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For each locus, the following are given: locus coordinate in GRCh37; inferred template-switch process (format similar to Fig. 1e-f) ; sequencing reads for HuRef (Li and Durbin , 2011) and for NA12878 (The 1000 Genomes Project Consortium, 2015); variation data from 1KG (The 1000 Genomes Project Consortium, 2015); and local annotation from Ensembl (Flicek et al., 2013).

[illegible]

HuRef

152808101 152808111 152808121 152808131 152808141 152808151      152808161 152808171 152808181 152808191 152808201  
TGTTGCCACACATCATGCTTTCCTCAATCGGCAGGAAGAAGGTGTGTGGTGGGACA...CAAATAACTGGGACAAATAAAGTTG-ACCTTCAGTCCGCTGGTAACCTCCC  
.K.K.....K.  
\*\*\*\*\*~::~~~~~~:::

[illegible]

[illegible]

```

// ===== g, g, t =====
// ===== g, g, t =====

```

[illegible]

[illegible]

=====

chr2:147332910-147332928

Switch process:  
 F: L TAACCTATTTTAAATGCACCTACTTTTAAAG 1  
 RF: 4 GGCACC-TCTCCACGCAATAATAGATAGATAAAATAA R  
 FR: TAACCTATTTTAAATGCACCTACTTTTAAAGACTCTTTATTTGGCGGGGGAAGGAGGCACCTTCTCCACGCAATAATAGATAGATAAAATAA  
 RR: ATTTGGGATAAAATTTACGTGAATGAAATTTCTAGATAAATAACCGCCCCCTCTCCGTGGGAAGAGGGTCGTATTATTCATCTATTTATT  
 FG: GTTGGATGGTCTTCTTATTTA 2

HuRef

[illegible]

chr2:177656645-177656662

Switch process:

```
F1: L TGGGGATGCTGGACAGGAGTGAATATTGCTCAA 1
R:                                     4 CAATGCTCAAGCTCTAACTAAATGGTCAGTAA R
F3: TGGGGATGCTGGACAGGAGTGAATATTGCTAAATGATGCTAACTATCATCAAGCTCGAAGCTCTAACTAAATGGTCAGTAA
RR: ACCCTTACCACCTGTCCTCTCACTTATAACAGTTATTCTATCGAGTATGATAGTTGTACGAGTTCGAGATTGAATTTACCAGCTATT
F2:                                     3 ACTACATAGCTAGATAGT
```

HuRef

[illegible][illegible][illegible]

Ensembl: 2 177656651 rs77039132 A T intron\_variant

| Variation data: |           |            |   |   |             |             |               |               |               |               |               |
|-----------------|-----------|------------|---|---|-------------|-------------|---------------|---------------|---------------|---------------|---------------|
| 1kg:            |           |            |   |   |             |             |               |               |               |               |               |
| 2               | 236077401 | rs56381894 | C | A | NA12878  01 | AF=0.363818 | AFR_AF=0.1982 | AMR_AF=0.4078 | EAS_AF=0.3393 | EUR_AF=0.4076 | SAS_AF=0.5368 |
| 2               | 236077402 | rs56401263 | T | G | NA12878  01 | AF=0.363818 | AFR_AF=0.1982 | AMR_AF=0.4078 | EAS_AF=0.3393 | EUR_AF=0.4076 | SAS_AF=0.5368 |





[illegible]

[illegible]

.....

chr3:163871744-163871758

```
Switch process:
F1: L CTCACCTACCTCTGCTCCAGCCCTATGATTAACCTG 1
F3:                                     4 TGTGATCACAATAACGTAATAAATAACAAA R
RF: CTCACCTACCTCTGCTCCAGCCCTATGATTAACCTGTGCTAGCAATATTTGGTGATCACAATAACATAAATAAATAACAAA
RR: GAGTGGATGGAGACGAAGTCGGATACATAATGAAACAGTGACGTATATATACACACTAGTGTATTGTATTTATTGTGTTT
F2:                                     3 GTATATACACACAT 2
```

HuRef

165354391 165354401 165354411 165354421 165354431 165354441 165354451 165354461 165354471 165354481 165354491  
ATGTTACTGGCCCTCACCATCTCTGCTCCAGCCTATGTTAACTGTGAC+ACATATATTTGGTGATCACATAAGCTAAATAAAC+AAAAAACTGATGT+TTTACTGAA+G  
.....  
T.....T..G...\*...T...T.....\*...A...G.G.....  
.....G.....  
.....TG.....A.....  
.....\*\*.....  
.....\*.....

[illegible]

| 1KG:     |           |             |   |    |             |                    |               |               |               |               |               |
|----------|-----------|-------------|---|----|-------------|--------------------|---------------|---------------|---------------|---------------|---------------|
| 3        | 163871747 | rs111902670 | C | CT | NA12878 0 0 | AF=0.546126        | AFR_AF=0.6377 | AMR_AF=0.4524 | EAS_AF=0.6687 | EUR_AF=0.4394 | SAS_AF=0.4724 |
| 3        | 163871748 | rs1470800   | A | G  | NA12878 0 0 | AF=0.546126        | AFR_AF=0.6377 | AMR_AF=0.4524 | EAS_AF=0.6687 | EUR_AF=0.4394 | SAS_AF=0.4724 |
| Ensembl: |           |             |   |    |             |                    |               |               |               |               |               |
| 3        | 163871748 | rs111902670 | - | T  | TG          | intergenic_variant |               |               |               |               |               |
| 3        | 163871748 | rs1470800   | A | G  | T           | intergenic_variant |               |               |               |               |               |

.....

