

EZH2 inhibition promotes tumor immunogenicity in lung squamous cell carcinomas**Supplementary Tables 1-6****Supplementary Figures 1-6****Supplemental Table 1: GSEA on RNAseq of Tumoroids, related to Figure 3
NES=Normalized Enrichment Score, FDR=False Discovery Rate**

MSigDB Signature Name	Patient 1		Patient 2		Patient 1		Patient 2	
	GSK126 vs Veh		GSK126 vs Veh		EPZ6438 vs Veh		EPZ6438 vs Veh	
	NES	FDR q-val	NES	FDR q-val	NES	FDR q-val	NES	FDR q-val
HALLMARK_MYC_TARGETS_V1	-2.274	0.000	-2.505	0.000		1.000	-2.127	0.000
HALLMARK_MYC_TARGETS_V2	-1.482	0.079	-1.940	0.014	-1.711	0.017	-1.743	0.026
HALLMARK_DNA_REPAIR	-1.356	0.085	-1.413	0.097	-0.833	0.644	-1.207	0.217
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	-1.360	0.096	-1.273	0.160	-1.542	0.039	-1.142	0.268
HALLMARK_E2F_TARGETS	-0.922	0.688	-1.357	0.117		1.000	-0.632	0.966
HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY	-1.868	0.008	-1.594	0.058	-1.818	0.007	-1.625	0.035
HALLMARK_OXIDATIVE_PHOSPHORYLATION	-2.657	0.000	-2.152	0.000	-2.161	0.004	-2.125	0.000
HALLMARK_INFLAMMATORY_RESPONSE	1.501	0.025	0.821	0.927	1.242	0.183	-1.659	0.036
HALLMARK_INTERFERON_GAMMA_RESPONSE	1.273	0.164	0.999	0.793	1.479	0.036	0.639	1.000
	GSK+IFN vs IFN		GSK+IFN vs IFN		EPZ+IFN vs IFN		EPZ+IFN vs IFN	
	NES	FDR q-val	NES	FDR q-val	NES	FDR q-val	NES	FDR q-val
HALLMARK_MYC_TARGETS_V1	-1.753	0.024	-2.284	0.000	-1.801	0.026	-2.111	0.000
HALLMARK_MYC_TARGETS_V2	-1.527	0.062	-2.244	0.000	-1.637	0.051	-2.139	0.000
HALLMARK_DNA_REPAIR	-1.064	0.420	-1.540	0.069	-1.121	0.361	-1.419	0.117
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	0.892	0.977	-0.829	0.814	0.716	1.000	-0.648	0.965
HALLMARK_E2F_TARGETS	-1.001	0.478	-1.530	0.054	-0.480	1.000	-0.730	0.984
HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY	-1.763	0.032	-1.321	0.149	-1.806	0.038	-1.398	0.096
HALLMARK_OXIDATIVE_PHOSPHORYLATION	-2.091	0.002	-1.393	0.107	-2.064	0.000	-1.557	0.067
HALLMARK_INFLAMMATORY_RESPONSE	1.503	0.036	0.882	0.934	1.178	0.421	-1.413	0.100
HALLMARK_INTERFERON_GAMMA_RESPONSE	1.722	0.002	1.066	0.698	1.385	0.118	0.912	1.000
	Mouse 1		Mouse 2		Mouse 1		Mouse 2	
	GSK126 vs Veh		GSK126 vs Veh		EPZ6438 vs Veh		EPZ6438 vs Veh	
	NES	FDR q-val	NES	FDR q-val	NES	FDR q-val	NES	FDR q-val
HALLMARK_MYC_TARGETS_V1	-1.948	0.001	-1.404	0.086	-1.701	0.089	-1.465	0.092
HALLMARK_MYC_TARGETS_V2	-1.635	0.017	-1.463	0.064	-1.543	0.110	-0.778	1.000
HALLMARK_DNA_REPAIR	-1.572	0.025	-0.815	0.981	-1.542	0.073	-1.315	0.167
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	-1.348	0.112	-1.000	0.690	-1.313	0.178	-0.693	0.931
HALLMARK_E2F_TARGETS	-2.393	0.000	-2.560	0.000	-0.597	0.980	-2.231	0.003
HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY	-1.054	0.424	0.979	0.591	-1.317	0.218	0.695	0.960
HALLMARK_OXIDATIVE_PHOSPHORYLATION	0.534	0.998	0.499	0.999	-1.198	0.258	-0.728	1.000
HALLMARK_INFLAMMATORY_RESPONSE	2.178	0.000	1.233	0.227	1.811	0.000	1.662	0.006
HALLMARK_INTERFERON_GAMMA_RESPONSE	1.772	0.014	1.614	0.032	1.775	0.001	1.811	0.000
	GSK+IFN vs IFN		GSK+IFN vs IFN		EPZ+IFN vs IFN		EPZ+IFN vs IFN	
	NES	FDR q-val	NES	FDR q-val	NES	FDR q-val	NES	FDR q-val
HALLMARK_MYC_TARGETS_V1	-1.618	0.050	-2.248	0.000	-2.003	0.008	-2.443	0.000
HALLMARK_MYC_TARGETS_V2	-2.020	0.007	-2.006	0.000	-1.930	0.007	-1.969	0.005
HALLMARK_DNA_REPAIR	-0.938	0.889	-1.046	0.469	-1.350	0.144	-1.591	0.030
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	-1.559	0.044	-1.936	0.001	-1.732	0.017	-1.955	0.004
HALLMARK_E2F_TARGETS	-1.185	0.458	-2.775	0.000	-1.024	0.392	-2.832	0.000
HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY	-0.911	0.884	0.768	0.945	-1.309	0.143	-0.828	0.799
HALLMARK_OXIDATIVE_PHOSPHORYLATION	0.510	0.998	-0.779	1.000	-1.114	0.294	-1.681	0.023
HALLMARK_INFLAMMATORY_RESPONSE	2.196	0.000	1.512	0.108	1.894	0.000	1.895	0.000
HALLMARK_INTERFERON_GAMMA_RESPONSE	1.888	0.001	1.426	0.121	1.663	0.007	1.937	0.000

Supplemental Table 2: GSEA on Genes That were Up-regulated and Lost H3K27me3 Peaks in Combination Treatment vs IFN γ alone, related to Figure 4

Group	MSigDB Signature Name	GeneRatio	BgRatio	P Value	Adj. P value	FDR q value
Inflammatory Responses	MANNE_COVID19_COMBINED_COHORT_VS_HEALTHY_DONOR_PLATELETS_DN	16/272	228/21697	3.32E-08	4.54878E-06	3.8288E-06
	MANNE_COVID19_ICU_VS_HEALTHY_DONOR_PLATELETS_DN	13/272	162/21697	1.4E-07	1.74026E-05	1.46481E-05
	REACTOME_INTERFERON_GAMMA_SIGNALING	8/272	93/21697	2.23E-05	0.001175233	0.000989219
	REACTOME_PD_1_SIGNALING	5/272	28/21697	2.32E-05	0.001175233	0.000989219
	REACTOME_MHC_CLASS_II_ANTIGEN_PRESENTATION	9/272	126/21697	3.07E-05	0.00150398	0.001265932
	KEGG_ASTHMA	5/272	30/21697	3.29E-05	0.001564249	0.001316661
	KEGG_ALLOGRAFT_REJECTION	5/272	37/21697	9.37E-05	0.003565296	0.003000985
	KEGG_GRAFT_VERSUS_HOST_DISEASE	5/272	41/21697	0.000155	0.005362662	0.004513866
Cell Adhesion and Signaling	KEGG_CELL_ADHESION_MOLECULES_CAMS	12/272	133/21697	1.18E-07	1.54175E-05	1.29773E-05
	ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY	50/272	1941/21697	7.24E-07	6.61582E-05	5.56867E-05
	ONDER_CDH1_TARGETS_2_UP	12/272	257/21697	0.000104	0.003918949	0.003298662
	KEGG_FOCAL_ADHESION	11/272	199/21697	4.51E-05	0.001992359	0.001677011
TP53 and Apoptosis	PEREZ_TP53_TARGETS	40/272	1198/21697	1.49E-08	2.39558E-06	2.01641E-06
	BRUINS_UVC_RESPONSE_VIA_TP53_GROUP_A	30/272	884/21697	7.99E-07	6.84384E-05	5.7606E-05
	PEREZ_TP53_AND_TP63_TARGETS	11/272	208/21697	6.73E-05	0.002792285	0.002350325
	HANN_RESISTANCE_TO_BCL2_INHIBITOR_UP	5/272	36/21697	8.19E-05	0.003298434	0.002776362
Nervous System	REACTOME_NEURONAL_SYSTEM	27/272	410/21697	2.36E-12	6.46166E-10	5.43892E-10
	REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES	16/272	269/21697	3.22E-07	3.39241E-05	2.85546E-05
	REACTOME_NERVOUS_SYSTEM_DEVELOPMENT	23/272	580/21697	1.28E-06	0.000103351	8.69924E-05
	REACTOME_NEUROTRANSMITTER_RECEPTORS_AND_POSTSYNAPTIC_SIGNAL	10/272	205/21697	0.000276	0.008316188	0.006999911
Polycomb Targets	BENPORATH_ES_WITH_H3K27ME3	76/272	1114/21697	3.02E-35	8.26451E-32	6.95641E-32
	BENPORATH_SUZ12_TARGETS	70/272	1033/21697	4.01E-32	5.49216E-29	4.62287E-29
	MIKKELSEN_MEF_HCP_WITH_H3K27ME3	51/272	590/21697	4.28E-28	3.9059E-25	3.28768E-25
	BENPORATH_EED_TARGETS	64/272	1058/21697	1.75E-26	1.19586E-23	1.00658E-23
	MEISSNER_BRAIN_HCP_WITH_H3K4ME3_AND_H3K27ME3	64/272	1073/21697	3.81E-26	2.08627E-23	1.75606E-23
	MIKKELSEN_MCV6_HCP_WITH_H3K27ME3	43/272	437/21697	5.7E-26	2.60336E-23	2.1913E-23
	BENPORATH_PRC2_TARGETS	49/272	649/21697	2.32E-24	9.07209E-22	7.63617E-22
	MIKKELSEN_NPC_HCP_WITH_H3K27ME3	26/272	345/21697	2.83E-13	9.6866E-11	8.15342E-11
	MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27ME3	26/272	350/21697	3.95E-13	1.20105E-10	1.01095E-10
	MEISSNER_BRAIN_HCP_WITH_H3K27ME3	20/272	271/21697	2.52E-10	6.27713E-08	5.28359E-08
	MIKKELSEN_NPC_HCP_WITH_H3K4ME3_AND_H3K27ME3	17/272	210/21697	1.42E-09	3.23121E-07	2.71978E-07
	MEISSNER_NPC_HCP_WITH_H3K4ME3_AND_H3K27ME3	13/272	143/21697	3.19E-08	4.54878E-06	3.8288E-06

Supplemental Table 3: Genes Highly Expressed in All 16 Clusters, Related to Figure 6
Log2FC=Log2-fold change between cluster and all others, pct=percentage of cells expressing

Cluster	Gene Symbol	Log2FC	pct.1	pct.2	P value	Adj P value	Cluster	Gene Symbol	Log2FC	pct.1	pct.2	P value	Adj P value
Tumor	Krt19	4.685	0.977	0.814	0.0E+00	0.0E+00	Dendritic	Cd74	4.390	0.964	0.555	0.0E+00	0.0E+00
	Ppbp	4.050	0.781	0.673	0.0E+00	0.0E+00		H2-Ab1	4.061	0.934	0.629	0.0E+00	0.0E+00
	S100a7a	3.910	0.908	0.872	0.0E+00	0.0E+00		C1qa	3.857	0.988	0.581	0.0E+00	0.0E+00
	S100a10	3.589	0.968	0.700	0.0E+00	0.0E+00		H2-Aa	3.618	0.918	0.556	0.0E+00	0.0E+00
	Ly6d	3.380	0.853	0.767	0.0E+00	0.0E+00		C1qb	3.455	0.982	0.503	0.0E+00	0.0E+00
	Prss27	3.341	0.899	0.825	0.0E+00	0.0E+00		Apoe	3.074	0.985	0.781	0.0E+00	0.0E+00
	Krt18	3.333	0.824	0.698	0.0E+00	0.0E+00		C1qc	2.985	0.988	0.640	0.0E+00	0.0E+00
	Plet1	3.301	0.954	0.684	0.0E+00	0.0E+00		Ms4a6c	2.243	0.930	0.407	0.0E+00	0.0E+00
	Nupr1	3.285	0.892	0.671	0.0E+00	0.0E+00		Ms4a7	2.238	0.969	0.433	0.0E+00	0.0E+00
	S100a16	3.221	0.951	0.730	0.0E+00	0.0E+00		Cts5	1.932	0.990	0.654	0.0E+00	0.0E+00
	Krt23	3.208	0.894	0.638	0.0E+00	0.0E+00		Cst3	1.844	0.987	0.817	0.0E+00	0.0E+00
	Ly6c1	2.943	0.832	0.652	0.0E+00	0.0E+00		Gatm	1.752	0.937	0.517	0.0E+00	0.0E+00
	Atp1b1	2.870	0.888	0.682	0.0E+00	0.0E+00		Lair1	1.530	0.895	0.546	0.0E+00	0.0E+00
	Irf7	2.800	0.937	0.588	0.0E+00	0.0E+00		Pld4	1.525	0.899	0.187	0.0E+00	0.0E+00
	Isg15	2.772	0.869	0.644	0.0E+00	0.0E+00		Tmem119	0.828	0.959	0.256	0.0E+00	0.0E+00
	Tspan1	2.562	0.857	0.516	0.0E+00	0.0E+00		Cxcl9	0.789	0.946	0.644	0.0E+00	0.0E+00
	Hspa5	2.539	0.951	0.818	0.0E+00	0.0E+00		Ccl8	0.651	0.962	0.382	0.0E+00	0.0E+00
	Glrx	2.448	0.869	0.594	0.0E+00	0.0E+00		Retnla	0.821	0.957	0.743	2.9E-289	4.4E-286
	Emp1	2.302	0.920	0.778	0.0E+00	0.0E+00		Cybb	1.677	0.924	0.514	1.9E-288	2.9E-285
	Hopx	2.294	0.766	0.477	0.0E+00	0.0E+00		Gngt2	1.535	0.964	0.637	4.8E-284	7.2E-281
	Cd81	2.276	0.909	0.547	0.0E+00	0.0E+00		Cxcl16	1.511	0.983	0.701	5.4E-279	8.1E-276
	Arg1	2.255	0.872	0.739	0.0E+00	0.0E+00		Fyb	1.709	0.949	0.688	1.7E-277	2.5E-274
	Scgb1a1	2.246	0.831	0.809	0.0E+00	0.0E+00		Pou2f2	1.956	0.849	0.421	1.4E-270	2.1E-267
	Lmo7	2.226	0.849	0.750	0.0E+00	0.0E+00		Acp5	1.404	0.968	0.607	4.2E-268	6.3E-265
	Ceacam1	2.214	0.888	0.649	0.0E+00	0.0E+00		Lgmn	1.372	0.964	0.624	2.1E-257	3.2E-254
	Dusp14	2.072	0.836	0.675	0.0E+00	0.0E+00		Air1	2.087	0.853	0.573	2.8E-255	4.3E-252
	Wnt4	2.037	0.882	0.722	0.0E+00	0.0E+00		Atp1a1	1.325	0.957	0.700	3.7E-254	5.6E-251
	Clu	2.031	0.918	0.761	0.0E+00	0.0E+00		Lyz2	0.748	0.994	0.755	9.3E-252	1.4E-248
	Epcam	2.006	0.848	0.601	0.0E+00	0.0E+00		Trf	1.377	0.891	0.499	4.4E-247	6.7E-244
	Anxa1	2.002	0.919	0.772	0.0E+00	0.0E+00		Ms4a6d	1.230	0.895	0.733	2.9E-240	4.4E-237
	Cldn3	1.963	0.803	0.773	0.0E+00	0.0E+00		Csf1r	1.731	0.824	0.437	2.0E-233	3.1E-230
	2310007B03Ril	1.887	0.861	0.663	0.0E+00	0.0E+00		Bcl2a1d	1.057	0.884	0.505	3.6E-223	5.4E-220
	Pdzk1ip1	1.882	0.850	0.786	0.0E+00	0.0E+00		Fcgr1	0.866	0.839	0.480	3.3E-217	5.0E-214
	Prss22	1.850	0.702	0.557	0.0E+00	0.0E+00		Napsa	1.159	0.904	0.579	1.7E-213	2.5E-210
	Aqp5	1.785	0.676	0.741	0.0E+00	0.0E+00		Ly86	1.085	0.807	0.287	7.3E-213	1.1E-209
	Cldn7	1.777	0.732	0.679	0.0E+00	0.0E+00		Ctsc	1.394	0.881	0.644	2.9E-207	4.4E-204
	Jdp2	1.736	0.810	0.711	0.0E+00	0.0E+00		Gm2a	1.234	0.909	0.624	5.8E-207	8.7E-204
	Plpp1	1.699	0.783	0.653	0.0E+00	0.0E+00		Malb	1.508	0.853	0.588	4.2E-199	6.3E-196
	Avp1	1.689	0.843	0.712	0.0E+00	0.0E+00		Ccr2	0.905	0.788	0.255	3.8E-195	5.7E-192
	Nccrp1	1.658	0.754	0.730	0.0E+00	0.0E+00		Ifitm3	1.495	0.943	0.695	1.8E-194	2.6E-191
	Errfi1	1.618	0.894	0.564	0.0E+00	0.0E+00		Pgls	0.758	0.921	0.629	5.1E-182	7.6E-179
	Plat	1.601	0.627	0.504	0.0E+00	0.0E+00		Itgb5	0.923	0.849	0.676	1.1E-177	1.6E-174
	Gsta4	1.599	0.796	0.689	0.0E+00	0.0E+00		Rpl3	1.055	0.970	0.708	1.1E-177	1.7E-174
	Tacstd2	1.567	0.736	0.538	0.0E+00	0.0E+00		Gpx1	0.883	0.965	0.833	4.2E-173	6.3E-170
	Calr	1.558	0.945	0.734	0.0E+00	0.0E+00		Clec4a3	1.528	0.770	0.440	5.1E-172	7.6E-169
	Tubb4b	1.556	0.918	0.674	0.0E+00	0.0E+00		Cd72	1.163	0.717	0.163	1.4E-171	2.1E-168
	Wwtr1	1.537	0.890	0.574	0.0E+00	0.0E+00		Cx3cr1	1.589	0.759	0.360	7.3E-171	1.1E-167
	Fxyd3	1.529	0.782	0.582	0.0E+00	0.0E+00		Tgfb1	0.964	0.915	0.601	2.9E-170	4.4E-167
	Csrp1	1.520	0.819	0.671	0.0E+00	0.0E+00		Asah1	0.779	0.879	0.564	1.0E-169	1.5E-166
	Spns3	1.512	0.823	0.552	0.0E+00	0.0E+00		Ptma	0.975	0.965	0.726	1.6E-165	2.4E-162
	Mall	1.506	0.859	0.721	0.0E+00	0.0E+00		Smpd3a	1.034	0.904	0.622	3.0E-163	4.5E-160
	Gprc5a	1.498	0.799	0.586	0.0E+00	0.0E+00		Ucp2	0.852	0.973	0.726	5.8E-162	8.7E-159
	Herpud1	1.429	0.790	0.560	0.0E+00	0.0E+00		Bcl2a1a	0.700	0.859	0.545	1.3E-159	1.9E-156
	Ddit3	1.405	0.820	0.723	0.0E+00	0.0E+00		Cd300e	1.156	0.727	0.244	4.8E-158	7.1E-155
	Clec2g	1.386	0.818	0.436	0.0E+00	0.0E+00		Ctsz	0.849	0.994	0.790	2.0E-152	3.1E-149
	Dnajb1	1.374	0.893	0.567	0.0E+00	0.0E+00		Laptm5	0.768	0.989	0.732	2.3E-151	3.5E-148
	Cidea	1.304	0.610	0.536	0.0E+00	0.0E+00		Rassf4	0.995	0.789	0.576	1.5E-149	2.3E-146
Lrrc26	1.302	0.812	0.724	0.0E+00	0.0E+00	Emp3	1.135	0.840	0.456	8.3E-148	1.2E-144		
Cldn23	1.294	0.734	0.615	0.0E+00	0.0E+00	Erp29	1.067	0.922	0.709	9.2E-146	1.4E-142		
Chac1	1.291	0.750	0.706	0.0E+00	0.0E+00	Sdf2l1	0.667	0.902	0.718	1.0E-143	1.5E-140		
Rdh10	1.290	0.787	0.518	0.0E+00	0.0E+00	Cd300c2	0.691	0.932	0.651	5.4E-142	8.1E-139		
Fam57a	1.279	0.733	0.754	0.0E+00	0.0E+00	Clec4a1	1.686	0.720	0.281	1.3E-141	1.9E-138		
Gadd45b	1.263	0.948	0.711	0.0E+00	0.0E+00	Ms4a6b	1.104	0.755	0.271	1.1E-138	1.6E-135		
Cops6	1.253	0.833	0.647	0.0E+00	0.0E+00	Tmem160	0.781	0.834	0.577	2.9E-137	4.4E-134		
Krt8	1.231	0.690	0.700	0.0E+00	0.0E+00	H2-DMa	1.252	0.756	0.394	3.1E-136	4.7E-133		
Gadd45g	1.225	0.659	0.573	0.0E+00	0.0E+00	Abhd12	0.845	0.790	0.432	6.7E-135	1.0E-131		
Fam110a	1.163	0.787	0.499	0.0E+00	0.0E+00	Hexb	1.403	0.863	0.751	6.5E-132	9.7E-129		
Pls3	1.149	0.784	0.594	0.0E+00	0.0E+00	S100a4	1.042	0.790	0.500	1.6E-130	2.3E-127		
Hbegf	1.114	0.731	0.762	0.0E+00	0.0E+00	Flna	0.830	0.835	0.487	2.2E-128	3.3E-125		

Phlda1	1.100	0.759	0.510	0.0E+00	0.0E+00	Unc93b1	0.755	0.848	0.511	1.4E-127	2.0E-124
Krt80	1.097	0.845	0.529	0.0E+00	0.0E+00	Pid1	0.802	0.765	0.585	1.5E-127	2.2E-124
Manf	1.096	0.869	0.829	0.0E+00	0.0E+00	Rras	0.921	0.760	0.544	7.2E-126	1.1E-122
Pamr1	1.078	0.778	0.721	0.0E+00	0.0E+00	Itgb2	0.950	0.910	0.585	2.3E-124	3.5E-121
Hsd17b2	1.076	0.686	0.537	0.0E+00	0.0E+00	Lilra5	1.100	0.724	0.321	2.1E-120	3.2E-117
Slco2a1	1.075	0.676	0.528	0.0E+00	0.0E+00	Mgst1	0.710	0.874	0.601	1.1E-119	1.6E-116
2610528A11Ril	1.070	0.701	0.641	0.0E+00	0.0E+00	Selenop	0.924	0.776	0.519	2.1E-115	3.2E-112
Apol7a	1.050	0.698	0.453	0.0E+00	0.0E+00	mt-Nd1	0.722	0.963	0.666	1.7E-114	2.6E-111
Mlph	1.045	0.754	0.665	0.0E+00	0.0E+00	Fcgrt	0.886	0.735	0.282	7.0E-114	1.0E-110
Sqstm1	1.023	0.873	0.581	0.0E+00	0.0E+00	Plekho1	0.926	0.756	0.553	7.7E-112	1.2E-108
Pmaip1	0.991	0.742	0.669	0.0E+00	0.0E+00	Ndufa4	0.708	0.879	0.666	2.0E-111	3.0E-108
Oasl1	0.984	0.620	0.575	0.0E+00	0.0E+00	Mef2c	1.025	0.724	0.384	3.3E-106	5.0E-103
Plac8	0.977	0.735	0.523	0.0E+00	0.0E+00	Irf8	1.231	0.760	0.635	2.2E-105	3.3E-102
Ifi202b	0.963	0.703	0.648	0.0E+00	0.0E+00	Npc2	0.824	0.958	0.889	2.4E-101	3.7E-98
Rbp1	0.960	0.608	0.545	0.0E+00	0.0E+00	Plac8	1.352	0.759	0.557	6.2E-100	9.3E-97
2010109I03Rik	0.930	0.607	0.662	0.0E+00	0.0E+00	H2-DMb1	1.111	0.707	0.428	3.2E-94	4.9E-91
Tspan8	0.903	0.766	0.646	0.0E+00	0.0E+00	Tifab	0.751	0.686	0.354	2.7E-81	4.1E-78
Yod1	0.898	0.649	0.569	0.0E+00	0.0E+00	Pltp	0.669	0.703	0.365	9.6E-81	1.4E-77
Cald1	0.888	0.677	0.690	0.0E+00	0.0E+00	Ccdc88a	1.007	0.688	0.547	2.3E-70	3.5E-67
Plk2	0.881	0.723	0.493	0.0E+00	0.0E+00	Ear2	1.003	0.647	0.320	8.7E-66	1.3E-62
Ephb3	0.877	0.717	0.631	0.0E+00	0.0E+00	Ms4a4c	0.756	0.630	0.135	1.7E-64	2.5E-61
Oit1	0.851	0.751	0.566	0.0E+00	0.0E+00	Ace	1.683	0.644	0.536	6.6E-64	9.9E-61
Hsp90aa1	0.846	0.911	0.832	0.0E+00	0.0E+00	Evl	0.693	0.688	0.340	1.6E-61	2.4E-58
Klk8	0.932	0.547	0.488	6.8E-289	1.0E-285	Ifi2712a	0.784	0.697	0.528	8.9E-55	1.3E-51
Hsp90b1	1.266	0.827	0.781	2.1E-272	3.1E-269	Gm15987	0.810	0.635	0.261	1.1E-54	1.6E-51
Tsc22d1	0.850	0.640	0.773	8.6E-178	1.3E-174	Klf4	0.724	0.648	0.422	4.9E-44	7.3E-41
Clic5	1.114	0.581	0.733	7.7E-159	1.2E-155	Slc12a2	1.262	0.706	0.578	4.8E-43	7.2E-40
Ifit1b1	1.446	0.487	0.470	6.4E-149	9.6E-146	Adgre4	0.930	0.597	0.375	2.9E-42	4.4E-39
Cxcl5	1.588	0.446	0.399	6.7E-125	1.0E-121	Bst2	0.727	0.651	0.506	1.1E-30	1.7E-27
Pigr	0.995	0.441	0.469	6.3E-68	9.5E-65	Tmem176b	1.272	0.622	0.568	1.4E-22	2.1E-19
Cxcl3	1.035	0.364	0.517	5.7E-03	1.0E+00	Krt80	0.745	0.634	0.587	1.1E-20	1.6E-17
Neu-1						B cells					
Cst3	1.532	0.929	0.800	0.0E+00	0.0E+00	Igkc	4.317	0.964	0.279	0.0E+00	0.0E+00
Gngt2	1.374	0.812	0.614	0.0E+00	0.0E+00	Ighm	3.141	0.908	0.317	0.0E+00	0.0E+00
Id2	1.172	0.925	0.753	0.0E+00	0.0E+00	Cd74	3.059	0.992	0.554	0.0E+00	0.0E+00
Ptgs1	1.172	0.772	0.678	0.0E+00	0.0E+00	H2-Ab1	2.828	0.975	0.628	0.0E+00	0.0E+00
Laptm5	0.838	0.829	0.722	0.0E+00	0.0E+00	H2-Aa	2.789	0.983	0.554	0.0E+00	0.0E+00
Gm19951	0.675	0.840	0.656	0.0E+00	0.0E+00	Cd79a	2.550	0.908	0.408	0.0E+00	0.0E+00
Ccl4	0.552	0.895	0.685	0.0E+00	0.0E+00	Cd79b	2.207	0.854	0.309	0.0E+00	0.0E+00
Hist1h1e	0.491	0.794	0.590	0.0E+00	0.0E+00	Ebf1	2.190	0.862	0.157	0.0E+00	0.0E+00
Asprv1	0.446	0.778	0.552	0.0E+00	0.0E+00	Igic2	2.133	0.870	0.147	0.0E+00	0.0E+00
Egr2	0.310	0.274	0.401	3.3E-290	5.0E-287	Cd72	1.409	0.846	0.159	0.0E+00	0.0E+00
B930036N10Ri	0.499	0.642	0.468	1.2E-283	1.8E-280	Serpina3g	0.465	0.972	0.560	0.0E+00	0.0E+00
Id1	1.043	0.832	0.665	4.7E-266	7.1E-263	Gatm	0.355	0.992	0.516	0.0E+00	0.0E+00
Gpx1	0.848	0.869	0.830	3.8E-265	5.7E-262	Ighd	2.304	0.799	0.270	1.4E-299	2.1E-296
Ms4a6d	0.565	0.805	0.725	7.4E-254	1.1E-250	Gm15987	0.802	0.838	0.255	1.2E-273	1.9E-270
Csf1r	0.366	0.280	0.483	9.3E-226	1.4E-222	Jchain	1.341	0.826	0.370	9.8E-271	1.5E-267
Gpc3	0.286	0.688	0.670	3.7E-198	5.5E-195	Ms4a1	1.914	0.819	0.197	6.8E-270	1.0E-266
Cd300c2	1.210	0.716	0.649	5.2E-190	7.8E-187	Ly6d	0.446	0.929	0.779	5.9E-245	8.9E-242
Hist1h1d	0.253	0.697	0.533	8.4E-188	1.3E-184	Rpl3	1.155	0.991	0.707	7.0E-233	1.1E-229
Ptgs2	0.526	0.234	0.306	4.4E-180	6.6E-177	Mef2c	1.562	0.830	0.381	8.7E-231	1.3E-227
Pmaip1	0.518	0.787	0.662	1.1E-178	1.6E-175	Bank1	1.757	0.792	0.348	2.6E-210	3.9E-207
Ccl3	0.592	0.738	0.624	1.2E-148	1.8E-145	Ptma	0.989	0.991	0.725	2.2E-205	3.3E-202
Osgin1	0.724	0.685	0.570	7.6E-146	1.1E-142	Igha	1.645	0.780	0.378	1.0E-200	1.5E-197
Olr1	0.348	0.328	0.404	8.3E-139	1.2E-135	Ighg1	1.025	0.772	0.364	8.7E-190	1.3E-186
Pi16	0.312	0.619	0.443	4.3E-134	6.5E-131	H2-DMa	0.962	0.810	0.392	7.6E-178	1.1E-174
Hexb	0.810	0.794	0.746	4.2E-133	6.3E-130	Fam96a	0.433	0.939	0.556	5.6E-177	8.5E-174
Fcgr4	0.354	0.750	0.685	1.7E-126	2.6E-123	Gpr65	0.440	0.838	0.448	3.8E-174	5.7E-171
Bcl2a1d	0.547	0.380	0.543	1.6E-123	2.4E-120	Igic3	1.588	0.712	0.157	2.9E-168	4.3E-165
Cd63	0.327	0.866	0.768	2.9E-120	4.4E-117	Napsa	1.338	0.843	0.582	3.3E-163	5.0E-160
Ier3	0.771	0.802	0.786	5.3E-113	8.0E-110	mt-Nd1	0.665	0.967	0.666	1.3E-152	1.9E-149
Atp1a1	0.853	0.779	0.694	1.1E-110	1.7E-107	Ets1	1.116	0.792	0.447	1.3E-150	1.9E-147
Hk2	0.263	0.470	0.609	5.4E-104	8.0E-101	Mzb1	1.617	0.728	0.330	2.9E-146	4.3E-143
P2ry6	0.401	0.710	0.682	1.5E-100	2.3E-97	Rps2	0.667	0.989	0.892	8.8E-135	1.3E-131
Lrg1	0.265	0.765	0.686	1.4E-95	2.1E-92	Fcmr	1.153	0.750	0.392	8.3E-132	1.2E-128
Gm12840	1.099	0.321	0.411	2.0E-95	3.0E-92	Gm31243	1.017	0.709	0.181	9.7E-121	1.5E-117
H1f0	0.599	0.700	0.568	2.2E-87	3.3E-84	H2-DMb2	1.138	0.718	0.272	2.2E-119	3.3E-116
Naaa	0.359	0.655	0.568	4.8E-75	7.2E-72	Ranbp1	0.695	0.826	0.642	4.2E-105	6.4E-102
Ltc4s	0.796	0.644	0.599	1.2E-72	1.9E-69	Gm8369	0.449	0.297	0.105	1.4E-101	2.1E-98
Reep5	0.646	0.749	0.711	5.2E-55	7.9E-52	Gimap6	1.256	0.710	0.321	1.5E-98	2.3E-95
Egr1	0.842	0.617	0.544	1.1E-51	1.6E-48	4930523C07R	1.050	0.716	0.510	6.0E-92	9.0E-89
Asah1	0.261	0.666	0.555	1.3E-49	2.0E-46	Ptprcap	0.932	0.716	0.524	7.3E-82	1.1E-78
Gm2a	0.855	0.637	0.632	1.0E-45	1.5E-42	Cd55	0.849	0.734	0.433	3.2E-81	4.8E-78
Hist1h4i	1.255	0.646	0.671	1.8E-45	2.8E-42	Fcer2a	1.434	0.669	0.501	4.6E-75	6.9E-72
Chil1	0.513	0.593	0.475	2.1E-43	3.2E-40	Erp29	0.518	0.910	0.710	1.4E-73	2.1E-70
Tgm2	0.664	0.463	0.641	5.8E-43	8.6E-40	Pax5	0.985	0.641	0.212	3.4E-73	5.1E-70

