

SUPPLEMENTAL MATERIAL

Supplemental Table 1. Location and extent of blocks of non-IBD containing genes of the immunoreceptor pathway and effects of ancestral variation on protein coding genes in block. The table indicates only genes with non-synonymous variation from the Brown-Norway (BN) reference genome in each block and omits the immunoglobulin heavy chain (chr 6) because of the extreme variation observed in this gene. The table also indicates confirmation of alleles in whole genome sequence from another SHR-A3 colony (Glasgow) and whether the variant allele is present in either of 2 injury-resistant (SHRSR) lines for which whole genome sequence data is available.

Gene name	Chr	Start position	End position	Variation from BN in	AA change	Confirm A3 genotype in SHRA3/Gla	Present in other SHRSR?
Block Non-IBD	3	158,090,000	161,780,000				
Ndr3	3	158,614,195	158,725,392	A3	Ser17Arg	Y	N
Tgm2	3	160,977,905	161,007,260	A3	Asp94Asn	Y	N
Tti1	3	161,113,415	161,140,919	A3	Thr663Ile	Y	Y
Tti1	3	161,113,415	161,140,919	A3	Lys665Phe	Y	Y
Block Non-IBD	6	146,030,000	154,190,000				
Gpr132	6	146,660,012	146,648,353	B2	Asp189Asn	Y	Y
Gpr132	6	146,660,012	146,648,353	A3	Thr26Met	Y	N
Gpr132	6	146,660,012	146,648,353	A3	Pro5Ser	Y	N
Adam6	6	147,426,645	147,429,132	B2	Val531Met	Y	Y
Wdr60	6	153,061,842	153,007,323	A3	Thr49Ala	Y	N
Block Non-IBD	16	17,650,000	23,470,000				
Dyc2	16	18,506,978	18,520,588	A3	Pro123Lys	Y	N
Cyp4f18	16	19,269,139	19,385,553	B2	Tyr242His	Y	Y
Myo9b	16	19,529,516	19,614,169	B2	Lys1175Gln	Y	Y
Slc27a1	16	19,859,540	19,876,619	A3	His357Arg	Y	N
Fam129c	16	19,887,776	19,899,606	A3	Cys7Ser	Y	N
B3gnt3	16	19,984,402	19,993,283	A3	Pro68Arg	Y	N
Crif1	16	20,541,796	20,530,521	B2	Lys32Phe	Y	1 of 2
Gdf1	16	20,712,564	20,698,125	A3	Ala173Thr	Y	N
Sugp2	16	20,789,858	20,760,491	B2	Ser298Gly	Y	Y
Armc6	16	20,789,624	20,799,784	B2	Ser263Asn	Y	Y
Tmem161a	16	20,846,231	20,836,630	B2	Arg98His	Y	Y
Rfxank	16	20,879,467	20,886,951	A3	Val39Ile	Y	Y
Gatad2a	16	21,093,916	21,184,110	B2	Ser235Gly	Y	Y
Cilp2	16	21,204,960	21,211,953	B2	Thr900Ala	Y	1 of 2
Sh2d4a	16	23,044,750	22,972,707	A3	Gly236Glu	Y	Y
Block Non-IBD	17	6,760,000	16,520,000				
Ntrk2	17	8,156,432	8,464,507	A3	Ala187Val	Y	N
Dok3	17	11,748,066	11,752,826	A3	Ile71Val	Y	N
Dok3	17	11,748,066	11,752,826	A3	Ala83Val	Y	N
Dbn1	17	11,788,597	11,802,569	B2	Ala618Val	Y	Y
Slc34a1	17	11,856,946	11,872,100	B2	Ala630Thr	Y	Y
Fgfr4	17	12,099,383	12,113,632	A3	Arg95Gly	Y	N
Hk3	17	12,246,816	12,261,635	B2	Ser770Asn	Y	Y
Ror2	17	14,050,995	14,228,982	A3	Gly744Ser	Y	N

Sema4d	17	15,590,977	15,613,214	B2	Gly35Glu	Y	Y
Sema4d	17	15,590,977	15,613,214	B2	Gly617Ser	Y	Y
Nxn12	17	16,120,216	16,124,963	B2	Ala147Thr	Y	Y

IgG Fc variants (positions from rn5):

1. Location: chr6:147108547 intron

SHR-A3 TAGGAGCTTGGGTCCAGACCTGTCAGACAAAAT

SHR-B2 TAGGAGCTTGGGTCCAAACCTGTCAGACAAAAT

SHR-B2 different from BN reference

2. Location: chr6:147107456 exon

SHR-A3 ACGTTCAGATGCAAGGTCACAGTGCAGCTTTCCCATCC

SHR-B2 ACGTTCAGATGCAAGGTCACAGTGCAGCTTTCCCATCC

SHR-B2 different from BN reference, synonymous

3. Location: chr6:147141845 intron

SHR-A3 AGACAAAATGATCACGCATACTTTTCTTGTAGCTGAAACAAC

SHR-B2 AGACAAAATGATCACGCATACTTTTCTTGTAGCTGAAACAAC

SHR-A3 different from BN reference

4. Location: chr6: 147141478 intron

SHR-A3 TAAGGCATTAGACTGCCTACACAACCAGGGTGGGCAGAC

SHR-B2 TAAGGCATTAGACTGCCTACACAACCAGGGTGGGCAGAC

SHR-A3 different from BN reference

5. Location: chr6: 147141081 intron

SHR-A3 ACAGCTATTGACCTATTTCCACCTTTCTTCTTCATCTA

SHR-B2 ACAGCTATTGACCTATTTCCACCTTTCTTCTTCATCTA

SHR-B2 different from BN reference

6. Location: chr6: 147141059 exon

SHR-A3 TTTCTTCTTCATCTACAGGCTCAGAAGTATCATCTGTC

SHR-B2 TTTCTTCTTCATCTACAGTCCCAGATATATCATCTGTC

SHR-A3 different from BN reference, non-synonymous, Gly to Val,

7. Location: chr6: 147141057 exon

SHR-A3 TCTTCTTCATCTACAGGCTCAGAAGTATCATCTGTCTTCATC

SHR-B2 TCTTCTTCATCTACAGTCCCAGATATATCATCTGTCTTCATC

SHR-A3 different from BN reference, non-synonymous, Ser to Pro

8. Location: chr6: 147141051-2 exon

SHR-A3 TCATCTACAGGCTCAGAAGTATCATCTGTCTTCATCTTCCCC

SHR-B2 TCATCTACAGTCCCAGATATATCATCTGTCTTCATCTTCCCC

SHR-A3 different from BN reference, non-synonymous, Glu to Asp, Val to Ile

9. Location: chr6: 147140508-9 exon

SHR-A3 TCTATCCCCCAGACATTTATGTGGAGTGGAAGATGAACG

SHR-B2 TCTATCCCCCAGACATTTATACGGAGTGGAAGATGAACG

SHR-A3 different from BN reference, non-synonymous, Tyr to Val

10. Location: chr6: 147086792 intron

SHR-A3 GACAGAAAGGATGCCTACACGCAGAAGGTGTAGGGTAGA

SHR-B2 GACAGAAAGGATGCCACACACAGAAGGTGTAGGGTAGA

SHR-A3 different from BN reference

11. Location: chr6: 147086612 intron

SHR-A3 CACTGAAAGATCAAGGCTCCTGGGGCTGGAGAGTTGGCTC
SHR-B2 CACTGAAAGATCAAGGCTCCTAGGGCTGGAGAGTTGGCTC
SHR-A3 different from BN reference

