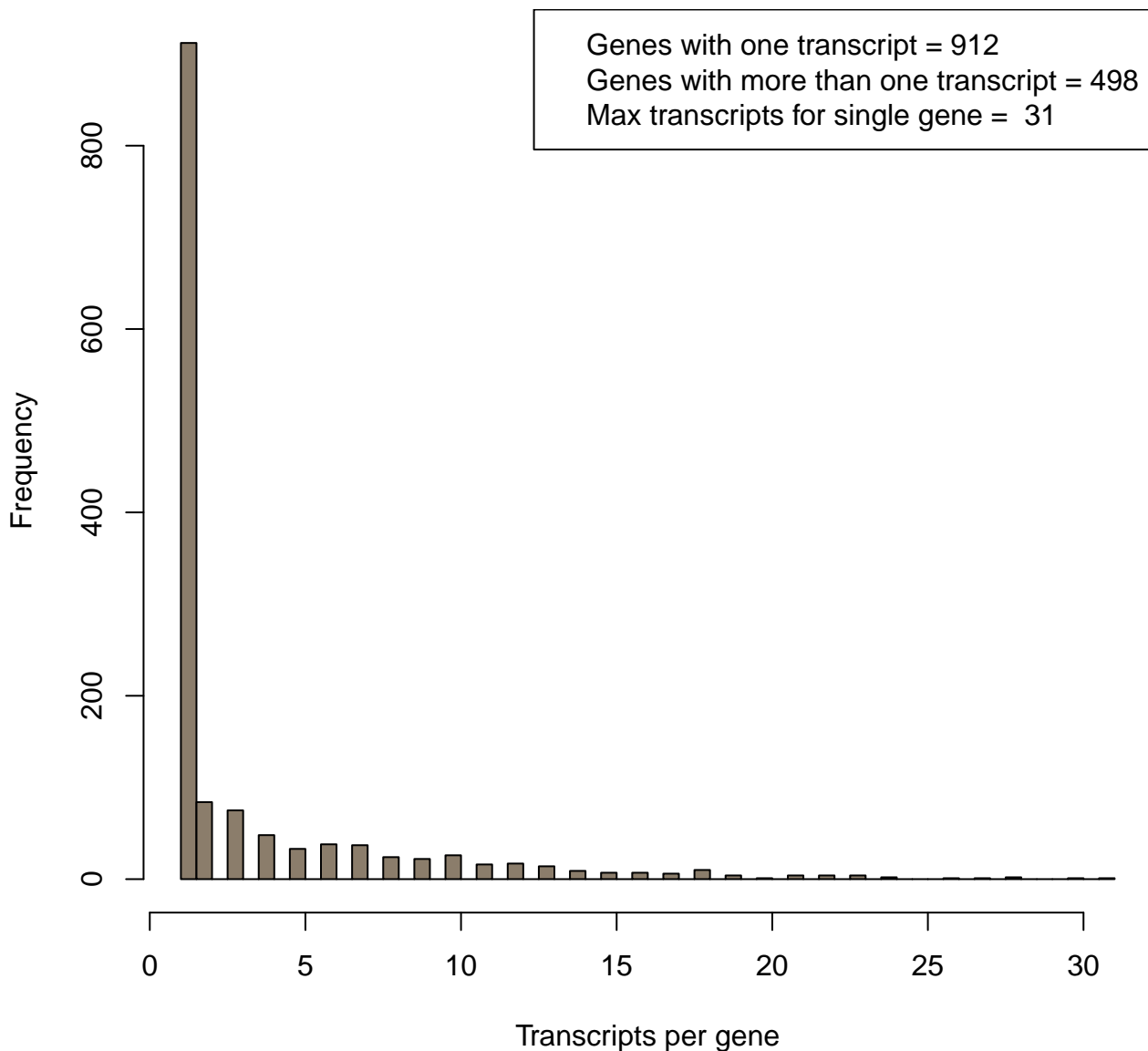
