

# Association of Encode Features with Integration

October 17, 2006

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# 1 Introduction

In this document, I examine the association of integration siting with various genomic features.

The data consist of both actual integration sites and sets of control sites, each set chosen to match the spacing (in bases) from the nearest restriction site (according to the direction in which the sequence was read) to an integration site. The numbers of insertion and matching sites for several data sets are shown below:

The numbers are shown below:

| Origin.of.data.set | type      |       |
|--------------------|-----------|-------|
|                    | insertion | match |
| AVR-E              | 416       | 4160  |
| MSE-E              | 450       | 4500  |

## 2 ENCODE

Here we examine the relative preference that insertions of the two types have for ENCODE annotations.

ENCODE ChIP tables follow one of two schemas. chrom chromStart chromEnd  
name span count offset lowerLimit dataRange validCount sumData sumSquares  
or chrom chromStart chromEnd dataValue



## 2.1 encodeAffyChIpHl60PvalBrg1Hr00

NULL

Affy Brg1 RA 0h

Affymetrix ChIP/Chip (Brg1 retinoic acid-treated HL-60, 0hrs) P-Value

|                                             | coef   | se    | z     | p      |
|---------------------------------------------|--------|-------|-------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.252  | 0.130 | 1.95  | 0.0518 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.247 | 0.124 | -1.99 | 0.0470 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

2870 3302

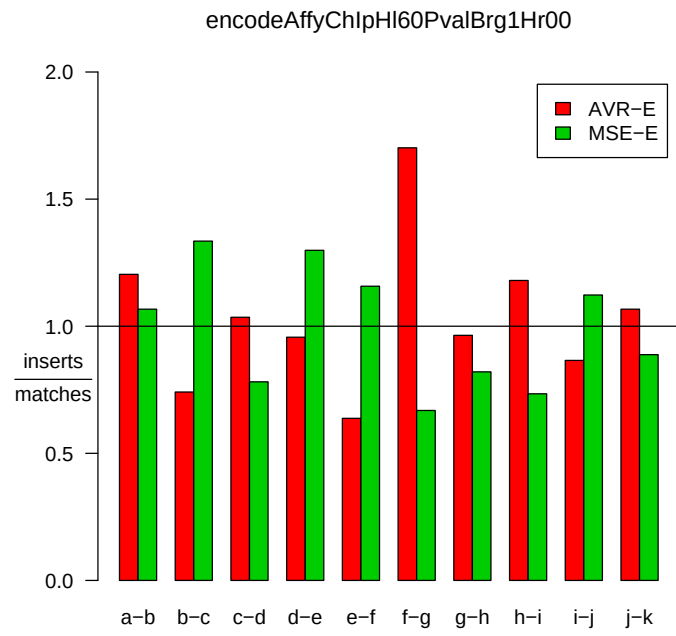
Category limits

|   | lower        | category  | upper     |
|---|--------------|-----------|-----------|
| 1 | 0.0009579175 | insertion | 0.3629349 |
| 2 | 0.3629348874 | match     | 0.8710244 |

0.000958 0.363 0.871 1.45 2.14 3 4.08 5.37 7.03

10 91.8

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 41  | 23  | 29  | 27  | 17  | 42  | 25  | 29  | 21  | 24  |
|       | match     |     | 327 | 298 | 269 | 271 | 256 | 237 | 249 | 236 | 233 | 216 |
| MSE-E | insertion |     | 25  | 36  | 24  | 38  | 37  | 22  | 27  | 25  | 38  | 32  |
|       | match     |     | 225 | 259 | 295 | 281 | 307 | 316 | 316 | 327 | 325 | 346 |



## 2.2 encodeAffyChIpHl60PvalBrg1Hr02

NULL

Affy Brg1 RA 2h

Affymetrix ChIP/Chip (Brg1 retinoic acid-treated HL-60, 2hrs) P-Value

|                                             | coef   | se    | z     | p      |
|---------------------------------------------|--------|-------|-------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.240  | 0.130 | 1.85  | 0.0649 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.157 | 0.125 | -1.26 | 0.2080 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

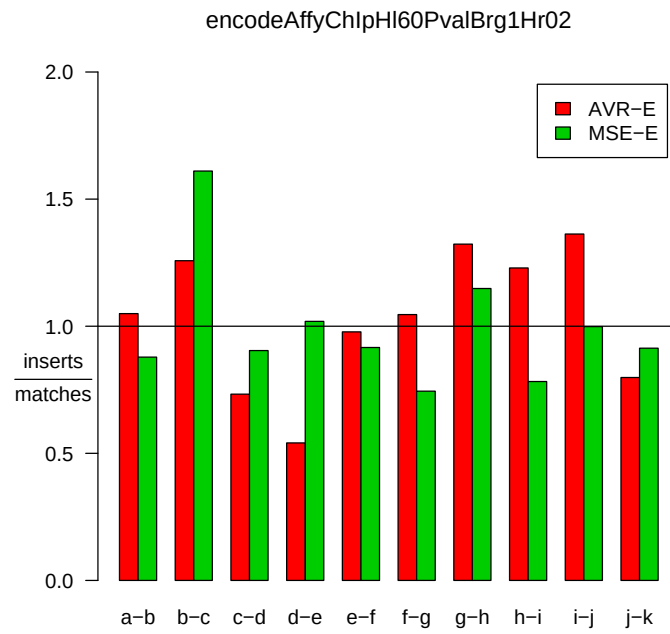
2870 3302

Category limits

|   | lower        | category  | upper      |
|---|--------------|-----------|------------|
| 1 | 1.368287e-06 | insertion | 0.08552034 |
| 2 | 8.552034e-02 | match     | 0.25119182 |

1.37e-06 0.0855 0.251 0.475 0.773 1.13 1.59 2.17  
3.01 4.6 32.9

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 36  | 40  | 23  | 14  | 25  | 25  | 33  | 29  | 33  | 19  |
|       | match     |     | 330 | 306 | 302 | 249 | 246 | 230 | 240 | 227 | 233 | 229 |
| MSE-E | insertion |     | 21  | 39  | 25  | 34  | 30  | 26  | 37  | 27  | 33  | 32  |
|       | match     |     | 230 | 233 | 266 | 321 | 315 | 336 | 310 | 332 | 318 | 337 |



## 2.3 encodeAffyChIpHl60PvalBrg1Hr08

NULL

Affy Brg1 RA 8h

Affymetrix ChIP/Chip (Brg1 retinoic acid-treated HL-60, 8hrs) P-Value

|                                             | coef   | se    | z      | p      |
|---------------------------------------------|--------|-------|--------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.219  | 0.131 | 1.670  | 0.0944 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.047 | 0.125 | -0.377 | 0.7060 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

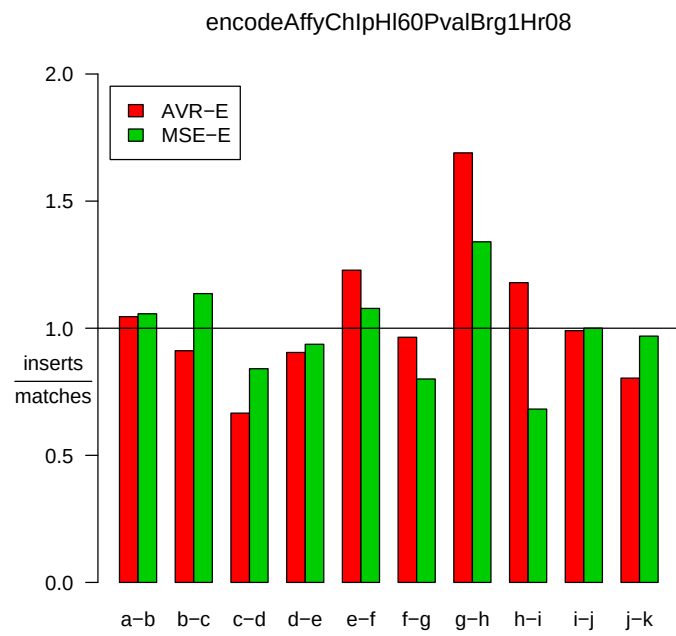
2870 3302

Category limits

|   | lower        | category  | upper     |
|---|--------------|-----------|-----------|
| 1 | 4.599796e-07 | insertion | 0.1356314 |
| 2 | 1.356314e-01 | match     | 0.4155342 |

4.6e-07 0.136 0.416 0.821 1.34 1.91 2.71 3.7 4.92  
7.21 74.9

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 38  | 28  | 19  | 26  | 33  | 23  | 41  | 28  | 23  | 19  |
|       | match     |     | 349 | 295 | 274 | 276 | 258 | 229 | 233 | 228 | 223 | 227 |
| MSE-E | insertion |     | 23  | 31  | 26  | 28  | 33  | 28  | 42  | 24  | 35  | 34  |
|       | match     |     | 209 | 262 | 297 | 287 | 294 | 336 | 301 | 338 | 336 | 337 |



## 2.4 encodeAffyChIPHL60PvalBrg1Hr32

NULL

Affy Brg1 RA 32h

Affymetrix ChIP/Chip (Brg1 retinoic acid-treated HL-60, 32hrs) P-Value

|                                             | coef   | se    | z      | p      |
|---------------------------------------------|--------|-------|--------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.228  | 0.129 | 1.760  | 0.0781 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.120 | 0.123 | -0.973 | 0.3310 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

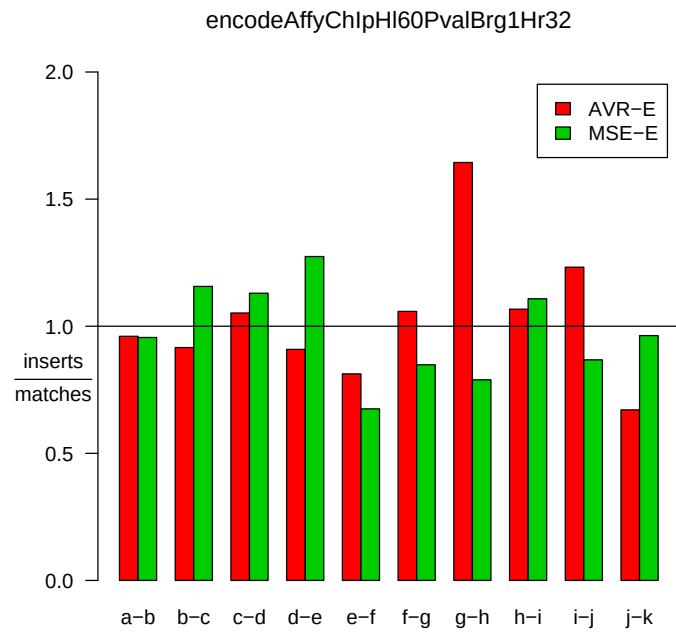
2870 3302

Category limits

|   | lower        | category  | upper      |
|---|--------------|-----------|------------|
| 1 | 1.274223e-07 | insertion | 0.07087296 |
| 2 | 7.087296e-02 | match     | 0.21960187 |

1.27e-07 0.0709 0.22 0.451 0.724 1.13 1.62 2.26  
3.2 4.93 84.9

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 35  | 27  | 31  | 23  | 22  | 27  | 44  | 24  | 29  | 16  |
|       | match     |     | 350 | 283 | 283 | 243 | 260 | 245 | 257 | 216 | 226 | 229 |
| MSE-E | insertion |     | 21  | 33  | 32  | 41  | 22  | 28  | 24  | 39  | 30  | 34  |
|       | match     |     | 211 | 274 | 272 | 309 | 313 | 317 | 292 | 338 | 332 | 339 |





## 2.5 encodeAffyChIpHl60PvalCebpeHr00

NULL

Affy CEBPe RA 0h

Affymetrix ChIP/Chip (CEBPe retinoic acid-treated HL-60, 0hrs) P-Value

|                                             | coef  | se    | z    | p       |
|---------------------------------------------|-------|-------|------|---------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.417 | 0.132 | 3.15 | 0.00164 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.375 | 0.126 | 2.99 | 0.00282 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

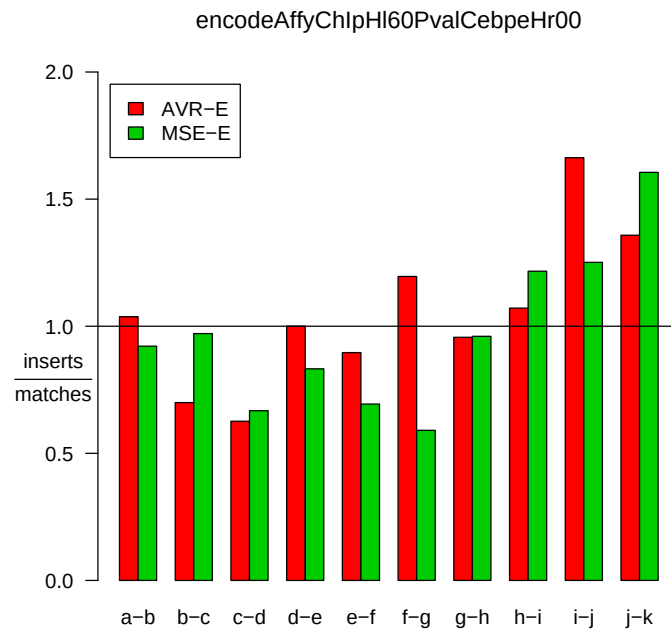
2870 3302

Category limits

|   | lower       | category  | upper     |
|---|-------------|-----------|-----------|
| 1 | 0.000841328 | insertion | 0.9524489 |
| 2 | 0.952448863 | match     | 2.1084406 |

0.000841 0.952 2.11 3.45 4.67 6 7.4 9.36 11.9  
18.2 210

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 39  | 22  | 18  | 25  | 21  | 32  | 25  | 28  | 40  | 28  |
|       | match     |     | 361 | 302 | 276 | 240 | 225 | 257 | 251 | 251 | 231 | 198 |
| MSE-E | insertion |     | 19  | 27  | 21  | 28  | 25  | 19  | 31  | 38  | 40  | 56  |
|       | match     |     | 198 | 267 | 302 | 323 | 346 | 309 | 310 | 300 | 307 | 335 |



## 2.6 encodeAffyChIpHl60PvalCebpeHr02

NULL

Affy CEBPe RA 2h

Affymetrix ChIP/Chip (CEBPe retinoic acid-treated HL-60, 2hrs) P-Value

|                                             | coef  | se    | z    | p      |
|---------------------------------------------|-------|-------|------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.333 | 0.130 | 2.56 | 0.0104 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.263 | 0.126 | 2.08 | 0.0375 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

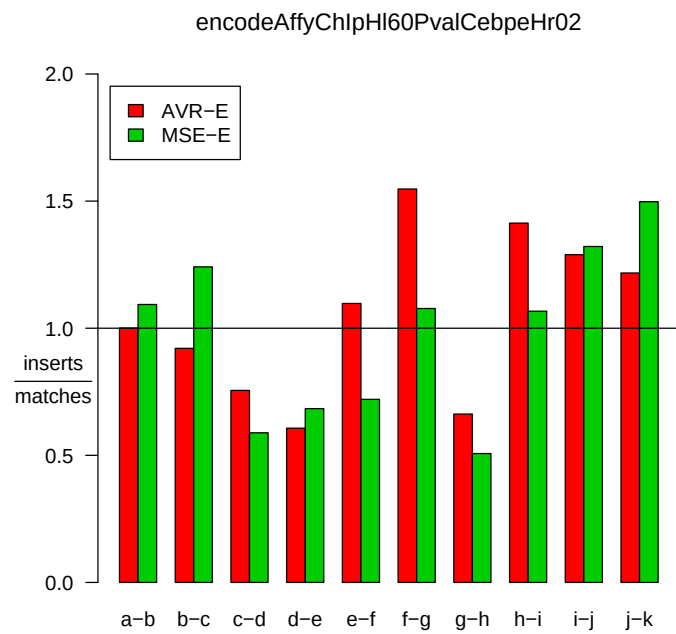
2870 3302

Category limits

|   | lower       | category  | upper     |
|---|-------------|-----------|-----------|
| 1 | 0.002349333 | insertion | 0.7564578 |
| 2 | 0.756457770 | match     | 1.7272394 |

0.00235 0.756 1.73 2.59 3.59 4.47 5.49 6.84 8.64  
12.1 198

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 37  | 28  | 21  | 17  | 28  | 39  | 18  | 34  | 29  | 27  |
|       | match     |     | 355 | 292 | 267 | 269 | 245 | 242 | 261 | 231 | 216 | 213 |
| MSE-E | insertion |     | 23  | 34  | 19  | 22  | 24  | 34  | 17  | 35  | 45  | 51  |
|       | match     |     | 202 | 263 | 310 | 309 | 320 | 303 | 322 | 315 | 327 | 327 |



## 2.7 encodeAffyChIpHl60PvalCebpeHr08

NULL

Affy CEBPe RA 8h

Affymetrix ChIP/Chip (CEBPe retinoic acid-treated HL-60, 8hrs) P-Value

|                                             | coef  | se    | z    | p       |
|---------------------------------------------|-------|-------|------|---------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.399 | 0.132 | 3.03 | 0.00247 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.224 | 0.124 | 1.80 | 0.07150 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

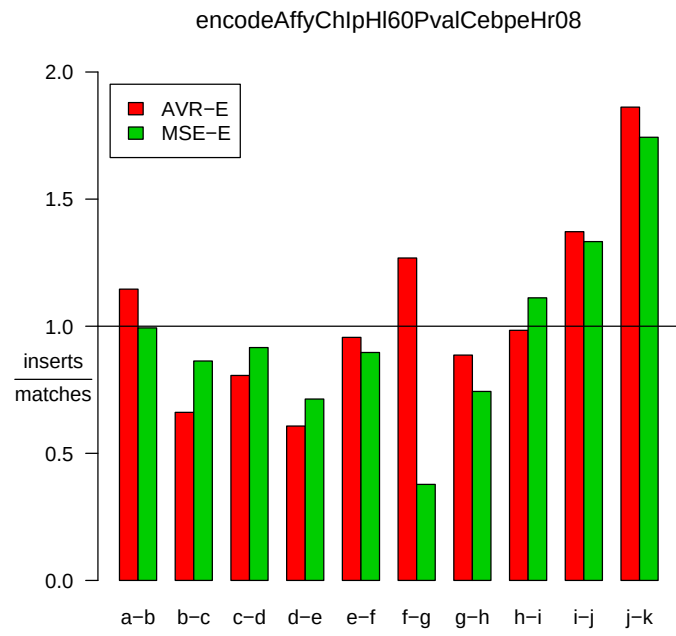
2870 3302

Category limits

|   | lower       | category  | upper     |
|---|-------------|-----------|-----------|
| 1 | 0.001237709 | insertion | 0.8586046 |
| 2 | 0.858604550 | match     | 1.9478641 |

0.00124 0.859 1.95 3.21 4.38 5.81 7.19 9.18 11.9  
17.5 235

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 42  | 21  | 22  | 16  | 23  | 35  | 24  | 25  | 32  | 38  |
|       | match     |     | 352 | 305 | 262 | 253 | 231 | 265 | 260 | 244 | 224 | 196 |
| MSE-E | insertion |     | 21  | 24  | 29  | 24  | 31  | 12  | 24  | 36  | 44  | 59  |
|       | match     |     | 203 | 267 | 304 | 323 | 332 | 305 | 310 | 311 | 317 | 325 |



## 2.8 encodeAffyChIpHl60PvalCebpeHr32

NULL

Affy CEBPe RA 32h

Affymetrix ChIP/Chip (CEBPe retinoic acid-treated HL-60, 32hrs) P-Value

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.396 | 0.131 | 3.04 | 0.002400 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.444 | 0.127 | 3.50 | 0.000472 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

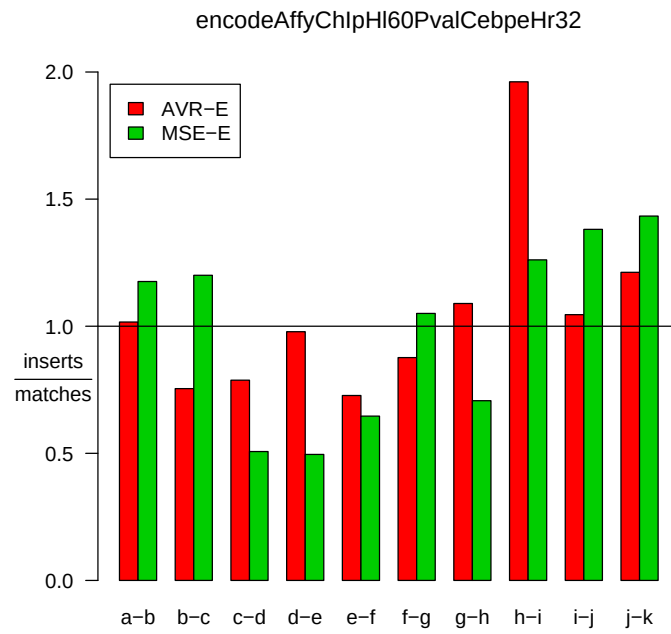
2870 3302

Category limits

|   | lower        | category  | upper     |
|---|--------------|-----------|-----------|
| 1 | 1.308827e-05 | insertion | 0.1904833 |
| 2 | 1.904833e-01 | match     | 0.5529355 |

1.31e-05 0.19 0.553 0.937 1.39 1.85 2.5 3.43 4.64  
7.64 199

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 38  | 22  | 21  | 27  | 20  | 22  | 27  | 48  | 27  | 26  |
|       | match     |     | 359 | 280 | 256 | 265 | 264 | 241 | 238 | 235 | 248 | 206 |
| MSE-E | insertion |     | 24  | 35  | 17  | 16  | 21  | 35  | 24  | 39  | 43  | 50  |
|       | match     |     | 196 | 280 | 322 | 310 | 312 | 320 | 326 | 297 | 299 | 335 |





## 2.9 encodeAffyChIpHl60PvalCtcfHr00

NULL

Affy CTCF RA Oh

Affymetrix ChIP/Chip (CTCF retinoic acid-treated HL-60, 0hrs) P-Value

|                                             | coef   | se    | z     | p      |
|---------------------------------------------|--------|-------|-------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.306  | 0.131 | 2.33  | 0.0199 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.202 | 0.124 | -1.62 | 0.1040 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

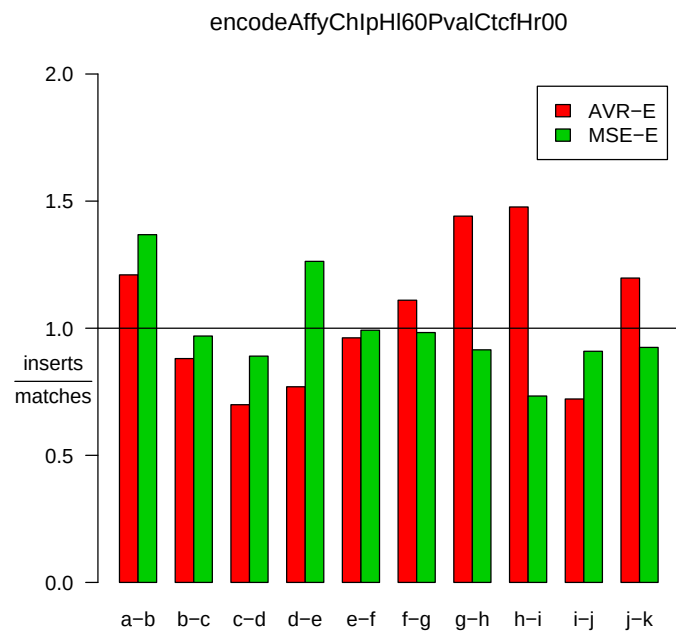
2870 3302

Category limits

|   | lower        | category  | upper     |
|---|--------------|-----------|-----------|
| 1 | 4.071542e-07 | insertion | 0.1514121 |
| 2 | 1.514121e-01 | match     | 0.5314385 |

4.07e-07 0.151 0.531 1.05 1.66 2.49 3.53 4.91  
6.67 9.74 33.3

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 42  | 27  | 21  | 24  | 24  | 27  | 31  | 35  | 18  | 28  |
|       | match     |     | 334 | 295 | 289 | 300 | 240 | 234 | 207 | 228 | 240 | 225 |
| MSE-E | insertion |     | 30  | 27  | 26  | 34  | 33  | 33  | 33  | 25  | 31  | 32  |
|       | match     |     | 211 | 268 | 281 | 259 | 320 | 323 | 347 | 328 | 328 | 333 |



## 2.10 encodeAffyChIpHl60PvalCtcfHr02

NULL

Affy CTCF RA 2h

Affymetrix ChIP/Chip (CTCF retinoic acid-treated HL-60, 2hrs) P-Value

|                                             | coef    | se    | z      | p      |
|---------------------------------------------|---------|-------|--------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.0187 | 0.132 | -0.142 | 0.8870 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.3030 | 0.124 | -2.440 | 0.0147 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

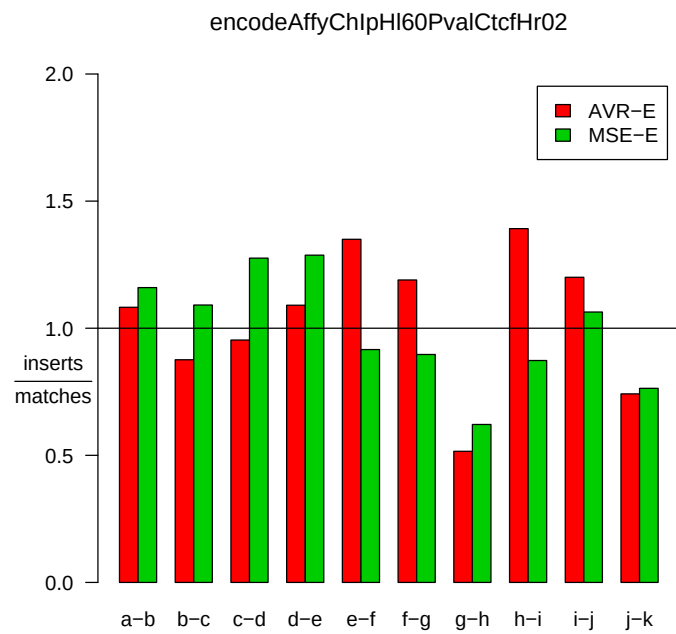
2870 3302

Category limits

|   | lower        | category  | upper     |
|---|--------------|-----------|-----------|
| 1 | 7.557698e-09 | insertion | 0.0331996 |
| 2 | 3.319960e-02 | match     | 0.1342575 |

7.56e-09 0.0332 0.134 0.308 0.537 0.847 1.25 1.83  
2.67 4.21 18.2

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 39  | 27  | 28  | 31  | 35  | 28  | 13  | 30  | 28  | 19  |
|       | match     |     | 346 | 296 | 282 | 273 | 249 | 226 | 242 | 207 | 224 | 246 |
| MSE-E | insertion |     | 25  | 30  | 36  | 37  | 29  | 31  | 22  | 32  | 36  | 26  |
|       | match     |     | 207 | 264 | 271 | 276 | 304 | 332 | 340 | 352 | 325 | 327 |



## 2.11 encodeAffyChIpHl60PvalCtcfHr08

NULL

Affy CTCF RA 8h

Affymetrix ChIP/Chip (CTCF retinoic acid-treated HL-60, 8hrs) P-Value

|                                             | coef   | se    | z     | p     |
|---------------------------------------------|--------|-------|-------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.141  | 0.130 | 1.08  | 0.279 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.172 | 0.125 | -1.38 | 0.169 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

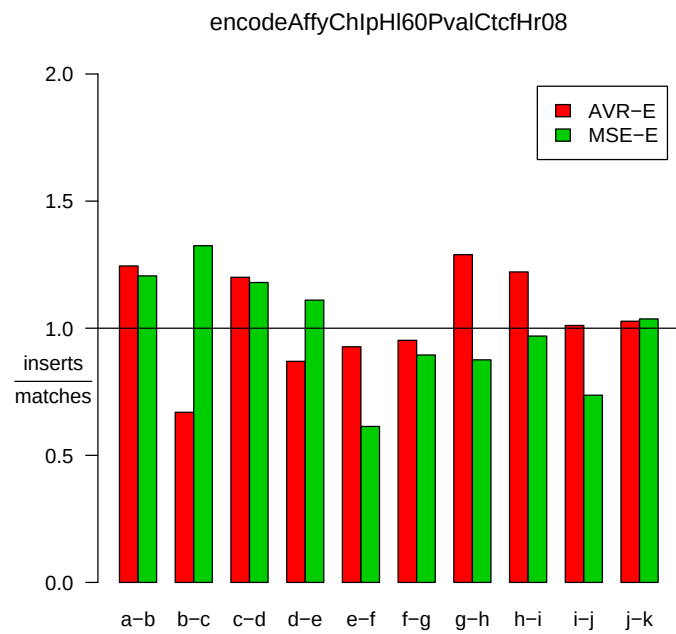
2870 3302

Category limits

|   | lower        | category  | upper      |
|---|--------------|-----------|------------|
| 1 | 1.566699e-07 | insertion | 0.06761207 |
| 2 | 6.761207e-02 | match     | 0.23110308 |

1.57e-07 0.0676 0.231 0.478 0.828 1.29 1.87 2.69  
3.81 6.03 43.7

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 42  | 23  | 32  | 24  | 25  | 24  | 29  | 29  | 24  | 26  |
|       | match     |     | 324 | 330 | 256 | 265 | 259 | 242 | 216 | 228 | 228 | 243 |
| MSE-E | insertion |     | 28  | 32  | 36  | 34  | 20  | 30  | 31  | 33  | 26  | 34  |
|       | match     |     | 223 | 232 | 293 | 294 | 313 | 322 | 340 | 327 | 339 | 315 |



## 2.12 encodeAffyChIpHl60PvalCtcfHr32

NULL

Affy CTCF RA 32h

Affymetrix ChIP/Chip (CTCF retinoic acid-treated HL-60, 32hrs) P-Value

|                                             | coef   | se    | z     | p     |
|---------------------------------------------|--------|-------|-------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.166  | 0.130 | 1.28  | 0.201 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.153 | 0.125 | -1.22 | 0.222 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

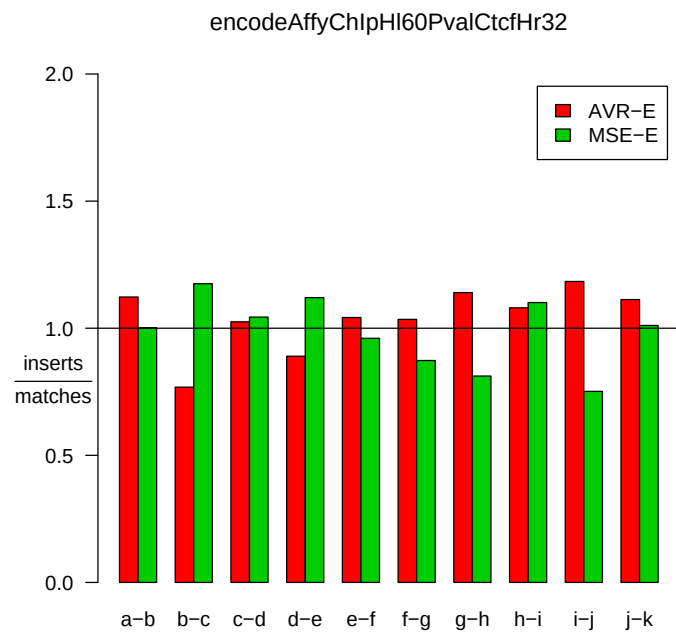
2870 3302

Category limits

|   | lower        | category  | upper      |
|---|--------------|-----------|------------|
| 1 | 1.419947e-08 | insertion | 0.07354394 |
| 2 | 7.354394e-02 | match     | 0.28445417 |

1.42e-08 0.0735 0.284 0.613 1.06 1.63 2.37 3.31  
4.56 7.03 26.1

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 38  | 26  | 30  | 24  | 28  | 25  | 26  | 27  | 27  | 27  |
|       | match     |     | 325 | 325 | 281 | 259 | 258 | 232 | 219 | 240 | 219 | 233 |
| MSE-E | insertion |     | 24  | 29  | 30  | 35  | 30  | 30  | 29  | 36  | 27  | 34  |
|       | match     |     | 230 | 237 | 276 | 300 | 300 | 330 | 343 | 314 | 345 | 323 |





## 2.13 encodeAffyChIPHL60PvalH3K27me3Hr00

NULL

Affy H3K27me3 RA 0h

Affymetrix ChIP/Chip (H3K27me3 retinoic acid-treated HL-60, 0hrs) P-Value

|                                             | coef   | se    | z     | p        |
|---------------------------------------------|--------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.281 | 0.134 | -2.09 | 3.65e-02 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.541 | 0.125 | -4.33 | 1.52e-05 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

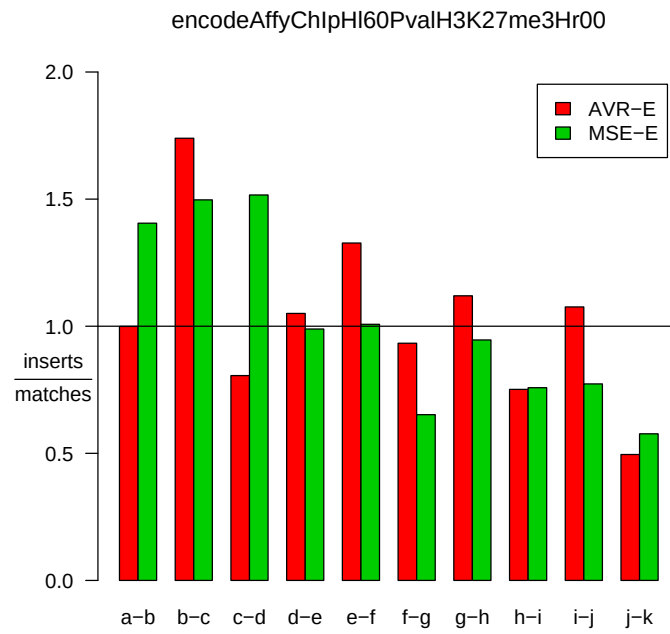
2870 3302

Category limits

|   | lower        | category  | upper     |
|---|--------------|-----------|-----------|
| 1 | 0.0004408875 | insertion | 0.7337749 |
| 2 | 0.7337748528 | match     | 1.4860557 |

0.000441 0.734 1.49 2.35 3.28 4.27 5.41 6.81 8.67  
12 122

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 36  | 48  | 24  | 28  | 34  | 24  | 26  | 18  | 27  | 13  |
|       | match     |     | 346 | 265 | 286 | 256 | 246 | 247 | 223 | 230 | 241 | 252 |
| MSE-E | insertion |     | 30  | 41  | 42  | 31  | 32  | 22  | 33  | 27  | 26  | 20  |
|       | match     |     | 205 | 263 | 266 | 301 | 305 | 324 | 335 | 342 | 323 | 333 |



## 2.14 encodeAffyChIpHl60PvalH3K27me3Hr02

NULL

Affy H3K27me3 RA 2h

Affymetrix ChIP/Chip (H3K27me3 retinoic acid-treated HL-60, 2hrs) P-Value

|                                             | coef   | se    | z     | p        |
|---------------------------------------------|--------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.338 | 0.134 | -2.52 | 0.011600 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.434 | 0.125 | -3.48 | 0.000494 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

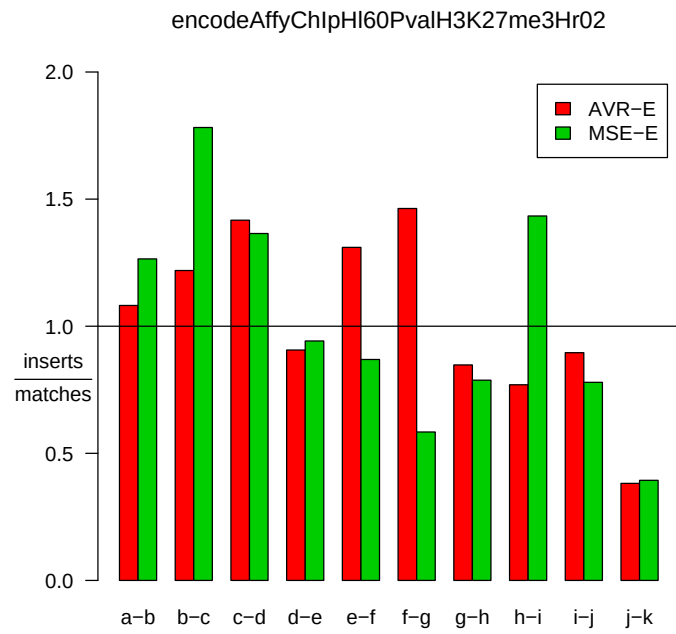
2870 3302

Category limits

|   | lower        | category  | upper     |
|---|--------------|-----------|-----------|
| 1 | 0.0001313269 | insertion | 0.6044279 |
| 2 | 0.6044279158 | match     | 1.3632351 |

0.000131 0.604 1.36 2.22 3.1 4.11 5.2 6.58 8.65  
12.3 183

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 38  | 37  | 38  | 26  | 32  | 33  | 20  | 20  | 23  | 10  |
|       | match     |     | 338 | 292 | 258 | 276 | 235 | 217 | 227 | 250 | 247 | 252 |
| MSE-E | insertion |     | 28  | 45  | 40  | 28  | 29  | 21  | 28  | 45  | 26  | 14  |
|       | match     |     | 213 | 243 | 282 | 286 | 321 | 346 | 342 | 302 | 321 | 342 |



## 2.15 encodeAffyChIpHl60PvalH3K27me3Hr08

NULL

Affy H3K27me3 RA 8h

Affymetrix ChIP/Chip (H3K27me3 retinoic acid-treated HL-60, 8hrs) P-Value

|                                             | coef   | se    | z     | p        |
|---------------------------------------------|--------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.555 | 0.136 | -4.08 | 4.59e-05 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.550 | 0.127 | -4.33 | 1.48e-05 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

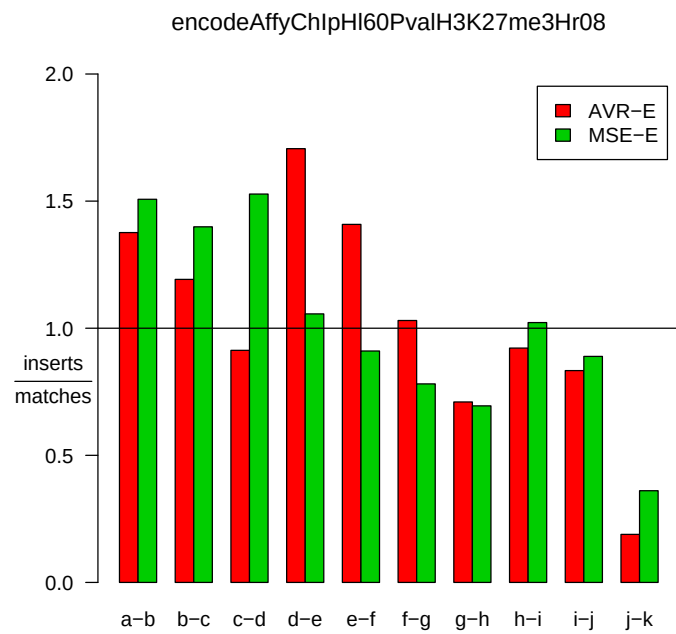
2870 3302

Category limits

|   | lower        | category  | upper    |
|---|--------------|-----------|----------|
| 1 | 0.0003988940 | insertion | 1.185297 |
| 2 | 1.1852966189 | match     | 2.432832 |

0.000399 1.19 2.43 3.7 5.05 6.55 8.21 10.3 13.1  
18.5 238

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 45  | 36  | 27  | 43  | 33  | 25  | 19  | 24  | 21  | 5   |
|       | match     |     | 314 | 290 | 284 | 242 | 225 | 233 | 257 | 250 | 242 | 254 |
| MSE-E | insertion |     | 35  | 37  | 42  | 33  | 31  | 27  | 23  | 33  | 30  | 13  |
|       | match     |     | 223 | 254 | 264 | 300 | 327 | 332 | 318 | 310 | 324 | 346 |



## 2.16 encodeAffyChIpHl60PvalH3K27me3Hr32

NULL

Affy H3K27me3 RA 32h

Affymetrix ChIP/Chip (H3K27me3 retinoic acid-treated HL-60, 32hrs) P-Value

|                                             | coef   | se    | z     | p        |
|---------------------------------------------|--------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.477 | 0.136 | -3.50 | 0.000468 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.537 | 0.126 | -4.25 | 0.000021 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

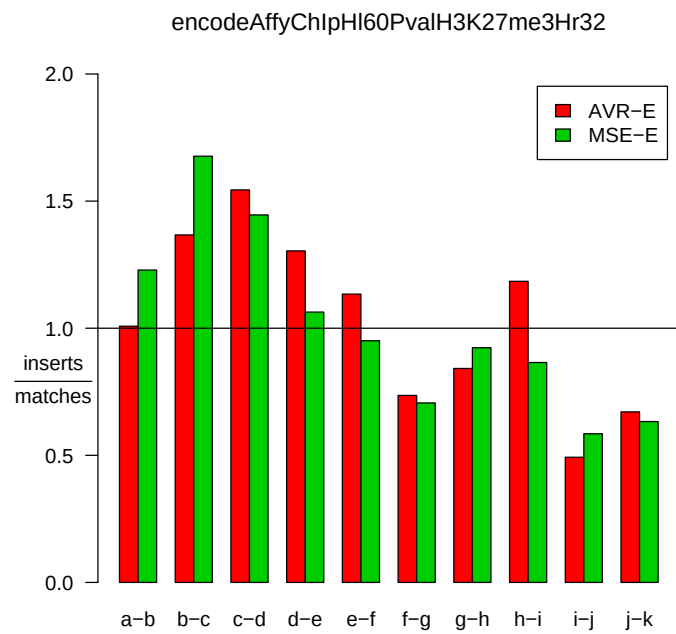
2870 3302

Category limits

|   | lower        | category  | upper     |
|---|--------------|-----------|-----------|
| 1 | 0.0002914343 | insertion | 0.9271227 |
| 2 | 0.9271226883 | match     | 1.7127155 |

0.000291 0.927 1.71 2.44 3.19 4.02 4.97 6.01 7.51  
10.2 197

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 36  | 40  | 41  | 33  | 30  | 18  | 22  | 28  | 14  | 16  |
|       | match     |     | 343 | 281 | 255 | 243 | 254 | 235 | 251 | 227 | 273 | 229 |
| MSE-E | insertion |     | 27  | 44  | 42  | 34  | 30  | 25  | 30  | 30  | 19  | 23  |
|       | match     |     | 211 | 252 | 279 | 307 | 303 | 340 | 312 | 333 | 312 | 349 |





## 2.17 encodeAffyChIPHL60PvalH4Kac4Hr00

NULL

Affy H4Kac4 RA 0h

Affymetrix ChIP/Chip (H4Kac4 retinoic acid-treated HL-60, 0hrs) P-Value

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.592 | 0.132 | 4.50 | 6.76e-06 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.711 | 0.132 | 5.39 | 7.16e-08 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

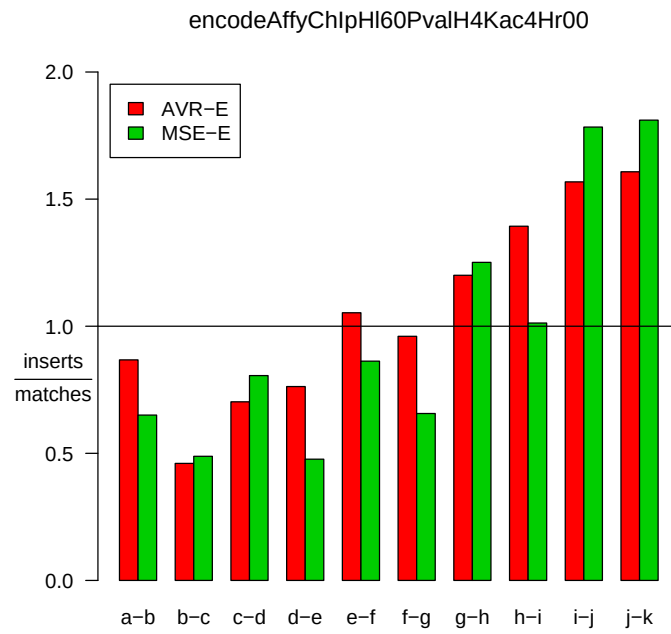
2870 3302

Category limits

|   | lower        | category  | upper     |
|---|--------------|-----------|-----------|
| 1 | 6.099925e-06 | insertion | 0.5759178 |
| 2 | 5.759178e-01 | match     | 1.3100501 |

6.1e-06 0.576 1.31 2.16 3.12 4.3 5.67 7.78 11  
18.9 456

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 29  | 14  | 21  | 22  | 25  | 22  | 30  | 37  | 40  | 38  |
|       | match     |     | 321 | 292 | 287 | 277 | 228 | 220 | 240 | 255 | 245 | 227 |
| MSE-E | insertion |     | 17  | 15  | 24  | 15  | 30  | 24  | 40  | 31  | 52  | 56  |
|       | match     |     | 251 | 295 | 286 | 302 | 334 | 351 | 307 | 294 | 280 | 297 |



## 2.18 encodeAffyChIPHL60PvalH4Kac4Hr02

NULL

Affy H4Kac4 RA 2h

Affymetrix ChIP/Chip (H4Kac4 retinoic acid-treated HL-60, 2hrs) P-Value

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.542 | 0.131 | 4.13 | 3.62e-05 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.603 | 0.128 | 4.73 | 2.26e-06 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

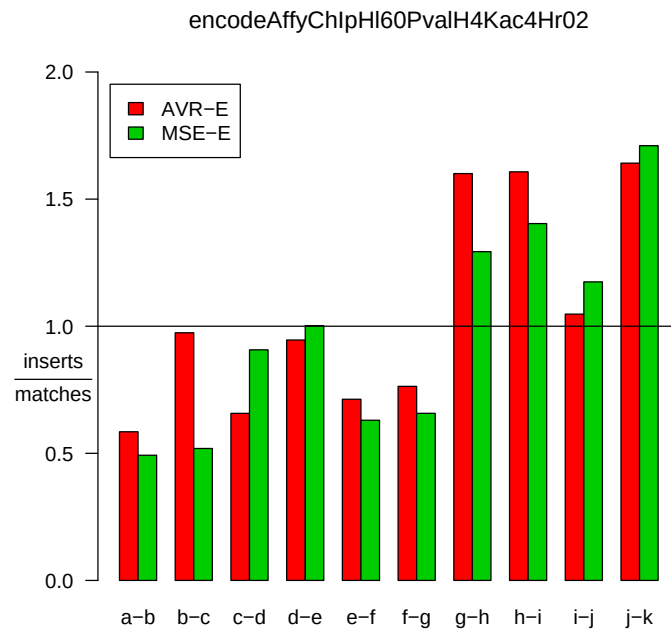
2870 3302

Category limits

|   | lower        | category  | upper     |
|---|--------------|-----------|-----------|
| 1 | 8.384675e-07 | insertion | 0.2075597 |
| 2 | 2.075597e-01 | match     | 0.4397663 |

8.38e-07 0.208 0.44 0.715 1.01 1.41 1.94 2.6 3.87  
7.03 351

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 19  | 28  | 18  | 26  | 19  | 19  | 40  | 39  | 30  | 40  |
|       | match     |     | 312 | 276 | 263 | 264 | 256 | 239 | 240 | 233 | 275 | 234 |
| MSE-E | insertion |     | 14  | 16  | 29  | 31  | 21  | 23  | 40  | 44  | 34  | 52  |
|       | match     |     | 273 | 296 | 307 | 297 | 320 | 336 | 297 | 301 | 278 | 292 |



## 2.19 encodeAffyChIpHl60PvalH4Kac4Hr08

NULL

Affy H4Kac4 RA 8h

Affymetrix ChIP/Chip (H4Kac4 retinoic acid-treated HL-60, 8hrs) P-Value

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.455 | 0.131 | 3.46 | 5.33e-04 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.678 | 0.131 | 5.19 | 2.11e-07 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

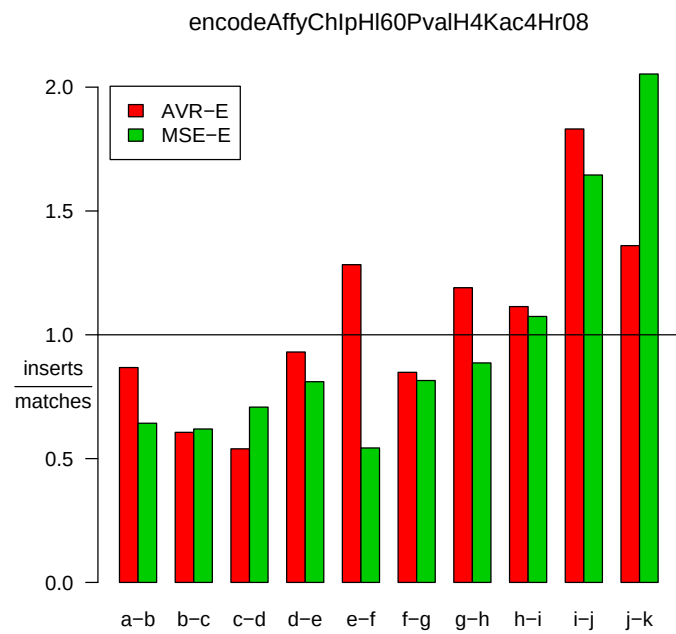
2870 3302

Category limits

|   | lower        | category  | upper     |
|---|--------------|-----------|-----------|
| 1 | 1.545812e-05 | insertion | 0.4872377 |
| 2 | 4.872377e-01 | match     | 1.1359094 |

1.55e-05 0.487 1.14 1.92 2.77 3.74 5.06 6.64 9.32  
15.8 436

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 30  | 19  | 15  | 25  | 31  | 22  | 29  | 29  | 45  | 33  |
|       | match     |     | 332 | 301 | 267 | 258 | 232 | 249 | 234 | 250 | 236 | 233 |
| MSE-E | insertion |     | 16  | 18  | 23  | 26  | 19  | 27  | 30  | 34  | 49  | 62  |
|       | match     |     | 239 | 279 | 312 | 308 | 336 | 318 | 325 | 304 | 286 | 290 |



## 2.20 encodeAffyChIPHL60PvalH4Kac4Hr32

NULL

Affy H4Kac4 RA 32h

Affymetrix ChIP/Chip (H4Kac4 retinoic acid-treated HL-60, 32hrs) P-Value

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.340 | 0.130 | 2.61 | 9.11e-03 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.545 | 0.127 | 4.28 | 1.83e-05 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

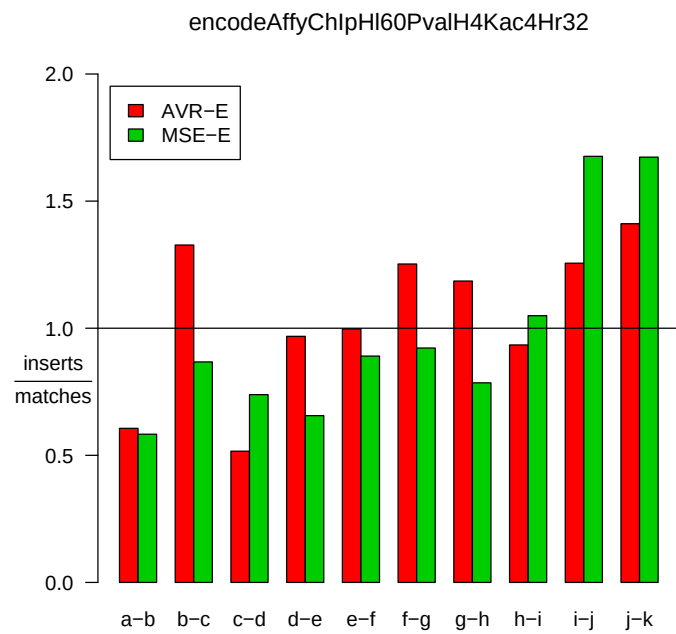
2870 3302

Category limits

|   | lower        | category  | upper     |
|---|--------------|-----------|-----------|
| 1 | 3.749116e-07 | insertion | 0.2867415 |
| 2 | 2.867415e-01 | match     | 0.5333240 |

3.75e-07 0.287 0.533 0.825 1.13 1.52 2.06 2.82  
4.22 8.72 421

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 19  | 34  | 15  | 25  | 27  | 33  | 30  | 25  | 34  | 36  |
|       | match     |     | 301 | 246 | 279 | 248 | 260 | 253 | 243 | 257 | 260 | 245 |
| MSE-E | insertion |     | 17  | 28  | 23  | 22  | 28  | 29  | 26  | 33  | 48  | 50  |
|       | match     |     | 280 | 310 | 299 | 322 | 302 | 302 | 318 | 302 | 275 | 287 |





## 2.21 encodeAffyChIpHl60PvalP300Hr00

NULL

Affy P300 RA 0h

Affymetrix ChIP/Chip (P300 retinoic acid-treated HL-60, 0hrs) P-Value

|                                             | coef    | se    | z      | p      |
|---------------------------------------------|---------|-------|--------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.2270  | 0.131 | 1.730  | 0.0829 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.0488 | 0.125 | -0.392 | 0.6950 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

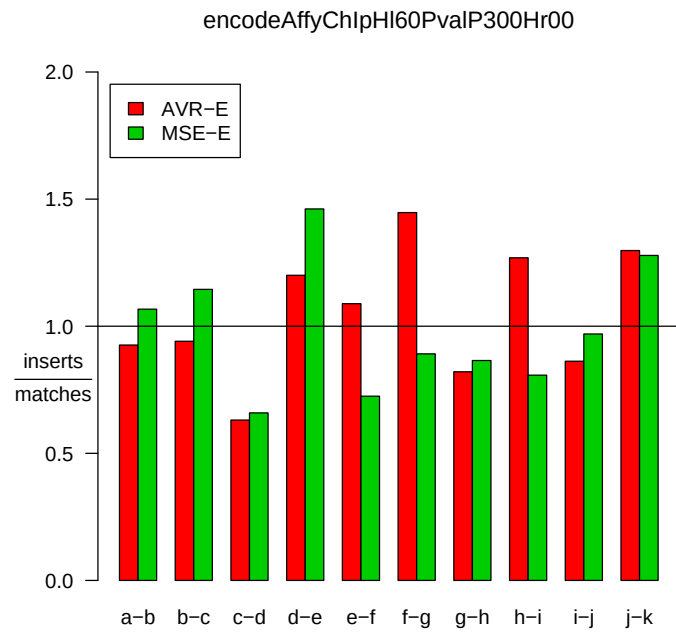
2870 3302

Category limits

|   | lower        | category  | upper     |
|---|--------------|-----------|-----------|
| 1 | 1.040694e-05 | insertion | 0.2395041 |
| 2 | 2.395041e-01 | match     | 0.7528426 |

1.04e-05 0.24 0.753 1.42 2.16 3.06 4.07 5.36 7.02  
9.94 46.1

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 35  | 29  | 18  | 33  | 28  | 33  | 20  | 30  | 22  | 30  |
|       | match     |     | 363 | 296 | 274 | 264 | 247 | 219 | 234 | 227 | 245 | 222 |
| MSE-E | insertion |     | 22  | 31  | 21  | 42  | 24  | 31  | 30  | 28  | 32  | 43  |
|       | match     |     | 198 | 260 | 306 | 276 | 318 | 334 | 333 | 333 | 317 | 323 |



## 2.22 encodeAffyChIpHl60PvalP300Hr02

NULL

Affy P300 RA 2h

Affymetrix ChIP/Chip (P300 retinoic acid-treated HL-60, 2hrs) P-Value

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.0165 | 0.132 | -0.125 | 0.901 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.1650  | 0.126 | 1.310  | 0.192 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

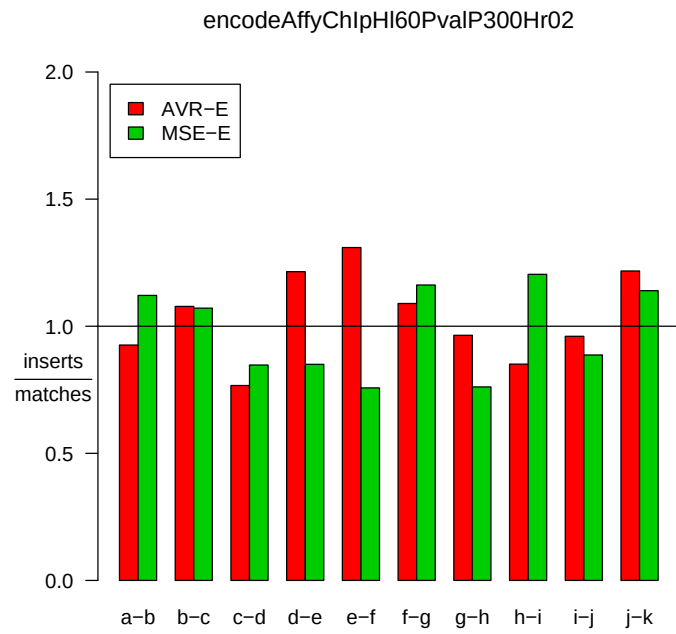
2870 3302

Category limits

|   | lower       | category  | upper    |
|---|-------------|-----------|----------|
| 1 | 0.001303843 | insertion | 1.095485 |
| 2 | 1.095484853 | match     | 2.258761 |

0.0013 1.1 2.26 3.6 4.84 6.24 7.83 9.67 12.3 16.7  
69.3

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 35  | 33  | 21  | 32  | 33  | 27  | 24  | 21  | 25  | 27  |
|       | match     |     | 363 | 294 | 263 | 253 | 242 | 238 | 239 | 237 | 250 | 213 |
| MSE-E | insertion |     | 23  | 29  | 27  | 27  | 25  | 38  | 26  | 40  | 29  | 40  |
|       | match     |     | 197 | 260 | 306 | 305 | 317 | 314 | 328 | 319 | 314 | 337 |



## 2.23 encodeAffyChIpHl60PvalP300Hr08

NULL

Affy P300 RA 8h

Affymetrix ChIP/Chip (P300 retinoic acid-treated HL-60, 8hrs) P-Value

|                                             | coef    | se    | z      | p      |
|---------------------------------------------|---------|-------|--------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.2690  | 0.131 | 2.060  | 0.0397 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.0173 | 0.125 | -0.138 | 0.8900 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

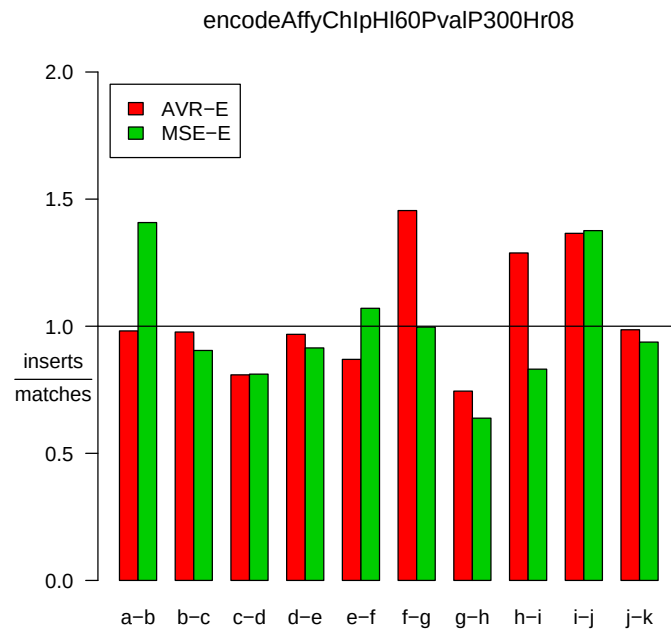
2870 3302

Category limits

|   | lower        | category  | upper    |
|---|--------------|-----------|----------|
| 1 | 0.0003482224 | insertion | 0.567760 |
| 2 | 0.5677599907 | match     | 1.467381 |

0.000348 0.568 1.47 2.55 3.68 4.97 6.41 8.26 10.6  
14.3 70.2

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 37  | 29  | 24  | 25  | 23  | 35  | 19  | 33  | 30  | 23  |
|       | match     |     | 362 | 285 | 285 | 248 | 254 | 231 | 245 | 246 | 211 | 224 |
| MSE-E | insertion |     | 28  | 26  | 24  | 30  | 34  | 33  | 22  | 27  | 47  | 33  |
|       | match     |     | 191 | 276 | 284 | 315 | 305 | 318 | 331 | 312 | 328 | 338 |



## 2.24 encodeAffyChIpHl60PvalP300Hr32

NULL

Affy P300 RA 32h

Affymetrix ChIP/Chip (P300 retinoic acid-treated HL-60, 32hrs) P-Value

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.1660  | 0.130 | 1.270  | 0.202 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.0595 | 0.125 | -0.478 | 0.633 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

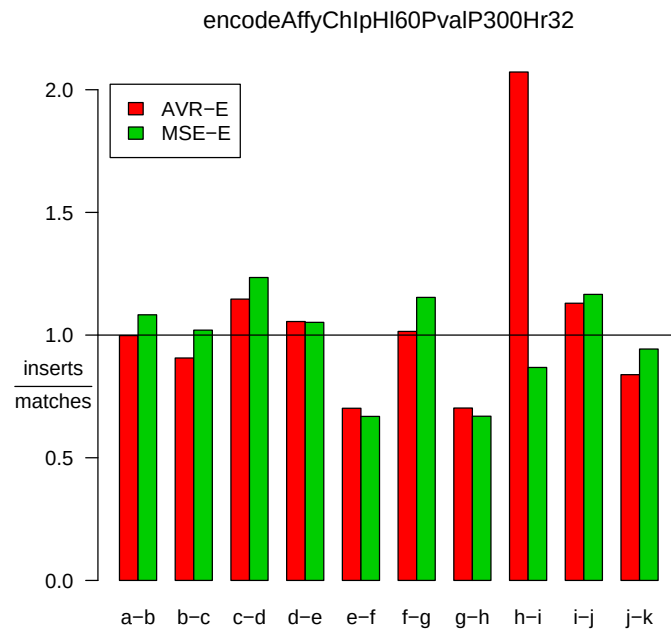
2870 3302

Category limits

|   | lower        | category  | upper     |
|---|--------------|-----------|-----------|
| 1 | 2.116548e-05 | insertion | 0.1827867 |
| 2 | 1.827867e-01 | match     | 0.6245136 |

2.12e-05 0.183 0.625 1.18 1.77 2.48 3.33 4.39  
5.75 7.93 60

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 37  | 27  | 32  | 30  | 19  | 26  | 18  | 41  | 28  | 20  |
|       | match     |     | 356 | 286 | 268 | 273 | 260 | 246 | 246 | 190 | 238 | 229 |
| MSE-E | insertion |     | 23  | 29  | 36  | 31  | 22  | 37  | 23  | 32  | 38  | 33  |
|       | match     |     | 204 | 273 | 280 | 283 | 316 | 308 | 330 | 354 | 313 | 336 |





## 2.25 encodeAffyChIpHL60PvalPu1Hr00

NULL

Affy PU1 RA 0h

Affymetrix ChIP/Chip (PU1 retinoic acid-treated HL-60, 0hrs) P-Value

|                                             | coef   | se    | z     | p     |
|---------------------------------------------|--------|-------|-------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.0901 | 0.129 | 0.701 | 0.484 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.1490 | 0.124 | 1.200 | 0.232 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

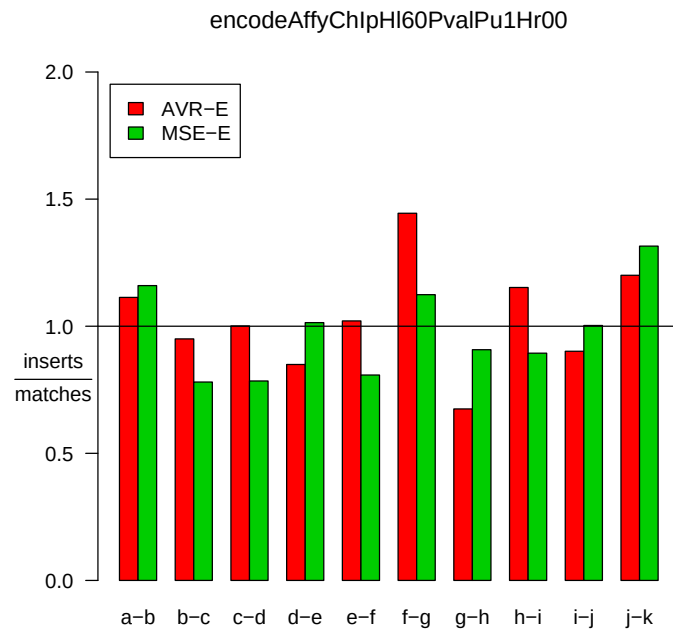
2870 3302

Category limits

|   | lower        | category  | upper     |
|---|--------------|-----------|-----------|
| 1 | 2.843335e-05 | insertion | 0.2037685 |
| 2 | 2.037685e-01 | match     | 0.5576946 |

2.84e-05 0.204 0.558 0.96 1.39 1.92 2.5 3.36 4.62  
7.04 92.7

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 40  | 28  | 27  | 23  | 27  | 37  | 17  | 27  | 23  | 29  |     |
|       | match     | 345 | 283 | 259 | 260 | 254 | 246 | 242 | 225 | 245 | 232 |     |
| MSE-E | insertion | 25  | 23  | 25  | 32  | 26  | 35  | 31  | 31  | 33  | 43  |     |
|       | match     | 207 | 283 | 306 | 303 | 309 | 299 | 328 | 333 | 316 | 314 |     |



## 2.26 encodeAffyChIpHl60PvalPu1Hr02

NULL

Affy PU1 RA 2h

Affymetrix ChIP/Chip (PU1 retinoic acid-treated HL-60, 2hrs) P-Value

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.1380 | 0.131 | -1.060 | 0.291 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.0292 | 0.123 | -0.238 | 0.812 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

2870 3302

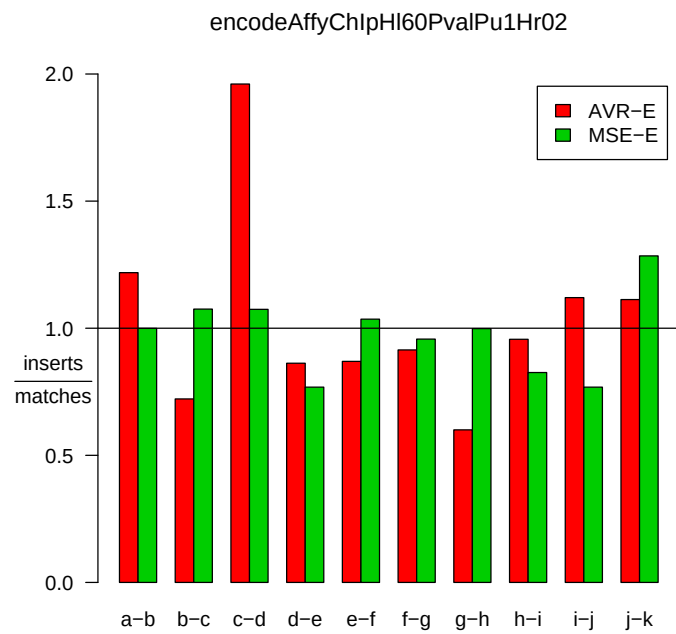
Category limits

|   | lower        | category  | upper     |
|---|--------------|-----------|-----------|
| 1 | 0.0000934002 | insertion | 0.2713364 |
| 2 | 0.2713363856 | match     | 0.6120725 |

9.34e-05 0.271 0.612 0.965 1.42 1.9 2.49 3.32

4.53 6.68 102

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 42  | 23  | 49  | 22  | 23  | 24  | 15  | 25  | 28  | 27  |
|       | match     |     | 331 | 306 | 240 | 245 | 254 | 252 | 240 | 251 | 240 | 233 |
| MSE-E | insertion |     | 23  | 29  | 33  | 26  | 33  | 31  | 34  | 27  | 26  | 42  |
|       | match     |     | 221 | 259 | 295 | 325 | 306 | 311 | 327 | 314 | 325 | 314 |



## 2.27 encodeAffyChIPHL60PvalPu1Hr08

NULL

Affy PU1 RA 8h

Affymetrix ChIP/Chip (PU1 retinoic acid-treated HL-60, 8hrs) P-Value

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.0232 | 0.130 | -0.179 | 0.858 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.1680 | 0.125 | -1.350 | 0.178 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

