

Gene Set	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	35	0.725	2.434	0	0	0	1026	tags=43%, list=14%, signal=50%
HALLMARK_INTERFERON_ALPHA_RESPONSE	29	0.626	2.026	0	0.026	0.293	1342	tags=55%, list=18%, signal=67%
RADAEVA_RESPONSE_TO_IFNA1_UP	18	0.695	2.016	0.003	0.027	0.323	1342	tags=61%, list=18%, signal=75%
GO_ANTIGEN_BINDING	147	0.451	2.001	0	0.031	0.379	1053	tags=34%, list=14%, signal=39%
GO_CELL_MIGRATION_INVOLVED_IN_SPROUTING_ANGIOGENESIS	31	0.595	1.979	0	0.040	0.493	836	tags=42%, list=11%, signal=47%
REACTOME_INTERFERON_ALPHA_BETA_SIGNALING	18	0.668	1.967	0	0.044	0.547	1261	tags=61%, list=17%, signal=74%
GO_REGULATION_OF_EPITHELIAL_CELL_APOPTOTIC_PROCESS	34	0.575	1.954	0	0.049	0.61	859	tags=41%, list=12%, signal=46%
HALLMARK_INTERFERON_GAMMA_RESPONSE	60	0.511	1.940	0	0.055	0.669	1691	tags=45%, list=23%, signal=58%
GO_CELLULAR_RESPONSE_TO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_S TIMULUS	28	0.598	1.904	0	0.076	0.808	1290	tags=64%, list=18%, signal=78%
GSE10325_CD4_TCELL_VS_BCELL_UP	79	0.480	1.897	0	0.078	0.832	1494	tags=35%, list=20%, signal=44%
GO_REGULATION_OF_CELL_MIGRATION_INVOLVED_IN_SPROUTING_ANGIOE NESIS	22	0.633	1.890	0.003	0.079	0.86	836	tags=41%, list=11%, signal=46%
GO_ENDOTHELIAL_CELL_APOPTOTIC_PROCESS	28	0.594	1.879	0	0.083	0.895	859	tags=43%, list=12%, signal=48%
HALLMARK_TGF_BETA_SIGNALING	26	0.597	1.867	0.003	0.088	0.92	1616	tags=58%, list=22%, signal=74%
PHONG_TNF_TARGETS_UP	32	0.568	1.862	0	0.088	0.929	1086	tags=44%, list=15%, signal=51%
GO_ADAPTIVE_IMMUNE_RESPONSE	289	0.387	1.828	0	0.113	0.978	1261	tags=31%, list=17%, signal=37%
GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION	45	0.519	1.817	0	0.113	0.987	1693	tags=47%, list=23%, signal=60%
GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERATION	49	0.488	1.802	0	0.125	0.994	797	tags=37%, list=11%, signal=41%
GO_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION	78	0.456	1.791	0	0.131	0.994	836	tags=29%, list=11%, signal=33%
GO_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	25	0.571	1.788	0	0.132	0.995	701	tags=32%, list=10%, signal=35%
GO_EPITHELIAL_CELL_APOPTOTIC_PROCESS	42	0.515	1.784	0.004	0.137	0.995	859	tags=36%, list=12%, signal=40%
HALLMARK_TNFA_SIGNALING_VIA_NFKB	80	0.443	1.778	0	0.142	0.996	1089	tags=31%, list=15%, signal=36%
GO_SPROUTING_ANGIOGENESIS	65	0.450	1.756	0	0.160	1	1348	tags=46%, list=18%, signal=56%
GO_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	109	0.419	1.756	0	0.159	1	1693	tags=41%, list=23%, signal=53%
GO_ENDOTHELIAL_CELL_MIGRATION	99	0.430	1.747	0	0.164	1	836	tags=29%, list=11%, signal=33%
GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	66	0.442	1.739	0	0.164	1	1693	tags=44%, list=23%, signal=57%
GSE34006_A2AR_KO_VS_A2AR_AGONIST_TREATED_TREG_UP	64	0.448	1.738	0	0.162	1	1453	tags=34%, list=20%, signal=43%
BROWNE_INTERFERON_RESPONSIVE_GENES	31	0.520	1.738	0	0.161	1	1342	tags=52%, list=18%, signal=63%
PID_VEGFR1_2_PATHWAY	18	0.608	1.736	0.015	0.162	1	1641	tags=50%, list=22%, signal=64%
AMIT_EGF_RESPONSE_40_HELA	21	0.580	1.736	0.003	0.162	1	1091	tags=38%, list=15%, signal=45%
GSE22886_DAY0_VS_DAY7_MONOCYTE_IN_CULTURE_UP	83	0.422	1.734	0	0.162	1	2508	tags=59%, list=34%, signal=89%
CHR17Q23	15	0.634	1.731	0.011	0.165	1	1180	tags=47%, list=16%, signal=56%
GSE41867_NAIVE_VS_DAY8_LCMV_EFFECTOR_CD8_TCELL_DN	75	0.433	1.729	0	0.167	1	2553	tags=55%, list=35%, signal=83%
GO_CAVEOLA	35	0.508	1.727	0	0.168	1	986	tags=37%, list=13%, signal=43%