chr3:170821849-170821880

Switch process:  
F1: L GTGTTACTAAAAGCTCTCTGCGCTGAACCAATTAGAA 1 4 ACAGTTTGGAGGGGAGACATATACCAAGATCCCTATG R  
RF:   
F2: GTGTTACTAAAAGCTCTCTGCGCTGAACCAATTAGAAATTCCTTTAAGTTTAATGTGAACAGTTTGGAGGGGAGACATATACCAAGATCCCTATG R  
RR: CACAATGATTTTCGAGAGAGGGGACTTGTAACTTTTAACTTATTTTAAAGGAATTCAAATTAACAAATGTCCAACTCCGCTCTGTATATGGCTTAGGGATC  
F3: 3 ATTAACTTTTAAAGGAATTCAAATTAACAAAT 2

HuRef

172304501 172304511 17174521 172304531 172304541 1724551 172304561 172304571 172304581 172304591 172304601  
TTTTCGCTCTGCTGTTACTAAAGAGCTCTCGCCCTGAACATTAGAAATAACCTAAATCAAGAGAAATTTCA-ATTAACAGTTTGAGGGCGAGACATATACCAGAAATCCCTGAT  
.....K.T.G..A..TCCTTT..G...A..G.....  
.....G.....  
.....T.G..G...TCccttt..g..g..A..ttg.....  
.....T.G...A..TCCTTT..G...A..TTG.....  
.....T.G...A..TCCTTT..G...A..TTG.....  
.....T.G...A..TCCTTT..G...A..TTG.....  
.....T.G...A..TCccttt..g..g..A..ttg.....

[illegible]



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chr4:84454349-84454369

Lastz alignment:

```
GRCh37 ATATATATACAGGTGTGTATATATATTCATAGTTACGGGTGtTAGGACTTgACATATCTTTTGGGGAGGCATGtATATATATACATGCCTG
HuRef  ATATATATACAGGTGTGTATATATATTCATAGTTACGGGTGGGAGGACTTGAACATATCTTTTGGGGAGGCATGTGTATATATACATGCCTG
```

F1: L ATATATATACAGGTGTGTATATATATATCATAGTTAC 1  
E3:

RF: ATATATATACAGGTGTGATATATATTACATAGTTACGGGTGGGAGGACATGAATATATCTTTTGGGAGGACATGTGTATATATACATGCCTGGATTAAATAGTAAAAAACAGGATTATGGATAAATTCATTACTAAGCATTTGACTATCAACTACCCATTAAATACATACCTCCCAATCCCAATACAAACCTCTGCAGGTAGGTGTTATATCTCTCATTTTACAGAGAT  
RR: TATATATATGTCCACATATATATAAGTATCAATGCCACCCTCCTGAACCTGTATAGAAAAACCCCTCCGTACACATATATATACGGACCTAAATATCCATTTTTTGTGCTTAATACCTATTTAAGTAATGATTCGTAACGTAGATTGATGGTAAATATGATGAGAGGTTAGGGTTATTGTTGGAGACGTCATCCACAATAATAGGAGTAAATGTCTCTA  
F2:

HuRef

84673331 84673341 84673411 84673361 84673371 84673381 84673391 84673401 84673411 84673421 84673431  
TGTGTAAGTGATATATACAGGTGTGTATATATCATAGTCAGGGTGTAGGACTTGGACATATCTTTGGGAGAGCATGTATATATACATCGCTGGATATATAGTATAAA  
.....K.T.....  
.....G.....  
.....GG.....  
.....C.....  
.....

NA12878

[illegible]

Variation data:

.....

Template-switch process:

Lastz alignment:

```

Grch37  CAAGGAGTAGGAGTGAAACATCTATGATGGATGTTtATCACAGTgcGTtTgtAaTaGTgaACActGCAAATATTACACCAAGGGACGTAGGTAAT
HuRef   CAAGGAGTAGGAGTGAAACATCTATGATGGATGTTAATCACAGCTATGACCCAGTGGGGCTACAAGCAAAATATTACACCAAGGGACGTAGGTAAT

```

F1: L GAGAACCAAGGAGTAGGAGTGAACATCTATGATGGATGTTTATCA 1  
F2:

RF: GAGAACCAAGGAGTAGGAGTGAACATCATATGATGGATGTTAATCACAGCATATACCCGACGGGGCTACAAGCAAAATATTACACCAAGGGAGCTAGGTAAATATGGTTACATCGATTTCATGTAATCATGATAATACATAGAATATTTGTTAAATGAAAAGTGGTTTCTAATACTTAAGCGGGAAAAACAAATTACAAAGAACACTG  
RR: CTCCTGGTCCCTCATCTCCACTTTGTAGATACATACCAATAGTGTGCGATCTGGGGTCACCCGATGTTTCGTTATATATGGTTCCTCGATCCATTATACCAATGTAGCTAAAGTACATTAGTACTATATGATTCTTATAACCAATTTTACTTTTCACCAAGAGATTATGAATCGCCCTTTTGTGTTAAATGTTCTTGTGGAC  
F2: 3 ATAATGTTTGTGCTGAC 2

Sequencing data:

HuRef

[illegible]

NA12878

[illegible]

Variation data:

.....

