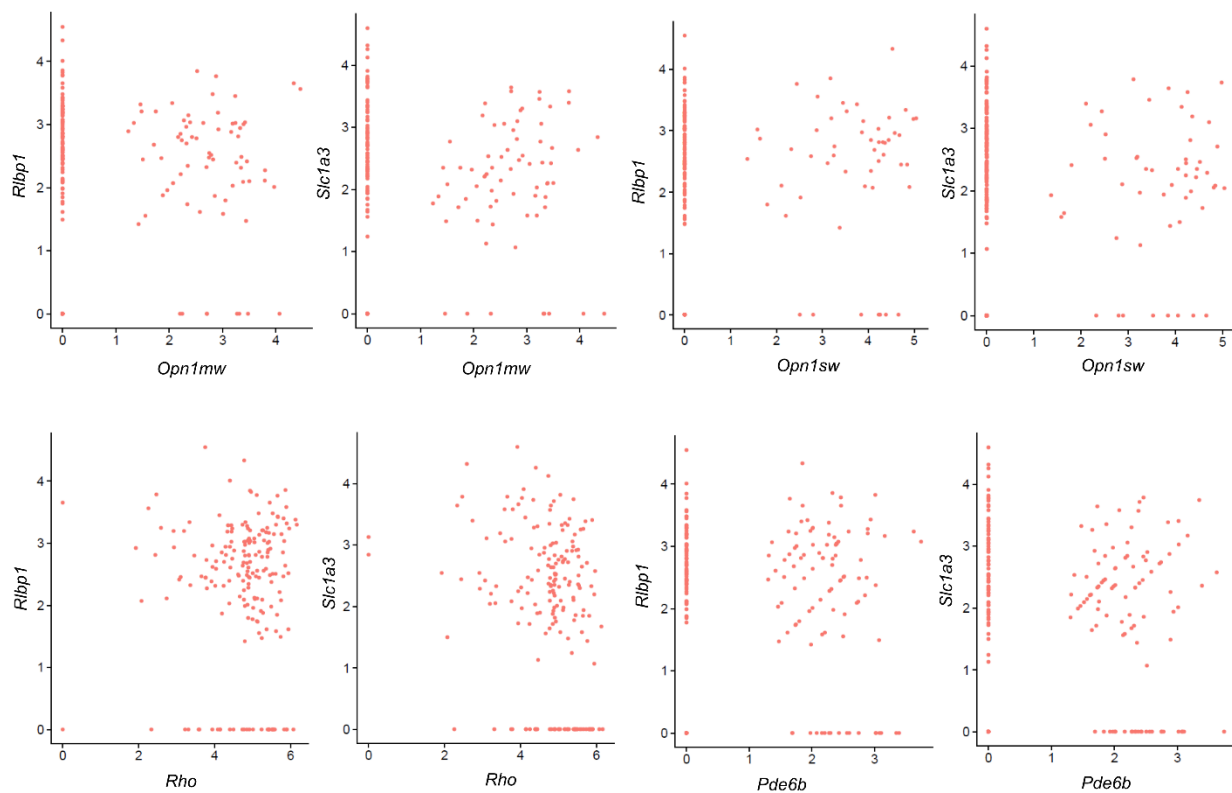




Supplementary Figure 1: X-Y scatter plots of normalized expression of marker genes for rod (*Rho*, *Pde6b*), cone (*Opn1mw*, *Opn1sw*) and Müller glial (*Rlbp1*, *Slc1a3*) in cluster 12 cells.

Supplementary Table 1, Cell number from each mouse sample.

Sample	Number of cells
WT_1	1651
WT_2	1539
WT_3	576
WT_4	419
Het_1	2031
Het_2	761
Het_3	880
Het_4	970

Supplementary Table 2, number of cells with >500 detectable genes in each cluster.

tSNE group	Cell type	Number of cells
0	Rods	1491
1	Bipolar cells	1063
2	Rods	942
3	Cones	831
4	Bipolar cells	772
5	Rods	702
6	Rods	647
7	Amacrine cells	529
8	Amacrine cells	517
9	Muller glia	443
10	Muller glia	398
11	Amacrine cells	198
12	Mixed	19
13	Macrophage Microglia	46
14	Endothelial cells	34
15	Retinal ganglion cells	24

