

# APPENDIX A

A.1 Table 1: gRNA sequences targeting 12 cell surface proteins

ID	Gene symbol	Transcript	sgRNA sequence	Chr	Location
SLC4A1-sg1	SLC4A1	NM_000342	GGGTTTGCAGCTGCCCTG	17	42345519
SLC4A1-sg2	SLC4A1	NM_000342	GCCAGTGGGGCGGGCAGATT	17	42345561
SLC4A1-sg3	SLC4A1	NM_000342	AAGAGATAACTCTGTTTACT	17	42345629
SLC4A1-sg4	SLC4A1	NM_000342	ACTCACAGCTGTCCAGATGT	17	42345653
SLC4A1-sg5	SLC4A1	NM_000342	GACTCTTCCTTTGTGGATGA	17	42345743
SLC4A1-sg6	SLC4A1	NM_000342	GTTTGATCGCTCTGTCCTCA	17	42345765
SLC4A1-sg7	SLC4A1	NM_000342	GGGAACTGCTCAGCACTCAC	17	42345964
SLC4A1-sg8	SLC4A1	NM_000342	AGTCTGGATCAAGGAGGGGA	17	42346002
RHD-sg1	RHD	NM_001127691	GCCTGAGATAAGGCCTTTGG	1	25598918
RHD-sg2	RHD	NM_001127691	TCCGTGTAACTCCATAGAG	1	25598875
RHD-sg3	RHD	NM_001127691	GCACAGCAGGAACCTGTAAC	1	25598775
RHD-sg4	RHD	NM_001127691	GGATTATGTTGGGTGTCAA	1	25598727
RHD-sg5	RHD	NM_001127691	CATTGTTGTTAAGAGCTCAC	1	25598559
RHD-sg6	RHD	NM_001127691	GCCCTCTCTGTCATGTAGTA	1	25598584
RHD-sg7	RHD	NM_001127691	TGGTTGTGCTGGCCTCTCTA	1	25598890
RHD-sg8	RHD	NM_001127691	ATTTCAACTGTGTAACTATG	1	25598456

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P2RX7-sg1	P2RX7	NM_002562	GTTTATCACAGCCACATGTG	12	121570578
P2RX7-sg2	P2RX7	NM_002562	GGTGAGGTCATCTGCCAGCC	12	121570533
P2RX7-sg3	P2RX7	NM_002562	ACCATCTTTGTGTAGGCATC	12	121570496
P2RX7-sg4	P2RX7	NM_002562	GACCAAAAAAGTGAAAGGAA	12	121570433
P2RX7-sg5	P2RX7	NM_002562	CTCATGTCTCTTGGGAGAAA	12	121570414
P2RX7-sg6	P2RX7	NM_002562	AGTCCTTTTCTGAGGCATAA	12	121570355
P2RX7-sg7	P2RX7	NM_002562	AGCGCCAAGTCCTACGGGCC	12	121570554
P2RX7-sg8	P2RX7	NM_002562	GCATCTGGGGGAGGCCAGCT	12	121570511
ENG-sg1	ENG	NM_000118	CCACCCAGTGACAAAGCCCG	9	130617056
ENG-sg2	ENG	NM_000118	AGCCTTGGAGAGGGTGGGAT	9	130617155
ENG-sg3	ENG	NM_000118	GGCCCCCTGAAAGTTCCCCT	9	130617235
ENG-sg4	ENG	NM_000118	GGAACTACTTTAGCCAAGAC	9	130617256
ENG-sg5	ENG	NM_000118	ATGGGATCAGTGAGCTCAGG	9	130617294
ENG-sg6	ENG	NM_000118	AACCAGTGATCTCAACACAT	9	130617340
ENG-sg7	ENG	NM_000118	ATGCCCGACAAGACGTGAAG	9	130617400
ENG-sg8	ENG	NM_000118	GTCAACTGCACTTAGTAGGC	9	130617428
CD2-sg1	CD2	NM_001767	AGGAACTGAAGTGAGACTGG	1	117297049
CD2-sg2	CD2	NM_001767	GAGGCACGTGGTTAAGCTCT	1	117297013
CD2-sg3	CD2	NM_001767	ACTGTAAAAGATGTAAAGAG	1	117296994
CD2-sg4	CD2	NM_001767	GGCAAAGGAGCACATCAGAA	1	117296920
CD2-sg5	CD2	NM_001767	AATTCTCACACAAAAAAATT	1	117296857
CD2-sg6	CD2	NM_001767	ACTCATAAACACATCTGCTT	1	117296899
CD2-sg7	CD2	NM_001767	AGAGGCTAAGTAGATCACTA	1	117296792
CD2-sg8	CD2	NM_001767	AGTATACCTAAGTGGATAAA	1	117296725
VCAM1-sg1	VCAM1	NM_001078	CTTCCAAGACTATAAAATAC	1	101185088
VCAM1-sg2	VCAM1	NM_001078	TCCTCATCTTCGACTCCAAA	1	101185061
VCAM1-sg3	VCAM1	NM_001078	TATCTTTACTGGAAAGATAA	1	101185037
VCAM1-sg4	VCAM1	NM_001078	GAATCCAATGTGGGTAAAG	1	101184985
VCAM1-sg5	VCAM1	NM_001078	GAAGCTTTCTGAATCCAATG	1	101184995
VCAM1-sg6	VCAM1	NM_001078	TTCTACTCTGGTTTTTGAAC	1	101184929
VCAM1-sg7	VCAM1	NM_001078	TGAAGCTCCTCTCTGTCC	1	101185123
VCAM1-sg8	VCAM1	NM_001078	TGAAATTGCTGCCAAAACAA	1	101184660
PROM1-sg1	PROM1	NM_001145847	GACTGAGGCAGATCCCCACG	4	16085635
PROM1-sg2	PROM1	NM_001145847	ATCAGAGTGCGTCCAGGGCT	4	16085676
PROM1-sg3	PROM1	NM_001145847	GCGTTGCAAGAAGGGAGTGC	4	16085790
PROM1-sg4	PROM1	NM_001145847	ATTCTAAGTAAGGGACTCTG	4	16085830
PROM1-sg5	PROM1	NM_001145847	CAGAAGGGTCTAATGCGGCC	4	16085886
PROM1-sg6	PROM1	NM_001145847	GAGGCGCAAGCGTTGCAAGA	4	16085799
PROM1-sg7	PROM1	NM_001145849	GCAAGGCCTCCAGCCTAATC	4	16077832