Template-switch process:

Lastz alignment:

```
GRCh37  CACCACCTAATATTCTATTATATTAGGTTGGTGCAAAAgTA-----AcAGATCAATTGATAATTGCACCATCAAATTACTTCTGCAC
HuRef   CACCACCTAATATTCTATTATATTAGGTTGGTGCAAAAATATATCAAAGATCAATTGATAATTGCACCATCAAATTACTTCTGCAC
```

Switch process:

F1: L CACCAACCTAATATTCATTTT T  
F3: 4 AATTGATAATTTGCACCATCAAAATTACTTCTGCAC R  
RF: GATCTGTTACTTTTGCCACCACTTAATATTTCTATTATATTAGTGTGGTGCAAAAATATATCAAAAGATCAATTGATAATTTGCACCATCAAAATTACTTCTGCAC  
RR: CTAGACAATGAAAACTGGTGTGGATTATAAAGATAAAATATAATCAACCAACCGTITTTATATAGTTTTCTAGTTAACTATTAACCGTGGTAGTTTAAATGAAGCGTG  
F2: 3 CTAGACAATGAAAACTGGTGTGGATTATA 2

Sequencing data:

HuRef

TGTTACTTTTGACCACCACTAATATTTCATA-TTATA-TTAGGTGGTGC-\*\*\*\*\*GTACAG-ATC-AATTGATAATTGCACCATCAAATTACTTCTCGACCAATCTAAATATTC

\*\*\* \*\*.....C.G+...C.....

\*\*\*\*\*.\*.....\*\*..\*

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182127551 182127561 182127571 182127581 182127591 182127601 182127611 182127621 182127631 182127641 182127651  
ACACCTCTAAATGCACGACAGACAACACTCAGAAGAGTGTCTGCTATGAAAAACATATATT\*\*\*TATGGAAGGATCTGTAATCTATTATAAAATTTGTTGATACTGAGTCATTATGAT

[illegible]



Variation data:

Template-switch process:

chr5:70120774-70120787

Lastz alignment:

```
GRCh37 TAAATATGCAATTGTGCTTTTAACTCTGAAAACCTGAATAccTATTCAACTGTTGATTCTGAGTATTACAGAACTTTATTT
HuRef  TAAATATGCAATTGTGCTTTTAACTCTGAAAACCTGAATAGGTATTCAACTGTTGATTCTGAGTATTACAGAACTTTATTT
```

Switch process:

```
F1: L TAAATATGACATTGTGCTTTTAACTCTGAAACC 1
R:                                     4 ACTGTGTATCTGAGTATTACAGAACTTTATT R
F3: TAAATATGACATTGTGCTTTTAACTCTGAAACCCTGAATAGGTATTCACGTGTGATCTGAGTATTACAGAACTTTATT
RR: ATTTTATACGTAAACAGAAAATTGAGACTTTGGCACTTATCTGCAATAGGTGACACTAAGACTCATAAATGCTTGGAAATAA
F2:                                     3 ACTTATCATAGT 2
```

Sequencing data:

HuRef

[illegible]

NA12878

[illegible]

Variation data:

Template-switch process:

chr5:107452444-1074524

Lastz alignment:

```

GRCh37  GATAGATGAATAATACCGTTTTCAAAGAAATTATGTGCAC-AtAATTTCTTATCACTCAAAAAACAGCTCAGATAGATCCAT
HuRef   GATAGATGAATAATACCGTTTTCAAAGAAATTATGTGCACAAAAATTTCTTATCACTCAAAAAACAGCTCAGATAGATCCAT

```

```
Switch process:
F1: L GATGATGAATAATACCGTTTCAAAGAAATTA 1
R: 4 ATCACTCAAAAAAACAGCTCAGATAGATCCAT
F2: GATGATGAATAATACCGTTTCAAAGAAATTTATGGCAAAAAATTTCTTATCACTCAAAAAACAGCTCAGATAGATCCAT
R: CTATCTACTTATTATGGCAAAAGTTTCTTTAATACCGTGTGTTTTAAGSATAAGTGAAGTTTTTTGTGCGAGTCTATCTAGTA
F2: 3 TCTTCTATCAACAGCTG 2
```

Sequencing data:

HuRef

[illegible]

NA12878

[illegible]

[illegible]

[illegible]

Variation data:

[illegible]

.....a,a,\*,c,t,t,c,c.....

[illegible]

Switch process:  
 F: L GCTCTCTGCGGCCCATCTTCCACCCACACAGGTC 1  
 R: 4 TCAATCAACATGGTTGGTGACAAACCAATATATAC  
 RF: GCTCTCTGCGGCCCATCTTCCACCCACACAGGTC1TTGTAAGCACTCTGGGAGTAGATGAAGCAGGCATCAATCAACATGGTTGGTGACAAACCAATATATAC  
 RR: CGAGAGACGCGGGGTGAAGGGTGGGTGTGTGCAAGAACTCTGGTGGAACCTCATCTACTCTGCGGTAGTGTGACCAACCACTGTTGGTATATAATG  
 F2: 3 AACACTCTGGTGGAACCTCATCTACTCTGCGGT 2

Sequencing data:

HuRef

[illegible]

NA12878

[illegible]

Variation data:

1kG:

Ensembl: 7 117357037 rs386717124 CCGTTCTCATCTACTCCCAAGGTGGCTTA TAAGCCACCTTGGGAGTAGATGAGAACGG TAAGCCACCTTGGGAGTAGATGAGAATGG intron\_variant

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Template-switch process:

chr7:118367022-118367036

Lastz alignment:

```
GRCh37 AACAAAGAAGTGACAACCTGAAGGAGATTAATGGATgtgTAGTATTTAA-----CTACAAAAGCAGGAACAAAGTTATCTCTAGTGAATAAAA
HuRef AACAAAGAAGTGACAACCTGAAGGAGATTAATGGATTTAAAGTAGTTAAATACTACTACCAAAAAGCAGGAACAAAGTTATCTCTAGTGAATAAAA
```

Switch process:

F1: L GTCACAAAAGAGTGACAACTGAAAGGAGATTAATGGATGT 1  
F3: 4 CAAAGCAGGACCAAAAGTTATCTCTAGTGAATAAAA R  
RF: GTCACAAAAGAGTGACAACTGAAAGGAGATTAATGGAT-TAAAAGTAGTTAAATACTACTACCAAAAGCAGGAACAAAGTTATCTCTAGTGAATAAAA  
RR: CAGTGTGTTCTCTCACTGTGACTTTCCTCTAAHTACCTA-ATTTTCACTCAATTTAATGATGATGGTTTCGTCTTGTTTCAATAGAGATCACTTATTTT  
F2: 3 CATCAATTTATGAT 2

Sequencing data:

HuRef

[illegible]

NA12878

[illegible]

Variation data:

1kG:

|   |           |             |   |   |             |             |               |               |               |               |               |
|---|-----------|-------------|---|---|-------------|-------------|---------------|---------------|---------------|---------------|---------------|
| 7 | 118367020 | rs370899603 | G | T | NA12878-0 0 | AF=0.212661 | AFR_AF=0.4077 | AMR_AF=0.1643 | EAS_AF=0.1935 | EUR_AF=0.1123 | SAS_AF=0.1033 |
| 7 | 118367021 | rs373797747 | T | A | NA12878-0 0 | AF=0.212661 | AFR_AF=0.4077 | AMR_AF=0.1643 | EAS_AF=0.1935 | EUR_AF=0.1123 | SAS_AF=0.1033 |
| 7 | 118367022 | rs375625255 | G | A | NA12878-0 0 | AF=0.212661 | AFR_AF=0.4077 | AMR_AF=0.1643 | EAS_AF=0.1935 | EUR_AF=0.1123 | SAS_AF=0.1033 |
| 7 | 118367023 | rs370880789 | T | A | NA12878-0 0 | AF=0.212661 | AFR_AF=0.4077 | AMR_AF=0.1643 | EAS_AF=0.1935 | EUR_AF=0.1123 | SAS_AF=0.1033 |

| Ensembl: |          |             |   |        |                    |
|----------|----------|-------------|---|--------|--------------------|
| 7        | 18367020 | rs370899603 | G | T      | intergenic_variant |
| 7        | 18367021 | rs373797747 | T | A      | intergenic_variant |
| 7        | 18367022 | rs375625255 | G | A      | intergenic_variant |
| 7        | 18367023 | rs370880789 | T | A      | intergenic_variant |
| 7        | 18367032 | rs111404281 | - | AATACT | intergenic_variant |

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Template-switch process:

chr8:3212293-3212315

F2: 3 ACTATATATATATAGTGATTGA 2

[illegible][illegible]

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RR: TTTTAAGACACAATGACCTTTTATATTTATCCAATATTTAAACCCTTAAATATTGGATATT

78337391 78337401 78337411 78337421 78337431 78337441 78337451 78337461 78337471 78337481 78337491  
 CATGTAGAGAGAAATCTGTGTTACT-GGGAAATATAAATAGGTTATAAATCCCAAAATTATAACCTATAAAGAGATATACATCAATAATAAATTTAAATATGGTTGTGTGGT  
 .....YSR  
 .....C999  
 .....C999  
 .....G.....

[illegible]

.....



RF: A A A T T G C T G C C G A G G A T G T A G A T C A G G T G T T C A T T G A C A C T A T A G C C A C T G G C T A A G C C T T G G C T G A C A C C A G C C A G G T G A T A C T G C A A C T T T C A G A A G G C T C T T T G A C C C C T T G T G T C T G A G A A A A T T T C A T C C A C T A C C T G A A A G T C A C A G T G T C A T C T G C A T G G G T G C A G C C A A G G C T T A G C C A G T A G C T C T G T G T C A A T G A A C A C T A  
RR: T T T A A C G A C G G C T C C T A C A T C T A G A T C C A A G T A A C T G T G A T A C G G T G A C A G A T C G G A A C C G A C T G T G G G T C G G T C C A T A T G A C G T T G A A A G T T C C C G A G A A A C T G G G A A A C A C A G A C T T T T A A G A A G T A G G T G A T G G A C T T T C A G T G C C A G T A G A C T A C C C A C A G C T G G T T C C G A A T G G T C A T C A G A G A C A G T T A C T T G T G A T  
F2: 3 C G G T G A C C A T G G T C A A T G A G G A C A C A G A C T T A C T T G G G A T 2

Sequencing data:

HuRef

CTAAGCTGCAGAAATTTGTCGCCAGGATGTAGATCATAGGTGTCATTGACACGAGACTCAATGGCTTAAGCCTTGGCGTGACACCCAGCAGGTGATATGCAATTTCAAGAAGCTCTT  
.....T.T..C.....  
T.T.T.C.....  
.....T.T..C.....

NA12878

[illegible]

Variation data:

| 1kG: |           |            |   |   |             |      |          |          |          |          |          |  |  |
|------|-----------|------------|---|---|-------------|------|----------|----------|----------|----------|----------|--|--|
| 8    | 139290469 | rs10093441 | G | T | NA12878-1 1 | AF-1 | AFR_AF-1 | AMR_AF-1 | EAS_AF-1 | EUR_AF-1 | SAS_AF-1 |  |  |
| 8    | 139290471 | rs62529144 | G | T | NA12878-1 1 | AF-1 | AFR_AF-1 | AMR_AF-1 | EAS_AF-1 | EUR_AF-1 | SAS_AF-1 |  |  |
| 8    | 139290475 | rs10111646 | T | C | NA12878-1 1 | AF-1 | AFR_AF-1 | AMR_AF-1 | EAS_AF-1 | EUR_AF-1 | SAS_AF-1 |  |  |

|          |           |             |     |     |                |
|----------|-----------|-------------|-----|-----|----------------|
| Ensembl: |           |             |     |     |                |
| 8        | 139290469 | rs386730637 | GAG | TAT | intron_variant |
| 8        | 139290475 | rs10111646  | T   | C   | intron_variant |