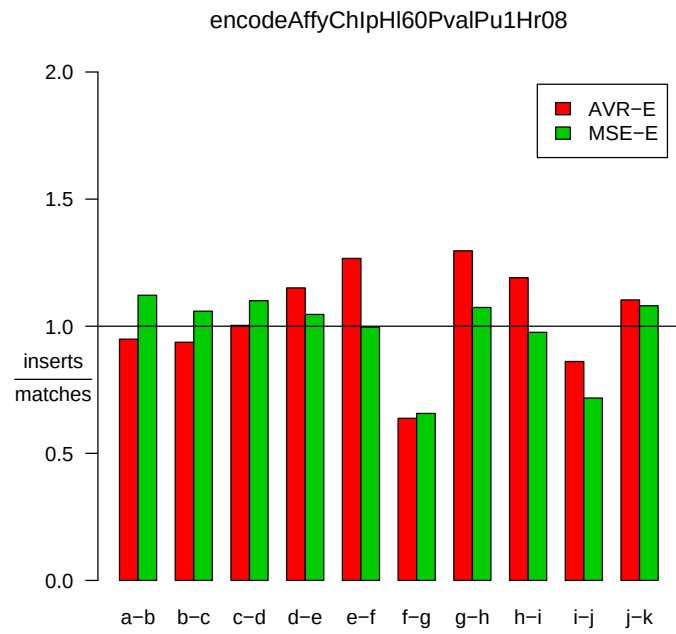
2870 3302

Category limits

|   | lower        | category  | upper      |
|---|--------------|-----------|------------|
| 1 | 1.884602e-06 | insertion | 0.06538057 |
| 2 | 6.538057e-02 | match     | 0.21942567 |

1.88e-06 0.0654 0.219 0.396 0.641 0.957 1.34 1.85  
2.67 4.42 74.5

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 34  | 28  | 28  | 29  | 31  | 18  | 32  | 31  | 20  | 27  |
|       | match     |     | 344 | 287 | 268 | 242 | 235 | 271 | 237 | 250 | 223 | 235 |
| MSE-E | insertion |     | 25  | 30  | 33  | 34  | 33  | 21  | 35  | 31  | 26  | 36  |
|       | match     |     | 214 | 272 | 288 | 312 | 318 | 307 | 313 | 305 | 348 | 320 |



## 2.28 encodeAffyChIpHl60PvalPu1Hr32

NULL

Affy PU1 RA 32h

Affymetrix ChIP/Chip (PU1 retinoic acid-treated HL-60, 32hrs) P-Value

|                                             | coef   | se    | z     | p     |
|---------------------------------------------|--------|-------|-------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.1520 | 0.130 | 1.170 | 0.243 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.0393 | 0.124 | 0.316 | 0.752 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

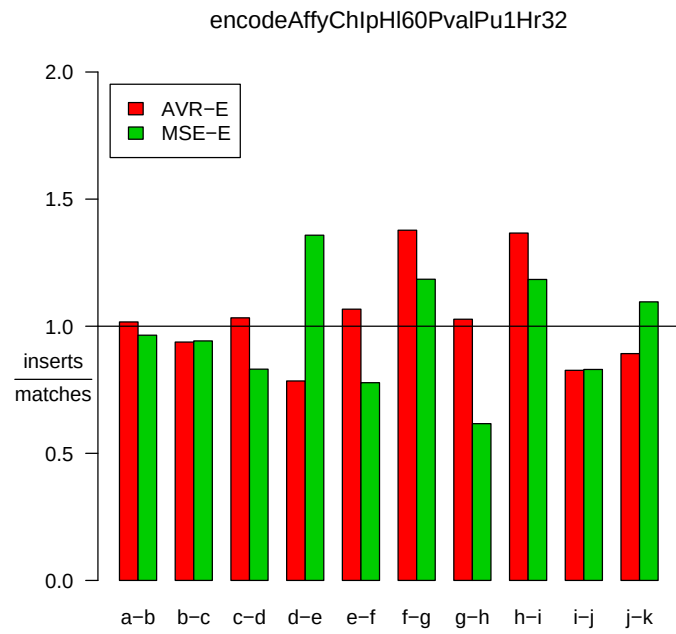
2870 3302

Category limits

|   | lower        | category  | upper     |
|---|--------------|-----------|-----------|
| 1 | 1.817379e-05 | insertion | 0.1506503 |
| 2 | 1.506503e-01 | match     | 0.4192069 |

1.82e-05 0.151 0.419 0.735 1.13 1.62 2.19 2.94  
3.91 5.83 71

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 36  | 29  | 27  | 21  | 27  | 34  | 26  | 36  | 21  | 21  |
|       | match     |     | 340 | 297 | 251 | 257 | 243 | 237 | 243 | 253 | 244 | 226 |
| MSE-E | insertion |     | 22  | 26  | 27  | 42  | 26  | 38  | 21  | 36  | 28  | 38  |
|       | match     |     | 219 | 265 | 312 | 297 | 321 | 308 | 327 | 292 | 324 | 333 |





## 2.29 encodeAffyChIpHl60PvalRaraHr00

NULL

Affy RARA RA Oh

Affymetrix ChIP/Chip (RARA retinoic acid-treated HL-60, 0hrs) P-Value

|                                             | coef  | se    | z    | p     |
|---------------------------------------------|-------|-------|------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.215 | 0.131 | 1.63 | 0.103 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.185 | 0.125 | 1.48 | 0.140 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

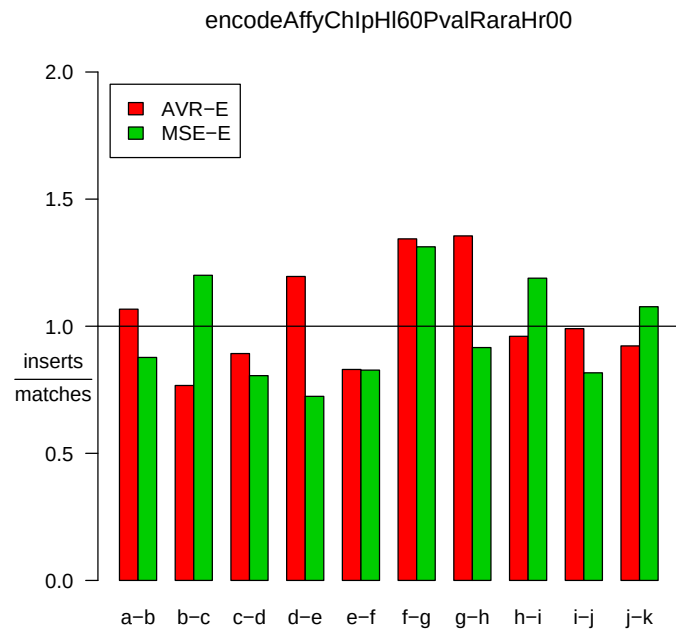
2870 3302

Category limits

|   | lower        | category  | upper     |
|---|--------------|-----------|-----------|
| 1 | 0.0001713477 | insertion | 0.6155971 |
| 2 | 0.6155971408 | match     | 1.6639974 |

0.000171 0.616 1.66 2.73 3.94 5.08 6.44 8.4 10.5  
14.1 144

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 39  | 23  | 25  | 32  | 21  | 34  | 35  | 24  | 23  | 22  |
|       | match     |     | 351 | 288 | 269 | 257 | 243 | 243 | 248 | 240 | 223 | 229 |
| MSE-E | insertion |     | 19  | 34  | 25  | 23  | 28  | 41  | 29  | 39  | 29  | 37  |
|       | match     |     | 208 | 272 | 298 | 305 | 325 | 300 | 304 | 315 | 341 | 330 |



## 2.30 encodeAffyChIpHl60PvalRaraHr02

NULL

Affy RARA RA 2h

Affymetrix ChIP/Chip (RARA retinoic acid-treated HL-60, 2hrs) P-Value

|                                             | coef    | se    | z     | p      |
|---------------------------------------------|---------|-------|-------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.0223 | 0.132 | -0.17 | 0.8650 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.2170 | 0.123 | -1.76 | 0.0776 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

2870 3302

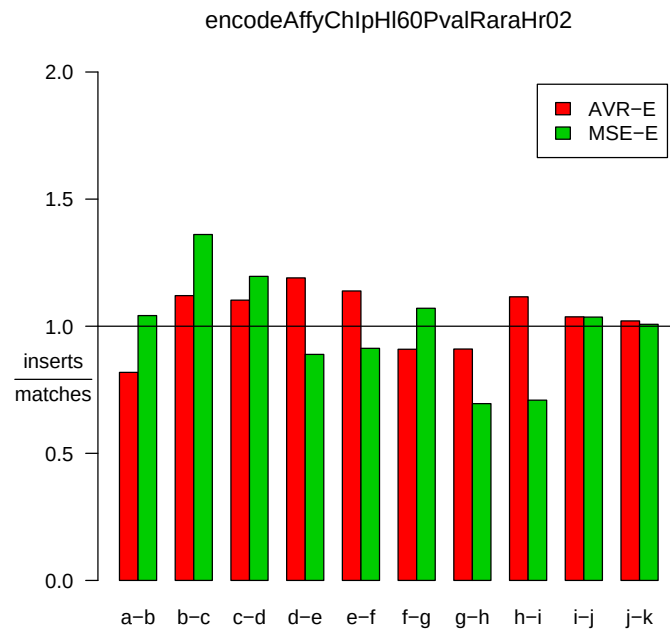
Category limits

|   | lower        | category  | upper      |
|---|--------------|-----------|------------|
| 1 | 8.681510e-08 | insertion | 0.02489982 |
| 2 | 2.489982e-02 | match     | 0.09986559 |

8.68e-08 0.0249 0.0999 0.202 0.338 0.52 0.76 1.09

1.59 2.56 19.8

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 30  | 35  | 31  | 29  | 30  | 25  | 20  | 28  | 23  | 27  |
|       | match     |     | 352 | 300 | 270 | 234 | 253 | 264 | 211 | 241 | 213 | 254 |
| MSE-E | insertion |     | 23  | 35  | 35  | 30  | 29  | 33  | 26  | 24  | 37  | 32  |
|       | match     |     | 212 | 247 | 281 | 324 | 305 | 296 | 359 | 325 | 343 | 305 |



## 2.31 encodeAffyChIpHl60PvalRaraHr08

NULL

Affy RARA RA 8h

Affymetrix ChIP/Chip (RARA retinoic acid-treated HL-60, 8hrs) P-Value

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.0428 | 0.132 | -0.325 | 0.745 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.0371 | 0.124 | -0.300 | 0.764 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

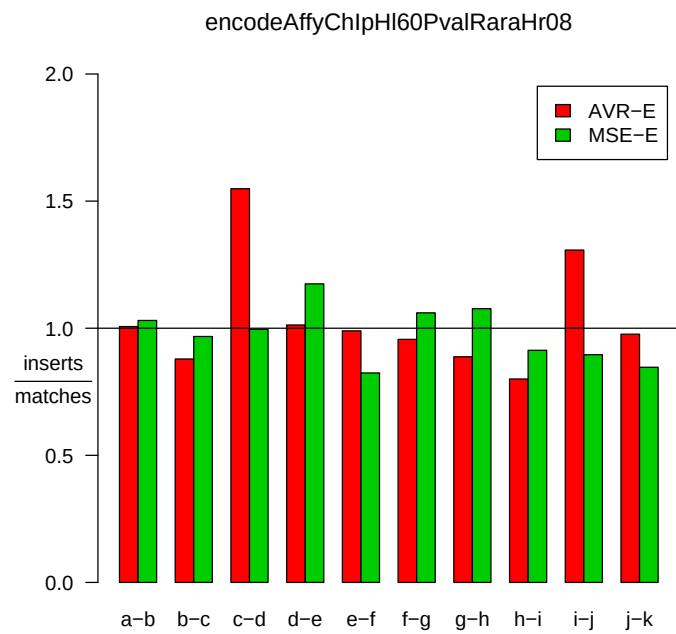
2870 3302

Category limits

|   | lower        | category  | upper      |
|---|--------------|-----------|------------|
| 1 | 2.329234e-07 | insertion | 0.08890306 |
| 2 | 8.890306e-02 | match     | 0.37204141 |

2.33e-07 0.0889 0.372 0.765 1.3 1.91 2.61 3.54  
4.91 7.1 77.1

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 37  | 27  | 40  | 29  | 27  | 23  | 22  | 20  | 29  | 24  |
|       | match     |     | 353 | 295 | 248 | 275 | 262 | 231 | 238 | 240 | 213 | 236 |
| MSE-E | insertion |     | 22  | 27  | 31  | 34  | 26  | 36  | 36  | 31  | 32  | 29  |
|       | match     |     | 205 | 268 | 299 | 278 | 303 | 326 | 321 | 326 | 343 | 329 |



## 2.32 encodeAffyChIpHl60PvalRaraHr32

NULL

Affy RARA RA 32h

Affymetrix ChIP/Chip (RARA retinoic acid-treated HL-60, 32hrs) P-Value

|                                             | coef  | se    | z     | p      |
|---------------------------------------------|-------|-------|-------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.381 | 0.131 | 2.890 | 0.0038 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.125 | 0.126 | 0.993 | 0.3210 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

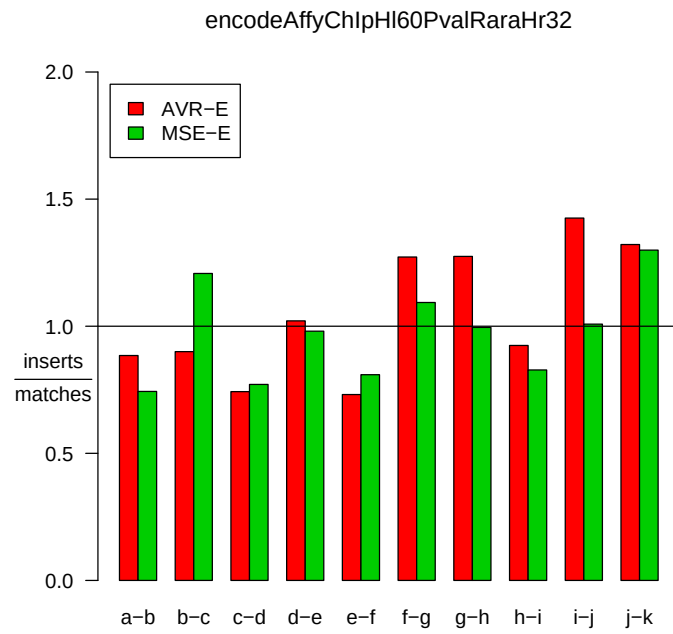
2870 3302

Category limits

|   | lower        | category  | upper      |
|---|--------------|-----------|------------|
| 1 | 1.623675e-06 | insertion | 0.05409775 |
| 2 | 5.409775e-02 | match     | 0.17870181 |

1.62e-06 0.0541 0.179 0.36 0.594 0.857 1.24 1.73  
2.45 3.69 42.2

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 32  | 29  | 22  | 26  | 19  | 32  | 31  | 22  | 32  | 32  |
|       | match     |     | 348 | 310 | 285 | 245 | 250 | 242 | 234 | 229 | 216 | 233 |
| MSE-E | insertion |     | 17  | 31  | 23  | 32  | 27  | 35  | 33  | 29  | 35  | 42  |
|       | match     |     | 220 | 247 | 287 | 314 | 321 | 308 | 319 | 337 | 334 | 311 |





## 2.33 encodeAffyChIpHl60PvalRnapHr00

NULL

Affy Pol2 RA 0h

Affymetrix ChIP/Chip (Pol2 8WG16 antibody, retinoic acid-treated HL-60, 0hrs) P-Value

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.546 | 0.132 | 4.14 | 3.42e-05 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.460 | 0.126 | 3.64 | 2.70e-04 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

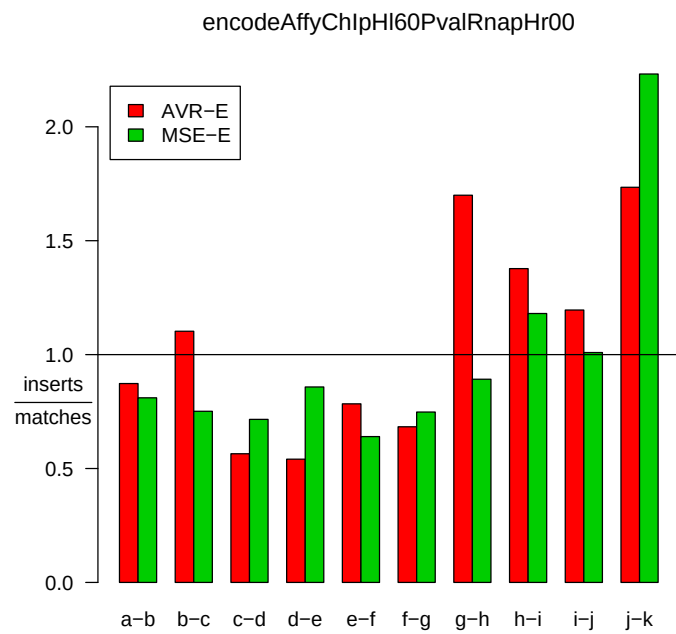
2870 3302

Category limits

|   | lower      | category  | upper    |
|---|------------|-----------|----------|
| 1 | 0.00954703 | insertion | 1.241957 |
| 2 | 1.24195690 | match     | 1.972065 |

0.00955 1.24 1.97 2.57 3.15 3.81 4.61 5.59 6.92  
9.94 148

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 30  | 31  | 15  | 16  | 20  | 18  | 40  | 35  | 32  | 41  |
|       | match     |     | 330 | 270 | 255 | 284 | 245 | 253 | 226 | 244 | 257 | 227 |
| MSE-E | insertion |     | 20  | 23  | 24  | 26  | 22  | 25  | 30  | 37  | 31  | 66  |
|       | match     |     | 237 | 294 | 322 | 291 | 330 | 321 | 323 | 301 | 295 | 284 |



## 2.34 encodeAffyChIpHl60PvalRnapHr02

NULL

Affy Pol2 RA 2h

Affymetrix ChIP/Chip (Pol2 8WG16 antibody, retinoic acid-treated HL-60, 2hrs) P-Value

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.487 | 0.132 | 3.70 | 0.000214 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.483 | 0.127 | 3.81 | 0.000140 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

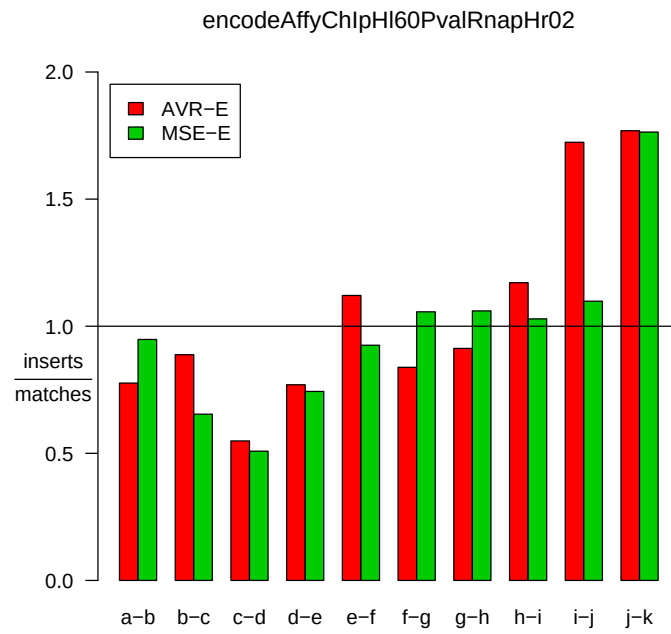
2870 3302

Category limits

|   | lower       | category  | upper     |
|---|-------------|-----------|-----------|
| 1 | 0.002025761 | insertion | 0.4260847 |
| 2 | 0.426084661 | match     | 0.7051428 |

0.00203 0.426 0.705 0.963 1.24 1.56 1.89 2.35  
3.02 4.45 93.2

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 27  | 27  | 14  | 21  | 30  | 22  | 23  | 30  | 42  | 42  |
|       | match     |     | 334 | 292 | 245 | 262 | 257 | 252 | 242 | 246 | 234 | 228 |
| MSE-E | insertion |     | 23  | 19  | 18  | 24  | 29  | 34  | 35  | 33  | 35  | 54  |
|       | match     |     | 233 | 279 | 340 | 310 | 301 | 309 | 317 | 308 | 306 | 294 |



## 2.35 encodeAffyChIpHl60PvalRnapHr08

NULL

Affy Pol2 RA 8h

Affymetrix ChIP/Chip (Pol2 8WG16 antibody, retinoic acid-treated HL-60, 8hrs) P-Value

|                                             | coef  | se    | z    | p       |
|---------------------------------------------|-------|-------|------|---------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.400 | 0.133 | 3.02 | 0.00257 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.462 | 0.128 | 3.62 | 0.00029 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

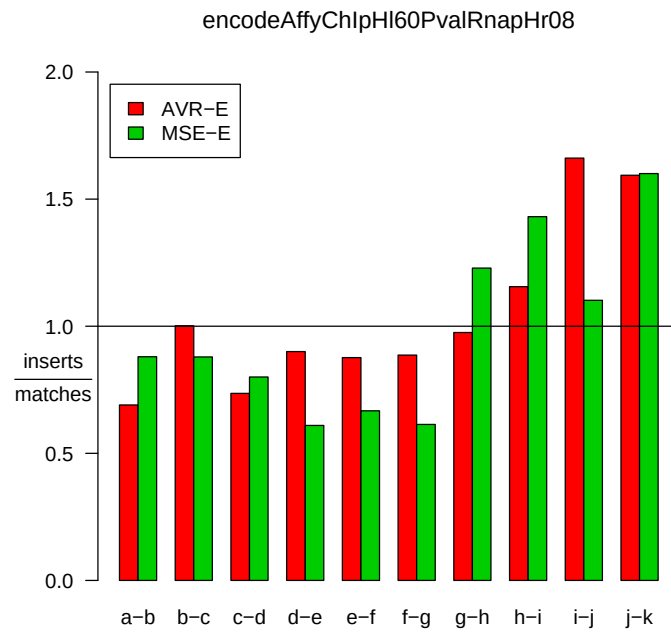
2870 3302

Category limits

|   | lower       | category  | upper     |
|---|-------------|-----------|-----------|
| 1 | 0.004352912 | insertion | 0.7988975 |
| 2 | 0.798897487 | match     | 1.2431162 |

0.00435 0.799 1.24 1.62 2.03 2.49 3.03 3.71 4.73  
6.71 101

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 23  | 29  | 20  | 24  | 22  | 24  | 26  | 29  | 41  | 40  |
|       | match     |     | 320 | 278 | 261 | 256 | 241 | 260 | 256 | 241 | 237 | 241 |
| MSE-E | insertion |     | 23  | 26  | 26  | 20  | 23  | 20  | 38  | 45  | 35  | 48  |
|       | match     |     | 251 | 284 | 312 | 315 | 331 | 313 | 297 | 302 | 305 | 288 |



## 2.36 encodeAffyChIpHl60PvalRnapHr32

NULL

Affy Pol2 RA 32h

Affymetrix ChIP/Chip (Pol2 8WG16 antibody, retinoic acid-treated HL-60, 32hrs) P-Value

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.556 | 0.131 | 4.23 | 2.37e-05 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.767 | 0.132 | 5.82 | 5.98e-09 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

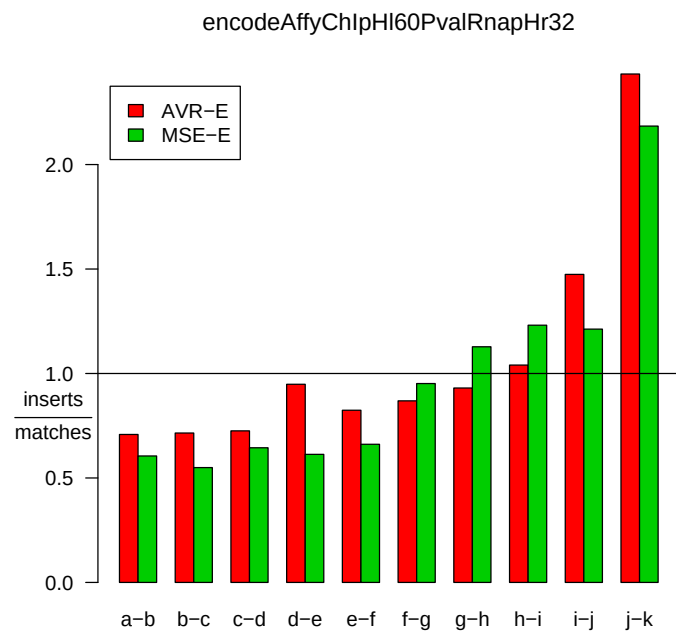
2870 3302

Category limits

|   | lower        | category  | upper    |
|---|--------------|-----------|----------|
| 1 | 0.0002234662 | insertion | 0.483001 |
| 2 | 0.4830009699 | match     | 0.958474 |

0.000223 0.483 0.958 1.44 1.97 2.52 3.24 4.12  
5.54 8.45 135

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 25  | 21  | 21  | 24  | 23  | 20  | 25  | 26  | 37  | 56  |
|       | match     |     | 339 | 282 | 278 | 243 | 268 | 221 | 258 | 240 | 241 | 221 |
| MSE-E | insertion |     | 15  | 17  | 20  | 21  | 21  | 34  | 35  | 40  | 38  | 63  |
|       | match     |     | 238 | 297 | 298 | 329 | 305 | 343 | 298 | 312 | 301 | 277 |





## 2.37 encodeAffyChIpHL60PvalSirt1Hr00

NULL

Affy SIRT1 RA 0h

Affymetrix ChIP/Chip (SIRT1 retinoic acid-treated HL-60, 0hrs) P-Value

|                                             | coef   | se    | z     | p      |
|---------------------------------------------|--------|-------|-------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.2670 | 0.129 | 2.070 | 0.0384 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.0223 | 0.124 | 0.179 | 0.8580 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

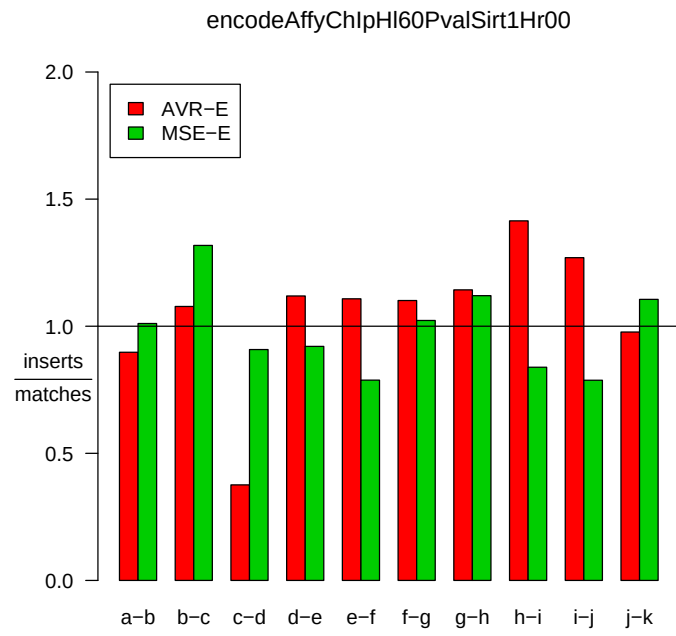
2870 3302

Category limits

|   | lower        | category  | upper     |
|---|--------------|-----------|-----------|
| 1 | 1.186480e-09 | insertion | 0.0246570 |
| 2 | 2.465700e-02 | match     | 0.1408830 |

1.19e-09 0.0247 0.141 0.345 0.635 1.06 1.63 2.45  
3.65 5.62 33.8

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 33  | 33  | 11  | 31  | 27  | 25  | 30  | 33  | 32  | 23  |
|       | match     |     | 353 | 294 | 281 | 266 | 234 | 218 | 252 | 224 | 242 | 226 |
| MSE-E | insertion |     | 22  | 35  | 28  | 28  | 27  | 36  | 35  | 29  | 26  | 38  |
|       | match     |     | 209 | 255 | 296 | 292 | 329 | 338 | 300 | 332 | 317 | 330 |



## 2.38 encodeAffyChIpHl60PvalSirt1Hr02

NULL

Affy SIRT1 RA 2h

Affymetrix ChIP/Chip (SIRT1 retinoic acid-treated HL-60, 2hrs) P-Value

|                                             | coef   | se    | z     | p     |
|---------------------------------------------|--------|-------|-------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.189  | 0.131 | 1.44  | 0.151 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.154 | 0.125 | -1.24 | 0.217 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

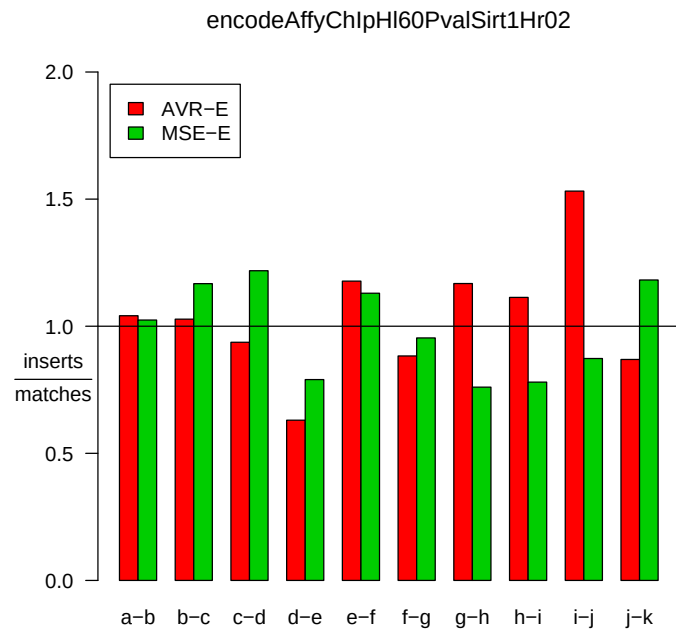
2870 3302

Category limits

|   | lower        | category  | upper      |
|---|--------------|-----------|------------|
| 1 | 1.312837e-08 | insertion | 0.05006252 |
| 2 | 5.006252e-02 | match     | 0.23393033 |

1.31e-08 0.0501 0.234 0.534 0.944 1.6 2.48 3.57  
5.15 7.78 37.3

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 36  | 32  | 28  | 17  | 32  | 24  | 27  | 24  | 37  | 21  |
|       | match     |     | 332 | 299 | 287 | 259 | 261 | 261 | 222 | 207 | 232 | 232 |
| MSE-E | insertion |     | 24  | 31  | 34  | 26  | 34  | 30  | 27  | 29  | 29  | 40  |
|       | match     |     | 225 | 255 | 268 | 316 | 289 | 302 | 341 | 357 | 319 | 325 |



## 2.39 encodeAffyChIpHl60PvalSirt1Hr08

NULL

Affy SIRT1 RA 8h

Affymetrix ChIP/Chip (SIRT1 retinoic acid-treated HL-60, 8hrs) P-Value

|                                             | coef   | se    | z     | p      |
|---------------------------------------------|--------|-------|-------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.164  | 0.131 | 1.25  | 0.2110 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.270 | 0.124 | -2.17 | 0.0299 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

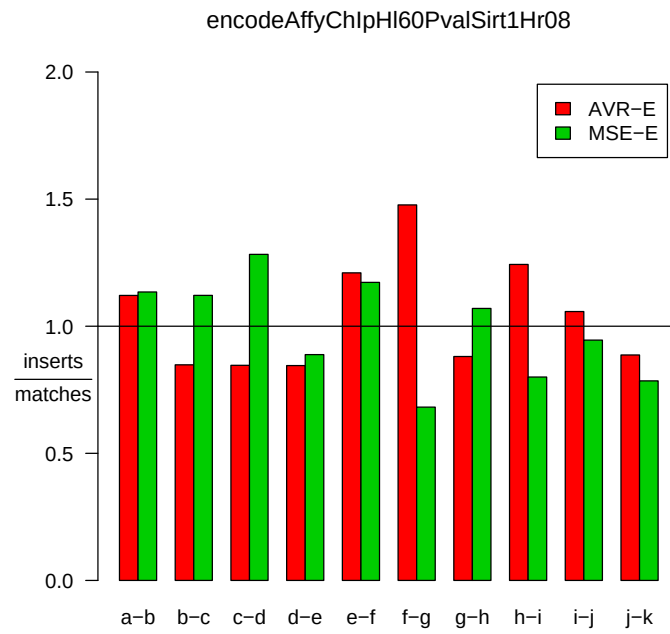
2870 3302

Category limits

|   | lower        | category  | upper       |
|---|--------------|-----------|-------------|
| 1 | 3.212079e-10 | insertion | 0.005043896 |
| 2 | 5.043896e-03 | match     | 0.033053715 |

3.21e-10 0.00504 0.0331 0.096 0.212 0.423 0.708  
1.14 1.85 3.46 36.8

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 39  | 25  | 26  | 25  | 31  | 34  | 20  | 29  | 26  | 23  |
|       | match     |     | 334 | 283 | 295 | 284 | 246 | 221 | 218 | 224 | 236 | 249 |
| MSE-E | insertion |     | 26  | 32  | 35  | 26  | 37  | 24  | 38  | 28  | 32  | 26  |
|       | match     |     | 220 | 274 | 262 | 281 | 303 | 338 | 341 | 336 | 325 | 318 |



## 2.40 encodeAffyChIPHL60PvalSirt1Hr32

NULL

Affy SIRT1 RA 32h

Affymetrix ChIP/Chip (SIRT1 retinoic acid-treated HL-60, 32hrs) P-Value

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.0695  | 0.131 | 0.529  | 0.597 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.1820 | 0.125 | -1.460 | 0.144 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

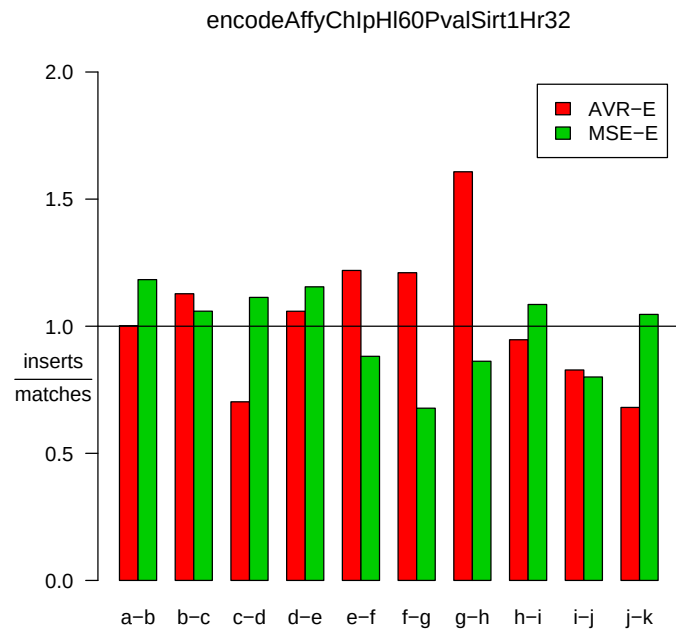
2870 3302

Category limits

|   | lower        | category  | upper      |
|---|--------------|-----------|------------|
| 1 | 2.997653e-09 | insertion | 0.03003603 |
| 2 | 3.003603e-02 | match     | 0.15336715 |

3e-09 0.03 0.153 0.386 0.734 1.25 1.86 2.75 4.07  
6.41 35.6

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 36  | 33  | 21  | 29  | 32  | 30  | 38  | 21  | 20  | 18  |
|       | match     |     | 345 | 281 | 287 | 263 | 252 | 238 | 227 | 213 | 232 | 254 |
| MSE-E | insertion |     | 26  | 30  | 32  | 35  | 28  | 23  | 29  | 39  | 28  | 34  |
|       | match     |     | 211 | 272 | 276 | 291 | 305 | 326 | 323 | 345 | 336 | 312 |





## 2.41 encodeAffyChIpHl60PvalStrictH3K9K14DHr00

NULL

Affy H3K9ac2 0h

Affymetrix ChIP/Chip (H3K9K14ac2, retinoic acid-treated HL-60, 0hrs) Strict P-Value

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.849 | 0.139 | 6.11 | 9.95e-10 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.956 | 0.135 | 7.06 | 1.66e-12 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

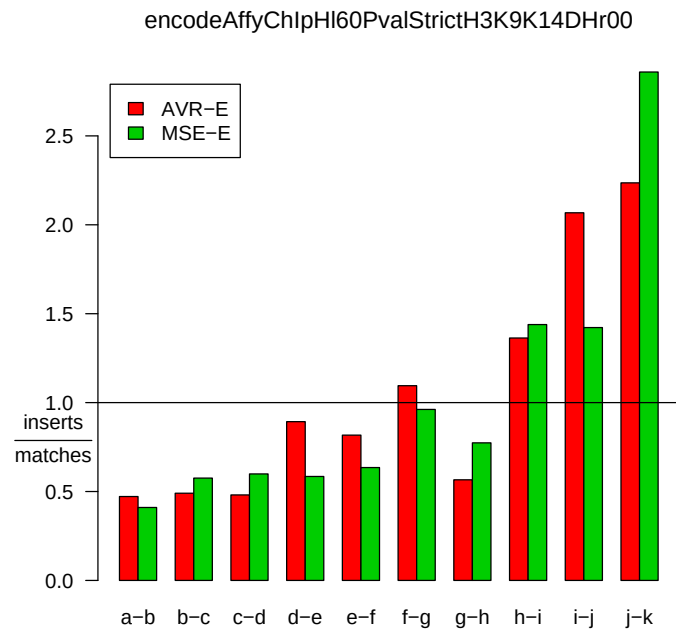
2874 3307

Category limits

|   | lower      | category  | upper    |
|---|------------|-----------|----------|
| 1 | 0.04775261 | insertion | 1.696272 |
| 2 | 1.69627190 | match     | 2.538049 |

0.0478 1.7 2.54 3.24 4.01 4.79 5.68 6.86 8.51  
11.8 262

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 13  | 13  | 14  | 26  | 22  | 32  | 15  | 35  | 52  | 56  |
|       | match     |     | 264 | 254 | 279 | 279 | 258 | 280 | 254 | 246 | 241 | 240 |
| MSE-E | insertion |     | 14  | 20  | 19  | 18  | 21  | 28  | 26  | 44  | 42  | 74  |
|       | match     |     | 327 | 333 | 304 | 295 | 317 | 279 | 322 | 293 | 283 | 248 |



## 2.42 encodeAffyChIPHL60PvalStrictH3K9K14DHr02

NULL

Affy H3K9ac2 2h

Affymetrix ChIP/Chip (H3K9K14ac2, retinoic acid-treated HL-60, 2hrs) Strict P-Value

|                                             | coef | se    | z    | p        |
|---------------------------------------------|------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 1.08 | 0.146 | 7.38 | 1.53e-13 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.04 | 0.137 | 7.64 | 2.16e-14 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

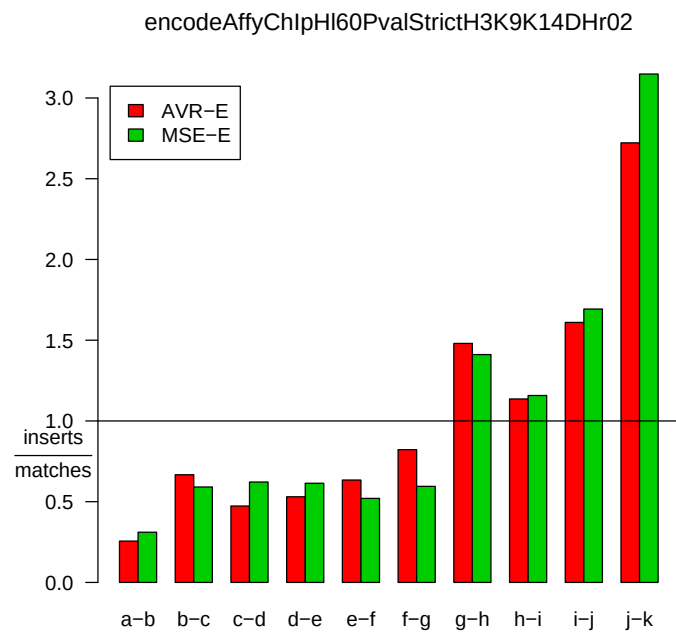
2874 3307

Category limits

|   | lower        | category  | upper     |
|---|--------------|-----------|-----------|
| 1 | 0.0008835184 | insertion | 0.3294787 |
| 2 | 0.3294786811 | match     | 0.5462796 |

0.000884 0.329 0.546 0.771 0.994 1.27 1.59 1.99  
2.64 4.25 257

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 7   | 19  | 12  | 15  | 18  | 23  | 38  | 30  | 41  | 75  |
|       | match     |     | 262 | 273 | 243 | 271 | 272 | 268 | 246 | 253 | 244 | 264 |
| MSE-E | insertion |     | 11  | 19  | 22  | 20  | 17  | 19  | 43  | 36  | 50  | 69  |
|       | match     |     | 339 | 308 | 339 | 312 | 313 | 306 | 292 | 298 | 283 | 210 |



## 2.43 encodeAffyChIpHl60PvalStrictH3K9K14DHr08

NULL

Affy H3K9ac2 8h

Affymetrix ChIP/Chip (H3K9K14ac2, retinoic acid-treated HL-60, 8hrs) Strict P-Value

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.999 | 0.146 | 6.83 | 8.75e-12 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.865 | 0.131 | 6.59 | 4.32e-11 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

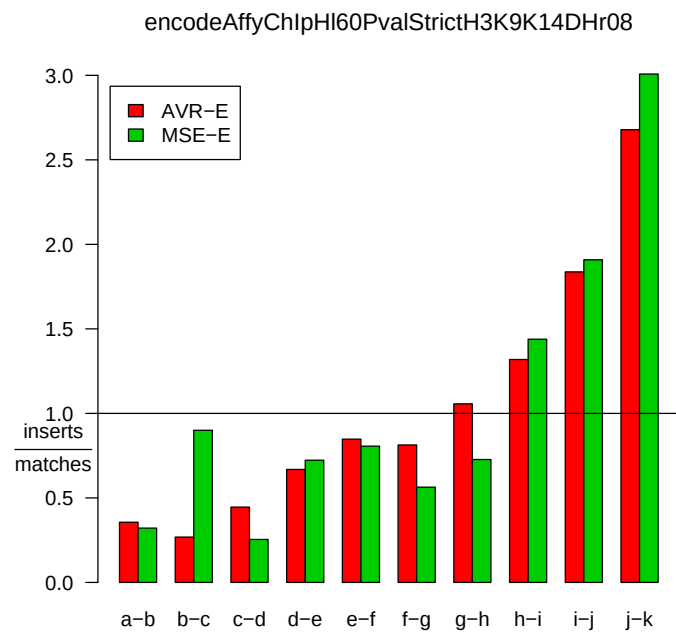
2874 3307

Category limits

|   | lower      | category  | upper     |
|---|------------|-----------|-----------|
| 1 | 0.01860871 | insertion | 0.8697054 |
| 2 | 0.86970538 | match     | 1.2902136 |

0.0186 0.87 1.29 1.69 2.1 2.53 3.07 3.77 4.75  
7.18 306

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 10  | 7   | 12  | 18  | 23  | 23  | 29  | 34  | 51  | 71  |
|       | match     |     | 269 | 250 | 258 | 258 | 260 | 271 | 263 | 247 | 266 | 254 |
| MSE-E | insertion |     | 11  | 31  | 9   | 24  | 26  | 18  | 23  | 44  | 50  | 70  |
|       | match     |     | 328 | 330 | 339 | 318 | 309 | 306 | 303 | 293 | 251 | 223 |



## 2.44 encodeAffyChIpHl60PvalStrictH3K9K14DHr32

NULL

Affy H3K9ac2 32h

Affymetrix ChIP/Chip (H3K9K14ac2, retinoic acid-treated HL-60, 32hrs) Strict P-Value

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.982 | 0.142 | 6.92 | 4.41e-12 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.870 | 0.132 | 6.61 | 3.78e-11 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

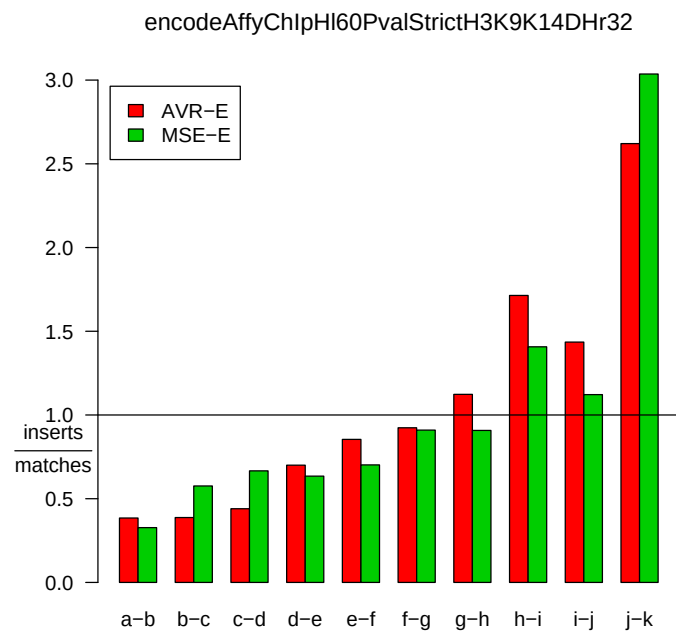
2874 3307

Category limits

|   | lower        | category  | upper     |
|---|--------------|-----------|-----------|
| 1 | 0.0006174378 | insertion | 0.4660956 |
| 2 | 0.4660955667 | match     | 0.7891073 |

0.000617 0.466 0.789 1.09 1.41 1.77 2.22 2.74  
3.61 5.56 317

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 11  | 11  | 13  | 19  | 23  | 24  | 32  | 44  | 37  | 64  |
|       | match     |     | 274 | 272 | 283 | 260 | 258 | 249 | 273 | 246 | 247 | 234 |
| MSE-E | insertion |     | 11  | 19  | 21  | 21  | 23  | 30  | 27  | 42  | 35  | 77  |
|       | match     |     | 322 | 316 | 302 | 317 | 314 | 316 | 285 | 286 | 299 | 243 |





## 2.45 encodeAffyChIpHl60PvalStrictHisH4Hr00

NULL

Affy H4Kac4 0h

Affymetrix ChIP/Chip (H4Kac4, retinoic acid-treated HL-60, 0hrs) Strict P-Value

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.696 | 0.138 | 5.06 | 4.15e-07 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.000 | 0.132 | 7.55 | 4.44e-14 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

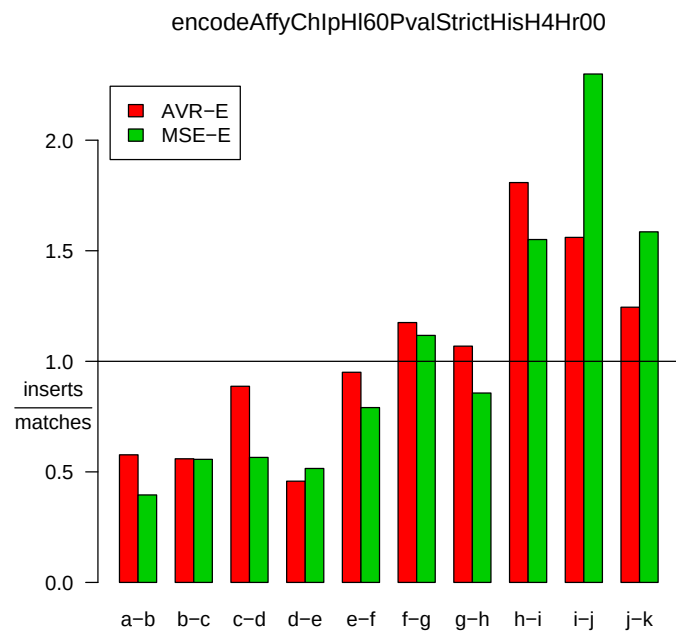
2874 3307

Category limits

|   | lower     | category  | upper    |
|---|-----------|-----------|----------|
| 1 | 0.1182174 | insertion | 2.433435 |
| 2 | 2.4334347 | match     | 3.583776 |

0.118 2.43 3.58 4.64 5.75 7.04 8.63 11.4 15.6  
27.6 467

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 15  | 15  | 25  | 13  | 25  | 33  | 29  | 47  | 43  | 33  |
|       | match     |     | 249 | 257 | 270 | 272 | 252 | 269 | 260 | 249 | 264 | 254 |
| MSE-E | insertion |     | 14  | 19  | 18  | 17  | 26  | 33  | 27  | 45  | 60  | 47  |
|       | match     |     | 339 | 327 | 305 | 316 | 315 | 283 | 302 | 278 | 250 | 284 |



## 2.46 encodeAffyChIPHL60PvalStrictHisH4Hr02

NULL

Affy H4Kac4 2h

Affymetrix ChIP/Chip (H4Kac4, retinoic acid-treated HL-60, 2hrs) Strict P-Value

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.591 | 0.135 | 4.38 | 1.19e-05 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.765 | 0.128 | 5.97 | 2.31e-09 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

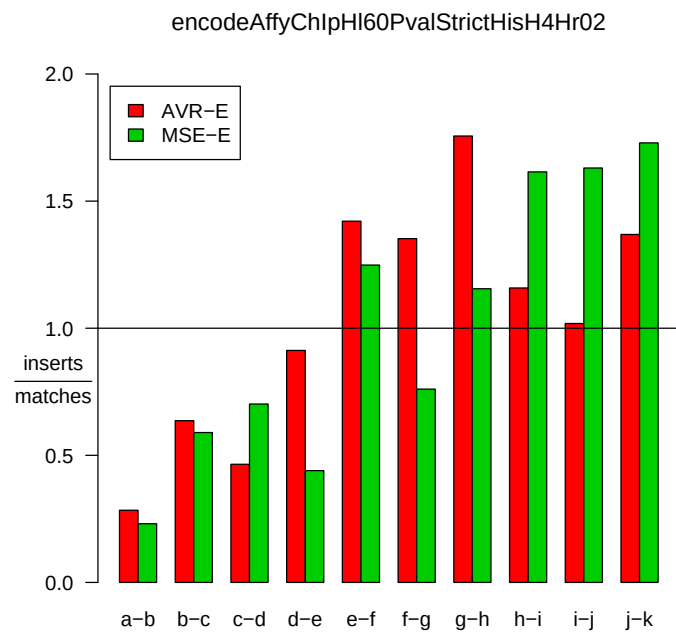
2874 3307

Category limits

|   | lower       | category  | upper     |
|---|-------------|-----------|-----------|
| 1 | 0.002139235 | insertion | 0.9014346 |
| 2 | 0.901434600 | match     | 1.3822458 |

0.00214 0.901 1.38 1.87 2.33 2.96 3.73 4.82 6.77  
13.2 368

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 8   | 17  | 13  | 26  | 35  | 35  | 46  | 33  | 27  | 38  |
|       | match     |     | 270 | 256 | 268 | 273 | 236 | 248 | 251 | 273 | 254 | 266 |
| MSE-E | insertion |     | 8   | 20  | 23  | 14  | 40  | 25  | 34  | 45  | 49  | 48  |
|       | match     |     | 332 | 325 | 314 | 305 | 307 | 315 | 282 | 267 | 288 | 266 |



## 2.47 encodeAffyChIpHl60PvalStrictHisH4Hr08

NULL

Affy H4Kac4 8h

Affymetrix ChIP/Chip (H4Kac4, retinoic acid-treated HL-60, 8hrs) Strict P-Value

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.342 | 0.133 | 2.58 | 9.95e-03 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.754 | 0.129 | 5.85 | 4.88e-09 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

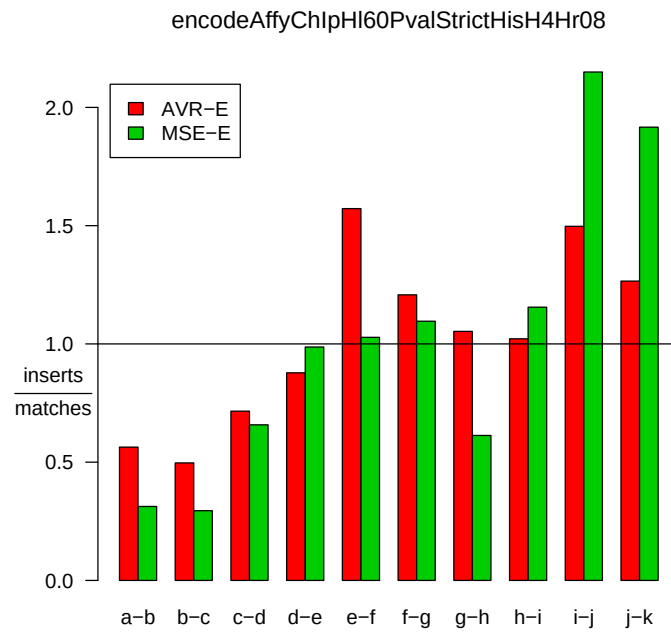
2874 3307

Category limits

|   | lower      | category  | upper    |
|---|------------|-----------|----------|
| 1 | 0.03229449 | insertion | 1.776222 |
| 2 | 1.77622223 | match     | 2.654654 |

0.0323 1.78 2.65 3.44 4.32 5.29 6.45 8 11.2 21.5  
435

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 15  | 14  | 18  | 24  | 42  | 31  | 30  | 29  | 40  | 35  |
|       | match     |     | 255 | 270 | 241 | 262 | 256 | 246 | 273 | 272 | 256 | 265 |
| MSE-E | insertion |     | 11  | 10  | 23  | 31  | 31  | 35  | 19  | 34  | 59  | 53  |
|       | match     |     | 337 | 325 | 335 | 301 | 289 | 306 | 297 | 282 | 263 | 265 |



## 2.48 encodeAffyChIpHl60PvalStrictHisH4Hr32

NULL

Affy H4Kac4 32h

Affymetrix ChIP/Chip (H4Kac4, retinoic acid-treated HL-60, 32hrs) Strict P-Value

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.390 | 0.132 | 2.95 | 3.16e-03 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.815 | 0.129 | 6.34 | 2.24e-10 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

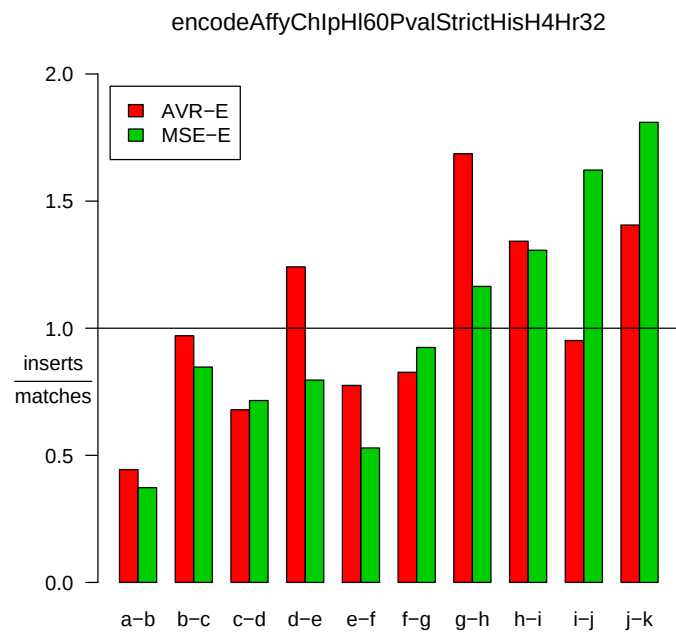
2874 3307

Category limits

|   | lower       | category  | upper     |
|---|-------------|-----------|-----------|
| 1 | 0.003288884 | insertion | 0.7483953 |
| 2 | 0.748395324 | match     | 1.1937439 |

0.00329 0.748 1.19 1.62 2.04 2.54 3.25 4.25 6.36  
13.9 427

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 12  | 24  | 19  | 32  | 22  | 22  | 44  | 36  | 29  | 38  |
|       | match     |     | 259 | 237 | 268 | 247 | 272 | 255 | 250 | 257 | 292 | 259 |
| MSE-E | insertion |     | 13  | 29  | 23  | 26  | 17  | 30  | 35  | 39  | 43  | 51  |
|       | match     |     | 334 | 328 | 308 | 313 | 308 | 311 | 288 | 286 | 254 | 270 |





## 2.49 encodeAffyChIPHL60PvalStrictPol2Hr00

NULL

Affy Pol2 0h

Affymetrix ChIP/Chip (Pol2, retinoic acid-treated HL-60, 0hrs) Strict P-Value

|                                             | coef  | se    | z    | p       |
|---------------------------------------------|-------|-------|------|---------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.333 | 0.130 | 2.56 | 0.01040 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.451 | 0.126 | 3.58 | 0.00034 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

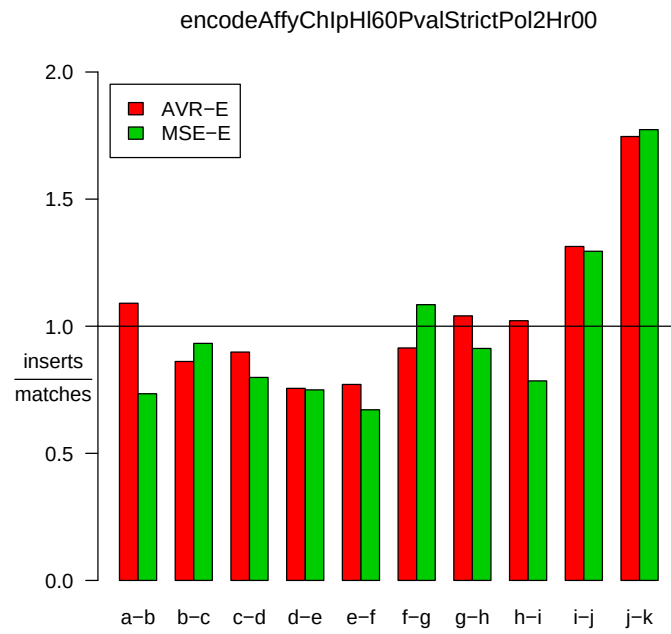
2874 3307

Category limits

|   | lower    | category  | upper    |
|---|----------|-----------|----------|
| 1 | 0.128816 | insertion | 2.284083 |
| 2 | 2.284083 | match     | 3.237469 |

0.129 2.28 3.24 4.06 4.94 5.88 7.03 8.51 10.6  
14.2 188

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 33  | 24  | 24  | 22  | 21  | 23  | 29  | 29  | 34  | 39  |
|       | match     |     | 290 | 267 | 256 | 279 | 261 | 241 | 267 | 272 | 248 | 214 |
| MSE-E | insertion |     | 21  | 29  | 26  | 23  | 22  | 36  | 28  | 24  | 40  | 57  |
|       | match     |     | 274 | 298 | 312 | 294 | 314 | 318 | 294 | 293 | 296 | 308 |



## 2.50 encodeAffyChIPHL60PvalStrictPol2Hr02

NULL

Affy Pol2 2h

Affymetrix ChIP/Chip (Pol2, retinoic acid-treated HL-60, 2hrs) Strict P-Value

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.265 | 0.130 | 2.04 | 0.041500 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.470 | 0.126 | 3.73 | 0.000188 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

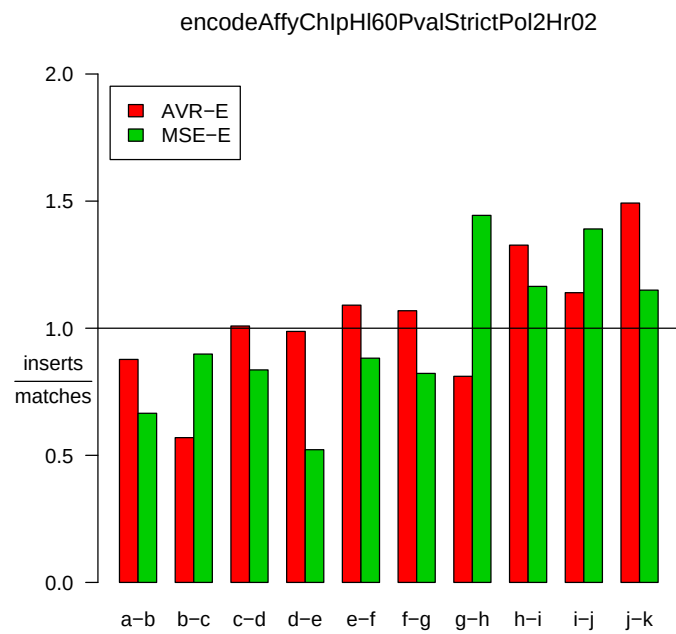
2874 3307

Category limits

|   | lower      | category  | upper     |
|---|------------|-----------|-----------|
| 1 | 0.02180612 | insertion | 0.5740666 |
| 2 | 0.57406664 | match     | 0.9203594 |

0.0218 0.574 0.92 1.23 1.53 1.87 2.35 2.89 3.71  
5.24 99.1

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 26  | 17  | 28  | 27  | 28  | 29  | 22  | 36  | 27  | 38  |
|       | match     |     | 284 | 286 | 266 | 262 | 246 | 260 | 260 | 260 | 227 | 244 |
| MSE-E | insertion |     | 20  | 27  | 26  | 17  | 29  | 26  | 44  | 35  | 46  | 36  |
|       | match     |     | 288 | 288 | 298 | 312 | 315 | 303 | 292 | 288 | 317 | 300 |



## 2.51 encodeAffyChIPHL60PvalStrictPol2Hr08

NULL

Affy Pol2 8h

Affymetrix ChIP/Chip (Pol2, retinoic acid-treated HL-60, 8hrs) Strict P-Value

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.357 | 0.130 | 2.74 | 0.006100 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.418 | 0.124 | 3.36 | 0.000777 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

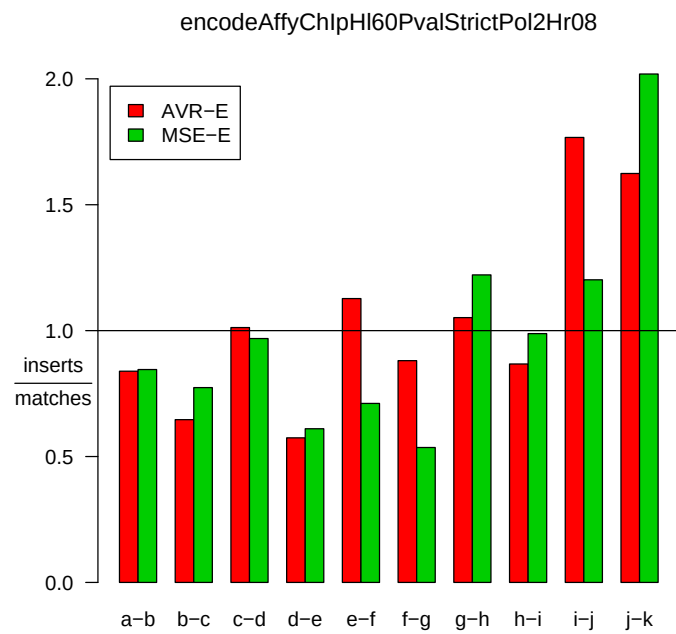
2874 3307

Category limits

|   | lower      | category  | upper    |
|---|------------|-----------|----------|
| 1 | 0.05265029 | insertion | 1.581805 |
| 2 | 1.58180499 | match     | 2.211423 |

0.0527 1.58 2.21 2.74 3.28 3.87 4.52 5.52 6.84  
9.44 119

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 26  | 17  | 30  | 16  | 30  | 25  | 27  | 22  | 45  | 40  |
|       | match     |     | 297 | 252 | 284 | 267 | 255 | 272 | 246 | 243 | 244 | 236 |
| MSE-E | insertion |     | 24  | 26  | 28  | 20  | 23  | 17  | 39  | 33  | 37  | 59  |
|       | match     |     | 272 | 322 | 277 | 314 | 310 | 304 | 306 | 320 | 295 | 280 |



## 2.52 encodeAffyChIPHL60PvalStrictPol2Hr32

NULL

Affy Pol2 32h

Affymetrix ChIP/Chip (Pol2, retinoic acid-treated HL-60, 32hrs) Strict P-Value

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.657 | 0.133 | 4.93 | 8.40e-07 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.856 | 0.133 | 6.43 | 1.26e-10 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

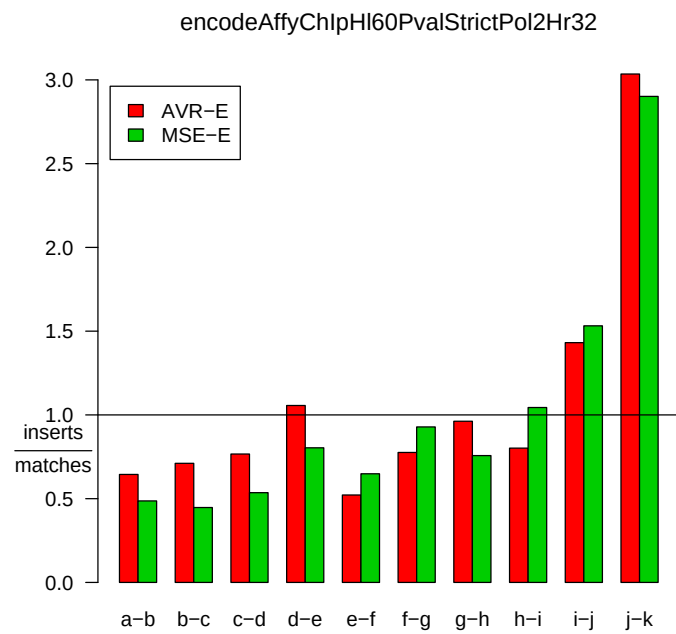
2874 3307

Category limits

|   | lower        | category  | upper     |
|---|--------------|-----------|-----------|
| 1 | 0.0003385733 | insertion | 0.6840369 |
| 2 | 0.6840369105 | match     | 1.2834417 |

0.000339 0.684 1.28 1.91 2.53 3.31 4.27 5.56 7.58  
12.4 283

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 22  | 21  | 22  | 28  | 14  | 20  | 24  | 21  | 36  | 70  |
|       | match     |     | 327 | 283 | 275 | 254 | 257 | 247 | 239 | 251 | 241 | 221 |
| MSE-E | insertion |     | 13  | 14  | 17  | 26  | 22  | 31  | 26  | 34  | 47  | 76  |
|       | match     |     | 256 | 300 | 304 | 310 | 325 | 320 | 329 | 312 | 294 | 251 |





## 2.53 encodeAffyChIpHl60PvalTfibHr32

NULL

Affy TFIIB RA 32h

Affymetrix ChIP/Chip (TFIIB retinoic acid-treated HL-60, 32hrs) P-Value

|                                             | coef  | se    | z    | p      |
|---------------------------------------------|-------|-------|------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.308 | 0.130 | 2.37 | 0.0179 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.260 | 0.125 | 2.08 | 0.0374 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3354

Origin.of.data.set

AVR-E MSE-E

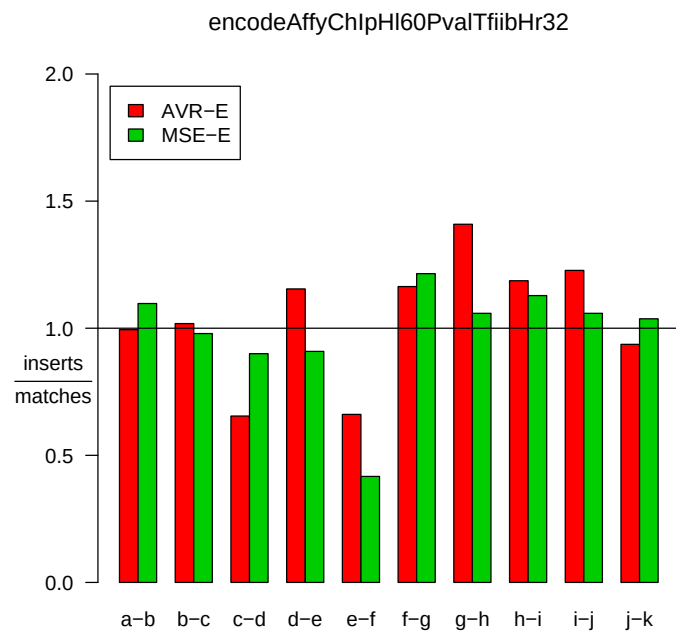
2870 3302

Category limits

|   | lower        | category  | upper    |
|---|--------------|-----------|----------|
| 1 | 6.428146e-05 | insertion | 0.290568 |
| 2 | 2.905680e-01 | match     | 0.697171 |

6.43e-05 0.291 0.697 1.22 1.84 2.53 3.38 4.47  
5.92 8.69 64.1

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 34  | 29  | 20  | 30  | 18  | 30  | 35  | 28  | 31  | 22  |
|       | match     |     | 329 | 274 | 294 | 250 | 262 | 248 | 239 | 227 | 243 | 226 |
| MSE-E | insertion |     | 26  | 29  | 26  | 29  | 14  | 38  | 34  | 38  | 34  | 36  |
|       | match     |     | 228 | 285 | 278 | 307 | 323 | 301 | 309 | 324 | 309 | 334 |



NULL

NULL

## 2.54 encodeAffyChIpHl60SignalStrictH3K9K14DHr00

NULL

Affy H3K9ac2 0h

Affymetrix ChIP/Chip (H3K9K14ac2, retinoic acid-treated HL-60, 0hrs) Strict Signal

|                                             | coef | se    | z    | p        |
|---------------------------------------------|------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 1.01 | 0.211 | 4.76 | 1.91e-06 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.25 | 0.198 | 6.30 | 3.03e-10 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

