

Supplementary Table 15. *Enriched pathways of Pattern IV genes* . Columns are the same as Table S10.

path	desc	p	m	P	M	nrich	log2FC	pval	fdr
GO:0042391	regulation of membrane potential	6	65	427	17583	3.80	1.93	9.81E-04	1.90E-02
GO:0097190	apoptotic signaling pathway	5	65	312	17583	4.34	2.12	1.02E-03	1.90E-02
GO:0031647	regulation of protein stability	5	65	322	17583	4.20	2.07	1.20E-03	1.90E-02
GO:0016310	phosphorylation	8	65	897	17583	2.41	1.27	5.51E-03	2.35E-02
GO:0022402	cell cycle process	8	65	899	17583	2.41	1.27	5.59E-03	2.35E-02
GO:0044238	primary metabolic process	36	65	7194	17583	1.35	0.44	6.55E-03	2.35E-02
GO:0048513	animal organ development	18	65	2895	17583	1.68	0.75	7.10E-03	2.35E-02
GO:0048869	cellular developmental process	21	65	3579	17583	1.59	0.67	7.64E-03	2.42E-02
GO:0007420	brain development	7	65	778	17583	2.43	1.28	7.70E-03	2.44E-02
GO:0030001	metal ion transport	6	65	624	17583	2.60	1.38	8.03E-03	2.54E-02
GO:0035556	intracellular signal transduction	11	65	1517	17583	1.96	0.97	8.95E-03	2.80E-02
GO:0061061	muscle structure development	5	65	498	17583	2.72	1.44	1.01E-02	2.80E-02
GO:0065008	regulation of biological quality	17	65	2788	17583	1.65	0.72	1.06E-02	2.80E-02
GO:0060322	head development	7	65	826	17583	2.29	1.20	1.08E-02	2.80E-02
GO:0006886	intracellular protein transport	6	65	688	17583	2.36	1.24	1.33E-02	3.23E-02
GO:0007417	central nervous system development	8	65	1041	17583	2.08	1.06	1.39E-02	3.23E-02
GO:0044085	cellular component biogenesis	16	65	2651	17583	1.63	0.71	1.41E-02	3.23E-02
GO:0030154	cell differentiation	20	65	3556	17583	1.52	0.61	1.47E-02	3.24E-02
GO:0071704	organic substance metabolic process	36	65	7534	17583	1.29	0.37	1.54E-02	3.38E-02
GO:0006468	protein phosphorylation	6	65	712	17583	2.28	1.19	1.58E-02	3.46E-02
GO:0043170	macromolecule metabolic process	29	65	5792	17583	1.35	0.44	1.80E-02	3.66E-02
GO:0008152	metabolic process	37	65	7967	17583	1.26	0.33	2.25E-02	4.17E-02
GO:0048646	anatomical structure formation involved in morphoge	7	65	945	17583	2.00	1.00	2.26E-02	4.20E-02
GO:0098662	inorganic cation transmembrane transport	5	65	602	17583	2.25	1.17	2.36E-02	4.36E-02
GO:0006807	nitrogen compound metabolic process	32	65	6674	17583	1.30	0.38	2.37E-02	4.39E-02
GO:0006325	chromatin organization	5	65	608	17583	2.22	1.15	2.46E-02	4.46E-02
GO:0048731	system development	19	65	3507	17583	1.47	0.55	2.52E-02	4.46E-02
GO:0022607	cellular component assembly	14	65	2411	17583	1.57	0.65	2.76E-02	4.81E-02

GO:0036211	protein modification process	15	65	2645	17583	1.53	0.62	2.89E-02	4.86E-02
GO:0070925	organelle assembly	6	65	827	17583	1.96	0.97	3.25E-02	5.26E-02
GO:0006915	apoptotic process	7	65	1028	17583	1.84	0.88	3.50E-02	5.60E-02
GO:0035239	tube morphogenesis	5	65	667	17583	2.03	1.02	3.63E-02	5.65E-02
GO:0044260	cellular macromolecule metabolic process	14	65	2498	17583	1.52	0.60	3.65E-02	5.67E-02