12. Location: chr6: 147086388 intron
SHR-A3 AAGGTCAGAGTGCAGGGTCTAGAGGTGGAAGCTGCTGACACCACTTA
SHR-B2 AAGGTCAGAGTGCAGGGTCTAGAAAGTGAAGCTGCTGACACCACTTA
SHR-A3 different from BN reference

13. Location: chr6: 147086179 exon
SHR-A3 GATACAACCAGCTCCACGGTGACCTGGGATGCCTGGTCAAGGG
SHR-B2 GATACAACCAGCTCCACGGTGACTCTGGGATGCCTGGTCAAGGG
SHR-A3 different from BN reference, synonymous

14. Location: chr6: 147086108 exon
SHR-A3 CCGTGACCTGGAACCTCTGGAGCCCTGTCCAGCGATGTG
SHR-B2 CCGTGACCTGGAACCTCTGGAGCCCTGTCCAGCGATGTG
SHR-A3 different from BN reference, non-synonymous, Ala to Pro

15. Location: chr6: 147086092 exon
SHR-A3 GTCCAGCGATGTGCACACCTTCCAGCTGTCCTGCAGTCTGGGC
SHR-B2 GTCCAGCGATGTGCACACCTTCCAGCTGTCCTGCAGTCTGGGC
SHR-A3 different from BN reference, synonymous

16. Location: chr6: 147086065 exon
SHR-A3 CTGTCCTGCAGTCTGGGCTCTACTCTCACCAGCTCAGTGA
SHR-B2 CTGTCCTGCAGTCTGGGCTCTACTCTCACCAGCTCAGTGA
SHR-B2 different from BN reference, synonymous

17. Location: chr6: 147085968 exon
SHR-A3 CACCAAGGTGGACAAGAAAATTGGTGAGAGGACAACCA
SHR-B2 CACCAAGGTGGACAAGAAAGTTGGTGAGAGAACAACCA
SHR-A3 different from BN reference, non-synonymous Val to Ile

18. Location: chr6: 147085957 intron
SHR-A3 GGACAAGAAAATTGGTGAGAGGACAACCAAGGGACGAGG
SHR-B2 GGACAAGAAAGTTGGTGAGAGACAACCAGGGGACGAGG
SHR-B2 different from BN reference

19. Location: chr6: 147085949 intron
SHR-A3 TTGGTGAGAGGACAACCAAGGGACGAGGGGCTCACTAGAC
SHR-B2 TTGGTGAGAGAACAACCAGGGGACGAGGGGCTCACTAGAC
SHR-A3 different from BN reference

20. Location: chr6: 147085908 intron
SHR-A3 GTGAGGATAAGGCATTAGATGCCTACACCAACCAGGGT
SHR-B2 GTGAGGATAAGGCATTAGATTGCCTACACCAACCAGGGT
SHR-A3 different from BN reference

21. Location: chr6: 147085842 intron
SHR-A3 GGGGGCCTCAGCCCGGGAGACACTGTCACTGCCTCCCTCCTGGAGGCCTC
SHR-B2 GGGGGCCTCAGCCCGGGAGACACTGTCTCTGCCTCCCTCCTGGAGGCCTC
SHR-A3 different from BN reference

22. Location: chr6: 147085758 intron
SHR-A3 AGACATGATCCTCTGGTATAGATGTCTATGTGCATGTATAGGATCATAAC
SHR-B2 AGACATGATCCTCTGGTATAGATGTCTGTGTGCATGCATAGGATCATAAC
SHR-A3 different from BN reference

23. Location: chr6: 147085750 intron
SHR-A3 TGGTATAGATGTCTATGTGCATGTATAGGATCATAACCAGGGACAAA
SHR-B2 TGGTATAGATGTCTGTGTGCATGCATAGGATCATAACCAGGGACAAA
SHR-A3 different from BN reference

24. Location: chr6: 147085643 exon
SHR-A3 CTCTACAGAGCGCAGAAATGGCGGCAATGGACACAAATG
SHR-B2 CTCTACAGAGCGCAGAAATGGCGGCAATGGACACAAATG
SHR-B2 different from BN reference, non-synonymous, Ile to Asn

25. Location: chr6: 147085580 intron
SHR-A3 GCCCAGGTAAGTCACTAGACCTGGGCCCCAGCTCCACAATGATGGCA
SHR-B2 GCCCAGGTAAGTCACTAGACCTGGGCCCCAGCTCCACAATGATGGCA
SHR-A3 different from BN reference

26. Location: chr6: 147085489 exon
SHR-A3 CATTCTATCTCTCCTCATCAGTTCCTGAACTCTTGGGTGGACCAT
SHR-B2 CATTCTATCTCTCCTCATCAGTTCCTGAACTCTTGGGTGGACCAT
SHR-A3 different from BN reference, non-synonymous, Val to Ala

27. Location: chr6: 147085464 exon
SHR-A3 TCCTGAACTCTTGGGTGGACCATCTGTCTTCATCTTCCCCCCTAAA
SHR-B2 TCCTGAACTCTTGGGTGGACCATCTGTCTTCATCTTCCCCCCTAAA
SHR-A3 different from BN reference, synonymous

28. Location: chr6: 147085449 exon
SHR-A3 CCATCCGTCTTCATCTTCCCCTCAAAGCCCAAGGACATCCTCTTGA
SHR-B2 CCATCTGTCTTCATCTTCCCCTCAAAGCCCAAGGACATCCTCTTGA
SHR-A3 different from BN reference, synonymous

29. Location: chr6: 147085379 exon
SHR-A3 ACGTGTGTGGTGGTGGATGTGAGTGAGGAGGAGCCGACGTCCAG
SHR-B2 ACGTGTGTGGTGGTGGATGTGAGTGAGGAGGAGCCGACGTCCAG
SHR-B2 different from BN reference, synonymous

30. Location: chr6: 147085368 exon
SHR-A3 TGGATGTGAGCGAGGAGGAGCCGACGTCCAGTTCAGCTGGTTT
SHR-B2 TGGATGTGAGTGAGGAGGAGCCGACGTCCAGTTCAGCTGGTTT
SHR-A3 different from BN reference, synonymous

31. Location: chr6: 147085102 intron
SHR-A3 CTGGGATAGGTATAAGAATGAATGCCCGGTGGACGGCCATGACCTCTGT
SHR-B2 CTGGGATAGGTATAAGAATGAATGCCCGGTGGACGGCCATGACCTCTGT
SHR-A3 different from BN reference

