



Figure S1. Expression of Lhx4, Pias3, Blimp1, Rgs9, Rtbdn, and Tbx2 in the mouse retina from embryonic day 11 to postnatal day 28

GO_Biological process				GO_Cellular component			
GO.ID	Description	p-Value	FDR	GO.ID	Description	p-Value	FDR
GO:0065007	biological regulation	3.49E-38	3.49E-38	GO:0005737	cytoplasm	1.79E-97	1.79E-97
GO:0050789	regulation of biological process	2.00E-33	2.00E-33	GO:0016020	membrane	1.10E-46	1.10E-46
GO:0050896	response to stimulus	8.95E-32	8.95E-32	GO:0012505	endomembrane system	1.93E-42	1.93E-42
GO:0050794	regulation of cellular process	2.67E-27	2.67E-27	GO:0005773	vacuole	4.05E-31	4.05E-31
GO:0051716	cellular response to stimulus	1.21E-25	1.21E-25	GO:0031090	organelle membrane	9.23E-31	9.23E-31
GO:0051179	localization	1.40E-25	1.40E-25	GO:0000323	lytic vacuole	8.02E-26	8.02E-26
GO:0009056	catabolic process	1.04E-24	1.04E-24	GO:0005764	lysosome	8.02E-26	8.02E-26
GO:0051234	establishment of localization	3.91E-21	3.91E-21	GO:0005783	endoplasmic reticulum	3.46E-23	3.46E-23
GO:0006810	transport	7.82E-21	7.82E-21	GO:0005774	vacuolar membrane	1.99E-22	1.99E-22
GO:0044281	small molecule metabolic process	5.65E-20	5.65E-20	GO:0098852	lytic vacuole membrane	3.88E-19	3.88E-19
GO:0006950	response to stress	3.08E-18	3.08E-18	GO:0005765	lysosomal membrane	3.88E-19	3.88E-19
GO:0048583	regulation of response to stimulus	2.61E-17	2.61E-17	GO:0031982	vesicle	4.06E-19	4.06E-19
GO:0032501	multicellular organismal process	4.67E-17	4.67E-17	GO:0098588	bounding membrane of organelle	1.24E-18	1.24E-18
GO:0048518	positive regulation of biological process	4.71E-17	4.71E-17	GO:0031410	cytoplasmic vesicle	2.01E-18	2.01E-18
GO:0007154	cell communication	7.96E-17	7.96E-17	GO:0071944	cell periphery	2.06E-18	2.06E-18
GO:0023052	signaling	1.23E-16	1.23E-16	GO:0097708	intracellular vesicle	2.65E-18	2.65E-18
GO:0007165	signal transduction	3.87E-15	3.87E-15	GO:0005886	plasma membrane	9.84E-18	9.84E-18
GO:0048522	positive regulation of cellular process	1.22E-14	1.22E-14	GO:0005794	Golgi apparatus	4.27E-13	4.27E-13
GO:0006629	lipid metabolic process	4.28E-14	4.28E-14	GO:0005768	endosome	1.39E-12	1.39E-12
GO:0032502	developmental process	6.66E-14	6.66E-14	GO:0031984	organelle subcompartment	2.45E-12	2.45E-12
GO:0023051	regulation of signaling	6.53E-13	6.53E-13	GO:0005829	cytosol	5.79E-12	5.79E-12
GO:0010646	regulation of cell communication	7.74E-13	7.74E-13	GO:0005739	mitochondrion	5.35E-11	5.35E-11
GO:0006082	organic acid metabolic process	7.88E-13	7.88E-13	GO:0042175	nuclear outer membrane-endoplasmic reticulum membrane network	7.59E-11	7.59E-11
GO:0019752	carboxylic acid metabolic process	1.19E-12	1.19E-12	GO:0042995	cell projection	2.37E-10	2.37E-10
GO:0043436	oxoacid metabolic process	1.33E-12	1.33E-12	GO:0098827	endoplasmic reticulum subcompartment	3.50E-10	3.50E-10
GO:0009966	regulation of signal transduction	1.59E-12	1.59E-12	GO:0005789	endoplasmic reticulum membrane	3.82E-10	3.82E-10
GO:0048856	anatomical structure development	5.75E-12	5.75E-12	GO:0120025	plasma membrane bounded cell projection	6.19E-10	6.19E-10
GO:0005975	carbohydrate metabolic process	6.72E-11	6.72E-11	GO:0012506	vesicle membrane	7.20E-09	7.20E-09
GO:0051641	cellular localization	8.93E-11	8.93E-11	GO:0030659	cytoplasmic vesicle membrane	7.74E-09	7.74E-09
GO:0070887	cellular response to chemical stimulus	2.59E-10	2.59E-10	GO:0031902	late endosome membrane	1.08E-07	1.08E-07
GO:0042221	response to chemical	7.01E-10	7.01E-10	GO:0005770	late endosome	1.54E-07	1.54E-07

