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Appendix Table S1— sgRNA sequences with properties

#	sgRNA Sequence	PAM	Score	off-target sites (counts)	
				outside genes	within genes
1	TGTTGAGCCACGTGTCACCG	TGG	82	82	13
2	CCTTCTGTTTGGAGCTCTCC	AGG	59	335	59
3	CTACTGGTACTTCGATGTCT	GGG	90	76	4
4	ACTGGGACCACGGTGACACG	TGG	86	90	12
5	CGCTAAAGTTCTCGAGCCTG	TGG	89	56	7
6	TCCCTGACTCAAGAGATGAC	TGG	66	196	13
7	AGTCTGACTAGAAATCACCCC	TGG	82	110	9
8	GGGGTTTTTGTCTGGGTATAG	AGG	88	73	4
9	TCCTGGCCAGCATTGCCGCT	AGG	85	153	28
10	CACAAGAGTCCGATAGACCC	TGG	89	70	5
11	ACCTAGCGGCAATGCTGGCC	AGG	80	85	16

Appendix Table S2—Off-Target genes

Off-targeted gene name	sequence	mismatches
Apoptosis-associated tyrosine kinase (Aatk)	TGCTCAGCCACGTGTCACTGTGG	3MMs
Mitogen-activated protein kinase kinase kinase 10 (Map3k10)	TCTTGAGCACCGTGTGTCAGCGAGG	4MMs
NOP9 nucleolar protein (Nop9)	GGACTTGTACTIONCGAAGTCTGAG	4MMs

Appendix Table S3— Primer sequences

	Name	Sequences
sgRNA	Frag.1 F	AGCAAAGAGCAGTATGAGTG
	Frag.1 R	AGGAGAAAGGAAACAAGAGA
	Frag.2 F	TGATGTCTAGGACCAGGGGG
	Frag.2 R	AGGCACATTGTGACAACAAT
	Frag.3 F	GACCAAGATTCTCTGCAAAC
	Frag.3 R	ACTCCACCAACACCATCACA
	Frag.4 F	GGACCTCCATCTGCTCTTAT
	Frag.4 R	ACTCCACCAACACCATCACA
sgRNA Off-targets	Aakt F	TAACCTGCCCTCCGGGGACA
	Aakt R	ACTGCCTTGACAGTCAAGGG
	Map3k10 F	ATAGCTACAAGAATGGCTGC
	Map3k10 R	GCAGCGTTGACTGTGTTGAA
	Nop9 F	GTCTTCCTATCTAGGCATTT
	Nop9 R	AAGTACACAGGTGTGTTCTG
Long range PCR	Fo.1F	CCTGTCAGTAACTGAAGGTAAG
	Fo.2F	TACTACTACTACATGGACGTCT
	Re.1R	AGAGTAATCACCTCAGTTTAGC

Appendix Table S4—PCR primers for amplification of IGH sequences.

Tables show the names of primers used for IGH cDNA amplification via nested PCR from WT and knock-in mice. Primers were used and/or adapted from: von Boehmer *et al.* (Nat Prot 2016), Escolano *et al.* (Cell, 2016) and Ho *et al.*; J Immunol Methods 2016. The corresponding pubmed identifiers (PMID) are listed in the table.

FIRST PCR – IgM HEAVY CHAIN			
Primer	Name	Sequence 5' -> 3'	PMID
Forward	1mFH_I	AGGAACTGCAGGTGTCC	27600311
	1mFH_II	CAGCTACAGGTGTCCACTCC	
	1mFH_III	TGGCAGCARCAGCTACAGG	
	1mFH_IV	CTGCCTGGTGACATTCCCA	
	1mFH_V	CCAAGCTGTGTCCTGTC	
	1mFH_VI	TTTTAAAAGGTGTCCAGKGT	
	1mFH_VII	CCTGTCAGTAACTRCAGGTGTCC	
	1mFH_VIII	TTTTAAAAGGGGTCCAGTGT	
	1mFH_IX	CGTTCCTGGTATCCTGTCT	
	1mFH_X	ATGAAGTTGTGGYTRAACTGG	
	1mFH_XI	TGTTGGGGCTKAAGTGGG	
Reverse	R-Cm	AGGGGGCTCTCGCAGGAGACGAGG	27600311