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Template-switch process:

chr9:13322919-13322940

Lastz alignment:

```
GRCh37  CACTGGCCCTTTGGTTTATGACTGAGTCCCAGACTCAGTCA-TAAACcaAAGGGAAGTGAGGCCACTCCCTGGGGCACTCGTGGTTGT
HuRef   CACTGGCCCTTTGGTTTATGACTGAGTCCCAGACTCAGTCAATAAACACaAAGGGAAGTGAGGCCACTCCCTGGGGCACTCGTGGTTGT
```

Switch process:

F1: L CACTGCCCTTTGGTTTATGACTGAGTCCCA 1  
F3: 4 AAGTAGGAGGCCACTCCTCGGGGCACTCGTGGTTGT R  
RF: CACTGCCCTTTGGTTTATGACTGAGTCCCGACCTAGTCAATAAACACAGGGAAGTGAGGCCACTCCTCGGGGCACTCGTGGTTGT  
RR: GTGACCGGACCAACAAATGACTGACTGAGGTTGAGTCAGTTATTGTGTTCCCTCACTCCCGTGAGGAGCCCGTGAGACCAACAA  
F2: 3 GGGGAACCAATGACTGAGTCCAG 2

## Sequencing data:

HuRef

[illegible]

NA12878

[illegible]

Variation data:

Template-switch process:

chr9:73792526-73792553

Last2 alignment:

```
GRCh37    ACATTAAAGACCTAAGTTTTCACACATGTAACAGAACTTgaGtcaTtCatgTattaGgAaaaCctATCTTTTCACATACTTAAATATTCAACTTAAAGAGGGCCC
HucRef     ACATTAAAGACCTAAGTTTTCACACATGTAACAGAACTTtagTttTCTCAATACAGAAAGACTCATCTTTTCACATACTTAAATATTCAACTTAAAGAGGGCCC
```

## Switch process:

F1: L ACATTAAAGACCTTAGTITTTACACATGTAAACAGAATCT 1  
4 TCTTTTCACATACTTAAATATTCAACTTAAAGAGGCC R  
RF: ACATTAAAGACCTTAGTITTTACACATGTAAACAGAATCTTAGTITTTCTTAATACATGAATGACTCATCTTTTCACATACTTAAATATTCAACTTAAAGAGGCC R  
FR: TGTAAITTCGGATTCAAAGTGTGTACATTTCGTCTAGACTCAAAAGGATTATGACTTACTGAGTAGAAGAGTGATGAATTATAAGTGAATTCTCCGGG  
F2: 3 ATCCAAAGGATTATGACTTACTGAGT 2

## Sequencing data:

HuRef

[illegible]

```

HsRef
      121707101 121707111 121707121 121707131 121707141 121707151          121707161 121707171 121707181 121707191
GTGGTTCACCAAGACCAGGAGTTCCACAGGGGGCTCCACAGGTGAATACTTTCATTGAAGA+-----TTTCTATCCAAGATCAGTGACTGATGCAGCGACAGGCCCAAGGCCCTCGCA
.....W.W.....
..G.....GA....G.....*****
.....
.....A.A.....TTACCC.....
.....A,A.....TTACCC.....
.....A.A.....TTACCC.....
.....A,A.....TTACCC.....
.....A.A.....TTACCC.....
.....A.A.....TTACCC.....
.....A.A.....TTACCC.....

```

| Variation data: |           |            |        |                   |             |                  |                      |                      |                 |                     |                 |
|-----------------|-----------|------------|--------|-------------------|-------------|------------------|----------------------|----------------------|-----------------|---------------------|-----------------|
| 1kg:            |           |            |        |                   |             |                  |                      |                      |                 |                     |                 |
| 9               | 122667323 | rs7046056  | T      | A                 | NA12878-1 1 | AF=0.507987      | AFR_AF=0.5454        | AMR_AF=0.6182        | EAS_AF=0.3026   | EUR_AF=0.6074       | SAS_AF=0.4888   |
| 9               | 122667326 | rs62569069 | T      | A                 | NA12878-1 1 | AF=0.507987      | AFR_AF=0.5454        | AMR_AF=0.6182        | EAS_AF=0.3026   | EUR_AF=0.6074       | SAS_AF=0.4888   |
| 9               | 122667333 | rs11283633 | A      | ATTACCTA,ATTACCTT | NA12878-2 2 | AF=0.0623,0.4447 | AFR_AF=0.2254,0.3207 | AMR_AF=0.0173,0.5994 | EAS_AF=0.0.3026 | EUR_AF=0.002,0.6044 | SAS_AF=0.0.4847 |
| Ensembl:        |           |            |        |                   |             |                  |                      |                      |                 |                     |                 |
| 9               | 122667323 | rs7046056  | T      | A                 |             |                  | intergenic_variant   |                      |                 |                     |                 |
| 9               | 122667326 | rs62569069 | T      | A                 |             |                  | intergenic_variant   |                      |                 |                     |                 |
| 9               | 122667334 | -          | TTCACC | TTCACCTA TTCACCTT |             |                  | intergenic_variant   |                      |                 |                     |                 |

[illegible]

```

Sequencing data:
HuRef
138241301 138241311 138241321 138241331 138241341 138241351 138241361 138241371 138241381 138241391 138241401
TCTCCGCACAGTGTGCCTGTGTGCCCTCCCCACCTCTGCCCTCTGCCCTTCTCGAGGGTGACCACTAGAGGCCACACTACTACAGACCCCGGGACCTGGGTGCTATGAGCACTG
.....
.....GA.....
.....A.....
.....C.....
.....T.....