Dpep2	0.374	0.652	0.687	7.8E-43	1.2E-39	Ndufa4	0.509	0.843	0.667	4.6E-69	6.9E-66	
Ctsa	0.381	0.744	0.697	2.0E-42	2.9E-39	Sdc4	0.893	0.745	0.674	2.2E-67	3.3E-64	
Fgd4	0.251	0.688	0.624	1.5E-41	2.3E-38	Tnfrsf13c	0.888	0.622	0.177	2.7E-67	4.1E-64	
Fam20c	0.442	0.792	0.763	5.8E-41	8.7E-38	Scd1	1.063	0.661	0.348	8.6E-65	1.3E-61	
Pou2f2	0.312	0.387	0.444	1.9E-34	2.9E-31	Hmg1	0.833	0.723	0.652	7.2E-61	1.1E-57	
Cks2	1.189	0.534	0.460	3.2E-33	4.8E-30	Hspe1	0.691	0.777	0.674	5.8E-60	8.7E-57	
Rhoc	0.380	0.529	0.605	3.6E-33	5.3E-30	Hes1	0.392	0.338	0.532	7.1E-59	1.1E-55	
Fyb	0.514	0.751	0.686	7.6E-32	1.1E-28	Pxdc1	0.899	0.660	0.339	2.1E-58	3.2E-55	
Fcgr2b	0.347	0.713	0.648	2.8E-31	4.1E-28	Cd180	0.448	0.352	0.326	1.2E-54	1.8E-51	
C3	0.875	0.585	0.551	5.4E-30	8.1E-27	Pgls	0.647	0.753	0.634	2.2E-54	3.3E-51	
Slc7a11	0.272	0.428	0.478	6.5E-28	9.7E-25	Nap111	0.555	0.726	0.561	1.5E-44	2.2E-41	
Hist1h1c	0.763	0.664	0.606	5.7E-26	8.5E-23	Blk	0.482	0.380	0.328	1.6E-43	2.3E-40	
Tcirg1	0.280	0.550	0.636	9.7E-26	1.5E-22	Bcar3	0.432	0.387	0.408	3.1E-43	4.7E-40	
Abca1	0.438	0.768	0.731	1.2E-25	1.7E-22	Gimap3	0.924	0.632	0.218	1.3E-42	2.0E-39	
Rgs1	1.284	0.650	0.628	1.6E-25	2.4E-22	AC149090.1	1.234	0.659	0.455	1.3E-41	1.9E-38	
Csf2rb	0.693	0.676	0.689	3.6E-25	5.5E-22	Irf8	0.826	0.671	0.638	8.6E-38	1.3E-34	
Bcl2a1b	0.872	0.640	0.631	2.0E-23	2.9E-20	Pou2f2	0.590	0.656	0.428	5.8E-36	8.7E-33	
Ccng1	0.266	0.520	0.595	7.3E-23	1.1E-19	Ms4a4c	0.498	0.386	0.143	8.2E-36	1.2E-32	
Agap1	0.867	0.586	0.610	2.6E-22	3.9E-19	Tubb5	0.433	0.727	0.599	1.1E-33	1.7E-30	
Erp29	0.301	0.600	0.739	1.2E-21	1.7E-18	Ly86	0.735	0.619	0.293	8.3E-27	1.2E-23	
Slc6a6	0.338	0.463	0.522	2.5E-21	3.7E-18	Aldh2	0.584	0.639	0.517	2.6E-26	3.9E-23	
Tnf	0.725	0.327	0.308	9.4E-19	1.4E-15	S1pr1	0.415	0.391	0.514	1.3E-24	1.9E-21	
Hist1h2ap	0.263	0.508	0.479	6.2E-18	9.3E-15	Id3	0.855	0.605	0.569	1.8E-24	2.7E-21	
Gm20186	0.564	0.404	0.440	6.6E-18	9.9E-15	Pou2af1	1.186	0.585	0.245	5.4E-24	8.1E-21	
Cfp	0.354	0.543	0.434	1.4E-17	2.2E-14	Lmo2	0.870	0.616	0.400	1.0E-23	1.5E-20	
Unc93b1	0.643	0.570	0.512	3.2E-16	4.8E-13	Gimap1	0.903	0.615	0.455	3.2E-23	4.9E-20	
Ptma	0.282	0.760	0.728	3.5E-15	5.2E-12	C1qbp	0.416	0.684	0.663	3.0E-22	4.5E-19	
Itgax	0.746	0.468	0.563	2.5E-14	3.8E-11	Slc25a4	0.458	0.662	0.537	2.2E-21	3.3E-18	
Aprt	0.365	0.639	0.761	2.1E-12	3.1E-09	Gimap7	0.681	0.581	0.231	4.9E-21	7.3E-18	
Itgb2	0.303	0.503	0.614	2.2E-12	3.3E-09	Myo1e	0.370	0.454	0.610	3.7E-20	5.5E-17	
Ucp2	0.280	0.743	0.732	4.5E-11	6.8E-08	Siglecg	0.415	0.590	0.505	4.4E-17	6.6E-14	
Bcl2a1a	0.956	0.592	0.547	7.5E-10	1.1E-06	Eprs	0.470	0.654	0.584	2.2E-16	3.3E-13	
Arhgap25	0.475	0.546	0.497	4.7E-08	7.1E-05	Nucks1	0.526	0.636	0.534	2.7E-15	4.0E-12	
G0s2	0.960	0.524	0.494	1.9E-06	2.8E-03	Plekho1	0.670	0.621	0.557	1.2E-14	1.9E-11	
Gm26870	0.339	0.577	0.569	5.6E-05	8.3E-02	Zbtb20	0.422	0.454	0.546	7.7E-14	1.2E-10	
Cdkn1a	0.436	0.825	0.760	5.5E-04	8.2E-01	Evl	0.561	0.600	0.343	3.7E-13	5.6E-10	
Tgfb	0.656	0.586	0.616	5.7E-04	8.5E-01	Snx5	0.608	0.621	0.551	2.3E-12	3.5E-09	
Mpeg1	0.405	0.595	0.629	6.4E-04	9.6E-01	Ciita	0.638	0.441	0.281	1.7E-11	2.6E-08	
Csf2ra	0.674	0.543	0.575	1.5E-03	1.0E+00	Blnk	0.663	0.596	0.738	2.1E-10	3.2E-07	
Tnfrsf23	0.465	0.654	0.712	5.8E-03	1.0E+00	Sptbn1	0.654	0.623	0.580	6.2E-10	9.3E-07	
Neu-2						Igcl1	1.620	0.546	0.204	9.9E-09	1.5E-05	
Gm5483	2.762	0.938	0.564	0.0E+00	0.0E+00	Ms4a6c	0.618	0.593	0.418	1.4E-08	2.1E-05	
BC100530	2.671	0.815	0.520	0.0E+00	0.0E+00	Cd2ap	0.534	0.624	0.597	1.7E-08	2.6E-05	
Wfdc17	2.485	0.993	0.744	0.0E+00	0.0E+00	Cd69	0.605	0.558	0.334	5.9E-08	8.8E-05	
Cxcl2	2.340	0.951	0.469	0.0E+00	0.0E+00	Ms4a6b	0.387	0.469	0.280	2.3E-07	3.4E-04	
Ifitm1	2.087	0.963	0.701	0.0E+00	0.0E+00	Bin1	0.731	0.578	0.566	2.8E-07	4.2E-04	
Retnlg	2.057	0.960	0.576	0.0E+00	0.0E+00	Kcnq1ot1	0.583	0.624	0.657	3.6E-07	5.4E-04	
Wfdc21	1.768	0.945	0.605	0.0E+00	0.0E+00	Odc1	0.433	0.478	0.572	3.6E-07	5.4E-04	
Lrg1	1.760	0.929	0.661	0.0E+00	0.0E+00	Vpreb3	1.232	0.539	0.135	4.7E-07	7.1E-04	
G0s2	1.756	0.819	0.446	0.0E+00	0.0E+00	Nr4a1	0.505	0.424	0.317	1.1E-06	1.7E-03	
Egr1	1.705	0.912	0.497	0.0E+00	0.0E+00	Rftn1	0.435	0.495	0.627	2.7E-06	4.1E-03	
Lcn2	1.667	0.911	0.561	0.0E+00	0.0E+00	Pdia4	0.591	0.566	0.537	7.0E-06	1.1E-02	
Ier3	1.643	0.972	0.758	0.0E+00	0.0E+00	Gpr171	0.531	0.481	0.578	3.9E-05	5.9E-02	
Slpi	1.397	0.904	0.602	0.0E+00	0.0E+00	Ikzf3	0.915	0.544	0.267	4.1E-05	6.2E-02	
Adam8	1.286	0.729	0.572	0.0E+00	0.0E+00	Gpr183	0.771	0.535	0.267	4.2E-04	6.2E-01	
Ccl4	1.276	0.981	0.676	0.0E+00	0.0E+00	Cd38	0.484	0.588	0.584	8.6E-03	1.0E+00	
F630028O10Ri	1.234	0.798	0.503	0.0E+00	0.0E+00	Lung Ep.	Il33	1.978	0.892	0.537	0.0E+00	0.0E+00
Sifn4	1.160	0.942	0.505	0.0E+00	0.0E+00	Areg	1.182	0.853	0.425	1.7E-291	2.6E-288	
Id1	0.989	0.915	0.655	0.0E+00	0.0E+00	Fxyd3	2.925	0.930	0.612	1.3E-275	2.0E-272	
Csf2rb	0.976	0.921	0.648	0.0E+00	0.0E+00	Wfdc2	4.063	0.911	0.760	1.7E-275	2.5E-272	
Steap4	0.965	0.732	0.447	0.0E+00	0.0E+00	Col1a1	1.424	0.721	0.220	4.9E-249	7.3E-246	
Hcar2	0.955	0.882	0.648	0.0E+00	0.0E+00	Dapl1	1.474	0.823	0.391	1.1E-243	1.6E-240	
Prok2	0.868	0.790	0.548	0.0E+00	0.0E+00	Col1a2	1.973	0.756	0.381	8.7E-239	1.3E-235	
Olfm4	0.701	0.793	0.426	0.0E+00	0.0E+00	Btb3	1.083	0.834	0.570	1.3E-220	1.9E-217	
Dgat2	0.563	0.795	0.603	0.0E+00	0.0E+00	Ly6d	1.756	0.948	0.779	8.8E-220	1.3E-216	
Tceal9	0.557	0.888	0.641	0.0E+00	0.0E+00	Hspb1	1.934	0.823	0.582	6.5E-217	9.7E-214	
Cxcl3	0.533	0.840	0.429	0.0E+00	0.0E+00	Wfdc3	1.449	0.821	0.682	5.9E-205	8.8E-202	
Cd177	0.461	0.740	0.458	0.0E+00	0.0E+00	Ckmt1	1.370	0.883	0.732	1.1E-200	1.7E-197	
Tnfrsf23	0.440	0.910	0.668	0.0E+00	0.0E+00	Gpx2	1.928	0.819	0.571	1.7E-198	2.6E-195	
Hk2	0.430	0.884	0.536	0.0E+00	0.0E+00	Cdh1	1.240	0.859	0.604	1.2E-197	1.8E-194	
Ccl6	0.398	0.910	0.592	0.0E+00	0.0E+00	Tmem176a	2.040	0.873	0.582	7.6E-197	1.1E-193	
Cdkn1a	0.298	0.945	0.742	0.0E+00	0.0E+00	Ehf	2.134	0.855	0.799	5.1E-196	7.6E-193	
Rgcc	0.260	0.926	0.710	0.0E+00	0.0E+00	Gsta4	2.610	0.871	0.705	1.8E-191	2.7E-188	
Slc7a11	0.868	0.715	0.429	1.1E-307	1.6E-304	Them5	1.260	0.732	0.268	1.7E-187	2.5E-184	
Mmp8	0.729	0.731	0.597	8.0E-292	1.2E-288	Cldn7	1.072	0.896	0.684	1.1E-182	1.6E-179	
Stfa211	2.238	0.682	0.448	1.4E-272	2.1E-269							

Osgin1	0.516	0.765	0.560	5.6E-269	8.5E-266	Clu	2.509	0.912	0.787	1.7E-182	2.5E-179
Stfa2	1.396	0.680	0.497	3.6E-261	5.4E-258	Api1	1.828	0.900	0.732	2.4E-182	3.6E-179
Il1f9	0.937	0.718	0.534	1.0E-248	1.6E-245	Cp	1.550	0.766	0.560	1.4E-168	2.1E-165
Gadd45a	0.936	0.731	0.606	1.1E-241	1.7E-238	Cald1	1.304	0.837	0.684	1.2E-164	1.8E-161
Ifitm3	0.397	0.844	0.679	2.8E-228	4.3E-225	Mgp	2.757	0.817	0.644	3.8E-162	5.7E-159
Hip1	0.280	0.812	0.586	5.1E-221	7.7E-218	Cbr2	3.030	0.806	0.745	6.7E-160	1.0E-156
Ifitm6	0.479	0.683	0.435	1.5E-216	2.2E-213	Ybx3	1.340	0.857	0.598	6.7E-160	1.0E-156
Chil1	0.781	0.691	0.462	2.0E-216	2.9E-213	Far1	1.422	0.882	0.509	6.9E-160	1.0E-156
Asprv1	1.206	0.707	0.570	1.3E-199	1.9E-196	Plac8	1.530	0.919	0.554	8.7E-160	1.3E-156
Tgm2	0.428	0.758	0.587	5.2E-159	7.8E-156	Serping1	1.481	0.693	0.306	5.8E-159	8.7E-156
Acod1	0.849	0.624	0.389	1.6E-127	2.5E-124	Akr1b3	1.620	0.866	0.517	1.5E-157	2.2E-154
Fyb	0.331	0.786	0.682	1.7E-118	2.6E-115	Cd81	1.439	0.922	0.607	1.0E-155	1.5E-152
Saa3	0.560	0.748	0.606	4.7E-83	7.1E-80	Scgb1a1	3.980	0.915	0.811	7.6E-155	1.1E-151
Ly6g	0.520	0.596	0.425	4.1E-82	6.1E-79	Id3	1.470	0.769	0.565	1.6E-149	2.5E-146
Tgfb1	0.391	0.696	0.596	1.9E-80	2.8E-77	Perp	1.659	0.834	0.733	1.2E-147	1.8E-144
Gm5416	0.363	0.605	0.486	5.7E-76	8.5E-73	Ppp1r14b	1.481	0.892	0.660	6.9E-146	1.0E-142
Pi16	0.460	0.605	0.450	1.1E-70	1.6E-67	Tpm2	1.173	0.815	0.658	4.9E-138	7.4E-135
Fcgr4	0.341	0.715	0.693	1.4E-60	2.0E-57	Ceacam1	1.300	0.918	0.689	2.4E-135	3.5E-132
Slc6a6	0.335	0.651	0.489	4.4E-51	6.6E-48	Igfbp4	1.213	0.714	0.516	3.6E-125	5.4E-122
Csf2ra	0.339	0.671	0.553	1.6E-47	2.4E-44	Rpl3	1.482	0.892	0.712	1.4E-118	2.1E-115
Fgd4	0.308	0.677	0.628	5.9E-39	8.9E-36	Ptprf	1.412	0.746	0.622	2.3E-117	3.4E-114
Stfa3	0.456	0.528	0.544	1.1E-08	1.7E-05	Rps2	1.263	0.934	0.894	1.5E-115	2.2E-112
Hacd4	0.323	0.496	0.524	8.5E-08	1.3E-04	Nenf	1.188	0.790	0.520	6.5E-109	9.7E-106
Ptgs2	0.592	0.407	0.275	1.3E-07	2.0E-04	Arg1	1.174	0.919	0.760	1.7E-105	2.6E-102
Fosb	0.422	0.476	0.366	3.8E-03	1.0E+00	Nedd4	1.526	0.696	0.323	1.8E-105	2.8E-102
Neu-3						Dmkn	1.828	0.776	0.719	1.0E-104	1.6E-101
Ccl3	2.965	0.920	0.610	0.0E+00	0.0E+00	Fabp5	2.134	0.923	0.803	7.8E-103	1.2E-99
Hcar2	2.705	0.884	0.657	0.0E+00	0.0E+00	Gm26870	1.224	0.813	0.564	1.2E-101	1.8E-98
Ccl4	2.320	0.868	0.702	0.0E+00	0.0E+00	Ein	1.022	0.671	0.350	3.1E-100	4.6E-97
Nceh1	2.161	0.856	0.686	0.0E+00	0.0E+00	Scgb3a1	4.567	0.740	0.635	1.2E-99	1.8E-96
Gadd45b	2.109	0.877	0.741	0.0E+00	0.0E+00	Pam	1.544	0.788	0.651	1.9E-97	2.9E-94
lfrd1	1.995	0.819	0.702	0.0E+00	0.0E+00	Aqp5	1.174	0.777	0.728	4.3E-96	6.5E-93
Hilpda	1.887	0.836	0.728	0.0E+00	0.0E+00	Phlda1	1.105	0.823	0.551	4.7E-95	7.1E-92
Atp6v1c1	1.859	0.857	0.741	0.0E+00	0.0E+00	Prdx2	1.395	0.805	0.642	2.1E-89	3.1E-86
Zeb2	1.831	0.829	0.607	0.0E+00	0.0E+00	Epcam	1.512	0.786	0.644	4.0E-89	6.0E-86
Cd63	1.769	0.936	0.766	0.0E+00	0.0E+00	Dcxr	1.400	0.768	0.619	4.5E-87	6.8E-84
Ftl1	1.745	1.000	0.953	0.0E+00	0.0E+00	Serpinb6b	1.063	0.769	0.688	5.7E-86	8.6E-83
Id2	1.629	0.874	0.771	0.0E+00	0.0E+00	Rbp1	1.619	0.722	0.552	4.9E-85	7.3E-82
F10	1.608	0.863	0.694	0.0E+00	0.0E+00	Muc5b	2.403	0.675	0.506	7.2E-84	1.1E-80
Ctsz	1.414	0.936	0.780	0.0E+00	0.0E+00	Scd1	1.002	0.226	0.360	1.4E-83	2.2E-80
Ctsb	1.241	0.977	0.941	0.0E+00	0.0E+00	Tsc22d1	1.408	0.780	0.747	1.2E-81	1.9E-78
Gas2l3	1.116	0.818	0.634	0.0E+00	0.0E+00	Socs2	1.111	0.732	0.667	2.5E-80	3.8E-77
Dhfr	0.942	0.789	0.739	0.0E+00	0.0E+00	Selenbp1	2.144	0.707	0.645	4.2E-80	6.3E-77
Lhfp12	0.915	0.784	0.664	0.0E+00	0.0E+00	Krt8	1.959	0.720	0.698	5.2E-77	7.9E-74
Ctsd	0.494	0.987	0.963	0.0E+00	0.0E+00	Atp5g1	1.265	0.834	0.645	8.9E-76	1.3E-72
Fcgr2b	0.726	0.838	0.637	1.2E-307	1.8E-304	Prdx1	1.233	0.822	0.667	1.8E-74	2.6E-71
Chka	0.537	0.738	0.519	3.0E-302	4.5E-299	Stfb	1.227	0.664	0.439	2.9E-74	4.4E-71
H2-Eb1	1.000	0.683	0.519	1.0E-285	1.5E-282	Retnla	1.246	0.738	0.750	1.6E-71	2.3E-68
Cd274	1.549	0.725	0.579	2.4E-265	3.6E-262	Nfib	1.180	0.680	0.619	2.7E-70	4.1E-67
Plcx2	0.637	0.728	0.653	3.2E-265	4.8E-262	Aldh1a1	1.071	0.648	0.384	9.0E-69	1.3E-65
Hexa	0.947	0.839	0.688	1.1E-248	1.7E-245	Nupr1	1.463	0.795	0.711	1.2E-68	1.8E-65
Dock10	0.893	0.783	0.666	2.7E-239	4.1E-236	Ifitm3	1.335	0.809	0.700	6.7E-68	1.0E-64
Pdxk	0.597	0.726	0.574	7.5E-236	1.1E-232	Sdc4	1.174	0.760	0.674	1.7E-65	2.5E-62
Cxcl2	1.230	0.759	0.512	6.9E-233	1.0E-229	Cldn3	1.119	0.776	0.778	5.3E-64	8.0E-61
Psap	0.760	0.852	0.749	1.3E-230	1.9E-227	Scd2	1.073	0.705	0.541	6.5E-63	9.7E-60
Gns	1.339	0.782	0.688	1.3E-230	2.0E-227	Timp3	1.525	0.657	0.569	1.1E-59	1.6E-56
Lamp1	1.194	0.885	0.861	2.6E-229	3.9E-226	Scgb3a2	2.769	0.668	0.618	4.3E-58	6.5E-55
Atf3	1.754	0.679	0.548	3.1E-224	4.7E-221	Dbi	1.376	0.776	0.646	7.1E-52	1.1E-48
Npc1	1.211	0.749	0.677	5.2E-220	7.8E-217	Tmem176b	1.986	0.660	0.567	2.6E-51	3.9E-48
Ccnf	0.536	0.662	0.612	4.8E-210	7.3E-207	Sdc1	1.649	0.700	0.709	1.3E-43	2.0E-40
Plekha2	1.096	0.785	0.726	1.7E-206	2.5E-203	Cyp2f2	2.315	0.663	0.704	2.5E-42	3.7E-39
Rgs1	1.675	0.774	0.615	1.1E-205	1.6E-202	Bgn	1.569	0.550	0.243	1.1E-39	1.7E-36
Ier3	1.085	0.810	0.786	1.8E-195	2.7E-192	Trf	1.356	0.684	0.507	1.6E-37	2.5E-34
9130230L23Rik	0.335	0.648	0.524	1.2E-192	1.8E-189	Wfdc18	1.473	0.361	0.563	6.2E-34	9.4E-31
P2rx7	0.626	0.760	0.609	9.9E-177	1.5E-173	Sparc	2.443	0.542	0.358	1.0E-32	1.6E-29
Fam20c	0.499	0.847	0.758	1.7E-170	2.6E-167	Foxq1	1.159	0.583	0.537	2.1E-25	3.2E-22
Gstm1	0.562	0.697	0.550	1.0E-164	1.6E-161	Tff2	1.506	0.544	0.381	1.1E-24	1.7E-21
Hmox1	1.389	0.790	0.754	7.4E-133	1.1E-129	Ndufc2	1.065	0.660	0.625	1.1E-23	1.7E-20
Aprt	0.932	0.820	0.731	3.6E-132	5.4E-129	Chchd10	1.241	0.644	0.644	2.8E-22	4.3E-19
Tnfrsf12a	0.301	0.721	0.595	1.8E-125	2.7E-122	Igfbp5	1.952	0.347	0.441	9.8E-22	1.5E-18
Tpp1	0.909	0.716	0.608	4.3E-113	6.5E-110	Ccnd1	1.370	0.572	0.514	2.1E-19	3.2E-16
Inhba	0.910	0.622	0.550	4.4E-112	6.5E-109	Tagln2	1.084	0.659	0.593	5.6E-18	8.5E-15
Tst	0.398	0.688	0.590	1.2E-95	1.9E-92	Hmg1	1.450	0.616	0.655	9.1E-17	1.4E-13
Tcirg1	1.119	0.670	0.616	9.4E-90	1.4E-86	Snhg18	1.056	0.551	0.593	1.2E-10	1.7E-07
Canx	0.712	0.769	0.666	1.2E-87	1.8E-84	C3	1.081	0.651	0.554	3.2E-06	4.8E-03
Mpeg1	0.696	0.701	0.614	6.5E-80	9.7E-77						

