

## SUPPLEMENTARY DATA LEGENDS

**Figure S1. Transcriptional regulator overlap with genomic regions.** Heatmap representing the fraction of TF binding overlapping the following genomic regions: Promoter (transcription start site; within 1kb upstream of a transcription start site or overlapping 5' UTR), Coding (coding sequence), Downstream (transcription stop site; 3' UTR or 200bp downstream of gene), intron, intergenic regions.

**Figure S2. Chromatin states across developmental stages.** Boxplots represent the distribution of histone H3 lysine 27 trimethylation (H3K27me3) or lysine 4 trimethylation (H3K4me3) ChIP-seq signals within each chromatin state across developmental stages.

**Figure S3. DNA Motifs in HOT, WARM, and COLD regions.** (A) For all TFs with a well-defined DNA binding motif, enrichment for the motif in all peaks was calculated relative to background ("All" column, see Methods for details). Datasets in which the expected motif is enriched are represented here (red represents enrichment and blue represents depletion). For the columns labeled HOT, WARM, and COLD, motif enrichment was calculated for peaks falling into one of three occupancy categories relative to the union of the three. To explore enrichment of individual TF motifs in corresponding datasets (Figure 6), we collected 536 regulatory motifs from the literature, each having an annotated corresponding fly TF (Matys et al. 2003; Wasserman and Sandelin 2004; Down et al. 2007; Ivan et al. 2008; Noyes et al. 2008a; Noyes et al. 2008b; Reed et al. 2008; MacArthur et al. 2009; Sen et al. 2010). Up to 10 shuffled control motifs were generated for each motif as previous described (Kheradpour et al. 2007; Lindblad-Toh et al. 2011). Each motif (or control motif) was matched to the fly genome using a PWM threshold corresponding to a p-value of  $4^{-7}$  as determined by TFM-Pvalue (Touzet and Varre 2007), while excluding coding exons, repeats, transposons, 3' untranslated regions and non-coding RNAs

(FlyBase v5.54), due to their prevalence of confounding patterns due to non-TF sources. Enrichments were computed for each motif and dataset as the fraction of motif instances bound divided by the fraction of control instances bound. When more than one literature motif exists for a given factor, the one with the highest enrichment was selected for further analysis. The association of the motif with regions different complexity (HOT, WARM, or COLD) was computed for each dataset as the motif enrichment in the subset of peaks for one complexity class compared to bound regions of any complexity class. (B) Boxplot represents the range of enrichment values seen in COLD, WARM, and HOT regions for TF datasets in which the expected motif is enriched in the overall set of binding peaks. (C) Same as A, only all TF datasets are included regardless of whether or not the expected motif is enriched in the overall set of binding peaks. In both cases, most TFs' DNA binding motifs are less enriched in HOT regions.

**Figure S4. Conservation of HOT promoter regions.** (A) Mean phastCons score (10bp window) across HOT regions within 1kb of a TSS ("Promoter-proximal HOT regions") and HOT regions that are not within 1kb of a TSS ("Promoter-distal HOT regions"). (B) Mean phastCons score (10bp window) across promoters (-500bp to TSS) that overlap a HOT region ("HOT Promoter Regions") and promoters that do not overlap a HOT region ("non-HOT Promoter Regions"). For both A and B, the difference in phastCons score within the boxed regions (dashed lines) was found to be statistically significant ( $p < 1 \times 10^{-15}$ ; Wilcoxon rank sum test).

**Figure S5. Patterned HOT enhancers and chromatin state.** As in Figure 6, the first four columns of the chart represent the fraction of HOT, WARM, and COLD binding across chromatin states, as well as the fraction of the genome covered by each chromatin state. The final column ("Kvon et al.") represents the fraction of patterned HOT enhancers identified by Kvon et al. that overlap each chromatin state.

**Figure S6. SNP density in HOT, WARM, and COLD regions.** Mean (10% trimmed mean) SNM density +/- confidence interval (95%) for the central 100bp of HOT, WARM, and COLD regions. Asterisks represent significant divergence from random (\*\* $p < 1 \times 10^{-16}$ ; Wilcoxon rank sum test). All line-specific bam files were downloaded from the Drosophila Genetic Reference Panel website (Mackay et al. 2012), and variants were called using SAMtools mpileup command with the -u option (Li et al. 2009). SNP calls were made on each individual iso female line separately. SNP density was derived by using BEDTools' coverageBed command (Quinlan and Hall 2010), and counting the resulting number of variant positions per each hot, warm, and cold region.

**Table S1. Data summary table.**

**Table S2. Genomic regions and chromatin states targeted by TRFs**

**Table S3. TRF interaction matrix (HOT regions subtracted)**

**Table S4. TRF overlap and motif enrichment in HOT regions.**

**Table S5. Catalog of STARR-seq enhancers and bound TFs.**

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Figure S1 - Slattery et al.

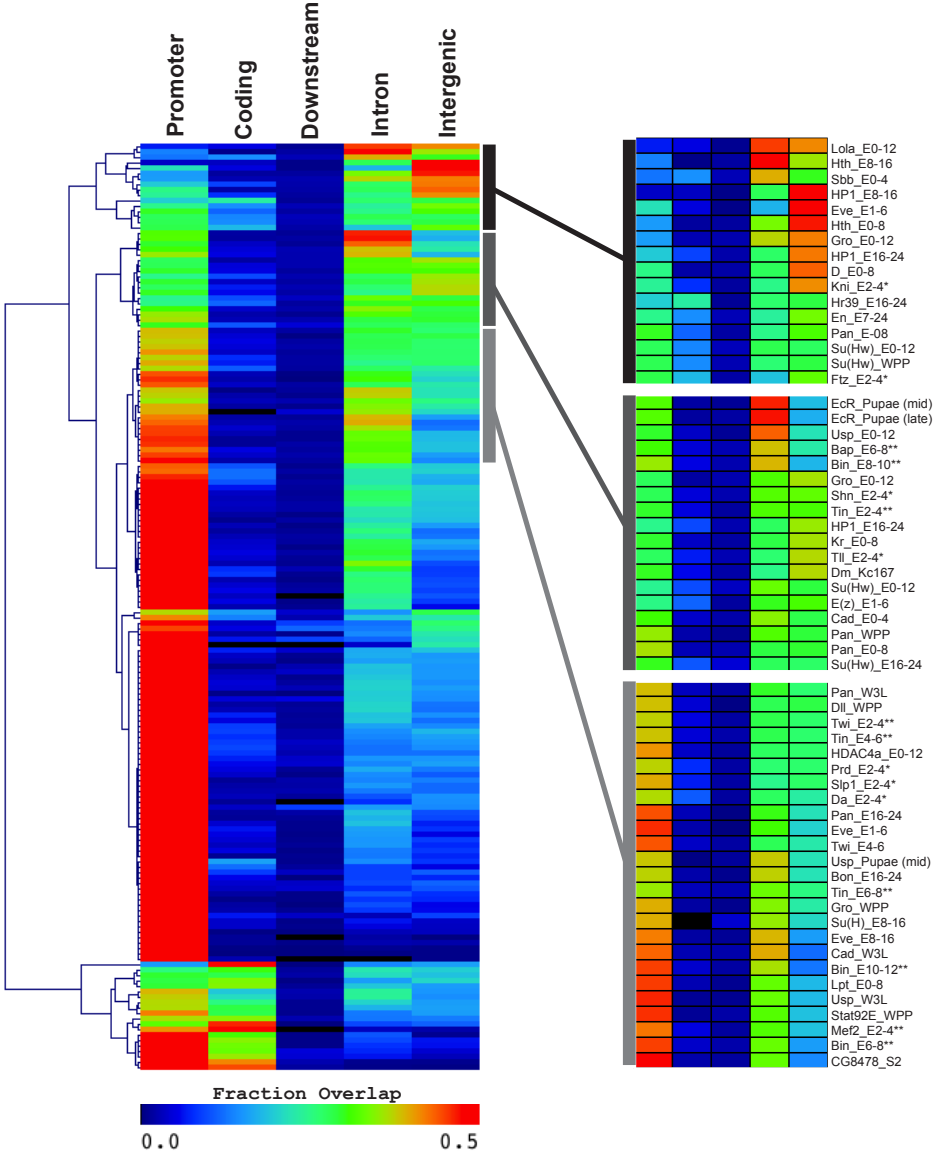


Figure S2 - Slattery et al.