GO:0032787	monocarboxylic acid metabolic process	7.04E-10	7.04E-10	GO:0010008	endosome membrane	1.60E-07	1.60E-07
GO:0019637	organophosphate metabolic process	1.46E-09	1.46E-09	GO:0005929	cilium	1.29E-06	1.29E-06
GO:0006793	phosphorus metabolic process	2.77E-09	2.77E-09	GO:0090533	cation-transporting ATPase complex	6.27E-06	6.27E-06
GO:0006796	phosphate-containing compound metabolic process	2.88E-09	2.88E-09	GO:0098590	plasma membrane region	7.08E-06	7.08E-06
GO:0048584	positive regulation of response to stimulus	3.20E-09	3.20E-09	GO:0022626	cytosolic ribosome	7.20E-06	7.20E-06
GO:0007166	cell surface receptor signaling pathway	5.15E-09	5.15E-09	GO:0030054	cell junction	8.00E-06	8.00E-06
GO:1901136	carbohydrate derivative catabolic process	2.73E-08	2.73E-08	GO:0033176	proton-transporting V-type ATPase complex	9.27E-06	9.27E-06
GO:0042592	homeostatic process	3.99E-08	3.99E-08	GO:0045202	synapse	2.58E-05	2.58E-05
GO:0048731	system development	5.56E-08	5.56E-08	GO:0098533	ATPase dependent transmembrane transport complex	3.56E-05	3.56E-05
GO:1901135	carbohydrate derivative metabolic process	1.17E-07	1.17E-07	GO:0005776	autophagosome	7.45E-05	7.45E-05
GO:0006996	organelle organization	1.18E-07	1.18E-07	GO:0110165	cellular anatomical structure	2.47E-04	2.47E-04
GO:0033554	cellular response to stress	2.01E-07	2.01E-07	GO:0033178	proton-transporting two-sector ATPase complex, catalytic domain	4.28E-04	4.28E-04
GO:0046434	organophosphate catabolic process	2.63E-07	2.63E-07	GO:0033180	proton-transporting V-type ATPase, V1 domain	4.28E-04	4.28E-04
GO:0019538	protein metabolic process	2.64E-07	2.64E-07	GO:0005856	cytoskeleton	4.47E-04	4.47E-04
GO:0030030	cell projection organization	2.73E-07	2.73E-07	GO:0005740	mitochondrial envelope	6.31E-04	6.31E-04
GO:0016052	carbohydrate catabolic process	3.04E-07	3.04E-07	GO:0005811	lipid droplet	1.06E-03	1.06E-03
GO:0120036	plasma membrane bounded cell projection organization	3.35E-07	3.35E-07	GO:0043005	neuron projection	1.55E-03	1.55E-03
GO:0044282	small molecule catabolic process	6.72E-07	6.72E-07	GO:0031966	mitochondrial membrane	1.77E-03	1.77E-03
GO:0071705	nitrogen compound transport	8.21E-07	8.21E-07	GO:0022627	cytosolic small ribosomal subunit	2.07E-03	2.07E-03
GO:0007275	multicellular organism development	1.04E-06	1.04E-06	GO:0016469	proton-transporting two-sector ATPase complex	2.47E-03	2.47E-03
GO:0065008	regulation of biological quality	1.08E-06	1.08E-06	GO:0005576	extracellular region	2.49E-03	2.49E-03
GO:0010647	positive regulation of cell communication	1.1E-06	1.1E-06	GO:0015630	microtubule cytoskeleton	3.96E-03	3.96E-03
GO:0009967	positive regulation of signal transduction	1.14E-06	1.14E-06	GO:0005815	microtubule organizing center	4.74E-03	4.74E-03
GO:0006631	fatty acid metabolic process	1.8E-06	1.8E-06	GO:0022625	cytosolic large ribosomal subunit	4.78E-03	4.78E-03
GO:0043603	amide metabolic process	2.43E-06	2.43E-06	GO:0099503	secretory vesicle	6.78E-03	6.78E-03
GO:0048869	cellular developmental process	2.52E-06	2.52E-06	GO:0031967	organelle envelope	6.91E-03	6.91E-03
GO:0030154	cell differentiation	2.52E-06	2.52E-06	GO:0005813	centrosome	7.01E-03	7.01E-03
GO:0023056	positive regulation of signaling	2.75E-06	2.75E-06	GO:0098794	postsynapse	8.87E-03	8.87E-03
GO:0048585	negative regulation of response to stimulus	3.38E-06	3.38E-06	GO:0030496	midbody	1.37E-02	1.37E-02
GO:0051239	regulation of multicellular organismal process	3.4E-06	3.4E-06	GO:0035869	ciliary transition zone	1.38E-02	1.38E-02