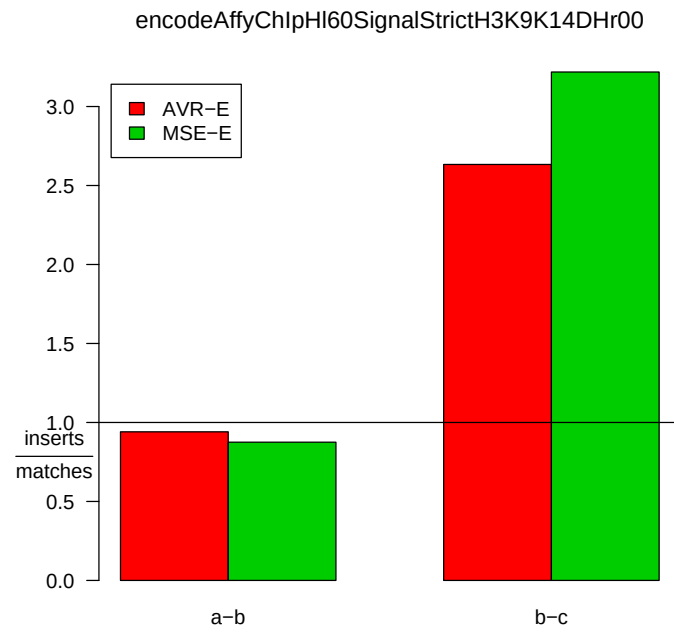
2874 3307

Category limits

|   | lower     | category  | upper    |
|---|-----------|-----------|----------|
| 1 | -0.659166 | insertion | 0.000000 |
| 2 | 0.000000  | match     | 2.270191 |

-0.659 0 2.27

| set   | type      | brk | a-b  | b-c |
|-------|-----------|-----|------|-----|
| AVR-E | insertion |     | 242  | 36  |
|       | match     |     | 2465 | 131 |
| MSE-E | insertion |     | 262  | 44  |
|       | match     |     | 2869 | 131 |



## 2.55 encodeAffyChIpHl60SignalStrictH3K9K14DHr02

NULL

Affy H3K9ac2 2h

Affymetrix ChIP/Chip (H3K9K14ac2, retinoic acid-treated HL-60, 2hrs) Strict Signal

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.914 | 0.317 | 2.88 | 3.94e-03 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.270 | 0.273 | 4.67 | 3.08e-06 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

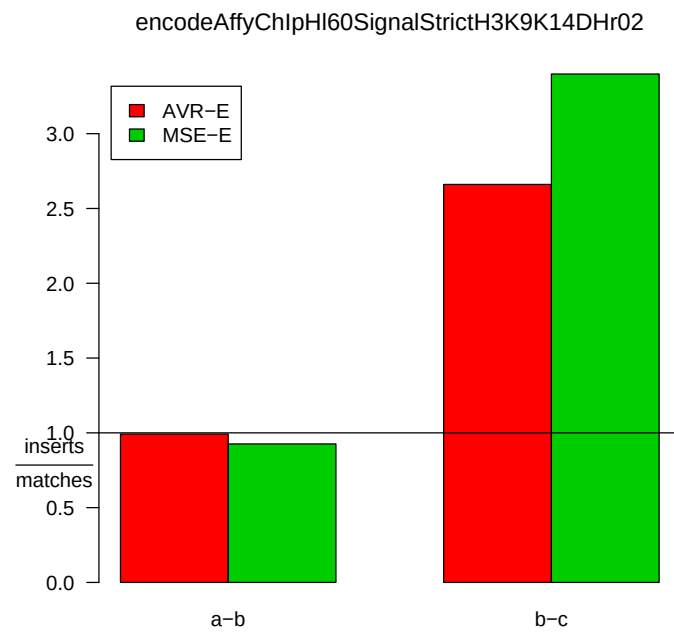
2874 3307

Category limits

|   | lower      | category  | upper    |
|---|------------|-----------|----------|
| 1 | -0.6630087 | insertion | 0.000000 |
| 2 | 0.0000000  | match     | 2.021613 |

-0.663 0 2.02

| set   | type      | brk | a-b  | b-c |
|-------|-----------|-----|------|-----|
| AVR-E | insertion |     | 263  | 15  |
|       | match     |     | 2540 | 54  |
| MSE-E | insertion |     | 284  | 22  |
|       | match     |     | 2938 | 62  |



## 2.56 encodeAffyChIpHL60SignalStrictH3K9K14DHR08

NULL

Affy H3K9ac2 8h

Affymetrix ChIP/Chip (H3K9K14ac2, retinoic acid-treated HL-60, 8hrs) Strict Signal

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.926 | 0.247 | 3.75 | 1.77e-04 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.060 | 0.236 | 4.50 | 6.66e-06 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

2874 3307

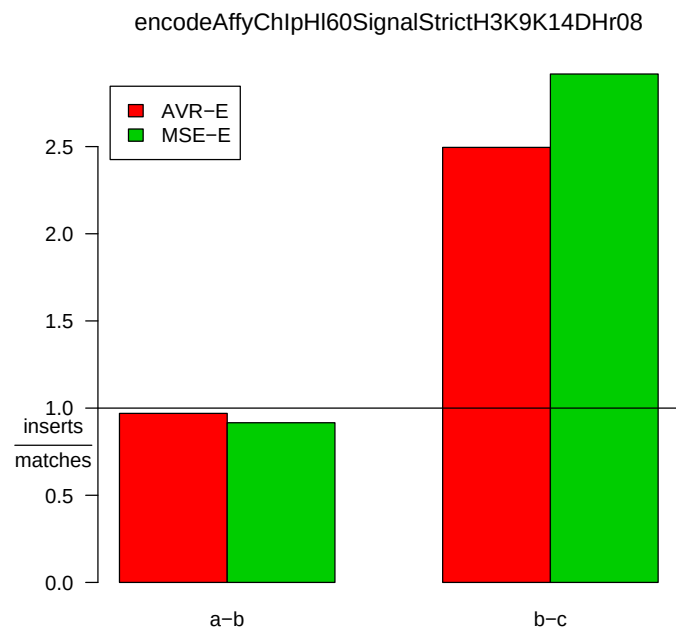
Category limits

|   | lower    | category  | upper    |
|---|----------|-----------|----------|
| 1 | -0.78345 | insertion | 0.000000 |
| 2 | 0.00000  | match     | 2.368809 |

-0.783 0 2.37

| set   | type      | brk | a-b  | b-c |
|-------|-----------|-----|------|-----|
| AVR-E | insertion |     | 253  | 25  |
|       | match     |     | 2500 | 96  |
| MSE-E | insertion |     | 278  | 28  |
|       | match     |     | 2908 | 92  |





## 2.57 encodeAffyChIpHl60SignalStrictH3K9K14DHr32

NULL

Affy H3K9ac2 32h

Affymetrix ChIP/Chip (H3K9K14ac2, retinoic acid-treated HL-60, 32hrs) Strict Signal

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.921 | 0.278 | 3.31 | 0.000933 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.010 | 0.268 | 3.79 | 0.000149 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

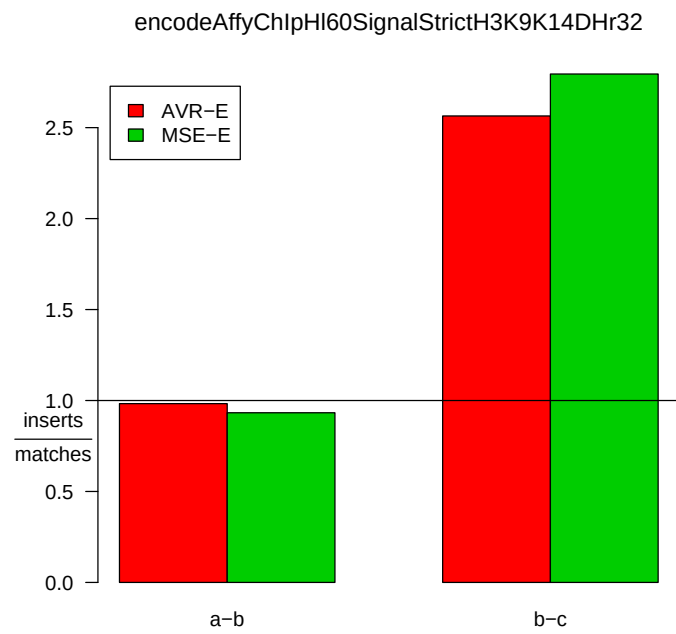
2874 3307

Category limits

|   | lower      | category  | upper    |
|---|------------|-----------|----------|
| 1 | -0.7056116 | insertion | 0.000000 |
| 2 | 0.0000000  | match     | 2.502447 |

-0.706 0 2.5

| set   | type      | brk | a-b  | b-c |
|-------|-----------|-----|------|-----|
| AVR-E | insertion |     | 259  | 19  |
|       | match     |     | 2525 | 71  |
| MSE-E | insertion |     | 285  | 21  |
|       | match     |     | 2928 | 72  |



## 2.58 encodeAffyChIpHL60SignalStrictHisH4Hr00

NULL

Affy H4Kac4 0h

Affymetrix ChIP/Chip (H4Kac4, retinoic acid-treated HL-60, 0hrs) Strict Signal

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.396 | 0.156 | 2.53 | 1.13e-02 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.721 | 0.145 | 4.96 | 7.01e-07 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

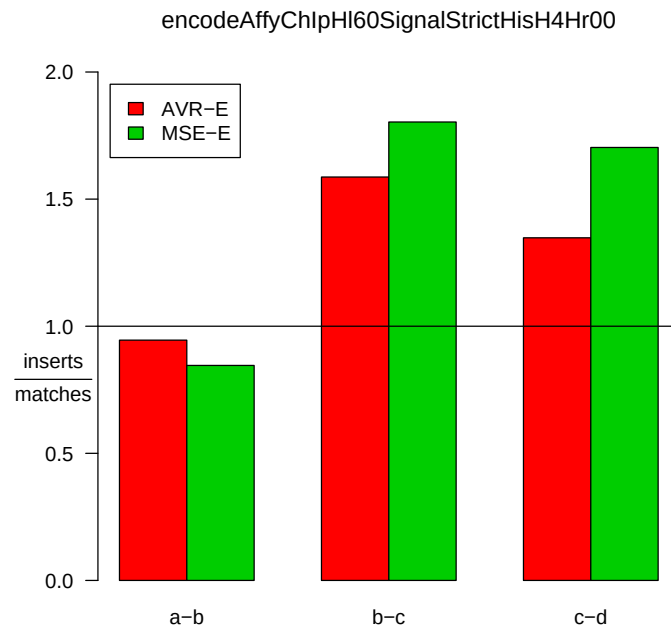
2874 3307

Category limits

|   | lower     | category  | upper     |
|---|-----------|-----------|-----------|
| 1 | -0.730285 | insertion | 0.0000000 |
| 2 | 0.000000  | match     | 0.1343497 |

-0.73 0 0.134 3.26

| set   | type      | brk | a-b  | b-c | c-d |
|-------|-----------|-----|------|-----|-----|
| AVR-E | insertion |     | 214  | 27  | 37  |
|       | match     |     | 2169 | 163 | 263 |
| MSE-E | insertion |     | 226  | 32  | 48  |
|       | match     |     | 2560 | 170 | 270 |



## 2.59 encodeAffyChIpHL60SignalStrictHisH4Hr02

NULL

Affy H4Kac4 2h

Affymetrix ChIP/Chip (H4Kac4, retinoic acid-treated HL-60, 2hrs) Strict Signal

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.548 | 0.198 | 2.77 | 5.54e-03 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.707 | 0.181 | 3.92 | 8.96e-05 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

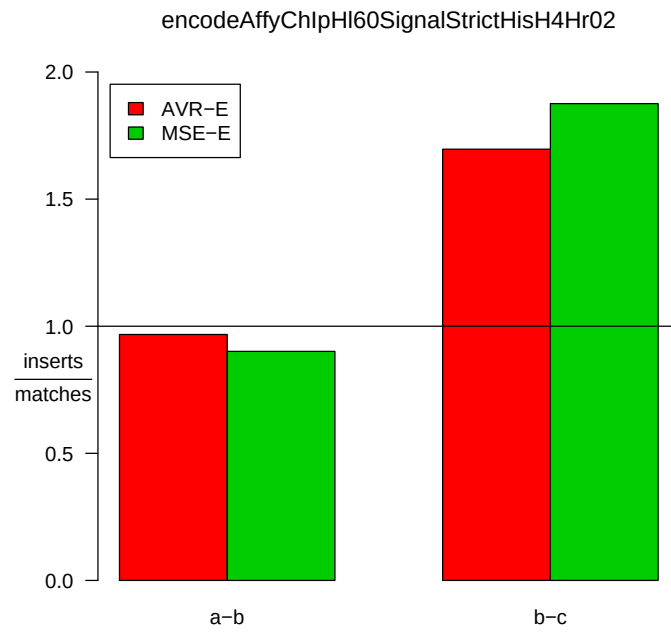
2874 3307

Category limits

|   | lower      | category  | upper   |
|---|------------|-----------|---------|
| 1 | -0.9831507 | insertion | 0.00000 |
| 2 | 0.0000000  | match     | 2.50048 |

-0.983 0 2.5

| set   | type      | brk | a-b  | b-c |
|-------|-----------|-----|------|-----|
| AVR-E | insertion |     | 241  | 37  |
|       | match     |     | 2387 | 209 |
| MSE-E | insertion |     | 260  | 46  |
|       | match     |     | 2765 | 235 |



## 2.60 encodeAffyChIpHL60SignalStrictHisH4Hr08

NULL

Affy H4Kac4 8h

Affymetrix ChIP/Chip (H4Kac4, retinoic acid-treated HL-60, 8hrs) Strict Signal

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.336 | 0.174 | 1.93 | 5.41e-02 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.760 | 0.155 | 4.90 | 9.57e-07 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

2874 3307

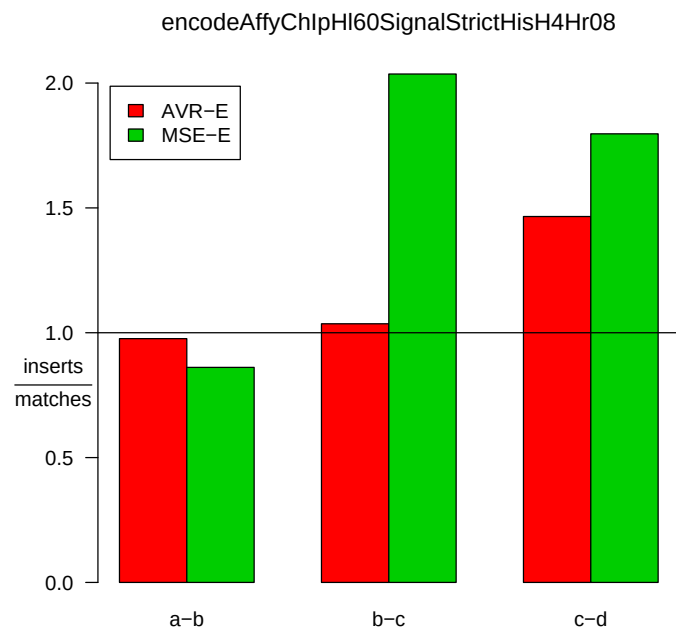
Category limits

|   | lower      | category  | upper      |
|---|------------|-----------|------------|
| 1 | -0.5824551 | insertion | 0.00000000 |
| 2 | 0.0000000  | match     | 0.05236103 |

-0.582 0 0.0524 3.13

| set   | type      | brk | a-b  | b-c | c-d |
|-------|-----------|-----|------|-----|-----|
| AVR-E | insertion |     | 231  | 8   | 39  |
|       | match     |     | 2267 | 74  | 255 |
| MSE-E | insertion |     | 238  | 17  | 51  |
|       | match     |     | 2648 | 80  | 272 |





## 2.61 encodeAffyChIpHl60SignalStrictHisH4Hr32

NULL

Affy H4Kac4 32h

Affymetrix ChIP/Chip (H4Kac4, retinoic acid-treated HL-60, 32hrs) Strict Signal

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.587 | 0.183 | 3.21 | 1.35e-03 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.711 | 0.174 | 4.09 | 4.24e-05 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

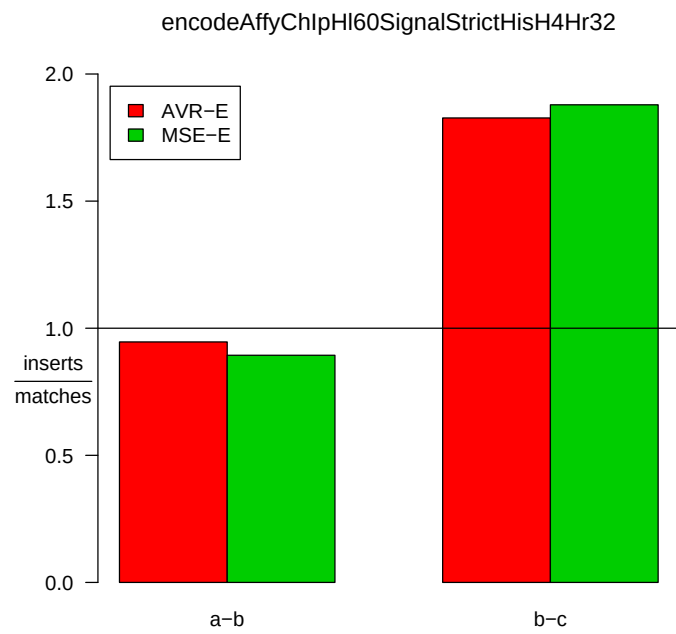
2874 3307

Category limits

|   | lower      | category  | upper   |
|---|------------|-----------|---------|
| 1 | -0.9099898 | insertion | 0.00000 |
| 2 | 0.0000000  | match     | 3.07848 |

-0.91 0 3.08

| set   | type      | brk | a-b  | b-c |
|-------|-----------|-----|------|-----|
| AVR-E | insertion |     | 233  | 45  |
|       | match     |     | 2360 | 236 |
| MSE-E | insertion |     | 256  | 50  |
|       | match     |     | 2745 | 255 |



## 2.62 encodeAffyChIpHl60SignalStrictp63<sub>ActD</sub>

NULL

Affy p63-ActD

Affymetrix ChIP/Chip (actinomycin-D treated p63 HL-60) Strict Signal

|                                             | coef    | se    | z       | p     |
|---------------------------------------------|---------|-------|---------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.7720 | 0.605 | -1.2800 | 0.201 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.0449  | 0.484 | 0.0927  | 0.926 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

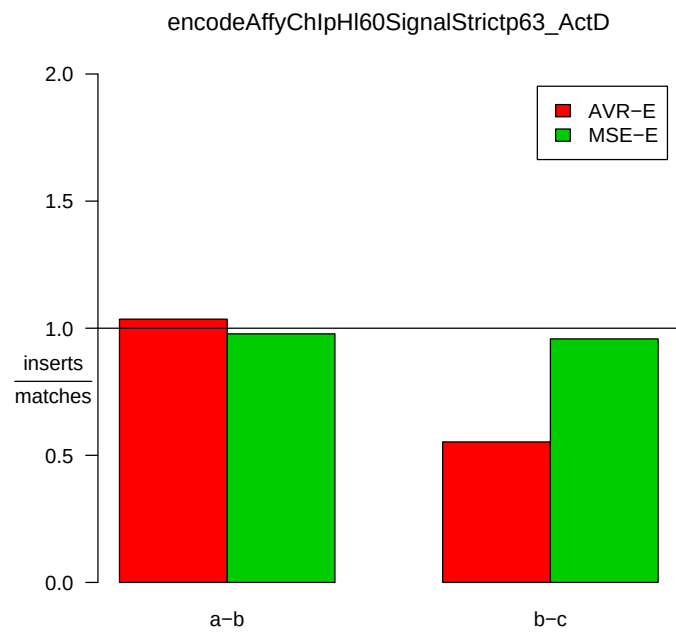
2874 3307

Category limits

|   | lower      | category  | upper    |
|---|------------|-----------|----------|
| 1 | -0.6931466 | insertion | 0.000000 |
| 2 | 0.0000000  | match     | 1.166497 |

-0.693 0 1.17

| set   | type      | brk | a-b  | b-c |
|-------|-----------|-----|------|-----|
| AVR-E | insertion |     | 275  | 3   |
|       | match     |     | 2544 | 52  |
| MSE-E | insertion |     | 301  | 5   |
|       | match     |     | 2949 | 50  |



## 2.63 encodeAffyChIpHl60SignalStrictp63<sub>m</sub>ActD

NULL

Affy p63

Affymetrix ChIP/Chip (p63, HL-60) Strict Signal

|                                             | coef     | se       | z       | p     |
|---------------------------------------------|----------|----------|---------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -15.2000 | 1430.000 | -0.0106 | 0.992 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.0884  | 0.758    | -0.1170 | 0.907 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

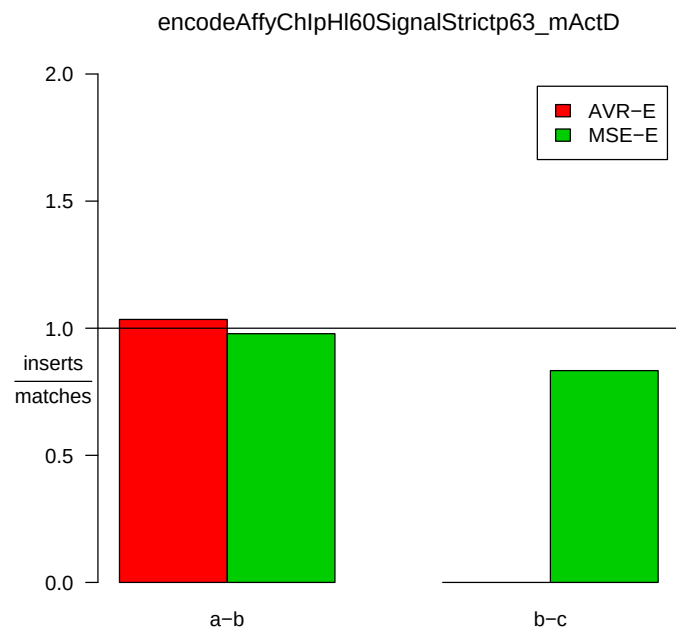
2874 3307

Category limits

|   | lower    | category  | upper    |
|---|----------|-----------|----------|
| 1 | -1.09861 | insertion | 0.000000 |
| 2 | 0.00000  | match     | 1.227622 |

-1.1 0 1.23

| set   | type      | brk | a-b  | b-c |
|-------|-----------|-----|------|-----|
| AVR-E | insertion |     | 278  | 0   |
|       | match     |     | 2575 | 21  |
| MSE-E | insertion |     | 304  | 2   |
|       | match     |     | 2977 | 23  |



## 2.64 encodeAffyChIPHL60SignalStrictPol2Hr00

NULL

Affy Pol2 0h

Affymetrix ChIP/Chip (Pol2, retinoic acid-treated HL-60, 0hrs) Strict Signal

|                                             | coef  | se    | z     | p      |
|---------------------------------------------|-------|-------|-------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.431 | 0.221 | 1.950 | 0.0514 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.136 | 0.231 | 0.591 | 0.5550 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

2874 3307

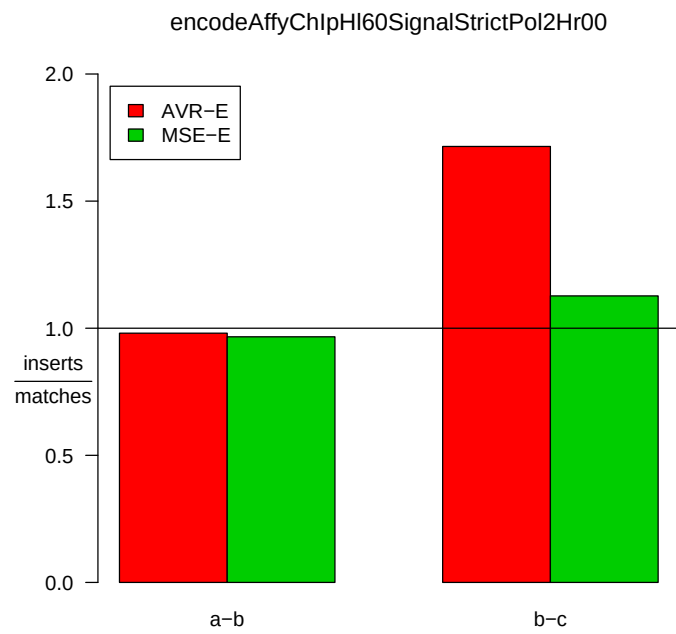
Category limits

|   | lower     | category  | upper    |
|---|-----------|-----------|----------|
| 1 | -0.658425 | insertion | 0.000000 |
| 2 | 0.000000  | match     | 1.605334 |

-0.658 0 1.61

| set   | type      | brk | a-b  | b-c |
|-------|-----------|-----|------|-----|
| AVR-E | insertion |     | 249  | 29  |
|       | match     |     | 2433 | 162 |
| MSE-E | insertion |     | 282  | 24  |
|       | match     |     | 2796 | 204 |





## 2.65 encodeAffyChIpHl60SignalStrictPol2Hr02

NULL

Affy Pol2 2h

Affymetrix ChIP/Chip (Pol2, retinoic acid-treated HL-60, 2hrs) Strict Signal

|                                             | coef  | se    | z     | p        |
|---------------------------------------------|-------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 1.350 | 0.332 | 4.070 | 4.66e-05 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.233 | 0.369 | 0.632 | 5.27e-01 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

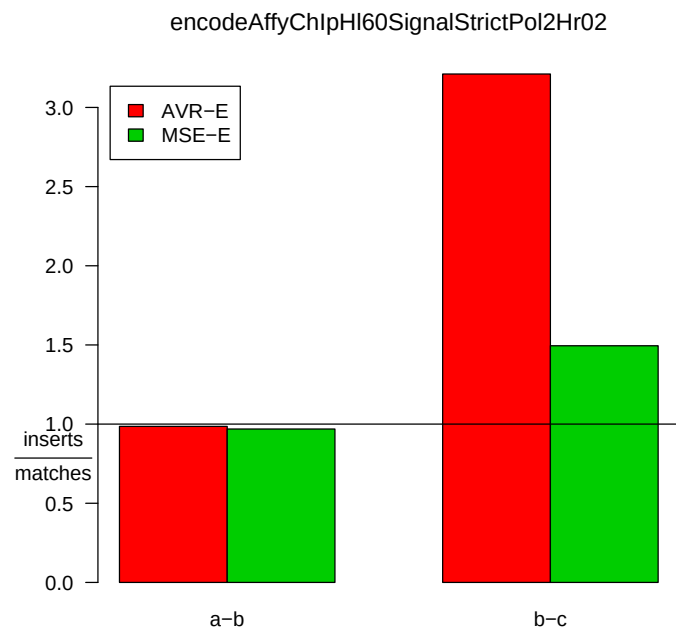
2874 3307

Category limits

|   | lower      | category  | upper    |
|---|------------|-----------|----------|
| 1 | -0.8351733 | insertion | 0.000000 |
| 2 | 0.0000000  | match     | 1.330286 |

-0.835 0 1.33

| set   | type      | brk | a-b  | b-c |
|-------|-----------|-----|------|-----|
| AVR-E | insertion |     | 261  | 15  |
|       | match     |     | 2551 | 45  |
| MSE-E | insertion |     | 296  | 9   |
|       | match     |     | 2943 | 58  |



## 2.66 encodeAffyChIpHl60SignalStrictPol2Hr08

NULL

Affy Pol2 8h

Affymetrix ChIP/Chip (Pol2, retinoic acid-treated HL-60, 8hrs) Strict Signal

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.859 | 0.251 | 3.42 | 0.000623 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.470 | 0.260 | 1.81 | 0.070500 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

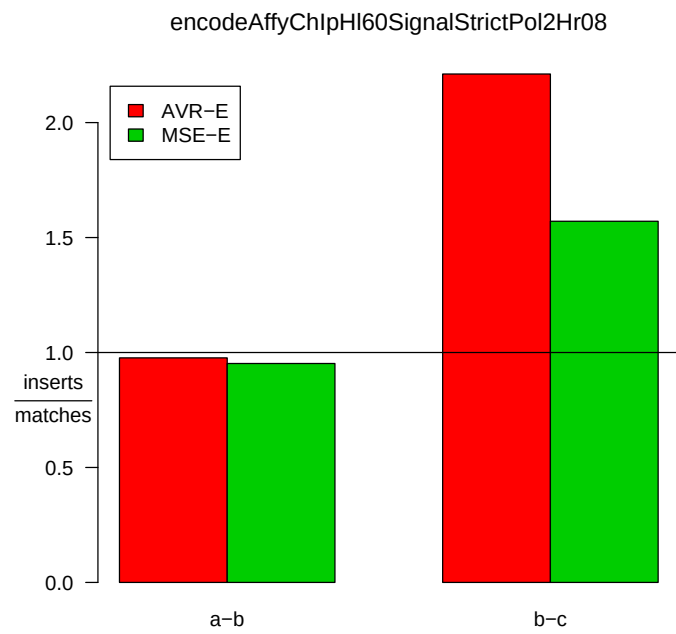
2874 3307

Category limits

|   | lower      | category  | upper    |
|---|------------|-----------|----------|
| 1 | -0.6622696 | insertion | 0.000000 |
| 2 | 0.0000000  | match     | 1.482243 |

-0.662 0 1.48

| set   | type      | brk | a-b  | b-c |
|-------|-----------|-----|------|-----|
| AVR-E | insertion |     | 254  | 24  |
|       | match     |     | 2492 | 104 |
| MSE-E | insertion |     | 286  | 20  |
|       | match     |     | 2878 | 122 |



## 2.67 encodeAffyChIpHl60SignalStrictPol2Hr32

NULL

Affy Pol2 32h

Affymetrix ChIP/Chip (Pol2, retinoic acid-treated HL-60, 32hrs) Strict Signal

|                                             | coef | se    | z    | p        |
|---------------------------------------------|------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 1.11 | 0.201 | 5.55 | 2.79e-08 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.00 | 0.195 | 5.13 | 2.86e-07 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

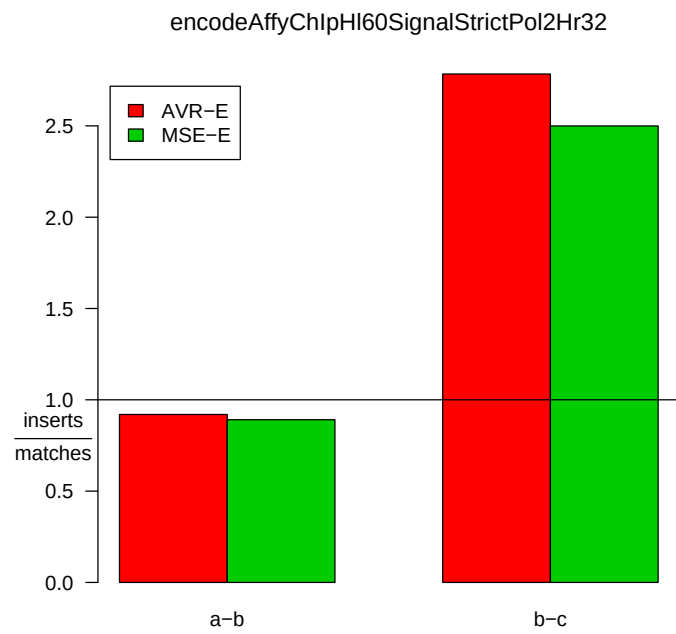
2874 3307

Category limits

|   | lower     | category  | upper    |
|---|-----------|-----------|----------|
| 1 | -1.165199 | insertion | 0.000000 |
| 2 | 0.000000  | match     | 1.982326 |

-1.17 0 1.98

| set   | type      | brk | a-b  | b-c |
|-------|-----------|-----|------|-----|
| AVR-E | insertion |     | 235  | 43  |
|       | match     |     | 2448 | 148 |
| MSE-E | insertion |     | 264  | 42  |
|       | match     |     | 2839 | 161 |



## 2.68 encodeAffyRnaGm06990Signal

NULL

Affy RNA GM06990

Affymetrix PolyA+ RNA (GM06990) Signal

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.812 | 0.139 | 5.86 | 4.57e-09 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.030 | 0.134 | 7.72 | 1.16e-14 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

2874 3307

Category limits

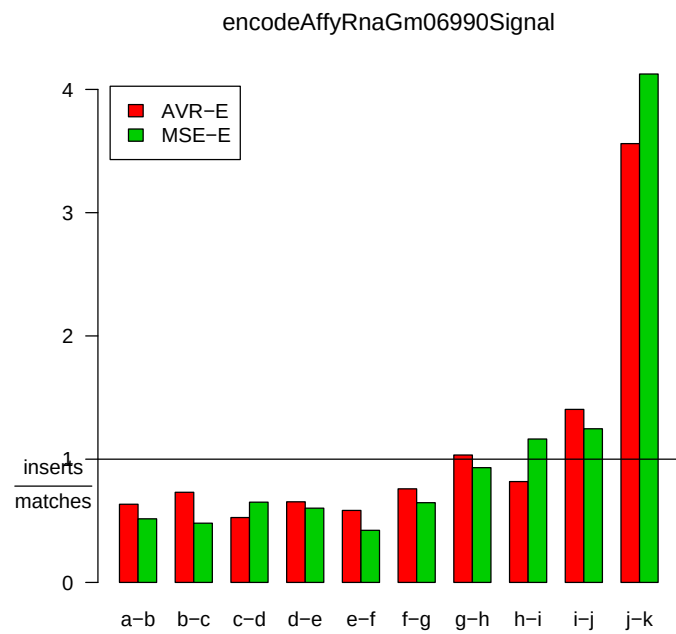
|   | lower      | category  | upper      |
|---|------------|-----------|------------|
| 1 | -8.7638893 | insertion | -0.8181818 |
| 2 | -0.8181818 | match     | -0.3181818 |

-8.76 -0.818 -0.318 -0.0345 0.214 0.479 0.798

1.22 2.06 4.95 471

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 19  | 20  | 15  | 17  | 15  | 21  | 26  | 24  | 40  | 81  |
|       | match     |     | 287 | 262 | 273 | 249 | 246 | 265 | 241 | 281 | 273 | 218 |
| MSE-E | insertion |     | 16  | 16  | 21  | 21  | 15  | 21  | 31  | 34  | 35  | 96  |
|       | match     |     | 297 | 319 | 309 | 334 | 340 | 311 | 319 | 280 | 269 | 223 |





## 2.69 encodeAffyRnaHeLaSignal

NULL

Affy RNA HeLa

Affymetrix PolyA+ RNA (HeLa) Signal

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.563 | 0.134 | 4.19 | 2.80e-05 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.795 | 0.129 | 6.15 | 7.79e-10 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

2874 3307

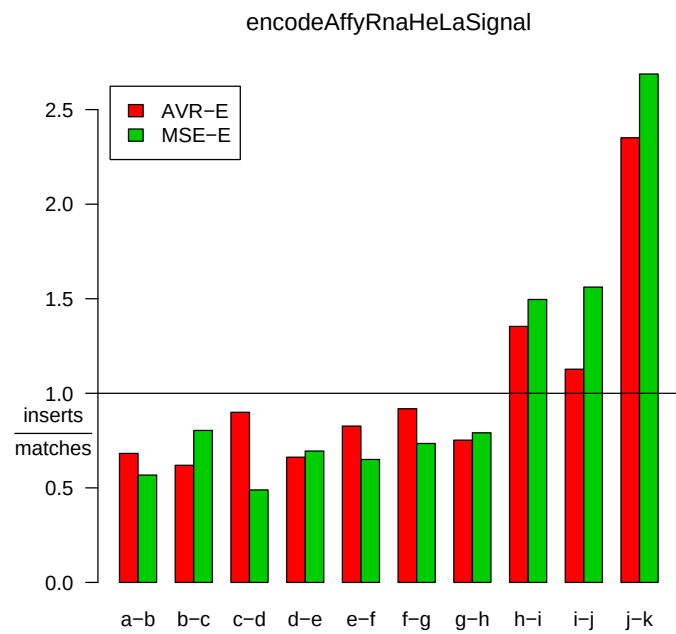
Category limits

|   | lower       | category  | upper      |
|---|-------------|-----------|------------|
| 1 | -13.6666670 | insertion | -0.5454546 |
| 2 | -0.5454546  | match     | -0.1938775 |

-13.7 -0.545 -0.194 -0.02 0.103 0.25 0.438 0.735

1.33 2.77 190

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 21  | 17  | 23  | 17  | 22  | 23  | 19  | 38  | 32  | 66  |
|       | match     |     | 295 | 263 | 245 | 246 | 255 | 240 | 242 | 269 | 272 | 269 |
| MSE-E | insertion |     | 17  | 26  | 17  | 24  | 23  | 24  | 27  | 42  | 44  | 62  |
|       | match     |     | 287 | 310 | 333 | 331 | 339 | 313 | 327 | 269 | 270 | 221 |



## 2.70 encodeAffyRnaHl60SignalHr00

NULL

Affy RNA RA Oh

Affymetrix PolyA+ RNA (retinoic acid-treated HL-60, 0hrs) Signal

|                                             | coef | se    | z    | p        |
|---------------------------------------------|------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 1.08 | 0.145 | 7.42 | 1.19e-13 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.25 | 0.139 | 9.03 | 1.76e-19 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

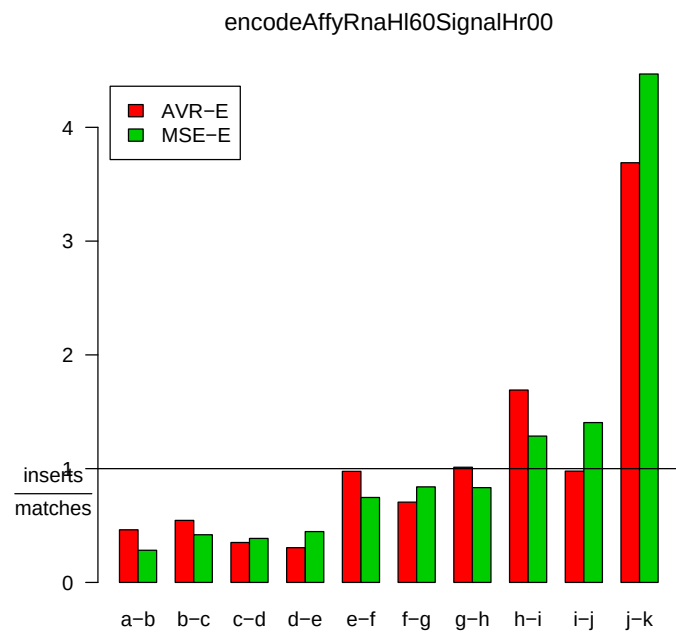
2874 3307

Category limits

|   | lower       | category  | upper      |
|---|-------------|-----------|------------|
| 1 | -12.0833330 | insertion | -0.8010204 |
| 2 | -0.8010204  | match     | -0.2833333 |

-12.1 -0.801 -0.283 0.069 0.41 0.75 1.2 1.79 2.79  
5.16 269

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 14  | 14  | 10  | 8   | 27  | 19  | 28  | 42  | 29  | 87  |
|       | match     |     | 290 | 246 | 273 | 251 | 265 | 258 | 265 | 238 | 284 | 226 |
| MSE-E | insertion |     | 9   | 15  | 13  | 16  | 24  | 27  | 26  | 40  | 39  | 97  |
|       | match     |     | 305 | 343 | 322 | 343 | 308 | 308 | 299 | 298 | 266 | 208 |



## 2.71 encodeAffyRnaHl60SignalHr02

NULL

Affy RNA RA 2h

Affymetrix PolyA+ RNA (retinoic acid-treated HL-60, 2hrs) Signal

|                                             | coef | se    | z    | p        |
|---------------------------------------------|------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 1.29 | 0.154 | 8.36 | 6.50e-17 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.37 | 0.143 | 9.56 | 1.17e-21 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

2874 3307

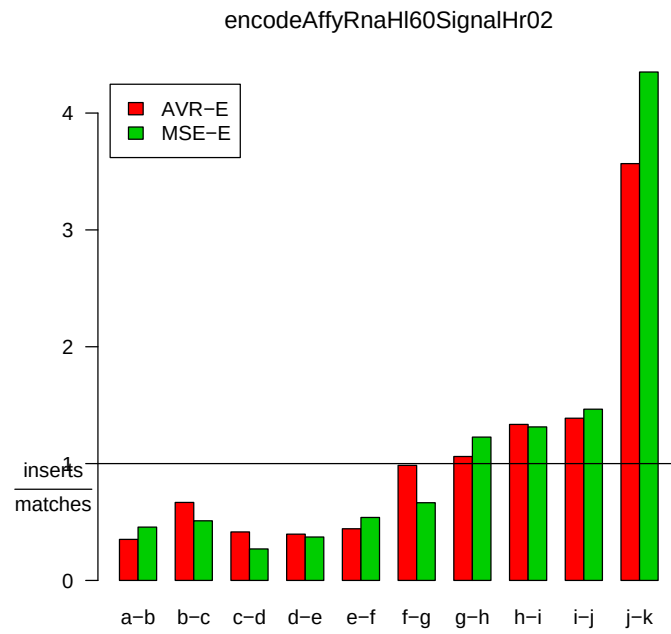
Category limits

|   | lower       | category  | upper       |
|---|-------------|-----------|-------------|
| 1 | -11.1666670 | insertion | -0.42857143 |
| 2 | -0.4285714  | match     | -0.05319149 |

-11.2 -0.429 -0.0532 0.17 0.375 0.619 0.934 1.39

2.14 4.32 265

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 11  | 17  | 12  | 10  | 12  | 26  | 29  | 34  | 41  | 86  |
|       | match     |     | 300 | 244 | 277 | 242 | 260 | 253 | 262 | 244 | 283 | 231 |
| MSE-E | insertion |     | 14  | 18  | 9   | 14  | 18  | 22  | 37  | 41  | 39  | 94  |
|       | match     |     | 294 | 338 | 320 | 361 | 320 | 317 | 289 | 299 | 255 | 207 |



## 2.72 encodeAffyRnaHl60SignalHr08

NULL

Affy RNA RA 8h

Affymetrix PolyA+ RNA (retinoic acid-treated HL-60, 8hrs) Signal

|                                             | coef | se    | z     | p        |
|---------------------------------------------|------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 1.25 | 0.152 | 8.19  | 2.67e-16 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.45 | 0.145 | 10.00 | 1.43e-23 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

2874 3307

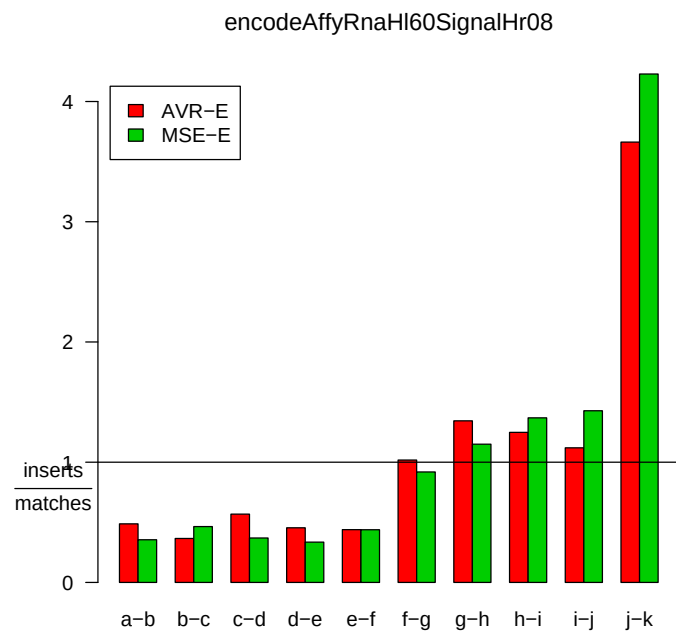
Category limits

|   | lower       | category  | upper      |
|---|-------------|-----------|------------|
| 1 | -12.0833330 | insertion | -0.6333333 |
| 2 | -0.6333333  | match     | -0.1829268 |

-12.1 -0.633 -0.183 0.133 0.423 0.771 1.18 1.73  
2.7 5.1 229

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 15  | 10  | 15  | 12  | 12  | 29  | 31  | 34  | 34  | 86  |
|       | match     |     | 295 | 262 | 253 | 253 | 262 | 273 | 221 | 261 | 291 | 225 |
| MSE-E | insertion |     | 11  | 16  | 13  | 12  | 15  | 28  | 39  | 40  | 38  | 94  |
|       | match     |     | 297 | 330 | 337 | 343 | 328 | 292 | 325 | 280 | 255 | 213 |





## 2.73 encodeAffyRnaHl60SignalHr32

NULL

Affy RNA RA 32h

Affymetrix PolyA+ RNA (retinoic acid-treated HL-60, 32hrs) Signal

|                                             | coef | se    | z    | p        |
|---------------------------------------------|------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 1.12 | 0.148 | 7.61 | 2.73e-14 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.31 | 0.141 | 9.34 | 1.00e-20 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3345

Origin.of.data.set

AVR-E MSE-E

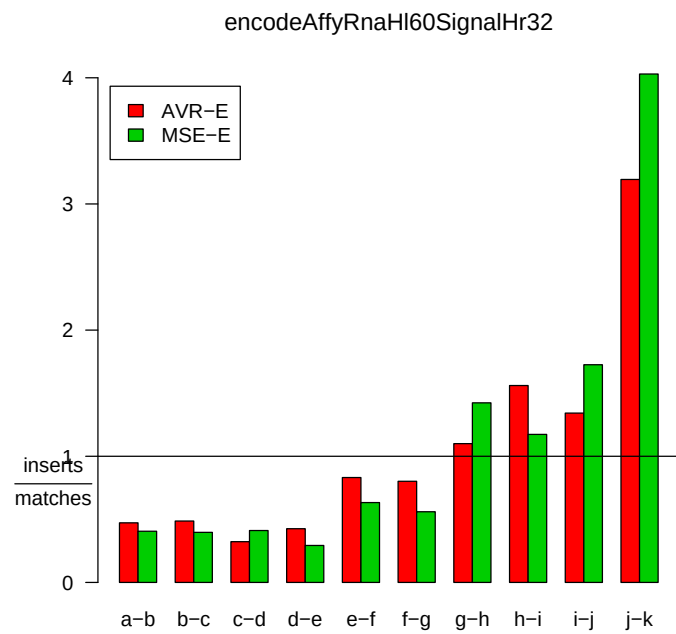
2874 3307

Category limits

|   | lower       | category  | upper       |
|---|-------------|-----------|-------------|
| 1 | -10.3472223 | insertion | -0.42857143 |
| 2 | -0.4285714  | match     | -0.07352941 |

-10.3 -0.429 -0.0735 0.118 0.32 0.55 0.849 1.28 2  
3.8 209

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 14  | 13  | 9   | 12  | 21  | 21  | 31  | 43  | 36  | 78  |
|       | match     |     | 284 | 256 | 267 | 270 | 242 | 251 | 270 | 264 | 257 | 234 |
| MSE-E | insertion |     | 13  | 14  | 14  | 10  | 22  | 19  | 41  | 36  | 47  | 90  |
|       | match     |     | 307 | 338 | 326 | 327 | 333 | 325 | 276 | 294 | 261 | 214 |



## 2.74 encodeBu<sub>o</sub> *RChID1*

NULL

BU ORChID

Boston University ORChID (OH Radical Cleavage Intensity Database)

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.158 | 0.104 | 1.52 | 0.130000 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.355 | 0.100 | 3.54 | 0.000408 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 0

Origin.of.data.set

AVR-E MSE-E

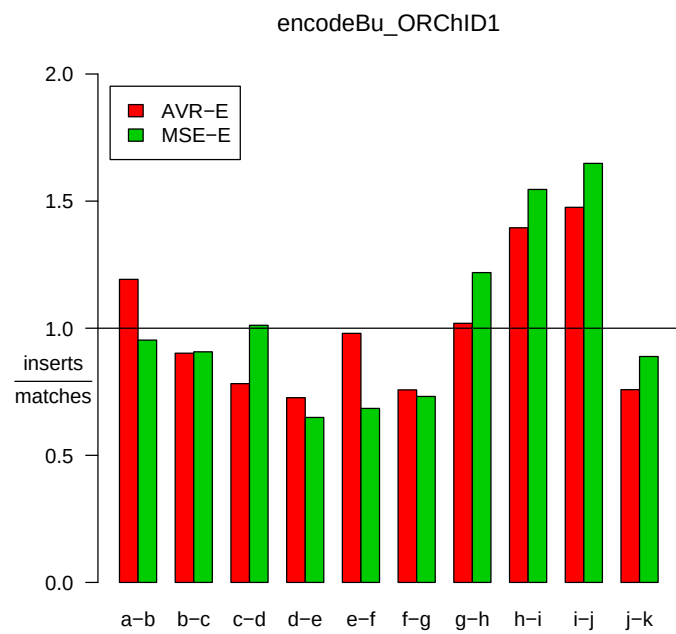
4576 4950

Category limits

|   | lower     | category  | upper     |
|---|-----------|-----------|-----------|
| 1 | 0.1588242 | insertion | 0.2273291 |
| 2 | 0.2273291 | match     | 0.2445439 |

0.159 0.227 0.245 0.259 0.271 0.283 0.295 0.307  
0.324 0.347 0.508

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 44  | 34  | 28  | 29  | 39  | 30  | 42  | 60  | 67  | 43  |
|       | match     |     | 369 | 377 | 358 | 399 | 398 | 396 | 412 | 430 | 454 | 567 |
| MSE-E | insertion |     | 47  | 45  | 52  | 32  | 33  | 36  | 54  | 62  | 61  | 28  |
|       | match     |     | 493 | 496 | 514 | 493 | 482 | 492 | 443 | 401 | 370 | 315 |



## 2.75 encodeGisChipPetStat1Gif

NULL

GIS STAT1 +gIF

Genome Institute of Singapore ChIP-PET: STAT1 Ab on gIF treated HeLa cells

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.0987 | 0.387 | -0.255 | 0.799 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.0773 | 0.496 | -0.156 | 0.876 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 8029

Origin.of.data.set

AVR-E MSE-E

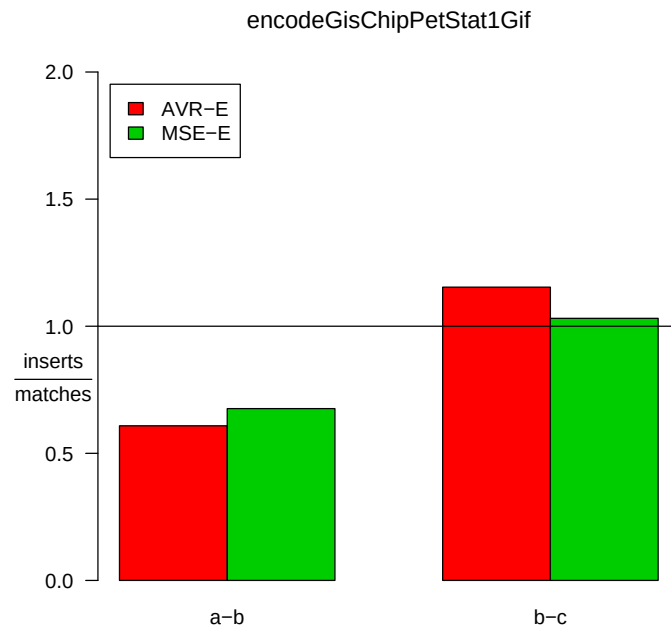
756 741

Category limits

|   | lower | category  | upper  |
|---|-------|-----------|--------|
| 1 | 333.0 | insertion | 566.5  |
| 2 | 566.5 | match     | 1000.0 |

333 567 1000

| set   | type      | brk | a-b | b-c |
|-------|-----------|-----|-----|-----|
| AVR-E | insertion | 2   | 11  |     |
|       | match     | 20  | 58  |     |
| MSE-E | insertion | 1   | 10  |     |
|       | match     | 9   | 59  |     |



## 2.76 encodeGisChipPetStat1NoGif

NULL

GIS STAT1 -gIF

Genome Institute of Singapore ChIP-PET: STAT1 Ab on untreated HeLa cells

|                                             | coef   | se    | z      | p     |
|---------------------------------------------|--------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.264 | 0.416 | -0.634 | 0.526 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.370 | 0.367 | -1.010 | 0.313 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 8048

Origin.of.data.set

AVR-E MSE-E

699 779

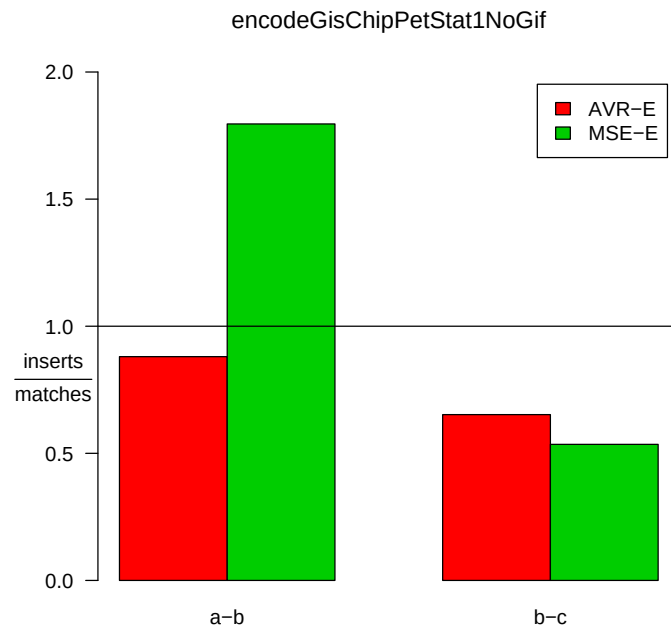
Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 333   | insertion | 800   |
| 2 | 800   | match     | 1000  |

333 800 1000

| set   | type      | brk a-b | b-c |
|-------|-----------|---------|-----|
| AVR-E | insertion | 7       | 5   |
|       | match     | 83      | 80  |
| MSE-E | insertion | 16      | 4   |
|       | match     | 93      | 78  |





NULL

NULL

## 2.77 encodeRegulomeAmpliconEven

NULL

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.655 | 0.327 | 2.00 | 0.045100 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.600 | 0.456 | 3.51 | 0.000441 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 8445

Origin.of.data.set

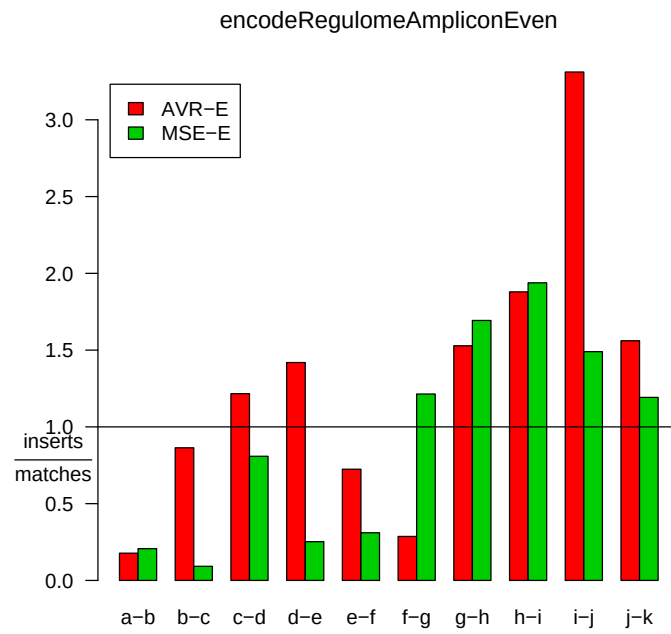
| AVR-E | MSE-E |
|-------|-------|
| 526   | 555   |

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 227   | insertion | 786   |
| 2 | 786   | match     | 888   |

227 786 888 928 954 976 1000 1030 1050 1100 1730

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 2   | 8   | 12  | 10  | 7   | 3   | 12  | 14  | 20  | 11  |     |
|       | match     | 56  | 46  | 49  | 35  | 48  | 52  | 39  | 37  | 30  | 35  |     |
| MSE-E | insertion | 2   | 1   | 7   | 3   | 3   | 11  | 15  | 16  | 12  | 12  |     |
|       | match     | 48  | 54  | 43  | 59  | 48  | 45  | 44  | 41  | 40  | 50  |     |



## 2.78 encodeRegulomeAmpliconOdd

NULL

```

                                coef    se    z      p
AVR-E:as.numeric(dens.med < eval(dens.var)) 0.407 0.335 1.22 0.22400
MSE-E:as.numeric(dens.med < eval(dens.var)) 1.010 0.361 2.80 0.00508

```

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 8413

Origin.of.data.set

AVR-E MSE-E  
525 588

Category limits

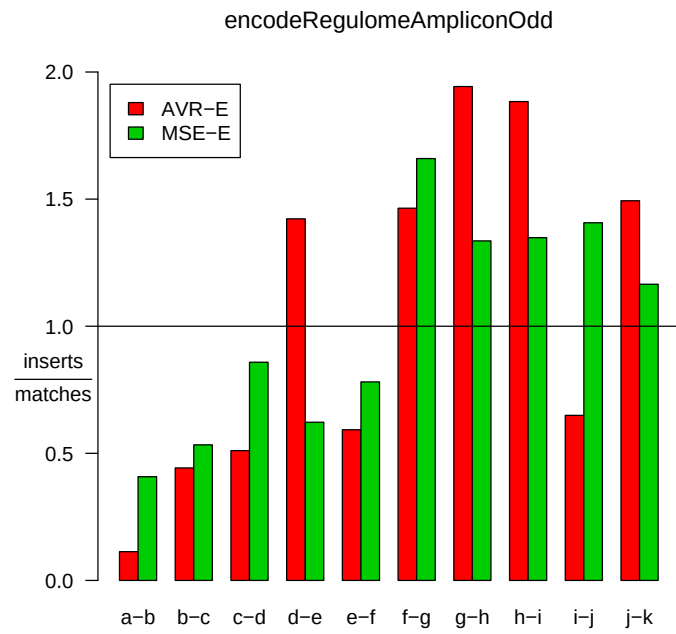
```

    lower category upper
1 213.0 insertion 790.2
2 790.2      match 886.4

```

213 790 886 929 957 980 1000 1020 1050 1100 1720

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 1   | 4   | 4   | 14  | 5   | 15  | 16  | 14  | 6   | 12  |     |
|       | match     | 44  | 45  | 39  | 49  | 42  | 51  | 41  | 37  | 46  | 40  |     |
| MSE-E | insertion | 5   | 6   | 10  | 6   | 8   | 12  | 11  | 13  | 13  | 11  |     |
|       | match     | 61  | 56  | 58  | 48  | 51  | 36  | 41  | 48  | 46  | 47  |     |



## 2.79 encodeRegulomeBaseCACO2

NULL

CACO2

CACO2 DNaseI Sensitivity

|                                             | coef   | se    | z     | p        |
|---------------------------------------------|--------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.799 | 0.200 | -3.99 | 6.54e-05 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -1.210 | 0.218 | -5.58 | 2.37e-08 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 7439

Origin.of.data.set

AVR-E MSE-E

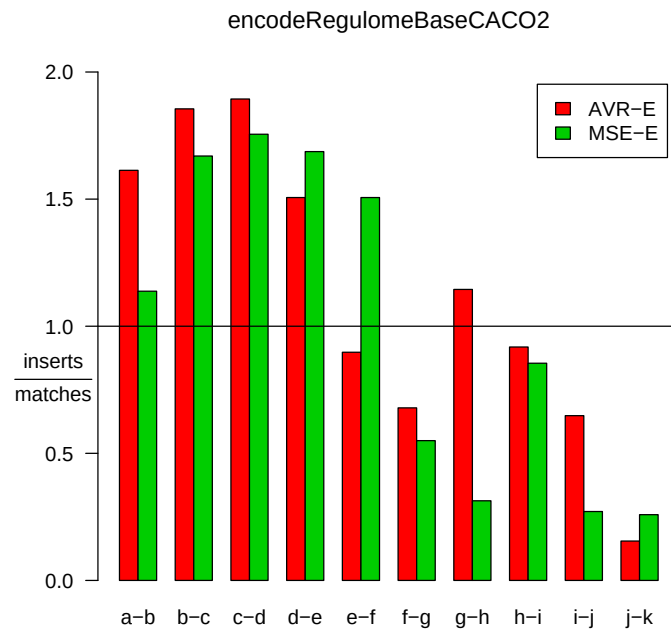
997 1090

Category limits

|   | lower     | category  | upper     |
|---|-----------|-----------|-----------|
| 1 | 0.5769340 | insertion | 0.9173638 |
| 2 | 0.9173638 | match     | 0.9531798 |

0.577 0.917 0.953 0.978 0.998 1.02 1.05 1.07 1.12  
1.26 4.69

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 23  | 30  | 27  | 25  | 17  | 13  | 19  | 17  | 12  | 3   |     |
|       | match     | 67  | 76  | 67  | 78  | 89  | 90  | 78  | 87  | 87  | 91  |     |
| MSE-E | insertion | 23  | 27  | 31  | 28  | 25  | 11  | 7   | 16  | 6   | 6   |     |
|       | match     | 95  | 76  | 83  | 78  | 78  | 94  | 105 | 88  | 104 | 109 |     |





## 2.80 encodeRegulomeBaseGM06990

NULL

GM06990

GM06990 DNaseI Sensitivity

|                                             | coef   | se    | z      | p      |
|---------------------------------------------|--------|-------|--------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.396  | 0.177 | 2.240  | 0.0249 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.174 | 0.192 | -0.904 | 0.3660 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 7200

Origin.of.data.set

AVR-E MSE-E

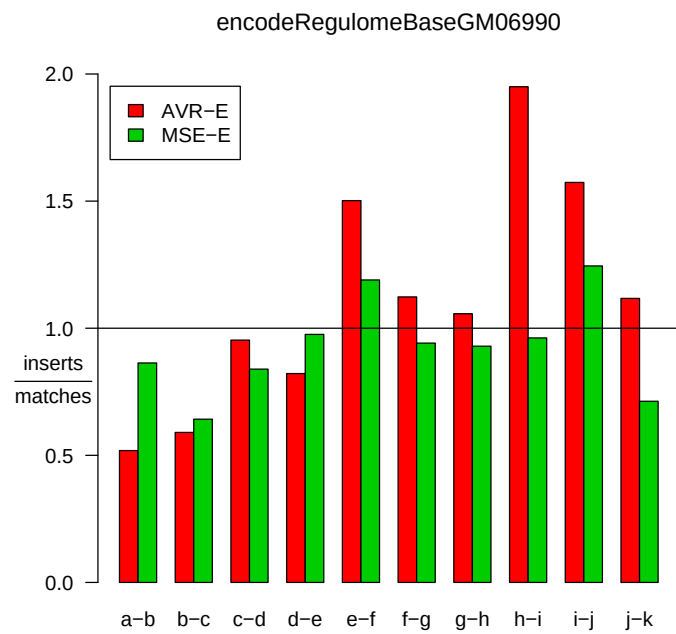
1127 1199

Category limits

|   | lower    | category  | upper    |
|---|----------|-----------|----------|
| 1 | 0.588478 | insertion | 0.904977 |
| 2 | 0.904977 | match     | 0.941088 |

0.588 0.905 0.941 0.965 0.986 1 1.02 1.04 1.06  
1.11 7.66

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 10  | 13  | 18  | 16  | 26  | 19  | 21  | 28  | 26  | 20  |     |
|       | match     | 98  | 112 | 96  | 99  | 88  | 86  | 101 | 73  | 84  | 91  |     |
| MSE-E | insertion | 18  | 12  | 17  | 19  | 22  | 20  | 17  | 21  | 24  | 15  |     |
|       | match     | 106 | 95  | 103 | 99  | 94  | 108 | 93  | 111 | 98  | 107 |     |



## 2.81 encodeRegulomeBaseSKNSH

NULL

SKNSH

SKNSH DNaseI Sensitivity

|                                             | coef   | se    | z     | p        |
|---------------------------------------------|--------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.611 | 0.252 | -2.42 | 0.015400 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.988 | 0.267 | -3.69 | 0.000221 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 8249

Origin.of.data.set

AVR-E MSE-E

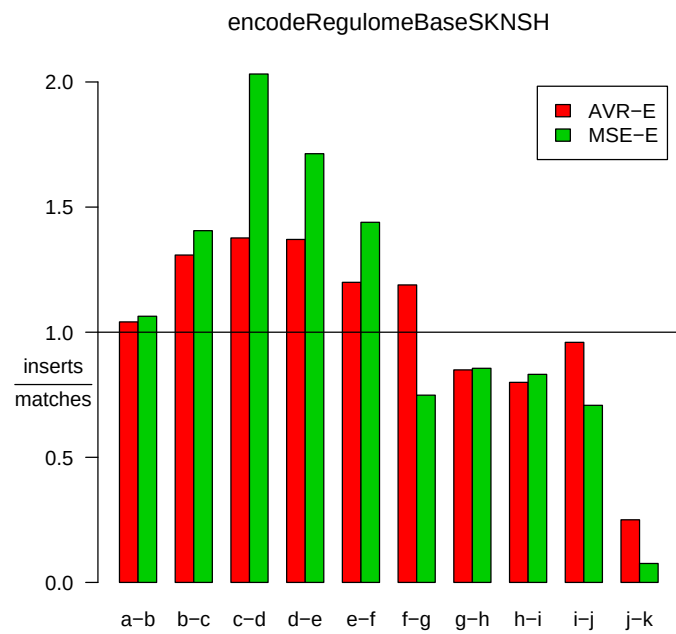
642 635

Category limits

|   | lower     | category  | upper     |
|---|-----------|-----------|-----------|
| 1 | 0.6331120 | insertion | 0.9024466 |
| 2 | 0.9024466 | match     | 0.9404154 |

0.633 0.902 0.94 0.963 0.983 1 1.02 1.05 1.08  
1.17 3.58

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 17  | 20  | 22  | 20  | 20  | 19  | 18  | 15  | 13  | 4   |     |
|       | match     | 47  | 44  | 46  | 42  | 48  | 46  | 61  | 54  | 39  | 46  |     |
| MSE-E | insertion | 17  | 21  | 24  | 25  | 20  | 13  | 11  | 13  | 15  | 2   |     |
|       | match     | 46  | 43  | 34  | 42  | 40  | 50  | 37  | 45  | 61  | 76  |     |



## 2.82 encodeRegulomeQualityCACO2

NULL

CACO2

CACO2 Quality

|                                             | coef   | se    | z     | p        |
|---------------------------------------------|--------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.592 | 0.169 | -3.51 | 0.000442 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.631 | 0.180 | -3.51 | 0.000456 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 6876

Origin.of.data.set

AVR-E MSE-E

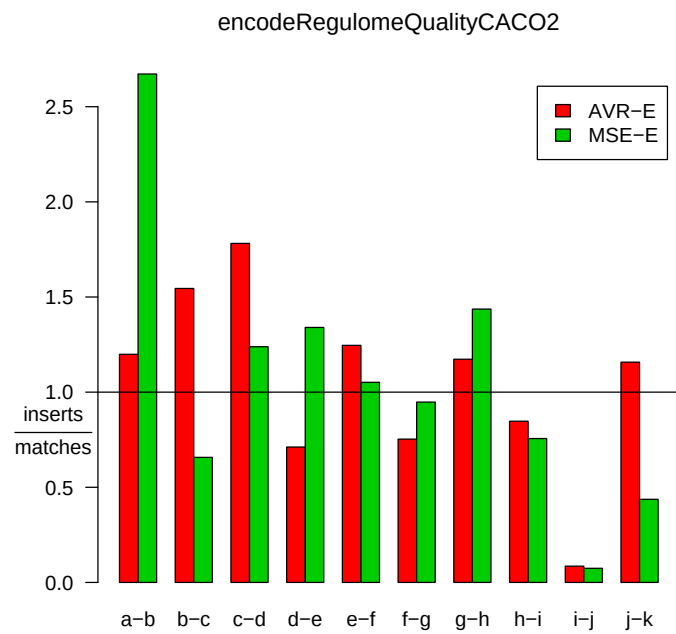
1290 1360

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0     | insertion | 23.0  |
| 2 | 23    | match     | 65.6  |

0 23 65.6 125 284 456 580 719 840 937 990

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 25  | 31  | 34  | 14  | 25  | 16  | 27  | 19  | 2   | 23  |
|       | match     |     | 106 | 102 | 97  | 100 | 102 | 108 | 117 | 114 | 119 | 101 |
| MSE-E | insertion |     | 41  | 15  | 29  | 29  | 24  | 22  | 26  | 18  | 2   | 11  |
|       | match     |     | 78  | 116 | 119 | 110 | 116 | 118 | 92  | 121 | 137 | 128 |



## 2.83 encodeRegulomeQualityGM06990

NULL

GM06990

GM06990 Quality

|                                             | coef   | se    | z     | p        |
|---------------------------------------------|--------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.423 | 0.154 | -2.74 | 6.10e-03 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.707 | 0.166 | -4.25 | 2.11e-05 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 6389

