

Supplementary Material

Supplementary Figures

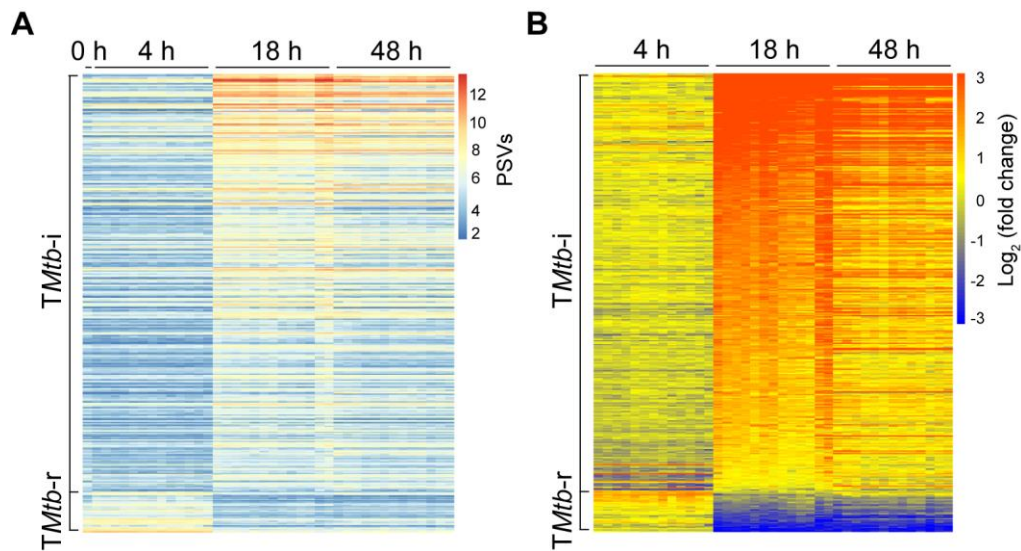


Figure S1: PSVs of the perturbed genes in homogeneous THP-1 cells responding to *Mtb* infection.

(A) The PSVs of TMtb-i and TMtb-r genes.

(B) The relative expression of each gene after *Mtb* infection compared to its expression prior to *Mtb* infection (0 h, panel A). The genes and samples in panel A and panel B are laid out in exactly the same way, except that time point 0 h was omitted in panel B since it served as a control.

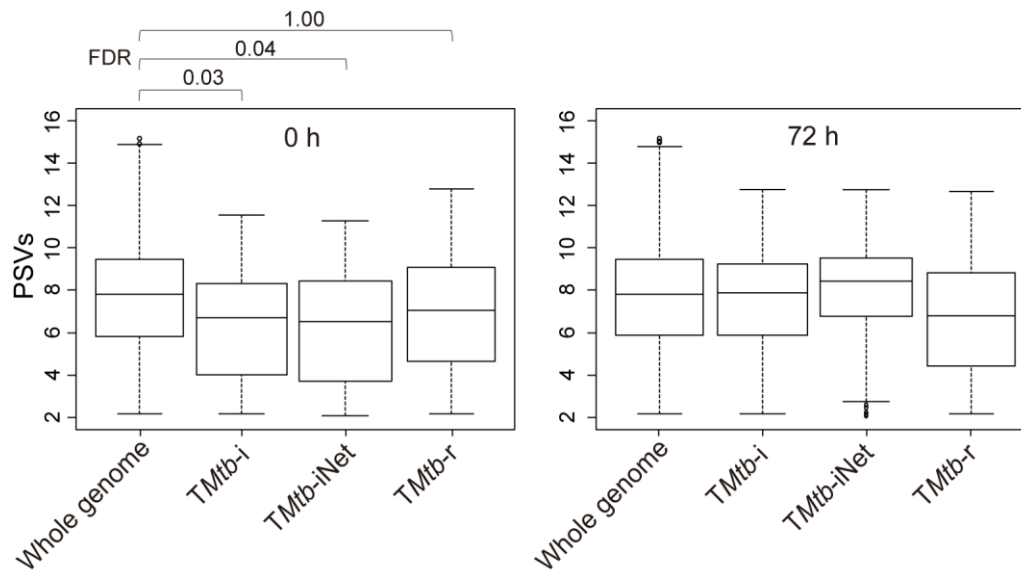


Figure S2: Box plots of the PSVs of THP-1 cells before and 72 h after infection.

TMtb-i data is from matched 212 out of 367 gene-specific DNA fragments, its derived network-based signature *TMtb-iNet* is from matched 122 out of 165 gene-specific DNA fragments and *TMtb-r* is from matched 15 out of 32 gene-specific DNA fragments. Data are shown as in Figure 1.

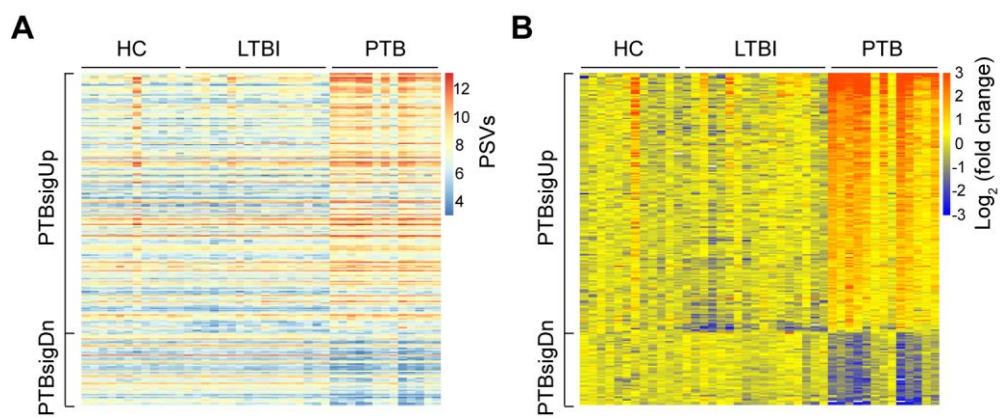


Figure S3: PSVs of PTB-specific signature genes in human whole blood.

(A) PSVs of each gene.

(B) Relative expressions of each gene compared to its median expression level in HC donors.

Data are shown as in Figure S1.

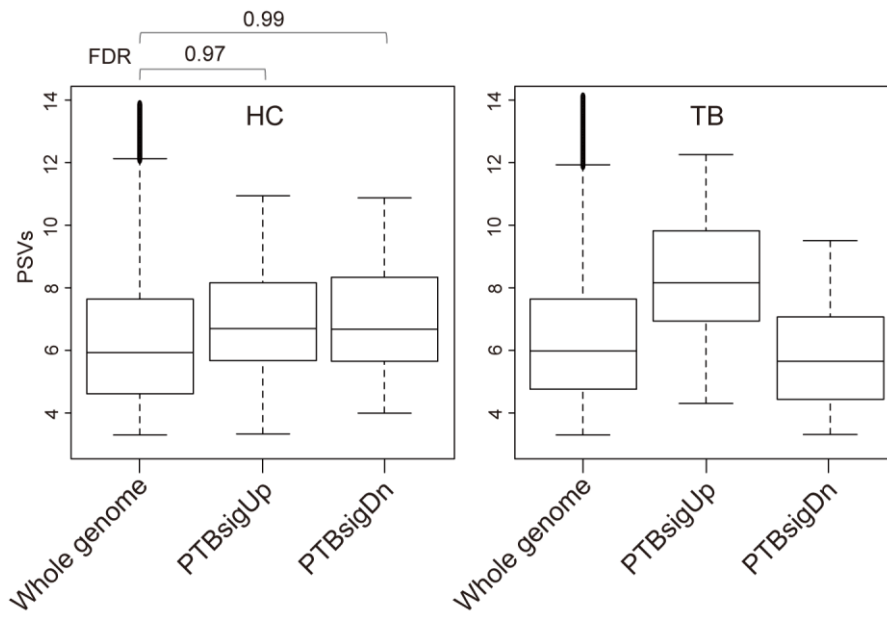


Figure S4: Box plots of the PSVs of the filtered whole genome and signature genes of whole blood.

PTBsigUp data is from matched 302 out of 306 gene-specific DNA fragments and PTBsigDn is from matched 85 out of 87 gene-specific DNA fragments matched between HC donors and TB patients. HC, healthy control donors; TB, tuberculosis patients. The data are shown as in Figure 1.

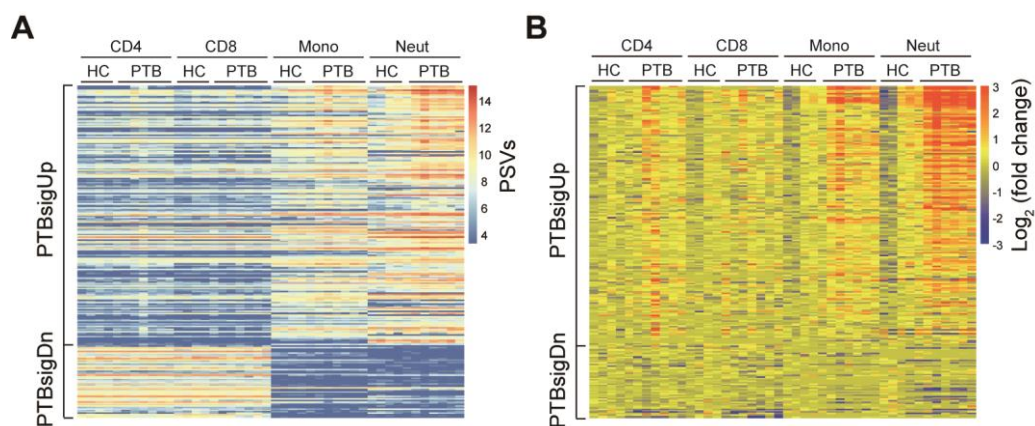


Figure S5: PSVs of PTB-specific signature genes in separated cell populations of human whole blood.

(A) PSVs of each gene.

(B) Relative expressions in different cell populations compared to the cognate median expression level in that cell population from HC donors.

The genes and samples in panel A and panel B are laid out identically.

		Section 1				
		(1)	1	10	20	30 45
FCGR1A_NM_000566.3	(1)	AATATCTTGCATGTTACAGATTTCAC				
FCGR1A_XM_005244957.3	(1)	AATATCTTGCATGTTACAGATTTCAC				
FCGR1A_XM_005244958.4	(1)	AATATCTTGCATGTTACAGATTTCAC				
FCGR1B_NM_001244910.1	(1)	AATATCTTGCATGTTACAGATTTCAC				
FCGR1B_NM_001017986.3	(1)	AATATCTTGCATGTTACAGATTTCAC				
FCGR1B_NM_001004340.3	(1)	AATATCTTGCATGTTACAGATTTCAC				
FCGR1B_XM_017000662.1	(1)	AATATCTTGCATGTTACAGATTTCAC				
FCGR1B_XM_017000661.1	(1)	AATATCTTGCATGTTACAGATTTCAC				
FCGR1B_XR_001737041.1	(1)	AATATCTTGCATGTTACAGATTTCAC				
FCGR1B_XR_001737040.1	(1)	AATATCTTGCATGTTACAGATTTCAC				
FCGR1B_NR_045213.1	(1)	AATATCTTGCATGTTACAGATTTCAC				
FCGR1CP_NR_027484.2	(1)	AATATCTTGCATGTTACAGATTTCAC				
Consensus	(1)	AATATCTTGCATGTTACAGATTTCAC				
		Section 2				
		(46)	46	60	70	80 90
FCGR1A_NM_000566.3	(46)	ACAACATGTGGTTCTTGACAACTCTGCTCCTTTGGGTTCCAGTTG				
FCGR1A_XM_005244957.3	(46)	ACAACATGTGGTTCTTGACAACTCTGCTCCTTTGGGTTCCAGTTG				
FCGR1A_XM_005244958.4	(1)	ACAACATGTGGTTCTTGACAACTCTGCTCCTTTGGGTTCCAGTTG				
FCGR1B_NM_001244910.1	(46)	ACAACATGTGGTTCTTGACAACTCTGCTCCTTTGGGTTCCAGTTG				
FCGR1B_NM_001017986.3	(46)	ACAACATGTGGTTCTTGACAACTCTGCTCCTTTGGGTTCCAGTTG				
FCGR1B_NM_001004340.3	(1)	ACAACATGTGGTTCTTGACAACTCTGCTCCTTTGGGTTCCAGTTG				
FCGR1B_XM_017000662.1	(1)	ACAACATGTGGTTCTTGACAACTCTGCTCCTTTGGGTTCCAGTTG				
FCGR1B_XM_017000661.1	(46)	ACAACATGTGGTTCTTGACAACTCTGCTCCTTTGGGTTCCAGTTG				
FCGR1B_XR_001737041.1	(46)	ACAACATGTGGTTCTTGACAACTCTGCTCCTTTGGGTTCCAGTTG				
FCGR1B_XR_001737040.1	(46)	ACAACATGTGGTTCTTGACAACTCTGCTCCTTTGGGTTCCAGTTG				
FCGR1B_NR_045213.1	(46)	ACAACATGTGGTTCTTGACAACTCTGCTCCTTTGGGTTCCAGTTG				
FCGR1CP_NR_027484.2	(46)	ACAACATGTGGTTCTTGACAACTCTGCTCCTTTGGGTTCCAGTTG				
Consensus	(46)	ACAACATGTGGTTCTTGACAACTCTGCTCCTTTGGGTTCCAGTTG				
		Section 3				
		(91)	91	100	110	120 135
FCGR1A_NM_000566.3	(91)	ATGGGCAAGTGG---ACACCACAAAGGCAGTGATCACTTTGCAGC				
FCGR1A_XM_005244957.3	(91)	ATGGGCAAGTGGTAGACACCACAAAGGCAGTGATCACTTTGCAGC				
FCGR1A_XM_005244958.4	(1)	ATGGGCAAGTGG---ACACCACAAAGGCAGTGATCACTTTGCAGC				
FCGR1B_NM_001244910.1	(91)	ATGGGCAAGTGG---ACACCACAAAGGCAGTGATCACTTTGCAGC				
FCGR1B_NM_001017986.3	(91)	ATGGGCAAGTGG---ACACCACAAAGGCAGTGATCACTTTGCAGC				
FCGR1B_NM_001004340.3	(1)	ATGGGCAAGTGG---ACACCACAAAGGCAGTGATCACTTTGCAGC				
FCGR1B_XM_017000662.1	(1)	ATGGGCAAGTGG---ACACCACAAAGGCAGTGATCACTTTGCAGC				
FCGR1B_XM_017000661.1	(91)	ATGGGCAAGTGGTAGACACCACAAAGGCAGTGATCACTTTGCAGC				
FCGR1B_XR_001737041.1	(91)	ATGGGCAAGTGGTAGACACCACAAAGGCAGTGATCACTTTGCAGC				
FCGR1B_XR_001737040.1	(91)	ATGGGCAAGTGGTAGACACCACAAAGGCAGTGATCACTTTGCAGC				
FCGR1B_NR_045213.1	(91)	ATGGGCAAGTGG---ACACCACAAAGGCAGTGATCACTTTGCAGC				
FCGR1CP_NR_027484.2	(91)	ATGGGCAAGTGG---ACACCACAAAGGCAGTGATCACTTTGCAGC				
Consensus	(91)	ATGGGCAAGTGGACACCACAAAGGCAGTGATCACTTTGCAGC				

		Section 4						
		(136)	136	150	160	170	180	
FCGR1A_NM_000566.3	(133)		CTCCATGGGTCAGCGTGTTC				CAAGAGGAAACCGTAACCTTGC	
FCGR1A_XM_005244957.3	(136)		CTCCATGGGTCAGCGTGTTC				CAAGAGGAAACCGTAACCTTGC	
FCGR1A_XM_005244958.4	(1)		-----				-----	
FCGR1B_NM_001244910.1	(133)		CTCCATGGGTCAGCGTGTTC				CAAGAGGAAACCGTAACCTTGC	
FCGR1B_NM_001017986.3	(133)		CTCCATGGGTCAGCGTGTTC				CAAGAGGAAACCGTAACCTTGC	
FCGR1B_NM_001004340.3	(1)		-----				-----	
FCGR1B_XM_017000662.1	(1)		-----				-----	
FCGR1B_XM_017000661.1	(136)		CTCCATGGGTCAGCGTGTTC				CAAGAGGAAACCGTAACCTTGC	
FCGR1B_XR_001737041.1	(136)		CTCCATGGGTCAGCGTGTTC				CAAGAGGAAACCGTAACCTTGC	
FCGR1B_XR_001737040.1	(136)		CTCCATGGGTCAGCGTGTTC				CAAGAGGAAACCGTAACCTTGC	
FCGR1B_NR_045213.1	(133)		CTCCATGGGTCAGCGTGTTC				CAAGAGGAAACCGTAACCTTGC	
FCGR1CP_NR_027484.2	(133)		CTCCATGGGTCAGCGTGTTC				CAAGAGGAAACCGTAACCTTGC	
Consensus	(136)		CTCCATGGGTCAGCGTGTTC				CAAGAGGAAACCGTAACCTTGC	
		Section 5						
		(181)	181	190	200	210	225	
FCGR1A_NM_000566.3	(178)		GTGAGGTGCTCCATCTGCCT				GGGAGCAGCTCT	ACACAGTGGTTTC
FCGR1A_XM_005244957.3	(181)		GTGAGGTGCTCCATCTGCCT				GGGAGCAGCTCT	ACACAGTGGTTTC
FCGR1A_XM_005244958.4	(1)		-----				-----	-----
FCGR1B_NM_001244910.1	(178)		GTGAGGTGCTCCATCTGCCT				GGGAGCAGCTCC	ACACAGTGGTTTC
FCGR1B_NM_001017986.3	(178)		GTGAGGTGCTCCATCTGCCT				GGGAGCAGCTCC	ACACAGTGGTTTC
FCGR1B_NM_001004340.3	(1)		-----				-----	-----
FCGR1B_XM_017000662.1	(1)		-----				-----	-----
FCGR1B_XM_017000661.1	(181)		GTGAGGTGCTCCATCTGCCT				GGGAGCAGCTCC	ACACAGTGGTTTC
FCGR1B_XR_001737041.1	(181)		GTGAGGTGCTCCATCTGCCT				GGGAGCAGCTCC	ACACAGTGGTTTC
FCGR1B_XR_001737040.1	(181)		GTGAGGTGCTCCATCTGCCT				GGGAGCAGCTCC	ACACAGTGGTTTC
FCGR1B_NR_045213.1	(178)		GTGAGGTGCTCCATCTGCCT				GGGAGCAGCTCC	ACACAGTGGTTTC
FCGR1CP_NR_027484.2	(178)		GTGAGGTGCTCCATCTGCCT				GGGAGCAGCTCC	ACACAGTGGTTTC
Consensus	(181)		GTGAGGTGCTCCATCTGCCT				GGGAGCAGCTCC	ACACAGTGGTTTC
		Section 6						
		(226)	226	240	250	260	270	
FCGR1A_NM_000566.3	(223)		TCAATGGCACAGGCCACTCAGACCTCGACCCCCAGCTACAG				AATCA	
FCGR1A_XM_005244957.3	(226)		TCAATGGCACAGGCCACTCAGACCTCGACCCCCAGCTACAG				AATCA	
FCGR1A_XM_005244958.4	(1)		-----A C C A G A A C C T C T T C A A T - A				-----	
FCGR1B_NM_001244910.1	(223)		TCAATGGCACAGGCCACTCAGACCTCGACCCCCAGCTACAG				AATCA	
FCGR1B_NM_001017986.3	(223)		TCAATGGCACAGGCCACTCAGACCTCGACCCCCAGCTACAG				AATCA	
FCGR1B_NM_001004340.3	(1)		-----				AAT-A	
FCGR1B_XM_017000662.1	(1)		-----				AAT-A	
FCGR1B_XM_017000661.1	(226)		TCAATGGCACAGGCCACTCAGACCTCGACCCCCAGCTACAG				AATCA	
FCGR1B_XR_001737041.1	(226)		TCAATGGCACAGGCCACTCAGACCTCGACCCCCAGCTACAG				AATCA	
FCGR1B_XR_001737040.1	(226)		TCAATGGCACAGGCCACTCAGACCTCGACCCCCAGCTACAG				AATCA	
FCGR1B_NR_045213.1	(223)		TCAATGGCACAGGCCACTCAGACCTCGACCCCCAGCTACAG				AATCA	
FCGR1CP_NR_027484.2	(223)		TCAATGGCACAGGCCACTCAGACCTCGACCCCCAGCTACAG				AATCA	
Consensus	(226)		TCAATGGCACAGGCCACTCAGACCTCGACCCCCAGCTACAG				AATCA	