PROM1-sg8	PROM1	NM_001145849	GCGTGTAAACTGCCTGCACC	4	16077776
SEMA7A-sg1	SEMA7A	NM_001146029	CGCTTGGGTCTGCCTGCGGC	15	74726312
SEMA7A-sg2	SEMA7A	NM_001146029	AGGCGAGAAAAGGCTGCGAG	15	74726380
SEMA7A-sg3	SEMA7A	NM_001146029	AGCGAGAGCGGAACTGCTGG	15	74726414
SEMA7A-sg4	SEMA7A	NM_001146029	GAACCTTCGCCACCCTCTCC	15	74726436
SEMA7A-sg5	SEMA7A	NM_001146029	GCTTTCCCCGTAGAGTTGCC	15	74726458
SEMA7A-sg6	SEMA7A	NM_001146029	AGTCTGGCTTGTCCGCAGCT	15	74726480
SEMA7A-sg7	SEMA7A	NM_001146029	GATTGGCGTAGAAGTCGTGG	15	74726575
SEMA7A-sg8	SEMA7A	NM_001146029	ACCTCTCTCCAAGGGCGCAG	15	74726598
CD200-sg1	CD200	NM_001004196	GACAGCCTCCGCTCCTGTGA	3	112051884
CD200-sg2	CD200	NM_001004196	GAGCGGAGGCTGTCTGTGTG	3	112051878
CD200-sg3	CD200	NM_005944	GAGAAAGGAAATGAGGTGGG	3	112051716
CD200-sg4	CD200	NM_001004196	CACTTTGTCAGTTTCCCAG	3	112051787
CD200-sg5	CD200	NM_001004196	AGCTCTTGATGTAGTGCCAA	3	112051667
CD200-sg6	CD200	NM_001004196	CAGTCCAGGTAGCAGGAAAA	3	112051735
CD200-sg7	CD200	NM_001004196	ATCCTCATCATTAATGCAAG	3	112051485
CD200-sg8	CD200	NM_001004196	AGAATTGATCACATCATGAA	3	112051526
ICAM1-sg1	ICAM1	NM_000201	ACTTAATAAACCGCTTAGCG	19	10381479
ICAM1-sg2	ICAM1	NM_000201	GAGGCCTGCGTAAGCTGGAG	19	10381346
ICAM1-sg3	ICAM1	NM_000201	ATAACAGTCTCCACTCTCCG	19	10381435
ICAM1-sg4	ICAM1	NM_000201	GTTCGGACCCCTCGCAGCC	19	10381379
ICAM1-sg5	ICAM1	NM_000201	GTCATCCACTCGATTAAAG	19	10381327
ICAM1-sg6	ICAM1	NM_000201	GGGAGCCCGGGGAGGATTCC	19	10381285
ICAM1-sg7	ICAM1	NM_000201	ACGTCCACACCTAGCTGACA	19	10381235
ICAM1-sg8	ICAM1	NM_000201	ATCCCTCAGTGGAGGGAGCC	19	10381272
SELE-sg1	SELE	NM_000450	AAGCAATCCCTCCTATAAAA	1	169703243
SELE-sg2	SELE	NM_000450	AATATCCTCCTATTATTCAC	1	169703266
SELE-sg3	SELE	NM_000450	ATTGTCCACATCCAGTAAAG	1	169703283
SELE-sg4	SELE	NM_000450	GAAAGTTTTTGGATGCCATT	1	169703314
SELE-sg5	SELE	NM_000450	GATATTCCC GGAAAGTTTT	1	169703325
SELE-sg6	SELE	NM_000450	GCATATACGATATAAAGGCA	1	169703410
SELE-sg7	SELE	NM_000450	ATTAGAATTTTCAGAAACAGA	1	169703548
SELE-sg8	SELE	NM_000450	GATTTCTCTTTACTGGATG	1	169703291
KEL-sg1	KEL	NM_000420	CAGCTTCTCAGGGGAGAAGA	7	142659512
KEL-sg2	KEL	NM_000420	GACCAAGGGCAAGATTGCTT	7	142659553
KEL-sg3	KEL	NM_000420	AATACAGAAGAAATGAGAGA	7	142659638
KEL-sg4	KEL	NM_000420	GGGAGCACCAGACCGACAA	7	142659723
KEL-sg5	KEL	NM_000420	ACACTAAACCTTTGTTCGGTC	7	142659734
KEL-sg6	KEL	NM_000420	GAGTCACAGTGCAAGACAAA	7	142659580

