

SUPPLEMENTAL TABLES

Supplemental Table 1: Characteristics of peripheral blood prior to electrotransfer of SB plasmids and numeric expansion on γ -irradiated AaPC and cytokines

P#	Auto or Allo	Day 0 (Day of electroporation)					
		WBC [K/mL]	ALC [K/mL]	CD3 (ATC) [% & K/mL]	CD4 [% & K/mL]	CD8 [% & K/mL]	ABC [% & K/mL]
P446	Auto	5.4	1.46	81% 1.18	60% 0.88	19% 0.28	ND
P458	Auto	9	0.27	23% 0.06	17% 0.05	2% 0.005	ND
P468	Auto	4.7	0.9	17% 0.15	12% 0.11	5% 0.04	ND
P471	Auto	11.4	0.93	47% 0.44	35% 0.32	5% 0.04	ND
P509	Auto	7.2	1.46	78% 1.14	67% 0.98	9% 0.13	ND
P747	Auto	6.1	1.38	82% 1.13	47% 0.65	32% 0.44	0
P708	Auto	4.6	2.78	88% 2.45	44% 1.22	47% 1.31	0% 0.05
P396	Allo	8.1	1.54	58% 0.89	47% 0.72	20% 0.31	21% 1.7
P410	Allo	5.9	2.81	70% 1.97	31% 0.87	32% 0.90	ND
P411	Allo	4.5	1.72	80% 1.38	48% 0.83	32% 0.55	ND
P513	Allo	6.7	2.27	41% 0.93	24% 0.54	15% 0.34	ND
P580	Allo	6.1	2.1	86% 1.81	68% 1.43	15% 0.32	5% 0.29
P459	Allo	10.6	2.29	82% 1.88	51% 1.17	28% 0.64	ND
P564	Allo	4.4	1.3	64% 0.83	52% 0.68	12% 0.16	18% 0.81
P617	Allo	7.1	1.55	82% 1.27	61% 0.94	17% 0.26	8% 0.58
P671	Allo	5.4	1.7	78% 1.33	53% 0.90	24% 0.41	3% 0.17
P723	Allo	8.6	2.61	69% 1.80	50% 1.30	20% 0.52	7% 0.59
P732	Allo	6.7	1.68	78% 1.31	52% 0.87	22% 0.37	6% 0.39
P641	Allo	9.0	2.13	74% 1.58	57% 1.21	15% 0.32	9% 0.78
P647	Allo	12.1	2.29	73% 1.67	54% 1.24	18% 0.41	9% 1.11

P716	Allo	3.0	1.83	75% 1.37	59% 1.08	11% 0.20	0
P718	Allo	6.2	1.99	87% 1.73	73% 1.45	12% 0.24	1% 0.07
P771	Allo	13.1	3.23	83% 2.68	69% 2.23	13% 0.42	6% 0.79
P783	Allo	8.1	1.54	73% 1.12	42% 0.65	27% 0.42	6% 0.52

WBC = white blood cell count (automated complete blood counts)

ALC = absolute lymphocyte count (automated complete blood counts)

ATC = absolute T-cell count (ALC x %CD3)

CD4 & CD8 = ALC x %(CD4 or CD8)

ABC = absolute B-cell count (ALC x %CD19)

ND = not detected

% CD3, %CD4, %CD8 and %CD19 (ABC) were calculated from lymphocyte gate (FSC/SSC) using flow cytometry

Supplemental Table 2: Characterization of T cells during and after SB electrotransfer and expansion on AaPC/cytokines

UPN	Auto or Allo	Day 1 after electroporation (%)*		Day 7 of co-culture (%)		Day 14 of co-culture (%)		Day 21 of co-culture (%)		Day 28 of co-culture (%)				**CD56 depletion	SB11 PCR				G-banding Karyotype
		CD3	CAR	CD3	CAR	CD3	CAR	CD3	CAR	CD3	CAR	CD4	CD8		GAPDH Control	Day 14	Day 21	Day 28	
P446	Auto	83	67	79	43	99	65	99	85	99	88	6	95	Days 7, 10	+			-	Normal
P458	Auto	48	47	87	44	99	93	99	85	99	77	38	47	Day 9	+			-	Normal
P468	Auto	61	38	86	34	97	79	97	69	98	86	1	91	Day 10	+			-	Normal
P471	Auto	84	38	75	34	99	53	99	89	99	96	7	87	None	+			-	Normal
P509	Auto	90	38	79	57	97	85	99	87	99	96	10	84	None	+			-	Normal
P747	Auto	90	75	96	26	80	40	97	79	99	88	3	86	Day 15	+		+	-	ND
P708	Auto	78	87	73	18	86	46	99	78	100	91	3	95	Days 7, 14	+			-	ND
P396	Allo	84	55	92	78	97	86	99	88	99	97	3	97	None	+			-	Normal
P410	Allo	61	48	88	54	94	70	98	84	99	90	4	92	None	+			-	Normal
P411	Allo	85	49	61	59	81	54	85	60	99	71	42	52	Day 7	+			-	Normal
P513	Allo	83	29	69	26	99	86	99	92	99	88	1	96	None	+			-	ND
P580	Allo	79	77	95	54	97	78	97	66	99	70	12	85	Day 14	+			-	ND
P459	Allo	91	40	93	39	96	81	98	95	99	91	30	64	None	+			-	Normal
P564	Allo	74	67	84	40	79	93	99	92	99	91	6	92	Day 14	+			-	ND
P617	Allo	93	77	68	20	94	50	97	61	99	67	3	64	Day 7	+			-	ND
P671	Allo	86	82	NA	NA	81	45	98	81	100	95	8	91	Day 11	+			-	ND
P723	Allo	85	61	84	54	97	34	97	26	95	47	10	71	Day 14	+		+	-	ND
P732	Allo	76	66	93	50	93	29	96	68	98	84	11	75	None	+		-	-	ND
P641	Allo	87	80	46	32	95	60	92	72	96	75	13	70	None	+		-	-	ND
P647	Allo	79	76	62	27	80	56	99	82	99	87	27	72	Days 7, 14	+		-	-	ND
P716	Allo	13	15	44	33	98	84	99	73	97	65	6	91	Day 7	+			-	ND
P718	Allo	90	77	87	34	87	57	99	65	99	92	14	75	Day 14	+		+	-	ND

P771	Allo	83	75	84	45	98	71	97	75	97	93	31	66	Day 15	+		+	-	ND
P783	Allo	33	38	86	51	98	68	99	78	99	94	4	92	Day 15	+		+	-	ND

*Day of electroporation, defined as Day 0

**Day of culture

ND=Not done

Supplemental Table 3: Genes measured using digital bar-coded probes (for nCounter Analysis

System)

CODESET DETAILS			
Gene	Accession	Target Region	Target Sequence
ABCB1	NM_0009 27.3	3911- 4010	TATAGCACTAAAGTAGGAGACAAAGGAACTCAGCTCTCTGGTGGCCAGAAACAACG CATTGCCATAGCTCGTGCCCTTGTTAGACAGCCTCATATTTTGC
ABCG2	NM_0048 27.2	286-385	AGGATTTAGGAACGCACCGTGCACATGCTTGGTGGTCTTGTTAAGTGGAACTGCTG CTTTAGAGTTTGTGGGAAGGTCCGGGTGACTCATCCCAACAT
CCR10	NM_0012 96.3	1346- 1445	GAACAGATGGGAACCAGCTCAATTGGGTGTCCACTCAAAGTGCTCTCTCCAGGGGCC TCAGTGACTGTGTTGCTAAACCCAGTGGTCAGTTCTCAGTTCT
ACTB	NM_0011 01.2	1011- 1110	TGCAGAAGGAGATCACTGCCCTGGCACCCAGCACAAATGAAGATCAAGATCATTGCTC CTCCTGAGCGCAAGTACTCCGTGTGGATCGGCGGCTCCATCCT
ADAM19	NM_0230 38.3	1691- 1790	GAGAAGGTGAATGTGGCAGGAGACACCTTTGGAACTGTGGAAAGGACATGAATG GTGAACACAGGAAGTGCAACATGAGAGATGCGAAGTGTGGGAAGA
AGER	NM_0011 36.3	341-440	GAAAGGAGACCAAGTCCAACCTACCGAGTCCGTGTCTACCAGATTCTGGGAAGCCAG AAATTGTAGATTCTGCCTCTGAACTCACGGCTGGTGTTCCTCAA
AHNAK	NM_0016 20.1	15421- 15520	GGATTTGACCTGAATGTTCTGGGGGTGAAATTGATGCCAGCCTCAAGGCTCCGGAT GTAGATGTCAACATCGCAGGGCCGGATGCTGCACTCAAAGTCG
AIF1	NM_0329 55.1	316-415	AAAAGCGAGAGAAAAGGAAAAGCCAACAGGCCCCCCAGCCAAGAAAGCTATCTCTG AGTTGCCCTGATTTGAAGGGAAAAGGGATGATGGGATTGAAGGG
AIM2	NM_0048 33.1	608-707	ACGTGCTGCACAAAAGTCTCTCCTCATGTTAAGCCTGAACAGAAACAGATGGTGGC CCAGCAGGAATCTATCAGAGAAGGGTTTCAGAAGCGCTGTTTG
p38	NM_0063 03.3	508-607	CCCTCTCCCTGCTTGTGCTGCACAGGCTGCTCTGTGAGCACTTCAGGGTCTGTCCAC GGTGCACACGCACTCCTCGGTCAAGAGCGTGCCTGAAAACCT
C11ORF17	NM_0206 42.3	571-670	GAACATCTTAAGGACCTCTACATAGAAGTATATCCAGGGACCTATTCTGCACTGTG GGCTCAAATGACTTAACCAAGAAGACTCATGTGGTAGCAGTT
AKT1	NM_0051 63.2	1773- 1872	TTCTTTGCCGGTATCGTGTGGCAGCACGTGTACGAGAAGAAGCTCAGCCCACCTTC AAGCCCCAGGTCAGTTCGGAGACTGACACCAGGTATTTTGATG
ALDH1A1	NM_0006 89.4	277-376	TTGCTGAGCCAGTCACCTGTGTTCCAGGAGCCGAATCAGAAATGTCATCCTCAGGCA CGCCAGACTTACCTGTCTACTACCGATTTGAAGATTCAATA
ANXA1	NM_0007 00.1	516-615	GAAATCAGAGACATTAACAGGGTCTACAGAGAGGAACTGAAGAGAGATCTGGCCAA AGACATAACCTCAGACACATCTGGAGATTTTCGGAACGCTTTGC
ANXA2P2	NR_00357 3.1	258-357	ATATTGTCTTCTCTACCAGAGAAGGACCAAAAAGGAACTGCATCAGCACTGAAGT CAGCCTTATCTGGCCACCTGGAGACGGTGATTTTGGGCCTATT
Apaf1	NM_1818 69.1	1161- 1260	TTCTGATGAACTGCAGAATCTTTGCACACGGTTGGATCAGGATGAGAGTTTTTCCA GAGGCTTCCACTTAATATTGAAGAGGCTAAAGACCGTCTCCG
aqp9	NM_0209 80.3	1503- 1602	TCATCCTCGATGGGAATTCTTGCTAGGTAAGCACTAATAACTCGGCATCTTGACGATA GTCCCATTTGGGTGGTTTCAGCTGCACTATCTGTATGAAATG
ARG1	NM_0000 45.2	506-605	AAGGAACTAAAAGGAAAGATTCCCAGTGTGCCAGGATTCTCTGGGTGACTCCCTGT ATATCTGCCAAGGATATTGTGTATATTGGCTTGAGAGACGTGG
Arntl	NM_0010 30272.1	841-940	GATGTGACCGAGGGAAGATACTCTTTGTCTCAGAGTCTGTCTTCAAGATCCTCAACTA CAGCCAGAATGATCTGATTGGTCAGAGTTTGTGTTGACTACCT
Beta-arrestin (ARRB2 and ARRB2)	NM_0043 13.3	1653- 1752	CATTAATTTTTTACTGCTGCTTCTCCAGCCCCGCGTGGGTGGCAAGCTGTG TTCATACCTAAATTTCTGGAAGGGGACAGTGAAAAGAGGAG
ATF3	NM_0010	601-700	GGCTCAGAATGGGAGGACTCCAGAAGATGAGAGAAACCTCTTTATCCAACAGATAA

	30287.2		AAGAAGGAACATTGCAGAGCTAAGCAGTCGTGGTATGGGGGCGA
ATM	NM_0000 51.3	31-130	ACGCTAAGTCGCTGGCCATTGGTGGACATGGCGCAGGCGGTTTGTCCGACGGGC CGAATGTTTTGGGGCAGTGTGTTGAGCGCGGAGACCGCGTGATA
atn1	NM_0010 07026.1	2857- 2956	CCCTACCTGGGTCTGACACTCCAGCCTTGCGCACTCTCAGTGAATATGCCCGGCCTC ATGTCATGTCTCCTGGCAATCGCAACCATCCATTCTACGTGC
ATP2B4	NM_0016 84.3	7641- 7740	CTTCCCATAGTATCATCTGTCTCTGGAATGACTCTCTGTCCCTAAAGGGGTTAAGA GAGAGATCACCTAGAAATCCCTCTGGACACTTGTGGGTTCTT
Axin2	NM_0046 55.3	1036- 1135	CTTGTCCAGCAAACTCTGAGGGCCACGGCGAGTGTGAGTCCACGGAACTGTTG ACAGTGGATACAGGTCCTTCAAGAGGAGCGATCCTGTTAATCCT
B2M	NM_0040 48.2	236-335	TACTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCATTCCAGACTTGTCTTTCAGCA AGGACTGGTCTTTCTATCTCTTGTACTACACTGAATTCACCCC
CD57/B3GA T1	NM_0186 44.3	146-245	CTGGACAGCGACCCCTTCTCAGACTCCAGTTGGGCCGGACTCTCAAACCTGCTCCG CAATGGGTGGGTTGTGAGTGTGGTAATGAGGAGCCGTGGGT
BACH2	NM_0218 13.2	3396- 3495	TGTGGCACTGTTTCATCTGCTGTCCCAGAAACCGAGAACACATTTGGTGCACACTA CAGCGGTCTTAGCAGCAATACTGTTCCGAAGTATCCTCTCCTC
BAD	NM_0043 22.2	196-295	CAGCTGTGCCTTGACTACGTAACATCTTGTCTCACAGCCCAGAGCATGTTCCAGATC CCAGAGTTTGAGCCGAGTGAGCAGGAAGACTCCAGCTCTGCA
RAP46	NM_0043 23.3	1491- 1590	CTCTTGATCGTGTAGTCCCATAGCTGTAAAACCAGAATCACCAGGAGGTTGCACCT AGTCAGGAATATTGGGAATGGCCTAGAACAAGGTGTTTGGCA
BATF	NM_0063 99.3	294-393	CCTGGCAAACAGGACTCATCTGATGATGTGAGAAGAGTTCAGAGGAGGGAGAAAAA TCGATTGCCGCCAGAAGAGCCGACAGAGGCAGACACAGAAGG
BAX	NM_1387 61.2	695-794	ATTTTTCTGGGAGGGGTGGGGATTGGGGACATGGGCATTTTTCTACTTTTGTAAAT ATTGGGGGGTGTGGGGAAGAGTGGTCTTGAGGGGGTAATAAA
BCL10	NM_0039 21.2	1251- 1350	TGAAAATACCATCTTCTCTTCAACTACACTCCCAGACCTGGGGACCCAGGGGCTCCT CCTTGGCCACCAGATCTACAGTTAGAAGAAGAAGGAAGTGT
Bcl11b	NM_0228 98.1	3421- 3520	GAGATGTAGCACTCATGTCTCCGAGTCAAGCGGCCTTTTCTGTGTTGATTCGGCT TTCATATTACATAAGGGAAACCTTGAGTGGTGGTGTCTGGGGG
Bcl2	NM_0006 33.2	1526- 1625	CCAAGCACCGCTTCGTGTGGCTCCACCTGGATGTTCTGTGCCTGTAAACATAGATTCCG CTTCCATGTTGTTGGCCGGATCACCATCTGAAGAGCAGACG
BCL2L1	NM_1385 78.1	1561- 1660	CTAAGAGCCATTTAGGGGCCACTTTTACTAGGGATTAGGCTGCTGGGATAAAGA TGCAAGGACCAGGACTCCCTCCTCACCTCTGGACTGGCTAGAG
BCLxL	NM_0011 91.2	261-360	ATCTTGGCTTTGGATCTTAGAAGAGAATCACTAACCAGAGACGAGACTCAGTGAGTG AGCAGGTGTTTTGGACAATGGACTGGTTGAGCCCATCCCTATT
BCL2L11	NM_1386 21.2	2826- 2925	TGTTGGCACCAGAACTTAAAGCGATGACTGGATGTCTCTGTACTGTATGTATCTGGTT ATCAAGATGCCTCTGTGCAGAAAGTATGCCTCCCGTGGGTAT
Bim	NM_1386 21.4	258-357	CGGACTGAGAAACGCAAGAAAAAAGACCAAATGGCAAAGCAACCTTCTGATGTAA GTTCTGAGTGTGACCGAGAAGGTAGACAATTGCAGCCTGCGGAG
Bcl6	NM_0017 06.2	676-775	GTTGTGGCACTTGCCGGAAGTTTATTAAGGCCAGTGAAGCAGAGATGGTTTCTGCC ATCAAGCCTCCTCGTGAAGAGTTCCTCAACAGCCGGATGCTGA
Bcl6b	NM_1818 44.3	2136- 2235	CTTTATTTGTTCTAGGGCAGCTCTGGGAACATGCGGGATTGTGGAATTGGGTCAGGA ACCCTCTCTGGTATTCTGGATGTTGTAGGTTCTCTAGCAGTCT
BHLHE41	NM_0307 62.2	656-755	CGCCCATTCAGTCCGACTTGGATGCGTTCCTCGGGATTTCAAACATGCGCCAAAG AAGTCTTGCAATACCTCTCCCGGTTTGGAGAGCTGGACACCCAG
BID	NM_1979 66.1	2096- 2195	GCTTAGCTTTAGAAACAGTGAACAACACTGGTCTGCTGTTCCAGTGGTAAGCTATGTCCC AGGAATCAGTTTAAAAGCACGACAGTGGATGCTGGGTCCATA
BIRC2	NM_0011 66.3	1761- 1860	TGGGATCCACCTCTAAGAATACGTCTCCAATGAGAAACAGTTTTGCACATTCATTATC TCCACCTTGGAAACATAGTAGCTTGTTCAGTGGTTCTTACTC
Blk	NM_0017 15.2	991-1090	AGCTTCTTGCTCCAATCAACAAGGCCGGCTCCTTTCTTATCAGAGAGAGTGAAACCAA CAAAGGTGCCTTCTCCCTGTCTGTGAAGGATGTCACCACCCA
BMI1	NM_0051 80.5	1146- 1245	CCTGGAGAAGGAATGGTCCACTTCCATTGAAATACAGAGTTCGACCTACTTGTAAAA GAATGAAGATCAGTCACCAGAGAGATGGACTGACAAATGCTGG
BNIP3	NM_0040	326-425	CACCTCGCTCGCAGACACCACAAGATACCAACAGGGCTTCTGAAACAGATACCCATA

	52.2		GCATTGGAGAGAAAAACAGCTCACAGTCTGAGGAAGATGATAT
BTLA	NM_0010 85357.1	891-990	GCACCAACAGAATATGCATCCATATGTGTGAGGAGTTAAGTCTGTTTCTGACTCCAAC AGGGACCATTGAATGATCAGCATGTTGACATCATTGTCTGGG
HES1	NM_0046 49.5	1341- 1440	TTGAGTTAATCAGCGTAAGGGGATTTCTAAAGCAGGCAATCCCTGTAGCCGCAGAGA ATAAACGCCTTCCCAAATGGCAACTTCCACAGCCACATTTT
Car2	NM_0000 67.2	576-675	AGCTGTGCAGCAACCTGATGGACTGGCCGTTCTAGGTATTTTTTTGAAGGTTGGCAG CGCTAAACCGGGCCTTCAGAAAGTTGTTGATGTGCTGGATTCC
CA9	NM_0012 16.2	961-1060	CAGGTCCCAGGACTGGACATATCTGCACTCCTGCCCTCTGACTTCAGCCGCTACTTCC AATATGAGGGGTCTCTGACTACACCGCCCTGTGCCAGGGTG
Caspase 9	NM_0528 13.2	1851- 1950	CGCTGACTTGGCCTGGAACGAGGAATCTGGTGCCTGAAAGGCCAGCCGGACTGC CGGGCATTGGGGCCGTTTGTAAAGCGGCACTATTTTGC GGAGG
CASP1	NM_0332 92.2	576-675	ACAGGCATGACAAATGCTGCTACAAAATCTGGGGTACAGCGTAGATGTGAAAAAAA TCTCACTGCTTCGGACATGACTACAGAGCTGGAGGCATTTGCAC
CAT	NM_0017 52.2	1131- 1230	ATGCTTCAGGGCCGCTTTTTGCCTATCTGCACTCACCGCCATCGCTGGGACCCA ATTATCTCATATACCTGTGAACTGTCCCTACCGTGCTCGAG
CBLB	NM_1706 62.3	3196- 3295	TAATGTGCAAGTTGCCCGAGCATCCTCCGAGAATTTGCCTTCCCTCCTCCAGTATCC CCACGTCTAAATCTATAGCAGCCAGAAGTGTAGACACCAAAA
Cbx2	NM_0326 47.3	86-185	CAGGTCTTCGCCGCCGAGTGCATCCTGAGCAAGCGGCTCCGCAAGGGCAAGCTGGA GTACCTGGTCAAGTGGCGCGGCTGGTCTCCAAACATAACAGCT
Cbx5	NM_0121 17.1	636-735	TATGAAGAGAGACTGACATGGCATGCATATCTGAGGATGCGGAAAACAAAGAGAA AGAAACAGCAAAGAGCTAAAGGAGGGGATGGTCTCTGTCAATTT
CCL11	NM_0029 86.2	379-478	TGGGTGCAGGATTCATGAAGTATCTGGACAAAATCTCCAACCTCAAAGCCATAA ATAATCACCATTTTTGAAACCAAACCAGAGCCTGAGTGTGTC
CCL20	NM_0045 91.1	36-135	ATCTGTTCTTTGAGCTAAAACCATGTGCTGTACCAAGAGTTTGTCTCTGGCTGCTTT GATGTCAGTGCTGCTACTCCACCTCTGCGGCAATCAGAAGC
CCL3	NM_0029 83.2	160-259	CAGTTCTCTGCATCACTTGCTGCTGACACGCCGACCGCTGCTGCTTCAGCTACACCT CCCGGCAGATTCCACAGAATTTTCATAGCTGACTACTTTGAGA
CCL4	NM_0029 84.2	36-135	TTCTGCAGCCTCACCTCTGAGAAAACCTCTTTGCCACCAATACCATGAAGCTCTGCGT GACTGTCTGTCTCTCTCATGCTAGTAGCTGCCTTCTGCTC
CCL5	NM_0029 85.2	281-380	AGTGTGTGCCAACCCAGAGAAGAAATGGTTTCGGGAGTACATCAACTCTTTGGAGA TGAGCTAGGATGGAGAGTCCTTGAACCTGAACTTACACAAATTT
CCNB1	NM_0319 66.2	716-815	AACTTGAGGAAGAGCAAGCAGTCAGACCAAAAATACCTACTGGGTCCGGGAAGTCACT GGAAACATGAGAGCCATCCTAATTGACTGGCTAGTACAGGTTCA
CCND1	NM_0530 56.2	691-790	TTGAACACTTCTCTCCAAAATGCCAGAGGCGGAGGAGAACAACAGATCATCCGCA AACACGCGCAGACCTTCGTTGCCCTCTGTGCCACAGATGTGAA
CCR1	NM_0012 95.2	536-635	CATCATTTGGGCCCTGGCCATCTTGCTTCCATGCCAGGCTTATACTTTTCCAAGACCC AATGGGAATTCACTCACACACCTGCAGCCTTCACTTTCT
CCR2	NM_0006 47.3	2011- 2110	ATGCAAGCAAGAAACTGGGCTTCTAGAACCAGGCAACTGGGAACTAGACTCCCA AGCTGGACTATGGCTCTACTTTAGGCCACATGGCTAAAGAAG
CCR4	NM_0055 08.4	36-135	GGTCCTTCTTAGCATCGTGCTTCTGAGCAAGCCTGGCATTGCCTCACAGACCTTCT CAGAGCCGCTTTCAGAAAAGCAAGCTGCTTCTGGTTGGGCC
CCR5	NM_0005 79.1	2731- 2830	TAGGAACATACTTCAGCTCACACATGAGATCTAGGTGAGGATTGATTACCTAGTAGT CATTTTCATGGGTTGTTGGGAGGATTCTATGAGGCAACCACAGG
CCR6	NM_0314 09.2	936-1035	CTTTAACTGCGGGATGCTGCTCCTGACTTGCATTAGCATGGACCGGTACATCGCCATT GTACAGGCGACTAAGTCATTCCGGCTCCGATCCAGAACACTA
CCR7	NM_0018 38.2	1611- 1710	TTCCGAAAACCAGGCCTTATCTCCAAGACCAGAGATAGTGGGGAGACTTCTTGCTT GGTGAGGAAAAGCGGACATCAGCTGGTCAAACAACTCTCTGA
CD160	NM_0070 53.2	501-600	TTGATGTTACCATAAGCCAAGTCACACCGTTGCACAGTGGGACCTACCAGTGTGT GCCAGAAGCCAGAAGTCAGGTATCCGCTTCAGGGCCATTTT
CD163	NM_0042 44.4	1631- 1730	CATCTGTGATTTCGACTTCTCTCTGGAAGCTGCCAGGCTTCTATGCAGGGAATTACAG TGTGGCACAGTTGCTCTATCCTGGGGGAGCTCACTTTGGA
CD19	NM_0017	1771-	AGATTCACACCTGACTCTGAAATCTGAAGACCTCGAGCAGATGATGCCAACCTCTGG

	70.4	1870	AGCAATGTTGCTTAGGATGTGTGCATGTGTGTAAGTGTGTGTG
CD19R_scfv	SCFV013.1	157-256	AGCCGGCTGCACAGCGGCGTGCCAGCCGTTTAGCGGCAGCGGCTCCGGCACCGA CTACAGCCTGACCATCTCCAACCTGGAGCAGGAGGACATCGCCA
CD19RCD28 CAR	MDA_000 02.1	3-102	CAGGTGTTCTGAAGATGAACAGCCTGCAGACCGACGACACCCGCATCTACTACTGT GCCAAGCACTACTACTACGGCGGCAGCTACGCCATGGACTACT
CD2	NM_0017 67.3	688-787	GCAGCCTCTTGATGGTCTTTGTGGCACTGCTCGTTTTCTATATCACAAAAGGAAAA ACAGAGGAGTCGGAGAAATGATGAGGAGCTGGAGACAAGAGC
CD20_scfv_r utuximab	SCFV002.1	9-108	GCTGTCCAGAGCCCCGCCATCCTGAGCGCCAGCCCTGGCGAGAAGGTGACCATGA CCTGCCGGGCCAGCAGCTCTGTGAGCTACATGCACTGGTATCAG
DNAM-1	NM_0065 66.2	164-263	TAAACAGGATACGATAAAAAGTCCTTAACCAAGACGCAGATGGGAAGAAGCGTTAGA GCGAGCAGCACTCACATCTCAAGAACCAGCCTTTCAAACAGTTT
CD244	NM_0163 82.2	1151- 1250	AAGAGGAACCACAGCCCTTCCTTCAATAGCACTATCTATGAAGTGATTGGAAGAGT CAACCTAAAGCCCAGAACCCTGCTCGATTGAGCCGCAAAGAGC
CD247	NM_1980 53.1	1491- 1590	TGGCAGGACAGGAAAAACCCGTCATGTACTAGGATACTGCTGCGTCATTACAGGGC ACAGGCCATGGATGGAAAACGCTCTCTGCTCTGCTTTTTTTCT
TNFRSF7 (CD27)	NM_0012 42.4	331-430	CCAGATGTGTGAGCCAGGAACATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGG CTGCTCAGTGTGATCCTTGCATACCGGGGGTCTCCTTCTCTCT
CD274	NM_0141 43.2	685-784	TAGGAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAACTACC TCTGGCACATCCTCAAATGAAAGGACTCACTTGGTAATTCTG
CD276	NM_0010 24736.1	2121- 2220	ACATTTCTTAGGGACACAGTACACTGACCACATCACACCCTCTTCTCCAGTGCTGC GTGGACCATCTGGCTGCCTTTTTTCTCCAAAAGATGCAATAT
CD28	NM_0061 39.1	306-405	GCTGTAGCGTACGACAATGCGGTCAACCTTAGCTGCAAGTATTCTACAATCTCTTC TCAAGGGAGTTCCGGGCATCCCTTCACAAAGGACTGGATAGT
CMRF-35H	NM_0072 61.3	903-1002	GGGGCCTCCCTGCTAGCCTGGAGGATGTTTCAGAAATGGATCAAAGCTGGTGACC ATTCAGAGCTGTCCCAGAACCCCAAGCAGGCTGCCACGCAGAGT
CD38	NM_0017 75.2	1036- 1135	CCTTGACTCCTTGTGGTTTATGTCATCATACATGACTCAGCATACCTGCTGGTGCAGA GCTGAAGATTTTGGAGGGTCTCCACAATAAGGTCAATGCCA
CD3D	NM_0007 32.4	111-210	TATCTACTGGATGAGTTCGGCTGGGAGATGGAACATAGCACGTTTCTCTGCGCTG GTACTGGCTACCCTTCTCTCGCAAGTGAGCCCTTCAAGATAC
CD3E	NM_0007 33.2	76-175	AAGTAACAGTCCCATGAAACAAAGATGCAGTCGGCACTCACTGGAGAGTTCTGGG CCTCTGCCTTATCAGTTGGCGTTGGGGCAAGATGGTAATG
CD4	NM_0006 16.3	836-935	AGACATCGTGGTGCTAGCTTTCAGAAAGCCTCCAGCATAGTCTATAAGAAAGAGGG GGAACAGGTGGAGTTCTCCTTCCCACTCGCCTTACAGTTGAA
CD40LG	NM_0000 74.2	1226- 1325	GCATTTGATTTATCAGTGAAGATGCAGAAAGGAAATGGGGAGCCTCAGCTCACATTC AGTTATGGTTGACTCTGGGTTCTATGGCCTTGTTGGAGGGGG
CD44	NM_0006 10.3	2461- 2560	GTGGGCAGAAGAAAAAGCTAGTGATCAACAGTGGCAATGGAGCTGTGGAGGACAG AAAGCCAAGTGGACTCAACGGAGAGGCCAGCAAGTCTCAGGAAAT
CD45R_scfv	SCFV006.1	159-258	CCTGGCCAGCAACCTGAAAGCGGCGTGCTGCCAGATTTTCTGGCTCTGGCAGCGG CACCGACTTCACCCTGAACATCCACCCCGTGGAGGAAGAGGAC
IAP	NM_0017 77.3	898-997	GCCATATTGGTTATTCAGGTGATAGCCTATATCCTCGCTGTGGTTGGACTGAGTCTCT GTATTGCGGCGTGTATACCAATGCATGGCCCTCTTCTGATTT
CD56R_scfv	SCFV008.1	198-297	ATTCAGCGGCTCTGGCTCCGGCACCGACTTCACTCTGATGATCTCTCGGGTGGAGGC CGAGGACCTGGGCGTGTACTACTGCTTTCAGGGCAGCCACGTG
CD58	NM_0017 79.2	479-578	GTGCTTGAGTCTCTTCCATCTCCACACTAATTGTGCATTGACTAATGGAAGCATTG AAGTCCAATGCATGATACCAGAGCATTACAACAGCCATCGAG
CD63	NM_0017 80.4	351-450	GTCATCATCGCAGTGGGTGCTTCTCTTCTGCTGGTGGCTTTTGTGGGCTGCTGCGGGG CCTGCAAGGAGAACTATTGTCTTATGATCACGTTTGCATCT
CD69	NM_0017 81.1	461-560	AGGACATGAACTTTCTAAAACGATACGCAGGTAGAGAGGAACACTGGGTTGGACTG AAAAAGGAACCTGGTACCATGGAAGTGGTCAAATGGCAAAGA
CD7	NM_0061 37.6	441-540	CCTACACCTGCCAGGCCATCACGGAGGTCAATGTCTACGGCTCCGGCACCCCTGGTCC TGGTGACAGAGGAACAGTCCAAGGATGGCACAGATGCTCGGA
CD70	NM_0012	191-290	CCTATGGGTGCGTCTGCGGGCTGCTTTGGTCCCATTGGTCGCGGGCTTGGTGATCT

	52.2		GCCTCGTGGTGTGCATCCAGCGCTTCGCACAGGCTCAGCAGCA
CD80	NM_0051 91.3	1289- 1388	AAAGATCTGAAGGTCCCACCTCCATTTGCAATTGACCTCTTCTGGGAACTTCTCAGA TGGACAAGATTACCCACCTTGCCCTTTACGTATCTGCTCTT
CD86	NM_0068 89.3	147-246	TATGGGACTGAGTAACATTCTCTTTGTGATGGCCTTCTGCTCTCTGGTGCTGCTCCTC TGAAGATTCAAGCTTATTTCAATGAGACTGCAGACCTGCCA
CD8A	NM_0017 68.5	1321- 1420	GCTCAGGGCTCTTCTCCACACCATTGAGGTCTTCTTTCCGAGGGCCCCTGTCTCAGG GTGAGGTGCTTGAGTCTCCAACGGCAAGGGAACAAGTACTT
CB8B	NM_1720 99.2	440-539	TCAGCTGAGTGTGGTTGATTTCTTCCCACTGCCCAGCCCACCAAGAAGTCCACC CTCAAGAAGAGAGTGTGCCGTTACCCAGGCCAGAGACCCAG
cdc45	NM_0035 04.3	1676- 1775	AGCTCCCGGATGCTGCACAACCATTTTACCTCTCAGTAATTGAGCTGAAAGCTGAG GATCGGAGCAAGTTTCTGGACGCACTTATTTCCCTCTGTCTT
CDCA7	NM_0319 42.4	771-870	GAATTAGAAAGCTTCCCTGGCTCGTTCCGTGGAAGACATCCCCTCCCAGGCTCCGACT CACAATCAAGGAGACCSCGAAGGCGTACATTCCCGGGTGTG
CDH1	NM_0043 60.2	1231- 1330	CGATAATCTCCGATCTTCAATCCCACCACGTACAAGGGTCAGGTGCCTGAGAACGA GGCTAACGTCGTAATCACCACTGAAAGTGACTGATGCTGAT
cdk1	NM_0017 86.4	179-278	GGTACCTATGGAGTTGTGTATAAGGGTAGACACAAAACCTACAGGTCAAGTGGTAGC CATGAAAAAATCAGACTAGAAAAGTGAAGAGGAAGGGGTTCTTA
CDK2	NM_0017 98.2	221-320	TCGCTGGCGCTTCATGGAGAACTTCCAAAAGGTGGAAGATCGGAGAGGGCACGT ACGGAGTTGTGTACAAAGCCAGAAACAAGTTGACGGGAGAGGTTG
CDK4	NM_0000 75.2	1056- 1155	ACTTTTAACCCACACAAGCGAATCTCTGCCTTTCGAGCTCTGCAGCACTTATCTACA TAAGGATGAAGGTAATCCGGAGTGAGCAATGGAGTGGCTGC
CDKN1A	NM_0003 89.2	1976- 2075	CATGTGCTCTGGTTCCCGTTTCTCCACCTAGACTGTAAACCTCTCGAGGGCAGGGACC ACACCCTGACTGTTCTGTGTCTTTCACAGCTCCTCCACAA
CDKN1B	NM_0040 64.2	366-465	GCTTCCGAGAGGGGTTCCGGCCGCGTAGGGGCGCTTTGTTTTGTTCCGTTTTGTTTT TTGAGAGTGCAGAGAGGGCGTCTGCAGACCCGGGAGAAAAG
p16	NM_0000 77.3	976-1075	AAGCGCACATTCATGTGGGCATTTCTTTCGAGCCTCGCAGCCTCCGGAAGCTGTCTGA CTTCATGACAAGCATTTTGTGAACTAGGGAAGCTCAGGGGGGT
CDKN2C	NM_0012 62.2	1296- 1395	ATAATGTAAACGTCAATGCACAAAATGGATTTGGAAGGACTGCGCTGCAGGTTATGA AACTTGGAATCCCGAGATTGCCAGGAGACTGCTACTTAGAGG
CD66b	NM_0018 16.3	826-925	ATTTCCCCTTCAGACACCTATTACCATGCAGGGGTAATCTCAACCTCTCTGCCATGC GGCCTCTAATCCACCCTCACAGTATTCTTGGTCTGTCAATG
CEBPA	NM_0043 64.2	1321- 1420	GAGCTGGGAGCCCGCAACTCTAGTATTTAGGATAACCTTGTGCCTTGGAAATGCAA ACTCACCGCTCCAATGCCTACTGAGTAGGGGGAGCAAATCGTG
Cebpb	NM_0051 94.2	1421- 1520	CAACCGCACATGCAGATGGGGCTCCCGCCCGTGGTGTTATTTAAGAAGAAACGTCT ATGTGTACAGATGAATGATAAACTCTGCTTCTCCCTCTGCC
CFLAR	NM_0038 79.3	446-545	CAAGACCCTGTGAGCTTCCCTAGTCTAAGAGTAGGATGTCTGCTGAAGTCATCCATC AGGTTGAAGAAGCACTTGATACAGATGAGAAGGAGATGCTGC
C-flip	NM_0011 27183.1	654-753	TAGAGTGCTGATGGCAGAGATTGGTGAGGATTTGGATAAATCTGATGTGTCCTCATT AATTTTCTCATGAAGGATTACATGGGCCGAGGCAAGATAAGC
Chd7	NM_0177 80.3	3076- 3175	AAGCAGGGCCAGAACAAGTTCCTTTCAGAGATTGAGGATGAGCTTTTTAATCCAGAT TATGTGGAGTTGACCGGATAATGGACTTTGCACGTAGCACAG
Cpt1	NM_0202 44.2	1304- 1403	GATATGGTGATATACTTTAGTGCTTTGTGCTGCAAATTTCAAGACACCTTCATCTAA ATATATCAAGACTGCATGTCATCAAGCACCTGAACAGGTTT
Churc1	NM_1451 65.2	21-120	GAGTTTTCTGCTTCCCGGAAGCGTTGGAGGACATTCCCTGTTGACTGCGTCGCGATG TGTGGCGACTGTGTGGAGAAGGAATATCCCAACCGGGTAATA
CIITA	NM_0002 46.3	471-570	GCCTGAGCAAGGACATTTTCAAGCACATAGGACCAGATGAAGTATCGGTGAGAGT ATGGAGATGCCAGCAGAAGTTGGGCAGAAAAGTCAGAAAAGACC
CITED2	NM_0060 79.3	966-1065	AGGAGCTGCCGAACCTGGCTGGGGCAAACGAGTTTATTTTATGACGGACTTCG TGTGCAAACAGCAGCCAGCAGAGTGAGCTGTTGACTCGATCG
CLIC1	NM_0012 88.4	311-410	GTGATGGGGCCAAGATTGGGAACTGCCATTCTCCAGAGACTGTTTATGGTACTGT GGCTCAAGGGAGTCACCTTCAATGTTACCACCGTTGACACCAA
Clnk	NM_0529	1109-	GAAGGAGAACAAGGATGGTAGTTTCTTGGTCCGAGATTGTTCCACAAAATCCAAGGA

	64.2	1208	AGAGCCCTATGTTTTGGCTGTGTTTTATGAGAACAAAGTCTAC
c-MET_scfv	SCFV004.1	139-238	CTGATCTACGCCGCCAGCAGCCTGAAGAGCGGCGTGCCAGCCGTTTAGCGGCTCT GGCTCTGGCGCCGACTTCACCCTGACCATCAGCAGCCTGCAGC
Cnbp	NM_0034 18.4	646-745	CCATCAACTGCAGCAAGACAAGTGAAGTCAACTGTTACCGCTGTGGCGAGTCAGGGC ACCTTGCACGGGAATGCACAATTGAGGCTACAGCCTAATTATT
cnr2	NM_0018 41.1	1571- 1670	AATGGGTTGTTCTCTTGGGAAGTCAGGGTATCAGATGGGATGGACATCCAGGTCTC TCTCTGCCTAATTGTCAAGGCCTCCTTGGCTCTGGAGCTATGA
cnrip1	NM_0011 11101.1	817-916	ACGCTGCAGGTCGAGAATATTTCCATTGGTGGTGTGCTTGTCCCCTGGAAGTGAAG TCTAAAGAGCCTGATGGGGACAGAGTTGTTTATACGGGTACAT
CREB1	NM_0043 79.3	4856- 4955	TTTGATGGTAGGTGAGCAGCAGTGTAGTCTCTGAAAGCACAATACCAGTCAGGCAG CCTATCCCATCAGATGTCATCTGGCTGAAGTTTATCTCTGTCT
Crem	NM_0018 81.2	261-360	CTCCACCTCCTCGCGTCCGTAATCAGTGACGAGGTCCGCTACGTAAATCCCTTTGCGG CGGACAAATGACCATGGAAACAGTTGAATCCCAGCATGATGG
CRIP1	NM_0013 11.4	270-369	CAACCACCCCTGCTACGCAGCCATGTTTGGGCTAAAGGCTTTGGGCGGGGCGGAG CCGAGAGCCACACTTTCAAGTAAACCAGGTGGTGGAGACCCCAT
TSLP-R	NM_0221 48.2	1421- 1520	CAAGGCAGCACGTCCAAAATGCTGTAACCATCTTCCCCTCTGTGAGTCCCAGTT CCGTCCATGTACCTGTTCCATAGCATTGGATTCTCGGAGGAT
CSAD	NM_0159 89.4	206-305	TCAAATCTTCTGCCTAGCCTTAGCCATTAGAGAGAGGTCTGCTAAAGATGGACTGC AAATGCGCTTGATGGAAGGAGATGTCAATCCACTGAAGTCC
CSF2	NM_0007 58.2	476-575	AGATGAGGCTGGCCAAGCCGGGAGCTGCTCTCTCATGAAACAAGAGCTAGAACT CAGGATGGTCATCTTGGAGGGACCAAGGGGTGGGCCACAGCCAT
CSNK2A1	NM_1775 59.2	1931- 2030	CCATCCCACCATTGTTCTCCACCGTCCCACACTTTAGGGGGTTGGTATCTCGTGCTC TTCTCCAGAGATTACAAAATGTAGCTTCTCAGGGGAGGCA
CTGF	NM_0019 01.2	1101- 1200	ACCACCCTGCCGGTGGAGTTCAAGTGCCCTGACGGCGAGGTCATGAAGAAGAACAT GATGTTTCATCAAGACCTGTGCCTGCCATTACAACGTCCCGGAG
CTLA4	NM_0052 14.3	406-505	AGTCTGTGCGGCAACCTACATGATGGGAATGAGTTGACCTTCTAGATGATTCCAT CTGCACGGGCACCTCCAGTGGAATCAAGTGAACCTCACTATC
CTNNA1	NM_0019 03.2	76-175	TCGCCCAGCTAGCCGAGAAATGACTGCTGTCCATGCAGGCAACATAAACTTCAAGT GGGATCCTAAAAGTCTAGAGATCAGGACTCTGGCAGTTGAGAG
CTNNB1	NM_0010 98210.1	1816- 1915	TCTTGCCCTTTGCCGCAAATCATGCACCTTTGCGTGAGCAGGGTGCCATTCCACGA CTAGTTCAGTTGCTTGTTCGTGCACATCAGGATACCCAGCGC
CTNNB1	NM_0308 77.3	856-955	TGATGCCAACAACTGTATTGCAGTGAAGTGTGGCCATATTGCTCCAGGACAATGA TGAAAACAGGGAATTGCTTGGGGAGCTGGATGGAATCGATGTG
cathepsinC	NM_0011 14173.1	261-360	TGCTCGGTTATGGGACCACAAGAAAAAAAGTAGTGGTGTACCTTCAGAAGCTGGAT ACAGCATATGATGACCTTGGCAATTCTGGCCATTTACCATCA
CathepsinD	NM_0019 09.4	1271- 1370	GGGCCACTCTGGATCCTGGGCGACGTCTTCATCGGCCGCTACTACACTGTGTTTGACC GTGACAACAACAGGGTGGGCTTCGCCGAGGCTGCCCGCTCT
CTSW	NM_0013 35.3	1076- 1175	TGCACCGAGGGAGCAATACCTGTGGCATCACCAAGTTCCCGCTCACTGCCCGTGTGC AGAAACCGGATATGAAGCCCCGAGTCTCCTGCCCTCCCTGAAC
CX3C1	NM_0029 96.3	141-240	AGCACCACGGTGTGACGAAATGCAACATCACGTGCAGCAAGATGACATCAAAGATA CCTGTAGCTTTGCTCATCCACTATCAACAGAACCAGGCATCATG
CX3CR1	NM_0013 37.3	1041- 1140	GGGCGCTCAGTCCACGTTGATTTCTCTCATCTGAATCACAAGGAGCAGGCATGGA AGTGTCTGAGCAGCAATTTACTTACCACACGAGTGATGGAG
CXCL10	NM_0015 65.1	41-140	GCAGAGGAACCTCCAGTCTCAGCACCATGAATCAAAGTGCAGTCTGATTTGCTGCCT TATCTTTCTGACTCTAAGTGGCATTCAAGGAGTACCTCTCTC
CXCL12	NM_1991 68.2	506-605	GGGCTGAGGTTTGCCAGCATTTAGACCCTGCATTTATAGCATACGGTATGATATTGC AGCTTATATTCATCCATGCCCTGTACCTGTGCACGTTGGAAC
CXCL9	NM_0024 16.1	1976- 2075	CACCATCTCCATGAAGAAAGGGAACGGTGAAGTACTAAGCGCTAGAGGAAGCAGC CAAGTCGGTTAGTGAAGCATGATTGGTCCCAGTTAGCCTCTG
CXCCR1	NM_0006 34.2	1951- 2050	GCAGCCACCAGTCCATTGGGCAGGCAGATGTTCTAATAAAGCTTCTGTTCCGTGCTT GTCCCTGTGGAAGTATCTTGGTTGTGACAGAGTCAAGGGTGT
CXCR3	NM_0015	81-180	GTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAAGTTC

	04.1		AGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGTGCT
CXCR4	NM_0010 08540.1	136-235	GTCCTATGGGAAAAGATGGGGAGGAGAGTTGTAGGATTCTACATTAATTCTCTTGT GCCCTTAGCCACTACTTCAGAATTTCTGAAGAAAGCAAGCC
CXCR6	NM_0065 64.1	96-195	TTACCATGAAGACTATGGGTTTCAGCAGTTTCAATGACAGCAGCCAGGAGGAGCATCA AGACTTCTGCAGTTCAGCAAGGTCCTTCTGCCCTGCATGTAC
Dapl 1	NM_0010 17920.2	191-290	CGAGAAAACAAGTGCCATTGCAAATGTTGCCAAAATACAGACTGGATGCCCTGAA TGACGCACTGGAGAAGCTCAACTATAAATTTCCAGCAACAGTG
1-Dec	NM_0174 18.2	191-290	AGGCCTTACTTTCCAGATCCAGATCCTTGTGCATACAACACTGACTTGTGTGGGTGAGGC TTGCAGAAAAAATCAGCTAGAACAGCCTTGGGGGTAGTGGCA
DECTIN-1R	SCFV010.1	271-370	CTGAAGATCGACAGCAGCAACGAGCTGGGCTTCATCGTGAAGCAGGTGTCCAGCCA GCCCCACAACCTCTTCTGGATCGGCCTGAGCAGGCCCCAGACCG
DGKA	NM_0013 45.4	1376- 1475	TTCCTAACACCCACCCACTTCTCGTCTTTGTCAATCCTAAGAGTGCGGGGAAGCAGGG GCAAAGGGTGCTCTGGAAGTTCCAGTATATATTAACCCCTCG
dmrta1	NM_0221 60.2	1516- 1615	AGAGTAGGTATCAGTCCATTAAGGCTGGCATATTCTTCTGCAGGAAGAGGGTTATCT GGTTTTATGTCACCCTACCTAACACCTGGGTTAGTACCAACCT
Dnmt1	NM_0013 79.2	1496- 1595	CAAAACCAATCTATGATGATGACCCATCTCTTGAAGGTGGTGTAAATGGCAAAAATCT TGGCCCCATAAATGAATGGTGGATCACTGGCCTTGTATGGAGG
Dock5	NM_0249 40.6	631-730	TGCGAGATGACAATGGGAACATCCTAGACCCTGACGAAACCAGCACCATTGCCCTCT TCAAGGCCCATGAGGTGGCCTCCAAAAGGATTGAGGAAAAGAT
dock9	NM_0011 30048.1	1021- 1120	CTTTGAAGCTGCAATGCAAGAAAAGCGAAATGGCGACTCTCACGAAGATGATGAAC AAAGCAAATTGGAAGGTTCTGGTCCGGTTTAGATAGCTACCTG
Dok2	NM_0039 74.2	651-750	GCCAGGGACCCAGCTGTACGACTGGCCCTACAGGTTTCTGCGGCCTTTGGGCGGG ACAAGGTAACCTTTTTCTTTGAGGCAGGCCGTGCTGCGTCTCT
DPP4	NM_0019 35.3	2701- 2800	CAGCAGTCAGCTCAGATCTCAAAGCCCTGGTCGATGTTGGAGTGGATTTCCAGGCA ATGTGGTATACTGATGAAGACCATGGAATAGCTAGCAGCACAG
DUSP16	NM_0306 40.2	616-715	ATGGGTTTAACTCTCCTTTTGCCAGTACCACCAGCCTGACCTCATACACTTTTAGTAC AATGGAGTGGCTGAGCCTTTGAGCACACCACCATTACATCA
E2f1	NM_0052 25.1	936-1035	CCAGCTCCAAGCCGTGGACTCTTCGGAGAACTTTCAGATCTCCCTAAGAGCAAACAA GGCCCCGATCGATGTTTTCTGTGCCCTGAGGAGACCGTAGGT
E2f4	NM_0019 50.3	221-320	GCCAGAAGCGGCGGATTTACGACATTACCAATGTTTTGGAAGGTATCGGGCTAATCG AGAAAAAGTCCAAGAACAGCATCCAGTGAAGGGTGTGGGGCC
E2f6	NM_1983 25.1	2181- 2280	TGTATGCAGCCTTGCTGTTGAGTCAGTCCAAGGGGTTTTACTTAGGACAAGTTGTACC TTGCCCTCTCTCAGCTGCTCCACATTTTACATACCTA
Edaradd	NM_0807 38.3	396-495	AAAATCAGGGAGAAGAAAATGGCTTTCCAGATAGCACTGGAGATCCTCTTCCAGAGA TCAGCAAGGACAACCTCTGCAAAGAAAAGTACTTGTTCCTC
EGFR_scfv_ NIMO_CAR	SCFV015.1	162-261	CAAGGTGTCCAACAGATTTCAGCGCGTGCCAGCAGATTTTCAGGAAGCGGCAGCG GCACCGACTTCACCTTACCATCAGCTCACTGCAGCCGAAGAT
EGLN1	NM_0220 51.1	3976- 4075	AGCAGCATGGACGACCTGATACGCCACTGTAACGGGAAGCTGGGCAGCTACAAAAT CAATGGCCGGACGAAAGCCATGGT
EGLN3	NM_0220 73.3	801-900	AAGCTACATGGTGGGATCCTGCGGATATTTCCAGAGGGGAAATCATTATAGCAGAT GTGGAGCCATTTTTGACAGACTCCTGTTCTTCTGGTCAGATC
egr2	NM_0003 99.3	1892- 1991	GGTGGAGCTAGCACTGCCCCCTTCCACCTAGAAGCAGGTTCTTCTAAAACCTTAGCC CATTCTAGTCTCTTAGGTGAGTTGACTATCAACCCAAGGC
EIF1	NM_0058 01.3	870-969	CCTGAACAGTCTCGGTGAATCTGAGAGGAGAGGATGGGGTAAGGCAGAAGCACCA GCTGTACTACTAGAAGGGAGCTTTTGGTGGTAGATCCCCTGGTG
ELF4	NM_0014 21.3	336-435	AGCTCTGGAGGGCTCTGATAATCCCGTTGTCAGCTCTGAAAAGACAGCATGGCTA TTACCCTACAGCCCAGTGACCTGATCTTTGAGTTGCGAAGCAA
ELF1	NM_0323 77.3	126-225	AGACCCAGTTCACCTGCCCCCTTGTCAACCACGAGAAATCCTGTGATGTGAAAATGG ACCGTGCCCGCAACACCGGAGTCATCTTGTACCGTGTGCCT
CD39	NM_0010 98175.1	8831- 8930	AGTGTATTAGATGTATTACCTCCATGCTCTCAGTAGAGGCCATAGGAAAGAGTAGG TAGGTTATGCCAGCTCACACGCATCCTTTAAAATGGTTTAGA
ENTPD1	NM_0017	226-325	TTCGAGTAACTTTAGGAAAATGAGCTGCTGGACTCCTCAGTCAATCTGTCCTTTCTAG

	76.4		TCAATGAAAAAGACAGGGTTTGAGGTTCTTCCGAAACGGGG
Eomes	NM_0054 42.2	1671- 1770	ATCCCATGCCCTGGGGTATTACCCAGACCCAACCTTTCTGCAATGGCAGGGTGGGG AGGTCGAGGTTCTTACCAGAGGAAGATGGCAGCTGGACTACCA
EphA2	NM_0044 31.2	1526- 1625	GAGCCGAGTGTGGAAGTACGAGGTCACTTACCGCAAGAAGGGGAGACTCCAACAGCT ACAATGTGCGCCGACCGAGGGTTTCTCCGTGACCCTGGACGAC
EPHA4	NM_0044 38.3	21-120	GCAGCGTTGGCACC GGCGAACCATGGCTGGGATTTCTATTTCCGCCTATTTTCGTGT CTCTTCGGGATTTGCGACGCTGTACAGGTTCCAGGGTATAC
ERK	NM_0174 49.2	786-885	CAAAGCAGGCTTCGAGGCCGTTGAGAATGGCACCGTCTGCCGAGGTTGTCCATCTGG GACTTTCAAGGCCAACCAAGGGGATGAGGCCTGTACCCACTGT
ets1	NM_0052 38.3	4626- 4725	GGTTTTACAGCATTAACTGCCTAACCTTCATGGTGAGAAATACACCATCTCTTTCTA GTCATGCTGTGCATGCCGCTTACTCTGTTGGGGTCTATATA
Etv3	NM_0011 45312.1	272-371	AAGAGCAGCGGGTGA AAATGAAAGCCGGCTGTAGCATCGTGAAAAGCCAGAAG GAGGTGGAGGGTATCAGTTTCTGACTGGGCCTACAAAACAGAGT
ETV6	NM_0019 87.4	3841- 3940	GTATGAATATGAAATCAGAGACCAGGGCATGATGTTGCTAGGATTAGAGCCTCTCAG TCTGGCCTCTTACCCAAGTGCAAGAACTCAGTCTCTTACTGT
FADD	NM_0038 24.2	1561- 1660	TGAGACTGCTAAGTAGGGCAGTGATGGTTGCCAGGACGAATTGAGATAATATCTG TGAGGTGCTGATGAGTGATTGACACACAGCACTCTCTAAATCTT
C10RF24	NM_0529 66.2	3527- 3626	TGCCAATAGATTCAAGAGAAGCTAAGCGGAAATGGAGGGTGAAGGTGTGATCTG TGGGACTGTCTGGGCCTGTTACTCATCCTGCTATCAATTTCTTA
FANCC	NM_0001 36.2	2131- 2230	GACTCAGTCAGACATGTTCACTAATGACTCAAGTGAGCCTTCGGTACTCCTGGTGCCC GCCCGGCCAGACCGTCAGCTTGATAATTACTAAAGCAAAGGC
FAS	NM_0000 43.3	91-190	CACCGGGCTTTTCGTGAGCTCGTCTCTGATCTCGCGCAAGAGTGACACACAGGTGT TCAAAGACGCTTCTGGGAGTGAGGGAAGCGGTTTACGAGTGA
FASLG	NM_0006 39.1	626-725	TCCATGCCTCTGGAATGGGAAGACACCTATGGAATTGCTCTGCTTTCTGGAGTGAAG TATAAGAAGGGTGGCCTTGATCAATGAAACTGGGCTGTACT
CD16	NM_0005 70.3	74-173	CCTATTCCTGTTCTATGGTGGGGCTCCATTGCGAGACTTCAGATTGAGAAATCAGATG AAGTTTCAAGAAAAGGAAACTGGCAGGTGACAGAGATGGGGT
Fgl2	NM_0066 82.2	251-350	CAATTCAGCAGGATCGAGGAGGTGTTCAAAGAAGTCCAAAACCTCAAGGAAATCGT AAATAGTCTAAAGAAATCTTGCCAAGACTGCAAGCTGCAGGCTG
FLT1	NM_0020 19.2	5616- 5715	TTCAACTGCTTTGAACTTGCCTGGGGTCTGAGCATGATGGGAATAGGGAGACAGG GTAGGAAAGGGCGCCTACTCTTCAGGGTCTAAAGATCAAGTGGG
FLT3LG	NM_0014 59.3	361-460	AGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAAC ACGGAGATACACTTTGTCAACAAATGTGCCTTTTCAGCCCCCCCC
FOS	NM_0052 52.2	1476- 1575	ACTCAAGTCCTTACCTCTCCGGAGATGTAGCAAAACGCATGGAGTGTGTATTGTTCC CAGTGACACTTCAGAGAGCTGGTAGTTAGTAGCATGTTGAGC
Foxd4	NM_2073 05.4	354-453	ACTCCGATGGGGAAGACGGTAAATCGATGTCCTGGGAGAGGAGGAAGATGAAGA CGAGGAGGAGGCGGCGAGCCAGCAGTTCCTAGAGCAGTCGCTCCA
Foxm1	NM_0219 53.2	3209- 3308	AAGTCTTTTGTATTGGGTCAGGAGTTGAATTTGGGGTGGGAGGATGGATGCAACTG AAGCAGAGTGTGGGTGCCAGATGTGCGCTATTAGATGTTTCTC
Foxo1	NM_0020 15.3	1527- 1626	TCTCATACCAACATCATTAACTGTTTCGACCCAGTCTCACCTGGCACCATGATGCA GCAGACGCCGTGCTACTCGTTTGCGCCACCAAACACCAGTTT
Foxo3	NM_0014 55.2	1861- 1960	CCGGAACGTGATGCTTCGCAATGATCCGATGATGTCCTTTGCTGCCAGCCTAACCA GGAAGTTTGGTCAATCAGA ACTTGCTCCACCACCAGCACCAA
FoxP1	NM_0326 82.5	6759- 6858	CCTGAAAATCAGATTTACAATGCTGAAGCATTTCCTTGGGCCAGTGTAGCTCACGC AATCTCTGCTACCATAAGCCTTGATGAAGATGATACAGTCCG
FOXP3	NM_0140 09.3	1231- 1330	GGGCCATCCTGGAGGCTCCAGAGAAGCAGCGGCACTCAATGAGATCTACCACTGG TTCACACGCATGTTTGCCTTCTCAGAAACCATCCTGCCACCTG
FYN	NM_0020 37.3	766-865	GTCTTTGGAGGTGTGAACTCTTCGTCTCATAACGGGGACCTTGCCTACGAGAGGAGGA ACAGGAGTGACACTCTTGTGGCCCTTATGACTATGAAGCAC
FZD1	NM_0035 05.1	2431- 2530	GTGCCAATCCTGACATCTCGAGGTTTCTCACTAGACA ACTCTCTTTCCGAGGCTCCTT TGAACAACTCAGCTCCTGCAAAAGCTTCCGTCCTGAGGCA
G6PD	NM_0004	1156-	ACAACATCGCTGCGTTATCTCACCTTCAAGGAGCCCTTTGGCACTGAGGGTCCGG

	02.2	1255	GGGGCTATTTTCGATGAATTTGGGATCATCCGGGACGTGATGCA
GABPa	NM_0020 40.3	1161- 1260	GACCAAGTCCTGCATTGGGTGGTTTGGGTAATGAAGGAATTCAGCATGACCGATATA GACCTCACCACACTCAACATTTCCGGGAGAGAATTATGTAGTC
GADD45alp ha	NM_0019 24.2	866-965	GTTACTCCCTACACTGATGCAAGGATTACAGAACTGATGCCAAGGGGCTGAGTGAG TTCAACTACATGTTCTGGGGGCCCGGAGATAGATGACTTTGCA
GADD45bet a	NM_0156 75.2	366-465	TGTGGACCCAGACAGCGTGGTCCTCTGCCTCTTGCCATTGACGAGGAGGAGGAGG ATGACATCGCCTGCAAATCCACTTCACGCTCATCCAGTCCTTC
GAL3ST4	NM_0246 37.4	1141- 1240	CGAGCCCAAACCTCAATCCCAATGCCCTCATCCATCCTGTTTCCACTGTTACTGATCA TCGCAGCCAGATATCAAGCCCTGCCTCTTTCGATTTGGGGT
GAS2	NM_0052 56.3	916-1015	GATCTCCCGTGTGGATGGCAAACATCCCCTATCCAAAGCAAATCTCCAACCTAAAG GACATGAATCCAGATAACTACTTGGTGGTCTCTGCCAGTTAT
GATA2	NM_0326 38.3	1496- 1595	GAAGAAGGAAGGGATCCAGACTCGGAACCGGAAGATGTCCAACAAGTCCAAGAAG AGCAAGAAAGGGGCGGAGTGCTTCGAGGAGCTGTCAAAGTGCATG
GATA3	NM_0010 02295.1	2836- 2935	AAGAGTCCGGCGGCATCTGTCTTGTCCCTATTCTGCAGCCTGTGCTGAGGGTAGCA GTGTATGAGCTACCAGCGTGCATGTCAGCGACCCTGGCCCCGAC
gBAD- 1R_scfv	SCFV001.1	270-369	CCTGACCATCAGCAGCGTGAAGGCCGAGGATCTGGCCGTGTACTACTGCCAGCAGTA CTACAGATACCCCTACACCTTCGGCGGAGGCACCAAGCTGGAA
SIP1	NM_0010 09182.1	538-637	ACAAGCAACAGTAACTAGTGTCTTGGAAATATCTGAGTAATTGTTTGGAGAAAGAGA CTTTACTCCAGAATTGGGAAGATGGCTTTATGCTTTATTGGCT
Gfi1	NM_0052 63.2	2236- 2335	TCATCACTGGAGGTAAAAGCACAAAGCAATGCCTGTGGACAAGATGTCATTCATTAC TCAGCAAATGTTTCATGGATCACCGGCTACCAAGGTACCAGGCA
GIMAP4	NM_0183 26.2	316-415	AACAGAACTTGTCTAGTTGACACACCAGGCATTTTCGACACAGAGGTGCCCAATGC TGAAACGTCCAAGGAGATTATTCGCTGCATTCTTCTGACCTCC
GIMAP6	NR_02411 5.1	2176- 2275	CTGCCTGGTTTATGGGAGAACTCTGAAGCCCATGATGTTTTCTGGAAGGCTGTTCT ACAGACGGGGTTTATAAGTACTGATACTGGACAGGATGAGAA
GLIPR1	NM_0068 51.2	256-355	CTGCGTTCGAATCCATAACAAGTTCCGATCAGAGGTGAAACCAACAGCCAGTGATAT GCTATACATGACTTGGGACCCAGCACTAGCCCAAATTGCAAAA
GLO1	NM_0067 08.1	1241- 1340	GGAAATGATATGGTACCCAGACACTGGGCTAGGCTGCAACTTTATCTCATTTAATACT CCCAGCTGTCTGTGAGAAAGAAAGCAGGCTAGGCATGTGAA
GNLY	NM_0064 33.2	306-405	CAGGAGCTGGCCGTGACTACAGGACCTGTCTGACGATAGTCCAAAACTGAAGAA GATGGTGGATAAGCCCACCCAGAGAAGTGTTCCAATGCTGCGA
GSK3B	NM_0020 93.2	926-1025	ACTGATTACCTCTAGTATAGATGTATGGTCTGCTGGCTGTGTGTTGGCTGAGCTGT TACTAGGACAACCAATATTTCCAGGGGATAGTGGTGTGGATC
GZMA	NM_0061 44.2	156-255	AGACCCTACATGGTCTACTTACTTGTCTTACAGAAAAACCATCTGTGCTGGGGCTTTGA TTGCAAAAGACTGGGTGTTGACTGCAGCTCACTGTAACCTTGA
GZMB	NM_0041 31.3	541-640	ACACTACAAGAGGTGAAGATGACAGTGCAGGAAGATCGAAAGTGCGAATCTGACTT ACGCCATTATTACGACAGTACCATTGAGTTGTGCGTGGGGGACC
GzmH	NM_0334 23.3	706-805	AAAAAAGGGACACCTCCAGGAGTCTACATCAAGGTCTCACACTTCTGCCCTGGATA AAGAGAACAATGAAGCGCCTCTAACAGCAGGCATGAGACTAAC
GZMK	NM_0021 04.2	701-800	CTGTAAAGGTGCTTCCACGCTATAGTCTCTGGAGGTCATGAATGTGGTGTGCCACA AAGCCTGGAATCTACACCCTGTAAACCAAGAAATACCAGACT
Hat1	NM_0036 42.2	686-785	TGGAGCTACGCTCTTTGCGACCGTAGGCTACATGACAGTCTATAATTACTATGTGTAC CCAGACAAAACCCGGCCACGTGTAAGTCAGATGCTGATTTTG
TIM-3	NM_0327 82.3	956-1055	TATATGAAGTGGAGGAGCCCAATGAGTATTATTGCTATGTCAGCAGCAGGCAGCAAC CCTCACAACCTTTGGGTTGTGCTTTGCAATGCCATAGATCCA
DAP10	NM_0010 07469.1	133-232	ATCCTCTTCTGCTTTTGTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAGAGAT CATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTT
HDAC1	NM_0049 64.2	786-885	CAAGCCGGTCATGTCCAAAGTAATGGAGATGTTCCAGCCTAGTGCGGTGGTCTTACA GTGTGGCTCAGACTCCCTATCTGGGGATCGGTTAGGTTGCTTC
HDAC2	NM_0015 27.1	931-1030	AAGCCTATTATCTCAAAGGTGATGGAGATGTATCAACCTAGTGTGTGGTATTACAG TGTGGTGCAGACTCATTATCTGGTGATAGACTGGGTTGTTTCA
Hdac6	NM_0060	537-636	ATATATTGATCTGATGGAAACAACCCAGTACATGAATGAGGGAGAACTCCGTGTCTCT

	44.2		AGCAGACACCTACGACTCAGTTTATCTGCATCCGAACCTACATC
HER2_scfv	SCFV014.1	65-164	CCTGCAGCGCCAGCAGCAGCGTGTCTACATGCACTGGTATCAGCAGAAGTCCGGCA CTAGCCCCAAGCGGTGGATCTACGACACCTACAAGCTCGCCAG
HERV-K_6H5_scfv	SCFV012.1	138-237	CGGCGGCACCAGCTACAACCAGAAGTTCAAGGACAAGGCCATCCTGACCGTGGACA AGAGCAGCAGCACCCGCTACATGGAAGTGCAGGAGCCTGACCAGC
HLA-A	NM_0021 16.5	1001- 1100	GGAAGAGCTCAGATAGAAAAGGAGGGAGTTACACTCAGGCTGCAAGCAGTGACAG TGCCAGGGCTCTGATGTGTCCCTCACAGCTTGAAAAGTGTGAGA
Hmgb2	NM_0011 30688.1	126-225	CTGTCAACATGGGTAAAGGAGACCCCAACAAGCCGCGGGGCAAATGTCCTCGTAC GCCTTCTTCGTGCAGACCTGCCGGGAAGAGCACAAGAAGAAACA
nsg2	NM_0159 80.3	366-465	TCCTGTGCAGCCTGGCCCTAGCTTTCCTTGCCTGCATCGTGTTCCTGGTGGTTTACAAA GCCTTACCTATGATCACAGCTGCCAGAGGGATTCTGCTA
HopX	NM_0011 45460.1	1118- 1217	AACAATAGGAAGCTATGTGTATCTTCTGTGTAAGCAGTGGCTTCACTGGAAAAATG GTGTGGCTAGCATTTCCTTTGAGTCATGATGACAGATGGTGT
HOXA10	NM_0189 51.3	1504- 1603	TTCTATAGAGATAGATATTGTCCTAAGTGTCAAGTCTGACTGGGCTGGGTTTGCTGT CTTGGGGTCCCCTGCTCGAAATGGCCCTGTCTTCGGCCGA
HOXA9	NM_1527 39.3	1016- 1115	GGCTCTAAACCTCAGGCCACATCTTTTCCAAGGCAAACCTGTTTCAGGCTGGCTCGTA GGCCTGCCGCTTTGATGGAGGAGGTATTGTAAGCTTTCCATT
HOXB3	NM_0021 46.4	61-160	TGTCCGTTTAAATGCTGCTGGGAGACTCGTAAAAAATCATCGTGGACCTGGAGGAT GAGAGGGGCGAGCTTTATTTTCGGTTCGGATTGCGGTGTGGTGGT
HOXB4	NM_0240 15.4	1341- 1440	CCTTTCTTTGTCCTCCACTCCCAGTACCCAGCGAAAGCACCTCTGACTGCCAGATAG TGCAGTGTGGTTCACGGTAACACACACACTCTCCCTCA
HPRT1	NM_0001 94.1	241-340	TGTGATGAAGGAGATGGGAGGCCATCACATTGTAGCCCTCTGTGTGCTCAAGGGGG GCTATAAATTCTTTGCTGACCTGCTGGATTACATCAAAGCACTG
HRH1	NM_0008 61.2	3056- 3155	GTGGCAGCTCAAAATGATATGTTTGTAGTAGACGAACAGCTGACATGGAGTTCCCGTG CACCTACGGAAGGGGACGCTTTGAAGGAACCAAGTGCATTTTT
HRH2	NM_0223 04.1	601-700	GCGGTCTCATCTCATCACCGTTGCTGGCAATGTGGTCGTCTGTCTGGCCGTGGGCT TGAACCGCCGCTCCGCAACCTGACCAATTGTTTCATCGTGT
Human_CD19R_scfv	SCFV009.1	216-315	CTTACCATCAGCAGCCTGCAGCCCAGGACATCGCCACCTACTACTGCCAGCAGTAC CAGAGCCTGCCCTACACCTTCGGCCAGGGCACCAAGCTGCAG
ICOS	NM_0120 92.2	641-740	AACTCTGGCACCCAGGCATGAAGCACGTTGGCCAGTTTTCTCAACTGAAGTGCAA GATTCTCTTATTTCCGGGACCACGGAGAGTCTGACTTAACTAC
ICOSLG	NM_0152 59.4	1191- 1290	CTGCTGGCGTTGGCTGTGATCCTGGAATGAGGCCCTTTCAAAGCGTCATCCACACC AAAGGCAAATGTCCCAAGTGAGTGGGCTCCCCGCTGTCACTG
ID2	NM_0021 66.4	506-605	CGGATATCAGCATCCTGTCTTGCAGGCTTCTGAATTCCTTCTGAGTTAATGTCAAAT GACAGCAAAGCACTGTGTGGCTGAATAAGCGGTGTTTCATGA
ID3	NM_0021 67.3	196-295	AGGAAGCCTGTTTGAATTTAAGCGGGCTGTGAACGCCAGGGCCGGCGGGGGCAG GGCCGAGGCGGGCCATTTTGAATAAAGAGGCGTGCCTTCCAGGC
INDO	NM_0021 64.3	51-150	CTATTATAAGATGCTCTGAAAACCTTTCAGACACTGAGGGGCACCAGAGGAGCAGAC TACAAGAATGGCACACGCTATGGAAAACCTCTGGACAATCAGT
IFNa1	NM_0240 13.1	586-685	ATCCCTCTTTTATCAACAACTTGAAGAAAGATTAAGGAGGAAGGAATAACATCT GGTCCAACATGAAAACAATTCTTATTGACTCATAACACCAGGTC
IFNG	NM_0006 19.2	971-1070	ATACTATCCAGTTACTGCCGTTTGAATAATGCCTGCAATCTGAGCCAGTGCTTTAA TGGCATGTCAGACAGAAGTGAATGTGTGAGGTGACCCTGAT
IFNGR1	NM_0004 16.1	1141- 1240	CCCGGGCAGCCATCTGACTCCAATAGAGAGAGAGAGTTCTTCACCTTTAAGTAGTAA CCAGTCTGAACCTGGCAGCATCGCTTTAAACTCGTATCACTCC
IGF1R	NM_0008 75.2	456-555	TCGGGGGGCCATCAGGATTGAGAAAAATGCTGACCTCTGTTACCTCTCCACTGTGGA CTGGTCCCTGATCCTGGATGCGGTGTCCAATAACTACATTGTG
IKZF1	NM_0060 60.3	4486- 4585	CCGCTGTGTACTACTGTGTGCCTAGATTCCATGCACTCTCGTTGTGTTTGAAGTAAAT ATTGGAGACCGGAGGGTAACAGTTGGCCTGTTGATTACAGC
IKZF2	NM_0010 79526.1	946-1045	CCATGTACCTCCTATGGAAGATTGTAAGGAACAAGAGCCTATTATGGACAACAATAT TTCTCTGGTGCCTTTTGTAGAGACCTGCTGTCATAGAGAAGCTC
IL10	NM_0005	231-330	AAGGATCAGCTGGACAACCTGTTGTTAAAGGAGTCCTTGTGAGGACTTTAAGGGT

	72.2		TACCTGGGTTGCCAAGCCTTGCTGAGATGATCCAGTTTTACC
IL10RA	NM_0015 58.2	151-250	TGCCCAGCCCTCCGTCTGTGTGGTTTGAAGCAGAATTTTCCACCACATCCTCCACTG GACACCCATCCCAAATCAGTCTGAAAGTACCTGCTATGAAGT
IL12A	NM_0008 82.2	776-875	CTTTCTAGATCAAACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTC AACAGTGAGACTGTGCCACAAAATCCTCCCTGAAGAACCG
IL-12p40	NM_0021 87.2	1436- 1535	GCAAGGCTGCAAGTACATCAGTTTTATGACAATCAGGAAGAATGCAGTGTCTGATA CCAGTGCCATCATACTTGTGATGGATGGGAACGCAAGAGAT
IL12RB1	NM_0055 35.1	1293- 1392	AGGAAAAGTGTTACTACATTACCATCTTTGCCTCTGCGACCCCGAGAAGCTCACCTT GTGGTCTACGGTCTGTCCACCTACCCTTTGGGGCAATGC
IL12RB2	NM_0015 59.2	1316- 1415	CCTCCGTGGGACATTAGAATCAAATTTCAAAGGCTTCTGTGAGCAGATGTACCCTTT ATTGGAGAGATGAGGGACTGGTACTGCTTAATCGACTCAGAT
IL13	NM_0021 88.2	517-616	TTTCTTTCTGATGTCAAAAATGTCTTGGGTAGGCGGGAAGGAGGGTTAGGGAGGGG TAAATTCCTTAGCTTAGACCTCAGCCTGTGCTGCCCGTCTTCA
IL15	NM_1721 74.1	1686- 1785	AGGGTGATAGTCAAATTATGTATTGGTGGGGCTGGGTACCAATGCTGCAGGTCAAC AGCTATGCTGGTAGGCTCTGCCAGTGTGGAACCACTGACTACT
IL15Ra	NM_0021 89.2	40-139	CGCTCGCCCGGGGAGTCCAGCGGTGTCTGTGGAGCTGCCCCATGGCCCCGCGGC GGGCGCGGGTCCCGGACCCTCGGTCTCCCGCGCTGCTACTG
IL17A	NM_0021 90.2	241-340	TACTACAACCGATCCACCTCACCTTGGAAATCTCCACCGCAATGAGGACCCTGAGAGAT ATCCCTCTGTGATCTGGGAGGCAAAGTGCCGCCACTTGGGCT
IL17F	NM_0528 72.3	211-310	GCCCGCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGCATCATCAATGAAAACC AGCGCGTTTCCATGTACGTAACATCGAGAGCCGCTCCACCTC
IL17RA	NM_0143 39.4	3021- 3120	CTACTATGTGGCGGGCATTGGGATACCAAGATAAATTGCATGCGGCATGGCCCCAG CCATGAAGGAACTTAACCGCTAGTGCCGAGGACACGTTAAACG
IL18	NM_0015 62.2	49-148	GACAGTCAGCAAGGAATTGTCTCCAGTGCATTTGCCCTCCTGGCTGCCAACTCTGG CTGCTAAAGCGGCTGCCACCTGCTGCAGTCTACACAGCTTCG
IL18R1	NM_0038 55.2	2026- 2125	GAATGAGGGGATTTAAGTGTCTGAAGAGGCATTTTCTAGGGACCAGTGGGTGACT GAGTAACTGAAATGCTGCTTTCCTCCCTAACACCATGGATCTG
IL18RAP	NM_0038 53.2	2413- 2512	GCTTGATGGACAATGGAGTGGGATTGAGACTGTGGTTAGAGCCTTTGATTTCTGG ACTGGACTGACGGCGAGTGAATTCTTAGACCTTGGGTACTTT
IL-1alpha	NM_0005 75.3	1086- 1185	ACTCCATGAAGGCTGCATGGATCAATCTGTGTCTCTGAGTATCTCTGAAACCTCTAAA ACATCCAAGCTTACCTTCAAGGAGAGCATGGTGGTAGTAGCA
IL-1beta	NM_0005 76.2	841-940	GGGACCAAAGGCGGCCAGGATATAACTGACTTCACCATGCAATTTGTGTCTTCTTAA AGAGAGCTGTACCCAGAGAGTCTGTGCTGAATGTGGACTCAA
IL2	NM_0005 86.2	301-400	AGGATGCAACTCCTGTCTTGCACTTGCATAAGTCTTGCACTTGTACAAACAGTGCAC CTACTTCAAGTTCTACAAAGAAAACACAGCTACAACCTGGAGC
IL21R	NM_0217 98.2	2081- 2180	CGTGTGTGTGGTCAACAGATGACAACAGCCGTCCTCCCTCCTAGGGTCTTGTGTTGCA AGTTGGTCCACAGCATCTCCGGGGCTTTGTGGGATCAGGGCA
IL22	NM_0205 25.4	320-419	CTATCTGATGAAGCAGGTGCTGAACTCACCTTGAAGAAGTGTGTTCCCTCAATCT GATAGGTTCCAGCCTTATATGCAGGAGGTGGTGCCTTCTCTG
IL-23p19	NM_0165 84.2	412-511	CAGGGACAACAGTCAAGTCTGCTTGCAAAGGATCCACCAGGGTCTGATTTTTATGA GAAGCTGCTAGGATCGGATATTTTACAGGGGAGCCTTCTCTG
IL23R	NM_1447 01.2	711-810	AACTGCAAATTCACCTGGATGATATAGTGATACCTTCTGCAGCCGTCATTTCCAGGGC TGAGACTATAAATGCTACAGTGCCCAAGACCATAATTTATTG
IL27	NM_1456 59.3	144-243	CAGGAGCTGCGGAGGGAGTTCACAGTCAAGCTGCATCTCGCCAGGAAGCTGCTCTCC GAGGTTCCGGGGCCAGGCCACCGCTTTGCGGAATCTCACCTGC
IL2RA	NM_0004 17.1	1001- 1100	CTTGGAAGAAGCCGGGAACAGACAACAGAAGTCATGAAGCCCAAGTGAAATCAAA GGTGCTAAATGGTCCGCCAGGAGACATCCGTTGTGCTTGCCTGC
IL2RB	NM_0008 78.2	1981- 2080	GTCCTGCTGCCCAGCCAGGAAGTGTGTGTGTTGCAGGGGGGCGAGTAACTCCCAAC TCCCTCGTTAATCACAGGATCCCACGAATTTAGGCTCAGAAGC
IL2RG	NM_0002 06.1	596-695	CCACAGCTGGACTGAACAATCAGTGGATTATAGACATAAGTTCTCCTTGCCTAGTGTG GATGGGCAGAAACGCTACACGTTTTCGTGTTCGGAGCCGCTTT
IL4	NM_0005	626-725	GACACTCGCTGCCTGGGTGCGACTGCACAGCAGTTCCACAGGCACAAGCAGCTGATC

	89.2		CGATTCTGAAACGGCTCGACAGGAACCTCTGGGGCCTGGCGG
IL4R	NM_0004 18.2	706-805	ATCATCTCACCTATGCAGTCAACATTTGGAGTGAAAACGACCCGGCAGATTTTCAGAAT CTATAACGTGACCTACCTAGAACCCTCCCTCCGCATCGCAGC
IL5	NM_0008 79.2	106-205	CCACAGAAATCCCACAAGTGCATTGGTGAAAGAGACCTTGGCACTGCTTTCTACTCA TCGAACTCTGCTGATAGCCAATGAGACTCTGAGGATTCCTGT
IL6	NM_0006 00.1	221-320	TGACAAACAAATTCGGTACATCCTCGACGGCATCTCAGCCCTGAGAAAGGAGACATG TAACAAGAGTAACATGTGTGAAAGCAGCAAAGAGGCACTGGCA
IL6R	NM_0005 65.2	994-1093	CTTTCTACATAGTGTCCATGTGCGTCGCCAGTAGTGTGCGGAGCAAGTTCAGCAAAA CTCAAACCTTTTCAGGGTTGTGGAATCTTGACGCTGATCCGCC
IL7R	NM_0021 85.2	1611- 1710	TTGCTTTGACCACTCTTCTGAGTTTCAGTGGCACTCAACATGAGTCAAGAGCATCCTG CTTCTACCATGTGGATTTGGTCACAAGGTTTAAGGTGACCCA
IL9	NM_0005 90.1	301-400	AAGTACTAAAGAACAACAAGTGTCCATATTTTTCTGTGAACAGCCATGCAACCAAAC CACGGCAGGCAACGCGCTGACATTTCTGAAGAGTCTTCTGGA
Insm1	NM_0021 96.2	1981- 2080	AAGCCTCCCCTTGGCGGGGAGAAGCTTTTTTTCTTGCTAGTATTGCTGTGTTTCATGG TCTAGAAATGCGGTCTGGTCTCGCCTCGCCTACCAATCTCTG
IRF1	NM_0021 98.1	511-610	CTGTGCGAGTGTACCGGATGCTTCCACCTCTCACCAAGAACCAGAGAAAAGAAAGAA AGTCGAAGTCCAGCCGAGATGCTAAGAGCAAGGCCAAGAGGAA
IRF2	NM_0021 99.2	1376- 1475	CAGTACCTGGAGCTTCTCTTTAACTCAGGACTCCAGCCCATTGGTAGACGTGTGTTTC TAGAGCCTGCTGGATCTCCAGGGCTACTCACTCAAGTTCAA
IRF4	NM_0024 60.1	326-425	GGGCACTGTTTAAAGGAAAGTTCGAGAAGGCATCGACAAGCCGGACCTCCCACCT GGAAGACGCGCCTGCGGTGCGCTTTGAACAAGAGCAATGACTT
Irf5	NM_0022 00.3	1846- 1945	GCCTGGCTCTCGGGAAATTCAGCCATGAGCAGGGAAAGAACTCTCCCAACCCTGGG GCCTAGCTGTATAGGAGGAATTGCCTAAGGGTGGCCCACTCTTG
Irf7	NM_0015 72.3	1764- 1863	CGCAGCGTGAGGGTGTGTCTTCCCTGGATAGCAGCAGCCTCAGCCTCTGCCTGTCCA GCGCCAACAGCCTCTATGACGACATCGAGTGCTTCTTATGGA
ITCH	NM_0314 83.4	156-255	ACTGTGAGAACTTCAGGTTTTCCAACCTATTGGTGGTATGTCTGACAGTGGATCACAA CTTGGTTCAATGGGTAGCCTCACCATGAAATCACAGTTCAG
ITGA1	NM_1815 01.1	1876- 1975	AAGTGGCAAGACTATAAGGAAAGAGTATGCACAACGTATTCCATCAGGTGGGGATG GTAAGACACTGAAATTTTTGGCCAGTCTATCCACGGAGAAATG
ITGA4	NM_0008 85.4	976-1075	GCCCACTGCCAACTGGCTCGCCAACGCTTCAGTGATCAATCCCGGGGCGATTTACAG ATGCAGGATCGGAAAGAATCCCGGCCAGACGTGCGAACAGCTC
ITGA5	NM_0022 05.2	926-1025	AGAAGACTTTGTTGCTGGTGTGCCCAAAGGGAACTCACTTACGGCTATGTCACCAT CCTTAATGGCTCAGACATTCGATCCCTCTACAACCTTCTCAGGG
ITGAL	NM_0022 09.2	3906- 4005	GTGAGGGCTTGTCAATACCAGACGGTTCACCAGCCTCTCTTGTTTCCTTCTTGGAA GAGAATGTCTGATCTAAATGTGGAGAACTGTAGTCTCAGGA
CD11b	NM_0006 32.3	516-615	GCCCTCCGAGGGTGTCTCAAGAGGATAGTGACATTGCCTTCTTGATTGATGGCTCT GGTAGCATCATCCACATGACTTTCGGCGGATGAAGGAGTTTG
CD11c	NM_0008 87.3	701-800	CCCCTCAGCCTGTTGGCTTCTGTTACCAGCTGCAAGGGTTACATACACGGCCACCG CCATCCAAAATGTCGTGCACCGATTGTTCCATGCCTCATATG
ITGB1	NM_0336 66.2	2001- 2100	TTTTAACATTACCAAGGTAGAAAGTCGGGACAAATTACCCAGCCGGTCCAACCTGA TCCTGTGTCCATTGTAAGGAGAAGGATGTTGACGACTGTTGG
ITGB7	NM_0008 89.1	1279- 1378	CAACGTGGTACAGCTCATCATGGATGCTTATAATAGCCTGTCTCCACCGTGACCCTT GAACACTCTTCACTCCCTCCTGGGGTCCACATTTCTTACGAA
ITK	NM_0055 46.3	3431- 3530	GCCAGTAAAGAAGTCAGTATAGAACCCTAGCGAATAGTGTGCTCTGGCACAGACC ACTGTGGTTGATGGCATGGCCCTCCAACCTTGAATAGGATTTT
JAK1	NM_0022 27.1	286-385	GAGAACACCAAGCTCTGGTATGCTCCAAATCGACCATCACCGTTGATGACAAGATG TCCCTCCGGCTCCACTACCGGATGAGGTTCTATTTACCAATT
JAK2	NM_0049 72.2	456-555	CTCCTCCCGCAGCGCAAATGTTCTGAAAAAGACTCTGCATGGGAATGGCCTGCCTT ACGATGACAGAAATGGAGGGAACATCCACCTCTTCTATATATC
JAK3	NM_0002 15.2	1716- 1815	GTGCTGCTGAAGGTCATGGATGCCAAGCACAAGAACTGCATGGAGTCATTCTGGGA AGCAGCGAGCTTGTGAGCCAAGTGTGCTACCGGCATCTCGTGC
AP1	NM_0022	141-240	ACACAGCCAGCCAGCCAGGTCGGCAGTATAGTCCGAACTGCAAATCTATTTTCTTTT

	28.3		CACCTTCTCTCTAACTGCCAGAGCTAGCGCCTGTGGCTCCC
JunB	NM_0022 29.2	1156- 1255	GCGCGCCTGGAGGACAAGGTGAAGACGCTCAAGGCCGAGAACCGGGGCTGTCTGA GTACCGCCGGCCTCCTCCGGGAGCAGGTGGCCAGCTCAAACAGA
KIAA0101	NM_0147 36.4	66-165	TGTCCAGTGA AACACCCTCGGCTGGGAAGTCAGTTCTCTCTCTCTCTCTCTCTCT GTTTGAACATGGTGCGGACTAAAGCAGACAGTGTTCAGGC
KIR2DL1 (NKAT1)/CD 158a	NM_0142 18.2	882-981	GCAGGAAACAGAACAGCGAATAGCGAGGACTCTGATGAACAAGACCCTCAGGAGGT GACATACACACAGTTGAATCACTGCGTTTTTCACACAGAGAAAAA
KIR2DL2 (NKAT6)/CD 158b	NM_0142 19.2	815-914	TCTCCTTCATCGCTGGTGCTCCAACAAAAAATGCTGCGGTAATGGACCAAGAGTC TGCAGGGAACAGAACAGCGAATAGCGAGGACTCTGATGAACAA
KIR2DL3 (NKAT2)/CD 158b	NM_0158 68.2	742-841	CTCCGAAACCGGTAACCCAGACACCTGCATGTTCTGATTGGGACCTCAGTGGTCATC ATCCTCTTCATCCTCCTCCTCTTTCTCCTTCATCGCTGG
KIR2DL4 (p49 CD158d)	NM_0010 80770.1	842-941	TTGGATCACTGCATTTTCACACAGAGAAAAATCACTGGCCCTTCTCAGAGGAGCAAG AGACCCTCAACAGATACCAGCGTGTGTATAGA ACTTCCAAATG
KIR2DL5A	NM_0205 35.3	1452- 1551	GACACGTGCTGTTCCACCTTCCCTCATGCTGTTTACCTTTCTCAGACTATTTCCAGC CTTCTGTGAGTCAGCAGTGA AACTTATAAAATTTTTGTG
KIR2DS1	NM_0145 12.1	699-798	CTTCAACCACTGAACCAAGCTCCGAAACCGGTAACCCAGACACCTACATGTTCTGAT TGGGACCTCAGTGGTCAAATCCCTTTCACCATCCTCCTCT
KIR2DS2 (NKAT5)/CD 158b	NM_0123 12.2	857-956	CAAGAGCCTGCAGGGAACAGAACAGTGAACAGCGAGGATTCTGATGAACAAGACCA TCAGGAGGTGTCATACGCATAATTGGATCACTGTGTTTTACAC
KIR2DS3 (NKAT7)	NM_0123 13.1	694-793	GGCCTTCAACCACTGAACCAAGCTCCAAAACCGGTAACCCAGACACCTACACGTTCT GATTGGGACCTCAGTGGTCAAACCTCCCTTTCACCATCCTCCT
KIR2DS4 (NKAT8)	NM_0123 14.3	1428- 1527	ACATACAAGAGGCTGCCTTTAACACAGCACTTAGACACGTGCTGTTCCACCTCCCTT CAGACTATCTTTCAGCCTTCTGCCAGCAGTAAACTTATAAA
KIR2DS5 (NKAT9)	NM_0145 13.2	205-304	CTTCTTCTGCACAGAGAGGGGACGTTTAAACCACTTTGCGCCTCATTGGAGAGCA CATTGATGGGGTCTCCAAGGGCAACTTCTCCATCGGTGCGATG
KIR3DL1 (NKAT3/NKB 1)	NM_0132 89.2	1055- 1154	CCAAATCTGGTAACCCAGACACCTGCACATTCTGATTGGGACCTCAGTGGTCATCAT CCTCTTCATCCTCCTCCTCTTTCTCCTTCATCTCTGGTG
KIR3DL2 (NKAT4)	NM_0067 37.2	885-984	TGCCACCCACGGAGGGACCTACAGATGCTTCGGCTCTTCCGTGCCCTGCCCTGCGTG TGGTCAAACCTCAAGTGACCCACTGCTTGTCTGTGTCACAGGA
KIR3DL3 (KIRC1 CD158z)	NM_1534 43.3	509-608	CCTTGCGCCTCGTTGGACAGCTCCACGATGCGGGTCCAGGTCAACTATTCCATGG GTCCCATGACACCTGCCCTTGAGGGACCTACAGATGCTTTGG
KIR3DS1 (NKAT10)	NM_0010 83539.1	1001- 1100	CTCAAATCTGGTAACCTCAGACACCTGCACATTCTGATTGGGACCTCAGTGGTCAAA ATCCCTTTCACCATCCTCCTCTTTCTCCTTCATCGCTGG
KIT	NM_0002 22.2	2645- 2744	GGTCTATGGGATTTTTCTTTGGGAGCTGTTCTCTTTAGGAAGCAGCCCTATCCTGG AATGCCGGTTCGATTCTAAGTTCTACAAGATGATCAAGGAAGG
KLF10	NM_0056 55.1	571-670	GCTCAGGCAACAAGTGTGATTCTGCATACAGCTGATGCCAGCTATGTAACCACAG ACCTGCCAATGAAAGCAGCCAGCATCCTCAACTATCAGAACA
Klf12	NM_0072 49.4	951-1050	TGACCTGCCAAATGTGACCTTAGATAGCGTTAATGAAACTGGATCTACGGCCCTTCC ATAGCCAGAGCAGTACAAGAGGTACATCCGTCCCCAGTATCA
Klf2	NM_0162 70.2	1016- 1115	GGAAGTTTGC GCGCTCAGACGAGCTCACGCGCCACTACCGAAAGCACACGGGCCAC CGGCCATTCCAGTGCCATCTGTGCGATCGTGCTTCTCGCGCTC
klf3	NM_0165 31.3	276-375	ACCAGAGCACCTAGAAAGTTTAACTAAAAGAATGCTCATGTTTGACCCAGTTCTGT CAAGCAAGAGGCCATGGACCCTGTCTCAGTGTACATCCCATC
KLF4	NM_0042 35.4	1981- 2080	CGAGCATTTTCCAGGTGCGACCCTCGCCTTACACATGAAGAGGCATTTTTAAATCC CAGACAGTGGATATGACCCCACTGCCAGAAGAGAATTCAGT

KLF6	NM_0010 08490.1	1166- 1265	GGGATGCGTGTTCAGCCAAAGCATGCCGTTCTGCACCCTACCCAGTTGCCTCCAGG GCCTCTCCTTGGAAAGTCTTTTGAGGGCTAAAAAGGTCCTGTA
KLF7	NM_0012 70943.1	1547- 1646	GTACTATTGAGATCTTTTCGCGTCGATCCCAACGGCCTTAGCGGCGGCAGACTGGAAT AACACCTTACACCTTTCTGGCCTGCATTTCTGTAGACTTCACT
Klra5 (Ly49E)	NR_02804 5.1	415-514	CCTTCAGAGTCACAGAATAGATTAAGGCCTGATGATACTCAAAGGCCTGGGAAA GATGACAAAGAATTTTCAGTGCCCTGGCACCTCATTGCAGTGA
KLRB1	NM_0022 58.2	86-185	TGAGTTAAACTTACCCACAGACTCAGGCCAGAAAAGTTCTTACCTTCATCTCTTCTC GGGATGTCTGTCAGGGTTCACCTTGGCATCAATTTGCCCTG
KLRC1	NM_0022 59.3	336-435	ACCTATCACTGCAAAGATTTACCATCAGCTCCAGAGAAGCTCATTGTTGGGATCCTGG GAATTATCTGTCTTATCTTAATGGCCTCTGTGGTAACGATAG
NKG2C	NM_0022 60.3	943-1042	TATGTGAGTCAGCTTATAGGAAGTACCAAGAACAGTCAAACCCATGGAGACAGAAA GTAGAATAGTGTTGCCAATGTCTCAGGGAGGTTGAAATAGGAG
NKG2E	NM_0022 61.2	761-860	ACTCCTGAGCTCAAGAAATCAACACATCTTGGCCTCCCAAGTTGCTGGGATTACTGAC ACAAGCCACCGCCCTGAGTGCTCATGTACCATTTAGCTTGT
NKG2F	NM_0134 31.2	277-376	CAGGAACCAAACAGGAAATATTCCAAGTAGAATTAACCTTCAAATGCTTCTTCGG ATCATCAAGGGAATGACAAGACATATCACTGCAAAGGTTTACT
KLRD1 (CD94)	NM_0022 62.3	543-642	AGCCTGCTTCAGCTTCAAACACAGATGAACTGGATTTTATGAGCTCCAGTCAACAAT TTTACTGGATTGGACTCTTACAGTGAGGAGCACACCCGCT
NKp80	NM_0165 23.1	276-375	AAAAAGGAAGTTGTTCAAATGCCACTCAGTATGAGGACACTGGAGATCTAAAAGTG AATAATGGCACAAGAAGAAATATAAGTAATAAGGACCTTTGTGC
KLRG1	NM_0058 10.3	66-165	CAGAATGACTATGGACCACAGCAAAAATCTTCTCTTCCAGGCCTTCTTGTCTTGCCT TGTGGCAATAGCTTTGGGGCTTCTGACTGCAGTTCTTCTGA
NKG2D	NM_0073 60.1	761-860	GGACCAGGATTTACTTAAACTGGTGAAGTCATATCATTGGATGGGACTAGTACACAT TCCAACAAATGGATCTTGGCAGTGGGAAGATGGCTCCATTCTC
CD223 (LAG3)	NM_0022 86.5	1736- 1835	CTTTTGGTGACTGGAGCCTTTGGCTTTACCTTTGGAGAAGACAGTGGCGACCAAGA CGATTTTCTGCCTTAGAGCAAGGGATTACCCCTCCGACGGCTC
LAIR1	NM_0022 87.3	1196- 1295	GCACCTGAGGGTAGAAAGTCACTCTAGGAAAAGCCTGAAGCAGCCATTTGGAAGGC TTCCTGTTGGATTCTTCTCATCTAGAAAGCCAGCCAGGCAGCT
CD208 (DC- LAMP)	NM_0143 98.3	1401- 1500	GGTCTCTGCCTTATGGGTATGGGTGTCTATAAAATCCGCCTAAGGTGTCAATCATCTG GATACCAGAGAATCTAATTGTTGCCCGGGGGAATGAAAATA
Lat	NM_0010 14987.1	1291- 1390	TGTGTAATAGAATAAAGGCCTGCGTGTGTCTGTGTTGAGCGTGCGTCTGTGTGTGCC TGTGTGCGAGTCTGAGTCAGAGATTTGGAGATGTCTCTGTGTG
Lat2	NM_0141 46.3	1864- 1963	TGCAGAGCTGATTAACAGTGTGTGACTGTCTCATGGGAAGAGCTGGGGCCCAGA GGGACCTTGAGTCAGAAATGTTGCCAGAAAAAGTATCTCCTCCA
LCK	NM_0053 56.2	1261- 1360	ATTAAGTGGACAGCGCCAGAAGCCATTAACACTACGGGACATTACCCATCAAGTCAGAT GTGTGGTCTTTTGGGATCCTGCTGACGGAAATTGTCACCCACG
LDB2	NM_0012 90.3	196-295	CTCTGTGTGTGTGAGCGTGTGTGCGTGCCTACTTTGTAAGGAGGAAACACAG CCCATGTGCTCTGCATGGACGTTACTGATACTCTGTTAGCTT
LDHA	NM_0055 66.1	986-1085	CAGAATGGAATCTCAGACCTTGTGAAGGTGACTCTGACTTCTGAGGAAGAGGCCCGT TTGAAGAAGAGTGCAGATACACTTTGGGGGATCCAAAAGGAGC
Lef1	NM_0162 69.3	1166- 1265	CCGTCACACATCCCATCAGATGTCAACTCAAACAAGGCATGTCCAGACATCCTCCAG CTCCTGATATCCCTACTTTTTATCCCTTGTCTCCGGGTGGTG
Lgals1	NM_0023 05.3	61-160	GGTGCGCCTGCCCGGAACATCCTCCTGGACTCAATCATGGCTTGTGGTCTGGTCCG CAGCAACCTGAATCTCAAACCTGGAGAGTGCCTTCGAGTGCAG
LGALS3	NM_0023 06.2	121-220	CAGCCGTCCGGAGCCAGCCAACGAGCGGAAAATGGCAGACAATTTTCGCTCCATGA TGCGTTATCTGGGTCTGGAAACCCAAACCCTCAAGGATGGCCT
CD118	NM_0023 10.3	2996- 3095	CCTATTGTCCACCCATCATTGAGGAAGAAATACCAAACCCAGCCGAGATGAAGCTG GAGGGACTGCACAGGTTATTTACATTGATGTTTCAGTCGATGTA
CD85/LILRB 1	NM_0010 81637.1	2333- 2432	AGCTGAGAAAATAAGTCAGAAAGTGCATTAACCTGAATCACAATGTAAATATTACA CATCAAGCGATGAAACTGGAAAATAACAAGCCACGAATGAATG
Lmo2	NM_0055 74.3	1416- 1515	AAGCATTTCTGTGTAGGTGACAGATACCTCCTCATCAACTCTGACATAGTGTGCGAAC AGGACATCTACGAGTGGACTAAGATCAATGGGATGATATAGG

LRP5	NM_0023 35.1	2516- 2615	TGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTGAGGAGCGGGTCTGTGATT GCCGACGATCTCCCGCACCCGTTCCGGTCTGACGACAGTACAGCGA
LRP6	NM_0023 36.1	2186- 2285	CTTAGATTATCCAGAAGGCATGGCAGTAGACTGGCTTGGGAAGAACTGTACTGGGC AGACACAGGAACGAATCGAATTGAGGTGTCAAAGTTGGATGGG
LRRC32	NM_0055 12.2	3471- 3570	CACCCTGGTGTGGGTTCTCCTGTTCTCTGTGCTCTTGCACTTCTCATTCCCTTTTCC TCTATTGAGCAGAGCCTGGAGTTGAGACTATGGAATCCA
LRRN3	NM_0010 99660.1	2941- 3040	GTCTTGGAGGCCTTCTGGGGATTATTGGTGTGATATGTCTTATCAGCTGCCTCTCTCC AGAAATGAACTGTGATGGTGGACACAGCTATGTGAGGAATTA
LTA	NM_0005 95.2	886-985	CTGATCAAGTCACCGGAGCTTTCAAAGAAGGAATTCTAGGCATCCCAGGGGACCACA CCTCCCTGAACCATCCCTGATGTCTGTCTGGCTGAGGATTTCA
LTbR	NM_0023 42.1	1436- 1535	CTAACAGGGGCCAAGGAACCAATTTATCACCCATGACTGACGGAGTCTGAGAAAA GGCAGAAGAAGGGGGGCACAAGGGCACTTTCTCCCTTGAGGCTG
Lyn	NM_0023 50.1	1286- 1385	TCCTGAAGAGCGATGAAGGTGGCAAAGTGCTGCTTCCAAAGCTCATTGACTTTTTCTG CTCAGATTGCAGAGGGAATGGCATAACATCGAGCGGAAGAACTA
MAD1L1	NM_0035 50.2	307-406	GAAGACCTGGGGGAAAACACCATGGTTTTATCCACCCTGAGATCTTTGAACAACCTC ATCTCTCAGCGTGTGGAGGGAGGCTCTGGACTGGATATTTCTA
Maf	NM_0010 31804.2	6161- 6260	TTCCAATTACAGAAGTGGAGCCACTCGCAAGTTGGAGCCATCAGTGGGATACGCCAC ATTTTGGAAAGCCCCAGCATCGTGTACTTACCAGTGTGTTTACA
MAP2K1	NM_0027 55.2	971-1070	ACGGAATGGACAGCCGACCTCCCATGGCAATTTTTGAGTTGTTGGATTACATAGTCA ACGAGCCTCCTCCAAAACCTGCCAGTGGAGTGTTCAGTCTGGA
MAPK14	NM_0013 15.1	451-550	TGGGCTCTGGCGCCTATGGCTCTGTGTGTGCTGCTTTTGACACAAAACGGGGTTAC GTGTGGCAGTGAAGAAGCTCTCCAGACCATTTTCAGTCCATCAT
MAPK3	NM_0027 46.2	581-680	AACGTGCTCCACCAGATCTAAAGCCCTCAACCTGCTCATCAACACCACCTGCGACC TTAAGATTTGTGATTTCCGGCTGGCCCGGATTGCCGATCCTG
MAPK8	NM_1390 49.1	946-1045	TCTCTGTAGATGAAGCTCTCCAACACCCGTACATCAATGTCTGGTATGATCCTTCTGA AGCAGAAGTCCACCACCAAAGATCCCTGACAAGCAGTTAGA
MBD2	NM_0039 27.3	2016- 2115	ATTTACATTTCAACTCTGATCCCTGGGCCTTAGGTTTGACATGGAGGTGGAGGAAGAT AGCGCATATATTTGCAGTATGAACTATTGCCTCTGGACGTTGT
MCL1	NM_0219 60.3	1261- 1360	GCTGTAACCTCCTAGAGTTGCACCCTAGCAACCTAGCCAGAAAAGCAAGTGGCAAGA GGATTATGGCTAACAAAGAATAAATACATGGGAAGAGTGCTCCC
MIF	NM_0024 15.1	320-419	TCCTACAGCAAGCTGCTGTGCGCCTGCTGGCCGAGCGCCTGCGCATCAGCCCGGAC AGGGTCTACATCAACTATTACGACATGAACGCGGCAATGTGG
MMP14	NM_0049 95.2	1471- 1570	GACAAGATTGATGCTGCTCTTCTGGATGCCAATGAAAAGACCTACTTCTTCCGTG GAAACAAGTACTACCGTTTCAACGAAGAGCTCAGGGCAGTGG
MPL	NM_0053 73.2	896-995	CAGTGGCACTTGGACTGCAATGCTTTACCTTGGACCTGAAGAATGTTACCTGTCAATG GCAGCAACAGGACCATGCTAGCTCCCAAGGCTTCTTCTACCA
mTOR	NM_0049 58.2	5096- 5195	TTAGTGTGCTCCTGGGAGTTGATCCGTCTCGGCAACTTGACCATCCTCTGCCAACAG TTCACCCTCAGGTGACCTATGCCTACATGAAAAACATGTGGA
MAD	NM_0023 57.2	881-980	GAGAATAAAGCTGCAGGACAGTCAAAAGCGTGTCTTGGTCTTAAGAGAGTGGGC ACTGCGGCTGTCTCCTTGAAGTTCTCCCTGTTGGTTCTGATTA
MYB	NM_0053 75.2	3146- 3245	AACTGTTGCATGGATCCTGTGTTTGAACCTGGGAGACAGAACTGTGGTTGATAGC CAGTCACTGCCTTAAAGAACATTTGATGCAAGATGGCCAGCACT
MYBL1	NM_0010 80416.2	1431- 1530	GCCGTGGAGGCAAACGCTGTGTTATCCTCTTTGCAGACCATCCAGAATTTGCAGAG ACTCTAGAACTTATTGAATCTGATCCTGTAGCATGGAGTGACG
Myc	NM_0024 67.3	1611- 1710	TCGGACACCGAGGAGAATGTCAAGAGGCGAACACACAACGTCTTGGAGCGCCAGAG GAGGAACGAGCTAAAACGGAGCTTTTTTGCCTGCGTGACCAGA
Mycl1	NM_0010 33081.2	569-668	GCAGGGAGCGGACATGGACTACGACTCGTACCAGCACTATTTCTACGACTATGACTG CGGGGAGGATTTCTACCGCTCCACGGCGCCAGCGAGGACATC
Mycn	NM_0053 78.4	1546- 1645	AAGGCCGCCAAGGTGGTCATTTTGA AAAAAGGCCACTGAGTATGTCCACTCCCTCCAG GCCGAGGAGCACCAGCTTTTGTGGAAAAGGAAAAATTGCAGG
myo3b	NM_0010 83615.1	216-315	GACACCTGGGAAATTATAGAGACCATTGGTAAAGGCACCTATGGCAAAGTCTACAAG GTAACATAACAAGAGAGATGGGAGCCTGGCTGCAGTGAAAATTC

MYO6	NM_0049 99.3	6656- 6755	AAGTTGGGGAGATGGCACCTTCTCAGAGGATTGTGAAAATATGAGGAAGAAACAAA ACAGTGCATGTAGGAGCACAGGGCCACACAAAGGCATTCTATTG
Nab1	NM_0059 66.3	250-349	GTTTTACATGGAAGTGGCTTACAGAACTTGGCGCTGAGGTGCAGGGAAGCCAGAA ACTCTTTGTGTCTCTAAGGCCGATGAGGAATTTGAAACACATG
Nab2	NM_0059 67.3	1206- 1305	GAGCGTTGGGCACATCTTTGAGATGGATGATAATGACAGCCAGAAGGAAGAGGAGA TCCGCAAATACAGCATCATCTATGGCCGTTTCGACTCTAAGCGG
Nanog	NM_0248 65.2	1101- 1200	CTACTCCATGAACATGCAACCTGAAGACGTGTGAAGATGAGTAAAAGTATATTACT CAATTTAGTCTGGACACTGGCTGAATCCTTCTCTCCCCTCC
NBEA	NM_0156 78.3	8646- 8745	CTGAGAGCCCTGAAGGACCAGAAAAGTCTTATTCCCACGCTTGATATCTGTCTCCA GCGAAGGCCACTGTATCATATACTATGAACGAGGGCGATTCA
NCAM1	NM_0006 15.5	1621- 1720	GGTATTTGCCTATCCCAGTGCCACGATCTCATGGTTTCGGGATGGCCAGCTGCTGCCA AGCTCCAATTACAGCAATATCAAGATCTACAACACCCCTCT
NCL	NM_0053 81.2	1493- 1592	GAACAGAGATCGATGGGCGATCTATTTCCCTGTAATACTGGAGAGAAAGGTCAAA ATCAAGACTATAGAGGTGGAAGAATAGCACTTGGAGTGGTGA
NKp46 (CD335)	NM_0011 45457.1	146-245	TTTCATGGTTCCAAAGGAAAAGCAAGTGACCATCTGTTGCCAGGGAAATTATGGGGC TGTTGAATACCAGCTGCACTTTGAAGGAAGCCTTTTTGCCGTG
NKp44 (CD336)	NM_0048 28.3	307-406	ACGATGGCTTGGACCTCTCGATTACAATCTGGGACGACCCTGATGCTGGCTTCTTCA CTGTCACCATGACTGATCTGAGAGAGGAAGACTCAGGACATT
NKp30 (CD337)	NM_1471 30.1	51-150	GCATCTGTCTCTCTCCTCAGGGAGGCAAGCATTGATGCTCGAGGTCCCTGGCAGTT GTGGTCTTGGCAAGTATGTGTGAGTCCCCTGTGTCATAGG
CYORF14	NR_00154 4.2	144-243	GAGGCTGTCTGCCAACATCTTTCATCACTCTGCCTGCAACTATGAAAAATTTAGTTCTA AAAAATGCAACCTTGCTAAATTGAGTACTAATAGGATTGGT
Neil1	NM_0246 08.2	1676- 1775	TTAGCAGGAGGCTCTCCTTGCTTGCCTCACCCTTCTTATTGTCTTGCCTGCATCTG GGGGTCTGAATTTTTGGGAGCAGGCAATATCTGAAGGTGCA
Neil2	NM_1450 43.2	2571- 2670	GCCCGGTGGTGTGTAGAGAAAAGCTGCTTGTACTCTTAAGTCAATGTATTGGTG ACTGTTGATTTGTTGAACAATCAGGAATCAAGGGCTGTGGAG
NFAT5	NM_1732 14.1	3291- 3390	CCCTGACAACCTATTCAAACCCAGGACATCTCACAGCCTGGTACTTTTCCAGCAGTTTCT GCTTCTAGTCAGCTGCCAACAGCGATGCACTATTGCAGCA
NFATC1	NM_1723 90.1	2511- 2610	CCAGTACCAGCGTTTACCTACCTTCCCGCCAACGGTAACGCCATCTTCTAACCCTA AGCCGTGAACATGAGCGCGTGGGGTGCTTTTTCTAAAGACGC
NFATC2	NM_0123 40.3	1816- 1915	GACGGACATTGGAAGAAAGAACACGCGGGTGAGACTGGTTTTCCGAGTTCACATCC CAGAGTCCAGTGGCAGAATCGTCTTTACAGACTGCATCTAAC
NFATC3	NM_0045 55.2	2191- 2290	GTCCTTGAAGTTCCTCCATATCATAACCCAGCAGTTACAGCTGCAGTGCAGGTGCACT TTTATCTTTGCAATGGCAAGAGGAAAAAAGCCAGTCTCAAC
Nfix	NM_0025 01.2	586-685	AAGAACTGGATCTTTATCTGGCTTACTTTGTCCACACTCCGGAATCCGGACAATCAGA TAGTTCAAACCAGCAAGGAGATGCGGACATCAAACCACTGCC
NFkB	NM_0011 65412.1	2306- 2405	CTTGGGTAACCTCTGTTTTGCACCTAGCTGCCAAGAAGGACATGATAAAGTTCTCAGT ATCTTACTCAAGCACAAAAGGCAGCACTACTTCTTGACCAC
NKG7	NM_0056 01.3	633-732	CTGTGGCGGTCCCCGTCCTGGCTATGAAACCTTGTGAGCAGAAGGCAAGAGCGGCA AGATGAGTTTTGAGCGTTGATTCCAAAGGCCTCATCTGGAGCC
NOS2	NM_0006 25.4	606-705	TTGCCTGGGGTCCATTATGACTCCCAAAAGTTTGACCAGAGGACCCAGGGACAAGCC TACCCCTCCAGATGAGCTTCTACCTCAAGCTATCGAATTTGTC
Notch1	NM_0176 17.3	736-835	CTGCCAGGCTTACCCGGCCAGAAGTGTGAGGAAAATATCGACGATTGTCCAGGAAAC AACTGCAAGAACGGGGGTGCTGTGTGGACGGCGTGAACACCT
Notch3	NM_0004 35.2	1966- 2065	CTTTGGAGTCTGCCGTGATGGCATCAACCGCTACGACTGTGTCTGCCAACCTGGCTTC ACAGGGCCCCTTTGTAACGTGGAGATCAATGAGTGTGCTTCC
NR3C1	NM_0010 18077.1	1666- 1765	GCTTTCTCTCTGGCGGGAGAAGACGATTCTTCTTTTGAAGGAAACTCGAATGA GGACTGCAAGCCTCTCATTTTACCGGACACTAAACCCAAAATT
NR4A1	NM_0021 35.3	156-255	CGGCCGGGTAGGGTGCAGCCTGAGGCTTGTTCAGCAGAACAGGTGCAAGCCACATT GTTGCCAAGACCTGCCTGAAGCCGATTCTCCCACTGCCTCT
C5ORF13	NM_0011 42474.1	716-815	GTGAATCCACGTTTACAACCTTACAGGTGGGCCTTCAGGCCTGGTTGCTACAACAA TGCTTCCACAACCTCAAACCTCCACCGCGCTCACACAACCGG

NRIP1	NM_0034 89.2	336-435	TGACTCATGGAGAAGAGCTTGGCTCTGATGTGCACCAGGATTCTATTGTTTTAACTTA CCTAGAAGGACTACTAATGCATCAGGCAGCAGGGGATCAGG
Nrp1	NM_0038 73.5	371-470	GCCTCGCTGCTTTCTTTCTCCAAGACGGGCTGAGGATTGTACAGCTCTAGGCGGAGT TGGGGCTCTTCGGATCGCTTAGATTCTCCTCTTTGCTGCATT
NT5E	NM_0025 26.2	1215- 1314	ATTCGGGTTTTGAAATGGATAAACTCATCGCTCAGAAAGTGAGGGGTGTGGACGTC GTGGTGGGAGGACACTCCAACACATTTCTTTACACAGGCAATCC
OAZ1	NM_0041 52.2	314-413	GGTGGGCGAGGGAATAGTCAGAGGGATCACAATCTTTAGCTAACTTATTCTACTCC GATGATCGGCTGAATGTAACAGAGGAACTAACGTCCAACGACA
OPTN	NM_0010 08211.1	626-725	TGAAGCTAAATAATCAAGCCATGAAAGGGAGATTTGAGGAGCTTTGAGGCTGGACA GAGAAACAGAAGGAAGAACGCCAGTTTTTTGAGATACAGAGCAA
P2RX7	NM_0025 62.4	341-440	AGTTGGTGCACAGTGTCTTTGACACCGCAGACTACACCTTCCCTTTGCAGGGGAACTC TTTCTTCGTGATGACAACTTTCTCAAACAGAAGGCCAAGA
Pax5	NM_0167 34.1	2289- 2388	CTCCAAGAGGAGCACACTTTGGGGAGATGTCTGGTTTCTGCCTCCATTTCTCTGGG ACCGATGCAGTATCAGCAGCTTTTTCCAGATCAAAGAACTC
PDCD1	NM_0050 18.1	176-275	CTTCTTCCAGCCCTGCTCGTGGTGACCGAAGGGGACAACGCCACCTTCACCTGCAG CTTCTCCAACACATCGGAGAGCTTCGTGCTAAACTGGTACCGC
PDCD1LG2	NM_0252 39.3	236-335	TGTGGAGCTGTGGCAAGTCTCATATCAAATACAGAACATGATCTTCTCCTGCTAAT GTTGAGCCTGGAATTGCAGCTTACCAGATAGCAGCTTTATT
LOC282997	NR_02693 2.1	666-765	TGATCACATTCTACCTGGCATTATTTTCATCTGAGTCCCTGTCTAGCCCTTCTGCCATT AGACTGTAACCTTGTTTAGGGAAAGACCTGTGTCTTACTC
PDE3	NM_0009 21.3	3011- 3110	CTGGCCAACCTTCAGGAATCCTTCATCTCTCACATTGTGGGGCCTCTGTGCAACTCCT ATGATTGAGCAGGACTAATGCCTGGAAAATGGGTGGAAGACA
PDE4	NM_0011 11307.1	3856- 3955	AATAATGGTGTATACCCTCATTCTCATTCTGGGCAGCCCTTCTTCCACCTGGCACC AAAATAATTTCTCCTCCATCCGTACCTTGCTAGCCTCTCC
PDE7	NM_0026 04.2	2211- 2310	GTAGCTCAACAAGGAATAGAGGGAGGAGTGAATTTGGTAGCTGGTGTGAATAG GGCCTTTGAGAATCAGACTGAACACAGTGAATATGTGCCAAA
PKD1	NM_0026 10.3	1171- 1270	TGGATTGCCATATCACGTCTTTACGCACAATACTTCCAAGGAGACCTGAAGCTGTAT TCCCTAGAGGGTTACGGGACAGATGCAGTTATCTACATTAAG
PNK	NM_0036 81.3	581-680	TCCCGGAGGACCTCCTTCCCGTCTACAAAGAAAAAGTGGTGCCGCTTCAGACATTA TCACGCCCAACCAGTTTGAGGCCGAGTTACTGAGTGGCCGGAA
PECAM1	NM_0004 42.3	1366- 1465	ATCTGCACTGCAGGTATTGACAAAGTGGTCAAGAAAAGCAACACAGTCCAGATAGTC GTATGTGAAATGCTCTCCAGCCCAGGATTTCTTATGATGCC
PHACTR2	NM_0011 00165.1	1861- 1960	AGAGAGTCGACAGTTTACAAGTTTTATCGTCCATAACGAAGAGTGAGACTATTTGG AAACAGAGACTGATCATCTTTGGGGGAAGCCCTGCTTCTGAA
PHC1	NM_0044 26.2	2906- 3005	ATACAGCTCCACCTACACCGGAATTACATGGCATCAACCCTGTGTTCTGTCCAGTAA TCCAGCCGTTGGAGTGTAGAGGAGGTGTACGAGTTTATTGC
Pias3	NM_0060 99.3	836-935	CGACTCTCAGCCACTGTTCCCAACACCATTGTGGTCAATTGGTCATCTGAGTTCGGAC GGAATTACTCCTGTCTGTGTACCTGGTGAGGCAGTTGACTG
pkm2	NM_1824 71.1	2106- 2205	ATGGCAAGAGGGTGACAGCTTCTTTCTGTGTGTACTCTGTCCAGTTCCTTAGAAA AAATGGATGCCAGAGGACTCCAACCCTGGCTTGGGGTCAA
POLR1B	NM_0190 14.3	3321- 3420	GGAGAACTCGGCCTTAGAATACTTTGGTGAGATGTTAAAGGCTGCTGGCTACAATTT CTATGGCACCGAGAGGTTATATAGTGGCATCAGTGGGCTAGAA
POLR2A	NM_0009 37.2	3776- 3875	TTCCAAGAAGCCAAAGACTCCTTCGCTTACTGTCTTCTGTTGGGCCAGTCCGCTCGA GATGCTGAGAGAGCCAAGGATATTCTGTGCCGTCTGGAGCAT
POP5	NM_0159 18.3	561-660	GCTTCAGGCCCACTTGTTGAACAGAACAATCTGGGTAGCAACAGCATCTTCCACAGTT TTCCAAACTGGATAGCTGCCAACCAGCAGACATTACCACTT
Pou2af1	NM_0062 35.2	1676- 1775	CCCTGATGCCAGAGTCTTGAGCTGTCAGTTCACAGTTGCTCCTTTGTTGCTCTTC TCAGCCTCGGCCAGATTTACAGTCCAGGCAGCAAATCTCA
4-Oct	NM_0027 01.4	1226- 1325	AAGTTCTTACTTAAGGAAGGAATTGGGAACACAAAGGGTGGGGCAGGGGA GTTTGGGGCAACTGTTGGAGGGAAAGGTGAAGTTCAATGATGCTC
PPARA	NM_0010 01928.2	5221- 5320	GGGTGTGTTTGCTATACGAACATAATGGACGTGAAGTGGGGCAGAAACCCAGA CAGATTCAAGGATGCCAGGAGAGCTGTCCCTGTTTTAAAGAG

Pparg	NM_0158 69.3	1036- 1135	GAGCAAAGAGGTGGCCATCCGCATCTTTCAGGGCTGCCAGTTTCGCTCCGTGGAGGC TGTGCAGGAGATCACAGAGTATGCCAAAAGCATTCTGTTTT
PPP2R1A	NM_0142 25.3	1441- 1540	AACTTAACTCCTTGTGCATGGCCTGGCTTGTGGATCATGTATATGCCATCCGCGAGGC AGCCACCAGCAACCTGAAGAAGCTAGTGGAAAAGTTTGGGAA
PRDM1	NM_1829 07.1	311-410	CATCCCTGCCAACCAGGAACCTTCTTGTGTGGTATTGTCGGGACTTTGCAGAAAGGCTT CACTACCCTTATCCCGGAGAGCTGACAATGATGAATCTCACA
PRF1	NM_0050 41.3	2121- 2220	ACTGTTTTTCAGGGAGGTGGCTGGGTTTACACGCTAATCCCGATTACCCCTGTCCAAA CTGCCTAAGCCCTCCGCCATTCTCAAGCCCTGCAGTCACAGC
AMPK	NM_0062 52.2	976-1075	ATAGTGGTGACCCTCAAGACCAGCTTGCAGTGGCTTATCATCTTATCATTGACAATCG GAGAATAATGAACCAAGCCAGTGAGTTCTACCTCGCCTCTAG
PRKCA	NM_0027 37.2	5561- 5660	CCGGCAGTGCTTCCCTTCTTTCATCCACTGGCCTCGTGTGGTCCATGCAGGGCCACT GTCTGCCCTTCTGATGCCACGTATTAGGCTTCTTACTCAG
Prkcq	NM_0062 57.2	1326- 1425	GATGGACGATGATGTTGAGTGCACGATGGTAGAGAAGAGAGTTCTTTCCTTGGCCTG GGAGCATCCGTTTCTGACGCACATGTTTTGTACATTCCAGACC
Prmt5	NM_0061 09.3	1696- 1795	TTGCACCTTGAATTTCTGTGGAGGTGAACACAGTACTACATGGCTTTCGCCGGCTAC TTGAGACTGTGCTTATCAGGACATCACTCTGAGTATCCGT
PROM1	NM_0060 17.1	926-1025	AGCCTGCGGTCATCTCTCAATGACCCTCTGTGCTTGGTGCATCCATCAAGTGAAACCT GCAACAGCATCAGATTGTCTCTAAGCCAGCTGAATAGCAACC
prss12	NM_0036 19.3	2161- 2260	AAGAAATTGGAGTTCAACAGATTGTGATTATCGGGAGTATCGACCCGACCGCAGTG ATTATGACATAGCCCTGGTTAGATTACAAGGACCAGAAGAGCA
PTGER2	NM_0009 56.2	1411- 1510	GTCAGAAGGAGCTACAAAACCTACCCTCAGTGAGCATGGTACTTGGCCTTGGAGGA ACAATCGGCTGCATTGAAGATCCAGCTGCCTATTGATTTAAGC
PTK2	NM_0056 07.3	1006- 1105	GGTTCAAGCTGGATTATTTTCAGTGGAACTGGCAATCGGCCAGAAGAAGGAATCAG TTACCTAACGGACAAGGGCTGCAATCCCACACATCTTGCTGACT
SHP2	NM_0028 34.3	4651- 4750	TAGTCCCTAGGTTGCTACGGCTTATCATGTGCTTGGTAAAAGGTGATCGCAGGTTCTC AGACGAGTTTACTTTACATGAGATGGAATCAGGCAGAGAGGC
Ptpn4	NM_0028 30.2	706-805	TCGAGGCTTTTTTCTCCAGCCGAGAGGACGCGGCTGTGATATACGAAGACTTTGTG TGGACAGTAATGACCTCACGTTTCCGATTGCCTGCTGGCAGAA
SHP-1	NM_0028 31.5	1735- 1834	TGGTGCAGACGGAGGCGCAGTACAAGTTCATCTACGTGGCCATCGCCAGTTCATTG AAACCACTAAGAAGAAGCTGGAGGTCCTGCAGTCGCAGAAGGG
PTPRK	NM_0011 35648.1	4316- 4415	GTGATCAACCGGATTTTTAGGATATGCAATCTAACAGACCACAGGAAGGTTATCTG ATGGTGCAACAGTTTCAGTACCTAGGATGGGCTTCTCATCGAG
Rab31	NM_0068 68.3	3801- 3900	TTTTGTAAAGAGCTTCCATCTGGGCTGGACCCAGTTCTTGCACATACAAGACACCGCT GCAGTCAGCTAGGACCTTCCGCCATGTATTCTATTCTGTAG
RAC1	NM_1988 29.1	1251- 1350	AAAGACCTTCGTCTTTGAGAAGACGGTAGCTTCTGCAGTTAGGAGGTGCAGACACTT GCTCTCCTATGTAGTTCTCAGATGCGTAAAGCAGAACAGCCTC
RAC2	NM_0028 72.3	1070- 1169	GCTGCCACAACCTGTGTACCTCAGGGATGGGGCTTACTCCCTCCTGAGGCCAGCT GCTCTAATATCGATGGTCTGCTTGCCAGAGAGTTCCTCTAC
Raf-1	NM_0028 80.2	1991- 2090	CCTATGGCATCGTATTGTATGAACTGATGACGGGGGAGCTTCTTATTCTCACATCAA CAACCGAGATCAGATCATCTTCATGGTGGGCCGAGGATATGC
GARNL4	NM_0150 85.4	4141- 4240	CCCACGGCTGGAAAGAGGCCTGTACGTTCTGGACGCGTTTTGTTGGCTGGGCTTCTG GAGGCACTGGCAAGGTCAAACCTGCATTTCTTAAAGAACAGTTG
RARA	NM_0009 64.2	116-215	AGCCACCTAGCTGGGGCCCATCTAGGAGTGGCATCTTTTTTGGTGCCTGAAGGCCA GCTCTGGACCTTCCAGGAAAAGTGCCAGCTCACAGAACTGCT
Rbpms	NM_0010 08710.1	843-942	AAACAGCCTGTAGTTTTTGTAGTTTTGACAGTCGCTCAGAAGCAGAGGCTGCAAAG AATGCTTTGAATGGCATCCGCTTCGATCCTGAAATTCCGCAA
Relb	NM_0065 09.2	251-350	CACTCTCGCTCGCCGTTTCCAGGAGCACAGATGAATTGGAGATCATCGACGAGTACA TCAAGGAGAACGGCTTCGGCCTGGACGGGGGACAGCCGGGCC
RHOA	NM_0016 64.2	1231- 1330	GGTACTCTGGTGAAGTACCACCTTCAGGGCTTACTCCGTAACAGATTTTGTGGCATA GCTCTGGGGTGGGCAGTTTTTGAATGGGCTCAACCAGAA
RNF125	NM_0178 31.3	791-890	GCAAGGTGTGTATGTCCCTTTTGTGAGAGGGAAGTGTATGAAGACAGCTTGCTGGAT CATTGTATTACTCATCACAGATCGGAACGGAGGCCTGTGTTCT

RORA	NM_1342 61.2	1716- 1815	AAAATTAACCGAGACACTTTATATGGCCCTGCACAGACCTGGAGCGCCACACACTGC ACATCTTTTGGTGATCGGGGTCAGGCAAAGGAGGGGAAACAAT
RORC	NM_0010 01523.1	1351- 1450	CTCATCAATGCCATCGGCCAGGGCTCCAAGAGAAAAGGAAAAGTAGAACAGCTGCA GTACAATCTGGAGCTGGCCTTTCATCATCATCTCTGCAAGACTC
RPL27	NM_0009 88.3	24-123	GGGCCGGGTGGTTGCTGCCGAAATGGGCAAGTTCATGAAACCTGGGAAGGTGGTGC TTGTCCTGGCTGGACGCTACTCCGGACGCAAAGCTGTCATCGTG
Rps13	NM_0010 17.2	332-431	GCATCTTGAGAGGAACAGAAAGGATAAGGATGCTAAATCCGTCTGATTCTAATAGA GAGCCGATTACCGTTTGGCTCGATATTATAAGACCAAGCGA
RRM2	NM_0010 34.1	1616- 1715	AGGGGTGACCCCTTAGTGAGCTTAGCACAGCGGGATTAAACAGTCCTTTAACCAGCA CAGCCAGTTAAAAGATGCAGCCTCACTGCTTCAACGCAGATTT
RUNX1	NM_0017 54.4	636-735	CAGCCATGAAGAACCAGGTTGCAAGATTTAATGACCTCAGGTTTGTGCGTCGAAGTG GAAGAGGGAAAAGCTTCACTCTGACCATCACTGTCTTACAAA
RUNX2	NM_0043 48.3	1851- 1950	GAAGCCACAGCAGTTCCTCAACTGTTTTGAATTCTAGTGGCAGAATGGATGAATCTG TTTGGCGACCATATTGAAATTCCTCAGCAGTGGCCAGTGTA
RUNX3	NM_0043 50.1	2086- 2185	GTGGTCTCATAATTCATTTGTGGAGAGAACAGGAGGGCCAGATAGATAGGTCCTA GCAGAAGGCATTGAGGTGAGGGATCATTTTGGGTCAGACATCAA
S100A4	NM_0029 61.2	264-363	CAGGGACAACGAGGTGGACTTCCAAGAGTACTGTGTCTTCTGTCTGCATCGCCAT GATGTGTAACGAATCTTTGAAGGCTTCCAGATAAGCAGCCC
S100A6	NM_0146 24.3	407-506	GAAGGAGCTGAAGGAGCTGATCCAGAAGGAGCTCACCATTGGCTCGAAGCTGCAGG ATGCTGAAATTGCAAGGCTGATGGAAGACTTGACCCGGAACAAG
s1pr1	NM_0014 00.3	1066- 1165	CCTGACGTTCCGCAAGAACATTTCCAAGGCCAGCCGAGCTCTGAGAAGTCGCTGGC GCTGCTCAAGACCGTAATTATCGTCTGAGCGTCTTCATCGCC
s1pr4	NM_0037 75.2	496-595	CAAGACCAGCCGCTTACGGCTTCATCGGCCTGCTGGCTGCTGGCCGCGCTGCT GGGGATGCTGCCTTTGCTGGGCTGGAAGTGCCTGTGCGCCTTT
s1pr5	NM_0307 60.3	1416- 1515	TGCCCTCGTGAATTGACGTTCTGCTTGGGAACACAGAAAAGAAGTCCGGTGATGAAA TAATGGAGATGATTCCAGTGACAAACGACAGAGATGGTGATGG
SATB1	NM_0011 31010.1	1336- 1435	TTCCGAAATCTACCAGTGGGTACGCGATGAACTGAAACGAGCAGGAATCTCCCAGGC GGTATTTGCACGTGTGGCTTTAACAGAACTCAGGGCTTGCTT
Scmh1	NM_0122 36.2	881-980	AACCCTCATTTCAATTTGCCAGCCACTATTGGGGAGGTTCCGGGCTCAGAGGTGCTT GTCATTTTGATGGGTGGCGAGGGGCTTTGACTACTGGTGCC
SCML1	NM_0010 37540.1	926-1025	GCAACGTATGGTTCTTCTCAGGGCTCTGCCTTGGCAACCTCGGGCTGACAGCATCC ACAACACTTACTCAACTGACCATGCTTCTGCAGCACACCTT
SCML2	NM_0060 89.2	361-460	ATTGGAAGCCCGTGACCCTCGCAATGCCACTTCAGTATGTATTGCTACGGTTATTGGA ATTACTGGGGCCAGGTTACGGTTACGACTGGATGGTAGTGAC
SEL1L	NM_0050 65.4	981-1080	GGGCAATCTAATAGCCACATGGTTTTGGGTTACAGATACTGGGCTGGCATCGGCGT CCTCCAGAGTTGTGAATCTGCCCTGACTCACTATCGTCTTGTT
SELL	NM_0006 55.3	111-210	CTCCCTTTGGGCAAGGACCTGAGACCTTGTGCTAAGTCAAGAGGCTCAATGGGCTG CAGAAGAACTAGAGAAGGACCAAGCAAAGCCATGATATTTCCA
CLA	NM_0030 06.3	2298- 2397	CATGGGCTGTTAGGTTGACTTCAGTTTTGCCTCTTGGACAACAGGGGGTCTTGACAT CCTTGGGTGACCAGGAAAAGTTCAGGCTATGGGGGGCCAAAG
SERPINE2	NM_0062 16.2	241-340	CGCTGCCTTCCATCTGCTCCCACTTCAATCCTCTGTCTCTCGAGGAACTAGGCTCCAAC ACGGGGATCCAGGTTTTCAATCAGATTGTGAAGTCGAGGCC
LNK	NM_0054 75.2	4286- 4385	CCTCCAGCCAGAAGTTAAACATCTGGGATATGACGTCTTCATGCCAGGGGCACTCAT TTCTTAGCAGCCTCTACATACTCTCAGGTGGTGCCAAG
Sh2d2a	NM_0011 61443.1	342-441	TGCTGGAGCCCAAGCCTCAGGGGTGCTACTTGGTGCAGGTTACAGGAGAGCGCGGTG ACCTTCGTGCTGACTTACAGGAGCCGACTTGCTGCCGCCACTT
SIRT3	NM_0122 39.5	1546- 1645	GAATCAGACCAACTGGAATCCCAGACCGAGTCTGCTTTCTGTGCCTAGTTGAACGGC AAGCTCGGCATCTGTTGGTTACAAGATCCAGACTTGGGCCGAG
SIT1	NM_0144 50.2	721-820	GCCCCAGCCCCCGTAGCAGGGGCATGACTGTTTCCAACCAGCACCCAAAGACGGG CGCCATTGCAAGTACAGGATGTGATCTACCCCGACTTCTT
Skap1	NM_0037 26.3	1361- 1460	AAGTGGGAAGAGGCAGTTCATCAAACCTGTTACTAAACCAGCCTAGTCATAGCTCA TCCCATCTCTAAATGTGTCCACACAACCACATCTGCCTTTTC