		Section 7				
		(271)	271	280	290	300 315
FCGR1A_NM_000566.3	(268)	CCTCTGCCAGTGTCA	-	ATGACAGTGGTGAATACAGGTGCCAGAGA		
FCGR1A_XM_005244957.3	(271)	CCTCTGCCAGTGTCA	-	ATGACAGTGGTGAATACAGGTGCCAGAGA		
FCGR1A_XM_005244958.4	(22)	TCT-TGGATGTTACAGATTTCACTGCTCCAC	CAGCTTGGAGACA			
FCGR1B_NM_001244910.1	(268)	CCTCTGCCAGTGTCA	-	ATGACAGTGGTGAATACAGGTGCCAGAGA		
FCGR1B_NM_001017986.3	(268)	CCTCTGCCAGTGTCA	-	ATGACAGTGGTGAATACAGGTGCCAGAGA		
FCGR1B_NM_001004340.3	(5)	TCT-TGGATGTTACAGATTTCACTACTCCAC	CAGCTTGGAGACA			
FCGR1B_XM_017000662.1	(5)	TCT-TGGATGTTACAGATTTCACTACTCCAC	CAGCTTGGAGACA			
FCGR1B_XM_017000661.1	(271)	CCTCTGCCAGTGTCA	-	ATGACAGTGGTGAATACAGGTGCCAGAGA		
FCGR1B_XR_001737041.1	(271)	CCTCTGCCAGTGTCA	-	ATGACAGTGGTGAATACAGGTGCCAGAGA		
FCGR1B_XR_001737040.1	(271)	CCTCTGCCAGTGTCA	-	ATGACAGTGGTGAATACAGGTGCCAGAGA		
FCGR1B_NR_045213.1	(268)	CCTCTGCCAGTGTCA	-	ATGACAGTGGTGAATACAGGTGCCAGAGA		
FCGR1CP_NR_027484.2	(268)	CCTCTGCCAGTGTCA	-	ATGACAGTGGTGAATACAGGTGCCAGAGA		
Consensus	(271)	CCTCTGCCAGTGTCA	-	ATGACAGTGGTGAATACAGGTGCCAGAGA		
		Section 8				
		(316)	316	330	340	350 360
FCGR1A_NM_000566.3	(312)	---GGTCTCTCAGGCGGAAGTGACCCCATACAGCTGGAAATC---				
FCGR1A_XM_005244957.3	(315)	---GGTCTCTCAGGCGGAAGTGACCCCATACAGCTGGAAATC---				
FCGR1A_XM_005244958.4	(66)	ACATGTGGTTCCTTACAACTCTGCTCCTTTGGG-----				
FCGR1B_NM_001244910.1	(312)	---GGTCTCTCAGGCGGAAGTGACCCCATACAGCTGGAAATC---				
FCGR1B_NM_001017986.3	(312)	---GGTCTCTCAGGCGGAAGTGACCCCATACAGCTGGAAATC---				
FCGR1B_NM_001004340.3	(49)	ACATGTGGTTCCTTACAACTCTGCTCCTTTGGG-----				
FCGR1B_XM_017000662.1	(49)	ACATGTGGTTCCTTACAACTCTGCTCCTTTGGGTTCCAGTGGATG				
FCGR1B_XM_017000661.1	(315)	---GGTCTCTCAGGCGGAAGTGACCCCATACAGCTGGAAATC---				
FCGR1B_XR_001737041.1	(315)	---GGTCTCTCAGGCGGAAGTGACCCCATACAGCTGGAAATC---				
FCGR1B_XR_001737040.1	(315)	---GGTCTCTCAGGCGGAAGTGACCCCATACAGCTGGAAATC---				
FCGR1B_NR_045213.1	(312)	---GGTCTCTCAGGCGGAAGTGACCCCATACAGCTGGAAATC---				
FCGR1CP_NR_027484.2	(312)	---GGTCTCTCAGGCGGAAGTGACCCCATACAGCTGGAAATC---				
Consensus	(316)	GGTCTCTCAGGCGGAAGTGACCCCATACAGCTGGAAATC				
		Section 9				
		(361)	361	370	380	390 405
FCGR1A_NM_000566.3	(351)	---CACAGAGGCTGGCTACTACTGCAGGTCTCCAGCAGAGTCTTCA				
FCGR1A_XM_005244957.3	(354)	---CACAGAGGCTGGCTACTACTGCAGGTCTCCAGCAGAGTCTTCA				
FCGR1A_XM_005244958.4	(99)	-----GCTGGCTACTACTGCAGGTCTCCAGCAGAGTCTTCA				
FCGR1B_NM_001244910.1	(351)	---CACAGAGGCTGGCTACTACTGCAGGTCTCCAGCAGAGTCTTCA				
FCGR1B_NM_001017986.3	(351)	---CACAGAGGCTGGCTACTACTGCAGGTCTCCAGCAGAGTCTTCA				
FCGR1B_NM_001004340.3	(82)	-----GCTGGCTACTACTGCAGGTCTCCAGCAGAGTCTTCA				
FCGR1B_XM_017000662.1	(94)	GGCAAGTGGCTGGCTACTACTGCAGGTCTCCAGCAGAGTCTTCA				
FCGR1B_XM_017000661.1	(354)	---CACAGAGGCTGGCTACTACTGCAGGTCTCCAGCAGAGTCTTCA				
FCGR1B_XR_001737041.1	(354)	---CACAGAGGCTGGCTACTACTGCAGGTCTCCAGCAGAGTCTTCA				
FCGR1B_XR_001737040.1	(354)	---CACAGAGGCTGGCTACTACTGCAGGTCTCCAGCAGAGTCTTCA				
FCGR1B_NR_045213.1	(351)	---CACAGAGGCTGGCTACTACTGCAGGTCTCCAGCAGAGTCTTCA				
FCGR1CP_NR_027484.2	(351)	---CACAGAGGCTGGCTACTACTGCAGGTCTCCAGCAGAGTCTTCA				
Consensus	(361)	CACAGAGGCTGGCTACTACTGCAGGTCTCCAGCAGAGTCTTCA				

		Section 10				
		(406)	406	420	430	440 450
FCGR1A_NM_000566.3	(394)	C	GGAAGGAGAACCTCTGGCCTTGAGGTGTCATGCGTGGAAGGATA			
FCGR1A_XM_005244957.3	(397)	C	GGAAGGAGAACCTCTGGCCTTGAGGTGTCATGCGTGGAAGGATA			
FCGR1A_XM_005244958.4	(135)	C	GGAAGGAGAACCTCTGGCCTTGAGGTGTCATGCGTGGAAGGATA			
FCGR1B_NM_001244910.1	(394)	T	GGAAGGAGAACCTCTGGCCTTGAGGTGTCATGCGTGGAAGGATA			
FCGR1B_NM_001017986.3	(394)	T	GGAAGGAGAACCTCTGGCCTTGAGGTGTCATGCGTGGAAGGATA			
FCGR1B_NM_001004340.3	(118)	T	GGAAGGAGAACCTCTGGCCTTGAGGTGTCATGCGTGGAAGGATA			
FCGR1B_XM_017000662.1	(139)	T	GGAAGGAGAACCTCTGGCCTTGAGGTGTCATGCGTGGAAGGATA			
FCGR1B_XM_017000661.1	(397)	T	GGAAGGAGAACCTCTGGCCTTGAGGTGTCATGCGTGGAAGGATA			
FCGR1B_XR_001737041.1	(397)	T	GGAAGGAGAACCTCTGGCCTTGAGGTGTCATGCGTGGAAGGATA			
FCGR1B_XR_001737040.1	(397)	T	GGAAGGAGAACCTCTGGCCTTGAGGTGTCATGCGTGGAAGGATA			
FCGR1B_NR_045213.1	(394)	T	GGAAGGAGAACCTCTGGCCTTGAGGTGTCATGCGTGGAAGGATA			
FCGR1CP_NR_027484.2	(394)	C	GGAAGGAGAACCTCTGGCCTTGAGGTGTCATGCGTGGAAGGATA			
Consensus	(406)	T	GGAAGGAGAACCTCTGGCCTTGAGGTGTCATGCGTGGAAGGATA			
		Section 11				
		(451)	451	460	470	480 495
FCGR1A_NM_000566.3	(439)	AGCTGGTGTACAATGTGCTTTACTATCGAAATGGCAAAGCCTTTA				
FCGR1A_XM_005244957.3	(442)	AGCTGGTGTACAATGTGCTTTACTATCGAAATGGCAAAGCCTTTA				
FCGR1A_XM_005244958.4	(180)	AGCTGGTGTACAATGTGCTTTACTATCGAAATGGCAAAGCCTTTA				
FCGR1B_NM_001244910.1	(439)	AGCTGGTGTACAATGTGCTTTACTATCGAAATGGCAAAGCCTTTA				
FCGR1B_NM_001017986.3	(439)	AGCTGGTGTACAATGTGCTTTACTATCGAAATGGCAAAGCCTTTA				
FCGR1B_NM_001004340.3	(163)	AGCTGGTGTACAATGTGCTTTACTATCGAAATGGCAAAGCCTTTA				
FCGR1B_XM_017000662.1	(184)	AGCTGGTGTACAATGTGCTTTACTATCGAAATGGCAAAGCCTTTA				
FCGR1B_XM_017000661.1	(442)	AGCTGGTGTACAATGTGCTTTACTATCGAAATGGCAAAGCCTTTA				
FCGR1B_XR_001737041.1	(442)	AGCTGGTGTACAATGTGCTTTACTATCGAAATGGCAAAGCCTTTA				
FCGR1B_XR_001737040.1	(442)	AGCTGGTGTACAATGTGCTTTACTATCGAAATGGCAAAGCCTTTA				
FCGR1B_NR_045213.1	(439)	AGCTGGTGTACAATGTGCTTTACTATCGAAATGGCAAAGCCTTTA				
FCGR1CP_NR_027484.2	(439)	AGCTGGTGTACAATGTGCTTTACTATCGAAATGGCAAAGCCTTTA				
Consensus	(451)	AGCTGGTGTACAATGTGCTTTACTATCGAAATGGCAAAGCCTTTA				
		Section 12				
		(496)	496	510	520	530 540
FCGR1A_NM_000566.3	(484)	AGTTTTTCCACTGGAATTCTAACCTCACCATTCTGAAAACCAACA				
FCGR1A_XM_005244957.3	(487)	AGTTTTTCCACTGGAATTCTAACCTCACCATTCTGAAAACCAACA				
FCGR1A_XM_005244958.4	(225)	AGTTTTTCCACTGGAATTCTAACCTCACCATTCTGAAAACCAACA				
FCGR1B_NM_001244910.1	(484)	AGTTTTTCCACTGGAATTCTAACCTCACCATTCTGAAAACCAACA				
FCGR1B_NM_001017986.3	(484)	AGTTTTTCCACTGGAATTCTAACCTCACCATTCTGAAAACCAACA				
FCGR1B_NM_001004340.3	(208)	AGTTTTTCCACTGGAATTCTAACCTCACCATTCTGAAAACCAACA				
FCGR1B_XM_017000662.1	(229)	AGTTTTTCCACTGGAATTCTAACCTCACCATTCTGAAAACCAACA				
FCGR1B_XM_017000661.1	(487)	AGTTTTTCCACTGGAATTCTAACCTCACCATTCTGAAAACCAACA				
FCGR1B_XR_001737041.1	(487)	AGTTTTTCCACTGGAATTCTAACCTCACCATTCTGAAAACCAACA				
FCGR1B_XR_001737040.1	(487)	AGTTTTTCCACTGGAATTCTAACCTCACCATTCTGAAAACCAACA				
FCGR1B_NR_045213.1	(484)	AGTTTTTCCACTGGAATTCTAACCTCACCATTCTGAAAACCAACA				
FCGR1CP_NR_027484.2	(484)	AGTTTTTCCACTGGAATTCTAACCTCACCATTCTGAAAACCAACA				
Consensus	(496)	AGTTTTTCCACTGGAATTCTAACCTCACCATTCTGAAAACCAACA				

		Section 13				
		(541)	541	550	560	570 585
FCGR1A_NM_000566.3	(529)		TAAGTCACAATGGCACCTACCATTGCTCAGGCAT	GGGAAAAGCATC		
FCGR1A_XM_005244957.3	(532)		TAAGTCACAATGGCACCTACCATTGCTCAGGCAT	GGGAAAAGCATC		
FCGR1A_XM_005244958.4	(270)		TAAGTCACAATGGCACCTACCATTGCTCAGGCAT	GGGAAAAGCATC		
FCGR1B_NM_001244910.1	(529)		TAAGTCACAATGGCACCTACCATTGCTCAGGCAT	GGGAAAAGCATC		
FCGR1B_NM_001017986.3	(529)		TAAGTCACAATGGCACCTACCATTGCTCAGGCAT	GGGAAAAGCATC		
FCGR1B_NM_001004340.3	(253)		TAAGTCACAATGGCACCTACCATTGCTCAGGCAT	GGGAAAAGCATC		
FCGR1B_XM_017000662.1	(274)		TAAGTCACAATGGCACCTACCATTGCTCAGGCAT	GGGAAAAGCATC		
FCGR1B_XM_017000661.1	(532)		TAAGTCACAATGGCACCTACCATTGCTCAGGCAT	GGGAAAAGCATC		
FCGR1B_XR_001737041.1	(532)		TAAGTCACAATGGCACCTACCATTGCTCAGGCAT	GGGAAAAGCATC		
FCGR1B_XR_001737040.1	(532)		TAAGTCACAATGGCACCTACCATTGCTCAGGCAT	GGGAAAAGCATC		
FCGR1B_NR_045213.1	(529)		TAAGTCACAATGGCACCTACCATTGCTCAGGCAT	GGGAAAAGCATC		
FCGR1CP_NR_027484.2	(529)		TAAGTCACAATGGCACCTACCATTGCTCAGGCAT	GGGAAAAGCATC		
Consensus	(541)		TAAGTCACAATGGCACCTACCATTGCTCAGGCAT	GGGAAAAGCATC		
		Section 14				
		(586)	586	600	610	620 630
FCGR1A_NM_000566.3	(574)		GCTACACATCAGCAGGAATATC	TGT---	CACTGTGAAAG	AGCTAT
FCGR1A_XM_005244957.3	(577)		GCTACACATCAGCAGGAATATC	TGT---	CACTGTGAAAG	AGCTAT
FCGR1A_XM_005244958.4	(315)		GCTACACATCAGCAGGAATATC	TGT---	CACTGTGAAAG	AGCTAT
FCGR1B_NM_001244910.1	(574)		GCTACACATCAGCAGGAATATC	ACAATA	CACTGTGAAAG	AGCTAT
FCGR1B_NM_001017986.3	(574)		GCTACACATCAGCAGGAATATC	ACAATA	CACTGTGAAAG	-----
FCGR1B_NM_001004340.3	(298)		GCTACACATCAGCAGGAATATC	ACAATA	CACTGTGAAAG	-----
FCGR1B_XM_017000662.1	(319)		GCTACACATCAGCAGGAATATC	ACAATA	CACTGTGAAAG	-----
FCGR1B_XM_017000661.1	(577)		GCTACACATCAGCAGGAATATC	ACAATA	CACTGTGAAAG	-----
FCGR1B_XR_001737041.1	(577)		GCTACACATCAGCAGGAATATC	ACAATA	CACTGTGAAAG	AGCTAT
FCGR1B_XR_001737040.1	(577)		GCTACACATCAGCAGGAATATC	ACAATA	CACTGTGAAAG	AGCTAT
FCGR1B_NR_045213.1	(574)		GCTACACATCAGCAGGAATATC	ACAATA	CACTGTGAAAG	AGCTAT
FCGR1CP_NR_027484.2	(574)		GCTACACATCAGCAGGAATATC	ACAATA	CACTGTGAAAG	AGCTAT
Consensus	(586)		GCTACACATCAGCAGGAATATC	ACAATA	CACTGTGAAAG	AGCTAT
		Section 15				
		(631)	631	640	650	660 675
FCGR1A_NM_000566.3	(616)		TTCCAGCTCCAGTGCTGAATGCATCTGTGACATCCCCACTCCTGG			
FCGR1A_XM_005244957.3	(619)		TTCCAGCTCCAGTGCTGAATGCATCTGTGACATCCCCACTCCTGG			
FCGR1A_XM_005244958.4	(357)		TTCCAGCTCCAGTGCTGAATGCATCTGTGACATCCCCACTCCTGG			
FCGR1B_NM_001244910.1	(619)		TTCCAGCTCCAGTGCTGAATGCATCTGTGACATCCCCACTCCTGG			
FCGR1B_NM_001017986.3	(613)		-----			
FCGR1B_NM_001004340.3	(337)		-----			
FCGR1B_XM_017000662.1	(358)		-----			
FCGR1B_XM_017000661.1	(616)		-----			
FCGR1B_XR_001737041.1	(622)		TTCCAGCTCCAGTGCTGAATGCATCTGTGACATCCCCACTCCTGG			
FCGR1B_XR_001737040.1	(622)		TTCCAGCTCCAGTGCTGAATGCATCTGTGACATCCCCACTCCTGG			
FCGR1B_NR_045213.1	(619)		TTCCAGCTCCAGTGCTGAATGCATCTGTGACATCCCCACTCCTGG			
FCGR1CP_NR_027484.2	(619)		TTCCAGCTCCAGTGCTGAATGCATCTGTGACATCCCCACTCCTGG			
Consensus	(631)		TTCCAGCTCCAGTGCTGAATGCATCTGTGACATCCCCACTCCTGG			

