

Table S1 qRT-PCR primer

Gene Symbol	Forward Primer	Reverse Primer
<i>ARNTL</i>	AAGGGAAGCTCACAGTCAGAT	GGACATTGCGTTGCATGTTGG
<i>BCL6</i>	ACACATCTCGGCTCAATTTGC	AGTGTCCACAACATGCTCCAT
<i>BHLHE40</i>	ACACATCTCGGCTCAATTTGC	AGTGTCCACAACATGCTCCAT
<i>TRIM28</i>	TGAGACCTGTGTAGAGGCG	CGTTCACCATCCCCGAGACTT
<i>FOXA1</i>	GCAATACTCGCCTTACGGCT	TACACACCTTGGTAGTACGCC
<i>GTF2I</i>	TTGTCGTCGGAAGTAAAGAG	CGATTTGCCTGGGTTGTAGAT
<i>AHR</i>	ACATCACCTACGCCAGTGC	CGCTTGAAGGATTTGACTTGA
<i>EZH2</i>	AATCAGAGTACATGCGACTGAGA	GCTGTATCCTTCGCTGTTTCC
<i>CTCF</i>	ATGTGCGATTACGCCAGTGTA	TGAAACGGACGCTCTCCAGTA
<i>BCOR</i>	TGGTGACGCTTCAAAAAGCCA	GCTAGAATAGACGATGTTTCCCG
<i>BRD4</i>	ACCTCCAACCCTAACAAGCC	TTTCCATAGTGTCTTGAGCACC
<i>EGR1</i>	GGTCAGTGGCCTAGTGAGC	GTGCCGCTGAGTAAATGGGA
<i>FOSL1</i>	CAGGCGGAGACTGACAAAAGT	TCCTTCCGGGATTTTGCAGAT
<i>AR</i>	GACGACCAGATGGCTGTCATT	GGGCGAAGTAGAGCATCCT
<i>AFF4</i>	AAAGGCCAGCATGGATCAGAA	GTGATTTGGAGCGTTGATGTTT
<i>ASXL1</i>	CGCGCCTGGTATTAGAAAAGT	GCATCCTTCTTGAGCGTGAAAAG
<i>BRD2</i>	GAGGTGTCCAATCCCAAAAAGC	ATGCGAACTGATGTTTCCACA
<i>EP300</i>	AGCCAAGCGGCCTAAAGT	TCACCACCATTGGTTAGTCCC
<i>FOXO3</i>	CGGACAAACGGCTCACTCT	GGACCCGCATGAATCGACTAT

qRT-PCR, quantitative real time polymerase chain reaction.

Table S2 GO analysis of blue module genes

ONTOLOGY	ID	Description	Gene Ratio	BgRatio	p value	p.adjust	q value	Gene ID	Count
BP	GO:0006971	hypotonic response	2/77	11/18800	0.000889	0.363992	0.351502	SLC4A11/TRPV4	2
BP	GO:0006692	prostanoid metabolic process	3/77	50/18800	0.001127	0.363992	0.351502	GSTA1/PIBF1/DAGLB	3
BP	GO:0006693	prostaglandin metabolic process	3/77	50/18800	0.001127	0.363992	0.351502	GSTA1/PIBF1/DAGLB	3
BP	GO:0051451	myoblast migration	2/77	13/18800	0.001254	0.363992	0.351502	NET1/SIX4	2
BP	GO:0043584	nose development	2/77	14/18800	0.001459	0.363992	0.351502	RPGRIP1L/SIX4	2
BP	GO:0060271	cilium assembly	6/77	355/18800	0.003342	0.437601	0.422586	WDR35/DZIP1L/PIBF1/UBXN10/BBS5/PPGRIP1L	6
BP	GO:0006970	response to osmotic stress	3/77	79/18800	0.004178	0.437601	0.422586	SLC4A11/TRPV4/SORD	3
BP	GO:0060219	camera-type eye photoreceptor cell differentiation	2/77	25/18800	0.004673	0.437601	0.422586	PROM1/PPGRIP1L	2
BP	GO:0044782	cilium organization	6/77	384/18800	0.004894	0.437601	0.422586	WDR35/DZIP1L/PIBF1/UBXN10/BBS5/PPGRIP1L	6
BP	GO:0007156	homophilic cell adhesion via plasma membrane adhesion molecules	4/77	168/18800	0.005018	0.437601	0.422586	DSG3/DSC3/CDH26/IGSF9	4
BP	GO:0045104	intermediate filament cytoskeleton organization	3/77	88/18800	0.005648	0.437601	0.422586	KRT5/KRT15/DST	3
BP	GO:0045103	intermediate filament-based process	3/77	89/18800	0.005828	0.437601	0.422586	KRT5/KRT15/DST	3
BP	GO:0035116	embryonic hindlimb morphogenesis	2/77	28/18800	0.005842	0.437601	0.422586	TP63/PPGRIP1L	2
BP	GO:0021591	ventricular system development	2/77	30/18800	0.006687	0.437601	0.422586	MNAT1/PPGRIP1L	2