KEL-sg7	KEL	NM_000420	TTAGAAATAAAGGAACTTCA	7	142659606
KEL-sg8	KEL	NM_000420	GTCTTTGGCTTTGTTTGCCT	7	142660016

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## A.2 Table 2: PCR and sequencing primers, gblock sequences

Name	Sequence (5' - 3')
<b>p300 core domain gBlock sequences</b>	
C-terminal insertion 5' fragment 1 (replace VP64)	aagaggaaggtggcgggaggtggaagcggaggaATTTTCAAACCAGAA GAACTACGACAGGCACTGATGCCAACTTTGGAGGCAC TTTACCGTCAGGATCCAGAATCCCTTCCCTTTCGTCAA CCTGTGGACCCTCAGCTTTTAGGAATCCCTGATTACTTT GATATTGTGAAGAGCCCCATGGATCTTTCTACCATTAA GAGGAAGTTAGACACTGGACAGTATCAGGAGCCCTGG CAGTATGTCGATGATATTTGGCTTATGTTCAATAATGC CTGGTTATATAACCGGAAAACATCACGGGTATACAAA TACTGCTCCAAGCTCTCTGAGGTCTTTGAACAAGAAAT TGACCCAGTGATGCAAAGCCTTGGATACTGTTGTGGCA GAAAGTTGGAGTTCTCTCCACAGACACTGTGTTGCTAC GGCAAACAGTTGTGCACAATACCTCGTGATGCCACTTA TTACAGTTACCAGAACAGGTATCATTTCTGTGAGAAGT GTTTCAATGAGATCCAAGGGGAGAGCGTTTCTTTGGGG GATGACC
C-terminal insertion 5' fragment 2 (after VP64)	gacctggacatgctgggaggtggaagcggaggaggaggtggaagcggaggaATTT TCAAACCAGAAGAACTACGACAGGCACTGATGCCAAC TTTGGAGGCACTTTACCGTCAGGATCCAGAATCCCTTC CCTTTCGTCAACCTGTGGACCCTCAGCTTTTAGGAATC CCTGATTACTTTGATATTGTGAAGAGCCCCATGGATCT TTCTACCATTAAGAGGAAGTTAGACACTGGACAGTATC AGGAGCCCTGGCAGTATGTCGATGATATTTGGCTTATG TTCAATAATGCCTGGTTATATAACCGGAAAACATCACG GGTATACAAATACTGCTCCAAGCTCTCTGAGGTCTTTG AACAAGAAATTGACCCAGTGATGCAAAGCCTTGGATA CTGTTGTGGCAGAAAGTTGGAGTTCTCTCCACAGACAC TGTGTTGCTACGGCAAACAGTTGTGCACAATACCTCGT GATGCCACTTATTACAGTTACCAGAACAGGTATCATTT CTGTGAGAAGTGTTTCAATGAGATCCAAGGGGAGAGC GTTTCTTTGGGGGATGACC