		Section 16				
		(676)	676	690	700	710 720
FCGR1A_NM_000566.3	(661)	AGGGGAATCTGGTCACCCTGAGCTGTGAAACAAAGTTGCTCTTGC				
FCGR1A_XM_005244957.3	(664)	AGGGGAATCTGGTCACCCTGAGCTGTGAAACAAAGTTGCTCTTGC				
FCGR1A_XM_005244958.4	(402)	AGGGGAATCTGGTCACCCTGAGCTGTGAAACAAAGTTGCTCTTGC				
FCGR1B_NM_001244910.1	(664)	AGGGGAATCTGGTCACCCTGAGCTGTGAAACAAAGTTGCTCTTGC				
FCGR1B_NM_001017986.3	(613)	-----				
FCGR1B_NM_001004340.3	(337)	-----				
FCGR1B_XM_017000662.1	(358)	-----				
FCGR1B_XM_017000661.1	(616)	-----				
FCGR1B_XR_001737041.1	(667)	AGGGGAATCTGGTCACCCTGAGCTGTGAAACAAAGTTGCTCTTGC				
FCGR1B_XR_001737040.1	(667)	AGGGGAATCTGGTCACCCTGAGCTGTGAAACAAAGTTGCTCTTGC				
FCGR1B_NR_045213.1	(664)	AGGGGAATCTGGTCACCCTGAGCTGTGAAACAAAGTTGCTCTTGC				
FCGR1CP_NR_027484.2	(664)	-AGGGGAATCTGGTCACCCTGAGCTGTGAAACAAAGTTGCTCTTGC				
Consensus	(676)	AGGGGAATCTGGTCACCCTGAGCTGTGAAACAAAGTTGCTCTTGC				
		Section 17				
		(721)	721	730	740	750 765
FCGR1A_NM_000566.3	(706)	AGAGGCCTGGTTTGCAGCTTTACTTCTCCTTCTACATGGGCAGCA				
FCGR1A_XM_005244957.3	(709)	AGAGGCCTGGTTTGCAGCTTTACTTCTCCTTCTACATGGGCAGCA				
FCGR1A_XM_005244958.4	(447)	AGAGGCCTGGTTTGCAGCTTTACTTCTCCTTCTACATGGGCAGCA				
FCGR1B_NM_001244910.1	(709)	AGAGGCCTGGTTTGCAGCTTTACTTCTCCTTCTACATGGGCAGCA				
FCGR1B_NM_001017986.3	(613)	-----				
FCGR1B_NM_001004340.3	(337)	-----				
FCGR1B_XM_017000662.1	(358)	-----				
FCGR1B_XM_017000661.1	(616)	-----				
FCGR1B_XR_001737041.1	(712)	AGAGGCCTGGTTTGCAGCTTTACTTCTCCTTCTACATGGGCAGCA				
FCGR1B_XR_001737040.1	(712)	AGAGGCCTGGTTTGCAGCTTTACTTCTCCTTCTACATGGGCAGCA				
FCGR1B_NR_045213.1	(709)	AGAGGCCTGGTTTGCAGCTTTACTTCTCCTTCTACATGGGCAGCA				
FCGR1CP_NR_027484.2	(708)	AGAGGCCTGGTTTGCAGCTTTACTTCTCCTTCTACATGGGCAGCA				
Consensus	(721)	AGAGGCCTGGTTTGCAGCTTTACTTCTCCTTCTACATGGGCAGCA				
		Section 18				
		(766)	766	780	790	800 810
FCGR1A_NM_000566.3	(751)	AGACCCTGCGAGGCAGGAACACATCCTCTGAATACCAAATACTAA				
FCGR1A_XM_005244957.3	(754)	AGACCCTGCGAGGCAGGAACACATCCTCTGAATACCAAATACTAA				
FCGR1A_XM_005244958.4	(492)	AGACCCTGCGAGGCAGGAACACATCCTCTGAATACCAAATACTAA				
FCGR1B_NM_001244910.1	(754)	AGACCCTGCGAGGCAGGAACACATCCTCTGAATACCAAATACTAA				
FCGR1B_NM_001017986.3	(613)	-----				
FCGR1B_NM_001004340.3	(337)	-----				
FCGR1B_XM_017000662.1	(358)	-----				
FCGR1B_XM_017000661.1	(616)	-----				
FCGR1B_XR_001737041.1	(757)	AGACCCTGCGAGGCAGGAACACATCCTCTGAATACCAAATACTAA				
FCGR1B_XR_001737040.1	(757)	AGACCCTGCGAGGCAGGAACACATCCTCTGAATACCAAATACTAA				
FCGR1B_NR_045213.1	(754)	AGACCCTGCGAGGCAGGAACACATCCTCTGAATACCAAATACTAA				
FCGR1CP_NR_027484.2	(753)	AGACCCTGCGAGGCAGGAACACATCCTCTGAATAGTAAATACTAA				
Consensus	(766)	AGACCCTGCGAGGCAGGAACACATCCTCTGAATACCAAATACTAA				

		Section 19				
		(811)	811	820	830	840 855
FCGR1A_NM_000566.3	(796)		CTGCTAGAAGAGAAGACTCTGGGTTTACTGGTGCGAGGCTGCCA			
FCGR1A_XM_005244957.3	(799)		CTGCTAGAAGAGAAGACTCTGGGTTTACTGGTGCGAGGCTGCCA			
FCGR1A_XM_005244958.4	(537)		CTGCTAGAAGAGAAGACTCTGGGTTTACTGGTGCGAGGCTGCCA			
FCGR1B_NM_001244910.1	(799)		CTGCTAGAAGAGAAGACTCTGGGTTTACTGGTGCGAGGCTGCCA			
FCGR1B_NM_001017986.3	(613)		-----			
FCGR1B_NM_001004340.3	(337)		-----			
FCGR1B_XM_017000662.1	(358)		-----			
FCGR1B_XM_017000661.1	(616)		-----			
FCGR1B_XR_001737041.1	(802)		CTGCTAGAAGAGAAGACTCTGGGTTTACTGGTGCGAGGCTGCCA			
FCGR1B_XR_001737040.1	(802)		CTGCTAGAAGAGAAGACTCTGGGTTTACTGGTGCGAGGCTGCCA			
FCGR1B_NR_045213.1	(799)		CTGCTAGAAGAGAAGACTCTGGGTTTACTGGTGCGAGGCTGCCA			
FCGR1CP_NR_027484.2	(798)		CTGCTAGAAGAGAAGACTCTGGGTTTACTGGTGCGAGGCTGCCA			
Consensus	(811)		CTGCTAGAAGAGAAGACTCTGGGTTTACTGGTGCGAGGCTGCCA			
		Section 20				
		(856)	856	870	880	890 900
FCGR1A_NM_000566.3	(841)		CAGAGGATGGAAATGTCCTTAAGC	G	CAGCCCTGAGTTGGAGCTTC	
FCGR1A_XM_005244957.3	(844)		CAGAGGATGGAAATGTCCTTAAGC	G	CAGCCCTGAGTTGGAGCTTC	
FCGR1A_XM_005244958.4	(582)		CAGAGGATGGAAATGTCCTTAAGC	G	CAGCCCTGAGTTGGAGCTTC	
FCGR1B_NM_001244910.1	(844)		CAGAGGATGGAAATGTCCTTAAGC	A	CAGCCCTGAGTTGGAGCTTC	
FCGR1B_NM_001017986.3	(613)		-----			
FCGR1B_NM_001004340.3	(337)		-----			
FCGR1B_XM_017000662.1	(358)		-----			
FCGR1B_XM_017000661.1	(616)		-----			
FCGR1B_XR_001737041.1	(847)		CAGAGGATGGAAATGTCCTTAAGC	A	CAGCCCTGAGTTGGAGCTTC	
FCGR1B_XR_001737040.1	(847)		CAGAGGATGGAAATGTCCTTAAGC	A	CAGCCCTGAGTTGGAGCTTC	
FCGR1B_NR_045213.1	(844)		CAGAGGATGGAAATGTCCTTAAGC	A	CAGCCCTGAGTTGGAGCTTC	
FCGR1CP_NR_027484.2	(843)		CAGAGGATGGAAATGTCCTTAAGC	G	CAGCCCTGAGTTGGAGCTTC	
Consensus	(856)		CAGAGGATGGAAATGTCCTTAAGC		CAGCCCTGAGTTGGAGCTTC	
		Section 21				
		(901)	901	910	920	930 945
FCGR1A_NM_000566.3	(886)		AAGTGCTTG	-----		
FCGR1A_XM_005244957.3	(889)		AAGTGCTTG	-----		
FCGR1A_XM_005244958.4	(627)		AAGTGCTTG	-----		
FCGR1B_NM_001244910.1	(889)		AAGTGCTTG	GTGAGAATGACGGGAAGCCACTGGCACAGAAGAAGG		
FCGR1B_NM_001017986.3	(613)		-----			
FCGR1B_NM_001004340.3	(337)		-----			
FCGR1B_XM_017000662.1	(358)		-----			
FCGR1B_XM_017000661.1	(616)		-----			
FCGR1B_XR_001737041.1	(892)		AAGTGCTTG	GTGAGAATGACGGGAAGCCACTGGCACAGAAGAAGG		
FCGR1B_XR_001737040.1	(892)		AAGTGCTTG	-----		
FCGR1B_NR_045213.1	(889)		AAGTGCTTG	-----		
FCGR1CP_NR_027484.2	(888)		AAGTGCTTG	-----		
Consensus	(901)		AAGTGCTTG			

		Section 22				
		(946)	946	960	970	980 990
FCGR1A_NM_000566.3	(895)	-----	-----	-----	GCCTCCA	GTACCA----
FCGR1A_XM_005244957.3	(898)	-----	-----	-----	GCCTCCA	GTACCA----
FCGR1A_XM_005244958.4	(636)	-----	-----	-----	GCCTCCA	GTACCA----
FCGR1B_NM_001244910.1	(934)	GAC-----	-----	-----	TCCCTTA	TCTCCCATGGG
FCGR1B_NM_001017986.3	(613)	-----	-----	-----	GCCTCCA	GTACCA----
FCGR1B_NM_001004340.3	(337)	-----	-----	-----	GCCTCCA	GTACCA----
FCGR1B_XM_017000662.1	(358)	-----	-----	-----	GCCTCCA	GTACCA----
FCGR1B_XM_017000661.1	(616)	-----	-----	-----	GCCTCCA	GTACCA----
FCGR1B_XR_001737041.1	(937)	GACTCCCTTATCTCCCATGGGACTGAG	-----	-----	GCCTCCA	GTACCA----
FCGR1B_XR_001737040.1	(901)	-----	-----	-----	GCCTCCA	GTACCA----
FCGR1B_NR_045213.1	(898)	-----	-----	-----	GCCTCCA	GTACCA----
FCGR1CP_NR_027484.2	(897)	-----	-----	-----	GCCTCCA	GTACCA----
Consensus	(946)	GCCTCCAGTTACCA				
		Section 23				
		(991)	991	1000	1010	1020 1035
FCGR1A_NM_000566.3	(909)	ACTCCTGTC	TGGTTTCATGTCCTTTTCTATCTGGCA	-----	GTGGGAAT	
FCGR1A_XM_005244957.3	(912)	ACTCCTGTC	TGGTTTCATGTCCTTTTCTATCTGGCA	-----	GTGGGAAT	
FCGR1A_XM_005244958.4	(650)	ACTCCTGTC	TGGTTTCATGTCCTTTTCTATCTGGCA	-----	GTGGGAAT	
FCGR1B_NM_001244910.1	(955)	ACTGAGGTTTG--	TTCAAGGGTTTTGGCC	CAGACAGAGGGGAA		
FCGR1B_NM_001017986.3	(627)	ACTCCTGTC	TGGTTTCATGTCCTTTTCTATCTGGCA	-----	GTGGGAAT	
FCGR1B_NM_001004340.3	(351)	ACTCCTGTC	TGGTTTCATGTCCTTTTCTATCTGGCA	-----	GTGGGAAT	
FCGR1B_XM_017000662.1	(372)	ACTCCTGTC	TGGTTTCATGTCCTTTTCTATCTGGCA	-----	GTGGGAAT	
FCGR1B_XM_017000661.1	(630)	ACTCCTGTC	TGGTTTCATGTCCTTTTCTATCTGGCA	-----	GTGGGAAT	
FCGR1B_XR_001737041.1	(978)	ACTCCTGTC	TGGTTTCATGTCCTTTTCTATCTGGCA	-----	GTGGGAAT	
FCGR1B_XR_001737040.1	(915)	ACTCCTGTC	TGGTTTCATGTCCTTTTCTATCTGGCA	-----	GTGGGAAT	
FCGR1B_NR_045213.1	(912)	ACTCCTGTC	TGGTTTCATGTCCTTTTCTATCTGGCA	-----	GTGGGAAT	
FCGR1CP_NR_027484.2	(911)	ACTCCTGTC	TGGTTTCATGTCCTTTTCTATCTGGCA	-----	GTGGGAAT	
Consensus	(991)	ACTCCTGTCTGGTTTCATGTCCTTTTCTATCTGGCA				
		Section 24				
		(1036)	1036	1050	1060	1070 1080
FCGR1A_NM_000566.3	(953)	AATGTTTTT	AGTGAACACTGTTCTCTGGG--	TGACAATACGTAAA		
FCGR1A_XM_005244957.3	(956)	AATGTTTTT	AGTGAACACTGTTCTCTGGG--	TGACAATACGTAAA		
FCGR1A_XM_005244958.4	(694)	AATGTTTTT	AGTGAACACTGTTCTCTGGG--	TGACAATACGTAAA		
FCGR1B_NM_001244910.1	(998)	AGTCTCTTCAGGAAAAGC	CCACAAGCAGGCC	TTTGCATCCTTGAT		
FCGR1B_NM_001017986.3	(671)	AATGTTTTT	AGTGAACACTGTTCTCTGGG--	TGACAATACGTAAA		
FCGR1B_NM_001004340.3	(395)	AATGTTTTT	AGTGAACACTGTTCTCTGGG--	TGACAATACGTAAA		
FCGR1B_XM_017000662.1	(416)	AATGTTTTT	AGTGAACACTGTTCTCTGGG--	TGACAATACGTAAA		
FCGR1B_XM_017000661.1	(674)	AATGTTTTT	AGTGAACACTGTTCTCTGGG--	TGACAATACGTAAA		
FCGR1B_XR_001737041.1	(1022)	AATGTTTTT	AGTGAACACTGTTCTCTGGG--	TGACAATACGTAAA		
FCGR1B_XR_001737040.1	(959)	AATGTTTTT	AGTGAACACTGTTCTCTGGG--	TGACAATACGTAAA		
FCGR1B_NR_045213.1	(956)	AATGTTTTT	AGTGAACACTGTTCTCTGGG--	TGACAATACGTAAA		
FCGR1CP_NR_027484.2	(955)	AATGTTTTT	AGTGAACACTGTTCTCTGGG--	TGACAATACGTAAA		
Consensus	(1036)	AATGTTTTTAGTGAACACTGTTCTCTGGG				

		Section 25				
	(1081)	1081	1090	1100	1110	1125
FCGR1A_NM_000566.3	(996)	GA	ACTG	AAAG	AAAAAGTGG	--GATTTAGAAATCTC-TTTG
FCGR1A_XM_005244957.3	(999)	GA	ACTG	AAAG	AAAAAGTGG	--GATTTAGAAATCTC-TTTG
FCGR1A_XM_005244958.4	(737)	GA	ACTG	AAAG	AAAAAGTGG	--GATTTAGAAATCTC-TTTG
FCGR1B_NM_001244910.1	(1043)	TC	ACA-AC	ATCACT	CTTCTCCTCGCA	AACTGTTAAATTTCTTTTC
FCGR1B_NM_001017986.3	(714)	GA	ACTG	AAAG	AAAAAGTGG	--AATTTAGAAATCTC-TTTG
FCGR1B_NM_001004340.3	(438)	GA	ACTG	AAAG	AAAAAGTGG	--AATTTAGAAATCTC-TTTG
FCGR1B_XM_017000662.1	(459)	GA	ACTG	AAAG	AAAAAGTGG	--AATTTAGAAATCTC-TTTG
FCGR1B_XM_017000661.1	(717)	GA	ACTG	AAAG	AAAAAGTGG	--AATTTAGAAATCTC-TTTG
FCGR1B_XR_001737041.1	(1065)	GA	ACTG	AAAG	AAAAAGTGG	--AATTTAGAAATCTC-TTTG
FCGR1B_XR_001737040.1	(1002)	GA	ACTG	AAAG	AAAAAGTGG	--AATTTAGAAATCTC-TTTG
FCGR1B_NR_045213.1	(999)	GA	ACTG	AAAG	AAAAAGTGG	--AATTTAGAAATCTC-TTTG
FCGR1CP_NR_027484.2	(998)	GA	ACTG	AAAG	AAAAAGTGG	--AATTTAGAAATCTC-TTTG
Consensus	(1081)	GA				
		Section 26				
	(1126)	1126	1140	1150	1160	1170
FCGR1A_NM_000566.3	(1038)	G	ATTC	TGGT	CATG	AGAAGAAGGTAATTTCCAGCCTTCAAGAAGAC
FCGR1A_XM_005244957.3	(1041)	G	ATTC	TGGT	CATG	AGAAGAAGGTAATTTCCAGCCTTCAAGAAGAC
FCGR1A_XM_005244958.4	(779)	G	ATTC	TGGT	CATG	AGAAGAAGGTAATTTCCAGCCTTCAAGAAGAC
FCGR1B_NM_001244910.1	(1087)	C	T	TTC	T	TTTTCCTTCC-TTTCCCTTCTCTATTTCTTT
FCGR1B_NM_001017986.3	(756)	G	ATTC	TGGT	CATG	AGAAGAAGGTAATTTCCAGCCTTCAAGAAGAC
FCGR1B_NM_001004340.3	(480)	G	ATTC	TGGT	CATG	AGAAGAAGGTAATTTCCAGCCTTCAAGAAGAC
FCGR1B_XM_017000662.1	(501)	G	ATTC	TGGT	CATG	AGAAGAAGGTAATTTCCAGCCTTCAAGAAGAC
FCGR1B_XM_017000661.1	(759)	G	ATTC	TGGT	CATG	AGAAGAAGGTAATTTCCAGCCTTCAAGAAGAC
FCGR1B_XR_001737041.1	(1107)	G	ATTC	TGGT	CATG	AGAAGAAGGTAATTTCCAGCCTTCAAGAAGAC
FCGR1B_XR_001737040.1	(1044)	G	ATTC	TGGT	CATG	AGAAGAAGGTAATTTCCAGCCTTCAAGAAGAC
FCGR1B_NR_045213.1	(1041)	G	ATTC	TGGT	CATG	AGAAGAAGGTAATTTCCAGCCTTCAAGAAGAC
FCGR1CP_NR_027484.2	(1040)	G	ATTC	TGGT	CATG	AGAAGAAGGTAATTTCCAGCCTTCAAGAAGAC
Consensus	(1126)	G				
		Section 27				
	(1171)	1171	1180	1190	1200	1215
FCGR1A_NM_000566.3	(1083)	AG	ACAT	T	TAGA	AGAAGAGCTGAAATGTCAGGAACAAAAAGAAGAA
FCGR1A_XM_005244957.3	(1086)	AG	ACAT	T	TAGA	AGAAGAGCTGAAATGTCAGGAACAAAAAGAAGAA
FCGR1A_XM_005244958.4	(824)	AG	ACAT	T	TAGA	AGAAGAGCTGAAATGTCAGGAACAAAAAGAAGAA
FCGR1B_NM_001244910.1	(1131)	C	C	T	T	C
FCGR1B_NM_001017986.3	(801)	AG	ACAT	T	TAGA	AGAAGAGCTGAAATGTCAGGAACAAAAAGAAGAA
FCGR1B_NM_001004340.3	(525)	AG	ACAT	T	TAGA	AGAAGAGCTGAAATGTCAGGAACAAAAAGAAGAA
FCGR1B_XM_017000662.1	(546)	AG	ACAT	T	TAGA	AGAAGAGCTGAAATGTCAGGAACAAAAAGAAGAA
FCGR1B_XM_017000661.1	(804)	AG	ACAT	T	TAGA	AGAAGAGCTGAAATGTCAGGAACAAAAAGAAGAA
FCGR1B_XR_001737041.1	(1152)	AG	ACAT	T	TAGA	AGAAGAGCTGAAATGTCAGGAACAAAAAGAAGAA
FCGR1B_XR_001737040.1	(1089)	AG	ACAT	T	TAGA	AGAAGAGCTGAAATGTCAGGAACAAAAAGAAGAA
FCGR1B_NR_045213.1	(1086)	AG	ACAT	T	TAGA	AGAAGAGCTGAAATGTCAGGAACAAAAAGAAGAA
FCGR1CP_NR_027484.2	(1085)	AG	ACAT	T	TAGA	AGAAGAGCTGAAATGTCAGGAACAAAAAGAAGAA
Consensus	(1171)	AG				