31. Location: chr6: 1470850352 exon
SHR-A3 GTCAGAAAACCACAGGTATATGTCATGGGTCCACCGACAGAGCAG
SHR-B2 GTCAGAAAACCACAGGTATATGTCATGGGTCCACCGACAGAGCAG
SHR-A3 different from BN reference, synonymous

32. Location: chr6: 147084991-5001 exon
SHR-A3 GACAGAGCAGTTGACTGAGAAAGCGGTCATTTTGACCTGCTTGA
SHR-B2 GACAGAGCAGTTGACTGAGCAAACGGTCAGTTTGACCTGCTTGA
SHR-A3 different from BN reference, non-synonymous Gln to Lys

33. Location: chr6: 147084818 exon
SHR-A3 GGAGCAGGTGGGATAGCAGAGCGTCCTTCGTCTGCTCCGTGGTCCACGA
SHR-B2 GGAGCAGGTGGGATAGCAGAGCGTCCTTCGTCTGCTCCGTGGTCCACGA
SHR-A3 different from BN reference, non-synonymous, Pro to Ser

34. Location: chr6: 147084778 exon
SHR-A3 GTCCACGAGGGTCTGCACAATCCACCACGTGGAGAAGAGCATCTC
SHR-B2 GTCCACGAGGGTCTGCACAATCCACCACGTGGAGAAGAGCATCTC
SHR-A3 different from BN reference, non-synonymous, His to Arg

35. Location: chr6: 147084600 intron
SHR-A3 TTCTTTCCGGGTATAGAGCCTAAGTCACGGGCTT
SHR-B2 TTCTTTCCGGGTATAGAGCCTAAGTCACGGGCTT
SHR-A3 different from BN reference

36. Location: chr6: 147189280 exon
SHR-A3 AGCCGGTAACCGTAAAATGGAACCTGGAGCCCTGTCCAGCGGTGTG
SHR-B2 AGCCGGTAACCGTAAAATGGAACCTGGAGCCCTGTCCAGCGGTGTG
SHR-B2 different from BN reference, non-synonymous Ser to Tyr

37. Location: chr6: 147189135 exon
SHR-A3 AGCCACCCAGCCACCAAAAGCACTTGATCAAGAGAATTGGTA
SHR-B2 AGCCACCCAGCCACCAAAAGCACTTGATCAAGAGAATTGGTA
SHR-B2 different from BN reference, non-synonymous Asp to Asn

38. Location: chr6: 147189069 intron
SHR-A3 AATATTTAATCAGGAGGTCAGGCTGGGGTCAACCCCTTGTATAGAACA
SHR-B2 AATATTTAATCAGGAGGTCAGGCTGGGGTCAACCCCTTGTATAGAACA
SHR-B2 different from BN reference

39. Location: chr6: 147188923 intron
SHR-A3 CAGAAAGTGGTCCTCTGGAATGACTACCAGTAGCTCACATCAGGGACA
SHR-B2 CAGAAAGTGGTCCTCTGGAATGACTACCAGTATCTCACATCAGGGACA
SHR-B2 different from BN reference

40. Location: chr6: 147188913 intron
SHR-A3 CTCTGGAATGACTACCAGTAGCTCACATCAGGGACACACAGA
SHR-B2 CTCTGGAATGACTACCAGTATCTCACATCAGGGACACACAGA
SHR-B2 different from BN reference

41. Location: chr6: 147188770 intron
SHR-A3 TCTCCCTTCCAGGCCCATTAATGCCAGTCTTTTCTCTGC
SHR-B2 TCTCCCTTCCAGGCCCATTAATGCCAGTCTTTTCTCTGC
SHR-B2 different from BN reference

42. Location: chr6: 147188379 exon
SHR-A3 GTCAGTACCCTCCATATCCAGCACCAGGACTGGA
SHR-B2 GTCAGTACCCTCCATATCCAGCACCAGGACTGGA

SHR-B2 different from BN reference, synonymous

43. Location: chr6: 147188230 intron

SHR-A3 CTGGGATGGGCGTAAGAATAAATGCCTGCGTGGACG

SHR-B2 CTGGGATGGGCGTAAGAATAAATGCCTGCGTGGACG

SHR-B2 different from BN reference

44. Location: chr6: 147188078 exon

SHR-A3 ACCAGCTTCTACCCCGCATCCATCAGTGTGGAGT

SHR-B2 ACCAGCTTCTACCCCGCATCCATCAGTGTGGAGT

SHR-A3 different from BN reference (Ala to Pro)

45. Location: chr6: 147187959 exon

SHR-A3 ACAGCAAGCTCAGTGTGGACACGGACAGTTGGATGCGAG

SHR-B2 ACAGCAAGCTCAGTGTGGACACAGACAGTTGGATGCGAG

SHR-B2 different from BN reference, synonymous

Haplotype structure in SHR strains across this region. SHR-A3 and SHRSP/Gla are injury-prone strains. SHR-B2, SHR and SHR/NHsd are injury resistant strains. SHR lines with the same genotype as SHR-A3 at each variant site are colored pink at that site. SHR lines with the same genotype as SHR-B2 are shaded green when this genotype differs from the injury-prone lines. Genome sequence variation for SHRSP/Gla, SHR, SHR/NHsd was provided by the Rat Genome Database.

Variant #	SHR-A3	SHRSP/Gla	SHR-B2	SHR	SHR/NHsd
1	G	G	A	A	A
2	C	C	T	T	T
3	A	A	T	T	T
4	A	A	C	C	C
5	T	T	C	C	C
6	G	G	T	T	T
7	T	T	C	C	C
8	AG	AG	TA	TA	TA
9	GT	GT	AC	AC	AC
10	G	G	A	A	A
11	G	G	A	A	A
12	G	G	A	A	A
13	C	C	T	T	T
14	C	C	G	G	G
15	C	C	T	T	T
16	C	C	T	T	T
17	A	A	G	G	G
18	G	G	A	A	A
19	A	A	G	G	G
20	C	C	T	T	T
21	A	A	T	T	T
22	A	A	G	G	G
23	T	T	C	C	C
24	A	A	T	T	T
25	G	G	A	A	A
26	C	C	T	T	T
27	C	C	T	T	T

28	C	C	G	G	G
29	C	C	T	T	T
30	A	A	C	C	C
31	C	C	T	T	T
32	A	A	C	C	C
33	T	T	C	C	C
34	G	G	A	A	A
35	A	A	G	G	G
36	C	C	A	A	A
37	A	A	G	G	G
38	G	G	A	A	A
39	A	A	G	G	G
40	G	G	T	T	T
41	C	C	A	A	A
42	T	T	C	C	C
43	A	A	G	G	G
44	C	C	G	G	G
45	G	G	A	A	A

Dok3 variants (positions from rn5):