SECOND PCR – IgM HEAVY CHAIN			
Primer	Name	Sequence 5' -> 3'	PMID
Forward	1mFH_I	AGGAACTGCAGGTGTCC	27600311
	1mFH_II	CAGCTACAGGTGTCCACTCC	
	1mFH_III	TGGCAGCARCAGCTACAGG	
	1mFH_IV	CTGCCTGGTGACATTCCCA	
	1mFH_V	CCAAGCTGTGTCCTGTC	
	1mFH_VI	TTTTAAAAGGTGTCCAGKGT	
	1mFH_VII	CCTGTCAGTAACTRCAGGTGTCC	
	1mFH_VIII	TTTTAAAAGGGGTCCAGTGT	
	1mFH_IX	CGTTCCTGGTATCCTGTCT	
	1mFH_X	ATGAAGTTGTGGYTRAACTGG	
	1mFH_XI	TGTTGGGGCTKAAGTGGG	
Reverse	R-Cm2	AGGGGGAAGACATTTGGGAAGGAC	27610569

Bone Marrow: Seq. from PGT121 knock-in mice

STables1-3: Summary of IGHV/ IGHD/ IGHJ family usage and HCDR3 for IGH sequences isolated from the bone marrow of PGT121 knock-in mice.

Mouse 1

Mouse-ID	BM B cell	Well-ID	IGHV	IGHD	IGHJ	HCDR3(aa)	Length	Species
PGT121.1	Early	A01	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	A05	1-26*01	2-1*01	1*03	CAIHYGNYGGYFDVW	13	mu
	Early	B03	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	B05	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	C01	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	C02	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	C03	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	C05	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	D01	1-64*01	2-4*01	2*01	CARLGGYDNDGDYW	12	mu
	Early	D02	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	D05	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	E01	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	E03	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	E04	1-64*01	2-2*01	1*03	CARGGYGYRWYFDVW	13	mu
	Early	F01	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	F03	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	F06	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	G01	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	G02	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	G04	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	G05	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	G06	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Late	A08	1-82*01	2-4*01	4*01	CARGGLREGYYYAMDYW	15	mu
	Late	C08	1-64*01	2-5*01	3*01	CARGDRNWFAYW	10	mu
	Late	D07	1-26*01	2-3*01	3*01	CARLDGSPYW	8	mu
	Late	D09	1-55*01	2-5*01	1*03	CARKDIVTTTRTLHGITIFGVVAFKEYYYYYYMDVW	34	mu
	Late	E11	1-22*01	3-2*02	3*01	CASPDSQATFAYW	11	mu
	Late	F08	1-15*01	2-1*01	1*03	CTRNLYGNSRRTLHGITIFGVVAFKEYYYYYYMDVW	34	mu
	Late	G07	1-62-2*01	2-1*01	3*01	CARHGAYGNYGFAYW	13	mu

Mouse 2

Mouse-ID	BM B cell	Well-ID	IGHV	IGHD	IGHJ	HCDR3(aa)	Length	Species
PGT121.2	Early	A04	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	B02	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	B03	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	B05	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	B06	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	C01	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	C05	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	C06	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	D01	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	D04	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	D05	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	E03	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	E05	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	E06	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	G01	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	G04	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Early	H06	4-59*01	3-3*01	6*03	CARTLHGITIFGVVAFKEYYYYYYMDVW	26	hu
	Late	A10	1-58*01	4-1*01	2*01	CARREELGGSGYFDYW	14	mu
	Late	B07	1-7*01	1-1*01	4*01	CARTDYYGSSYYAMDYW	15	mu
	Late	B08	1-81*01	1-2*01	1*03	CASRGHGITIFGVVAFKEYYYYYYMDVW	26	mu
	Late	E09	1-72*01	1-1*01	4*01	CASTTVVAKGAMDYW	13	mu
	Late	F09	5-9-1*02	2-12*01	1*03	CTDRLYYSQPAYWYFDVW	17	mu
	Late	F10	1-78*01	1-1*02	1*02	CARRDYYGTLHGITIFGVVAFKEYYYYYYMDVW	31	mu
	Late	G07	1-72*01	1-1*02	4*01	CARRWFYAMDYW	10	mu
	Late	G08	1-82*01	1-1*01	2*01	CARGGRFTTDYFDYW	13	mu
	Late	H07	5-16*01	1-1*01	1*03	CARVLLRWYFDVW	12	mu