		Section 28				
		(1216)	1216	1230	1240	1250 1260
FCGR1A_NM_000566.3	(1128)		CAGCTGCAGGAAGGGGTGCACCGGAAGGAGCCCCAGGGGGCCACG			
FCGR1A_XM_005244957.3	(1131)		CAGCTGCAGGAAGGGGTGCACCGGAAGGAGCCCCAGGGGGCCACG			
FCGR1A_XM_005244958.4	(869)		CAGCTGCAGGAAGGGGTGCACCGGAAGGAGCCCCAGGGGGCCACG			
FCGR1B_NM_001244910.1	(1176)		CTTCTCCTTCATTTTATTTTCCCTCCCTCCAGTCTTCCCTCCA			
FCGR1B_NM_001017986.3	(846)		CAGCTGCAGGAAGGGGTGCACCGGAAGGAGCCCCAGGGGGCCACG			
FCGR1B_NM_001004340.3	(570)		CAGCTGCAGGAAGGGGTGCACCGGAAGGAGCCCCAGGGGGCCACG			
FCGR1B_XM_017000662.1	(591)		CAGCTGCAGGAAGGGGTGCACCGGAAGGAGCCCCAGGGGGCCACG			
FCGR1B_XM_017000661.1	(849)		CAGCTGCAGGAAGGGGTGCACCGGAAGGAGCCCCAGGGGGCCACG			
FCGR1B_XR_001737041.1	(1197)		CAGCTGCAGGAAGGGGTGCACCGGAAGGAGCCCCAGGGGGCCACG			
FCGR1B_XR_001737040.1	(1134)		CAGCTGCAGGAAGGGGTGCACCGGAAGGAGCCCCAGGGGGCCACG			
FCGR1B_NR_045213.1	(1131)		CAGCTGCAGGAAGGGGTGCACCGGAAGGAGCCCCAGGGGGCCACG			
FCGR1CP_NR_027484.2	(1130)		CAGCTGCAGGAAGGGGTGCACCGGAAGGAGCCCCAGGGGGCCACG			
Consensus (1216)			CAGCTGCAGGAAGGGGTGCACCGGAAGGAGCCCCAGGGGGCCACG			
		Section 29				
		(1261)	1261	1270	1280	1290 1305
FCGR1A_NM_000566.3	(1173)		TAGCAG--CGGCTCAGTTGGTGGCCATCGATCTGGACCGTCCCT			
FCGR1A_XM_005244957.3	(1176)		TAGCAG--CGGCTCAGTTGGTGGCCATCGATCTGGACCGTCCCT			
FCGR1A_XM_005244958.4	(914)		TAGCAG--CGGCTCAGTTGGTGGCCATCGATCTGGACCGTCCCT			
FCGR1B_NM_001244910.1	(1221)		CTCCATGACCCCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT			
FCGR1B_NM_001017986.3	(891)		TAGCAG--CGGCTCAGTTGGTGGCCATCGATCTGGACCGTCCCT			
FCGR1B_NM_001004340.3	(615)		TAGCAG--CGGCTCAGTTGGTGGCCATCGATCTGGACCGTCCCT			
FCGR1B_XM_017000662.1	(636)		TAGCAG--CGGCTCAGTTGGTGGCCATCGATCTGGACCGTCCCT			
FCGR1B_XM_017000661.1	(894)		TAGCAG--CGGCTCAGTTGGTGGCCATCGATCTGGACCGTCCCT			
FCGR1B_XR_001737041.1	(1242)		TAGCAG--CGGCTCAGTTGGTGGCCATCGATCTGGACCGTCCCT			
FCGR1B_XR_001737040.1	(1179)		TAGCAG--CGGCTCAGTTGGTGGCCATCGATCTGGACCGTCCCT			
FCGR1B_NR_045213.1	(1176)		TAGCAG--CGGCTCAGTTGGTGGCCATCGATCTGGACCGTCCCT			
FCGR1CP_NR_027484.2	(1175)		TAGCAG--CGGCTCAGTTGGTGGCCATCGATCTGGACCGTCCCT			
Consensus (1261)			TAGCAG--CGGCTCAGTTGGTGGCCATCGATCTGGACCGTCCCT			
		Section 30				
		(1306)	1306	1320	1330	1340 1350
FCGR1A_NM_000566.3	(1216)		GCCCACTTGCTCCCGGTGAGCACTGCGTACAAACATCCAA--AAGT			
FCGR1A_XM_005244957.3	(1219)		GCCCACTTGCTCCCGGTGAGCACTGCGTACAAACATCCAA--AAGT			
FCGR1A_XM_005244958.4	(957)		GCCCACTTGCTCCCGGTGAGCACTGCGTACAAACATCCAA--AAGT			
FCGR1B_NM_001244910.1	(1266)		GCCTCCCTCCTCCTCCTGACCAACAATCTCACCACAATTTATCAAGT			
FCGR1B_NM_001017986.3	(934)		GCCCACTTGCTCCCGGTGAGCACTGCGTACAAACATCCAA--AAGT			
FCGR1B_NM_001004340.3	(658)		GCCCACTTGCTCCCGGTGAGCACTGCGTACAAACATCCAA--AAGT			
FCGR1B_XM_017000662.1	(679)		GCCCACTTGCTCCCGGTGAGCACTGCGTACAAACATCCAA--AAGT			
FCGR1B_XM_017000661.1	(937)		GCCCACTTGCTCCCGGTGAGCACTGCGTACAAACATCCAA--AAGT			
FCGR1B_XR_001737041.1	(1285)		GCCCACTTGCTCCCGGTGAGCACTGCGTACAAACATCCAA--AAGT			
FCGR1B_XR_001737040.1	(1222)		GCCCACTTGCTCCCGGTGAGCACTGCGTACAAACATCCAA--AAGT			
FCGR1B_NR_045213.1	(1219)		GCCCACTTGCTCCCGGTGAGCACTGCGTACAAACATCCAA--AAGT			
FCGR1CP_NR_027484.2	(1218)		GTCCACTTGCTCCCGGTGAGCACTGCGTACAAACATCCAA--AAGT			
Consensus (1306)			GCCCACTTGCTCCCGGTGAGCACTGCGTACAAACATCCAA--AAGT			

		Section 31				
	(1351)	1351	1360	1370	1380	1395
FCGR1A_NM_000566.3 (1260)		TCAAC	AACAC	CAGAACTGTGTGTCTCATGGTATGTA	ACTCTTAAA	
FCGR1A_XM_005244957.3 (1263)		TCAAC	AACAC	CAGAACTGTGTGTCTCATGGTATGTA	ACTCTTAAA	
FCGR1A_XM_005244958.4 (1001)		TCAAC	AACAC	CAGAACTGTGTGTCTCATGGTATGTA	ACTCTTAAA	
FCGR1B_NM_001244910.1 (1311)		TCTT	CTATCTGTTGTCA	TACSTCTGGG	ATATAGACATTGA	
FCGR1B_NM_001017986.3 (978)		TCAAC	AACAC	CAGAACTGTGTGTCTCATGGTATATA	ACTCTTAAA	
FCGR1B_NM_001004340.3 (702)		TCAAC	AACAC	CAGAACTGTGTGTCTCATGGTATATA	ACTCTTAAA	
FCGR1B_XM_017000662.1 (723)		TCAAC	AACAC	CAGAACTGTGTGTCTCATGGTATATA	ACTCTTAAA	
FCGR1B_XM_017000661.1 (981)		TCAAC	AACAC	CAGAACTGTGTGTCTCATGGTATATA	ACTCTTAAA	
FCGR1B_XR_001737041.1 (1329)		TCAAC	AACAC	CAGAACTGTGTGTCTCATGGTATATA	ACTCTTAAA	
FCGR1B_XR_001737040.1 (1266)		TCAAC	AACAC	CAGAACTGTGTGTCTCATGGTATATA	ACTCTTAAA	
FCGR1B_NR_045213.1 (1263)		TCAAC	AACAC	CAGAACTGTGTGTCTCATGGTATATA	ACTCTTAAA	
FCGR1CP_NR_027484.2 (1262)		TCAAC	AACAC	CAGAACTGTGTGTCTCATGGTATATA	ACTCTTAAAG	
Consensus (1351)		TCAAC	AACAC	CAGAACTGTGTGTCTCATGGTATATA	ACTCTTAAA	
		Section 32				
	(1396)	1396	1410	1420	1430	1440
FCGR1A_NM_000566.3 (1305)		GCAAA	----	TAAATGA	ACTGACTTCAACTGGGATACATTTGGAAA	
FCGR1A_XM_005244957.3 (1308)		GCAAA	----	TAAATGA	ACTGACTTCAACTGGGA	-----
FCGR1A_XM_005244958.4 (1046)		GCAAA	----	TAAATGA	ACTGACTTCAACTGGGA	-----
FCGR1B_NM_001244910.1 (1356)		GTATA	GTTC	TGCTCAAG	GAGCTCA	CAAGGTGGATTATCAGATC
FCGR1B_NM_001017986.3 (1023)		GCAAA	----	TAAATGA	ACTGACTTCAACTGGGATACATTTGGAAA	
FCGR1B_NM_001004340.3 (747)		GCAAA	----	TAAATGA	ACTGACTTCAACTGGGATACATTTGGAAA	
FCGR1B_XM_017000662.1 (768)		GCAAA	----	TAAATGA	ACTGACTTCAACTGGGATACATTTGGAAA	
FCGR1B_XM_017000661.1 (1026)		GCAAA	----	TAAATGA	ACTGACTTCAACTGGGATACATTTGGAAA	
FCGR1B_XR_001737041.1 (1374)		GCAAA	----	TAAATGA	ACTGACTTCAACTGGGATACATTTGGAAA	
FCGR1B_XR_001737040.1 (1311)		GCAAA	----	TAAATGA	ACTGACTTCAACTGGGATACATTTGGAAA	
FCGR1B_NR_045213.1 (1308)		GCAAA	----	TAAATGA	ACTGACTTCAACTGGGATACATTTGGAAA	
FCGR1CP_NR_027484.2 (1307)		GCAAA	----	TAAATGA	ACTGACTTCAACTGGGA	AAAAAAAAAA
Consensus (1396)		GCAAA		TAAATGA	ACTGACTTCAACTGGGATACATTTGGAAA	
		Section 33				
	(1441)	1441	1450	1460	1470	1485
FCGR1A_NM_000566.3 (1346)		TGTGGTCATCAAAGATGACTTGAAATGAGGCCTACTCTAAAGAAT				
FCGR1A_XM_005244957.3 (1337)		-----				
FCGR1A_XM_005244958.4 (1075)		-----				
FCGR1B_NM_001244910.1 (1401)		AGTGA	TTTGTAA	----	ACTGC	AAATCCCACTCCCAAGTATC
FCGR1B_NM_001017986.3 (1064)		TGTGGTCATCAAAGATGACTTGAAATGAGGCCTACTCTAAAGAAT				
FCGR1B_NM_001004340.3 (788)		TGTGGTCATCAAAGATGACTTGAAATGAGGCCTACTCTAAAGAAT				
FCGR1B_XM_017000662.1 (809)		TGTGGTCATCAAAGATGACTTGAAATGAGGCCTACTCTAAAGAAT				
FCGR1B_XM_017000661.1 (1067)		TGTGGTCATCAAAGATGACTTGAAATGAGGCCTACTCTAAAGAAT				
FCGR1B_XR_001737041.1 (1415)		TGTGGTCATCAAAGATGACTTGAAATGAGGCCTACTCTAAAGAAT				
FCGR1B_XR_001737040.1 (1352)		TGTGGTCATCAAAGATGACTTGAAATGAGGCCTACTCTAAAGAAT				
FCGR1B_NR_045213.1 (1349)		TGTGGTCATCAAAGATGACTTGAAATGAGGCCTACTCTAAAGAAT				
FCGR1CP_NR_027484.2 (1348)		AAAAA	-----			
Consensus (1441)		TGTGGTCATCAAAGATGACTTGAAATGAGGCCTACTCTAAAGAAT				

		Section 34				
		(1486)	1486	1500	1510	1520 1530
FCGR1A_NM_000566.3	(1391)	TCT	--	TGAAAAA	CTTACAAGTCAAGCCTAGCCTGATAATCCTAT	--
FCGR1A_XM_005244957.3	(1337)	-----	-----	-----	-----	-----
FCGR1A_XM_005244958.4	(1075)	-----	-----	-----	-----	-----
FCGR1B_NM_001017986.3	(1109)	TCT	GT	TAA	CTGAGGCAGAGGG	ATTGTGAGCTCTAGAA
FCGR1B_NM_001004340.3	(833)	TCT	--	TGAAAAA	CTTACAAGTCAAGCCTAGCCTGATAATCCTAT	--
FCGR1B_XM_017000662.1	(854)	TCT	--	TGAAAAA	CTTACAAGTCAAGCCTAGCCTGATAATCCTAT	--
FCGR1B_XM_017000661.1	(1112)	TCT	--	TGAAAAA	CTTACAAGTCAAGCCTAGCCTGATAATCCTAT	--
FCGR1B_XR_001737041.1	(1460)	TCT	--	TGAAAAA	CTTACAAGTCAAGCCTAGCCTGATAATCCTAT	--
FCGR1B_XR_001737040.1	(1397)	TCT	--	TGAAAAA	CTTACAAGTCAAGCCTAGCCTGATAATCCTAT	--
FCGR1B_NR_045213.1	(1394)	TCT	--	TGAAAAA	CTTACAAGTCAAGCCTAGCCTGATAATCCTAT	--
FCGR1CP_NR_027484.2	(1353)	-----	-----	-----	-----	-----
Consensus (1486)		TCT		TGAAAAA	CTTACAAGTCAAGCCTAGCCTGATAATCCTAT	
		Section 35				
		(1531)	1531	1540	1550	1560 1575
FCGR1A_NM_000566.3	(1433)	TACATAGTTT	TGAAAAA	TAGTATTTTATTTCTCAGAACAAGGTAAA		
FCGR1A_XM_005244957.3	(1337)	-----	-----	-----	-----	-----
FCGR1A_XM_005244958.4	(1075)	-----	-----	-----	-----	-----
FCGR1B_NM_001244910.1	(1487)	TCT	TTGGGGG	GAAGT	TCA	TCTCAACCAATTCAT
FCGR1B_NM_001017986.3	(1151)	TACATAGTTT	TGAAAAA	TAGTATTTTATTTCTCAGAACAAGGTAAA		
FCGR1B_NM_001004340.3	(875)	TACATAGTTT	TGAAAAA	TAGTATTTTATTTCTCAGAACAAGGTAAA		
FCGR1B_XM_017000662.1	(896)	TACATAGTTT	TGAAAAA	TAGTATTTTATTTCTCAGAACAAGGTAAA		
FCGR1B_XM_017000661.1	(1154)	TACATAGTTT	TGAAAAA	TAGTATTTTATTTCTCAGAACAAGGTAAA		
FCGR1B_XR_001737041.1	(1502)	TACATAGTTT	TGAAAAA	TAGTATTTTATTTCTCAGAACAAGGTAAA		
FCGR1B_XR_001737040.1	(1439)	TACATAGTTT	TGAAAAA	TAGTATTTTATTTCTCAGAACAAGGTAAA		
FCGR1B_NR_045213.1	(1436)	TACATAGTTT	TGAAAAA	TAGTATTTTATTTCTCAGAACAAGGTAAA		
FCGR1CP_NR_027484.2	(1353)	-----	-----	-----	-----	-----
Consensus (1531)		TACATAGTTT	TGAAAAA	TAGTATTTTATTTCTCAGAACAAGGTAAA		
		Section 36				
		(1576)	1576	1590	1600	1610 1620
FCGR1A_NM_000566.3	(1478)	AAGGTGAGTGGGTGCATATGTA	--	CAGAAGATTAAGACAGAGAAAC		
FCGR1A_XM_005244957.3	(1337)	-----	-----	-----	-----	-----
FCGR1A_XM_005244958.4	(1075)	-----	-----	-----	-----	-----
FCGR1B_NM_001244910.1	(1532)	AGTA	TTAATGG	CACAG	AGATATCAGTTCTCTCT	-----GAACT
FCGR1B_NM_001017986.3	(1196)	AAGGTGAGTGGGTGCATATGTA	--	CAGAAGATTAAGACAGAGAAAC		
FCGR1B_NM_001004340.3	(920)	AAGGTGAGTGGGTGCATATGTA	--	CAGAAGATTAAGACAGAGAAAC		
FCGR1B_XM_017000662.1	(941)	AAGGTGAGTGGGTGCATATGTA	--	CAGAAGATTAAGACAGAGAAAC		
FCGR1B_XM_017000661.1	(1199)	AAGGTGAGTGGGTGCATATGTA	--	CAGAAGATTAAGACAGAGAAAC		
FCGR1B_XR_001737041.1	(1547)	AAGGTGAGTGGGTGCATATGTA	--	CAGAAGATTAAGACAGAGAAAC		
FCGR1B_XR_001737040.1	(1484)	AAGGTGAGTGGGTGCATATGTA	--	CAGAAGATTAAGACAGAGAAAC		
FCGR1B_NR_045213.1	(1481)	AAGGTGAGTGGGTGCATATGTA	--	CAGAAGATTAAGACAGAGAAAC		
FCGR1CP_NR_027484.2	(1353)	-----	-----	-----	-----	-----
Consensus (1576)		AAGGTGAGTGGGTGCATATGTA		CAGAAGATTAAGACAGAGAAAC		

		Section 37				
		(1621)	1621	1630	1640	1650 1665
FCGR1A_NM_000566.3	(1522)		AGACAGAAAGAGACACACACACAGCCAGGAGTGGGTAGATTTCAG			
FCGR1A_XM_005244957.3	(1337)		-----			
FCGR1A_XM_005244958.4	(1075)		-----			
FCGR1B_NM_001244910.1	(1572)		AGGGAGTAAG-----			
FCGR1B_NM_001017986.3	(1240)		AGACAGAAAGAGACACACACACAGCCAGGAGTGGGTAGATTTCAG			
FCGR1B_NM_001004340.3	(964)		AGACAGAAAGAGACACACACACAGCCAGGAGTGGGTAGATTTCAG			
FCGR1B_XM_017000662.1	(985)		AGACAGAAAGAGACACACACACAGCCAGGAGTGGGTAGATTTCAG			
FCGR1B_XM_017000661.1	(1243)		AGACAGAAAGAGACACACACACAGCCAGGAGTGGGTAGATTTCAG			
FCGR1B_XR_001737041.1	(1591)		AGACAGAAAGAGACACACACACAGCCAGGAGTGGGTAGATTTCAG			
FCGR1B_XR_001737040.1	(1528)		AGACAGAAAGAGACACACACACAGCCAGGAGTGGGTAGATTTCAG			
FCGR1B_NR_045213.1	(1525)		AGACAGAAAGAGACACACACACAGCCAGGAGTGGGTAGATTTCAG			
FCGR1CP_NR_027484.2	(1353)		-----			
Consensus (1621)			AGACAGAAAGAGACACACACACAGCCAGGAGTGGGTAGATTTCAG			
		Section 38				
		(1666)	1666	1680	1690	1700 1710
FCGR1A_NM_000566.3	(1567)		GGAGACAAGAGGGAATAGTATAGACAATAAGGAAGGAAATAGTAC			
FCGR1A_XM_005244957.3	(1337)		-----			
FCGR1A_XM_005244958.4	(1075)		-----			
FCGR1B_NM_001244910.1	(1582)		-----			
FCGR1B_NM_001017986.3	(1285)		GGAGACAAGAGGGAATAGTATAGACAATAAGGAAGGAAATAGTAC			
FCGR1B_NM_001004340.3	(1009)		GGAGACAAGAGGGAATAGTATAGACAATAAGGAAGGAAATAGTAC			
FCGR1B_XM_017000662.1	(1030)		GGAGACAAGAGGGAATAGTATAGACAATAAGGAAGGAAATAGTAC			
FCGR1B_XM_017000661.1	(1288)		GGAGACAAGAGGGAATAGTATAGACAATAAGGAAGGAAATAGTAC			
FCGR1B_XR_001737041.1	(1636)		GGAGACAAGAGGGAATAGTATAGACAATAAGGAAGGAAATAGTAC			
FCGR1B_XR_001737040.1	(1573)		GGAGACAAGAGGGAATAGTATAGACAATAAGGAAGGAAATAGTAC			
FCGR1B_NR_045213.1	(1570)		GGAGACAAGAGGGAATAGTATAGACAATAAGGAAGGAAATAGTAC			
FCGR1CP_NR_027484.2	(1353)		-----			
Consensus (1666)			GGAGACAAGAGGGAATAGTATAGACAATAAGGAAGGAAATAGTAC			
		Section 39				
		(1711)	1711	1720	1730	1740 1755
FCGR1A_NM_000566.3	(1612)		TTACAAATGACTCCTAAGGGACTGTGAGACTGAGAGGGCTCACGC			
FCGR1A_XM_005244957.3	(1337)		-----			
FCGR1A_XM_005244958.4	(1075)		-----			
FCGR1B_NM_001244910.1	(1582)		-----			
FCGR1B_NM_001017986.3	(1330)		TTACAAATGACTCCTAAGGGACTGTGAGACTGAGAGGGCTCACGC			
FCGR1B_NM_001004340.3	(1054)		TTACAAATGACTCCTAAGGGACTGTGAGACTGAGAGGGCTCACGC			
FCGR1B_XM_017000662.1	(1075)		TTACAAATGACTCCTAAGGGACTGTGAGACTGAGAGGGCTCACGC			
FCGR1B_XM_017000661.1	(1333)		TTACAAATGACTCCTAAGGGACTGTGAGACTGAGAGGGCTCACGC			
FCGR1B_XR_001737041.1	(1681)		TTACAAATGACTCCTAAGGGACTGTGAGACTGAGAGGGCTCACGC			
FCGR1B_XR_001737040.1	(1618)		TTACAAATGACTCCTAAGGGACTGTGAGACTGAGAGGGCTCACGC			
FCGR1B_NR_045213.1	(1615)		TTACAAATGACTCCTAAGGGACTGTGAGACTGAGAGGGCTCACGC			
FCGR1CP_NR_027484.2	(1353)		-----			
Consensus (1711)			TTACAAATGACTCCTAAGGGACTGTGAGACTGAGAGGGCTCACGC			