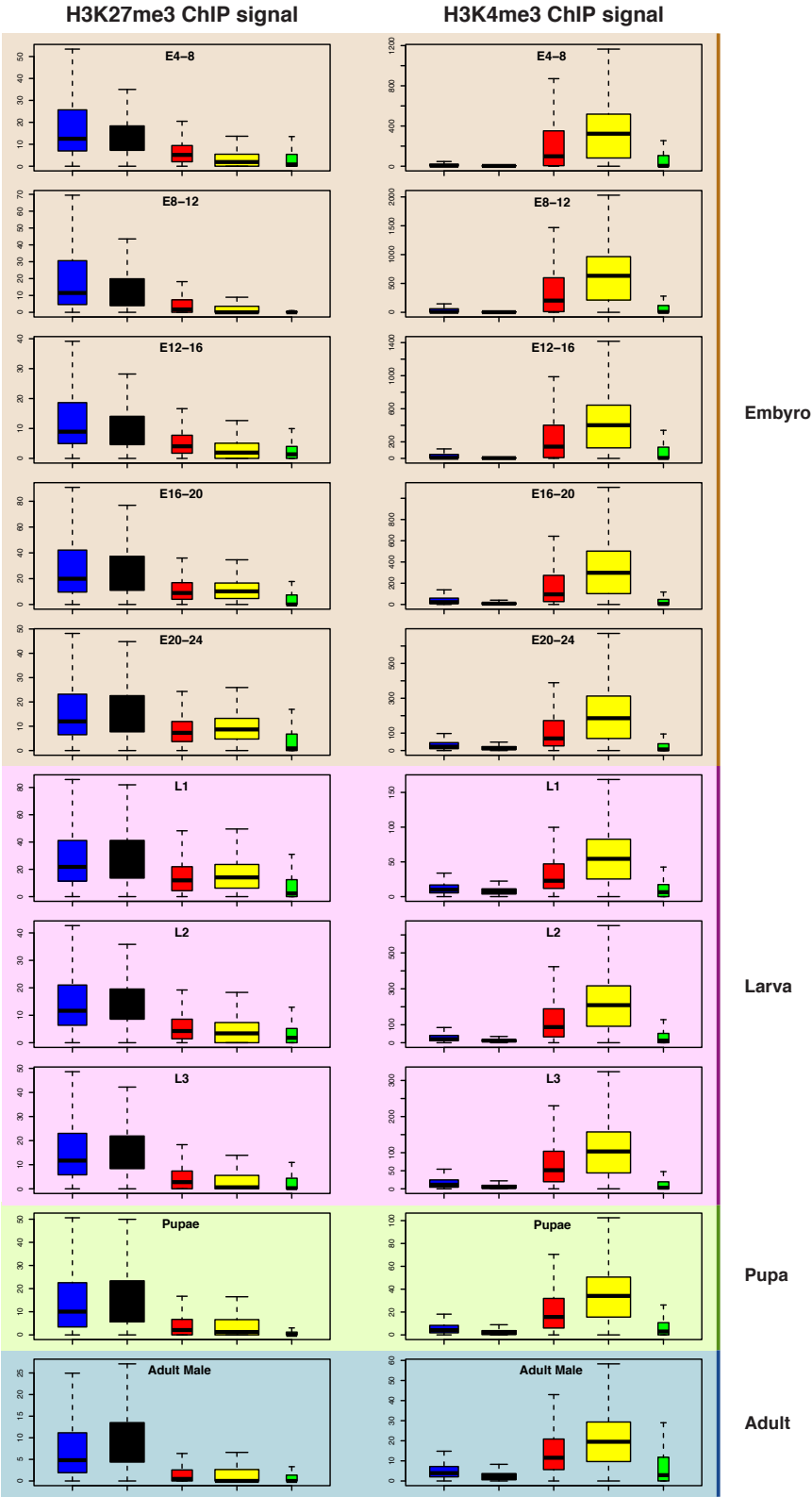


Figure S3 - Slattery et al.

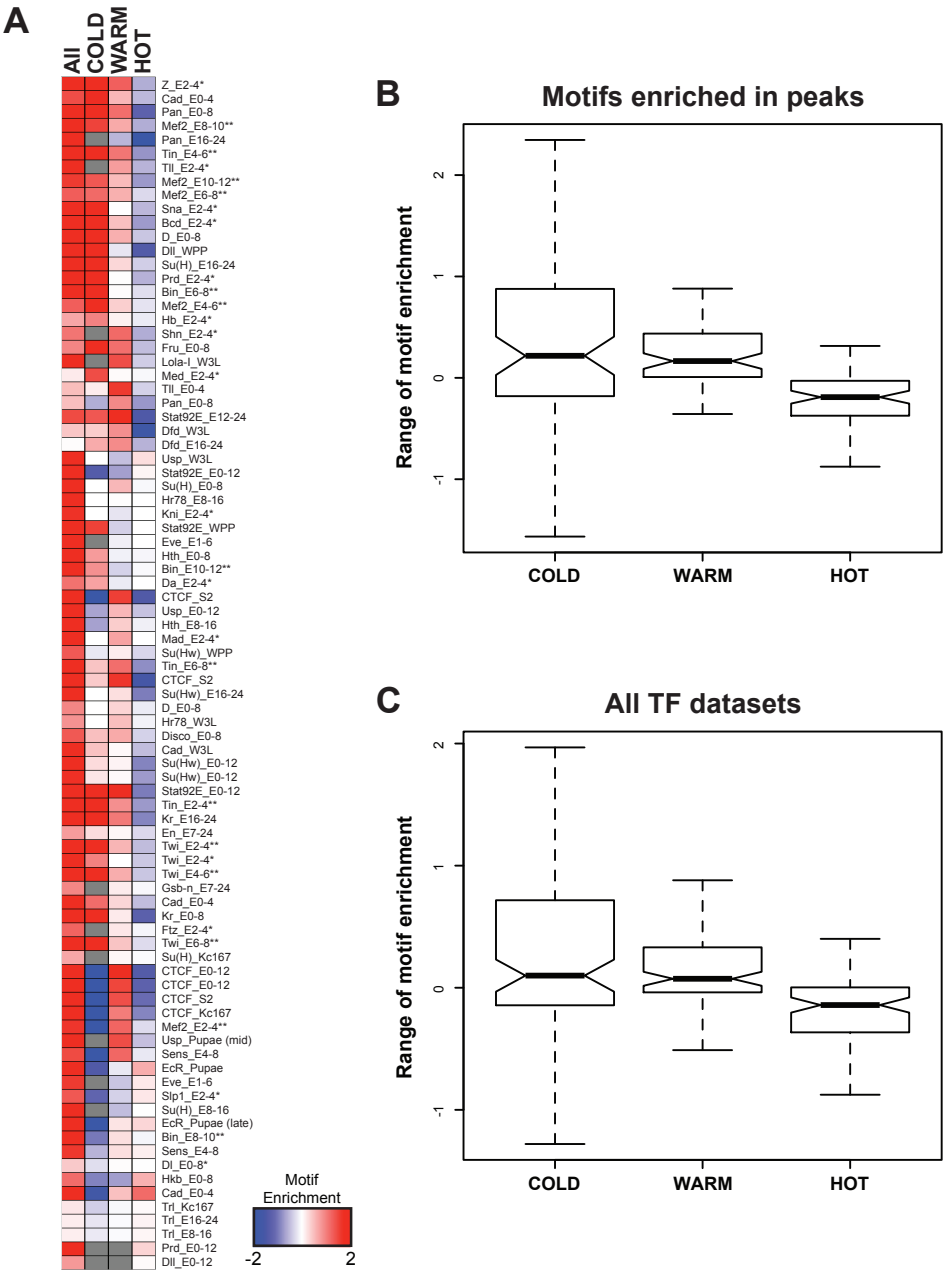


Figure S4 - Slattery et al.

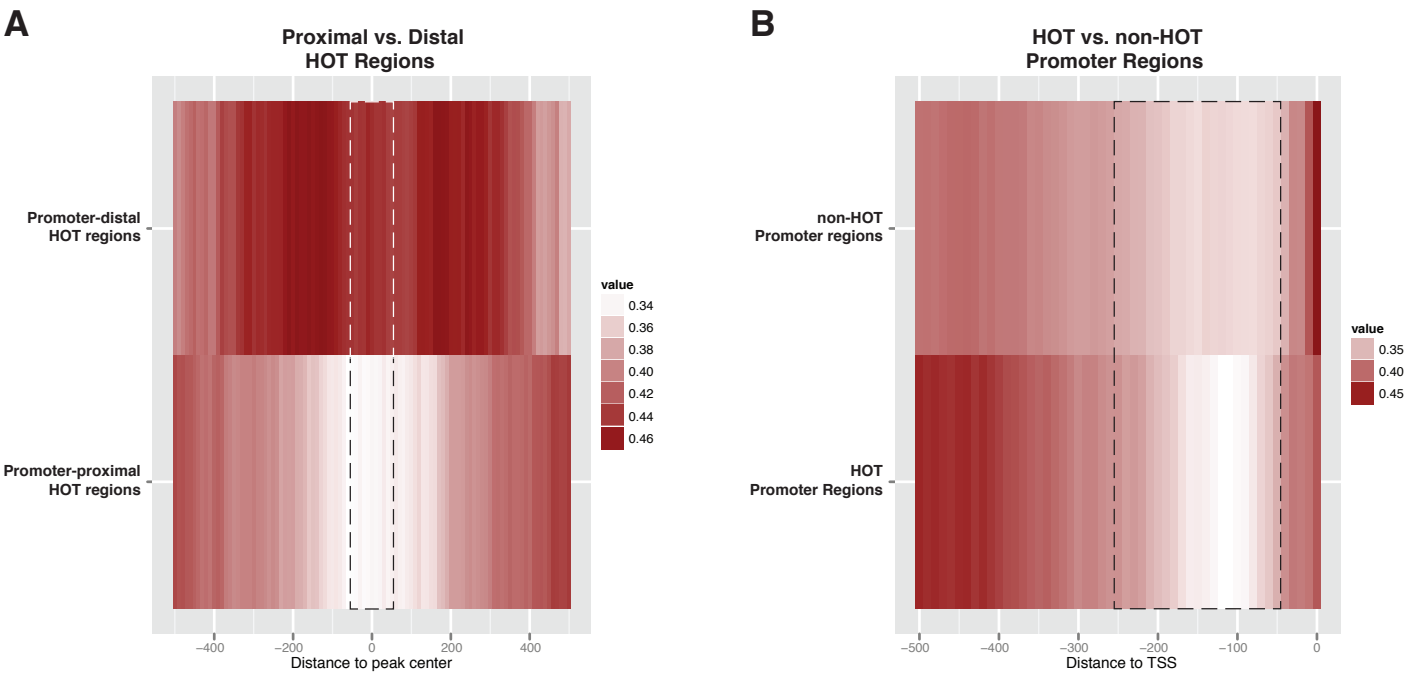


Figure S5 - Slattery et al.