Origin.of.data.set

AVR-E MSE-E

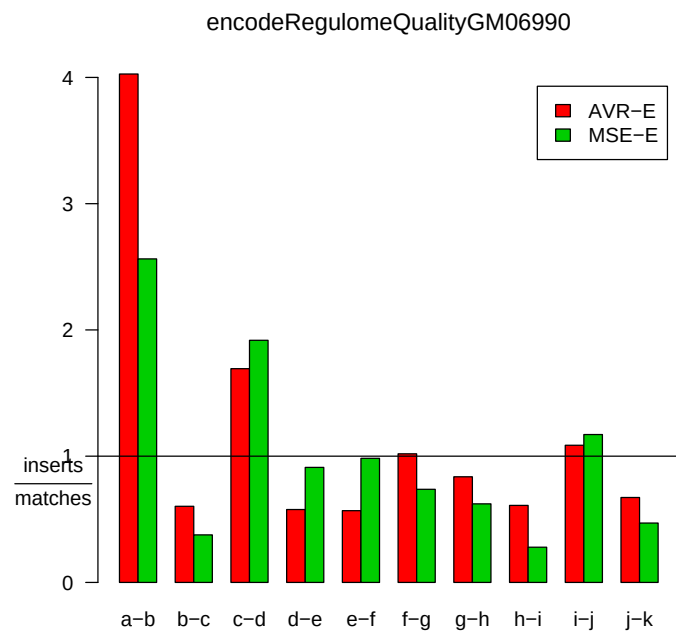
1527 1610

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0     | insertion | 110.0 |
| 2 | 110   | match     | 375.1 |

0 110 375 606 823 888 931 949 963 973 988

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 55  | 14  | 37  | 14  | 13  | 24  | 17  | 15  | 23  | 17  |     |
|       | match     | 80  | 136 | 128 | 142 | 134 | 138 | 119 | 144 | 124 | 148 |     |
| MSE-E | insertion | 56  | 9   | 37  | 21  | 24  | 17  | 17  | 7   | 28  | 11  |     |
|       | match     | 128 | 140 | 113 | 135 | 143 | 135 | 160 | 147 | 140 | 137 |     |





## 2.84 encodeRegulomeQualitySKNSH

NULL

SKNSH

SKNSH Quality

|                                             | coef   | se    | z     | p      |
|---------------------------------------------|--------|-------|-------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.496 | 0.199 | -2.49 | 0.0127 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.241  | 0.209 | 1.15  | 0.2490 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 7904

Origin.of.data.set

AVR-E MSE-E

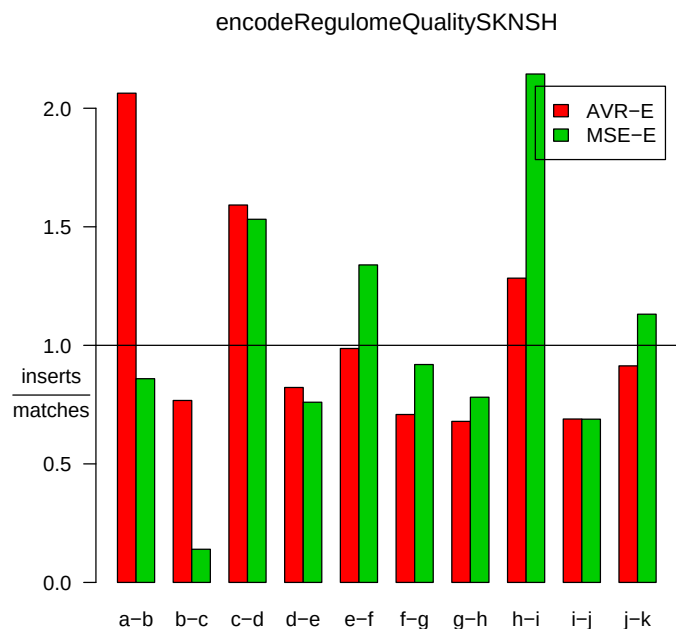
808 814

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0     | insertion | 48    |
| 2 | 48    | match     | 153   |

0 48 153 285 515 753 841 892 929 955 985

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 35  | 14  | 27  | 15  | 18  | 17  | 15  | 23  | 15  | 19  |
|       | match     |     | 53  | 57  | 53  | 57  | 57  | 75  | 69  | 56  | 68  | 65  |
| MSE-E | insertion |     | 22  | 3   | 25  | 18  | 27  | 15  | 16  | 35  | 13  | 21  |
|       | match     |     | 80  | 67  | 51  | 74  | 63  | 51  | 64  | 51  | 59  | 58  |



## 2.85 encodeRegulomeDnaseGM06990Sens

NULL

DnaseI Sens

UW DNase/Array GM06990 Sensitivity

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.476 | 0.144 | 3.30 | 0.000967 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.299 | 0.130 | 2.31 | 0.021100 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3993

Origin.of.data.set

AVR-E MSE-E

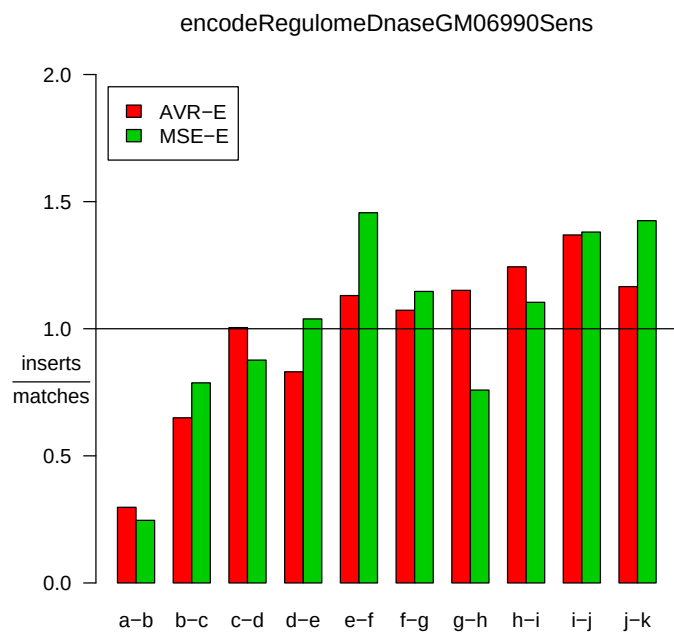
2617 2916

Category limits

|   | lower  | category  | upper  |
|---|--------|-----------|--------|
| 1 | -4.092 | insertion | -1.452 |
| 2 | -1.452 | match     | -1.286 |

-4.09 -1.45 -1.29 -1.17 -1.07 -0.97 -0.874 -0.761  
-0.597 -0.161 7.53

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 8   | 17  | 23  | 18  | 26  | 25  | 30  | 30  | 34  | 28  |
|       | match     |     | 263 | 256 | 224 | 212 | 225 | 228 | 255 | 236 | 243 | 235 |
| MSE-E | insertion |     | 7   | 21  | 25  | 31  | 39  | 32  | 19  | 29  | 34  | 37  |
|       | match     |     | 278 | 261 | 279 | 292 | 262 | 273 | 245 | 257 | 241 | 254 |



NULL

NULL

## 2.86 encodeSangerChipH3ac

NULL

SI H3ac GM06990

Sanger Institute ChIP/Chip (H3ac ab, GM06990 cells)

|                                             | coef | se    | z    | p        |
|---------------------------------------------|------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 1.02 | 0.142 | 7.21 | 5.58e-13 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.24 | 0.134 | 9.20 | 3.53e-20 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 2716

Origin.of.data.set

AVR-E MSE-E

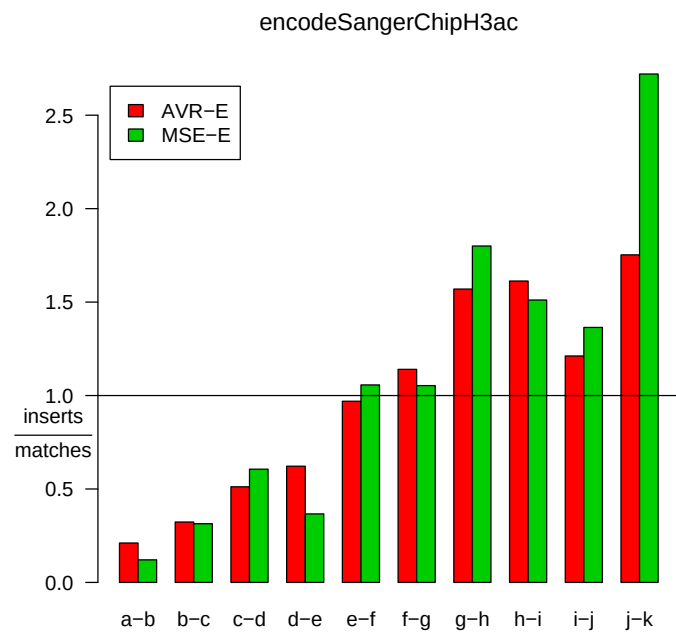
3194 3616

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.11  | insertion | 0.55  |
| 2 | 0.55  | match     | 0.66  |

0.11 0.55 0.66 0.73 0.788 0.84 0.9 0.98 1.1 1.37  
14.7

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 6   | 10  | 14  | 18  | 27  | 33  | 42  | 47  | 37  | 53  |
|       | match     |     | 286 | 311 | 275 | 291 | 280 | 291 | 269 | 293 | 307 | 304 |
| MSE-E | insertion |     | 5   | 11  | 22  | 12  | 37  | 33  | 53  | 49  | 38  | 69  |
|       | match     |     | 416 | 352 | 365 | 329 | 352 | 315 | 296 | 326 | 280 | 255 |



## 2.87 encodeSangerChipH3acHeLa

NULL

SI H3ac HeLa

Sanger Institute ChIP/Chip (H3ac ab, HeLa cells)

|                                             | coef | se    | z    | p        |
|---------------------------------------------|------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 1.73 | 0.162 | 10.7 | 1.51e-26 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.75 | 0.148 | 11.9 | 1.47e-32 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 2191

Origin.of.data.set

AVR-E MSE-E

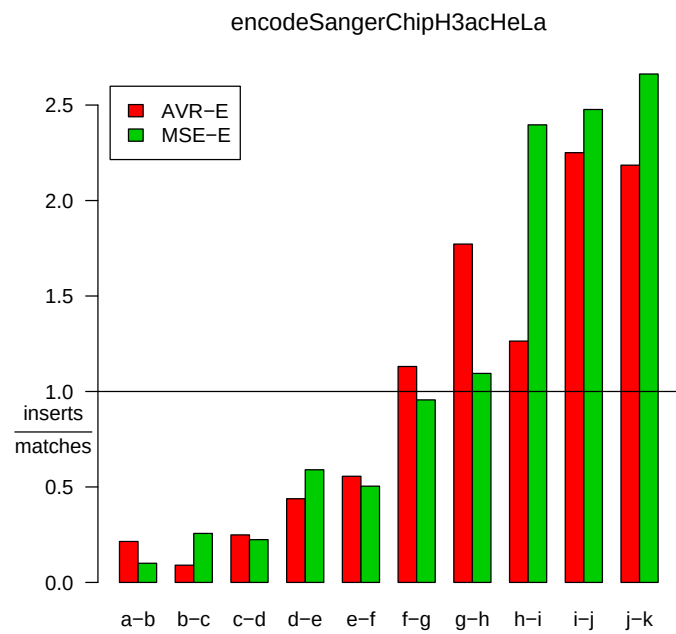
3452 3883

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.290 | insertion | 0.585 |
| 2 | 0.585 | match     | 0.670 |

0.29 0.585 0.67 0.75 0.82 0.895 0.983 1.08 1.21  
1.44 18.8

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 7   | 3   | 8   | 15  | 16  | 34  | 51  | 40  | 65  | 67  |
|       | match     |     | 330 | 336 | 325 | 346 | 291 | 304 | 291 | 320 | 292 | 310 |
| MSE-E | insertion |     | 4   | 10  | 9   | 22  | 18  | 33  | 38  | 73  | 73  | 74  |
|       | match     |     | 403 | 394 | 406 | 377 | 361 | 349 | 351 | 308 | 298 | 281 |



## 2.88 encodeSangerChipH3acHFL1

NULL

SI H3ac HFL-1

Sanger Institute ChIP/Chip (H3ac ab, HFL-1 cells)

|                                             | coef | se    | z    | p        |
|---------------------------------------------|------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 1.35 | 0.147 | 9.2  | 3.60e-20 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.50 | 0.137 | 10.9 | 1.41e-27 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 2189

Origin.of.data.set

AVR-E MSE-E

3453 3884

Category limits

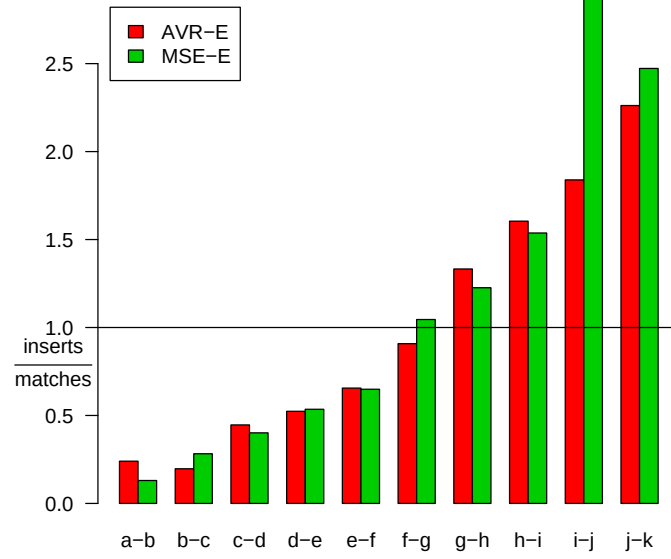
|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.15  | insertion | 0.54  |
| 2 | 0.54  | match     | 0.65  |

0.15 0.54 0.65 0.735 0.805 0.875 0.95 1.05 1.18  
1.48 10.3

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 8   | 6   | 15  | 16  | 21  | 29  | 39  | 46  | 54  | 72  |     |
|       | match     | 337 | 308 | 340 | 309 | 324 | 323 | 296 | 290 | 297 | 322 |     |
| MSE-E | insertion | 5   | 12  | 14  | 20  | 24  | 37  | 44  | 50  | 82  | 66  |     |
|       | match     | 388 | 430 | 353 | 378 | 374 | 358 | 363 | 329 | 287 | 270 |     |



encodeSangerChipH3acHFL1



## 2.89 encodeSangerChipH3acK562

NULL

SI H3ac K562

Sanger Institute ChIP/Chip (H3ac ab, K562 cells)

|                                             | coef | se    | z    | p        |
|---------------------------------------------|------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 1.80 | 0.168 | 10.7 | 9.09e-27 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 2.27 | 0.170 | 13.3 | 2.08e-40 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 2199

Origin.of.data.set

AVR-E MSE-E

3447 3880

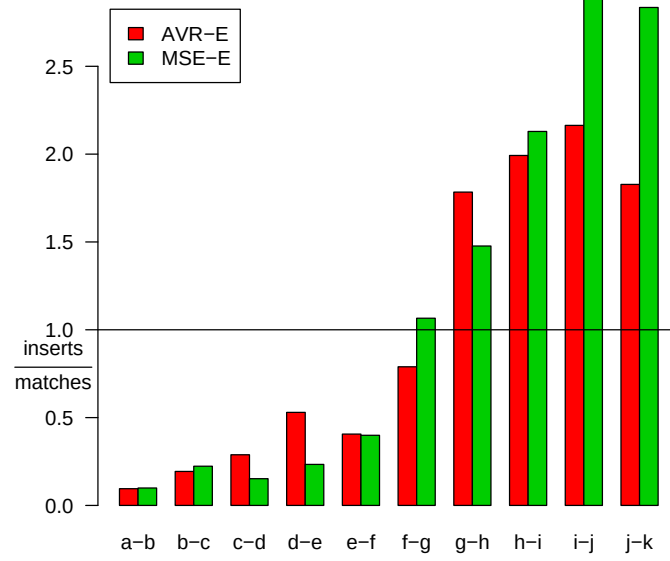
Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.120 | insertion | 0.355 |
| 2 | 0.355 | match     | 0.480 |

0.12 0.355 0.48 0.601 0.715 0.836 0.957 1.11 1.33  
1.75 18.6

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 3   | 6   | 9   | 17  | 14  | 24  | 53  | 59  | 60  | 61  |
|       | match     |     | 318 | 313 | 315 | 324 | 348 | 307 | 300 | 299 | 280 | 337 |
| MSE-E | insertion |     | 4   | 9   | 6   | 9   | 14  | 38  | 49  | 66  | 86  | 73  |
|       | match     |     | 407 | 407 | 398 | 389 | 354 | 360 | 335 | 313 | 300 | 260 |

encodeSangerChipH3acK562



## 2.90 encodeSangerChipH3K4me1

NULL

SI H3K4m1 GM6990

Sanger Institute ChIP/Chip (H3K4me1 ab, GM06990 cells)

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.871 | 0.135 | 6.44 | 1.18e-10 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.180 | 0.133 | 8.88 | 6.64e-19 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 2629

Origin.of.data.set

AVR-E MSE-E

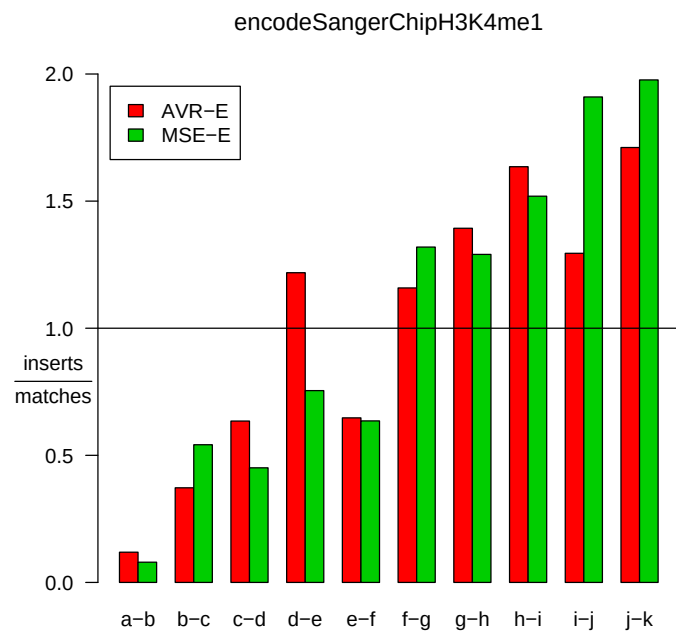
3231 3666

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.020 | insertion | 0.355 |
| 2 | 0.355 | match     | 0.440 |

0.02 0.355 0.44 0.53 0.625 0.74 0.89 1.07 1.43  
2.43 12.2

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 4   | 11  | 18  | 36  | 19  | 34  | 42  | 41  | 38  | 48  |     |
|       | match     | 338 | 297 | 285 | 297 | 295 | 295 | 303 | 252 | 295 | 282 |     |
| MSE-E | insertion | 3   | 18  | 17  | 25  | 22  | 42  | 38  | 52  | 57  | 59  |     |
|       | match     | 379 | 334 | 379 | 333 | 348 | 320 | 296 | 344 | 300 | 300 |     |



## 2.91 encodeSangerChipH3K4me1HeLa

NULL

SI H3K4me1 HeLa

Sanger Institute ChIP/Chip (H3K4me1 ab, HeLa cells)

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.829 | 0.130 | 6.36 | 2.01e-10 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.951 | 0.123 | 7.73 | 1.12e-14 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 2189

Origin.of.data.set

AVR-E MSE-E

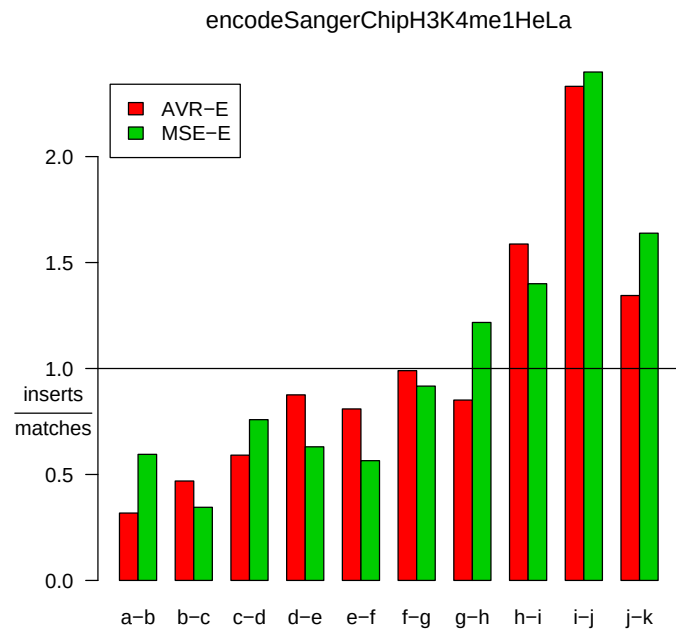
3453 3884

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.140 | insertion | 0.465 |
| 2 | 0.465 | match     | 0.540 |

0.14 0.465 0.54 0.615 0.69 0.77 0.865 0.98 1.18  
1.79 11.8

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 11  | 16  | 18  | 29  | 24  | 32  | 26  | 43  | 65  | 42  |
|       | match     |     | 350 | 345 | 308 | 335 | 300 | 327 | 309 | 274 | 282 | 316 |
| MSE-E | insertion |     | 21  | 13  | 27  | 24  | 20  | 32  | 42  | 49  | 74  | 52  |
|       | match     |     | 357 | 381 | 360 | 385 | 358 | 353 | 349 | 354 | 312 | 321 |



## 2.92 encodeSangerChipH3K4me1HFL1

NULL

SI H3K4me1 HFL-1

Sanger Institute ChIP/Chip (H3K4me1 ab, HFL-1 cells)

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.598 | 0.126 | 4.76 | 1.98e-06 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.874 | 0.122 | 7.14 | 9.17e-13 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 2189

Origin.of.data.set

AVR-E MSE-E

3453 3884

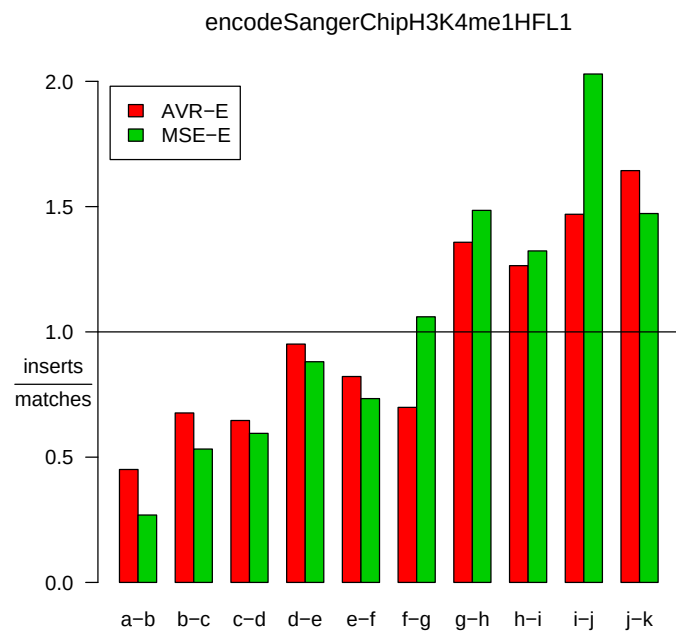
Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.17  | insertion | 0.51  |
| 2 | 0.51  | match     | 0.61  |

0.17 0.51 0.61 0.69 0.776 0.86 0.96 1.09 1.33  
1.89 8.49

|       | set       | type | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |      | 16  | 22  | 20  | 30  | 26  | 21  | 40  | 36  | 43  | 52  |     |
|       | match     |      | 359 | 329 | 313 | 319 | 320 | 304 | 298 | 288 | 296 | 320 |     |
| MSE-E | insertion |      | 10  | 20  | 21  | 29  | 28  | 37  | 53  | 45  | 65  | 46  |     |
|       | match     |      | 376 | 380 | 357 | 333 | 386 | 353 | 361 | 344 | 324 | 316 |     |





## 2.93 encodeSangerChipH3K4me2

NULL

SI H3K4m2 GM6990

Sanger Institute ChIP/Chip (H3K4me2 ab, GM06990 cells)

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.727 | 0.131 | 5.54 | 3.10e-08 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.840 | 0.125 | 6.69 | 2.21e-11 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 2671

Origin.of.data.set

AVR-E MSE-E

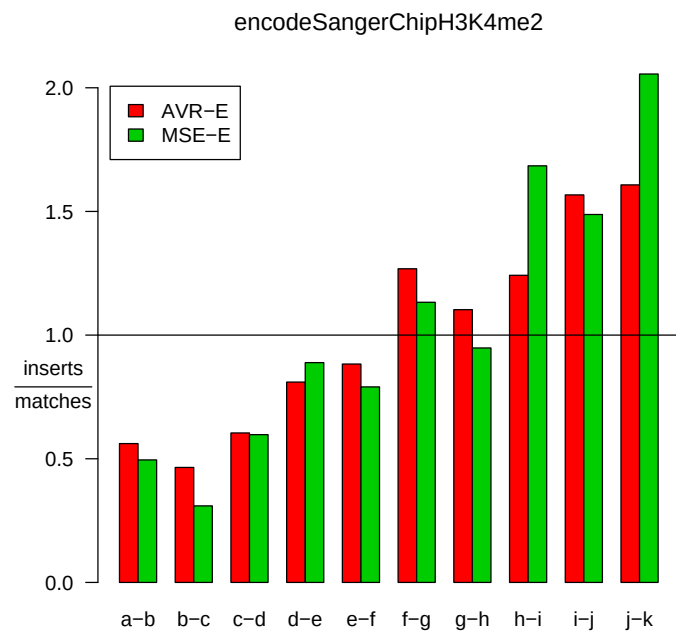
3208 3647

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.16  | insertion | 0.39  |
| 2 | 0.39  | match     | 0.44  |

0.16 0.39 0.44 0.49 0.54 0.61 0.69 0.79 0.965  
1.85 27.4

|       | set       | type | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |      | 17  | 15  | 18  | 23  | 27  | 35  | 30  | 36  | 42  | 45  |     |
|       | match     |      | 305 | 325 | 300 | 286 | 308 | 278 | 274 | 292 | 270 | 282 |     |
| MSE-E | insertion |      | 18  | 11  | 21  | 27  | 27  | 37  | 32  | 50  | 48  | 60  |     |
|       | match     |      | 366 | 358 | 354 | 306 | 344 | 329 | 340 | 299 | 325 | 294 |     |



## 2.94 encodeSangerChipH3K4me2HeLa

NULL

SI H3K4me2 HeLa

Sanger Institute ChIP/Chip (H3K4me2 ab, HeLa cells)

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.558 | 0.125 | 4.47 | 7.92e-06 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.556 | 0.117 | 4.73 | 2.19e-06 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 2189

Origin.of.data.set

AVR-E MSE-E

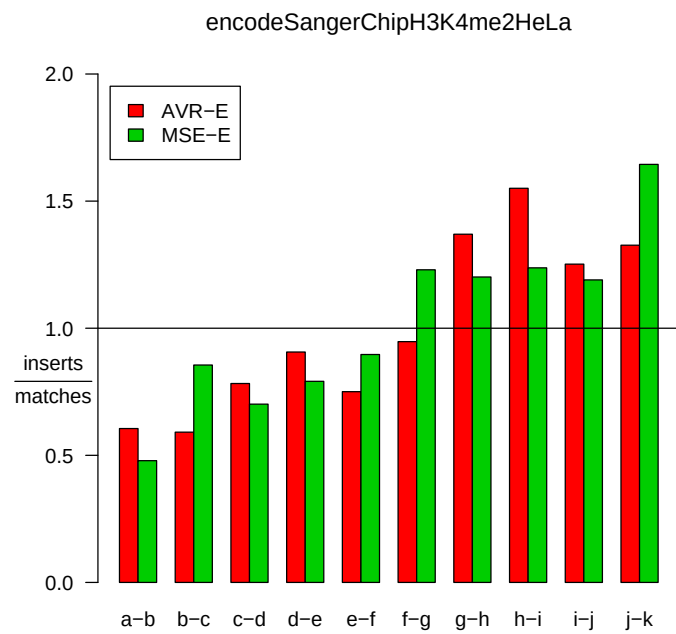
3453 3884

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.315 | insertion | 0.565 |
| 2 | 0.565 | match     | 0.615 |

0.315 0.565 0.615 0.66 0.7 0.745 0.795 0.86 0.96  
1.17 26.7

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 24  | 18  | 27  | 25  | 25  | 28  | 39  | 42  | 38  | 40  |     |
|       | match     | 401 | 308 | 349 | 279 | 337 | 299 | 288 | 274 | 307 | 305 |     |
| MSE-E | insertion | 17  | 29  | 26  | 28  | 32  | 40  | 43  | 46  | 40  | 53  |     |
|       | match     | 359 | 343 | 375 | 358 | 361 | 329 | 362 | 376 | 340 | 326 |     |



## 2.95 encodeSangerChipH3K4me2HFL1

NULL

SI H3K4me2 HFL-1

Sanger Institute ChIP/Chip (H3K4me2 ab, HFL-1 cells)

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.514 | 0.125 | 4.11 | 3.91e-05 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.691 | 0.118 | 5.85 | 4.95e-09 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 2189

Origin.of.data.set

AVR-E MSE-E

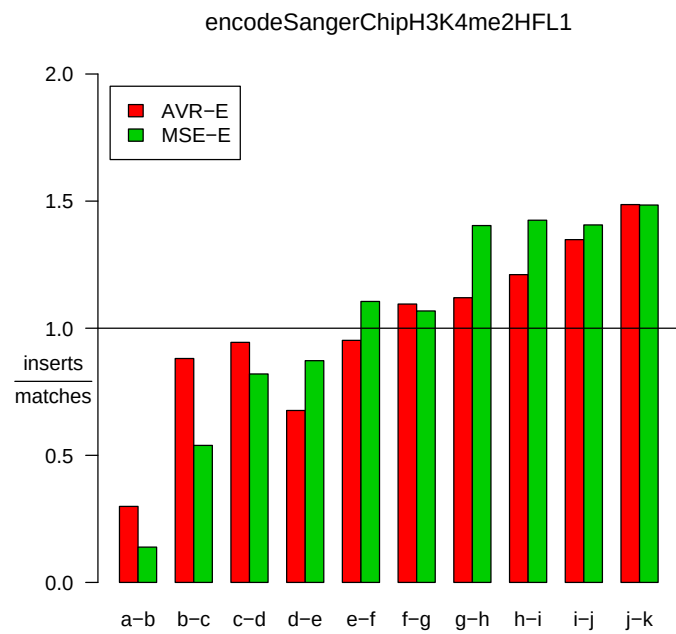
3453 3884

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.245 | insertion | 0.475 |
| 2 | 0.475 | match     | 0.550 |

0.245 0.475 0.55 0.615 0.68 0.75 0.83 0.945 1.09  
1.42 23.5

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 11  | 27  | 31  | 21  | 29  | 34  | 33  | 34  | 40  | 46  |     |
|       | match     | 372 | 310 | 332 | 314 | 308 | 314 | 298 | 284 | 300 | 313 |     |
| MSE-E | insertion | 5   | 21  | 27  | 32  | 40  | 34  | 49  | 51  | 47  | 48  |     |
|       | match     | 364 | 394 | 333 | 371 | 366 | 322 | 353 | 362 | 338 | 327 |     |



## 2.96 encodeSangerChipH3K4me2K562

NULL

SI H3K4me2 K562

Sanger Institute ChIP/Chip (H3K4me2 ab, K562 cells)

|                                             | coef  | se    | z    | p      |
|---------------------------------------------|-------|-------|------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.186 | 0.124 | 1.49 | 0.1350 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.254 | 0.117 | 2.16 | 0.0309 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 2548

Origin.of.data.set

AVR-E MSE-E

3271 3707

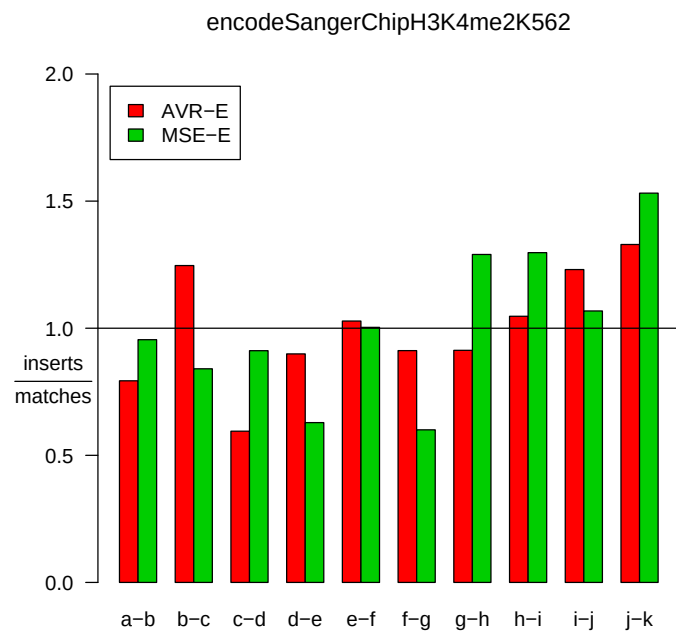
Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.175 | insertion | 0.660 |
| 2 | 0.660 | match     | 0.735 |

0.175 0.66 0.735 0.79 0.84 0.89 0.94 1 1.1 1.39  
27.3

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 24  | 36  | 19  | 28  | 30  | 24  | 27  | 29  | 37  | 38  |
|       | match     |     | 307 | 293 | 324 | 316 | 296 | 267 | 300 | 281 | 305 | 290 |
| MSE-E | insertion |     | 32  | 28  | 31  | 22  | 36  | 20  | 44  | 39  | 34  | 48  |
|       | match     |     | 340 | 338 | 345 | 355 | 364 | 338 | 346 | 305 | 323 | 318 |





## 2.97 encodeSangerChipH3K4me3

NULL

SI H3K4m3 GM6990

Sanger Institute ChIP/Chip (H3K4me3 ab, GM06990 cells)

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.427 | 0.128 | 3.34 | 0.000835 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.421 | 0.119 | 3.53 | 0.000418 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 2694

Origin.of.data.set

AVR-E MSE-E

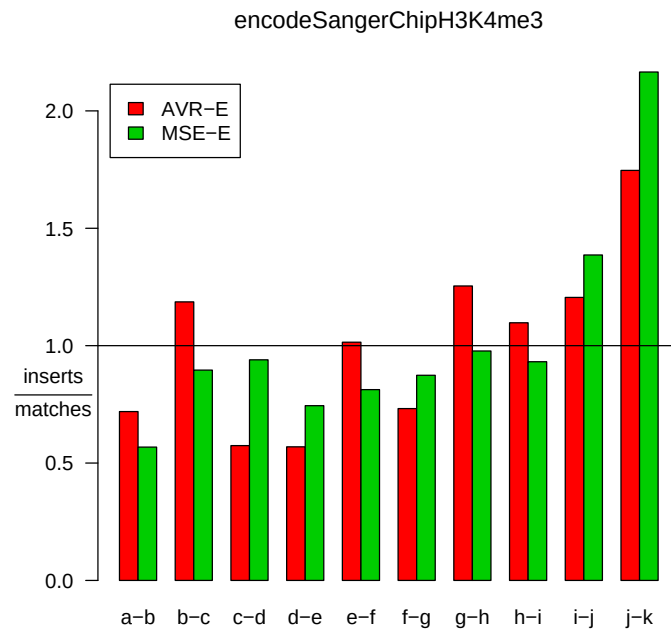
3206 3626

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.16  | insertion | 0.410 |
| 2 | 0.41  | match     | 0.475 |

0.16 0.41 0.475 0.525 0.58 0.63 0.695 0.77 0.89  
1.29 46.7

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 20  | 35  | 17  | 19  | 27  | 24  | 35  | 28  | 34  | 51  |
|       | match     |     | 279 | 296 | 297 | 335 | 267 | 329 | 280 | 256 | 283 | 293 |
| MSE-E | insertion |     | 21  | 30  | 31  | 25  | 26  | 29  | 30  | 35  | 42  | 60  |
|       | match     |     | 371 | 336 | 331 | 337 | 321 | 333 | 308 | 377 | 304 | 278 |



## 2.98 encodeSangerChipH3K4me3HeLa

NULL

SI H3K4me3 HeLa

Sanger Institute ChIP/Chip (H3K4me3 ab, HeLa cells)

|                                             | coef   | se    | z      | p     |
|---------------------------------------------|--------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.0301 | 0.122 | 0.2480 | 0.804 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.0082 | 0.113 | 0.0725 | 0.942 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 2189

Origin.of.data.set

AVR-E MSE-E

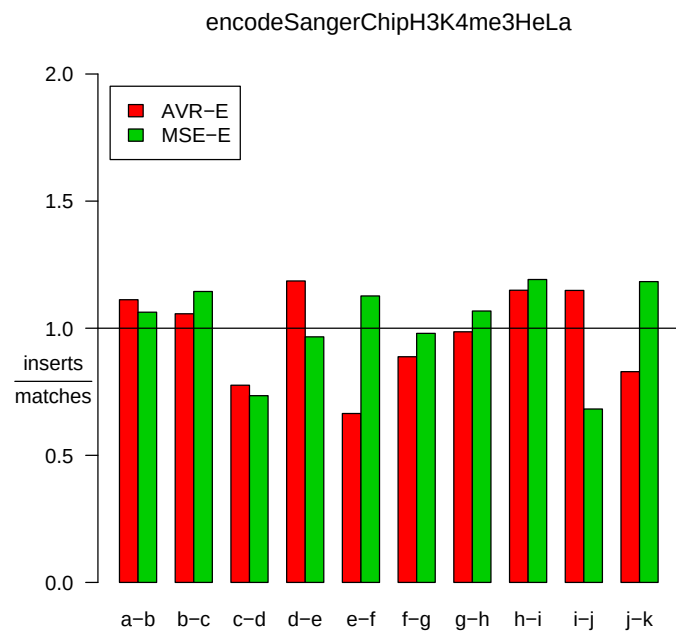
3453 3884

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.195 | insertion | 0.54  |
| 2 | 0.540 | match     | 0.61  |

0.195 0.54 0.61 0.67 0.72 0.77 0.835 0.905 1.01  
1.22 48.5

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 42  | 35  | 26  | 34  | 18  | 28  | 27  | 35  | 36  | 25  |     |
|       | match     | 382 | 335 | 339 | 290 | 274 | 319 | 277 | 308 | 317 | 305 |     |
| MSE-E | insertion | 33  | 37  | 26  | 34  | 41  | 37  | 38  | 43  | 23  | 42  |     |
|       | match     | 314 | 327 | 358 | 356 | 368 | 382 | 360 | 365 | 341 | 359 |     |



## 2.99 encodeSangerChipH3K4me3HFL1

NULL

SI H3K4me3 HFL-1

Sanger Institute ChIP/Chip (H3K4me3 ab, HFL-1 cells)

|                                             | coef   | se    | z     | p     |
|---------------------------------------------|--------|-------|-------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.1650 | 0.122 | 1.360 | 0.175 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.0727 | 0.113 | 0.644 | 0.520 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 2189

Origin.of.data.set

AVR-E MSE-E

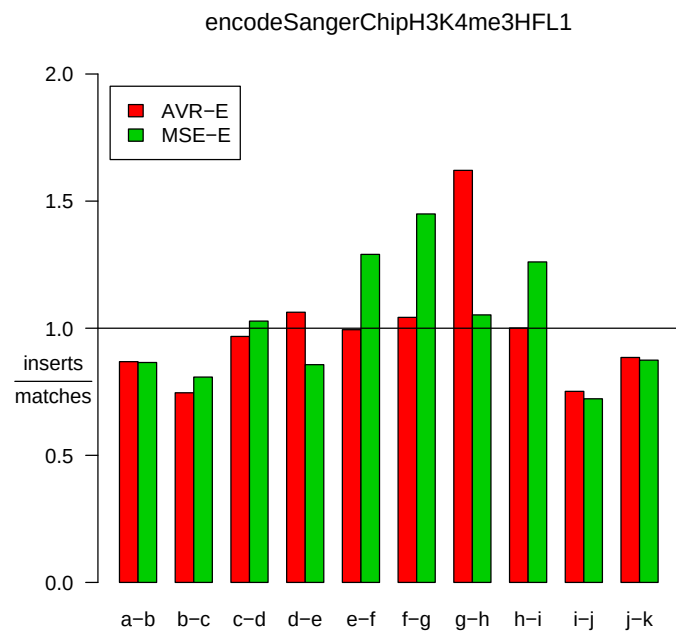
3453 3884

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.235 | insertion | 0.56  |
| 2 | 0.560 | match     | 0.64  |

0.235 0.56 0.64 0.71 0.78 0.85 0.925 1.02 1.17  
1.45 18

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 31  | 27  | 31  | 33  | 29  | 30  | 46  | 29  | 22  | 28  |
|       | match     |     | 361 | 366 | 324 | 314 | 295 | 291 | 287 | 293 | 296 | 320 |
| MSE-E | insertion |     | 29  | 25  | 37  | 31  | 43  | 44  | 41  | 46  | 28  | 30  |
|       | match     |     | 339 | 313 | 364 | 366 | 337 | 307 | 394 | 369 | 392 | 347 |



## 2.100 encodeSangerChipH3K4me3K562

NULL

SI H3K4me3 K562

Sanger Institute ChIP/Chip (H3K4me3 ab, K562 cells)

|                                             | coef   | se    | z     | p       |
|---------------------------------------------|--------|-------|-------|---------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.229 | 0.123 | -1.87 | 0.06150 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.298 | 0.114 | -2.62 | 0.00888 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 2199

Origin.of.data.set

AVR-E MSE-E

3447 3880

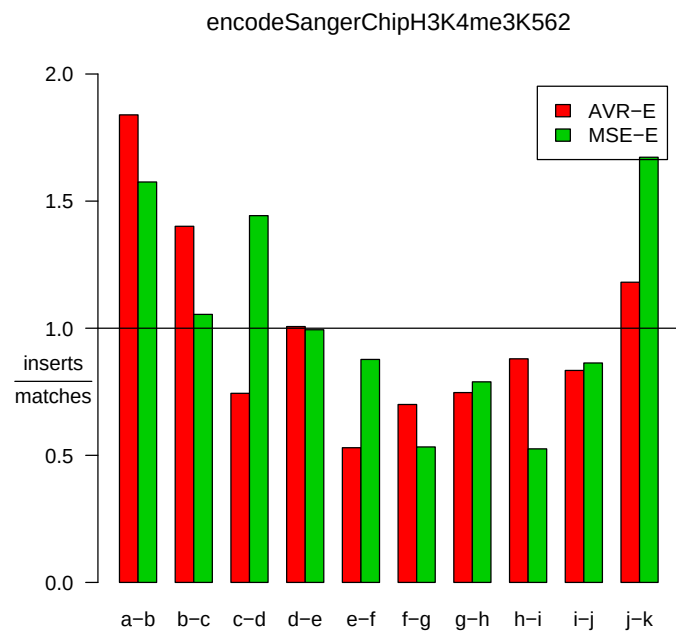
Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.125 | insertion | 0.415 |
| 2 | 0.415 | match     | 0.495 |

0.125 0.415 0.495 0.55 0.595 0.65 0.705 0.78 0.91  
1.39 48.8

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 57  | 43  | 26  | 29  | 17  | 21  | 21  | 27  | 27  | 38  |
|       | match     |     | 313 | 310 | 353 | 291 | 324 | 303 | 284 | 310 | 327 | 325 |
| MSE-E | insertion |     | 51  | 38  | 49  | 31  | 35  | 20  | 30  | 18  | 30  | 52  |
|       | match     |     | 327 | 364 | 343 | 315 | 403 | 379 | 384 | 346 | 351 | 314 |





## 2.101 encodeSangerChipH4ac

NULL

SI H4ac GM06990

Sanger Institute ChIP/Chip (H4ac ab, GM06990 cells)

|                                             | coef | se    | z    | p        |
|---------------------------------------------|------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 2.25 | 0.202 | 11.1 | 9.41e-29 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.74 | 0.150 | 11.5 | 7.99e-31 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 2665

Origin.of.data.set

AVR-E MSE-E

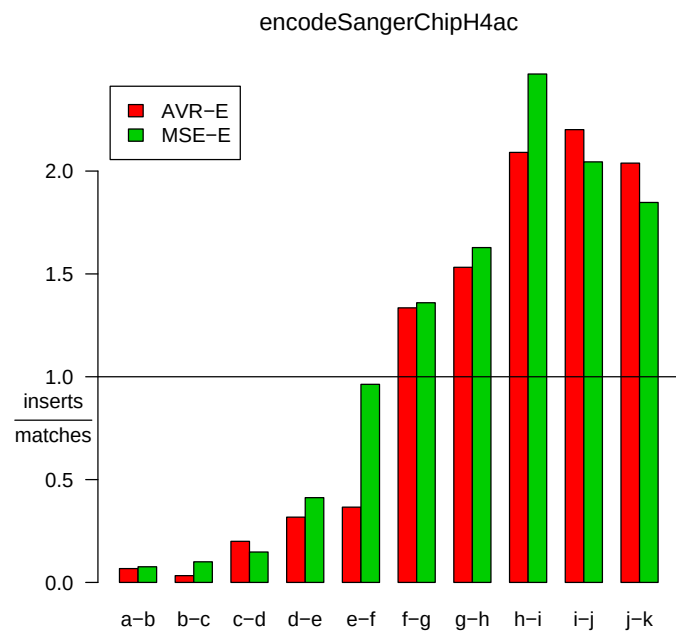
3212 3649

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.165 | insertion | 0.435 |
| 2 | 0.435 | match     | 0.515 |

0.165 0.435 0.515 0.592 0.675 0.78 0.905 1.04  
1.22 1.71 8.63

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 2   | 1   | 6   | 10  | 10  | 41  | 44  | 59  | 54  | 62  |     |
|       | match     | 298 | 304 | 301 | 316 | 274 | 308 | 288 | 283 | 246 | 305 |     |
| MSE-E | insertion | 3   | 4   | 5   | 15  | 34  | 40  | 50  | 70  | 63  | 49  |     |
|       | match     | 395 | 400 | 339 | 365 | 354 | 295 | 308 | 284 | 309 | 266 |     |



## 2.102 encodeSangerChipH4acHeLa

NULL

SI H4ac HeLa

Sanger Institute ChIP/Chip (H4ac ab, HeLa cells)

|                                             | coef | se    | z    | p        |
|---------------------------------------------|------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 1.31 | 0.145 | 9.01 | 1.99e-19 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.29 | 0.131 | 9.84 | 7.29e-23 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 2189

Origin.of.data.set

AVR-E MSE-E

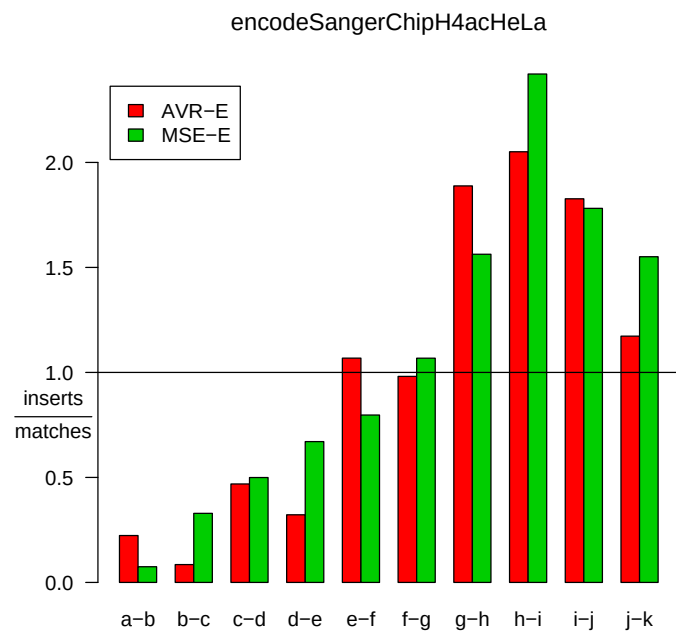
3453 3884

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.270 | insertion | 0.588 |
| 2 | 0.588 | match     | 0.680 |

0.27 0.588 0.68 0.76 0.835 0.91 0.985 1.07 1.2  
1.45 9.94

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 7   | 3   | 14  | 10  | 34  | 29  | 56  | 59  | 54  | 40  |
|       | match     |     | 317 | 357 | 302 | 314 | 322 | 299 | 300 | 291 | 299 | 345 |
| MSE-E | insertion |     | 3   | 12  | 20  | 24  | 29  | 36  | 55  | 73  | 56  | 46  |
|       | match     |     | 406 | 369 | 405 | 362 | 368 | 341 | 356 | 305 | 318 | 300 |



## 2.103 encodeSangerChipH4acHFL1

NULL

SI H4ac HFL-1

Sanger Institute ChIP/Chip (H4ac ab, HFL-1 cells)

|                                             | coef | se    | z    | p        |
|---------------------------------------------|------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 1.23 | 0.140 | 8.82 | 1.12e-18 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.23 | 0.128 | 9.57 | 1.06e-21 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 2189

Origin.of.data.set

AVR-E MSE-E

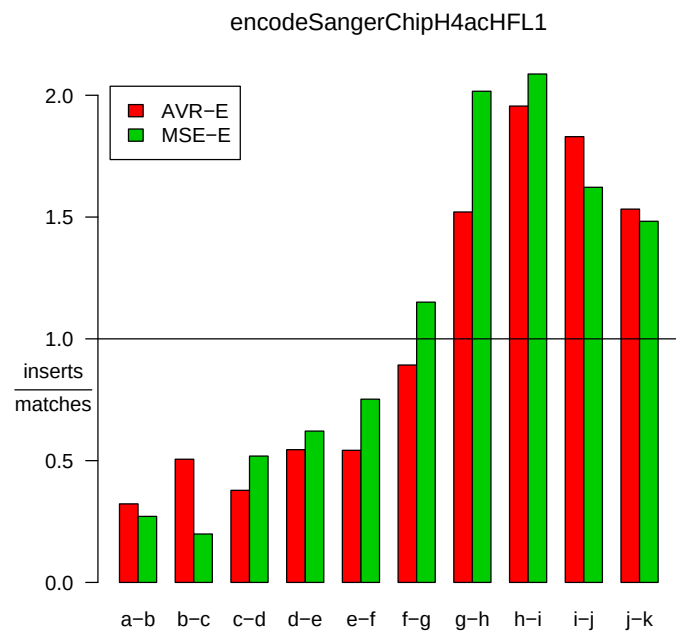
3453 3884

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.20  | insertion | 0.470 |
| 2 | 0.47  | match     | 0.565 |

0.2 0.47 0.565 0.645 0.725 0.805 0.89 0.975 1.12  
1.4 12.9

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 11  | 17  | 12  | 16  | 17  | 27  | 43  | 58  | 55  | 50  |
|       | match     |     | 345 | 340 | 321 | 297 | 317 | 306 | 286 | 300 | 304 | 330 |
| MSE-E | insertion |     | 10  | 8   | 18  | 25  | 27  | 43  | 62  | 65  | 51  | 45  |
|       | match     |     | 373 | 407 | 351 | 407 | 363 | 378 | 311 | 315 | 318 | 307 |



## 2.104 encodeSangerChipH4acK562

NULL

SI H4ac K562

Sanger Institute ChIP/Chip (H4ac ab, K562 cells)

|                                             | coef | se    | z    | p        |
|---------------------------------------------|------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 1.69 | 0.162 | 10.4 | 2.28e-25 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.90 | 0.151 | 12.6 | 3.13e-36 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 2199

Origin.of.data.set

AVR-E MSE-E

3447 3880

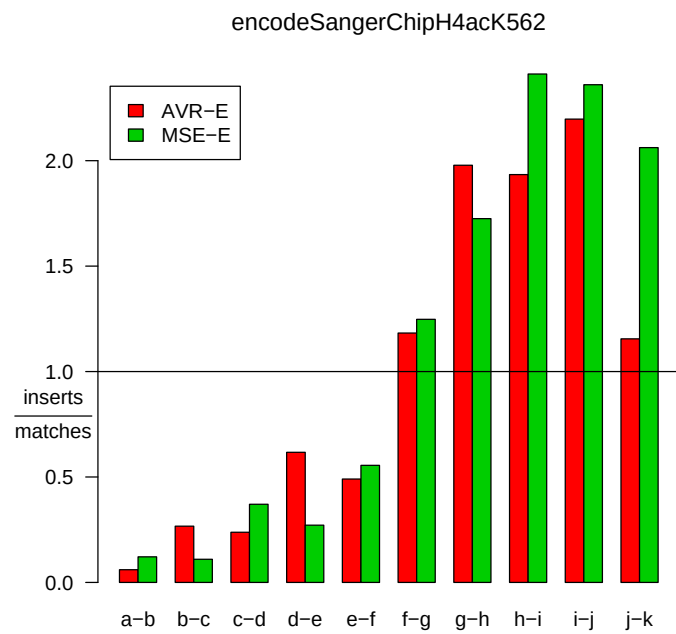
Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.11  | insertion | 0.360 |
| 2 | 0.36  | match     | 0.425 |

0.11 0.36 0.425 0.5 0.58 0.665 0.76 0.885 1.11  
1.66 23.1

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 2   | 7   | 9   | 19  | 15  | 37  | 57  | 54  | 67  | 39  |
|       | match     |     | 335 | 265 | 382 | 311 | 309 | 316 | 291 | 282 | 308 | 341 |
| MSE-E | insertion |     | 5   | 4   | 16  | 10  | 21  | 42  | 55  | 74  | 68  | 59  |
|       | match     |     | 416 | 368 | 436 | 372 | 382 | 340 | 322 | 310 | 291 | 289 |





## 2.105 encodeSangerChipHitH3acGM06990

NULL

SI H3ac GM06990

Sanger Institute ChIP/Chip Hits (H3ac ab, GM06990 cells)

|                                             | coef  | se    | z    | p       |
|---------------------------------------------|-------|-------|------|---------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.403 | 0.323 | 1.25 | 0.21200 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.280 | 0.396 | 3.23 | 0.00125 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 8266

Origin.of.data.set

AVR-E MSE-E

606 654

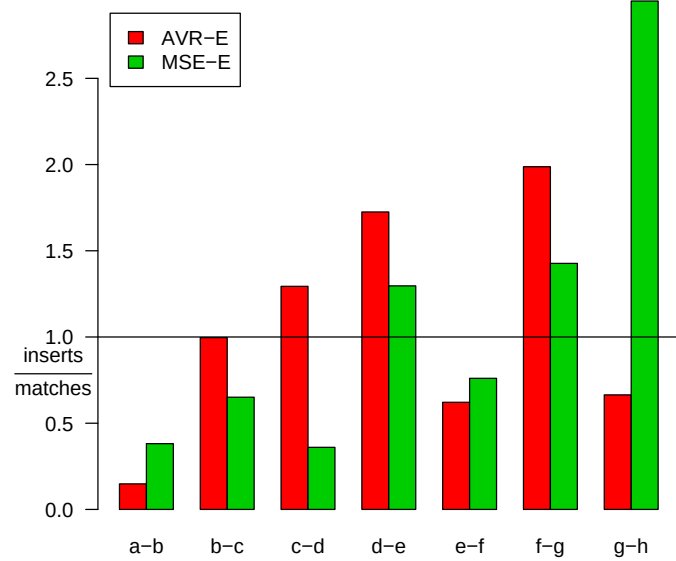
Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.193 | insertion | 0.90  |
| 2 | 0.900 | match     | 1.05  |

0.193 0.9 1.05 1.23 1.44 1.61 1.95 2.47

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 1   | 6   | 9   | 12  | 4   | 13  | 4   |     |
|       | match     | 65  | 58  | 67  | 67  | 62  | 63  | 58  |     |
| MSE-E | insertion | 4   | 5   | 4   | 7   | 3   | 8   | 15  |     |
|       | match     | 101 | 74  | 107 | 52  | 38  | 54  | 49  |     |

encodeSangerChipHitH3acGM06990



## 2.106 encodeSangerChipHitH3acHeLa

NULL

SI H3ac HeLa

Sanger Institute ChIP/Chip Hits (H3ac ab, HeLa cells)

|                                             | coef   | se    | z      | p      |
|---------------------------------------------|--------|-------|--------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.351 | 0.451 | -0.777 | 0.4370 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.230  | 0.479 | 2.560  | 0.0104 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 8634

Origin.of.data.set

AVR-E MSE-E

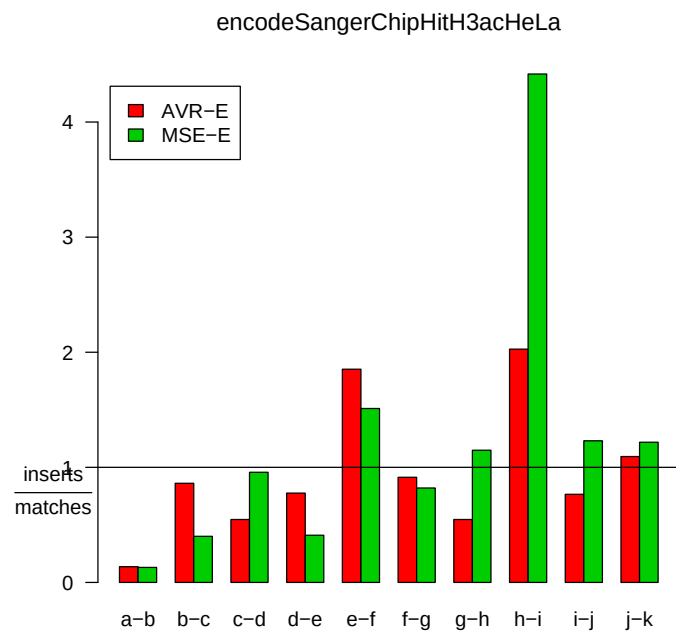
446 446

Category limits

|   | lower    | category  | upper    |
|---|----------|-----------|----------|
| 1 | 0.556355 | insertion | 0.981332 |
| 2 | 0.981332 | match     | 1.073110 |

0.556 0.981 1.07 1.18 1.35 1.58 1.91 2.39 2.91  
3.73 9.1

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 1   | 6   | 4   | 5   | 10  | 7   | 4   | 12  | 4   | 8   |     |
|       | match     | 42  | 40  | 42  | 37  | 31  | 44  | 42  | 34  | 30  | 42  |     |
| MSE-E | insertion | 1   | 3   | 6   | 3   | 10  | 5   | 7   | 20  | 9   | 7   |     |
|       | match     | 44  | 43  | 36  | 42  | 38  | 35  | 35  | 26  | 42  | 33  |     |



## 2.107 encodeSangerChipHitH3acK562

NULL

SI H3ac K562

Sanger Institute ChIP/Chip Hits (H3ac ab, K562 cells)

|                                             | coef | se    | z    | p        |
|---------------------------------------------|------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 1.08 | 0.303 | 3.57 | 3.63e-04 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.49 | 0.268 | 5.55 | 2.90e-08 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 7278

Origin.of.data.set

AVR-E MSE-E

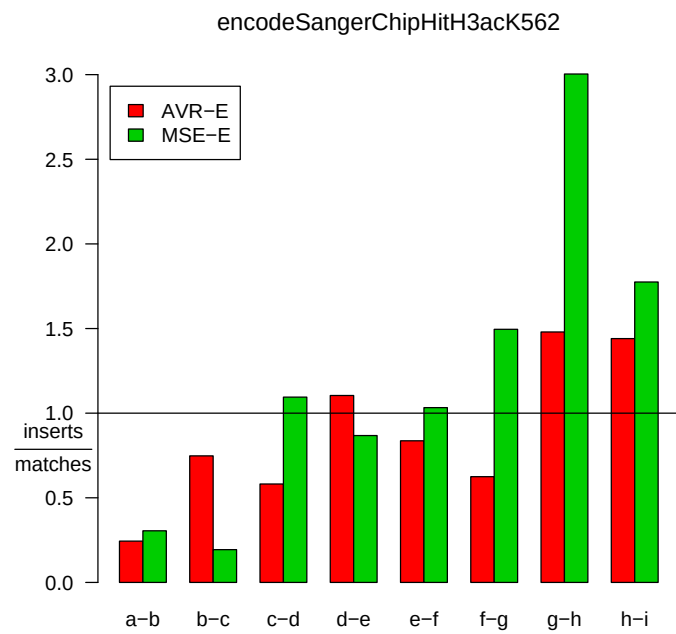
1031 1217

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.590 | insertion | 0.762 |
| 2 | 0.762 | match     | 1.040 |

0.59 0.762 1.04 1.26 1.54 1.87 2.33 3.33 11.2

|       | set       | type | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i |
|-------|-----------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |      | 3   | 9   | 7   | 14  | 9   | 8   | 18  | 19  |     |
|       | match     |      | 96  | 94  | 94  | 99  | 84  | 100 | 95  | 103 |     |
| MSE-E | insertion |      | 5   | 3   | 15  | 11  | 16  | 18  | 30  | 20  |     |
|       | match     |      | 128 | 121 | 107 | 99  | 121 | 94  | 78  | 88  |     |



## 2.108 encodeSangerChipHitH3K4me1GM06990

NULL

SI H3K4m1 GM6990

Sanger Institute ChIP/Chip Hits (H3K4me1 ab, GM06990 cells)

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.713 | 0.223 | 3.20 | 1.39e-03 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.090 | 0.213 | 5.13 | 2.92e-07 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 6986

Origin.of.data.set

AVR-E MSE-E

1177 1363

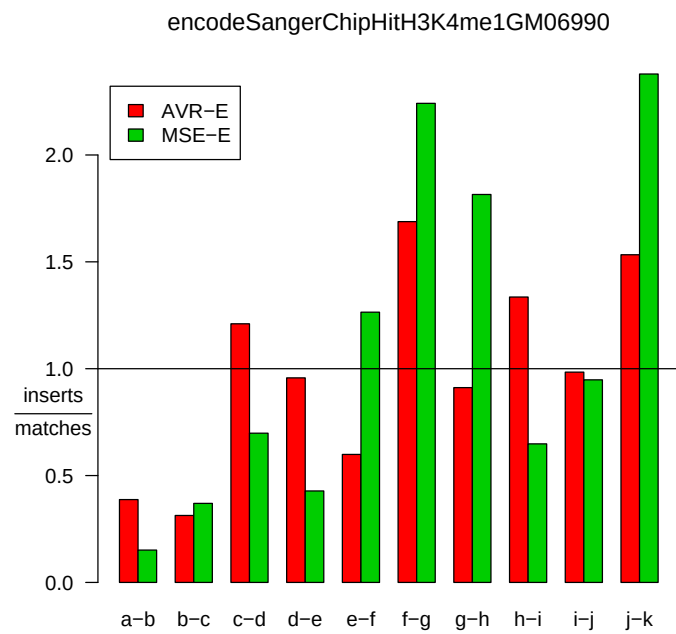
Category limits

|   | lower    | category  | upper     |
|---|----------|-----------|-----------|
| 1 | 0.183620 | insertion | 0.6785350 |
| 2 | 0.678535 | match     | 0.9678552 |

0.184 0.679 0.968 1.22 1.44 1.7 2.01 2.31 2.74  
3.62 8.44

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 5   | 5   | 14  | 14  | 9   | 22  | 12  | 19  | 14  | 21  |
|       | match     |     | 97  | 120 | 87  | 110 | 113 | 98  | 99  | 107 | 107 | 103 |
| MSE-E | insertion |     | 3   | 6   | 13  | 7   | 19  | 31  | 28  | 10  | 15  | 31  |
|       | match     |     | 149 | 122 | 140 | 123 | 113 | 104 | 116 | 116 | 119 | 98  |





## 2.109 encodeSangerChipHitH3K4me1HeLa

NULL

SI H3K4me1 HeLa

Sanger Institute ChIP/Chip Hits (H3K4me1 ab, HeLa cells)

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.339 | 0.258 | 1.31 | 0.189000 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.929 | 0.275 | 3.38 | 0.000737 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 7902

Origin.of.data.set

AVR-E MSE-E

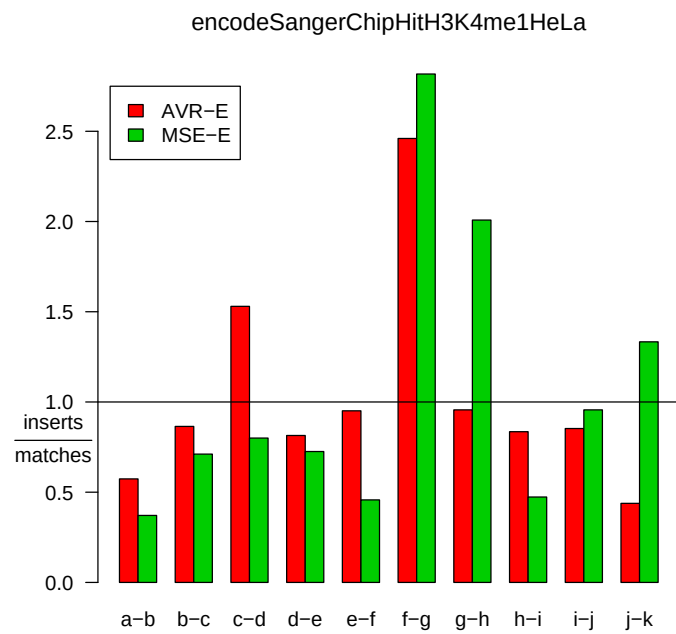
787 837

Category limits

|   | lower     | category  | upper     |
|---|-----------|-----------|-----------|
| 1 | 0.5359200 | insertion | 0.9792986 |
| 2 | 0.9792986 | match     | 1.2231160 |

0.536 0.979 1.22 1.41 1.63 1.82 2.01 2.38 2.75  
3.31 6.26

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 6   | 10  | 16  | 8   | 11  | 23  | 10  | 9   | 10  | 5   |     |
|       | match     | 66  | 73  | 66  | 62  | 73  | 59  | 66  | 68  | 74  | 72  |     |
| MSE-E | insertion | 5   | 8   | 9   | 10  | 5   | 25  | 21  | 6   | 10  | 15  |     |
|       | match     | 85  | 71  | 71  | 87  | 69  | 56  | 66  | 80  | 66  | 71  |     |



## 2.110 encodeSangerChipHitH3K4me2GM06990

NULL

SI H3K4m2 GM6990

Sanger Institute ChIP/Chip Hits (H3K4me2 ab, GM06990 cells)

|                                             | coef  | se    | z    | p       |
|---------------------------------------------|-------|-------|------|---------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.607 | 0.242 | 2.51 | 0.01200 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.543 | 0.202 | 2.69 | 0.00717 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 7296

Origin.of.data.set

AVR-E MSE-E

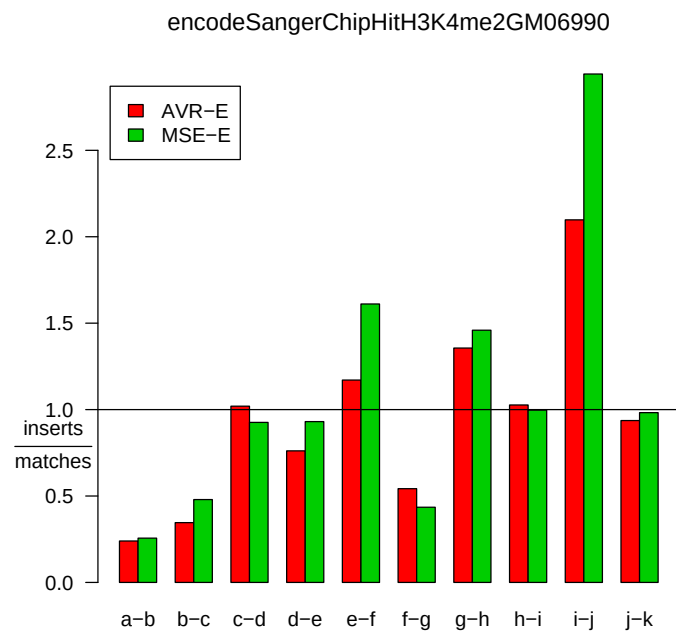
1037 1193

Category limits

|   | lower    | category  | upper     |
|---|----------|-----------|-----------|
| 1 | 0.000000 | insertion | 0.6870060 |
| 2 | 0.687006 | match     | 0.8211478 |

0 0.687 0.821 1 1.28 1.58 2.02 2.76 3.84 5.99  
18.1

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 3   | 5   | 12  | 11  | 15  | 8   | 20  | 13  | 30  | 12  |
|       | match     |     | 84  | 97  | 79  | 97  | 86  | 99  | 99  | 85  | 96  | 86  |
| MSE-E | insertion |     | 5   | 8   | 16  | 14  | 24  | 7   | 20  | 15  | 39  | 12  |
|       | match     |     | 131 | 112 | 116 | 101 | 100 | 108 | 92  | 101 | 89  | 82  |



## 2.111 encodeSangerChipHitH3K4me2HeLa

NULL

SI H3K4me2 HeLa

Sanger Institute ChIP/Chip Hits (H3K4me2 ab, HeLa cells)

|                                             | coef   | se    | z      | p      |
|---------------------------------------------|--------|-------|--------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.767  | 0.416 | 1.840  | 0.0654 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.228 | 0.392 | -0.581 | 0.5610 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 8679

