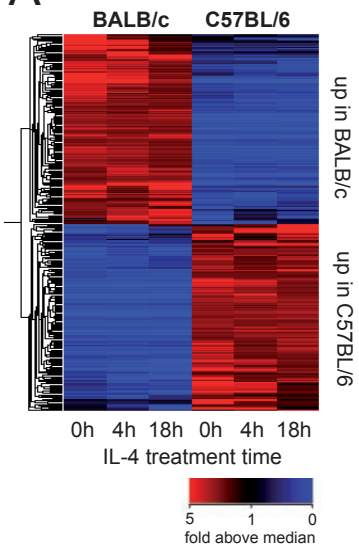
Supplemental Figure S1

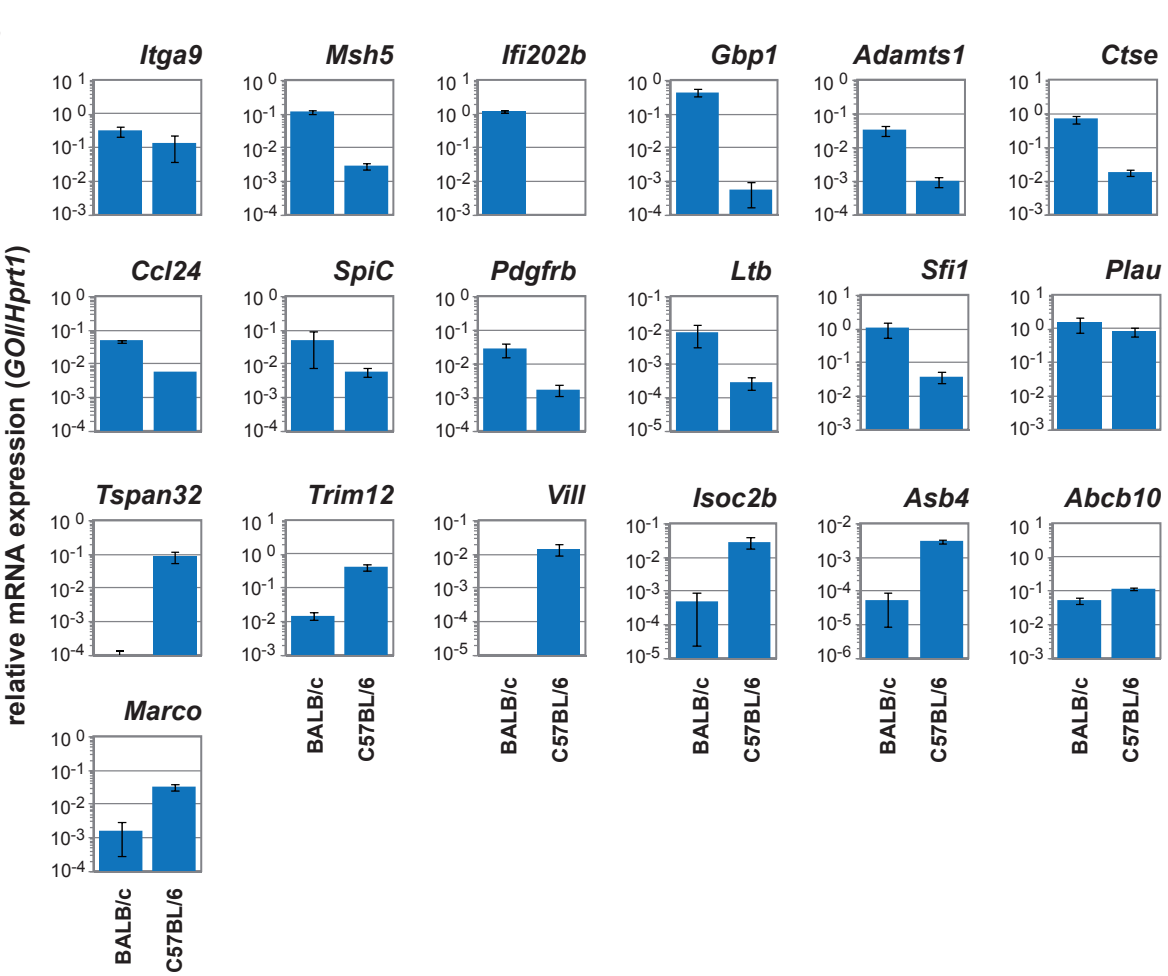
A



Term	GO ID	P-value	
C-type_lectin	IPR001304	2.461e-04	(99/5/14438/82)
Immune response	GO:0006955	5.173e-04	(339/8/12558/69)
Carbohydrate binding	GO:0030246	5.386e-04	(254/7/13943/78)

Term	GO ID	P-value	
Cellular polysaccharide metabolic process	GO:0044264	8.525e-05	(46/4/12558/64)
Carbohydrate metabolic process	GO:0005975	1.127e-03	(318/7/12558/64)

B



Supplemental Figure S2:

A

md_1

chr8: 124,744,953-124,745,822

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C57BL/6  ---------------------------------GAATGCCTAGGAGGGAA-CGCCCAGATGGTCAAGGAGTACTGACACGTCCTACGTCACTGTACACTG
BALB/c   ---------------------------------GAGATGCTAGGAGGGAA-CGCCCAGATGGTCAAGGAGTACTGACACGTCCTACGACACTGTACACCG

C57BL/6  AGCATCACACAGTGCATGGGGACCGTGGCTGCTCTCAGCAGGTGGCAGAGCAGGGCCAAGAGGGAATCAAAATCTTAACCTCCTTCATGAACCAGAAGTA
BALB/c   AGCATCACACGGTGCATGGGGACCGTGGCTGCTCTCAGCATGTGGCAGAGT------------GAATCAAAATCTTAACCTCCTTCATGAACCAGAAGTA

C57BL/6  GCAATGGAAAAGAAATTCCAGGGAGGA-TGGGAGGTGGTGGCAGGCTCAGCATGGGCTGGGGGACATGGCGGCTCTCTCCCTCTGTCCTCCCTTACATAT
BALB/c   GCAATGGAAGAGAAATTCCAGGGAGGACTGGGAGGTGGTGGCAGGCTCAGCCTGGGCTGGGGGACATGGCGGCTCTCTCCCTCTGTCCTCCCTTCCATAT

C57BL/6  GGC----------CCCCCCTGGTCTGCACCTCTGTGCTCTAACTACCCCGGGGACCTTTCTGTTCTTACATGTCACTAATCAGAAAATTGGGCTGGAGAG
BALB/c   GGCGGCGCCCCCCCCCCCCCCGTCTGCACCTCTGTGCTCTAACTGCCCCAGGGACCTTTCTGTTCTTACATGCCACTAATCAGAAAATTGGGCTGGAGAG

C57BL/6  ATGGCTCACAGTTAAGAGAACTGGCTGCTCTTCCACAGGACCCAGTGTTAATTCCCAGCGCCCACAGGAAGCTCACAACCATCTGTAACTCTAGCACTAG
BALB/c   ATGGCTCACAGTTAAGAGAACTGGCTGCTCTTCCACAGGACCCAGTGTTAATTCCCAGCGCCCACAGGAAGCTCACAACCATCTGTAACTCTAGCACTAG

C57BL/6  GGGAATCCAATGCCCTTAGTGCCCGGCGAACGCATGATGCACAGGCATATATGCAGACAAATCCCCCATGCACATAAAGAATGGGGAGGAAGAGGAGGGG
BALB/c   GGGA-TCCAATGCCCTTAGTGCCCGGCATACGCATGATGCACAGGCATATATGTAGACAAATCCCCCATGCACATAAAGAATGGGGAGGAAGAGGAGGGG

C57BL/6  GGGCAAGGGGA-GGAGAAGGGGAGGGGGATAGGGAGGAGGAAGAGAAAGAAGAAGGGGAAGGAAGAAGAGGAGGGGGAGAGAAAAAGGAGGGGGAAGAGG
BALB/c   GTGCAAGGGGAAGGAGAAGGGGAGGGGGATAGGGAGGAGGAAGAGAAAGAAGAAGGGGAAGGAAGAAGAGGAGGGGGAGAGAAAAAGGAGGGGGAAGAGG

C57BL/6  AAGAGAAGGAAGAGAAGAGAAAGAAGAAGAGGAGGAGGAGG------GGAAGGAGGAGGAAATGGAAAAAAAAAAAACTCTTTGGGTCCCAAAGTCAGAT
BALB/c   AAGAGAAGGAAGAGAAGAGAAAGAAGAAGAAGAGAGGAGGAGGAGGAGGGGAAGGAGGAGGAAATGGAAAA--CAAAACCTCTTTGGGTCCCAAAGTCAGAT

C57BL/6  ACTTTCCATAGACCCCAACTGTATAACAAGACAGAGCCAGGTGTCAAGAAGAGCAGAGCCCAGGGCCACAGCACCAATGACGAGAGCTTGTGAGACACAC
BALB/c   ACTTTCCAGAGACCCCAACTATATAACAAGACAGAGCCAGGTGTCAAGAAGAGCAGAGCCCAGGGCCACAGCACCAATGACGAGAGCTTGTGAGACACAC

C57BL/6  TCACCTGCCACAGACTCACCA
BALB/c   TCATCTGCCACAG-CTCACCA
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B

md_3

chr7:59,714,748-59,715,117

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BALB/c   ---------------------------------CTGAATT-ACTCTGTACACTTACTTTCTTAATGCCACATTGGAATCCCCTTTCCTGTATTATAAGTA

C57BL/6  TCAAAGTGTCAAAACACGTATTTACCGGTTCCTCCTATCCCTTTAGAAACTGGGAGGTGCAAATCACCATTATCTGTTGTGATTTCCCTCTGAAAAAAAT
BALB/c   TCAAAGTGTCAAAACACATATTTACCTGTTCCTCCTATCCCTTTAGAAACTGGGAGCTGCAAATCACCATTATCTGTTATGATTTTCCTCTGAAAATGAT

C57BL/6  CTGCATGTTAACTCTCAAGTGCTTTTATCCCTTCCCATCATTAATTATATTCACAGCAAGGCACAATATAATTTTAATTCCTTTAGGAATATTATTATTG
BALB/c   CTGCATGTTAACTCTCAAGTGCTTTTATCCCTTCC-ATCACTAATTATATTCACAGCAAGGCACAATATAATTTCAATTCCTTTAGGAATATTATTTTTA

C57BL/6  TGCAACACCCATATACCAAAATAAATGTTCTTTTTTTCTGTCTGCCTTTAATTTCCACACACCTTTAATCCACAATACTGTCTGTTCTTTGAAATATTAA
BALB/c   TGCAACACCCATGTACCAAAATAAATGTTCTTTTTTTCTGTCTGCCTTTAATTTCCACACACGTTTAATCCACAATACTGTCTGTTCTTTGAAATATTAA

C57BL/6  TGT
BALB/c   TGT
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C

md_4

chr7:104,152,267-104,153,014

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C57BL/6  ---------------------------------ATCTTTCAG--TTTCAAATTCTTTCTTATCTGCCATCAGCCTTTGCAGAACTACCTGCAGCTGCTCC
BALB/c   ---------------------------------ACCTTTCGA--TTTC-AATTCTTTCTTGTCTGCCATCAGCCTTTGCAGAACTACCTGCAGCTGCTCC

C57BL/6  TGTAAGAAAGGAATTGTAGCAGAGTCAAGCTGTGTGCTTAGTAGGACTGTTGTTCTATCCAAAGGCCAAAACCTTCTGGAAAGATAGAAAGCTAAGGATT
BALB/c   TGTAAGAAAGGAATTGTAGCAGAGTCAAGCTGTGTGCTTAGTAGGACTGTTGTTCTATCCAAAGGCCAAAACCTTCTGGAAAGATAGAAAGTTAAGGATT

C57BL/6  TCTACCTTTCTTTTAAAGGATTGTGATATGAATTCTTTACATAACAATTATATACACATATAGTTTTAATCTATTATGAATAAGTAGATAAGAAACTTTT
BALB/c   TCTACCTTTCTTTTAAAGGATTGTGATATGAATTCTTTACATAACAATTATATACACATATAGTTTTAATCTATTATGAATAAGTAGATAAGACACTTTT

C57BL/6  GGAAACAAGGCAAACAGGGACAAAATCAACTTGGTCTGGAAAGTTTACAGAAACCCAGGGAATGGCAACTAGAGTCTAGGAGTAGGAAGAAAATAATAAG
BALB/c   GAAATGAAGGCAAACAGGGACAAAATCAACTTGGTCTGGGAAGTTTACAGAAACCCAGGGAATGGCAACTAGAGTCTAGGAGTAGGAAGAAAATAATAAG

C57BL/6  GGATAGCCATGTACTTGGAAAAAGATTCCCCATCTTCTTTCAAAAAGGTGGTCTCAAGCCATGCCAGGTATGTAGATATCAGAGAATAATTTGCAACTTG
BALB/c   GAATAACCATCTACTTGGAAAAGGATTCCCCATCTTCTATCCAAATGGTGGTCTCAAGCCATGCCAGGTATGTAGATATCAGAGAATAATTTGCAACTTG

C57BL/6  CAGCCATCAGTTTTCTCCTTCAGTGGTCTGGTTTCTGAGTTCAGACTCAGGCCGATATACTTGGCAACAAGCCATTGAGGCATTGTTCCCAACACTCATC
BALB/c   CAGCCATCAGTTCTCTCCTTCAGTGGTCTGGTTTCTGATTTCAGACTCAGGCCGTTATACTTGGCAACAAGCCATTAAGGCATTGCTCCCAACCCTCATC

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BALB/c   TTATTTACTTTGACACGTAAAGTATAATCAGAGCTTTTCGTGGACATAAAATCTCAACAGTATACAACAAACTGTAAAAACACTTGCTATTGTTCTAGAG

C57BL/6  TTTGTCGCCCCTGGTAGATTCTCTTAGGATTAAGCTCAATGGATAGTCCCATTCTTTCAGGCCTCAGAAGGTAACAGGATG
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D

md_5

chr7:29,621,365-29,622,278

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C57BL/6  ATTGGTAAAGAGCTTACAAGAGGCCTGTGCTCGGGTAAGTGAGAAGCATTGCGCAGAGCGGTGCCCACGGGGACAACTCGCTGGTAATCCAGGAAACTGC
BALB/c   ATTGGTAAAGAGCTTACAAGAGGCCTGTGCTCGGGTAAGTGAGAAGCATTGCGCAGAGCGGTGCCCACGGGGACAACTCGCTGGTAATCCAGGAAACTGC

C57BL/6  ACCTTTCCCATGTTATTTTGTTTTTTTTTTTTTTTTTTATTTTTTTTTTTTTTTAAAAATTTTTTTTTTTTTTATTTGAAAGTACACTGTAGCTGTCTTCA
BALB/c   ACCTTTCCCATGTTATTTTGTTTT----------------------------------------------------------------------------

C57BL/6  GACACTCCAGAAGAGAGAGTCAGATCTCCTTACGGATGGTTGTGAGCCACCATGTGGTTGCTGGGATTTGAACTCCTGACCTTCGGAAGAGCAGTCGGGT
BALB/c   ----------------------------------------------------------------------------------------------------

C57BL/6  GCTCTTACCCACTGAGCCATCTCACCAGCCCGTTATTTTGTTTTAAAGAGTATTTCCTAATGTTATGTAGACGAGTGCTCTGTCTGCATGTACACCTGCG
BALB/c   ---------------------------------------------AAAGAGTATTTCCTAATGTTATGTAGACGAGTGCTCTGTCTGCATGCACACCTGCG

C57BL/6  TGCCAGAAGAGAACATCAACTCCCATTATAGATGGCTGTGAGCCACCATGTGGTTGCTGGAAAGTGACCTCTTAACAGCTGAGCCATCTCTCCTGCCCAT
BALB/c   TGCCAGAAGAGAACATCAACTCCCACTATAGATGGCTGTGAGCCACCATGTGGTTGCTGGAAAGTGACCTCTTAACAGCTGAGCCATCTCTCCTGCCCAT

C57BL/6  TGGTTGTTATTTTGTAAGCTTCTGCCAAAAACTTGGGTCTAAGTGAGAAAAGCAAGTTCTTTTTTTAAAAAAAG-AGCATTATTATTATTATTATTTTGT
BALB/c   TGGTTGTTATTTTGTAAGCTTCTGCCAAAAACTTAGATCTAAGTGAGAAAAGCAAGTTCTTTTTTTAAAAAGAGCATTATTATTATTATTATTTTGT

C57BL/6  TTCATGTATTGATTGATTGATTGATTGATTGCATGGGGCGAATTGGGGGGGGTCAAAGGACAACTGTGAGAGTTCGTTTTCTCTGTGCATGGTGTTGGTC
BALB/c   TTCATGTATTGATTGATTGATTGATTGATTGCATGGGGCGAGTTGGGGGGG-TCAAAGGACAACTGTGAGAGTTCGTTTTCTCTGTGCATGGTGTTGGCC

C57BL/6  TGGGGATCAGACTCAGGTCATCATTGGTTTTGTTTTCACATAGGAACGGTTTTATAACTGGCTTATCAGTCTTTACCTTCTCTTGTCCATCCAGAGGTCG
BALB/c   TGGGGATCAGACTCAGGTCATCATTGGTTTTGTTTTCACATAGGAACGGTTTTATAGCTGGCTTCTCAGTCTTTACCTTCTCTTGTCCATCCAGAGGTCG

C57BL/6  GATGCCTAAAATCCCAACCTCCTAACAACCTGAGTTACCCTCTGGTGACCAGGCTCAATACTAGAGCT
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E

Tbc1d2

chr4:46,658,967-46,659,728

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C57BL/6  AGACTCTTCACGAACACGCAGGCCACAGGTGACTCTGTATCTGATAAGCCATTTTAAAAAAAGAGTCTGAAATGTACCAAAAACTTGATGTGCCAAGGTG
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BALB/c   TCTATCCTAGGGTCATGTACAGTACCTTAAAGTGGAAATAACTTTCCCCAGGTTTCTGTTGCTGTTGTTGTTTTATTTTTATCATGTGTATGTATGTATT

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BALB/c   GGAGGGAGCATATATAATGTTTGTTCACATGTGTATGAACACACATGCACATGCATGTGCTATGTGTGGTGCCCAGAGGTTGATGTCAGATATCTTCTTG

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BALB/c   TGCCTCCCCAGGAATACCTGAGCACAAGGTACCACGCCCACCTGGCTTTCCCATGCACTCTGGGGAAATCTGCATGCTGTTTCTCAGGCTTGCATGGCAA

C57BL/6  TCCTTTATCTATGGAGCCATCTCTCTAGACATCCTCCTTTTTTGGGGGGGGGGGGTAGAGTCTCACTAAATTACTCAGACCTGGCCTGGATCTTGAAAT
BALB/c   TCCTTTATCTATGGAGCCATCTCTCTAGACATCCCCCTTTTTTGGGGGGG------CAGAGTCTCACTAAATTACTCATACCTGGCCTGGATCTTGAAAT

C57BL/6  CCATATTCCAGCGCTCAAGAACCTAGGATTACAGGTGCACACCACCAAGCCCGGCCAGAAATGAAGACTTGACAGCCCAGGAGGAGGCTGGGTAAAGCAA
BALB/c   CCATATTCCAATGCTCAAGAACCTAGGATTACAAGTGCACACCACAAAGCCCGGCTGGAAATGAAGACTTGACAGCCCAGGAGGAGGCTGGGTAAAGCAA

C57BL/6  GA
BALB/c   GA
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F

Cd48

chr1:173,518,415-173,518,932

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BALB/c   ----------------------------------------------------------CTCCCCTCTGCGACGCTGGTGGTCTCTGCCCAGTCACAGCCTCTCC

C57BL/6  TTACTCCCCACAGGCAACAGCAGATTCGGCCTCAGTGCTCAAAGTGCACTGCTGAAAAATCCATTCTTTTAAGCCAAGCTATTTTTCTTGTTGATCTCTA
BALB/c   TTACTCCCCACAGGCGACAGCAGATTCGGCCTCAGTGCTCAAAGTGCACTGCTGAAAAATCCATTCTTTTAAGCCAAGCTATTTTTCTTGTTGATCTCTA

C57BL/6  GTGGGTAGGAGAATTTGAAATCTCATTCCATGTGGTGTGATGGTAGTGGTCTGCTTTCCTGTTGTGTATGGTAATTCGTGAAATAGAGAAAAAACAGAAA
BALB/c   GTGGGTAGGAGAATTTTAAATCTCATTCCATGTGGTGTGATGGTAGTG-----CTTTCCTGTTGTGTATGGTAATTCGTAAGATAGAGAAAAAACAGAAA

C57BL/6  AACCTCATACGACTTCCGGTTTTGGGTTTTGCTTCCTGATTGAAGGGCAGGCGCCCTGACTTCTCTTACAGTTGTCTCCAGTGTTCTGGGGAAGCTTCTC
BALB/c   AACCTCATACAACTTCCGGGTTTGGGTTTTGCTTCCTGATTGAAGGGCAGGCGCCCTGCCTTCTCTTACAGTTGTCTCAAGTGTTTCGGGGAAGCTTCTC

C57BL/6  TAAGTATTATGTGCTTCATAAAACAGGGATGGTGTCTGGTCCTGGAACTGCTACTGCTGCCCTTGGGAACTGGATTTCAAGGTAGCTTCCTCCAAGTGTC
BALB/c   TAAGTATTATGTGCTTCAGAAAACAGGGATGGTGTCTGGTCCTGGAACTGCTACTGCTGCCCTTGGGAACTGGATTTCAAGGTAGCTTCCACCAAGTGTC

C57BL/6  CGGCTGTGCACTGAAGGCATGGCCAGCTGGGAAAGGGGAGGTGGGATGTAGCTCAACCCTGGAAATGAGCAT
BALB/c   CGGCTGTGCACTGAAGGCATGGCCAGCTGGGAAAGGGGAGGTGTGATGTAGCTCAACCCTGGAAATGAGCAT
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G

Tmtc2

chr10:104,969,448-104,970,451

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BALB/c    -------------------TTTGTTGT-CTGTTAA-TGTGTGG--CTTCAAATTCCTGAGGACTTGGT--GTTCTGCCTCCCATCTTCTCAGGGAAGTAG

C57BL/6   TCCTTCATTGAGGATTCAAGAGGATTTACAGACATTCATGTTATGCTT-TTTTTTTTTTTCTGTAGGTCTGGAAGATGCAAATTTAGGTCCTCAGGCTTG
BALB/c    TCCTTCAT-GAGGATTCAAGAGGATTTACAGACATTCATGTTATACTTCTTTTTTTTTTTCTGTAGTTCTGGAAGATGCAAATTTAGGTC-TCAGGCTTG

C57BL/6   GGTACCAAGTGCTTCTATCCACTGAACCCTCCCTCCACCCAGCTTCAAGGAAATATTTTTAAGGTTTCCTAACAAAATAAAGCAAAATTGAAAACTATGT
BALB/c    GGTACCAAGTGCTTCTATCCACTGGAACCTTCCTTCCACCAGCTTCAAGGAAATATTTTTAAGGTTTCCTAACAAAATAAAGCAAAATTAAAAACTATGT

C57BL/6   TGATTTTTTTTTTGCTAGGGTTATGTAAGAAGAGAGAATATCCATTGAGACAACACTTCCATCAAATTGGCCTGTAAATAAGTCTGTGGGAGGCATTTTC
BALB/c    TGATTTTTTTT--GCTAGGGTTATGTAAGAAGAAAGAATATCCATTGAGACAACACTTCCATCAAATTGGCCTGTAAATAAGTCTGTGGGAGGCATTTTC

C57BL/6   TTGGTTAAAAGTTGATGTGGGAGGGCTCAGCCCATTGCAGGTGCTATCACACATAGGCTAGTGGTCCTGGATGCTATAAGAGGAGGTTATGCAAGCCATC
BALB/c    TTGGTAAAAAGTTGATGTGGGAGGGTCCAGCCCATTGTAGGGGCTATCACACATAGGCTAGTGGTCCTGGATGCTATAAGAGTAGGTTACACAAGCCATC