Gene Set	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
GSE17974_OH_VS_1H_IN_VITRO_ACT_CD4_TCELL_DN	58	0.457	1.727	0	0.167	1	1532	tags=33%, list=21%, signal=41%
GSE22886_TCELL_VS_BCELL_NAIVE_UP	69	0.440	1.726	0	0.168	1	2526	tags=54%, list=34%, signal=81%
GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_APOPTOTIC_PROCESS	18	0.597	1.722	0.009	0.172	1	633	tags=44%, list=9%, signal=49%
REACTOME_INTERFERON_SIGNALING	54	0.458	1.705	0.004	0.188	1	1691	tags=43%, list=23%, signal=55%
SANA_RESPONSE_TO_IFNG_UP	19	0.578	1.704	0.013	0.188	1	1026	tags=47%, list=14%, signal=55%
GO_BLOOD_VESSEL_ENDOTHELIAL_CELL_PROLIFERATION_INVOLVED_IN_SPROUTING_ANGIOGENESIS	15	0.627	1.703	0.013	0.187	1	797	tags=60%, list=11%, signal=67%
PID_TGFBR_PATHWAY	22	0.572	1.700	0.003	0.188	1	2253	tags=68%, list=31%, signal=98%
HECKER_IFNB1_TARGETS	32	0.515	1.697	0.003	0.187	1	1342	tags=50%, list=18%, signal=61%
GO_NEGATIVE_REGULATION_OF_SPROUTING_ANGIOGENESIS	17	0.588	1.685	0.020	0.196	1	1841	tags=65%, list=25%, signal=86%
REACTOME_SIGNALING_BY_FGFR	21	0.559	1.685	0.006	0.196	1	599	tags=19%, list=8%, signal=21%
GO_ENDOTHELIAL_CELL_PROLIFERATION	74	0.428	1.673	0.009	0.202	1	797	tags=30%, list=11%, signal=33%
REACTOME_FCERI_MEDIATED_MAPK_ACTIVATION	64	0.441	1.672	0	0.203	1	1931	tags=44%, list=26%, signal=59%
GO_RESPONSE_TO_INTERFERON_GAMMA	61	0.423	1.657	0.008	0.218	1	1680	tags=39%, list=23%, signal=51%
GO_REGULATION_OF_NIK_NF_KAPPAB_SIGNALING	34	0.496	1.650	0.007	0.215	1	1693	tags=38%, list=23%, signal=49%
GO_NIK_NF_KAPPAB_SIGNALING	38	0.478	1.648	0	0.217	1	1693	tags=34%, list=23%, signal=44%
GSE3920_IFNA_VS_IFNB_TREATED_ENDOTHELIAL_CELL_DN	73	0.424	1.646	0	0.217	1	1116	tags=27%, list=15%, signal=32%
GO_FRIZZLED_BINDING	17	0.567	1.645	0.014	0.218	1	1088	tags=47%, list=15%, signal=55%
LI_INDUCED_T_TO_NATURAL_KILLER_UP	138	0.370	1.642	0	0.217	1	1252	tags=25%, list=17%, signal=30%
GSE13229_IMM_VS_MATURE_NKCELL_DN	71	0.412	1.633	0	0.224	1	2160	tags=52%, list=29%, signal=73%
GO_LEUKOCYTE_MEDIATED_CYTOTOXICITY	41	0.460	1.624	0.007	0.233	1	1269	tags=39%, list=17%, signal=47%
BROCKE_APOPTOSIS_REVERSED_BY_IL6	59	0.436	1.622	0	0.234	1	1023	tags=29%, list=14%, signal=33%
GO_INTERFERON_GAMMA_MEDIATED_SIGNALING_PATHWAY	21	0.532	1.611	0.021	0.237	1	1502	tags=43%, list=20%, signal=54%
GO_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	22	0.535	1.610	0.02	0.237	1	1269	tags=45%, list=17%, signal=55%
GO_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGRATION	52	0.449	1.606	0.008	0.237	1	1693	tags=48%, list=23%, signal=62%
GO_RESPONSE_TO_TYPE_I_INTERFERON	27	0.507	1.606	0.020	0.237	1	1261	tags=44%, list=17%, signal=53%
GO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_SIGNALING_PATHWAY	21	0.534	1.599	0.026	0.239	1	1290	tags=62%, list=18%, signal=75%

Supplementary file 5: Significantly enriched gene sets in IPF tissues with IL7=AC083837.1 gene fusion.

Columns: Size: Number of genes in the gene set that included in the expression matrix; ES: enrichment score; NES: Normalized enrichment score; NOM p-value: Nominal p-value; FDR q-value: False discovery rate; FWER p-value: Familywise-error rate; RANK AT MAX: The position in the ranked list at which the maximum enrichment score occurred; LEADING EDGE: three statistics used to define the leading-edge subsets (<https://www.gsea-msigdb.org/gsea/doc/GSEAUserGuideFrame.html>).