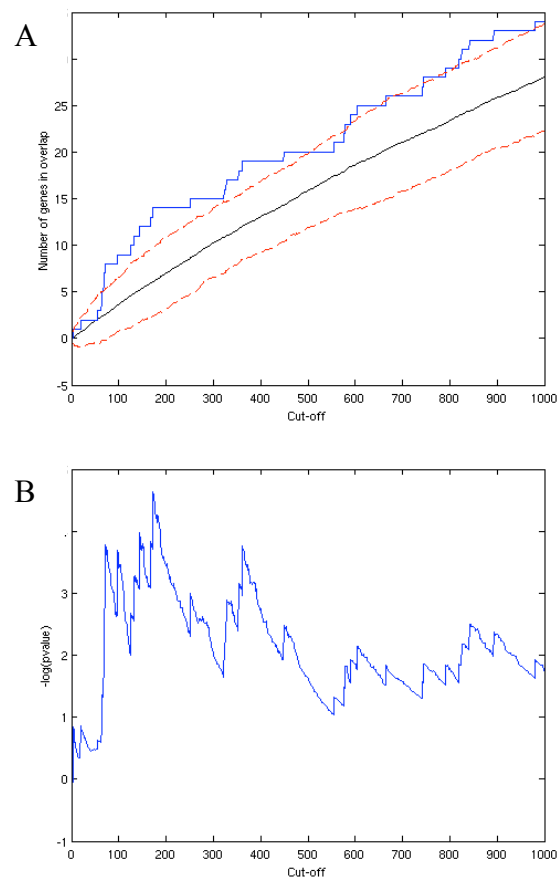


### Supplementary Figure 3: Overlap between Ey candidate targets obtained from microarray data and from genome-wide binding site prediction

At different cut-offs  $N$  (x-axis), the  $N$  top scoring Ey candidate targets, based on motif detection, are compared with the 188 Ey candidate targets obtained from gene expression studies [1]. The same is done for each of 100 randomized rankings (obtained by using a randomized Ey PWM).

(A) For each cut-off value, the number of genes in common between the two sets is plotted on the y-axis. The values for the true Ey PWM are in blue, while the mean values of the randomized PWMs are in black. A 95% confidence interval is plotted in red dashed lines.

(B) A p-value for each cut-off value is plotted on the y-axis. The p-values are calculated using a normal distribution based on the mean and standard deviation from the randomized rankings. The optimal p-value is obtained by using a cut-off value of 171.



### References

1. Ostrin JE, Li Y, Hoffman K, Liu J, Wang K, et al. (2006) Genome-wide identification of direct targets of the Drosophila retinal determination protein Eyeless. *Genome Res* 16: 466-476.