hu - human; mu - murine

aa - amino acids

blue - human PGT121 germline sequences

Blood: Seq. from PGT121 knock-in mice

STables1-3: Summary of IGHV/ IGHD/ IGHJ family usage and HCDR3 for IGH sequences isolated from blood of PGT121 knock-in mice.

Mouse 1

Mouse-ID	Well-ID	IGHV	IGHD	IGHJ	HCDR3(aa)	Length	Species
PGT121.1	A01	1-59*01	1-1*01	2*03	CARYYYGSSWDYW	11	mu
	A04	1-69*01	1-1*01	1*03	CARSEGSNSDWYFDVW	14	mu
	A05	1-7*01	1-1*01	2*01	CARRITTVDYFDYW	13	mu
	A07	1-26*01	4-1*01	2*01	CARSGLGDIW	8	mu
	A08	15-2*01	1-1*01	2*01	CARGDYYGSSYYW	11	mu
	A10	5-6*01	4-1*01	2*01	CARPNWDGGFDYW	11	mu
	B01	1-82*01	3-3*01	2*03	CARRGGVDYW	8	mu
	B02	1-64*01	2-4*01	2*01	CARWDDYDDYFDYW	12	mu
	B03	1-69*01	2-3*01	2*01	CARGGGYWSIYW	10	mu
	B11	1-39*01	2-5*01	4*01	CARGDYYSNYYAMDYW	14	mu
	C04	5-4*01	2-4*01	3*01	CARDRGYDYDSWFAYW	14	mu
	C05	1-80*01	2-5*01	3*01	CAREGYSNYPSSYPSPDAWFAYW	21	mu
	C09	1-64*01	1-1*01	2*01	CAITTVVATDIW	10	mu
	C10	1-69*01	1-1*01	3*01	CARSGYYGSIRPAWFAYW	17	mu
	C11	1-18*01	2-13*01	1*03	CARGEYGWYFDVW	11	mu
	C12	1-12*01	1-1*01	4*01	CARNYGSSYYYAMDYW	14	mu
	D03	1-26*01	2-3*01	3*01	CARKGYDGYAWFAYW	14	mu
	D04	3-6*01	2-13*01	2*02	CAREDSNYFDYW	10	mu
	D09	1-75*01	2-5*01	4*01	CARSRAYYSNYDAMDYW	15	mu
	D11	1-18*01	2-5*01	1*03	CARDSNYLGGYFDVW	13	mu
	E04	1-59*01	1-1*02	2*01	CARGGGGNFDYW	10	mu
	E06	5-4*01	1-1*01	1*03	CASLYYGSSYGYWYFDVW	16	mu
	E08	1-82*01	2-3*01	3*01	CARGGDGYSSWFAIW	14	mu
	E09	5-16*01	4-1*01	2*01	CARDRGANWDSYYFDYW	15	mu
	E11	1-72*01	2-3*01	2*01	CARSGDGYPIYFDYW	13	mu
	E12	1-22*01	1-2*01	3*01	CARGYYGPAWFAYW	12	mu
	F01	1-81*01	1-1*01	1*03	CAIPSDYYGSSYWYFDVW	16	mu
	F05	1-82*01	2-5*01	1*03	CARYSNPWYFDVW	11	mu
	F06	1-61*01	1-1*02	1*03	CARHRAWTPYWYFDVW	14	mu
	F08	1-18*01	1-1*01	4*01	CARCDYGSSYDYYAMDYW	16	mu
	G01	1-82*01	5-1*01	2*01	CASTLDYW	6	mu
	G05	1-39*01	2-1*01	3*01	CASYGNYAFAYW	10	mu
	G10	13-2*01	1-1*01	4*01	CSRGYYGSSYAMDYW	13	mu
	H03	1-82*01	4-1*01	4*01	CARDRLTGGFYAMDYW	14	mu
	H09	1-22*01	1-1*01	2*01	CASSYGSSYLDYW	11	mu
	H10	5-16*01	2-4*01	1*03	CARGHYDYDASYWYFDVW	16	mu