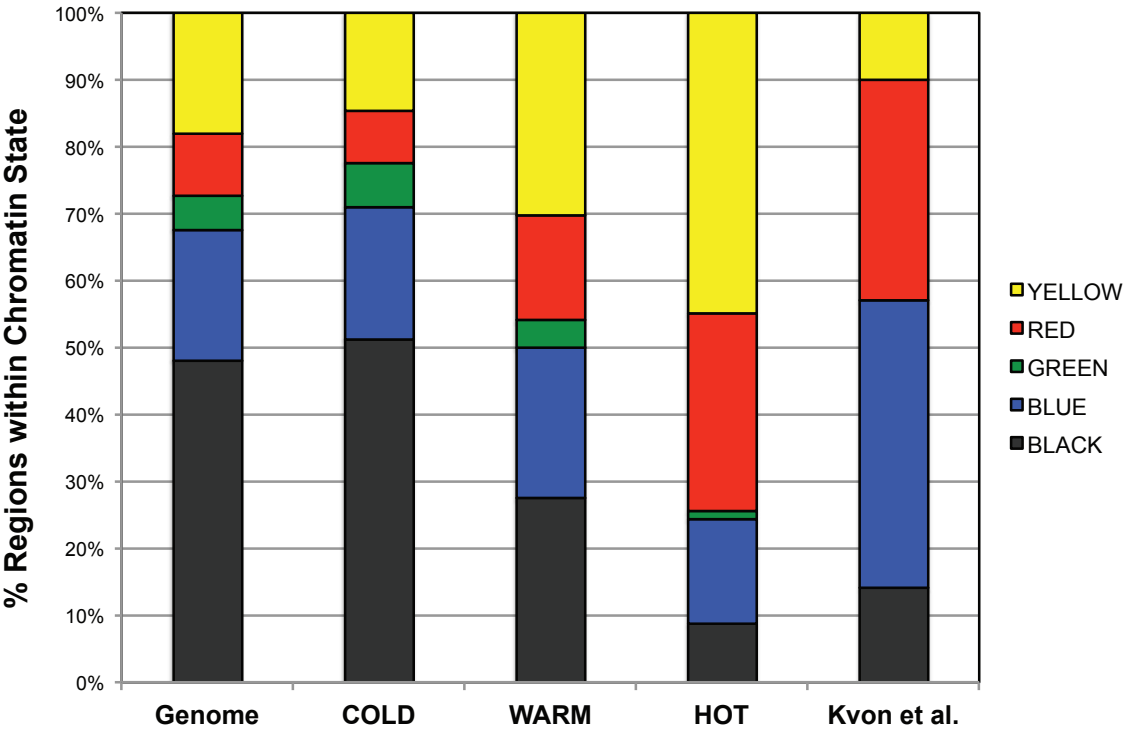
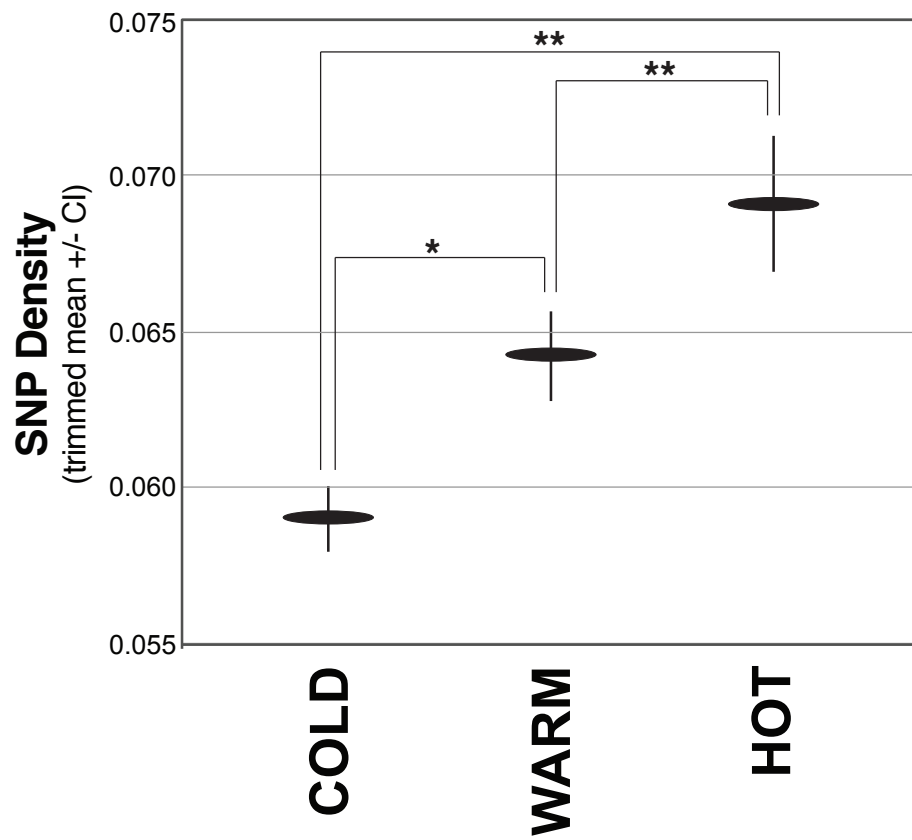


Figure S6 - Slattery et al.



| #EXP     | ChIPped TRF FBID | ChIPped TRF Symbol | ChIPped TRF Name | STAGE  | STRAIN      | modENCODE DCC ID | GEO submission, if DCC pending | Published                   |
|----------|------------------|--------------------|------------------|--------|-------------|------------------|--------------------------------|-----------------------------|
| ChIP-seq | FBgn0085432      | pan                | TCF              | WPP    | Iso1        | pending, ID=5025 | GSE49780                       | modENCODE - New, this study |
| ChIP-seq | FBgn0085432      | pan                | TCF              | W3L    | Iso1        | pending, ID=5024 | GSE49779                       | modENCODE - New, this study |
| ChIP-seq | FBgn0085432      | pan                | TCF              | E0-8   | Hr46-GFP    | pending, ID=5023 | GSE49778                       | modENCODE - New, this study |
| ChIP-seq | FBgn0003687      | Tbp                | TBP              | E0-8   | Exd-GFP     | pending, ID=5022 | GSE49777                       | modENCODE - New, this study |
| ChIP-seq | FBgn0004837      | Su(H)              | SuH              | Kc167  | Kc167       | pending, ID=5018 | GSE49899                       | modENCODE - New, this study |
| ChIP-seq | FBgn0004837      | Su(H)              | SuH              | E0-8   | Iso1        | pending, ID=5017 | GSE49776                       | modENCODE - New, this study |
| ChIP-seq | FBgn0016917      | Stat92E            | Stat92E          | E12-24 | Stat92E-GFP | pending, ID=5014 | GSE49775                       | modENCODE - New, this study |
| ChIP-seq | FBgn0016917      | Stat92E            | Stat92E          | E0-12  | Stat92E-GFP | pending, ID=5013 | GSE49899                       | modENCODE - New, this study |
| ChIP-seq | FBgn0004647      | N                  | Notch            | W3L    | Notch-GFP   | pending, ID=5011 | GSE49899                       | modENCODE - New, this study |
| ChIP-seq | FBgn0262656      | dm                 | Myc              | W3L    | Iso1        | pending, ID=5008 | GSE49774                       | modENCODE - New, this study |
| ChIP-seq | FBgn0262656      | dm                 | Myc              | Kc167  | Kc167       | pending, ID=5006 | GSE49899                       | modENCODE - New, this study |
| ChIP-seq | FBgn0005630      | lola               | LolaJ            | E12-24 | LolaJ-GFP   | pending, ID=5005 | GSE49773                       | modENCODE - New, this study |
| ChIP-seq | FBgn0005630      | lola               | LolaJ            | E0-12  | LolaJ-GFP   | pending, ID=5004 | GSE49772                       | modENCODE - New, this study |
| ChIP-seq | FBgn0005630      | lola               | LolaI            | W3L    | LolaI-GFP   | pending, ID=5003 | GSE49899                       | modENCODE - New, this study |
| ChIP-seq | FBgn0031434      | insv               | insv             | Kc167  | Kc167       | pending, ID=5001 | GSE49899                       | modENCODE - New, this study |
| ChIP-seq | FBgn0015239      | Hr78               | Hr78             | W3L    | Hr78-GFP    | pending, ID=5000 | GSE49899                       | modENCODE - New, this study |
| ChIP-seq | FBgn0015239      | Hr78               | Hr78             | E8-16  | Hr78-GFP    | pending, ID=4998 | GSE49899                       | modENCODE - New, this study |
| ChIP-seq | FBgn0001168      | h                  | H                | Kc167  | Kc167       | pending, ID=4983 | GSE49899                       | modENCODE - New, this study |
| ChIP-seq | FBgn0001168      | h                  | H                | E0-8   | Iso1        | pending, ID=4982 | GSE49771                       | modENCODE - New, this study |
| ChIP-seq | FBgn0001139      | gro                | Gro              | WPP    | Iso1        | pending, ID=4981 | GSE49770                       | modENCODE - New, this study |
| ChIP-seq | FBgn0000567      | Eip74EF            | Eip74            | E8-16  | Eip74-GFP   | pending, ID=4976 | GSE49769                       | modENCODE - New, this study |