Origin.of.data.set

AVR-E MSE-E

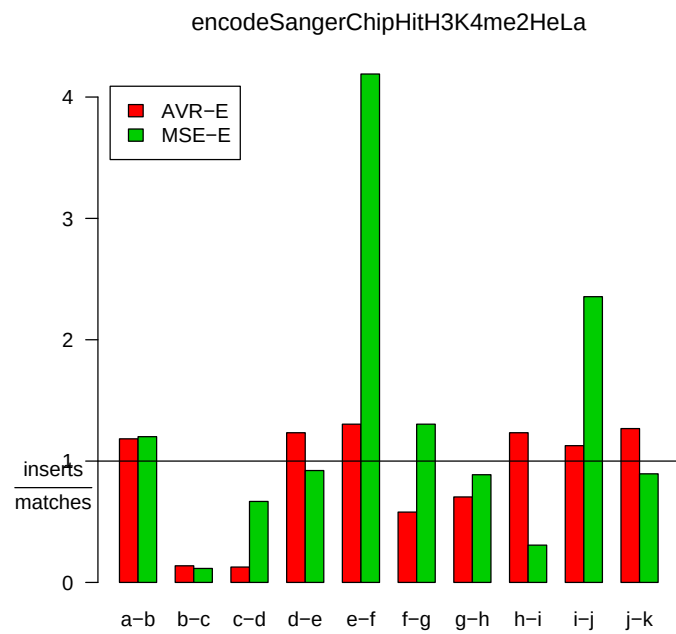
423 424

Category limits

|   | lower    | category  | upper    |
|---|----------|-----------|----------|
| 1 | 0.564986 | insertion | 1.014820 |
| 2 | 1.014820 | match     | 1.234626 |

0.565 1.01 1.23 1.49 1.9 2.27 2.91 3.99 4.91 5.85  
13.8

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 7   | 1   | 1   | 9   | 9   | 4   | 5   | 9   | 8   | 9   |     |
|       | match     | 30  | 37  | 40  | 37  | 35  | 35  | 36  | 37  | 36  | 36  |     |
| MSE-E | insertion | 9   | 1   | 5   | 6   | 19  | 9   | 7   | 2   | 13  | 6   |     |
|       | match     | 38  | 44  | 38  | 33  | 23  | 35  | 40  | 33  | 28  | 34  |     |



## 2.112 encodeSangerChipHitH3K4me2K562

NULL

SI H3K4me2 K562

Sanger Institute ChIP/Chip Hits (H3K4me2 ab, K562 cells)

|                                             | coef   | se    | z     | p      |
|---------------------------------------------|--------|-------|-------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.7770 | 0.392 | 1.980 | 0.0476 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.0935 | 0.326 | 0.287 | 0.7740 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 8345

Origin.of.data.set

AVR-E MSE-E

571 610

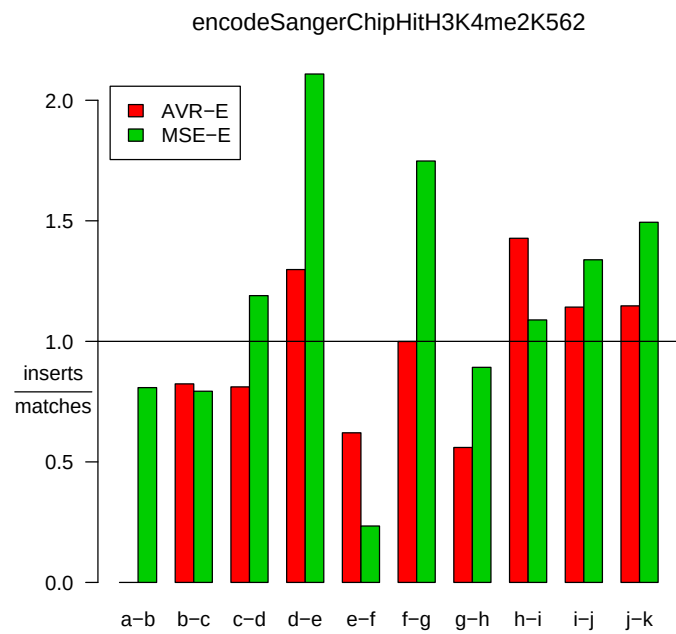
Category limits

|   | lower    | category  | upper   |
|---|----------|-----------|---------|
| 1 | 0.605626 | insertion | 1.12381 |
| 2 | 1.123810 | match     | 1.30502 |

0.606 1.12 1.31 1.47 1.68 2 2.45 3.5 5.11 6.95  
20.4

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 0   | 6   | 5   | 10  | 4   | 7   | 4   | 9   | 8   | 9   |     |
|       | match     | 59  | 52  | 44  | 55  | 46  | 50  | 51  | 45  | 50  | 56  |     |
| MSE-E | insertion | 6   | 6   | 10  | 13  | 2   | 12  | 7   | 9   | 9   | 9   |     |
|       | match     | 53  | 54  | 60  | 44  | 61  | 49  | 56  | 59  | 48  | 43  |     |





## 2.113 encodeSangerChipHitH3K4me3GM06990

NULL

SI H3K4m3 GM6990

Sanger Institute ChIP/Chip (H3K4me3 ab, GM06990 cells)

|                                             | coef  | se    | z   | p        |
|---------------------------------------------|-------|-------|-----|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.975 | 0.315 | 3.1 | 1.96e-03 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.020 | 0.261 | 3.9 | 9.63e-05 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 7832

Origin.of.data.set

AVR-E MSE-E

811 883

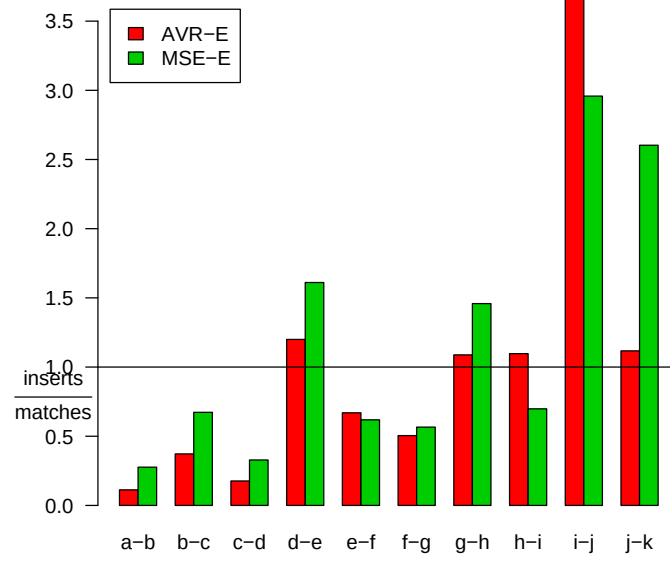
Category limits

|   | lower     | category  | upper     |
|---|-----------|-----------|-----------|
| 1 | 0.0000000 | insertion | 0.7019794 |
| 2 | 0.7019794 | match     | 0.8246470 |

0 0.702 0.825 0.96 1.13 1.39 1.91 3.08 5.22 6.78  
23.7

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 1   | 4   | 2   | 11  | 7   | 6   | 12  | 11  | 30  | 12  |     |
|       | match     | 62  | 75  | 79  | 64  | 73  | 83  | 77  | 70  | 57  | 75  |     |
| MSE-E | insertion | 4   | 8   | 4   | 18  | 7   | 6   | 14  | 8   | 25  | 22  |     |
|       | match     | 101 | 83  | 85  | 78  | 79  | 74  | 67  | 80  | 59  | 59  |     |

encodeSangerChipHitH3K4me3GM06990



## 2.114 encodeSangerChipHitH3K4me3HeLa

NULL

SI H3K4me3 HeLa

Sanger Institute ChIP/Chip Hits (H3K4me3 ab, HeLa cells)

|                                             | coef   | se    | z      | p     |
|---------------------------------------------|--------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.174  | 0.401 | 0.435  | 0.664 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.209 | 0.410 | -0.509 | 0.611 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 8693

Origin.of.data.set

AVR-E MSE-E

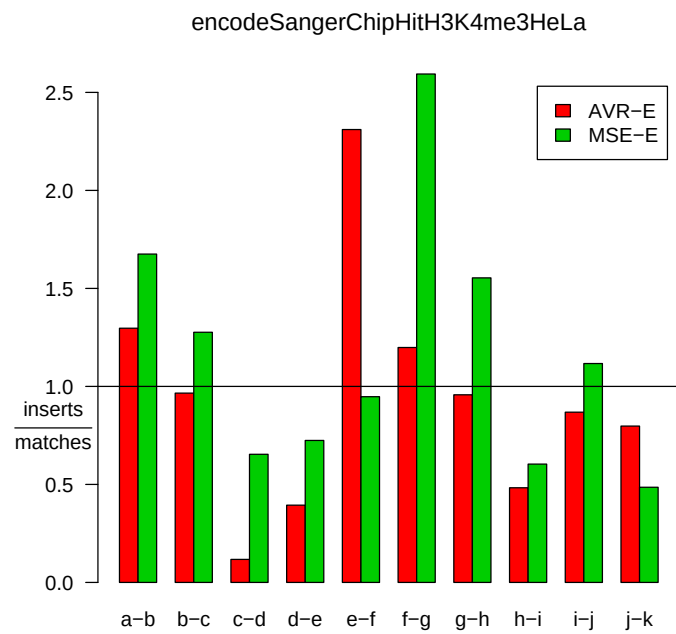
410 423

Category limits

|   | lower    | category  | upper    |
|---|----------|-----------|----------|
| 1 | 0.296888 | insertion | 0.941106 |
| 2 | 0.941106 | match     | 1.071322 |

0.297 0.941 1.07 1.2 1.46 2.02 3.08 4.51 6.07  
7.75 31.7

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 9   | 8   | 1   | 3   | 15  | 11  | 6   | 4   | 7   | 5   |
|       | match     |     | 31  | 37  | 38  | 34  | 29  | 41  | 28  | 37  | 36  | 28  |
| MSE-E | insertion |     | 12  | 8   | 6   | 6   | 7   | 18  | 8   | 5   | 8   | 5   |
|       | match     |     | 32  | 28  | 41  | 37  | 33  | 31  | 23  | 37  | 32  | 46  |



## 2.115 encodeSangerChipHitH3K4me3K562

NULL

SI H3K4me3 K562

Sanger Institute ChIP/Chip Hits (H3K4me3 ab, K562 cells)

|                                             | coef  | se    | z    | p       |
|---------------------------------------------|-------|-------|------|---------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.939 | 0.352 | 2.66 | 0.00773 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.070 | 0.389 | 2.76 | 0.00577 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 8048

Origin.of.data.set

AVR-E MSE-E

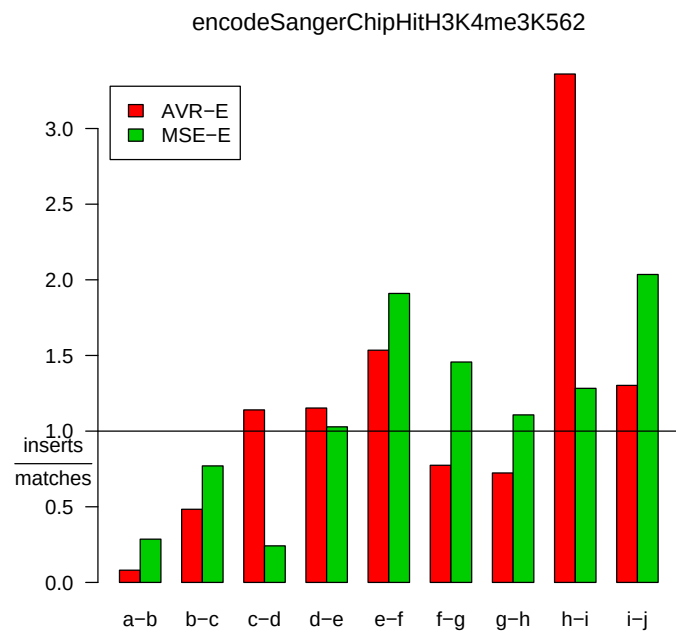
707 771

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.238 | insertion | 0.775 |
| 2 | 0.775 | match     | 0.876 |

0.238 0.775 0.876 1.04 1.16 1.48 2.19 5 9.19 49.5

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 1   | 4   | 8   | 7   | 9   | 6   | 5   | 19  | 9   |     |
|       | match     | 118 | 79  | 67  | 58  | 56  | 74  | 66  | 54  | 66  |     |
| MSE-E | insertion | 5   | 5   | 2   | 7   | 14  | 9   | 8   | 9   | 13  |     |
|       | match     | 167 | 62  | 79  | 65  | 70  | 59  | 69  | 67  | 61  |     |



## 2.116 encodeSangerChipHitH4acGM06990

NULL

SI H4ac GM06990

Sanger Institute ChIP/Chip Hits (H4ac ab, GM06990 cells)

|                                             | coef  | se    | z    | p      |
|---------------------------------------------|-------|-------|------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.344 | 0.226 | 1.53 | 0.1270 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.444 | 0.246 | 1.81 | 0.0708 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 7417

Origin.of.data.set

AVR-E MSE-E

1016 1093

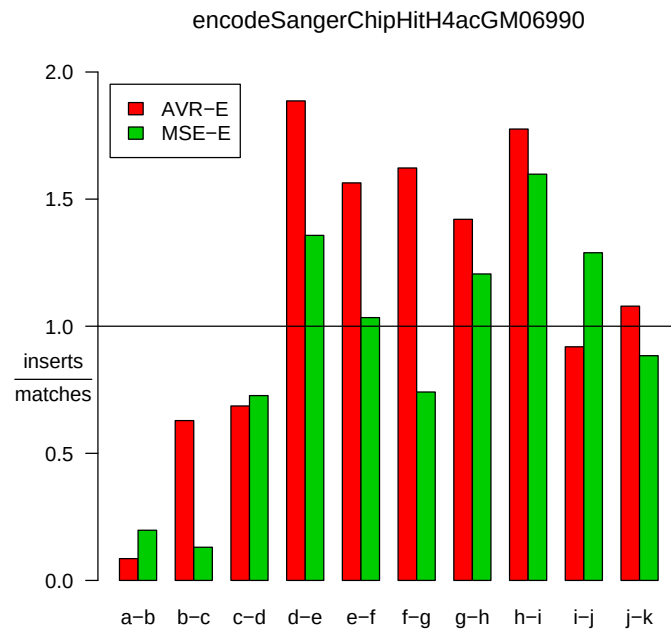
Category limits

|   | lower     | category  | upper     |
|---|-----------|-----------|-----------|
| 1 | 0.0000000 | insertion | 0.6869694 |
| 2 | 0.6869694 | match     | 0.8789498 |

0 0.687 0.879 1.01 1.11 1.28 1.5 1.67 1.99 2.53  
5.86

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 1   | 7   | 8   | 21  | 17  | 17  | 16  | 20  | 13  | 13  |     |
|       | match     | 89  | 85  | 89  | 85  | 83  | 80  | 86  | 86  | 108 | 92  |     |
| MSE-E | insertion | 3   | 2   | 10  | 16  | 13  | 10  | 15  | 18  | 13  | 11  |     |
|       | match     | 116 | 117 | 105 | 90  | 96  | 103 | 95  | 86  | 77  | 95  |     |





## 2.117 encodeSangerChipHitH4acHeLa

NULL

SI H4ac HeLa

Sanger Institute ChIP/Chip Hits (H4ac ab, HeLa cells)

|                                             | coef   | se    | z      | p      |
|---------------------------------------------|--------|-------|--------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -1.040 | 0.624 | -1.670 | 0.0955 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.174  | 0.478 | 0.364  | 0.7160 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 8547

Origin.of.data.set

AVR-E MSE-E

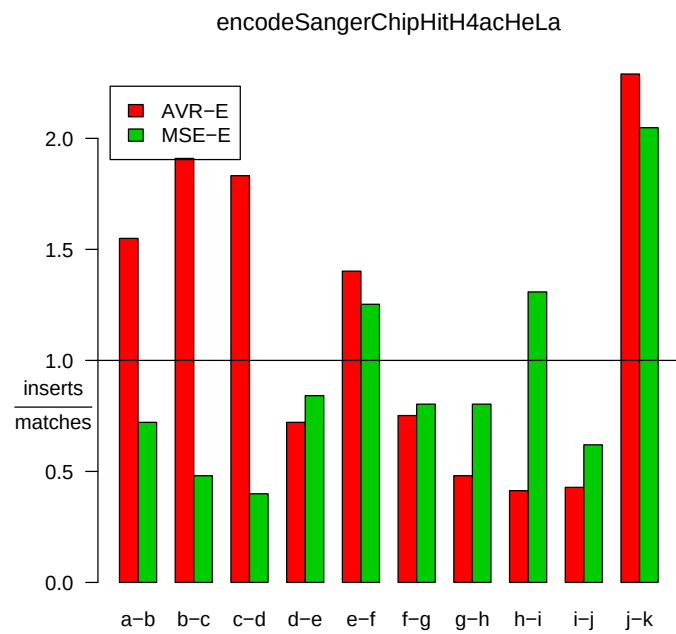
501 478

Category limits

|   | lower    | category  | upper   |
|---|----------|-----------|---------|
| 1 | 0.669009 | insertion | 1.01081 |
| 2 | 1.010810 | match     | 1.12366 |

0.669 1.01 1.12 1.24 1.34 1.5 1.65 1.84 2.09 2.5  
6.6

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 5   | 6   | 7   | 3   | 5   | 3   | 2   | 2   | 2   | 7   |
|       | match     |     | 38  | 37  | 45  | 49  | 42  | 47  | 49  | 57  | 55  | 36  |
| MSE-E | insertion |     | 3   | 2   | 2   | 2   | 5   | 3   | 3   | 4   | 2   | 8   |
|       | match     |     | 49  | 49  | 59  | 28  | 47  | 44  | 44  | 36  | 38  | 46  |



## 2.118 encodeSangerChipHitH4acK562

NULL

SI H4ac K562

Sanger Institute ChIP/Chip Hits (H4ac ab, K562 cells)

|                                             | coef  | se    | z    | p       |
|---------------------------------------------|-------|-------|------|---------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.816 | 0.301 | 2.71 | 0.00673 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.985 | 0.276 | 3.58 | 0.00035 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 7575

Origin.of.data.set

AVR-E MSE-E

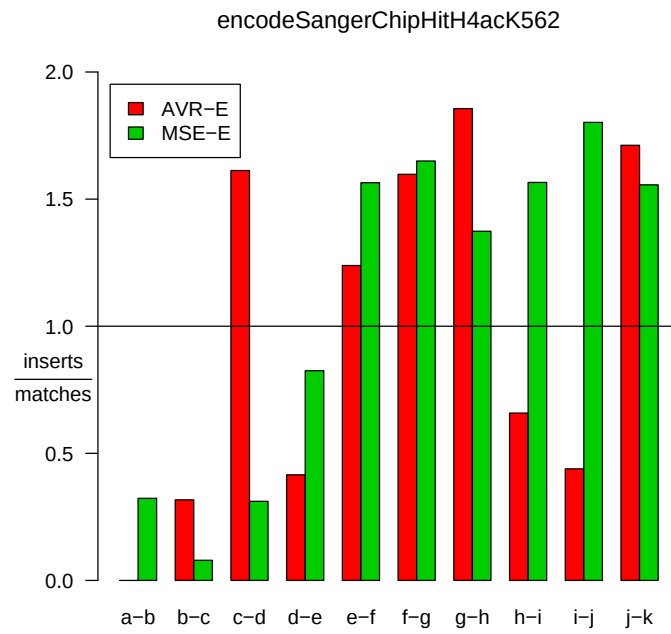
921 1030

Category limits

|   | lower    | category  | upper    |
|---|----------|-----------|----------|
| 1 | 0.122115 | insertion | 0.526304 |
| 2 | 0.526304 | match     | 0.659724 |

0.122 0.526 0.66 0.858 0.993 1.17 1.43 1.74 2.25  
3.28 11.7

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 0   | 3   | 13  | 5   | 11  | 14  | 18  | 7   | 4   | 17  |     |
|       | match     | 87  | 81  | 69  | 103 | 76  | 75  | 83  | 91  | 78  | 85  |     |
| MSE-E | insertion | 4   | 1   | 4   | 8   | 17  | 16  | 13  | 15  | 20  | 14  |     |
|       | match     | 106 | 108 | 110 | 83  | 93  | 83  | 81  | 82  | 95  | 77  |     |



NULL

NULL

## 2.119 encodeStanfordChipHCT116Sp1

NULL

Stan HCT116 Sp1

Stanford ChIP/chip (HCT116 cells, Sp1 ChIP)

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.0572 | 0.154 | -0.372 | 0.710 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.0777 | 0.148 | -0.527 | 0.598 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4978

Origin.of.data.set

AVR-E MSE-E

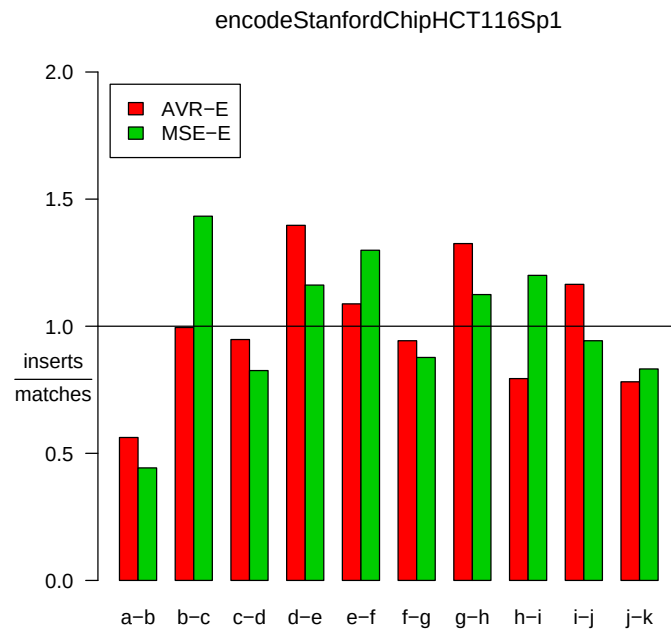
2143 2405

Category limits

|   | lower  | category  | upper   |
|---|--------|-----------|---------|
| 1 | 0.0797 | insertion | 0.42470 |
| 2 | 0.4247 | match     | 0.58098 |

0.0797 0.425 0.581 0.734 0.873 1.04 1.23 1.45  
1.76 2.24 29.7

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 13  | 21  | 20  | 28  | 24  | 20  | 26  | 16  | 21  | 15  |
|       | match     |     | 218 | 199 | 199 | 189 | 208 | 200 | 185 | 190 | 170 | 181 |
| MSE-E | insertion |     | 10  | 31  | 19  | 26  | 27  | 20  | 26  | 28  | 24  | 21  |
|       | match     |     | 213 | 204 | 217 | 211 | 196 | 215 | 218 | 220 | 240 | 238 |





## 2.120 encodeStanfordChipHCT116Sp3

NULL

Stan HCT116 Sp3

Stanford ChIP/chip (HCT116 cells, Sp3 ChIP)

|                                             | coef   | se    | z     | p      |
|---------------------------------------------|--------|-------|-------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.3430 | 0.157 | 2.180 | 0.0293 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.0657 | 0.143 | 0.458 | 0.6470 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4930

Origin.of.data.set

AVR-E MSE-E

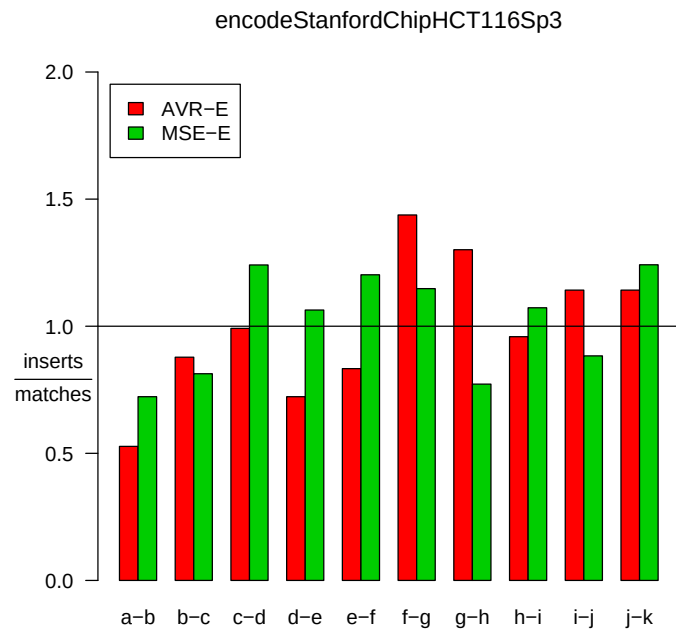
2162 2434

Category limits

|   | lower  | category  | upper  |
|---|--------|-----------|--------|
| 1 | 0.0909 | insertion | 0.5418 |
| 2 | 0.5418 | match     | 0.6820 |

0.0909 0.542 0.682 0.805 0.919 1.04 1.17 1.34  
1.57 1.92 28.8

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 11  | 20  | 21  | 16  | 18  | 28  | 27  | 20  | 22  | 22  |
|       | match     |     | 196 | 214 | 199 | 208 | 203 | 183 | 195 | 196 | 181 | 181 |
| MSE-E | insertion |     | 18  | 18  | 28  | 24  | 27  | 27  | 18  | 25  | 22  | 30  |
|       | match     |     | 234 | 208 | 212 | 212 | 211 | 221 | 219 | 219 | 234 | 227 |



## 2.121 encodeStanfordChipJurkatSp1

NULL

Stan Jurkat Sp1

Stanford ChIP/chip (Jurkat cells, Sp1 ChIP)

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.276 | 0.159 | 1.74 | 0.082600 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.557 | 0.150 | 3.72 | 0.000198 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4985

Origin.of.data.set

AVR-E MSE-E

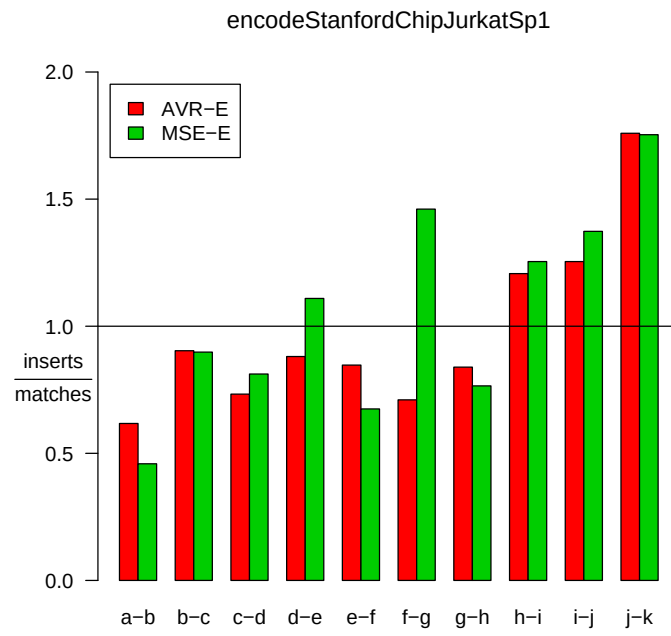
2143 2398

Category limits

|   | lower  | category  | upper  |
|---|--------|-----------|--------|
| 1 | 0.0673 | insertion | 0.3756 |
| 2 | 0.3756 | match     | 0.5388 |

0.0673 0.376 0.539 0.688 0.821 0.967 1.16 1.35  
1.63 2.16 22.7

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 11  | 16  | 14  | 19  | 18  | 17  | 19  | 25  | 28  | 37  |
|       | match     |     | 166 | 165 | 178 | 201 | 198 | 223 | 211 | 193 | 208 | 196 |
| MSE-E | insertion |     | 13  | 24  | 21  | 25  | 16  | 29  | 17  | 28  | 28  | 35  |
|       | match     |     | 264 | 249 | 241 | 210 | 221 | 185 | 207 | 208 | 190 | 186 |



## 2.122 encodeStanfordChipJurkatSp3

NULL

Stan Jurkat Sp3

Stanford ChIP/chip (Jurkat cells, Sp3 ChIP)

|                                             | coef  | se    | z    | p       |
|---------------------------------------------|-------|-------|------|---------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.283 | 0.158 | 1.79 | 0.07300 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.461 | 0.149 | 3.09 | 0.00202 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4992

Origin.of.data.set

AVR-E MSE-E

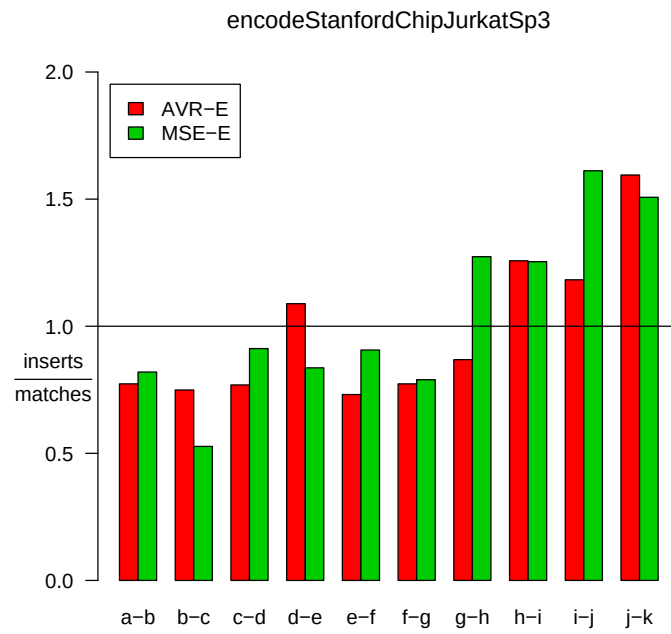
2138 2396

Category limits

|   | lower    | category  | upper    |
|---|----------|-----------|----------|
| 1 | 0.089100 | insertion | 0.413465 |
| 2 | 0.413465 | match     | 0.554400 |

0.0891 0.413 0.554 0.695 0.837 0.981 1.15 1.35  
1.66 2.26 15.5

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 14  | 13  | 15  | 21  | 16  | 19  | 19  | 29  | 26  | 33  |
|       | match     |     | 168 | 161 | 181 | 179 | 203 | 228 | 203 | 214 | 204 | 192 |
| MSE-E | insertion |     | 22  | 15  | 23  | 21  | 21  | 16  | 28  | 25  | 33  | 32  |
|       | match     |     | 249 | 264 | 234 | 233 | 215 | 188 | 204 | 185 | 190 | 197 |



## 2.123 encodeStanfordChipK562Sp1

NULL

Stan K562 Sp1

Stanford ChIP/chip (K562 cells, Sp1 ChIP)

|                                             | coef  | se    | z    | p       |
|---------------------------------------------|-------|-------|------|---------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.304 | 0.157 | 1.94 | 0.05230 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.384 | 0.145 | 2.64 | 0.00827 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4984

Origin.of.data.set

AVR-E MSE-E

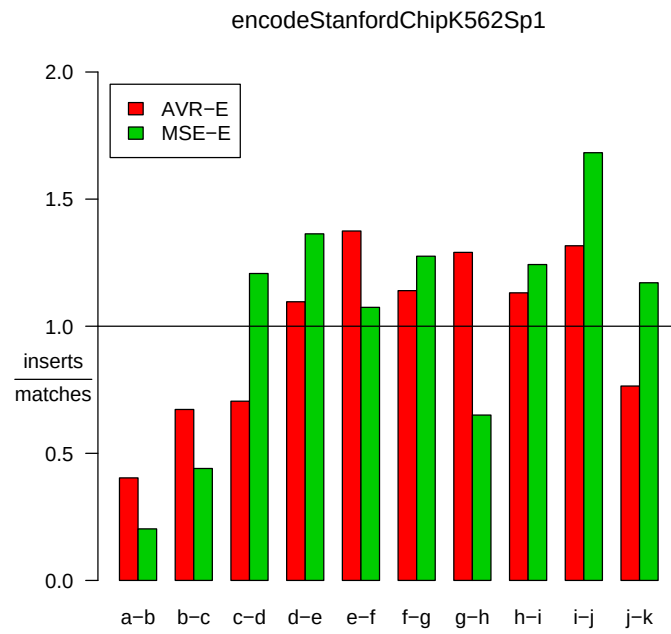
2138 2404

Category limits

|   | lower    | category  | upper    |
|---|----------|-----------|----------|
| 1 | 0.074100 | insertion | 0.386515 |
| 2 | 0.386515 | match     | 0.546760 |

0.0741 0.387 0.547 0.712 0.871 1.04 1.22 1.41  
1.68 2.16 11.9

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 9   | 14  | 14  | 22  | 27  | 23  | 27  | 25  | 26  | 16  |
|       | match     |     | 209 | 195 | 186 | 188 | 184 | 189 | 196 | 207 | 185 | 196 |
| MSE-E | insertion |     | 5   | 11  | 29  | 31  | 25  | 29  | 15  | 26  | 37  | 27  |
|       | match     |     | 231 | 234 | 225 | 213 | 218 | 213 | 216 | 196 | 206 | 216 |





## 2.124 encodeStanfordChipK562Sp3

NULL

Stan K562 Sp3

Stanford ChIP/chip (K562 cells, Sp3 ChIP)

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.644 | 0.161 | 4.01 | 6.17e-05 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.650 | 0.151 | 4.29 | 1.77e-05 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4989

Origin.of.data.set

AVR-E MSE-E

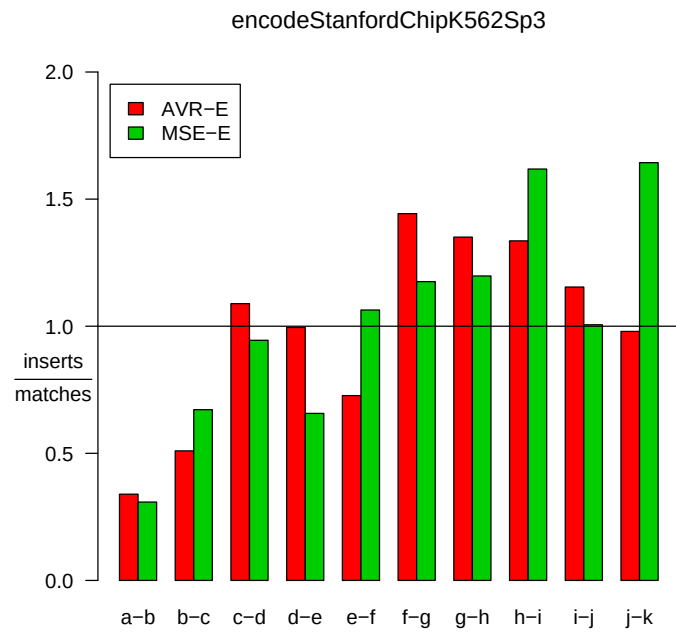
2138 2399

Category limits

|   | lower   | category  | upper   |
|---|---------|-----------|---------|
| 1 | 0.06880 | insertion | 0.42767 |
| 2 | 0.42767 | match     | 0.58184 |

0.0688 0.428 0.582 0.731 0.882 1.03 1.2 1.4 1.71  
2.24 43.6

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 7   | 11  | 22  | 20  | 15  | 29  | 27  | 25  | 27  | 20  |
|       | match     |     | 194 | 203 | 190 | 189 | 194 | 189 | 188 | 176 | 220 | 192 |
| MSE-E | insertion |     | 8   | 16  | 22  | 16  | 25  | 26  | 27  | 37  | 20  | 36  |
|       | match     |     | 244 | 224 | 219 | 229 | 221 | 208 | 212 | 215 | 187 | 206 |



## 2.125 encodeStanfordChipSmoothedHCT116Sp1

NULL

Stan Sc HCT116 Sp1

Stanford ChIP/chip Smoothed Score (HCT116 cells, Sp1 ChIP)

|                                             | coef    | se    | z      | p      |
|---------------------------------------------|---------|-------|--------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.3310  | 0.185 | 1.790  | 0.0727 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.0228 | 0.179 | -0.127 | 0.8990 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 6225

Origin.of.data.set

AVR-E MSE-E

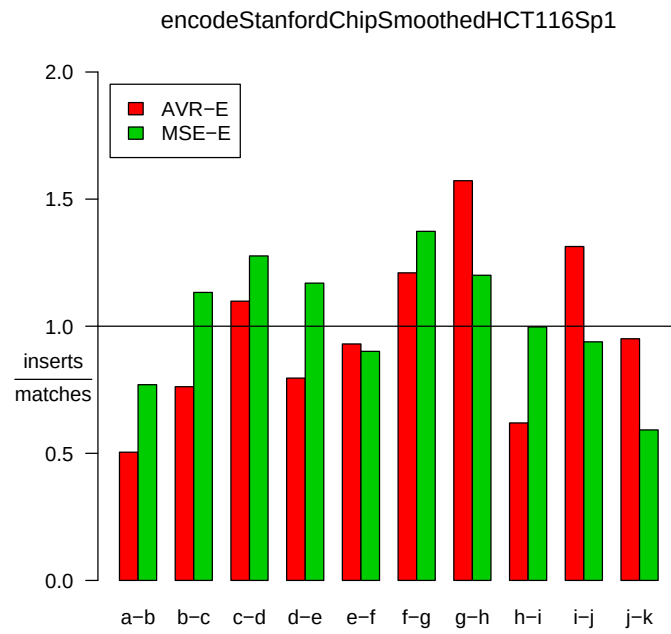
1598 1703

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0     | insertion | 1     |
| 2 | 1     | match     | 3     |

0 1 3 4 7 10 15 23 35 63 5830

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 6   | 16  | 10  | 17  | 14  | 21  | 25  | 10  | 22  | 15  |
|       | match     |     | 98  | 173 | 75  | 176 | 124 | 143 | 131 | 133 | 138 | 130 |
| MSE-E | insertion |     | 10  | 22  | 11  | 22  | 14  | 24  | 22  | 19  | 18  | 12  |
|       | match     |     | 107 | 160 | 71  | 155 | 128 | 144 | 151 | 157 | 158 | 167 |



## 2.126 encodeStanfordChipSmoothedHCT116Sp3

NULL

Stan Sc HCT116 Sp3

Stanford ChIP/chip Smoothed Score (HCT116 cells, Sp3 ChIP)

|                                             | coef  | se    | z    | p      |
|---------------------------------------------|-------|-------|------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.328 | 0.179 | 1.83 | 0.0673 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.251 | 0.171 | 1.47 | 0.1420 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 6225

Origin.of.data.set

AVR-E MSE-E

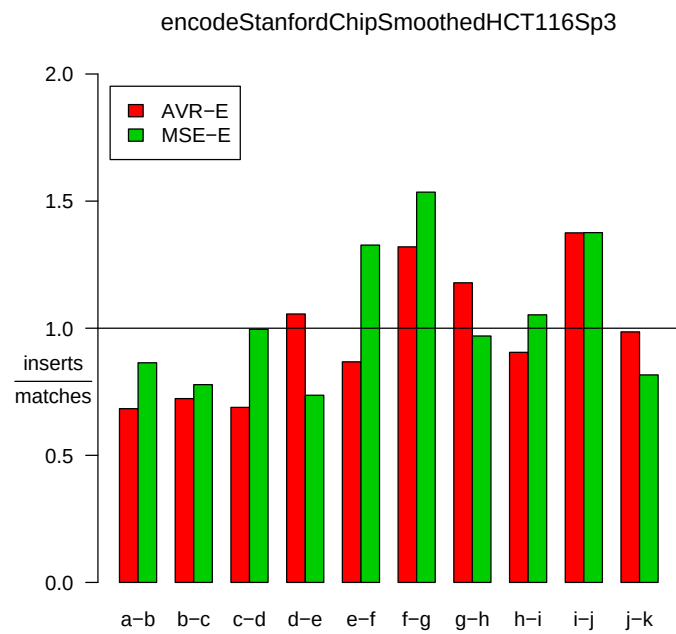
1598 1703

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0     | insertion | 1     |
| 2 | 1     | match     | 3     |

0 1 3 5 8 10 13 18 26 44 123000

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 6   | 14  | 13  | 24  | 12  | 20  | 18  | 16  | 21  | 16  |     |
|       | match     | 73  | 161 | 157 | 189 | 115 | 126 | 127 | 147 | 127 | 135 |     |
| MSE-E | insertion | 8   | 16  | 17  | 17  | 15  | 24  | 19  | 20  | 23  | 16  |     |
|       | match     | 77  | 171 | 142 | 192 | 94  | 130 | 163 | 158 | 139 | 163 |     |



## 2.127 encodeStanfordChipSmoothedJurkatSp1

NULL

Stan Sc Jurkat Sp1

Stanford ChIP/chip Smoothed Score (Jurkat cells, Sp1 ChIP)

|                                             | coef  | se    | z    | p       |
|---------------------------------------------|-------|-------|------|---------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.514 | 0.195 | 2.64 | 0.00829 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.308 | 0.178 | 1.73 | 0.08340 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 6225

Origin.of.data.set

AVR-E MSE-E

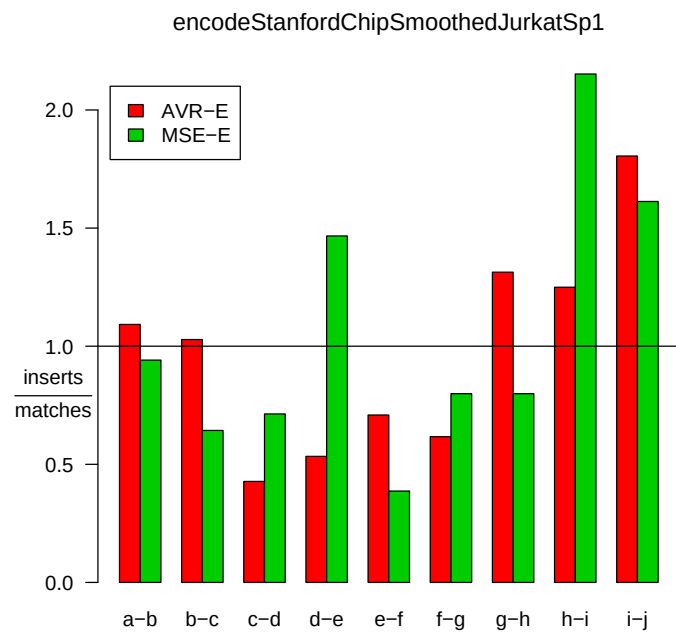
1598 1703

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0     | insertion | 1     |
| 2 | 1     | match     | 2     |

0 1 2 5 9 15 23 38 73 24600

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 16  | 10  | 8   | 9   | 13  | 12  | 27  | 24  | 30  |     |
|       | match     | 119 | 79  | 152 | 137 | 149 | 158 | 167 | 156 | 135 |     |
| MSE-E | insertion | 19  | 8   | 18  | 26  | 7   | 12  | 12  | 31  | 27  |     |
|       | match     | 164 | 101 | 205 | 144 | 147 | 122 | 122 | 117 | 136 |     |





## 2.128 encodeStanfordChipSmoothedJurkatSp3

NULL

Stan Sc Jurkat Sp3

Stanford ChIP/chip Smoothed Score (Jurkat cells, Sp3 ChIP)

|                                             | coef  | se    | z    | p       |
|---------------------------------------------|-------|-------|------|---------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.386 | 0.188 | 2.05 | 0.04030 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.708 | 0.183 | 3.87 | 0.00011 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 6225

Origin.of.data.set

AVR-E MSE-E

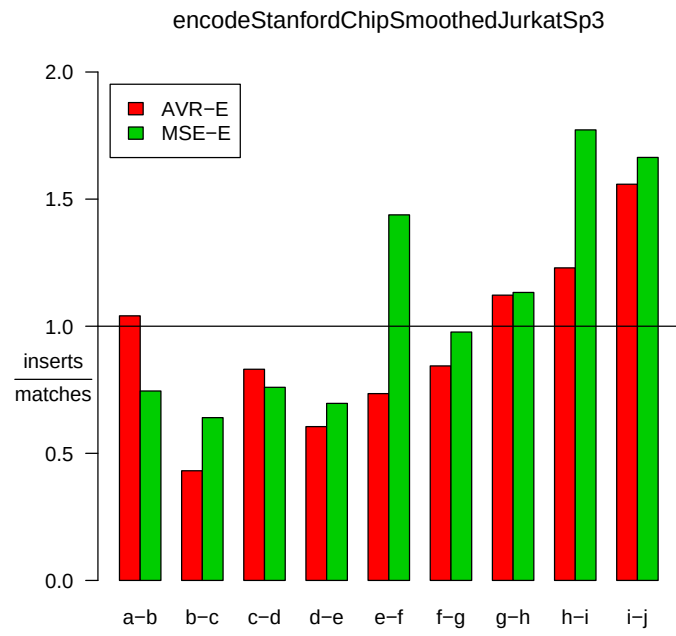
1598 1703

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0     | insertion | 1     |
| 2 | 1     | match     | 2     |

0 1 2 5 9 14 23 41 89 12500

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 16  | 5   | 15  | 11  | 13  | 14  | 23  | 24  | 27  |     |
|       | match     | 126 | 95  | 148 | 149 | 145 | 136 | 168 | 160 | 142 |     |
| MSE-E | insertion | 14  | 10  | 19  | 13  | 20  | 18  | 17  | 24  | 27  |     |
|       | match     | 154 | 128 | 205 | 153 | 114 | 151 | 123 | 111 | 133 |     |



## 2.129 encodeStanfordChipSmoothedK562Sp1

NULL

Stan Sc K562 Sp1

Stanford ChIP/chip Smoothed Score (K562 cells, Sp1 ChIP)

|                                             | coef  | se    | z    | p       |
|---------------------------------------------|-------|-------|------|---------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.573 | 0.193 | 2.96 | 0.00304 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.465 | 0.172 | 2.70 | 0.00699 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 6225

Origin.of.data.set

AVR-E MSE-E

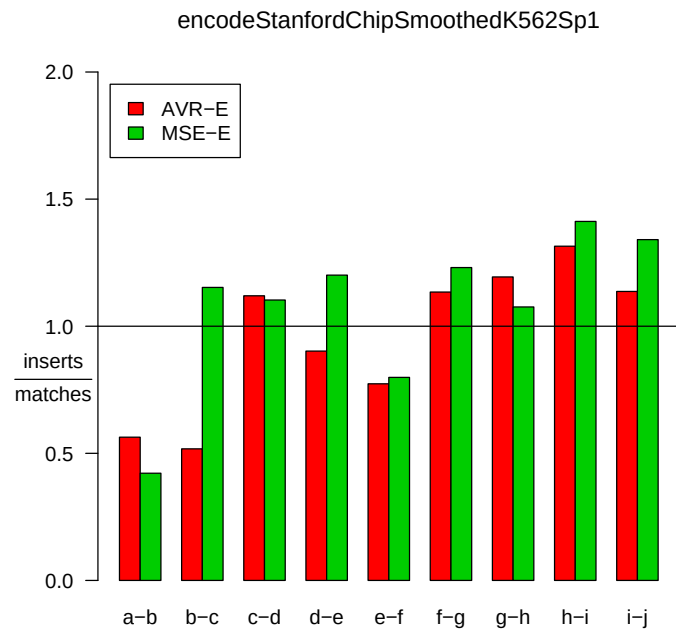
1598 1703

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0     | insertion | 2     |
| 2 | 2     | match     | 4     |

0 2 4 7 11 17 25 39 67 5890

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 11  | 7   | 16  | 16  | 15  | 22  | 23  | 26  | 19  |     |
|       | match     | 153 | 106 | 112 | 139 | 152 | 152 | 151 | 155 | 131 |     |
| MSE-E | insertion | 12  | 20  | 19  | 19  | 16  | 19  | 21  | 20  | 26  |     |
|       | match     | 223 | 136 | 135 | 124 | 157 | 121 | 153 | 111 | 152 |     |



## 2.130 encodeStanfordChipSmoothedK562Sp3

NULL

Stan Sc K562 Sp3

Stanford ChIP/chip Smoothed Score (K562 cells, Sp3 ChIP)

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.392 | 0.188 | 2.09 | 3.70e-02 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.731 | 0.177 | 4.13 | 3.67e-05 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 6225

Origin.of.data.set

AVR-E MSE-E

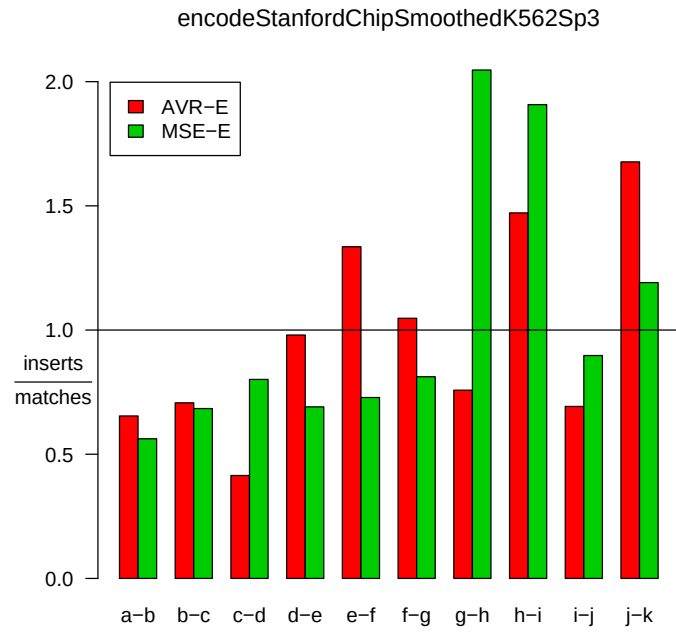
1598 1703

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0     | insertion | 1     |
| 2 | 1     | match     | 2     |

0 1 2 5 8 11 16 23 34 57 5670

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 8   | 6   | 9   | 17  | 17  | 20  | 14  | 27  | 14  | 27  |     |
|       | match     | 98  | 68  | 174 | 139 | 102 | 153 | 148 | 147 | 162 | 129 |     |
| MSE-E | insertion | 8   | 7   | 20  | 15  | 10  | 15  | 35  | 30  | 14  | 22  |     |
|       | match     | 114 | 82  | 200 | 174 | 110 | 148 | 137 | 126 | 125 | 148 |     |



## 2.131 encodeStanfordMethBe2C

NULL

Stan Meth Be2C

Stanford Methylation Digest (Be2C cells)

|                                             | coef   | se    | z     | p        |
|---------------------------------------------|--------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.875 | 0.169 | -5.17 | 2.31e-07 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.621 | 0.150 | -4.13 | 3.55e-05 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4942

Origin.of.data.set

AVR-E MSE-E

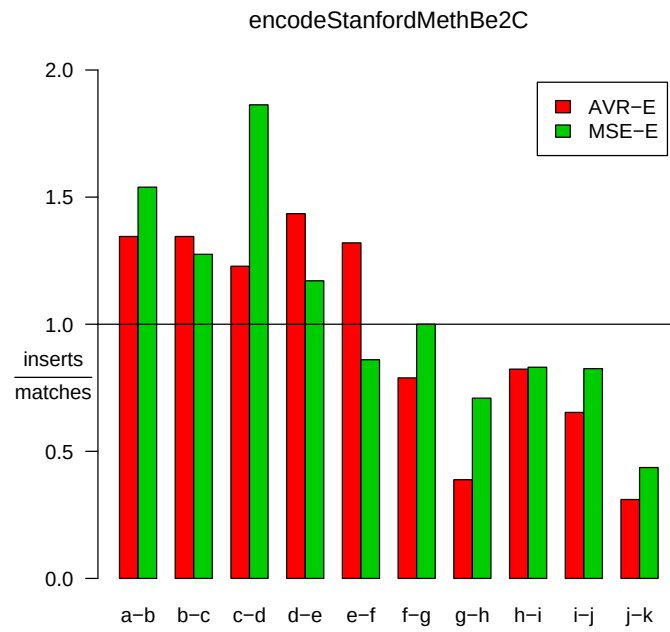
2157 2427

Category limits

|   | lower    | category  | upper    |
|---|----------|-----------|----------|
| 1 | 0.026500 | insertion | 0.429305 |
| 2 | 0.429305 | match     | 0.607460 |

0.0265 0.429 0.607 0.745 0.88 1.01 1.17 1.3 1.48  
1.71 8.28

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 27  | 30  | 27  | 32  | 30  | 16  | 8   | 16  | 12  | 6   |
|       | match     |     | 189 | 210 | 207 | 210 | 214 | 191 | 194 | 183 | 173 | 182 |
| MSE-E | insertion |     | 34  | 26  | 37  | 24  | 18  | 24  | 18  | 21  | 22  | 12  |
|       | match     |     | 208 | 192 | 187 | 193 | 197 | 226 | 239 | 238 | 251 | 259 |





## 2.132 encodeStanfordMethCRL1690

NULL

Stan Meth CRL1690

Stanford Methylation Digest (CRL1690 cells)

|                                             | coef   | se    | z     | p        |
|---------------------------------------------|--------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.600 | 0.162 | -3.69 | 2.24e-04 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.737 | 0.152 | -4.86 | 1.19e-06 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4947

Origin.of.data.set

AVR-E MSE-E

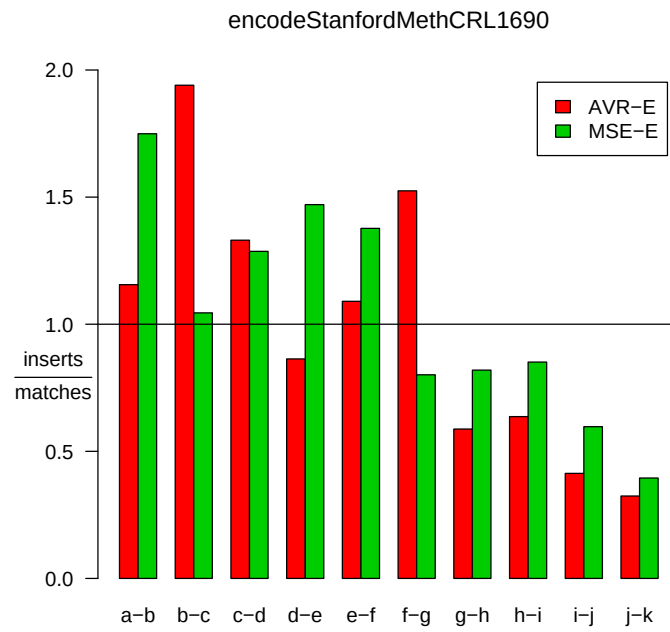
2157 2422

Category limits

|   | lower   | category  | upper   |
|---|---------|-----------|---------|
| 1 | 0.04320 | insertion | 0.43598 |
| 2 | 0.43598 | match     | 0.63802 |

0.0432 0.436 0.638 0.776 0.898 1.03 1.17 1.33  
1.54 1.84 18.5

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 22  | 39  | 30  | 18  | 24  | 30  | 13  | 13  | 8   | 7   |
|       | match     |     | 179 | 189 | 212 | 196 | 207 | 185 | 208 | 192 | 182 | 203 |
| MSE-E | insertion |     | 40  | 23  | 26  | 33  | 29  | 19  | 19  | 21  | 16  | 10  |
|       | match     |     | 215 | 207 | 190 | 211 | 198 | 223 | 218 | 232 | 252 | 238 |



## 2.133 encodeStanfordMethHCT116

NULL

Stan Meth HCT116

Stanford Methylation Digest (HCT116 cells)

|                                             | coef   | se    | z     | p        |
|---------------------------------------------|--------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.491 | 0.161 | -3.04 | 2.36e-03 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.601 | 0.150 | -4.01 | 6.11e-05 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4936

Origin.of.data.set

AVR-E MSE-E

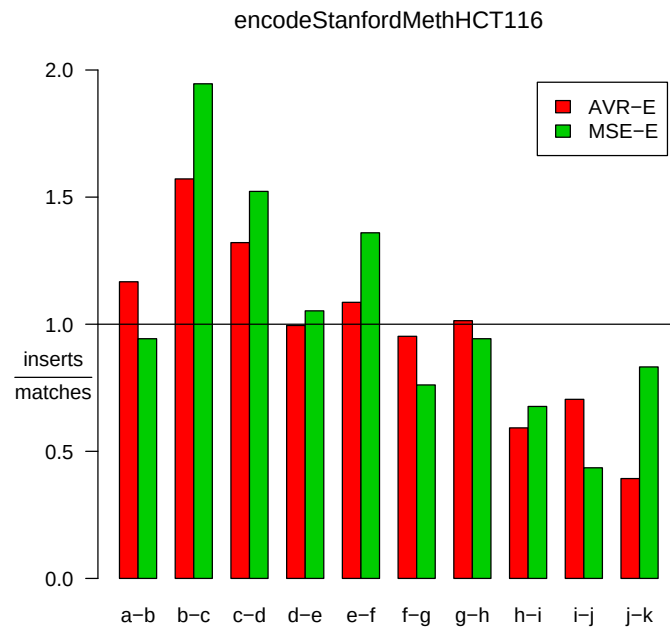
2159 2431

Category limits

|   | lower   | category  | upper   |
|---|---------|-----------|---------|
| 1 | 0.04060 | insertion | 0.53169 |
| 2 | 0.53169 | match     | 0.70749 |

0.0406 0.532 0.707 0.827 0.921 1.01 1.12 1.26  
1.49 1.92 14.6

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 25  | 33  | 29  | 21  | 22  | 20  | 20  | 13  | 13  | 8   |
|       | match     |     | 202 | 198 | 207 | 199 | 191 | 198 | 186 | 207 | 174 | 192 |
| MSE-E | insertion |     | 21  | 39  | 31  | 24  | 31  | 18  | 23  | 16  | 12  | 21  |
|       | match     |     | 210 | 189 | 192 | 215 | 215 | 223 | 230 | 223 | 260 | 238 |



## 2.134 encodeStanfordMethHepG2

NULL

Stan Meth HepG2

Stanford Methylation Digest (HepG2 cells)

|                                             | coef   | se    | z     | p        |
|---------------------------------------------|--------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.410 | 0.160 | -2.57 | 0.010200 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.614 | 0.149 | -4.13 | 0.000036 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4936

Origin.of.data.set

AVR-E MSE-E

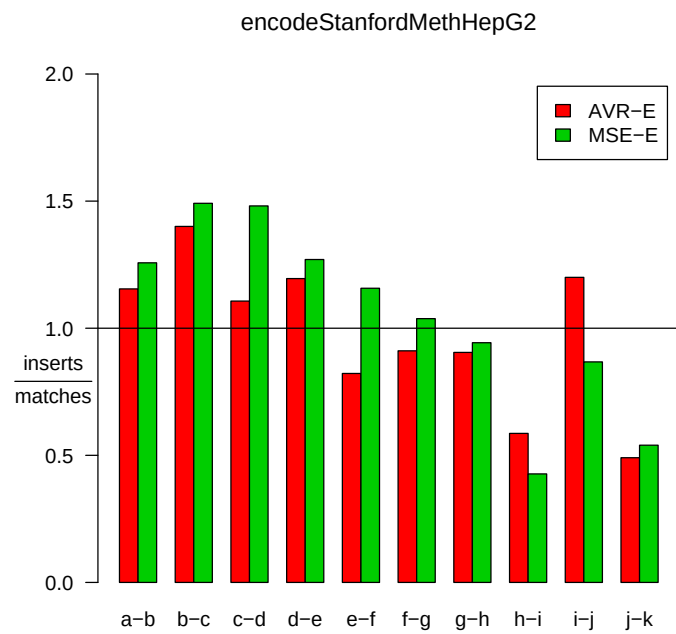
2159 2431

Category limits

|   | lower   | category  | upper   |
|---|---------|-----------|---------|
| 1 | 0.02570 | insertion | 0.49529 |
| 2 | 0.49529 | match     | 0.68150 |

0.0257 0.495 0.681 0.814 0.93 1.04 1.15 1.29 1.46  
1.76 12.3

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 24  | 30  | 25  | 27  | 17  | 20  | 19  | 12  | 21  | 9   |
|       | match     |     | 196 | 202 | 213 | 213 | 195 | 207 | 198 | 193 | 165 | 173 |
| MSE-E | insertion |     | 28  | 31  | 30  | 26  | 27  | 23  | 22  | 11  | 23  | 15  |
|       | match     |     | 210 | 196 | 191 | 193 | 220 | 209 | 220 | 243 | 250 | 262 |



## 2.135 encodeStanfordMethHT1080

NULL

Stan Meth HT1080

Stanford Methylation Digest (HT1080 cells)

|                                             | coef   | se    | z     | p        |
|---------------------------------------------|--------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.385 | 0.158 | -2.43 | 0.015000 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.514 | 0.146 | -3.53 | 0.000412 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4935

Origin.of.data.set

AVR-E MSE-E

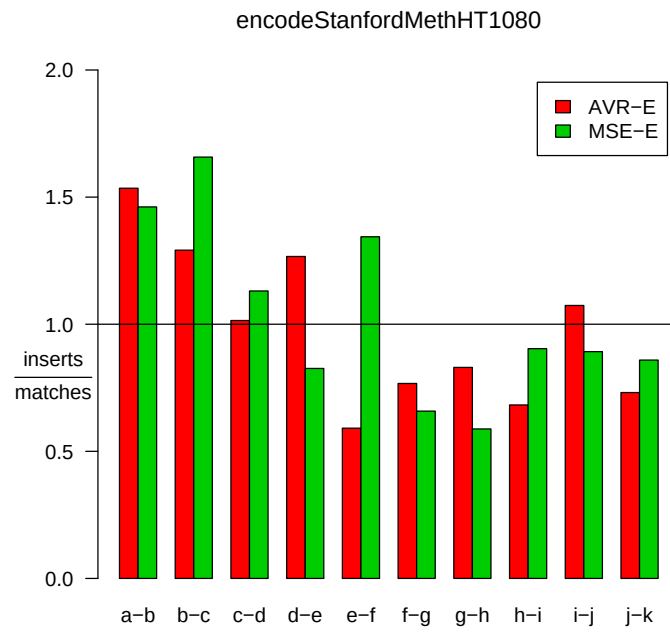
2159 2432

Category limits

|   | lower  | category  | upper  |
|---|--------|-----------|--------|
| 1 | 0.0214 | insertion | 0.5240 |
| 2 | 0.5240 | match     | 0.6944 |

0.0214 0.524 0.694 0.818 0.936 1.04 1.16 1.29  
1.45 1.73 6.99

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 31  | 28  | 22  | 28  | 12  | 15  | 18  | 14  | 21  | 15  |
|       | match     |     | 190 | 204 | 204 | 208 | 191 | 184 | 204 | 193 | 184 | 193 |
| MSE-E | insertion |     | 32  | 34  | 25  | 18  | 32  | 17  | 14  | 22  | 22  | 21  |
|       | match     |     | 206 | 193 | 208 | 205 | 224 | 243 | 224 | 229 | 232 | 230 |





## 2.136 encodeStanfordMethJEG3

NULL

Stan Meth JEG3

Stanford Methylation Digest (JEG3 cells)

|                                             | coef   | se    | z     | p       |
|---------------------------------------------|--------|-------|-------|---------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.404 | 0.160 | -2.53 | 0.01130 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.410 | 0.147 | -2.79 | 0.00531 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4936

Origin.of.data.set

AVR-E MSE-E

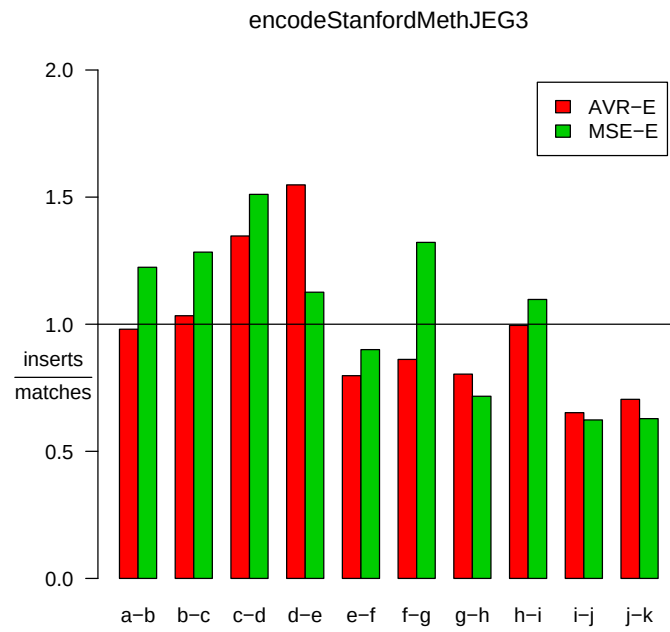
2159 2431

Category limits

|   | lower    | category  | upper    |
|---|----------|-----------|----------|
| 1 | 0.045300 | insertion | 0.448955 |
| 2 | 0.448955 | match     | 0.626800 |

0.0453 0.449 0.627 0.78 0.91 1.05 1.18 1.34 1.51  
1.77 3.43

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 21  | 24  | 31  | 33  | 17  | 18  | 15  | 19  | 13  | 13  |
|       | match     |     | 202 | 219 | 217 | 201 | 201 | 197 | 176 | 180 | 188 | 174 |
| MSE-E | insertion |     | 27  | 26  | 29  | 24  | 21  | 30  | 19  | 27  | 16  | 17  |
|       | match     |     | 208 | 191 | 181 | 201 | 220 | 214 | 250 | 232 | 242 | 255 |



## 2.137 encodeStanfordMethSmoothedBe2C

NULL

Stan Meth Sc Be2C

Stanford Methylation Digest Smoothed Score (Be2C cells)

|                                             | coef   | se    | z     | p        |
|---------------------------------------------|--------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.754 | 0.198 | -3.81 | 1.41e-04 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.781 | 0.183 | -4.27 | 1.96e-05 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 6225

Origin.of.data.set

AVR-E MSE-E

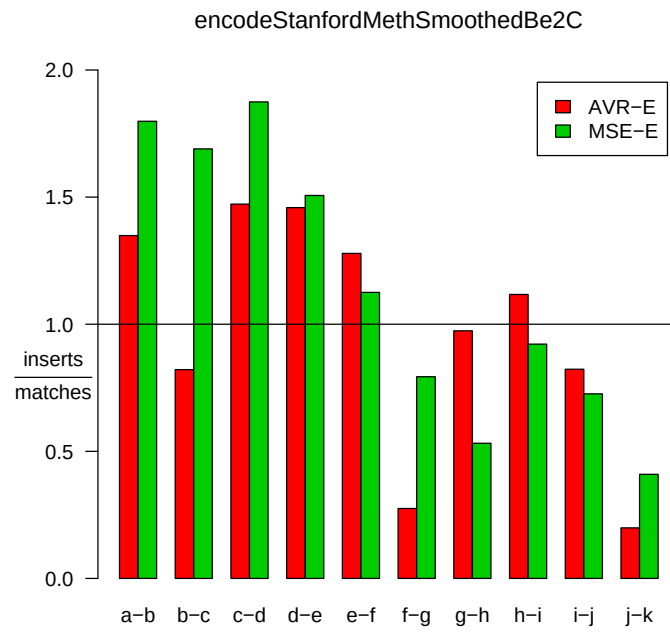
1598 1703

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0     | insertion | 1     |
| 2 | 1     | match     | 2     |

0 1 2 4 6 10 15 21 30 43.5 1710

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 12  | 9   | 27  | 22  | 24  | 4   | 13  | 16  | 10  | 3   |     |
|       | match     | 82  | 101 | 169 | 139 | 173 | 134 | 123 | 132 | 112 | 139 |     |
| MSE-E | insertion | 16  | 11  | 24  | 17  | 21  | 13  | 9   | 19  | 13  | 8   |     |
|       | match     | 82  | 60  | 118 | 104 | 172 | 151 | 156 | 190 | 165 | 180 |     |



## 2.138 encodeStanfordMethSmoothedCRL1690

NULL

Stan Meth Sc CRL1690

Stanford Methylation Digest Smoothed Score (CRL1690 cells)

|                                             | coef   | se    | z     | p        |
|---------------------------------------------|--------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.656 | 0.194 | -3.38 | 7.27e-04 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.797 | 0.185 | -4.32 | 1.57e-05 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 6225

Origin.of.data.set

AVR-E MSE-E

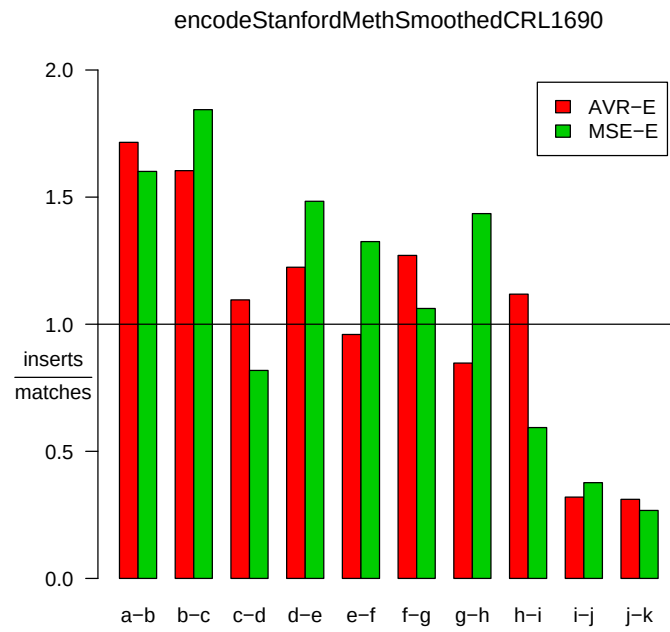
1598 1703

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0     | insertion | 1     |
| 2 | 1     | match     | 3     |

