

**Table S1**

	Ensembl_gene_identifier	Gene_symbol	Donor #1				Donor #2				Donor #3				Score
			K562/A*0201		PBMC		K562/A*0201		PBMC		K562/A*0201		PBMC		
			cognate vs.		cognate vs.		cognate vs.		cognate vs.		cognate vs.		cognate vs.		
			DMSO	mock											
1	ENSG0000049249	TNFRSF9	S	S	S	S	S	S	S	S	S	S	S	S	18
2	ENSG00000162924	REL	S	S	S	S	S	S	S	S	S	S	S	S	18
3	ENSG00000122877	EGR2	S	S	S	S	S	S	S	S	S	S	S	S	18
4	ENSG00000140319	SRP14	S	S	S	S	S	S	S	S	S	S	S	S	18
5	ENSG00000117560	FASLG	S	S	S	S	S	S	S	S	S	S	S	S	18
6	ENSG00000100453	GZMB	S	S	S	S	S	S	S	S	S	S	S	S	18
7	ENSG00000111537	IFNG	S	S	S	S	S	S	S	S	S	S	NS	S	16.5
8	ENSG00000189403	HMGB1	S	S	S	S	S	S	S	S	S	S	NS	S	16.5
9	ENSG00000110848	CD69	S	S	S	S	NS	S	S	S	S	S	S	S	16.5
10	ENSG00000168685	IL7R	S	S	S	S	S	S	S	S	S	NS	S	S	16.5
11	ENSG00000166886	NAB2	S	S	S	S	NS	S	S	S	S	S	S	S	16.5
12	ENSG00000143333	RGS16	S	S	S	S	S	S	S	S	NS	NS	S	S	15
13	ENSG00000172116	CD8B	S	S	S	S	S	S	S	S	S	S	NS	NS	15
14	ENSG00000140968	IRF8	S	S	S	S	S	S	S	S	S	S	NS	NS	15
15	ENSG00000168610	STAT3	S	S	S	S	S	S	NS	S	S	S	NS	NS	13.5
16	ENSG00000198851	CD3E	S	S	S	S	S	S	S	S	NS	S	NS	NS	13.5
17	ENSG00000134460	IL2RA	S	S	NS	NS	S	S	S	S	NS	S	S	S	13.5
18	ENSG00000171791	BCL2	S	S	S	S	NS	S	NS	NS	S	S	NS	S	12
19	ENSG00000139193	CD27	S	S	S	S	S	S	S	S	NS	NS	NS	NS	8
20	ENSG00000271503	CCL5	S	S	NS	S	NS	S	NS	NS	NS	S	NS	NS	7.5
21	ENSG00000275302	CCL4	S	S	S	S	S	S	S	NS	NS	NS	NS	NS	7
22	ENSG00000180644	PRF1	S	S	NS	S	NS	NS	NS	NS	S	S	S	S	7
23	ENSG00000169442	CD52	S	S	S	S	S	S	NS	NS	NS	NS	NS	NS	6
24	ENSG00000073861	TBX21	S	S	S	S	NS	NS	NS	NS	S	S	NS	NS	6
25	ENSG00000228978	TNF	S	NS	S	S	S	S	NS	S	NS	NS	NS	NS	6
26	ENSG00000135048	CEMP2	S	S	NS	NS	S	NS	NS	NS	S	NS	NS	NS	6
27	ENSG00000075426	FOSL2	S	S	NS	NS	S	NS	NS	NS	S	NS	NS	NS	6
28	ENSG00000188486	H2AFX	S	S	S	NS	NS	NS	S	S	NS	NS	NS	NS	5
29	ENSG00000115607	IL18RAP	S	S	S	NS	NS	NS	NS	NS	S	NS	S	NS	5
30	ENSG00000142166	IFNAR1	S	S	NS	S	NS	NS	NS	NS	S	S	NS	NS	5
31	ENSG00000163513	TGFBR2	S	NS	S	S	NS	NS	S	S	NS	NS	NS	NS	5
32	ENSG00000121858	TNFSF10	S	S	S	S	NS	NS	NS	NS	NS	NS	NS	NS	2
33	ENSG00000087586	AURKA	S	NS	NS	NS	NS	NS	NS	S	NS	NS	NS	NS	2
34	ENSG00000109471	IL2	S	S	NS	NS	1								
35	ENSG00000100450	GZMH	NS	S	S	NS	NS	NS	NS	NS	NS	NS	NS	NS	1
36	ENSG00000164400	CSF2	S	S	NS	NS	1								
37	ENSG00000126353	CCR7	S	S	NS	NS	1								
38	ENSG00000170345	FOS	S	S	NS	NS	1								
39	ENSG00000124813	RUNX2	S	NS	NS	NS	0.5								