|          |             |           |         |        |          |                     |          |                                |
|----------|-------------|-----------|---------|--------|----------|---------------------|----------|--------------------------------|
| ChIP-seq | FBgn0000157 | Dll       | Dll     | WPP    | Iso1     | pending,<br>ID=4974 | GSE49768 | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0263667 | Lpt       | Cmi     | E0-8   | Exd-GFP  | pending,<br>ID=4967 | GSE49899 | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0037746 | CG8478    | CG8478  | S2     | S2       | pending,<br>ID=4966 | GSE49899 | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0000015 | Abd-B     | AbdB    | W3L    | AbdB-GFP | pending,<br>ID=4962 | GSE49899 | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0003964 | usp       | USP     | E0-12  | USP-GFP  | pending,<br>ID=4114 | GSE34598 | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0003964 | usp       | USP     | WPP12  | USP-GFP  | pending,<br>ID=4113 | GSE34703 | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0003870 | ttk       | Ttk     | Kc167  | Kc167    | pending,<br>ID=4110 | GSE34698 | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0003964 | usp       | Usp     | W3L    | Iso1     | pending,<br>ID=4109 | GSE34707 | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0085432 | pan       | TCF     | E16-24 | Iso1     | pending,<br>ID=4107 | GSE34693 | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0003567 | su(Hw)    | SuHw    | WPP    | Iso1     | pending,<br>ID=4105 | GSE34706 | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0003567 | su(Hw)    | SuHw    | E16-24 | Iso1     | pending,<br>ID=4104 | GSE34611 | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0016917 | Stat92E   | Stat92E | WPP    | Iso1     | pending,<br>ID=4103 | GSE34386 | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0022764 | Sin3A     | Sin3A   | Kc167  | Kc167    | pending,<br>ID=4100 | GSE34376 | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0004170 | sc        | sc      | E0-12  | Iso1     | pending,<br>ID=4099 | GSE34347 | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0263102 | psq       | psq     | WPP    | Iso1     | pending,<br>ID=4098 | GSE34385 | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0263102 | psq       | psq     | Kc167  | Kc167    | pending,<br>ID=4097 | GSE34374 | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0003145 | prd       | Prd     | E0-12  | Iso1     | pending,<br>ID=4096 | GSE49899 | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0003145 | prd       | Prd     | E0-12  | Iso1     | pending,<br>ID=4095 | GSE49899 | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0002781 | mod(mdg4) | modMDG4 | W3L    | Iso1     | pending,<br>ID=4094 | GSE34701 | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0030082 | HP1b      | HP1     | E8-16  | Iso1     | pending,<br>ID=4091 | GSE34360 | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0004652 | fru       | Fru     | E0-8   | Iso1     | pending,<br>ID=4089 | GSE34710 | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0001235 | hth       | Hth     | E8-16  | Iso1     | pending,<br>ID=4085 | GSE34361 | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0262975 | cnc       | CNC     | WPP    | Iso1     | pending,<br>ID=4084 | GSE32661 | modENCODE -<br>New, this study |

|          |             |            |          |           |            |                        |          |                                                   |
|----------|-------------|------------|----------|-----------|------------|------------------------|----------|---------------------------------------------------|
| ChIP-seq | FBgn0262975 | cnc        | CNC      | Adult(M)  | Iso1       | pending,<br>ID=4083    | GSE34342 | modENCODE -<br>New, this study                    |
| ChIP-seq | FBgn0262975 | cnc        | CNC      | Adult(F)  | Iso1       | pending,<br>ID=4082    | GSE49899 | modENCODE -<br>New, this study                    |
| ChIP-seq | FBgn0262975 | cnc        | CNC      | E16-24    | Iso1       | pending,<br>ID=4081    | GSE34354 | modENCODE -<br>New, this study                    |
| ChIP-seq | FBgn0037746 | CG8478     | CG8478   | WPP       | Iso1       | pending,<br>ID=4080    | GSE34352 | modENCODE -<br>New, this study                    |
| ChIP-seq | FBgn0003715 | CG16778    | CG16778  | E0-8      | Iso1       | pending,<br>ID=4078    | GSE34601 | modENCODE -<br>New, this study                    |
| ChIP-seq | FBgn0000210 | br         | br-core  | E0-8      | Iso1       | pending,<br>ID=4077    | GSE49899 | modENCODE -<br>New, this study                    |
| ChIP-seq | FBgn0000439 | Dfd        | Dfd      | E0-8      | Dfd-GFP    | pending,<br>ID=4075    | GSE34613 | modENCODE -<br>New, this study                    |
| ChIP-seq | FBgn0085432 | pan        | TCF      | E0-8      | Iso1       | pending,<br>ID=4074    | GSE34609 | modENCODE -<br>New, this study                    |
| ChIP-seq | FBgn0004170 | sc         | sc       | E0-8      | Iso1       | pending,<br>ID=4071    | GSE34712 | modENCODE -<br>New, this study                    |
| ChIP-seq | FBgn0001235 | hth        | Hth      | E0-8      | Iso1       | pending,<br>ID=4070    | GSE34604 | modENCODE -<br>New, this study                    |
| ChIP-seq | FBgn0004837 | Su(H)      | SuH      | E16-24    | Iso1       | pending,<br>ID=4069    | GSE34359 | modENCODE -<br>New, this study                    |
| ChIP-seq | FBgn0004837 | Su(H)      | SuH      | E8-16     | Iso1       | pending,<br>ID=4068    | GSE34371 | modENCODE -<br>New, this study                    |
| ChIP-seq | FBgn0013263 | Trl        | Trl      | Wing disc | Iso1       | pending,<br>ID=pending | GSE38594 | modENCODE -<br>New, Oh et al.<br>(PMID: 23395637) |
| ChIP-seq | FBgn0034970 | yki        | Yki      | E8-16     | Iso1       | pending,<br>ID=5029    | GSE38594 | modENCODE -<br>New, Oh et al.<br>(PMID: 23395637) |
| ChIP-seq | FBgn0013263 | Trl        | Trl      | E8-16     | Iso1       | pending,<br>ID=5028    | GSE38594 | modENCODE -<br>New, Oh et al.<br>(PMID: 23395637) |
| ChIP-seq | FBgn0000251 | cad        | Caudal   | W3L       | 7T-CAD-GFP | 3403                   |          | modENCODE -<br>New, this study                    |
| ChIP-seq | FBgn0000606 | eve        | eve      | E8-16     | 5T-GFP     | 3401                   |          | modENCODE -<br>New, this study                    |
| ChIP-seq | FBgn0000606 | eve        | eve      | E1-6      | R13-YFP    | 3400                   |          | modENCODE -<br>New, this study                    |
| ChIP-seq | FBgn0038767 | trem       | trem     | Adult(F)  | Iso1       | 3399                   |          | modENCODE -<br>New, this study                    |
| ChIP-seq | FBgn0263755 | Su(var)3-9 | SuVar3-9 | E0-12     | Iso1       | 3396                   |          | modENCODE -<br>New, this study                    |
| ChIP-seq | FBgn0000411 | D          | Dichaete | E0-8      | Iso1       | 3395                   |          | modENCODE -<br>New, this study                    |

|          |             |        |           |           |             |      |  |                                |
|----------|-------------|--------|-----------|-----------|-------------|------|--|--------------------------------|
| ChIP-seq | FBgn0001325 | Kr     | Kruppel   | E16-24    | Iso1        | 3394 |  | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0023097 | bon    | bonus     | E16-24    | Iso1        | 3393 |  | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0030082 | HP1b   | HP1       | E16-24    | Iso1        | 3392 |  | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0030082 | HP1b   | HP1       | E16-24    | Iso1        | 3391 |  | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0261239 | Hr39   | Hr39      | E16-24    | Iso1        | 3390 |  | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0015805 | HDAC1  | HDAC1     | E0-12     | Iso1        | 2636 |  | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0025825 | HDAC3  | HDAC3     | E0-12     | Iso1        | 2634 |  | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0025825 | HDAC3  | HDAC3     | E0-12     | Iso1        | 2633 |  | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0051119 | HDAC11 | HDAC11    | E0-12     | Iso1        | 2630 |  | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0051119 | HDAC11 | HDAC11    | E0-12     | Iso1        | 2629 |  | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0041210 | HDAC4a | HDAC4a    | E0-12     | Iso1        | 2627 |  | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0037746 | CG8478 | CG8478    | E8-16     | Iso1        | 3240 |  | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0003720 | tll    | tll       | E0-4      | 8T-GFP      | 3234 |  | modENCODE -<br>New, this study |
| ChIP-seq | FBgn0001320 | kni    | KNI       | E8-16     | Iso1        | 3243 |  | modENCODE -<br>Negre et al.    |
| ChIP-seq | FBgn0261434 | hkb    | Huckebein | E8-16     | Iso1        | 3242 |  | modENCODE -<br>Negre et al.    |
| ChIP-seq | FBgn0000606 | eve    | eve       | E1-6      | eve-YFP     | 3239 |  | modENCODE -<br>Negre et al.    |
| ChIP-seq | FBgn0013263 | Trl    | GAF       | E16-24    | Iso1        | 3238 |  | modENCODE -<br>Negre et al.    |
| ChIP-seq | FBgn0003044 | Pcl    | PCL       | E0-8      | Iso1        | 3237 |  | modENCODE -<br>Negre et al.    |
| ChIP-seq | FBgn0022764 | Sin3A  | Sin3A     | E0-12     | Iso1        | 3232 |  | modENCODE -<br>Negre et al.    |
| ChIP-seq | FBgn0000439 | Dfd    | dfd       | W3L       | 10T-DFD-GFP | 3230 |  | modENCODE -<br>Negre et al.    |
| ChIP-seq | FBgn0000439 | Dfd    | dfd       | E16-24    | 10T-DFD-GFP | 3229 |  | modENCODE -<br>Negre et al.    |
| ChIP-seq | FBgn0000546 | EcR    | EcR       | WPP.30-33 | EcR-GFP     | 2642 |  | modENCODE -<br>Negre et al.    |
| ChIP-seq | FBgn0000546 | EcR    | EcR       | WPP.10-11 | EcR-GFP     | 2641 |  | modENCODE -<br>Negre et al.    |