Supplementary Table 3, GO pathway analysis with downregulated genes in rods

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count	GO_type	minus log10	gene rati
GO:0022626	cytosolic ribosome	33/268	111/18982	8.04E-35	2.69E-32	2.42E-32	Rpl18a/U	33 CC		34.09455	0.123
GO:0003735	structural constituent of ribosome	32/260	153/18634	1.32E-28	6.90E-26	6.30E-26	Rpl18a/R	32 MF		27.879034	0.123
GO:0044391	ribosomal subunit	33/268	190/18982	1.63E-26	2.14E-24	1.93E-24	Rpl18a/U	33 CC		25.787632	0.123
GO:0005840	ribosome	35/268	224/18982	1.92E-26	2.14E-24	1.93E-24	Rpl18a/U	35 CC		25.716661	0.131
GO:0007601	visual perception	27/264	157/18773	8.62E-22	1.91E-18	1.86E-18	Rho/Opn:	27 BP		21.064243	0.102
GO:0001750	photoreceptor outer segment	21/268	76/18982	9.24E-22	7.71E-20	6.95E-20	Rho/Opn:	21 CC		21.034545	0.078
GO:0050953	sensory perception of light stimulus	27/264	161/18773	1.72E-21	1.91E-18	1.86E-18	Rho/Opn:	27 BP		20.763452	0.102
GO:0009583	detection of light stimulus	18/264	49/18773	2.02E-21	1.91E-18	1.86E-18	Rho/Opn:	18 BP		20.694281	0.068
GO:0022627	cytosolic small ribosomal subunit	17/268	46/18982	2.56E-20	1.71E-18	1.54E-18	Uba52/Rf	17 CC		19.590945	0.063
GO:0097733	photoreceptor cell cilium	22/268	110/18982	2.09E-19	1.16E-17	1.05E-17	Rho/Opn:	22 CC		18.680007	0.082
GO:0097731	9+0 non-motile cilium	22/268	116/18982	7.06E-19	3.37E-17	3.04E-17	Rho/Opn:	22 CC		18.151017	0.082
GO:0022625	cytosolic large ribosomal subunit	17/268	60/18982	4.76E-18	1.99E-16	1.79E-16	Rpl18a/U	17 CC		17.322453	0.063
GO:0097730	non-motile cilium	23/268	148/18982	1.18E-17	4.38E-16	3.95E-16	Rho/Opn:	23 CC		16.928268	0.086
GO:0015935	small ribosomal subunit	17/268	75/18982	3.02E-16	1.01E-14	9.09E-15	Uba52/Rf	17 CC		15.52002	0.063
GO:0007602	phototransduction	12/264	28/18773	1.16E-15	8.23E-13	8.00E-13	Rho/Opn:	12 BP		14.935309	0.045
GO:0009582	detection of abiotic stimulus	19/264	127/18773	1.64E-14	8.99E-12	8.73E-12	Rho/Slc1	19 BP		13.78538	0.072
GO:0009581	detection of external stimulus	19/264	128/18773	1.90E-14	8.99E-12	8.73E-12	Rho/Slc1	19 BP		13.72103	0.072
GO:0042622	photoreceptor outer segment membrane	9/268	14/18982	3.67E-14	1.11E-12	1.00E-12	Rho/Pde	9 CC		13.435381	0.034
GO:0002181	cytoplasmic translation	16/264	88/18773	8.70E-14	3.53E-11	3.43E-11	Rpl18a/Pl	16 BP		13.060424	0.061
GO:0009416	response to light stimulus	25/264	285/18773	3.24E-13	1.15E-10	1.12E-10	Rho/Opn:	25 BP		12.489558	0.095
GO:0015934	large ribosomal subunit	17/268	120/18982	1.10E-12	3.05E-11	2.75E-11	Rpl18a/U	17 CC		11.95982	0.063
GO:0009584	detection of visible light	10/264	30/18773	5.99E-12	1.89E-09	1.83E-09	Rho/Prph	10 BP		11.222915	0.038
GO:0042461	photoreceptor cell development	12/264	59/18773	2.90E-11	8.23E-09	8.00E-09	Nr2e3/Nr	12 BP		10.537301	0.045
GO:0051606	detection of stimulus	20/264	236/18773	1.53E-10	3.95E-08	3.84E-08	Rho/Slc1	20 BP		9.8145251	0.076
GO:0009314	response to radiation	25/264	387/18773	2.56E-10	6.04E-08	5.87E-08	Rho/Opn:	25 BP		9.59252	0.095
GO:0046530	photoreceptor cell differentiation	12/264	78/18773	8.89E-10	1.94E-07	1.88E-07	Nr2e3/Nr	12 BP		9.0513024	0.045
GO:0060041	retina development in camera-type eye	15/264	154/18773	4.81E-09	9.74E-07	9.47E-07	Rho/Nr2e	15 BP		8.3178647	0.057
GO:0000028	ribosomal small subunit assembly	7/264	20/18773	6.66E-09	1.26E-06	1.22E-06	Rps27/Rp	7 BP		8.1764447	0.027
GO:0001917	photoreceptor inner segment	10/268	59/18982	9.10E-09	2.34E-07	2.11E-07	Rho/Gnat	10 CC		8.0410304	0.037
GO:0060170	ciliary membrane	9/268	47/18982	1.66E-08	3.97E-07	3.57E-07	Rho/Pde	9 CC		7.779326	0.034
GO:0042274	ribosomal small subunit biogenesis	10/264	69/18773	4.18E-08	7.42E-06	7.21E-06	Rps27/Rp	10 BP		7.3784149	0.038
GO:0005844	polysome	10/268	70/18982	5.01E-08	1.12E-06	1.01E-06	Rpl18a/R	10 CC		7.2999475	0.037
GO:0042788	polysomal ribosome	7/268	29/18982	1.24E-07	2.58E-06	2.33E-06	Rpl18a/R	7 CC		6.9074454	0.026
GO:0007603	phototransduction, visible light	5/264	10/18773	1.26E-07	2.05E-05	2.00E-05	Rho/Grk1	5 BP		6.899639	0.019
GO:0045494	photoreceptor cell maintenance	8/264	43/18773	1.30E-07	2.05E-05	2.00E-05	Rho/Abca	8 BP		6.8850087	0.030
GO:0050908	detection of light stimulus involved in visual perception	6/264	20/18773	2.40E-07	3.40E-05	3.31E-05	Prph2/Ro	6 BP		6.6196716	0.023
GO:0050962	detection of light stimulus involved in sensory perception	6/264	20/18773	2.40E-07	3.40E-05	3.31E-05	Prph2/Ro	6 BP		6.6196716	0.023
GO:0001895	retina homeostasis	8/264	53/18773	7.05E-07	9.53E-05	9.26E-05	Rho/Abca	8 BP		6.151561	0.030
GO:0030507	spectrin binding	6/260	29/18634	2.53E-06	0.00065964	0.0006026	Rho/Pde	6 MF		5.5973354	0.023
GO:0001654	eye development	19/264	387/18773	2.60E-06	0.00033489	0.0003255	Rho/Nr2e	19 BP		5.5853774	0.072
GO:0150063	visual system development	19/264	391/18773	3.02E-06	0.00036427	0.0003541	Rho/Nr2e	19 BP		5.5202772	0.072
GO:0042255	ribosome assembly	8/264	64/18773	3.08E-06	0.00036427	0.0003541	Rps27/Rp	8 BP		5.5110764	0.030
GO:0048880	sensory system development	19/264	395/18773	3.50E-06	0.0003969	0.0003858	Rho/Nr2e	19 BP		5.4560823	0.072
GO:0019843	rRNA binding	8/260	69/18634	5.17E-06	0.00089978	0.0008219	Rpl9/Rps:	8 MF		5.2864127	0.031
GO:0046034	ATP metabolic process	14/264	233/18773	5.80E-06	0.00063299	0.0006153	Pgam1/Es	14 BP		5.2363368	0.053
GO:0043010	camera-type eye development	17/264	340/18773	6.95E-06	0.00073045	0.0007101	Rho/Nr2e	17 BP		5.1577519	0.064
GO:0071482	cellular response to light stimulus	9/264	95/18773	7.69E-06	0.00077841	0.0007567	Rho/Opn:	9 BP		5.1143426	0.034
GO:0001754	eye photoreceptor cell differentiation	7/264	53/18773	8.91E-06	0.0008717	0.0008474	Nr2e3/Nr	7 BP		5.0499424	0.027
GO:0042462	eye photoreceptor cell development	6/264	39/18773	1.62E-05	0.00152672	0.0014841	Nr2e3/Nr	6 BP		4.7918263	0.023
GO:0004114	3',5'-cyclic-nucleotide phosphodiesterase activity	5/260	24/18634	1.74E-05	0.00196872	0.0017984	Pde6g/Pd	5 MF		4.7592209	0.019
GO:0008081	phosphoric diester hydrolase activity	8/260	82/18634	1.89E-05	0.00196872	0.0017984	Pde6g/Pd	8 MF		4.7245169	0.031
GO:0004112	cyclic-nucleotide phosphodiesterase activity	5/260	26/18634	2.63E-05	0.00229116	0.0020929	Pde6g/Pd	5 MF		4.5794647	0.019
GO:0035845	photoreceptor cell outer segment organization	4/264	14/18773	3.42E-05	0.00313314	0.0030457	Prph2/Ro	4 BP		4.4653647	0.015
GO:0047555	3',5'-cyclic-GMP phosphodiesterase activity	4/260	15/18634	4.48E-05	0.00334004	0.0030511	Pde6g/Pd	4 MF		4.3488209	0.015
GO:0042254	ribosome biogenesis	14/264	283/18773	5.08E-05	0.00450602	0.0043803	Rps27/Rp	14 BP		4.2937629	0.053
GO:0031253	cell projection membrane	14/268	293/18982	7.72E-05	0.00151645	0.0013669	Rho/Kcnc	14 CC		4.1124684	0.052
GO:0043209	myelin sheath	11/268	205/18982	0.0001662	0.00308399	0.0027798	Pgam1/Gi	11 CC		3.779361	0.041

Supplementary Table 4, GO pathway analysis with upregulated genes in rods

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count	GO_type	minus log10	GeneRatio
GO:0000979	RNA polymerase II core promoter sequence-specific DNA binding	5/156	22/18634	9.05E-07	0.00019757	0.00018436	Stat1/Gtf2a1/Fos/Egr1/H3f3a	5	MF	6.04324749	0.03205128
GO:0031720	haptoglobin binding	4/156	10/18634	9.54E-07	0.00019757	0.00018436	Hbb-bt/Hba-a1/Hba-a2/Hbb-bs	4	MF	6.02025081	0.02564103
GO:0005833	hemoglobin complex	4/162	10/18982	1.03E-06	0.00016691	0.00015253	Hbb-bt/Hba-a1/Hba-a2/Hbb-bs	4	CC	5.98655634	0.02469136
GO:0043209	myelin sheath	11/162	205/18982	1.54E-06	0.00016691	0.00015253	Ubb/Nefh/Ckb/Eef1a1/Fscn1/Nme2/Ppl	11	CC	5.81357775	0.06790123
GO:0031838	haptoglobin-hemoglobin complex	4/162	11/18982	1.61E-06	0.00016691	0.00015253	Hbb-bt/Hba-a1/Hba-a2/Hbb-bs	4	CC	5.79315979	0.02469136
GO:0019825	oxygen binding	4/156	23/18634	3.70E-05	0.00461025	0.00430196	Hbb-bt/Hba-a1/Hba-a2/Hbb-bs	4	MF	4.43215008	0.02564103
GO:0001046	core promoter sequence-specific DNA binding	5/156	47/18634	4.45E-05	0.00461025	0.00430196	Stat1/Gtf2a1/Fos/Egr1/H3f3a	5	MF	4.35121571	0.03205128
GO:0097440	apical dendrite	4/162	28/18982	8.92E-05	0.0069357	0.00633826	Slc1a1/Nefh/Neurl1a/Clu	4	CC	4.04961009	0.02469136