Tmem86a	0.586	0.724	0.687	1.8E-78	2.7E-75	Tst	1.319	0.571	0.602	1.0E-05	1.6E-02	
Osm	0.502	0.286	0.341	5.9E-76	8.8E-73	Pmepa1	1.556	0.563	0.622	5.8E-05	8.7E-02	
C3	0.873	0.632	0.548	3.4E-72	5.1E-69	Fmo2	1.044	0.413	0.343	2.5E-04	3.8E-01	
Slc7a11	1.622	0.565	0.458	4.8E-70	7.2E-67	Crip2	1.269	0.502	0.560	1.6E-03	1.0E+00	
Acod1	1.455	0.548	0.408	1.2E-65	1.8E-62	Igfbp7	1.823	0.413	0.473	5.7E-03	1.0E+00	
Ftl1-ps1	0.517	0.338	0.440	5.7E-65	8.5E-62	Sftpd	1.945	0.489	0.461	8.2E-03	1.0E+00	
Naglu	0.833	0.616	0.547	7.7E-61	1.2E-57	T cells 2	Ccl5	6.355	0.988	0.505	0.0E+00	0.0E+00
Gm5416	0.294	0.605	0.491	3.2E-55	4.8E-52	Nkg7	4.438	0.997	0.532	0.0E+00	0.0E+00	
Prok2	0.362	0.643	0.575	3.5E-50	5.2E-47	AW112010	3.298	0.997	0.502	0.0E+00	0.0E+00	
Cd300c2	0.878	0.675	0.658	2.2E-49	3.3E-46	Cd3g	2.927	0.963	0.453	0.0E+00	0.0E+00	
Hk2	0.718	0.466	0.600	6.9E-44	1.0E-40	Klrd1	2.649	0.930	0.383	0.0E+00	0.0E+00	
Slc43a3	0.347	0.577	0.585	8.1E-44	1.2E-40	Gimap4	2.407	0.904	0.222	0.0E+00	0.0E+00	
Creg1	1.161	0.702	0.668	6.8E-39	1.0E-35	Cxcr6	2.039	0.977	0.308	0.0E+00	0.0E+00	
Cldn1	0.605	0.582	0.623	1.3E-37	2.0E-34	Ikzf3	1.577	0.956	0.261	0.0E+00	0.0E+00	
Hspa1b	0.760	0.659	0.609	2.5E-37	3.8E-34	Pdcd1	1.413	0.989	0.234	0.0E+00	0.0E+00	
G0s2	0.733	0.597	0.488	6.5E-37	9.7E-34	Rgs16	0.578	0.966	0.464	0.0E+00	0.0E+00	
Tgm2	0.386	0.453	0.630	1.1E-35	1.7E-32	Bcl2	2.127	0.963	0.426	1.1E-305	1.6E-302	
Ctsa	0.424	0.748	0.700	1.5E-35	2.2E-32	Klre1	1.502	0.905	0.518	5.3E-294	8.0E-291	
Cxcr1	0.882	0.643	0.718	9.1E-35	1.4E-31	Gimap1	2.138	0.918	0.450	1.1E-276	1.6E-273	
Gadd45g	0.961	0.634	0.584	2.1E-31	3.2E-28	Ptprcap	2.054	0.919	0.521	6.8E-265	1.0E-261	
Cd68	0.694	0.714	0.715	6.3E-31	9.4E-28	Gzma	3.710	0.885	0.291	3.3E-263	5.0E-260	
Tnfrsf23	0.997	0.661	0.707	8.2E-31	1.2E-27	Serpib9	1.165	0.887	0.348	3.6E-245	5.4E-242	
Hal	0.570	0.514	0.710	1.2E-30	1.8E-27	Wls	1.997	0.925	0.525	5.8E-242	8.8E-239	
Syng1	0.408	0.721	0.777	1.4E-28	2.0E-25	Ctsw	2.064	0.826	0.206	9.3E-235	1.4E-231	
Ptgs2	0.446	0.299	0.293	4.0E-27	6.0E-24	Gpr171	0.922	0.902	0.568	2.0E-234	3.1E-231	
Slc37a2	0.659	0.609	0.589	5.6E-27	8.4E-24	Camk2n1	0.674	0.893	0.584	6.5E-232	9.8E-229	
Dpp7	0.410	0.624	0.628	5.7E-25	8.6E-22	Klrb1c	0.994	0.792	0.241	1.3E-217	2.0E-214	
Laptm5	0.357	0.748	0.739	3.4E-23	5.1E-20	Thy1	1.399	0.805	0.194	2.8E-212	4.2E-209	
Hpgds	0.365	0.680	0.634	4.8E-21	7.2E-18	Itga1	1.174	0.858	0.540	2.9E-207	4.3E-204	
Rps6ka2	0.407	0.521	0.487	7.5E-20	1.1E-16	Lck	1.936	0.843	0.282	9.4E-198	1.4E-194	
Slc6a6	0.352	0.448	0.520	6.6E-18	9.9E-15	Cd3e	1.702	0.850	0.307	4.9E-196	7.4E-193	
Syne1	0.775	0.511	0.619	2.1E-17	3.1E-14	Bin1	1.028	0.889	0.559	4.2E-175	6.3E-172	
Vegfa	0.957	0.495	0.433	7.9E-17	1.2E-13	Rpl3	1.327	0.992	0.710	1.8E-173	2.7E-170	
Asprv1	0.304	0.639	0.584	1.2E-14	1.8E-11	mt-Nd1	1.057	0.991	0.669	1.2E-168	1.8E-165	
Sqstm1	0.695	0.608	0.639	3.5E-14	5.2E-11	Ctla2a	1.995	0.849	0.746	4.1E-167	6.2E-164	
Tnf	0.606	0.311	0.311	1.1E-12	1.6E-09	Gbp4	0.491	0.908	0.599	6.1E-164	9.2E-161	
Gm26870	0.659	0.567	0.570	1.1E-11	1.7E-08	Skap1	1.419	0.785	0.187	8.8E-160	1.3E-156	
Hspa9	0.318	0.651	0.648	1.1E-09	1.6E-06	Lgals1	1.245	0.915	0.575	1.1E-159	1.6E-156	
Osgin1	0.594	0.500	0.600	5.8E-08	8.7E-05	Gimap3	1.887	0.779	0.219	8.9E-157	1.3E-153	
Cst2rb	0.453	0.681	0.687	7.0E-07	1.1E-03	Gpr65	0.821	0.870	0.451	4.5E-153	6.7E-150	
Egr1	0.431	0.574	0.554	8.2E-07	1.2E-03	Ets1	1.314	0.838	0.449	9.4E-153	1.4E-149	
Dhrs3	0.461	0.674	0.676	1.1E-06	1.7E-03	Ptma	1.057	0.983	0.728	1.0E-151	1.5E-148	
Thbs1	1.309	0.451	0.550	7.4E-06	1.1E-02	Il2rb	1.677	0.756	0.242	1.1E-147	1.7E-144	
Cdkn1a	0.339	0.776	0.770	4.9E-05	7.3E-02	Crip1	0.729	0.947	0.503	4.0E-140	5.9E-137	
Gadd45a	0.424	0.639	0.622	1.8E-04	2.6E-01	Hspe1	0.981	0.928	0.671	4.3E-139	6.5E-136	
Hist1h4i	0.531	0.648	0.669	3.2E-04	4.8E-01	Gzmb	2.047	0.733	0.217	1.6E-136	2.4E-133	
Slpi	0.477	0.653	0.644	3.7E-04	5.5E-01	Bcl2a1d	0.761	0.902	0.508	6.0E-129	9.1E-126	
Ddit3	0.444	0.598	0.758	3.7E-04	5.6E-01	Ly9	0.743	0.798	0.321	9.2E-125	1.4E-121	
Il1f9	0.929	0.529	0.564	5.8E-04	8.7E-01	Laptm5	0.968	0.994	0.735	1.4E-124	2.2E-121	
Sirpa	0.299	0.560	0.634	5.2E-03	1.0E+00	Trbc2	2.552	0.763	0.257	3.1E-120	4.7E-117	
T cells	Cd3g	2.602	0.918	0.436	0.0E+00	0.0E+00	Gimap6	1.119	0.771	0.323	5.1E-115	7.7E-112
	Trbc2	2.530	0.904	0.229	0.0E+00	0.0E+00	Rps2	0.852	0.998	0.893	4.5E-114	6.7E-111
	Il7r	2.308	0.820	0.669	0.0E+00	0.0E+00	Trac	1.458	0.734	0.151	8.0E-114	1.2E-110
	Bcl2	2.093	0.817	0.414	0.0E+00	0.0E+00	AU020206	0.620	0.934	0.698	2.9E-110	4.4E-107
	Rpl3	1.972	0.988	0.699	0.0E+00	0.0E+00	Irf8	0.532	0.853	0.635	3.3E-106	4.9E-103
	Cd3e	1.953	0.856	0.286	0.0E+00	0.0E+00	H2afz	0.948	0.944	0.804	2.5E-104	3.7E-101
	Cd3d	1.904	0.890	0.375	0.0E+00	0.0E+00	Ccnd2	1.530	0.785	0.608	3.8E-104	5.7E-101
	Ptprcap	1.902	0.828	0.511	0.0E+00	0.0E+00	Dut	0.533	0.774	0.448	1.5E-98	2.3E-95
	Gimap1	1.875	0.851	0.436	0.0E+00	0.0E+00	Emp3	0.746	0.876	0.460	5.1E-97	7.6E-94
	Cxcr6	1.867	0.946	0.284	0.0E+00	0.0E+00	Id2	0.628	0.977	0.778	1.4E-96	2.0E-93
	Ctla2a	1.782	0.926	0.738	0.0E+00	0.0E+00	Ebpl	0.549	0.782	0.407	2.9E-88	4.4E-85
	Trac	1.722	0.781	0.126	0.0E+00	0.0E+00	Ndufa4	0.747	0.879	0.668	4.0E-88	6.0E-85
	Gimap3	1.701	0.790	0.197	0.0E+00	0.0E+00	Cd2	1.412	0.725	0.421	1.2E-85	1.8E-82
	AW112010	1.634	0.891	0.489	0.0E+00	0.0E+00	Ilf47	0.906	0.766	0.648	1.7E-82	2.6E-79
	Ets1	1.568	0.849	0.434	0.0E+00	0.0E+00	Klrk1	1.640	0.666	0.100	2.0E-81	3.0E-78
	Ms4a6b	1.553	0.803	0.254	0.0E+00	0.0E+00	Serpib6b	0.741	0.769	0.688	8.2E-73	1.2E-69
	Skap1	1.513	0.806	0.163	0.0E+00	0.0E+00	Cx3cr1	0.855	0.716	0.365	3.6E-72	5.4E-69
	Lck	1.488	0.779	0.264	0.0E+00	0.0E+00	Reep5	0.686	0.904	0.713	1.6E-71	2.4E-68
	Ramp1	1.368	0.783	0.405	0.0E+00	0.0E+00	Pla2g16	0.823	0.780	0.548	3.0E-65	4.5E-62
	Rps2	1.301	0.993	0.889	0.0E+00	0.0E+00	Racgap1	0.500	0.689	0.255	1.8E-63	2.7E-60
	Nkg7	1.264	0.876	0.521	0.0E+00	0.0E+00	Cd7	1.311	0.653	0.123	3.7E-59	5.5E-56
	Ptma	1.233	0.983	0.718	0.0E+00	0.0E+00	F2r	1.007	0.699	0.655	1.7E-57	2.5E-54
	Maf	1.184	0.936	0.701	0.0E+00	0.0E+00	Iitm2c	0.598	0.789	0.595	2.3E-57	3.5E-54
	Thy1	1.172	0.878	0.165	0.0E+00	0.0E+00	Maf	0.484	0.773	0.713	6.1E-56	9.2E-53
	Hspe1	1.096	0.879	0.665	0.0E+00	0.0E+00	Sh2d1a	1.028	0.637	0.160	4.7E-49	7.0E-46

Ccl5	1.061	0.893	0.492	0.0E+00	0.0E+00	Cd3d	1.570	0.660	0.399	1.5E-48	2.3E-45
Pdcd1	1.058	0.965	0.206	0.0E+00	0.0E+00	Nme1	0.638	0.798	0.715	6.0E-44	9.0E-41
Icos	1.040	0.721	0.224	0.0E+00	0.0E+00	Cd48	1.146	0.658	0.445	9.0E-42	1.3E-38
Il2rb	0.938	0.822	0.219	0.0E+00	0.0E+00	Pycard	0.597	0.864	0.778	3.7E-39	5.5E-36
Trdc	0.926	0.888	0.260	0.0E+00	0.0E+00	Zbp1	0.508	0.708	0.633	3.6E-36	5.5E-33
Ikzf3	0.876	0.895	0.238	0.0E+00	0.0E+00	Itgb7	0.911	0.655	0.528	4.8E-34	7.2E-31
F2r	0.833	0.807	0.646	0.0E+00	0.0E+00	Gimap7	1.216	0.618	0.234	2.7E-31	4.0E-28
mt-Nd1	0.778	0.971	0.657	0.0E+00	0.0E+00	Tmem160	0.727	0.687	0.583	2.4E-28	3.7E-25
Tcrg-C1	0.619	0.895	0.175	0.0E+00	0.0E+00	Phf11b	0.550	0.623	0.316	8.7E-28	1.3E-24
Cd163l1	0.484	0.811	0.167	0.0E+00	0.0E+00	Dock10	0.734	0.696	0.678	3.1E-27	4.7E-24
Camk2n1	0.476	0.974	0.567	0.0E+00	0.0E+00	Klra4	1.070	0.347	0.141	2.8E-26	4.2E-23
Il2ra	0.462	0.861	0.138	0.0E+00	0.0E+00	Kcnq1ot1	0.612	0.692	0.655	1.8E-18	2.6E-15
Gbp4	0.441	0.879	0.589	0.0E+00	0.0E+00	Nucks1	0.618	0.643	0.535	1.4E-17	2.1E-14
AU020206	0.440	0.957	0.687	0.0E+00	0.0E+00	Ranbp1	0.579	0.682	0.647	3.9E-15	5.9E-12
Nrp1	0.439	0.886	0.725	0.0E+00	0.0E+00	Trbc1	1.609	0.582	0.216	9.1E-15	1.4E-11
Gpr171	0.417	0.782	0.562	3.2E-288	4.8E-285	Osbp13	0.642	0.631	0.611	1.3E-13	1.9E-10
S100a4	1.528	0.865	0.488	9.4E-267	1.4E-263	AC149090.1	0.829	0.602	0.458	1.3E-12	2.0E-09
Crip1	0.519	0.881	0.490	1.0E-230	1.6E-227	Bcl11b	1.186	0.573	0.347	3.4E-12	5.1E-09
Ctsw	0.610	0.694	0.191	3.5E-222	5.3E-219	Sept9	0.475	0.618	0.475	1.9E-10	2.8E-07
Slc25a4	0.912	0.791	0.526	7.1E-222	1.1E-218	Il18r1	0.691	0.586	0.426	6.5E-10	9.8E-07
Lat	0.926	0.715	0.457	1.0E-202	1.6E-199	Il7r	0.709	0.631	0.679	2.1E-09	3.1E-06
Gimap4	1.294	0.695	0.208	3.3E-200	5.0E-197	S100a4	1.032	0.598	0.508	3.6E-09	5.4E-06
Tcf7	0.897	0.659	0.050	2.1E-199	3.1E-196	Ev1	0.553	0.597	0.346	4.4E-08	6.6E-05
Gimap6	0.852	0.713	0.309	4.4E-194	6.6E-191	Dok2	0.675	0.563	0.438	3.4E-07	5.0E-04
Cd28	1.003	0.702	0.529	1.9E-184	2.8E-181	Sms	0.505	0.435	0.441	5.8E-07	8.7E-04
Bcl11b	1.081	0.686	0.332	1.0E-181	1.6E-178	Ms4a6b	0.880	0.574	0.280	7.1E-07	1.1E-03
Ebpl	0.434	0.744	0.395	1.2E-177	1.7E-174	Ybx3	0.569	0.449	0.607	4.5E-06	6.7E-03
Itgb7	1.071	0.709	0.520	5.7E-170	8.5E-167	Cblb	0.518	0.449	0.632	7.0E-06	1.0E-02
Wls	0.694	0.775	0.518	1.0E-164	1.6E-161	Esyt1	0.697	0.566	0.420	1.5E-05	2.2E-02
Cd2	1.084	0.694	0.411	6.8E-162	1.0E-158	Sept11	0.805	0.568	0.594	8.0E-05	1.2E-01
Gpr65	0.404	0.737	0.442	2.0E-150	3.0E-147	Slamf7	0.845	0.534	0.547	8.7E-03	1.0E+00
4930523C07Ril	0.862	0.693	0.505	1.3E-137	1.9E-134	Prol. Pclaf	2.491	0.958	0.145	0.0E+00	0.0E+00
Pla2g16	0.610	0.767	0.540	8.1E-130	1.2E-126	Tpx2	1.659	0.979	0.461	0.0E+00	0.0E+00
Pgls	0.429	0.820	0.627	5.4E-121	8.1E-118	Hmmr	1.416	0.965	0.417	0.0E+00	0.0E+00
Dut	0.633	0.647	0.443	7.5E-88	1.1E-84	Cks1b	1.929	0.966	0.434	5.1E-307	7.7E-304
Cd7	0.448	0.374	0.119	7.0E-70	1.1E-66	Ccnb1	1.412	0.897	0.279	9.5E-295	1.4E-291
Ifi203	0.760	0.642	0.560	2.2E-69	3.3E-66	Sp25	1.049	0.954	0.304	7.3E-293	1.1E-289
Il18r1	0.468	0.359	0.433	9.1E-69	1.4E-65	Stmn1	2.414	0.965	0.511	2.1E-290	3.1E-287
Ranbp1	0.564	0.715	0.643	6.1E-68	9.1E-65	Mki67	2.558	0.959	0.570	2.8E-289	4.3E-286
Mllt3	0.629	0.666	0.631	2.6E-67	3.8E-64	Nusap1	1.629	0.920	0.239	1.2E-271	1.7E-268
Ar	0.464	0.380	0.208	8.1E-65	1.2E-61	Cdca8	1.719	0.927	0.543	1.2E-265	1.8E-262
Ccnd2	0.721	0.677	0.608	5.6E-64	8.3E-61	Tuba1b	2.789	0.975	0.597	1.6E-247	2.4E-244
Tmem176a	0.693	0.737	0.580	1.5E-62	2.3E-59	Cenpe	1.483	0.904	0.409	3.6E-245	5.4E-242
Igfbp4	0.442	0.371	0.530	4.0E-61	6.0E-58	Racgap1	1.111	0.892	0.252	2.0E-234	3.0E-231
Hmgn1	0.444	0.702	0.651	8.9E-57	1.3E-53	Ptma	2.106	0.961	0.729	9.1E-234	1.4E-230
Nucks1	0.698	0.651	0.530	2.2E-56	3.2E-53	Lig1	1.309	0.922	0.604	1.5E-224	2.2E-221
Ifi27l2a	0.810	0.649	0.527	1.1E-55	1.7E-52	Comt	1.054	0.981	0.624	1.5E-214	2.2E-211
Nrip1	0.824	0.664	0.612	7.0E-54	1.1E-50	Fn1	1.115	0.950	0.408	2.4E-214	3.6E-211
Esyt1	0.550	0.636	0.410	6.1E-53	9.1E-50	Mt1	1.467	0.989	0.771	5.7E-214	8.6E-211
Ifi47	0.471	0.662	0.649	1.9E-50	2.9E-47	Tacc3	1.088	0.885	0.465	6.6E-212	1.0E-208
Dock10	0.556	0.688	0.678	8.2E-47	1.2E-43	Nucks1	2.033	0.961	0.529	6.2E-211	9.3E-208
Trbc1	1.908	0.580	0.202	3.3E-44	4.9E-41	H2afz	1.932	0.933	0.805	2.0E-204	3.0E-201
C1qbp	0.468	0.666	0.664	9.5E-43	1.4E-39	Tagln2	2.069	0.991	0.587	7.3E-196	1.1E-192
Ms4a4b	0.952	0.551	0.088	2.1E-41	3.2E-38	Snx5	1.077	0.986	0.545	5.5E-194	8.2E-191
Gm12840	1.196	0.572	0.386	9.3E-39	1.4E-35	Tubb5	2.638	0.927	0.597	1.1E-193	1.6E-190
Gimap7	0.743	0.566	0.222	1.6E-32	2.4E-29	Hmgn1	1.810	0.970	0.649	2.7E-191	4.0E-188
Klk8	0.546	0.598	0.493	8.8E-32	1.3E-28	Atad2	1.082	0.929	0.479	9.4E-191	1.4E-187
Rexo2	0.515	0.636	0.637	1.1E-25	1.6E-22	Ppp1r14b	1.888	0.981	0.660	1.3E-189	1.9E-186
Zbtb20	0.641	0.604	0.540	1.0E-24	1.5E-21	Lgals1	1.754	0.982	0.574	1.6E-188	2.4E-185
Ev1	0.589	0.582	0.337	5.4E-18	8.2E-15	Slc25a4	1.447	0.961	0.533	1.2E-185	1.8E-182
Las1l	0.388	0.576	0.490	5.6E-17	8.4E-14	Ccnb2	1.586	0.846	0.228	4.4E-185	6.7E-182
Kcnq1ot1	0.582	0.619	0.658	8.6E-16	1.3E-12	Hebp1	1.259	0.989	0.644	2.7E-183	4.1E-180
S1pr1	0.739	0.552	0.507	8.8E-16	1.3E-12	Ezh2	1.288	0.869	0.522	1.3E-180	2.0E-177
Lef1	0.517	0.517	0.035	3.6E-14	5.4E-11	Crip1	1.624	0.982	0.504	1.2E-176	1.8E-173
Gpr183	0.598	0.436	0.265	9.7E-11	1.5E-07	Tmem256	1.475	0.968	0.545	1.8E-173	2.7E-170
Kcnn4	0.510	0.468	0.579	5.0E-10	7.6E-07	Prdx1	1.850	0.996	0.665	5.2E-173	7.7E-170
Gm8369	0.566	0.443	0.091	1.8E-09	2.8E-06	Selenoh	1.849	0.871	0.469	1.9E-168	2.8E-165
Tnfrsf8	0.669	0.451	0.396	5.5E-09	8.3E-06	Cenpa	1.756	0.867	0.426	3.0E-166	4.4E-163
Ramp3	0.410	0.540	0.413	1.2E-07	1.8E-04	Cenpx	1.309	0.959	0.664	6.9E-165	1.0E-161
Ccr2	0.445	0.449	0.261	4.5E-07	6.8E-04	Rexo2	1.263	0.965	0.631	8.8E-164	1.3E-160
Tmem160	0.367	0.600	0.584	5.6E-07	8.5E-04	Ndufa4	2.100	0.982	0.667	3.8E-158	5.8E-155
Dapl1	0.839	0.526	0.394	4.6E-06	6.9E-03	Pycard	1.529	0.989	0.776	2.6E-157	4.0E-154
Cblb	0.388	0.487	0.637	1.4E-04	2.1E-01	Smc4	1.764	0.924	0.614	5.8E-155	8.7E-152
Odc1	0.426	0.573	0.569	1.2E-03	1.0E+00	Fabp5	1.449	0.993	0.803	1.1E-154	1.7E-151
Tmem176b	0.675	0.581	0.569	5.8E-03	1.0E+00	Cks2	1.430	0.931	0.464	1.4E-152	2.2E-149

Igfbp4	0.442	0.371	0.530	4.0E-61	6.0E-58	Racgap1	1.111	0.892	0.252	2.0E-234	3.0E-231
Hmgn1	0.444	0.702	0.651	8.9E-57	1.3E-53	Ptma	2.106	0.961	0.729	9.1E-234	1.4E-230
Nucks1	0.698	0.651	0.530	2.2E-56	3.2E-53	Lig1	1.309	0.922	0.604	1.5E-224	2.2E-221
Ifi2712a	0.810	0.649	0.527	1.1E-55	1.7E-52	Comt	1.054	0.981	0.624	1.5E-214	2.2E-211
Nrip1	0.824	0.664	0.612	7.0E-54	1.1E-50	Fn1	1.115	0.950	0.408	2.4E-214	3.6E-211
Esyt1	0.550	0.636	0.410	6.1E-53	9.1E-50	Mt1	1.467	0.989	0.771	5.7E-214	8.6E-211
Ifi47	0.471	0.662	0.649	1.9E-50	2.9E-47	Tacc3	1.088	0.885	0.465	6.6E-212	1.0E-208
Dock10	0.556	0.688	0.678	8.2E-47	1.2E-43	Nucks1	2.033	0.961	0.529	6.2E-211	9.3E-208
Trbc1	1.908	0.580	0.202	3.3E-44	4.9E-41	H2afz	1.932	0.933	0.805	2.0E-204	3.0E-201
C1qbp	0.468	0.666	0.664	9.5E-43	1.4E-39	Tagln2	2.069	0.991	0.587	7.3E-196	1.1E-192
Ms4a4b	0.952	0.551	0.088	2.1E-41	3.2E-38	Snx5	1.077	0.986	0.545	5.5E-194	8.2E-191
Gm12840	1.196	0.572	0.386	9.3E-39	1.4E-35	Tubb5	2.638	0.927	0.597	1.1E-193	1.6E-190
Gimap7	0.743	0.566	0.222	1.6E-32	2.4E-29	Hmgn1	1.810	0.970	0.649	2.7E-191	4.0E-188
Klk8	0.546	0.598	0.493	8.8E-32	1.3E-28	Atad2	1.082	0.929	0.479	9.4E-191	1.4E-187
Rexo2	0.515	0.636	0.637	1.1E-25	1.6E-22	Ppp1r14b	1.888	0.981	0.660	1.3E-189	1.9E-186
Zbtb20	0.641	0.604	0.540	1.0E-24	1.5E-21	Lgals1	1.754	0.982	0.574	1.6E-188	2.4E-185
Evi	0.589	0.582	0.337	5.4E-18	8.2E-15	Slc25a4	1.447	0.961	0.533	1.2E-185	1.8E-182
Las1l	0.388	0.576	0.490	5.6E-17	8.4E-14	Ccnb2	1.586	0.846	0.228	4.4E-185	6.7E-182
Kcnq1ot1	0.582	0.619	0.658	8.6E-16	1.3E-12	Hebp1	1.259	0.989	0.644	2.7E-183	4.1E-180
S1pr1	0.739	0.552	0.507	8.8E-16	1.3E-12	Ezh2	1.288	0.869	0.522	1.3E-180	2.0E-177
Lef1	0.517	0.517	0.035	3.6E-14	5.4E-11	Crip1	1.624	0.982	0.504	1.2E-176	1.8E-173
Gpr183	0.598	0.436	0.265	9.7E-11	1.5E-07	Tmem256	1.475	0.968	0.545	1.8E-173	2.7E-170
Kcnn4	0.510	0.468	0.579	5.0E-10	7.6E-07	Prdx1	1.850	0.996	0.665	5.2E-173	7.7E-170
Gm8369	0.566	0.443	0.091	1.8E-09	2.8E-06	Selenoh	1.849	0.871	0.469	1.9E-168	2.8E-165
Tnfrsf8	0.669	0.451	0.396	5.5E-09	8.3E-06	Cenpa	1.756	0.867	0.426	3.0E-166	4.4E-163
Ramp3	0.410	0.540	0.413	1.2E-07	1.8E-04	Cenpx	1.309	0.959	0.664	6.9E-165	1.0E-161
Ccr2	0.445	0.449	0.261	4.5E-07	6.8E-04	Rexo2	1.263	0.965	0.631	8.8E-164	1.3E-160
Tmem160	0.367	0.600	0.584	5.6E-07	8.5E-04	Ndufa4	2.100	0.982	0.667	3.8E-158	5.8E-155
Dapl1	0.839	0.526	0.394	4.6E-06	6.9E-03	Pycard	1.529	0.989	0.776	2.6E-157	4.0E-154
Cblb	0.388	0.487	0.637	1.4E-04	2.1E-01	Smc4	1.764	0.924	0.614	5.8E-155	8.7E-152
Odc1	0.426	0.573	0.569	1.2E-03	1.0E+00	Fabp5	1.449	0.993	0.803	1.1E-154	1.7E-151
Tmem176b	0.675	0.581	0.569	5.8E-03	1.0E+00	Cks2	1.430	0.931	0.464	1.4E-152	2.2E-149
Mac 1						Nap111	1.688	0.954	0.558	1.7E-148	2.5E-145
ApoE	3.645	0.999	0.776	0.0E+00	0.0E+00	Hspa9	1.285	0.938	0.643	9.9E-148	1.5E-144
Ctss	3.156	1.000	0.646	0.0E+00	0.0E+00	Nme1	1.906	0.965	0.712	1.0E-146	1.5E-143
Fn1	3.070	0.961	0.389	0.0E+00	0.0E+00	Prdx2	1.788	0.940	0.640	2.6E-141	3.9E-138
Lyz2	2.912	1.000	0.750	0.0E+00	0.0E+00	Rpl3	1.645	0.952	0.712	2.0E-140	3.0E-137
Trem2	2.398	0.999	0.563	0.0E+00	0.0E+00	Rps2	1.458	0.940	0.894	2.3E-130	3.5E-127
Lgals1	2.386	1.000	0.559	0.0E+00	0.0E+00	Spp1	1.101	0.991	0.788	3.2E-128	4.8E-125
Spp1	2.356	0.996	0.780	0.0E+00	0.0E+00	Tubb4b	1.816	0.977	0.715	3.8E-128	5.6E-125
Ma1b	2.251	0.977	0.576	0.0E+00	0.0E+00	Cybb	1.037	0.947	0.519	8.9E-128	1.3E-124
C1qa	2.202	0.980	0.573	0.0E+00	0.0E+00	Vim	1.633	0.988	0.644	2.4E-125	3.5E-122
Fabp5	2.165	0.994	0.796	0.0E+00	0.0E+00	Mcm7	1.071	0.851	0.556	1.5E-124	2.2E-121
C1qb	2.126	0.982	0.493	0.0E+00	0.0E+00	Ybx3	1.869	0.865	0.599	1.9E-123	2.8E-120
Psap	2.095	1.000	0.747	0.0E+00	0.0E+00	Siva1	1.363	0.931	0.730	6.4E-120	9.6E-117
Ctsl	2.035	0.999	0.840	0.0E+00	0.0E+00	Pgls	1.338	0.950	0.632	5.3E-119	8.0E-116
C1qc	2.002	0.983	0.633	0.0E+00	0.0E+00	Ptms	1.038	0.988	0.620	2.7E-116	4.1E-113
Gpnmb	1.975	0.994	0.642	0.0E+00	0.0E+00	Fkbp2	1.125	0.931	0.533	4.2E-114	6.3E-111
Vim	1.894	0.998	0.631	0.0E+00	0.0E+00	Tyms	1.094	0.796	0.470	1.6E-111	2.5E-108
Ms4a6c	1.887	0.981	0.393	0.0E+00	0.0E+00	Lamtor4	1.288	0.982	0.702	9.9E-107	1.5E-103
Emp3	1.866	0.993	0.440	0.0E+00	0.0E+00	Hist1h4d	1.284	0.839	0.676	1.0E-105	1.5E-102
Plin2	1.859	1.000	0.843	0.0E+00	0.0E+00	Dbi	1.394	0.936	0.644	2.0E-103	3.0E-100
Cd68	1.847	0.999	0.699	0.0E+00	0.0E+00	Top2a	2.140	0.749	0.304	1.5E-100	2.3E-97
F13a1	1.817	0.892	0.611	0.0E+00	0.0E+00	mt-Nd1	1.535	0.881	0.672	2.2E-98	3.2E-95
Lgmn	1.795	0.994	0.615	0.0E+00	0.0E+00	Birc5	2.119	0.756	0.487	3.7E-96	5.6E-93
Gm	1.771	1.000	0.840	0.0E+00	0.0E+00	Hsp90b1	1.288	0.991	0.786	4.3E-96	6.5E-93
S100a4	1.755	0.940	0.486	0.0E+00	0.0E+00	Cdca3	1.395	0.733	0.222	6.4E-91	9.6E-88
Lrp1	1.691	0.995	0.503	0.0E+00	0.0E+00	Reep5	1.089	0.966	0.713	1.3E-90	2.0E-87
Ms4a7	1.620	0.981	0.421	0.0E+00	0.0E+00	Gm26917	1.427	0.839	0.566	1.8E-88	2.7E-85
mt-Nd1	1.606	0.996	0.658	0.0E+00	0.0E+00	Aprt	1.160	0.943	0.737	1.0E-83	1.6E-80
Hexa	1.594	0.999	0.688	0.0E+00	0.0E+00	Gzma	1.044	0.791	0.294	5.1E-75	7.7E-72
Npc2	1.576	1.000	0.885	0.0E+00	0.0E+00	C1qbp	1.452	0.809	0.661	1.8E-71	2.7E-68
Hexb	1.575	0.998	0.741	0.0E+00	0.0E+00	Ranbp1	1.666	0.798	0.645	3.8E-71	5.8E-68
Crip1	1.546	0.994	0.486	0.0E+00	0.0E+00	Cdc20	1.193	0.713	0.484	2.7E-70	4.1E-67
Lamp1	1.530	1.000	0.856	0.0E+00	0.0E+00	Tmed3	1.101	0.873	0.617	4.5E-69	6.7E-66
Saa3	1.523	0.868	0.613	0.0E+00	0.0E+00	Pdia6	1.130	0.973	0.783	2.8E-67	4.2E-64
Mgst1	1.502	0.992	0.589	0.0E+00	0.0E+00	Cenpf	1.498	0.697	0.197	9.5E-65	1.4E-61
Syng1	1.501	0.994	0.759	0.0E+00	0.0E+00	Calr	1.114	0.973	0.770	1.3E-59	1.9E-56
Ctsz	1.495	1.000	0.786	0.0E+00	0.0E+00	Ramp1	1.043	0.756	0.421	6.4E-56	9.5E-53
Ctsb	1.482	1.000	0.942	0.0E+00	0.0E+00	Atp5g1	1.539	0.749	0.648	3.7E-50	5.5E-47
Ccl9	1.476	0.919	0.528	0.0E+00	0.0E+00	Hspd1	1.695	0.731	0.563	1.7E-49	2.6E-46
C3ar1	1.475	0.992	0.552	0.0E+00	0.0E+00	Igkc	2.677	0.216	0.301	7.5E-49	1.1E-45
Pycard	1.449	0.984	0.769	0.0E+00	0.0E+00	Igha	1.754	0.694	0.385	6.0E-45	9.0E-42
Ctsd	1.430	1.000	0.964	0.0E+00	0.0E+00	Hspe1	1.292	0.779	0.675	1.7E-44	2.6E-41
Smpd13a	1.420	0.995	0.611	0.0E+00	0.0E+00	Dtymk	1.346	0.694	0.574	2.7E-43	4.1E-40
Anxa5	1.419	0.999	0.669	0.0E+00	0.0E+00						