BP	GO:0035115	embryonic forelimb morphogenesis	2/77	31/18800	0.00713	0.437601	0.422586	TP63/PPGRIP1L	2
BP	GO:0060351	cartilage development involved in endochondral bone morphogenesis	2/77	31/18800	0.00713	0.437601	0.422586	MMP13/TRPV4	2
BP	GO:0001516	prostaglandin biosynthetic process	2/77	32/18800	0.007585	0.437601	0.422586	PIBF1/DAGLB	2
BP	GO:0046457	prostanoid biosynthetic process	2/77	32/18800	0.007585	0.437601	0.422586	PIBF1/DAGLB	2
BP	GO:0060795	cell fate commitment involved in formation of primary germ layer	2/77	32/18800	0.007585	0.437601	0.422586	EYA2/SOX2	2
BP	GO:0035137	hindlimb morphogenesis	2/77	35/18800	0.009027	0.437601	0.422586	TP63/PPGRIP1L	2
BP	GO:0021532	neural tube patterning	2/77	36/18800	0.009533	0.437601	0.422586	DZIP1L/PPGRIP1L	2
BP	GO:0006805	xenobiotic metabolic process	3/77	108/18800	0.009913	0.437601	0.422586	GSTA1/ALDH3A1/GSTA2	3
BP	GO:0035136	forelimb morphogenesis	2/77	38/18800	0.010581	0.437601	0.422586	TP63/PPGRIP1L	2
BP	GO:0001676	long-chain fatty acid metabolic process	3/77	111/18800	0.010677	0.437601	0.422586	GSTA1/SLC27A2/DAGLB	3
BP	GO:0071470	cellular response to osmotic stress	2/77	39/18800	0.011124	0.437601	0.422586	SLC4A11/TRPV4	2
BP	GO:0033559	unsaturated fatty acid metabolic process	3/77	115/18800	0.011748	0.437601	0.422586	GSTA1/PIBF1/DAGLB	3
BP	GO:0035019	somatic stem cell population maintenance	2/77	43/18800	0.013414	0.437601	0.422586	TP63/SOX2	2
BP	GO:0045214	sarcomere organization	2/77	43/18800	0.013414	0.437601	0.422586	SIX4/FHOD3	2
BP	GO:0006690	icosanoid metabolic process	3/77	121/18800	0.013465	0.437601	0.422586	GSTA1/PIBF1/DAGLB	3
BP	GO:0001754	eye photoreceptor cell differentiation	2/77	45/18800	0.014629	0.437601	0.422586	PROM1/PPGRIP1L	2
BP	GO:0001655	urogenital system development	5/77	352/18800	0.014732	0.437601	0.422586	PROM1/TP63/HSPB11/PPGRIP1L/SIX4	5
BP	GO:0051402	neuron apoptotic process	4/77	241/18800	0.017194	0.437601	0.422586	PTPRZ1/CHL1/TP63/SIX4	4
BP	GO:0006636	unsaturated fatty acid biosynthetic process	2/77	52/18800	0.019237	0.437601	0.422586	PIBF1/DAGLB	2
BP	GO:0007224	smoothed signaling pathway	3/77	140/18800	0.019808	0.437601	0.422586	DZIP1L/HSPB11/PPGRIP1L	3
BP	GO:0043524	negative regulation of neuron apoptotic process	3/77	145/18800	0.021708	0.437601	0.422586	PTPRZ1/CHL1/SIX4	3
BP	GO:0043903	regulation of biological process involved in symbiotic interaction	2/77	56/18800	0.022109	0.437601	0.422586	TMPRSS4/CXCL6	2
BP	GO:0031122	cytoplasmic microtubule organization	2/77	57/18800	0.022853	0.437601	0.422586	DST/TRPV4	2
BP	GO:0046456	icosanoid biosynthetic process	2/77	57/18800	0.022853	0.437601	0.422586	PIBF1/DAGLB	2
BP	GO:0060042	retina morphogenesis in camera-type eye	2/77	57/18800	0.022853	0.437601	0.422586	PROM1/PPGRIP1L	2
BP	GO:0060350	endochondral bone morphogenesis	2/77	57/18800	0.022853	0.437601	0.422586	MMP13/TRPV4	2