Supplementary Table 5, GO pathway analysis with downregulated genes in cones

ID	Description	GeneRatio	lgRatio	pvalue	p.adjust	qvalue	geneID	GO_type	minus log10	GeneRatio
GO:0042622	photoreceptor outer segment membrane	10/112	14/18982	3.33E-20	7.02E-18	5.78E-18	Rho/Gnat1/Cnga1/Pde6a/Pde6b/Rom1/Pde6g/Cdhrl/Prctd/Pde6h	CC	19.4779339	0.08928571
GO:0001750	photoreceptor outer segment	14/112	76/18982	1.36E-17	1.43E-15	1.18E-15	Rho/Gnat1/Gnb1/Cnga1/Pde6a/Prph2/Pde6b/Rom1/Pde6g/Cdhrl/Prctd/Gngt1/Pde6h/Gna	CC	16.8667605	0.125
GO:0007601	visual perception	17/107	157/18773	2.41E-17	2.61E-14	2.39E-14	Rho/Gnat1/Reep6/Cnga1/Pde6a/Prph2/Pde6b/Rom1/Pde6g/Rcvrn/Unc119/Prctd/Rbp3/Cat	BP	16.617949	0.1588785
GO:0050953	sensory perception of light stimulus	17/107	161/18773	3.71E-17	2.61E-14	2.39E-14	Rho/Gnat1/Reep6/Cnga1/Pde6a/Prph2/Pde6b/Rom1/Pde6g/Rcvrn/Unc119/Prctd/Rbp3/Cat	BP	16.4300858	0.1588785
GO:0005853	detection of light stimulus	12/107	49/17773	4.82E-17	2.61E-14	2.39E-14	Rho/Gnat1/Gnb1/Reep6/Prph2/Pde6b/Rom1/Rcvrn/Cabp4/Gngt1/Aiopl1/Gnat2	BP	16.3165846	0.1214953
GO:0007733	photoreceptor cell cilium	14/112	110/18982	3.08E-15	2.17E-13	1.78E-13	Rho/Gnat1/Gnb1/Cnga1/Pde6a/Prph2/Pde6b/Rom1/Pde6g/Cdhrl/Prctd/Gngt1/Pde6h/Gna	CC	14.5112719	0.125
GO:0007731	9+0 non-motile cilium	14/112	116/18982	6.60E-15	3.48E-13	2.86E-13	Rho/Gnat1/Gnb1/Cnga1/Pde6a/Prph2/Pde6b/Rom1/Pde6g/Cdhrl/Prctd/Gngt1/Pde6h/Gna	CC	14.1807759	0.125
GO:0022626	cytosolic ribosome	13/112	111/18982	9.54E-14	4.02E-12	3.31E-12	Rpl23a/Rps18/Rpl6/Rps13/Rpl21/Rpl18a/Rps2/Rpl35a/Rps29/Rps27/Rps25/Rplp1/Rps14	CC	13.020614	0.1607143
GO:0060170	ciliary membrane	10/112	47/18982	1.46E-13	5.15E-12	4.24E-12	Rho/Gnb1/Cnga1/Pde6a/Pde6b/Rom1/Pde6g/Cdhrl/Prctd/Pde6h	CC	12.8344294	0.08928571
GO:0007730	non-motile cilium	14/112	148/18982	2.05E-13	6.19E-12	5.09E-12	Rho/Gnat1/Gnb1/Cnga1/Pde6a/Prph2/Pde6b/Rom1/Pde6g/Cdhrl/Prctd/Gngt1/Pde6h/Gna	CC	12.6877187	0.125
GO:0005852	detection of abiotic stimulus	13/107	127/18773	3.52E-13	1.26E-10	1.16E-10	Rho/Gnat1/Gnb1/Reep6/Prph2/Pde6b/Rom1/Slc12a2/Rcvrn/Cabp4/Gngt1/Aiopl1/Gnat2	BP	12.4538293	0.1214953
GO:0005851	detection of external stimulus	13/107	128/18773	3.90E-13	1.26E-10	1.16E-10	Rho/Gnat1/Gnb1/Reep6/Prph2/Pde6b/Rom1/Slc12a2/Rcvrn/Cabp4/Gngt1/Aiopl1/Gnat2	BP	12.4093483	0.1214953
GO:0007602	phototransduction	8/107	28/18773	2.41E-12	6.53E-10	5.99E-10	Rho/Gnat1/Gnb1/Rcvrn/Cabp4/Gngt1/Aiopl1/Gnat2	BP	11.6172795	0.07476636
GO:0005854	detection of visible light	8/107	30/18773	4.50E-12	1.04E-09	9.58E-10	Rho/Gnat1/Gnb1/Reep6/Prph2/Rom1/Aiopl1/Gnat2	BP	11.3464841	0.07476636
GO:0007375	structural constituent of ribosome	13/108	153/18634	4.85E-12	1.42E-09	1.16E-09	Rpl23a/Rps18/Rpl6/Rps13/Rpl21/Rpl18a/Rps2/Rpl35a/Rps29/Rps27/Rps25/Rplp1/Rps14	MF	11.3143703	0.1203707
GO:0042461	photoreceptor cell development	9/107	59/18773	4.47E-11	9.07E-09	8.31E-09	Gnat1/Nrl/Nr2e3/Prph2/Rom1/Cabp4/Gngt1/Gnat2	BP	10.3497889	0.08411215
GO:0001917	photoreceptor inner segment	9/112	59/18982	6.14E-11	1.62E-09	1.33E-09	Rho/Gnat1/Gnb1/Reep6/Pkm/Guk1/Gngt1/Aiopl1/Gnat2	CC	10.2117215	0.08035714
GO:0044391	ribosomal subunit	13/112	190/18982	9.59E-11	2.25E-09	1.85E-09	Rpl23a/Rps18/Rpl6/Rps13/Rpl21/Rpl18a/Rps2/Rpl35a/Rps29/Rps27/Rps25/Rplp1/Rps14	CC	10.0182248	0.1607143
GO:0009135	purine nucleoside diphosphate metabolic process	10/107	100/18773	2.66E-10	4.32E-08	3.96E-08	Aldoa/Esrrb/Pkm/Pfkl/Pgam1/Tp1/Guk1/Eno1/Eno1b/Mif	BP	9.57465922	0.09345794
GO:0009179	purine ribonucleoside diphosphate metabolic process	10/107	100/18773	2.66E-10	4.32E-08	3.96E-08	Aldoa/Esrrb/Pkm/Pfkl/Pgam1/Tp1/Guk1/Eno1/Eno1b/Mif	BP	9.57465922	0.09345794
GO:0046939	nucleotide phosphorylation	10/107	103/18773	3.58E-10	5.28E-08	4.84E-08	Aldoa/Esrrb/Pkm/Pfkl/Pgam1/Tp1/Guk1/Eno1/Eno1b/Mif	BP	9.44635479	0.09345794
GO:0009185	ribonucleoside diphosphate metabolic process	10/107	104/18773	3.94E-10	5.33E-08	4.89E-08	Aldoa/Esrrb/Pkm/Pfkl/Pgam1/Tp1/Guk1/Eno1/Eno1b/Mif	BP	9.40449672	0.09345794
GO:0046530	photoreceptor cell differentiation	9/107	78/18773	5.93E-10	7.40E-08	6.79E-08	Gnat1/Nrl/Nr2e3/Prph2/Rom1/Cabp4/Gngt1/Gnat2	BP	9.22697429	0.08411215
GO:0005840	ribosome	13/112	224/18982	7.37E-10	1.55E-08	1.28E-08	Rpl23a/Rps18/Rpl6/Rps13/Rpl21/Rpl18a/Rps2/Rpl35a/Rps29/Rps27/Rps25/Rplp1/Rps14	CC	9.13263354	0.1607143
GO:0051606	detection of stimulus	13/107	236/18773	8.97E-10	1.04E-07	9.53E-08	Rho/Gnat1/Gnb1/Reep6/Prph2/Pde6b/Rom1/Slc12a2/Rcvrn/Cabp4/Gngt1/Aiopl1/Gnat2	BP	9.04729674	0.1214953
GO:0060041	retina development in camera-type eye	11/107	154/18773	1.25E-09	1.35E-07	1.24E-07	Rho/Gnat1/Nrl/Gnb1/Nr2e3/Pde6a/Prph2/Pde6b/Rom1/Cabp4/Gnat2	BP	8.90476349	0.1280374
GO:0009132	nucleoside diphosphate metabolic process	10/107	118/18773	1.38E-09	1.40E-07	1.28E-07	Aldoa/Esrrb/Pkm/Pfkl/Pgam1/Tp1/Guk1/Eno1/Eno1b/Mif	BP	8.86101477	0.09345794
GO:0006096	glycolytic process	9/107	89/18773	1.96E-09	1.77E-07	1.62E-07	Aldoa/Esrrb/Pkm/Pfkl/Pgam1/Tp1/Eno1/Eno1b/Mif	BP	8.70715574	0.08411215
GO:0006757	ATP generation from ADP	9/107	89/18773	1.96E-09	1.77E-07	1.62E-07	Aldoa/Esrrb/Pkm/Pfkl/Pgam1/Tp1/Eno1/Eno1b/Mif	BP	8.70715574	0.08411215
GO:0046031	ADP metabolic process	9/107	95/18773	3.53E-09	3.01E-07	2.76E-07	Aldoa/Esrrb/Pkm/Pfkl/Pgam1/Tp1/Eno1/Eno1b/Mif	BP	8.45259946	0.08411215
GO:0006165	nucleoside diphosphate phosphorylation	9/107	101/18773	6.09E-09	4.95E-07	4.54E-07	Aldoa/Esrrb/Pkm/Pfkl/Pgam1/Tp1/Eno1/Eno1b/Mif	BP	8.21511352	0.08411215
GO:0009416	response to light stimulus	13/107	285/18773	7.87E-09	6.79E-07	6.22E-07	Rho/Gnat1/Gnb1/Reep6/Prph2/Pde6b/Rom1/Rcvrn/Stk11/Cabp4/Gngt1/Aiopl1/Gnat2	BP	8.05649226	0.1214953
GO:0026277	cytosolic small ribosomal subunit	7/112	46/18982	9.12E-09	1.75E-07	1.44E-07	Rps18/Rps13/Rps2/Rps29/Rps27/Rps25/Rps14	CC	8.04004517	0.0625
GO:0001754	eye photoreceptor cell differentiation	7/107	53/18773	1.99E-08	1.47E-06	1.35E-06	Gnat1/Nrl/Nr2e3/Rom1/Cabp4/Gngt1/Gnat2	BP	7.70096249	0.06542056
GO:0006090	pyruvate metabolic process	9/107	117/18773	2.23E-08	1.58E-06	1.45E-06	Aldoa/Esrrb/Pkm/Pfkl/Pgam1/Tp1/Eno1/Eno1b/Mif	BP	7.65027316	0.08411215