GO:0008219	cell death	4.25E-06	4.25E-06	GO:0005615	extracellular space	1.49E-02	1.49E-02
GO:0012501	programmed cell death	4.25E-06	4.25E-06	GO:0030424	axon	2.14E-02	2.14E-02
GO:0051649	establishment of localization in cell	4.37E-06	4.37E-06	GO:0048471	perinuclear region of cytoplasm	2.75E-02	2.75E-02
GO:0055085	transmembrane transport	5.13E-06	5.13E-06	GO:0016471	vacuolar proton- transporting V-type ATPase complex	3.38E-02	3.38E-02
GO:0035556	intracellular signal transduction	5.5E-06	5.5E-06	GO:0030990	intraciliary transport particle	3.91E-02	3.91E-02
GO:0033036	macromolecule localization	5.64E-06	5.64E-06	GO:0014069	postsynaptic density	4.16E-02	4.16E-02
GO:0080134	regulation of response to stress	5.97E-06	5.97E-06	GO:0030133	transport vesicle	4.70E-02	4.70E-02
GO:1902531	regulation of intracellular signal transduction	6.81E-06	6.81E-06	GO:0098978	glutamatergic synapse	4.95E-02	4.95E-02

Table S1. Gene Ontogeny terms of upregulated gene

GO_Biological process				GO_Cellular component			
GO.ID	Description	p-Value	FDR	GO.ID	Description	p-Value	FDR
GO:0050789	regulation of biological process	2.35E-103	2.35E-103	GO:0005654	nucleoplasm	1.08E-97	1.08E-97
GO:0050794	regulation of cellular process	1.07E-101	1.07E-101	GO:0005694	chromosome	2.66E-68	2.66E-68
GO:0065007	biological regulation	4.57E-99	4.57E-99	GO:0005737	cytoplasm	4.54E-57	4.54E-57
GO:0080090	regulation of primary metabolic process	1.43E-78	1.43E-78	GO:0005829	cytosol	2.79E-44	2.79E-44
GO:0019219	regulation of nucleobase-containing compound metabolic process	9.38E-63	9.38E-63	GO:1902494	catalytic complex	7.04E-42	7.04E-42
GO:0060255	regulation of macromolecule metabolic process	1.38E-61	1.38E-61	GO:0000785	chromatin	3.45E-35	3.45E-35
GO:0048518	positive regulation of biological process	1.09E-60	1.09E-60	GO:0005856	cytoskeleton	1.79E-28	1.79E-28
GO:0007049	cell cycle	1.21E-59	1.21E-59	GO:0098687	chromosomal region	1.75E-26	1.75E-26
GO:0048522	positive regulation of cellular process	9.82E-58	9.82E-58	GO:1990234	transferase complex	1.07E-24	1.07E-24
GO:0019222	regulation of metabolic process	1.30E-57	1.30E-57	GO:0140535	intracellular protein-containing complex	3.05E-24	3.05E-24
GO:0022402	cell cycle process	2.24E-56	2.24E-56	GO:0000775	chromosome, centromeric region	1.78E-23	1.78E-23
GO:0051252	regulation of RNA metabolic process	5.84E-50	5.84E-50	GO:0099080	supramolecular complex	5.04E-21	5.04E-21
GO:0010556	regulation of macromolecule biosynthetic process	3.99E-45	3.99E-45	GO:0000793	condensed chromosome	1.77E-18	1.77E-18
GO:0009889	regulation of biosynthetic process	1.59E-44	1.59E-44	GO:0015630	microtubule cytoskeleton	1.90E-17	1.90E-17
GO:0048523	negative regulation of cellular process	1.26E-43	1.26E-43	GO:0016604	nuclear body	7.29E-17	7.29E-17
GO:0006996	organelle organization	8.02E-43	8.02E-43	GO:0005681	spliceosomal complex	1.76E-16	1.76E-16
GO:0051716	cellular response to stimulus	3.77E-42	3.77E-42	GO:0000228	nuclear chromosome	2.03E-15	2.03E-15
GO:0010468	regulation of gene expression	5.50E-42	5.50E-42	GO:0000779	condensed chromosome, centromeric region	5.57E-15	5.57E-15
GO:0048519	negative regulation of biological process	1.15E-41	1.15E-41	GO:0043233	organelle lumen	6.82E-15	6.82E-15
GO:1903047	mitotic cell cycle process	5.53E-41	5.53E-41	GO:0070013	intracellular organelle lumen	6.82E-15	6.82E-15
GO:0000278	mitotic cell cycle	1.10E-40	1.10E-40	GO:0031974	membrane-enclosed lumen	6.82E-15	6.82E-15
GO:0006351	DNA-templated transcription	1.83E-40	1.83E-40	GO:0000776	kinetochore	2.54E-14	2.54E-14
GO:0006259	DNA metabolic process	6.91E-38	6.91E-38	GO:0005819	spindle	4.75E-14	4.75E-14
GO:0010604	positive regulation of macromolecule metabolic process	2.77E-37	2.77E-37	GO:0005622	intracellular anatomical structure	2.54E-13	2.54E-13
GO:2001141	regulation of RNA biosynthetic process	1.57E-36	1.57E-36	GO:0031981	nuclear lumen	4.57E-13	4.57E-13
GO:0050896	response to stimulus	4.79E-36	4.79E-36	GO:0071013	catalytic step 2 spliceosome	1.26E-12	1.26E-12
GO:0006355	regulation of DNA-templated transcription	5.32E-36	5.32E-36	GO:0015629	actin cytoskeleton	2.20E-12	2.20E-12
GO:0009893	positive regulation of metabolic process	1.29E-35	1.29E-35	GO:0005813	centrosome	2.27E-12	2.27E-12

