

SUPPLEMENTAL FIGURES & TABLES

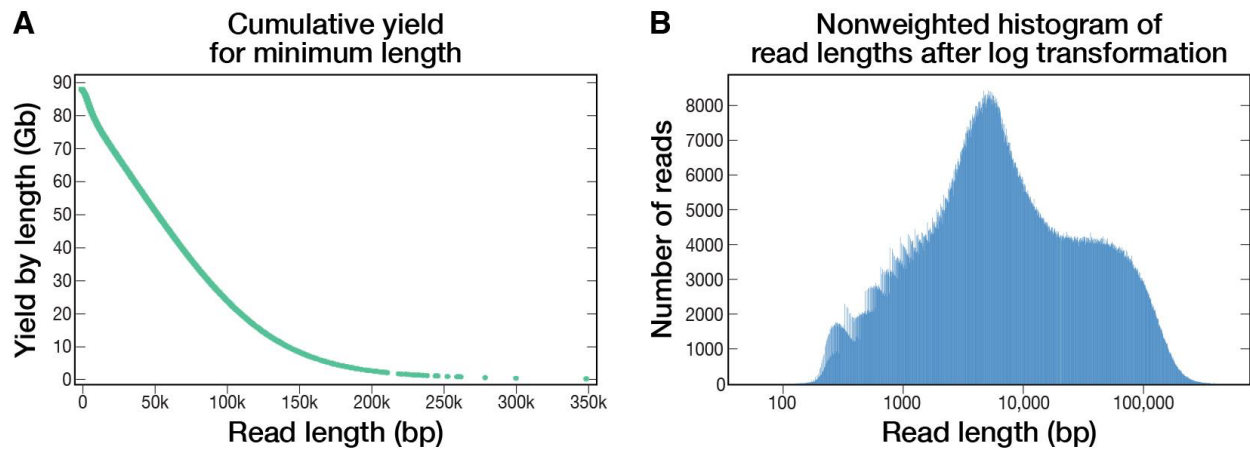


Figure S1. Read statistics after basecalling, generated with NanoPlot (De Coster *et al.* 2018). **(A)** Cumulative yield (in Gb) by read length. **(B)** Count of reads by length.

