Table S6. Mean number of matches to the 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	2.18	2.24	2.38	2.76	3.60
Non-significant	0.79	0.85	1.01	1.58	2.68
P-value[†]	$1.23{\times}10^{-7}$	$2.55{\times}10^{-6}$	$6.01{\times}10^{-5}$	$1.16{\times}10^{-2}$	$2.53{\times}10^{-2}$
P6					
Significant	1.21	1.28	1.48	2.04	3.02
Non-significant	0.78	0.85	1.01	1.58	2.68
P-value	$1.11{\times}10^{-8}$	$2.38{\times}10^{-8}$	$3.30{\times}10^{-8}$	$1.35{\times}10^{-5}$	$1.09{\times}10^{-2}$
P20					
Significant	1.15	1.22	1.46	2.07	3.20
Non-significant	0.78	0.85	1.00	1.57	2.67
P-value	$6.34{\times}10^{-4}$	$4.02{\times}10^{-4}$	$4.06{\times}10^{-6}$	$1.30{\times}10^{-5}$	$2.36{\times}10^{-4}$
ALL[‡]					
Significant	1.16	1.24	1.45	2.03	3.09
Non-significant	0.78	0.84	1.00	1.57	2.67
P-value	$7.58{\times}10^{-9}$	$7.20{\times}10^{-9}$	$1.74{\times}10^{-10}$	$2.49{\times}10^{-8}$	$9.83{\times}10^{-5}$

*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 P-value is based on a two-sided Wilcoxon rank sum test of the hypothesis that the number 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.