0 1 3 5 7 10 13 20 29 47 24100

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 12  | 27  | 20  | 19  | 15  | 15  | 15  | 11  | 5   | 5   |     |
|       | match     | 64  | 154 | 167 | 142 | 143 | 108 | 162 | 90  | 143 | 147 |     |
| MSE-E | insertion | 14  | 26  | 11  | 18  | 21  | 13  | 24  | 12  | 7   | 5   |     |
|       | match     | 80  | 129 | 123 | 111 | 145 | 112 | 153 | 185 | 170 | 171 |     |



## 2.139 encodeStanfordMethSmoothedHCT116

NULL

Stan Meth Sc HCT116

Stanford Methylation Digest Smoothed Score (HCT116 cells)

|                                             | coef   | se    | z     | p        |
|---------------------------------------------|--------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.634 | 0.196 | -3.23 | 1.25e-03 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.755 | 0.186 | -4.05 | 5.03e-05 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 6225

Origin.of.data.set

AVR-E MSE-E

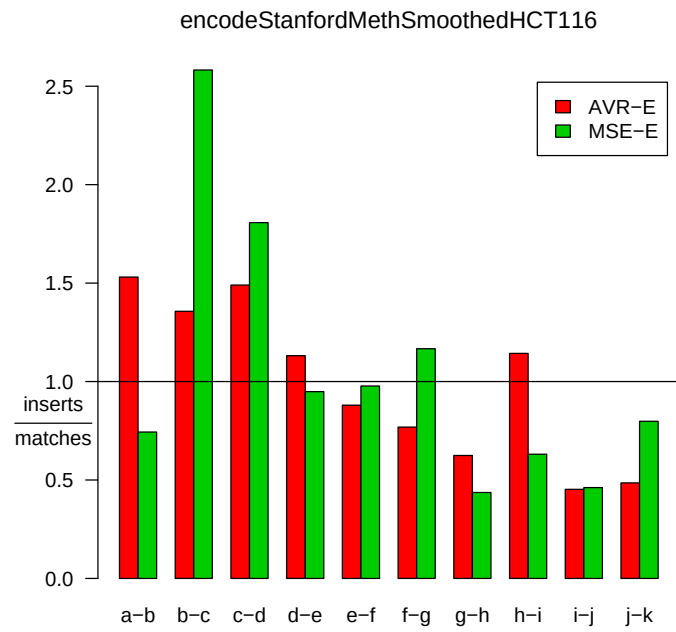
1598 1703

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0     | insertion | 1     |
| 2 | 1     | match     | 3     |

0 1 3 5 7 10 15 21 34 65 2900

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 12  | 28  | 28  | 18  | 14  | 14  | 9   | 17  | 6   | 8   |     |
|       | match     | 68  | 179 | 163 | 138 | 138 | 158 | 125 | 129 | 115 | 143 |     |
| MSE-E | insertion | 6   | 39  | 25  | 14  | 16  | 23  | 8   | 12  | 10  | 15  |     |
|       | match     | 70  | 131 | 120 | 128 | 142 | 171 | 159 | 165 | 188 | 163 |     |





## 2.140 encodeStanfordMethSmoothedHepG2

NULL

Stan Meth Sc HepG2

Stanford Methylation Digest Smoothed Score (HepG2 cells)

|                                             | coef   | se    | z     | p        |
|---------------------------------------------|--------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.407 | 0.189 | -2.16 | 3.08e-02 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -1.010 | 0.193 | -5.23 | 1.66e-07 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 6225

Origin.of.data.set

AVR-E MSE-E

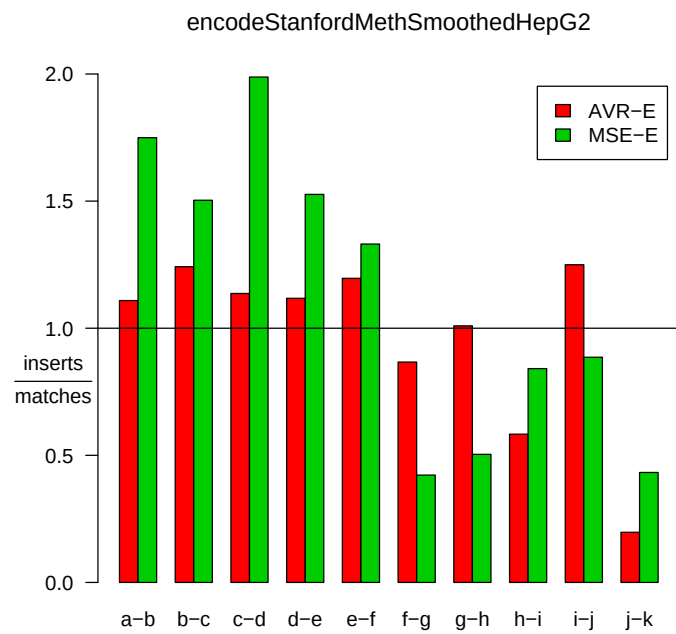
1598 1703

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0     | insertion | 1     |
| 2 | 1     | match     | 3     |

0 1 3 5 8 11 14 19 26 42 2790

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 9   | 23  | 23  | 23  | 16  | 11  | 18  | 8   | 17  | 3   |
|       | match     |     | 71  | 162 | 177 | 180 | 117 | 111 | 156 | 120 | 119 | 133 |
| MSE-E | insertion |     | 14  | 22  | 25  | 26  | 21  | 7   | 11  | 15  | 16  | 9   |
|       | match     |     | 70  | 128 | 110 | 149 | 138 | 145 | 191 | 156 | 158 | 182 |



## 2.141 encodeStanfordMethSmoothedHT1080

NULL

Stan Meth Sc HT1080

Stanford Methylation Digest Smoothed Score (HT1080 cells)

|                                             | coef   | se    | z     | p        |
|---------------------------------------------|--------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.368 | 0.183 | -2.01 | 0.044700 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.771 | 0.189 | -4.08 | 0.000045 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 6225

Origin.of.data.set

AVR-E MSE-E

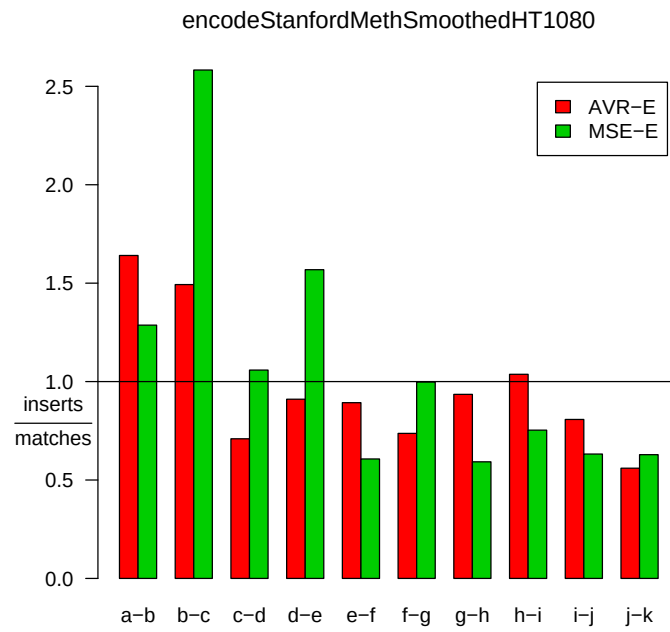
1598 1703

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0     | insertion | 1     |
| 2 | 1     | match     | 4     |

0 1 4 6 8 11 13 17 22 30 182

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 12  | 36  | 12  | 18  | 15  | 8   | 14  | 16  | 12  | 8   |     |
|       | match     | 64  | 211 | 148 | 173 | 147 | 95  | 131 | 135 | 130 | 125 |     |
| MSE-E | insertion | 10  | 49  | 15  | 19  | 12  | 13  | 13  | 13  | 13  | 12  |     |
|       | match     | 68  | 166 | 124 | 106 | 173 | 114 | 192 | 151 | 180 | 167 |     |



## 2.142 encodeStanfordMethSmoothedJEG3

NULL

Stan Meth Sc JEG3

Stanford Methylation Digest Smoothed Score (JEG3 cells)

|                                             | coef   | se    | z     | p        |
|---------------------------------------------|--------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.415 | 0.188 | -2.21 | 2.70e-02 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.763 | 0.190 | -4.02 | 5.71e-05 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 6225

Origin.of.data.set

AVR-E MSE-E

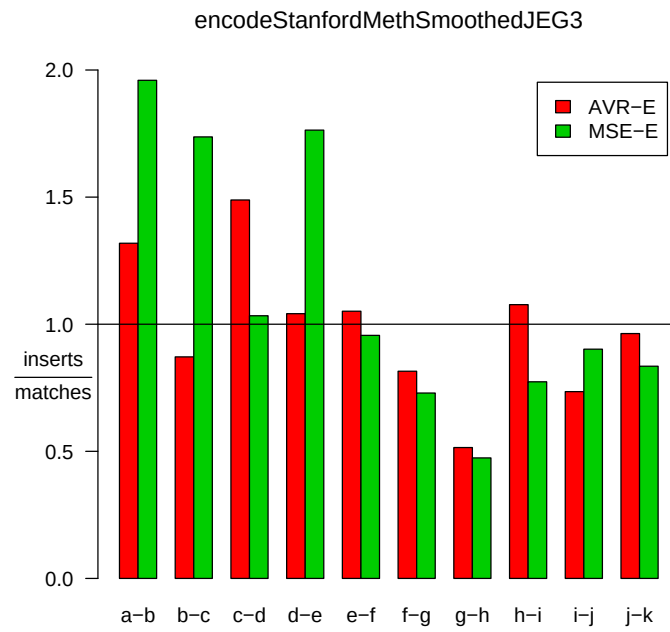
1598 1703

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0     | insertion | 1     |
| 2 | 1     | match     | 3     |

0 1 3 5 7 11 15 22 30 43 665

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 16  | 17  | 26  | 15  | 18  | 11  | 8   | 16  | 10  | 13  |     |
|       | match     | 107 | 172 | 154 | 127 | 151 | 119 | 137 | 131 | 120 | 119 |     |
| MSE-E | insertion | 16  | 26  | 15  | 18  | 18  | 11  | 10  | 15  | 18  | 16  |     |
|       | match     | 72  | 132 | 128 | 90  | 166 | 133 | 186 | 171 | 176 | 169 |     |



## 2.143 encodeStanfordMethSmoothedSnu182

NULL

Stan Meth Sc Snu182

Stanford Methylation Digest Smoothed Score (Snu182 cells)

|                                             | coef   | se    | z     | p        |
|---------------------------------------------|--------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.740 | 0.193 | -3.83 | 1.27e-04 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.734 | 0.185 | -3.96 | 7.54e-05 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 6225

Origin.of.data.set

AVR-E MSE-E

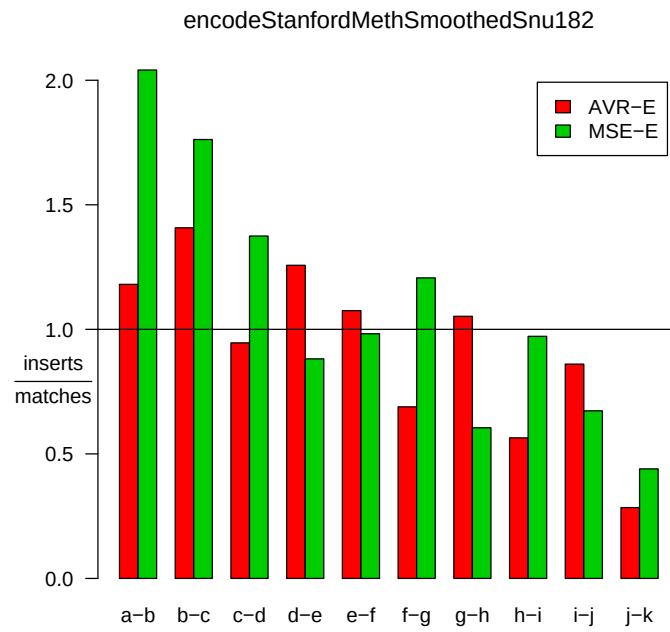
1598 1703

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0     | insertion | 2     |
| 2 | 2     | match     | 4     |

0 2 4 5 7 10 13 17 22 32 4760

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 22  | 28  | 8   | 24  | 22  | 10  | 16  | 8   | 12  | 4   |
|       | match     |     | 163 | 174 | 74  | 167 | 179 | 127 | 133 | 124 | 122 | 123 |
| MSE-E | insertion |     | 28  | 28  | 11  | 13  | 21  | 20  | 13  | 16  | 12  | 9   |
|       | match     |     | 120 | 139 | 70  | 129 | 187 | 145 | 188 | 144 | 156 | 179 |





## 2.144 encodeStanfordMethSmoothedU87

NULL

Stan Meth Sc U87

Stanford Methylation Digest Smoothed Score (U87 cells)

|                                             | coef   | se    | z     | p        |
|---------------------------------------------|--------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.419 | 0.186 | -2.26 | 0.024000 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.627 | 0.181 | -3.45 | 0.000554 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 6225

Origin.of.data.set

AVR-E MSE-E

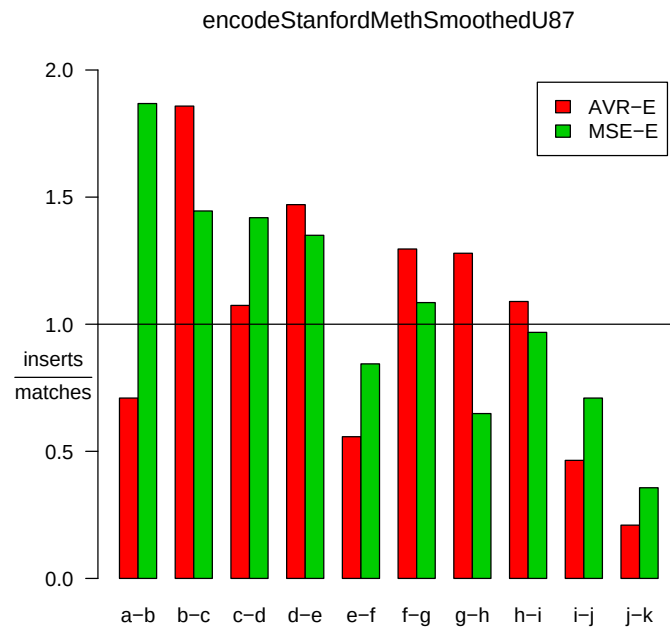
1598 1703

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0     | insertion | 1     |
| 2 | 1     | match     | 3     |

0 1 3 5 7 10 13 17 24 37 4810

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 5   | 28  | 17  | 22  | 11  | 17  | 19  | 15  | 7   | 3   |     |
|       | match     | 65  | 139 | 146 | 138 | 182 | 121 | 137 | 127 | 139 | 132 |     |
| MSE-E | insertion | 16  | 21  | 20  | 18  | 14  | 16  | 9   | 17  | 13  | 7   |     |
|       | match     | 79  | 134 | 130 | 123 | 153 | 136 | 128 | 162 | 169 | 181 |     |



## 2.145 encodeStanfordMethSnu182

NULL

Stan Meth Snu182

Stanford Methylation Digest (Snu182 cells)

|                                             | coef   | se    | z     | p        |
|---------------------------------------------|--------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.308 | 0.157 | -1.96 | 4.98e-02 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.596 | 0.146 | -4.07 | 4.62e-05 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4939

Origin.of.data.set

AVR-E MSE-E

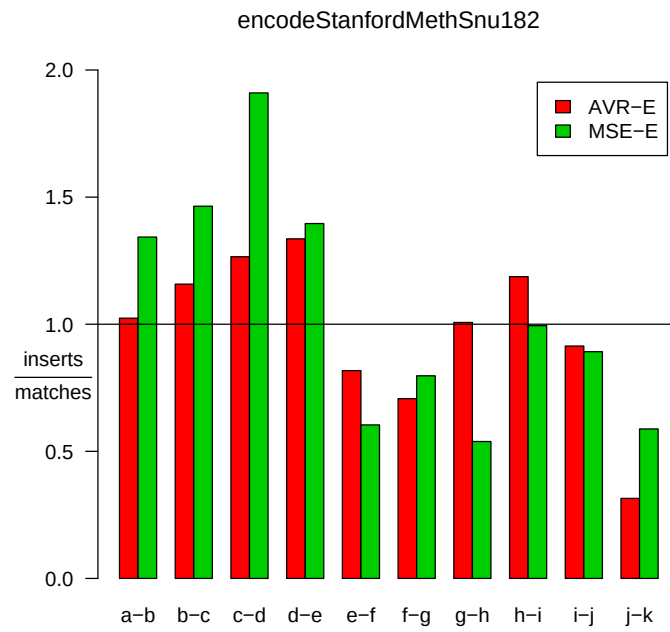
2159 2428

Category limits

|   | lower  | category  | upper  |
|---|--------|-----------|--------|
| 1 | 0.0468 | insertion | 0.4881 |
| 2 | 0.4881 | match     | 0.6784 |

0.0468 0.488 0.678 0.805 0.911 1.02 1.13 1.24  
1.38 1.64 15.1

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 22  | 25  | 28  | 28  | 18  | 14  | 21  | 23  | 18  | 6   |
|       | match     |     | 203 | 204 | 209 | 198 | 208 | 187 | 197 | 183 | 186 | 180 |
| MSE-E | insertion |     | 29  | 31  | 37  | 30  | 14  | 20  | 13  | 24  | 22  | 16  |
|       | match     |     | 204 | 200 | 183 | 203 | 219 | 237 | 228 | 228 | 233 | 257 |



## 2.146 encodeStanfordMethU87

NULL

Stan Meth U87

Stanford Methylation Digest (U87 cells)

|                                             | coef   | se    | z     | p        |
|---------------------------------------------|--------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.608 | 0.160 | -3.79 | 1.49e-04 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.623 | 0.149 | -4.19 | 2.73e-05 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4940

Origin.of.data.set

AVR-E MSE-E

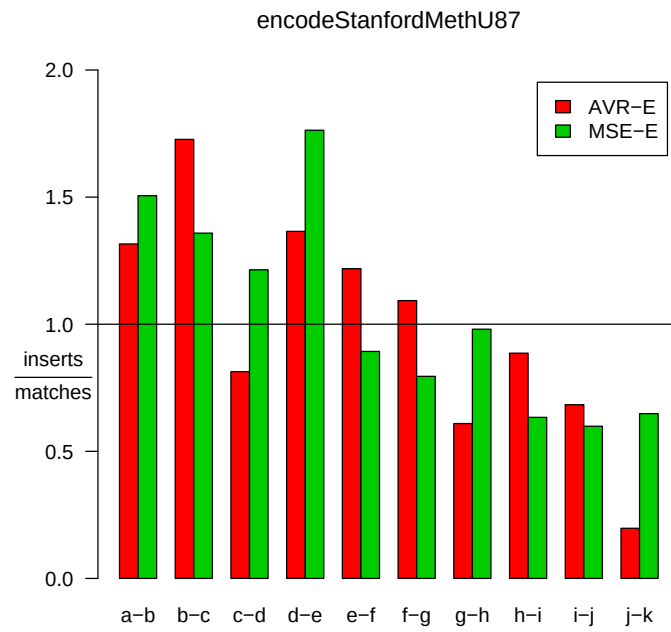
2159 2427

Category limits

|   | lower   | category  | upper   |
|---|---------|-----------|---------|
| 1 | 0.02310 | insertion | 0.43465 |
| 2 | 0.43465 | match     | 0.62880 |

0.0231 0.435 0.629 0.767 0.892 1.02 1.16 1.31  
1.47 1.72 15.3

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 25  | 33  | 19  | 30  | 26  | 21  | 13  | 19  | 14  | 4   |
|       | match     |     | 179 | 180 | 220 | 207 | 201 | 181 | 201 | 202 | 193 | 191 |
| MSE-E | insertion |     | 35  | 31  | 25  | 35  | 20  | 20  | 23  | 15  | 15  | 17  |
|       | match     |     | 219 | 215 | 194 | 187 | 211 | 237 | 221 | 223 | 236 | 247 |



NULL

NULL

## 2.147 encodeUCDavisChipMyc

NULL

UCD C-Myc

UC Davis ChIP/Chip NimbleGen (C-Myc ab, HeLa Cells)

|                                             | coef   | se    | z    | p      |
|---------------------------------------------|--------|-------|------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.0731 | 0.156 | 0.47 | 0.6380 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.2480 | 0.141 | 1.76 | 0.0776 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4826

Origin.of.data.set

AVR-E MSE-E

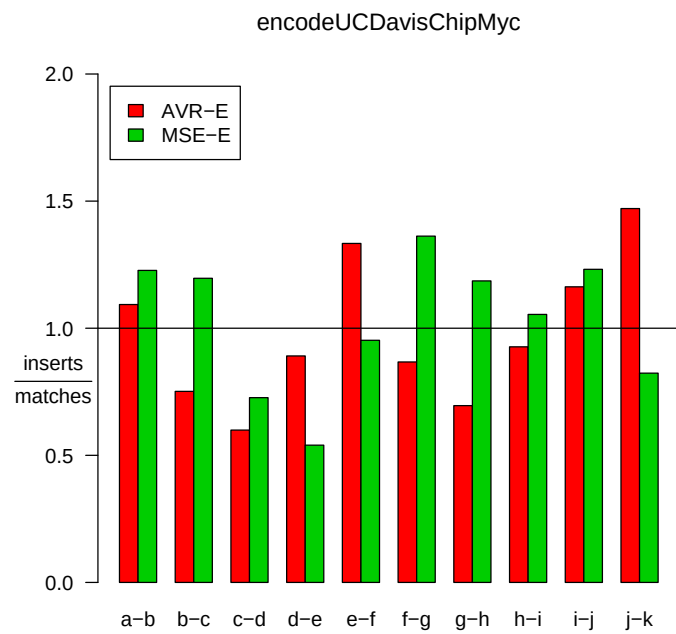
2210 2490

Category limits

|   | lower   | category  | upper   |
|---|---------|-----------|---------|
| 1 | -3.0000 | insertion | -0.6155 |
| 2 | -0.6155 | match     | -0.3500 |

-3 -0.616 -0.35 -0.2 -0.1 0 0.08 0.185 0.32 0.65  
3.51

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 25  | 16  | 12  | 20  | 26  | 17  | 14  | 21  | 25  | 31  |
|       | match     |     | 217 | 202 | 190 | 213 | 185 | 186 | 191 | 215 | 204 | 200 |
| MSE-E | insertion |     | 26  | 29  | 18  | 14  | 26  | 29  | 29  | 24  | 27  | 19  |
|       | match     |     | 201 | 230 | 235 | 246 | 259 | 202 | 232 | 216 | 208 | 219 |





## 2.148 encodeUCDavisE2F1Median

NULL

UCD E2F1

UC Davis ChIP/Chip NimbleGen (E2F1 ab, HeLa Cells)

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.2290 | 0.155 | -1.480 | 0.140 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.0645  | 0.144 | 0.447  | 0.655 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4857

Origin.of.data.set

AVR-E MSE-E

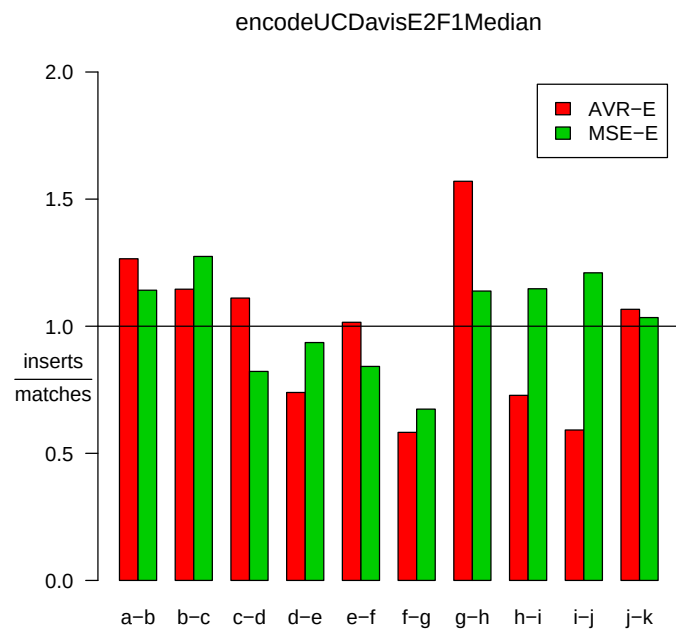
2199 2470

Category limits

|   | lower | category  | upper  |
|---|-------|-----------|--------|
| 1 | -1.65 | insertion | -0.330 |
| 2 | -0.33 | match     | -0.195 |

-1.65 -0.33 -0.195 -0.11 -0.05 0 0.055 0.11 0.17  
0.28 2.89

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 27  | 23  | 23  | 15  | 19  | 12  | 34  | 15  | 13  | 25  |     |
|       | match     | 203 | 191 | 197 | 193 | 178 | 196 | 206 | 196 | 209 | 223 |     |
| MSE-E | insertion | 27  | 28  | 21  | 24  | 20  | 17  | 28  | 24  | 29  | 20  |     |
|       | match     | 225 | 209 | 243 | 244 | 226 | 240 | 234 | 199 | 228 | 184 |     |



## 2.149 encodeUcsdChipAch3Imr90<sub>f</sub>

NULL

LI H3ac IMR90

Ludwig Institute ChIP/Chip: H3ac ab, IMR90 cells

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.387 | 0.170 | 2.27 | 0.023100 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.528 | 0.157 | 3.37 | 0.000753 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5397

Origin.of.data.set

AVR-E MSE-E

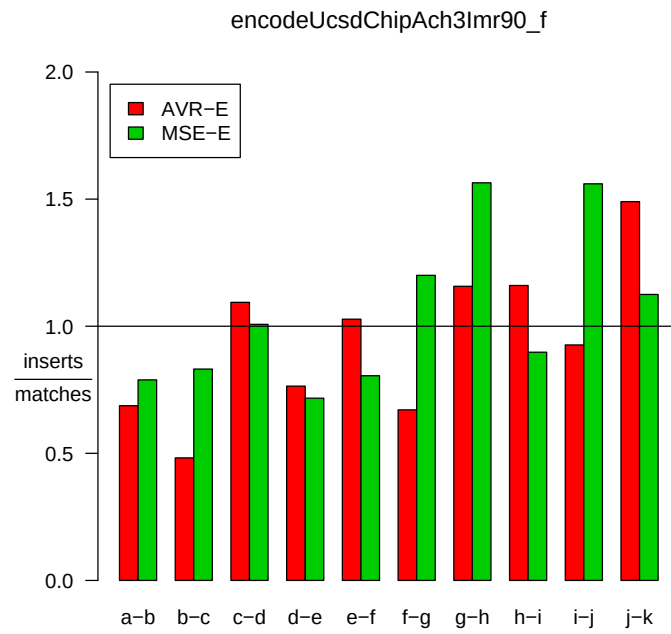
1973 2156

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.00  | insertion | 0.01  |
| 2 | 0.01  | match     | 0.03  |

0 0.01 0.03 0.06 0.11 0.19 0.3 0.48 0.79 1.34  
14.3

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 8   | 9   | 15  | 17  | 18  | 15  | 24  | 25  | 19  | 34  |
|       | match     |     | 101 | 162 | 119 | 193 | 152 | 194 | 180 | 187 | 178 | 198 |
| MSE-E | insertion |     | 17  | 16  | 13  | 19  | 18  | 26  | 31  | 18  | 32  | 21  |
|       | match     |     | 187 | 167 | 112 | 230 | 194 | 188 | 172 | 174 | 178 | 162 |



## 2.150 encodeUcsdChipH3K27me3

NULL

LI H3K27me3 HeLa

Ludwig Institute ChIP/Chip: H3K27me3 ab, HeLa cells

|                                             | coef   | se    | z     | p        |
|---------------------------------------------|--------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.888 | 0.172 | -5.17 | 2.33e-07 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.912 | 0.162 | -5.64 | 1.69e-08 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5380

Origin.of.data.set

AVR-E MSE-E

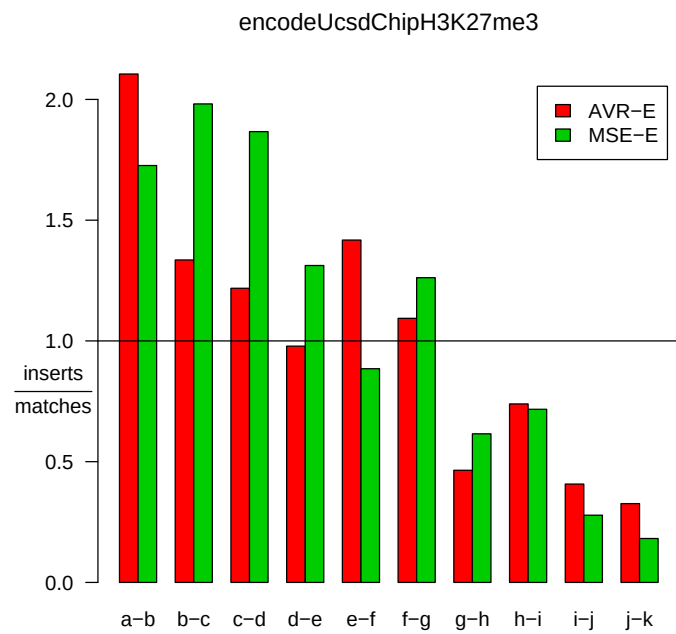
1985 2161

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.00  | insertion | 0.04  |
| 2 | 0.04  | match     | 0.09  |

0 0.04 0.09 0.15 0.22 0.3 0.38 0.52 0.78 1.63 16

|       | set       | type | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |      | 33  | 25  | 24  | 18  | 25  | 20  | 9   | 14  | 9   | 7   |     |
|       | match     |      | 144 | 172 | 181 | 169 | 162 | 168 | 178 | 174 | 203 | 197 |     |
| MSE-E | insertion |      | 28  | 33  | 38  | 28  | 21  | 25  | 14  | 16  | 6   | 4   |     |
|       | match     |      | 149 | 153 | 187 | 196 | 218 | 182 | 209 | 205 | 198 | 202 |     |



## 2.151 encodeUcsdChipHeLaH3H4acH3<sub>p</sub>0

NULL

LI H3ac -gIF

Ludwig Institute ChIP/Chip: H3ac ab, HeLa cells, no gamma interferon

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.727 | 0.170 | 4.28 | 1.83e-05 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.616 | 0.155 | 3.96 | 7.48e-05 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5380

Origin.of.data.set

AVR-E MSE-E

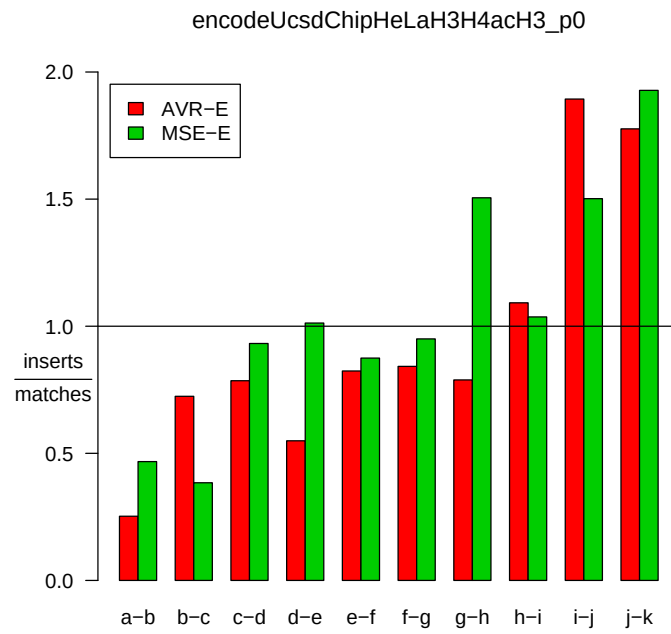
1985 2161

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.00  | insertion | 0.05  |
| 2 | 0.05  | match     | 0.10  |

0 0.05 0.1 0.16 0.22 0.29 0.37 0.47 0.66 1.25 16

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 5   | 15  | 16  | 10  | 18  | 16  | 14  | 21  | 39  | 38  |
|       | match     |     | 174 | 182 | 179 | 160 | 192 | 167 | 156 | 169 | 181 | 188 |
| MSE-E | insertion |     | 10  | 8   | 21  | 25  | 21  | 24  | 31  | 23  | 27  | 34  |
|       | match     |     | 188 | 183 | 198 | 217 | 211 | 222 | 181 | 195 | 158 | 155 |





## 2.152 encodeUcsdChipHeLaH3H4acH3<sub>p</sub>30

NULL

LI H3ac +gIF

Ludwig Institute ChIP/Chip: H3ac ab, HeLa cells, 30 min. after gamma interferon

|                                             | coef | se    | z    | p        |
|---------------------------------------------|------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.55 | 0.167 | 3.30 | 0.000961 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.56 | 0.154 | 3.63 | 0.000286 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5380

Origin.of.data.set

AVR-E MSE-E

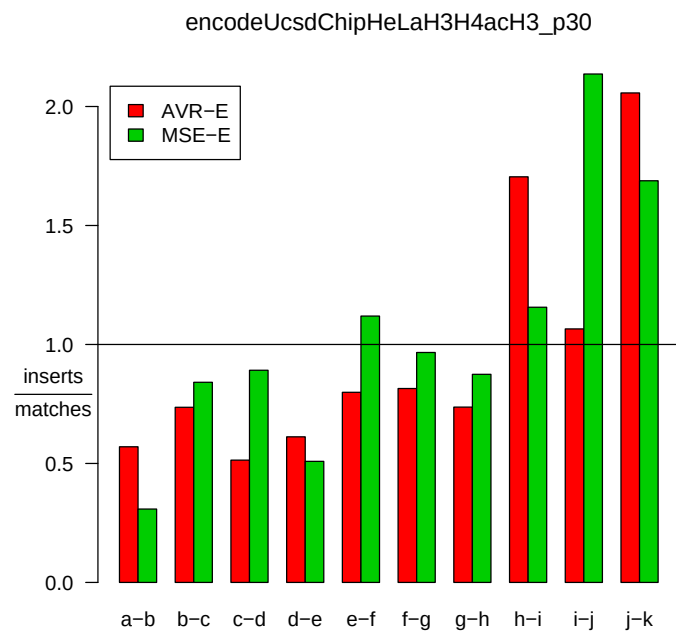
1985 2161

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.00  | insertion | 0.05  |
| 2 | 0.05  | match     | 0.11  |

0 0.05 0.11 0.17 0.23 0.3 0.37 0.48 0.66 1.28 16

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 12  | 17  | 10  | 11  | 19  | 14  | 14  | 32  | 20  | 44  |
|       | match     |     | 185 | 203 | 171 | 158 | 209 | 151 | 167 | 165 | 165 | 188 |
| MSE-E | insertion |     | 6   | 20  | 21  | 11  | 27  | 21  | 20  | 25  | 44  | 29  |
|       | match     |     | 171 | 209 | 207 | 190 | 212 | 191 | 201 | 190 | 181 | 151 |



## 2.153 encodeUcsdChipHeLaH3H4acH4<sub>p</sub>0

NULL

LI H4ac -gIF

Ludwig Institute ChIP/Chip: H4ac ab, HeLa cells, no gamma interferon

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.1380 | 0.164 | -0.839 | 0.402 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.0195 | 0.150 | -0.130 | 0.896 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5380

Origin.of.data.set

AVR-E MSE-E

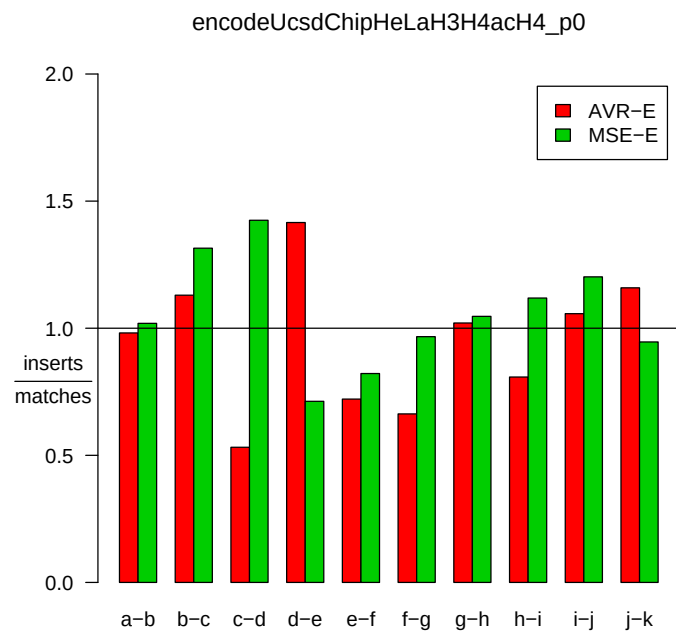
1985 2161

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.00  | insertion | 0.04  |
| 2 | 0.04  | match     | 0.09  |

0 0.04 0.09 0.15 0.21 0.28 0.35 0.45 0.58 0.94 16

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 19  | 20  | 11  | 26  | 15  | 11  | 21  | 16  | 20  | 25  |
|       | match     |     | 175 | 160 | 187 | 166 | 188 | 150 | 186 | 179 | 171 | 195 |
| MSE-E | insertion |     | 23  | 24  | 29  | 16  | 19  | 20  | 22  | 25  | 25  | 18  |
|       | match     |     | 204 | 165 | 184 | 203 | 209 | 187 | 190 | 202 | 188 | 172 |



## 2.154 encodeUcsdChipHeLaH3H4acH4<sub>p</sub>30

NULL

LI H4ac +gIF

Ludwig Institute ChIP/Chip: H4ac ab, HeLa cells, 30 min. after gamma interferon

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.0788  | 0.163 | 0.484  | 0.628 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.1890 | 0.149 | -1.270 | 0.204 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5380

Origin.of.data.set

AVR-E MSE-E

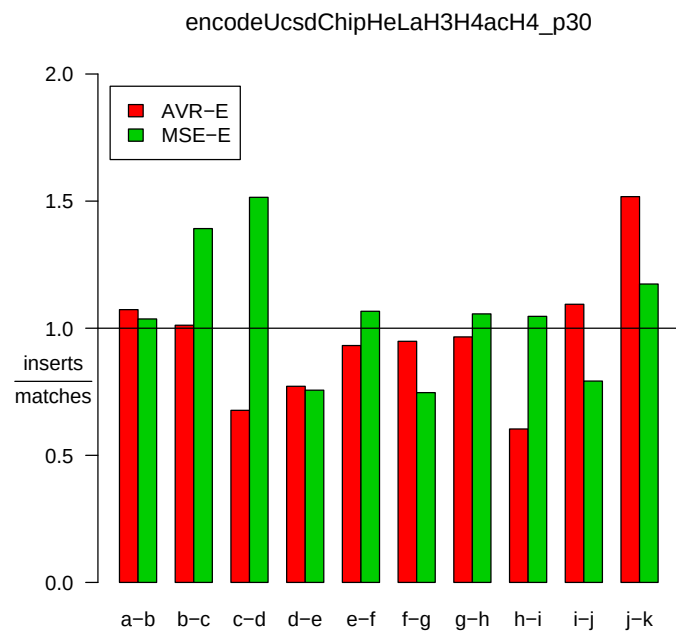
1985 2161

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.00  | insertion | 0.04  |
| 2 | 0.04  | match     | 0.07  |

0 0.04 0.07 0.11 0.16 0.21 0.29 0.39 0.6 1.03  
11.2

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 24  | 16  | 13  | 19  | 18  | 18  | 18  | 12  | 22  | 30  |     |
|       | match     | 198 | 140 | 170 | 218 | 171 | 168 | 165 | 176 | 178 | 175 |     |
| MSE-E | insertion | 24  | 25  | 32  | 17  | 20  | 21  | 21  | 24  | 17  | 24  |     |
|       | match     | 205 | 159 | 187 | 199 | 166 | 249 | 176 | 203 | 190 | 181 |     |



## 2.155 encodeUcsdChipHeLaH3H4dmH3K4<sub>p</sub>0

NULL

LI H3K4me2 -gIF

Ludwig Institute ChIP/Chip: H3K4me2 ab, HeLa cells, no gamma interferon

|                                             | coef   | se    | z     | p     |
|---------------------------------------------|--------|-------|-------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.172  | 0.162 | 1.06  | 0.288 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.179 | 0.151 | -1.19 | 0.235 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5380

Origin.of.data.set

AVR-E MSE-E

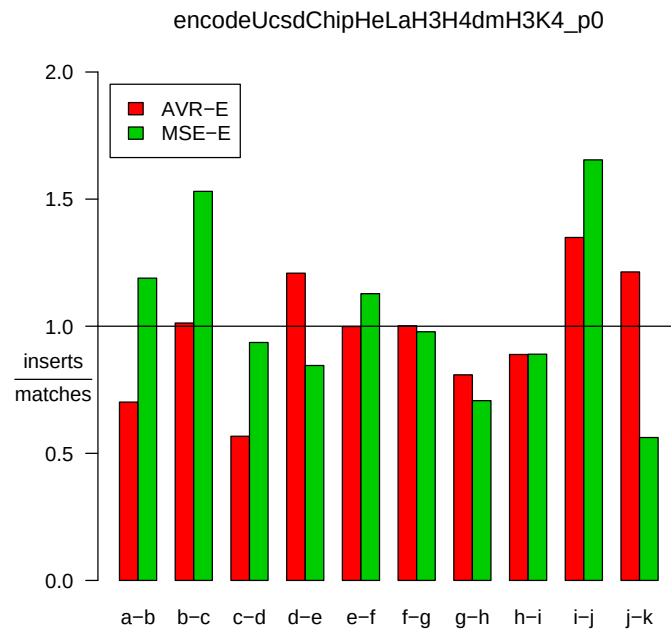
1985 2161

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.00  | insertion | 0.05  |
| 2 | 0.05  | match     | 0.10  |

0 0.05 0.1 0.15 0.2 0.27 0.34 0.47 0.71 1.16 13.1

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 16  | 18  | 13  | 20  | 22  | 14  | 17  | 16  | 27  | 27  |
|       | match     |     | 204 | 159 | 205 | 148 | 197 | 125 | 188 | 161 | 179 | 199 |
| MSE-E | insertion |     | 23  | 32  | 18  | 19  | 28  | 21  | 17  | 20  | 32  | 11  |
|       | match     |     | 173 | 187 | 172 | 201 | 222 | 192 | 215 | 201 | 173 | 175 |





## 2.156 encodeUcsdChipHeLaH3H4dmH3K4<sub>p</sub>30

NULL

LI H3K4me2 +gIF

Ludwig Institute ChIP/Chip: H3K4me2 ab, HeLa cells, 30 min. after gamma interferon

|                                             | coef   | se   | z     | p     |
|---------------------------------------------|--------|------|-------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.1310 | 0.16 | 0.815 | 0.415 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.0325 | 0.15 | 0.216 | 0.829 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5380

Origin.of.data.set

AVR-E MSE-E

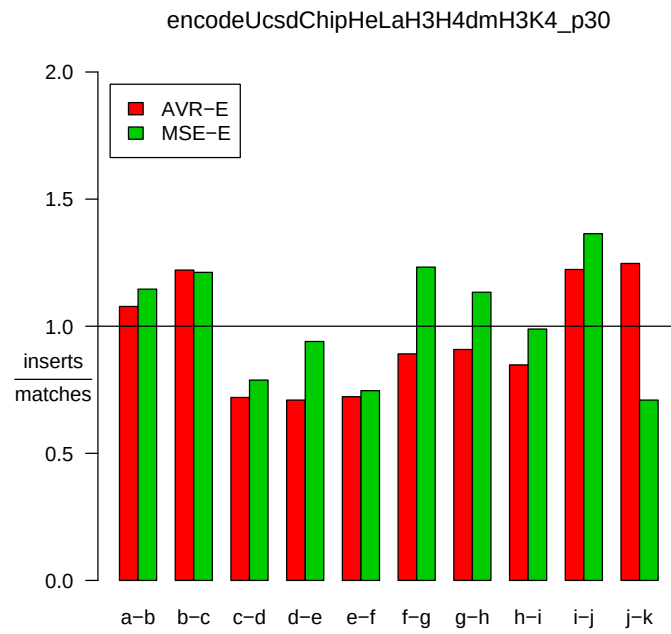
1985 2161

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.00  | insertion | 0.05  |
| 2 | 0.05  | match     | 0.11  |

0 0.05 0.11 0.16 0.22 0.29 0.38 0.52 0.77 1.39 16

|       | brk       | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| set   | type      |     |     |     |     |     |     |     |     |     |     |
| AVR-E | insertion | 22  | 27  | 12  | 14  | 15  | 19  | 17  | 15  | 24  | 28  |
|       | match     | 180 | 195 | 147 | 174 | 183 | 188 | 165 | 156 | 173 | 198 |
| MSE-E | insertion | 23  | 29  | 16  | 21  | 16  | 26  | 27  | 24  | 28  | 14  |
|       | match     | 177 | 211 | 179 | 197 | 189 | 186 | 210 | 214 | 181 | 174 |



## 2.157 encodeUcsdChipHeLaH3H4RNAP<sub>p</sub>0

NULL

LI Pol2 -gIF

Ludwig Institute ChIP/Chip: RNA Pol2, HeLa cells, no gamma interferon

|                                             | coef  | se    | z    | p      |
|---------------------------------------------|-------|-------|------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.335 | 0.163 | 2.06 | 0.0393 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.278 | 0.149 | 1.86 | 0.0628 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5380

Origin.of.data.set

AVR-E MSE-E

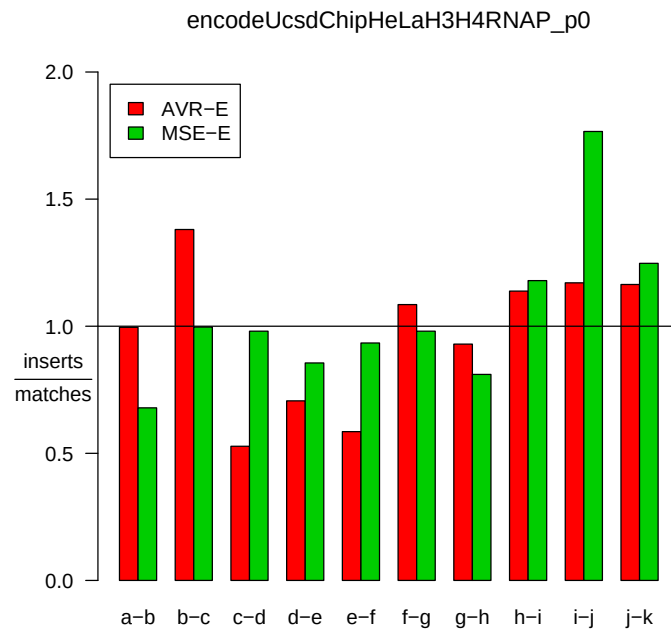
1985 2161

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.00  | insertion | 0.04  |
| 2 | 0.04  | match     | 0.08  |

0 0.04 0.08 0.13 0.18 0.24 0.32 0.42 0.59 0.98 16

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 22  | 25  | 11  | 14  | 12  | 22  | 18  | 21  | 24  | 24  |
|       | match     |     | 194 | 159 | 183 | 174 | 180 | 178 | 170 | 162 | 180 | 181 |
| MSE-E | insertion |     | 15  | 21  | 22  | 19  | 20  | 22  | 18  | 27  | 35  | 26  |
|       | match     |     | 194 | 185 | 197 | 195 | 188 | 197 | 195 | 201 | 174 | 183 |



## 2.158 encodeUcsdChipHeLaH3H4RNAP<sub>p</sub>30

NULL

LI Pol2 +gIF

Ludwig Institute ChIP/Chip: RNA Pol2, HeLa cells, 30 min. after gamma interferon

|                                             | coef  | se    | z    | p      |
|---------------------------------------------|-------|-------|------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.284 | 0.159 | 1.79 | 0.0742 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.556 | 0.154 | 3.62 | 0.0003 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5380

Origin.of.data.set

AVR-E MSE-E

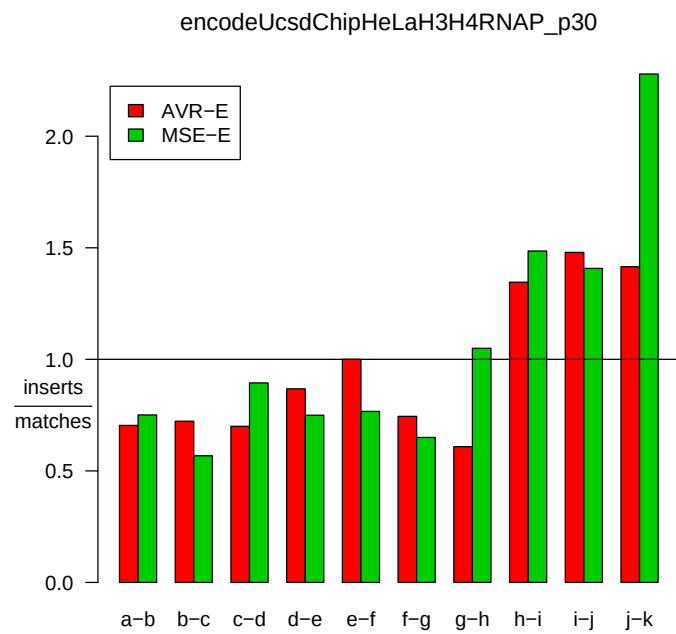
1985 2161

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.00  | insertion | 0.04  |
| 2 | 0.04  | match     | 0.08  |

0 0.04 0.08 0.13 0.18 0.25 0.32 0.42 0.56 0.92 16

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 15  | 14  | 13  | 18  | 22  | 14  | 12  | 25  | 29  | 30  |     |
|       | match     | 187 | 170 | 163 | 182 | 193 | 165 | 173 | 163 | 172 | 186 |     |
| MSE-E | insertion | 16  | 11  | 21  | 17  | 18  | 14  | 25  | 32  | 30  | 40  |     |
|       | match     | 187 | 170 | 206 | 199 | 206 | 189 | 209 | 189 | 187 | 154 |     |



## 2.159 encodeUcsdChipHeLaH3H4stat1<sub>p</sub>0

NULL

LI STAT1 -gIF

Ludwig Institute ChIP/Chip: STAT1 ab, HeLa cells, no gamma interferon

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.0578 | 0.159 | -0.364 | 0.716 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.1300 | 0.149 | -0.871 | 0.384 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5380

Origin.of.data.set

AVR-E MSE-E

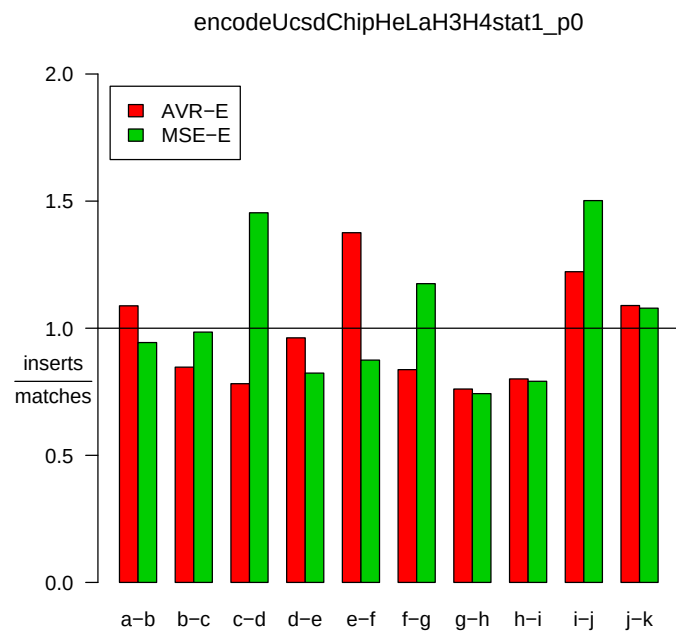
1985 2161

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.00  | insertion | 0.04  |
| 2 | 0.04  | match     | 0.10  |

0 0.04 0.1 0.15 0.2 0.26 0.33 0.43 0.57 0.855  
3.82

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 21  | 21  | 15  | 19  | 23  | 17  | 14  | 15  | 24  | 22  |     |
|       | match     | 172 | 221 | 171 | 176 | 149 | 181 | 164 | 167 | 175 | 180 |     |
| MSE-E | insertion | 18  | 20  | 31  | 17  | 21  | 24  | 17  | 19  | 30  | 23  |     |
|       | match     | 170 | 181 | 190 | 184 | 214 | 182 | 204 | 214 | 178 | 190 |     |





## 2.160 encodeUcsdChipHeLaH3H4stat1<sub>p</sub>30

NULL

LI STAT1 +gIF

Ludwig Institute ChIP/Chip: STAT1 ab, HeLa cells, 30 min. after gamma interferon

|                                             | coef  | se    | z    | p      |
|---------------------------------------------|-------|-------|------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.121 | 0.160 | 0.76 | 0.4470 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.278 | 0.151 | 1.84 | 0.0655 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5380

Origin.of.data.set

AVR-E MSE-E

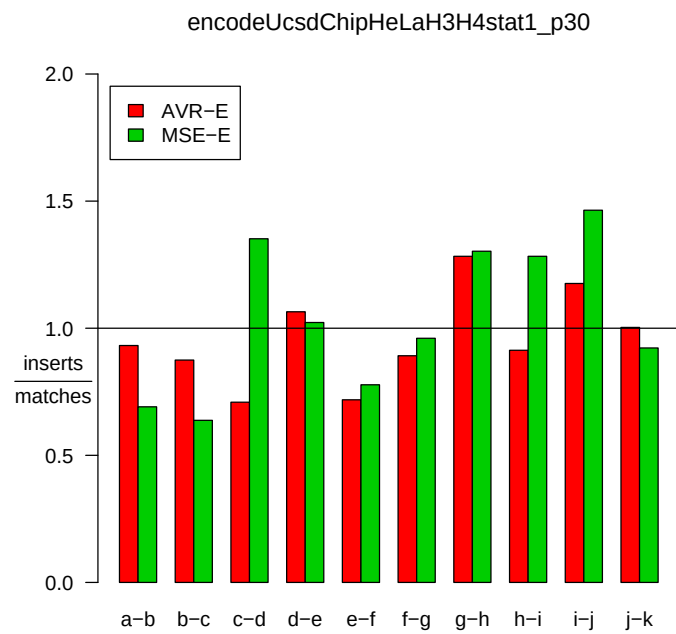
1985 2161

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.00  | insertion | 0.05  |
| 2 | 0.05  | match     | 0.09  |

0 0.05 0.09 0.14 0.2 0.27 0.34 0.46 0.65 1 16

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 22  | 15  | 15  | 23  | 14  | 14  | 24  | 18  | 22  | 21  |
|       | match     |     | 212 | 154 | 190 | 194 | 175 | 141 | 168 | 177 | 168 | 188 |
| MSE-E | insertion |     | 14  | 12  | 28  | 23  | 20  | 20  | 28  | 28  | 30  | 19  |
|       | match     |     | 182 | 169 | 186 | 202 | 231 | 187 | 193 | 196 | 184 | 185 |



## 2.161 encodeUcsdChipHeLaH3H4TAF250<sub>p</sub>0

NULL

LI TAF1 -gIF

Ludwig Institute ChIP/Chip: TAF1, HeLa cells, no gamma interferon

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.0511  | 0.161 | 0.317  | 0.751 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.0983 | 0.149 | -0.661 | 0.509 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5380

Origin.of.data.set

AVR-E MSE-E

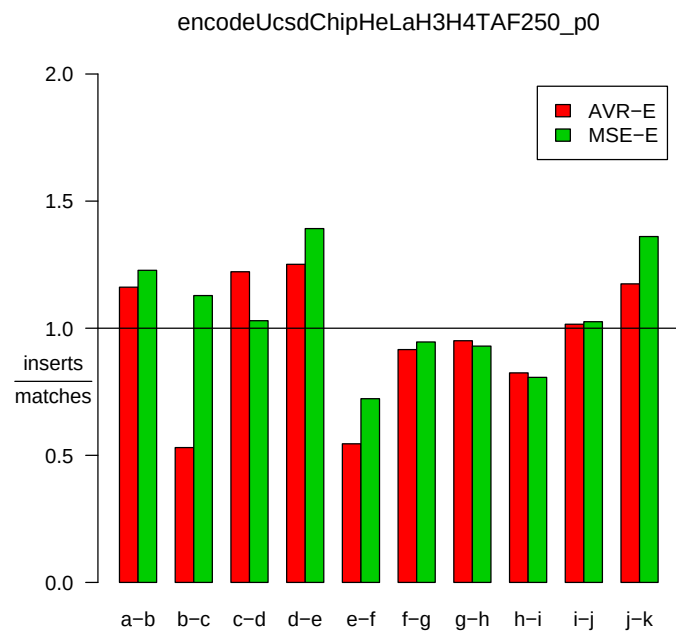
1985 2161

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.00  | insertion | 0.04  |
| 2 | 0.04  | match     | 0.09  |

0 0.04 0.09 0.14 0.19 0.25 0.31 0.4 0.57 0.87  
15.6

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 25  | 11  | 23  | 22  | 11  | 16  | 18  | 17  | 19  | 27  |     |
|       | match     | 191 | 184 | 167 | 156 | 179 | 155 | 168 | 183 | 166 | 204 |     |
| MSE-E | insertion | 22  | 22  | 21  | 32  | 18  | 21  | 22  | 19  | 23  | 23  |     |
|       | match     | 159 | 173 | 181 | 204 | 221 | 197 | 210 | 209 | 199 | 150 |     |



## 2.162 encodeUcsdChipHeLaH3H4TAF250<sub>p</sub>30

NULL

LI TAF1 +gIF

Ludwig Institute ChIP/Chip: TAF1, HeLa cells, 30 min. after gamma interferon

|                                             | coef  | se    | z     | p     |
|---------------------------------------------|-------|-------|-------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.072 | 0.160 | 0.449 | 0.654 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.141 | 0.148 | 0.954 | 0.340 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5380

Origin.of.data.set

AVR-E MSE-E

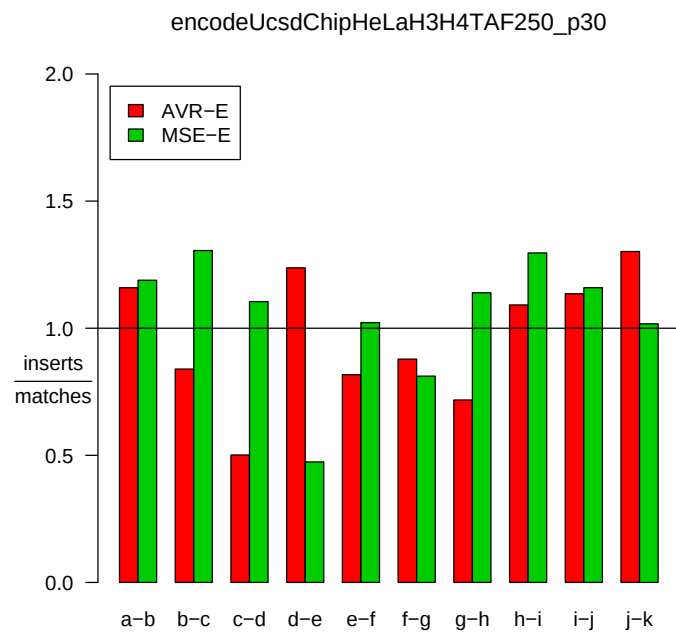
1985 2161

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.00  | insertion | 0.04  |
| 2 | 0.04  | match     | 0.09  |

0 0.04 0.09 0.14 0.2 0.26 0.34 0.44 0.62 1.05 16

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 21  | 17  | 11  | 22  | 16  | 17  | 13  | 21  | 23  | 29  |
|       | match     |     | 161 | 180 | 195 | 158 | 174 | 172 | 161 | 171 | 180 | 198 |
| MSE-E | insertion |     | 21  | 26  | 22  | 12  | 23  | 21  | 25  | 28  | 24  | 19  |
|       | match     |     | 157 | 177 | 177 | 225 | 200 | 230 | 195 | 192 | 184 | 166 |



## 2.163 encodeUcsdChipHeLaH3H4tmH3K4<sub>p</sub>0

NULL

LI H3K4me3 -gIF

Ludwig Institute ChIP/Chip: H3K4me3 ab, HeLa cells, no gamma interferon

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.0597 | 0.161 | -0.370 | 0.711 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.0597  | 0.148 | 0.403  | 0.687 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5380

Origin.of.data.set

AVR-E MSE-E

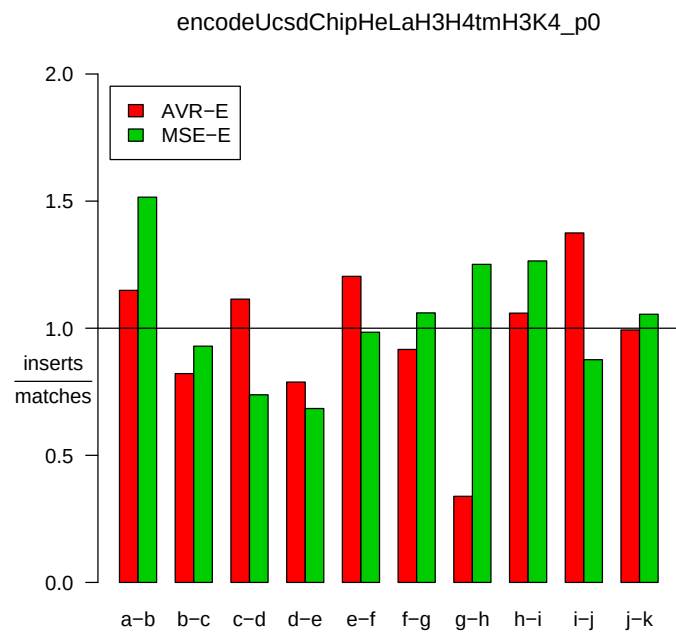
1985 2161

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.00  | insertion | 0.04  |
| 2 | 0.04  | match     | 0.09  |

0 0.04 0.09 0.14 0.2 0.26 0.35 0.48 0.77 1.33 16

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 24  | 18  | 21  | 17  | 19  | 18  | 7   | 19  | 27  | 23  |     |
|       | match     | 184 | 193 | 166 | 190 | 139 | 173 | 182 | 158 | 173 | 204 |     |
| MSE-E | insertion | 32  | 23  | 15  | 16  | 20  | 26  | 25  | 29  | 19  | 20  |     |
|       | match     | 186 | 218 | 179 | 206 | 179 | 216 | 176 | 202 | 191 | 167 |     |





## 2.164 encodeUcsdChipHeLaH3H4tmH3K4<sub>p</sub>30

NULL

LI H3K4me3 +gIF

Ludwig Institute ChIP/Chip: H3K4me3 ab, HeLa cells, 30 min. after gamma interferon

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.0911  | 0.163 | 0.559  | 0.576 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.2430 | 0.148 | -1.640 | 0.101 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5380

Origin.of.data.set

AVR-E MSE-E

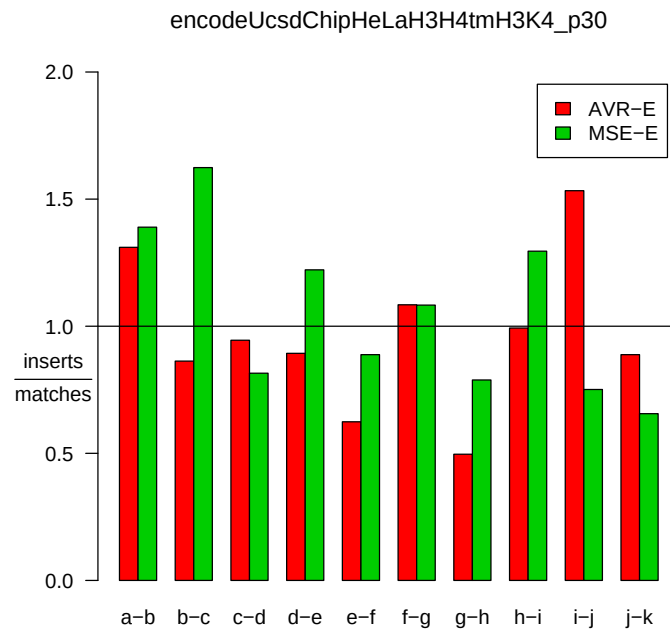
1985 2161

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.00  | insertion | 0.04  |
| 2 | 0.04  | match     | 0.09  |

0 0.04 0.09 0.15 0.21 0.28 0.37 0.47 0.61 0.95 16

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 27  | 17  | 20  | 17  | 13  | 21  | 9   | 18  | 29  | 20  |     |
|       | match     | 183 | 175 | 188 | 169 | 185 | 172 | 161 | 161 | 168 | 200 |     |
| MSE-E | insertion | 23  | 32  | 19  | 26  | 20  | 25  | 19  | 28  | 17  | 13  |     |
|       | match     | 147 | 175 | 207 | 189 | 200 | 205 | 214 | 192 | 201 | 176 |     |



## 2.165 encodeUcsdChipRnapHCT116<sub>f</sub>

NULL

LI Pol2 HCT116

Ludwig Institute ChIP/Chip: Pol2 8WG16 ab, HCT116 cells

|                                             | coef  | se    | z    | p      |
|---------------------------------------------|-------|-------|------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.322 | 0.166 | 1.94 | 0.0519 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.348 | 0.155 | 2.25 | 0.0244 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5409

Origin.of.data.set

AVR-E MSE-E

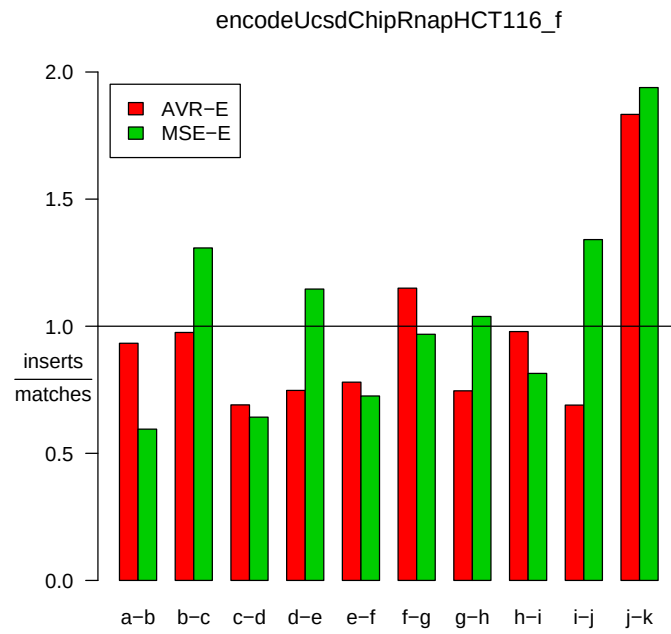
1969 2148

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.00  | insertion | 0.02  |
| 2 | 0.02  | match     | 0.05  |

0 0.02 0.05 0.08 0.12 0.18 0.27 0.42 0.7 1.34  
15.1

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 17  | 18  | 9   | 15  | 17  | 24  | 16  | 21  | 14  | 37  |
|       | match     |     | 158 | 160 | 113 | 174 | 189 | 181 | 186 | 186 | 176 | 175 |
| MSE-E | insertion |     | 14  | 27  | 10  | 23  | 20  | 22  | 20  | 17  | 30  | 36  |
|       | match     |     | 204 | 179 | 135 | 174 | 239 | 197 | 167 | 181 | 194 | 161 |



## 2.166 encodeUcsdChipRnapHela<sub>f</sub>

NULL

LI Pol2 HeLa

Ludwig Institute ChIP/Chip: Pol2 8WG16 ab, HeLa cells

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.0869  | 0.164 | 0.531  | 0.595 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.0153 | 0.149 | -0.103 | 0.918 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5409

Origin.of.data.set

AVR-E MSE-E

1969 2148

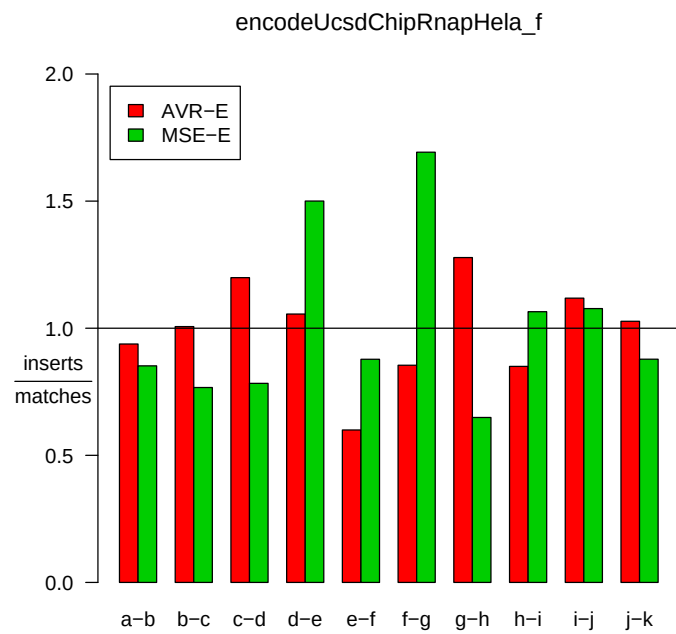
Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.00  | insertion | 0.01  |
| 2 | 0.01  | match     | 0.03  |