GO:0051726	regulation of cell cycle	2.32E-35	2.32E-35	GO:0005815	microtubule organizing center	2.22E-11	2.22E-11
GO:0045935	positive regulation of nucleobase-containing compound metabolic process	3.00E-35	3.00E-35	GO:0005635	nuclear envelope	2.47E-11	2.47E-11
GO:0051276	chromosome organization	1.13E-32	1.13E-32	GO:0072686	mitotic spindle	1.78E-10	1.78E-10
GO:0032502	developmental process	2.81E-31	2.81E-31	GO:0000502	proteasome complex	9.79E-10	9.79E-10
GO:0048856	anatomical structure development	1.25E-30	1.25E-30	GO:0035770	ribonucleoprotein granule	1.90E-09	1.90E-09
GO:0045934	negative regulation of nucleobase-containing compound metabolic process	8.28E-30	8.28E-30	GO:0070161	anchoring junction	2.65E-09	2.65E-09
GO:0007059	chromosome segregation	9.46E-30	9.46E-30	GO:0016607	nuclear speck	4.13E-09	4.13E-09
GO:0035556	intracellular signal transduction	9.95E-30	9.95E-30	GO:0036464	cytoplasmic ribonucleoprotein granule	4.78E-09	4.78E-09
GO:0051254	positive regulation of RNA metabolic process	1.99E-29	1.99E-29	GO:0010494	cytoplasmic stress granule	7.83E-09	7.83E-09
GO:0007165	signal transduction	2.08E-29	2.08E-29	GO:0032991	protein-containing complex	1.32E-08	1.32E-08
GO:0010564	regulation of cell cycle process	3.52E-29	3.52E-29	GO:0022624	proteasome accessory complex	1.45E-08	1.45E-08
GO:0010605	negative regulation of macromolecule metabolic process	9.91E-28	9.91E-28	GO:0034708	methyltransferase complex	7.07E-08	7.07E-08
GO:0009891	positive regulation of biosynthetic process	3.81E-27	3.81E-27	GO:0061695	transferase complex, transferring phosphorus-containing groups	2.00E-07	2.00E-07
GO:0006950	response to stress	6.80E-27	6.80E-27	GO:0030684	preribosome	4.57E-07	4.57E-07
GO:0009892	negative regulation of metabolic process	7.02E-27	7.02E-27	GO:0110165	cellular anatomical structure	4.95E-07	4.95E-07
GO:0010557	positive regulation of macromolecule biosynthetic process	1.16E-26	1.16E-26	GO:0031965	nuclear membrane	1.27E-06	1.27E-06
GO:0007010	cytoskeleton organization	7.50E-26	7.50E-26	GO:0005684	U2-type spliceosomal complex	1.32E-06	1.32E-06
GO:0023052	signaling	1.47E-25	1.47E-25	GO:1905368	peptidase complex	1.48E-06	1.48E-06
GO:0007154	cell communication	1.57E-25	1.57E-25	GO:0032040	small-subunit processome	1.67E-06	1.67E-06
GO:0051128	regulation of cellular component organization	1.76E-25	1.76E-25	GO:1905369	endopeptidase complex	1.70E-06	1.70E-06
