

Supplemental Table 4: List of genes that share genetic correlations among the Gap43/Pten network within the retina.

Target Database: Illum_Retina_BXD_RankInv0410: Correlation Comparison from WebQTL and UTHSC initiated Feb 8 15:34:36 2011

Correlation Type: Pearson

Threshold 0.7

Selected Traits:

ILMN_1228141 (Neurod1 on Chr 2 @ 79.292819 Mb): neurogenic differentiation 1

ILMN_2594450 (Pten on Chr 19 @ 32.892434 Mb): phosphatase and tensin homolog

ILMN_1234990 (Gap43 on Chr 16 @ 42.248876 Mb): growth associated protein 43

ILMN_2418222 (Zbed4 on Chr 15 @ 88.614869 Mb): zinc finger, BED domain containing 4

ILMN_2762026 (Pcna on Chr 2 @ 132.075169 Mb): proliferating cell nuclear antigen

ILMN_1248711 (Sox2 on Chr 3 @ 34.551049 Mb): SRY-box containing gene 2

ILMN_2504978 (Pax6 on Chr 2 @ 105.537316 Mb): paired box gene 6

ILMN_1228557 (Id2 on Chr 12 @ 25.779264 Mb): inhibitor of DNA binding 2

Summary: 88 genes

Name	Symbol	Description	Chr	Position (Mb)	Neurod1	Pten	Gap43	Zbed4	Pcna	Sox2	Pax6	Id2
ILMN_1238326	Nkiras1	NFKB inhibitor interacting Ras-like protein 1	14	19.12	0.896	0.764	0.804	0.894	0.908	0.923	0.950	0.771
ILMN_2765741	Mxi1	Max interacting protein 1	19	53.45	0.921	0.778	0.778	0.900	0.930	0.908	0.936	0.758
ILMN_2615628	Ttc33	tetratricopeptide repeat domain 33	15	5.17	0.928	0.796	0.808	0.895	0.893	0.885	0.907	0.760
ILMN_2519780	Fin14		6	102.89	0.887	0.797	0.771	0.858	0.948	0.901	0.915	0.782
ILMN_2449466	Hipk1	homeodomain interacting protein kinase 1	3	103.54	0.899	0.707	0.774	0.932	0.910	0.940	0.964	0.729
ILMN_2598420	Rbm16	RNA binding motif protein 16	17	3.2	0.912	0.746	0.778	0.940	0.906	0.905	0.943	0.723
ILMN_2683732	Morf4l1	mortality factor 4 like 1	16	24.53	0.860	0.731	0.755	0.887	0.923	0.952	0.964	0.776
ILMN_2626779	Nono	non-POU-domain-containing, octamer binding protein	X	98.64	0.873	0.748	0.734	0.879	0.940	0.941	0.953	0.765
ILMN_2771074	Hnrpa2b1	heterogeneous nuclear ribonucleoprotein A2/B1	6	51.41	0.919	0.725	0.800	0.921	0.877	0.915	0.945	0.703
ILMN_3155380	Cycs	cytochrome c, somatic	6	50.51	0.930	0.764	0.808	0.896	0.878	0.883	0.904	0.743
ILMN_2605465	Snx1	sorting nexin 1	9	65.94	0.884	0.720	0.804	0.896	0.897	0.914	0.938	0.753
ILMN_2775885	Calm2	calmodulin 2	17	87.83	0.885	0.742	0.818	0.925	0.866	0.898	0.933	0.730
ILMN_2707308	Cct5	chaperonin subunit 5 (epsilon)	15	31.52	0.902	0.755	0.742	0.896	0.914	0.921	0.936	0.730

