

TABLE S4**Top 10 additional strains for resequencing**

All 94 strains		73 classical inbred strains	
Strain name	Coverage increase (avg)	Strain name	Coverage increase (avg.)
PERC/EjJ	0.012039	NZL/LtJ	0.004697
ZALENDE/EjJ	0.006353	P/J	0.003432
SPRET/EjJ	0.004942	DDK/Pas	0.002914
IS/CamRkJ	0.002984	LG/J	0.002070
NZL/LtJ	0.002416	C57/L	0.001928
LEWES/EjJ	0.001931	SJL/J	0.001574
P/J	0.001624	O20	0.001359
DDK/Pas	0.001354	RIIS/J	0.001184
C57/L	0.001013	I/LnJ	0.000985
LG/J	0.000919	SM/J	0.000789

Top 10 strains greedily targeted for resequencing in addition to 16 resequenced strains in order to improve the genomic coverage over mouse HapMap strains.