

Table S7. Mean density of matches to consensus Dsx binding sequence per significant and non-significant gene

Category	Distance from gene*				
	≤500 bp	≤1000 bp	≤2000 bp	≤5000 bp	≤10,000 bp
L3					
Significant	0.131	0.125	0.123	0.122	0.128
Non-significant	0.097	0.102	0.106	0.112	0.117
<i>P</i> -value [†]	1.14×10^{-4}	3.66×10^{-3}	1.08×10^{-1}	5.11×10^{-1}	3.39×10^{-1}
P6					
Significant	0.107	0.110	0.122	0.126	0.123
Non-significant	0.097	0.102	0.106	0.112	0.117
<i>P</i> -value	8.12×10^{-5}	5.85×10^{-4}	2.03×10^{-3}	3.32×10^{-2}	3.83×10^{-1}
P20					
Significant	0.099	0.109	0.126	0.130	0.132
Non-significant	0.097	0.102	0.106	0.111	0.116
<i>P</i> -value	1.94×10^{-2}	1.47×10^{-2}	2.20×10^{-3}	9.48×10^{-4}	3.57×10^{-3}
ALL[‡]					
Significant	0.100	0.107	0.121	0.126	0.127
Non-significant	0.097	0.101	0.106	0.111	0.116
<i>P</i> -value	1.07×10^{-4}	3.04×10^{-4}	3.45×10^{-4}	1.20×10^{-3}	2.57×10^{-2}

*Only non-coding sequences are considered. If a match to the consensus Dsx binding sequence lies between the start and end of a gene (as annotated in FlyBase R5.29), its distance is recorded as 0 bp. Otherwise, its distance is recorded as the number of bp between it and the start of the gene. The density is calculated as the number of matches divided by the length (in kb) of the considered region for each gene. This length is the sum of the upstream length (which is equal to the window size of 0.5, 1, 2, 5 or 10 kb) and the downstream length (which is equal to whichever is the greater of the window size or the length of the gene).

[†]The *P*-value is based on a two-sided Wilcoxon rank sum test of the hypothesis that the density of matches is the same for 'significant' (differentially expressed at FDR threshold of 0.05) and 'non-significant' (not differentially expressed at FDR threshold of 0.05) genes.

[‡]For the category 'ALL', 'significant' genes are those that are differentially expressed at FDR threshold of 0.05 at at least one developmental stage.