ILMN_2596761	Cip29	cytokine induced protein 29 kDa	10	128.31	0.902	0.805	0.810	0.864	0.894	0.853	0.888	0.770
ILMN_2755059	2900064A13Rik	RIKEN cDNA 2900064A13 gene	2	112.31	0.947	0.769	0.756	0.918	0.918	0.858	0.903	0.710
ILMN_1237846	Brp44	brain protein 44	1	167.41	0.880	0.803	0.766	0.833	0.956	0.876	0.884	0.780
ILMN_2669869	Lin7c	lin-7 homolog C (C. elegans)	2	109.74	0.924	0.754	0.769	0.904	0.885	0.885	0.918	0.736
ILMN_2604080	Smc3	structural maintenace of chromosomes 3	19	53.72	0.923	0.721	0.779	0.940	0.905	0.880	0.923	0.704
ILMN_2783918	Rab9	RAB9, member RAS oncogene family	13	99.04	0.904	0.749	0.823	0.895	0.878	0.881	0.900	0.734
ILMN_2714534	Map2k1	mitogen activated protein kinase kinase 1	9	64.03	0.892	0.705	0.773	0.934	0.866	0.919	0.960	0.705
ILMN_2587859	Atp5l	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g	9	44.72	0.877	0.758	0.790	0.852	0.923	0.880	0.893	0.779
ILMN_1232951	Rps6	ribosomal protein S6	X	66.86	0.883	0.707	0.766	0.937	0.885	0.902	0.938	0.722
ILMN_1243256	LOC214738		8	91.33	0.840	0.799	0.724	0.842	0.937	0.903	0.912	0.781
ILMN_2670352	Chmp5	chromatin modifying protein 5	4	40.91	0.933	0.759	0.815	0.871	0.874	0.867	0.884	0.718
ILMN_2710166	Ddx3x	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked	X	12.87	0.871	0.755	0.742	0.896	0.914	0.921	0.936	0.730
ILMN_2655555	Taf9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor	13	101.43	0.897	0.805	0.810	0.864	0.894	0.853	0.888	0.770
ILMN_1248711	Sox2	SRY-box containing gene 2	3	34.55	0.800	0.769	0.756	0.918	0.918	0.858	0.903	0.710
ILMN_2678755	Rpl22l1	ribosomal protein L22 like 1	3	28.71	0.867	0.803	0.766	0.833	0.956	0.876	0.884	0.780
ILMN_2639035	C1orf52	human chromosome 1 open reading frame 52, RIKEN cDNA 2410004B18 gene	3	145.61	0.930	0.754	0.769	0.904	0.885	0.885	0.918	0.736
ILMN_1240067	Tsn	translin	1	120.2	0.880	0.721	0.779	0.940	0.905	0.880	0.923	0.704
ILMN_2743668	Lias	lipoic acid synthetase	5	65.8	0.848	0.749	0.823	0.895	0.878	0.881	0.900	0.734
ILMN_2512541	Ube2n	ubiquitin-conjugating enzyme E2N	10	95.01	0.832	0.705	0.773	0.934	0.866	0.919	0.960	0.705
ILMN_1239438	LOC381850		7	17.31	0.856	0.758	0.790	0.852	0.923	0.880	0.893	0.779
ILMN_1243273	Pcmt1	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	10	7.35	0.917	0.812	0.791	0.853	0.875	0.833	0.869	0.724