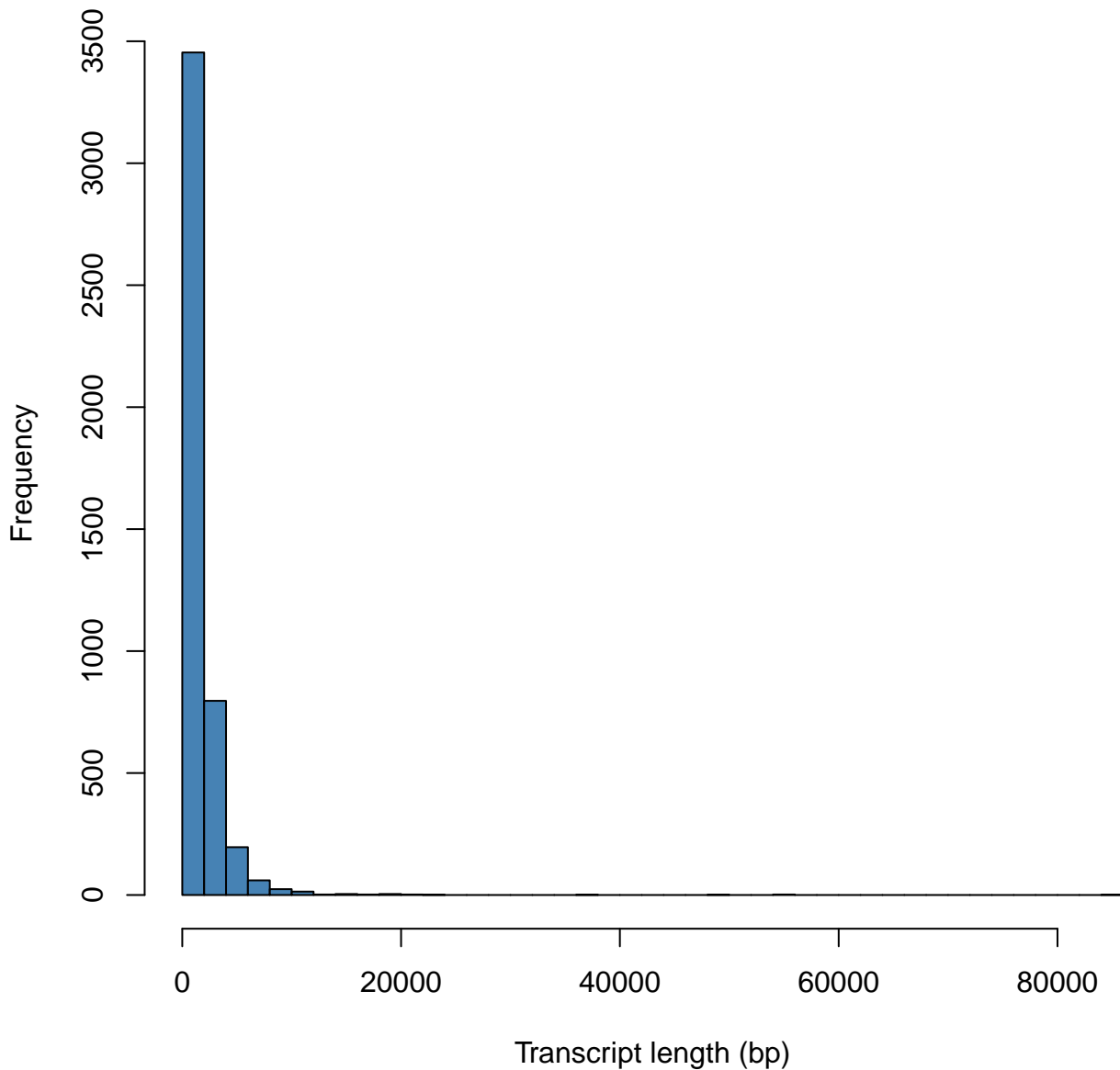