BP	GO:0006631	fatty acid metabolic process	5/77	395/18800	0.02299	0.437601	0.422586	GSTA1/SLC27A2/CROT/PIBF1/DAGLB	5
BP	GO:0050891	multicellular organismal water homeostasis	2/77	59/18800	0.024371	0.437601	0.422586	TP63/TRPV4	2
BP	GO:0030865	cortical cytoskeleton organization	2/77	61/18800	0.02593	0.437601	0.422586	TRPV4/FHOD3	2
BP	GO:0046530	photoreceptor cell differentiation	2/77	62/18800	0.026725	0.437601	0.422586	PROM1/PPGRIP1L	2
BP	GO:1905515	non-motile cilium assembly	2/77	63/18800	0.027529	0.437601	0.422586	PIBF1/PPGRIP1L	2
BP	GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	4/77	279/18800	0.027617	0.437601	0.422586	DSG3/DSC3/CDH26/IGSF9	4
BP	GO:0043329	cell junction assembly	5/77	420/18800	0.028948	0.437601	0.422586	DNER/COL17A1/DST/TRPV4/SIX4	5
BP	GO:0006749	glutathione metabolic process	2/77	65/18800	0.029166	0.437601	0.422586	GSTA1/GSTA2	2
BP	GO:0030104	water homeostasis	2/77	66/18800	0.029999	0.437601	0.422586	TP63/TRPV4	2
BP	GO:0030239	myofibril assembly	2/77	66/18800	0.029999	0.437601	0.422586	SIX4/FHOD3	2
BP	GO:0055002	striated muscle cell development	2/77	67/18800	0.030841	0.437601	0.422586	SIX4/FHOD3	2
BP	GO:0071466	cellular response to xenobiotic stimulus	3/77	168/18800	0.031689	0.437601	0.422586	GSTA1/ALDH3A1/GSTA2	3
BP	GO:0045109	intermediate filament organization	2/77	68/18800	0.031693	0.437601	0.422586	KRT5/KRT15	2
BP	GO:0003407	neural retina development	2/77	70/18800	0.033424	0.437601	0.422586	PROM1/PPGRIP1L	2
BP	GO:1904888	cranial skeletal system development	2/77	70/18800	0.033424	0.437601	0.422586	TP63/SIX4	2
BP	GO:0001736	establishment of planar polarity	2/77	72/18800	0.035192	0.437601	0.422586	TP63/PPGRIP1L	2
BP	GO:0007164	establishment of tissue polarity	2/77	72/18800	0.035192	0.437601	0.422586	TP63/PPGRIP1L	2
BP	GO:0001822	kidney development	4/77	303/18800	0.035793	0.437601	0.422586	PROM1/HSPB11/PPGRIP1L/SIX4	4
BP	GO:0061512	protein localization to cilium	2/77	75/18800	0.037909	0.437601	0.422586	WDR35/DZIP1L	2
BP	GO:0006635	fatty acid beta-oxidation	2/77	76/18800	0.038833	0.437601	0.422586	SLC27A2/CROT	2
BP	GO:0072001	renal system development	4/77	312/18800	0.039185	0.437601	0.422586	PROM1/HSPB11/PPGRIP1L/SIX4	4
BP	GO:0055001	muscle cell development	3/77	183/18800	0.039289	0.437601	0.422586	DNER/SIX4/FHOD3	3
BP	GO:0033504	floor plate development	1/77	10/18800	0.04022	0.437601	0.422586	DZIP1L	1
BP	GO:0043587	tongue morphogenesis	1/77	10/18800	0.04022	0.437601	0.422586	SIX4	1
BP	GO:0060742	epithelial cell differentiation involved in prostate gland development	1/77	10/18800	0.04022	0.437601	0.422586	TP63	1
BP	GO:0098917	retrograde trans-synaptic signaling	1/77	10/18800	0.04022	0.437601	0.422586	DAGLB	1
BP	GO:1902459	positive regulation of stem cell population maintenance	1/77	10/18800	0.04022	0.437601	0.422586	TP63	1