ILMN_2510364	Trip12	thyroid hormone receptor interactor 12	1	84.72	0.919	0.728	0.751	0.910	0.883	0.860	0.893	0.726
ILMN_2491526	Zkscan3	zinc finger with KRAB and SCAN domains 3	13	21.48	0.898	0.767	0.772	0.888	0.871	0.851	0.887	0.728
ILMN_2751228	Nudcd2	NudC domain containing 2	11	40.55	0.875	0.770	0.802	0.864	0.850	0.894	0.878	0.724
ILMN_2510122	Ankhd1	ankyrin repeat and KH domain containing 1	18	36.82	0.878	0.703	0.792	0.877	0.878	0.900	0.888	0.740
ILMN_2485148	Vapa	vesicle-associated membrane protein, associated protein A	17	65.93	0.877	0.710	0.809	0.916	0.863	0.871	0.901	0.707
ILMN_2755660	Ptma	prothymosin alpha	1	88.43	0.928	0.726	0.817	0.896	0.834	0.844	0.893	0.710
ILMN_2701837	Srp72	signal recognition particle 72	5	77.43	0.904	0.766	0.767	0.879	0.893	0.858	0.864	0.708
ILMN_1248132	Stmn1	stathmin 1	4	134.03	0.813	0.707	0.821	0.822	0.875	0.892	0.891	0.804
ILMN_1227815	Idh3a	isocitrate dehydrogenase 3 (NAD+) alpha	9	54.45	0.854	0.716	0.733	0.869	0.926	0.890	0.917	0.719
ILMN_2817371	Gtf2e2	general transcription factor II E, polypeptide 2 (beta subunit)	8	34.89	0.887	0.738	0.732	0.862	0.911	0.862	0.886	0.743
ILMN_3009572	Txn1	thioredoxin 1	1	44.52	0.816	0.745	0.775	0.830	0.885	0.889	0.889	0.782
ILMN_1225312	Slc25a4	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 4	8	47.29	0.855	0.812	0.791	0.853	0.875	0.833	0.869	0.724
ILMN_1251499	Tspan3	tetraspanin 3	9	55.98	0.837	0.728	0.751	0.910	0.883	0.860	0.893	0.726
ILMN_2540475	LOC386564		X	71.51	0.888	0.767	0.772	0.888	0.871	0.851	0.887	0.728
ILMN_1249407	Mrpl39	mitochondrial ribosomal protein L39	16	84.72	0.865	0.770	0.802	0.864	0.850	0.894	0.878	0.724
ILMN_1220522	Dnm1l	dynamamin 1-like GTPase (mitochondrial and peroxisome division)	16	16.31	0.843	0.703	0.792	0.877	0.878	0.900	0.888	0.740
ILMN_1239143	Sdhd	succinate dehydrogenase complex, subunit D, integral membrane protein	9	50.4	0.872	0.710	0.809	0.916	0.863	0.871	0.901	0.707
ILMN_3137920	Sel1l	sel-1 suppressor of lin-12-like (C. elegans)	12	93.04	0.876	0.726	0.817	0.896	0.834	0.844	0.893	0.710
ILMN_2633439	Jam3	junction adhesion molecule 3	9	26.91	0.798	0.766	0.767	0.879	0.893	0.858	0.864	0.708
ILMN_2465770	Usp14	ubiquitin specific peptidase 14	15	97.03	0.883	0.707	0.821	0.822	0.875	0.892	0.891	0.804
ILMN_1217625	7-Sep	septin 7	9	25.12	0.826	0.701	0.722	0.869	0.859	0.930	0.943	0.725