Section 40					
	(1756)	1756	1770	1780	1790 1800
FCGR1A_NM_000566.3 (1657)		CTCTGTGTTTCAGGATACTTAGTTCATGGCTTTTCTCTTTGACTTT			
FCGR1A_XM_005244957.3 (1337)		-----			
FCGR1A_XM_005244958.4 (1075)		-----			
FCGR1B_NM_001244910.1 (1582)		-----			
FCGR1B_NM_001017986.3 (1375)		CTCTGTGTTTCAGGATACTTAGTTCATGGCTTTTCTCTTTGACTTT			
FCGR1B_NM_001004340.3 (1099)		CTCTGTGTTTCAGGATACTTAGTTCATGGCTTTTCTCTTTGACTTT			
FCGR1B_XM_017000662.1 (1120)		CTCTGTGTTTCAGGATACTTAGTTCATGGCTTTTCTCTTTGACTTT			
FCGR1B_XM_017000661.1 (1378)		CTCTGTGTTTCAGGATACTTAGTTCATGGCTTTTCTCTTTGACTTT			
FCGR1B_XR_001737041.1 (1726)		CTCTGTGTTTCAGGATACTTAGTTCATGGCTTTTCTCTTTGACTTT			
FCGR1B_XR_001737040.1 (1663)		CTCTGTGTTTCAGGATACTTAGTTCATGGCTTTTCTCTTTGACTTT			
FCGR1B_NR_045213.1 (1660)		CTCTGTGTTTCAGGATACTTAGTTCATGGCTTTTCTCTTTGACTTT			
FCGR1CP_NR_027484.2 (1353)		-----			
Consensus (1756)		CTCTGTGTTTCAGGATACTTAGTTCATGGCTTTTCTCTTTGACTTT			
Section 41					
	(1801)	1801	1810	1820	1830 1845
FCGR1A_NM_000566.3 (1702)		ACTAAAAGAGAATGTCTCCATACGCGTTCTAGGCATACAAGGGGG			
FCGR1A_XM_005244957.3 (1337)		-----			
FCGR1A_XM_005244958.4 (1075)		-----			
FCGR1B_NM_001244910.1 (1582)		-----			
FCGR1B_NM_001017986.3 (1420)		ACTAAAAGAGAATGTCTCCATACGCGTTCTAGGCATACAAGGGGG			
FCGR1B_NM_001004340.3 (1144)		ACTAAAAGAGAATGTCTCCATACGCGTTCTAGGCATACAAGGGGG			
FCGR1B_XM_017000662.1 (1165)		ACTAAAAGAGAATGTCTCCATACGCGTTCTAGGCATACAAGGGGG			
FCGR1B_XM_017000661.1 (1423)		ACTAAAAGAGAATGTCTCCATACGCGTTCTAGGCATACAAGGGGG			
FCGR1B_XR_001737041.1 (1771)		ACTAAAAGAGAATGTCTCCATACGCGTTCTAGGCATACAAGGGGG			
FCGR1B_XR_001737040.1 (1708)		ACTAAAAGAGAATGTCTCCATACGCGTTCTAGGCATACAAGGGGG			
FCGR1B_NR_045213.1 (1705)		ACTAAAAGAGAATGTCTCCATACGCGTTCTAGGCATACAAGGGGG			
FCGR1CP_NR_027484.2 (1353)		-----			
Consensus (1801)		ACTAAAAGAGAATGTCTCCATACGCGTTCTAGGCATACAAGGGGG			
Section 42					
	(1846)	1846	1860	1870	1880 1890
FCGR1A_NM_000566.3 (1747)		TAACTCATGATGAGAAATGGATGTGTTATTCTTGCCCTCTCTTTT			
FCGR1A_XM_005244957.3 (1337)		-----			
FCGR1A_XM_005244958.4 (1075)		-----			
FCGR1B_NM_001244910.1 (1582)		-----			
FCGR1B_NM_001017986.3 (1465)		TAACTCATGATGAGAAATGGATGTGTTATTCTTGCCCTCTCTTTT			
FCGR1B_NM_001004340.3 (1189)		TAACTCATGATGAGAAATGGATGTGTTATTCTTGCCCTCTCTTTT			
FCGR1B_XM_017000662.1 (1210)		TAACTCATGATGAGAAATGGATGTGTTATTCTTGCCCTCTCTTTT			
FCGR1B_XM_017000661.1 (1468)		TAACTCATGATGAGAAATGGATGTGTTATTCTTGCCCTCTCTTTT			
FCGR1B_XR_001737041.1 (1816)		TAACTCATGATGAGAAATGGATGTGTTATTCTTGCCCTCTCTTTT			
FCGR1B_XR_001737040.1 (1753)		TAACTCATGATGAGAAATGGATGTGTTATTCTTGCCCTCTCTTTT			
FCGR1B_NR_045213.1 (1750)		TAACTCATGATGAGAAATGGATGTGTTATTCTTGCCCTCTCTTTT			
FCGR1CP_NR_027484.2 (1353)		-----			
Consensus (1846)		TAACTCATGATGAGAAATGGATGTGTTATTCTTGCCCTCTCTTTT			

		Section 43				
	(1891)	1891	1900	1910	1920	1935
FCGR1A_NM_000566.3 (1792)		GAGGCTCTCTCATAACCCCTCTATTTCTAGAGACAACAAAAATGC				
FCGR1A_XM_005244957.3 (1337)		-----				
FCGR1A_XM_005244958.4 (1075)		-----				
FCGR1B_NM_001244910.1 (1582)		-----				
FCGR1B_NM_001017986.3 (1510)		GAGGCTCTCTCATAACCCCTCTATTTCTAGAGACAACAAAAATGT				
FCGR1B_NM_001004340.3 (1234)		GAGGCTCTCTCATAACCCCTCTATTTCTAGAGACAACAAAAATGT				
FCGR1B_XM_017000662.1 (1255)		GAGGCTCTCTCATAACCCCTCTATTTCTAGAGACAACAAAAATGT				
FCGR1B_XM_017000661.1 (1513)		GAGGCTCTCTCATAACCCCTCTATTTCTAGAGACAACAAAAATGT				
FCGR1B_XR_001737041.1 (1861)		GAGGCTCTCTCATAACCCCTCTATTTCTAGAGACAACAAAAATGT				
FCGR1B_XR_001737040.1 (1798)		GAGGCTCTCTCATAACCCCTCTATTTCTAGAGACAACAAAAATGT				
FCGR1B_NR_045213.1 (1795)		GAGGCTCTCTCATAACCCCTCTATTTCTAGAGACAACAAAAATGT				
FCGR1CP_NR_027484.2 (1353)		-----				
Consensus (1891)		GAGGCTCTCTCATAACCCCTCTATTTCTAGAGACAACAAAAATGT				
		Section 44				
	(1936)	1936	1950	1960	1970	1980
FCGR1A_NM_000566.3 (1837)		TGCCAGTCCTAGGCCCTGCCCTGTAGGAAGGCAGAATGTAACTG				
FCGR1A_XM_005244957.3 (1337)		-----				
FCGR1A_XM_005244958.4 (1075)		-----				
FCGR1B_NM_001244910.1 (1582)		-----				
FCGR1B_NM_001017986.3 (1555)		TGCCAGTCCTAGGCCCTGCCCTGTAGGAAGGCAGAATGTAACTG				
FCGR1B_NM_001004340.3 (1279)		TGCCAGTCCTAGGCCCTGCCCTGTAGGAAGGCAGAATGTAACTG				
FCGR1B_XM_017000662.1 (1300)		TGCCAGTCCTAGGCCCTGCCCTGTAGGAAGGCAGAATGTAACTG				
FCGR1B_XM_017000661.1 (1558)		TGCCAGTCCTAGGCCCTGCCCTGTAGGAAGGCAGAATGTAACTG				
FCGR1B_XR_001737041.1 (1906)		TGCCAGTCCTAGGCCCTGCCCTGTAGGAAGGCAGAATGTAACTG				
FCGR1B_XR_001737040.1 (1843)		TGCCAGTCCTAGGCCCTGCCCTGTAGGAAGGCAGAATGTAACTG				
FCGR1B_NR_045213.1 (1840)		TGCCAGTCCTAGGCCCTGCCCTGTAGGAAGGCAGAATGTAACTG				
FCGR1CP_NR_027484.2 (1353)		-----				
Consensus (1936)		TGCCAGTCCTAGGCCCTGCCCTGTAGGAAGGCAGAATGTAACTG				
		Section 45				
	(1981)	1981	1990	2000	2010	2025
FCGR1A_NM_000566.3 (1882)		TTCTGTTTGTGTTTAACGATTAAGTCCAAATCTCCAAGTGCGGCACT				
FCGR1A_XM_005244957.3 (1337)		-----				
FCGR1A_XM_005244958.4 (1075)		-----				
FCGR1B_NM_001244910.1 (1582)		-----				
FCGR1B_NM_001017986.3 (1600)		TTCTTTTGTGTTTAACGATTAAGTCCAAATCTCCAAGTGCGGCACT				
FCGR1B_NM_001004340.3 (1324)		TTCTTTTGTGTTTAACGATTAAGTCCAAATCTCCAAGTGCGGCACT				
FCGR1B_XM_017000662.1 (1345)		TTCTTTTGTGTTTAACGATTAAGTCCAAATCTCCAAGTGCGGCACT				
FCGR1B_XM_017000661.1 (1603)		TTCTTTTGTGTTTAACGATTAAGTCCAAATCTCCAAGTGCGGCACT				
FCGR1B_XR_001737041.1 (1951)		TTCTTTTGTGTTTAACGATTAAGTCCAAATCTCCAAGTGCGGCACT				
FCGR1B_XR_001737040.1 (1888)		TTCTTTTGTGTTTAACGATTAAGTCCAAATCTCCAAGTGCGGCACT				
FCGR1B_NR_045213.1 (1885)		TTCTTTTGTGTTTAACGATTAAGTCCAAATCTCCAAGTGCGGCACT				
FCGR1CP_NR_027484.2 (1353)		-----				
Consensus (1981)		TTCTTTTGTGTTTAACGATTAAGTCCAAATCTCCAAGTGCGGCACT				

		Section 46					
		(2026)	2026	2040	2050	2060	2070
FCGR1A_NM_000566.3	(1927)		GCAAAGAGACGCTTCAAGTGGGGAGAAGCGGCGATACCATAGAGT				
FCGR1A_XM_005244957.3	(1337)		-----				
FCGR1A_XM_005244958.4	(1075)		-----				
FCGR1B_NM_001244910.1	(1582)		-----				
FCGR1B_NM_001017986.3	(1645)		GCAAAGAGACGCTTCAAGTGGGGAGAAGCGGCGATATCATAGAGT				
FCGR1B_NM_001004340.3	(1369)		GCAAAGAGACGCTTCAAGTGGGGAGAAGCGGCGATATCATAGAGT				
FCGR1B_XM_017000662.1	(1390)		GCAAAGAGACGCTTCAAGTGGGGAGAAGCGGCGATATCATAGAGT				
FCGR1B_XM_017000661.1	(1648)		GCAAAGAGACGCTTCAAGTGGGGAGAAGCGGCGATATCATAGAGT				
FCGR1B_XR_001737041.1	(1996)		GCAAAGAGACGCTTCAAGTGGGGAGAAGCGGCGATATCATAGAGT				
FCGR1B_XR_001737040.1	(1933)		GCAAAGAGACGCTTCAAGTGGGGAGAAGCGGCGATATCATAGAGT				
FCGR1B_NR_045213.1	(1930)		GCAAAGAGACGCTTCAAGTGGGGAGAAGCGGCGATATCATAGAGT				
FCGR1CP_NR_027484.2	(1353)		-----				
Consensus (2026)			GCAAAGAGACGCTTCAAGTGGGGAGAAGCGGCGATATCATAGAGT				
		Section 47					
		(2071)	2071	2080	2090	2100	2115
FCGR1A_NM_000566.3	(1972)		CCAGATCTTGCCTCCAGAGATTTGCTTTACCTTCCTGATTTTCTG				
FCGR1A_XM_005244957.3	(1337)		-----				
FCGR1A_XM_005244958.4	(1075)		-----				
FCGR1B_NM_001244910.1	(1582)		-----				
FCGR1B_NM_001017986.3	(1690)		CCAGATCTTGCCTCCAGAGATTTGCTTTACCTTCCTGATTTTCTG				
FCGR1B_NM_001004340.3	(1414)		CCAGATCTTGCCTCCAGAGATTTGCTTTACCTTCCTGATTTTCTG				
FCGR1B_XM_017000662.1	(1435)		CCAGATCTTGCCTCCAGAGATTTGCTTTACCTTCCTGATTTTCTG				
FCGR1B_XM_017000661.1	(1693)		CCAGATCTTGCCTCCAGAGATTTGCTTTACCTTCCTGATTTTCTG				
FCGR1B_XR_001737041.1	(2041)		CCAGATCTTGCCTCCAGAGATTTGCTTTACCTTCCTGATTTTCTG				
FCGR1B_XR_001737040.1	(1978)		CCAGATCTTGCCTCCAGAGATTTGCTTTACCTTCCTGATTTTCTG				
FCGR1B_NR_045213.1	(1975)		CCAGATCTTGCCTCCAGAGATTTGCTTTACCTTCCTGATTTTCTG				
FCGR1CP_NR_027484.2	(1353)		-----				
Consensus (2071)			CCAGATCTTGCCTCCAGAGATTTGCTTTACCTTCCTGATTTTCTG				
		Section 48					
		(2116)	2116	2130	2140	2150	2160
FCGR1A_NM_000566.3	(2017)		GTTACTAATTAGCTTCAGGATACGCTGCTCTCATACTTGGGCTGT				
FCGR1A_XM_005244957.3	(1337)		-----				
FCGR1A_XM_005244958.4	(1075)		-----				
FCGR1B_NM_001244910.1	(1582)		-----				
FCGR1B_NM_001017986.3	(1735)		GTTACTAATTAGCTTCAGGATACGCTGCTCTCATACTTGGGCTGT				
FCGR1B_NM_001004340.3	(1459)		GTTACTAATTAGCTTCAGGATACGCTGCTCTCATACTTGGGCTGT				
FCGR1B_XM_017000662.1	(1480)		GTTACTAATTAGCTTCAGGATACGCTGCTCTCATACTTGGGCTGT				
FCGR1B_XM_017000661.1	(1738)		GTTACTAATTAGCTTCAGGATACGCTGCTCTCATACTTGGGCTGT				
FCGR1B_XR_001737041.1	(2086)		GTTACTAATTAGCTTCAGGATACGCTGCTCTCATACTTGGGCTGT				
FCGR1B_XR_001737040.1	(2023)		GTTACTAATTAGCTTCAGGATACGCTGCTCTCATACTTGGGCTGT				
FCGR1B_NR_045213.1	(2020)		GTTACTAATTAGCTTCAGGATACGCTGCTCTCATACTTGGGCTGT				
FCGR1CP_NR_027484.2	(1353)		-----				
Consensus (2116)			GTTACTAATTAGCTTCAGGATACGCTGCTCTCATACTTGGGCTGT				

Section 49						
	(2161)	2161	2170	2180	2190	2205
FCGR1A_NM_000566.3 (2062)		AGTTTGGAGACAAAATATTTTCCTGCCACTGTGTAACATAGCTGA				
FCGR1A_XM_005244957.3 (1337)		-----				
FCGR1A_XM_005244958.4 (1075)		-----				
FCGR1B_NM_001244910.1 (1582)		-----				
FCGR1B_NM_001017986.3 (1780)		AGTTTGGAGACAAAATATTTTCCTGCCACTGTGTAACATAGCTGA				
FCGR1B_NM_001004340.3 (1504)		AGTTTGGAGACAAAATATTTTCCTGCCACTGTGTAACATAGCTGA				
FCGR1B_XM_017000662.1 (1525)		AGTTTGGAGACAAAATATTTTCCTGCCACTGTGTAACATAGCTGA				
FCGR1B_XM_017000661.1 (1783)		AGTTTGGAGACAAAATATTTTCCTGCCACTGTGTAACATAGCTGA				
FCGR1B_XR_001737041.1 (2131)		AGTTTGGAGACAAAATATTTTCCTGCCACTGTGTAACATAGCTGA				
FCGR1B_XR_001737040.1 (2068)		AGTTTGGAGACAAAATATTTTCCTGCCACTGTGTAACATAGCTGA				
FCGR1B_NR_045213.1 (2065)		AGTTTGGAGACAAAATATTTTCCTGCCACTGTGTAACATAGCTGA				
FCGR1CP_NR_027484.2 (1353)		-----				
Consensus (2161)		AGTTTGGAGACAAAATATTTTCCTGCCACTGTGTAACATAGCTGA				
Section 50						
	(2206)	2206	2220	2230	2240	2250
FCGR1A_NM_000566.3 (2107)		GGTAAAAACTGAACATATGTAATGACTCTACTAAAAGTTTAGGGA				
FCGR1A_XM_005244957.3 (1337)		-----				
FCGR1A_XM_005244958.4 (1075)		-----				
FCGR1B_NM_001244910.1 (1582)		-----				
FCGR1B_NM_001017986.3 (1825)		GGTAAAAACTGAACATATGTAATGACTCTACTAAAAGTTTAGGGA				
FCGR1B_NM_001004340.3 (1549)		GGTAAAAACTGAACATATGTAATGACTCTACTAAAAGTTTAGGGA				
FCGR1B_XM_017000662.1 (1570)		GGTAAAAACTGAACATATGTAATGACTCTACTAAAAGTTTAGGGA				
FCGR1B_XM_017000661.1 (1828)		GGTAAAAACTGAACATATGTAATGACTCTACTAAAAGTTTAGGGA				
FCGR1B_XR_001737041.1 (2176)		GGTAAAAACTGAACATATGTAATGACTCTACTAAAAGTTTAGGGA				
FCGR1B_XR_001737040.1 (2113)		GGTAAAAACTGAACATATGTAATGACTCTACTAAAAGTTTAGGGA				
FCGR1B_NR_045213.1 (2110)		GGTAAAAACTGAACATATGTAATGACTCTACTAAAAGTTTAGGGA				
FCGR1CP_NR_027484.2 (1353)		-----				
Consensus (2206)		GGTAAAAACTGAACATATGTAATGACTCTACTAAAAGTTTAGGGA				
Section 51						
	(2251)	2251	2260	2270	2280	2295
FCGR1A_NM_000566.3 (2152)		AAAAAAACAGGAGGAGTATGACACAA		AAAA	AAAA	AAAAAAAAAAAA
FCGR1A_XM_005244957.3 (1337)		-----				
FCGR1A_XM_005244958.4 (1075)		-----				
FCGR1B_NM_001244910.1 (1582)		-----				
FCGR1B_NM_001017986.3 (1870)		AAAAAAACAGGAGGAGTATGACACACACAGCAA				AAAAAAAAAAAA
FCGR1B_NM_001004340.3 (1594)		AAAAAAACAGGAGGAGTATGACACACACAGCAA				AAAAAAAAAAAA
FCGR1B_XM_017000662.1 (1615)		AAAAAAACAGGAGGAGTATGACACACACAGCAA				-----
FCGR1B_XM_017000661.1 (1873)		AAAAAAACAGGAGGAGTATGACACACACAGCAA				-----
FCGR1B_XR_001737041.1 (2221)		AAAAAAACAGGAGGAGTATGACACACACAGCAA				-----
FCGR1B_XR_001737040.1 (2158)		AAAAAAACAGGAGGAGTATGACACACACAGCAA				-----
FCGR1B_NR_045213.1 (2155)		AAAAAAACAGGAGGAGTATGACACACACAGCAA				AAAAAAAAAAAA
FCGR1CP_NR_027484.2 (1353)		-----				
Consensus (2251)		AAAAAAACAGGAGGAGTATGACACACACAGCAA				
Section 52						
	(2296)	2296	2310	2320	2330	2340
FCGR1A_NM_000566.3 (2197)		AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA				
FCGR1A_XM_005244957.3 (1337)		-----				
FCGR1A_XM_005244958.4 (1075)		-----				
FCGR1B_NM_001244910.1 (1582)		-----				
FCGR1B_NM_001017986.3 (1915)		AAA-----				
FCGR1B_NM_001004340.3 (1639)		AAA-----				
FCGR1B_XM_017000662.1 (1648)		-----				
FCGR1B_XM_017000661.1 (1906)		-----				
FCGR1B_XR_001737041.1 (2254)		-----				
FCGR1B_XR_001737040.1 (2191)		-----				
FCGR1B_NR_045213.1 (2200)		AAA-----				
FCGR1CP_NR_027484.2 (1353)		-----				
Consensus (2296)		-----				
Section 53						
	(2341)	2341	2350	2367		
FCGR1A_NM_000566.3 (2242)		AAAAAAAAAAAAAAAAAAAAAAAAAAAA				
FCGR1A_XM_005244957.3 (1337)		-----				
FCGR1A_XM_005244958.4 (1075)		-----				
FCGR1B_NM_001244910.1 (1582)		-----				
FCGR1B_NM_001017986.3 (1918)		-----				
FCGR1B_NM_001004340.3 (1642)		-----				
FCGR1B_XM_017000662.1 (1648)		-----				
FCGR1B_XM_017000661.1 (1906)		-----				
FCGR1B_XR_001737041.1 (2254)		-----				
FCGR1B_XR_001737040.1 (2191)		-----				
FCGR1B_NR_045213.1 (2203)		-----				
FCGR1CP_NR_027484.2 (1353)		-----				
Consensus (2341)		-----				

