

**Table S13: Evolutionary groups of CTCF binding events at high sequence coverage sites**

With all four species

| Boolean conservation score | All sites | FWOB sites |
|----------------------------|-----------|------------|
| (1,1,1,1)                  | 390       | 271        |
| (1,1,1,0)                  | 594       | 379        |
| (1,1,0,1)                  | 26        | 16         |
| (1,1,0,0)                  | 167       | 106        |
| (1,0,1,1)                  | 5         | 3          |
| (1,0,0,1)                  | 16        | 13         |
| (1,0,1,0)                  | 61        | 37         |
| (1,0,0,0)                  | 103       | 63         |
| (0,1,1,1)                  | 0         | 0          |
| (0,1,1,0)                  | 22        | 12         |
| (0,1,0,1)                  | 1         | 1          |
| (0,1,0,0)                  | 94        | 76         |
| (0,0,1,1)                  | 2         | 2          |
| (0,0,0,1)                  | 112       | 84         |
| (0,0,1,0)                  | 152       | 105        |

With three *D.melanogster* group species

| Boolean conservation score | All sites | FWOB |
|----------------------------|-----------|------|
| (1,1,1)                    | 1368      | 1346 |
| (1,1,0)                    | 288       | 278  |
| (1,0,1)                    | 107       | 103  |
| (1,0,0)                    | 201       | 195  |
| (0,1,1)                    | 23        | 15   |
| (0,1,0)                    | 117       | 74   |
| (0,0,1)                    | 194       | 105  |

Note: the number of binding events shown here are obtained after filtering out binding peaks with input sequence coverage  $<0.5$ . All notations for the tables are the same as for Figure 2 and Figure S7.