GO:0002181	cytoplasmic translation	8/107	88/18773	3.77E-08	2.55E-06	2.34E-06	Pkm/Tmat7/Rpl6/Rpl18a/Rps2/Rpl35a/Rps29/Rplp1	BP	7.42413211	0.07476636
GO:0050908	detection of light stimulus involved in visual perception	5/107	20/18773	7.93E-08	4.95E-06	4.54E-06	Gnat1/Reep6/Prph2/Rom1/Gnat2	BP	7.10079686	0.04672897
GO:0050962	detection of light stimulus involved in sensory perception	5/107	20/18773	7.93E-08	4.95E-06	4.54E-06	Gnat1/Reep6/Prph2/Rom1/Gnat2	BP	7.10079686	0.04672897
GO:0042462	eye photoreceptor cell development	6/107	39/18773	8.33E-08	5.01E-06	4.59E-06	Gnat1/Nrl/Nr2e3/Cabp4/Gngt1/Gnat2	BP	7.07914885	0.06504777
GO:0046034	ATP metabolic process	11/107	233/18773	9.26E-08	5.36E-06	4.92E-06	Aldoa/Esrrb/Pkm/Pfkl/Pgam1/Tp1/Guk1/Uqcrh/Eno1/Eno1b/Mif	BP	7.03361957	0.1280374
GO:0016052	carbohydrate catabolic process	9/107	139/18773	1.00E-07	5.59E-06	5.13E-06	Aldoa/Esrrb/Pkm/Pfkl/Pgam1/Tp1/Eno1/Eno1b/Mif	BP	7.00012639	0.08411215
GO:0007603	phototransduction, visible light	4/107	10/18773	2.04E-07	1.10E-05	1.01E-05	Rho/Gnat1/Gnb1/Aiopl1	BP	6.69032599	0.03738318
GO:0019535	small ribosomal subunit	7/112	75/18982	2.94E-07	5.17E-06	4.25E-06	Rps18/Rps13/Rps2/Rps29/Rps27/Rps25/Rps14	CC	6.53189975	0.0625
GO:0047555	eye development	13/107	387/18773	3.12E-07	1.58E-05	1.45E-05	Rho/Gnat1/Nrl/Gnb1/Nr2e3/Pde6a/Prph2/Pde6b/Rom1/Cabp4/Gngt1/Sh3pxd2b/Gnat2	BP	6.50521172	0.1214953
GO:0009314	response to radiation	13/107	387/18773	3.12E-07	1.58E-05	1.45E-05	Rho/Gnat1/Gnb1/Reep6/Prph2/Pde6b/Rom1/Rcvrn/Stk11/Cabp4/Gngt1/Aiopl1/Gnat2	BP	6.50521572	0.1214953
GO:0150063	visual system development	13/107	391/18773	3.51E-07	1.73E-05	1.58E-05	Rho/Gnat1/Nrl/Gnb1/Nr2e3/Pde6a/Prph2/Pde6b/Rom1/Cabp4/Gngt1/Sh3pxd2b/Gnat2	BP	6.45441567	0.1214953
GO:0048880	sensory system development	13/107	395/18773	3.94E-07	1.88E-05	1.73E-05	Rho/Gnat1/Nrl/Gnb1/Nr2e3/Pde6a/Prph2/Pde6b/Rom1/Cabp4/Gngt1/Sh3pxd2b/Gnat2	BP	6.40422588	0.1214953
GO:0031253	cell projection membrane	11/112	293/18982	1.30E-06	2.10E-05	1.73E-05	Rho/Gnb1/Cnga1/Pde6a/Pde6b/Rom1/Pde6g/Kcnb1/Cdhrl/Prctd/Pde6h	CC	5.887634	0.09821429
GO:0047555	3',5'-cyclic-GMP phosphodiesterase activity	4/108	15/18634	1.39E-06	0.00020246	0.0001664	Pde6a/Pde6b/Pde6g/Pde6h	MF	5.85801638	0.03703704
GO:0022625	cytosolic large ribosomal subunit	6/112	60/18982	1.42E-06	2.15E-05	1.77E-05	Rpl23a/Rpl6/Rpl21/Rpl18a/Rpl35a/Rplp1	CC	5.84604032	0.05357143
GO:0042255	ribosome assembly	6/107	64/18773	1.71E-06	7.91E-05	7.26E-05	Rpl23a/Rpl6/Rps2/Rps27/Rps25/Rps14	BP	5.76788494	0.06507477
GO:0019843	rRNA binding	6/108	69/18634	2.94E-06	0.00028588	0.00023497	Rpl23a/Rps18/Rpl6/Rps13/Ncl/Rps14	MF	5.52037832	0.05555556
GO:0043010	camera-type eye development	11/107	340/18773	3.85E-06	0.00017363	0.00015924	Rho/Gnat1/Nrl/Gnb1/Nr2e3/Pde6a/Prph2/Pde6b/Rom1/Cabp4/Gnat2	BP	5.41438429	0.1280374
GO:0000028	ribosomal small subunit assembly	4/107	20/18773	4.50E-06	0.0001976	0.00018121	Rps2/Rps27/Rps25/Rps14	BP	5.34633111	0.03738318
GO:0022618	ribonucleoprotein complex assembly	8/107	166/18773	4.90E-06	0.0002091	0.00019176	Rpl23a/Rpl6/Prph8/Rps2/Rps27/Rps25/Rps14/Isy1	BP	5.31018479	0.07476636
GO:0071826	ribonucleoprotein complex subunit organization	8/107	173/18773	6.64E-06	0.0002763	0.00025399	Rpl23a/Rpl6/Prph8/Rps2/Rps27/Rps25/Rps14/Isy1	BP	5.17788026	0.07476636
GO:0041144	3',5'-cyclic-nucleotide phosphodiesterase activity	4/108	24/18634	1.04E-05	0.00075698	0.00062218	Pde6a/Pde6b/Pde6g/Pde6h	MF	4.98423619	0.03703704
GO:0009150	purine ribonucleotide metabolic process	10/107	311/18773	1.15E-05	0.00046502	0.00042646	Aldoa/Esrrb/Pkm/Pfkl/Pgam1/Tp1/Guk1/Eno1/Eno1b/Mif	BP	4.94078789	0.09345794
GO:0001895	retina homeostasis	5/107	53/18773	1.26E-05	0.00050032	0.0004883	Rho/Pde6a/Esrrb/Cdhrl/Aiopl1	BP	4.89828657	0.04672897
GO:0050906	detection of stimulus involved in sensory perception	7/107	137/18773	1.34E-05	0.00051893	0.0004759	Rho/Gnat1/Reep6/Prph2/Rom1/Slc12a2/Gnat2	BP	4.87196056	0.06542056
GO:0004112	cyclic-nucleotide phosphodiesterase activity	4/108	26/18634	1.45E-05	0.00084445	0.00069407	Pde6a/Pde6b/Pde6g/Pde6h	MF	4.83984101	0.03703704
GO:0009259	ribonucleotide metabolic process	10/107	321/18773	1.51E-05	0.00056888	0.00052171	Aldoa/Esrrb/Pkm/Pfkl/Pgam1/Tp1/Guk1/Eno1/Eno1b/Mif	BP	4.82182823	0.09345794
GO:0019693	ribose phosphate metabolic process	10/107	332/18773	2.01E-05	0.00074284	0.00068124	Aldoa/Esrrb/Pkm/Pfkl/Pgam1/Tp1/Guk1/Eno1/Eno1b/Mif	BP	4.69597302	0.09345794
GO:0006163	purine nucleotide metabolic process	10/107	339/18773	2.41E-05	0.00086826	0.00079626	Aldoa/Esrrb/Pkm/Pfkl/Pgam1/Tp1/Guk1/Eno1/Eno1b/Mif	BP	4.61845644	0.09345794
GO:0060219	camera-type eye photoreceptor cell differentiation	4/107	33/18773	3.59E-05	0.00126797	0.00116283	Nrl/Rom1/Cabp4/Gnat2	BP	4.44445265	0.03738318
GO:0005834	heterotrimeric G-protein complex	4/112	33/18982	4.12E-05	0.0005431	0.00044705	Gnat1/Gnb1/Gngt1/Gnat2	CC	4.38528416	0.03571429
GO:1905360	GTPase complex	4/112	33/18982	4.12E-05	0.0005431	0.00044705	Gnat1/Gnb1/Gngt1/Gnat2	CC	4.38528416	0.03571429
GO:0019318	hexose metabolic process	8/107	224/18773	4.29E-05	0.00148114	0.00135832	Aldoa/Fam3c/Esrrb/Pkm/Pfkl/Tp1/G6pc3/Stk11	BP	4.36762462	0.07476636
GO:0006091	generation of precursor metabolites and energy	10/107	375/18773	5.65E-05	0.00190913	0.00175083	Aldoa/Esrrb/Pkm/Pfkl/Pgam1/Tp1/Uqcrh/Eno1/Eno1b/Mif	BP	4.24824145	0.09345794
GO:0048592	eye morphogenesis	7/107	174/18773	6.23E-05	0.00203202	0.00186352	Gnat1/Nrl/Nr2e3/Rom1/Cabp4/Gngt1/Gnat2	BP	4.20532457	0.06542056
GO:0035845	photoreceptor cell outer segment organization	3/107	14/18773	6.26E-05	0.00203202	0.00186352	Prph2/Rom1/Cdhrl	BP	4.20342123	0.02803738
GO:0072521	purine-containing compound metabolic process	10/107	381/18773	6.45E-05	0.00205112	0.00188104	Aldoa/Esrrb/Pkm/Pfkl/Pgam1/Tp1/Guk1/Eno1/Eno1b/Mif	BP	4.19075781	0.09345794
GO:0015934	large ribosomal subunit	6/112	120/18982	7.80E-05	0.00096845	0.00079718	Rpl23a/Rpl6/Rpl21/Rpl18a/Rpl35a/Rplp1	CC	4.07175717	0.05357143
GO:0022613	ribonucleoprotein complex biogenesis	10/107	392/18773	8.16E-05	0.00254744	0.0023				