40	ENSG00000159216	RUNX1	S	NS	NS	NS	0.5								
41	ENSG00000105329	TGFB1	NS	NS	NS	NS	NS	NS	NS	S	NS	NS	NS	NS	0.5
42	ENSG00000198821	CD247	NS	NS	NS	NS	NS	NS	NS	S	NS	NS	NS	NS	0.5
43	ENSG00000113916	BCL6	NS	NS	NS	S	0.5								
44	ENSG00000145649	GZMA	NS	NS	NS	NS	NS	NS	NS	S	NS	NS	NS	NS	0.5
45	ENSG00000026103	FAS	NS	NS	NS	NS	NS	S	NS	NS	NS	NS	NS	NS	0.5
46	ENSG00000126456	IRF3	NS	NS	NS	NS	NS	NS	NS	NS	S	NS	NS	NS	0.5
47	ENSG00000163600	ICOS	NS	NS	0										
48	ENSG00000163599	CTLA4	NS	NS	0										
49	ENSG00000160791	CCR5	NS	NS	0										
50	ENSG00000177606	JUN	NS	NS	0										
51	ENSG00000106546	AHR	NS	NS	0										
52	ENSG00000197919	IFNA1	NS	NS	0										
53	ENSG00000150907	FOXO1	NS	NS	0										
54	ENSG00000163508	EOMES	NS	NS	0										
55	ENSG00000183813	CCR4	NS	NS	0										
56	ENSG00000178573	MAF	NS	NS	0										
57	ENSG00000069667	RORA	NS	NS	0										
58	ENSG00000160712	IL6R	NS	NS	0										
59	ENSG00000102245	CD40LG	NS	NS	0										
60	ENSG00000030419	IKZF2	NS	NS	0										
61	ENSG00000136634	IL10	NS	NS	0										
62	ENSG00000049768	FOXP3	NS	NS	0										
63	ENSG00000186891	TNFRSF18	NS	NS	0										
64	ENSG00000127318	IL22	NS	NS	0										
65	ENSG00000120738	EGR1	NS	NS	0										
66	ENSG00000175063	UBE2C	NS	NS	0										
67	ENSG00000112116	IL17F	NS	NS	0										
68	ENSG00000105639	JAK3	NS	NS	0										
69	ENSG00000145839	IL9	NS	NS	0										
70	ENSG00000113520	IL4	NS	NS	0										
71	ENSG00000112486	CCR6	NS	NS	0										
72	ENSG00000112115	IL17A	NS	NS	0										
73	ENSG00000138684	IL21	NS	NS	0										
74	ENSG00000169194	IL13	NS	NS	0										
75	ENSG00000010610	CD4	NS	NS	0										

**Table S1: Overview of statistical results of the targeted gene expression analysis.** qPCR-based single-cell gene expression data of Flu MP<sub>58-66</sub>-directed cells from donors #1–3 stimulated with cognate peptide or control stimuli (solvent DMSO or mock peptide) in the dye-based CD8<sup>+</sup> T cell activation assay were compared using the Hurdle model (40). Genes were ranked using scores that considered the number of comparisons suggesting significantly different gene expression levels and the number of donors with statistically significant comparisons. Genes with the same score were ranked based on the delta for their median expression differences between the cognate and control stimuli. S = significant; NS = not significant.