GO:0006812	cation transport	6	65	849	17583	1.91	0.93	3.67E-02	5.70E-02
GO:0019538	protein metabolic process	20	65	3891	17583	1.39	0.48	3.76E-02	5.85E-02
GO:0098655	cation transmembrane transport	5	65	677	17583	2.00	1.00	3.86E-02	5.99E-02
GO:0042981	regulation of apoptotic process	9	65	1446	17583	1.68	0.75	3.87E-02	6.00E-02
GO:0030182	neuron differentiation	7	65	1052	17583	1.80	0.85	3.93E-02	6.03E-02
GO:0035295	tube development	6	65	876	17583	1.85	0.89	4.23E-02	6.37E-02
GO:0012501	programmed cell death	7	65	1070	17583	1.77	0.82	4.28E-02	6.40E-02
GO:0006996	organelle organization	16	65	3011	17583	1.44	0.52	4.36E-02	6.41E-02
GO:0008285	negative regulation of cell population proliferation	5	65	698	17583	1.94	0.95	4.38E-02	6.44E-02
GO:0098660	inorganic ion transmembrane transport	5	65	699	17583	1.93	0.95	4.40E-02	6.48E-02
GO:0043067	regulation of programmed cell death	9	65	1479	17583	1.65	0.72	4.41E-02	6.48E-02
GO:0043066	negative regulation of apoptotic process	6	65	886	17583	1.83	0.87	4.45E-02	6.55E-02
GO:0032502	developmental process	27	65	5685	17583	1.28	0.36	4.47E-02	6.58E-02
GO:0007049	cell cycle	8	65	1283	17583	1.69	0.75	4.55E-02	6.70E-02
GO:0008283	cell population proliferation	5	65	707	17583	1.91	0.94	4.61E-02	6.77E-02
GO:0044237	cellular metabolic process	30	65	6489	17583	1.25	0.32	4.83E-02	6.95E-02
GO:0008219	cell death	7	65	1103	17583	1.72	0.78	4.96E-02	7.13E-02
GO:1901564	organonitrogen compound metabolic process	24	65	4982	17583	1.30	0.38	4.96E-02	7.13E-02
GO:0043069	negative regulation of programmed cell death	6	65	908	17583	1.79	0.84	4.96E-02	7.13E-02
GO:0051179	localization	22	65	4502	17583	1.32	0.40	5.11E-02	7.20E-02
GO:0120036	plasma membrane bounded cell projection organiza	7	65	1112	17583	1.70	0.77	5.16E-02	7.28E-02
GO:0048699	generation of neurons	7	65	1121	17583	1.69	0.76	5.37E-02	7.49E-02
GO:0043412	macromolecule modification	15	65	2865	17583	1.42	0.50	5.47E-02	7.58E-02
GO:0007399	nervous system development	12	65	2189	17583	1.48	0.57	5.52E-02	7.64E-02
GO:0006974	cellular response to DNA damage stimulus	5	65	743	17583	1.82	0.86	5.62E-02	7.77E-02
GO:0046907	intracellular transport	8	65	1358	17583	1.59	0.67	6.12E-02	8.26E-02

GO:0030030	cell projection organization	7	65	1158	17583	1.64	0.71	6.26E-02	8.44E-02
GO:0009653	anatomical structure morphogenesis	12	65	2232	17583	1.45	0.54	6.27E-02	8.45E-02
GO:0006259	DNA metabolic process	5	65	778	17583	1.74	0.80	6.71E-02	8.93E-02
GO:0015031	protein transport	7	65	1176	17583	1.61	0.69	6.73E-02	8.95E-02
GO:0007275	multicellular organism development	19	65	3903	17583	1.32	0.40	6.84E-02	9.02E-02
GO:0044265	cellular macromolecule catabolic process	5	65	786	17583	1.72	0.78	6.98E-02	9.19E-02
GO:0006796	phosphate-containing compound metabolic process	10	65	1826	17583	1.48	0.57	7.01E-02	9.23E-02
GO:0006811	ion transport	7	65	1194	17583	1.59	0.67	7.22E-02	9.40E-02
