Elys and Lamin B/C depletions in spermatogonia and spermatocytes

1. RNA-seq in larval testes. Differential expresion and TPM comparison.

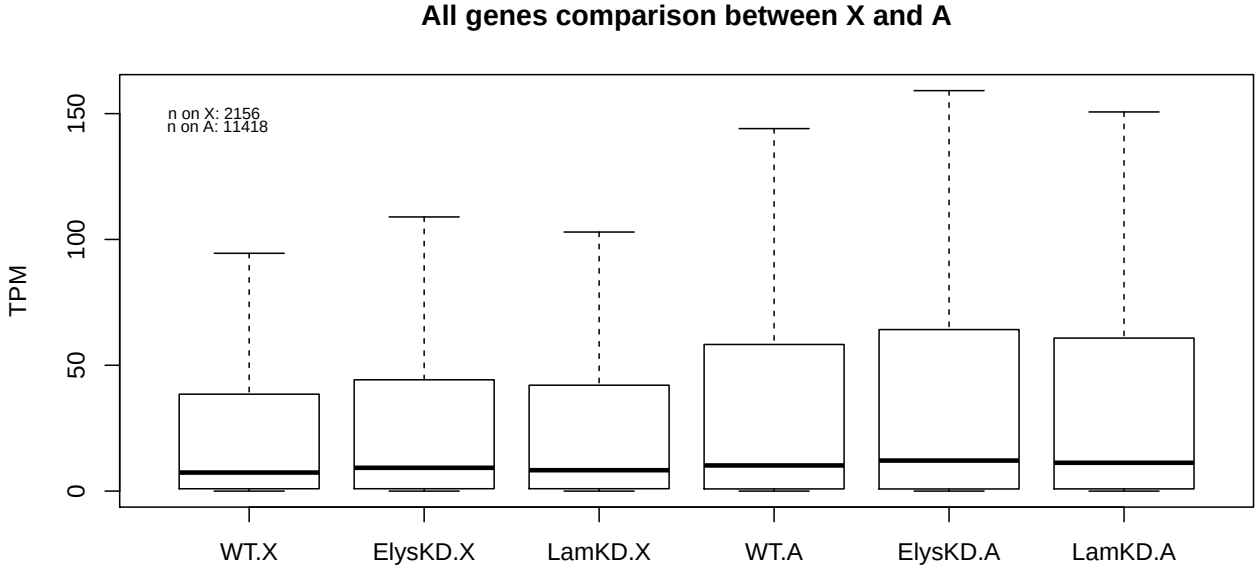
We used a BDGP5.78 annotation for *Drosophila* genes:

chr	start	end	strand	id	gene_name	tss
chr2L	7529	9484	+	FBgn0031208	CG11023	7529
chr2L	9839	21376	-	FBgn0002121	l(2)gl	21376
chr2L	21823	25155	-	FBgn0031209	Ir21a	25155
chr2L	21952	24237	+	FBgn0263584	CR43609	21952
chr2L	25402	65404	-	FBgn0051973	Cda5	65404
chr2L	65999	66242	+	FBgn0266878	CR45339	65999

Using salmon we obtained read counts per gene and normalized TPM values:

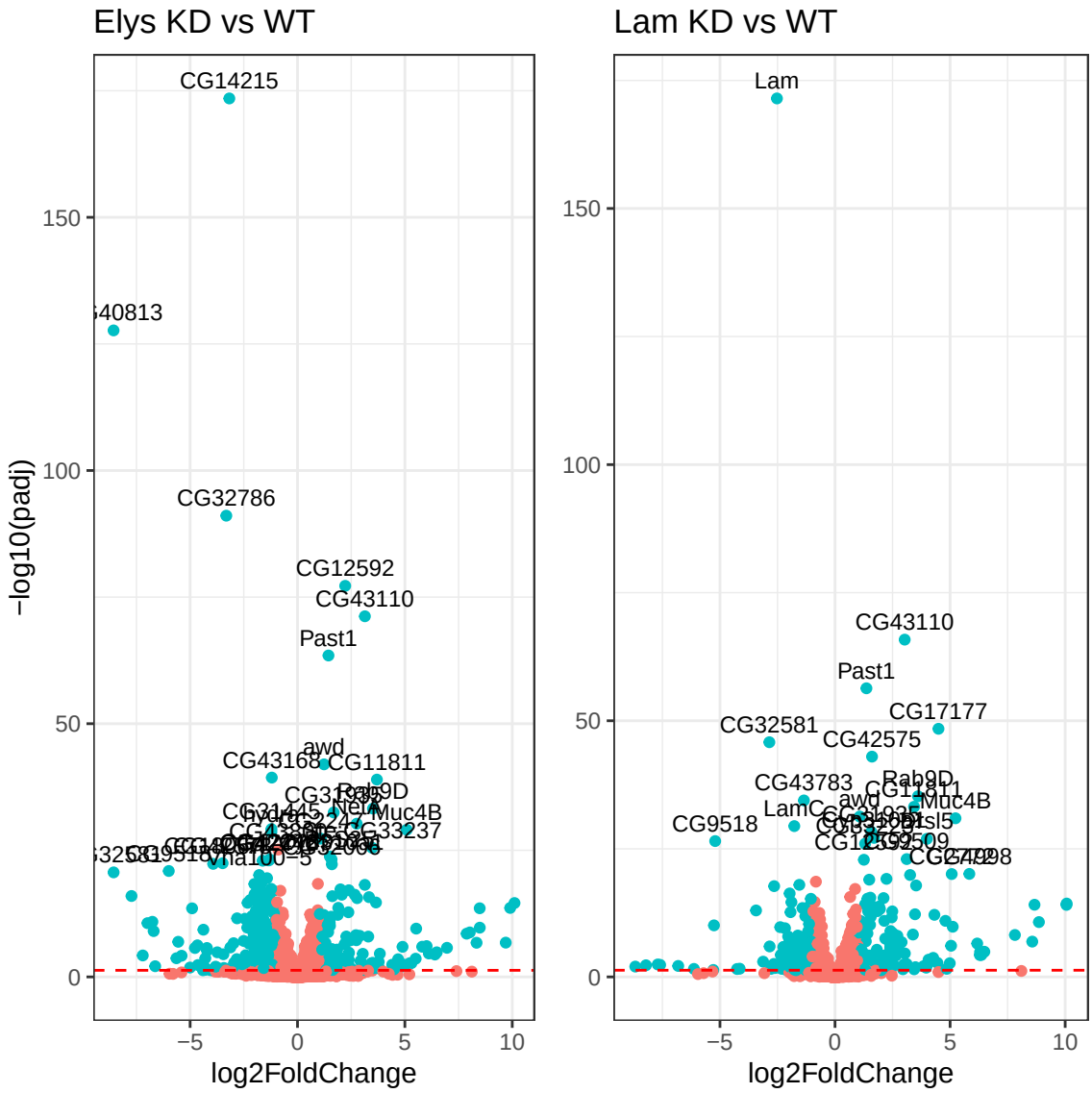
chr	start	end	strand	gene_name	WT	ElysKD	LamKD
chr2R	18024473	18060339	+	a	6.7153633	5.6267533	5.894823
chr3R	12632936	12655771	-	abd-A	7.6534000	9.6282000	9.564213
chr3R	12752932	12797958	-	Abd-B	0.4616433	0.6147677	0.604028
chr3L	16608966	16640982	-	Abl	9.4840567	12.5862000	10.405730
chr2L	10973443	10975293	-	abo	27.6684000	41.1312667	36.629433
chrX	264064	264980	+	ac	0.2590723	0.0000000	0.000000

The main question that we investigate is whether the expression of genes on X-chromosome is higher than of those on autosomes in spermatocytes? And do Elys and/or Lamins knockdowns alter this discordance?