GO:0098813	nuclear chromosome segregation	2.42E-25	2.42E-25	GO:0001650	fibrillar center	1.71E-06	1.71E-06
GO:0051253	negative regulation of RNA metabolic process	4.04E-25	4.04E-25	GO:0031248	protein acetyltransferase complex	2.10E-06	2.10E-06
GO:0033043	regulation of organelle organization	7.25E-25	7.25E-25	GO:1902493	acetyltransferase complex	2.10E-06	2.10E-06
GO:0048583	regulation of response to stimulus	7.56E-25	7.56E-25	GO:0031252	cell leading edge	2.29E-06	2.29E-06
GO:0033554	cellular response to stress	2.62E-24	2.62E-24	GO:0099512	supramolecular fiber	3.41E-06	3.41E-06
GO:0006366	transcription by RNA polymerase II	9.31E-24	9.31E-24	GO:0099081	supramolecular polymer	7.52E-06	7.52E-06
GO:0007275	multicellular organism development	1.21E-23	1.21E-23	GO:0000922	spindle pole	8.05E-06	8.05E-06
GO:0051641	cellular localization	1.33E-23	1.33E-23	GO:0099513	polymeric cytoskeletal fiber	9.25E-06	9.25E-06
GO:0006260	DNA replication	2.82E-23	2.82E-23	GO:0031967	organelle envelope	9.41E-06	9.41E-06

GO:0140694	membraneless organelle assembly	5.46E-23	5.46E-23	GO:0005643	nuclear pore	1.05E-05	1.05E-05
GO:0140014	mitotic nuclear division	7.55E-23	7.55E-23	GO:0005911	cell-cell junction	1.24E-05	1.24E-05
GO:0033036	macromolecule localization	8.13E-23	8.13E-23	GO:0005667	transcription regulator complex	1.62E-05	1.62E-05
GO:0006325	chromatin organization	9.61E-23	9.61E-23	GO:0005838	proteasome regulatory particle	1.71E-05	1.71E-05
GO:0044770	cell cycle phase transition	1.48E-22	1.48E-22	GO:0030054	cell junction	2.61E-05	2.61E-05
GO:0051052	regulation of DNA metabolic process	1.49E-22	1.49E-22	GO:0030055	cell-substrate junction	2.97E-05	2.97E-05
GO:0000819	sister chromatid segregation	6.47E-22	6.47E-22	GO:0000792	heterochromatin	3.23E-05	3.23E-05
GO:0010558	negative regulation of macromolecule biosynthetic process	8.04E-22	8.04E-22	GO:0000940	outer kinetochore	4.13E-05	4.13E-05
GO:0000070	mitotic sister chromatid segregation	8.74E-22	8.74E-22	GO:0005925	focal adhesion	5.63E-05	5.63E-05
GO:0006974	DNA damage response	1.01E-21	1.01E-21	GO:0005657	replication fork	6.05E-05	6.05E-05
GO:0006357	regulation of transcription by RNA polymerase II	1.75E-21	1.75E-21	GO:0070603	SWI/SNF superfamily-type complex	1.13E-04	1.13E-04
GO:0009890	negative regulation of biosynthetic process	1.78E-21	1.78E-21	GO:0000781	chromosome, telomeric region	1.31E-04	1.31E-04