Mouse 2

Mouse-ID	Well-ID	IGHV	IGHD	IGHJ	HCDR3(aa)	Length	Species
	A02	1-26*01	1-1*01	2*01	CARRDYYSYFDYW	13	mu
	A06	1-18*01	2-1*01	1*03	CARYGNWYFDVW	11	mu
	A08	3-6*01	2-4*01	4*01	CARYDYDAMDYW	10	mu
	B02	1-72*01	4-1*01	2*01	LSNWDGILLHYW	10	mu
	B04	1-64*01	1-2*01	2*01	CARYGPYFDYW	10	mu
	B05	6-3*01	2-4*01	2*01	CTTYDYLDYW	9	mu
	B07	3-6*01	1-1*01	1*03	CARDTFWYFDVW	10	mu
	B08	5-4*01	2-5*01	2*01	CAREHSNLDYW	9	mu
	B12	1-47*01	2-5*01	2*01	CARTSNYVFDYW	10	mu
	C01	1-78*01	2-4*01	1*03	CARWGEYYDYDVGYFDVW	16	mu
	C04	1-26*01	1-2*01	1*03	CARHYGGFDVW	10	mu
	C06	1-78*01	4-1*01	3*01	CARNGLAWFAYW	11	mu

PGT121.2	C07	1-15*01	2-3*01	2*01	CTRPGYYYFDYW	10	mu
	C08	1-26*01	1-1*02	4*01	CASRGGSLYAMDYS	12	mu
	D04	1-76*01	4-1*01	2*01	CARELAYFDYW	9	mu
	D09	1-50*01	4-1*01	1*03	CARSGTGYFDVW	10	mu
	E07	1-9*01	2-5*01	2*01	CARGPYYSNLYYFDYW	15	mu
	E08	1-82*01	2-4*01	4*01	CARDDYDGSYAMDYW	13	mu
	E09	5-9*01	4-1*01	3*01	CARHLNWAWFAYW	11	mu
	F01	6-6*01	1-1*01	1*03	CTPHYYGSRNWYFDVW	14	mu
	F02	1-18*01	3-1*01	4*01	CARSDPYAMDYW	10	mu
	F04	1-39*01	2-2*01	2*01	CARGGLRQNSHFDYW	13	mu
	F06	6-3*01	3-1*01	1*03	CTEGPDWYFDVW	10	mu
	F07	1-18*01	6-2*02	2*01	CARSMGLLSYYFDYW	13	mu
	F08	3-6*01	1-1*01	1*03	CASYYYGSSRYWYFDVW	15	mu
	F09	3-6*01	1-1*01	2*01	CASGYYGSSYDYW	11	mu
	F11	7-3*01	5-5*01	2*01	CARSNFHFDYW	9	mu
	G01	1-18*01	2-5*01	2*01	CARSAYYSNYADYW	12	mu
	G03	1-59*01	1-1*01	1*03	CARCPHYYGSSPRYFDVW	16	mu
	G05	3-6*01	2-1*01	1*03	CASGLTTYWYFDVW	12	mu
	G06	5-9*01	4-1*01	2*01	CARHWDEVYFDYW	11	mu
	G07	1-26*01	2-4*01	3*01	CASYDYDAFAYW	10	mu
	G09	1-39*01	2-2*01	2*01	CAREGSTMTTPYYFDYW	16	mu
	G10	1-19*01	4-1*01	3*01	CAREGGPAYW	8	mu
	H04	1-15*01	2-4*01	4*01	CTRGGGLRRRPNYAMDYW	15	mu
	H09	1-81*01	3-2*02	3*01	CAKTAQAAWFAYW	11	mu
	H10	1-81*01	3-2*02	2*01	CAREGGTAQATYYFDYW	15	mu

hu - human; mu - murine

aa - amino acids

blue - human PGT121 germline sequences

Spleen: Seq. from PGT121 knock-in mice

STables1-3: Summary of IGHV/ IGHD/ IGHJ family usage and HCDR3 for IGH sequences isolated from spleens of PGT121 knock-in mice.