0 0.01 0.03 0.06 0.104 0.17 0.26 0.42 0.71 1.38

16

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 13  | 9   | 26  | 19  | 12  | 17  | 25  | 19  | 21  | 24  |     |
|       | match     | 124 | 80  | 194 | 161 | 179 | 178 | 175 | 200 | 168 | 209 |     |
| MSE-E | insertion | 12  | 9   | 26  | 27  | 21  | 35  | 14  | 20  | 23  | 16  |     |
|       | match     | 126 | 105 | 297 | 161 | 214 | 185 | 193 | 168 | 191 | 163 |     |



## 2.167 encodeUcsdChipRnapImr90<sub>f</sub>

NULL

LI Pol2 IMR90

Ludwig Institute ChIP/Chip: Pol2 8WG16 ab, IMR90 cells

|                                             | coef   | se    | z     | p     |
|---------------------------------------------|--------|-------|-------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.0808 | 0.165 | 0.489 | 0.625 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.1080 | 0.153 | 0.706 | 0.480 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5409

Origin.of.data.set

AVR-E MSE-E

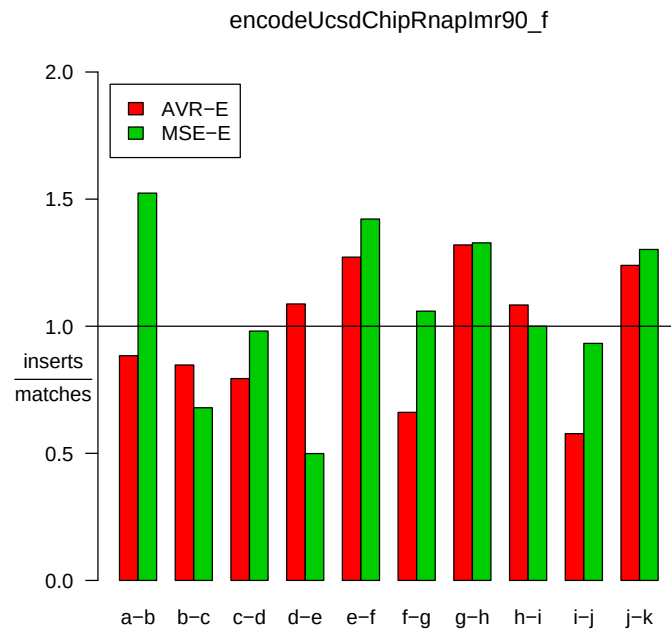
1969 2148

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.00  | insertion | 0.01  |
| 2 | 0.01  | match     | 0.04  |

0 0.01 0.04 0.08 0.14 0.21 0.3 0.46 0.68 1.21 16

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 8   | 16  | 11  | 26  | 26  | 13  | 23  | 23  | 12  | 27  |     |
|       | match     | 81  | 169 | 124 | 214 | 183 | 176 | 156 | 190 | 186 | 195 |     |
| MSE-E | insertion | 16  | 17  | 16  | 15  | 27  | 20  | 27  | 21  | 20  | 24  |     |
|       | match     | 94  | 224 | 146 | 269 | 170 | 169 | 182 | 188 | 192 | 165 |     |





## 2.168 encodeUcsdChipRnapThp1<sub>f</sub>

NULL

LI Pol2 THP1

Ludwig Institute ChIP/Chip: Pol2 8WG16 ab, THP1 cells

|                                             | coef   | se    | z      | p      |
|---------------------------------------------|--------|-------|--------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.273  | 0.165 | 1.650  | 0.0982 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.053 | 0.153 | -0.347 | 0.7290 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5409

Origin.of.data.set

AVR-E MSE-E

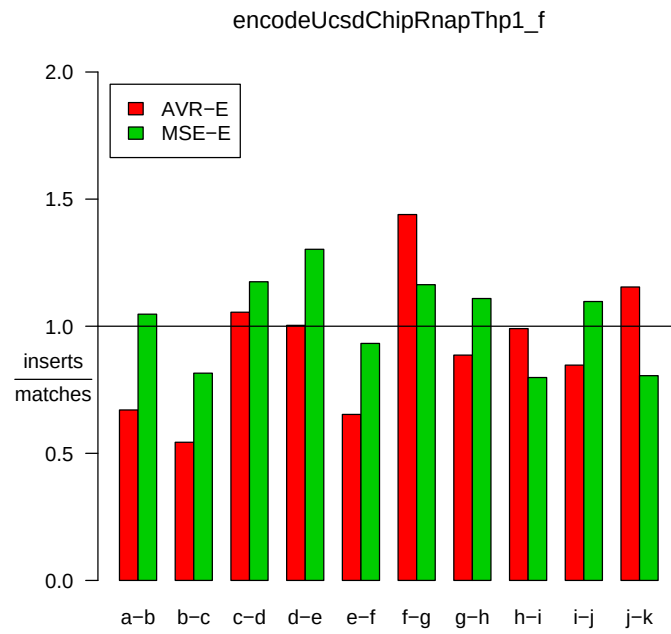
1969 2148

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.00  | insertion | 0.01  |
| 2 | 0.01  | match     | 0.03  |

0 0.01 0.03 0.06 0.1 0.16 0.25 0.38 0.62 1.01 16

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 8   | 4   | 26  | 16  | 15  | 26  | 17  | 19  | 17  | 26  |     |
|       | match     | 107 | 66  | 221 | 143 | 206 | 162 | 172 | 172 | 180 | 202 |     |
| MSE-E | insertion | 16  | 7   | 30  | 26  | 21  | 24  | 23  | 17  | 23  | 15  |     |
|       | match     | 137 | 77  | 229 | 179 | 202 | 185 | 186 | 191 | 188 | 167 |     |



## 2.169 encodeUcsdChipTaf250HCT116<sub>f</sub>

NULL

LI TAF1 HCT116

Ludwig Institute ChIP/Chip: TAF1 ab, HCT116 cells

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.0708  | 0.161 | 0.439  | 0.660 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.1130 | 0.152 | -0.742 | 0.458 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5409

Origin.of.data.set

AVR-E MSE-E

1969 2148

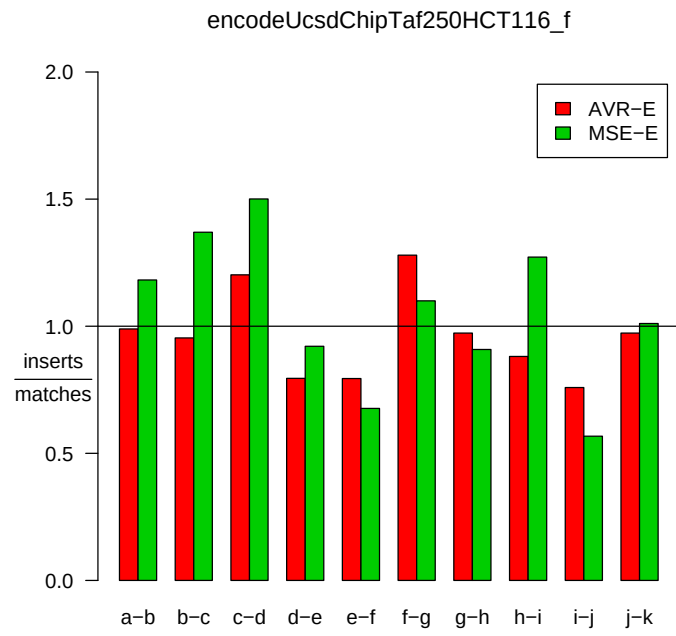
Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.00  | insertion | 0.01  |
| 2 | 0.01  | match     | 0.03  |

0 0.01 0.03 0.07 0.12 0.18 0.276 0.41 0.63 1.03

16

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 12  | 6   | 32  | 10  | 19  | 24  | 20  | 19  | 15  | 20  |     |
|       | match     | 108 | 56  | 237 | 112 | 213 | 167 | 183 | 192 | 176 | 183 |     |
| MSE-E | insertion | 15  | 12  | 45  | 15  | 19  | 21  | 20  | 25  | 13  | 21  |     |
|       | match     | 113 | 78  | 267 | 145 | 250 | 170 | 196 | 175 | 204 | 185 |     |



## 2.170 encodeUcsdChipTaf250Hela<sub>f</sub>

NULL

LI TAF1 HeLa

Ludwig Institute ChIP/Chip: TAF1 ab, HeLa cells

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.14300 | 0.163 | 0.8750 | 0.382 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.00458 | 0.155 | 0.0296 | 0.976 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5409

Origin.of.data.set

AVR-E MSE-E

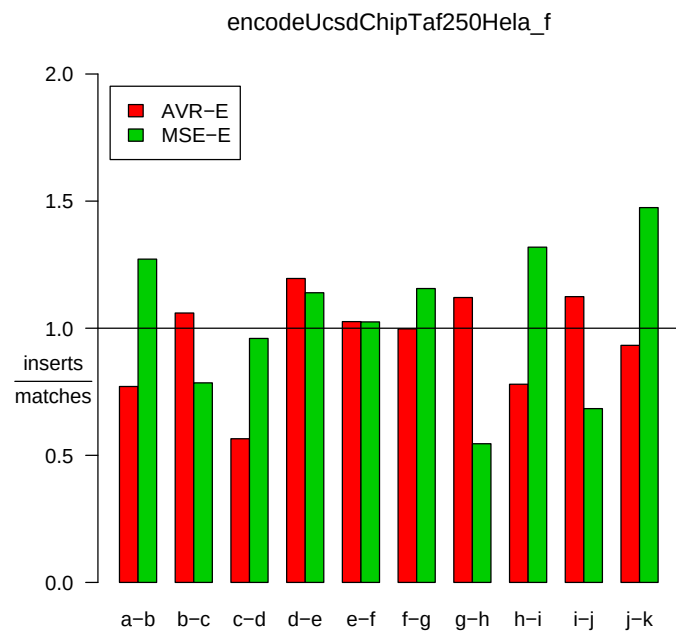
1969 2148

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.00  | insertion | 0.01  |
| 2 | 0.01  | match     | 0.02  |

0 0.01 0.02 0.04 0.08 0.14 0.25 0.45 0.68 1.04 16

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 13  | 11  | 9   | 22  | 19  | 24  | 23  | 16  | 24  | 22  |     |
|       | match     | 143 | 88  | 135 | 156 | 157 | 204 | 174 | 174 | 181 | 200 |     |
| MSE-E | insertion | 27  | 10  | 18  | 25  | 22  | 24  | 13  | 28  | 15  | 28  |     |
|       | match     | 180 | 108 | 159 | 186 | 182 | 176 | 202 | 180 | 186 | 161 |     |



## 2.171 encodeUcsdChipTaf250Imr90<sub>f</sub>

NULL

LI TAF1 IMR90

Ludwig Institute ChIP/Chip: TAF1 ab, IMR90 cells

|                                             | coef  | se    | z     | p     |
|---------------------------------------------|-------|-------|-------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.057 | 0.164 | 0.348 | 0.728 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.177 | 0.154 | 1.150 | 0.251 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5409

Origin.of.data.set

AVR-E MSE-E

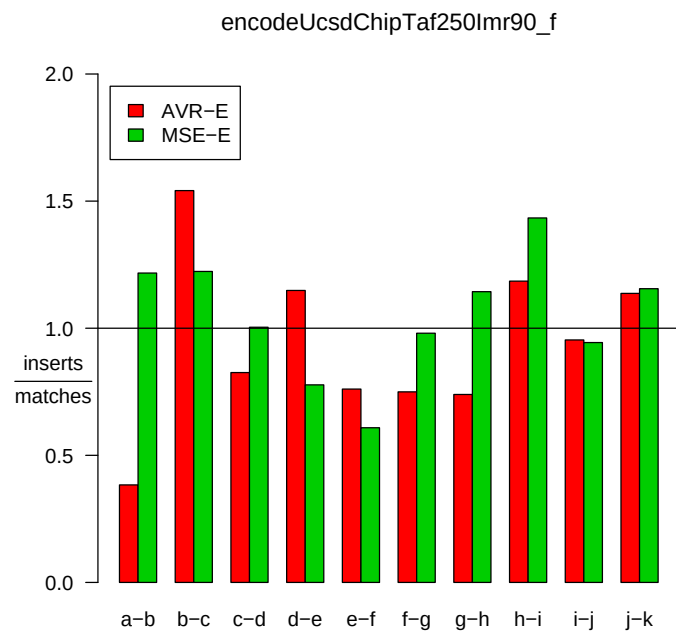
1969 2148

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.00  | insertion | 0.01  |
| 2 | 0.01  | match     | 0.05  |

0 0.01 0.05 0.09 0.14 0.2 0.28 0.382 0.55 0.9 16

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 4   | 29  | 16  | 22  | 15  | 13  | 15  | 27  | 20  | 25  |
|       | match     |     | 92  | 166 | 171 | 169 | 174 | 153 | 179 | 201 | 185 | 194 |
| MSE-E | insertion |     | 12  | 33  | 19  | 17  | 16  | 24  | 21  | 26  | 20  | 22  |
|       | match     |     | 87  | 238 | 167 | 193 | 232 | 216 | 162 | 160 | 187 | 168 |





## 2.172 encodeUcsdChipTaf250Thp1<sub>f</sub>

NULL

LI TAF1 THP1

Ludwig Institute ChIP/Chip: TAF1 ab, THP1 cells

|                                             | coef   | se    | z     | p      |
|---------------------------------------------|--------|-------|-------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.2910 | 0.164 | 1.770 | 0.0763 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.0323 | 0.149 | 0.217 | 0.8280 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5409

Origin.of.data.set

AVR-E MSE-E

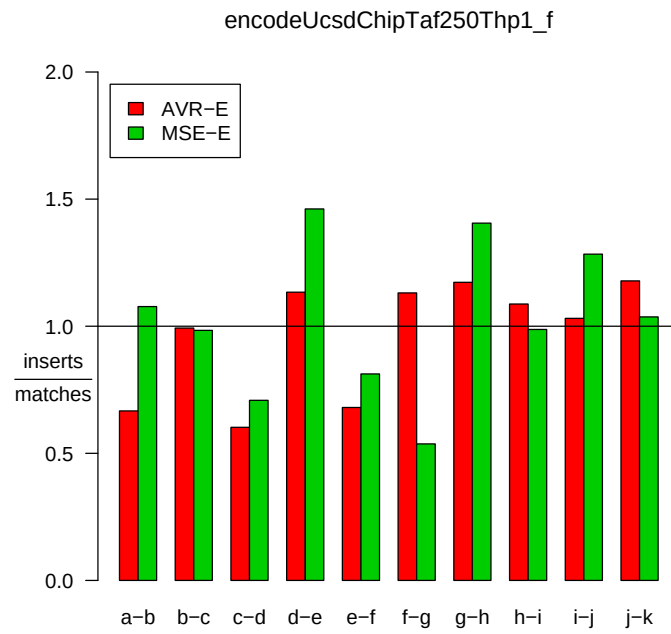
1969 2148

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.00  | insertion | 0.01  |
| 2 | 0.01  | match     | 0.03  |

0 0.01 0.03 0.05 0.1 0.16 0.25 0.4 0.67 1.25 16

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 10  | 10  | 12  | 25  | 15  | 20  | 21  | 23  | 21  | 24  |     |
|       | match     | 134 | 90  | 178 | 197 | 197 | 158 | 160 | 189 | 182 | 182 |     |
| MSE-E | insertion | 17  | 12  | 18  | 35  | 17  | 11  | 28  | 20  | 26  | 21  |     |
|       | match     | 141 | 109 | 227 | 214 | 187 | 183 | 178 | 181 | 181 | 181 |     |



## 2.173 encodeUcsdNgChipSignal

NULL

LI Ng TAF1 IMR90

Ludwig Institute NimbleGen ChIP/Chip: TAF1 antibody, IMR90 cells

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.2620 | 0.155 | -1.690 | 0.091 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.0294 | 0.142 | -0.207 | 0.836 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4802

Origin.of.data.set

AVR-E MSE-E

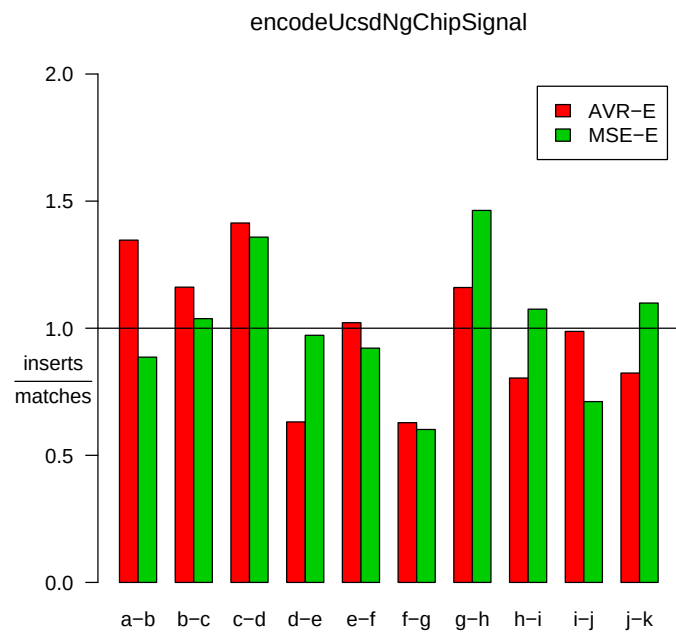
2236 2488

Category limits

|   | lower      | category  | upper      |
|---|------------|-----------|------------|
| 1 | -1.6000000 | insertion | -0.2081410 |
| 2 | -0.2081410 | match     | -0.1250000 |

-1.6 -0.208 -0.125 -0.0833 -0.0482 -0.0154 0.0175  
0.0503 0.0974 0.171 3.22

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 27  | 26  | 27  | 14  | 22  | 14  | 24  | 18  | 22  | 18  |
|       | match     |     | 189 | 211 | 180 | 209 | 203 | 210 | 195 | 211 | 210 | 206 |
| MSE-E | insertion |     | 22  | 24  | 33  | 23  | 22  | 15  | 34  | 26  | 16  | 26  |
|       | match     |     | 234 | 218 | 229 | 223 | 225 | 235 | 219 | 228 | 212 | 223 |



## 2.174 encodeUcsdNgHeLaAcH3<sub>p</sub>0

NULL

LI H3ac -gIF

Ludwig Institute/UCSD ChIP/Chip Ng: HeLa, H3ac, no gamma interferon

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.905 | 0.167 | 5.41 | 6.45e-08 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.593 | 0.151 | 3.93 | 8.53e-05 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4826

Origin.of.data.set

AVR-E MSE-E

2210 2490

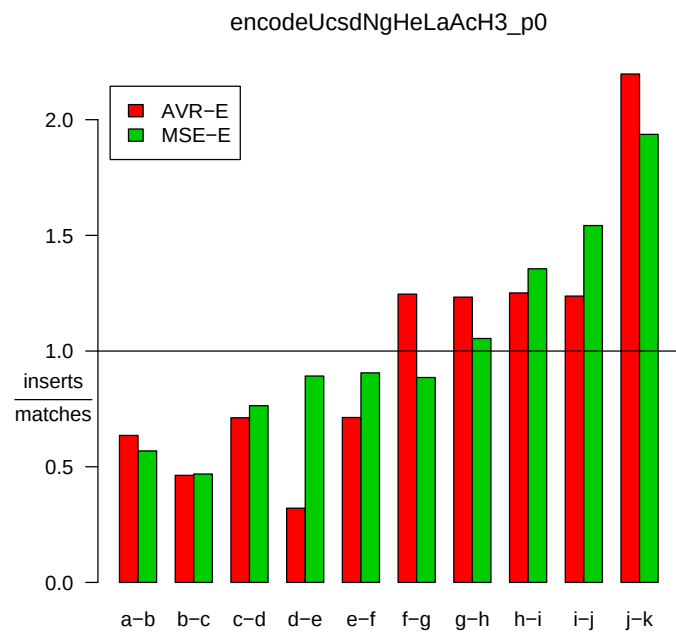
Category limits

|   | lower      | category  | upper      |
|---|------------|-----------|------------|
| 1 | -2.8063400 | insertion | -0.3709361 |
| 2 | -0.3709361 | match     | -0.2144300 |

-2.81 -0.371 -0.214 -0.131 -0.0562 0.00433 0.0614

0.13 0.212 0.371 3.58

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 15  | 10  | 15  | 7   | 16  | 26  | 23  | 24  | 27  | 44  |
|       | match     |     | 224 | 205 | 200 | 207 | 213 | 198 | 177 | 182 | 207 | 190 |
| MSE-E | insertion |     | 13  | 12  | 19  | 22  | 21  | 21  | 27  | 33  | 33  | 40  |
|       | match     |     | 217 | 243 | 236 | 234 | 220 | 225 | 243 | 231 | 203 | 196 |



## 2.175 encodeUcsdNgHeLaAcH3<sub>p</sub>30

NULL

LI H3ac +gIF

Ludwig Institute/UCSD ChIP/Chip Ng: HeLa, H3ac, 30 min after gamma interferon

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.768 | 0.166 | 4.63 | 3.71e-06 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.794 | 0.149 | 5.34 | 9.41e-08 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4826

Origin.of.data.set

AVR-E MSE-E

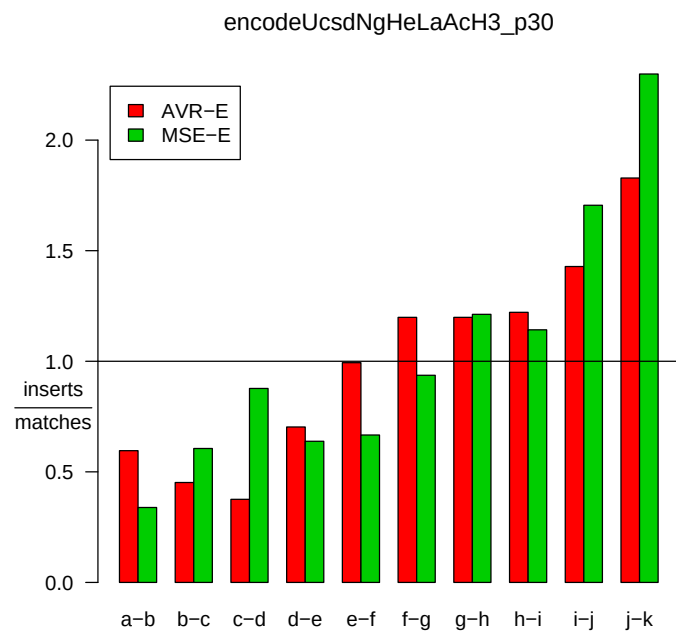
2210 2490

Category limits

|   | lower      | category  | upper      |
|---|------------|-----------|------------|
| 1 | -2.5447850 | insertion | -0.3798279 |
| 2 | -0.3798279 | match     | -0.2363438 |

-2.54 -0.38 -0.236 -0.132 -0.0587 0.0125 0.0744  
0.148 0.24 0.442 3.28

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 14  | 10  | 8   | 16  | 20  | 24  | 24  | 26  | 28  | 37  |
|       | match     |     | 223 | 210 | 202 | 216 | 191 | 190 | 190 | 202 | 186 | 192 |
| MSE-E | insertion |     | 8   | 15  | 22  | 15  | 17  | 23  | 29  | 26  | 39  | 47  |
|       | match     |     | 224 | 235 | 238 | 223 | 242 | 233 | 227 | 216 | 217 | 194 |





## 2.176 encodeUcsdNgHeLaAcH4<sub>p</sub>0

NULL

LI H4ac -gIF

Ludwig Institute/UCSD ChIP/Chip Ng: HeLa, H4ac, no gamma interferon

|                                             | coef   | se    | z     | p       |
|---------------------------------------------|--------|-------|-------|---------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.177 | 0.154 | -1.15 | 0.25200 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.430 | 0.145 | -2.97 | 0.00302 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4826

Origin.of.data.set

AVR-E MSE-E

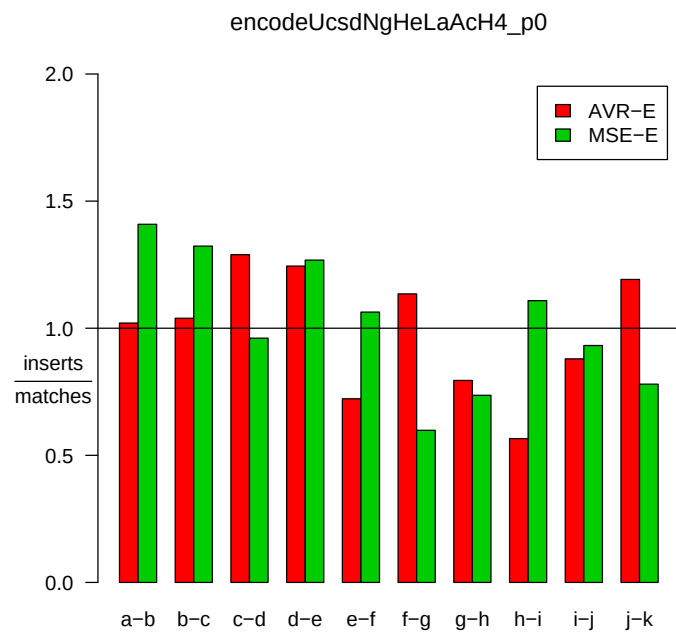
2210 2490

Category limits

|   | lower      | category  | upper      |
|---|------------|-----------|------------|
| 1 | -1.7294500 | insertion | -0.3830906 |
| 2 | -0.3830906 | match     | -0.2272920 |

-1.73 -0.383 -0.227 -0.131 -0.0557 0.0093 0.069  
0.134 0.211 0.353 2.55

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 20  | 23  | 25  | 24  | 15  | 25  | 17  | 13  | 19  | 26  |
|       | match     |     | 186 | 210 | 184 | 183 | 197 | 209 | 203 | 218 | 205 | 207 |
| MSE-E | insertion |     | 34  | 29  | 24  | 31  | 26  | 14  | 18  | 25  | 22  | 18  |
|       | match     |     | 229 | 208 | 237 | 232 | 232 | 222 | 232 | 214 | 224 | 219 |



## 2.177 encodeUcsdNgHeLaDmH3K4<sub>p</sub>0

NULL

LI H3K4me2 -gIF

Ludwig Institute/UCSD ChIP/Chip Ng: HeLa, H3K4me2, no gamma interferon

|                                             | coef    | se    | z     | p     |
|---------------------------------------------|---------|-------|-------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.2020  | 0.154 | 1.31  | 0.190 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.0681 | 0.145 | -0.47 | 0.638 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4826

Origin.of.data.set

AVR-E MSE-E

2210 2490

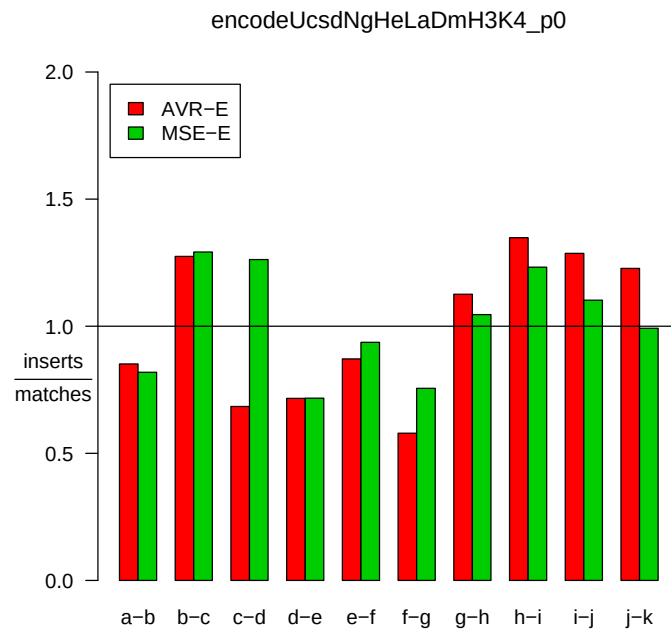
Category limits

|   | lower      | category  | upper      |
|---|------------|-----------|------------|
| 1 | -1.9931000 | insertion | -0.3812886 |
| 2 | -0.3812886 | match     | -0.2217950 |

-1.99 -0.381 -0.222 -0.13 -0.0554 0.011 0.0773

0.143 0.227 0.379 3

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 21  | 27  | 15  | 16  | 18  | 13  | 21  | 26  | 24  | 26  |
|       | match     |     | 234 | 201 | 208 | 212 | 196 | 213 | 177 | 183 | 177 | 201 |
| MSE-E | insertion |     | 17  | 29  | 29  | 17  | 23  | 18  | 27  | 30  | 28  | 23  |
|       | match     |     | 197 | 213 | 218 | 225 | 233 | 226 | 245 | 231 | 241 | 220 |



## 2.178 encodeUcsdNgHeLaDmH3K4<sub>p</sub>30

NULL

LI H3K4me2 +gIF

Ludwig Institute/UCSD ChIP/Chip Ng: HeLa, H3K4me2, 30 min after gamma interferon

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.0336 | 0.155 | -0.218 | 0.828 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.1990  | 0.146 | 1.360  | 0.173 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4826

Origin.of.data.set

AVR-E MSE-E

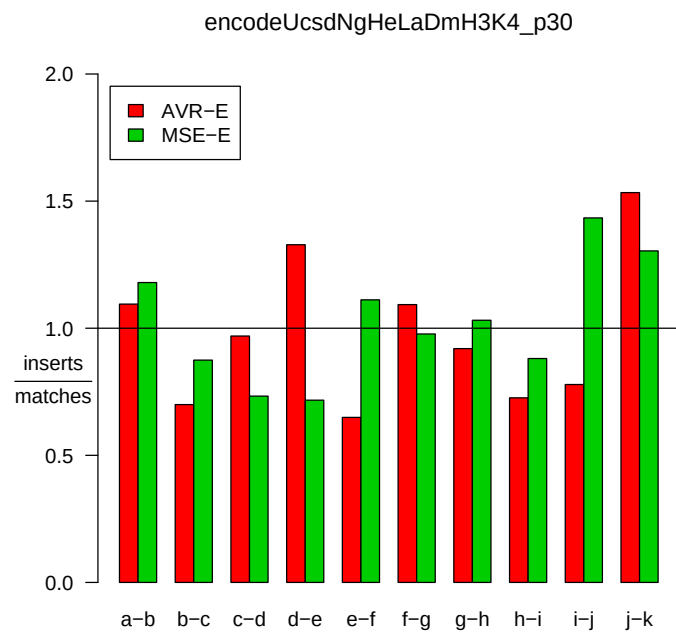
2210 2490

Category limits

|   | lower      | category  | upper      |
|---|------------|-----------|------------|
| 1 | -2.0401399 | insertion | -0.3388628 |
| 2 | -0.3388628 | match     | -0.1910088 |

-2.04 -0.339 -0.191 -0.111 -0.0472 0.00827 0.0643  
0.128 0.209 0.389 3.24

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 27  | 16  | 19  | 28  | 13  | 22  | 19  | 15  | 16  | 32  |
|       | match     |     | 234 | 217 | 186 | 200 | 190 | 191 | 196 | 196 | 195 | 198 |
| MSE-E | insertion |     | 23  | 20  | 19  | 17  | 28  | 24  | 25  | 22  | 34  | 29  |
|       | match     |     | 185 | 217 | 246 | 225 | 239 | 233 | 230 | 237 | 225 | 211 |



## 2.179 encodeUcsdNgHeLaH3K4me3<sub>p</sub>0

NULL

LI H3K4me3 -gIF

Ludwig Institute/UCSD ChIP/Chip Ng: HeLa, H3K4me3, no gamma interferon

|                                             | coef   | se    | z      | p     |
|---------------------------------------------|--------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.116 | 0.156 | -0.743 | 0.457 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.134 | 0.142 | -0.947 | 0.344 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4826

Origin.of.data.set

AVR-E MSE-E

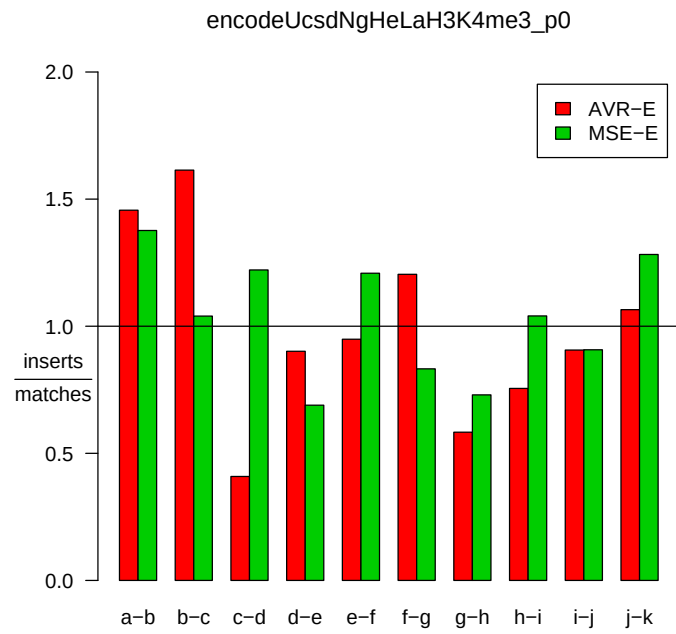
2210 2490

Category limits

|   | lower      | category  | upper      |
|---|------------|-----------|------------|
| 1 | -3.1064200 | insertion | -0.3869901 |
| 2 | -0.3869901 | match     | -0.2247926 |

-3.11 -0.387 -0.225 -0.124 -0.0518 0.0121 0.0738  
0.14 0.231 0.398 4.11

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 33  | 33  | 10  | 19  | 21  | 25  | 11  | 16  | 17  | 22  |
|       | match     |     | 215 | 194 | 232 | 200 | 210 | 197 | 179 | 201 | 178 | 196 |
| MSE-E | insertion |     | 28  | 24  | 26  | 17  | 27  | 20  | 20  | 25  | 24  | 30  |
|       | match     |     | 193 | 219 | 202 | 234 | 212 | 228 | 260 | 228 | 251 | 222 |





## 2.180 encodeUcsdNgHeLaH3K4me3<sub>p</sub>30

NULL

LI H3K4m3 +gIF

Ludwig Institute/UCSD ChIP/Chip Ng: HeLa, H3K4me3, 30 min after gamma interferon

|                                             | coef   | se    | z      | p     |
|---------------------------------------------|--------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.059 | 0.153 | -0.386 | 0.699 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.129 | 0.142 | -0.910 | 0.363 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4826

Origin.of.data.set

AVR-E MSE-E

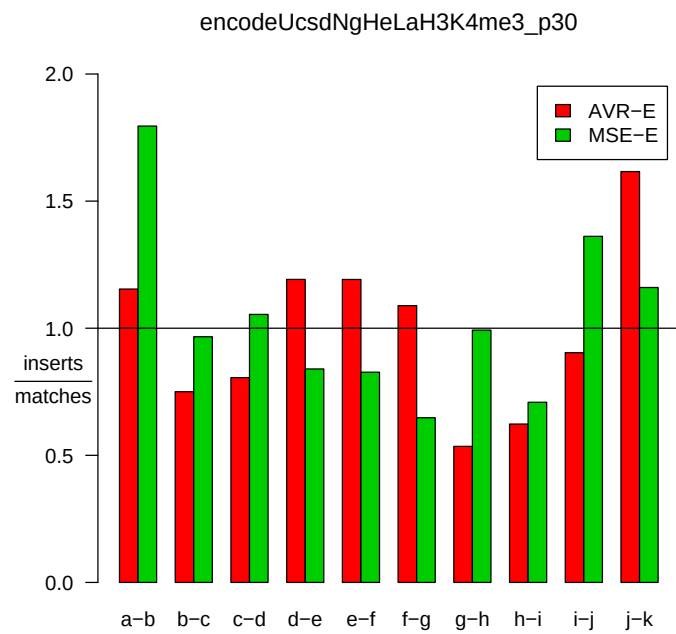
2210 2490

Category limits

|   | lower      | category  | upper      |
|---|------------|-----------|------------|
| 1 | -1.6181400 | insertion | -0.3472243 |
| 2 | -0.3472243 | match     | -0.2088045 |

-1.62 -0.347 -0.209 -0.119 -0.0525 0.00854 0.0734  
0.133 0.209 0.335 4.2

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 27  | 17  | 18  | 25  | 26  | 21  | 11  | 13  | 18  | 31  |
|       | match     |     | 222 | 215 | 212 | 199 | 207 | 183 | 195 | 198 | 189 | 182 |
| MSE-E | insertion |     | 35  | 22  | 24  | 20  | 19  | 17  | 25  | 18  | 33  | 28  |
|       | match     |     | 185 | 216 | 216 | 226 | 218 | 249 | 239 | 241 | 230 | 229 |



## 2.181 encodeUcsdNgHeLaRnap<sub>p</sub>0

NULL

LI Pol2 -gIF

Ludwig Institute/UCSD ChIP/Chip Ng: HeLa, Pol2, no gamma interferon

|                                             | coef   | se    | z     | p      |
|---------------------------------------------|--------|-------|-------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.0468 | 0.155 | 0.302 | 0.7630 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.2810 | 0.144 | 1.950 | 0.0509 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4826

Origin.of.data.set

AVR-E MSE-E

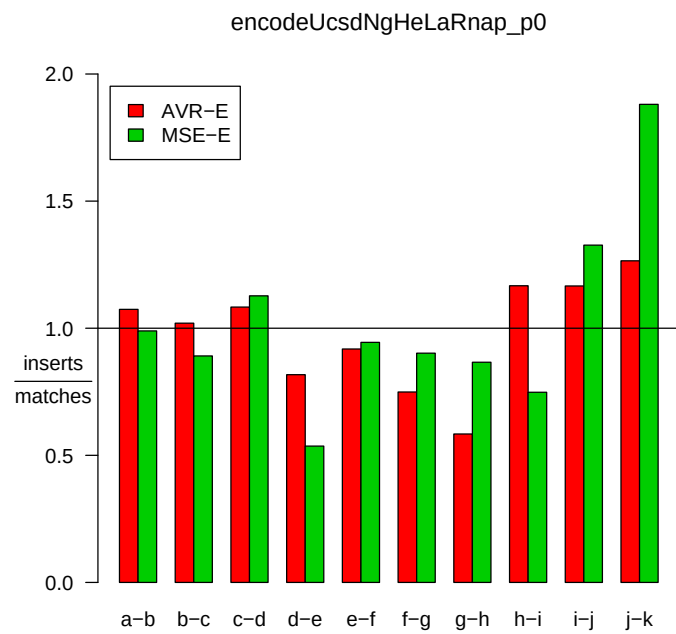
2210 2490

Category limits

|   | lower      | category  | upper      |
|---|------------|-----------|------------|
| 1 | -1.8029000 | insertion | -0.3755987 |
| 2 | -0.3755987 | match     | -0.2147798 |

-1.8 -0.376 -0.215 -0.122 -0.0486 0.0166 0.0906  
0.165 0.264 0.44 2.73

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 24  | 23  | 25  | 18  | 21  | 15  | 12  | 23  | 22  | 24  |
|       | match     |     | 212 | 214 | 219 | 209 | 217 | 190 | 195 | 187 | 179 | 180 |
| MSE-E | insertion |     | 22  | 20  | 24  | 13  | 21  | 23  | 22  | 19  | 33  | 44  |
|       | match     |     | 211 | 213 | 202 | 230 | 211 | 242 | 241 | 241 | 236 | 222 |



## 2.182 encodeUcsdNgHeLaRnap<sub>p</sub>30

NULL

LI Pol2 +gIF

Ludwig Institute/UCSD ChIP/Chip Ng: HeLa, Pol2, 30 min after gamma interferon

|                                             | coef  | se    | z    | p     |
|---------------------------------------------|-------|-------|------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.380 | 0.153 | 2.48 | 0.013 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.213 | 0.143 | 1.50 | 0.135 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4826

Origin.of.data.set

AVR-E MSE-E

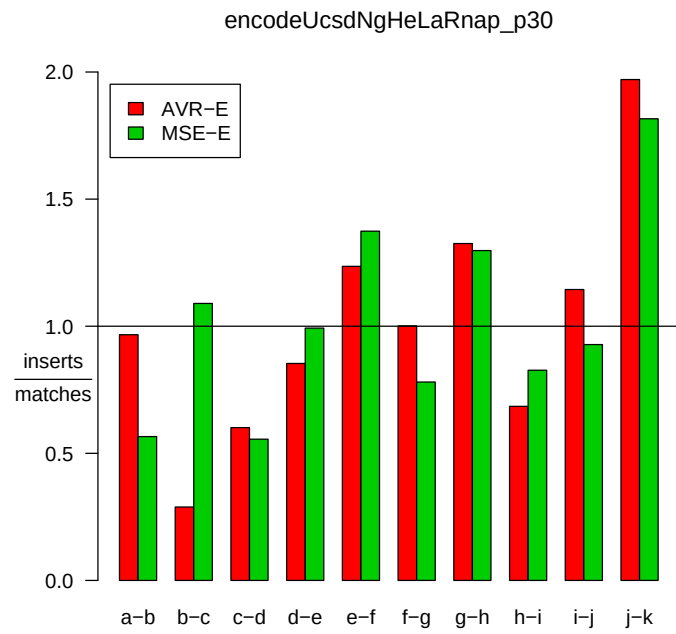
2210 2490

Category limits

|   | lower      | category  | upper      |
|---|------------|-----------|------------|
| 1 | -2.1246600 | insertion | -0.4033353 |
| 2 | -0.4033353 | match     | -0.2402736 |

-2.12 -0.403 -0.24 -0.137 -0.0578 0.0158 0.0892  
0.179 0.301 0.511 3.01

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 22  | 7   | 14  | 17  | 25  | 21  | 25  | 14  | 24  | 38  |     |
|       | match     | 216 | 230 | 221 | 189 | 192 | 199 | 179 | 194 | 199 | 183 |     |
| MSE-E | insertion | 13  | 24  | 13  | 25  | 32  | 19  | 32  | 21  | 22  | 40  |     |
|       | match     | 218 | 209 | 222 | 239 | 221 | 231 | 234 | 241 | 225 | 209 |     |



## 2.183 encodeUcsdNgHeLaStat1<sub>p</sub>30

NULL

LI STAT1 +gIF

Ludwig Institute/UCSD ChIP/Chip Ng: HeLa, STAT1, 30 min after gamma interferon

|                                             | coef   | se    | z      | p     |
|---------------------------------------------|--------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.040 | 0.153 | -0.262 | 0.793 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.025  | 0.143 | 0.175  | 0.861 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4857

Origin.of.data.set

AVR-E MSE-E

2199 2470

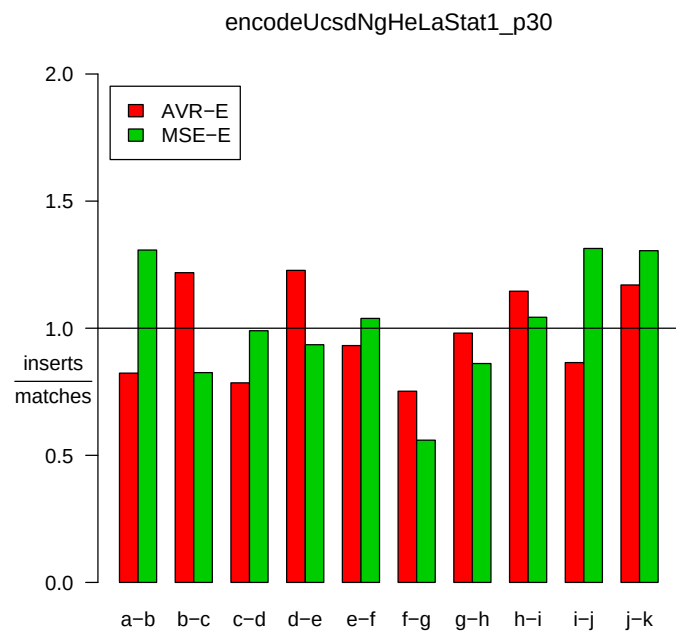
Category limits

|   | lower      | category  | upper      |
|---|------------|-----------|------------|
| 1 | -2.8022299 | insertion | -0.3756546 |
| 2 | -0.3756546 | match     | -0.2197356 |

-2.8 -0.376 -0.22 -0.132 -0.0583 0.00659 0.0703

0.138 0.229 0.387 1.87

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 18  | 26  | 17  | 24  | 19  | 17  | 20  | 23  | 19  | 23  |
|       | match     |     | 208 | 203 | 206 | 186 | 194 | 215 | 194 | 191 | 209 | 187 |
| MSE-E | insertion |     | 29  | 19  | 23  | 23  | 25  | 13  | 21  | 25  | 29  | 31  |
|       | match     |     | 211 | 219 | 221 | 234 | 229 | 221 | 232 | 228 | 210 | 226 |



NULL

NULL



## 2.184 encodeUncFairePeaks

NULL

UNC FAIRE PeakFinder

UNC FAIRE Peaks (Formaldehyde Assisted Isolation of Regulatory Elements) (PeakFinder)

|                                             | coef  | se    | z    | p      |
|---------------------------------------------|-------|-------|------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.865 | 0.377 | 2.29 | 0.0219 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.584 | 0.397 | 1.47 | 0.1410 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 8173

Origin.of.data.set

AVR-E MSE-E

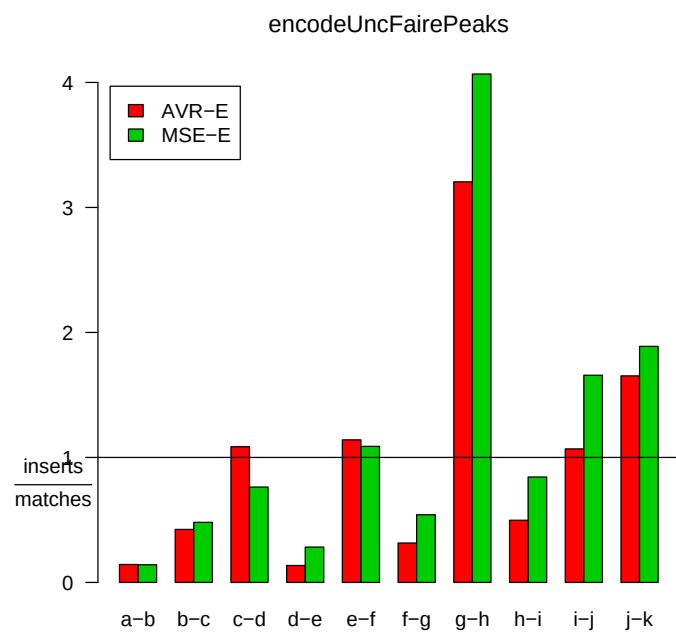
676 677

Category limits

|   | lower | category  | upper  |
|---|-------|-----------|--------|
| 1 | 0.61  | insertion | 1.5300 |
| 2 | 1.53  | match     | 1.7875 |

0.61 1.53 1.79 1.87 1.97 2.04 2.13 2.23 2.37 2.51  
3.13

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 1   | 3   | 7   | 1   | 7   | 2   | 17  | 3   | 6   | 11  |     |
|       | match     | 67  | 68  | 62  | 71  | 59  | 61  | 51  | 58  | 54  | 64  |     |
| MSE-E | insertion | 1   | 3   | 5   | 2   | 6   | 4   | 22  | 5   | 10  | 11  |     |
|       | match     | 68  | 60  | 63  | 68  | 53  | 71  | 52  | 57  | 58  | 56  |     |



## 2.185 encodeUncFaireSignal

NULL

UNC FAIRE Signal

UNC FAIRE Signal (Formaldehyde Assisted Isolation of Regulatory Elements)

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.396 | 0.111 | 3.58 | 3.45e-04 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.854 | 0.113 | 7.56 | 4.02e-14 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 884

Origin.of.data.set

AVR-E MSE-E

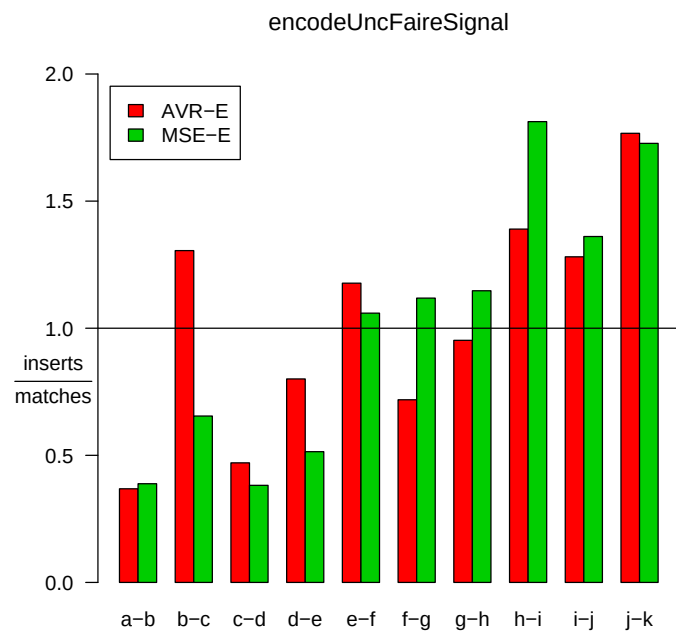
4165 4477

Category limits

|   | lower      | category  | upper       |
|---|------------|-----------|-------------|
| 1 | -1.3525000 | insertion | -0.12471483 |
| 2 | -0.1247148 | match     | -0.08718894 |

-1.35 -0.125 -0.0872 -0.0436 0.00235 0.0502  
0.0885 0.136 0.175 0.253 1.95

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 15  | 47  | 18  | 30  | 41  | 27  | 37  | 48  | 47  | 65  |
|       | match     |     | 415 | 367 | 390 | 382 | 355 | 383 | 396 | 352 | 374 | 375 |
| MSE-E | insertion |     | 16  | 28  | 16  | 22  | 45  | 44  | 43  | 69  | 53  | 61  |
|       | match     |     | 420 | 436 | 427 | 436 | 433 | 401 | 382 | 388 | 397 | 360 |



## 2.186 encodeUppsalaChipAch3

NULL

UU H3ac HepG2

University of Uppsala, Sweden ChIP/Chip (H3ac, HepG2)

|                                             | coef | se    | z    | p        |
|---------------------------------------------|------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 1.14 | 0.156 | 7.32 | 2.57e-13 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.10 | 0.133 | 8.31 | 9.50e-17 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 2986

Origin.of.data.set

AVR-E MSE-E

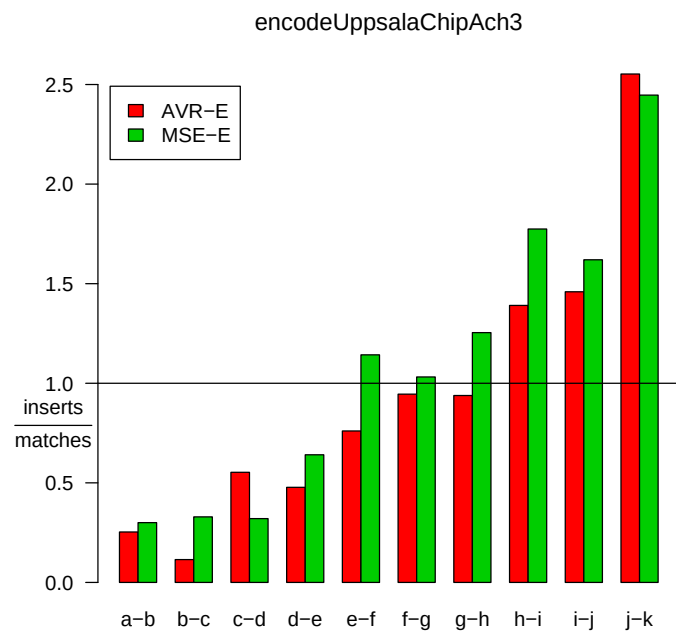
3028 3512

Category limits

|   | lower  | category  | upper  |
|---|--------|-----------|--------|
| 1 | 0.5000 | insertion | 0.6529 |
| 2 | 0.6529 | match     | 0.7460 |

0.5 0.653 0.746 0.821 0.886 0.95 1.02 1.13 1.3  
1.63 11.5

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 5   | 3   | 15  | 13  | 21  | 25  | 24  | 38  | 42  | 69  |
|       | match     |     | 203 | 269 | 279 | 280 | 284 | 272 | 263 | 281 | 296 | 278 |
| MSE-E | insertion |     | 8   | 12  | 11  | 21  | 35  | 32  | 40  | 49  | 43  | 59  |
|       | match     |     | 274 | 375 | 353 | 337 | 315 | 319 | 328 | 284 | 273 | 248 |



## 2.187 encodeUppsalaChipHnf3b

NULL

UU HNF-3b HepG2

University of Uppsala, Sweden ChIP/Chip (HNF-3b, HepG2)

|                                             | coef     | se    | z       | p     |
|---------------------------------------------|----------|-------|---------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.00874  | 0.135 | 0.0646  | 0.949 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.15200 | 0.122 | -1.2500 | 0.212 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3094

Origin.of.data.set

AVR-E MSE-E

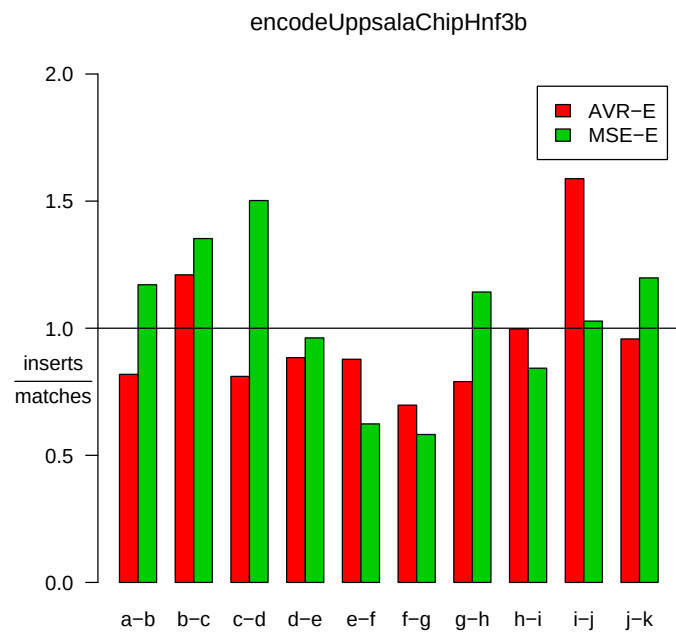
2970 3462

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.500 | insertion | 0.723 |
| 2 | 0.723 | match     | 0.793 |

0.5 0.723 0.793 0.857 0.918 0.979 1.05 1.14 1.26  
1.49 15

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 19  | 31  | 21  | 23  | 23  | 18  | 21  | 27  | 41  | 25  |     |
|       | match     | 241 | 266 | 269 | 270 | 272 | 268 | 276 | 281 | 268 | 271 |     |
| MSE-E | insertion | 30  | 40  | 45  | 29  | 20  | 19  | 34  | 25  | 30  | 36  |     |
|       | match     | 266 | 307 | 311 | 313 | 333 | 339 | 309 | 308 | 303 | 312 |     |





## 2.188 encodeUppsalaChipHnf4a

NULL

UU HNF-4a HepG2

University of Uppsala, Sweden ChIP/Chip (HNF-4a, HepG2)

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.0640 | 0.134 | -0.478 | 0.633 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.0345  | 0.121 | 0.285  | 0.775 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3047

Origin.of.data.set

AVR-E MSE-E

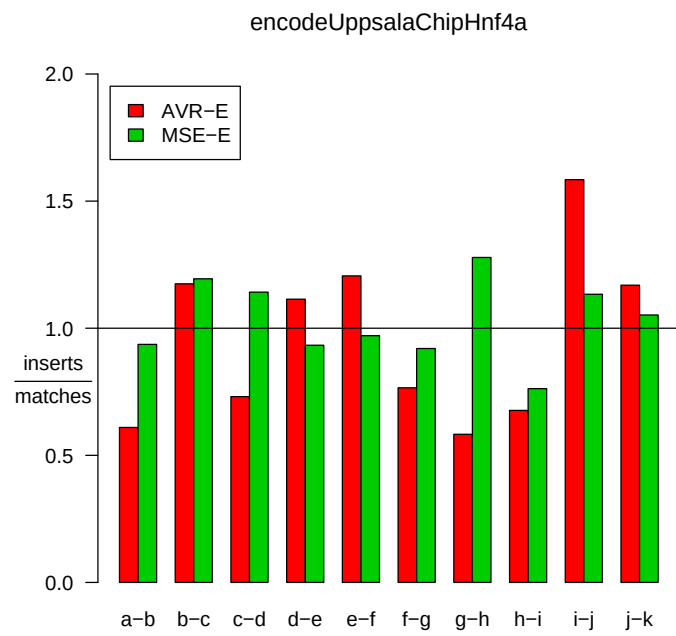
2992 3487

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.500 | insertion | 0.712 |
| 2 | 0.712 | match     | 0.784 |

0.5 0.712 0.784 0.842 0.901 0.959 1.03 1.12 1.24  
1.48 15

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 14  | 29  | 20  | 29  | 30  | 20  | 15  | 18  | 42  | 32  |
|       | match     |     | 240 | 258 | 286 | 272 | 260 | 273 | 269 | 278 | 277 | 286 |
| MSE-E | insertion |     | 25  | 36  | 33  | 30  | 30  | 28  | 40  | 24  | 32  | 30  |
|       | match     |     | 279 | 315 | 302 | 336 | 323 | 318 | 327 | 329 | 295 | 298 |



## 2.189 encodeUppsalaChipUsf1

NULL

UU USF-1 HepG2

University of Uppsala, Sweden ChIP/Chip (USF-1, HepG2)

|                                             | coef   | se    | z      | p       |
|---------------------------------------------|--------|-------|--------|---------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.109 | 0.140 | -0.775 | 0.43800 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.403 | 0.128 | -3.140 | 0.00171 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3377

Origin.of.data.set

AVR-E MSE-E

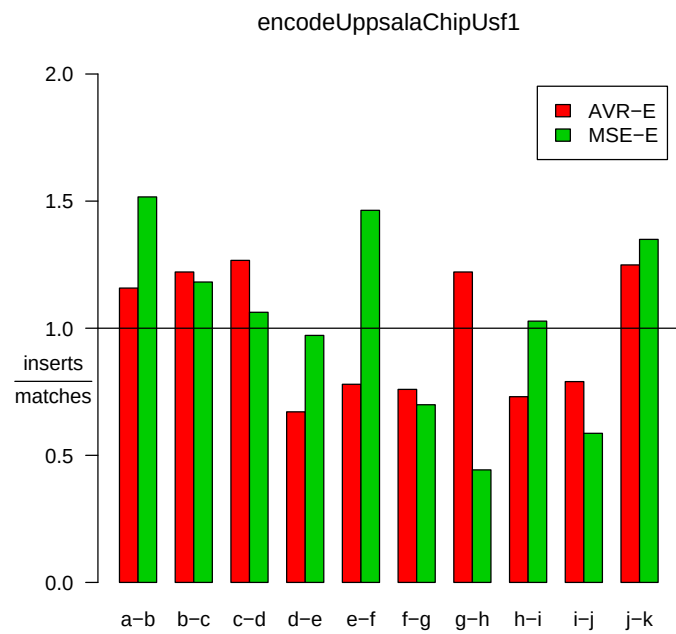
2833 3316

Category limits

|   | lower | category  | upper  |
|---|-------|-----------|--------|
| 1 | 0.500 | insertion | 0.7560 |
| 2 | 0.756 | match     | 0.8176 |

0.5 0.756 0.818 0.872 0.926 0.977 1.04 1.11 1.22  
1.41 10.7

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 24  | 30  | 31  | 17  | 19  | 18  | 30  | 19  | 21  | 32  |
|       | match     |     | 216 | 256 | 255 | 264 | 254 | 247 | 256 | 271 | 277 | 267 |
| MSE-E | insertion |     | 39  | 33  | 31  | 29  | 42  | 22  | 13  | 29  | 17  | 36  |
|       | match     |     | 268 | 291 | 304 | 311 | 299 | 328 | 306 | 294 | 302 | 278 |



## 2.190 encodeUtexChip2091fibE2F4Raw

NULL

UT E2F4 Fb

University of Texas, Austin ChIP/Chip (E2F4, 2091 fibroblasts)

|                                             | coef  | se    | z    | p      |
|---------------------------------------------|-------|-------|------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.274 | 0.154 | 1.78 | 0.0755 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.171 | 0.144 | 1.19 | 0.2330 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4836

Origin.of.data.set

AVR-E MSE-E

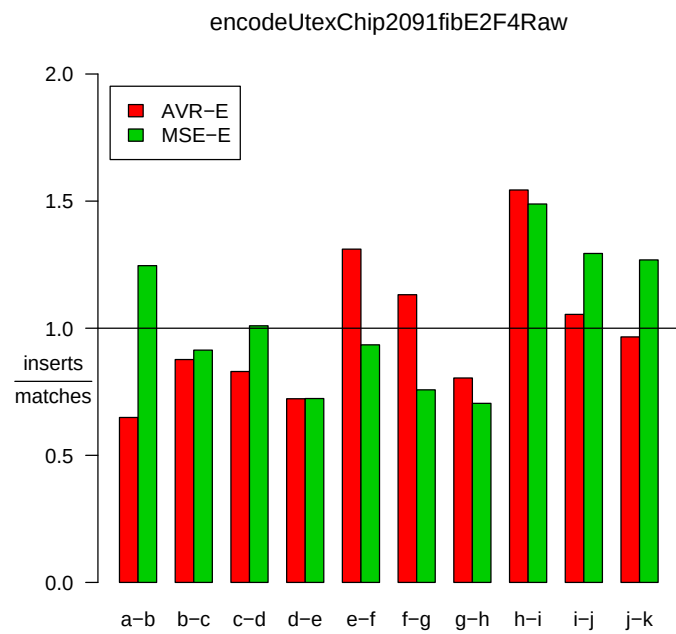
2204 2486

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | -2.40 | insertion | -0.48 |
| 2 | -0.48 | match     | -0.32 |

-2.4 -0.48 -0.32 -0.23 -0.15 -0.055 0.06 0.195  
0.38 0.65 2.91

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 16  | 17  | 16  | 15  | 21  | 26  | 15  | 34  | 24  | 23  |
|       | match     |     | 234 | 184 | 183 | 197 | 152 | 218 | 177 | 209 | 216 | 226 |
| MSE-E | insertion |     | 26  | 26  | 25  | 17  | 26  | 19  | 17  | 32  | 27  | 25  |
|       | match     |     | 198 | 270 | 235 | 223 | 264 | 238 | 229 | 204 | 198 | 187 |



## 2.191 encodeUtexChip2091fibMycRaw

NULL

UT Myc Fb

University of Texas, Austin ChIP/Chip (c-Myc, 2091 fibroblasts)

|                                             | coef   | se    | z      | p     |
|---------------------------------------------|--------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.133 | 0.154 | -0.868 | 0.385 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.203  | 0.144 | 1.420  | 0.157 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4836

Origin.of.data.set

AVR-E MSE-E

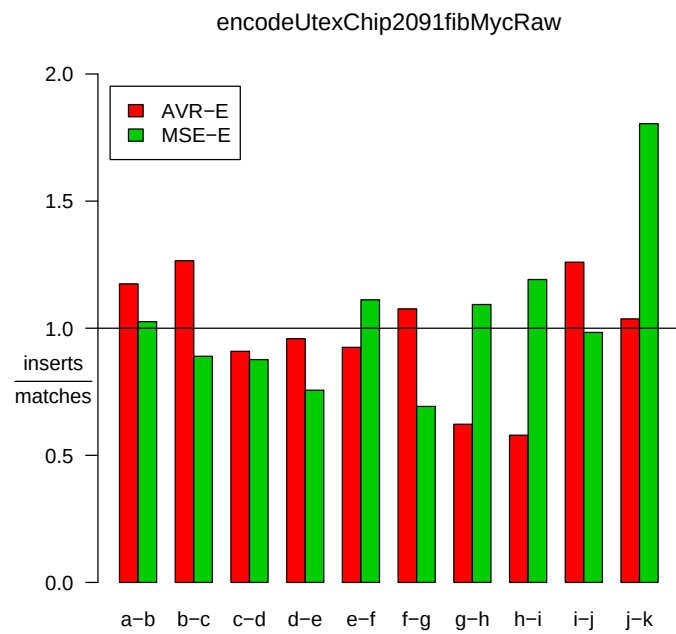
2204 2486

Category limits

|   | lower  | category  | upper |
|---|--------|-----------|-------|
| 1 | -1.835 | insertion | -0.34 |
| 2 | -0.340 | match     | -0.22 |

-1.83 -0.34 -0.22 -0.15 -0.09 -0.03 0.04 0.12  
0.24 0.43 1.65

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 25  | 24  | 16  | 20  | 19  | 22  | 12  | 13  | 30  | 26  |
|       | match     |     | 202 | 180 | 167 | 198 | 195 | 194 | 183 | 213 | 226 | 238 |
| MSE-E | insertion |     | 24  | 24  | 23  | 20  | 28  | 17  | 25  | 28  | 20  | 31  |
|       | match     |     | 222 | 256 | 249 | 251 | 239 | 233 | 217 | 223 | 193 | 163 |





## 2.192 encodeUtexChip2091fibMycStimRaw

NULL

UT Myc st-Fb

University of Texas, Austin ChIP/Chip (c-Myc, FBS-stimulated 2091 fibroblasts)

|                                             | coef   | se    | z     | p     |
|---------------------------------------------|--------|-------|-------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.0815 | 0.155 | 0.527 | 0.598 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.1590 | 0.146 | 1.090 | 0.276 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4836

Origin.of.data.set

AVR-E MSE-E

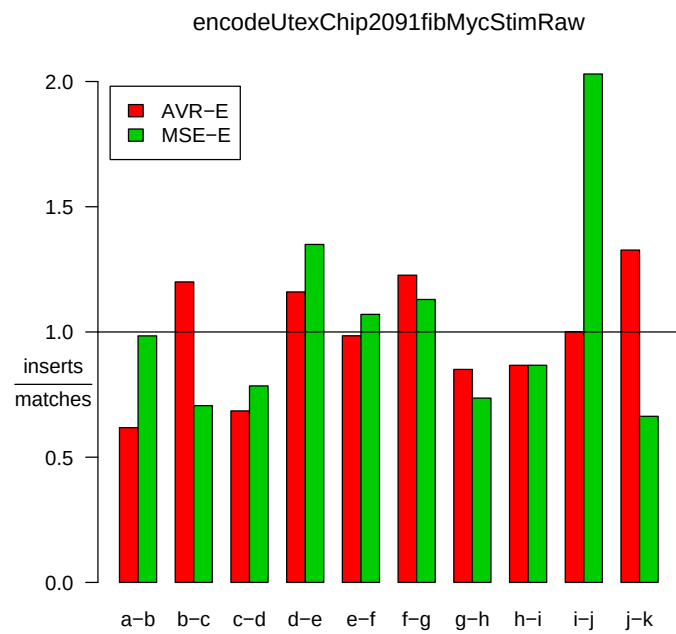
2204 2486

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | -1.13 | insertion | -0.26 |
| 2 | -0.26 | match     | -0.18 |

-1.13 -0.26 -0.18 -0.12 -0.07 -0.01 0.045 0.12  
0.235 0.465 2.65

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 14  | 22  | 14  | 22  | 22  | 19  | 19  | 19  | 23  | 33  |
|       | match     |     | 215 | 174 | 194 | 180 | 212 | 147 | 212 | 208 | 218 | 236 |
| MSE-E | insertion |     | 25  | 18  | 21  | 31  | 30  | 25  | 19  | 18  | 40  | 13  |
|       | match     |     | 241 | 242 | 254 | 218 | 266 | 210 | 245 | 197 | 187 | 186 |



## 2.193 encodeUtexChipHeLaMycRaw

NULL

UT Myc HeLa

University of Texas, Austin ChIP/Chip (c-Myc, HeLa)

|                                             | coef  | se    | z     | p      |
|---------------------------------------------|-------|-------|-------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.143 | 0.156 | 0.919 | 0.3580 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.362 | 0.145 | 2.500 | 0.0123 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4836

Origin.of.data.set

AVR-E MSE-E

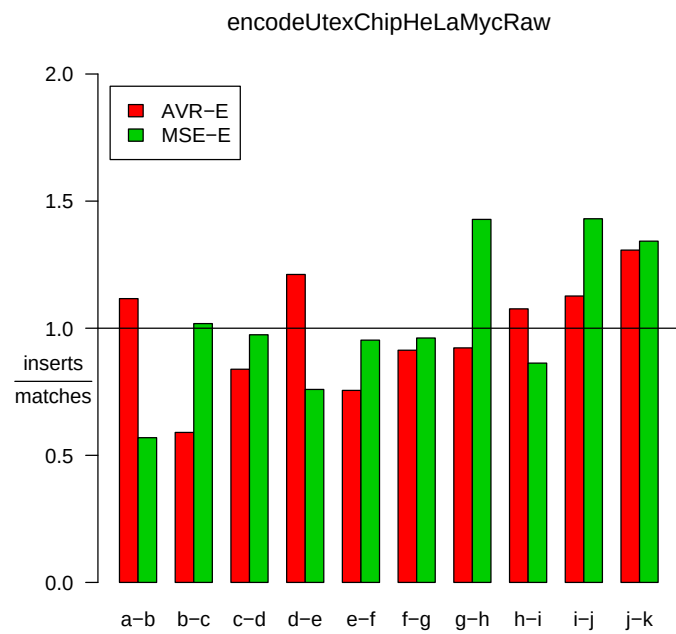
2204 2486

Category limits

|   | lower  | category  | upper  |
|---|--------|-----------|--------|
| 1 | -1.360 | insertion | -0.335 |
| 2 | -0.335 | match     | -0.226 |