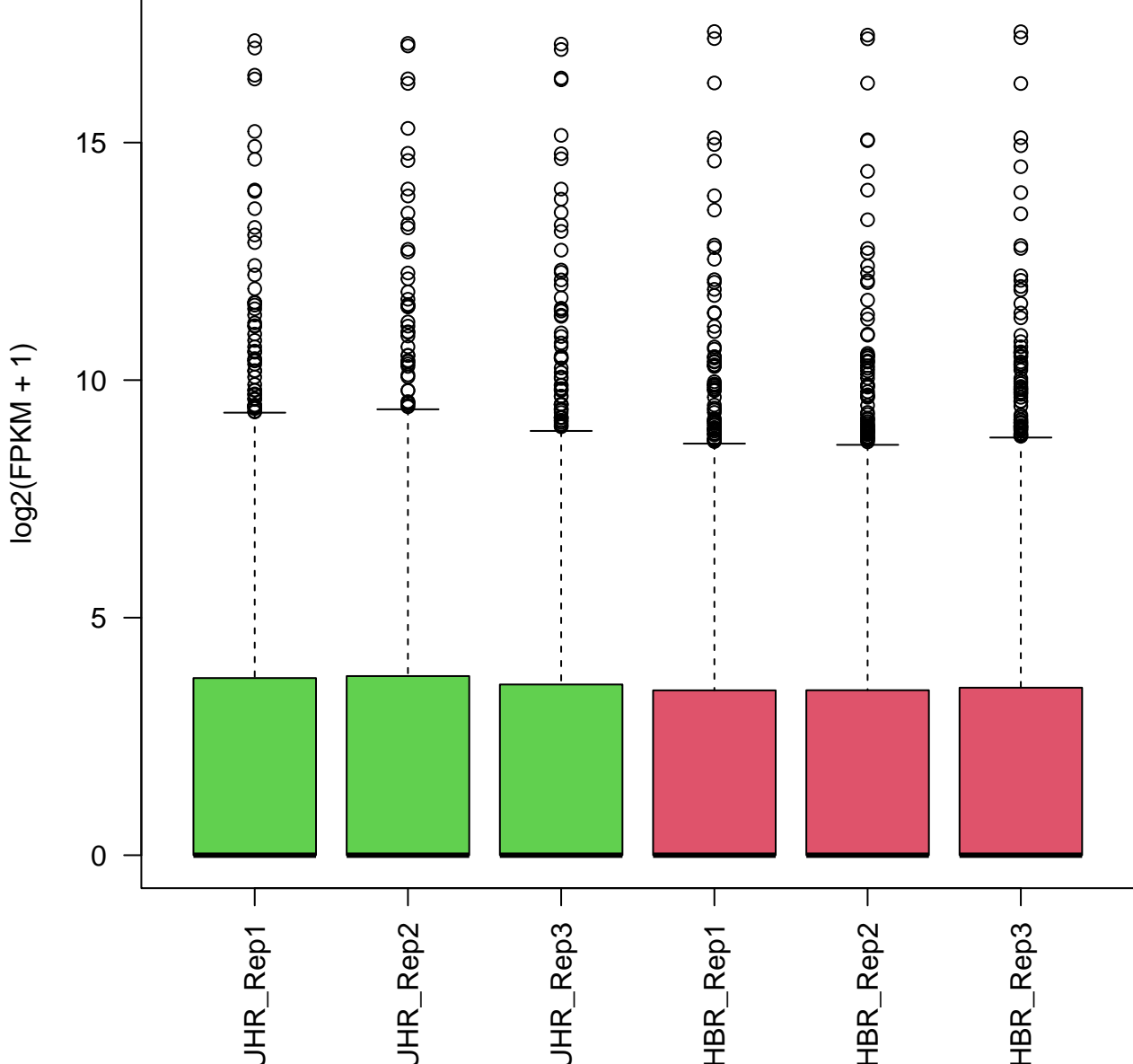