Cybb	1.397	0.993	0.501	0.0E+00	0.0E+00	Camp	4.266	0.267	0.373	3.4E-41	5.1E-38
Ctsa	1.395	0.999	0.689	0.0E+00	0.0E+00	Hist1h2ap	1.712	0.662	0.481	8.0E-37	1.2E-33
Fcgr2b	1.362	0.991	0.641	0.0E+00	0.0E+00	Erp29	1.042	0.758	0.715	5.1E-28	7.7E-25
Ms4a6d	1.355	0.957	0.726	0.0E+00	0.0E+00	Ube2c	1.866	0.621	0.424	1.2E-24	1.7E-21
Ctsc	1.326	0.970	0.634	0.0E+00	0.0E+00	Serpnb1a	1.100	0.363	0.542	1.4E-23	2.2E-20
Rpl3	1.324	0.999	0.701	0.0E+00	0.0E+00	Ngp	3.416	0.294	0.366	1.9E-22	2.8E-19
Tmem256	1.321	0.978	0.530	0.0E+00	0.0E+00	H2afx	1.423	0.598	0.441	1.4E-15	2.1E-12
Erp29	1.320	0.994	0.701	0.0E+00	0.0E+00	Prc1	1.160	0.595	0.429	2.0E-15	2.9E-12
Lrpap1	1.315	0.993	0.571	0.0E+00	0.0E+00	Hist1h2ae	1.473	0.600	0.599	3.2E-09	4.8E-06
Gpx1	1.307	1.000	0.828	0.0E+00	0.0E+00	Hist1h1b	2.008	0.556	0.500	1.6E-06	2.4E-03
Prdx1	1.306	0.998	0.653	0.0E+00	0.0E+00	Car2	1.424	0.451	0.501	5.3E-05	7.9E-02
Selenop	1.301	0.939	0.505	0.0E+00	0.0E+00	Smc2	1.419	0.545	0.391	1.3E-04	2.0E-01
Ccl6	1.287	0.993	0.618	0.0E+00	0.0E+00	Jchain	1.375	0.566	0.380	9.6E-04	1.0E+00
Itgb5	1.270	0.995	0.664	0.0E+00	0.0E+00	Neu-5					
Snx5	1.244	0.989	0.529	0.0E+00	0.0E+00	IFN					
Gusb	1.240	0.981	0.609	0.0E+00	0.0E+00	Rsad2	3.882	0.893	0.683	2.2E-159	3.2E-156
Aprt	1.235	0.992	0.727	0.0E+00	0.0E+00	lsg15	2.862	0.914	0.683	9.1E-136	1.4E-132
Dbi	1.213	0.986	0.631	0.0E+00	0.0E+00	lfitm3	2.426	0.937	0.699	9.8E-131	1.5E-127
Rps2	1.206	0.998	0.889	0.0E+00	0.0E+00	Gbp2	3.508	0.883	0.647	3.1E-123	4.6E-120
Cst3	1.200	0.999	0.812	0.0E+00	0.0E+00	Slfn4	3.032	0.848	0.564	3.0E-118	4.5E-115
Atp5g1	1.188	0.996	0.631	0.0E+00	0.0E+00	lfi47	2.533	0.858	0.647	4.5E-108	6.7E-105
Plekho1	1.164	0.955	0.538	0.0E+00	0.0E+00	lfit2	1.494	0.827	0.689	1.6E-98	2.5E-95
Myof	1.160	0.994	0.484	0.0E+00	0.0E+00	Rtp4	2.650	0.820	0.679	1.4E-96	2.1E-93
Abca1	1.158	0.989	0.723	0.0E+00	0.0E+00	lfit1bl2	1.106	0.794	0.562	1.8E-92	2.6E-89
Mpeg1	1.121	0.999	0.603	0.0E+00	0.0E+00	Slfn5	2.500	0.787	0.570	5.6E-89	8.5E-86
Creg1	1.120	0.999	0.654	0.0E+00	0.0E+00	lfit3b	2.020	0.698	0.421	5.4E-66	8.2E-63
Irf8	1.119	0.934	0.623	0.0E+00	0.0E+00	Ccl4	1.652	0.921	0.717	1.5E-61	2.2E-58
Cd93	1.117	0.916	0.618	0.0E+00	0.0E+00	Acod1	1.515	0.764	0.419	5.1E-59	7.7E-56
Lamtor4	1.117	0.985	0.692	0.0E+00	0.0E+00	lfit1	2.933	0.693	0.445	1.8E-55	2.7E-52
Pdia6	1.103	0.993	0.775	0.0E+00	0.0E+00	lsg20	2.176	0.731	0.572	2.0E-51	3.0E-48
Fam20c	1.100	0.997	0.755	0.0E+00	0.0E+00	Cldn1	0.347	0.777	0.616	3.0E-47	4.4E-44
Hebp1	1.091	0.971	0.633	0.0E+00	0.0E+00	Fcgr4	1.090	0.812	0.694	1.6E-45	2.3E-42
Hspe1	1.089	0.996	0.660	0.0E+00	0.0E+00	Zbp1	1.271	0.789	0.633	5.8E-45	8.7E-42
Fam96a	1.086	0.958	0.547	0.0E+00	0.0E+00	Cmpk2	1.335	0.647	0.457	6.9E-42	1.0E-38
Tubb5	1.084	0.991	0.582	0.0E+00	0.0E+00	Wfdc17	0.879	0.916	0.778	1.7E-38	2.6E-35
Sash1	1.076	0.988	0.700	0.0E+00	0.0E+00	Oas1	2.003	0.668	0.582	1.0E-34	1.5E-31
Msr1	1.069	0.965	0.286	0.0E+00	0.0E+00	Hcar2	0.498	0.830	0.679	1.6E-30	2.4E-27
Nme1	1.065	0.992	0.702	0.0E+00	0.0E+00	Gbp5	1.549	0.660	0.546	6.0E-30	9.0E-27
Fkbp2	1.048	0.993	0.516	0.0E+00	0.0E+00	lfit3	2.987	0.612	0.399	9.5E-30	1.4E-26
Tmem160	1.046	0.970	0.564	0.0E+00	0.0E+00	Gm4316	0.371	0.279	0.493	1.4E-29	2.1E-26
Gyg	1.041	0.960	0.639	0.0E+00	0.0E+00	Gm12840	0.275	0.201	0.399	4.9E-28	7.3E-25
Gatm	1.037	0.904	0.510	0.0E+00	0.0E+00	Retnlg	0.406	0.835	0.628	9.9E-28	1.5E-24
Anxa4	1.008	0.987	0.484	0.0E+00	0.0E+00	G0s2	1.012	0.711	0.497	7.3E-27	1.1E-23
Pgls	1.005	0.988	0.619	0.0E+00	0.0E+00	Fyb	0.799	0.835	0.695	1.1E-26	1.6E-23
Pid1	1.002	0.863	0.576	0.0E+00	0.0E+00	Ffar2	0.272	0.701	0.484	2.4E-26	3.6E-23
Ppp1r14b	1.000	0.991	0.648	0.0E+00	0.0E+00	Cd274	1.280	0.736	0.593	5.4E-26	8.2E-23
Ucp2	0.994	0.999	0.719	0.0E+00	0.0E+00	Bst2	1.457	0.657	0.508	1.2E-23	1.7E-20
Aldh2	0.986	0.970	0.496	0.0E+00	0.0E+00	Egr1	0.572	0.756	0.554	1.1E-22	1.7E-19
Tuba1b	0.983	0.991	0.583	0.0E+00	0.0E+00	Ccl3	0.827	0.799	0.641	1.1E-22	1.7E-19
Timp2	0.980	0.994	0.767	0.0E+00	0.0E+00	Cxcl2	1.001	0.741	0.536	4.1E-22	6.2E-19
Tmed3	0.973	0.994	0.602	0.0E+00	0.0E+00	Cxcl10	1.921	0.551	0.311	1.4E-21	2.2E-18
Zeb2	0.969	0.991	0.611	0.0E+00	0.0E+00	ler3	0.726	0.820	0.788	1.7E-21	2.5E-18
Sgk1	0.967	0.986	0.632	0.0E+00	0.0E+00	Gm20234	0.309	0.609	0.491	1.1E-18	1.6E-15
Lat2	0.960	0.968	0.664	0.0E+00	0.0E+00	Ly6i	0.652	0.586	0.455	1.5E-18	2.2E-15
Hai	0.960	0.984	0.673	0.0E+00	0.0E+00	Usp18	1.392	0.604	0.553	2.2E-18	3.4E-15
Ccr2	0.957	0.715	0.248	2.0E-241	3.0E-238	Clec4a3	0.263	0.614	0.448	7.7E-17	1.1E-13
Ccl2	1.048	0.587	0.454	4.3E-39	6.5E-36	Slpi	0.712	0.797	0.643	1.8E-16	2.6E-13
Macs 2						Gm5483	0.695	0.728	0.616	2.9E-16	4.3E-13
Chil3	4.719	0.975	0.671	0.0E+00	0.0E+00	Olfm4	0.430	0.635	0.476	1.4E-15	2.1E-12
GpnmB	3.826	1.000	0.645	0.0E+00	0.0E+00	Saa3	0.296	0.764	0.624	1.7E-15	2.6E-12
Lpl	3.697	0.989	0.496	0.0E+00	0.0E+00	Asprv1	0.545	0.734	0.588	2.1E-15	3.1E-12
Ctsk	3.692	0.959	0.550	0.0E+00	0.0E+00	Gm19951	0.676	0.769	0.685	5.5E-15	8.3E-12
Mmp12	3.321	0.870	0.537	0.0E+00	0.0E+00	lfi202b	0.285	0.739	0.658	5.6E-15	8.4E-12
Lyz2	3.173	1.000	0.752	0.0E+00	0.0E+00	lfitm1	0.593	0.807	0.738	8.3E-15	1.2E-11
Psap	3.172	1.000	0.749	0.0E+00	0.0E+00	Osgin1	0.663	0.678	0.588	7.4E-14	1.1E-10
Cybb	2.910	1.000	0.504	0.0E+00	0.0E+00	Fgd4	0.355	0.713	0.634	7.6E-14	1.1E-10
Crip1	2.846	0.996	0.490	0.0E+00	0.0E+00	Lcn2	0.607	0.683	0.610	1.0E-11	1.5E-08
Atp6v0d2	2.784	0.999	0.677	0.0E+00	0.0E+00	Cst3	0.478	0.858	0.821	2.9E-11	4.3E-08
Spp1	2.744	0.996	0.782	0.0E+00	0.0E+00	Fam20c	0.267	0.858	0.766	2.1E-10	3.2E-07
Mfge8	2.720	0.895	0.672	0.0E+00	0.0E+00	Bcl2a1a	0.523	0.398	0.556	5.1E-10	7.6E-07
Ctss	2.600	0.999	0.649	0.0E+00	0.0E+00	ld2	0.498	0.881	0.780	1.8E-09	2.6E-06
Fabp5	2.562	0.999	0.797	0.0E+00	0.0E+00	Wfdc21	0.437	0.713	0.653	1.8E-09	2.6E-06
Ctsl	2.553	0.996	0.841	0.0E+00	0.0E+00	lfi19	0.718	0.632	0.560	2.7E-09	4.0E-06
Ctsd	2.452	1.000	0.964	0.0E+00	0.0E+00	Laptm5	0.349	0.812	0.739	3.7E-08	5.6E-05
						ld1	0.788	0.688	0.693	5.4E-08	8.1E-05

Fabp4	2.405	0.976	0.611	0.0E+00	0.0E+00	Csf2rb	0.657	0.721	0.686	8.4E-08	1.3E-04
Lipa	2.389	0.997	0.513	0.0E+00	0.0E+00	Bcl2a1b	0.643	0.751	0.631	3.8E-07	5.7E-04
Mgll	2.382	0.973	0.587	0.0E+00	0.0E+00	Ddx60	1.401	0.528	0.488	5.3E-07	8.0E-04
Trem2	2.379	0.995	0.566	0.0E+00	0.0E+00	Mpeg1	0.362	0.726	0.622	1.2E-06	1.7E-03
Mpeg1	2.367	0.999	0.606	0.0E+00	0.0E+00	Tnfrsf23	0.333	0.741	0.702	5.0E-06	7.5E-03
Vim	2.330	0.999	0.634	0.0E+00	0.0E+00	Osm	0.260	0.475	0.334	5.3E-06	8.0E-03
Sgk1	2.323	0.999	0.634	0.0E+00	0.0E+00	Ifi2712a	2.007	0.553	0.533	5.5E-06	8.2E-03
mt-Nd1	2.303	0.998	0.660	0.0E+00	0.0E+00	Cdc42ep3	0.290	0.622	0.527	7.5E-06	1.1E-02
S100a1	2.291	0.994	0.634	0.0E+00	0.0E+00	Il18bp	0.429	0.508	0.450	1.3E-05	2.0E-02
Ccl6	2.274	0.994	0.621	0.0E+00	0.0E+00	Irf7	0.399	0.642	0.654	2.9E-05	4.4E-02
Abcg1	2.256	0.997	0.645	0.0E+00	0.0E+00	Lrg1	0.382	0.668	0.699	2.1E-04	3.1E-01
Mrc1	2.227	0.894	0.408	0.0E+00	0.0E+00	Cd300c2	0.587	0.657	0.660	2.3E-04	3.4E-01
Myof	2.219	0.995	0.488	0.0E+00	0.0E+00	Hk2	0.508	0.497	0.587	2.8E-04	4.2E-01
Selenop	2.137	0.991	0.506	0.0E+00	0.0E+00	Steap4	0.298	0.586	0.487	3.4E-04	5.1E-01
Pld3	2.132	0.995	0.574	0.0E+00	0.0E+00	Ifi209	0.898	0.563	0.599	4.8E-04	7.3E-01
Plin2	2.121	0.999	0.844	0.0E+00	0.0E+00	Ly6c2	1.077	0.482	0.398	5.2E-04	7.8E-01
Apoe	2.006	0.979	0.778	0.0E+00	0.0E+00	Chil1	0.308	0.429	0.495	7.0E-04	1.0E+00
Anxa5	1.983	0.999	0.671	0.0E+00	0.0E+00	Il18	0.297	0.556	0.516	8.5E-04	1.0E+00
Cd68	1.963	0.998	0.702	0.0E+00	0.0E+00	Ly6g	0.309	0.497	0.449	1.5E-03	1.0E+00
Aig1	1.926	0.981	0.665	0.0E+00	0.0E+00	Rgs1	0.948	0.627	0.632	1.9E-03	1.0E+00
Mgst1	1.906	0.996	0.592	0.0E+00	0.0E+00	Unc93b1	0.563	0.569	0.521	2.0E-03	1.0E+00
Slc7a2	1.859	0.953	0.593	0.0E+00	0.0E+00	Hist1h1c	0.327	0.497	0.617	2.6E-03	1.0E+00
Ear2	1.849	0.881	0.305	0.0E+00	0.0E+00	Ifitm6	0.346	0.391	0.472	4.6E-03	1.0E+00
Sh3bgrl	1.816	0.991	0.540	0.0E+00	0.0E+00	Eryth. Hbb-bs	9.669	1.000	0.782	0.0E+00	0.0E+00
Lrp1	1.810	0.995	0.507	0.0E+00	0.0E+00	Hba-a1	8.916	1.000	0.499	0.0E+00	0.0E+00
Hexa	1.807	0.999	0.690	0.0E+00	0.0E+00	Hbb-bt	8.788	0.996	0.481	0.0E+00	0.0E+00
Gns	1.748	1.000	0.684	0.0E+00	0.0E+00	Hba-a2	8.609	1.000	0.450	0.0E+00	0.0E+00
Abhd12	1.739	0.990	0.418	0.0E+00	0.0E+00	Bpgm	4.001	0.837	0.481	0.0E+00	0.0E+00
Ahnak2	1.738	0.981	0.542	0.0E+00	0.0E+00	Alas2	3.365	0.939	0.531	0.0E+00	0.0E+00
Creg1	1.723	0.999	0.657	0.0E+00	0.0E+00	Snca	2.876	0.949	0.366	0.0E+00	0.0E+00
Prdx1	1.712	0.996	0.656	0.0E+00	0.0E+00	Fech	2.293	0.957	0.604	0.0E+00	0.0E+00
Lgals1	1.693	0.991	0.563	0.0E+00	0.0E+00	Fam46c	1.861	0.916	0.610	0.0E+00	0.0E+00
Lgmn	1.687	0.991	0.618	0.0E+00	0.0E+00	Rsad2	1.161	0.865	0.679	0.0E+00	0.0E+00
Gstm1	1.679	0.977	0.546	0.0E+00	0.0E+00	Gypa	0.702	0.791	0.028	0.0E+00	0.0E+00
Trf	1.674	0.974	0.490	0.0E+00	0.0E+00	Slc4a1	0.430	0.640	0.027	0.0E+00	0.0E+00
Gm26917	1.673	0.905	0.556	0.0E+00	0.0E+00	Prdx2	1.533	0.891	0.636	2.0E-288	3.0E-285
Gusb	1.658	0.988	0.611	0.0E+00	0.0E+00	Fam213a	0.874	0.916	0.568	2.3E-282	3.5E-279
Lamp1	1.650	0.999	0.858	0.0E+00	0.0E+00	Isg20	1.050	0.910	0.561	2.0E-245	2.9E-242
Acp5	1.634	0.995	0.601	0.0E+00	0.0E+00	Ncoa4	0.766	0.907	0.558	3.4E-228	5.0E-225
Vat1	1.632	0.981	0.642	0.0E+00	0.0E+00	Aldh1a1	0.377	0.748	0.376	5.6E-212	8.4E-209
F7	1.632	0.925	0.406	0.0E+00	0.0E+00	Car2	0.406	0.781	0.489	6.8E-212	1.0E-208
Axl	1.612	0.892	0.422	0.0E+00	0.0E+00	Ube2c	0.553	0.642	0.419	4.5E-87	6.8E-84
Ctsb	1.608	1.000	0.943	0.0E+00	0.0E+00	Gpx1	0.918	0.898	0.834	2.7E-17	4.0E-14
Ctsz	1.605	1.000	0.787	0.0E+00	0.0E+00	Macs 3 Lyz2	3.103	0.994	0.755	0.0E+00	0.0E+00
Snx5	1.602	0.992	0.532	0.0E+00	0.0E+00	Atp6v0d2	2.835	0.929	0.683	0.0E+00	0.0E+00
Ctsa	1.599	0.999	0.692	0.0E+00	0.0E+00	Fabp5	2.818	0.976	0.801	0.0E+00	0.0E+00
Dusp3	1.564	0.986	0.628	0.0E+00	0.0E+00	Fabp4	2.446	0.907	0.618	0.0E+00	0.0E+00
Cd36	1.561	0.877	0.480	0.0E+00	0.0E+00	Trem2	2.287	0.948	0.573	0.0E+00	0.0E+00
Myo5a	1.560	0.983	0.491	0.0E+00	0.0E+00	Mmp12	2.260	0.889	0.540	0.0E+00	0.0E+00
Aplp2	1.550	0.995	0.630	0.0E+00	0.0E+00	Vim	2.236	0.943	0.640	0.0E+00	0.0E+00
Il11ra1	1.532	0.958	0.470	0.0E+00	0.0E+00	Gpnmb	2.203	0.955	0.651	0.0E+00	0.0E+00
Kcnq1ot1	1.510	0.945	0.642	0.0E+00	0.0E+00	Ftl1	1.976	1.000	0.956	0.0E+00	0.0E+00
Sirpa	1.506	0.996	0.609	0.0E+00	0.0E+00	C1qa	1.299	0.907	0.583	0.0E+00	0.0E+00
Ilgax	1.499	0.986	0.527	0.0E+00	0.0E+00	Il11ra1	1.068	0.868	0.479	1.4E-302	2.1E-299
Anxa4	1.494	0.988	0.487	0.0E+00	0.0E+00	Lgals1	2.459	0.899	0.571	2.8E-293	4.2E-290
Fstl1	1.486	0.862	0.466	0.0E+00	0.0E+00	C1qb	1.319	0.890	0.505	4.2E-288	6.2E-285
Dnmt3a	1.473	0.946	0.462	0.0E+00	0.0E+00	Lpl	2.532	0.875	0.506	1.6E-278	2.4E-275
Cdo1	1.466	0.918	0.461	0.0E+00	0.0E+00	Cdkn2a	0.952	0.852	0.657	1.9E-278	2.9E-275
Shtn1	1.463	0.978	0.464	0.0E+00	0.0E+00	Pld3	1.832	0.903	0.582	6.5E-275	9.7E-272
Laptn5	1.462	0.999	0.728	0.0E+00	0.0E+00	Crip1	2.187	0.866	0.500	1.9E-269	2.8E-266
Grn	1.460	0.996	0.841	0.0E+00	0.0E+00	Serpnb6a	2.298	0.917	0.672	1.5E-268	2.3E-265
Mertk	1.458	0.955	0.387	0.0E+00	0.0E+00	Spp1	2.531	0.948	0.786	4.3E-264	6.4E-261
Slc6a6	1.456	0.997	0.490	0.0E+00	0.0E+00	Prdx1	2.470	0.877	0.664	4.4E-258	6.7E-255
Smpd3a	1.454	0.996	0.614	0.0E+00	0.0E+00	Sdc3	1.041	0.862	0.567	9.7E-254	1.5E-250
Il18	1.438	0.916	0.498	0.0E+00	0.0E+00	S100a1	2.732	0.862	0.643	1.9E-248	2.8E-245
Abcc5	1.434	0.946	0.408	0.0E+00	0.0E+00	Myof	1.428	0.860	0.499	6.7E-247	1.0E-243
Colgalt1	1.434	0.980	0.501	0.0E+00	0.0E+00	Ctsk	2.393	0.836	0.559	2.3E-238	3.5E-235

	Ucp2	1.423	0.999	0.721	0.0E+00	0.0E+00		Mt2	1.490	0.817	0.645	2.6E-238	3.8E-235
	Serpinb6a	1.419	0.997	0.665	0.0E+00	0.0E+00		Ccl6	2.295	0.913	0.628	1.9E-236	2.9E-233
	Itgb2	1.419	0.996	0.577	0.0E+00	0.0E+00		Cd63	2.069	0.968	0.778	4.8E-228	7.2E-225
	Cd63	1.419	0.999	0.774	0.0E+00	0.0E+00		Apoe	1.530	0.947	0.782	7.2E-227	1.1E-223
	Dbi	1.415	0.987	0.634	0.0E+00	0.0E+00		Chil3	2.328	0.881	0.677	1.7E-224	2.5E-221
	Tgfb2	1.413	0.988	0.488	0.0E+00	0.0E+00		C1qc	1.093	0.861	0.644	9.6E-215	1.4E-211
	Sdc3	1.412	0.957	0.559	0.0E+00	0.0E+00		Lgmn	1.340	0.917	0.625	6.9E-209	1.0E-205
	Npc2	1.410	1.000	0.886	0.0E+00	0.0E+00		Plin2	1.944	0.957	0.847	9.8E-201	1.5E-197
	Dhrs3	1.394	0.995	0.661	0.0E+00	0.0E+00		Mfge8	2.225	0.887	0.675	2.6E-200	3.9E-197
	Serpine1	1.356	0.860	0.281	0.0E+00	0.0E+00		Gngt2	2.023	0.880	0.639	1.5E-198	2.2E-195
	Syng1	1.354	0.971	0.762	0.0E+00	0.0E+00		Cd36	1.210	0.816	0.487	1.8E-196	2.6E-193
	Atp13a2	1.353	0.978	0.468	0.0E+00	0.0E+00		Bhlhe41	1.075	0.805	0.561	8.0E-189	1.2E-185
	Tcf7l2	1.342	0.915	0.455	0.0E+00	0.0E+00		Syng1	1.161	0.875	0.768	9.8E-184	1.5E-180
	Sort1	1.301	0.946	0.559	0.0E+00	0.0E+00		Mt1	2.231	0.865	0.772	4.2E-183	6.3E-180
	Lrpap1	1.294	0.948	0.577	0.0E+00	0.0E+00		Psap	1.901	0.939	0.754	5.8E-181	8.4E-178
	Bhlhe41	1.284	0.943	0.552	0.0E+00	0.0E+00		Comt	1.663	0.818	0.624	8.2E-180	1.2E-176
	AU020206	1.254	0.941	0.692	0.0E+00	0.0E+00		Ucp2	1.750	0.878	0.729	1.1E-168	1.6E-165
Neu-4 classic	Retnlg	4.320	0.993	0.616	0.0E+00	0.0E+00		Ctsz	1.495	0.959	0.791	1.0E-166	1.5E-163
	lfitm6	3.584	0.992	0.450	0.0E+00	0.0E+00		Vat1	1.214	0.850	0.651	4.9E-166	7.4E-163
	Lcn2	3.566	0.999	0.596	0.0E+00	0.0E+00		Ctss	1.571	0.856	0.658	2.9E-164	4.3E-161
	Wfdc21	3.439	0.999	0.640	0.0E+00	0.0E+00		Rps2	1.322	0.923	0.894	6.8E-152	1.0E-148
	Mmp8	2.882	0.971	0.602	0.0E+00	0.0E+00		Mgll	1.555	0.775	0.599	2.6E-149	3.9E-146
	Wfdc17	2.808	0.997	0.771	0.0E+00	0.0E+00		Lipa	1.354	0.858	0.524	4.6E-147	6.9E-144
	lfitm1	2.636	0.992	0.728	0.0E+00	0.0E+00		Nme1	1.536	0.864	0.712	2.6E-139	3.8E-136
	Lrg1	2.580	0.992	0.687	0.0E+00	0.0E+00		Npc2	1.668	0.952	0.889	1.9E-138	2.9E-135
	Prok2	2.540	0.960	0.568	0.0E+00	0.0E+00		Cd68	1.715	0.860	0.710	4.7E-137	7.0E-134
	Ly6g	2.372	0.944	0.430	0.0E+00	0.0E+00		Ndufc2	1.120	0.806	0.620	1.0E-130	1.6E-127
	Slpi	1.882	0.978	0.632	0.0E+00	0.0E+00		Ctsd	1.460	0.982	0.965	5.3E-126	8.0E-123
	lfitm3	1.752	0.989	0.691	0.0E+00	0.0E+00		Chchd10	0.992	0.770	0.640	1.8E-116	2.7E-113
	Stfa2	1.639	0.909	0.508	0.0E+00	0.0E+00		Acp5	1.333	0.859	0.610	1.3E-111	2.0E-108
	Cd177	1.499	0.907	0.482	0.0E+00	0.0E+00		Blvra	1.204	0.765	0.688	3.1E-107	4.6E-104
	Chil1	1.440	0.942	0.477	0.0E+00	0.0E+00		Ckb	1.006	0.730	0.512	4.7E-105	7.1E-102
	Anxa1	1.274	0.997	0.792	0.0E+00	0.0E+00		Lrpap1	1.029	0.784	0.587	1.6E-100	2.4E-97
	Steap4	1.122	0.940	0.470	0.0E+00	0.0E+00		Marco	1.092	0.638	0.382	1.4E-99	2.1E-96
	Ggt1	1.101	0.897	0.480	0.0E+00	0.0E+00		Hebp1	1.673	0.752	0.647	4.2E-98	6.3E-95
	Il1f9	0.835	0.940	0.545	3.3E-294	4.9E-291		Mrc1	1.060	0.678	0.421	4.6E-96	6.8E-93
	Silfn4	0.805	0.912	0.554	3.6E-286	5.4E-283		Creg1	1.335	0.866	0.665	2.1E-95	3.1E-92
	Tgm1	0.511	0.865	0.592	3.6E-260	5.4E-257		Mpeg1	1.104	0.872	0.615	1.0E-91	1.5E-88
	Ngp	1.375	0.786	0.348	1.6E-249	2.3E-246		Rpl3	1.021	0.848	0.712	2.1E-91	3.2E-88
	Gm5483	1.224	0.916	0.606	2.1E-249	3.2E-246		Ear2	1.521	0.627	0.320	7.5E-87	1.1E-83
	Gbp2	0.381	0.899	0.640	3.9E-247	5.9E-244		Gpx1	1.184	0.891	0.835	1.3E-82	2.0E-79
	BC100530	2.269	0.877	0.550	4.7E-247	7.0E-244		Ctsl	1.931	0.937	0.845	3.9E-82	5.8E-79
	Tgfb1	0.991	0.922	0.598	1.6E-246	2.5E-243		Anxa4	1.516	0.722	0.503	2.2E-78	3.2E-75
	Flna	0.907	0.875	0.483	5.7E-215	8.5E-212		Gyg	1.106	0.792	0.651	6.1E-76	9.1E-73
	Csf2rb	0.767	0.972	0.676	1.4E-214	2.1E-211		Akr1b3	1.361	0.704	0.519	2.5E-74	3.7E-71
	Hacd4	1.020	0.822	0.508	3.9E-214	5.8E-211		Abcg1	1.286	0.825	0.655	1.8E-73	2.7E-70
	Ccl6	0.890	0.959	0.624	1.5E-213	2.3E-210		Cybb	1.621	0.701	0.520	1.8E-71	2.7E-68
	Gyg	0.741	0.863	0.647	1.3E-200	2.0E-197		Anxa5	1.578	0.758	0.684	1.8E-70	2.7E-67
	Stfa2l1	1.303	0.835	0.467	2.0E-193	2.9E-190		Il18	1.245	0.662	0.512	9.3E-69	1.4E-65
	Pi16	0.851	0.785	0.460	4.3E-188	6.4E-185		Fit1-ps1	0.990	0.663	0.422	6.5E-67	9.7E-64
	Tceal9	0.260	0.937	0.666	1.7E-185	2.6E-182		Lamtor4	1.225	0.821	0.703	5.3E-66	7.9E-63
	Id1	0.309	0.894	0.685	8.3E-174	1.2E-170		Mgst1	1.663	0.691	0.607	2.6E-64	4.0E-61
	Syne1	0.622	0.810	0.599	1.2E-162	1.8E-159		Hexa	1.098	0.839	0.699	4.3E-62	6.4E-59
	F630028O10Ri	0.753	0.828	0.534	8.0E-158	1.2E-154		Sh3bgrl	1.604	0.671	0.556	1.4E-58	2.1E-55
	Mgst1	0.476	0.870	0.599	2.7E-148	4.1E-145		Cndp2	1.101	0.673	0.547	2.4E-57	3.5E-54
	Gadd45a	0.597	0.832	0.616	9.7E-141	1.5E-137		Lmna	1.256	0.730	0.630	2.9E-50	4.4E-47
	Tuba1a	0.562	0.780	0.518	2.4E-137	3.7E-134		Gstm1	1.617	0.640	0.563	2.5E-49	3.7E-46
Napsa	0.305	0.855	0.579	6.0E-121	9.0E-118		Ptms	1.387	0.727	0.623	3.7E-49	5.5E-46	
Adam8	0.628	0.807	0.586	3.7E-118	5.5E-115		Sept9	1.139	0.627	0.473	6.6E-45	9.8E-42	
Ly6c2	0.635	0.708	0.387	1.9E-116	2.9E-113		Lamp1	0.986	0.887	0.863	7.9E-42	1.2E-38	
Arhgap25	0.285	0.808	0.494	8.0E-109	1.2E-105		Nenf	0.948	0.658	0.522	8.2E-42	1.2E-38	
Fgd4	0.382	0.790	0.629	7.6E-99	1.1E-95		Selenop	1.239	0.639	0.523	4.1E-40	6.2E-37	
Lmo4	0.595	0.715	0.404	6.3E-96	9.5E-93		Ctsb	1.179	0.945	0.945	9.1E-39	1.4E-35	
Smpd3a	0.448	0.826	0.623	7.2E-91	1.1E-87		Dbi	1.285	0.650	0.649	5.4E-32	8.1E-29	
Itgb2	0.339	0.867	0.585	4.4E-86	6.6E-83		Ccl9	1.120	0.623	0.545	1.0E-31	1.5E-28	
Acv11	0.628	0.673	0.488	1.1E-76	1.7E-73		Ctsa	0.950	0.810	0.702	4.3E-31	6.5E-28	
Saa3	0.352	0.854	0.617	1.3E-74	2.0E-71		Camk1	1.023	0.632	0.532	6.6E-31	9.9E-28	
Sirpa	0.296	0.858	0.617	5.0E-72	7.5E-69		Hspe1	1.301	0.691	0.676	9.4E-31	1.4E-27	
Olfm4	1.468	0.683	0.470	6.3E-67	9.5E-64		Smpd3a	0.946	0.721	0.628	2.8E-25	4.3E-22	
Asprv1	0.875	0.706	0.585	2.1E-58	3.2E-55		Pgls	1.000	0.682	0.636	5.1E-23	7.6E-20	