Figure S6. Sequence alignment of transcripts of *FCGR1A*, *FCGR1B*, and *FCGR1CP*.

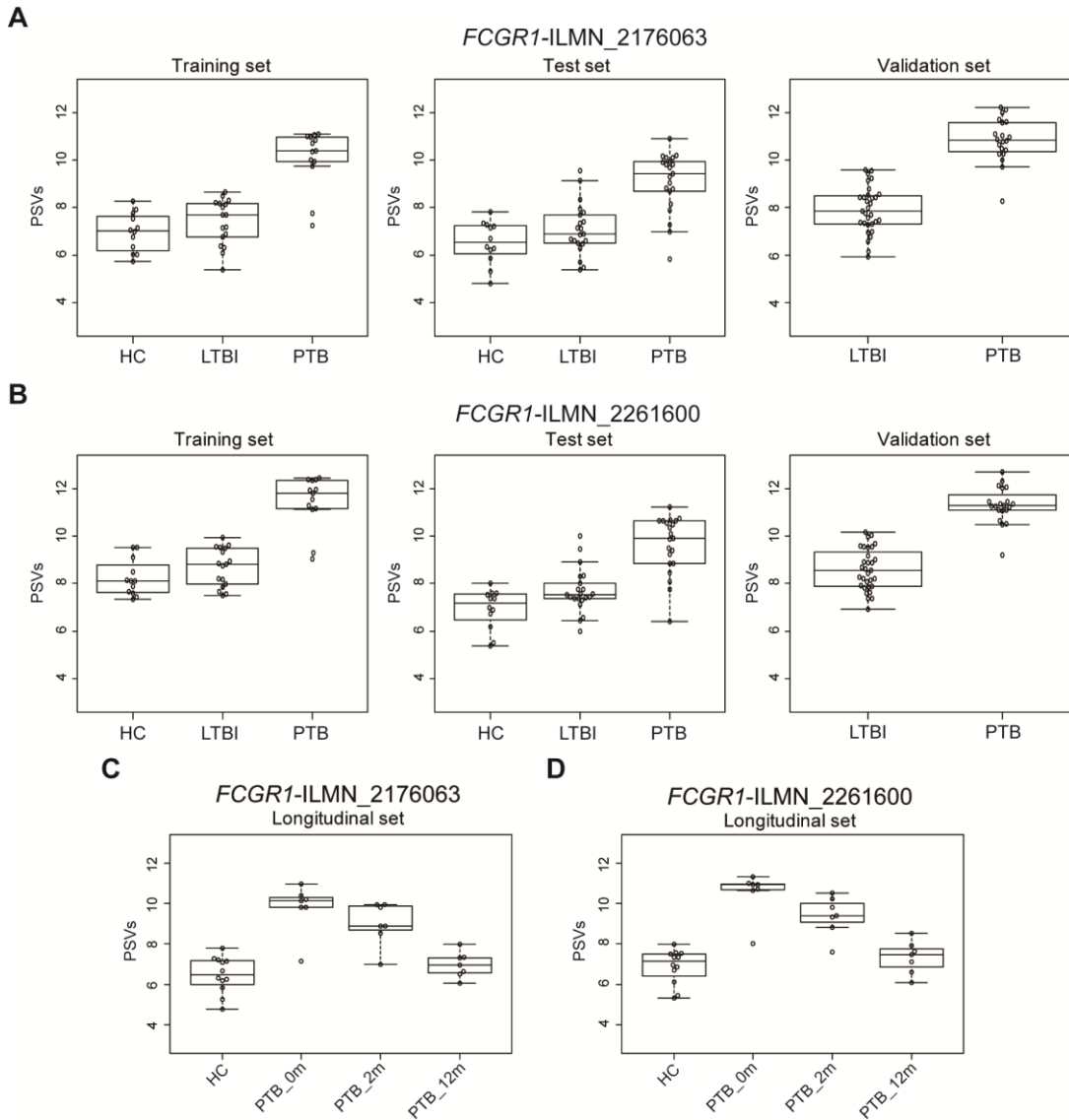


Figure S7: The box plots of the PSVs of *FCGR1* in whole blood.

(A & B) The PSVs from ILMN_2176063 and ILMN_2261600 respectively in whole blood of HC donors, LTBI donors and PTB patients from different cohorts.

(C & D) The PSVs from ILMN_2176063 and ILMN_2261600 respectively in whole blood of HC donors or PTB patients at different stages of chemotherapy. PTB_0m, PTB patients without chemotherapy; PTB_2m, PTB patients at 2 months post drug initiation; PTB_12m, PTB patients at 12 months post drug initiation.

		Section 1			
	(1)	1	10	20	38
promoter of FCGR1A other transcripts	(1)	-----TATA			
promoter of FCGR1A XM_005244958.4	(1)	-----ATTTTATCCTTCCAGGC			
promoter of FCGR1B all transcripts	(1)	CTTATTAGAAAGAAAGTATTTTATCCTTCCAGGC			
promoter of FCGR1CP	(1)	CTTATTAGAAAGAAAGTATTTTATCCTTCCAGGC			
Consensus	(1)	CTTATTAGAAAGAAAGTATTTTATCCTTCCAGGC			
		Section 2			
	(39)	39	50	60	76
promoter of FCGR1A other transcripts	(5)	GATCTTACATTCTCTTACACAACAATCCTAATTCCT			
promoter of FCGR1A XM_005244958.4	(22)	GATCTTACATTCTCTTACACAACAATCCTAATTCCT			
promoter of FCGR1B all transcripts	(39)	GATCTTACATTCTCTTACACAACAATCCTAATTCCT			
promoter of FCGR1CP	(39)	GATCTTACATTCTCTTACACAACAATCCTAATTCCT			
Consensus	(39)	GATCTTACATTCTCTTACACAACAATCCTAATTCCT			
		Section 3			
	(77)	77	90	100	114
promoter of FCGR1A other transcripts	(43)	CATGTTATCCTGATCAATGAAATGATTTCACCTATTTT			
promoter of FCGR1A XM_005244958.4	(60)	CATGTTATCCTGATCAATGAAATGATTTCACCTATTTT			
promoter of FCGR1B all transcripts	(77)	CATGTTATCCTGATCAATGAAATGATTTCACCTATTTT			
promoter of FCGR1CP	(77)	CATGTTATCCTGATCAATGAAATGATTTCACCTATTTT			
Consensus	(77)	CATGTTATCCTGATCAATGAAATGATTTCACCTATTTT			
		Section 4			
	(115)	115	120	130	152
promoter of FCGR1A other transcripts	(81)	TCAAAGAAGTAGCTATTTTACTACAAAGCAGGAATCG			
promoter of FCGR1A XM_005244958.4	(98)	TCAAAGAAGTAGCTATTTTACTACAAAGCAGGAATCG			
promoter of FCGR1B all transcripts	(115)	TCAAAGAAGTAGCTATTTTACTACAAAGCAGGAATCG			
promoter of FCGR1CP	(115)	TCAAAGAAGTAGCTATTTTACTACAAAGCAGGAATCG			
Consensus	(115)	TCAAAGAAGTAGCTATTTTACTACAAAGCAGGAATCG			
		Section 5			
	(153)	153	160	170	190
promoter of FCGR1A other transcripts	(119)	AAGGCATGGGGTGGGCACCTGTTATACATCCATCAGTGAG			
promoter of FCGR1A XM_005244958.4	(136)	AAGGCATGGGGTGGGCACCTGTTATACATCCATCAGTGAG			
promoter of FCGR1B all transcripts	(153)	AAGGCATGGGGTGGGCACCTGTTATACATCCATCAGTGAG			
promoter of FCGR1CP	(153)	AAGGCATGGGGTGGGCACCTGTTATACATCCATCAGTGAG			
Consensus	(153)	AAGGCATGGGGTGGGCACCTGTTATACATCCATCAGTGAG			
		Section 6			
	(191)	191	200	210	228
promoter of FCGR1A other transcripts	(157)	TACGTAAAGGAAATCAAACCTGTCTGATTTTGAATCCTG			
promoter of FCGR1A XM_005244958.4	(174)	TACGTAAAGGAAATCAAACCTGTCTGATTTTGAATCCTG			
promoter of FCGR1B all transcripts	(191)	TACGTAAAGGAAATCAAACCTGTCTGATTTTGAATCCTG			
promoter of FCGR1CP	(191)	TACGTAAAGGAAATCAAACCTGTCTGATTTTGAATCCTG			
Consensus	(191)	TACGTAAAGGAAATCAAACCTGTCTGATTTTGAATCCTG			
		Section 7			
	(229)	229	240	250	266
promoter of FCGR1A other transcripts	(195)	CTTCTATTTTTTACAACCTTGGACAAATTACTGATTTC			
promoter of FCGR1A XM_005244958.4	(212)	CTTCTATTTTTTACAACCTTGGACAAATTACTGATTTC			
promoter of FCGR1B all transcripts	(229)	CTTCTATTTTTTACAACCTTGGACAAATTACTGATTTC			
promoter of FCGR1CP	(229)	CTTCTATTTTTTACAACCTTGGACAAATTACTGATTTC			
Consensus	(229)	CTTCTATTTTTTACAACCTTGGACAAATTACTGATTTC			

		Section 8			
	(267)	267	280	290	304
promoter of FCGR1A other transcripts	(233)	CTCTTTCACTAGGTTTATCATTGTGTAATAATGGAGATAC			
promoter of FCGR1A XM_005244958.4	(250)	CTCTTTCACTAGGTTTATCATTGTGTAATAATGGAGATAC			
promoter of FCGR1B all transcripts	(267)	CTCTTTCACTAGGTTTATCATTGTGTAATAATGGAGATAC			
promoter of FCGR1CP	(267)	CTCTTTCACTAGGTTTATCATTGTGTAATAATGGAGATAC			
Consensus	(267)	CTCTTTCACTAGGTTTATCATTGTGTAATAATGGAGATAC			
		Section 9			
	(305)	305	310	320	342
promoter of FCGR1A other transcripts	(271)	TAGTGTCTACTCATGGATTATTGTGAGGCTTAAATAAG			
promoter of FCGR1A XM_005244958.4	(288)	TAGTGTCTACTCATGGATTATTGTGAGGCTTAAATAAG			
promoter of FCGR1B all transcripts	(305)	TAGTGTCTACTCATGGATTATTGTGAGGCTTAAATAAG			
promoter of FCGR1CP	(305)	TAGTGTCTACTCATGGATTATTGTGAGGCTTAAATAAG			
Consensus	(305)	TAGTGTCTACTCATGGATTATTGTGAGGCTTAAATAAG			
		Section 10			
	(343)	343	350	360	380
promoter of FCGR1A other transcripts	(309)	AAAACATGTATCAAGCATATTTGTCTGGCATTGTAATAA			
promoter of FCGR1A XM_005244958.4	(326)	AAAACATGTATCAAGCATATTTGTCTGGCATTGTAATAA			
promoter of FCGR1B all transcripts	(343)	AAAACATGTATCAAGCATATTTGTCTGGCATTGTAATAA			
promoter of FCGR1CP	(343)	AAAACATGTATCAAGCATATTTGTCTGGCATTGTAATAA			
Consensus	(343)	AAAACATGTATCAAGCATATTTGTCTGGCATTGTAATAA			
		Section 11			
	(381)	381	390	400	418
promoter of FCGR1A other transcripts	(347)	GCACTCTAAAAATTTATGCAGCGATGAGGATAATGATCA			
promoter of FCGR1A XM_005244958.4	(364)	GCACTCTAAAAATTTATGCAGCGATGAGGATAATGATCA			
promoter of FCGR1B all transcripts	(381)	GCACTCTAAAAATTTATGCAGCGATGAGGATAATGATCA			
promoter of FCGR1CP	(381)	GCACTCTAAAAATTTATGCAGCGATGAGGATAATGATCA			
Consensus	(381)	GCACTCTAAAAATTTATGCAGCGATGAGGATAATGATCA			
		Section 12			
	(419)	419	430	440	456
promoter of FCGR1A other transcripts	(385)	TAGACAATCTGATAGCATCTTATCCAAAGGAAAAAATG			
promoter of FCGR1A XM_005244958.4	(402)	TAGACAATCTGATAGCATCTTATCCAAAGGAAAAAATG			
promoter of FCGR1B all transcripts	(419)	TAGACAATCTGATAGCATCTTATCCAAAGGAAAAAATG			
promoter of FCGR1CP	(419)	TAGACAATCTGATAGCATCTTATCCAAAGGAAAAAATG			
Consensus	(419)	TAGACAATCTGATAGCATCTTATCCAAAGGAAAAAATG			
		Section 13			
	(457)	457	470	480	494
promoter of FCGR1A other transcripts	(423)	CGCATTTTCCTTTGAGTAAGCACTACTGATTCTAGGAAT			
promoter of FCGR1A XM_005244958.4	(440)	CGCATTTTCCTTTGAGTAAGCACTACTGATTCTAGGAAT			
promoter of FCGR1B all transcripts	(457)	CGCATTTTCCTTTGAGTAAGCACTACTGATTCTAGGAAT			
promoter of FCGR1CP	(457)	CGCATTTTCCTTTGAGTAAGCACTACTGATTCTAGGAAT			
Consensus	(457)	CGCATTTTCCTTTGAGTAAGCACTACTGATTCTAGGAAT			
		Section 14			
	(495)	495	500	510	532
promoter of FCGR1A other transcripts	(461)	GTGTCCTAAGGAAAAAATAAGTCAAAATGTTTAAAGGTA			
promoter of FCGR1A XM_005244958.4	(478)	GTGTCCTAAGGAAAAAATAAGTCAAAATGTTTAAAGGTA			
promoter of FCGR1B all transcripts	(495)	GTGTCCTAAGGAAAAAATAAGTCAAAATGTTTAAAGGTA			
promoter of FCGR1CP	(495)	GTGTCCTAAGGAAAAAATAAGTCAAAATGTTTAAAGGTA			
Consensus	(495)	GTGTCCTAAGGAAAAAATAAGTCAAAATGTTTAAAGGTA			

Section 15						
	(533)	533	540	550	560	570
promoter of FCGR1A other transcripts	(499)	GTCACAAGACTATTTTGGTAGTAAGCAGTCTTTTTTAC				
promoter of FCGR1A XM_005244958.4	(516)	GTCACAAGACTATTTTGGTAGTAAGCAGTCTTTTTTAC				
promoter of FCGR1B all transcripts	(533)	GTCACAAGACTATTTTGGTAGTAAGCAGTCTTTTTTAC				
promoter of FCGR1CP	(533)	GTCACAAGACTATTTTGGTAGTAAGCAGTCTTTTTTAC				
Consensus	(533)	GTCACAAGACTATTTTGGTAGTAAGCAGTCTTTTTTAC				
Section 16						
	(571)	571	580	590	608	
promoter of FCGR1A other transcripts	(537)	TGGTCACACAGTAAAAAATTAGAAATAACCTACATGTT				
promoter of FCGR1A XM_005244958.4	(554)	TGGTCACACAGTAAAAAATTAGAAATAACCTACATGTT				
promoter of FCGR1B all transcripts	(571)	TGGTCACACAGTAAAAAATTAGAAATAACCTACATGTT				
promoter of FCGR1CP	(571)	TGGTCACACAGTAAAAAATTAGAAATAACCTACATGTT				
Consensus	(571)	TGGTCACACAGTAAAAAATTAGAAATAACCTACATGTT				
Section 17						
	(609)	609	620	630	646	
promoter of FCGR1A other transcripts	(575)	CATGAAGAGAAGTTGGTGAAATAAATTATGGTACATGC				
promoter of FCGR1A XM_005244958.4	(592)	CATGAAGAGAAGTTGGTGAAATAAATTATGGTACATGC				
promoter of FCGR1B all transcripts	(609)	CATGAAGAGAAGTTGGTGAAATAAATTATGGTACATGC				
promoter of FCGR1CP	(609)	CATGAAGAGAAGTTGGTGAAATAAATTATGGTACATGC				
Consensus	(609)	CATGAAGAGAAGTTGGTGAAATAAATTATGGTACATGC				
Section 18						
	(647)	647	660	670	684	
promoter of FCGR1A other transcripts	(613)	ATACAGTAGAAAACCTTTGGAGACAAAATAGTAAATAG				
promoter of FCGR1A XM_005244958.4	(630)	ATACAGTAGAAAACCTTTGGAGACAAAATAGTAAATAG				
promoter of FCGR1B all transcripts	(647)	ATACAGTAGAAAACCTTTGGAGACAAAATAGTAAATAG				
promoter of FCGR1CP	(647)	ATACAGTAGAAAACCTTTGGAGACAAAATAGTAAATAG				
Consensus	(647)	ATACAGTAGAAAACCTTTGGAGACAAAATAGTAAATAG				
Section 19						
	(685)	685	690	700	710	722
promoter of FCGR1A other transcripts	(651)	TTACAGATATAGGCTTTGAATATAAATTTTAACAAGCT				
promoter of FCGR1A XM_005244958.4	(668)	TTACAGATATAGGCTTTGAATATAAATTTTAACAAGCT				
promoter of FCGR1B all transcripts	(685)	TTACAGATATAGGCTTTGAATATAAATTTTAACAAGCT				
promoter of FCGR1CP	(685)	TTACAGATATAGGCTTTGAATATAAATTTTAACAAGCT				
Consensus	(685)	TTACAGATATAGGCTTTGAATATAAATTTTAACAAGCT				
Section 20						
	(723)	723	730	740	750	760
promoter of FCGR1A other transcripts	(689)	GAGGCTTCTCTCTCTCTCTCAGAACACCCTGAGTTCTT				
promoter of FCGR1A XM_005244958.4	(706)	GAGGCTTCTCTCTCTCTCTCAGAACACCCTGAGTTCTT				
promoter of FCGR1B all transcripts	(723)	GAGGCTTCTCTCTCTCTCTCAGAACACCCTGAGTTCTT				
promoter of FCGR1CP	(723)	GAGGCTTCTCTCTCTCTCTCAGAACACCCTGAGTTCTT				
Consensus	(723)	GAGGCTTCTCTCTCTCTCTCAGAACACCCTGAGTTCTT				
Section 21						
	(761)	761	770	780	798	
promoter of FCGR1A other transcripts	(727)	CCCGGCCCTTTCTTCCTTGCTTTTCATTTGTGTCA				
promoter of FCGR1A XM_005244958.4	(744)	CCCGGCCCTTTCTTCCTTGCTTTTCATTTGTGTCA				
promoter of FCGR1B all transcripts	(761)	CCCGGCCCTTTCTTCCTTGCTTTTCATTTGTGTCA				
promoter of FCGR1CP	(761)	CCCGGCCCTTTCTTCCTTGCTTTTCATTTGTGTCA				
Consensus	(761)	CCCGGCCCTTTCTTCCTTGCTTTTCATTTGTGTCA				

