

All Enrichment of Significant Genes						All Enrichment of Genes Thresholded at 95 percentile					
term	N-term	N-query	overlap	p.value	domain	term	N-term	N-query	overlap	p.value	domain
ion binding	6165	1252	492	2.21e-09	MF	protein binding	11522	836	597	2.76e-16	MF
anatomical structure morphogenesis	2598	617	143	3.2e-09	BP	intracellular part	14266	834	692	6.61e-16	CC
intracellular	14606	386	333	1.25e-08	CC	cellular component organization or biogenesis	6297	832	342	7.88e-07	BP
kinase activity	900	758	67	0.000297	MF	cellular protein localization	1686	832	112	0.000766	BP
establishment of cell polarity	122	1101	23	0.000458	BP	poly(u) rna binding	20	2	2	0.00333	MF
cell junction	1253	458	57	0.00142	CC	filopodium	97	816	16	0.00521	CC
response to growth factor	713	1128	72	0.00192	BP	movement of cell or subcellular component	2064	836	127	0.00868	BP
poly(u) rna binding	20	2	2	0.00312	MF	actin filament-based process	714	832	56	0.00973	BP
extracellular matrix component	47	617	10	0.00409	CC	enzyme linked receptor protein signaling pathway	1031	836	72	0.0298	BP
microtubule-based process	722	269	27	0.00455	BP	cellular protein modification process	4097	839	220	0.0371	BP
regulation of gtpase activity	482	708	39	0.00455	BP	hemopoiesis	827	811	59	0.0446	BP
ventricular septum morphogenesis	45	1227	13	0.00473	BP	response to ozone	5	24	2	0.0483	BP
intraciliary transport particle b	21	938	8	0.00761	CC						
coreceptor activity involved in wnt signaling pathway	8	71	3	0.00799	MF						
phosphatidylinositol-4,5-bisphosphate binding	64	868	13	0.00836	MF						
gtpase binding	632	264	24	0.00992	MF						
gtpase activator activity	284	708	27	0.0103	MF						
extracellular matrix structural constituent	126	655	16	0.0111	MF						
plasma membrane region	1068	1284	104	0.0159	CC						
regulation of primary metabolic process	6175	614	239	0.0226	BP						
regulation of mapk cascade	747	589	44	0.0303	BP						
laminin-10 complex	3	434	3	0.031	CC						
rho gtpase binding	170	252	11	0.0316	MF						
epithelial tube branching involved in lung morphogenesis	29	1372	10	0.0328	BP						
positive regulation of molecular function	1718	710	94	0.0438	BP						
wnt-activated receptor activity	21	836	7	0.0446	MF						
cellular response to endogenous stimulus	1347	1128	111	0.0479	BP						

Autoimmune Enrichment of Significant Genes					
term	N-term	N-query	overlap	p.value	domain
multicellular organism development	5321	1267	470	1.9e-18	BP
plasma membrane part	2740	1352	272	7.15e-11	CC
cell adhesion	1343	1169	140	7.71e-10	BP
transcription activator activity, rna polymerase ii-specific	414	1370	64	2.75e-07	MF
extracellular matrix	376	1240	55	1.55e-06	CC
cell projection	2002	697	116	7.77e-06	CC
cell junction	1253	1112	114	3.43e-05	CC
receptor regulator activity	485	997	52	0.000137	MF
sarcomere	198	1311	34	0.000225	CC
ion channel activity	428	1398	59	0.00023	MF
ion transport	1609	627	86	0.000381	BP
regulation of signaling receptor activity	546	997	55	0.000457	BP
extracellular matrix structural constituent	126	1198	24	0.000523	MF
calcium ion binding	707	1322	80	0.000752	MF
negative regulation of hormone biosynthetic process	11	133	4	0.00155	BP
sequence-specific dna binding	1076	1257	104	0.00292	MF
poly(u) rna binding	20	2	2	0.00312	MF
negative regulation of alcohol biosynthetic process	13	133	4	0.00333	BP
metal ion transmembrane transporter activity	457	1350	57	0.00364	MF
heparan sulfate sulfotransferase activity	16	1248	8	0.00412	MF
cell junction organization	272	734	27	0.00449	BP
extracellular structure organization	385	1240	47	0.00653	BP
regulation of hormone levels	510	1258	57	0.0153	BP
potassium ion transport	245	627	22	0.0173	BP
positive regulation of transcription by rna polymerase ii	1112	1258	103	0.0228	BP
cyclic nucleotide metabolic process	49	586	9	0.0238	BP
fibroblast growth factor receptor binding	27	597	7	0.0255	MF
actin binding	415	246	17	0.0262	MF
proteoglycan metabolic process	85	1248	17	0.029	BP
negative regulation of steroid biosynthetic process	23	133	4	0.0393	BP
RNA polymerase ii regulatory region sequence-specific dna binding	674	1370	73	0.0396	MF
epithelial cell proliferation	424	1282	49	0.0446	BP