Olfm4	1.468	0.683	0.470	6.3E-67	9.5E-64	Smpd3a	0.946	0.721	0.628	2.8E-25	4.3E-22
Asprv1	0.875	0.706	0.585	2.1E-58	3.2E-55	Pgls	1.000	0.682	0.636	5.1E-23	7.6E-20
Camp	0.968	0.597	0.362	2.9E-50	4.4E-47	Atp5g1	1.239	0.649	0.649	5.3E-21	8.0E-18
Serpinb1a	0.640	0.616	0.536	9.8E-38	1.5E-34	Trf	0.948	0.589	0.509	6.0E-18	9.0E-15
Cfp	0.367	0.625	0.445	1.9E-37	2.9E-34	Fam96a	0.940	0.409	0.573	6.5E-15	9.8E-12
Sitfa3	0.514	0.382	0.548	5.2E-34	7.8E-31	Ppp1r14b	1.198	0.602	0.668	1.6E-10	2.4E-07
Abcd2	0.264	0.621	0.524	2.9E-28	4.3E-25	Rexo2	1.352	0.558	0.640	1.2E-09	1.8E-06
Dgat2	0.299	0.683	0.628	9.4E-26	1.4E-22	Aig1	1.010	0.561	0.683	5.7E-03	1.0E+00
Rab27a	0.295	0.545	0.430	4.6E-11	6.8E-08						
Osm	0.446	0.514	0.328	4.6E-06	7.0E-03						

Supplemental Table 4: GSEA on scRNAseq Populations, related to Figure 6
NES=Normalized Enrichment Score, FDR=False Discovery Rate

Group	MSigDB Signature Name	Combo vs aPD1								
		Macs/Dend			Neus			Tumor		
		NES	FDR q	-Log(q)	NES	FDR q	-Log(q)	NES	FDR q	-Log(q)
DNA Replication and Damage	REACTOME_G1_S_DNA_DAMAGE_CHECKPOINTS.v2022.1.Hs.grp	1.64	0.02	1.65	1.30	0.18	0.74	1.46	0.03	1.57
	REACTOME_ORC1_REMOVAL_FROM_CHROMATIN.v2022.1.Hs.grp	1.51	0.04	1.36	1.64	0.04	1.39	1.49	0.02	1.68
	REACTOME_SWITCHING_OF_ORIGINS_TO_A_POST_REPLICATIVE_STATE.v2022.1.Hs.grp	1.42	0.07	1.15	1.59	0.05	1.33	1.43	0.03	1.46
	REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_ORIGIN_COMPLEX.v2022.1.Hs.grp	1.55	0.03	1.46	1.69	0.04	1.40	1.41	0.04	1.36
	REACTOME_SYNTHESIS_OF_DNA.v2022.1.Hs.grp	1.37	0.10	1.01	1.63	0.04	1.39	1.37	0.06	1.23
	REACTOME_APC_C_MEDIATED_DEGRADATION_OF_CELL_CYCLE_PROTEINS.v2022.1.Hs.grp	1.45	0.06	1.24	1.52	0.07	1.18	1.40	0.05	1.34
Protein and RNA Processing	KEGG_RIBOSOME.v2022.1.Hs.grp	2.56	0.00	4.00	1.61	0.04	1.37	-2.28	0.00	4.00
	REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION.v2022.1.Hs.grp	2.56	0.00	4.00	1.52	0.07	1.17	-2.42	0.00	4.00
	Hs.grp	2.54	0.00	4.00	1.64	0.04	1.39	-2.02	0.00	2.85
	REACTOME_RESPONSE_OF_EIF2AK4_GCN2_TO_AMINO_ACID_DEFICIENCY.v2022.1.Hs.grp	2.41	0.00	4.00	1.36	0.14	0.84	-2.12	0.00	3.34
	REACTOME_EUKARYOTIC_TRANSLATION_INITIATION.v2022.1.Hs.grp	2.40	0.00	4.00	1.25	0.22	0.65	-2.11	0.00	3.37
	REACTOME_INFLUENZA_INFECTION.v2022.1.Hs.grp	2.40	0.00	4.00	1.27	0.21	0.67	-2.19	0.00	3.84
	GOBP_CYTOPLASMIC_TRANSLATION.v2022.1.Hs.grp	2.24	0.00	4.00	1.04	0.45	0.34	-1.94	0.00	2.60
	REACTOME_TRANSLATION.v2022.1.Hs.grp	2.01	0.00	3.05	1.23	0.24	0.61	-1.62	0.02	1.69
	REACTOME_SELENOAMINO_ACID_METABOLISM.v2022.1.Hs.grp	2.38	0.00	4.00	1.51	0.07	1.17	-2.38	0.00	4.00
	REACTOME_CELLULAR_RESPONSE_TO_STARVATION.v2022.1.Hs.grp	2.30	0.00	4.00	1.04	0.45	0.35	-1.80	0.01	2.14
	REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES.v2022.1.Hs.grp	1.98	0.00	2.99	1.22	0.25	0.61	-1.56	0.03	1.54
	REACTOME_NONSENSE_MEDIATED_DECAY_NMD.v2022.1.Hs.grp	2.48	0.00	4.00	1.42	0.11	0.96	-2.21	0.00	4.00
	REACTOME_RRNA_PROCESSING.v2022.1.Hs.grp	2.19	0.00	4.00	1.40	0.12	0.91	-2.01	0.00	2.79
Oxidative Phosphorylation	GOBP_AEROBIC_RESPIRATION.v2022.1.Hs.grp	1.77	0.01	2.11	2.53	0.00	4.00	1.63	0.01	2.28
	GOBP_OXIDATIVE_PHOSPHORYLATION.v2022.1.Hs.grp	1.95	0.00	2.80	2.62	0.00	4.00	1.72	0.00	2.67
	GOBP_ATP_SYNTHESIS_COUPLED_ELECTRON_TRANSPORT.v2022.1.Hs.grp	2.02	0.00	3.01	2.64	0.00	4.00	1.62	0.01	2.22
	GOBP_RESPIRATORY_ELECTRON_TRANSPORT_CHAIN.v2022.1.Hs.grp	1.89	0.00	2.60	2.48	0.00	4.00	1.67	0.00	2.42
	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS.v2022.1.Hs.grp	1.81	0.01	2.27	2.69	0.00	4.00	1.74	0.00	2.77
	GOBP_ATP_BIOSYNTHETIC_PROCESS.v2022.1.Hs.grp	1.76	0.01	2.05	2.08	0.00	3.19	1.66	0.00	2.38
	Hs.grp	1.54	0.04	1.44	2.31	0.00	4.00	1.60	0.01	2.16
	GOBP_ELECTRON_TRANSPORT_CHAIN.v2022.1.Hs.grp	1.59	0.03	1.52	2.30	0.00	4.00	1.72	0.00	2.69
	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT.v2022.1.Hs.grp	1.83	0.00	2.36	2.53	0.00	4.00	1.62	0.01	2.22
	KEGG_OXIDATIVE_PHOSPHORYLATION.v2022.1.Hs.grp	1.85	0.00	2.41	2.31	0.00	4.00	1.69	0.00	2.57
	REACTOME_COMPLEX_I_BIOGENESIS.v2022.1.Hs.grp	1.83	0.00	2.37	2.13	0.00	3.23	1.58	0.01	2.10
Myeloid Migration	GOBP_NEUTROPHIL_MIGRATION.v2022.1.Hs.grp	2.02	0.00	3.03	-0.94	0.81	0.09	1.97	0.00	4.00
	GOBP_MYELOID_LEUKOCYTE_MIGRATION.v2022.1.Hs.grp	1.99	0.00	2.98	-0.95	0.83	0.08	1.84	0.00	3.20
	GOBP_NEUTROPHIL_CHEMOTAXIS.v2022.1.Hs.grp	1.99	0.00	3.00	0.88	0.72	0.14	2.12	0.00	4.00
	GOBP_GRANULOCYTE_MIGRATION.v2022.1.Hs.grp	1.97	0.00	2.99	1.08	0.42	0.38	1.94	0.00	4.00
	GOBP_LEUKOCYTE_CHEMOTAXIS.v2022.1.Hs.grp	1.90	0.00	2.61	-0.94	0.79	0.10	1.73	0.00	2.68
	GOBP_GRANULOCYTE_CHEMOTAXIS.v2022.1.Hs.grp	1.90	0.00	2.59	1.06	0.43	0.37	2.07	0.00	4.00
	GOBP_CELL_CHEMOTAXIS.v2022.1.Hs.grp	1.89	0.00	2.61	1.05	0.44	0.35	1.72	0.00	2.68
	GOBP_LEUKOCYTE_MIGRATION.v2022.1.Hs.grp	1.81	0.01	2.26	-1.04	0.76	0.12	1.68	0.00	2.45
	GOBP_TAXIS.v2022.1.Hs.grp	1.69	0.01	1.85	1.04	0.45	0.34	1.62	0.01	2.22
		GOBP_GRANULOCYTE_ACTIVATION.v2022.1.Hs.grp	1.47	0.06	1.26	1.16	0.31	0.50	1.52	0.02
Myeloid Activation	GOBP_POSITIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION.v2022.1.Hs.grp	1.53	0.04	1.39	1.03	0.47	0.33	1.49	0.02	1.69
	GOBP_REGULATION_OF_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY.v2022.1.Hs.grp	0.91	0.64	0.19	-0.80	0.92	0.03	1.48	0.02	1.65
	GOBP_LEUKOCYTE_MEDIATED_CYTOTOXICITY.v2022.1.Hs.grp	1.29	0.15	0.82	-0.85	0.89	0.05	1.88	0.00	3.52
	GOBP_FC_RECEPTOR_SIGNALING_PATHWAY.v2022.1.Hs.grp	1.12	0.33	0.48	-0.99	0.80	0.09	1.39	0.05	1.30
	GOBP_REGULATION_OF_LEUKOCYTE_MEDIATED_CYTOTOXICITY.v2022.1.Hs.grp	1.16	0.28	0.55	-1.03	0.73	0.14	1.72	0.00	2.66
		GOBP_RESPONSE_TO_CHEMOKINE.v2022.1.Hs.grp	1.75	0.01	2.02	-1.26	0.38	0.42	1.69	0.00
Inflammation	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION.v2022.1.Hs.grp	1.56	0.04	1.46	-1.40	0.24	0.62	1.52	0.02	1.79
	HALLMARK_IL6_JAK_STAT3_SIGNALING.v2022.1.Hs.grp	1.55	0.04	1.45	-1.48	0.17	0.77	1.48	0.02	1.63
	GOBP_POSITIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION.v2022.1.Hs.grp	1.57	0.03	1.47	-1.26	0.37	0.44	1.59	0.01	2.12
	GOBP_NEGATIVE_REGULATION_OF_VIRAL_GENOME_REPLICATION.v2022.1.Hs.grp	1.93	0.00	2.72	1.53	0.06	1.20	1.35	0.07	1.17
	GOBP_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION.v2022.1.Hs.grp	1.81	0.01	2.26	0.97	0.56	0.25	1.56	0.01	1.98
	HALLMARK_TNFA_SIGNALING_VIA_NFKB.v2022.1.Hs.grp	1.61	0.03	1.58	-2.35	0.00	4.00	1.44	0.03	1.49
	REACTOME_INTERFERON_ALPHA_BETA_SIGNALING.v2022.1.Hs.grp	1.96	0.00	2.88	1.87	0.01	2.14	1.58	0.01	2.09
	HALLMARK_INTERFERON_ALPHA_RESPONSE.v2022.1.Hs.grp	2.17	0.00	3.82	1.79	0.02	1.76	1.57	0.01	2.06
	HALLMARK_INTERFERON_GAMMA_RESPONSE.v2022.1.Hs.grp	2.04	0.00	3.09	0.92	0.64	0.19	1.47	0.03	1.60
	GOBP_ACUTE_INFLAMMATORY_RESPONSE.v2022.1.Hs.grp	2.02	0.00	2.99	1.41	0.12	0.93	1.76	0.00	2.79
	HALLMARK_ALLOGRAFT_REJECTION.v2022.1.Hs.grp	1.72	0.01	1.92	-0.92	0.80	0.10	1.59	0.01	2.11
	HALLMARK_INFLAMMATORY_RESPONSE.v2022.1.Hs.grp	1.97	0.00	2.96	-1.51	0.15	0.82	1.49	0.02	1.67

Supplemental Table 4 Continued: GSEA on scRNAseq Populations, related to Figure 6
NES=Normalized Enrichment Score, FDR=False Discovery Rate

Group	MSigDB Signature Name	Combo vs GSK								
		Macs/Dend			Neus			Tumor		
		NES	FDR q	-Log(q)	NES	FDR q	-Log(q)	NES	FDR q	-Log(q)
DNA Replication and Damage	REACTOME_G1_S_DNA_DAMAGE_CHECKPOINTS.v2022.1.Hs.grp	1.72	0.01	2.20	1.09	0.39		1.30	0.12	0.92
	REACTOME_ORC1_REMOVAL_FROM_CHROMATIN.v2022.1.Hs.grp	1.76	0.00	2.38	1.29	0.20	0.69	1.27	0.14	0.84
	REACTOME_SWITCHING_OF_ORIGINS_TO_A_POST_REPLICATIVE_STATE.v2022.1.Hs.grp	1.65	0.01	1.96	1.20	0.26	0.58	1.23	0.18	0.75
	REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_ORIGIN_COMPLEX.v2022.1.Hs.grp	1.76	0.00	2.37	1.30	0.20	0.69	1.21	0.19	0.71
	REACTOME_SYNTHESIS_OF_DNA.v2022.1.Hs.grp	1.62	0.01	1.84	1.18	0.29	0.54	1.20	0.20	0.69
REACTOME_APC_C_MEDIATED_DEGRADATION_OF_CELL_CYCLE_PROTEINS.v2022.1.Hs.grp	1.66	0.01	2.00	1.22	0.25	0.60	1.20	0.20	0.69	
Protein and RNA Processing	KEGG_RIBOSOME.v2022.1.Hs.grp	2.59	0.00	4.00	-1.30	0.31	0.50	-2.15	0.00	3.86
	REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION.v2022.1.Hs.grp	2.61	0.00	4.00	-1.43	0.28	0.55	-2.28	0.00	4.00
	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE.v2022.1.Hs.grp	2.51	0.00	4.00	-1.25	0.33	0.48	-2.12	0.00	3.70
	REACTOME_RESPONSE_OF_EIF2AK4_GCN2_TO_AMINO_ACID_DEFICIENCY.v2022.1.Hs.grp	2.63	0.00	4.00	-1.40	0.33	0.49	-2.27	0.00	4.00
	REACTOME_EUKARYOTIC_TRANSLATION_INITIATION.v2022.1.Hs.grp	2.52	0.00	4.00	-1.38	0.27	0.57	-2.09	0.00	3.48
	REACTOME_INFLUENZA_INFECTION.v2022.1.Hs.grp	2.53	0.00	4.00	-1.40	0.30	0.52	-2.18	0.00	3.76
	GOBP_CYTOPLASMIC_TRANSLATION.v2022.1.Hs.grp	2.41	0.00	4.00	-1.46	0.25	0.60	-2.18	0.00	3.81
	REACTOME_TRANSLATION.v2022.1.Hs.grp	2.29	0.00	4.00	-1.29	0.33	0.48	-2.02	0.00	3.36
	REACTOME_SELENOAMINO_ACID_METABOLISM.v2022.1.Hs.grp	2.56	0.00	4.00	-1.36	0.29	0.54	-2.24	0.00	4.00
	REACTOME_CELLULAR_RESPONSE_TO_STARVATION.v2022.1.Hs.grp	2.39	0.00	4.00	-1.59	0.24	0.61	-2.05	0.00	3.31
	REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES.v2022.1.Hs.grp	2.21	0.00	4.00	-1.09	0.54	0.27	-1.66	0.01	1.85
	REACTOME_NONSENSE_MEDIATED_DECAY_NMD.v2022.1.Hs.grp	2.58	0.00	4.00	-1.34	0.32	0.49	-2.14	0.00	3.90
REACTOME_RRNA_PROCESSING.v2022.1.Hs.grp	2.39	0.00	4.00	-1.38	0.28	0.55	-2.13	0.00	3.67	
Oxidative Phosphorylation	GOBP_AEROBIC_RESPIRATION.v2022.1.Hs.grp	2.05	0.00	3.93	1.93	0.09	1.06	1.82	0.00	3.70
	GOBP_OXIDATIVE_PHOSPHORYLATION.v2022.1.Hs.grp	2.14	0.00	4.00	1.90	0.06	1.26	1.92	0.00	3.82
	GOBP_ATP_SYNTHESIS_COUPLED_ELECTRON_TRANSPORT.v2022.1.Hs.grp	2.14	0.00	4.00	1.83	0.06	1.23	1.88	0.00	3.97
	GOBP_RESPIRATORY_ELECTRON_TRANSPORT_CHAIN.v2022.1.Hs.grp	2.06	0.00	3.91	1.81	0.05	1.28	1.88	0.00	3.94
	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS.v2022.1.Hs.grp	2.07	0.00	3.88	1.78	0.06	1.19	1.96	0.00	4.00
	GOBP_ATP_BIOSYNTHETIC_PROCESS.v2022.1.Hs.grp	2.08	0.00	3.85	1.72	0.06	1.24	1.98	0.00	4.00
	REACTOME_THE_CITRIC_ACID_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT.v2022.1.Hs.grp	1.96	0.00	3.45	1.72	0.05	1.26	1.87	0.00	4.04
	GOBP_ELECTRON_TRANSPORT_CHAIN.v2022.1.Hs.grp	1.84	0.00	2.70	1.71	0.05	1.26	1.88	0.00	4.19
	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT.v2022.1.Hs.grp	1.95	0.00	3.41	1.70	0.05	1.30	1.91	0.00	4.04
	KEGG_OXIDATIVE_PHOSPHORYLATION.v2022.1.Hs.grp	2.07	0.00	3.87	1.65	0.06	1.21	2.05	0.00	4.00
REACTOME_COMPLEX_I_BIOGENESIS.v2022.1.Hs.grp	1.85	0.00	2.77	1.58	0.08	1.09	1.80	0.00	3.38	
Myeloid Migration	GOBP_NEUTROPHIL_MIGRATION.v2022.1.Hs.grp	1.81	0.00	2.59	1.43	0.14	0.84	1.83	0.00	3.72
	GOBP_MYELOID_LEUKOCYTE_MIGRATION.v2022.1.Hs.grp	1.88	0.00	2.95	1.38	0.17	0.78	1.84	0.00	3.72
	GOBP_NEUTROPHIL_CHEMOTAXIS.v2022.1.Hs.grp	1.84	0.00	2.70	1.26	0.21	0.68	1.75	0.00	3.07
	GOBP_GRANULOCYTE_MIGRATION.v2022.1.Hs.grp	1.89	0.00	2.99	1.54	0.09	1.03	1.75	0.00	3.07
	GOBP_LEUKOCYTE_CHEMOTAXIS.v2022.1.Hs.grp	1.91	0.00	3.14	1.35	0.17	0.76	1.51	0.02	1.72
	GOBP_GRANULOCYTE_CHEMOTAXIS.v2022.1.Hs.grp	1.90	0.00	3.05	1.39	0.16	0.79	1.71	0.00	2.84
	GOBP_CELL_CHEMOTAXIS.v2022.1.Hs.grp	1.98	0.00	3.60	1.58	0.08	1.11	1.64	0.00	2.41
	GOBP_LEUKOCYTE_MIGRATION.v2022.1.Hs.grp	1.80	0.00	2.54	1.43	0.14	0.84	1.68	0.00	2.68
	GOBP_TAXIS.v2022.1.Hs.grp	1.76	0.00	2.38	1.50	0.12	0.91	1.62	0.01	2.29
	GOBP_REGULATION_OF_LEUKOCYTE_MIGRATION.v2022.1.Hs.grp	1.81	0.00	2.59	1.43	0.14	0.84	1.83	0.00	3.72
Myeloid Activation	GOBP_GRANULOCYTE_ACTIVATION.v2022.1.Hs.grp	1.57	0.02	1.66	1.55	0.09	1.03	1.73	0.00	3.01
	GOBP_POSITIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION.v2022.1.Hs.grp	1.29	0.15	0.83	1.08	0.39	0.41	1.76	0.00	3.16
	GOBP_REGULATION_OF_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY.v2022.1.Hs.grp	1.39	0.08	1.10	1.19	0.28	0.55	1.79	0.00	3.35
	GOBP_LEUKOCYTE_MEDIATED_CYTOTOXICITY.v2022.1.Hs.grp	1.35	0.10	1.00	0.91	0.65	0.19	1.72	0.00	2.95
	GOBP_FC_RECEPTOR_SIGNALING_PATHWAY.v2022.1.Hs.grp	1.39	0.08	1.10	0.94	0.60	0.22	1.77	0.00	3.19
	GOBP_REGULATION_OF_LEUKOCYTE_MEDIATED_CYTOTOXICITY.v2022.1.Hs.grp	1.12	0.31	0.50	-0.69	0.99	0.00	1.79	0.00	3.39
Inflammation	GOBP_RESPONSE_TO_CHEMOKINE.v2022.1.Hs.grp	1.61	0.02	1.82	-0.90	0.79	0.10	1.73	0.00	3.00
	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION.v2022.1.Hs.grp	1.62	0.01	1.83	0.84	0.78	0.11	1.64	0.00	2.37
	HALLMARK_IL6_JAK_STAT3_SIGNALING.v2022.1.Hs.grp	1.67	0.01	2.02	0.66	0.96	0.02	1.50	0.02	1.66
	GOBP_POSITIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION.v2022.1.Hs.grp	1.24	0.18	0.75	-1.12	0.48	0.32	1.89	0.00	4.15
	GOBP_NEGATIVE_REGULATION_OF_VIRAL_GENOME_REPLICATION.v2022.1.Hs.grp	1.52	0.03	1.51	1.66	0.06	1.26	1.83	0.00	3.70
	GOBP_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION.v2022.1.Hs.grp	1.38	0.08	1.09	-0.87	0.83	0.08	1.77	0.00	3.17
	HALLMARK_TNFA_SIGNALING_VIA_NFKB.v2022.1.Hs.grp	1.65	0.01	1.96	-1.33	0.32	0.49	1.38	0.06	1.20
	REACTOME_INTERFERON_ALPHA_BETA_SIGNALING.v2022.1.Hs.grp	1.67	0.01	2.01	1.12	0.35	0.46	1.73	0.00	3.01
	HALLMARK_INTERFERON_ALPHA_RESPONSE.v2022.1.Hs.grp	1.83	0.00	2.69	1.43	0.15	0.84	1.84	0.00	3.74
	HALLMARK_INTERFERON_GAMMA_RESPONSE.v2022.1.Hs.grp	1.98	0.00	3.57	1.30	0.20	0.70	1.78	0.00	3.28
	GOBP_ACUTE_INFLAMMATORY_RESPONSE.v2022.1.Hs.grp	1.85	0.00	2.74	1.68	0.06	1.24	1.71	0.00	2.83
	HALLMARK_ALLOGRAFT_REJECTION.v2022.1.Hs.grp	1.94	0.00	3.33	0.96	0.57	0.24	1.53	0.02	1.78
HALLMARK_INFLAMMATORY_RESPONSE.v2022.1.Hs.grp	1.82	0.00	2.66	1.07	0.40	0.39	1.71	0.00	2.84	

Supplemental Table 5: GSEA on scRNAseq Populations, related to Figure 6
NES=Normalized Enrichment Score, FDR=False Discovery Rate