C57BL/6   AAGAGCTTGCCTTGTAAGCAGCACTCTCCCAGGTCTTCTACAGAAGTTCTGTCTCCAGGTACCTGCCTTGAATTCCTGTCCTGACTTCCTTCAGTGATGG
BALB/c    AAGAGCTTGCCTTGTAAGCAGCACTCTTCCAGGTCTTCTACAGAAGTTCTGTCTCCAGGTCCCTGCCTTGAATTCCTGTCCTGACTTCCTTCAGTGATGG

C57BL/6   ACTGTGACGTGAAAATATAAACCAAATAAACCCTCTCCAAGTTGCTTTTGATCAGAAGGCTTTACCATAGCAAGTGAAAATGAACAAGGACATGTACCTA
BALB/c    ACAGTGACGTGAAAATATAAACCAAATAAACCCTCTCCAAGTTGCTTTTGGTCAGAAGGCTTCACCATAGCAAGTGAAAATGAACAAGGACATGGACCTA

C57BL/6   CATTGATCCCATTTTTATAAACTTGTTGCTTCTAAGAAAAATTGCAAATGTATTGTGAAGATCTCCCCAGAAAGGGCGATTAGTCATCAAAAGCAGAGAT
BALB/c    CATTGATCCCATTTTTATAAACGTGTTGCTTCTAAGAAAAATTGCAAATGTATTGTGAAAATCTCCCCAGAAAGGGCGATTAGTCATCAAAAGCAGAGAT

C57BL/6   TTGACAAAAACAACAACAACAAACAAACAAACAAAAACAACAACAACAACAAACTTTTTT------AACTGATCACACCACCTAGCACAGAGGCACAAGT
BALB/c    TTGACAAAAACAACAACAACAAACAAACAAACAAAAACAACAACAAAAAAAACCCTTTTTTCCTTTAACTGATCACACCACCTAGCACAGAGGCACACGT

C57BL/6   TCATAGGC-AGGACCATGTTTCATTTGACAAACCAGGAATTCAGACTTGAGAGCAGTCTAGGCCACACCTCCTACCTTACCTCTCACAGATACCACAAAG
BALB/c    TCATAGGCGAGGACCGTGTTTCATTTGACAA-CCAGGAATTCAGACTTGAGAGCAGTCTAGGCCACGCCCCTACCCTACCTCTCACAGATACCACAAAG

C57BL/6   TGACCTACTGGTTGAATCAAGAAACAAAAGC
BALB/c    TGACCTACTGGT-GAATCGAGAAC--GAAGC
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H

Pgbd5

chr8:127,300,507-127,300,973

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C57BL/6   ------------------------------------CACTCTACCCACAGCTT-CTCAACAAATGCCCCTCACAAAACAAGCTTTCTATCTTTCAATTT
BALB/c    ------------------------------------CATCTCCAGCACAGTTTTCTCAACAAACACCCCTT-CAAAACAAGCTTTCTACCTTTCAATTT

C57BL/6   CCCTGTCTTCATTTTGACCAAGCC-TTGGTTAGGGCCAC-TCCACAC-TCAGGCATGGAAGGCATGCCTTACACTGACCAAGACCAAGCCATGCCCAATC
BALB/c    CCCTGCCTTCATTTTGACCAAGCCATTGGTTAGGGCCACCTCCACACATCAGGCATGGAAGGCATGCCTTACACTGACCAAGACCAAGCCATGCCCAGTC

C57BL/6   GCCCATTAAGCGCCCACAGGAATGAACTCTAGCTTTGACCCTACACTCTCAGACTGACCTGAGAATTAAAGCTGGTCACTGCCCTCTCAGAGCCCGGTCT
BALB/c    GCCCATTAAGCGCCCACAGGAATGAACTCAAGCTTTAACCCTACGCTCTCAGACTGACCTGAGAATTAAAGCCGGTCACTGCCCTCTCAGAGCCCGGTCT

C57BL/6   CCCTGCAGAAAACACCCAAAGAAGG------ACCCTGAAGGTGTCGGTCGGATCAGGTTGAAGAGTGGCACGAGCCAAGTGGTCCCTAATGTTCTAACGT
BALB/c    CCCTGCAGAAAACACCCAAAGGAGAGAGCCTAATCTGAAGATGTCGGTCGGATCAGGTTGAAGAGTGTCACGAGCCAAGTGGTCCCTAATGTTCTAACAT

C57BL/6   CTTTCTGTAAACCCAGTGGTTCCCTGCAACTTCACGTACCCGTGAGCCTCCTTAAAAGTCTAGAGACCAGTTGGTTGTGGTCCCAGGATCCAGGAATCAC
BALB/c    CTTTCTGTAAACCCAGTGGTTCCCTGCAACTTCACGTACCCATGACCCTCCTTAAAAGTCTAGAGGCCAGTTGGTTGTGGTCCCAGGATCCAGGAATCAT

C57BL/6   ACTCTACCAGGATC
BALB/c    ACTCTAACAGGATC
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I

Ttc12

chr9:49,224,882-49,225,570

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C57BL/6   ----------------------------------AAAGGAGAAGAAGGTACTAGGAAAGACCAGTGAATCGCTGGGACTAATGTGAGACAATTAGGAAGA
BALB/c    ----------------------------------AAAGGAGAAGAAGGTACTAGGAA-GACCAGTGAATCGCTGGGACTAATGTGAGTCAATTAGGAAGA

C57BL/6   AAAAGAAATAGCAAGAGAATTTAATACTGGGCTTCCAGGAACAGAGCTTTAAGTCACTAGCCAACTCTAGTAATTTATGGACGGCTTATCAGGAGTTGTA
BALB/c    AAAAGAAATAGCAAGAGAATTTAATACCGGGCTTCCAGGAACAGAGCTTTAAGTCACTAGCCAACTCTAGTAATTTATGGACGGCTTATCAGGAGTTGTA

C57BL/6   TGCTTTGCTGAGTATCAGGGAAAGTGGTGAATAAAAAACAAAATCCTTTTGTTTTGTTTGAAAAGCTTGTGATCTTGTGTGGGAGACAAACGTTAACACA
BALB/c    TGCTTTGCTGAGTATCAGGGAAAGTGGTGAATAAAAAACAAAATCCTTTTGTTTTGTTTGAAAAGCTTGTGATCTTGTGTGGGAGACAAACGTTAACACA

C57BL/6   AGCAGCTCTGAGATTCCTAAAACAGAAGCCTTCAGCTGTCTCCCTGCCTCTCTTCACTGTGTTGTCTACGCAGATTGGCATTCATAGACTGTCCTTTAGA
BALB/c    AGCAGCTCTGAGATTCCTAAAACAGAAGCCTTCAGCTGTCTCCCTGCCTCTCTTCACTGTGTTGTCTACCCAGATTGGCAATCATAGACTGTCCTTTAGA

C57BL/6   GGGATCACTCTACCCTCACACCCCACCTAAACAGATAAATTTGTTCACCTCACTCCAATTTCAGATCAATCTAATTATCCATATCTAGCAGCCTTGACTA
BALB/c    GGGATCACTCTACCCTCACACCCCACCTAAACAGATAAATTTGTTCACCTCACTCCAATTTCAGATCAATCTAATTATCCATATCTAGCAGCCTTGACTA

C57BL/6   GGGAGGCTAAACATTGATGAAGAAAAATGGATAAATATCTGGGGGGGGGGGGACTTACTGGTCTGTCAGTGACCCTCACTCTCCCAGATCCTTTACTATG
BALB/c    GGGAGGCTAAACATTGATGAAGAAAACTGGATAAATATCTGTGGGGGG---AACTTACTGGTCTGTCAGTGACCCTCACTCTCCCAGATCCTCTACTATG

C57BL/6   TCATCCTAGGTAGTCTATTATCCTCTCAAACACTTTCAAGTTTTGGACAATCTAAACCTGACGATTCCAAATAGAGGATTCTGCTTATTCATTCGGTGAG
BALB/c    TCATCCTAGGTAGTCTATTATCCTCTCAAACACTTTCAAGTTTTGGACAATCTAAACCTGACGATTCCAAATAGAGGATTCTGCTTATTCATTCGGTGAG

C57BL/6   GAAAGGGATGGTGTTAAGAAAGAG
BALB/c    GAAAGGGATGGTGTTAAGAAAGAG
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J

1600021P15Rik

chr16:28,833,612-28,834,468

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C57BL/6   ----------------------GTAGTCAACAATGTGTTGACAGAATGTTTCCCCAGAGAACGGAGGGGACCCAAGCACACAGCTCTCCCTCCTTTGTGC
BALB/c    ----------------------GTAGTCAACAATGTGTTGACAGAATGTTTCCCCAGAGAACGGAGGGGACCCAAGCACACAGCTCTCCCTCCTTTGTGC

C57BL/6   TCAGGCTGCTACACTGATCTCAGCTTGGGAGGAGGAAGTATGGCGGTTGAGGGAAAAGGTTTCACATGGAGAGCGCCTAATATCCTGTGTACCTCAGATA
BALB/c    TCAGGCTGCTACACTGATCTCAGCTTGGGAGGAGGAAGCATGGCGGTTGAGGGAAAAGGTTTCCCATGGAGAGCGCCTAATATCCTGTGTACCTCAGATA

C57BL/6   ATACACACATAACCACTGCTGGGCTTTAACGGAAGCCTATACTCTTAGCTTTGCCCTTCATAAACTTAGCTTTGTCCTTAGAGATCTTTAGGACCTACAA
BALB/c    ATACACACACAACCACTGCTGGGCTTTAACGGAAGCCTATACTCTTAGCTTTGCCCTTCATAAACTTAGCTTCGTCCTTAGAGATCTTTAGGACCTACAA

C57BL/6   CAGGCTATGGAATGATGAAGCTAACACGATCTGTCCGGCCCCAGGGCCGTGTTCTCCCATCTCACTGCATCCTCACTTCTTCCGTGACAACTCTATCTCT
BALB/c    CAGGCTATGGAATGATGAAGCTAACACGGTCTGTCCGGCCCCAGGGCCGTGTTCTCCCATCTCACTGCATCCTCACTTCTTCCGTGACAACTCTCTCTCT

C57BL/6   CCCGTGCAGCCACAGAAGGATGGCTACTGTTTACCTCAGACAACGGAACTTAACACAGGAACTACAGATTTTGCCTAAACCACAGCTAAAAGACAAATCT
BALB/c    CCCGTGCAGCCACAGAAGGATGGCTACTGTTTACCTCAGACAACGGAGCTTAACACAGGAACTACAGATTTTGCCTAAACCACAGCTAAAAGCCAAATCT

C57BL/6   GCCAAGCCAGCTTTGTTCCCATTAGCAAAATTTAGCAACAGCACTATTCCTTAGTCACCAAAACTCTATGTCAACAATCACCTGAGCACGAGTCTTTCAT
BALB/c    GCCAAGCCAGCTTTGTTCCCATTAGCAAAATTTAGCAACAGCACTATTCCTTAGTCACCAAGACTCTATGTCAACAATCACCTGAGCACGAGTCTTTCAT

C57BL/6   ATTTGGGGAAATTTCTCACATTAGGTTATCTTGGGCCACTGTGGGAACTGCCATAGATTGTCATCAATGACAAACATCCAACAAACAGCCCAAGTTCTGA
BALB/c    ATTTGGGGAAATTTCTCACATTAGGGTGTCTTGGGCCACTGTGGGAACTGCCATAGATTGTCATCAATGACAAACATCCAACAAACAGCCCAAGTTCTGA

C57BL/6   ACAAAAACAAAATCAGTAATATTAGCAAGATCTGTTGAGGACCTCTCAAATCTCCACTGAACTGTGTTCCAGACATGCAAAAGAGAAACAACAGCATATC
BALB/c    ACAAAAACAAAATCAGTAATATTAGCAAGATCTGTTGAGGCCCTCTCAAATCTCCACTGAACTGTGTTCCAGACATGCAAAAGAGAAACAACAGCATATC

C57BL/6   CGTGAAGGGCATCTTTGGGATGTTAAGTAGTGGGAAACATCAGACATTGGTCACTAACAATTAGAAATTCATAACTGAC
BALB/c    CGTGAAGGGCATCTTTGGGATGTTAAGTAGTGGGAAACATCAGACACTGGTCACTAACAATTAGAAATTCATAACTGAC
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K

Fggy (2310009E04Rik)

chr4:95,071,096-95,072,198

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C57BL/6   ----------------------------------------CCAGGCTACAAAGCTGAGGAGGAGTGGGCTGTCATAGAAGACAGCCTTTTACTTTAAG
BALB/c    ----------------------------------------CCAGGCTACAAAGCTGAGGAGGAGTGGGCTGTCATAGAAGACAGCCTTTTATTTTAAG

C57BL/6   AGGAAGAAAGATCCTGAATATGCTGAGAGAAGCCATAGAGAATCAGGTATTATTGTCATGTTGACTCCTTCCTTCCTGTACAAAATTTTCTCACCATCTT
BALB/c    AGGAAGAAAGATCCTGAATATGCTGAGAGAAGCCATAGAGAATCAGGTATTATTGTCATGTTGACTCCTTCCTTCCTGTACAAAATTTTCTCACCATCTT

C57BL/6   AGAGCATGTGGGAGACTTGCAGGACTATTCACTCTTATAGGAGCGGCGAATCTTTTCTGTTAATAAGACTGAAGTGCGCAGTACAGGCCTACTTGTTGCT
BALB/c    AGAGCATGTGGGAGACTTGCAGGACTACTCACTCTTATAGGAGCGGCGAATCTTTTCTGTTAATAAGACCGAAGTGAGCAGTACAGGCCTACTTGTTGCT

C57BL/6   TGTCCTCATCTCCCCTGCTTACCTAAACCGGATTACAATGTAACCAAAAACTAAATTGCATGAGGCTGGAACACATGAGCTCCCAGTAGAGTTCAAAGAT
BALB/c    TGTCCTCATCTCCCCTTCTTACCTAAACCGGATTACAATGTAACCAAAAACTAAATTGCATGAGGCTGGAACACATGAGCTCCCAGTAGAGTTCAAAGAT

C57BL/6   CACTGTTAAAAGAGGACACTGAGTTGAGTTTTCTCCCCTGGCCTGGGACTTACTTTCTGTAGGCTGTCACCAACGAAACTGAACCTGGAGGAGTGGTTCT
BALB/c    CACTGTTAAAAGAGGACACTGAGTTGAGTTTTCTCCCCTGGCCTGGGACTTAATTTCTGTAGGCTGTCACCAACGAAACTGAACCTGGAGGAGTGGTTCT

C57BL/6   TTAAGAAGCAGAATCTAAGGTAAGCCCCTCCATTTTCCAGGGATGTGGTGCTGTGAAGTAGTCATCACTGTGACTAAGTTATTTGAGGGGAAAG------
BALB/c    TTAAGAAGCAGAATCTAAGGTAAGCCCCTCCATTTTCCAGGGATGTGGTGCTGTGAAGTAGTCATCACTGTGACTAGGTTATTTGAGGGGAAAGAAAGGG

C57BL/6   ----------------------------------------------------------------------------------------------------
BALB/c    AATACAGGGACAGCACAATTCCCTAGGGTTGTTTTTGAGCAGAGAGTTTGTAGCATTTACCCCCTTCTAGGGATGGCTGAAATAGTTTTGCAGAGAGCAG

C57BL/6   ----------------------------------------------------------------------------------------------------
BALB/c    TCCCAGTTTCCAGGTCTCCCGCCTATCCTCATATGGCATTTGAATAAGCTTGTACATTTGCTAAACAATTAGCTGTGAAATCTATGACTTCCTGTGGTAC

C57BL/6   ----------------------------------------------------------------------------------------------------
BALB/c    ACTTCTCACAATATTTATACAGGCCATCATTTAGTGAACTGTATAAATATTTATGGCATGGAACAGCCTTTTGATCATAAATAGGGGCCAGGAGTCAGTG

C57BL/6   --------------------GCTTGGTATTACCTGAGTTTTAAGGCATCTTGTAGCCTGAGATATTAGGTATGTCTCAGGACTTGTGCACAGCTTGAATTT
BALB/c    TCGCCCATGCTGGGGACTGGCTTGGTATTACCTGAGTTTTAAGGCATCTTGTAGCCTGAGATATTAGGTATGTCTCAGGACTTGTGCACAGCTTGAATTT

C57BL/6   CTCTTCATTATTTTTCTATCTCTTTGCCATTTATTTTTCTATCTCTTTGCCATCGAGAGGCCATGAGCTTATTTTTCCTGAATGCCCTCCTCTACAACTG
BALB/c    CTCTTCATTATTTTTCTATCTCTTTGCCAT----------------------CGAGAGGCCATGGGCTTATTTTTCCTGAATGCTCTCCTCTAAAACTG

C57BL/6   TTTTTCTTTTTAGAGTATTCCTCTTTGCCCCAAAATAGTGAGTTGAAACCCAAGTTCCATTCCTCATTATTCATAAAGCAGGCTGTGGAATTTCCGTGAC
BALB/c    TTTTTCTTTTTAGAGTATTCCTCTTTGCCCCAAAATAGTGAGTTGAAACCCAAGTTCCATTCCTCATTATTCATAAAGCAGGCTGTGGAATTTCCGTGAC

C57BL/6   CTGACCTGGAATTATAGCCCCTCTGTTGCTGCTATGCTTTACCTAGTGCTGTCTTTGAATACCTCAGCTCATTTTCCTGAGAAATGGGGCTTCCACACTG
BALB/c    CTGACCTGGAATTATAGCCCCTCTGTTGCTGCTATGCTTTACCTAGTGCTGTCTTTGAATACCTCAGCTCATTTTCCTGAGAAATGGGGCTTCCACACTG

C57BL/6   CCTACTTGCTCAGCTAAAGATGAAATGAGATCATAGAGTCAGGTGGGCAGTTTGCTCAAGAAAGACCAGCTTTTGTGGCATTTGTTGTTTGTTATTGAAG
BALB/c    CCTACTTGCTCAGCTAAAGATGAAATGAGATCATAGAGTCAGGTGGGCAGTTTGCTCAAGAAAGACCAGCTTTTGTGGCATTTGTTG----TTATTGAAG

C57BL/6   TTGCAAAGGCTTTGATTTTCAGTTTTAGCTGAATGTTGTGGAAAGTGTCCGAAACTCACTACTGTATGCT
BALB/c    TTGCAAAGGCTTTGATTTTCAGTTTTAGCTGAATGTTGTGGAAAGTGTCCGAAACTCACTACTGTATGCT
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L

Fggy (2310009E04Rik)

chr4:95,074,498-95,075,968

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C57BL/6  ----------------------------------------CATGCCTCTGGGAATGCCCGTGTTCTCCCTTCTAGCTTTCTGTAAGCACAGCTTATGATGCA
BALB/c   ----------------------------------------CATGCCTCTGGGA-TGCCCGTGTTCTCCCTTCTAGCTTTCTGTAAGCACAGCTTATGATGCA

C57BL/6  TTCTCAAAGCGGACATCATCTACTGCATTTCTCAGAAAGGAACCCTGTTAAGTGACACATGATTGTACAAGCACAGACTGAGAAAGTCAAATAACTAAGG
BALB/c   TTCTCAAAGCGGACATCATCTACTGCATTTCTCAGAAAGGAACCCTGTTAAGTGACACATGATTGTACAAGCACAGACTGAGAAAGTCAAATAACTAAGG

C57BL/6  GATGGCTCTTTTCGCTTTTTTTT-CCTATTGGTTCACTGATAAAGGAGTTTACTTTAGAAAACCACCGCTGGAAACCAATTATATTGCAAGCACTGGAAG
BALB/c   GATGGCTCTTTTCGCTTTTTTTTTCCTATGGGTTCACTGATAAAGGAGTTTACTTTAGAAAACCACCGCTGGAAACCAACTATATTGCAAGCACTGGAAG

C57BL/6  GGAGTGGGGATGCAGCAATCAGTAACATCCCCTTTTCTCCAGGTTCAGTCCAATGAGGAGATGGACATACCACCAAAAACATGGTCCAGAGCGAACATTT
BALB/c   GGAGTGGGGATGCAGCAATCAGTAACATCCCCTTTTCTCCAGGTTCCGTCCAATGAGGAGATGGACATACCACCAAAAACATGGTCCAGAGCGAACATTT

C57BL/6  GAAATGAAAATACAGACACTGTACATATTGACAGCCTTTGTACATGTGCAAGAAAAGTGATAAGGTCCCCCTTAGAGAAGTAGAGGATGGAATTGGGAAG
BALB/c   GAAATGAAAATACAGACACTGTACATATTGACAGCCTTTGTACATGTGCAAGAAAAGTGATAAGGTCCCCCTTAGAGAAGTAGAGGATGGAATTGGGAAG

C57BL/6  GGAAGAGCAAGTGATGGGGGAGGACCTCCATCAGTGCAAAGCACAAGTATACTTCCAGGACTGTGGGAATATCTAGGATCCCAGTGGGCAGGGCCAGGGT
BALB/c   GGAAGAGCAAGTGATGGGGGAGGACCTCCATCAGTGCAAAACACAAGTATACTTCCAGGACTGTGGGAATATCTAGGACCCCAGTGGGCAGGGCCAGGGT

C57BL/6  AGCATTCATTCGGGTTAAGAAGCTCACAGAAAGTCTCACTTGAGGAAGACCTTAGGGTGTCTTATTCTATCTATTTCTATCTATTGTGATGATATACTGC
BALB/c   AGCGTTCATTCGGGTTAAGAAGCTCACAGAAAGTCTCACTTGAGGAAGACCTTAGGCTGTCTTATTCTATCTATTTCTATCTATTGTGATGATATTCTGC

C57BL/6  TGCCCCAAGAAAGAGTCTAGCACAGTAATCACTATGGTGTTCATCTGGCTTGACCCAGGATATCTGACTTGGGGTACTAGGACACAAAAGGACAGACAAA
BALB/c   TGCCCCGAGAAAGAGCCTAGCACAGTAATCACTATGGTGTTCATCTGGCTTGACCCAGGATATCTGACATGGGGTACTAGGACACAAAAGGACAGACACA

C57BL/6  CAGATACAAGTACAGGAAAGCCAGGACTGCATGGACCACACACACTCTGATAAAGATGCGCCATCAGAGTCTGCACTGTGCAGGTTGCAGTTATATATAG
BALB/c   CAGATGCAAGTACAGGAAAGCCAGGACTGCATGGACCACACACACTCTGATAAAGATGCGCCATCAGAGTCGGCACTGTGCAGGTTGCAGTTATATATAG

C57BL/6  TTGCAGGAGGAGCTGGGATTACTGTATAAATTTGCAAGAGATGGTGAGGTTATTCTATACACTTGTAGTGAGAGGCAGGGTTATTGTATACAGTTGTCCA
BALB/c   TTGCAGGAGGAGCTGGGATTATTGTATAAAGTTGCAGAAGATGGTGAGGTTATTCTATACACTTGTAGTGAGAGGCAGGGTTATTGTATACAGTTGTCCA

C57BL/6  AGAAGGCAGGACTATTATATATGTAGCTGAGCAAGGAGGCAGGCTTAGCTAATCTTGGTAGGGGAGTCTCTATAGGGGAACCGGCTCAGACTGTAAGCAT
BALB/c   AGAAGGCAGGGCTATTATAGATGTAGCTGAGCAAGGAGGCAAGCTTAGCTAATCTTGGTAGGGGAGTCTCTATAGGGGAACCGGCTCAGACTGTAAGCAT

C57BL/6  CTTGGATGAAGTTATTGCACTTGACCTATTTTTAAGGACCAGGGTAAGGTCTTGACTTTCCCATGGGTCTGAGGCATGTGGACATTAACATGGTCATACT
BALB/c   CTTGGATGAAGTTATTGCACTTGACCTATTTTTAAGGACCAGGGTAAGGTTTTGACTTTCCCATGGGTCTGAGGCATGTGGACATTGACATGGTCATACT