|           |             |           |                   |       |            |      |  |                             |
|-----------|-------------|-----------|-------------------|-------|------------|------|--|-----------------------------|
| ChIP-seq  | FBgn0035769 | CTCF      | CTCF              | S2    | S2         | 2639 |  | modENCODE -<br>Negre et al. |
| ChIP-seq  | FBgn0035769 | CTCF      | CTCF              | S2    | S2         | 2638 |  | modENCODE -<br>Negre et al. |
| ChIP-seq  | FBgn0000251 | cad       | Caudal            | E0-4  | 7T-CAD-GFP | 2626 |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0000629 | eve       | eGFP              | E1-6  | R13-GFP    | 2603 |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0002781 | mod(mdg4) | mod(mdg4)         | E8-16 | Iso1       | 2602 |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0000629 | E(z)      | enhancer of zeste | E8-16 | Iso1       | 2585 |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0002573 | sens      | senseless         | E4-8  | Iso1       | 2577 |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0015396 | jumu      | Jumeau            | E0-8  | Iso1       | 2576 |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0261434 | hkb       | Huckebein         | E0-8  | Iso1       | 2575 |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0038391 | GATAe     | GATAe             | E0-8  | Iso1       | 2573 |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0000459 | disco     | Disco             | E0-8  | Iso1       | 2572 |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0000411 | D         | Dichaete          | E0-8  | Iso1       | 2571 |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0000251 | cad       | Caudal            | E0-4  | Iso1       | 2570 |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0010575 | sbb       | Brakeless         | E0-4  | Iso1       | 2569 |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0013263 | Trl       | GAF               | Kc167 | Kc167      | 2568 |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0051119 | HDAC11    | HDAC11-495        | E0-12 | Iso1       | 2567 |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0026428 | HDAC6     | HDAC6-497         | E0-12 | Iso1       | 2566 |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0026428 | HDAC6     | HDAC6-496         | E0-12 | Iso1       | 2565 |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0041210 | HDAC4a    | HDAC4a-493        | E0-12 | Iso1       | 2564 |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0041210 | HDAC4a    | HDAC4a-492        | E0-12 | Iso1       | 2563 |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0025825 | HDAC3     | HDAC3-499         | E0-12 | Iso1       | 2562 |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0025825 | HDAC3     | HDAC3-498         | E0-12 | Iso1       | 2561 |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0015805 | HDAC1     | HDAC1-501         | E0-12 | Iso1       | 2560 |  | modENCODE -<br>Negre et al. |

|           |             |         |            |       |          |      |  |                             |
|-----------|-------------|---------|------------|-------|----------|------|--|-----------------------------|
| ChIP-chip | FBgn0015805 | HDAC1   | HDAC1-500  | E0-12 | Iso1     | 2559 |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0051119 | HDAC11  | HDAC11-494 | E0-12 | Iso1     | 2558 |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0002573 | sens    | senseless  | E4-8  | SENS-GFP | 978  |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0035769 | CTCF    | CTCF       | S2    | S2       | 913  |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0035769 | CTCF    | CTCF       | Kc167 | Kc167    | 908  |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0000251 | cad     | Caudal     | E0-4  | 7T-GFP   | 902  |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0003567 | su(Hw)  | Su(Hw)-PG  | E0-12 | Iso1     | 901  |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0001325 | Kr      | Kruppel    | E0-8  | Iso1     | 898  |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0035769 | CTCF    | CTCF-N     | E0-12 | Iso1     | 770  |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0035769 | CTCF    | CTCF-C     | E0-12 | Iso1     | 769  |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0004870 | bab1    | BAB-1      | E0-12 | Iso1     | 628  |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0262975 | cnc     | cnc        | E0-12 | Iso1     | 627  |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0000577 | en      | ENGRAILED  | E0-12 | Iso1     | 625  |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0001139 | gro     | GRO        | E0-12 | Iso1     | 623  |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0001319 | kn      | KNOT       | E0-12 | Iso1     | 618  |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0016917 | Stat92E | Stat92E    | E0-12 | Iso1     | 616  |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0003870 | ttk     | TRAMTRACK  | E0-12 | Iso1     | 615  |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0003944 | Ubx     | UBX        | E0-12 | Iso1     | 614  |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0003944 | Ubx     | UBX-2      | E3-8  | Iso1     | 612  |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0000577 | en      | ENGRAILED  | E7-24 | Iso1     | 611  |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0001147 | gsb-n   | GSBN       | E7-24 | Iso1     | 610  |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0086758 | chinmo  | chinmo     | E0-12 | Iso1     | 608  |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0026144 | CBP     | cbp        | E0-12 | Iso1     | 607  |  | modENCODE -<br>Negre et al. |

|           |             |           |           |        |      |         |  |                             |
|-----------|-------------|-----------|-----------|--------|------|---------|--|-----------------------------|
| ChIP-chip | FBgn0000157 | Dll       | DLL       | E0-12  | Iso1 | 606     |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0004606 | zfh1      | ZFH1      | E0-12  | Iso1 | 604     |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0003944 | Ubx       | UBX-7701  | E3-8   | Iso1 | 603     |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0000212 | brm       | brahma    | Pupae  | Iso1 | 602     |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0011715 | Snr1      | SNR1      | Pupae  | Iso1 | 601     |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0001139 | gro       | GROUCHO   | E0-12  | Iso1 | 597     |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0003567 | su(Hw)    | Su(Hw)    | E0-12  | Iso1 | 27      |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0002781 | mod(mdg4) | mod(mdg4) | E0-12  | Iso1 | 24      |  | modENCODE -<br>Negre et al. |
| ChIP-chip | FBgn0000166 | bcd       | bcd       | E2-4   | Iso1 | BDTNP   |  | Berkeley Group              |
| ChIP-chip | FBgn0000413 | da        | da        | E2-4   | Iso1 | BDTNP   |  | Berkeley Group              |
| ChIP-chip | FBgn0260632 | dl        | dl        | E2-4   | Iso1 | BDTNP   |  | Berkeley Group              |
| ChIP-chip | FBgn0001077 | ftz       | ftz       | E2-4   | Iso1 | BDTNP   |  | Berkeley Group              |
| ChIP-chip | FBgn0001180 | hb        | hb        | E2-4   | Iso1 | BDTNP   |  | Berkeley Group              |
| ChIP-chip | FBgn0001320 | kni       | kni       | E2-4   | Iso1 | BDTNP   |  | Berkeley Group              |
| ChIP-chip | FBgn0011648 | Mad       | Mad       | E2-4   | Iso1 | BDTNP   |  | Berkeley Group              |
| ChIP-chip | FBgn0011655 | Med       | Med       | E2-4   | Iso1 | BDTNP   |  | Berkeley Group              |
| ChIP-chip | FBgn0003145 | prd       | prd       | E2-4   | Iso1 | BDTNP   |  | Berkeley Group              |
| ChIP-chip | FBgn0003396 | shn       | shn       | E2-4   | Iso1 | BDTNP   |  | Berkeley Group              |
| ChIP-chip | FBgn0003430 | slp1      | slp1      | E2-4   | Iso1 | BDTNP   |  | Berkeley Group              |
| ChIP-chip | FBgn0003448 | sna       | sna       | E2-4   | Iso1 | BDTNP   |  | Berkeley Group              |
| ChIP-chip | FBgn0003720 | tll       | tll       | E2-4   | Iso1 | BDTNP   |  | Berkeley Group              |
| ChIP-chip | FBgn0003900 | twi       | twi       | E2-4   | Iso1 | BDTNP   |  | Berkeley Group              |
| ChIP-chip | FBgn0004050 | z         | z         | E2-4   | Iso1 | BDTNP   |  | Berkeley Group              |
| ChIP-chip | FBgn0004862 | bap       | bap       | E6-8   | Iso1 | Furlong |  | Furlong Group               |
| ChIP-chip | FBgn0045759 | bin       | bin       | E10-12 | Iso1 | Furlong |  | Furlong Group               |
| ChIP-chip | FBgn0045759 | bin       | bin       | E6-8   | Iso1 | Furlong |  | Furlong Group               |
| ChIP-chip | FBgn0045759 | bin       | bin       | E8-10  | Iso1 | Furlong |  | Furlong Group               |
| ChIP-chip | FBgn0011656 | Mef2      | mef2      | E10-12 | Iso1 | Furlong |  | Furlong Group               |
| ChIP-chip | FBgn0011656 | Mef2      | mef2      | E2-4   | Iso1 | Furlong |  | Furlong Group               |
| ChIP-chip | FBgn0011656 | Mef2      | mef2      | E4-6   | Iso1 | Furlong |  | Furlong Group               |
| ChIP-chip | FBgn0011656 | Mef2      | mef2      | E6-8   | Iso1 | Furlong |  | Furlong Group               |
| ChIP-chip | FBgn0011656 | Mef2      | mef2      | E8-10  | Iso1 | Furlong |  | Furlong Group               |
| ChIP-chip | FBgn0004110 | tin       | tin       | E2-4   | Iso1 | Furlong |  | Furlong Group               |
| ChIP-chip | FBgn0004110 | tin       | tin       | E4-6   | Iso1 | Furlong |  | Furlong Group               |
| ChIP-chip | FBgn0004110 | tin       | tin       | E6-8   | Iso1 | Furlong |  | Furlong Group               |
| ChIP-chip | FBgn0003900 | twi       | twi       | E2-4   | Iso1 | Furlong |  | Furlong Group               |
| ChIP-chip | FBgn0003900 | twi       | twi       | E4-6   | Iso1 | Furlong |  | Furlong Group               |
| ChIP-chip | FBgn0003900 | twi       | twi       | E6-8   | Iso1 | Furlong |  | Furlong Group               |