1. Location: chr17:11747889 proximal promoter

SHR-A3 AAGCTCCCCATAGGCAGGTACGGTTTCTTGGAACAGCAAGG

SHR-B2 AAGCTCCCCATAGGCAGGTATGGTTTCTTGGAACAGCAAGG

SHR-B2 differs from BN reference seq

2. Location: chr17:11748271 intron

SHR-A3 GTGAAGTGAAAGCTGGAGACGGGAGGTTCTTGGCCCAAGAA

SHR-B2 GTGAAGTGAAAGCTGGAGACAGGAGGTTCTTGGCCCAAGAA

SHR-A3 differs from BN reference seq

3. Location: chr17:11748474 proximal promoter

SHR-A3 CAGGCTGGTTCTCCTGGAGAGAGATGGGCTGGGAATCTAT

SHR-B2 CAGGCTGGTTCTCCTGGAGAGAGATGGGCTGGGAATCTAT

SHR-A3 differs from BN reference seq

4. Location: chr17:11749072 exon 2

SHR-A3 GCCGTAGAGGGGAACGCCGGGTCATACGCTTGCTGACTGT

SHR-B2 GCCGTAGAGGGGAACGCCGGATCATACGCTTGCTGACTGT

SHR-A3 differs from BN reference seq, non-synon Ile to Val (I71V)

5. Location: chr17:11749109 exon 2

SHR-A3 CTGTGTATCTGTTCTGCCGGTGGATGGTGAGAGTTGCCCA

SHR-B2 CTGTGTATCTGTTCTGCCGGCGGATGGTGAGAGTTGCCCA

SHR-A3 differs from BN reference seq, non-synon Ala to Val (A83V)

6. Location: chr17:11749790 intron

SHR-A3 TCCTACCAAGTTGCTCATGGAGCAGCTGGAGAGGTGCTGC

SHR-B2 TCCTACCAAGTTGCTCATGTTGCAGCTGGAGAGGTGCTGC

SHR-B2 differs from BN reference seq

7. Location: chr17:11750490 intron

SHR-A3 CTAAAACCCACTGAACTGGGTACCTTAAAATAGTAATGTCC

SHR-B2 CTAAAACCCACTGAACTGGGAACCTTAAAATAGTAATGTCC

SHR-B2 differs from BN reference seq

8. Location: chr17:11750514 intron

SHR-A3 TTAAAATAGTAATGTCCAGGGCTTGAGAAATGACTCCGTAG

SHR-B2 TTAAAATAGTAATGTCCAGGACTTGAGAAATGACTCCGTAG

SHR-B2 differs from BN reference seq

9. Location: chr17:11750578 intron

SHR-A3 AGAGTAGTAGAGTTCAATTCACAGCAACCACATGGCAGCTC

SHR-B2 AGAGTAGTAGAGTTCAATTCACAGCAACCACATGGCAGCTC

SHR-B2 differs from BN reference seq

10. Location: chr17:11750642 intron

SHR-A3 AGAGGACCTGACACCCTCACCCAATCCAATACACACAAAA

SHR-B2 AGAGGACCTGACACCCTCACCCAATCCAATACACACAAAA

SHR-B2 differs from BN reference seq

11. Location: chr17:11750740 intron

SHR-A3 TGTAGACAAGGTTTCTCCATATAGCCCTGGCTGTTCTAGAA
 SHR-B2 TGTAGACAAGGTTTCTCCATGTAGCCCTGGCTGTTCTAGAA
 SHR-B2 differs from BN reference seq

12. Location: chr17:11751049 intron
 SHR-A3 CTGTCTTGAAAACAAAAAAGGAAAAAAAAAAGTGCAGGTAG
 SHR-B2 CTGTCTTGAAAACAAAAAAGGAAAAAAAAAAGTGCAGGTAG
 SHR-B2 differs from BN reference seq

13. Location: chr17:11751393 intron
 SHR-A3 CCCTGGAGTGTGGGTGAGAGTGGAGACTGATGGCGGAGAGTG
 SHR-B2 CCCTGGAGTGTGGGTGAGAGTGGAGACTGATGGCGGAGAGTG
 SHR-B2 differs from BN reference seq

14. Location: chr17:11752923 3'-UTR
 SHR-A3 TGCTCAGTGTAGCAAACGCCGGCCTCGGCTGGACCCTGAG
 SHR-B2 TGCTCAGTGTAGCAAACGCCGGCCTCGGCTGGACCCTGAG
 SHR-A3 differs from BN reference seq

Haplotype structure in SHR strains across this region. SHR-A3 and SHRSP/Gla are injury-prone strains. SHR-B2, SHR and SHR/NHsd are injury resistant strains. SHR lines with the same genotype as SHR-A3 at each variant site are colored pink at that site. SHR lines with the same genotype as SHR-B2 are shaded green when this genotype differs from the injury-prone lines. Genome sequence variation for SHRSP/Gla, SHR, SHR/NHsd was provided by the Rat Genome Database.

Variant #	SHR-A3	SHRSP/Gla	SHR-B2	SHR	SHR/NHsd
1	C	C	T	T	T
2	G	G	A	A	A
3	A	A	G	G	G
4	G	G	A	A	A
5	T	T	C	C	C
6	GA	GA	TT	TT	TT
7	T	T	A	A	A
8	G	G	A	A	A
9	C	C	T	T	T
10	G	G	A	A	A
11	A	A	G	G	G
12	A	A	-	-	-
13	T	T	C	C	C
14	G	G	A	A	A

Src variants (positions are rn5):