Group	MSigDB Signature Name	Combo vs Placebo								
		Macs/Dend		Neus		Tumor				
		NES	FDR q -Log(q)	NES	FDR q -Log(q)	NES	FDR q -Log(q)			
DNA Replication and Damage	REACTOME_G1_S_DNA_DAMAGE_CHECKPOINTS.v2022.1.Hs.grp	2.19	0.00	4.00	1.86	0.00	2.76	1.50	0.03	1.60
	REACTOME_ORC1_REMOVAL_FROM_CHROMATIN.v2022.1.Hs.grp	2.27	0.00	4.00	1.95	0.00	3.16	1.44	0.04	1.39
	REACTOME_SWITCHING_OF_ORIGINS_TO_A_POST_REPLICATIVE_STATE.v2022.1.Hs.grp	2.18	0.00	4.00	1.95	0.00	3.16	1.42	0.05	1.33
	REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_ORIGIN_COMPLEX.v2022.1.Hs.grp	2.22	0.00	4.00	1.88	0.00	2.86	1.47	0.03	1.52
	REACTOME_SYNTHESIS_OF_DNA.v2022.1.Hs.grp	2.06	0.00	4.01	2.01	0.00	3.50	1.39	0.06	1.23
	REACTOME_APC_C_MEDIATED_DEGRADATION_OF_CELL_CYCLE_PROTEINS.v2022.1.Hs.grp	2.18	0.00	4.00	1.96	0.00	3.18	1.47	0.03	1.52
Protein and RNA Processing	KEGG_RIBOSOME.v2022.1.Hs.grp	3.06	0.00	4.00	3.34	0.00	4.00	1.61	0.01	2.04
	REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION.v2022.1.Hs.grp	3.06	0.00	4.00	3.33	0.00	4.00	1.57	0.01	1.90
	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE.v2022.1.Hs.grp	3.03	0.00	4.00	3.34	0.00	4.00	1.58	0.01	1.92
	REACTOME_RESPONSE_OF_EIF2AK4_GCN2_TO_AMINO_ACID_DEFICIENCY.v2022.1.Hs.grp	3.06	0.00	4.00	3.32	0.00	4.00	1.52	0.02	1.68
	REACTOME_EUKARYOTIC_TRANSLATION_INITIATION.v2022.1.Hs.grp	2.94	0.00	4.00	3.36	0.00	4.00	1.58	0.01	1.92
	REACTOME_INFLUENZA_INFECTION.v2022.1.Hs.grp	2.89	0.00	4.00	3.23	0.00	4.00	1.33	0.09	1.02
	GOBP_CYTOPLASMIC_TRANSLATION.v2022.1.Hs.grp	2.81	0.00	4.00	3.26	0.00	4.00	1.48	0.03	1.53
	REACTOME_TRANSLATION.v2022.1.Hs.grp	2.81	0.00	4.00	3.21	0.00	4.00	1.35	0.08	1.11
	REACTOME_SELENOAMINO_ACID_METABOLISM.v2022.1.Hs.grp	3.04	0.00	4.00	3.36	0.00	4.00	1.50	0.02	1.61
	REACTOME_CELLULAR_RESPONSE_TO_STARVATION.v2022.1.Hs.grp	2.86	0.00	4.00	3.22	0.00	4.00	1.54	0.02	1.72
	REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES.v2022.1.Hs.grp	2.72	0.00	4.00	3.06	0.00	4.00	1.41	0.05	1.32
	REACTOME_NONSENSE_MEDIATED_DECAY_NMD.v2022.1.Hs.grp	2.93	0.00	4.00	3.33	0.00	4.00	1.50	0.02	1.61
	REACTOME_RRNA_PROCESSING.v2022.1.Hs.grp	2.93	0.00	4.00	3.28	0.00	4.00	1.48	0.03	1.55
Oxidative Phosphorylation	GOBP_AEROBIC_RESPIRATION.v2022.1.Hs.grp	1.70	0.01	2.12	2.59	0.00	4.00	1.86	0.00	3.69
	GOBP_OXIDATIVE_PHOSPHORYLATION.v2022.1.Hs.grp	1.88	0.00	2.91	2.66	0.00	4.00	1.96	0.00	4.13
	GOBP_ATP_SYNTHESIS_COUPLED_ELECTRON_TRANSPORT.v2022.1.Hs.grp	1.83	0.00	2.73	2.54	0.00	4.00	1.92	0.00	3.99
	GOBP_RESPIRATORY_ELECTRON_TRANSPORT_CHAIN.v2022.1.Hs.grp	1.71	0.01	2.15	2.47	0.00	4.00	1.91	0.00	3.86
	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMOSMOTIC_COUPLING_AND_HEAT_PRODUCED_BY_UNCOUPLING_PROTEINS.v2022.1.Hs.grp	1.75	0.00	2.32	2.69	0.00	4.00	2.10	0.00	4.00
	GOBP_ATP_BIOSYNTHETIC_PROCESS.v2022.1.Hs.grp	1.84	0.00	2.73	2.45	0.00	4.00	2.06	0.00	4.00
	REACTOME_THE_CITRIC_ACID_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT.v2022.1.Hs.grp	1.48	0.04	1.43	2.64	0.00	4.00	1.92	0.00	3.97
	GOBP_ELECTRON_TRANSPORT_CHAIN.v2022.1.Hs.grp	1.46	0.04	1.36	2.27	0.00	4.00	1.90	0.00	3.77
	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT.v2022.1.Hs.grp	1.70	0.01	2.13	2.53	0.00	4.00	2.01	0.00	3.79
	KEGG_OXIDATIVE_PHOSPHORYLATION.v2022.1.Hs.grp	1.69	0.01	2.12	2.63	0.00	4.00	2.13	0.00	4.00
	REACTOME_COMPLEX_I_BIOGENESIS.v2022.1.Hs.grp	1.82	0.00	2.63	2.20	0.00	4.00	1.90	0.00	3.75
Myeloid Migration	GOBP_NEUTROPHIL_MIGRATION.v2022.1.Hs.grp	-1.43	0.06	1.25	-1.49	0.08	1.11	1.16	0.27	0.57
	GOBP_MYELOID_LEUKOCYTE_MIGRATION.v2022.1.Hs.grp	-1.51	0.04	1.43	-1.43	0.10	1.00	1.30	0.11	0.94
	GOBP_NEUTROPHIL_CHEMOTAXIS.v2022.1.Hs.grp	-1.41	0.07	1.18	-1.50	0.07	1.13	1.20	0.22	0.66
	GOBP_GRANULOCYTE_MIGRATION.v2022.1.Hs.grp	-1.49	0.04	1.40	-1.43	0.10	0.99	1.23	0.18	0.74
	GOBP_LEUKOCYTE_CHEMOTAXIS.v2022.1.Hs.grp	-1.50	0.04	1.43	-1.76	0.01	1.84	1.09	0.37	0.43
	GOBP_GRANULOCYTE_CHEMOTAXIS.v2022.1.Hs.grp	-1.50	0.04	1.43	-1.46	0.09	1.06	1.25	0.17	0.78
	GOBP_CELL_CHEMOTAXIS.v2022.1.Hs.grp	-1.50	0.04	1.43	-1.84	0.01	2.03	1.19	0.23	0.64
	GOBP_LEUKOCYTE_MIGRATION.v2022.1.Hs.grp	-1.60	0.02	1.64	-1.78	0.01	1.89	1.13	0.31	0.51
	GOBP_TAXIS.v2022.1.Hs.grp	-1.65	0.02	1.81	-1.72	0.02	1.77	1.14	0.31	0.51
Myeloid Activation	GOBP_GRANULOCYTE_ACTIVATION.v2022.1.Hs.grp	-1.19	0.22	0.65	-1.21	0.24	0.62	1.04	0.47	0.33
	GOBP_POSITIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION.v2022.1.Hs.grp	-1.44	0.05	1.28	-1.80	0.01	1.91	0.75	0.88	0.06
	GOBP_REGULATION_OF_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY.v2022.1.Hs.grp	-0.84	0.78	0.11	-1.05	0.45	0.35	-1.00	0.47	0.33
	GOBP_LEUKOCYTE_MEDIATED_CYTOTOXICITY.v2022.1.Hs.grp	1.23	0.16	0.79	-1.33	0.16	0.81	1.42	0.05	1.33
	GOBP_FC_RECEPTOR_SIGNALING_PATHWAY.v2022.1.Hs.grp	-0.91	0.66	0.18	-1.51	0.07	1.14	0.67	0.93	0.03
	GOBP_REGULATION_OF_LEUKOCYTE_MEDIATED_CYTOTOXICITY.v2022.1.Hs.grp	1.22	0.17	0.77	-1.58	0.05	1.32	0.97	0.58	0.23
Inflammation	GOBP_RESPONSE_TO_CHEMOKINE.v2022.1.Hs.grp	-1.90	0.00	2.76	-2.13	0.00	4.00	-1.25	0.16	0.81
	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION.v2022.1.Hs.grp	-1.56	0.03	1.56	-1.79	0.01	1.93	-1.97	0.00	2.45
	HALLMARK_IL6_JAK_STAT3_SIGNALING.v2022.1.Hs.grp	-1.55	0.03	1.53	-1.97	0.00	2.37	-1.15	0.24	0.61
	p	0.94	0.58	0.24	-0.99	0.52	0.28	1.38	0.06	1.19
	GOBP_NEGATIVE_REGULATION_OF_VIRAL_GENOME_REPLICATION.v2022.1.Hs.grp	1.30	0.11	0.97	1.12	0.29	0.54	-2.23	0.00	2.47
	GOBP_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION.v2022.1.Hs.grp	-1.04	0.43	0.37	-0.99	0.53	0.28	1.08	0.39	0.41
	HALLMARK_TNFA_SIGNALING_VIA_NFKB.v2022.1.Hs.grp	-2.36	0.00	4.00	-3.21	0.00	4.00	-1.41	0.07	1.18
	REACTOME_INTERFERON_ALPHA_BETA_SIGNALING.v2022.1.Hs.grp	1.52	0.03	1.52	1.22	0.18	0.74	-2.17	0.00	2.77
	HALLMARK_INTERFERON_ALPHA_RESPONSE.v2022.1.Hs.grp	1.44	0.05	1.34	1.39	0.08	1.11	-2.14	0.00	2.93
	HALLMARK_INTERFERON_GAMMA_RESPONSE.v2022.1.Hs.grp	1.32	0.10	1.00	-0.98	0.54	0.27	-1.44	0.06	1.21
	GOBP_ACUTE_INFLAMMATORY_RESPONSE.v2022.1.Hs.grp	1.63	0.01	1.87	-1.54	0.06	1.21	1.36	0.08	1.12
	HALLMARK_ALLOGRAFT_REJECTION.v2022.1.Hs.grp	1.36	0.08	1.11	-1.03	0.47	0.33	1.06	0.43	0.36
	HALLMARK_INFLAMMATORY_RESPONSE.v2022.1.Hs.grp	-1.55	0.03	1.52	-1.90	0.01	2.28	-1.47	0.06	1.22

Supplemental Table 5 Continued: GSEA on scRNAseq Populations, related to Figure 6
NES=Normalized Enrichment Score, FDR=False Discovery Rate

Group	MSigDB Signature Name	GSK vs Placebo								
		Macs/Dend		Neus		Tumor				
		NES	FDR q-Log(q)	NES	FDR q-Log(q)	NES	FDR q-Log(q)			
DNA Replication and Damage	REACTOME_G1_S_DNA_DAMAGE_CHECKPOINTS.v2022.1.Hs.grp	1.87	0.00	2.68	1.83	0.00	2.66	1.14	0.35	0.46
	REACTOME_ORC1_REMOVAL_FROM_CHROMATIN.v2022.1.Hs.grp	2.09	0.00	4.15	1.89	0.00	2.83	1.19	0.32	0.49
	REACTOME_SWITCHING_OF_ORIGINS_TO_A_POST_REPLICATIVE_STATE.v2022.1.Hs.grp	2.02	0.00	3.39	1.97	0.00	3.13	1.13	0.36	0.45
	REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_ORIGIN_COMPLEX.v2022.1.Hs.grp	2.22	0.00	4.00	1.86	0.00	2.74	1.21	0.30	0.52
	REACTOME_SYNTHESIS_OF_DNA.v2022.1.Hs.grp	1.87	0.00	2.69	1.95	0.00	3.06	1.14	0.34	0.46
	REACTOME_APC_C_MEDIATED_DEGRADATION_OF_CELL_CYCLE_PROTEINS.v2022.1.Hs.grp	2.02	0.00	3.41	1.95	0.00	3.06	1.09	0.41	0.39
Protein and RNA Processing	KEGG_RIBOSOME.v2022.1.Hs.grp	2.45	0.00	4.00	3.46	0.00	4.00	2.46	0.00	4.00
	REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION.v2022.1.Hs.grp	2.53	0.00	4.00	3.51	0.00	4.00	2.47	0.00	4.00
	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE.v2022.1.Hs.grp	2.50	0.00	4.00	3.46	0.00	4.00	2.37	0.00	4.00
	REACTOME_RESPONSE_OF_EIF2AK4_GCN2_TO_AMINO_ACID_DEFICIENCY.v2022.1.Hs.grp	2.32	0.00	4.00	3.45	0.00	4.00	2.44	0.00	4.00
	REACTOME_EUKARYOTIC_TRANSLATION_INITIATION.v2022.1.Hs.grp	2.27	0.00	4.00	3.46	0.00	4.00	2.44	0.00	4.00
	REACTOME_INFLUENZA_INFECTION.v2022.1.Hs.grp	2.00	0.00	3.24	3.42	0.00	4.00	2.20	0.00	4.00
	GOBP_CYTOPLASMIC_TRANSLATION.v2022.1.Hs.grp	2.16	0.00	4.00	3.36	0.00	4.00	2.43	0.00	4.00
	REACTOME_TRANSLATION.v2022.1.Hs.grp	2.06	0.00	4.19	3.47	0.00	4.00	2.29	0.00	4.00
	REACTOME_SELENOAMINO_ACID_METABOLISM.v2022.1.Hs.grp	2.37	0.00	4.00	3.48	0.00	4.00	2.38	0.00	4.00
	REACTOME_CELLULAR_RESPONSE_TO_STARVATION.v2022.1.Hs.grp	2.31	0.00	4.00	3.38	0.00	4.00	2.38	0.00	4.00
	REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES.v2022.1.Hs.grp	2.13	0.00	4.00	3.29	0.00	4.00	1.88	0.00	3.25
	REACTOME_NONSENSE_MEDIATED_DECAY_NMD.v2022.1.Hs.grp	2.21	0.00	4.00	3.47	0.00	4.00	2.35	0.00	4.00
	REACTOME_RRNA_PROCESSING.v2022.1.Hs.grp	2.18	0.00	4.00	3.41	0.00	4.00	2.37	0.00	4.00
Oxidative Phosphorylation	GOBP_AEROBIC_RESPIRATION.v2022.1.Hs.grp	-1.23	0.21	0.67	1.94	0.00	3.03	1.14	0.35	0.46
	GOBP_OXIDATIVE_PHOSPHORYLATION.v2022.1.Hs.grp	-1.13	0.32	0.49	2.05	0.00	3.80	1.25	0.27	0.58
	GOBP_ATP_SYNTHESIS_COUPLED_ELECTRON_TRANSPORT.v2022.1.Hs.grp	-1.20	0.24	0.61	2.04	0.00	3.71	1.08	0.42	0.37
	GOBP_RESPIRATORY_ELECTRON_TRANSPORT_CHAIN.v2022.1.Hs.grp	-1.09	0.36	0.44	2.00	0.00	3.42	1.18	0.33	0.48
	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMOSMOTIC_COUPLING_AND_HEAT_PRODUCED_BY_UNCOUPLING_PROTEINS.v2022.1.Hs.grp	-1.34	0.13	0.90	2.14	0.00	4.10	1.31	0.20	0.70
	GOBP_ATP_BIOSYNTHETIC_PROCESS.v2022.1.Hs.grp	-1.22	0.22	0.66	1.87	0.00	2.74	1.04	0.48	0.32
	REACTOME_THE_CITRIC_ACID_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT.v2022.1.Hs.grp	-1.36	0.12	0.93	2.04	0.00	3.81	1.16	0.34	0.47
	GOBP_ELECTRON_TRANSPORT_CHAIN.v2022.1.Hs.grp	-1.10	0.36	0.44	1.54	0.03	1.54	1.17	0.34	0.46
	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT.v2022.1.Hs.grp	-1.22	0.22	0.66	1.99	0.00	3.34	1.16	0.33	0.48
	KEGG_OXIDATIVE_PHOSPHORYLATION.v2022.1.Hs.grp	-1.40	0.09	1.05	2.18	0.00	4.00	1.18	0.33	0.48
	REACTOME_COMPLEX_I_BIOGENESIS.v2022.1.Hs.grp	-0.99	0.51	0.29	1.62	0.02	1.82	0.96	0.59	0.23
Myeloid Migration	GOBP_NEUTROPHIL_MIGRATION.v2022.1.Hs.grp	-2.04	0.00	3.50	-1.70	0.02	1.73	-2.20	0.00	4.00
	GOBP_MYELOID_LEUKOCYTE_MIGRATION.v2022.1.Hs.grp	-2.02	0.00	3.64	-1.75	0.01	1.93	-2.08	0.00	3.48
	GOBP_NEUTROPHIL_CHEMOTAXIS.v2022.1.Hs.grp	-2.02	0.00	3.75	-1.59	0.04	1.46	-2.10	0.00	3.43
	GOBP_GRANULOCYTE_MIGRATION.v2022.1.Hs.grp	-2.11	0.00	3.59	-1.86	0.01	2.10	-2.07	0.00	3.52
	GOBP_LEUKOCYTE_CHEMOTAXIS.v2022.1.Hs.grp	-2.02	0.00	3.70	-1.90	0.01	2.26	-1.87	0.00	2.61
	GOBP_GRANULOCYTE_CHEMOTAXIS.v2022.1.Hs.grp	-2.09	0.00	3.72	-1.66	0.02	1.62	-2.02	0.00	3.44
	GOBP_CELL_CHEMOTAXIS.v2022.1.Hs.grp	-2.02	0.00	3.80	-2.09	0.00	3.02	-1.94	0.00	3.05
	GOBP_LEUKOCYTE_MIGRATION.v2022.1.Hs.grp	-2.01	0.00	3.84	-2.04	0.00	2.77	-1.98	0.00	3.34
	GOBP_TAXIS.v2022.1.Hs.grp	-1.98	0.00	3.76	-2.04	0.00	2.74	-1.77	0.01	2.24
Myeloid Activation	GOBP_GRANULOCYTE_ACTIVATION.v2022.1.Hs.grp	-1.60	0.02	1.71	-1.64	0.03	1.60	-1.99	0.00	3.33
	GOBP_POSITIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION.v2022.1.Hs.grp	-1.65	0.02	1.80	-2.07	0.00	2.88	-2.16	0.00	3.73
	GOBP_REGULATION_OF_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY.v2022.1.Hs.grp	-1.26	0.19	0.71	-1.34	0.13	0.90	-2.04	0.00	3.54
	GOBP_LEUKOCYTE_MEDIATED_CYTOTOXICITY.v2022.1.Hs.grp	-1.09	0.36	0.44	-1.25	0.19	0.73	-1.57	0.03	1.55
	GOBP_FC_RECEPTOR_SIGNALING_PATHWAY.v2022.1.Hs.grp	-1.43	0.08	1.12	-1.34	0.13	0.90			
	GOBP_REGULATION_OF_LEUKOCYTE_MEDIATED_CYTOTOXICITY.v2022.1.Hs.grp	-0.93	0.62	0.21	-1.18	0.24	0.61	-1.84	0.00	2.54
Inflammation	GOBP_RESPONSE_TO_CHEMOKINE.v2022.1.Hs.grp	-2.00	0.00	3.73	-1.86	0.01	2.11	-1.85	0.00	2.58
	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION.v2022.1.Hs.grp	-1.96	0.00	3.85	-1.85	0.01	2.13	-2.34	0.00	4.00
	HALLMARK_IL6_JAK_STAT3_SIGNALING.v2022.1.Hs.grp	-2.01	0.00	3.88	-1.98	0.00	2.58	-2.16	0.00	3.76
	GOBP_NEGATIVE_REGULATION_OF_VIRAL_GENOME_REPLICATION.v2022.1.Hs.grp	-1.10	0.36	0.44	-1.00	0.49	0.31	-1.74	0.01	2.14
	GOBP_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION.v2022.1.Hs.grp	-1.22	0.23	0.65	-1.23	0.20	0.69	-2.37	0.00	4.00
	GOBP_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION.v2022.1.Hs.grp	-1.35	0.12	0.92	-1.20	0.23	0.64	-2.08	0.00	3.50
	HALLMARK_TNFA_SIGNALING_VIA_NFKB.v2022.1.Hs.grp	-2.43	0.00	4.00	-3.00	0.00	4.00	-1.93	0.00	3.05
	REACTOME_INTERFERON_ALPHA_BETA_SIGNALING.v2022.1.Hs.grp	-1.00	0.50	0.30	0.99	0.50	0.30	-2.38	0.00	4.00
	HALLMARK_INTERFERON_ALPHA_RESPONSE.v2022.1.Hs.grp	-1.17	0.27	0.57	1.05	0.40	0.40	-2.66	0.00	4.00
	HALLMARK_INTERFERON_GAMMA_RESPONSE.v2022.1.Hs.grp	-1.44	0.07	1.14	-1.52	0.05	1.30	-2.39	0.00	4.00
	GOBP_ACUTE_INFLAMMATORY_RESPONSE.v2022.1.Hs.grp	-1.41	0.09	1.07	-1.91	0.01	2.24	-2.10	0.00	3.49
	HALLMARK_ALLOGRAFT_REJECTION.v2022.1.Hs.grp	-1.61	0.02	1.70	-1.39	0.10	1.00	-1.43	0.06	1.20
HALLMARK_INFLAMMATORY_RESPONSE.v2022.1.Hs.grp	-2.12	0.00	3.42	-2.32	0.00	4.00	-2.23	0.00	4.00	

Supplemental Table 5 Continued: GSEA on scRNAseq Populations, related to Figure 6
NES=Normalized Enrichment Score, FDR=False Discovery Rate

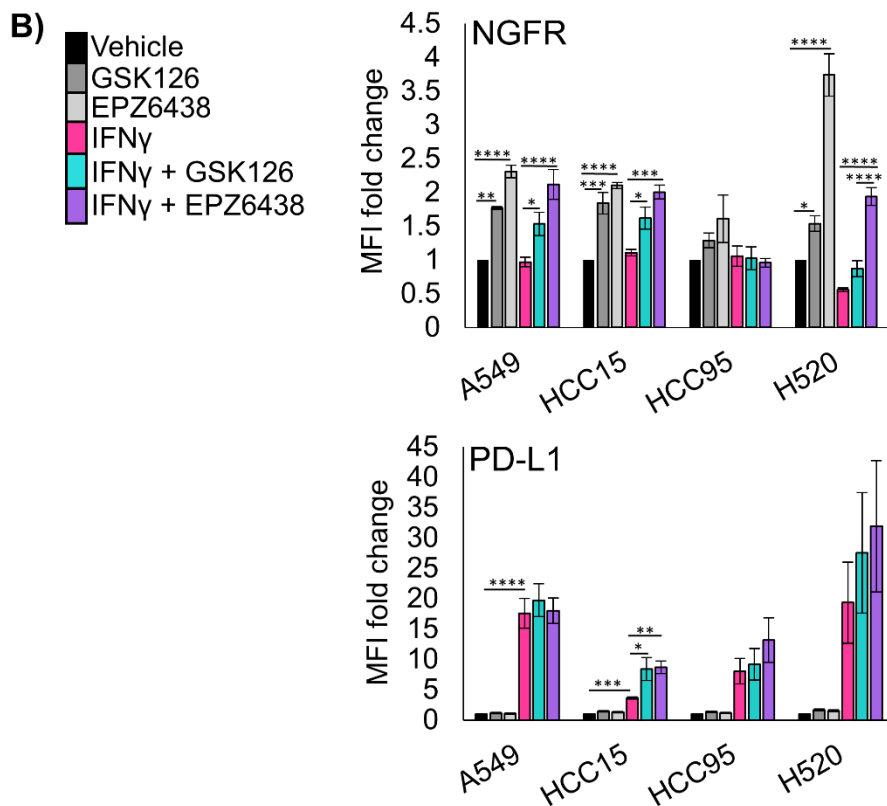
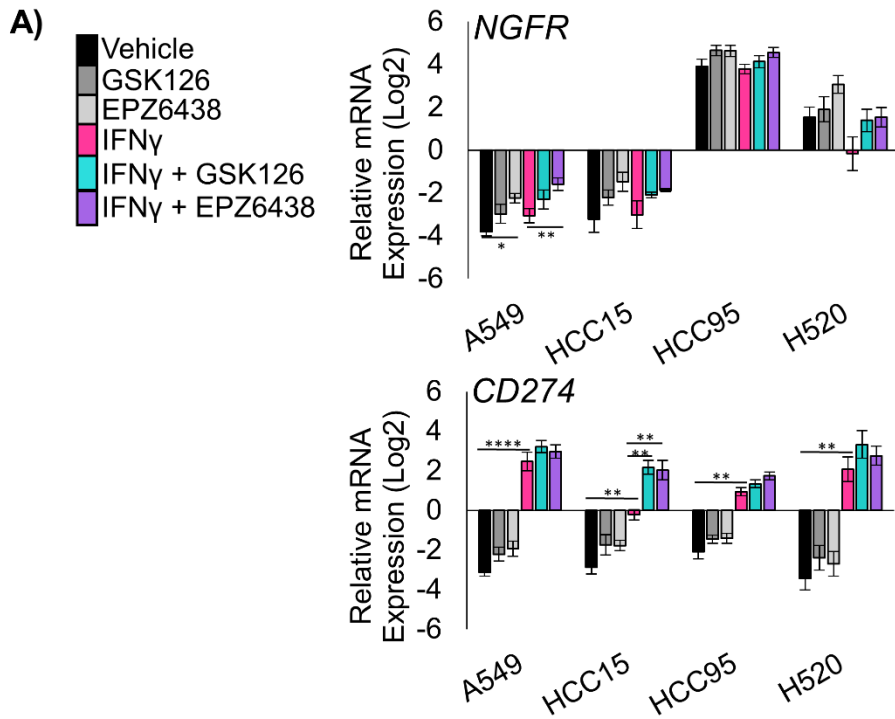
Group	MSigDB Signature Name	aPD1 vs Placebo								
		Macs/Dend		Neus		Tumor				
		NES	FDR q-Log(q)	NES	FDR q-Log(q)	NES	FDR q-Log(q)			
DNA Replication and Damage	REACTOME_G1_S_DNA_DAMAGE_CHECKPOINTS.v2022.1.Hs.grp	2.15	0.00	4.00	1.81	0.00	2.45	0.83	0.81	0.09
	REACTOME_ORC1_REMOVAL_FROM_CHROMATIN.v2022.1.Hs.grp	2.32	0.00	4.00	1.73	0.01	2.06	0.80	0.84	0.07
	REACTOME_SWITCHING_OF_ORIGINS_TO_A_POST_REPLICATIVE_STATE.v2022.1.Hs.grp	2.24	0.00	4.00	1.65	0.02	1.81	0.75	0.88	0.05
	REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_ORIGIN_COMPLEX.v2022.1.Hs.grp	2.39	0.00	4.00	1.70	0.01	1.96	0.94	0.65	0.18
	REACTOME_SYNTHESIS_OF_DNA.v2022.1.Hs.grp	2.16	0.00	4.00	1.63	0.02	1.74	0.79	0.86	0.07
	REACTOME_APC_C_MEDIATED_DEGRADATION_OF_CELL_CYCLE_PROTEINS.v2022.1.Hs.grp	2.33	0.00	4.00	1.66	0.01	1.83	0.84	0.80	0.10
Protein and RNA Processing	KEGG_RIBOSOME.v2022.1.Hs.grp	3.25	0.00	4.00	3.40	0.00	4.00	2.48	0.00	4.00
	REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION.v2022.1.Hs.grp	3.17	0.00	4.00	3.35	0.00	4.00	2.50	0.00	4.00
	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE.v2022.1.Hs.grp	3.04	0.00	4.00	3.33	0.00	4.00	2.46	0.00	4.00
	REACTOME_RESPONSE_OF_EIF2AK4_GCN2_TO_AMINO_ACID_DEFICIENCY.v2022.1.Hs.grp	3.00	0.00	4.00	3.28	0.00	4.00	2.22	0.00	4.00
	REACTOME_EUKARYOTIC_TRANSLATION_INITIATION.v2022.1.Hs.grp	2.91	0.00	4.00	3.37	0.00	4.00	2.41	0.00	4.00
	REACTOME_INFLUENZA_INFECTION.v2022.1.Hs.grp	2.63	0.00	4.00	3.27	0.00	4.00	2.34	0.00	4.00
	GOBP_CYTOPLASMIC_TRANSLATION.v2022.1.Hs.grp	2.67	0.00	4.00	3.32	0.00	4.00	2.39	0.00	4.00
	REACTOME_TRANSLATION.v2022.1.Hs.grp	2.54	0.00	4.00	3.23	0.00	4.00	2.29	0.00	4.00
	REACTOME_SELENOAMINO_ACID_METABOLISM.v2022.1.Hs.grp	3.05	0.00	4.00	3.35	0.00	4.00	2.41	0.00	4.00
	REACTOME_CELLULAR_RESPONSE_TO_STARVATION.v2022.1.Hs.grp	2.85	0.00	4.00	3.25	0.00	4.00	2.17	0.00	4.00
	REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES.v2022.1.Hs.grp	2.58	0.00	4.00	3.16	0.00	4.00	2.00	0.00	4.00
	REACTOME_NONSENSE_MEDIATED_DECAY_NMD.v2022.1.Hs.grp	2.90	0.00	4.00	3.38	0.00	4.00	2.42	0.00	4.00
	REACTOME_RRNA_PROCESSING.v2022.1.Hs.grp	2.62	0.00	4.00	3.29	0.00	4.00	2.38	0.00	4.00
Oxidative Phosphorylation	GOBP_AEROBIC_RESPIRATION.v2022.1.Hs.grp	-1.04	0.47	0.33	0.98	0.58	0.24	1.64	0.01	1.96
	GOBP_OXIDATIVE_PHOSPHORYLATION.v2022.1.Hs.grp	-1.05	0.45	0.34	0.96	0.61	0.21	1.71	0.00	2.32
	GOBP_ATP_SYNTHESIS_COUPLED_ELECTRON_TRANSPORT.v2022.1.Hs.grp	-1.14	0.32	0.49	0.87	0.75	0.12	1.62	0.01	1.89
	GOBP_RESPIRATORY_ELECTRON_TRANSPORT_CHAIN.v2022.1.Hs.grp	-1.15	0.32	0.50	1.03	0.50	0.30	1.61	0.01	1.85
	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCED_BY_UNCOUPLING_PROTEINS.v2022.1.Hs.grp	-1.11	0.36	0.44	0.93	0.66	0.18	1.77	0.00	2.64
	GOBP_ATP_BIOSYNTHETIC_PROCESS.v2022.1.Hs.grp	-0.98	0.55	0.26	1.12	0.38	0.42	1.73	0.00	2.44
	REACTOME_THE_CITRIC_ACID_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT.v2022.1.Hs.grp	-1.19	0.27	0.57	1.08	0.43	0.36	1.69	0.01	2.18
	GOBP_ELECTRON_TRANSPORT_CHAIN.v2022.1.Hs.grp	-1.17	0.29	0.54	0.74	0.93	0.03	1.57	0.02	1.64
	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT.v2022.1.Hs.grp	-1.14	0.32	0.50	0.75	0.92	0.04	1.65	0.01	1.97
	KEGG_OXIDATIVE_PHOSPHORYLATION.v2022.1.Hs.grp	-1.26	0.19	0.72	1.39	0.09	1.03	1.75	0.00	2.56
	REACTOME_COMPLEX_I_BIOGENESIS.v2022.1.Hs.grp	-1.04	0.46	0.34	0.64	0.98	0.01	1.38	0.10	1.00
Myeloid Migration	GOBP_NEUTROPHIL_MIGRATION.v2022.1.Hs.grp	-2.07	0.00	4.00	-1.38	0.13	0.89	-2.21	0.00	4.00
	GOBP_MYELOID_LEUKOCYTE_MIGRATION.v2022.1.Hs.grp	-2.11	0.00	4.00	-1.61	0.05	1.28	-1.91	0.00	2.81
	GOBP_NEUTROPHIL_CHEMOTAXIS.v2022.1.Hs.grp	-2.06	0.00	4.00	-1.45	0.10	1.00	-2.14	0.00	4.00
	GOBP_GRANULOCYTE_MIGRATION.v2022.1.Hs.grp	-2.16	0.00	4.00	-1.62	0.05	1.27	-2.08	0.00	3.99
	GOBP_LEUKOCYTE_CHEMOTAXIS.v2022.1.Hs.grp	-1.95	0.00	3.67	-1.86	0.01	1.85	-1.98	0.00	3.28
	GOBP_GRANULOCYTE_CHEMOTAXIS.v2022.1.Hs.grp	-2.15	0.00	4.00	-1.73	0.03	1.55	-2.01	0.00	3.44
	GOBP_CELL_CHEMOTAXIS.v2022.1.Hs.grp	-1.91	0.00	3.35	-2.09	0.00	2.62	-1.83	0.00	2.51
	GOBP_LEUKOCYTE_MIGRATION.v2022.1.Hs.grp	-1.97	0.00	3.86	-1.91	0.01	1.99	-1.81	0.00	2.38
	GOBP_TAXIS.v2022.1.Hs.grp	-1.87	0.00	3.06	-1.96	0.01	2.07	-1.75	0.01	2.18
Myeloid Activation	GOBP_GRANULOCYTE_ACTIVATION.v2022.1.Hs.grp	-1.56	0.03	1.55	-1.50	0.09	1.06	-1.51	0.04	1.39
	GOBP_POSITIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION.v2022.1.Hs.grp	-1.67	0.01	2.02	-2.28	0.00	3.23	-1.78	0.00	2.31
	GOBP_REGULATION_OF_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY.v2022.1.Hs.grp	-0.87	0.72	0.15	0.69	0.96	0.02	-1.87	0.00	2.65
	GOBP_LEUKOCYTE_MEDIATED_CYTOTOXICITY.v2022.1.Hs.grp	-0.84	0.75	0.13	-1.13	0.32	0.49	-1.68	0.01	1.92
	GOBP_FC_RECEPTOR_SIGNALING_PATHWAY.v2022.1.Hs.grp	-0.95	0.60	0.22				-1.27	0.15	0.83
	GOBP_REGULATION_OF_LEUKOCYTE_MEDIATED_CYTOTOXICITY.v2022.1.Hs.grp	1.01	0.42	0.38	-1.17	0.30	0.52	-1.87	0.00	2.66
Inflammation	GOBP_RESPONSE_TO_CHEMOKINE.v2022.1.Hs.grp	-2.07	0.00	4.00	-1.68	0.03	1.46	-1.80	0.00	2.31
	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION.v2022.1.Hs.grp	-1.80	0.00	2.60	-1.69	0.03	1.48	-2.23	0.00	4.00
	HALLMARK_IL6_JAK_STAT3_SIGNALING.v2022.1.Hs.grp	-1.72	0.01	2.23	-1.56	0.06	1.19	-1.91	0.00	2.80
		-1.15	0.30	0.52	0.73	0.93	0.03	-1.34	0.10	1.00
	GOBP_NEGATIVE_REGULATION_OF_VIRAL_GENOME_REPLICATION.v2022.1.Hs.grp	-1.48	0.06	1.24	-1.60	0.05	1.28	-2.10	0.00	4.00
	GOBP_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION.v2022.1.Hs.grp	-1.41	0.08	1.07	-1.08	0.38	0.42	-1.48	0.05	1.32
	HALLMARK_TNFA_SIGNALING_VIA_NFKB.v2022.1.Hs.grp	-2.32	0.00	4.00	-2.33	0.00	2.93	-1.87	0.00	2.63
	REACTOME_INTERFERON_ALPHA_BETA_SIGNALING.v2022.1.Hs.grp	-1.29	0.16	0.79	-1.79	0.02	1.70	-2.28	0.00	4.00
	HALLMARK_INTERFERON_ALPHA_RESPONSE.v2022.1.Hs.grp	-1.39	0.09	1.04	-1.15	0.32	0.49	-2.46	0.00	4.00
	HALLMARK_INTERFERON_GAMMA_RESPONSE.v2022.1.Hs.grp	-1.43	0.08	1.12	-1.04	0.41	0.38	-2.18	0.00	4.00
	GOBP_ACUTE_INFLAMMATORY_RESPONSE.v2022.1.Hs.grp	-1.37	0.11	0.98	-1.90	0.01	2.01	-1.77	0.01	2.24
	HALLMARK_ALLOGRAFT_REJECTION.v2022.1.Hs.grp	-1.40	0.09	1.06	-1.13	0.32	0.49	-1.62	0.02	1.75
	HALLMARK_INFLAMMATORY_RESPONSE.v2022.1.Hs.grp	-2.14	0.00	4.00	-1.61	0.05	1.29	-1.88	0.00	2.65

