

**TABLE S2****Total number of imputed missing genotypes in resequenced strains**

Strain name	# imputed genotypes	# high-confidence genotypes	Overall imputation error	High-confidence imputation error
129S1/SvImJ	923,959	245,792	0.02505	0.00379
A/J	797,363	164,028	0.01473	0.00195
AKR/J	899,745	213,076	0.01976	0.00288
BALB/cByJ	856,126	225,381	0.01172	0.00211
BTBRT<+>tf/J	905,104	270,244	0.02092	0.00430
C3H/HeJ	987,508	282,717	0.01181	0.00289
C57BL/6J	14	0	0.03854	0.00369
CAST/EiJ	1,257,795	0	0.34073	N/A
DBA/2J	956,054	272,074	0.01874	0.00341
FVB/NJ	914,948	208,107	0.02886	0.00395
KK/HIJ	908,091	211,090	0.03628	0.00674
MOLF/EiJ	1,226,418	0	0.15148	N/A
NOD/LtJ	929,392	224,838	0.02584	0.00379
NZW/LacJ	905,125	214,152	0.03395	0.00542
PWD/PhJ	1,312,167	0	0.16713	N/A
WSB/EiJ	943,362	5,665	0.13027	N/A
<b>Total (or Avg.)</b>	<b>14,733,063</b>	<b>2,542,320</b>	<b>0.06156</b>	<b>0.00367</b>

Total number of imputed genotypes of 16 resequenced strains missing in NIEHS/Perlegen SNPs, mouse HapMap SNPs, WTCHG SNPs, and the gap-filling NIEHS/Perlegen SNPs, in addition to the estimation of imputation errors using leave-one-out cross-validation.