1. Location: chr3:158138524 Promoter

SHR-A3 CAGGACCTTAGTCTGCCTATCTGCTTAGTGGGTAGGGTGTCTTGTCTGTT

SHR-B2 CAGGACCTTAGTCTGCCTATCTGCTTAGTGGGTAGGGTGTCTTGTCTGTT

SHR-A3 differs from BN reference sequence

2. Location: chr3:158138450 Promoter Kozak consensus sequence

SHR-A3 GGGATTTCTGTGCGCCCCAGCCAGGACCATGGGCAGCAACAAGAGCAAGC

SHR-B2 GGGATTTCTGTGCGCCCCAGCCAGGACCATGGGCAGCAACAAGAGCAAGC

SHR-A3 differs from BN reference sequence

3. Location: chr3:158136014 Intron

SHR-A3 TATTCACCCCTCAAGATCCAGGGTGGGGCTGCCCTCCCTGCAAGCAGGT

SHR-B2 TATTCACCCCTCAAGATCCAGGGTGGGGCTGCCCTCCCTGCAAGCAGGT

SHR-A3 differs from BN reference sequence

4. Location: chr3:158134950 Intron

SHR-A3 ACAGTGTTCCTCCAGGAAGTACTGAGCTCTGGGGGGCCGGGGCAGTACAG

SHR-B2 ACAGTGTTCCTCCAGGAAGTACTGAGCTCTGGGGGGCCGGGGCAGTACAG

SHR-A3 differs from BN reference sequence

5. Location: chr3:158131765 Intron

SHR-A3 ATGGCAACCAAGCCAGGCTGCTTCCTGTGGGCCTGGGGCTCAGCAGGAGA

SHR-B2 ATGGCAACCAAGCCAGGCTGCTTCCTGTGGGCCTGGGGCTCAGCAGGAGA

SHR-A3 differs from BN reference sequence

6. Location: chr3:158129031 Intron

SHR-A3 TGTGGCCAGGTCTCACACCAAGCCTCAGCCTCCTGATGTGAACAC

SHR-B2 TGTGGCCAGGTCTCACACCAAGCCTCAGCCTCCTGATGTGAACAC

SHR-A3 differs from BN reference sequence

7. Location: chr3:158128929 Intron

SHR-A3 AGTGCTGTGCGGAGGGAGTAGTGGGAAGTAGGTGTCCGGTCTCCCG

SHR-B2 AGTGCTGTGCGGAGGGAGTAATGGGAAGTAGGTGTCCGGTCTCCCG

SHR-A3 differs from BN reference sequence

8. Location: chr3:158127846 Intron

SHR-A3 CAGGCTGACCTCTGCTCAGATGCCCCACCGGCAGACTGAGGGTAAC

SHR-B2 CAGGCTGACCTCTGCTCAGATGCCCCACCGGCAGACTGAGGGTAAC

SHR-A3 differs from BN reference sequence

9. Location: chr3:158127694 Intron

SHR-A3 TCTTTTGTCCCTTACCACTGACAAAGATCCCTGTTGTTGCTGGTGTG

SHR-B2 TCTTTTGTCCCTTACCACTGACAAAGATCCCTGTTGTTGCTGGTGTG

SHR-A3 differs from BN reference sequence

10. Location: chr3:158127366 Intron

SHR-A3 GCCTCCGTTGCACCTTGAGTTGGTTTACGGTGAGACCCTGTCTCAGAACAA

SHR-B2 GCCTCCGTTGCACCTTGAGTTGGTTTACGGTGAGACCCTGTCTCAGAACAA

SHR-A3 differs from BN reference sequence

11. Location: chr3:158126261 Intron

SHR-A3 TACACAGCTCGGCAAGGTGGGAGTTCCTGGCGGTTATCTGATGGTATCGG

SHR-B2 TACACAGCTCGGCAAGGTGGGAGTGCCTGGCGGTTATCTGATGGTATCGG
SHR-A3 differs from BN reference sequence

12. Location: chr3:158125852 Intron

SHR-A3 TGCCTCTGGTCAGGACTCTTAGCCTCCAAGACAGTGTCTGTACAGCATA

SHR-B2 TGCCTCTGGTCAGGACTCTTAGCCTCCAAGCCAGTGTCTGTACAGCATA

SHR-A3 differs from BN reference sequence

Haplotype structure in SHR strains across this region. SHR-A3 and SHRSP/Gla are injury-prone strains. SHR-B2, SHR and SHR/NHsd are injury resistant strains. SHR lines with the same genotype as SHR-A3 at each variant site are colored pink at that site. SHR lines with the same genotype as SHR-B2 are shaded green when this genotype differs from the injury-prone lines. Genome sequence variation for SHRSP/Gla, SHR, SHR/NHsd was provided by the Rat Genome Database.

Variant #	SHR-A3	SHRSP/Gla	SHR-B2	SHR	SHR/NHsd
1	C	C	T	T	T
2	G	G	A	A	A
3	G	G	A	G	G
4	G	G	C	C	C
5	C	C	T	T	T
6	A	A	C	C	C
7	G	G	A	A	A
8	A	A	G	A	A
9	A	A	G	G	G
10	C	C	T	T	T
11	T	T	G	T	T
12	A	A	G	G	G

Syk variants (positions from rn5):

1. Location: chr17:14759592 proximal promoter

SHR-A3 GTTTCCTATTTTTAGCTTCAGAGTTTTTTTTTTTCATGTTACT

SHR-B2 GTTTCCTATTTTTAGCTTCAGAGTTTTTTTTTTTCATGTTACT

SHR-A3 differs from BN reference seq

2. Location: chr17:14730906 Intron

SHR-A3 GTGTTCAATCCCAGCATTACAAGGCAGAGTAGGGAATCTGTTC

SHR-B2 GTGTTCAATCCCAGCATTACAAGGCAGAGTAGGGAATCTGTTC

SHR-B2 differs from BN reference seq

3. Location: chr17:14728977 Intron

SHR-A3 CTGAGCCTCGCTGCCCCTGCACACCGCATGCCTGCTCCGGTTGTG

SHR-B2 CTGAGCCTCGCTGCCCCTGCACACCGCATGCCTGCTCCGGTTGTG

SHR-B2 differs from BN reference seq

4. Location: chr17:14721420 Exon

SHR-A3 GCCTGCCATGGACACCGAGGTATATGAGAGTCCTTACGCTG

SHR-B2 GCCTGCCATGGACACTGAGGTATATGAGAGTCCTTACGCTG

Synonymous, codon is Thr, third base of codon affected

SHR-A3 differs from BN reference seq

5. Location: chr17:14706170 3'UTR

SHR-A3 GGTACACGTGGTATCCACACAGAGGAAGCGAAGAATGAACAGGAA

SHR-B2 GGTACACGTGGTATCCACACTGAGGAAGCGAAGAATGAACAGGAA

SHR-A3 differs from BN reference seq

6. Location: chr17:14704598 3'UTR

SHR-A3 GGGTTGGGACTGACCATTTCGTTATCCGGATGTGACCAAGCAGAACGGAGG

SHR-B2 GGGTTGGGACTGACCATTTCGTTATCCGGATGTGACCAAGCAGAACGGAGG

SHR-B2 differs from BN reference seq

7. Location: chr17:14704464 3'UTR

SHR-A3 TCTGTTGAAAACGTGTCTTGCTGTCAAGATTAATTCTCTCCCCTG

SHR-B2 TCTGTTGAAAACGTGTCTTGCTGTCAAGATTAATTCTCTCCCCTG

SHR-B2 differs from BN reference seq

8. Location: chr17:14704198 3'UTR

SHR-A3 CCCTAATCTGCCTCGCCACATCCTACTGACCTCGCCACACCACATAACC

SHR-B2 CCCTAATCTGCCTCGCCACATACCACTGACCTCGCCACACCACATAACC

SHR-B2 differs from BN reference seq

9. Location: chr17:14704196 3'UTR

SHR-A3 CCCTAATCTGCCTCGCCACATCCTACTGACCTCGCCACACCACATAACC

SHR-B2 CCCTAATCTGCCTCGCCACATACCACTGACCTCGCCACACCACATAACC

SHR-A3 differs from BN reference seq

Haplotype structure in SHR strains across this region. SHR-A3 and SHRSP/Gla are injury-prone strains. SHR-B2, SHR and SHR/NHsd are injury resistant strains. SHR lines with the same genotype as SHR-A3 at each variant site are colored pink at that site. SHR lines with the same genotype as SHR-B2 are shaded green when this genotype differs from the injury-prone lines. Uncolored boxes indicate no genomic sequence variation data for SHRSP/Gla, SHR or SHR/NHsd. Genome sequence variation for SHRSP/Gla, SHR, SHR/NHsd was provided by the Rat Genome Database.