Distribution of transcript count per gene

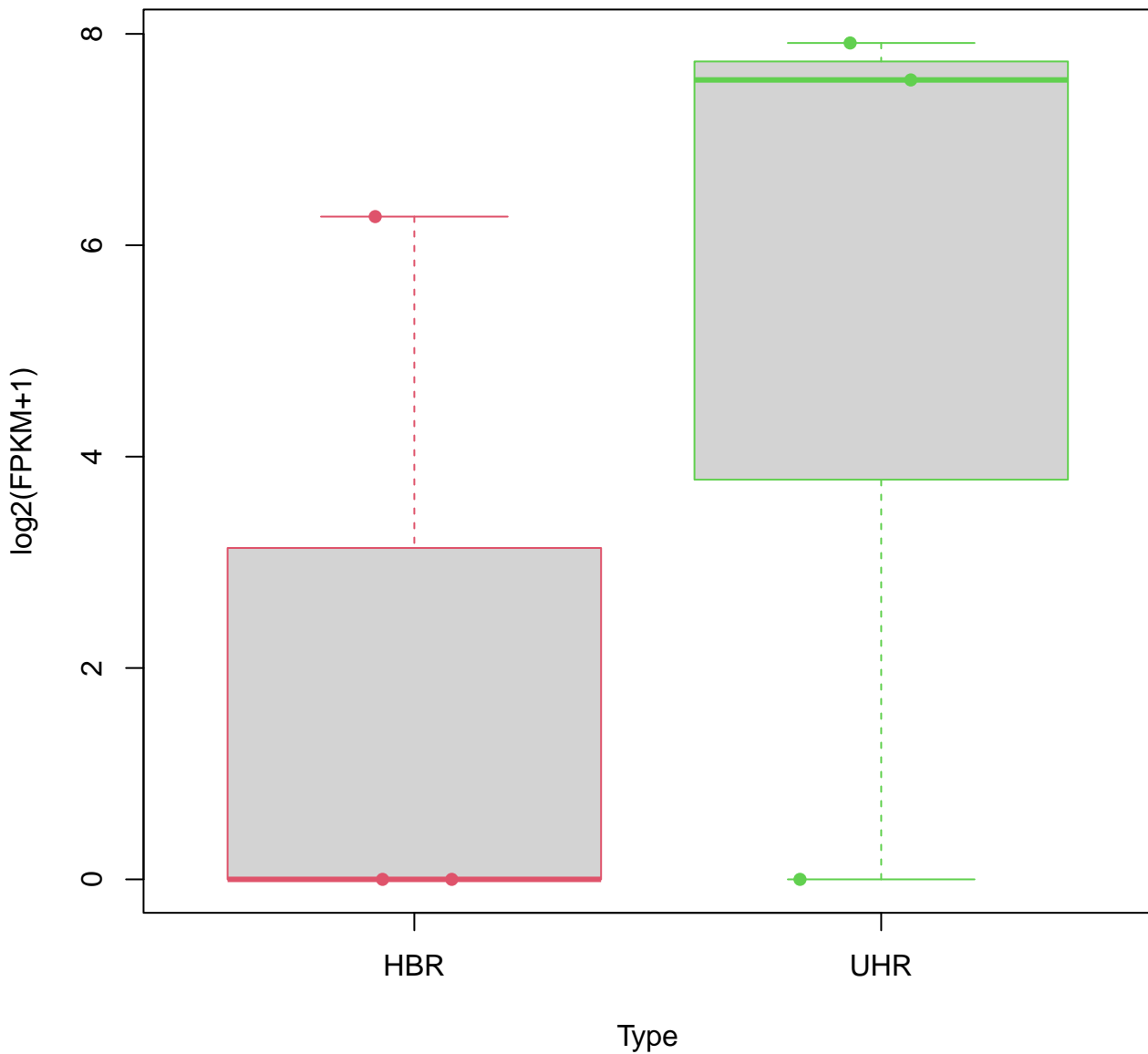


Distribution of transcript lengths





TST : ENST00000249042



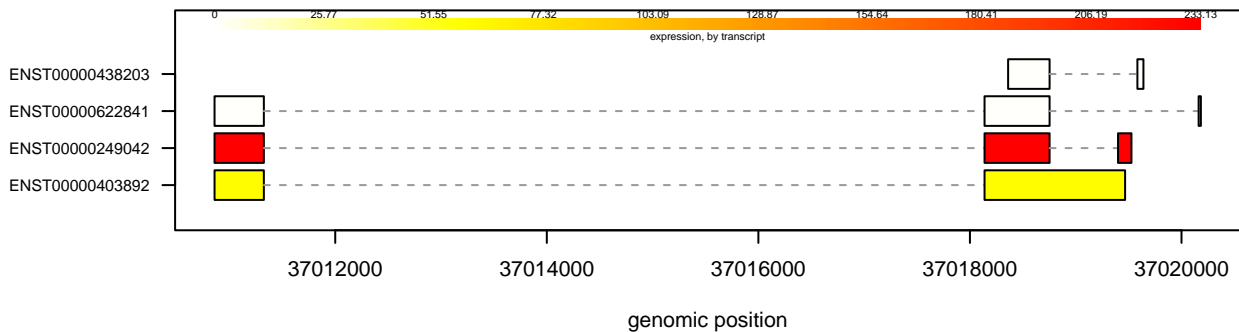
t_id	chr	strand	start	end	t_name	num_exons	length	gene_id	gene_name
2762	22	-	37010859	37019467	ENST000000403892	2	1797	ENSG000000128311	TST
2763	22	-	37010859	37019527	ENST000000249042	3	1211	ENSG000000128311	TST
2764	22	-	37010859	37020183	ENST000000622841	3	1105	ENSG000000128311	TST
2766	22	-	37018361	37019640	ENST000000438203	2	451	ENSG000000128311	TST

cov.UHR_Rep1	FPKM.UHR_Rep1	cov.UHR_Rep2	FPKM.UHR_Rep2	cov.UHR_Rep3	FPKM.UHR_Rep3