C57BL/6  CATGTCAAACAATCCATGTTCACTCAGGACTTCCTCTACTCCCTGTGAACCACTAAGAGCAAACAGGGAGGATGGGAATGACAACTCAACAGGTGTCTGG
BALB/c   CATGTCAAACAATACATGTTCACTCAGGACTTCCTCTACTCCCTGTGAACCACTAAGAGCAAACAGGGAGGATGGGAATGACAACTCAACAGGTGTCTGG

C57BL/6  GTTATTTAAAAATCTGCTTTTATTGGTTACTGGCTTAAAGAGAAGGTATCACTCCCAAGTGAATGAAAGAATGAAAGCTGGTACTCATGTTTATGTGAGC
BALB/c   GTTATTTAAAAATCTGCTTTTATTGGTTACTGGCTTAAAGAGAAGGTATCACTCCCAAGTGAATGAAAGAATGAAAGCTGGTACTCATGTTTATGTGAGC

C57BL/6  TCTCGAGGGGAAAAAAGTCAGGGACCCAGGGAGCCAGGAAGACCCACCTGCTGAGCCTGGGAGCCCTGTCATGCTCAGGGGAGGCTGTGAGCTTTATTAT
BALB/c   TCTCGAGGGGAAAAAAGTCAGGGACCCAGGGAGCCAGGAAGACCCACCTGCTGAGCCTGGGAGCCCTGTCATGCTCAGGGGAGGCTGTGAGCTTTATTAT

C57BL/6  TCTTGCTTCT
BALB/c   TCTTGCTTCT
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M

3110007F17Rik

chrX:119,220,163-119,220,873

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C57BL/6  ------------------TCTCGTTCAGCTGTTCTACCCACTGGTCTAGCTCCTTGGTGAATGCCTTGTCGTCTATGGCGGTGAGCTGCTCATCTCCGCC
BALB/c   ------------------TCTCGTTCAGCTGTTCTACCCACTGGTCTAGCTCCTTGGTGAATGCCTTGTCGTCTGTGGCGGTGAGCTGCTCATCTCCGCC

C57BL/6  GCCTCCCCCTCCGCTGATCCCCTGGCGGGACCGCTAAGCTGCAGAGAGCGCAGCCCGCGCCCCGCCCAAGCCCAGCCATTATCTTCGGGTCCCTGCTGTT
BALB/c   GCCTCCCCCTCCGCTGATCCCCTGGCGGGACCGCTAAGCTGCAGAGAGCGCAGCCCGCGCCCTGCCCAAGCCCAGCCATTATCTTCGGGTCCCTGCTGTT

C57BL/6  TGCCTCTAAGTCTGTGGCGGTTCCGTAGCTGTAGTGCCTGGCGGCCCCAGCCCCGCCCACGCGCTTCTGTCGCACCGCCCCCTGCGCTGTTGTCAGAGCG
BALB/c   TGCCTCTAAGTCTGTGGCGGTTCCGTAGCTGTAGTGCCTGGCGGCCCCAGCCCCGCCCACGAGCTTCTGTCGCACCGCCCCCTGCGCTGTTGTCAGAGCG

C57BL/6  CGGGACACAGTGAGGGAGGGGGGAATGGGCGAGCGGTCGCGCCGTTGGGAGGAGCAGTCCGGACCCATGCCCGTGCAGGCAGGACATGGGGAGAGCACGC
BALB/c   CGGGACACAGTGAGGGAGGGGGGAATGGGCGAGCGGTCGCGCCATTGGGAGGAGCAGTCCGGACCCCTGCCCGTGCAGGCGGGACGTGGGGAGAGCACGC

C57BL/6  AGCGACAGGCATCTGGCTTTCTGAGCCCTGGGATTTGGTGAGCGAACACTCGGAGTGGGATGGTTCGGCGCGCGCTGAGACCCGCTATCCCGGCCCCCGC
BALB/c   AGCGACAGGCATCTGGCTTTCTGAGCCCTGGGATTTGGCGAGCGAACACTCGGAGTGGGA----------------AGACCCGCTATCCCGGCCCCCGC

C57BL/6  CCACCTTTCCCAGCGGGCCTTTCCAGCGGTCCCGGGGCGGTCTTGGTGTACTGCCATGGTGGGTGGAGGTGCGCTTGGGGCCTGGTCGCTGGCCAGGGGG
BALB/c   CCACCTTTCCCAGCGGGCCTTTCCAGCCGTCCCAGGGCGGTCGAGGTGTACCGCCATGGTGG----AGGTGCGCTTGGGGCCTGGTCGCTGGCCAGGGGG

C57BL/6  GGCAGTCCCCCGCCGACCCCAGCCTGGCCCTGCCCGCGAGCCCGCCACCAGAGCACGGGACGCAGGAAAAGGGGGCGGGGAATGACGCGCGGGTGGAGGA
BALB/c   GGCAGTCCCCAGCCGACCCCAGCCTGGCCCTGCCCGCGCGCCGGCCGCCAGAGCACTGGACGCAGGAAAAGGGGACGGGGAATGACGCGCGGGTGGAGGA

C57BL/6  GTTTTCGCTGTGCGCCGCCAGCACAGTTG
BALB/c   GTTTTCACTGTGCGCCGCCAGCACAGTAG
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N

Arhgdib

chr6:136,897,634-136,898,449

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C57BL/6   ----------------------------------------TAATTATACAATCCATGACCTTAGGCAGCAGGGTACAGATGGTGCCTCACCCACCTAACC
BALB/c    ----------------------------------------TAATTATACAATCCATGACCTTAGGCAGCAGG-TACAGATGGTGCCTCACCCACCTAACC

C57BL/6   AGGAAGCCCTTTGCTCCTGACTGTGGGTGACAGCAATTGCATGTCTCCGTGGAGGCCTTGCCCTGACCCATCCCTACACGCACACACCTGCTACCACAGG
BALB/c    AGGAAGCCCTTTGCTCCTGACTGTGGGTGACAGCAATTGCATGTCTCCGTGGAGGCCTTGCCCTGACCCAACCCTACACGCACACACCTGCTACCACAGG

C57BL/6   GACATCTCCCAGCAGTGTTTTCTTGTACTTGGTTAGACTCTCGTCATCCTTGTCCATCTCCTGCAGCTCCTTCAAGGACTTCTGAGGGGGTGGCTTATAA
BALB/c    GACATCTCCCAGCAGTGTTTTCTTGTACTTGGTTAGACTCTCGTCATCCTTGTCCATCTCCTGCAGCTCCTTCAAGGACTTCTGAGGGGGTGGCTTATAA

C57BL/6   TTGAGCTTGCTGTCCAGGTCGTCGTCCGCCTCTTCCAGCTGTGGCTGTGCATCCTTCTCCGTCATCTTGATTGCTCTCTATTTCAGAGAGAGAATGATGG
BALB/c    TTGAGCTTGCTGTCCAGGTCGTCATCCGCCTCTTCCAGCTGTGGCTGTGCATCCTTCTCCGTCATCTTGATTGTTCTCTATTTCAGAGAGAGAATGATGG

C57BL/6   TTCATTAGGCGCTGGGGTTGCTACTGGTACCACCTTAGTGGAGATCTGTATTCATCGGTGATTTTCAAATTGTTCCTCAACACAGATATTCCATGAAATA
BALB/c    TTCATTAGGCGCTGGGGTTGCTACTGGTACCACCTTAGTGGAGATCTGTATTCATCGGTGATTTTCAAATTGTTCCTCAACACATATATTCCATGAAATA

C57BL/6   GATAGTATTTCCAGTCATTTCTCTGACTTGTCTTAATTTTTGCTTATAGAATAAAGCTATAAGAATGAACAGCTTTTCTGTGAGCCATGCACTACAGTGA
BALB/c    GATAGTATTTCCAGTCATTTCTCTGACTTGTCTTAATTTTTGCTTATAGAATAAAGCTGTAAGAATGAACAGCTTTTCTGTGAGCCATGCACTACAGTGA

C57BL/6   AGAAAGGTAACATAAACAATCCCAGCGATCGACCATTCTAGCTTAGCCC----------------------------------------------------
BALB/c    AGAAAGGTAACATAAACAATCCCAGCGATCGACCATTCTAGCTTAGCCCATTGCTATTCCCAGCGATCGACCATTCTAGCTTAGCCCATTGCTATTCCCA

C57BL/6   ----------------------------------------------------------------------------------------------------
BALB/c    GCGATCGACCATTCTAGCTTAGCCCCATTGCTATTCCCAGCGATCGACCATTCTAGCTTAGCCCATTGCTATTCCCAGCGATCGACCATTCTAGCTTAGC

C57BL/6   ----------------------------------------CATTGCTATTCCCAGTATGCGCAATCTGAGTTTTGCTGACTTCTGGACACTGGTCAATT
BALB/c    CCCATTGCTATTCCCAGCGATCGACCATTCTAGCTTAGCCCCATTGCTATTCCCAGTATGCGCAATCTGAGTTTTGCTGACTTCTGGACACTGGTCAATT

C57BL/6   ATCTGTGGTCAAAAGGCTGGTTTCTTCTTATTAATGTATTCTTTCGTTGAATACTTATCAGACCTTAAAGGGGAACCCTGGGGAAAACAGACCTCTAATG
BALB/c    ATCTGTGGTCAAAAGGCTGGTTTCTTCTTATTAACGTATTCTTTCCTTGAATACTTATCAGACCTTAAAGGGGAACCCTGGGGAAAACAGACCTCTAATG

C57BL/6   CCTGCCTGGCGGGTATGAACGGTTCTGCTCCATGCTGTTAATCATAGCT
BALB/c    CCTGCCTGGCGGGTATGAACGGTTCTGCTCCATGCTGTTAATCATAGCT
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O

Asb4

chr6:5,331,766-5,333,016

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C57BL/6   ---------------------------------CTGTCTCTTGGCTTCAGCCTGGTGGATCCCAGTAGCATACAGCAATAACTCAAGTCCATAGCCATTG
BALB/c    ---------------------------------CTGTCTCTTGGCT-CAGCCTGGTGGATCCCAGTAGCATACAGCAATAACTCAAGTCCATAGCCATTG

C57BL/6   AGTTATGGTATGTGGAGGCAGGGCTTCCAGCCAAGCCAGAAATGTATCAGATAGCTTTCAGCCAAGGCAATTTATTGTAGCATGTTGGTGTTTGTTCCTA
BALB/c    AGTTATGGTATGTGGAGGCAGGGCTTCCAGCCAAGCCAGAAATGTATCAGATAGCTTTCAGCCAAGGCAATTTATTGTAGCATGTTGGTGTTTGTTCCTA

C57BL/6   AGTCGCCTTTGCTGGTGACTGATGTACCATCCTTCTAACACTCCTGAAAACCTCATAGTCATGCTGAAGAAAGAAATTCACCCAGGAGAAACGCCAGACG
BALB/c    AGTCGCCTTTGCTGGTGACTGATGTACCATCCTTCTAACACTCCTGAAAACCTCATAGTCATGCTGAAGAAAGAAATTCACCCAGGAGAAACGCCAGACG

C57BL/6   GATCAGGAGTACAAGCTCCCCGCCCTTTTATGCCCTGGAGCTATCAAAGGCCACCTAGCAACATTATCAGACAGGGAAAGGAGGGCATATCTTTGATTTC
BALB/c    GATCAGGAGTACAAGCTCCCCGCCCTTTTATGCCCTGGAGCTATCAAAGGCCACCTAGCAAGATTATCAGACAGGGAAAGGAGGGCATATCTTTGATTTC

C57BL/6   TCAGTCTTGCCTGGGGCCTTGACTGACAGTAGCTGCTGTTTTAACCTCCATCTGTGTCTTCGTGCCTTTTTAGAAGGGACTCAGGAAAGCTTGCTCTGGC
BALB/c    TCAGTCTTGCCTGGGGCCTTGACTGACAGTAGCTGCTGTTTTAACCTCCATCTGTGTCTTCATGCCTTTTTAGAAGGGACTCAGGAAAGCTTGCTCTGGC

C57BL/6   ATTATGGGGAATATCATCAACCTAGGAGGAGAATTCTGAACATGAGATGCAAGCTTGTCTTGCTTTCCCACAGCCCAAAACAGACGTATATGACAGTGAG
BALB/c    ATTATGGGGAATATCATCAACCTAGGAGGAGAATTCTGAACATGAGATGCAAGCTTGTCTTGCTTTCCCACAGCCCAAAACAGACGTATATGACAGTGAG

C57BL/6   TATGGGAAATAAACATATAGAAGAAAACACGTCTAGTTCGTTTACAGAACGCTTCTTAATACCAGTGACGTAGGAGCAAAGGATCGTGGGTGGGCGGCTA
BALB/c    TATGGGAAATAAACATATAGAAGAAAACACGTCTAGTTCGTTTACAGAACGCTTCTTAATACCAGTGACGTAGGAGCAAAGGATCGTGGGTGGGCGGCTA

C57BL/6   CTCCTCCCTGACAAGCCTTAATTACTTTTATATTTATTAGACATACATCTTGAAATGATTCTATAGAATCATAGGCAAACCTATGGTAAAATTTCAGCAG
BALB/c    CTCCTCCCTGACAAGCCTTAATTACTTTTATATTTATTAGACATACATCTTGAAATGATTCTATAGAATCATAGGCAAACCTATGGTAAAATTTCAGCAG

C57BL/6   AGAAATTCATCCTCGAAGCAAAATTTAATCAGCAAGGATAATGGTTTATATGGATTAAAACACATTTTTAAAATCTGCGTTTGATTTCATCTAGACCTCG
BALB/c    AGAAATTCATCCTCGAAGCAAAATTTAATCAGCAAGGATAATGGTTTATATGGATTAAAACACATTTTTAAAATCTGCGTTTGATTTCATCTAGACCTCG

C57BL/6   TTTT-ATCTGCATTGGCTCATTTCTCCCATTTTTGAGAGATTTTGCAGCTGGTCTTTCAGGTTCATTTTTCAAGGAATACTGCCCTCATGCGGCCGGGTG
BALB/c    TTTTTATCTGCATTGGCTCATTTCTCCCATTTTTGAGAGATTTTGCAGCTGGTCTTTCAGGTTCATTTTTCAAGGAATACTGCCCTCATGCGGCCGGGTG

C57BL/6   TGCCAAGACCGCTCACTCTCTGATTCCCTCCAGAGGACGGTCTGTGTGGCTCTGTGAGAGAGAGCTTTTGCTGCTTGAGGCTGTGTCTGTGGGTTCCTTT
BALB/c    TGCCAAGACCGCTCACTCTCTGATTCCCTCCAGAGGACGGTCTGTGTGGCTCTGTGAGAG----CTTTTGCTGCTTGAGGTTGTGTCTGTGGGTTCCTTT

C57BL/6   CGAAAACATGAATCCTTAAAATGCTTGCCAGGGGATGCACTCTGGTGCAGCTTTTGACTCAATTATCTGCTTACTGCATCAATAACCAACACATGCAAAA
BALB/c    CGAAAACATGAATCCTTAAAATGCTTGCCAGGGGATGCACTCTGGTGCAGCTTTTGACTCAATTATCTGCTTACTGCATCAATAACCAACACATGCAAAA

C57BL/6   ATAATCAGTCGCTGATCATTTTACACACTCGGAAAGTCCTCACAAACCCGACTCCTTTAAAGTCAGTAGAACGCGTTAGCCTTG
BALB/c    ATAATCAGTCGCTGATCATTTTACACACTCGGAAAGTCCTCACAAACCCGACTCCTTTAAAGTCAGTAGAACGCGTTAGCCTTG
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P

Asb4

chr6:5,333,153-5,335,375

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C57BL/6  --------------------AGTGGAACAAACAACGGAGGTGGGCTCTGTACTTTCTTAAAAAGACAAGGTTTGACAAGATACTGTTTCTCAGCTCCAAT
BALB/c   --------------------AGTGGAACAAACAACGGAGGTGGGCTCTGTACTTTCTTAAAAAGACAAGGTTTGACAAGATACTGTTTCTCAGCTCCAAT

C57BL/6  TCAGCCGTTCTATAGCAAGAATATCTGTAAGCAGACAGAAAATATGCAACCCTTCTCTCCACTCTTCCCGGGTCCTGCAGCTTCATTTGCATGATACACT
BALB/c   TCAGCCGTTCTATAGCAAGAATATCTGTAAGCAGACAGAAAATATGCAACCCTTCTCTCCACTCTTCCCGGGTCCTGCAGCTTCATTTGCATGATACACT

C57BL/6  CCAAACAAATTCTCTGCAAGAATGTCGATTTTACATTATATCCAGGGAAATGCGCAAAGTGCTACCCCAAAAGGTAAAATCAAATCGATGAATCTTTGCA
BALB/c   CCAAACAAATTCTCTGCAAGAATGTCGATTTTACATTATATCCAGGGAAATGCGCAAAGTGCTACCCCAAAAGGTAAAATCAAATCGATGAATCTTTGCA

C57BL/6  ACTGGTAAACTGCTTCTTGGTTTCTGTGAACTCTGAGGGCTAAAGGGCATCCTGGGATCTTAGGAAAGAAGGCTTAGAAGCCTGCCATATTTCTTTCCCA
BALB/c   ACTGGTAAACTGCTTCTTGGTTTCTGTGAACTCTGAGGGCTAAAGGGCATCCTGGGATCTTAGGAAAGAAGGCTTAGAAGCCTGCCATATTTCTTTCCCA

C57BL/6  CATGAAGGGCAATTTTCTTCCCTAGCTATACTTTGCCTTCAAAAATTTGTCAGAGGTAAAGAAAGAATGCAAACGCTGCCTGGAGTACAATTGCGGGGTC
BALB/c   CATGAAGGGCAATTTTCTTCCCTAGCTATACTTTGCCTTCAAAAATTTGTCAGAGGTAAAGAAAGAATGCAAACGCTGCCTGGAGTACAATTGCGGGGTC

C57BL/6  AGTGTTCTGATTGAGACAGAATTATGGCGAATTATTCCCATGAGTTGATTTTGTGAAGTGTGTGCTGGTG-TGAGGGTGGAAATACAAGCCGGCGCTAGT
BALB/c   AGTGTTCTGATTGAGACAGAATTATGGCGAATTATTCCCATGAGTTGATTTTGTGAAGTGTGTGCTGGTG-TGAGGGTGGAAATACAAGCCGGCGCTAGT

C57BL/6  GTTTAAACAAGGCTGCAAGGGCAGTTGCTAGGAGACCCTGCACACAGCTGATGCCCCCACTGCGGGCTCAGACGTGCTTTGTCTGAAGAACCCGGCCTTT
BALB/c   GTTTAAACAAGGCTGCAAGGGCAGTTGCTAGGAGACCCTGCACACAGCTGATGCCCCCACTGCGGGCTCAGACGTGCTTTGTCTGAAGAACCCGGCCTTT

C57BL/6  CGCAGTCAAAGATGACATTAAATGTATAGTCTGTCAAAATTTAGGTGGAGGAAAAATTCAGGTGGACCAGGGCTCGGTTATTGCTTGTGTCAATCTAGCT
BALB/c   CGCAGTCAAAGATGACATTAAATGTATAGTCTGTCAAAATTTAGGTGGAGGAAAAATTCAGGTGGACCAGGGCTCGGTTATTGCTTGTGTCAATCTAGCT

C57BL/6  ATTCTGACGTCCATCACCCATTAAGGATGGGTTTTGAAAGGGAAAATATAGCATTGTGCCAGGAACCAAGAGCCTCCGGAAACGCTCAAGGGAATTTAGT
BALB/c   ATTCTGACGTCCATCACCCATTAAGGATGGGTTTTGAAAGGGAAAATATAGCATTGTGCCAGGAACCAAGAGCCTCCGGAAACGCTCAAGGGAATTTAGT

C57BL/6  TACAAATGCAGTTTGAATACCCCGATATGAAAGGCAGATGGTCTGGGTACCAGTTCCGGGAAGCAGGCGGCCCCAGCTAAGTAATCACTTCAATGTTCCA
BALB/c   TACAAATGCAGTTTGAATACCCCGATATGAAAGGCAGATGGTCTGGGTACCAGTTCCGGGAAGCAGGCGGCCCCAGCTAAGTGATCACTTCAATGTTCCA

C57BL/6  AATAGAGGACCTTGAGTCCACAAACAGAGACTTCTAAGAGGAAAGGCGCGCGAGTGTGATTTTAGATCCCGCCGTTTACAAACAACCATTTCAGTCATTT
BALB/c   AATAGAAGACCTTGAGTCCACAAACAGAGACTTCTAAGAGGAAAGGCGCGCGAGTGTGATTTTAGATCCCGCCGTTTACAAACAACCATTTCAGTCATTT

C57BL/6  GTGGGAACCGTTTAATAGACTTTTATGAGAAACACATAGGCTTCCAGTTTGTAATTTAGACCTTAGAGATGCATCGAACTCGAGAGCTGAAAGTGGCTTA
BALB/c   GTGGGAACCGTTTAATAGACTTTTATGAGAAACACATAGGCTTCCAGTTTGTAATTTAGACCTTAGAGATGCATCGAACTCGAGAGCTGAAAGTGGCTTA

C57BL/6  GAAGTTCCTCAAGCGCCCCCAACTGGTGGAAGGAGAAAACTGACCCGCTTTGTGGATAAGTGCAGTCTAAAAAAAACGTTGCTTTCTTGGTTTTCAGAAA
BALB/c   GAAGTTCCTCAAGCGCCCCCAACTGGTGGAAGGAGAAAACTGACCCGCTTTGTGGATAAGTGCAGTCTAAAAAAAACGTTGCTTTCTTGGTTTTCAGAAA

C57BL/6  CTCAGGCAAGACTACTTGCCTTTGTAAAATAGTATCACCCACCCTCTGCCAATGCTCAAGATATGATACCCGGTGAGGAGTAAAGTAGAGGAAAGAGGAA
BALB/c   CTCAGGCAAGACTACTTGCCTTTGTAAAATAGTATCACCCACCCTCTGCCAATGCTCAAGATATGATACCCGGTGAGGAGTAAAGTAGAGGAAAGAGGAA

C57BL/6  CATTTTGAATTTTGTGTTTTGAATATCAGTAGCACGGGAGCCAGAGACACAGTCAGTTAAGATTGCCTGTCTTCTCCAGGAGAGTCATGTTGTTCTGTGA
BALB/c   CATTTTGAATTTTGTGTTTTGAATATCAGTAGCACGGGAGCCAGAGACACAGTCAGTTAAGATTGCCTGTCTTCTCCAGGAGAGTCATGTTGTTCTGTGA

C57BL/6  GCATCGAGACCAGAATCATCCACAACTCTTTGTAGTGCTTTTCCGTGTACAAGCACATTCTGTGTATTAATTTTTTTCATTTGTTTCATAAAGTCTGACA
BALB/c   GCATCGAGACCAGAATCATCCACAACTCTTTGTAGTGCTTTTCCGTGTACAAGCACATTCTGTGTATTAATTTTTTTCATTTGTTTCATAAAGTCTGACA

C57BL/6  ATTGCTCTTACACGCTGGTGGTGAAACTAATAAGGATTTGATACAAGGTTTAGTTGTAACTCCACTACCCTACCTCCAAATAAGGAATAACTTCCTTGGC
BALB/c   ATTGCTCTTACACGCTGGTGGTGAAACTAATAAGGATTTGATACAAGGTTTAGTTGTAACTCCACTACCCTACCTCCAAATAAGGAATAACTTCCTTGGC

C57BL/6  CAGTGATCTCACAGAATAGCTAATTGAAATCTCAAAGTGGTTTGAATTTTTAATTTTGTTTGTTTTGTATTTATACTTCATAGCCAGGAAAAACAAAAAC
BALB/c   CAGTGATCTCACAGAATAGCTAATTGAAATCTCAAAGTGGTTTGAATTTTTAATTTTGTTTGTTTTGTATTTATACTTCATAGCCAGGAAAAACAAAAAC

C57BL/6  AAAACAAAAAAACCTCTGTACTTTTTTTGCTTTTTTATGAAAAAAAAAAAAAAAGAAACCCCATCAGCACTTCCCATGTTGGAGAAATTAGTATTACTAA
BALB/c   AAAACAAAAAAACCTCTGTACTTTTTTTGCTTTTTTATGAAAAAAAAAAAAAA-GAAACCCCATCAGCACTTCCCATGTTGGAGAAATTAGTATTACTAA