ILMN_2909336	Gpm6a	glycoprotein m6a downstream element, RIKEN cDNA 9330121K16	8	56.15	0.842	0.720	0.839	0.868	0.831	0.860	0.899	0.715
ILMN_2895339	B930006L02Rik	RIKEN cDNA B930006L02 gene	7	107.99	0.878	0.736	0.805	0.839	0.876	0.843	0.860	0.734
ILMN_2671689	Cox7b	cytochrome c oxidase subunit VIIb	X	103.22	0.851	0.705	0.752	0.872	0.887	0.883	0.903	0.713
ILMN_2526572	LOC381300		1	144.99	0.830	0.778	0.730	0.870	0.872	0.853	0.870	0.753
ILMN_1241910	Psmid6	proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	14	14.95	0.890	0.731	0.799	0.845	0.816	0.863	0.876	0.707
ILMN_2743082	Bhlhb5	basic helix-loop-helix domain containing, class B5 (GABAergic amacrine and type 2 OFF-cone bipolar cell expression signature)	3	17.96	0.848	0.737	0.845	0.832	0.787	0.868	0.878	0.721
ILMN_2746167	Prmt8	protein arginine N-methyltransferase 8	6	127.64	0.846	0.718	0.862	0.833	0.820	0.857	0.869	0.708
ILMN_1240425	Tra2a	transformer 2 alpha homolog (Drosophila)	6	49.21	0.812	0.739	0.703	0.860	0.865	0.897	0.882	0.744
ILMN_1259482	Pabpc1	poly A binding protein, cytoplasmic 1	3	59.24	0.876	0.765	0.805	0.845	0.820	0.807	0.817	0.763
ILMN_2982652	Abce1	ATP-binding cassette, sub-family E (OABP), member 1	8	82.21	0.828	0.748	0.721	0.836	0.879	0.850	0.881	0.718
ILMN_1228850	Ccn1	cyclin L1	3	65.75	0.863	0.736	0.768	0.880	0.809	0.827	0.854	0.719
ILMN_2663694	Ndufs4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	13	115.08	0.878	0.701	0.722	0.869	0.859	0.930	0.943	0.725
ILMN_1215717	Nap1l1	nucleosome assembly protein 1-like 1	10	110.93	0.796	0.720	0.839	0.868	0.831	0.860	0.899	0.715
ILMN_2816315	Erlin2	ER lipid raft associated 2	8	28.15	0.813	0.736	0.805	0.839	0.876	0.843	0.860	0.734
ILMN_2654296	Rab10	RAB10, member RAS oncogene family	12	3.25	0.860	0.705	0.752	0.872	0.887	0.883	0.903	0.713
ILMN_1248892	Tmem34	transmembrane protein 34	8	80.12	0.894	0.778	0.730	0.870	0.872	0.853	0.870	0.753
ILMN_1224268	Mrps15	mitochondrial ribosomal protein S15	4	125.73	0.830	0.731	0.799	0.845	0.816	0.863	0.876	0.707
ILMN_1221592	Sec11c	SEC11 homolog C (S. cerevisiae)	18	65.98	0.846	0.737	0.845	0.832	0.787	0.868	0.878	0.721
ILMN_1226709	Bxdc1	brix domain containing 1	10	39.94	0.851	0.718	0.862	0.833	0.820	0.857	0.869	0.708
ILMN_2854983	Gpr85	G protein-coupled receptor 85	6	13.79	0.797	0.739	0.703	0.860	0.865	0.897	0.882	0.744
ILMN_2698958	Arpc2	actin related protein 2/3 complex, subunit 2	1	74.31	0.771	0.777	0.812	0.779	0.822	0.800	0.791	0.772

ILMN_1224076	MGC12966	protein LOC84792 (MGC12966)	5	144.33	0.828	0.723	0.867	0.816	0.735	0.819	0.816	0.710
ILMN_2636435	Ndufb2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2	6	39.55	0.795	0.752	0.713	0.817	0.860	0.803	0.826	0.740
ILMN_3155274	Ube3a	ubiquitin protein ligase E3A (Angelman syndrome)	7	66.54	0.793	0.781	0.755	0.807	0.842	0.806	0.797	0.712
ILMN_1253681	LOC241737		2	156.62	0.777	0.727	0.700	0.822	0.885	0.818	0.828	0.723
ILMN_2608016	Gclc	glutamate-cysteine ligase, catalytic subunit	9	77.64	0.763	0.738	0.754	0.728	0.806	0.890	0.833	0.751
ILMN_1234143	EG384525	predicted gene, EG384525	7	5.97	0.770	0.702	0.710	0.820	0.851	0.838	0.836	0.719
ILMN_1260446	Ttc3	tetratricopeptide repeat domain 3	16	94.66	0.720	0.821	0.757	0.726	0.828	0.812	0.769	0.776
ILMN_2540573	LOC385505		X	120.63	0.762	0.743	0.759	0.804	0.798	0.791	0.806	0.739
ILMN_2719794	BC003331	cDNA sequence BC003331	1	152.21	0.783	0.750	0.761	0.840	0.740	0.797	0.798	0.700
ILMN_2696207	Pcdhb21	protocadherin beta 21	18	37.68	0.701	0.733	0.723	0.731	0.796	0.857	0.835	0.777
ILMN_2631953	Etv1	ets variant gene 1	12	39.59	0.736	0.728	0.812	0.754	0.765	0.811	0.801	0.702
ILMN_1254684	Nmd3	NMD3 homolog (S. cerevisiae)	3	69.55	0.803	0.790	0.752	0.704	0.777	0.733	0.723	0.714
