Table S7 eQTL simulation summary showing the classification of eQTL calls that differ between alignment strategies differentiated by gene biotype

	Correct Calls			Incorrect Calls		
Gene Biotype	True Local	True Distant	True No eQTL	False Negative	False Positive Local	False Positive Distant
Antisense	2	3	15	-2	-16	-2
IG_C_gene	0	0	1	0	-1	0
lincRNA	6	3	15	-7	-15	-2
misc_RNA	2	0	2	-2	-1	-1
Mt_rRNA	0	0	0	0	0	0
non_coding	0	0	0	0	0	0
polymorphic pseudogene	1	0	0	-1	0	0
processed_transcript	3	0	2	-3	-2	0
protein_coding	336	94	981	-353	-980	-78
pseudogene	23	3	32	-10	-7	-41
retrotransposed	3	-1	1	-2	1	-2
sense_intronic	0	0	1	0	-1	0
sense_overlapping	0	0	0	0	0	0
snoRNA	0	0	0	0	0	0
Total	**376**	**102**	**1050**	**-380**	**-1022**	**-126**

Choice of read alignment strategy affects ten percent of genes (n = 1,528/15,027 total) in our simulation study. Alignment to individualized DO transcriptomes yields the correct eQTL assignment for all but one gene with a discordant call. Many gene biotypes yield incorrect eQTL calls after alignment to GRCm38 but pseudogenes in particular appear to be sensitive to false positive distant associations.