Mouse 1

Mouse-ID	Well-ID	IGHV	IGHD	IGHJ	HCDR3(aa)	Length	Species
PGT121.1	A11	1-69*01	2-1*01	4*01	CARGEPYAMDYW	10	mu
	A03	1-55*01	2-4*01	4*01	CARGDYDYDGGAMDYW	14	mu
	B11	5-17*01	3-1*01	4*01	CARRGAMDYW	8	mu
	B03	1-75*01	3-3*01	4*01	CARRGVSDAMDYW	11	mu
	B04	1-82*01	1-1*01	2*01	CAQEGDYYGSSYW	11	mu
	C01	2-2*01	2-2*01	2*01	CARATGVNYFDYW	11	mu
	C02	1-64*01	1-1*01	4*01	CARKNYGSSPLYAMDYW	15	mu
	C03	1-55*01	2-2*01	4*01	CARDVYGYGLYYYAMDYW	16	mu
	C04	1-18*01	2-4*01	2*01	CARRGYDYPPYFDYW	14	mu
	C05	1-62-2*01	3-3*01	3*01	CARHEEGGVFAYW	11	mu
	C08	1-59*01	2-3*01	4*01	CARRGLYDGYSYYAMDYW	16	mu
	D10	1-80*01	2-1*01	4*01	CASTPPYAMDYW	10	mu
	D02	5-17*01	2-3*01	3*01	CARPRIYDGYSAWFAYW	15	mu
	D03	1-18*01	2-2*01	4*01	CARGGYAYYYAMDYW	13	mu
	D04	6-6*01	1-1*01	2*01	CTRRHYYGSSYHFFDYW	15	mu
	D09	5-17*01	2-4*01	3*01	CARGLRPYW	7	mu
	E01	1-78*01	1-1*01	2*01	CARSATTVVSHFDYW	13	mu
	E11	5-4*01	1-1*01	2*01	CARSGSSYVAFW	10	mu
	E03	13-2*01	2-12*01	2*01	CSRSYYFDYW	8	mu
	E07	1-75*01	2-4*01	1*03	CARSKYDWDWYFDVW	13	mu
	F01	1-75*01	2-5*01	4*01	CARRDSNRPYAMDYW	13	mu
	F02	5-9-1*02	2-3*01	2*01	CTREGYKGFYW	10	mu
	F04	3-6*01	2-2*01	4*01	CAYYGYDDAMDYW	11	mu
	F06	1-64*01	1-1*01	4*01	CARNYGSSWDAMDYW	13	mu
	F08	1-18*01	1-1*01	2*01	CARDDGGNYFDYW	11	mu
	G01	1-80*01	1-1*01	2*01	CASITTVVALDYW	11	mu
	G11	1-82*01	4-1*02	4*01	CARKSQLGSYYYAMDYW	15	mu
	G12	1-78*01	1-1*01	3*01	CARLMDYGSSFAYW	12	mu
	G03	1-78*01	2-3*01	3*01	CARSNDGYFSWFAYW	13	mu
	G04	1-80*01	2-4*01	2*01	CARKDDYDERLGFYW	14	mu
	G05	1-53*01	1-3*01	4*01	CARESQYGELQYYYAMDYW	17	mu
	G06	2-3*01	1-1*01	4*01	CAKLSTVVAVYYAMDYW	15	mu
	G08	1-80*01	2-1*01	2*01	CARIGIYYGIDYW	11	mu
	G09	5-17*01	1-1*02	4*01	CARRGGNYENAMDYW	13	mu
	H01	1-53*01	2-3*01	3*01	CARADDGYEFAFW	12	mu
	H03	5-17*01	1-1*01	2*01	CARYYYSFDYW	9	mu
	H04	1-15*01	3-2*02	3*01	CTRDSSGYWFAYW	11	mu