Supplementary Table 6, GO pathway analysis with upregulated genes in Müller glia

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count	GO_type	minus log10	GeneRatio
GO:0001750	photoreceptor outer segment	20/214	76/18982	2.80E-22	1.03E-19	8.16E-20	Gucy2e/Tulp1/P	20	CC	21.5529657	0.09345794
GO:0007601	visual perception	25/210	157/18773	7.25E-22	2.13E-18	1.81E-18	Gucy2e/Nxn12/I	25	BP	21.1397282	0.11904762
GO:0050953	sensory perception of light stimulus	25/210	161/18773	1.38E-21	2.13E-18	1.81E-18	Gucy2e/Nxn12/I	25	BP	20.8601999	0.11904762
GO:0097733	photoreceptor cell cilium	21/214	110/18982	3.59E-20	6.60E-18	5.23E-18	Gucy2e/Tulp1/P	21	CC	19.4451618	0.09813084
GO:0097731	9+0 non-motile cilium	21/214	116/18982	1.16E-19	1.42E-17	1.12E-17	Gucy2e/Tulp1/P	21	CC	18.9373981	0.09813084
GO:0097730	non-motile cilium	21/214	148/18982	2.18E-17	2.01E-15	1.59E-15	Gucy2e/Tulp1/P	21	CC	16.661359	0.09813084
GO:0042622	photoreceptor outer segment membrane	9/214	14/18982	4.74E-15	3.49E-13	2.76E-13	Gucy2e/Phlpp2/	9	CC	14.324329	0.04205607
GO:0060041	retina development in camera-type eye	17/210	154/18773	1.58E-12	1.63E-09	1.38E-09	Tulp1/Hif1a/Rp/	17	BP	11.8011483	0.08095238
GO:0001917	photoreceptor inner segment	12/214	59/18982	2.17E-12	1.33E-10	1.06E-10	Tulp1/Phlpp2/R	12	CC	11.662589	0.05607477
GO:0048592	eye morphogenesis	16/210	174/18773	1.19E-10	8.60E-08	7.29E-08	Tulp1/Bdnf/Hif1/	16	BP	9.92539873	0.07619048
GO:0009583	detection of light stimulus	10/210	49/18773	1.39E-10	8.60E-08	7.29E-08	Tulp1/Rom1/Rs/	10	BP	9.85666562	0.04761905
GO:0001754	eye photoreceptor cell differentiation	10/210	53/18773	3.17E-10	1.64E-07	1.39E-07	Tulp1/Rpgrip1/C	10	BP	9.49829929	0.04761905
GO:0007602	phototransduction	8/210	28/18773	5.50E-10	2.43E-07	2.06E-07	Rs1/Gnb1/Gngt/	8	BP	9.25943262	0.03809524
GO:0060170	ciliary membrane	9/214	47/18982	2.34E-09	1.23E-07	9.74E-08	Gucy2e/Phlpp2/	9	CC	8.63129989	0.04205607
GO:0001654	eye development	21/210	387/18773	2.67E-09	1.03E-06	8.76E-07	Tulp1/Bdnf/Hif1/	21	BP	8.57295479	0.1
GO:0150063	visual system development	21/210	391/18773	3.21E-09	1.10E-06	9.35E-07	Tulp1/Bdnf/Hif1/	21	BP	8.49363691	0.1
GO:0048880	sensory system development	21/210	395/18773	3.84E-09	1.19E-06	1.01E-06	Tulp1/Bdnf/Hif1/	21	BP	8.41532662	0.1
GO:0003407	neural retina development	10/210	70/18773	5.48E-09	1.54E-06	1.31E-06	Rpgrip1/Cas21/f	10	BP	8.26160591	0.04761905
GO:0001895	retina homeostasis	9/210	53/18773	6.69E-09	1.72E-06	1.46E-06	Nxn12/Tulp1/Pc/	9	BP	8.17482081	0.04285714
GO:0090596	sensory organ morphogenesis	18/210	301/18773	8.62E-09	2.05E-06	1.74E-06	Tulp1/Pcdh15/B	18	BP	8.06432199	0.08571429
GO:0043010	camera-type eye development	19/210	340/18773	9.87E-09	2.18E-06	1.85E-06	Tulp1/Hif1a/Rp/	19	BP	8.00552673	0.09047619
GO:0046530	photoreceptor cell differentiation	10/210	78/18773	1.61E-08	3.31E-06	2.81E-06	Tulp1/Rpgrip1/C	10	BP	7.79403529	0.04761905
GO:0009582	detection of abiotic stimulus	12/210	127/18773	1.95E-08	3.77E-06	3.20E-06	Prrx1/Tulp1/Pc/	12	BP	7.70941841	0.05714286
GO:0009581	detection of external stimulus	12/210	128/18773	2.13E-08	3.82E-06	3.24E-06	Prrx1/Tulp1/Pc/	12	BP	7.67091113	0.05714286
GO:0045494	photoreceptor cell maintenance	8/210	43/18773	2.22E-08	3.82E-06	3.24E-06	Nxn12/Tulp1/Pc/	8	BP	7.65304036	0.03809524
GO:0060219	camera-type eye photoreceptor cell differentiation	7/210	33/18773	6.62E-08	1.08E-05	9.13E-06	Rpgrip1/Cas21/f	7	BP	7.17920686	0.03333333
GO:0060042	retina morphogenesis in camera-type eye	9/210	72/18773	1.07E-07	1.65E-05	1.40E-05	Rpgrip1/Cas21/f	9	BP	6.97109325	0.04285714
GO:0031253	cell projection membrane	16/214	293/18982	2.32E-07	1.07E-05	8.44E-06	Pdpn/Gucy2e/N	16	CC	6.63529669	0.07476636
GO:0048593	camera-type eye morphogenesis	11/210	143/18773	6.28E-07	9.25E-05	7.85E-05	Hif1a/Rpgrip1/C	11	BP	6.20182066	0.05238095
GO:0030507	spectrin binding	6/207	29/18634	6.71E-07	0.00029048	0.00025069	Myo10/Epab41/f	6	MF	6.17336542	0.02898551
GO:0009584	detection of visible light	6/210	30/18773	8.66E-07	0.00012168	0.00010318	Tulp1/Rom1/Rs/	6	BP	6.06261092	0.02857143
GO:0051606	detection of stimulus	13/210	236/18773	2.69E-06	0.00036052	0.00030573	Prrx1/Tulp1/Pc/	13	BP	5.57079543	0.06190476
GO:0034643	establishment of mitochondrion localization, microtubule-mediated	5/210	21/18773	2.94E-06	0.00036052	0.00030573	Ubb/Kif1b/Hif1a	5	BP	5.53206184	0.02380952
GO:0047497	mitochondrion transport along microtubule	5/210	21/18773	2.94E-06	0.00036052	0.00030573	Ubb/Kif1b/Hif1a	5	BP	5.53206184	0.02380952
GO:0097499	protein localization to non-motile cilium	4/210	10/18773	3.03E-06	0.00036052	0.00030573	Tulp1/Rom1/Ar/	4	BP	5.51833936	0.01904762
GO:0042461	photoreceptor cell development	7/210	59/18773	4.13E-06	0.00046506	0.00039438	Tulp1/Rpgrip1/f	7	BP	5.38382873	0.03333333
GO:0009416	response to light stimulus	14/210	285/18773	4.21E-06	0.00046506	0.00039438	Tulp1/Hif1a/Ro/	14	BP	5.37557562	0.06666667
GO:0042462	eye photoreceptor cell development	6/210	39/18773	4.37E-06	0.00046639	0.00039551	Tulp1/Rpgrip1/C	6	BP	5.35909535	0.02857143