GO:0009887	animal organ morphogenesis	6	65	992	17583	1.64	0.71	7.27E-02	9.47E-02
GO:0009057	macromolecule catabolic process	6	65	992	17583	1.64	0.71	7.27E-02	9.47E-02
GO:0006793	phosphorus metabolic process	10	65	1852	17583	1.46	0.55	7.60E-02	9.79E-02
GO:0010941	regulation of cell death	9	65	1634	17583	1.49	0.58	7.62E-02	9.82E-02
GO:0060548	negative regulation of cell death	6	65	1009	17583	1.61	0.69	7.81E-02	1.00E-01
GO:0010604	positive regulation of macromolecule metabolic proc	17	65	3487	17583	1.32	0.40	7.93E-02	1.01E-01
GO:0009719	response to endogenous stimulus	8	65	1431	17583	1.51	0.60	7.95E-02	1.01E-01
GO:1901360	organic cyclic compound metabolic process	16	65	3255	17583	1.33	0.41	8.05E-02	1.03E-01
GO:0033036	macromolecule localization	12	65	2323	17583	1.40	0.48	8.08E-02	1.03E-01
GO:0018193	peptidyl-amino acid modification	5	65	828	17583	1.63	0.71	8.49E-02	1.07E-01
GO:0048666	neuron development	5	65	832	17583	1.63	0.70	8.64E-02	1.09E-01
GO:0045944	positive regulation of transcription by RNA polymera	7	65	1246	17583	1.52	0.60	8.75E-02	1.10E-01
GO:0007010	cytoskeleton organization	7	65	1247	17583	1.52	0.60	8.78E-02	1.10E-01
GO:0080090	regulation of primary metabolic process	26	65	5782	17583	1.22	0.28	8.92E-02	1.11E-01
GO:0009790	embryo development	6	65	1044	17583	1.55	0.64	8.98E-02	1.12E-01
GO:0009893	positive regulation of metabolic process	18	65	3796	17583	1.28	0.36	9.17E-02	1.14E-01
GO:0010557	positive regulation of macromolecule biosynthetic pr	10	65	1920	17583	1.41	0.49	9.27E-02	1.15E-01
GO:0045184	establishment of protein localization	7	65	1264	17583	1.50	0.58	9.32E-02	1.15E-01
GO:1903508	positive regulation of nucleic acid-templated transcri	9	65	1700	17583	1.43	0.52	9.36E-02	1.16E-01
GO:0045893	positive regulation of DNA-templated transcription	9	65	1700	17583	1.43	0.52	9.36E-02	1.16E-01
GO:1902680	positive regulation of RNA biosynthetic process	9	65	1706	17583	1.43	0.51	9.53E-02	1.17E-01
GO:0022008	neurogenesis	7	65	1281	17583	1.48	0.56	9.88E-02	1.20E-01
GO:0051173	positive regulation of nitrogen compound metabolic	15	65	3112	17583	1.30	0.38	9.99E-02	1.22E-01

GO:0010646	regulation of cell communication	16	65	3362	17583	1.29	0.36	1.02E-01	1.23E-01
GO:0071702	organic substance transport	10	65	1956	17583	1.38	0.47	1.02E-01	1.24E-01
GO:0051171	regulation of nitrogen compound metabolic process	25	65	5628	17583	1.20	0.26	1.07E-01	1.29E-01
GO:0060255	regulation of macromolecule metabolic process	27	65	6147	17583	1.19	0.25	1.08E-01	1.30E-01
GO:0034220	ion transmembrane transport	5	65	885	17583	1.53	0.61	1.08E-01	1.30E-01
GO:0048856	anatomical structure development	23	65	5143	17583	1.21	0.27	1.12E-01	1.33E-01
GO:0051649	establishment of localization in cell	9	65	1764	17583	1.38	0.46	1.13E-01	1.34E-01
GO:0010556	regulation of macromolecule biosynthetic process	18	65	3907	17583	1.25	0.32	1.15E-01	1.36E-01