Mouse 2

Mouse-ID	Well-ID	IGHV	IGHD	IGHJ	HCDR3(aa)	Length	Species
	A10	5-16*01	3-3*01	2*01	CARDRTEGYFDYW	11	mu
	A03	1-50*01	1-3*01	2*01	CANDYRGNYW	8	mu
	B11	1-72*01	3-2*02	3*01	CARWDSSGYDWFAYW	13	mu
	B02	6-3*01	2-14*01	2*01	TTGVHSRYW	7	mu
	C02	1-36*01	3-1*01	2*01	CARYRDYFDYW	9	mu
	C05	1-62-2*01	2-2*01	4*01	CARHEGGIGYDYAMDYW	15	mu
	C08	1-72*01	1-1*01	2*01	CAREGDYGSTDYW	11	mu
	D01	1-72*01	2-3*01	4*01	CARLVDGYAMDYW	12	mu

PGT121.2	D10	1-47*01	3-2*02	2*01	CARRAQADGYFFDYW	13	mu
	D02	1-59*01	1-1*01	2*01	CARGDYGSSSYFFDYW	14	mu
	D04	1-53*01	3-2*02	3*01	CARWDSSGYWFAYW	12	mu
	D09	1-53*01	2-3*01	4*01	CARMRDGYCFYAMDYW	15	mu
	E01	1-78*01	2-3*01	4*01	CAIYVPIFYAMDYW	12	mu
	E03	1-9*01	1-1*01	3*01	CARGYSGFAYW	9	mu
	F01	5-9-1*02	2-2*01	3*01	CTRDRGYAWFAYW	11	mu
	F04	1-54*01	2-4*01	3*01	CARRFYDYDAFAYW	13	mu
	F06	1-82*01	2-4*01	4*01	CARDGVYYDFYYAMDYW	15	mu
	G11	5-17*01	1-1*02	4*01	CARRGFYAMDYW	10	mu
	G12	5-4*01	2-5*01	2*01	CAREGTGYSNRYFFDYW	15	mu
	G02	7-3*01	1-1*02	4*01	CARPMGDSLYAMDYW	13	mu
	G03	1-55*01	6-3*01	1*02	CATPKGYFDVW	9	mu
	G04	1-59*01	2-5*01	2*01	CARSDSNVVGyw	10	mu
	G05	6-3*01	1-1*01	4*01	CTGPTTVVASYYYAMDYW	16	mu
	G08	1-18*01	1-1*01	3*01	CARGDYYGSSYGfAYW	14	mu
	G09	1-4*01	4-1*01	1*03	CAREGGTGSYFDVW	12	mu
	H03	1-26*01	1-1*01	1*03	CARRYYGSSLWYFDVW	14	mu
	H04	2-5*01	2-14*01	4*01	CAKKDDLPEAMDYW	12	mu

hu - human; mu - murine

aa - amino acids

blue - human PGT121 germline sequences

Spleen: Seq. from BG18 knock-in mice

Stables1-3: Summary of IGHV/ IGHD/ IGHV family usage and HCDR3 for IGH sequences isolated from the spleens of BG18 knock-in mice.

Mouse 1

(BG18+/WT)

