

Supplementary Table 10: **Characterisation of genes with a percentile X/A divergence ratio greater than 1.015 in adult males.**

ID	Term	#	Sig.	Exp.	P -value	P_{adj} -value
GO:0007538	primary sex determination	11	5	0.6	8.9×10^{-5}	0.312
GO:0019748	secondary metabolic process	24	7	1.32	1.6×10^{-4}	0.312
GO:0030534	adult behavior	34	7	1.86	6.2×10^{-4}	0.625
GO:0007362	terminal region determination	10	3	0.5	0.0062	0.625
GO:0046152	ommochrome metabolic process	13	4	0.71	0.0076	1.0

Enrichment is based on the ‘parent-child’ algorithm in the topGO R package and Fisher’s exact test applied to 352 genes that have an X/A percentile divergence ratio of > 1.015 against the background of the genes in the dataset. # - total number of genes with this annotation in the dataset. Sig. - significant, Exp. - expected. P_{adj} -value - adjusted according to the Benjamini-Hochberg false discovery rate.