		Section 22			
	(799)	799	810	820	836
promoter of FCGR1A other transcripts	(765)	GCTCTTGCTCGTATAGCAATCTCAAATCTCAGTAGCA			
promoter of FCGR1A XM_005244958.4	(782)	GCTCTTGCTCGTATAGCAATCTCAAATCTCAGTAGCA			
promoter of FCGR1B all transcripts	(799)	GCTCTTGCTCGTATAGCAATCTCAAATCTCAGTAGCA			
promoter of FCGR1CP	(799)	GCTCTTGCTCGTATAGCAATCTCAAATCTCAGTAGCA			
Consensus	(799)	GCTCTTGCTCGTATAGCAATCTCAAATCTCAGTAGCA			
		Section 23			
	(837)	837	850	860	874
promoter of FCGR1A other transcripts	(803)	TATAAAGGTAAGCATTAGTTCTCACTTACAAGTTTGC			
promoter of FCGR1A XM_005244958.4	(820)	TATAAAGGTAAGCATTAGTTCTCACTTACAAGTTTGC			
promoter of FCGR1B all transcripts	(837)	TATAAAGGTAAGCATTAGTTCTCACTTACAAGTTTGC			
promoter of FCGR1CP	(837)	TATAAAGGTAAGCATTAGTTCTCACTTACAAGTTTGC			
Consensus	(837)	TATAAAGGTAAGCATTAGTTCTCACTTACAAGTTTGC			
		Section 24			
	(875)	875	880	890	912
promoter of FCGR1A other transcripts	(841)	AGGGCAGGTGAGGCAGCTCTGCCTCAAGCCACAATGTC			
promoter of FCGR1A XM_005244958.4	(858)	AGGGCAGGTGAGGCAGCTCTGCCTCAAGCCACAATGTC			
promoter of FCGR1B all transcripts	(875)	AGGGCAGGTGAGGCAGCTCTGCCTCAAGCCACAATGTC			
promoter of FCGR1CP	(875)	AGGGCAGGTGAGGCAGCTCTGCCTCAAGCCACAATGTC			
Consensus	(875)	AGGGCAGGTGAGGCAGCTCTGCCTCAAGCCACAATGTC			
		Section 25			
	(913)	913	920	930	950
promoter of FCGR1A other transcripts	(879)	TAGGACAGCTCTGTTTCACAGTGGGTGACTAGCTAA			
promoter of FCGR1A XM_005244958.4	(896)	TAGGACAGCTCTGTTTCACAGTGGGTGACTAGCTAA			
promoter of FCGR1B all transcripts	(913)	TAGGACAGCTCTGTTTCACAGTGGGTGACTAGCTAA			
promoter of FCGR1CP	(913)	TAGGACAGCTCTGTTTCACAGTGGGTGACTAGCTAA			
Consensus	(913)	TAGGACAGCTCTGTTTCGCACTGTGGGTGACTAGCTAA			
		Section 26			
	(951)	951	960	970	988
promoter of FCGR1A other transcripts	(917)	AAAATGTTCTTGTCTCAGCAATCACAGGAGAACAAGAG			
promoter of FCGR1A XM_005244958.4	(934)	AAAATGTTCTTGTCTCAGCAATCACAGGAGAACAAGAG			
promoter of FCGR1B all transcripts	(951)	AAAATGTTCTTGTCTCAGCAATCACAGGAGAACAAGAG			
promoter of FCGR1CP	(951)	AAAATGTTCTTGTCTCAGCAATCACAGGAGAACAAGAG			
Consensus	(951)	AAAATGTTCTTGTCTCAGCAATCACAGGAGAACAAGAG			
		Section 27			
	(989)	989	1000	1010	1026
promoter of FCGR1A other transcripts	(955)	GGTGAGAGATAATGTGTGAAGCTTCCTAAGTGCTAAGT			
promoter of FCGR1A XM_005244958.4	(972)	GGTGAGAGATAATGTGTGAAGCTTCCTAAGTGCTAAGT			
promoter of FCGR1B all transcripts	(989)	GGTGAGAGATAATGTGTGAAGCTTCCTAAGTGCTAAGT			
promoter of FCGR1CP	(989)	GGTGAGAGATAATGTGTGAAGCTTCCTAAGTGCTAAGT			
Consensus	(989)	GGTGAGAGATAATGTGTGAAGCTTCCTAAGTGCTAAGT			
		Section 28			
	(1027)	1027	1040	1050	1064
promoter of FCGR1A other transcripts	(993)	TTGAAATTAGCACCATGTCATTTCCATTACATTTTCGC			
promoter of FCGR1A XM_005244958.4	(1010)	TTGAAATTAGCACCATGTCATTTCCATTACATTTTCGC			
promoter of FCGR1B all transcripts	(1027)	TTGAAATTAGCACCATGTCATTTCCATTACATTTTCGC			
promoter of FCGR1CP	(1027)	TTGAAATTAGCACCATGTCATTTCCATTACATTTTCGC			
Consensus	(1027)	TTGAAATTAGCACCATGTCATTTCCATTACATTTTCGC			

		Section 29				
	(1065)	1065	1070	1080	1090	1102
promoter of FCGR1A other transcripts (1031)		TGGCCAATGAAAGTCTCATGATGAGCCACAGTCAAGAG				
promoter of FCGR1A XM_005244958.4 (1048)		TGGCCAATGAAAGTCTCATGATGAGCCACAGTCAAGAG				
promoter of FCGR1B all transcripts (1065)		TGGCCAATGAAAGTCTCATGATGAGCCACAGTCAAGAG				
promoter of FCGR1CP (1065)		TGGCCAATGAAAGTCTCATGATGAGCCACAGTCAAGAG				
Consensus (1065)		TGGCCAATGAAAGTCTCATGATGAGCCACAGTCAAGAG				
		Section 30				
	(1103)	1103	1110	1120	1130	1140
promoter of FCGR1A other transcripts (1069)		TCAGAGACATACCCTCATGAGGCTGTGGAGAGAGTGTA				
promoter of FCGR1A XM_005244958.4 (1086)		TCAGAGACATACCCTCATGAGGCTGTGGAGAGAGTGTA				
promoter of FCGR1B all transcripts (1103)		TCAGAGATGTACCCTCATGAGGCTGTGGAGAGAGTGTA				
promoter of FCGR1CP (1103)		TCAGAGACATACCCTCATGAGGCTGTGGAGAGAGTGTA				
Consensus (1103)		TCAGAGACGTACCCTCATGAGGCTGTGGAGAGAGTGTA				
		Section 31				
	(1141)	1141	1150	1160		1178
promoter of FCGR1A other transcripts (1107)		GATTTCAGGGAGCGGTGAGAACTGGGGCCAGTACACCA				
promoter of FCGR1A XM_005244958.4 (1124)		GATTTCAGGGAGCGGTGAGAACTGGGGCCAGTACACCA				
promoter of FCGR1B all transcripts (1141)		GATTTCAGGGAGCGGTGAGAACTGGGGCCAGTACACCA				
promoter of FCGR1CP (1141)		GATTTCAGGGAGCGGTGAGAACTGGGGCCAGTACACCA				
Consensus (1141)		GATTTCAGGGAGCGGTGAGAACTGGGGCCAGTACACCA				
		Section 32				
	(1179)	1179	1190	1200		1216
promoter of FCGR1A other transcripts (1145)		ACTTACAGCATGATTGTGTCATCATTTTTCATTCTCTGC				
promoter of FCGR1A XM_005244958.4 (1162)		ACTTACAGCATGATTGTGTCATCATTTTTCATTCTCTGC				
promoter of FCGR1B all transcripts (1179)		ACTTACAGCATGATTGTGTCATCATTTTTCATTCTCTGC				
promoter of FCGR1CP (1179)		ACTTACAGCATGATTGTGTCATCATTTTTCATTCTCTGC				
Consensus (1179)		ATTTACAGCATGATTGTGTCATCATTTTTCATTCTCTGC				
		Section 33				
	(1217)	1217	1230	1240		1254
promoter of FCGR1A other transcripts (1183)		TAGTAAGATTGCCAAAGTCTCTCTGCACTCATTGAATT				
promoter of FCGR1A XM_005244958.4 (1200)		TAGTAAGATTGCCAAAGTCTCTCTGCACTCATTGAATT				
promoter of FCGR1B all transcripts (1217)		TAGTAAGATTGCCAAAGTCTCTCTGCACTCATTGAATT				
promoter of FCGR1CP (1217)		TAGTAAGATTGCCAAAGTCTCTCTGCACTCATTGAATT				
Consensus (1217)		TAGTAAGATTGCCAAAGTCTCTCTGCACTCATTGAATT				
		Section 34				
	(1255)	1255	1260	1270	1280	1292
promoter of FCGR1A other transcripts (1221)		CATTTAGCTCTCTTTAGCTCTCTTTTTTTAGCTCTCAT				
promoter of FCGR1A XM_005244958.4 (1238)		CATTTAGCTCTCTTTAGCTCTCTTTTTTTAGCTCTCAT				
promoter of FCGR1B all transcripts (1255)		CATCC-----				
promoter of FCGR1CP (1255)		CATCC-----				
Consensus (1255)		CATTTAGCTCTCTTTAGCTCTCTTTTTTTAGCTCTCAT				
		Section 35				
	(1293)	1293	1300	1310	1320	1330
promoter of FCGR1A other transcripts (1259)		TAGTTTCCATTTAGCTCTCTTTCTCTCTTACCACAAT				
promoter of FCGR1A XM_005244958.4 (1276)		TAGTTTCCATTTAGCTCTCTTTCTCTCTTACCACAAT				
promoter of FCGR1B all transcripts (1260)		-TAGTTTCCATTTAGCTCTCTTTCTCTCTTACCACAAT				
promoter of FCGR1CP (1260)		-TAGTTTCCATTTAGCTCTCTTTCTCTCTTACCACAAT				
Consensus (1293)		TAGTTTCCATTTAGCTCTCTTTCTCTCTTACCACAAT				

		Section 36			
	(1331)	1331	1340	1350	1368
promoter of FCGR1A other transcripts (1297)		ACCTAAAAATCTTTTATGGGGTTACAACCTCTGTCTCA			
promoter of FCGR1A XM_005244958.4 (1314)		ACCTAAAAATCTTTTATGGGGTTACAACCTCTGTCTCA			
promoter of FCGR1B all transcripts (1297)		ACCTAAAAATCTTTTATGGGGTTACAACCTCTGTCTCA			
promoter of FCGR1CP (1297)		ACCTAAAAATCTTTTATGGGGTTACAACCTCTGTCTCA			
Consensus (1331)		ACCTAAAAATCTTTTATGGGGTTACAACCTCTGTCTCA			
		Section 37			
	(1369)	1369	1380	1390	1406
promoter of FCGR1A other transcripts (1335)		GGAGCCACCTCAGTTTGGTGGCACAGAGCTCCCCACTT			
promoter of FCGR1A XM_005244958.4 (1352)		GGAGCCACCTCAGTTTGGTGGCACAGAGCTCCCCACTT			
promoter of FCGR1B all transcripts (1335)		GGAGCCACCTCAGTTTGGTGGCACAGAGCTCCCCACTT			
promoter of FCGR1CP (1335)		GGAGCCACCTCAGTTTGGTGGCACAGAGCTCCCCACTT			
Consensus (1369)		GGAGCCACCTCAGTTTGGTGGCACAGAGCTCCCCACTT			
		Section 38			
	(1407)	1407	1420	1430	1444
promoter of FCGR1A other transcripts (1373)		GTACTCTGAAACTCTTTTCTTGAAGATATTGCTATCCA			
promoter of FCGR1A XM_005244958.4 (1390)		GTACTCTGAAACTCTTTTCTTGAAGATATTGCTATCCA			
promoter of FCGR1B all transcripts (1373)		GTACTCTGAAACTCTTTTCTTGAAGATATTGCTATCCA			
promoter of FCGR1CP (1373)		GTACTCTGAAACTCTTTTCTTGAAGATATTGCTATCCA			
Consensus (1407)		GTACTCTGAAACTCTTTTCTTGAAGATATTGCTATCCA			
		Section 39			
	(1445)	1445	1450	1460	1482
promoter of FCGR1A other transcripts (1411)		TGTGCATGAGTTATTTTCTTCTCCATAGCATCCACAT			
promoter of FCGR1A XM_005244958.4 (1428)		TGTGCATGAGTTATTTTCTTCTCCATAGCATCCACAT			
promoter of FCGR1B all transcripts (1411)		TGTGCATGAGTTATTTTCTTCTCCATAGCATCCACAT			
promoter of FCGR1CP (1411)		TGTGCATGAGTTATTTTCTTCTCCATAGCATCCACAT			
Consensus (1445)		TGTGCATGAGTTATTTTCTTCTCCATAGCATCCACAT			
		Section 40			
	(1483)	1483	1490	1500	1520
promoter of FCGR1A other transcripts (1449)		TAAACAATTAATTACCTTGGATTTAGCCAAAATAAACA			
promoter of FCGR1A XM_005244958.4 (1466)		TAAACAATTAATTACCTTGGATTTAGCCAAAATAAACA			
promoter of FCGR1B all transcripts (1449)		TAAACAATTAATTACCTTGGATTTAGCCAAAATAAACA			
promoter of FCGR1CP (1449)		TAAACAATTAATTACCTTGGATTTAGCCAAAATAAACA			
Consensus (1483)		TAAACAATTAATTACCTTGGATTTAGCCAAAATAAACA			
		Section 41			
	(1521)	1521	1530	1540	1558
promoter of FCGR1A other transcripts (1487)		CTCCAAATTCATGATGTCTTTCAGGAAGAGAGTTTGTT			
promoter of FCGR1A XM_005244958.4 (1504)		CTCCAAATTCATGATGTCTTTCAGGAAGAGAGTTTGTT			
promoter of FCGR1B all transcripts (1487)		CTCCAAATTCATGATGTCTTTCAGGAAGAGAGTTTGTT			
promoter of FCGR1CP (1487)		CTCCAAATTCATGATGTCTTTCAGGAAGAGAGTTTGTT			
Consensus (1521)		CTCCAAATTCATGATGTCTTTCAGGAAGAGAGTTTGTT			
		Section 42			
	(1559)	1559	1570	1580	1596
promoter of FCGR1A other transcripts (1525)		TTCTTTTTTAACCAAAATGGGAGATTGATCCTGTCTGT			
promoter of FCGR1A XM_005244958.4 (1542)		TTCTTTTTTAACCAAAATGGGAGATTGATCCTGTCTGT			
promoter of FCGR1B all transcripts (1525)		TTCTTTTTTAACCAAAATGGGAGATTGATCCTGTCTGT			
promoter of FCGR1CP (1525)		TTCTTTTTTAACCAAAATGGGAGATTGATCCTGTCTGT			
Consensus (1559)		TTCTTTTTTAACCAAAATGGGAGATTGATCCTGTCTGT			

Section 43				
	(1597)	1597	1610	1620 1634
promoter of FCGR1A other transcripts (1563)		GTCCCCTAGAGGAGCAGAGGCTGGTTTGTATTAGGGCA		
promoter of FCGR1A XM_005244958.4 (1580)		GTCCCCTAGAGGAGCAGAGGCTGGTTTGTATTAGGGCA		
promoter of FCGR1B all transcripts (1563)		GTCCCCTAGAGGAGCAGAGGCTGGTTTGTATTAGGGCA		
promoter of FCGR1CP (1563)		GTCCCCTAGAGGAGCAGAGGCTGGTTTGTATTAGGGCA		
Consensus (1597)		GTCCCCTAGAGGAGCAGAGGCTGGTTTGTATTAGGGCA		
Section 44				
	(1635)	1635	1640	1650 1660 1672
promoter of FCGR1A other transcripts (1601)		GCTCTTGTAGATGAGTAACTTTTCCCATGGCCTCATAG		
promoter of FCGR1A XM_005244958.4 (1618)		GCTCTTGTAGATGAGTAACTTTTCCCATGGCCTCATAG		
promoter of FCGR1B all transcripts (1601)		GCTCTTGTAGATGAGTAACTTTTCCCATGGCCTCATAG		
promoter of FCGR1CP (1601)		GCTCTTGTAGATGAGTAACTTTTCCCATGGCCTCATAG		
Consensus (1635)		GCTCTTGTAGATGAGTAACTTTTCCCATGGCCTCATAG		
Section 45				
	(1673)	1673	1680	1690 1700 1710
promoter of FCGR1A other transcripts (1639)		AGGCTGATATAGAACTTCTGGATTCAAATGATTGTTT		
promoter of FCGR1A XM_005244958.4 (1656)		AGGCTGATATAGAACTTCTGGATTCAAATGATTGTTT		
promoter of FCGR1B all transcripts (1639)		AGGCTGATATAGAACTTCTGGATTCAAATGATTGTTT		
promoter of FCGR1CP (1639)		AGGCTGATATAGAACTTCTGGATTCAAATGATTGTTT		
Consensus (1673)		AGGCTGATATAGAACTTCTGGATTCAAATGATTGTTT		
Section 46				
	(1711)	1711	1720	1730 1748
promoter of FCGR1A other transcripts (1677)		GGAGGCATTAGCCAGGCATTGAACCAATTATAAAGAGT		
promoter of FCGR1A XM_005244958.4 (1694)		GGAGGCATTAGCCAGGCATTGAACCAATTATAAAGAGT		
promoter of FCGR1B all transcripts (1677)		GGAGGCATTAGCCAGGCATTGAACCAATTATAAAGAGT		
promoter of FCGR1CP (1677)		GGAGGCATTAGCCAGGCATTGAACCAATTATAAAGAGT		
Consensus (1711)		GGAGGCATTAGCCAGGCATTGAACCAATTATAAAGAGT		
Section 47				
	(1749)	1749	1760	1770 1786
promoter of FCGR1A other transcripts (1715)		GAGGTTTTGCCATATTCTAACCCTAAGAAACAGAAACG		
promoter of FCGR1A XM_005244958.4 (1732)		GAGGTTTTGCCATATTCTAACCCTAAGAAACAGAAACG		
promoter of FCGR1B all transcripts (1715)		GAGGTTTTGCCATATTCTAACCCTAAGAAACAGAAACG		
promoter of FCGR1CP (1715)		GAGGTTTTGCCATATTCTAACCCTAAGAAACAGAAACG		
Consensus (1749)		GAGGTTTTGCCATATTCTAACCCTAAGAAACAGAAACG		
Section 48				
	(1787)	1787	1800	1810 1824
promoter of FCGR1A other transcripts (1753)		GTAGAGGGTAAAAATAGAATAGAATGTCAATACAACCTT		
promoter of FCGR1A XM_005244958.4 (1770)		GTAGAGGGTAAAAATAGAATAGAATGTCAATACAACCTT		
promoter of FCGR1B all transcripts (1753)		GTAGAGGGTAAAAATAGAATAGAATGTCAATACAACCTT		
promoter of FCGR1CP (1753)		GTAGAGGGTAAAAATAGAATAGAATGTCAATACAACCTT		
Consensus (1787)		GTAGAGGGTAAAAATAGAATAGAATGTCAATACAACCTT		
Section 49				
	(1825)	1825	1830	1840 1850 1862
promoter of FCGR1A other transcripts (1791)		TAGCCTTTTCCCTGGATTCTGAGAGTTCATAACCTGAA		
promoter of FCGR1A XM_005244958.4 (1808)		TAGCCTTTTCCCTGGATTCTGAGAGTTCATAACCTGAA		
promoter of FCGR1B all transcripts (1791)		TAGCCTTTTCCCTGGATTCTGAGAGTTCATAACCTGAA		
promoter of FCGR1CP (1791)		TAGCCTTTTCCCTGGATTCTGAGAGTTCATAACCTGAA		
Consensus (1825)		TAGCCTTTTCCCTGGATTCTGAGAGTTCATAACCTGAA		