BP	GO:1904672	regulation of somatic stem cell population maintenance	1/77	10/18800	0.04022	0.437601	0.422586	TP63	1
BP	GO:0007492	endoderm development	2/77	78/18800	0.040705	0.437601	0.422586	SOX2/PAX9	2
BP	GO:0007389	pattern specification process	5/77	463/18800	0.041325	0.437601	0.422586	TP63/DZIP1L/HSPB11/BBS5/PPGRIP1L	5
BP	GO:0060249	anatomical structure homeostasis	4/77	319/18800	0.041946	0.437601	0.422586	NELL2/PROM1/PIP/MUC4	4
BP	GO:0006575	cellular modified amino acid metabolic process	3/77	188/18800	0.042011	0.437601	0.422586	GSTA1/CROT/GSTA2	3
BP	GO:1902806	regulation of cell cycle G1/S phase transition	3/77	188/18800	0.042011	0.437601	0.422586	MNAT1/MLF1/SOX2	3
BP	GO:0001895	retina homeostasis	2/77	80/18800	0.042611	0.437601	0.422586	PROM1/PIP	2
BP	GO:0002924	negative regulation of humoral immune response mediated by circulating immunoglobulin	1/77	11/18800	0.044153	0.437601	0.422586	SUSD4	1
BP	GO:0039532	negative regulation of viral-induced cytoplasmic pattern recognition receptor signaling pathway	1/77	11/18800	0.044153	0.437601	0.422586	TSPAN6	1
BP	GO:0043589	skin morphogenesis	1/77	11/18800	0.044153	0.437601	0.422586	TP63	1
BP	GO:0046598	positive regulation of viral entry into host cell	1/77	11/18800	0.044153	0.437601	0.422586	TMPRSS4	1
BP	GO:0060221	retinal rod cell differentiation	1/77	11/18800	0.044153	0.437601	0.422586	PPGRIP1L	1
BP	GO:0060601	lateral sprouting from an epithelium	1/77	11/18800	0.044153	0.437601	0.422586	TP63	1
BP	GO:0070944	neutrophil-mediated killing of bacterium	1/77	11/18800	0.044153	0.437601	0.422586	CXCL6	1
BP	GO:0071472	cellular response to salt stress	1/77	11/18800	0.044153	0.437601	0.422586	TRPV4	1
BP	GO:0071609	chemokine (C-C motif) ligand 5 production	1/77	11/18800	0.044153	0.437601	0.422586	TRPV4	1
BP	GO:0071649	regulation of chemokine (C-C motif) ligand 5 production	1/77	11/18800	0.044153	0.437601	0.422586	TRPV4	1
BP	GO:0072584	caveolin-mediated endocytosis	1/77	11/18800	0.044153	0.437601	0.422586	PROM2	1
BP	GO:0075294	positive regulation by symbiont of entry into host	1/77	11/18800	0.044153	0.437601	0.422586	TMPRSS4	1
BP	GO:0048839	inner ear development	3/77	192/18800	0.044256	0.437601	0.422586	SOX2/PPGRIP1L/SIX4	3
BP	GO:0002024	diet induced thermogenesis	1/77	12/18800	0.048071	0.437601	0.422586	TRPV4	1
BP	GO:0007501	mesodermal cell fate specification	1/77	12/18800	0.048071	0.437601	0.422586	EYA2	1
BP	GO:0021670	lateral ventricle development	1/77	12/18800	0.048071	0.437601	0.422586	PPGRIP1L	1
BP	GO:0021781	glial cell fate commitment	1/77	12/18800	0.048071	0.437601	0.422586	SOX2	1
BP	GO:0033540	fatty acid beta-oxidation using acyl-CoA oxidase	1/77	12/18800	0.048071	0.437601	0.422586	CROT	1
BP	GO:0035112	genitalia morphogenesis	1/77	12/18800	0.048071	0.437601	0.422586	TP63	1