Mouse-ID	Well-ID	IGHV	IGHD	IGHJ	HCDR3(aa)	Length	Species
n18P2_HC	A01	14-2*01	1-1*01	3*01	CARSDYYGSRPWFAYW	14	mu
	A02	10-3*01	1-1*01	2*01	CVRAFYLRGFDYW	11	mu
	A07	6-3*01	2-5*01	4*01	CTGGDYSNYGGMDYW	14	mu
	A09	1-52*01	2-4*01	4*01	CARGIYYDYDARNAITIFGVVALGEYYYYGMDVW	32	mu
	A10	1-64*01	1-1*01	1*03	CARGEVLLPLRGYFDVW	15	mu
	A12	1-18*01	2-2*01	3*01	CARGMDGYDRWFAYW	13	mu
	B01	1-12*01	2-3*01	3*01	CASHDSSWFAYW	10	mu
	B02	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	B04	1-55*01	4-1*01	2*01	CARGRTGTDYW	9	mu
	B05	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	B06	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	B08	5-17*01	3-1*01	2*01	CARQLEFDYW	8	mu
	B09	10-1*01	1-2*01	1*03	CVRPTAWYFDVW	10	mu
	B11	1-18*01	3-3*01	4*01	CARFGWDDAMDYW	11	mu
	B12	1-64*01	1-1*01	3*01	CARTTTVVARVPFAYW	14	mu
	C05	1-9*01	2-4*01	4*01	CARYDYDESFYAMDYW	14	mu
	C06	2-9-1*01	4-1*01	2*01	CAREGLTGTFDYW	11	mu
	C11	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	C12	1-22*01	1-1*01	1*02	CARGDYGRWYFDVW	12	mu
	D04	1-9*01	2-4*01	1*03	CARGIYYDYDGGWYFDVW	16	mu
	D06	1-82*01	1-1*01	1*03	CASITTVVATEYFDVW	14	mu
	D10	5-6*01	2-4*01	3*01	CARQEDYGFAYW	10	mu
	D11	1-64*01	1-1*01	1*02	CARGGLLLRIYWYFDVW	15	mu
	D12	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	E01	3-1*01	1-1*01	2*01	CARGDYSYYYGSSPFDYW	16	mu
	E04	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	E05	1-9*01	2-4*01	2*01	CARGGYDYPYFDYW	12	mu
	E06	3-2*02	1-1*01	4*01	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	E10	2-2*01	1-1*01	4*01	CARNYGHYAMDYW	12	mu
	E12	1-74*01	6-3*01	2*01	CAICPSLYYFDWF	11	mu
	F01	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	F02	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	F04	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	F05	1-42*01	2-4*01	4*01	CARQAIYYDYDEGNAITIFGVVALGEYYYYGMDVW	33	mu
	F07	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	F08	5-16*01	3-2*02	4*01	CARDRDSSSGFWAMDYW	14	mu
	F09	2-2*01	4-1*01	4*01	CARTTGTGYAMDYW	12	mu
	F12	1-19*01	3-3*01	2*01	CARRGGDGYFDYW	12	mu
	G02	1-69*01	2-3*01	3*01	CARWDGYMFAYW	11	mu
	G08	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	G09	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	G10	1-59*01	2-4*01	4*01	CARRGYDYDGYAMDYW	15	mu
	G11	1-62-2*01	2-4*01	3*01	CARHEGYDYDPWFAYW	14	mu

hu - human; mu - murine

aa - amino acids

green - human BG18 germline sequences

Mouse 2

(BG18+/WT)

Mouse-ID	Well-ID	IGHV	IGHD	IGHJ	HCDR3(aa)	Length	Species
BG18.3	A02	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	A03	10-1*01	4-1*01	2*01	CVRQTGRGDFDYW	11	mu
	A04	1-80*01	2-5*01	4*01	CARSGYSNPPRNAITIFGVVALGEYYYYGMDVW	31	mu
	A07	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	A09	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	A10	1-85*01	1-1*01	2*01	CARGGSNYGYFDYW	13	mu
	A11	10-1*01	1-1*02	4*01	CVRHVGDFAMDYW	11	mu
	B01	5-9-1*02	2-4*01	4*01	CTRGCDYEDAMDYW	12	mu
	B04	5-4*01	2-2*01	3*01	CARAGYDLFAYW	10	mu
	B05	15-2*01	2-2*01	3*01	CARGENGHEEAWFAYW	14	mu
	B07	2-2*01	2-1*01	1*03	CASIYGNIGYFDVW	12	mu
	B08	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	B09	1-64*01	2-1*01	3*01	CAPFYYGKSLVAYW	12	mu
	B10	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	B11	1-72*01	4-1*01	3*01	CARSGTTAWFAYW	11	mu
	C01	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	C02	3-6*01	3-2*01	2*01	CARDRTARGDFDYW	12	mu
	C03	1-76*01	6-2*02	4*01	CAREEDGPHYAMDYW	12	mu
	C05	5-6*01	3-3*01	3*01	CGEEQGFAYW	9	mu
	C06	5-4*01	2-5*01	3*01	CARGRSNYEFAYW	11	mu
	C07	1-4*01	2-3*01	4*01	CARRIDGYAMDYW	12	mu
	C08	3-6*01	2-5*01	4*01	CARGTSYSSNYGAMDYW	15	mu
	C09	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	C12	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	D01	1-9*01	4-1*01	2*01	CARKANWEDW	8	mu
	D03	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	D10	2-9-1*01	2-4*01	3*01	CARDDYDAWFAYW	11	mu
	E01	1-62-2*01	1-1*01	2*01	CARHEVTVLTDYW	11	mu