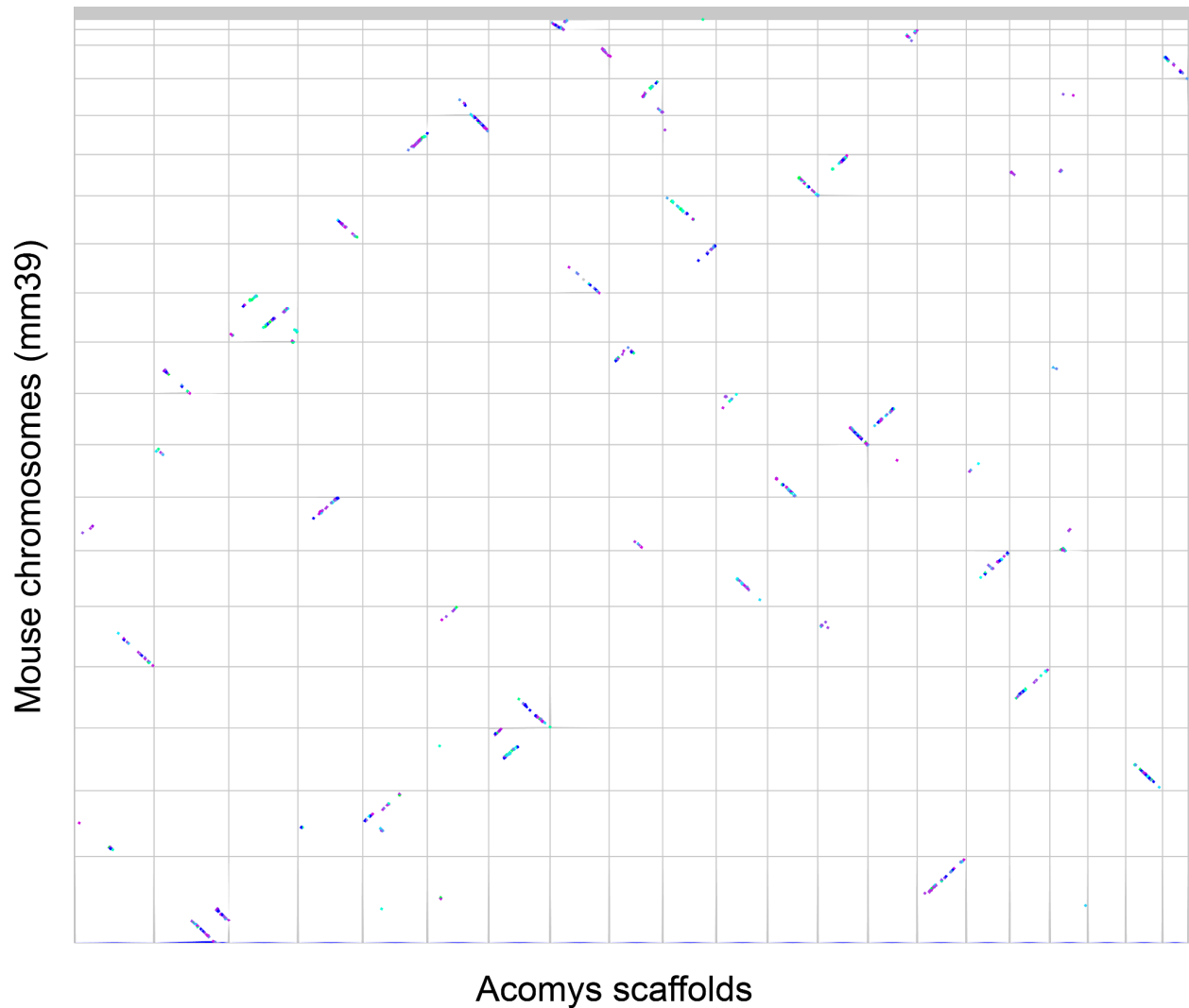


Figure S2. Syntenic dot plot with Kn/Ks coloration. The latest *Mus musculus* reference (mm39) is represented on the y-axis, and *Acomys cahirinus* scaffolds are on the x-axis. Grey lines separate chromosomes/scaffolds in each genome. Syntenic gene pairs are colored by the ratio of the rate of nonsynonymous to synonymous mutations (Kn/Ks), with the smallest values dark blue, followed in increasing value by violet, light blue, green, red, and orange (orange denotes \sim Kn/Ks > 1.1, which is rare in the *Acomys-Mus* comparison - see Results).