GO:0051654	establishment of mitochondrion localization	5/210	24/18773	5.97E-06	0.00061528	0.00052178	Ubb/Kif1b/Hif1a	5	BP	5.22404373	0.02380952
GO:0005516	calmodulin binding	11/207	183/18634	6.55E-06	0.00141822	0.00122394	Akap12/Myo10/	11	MF	5.1837154	0.0531401
GO:0061351	neural precursor cell proliferation	11/210	182/18773	6.65E-06	0.00066344	0.00056262	Wnt7b/Insm1/C	11	BP	5.17707483	0.05238095
GO:0042670	retinal cone cell differentiation	4/210	12/18773	7.02E-06	0.00067841	0.00057531	Cas21/Gnat2/Ca	4	BP	5.15359737	0.01904762
GO:0008277	regulation of G protein-coupled receptor signaling pathway	9/210	124/18773	1.08E-05	0.00101145	0.00085774	Usp33/Frmpd1/	9	BP	4.96678051	0.04285714
GO:0032103	positive regulation of response to external stimulus	16/210	401/18773	1.22E-05	0.00110945	0.00094085	Lgals9/Cdh13/O	16	BP	4.91365283	0.07619048
GO:0010970	transport along microtubule	10/210	162/18773	1.46E-05	0.00129128	0.00109504	Ubb/Kif1b/Map	10	BP	4.83515036	0.04761905
GO:0001894	tissue homeostasis	12/210	244/18773	2.05E-05	0.00175823	0.00149103	Nxn12/Tulp1/Pc/	12	BP	4.68886081	0.05714286
GO:0099568	cytoplasmic region	11/214	210/18982	2.75E-05	0.00112255	0.00088943	Map2/Gpsm2/D	11	CC	4.56140111	0.05140187
GO:2000177	regulation of neural precursor cell proliferation	8/210	111/18773	3.53E-05	0.00295259	0.00250388	insm1/Bdnf/	8	BP	4.45183462	0.03809524
GO:0019897	extrinsic component of plasma membrane	10/214	179/18982	3.70E-05	0.00136161	0.00107885	Cdh13/Rs1/Rtbc	10	CC	4.43179585	0.04672897
GO:0051607	defense response to virus	11/210	226/18773	4.99E-05	0.00406132	0.00344411	Ifi441/Trim30a/f	11	BP	4.30178913	0.05238095
GO:0099111	microtubule-based transport	10/210	188/18773	5.24E-05	0.0041555	0.00352398	Ubb/Kif1b/Map	10	BP	4.2805515	0.04761905
GO:0050839	cell adhesion molecule binding	12/207	271/18634	5.32E-05	0.00768237	0.00662998	Cd9/Cdh13/Anx	12	MF	4.27387151	0.05797101
GO:0009615	response to virus	12/210	270/18773	5.50E-05	0.00425292	0.0036066	Lgals9/Ifi441/Tri	12	BP	4.25949184	0.05714286
GO:0030705	cytoskeleton-dependent intracellular transport	10/210	191/18773	5.99E-05	0.00451612	0.0038298	Ubb/Kif1b/Map	10	BP	4.22268991	0.04761905
GO:1902904	negative regulation of supramolecular fiber organization	9/210	155/18773	6.34E-05	0.0046701	0.00396038	Capg/Clu/Map2	9	BP	4.19766394	0.04285714
GO:0030659	cytoplasmic vesicle membrane	13/214	323/18982	8.07E-05	0.00232428	0.00184161	Slc10a4/Kif1b/A	13	CC	4.09287582	0.06074766
GO:0042611	MHC protein complex	4/214	21/18982	8.09E-05	0.00232428	0.00184161	H2-DMb2/H2-D	4	CC	4.09222745	0.01869159
GO:0032838	plasma membrane bounded cell projection cytoplasm	9/214	159/18982	8.21E-05	0.00232428	0.00184161	Map2/Dynl1/Pi	9	CC	4.08561565	0.04205607
GO:0006836	neurotransmitter transport	11/210	241/18773	8.89E-05	0.00639104	0.00541979	Slc10a4/Cspg5/i	11	BP	4.05119931	0.05238095
GO:0051291	protein heterooligomerization	4/210	22/18773	9.50E-05	0.00667814	0.00566326	Krt1/Mat2a/Ror	4	BP	4.02213111	0.01904762
GO:0045185	maintenance of protein location	7/210	96/18773	0.00010183	0.00693336	0.00587969	Lgals9/Pfn1/Nfk	7	BP	3.99211302	0.03333333
GO:2000179	positive regulation of neural precursor cell proliferation	6/210	67/18773	0.00010315	0.00693336	0.00587969	Insm1/Optn/Hif	6	BP	3.98653792	0.02857143
GO:0035455	response to interferon-alpha	4/210	23/18773	0.00011403	0.00750201	0.00636192	Bst2/Ifttm3/Iftt1	4	BP	3.94296406	0.01904762
GO:0009314	response to radiation	14/210	387/18773	0.00012266	0.00790125	0.00670049	Tulp1/Hif1a/Ro/	14	BP	3.91130248	0.06666667
GO:0051646	mitochondrion localization	5/210	45/18773	0.0001418	0.0089476	0.00758782	Ubb/Kif1b/Hif1a	5	BP	3.84833702	0.02380952
GO:0007603	phototransduction, visible light	3/210	10/18773	0.00015627	0.00966357	0.00819499	Rs1/Gnb1/Aip1	3	BP	3.80613172	0.01428571
GO:0012506	vesicle membrane	13/214	349/18982	0.00017423	0.0045798	0.00362873	Slc10a4/Kif1b/A	13	CC	3.75887323	0.06074766
GO:0042612	MHC class I protein complex	3/214	11/18982	0.00021808	0.00535026	0.00423919	H2-D1/B2m/H2-	3	CC	3.66138203	0.01401869
GO:0150034	distal axon	13/214	374/18982	0.00034011	0.00782262	0.00619813	Clu/Map2/Tulp	13	CC	3.46837582	0.06074766
GO:0005930	axoneme	7/214	117/18982	0.00036484	0.00789768	0.0062576	Prkar2a/Rpgrip1	7	CC	3.43789918	0.03271028
GO:0097014	ciliary plasm	7/214	119/18982	0.00040436	0.00826698	0.00655021	Prkar2a/Rpgrip1	7	CC	3.39322829	0.03271028
GO:0005834	heterotrimeric G-protein complex	4/214	33/18982	0.00049734	0.00915114	0.00725076	Gnb1/Gngt1/Gn	4	CC	3.30334269	0.01869159
GO:1905360	GTPase complex	4/214	33/18982	0.00049734	0.00915114	0.00725076	Gnb1/Gngt1/Gn	4	CC	3.30334269	0.01869159
GO:0042824	MHC class I peptide loading complex	3/214	15/18982	0.00058166	0.00979949	0.00776447	H2-D1/B2m/H2-	3	CC	3.23532753	0.01401869
GO:0044306	neuron projection terminus	9/214	207/18982	0.00058584	0.00979949	0.00776447	Tulp1/Bdnf/Pac	9	CC	3.23222179	0.04205607

