

Supplementary Table 1. Gene ontology (GO) categories in which ILT3-Fc treatment induced significant modulation of gene expression in CD8+ T cells

Gene Ontology Term	Count	%	#UP	%UP	#DOWN	%DOWN	Total	PValue	FDR
GO:0007049~cell cycle	241	24.32%	121	12.16%	121	12.16%	995	2.80E-12	5.3E-11
GO:0022402~cell cycle process	171	25.99%	74	11.25%	97	14.74%	658	4.34E-08	8.2E-07
GO:0000278~mitotic cell cycle	116	23.97%	41	8.47%	75	15.50%	484	1.18E-06	2.2E-05
GO:0016481~negative regulation of transcription	137	27.96%	110	22.45%	27	5.51%	490	2.49E-06	4.7E-05
GO:0051726~regulation of cell cycle	103	27.81%	58	15.51%	46	12.30%	374	7.11E-06	0.0001
GO:0046649~lymphocyte activation	66	23.43%	44	15.38%	23	8.04%	286	4.62E-05	0.0009
GO:0045321~leukocyte activation	76	22.32%	52	15.07%	25	7.25%	345	9.06E-05	0.0017
GO:0002520~immune system development	82	23.66%	54	15.21%	30	8.45%	355	3.54E-04	0.0067
GO:0002521~leukocyte differentiation	45	23.47%	34	17.35%	12	6.12%	196	3.73E-04	0.0070
GO:0042110~T cell activation	43	22.22%	30	15.15%	14	7.07%	198	5.98E-04	0.0113
GO:0006916~anti-apoptosis	61	25.96%	35	14.89%	26	11.06%	235	0.0023463	0.0435
GO:0045786~negative regulation of cell cycle	29	33.72%	18	20.93%	11	12.79%	86	0.0025288	0.0468
GO:0001775~cell activation	80	20.66%	55	14.03%	26	6.63%	392	0.0030684	0.0565
GO:0016055~Wnt receptor signaling pathway	42	23.20%	40	22.10%	2	1.10%	181	0.0036367	0.0666
GO:0050670~regulation of lymphocyte proliferation	29	31.18%	13	13.98%	16	17.20%	93	0.0037673	0.0689
GO:0043066~negative regulation of apoptosis	95	23.70%	50	12.35%	46	11.36%	405	0.0042326	0.0771
GO:0030098~lymphocyte differentiation	34	25.37%	27	20.15%	7	5.22%	134	0.0044462	0.0808
GO:0000279~M phase	89	22.31%	31	7.77%	58	14.54%	399	0.0044613	0.0811
GO:0022403~cell cycle phase	108	21.51%	41	8.17%	67	13.35%	502	0.0058707	0.1054

Count, Number of genes significantly modulated in CD8 T cells by ILT3-Fc treatment in each GO category as determined by gene chip analysis, %, percentage of genes in the GO significantly modulated by ILT3-Fc treatment, #UP, #DOWN, number of genes significantly up- or down-regulated by ILT3-Fc treatment in each GO category, %UP, %DOWN, percentage of genes in a GO category significantly up- or down-regulated by ILT3-Fc treatment, Total, the total number of genes belonging to a GO category, and FDR, false discovery rate.