E02	1-80*01	2-1*01	2*01	CARSTRGYW	7	mu
E04	1-81*01	4-1*01	4*01	CARSLGQGDYAMDYW	13	mu
E05	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
E06	1-18*01	1-1*02	2*01	CARGGGYGYFDYW	11	mu
E07	1-9*01	3-3*01	4*01	CARGGAGPSYYYAMDYW	15	mu
E09	1-69*01	1-1*01	2*01	CARYGLLRYPDYW	11	mu
E10	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
E11	1-26*01	1-1*02	3*01	CARGGNYEDWFAYW	12	mu
F02	3-6*01	2-4*01	3*01	CARDDPYDYRDLDFAYW	16	mu
F05	1-47*01	4-1*01	4*01	CARNWDGAMDYW	10	mu
F06	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
F08	5-17*01	1-1*01	3*01	CARIYGSETFAYW	11	mu
F09	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
F10	1-53*01	4-1*01	2*01	CASGEDWDRDYW	10	mu
F11	1-80*01	3-3*01	3*01	CARLDWFAYW	9	mu
F12	1-55*01	1-1*01	4*01	CARRDYGSSWGAMDYW	14	mu
G03	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
G04	2-3*01	4-1*01	3*01	CAKTGPSFAYW	9	mu
G07	1-74*01	2-1*01	2*01	CAIDYYGNLYYFDYW	13	mu
G10	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
G12	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
H03	5-6*01	4-1*01	4*01	CARKGLGREDYYAMDYW	15	mu
H04	1-42*01	1-1*01	2*01	CARGSSSSGYFDYW	12	mu
H11	5-17*01	4-1*02	4*01	CANQLRHAMDYW	10	mu
H12	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu

Mouse 3

(BG18+/-)						
Mouse-ID	Well-ID	IGHV	IGHD	IGHJ	HCDR3(aa)	Length Species
BG18.1	A02	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	A03	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	A04	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	A06	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	A07	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	A09	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	A11	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	A12	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	B01	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	B02	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	B03	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	B04	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	B05	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	B07	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	B08	2-2*01	1-1*01	4*01	CARGGLPRNAITIFGVVALGEYYYYGMDVW	28 mu
	B10	3-6*01	1-1*01	4*01	CARGRGVVALGEYYYYGMDVW	19 mu
	B11	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	B12	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	C01	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	C04	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	C05	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	C06	1-75*01	1-1*01	4*01	CARSLTIFGVVALGEYYYYGMDVW	23 mu
	C08	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	C09	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	C10	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	C11	5-17*01	2-10*02	4*01	CARGMGYGNITIFGVVALGEYYYYGMDVW	27 mu
	C12	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	D03	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	D04	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	D09	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	D12	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	E02	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	E05	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	E06	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	E07	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	E08	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	E09	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	E11	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	F01	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	F02	1-55*01	1-1*01	4*01	CARAPIYYYGVVALGEYYYYGMDVW	23 mu
	F03	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	F04	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	F05	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	F06	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	F09	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	F11	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	F12	1-47*01	3-3*01	4*01	CARMGDYFGMDVW	11 mu
	G01	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	G02	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	G05	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	G07	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu
	G08	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23 hu

	G09	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	G10	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	G11	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	G12	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	H03	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	H04	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	H09	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu
	H11	4-4*02	3-3*01	6*02	CARNAITIFGVVALGEYYYYGMDVW	23	hu