Supplementary Table 7, GO pathway analysis with downregulated genes in bipolar cells

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count	GO_type	minus log10	GeneRatio
GO:0003735	structural constituent of ribosome	14/126	153/18634	2.17E-12	7.11E-10	6.76E-10	Rps3/Mrpl9/	14	MF	11.6638891	0.11111111
GO:0022626	cytosolic ribosome	12/126	111/18982	9.72E-12	2.72E-09	2.33E-09	Rps3/Rpl18a	12	CC	11.0123307	0.0952381
GO:0005840	ribosome	15/126	224/18982	2.42E-11	3.03E-09	2.59E-09	Rps3/Mrpl9/	15	CC	10.6154884	0.11904762
GO:0044391	ribosomal subunit	14/126	190/18982	3.24E-11	3.03E-09	2.59E-09	Rps3/Mrpl9/	14	CC	10.4892698	0.11111111
GO:0070181	small ribosomal subunit rRNA binding	4/126	10/18634	4.06E-07	6.65E-05	6.32E-05	Cirbp/Rps3/f	4	MF	6.391939	0.03174603
GO:0022627	cytosolic small ribosomal subunit	6/126	46/18982	5.72E-07	4.00E-05	3.43E-05	Rps3/Rps14/	6	CC	6.24265386	0.04761905
GO:0015934	large ribosomal subunit	8/126	120/18982	1.36E-06	7.62E-05	6.53E-05	Mrpl9/Rpl18	8	CC	5.86646049	0.06349206
GO:0002181	cytoplasmic translation	7/124	88/18773	1.89E-06	0.00389132	0.00377264	Rpl18a/Rpl1	7	BP	5.72461293	0.05645161
GO:0022625	cytosolic large ribosomal subunit	6/126	60/18982	2.83E-06	0.00013224	0.00011334	Rpl18a/Rplp	6	CC	5.54765895	0.04761905
GO:0015935	small ribosomal subunit	6/126	75/18982	1.05E-05	0.00042034	0.00036029	Rps3/Rps14/	6	CC	4.97846236	0.04761905
GO:0042788	polysomal ribosome	4/126	29/18982	3.87E-05	0.00135289	0.00115962	Rpl18a/Rpl1	4	CC	4.41280562	0.03174603
GO:0005844	polysome	5/126	70/18982	0.00010198	0.00317278	0.00271953	Rps3/Rpl18a	5	CC	3.9914755	0.03968254

Supplementary Table 8, GO pathway analysis with downregulated genes in Amacrine cells

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count	GO_type	minus log10	GeneRatio
GO:0043209	myelin sheath	13/175	205/18982	5.89E-08	2.12E-05	1.70E-05	Atp6v1b2/M	13	CC	7.22992979	0.07428571
GO:0022626	cytosolic ribosome	9/175	111/18982	8.84E-07	0.00015905	0.00012743	Rpl37a/Rpl2	9	CC	6.05373931	0.05142857
GO:0003735	structural constituent of ribosome	10/172	153/18634	1.59E-06	0.00060807	0.00054457	Rpl37a/Rpl2	10	MF	5.79810819	0.05813953
GO:0150034	distal axon	15/175	374/18982	2.07E-06	0.00024881	0.00019934	Ptprf/Cplx3/	15	CC	5.68330675	0.08571429
GO:0044391	ribosomal subunit	10/175	190/18982	1.09E-05	0.00098272	0.00078733	Rpl37a/Rpl2	10	CC	4.96181163	0.05714286
GO:0070382	exocytic vesicle	11/175	254/18982	2.47E-05	0.00177553	0.0014225	Cplx3/Cdk16	11	CC	4.6080042	0.06285714
GO:0005840	ribosome	10/175	224/18982	4.49E-05	0.00269663	0.00216046	Rpl37a/Rpl2	10	CC	4.3473296	0.05714286
GO:0008021	synaptic vesicle	10/175	232/18982	6.04E-05	0.00285688	0.00228885	Cplx3/Cdk16	10	CC	4.2192414	0.05714286
GO:0022627	cytosolic small ribosomal subunit	5/175	46/18982	6.35E-05	0.00285688	0.00228885	Rps29/Rps28	5	CC	4.19731985	0.02857143
GO:0044306	neuron projection terminus	9/175	207/18982	0.0001326	0.00530409	0.00424948	Cplx3/Slc32a	9	CC	3.87744878	0.05142857
GO:0030659	cytoplasmic vesicle membrane	11/175	323/18982	0.0002106	0.00751327	0.0060194	Cplx3/Slc6a9	11	CC	3.67655027	0.06285714
GO:0031252	cell leading edge	12/175	382/18982	0.00022957	0.00751327	0.0060194	Atp6v1b2/Th	12	CC	3.63908071	0.06857143
GO:0030133	transport vesicle	11/175	330/18982	0.00025319	0.00759566	0.00608541	Cplx3/Cdk16	11	CC	3.59655558	0.06285714
GO:0098563	intrinsic component of synaptic vesicle membrane	5/175	64/18982	0.00030894	0.00855533	0.00685427	Cplx3/Slc6a9	5	CC	3.5101226	0.02857143
GO:0043679	axon terminus	8/175	187/18982	0.00034971	0.00899262	0.00720461	Cplx3/Slc32a	8	CC	3.45628834	0.04571429
GO:0012506	vesicle membrane	11/175	349/18982	0.00040709	0.00977015	0.00782755	Cplx3/Slc6a9	11	CC	3.39030996	0.06285714

Supplementary Table 9, GSEA of rod and Müller glia clusters in P23H vs WT retinas