Supplemental Table 6: Genes Highly Expressed in Neutrophil Clusters, Related to Figure 6
Log2FC=Log2-fold change between cluster and all others, pct=percentage of cells expressing

Gene							Gene						
Cluster	Symbol	Log2FC	pct.1	pct.2	P value	Adj P value	Cluster	Symbol	Log2FC	pct.1	pct.2	P value	Adj P value
Neu-1	Cst3	2.050	0.929	0.784	0.0E+00	0.0E+00	Neu-3	Gadd45b	2.421	0.877	0.664	0.0E+00	0.0E+00
	Gngt2	1.920	0.812	0.557	0.0E+00	0.0E+00		Nceh1	2.367	0.856	0.760	0.0E+00	0.0E+00
	Hexb	1.393	0.794	0.754	0.0E+00	0.0E+00		Gpnmb	2.274	0.781	0.565	0.0E+00	0.0E+00
	Gpx1	1.277	0.869	0.823	0.0E+00	0.0E+00		Psap	2.244	0.852	0.718	0.0E+00	0.0E+00
	Ptgs1	1.126	0.772	0.702	0.0E+00	0.0E+00		Ifrd1	2.039	0.819	0.707	0.0E+00	0.0E+00
	Ms4a6d	0.881	0.805	0.780	0.0E+00	0.0E+00		Hilpda	2.038	0.836	0.799	0.0E+00	0.0E+00
	Gm19951	0.635	0.840	0.837	0.0E+00	0.0E+00		Ccl3	1.982	0.920	0.759	0.0E+00	0.0E+00
	Cenpx	0.430	0.745	0.593	0.0E+00	0.0E+00		Atp6v1c1	1.914	0.857	0.766	0.0E+00	0.0E+00
	Hist1h4d	0.351	0.793	0.747	0.0E+00	0.0E+00		Lamp1	1.832	0.885	0.784	0.0E+00	0.0E+00
	Ranbp1	0.333	0.704	0.546	0.0E+00	0.0E+00		Hcar2	1.829	0.884	0.824	0.0E+00	0.0E+00
	Card11	0.298	0.831	0.810	0.0E+00	0.0E+00		Ctsb	1.789	0.977	0.916	0.0E+00	0.0E+00
	Hist1h1d	0.297	0.697	0.506	0.0E+00	0.0E+00		Cd63	1.786	0.936	0.864	0.0E+00	0.0E+00
	Dmkn	0.263	0.794	0.646	0.0E+00	0.0E+00		Zeb2	1.742	0.829	0.553	0.0E+00	0.0E+00
	Cpt1a	0.256	0.724	0.482	0.0E+00	0.0E+00		Ctsz	1.678	0.936	0.850	0.0E+00	0.0E+00
	H1f0	0.809	0.700	0.554	4.0E-279	5.9E-276		Ftl1	1.590	1.000	0.999	0.0E+00	0.0E+00
	Laptm5	0.807	0.829	0.784	8.0E-255	1.2E-251		F10	1.513	0.863	0.864	0.0E+00	0.0E+00
	Asah1	0.427	0.666	0.444	2.5E-208	3.7E-205		Gas2l3	1.194	0.818	0.737	0.0E+00	0.0E+00
	Atp1a1	1.115	0.779	0.714	3.2E-204	4.8E-201		Dock10	1.193	0.783	0.789	0.0E+00	0.0E+00
	Pmaip1	0.631	0.787	0.697	2.3E-202	3.5E-199		Lhfp12	1.059	0.784	0.606	0.0E+00	0.0E+00
	Hist1h1e	0.525	0.794	0.723	2.0E-201	2.9E-198		P2rx7	0.743	0.760	0.628	0.0E+00	0.0E+00
	Atp5g1	0.535	0.667	0.503	3.9E-197	5.8E-194		Pdxk	0.707	0.726	0.490	0.0E+00	0.0E+00
	Ltc4s	0.855	0.644	0.562	2.4E-193	3.5E-190		Gstm1	0.948	0.697	0.537	5.0E-285	7.5E-282
	Ptma	1.199	0.760	0.667	4.4E-184	6.5E-181		Tst	0.523	0.688	0.501	9.7E-282	1.5E-278
	Reep5	0.947	0.749	0.636	1.4E-175	2.1E-172		Hexa	1.286	0.839	0.735	4.4E-268	6.5E-265
	Fam96a	0.381	0.589	0.440	2.4E-164	3.7E-161		Atp6v0d2	0.978	0.752	0.684	3.5E-267	5.3E-264
	Cd81	0.475	0.278	0.442	2.2E-155	3.3E-152		Dhfr	0.859	0.789	0.859	3.2E-265	4.7E-262
	Rps2	0.817	0.873	0.819	8.0E-152	1.2E-148		Chka	0.492	0.738	0.529	2.2E-261	3.2E-258
	Chil3	1.278	0.842	0.760	4.3E-130	6.4E-127		Plcx2	0.704	0.728	0.788	1.7E-250	2.5E-247
	Agap1	0.711	0.586	0.439	4.9E-117	7.3E-114		Fcgr2b	0.662	0.838	0.714	5.9E-241	8.8E-238
	Cd302	0.256	0.296	0.474	2.5E-116	3.8E-113		Gns	1.455	0.782	0.705	7.0E-240	1.1E-236
	Cd300c2	0.778	0.716	0.616	2.5E-111	3.8E-108		Ctsd	0.702	0.987	0.976	1.2E-220	1.8E-217
	Lrp1	0.630	0.529	0.374	2.7E-108	4.0E-105		Atf3	1.518	0.679	0.486	1.4E-214	2.2E-211
	Krt19	0.266	0.659	0.814	1.1E-103	1.7E-100		Npc1	1.184	0.749	0.753	6.1E-211	9.1E-208
	Hebp1	0.441	0.646	0.524	5.1E-103	7.6E-100		Aprt	1.030	0.820	0.695	1.5E-210	2.3E-207
	Ccnd2	0.297	0.487	0.674	3.5E-88	5.2E-85		Cd68	1.480	0.714	0.531	1.7E-208	2.6E-205
	Ssbp4	0.336	0.596	0.543	6.5E-87	9.8E-84		Canx	0.895	0.769	0.640	1.5E-207	2.3E-204
	Tcf4	0.262	0.442	0.288	1.4E-86	2.1E-83		Cd274	1.443	0.725	0.671	2.9E-205	4.3E-202
	Dpep2	0.452	0.652	0.764	1.9E-86	2.8E-83		Plekhm2	1.059	0.785	0.766	4.3E-197	6.4E-194
	Grn	0.508	0.869	0.830	2.0E-84	2.9E-81		Prdx1	1.174	0.673	0.462	6.6E-191	9.9E-188
	Calr	0.613	0.710	0.613	1.3E-82	1.9E-79		Tpp1	1.030	0.716	0.620	1.2E-185	1.8E-182
	B930036N10Ri	0.429	0.642	0.682	1.8E-82	2.7E-79		Naglu	0.956	0.616	0.469	3.1E-165	4.6E-162
	Naaa	0.466	0.655	0.600	1.6E-81	2.4E-78		H2-Eb1	0.929	0.683	0.729	7.5E-150	1.1E-146
	Pgls	0.322	0.607	0.512	2.7E-81	4.0E-78		Dhrs3	0.764	0.674	0.525	6.6E-145	9.9E-142
	Id2	0.400	0.925	0.882	1.7E-75	2.6E-72		Dnmt1	0.341	0.626	0.526	3.8E-137	5.7E-134
	Bcl2a1b	0.796	0.640	0.563	8.2E-75	1.2E-71		Npc2	1.027	0.875	0.886	1.8E-132	2.7E-129
Ctsa	0.531	0.744	0.686	2.7E-68	4.0E-65	Tmem86a	0.556	0.724	0.748	2.4E-128	3.5E-125		
Manf	0.354	0.814	0.794	6.8E-68	1.0E-64	Gadd45g	1.393	0.634	0.509	5.6E-122	8.4E-119		
Cybb	0.303	0.519	0.409	4.6E-65	6.8E-62	Id2	0.969	0.874	0.904	4.8E-121	7.2E-118		
Gm26917	0.282	0.585	0.474	1.5E-61	2.2E-58	Hpgds	0.522	0.680	0.724	9.2E-119	1.4E-115		
Ndufa4	0.667	0.623	0.564	1.9E-60	2.9E-57	Inhba	0.874	0.622	0.511	6.6E-114	9.9E-111		
Hist1h1c	0.752	0.664	0.572	3.1E-58	4.7E-55	Tcirg1	1.016	0.670	0.594	1.6E-112	2.5E-109		
Bcl2a1a	0.768	0.592	0.516	3.8E-58	5.7E-55	Lgmn	0.951	0.627	0.518	1.4E-111	2.1E-108		
Gm2a	0.892	0.637	0.616	1.3E-56	2.0E-53	Ccnf	0.540	0.662	0.781	5.7E-109	8.6E-106		
Phlda1	0.268	0.391	0.530	1.3E-55	1.9E-52	Creg1	1.377	0.702	0.577	1.2E-106	1.9E-103		
Mt1	0.286	0.750	0.734	4.5E-55	6.8E-52	Myo5a	0.533	0.480	0.319	2.3E-99	3.5E-96		
Hist1h4i	0.880	0.646	0.592	5.1E-54	7.6E-51	Mpeg1	0.803	0.701	0.585	5.7E-99	8.5E-96		

Nap1l1	0.311	0.514	0.434	7.4E-52	1.1E-48	Ccl4	1.163	0.868	0.935	3.7E-95	5.6E-92		
Ccng1	0.519	0.520	0.461	1.5E-51	2.2E-48	Syng1	0.793	0.721	0.791	7.6E-92	1.1E-88		
Unc93b1	0.566	0.570	0.493	1.8E-51	2.6E-48	Aplp2	0.334	0.718	0.588	7.3E-91	1.1E-87		
Pycard	0.298	0.870	0.846	2.1E-51	3.1E-48	Hmx1	1.205	0.790	0.778	9.1E-85	1.4E-81		
P2ry6	0.379	0.710	0.721	1.9E-50	2.9E-47	Hspa9	0.589	0.651	0.663	2.2E-81	3.4E-78		
Tubb5	0.364	0.356	0.505	2.0E-50	3.0E-47	Hspa5	0.742	0.800	0.740	2.0E-80	2.9E-77		
Tubb4b	0.403	0.662	0.575	5.7E-48	8.6E-45	Dpp7	0.502	0.624	0.692	1.0E-72	1.5E-69		
Pdia6	0.555	0.775	0.771	7.2E-48	1.1E-44	Hsp90b1	0.441	0.736	0.690	3.7E-72	5.5E-69		
Gm20186	0.390	0.404	0.535	4.5E-47	6.7E-44	Rgs1	0.942	0.774	0.774	7.5E-70	1.1E-66		
Ucp2	0.715	0.743	0.739	8.8E-42	1.3E-38	Hk2	0.381	0.466	0.660	4.3E-69	6.4E-66		
Clec12a	0.455	0.481	0.424	1.0E-39	1.6E-36	Sqstm1	0.921	0.608	0.494	1.2E-67	1.8E-64		
Colgalt1	0.261	0.486	0.423	4.1E-39	6.1E-36	Emp1	0.827	0.723	0.773	6.3E-65	9.4E-62		
Cks2	0.955	0.534	0.469	1.2E-36	1.8E-33	Rps2	0.628	0.867	0.830	3.3E-63	4.9E-60		
Rpn1	0.256	0.347	0.457	3.6E-31	5.3E-28	Hspa1b	0.866	0.659	0.604	4.8E-63	7.2E-60		
Id1	0.318	0.832	0.819	1.9E-28	2.8E-25	Fam20c	0.379	0.847	0.869	2.1E-60	3.1E-57		
Fam20c	0.332	0.792	0.904	6.0E-27	9.0E-24	Slc37a2	0.582	0.609	0.576	3.5E-55	5.3E-52		
Ctsc	0.283	0.661	0.629	8.2E-26	1.2E-22	Ctsl	0.651	0.807	0.742	5.6E-54	8.4E-51		
Lamtor4	0.498	0.641	0.610	1.3E-25	2.0E-22	Fabp5	0.488	0.626	0.784	3.1E-49	4.6E-46		
Csf1r	0.363	0.280	0.375	2.1E-25	3.2E-22	Ctsa	0.516	0.748	0.695	6.2E-49	9.3E-46		
Rhoc	0.353	0.529	0.648	1.6E-24	2.4E-21	Hsp90aa1	1.357	0.762	0.791	1.2E-48	1.8E-45		
Cdc42ep3	0.331	0.512	0.462	5.0E-23	7.5E-20	Tim2	1.159	0.724	0.658	9.5E-47	1.4E-43		
Krt18	0.259	0.611	0.616	1.1E-21	1.7E-18	Hal	0.601	0.514	0.776	7.5E-29	1.1E-25		
Rgs1	0.444	0.650	0.843	6.1E-21	9.2E-18	Cldn1	0.594	0.582	0.669	4.4E-28	6.6E-25		
H2afz	0.536	0.744	0.728	1.6E-19	2.5E-16	Jdp2	0.437	0.670	0.653	2.7E-25	4.0E-22		
Rpl3	0.306	0.538	0.517	1.6E-16	2.4E-13	Acod1	0.845	0.548	0.530	8.1E-24	1.2E-20		
Hist1h2ap	0.291	0.508	0.492	1.7E-16	2.5E-13	Slc7a11	0.925	0.565	0.555	1.8E-23	2.7E-20		
Mpeg1	0.501	0.595	0.621	2.6E-16	3.8E-13	Gm	0.382	0.873	0.835	1.8E-21	2.8E-18		
Cfp	0.260	0.543	0.504	1.5E-15	2.2E-12	Vegfa	0.831	0.495	0.452	1.0E-20	1.6E-17		
Tubb6	0.260	0.394	0.341	4.6E-14	7.0E-11	Gm26870	0.478	0.567	0.719	2.0E-19	3.0E-16		
Erp29	0.740	0.600	0.627	1.3E-13	2.0E-10	Gusb	0.335	0.618	0.634	2.3E-19	3.5E-16		
Fyb	0.264	0.751	0.780	2.7E-10	4.0E-07	Cd300c2	0.375	0.675	0.645	4.3E-19	6.5E-16		
Spp1	0.341	0.831	0.843	3.7E-09	5.5E-06	Hspe1	0.432	0.639	0.663	1.4E-15	2.1E-12		
Atad2	0.270	0.495	0.481	4.1E-09	6.2E-06	Slc43a3	0.361	0.577	0.707	1.5E-15	2.3E-12		
Bcl2a1d	0.651	0.380	0.413	7.1E-08	1.1E-04	Abcg1	0.435	0.571	0.559	2.1E-15	3.2E-12		
S100a10	0.397	0.513	0.610	3.7E-07	5.6E-04	Syne1	0.692	0.511	0.667	2.2E-14	3.3E-11		
Ctss	0.529	0.679	0.716	6.8E-07	1.0E-03	Rps6ka2	0.368	0.521	0.558	4.6E-14	6.8E-11		
Apoe	0.328	0.748	0.737	8.0E-06	1.2E-02	Flt1-ps1	0.479	0.338	0.347	1.7E-11	2.5E-08		
Tnf	0.345	0.327	0.311	8.5E-06	1.3E-02	C3	0.346	0.632	0.634	4.3E-11	6.5E-08		
Gm12840	1.062	0.321	0.302	6.5E-05	9.7E-02	Thbs1	1.191	0.451	0.593	1.1E-09	1.6E-06		
Pou2f2	0.584	0.387	0.411	7.3E-04	1.0E+00	Hbb-bs	0.414	0.804	0.812	3.3E-09	5.0E-06		
Aprt	0.360	0.639	0.770	1.4E-03	1.0E+00	Rpl3	0.505	0.532	0.522	5.9E-09	8.8E-06		
Abca1	0.524	0.768	0.829	4.0E-03	1.0E+00	Acp5	0.601	0.473	0.461	1.5E-03	1.0E+00		
Tgfb1	0.309	0.586	0.654	5.9E-03	1.0E+00	Hspa1a	0.817	0.527	0.564	1.7E-03	1.0E+00		
Acp5	0.644	0.451	0.471	7.0E-03	1.0E+00	Spp1	1.001	0.762	0.862	5.5E-03	1.0E+00		
Neu-2	BC100530	1.757	0.815	0.739	0.0E+00	0.0E+00	Neu-5-IFN	lsg15	3.959	0.914	0.574	8.6E-166	1.3E-162
	Gm5483	1.712	0.938	0.789	0.0E+00	0.0E+00		Rsad2	3.922	0.893	0.799	5.5E-153	8.3E-150
	Wfdc17	1.379	0.993	0.891	0.0E+00	0.0E+00		lfi47	2.686	0.858	0.765	3.1E-121	4.7E-118
	Cxcl2	1.173	0.951	0.703	0.0E+00	0.0E+00		lfitm3	2.227	0.937	0.742	1.4E-114	2.1E-111
	lfitm1	1.111	0.963	0.776	0.0E+00	0.0E+00		Gbp2	3.371	0.883	0.701	2.0E-112	3.0E-109
	Lrg1	0.856	0.929	0.751	0.0E+00	0.0E+00		lfit2	1.589	0.827	0.776	2.5E-109	3.8E-106
	Egr1	0.840	0.912	0.633	0.0E+00	0.0E+00		Rtp4	2.640	0.820	0.711	1.3E-94	1.9E-91
	Retnlg	0.817	0.960	0.812	0.0E+00	0.0E+00		Slfn4	2.454	0.848	0.736	8.9E-90	1.3E-86
	Wfdc21	0.764	0.945	0.788	0.0E+00	0.0E+00		Slfn5	2.495	0.787	0.619	1.1E-87	1.7E-84
	Ccl6	0.733	0.910	0.693	0.0E+00	0.0E+00		lfit1bl2	0.982	0.794	0.613	2.2E-77	3.3E-74
	Lcn2	0.710	0.911	0.736	0.0E+00	0.0E+00		lsg20	2.415	0.731	0.518	3.4E-64	5.1E-61
	Cxcl3	0.666	0.840	0.353	0.0E+00	0.0E+00		lfit1	3.118	0.693	0.425	1.5E-61	2.2E-58
	Tceal9	0.526	0.888	0.729	0.0E+00	0.0E+00		Zbp1	1.428	0.789	0.729	2.5E-60	3.7E-57
	Slfn4	0.469	0.942	0.649	0.0E+00	0.0E+00		lfi202b	0.654	0.739	0.617	3.0E-57	4.5E-54
	Id1	0.277	0.915	0.784	4.8E-284	7.2E-281		lfit3b	2.094	0.698	0.535	7.2E-57	1.1E-53
	Slpi	0.579	0.904	0.662	4.9E-284	7.3E-281		Oasl1	2.280	0.668	0.414	6.9E-56	1.0E-52
	Dgat2	0.449	0.795	0.605	5.1E-282	7.6E-279		lfit3	3.099	0.612	0.263	4.7E-39	7.0E-36
	Adam8	1.014	0.729	0.463	8.4E-262	1.3E-258		Cldn1	0.258	0.777	0.646	1.1E-38	1.6E-35
	Prok2	0.277	0.790	0.700	4.3E-239	6.4E-236		Bst2	1.698	0.657	0.525	6.1E-38	9.1E-35
	Vim	0.636	0.831	0.556	1.3E-219	2.0E-216		Ctss	1.414	0.764	0.701	7.1E-37	1.1E-33
	G0s2	0.703	0.819	0.568	3.6E-170	5.3E-167		Fcgr4	0.876	0.812	0.699	1.1E-32	1.6E-29
	Glrx	0.709	0.678	0.390	5.3E-170	7.9E-167		Cmpk2	1.332	0.647	0.692	9.6E-30	1.4E-26