2.272105	59.237762	5.319421	209.532623	0.711043	22.643164
9.212243	240.179337	0	0	5.911855	188.263016
0	0	0	0	0	0
0	0	0	0	0	0

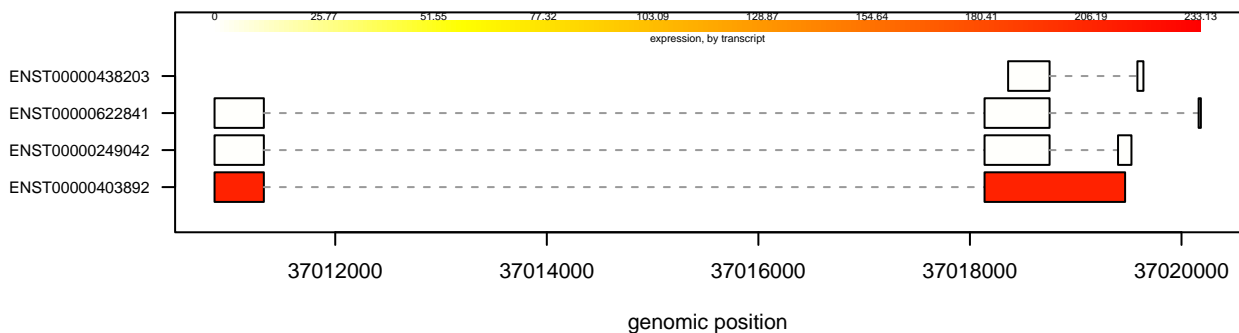
cov.HBR_Rep1	FPKM.HBR_Rep1	cov.HBR_Rep2	FPKM.HBR_Rep2	cov.HBR_Rep3	FPKM.HBR_Rep3
1.532554	78.781723	0.748703	31.307688	1.671675	78.555351
0	0	1.822941	76.227913	0	0
0	0	0	0	0	0
0	0	0	0	0	0

Data from this table is plotted in the plots in the next 2 pages. You can compare the value of FPKM.UHR_Rep1 (240.17934) and FPKM.HBR_Rep1 (0.00000) of t_name ENST000000249042 (t_id = 2763) in this table to the red and white rectangle boxes in the plots.