BP	GO:0045916	negative regulation of complement activation	1/77	12/18800	0.048071	0.437601	0.422586	SUSD4	1
BP	GO:0048548	regulation of pinocytosis	1/77	12/18800	0.048071	0.437601	0.422586	PROM2	1
BP	GO:0051095	regulation of helicase activity	1/77	12/18800	0.048071	0.437601	0.422586	MNAT1	1
BP	GO:0051639	actin filament network formation	1/77	12/18800	0.048071	0.437601	0.422586	FHOD3	1
BP	GO:0060788	ectodermal placode formation	1/77	12/18800	0.048071	0.437601	0.422586	SIX4	1
BP	GO:0070943	neutrophil-mediated killing of symbiont cell	1/77	12/18800	0.048071	0.437601	0.422586	CXCL6	1
BP	GO:0071697	ectodermal placode morphogenesis	1/77	12/18800	0.048071	0.437601	0.422586	SIX4	1
BP	GO:0072182	regulation of nephron tubule epithelial cell differentiation	1/77	12/18800	0.048071	0.437601	0.422586	PROM1	1
BP	GO:0072497	mesenchymal stem cell differentiation	1/77	12/18800	0.048071	0.437601	0.422586	SLC4A11	1
BP	GO:0030433	ubiquitin-dependent ERAD pathway	2/77	86/18800	0.048523	0.437601	0.422586	CLGN/UBXN10	2
CC	GO:0036064	ciliary basal body	6/80	161/19594	5.10E-05	0.007803	0.007194	WDR35/DZIP1L/MLF1/EFHC2/BBS5/PPGRIP1L	6
CC	GO:0005930	axoneme	5/80	131/19594	0.000199	0.01052	0.009698	WDR35/DZIP1L/EFHC2/BBS5/PPGRIP1L	5

Table S3 KEGG analysis of blue module genes

ID	Description	Gene Ratio	BgRatio	p value	p.adjust	q value	Gene ID	Count
hsa05418	Fluid shear stress and atherosclerosis	4/30	139/8159	0.00156715	0.08974693	0.08054849	CALML4/GSTA1/TRPV4/GSTA2	4
hsa00982	Drug metabolism - cytochrome P450	3/30	72/8159	0.00225502	0.08974693	0.08054849	GSTA1/ALDH3A1/GSTA2	3
hsa00980	Metabolism of xenobiotics by cytochrome P450	3/30	78/8159	0.00283411	0.08974693	0.08054849	GSTA1/ALDH3A1/GSTA2	3
hsa04657	IL-17 signaling pathway	3/30	94/8159	0.00480009	0.11400204	0.10231762	MMP13/CXCL6/MUC5B	3
hsa00480	Glutathione metabolism	2/30	57/8159	0.01840355	0.31255924	0.28052408	GSTA1/GSTA2	2
hsa05204	Chemical carcinogenesis - DNA adducts	2/30	69/8159	0.0263271	0.31255924	0.28052408	GSTA1/GSTA2	2
hsa01524	Platinum drug resistance	2/30	73/8159	0.02922643	0.31255924	0.28052408	GSTA1/GSTA2	2
hsa05133	Pertussis	2/30	76/8159	0.0314814	0.31255924	0.28052408	CALML4/CXCL6	2
hsa05202	Transcriptional misregulation in cancer	3/30	193/8159	0.03311686	0.31255924	0.28052408	PROM1/MLF1/SIX4	3
hsa00983	Drug metabolism - other enzymes	2/30	80/8159	0.03459216	0.31255924	0.28052408	GSTA1/GSTA2	2
hsa04146	Peroxisome	2/30	82/8159	0.03619107	0.31255924	0.28052408	SLC27A2/CROT	2
hsa04970	Salivary secretion	2/30	92/8159	0.044602	0.33904891	0.30429875	CALML4/MUC5B	2
hsa04750	Inflammatory mediator regulation of TRP channels	2/30	98/8159	0.0499651	0.33904891	0.30429875	CALML4/TRPV4	2
hsa04925	Aldosterone synthesis and secretion	2/30	98/8159	0.0499651	0.33904891	0.30429875	CALML4/DAGLB	2

KEGG, Kyoto Encyclopedia of Genes and Genomes; TRP, transient receptor potential.