Table S2. Gene Ontogeny terms of downregulated gene

	KEGG.ID	Description	P-Value	FDR
Upregulated	KEGG:01100	Metabolic pathways	2.10E-22	2.10E-22
	KEGG:04142	Lysosome	1.39E-17	1.39E-17
	KEGG:05171	Coronavirus disease - COVID-19	8.92E-07	8.92E-07
	KEGG:03010	Ribosome	7.70E-06	7.70E-06
	KEGG:04721	Synaptic vesicle cycle	5.38E-05	5.38E-05
	KEGG:00511	Other glycan degradation	5.90E-05	5.90E-05
	KEGG:00051	Fructose and mannose metabolism	1.79E-04	1.79E-04
	KEGG:00600	Sphingolipid metabolism	8.99E-04	8.99E-04
	KEGG:04146	Peroxisome	1.44E-03	1.44E-03
	KEGG:04966	Collecting duct acid secretion	1.85E-03	1.85E-03
	KEGG:00052	Galactose metabolism	8.93E-03	8.93E-03
	KEGG:00480	Glutathione metabolism	9.91E-03	9.91E-03
	KEGG:05323	Rheumatoid arthritis	1.10E-02	1.10E-02
	KEGG:00520	Amino sugar and nucleotide sugar metabolism	1.69E-02	1.69E-02
	KEGG:05152	Tuberculosis	2.29E-02	2.29E-02
	KEGG:04145	Phagosome	2.88E-02	2.88E-02
	KEGG:04144	Endocytosis	3.17E-02	3.17E-02
	KEGG:04932	Non-alcoholic fatty liver disease	4.18E-02	4.18E-02
	KEGG:00190	Oxidative phosphorylation	4.42E-02	4.42E-02
Downregulated	KEGG:04110	Cell cycle	2.64E-23	2.64E-23
	KEGG:03013	Nucleocytoplasmic transport	1.61E-22	1.61E-22
	KEGG:04390	Hippo signaling pathway	7.55E-11	7.55E-11
	KEGG:03008	Ribosome biogenesis in eukaryotes	1.19E-09	1.19E-09
	KEGG:04520	Adherens junction	2.10E-08	2.10E-08
	KEGG:05014	Amyotrophic lateral sclerosis	4.28E-08	4.28E-08
	KEGG:03040	Spliceosome	6.77E-08	6.77E-08
	KEGG:03082	ATP-dependent chromatin remodeling	6.44E-07	6.44E-07
	KEGG:04814	Motor proteins	8.86E-07	8.86E-07
	KEGG:04530	Tight junction	1.20E-06	1.20E-06
	KEGG:04810	Regulation of actin cytoskeleton	1.22E-06	1.22E-06
	KEGG:04120	Ubiquitin mediated proteolysis	1.94E-06	1.94E-06
	KEGG:03050	Proteasome	2.97E-06	2.97E-06
	KEGG:05203	Viral carcinogenesis	3.49E-06	3.49E-06
	KEGG:04350	TGF-beta signaling pathway	5.76E-06	5.76E-06
	KEGG:04218	Cellular senescence	8.73E-06	8.73E-06
	KEGG:05132	Salmonella infection	9.66E-06	9.66E-06
	KEGG:05017	Spinocerebellar ataxia	2.63E-05	2.63E-05