Autoimmune Enrichment of Genes Thresholded at 95 percentile					
term	N-term	N-query	overlap	p.value	domain
cytoplasmic part	9521	805	440	0.000269	CC
poly(u) rna binding	20	2	2	0.00312	MF
transport	4965	808	251	0.00336	BP
protein binding	11522	781	493	0.00666	MF
purine ribonucleotide catabolic process	32	799	9	0.00695	BP
small molecule metabolic process	1987	799	115	0.015	BP
lysosomal lumen	94	755	14	0.0233	CC
proximal/distal pattern formation	33	86	4	0.0339	BP
oxidation-reduction process	996	574	51	0.0486	BP

EMT Enrichment of Significant Genes							EMT Enrichment of Genes Thresholded at 95 percentile						
	term	N-term	N-query	overlap	p.value	domain		term	N-term	N-query	overlap	p.value	domain
	cytosol	5004	675	237	4.92e-06	CC		protein binding	11522	794	542	1.41e-06	MF
	protein binding	11522	718	481	0.000137	MF		organelle	13288	758	579	5.68e-06	CC
	catabolic process	2435	727	137	0.000265	BP		poly(u) rna binding	20	2	2	0.00333	MF
	vesicle	3788	694	182	0.00268	CC		catalytic activity, acting on dna	185	57	6	0.0491	MF
	poly(u) rna binding	20	2	2	0.00333	MF							
	transport	4965	699	227	0.00547	BP							
	catalytic complex	1367	97	21	0.00668	CC							
	dna dealkylation involved in dna repair	10	75	3	0.0198	BP							
	regulation of dna catabolic process	10	625	5	0.0216	BP							
	macromolecule modification	4292	134	51	0.0219	BP							
proteolysis involved in cellular protein catabolic process		678	127	16	0.0235	BP							
	adherens junction	513	911	46	0.0283	CC							
	protein catabolic process	882	101	16	0.0298	BP							
	protein localization	2600	697	130	0.0306	BP							
	peroxisome organization	80	456	10	0.0466	BP							

Fibrosis							Fibrosis						
Enrichment of Significant Genes							Enrichment of Genes Thresholded at 95 percentile						
	term	N-term	N-query	overlap	p.value	domain		term	N-term	N-query	overlap	p.value	domain
	cilium assembly	358	309	32	3.91e-12	BP		intracellular part	14266	351	293	4.53e-05	CC
	cilium	583	309	40	8.01e-12	CC		cilium assembly	358	348	24	5.41e-05	BP
	cytoskeletal protein binding	888	212	35	7.15e-08	MF		cytoskeletal protein binding	888	348	40	0.000102	MF
	nervous system development	2299	330	79	3.34e-07	BP		poly(u) rna binding	20	2	2	0.00278	MF
	heart development	555	301	28	8.4e-05	BP		regulation of protein depolymerization	74	337	9	0.0114	BP
	erase ii proximal promoter sequence-specific dna binding	402	227	19	0.000648	MF		brain development	712	345	30	0.0182	BP
	smoothened signaling pathway	132	299	12	0.00214	BP		enzyme activator activity	515	68	10	0.0235	MF
	poly(u) rna binding	20	2	2	0.00278	MF		negative regulation of microtubule depolymerization	20	337	5	0.0457	BP
	negative regulation of transcription by rna polymerase ii	798	220	25	0.00956	BP		dystrophin-associated glycoprotein complex	21	151	4	0.0467	CC
	rna polymerase ii transcription factor binding	119	206	9	0.0125	MF							
	outflow tract septum morphogenesis	27	82	4	0.0132	BP							
	nephron tubule epithelial cell differentiation	15	200	4	0.0358	BP							
	alpha-actinin binding	34	27	3	0.0382	MF							