Variant #	SHR-A3	SHRSP/Gla	SHR-B2	SHR	SHR/NHsd
1	-		T		
2	A	A	G	G	G
3	G		-		
4	C	C	T	T	T
5	A	A	T	T	T
6	G	G	A	A	A
7	C	C	T	T	T
8	C	C	A	A	A
9	T	T	C	C	C

JunD variants (positions from rn5):

1. Location: chr16:20344584 proximal promoter
 SHR-A3 TGAGATCTTGTCTTAAAAA**T**AACCCAAAACAAAGATTAAA
 SHR-B2 TGAGATCTTGTCTTAAAAA**C**AACCCAAAACAAAGATTAAA
 SHR-B2 differs from BN reference seq

2. Location: chr16:20344303 proximal promoter
 SHR-A3 ACCCTGGTTGGCGCC**CAGT**CCCCGAGGGGCGTGCCTAT
 SHR-B2 ACCCTGGTTGGCGCC**CAGC**CCCCGAGGGGCGTGCCTAT
 SHR-A3 differs from BN reference seq

3. Location: chr16:20344265 proximal promoter
 SHR-A3 CTATGGTGGGCGTGACGC**C**GGGCGTGGCTTCTCAGAGG
 SHR-B2 CTATGGTGGGCGTGACGC**C**GGGCGTGGCTTCTCAGAGG
 SHR-B2 differs from BN reference seq

4. Location: chr16:20344104-5 proximal promoter
 SHR-A3 GAGAGAGAGAGAGAGAGAGAG**GA**CAAGAAACAGCAGGGGA
 SHR-B2 GAGAGAGAGAGAGAGAGAG**A**CAAGAAACAGCAGGGGA
 SHR-A3 differs from BN reference seq

5. Location: chr16:20344084-5 proximal promoter
 SHR-A3 GGGAGGAAGAGAGAGGG**G**GAGAGAGAGAGAGAGAGA
 SHR-B2 GGGAGGAAGAGAGAGGG**T**AGAGAGAGAGAGAGAGAGA
 SHR-B2 differs from BN reference seq

6. Location: chr16:20343878 proximal promoter
 SHR-A3 CCCGCCCTTTATGCAAAT**C**CACGACGTCACCTCGAGCC
 SHR-B2 CCCGCCCTTTATGCAAAT**C**CACGACGTCACCTCGAGCC
 SHR-B2 differs from BN reference seq

7. Location: chr16:20342252-4 3'-UTR
 SHR-A3 TTTTAAAGAAACGGGAAG**A**AAAAAAAAAATCCTCCC
 SHR-B2 TTTTAAAGAAACGGGAAG**A**AAAAAAAAAATCCTCCC
 SHR-A3 differs from BN reference seq

Haplotype structure in SHR strains across this region. SHR-A3 and SHRSP/Gla are injury-prone strains. SHR-B2, SHR and SHR/NHsd are injury resistant strains. SHR lines with the same genotype as SHR-A3 at each variant site are colored pink at that site. SHR lines with the same genotype as SHR-B2 are shaded green when this genotype differs from the injury-prone lines. Uncolored boxes indicate no genomic sequence variation data for SHRSP/Gla, SHR or SHR/NHsd. Genome sequence variation for SHRSP/Gla, SHR, SHR/NHsd was provided by the Rat Genome Database.

Variant #	SHR-A3	SHRSP/Gla	SHR-B2	SHR	SHR/NHsd
1	T	T	C	C	C
2	T	T	C	C	C
3	G		-		
4	GA		--		
5	--		TA		

6	C	C	T	T	T
7	---		AAG		

Supplemental statistical analysis for Figure 6.

SHR-A3 ctrl BP vs time

Call:
lm(formula = sample1\$BP ~ poly(sample1\$Week, 2, raw = TRUE))

Residuals:

Min	1Q	Median	3Q	Max
-24.5763	-7.7596	-0.4215	7.9176	24.1168

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	198.1606	5.0170	39.498	< 2e-16 ***
poly(sample1\$Week, 2, raw = TRUE)1	8.6372	2.5579	3.377	0.00115 **
poly(sample1\$Week, 2, raw = TRUE)2	-0.6258	0.2774	-2.256	0.02693 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 11.37 on 77 degrees of freedom
Multiple R-squared: 0.3089, Adjusted R-squared: 0.2909
F-statistic: 17.21 on 2 and 77 DF, p-value: 6.644e-07

SHR-A3 +MMF BP vs time

Call:
lm(formula = sample2\$BP ~ poly(sample2\$Week, 2, raw = TRUE))

Residuals:

Min	1Q	Median	3Q	Max
-30.8104	-3.2991	0.8181	6.3479	28.5903

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	190.2577	4.9032	38.803	<2e-16 ***
poly(sample2\$Week, 2, raw = TRUE)1	3.0319	2.4999	1.213	0.229
poly(sample2\$Week, 2, raw = TRUE)2	-0.2889	0.2711	-1.065	0.290

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 11.11 on 77 degrees of freedom
Multiple R-squared: 0.02247, Adjusted R-squared: -0.002918
F-statistic: 0.8851 on 2 and 77 DF, p-value: 0.4168

SHR-B2 ctrl BP vs time

Call:
lm(formula = sample3\$BP ~ poly(sample3\$Week, 2, raw = TRUE))

Residuals:

Min	1Q	Median	3Q	Max
-24.0196	-5.0269	-0.6765	5.2464	13.5330

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	164.9447	3.4117	48.346	<2e-16 ***
poly(sample3\$Week, 2, raw = TRUE)1	4.1114	1.7395	2.364	0.0213 *
poly(sample3\$Week, 2, raw = TRUE)2	-0.3412	0.1887	-1.809	0.0754 .

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 6.917 on 61 degrees of freedom
Multiple R-squared: 0.1513, Adjusted R-squared: 0.1235
F-statistic: 5.437 on 2 and 61 DF, p-value: 0.006719

SHR-B2 +MMF BP vs time

Call:
lm(formula = sample4\$BP ~ poly(sample4\$Week, 2, raw = TRUE))

Residuals:
Min 1Q Median 3Q Max
-16.149 -7.277 -3.458 7.755 19.859

Coefficients:

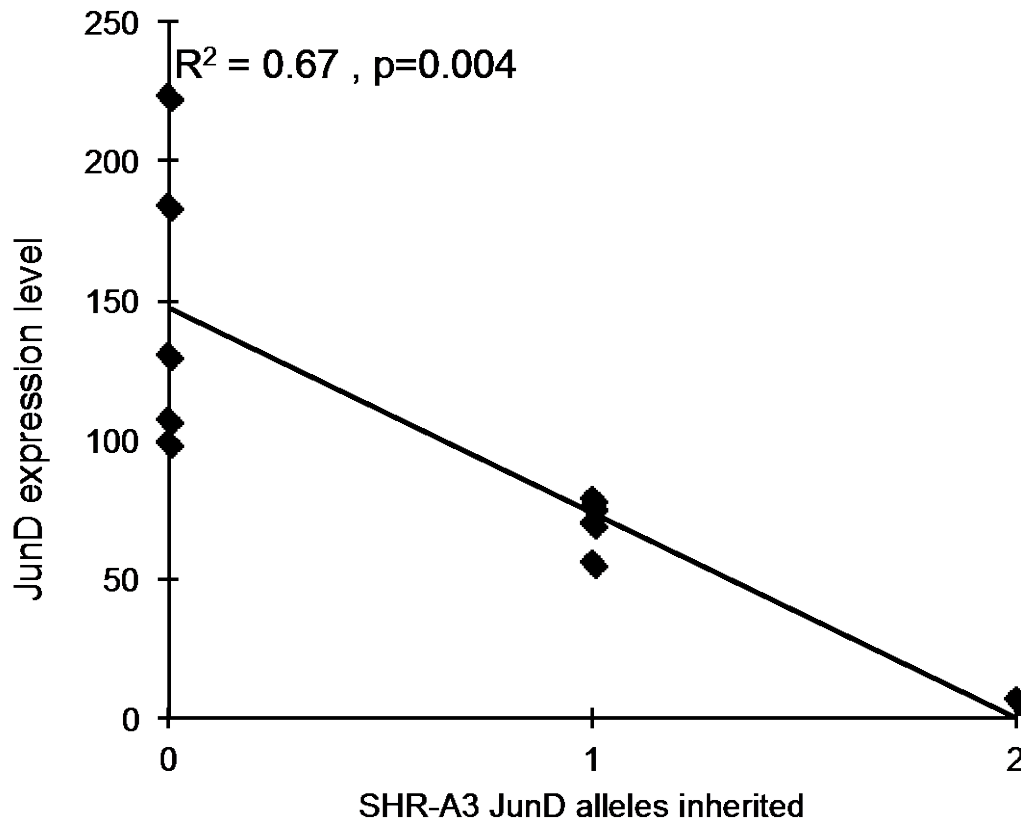
	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	164.9861	4.5248	36.462	<2e-16 ***
poly(sample4\$Week, 2, raw = TRUE)1	2.7700	2.3527	1.177	0.243
poly(sample4\$Week, 2, raw = TRUE)2	-0.3237	0.2573	-1.258	0.213

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 9.597 on 63 degrees of freedom
Multiple R-squared: 0.02533, Adjusted R-squared: -0.005608
F-statistic: 0.8188 on 2 and 63 DF, p-value: 0.4456

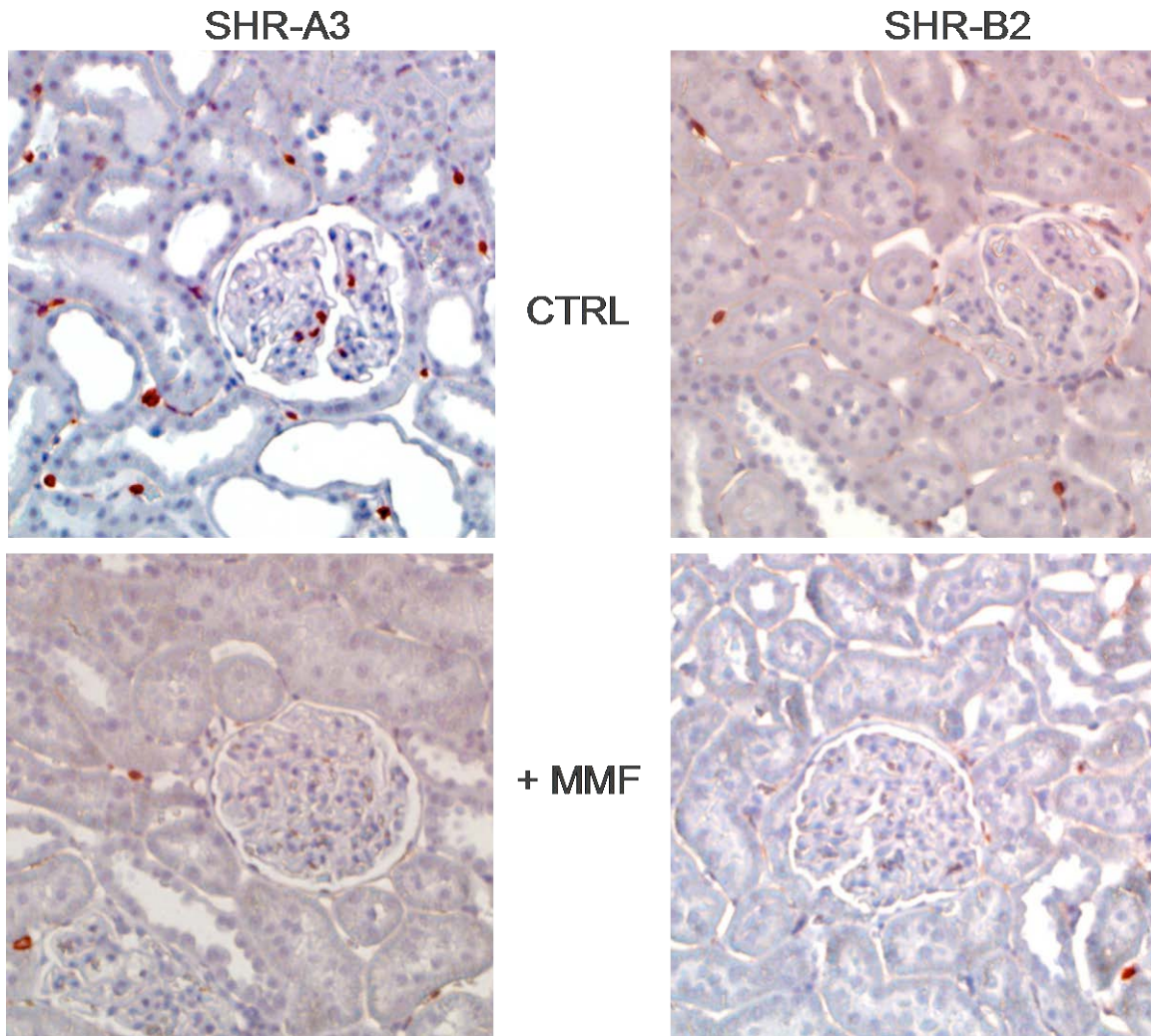
Supplemental Figure 1.

Renal JunD expression determined by Affymetrix array in F2 rats inheriting contrasting JunD alleles, is determined in cis by the JunD allele inherited.