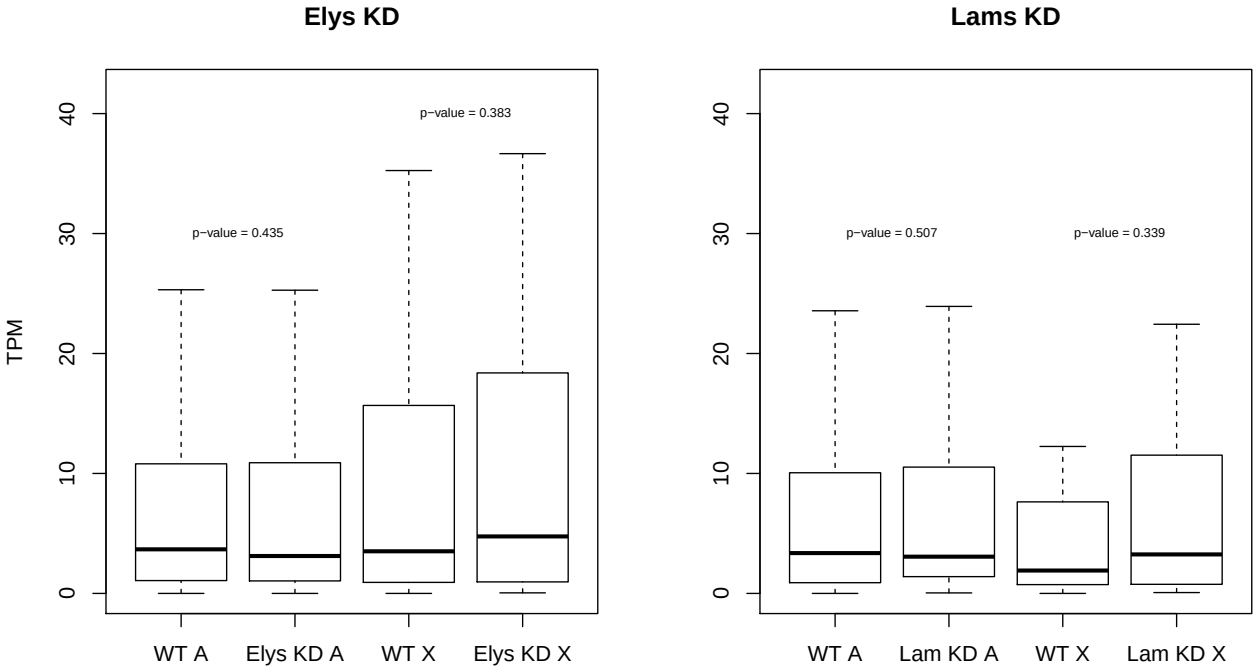


3. Differential expression analysis in HP1 knockdown in somatic ovarian cells

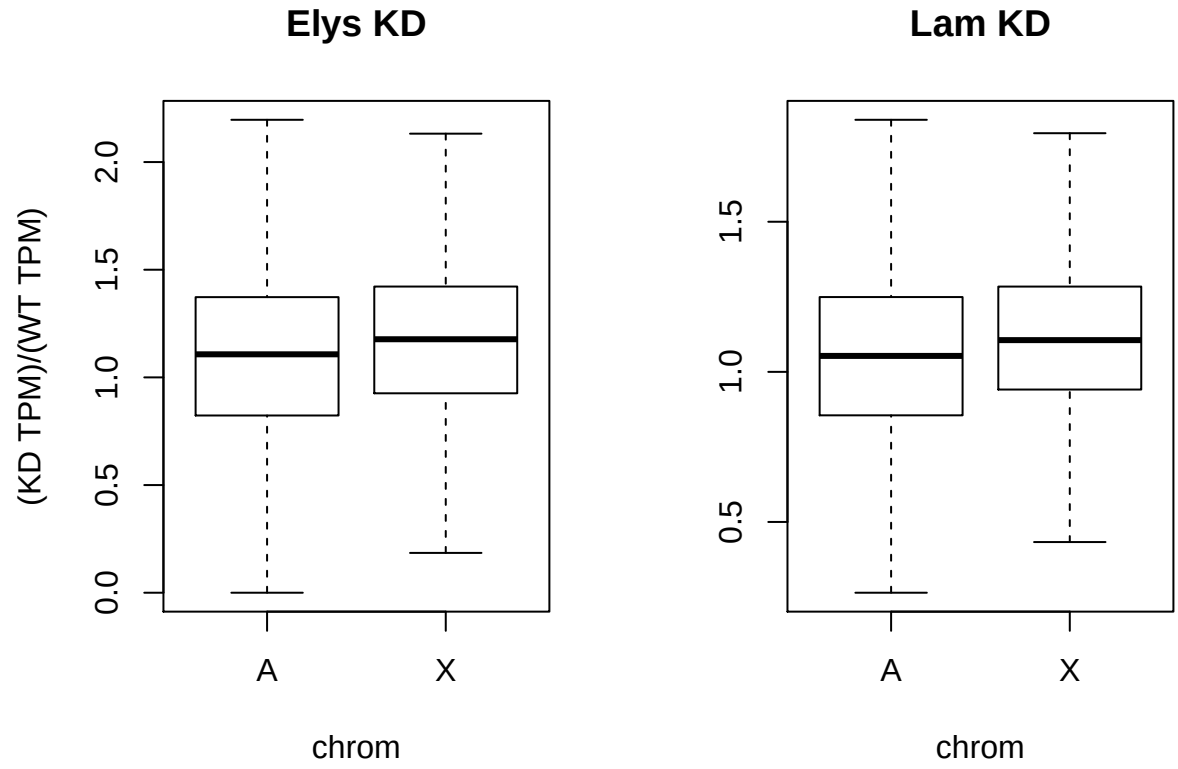
Differential analysis was performed using DESeq2 Volcano plot for Elys KD:



Here are similar boxplots but only for differentially expressed genes (via DESeq2 and TPM ratio > 2:



Let's represent the ratios between knockdowns and wild type:



Spermatocyte-specific genes

Boxplot with TPMs for SpC-specific genes: