

SUPPLEMENTAL MATERIAL

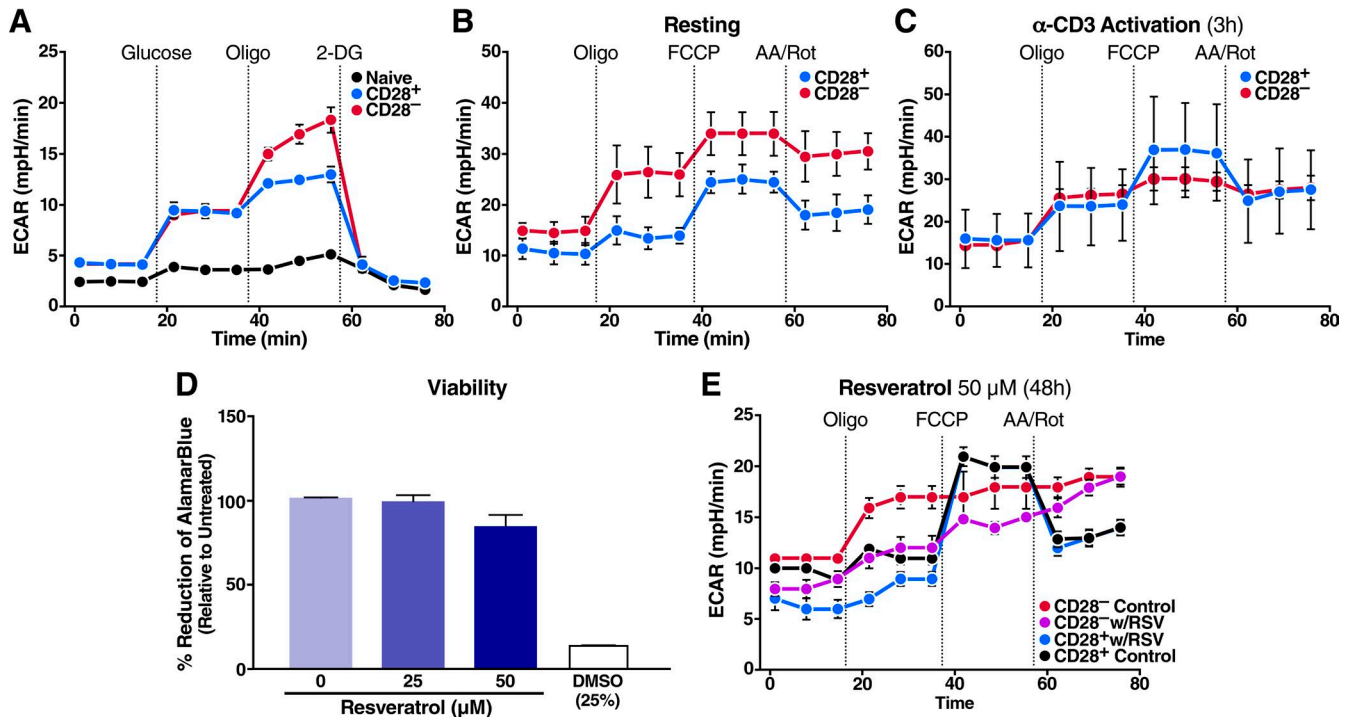
Jeng et al., <https://doi.org/10.1084/jem.20161066>

Figure S1. **Glycolytic capacity of resting CD8⁺CD28⁻ T cells depends on glucose and SIRT1.** Metabolism of sorted human T cell populations was assessed using an extracellular flux analyzer. (A) ECAR was measured in freshly isolated and glucose-deprived T cell populations after sequential addition of glucose, oligomycin, and 2-DG (representative, $n = 2$ biological replicates, $n = 6$ technical replicates). (B and C) ECAR measurement of resting (B) and activated (C) T cells (3 h with anti-CD3 antibody; mean of $n = 2$ biological replicates, $n = 6$ technical replicates). (D) Viability of human CD8⁺ T cells assessed by alamarBlue assay after RSV treatment for 48 h; 25% DMSO was used as toxicity control ($n = 2$ biological in technical triplicates). (E) ECAR analysis of CD28⁺ and CD28⁻ subsets in the presence of 50 μ M RSV (representative, $n = 2$ biological replicates, $n = 6$ technical replicates). Data are mean \pm SEM of technical replicates and individual donors.

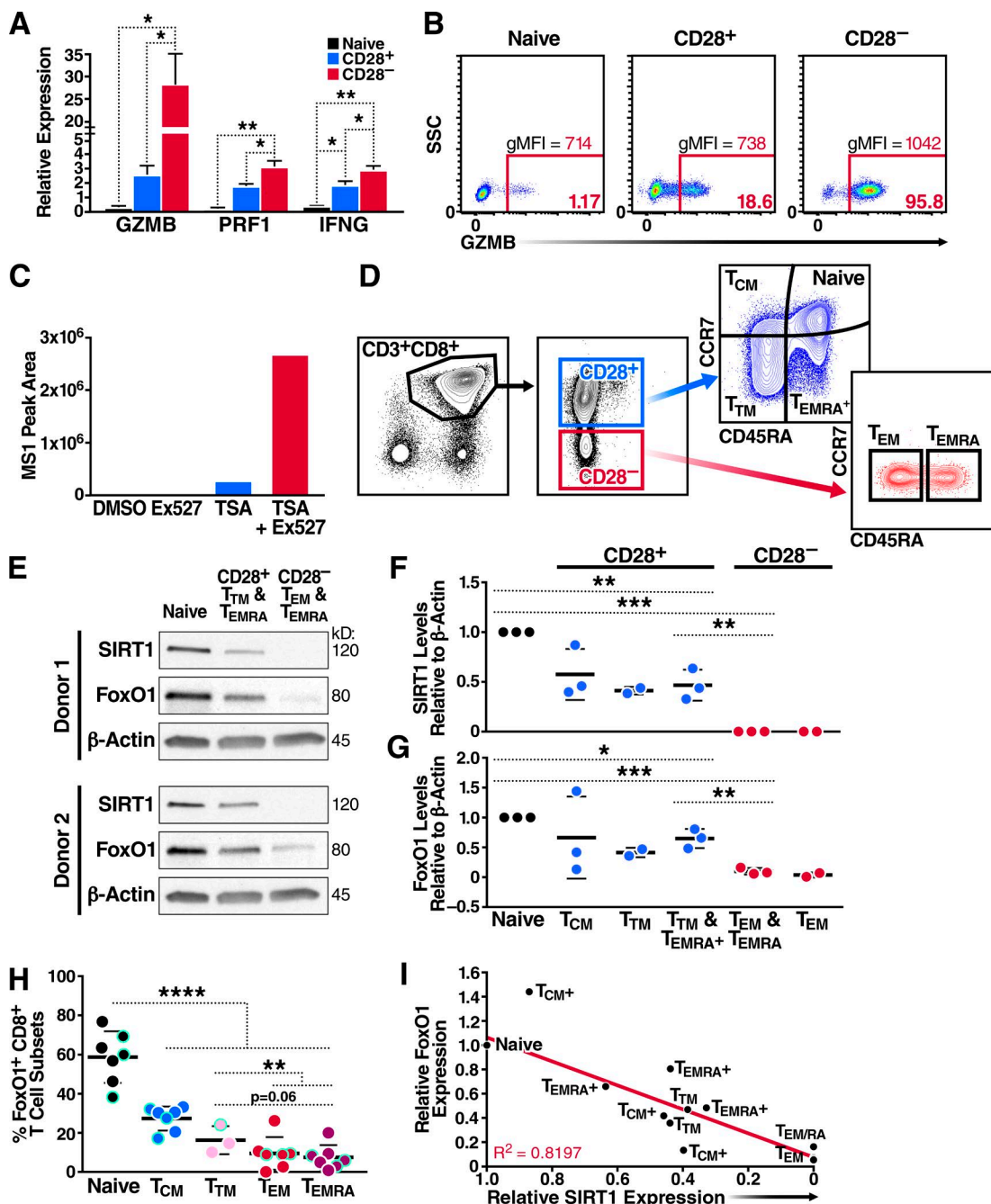


Figure S2. **Cytotoxicity and FoxO1 status in CD8⁺ T cell subsets.** (A) Cytotoxic gene expression assessed by qRT-PCR in freshly isolated human T cells relative to the mean expression in CD28⁺ cells ($n = 7$, two-way ANOVA). (B) GZMB intracellular staining was measured by flow cytometry in resting T cell populations treated with brefeldin A for 4 h (representative, $n = 3$, numbers show geometric median fluorescence intensity). (C) Freshly isolated CD8⁺ T cells were analyzed by mass spectrometry for AcK peptides (treated with 400 nM TSA and 25 μ M Ex-527 for 4 h). The integrated MS1 intensity for peptide AASMDNNSK(ac)FAK is shown ($n = 1$). (D) Representative sorting flow plot of CD8⁺CD28⁺ and CD28⁻ T cells stained for memory markers CCR7 and CD45RA. (E-G) Naive, CD28⁺ T_{CM}, T_{TM} + T_{EMRA}⁺, and CD28⁻ T_{EM} + T_{EMRA} were sorted as shown in D, probed for SIRT1 and FoxO1 expression by Western blot, and quantified by densitometry (F and G; $n = 3$ biological replicates). (H) CD8⁺ memory T cell subsets from CMV⁻ and CMV⁺ (green circles) blood donors were stained for intracellular FoxO1 protein and analyzed by flow cytometry ($n = 7$ biological replicates and $n = 3$ for T_{TM}, paired one-way ANOVA). (I) Linear regression analysis of SIRT1 and FoxO1 Western blots in sorted subsets ($R^2 = 0.819$). Data are mean \pm SEM of individual donors. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; ****, $P < 0.0001$.

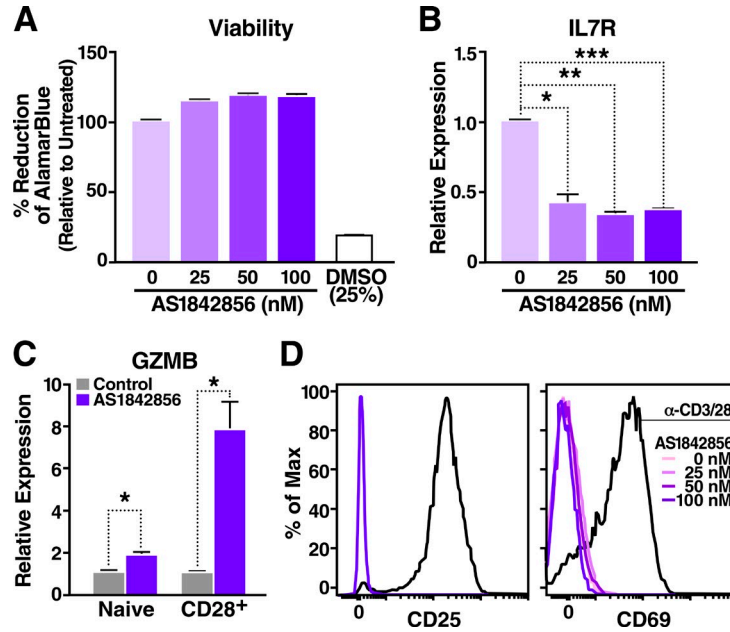


Figure S3. **FoxO1 inhibitor increases GZMB expression without T cell activation.** (A) Viability of human CD8⁺ T cells was assessed with an alamarBlue assay after AS1842856 treatment for 48 h; DMSO (25%) served as toxicity control ($n = 2$ biological replicates in technical duplicates). (B) IL7R mRNA was measured by qRT-PCR, normalized to RPL13A mRNA and to untreated control, in human CD8⁺ T cells after increasing doses of AS1842856 for 48 h ($n = 3$, paired two-tailed Student's t test). (C) GZMB mRNA was measured in sorted CD8⁺ naive and CD8⁺CD28⁺ memory T cells after treatment with 100 nM AS1842856 for 48 h ($n = 3$, paired two-tailed Student's t test). (D) Activation markers CD25 and CD69 were assessed by flow cytometry in CD8⁺ T cells after 48-h treatment of AS1842856 or α -CD3/28 activation (representative, $n = 2$). Data are mean \pm SEM of individual donors. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$.

Table S1. Microarray identifies 159 differentially regulated genes between CD8⁺CD28⁺ and CD8⁺CD28⁻ T cells

Gene name	entrez_ids	log ₂ fold change	P-value	FDR
Up-regulated in CD28⁻				
<i>GPR141</i>	353345	3.04618	0.00000	0.00000
<i>FCGR3A</i>	2214	2.91839	0.00002	0.00012
<i>CX3CR1</i>	1524	2.91351	0.00000	0.00001
<i>KLRF1</i>	51348	2.70094	0.00002	0.00008
<i>TXNDC3</i>	51314	2.38590	0.00000	0.00000
<i>GNLY</i>	10578	2.31302	0.00000	0.00005
<i>PLEK</i>	5341	2.04459	0.00032	0.00190
<i>PDGFD</i>	80310	2.02545	0.00011	0.00068
<i>ZEB2</i>	9839	2.01872	0.00000	0.00001
<i>FCRL6</i>	343413	1.81571	0.00329	0.00986
<i>GZMB</i>	3002	1.78378	0.00357	0.01430
<i>KLRD1</i>	3824	1.68624	0.00094	0.00564
<i>GZMH</i>	2999	1.65432	0.00000	0.00003
<i>KIR2DS2</i>	100132285	1.59739	0.00076	0.00306
<i>KIR2DL1</i>	3802	1.56286	0.00031	0.00186
<i>PRSS23</i>	11098	1.51952	0.00001	0.00004
<i>TGFBR3</i>	7049	1.49051	0.00002	0.00013
<i>NKG7</i>	4818	1.47231	0.00083	0.00500
<i>TNFRSF9</i>	3604	1.47152	0.01948	0.04680
<i>EPB41L4A</i>	64097	1.45895	0.00288	0.01730
<i>KLRA1</i>	10748	1.34042	0.00529	0.01590
<i>FGFBP2</i>	83888	1.33460	0.00013	0.00077
<i>LYN</i>	4067	1.33105	0.00000	0.00000
<i>GPR56</i>	9289	1.32119	0.00116	0.00464
<i>PTPN12</i>	5782	1.30337	0.00006	0.00034
<i>FAM49A</i>	81553	1.29781	0.00108	0.00648
<i>SUSD1</i>	64420	1.29745	0.00028	0.00170
<i>ST8SIA6</i>	338596	1.29096	0.00579	0.02090
<i>GALNT3</i>	2591	1.27587	0.00325	0.01950
<i>RHOBTB3</i>	22836	1.27035	0.00042	0.00316
<i>PIK3R3</i>	8503	1.26994	0.00358	0.01430
<i>CD244</i>	51744	1.26005	0.00034	0.00207
<i>TOX</i>	9760	1.23303	0.00000	0.00002
<i>BHLHE40</i>	8553	1.22762	0.01181	0.03540
<i>PRF1</i>	5551	1.22406	0.00001	0.00007
<i>RAP2A</i>	5911	1.21786	0.00184	0.01100
<i>UBE2F</i>	140739	1.20307	0.00046	0.00279
<i>SLCO4C1</i>	353189	1.16089	0.00062	0.00248
<i>DUSP10</i>	11221	1.15745	0.00120	0.00360
<i>CMKLR1</i>	1240	1.14464	0.00023	0.00091
<i>LYST</i>	1130	1.13964	0.00068	0.00407
<i>PIK3AP1</i>	118788	1.13478	0.00087	0.00524
<i>PRDM1</i>	639	1.13389	0.01228	0.04760
<i>RCAN2</i>	10231	1.12531	0.01148	0.03450
<i>PDLIM1</i>	9124	1.11957	0.00217	0.01620
<i>EGR2</i>	1959	1.09724	0.00768	0.01840
<i>F2R</i>	2149	1.09415	0.00027	0.00163
<i>OR7E13P</i>	10820	1.08994	0.00730	0.02920
<i>DDI1</i>	414301	1.07559	0.00056	0.00477
<i>USP28</i>	57646	1.06786	0.00007	0.00040
<i>KLRG1</i>	10219	1.04885	0.01903	0.04570
<i>PTMS</i>	5763	1.04800	0.00001	0.00004
<i>PTGDR</i>	5729	1.03258	0.01848	0.03700
<i>PRR5L</i>	79899	1.03002	0.00000	0.00002
<i>B4GALT5</i>	9334	1.02674	0.00057	0.00341
<i>KLRC4</i>	8302	1.01029	0.00058	0.00232
<i>JAKMIP2</i>	9832	1.00682	0.00187	0.01120
Down-regulated in CD28⁻				
<i>CD28</i>	940	-3.21368	0.00000	0.00000
<i>RCAN3</i>	11123	-3.09246	0.00000	0.00000
<i>LRRN3</i>	54674	-3.01606	0.00001	0.00003

Table S1. Microarray identifies 159 differentially regulated genes between CD8⁺CD28⁺ and CD8⁺CD28⁻ T cells (Continued)

Gene name	entrez_ids	log ₂ fold change	P-value	FDR
LEF1	51176	-2.88079	0.00000	0.00000
SCML1	6322	-2.85338	0.00000	0.00001
NELL2	4753	-2.75817	0.00069	0.00414
CCR7	1236	-2.75189	0.00000	0.00000
CCR4	1233	-2.73984	0.00010	0.00123
CD62L (SELL)	6402	-2.72432	0.00068	0.00407
VSIG1	340547	-2.64089	0.00000	0.00000
IFI44L	10964	-2.44298	0.00643	0.03860
SERINC5	256987	-2.40756	0.00000	0.00000
TXK	7294	-2.40674	0.00002	0.00012
ITGA6	3655	-2.25528	0.00000	0.00000
FCER1G	2207	-2.20898	0.00232	0.01390
HOOK1	51361	-1.98196	0.00001	0.00002
GCNT4	51301	-1.97421	0.00061	0.00147
GZMK	3003	-1.95871	0.00108	0.00647
ZNF204	7754	-1.93824	0.00005	0.00021
NRCAM	4897	-1.88703	0.00307	0.01230
AK5	26289	-1.85673	0.00018	0.00055
DSC1	1823	-1.83981	0.00094	0.00376
SESN3	143686	-1.83407	0.00321	0.03850
LOC100288114	100288114	-1.83211	0.00000	0.00003
SLC4A10	57282	-1.82461	0.00021	0.00246
SH3BGRL2	83699	-1.77375	0.00002	0.00022
IFI44	10561	-1.75209	0.00018	0.00109
CNKSR2	22866	-1.67434	0.00000	0.00000
FAAH2	158584	-1.63792	0.00020	0.00122
ABLIM1	3983	-1.63051	0.00138	0.00829
RASGRF2	5924	-1.56132	0.00002	0.00018
MAL	4118	-1.55220	0.00000	0.00000
NT5E	4907	-1.54542	0.00099	0.00396
DENND5A	23258	-1.54457	0.00002	0.00011
IL6ST	3572	-1.48902	0.00003	0.00016
IGF1R	3480	-1.46375	0.00001	0.00005
OR10AD1	121275	-1.42079	0.00000	0.00000
LASS6	253782	-1.41802	0.00196	0.01170
DOCK9	23348	-1.39609	0.00000	0.00000
KLF7	8609	-1.38395	0.00005	0.00056
SULT1B1	27284	-1.37986	0.00802	0.03210
IL26	55801	-1.37830	0.00093	0.01120
CAMK4	814	-1.36832	0.00001	0.00006
CCR2	729230	-1.34807	0.00097	0.01170
APP	351	-1.33761	0.00004	0.00026
C9orf135	138255	-1.33327	0.00771	0.04620
EFHA2	286097	-1.33119	0.00034	0.00202
INADL	10207	-1.32465	0.00000	0.00000
USP6NL	9712	-1.32055	0.00003	0.00042
LMO7	4008	-1.31889	0.00018	0.00109
GPR82	27197	-1.30788	0.00133	0.01300
PDE3B	5140	-1.30030	0.00060	0.00362
USP53	54532	-1.29765	0.00001	0.00004
CAMSAP1L1	23271	-1.29739	0.00006	0.00037
FAM117B	150864	-1.29393	0.00093	0.00560
PRKCA	5578	-1.28151	0.00001	0.00006
SLC16A10	117247	-1.26315	0.00699	0.04190
ACVR1C	130399	-1.25999	0.00001	0.00007
SLAMF1	6504	-1.25618	0.00177	0.01060
PDK1	5163	-1.25416	0.00006	0.00035
RAB3GAP1	22930	-1.25248	0.00001	0.00004
KDSR	2531	-1.24796	0.00027	0.00320
ALPK1	80216	-1.24721	0.00018	0.00217
GPR34	2857	-1.24673	0.00208	0.02500
SAMD12	401474	-1.24492	0.00001	0.00006
C9orf72	203228	-1.24421	0.00002	0.00017

Table S1. **Microarray identifies 159 differentially regulated genes between CD8⁺CD28⁺ and CD8⁺CD28⁻ T cells** (Continued)

Gene name	entrez_ids	log ₂ fold change	P-value	FDR
NBEA	26960	-1.23812	0.00012	0.00073
ZNF238	10472	-1.22531	0.00055	0.00333
C1orf162	128346	-1.21798	0.00012	0.00047
RALGPS2	55103	-1.21599	0.00003	0.00018
ZNF208	7757	-1.21537	0.00055	0.00659
CSGALNACT1	55790	-1.21343	0.00008	0.00033
LRRC16A	55604	-1.21062	0.00026	0.00105
CLUAP1	23059	-1.19804	0.00000	0.00000
GTSCR1	220158	-1.18521	0.00379	0.01520
ZFP28	140612	-1.17834	0.00001	0.00003
BACH2	60468	-1.17753	0.00064	0.00386
EPHX2	2053	-1.16847	0.00349	0.02090
SPG20	23111	-1.16119	0.00029	0.00115
OCM	654231	-1.15669	0.00057	0.00170
LOC283174	283174	-1.12311	0.00013	0.00078
OCM2	4951	-1.11977	0.00071	0.00213
RIC3	79608	-1.09937	0.00035	0.00211
RBM11	54033	-1.09596	0.00001	0.00005
ZFYVE9	9372	-1.09436	0.00000	0.00001
FAM102A	399665	-1.08628	0.00192	0.01150
IGSF9B	22997	-1.08560	0.00034	0.00409
CNN3	1266	-1.07971	0.00327	0.00981
NPCDR1	246734	-1.06681	0.01193	0.04770
VWDE	221806	-1.05085	0.00060	0.00241
OXNAD1	92106	-1.04769	0.00000	0.00003
C13orf15	28984	-1.03962	0.00896	0.03580
FAM134B	54463	-1.02815	0.00001	0.00004
TMEM14C	51522	-1.02783	0.00001	0.00006
DAPP1	27071	-1.02770	0.00000	0.00000
FLJ44048	401024	-1.02506	0.00068	0.00408
ME1	4199	-1.02438	0.00307	0.03680
ACVR2A	92	-1.02148	0.00056	0.00220
CASP10	843	-1.02041	0.00004	0.00025
DSEL	92126	-1.01814	0.00003	0.00013
P2RY14	9934	-1.01522	0.01979	0.03960
LY96	23643	-1.01413	0.00364	0.02190

Table S2. **Primer list for qRT-PCR**

Human gene	qRT-PCR forward primers (5'-3')	qRT-PCR reverse primers (5'-3')
RPL13A	CCTGGAGGAGAAGAGAAAGAGA	TTGAGGACCTCTGTGATTTGTCAA
SIRT1	GCCTCACATGCAAGCTCTAGTGAC	TTCGAGGATCTGTGCCAATCATAA
GZMB	CCCTGGGAAAACACTCACACA	GCACAACCTCAATGGTACTGTCC
PRF1	GGCTGGACGTGACTCCTAAG	CTGGGTGGAGGCGTTGAAG
IFNG	TCGGTAACTGACTTGAATGTCCA	TCGCTTCCCTGTTTTAGCTGC
CCR7	TGAGGTCACGGACGATTACAT	GTAGGCCACGAAACAAATGAT
CD62L	CTTTCACCAAGGGCGATTTA	GGCATTATCATTGGCTGG
IL7R	CCCTCGTGGAGGTAAGTGC	CCTTCCCGATAGACGACACTC
KLRG1	TCCATGTTAGAGTTGCCTACGG	AAGTGGAGTAGTTGGAGCCCT
FOXO1	TCGTCATAATCTGTCCTACACA	CGGCTTCGGCTCTTAGCAAA