ILD_PAH Enrichment of Significant Genes					
term	N-term	N-query	overlap	p.value	domain
extracellular matrix	376	1284	58	2.1e-07	CC
motile cilium	173	1297	35	1.19e-06	CC
mesonephros development	102	1256	25	3.32e-06	BP
regulation of biological quality	3656	1275	296	9.16e-05	BP
cellular component organization	6120	358	154	0.000124	BP
response to glucocorticoid	141	1164	26	0.000192	BP
cilium movement	68	841	15	0.000211	BP
negative regulation of signal transduction	1206	410	52	0.000345	BP
calcium ion binding	707	1361	82	0.000497	MF
biological adhesion	1351	1348	134	0.000619	BP
cilium assembly	358	844	37	0.00067	BP
cytoplasmic region	427	869	42	0.000912	CC
heart development	555	1189	61	0.00204	BP
poly(u) rna binding	20	2	2	0.00294	MF
cytoskeleton	2115	805	125	0.0032	CC
cellular response to stress	1870	138	32	0.00328	BP
regulation of animal organ morphogenesis	209	954	27	0.00364	BP
regulation of canonical wnt signaling pathway	226	392	17	0.00528	BP
extracellular matrix organization	332	728	30	0.00726	BP
extracellular matrix structural constituent	126	1205	22	0.00876	MF
actin binding	415	1374	52	0.0126	MF
multi-organism reproductive process	993	1379	100	0.0268	BP
cell adhesion via plasma membrane adhesion molecules	159	1343	26	0.0269	BP
branching involved in ureteric bud morphogenesis	60	1256	14	0.028	BP
synapse assembly	150	1343	25	0.0282	BP
protein catabolic process	882	149	20	0.0282	BP
striated muscle cell differentiation	283	920	30	0.029	BP
protein binding	11522	366	244	0.0333	MF
intrinsic component of plasma membrane	1661	1117	129	0.0347	CC
organonitrogen compound metabolic process	6908	181	90	0.0384	BP
protein maturation by iron-sulfur cluster transfer	9	13	2	0.0433	BP
protein k33-linked deubiquitination	3	44	2	0.0439	BP
response to organic substance	3180	195	54	0.0442	BP
tonic smooth muscle contraction	11	92	3	0.0449	BP
cytoskeleton organization	1235	459	51	0.0473	BP

ILD_PAH Enrichment of Genes Thresholded at 95 percentile					
term	N-term	N-query	overlap	p.value	domain
intracellular part	14266	860	683	1.55e-10	CC
protein binding	11522	836	551	5.47e-07	MF
cellular metabolic process	10713	860	526	1.71e-05	BP
poly(u) rna binding	20	2	2	0.00333	MF
t cell apoptotic process	48	704	10	0.014	BP
response to topologically incorrect protein	185	850	22	0.0274	BP
peptidyl-serine modification	317	356	18	0.0422	BP
transferase activity	2479	630	113	0.0432	MF

Lung Enrichment of Significant Genes						Lung Enrichment of Genes Thresholded at 95 percentile					
term	N-term	N-query	overlap	p.value	domain	term	N-term	N-query	overlap	p.value	domain
cytoplasm	11390	890	653	1.57e-20	CC	intracellular part	14266	840	709	2.12e-20	CC
anatomical structure morphogenesis	2598	1017	234	9.81e-16	BP	ncrna processing	346	837	60	7.51e-18	BP
protein binding	11522	1025	715	6.61e-13	MF	protein binding	11522	806	570	6.03e-14	MF
phosphorus metabolic process	3255	1089	263	1.37e-08	BP	ribonucleoprotein complex	825	816	80	9.14e-10	CC
anchoring junction	530	839	56	1.29e-06	CC	protein localization to cajal body	10	588	6	0.000397	BP
basement membrane	92	740	19	4.07e-06	CC	ulation of establishment of protein localization to telomere	10	588	6	0.000397	BP
cytoskeleton	2115	803	138	3.89e-05	CC	poly(u) rna binding	20	2	2	0.00333	MF
extracellular matrix structural constituent	126	676	20	3.98e-05	MF	'de novo' protein folding	38	763	10	0.0035	BP
regulation of hydrolase activity	1256	1060	112	0.000128	BP	rna localization to cajal body	19	656	7	0.00463	BP
gtpase activator activity	284	1044	37	0.00111	MF	protein stabilization	162	799	21	0.00569	BP
membrane docking	171	730	22	0.00138	BP	telomere maintenance via telomerase	67	826	13	0.00884	BP
transcription coregulator activity	529	503	34	0.00302	MF	chaperone-mediated protein folding	63	763	12	0.0123	BP
poly(u) rna binding	20	2	2	0.00357	MF	cellular response to endogenous stimulus	1347	628	72	0.0208	BP
establishment or maintenance of cell polarity	186	810	23	0.00888	BP	dna-templated transcription, initiation	258	78	8	0.0221	BP
insulin-like growth factor-activated receptor activity	3	23	2	0.0143	MF	mitotic sister chromatid separation	55	100	5	0.0262	BP
synaptic vesicle localization	121	1052	20	0.0181	BP	n-acyltransferase activity	99	817	15	0.0333	MF
negative regulation of vascular permeability	13	782	6	0.0184	BP	paraxial mesoderm development	19	607	6	0.0493	BP
ligase activity, forming carbon-carbon bonds	8	332	4	0.0186	MF						
phospholipid transporter activity	56	1063	13	0.0206	MF						
positive regulation of transcription of notch receptor target	18	884	7	0.0257	BP						
maintenance of mitotic sister chromatid cohesion, telomeric	2	58	2	0.03	BP						
anion transport	590	1005	55	0.0333	BP						
caveola	78	910	14	0.0408	CC						
positive regulation of apoptotic process	622	611	40	0.0429	BP						