| Sample          | Regions |       |       |        |            | Chromatin States |       |       |        |       |
|-----------------|---------|-------|-------|--------|------------|------------------|-------|-------|--------|-------|
|                 | TSS     | CDS   | TES   | Intron | Intergenic | BLUE             | BLACK | RED   | YELLOW | GREEN |
| Abd-B_W3L       | 0.605   | 0.037 | 0.009 | 0.194  | 0.155      | 0.215            | 0.139 | 0.305 | 0.319  | 0.022 |
| bab1_E0-12      | 0.678   | 0.086 | 0.033 | 0.091  | 0.111      | 0.222            | 0.214 | 0.144 | 0.405  | 0.015 |
| bap_E6-8        | 0.312   | 0.047 | 0.026 | 0.386  | 0.229      | 0.31             | 0.29  | 0.301 | 0.09   | 0.008 |
| bcd_E2-4        | 0.416   | 0.137 | 0.025 | 0.194  | 0.228      | 0.322            | 0.279 | 0.169 | 0.218  | 0.012 |
| bin_E10-12      | 0.45    | 0.041 | 0.019 | 0.363  | 0.128      | 0.252            | 0.18  | 0.346 | 0.214  | 0.009 |
| bin_E6-8        | 0.45    | 0.039 | 0.022 | 0.332  | 0.157      | 0.242            | 0.156 | 0.332 | 0.261  | 0.009 |
| bin_E8-10       | 0.355   | 0.053 | 0.024 | 0.391  | 0.177      | 0.269            | 0.21  | 0.336 | 0.172  | 0.012 |
| bon_E16-24      | 0.374   | 0.022 | 0.009 | 0.375  | 0.22       | 0.269            | 0.228 | 0.363 | 0.13   | 0.01  |
| br_E0-8         | 0.774   | 0.058 | 0.003 | 0.092  | 0.073      | 0.113            | 0.071 | 0.173 | 0.629  | 0.014 |
| brm_Pupae       | 0.644   | 0.007 | 0.004 | 0.196  | 0.148      | 0.212            | 0.119 | 0.316 | 0.349  | 0.004 |
| cad_E0-4        | 0.308   | 0.038 | 0.023 | 0.347  | 0.283      | 0.397            | 0.277 | 0.189 | 0.128  | 0.009 |
| cad_E0-4        | 0.481   | 0.036 | 0.012 | 0.274  | 0.197      | 0.298            | 0.172 | 0.263 | 0.258  | 0.008 |
| cad_E0-4        | 0.156   | 0.54  | 0.004 | 0.141  | 0.159      | 0.144            | 0.469 | 0.042 | 0.288  | 0.056 |
| cad_W3L         | 0.433   | 0.027 | 0.022 | 0.397  | 0.121      | 0.233            | 0.145 | 0.442 | 0.174  | 0.005 |
| CBP_E0-12       | 0.295   | 0.284 | 0.02  | 0.214  | 0.188      | 0.161            | 0.357 | 0.099 | 0.325  | 0.058 |
| CG16778_E0-8    | 0.62    | 0.053 | 0.007 | 0.233  | 0.087      | 0.176            | 0.088 | 0.365 | 0.365  | 0.007 |
| CG8478_E8-16    | 0.642   | 0.049 | 0.012 | 0.167  | 0.13       | 0.267            | 0.101 | 0.278 | 0.342  | 0.013 |
| CG8478_S2       | 0.488   | 0.022 | 0.017 | 0.33   | 0.143      | 0.19             | 0.036 | 0.558 | 0.205  | 0.011 |
| CG8478_WPP      | 0.589   | 0.029 | 0.019 | 0.236  | 0.127      | 0.241            | 0.085 | 0.374 | 0.292  | 0.009 |
| chinmo_E0-12    | 0.326   | 0.464 | 0.003 | 0.095  | 0.112      | 0.124            | 0.411 | 0.028 | 0.391  | 0.047 |
| cnc_AdultFemale | 0.574   | 0.055 | 0.018 | 0.261  | 0.092      | 0.1              | 0.053 | 0.485 | 0.358  | 0.004 |
| cnc_AdultMale   | 0.514   | 0.077 | 0.026 | 0.295  | 0.088      | 0.141            | 0.087 | 0.443 | 0.32   | 0.009 |
| cnc_E0-12       | 0.532   | 0.03  | 0.02  | 0.226  | 0.192      | 0.207            | 0.176 | 0.288 | 0.321  | 0.007 |
| cnc_E16-24      | 0.562   | 0.085 | 0.01  | 0.253  | 0.09       | 0.08             | 0.039 | 0.514 | 0.364  | 0.003 |
| cnc_WPP         | 0.728   | 0.054 | 0.007 | 0.156  | 0.054      | 0.048            | 0.028 | 0.614 | 0      | 0.31  |
| CTCF_E0-12      | 0.561   | 0.091 | 0.023 | 0.147  | 0.177      | 0.211            | 0.273 | 0.128 | 0.372  | 0.017 |
| CTCF_E0-12      | 0.599   | 0.079 | 0.022 | 0.14   | 0.16       | 0.193            | 0.248 | 0.134 | 0.407  | 0.018 |
| CTCF_Kc167      | 0.602   | 0.096 | 0.03  | 0.125  | 0.146      | 0.175            | 0.29  | 0.166 | 0.35   | 0.019 |
| CTCF_S2         | 0.535   | 0.069 | 0.04  | 0.167  | 0.188      | 0.235            | 0.27  | 0.136 | 0.344  | 0.015 |
| CTCF_S2         | 0.599   | 0.06  | 0.043 | 0.14   | 0.159      | 0.197            | 0.244 | 0.124 | 0.416  | 0.019 |
| CTCF_S2         | 0.641   | 0.086 | 0.024 | 0.125  | 0.124      | 0.149            | 0.217 | 0.18  | 0.43   | 0.023 |
| D_E0-8          | 0.252   | 0.02  | 0.02  | 0.275  | 0.434      | 0.427            | 0.34  | 0.135 | 0.096  | 0.003 |
| da_E2-4         | 0.367   | 0.109 | 0.016 | 0.274  | 0.234      | 0.302            | 0.265 | 0.191 | 0.229  | 0.013 |
| Dfd_E0-8        | 0.703   | 0.024 | 0.024 | 0.13   | 0.118      | 0.179            | 0.112 | 0.172 | 0.438  | 0.099 |
| Dfd_E16-24      | 0.391   | 0.193 | 0.025 | 0.24   | 0.151      | 0.139            | 0.257 | 0.267 | 0.311  | 0.026 |
| Dfd_W3L         | 0.257   | 0.307 | 0.014 | 0.224  | 0.198      | 0.238            | 0.439 | 0.127 | 0.175  | 0.021 |
| disco_E0-8      | 0.437   | 0.103 | 0.01  | 0.256  | 0.194      | 0.267            | 0.163 | 0.229 | 0.325  | 0.016 |
| dl_E2-4         | 0.486   | 0.104 | 0.018 | 0.224  | 0.168      | 0.236            | 0.197 | 0.192 | 0.351  | 0.024 |
| DLL_E0-12       | 0.76    | 0.013 | 0     | 0.08   | 0.147      | 0.149            | 0.054 | 0.446 | 0.338  | 0.014 |
| Dll_WPP         | 0.385   | 0.044 | 0.005 | 0.28   | 0.286      | 0.359            | 0.283 | 0.272 | 0.082  | 0.004 |
| dm_Kc167        | 0.3     | 0.06  | 0.02  | 0.25   | 0.37       | 0.267            | 0.333 | 0.217 | 0.15   | 0.033 |
| dm_W3L          | 0.71    | 0.042 | 0.037 | 0.096  | 0.115      | 0.151            | 0.176 | 0.155 | 0.494  | 0.025 |
| EcR_WPP+10-11   | 0.32    | 0.018 | 0.012 | 0.465  | 0.183      | 0.266            | 0.14  | 0.421 | 0.169  | 0.005 |
| EcR_WPP+30-33   | 0.323   | 0.017 | 0.018 | 0.472  | 0.171      | 0.278            | 0.169 | 0.406 | 0.142  | 0.006 |
| Eip74EF_E8-16   | 0.704   | 0.012 | 0.013 | 0.175  | 0.095      | 0.145            | 0.073 | 0.314 | 0.377  | 0.09  |
| en_E0-12        | 0.731   | 0     | 0     | 0.038  | 0.231      | 0.5              | 0.091 | 0     | 0      | 0.409 |
| en_E7-24        | 0.248   | 0.147 | 0.028 | 0.238  | 0.339      | 0.381            | 0.349 | 0.114 | 0.135  | 0.021 |
| eve_E1-6        | 0.46    | 0.023 | 0.003 | 0.311  | 0.203      | 0.299            | 0.172 | 0.26  | 0.263  | 0.006 |