```

[illegible]

```

Variation data:

#####

Template-switch process:

chr10:3173066-3173095

Last alignment:
GRCh37: CATGAGCCACCGCGCCGACACCATTTGCTCTTTAAAGTTaGGAAT--GtActGtTtCtGAgCAaLaAGATCAAGTAAAAAGGGCCTTGGCACTAATTATGTGCAT
HsRef: CATAGGACACCGCGCCGCGGACCATTTGCTCTTTAAAGTTtGGCTCGAGAAACAAGTAAC--ATCTCAACAGATCAAGTAAAAAGGGCCTTGGCACTAATTATGTGCAT

Switch process:
F1: L CATGAGCCACCGCGCCGACACCATTTGCTCTTTAAAAA 1
F2: 4 AGATCAAGTAAAAAGGGCCTTGGCACTAATTATGTGCAT R
RP: CATGAGCCACCGCGCCGCGGACCATTTGCTCTTTAAAGTTtGGCTCGAGAAACAAGTAACATCTCAACAGATCAAGTAAAAAGGGCCTTGGCACTAATTATGTGCAT
RR: GTACTCGGTGGCGCGGCGCGGTGAACAGAAATTTTCAAACCGAGTCTTTGTTGTCATTGTAGGATGTGTCTAGTCTATTTCCTCCGGAACCGTGATTAACACGTGA
F2: 3 TAAACCGAGTCTTTGTCATTGTAGGATTG 2

```

Sequencing data:

HuRef

3163021 3163031 3163041 3163051 3163061 3163071 3163081 3163091 3163101 3163111 3163121

GGGATTACAGGATCAGGCCAGCGGCCGACACACCATGTTCTTTAAAAAGTTAGGAT+GTTACTGTTTGTTCGACGAAATAGATCAGTAAAAAGGGCCTGGGACATAATATGTGACA  
.....G.....T.C..AA..AA..T.T.C.....  
.....  
.....G.....T,C,Ca,aa,,aa,,aa,,\*,T,,\*,C.....  
.....G.....T.C..CA..AA..AA..AA..\*,T.T.C.....  
.....G.....T.C..CA..AA..AA..AA..\*,T.T.C.....  
.....G.....T,C,Ca,aa,,aa,,aa,,\*,T,,\*,C.....  
.....G.....T.C..CA..AA..AA..AA..\*,T.T.C.....  
.....G.....T.C..CA..AA..AA..AA..\*,T.T.C.....  
.....G.....T.C..CA..AA..AA..AA..\*,T.T.C.....

[illegible]

[illegible]

Template-switch process:

```

last2 alignment:
GRCH37: TAGATAAAGAAGGAGGATCACTGACAAAAACAACAGATAGCT-TtttgcAGTg-ATGGAGAACAATGTTAAATATTTTATAGATATTTTAAAG
HuRef: TAGATAAAGAAGGAGGATCACTGACAAAAACAACAGATAGCTTGTGGTTCAGTACATGGAGAACAATGTTAAATATTTTATAGATATTTTAAAG

Switch process:
F1: L TAGATAAAGAAGGAGGATCACTGACAAAAACAACAGATAC 1
F3:                                     4 GGAGATAACAATGTTAAATATTTTATAGATATTTTAAAG
RF: TAGATAAAGAAGGAGGATCACTGACAAAAACAACAGATAGCTTGTGGTTCAGTACATGGAGAACAATGTTAAATATTTTATAGATATTTTAAAG
RE: ATCTATTTTCTTCTAGAGGCTTCTTCTTCTTCTGATGACATGACAGAGTCATGATGACATATGATGAATATATTAAGAAATCTCAAAAATTTT
      3 TAGTGAAGCTTTTGGT 2

```

[illegible]

.....

```

Last alignment:
GACB37  CGCTCTAATCATCGCTCTCTCTATTCTCATGTCTCTCTCTGAGAGAGAGAGATGCTGCTGCTAGGTTATCTCATGGATAT
HuRef  CGCTCTAATCATCGCTCTCTCTATTCTCATGTCTCTCTCTGAGAGAGAGATGCTGCTGCTAGGTTATCTCATGGATAT

Switch process:
F1: L CGCTCTAATCATCGCTCTCTCTATTCTCATGT 1
F3:                                     4 GATACTGCTGCTGCTAGGTTATCTCATGGATAT R
RF: CGCTCTAATCATCGCTCTCTCTATTCTCATGTCTCTCTCTGAGAGAGAGAGATGCTGCTGCTAGGTTATCTCATGGATAT
      GCGATGTTATTAGCGAAGAAGATAAAGAGATGAGAGAGAGAGCTCTGACGACGATGACCTCAATGAGATGACTCTATT
      3 AGAGAGAGAGCTCTCTCT

```

|    |          |           |   |   |             |             |               |               |               |               |               |
|----|----------|-----------|---|---|-------------|-------------|---------------|---------------|---------------|---------------|---------------|
| 10 | 72001959 | rs9415010 | G | T | NA12878-1 1 | AF=0.878195 | AFR_AF=0.8684 | AMR_AF=0.8718 | EAS_AF=0.8869 | EUR_AF=0.8956 | SAS_AF=0.8691 |
| 10 | 72001960 | rs9415011 | A | C | NA12878-1 1 | AF=0.854034 | AFR_AF=0.851  | AMR_AF=0.8458 | EAS_AF=0.8631 | EUR_AF=0.8738 | SAS_AF=0.8344 |

.....

chr11:63682312-63682327

HuRef AGAAGCATGCCAGCGCCTGGCCCCGGGGCAAGGGGCAGCTCAGGCTC-GCTGCCCCGGGCACCGTTCCACCCCATTCCCAAGTCCCTGG

[illegible]

[illegible]



[illegible]

[illegible]

.....