-1.36 -0.335 -0.226 -0.14 -0.07 0.01 0.09 0.19  
0.31 0.54 2.73

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 22  | 12  | 19  | 24  | 16  | 18  | 21  | 22  | 26  | 27  |
|       | match     |     | 187 | 193 | 215 | 188 | 201 | 187 | 216 | 194 | 219 | 196 |
| MSE-E | insertion |     | 15  | 25  | 27  | 18  | 23  | 23  | 31  | 19  | 30  | 29  |
|       | match     |     | 250 | 233 | 263 | 225 | 229 | 227 | 206 | 209 | 199 | 205 |



## 2.194 encodeYaleAffyNB4RARNATransMap

NULL

Yale RNA NB4 RA

Yale NB4 RNA Transcript Map, Treated with Retinoic Acid

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.681 | 0.133 | 5.13 | 2.88e-07 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.702 | 0.125 | 5.60 | 2.08e-08 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3174

Origin.of.data.set

AVR-E MSE-E

2968 3384

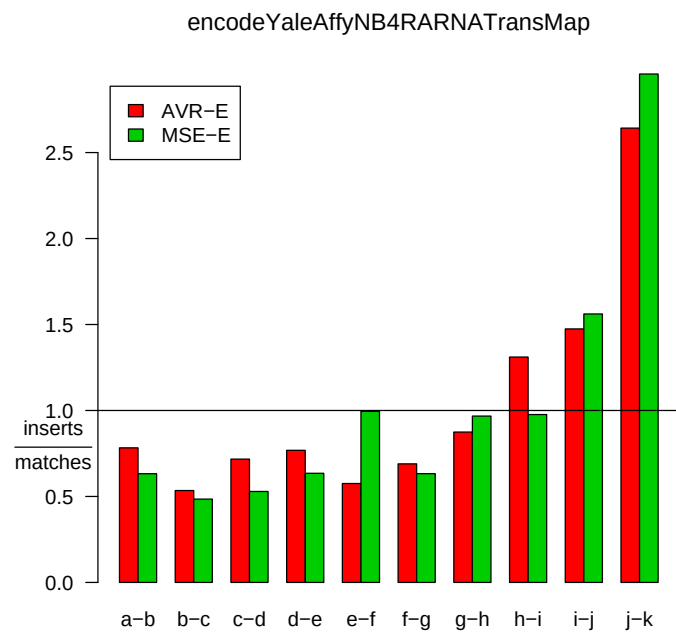
Category limits

|   | lower      | category  | upper     |
|---|------------|-----------|-----------|
| 1 | -43.674320 | insertion | -1.165522 |
| 2 | -1.165522  | match     | -0.401207 |

-43.7 -1.17 -0.401 0.00453 0.345 0.736 1.21 1.84

2.94 5.44 302

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 25  | 15  | 19  | 21  | 15  | 20  | 25  | 35  | 44  | 70  |
|       | match     |     | 305 | 268 | 253 | 261 | 249 | 277 | 273 | 255 | 285 | 253 |
| MSE-E | insertion |     | 19  | 17  | 19  | 22  | 35  | 21  | 31  | 32  | 43  | 74  |
|       | match     |     | 287 | 335 | 343 | 331 | 336 | 317 | 306 | 313 | 263 | 239 |



## 2.195 encodeYaleAffyNB4TPARNATransMap

NULL

Yale RNA NB4 TPA

Yale NB4 RNA Transcript Map, Treated with 12-0-tetradecanoylphorbol-13 Acetate (TPA)

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.538 | 0.130 | 4.15 | 3.30e-05 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.894 | 0.131 | 6.83 | 8.42e-12 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3174

Origin.of.data.set

AVR-E MSE-E

2968 3384

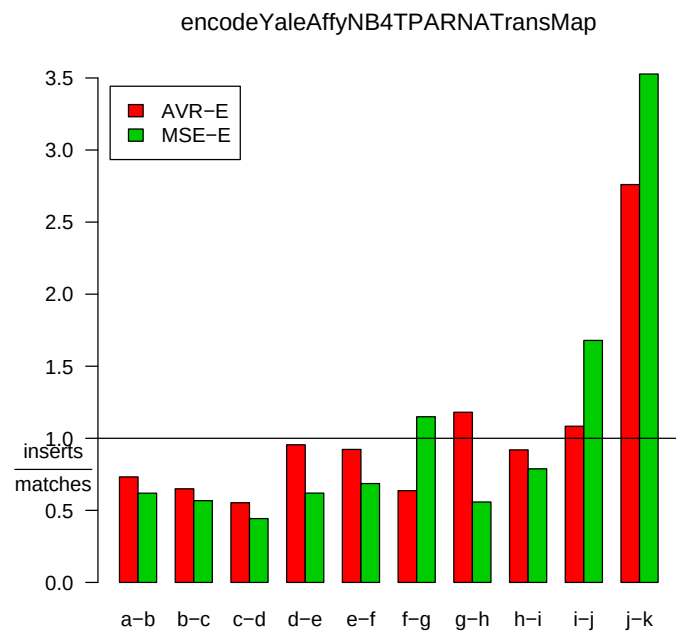
Category limits

|   | lower      | category  | upper      |
|---|------------|-----------|------------|
| 1 | -33.947433 | insertion | -1.1922924 |
| 2 | -1.192292  | match     | -0.4857754 |

-33.9 -1.19 -0.486 -0.0625 0.298 0.645 1.06 1.64

2.67 4.67 277

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 23  | 20  | 15  | 25  | 23  | 17  | 34  | 26  | 32  | 74  |
|       | match     |     | 300 | 294 | 259 | 250 | 238 | 255 | 275 | 270 | 282 | 256 |
| MSE-E | insertion |     | 19  | 18  | 16  | 22  | 25  | 39  | 18  | 26  | 48  | 82  |
|       | match     |     | 293 | 303 | 345 | 339 | 348 | 324 | 308 | 315 | 273 | 222 |





## 2.196 encodeYaleAffyNB4UntrRNATransMap

NULL

Yale RNA NB4 Un

Yale NB4 RNA Transcript Map, Untreated

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.695 | 0.133 | 5.21 | 1.87e-07 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.762 | 0.127 | 6.02 | 1.78e-09 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3174

Origin.of.data.set

AVR-E MSE-E

2968 3384

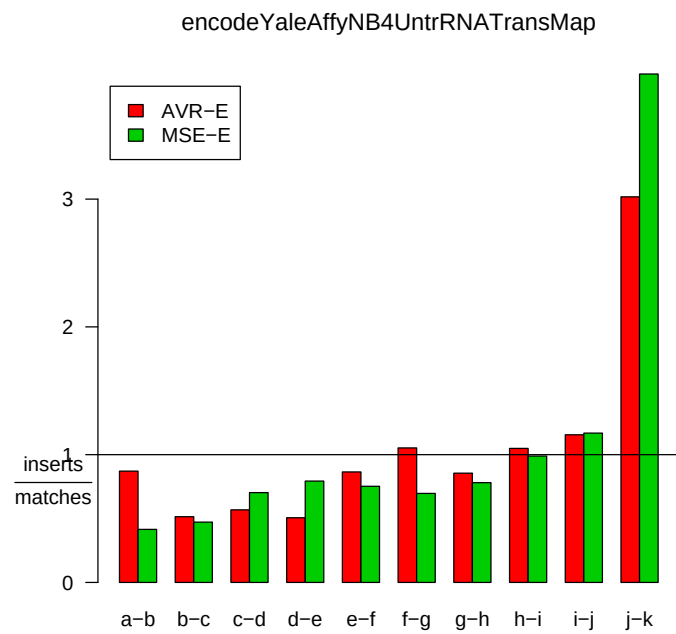
Category limits

|   | lower      | category  | upper      |
|---|------------|-----------|------------|
| 1 | -35.043808 | insertion | -1.1388443 |
| 2 | -1.138844  | match     | -0.3867652 |

-35 -1.14 -0.387 0.0062 0.364 0.732 1.16 1.74

2.82 5.29 366

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 27  | 14  | 16  | 15  | 23  | 28  | 24  | 29  | 34  | 79  |     |
|       | match     | 296 | 260 | 269 | 283 | 254 | 254 | 268 | 264 | 281 | 250 |     |
| MSE-E | insertion | 13  | 17  | 24  | 26  | 26  | 24  | 26  | 32  | 35  | 90  |     |
|       | match     | 299 | 344 | 326 | 313 | 330 | 329 | 318 | 309 | 286 | 216 |     |



## 2.197 encodeYaleAffyNeutRNATransMapAll

NULL

Yale RNA Neu Sum

Yale Neutrophil RNA Transcript Map, Summary

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.608 | 0.132 | 4.59 | 4.41e-06 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.823 | 0.127 | 6.47 | 9.90e-11 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3174

Origin.of.data.set

AVR-E MSE-E

2968 3384

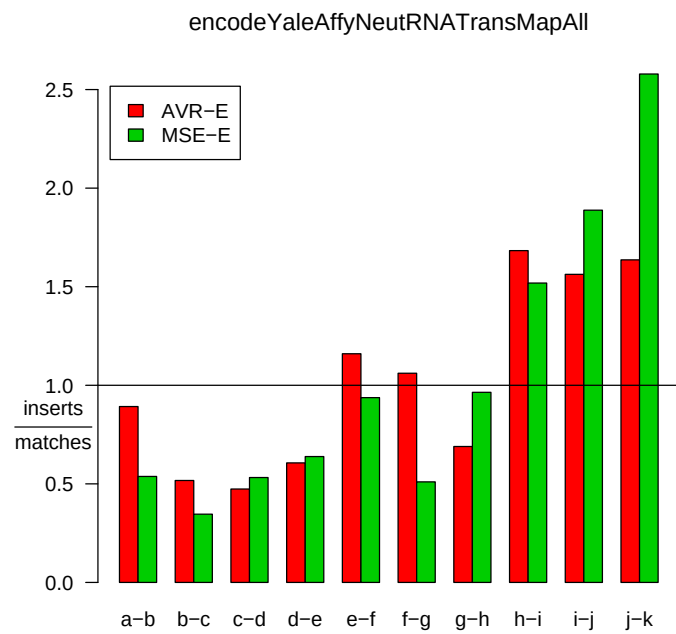
Category limits

|   | lower       | category  | upper       |
|---|-------------|-----------|-------------|
| 1 | -43.8968201 | insertion | -0.73993964 |
| 2 | -0.7399396  | match     | -0.07368087 |

-43.9 -0.74 -0.0737 0.347 0.761 1.22 1.88 2.88

4.44 8.54 371

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 27  | 15  | 13  | 16  | 30  | 28  | 20  | 46  | 45  | 49  |
|       | match     |     | 289 | 277 | 262 | 252 | 247 | 252 | 277 | 261 | 275 | 286 |
| MSE-E | insertion |     | 17  | 12  | 19  | 23  | 32  | 18  | 31  | 45  | 52  | 64  |
|       | match     |     | 302 | 331 | 341 | 344 | 326 | 337 | 307 | 283 | 263 | 237 |



## 2.198 encodeYaleAffyPlacRNATransMap

NULL

Yale RNA Plcnta

Yale Placenta RNA Transcript Map

|                                             | coef  | se    | z    | p        |
|---------------------------------------------|-------|-------|------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.862 | 0.139 | 6.22 | 4.83e-10 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 1.120 | 0.133 | 8.45 | 2.99e-17 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 3174

Origin.of.data.set

AVR-E MSE-E

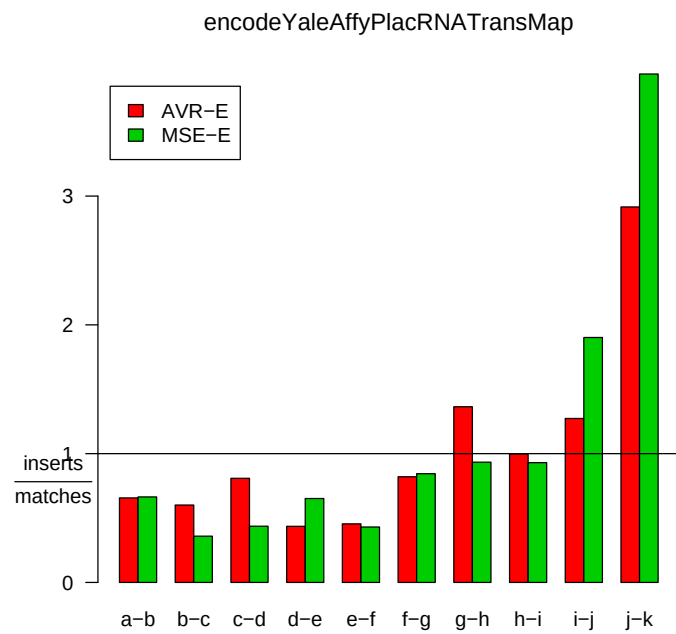
2968 3384

Category limits

|   | lower       | category  | upper      |
|---|-------------|-----------|------------|
| 1 | -47.4585190 | insertion | -0.7096193 |
| 2 | -0.7096193  | match     | -0.2229645 |

-47.5 -0.71 -0.223 0.0468 0.29 0.552 0.865 1.36  
2.32 5.61 848

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 20  | 18  | 21  | 12  | 12  | 22  | 36  | 28  | 40  | 80  |
|       | match     |     | 291 | 286 | 248 | 263 | 252 | 256 | 252 | 268 | 300 | 262 |
| MSE-E | insertion |     | 21  | 12  | 16  | 23  | 16  | 29  | 31  | 30  | 49  | 86  |
|       | match     |     | 302 | 319 | 350 | 337 | 355 | 328 | 317 | 308 | 246 | 208 |



## 2.199 encodeYaleChipPvalBaf155

NULL

Yale BAF155 Pval

Yale ChIP/Chip (BAF155 ab, HeLa cells) P-Value

|                                             | coef   | se    | z      | p     |
|---------------------------------------------|--------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.195 | 0.153 | -1.270 | 0.204 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.143  | 0.146 | 0.981  | 0.326 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4866

Origin.of.data.set

AVR-E MSE-E

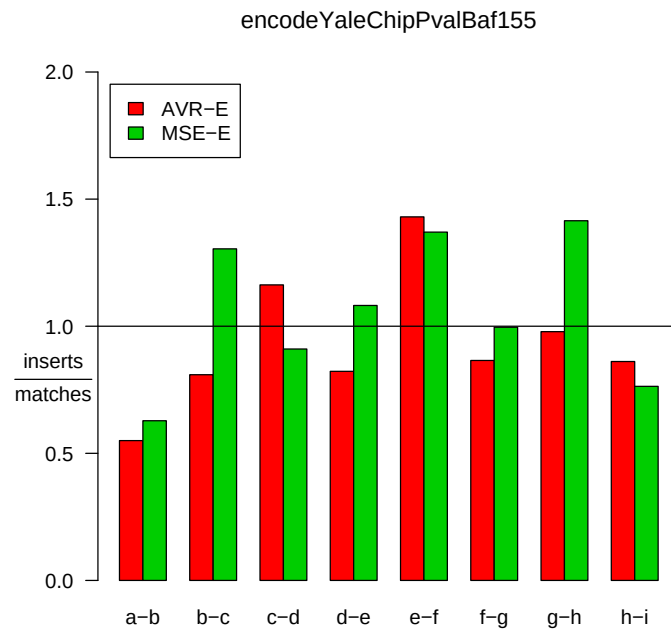
2194 2466

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.000 | insertion | 0.004 |
| 2 | 0.004 | match     | 0.023 |

0 0.004 0.023 0.0975 0.324 0.824 1.78 4.28 20

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 10  | 14  | 20  | 16  | 26  | 17  | 22  | 25  |
|       | match     |     | 186 | 177 | 176 | 199 | 186 | 201 | 230 | 297 |
| MSE-E | insertion |     | 14  | 32  | 21  | 24  | 30  | 22  | 26  | 10  |
|       | match     |     | 228 | 251 | 236 | 227 | 224 | 226 | 188 | 134 |





## 2.200 encodeYaleChipPvalBaf170

NULL

Yale BAF170 Pval

Yale ChIP/Chip (BAF170 ab, HeLa cells) P-Value

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.2340 | 0.154 | -1.520 | 0.127 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.0904  | 0.148 | 0.612  | 0.540 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4866

Origin.of.data.set

AVR-E MSE-E

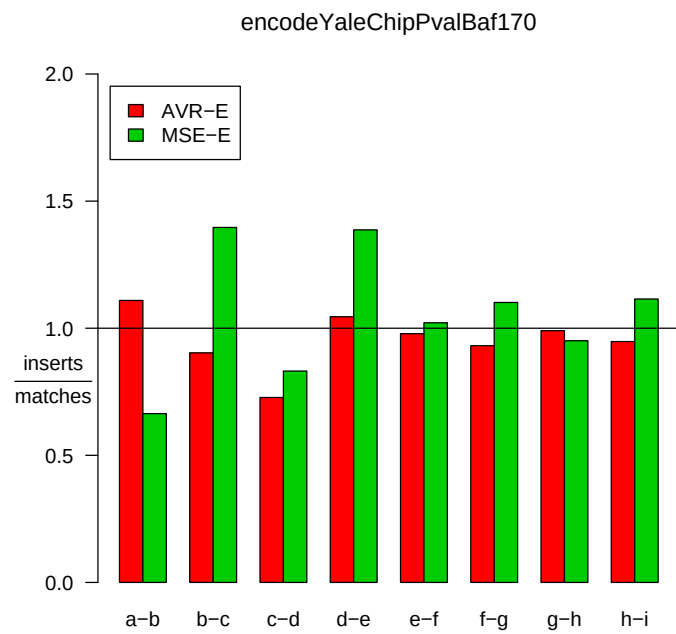
2194 2466

Category limits

|   | lower | category  | upper  |
|---|-------|-----------|--------|
| 1 | 0.000 | insertion | 0.0050 |
| 2 | 0.005 | match     | 0.0243 |

0 0.005 0.0243 0.114 0.371 0.933 2.17 4.6 20

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 21  | 13  | 13  | 21  | 19  | 17  | 22  | 27  |
|       | match     |     | 196 | 149 | 185 | 208 | 201 | 189 | 230 | 295 |
| MSE-E | insertion |     | 17  | 29  | 20  | 28  | 22  | 25  | 18  | 14  |
|       | match     |     | 265 | 215 | 249 | 209 | 223 | 235 | 196 | 130 |



## 2.201 encodeYaleChipPvalFos

NULL

Yale c-Fos Pval

Yale ChIP/Chip (c-Fos ab, HeLa cells) P-Value

|                                             | coef   | se    | z     | p       |
|---------------------------------------------|--------|-------|-------|---------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.343 | 0.157 | -2.18 | 0.02950 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.567 | 0.150 | -3.79 | 0.00015 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4866

Origin.of.data.set

AVR-E MSE-E

2194 2466

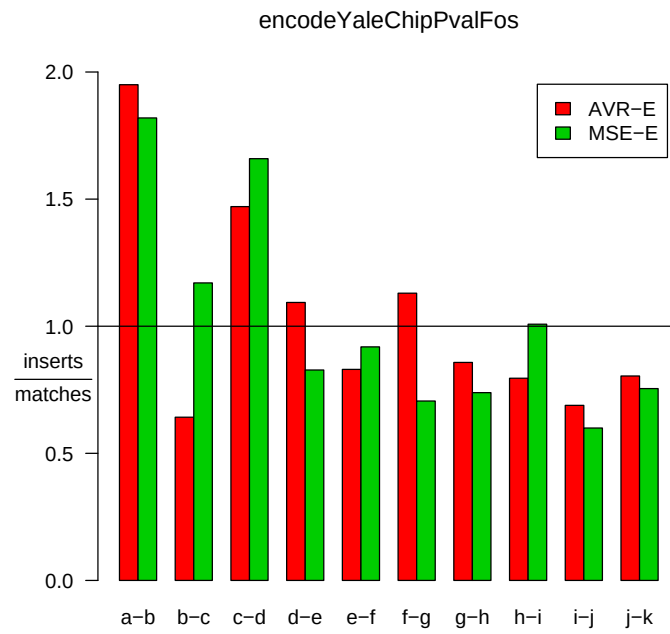
Category limits

|   | lower | category  | upper  |
|---|-------|-----------|--------|
| 1 | 0.000 | insertion | 0.0140 |
| 2 | 0.014 | match     | 0.0608 |

0 0.014 0.0608 0.139 0.262 0.419 0.644 0.952 1.43

2.3 8.98

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 30  | 12  | 29  | 21  | 15  | 21  | 17  | 17  | 16  | 23  |     |
|       | match     | 149 | 181 | 191 | 186 | 175 | 180 | 192 | 207 | 225 | 277 |     |
| MSE-E | insertion | 34  | 29  | 37  | 20  | 24  | 18  | 18  | 23  | 13  | 12  |     |
|       | match     | 181 | 240 | 216 | 234 | 253 | 247 | 236 | 221 | 210 | 154 |     |



## 2.202 encodeYaleChipPvalJun

NULL

Yale c-Jun Pval

Yale ChIP/Chip (c-Jun ab, HeLa cells) P-Value

|                                             | coef   | se    | z     | p      |
|---------------------------------------------|--------|-------|-------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.141 | 0.155 | -0.91 | 0.3630 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.377 | 0.147 | -2.56 | 0.0104 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4866

Origin.of.data.set

AVR-E MSE-E

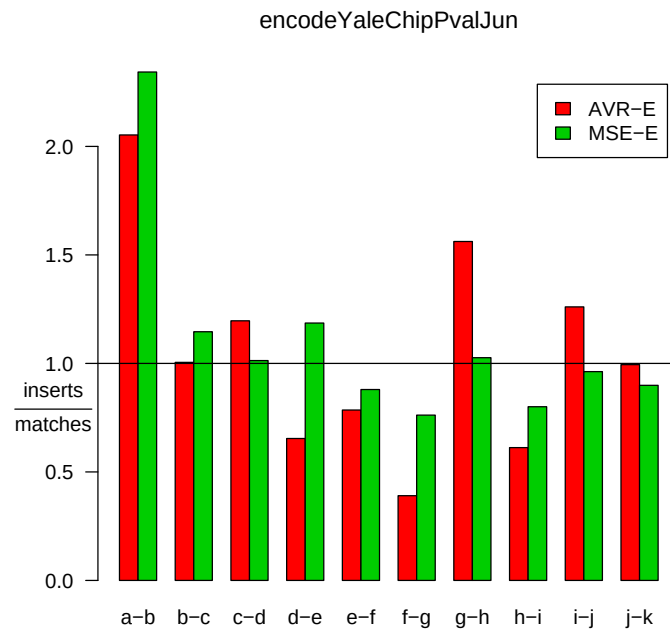
2194 2466

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.000 | insertion | 0.001 |
| 2 | 0.001 | match     | 0.008 |

0 0.001 0.008 0.029 0.082 0.192 0.387 0.732 1.43  
3.26 13.2

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 12  | 14  | 19  | 13  | 14  | 7   | 28  | 13  | 28  | 28  |     |
|       | match     | 60  | 143 | 163 | 204 | 183 | 184 | 184 | 218 | 228 | 289 |     |
| MSE-E | insertion | 21  | 23  | 23  | 26  | 21  | 19  | 23  | 17  | 18  | 12  |     |
|       | match     | 92  | 206 | 233 | 225 | 245 | 256 | 230 | 218 | 192 | 137 |     |



## 2.203 encodeYaleChipPvalTaf

NULL

Yale TAF1 Pval

Yale ChIP/Chip (TAF1 ab, HeLa cells) P-Value

|                                             | coef   | se    | z     | p      |
|---------------------------------------------|--------|-------|-------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.308 | 0.155 | -1.99 | 0.0465 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.307 | 0.147 | -2.09 | 0.0366 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4866

Origin.of.data.set

AVR-E MSE-E

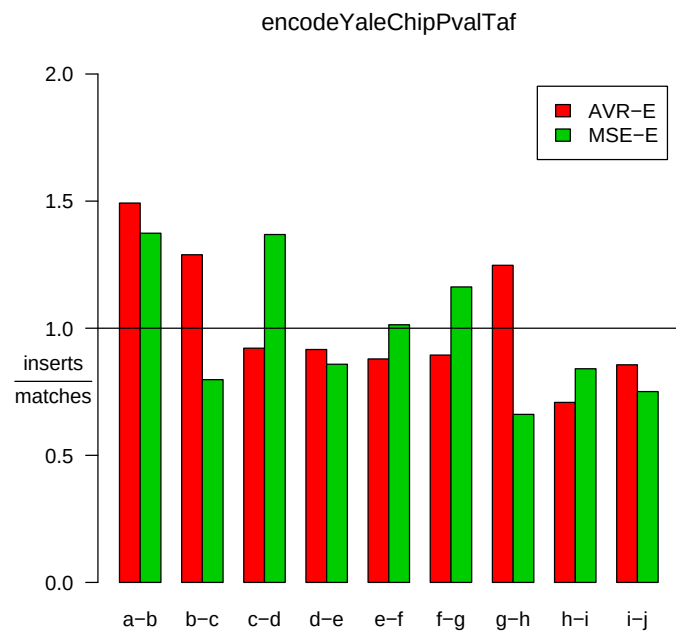
2194 2466

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.000 | insertion | 0.005 |
| 2 | 0.005 | match     | 0.021 |

0 0.005 0.021 0.065 0.163 0.348 0.663 1.32 2.86  
9.44

|       | brk       | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| set   | type      |     |     |     |     |     |     |     |     |     |
| AVR-E | insertion | 24  | 22  | 16  | 16  | 17  | 18  | 24  | 16  | 25  |
|       | match     | 163 | 173 | 176 | 177 | 196 | 204 | 195 | 229 | 296 |
| MSE-E | insertion | 37  | 17  | 32  | 21  | 23  | 25  | 15  | 17  | 10  |
|       | match     | 273 | 216 | 237 | 248 | 230 | 218 | 230 | 205 | 135 |





## 2.204 encodeYaleChipSignalBaf155

NULL

Yale BAF155 Sig

Yale ChIP/Chip (BAF155 ab, HeLa cells) Signal

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.0959 | 0.156 | -0.617 | 0.538 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.1310  | 0.152 | 0.862  | 0.389 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4866

Origin.of.data.set

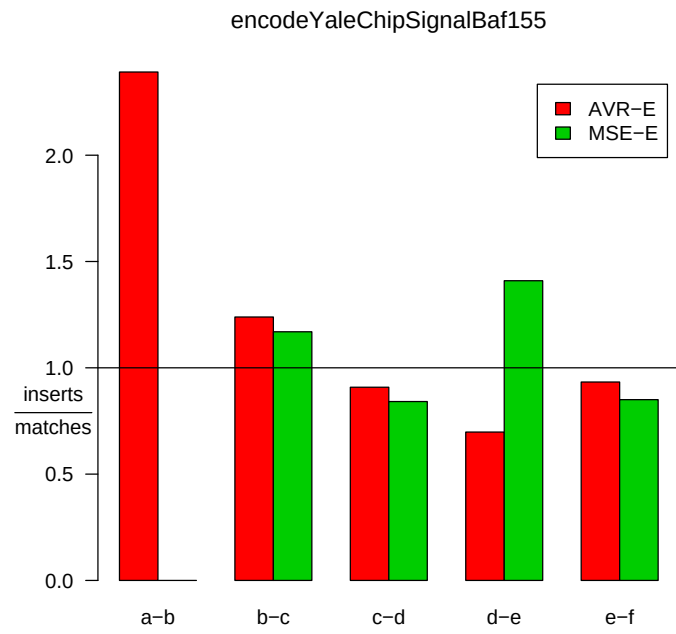
AVR-E MSE-E

2194 2466

Category limits

|   | lower | category  | upper            |
|---|-------|-----------|------------------|
| 1 | 0.000 | insertion | 0.002            |
| 2 | 0.002 | match     | 0.060            |
| 0 | 0.002 | 0.06      | 0.132 0.265 1.04 |

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f |
|-------|-----------|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 1   | 25  | 19  | 17  | 28  |     |
|       | match     | 4   | 193 | 200 | 233 | 287 |     |
| MSE-E | insertion | 0   | 28  | 19  | 28  | 12  |     |
|       | match     | 6   | 229 | 216 | 190 | 135 |     |



## 2.205 encodeYaleChipSignalBaf170

NULL

Yale BAF170 Sig

Yale ChIP/Chip (BAF170 ab, HeLa cells) Signal

|                                             | coef    | se    | z      | p      |
|---------------------------------------------|---------|-------|--------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.3300 | 0.155 | -2.130 | 0.0328 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.0911 | 0.155 | -0.588 | 0.5560 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4866

Origin.of.data.set

AVR-E MSE-E

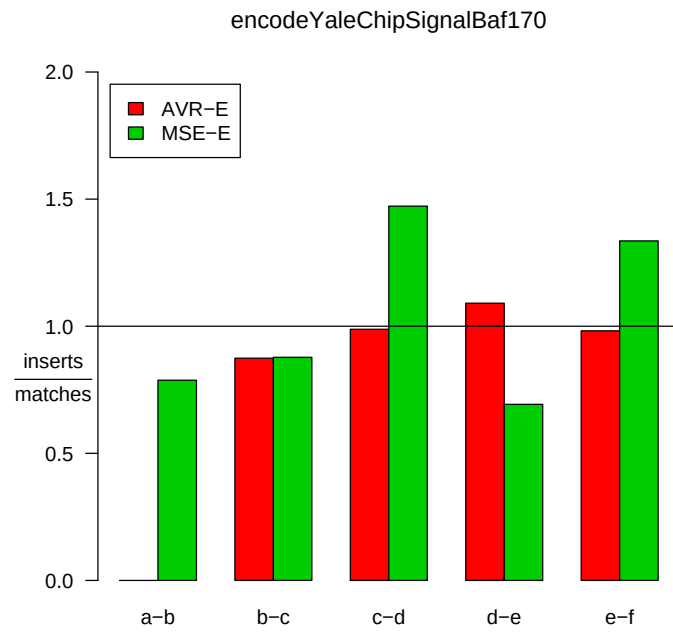
2194 2466

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.00  | insertion | 0.010 |
| 2 | 0.01  | match     | 0.073 |

0 0.01 0.073 0.155 0.305 1.13

|       | set       | type | brk | a-b | b-c | c-d | d-e | e-f |
|-------|-----------|------|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |      | 0   | 16  | 19  | 23  | 26  |     |
|       | match     |      | 35  | 197 | 207 | 227 | 285 |     |
| MSE-E | insertion |      | 3   | 19  | 29  | 13  | 17  |     |
|       | match     |      | 41  | 233 | 212 | 202 | 137 |     |



## 2.206 encodeYaleChipSignalFos

NULL

Yale c-Fos Sig

Yale ChIP/Chip (c-Fos ab, HeLa cells) Signal

|                                             | coef   | se    | z     | p        |
|---------------------------------------------|--------|-------|-------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.396 | 0.158 | -2.51 | 1.20e-02 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.594 | 0.151 | -3.94 | 8.25e-05 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4866

Origin.of.data.set

AVR-E MSE-E

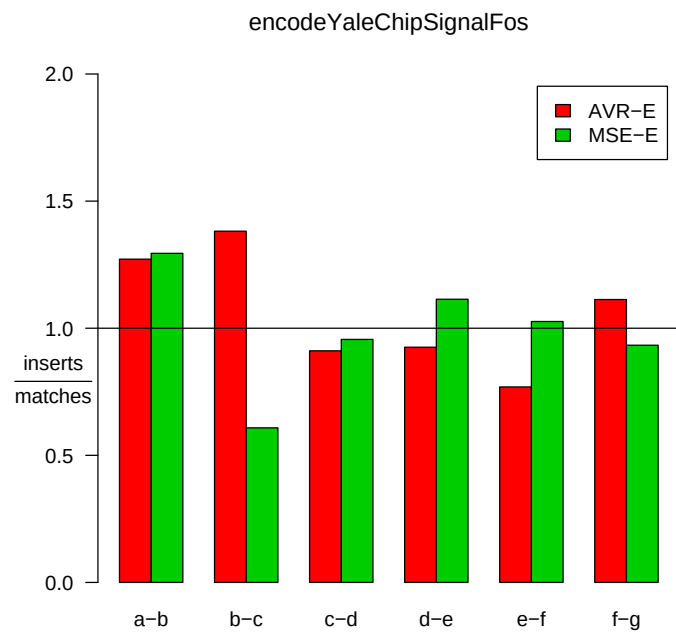
2194 2466

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.00  | insertion | 0.020 |
| 2 | 0.02  | match     | 0.055 |

0 0.02 0.055 0.092 0.143 0.22 1.38

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 12  | 21  | 14  | 17  | 14  | 25  |     |
|       | match     | 113 | 182 | 184 | 220 | 218 | 269 |     |
| MSE-E | insertion | 16  | 13  | 19  | 20  | 18  | 12  |     |
|       | match     | 148 | 256 | 238 | 215 | 210 | 154 |     |



## 2.207 encodeYaleChipSignalJun

NULL

Yale c-Jun Sig

Yale ChIP/Chip (c-Jun ab, HeLa cells) Signal

|                                             | coef     | se    | z       | p      |
|---------------------------------------------|----------|-------|---------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.00837  | 0.156 | 0.0537  | 0.9570 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.30400 | 0.154 | -1.9800 | 0.0478 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4866

Origin.of.data.set

AVR-E MSE-E

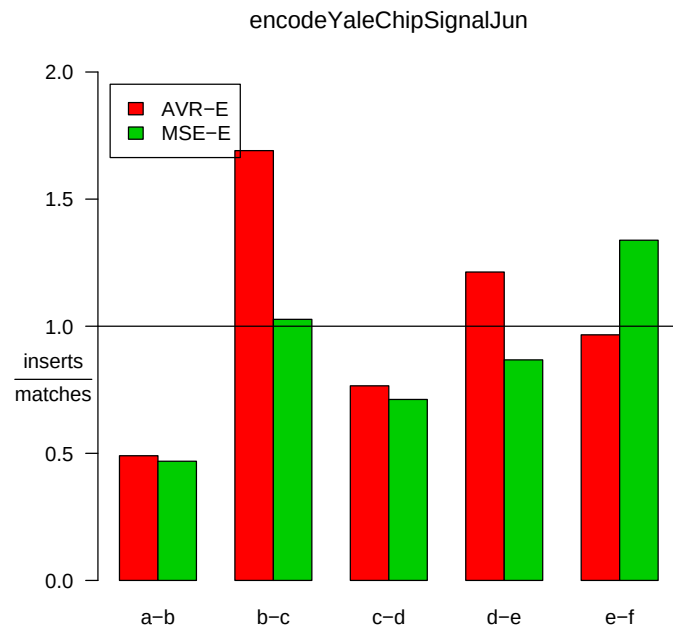
2194 2466

Category limits

|   | lower | category  | upper |
|---|-------|-----------|-------|
| 1 | 0.000 | insertion | 0.017 |
| 2 | 0.017 | match     | 0.068 |

0 0.017 0.068 0.145 0.297 1.23

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f |
|-------|-----------|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 3   | 28  | 17  | 25  | 26  |
|       | match     |     | 65  | 176 | 236 | 219 | 286 |
| MSE-E | insertion |     | 3   | 23  | 14  | 16  | 17  |
|       | match     |     | 68  | 238 | 209 | 196 | 135 |





## 2.208 encodeYaleChipSignalTaf

NULL

Yale TAF1 Sig

Yale ChIP/Chip (TAF1 ab, HeLa cells) Signal

|                                             | coef   | se    | z     | p      |
|---------------------------------------------|--------|-------|-------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.206 | 0.157 | -1.31 | 0.1900 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.262 | 0.157 | -1.67 | 0.0952 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4866

Origin.of.data.set

AVR-E MSE-E

2194 2466

Category limits

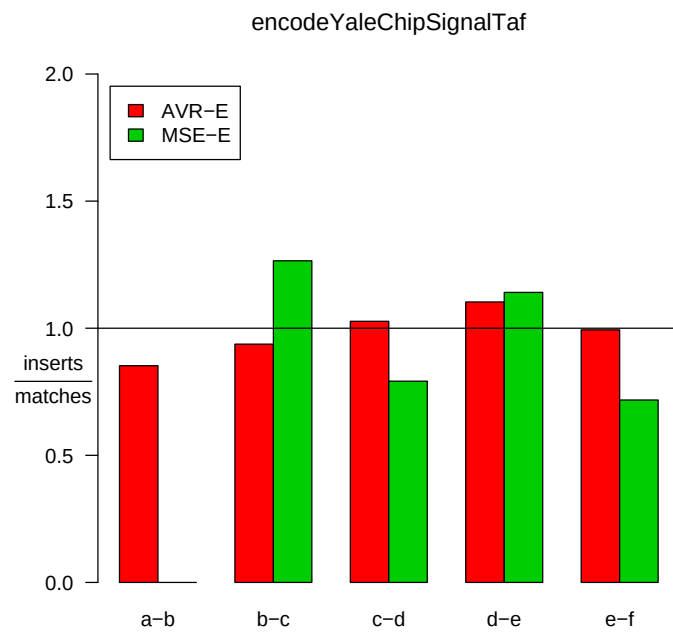
|  | lower | category | upper |
|--|-------|----------|-------|
|--|-------|----------|-------|

|   |       |           |       |
|---|-------|-----------|-------|
| 1 | 0.000 | insertion | 0.005 |
|---|-------|-----------|-------|

|   |       |       |       |
|---|-------|-------|-------|
| 2 | 0.005 | match | 0.098 |
|---|-------|-------|-------|

0 0.005 0.098 0.256 0.68 2.7

|       | set       | type | brk | a-b | b-c | c-d | d-e | e-f |
|-------|-----------|------|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |      | 1   | 17  | 19  | 22  | 26  |     |
|       | match     |      | 13  | 201 | 205 | 221 | 290 |     |
| MSE-E | insertion |      | 0   | 25  | 16  | 21  | 9   |     |
|       | match     |      | 13  | 219 | 224 | 204 | 139 |     |



## 2.209 encodeYaleChIPSTAT1HeLaBingRenPval

NULL

Yale LI PVal

Yale ChIP/Chip (STAT1 ab, HeLa cells) LI/UCSD PCR Amplicon, P-Value

|                                             | coef    | se    | z     | p     |
|---------------------------------------------|---------|-------|-------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.1130 | 0.163 | -0.69 | 0.490 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.0901 | 0.150 | -0.60 | 0.548 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5402

Origin.of.data.set

AVR-E MSE-E

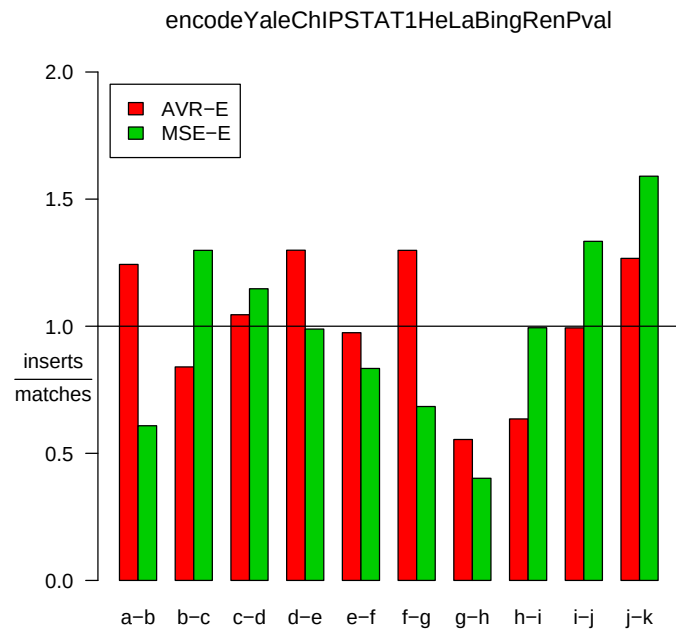
1973 2151

Category limits

|   | lower     | category  | upper      |
|---|-----------|-----------|------------|
| 1 | 0.0000000 | insertion | 0.02731140 |
| 2 | 0.0273114 | match     | 0.07727036 |

0 0.0273 0.0773 0.135 0.199 0.276 0.358 0.477  
0.639 0.942 5.24

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 11  | 17  | 20  | 25  | 18  | 27  | 13  | 13  | 20  | 22  |
|       | match     |     | 80  | 183 | 173 | 174 | 167 | 188 | 212 | 185 | 182 | 157 |
| MSE-E | insertion |     | 7   | 27  | 25  | 21  | 19  | 14  | 8   | 21  | 27  | 35  |
|       | match     |     | 104 | 188 | 197 | 192 | 206 | 185 | 180 | 191 | 183 | 199 |



## 2.210 encodeYaleChIPSTAT1HeLaBingRenSig

NULL

Yale LI Sig

Yale ChIP/Chip (STAT1 ab, HeLa cells) LI/UCSD PCR Amplicon, Signal

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.0978 | 0.160 | -0.613 | 0.540 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.0649  | 0.151 | 0.430  | 0.667 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5402

Origin.of.data.set

AVR-E MSE-E

1973 2151

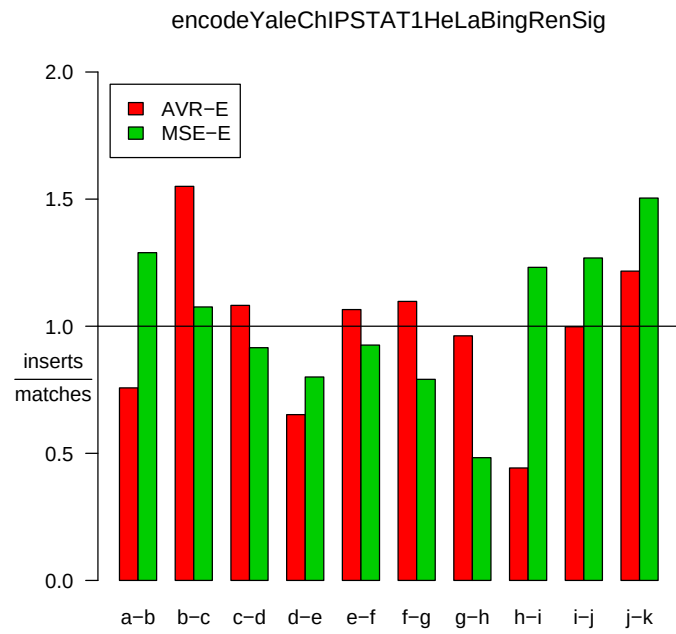
Category limits

|   | lower      | category  | upper      |
|---|------------|-----------|------------|
| 1 | -2.2021401 | insertion | -0.3527535 |
| 2 | -0.3527535 | match     | -0.2142504 |

-2.2 -0.353 -0.214 -0.124 -0.0425 0.0258 0.0793

0.14 0.219 0.316 1.03

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 14  | 29  | 20  | 13  | 21  | 22  | 21  | 10  | 21  | 21  |
|       | match     |     | 166 | 168 | 166 | 179 | 177 | 180 | 196 | 203 | 189 | 155 |
| MSE-E | insertion |     | 29  | 23  | 21  | 18  | 20  | 17  | 10  | 24  | 25  | 34  |
|       | match     |     | 202 | 192 | 206 | 202 | 194 | 193 | 186 | 175 | 177 | 203 |



## 2.211 encodeYaleChIPSTAT1HeLaMaskLess36mer36bpPval

NULL

Yale 36-36 PVal

Yale ChIP/Chip (STAT1 ab, HeLa cells) Maskless 36-mer, 36bp Win, P-Value

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.1300 | 0.153 | -0.854 | 0.393 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.0506 | 0.142 | -0.357 | 0.721 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5190

Origin.of.data.set

AVR-E MSE-E

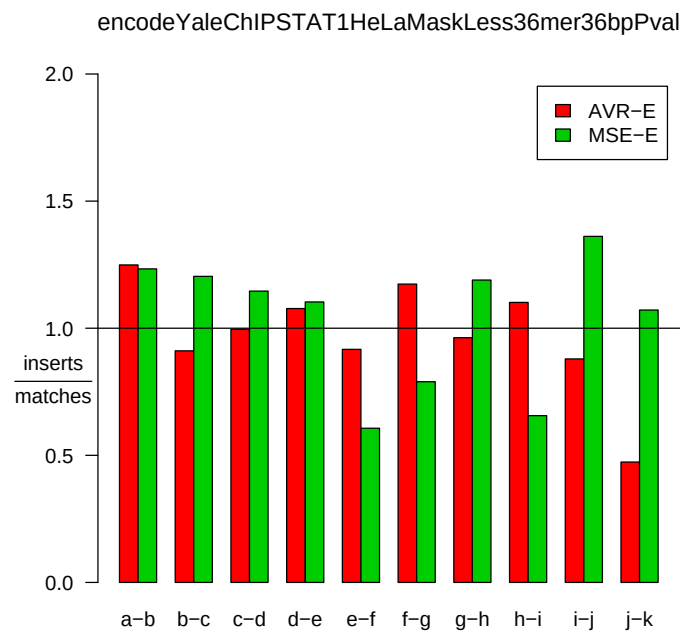
2044 2292

Category limits

|   | lower     | category  | upper     |
|---|-----------|-----------|-----------|
| 1 | 0.0000000 | insertion | 0.0274892 |
| 2 | 0.0274892 | match     | 0.0763068 |

0 0.0275 0.0763 0.138 0.203 0.284 0.386 0.523  
0.712 1.04 4.39

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 22  | 22  | 23  | 23  | 20  | 23  | 21  | 23  | 16  | 10  |
|       | match     |     | 151 | 207 | 198 | 183 | 187 | 168 | 187 | 179 | 156 | 181 |
| MSE-E | insertion |     | 20  | 25  | 25  | 26  | 15  | 21  | 29  | 15  | 37  | 26  |
|       | match     |     | 139 | 178 | 187 | 202 | 212 | 228 | 209 | 196 | 233 | 208 |





## 2.212 encodeYaleChIPSTAT1HeLaMaskLess36mer36bpSig

NULL

Yale 36-36 Sig

Yale ChIP/Chip (STAT1 ab, HeLa cells) Maskless 36-mer, 36bp Win, Signal

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.1680 | 0.153 | -1.090 | 0.274 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.0299 | 0.141 | -0.212 | 0.832 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 5190

Origin.of.data.set

AVR-E MSE-E

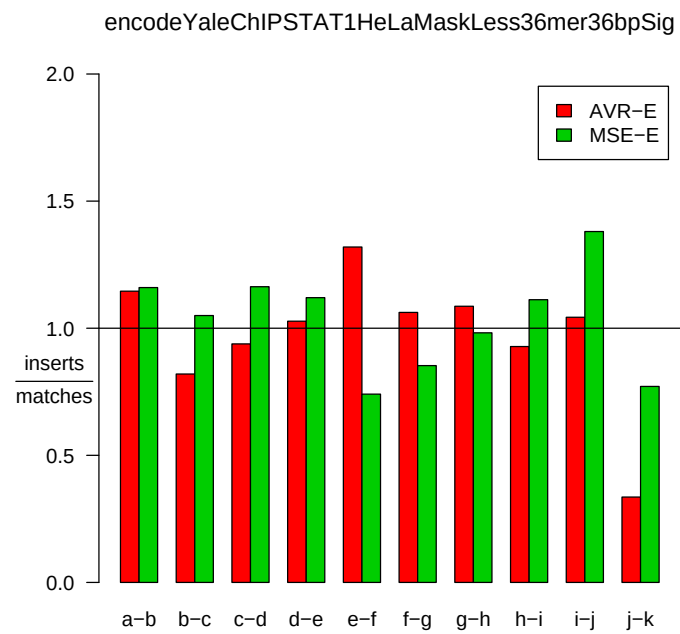
2044 2292

Category limits

|   | lower       | category  | upper       |
|---|-------------|-----------|-------------|
| 1 | -0.36805201 | insertion | -0.09599385 |
| 2 | -0.09599385 | match     | -0.06158160 |

-0.368 -0.096 -0.0616 -0.0374 -0.0163 0 0.018  
0.0384 0.0637 0.101 0.603

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 27  | 20  | 21  | 23  | 30  | 20  | 22  | 20  | 21  | 7   |
|       | match     |     | 199 | 206 | 189 | 189 | 192 | 159 | 171 | 182 | 170 | 176 |
| MSE-E | insertion |     | 25  | 23  | 27  | 26  | 20  | 20  | 25  | 27  | 34  | 21  |
|       | match     |     | 182 | 185 | 196 | 196 | 228 | 198 | 215 | 205 | 208 | 230 |



## 2.213 encodeYaleChIPSTAT1HeLaMaskLess50mer38bpPval

NULL

Yale 50-38 PVal

Yale ChIP/Chip (STAT1 ab, HeLa cells) Maskless 50-mer, 38bp Win, P-Value

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.0171 | 0.155 | -0.110 | 0.912 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.0844  | 0.145 | 0.584  | 0.560 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4858

Origin.of.data.set

AVR-E MSE-E

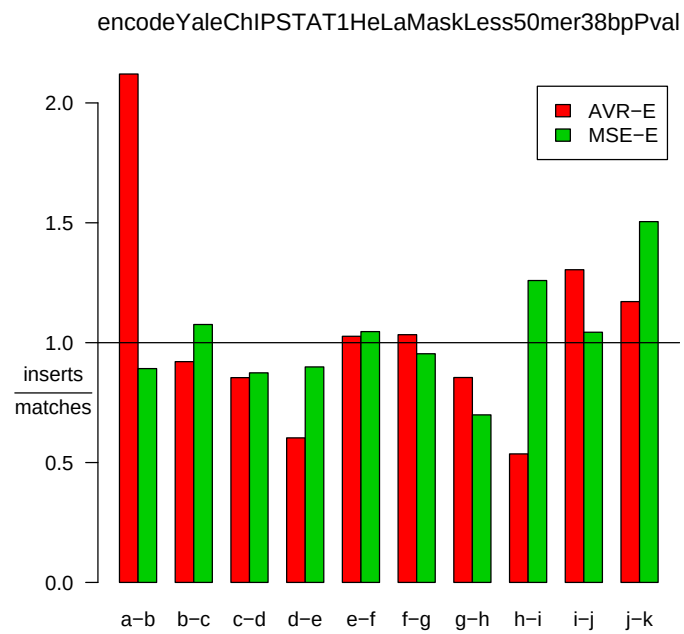
2197 2471

Category limits

|   | lower       | category  | upper        |
|---|-------------|-----------|--------------|
| 1 | 0.00000e+00 | insertion | 4.828390e-06 |
| 2 | 4.82839e-06 | match     | 1.000823e-03 |

0 4.83e-06 0.001 0.0217 0.138 0.472 1.18 2.34  
4.12 6.95 13.5

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 23  | 16  | 17  | 12  | 20  | 21  | 18  | 14  | 32  | 28  |
|       | match     |     | 103 | 165 | 189 | 189 | 185 | 193 | 200 | 248 | 233 | 227 |
| MSE-E | insertion |     | 17  | 29  | 22  | 23  | 26  | 23  | 17  | 24  | 20  | 29  |
|       | match     |     | 181 | 256 | 239 | 243 | 236 | 229 | 231 | 181 | 182 | 183 |



## 2.214 encodeYaleChIPSTAT1HeLaMaskLess50mer38bpSig

NULL

Yale 50-38 Sig

Yale ChIP/Chip (STAT1 ab, HeLa cells) Maskless 50-mer, 38bp Win, Signal

|                                             | coef     | se    | z       | p     |
|---------------------------------------------|----------|-------|---------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.00824 | 0.155 | -0.0533 | 0.958 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.17200  | 0.144 | 1.1900  | 0.233 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 4858

Origin.of.data.set

AVR-E MSE-E

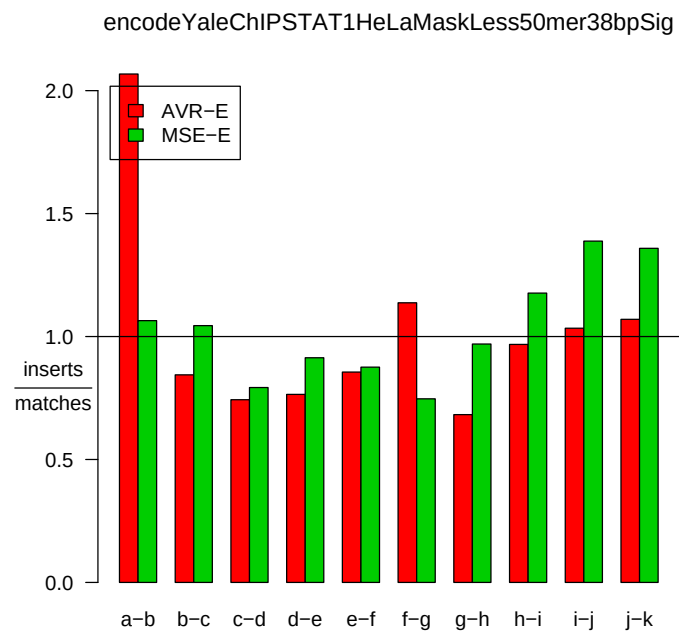
2197 2471

Category limits

|   | lower      | category  | upper      |
|---|------------|-----------|------------|
| 1 | -4.1852698 | insertion | -0.5163757 |
| 2 | -0.5163757 | match     | -0.2589998 |

-4.19 -0.516 -0.259 -0.119 -0.0268 0.0372 0.131  
0.24 0.374 0.607 2.91

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 30  | 15  | 15  | 16  | 17  | 22  | 16  | 23  | 25  | 27  |     |
|       | match     | 138 | 169 | 192 | 199 | 189 | 184 | 223 | 226 | 230 | 240 |     |
| MSE-E | insertion | 30  | 28  | 20  | 22  | 22  | 19  | 21  | 24  | 27  | 25  |     |
|       | match     | 268 | 255 | 240 | 229 | 239 | 242 | 206 | 194 | 185 | 175 |     |



## 2.215 encodeYaleChIPSTAT1HeLaMaskLess50mer50bpPval

NULL

Yale 50-50 PVal

Yale ChIP/Chip (STAT1 ab, HeLa cells) Maskless 50-mer, 50bp Win, P-Value

|                                             | coef    | se    | z      | p     |
|---------------------------------------------|---------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.2930 | 0.201 | -1.460 | 0.146 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | -0.0614 | 0.184 | -0.334 | 0.739 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 6608

Origin.of.data.set

AVR-E MSE-E

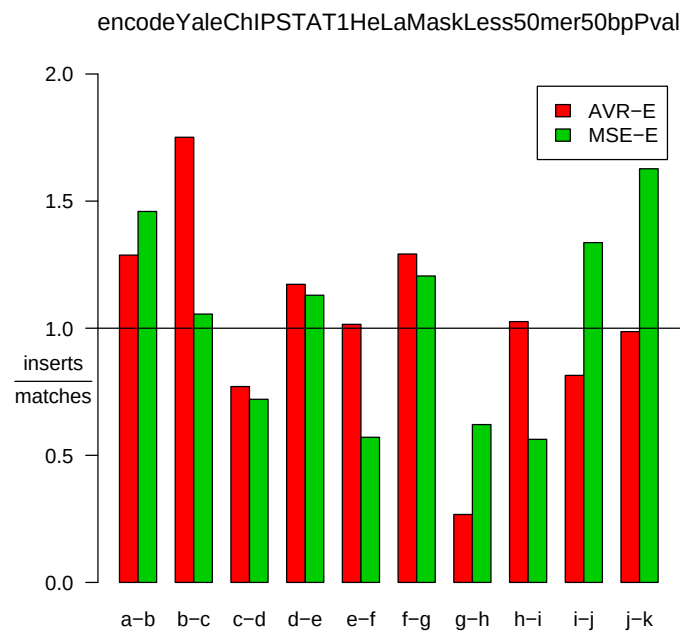
1393 1525

Category limits

|   | lower     | category  | upper      |
|---|-----------|-----------|------------|
| 1 | 0.0000000 | insertion | 0.02012770 |
| 2 | 0.0201277 | match     | 0.05821328 |

0 0.0201 0.0582 0.102 0.158 0.231 0.31 0.419  
0.566 0.828 5.42

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 10  | 22  | 11  | 15  | 16  | 18  | 4   | 15  | 12  | 16  |     |
|       | match     | 68  | 110 | 125 | 112 | 138 | 122 | 131 | 128 | 129 | 142 |     |
| MSE-E | insertion | 14  | 17  | 13  | 16  | 9   | 19  | 10  | 9   | 20  | 21  |     |
|       | match     | 84  | 141 | 158 | 124 | 138 | 138 | 141 | 140 | 131 | 113 |     |





## 2.216 encodeYaleChIPSTAT1HeLaMaskLess50mer50bpSig

NULL

Yale 50-50 Sig

Yale ChIP/Chip (STAT1 ab, HeLa cells) Maskless 50-mer, 50bp Win, Signal

|                                             | coef   | se    | z      | p     |
|---------------------------------------------|--------|-------|--------|-------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.209 | 0.202 | -1.030 | 0.301 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.155  | 0.188 | 0.825  | 0.409 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 6608

Origin.of.data.set

AVR-E MSE-E

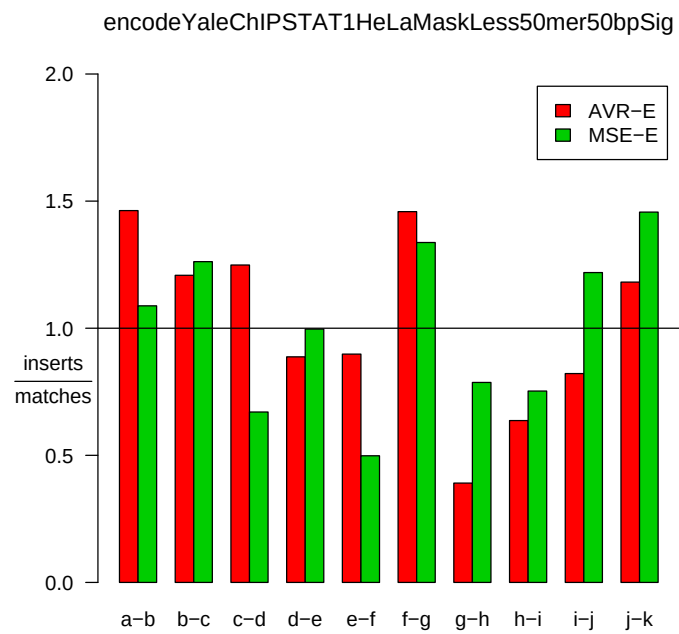
1393 1525

Category limits

|   | lower      | category  | upper      |
|---|------------|-----------|------------|
| 1 | -0.3760050 | insertion | -0.1490166 |
| 2 | -0.1490166 | match     | -0.1010494 |

-0.376 -0.149 -0.101 -0.0688 -0.0389 -0.00906  
0.00544 0.0349 0.071 0.119 1.17

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j | j-k |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 18  | 16  | 18  | 13  | 14  | 20  | 6   | 10  | 13  | 18  |
|       | match     |     | 105 | 113 | 123 | 125 | 133 | 117 | 131 | 134 | 135 | 130 |
| MSE-E | insertion |     | 19  | 21  | 11  | 16  | 8   | 21  | 13  | 12  | 18  | 21  |
|       | match     |     | 149 | 142 | 140 | 137 | 137 | 134 | 141 | 136 | 126 | 123 |



## 2.217 encodeYaleMASNB4RNANprotTMFWDMless36mer36bp

NULL

Yale NB4 NgF RNA

Yale NB4 RNA Trans Map, MAS Array, Forward Direction, NimbleGen Protocol

|                                             | coef   | se    | z     | p       |
|---------------------------------------------|--------|-------|-------|---------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.0733 | 0.230 | 0.318 | 0.75000 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.5960 | 0.217 | 2.750 | 0.00599 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 7500

Origin.of.data.set

AVR-E MSE-E

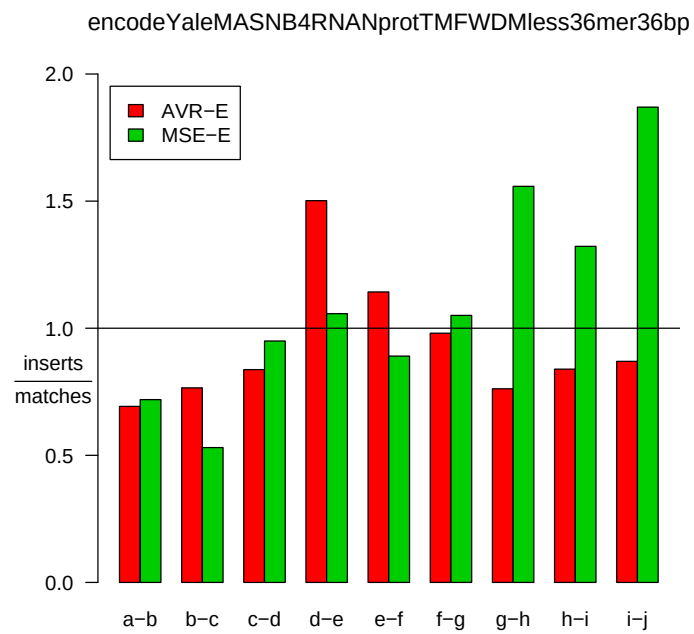
972 1054

Category limits

|   | lower | category  | upper  |
|---|-------|-----------|--------|
| 1 | 0e+00 | insertion | 0.0001 |
| 2 | 1e-04 | match     | 0.0011 |

0 1e-04 0.0011 0.0214 0.0866 0.242 0.743 1.95  
3.86 9.03

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 3   | 7   | 9   | 20  | 11  | 14  | 11  | 14  | 18  |     |
|       | match     | 27  | 57  | 67  | 83  | 60  | 89  | 90  | 104 | 129 |     |
| MSE-E | insertion | 6   | 8   | 16  | 19  | 11  | 15  | 20  | 14  | 12  |     |
|       | match     | 52  | 94  | 105 | 112 | 77  | 89  | 80  | 66  | 40  |     |



## 2.218 encodeYaleMASNB4RNANprotTMREVMless36mer36bp

NULL

Yale NB4 NgR RNA

Yale NB4 RNA Trans Map, MAS Array, Reverse Direction, NimbleGen Protocol

|                                             | coef  | se    | z    | p       |
|---------------------------------------------|-------|-------|------|---------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.392 | 0.246 | 1.59 | 0.11100 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.743 | 0.230 | 3.23 | 0.00122 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 7527

Origin.of.data.set

AVR-E MSE-E

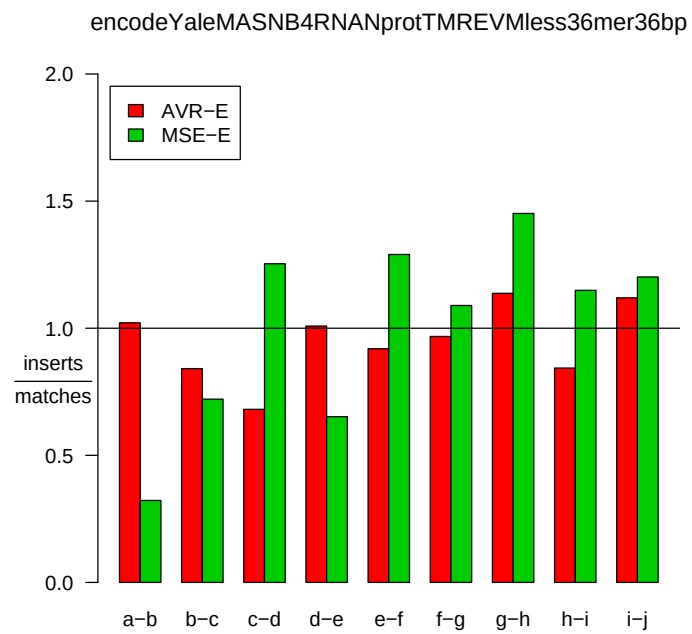
959 1040

Category limits

|   | lower | category  | upper  |
|---|-------|-----------|--------|
| 1 | 0e+00 | insertion | 0.0001 |
| 2 | 1e-04 | match     | 0.0011 |

0 1e-04 0.0011 0.0141 0.055 0.242 0.743 2.09 4.53  
9.03

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i | i-j |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion | 6   | 7   | 8   | 13  | 12  | 12  | 18  | 15  | 19  |     |
|       | match     | 36  | 51  | 72  | 79  | 80  | 76  | 97  | 109 | 104 |     |
| MSE-E | insertion | 2   | 10  | 18  | 10  | 20  | 16  | 18  | 12  | 10  |     |
|       | match     | 38  | 85  | 88  | 94  | 95  | 90  | 76  | 64  | 51  |     |



## 2.219 encodeYaleMASPlacRNANprotTMFWDMless36mer36bp

NULL

Yale Plc NgF RNA

Yale Placenta RNA Trans Map, MAS Array, Forward Direction, NimbleGen Protocol

|                                             | coef     | se    | z       | p        |
|---------------------------------------------|----------|-------|---------|----------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | -0.00561 | 0.229 | -0.0245 | 0.980000 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.80600  | 0.226 | 3.5700  | 0.000353 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 7500

Origin.of.data.set

AVR-E MSE-E

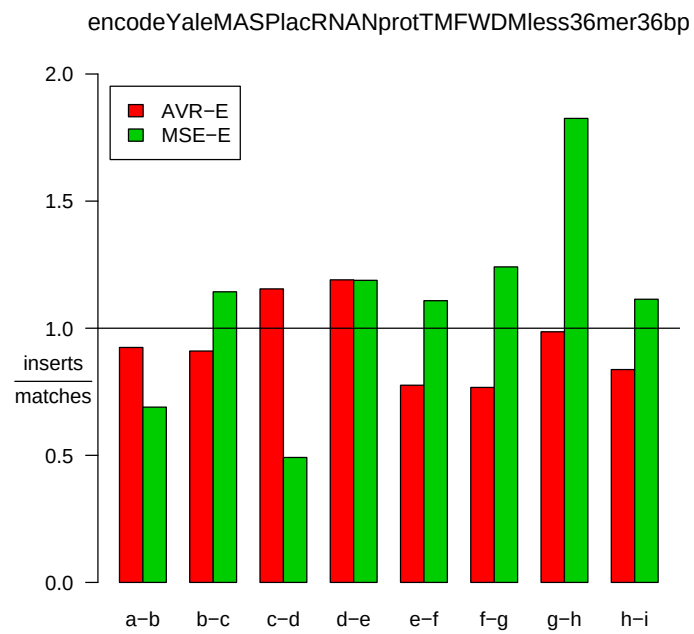
972 1054

Category limits

|   | lower | category  | upper  |
|---|-------|-----------|--------|
| 1 | 0e+00 | insertion | 0.0008 |
| 2 | 8e-04 | match     | 0.0174 |

0 8e-04 0.0174 0.0733 0.301 0.809 2.08 4.95 10.5

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 7   | 11  | 16  | 14  | 10  | 11  | 17  | 17  |
|       | match     |     | 47  | 75  | 86  | 73  | 80  | 89  | 107 | 126 |
| MSE-E | insertion |     | 10  | 21  | 8   | 18  | 15  | 16  | 20  | 7   |
|       | match     |     | 90  | 114 | 101 | 94  | 84  | 80  | 68  | 39  |





## 2.220 encodeYaleMASPlacRNANprotTMREVMless36mer36bp

NULL

Yale Plc NgR RNA

Yale Placenta RNA Trans Map, MAS Array, Reverse Direction, NimbleGen Protocol

|                                             | coef  | se    | z     | p      |
|---------------------------------------------|-------|-------|-------|--------|
| AVR-E:as.numeric(dens.med < eval(dens.var)) | 0.211 | 0.238 | 0.886 | 0.3750 |
| MSE-E:as.numeric(dens.med < eval(dens.var)) | 0.403 | 0.222 | 1.810 | 0.0699 |

ENCODE annotation is not contiguous. Non-NULL sites:

[1] 7527

Origin.of.data.set

AVR-E MSE-E

959 1040

Category limits

|   | lower | category  | upper   |
|---|-------|-----------|---------|
| 1 | 0e+00 | insertion | 0.00080 |
| 2 | 8e-04 | match     | 0.00927 |

0 8e-04 0.00927 0.0733 0.301 0.809 2.2 4.95 10.5

| set   | type      | brk | a-b | b-c | c-d | d-e | e-f | f-g | g-h | h-i |
|-------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AVR-E | insertion |     | 5   | 14  | 12  | 7   | 11  | 20  | 14  | 18  |
|       | match     |     | 57  | 69  | 87  | 83  | 70  | 84  | 125 | 99  |
| MSE-E | insertion |     | 11  | 15  | 17  | 9   | 21  | 15  | 7   | 14  |
|       | match     |     | 87  | 92  | 127 | 88  | 68  | 81  | 62  | 60  |