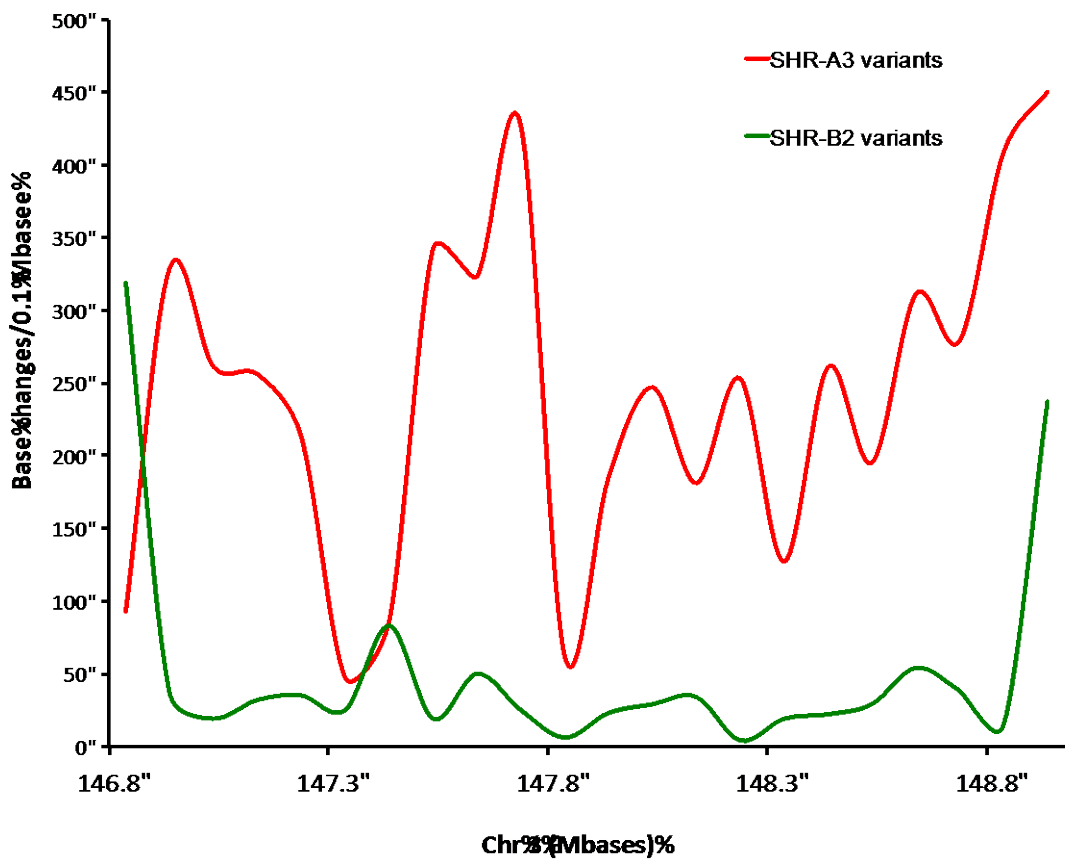
Supplemental Figure 2.

Representative photomicrographs of CD43 immunohistochemistry in SHR-A3 and SHR-B2 animals at 25 wks of age with (+ MMF) and without (CTRL) 8 weeks of MMF treatment



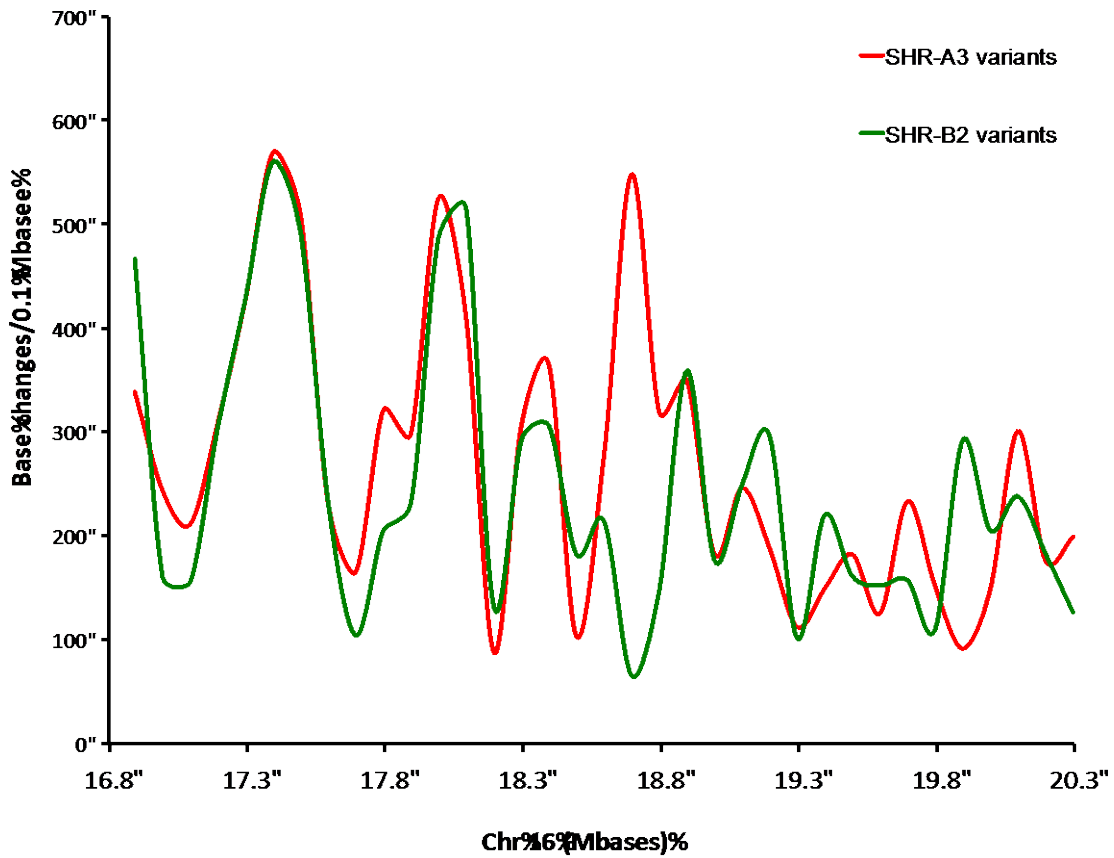
Supplemental Figure 3.

Divergence at the nucleotide level between the rat reference genome sequence derived from the Brown Norway strain and SHR-A3 and SHR-B2 in the haplotype block on chromosome 3 that contains *Src* (chr3:148,157,256-148,170,524). The vertical axis indicates the number of bases that differ in each rat strain compared to the reference. This value was calculated by dividing the region into bins of 100,000 bases and summing the number of variants for each bin across the entire region. In regions of identity by descent SHR-A3 and SHR-B2 are descended from a common ancestor and share the same divergence from the rat reference genome. In this block of non-identity by descent SHR-A3 is more divergent from the rat reference strain than SHR-B2 and differences in divergence vary across this region.



Supplemental Figure 4.

Divergence at the nucleotide level between the rat reference genome sequence derived from the Brown Norway strain and SHR-A3 and SHR-B2 in the haplotype block on chromosome 16 that contains JunD (chr16:19,239,694-19,241,529). In this block of non-identity by descent the degree of divergence is less between SHR-A3 and SHR-B2, possibly indicating that this region of the chromosome is derived from a more recent common ancestor that is shared by the two lines than is suggested by Supplemental Figure 3 where the nucleotide divergence is greater.



Supplemental Figure 5.

Divergence at the nucleotide level between the rat reference genome sequence derived from the Brown Norway strain and SHR-A3 and SHR-B2 in the haplotype block on chromosome 17 that contains Dok3 (chr17: 15,154,414-15,159,609) and Syk (chr17: 18,440,672-18,498,001).