KEGG:05200	Pathways in cancer	3.73E-05	3.73E-05
KEGG:05205	Proteoglycans in cancer	8.22E-05	8.22E-05
KEGG:05161	Hepatitis B	1.09E-04	1.09E-04
KEGG:04510	Focal adhesion	4.45E-04	4.45E-04
KEGG:03030	DNA replication	6.49E-04	6.49E-04
KEGG:03015	mRNA surveillance pathway	1.00E-03	1.00E-03
KEGG:05166	Human T-cell leukemia virus 1 infection	1.03E-03	1.03E-03
KEGG:04550	Signaling pathways regulating pluripotency of stem cells	1.46E-03	1.46E-03
KEGG:03083	Polycomb repressive complex	2.16E-03	2.16E-03
KEGG:05170	Human immunodeficiency virus 1 infection	2.21E-03	2.21E-03
KEGG:05165	Human papillomavirus infection	2.67E-03	2.67E-03
KEGG:05100	Bacterial invasion of epithelial cells	2.73E-03	2.73E-03
KEGG:03018	RNA degradation	2.79E-03	2.79E-03
KEGG:04310	Wnt signaling pathway	3.03E-03	3.03E-03
KEGG:05210	Colorectal cancer	3.68E-03	3.68E-03
KEGG:04114	Oocyte meiosis	3.89E-03	3.89E-03
KEGG:05211	Renal cell carcinoma	5.85E-03	5.85E-03
KEGG:04919	Thyroid hormone signaling pathway	6.92E-03	6.92E-03
KEGG:05022	Pathways of neurodegeneration - multiple diseases	1.04E-02	1.04E-02
KEGG:04141	Protein processing in endoplasmic reticulum	1.07E-02	1.07E-02
KEGG:03440	Homologous recombination	2.18E-02	2.18E-02
KEGG:04360	Axon guidance	2.30E-02	2.30E-02
KEGG:05225	Hepatocellular carcinoma	2.76E-02	2.76E-02
KEGG:05010	Alzheimer disease	3.44E-02	3.44E-02
KEGG:05169	Epstein-Barr virus infection	3.85E-02	3.85E-02
KEGG:04152	AMPK signaling pathway	4.33E-02	4.33E-02
KEGG:01524	Platinum drug resistance	4.67E-02	4.67E-02

Table S3. KEGG pathways of upregulated and downregulated genes

Sample ID	Total Sequences	% GC	Average Read Length	Adapter Contamination
Ctrl1_1.fq	20764657	48	150	PASS
Ctrl1_2.fq	20764657	49	150	PASS
Ctrl2_1.fq	23698911	48	150	PASS
Ctrl2_2.fq	23698911	49	150	PASS
Ctrl3_1.fq	21041746	48	150	PASS
Ctrl3_2.fq	21041746	49	150	PASS
PDM1_1.fq	22688421	49	variable(31-150)	PASS
PDM1_2.fq	22688421	50	variable(31-150)	PASS
PDM2_1.fq	24738849	49	variable(31-150)	PASS
PDM2_2.fq	24738849	50	variable(31-150)	PASS
PDM3_1.fq	22512738	49	150	PASS
PDM3_2.fq	22512738	50	150	PASS

Table S4. Summary of FastQC Results for Each Sample

Sample ID	Total Reads	Uniquely Mapped (%)	Multi-mapped (%)	Unmapped (%)	Overall Mapping Rate (%)
Ctrl_1	20764657	92.56	2.11	5.29	94.71
Ctrl_2	24738849	87.53	2.07	10.23	89.77
Ctrl_3	21041746	93.10	2.24	4.57	95.43
PDM_1	20263113	89.31	1.9	8.66	91.34
PDM_2	21654408	87.53	2.07	10.23	89.77
PDM_3	19788374	87.9	1.9	10.11	89.89

Table S5. Summary of STAR Alignment Results for Each Sample

Sample ID	Assigned Reads	%Assigned	Unassigned Multimapping	Unassigned No Feature	Unassigned Ambiguous
Ctrl_1	32634535	80.39	2159066	4807004	996983
Ctrl_2	36683798	79.34	2425776	6006865	1120331
Ctrl_3	33101824	79.63	2386066	5047952	1031762
PDM_1	34555242	80.74	2270630	4728855	1242129
PDM_2	37375826	81.11	2771318	4520290	1412700
PDM_3	33932825	81.14	2245330	4374939	1268984

Table S6. Summary of featureCounts Quantification Results for Each Sample