SCAP2	NM_0039 30.3	3375- 3474	TTTTACAGTTAATCCAGGAGAGGGAGTCCTTTGCCAACTGATGACCAACAGTTCCAA GCCAGATAGTCTCGTGAACAGTGACAATACAGAAATAAGGTGT
SLA2	NM_0322 14.2	1641- 1740	AAAGGAAAGCTGAGATGATGTCTTACCGTAGCAGCAGATCTTGATGGTCCAGGCTC TATGTGACCTCCAGAGCAAAGAGAAAGACTTCGGACAGTCTAG
SLAMF1	NM_0030 37.2	581-680	GTGTCTCTTGATCCATCCGAAGCAGGCCCTCCACGTTATCTAGGAGATCGCTACAAGT TTTATCTGGAGAATCTCACCTGGGGATACGGGAAAGCAGGA
SLAMF7	NM_0211 81.3	216-315	GGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATG GAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCA
SLC2A1	NM_0065 16.2	2501- 2600	AGGCTCCATTAGGATTTGCCCTTCCCATCTCTTCTACCCAACCACTCAAATTAATCT TTCTTTACCTGAGACCAGTTGGGAGCACTGGAGTGCAGGGA
slfn5	NM_1449 75.3	511-610	GAAGCTCTGGCATTCTCAAATGCAGGACTCAGACTCCAACGAATATTAATGTTTCCA ATTCATTAGGTCCACAGGCAGCTCAGGGTAGTGTACAATATG
SMAD3	NM_0059 02.3	4221- 4320	TTAAAGGACAGTTGAAAAGGGCAAGAGGAAACCAGGGCAGTTCTAGAGGAGTGCT GGTACTGGATAGCAGTTTTAAGTGGCGTTCACCTAGTCAACACG
SMAD4	NM_0053 59.3	1371- 1470	AGGTTGCACATAGGCAAAGGTGTGCAGTTGGAATGTAAAGGTGAAGGTGATGTTTG GGTCAGGTGCCTTAGTGACCACGCGGTCTTTGTACAGAGTTACT
Smad7	NM_0059 04.2	1836- 1935	AGCAGAAATCCAAGCACCAACACAGTGTATGAAGGGGGGCGGTATCATTTTC ACTTGTGAGGAGTGTGTGTGAGTGTGAGTGTGCGGCTGTGTGTG
Smyd1	NM_1982 74.3	654-753	TGCAGGCCGTGGGCGTAGGCATCTTCCCAACCTGGGCCTGGTGAACCATGACTGTT GGCCCAACTGTACTGTCATATTTAACAATGGCAATCATGAGGC
Smyd3	NM_0227 43.1	966-1065	TCAACCTCGGCCTGTTGGAGGAAGCCTTGTCTATGGTACTCGACCATGGAGCCAT ACAGGATTTTTTCCAGGAAGCCATCCCGTCAGAGGGGTTCA
SNAI1	NM_0059 85.2	64-163	GACCACTATGCCGCGCTCTTCTCGTCAGGAAGCCCTCCGACCCCAATCGGAAGCCT AACTACAGCGAGCTGCAGGACTCTAATCCAGAGTTTACCTTC
SOCS1	NM_0037 45.1	1026- 1125	TTAACTGTATCTGGAGCCAGGACCTGAACTCGCACCTCTACCTTTCATGTTTACATA TACCCAGTATCTTTCACAAACCAGGGTTGGGGGAGGGTC
SOCS3	NM_0039 55.3	1871- 1970	GGAGGATGGAGGAGACGGGACATCTTTCACCTCAGGCTCCTGGTAGAGAAGACAGG GGATTCTACTCTGTGCCTCCTGACTATGTCTGGCTAAGAGATTC
SOD1	NM_0004 54.4	36-135	GCCTATAAAGTAGTCGCGGAGACGGGGTGCTGGTTTGCCTGCTAGTCTCCTGCAGCG TCTGGGGTTTCCGTTGCAGTCTCGGAACCAGGACCTCGGCGT
SOX13	NM_0056 86.2	3040- 3139	ATTTATTGAGTGCCCACTACGTGCCAGGCACTGTTGCTGAGTTCCTGTGGGTGTGTCT CTCGATGCCACTCCTGCTTCTCTGGGGCCTCTTCTGTGCT
Sox2	NM_0031 06.2	152-251	CTTAAGCCTTTCCAAAAATAATAACAATCATCGGCGGCGGCAGGATCGGCCAG AGGAGGAGGGAAGCGCTTTTTTGTATCTGATTCCAGTTTGCC
SOX4	NM_0031 07.2	3041- 3140	GTTACGGTCAAACCTGAAATGGATTTGCACGTTGGGGAGCTGGCAGGCGGCGGCTGC TGGGCTCCGCCTTCTTCTACGTGAAATCAGTGAGGTGAGAC
Sox5	NM_1529 89.2	1886- 1985	TAGCCATGCAATGATGGATTTCAATCTGAGTGGAGATTCTGATGGAAGTGCTGGAGT CTCAGAGTCAAGAATTTATAGGGAATCCCGAGGGCGTGGTAGC
SPI1	NM_0031 20.1	731-830	CTCCGCAGCGGCGACATGAAGGACAGCATCTGGTGGTGGACAAGGACAAGGGCA CCTCCAGTTCTCGTCCAAGCACAAGGAGGCGTGGCGCACCGCT
CD43	NM_0010 30288.1	2799- 2898	AAGCCAGGCTTCATGGAAAGATCGTATGTGTGACCCAAATATGAGTTCTTCAGCTCA GCCATGGTAATCCCTTCTTGAAGTCTCCATTTCTGCAGTACA
Spry2	NM_0058 42.2	86-185	AAAGAGGAAATACTCCGCGTGCCTTGTAGAAGGGGAGTCGTCTCCAGCTCCGAAC CCCGGAGTGTTATCAGCGGGGAATCTGGCTCCGAATTCTCTTT
STAT1	NM_0073 15.2	206-305	TTTGCTGTATGCCATCCTCGAGAGCTGTCTAGGTTAACGTTCCGACTCTGTGTATATA ACCTCGACAGTCTTGGCACCTAACGTGCTGTGCGTAGCTGCT
Stat2	NM_0054 19.2	1966- 2065	CCGTACACGAAGGAGGTGCTGCAGTCACTCCCGCTGACTGAAATCATCCGCCATTAC CAGTTGCTCACTGAGGAGAATATACCTGAAAACCACTGCGCT
STAT3	NM_1392 76.2	4536- 4635	AGACTTGGGCTTACCATTGGGTTTAAATCATAGGGACCTAGGGCGAGGGTTCAGGG CTTCTCTGGAGCAGATATTGTCAAGTTCATGGCCTTAGGTAGCA
STAT4	NM_0031 51.2	790-889	AGACAATGGATCAGAGTGACAAGAATAGTGCCATGGTGAATCAGGAAGTTTTGACA CTGCAGGAAATGCTTAACAGCCTCGATTTCAAGAGAAAGGAGGC

STAT5A	NM_0031 52.2	3461- 3560	GAGACAGAGAGAGAGAAAAGAGAGAGTGTGTGGGTCTATGTAATGCATCTGTCCTC ATGTGTTGATGTAACCGATTCTCTCTCAGAAGGGAGGCTGGGG
STAT5B	NM_0124 48.3	201-300	AAGGAGAAGCCCTTCATCAGATGCAAGCGTTATATGGCCAGCATTTTCCCATTGAGG TGCGGCATTATTTATCCCAGTGGATTGAAAGCCAAGCATGGGA
Stat6	NM_0031 53.3	2031- 2130	AGAACATCCAGCCATTCTCTGCCAAAGACCTGTCCATTGCTCACTGGGGGACCGAA TCCGGGATCTTGCTCAGCTCAAAAATCTCTATCCCAAGAAGCC
STMN1	NM_2034 01.1	288-387	CGTGGGTGCGGCCAGGACTTTCCTTATCCCAGTTGATTGTGCAGAATACACTGCCTG TCGCTTGCTTCTATTACCATGGCTTCTTGATATCCAGGT
Syk	NM_0031 77.3	1686- 1785	CGGACTCTCAAAGCACTGCGTGCTGATGAAACTACTACAAGGCCAGACCCATGG AAAGTGGCCTGTCAAGTGGTACGCTCCGGAATGCATCAACTAC
SYNE2	NM_1829 14.2	20436- 20535	CTGGTAGAACGTCAACCTCAAGTGGACATGTTACAGGAGATTTCAAACAGCCTTCTC ATTAAGGGACATGGAGAAGACTGTATTGAAGCTGAAGAAAAGG
Taf2	NM_0031 84.3	3151- 3250	ACTTCACATGACTGGAGTTACGGTGTGGTGTGGACTGTACTTCACACTTTTTG GCCTCAGTAGACCTTCTGTTTACCCTTGCCAGAGCTTGGGT
Taf9	NM_0010 15891.1	316-415	CACCCTCCAACCTTTCGCGACGGAATGTGTCATCGAAAGCCAGGTACACCAGGGGTTG GAAAAACCACACTAGGCAAAGAAGTTCGCTCAAAAATCAGGACT
TAL1	NM_0031 89.2	4636- 4735	ACAGCATCTGTAGTCAGCCGACAACTATTTTCGGCCTTTTGGGGGTGGGTCTGGCCGT ACTTGTGATTTTCGATGGTACGTGACCCTCTGCTGAAGACTTGC
TBP	NM_0031 94.3	26-125	CGCCGGCTGTTAACTTCGCTTCCGCTGGCCCATAGTGATCTTTCAGTGACCCAGCA GCATCACTGTTTCTTGGCGTGTGAAGATAACCCAAGGAATTG
TBX21	NM_0133 51.1	891-990	ACACAGGAGCGCACTGGATGCGCCAGGAAGTTTCATTTGGGAACTAAAGCTCACA AACAACAAGGGGGCGTCCAACAATGTGACCCAGATGATTGTGCT
Tbx6	NM_0046 08.3	807-906	GACAGCTACCAGAACCCACAGATCACACAAGTGAAGATTGCAGCCAATCCCTTTGC CAAAGGCTTCCGGGAGAACGGCAGAACTGTAAGAGGGAGCGA
TBXA2R	NM_0010 60.3	386-485	CACACGCGCTCCTCCTTCTCACCTTCTCTGCGCCTCGTCTCACCGACTTCTGGG GCTGCTGGTGACCGGTACCATCGTGGTGTCCAGCACGCGG
Tcf12	NM_2070 37.1	1106- 1205	CACATGACCGCTTGAGTTATCCTCCACACTCAGTTTACCAACAGACATAAACACGAG TCTTCCACCAATGTCCAGCTTTCATCGCGGCAGTACCAGCAG
tcf19	NM_0071 09.2	2081- 2180	CATGGACACCAGAATATCTGTAGTCAGAGCACCTATCAGTTGCAAAGCCATGCCTG CAACCGATGGAAAATGTAAGAGGGAGTTCTTAAGTTCTTGGT
Tcf20	NM_0056 50.1	926-1025	CAATGTGAATGCTGGATCTCAGTATGAAGGACACAATGTGGGTTCTAATGCACAGGC TTATGGAACACAATCCAATTACAGCTATCAGCCTCAATCTATG
E2A	NM_0032 00.3	859-958	ACGTTTGGTGGCCTGCACCAGCACGAGCGTATGGGCTACCAGCTGCATGGAGCAGA GGTGAACGGTGGGCTCCCATCTGCATCCTCCTTCTCCTCAGCCC
Tcf4	NM_0031 99.1	1456- 1555	TGGAATCATTGGACCTTCTCATAATGGAGCCATGGGTGGTCTGGGCTCAGGGTATGG AACCGCCTTCTTTCAGCCAACAGACATTCACTCATGGTGGGG
Tcf7	NM_0032 02.2	2421- 2520	ATTCCATTTCCAGTTCATCTATGGCAGTCCAGCCAGCTCCTGGGCAGCTTGAGAGGGC AAACCCAAAACCTCATGACAGCCAGAGCCTGTCTTTCAGCAT
TDGF1	NM_0032 12.2	1568- 1667	AAGGAAAAGAAAACATCTTTAAGGGGAGGAACCAGAGTGTGAAGGAATGGAAGTC CATCTGCGTGTGTGCAGGGAGACTGGGTAGGAAAGAGGAAGCAAA
TDO2	NM_0056 51.2	496-595	AGAGTACTTATCTCCAGCATCAGGCTTCCAGAGTTTGCAATTCCGACTATTAGAAAAC AAGATAGGTGTTCTTTCAGAACATGAGAGTCCCTTATAACAGA
TEK	NM_0004 59.2	616-715	CGAGTTCGAGGAGAGGCAATCAGGATACGAACCATGAAGATGCGTCAACAAGCTTC CTTCTACCAGCTACTTTAACTATGACTGTGGACAAGGGAGATA
Trf	NM_0032 18.3	1038- 1137	CTGAAAGCAGAATACCTGTTTCAAAGAGTCAGCCGGTAACTCCTGAAAAACATCGAG CTAGAAAAAGACAGGCATGGCTTTGGGAAGAAGACAAGAATTT
TERT	NM_1982 53.1	2571- 2670	GGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACCTTTGGGGTCTTGCGGCTGAA GTGTACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGA
TF	NM_0010 63.2	641-740	CTGCTCCACCCTTAACCAATACTTCGGTACTCGGGAGCCTTCAAGTGTCTGAAGGAT GGTGTGGGGATGTGGCCTTTGTCAAGCACTCGACTATATTT
Tcfe3	NM_0065 21.3	2936- 3035	GGTATTAGTGGGGGACTGAGTTCAGGTTACCAGAACCAGTACCTCAGTATTCTTTTTC AACATGTAGGGCAAGAGGATGAAGGAAGGGGCTATCCTGGGA

TFRC	NM_0032 34.1	1221- 1320	CAGTTTCCACCATCTCGGTCATCAGGATTGCCTAATATACCTGTCCAGACAATCTCCA GAGCTGCTGCAGAAAAGCTGTTTGGGAATATGGAAGGAGACT
TGFA	NM_0032 36.2	781-880	TGCCACAGACCTTCTACTTGGCCTGTAATCACCTGTGCAGCCTTTTGTGGGCCTTCA AAACTCTGTCAAGAACTCCGTCTGCTTGGGGTTATTCAAGTGT
TGFB1	NM_0006 60.3	1261- 1360	TATATGTTCTTCAACACATCAGAGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCT CCCGGGCAGAGCTGCGTCTGCTGAGGCTCAAGTTAAAAGTGG
TGFB2	NM_0032 38.2	1126- 1225	AAGCCAGAGTGCCTGAACAACGGATTGAGCTATATCAGATTCTCAAGTCCAAAGATT TAACATCTCCAACCCAGCGCTACATCGACAGCAAAGTTGTGAA
TGFBR1	NM_0046 12.2	4281- 4380	GGGAAAATACGACTTAGTGAGGCATAGACATCCCTGGTCCATCCTTTCTGTCTCCAGC TGTTTCTTGGAACCTGCTCTCCTGCTTGCTGGTCCCTGACGC
Thymidine_ kinase	SCFV007.1	101-200	TCTACGTACCCGAGCCGATGACTTACTGGCAGGTGCTGGGGGCTCCGAGACAATCG CGAACATCTACACCACACAACACCGCTCGACCAGGGTGAGAT
TIE1	NM_0054 24.2	2611- 2710	CATCGGGGAGGGAACTTCGGCCAGTTCATCCGGGCCATGATCAAGAAGGACGGG CTGAAGATGAACGCAGCCATCAAATGCTGAAAGAGTATGCCTCT
TLR2	NM_0032 64.3	181-280	CTGCTTCAACTGGTAGTTGTGGGTTGAAGCACTGGACAATGCCACATACTTTGTGG ATGGTGTGGGTCTTGGGGTGCATCATCAGCCTCTCCAAGGAAG
TLR8	NM_1386 36.3	2796- 2895	GACAAAAACGTTCTCCTTGTCTAGAGGAGAGGGATTGGGATCCGGGATTGGCCATC ATCGACAACCTCATGCAGAGCATCAACCAAAGCAAGAAAACAG
TNF	NM_0005 94.2	1011- 1110	AGCAACAAGACCACCACTTCGAAACCTGGGATTGAGGAATGTGTGGCCTGCACAGTG AAGTGCTGGCAACCACTAAGAATCAAACCTGGGGCCTCCAGAA
HVEM	NM_0038 20.2	917-1016	CTCAGGGAGCCTCGTCATCGTCATTGTTTGTCCACAGTTGGCCTAATCATATGTGTG AAAAGAAGAAAGCCAAGGGGTGATGTAGTCAAGGTGATCGTC
TNFRSF18	NM_0041 95.2	446-545	AGGGGAAATTCAGTTTTGGCTTCCAGTGTATCGACTGTGCCTCGGGGACCTTCTCCG GGGGCCACGAAGGCCACTGCAAACCTTGGACAGACTGCACCCA
TNFRSF1B	NM_0010 66.2	836-935	CCCAGCTGAAGGGAGCACTGGCGACTTCGCTCTTCCAGTTGGACTGATTGTGGGTGT GACAGCCTTGGGTCTACTAATAATAGGAGTGGTGAAGTGTGTC
TNFRSF4	NM_0033 27.2	201-300	CCGTGCGGGCCGGGCTTCTACAACGACGTGGTCAGCTCCAAGCCGTGCAAGCCCTGC ACGTGGTGTAACCTCAGAAGTGGGAGTGAGCGGAAGCAGCTGT
TNFRSF9	NM_0015 61.4	256-355	AGATTTGCAGTCCCTGTCTCCAATAGTTTCTCCAGCGCAGGTGGACAAAGGACCT GTGACATATGCAGGCAGTGTAAGGTGTTTTCAGGACCAGGAA
TNFSF10	NM_0038 10.2	116-215	GGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTGATCTTCACAGTGCTCCT GCAGTCTCTGTGTGGCTGTAACCTTACGTGTACTTTACCAAC
CD254	NM_0037 01.2	491-590	TACCTGATTCATGTAGGAGAATTAACAGGCCTTTCAAGGAGCTGTGCAAAAGGAAT TACAACATATCGTTGGATCACAGCACATCAGAGCAGAGAAAGC
TNFSF14	NM_0038 07.2	271-370	ATTTTCAGAAGCCTCTGGAAAGTCGTGCACAGCCCAGGAGTGTGAGCAATTTCCGGT TTCCTCTGAGGTTGAAGGACCCAGGCGTGTGAGCCCTGCTCCA
CD252 (Ox40L)	NM_0033 26.2	546-645	GAAGGTCAGGTCTGTCAACTCCTTGATGGTGGCCTCTGACTTACAAAGACAAAGT CTACTTGAATGTGACCACTGACAATACCTCCCTGGATGACTTC
TOX	NM_0147 29.2	575-674	CACAGTCTCCAATATGCTGGGCCAGGATGGAACACTGCTTTCTAATTCCATTTCTGTG ATGCCAGATATACGAAACCCAGAAGGAAGTCAAGTACAGTTCC
TP53	NM_0005 46.2	1331- 1430	GGGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAGGGTCAAGTCTACCTCCC GCCATAAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC
TRAF1	NM_0056 58.3	3736- 3835	CGAGTGATGGGTCTAGGCCCTGAAACTGATGTCTAGCAATAACCTCTTGATCCCTAC TCACCGAGTGTTGAGCCCAAGGGGGGATTTGTAGAACAAGCC
TRAF2	NM_0211 38.3	1326- 1425	GTGGCCCTTCAACCAGAAGGTGACCTAATGCTGCTCGACCAGAATAACCGGGAGCA CGTGATTGACGCCTTCAAGCCCGACGTGACTTCATCCTCTTTT
TRAF3	NM_1457 25.1	1796- 1895	ATATGATGCCCTGCTTCTTGGCCGTTAAGCAGAAAGTGACACTCATGCTGATGGAT CAGGGGTCTCTCGACGTCAATTTGGGAGATGCATTCAAGCCC
GILZ	NM_1980 57.2	1401- 1500	TTAAGCAGAGGCAACCTCTCTTCTCTCTGTTTCGTGAAGGCAGGGGACACAGAT GGGAGAGATTGAGCCAAGTCAAGCCTTCTGTTGGTTAATATGGT
TSLP	NM_0330 35.3	396-495	CCGTCTTGTAGCAATCGGCCACATTGCCTTACTGAAATCCAGAGCCTAACCTTCAA TCCCACCGCCGGCTGCGCGTCTCGCCAAAGAAATGTTTCGC

Txk	NM_0033 28.1	801-900	ATGACTCGTCTCCGATATCCAGTTGGGCTGATGGGCAGTTGTTTACCAGCCACAGCT GGGTTTAGCTACGAAAAGTGGGAGATAGATCCATCTGAGTTGG
TYK2	NM_0033 31.3	486-585	TCATCGCTGACAGCTGAGGAAGTCTGCATCCACATTGCACATAAAGTTGGTATCACTC CTCCTTGCTTCAATCTCTTTGCCCTCTTCGATGCTCAGGCC
DAP12	NM_0033 32.3	362-461	TCCAGGGTCAGAGGTCGGATGTCTACAGCGACCTCAACACACAGAGGCCGTATTACA AATGAGCCCCGAATCATGACAGTCAGCAACATGATACCTGGATC
STS2 (Ubash3a)	NM_0010 01895.1	1971- 2070	GAGATGCTGCTGTTTCCAGAGGCGTCTTAGTCTCACCAATGTGATTTGTAGAAGCAC GAGACGCACTTTTATATCCCGGAATATTTCCCTCCGGCTTTC
Unc5a	NM_1333 69.2	1117- 1216	CTCATCGCCGTGGCCGTCTGCCTGGTCTGCTGCTGCTTGTCTCATCTCGTTTATTG CCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGT
Vax2	NM_0124 76.2	872-971	CAGCGCCAGCAGCTGCAAGAAAGCTAACACTTAAGACTCCCACCCTGTGACTGAG TCCCGAGCACAGCACCTTCCAGTCTCCTGTGCCCCAGCGGAC
VEGFA	NM_0010 25366.1	1326- 1425	GAGTCCAACATCACCATGCAGATTATGCGGATCAAACCTACCAAGGCCAGCACATA GGAGAGATGAGCTTCTACAGCACAACAATGTGAATGCAGAC
WEE1	NM_0033 90.3	1226- 1325	TATGCCATTAAGCGATCAAAAAAGCCATTGGCGGGCTCTGTTGATGAGCAGAACGCT TTGAGAGAAGTATATGCTCATGCAGTGCTTGGACAGATTCTC
Xbp1	NM_0010 79539.1	936-1035	ATTCATTGTCTCAGTGAAGGAAGAACCTGTAGAAGATGACCTCGTTCCGGAGCTGGG TATCTCAAATCTGCTTTCATCCAGCCACTGCCCAAAGCCATCT
XBP-1	NM_0050 80.2	441-540	GGAGTTAAGACAGCGCTTGGGGATGGATGCCCTGGTTGCTGAAGAGGAGGCGGAA GCCAAGGGGAATGAAGTGAGGCCAGTGCCGGGTCTGCTGAGTCC
XCL1	NM_0029 95.1	621-720	GTACCTCTTTGATGGTAACCATAATGGAAGAGATTCTGGCTAGTGTCTATCAGAG GTGAAAGCTATATCAATCTCTCTTAGAGTCCAGCTTGTAAATGG
YES1	NM_0054 33.3	266-365	ATACAGACCTGAAAATACTCCAGAGCCTGTCAAGTGTGAGCCATTATGGAGC AGAACCCACTACAGTGTCAACCATGTCCGTCATCTTCAGCAAAG
YAP	NM_1391 18.2	756-855	ATGGGAGCTATGCAGCTGATTGAAGACTTCAGCACACATGTCAGCATTGACTGCAGC CCTCATAAACTGTCAAGAAGACTGCCAATGAATTTCCCTGTT
ZAP70	NM_0010 79.3	1176- 1275	GGAGCTCAAGGACAAGAAGCTTTCCTGAAGCGCGATAACCTCCTCATAGCTGACAT TGAACCTGGCTGCGGCAACTTTGGCTCAGTGCGCCAGGGCGTG
PLZF	NM_0060 06.4	1586- 1685	TCCTGGATAGTTTTCGGCTGAGAATGCACCTACTGGCTCATTAGCGGGTGCCAAAG CCTTTGTCTGTGATCAGTGCGGTGCACAGTTTTTCGAAGGAGGA
Zbtb7	NM_0158 98.2	555-654	GACGCGGGCGCCGACGCGGGCAGCTGGACCTTGTAGATCAAATTGATCAGCGCAA CCTCCTCCGCGCAAGGAGTACCTCGAGTTCTTCAGAGCAACC
C80RF70	NM_0160 10.2	666-765	ACGATTACCGCAGCCAAGTGGCGCTGGCAAACTGTTGTAGGTGTTTCTTCAGGTAA AGTGTCTTCAAGTAGCAGCTCTTTGGGAAACAACTTCAGACC
ZEB2	NM_0011 71653.1	241-340	GTTTGTGTTTCTGGAGTGGCCGAAAGAGATCAGTTCTAACCTGCTCTGCAGGAATA ACGGTCTGCCTCCCGACACTCTTGGCGAGGTTTTGTACAGT
ZNF516	NM_0146 43.2	4831- 4930	GGTGGGGGACGGCTTCATATACCTCTTCTCAGTAATGCAAATGCGAGTTTTTGTGGT GGGGTTAAGGCCATAACAAAGGATCTTAAACCATGCAGTG

Supplemental Table 4:*Antigen-specific killing by CAR T cells used in the clinical trials*

Patient #	Effector : Target Ratio										% CAR
	20:1					5:1					
	Daudi β_2m	NALM-6	CD19 EL-4	EL-4	No DNA	Daudi β_2m	NALM-6	CD19 EL-4	EL-4	No DNA	
P446	64.8	52.4	45.1	13.1	4.7	65.8	58.2	42.7	7.7	3.0	88
P458	53.3	51.2	43.9	9.6	4.9	41.4	29.7	35.3	4.4	1.2	77
P468	54.0	46.8	41.6	8.5	1.7	44.4	33.3	31.3	3.8	-0.2	86
P471	53.0	49.6	52.7	16.9	1.3	45.6	35.3	45.3	7.7	0.4	96
P509	64.1	55.1	43.7	3.9	1.5	57.8	49.0	39.8	2.9	3.6	96
P747	56.3	50.6	36.4	4.3	2.0	52.4	40.9	32.9	1.4	1.9	88
P411			30.3	2.9	8.0			24.7	0.7	6.5	71
P580	52.5	38.2	38.4	9.1	8.8	40.7	24.5	30.4	5.1	9.2	70
P410	65.9	54.9	49.2	19.5	2.3	63.6	51.0	41.6	13.8	2	90
P396	64.3	58.0	55.7	15.9	2.4	54.6	44.5	47.5	9.8	2.2	97
P513	66.1	57.5	51.6	20.2	4.4	59.5	46.7	41.9	12.1	3.1	88
P732	57.5	54.2	51.8	24.7	5.4	56.3	50.2	48.0	14.8	4.9	84
P671	62.4	58.0	51.9	20.8	-0.5	54.8	51.6	47.4	10.6	-0.2	95
P617	57.2	48.6	31.4	9.7	29.0	55.5	41.7	33.9	7.3	26	67
P564	60.1	54.3	40.1	5.1	1.7	55.9	46.5	39.9	2.7	2.9	91
P723	60.6	51.9	52.8	15.7	-17.2	51.8	41.9	46.9	6.6	-13.1	47
P716	58.3	51.8	48.1	10.5	0.2	57.8	45.2	45.8	5.7	-0.3	65
P771	58.2	48.9	37.9	8.9	0.8	51.6	37.9	30.7	5.9	1.3	93
P718	59.4	52.9	43.4	8.2	0.5	58.7	46.1	40.6	5.4	1.5	92
P641	54.2	45.1	26.7	4.9	15.5	49.9	39.7	24.5	3.0	10.2	75
P647	63.7	45.3	34.8	4.4	3.4	52.9	36.7	30.1	2.3	2.5	87
P783	64.3	52.0	39.5	5.8	0.1	58.9	41.9	35.8	4.3	-0.2	94
P788	63.8	38.1	37.3	9.1	3.4	52.9	44.6	29.1	5.3	1	84
P753	58.9	47.6	35.7	7.1	18.4	52.2	36.4	27.7	2.2	16.2	58

The antigen-specific cytotoxicity of SB-modified CAR T cells was assessed using ⁵¹Cr-release assays via standard techniques. The human tumor lines Daudi (genetically modified to express b-2-microglobulin) and NALM-6 express endogenous CD19. The immortalized mouse T-cell line EL-4 does not express human CD19, but the sub-line CD19EL-4 has been genetically modified to homogeneously express human truncated CD19. CAR T cells were mixed with the designated targets at effector:target ratios of 20:1 and 5:1. The % specific cytolysis for each target by each cell product is shown. Parental EL-4 cells reflect antigen non-specific cytolysis of the manufactured product, while the “No DNA” column reflects the target cytolysis observed for mock-transformed T cells (cells undergoing the SB transformation process without plasmid DNA) that themselves serve as targets (from the same donor as the genetically modified effector T cells). The final column shows the percent CAR expression on each cell product.

Supplemental Table 5:*Characteristics of peripheral blood in recipient on day of T-cell infusion*

UPN	Auto or Allo	WBC at infusion [K/ μ L]	%lymph	CD3 (ATC) [% & K/ μ L]	CD4 [% & K/ μ L]	CD8 [% & K/ μ L]	CD19 (ABC) [% & K/ μ L]
P446	Auto	0.2	N/A	N/A	N/A	N/A	N/A
P458	Auto	1	5.8	N/A	N/A	N/A	N/A
P468	Auto	0.4	12	N/A	N/A	N/A	N/A
P471	Auto	0.4	40	N/A	N/A	N/A	N/A
P509	Auto	0.1	N/A	N/A	N/A	N/A	N/A
P747	Auto	0.2	N/A	N/A	N/A	N/A	N/A
P708	Auto	0.1	N/A	N/A	N/A	N/A	N/A
P396	Allo	4.7	25	73% 3.42	1% 4.64	33% 1.55	2% 0.11
P410	Allo	5.6	16	7% 0.38	7% 0.37	23% 1.26	0% 0.00
P411	Allo	1.2	11	39% 0.46	20% 0.24	19% 0.23	0% 0.00
P513	Allo	3.5	37	87% 3.04	13% 0.46	73% 2.54	0% 0.00
P580	Allo	5.8	12.3	ND	ND	ND	ND
P459	Allo	6.7	32.8	63% 4.19	27% 1.81	32% 2.12	2% 0.12
P564	Allo	2	32.3	62% 1.22	45% 0.9	16% 0.31	0% 0.00
P617	Allo	6.6	9.9	ND	ND	ND	ND
P671	Allo	6.1	6	2% 0.12	2% 0.11	0% 0.01	0% 0.00
P723	Allo	2.8	27	18% 0.51	8% 0.22	5% 0.13	0% 0.00
P732	Allo	3.8	5.3	9% 0.33	3% 0.12	5% 0.19	0% 0.00
P641	Allo	3	39.5	85% 2.55	26% 0.77	57% 1.71	0% 0.01
P647	Allo	9.2	44	71% 6.53	23% 2.11	45% 4.12	0% 0.00
P716	Allo	2.8	12.4	55% 1.52	34% 0.94	18% 0.50	0% 0.00
P718	Allo	1.3	44	56% 0.72	16% 0.20	39% 0.50	0% 0.00
P771	Allo	6.2	8.5	30% 1.85	18% 1.12	9% 0.54	0% 0.02
P783	Allo	4	3.5	1% 0.06	0% 0.02	1% 0.04	0% 0.00

WBC = white blood cell count, ATC = absolute T-cell count, ABC = absolute B-cell count, N/A= not available, ND= not done.

Supplemental Table 6: Timing of infusion of CAR T cells from venipuncture to after infusion of peripheral blood stem cells (PBSC)

UPN	Auto or Allo	^a Time to cryopreservation of genetically modified T cells (days)	^b Time to cryopreservation (days)	^a Time to infusion (days)	^b Time to infusion (days)	Days between PBSC and T-cell infusions
P446	Auto	29	29	77	77	2
P458	Auto	25	32	48	55	2
P468	Auto	29	30	60	61	3
P471	Auto	29	30	57	58	2
P509†	Auto	31	44	58	71	3
P747	Auto	29	29	69	69	2
P708	Auto	30	30	49	49	4
P396†	Allo	30	45	66	81	64
P410†	Allo	29	35	61	67	54
P411†	Allo	31	57	64	90	71
P513†	Allo	34	45	55	66	66
P580*	Allo	32	70	89	90	81
P459*†	Allo	35	54	84	90	62
P564	Allo	29	30	70	71	64
P617	Allo	30	30	69	69	43
P671	Allo	27	27	95	95	45
P723	Allo	34	35	61	62	54
P732	Allo	27	28	53	54	46
P641	Allo	22	23	88	89	68
P647	Allo	22	22	55	55	57
P716	Allo	27	28	63	64	56
P718	Allo	33	34	125	126	56
P771	Allo	29	30	67	68	67
P783	Allo	29	30	62	63	49

The time from genetic modification to end of culture period and T-cell preservation (time to cryopreservation), time to CAR⁺ T-cell infusion, and time from HSCT (infusion of PBSC) to CAR T-cell infusion

^a Time to T-cell cryopreservation or infusion from genetic modification/start of T-cell culture

^b Time to T-cell cryopreservation or infusion from phlebotomy

* Culture re-initiation at day 14/d20 (P580/P459) from in-process cryopreserved products

† Peripheral blood-derived samples were initially cryopreserved before subsequent SB-mediated genetic modification

Supplemental Table 7: Average time of CAR T-cell persistence in autologous and allogeneic recipients after infusion determined by ddPCR

T-cell Dose Level and recipients (allo versus auto)	Number of patients infused	Average time (days) transgene detected	Maximum time (days) transgene detected
A (allo)	5	78	180
B (allo)	6	65	90
C (allo)	8	24	90
MSD (allo)	11	49	90
Haplo (allo)	8	54	180
A (auto)	5	234	360
B (auto)	2	120	180
All Auto patients	7	201	360
All Allo patients	19	51	180

Supplemental Table 8: Recipients that received a second CAR T-cell infusion

Protocol	UPN	WBC [K/ μ L]	ALC [K/ μ L]	CD3 [% & K/ μ L]	CD4 [% & K/ μ L]	CD8 [% & K/ μ L]
Allo	P396 CIND	3.7	0.71	50% 0.36	26% 0.18	20% 0.14
Allo	P410 CIND	4.8	0.67	44% 0.29	9% 0.06	34% 0.23
Allo	P564 (2nd inf)	2.5	0.16	61% 0.1	45% 0.07	15% 0.02
Allo	P647 (2 nd inf)	8.7	3.96	89% 3.5	23% 0.91	37% 1.47
Allo	P671 (2 nd inf)	6.1	2.89	*49% 1.4	*23% 0.66	*24% 0.69

WBC = white blood cell count, at time of infusion (inf)

ALC = absolute lymphocyte count at time of infusion

%CD3, %CD4 and %CD8 were calculated from lymphocyte gate (FSC/SSC) using flow cytometry

*Percentages from last time point previous to second T cell infusion were used, as pre-infusion sample was not available.

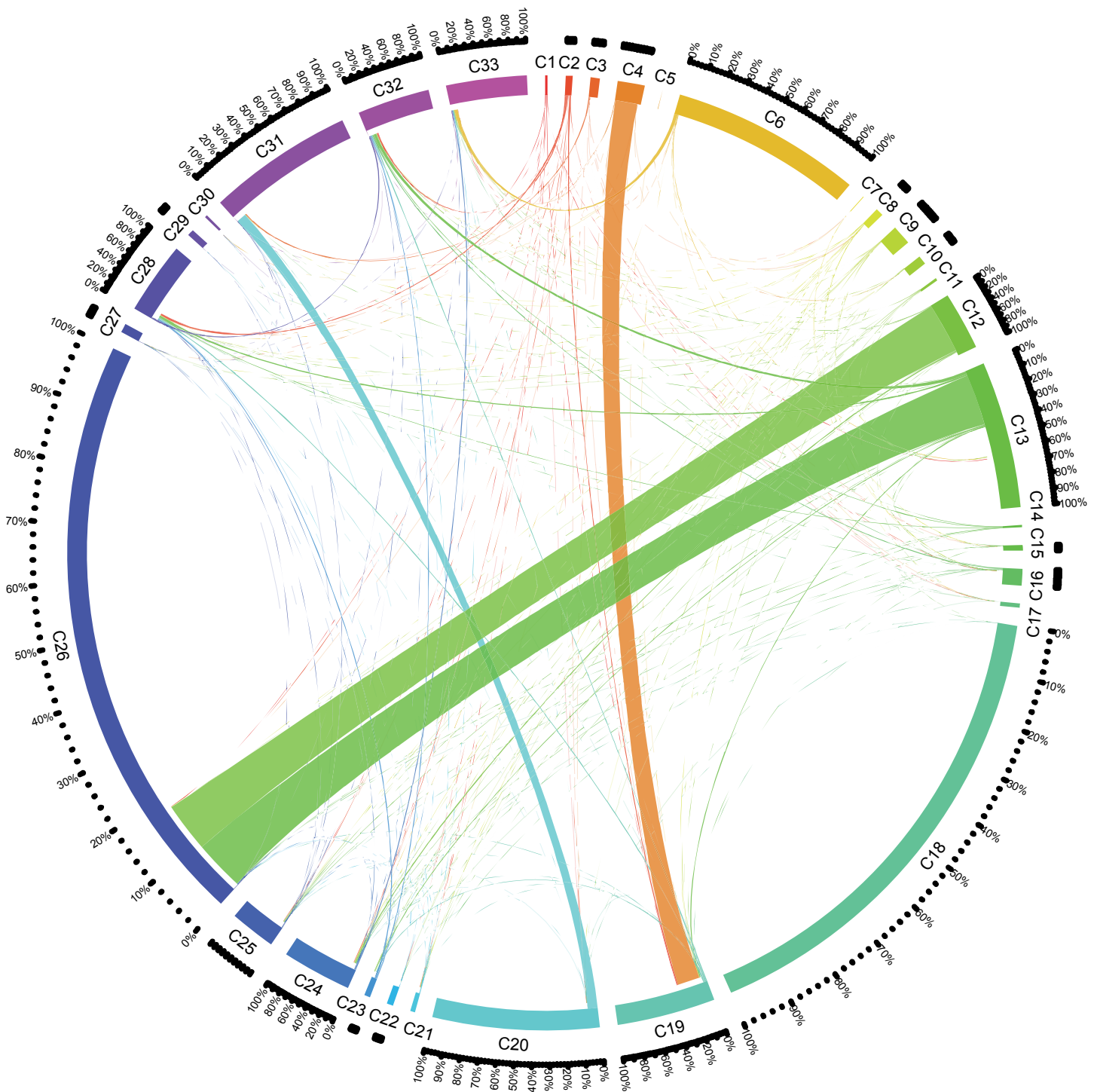
Supplemental Table 9: Genes that contain CAR within exons

Chromosome	Gene name	Exon
1	RP5-837M10.3	2
2	KCMF1	10
3	DAZL	12
3	TMF1	20
4	CCDC149	17
6	C6orf64	4
6	USP45	32
7	EPHA1	8
8	ERLIN2	16
11	GAS2	8
12	MDM2	11
14	RBM23	20
15	KIAA1370	15
16	SSU_rRNA_5	1
16	RFWD3	13
17	UNC45B	21
19	ZNF529	8
19	NAPA	5
20	ZGPAT	8
22	TMEM184B	5
22	TOMM22	4
X	WWC3	25
X	RPGR	26

Unique chromosomal positions are listed even though a particular positions can have many/multiple reads.

SUPPLEMENTAL FIGURES

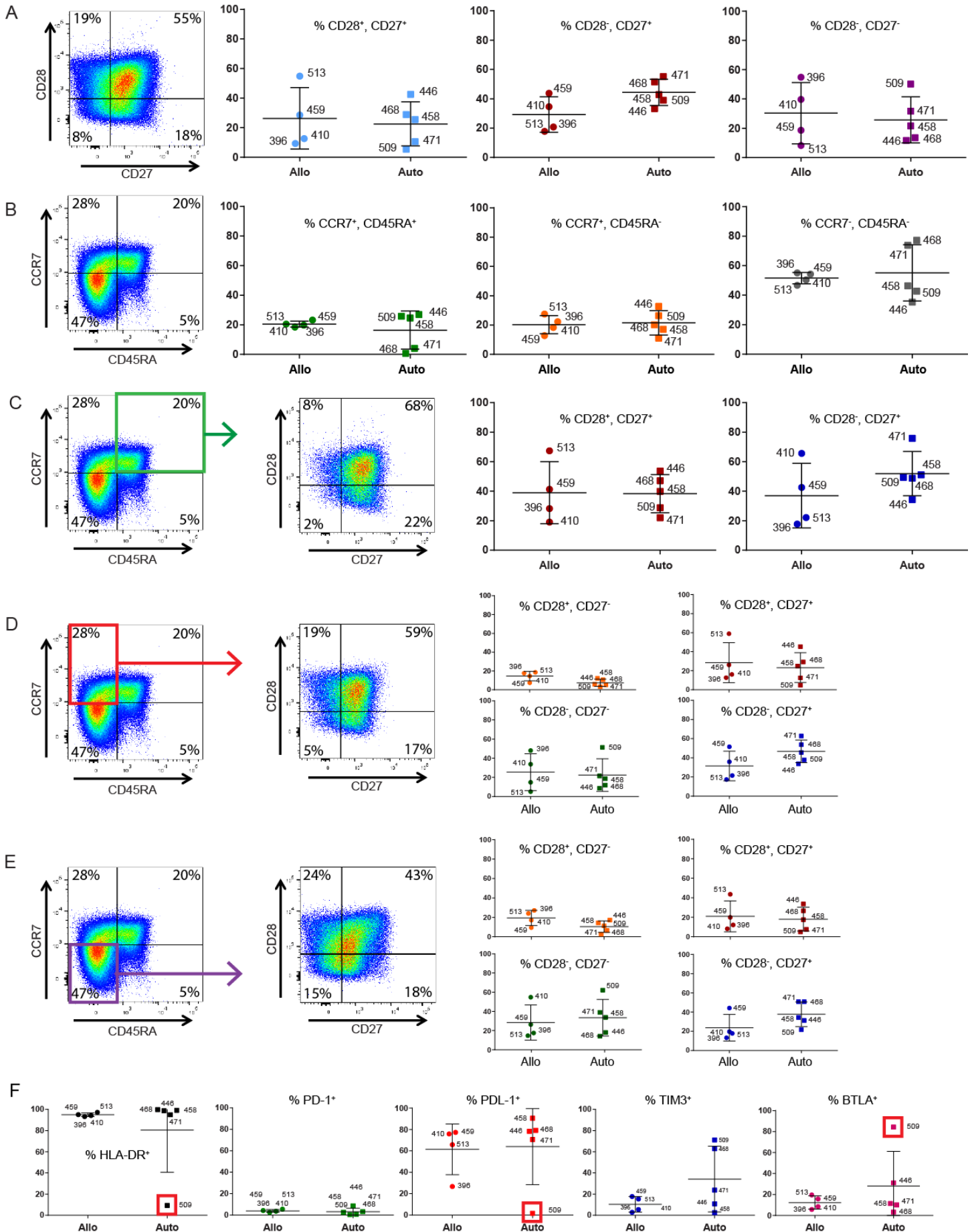
Supplemental Figure 1



High throughput sequencing to reveal distribution of CAR integrants after SB-mediated transposition in primary T cells. Genomic DNA libraries were made from independent polyclonal

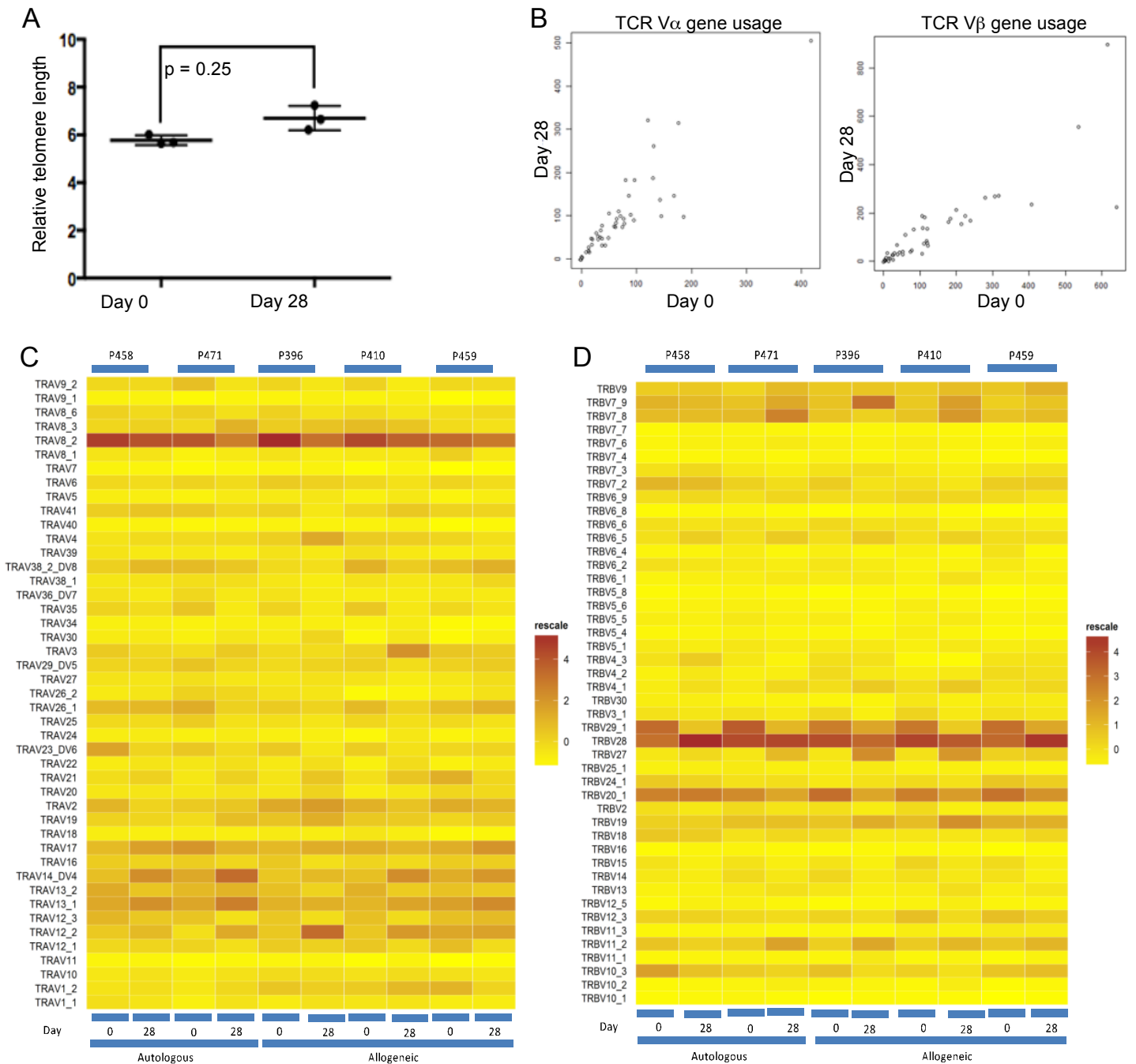
populations of T cells that had been genetically modified with the SB system to express CD19RCD28, and the precise integration site for each insertion was determined in each library. The figure consists of a circos plot of the CAR transgene common insertion sites (CIS). Each library is represented by colored bars around the periphery, sized in proportion to the number of insertion sites. The outer ring is populated by relative scales (0 to 100%) apportioning each library. The number of insertion sites common between libraries is linked by weight-sized ribbons, colored according to each origination library. Libraries C4, C12 and C13 have relatively large portions of insertion sites in common with other libraries (C19 and C26), while C18, which has a relatively large number of insertions, has relatively low or no insertion sites in common with other libraries. We matched insertions within exons using BLAST against human reference genome (hg19). Intragenic insertions are defined as insertions within either 5' UTR, exonic, intronic, or 3' UTR. The majority (96.5%) of intragenic insertions are within intronic regions while only 3.5% of integrants are within coding (exonic) and non-coding (5' UTR and 3' UTR) regions. Insertions with the same chromosomal coordinates were binned and unique insertions tabulated. **Supplemental Table 9** lists coding region (exonic) insertions.

Supplemental Figure 2



Phenotype of clinical-grade is no genetically modified T cells: Multi-parameter flow cytometry was used to evaluate co-expression of CD27, CD28, CCR7 and CD45RA on the CAR T cells, assessing the proportion of T_{SCM} or, T_N ($CCR7^+CD45RA^+CD28^+CD27^+$) T_{CM} ($CCR7^+CD45RA^{neg}CD28^+CD27^+$), T_{EM} ($CCR7^{neg}CD45RA^{neg}CD28^{\pm}CD27^{\pm}$) and exhausted/immune-incompetent T cells. **(A)** The color histogram displays the expression of CD27 and CD28 from a representative sample of CAR T cells (P513), and the panels to the right show the percentage of cells with each phenotype from the allogeneic (left side of each panel) and autologous (right side of each panel) patient infusion products tested. **(B)** Expression of CD45RA and CCR7 for the same cells shown in (A). The $CD3^+$, CAR^+ , $CCR7^+$, $CD45RA^{neg}$ subset was $20.2 \pm 6.2\%$ (autologous, $n = 5$) and $21.5 \pm 8.4\%$ (allogeneic, $n = 4$) of the total. Gating on the $CD45RA^+CCR7^+CAR^+$ lymphocytes **(C)**, the $CD45RA^{neg}CCR7^+CAR^+$ lymphocytes **(D)** and the $CD45RA^{neg}CCR7^{neg}CAR^+$ lymphocytes **(E)**, the expression of CD27 and CD28 for each subpopulation is shown for a representative sample, with panels showing the individual and mean \pm standard deviation for each quadrant displayed on the right. **(F)** Expression of HLA-DR, PD-1, PDL-1, TIM3 and BTLA is shown for each patient, as per similar panels in **Supplemental Fig. 2A-2E**. The red box outlining P509 highlights the reduced expression of activation markers on the infused cells of the one autologous patient who experienced relapsed disease.

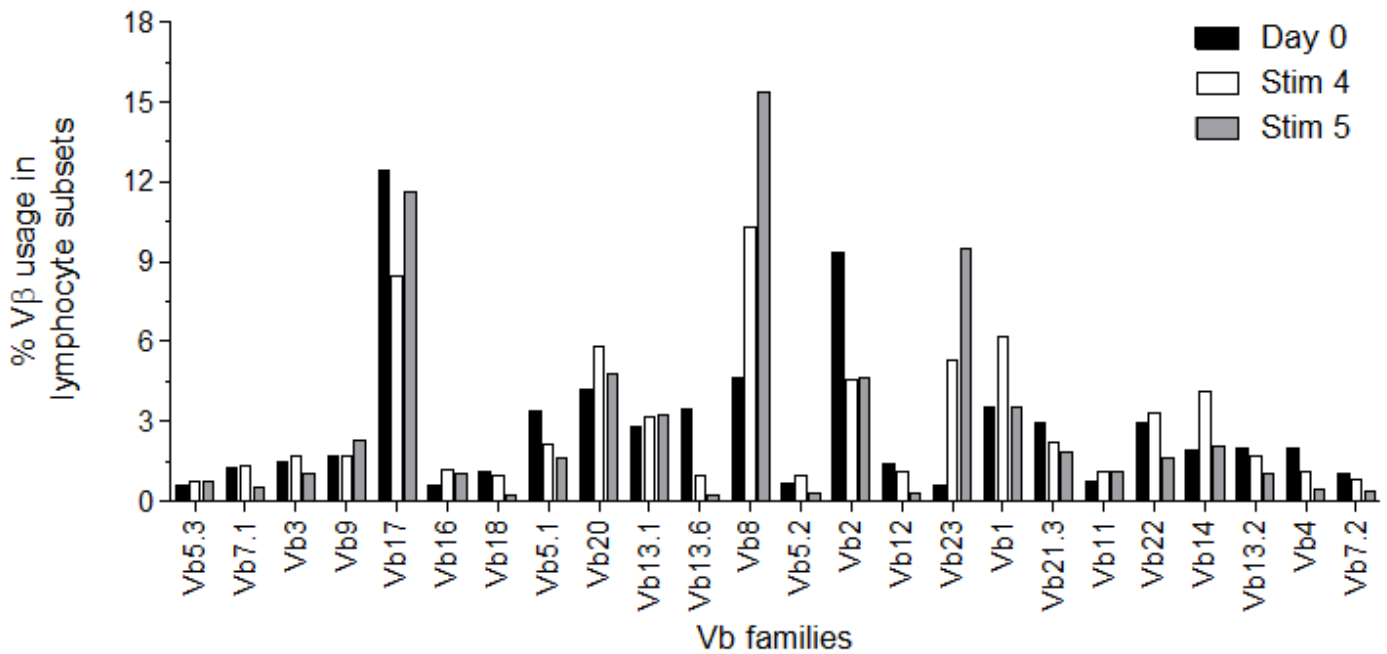
Supplemental Figure 3



Telomere length and molecular analysis of clinical-grade CAR T cells. (A) The relative telomere length was compared for three genetically modified T-cell products on Days 0 and 28 of tissue culture. mRNA from PBMC at day 0 and *ex vivo*-expanded CAR T cells harvested on day 28 of co-culture with AaPC/cytokines was used in digital multiplexed assay (using the NanoString nCounter) to quantify the amount of mRNA coding for 45 TCR V α and 46 TCR V β chains using direct TCR expression assay (DTEA). Cells harvested on Day 0 (unmodified T cells) were used as pre-

electroporation controls. **(B)** Scatter plots from a representative patient comparing day 0 and day 28 TCR V α and V β gene usage are shown. Heat maps display the relative expression of each of the 45 TCR V α **(C)** and TCR V β **(D)** genes on days 0 and 28 (P396; correlation coefficient (ρ) = 0.85; P410; ρ = 0.83; P458; ρ = 0.94; P459; ρ = 0.93 and P471; ρ = 0.87). All correlation coefficients are greater than 0.8, thus the TCR V α and TCR V β repertoire expression patterns are similar between day 0 and day 28 in these 5 patients.

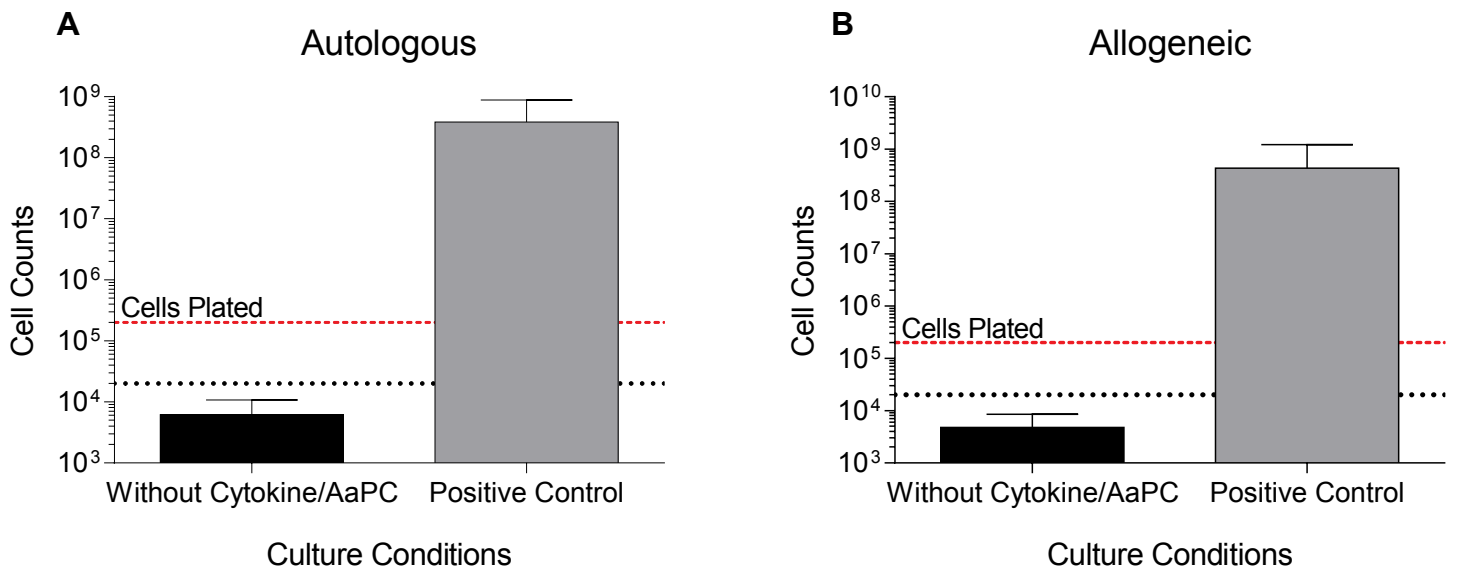
Supplemental Figure 4



Distribution of TCR Vβ before and after electroporation and extended *ex vivo* propagation.

