

Table s1. European Nucleotide Archive ERS IDs for all raw sequencing data for each strain. Jackson Laboratory stock numbers for each strain are also shown.

Strain	ERS ID	Stock number
BUB/BnJ	ERS661322	000653
C57BL/10J	ERS661323	000665
C57BR/cdJ	ERS661325	000667
C58/J	ERS661326	000669
DBA/1J	ERS661327	000670
I/LnJ	ERS661328	000674
KK/HiJ	ERS661329	002106
MOLF/EiJ	ERS661330	000550
NZB/B1NJ	ERS661331	000684
NZW/LacJ	ERS661332	001058
RF/J	ERS661333	000682
SEA/GnJ	ERS661334	000644
ST/bJ	ERS661335	000688

Table s2. Sensitivity estimates for all PCR validated structural variants.

Strain	Total PCR deletions	Missed	Sensitivity	Total PCR insertions	Missed	Sensitivity
AKR/J	132	9	93.18%	72	13	81.94%
A/J	149	11	92.62%	86	12	86.05%
BALB/cJ	138	9	93.48%	77	9	88.31%
C3H/HeJ	165	12	92.73%	93	11	88.17%
CBA/J	148	10	93.24%	87	5	94.25%
DBA/2J	151	12	92.05%	84	8	90.48%
DBA/1J*	151	20	86.75%	84	16	80.95%
LP/J	136	8	94.12%	68	8	88.24%

*Sensitivity estimated for DBA/1J using the PCR validated structural variants identified in DBA/2J. When true structural variant differences between the strains are removed from the sensitivity analysis, the sensitivity increases to 91.6% (131/143) which is similar to the number of SNP sites that are identical (90.72%).

Table s3. Library and sequencing statistics for each sample.

Strain	Gender	Raw total sequences:	Average quality	Insert size average	Insert size standard deviation
BUB/BnJ	M	1344667465	35.8	256.3	92.7
C57BL/10J	M	1098531348	35	344.6	854.8
C57BR/cdJ	M	1404238082	34.1	258.1	109
C58/J	M	1526927921	36	262.7	123.9
DBA/1J	M	1394978119	35.1	254.6	110
I/LnJ	M	1243880652	35.7	217.4	82.4
KK/HiJ	M	1505723009	36.3	258.5	104.5
MOLF/EiJ	M	1119348103	35.7	194.7	68.5
NZB/B1NJ	M	1324550888	35.1	287.6	104.1
NZW/LacJ	M	1592592167	34.2	281.8	87.5
RF/J	M	1466072740	36.4	244.6	94.9
SEA/GnJ	M	1332757895	35.7	258.2	91.9
ST/bJ	M	2215849093	35.3	238.2	90.3

Table s4. Filter and cut-off values used to soft-filter SNPs and indels.

Filter	Description	Tag(s)	Value
StrandBias	Min P-value for strand bias	PV4	0.0001
EndDistBias	Min P-value for end distance bias	PV4	0.0001
MaxDP	Maximum read depth	DP or DP4	150-350*
BaseQualBias	Min P-value for baseQ bias	PV4	0
MinMQ	Minimum RMS mapping quality for SNPs	MQ	20
MinAB	Minimum number of alternate bases	DP4	5
Qual	Minimum value of the QUAL field	QUAL	10
VDB	Minimum Variant Distance Bias	VDB	0
GapWin	Window size for filtering adjacent gaps	-	3
MapQualBias	Min P-value for mapQ bias	PV4	0
SnpGap	SNP within INT bp around a gap to be filtered	-	2
RefN	Reference base is N	-	-
MinDP	Minimum read depth	DP or DP4	5
Het	Genotype call is heterozygous	low quality	-

*MaxDP calculated for each strain separately as 5 times the coverage and then rounded to the nearest 50.

Table s5. Parameters for each tool used to identify structural variation deletions and insertions.

Software	SV type	Version	Parameters*
BreakDancerMax	Deletion	1.1	bam2cfg.pl: -c 3 -n50000 -q 25 BreakDancer: -c3 -m 10000000 -q 25 -r 2 -y 25
cnD	Copy number losses and gains	1.3	--repeat-cut-off=0.35 --smooth=100
LUMPY	Deletion	0.2.11	extractSplitReads_BwaMem: default extractDiscordants: samtools view -bh -F 1294 Lumpyexpress: -m 4 -r 0
Scalpel	Short novel sequence insertion	0.3.2	--window 600 --maxregcov 300
Manta	Novel sequence insertion	0.29.6	runWorkflow.py -m local
Retroseq	Transposable element insertion	1.5	Default

*A minimum of 10 support reads (read pairs or soft clipped reads) was required for all SVs to pass post-filtering