C57BL/6  CCCTGGTACATAGTAACTTTCGGAATGTTGTTCCAGGCAGCCTTGAGAGAACTGAGCTGGTTGGGTTCAAGAAACAGAAGGAAATAAAAATTACCCATCA
BALB/c   CCCTGGTACATAGTAACTTTCGGAATGTTGTTCCAGGCAGCCTTGAGAGAACTGAGCTGGTTGGGTTCAAGAAACAGAAGGAAATAAAAATTACCCATCA

C57BL/6  GTCCCACTCTTAAACTTTACTGCAAAGAGATGTCTTTAGAGAGATGGAACCCAGGGGCTGATATGGCTTCTTTGCATCCTCTTGGCAGAGCTTAGGGGCC
BALB/c   GTCCCACTCTTAAACTTTACTGCAAAGAGATGTCTTTAGAGAGATGGAACCCAGGGGCTGACATGGCTTCTTTGCATCCTCTTGGCAGAGCTTAGGGGCC

C57BL/6  CAGGACTTGTTGCTTTAGCCCACAAAGCTCTGTCCTTACAGAGAAAACCAGTCTCGATGTTCCCTCCCCTCCCCTTTTCCTTCGTTCTAGGAGATGCCAA
BALB/c   CAGGACTTGTTGCTTTAGCCCACAAAGCTCTGTCCTTACAGAGAAAACCAGTCTCGATGTTCCCTCCCCTCCCCTTTTCCTTCGTTCTAGGAGATGCCAA

C57BL/6  CCACCATGCGGGGAGGGTATTCAGACAGGCTCCTGGAGAGACTG
BALB/c   CCACCATGCGGGGAGGGTATTCAGACAGGCTCCTGGAGAGACTG
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Q

Cd48

chr1:173,509,829-173,510,806

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C57BL/6   --------------------------------------------------GACATGAGCATTAAGGCCTCCCTCTGCACTGGTCCTCATAAGCCCTGCTT
BALB/c    --------------------------------------------------GACATGAGCATTAAGGCCTCCCTCTGCACTGGTCCTCATAAGCCCTGCTT

C57BL/6   GCCTGCAGGTGCTGCTGGCTTGCAGGTCAGCTGGATCTCAGCTGCTCTGAGCCTTCTGTCACCTTCTGCTCATTGGTTTGCTAGGTTGCTAGGAAACCGT
BALB/c    GCCTGCAGGTGCTGCTGGCTTGCAGGTCAGCTGGATCTCAGCTGCTCTGAGCCTTCTGTCACCTTCTGCTCATTGGTTTGCTAGGTTGCTAGGAAACCGT

C57BL/6   GTCCCAGGCTTCCATGCTGGGCTTGGCCTAAAGCCTAGTCTGCCTAAGTTTAGATTTCTAGCCCTACATTTGGTGAGCCGAATACTGTTAGACCACCTCA
BALB/c    GTCCCAGGCTTCCGTGCTGGGCTTGGCCTAAAGCCTAGTCTGCCTAAGTTTAGATTTCTAGCCCTACATTTGGTGAGCTGAATACTGTTAGACCGCCTCA

C57BL/6   ACTCGCCAGCTCCCAATAATGACTTTTTACTAGTTATAAAAGCTGAGGCCTTTTATCTGTTTTTT----------------------------------
BALB/c    ACTCGCCAGCTCCCAATAATGACTTTTTACTAGTTATAAAAGCTGAGGCCTTTTATCTGTTTTTTTTTTCTCTTTGTCTTGTCTTGTTTTCCTGTATAAA

C57BL/6   ----------------------------------------------------------------------------------------------------
BALB/c    AAAGATCCCAGTATAAATCAGGGAGGGAAGAAGACAGATACACCTGCCCTTTAGTGTAGAGCTAGGGGAGGGTAATGGGGGTGAACCTCGTAAGGAGAGG

C57BL/6   ----------------------------------------------------------------------------------------------------
BALB/c    TGGGGACTTGTTATTTAAGGCTTAAAATATTCTCTGTAAAAAACGAGGATTCTCCACAGCCTTGGGGGAGACAGAGGCTGCCGCTTCAGTGAGGGTTTCT

C57BL/6   ----------------------------------------------------------------------------------------------------
BALB/c    CCACCAAGACTGGGAAAGGCAGCCCCTCTTCTCACTCTGCGTCGCTTTCCTCCTTGTGCAGGTAGGAGTGCTGCAGGGCTCGGAAGGCAGAGATTCGCTT

C57BL/6   ----------------------------------------------------------------------------------------------------
BALB/c    ATGTGGGTTAAAGGTCAGCATTTCCAGTAGCAGCTGCGCTCCAGACTCCTCCATCTCTGGCACCACTGACTGCACTGGCCGAGGCCCTCTGGGGGCAAAG

C57BL/6   ----------------------------------------------------------------------------------------------------
BALB/c    GCTCCTCGAGGTAGAGATACCTCTCGAGGCCAGTCGTCTTCTGGAGGCAATCCAATGAGATCAAAGATTTTCCCCAACTGGTGGGCTTCAGAGTTTCCAC

C57BL/6   ----------------------------------------------------------------------------------------------------
BALB/c    AGAAGAGAGGCTTCCGACGGAACATCTCTGCAAAGATACAGCCAACGCTCCACATGTCCACGGGTGTTGCGTATGTAGACTGCAGAAGAACTTCAGGAGC

C57BL/6   ----------------------------------------   ----------------------------------------------------
BALB/c    TCGGTACCAAAGCGTACCACCACAGGCGTGAGGCCATCTGG //GGAGTACACGACTCCTCACCGTCACATTGGAGTCAAAGGCTCCAGCTCCTAACAAG

C57BL/6   ----------------------------------------------------------------------------------------------------
BALB/c    CCACTCACGAACTGTGCT-GATGGAAGGCCCCTCCAGCTGCTCCTCCATTAGGACTCTCACACTTCTTGAGGCCACAAAGTGGCCACTGTGGGGATCTCG

C57BL/6   ----------------------------------------------------------------------------------------------------
BALB/c    GGTTTGTACACCGTCCCATAGGCACCGACACCAATTTCAGCCACGGGTTCATATCGAGTGGCAGCCATTCTCGAAGCAGGGGATCTTACGCTCGGCTAAG

C57BL/6   ----------------------------------------------------------------------------------------------------
BALB/c    AGCTCTGGAGGTGGCCCTTTATCTGGGCCCGGGAGCCGGTTCCTGCGGCGCCATACACCGGGGATCGGTCCCGGGCAGCTGGACGCTTCGGGCCAGACCA

C57BL/6   ------------------------ATGCAATGCAAATATTTACTCTTAATTCACATTGTCAAAATTTTTCAAGAAACAATCACAAAGGTTTATTTTAAA
BALB/c    --TAGACACAGTTATCTGTTTTTTTATGCAATGCAAATATTTACTCTTAATTCACATTGTCAAAAATTTTCAAGAAACAATCACAAAGGTTTATTTTAAA

C57BL/6   TGTGCTTTGTATCTTTGGCTTGTTCTCGACTAGCTTGTATAACTTAGTAACTCCACAGGTAGTCACTATGTCTGACTTTCTCCATGTCTGGCTGGAGCAT
BALB/c    TGTGCTTTGTATCTTTGGCTTGTTCTCGACTAGCTTGTATAACTTAGTAACTCCACAGGTAGTCACTATGTCTGACTTTCTCCATGTCTGGCTGGAGCAT

C57BL/6   TTCCCAGGCCTGATTCTTTCCCAGAGTTCCTATCTATACTCTGAAGTTTCACTTTTCTTCTCCTGTCCTGTTATAGACCATCAGATCTTTATTAAACCAA
BALB/c    TTCCCAGGCCTGATTCTTTCCCAGAGTTCCTATCTATATTCTGAAGTTCCGCTTTTCTTCTCCTGTCCTGTTATAGACCATCAGATCTTTATTAAACCAA

C57BL/6   TCAGAAGATGATGGAGAAAATGTTTACGAAATCTTTAGGCAGGTGTGATGATCCAATAAAAATAACAATACCAAGGTCAGGCCTGTAAACAGCTCTGCGG
BALB/c    TCAGAAGATGATGGAGAAAATGTTTACGAAATCTTTAGGCAGGTGTGATGATCCAATAAAAGTAACAATACCAAGGTCAGGCCTGTAAACAGCTCTGCGG

C57BL/6   GTAGGTAAACCAATATTTGAATAATACAAGGGTAACCTTTACACAGTGCACAAAAAGATTAACCCAACTGAGGAGGAGAGAGGAGGAAGGGAAGAAGGGT
BALB/c    GTAGATAAACCAATATTTGAATAATACAAGGGTAACCTTTACACAGTGCACAAAAAGATTAACCCAACTGAGGAGGAGAGAGGAGGAAGGGAAGAAGGGT

C57BL/6   AGAGACAAGAGCAGAGTGGGACAAAGGTGGCCTGCTAAATTGACTTTGGTATTAAAGGAGGAATCTGTGTAAATGAAAGAGCTGGATGAAAATCCAGTAC
BALB/c    AGAGACAAGAGCGGAGTGGGACAAAGGTGGCCTGCTAAATTGACTTTGGTATTAAAGGAGGAATCTGTGTAAATGAAAGAGCTGGATGAGAATCCAGTAC

C57BL/6   ATGAACACTGTCTGGTCTGTTTGCTTGGTTTAGTTTTGAGCCTCTCAGCATCCCTTCCTAGGTGTT-AGAAGTCCATCTCATCCCTGG
BALB/c    ATGAACGCTGTCTGGTCTGTTTGCTTGGTTTAGTTTTGAGCCTCTCAGCATCTCTTCCTAGGTGTT-AGAAGTCCATCTCATCCCTGG
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R

Coro2a

chr4:46,621,090-46,622,106

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C57BL/6  ---------------------------------------------GTTCGGTCGATTCGGTTTTGGGGATGGAACTCTGCCGACTGAGCTGCACCCTAGC
BALB/c   ---------------------------------------------GTTCGGTCGATTCGGTTTTGGGGATGGAACTCTGCCGACTGAGCTGCACCCTAGC

C57BL/6  TGCTAAGCACCCCATTCTTGGAATTAGGATTCCTGGCTGGTTTGTTGTGTGGCCTTTACCAGGCACACCCCCTCCTGGGACAGGTGATTATATGCCCATA
BALB/c   TGCTAAGCACCCCATTCTTGGAATTAGGATTCCTGGCTGGTTTGTTGTGTGGCCTTTACCAGGCACACCCCCTCCTGGGACAGGTGATTATATGCCCATA

C57BL/6  GAATACGAGCGTTGGATGAGATAGACGGTTTCTAGACTGCCCCTAGAATAAGGGCCTGGGATGAGATGGTTTCTAGAGACCCTTTCAGGTCAGAGAATCC
BALB/c   GAATACGAGCGTTGGATGAGATAGACGGTTTCTAGACTGCCCCTAGAATAAGGGCCTGGGATGAGATGGTTTCTAGAGACCCTTTCAGGTCAGAGAATCC

C57BL/6  ACAACTCCACAGTACATTTTTAAAGTTCGGGATGACTTTGTAATAATCAGGACCTGCCTGCTCATGCGCCATCACTGTAGCCTCCCAGATCACAAACGTT
BALB/c   ACAACTCCACAGTACATTTTTAAAGTTCGGGATGACTTTGTAATAATCAGGACCTGCCTGCTCATGCGCCATCACTGTAGCCTCCCAGATCACAAACGTT

C57BL/6  CCCAATGACAGGGGACTCAGGTGGTACTTAGGCTTTCGAGCTGGCGCTGGGCTCTGGCAGCCACACTTATACTTAGTCTCCCTTTATGAGGGGATAATAA
BALB/c   CCCAATGACAGGGGACTCAGGTGGTACTTAGGCTTTCTAGCTGGCGCTGGGCTCTGGCAGCCACACTTATACTTAGTCTCCCTTTATGAGGGGATAATAA

C57BL/6  CACTCATTTGCAGCGAAGCTCCAGGTTGGGGCCACAGGGCAAGGTCCCCTGCCACACTGCTTTGGCCCTGGCAACGCACAGCACCCTATGATGCCCACCC
BALB/c   CACTCATTTGCAGCGAAGCTCCAGGTTGGGGCCACAGGGCAAGGTCCCCTGCCACAGTGCTTTGGCCCTGGCAACGCACAGCACCCTATGATGCCCACCC

C57BL/6  AGCCCTCTGCCTGTACACTTAGATGACGTAGGGCTCACTACCGGCGCTGGCCTGGGGAAAGGGAAGGGTCTCCTCTTTTAGCCTTAAGAAAGTCCTTGGG
BALB/c   AGCCCTCTGCCTGTACACTTAGATGACGTAGGGCTCACTACCGGCGCTGGCCTGGAGAAAGGGAAGGGTCTCCTCTTTTAGCCTTAAGAAAGTCCTTGGG

C57BL/6  TGAGGGAGAGGGAGACAGGCGATCAGGAGGTGCTGAGCCTGTTCCTTAGTGGGGACAGATGTCAGGAAATGAGGCAGAAGTGTCCAGAGATGGGCTTAAG
BALB/c   TGAGGGAGAGGGAGACAGGCGATCAGGAGGTGCTGAGCCTGTTCCTTAGTGGGGACAGATGTCAGGAAATGAGGCAGAAGTGTCCAGAGATGGGCTTAAG

C57BL/6  CCTTTCTCTCCCTCCACATCCCTCAAGAGATGTCTGGAGGCGAGGGACGTGTAAGGACACATTCCTGTGCTGAGGCACAGGTGGTTATGAACAAGTCCCT
BALB/c   CCTTTCTCTCCCTCCACATCCCTCAAGAGATGTCTGGAGGCGAGGGACGTGTAAGGACACATTCCTGTGCTGAGGCACAGGTGGTTATGAACAAGTCCCT

C57BL/6  GGAGCATTCGCAGAAGAGCAGGCTCTGAGACAGAAGGGCCACATGCTAGCTAAGGGACACTATCAGGATTGCAGCCACAGTGGGACCAGATTCCCCAGTT
BALB/c   GGAGCATTCGCAGAAGAGCAGGCTCTGAGACAGAAGGGCCACATGCTAGCTAAGGGACACTATCAGGATTGCAGCCACAGTGGGACCAGATTCCCCAGTT

C57BL/6  TCGCTAGTGAGAGTCCCCATCTCGAGAAGAATGCAACATAAGACCT-CATCAAAAGGCATCT
BALB/c   TCGCTAGTGAGAGTCCCCATCTCGAGAAGAATGCAACATAAGACCT-CATCAAAAGGCATCT
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S

Eps8l1

chr7:4,081,175-4,081,945

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C57BL/6  --------------------GCCCCAGCACCTAGAGTGCGCACTCCCTCCCTTCCCGGTTTCCCTCCTGCAGAGAAATTCTCCCAGATGCTTTGTGTCAA
BALB/c   --------------------GCCCCAGCACCTAGAGTGCGCACTCCCTCCCTTCCCGGTTTCCCTCCTGCAGAGAAATTCTCCCAGATGCTTTGTGTCAA

C57BL/6  TGAGGAGCTGCAGTCGCGCCTGGCGCAGGGCCGTTCGGGTCCCAGCCGGGTAACCCCGGGGCCCCGAGCCCAAGAGCCCCAGCTCAGCCCGCGCTCTGAG
BALB/c   TGAGGAGCTGCAGTCGCGCCTGGCGCAGGGCCGTTCGGGTCCCAGCCGGGTAACCCCGGGGCCCCGAGCCCAAGAGCCCCAGCTCAGCCCGCGCTCTGAG

C57BL/6  GCCTCGGTGGTCCGTGCCTGGCTGCAGACCAAGGGCTTTAGCTCCGGGTGAGTGGGGTCCCGCTGCTACTTTGCAGAGACAGATAACAGACCTGGAAGTC
BALB/c   GCCTCGGTGGTCCGTGCCTGGCTGCAGACCAAGGGCTTTAGCTCCGGGTGAGTGGGGTCCCGCTGCTACTTTGCAGAGACAGATAACAGACCTGGAAGTC

C57BL/6  AAGGTTTTAGTTGGTCTGGGGGTGGGAGCGGGGAAAACTGTAGGGCAATTTGCTACGCCCAAAGACAGGCTCTGATTGGAGACCACAGGGAAGAGCATTC
BALB/c   AAGGTTTTAGTTGGTCTGGGGGTGGGAGCGGGGAAAACTGTAGGGCAATTTGCTACGCCCAAAGACAGGCTCTGATTGGAGACCACAGGGAAGAGCATTC

C57BL/6  CTTTTCTGAAATCTGACACCTCCGGAGCCTGAGCCTCTCCGTCCCAACTTCCTTGCTTGAGAGCTCTGATTGGACAAGCAGCTAGGTGGGTGCGATGTGA
BALB/c   CTTTTCTGAAATCTGACACCTCCGGAGCCTGAGCCTCTCCGTCCCAACTTCCTTGCTTGAGAGCTCTGATTGGACAAGCAGCTAGGTGGGTGCGATGTGA

C57BL/6  TTGGTGAAGCTGAAGGGGCTTGAGCTGTGATGGCCCCTGCTGCCTTCTTAGGACTGTGGAGGCGCTCGGTGTGCTGACCGGCGCACAGCTCTTCTCGCTG
BALB/c   TTGGTGAAGCTGAAGGGGCTTGAGCTGTGATGGCCCCTGCTGCCTTCTTAGGACTGTGGAGGCGCTCGGTGTGCTGACCGGCGCACAGCTCTTCTCGCTG

C57BL/6  CAAAAGGAAGAGTTGCGGGCGGTGTGCCCCGAGGAAGGGGCGCGAGTGTACAGCCAAGTCACTGTGCAGCGCGCGCTGCTGGAGGTGAGAGAATCGCCCA
BALB/c   CAAAAGGAAGAGTTGCGGGCGGTGTGCCCCGAGGAAGGGGCGCGAGTGTACAGCCAAGTCACTGTGCAGCGCGCGCTGCTGGAGGTGAGAGAATCGCCCA

C57BL/6  GGCCCTGACGAGGCGAGGGGTGGGGCGCCCAGGACTCACATACTAAGGTCTTGATTTCTACCCCACCCTCAAGGACAGAGAAAAAGTATCA
BALB/c   GGCCCTGACGAGGCGAGGGGTGGGGCGCCCAGGACTCACATACTAAGGTCTTGATTTCTACCCCACCCTCAAGGACAGAGAAAAAGTATCA
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T

Mtor (Frap1)

chr4:147,344,467-147,345,448

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C57BL/6   ------------------------------------------AGGAGCTGTGAACTTGTTTCCAGTTGCGCCTATTAGATTATGGCCTGCCAGCCACT
BALB/c    ------------------------------------------AGGAGCTGTGAACTTGTTCCCAGTTGCGCCTATTAGATTATGGCCTGCCAGCCACT

C57BL/6   GGCTCAGCTCTATCAGCAGACAGGCAGAGTGGAAGACTTTCCCAACTCCTGTCTGAAGGTTATATAACACAGATTGAGGGTGAGGTAGCAAGAAAGAGTT
BALB/c    GGCTCAGCTCTATCAGCAGACAGGCAGAGTGGAAGACTTTCCCAACTCCTGTCTGAAGGTTATATAACACAGACTGAGGGTGAGGTAGCAAGAAAGAGTT

C57BL/6   GGACTGGAGACTGCTGAGCCAGGGAGGCTGGCTAAGGTAATGCATGCTGTTTACTCCAGGTCCTGGTTTATCTGGGCTGAGATGAGTCTTAACAGGGCTT
BALB/c    GGACTGGAGACTGCTGAGCCAGGGAGGCTGGCTAAGGTAATGCATGCTGTTTACTCCAGGTCCTGGTTTATCTGGGCTGAGATGAGTCTTAACAGGGCTT

C57BL/6   TGTCTGGCCATCATTCGGTGTTCTTCAAAATCCTGTTGAACCTGATCCTTGGGCGTCAGGTGGTTTGCATCTGTGGGGCTGTCTTCCTCTTTACACATTC
BALB/c    TGTCTGGCCATCATTCGGTGTTCTTCAAAATCCTGTTGAACCTGATCCTTGGGCGTCAGGTGGTTTACATCTGTGGGGCTGTCTTCCTCTTTACACATTC

C57BL/6   TCCTTCTAAAACGATCTTTCAACATTTACAAGGAGTTGTCATAGTTTGGGGCAGAGAGAAAGTCTCAGCCATGCCAGGCGTGGTCTGGGGTTGGTCATCC
BALB/c    TCCTTCTAAAACGATCTTTCAACATTTACAAGGAGTTGTCATAGTTTGGGGCAGAGAGGAAGTCTCAGCCATGCCAGGCGTGGTCTGGGGTTGGTCATCC

C57BL/6   ACACTTCTGTCAGGTTCTGTCTGGGCAGCAGTGAGTGGGCCTGACCTTTACCCAAGGCTCAGACTCAGAGAGAAGATTCCCTAGTACATGCAGATCAGAA
BALB/c    ACACTTCTGTCAGGTTCTGTCTGGGCAGCAGTGAGTGGGCCTGACCTTTACCCAAGGCTCAGACTCAGAGAGAAGACTCCCTAGTACATGCAGATCAGAA

C57BL/6   GGCTCGATTCCCTCTGTGCCTGCAGCGTGGTTTGCAGCTTGATGCTGGCCCCTATACCTACGTACACAGTGTCTGAGAAAACGGGGGTGATGGCAGCTTTC
BALB/c    GGCTCGATTCCCTCTGTGCCTGCAGCGTGGTTTGCAGCTTGATGCTGGCCCCTATAGCTACGTACACAGTGTCTGAGAAAACGGGGGTGATGGCAGCTTTC

C57BL/6   ATACCTTTAATTGAAGGGCACTGCTCTTCTGAAATCATGTAAAAGATGGAACTTTCCCTATAACTGTACAAAGGTCCCTCTGTCCTTATGGCAGGAGCTC
BALB/c    ATACCTTTAAGTGAAGGGCACTGCTCTTCTGAAATCATGGAAAAGATGGAACTTTCCCTATAACTGTACAAAGGTCCCTCTGTCCTTATGGCAGGAGCTC

C57BL/6   TGTCTGACTTTATAGTGTGGGTCCTACAGCTTTGCCTACCCTGATCCCTCAGAGTCTTTCCCAGATGGGTTTCTGGCTCCTCGGAAAGTGATTTCTGCTC
BALB/c    TGTCTGACTTTATAGTGTGGGTCCTACAGCTTTGCCTACCCTGATCCCTCAGAGTCTTTCCCAGATGGGTTTCTGGCTCCTCGGAAAGTGATTTCTGCTC

C57BL/6   AGACAGCTGGAGTTACTTAGCAGGGACCCATTTCTGAATATAAGCATTGGGTGCTCAGACAGACGACTGTCTGTTTCCTCTCACTCCTGTCTTTTTTGCC
BALB/c    AGACAGCTGGAGTTACTTAGCAGGGACCCATTTCTGAATATAAGCATTGGGTGCTCAGACAGACGACTGTCTGTTTCCTCTCACTCCTGTCTTTTTTGCC

C57BL/6   TCCTTGGGCACCAGGTTGTTACTAAC
BALB/c    TCCTTGGGCACCAGGTTGTTACTAAC
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U

Pdgfrb

chr18:61,190,675-61,191,616

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C57BL/6   ----------------------------------------ACCTAGACTTCCCACCGAGCCTAGTTCATTCTCAACCCCTCAGTGCAGACCTTGACAGC
BALB/c    ----------------------------------------ACCTAGACTTCCCACCGAGCCTAGTTCATTCTCAACCCCTCAGTGCAGACCTTGACAGC

C57BL/6   CCCGTTGCCAGAGTCAACCTCTGCATTAGTTTGAAGTTCCCTTGCACCCTGTATATAATATAGACCCAGAATAGAAAACTTCAACTCCACTCCCAACCTC
BALB/c    CCCGTTGCCAGAGTCAACCTCTGCATTAGTTTGAAGTTCCCTTGCACCCTGTATATAATATAGACCCAGAATAGAAAACTTCAACTCCACTCCCAACCTC