|              |       |       |       |       |       |       |       |       |       |       |
|--------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| eve_E1-6     | 0.219 | 0.05  | 0.006 | 0.175 | 0.55  | 0.581 | 0.275 | 0.088 | 0.05  | 0.006 |
| eve_E8-16    | 0.42  | 0.019 | 0.014 | 0.391 | 0.157 | 0.255 | 0.155 | 0.379 | 0.183 | 0.029 |
| Ez_E1-6      | 0.253 | 0.114 | 0.016 | 0.303 | 0.314 | 0.298 | 0.383 | 0.126 | 0.175 | 0.019 |
| Ez_E8-16     | 0.688 | 0.063 | 0.008 | 0.16  | 0.081 | 0.102 | 0.08  | 0.304 | 0.506 | 0.008 |
| fru_E0-8     | 0.602 | 0.162 | 0.009 | 0.144 | 0.083 | 0.174 | 0.096 | 0.248 | 0.45  | 0.031 |
| ftz_E2-4     | 0.283 | 0.179 | 0.02  | 0.189 | 0.329 | 0.392 | 0.322 | 0.077 | 0.193 | 0.015 |
| GATAe_E0-8   | 0.377 | 0.213 | 0.022 | 0.242 | 0.146 | 0.184 | 0.234 | 0.181 | 0.359 | 0.042 |
| gro_E0-12    | 0.157 | 0.027 | 0.024 | 0.371 | 0.421 | 0.453 | 0.362 | 0.161 | 0.021 | 0.002 |
| gro_E0-12    | 0.276 | 0.019 | 0.024 | 0.318 | 0.363 | 0.42  | 0.264 | 0.244 | 0.07  | 0.002 |
| gro_WPP      | 0.396 | 0.018 | 0.008 | 0.346 | 0.232 | 0.278 | 0.166 | 0.429 | 0.124 | 0.003 |
| gsbn_E7-24   | 0.79  | 0.018 | 0.007 | 0.106 | 0.08  | 0.167 | 0.078 | 0.415 | 0.322 | 0.019 |
| h_E0-8       | 0.42  | 0.283 | 0.01  | 0.13  | 0.157 | 0.269 | 0.268 | 0.141 | 0.293 | 0.028 |
| h_Kc167      | 0.569 | 0.042 | 0.028 | 0.204 | 0.157 | 0.163 | 0.094 | 0.419 | 0.217 | 0.108 |
| hb_E2-4      | 0.475 | 0.064 | 0.015 | 0.245 | 0.202 | 0.258 | 0.255 | 0.23  | 0.245 | 0.012 |
| HDAC1_E0-12  | 0.707 | 0.045 | 0.008 | 0.152 | 0.088 | 0.135 | 0.078 | 0.217 | 0.549 | 0.021 |
| HDAC1_E0-12  | 0.726 | 0.05  | 0.008 | 0.132 | 0.085 | 0.133 | 0.061 | 0.213 | 0.572 | 0.022 |
| HDAC1_E0-12  | 0.775 | 0.01  | 0.011 | 0.131 | 0.073 | 0.121 | 0.064 | 0.23  | 0.564 | 0.021 |
| HDAC11_E0-12 | 0.572 | 0.028 | 0.007 | 0.236 | 0.156 | 0.178 | 0.123 | 0.246 | 0.427 | 0.025 |
| HDAC11_E0-12 | 0.557 | 0.02  | 0.006 | 0.228 | 0.189 | 0.212 | 0.139 | 0.28  | 0.352 | 0.017 |
| HDAC11_E0-12 | 0.717 | 0.123 | 0.014 | 0.091 | 0.054 | 0.169 | 0.207 | 0.094 | 0.509 | 0.02  |
| HDAC11_E0-12 | 0.512 | 0.337 | 0.007 | 0.082 | 0.062 | 0.073 | 0.064 | 0.138 | 0.711 | 0.013 |
| HDAC3_E0-12  | 0.504 | 0.332 | 0.048 | 0.074 | 0.042 | 0.048 | 0.089 | 0.078 | 0.688 | 0.098 |
| HDAC3_E0-12  | 0.505 | 0.356 | 0.045 | 0.064 | 0.029 | 0.041 | 0.062 | 0.074 | 0.723 | 0.101 |
| HDAC3_E0-12  | 0.54  | 0.417 | 0.025 | 0.008 | 0.009 | 0.018 | 0.027 | 0.028 | 0.806 | 0.121 |
| HDAC3_E0-12  | 0.526 | 0.447 | 0.016 | 0.006 | 0.005 | 0.017 | 0.02  | 0.03  | 0.818 | 0.114 |
| HDAC4a_E0-12 | 0.408 | 0.035 | 0.014 | 0.274 | 0.268 | 0.297 | 0.238 | 0.22  | 0.238 | 0.006 |
| HDAC4a_E0-12 | 0.63  | 0.036 | 0.01  | 0.17  | 0.154 | 0.225 | 0.111 | 0.223 | 0.432 | 0.01  |
| HDAC4a_E0-12 | 0.594 | 0.089 | 0.012 | 0.162 | 0.143 | 0.158 | 0.124 | 0.151 | 0.543 | 0.024 |
| HDAC6_E0-12  | 0.856 | 0.038 | 0.007 | 0.063 | 0.036 | 0.047 | 0.039 | 0.135 | 0.759 | 0.019 |
| HDAC6_E0-12  | 0.87  | 0.038 | 0.008 | 0.049 | 0.035 | 0.043 | 0.042 | 0.104 | 0.787 | 0.024 |
| hkb_E0-8     | 0.37  | 0.254 | 0.012 | 0.205 | 0.159 | 0.171 | 0.24  | 0.152 | 0.396 | 0.041 |
| hkb_E8-16    | 0.704 | 0.031 | 0.015 | 0.102 | 0.148 | 0.154 | 0.169 | 0.19  | 0.477 | 0.01  |
| HP1b_E16-24  | 0.249 | 0.098 | 0.024 | 0.274 | 0.356 | 0.01  | 0.064 | 0.036 | 0.209 | 0.681 |
| HP1b_E16-24  | 0.195 | 0.092 | 0.022 | 0.269 | 0.422 | 0.013 | 0.084 | 0.045 | 0.236 | 0.622 |
| HP1b_E8-16   | 0.036 | 0.034 | 0.007 | 0.278 | 0.646 | 0.004 | 0.033 | 0.012 | 0.011 | 0.941 |
| Hr39_E16-24  | 0.199 | 0.235 | 0.013 | 0.266 | 0.287 | 0.243 | 0.536 | 0.077 | 0.128 | 0.015 |
| Hr78_E8-16   | 0.687 | 0.021 | 0.021 | 0.153 | 0.119 | 0.172 | 0.088 | 0.233 | 0.419 | 0.088 |
| Hr78_W3L     | 0.676 | 0.015 | 0.021 | 0.186 | 0.102 | 0.118 | 0.056 | 0.332 | 0.438 | 0.057 |
| hth_E0-8     | 0.156 | 0.017 | 0.016 | 0.34  | 0.47  | 0.505 | 0.287 | 0.172 | 0.032 | 0.003 |
| hth_E8-16    | 0.135 | 0.007 | 0.019 | 0.48  | 0.358 | 0.48  | 0.258 | 0.232 | 0.027 | 0.002 |
| insv_Kc167   | 0.693 | 0.041 | 0.009 | 0.188 | 0.069 | 0.183 | 0.028 | 0.549 | 0.225 | 0.014 |
| jumu_E0-8    | 0.487 | 0.348 | 0.006 | 0.094 | 0.065 | 0.106 | 0.113 | 0.104 | 0.63  | 0.047 |
| kn_E0-12     | 0.578 | 0.035 | 0.087 | 0.158 | 0.141 | 0.147 | 0.161 | 0.238 | 0.403 | 0.051 |
| kni_E2-4     | 0.242 | 0.08  | 0.017 | 0.249 | 0.412 | 0.477 | 0.334 | 0.08  | 0     | 0.108 |
| kni_E8-16    | 0.742 | 0.035 | 0.041 | 0.078 | 0.104 | 0.143 | 0.195 | 0.179 | 0.466 | 0.018 |
| Kr_E0-8      | 0.296 | 0.037 | 0.02  | 0.285 | 0.362 | 0.387 | 0.327 | 0.164 | 0.12  | 0.002 |
| Kr_E16-24    | 0.515 | 0.064 | 0.091 | 0.114 | 0.216 | 0.294 | 0.303 | 0.109 | 0.251 | 0.043 |
| lola_E0-12   | 0.068 | 0.054 | 0.01  | 0.453 | 0.416 | 0.353 | 0.49  | 0.098 | 0.045 | 0.014 |
| lola_E12-24  | 0.692 | 0.014 | 0.022 | 0.139 | 0.134 | 0.172 | 0.106 | 0.218 | 0.391 | 0.115 |
| lola_W3L     | 0.724 | 0.033 | 0.012 | 0.155 | 0.076 | 0.069 | 0.062 | 0.363 | 0.448 | 0.059 |