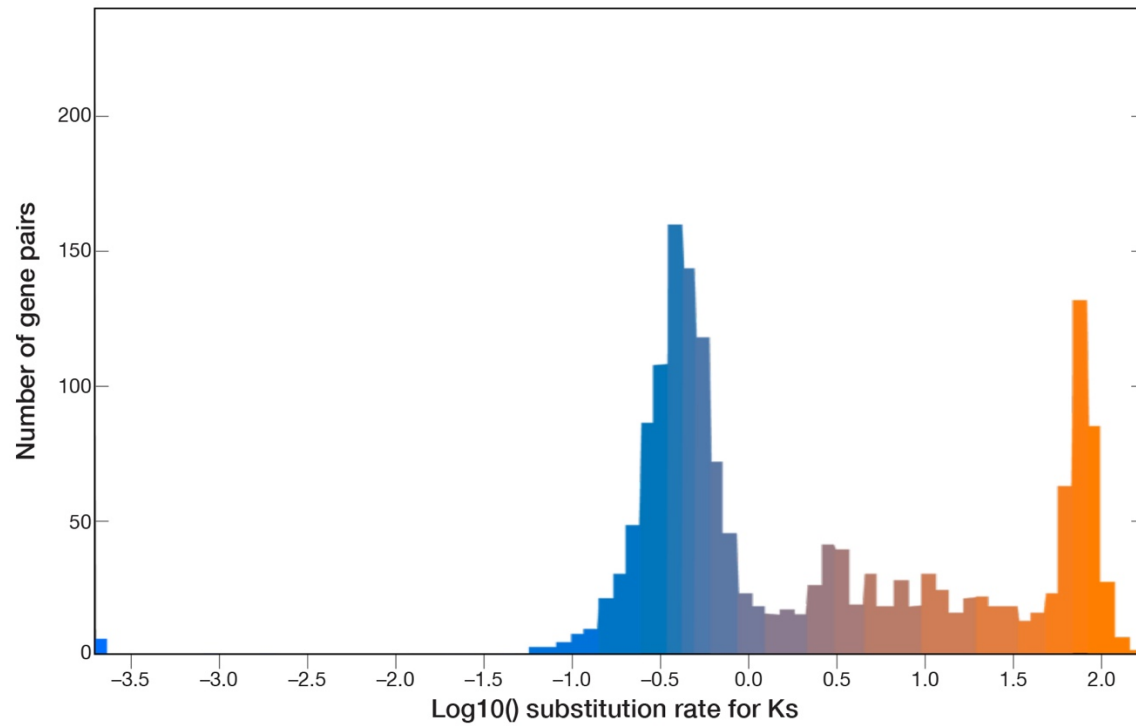


Figure S3. Histogram of the log10-transformed synonymous mutation (Ks) values of the syntenic gene pairs found between *Mus* (mm39) and *Acomys cahirinus*.

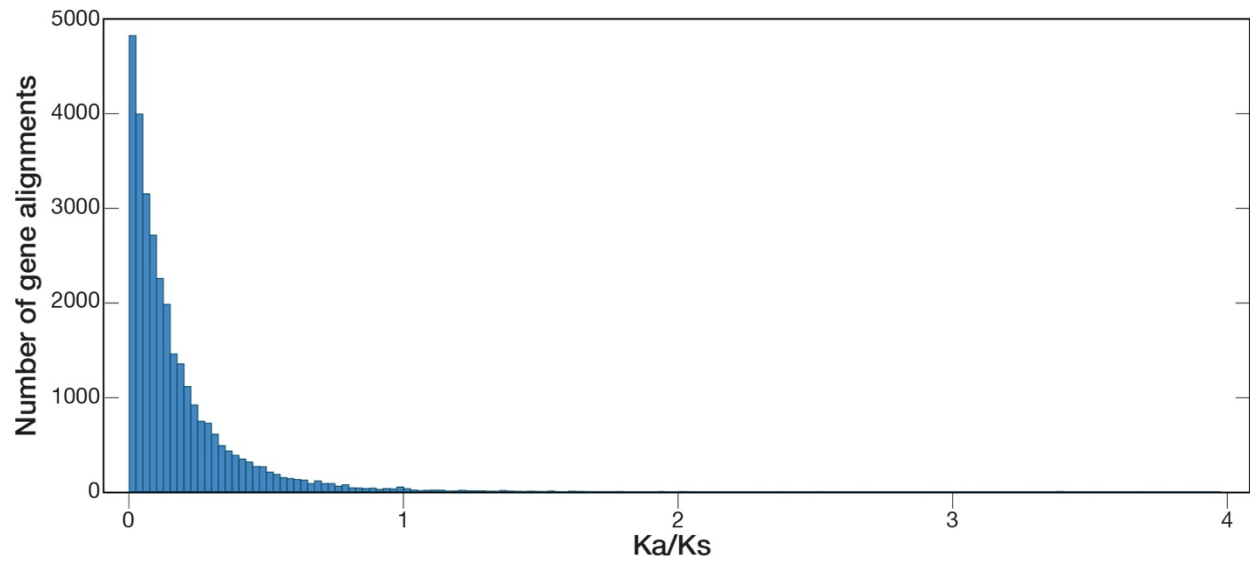


Figure S4. Distribution of Ka/Ks estimates for 33,197 protein-coding orthologs between *Acomys cahirinus* and *Mus musculus*. Multiple isoforms were tested for some genes.

