

Table S3: Summary of RNA-seq data mapping to reference genome

	Sample	Sample ID	Sex	read count	Uniquely mapped reads number	Number of reads mapped to multiple loci	total mapped reads	% mapped reads
WT (<i>Atp7b</i> ^{+/+})	1	WT614M_idx12*	male	36360686	26981727	4679367	31661094	87.1
	2	WT2_wild_type	female	15823058	13767853	1578894	15346747	97
	3	WT3_wild_type	female	8149631	6698957	1007821	7706778	94.6
KO (<i>Atp7b</i> ^{-/-})	1	ATP7B_1_K0204	male	22931967	18941053	2895805	21836858	95.2
	2	ATP7B_1_K0243	male	9538147	7676801	1403163	9079964	95.2
	3	KO620F_idx12*	female	38366743	30150835	4862158	35012993	91.3

*paired-end runs

Reads were mapped to Mus musculus genome assembly GRCm38