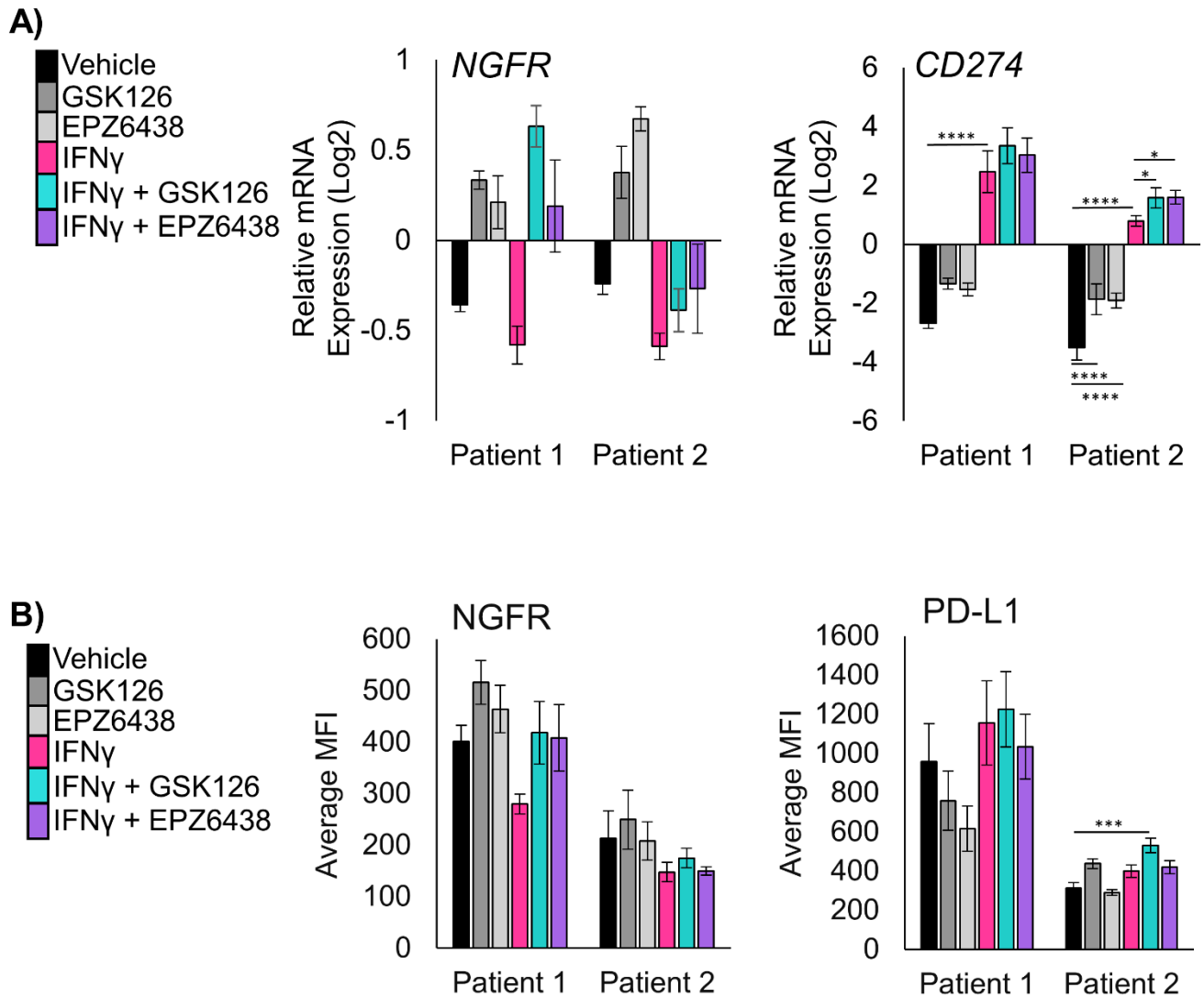
	F630028O10Ril	0.557	0.798	0.542	6.6E-167	9.8E-164		Clec4a3	0.377	0.614	0.450	1.1E-28	1.6E-25
	Ier3	0.594	0.972	0.826	5.5E-157	8.2E-154		Acod1	0.910	0.764	0.528	9.0E-26	1.3E-22
	Steap4	0.560	0.732	0.674	8.3E-127	1.2E-123		Ii18	0.463	0.556	0.366	4.8E-23	7.2E-20
	Gadd45a	0.551	0.731	0.616	2.4E-122	3.6E-119		Fxyd3	0.255	0.571	0.443	7.7E-23	1.2E-19
	Stfa2l1	1.367	0.682	0.553	2.0E-118	3.0E-115		Irf7	1.505	0.642	0.564	5.3E-21	7.9E-18
	Csf2rb	0.259	0.921	0.714	1.3E-114	1.9E-111		Ii18bp	0.433	0.508	0.318	7.1E-20	1.1E-16
	Stfa2	0.989	0.680	0.704	2.8E-87	4.2E-84		Cxcl10	1.827	0.551	0.388	8.9E-20	1.3E-16
	Ii1f9	0.250	0.718	0.540	2.8E-75	4.3E-72		Lair1	0.305	0.609	0.516	8.0E-19	1.2E-15
	Asprv1	0.555	0.707	0.722	3.9E-33	5.8E-30		Gm4316	0.443	0.279	0.343	1.0E-17	1.5E-14
	Saa3	0.387	0.748	0.691	3.2E-27	4.7E-24		Npc2	0.571	0.904	0.883	1.2E-17	1.9E-14
	Tacstd2	0.305	0.584	0.468	3.7E-24	5.5E-21		Gbp5	1.547	0.660	0.801	1.3E-17	1.9E-14
	Osm	0.506	0.460	0.331	1.0E-09	1.6E-06		AW112010	0.469	0.520	0.370	1.3E-17	1.9E-14
	Hacd4	0.294	0.496	0.406	4.6E-03	1.0E+00		Cd274	0.977	0.736	0.682	3.9E-16	5.9E-13
Neu-4-classic	Retnlg	3.329	0.993	0.845	0.0E+00	0.0E+00		Hes1	0.375	0.358	0.549	4.7E-16	7.0E-13
	Iifitn6	3.306	0.992	0.478	0.0E+00	0.0E+00		Iifi207	0.258	0.655	0.691	6.5E-15	9.7E-12
	Lcn2	2.827	0.999	0.771	0.0E+00	0.0E+00		Usp18	1.418	0.604	0.700	7.7E-15	1.2E-11
	Wfdc21	2.632	0.999	0.822	0.0E+00	0.0E+00		Abcg1	0.446	0.701	0.558	1.4E-13	2.2E-10
	Mmp8	2.622	0.971	0.633	0.0E+00	0.0E+00		Fyb	0.553	0.835	0.768	1.2E-12	1.8E-09
	Ly6g	2.187	0.944	0.567	0.0E+00	0.0E+00		Bcl2a1b	0.420	0.751	0.586	9.3E-11	1.4E-07
	Anxa1	2.167	0.997	0.716	0.0E+00	0.0E+00		Cxcl9	0.426	0.736	0.737	1.9E-08	2.8E-05
	Prok2	2.127	0.960	0.707	0.0E+00	0.0E+00		Iifi2712a	2.036	0.553	0.506	1.4E-07	2.1E-04
	Lrg1	1.793	0.992	0.789	0.0E+00	0.0E+00		Cybb	0.284	0.546	0.446	3.7E-07	5.5E-04
	Iifitn3	1.588	0.989	0.726	0.0E+00	0.0E+00		Ly6i	0.647	0.586	0.648	9.8E-07	1.5E-03
	Cd177	1.349	0.907	0.656	0.0E+00	0.0E+00		Plac8	1.572	0.533	0.491	1.0E-06	1.6E-03
	Ggt1	1.045	0.897	0.603	0.0E+00	0.0E+00		Mpeg1	0.339	0.726	0.608	2.2E-06	3.4E-03
	Glul	0.436	0.853	0.387	0.0E+00	0.0E+00		Emp3	0.292	0.447	0.314	2.4E-06	3.5E-03
	Gyg	0.996	0.863	0.596	8.3E-285	1.2E-281		Gm20234	0.310	0.609	0.679	2.7E-06	4.1E-03
	Wfdc17	1.832	0.997	0.916	2.1E-279	3.1E-276		Cst3	0.308	0.858	0.835	9.4E-06	1.4E-02
	Chil1	0.973	0.942	0.592	8.9E-269	1.3E-265		Ddx60	1.381	0.528	0.576	2.6E-05	3.9E-02
	Steap4	0.716	0.940	0.670	1.5E-254	2.2E-251		Iifi209	1.094	0.563	0.675	6.0E-05	9.0E-02
	Stfa2	1.185	0.909	0.678	2.8E-254	4.2E-251		Unc93b1	0.390	0.569	0.519	6.2E-05	9.3E-02
	Tgm1	0.493	0.865	0.635	2.0E-252	3.0E-249		Hba-a1	0.963	0.429	0.553	1.2E-04	1.7E-01
	Mgst1	0.981	0.870	0.580	2.4E-243	3.6E-240		Lyz2	0.310	0.838	0.771	1.9E-03	1.0E+00
	Flna	0.955	0.875	0.433	4.9E-242	7.4E-239		Ccl4	0.628	0.921	0.920	2.1E-03	1.0E+00
	Ngp	1.645	0.786	0.355	7.6E-234	1.1E-230		Ly6c2	1.048	0.482	0.460	3.0E-03	1.0E+00
	Slpi	1.162	0.978	0.715	2.2E-232	3.3E-229							
	Hacd4	1.004	0.822	0.400	5.4E-230	8.1E-227							
	Iifitn1	1.769	0.992	0.819	1.3E-203	2.0E-200							
	Ccl6	1.106	0.959	0.742	2.3E-188	3.5E-185							
	Smpd13a	0.852	0.826	0.558	3.0E-187	4.5E-184							
	Tuba1a	0.578	0.780	0.474	1.3E-175	1.9E-172							
	Vim	0.919	0.966	0.611	2.8E-175	4.1E-172							
	Syne1	0.469	0.810	0.615	7.0E-163	1.1E-159							
	Tgfb1	0.673	0.922	0.604	6.7E-159	1.0E-155							
	Glrx	0.596	0.853	0.445	1.3E-157	2.0E-154							
	Tacstd2	0.565	0.812	0.476	1.1E-141	1.7E-138							
	Pi16	0.611	0.785	0.543	5.7E-120	8.6E-117							
	Lyz2	0.426	0.978	0.755	2.3E-116	3.4E-113							
	Lmo4	0.573	0.715	0.315	5.2E-112	7.9E-109							
	Ly6c2	0.617	0.708	0.439	1.4E-109	2.1E-106							
	BC100530	1.364	0.877	0.752	3.0E-94	4.5E-91							
	Aldh2	0.324	0.698	0.433	2.9E-86	4.3E-83							
	Stfa2l1	0.440	0.835	0.571	5.3E-68	7.9E-65							
	Ceacam1	0.277	0.709	0.530	2.0E-64	3.0E-61							
	Plac8	0.327	0.668	0.476	5.6E-64	8.4E-61							
	Acvrl1	0.598	0.673	0.666	1.5E-62	2.3E-59							
	Camp	1.496	0.597	0.402	1.9E-49	2.9E-46							
	Serp1nb1a	0.774	0.616	0.519	1.8E-45	2.7E-42							
	Abcd2	0.289	0.621	0.535	1.2E-40	1.8E-37							
	Stfa3	0.395	0.382	0.646	1.5E-34	2.3E-31							
Sept9	0.260	0.546	0.375	1.8E-28	2.7E-25								
Olfm4	0.922	0.683	0.609	5.7E-22	8.6E-19								
Asprv1	0.255	0.706	0.718	2.2E-13	3.3E-10								
C130026I21Rik	0.253	0.399	0.417	2.3E-11	3.5E-08								



Supplementary Figure 1: Related to Figure 1

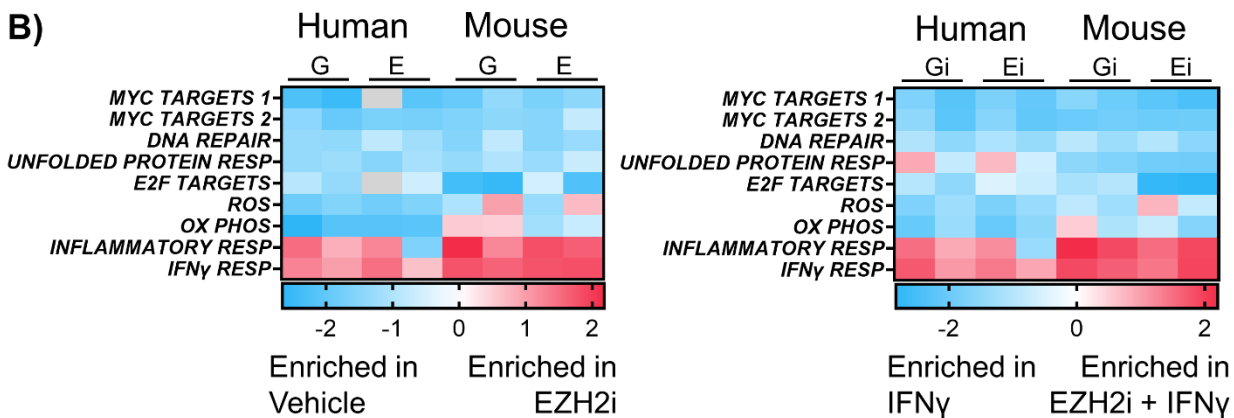
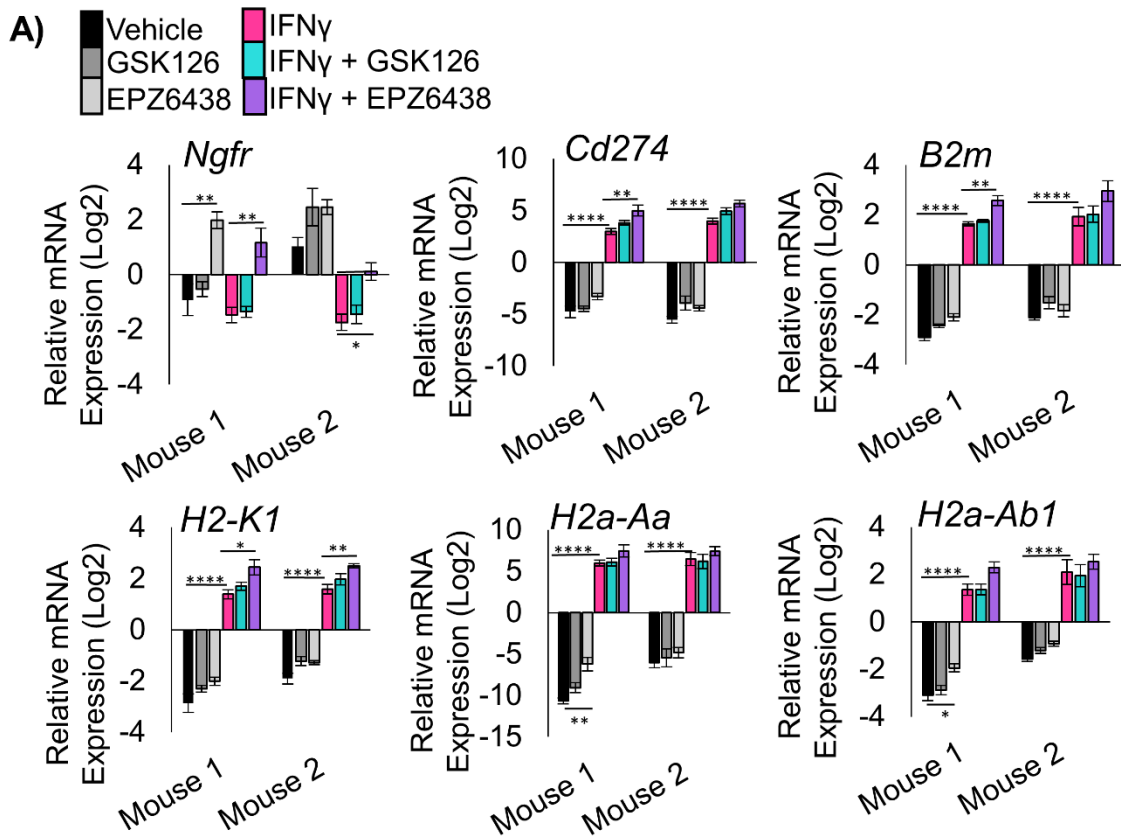
A) RT-qPCR in the indicated four human lung cancer cell lines treated for 7 days with vehicle or EZH2 inhibition with IFN γ added on day 5 for the genes *NGFR* and *CD274*, mean \pm SEM is graphed, n = 4 individual experiments, * indicated $p=0.0481$ ** $p<0.0098$, **** $p<0.0001$ by one-way ANOVA with pairwise comparisons and Holm-Šidák's *post hoc* test. **B)** Flow cytometry analysis of indicated four human lung cancer cell lines treated

for 6 days with vehicle or EZH2 inhibition with IFN γ added on day 5 for the cell surface proteins NGFR and PD-L1, mean \pm SEM is graphed, n = 4 individual experiments, * indicated p = 0.04, **p=0.0033, ***p<0.0003, ****p<0.0001 by one-way ANOVA with pairwise comparisons and Holm-Šidák's *post hoc* test.



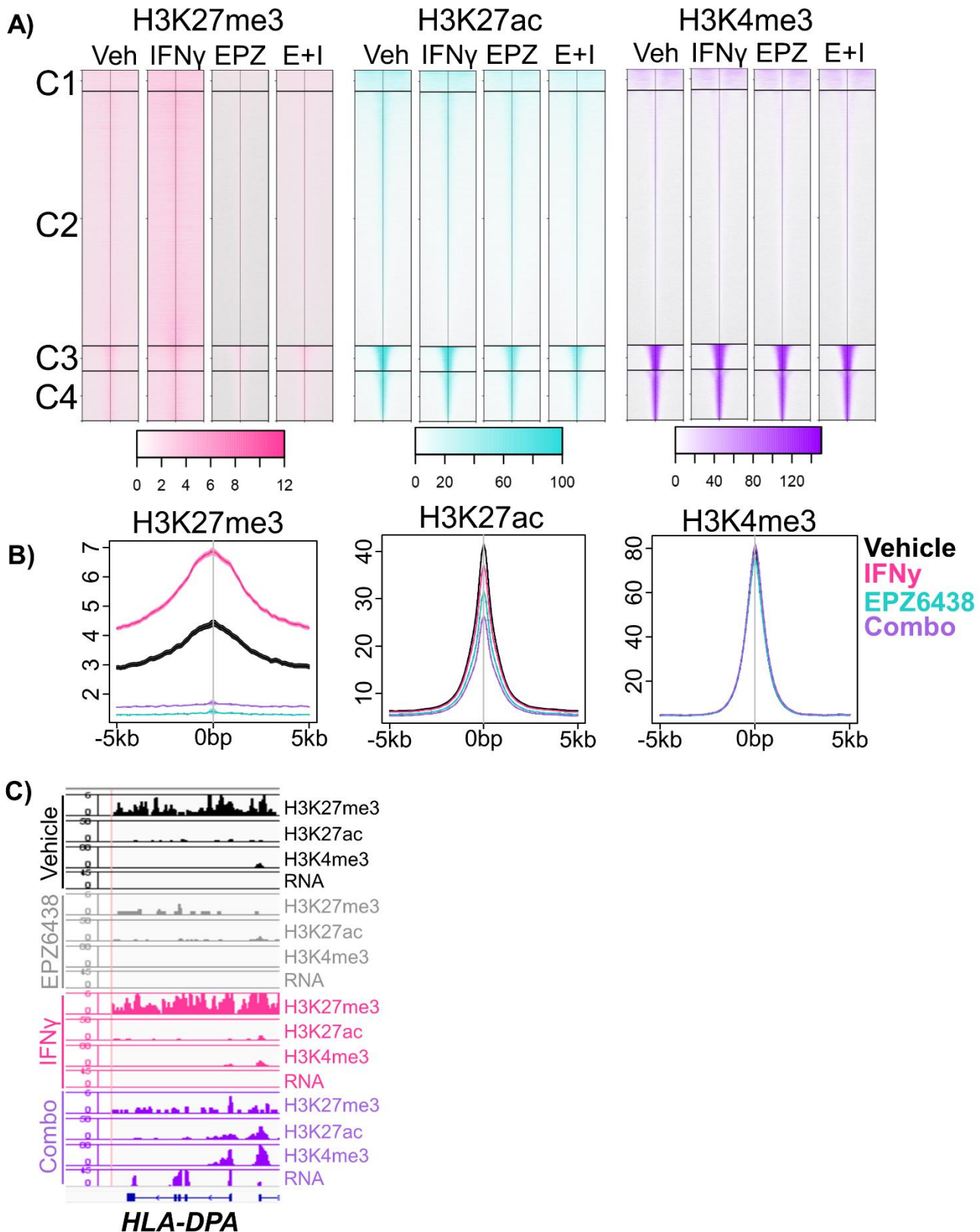
Supplementary Figure 2: Related to Figure 2

A) RT-qPCR in the indicated two unique patient-derived tumoroid cultures treated for 11 days and IFN γ added on day 9 for the genes *NGFR* and *CD274*, mean +/- SEM is graphed, n = 4 individual experiments, * indicates $p < 0.03$, **** $p < 0.0001$ by one-way ANOVA with pairwise comparisons and Holm-Šídák's *post hoc* test. **B)** Flow cytometry analysis of indicated two unique patient derived tumoroid cultures treated for 11 days and IFN γ added on day 9 for the cell surface proteins NGFR and PD-L1, mean +/- SEM is graphed, n = 4 individual experiments, *** indicates $p = 0.0002$ by one-way ANOVA with pairwise comparisons and Holm-Šídák's *post hoc* test.



Supplementary Figure 3: Related to Figure 3

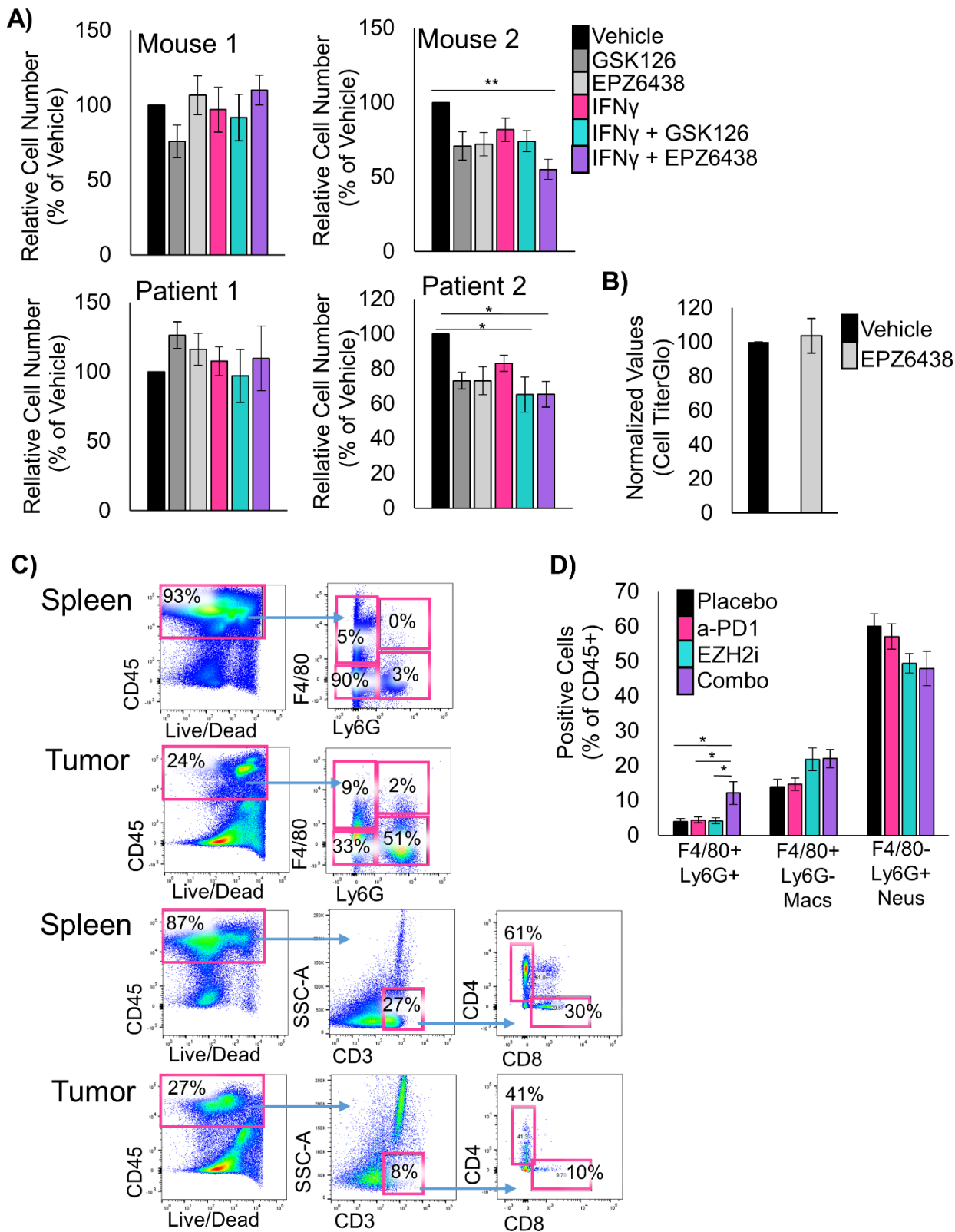
A) RT-qPCR in the indicated two unique murine tumoroid cultures treated for 11 days and IFN γ added on day 9 for the genes *Ngfr*, *B2m*, *H2-K1*, *Cd274*, and *H2a-Aa*, mean +/- SEM is graphed, n = 5 individual experiments for mouse 1, n=4 individual experiments for mouse 2, * indicates p<0.05, **p<0.009, ****p<0.0001 by one-way ANOVA with pairwise comparisons and Holm-Šidák's *post hoc* test. **B)** Heat map of Enrichment Scores using Gene Set Enrichment Analysis on human or murine tumoroids treated with the EZH2 inhibitors GSK126 (G) or EPZ6438 (E) contrasted to vehicle control, or treated with EZH2 inhibitor and IFN γ contrasted to IFN γ alone. See also Supp. Table 2.



Supplementary Figure 4: Related to Figure 4

A) Heatmap representation of H3K27me3-, H3K27ac- and H3K4me3-bound chromatin peaks centered across a ± 5 kb window that shows occupancy in tumoroids cultures of the indicated treatments. **B)** Histogram of merged

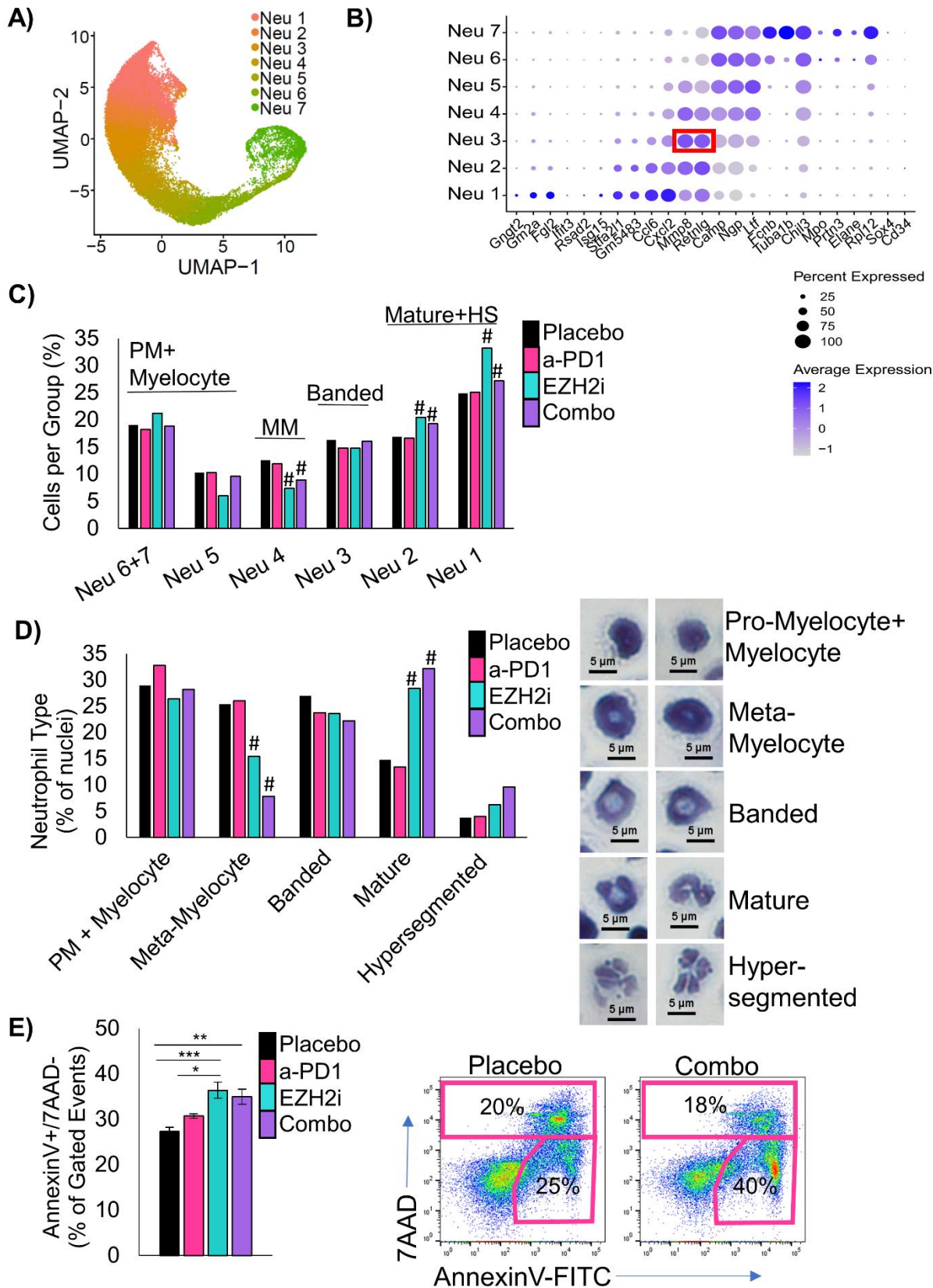
ChIP-seq peaks in the indicated 3D tumoroid samples. **C)** Wiggle plots for H3K27me3, H3K27ac, and H3K4me3 histone mark enrichments, and matched RNAseq tracks in patient-derived tumoroids from the indicated treatment groups for the gene *HLA-DPA*.



Supplementary Figure 5: Related to Figure 5

A) Relative counts of cells after dissociation of tumoroids treated with the indicated treatments, mean \pm s.e.m. is plotted, $n=4$ individual experiments for the human tumoroids, $n=7$ experiments for mouse 1 and $n=5$ experiments for mouse 2, * indicates $p<0.0250$, ** $p=0.0048$ by one-way ANOVA with multiple comparisons and

Holm-Šídák's *post-hoc* test. **B)** Relative luminescence from CellTiter Glo assayed tumoroid cultures treated with vehicle or EPZ6438, mean \pm s.e.m. is plotted, n=4 individual experiments. **C)** Representative flow cytometry plots with the indicated samples and markers. The left plots are gated on FSC/SSC and Live/Dead negative cells. Spleen samples are shown as staining controls. **D)** Flow cytometry analysis of dissociated tumors from the syngeneic grafts from the indicated treatment arms at day 14. Percentage of CD45+ cells expressing F4/80 or Ly6G are graphed, mean \pm s.e.m. is plotted, placebo n=8, EZH2 inhibitor n=8, anti-PD1 n=9, combo n=7, * indicates $p < 0.012$, by one-way ANOVA with multiple comparisons and Holm-Šídák's *post-hoc* test.



Supplementary Figure 6: Related to Figure 6

A) Annotated Uniform Manifold Approximation and Projection (UMAP) plot showing the 8 different populations of neutrophils within the bone marrow of tumor-bearing mice treated with placebo, GSK126, anti-PD1, or

combined GSK126 with anti-PD1. **B)** Dot plot showing the relative expression of marker genes (x-axis) in each neutrophil cluster (y-axis). Expression of *Mmp8* and *Rentlg* were shown to be enriched in banded neutrophils. **C)** Percentage of cells per treatment group graphed for the neutrophil populations, # indicates adjusted $p < 0.008$ by proportion z-test. **D)** Proportions of different nuclear morphologies in bone marrow cytopins, average of $n=2$ samples for Placebo, $n=1$ sample for others, 500 nuclei were counted, # indicates $p < 0.0004$ with Fisher's Exact test between Vehicle and EZH2 inhibitor or Vehicle and Placebo for meta-myelocyte vs mature neutrophils. Representative images of nuclei types shown, scale bar = $5\mu\text{m}$. **E)** Percentage of AnnexinV+/7AAD- cells in bone marrow cultures 48 hours post isolation from mice treated with the indicated therapies, $n=3$ biological replicates each with 2 experimental replicates for placebo, EPZ6438 and combo, $n=4$ biological replicates each with 2 experimental replicates for anti-PD1, * indicates $p=0.012$, ** $p=0.0017$, *** $p=0.0003$ by one-way ANOVA with pairwise comparisons and Holm-Šídák's *post-hoc* test. Representative flow plots of placebo and combination treated cultures shown.