C57BL/6   AGCTCTGACCCTAACACTATCAGTTAGGGTCAAATTCCATCCCTGTTTCCGTTCCAGTCAAAGCTTGCACTTCAGCTCTGTTGCCTAAAGAAACCGTGCC
BALB/c    AGCTCTGACCCTAACACTATCAGTTAGGGTCAAATTCCATCCCTGTTTCCGTTCCAGTCAAAGCTTGCACTTCAGCTCTGTTGCCTAAAGAAACCGTGCC

C57BL/6   CTAGTTTTTAGAAGCCCCCAGAAGGTGTTTATCTTGCATTTAGTCCGCGCTGGCCTCCAGGAACCCTCCACTAGAGATGGGCAGGATG--------CATT
BALB/c    CTAGTTTTTAGAAGCCCCCAGAAGGTGTTTATCTTGCATTTAGTCCGCGCTGGCCTCCAGGAACCCTCCACTAGAGATGGGCAGGATGCACATTCTCATT

C57BL/6   GGTGTCTGGGCATAACTCCGCCCACAGGGCCCGCCCCTAACTGTTGTACCTTCCGCAGAGAATGGCTACGTGCGGCTGCTGGAGACACTGGGAGATGTAG
BALB/c    GGTGTCTGGGCATAACTCCGCCCACAGGGCCCGCCCCTAACTGTTGTACCTTCCGCAGAGAATGGCTACGTGCGGCTGCTGGAGACACTGGGAGATGTAG

C57BL/6   AAATTGCTGAGCTGCACCGGAGTCGGACGCTGCGGGTGGTGTTCGAGGCTTATCCGATGCCTTCTGTCCTGTGGCTCAAGGACAACCGTACCTTGGGTGA
BALB/c    AAATTGCTGAGCTGCACCGGAGTCGGACGCTGCGGGTGGTGTTCGAGGCTTATCCGATGCCTTCTGTCCTGTGGCTCAAGGACAACCGTACCTTGGGTGA

C57BL/6   CTCCGGCGCTGGCGAGTTAGTTTTGTCTACTCGCAACATGTCTGAGACCCGGTGAGCACCAGTTAGTCCACTTATGTTGGAAGCTTCAAAGCTGCCAGGC
BALB/c    CTCCGGCGCTGGCGAGTTAGTTTTGTCTACTCGCAACATGTCTGAGACCCGGTGAGCACCAGTTAGTCCACTTATGTTGGAAGCTTCAAAGCTGCCAGGC

C57BL/6   AGCCTGGGGCCTTCAGTCACCAACAAACCTAGGACCTTCTTGTCTGAGAGCCTGTTGTGTGATGGACACATGCCAGGTACTAGGTATGATGCTCCTGCAG
BALB/c    AGCCTGGGGCCTTCAGTCACCAACAAACCTAGGACCTTCTTGTCTGAGAGCCTGTTGTGTGATGGACACATGCCAGGTACTAGGTATGATGCTCCTGCAG

C57BL/6   GAGCAACGCAGGCTGCTCTGCTCCTCCTAGTGGGGGTAGCAGACACTGACGACTTGGCCACTCAGAGGTTTAGTTAACCTTGTGATGAACAGAACCAGCA
BALB/c    GAGCAACGCAGGCTGCTCTGCTCCTCCTAGTGGGGGTAGCAGACACTGACGACTTGGCCACTCAGAGGTTTAGTTAACCTTGTGATGAACAGAACCAGCA

C57BL/6   GGTAATGGCCAAAAGCAAAAA-CACCGGATAGGAAGAGGATTTCCCCAAGGCTAGAGATCTGCAGACAGGCAAGAATGTGCCCCTCTGATGG
BALB/c    GGTAATGGCCAAAAGCAAAAAACACCGGATAGGAAGAGGATTTCCCCAAGGCTAGAGATCTGCAGACAGGCAAGAATGTGCCCCTCTGATGG
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V

Isoc2b

chr7:4,468,816-4,470,431

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C57BL/6  ------------------------------------------------------------------------ATGCTTTAGGGAGAGCGATACAGAGGA
BALB/c   ------------------------------------------------------------------------ATGCTTTAGGGAGAGCGATACAGAGGA

C57BL/6  GCACGTAATTGTGAGAGAAGCGGGGACCACAACTCCTGGAACCAGGAATTTCAGGCTGTGTGACCCTGGGTGAGTTTCCCTTCCTCTCTGGGTCTCTTTT
BALB/c   GCACGTAATTGTGAGAGAAGCGGGGACCACAACTCCTGGAACCAGGAATTTCAGGCTGTGTGACCCTGGGTGAGTTTCCCTTCCTCTCTGGGTCTCTTTT

C57BL/6  TTTCTCCAGGGTTAGCTCACTGGCGGGGTTGATGCAAAATTTGTCTCTAGAGAGGGTTGGGGACTCTCCCCGCGGGTCTATCCTGAGACCAAATGGAATG
BALB/c   TTTCTCCAGGGTTAGCTCACTGGCGGGGTTGATGCAAAATTTGTCTCTAGAGAGGGTTGGGGACTCTCCCCGCGGGTCTATCCTGAGACCAAATGGAATG

C57BL/6  CCATTCCAACCCCCGAACCCGACACCCTGCAAAGCTTCCGTTTCCCGGTCTGAATGACGGGATGGTGGGTTTGCAAACAGCCAGCAAGTAACGAACCGGA
BALB/c   CCATTCCAACCCCCGAACCCGACACCCTGCAAAGCTTCCGTTTCCCGGTCTGAATGACGGGATGGTGGGTTTGCAAACAGCCAGCAAGTAACGAACCGGA

C57BL/6  CTTACTCGAAGGTCCCAGGTTCGAGTTCGGGCCCCTTTTCCAAGAAGTCCCGTGACCTTTTCCCCGCTGGATTCCCACTGACCCCGTACTGGGCCTCCTT
BALB/c   CTTACTCGAAGGTCCCAGGTTCGAGTTCGGGCCCCTTTTCCAAGAAGTCCCGTGACCTTTTCCCCGCTGGATTCCCACTGACCCCGTACTGGGCCTCCTT

C57BL/6  TTTGCCCTTTGTAGACACGTAGTCAGAGCCGCGGGTCTACACCCCCGCGCCGAGCCAACCAATCGGCGTTCGCCTCACTCTGTTCTACTCCATCCTGTTA
BALB/c   TTTGCCCTTTGTAGACACGTAGTCAGAGCCGCGGGTCTACACCCCCGCGCCGAGCCAACCAATCGGCGTTCGCCTCACTCTGTTCTACTCCATCCTGTTA

C57BL/6  ATTCGATTGGTCTGAAGAAACTGGAGCAGGCGGAGAGACAGAGGGTAGGACCAATGAAAATCCACGGAGGGAGGGCCTTGGCTGAGAGCTCGGCTTCTAA
BALB/c   ATTCGATTGGTCTGAAGAAACTGGAGCAGGCGGAGAGACAGAGGGTAGGACCAATGAAAATCCACGGAGGGAGGGCCTTGGCTGAGAGCTCGGCTTCTAA

C57BL/6  CCCGGAAGGAGGGTGAAGAACGACCAGAGAGCTAGAGGCTCAATCTTGGCTAGTGTAGGGTTCATGGCACCATCCACTCCATCCGGGGCGACCGGGGAGA
BALB/c   CCCGGAAGGAGGGTGAAGAACGACCAGAGAGCTAGAGGCTCAATCTTGGCTAGTGTAGGGTTCATGGCACCATCCACTCCATCCGGGGCGACCGGGGAGA

C57BL/6  GGTGATGCTTTCTGTAACCTAGCTCTAGGAAGGCTGAAGCACGAGTATCGCCAGTTCGAGACTAGCCGGGACTGCGTGGTGAGACCCTGTCAACCAAAAC
BALB/c   GGTGATGCTTTCTGTAACCTAGCTCTAGGAAGGCTGAAGCACGAGTATCGCCAGTTCGAGACTAGCCGGGACTGCGTGGTGAGACCCTGTCAACCAAAAC

C57BL/6  AACAGCCGGGCATGGTGGCGCAAATGTTTAGTTCCAGTAATCATCATAAACCGATGATTTAGTTAATGGTTTAGTTCCAGTACTCAGGAGGCAGAGGCAG
BALB/c   AACAGCCGGGCATGGTGGCGCTAATGTTTAGTTCCAGTAATCATCATAAACCGATGATTTAGTTAATGGTTTAGTTCCAGTACTCAGGAGGCAGAGGCAG

C57BL/6  GCATAATTCTGACTCTACAACGCGAATTCCAGAATAGCCAGTACAACACGGAAGTAAGTCCTGTCTCGAAAACCCGAAAGTCAAACTAAGAAAACAAAAG
BALB/c   GCATAATTCTGACTCTACAACGCGAATTCCAGAATAGCCAGTACAACACGGAAGTAAGCCCTGTCTCGAAAACCCGAAAGTCAAACTAAGAAAACAAAAG

C57BL/6  AACAAGCCTCGTAAGACATTTTCCCCC-ACTGCTTGCCAGTTAGCTTTTTCTCCAGGAATTCAGGACTTGTCTCCTTGGGTGGTCTATATAGAAAACTGA
BALB/c   AACAAGCCTCGTAAGACATTTTCCCCCCACTGCTTGCCAGTTAGCTCTTTCTCCAGGAATTCAGGACTTGTCTCCTTGGGTGGTCTATATAGAAAACTGA

C57BL/6  CTCTGTACTTAGAAGTGGGGGTTAAGAGAGAGAGGATTACTTCATCCAGATATATAAACCTGGTATGGTGGCTCAGG-CCGGTAATCCCAGCGTTCTAGA
BALB/c   CTCTGTACTTAGAAGTGGGGGTTAAGAGAGAGAGGATTACTTCATCCAGATATATAAACCTGGTATGGTGGCTCAGG-CCGGTAATCCCAGCGTTCTAGA

C57BL/6  AGCTGAGGCCTTGAGTTCAATGAATAAGAAAACAAAAGCTGATTACGGTGGCTTAATACCCATGACCCCAAGTACTCAGAAGTGGAGACAGGAGGATTTC
BALB/c   AGCTGAGGCCTTGAGTTCAATGAATAAGAAAACAAAAGCTGATTACGGTGGCTTAATACCCATGACCCCAAGTACTCAGAAGTGGAGACAGGAGGATTTC

C57BL/6  TTCACCTTGAAGTTATGAGAAAAGGGCTAGGCATGGTGGCTAACGAGGACTGTAAACCCAGCACTTGGGAGGCTGAGTGTGGGTGAGGATCTTTTGGGGG
BALB/c   TTCACCTTGAAGTTATGAGAAAAGGGCTAGGCATGGTGGCTAACGAGGACTGTAAACCCAGCACTTGGGAGGCTGAGTGTGGGTGAGGATCTTTTGGGGG

C57BL/6  AGAGATATATATATACACAGAGTTCCAGGTTAGCCTGGGCCACAGAGTGTGACACTGTCGAACAAAGAAAAAGAAATAAGGCTGGAACTGTAGCTCAGGT
BALB/c   AGAGATATATATATACATAGAGTTCCAGGTTAGCCTGGGCCACAGAGTGTGACACTGTCGAACAAAGAAAAAGAAATAAGGCTGGAACTGTAGCTCAGGT

C57BL/6  GGCAGAGTCCTTGCCTGGCATGAATAAAGCCTTCGCTTTAGTGCCCAGCACTGTATGCATGGGGGTGGGGTGAGGGTGG-AGAGATGGGG
BALB/c   GGCAGAGTCCTTGCCTGGCATGAATAAAGCCTTCGCTTTAGTGCCCAGCACTGTATGCATGGGGGTGGGGTGAGGGTGGGAGAGATGGGG
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W

Pi4k2b

chr5:53,026,310-53,027,151

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C57BL/6  ------------------------AAGGCCACACAAGATATTTTAGAACTGAGCTTGGATAAGGGCAGTAACAATAGCAGTTGTGGTTGGCATCTGGAAT
BALB/c   ------------------------AAGGCCACACAAGATATTTTAGA-CTGAGCTTGGATAAGGGCAGTAACAATAGCAGTTGTGGTTGGCATCTGGAAT

C57BL/6  GCCCTCCTCCGCCGGCTCACGCTTTGTTCCCAGGCTGCTGATGTGAGAGGTGGTACAGCCTTTAGGAAGATGGGTCTGGTGGGCAGAAGTATGTGACTCT
BALB/c   GCCCTCCTCCGCCGGCTCACGCTTTGTTCCCAGGCTGCTGATGTGAGAGGTGGTACAGCCTTTAGGAAGATGGGTCTGGTGGGCAGAAGTATGTGACTCT

C57BL/6  GGAGGTGACAGTGCCTTTGATATGGGACATGGCTTTTGCTCCATGTCTTTCCTAATGGGGGGGGGGGAGGGGGGTGTCTCTGCCTCAGGCACCTCCTGTAA
BALB/c   GGAGGTGACAGTGCCTTTGATATGGGACATGGCTTTTGCTCCATGTCTTTCCTAATGGGGGGGGG-AGGGGGGTGTCTCTGCCTCAGGCACCTCCTGTAA

C57BL/6  GACCTTTTCCCACTCAGATGACTTGGAATTTCTGGAATCATAATTGAAAATGATCTTTCCTCTCCTGGGTTGTTTCCATCAGATGCTTTGGTCATGGTGG
BALB/c   GACCTTTTCCCACTCAGATGACTTGGAATTTCTGGAATCATAATTGAAAATGATCTTTCCTCTCCTGGGTTGTTTCCATCAGATGCTTTGGTCATGATGG

C57BL/6  CAAGAAAGGCGACCGACGTGCGATCCACGACCATTTGAAAATGCCGGTGAAATAAACCACCCCAAGTAAATAAAACCATAGACATCATCCCCAGATCTGT
BALB/c   CAAGAAAGGCGAGCGACGTGCGATCCACGACCATTTGAAAATGCCGGTGAAATAAACCACCCCAAGTAAATAAAACCATAGACATCATCCCCAGATCTGT

C57BL/6  GTTATAACTAACCGTGCTAATTTCTTCACTGGGAAGGAAAATGGTACTAGGTAGAAAATCAGACTTCTAAGAGGGAATAAAACAGGGGCTGGAGAGATGG
BALB/c   GTTATAACTAACCGTGCTAATTTCTTCACTGGGAAGGAAAACGGTACTAGGTAGAAAATCAGACTTCTAAGAGGGAATAAAACAGGGGCTGGAGAGATGG

C57BL/6  CTCAGCGAGTTAAGAGCACTGACTGCTCTTCAGAAGGTCCTGAGTTCAAATCCCAGCAACCACATGGTGGCTCACAACCAGATATGACGCCCTCTTCTGG
BALB/c   CTCAGCGAGTTAAGAGCACTGACTGCTCTTCAGAAGGTCCTGAGTTCAAATCCCAGCAACCACATGGTGGCTCACAACCAGATATGACGCCCTCTTCTGG

C57BL/6  TCTGTCTGAAGACAGCTACAGTGTACTTACATATAATGATAATGATGATGATAATAATAATAATAATTAATAAATAAAAGAGGTAATAAAACAGTACATT
BALB/c   TCTGTCTGAAGACAGCTACAGTGTACTTACATATAATGATAATGATGATGATAATAATAATAATAATTAATAAATAAAAGAGGTAATAAAACAGTACATT

C57BL/6  AGTAATTAGAGCCATCGTGTAATATTTATTTTAGGAAGAAGCTTCACAGGGAAAGGGAGGAGCATG
BALB/c   AGTAATTAGAGCCATCGTGTAATATTTATTTTAGGAAGAAGCTTCACAGGGAAAGGGAGGAACATG
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X

Pop4

chr7:37,961,843-37,962,567

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C57BL/6  ----------------------------------------CTGTTTCTATCTCTTTGGGGCTGCTGCCAGCAGGCCTAGGCTTCCCTATGCACTGGTCTAGA
BALB/c   ----------------------------------------CTGTTTCTATCTCTTTGGGGCTGCTGCCAGCAGGCCTAGGCTTCCCTATGCACTGGTCTAGA

C57BL/6  ATGCATGTCTCTCCTAGTAAGCCTTTCTGCCTTTAGGCCCTGGTTGTGGGTACACAAAGGTTCAAAGGGACAGAGATTGCGTTTCTGACACCGTGCTCAT
BALB/c   ATGCATGTCTCTCCTAGTAAGCCTTTCTGCCTTTAGGCCCTGGTTGTGGGTACACAAAGGTTCAAAGGGACAGAGATTGCGTTTCTGACACCGTGCTCAT

C57BL/6  GAGTACTGTTCCCATGCCTCATAACAATATCTGAGATGGCTGTGGTGGAATATAATATGCCTACAATCCTAGCATTTGGAAGGGTGAGGCAGAGAGATCC
BALB/c   GAGTACTGTTCCCATGCCTCATAACAATATCTGAGATGGCTGTGGTGGAATATAATATGCCTACAATCCTAGCATTTGGAAGGGTGAGGCAGAGAGATCC

C57BL/6  TGAGTTCCCAGATAGCCTGGTATATAGGGTAAGTTTCAGGCTAGCCTGTGCTGTAAAGCTAGAGACCCTATTTTAAAAAAAGAATCAAGCCGGGCGTGGT
BALB/c   TGAGTTCCCAGATAGCCTGGTATATAGGGTAAGTTTCAGGCTAGCCTGTGCTGTAAAGCTAGAGACCCTATTTTAAAAAAAGAATCAA----------

C57BL/6  GGCGCACGCCTTTAATCCCAGCACTTGGGAGGCAGAGACAGGCGGATTTCTGAGTTCGAGGCCAGCCTGGTCTACAAAGAGAGTTCCGGGACAGCCAAGA
BALB/c   ----------------------------------------------------------------------------------------------------

C57BL/6  CTATACAGAGAAACCCTGTCTCGAAAAACCAAAAAAAAAAAAAAAAAAAA----AAAGAATCAAAACTAATCAACTAATGAAAGATCAAAAAAGGCTGGG
BALB/c   ------------------------------------------------------------AACTAATCAACTAATGAAAGATCAAAAAAGGCTGGG

C57BL/6  AGTATGGGTCATGGTCACAGGCTCAATGGTGTTCGTTTCCTTCCCGGCATTCAAACAAACAACAAAGAAAACCTTTCTTCTGTGCATCTTCAATGCTGAC
BALB/c   AGTATGGGTCATGGTCACAGGCTCAATGGTGTTCGTTTCCTTCCCGGCATTCAAACAAACAACAAAGAAAACCTTTCTTCTGTGCATCTTCAATGCTGAC

C57BL/6  CCTGGTCTAGGATGCAGATATTCCTCACAGGCCAGAGCCACCTCCTCACTGGCATATGTTCTT
BALB/c   CCTGGTCTAGGATGCAGATATTCCTCACAGGCCAGAGCCACCTCCTCACTGGCATATGTTCTT
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Y

Ppp1r14d

chr2:118,921,131-118,922,245

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C57BL/6  ----------------------------------------------TCTGTGGACGATGCCCTCCTTCTCTTCTCAGAAGCCCAGTGGACCTTCTTGTCTGGG
BALB/c   ----------------------------------------------TCTGTGGACGATGCCCTCCTTCTCTTCTCAGAAGCCCAGTGGACCTTCTTGTCTGGG

C57BL/6  TTGTCTGTGCCAGGGCTGGGAGATGTACAGGAAGCAGGGCTTGAAGACAGCATGGAGAGATCAGACTGTGCAAGGTGCTGGGAGAAACTGCCAGTCTAGG
BALB/c   TTGTCTGTGCCAGGGCTGGGAGATGTACAGGAAGCAGGGCTTGAAGACAGCATGGAGAGATCGGACTGTGCAAGGTGCTGGGAGAAACTGCCAGTCTAGG

C57BL/6  CAAGAGAATAGAGGGAAATGAGGGGACAGAGAATGGAGGGAGAGGCCCACAAGGAAGAAAGGAGGTGGGAAGAGGGCCAAGGCTCTTGGGAGGGGCAGGG
BALB/c   CAAGAGAATAGAGGGAAATGAGGGGACCGAGAATGGAGGGAGAGGCCCACAAGGAAGAAAGGAGGTGGGAAGAGGGCCAAGGCTCTTGGGCGGGGCAGGG

C57BL/6  GTCAAAGATCAATAGGTCTCTAGTTAGTGCCGGGAATGAACTTCCTAGCCTCTCTCTGCCAGCCAGTGGCATTCAGAGCCATATCCCAGCCTCCATTCTG
BALB/c   GTCAAAGATCAATAGGTCTCTAGTTAGTGCCGGGAATGAACTTCCTAGCCTCTCTCTGCCAGCCAGTGGCATTCAGAGCCGTATCCCAGCCTCCATTCTG

C57BL/6  CAGCTGCTGGAGCCCACAGTAACATAAACCTCAAACAAGCAAATGTCAAGAGGCTAGCAAGCCTTGAGAAGAGGAAGAAGGAGCCTTTGAGTGCTGAAGG
BALB/c   CAGCTGCTGGAGCCCACGGTAACATAAACCTCACACAAGCAAATGTCAAGAGGCTAGCAAGCCTTGAGAAGAGGAAGAAGGAGCCTTTGAGTGCTGAAGG

C57BL/6  GTGTGGGGCTCCCACCTGTCTTCCGGGATAGCTCTAGACATACGGTGACTAGGCTCAATCAACTGAAGTCCCTCAGCATCCAATCTTCTAGGAACTAGAT
BALB/c   GTGTGGGGCTCCCACCTGTTTTCCAGGATAGCTCTAGACATACGGTGACTAGGCTCAATCAACTGAAGTCCCTCAGCATCCGATCTTCTAGGAACTAGAT

C57BL/6  AGTCTATTGCAGGCCTGAGCAGCTGTGGTCGGATAATTCTGGTTCCTGCAGGGGTAGGATTCCTCCTCAAGGTGAGGAGCCACCGAGGGCAATCTCAGCC
BALB/c   AGTCTATTGCAGGCCTGAGCAGCTGTGGTCGGATAATTCCGGTTCCTGCGGTGGTAGGATTCCTCCTCACAGTGAGGAGCCACCGAGGGCAATCTCAGCC

C57BL/6  AGTGGATAGAGTTCACAGATGGCTACTTCTGTCCTGTGTCTGGGTGTGTCTGGATATTGGCTTTGCTGCTGTGATTGTTAAAGGCAGATTTATGCAGCCT
BALB/c   AGTGGATAGAGTTCATAGATGGCTACTTCTGTCCTGTGTCTGGGTGTGTCTGGATATTGGCTTTGCTGCTGTGATTGTTAAAGGCAGATTTATGCAGCCT

C57BL/6  GGCCTACAAGACCTGTTGTCATTCTTAGAAGCCAAGTTTATGGTCATGTGACCCTCCCCTGATTCAGCTTCTTCCTGATAAAAGACACCTTCAGACCTGA
BALB/c   GGCCTACAAGACCTGTTGTCATTCTTAGAAGCCAAGTTTATGGTCATGTGACCCTCCCCTGATTCAGCTTCTTCCTGATAAAAGACACCTTCAGACCTGA

C57BL/6  CTTCACATAGGAATCCTGGACTGGTAAACAAGCTTGCCATTTAAAAGTACTTTCATTATTCAGTCCTTTATAAGAAAAAATTTAAATAACTTAATGTGGT
BALB/c   CTTCACATAGGAATCCTGGACTGGTAAACAAGCTTGCCATTTAAAAGTACTTTCATTATTCAGTCCTTTATAAGAAAAAATTTAAATAACTTAATGTGGT

C57BL/6  TCATTTTGTCTTGTTTTTCGTTTTAATGAACAGCTCAGAAAAACAGATAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAGAA
BALB/c   TCATTTTGTCTTGTTTTTCGTTTTAATGAACAGCTCAGAAAAAAAGATAGAA-GAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAGAG

C57BL/6  AGAAAGGAAGGAAGG--AAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG
BALB/c   AGAGAGAGAGAGAGGGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG
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Z

Rab6b

chr9:102,967,555-102,969,590

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C57BL/6   ----------------------------------TATCGTGGGGGCTGTTGGATGAAGAGACACAGAAACTTCCTGTACTATTTTTTGAAACCTCTATGT
BALB/c    ----------------------------------TATCGTGGGGGCTGTTGGATGAAGAGACACAGAAACTTCCTGTACTATTTTTTGAAACCTCTATGT

C57BL/6   AGTCTAAAACTATTTCAGGCTTTAAAAACTGGACACATTTTTACTGAAAATGGTTTCAAAATTGGGGCAGACGATGGAATGCTAAGCAGACACGGGAACC
BALB/c    AGTCTAAAACTATTTCAGGCTTTAAAAACTGGACACATTTTTACTGAAAATGGTTTCAAAATTGGGGCAGACGATGGAATGCTAAGCAGACACGGGAACC

C57BL/6   AAAGGCTCTGCTCTATGCATCAACAGGAATCTTGGGAGTACAGCGAGAAGGGAAGAGCAAGTCAGAAGACAGGGTTTGAAATATGAATTCAAAAGACTCA
BALB/c    AAAGGCTCTGCTCTATGCATCAACAGGAATCTTGGGAGTACAGCGAGAAGGGAAGAGCAAGTCAGAAGACAGGGTTTGAAATATGAATTCAAAAGACTCA

C57BL/6   AGAGAAATGAAAGTGTTGAGAGTTTGGGTTTTCTGCCTTGGGGAAGGAGGAAAAGGGGGAGGGGATAAAAGAAGAATTAGAAGACAGGTGTGTGTTCACT
BALB/c    AGAGAAATGAAAGTGTTGAGAGTTTGGGTTTTCTGCCTTGGGGAAGGAGGAAAAGGGGGAGGGGATAAAAGAAGAATTAGAAGACAGGTGTGTGTTCACT

C57BL/6   GCGATATGATGTCTTTCCATGTTCCTCATCCAGAGAACACACTCATCAGGAAGGGCAGAAAGATGCCATGCAGAAGAAACTCTTTCTAGTGAGACTACCA
BALB/c    GCGATATGATGTCTTTCCATGTTCCTCATCCAGAGAACACACTCATCAGGAAGGGCAGAAAGATGCCATGCAGAAGAAACTCTTTCTAGTGAGACTACCA

C57BL/6   AAAAGAGGCTTATAGTGGCTCTTTTTATCTATCACATGGGAAATGCCTGATATCCCAGGACAGAATAAAGATGATCCCTTCCCCTAAGAGACAAAGGAAT
BALB/c    AAAAGAGGCTTATAGTGGCTCTTTTTATCTATCACATGGGAAATGCCTGATATCCCAGGACAGAATAAAGATGATCCCTTCCCCTAAGAGACAAAGGAAT

C57BL/6   GGCAAGGGTAAGGGAGAGACTTGGAAGAGAGCAGAAGCATTCTAAGGTTAGGATTCACATACAGCATGAAGACCATGCTGTGTAGCTCTGCCCAGACTGC
BALB/c    GGCAAGGGTAAGGGAGAGACTTGGAAGAGAGCAGAAGCATTCTAAGGTTAGGATTCACATACAGCATGAAGACCATGCTGTGTAGCTCTGCCCAGACTGC

C57BL/6   AGGAGCCAACCCAGCCGACTGAACCAGTACAGATGAGGAAATGCTGGGTGGAAGGTGTGACACCCCCCAACCCCCTGAATGCCTTGACCTCCACAGGCAG
BALB/c    AGGAGCCAACCCAGCCGACTGAACCAGTACAGATGAGGAAATGCTGGGTGGAAGGTGTGACACCCCCCAACCCCCTGAATGCCTTGACCTCCACAGGCAG

C57BL/6   GGAGGGGTGTGGCTTAGGAGTAGTTCTTTCACTGCTGGAGTGTCCAACTTCTAGCTACGGAGACACAACATTGCAATCTACAAACTTCACAATGTAAAAC
BALB/c    GGAGGGGTGTGGCTTAGGAGTAGTTCTTTCACTGCTGGAGTGTCCAACTTCTAGCTACGGAGACACAACATTGCAATCTACAAACTTCACAATGTAAAAC

C57BL/6   CAGGCAATGGGATCAACAACAATAAACAAAAACTTGCCCCAAAAAATGTAGAAACCCATCCAGTATCTCATAATGTTCTACATAAGATTACAATATTGTG
BALB/c    CAGGCAATGGGATCAACAACAATAAACAAAAACTTGCCCCAAAAAATGTAGAAACCCATCCAGTATCTCATAATGTTCTACATAAGATTACAATATTGTG

C57BL/6   TTGTGCTGAATTCAAAGCTATCCTGCAAGGCATATGGCCTGTGGACAGTGGGTCGGACACACCTGCCAAAACTTTCCTCAGCCCATGCTGGATCCCGAGA
BALB/c    TTGTGCTGAATTCAAAGCTATCCTGCAAGGCATATGGCCTGTGGACAGTGGGTCGGACACACCTGCCAAAACTTTCCTCAGCCCATGCTGGATCCCGAGA

C57BL/6   CAGCAACACACTCGGGGCAAAAGTAGGGTGGAGTCTGAGTTATCTTAGTCTGGTGCCCAATCTGGCATGCTTATATGCTCAGAGGGATGACCTCCGACTC
BALB/c    CAGCAACACACTCGGGGCAAAAGTAGGGTGGAGTCTGAGTTATCTTAGTCTGGTGCCCAATCTGGCATGCTTATATGCTCAGAGGGATGACCTCCGACTC

C57BL/6   CAGGGACTTCAAACCGAAGAAGACCACAAGAATAGAACAGTTACTCTGATTTGAGAGTAGTTTTAGAGGTTAATTCGAGCATTCAGCAACTGTTTCCTAA
BALB/c    CAGGGACTTCAAACCGAAGAAGACCACAAGAATAGAACAGTTACTCTGATTTGAGAGTAGTTTTAGAGGTTAATTCGAGCATTCAGCAACTGTTTCCTAA

C57BL/6   ACTCTAGGTGAAGTGGAACCTCAGCTGCTTCCATGGAGTTTCCTGTGAGGGCTCAATGTGCGGTGGGAGACTCTAGTGGGTACATTCGGGGTAAATTCAT
BALB/c    ACTCTAGGTGAAGTGGAACCTCAGCTGCTTCCATGGAGTTTCCTGTGAGGGCTCAATGTGCGGTGGGAGACTCTAGTGGGTACATTCGGGGTAAATTCAT

C57BL/6   AAGTGTCCCCTGGGAAATCCGTAGGCACGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCATTTCACTCCTGGCTTGCTTTGTGTAACATACACTACACA
BALB/c    AAGTGTCCC-TGGGAAATCCGTAAGCACGGGTGTGTGTGTGTGTGTGTGTGTGTGTGCATTTCACTCCTGGCTTGCTTTGTGTAACATACACTACACA

C57BL/6   TTCCAAACAGTCCCAAACAAACATTCCCTGAATGGCCAGAGAAGGTCAAGACCAGCAAGTGGCTGGAGAGGAAGAGGGGAGGGGCTTTGTAAAGCCTCAA
BALB/c    TTCCAAACAGTCCCAAACAAACATTCCCTGAATGGCCAGAGAAGGTCAAGACCAGCAAGTGGCTGGAGAGGAAGAGGGGAGGGGCTTTGTAAAGCCTCAA

C57BL/6   TTAACCCGATGCCTTAGAGTGTACTGCTTGGGGACTGCGTTTAACCTTAGTCTGGCGTCTACTCCTTGCTCTCACGCTACTGTGTGTGCCCTGCAAACTT
BALB/c    TTAACCCGATGCCTTAGAGTGTACTGCTTGGGGACTGCGTTTAACCTTAGTCTGGCGTCTACTCCTTGCTCTCACGCTACTGTGTGTGCCCTGCAAACTT

C57BL/6   AGAGGTCGCTCTCTTATACTCTTGTAGCTCATTACCCGAATAAACCTAACTAGCAGGGCGCAGGAGTGTGGTTGGGCTGACGGTCTCAGGATCAAAAGAG
BALB/c    AGAGGTCGCTCTCTTATACTCTTGTAGCTCATTACCCGAATAAACCTAACTAGCAGGGCGCAGGAGTGTGGTTGGGCTGACGGTCTCAGGATCAAAAGAG

C57BL/6   GCAGGGCATTGTCTTTGGGTTAGTGGAGCTGTCTTCTACCAGGCAGGTTAGGTTTCAAACCCTAGTAGGCATATCCTGTAAGGGTGTCTTCTCTCTCACT
BALB/c    GCAGGGCATTGTCTTTGGGTTAGTGGAGCTGTCTTCTACCAGGCAGGTTAGGTTTCAAACCCTAGTAGGCATATCCTGTAAGGGTGTCTTCTCTCTCACT

C57BL/6   GGCCAGCTCCTCTGGGGACAACCACAGATCCCCTCCGCATGAAGAGTCTGAGCCTAGCTAGATAGGAGGTAAGCTAGAGGCCAGCAGGGGCCACCGAGGA
BALB/c    GGCCAGCTCCTCTGGGGACAACCACAGATCCCCTCCGCATGAAGAGTCTGAGCCTAGCTAGATAGGAGGTAAGCTAGAGGCCAGCAGGGGCCACCGAGGA

C57BL/6   GCCATACCCCAGGTCTGAGCCAGGTATCCGCACATCTTCCTACTCACCACCACACCACACACTGACCCTT
BALB/c    GCCATACCCCAGGTCTGAGCCAGGTATCCGCACATCTTCCTACTCACCACCACACCACACACTGACCCTT
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AA

Slc13a3

chr2:165,163,937-165,164,881

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C57BL/6   -------------------TAGAA---CGACATAGACTGATTCCTTTAT-TTCACCGTGAGCCTATGATGCGTTATCATATTCCCTCTTTCTGGGTAGGG
BALB/c    -------------------TAGCA---CGACATAGACTGATTCCTTTATCTTCACCGTGAGCCTATGATGCGTTATCATATTCCCTCTTTCTGGGTAGGG

C57BL/6   GGTACGCAAACCAAAGTTCAGAGAGGTTAAGTGACTGGCGACAGGTCACACAGTTGTTCTTCGGAAAGACTGTGAAGGGCTATATACCCCAGTAGCACCA
BALB/c    GGTAAGCAAACCAAAGTTCAGAGAGGTTAAGTGACTGGCGACAGGTCACACAGTTGTTCTTCGGAAAGACTGTGAAGGGCTATATACCCCAGTAGCACCA

C57BL/6   AGCAAGCCGTCAGAGCTCAAACTTTAGAAGAGTGGGAGGACCGAGAGAGGCAGACCAGGGAGAGGCAAGGAAGGGAGAAGGGGAGCGGGTGCTCCTAGGG
BALB/c    AGCAAGCCGTCAGAGCTCAAACTTTAGAAGAGTGGGAGGACCGAGAGAGGCAGACCAGGGAGAGGCAAGGAAGGGAGAAGGGGAGCGGGTGCTCCTAGGA

C57BL/6   GTAGGCAGGCTCAAGGCGGGAGGGTCTCGACCCGGGACCACCGTACCTTGGGCGGCAGGGCGAAGAGAATGGGCAGCAGAGCCAGCGGCACCAGCAGCAG
BALB/c    GTAGGCAGGCTCAAGGCGGGAGGGTCTCGACCCGGGACCACCGTACCTTGGGCGGCAGGGCGAAGAGAATGGGCAGCAGAGCCAGCGGCACCAGCAGCAG

C57BL/6   CACCAGGAGGCGCCGCGCGCTCCACACCTTCTTGGCCAGCGCCGCCAGCGCCGCCATCCGCGCGATCGCTGGAGACCAGGCGGCCCGACTGCCCCTCAGC
BALB/c    CACCAGGAGGCGCCGCGCGCTCCACACCTTTTGGCCAGCGCCGCCAGCGCCGCCATCCGCGCGATCGCTGGAGACCAGGCGGCCCGACTGCCCCTCAGC

C57BL/6   GGCCGCCGGCAGGGACCTAAAGCCCCAAGGGACGGGGAGGAGCCATGCGGAACCGCCCCGGGCCGCGCCTCCTTGGTCTGGACAAGGAGCAGGGAAGGGG
BALB/c    GGCCGCCGGCAGGGACCTAAAGCCCCAAGGGACGGGGAGGAGCCATGCGGAACCGCCCCGGGCCGCGCCTCCTTGGTCTGGACAAGGAGCAGGGAAGGGG

C57BL/6   CCCCAGAGCACCCCACCCGCCCCCGCGCCCCACTCTGGACTCACGTGGGAAATGGGGCAAAGCCCAGGTGGGACTAAAGGCCTCAGCACCGTCATCCCAC
BALB/c    CCCCAGAGCACCCCACCCGCCCCCGCGCCCCACTCTGGACTCACGTGGGAAATGGGGCAAAGCCCAGGTGGGACTAAAGGCCTCAGCACTGTCATCCCAC

C57BL/6   TGTCCAACCCTGTAGGGACAGACCAAGCTACTGAGACCTCTAGTGACCGTGGTTGCAGCCTCTTCCAGACTTGGAGGTTGGTGGGGGGG----TTTAAGT
BALB/c    TGTCCAACCCTGTAGGGACAGACCACGCTACTGAGACCTCTAGTGACCGTGGTTGCAGCCTCTTCCAGACTTGGAGGTTGGTGGGGGGGGGGGTTTAAGT

C57BL/6   GAGATAGTGCTTCGTGCAAAGGGCCGGGTCACCTGTGGGTAGGAGCTTTCCCTTCTCAGTGACAGATGCCACAACCTGCTTGATATTGTGTGTGTTGGGA
BALB/c    GAGATAGTGCTTCGTGCAAAGGGCCCGGTCACCTGTGGGTAGGAGCTTTCCCTTCTCAGTGACAGATGCCACAACCTGCTTGATATTGTGTGTGTTGGGA

C57BL/6   CAGGCTCTTATTTAGCCCAAGCTGGCCTGCATCTCCCTATGCTGCTGAGGACAACCTTGAACTCCCATCCTCCTGC
BALB/c    CAGGCTCTTATTTAGCCCAAGCTGGCCTGCATCTCCCTATGCTGCTGAGGACAACCTT-AACTCCC-TCCTCCTGC
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AB

Sfi1

chr11:3,092,948-3,093,861

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C57BL/6   ----------------------------------------AAACGCAACGTGAGCTCAGCTCCTTGCTTGGTCACTTGAGCTCAGTGTACCAACGAGC
BALB/c    ----------------------------------------AAACGCAACGTGAGCTCAGCTCCTTGCTTGGTCACTTGAGCTCAGTGTACCAACGAGC

C57BL/6   CCTACGCCCCGCCACACCCCTGAATCGAACGTGGATCTGCGCAGACTAGTAAGCGAAGCACGAGCTGGAGAATCACTCAGCGGAGCTCTCCACCAGGGGG
BALB/c    CCTACGCCCCGCCACACCCCTGAATCGAACGTGGATCTGCGCAGACTAGTAAGCGAAGCACGAGCTGGAGAATCACTCAGCGGAGCTCTCCACCAGGGGG

C57BL/6   AGAAGGATGCATAGACCCTGCAGAAACAGCGCGAGTGCAGCCGTGACTGCGAGCGACCTTACGCACGCCCTGCTCGCACTTCCACGCATGGACCAGAGCC
BALB/c    AGAAGGATGCATAGACCCTGCAGAAACAGCGCGAGTGCAGCCGTGACTGCGAGCGACCTTACGCACGCCCTGCTCGCACTTCCACGCATGGACCAGAGCC

C57BL/6   TTGTGGGTAGGCAGCATCTCCTGCACTTCTACAGAAGAAAGCAGAAGCCCCGACCAAGCCGTTCCAGGACAAAGTTCCTAGGAACGCGCGCTCCGCCAAC
BALB/c    TTGTGGGAAGGCAGCATCTCCTGCACTTCTACAGAAGAAAGCAGAAGCCCCGACCAAGCCGTTCCAGGACAAAGTTCCTAGGAACGCGCGCTCCGCCAAC

C57BL/6   TTCAAAACGCAAGGGCGAGCCAGTCAAAAGCTGGAGGCGCTAGGCCGGGCCTCGTACCTGAGGGAGGTGACTCCTCAGCAGACGCTAGACAGAGGTGGTA
BALB/c    TTCAAAACGCAAGGGCGAGCCAGTCAAAAGCTGGAGGCGCTAGGCCGGGCCTCGTACCTGAGGGAGGTGACTCCTCAGCAGACGCTAGACAGAGGTGGTA

C57BL/6   GCAAAGGGCCCCAGCCCAGAGTTTCCGGCCCTGCGCCGACGGCGGCTCCTCCCCCGTCTCCACGGCAACGCGACCCGCGCCGGAAGCTGCTCTGTCCAGC
BALB/c    GCAAAGGGCCCCAGCCCAGAGTTTCCGGCCCTGCGCCGACGGCGGCTCCTCCCCCGTCTCCACGGCAACGCGACCCGCGCCGGAAGCTGCTCTGTCCAGC

C57BL/6   TTAGTGCGCTCTGTCTTCCAGGAAACAGAGACTTCTCTCTAAGCTCGGCTTCCTACGGTTTTCTTGCCCTGAAGTTTCTGCGCTTCTGAGAAGCGGGTCA
BALB/c    TTAGTGCGCTCTGTCTTCCAGGAAACAGAGACTTCTCTCTAAGCTCGGCTTCCTACGGTTTTCTTGCCCTGAAGTTTCTGCGCTTCTGAGAAGCGGGTCA

C57BL/6   CTAGTTACAACTCCTGCATGGGACCGGTGTGAGACGGAAAAGTGTCTCTTTTCATTGCGTGGTGGCTCACGTCGGTAATCTCCGCATCAAACAGCCGAAT
BALB/c    CTAGTTACAACTCCTGCATGGGACCGGTGTGAGACGGAAAAGTGTCTCTTTTCATTGCGTGGTGGCTCACGTCGGTAATCTCCGCATCAAACAGCCGAAT

C57BL/6   CTTTAAAGAGAACTTTCAGAACAAAGTATGAAGTTTCATACTAAGAACAGTGAAAACTAGTGGGTGGGTGTCTGAAGACGAAAACCAAGGGGCAGGAGAT
BALB/c    CTTTAAAGAGAACTTTCAGAACAAAGTATGAAGTTTCATACTAAGAACAGTGAAAACTAGTGGGTGGGTGTCTGAAGACGAAAACCAAGGGGCAGGAGAT

C57BL/6   ATGACTCACCAGTTAAATGCACTTTTCATTCATCCAGACTCCCAATACCCACACGG
BALB/c    ATGACTCACCAGTTAAATGCACTTTTCATTCATCCAGACTCCCAATACCCACACGG
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AC

Sfi1 (pseudogene or duplication)
(location unknown)

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C57BL/6  ------------------------------------------------CAAATTAACCATGAAAAATCTCATCCTTGGGGCTGGAGAGATGGCTCAGTG
BALB/c   ------------------------------------------------CAAATTAACCATGAAAAATCTCATCCTTGGGGCTGGAGAGATGGCTCAGTG

C57BL/6  GTTAAGAGCACTGACTGCTCTTCCAGAGTTCCTGAGTTCAATTCCCAGCAACCACATGGTGGCTCACAACCATCTGTAATGGGATCTGATGCCCTCTTCT
BALB/c   GTTAAGAGCACTGACTGCTCTTCCAGAGTTCCTGAGTTCAATTCCCAGCAACCACATGGTGGCTCACAACCATCTGTAATGGGATCTGATGCCCTCTTCT

C57BL/6  GGTGTGTCTGAAGACAGCGACAGTGTACTCATATACATAAAATAAACAAATTGTTAAAAAAAAAAAAGAAAAGAAAAATCTCATCCTTGCAAGGCTAAGT
BALB/c   GGTGTGTCTGAAGACAGCGACAGTGTACTCATATACATAAAATAAACAAATTGTTAAAAAAAAAAAAGAAAAGAAAAATCTCATCCTTGCAAGGCTAAGT

C57BL/6  TTTTACTGATATATAATCTGCATTTAAGGCTGGAGATGGTTTAATTGTGCTTTTCCACCACAAAAAGAGCTCTAGGTTCAGTCATCAGCCCTGAATAGAA
BALB/c   TTTTACTGATATATAATCTGCATTTAAGGCTGGAGATGGTTTAATTGTGCTTTTCCACCACAAAAAGAGCTCTAGGTTCAGTCATCAGCCCTGAATAGAA

C57BL/6  CGGGGCATGGTGCCACACACCAGTAATCCCAGAGACAGGAGGATCTCTGCAAGCTTTTCTCTTTCTTTAAAATTTATGTATTCTGGAGCTGGAGAGATGG
BALB/c   CGGGGCATGGTGCCACACACCAGTAATCCCAGAGACAGGAGGATCTCTGCAAGCTTTTCTCTTTCTTTAAAATTTATGTATTCTGGAGCTGGAGAGATGG

C57BL/6  CTCAACAGTTAAAACCACTGATTGTTCCTTCAGAGATTCTGAGTTCAGTTCCCAGCAACCACATGGTGGCTCACAACCATCTATAATGGGATTCAATGCC
BALB/c   CTCAACAGTTAAGACCACTGATTGTTCCTTCAGAGATTCTGAGTTCAGTTCCCAGCAACCACATGGGGGCTCACAACCATCTATAAGGGGATTCAATGCC

C57BL/6  CTCTTCTGGTGTGTCTGGACAGCAACAGCGTACTCACATATATAAAATAAATCTTTTTTTAAAATTTTAAGAATTATGTATTCTGTGTATGTATAGAAGTG
BALB/c   CTCTTCTGGTGTGTCTGGACAGCAACAGCGTACTCACATATATAAAATAAATCTTTTTTAAAATTTTAAAATTATGTATTCTGTGTATGTATAGAAGTG

C57BL/6  CTTTGCCTACATGTGTGTACGAGTACCACATGAGTACATAGTTTCCTTGGAGGTCAAAAGAAGGTATCAGATTCCATGGAATTGGTGATATGAGCTTGAT
BALB/c   CTTTGCCTACATGTGTGTACGAGTACCACATGAGTACATAGTTTCCTTGGAGGTCAAAAGAAGGTATCAGATTCCATGGAATTGGTGATATGAGCTTGAT

C57BL/6  TTTTTTAATTCATTTTGGCCATATGTTTAGAAGCCTTTATACTCTTGTCAAAGTTTTCAAGACTCATCCCATATGGAGTCCTGACCTACAGTTTGAAAAG
BALB/c   TTTTTTAATTCATTTTGGCCATATGTTTAGAAGCCTTTATACTCTTGTCAAAGTTTTCAAGACTCATCCCATATGGAGTCCTGACCTACAGTTTGAAAAG

C57BL/6  CTGAGATCAGGGCTGGAGAAATACCCCAGCAGTTAACAACAGTACATGATATTCTAGCAGAGAAATGAAGTTTGGTTCCTACCACCCACAACCTGTAGTT
BALB/c   CTGAGATCAGGGCTGGAGAAATACCCCAGCAGTTAACAACAGTACATGATATTCTAGCAGAGAAATGAAGTTTGGTTCCTACCACCCACAACCTGTAGTT

C57BL/6  TCCAACCTCCTTTAACTACAGTTCCAAGGAATCCAATAAGAGATCGATCCAACACTCGTGGCTCCAAGAGAGCCTGTACAAATGCACATGTACCCCCACA
BALB/c   TCCAACCTCCTTTAACTACAGTTCCAAGGAATCCAATAAGAGATCGATCCAACACTCGTGGCTCCAAGAGAGCCTGTACAAATGCACATGTACCCCCACA

C57BL/6  AACACATAACTAAAAACAATAAAAGTAAATCTGTGTTGGGGGGGAGAGGGGCTGAAGTGATGGCTCAGCTGT----------
BALB/c   AACACATAACTAAAAACAATAAAAGTAAATCTGTGTTGGGGGGGAGAGGGGCTGAAGTGATGGCTCAGCTGT----------