rod upregulated genes-related TFs									
NAME	GS follow link to MSigDB	GS C SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
STAT1 HeLa-S3 hg19.grp	STAT1 HeLa-S3 hg19.grp	Detail 31	0.578262	2.281577	0	0.039234	0.033	40	tags=39%, list=8%, signal=39%
TEAD4 SK-N-SH hg19.grp	TEAD4 SK-N-SH hg19.grp	Detail 16	0.673964	2.18223	0.001664	0.072166	0.117	82	tags=69%, list=17%, signal=80%
BATF GM12878 hg19.grp	BATF GM12878 hg19.grp	Detail 15	0.697051	2.159325	0	0.058917	0.142	71	tags=67%, list=15%, signal=76%
TCF12 SK-N-SH hg19.grp	TCF12 SK-N-SH hg19.grp	Detail 18	0.616285	2.081809	0.001634	0.103581	0.3	54	tags=50%, list=11%, signal=54%
IKZF1 GM12878 hg19.grp	IKZF1 GM12878 hg19.grp	Detail 40	0.479374	2.014515	0.005594	0.1647	0.501	87	tags=45%, list=18%, signal=50%
EP300 HeLa-S3 hg19.grp	EP300 HeLa-S3 hg19.grp	Detail 37	0.480367	1.97442	0.004286	0.202274	0.641	75	tags=41%, list=15%, signal=44%
EP300 SK-N-SH hg19.grp	EP300 SK-N-SH hg19.grp	Detail 62	0.410986	1.870132	0.00267	0.458746	0.935	86	tags=37%, list=18%, signal=39%
TEAD4 ECC-1 hg19.grp	TEAD4 ECC-1 hg19.grp	Detail 62	0.408636	1.868547	0.002614	0.404734	0.936	73	tags=35%, list=15%, signal=36%
MEF2A GM12878 hg19.grp	MEF2A GM12878 hg19.grp	Detail 26	0.483251	1.847117	0.015038	0.429853	0.967	134	tags=62%, list=28%, signal=80%
EP300 ECC-1 hg19.grp	EP300 ECC-1 hg19.grp	Detail 23	0.512143	1.831156	0.012461	0.437107	0.976	46	tags=35%, list=9%, signal=37%
NR3C1 A549 hg19.grp	NR3C1 A549 hg19.grp	Detail 43	0.415577	1.777264	0.009859	0.597982	0.998	134	tags=53%, list=28%, signal=67%
SMC3 HepG2 hg19.grp	SMC3 HepG2 hg19.grp	Detail 44	0.413018	1.765342	0.008392	0.599381	0.999	86	tags=41%, list=18%, signal=45%
CTCF GM19240 hg19.grp	CTCF GM19240 hg19.grp	Detail 37	0.433418	1.761241	0.013314	0.57187	1	78	tags=41%, list=16%, signal=45%
STAT3 HeLa-S3 hg19.grp	STAT3 HeLa-S3 hg19.grp	Detail 67	0.371	1.74812	0.006443	0.582685	1	82	tags=34%, list=17%, signal=36%
rod downregulated genes-related TFs									
NAME	GS follow link to MSigDB	GS C SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
YY1 HepG2 hg19.grp	YY1 HepG2 hg19.grp	Detail 22	-0.373977	-1.617542	0.040107	1	0.996	220	tags=77%, list=45%, signal=135%
GABPA K562 hg19.grp	GABPA K562 hg19.grp	Detail 35	-0.307584	-1.55343	0.0625	1	1	185	tags=60%, list=38%, signal=90%
RELA GM12891 hg19.grp	RELA GM12891 hg19.grp	Detail 65	-0.259875	-1.54133	0.030172	1	1	200	tags=63%, list=41%, signal=93%
GABPA SK-N-SH hg19.grp	GABPA SK-N-SH hg19.grp	Detail 36	-0.293363	-1.469014	0.056604	1	1	258	tags=78%, list=53%, signal=154%
TCF12 ECC-1 hg19.grp	TCF12 ECC-1 hg19.grp	Detail 27	-0.308242	-1.42344	0.098901	1	1	174	tags=67%, list=36%, signal=98%
Retinal glia (Muller/astrocytes) upregulated genes-related TFs									
NAME	GS follow link to MSigDB	GS C SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
JUND H1-hESC hg19.grp	JUND H1-hESC hg19.grp	Detail 24	0.434206	1.731412	0.014002	1	0.999	108	tags=71%, list=36%, signal=102%
JUND HeLa-S3 hg19.grp	JUND HeLa-S3 hg19.grp	Detail 19	0.442398	1.64157	0.027027	1	1	83	tags=58%, list=28%, signal=75%
PRDM1 HeLa-S3 hg19.grp	PRDM1 HeLa-S3 hg19.grp	Detail 23	0.406584	1.624474	0.031432	1	1	82	tags=57%, list=28%, signal=72%
BCL11A GM12878 hg19.grp	BCL11A GM12878 hg19.grp	Detail 16	0.418579	1.524936	0.053284	1	1	92	tags=63%, list=31%, signal=86%
TCF12 myocyte mm9.grp	TCF12 myocyte mm9.grp	Detail 27	0.355985	1.502258	0.068927	1	1	78	tags=44%, list=26%, signal=55%
Retinal glia (Muller/astrocytes) downregulated genes-related TFs									
NAME	GS follow link to MSigDB	GS C SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
CTCF testis mm9.grp	CTCF testis mm9.grp	Detail 27	-0.310611	-2.005792	0	0.530678	0.209	171	tags=89%, list=58%, signal=190%
CTCF GM19240 hg19.grp	CTCF GM19240 hg19.grp	Detail 20	-0.311236	-1.661771	0.006024	1	0.833	188	tags=95%, list=63%, signal=241%
MAZ K562 hg19.grp	MAZ K562 hg19.grp	Detail 26	-0.278955	-1.645374	0.008264	1	0.852	126	tags=73%, list=42%, signal=116%
ZNF384 MEL cell line mm9.grp	ZNF384 MEL cell line mm9.grp	Detail 23	-0.264618	-1.58023	0.012658	1	0.92	164	tags=87%, list=55%, signal=179%
NELFE CH12.LX mm9.grp	NELFE CH12.LX mm9.grp	Detail 23	-0.268068	-1.557995	0.049645	1	0.936	208	tags=96%, list=70%, signal=294%
CHD1 H1-hESC hg19.grp	CHD1 H1-hESC hg19.grp	Detail 33	-0.21897	-1.557739	0.018349	1	0.936	187	tags=91%, list=63%, signal=218%
CTCF astrocyte of the spinal cord	CTCF astrocyte of the spinal cord	Detail 29	-0.241039	-1.521745	0.056604	1	0.964	179	tags=86%, list=60%, signal=196%
NFYB K562 hg19.grp	NFYB K562 hg19.grp	Detail 23	-0.259703	-1.516779	0.048276	1	0.969	46	tags=39%, list=15%, signal=43%
POLR2A liver mm9.grp	POLR2A liver mm9.grp	Detail 31	-0.226873	-1.504234	0.025	0.96177	0.973	168	tags=84%, list=57%, signal=173%
CTCF osteoblast hg19.grp	CTCF osteoblast hg19.grp	Detail 24	-0.256033	-1.491946	0.065041	0.922305	0.981	179	tags=88%, list=60%, signal=202%
CTCF skin fibroblast hg19.grp	CTCF skin fibroblast hg19.grp	Detail 17	-0.289571	-1.489897	0.034884	0.847565	0.982	165	tags=88%, list=56%, signal=187%
ZNF384 CH12.LX mm9.grp	ZNF384 CH12.LX mm9.grp	Detail 31	-0.220611	-1.483546	0.065421	0.799175	0.984	161	tags=81%, list=54%, signal=158%
UBTF MEL cell line mm9.grp	UBTF MEL cell line mm9.grp	Detail 35	-0.212534	-1.466708	0.07619	0.801737	0.988	231	tags=97%, list=78%, signal=386%
CTCF fibroblast of villous mesoderm	CTCF fibroblast of villous mesoderm	Detail 29	-0.219911	-1.450282	0.028846	0.799462	0.991	173	tags=83%, list=58%, signal=179%
Cone upregulated genes-related TFs									
NAME	GS follow link to MSigDB	GS C SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
GABPA HL-60 hg19.grp	GABPA HL-60 hg19.grp	Detail 22	0.299145	1.641659	0.007874	1	0.564	103	tags=100%, list=74%, signal=325%
ELK4 HEK293 hg19.grp	ELK4 HEK293 hg19.grp	Detail 18	0.322314	1.540951	0.071429	0.880385	0.715	99	tags=100%, list=71%, signal=303%
GATA3 SH-SY5Y hg19.grp	GATA3 SH-SY5Y hg19.grp	Detail 15	0.330645	1.49429	0.065574	0.726011	0.787	97	tags=100%, list=70%, signal=295%
MAX H1-hESC hg19.grp	MAX H1-hESC hg19.grp	Detail 17	0.308443	1.474285	0.059524	0.600318	0.824	88	tags=94%, list=63%, signal=225%
GABPA GM12878 hg19.grp	GABPA GM12878 hg19.grp	Detail 16	0.300813	1.438642	0.082278	0.559502	0.869	101	tags=100%, list=73%, signal=324%
Cone downregulated genes-related TFs									
NAME	GS follow link to MSigDB	GS C SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
MAX A549 hg19.grp	MAX A549 hg19.grp	Detail 18	-0.425527	-1.54213	0.057176	1	1	83	tags=94%, list=60%, signal=204%
POLR2A spleen mm9.grp	POLR2A spleen mm9.grp	Detail 18	-0.425258	-1.541406	0.048555	1	1	75	tags=89%, list=54%, signal=168%
CTCF astrocyte hg19.grp	CTCF astrocyte hg19.grp	Detail 15	-0.446529	-1.538345	0.058683	1	1	73	tags=87%, list=53%, signal=163%
MYC MEL cell line mm9.grp	MYC MEL cell line mm9.grp	Detail 20	-0.418045	-1.535843	0.052692	1	1	71	tags=80%, list=51%, signal=140%