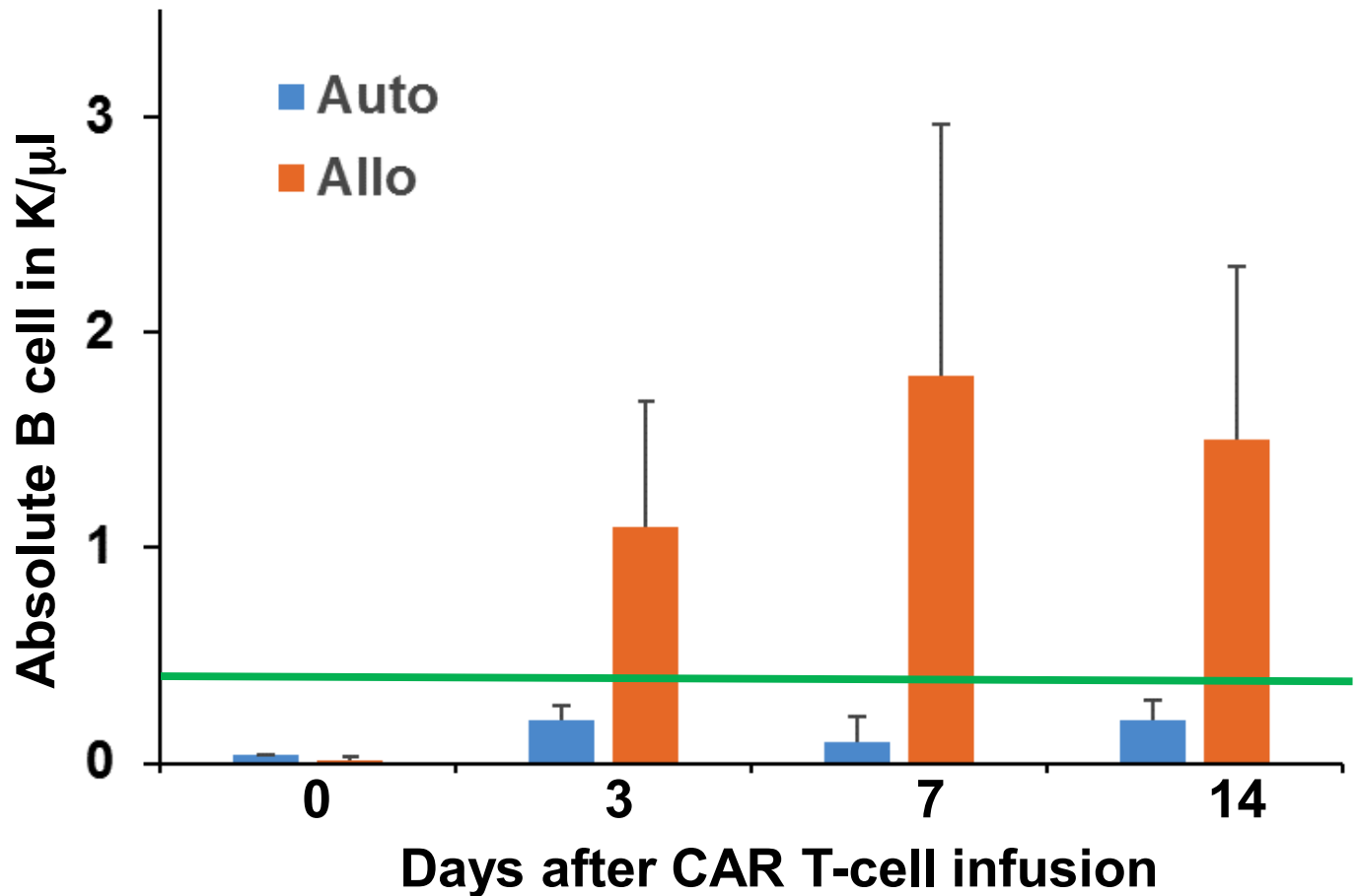
CAR T cells (P411) underwent five cycles of AaPC-mediated stimulation and numerically expanded in culture to day 35. The TCR Vβ repertoire was assessed by flow cytometry prior to SB gene modification, after four cycles of stimulation (*i.e.*, the cells that were infused into the patient, harvested at day 28 of culture time) and following 35 total days of culture. No significant differences in TCR Vβ use were observed, showing that SB gene modification did not cause outgrowth of an oligoclonal population of manufactured T cells.

Supplemental Figure 5



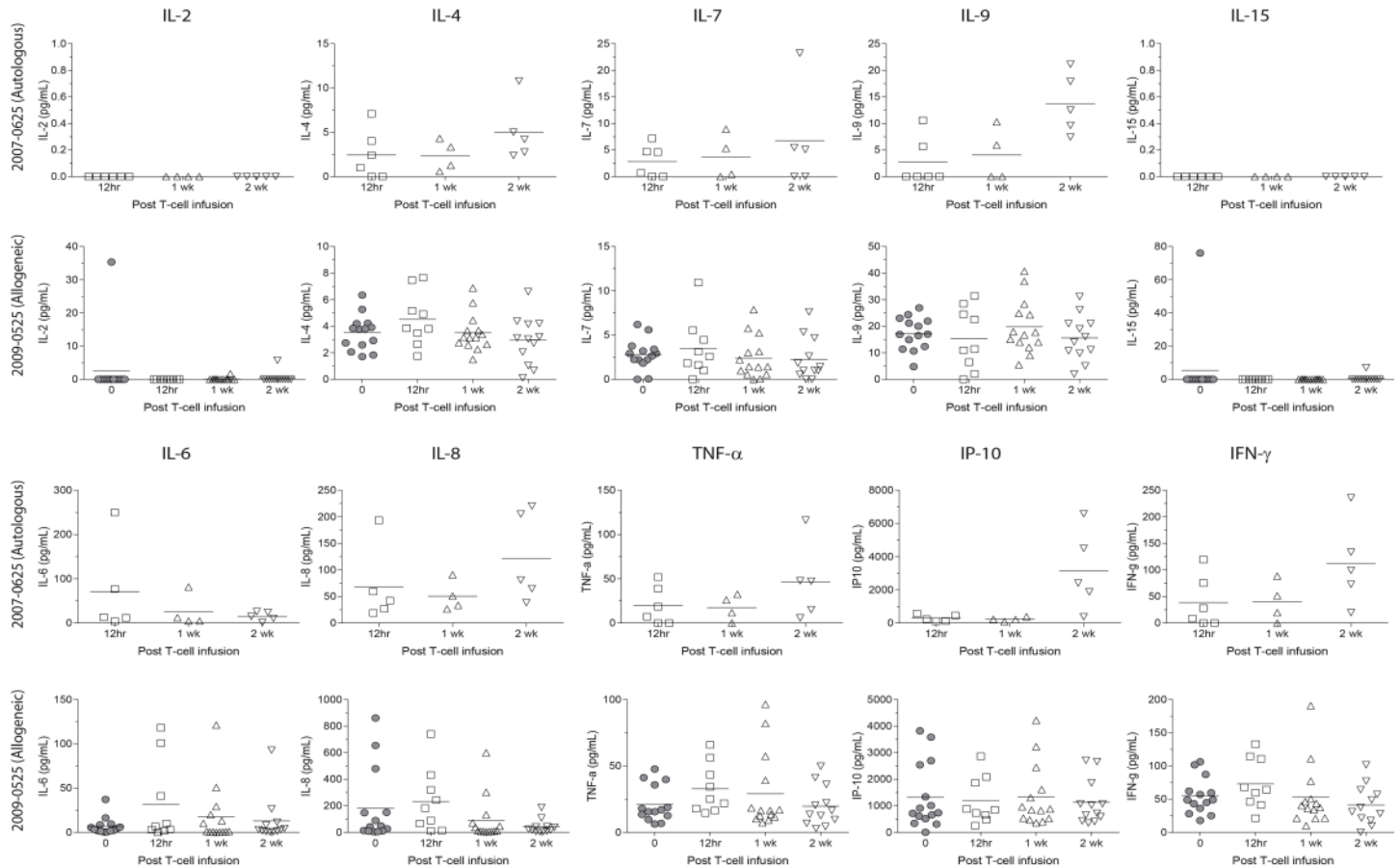
Confirmation of the absence of autonomous growth of clinical-grade CAR T cells. CAR T cells (2×10^5 , red dashed line) derived from (A) autologous patients ($n = 7$) and (B) allogeneic donors ($n = 16$) were continuously cultured for 18 days in the absence or presence of cytokines (IL-2 at 50U/mL, IL-21 at 30 ng/mL, cytokines added on a Monday-Wednesday-Friday schedule) and γ -irradiated AaPC (at 1:2 ratio of T cells to AaPC). Lack of autonomous growth for CAR T cells was defined when counts were $\leq 2 \times 10^4$ (black dotted line) at the end of 18 days in the absence of stimulation.

Supplemental Figure 6



Measurement of circulating CD19⁺ B cells in peripheral blood following infusion of CD19-specific CAR T cells. Average (\pm standard error of the mean) B cell number in peripheral blood was determined by multiplying the percentage of lymphocytes expressing CD19 (determined by flow cytometry) by the absolute lymphocyte number. The green line represents the average normal number of peripheral blood (CD19⁺) B cells, determined from allogeneic donor data presented in Supplemental Table 1. Values are shown in thousands per μL .

Supplemental Figure 7

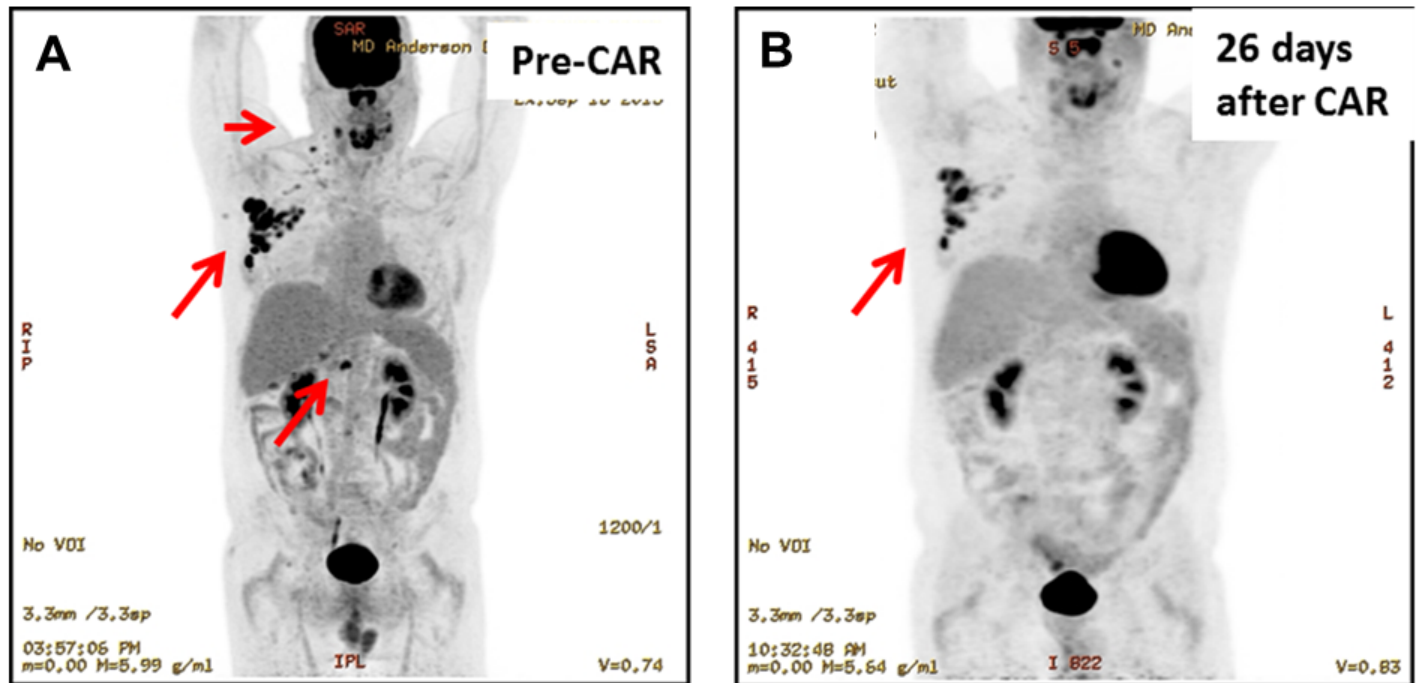


Level of cytokines that signal through common γ -chain receptor in recipients of autologous (n = 6) and allogeneic (n = 9) genetically modified CAR T cells. Serum was isolated at the times indicated after T-cell infusion and frozen in aliquots at -80°C . Samples were thawed, diluted 1:4 in complete media (10% FBS, 2mM Glutamax-1 in RPMI 1640) and evaluated using Bio-Plex Pro Human Cytokine 27-plex Assay (Bio-Rad, Hercules, CA) according to manufacturer's instruction using Luminex 100 or, Bio-Rad MAGPIX Multiplex Reader (Bio-Rad). The levels of each cytokine (in pg/mL) in patient serum are shown for each patient at each time point. Autologous patients are shown in the top panels and allogeneic patients in the bottom panels. The average value is designated by a heavy line. Note: the data for the 12 hour time point are the same as those shown in **Fig. 4B**. Several cytokines were elevated after infusion. IP-10 was markedly elevated in all allogeneic samples throughout follow-up and rose rapidly in the autologous patients and most patients had elevated

levels of IL-9 and interferon (IFN)- γ with low levels of IL-4. The role of the elevated cytokines in supporting the sustained persistence of the infused T cells is unclear, but it is notable that the infused T cells could be detected despite the low levels of cytokines that signal through the common cytokine γ -chain receptor.

Supplemental Figure 8

Patient P671



Clinical responses to CAR T cells administered to patients with bulky disease. A 52 year-old man (P671) with a history of follicular lymphoma transformed to DLBL in 2013. Prior to enrolling on this study, his treatment included rituximab plus CHOP x 6 followed by progression, rituximab-ifosfamide, carboplatin, and etoposide x 2 followed by progression, rituximab-DHAP x 2 followed by progression, and rituximab-hyperCytoxin and radiation therapy with partial response. At entrance to this study, he had bulky mesenteric disease that was refractory to chemotherapy. He received a haplo-identical donor HSCT from his son after conditioning with fludarabine, cyclophosphamide and total body irradiation. CAR T cells ($10^7/m^2$) were infused 45 days after haplo-identical HSCT, and he had no aGVHD, cGVHD or complications, and was in a CR 6 months later with 100% donor chimerism. **(A)** In 2015 he relapsed in multiple LN: R/L axillae, neck and abdomen. Gray scale image shows SUV from PET scan; red arrows indicate areas of relapse. He was reinfused with 5×10^7 CAR T cells without prior lymphodepletion or tumor cytoreduction. **(B)** Repeat PET scan one month after CAR T-cell infusion showed dramatic reduction in disease burden: clearance of tumor from all areas except right axilla, which showed a decrease in SUV from 13 to 7.9 with ongoing improvement.

Repeat right axilla FNA and core biopsy 2 months after CAR T-cell infusion revealed no evidence of NHL. Then, one month later, P671 was noted to have increased PET activity and received a third dose of haplo-identical donor-derived CAR T cells (also at 5×10^7 T cells/m²) without prior lymphodepleting chemotherapy and again a reduction in PET activity was observed.

SUPPLEMENTAL METHODS

T-cell manufacture in compliance with cGMP for phase I/II trials

The CD19RCD28 transgene is a second-generation CAR that activates T cells via chimeric CD28 and CD3- ζ . After electroporation with the two supercoiled SB system DNA plasmids, the genetically modified T cells were selectively propagated in a CAR-dependent manner on γ -irradiated K-562 cells (expressing endogenous CD32) that had been genetically modified by transduction with lentivirus (in collaboration with Dr. Carl June at the University of Pennsylvania, Philadelphia, PA) and cloned (designated clone #4 (also known as CJK64.86.41BBL.GFP.IL-15.CD19), homogeneously co-expressing truncated CD19, CD64, CD86, CD137L (4-1BBL), and a membrane bound form of IL-15 as coexpressed with EGFP) by limiting dilution to function as AaPC. The AaPC were manufactured as a Master Cell Bank (MCB) by Production Assistance for Cellular Therapies (PACT) under the auspices of the National Heart, Lung, and Blood Institute (NHLBI, Bethesda, MD). Subsequently, a Working Cell Bank (WCB) of clone #4 was derived at MD Anderson. The AaPC from MCB/WCB were continuously propagated in a WAVE (GE Healthcare) for up to 65 days under standard operating procedures and then γ -irradiated (100 Gy using a Cesium source as described (38)) prior to cryopreservation. Thawed AaPC were added at 1:2 (CAR T cells to AaPC) every 7 to 10 days to selectively propagate CAR T cells as cultured in the presence of soluble recombinant human IL-2 (50 U/mL) and IL-21 (30 ng/mL) added on a Monday-Wednesday-Friday schedule (34, 38). The validation studies describing phenotype and function of the CAR T cells manufactured in compliance with cGMP have been published (34, 36-38). In the event of an overgrowth of CD3^{neg}CD56⁺ lymphocytes early in the culturing process, these cells were removed using a CD56-specific monoclonal antibody and paramagnetic selection (**Supplemental Table 2**). The electroporation and propagation of clinical-grade T cells occurred at MD Anderson in compliance with cGMP for Phase I/II trials. The release criteria, undertaken in compliance with Clinical Laboratory Improvement Amendments (CLIA), for the manufactured T cells are (1) sterility (bacteria, fungi, mycoplasma, endotoxin), (2) chain of custody

(low-resolution HLA class I typing), (3) phenotype (presence of T cells (1), presence of transgene [CAR expression], absence of AaPC [CD32 expression], and absence of B cells [CD19 expression]), (4) safety (absence of autonomous cell growth) following our described methods (38), and (5) viability. T cells from PBMC were mock electroporated (without SB DNA plasmids) as “no DNA control” and propagated by cross-linking CD3 by the every-7-day addition of AaPC clone #4 preloaded with CD3-specific mAb (clone OKT3) in the presence of IL-2 and 21 (38).

Conditioning regimens for HSCT

Autologous trial: The conditioning regimen (BEAM) began on day -6 with intravenous carmustine (300 mg/m²) infused over 2 hours, followed by etoposide (200 mg/m²) infused over 3 hours and cytarabine (200 mg/m²) infused over 1 hour, given every 12 hours for 8 doses on days -5 through -2, followed by melphalan (140 mg/m²) infused over 30 minutes on day -1. Autologous PBSC were infused on day 0, premedicating only with diphenhydramine. *Allogeneic trial:* the preparative regimen was at the discretion of the treating physician. GVHD prophylaxis consisted of tacrolimus (from day -2 through 180 days post-transplant) and mini-dose methotrexate (5 mg/m² administered on days 1, 3, 6 and 11 after infusion of PBSC) as described for patients after HLA-matched-sibling HSCT (44) and tacrolimus, mycophenolate mofetil and post-HSCT cyclophosphamide (50 mg/kg infused on day 3 and 4 after infusion of PBSC) after haplo-identical HSCT (45). GVHD prophylaxis was tapered and discontinued by 6 months after HSCT as feasible.

Intravenous infusions of electroporated and propagated T cells

Autologous trial: T cells were administered no sooner than 48 hours and no later than 5 days after PBSC infusion. *Allogeneic trial:* T cells were administered 6 to 12 weeks following infusion of PBSC, based on a median time to occurrence of acute GVHD of 6 weeks post HSCT. T cells were intravenously infused at MD Anderson by principal investigator or designee. Initially, to enhance patient safety, the cryopreserved T-cell products for both trials were split over two days, with 25% of the thawed product initially administered and the remaining T-cell dose infused no sooner than

24 hours and no later than 72 hours after completion of the first portion. After patient safety was established, the study was amended to allow for administration of the entire genetically modified T-cell product as a single administration. Patients were premedicated with acetaminophen and diphenhydramine, and blood pressure, oxygen saturation, and temperature monitored for 4 hours following the infusion. Systemic corticosteroids and other immunosuppressive agents were contraindicated. If an adverse event (AE) of grade >2 (common terminology criteria [CTC], version 4) occurred involving cardiopulmonary, hepatic (excluding albumin), gastrointestinal, neurological, or renal toxicity probably or definitely attributed to T-cell administration, the patient could then receive corticosteroids and additional immunosuppressive agents if needed.

Quantitative PCR (Q-PCR) and droplet digital PCR (ddPCR) to measure T-cell persistence

The measurement of CAR was reported as transgene copy number per μg of total PBMC genomic DNA. Additionally, the ddPCR system was employed to determine presence and quantification of CAR T cells in patient-derived PB after infusion. ddPCR is a platform designed to provide improved sensitivity and precision for the detection and quantitation of infrequent target DNA molecules (35). gDNA from *ex vivo* numerically expanded day 28 “no DNA” autologous control T cells (used as negative control) and CD19-specific CAR T cells (used as positive control), as well as gDNA from serially collected patient-derived PBMC after infusion of genetically modified T cells, were isolated using a commercially available kit (Qiagen). gDNA (50 ng) from each of positive and negative control and serially collected sample was used for ddPCR. PCR droplets were generated according to manufacturer's recommendations (Bio-Rad). Briefly, a 20 μl of multiplex PCR mixture was prepared by mixing gDNA with the ddPCR 2x Master Mix and FAM labeled TaqMan primer/probe sets (CAR context sequence; 5'-TCTTTAGCTGCTCCGTGATGCACGAGGCCCTGCACAACCACTACACCCAGAAGAGCCTGTCCCTGAGCCTGGGCAAGATGTTCTGGGTGCTGGTcg-3') and the human HEX labeled house-keeping EIF2C1 gene (5'-GAGGGCTACTACCACCCGCTGGGGGGTGGGCGCGAGGTCTGGTTCGGCTTTCACCAGTCTGTG

CGCCCTGCCATGTGGAAGATGATGCTCAACATTGATGGTGAGTGGGGAGAGCTATGGAGC-3').

PCR droplets were generated in a DG8 cartridge (Bio-Rad, Hercules, CA) using the QX-100 droplet generator, where each 20 μ L PCR mixture was partitioned into approximately 20,000 nano-liter size droplets. PCR droplets were transferred into a 96-well PCR plate and sealed with foil. Standard PCR was performed with a Bio-Rad C1000 Thermal Cycler (95°C (60 sec), 40 cycles of 94°C (30 sec), 60°C (60 sec), 98°C (60 sec)). CAR DNA copy number was evaluated using the QX-100 Digital Droplet PCR system (Bio-Rad,). The PCR-positive and PCR-negative droplets for CAR and the eukaryotic initiation factor 2C1 (*EIF2C1*) reference gene were determined and template concentrations were calculated by Poisson analysis. CAR copy number was determined by normalizing CAR concentration to *EIF2C1* concentration. The formula used to determine transgene copy number/cell was:

$$\frac{Tg}{cell} = \left(\frac{[CAR]}{[EIF2C1]} - \frac{[neg]}{[EIF2C1]} \right) \times 2$$

Where [CAR], [EIF2C1], and [neg] are the concentrations of DNA from the CAR, EIF2C1, and negative control (the greater of the no DNA or baseline values) reactions.

Linker-mediated PCR (LM-PCR)

Briefly, genomic DNA was extracted from primary T cells using standard column purification methods. Genomic DNA was digested with *Bfal* and *NlaIII* separately to clone regions adjacent to the left and right sides of the transposon, respectively. After overnight digestion at 37°C, reactions were heat inactivated at 80°C for 20 minutes. Previously published linkers for the left and right sides were then prepared by annealing sense and antisense primers (71). The prepared linkers were then ligated overnight at 16°C to genomic DNA digested with the corresponding restriction enzyme. Ligated DNA was purified using Qiagen MinElute 96 UF Plates, following the manufacturer's instructions. Primary PCR was performed with an annealing temperature of 55°C for 30 cycles. The primary PCR reaction was then diluted 1:75 in water, and 1 μ L of this dilution was used for secondary PCR with Long-Range

Taq (Roche), applying an annealing temperature of 53°C for 35 cycles. The primers used for secondary PCR were barcoded and designed for Illumina sequencing; these have been published previously (71).

Direct TCR expression analysis to quantify TCRV α and V β gene expression

Cellular lysate (equivalent to ~30,000 cells) from each of the unmodified (day 0) and CAR-modified T cells (day 28) were analyzed. Spearman's non parametric correlation was performed on normalized transcript counts, and if the correlation coefficient was greater than or equal to 0.8 ($p \geq 0.8$) within the 95% confidence interval, then the two TCR repertoires were considered to be highly correlated.

Telomere length analysis by fluorescence in situ hybridization and flow cytometry (Flow-FISH)

Telomere length of the T cells was measured by using the DAKO Telomere PNA Kit/FITC for Flow Cytometry (DAKO) according to the manufacturer's instructions. Briefly, isolated cells and control cells (1301 cell line; ECACC catalogue no. 85112105) were mixed in equal measure in hybridization solution with or without FITC-labeled telomere PNA probe for 10 minutes at 82°C; hybridized overnight in the dark at room temperature; washed twice with wash solution at 40°C; resuspended in DNA staining solution containing propidium iodide and RNase A, and analyzed on a FACSCalibur flow cytometer (BD Biosciences). Relative telomere length (RTL) was determined by comparing NK cells with a CEM-1301 cell line in the following way:

$$RTL = \frac{(\text{GM FL1 sample cells with probe} - \text{GM FL1 sample cells without probe}) \times \text{DI of control cells}}{(\text{GM FL1 reference cells with probe} - \text{GM FL1 reference cells without probe}) \times \text{DI of sample cells}} \times 100$$

where GM is geometric means and DI is DNA index.

Multi-parameter flow cytometry

Multi-parameter flow cytometric analysis of different cell subsets was performed on banked samples. Four panels were used: the first panel had CD8-PB (cat# 558207), CD3-FITC (cat# 340042), CD4-PerCP-Cy5.5 (cat# 560650), CD19-PE-Cy7 (cat# 557835), CD20-APC-H7 (cat# 641396, BD Biosciences, CA) and LIVE/DEAD Fixable Aqua Dead Cell Stain (cat# L34957, Life Technologies,

NY). Panel 2 had CD3-AmCyan (cat# 339186), CD8-PerCP-Cy5.5 (cat# 341051), CD27-PE-Cy7 (cat# 560609), CD45RA-APC-H7 (cat# 560674), CD28-PE (cat# 555729), CD62L-V450 (cat# 560440), and CCR7-AF-647 (cat# 353217, BD Biosciences, CA). Panel 3 had PD1 (CD279)-BV421 (cat# 562516), PDL1 (CD274)-PE-Cy7 (cat# 558017), BTLA (CD272)-PE (cat# 558485), CD8-APC (cat# 340584), HLA-DR-APC-Cy7 (cat# 335796, BD Biosciences, CA), TIM3-PerCP-eFluor710 (cat# 46-3109-41, eBioscience, CA) and LIVE/DEAD Fixable Aqua Dead Cell Stain. The last panel had CD122 (IL-2R β)-BV510 (cat# 563093), CD132 (IL2R γ)-BV421 (cat# 562881), CD215 (IL-15R α)-PE (cat# 330208), CD3-PerCP-Cy5.5 (cat# 340949), CD360 (IL-21R)-APC (cat# 460331), CD127 (IL-7R α)-PE-Cy7 (cat# 560822) and CD8-APC-Cy7 (cat# 34879, BD Biosciences, CA). Acquisition was performed on a FACS Canto II (BD Biosciences, CA) and all analyses were carried with the software FlowJo (Tree Star, OR).

Assay to assess for unwanted autonomous growth

To monitor aberrant T-cell growth (as part of the release criteria), 2×10^5 CAR T cells, harvested after four γ -irradiated AaPC-mediated stimulation cycles (28 days after electroporation) were cultured in triplicate in a 24-well tissue culture plate for an additional 18 days. Positive control: cells were cultured in the presence of γ -irradiated AaPC at ratio of 1:2 (CAR T cell: AaPC) and cytokines (50 U/mL IL-2 and 30 ng/mL IL-21), as described (38). Experimental: cells were cultured in the absence of AaPC and cytokines. The assay was passed when total viable genetically modified cells at day 18 were (i) $>2 \times 10^5$ T cells cultured with AaPC and cytokines as well as (ii) $<2 \times 10^4$ cells T cells cultured without AaPC and cytokines.