C-terminal insertion  
common 3' fragment

TCTTTGGGGGATGACCCTTCCCAGCCTCAAACCTACAAT  
AAATAAAGAACAATTTTCCAAGAGAAAAAATGACACA  
CTGGATCCTGAACTGTTTGTGAATGTACAGAGTGCGG  
AAGAAAGATGCATCAGATCTGTGTCCTTCACCATGAGA  
TCATCTGGCCTGCTGGATTCGTCTGTGATGGCTGTTTA  
AAGAAAAGTGCACGAACTAGGAAAGAAAATAAGTTTT  
CTGCTAAAAGGTTGCCATCTACCAGACTTGGCACCTTT  
CTTGAGAATCGTGTGAATGACTTTCTGAGGCGACAGAA  
TCACCCTGAGTCAGGAGAGGTCAGTGTAGAGTAGTTC  
ATGCTTCTGACAAAACCGTGGAAGTAAAACCAGGCAT  
GAAAGCAAGGTTTGTGGACAGTGGAGAGATGGCAGAA  
TCCTTTCCATACCGAACCAAAGCCCTCTTTGCCTTTGA  
AGAAATTGATGGTGTGACCTGTGCTTCTTTGGCATGC  
ATGTTCAAGAGTATGGCTCTGACTGCCCTCCACCCAAC  
CAGAGGAGAGTATACATATCTTACCTCGATAGTGTTC  
TTTCTTCCGTCCTAAATGCTTGAGGACTGCAGTCTATC  
ATGAAATCCTAATTGGATATTTAGAATATGTCAAGAAA  
TTAGGTTACACAACAGGGCATATTTGGGCATGTCCACC  
AAGTGAGGGAGATGATTATATCTTCCATTGCCATCCTC  
CTGACCAGAAGATACCCAAGCCCAAGCGACTGCAGGA  
ATGGTACAAAAAATGCTTGACAAGGCTGTATCAGAG  
CGTATTGTCCATGACTACAAGGATATTTTTAAACAAGC  
TACTGAAGATAGATTAACAAGTGCAAAGGAATTGCCT  
TATTTTCGAGGGTGATTTCTGGCCCAATGTTCTGGAAGA  
AAGCATTAAAGAACTGGAACAGGAGGAAGAAGAGAG  
AAAACGAGAGGAAAACACCAGCAATGAAAGCACAGA  
TGTGACCAAGGGAGACAGCAAAAATGCTAAAAAGAAG  
AATAATAAGAAAACCAGCAAAAATAAGAGCAGCCTGA  
GTAGGGGCAACAAGAAGAAACCCGGGATGCCCAATGT  
ATCTAACGACCTCTCACAGAACTATATGCCACCATGG  
AGAAGCATAAAGAGGTCTTCTTTGTGATCCGCCTCATT  
GCTGGCCCTGCTGCCAACTCCCTGCCTCCCATTGTTGA  
TCCTGATCCTCTCATCCCCTGCGATCTGATGGATGGTC  
GGGATGCGTTTCTCACGCTGGCAAGGGACAAGCACCT  
GGAGTTCTTCTACTCCGAAGAGCCCAGTGGTCCACCA  
TGTGCATGCTGGTGGAGCTGCACACGCAGAGCCAGGA  
CGAGGGCAGAGGAAGTCTCCTAACATGCGGTGACGTG  
GAGGAGAATCCTGGCCCAaggaggtatggcttcaactttactcagtTCT  
AGAtgtctcctGTACATGAGgaattccgatatcaagcttatcgg