C57BL/6  ----------TGAGGACGAATCAGATTCAGCTGACCGCTTTTCCAAAGTACCCAGATTAAGTTCCCATAACCCAGGGGTGGCTCACAATCACCTGGAACT
BALB/c   ----------TGAGGACGAATCAGATTCAGCTGACCGCTTTTCCAAAGTACCCAGATTAAGTTCCCATAACCCAGGGGTGGCTCACAATCACCTGGAACT

C57BL/6  CCAGTTCTGAGGTTCCAATGCCCTCGTCTGACCTCTCCATTTGGGCTTCTGAGGGCAACAGGCAAGCAAAAGGTACCCAGACATCCATGCACGCAAAACA
BALB/c   CCAGTTCTGAGGTTCCAATGCCCTCGTCTGACCTCTCCATTTGGGCTTCTGAGGGCAACAGGCAAGCAAAAGGTACCCAGACATCCATGCACGCAAAACA

C57BL/6  GCCACACACATAAATCTTTTTTTTTTA-AATGTTTTTAAATAATCATGAATTGGAGGTTAGCCTGGATTCTGAGGCCAGTGTGAGCTAGCTTGTGTTATAG
BALB/c   GCCACACACATAAATCTTTTTTTTTTA-AATGTTTTTAAATAATCATGAATTGGAGGTTAGCCTGGATTCTGAGGCCAGTGTGAGCTAGCTTGTGTTATAG

C57BL/6  AGACGCCAGAAATGGAGCCCAAAGCCTTCAGGACACCAGACAATCAGTCTACCTATGAGCTGGCATTTCAGGTGTGTTGTGAGCCACCAGTGGTGGACGC
BALB/c   AGACGCCAGAAATGGAGCCCAAAGCCTTCAGGACACCAGACAATCAGTCTACCTATGAGCTGGCATTTCAGGTGTGTTGTGAGCCACCAGTGGTGGACGC

C57BL/6  TGGGAGTCCAACTGGTATTGTCTCAAAAAGGAGTAAGGGTTTCTTAAGCGCTGAGCCATCTCTCTGGCTCCTTTAATAAATCATCTTTCTTTTTAAAAAT
BALB/c   TGGGAGTCCAACTGGTATTGTCTCAAAAAGGAGTAAGGGTTTCTTAAGCGCTGAGCCATCTCTCTGGCTCCTTTAATAAATCATCTTTCTTTTTAAAAAT

C57BL/6  ATTTAATATTAAATTTTAAACCATGATAACTTCAAATTACTTGATAATTACCAGGCAATCTAAAGCCCAGGGACTACAATTAAGACAGCATTTACAGCAC
BALB/c   ATTTAATATTAAATTTTAAACCATGATAACTTCAAATTACTTGATAATTACCAGGCAATCTAAAGCCCAGGGACTACAATTAAGACAGCATTTACAGCAC

C57BL/6  GGGTTGCACACGTTTTTCTGAAGCACTTTTCATGAACGACCCACTCTAAGAACAGGCACCTCAGCTGGTGCTTATTGTCATTTTCCAGGCTGATGCTCAA
BALB/c   GGGTTGCACACGTTTTTCTGAAGCACTTTTCATGAACGACCCACTCTAAGAACAGGCACCTCAGCTGGTGCTTATTGTCATTTTCCAGGCTGATGCTCAA

C57BL/6  GACCATCAGCTAACAGG-TGGCAAAGGTGCCACTCTCATTCAAACCTCGATACACCTTCAGGAACTACACCAGGAGAGGTTCCATGGTACAAACGCAACG
BALB/c   GACCATCAGCTAACAGGCTGGCAAAGGTGCCACTCTCATTCAAACCTCGATACACCTTCAGGAACTACACCAGGAGAGGTTCCATGGTACAAACGCAACG

C57BL/6  TGAGCTCAG--------------------------TGTACCAACGAGCCCTACGCCCAGCCACACCCCTGAATCGAACGTGGATCTGCGCAGACTAGTAA
BALB/c   TGAGCTCAG--------------------------TGTACCAACGAGCCCTACGCCCAGCCACACCCCTGAATCGAACGTGGATCTGCGCAGACTAGTAA

C57BL/6  GCGAAGCACGAGCTGGAGAATCACTCAGCGGAGCTCTCCACCAGGGGGAGAAGGATGCATAGACCCTGCAGAAACAGCGCGAGTGCAGCCGTGACTGCGA
BALB/c   GCGAAGCACGAGCTGGAGAATCACTCAGCGGAGCTCTCCACCAGGGGGAGAAGGATGCATAGACCCTGCAGAAACAGCGCGAGTGCAGCCGTGACTGCGA

C57BL/6  GCGACCTTACGCACGCCCTGCTCGCACTTCCACGCATGGACCAGAGCCTTGTGGGTAGGCAGCATCTCCTGCACTTCTACAGAAGAAAGCGGAAGCCCCG
BALB/c   GCGACCTTACGCACGCCCTGCTCGCACTTCCACGCATGGACCAGAGCCTTGTGGGTAGGCAGCATCTCCTGCACTTCTACAGAAGAAAGCGGAAGCCCCG

C57BL/6  ACCAAGCCGTTCCAGGACAAAGTTCCTAGGAACGCGAGCTCCGCCAACTTCAAAACACAAGGGCGAGCCAGTCAAAAGCTGGAGGCGCTAGGCCGGGCCT
BALB/c   ACCAAGCCGTTCCAGGACAAAGTTCCTAGGAACGCGAGCTCCGCCAACTTCAAAACACAAGGGCGAGCCAGTCAAAAGCTGGAGGCGCTAGGCCGGGCCT

C57BL/6  CGTACCTGAGGGAGGTGACTCCTCAGCAGACGCTAGACAGAGGTGGTAGCAAAGGGCCCCAGCCCAGAGTTTCCGGCCCTGCGCCGACGGCGGCTCCTCC
BALB/c   CGTACCTGAGGGAGGTGACTCCTCAGCAGACGCTAGACAGAGGTGGTAGCAAAGGGCCCCAGCCCAGAGTTTCCGGCCCTGCGCCGACGGCGGCTCCTCC

C57BL/6  CCCGTCTCCACGGCAACGCGGCCCGCGCCGGAAGCTGCTCTGTCTTGCTTAGTGCGCTCTGTCTTCCAGGAAACCGAGACTTCTCTCTAAGCTCGGCTTC
BALB/c   CCCGTCTCCACGGCAACGCGGCCCGCGCCGGAAGCTGCTCTGTCTTGCTTAGTGCGCTCTGTCTTCCAGGAAACCGAGACTTCTCTCTAAGCTCGGCTTC

C57BL/6  CTACAGTTTTCTTGCCCTGAAGTTTCTGCGCTTCTGAGAAGCGGGTCACTAGTTACAACTCCTGCATGGGACCGGTGTGAGACGGAAAAGTGTCTCTTTT
BALB/c   CTACAGTTTTCTTGCCCTGAAGTTTCTGCGCTTCTGAGAAGCGGGTCACTAGTTACAACTCCTGCATGGGACCGGTGTGAGACGGAAAAGTGTCTCTTTT

C57BL/6  CATTGCGTGGTGGCTCACGTCGGTAATCTCCGCATCAAACAGCCGAATCTTTAAAGAGAACTTTCAGAACAGAGTATGAAGTTTCAAACTAAGAACAGTG
BALB/c   CATTGCGTGGTGGCTCACGTCGGTAATCTCCGCATCAAACAGCCGAATCTTTAAAGAGAACTTTCAGAACAGAGTATGAAGTTTCAAACTAAGAACAGTG

C57BL/6  AAAACTAGTGGGTGGGTGTCTGAAGACGAAAACCAAGGGGCAGGAGATATGACTCACCAGTTAAATGCACTTTTCATTCATCCAGACTCCCAATACCCAC
BALB/c   AAAACTAGTGGGTGGGTGTCTGAAGACGAAAACCAAGGGGCAGGAGATATGACTCACCAGTTAAATGCACTTTTCATTCATCCAGACTCCCAATACCCAC
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C57BL/6   ACGGTGGCTCTTAAAACAGTTGTGACTCCCAAGTCGCGCTCCCGTTTGACCTATATGCAAGCAAAACATTCATACTCAAAATTTTTAAAAAGATTAAACC
BALB/c    ACGGTGGCTCTTAAAACAGTTGTGACTCCCAAGTCGCGCTCCCGTTTGACCTATATGCAAGCAAAACATTCATACTCAAAATTTTTAAAAAGATTAAACC

C57BL/6   CAAGAAATATGGGTTTTGCCCTTTTACAAATGGTAATTTTGTAATCCAAAGATTTA
BALB/c    CAAGAAATATGGGTTTTGCCCTTTTACAAATGGTAATTTTGTAATCCAAAGATTTA
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AD

Slc27a6

chr18:58,681,397-58,682,391

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C57BL/6   ------------------------------------TTAGGCGGGGTTTTCAGAGGCAGCAAGAGGTGCTAAAGACATTCCCAGCTTGAAGCCCAGGG
BALB/c    ------------------------------------TTAGGCGGGGTTTTCAGAGGCAGCAAGAGGTGCTAAAGACATTCCCAGCTTGAAGCCCAGGG

C57BL/6   AGCTGCAAGGAGCCTGTTGGACAGCCGTGGAGGGTGGGTGCACTGAGCTGTGTTGGGCTCATTTCCAGCGCTGTGAGTGTTGTGAGTACAATAGCCCCCC
BALB/c    AGCTGCAAGGAGCCTGTTGGACAGCCGTGGAGGGTGGGTGCACTGTGCTGTGTTGGGCTCATTTCCAGCGCTGTGAGTGTTGTGAGTACAATAGCTCCCC

C57BL/6   CCCCCCCTCTTTTTTTAATCTAAGAAGACTCAGGGCTCTGCTCCACAACTGTCTAGCCCAATGCCCCAGGGCGTATCACCAGCGTTCTGTAGCTTTCTGG
BALB/c    CCCCCCCTCTTTTTTTAATCTAAGAAGACTCAGGGCTCTGCTCCACAACTGTCTAGCCCAATGCCCCAGGGCTTATCACCAGCATTCTGAAGCTTTCTGG

C57BL/6   GCGAAAACCTTTGATTTCTTTCATGGGATATACAAAGACATCTTGAGCCAGAACTACAGGTGCCAGCCTCTGAGCTTTCAGGACAGGAGTCTCCAGGGCA
BALB/c    GCGAAAACCTTTGATTTCTTTCATGGGATATACAAAGACATCTTGAGCCAGAACTACAGGTGCCAGCCTCTGAGCTTTCAGGACAGGAGTCTCCGGGGCA

C57BL/6   AAAAGAGGTGAAACTCTTGGAAAAGAAAGAGACACTGCTAGGACCCATCGGGTCTGCTGGAGGTCTGGGCACCCATGCTCCTGTCATGGCTCACAGGATT
BALB/c    AAAAGAGGTGAAACTCTTGGAAAAGAAAGAGACACTGCTAGGACCCATCGGGTCTGCTGGAGGTCTGGGCACCCATGCTCCTGTCATGGCTCACAGGATT

C57BL/6   GGGGGCTGGACTGCTCTCCCTGCATTTCCTGCAGAAACTTCTGTTCCCGTATTTCTGGGATGATTTCTGGTACTTGCTGAAGGTGGTGCGCTACGGAATT
BALB/c    TGGGGCTGGACTGCTCTCCCTGCATTTCCTGCAGAAACTTCTGTTCCCGTATTTCTGGGATGATTTCTGGTACTTGCTGAAGGTGGTGCGCTACGGAATT

C57BL/6   CAGATGGAGATGTACAAACTGAGGGGGGAGCTGGTCACGGTGCTGGATAAGTTCCTGAGCCACACCAGGAAGCAACCACGGAAAGCCTTCATCATTTATG
BALB/c    CAGATGGAGATGTACAAACTGAGGGGGGAGCTGGTCACGGTGCTGGATAAGTTCCTGAGCCACGCCAGGAAGCAACCACGGAAAGCCTTCATCATTTATG

C57BL/6   AGGGGGACGTCTACACCTACGAGGACGTGGACAAGAGGAGTAACAGAATAGCCCACGCTCTCCTGAACCACTCCTCGCTGAAAAGGGGGGACGTTGTGGC
BALB/c    AGGGGGACGTCTACACCTACGAGGACGTGGACAAGAGGAGTAACAGAATAGCCCACGCTCTCCTGAACCACTCCTCGCTGAAAAGGGGGGACGTTGTGGC

C57BL/6   TTTGTTGATGAGCAACGAGCCCGACTTCGTTCATGTGTGGTTTGGCCTGGCTAAACTGGGCTGCGTGGTGGCCTTCCTCAACTCCAACCTTCGCTTCGAT
BALB/c    TTTGTTGATGAGCAACGAGCCCGACTTCGTTCATGTGTGGTTTGGCCTGGCTAAACTGGGCTGCGTGGTGGCCTTCCTCAACTCCAACCTTCGCTTCGAT

C57BL/6   TCCCTCCTACACTGCATCAACACCTGTGAACCCACTGCCGTGGTGGTGGGCGGAGGTAGAGTATGGACTGTGGTCTGCTGTGCCCAAAGCAAACCAACCT
BALB/c    TCCCTCCTACACTGCATCAACACCTGTGAACCCACTGCCGTGGTGGTGGGCGGAGGTAGAGTATGGACTGTGGTCTGCTATGCCCAAAGCAAACCAACCT

C57BL/6   ATTTCCTGCCCTCCCCTTTCTATCCATACTTCC
BALB/c    ATTTCCTGCCCTCCCCTTTCTATCCATACTTCC
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AE

Slc27a6

chr18:58,685,847-58,687,080

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C57BL/6   ------------------------------------CTTCAGTA-GGTTGCATAACCAGG-ATCAAAATCTCGACTTCTGATGTGAGGTCTTGATTTGA
BALB/c    ------------------------------------CTTCAGTAAGGTTGCATAACCAGGGATCAAAATCTCGACTTCTGATGTGAGGTCTTGATTTGA

C57BL/6   TCACAATCCAGCTATGTGGGGACCGTCAGTTACATTGCACACAGTTATAAAAAAGTATATATGTTCAGGCTCTATGAAAACACTACAAAATGGCAACATC
BALB/c    TCACAATCCAGCTATGTGGGGACCGTCAGTTACATTGCACACAGTTATAAAAAAGTATATATGTTCAGGCTCTATGAAAACACTACAAAATGGCAACATC

C57BL/6   AAGATACCAGGCTTTTAATACACACTAATTAGAAAAATGTGTACGATATTATTCTTCCAACAGAGCTGAAGACTCAAATATACTTGCAAAGGGGTCTCCT
BALB/c    AAGATACCAGGCTTTTAATACACACTAATTAGAAAAATGTGTACGATATTATTCTTCCAACAGAGCTGAAGACTCAAATATACTTGCAAAGGGGTCTCCT

C57BL/6   AGCTATGCTCTGGTCTCGGGGTCTGGGTCAGGTTAGTGTTCTCTGCTAATCAAAGAATGGAAATGAAAAGACAGGAAAAATCTCAGGCAGGACAAGTGAC
BALB/c    AGCTATGCTCTGGTCTCGGGGTCTGGGTCAGGTTAGTGTTCTCTGCTAATCAAAGAATGGAAATGAAAAGACAGGAAAAATCTCAGGCAGGACAAGTGAC

C57BL/6   GACAGCCTGAAGATTCTCATTGAGGCTGACAGAAACTGCTGTTTAAAAAAAAAAAAAAAAAAAAAAAACTTTATCAGGGAAGAGGAAATGCTACTCATAA
BALB/c    GACAGCCTGAAGATTCTCATTGAGGCTGACAGAAACTGCTGTTTAAAAAAAAAAAAAAAAAAAA----CTTTATCAGGGAAGAGGAAATGCTACTCATAA

C57BL/6   TAAGATAAGAAATGTTGTGGGTCTACCAGGTGTCCACGGTTCCCTTGCTACACATTGCGCGTGCGCGTTGTTTGCTTTCTCGATACTCTGCCGCTTAAAT
BALB/c    TAAGATA-----TGTTGTGGGTCTACCAGGTGTCCACGGTTCCCTTGCTACACATTGCGCGTGCGCGTTGTTTGCTTTCTCGATACTCTGCCGCTTAAAT

C57BL/6   CTCTACAAACAGATGACTTTACAATTCTCCCGTTGCCCGTCTCCCCGTCTCCCCTACTTTAAATGTGACAGCACTTAGTGTGTGAGTTTATTTTAAAAGA
BALB/c    CTCTACAAACAGATGACTTTACAATTCTCCCGTTGCCCGTCTCCCCGTCTCCCCTACTTTAAATGTGACAGCACTTAGTGTGTGAGTTTATTTTAAAAGA

C57BL/6   CTTGAGATTTCTCTTCATGAGAAGTCATGACTTCCGTTCACAGTTAAGGAGCTAATGGTTACTGCCCTGCCCTGTTTTTATAAGCAGTTGCCCTCAGGCT
BALB/c    CTTGAGATTTCTCTTCATGAGAAGTCATGACTTCCGTTCACAGTTAAGGAGCTAATGGTTACTGCCCTGCCCTGTTTTTATAAGCAGTTGCCCTCAGGCT

C57BL/6   GTGCAGAGGAAATGTTCAGGTTAACAACTGATCTGTTGTAACCCTGCAATTACCCTTTAGCCATAAAGGTAATTATTAAAATCAACAGGAAGAGAGGGAA
BALB/c    GTGCAGAGGAAATGTTCAGGTTAACAATTGATCTGTTGTAACCCTGCAATTACCCTTTAGCCATAAAGGTAATTATTAAAATCAACAGGAAGAGAGGGAA

C57BL/6   CGAGCCCCTTTGCAGTTCATAGAAAATTATATGTACAGAGGTACAGAAAGCTAAGGGACCCTGTGAACTTTATTACCTACCCTGTGTTCCATGATACCCT
BALB/c    CGAGCCCCTTTGCAGTTCATAGAAAATTATATGTACAGAGGTACAGAAAGCTAAGGGACCCTGTGAACTTTATTATCTACCCTGTGTTCCGTGATACCCT

C57BL/6   CTCACAGGACACGAATATTTTTCCAGGACATGGCTATTTTTTTTCTTGTATTTATTAGAATGGCTGTTACCACATTCTTATTTTTTCCCCATCTTGGATT
BALB/c    CTCACAGGACACGAATATTTTTCCAGGACATGGCTATTTTTTTTCTTGTATTTATTAGAATGGCTGTTACCACATTCTTATTTTTTCCCCATCTTGGATT

C57BL/6   TAGCAGGGTCGAGAAAGTAACCTTGCTACAAAAGAAAATCATTTTATTAATTTAAATGTATAGTGTAATTTCAAAAGAAGAAATCTAGACAGAGAAGTGA
BALB/c    TAGCAGGGTCGAGAAAGTAACCTTGCTACAAAAGAAAATCATTTTATTAATTTAAATGTATAGTGTAATTTCAAAAGAAGAAACCTAGACAGAGAAGTGA

C57BL/6   ATGAAACAGCGTGGCTCATACCCATCTCTTCTCAATGGAAAGGGGAAAATGACTTAACACATCCTGTGGAGAC
BALB/c    ATGAAACAGCGTGGCTCATACCCATCTCTTCTCAATGGAAAGGGGAAAATGACTTAACACATCCTGTGGAGAC
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AF

Spint1

chr2:118,930,972-118,931,837

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C57BL/6  ------------------------------------------------CAGAACCAGAGTGTGGAGTGCAGGGAGCAGGACACATAGGGCCAGTGCGACA
BALB/c   ------------------------------------------------CAGAACCAGAGTGTGGAGTGCAGGGAGCAGGACACATAGGGCCAGTGCGACA

C57BL/6  GACCCTTTCTCTCCAGGCTTCTTCCTACTAGGACCTATGGTAGACTAAAGGTCTGCTCTTCTAACTGTCCAATAGCGTCCAATAGCTCTCCTTGATCTCT
BALB/c   GACCCTTTCTCTCCAGGCTTCTTCCTACTAGGACCTATGGTAGACTAAGGGTCTGCTCTTCTAACTGTCCAATAGCGTCCAATAGCTCTCCTTGATCTCT

C57BL/6  GGGGAGACCCCAGGTGGGGATTCTGGAAAGTGGGGGATGCTGTGAAGTAGGTATCTCACTTGGTTAGCATTGGAGCCTGTTCCACAAGAACCTTACAGGA
BALB/c   GGGGAGACCCCAGGTGGGGATTCTGGAAAATGGGGGATGCTGTGAAGTAGGTATCTCACTTGGTTAGCATTGGAGCCTGTTCCACAAGAACCTTACAGGA

C57BL/6  CTCCCTTCCCCGGCCAGAACCTGAGTCTCTGGATCTGGGCCCCTTAGTCCTAGGGCCAGCCTTCCTCTTTCGGAAACCCCCAGAAATGGTCCATTTGGCG
BALB/c   CTCCCTTCCCCGGCCAGAACCTGAGTCTCTGGATCTGGGCCGCTTAGTCCTAGGGCCAGCCTTCCTCTTTCGGAAACCCCCAGAAATGGTCCATTTGGCG

C57BL/6  TGAGATAGGCTAGAATGGGGATTTTCCTGGAACATTTGAGGAGCTGGGTAGGGCTCAGGTGTTGTGTGCACTCCCGGCCATTCTCGGCTGTATCAGGGAT
BALB/c   TGAGATAGGCTAGAATGGGGATTTTCCTGGAACATTCGAGGAGCTGGGTAGGGCTCAGGTGTTGTGTGCACTCCCGGCCATTCTCGGCTGTATCAGGGAT

C57BL/6  ACTGTAAGGAAGTCCAGAAGCTTCATGTCGGTGGTCCCCGTGTCAGCCAAGTAGCCTAGAGGGGATGTGTCAAGAAACCTAAGCTGTTGGTTGATTCCTG
BALB/c   ACTGTAAGGAAGTCCAGAAGCTTCATGTCGGTGGTCCCCGTGTCAGCCAAGTAGCCTAGAGGGGATGTGTCAAGAAACCTAAGCTGTTGGTTGATTCCTG

C57BL/6  TGTTGGATGAACGAATCCTTCCCAGAATGGGTGGCTTGGGTCCCTTTTCCCAGCTTGTGGTTAGGCCAGGCAAGAAGACTCCAGCCCAGTAACTTGTTCT
BALB/c   TGTTGGATGAACGAATCCTTCCCAGAATGGGTGGCTTGGGTCCCTTTTCCCAGCTTGTGGTTAGGCCAGGCAAGAAGACTCCAGCCCAGTAACTTGTTCT

C57BL/6  TTCCCTGTGTCTGTGTCCCCTCACCCTGGCTAGTGGCTTGGGAGGCGGAGTCTGCAGTTCCTCAGATATGTCCTGAGGCCTGGTTTTATTGCCATTCCAG
BALB/c   TTCCCTGTGTCTGTGTCCCCTCACCCTGGCTAGTGGCTTGGGAGGCGGAGTCTGCAGTTCCTCAGATATGTCCTGAGGCCTGGTTTTATTGCCATTCCAG

C57BL/6  CCCTTTGCTCTCTGAGGGTAGGAAGAAGGGAGTGGTAGGTAAGGGTAGGGCATTTGCCCCTTGGTCTTGGGGCTTGGTGAGAG----CAGATAGGGGTTG
BALB/c   CCCTTTGCTCTCTGAGGGTAGGAAGAAGGGAGTGGTAGGTTAGGGTAGGGCATTTGCCCCTTGGTCTTGGGGCTTGGTGAGAGAGAGCAGATAGGG-TTG

