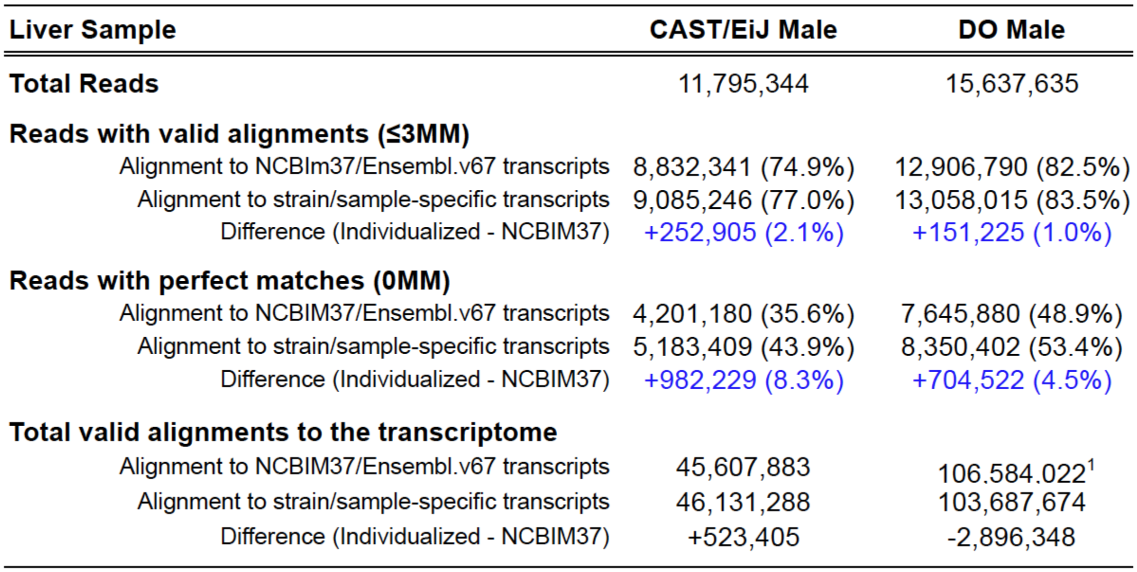
Table S6 Alignment statistics for real CAST and DO liver RNA-seq data



Liver Sample	CAST/EiJ Male	DO Male
Total Reads	11,795,344	15,637,635
Reads with valid alignments (≤3MM)		
Alignment to NCBIm37/Ensembl.v67 transcripts	8,832,341 (74.9%)	12,906,790 (82.5%)
Alignment to strain/sample-specific transcripts	9,085,246 (77.0%)	13,058,015 (83.5%)
Difference (Individualized - NCBIM37)	+252,905 (2.1%)	+151,225 (1.0%)
Reads with perfect matches (0MM)		
Alignment to NCBIM37/Ensembl.v67 transcripts	4,201,180 (35.6%)	7,645,880 (48.9%)
Alignment to strain/sample-specific transcripts	5,183,409 (43.9%)	8,350,402 (53.4%)
Difference (Individualized - NCBIM37)	+982,229 (8.3%)	+704,522 (4.5%)
Total valid alignments to the transcriptome		
Alignment to NCBIM37/Ensembl.v67 transcripts	45,607,883	106.584.022[1]
Alignment to strain/sample-specific transcripts	46,131,288	103,687,674
Difference (Individualized - NCBIM37)	+523,405	-2,896,348

Bowtie (version 0.12.8) parameters: -v 3 -a -m --best --strata

[1] For comparison to the diploid transcriptome alignments in DO samples, the total number of alignments to NCBIM37 were scaled by 2x.

Alignment of real data to individualized CAST- or DO-specific transcriptomes yields more reads with valid alignments (≤ 3 mismatches (MM)), and significantly more reads with perfect (0 MM) alignments. Reads align with greater specificity (i.e. fewer alignments per mapped read) to individualized transcriptomes than to NCBIM37.