Skin Enrichment of Significant Genes						Skin Enrichment of Genes Thresholded at 95 percentile							
	term	N-term	N-query	overlap	p.value	domain		term	N-term	N-query	overlap	p.value	domain
negative regulation of nucleic acid-templated transcription	protein binding	11522	633	439	8.44e-09	MF		intracellular	14606	816	671	4.94e-13	CC
		1219	1119	123	8.54e-08	BP		protein binding	11522	802	550	1.82e-11	MF
	intracellular	14606	737	596	1.07e-06	CC		organonitrogen compound metabolic process	6908	693	307	3.05e-06	BP
	cellular response to chemical stimulus	3116	810	189	1.73e-06	BP		cellular response to organic substance	2603	813	162	4.54e-06	BP
	renal system development	281	1253	44	2.43e-05	BP		organelle organization	3710	740	186	0.00138	BP
	protein modification by small protein conjugation	830	678	58	0.000257	BP		poly(u) rna binding	20	2	2	0.00333	MF
	response to other organism	935	913	77	0.000578	BP		oxidoreductase activity, acting on nad(p)h	110	653	15	0.00711	MF
	tube formation	147	1167	25	0.00298	BP		positive regulation of cellular process	5100	802	254	0.0114	BP
	tube development	1079	1059	93	0.00326	BP		regulation of programmed cell death	1554	811	97	0.0128	BP
	poly(u) rna binding	20	2	2	0.00333	MF		response to stress	3862	646	167	0.0158	BP
	nucleosome	108	1204	21	0.0037	CC		glial cell projection	21	756	7	0.0216	CC
	icosanoid metabolic process	107	737	16	0.00495	BP		nadh dehydrogenase (ubiquinone) activity	46	653	9	0.0407	MF
	intracellular signal transduction	2713	811	154	0.00762	BP		regulation of macromolecule biosynthetic process	4256	804	215	0.0463	BP
	aldehyde dehydrogenase (nad) activity	16	896	7	0.00839	MF							
	response to stress	3862	810	205	0.0105	BP							
	regulation of stem cell differentiation	66	1181	15	0.0137	BP							
	chromatin assembly or disassembly	187	960	24	0.0273	BP							
	oxidoreductase activity, acting on the aldehyde or oxo group of donors	46	999	11	0.0337	MF							
	circulatory system development	1128	814	75	0.0339	BP							
	organonitrogen compound metabolic process	6908	426	186	0.0345	BP							
	pattern specification process	423	1215	48	0.0388	BP							
	nucleosome assembly	143	879	19	0.0426	BP							
	peroxisome fission	9	847	5	0.0447	BP							
	regulation of cell-cell adhesion	374	1228	44	0.0467	BP							
	whole membrane	1617	578	75	0.0477	CC							

SSc Enrichment of Significant Genes							SSc Enrichment of Genes Thresholded at 95 percentile						
	term	N-term	N-query	overlap	p.value	domain		term	N-term	N-query	overlap	p.value	domain
	multicellular organismal process	7414	1071	469	2.27e-06	BP		ncrna metabolic process	523	832	73	3.01e-17	BP
	nucleosome	108	1081	24	3.01e-06	CC		nucleus	7234	810	395	1.28e-13	CC
	intrinsic component of plasma membrane	1661	962	129	5.19e-06	CC		nucleic acid binding	4267	831	263	3.72e-11	MF
	hemoglobin complex	13	826	8	2.25e-05	CC		catalytic activity, acting on rna	378	832	49	1.57e-09	MF
	striated muscle contraction	179	910	26	0.000233	BP		poly(u) rna binding	20	2	2	0.00333	MF
	extracellular matrix	376	966	40	0.00269	CC		cytosol	5004	833	259	0.00646	CC
	poly(u) rna binding	20	2	2	0.00333	MF							
	synaptic transmission, glutamatergic	81	285	9	0.00512	BP							
	oxygen binding	38	826	10	0.00557	MF							
	behavior	588	760	45	0.0102	BP							
	p granule	15	1059	7	0.012	CC							
	positive regulation of potassium ion transport	43	323	7	0.0127	BP							
	cell adhesion via plasma membrane adhesion molecules	159	1062	23	0.0169	BP							
	striated muscle cell development	164	620	17	0.0282	BP							
	positive regulation of cation transmembrane transport	133	412	12	0.0454	BP							
	oxygen carrier activity	15	826	6	0.0488	MF							