Last2 alignment:

```
GRCh37  CCTGAACACTTGTCTATAAAACCAAGGTGGATAAAATTAGAAAAATTTCTAATTTATCCTGAGATAAATTAGAGCCTGGGGAATAG
HuRef   CCTGAACACTTGTCTATAAAACCAAGGTGGATAAAATTAGAAATTTTCTAATTTATCCTGAGATAAATTAGAGCCTGGGGAATAG
```

F1: L CCTGAACACTTGTCTATAAAACCAAGT 1 4 TGAGATAAAATTAGACCTGGGGAATAG R  
RF: CCTGAACACTTGTCTATAAAACCAAGTGGAATAATTAGAATTTTCTAATTTATCCTGAGATAAAATTAGACCTGGGGAATAG  
FR: GGACTTGTGAACAGATATTTGGTTCACACTTAATTAATCTAAAAAGATTAATAGGACTCTATTATCTCGGACCCCTTATC  
R2: CTTAATTAATCTAAAAAGATTAAGAT 2

[illegible][illegible][illegible]

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Last2 alignment:

```
GRCh37  TCTATATATATCTCACATATATTGTATGCATTATATAGAG--GAACaATAAGAACTCTGTGCTTGACTACAGTGATAAATATATTT
HuRef   TCTATATATATCTCACATATATTGTATGCATTATATAGAGGGAACCAATAAGAACTCTGTGCTTGACTACAGTGATAAATATATTT
```

RF: TCTATATATATCTCACATATATTGTATGCATTATATAGAGAGGAACCATAGAATCCTGTGCTTGACTACAGTGATAAATATATTAT  
RR: AGATATATATAGGAGTGTATATAACATACGTAATATATCTCTCCTTGATTCTTAGGACACAGAACTGATGTCACTATTATATAAATA  
F2:

[illegible][illegible]

| 1KG:     |          |            |   |     |                |             |               |               |               |               |               |  |
|----------|----------|------------|---|-----|----------------|-------------|---------------|---------------|---------------|---------------|---------------|--|
| 14       | 39602391 | rs10677580 | T | TAG | NA12878 1      | AF=0.795327 | AFR_AF=0.6415 | AMR_AF=0.7349 | EAS_AF=0.9435 | EUR_AF=0.8479 | SAS_AF=0.8395 |  |
| 14       | 39602400 | rs71204288 | A | C   | NA12878 0      | AF=0.187101 | AFR_AF=0.0091 | AMR_AF=0.2017 | EAS_AF=0.2331 | EUR_AF=0.2793 | SAS_AF=0.2751 |  |
| Ensembl: |          |            |   |     |                |             |               |               |               |               |               |  |
| 14       | 39602396 | rs59803773 | - | AG  | intron_variant |             |               |               |               |               |               |  |
| 14       | 39602400 | rs71204288 | A | C   | intron_variant |             |               |               |               |               |               |  |

Last2 alignment:

```
GRCh37  GGTGATTAAATGTGCTGTTTAAAGTTTGATACCTTAATAtCctACAGTGCAAAATatGTAGaCaaGCTAACCCCCAGGATTAGC
HuRef   GGTGATTAAATGTGCTGTTTAAAGTTTGATACCTTAATACTAACAGTGCAAAATAGGTAGTCACGCTAACCCCCAGGATTAGC
```

Switch process:

F1: L GGTGATTAAAATGTGCTGTTTAAAGTTTGATACCTTAAT 1

F2: 4 CCCCCAGGATTAGC R

F3: GGTGATTAAAATGTGCTGTTTAAAGTTTGATACCTTAATACTAACAGTCGCAATAGTAGTCACGCTAACCCAGGATAGCTGTCTCATATTTGCACGTAGGAT

F4: CCACTAAATTTTACACAGCAAAATTTCAACATGGAAATTGATGTGTCAGCTTATCCATCAGTCGCTGGGGGCTCAATGCAGACAGATGTAAACGTCACATCTA

F5: 3 GGTACACAGAGATGTAAACGTCACATCTA 2

[illegible][illegible]

Last2 alignment:

```
GrCh37  AAAGGAATTACTTAAAGAATAACACAAACCACCATGAACATGcTTacAcaagggggaaGtcAAtCATGAGTGGATTATATGAAGATTGATTTAGTTTGGTTATC
HGHC8   AAAGGAATTACTTAAAGAATAACACAAACCACCATGAACATGATTTGACTTCCCCCTTGTTGAAGCATGAGTGGATTATATGAAGATTGATTTAGTTTGGTTATC
```

Switch process:

F1: L AAAGGAATACCTTAAGAATACACAACCAACCATGAA 1

F3: 4 AGTGATTATATGAAGATTGATTAGTTGGTTATC R

RF: AAAGGAATACCTTAAGAATACACAACCAACCATGAACATGATTGACTTCCCTTGTGTAGCATGATGGGATATATGAAGATTGATTAGTTGGTTATC

RR: TTTCCTTAATGAATCTTATTGTGTGGTGGTACTTGCTAAACTGCTGAAACCAACATCTGCTACTCAATTAATCTTCAACTAAATCAACCAATAG

F2: 3 GCTAACTAATGAAGGGGACACATCTGAT 2

34047031 34047041 34047051 34047061 34047071 34047081 34047091 34047101 34047111 34047121 34047131  
ATTGAAATGCAAGGAATTACTTAGAATACACAAACCCACATGAACATGCTTACACAGGGGGGAAGTCAATCATGAGTGGATTATATGAGAGATTGATTAGTTGGTTATCAAAAT  
.....A..TG..TCCCCCTT..GT..G.....  
.....A,g,t,tccccctt,gt,g.....  
.....A,g,t,tccccctt,gt,g.....