|                |       |       |       |       |       |       |       |       |       |       |
|----------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| Lpt_E0-8       | 0.453 | 0.027 | 0.01  | 0.331 | 0.179 | 0.222 | 0.143 | 0.439 | 0.189 | 0.007 |
| Mad_E2-4       | 0.366 | 0.348 | 0.025 | 0.129 | 0.133 | 0.276 | 0.226 | 0.154 | 0.283 | 0.061 |
| Med_E2-4       | 0.581 | 0.071 | 0.013 | 0.188 | 0.147 | 0.21  | 0.162 | 0.188 | 0.422 | 0.018 |
| Mef2_E10-12    | 0.51  | 0.051 | 0.02  | 0.294 | 0.125 | 0.238 | 0.191 | 0.336 | 0.225 | 0.01  |
| Mef2_E2-4      | 0.425 | 0.052 | 0.017 | 0.321 | 0.186 | 0.268 | 0.202 | 0.328 | 0.19  | 0.012 |
| Mef2_E4-6      | 0.501 | 0.034 | 0.02  | 0.255 | 0.19  | 0.291 | 0.192 | 0.294 | 0.216 | 0.007 |
| Mef2_E6-8      | 0.59  | 0.045 | 0.017 | 0.201 | 0.146 | 0.26  | 0.178 | 0.28  | 0.272 | 0.009 |
| Mef2_E8-10     | 0.532 | 0.043 | 0.014 | 0.282 | 0.13  | 0.269 | 0.169 | 0.331 | 0.224 | 0.007 |
| modmdg4_E0-12  | 0.592 | 0.089 | 0.036 | 0.131 | 0.152 | 0.192 | 0.29  | 0.169 | 0.336 | 0.014 |
| modmdg4_E8-16  | 0.589 | 0.069 | 0.037 | 0.151 | 0.153 | 0.197 | 0.253 | 0.207 | 0.335 | 0.008 |
| modmdg4_W3L    | 0.481 | 0.038 | 0.089 | 0.123 | 0.268 | 0.277 | 0.346 | 0.126 | 0.247 | 0.004 |
| N_W3L          | 0.599 | 0.026 | 0.036 | 0.186 | 0.153 | 0.19  | 0.148 | 0.277 | 0.346 | 0.04  |
| pan_E0-8       | 0.364 | 0.029 | 0.024 | 0.287 | 0.296 | 0.334 | 0.204 | 0.283 | 0.167 | 0.012 |
| pan_E0-8       | 0.301 | 0.115 | 0.019 | 0.249 | 0.316 | 0.249 | 0.373 | 0.213 | 0.146 | 0.019 |
| pan_E16-24     | 0.443 | 0.029 | 0.005 | 0.305 | 0.219 | 0.208 | 0.134 | 0.463 | 0.182 | 0.013 |
| pan_W3L        | 0.388 | 0.032 | 0.019 | 0.299 | 0.263 | 0.259 | 0.232 | 0.326 | 0.169 | 0.014 |
| pan_WPP        | 0.354 | 0.022 | 0.011 | 0.322 | 0.292 | 0.263 | 0.247 | 0.316 | 0.162 | 0.012 |
| Pcl_E0-8       | 0.288 | 0.343 | 0.005 | 0.158 | 0.206 | 0.482 | 0.3   | 0.057 | 0.153 | 0.008 |
| prd_E0-12      | 0.448 | 0.054 | 0.116 | 0.13  | 0.252 | 0.389 | 0.28  | 0.147 | 0.182 | 0.003 |
| prd_E2-4       | 0.374 | 0.077 | 0.019 | 0.263 | 0.267 | 0.345 | 0.28  | 0.175 | 0.187 | 0.013 |
| psq_Kc167      | 0.664 | 0.025 | 0.011 | 0.24  | 0.061 | 0.041 | 0.007 | 0.438 | 0.51  | 0.005 |
| psq_WPP        | 0.517 | 0.027 | 0.011 | 0.345 | 0.1   | 0.124 | 0.045 | 0.524 | 0.304 | 0.003 |
| sbb_E0-4       | 0.126 | 0.148 | 0.028 | 0.394 | 0.304 | 0.175 | 0.632 | 0.052 | 0.112 | 0.029 |
| sc_E0-12       | 0.617 | 0.035 | 0     | 0.244 | 0.104 | 0.236 | 0.01  | 0.349 | 0.395 | 0.01  |
| sc_E0-8        | 0.51  | 0.042 | 0.007 | 0.287 | 0.154 | 0.3   | 0.123 | 0.277 | 0.277 | 0.023 |
| sens_E4-8      | 0.293 | 0.346 | 0.012 | 0.192 | 0.157 | 0.194 | 0.253 | 0.124 | 0.38  | 0.048 |
| sens_E4-8      | 0.408 | 0.537 | 0     | 0.032 | 0.023 | 0.072 | 0.152 | 0.057 | 0.666 | 0.053 |
| shn_E2-4       | 0.278 | 0.048 | 0.024 | 0.322 | 0.328 | 0.432 | 0.342 | 0.136 | 0.086 | 0.004 |
| Sin3A_E0-12    | 0.982 | 0.003 | 0.003 | 0.006 | 0.006 | 0.014 | 0.016 | 0.092 | 0.854 | 0.024 |
| Sin3A_Kc167    | 0.966 | 0.012 | 0     | 0.019 | 0.003 | 0.012 | 0.007 | 0.103 | 0.864 | 0.014 |
| slp1_E2-4      | 0.397 | 0.067 | 0.018 | 0.248 | 0.27  | 0.308 | 0.241 | 0.174 | 0.267 | 0.01  |
| sna_E2-4       | 0.367 | 0.287 | 0.011 | 0.175 | 0.16  | 0.229 | 0.301 | 0.122 | 0.316 | 0.032 |
| Snr1_Pupae     | 0.821 | 0.018 | 0.004 | 0.1   | 0.057 | 0.101 | 0.06  | 0.165 | 0.509 | 0.165 |
| Stat92E_E0-12  | 0.573 | 0.01  | 0.019 | 0.214 | 0.184 | 0.305 | 0.171 | 0.314 | 0     | 0.21  |
| Stat92E_E0-12  | 0.6   | 0.019 | 0.01  | 0.143 | 0.229 | 0.263 | 0.184 | 0.179 | 0.235 | 0.14  |
| Stat92E_E12-24 | 0.628 | 0.006 | 0.024 | 0.189 | 0.152 | 0.25  | 0.115 | 0.196 | 0.297 | 0.142 |
| Stat92E_WPP    | 0.458 | 0.014 | 0.02  | 0.322 | 0.186 | 0.357 | 0.105 | 0.146 | 0     | 0.391 |
| SuH_E0-8       | 0.37  | 0.157 | 0.039 | 0.15  | 0.283 | 0.336 | 0.241 | 0.319 | 0.095 | 0.009 |
| SuH_E16-24     | 0.592 | 0.017 | 0.013 | 0.258 | 0.121 | 0.2   | 0.072 | 0.455 | 0.264 | 0.009 |
| SuH_E8-16      | 0.396 | 0     | 0.042 | 0.354 | 0.208 | 0.25  | 0.042 | 0.146 | 0     | 0.563 |
| SuH_Kc167      | 0.606 | 0.027 | 0.006 | 0.265 | 0.096 | 0.13  | 0.042 | 0.667 | 0.154 | 0.007 |
| SuHw_E0-12     | 0.245 | 0.099 | 0.034 | 0.332 | 0.289 | 0.196 | 0.627 | 0.081 | 0.09  | 0.007 |
| SuHw_E0-12     | 0.276 | 0.139 | 0.03  | 0.28  | 0.274 | 0.19  | 0.64  | 0.077 | 0.085 | 0.008 |
| suHw_E16-24    | 0.303 | 0.107 | 0.046 | 0.275 | 0.27  | 0.22  | 0.553 | 0.114 | 0.105 | 0.009 |
| suHw_WPP       | 0.279 | 0.145 | 0.027 | 0.262 | 0.287 | 0.174 | 0.678 | 0.064 | 0.077 | 0.007 |
| Suvar3-9_E0-12 | 0.702 | 0.038 | 0.007 | 0.145 | 0.109 | 0.186 | 0.125 | 0.213 | 0.465 | 0.011 |
| Tbp_E0-8       | 0.82  | 0.022 | 0.012 | 0.086 | 0.06  | 0.119 | 0.08  | 0.198 | 0.579 | 0.025 |
| tin_E2-4       | 0.298 | 0.053 | 0.017 | 0.318 | 0.314 | 0.39  | 0.28  | 0.245 | 0.082 | 0.003 |
| tin_E4-6       | 0.383 | 0.046 | 0.023 | 0.282 | 0.266 | 0.38  | 0.25  | 0.238 | 0.125 | 0.007 |
| tin_E6-8       | 0.356 | 0.031 | 0.025 | 0.334 | 0.254 | 0.365 | 0.203 | 0.306 | 0.119 | 0.006 |

|                  |       |       |       |       |       |       |       |       |       |       |
|------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| tll_E0-4         | 0.648 | 0.028 | 0.007 | 0.16  | 0.158 | 0.172 | 0.176 | 0.173 | 0.448 | 0.031 |
| tll_E2-4         | 0.273 | 0.067 | 0.027 | 0.264 | 0.369 | 0.439 | 0.308 | 0.162 | 0.086 | 0.005 |
| trem_AdultFemale | 0.932 | 0.013 | 0.006 | 0.025 | 0.023 | 0.038 | 0.04  | 0.121 | 0.746 | 0.056 |
| Trl_E16-24       | 0.623 | 0.029 | 0.016 | 0.208 | 0.124 | 0.191 | 0.228 | 0.315 | 0.248 | 0.017 |
| Trl_E8-16        | 0.496 | 0.039 | 0.017 | 0.283 | 0.165 | 0.247 | 0.232 | 0.331 | 0.166 | 0.025 |
| Trl_Kc167        | 0.581 | 0.043 | 0.015 | 0.259 | 0.102 | 0.144 | 0.063 | 0.456 | 0.322 | 0.015 |
| ttk_E0-12        | 0.779 | 0.065 | 0.036 | 0.029 | 0.091 | 0.072 | 0.096 | 0.08  | 0.72  | 0.032 |
| ttk_Kc167        | 0.564 | 0.312 | 0.007 | 0.106 | 0.011 | 0.008 | 0.002 | 0.183 | 0.763 | 0.044 |
| twi_E2-4         | 0.376 | 0.055 | 0.018 | 0.283 | 0.268 | 0.33  | 0.251 | 0.225 | 0.181 | 0.014 |
| twi_E2-4         | 0.431 | 0.123 | 0.018 | 0.228 | 0.201 | 0.249 | 0.276 | 0.156 | 0.297 | 0.022 |
| twi_E4-6         | 0.44  | 0.035 | 0.018 | 0.277 | 0.229 | 0.299 | 0.213 | 0.263 | 0.219 | 0.006 |
| twi_E6-8         | 0.49  | 0.03  | 0.015 | 0.27  | 0.195 | 0.298 | 0.169 | 0.27  | 0.257 | 0.007 |
| Ubx_E0-12        | 0.928 | 0.005 | 0.005 | 0.029 | 0.033 | 0.047 | 0.025 | 0.103 | 0.791 | 0.034 |
| Ubx_E3-8         | 0.974 | 0.005 | 0.003 | 0.011 | 0.007 | 0.025 | 0.006 | 0.938 | 0     | 0.031 |
| usp_E0-12        | 0.297 | 0.036 | 0.012 | 0.435 | 0.22  | 0.28  | 0.146 | 0.431 | 0.138 | 0.004 |
| usp_W3L          | 0.463 | 0.014 | 0.011 | 0.332 | 0.181 | 0.106 | 0.031 | 0.628 | 0.231 | 0.005 |
| usp_WPP+12       | 0.381 | 0.006 | 0.014 | 0.378 | 0.221 | 0.205 | 0.061 | 0.556 | 0.17  | 0.009 |
| yki_E8-16        | 0.637 | 0.018 | 0.013 | 0.205 | 0.127 | 0.219 | 0.135 | 0.423 | 0.211 | 0.012 |
| z_E2-4           | 0.622 | 0.05  | 0.015 | 0.191 | 0.123 | 0.228 | 0.105 | 0.339 | 0.316 | 0.013 |
| zfh1_E0-12       | 0.554 | 0.047 | 0.054 | 0.199 | 0.146 | 0.202 | 0.113 | 0.301 | 0.334 | 0.05  |