p300 core full

tcgtggGAAGCTTGGggccaccatgATTTTCAAACCAGAAGAA  
CTACGACAGGCACTGATGCCAACTTTGGAGGCACTTTA  
CCGTCAGGATCCAGAATCCCTTCCCTTTTCGTCAACCTG  
TGGACCCTCAGCTTTTAGGAATCCCTGATTACTTTGAT  
ATTGTGAAGAGCCCCATGGATCTTTCTACCATTAAGAG  
GAAGTTAGACACTGGACAGTATCAGGAGCCCTGGCAG  
TATGTCGATGATATTTGGCTTATGTTCAATAATGCCTG  
GTTATATAACCGGAAAACATCACGGGTATACAAATAC  
TGCTCCAAGCTCTCTGAGGTCTTTGAACAAGAAATTGA  
CCCAGTGATGCAAAGCCTTGGATACTGTTGTGGCAGAA  
AGTTGGAGTTCTCTCCACAGACACTGTGTTGCTACGGC  
AAACAGTTGTGCACAATACCTCGTGATGCCACTTATTA  
CAGTTACCAGAACAGGTATCATTCTGTGAGAAGTGTT  
TCAATGAGATCCAAGGGGAGAGCGTTTCTTTGGGGGA  
TGACCCTTCCAGCCTCAAACACTACAATAAATAAAGAA  
CAATTTTCCAAGAGAAAAAATGACACACTGGATCCTG  
AACTGTTTGTGAAATGTACAGAGTGCGGAAGAAAGAT  
GCATCAGATCTGTGTCCTTCACCATGAGATCATCTGGC  
CTGCTGGATTCGTCTGTGATGGCTGTTTAAAGAAAAGT  
GCACGAACTAGGAAAGAAAATAAGTTTTCTGCTAAAA  
GGTTGCCATCTACCAGACTTGGCACCTTTCTAGAGAAT  
CGTGTGAATGACTTTCTGAGGCGACAGAATCACCTGA  
GTCAGGAGAGGTCACTGTTAGAGTAGTTCATGCTTCTG  
ACAAAACCGTGGAAGTAAAACCAGGCATGAAAGCAAG  
GTTTGTGGACAGTGGAGAGATGGCAGAATCCTTTCCAT  
ACCGAACCAAAGCCCTCTTTGCCTTTGAAGAAATTGAT  
GGTGTGACCTGTGCTTCTTTGGCATGCATGTTCAAGA  
GTATGGCTCTGACTGCCCTCCACCCAACCAGAGGAGA  
GTATACATATCTTACCTCGATAGTGTTCAATTTCTTCCGT  
CCTAAATGCTTGAGGACTGCAGTCTATCATGAAATCCT  
AATTGGATATTTAGAATATGTCAAGAAATTAGGTTACA  
CAACAGGGCATATTTGGGCATGTCCACCAAGTGAGGG  
AGATGATTATATCTTCCATTGCCATCCTCCTGACCAGA  
AGATACCCAAGCCCAAGCGACTGCAGGAATGGTACAA  
AAAAATGCTTGACAAGGCTGTATCAGAGCGTATTGTCC  
ATGACTACAAGGATATTTTTAAACAAGCTACTGAAGAT  
AGATTAACAAGTGCAAAGGAATTGCCTTATTTTCGAGG  
GTGATTTCTGGCCCAATGTTCTGGAAGAAAGCATTAAAG  
GAACTGGAACAGGAGGAAGAAGAGAGAAAACGAGAG  
GAAAACACCAGCAATGAAAGCACAGATGTGACCAAGG  
GAGACAGCAAAAATGCTAAAAAGAAGAATAATAAGA  
AAACCAGCAAAAATAAGAGCAGCCTGAGTAGGGGCAA  
CAAGAAGAAACCCGGGATGCCCAATGTATCTAACGAC  
CTCTCACAGAACTATATGCCACCATGGAGAAGCATA  
AAGAGGTCTTCTTTGTGATCCGCCTCATTTGCTGGCCCT

**PCR primers for VP64 amplification**

VP64 Forward	TCGTGGGAAGCTTGGGGCCACCATGGACGCATTGGAC
VP64 Reverse	TCATGGTGGCCGTACATCCAGAACCTCCACCCAGCATGTCCAGGTC

**Sequencing primers for dCas9-activator constructs**

p300 F1	TGCCTCCCATTGTTGATCCT
p300 F2	TTGTGAAGAGCCCCATGGAT
p300 F3	CCCTTCCCAGCCTCAAATA
p300 F4	TGCTTCTGACAAAACCGTGG
N term dCas9 F1	TCTCAAGCCTCAGACAGTGG
N term dCas9 R1	TGTACTCGTCGGTGATCACG
C term dCas9 F1	ACTTTGACACCACCATCGAC
C term dCas9 R1	CGTCACCGCATGTTAGGAGA
post T2A F1	AGTCTCCTAACATGCGGTGA
post T2A R1	CACACCGGCCTTATTCCAAG