[illegible][illegible]

Ensembl: 15 36259783 rs386783006 CTTACACAAGGGGAAGTCAAAT ATTTGACTTCCCCTTGTGTAAG intron\_variant

=====

[illegible]

```
G.....G.....  
#####  
G.....C.....  
.....C.....C.....g.....  
#####A.....c  
G.....AG.....G.....  
  
#####  
#####S.....  
#####C.....  
#####G.....  
#####G.....
```

[illegible]

[illegible]

|    |          |           |   |   |           |            |               |          |          |          |          |
|----|----------|-----------|---|---|-----------|------------|---------------|----------|----------|----------|----------|
| 18 | 69556841 | rs7239836 | T | C | NA12878 1 | AF=0.99361 | AFR_AF=0.9758 | AMR_AF=1 | EAS_AF=1 | EUR_AF=1 | SAS_AF=1 |
| 18 | 69556842 | rs7239899 | G | C | NA12878 1 | AF=0.99361 | AFR_AF=0.9758 | AMR_AF=1 | EAS_AF=1 | EUR_AF=1 | SAS_AF=1 |

|          |          |             |    |    |                         |
|----------|----------|-------------|----|----|-------------------------|
| Ensembl: |          |             |    |    |                         |
| 18       | 69556841 | rs386804713 | TG | CC | downstream_gene_variant |

Template-switch process:

Lastz alignment:

```
GRCh37  CAGCAAACTACTCAGGGCTCCACCTCACATCTGTCCCAAGtcCTGGGGACTTGCTCACTCAGCAGAAGCAAGAGAAGGCC
HuRef   CAGCAAACTACTCAGGGCTCCACCTCACATCTGTCCCAAGGACTTGGGGACTTGCTCACTCAGCAGAAGCAAGAGAAGGCC
```

F1: L CAGCAAACTCACTCAGGGCTCCACCTCACAATCT 1  
F3: 4 TTGCTCACTCAGCAGAAGACCAAGAGAAGCC R  
RF: CAGCAAACTCACTCAGGGCTCCACCTCACAATCTGTCCCCAAGGACTTGGGACTTGTCTACTCAGCAGAAGACCAAGAGAAGCC  
RR: GTCTGTTTAGTGAGTCCCGAGGTGGAGTGTAGACAGGGGTTCTTGAAACCCCTGAACGAGTGAGTGTCTTCTGGTTCTCTCGG  
F2: 3 CAGGGGTTCTCGAACCCTG 2

```

chrRef
      718471  718481  718491  718501  718511  718521  718531  718541  718551  718561  718571
AG-AAGTCACTTCACG-AATCACTCA+GGGCTGCACCTATCTGTCCCAACCTCTGGGGACTGTCTCACTACGACAGAGACCAAGAGACGACAGATGCAGTGGCTCACACCTGTA
.....RM.....
..A.....TC.....
.....A.....G.....
.....GA.....
.....T.....G.....T.....CCT.....

```

| Ensembl: | chr    | pos       | ref | alt | variant                 |
|----------|--------|-----------|-----|-----|-------------------------|
| 19       | 767517 | rs8113085 | T   | G   | downstream_gene_variant |
| 19       | 767518 | rs8104002 | C   | A   | downstream_gene_variant |

Template-switch process:

Lastz alignment:

Lastz alignment:

```
GRCh37  ATATCTTTTTTTTATGATCTAAATTTTACCATTATCCAAATAG-ACTATATGgcCaTATTA-GtaCAT-TAGTcTcTATCTATCAATCACAACAAGAGAAAAATTCACATATC
HueRef  ATATCTTTTTTTTATGATCTAAATTTACCATTATCCAAATAGGACTA-ATGtAC-TAATTATGGCCATATAGTC-TATCTATCAATCACAATCAACAAGAGAAAAATTCACATATC
```

F1: L ATATCTTTTTTATGATCTAATTTACCAATTATCCA 1  
F3: 4 CTATCAATCACATCAACAATGAGAAAAATTCACATATC R  
RF: ATATCTTTTTTATGATCTAATTTACCAATTACCAATAGGACTAATGTACTAATTATGGCCATATAGTCTATCTATCAATCACATCAACAATGAGAAAAATTCACATATC  
R1: ATAGAAAAAATACTAGATTAAATGGTAATAGTTTATCTCTGATTACATGATTAATACCGGTATATCAGATAGATAGTTAGTGTAGTGTACTCTTTTAAAGTGATAG  
F2: TCTCTGATTACATGATTAATACCGGTATACGATA 2

38062861 38062871 38062881 38062891 38062901 38062911 38062921 38062931 38062941 38062951



73181844 73181851 7318181 73181871 73181818 7318181 73181820 73181821 73181822 73181823 73181824  
GGACATGGATGGAGGAAGCAGGACTCAATGTTTTCATCAGCCGCTCTGTATAGA-AGCGGCTTTCACAAAGTATAATAGCTTGAGTAAACCCACAGTTTATCTTGTATAGTGGG  
.....R.Y.....  
.....G.....  
.....R.G.C.....



## 1kg.