Table S1. Summary of Oxford Nanopore sequencing statistics generated by NanoPlot (De Coster *et al.* 2018).

Mean read length	20,158	
Mean read quality	12.6	
Median read length	6,129	
Median read quality	12.6	
Number of reads	4,345,343	
Read length N50	62,867	
STDEV read length	32,666	
Total bases	87,593,195,281	
Quality cutoff	Number of reads (%)	Read length
>Q5	4,345,343 (100.0%)	87,593.2 Mb
>Q7	4,345,166 (100.0%)	87,592.9 Mb
>Q10	3,444,710 (79.3%)	74,862.6 Mb
>Q12	2,483,116 (57.1%)	59,723.1 Mb
>Q15	930,916 (21.4%)	23,692.5 Mb
Top 5 longest reads	Mean base call quality score	
769,429	7.4	
730,505	7.3	
665,850	10.8	
661,387	11.2	
656,035	7.8	

Table S2. Quast and BUSCO scores after each step of assembly, polishing, or scaffolding.

	After purging duplicates	After polishing with medaka	After polishing with pilon	After scaffolding and annotation
Quast statistics				
# contigs (≥ 0 bp)	181	181	181	129
# contigs (≥ 1000 bp)	177	177	177	125
# contigs (≥ 5000 bp)	162	162	162	110
# contigs (≥ 10000 bp)	156	156	156	104
# contigs (≥ 25000 bp)	147	147	147	94
# contigs (≥ 50000 bp)	141	141	141	87
Total length (≥ 0 bp)	2,288,116,004	2,289,791,246	2,289,253,112	2,289,268,912
Total length (≥ 1000 bp)	2,288,113,194	2,289,788,406	2,289,250,289	2,289,266,089
Total length (≥ 5000 bp)	2,288,074,385	2,289,749,375	2,289,211,425	2,289,227,225
Total length (≥ 10000 bp)	2,288,033,368	2,289,707,944	2,289,170,056	2,289,185,856
Total length (≥ 25000 bp)	2,287,894,346	2,289,568,906	2,289,031,072	2,289,027,872
Total length (≥ 50000 bp)	2,287,707,297	2,289,381,919	2,288,844,248	2,288,790,854
# contigs	181	181	181	129
Largest contig	126,722,130	126,814,207	126,792,893	212,232,915
Total length	2,288,116,004	2,289,791,246	2,289,253,112	2,289,268,912
GC (%)	43	43	43	43
N50	58,763,166	58,809,824	58,791,706	127,770,522
N75	34,405,976	34,434,390	34,427,997	117,233,451
L50	16	16	16	8
L75	28	28	28	13
# N's per 100 kbp	0	0	0	1
BUSCO statistics				
Complete BUSCOs (C)	3,290 (98.0%)	3,300 (98.4%)	3,305 (98.6%)	3,304 (98.5%)
Complete and single-copy BUSCOs (S)	3,218 (95.9%)	3,225 (96.2%)	3,232 (96.4%)	3,233 (96.4%)
Complete and duplicated BUSCOs (D)	72 (2.1%)	75 (2.2%)	73 (2.2%)	71 (2.1%)
Fragmented BUSCOs (F)	25 (0.7%)	19 (0.6%)	15 (0.4%)	16 (0.5%)
Missing BUSCOs (M)	39 (1.3%)	35 (1.0%)	34 (1.0%)	34 (1.0%)

File S1. Concatenated output from KaKs_calculator2.0 analysis of mouse RefSeq transcripts.

File S2. RPKM values for RNA sequencing data from heart, liver, brain, and testis.