		Section 50				
	(1863)	1863	1870	1880	1890	1900
promoter of FCGR1A other transcripts (1829)		AATCAGAGATTCAAAC TGGAGAGATGGGCTAACAGGT				
promoter of FCGR1A XM_005244958.4 (1846)		AATCAGAGATTCAAAC TGGAGAGATGGGCTAACAGGT				
promoter of FCGR1B all transcripts (1829)		AATCAGAGATTCAAAC TGGAGAGATGGGCTAACAGGT				
promoter of FCGR1CP (1829)		AATCAGAGATTCAAAC TGGAGAGATGGGCTAACAGGT				
Consensus (1863)		AATCAGAGATTCAAAC TGGAGAGATGGGCTAACAGGT				
		Section 51				
	(1901)	1901	1910	1920		1938
promoter of FCGR1A other transcripts (1867)		ATGAGCATGGGAAAAGCATGTTTCAAG AATTTGAGATG				
promoter of FCGR1A XM_005244958.4 (1884)		ATGAGCATGGGAAAAGCATGTTTCAAG AATTTGAGATG				
promoter of FCGR1B all transcripts (1867)		ATGAGCATGGGAAAAGCATGTTTCAAG AATTTGAGATG				
promoter of FCGR1CP (1867)		ATGAGCATGGGAAAAGCATGTTTCAAG AATTTGAGATG				
Consensus (1901)		ATGAGCATGGGAAAAGCATGTTTCAAG AATTTGAGATG				
		Section 52				
	(1939)	1939	1950	1960		1976
promoter of FCGR1A other transcripts (1905)		TATTTCCAGAAAAGCAACATGATGAAAATGGTCAGAA				
promoter of FCGR1A XM_005244958.4 (1922)		TATTTCCAGAAAAGCAACATGATGAAAATGGTCAGAA				
promoter of FCGR1B all transcripts (1905)		TATTTCCAGAAAAGCAACATGATGAAAATGGTCAGAA				
promoter of FCGR1CP (1905)		TATTTCCAGAAAAGCAACATGATGAAAATGGTCAGAA				
Consensus (1939)		TATTTCCAGAAAAGCAACATGATGAAAATGGTCAGAA				
		Section 53				
	(1977)	1977	1990	2000		2014
promoter of FCGR1A other transcripts (1943)		AAGGCAATTTCTCCTCTTTTCTAATTTGGCTCTGGA				
promoter of FCGR1A XM_005244958.4 (1960)		AAGGCAATTTCTCCTCTTTTCTAATTTGGCTCTGGA				
promoter of FCGR1B all transcripts (1943)		AAGGCAATTTCTCCTCTTTTCTAATTTGGCTCTGGA				
promoter of FCGR1CP (1943)		AAGGCAATTTCTCCTCTTTTCTAATTTGGCTCTGGA				
Consensus (1977)		AAGGCAATTTCTCCTCTTTTCTAATTTGGCTCTGGA				
		Section 54				
	(2015)	2015	2020	2030	2040	2052
promoter of FCGR1A other transcripts (1981)		GCCACCAGCAGAACCTCTTCAATATCTTGCATGTTACA				
promoter of FCGR1A XM_005244958.4 (1998)		GCCACCAGCAGAACCTCTTCAATATCTTGCATGTTACA				
promoter of FCGR1B all transcripts (1981)		GCCACCAGCAGAACCTCTTCAATATCTTGCATGTTACA				
promoter of FCGR1CP (1981)		GCCACCAGCAGAACCTCTTCAATATCTTGCATGTTACA				
Consensus (2015)		GCCACCAGCAGAACCTCTTCAATATCTTGCATGTTACA				
		Section 55				
	(2053)	2053	2060	2070		2085
promoter of FCGR1A other transcripts (2019)		GATTTCACTGCTCCCAACCAGCTTGGAGACAACA				
promoter of FCGR1A XM_005244958.4 (2036)		GATTTCACTGCTCCCA-----				
promoter of FCGR1B all transcripts (2019)		GATTTCACTGCTCCCAACCAGCTTGGAGACAACA				
promoter of FCGR1CP (2019)		GATTTCACTGCTCCCAACCAGCTTGGAGACAACA				
Consensus (2053)		GATTTCACTGCTCCCAACCAGCTTGGAGACAACA				

Figure S8: Sequence alignment of the promoters of *FCGR1A*, *FCGR1B*, and *FCGR1CP*.

Sequences from 2000 bp upstream to -50 downstream of transcription start site were used for sequence alignment.

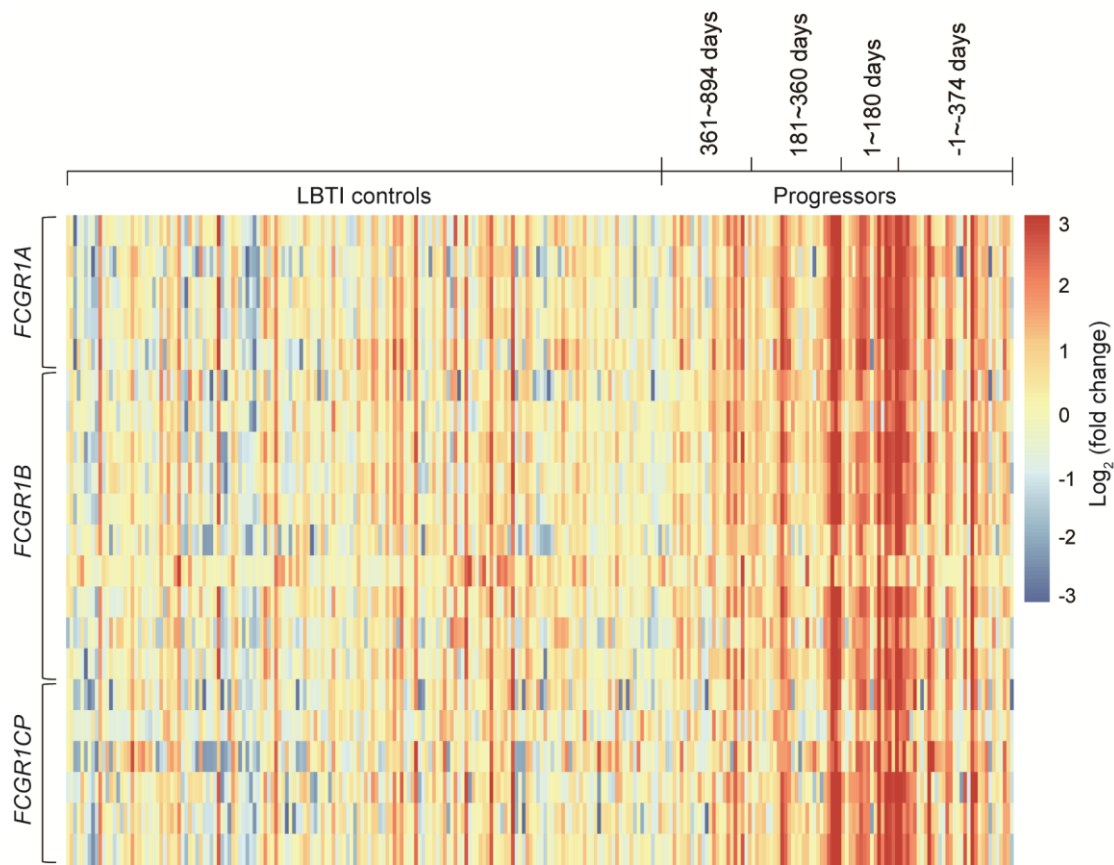


Figure S9: The relative expressions of *FCGR1A*, *FCGR1B*, and *FCGR1CP* in the whole blood of LTBI progressors compared to their expressions in the whole blood of LTBI controls.

This heat map is a visual representation of the data shown in Figures 5a-5c. Each row represents the relative expressions of a specific splice junction (1).

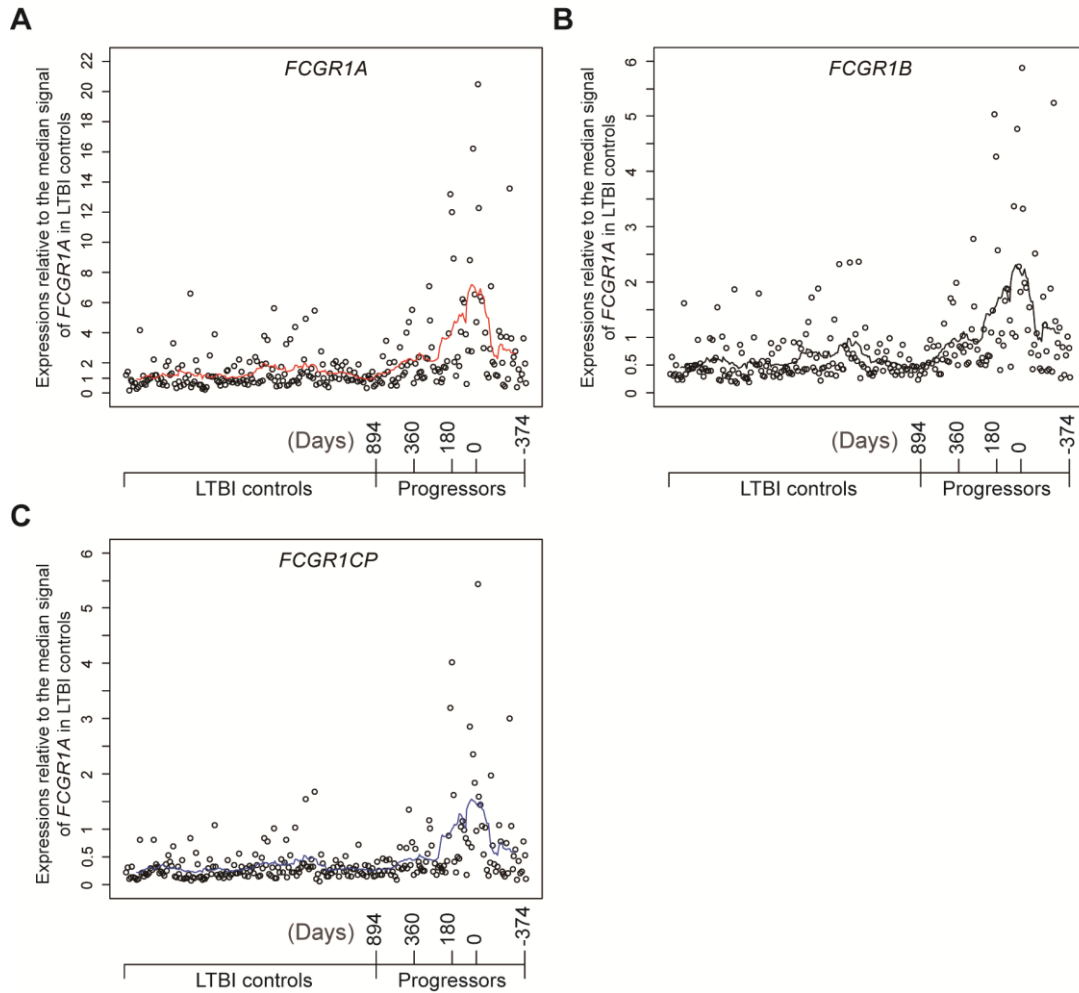


Figure S10: The PSVs of *FCGR1A* (A), *FCGR1B* (B) and *FCGR1CP* (C) relative to the median expression of *FCGR1A* in LTBI controls.

Data were from Figure S9, presented as described in Figure 5.

		Section 1									
		(1)	1	10	20	30	40	50			
FCGR1A	(1)	MWFL	TLL	LW	VPVDG	-Q	VDTTKAVITLQPPWVS	VFQEETVTLHCEV	LHLP		
FCGR1A isoform X1	(1)	MWFL	TLL	LW	VPVDG	QV	VDTTKAVITLQPPWVS	VFQEETVTLHCEV	LHLP		
FCGR1A isoform X2	(1)	MWFL	TLL	LW	G	-	VDTTKAVITLQPPWVS	VFQEETVTLHCEV	LHLP		
FCGR1B isoform 1	(1)	MWFL	TLL	LW	VPVDG	-Q	VDTTKAVITLQPPWVS	VFQEETVTLHCEV	LHLP		
FCGR1B isoform 2	(1)	MWFL	TLL	LW	G	-	VDTTKAVITLQPPWVS	VFQEETVTLHCEV	LHLP		
FCGR1B isoform 3	(1)	MWFL	TLL	LW	VPVDG	-Q	VDTTKAVITLQPPWVS	VFQEETVTLHCEV	LHLP		
FCGR1B isoform X1	(1)	MWFL	TLL	LW	VPVDG	QV	VDTTKAVITLQPPWVS	VFQEETVTLHCEV	LHLP		
FCGR1B isoform X2	(1)	MWFL	TLL	LW	VPVDG	-	VDTTKAVITLQPPWVS	VFQEETVTLHCEV	LHLP		
Consensus	(1)	MWFL	TLL	LW	VPVDG		VDTTKAVITLQPPWVS	VFQEETVTLHCEV	LHLP		
		Section 2									
		(51)	51	60	70	80	90	100			
FCGR1A	(50)	GSSSTQWFL	NGTATQTST	PSYRITSASV	ND	SGEYRCQRGL	SGRSDP	IQLE			
FCGR1A isoform X1	(51)	GSSSTQWFL	NGTATQTST	PSYRITSASV	ND	SGEYRCQRGL	SGRSDP	IQLE			
FCGR1A isoform X2	(12)	-----	-----	-----	-----	-----	-----	-----			
FCGR1B isoform 1	(50)	GSSSTQWFL	NGTATQTST	PSYRITSASV	ND	SGEYRCQRGL	SGRSDP	IQLE			
FCGR1B isoform 2	(12)	-----	-----	-----	-----	-----	-----	-----			
FCGR1B isoform 3	(50)	GSSSTQWFL	NGTATQTST	PSYRITSASV	ND	SGEYRCQRGL	SGRSDP	IQLE			
FCGR1B isoform X1	(51)	GSSSTQWFL	NGTATQTST	PSYRITSASV	ND	SGEYRCQRGL	SGRSDP	IQLE			
FCGR1B isoform X2	(16)	-----	-----	-----	-----	-----	-----	-----			
Consensus	(51)	GSSSTQWFL	NGTATQTST	PSYRITSASV	ND	SGEYRCQRGL	SGRSDP	IQLE			
		Section 3									
		(101)	101	110	120	130	140	150			
FCGR1A	(100)	IHRG	WLL	LQVSSRV	ET	EGEPLALRCHAWK	DKLVYNVLY	YRNGKAF	KFFFW		
FCGR1A isoform X1	(101)	IHRG	WLL	LQVSSRV	ET	EGEPLALRCHAWK	DKLVYNVLY	YRNGKAF	KFFFW		
FCGR1A isoform X2	(12)	----	WLL	LQVSSRV	ET	EGEPLALRCHAWK	DKLVYNVLY	YRNGKAF	KFFFW		
FCGR1B isoform 1	(100)	IHRG	WLL	LQVSSRV	ET	EGEPLALRCHAWK	DKLVYNVLY	YRNGKAF	KFFFW		
FCGR1B isoform 2	(12)	----	WLL	LQVSSRV	ET	EGEPLALRCHAWK	DKLVYNVLY	YRNGKAF	KFFFW		
FCGR1B isoform 3	(100)	IHRG	WLL	LQVSSRV	ET	EGEPLALRCHAWK	DKLVYNVLY	YRNGKAF	KFFFW		
FCGR1B isoform X1	(101)	IHRG	WLL	LQVSSRV	ET	EGEPLALRCHAWK	DKLVYNVLY	YRNGKAF	KFFFW		
FCGR1B isoform X2	(16)	-QV	WLL	LQVSSRV	ET	EGEPLALRCHAWK	DKLVYNVLY	YRNGKAF	KFFFW		
Consensus	(101)	IHRG	WLL	LQVSSRV	ET	EGEPLALRCHAWK	DKLVYNVLY	YRNGKAF	KFFFW		
		Section 4									
		(151)	151	160	170	180	190	200			
FCGR1A	(150)	NSNLTIL	KTNISHNGTYH	CSGMGKHRYT	SAGIS	VT	VKELFP	PAPVLNAS	VT		
FCGR1A isoform X1	(151)	NSNLTIL	KTNISHNGTYH	CSGMGKHRYT	SAGIS	VT	VKELFP	PAPVLNAS	VT		
FCGR1A isoform X2	(58)	NSNLTIL	KTNISHNGTYH	CSGMGKHRYT	SAGIS	VT	VKELFP	PAPVLNAS	VT		
FCGR1B isoform 1	(150)	NSNLTIL	KTNISHNGTYH	CSGMGKHRYT	SAGIS	-----	-----	-----	-----		
FCGR1B isoform 2	(58)	NSNLTIL	KTNISHNGTYH	CSGMGKHRYT	SAGIS	-----	-----	-----	-----		
FCGR1B isoform 3	(150)	NSNLTIL	KTNISHNGTYH	CSGMGKHRYT	SAGIS	-----	-----	-----	-----		
FCGR1B isoform X1	(151)	NSNLTIL	KTNISHNGTYH	CSGMGKHRYT	SAGIS	-----	-----	-----	-----		
FCGR1B isoform X2	(65)	NSNLTIL	KTNISHNGTYH	CSGMGKHRYT	SAGIS	-----	-----	-----	-----		
Consensus	(151)	NSNLTIL	KTNISHNGTYH	CSGMGKHRYT	SAGIS	-----	-----	-----	-----		

Figure S11: The sequence alignment of proteins of FCGR1A and FCGR1B.

Table S1. Genomic locations of *FCGR1* genes.

Organisms	Gene Symbol	Chromosome	Location	Genome Assembly
Human	<i>FCGR1A</i>	1	149782071- 149792518	GRCh38.p13
Human	<i>FCGR1B</i>	1	121087345- 121097161	GRCh38.p13

Human	<i>FCGR1CP</i>	1	143874743- 143883733	GRCh38.p13
Mouse	<i>Fcgr1</i>	3	96282909- 96293969, complement	GRCm38.p6

References

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