GO:0072359	circulatory system development	5	65	907	17583	1.49	0.58	1.18E-01	1.39E-01
GO:0090304	nucleic acid metabolic process	11	65	2247	17583	1.32	0.41	1.20E-01	1.41E-01
GO:0031328	positive regulation of cellular biosynthetic process	10	65	2016	17583	1.34	0.42	1.20E-01	1.41E-01
GO:0009966	regulation of signal transduction	14	65	2966	17583	1.28	0.35	1.22E-01	1.44E-01
GO:0033554	cellular response to stress	8	65	1576	17583	1.37	0.46	1.25E-01	1.46E-01
GO:0045935	positive regulation of nucleobase-containing compo	10	65	2034	17583	1.33	0.41	1.26E-01	1.47E-01
GO:0051234	establishment of localization	18	65	3956	17583	1.23	0.30	1.26E-01	1.47E-01
GO:0071705	nitrogen compound transport	8	65	1581	17583	1.37	0.45	1.27E-01	1.48E-01
GO:0009891	positive regulation of biosynthetic process	10	65	2055	17583	1.32	0.40	1.32E-01	1.53E-01
GO:0048519	negative regulation of biological process	23	65	5250	17583	1.19	0.24	1.34E-01	1.55E-01
GO:0051254	positive regulation of RNA metabolic process	9	65	1833	17583	1.33	0.41	1.35E-01	1.56E-01
GO:0016192	vesicle-mediated transport	7	65	1387	17583	1.37	0.45	1.38E-01	1.59E-01
GO:0016070	RNA metabolic process	8	65	1619	17583	1.34	0.42	1.41E-01	1.62E-01
GO:0010243	response to organonitrogen compound	5	65	967	17583	1.40	0.48	1.46E-01	1.67E-01
GO:0031325	positive regulation of cellular metabolic process	14	65	3060	17583	1.24	0.31	1.48E-01	1.69E-01
GO:0006810	transport	17	65	3800	17583	1.21	0.28	1.49E-01	1.70E-01
GO:0010468	regulation of gene expression	21	65	4813	17583	1.18	0.24	1.51E-01	1.71E-01
GO:0031326	regulation of cellular biosynthetic process	18	65	4057	17583	1.20	0.26	1.51E-01	1.71E-01
GO:0070887	cellular response to chemical stimulus	11	65	2350	17583	1.27	0.34	1.52E-01	1.72E-01
GO:0033043	regulation of organelle organization	6	65	1199	17583	1.35	0.44	1.53E-01	1.74E-01
GO:0006357	regulation of transcription by RNA polymerase II	12	65	2592	17583	1.25	0.32	1.53E-01	1.74E-01
GO:0008104	protein localization	9	65	1892	17583	1.29	0.36	1.57E-01	1.77E-01
GO:0055085	transmembrane transport	6	65	1209	17583	1.34	0.42	1.58E-01	1.78E-01

GO:0070727	cellular macromolecule localization	9	65	1898	17583	1.28	0.36	1.59E-01	1.79E-01
GO:0009894	regulation of catabolic process	5	65	995	17583	1.36	0.44	1.61E-01	1.81E-01
GO:0023051	regulation of signaling	15	65	3352	17583	1.21	0.28	1.62E-01	1.82E-01
GO:0019222	regulation of metabolic process	28	65	6669	17583	1.14	0.18	1.62E-01	1.82E-01
GO:0006629	lipid metabolic process	6	65	1221	17583	1.33	0.41	1.63E-01	1.83E-01
GO:0051128	regulation of cellular component organization	11	65	2384	17583	1.25	0.32	1.64E-01	1.84E-01
GO:1901575	organic substance catabolic process	8	65	1679	17583	1.29	0.37	1.64E-01	1.84E-01
GO:0051641	cellular localization	12	65	2639	17583	1.23	0.30	1.68E-01	1.88E-01
GO:0009889	regulation of biosynthetic process	18	65	4122	17583	1.18	0.24	1.69E-01	1.89E-01