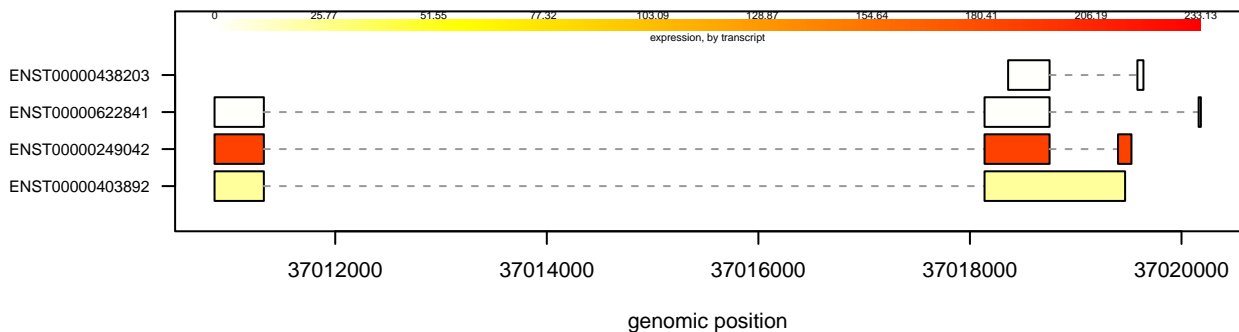
TST in UHR_Rep1



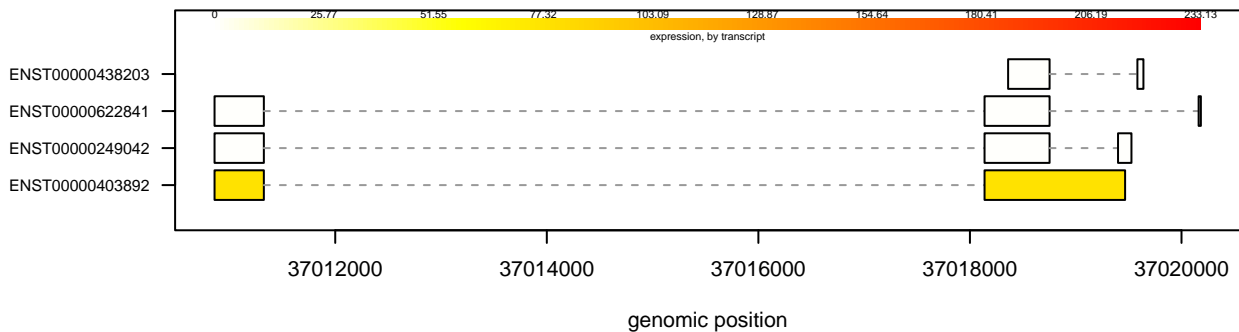
TST in UHR_Rep2



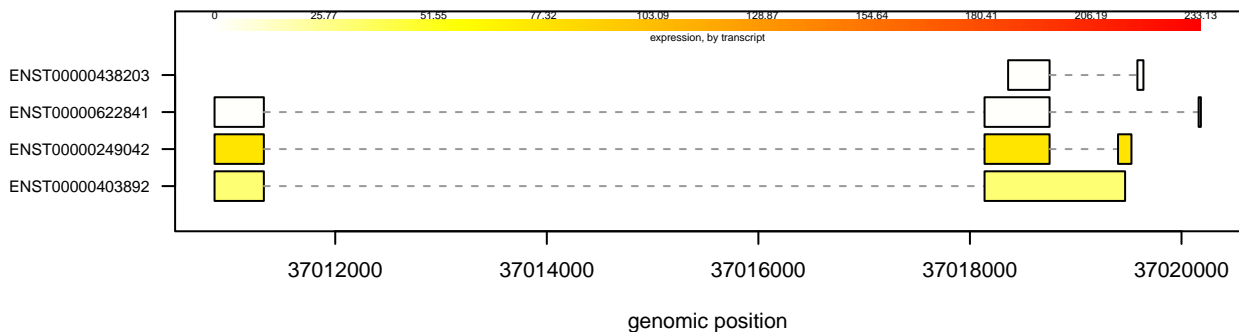
TST in UHR_Rep3



TST in HBR_Rep1



TST in HBR_Rep2



TST in HBR_Rep3