C57BL/6  GGGGTGGGGCTGCTCCTCAT
BALB/c   GGGGTGGGGCTGCTCCTCAT
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AG

Zfp568

chr7:29,691,813-29,692,926

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C57BL/6  ------------------------------------GCTATTCTAAGA-CAGAGGTCTTATCTCAGCCTTTAGGGAGCTCGCCCAGGCCTGGTGGTTTT
BALB/c   ------------------------------------GCTATTCTAAGAACGGAGGTCTTATCTCAGCCTTTAGGGAGCTCGCCCAGGCCTGGTGGTTTT

C57BL/6  ACTGCAGCTTGAAAGAAAGTAAGGCTTGCGGGCATGCAGTAAGATGGGGGCGGCCGTCCAATACCTGGGATCACTCTGGGCTCGGCACAAAGGAAAGCCC
BALB/c   ACTGCAGCTTGAAAGAAAGTAAGGCTTGCGGGCATGCAGTAAGATGGGGGCGGCTGTCCAATACCTGGGATCACTCTGGGCTCGGCACAAAGGAAAGCCC

C57BL/6  GGCTCTTTGTGGTTTGTAGTGCATTCTTTGCCTCTTTTGGGTAACTGACCTGGCAATGGGTAAAACTGGGAGTAGACATAAAAAAATTGTGACCCTCCAG
BALB/c   GGCTCTTTGTGGTTTGTAGTGCATTCTTTGCCTCTTTTGGGTAACTGACCTGGCAATGGGTAAAACTGGGAGTAGACATAAAAAAATTGTGACCCTCCAG

C57BL/6  GTCTTTCTTGGCCAGGCCAGAGATCATTACCAGCCTTGTCCCCATTATCCATCCTGCGTAGAGAATGGAGATTAGGAGAGAACTGGCACCCTGACCAATT
BALB/c   GTCTTTCTTGGCCAGGCCAGAGATCATTACCAGCCTTGTCCCCATTATCCATCCTGCGTAGAGAATGGAGATTAGGAGAGAACTGGCACCCTGACCAATT

C57BL/6  TGCGAATCTAAACCTCACCTCAGAGATTGTTCCCAGGAGCAGAGTTCTGAAGTCACAACCACTCGGGTGACAGGAGCCCCATGGTTACATGCAAGATGCC
BALB/c   TGCGAATCTAAACCTCACCTCAGAGATTGTTCCCAGGAGCAGAGTTCTGAAGTCACAACCACTCGGGTGACAGGAGCCCCATGGTTACATGCAAGATGCC

C57BL/6  ACATAGAGGTAGGCACAGTCTT----------------------------------------------------------------------------------
BALB/c   ACATAGAGGTAGGCACAGTCTTTTTTTTGTTTGTTTGTTTGTTTTTTGTTTTTTTTTGTTTGTTTTTGTTTTTTTGAGACAGGGTTTCTCTGTATAGCCC

C57BL/6  ----------------------------------------------------------------------------------------------------
BALB/c   TGGCTGTCCTGGAACTCACTCTGTAGACCAGGCTGGCCTCGAACTCAGAAATCCGCCTGCCTCTGCCTCCCGAGTGCTGAGATTAAAGGCGTGCGCCACC

C57BL/6  -------------------------ACACTTAAGCCACAACTCCACAACGACCAGACATTTCATGTCCTCATAGAAAAGCTATCAGAATGTATTACAAAC
BALB/c   ACGCCCGGCTGGTAGGCACAGTCTTACACTTAAGCCACAACTCCACAACGACCAGACATTTCATGTCCTCATAGAAAAGCTATCAGAATGTATTACAAAC

C57BL/6  AACCACAAAAACTATTCCAGGGCACTGCGTCCGCCCAGTCGCAAGGCTCCTGCCGAGAGGCTGGACAGGCCACTAGCCTTTCTGGGAAATGTAGTCCACA
BALB/c   AACCACAAAAACTATTCCAGGGCACTGCGTCCGCCCAGTCGCAAGGCTCCTGCCGAGAGGCTGGACAGGCCACTAGCCTTTCTGGGAAATGTAGTCCACA

C57BL/6  AAGGGACAGCCACCTAGCGCCCCCAGCGCCTCCTCTGGTTGTTCCGGAAAAGACCGTCCCCGCAGCTGCTCACGTCCAGCGCTGCTTCGCCGGCGGCGTC
BALB/c   AAGGGACAGCCACCTAGCGCCCCCAGCGCCTCCTCTGGTTGTTCCGGAAAAGACCGTCCCCACAGCTGCTCACGTCCAGCGCTGCTTCGCCGCCGGCGTC

C57BL/6  ACCGTCTCGCCGCGCTAATGGGCTCAGCCACCTCGGCGCCTTCGGCCATGACTCCTGTCCCTAGCACAGGAAACGCCAGCCGAGCTCTGACCGGAAGTTG
BALB/c   ACCGTCTCGCGGCGCTAATGGGCTCAGCCACCTCCGCGCCTTCGGCCATGACTCCTGTCCCTAGTACAGGAAACGCCAGCGGAGCTCTGACCGGAAGTTG

C57BL/6  GGTCGGGCCGCGGGTCCTTCTGGGAGCACCTGTGCTCTGGGACATAACGGGCGCGCGCTGCCGCCCGAGTGGAGGGGCTGGCCGTGCGTGGCCCGCATGC
BALB/c   GGTCGGGCCGCGGGTCCTTCTGGGAGCACCTGTGCTCTGGGACATAACGGGCGCGCGCTGCTGCCCGAGTGGAGGGGCTGGCCGTGCGTGGCCCGCATGC

C57BL/6  CGCGTCTCTGAGGTTGCGTCTCGGGAGGTTTTGGCTGGTGGCGCTGCGGGGACCTCTCCACGGGAGAGGCACGGGTGGTCCGGTTTGCGCCGGCCGTGGG
BALB/c   CGCGTCTCTGAGGTTGAGTCTCGGGAGGTTTTGGCTGGTGACGCTGCGGGGACCTCTCCACGGGAGAGGCACGGGTGGTCCGGTTTGCGCCGGCCGTGGG

C57BL/6  CTTCGGGCTGGGCGCGGGCTCTCGGGGGGCTCGGAGTATCCCGGGTCACAGCTTT
BALB/c   CTTCGGGCTGGGCGCGGGCTCTCGGGGGGCTCGGAGTATCCCGG-TCACAGTTTT
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AH

Tiam2

chr17:3,352,121-3,353,556

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C57BL/6  ----------------------------------------TATTGTTCTCAATGTGGGTTCATATGTGTGAATGTATACATGTCAACAAGATATGTCT
BALB/c   ----------------------------------------TATTGTTCTCAATGTGGGTTCATATGTGTGAATGTATACATGTCAACAAGATATGTCT

C57BL/6  TAAAATCCAAATAGGGAATTACAAGTTTATCTAACTATAGTAGAATCTGGTCCTTAATAACTCACCAATGGCATATTTAGCTCAGTTCACTTTTTAAAAA
BALB/c   TAAAATCCAAATAGGGAATTACAAGTTTATCTAACTATAGTAGAATCTGGTCCTTAATAACTCACCAATGGCATATTTAGCTCAGTTCACTTTTTAAAAA

C57BL/6  ATTATTGGATATGTGCACTTATGCCACAGTGTGTGTATGGTCAGTGACAGATATCGGTGTCAGTTTGTCCTTCTACCTTGCTGAGGTAGGTGCTGGGTAC
BALB/c   GTTATTGGATATGTGCACTTATGCCACAGTGTGTGTATGGTCAGTGACAGATATCGGTGTCAGTTTGTCCTTCTACCTTGCTGAGGTAGGTGCTGGGTAC

C57BL/6  TGCAGTCTAGCCAGCTTGAGAGCTTTCCGGAGATTTCTTCCTGTCTCAATGTAGAAGTACCAGGATTACAGATGTACCCCACTGTATCTGGCCATTTTAT
BALB/c   TGCAGTCTAGCCAGCTTGAGAGCTTTCCGGAGATTTCTTCCTGTCTCAATGTAGAAGTACCAGGATTACAGATGTACCCCACTGTATCTGGCCATTTTAT

C57BL/6  GTGGCTTCCAGGGTTCATGATGTTTGTACCAGCAAGAAAGTTAATTCACTGAGCCATCTGAAGGACTTCTGTCACATTTTAAAATTAAGAATGTTACCAT
BALB/c   GTGGCTTCCAGGGTTCATGATGTTTGTACCAGCAAGAAAGTTAATTCACTGAGCCATCTGAAGGACTTCTGTCACATTTTAAAAATAAGAATGTTACCAT

C57BL/6  TATAAAGCTCTTGCCACATGTTCAGGATGGTTCAGGATGGGTTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTATTTATATG
BALB/c   TATAAAGCTCTTGCCACATGTTCAGGATGGTTCAGGATGGGTTGAG--------TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTATTTATATG

C57BL/6  TCTGAAAATGTAGGACTTTTGGTCATTCTGTGGAATATAAACACATAAATTTAAGCATGACAACAGAAATGTAATTTGATTCTATTCATCATAAAACAAC
BALB/c   TCTGAAAATGTAAGACTTTTGGTCATTCTGTGGAATATACACACATAAATTTAAGCATGACAACAGAAATGTAATTTGATTCTATTCATCATAAAACAAC

C57BL/6  AACAACAA---AAATCTAGTATAGAAATAACCTAGGGGCTGGAGAGATGGCTCAGAGGTTAAGAGCACTGGCTGCTTCTCCAGAGGTCCTGAGTTCAATT
BALB/c   AACAACAACAAAAATCTAGTATAGAAATAACCTAGGGGCTGGAGAGATGGCTCAGAGGTTAAGAGCACTGGCTGCTTCTCCAGAGGTCCTGAGTTCAATT

C57BL/6  CCCAGCAACCACATGGTGGCTCACAACCATCGGTAATGGGATCTGGTTTCTTCTTCTGGTATGCAGGTATACATACAGGCAGAACACTGTATCCATAGTA
BALB/c   CCCAGCAACCACATGGTGGCTCACAACCATCGGTAATGGGATCTGGTTTCTTCTTCTGGTATGCAGGTATACATACAGGCAGAACACTGTATCCATAGTA

C57BL/6  AATAAAAAAAT----------------------------------------------------------------------------------------
BALB/c   AATAAAAAAAATCTTTTTTTTGGGCTGGAGAGATGGCTCAGTGGTTAAGTAATGGCTGCTCAGCCAGGCATGGTGGAACACGCCTTTATCCCAGCACTCG

C57BL/6  ----------------------------------------------------------------------------------------------------
BALB/c   GGAGGCAGAACAGGCAGATTTCTGAGTTCGAGGCCAGCCTGGTCTACAAAGTGAGTTCCAGGACAGCCAGGGCTACATAGAGAAACCCTGTCTCAAAAAA

C57BL/6  ----------------------------------------------------CTTTTTAAAAAATGACTTGAAAAAAATCTTGTATATTTTTAACATCTTT
BALB/c   CAAACAAACAAACAAACCCAAAAAACAAAAAAACAAAAACAAAAAAAAAAACTTTTTAAAAAATGACTTGAAAAAAATCTTGTATATTTTTAACATCTTT

C57BL/6  CATCAATGGTTACAGTGAGACTTCAAAATACTCTGCCTCTGTTGTATAGCCTTAATTTACAGTAATGTAATACATACTCTGGATAAAATGGCTCCGCATT
BALB/c   CATCAATGGTTACAGTGAGACTTCAAAATACTCTGCCTCTGTTGTATAGCCTTAATTTACAGTAATGTAATACATACTCTGGATAAAATGGCTCCGCATT

C57BL/6  TAGTTTCCAAGGACTTTGAGTGTAAGACTCTGTTGTGCTAACTTAAGGGGGGTGGGAAGCCCGATTCCAACAAGGAACACAGAATGAGGGTATACTCGAT
BALB/c   TAGTTTCCAAGGACTTTGAGTGTAAGACTCTGTTGTGCTAACTTAAGGGGGGTGGGAAGCCCGATTCCAACAAGGAACACAGAATGAGGGTATACTCGAT

C57BL/6  ATTCTGCAAACCATGGCAGCATTTCCTGGGGCTGTTCTAAAGGCAGTTCTGACCATAACATTCCATCTGTGGTTTTCACTGCTTCCCCAAACACAAGGAT
BALB/c   ATTCTGCAAACCATGGCAGCATTTCCTGGGGCTGTTCTAAAGGCAGTTCTGACCATAACATTCCATCTGTGGTTTTCACTGCTTCCCCAAACACAAGGAT

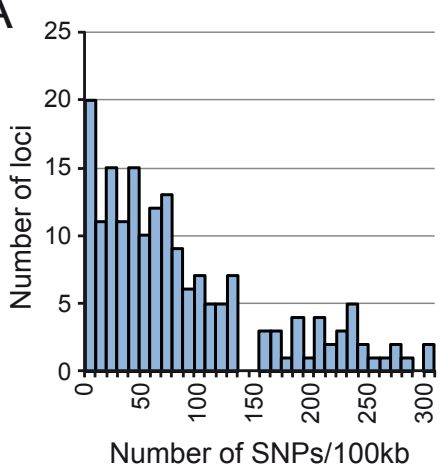
C57BL/6  GATAGGTGTGTATTCTCAGTGCTACAGGGCTTTATAAATGACGCCAGGGCAGCCCTGGTGAGTAGGGCTTTATTCTGTAACCCTTGGAGCCAGACTCCTA
BALB/c   GATAGGTGTGTATTCTCAGTGCTACAGGGCTTTATAAATGACGCCAGGGCAGCCCTGGTGAGTAGGGCTTTATTCTGTAACCCTTGGAGCCAGACTCCTA

C57BL/6  TGGAACTTCGGTGGTCATGGTGGATTGCTGGCCCAACAAGAGCCTAGTCATGGGCAGCCCCGTGTCTCTGAGGCGAGCATGGTGGCAGGCTGTCCCGGGT
BALB/c   TGGAACTTCGGTGGTCATGGTGGATTGCTGGCCCAACAAGAGCCTAGTCATGGGCAGCCCCGTGTCTCTGAGGCGAGCATGGTGGCAGGCTGTCCCGGGT

C57BL/6  AATCACTCCAGGCAGCCCATG
BALB/c   AACCACTCCAGGCAGCCCATG
```

Supplemental Figure S3

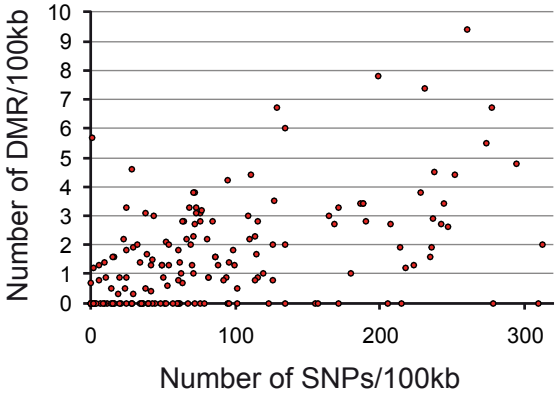
A



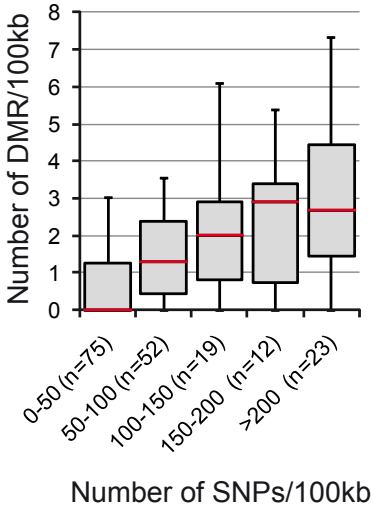
B

Origin of DMR	Number of DMR	Number of loci with DMR
intersubspecific	211	80
intrasubspecific	131	66
same haplotype	52 (43)	32
not classified	39 (36)	26

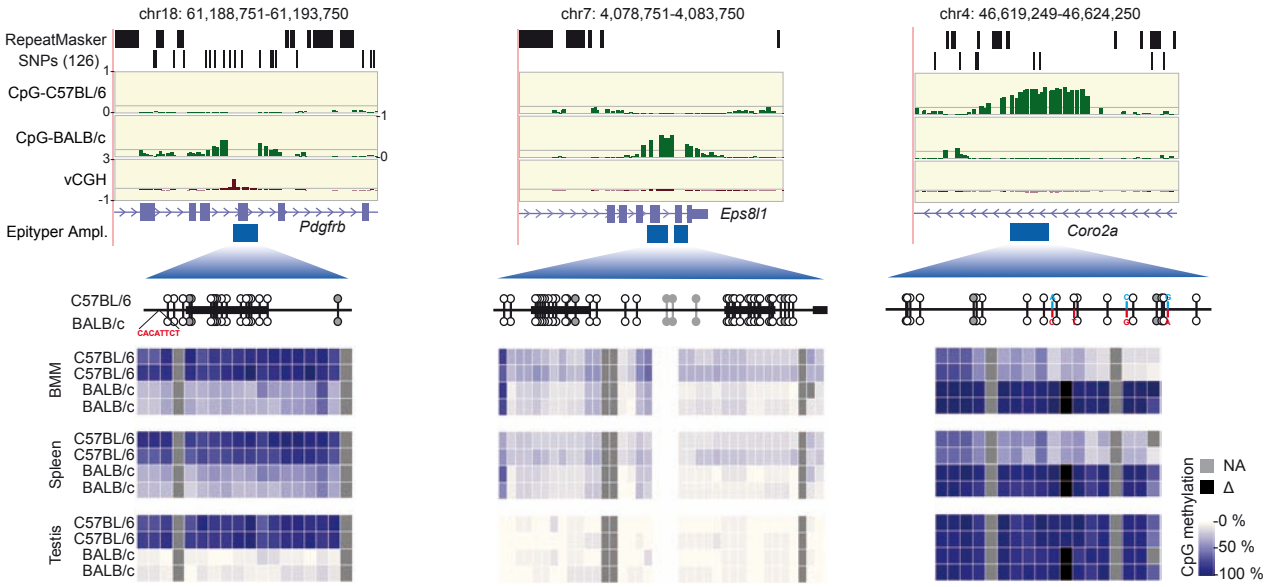
C



D



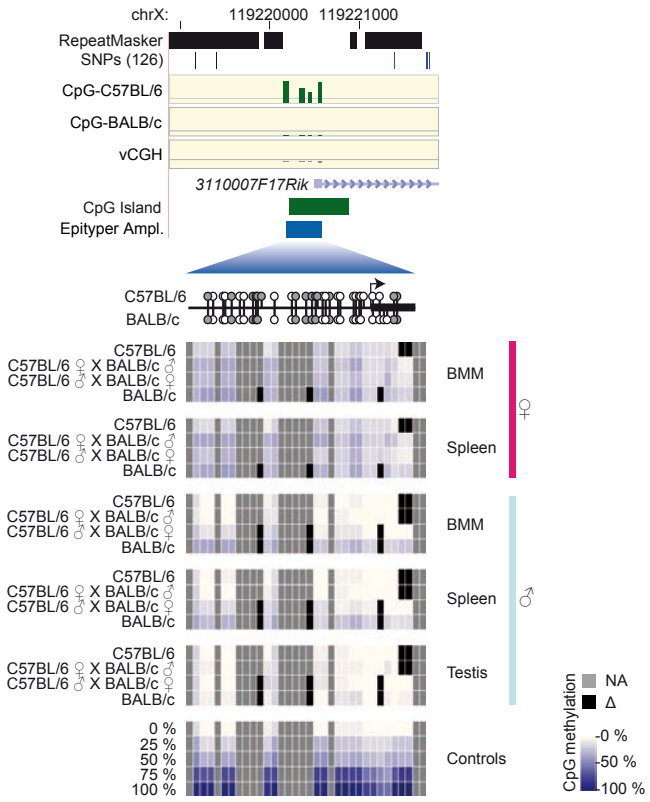
Supplemental Figure S4



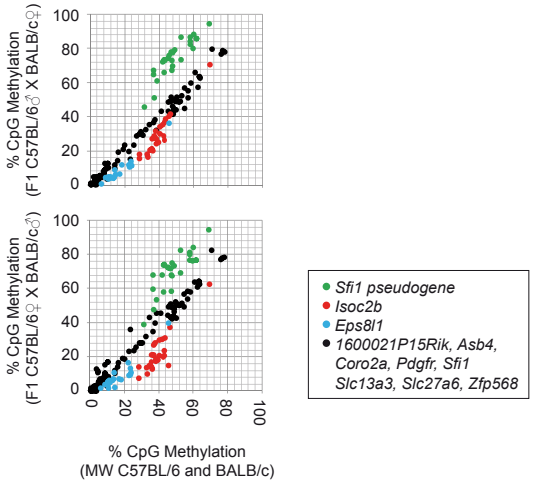
Supplemental Figure S5

	C57BL/6 BMM male (n=3)	C57BL/6 BMM female (n=3)	F1 (Cmother) BMM male (n=1)	F1 (Bmother) BMM male (n=3)	F1 (Cmother) BMM female (n=2)	F1 (Bmother) BMM female (n=2)	BALB/c BMM male (n=3)	BALB/c BMM female (n=3)	C57BL/6 spleen male (n=3)	C57BL/6 spleen female (n=3)	F1 (Cmother) spleen male (n=2)	F1 (Bmother) spleen male (n=3)	F1 (Cmother) spleen female (n=2)	F1 (Bmother) spleen female (n=2)	BALB/c spleen male (n=3)	BALB/c spleen female (n=3)	C57BL/6 testis male (n=3)	F1 (Cmother) testis male (n=2)	F1 (Bmother) testis male (n=2)	BALB/c testis male (n=3)
C57BL/6 BMM male	1.00	0.99	0.66	0.71	0.60	0.63	0.00	0.01	0.95	0.94	0.65	0.60	0.55	0.63	0.01	0.01	0.43	0.37	0.34	0.05
C57BL/6 BMM female		1.00	0.60	0.66	0.56	0.58	0.01	0.01	0.94	0.95	0.60	0.55	0.51	0.59	0.01	0.02	0.41	0.34	0.31	0.03
F1 (Cmother) BMM male			1.00	0.97	0.96	0.97	0.15	0.13	0.67	0.66	0.95	0.94	0.93	0.95	0.13	0.12	0.32	0.43	0.39	0.23
F1 (Bmother) BMM male				1.00	0.95	0.98	0.16	0.15	0.74	0.72	0.97	0.95	0.92	0.96	0.14	0.13	0.42	0.51	0.48	0.30
F1 (Cmother) BMM female					1.00	0.97	0.23	0.22	0.64	0.63	0.95	0.93	0.97	0.94	0.22	0.20	0.35	0.44	0.42	0.28
F1 (Bmother) BMM female						1.00	0.21	0.20	0.65	0.65	0.95	0.93	0.94	0.95	0.19	0.18	0.35	0.46	0.43	0.30
BALB/c BMM male							1.00	0.99	0.00	0.00	0.13	0.17	0.24	0.16	0.98	0.97	0.00	0.01	0.01	0.24
BALB/c BMM female								1.00	0.00	0.00	0.12	0.16	0.22	0.16	0.98	0.98	0.00	0.01	0.01	0.27
C57BL/6 spleen male									1.00	0.97	0.72	0.68	0.63	0.70	0.00	0.01	0.53	0.46	0.43	0.08
C57BL/6 spleen female										1.00	0.70	0.66	0.61	0.68	0.00	0.01	0.52	0.48	0.44	0.09
F1 (Cmother) spleen male											1.00	0.96	0.96	0.98	0.12	0.11	0.43	0.54	0.51	0.32
F1 (Bmother) spleen male												1.00	0.94	0.97	0.17	0.16	0.43	0.55	0.51	0.33
F1 (Cmother) spleen female													1.00	0.94	0.23	0.21	0.35	0.46	0.44	0.29
F1 (Bmother) spleen female														1.00	0.16	0.15	0.44	0.54	0.50	0.33
BALB/c spleen male															1.00	0.98	0.00	0.01	0.01	0.26
BALB/c spleen female																1.00	0.00	0.01	0.01	0.28
C57BL/6 testis male																	1.00	0.88	0.87	0.39
F1 (Cmother) testis male																		1.00	0.99	0.61
F1 (Bmother) testis male																			1.00	0.62
BALB/c testis male																				1.00

Supplemental Figure S6



Supplemental Figure S7



Supplemental Figure S8