

Supplementary Table 1. Summary of RIIS/J polymorphism screening data for all mouse strains tested. Data for all mouse strains screened by PCR for RIIS/J size polymorphisms, small bowel DBA lectin staining patterns, and plasma VWF levels. “wt” = wild-type (similar to C57BL6/J); “ins*” = intermediate PCR size with *Mvwf1* SNPs; “del” = deletion, “ins” = insertion; “nd”= not determined; “nr” = no results.

Strain ID#	Strain Name	2.7kb del (15kb upstream)	6.4kb del (10kb upstream)	120bp ins (5kb upstream)	900bp del (intron 1)	DBA Lectin Staining Pattern	Plasma VWF+/-1SD (in arbitrary units)
1	129x1/SvJ	nd	wt	wt	nr	bowel+, vessel-	nd
2	A/J	nd	wt	wt	nr	bowel+, vessel-	nd
3	AKR/J	nd	wt	wt	del	nd	nd
4	AuSs/J	nd	wt	wt	nr	nd	nd
5	BALB/cByJ	nd	wt	wt	nr	nd	nd
6	BALB/cJ	nd	wt	wt	nr	nd	nd
7	C3H/HeJ	nd	wt	wt	nd	nd	nd
8	C57BL/10J	nd	wt	wt	nr	nd	nd
9	C57BL/6J	wt	wt	wt	wt	bowel+, vessel-	nd
10	C57BL/Ks-Bst+	nd	wt	wt	nr	nd	nd
11	c57BLKs/J	nd	wt	wt	wt	nd	nd
12	C57BR/cdJ	nd	wt	wt	wt	nd	nd
13	C58/J	nd	wt	wt	nr	nd	nd
14	CALB/Rk	nd	wt	wt	wt	nd	nd
15	CASA/Rk	nd	nr	wt	wt	bowel+, vessel-	18.87+/-2.37
16	CAST/Ei	nd	wt	wt	wt	nd	nd
17	CBA/J	nd	wt	wt	nr	nd	nd
18	CD1 #1	nd	wt	wt	nd	nd	nd
19	CD1 #2	nd	nd	wt	del	nd	nd
20	CHD/Ms	nd	nd	wt	nd	nd	nd
21	CZECHI/Ei	nd	wt	wt	nr	nd	nd
22	CZECHII/Ei	nd	wt	wt	nr	nd	nd
23	DBA/2J	nd	wt	wt	nr	nd	nd
24	DDK	nd	del	ins	nd	bowel-, vessel+	1.47+/-0.80
25	FVB/NJ	wt	nd	wt	nd	nd	nd
26	GR	nd	nd	ins	nd	bowel-, vessel+	nd
27	HMI/MsfB6C3F1	nd	nd	wt	nd	nd	nd
28	Id12b	nd	nd	wt	nd	bowel+, vessel-	nd

29	Ih12b	nd	nd	ins	nd	bowel-, vessel+	nd
30	Is/CamRk	nd	wt	wt	nr	nd	nd
31	KJR/Ms	nd	nd	wt	nd	nd	nd
32	KK/H1J	del	del	ins	del	bowel-, vessel+	6.26+/-0.74
33	LEWES/Ei	del	del	ins	del	bowel-, vessel+	3.65+/-0.32
34	LT/ChRe	nd	wt	wt	nr	nd	nd
35	MA	nd	nd	ins	nd	bowel-, vessel+	nd
36	M.MUS-NJL	nd	nd	wt	nd	nd	nd
37	MOLF/Ei	wt	nr	wt	del	bowel+, vessel-	17.81+/- 0.80
38	Mol-KOR7/Stm	nd	nd	wt	nd	nd	nd
39	Mor/Rk	nd	wt	wt	nr	nd	nd
40	MSM/Ms	nd	nd	wt	nd	nd	nd
41	Mus caroli	nd	nr	nr	nr	nd	nd
42	Mus pahari	nd	nr	nr	nr	nd	nd
43	NJL	nd	nd	wt	nd	nd	nd
44	NZB/B1NJ	nd	wt	wt	nr	nd	nd
45	Pancevo/Ei	nd	wt	wt	nr	nd	nd
46	PERA/Ei	del	del	ins	del	bowel-, vessel+	1.70+/-0.61
47	PERC/Ei	del	del	ins	del	bowel-, vessel+	11.72+/- 1.67
48	PL/J	nd	wt	wt	wt	nd	nd
49	PWK/Ph	wt	nr	wt	wt	nd	nd
50	RBA/Dn	nd	wt	wt	nr	nd	nd
51	RF/J	del	del	ins	del	bowel-, vessel+	3.53+/-1.00
52	RIIS/J	del	del	ins	del	bowel-, vessel+	2.36+/-0.18
53	SF/CamEi	del	del	ins	del	bowel-, vessel+	2.48+/-0.22
54	SJL/J	nd	wt	wt	nr	nd	nd
55	SKIVE/Ei	nd	wt	wt	nr	nd	nd
56	SM/J	wt	nd	wt	nd	nd	nd
57	SPRET/Ei	nr	nr	wt	nr	nd	nd
58	SPRET(RIKEN)	nd	nd	wt	nd	nd	nd
59	STS	nd	nd	ins	nd	nd	nd
60	SWR/J	del	del	ins	del	bowel-, vessel+	nd
61	TIRANO/Ei	nd	wt	nr	nr	nd	nd
62	WMP/Pas	nd	wt	wt	nr	nd	nd
63	WSA	del	nd	ins	nd	bowel-, vessel+	nd
64	WSB/Ei	wt	del	ins*	wt	bowel-, vessel-	22.35+/- 1.52
65	ZALENDE/Ei	nd	wt	wt	nr	nd	nd

Supplementary Table 2. Primers.

Genotyping	ID	Primer Sequence
118bp ins (-5kb upstream)	1F	5'-GTCCCACGATGTCTCCATTT-3'
	1R	5'-GAGCAAGTTACAGGCCAAGC-3'
6.4kb del (-10kb upstream)	2F	5'-GCCAGCAAATAGAGAGACCC-3'
	2R	5'-AGTGAGGTCCATTTCGCAAAC-3'
2.7kb del (-15kb upstream)	3F	5'-GCTAGCCCAGCACCTACAAG-3'
	3R	5'-AAGTAGTGCCCTGCCTTTCA-3'
0.9kb del (intron 1)	4F	5'-TCTCTCATCACGTGACCTGG-3'
	4R	5'-TGGCTGTCTGTGAAGGAGTG-3'
BAC vector	5F	5'-CTCCGCACCCGACATAGATA-3'
	5R	5'-GAGAGCCTTCAACCCAGTCAGC-3'
<i>B4galnt2</i> null allele	6F1	5'-CTGGTTTGCTGGGAGGAAC-3'
	6F2	5'-CGCCTTCTATCGCCTTCTTGACGAGTTCTT-3'
	6R	5'-GTGACCGAACAAGAACATGG-3'
RIIS/J BAC insert	7F	5'-GCCAAGCAAAACTACACAG-3'
	7R	5'-GACTAAGGAGGCAAAAGCA-3'
RIIS/J BACs		
	8F	5'-GCCTGGTTACCCAAGTTCAA-3'
	8R	5'-TTGGTACATGGATGGTGGTG-3'
	9F	5'-TACAAAGGCCATGTGAGCTG-3'
	9R	5'-GACTCGGGTGGTGTGCTTAT-3'
	10F	5'-TGCTAGAACAGGCTGGAGGT-3'
	10R	5'-CACCCCGCACTCTGTTATTT-3'
	11F	5'-AAACAGGCACTATCCCATGC-3'
	11R	5'-TCACAGGAAAACAGCACAGG-3'
	12F	5'-GTCTTCTGGCATTACAGC-3'
	12R	5'-TCTTTTGCCAGCTTCAGGTT-3'
	13F	5'-CCCCAAAGCAAACAAAAGA-3'
	13R	5'-GCTAGGGGTAGGATCGGAAG-3'
	14F	5'-CACTCCTTACAGACAGCCA-3'
	14R	5'-TTGGCTGGGAGTTTAGGGTA-3'
	15F	5'-GCAGACTTCCTCAGTTTCACAA-3'
	15R	5'-CACAGCTGACCTGTCTAGGAAA-3'
	16F	5'-GCCAAGCAAAACTACACAG -3'
	16R	5'-GACTAAGGAGGCAAAAGCA -3'
	17F	5'-GCCAGCAAATAGAGAGACCC-3'
	17R	5'-AGTGAGGTCCATTTCGCAAAC-3'
	18F	5'-GCTAGCCCCAACACACAGTT-3'
	18R	5'-CACCACCAGGTTTTTGGTGT-3'
	19F	5'-CCCAGCCCAGTCTTTCTTTC-3'
	19R	5'-GGCTCCTTGCCAGAACTGT-3'
	20F	5'-CACACGTCACGGTAGCTTTG-3'

	20R	5'-TGGCTTCTATCCTTGGCATC-3'
	21F	5'-GCTGAAGTTGGGATCCTTCA-3'
	21R	5'-GTGTTCCACACAGACGGAGTT-3'
	22F	5'-CTTACGGGTCCCAAGAATGA-3'
	22R	5'-ACCTGTTCAACGGTCTCACC-3'
	23F	5'-GCCCTCTTCTGCTGTTTCTG-3'
	23R	5'-ACAGGGTTGGGAGACAGATG-3'
<u>Southern blot probe</u>		
	24F	5'-GGTGAGGTCCTGTCAGAATCA-3'
	24R	5'-CAAGAAGTCAGGCTGTTTTGG-3'
<u>RNase Protection Assay Probe</u> (promoter binding sites are lowercase)		
Genomic DNA fragment:	25F1	5'taatacgactcactatgggcgaAACTTGCCTAGATTTCTTCACCTG-3'
	25R1	5'-CTGGAAGTCATCGCAGCTC-3'
Exons 1-2 from cDNA:	25F2	5'-GTAGGCAGTCTGCAGAAGTGGCT-3'
	25R2	5'-aaattaaccctcactaaaggaatAGATGTCAGTGTAGGTAAAGA-3'
<u>5'-RACE</u>		
	26F	5'-CAGATGTCAGTGTAGGTAAAGAGT-3'
	26R	5'-TCCTCTGGTAGAAGCTTCAGC-3'
<u>Northern blot probe</u>		
	27	5'-TTGTTGCCCGCCGCTAATCTGTT-3'
<u>RIIS/J BAC Library Probe</u>		
	28F	5'-GCAGACTTCCTCAGTTTCACAA-3'
	28R	5'-CACAGCTGACCTGTCTAGGAAA-3'
<u>Mvwf1 Haplotype</u>		
	29F	5'-ACTTGGGAGGTAGCAGCAGA-3'
	29R	5'-GCATCTCCAGCTACCAGAG-3'
	30F	5'-GCCCTCTTCTGCTGTTTCTG-3'
	30R	5'-ACAGGGTTGGGAGACAGATG-3'
	31F	5'-CTTACGGGTCCCAAGAATGA-3'
	31R	5'-ACCTGTTCAACGGTCTCACC-3'
	32F	5'-ATGGGAACACACTGGGGATA-3'
	32R	5'-GTGGGTCCAGGCTTCTGATA-3'
	33F	5'-GCTGAAGTTGGGATCCTTCA-3'
	33R	5'-GTGTTCCACACAGACGGAGTT-3'
	34F	5'-TTGAATGGGAACAAAGCACA-3'
	34R	5'-GCTACCCTGGACAATGCTGT-3'
	35F	5'-CCGGCCATAACTTTCCTTTT-3'
	35R	5'-ACTTCTGTTCCAGCACGAT-3'
	36F	5'-CCCAGGACCTCTGGAAGAAT-3'
	36R	5'-AAGTAGTGCCCTGCCTTCA-3'
	37F	5'-GCTAGCCCCAACACACAGTT-3'
	37R	5'-CACCACCAGTTTTTGGTGT-3'
	38F	5'-TCAACCCAAGTCCAAGGAAG-3'
	38R	5'-CCAGCATTTGATCCCTGAGT-3'
	39F	5'-GCACAGAAAAGCCAAGAAGA-3'

	39R	5'-AGCTTCCTGAGCTGGGATTA-3'
	40F	5'-GTCCCACGATGTCTCCATTT-3'
	40R	5'-CGTGGACGGGAATCTACTGT-3'
	41F	5'-GCCTGGCTTCCTAACTGAAC-3'
	41R	5'-AGAGACAGCAGGGACAAGGA-3'
	42F	5'-AAATGCAAGCCATCTCTGCT-3'
	42R	5'-GATCCTCCTGCCTCAGTGAC-3'
	43F	5'-CTCCTTCCAGCATGGTTCTC-3'
	43R	5'-TAGCTTCCTGCTTCCTGCAT-3'
	44F	5'-CACTCCTTACAGACAGCCA-3'
	44R	5'-TTGGCTGGGAGTTTAGGGTA-3'
	45F	5'-TCTTCATCACGTGACCTGG-3'
	45R	5'-TGGCTGTCTGTGAAGGAGTG-3'
	46F	5'-GCCTGAACTGTGAACAGCA-3'
	46R	5'-GTCCATCTTGACTGGCCTTCAAG-3'
	47F	5'-CAAGGCGACAAGAAGAGAGA-3'
	47R	5'-GTTGTTTGGGCAGTTGCTTT-3'
	48F	5'-ATTCTAAATGCCACGGATGG-3'
	48R	5'-ACATGTGCCACCAAAGTGA-3'
	49F	5'-TGCTAGAACAGGCTGGAGGT-3'
	49R	5'-CACCCCGCACTCTGTTATTT-3'
	50F	5'-GCTCCCATGTAAAGCTCGTC-3'
	50R	5'-CCCCAGTGACGTGATGTATG-3'
	51F	5'-GGCTTCTTGAATCCCAGTG-3'
	51R	5'-AGAAACCTGGTGACCATTGC-3'
	52F	5'-GCTGGGTCACTGAATCCCTA-3'
	52R	5'-AGTGGTGAGGAATGGTGGAG-3'
	53F	5'-AGCCACCGTATTTGTTCTGG-3'
	53R	5'-AGCTACTGTGCTGGCTGGTT-3'

Supplementary Table 3. Haplotype block SNPs. Summary of SNPs from the *MvwfI* haplotype analysis. Most, but not all, sites are polymorphic between C57BL6/J and RIIS/J.

Primer Set	No. of SNPs	sequence length (bps)
29	4	856
30	2	759
31	0	910
32	1	899
33	2	896
34	3	1082
35	8	1096
36	3	909
37	65	1140
38	41	766
39	47	900
40	37	1048
41	48	846
42	23	1195
43	33	793
44	31	739
45	14	365
46	16	259
47	21	677
48	21	706
49	17	812
50	4	918
51	12	888
52	6	877
53	3	918