**Primers for initial amplification of gRNA library**

77-mer_U1	GCAGATGGCTCTTTGTCCTA
77-mer_L1	GCGACGAGAAGACTAAAAC

**Primers for q-RT-PCR**

SLC4A1 F	GGGCTCAGATCACCGTAGAC
SLC4A1 R	AGGAGGACAGTACCCTTGGT
RHD F	AGGATCAAAAGGGGCTCGTG
RHD R	TGTTTCATGTGGTAGTCTGTGTTG
SELE F	GCCTGCAATGTGGTTGAGTG
SELE R	ATTCATGTAGCCTCGCTCGG
KEL F	CTGATAAGCAGGCTCCACCC
KEL R	CTGGAGTGCTCTCTTGGCTC

**Primers for amplification of RTN4R family ectodomains**

RTN4R F	CCAAGTTTAAACTGCGGCCGCCACCATGAAGAGGGCGTCCGCTG
RTN4R R	TGGAGGTCGACGGCGCGGGCGCGCCTGAGCCTTCTGAGTCACCAG
RTN4RL1 F	CCAAGTTTAAACTGCGGCCGCCACCATGCTTCGCAAAGGGTGCT
RTN4RL1 R	TGGAGGTCGACGGCGCGGGCGCGCCGCTGGGGGACAG
RTN4RL2 F	CCAAGTTTAAACTGCGGCCGCCACCATGCTGCCCGGGCTCA
RTN4RL2 R	TGGAGGTCGACGGCGCGGGCGCGCCGAGTCCGGGGGCGCCTGG



**Primers for Illumina library preparation and sequencing****First PCR**

SAMlibrary-	ACACTCTTTCCCTACACGACGCTCTTCCGATATATCTTG
HiSeq_50bp-F1	TGGAAAGGACGAAACA
SAMlibrary-	TCGGCATTCCCTGCTGAACCGCTCTTCCGATCTCAGACT
HiSeq_50bp-R1	GCCTTGGGAAAAG

**Second PCR**

HiSeq-PE 1.0	AATGATACGGCGACCACCGAGATCTACACTCTTTCCCT ACACGACGCTCTTCCGATC*T
HiSeq-iPCRTag- 11mer	CAAGCAGAAGACGGCATACGAGATNNNNNNNNNNNG AGATCGGTCTCGGCATTCCTGCTGAACCGCTCTCCGA TC*T

\* indicates phosphorothioate

**Sequencing primer**

U6-SAMlibrary-	TATATCTTGTGGAAAGGACGAAACACCG
Illumina-seq (19bp- SE)	

## A.3 Table 3: Primary and secondary antibodies

**Primary monoclonal antibodies**

Clone	Source	Cat No.	Antigen gene symbol	Antigen gene name
BRAC18	IBGRL		SLC4A1	Solute Carrier Family 4 Member 1
BRAD2	IBGRL		RHD	Rh blood group D antigen
BRIC18	IBGRL		KEL	Kell blood group glycoprotein
P2X7-L4	DSHB		P2RX7	P2X purinoceptor 7
P3D1	DSHB		ENG	Endoglin
TS2/18.1.1	DSHB		CD2	Cluster of differentiation 2
P3C4	DSHB		VCAM1	Vascular cell adhesion molecule 1
HB#7/HC7	DSHB		PROM1	Prominin 1
MEM-150	Abcam	ab26012	SEMA7A	Semaphorin 7A
OX-104	Bioline	329202	CD200	Cluster of differentiation 200
P2A4	DSHB		ICAM1	Intercellular Adhesion Molecule 1
1.2B6	Santa Cruz	sc-18852	SELE	E-selectin
OX68	from hybridoma		rCD4 (d3/4)	Rat CD4 (Domains 3 and 4)
LM609	Merck Millipore	MAB1976	avb3	Integrin avb3

IBGRL - International Blood Group Reference Laboratory

DSHB - Developmental Studies Hybridoma Bank

**Secondary antibodies and other flow cytometry reagents**

<b>Antibody description</b>	<b>Source</b>	<b>Cat No.</b>
anti-mouse-PE	Abcam	ab7002
anti-mouse-AP	Sigma Aldrich	A4656
Streptavidin-PE	Biolegend	405204
Annexin V-FITC	eBioscience	BMS306F1

