Supplementary Table S1

Vertebrate Pigmentation Genes

no.	gene	mouse coat color mutant	teleost pigment. mutants	FSGD[1]	LSGD[2]	References
a) melanophore development (FSGD duplicate retention ratio: 22/45 = 48.9%)						
1	*Adam17*			■		1
2	*Adamts20*	*belted*				1
3	*Apc*					1
4	*Creb1**			■	◊	2
5	*Eda*	*Tabby*				1
6	*Edn3**	*lethal spotting*		■		1
7	*Ednrb1**	*piebald spotting*	*rose* (*ednrb1a*)[Dre]	■		1, 3, 4
8	*Ednrb2*					5
9	*Ece1*					1
10	*Egfr*	*dark skin 5*		■		1, 6
11	*En1*			■		1
12	*Erbb3*		*picasso* (*erbb3b*)[Dre]	■		3, 7
13	*Fgfr2*					1
14	*Foxd3**		*mother superior*[Dre]			3, 8
15	*Frem2*			■		1
16	*Fzd4*					1
17	*Gnaq*	*dark skin 1, dark skin 10*		■	◊	1
18	*Gna11*	*dark skin7*		■		1
19	*Gpc3*					1
20	*Gpr161*					1
21	*Hdac1*		*colgate* (*hdac1a*)[Dre]	■		3, 9
22	*Ikbkg*					1
23	*Itgb1*			■	◊	1
24	*Kit*	*dominant white-spotting*	*sparse* (*kita*)[Dre]	■		1, 3, 10
25	*Kitl*	*steel*		■		1, 11
26	*Lef1*					1
27	*Lmx1a*	*dreher*				1
28	*Mbtps1*					1
29	*Mcoln3*	*varitint-waddler*		■		1
30	*Mitf*	*microphthalmia*	*nacre* (*mitfa*)[Dre]	■		1, 3, 12
31	*Mreg*	*dilute supressor*				1
32	*Myc*			■		1
33	*Pax3**	*splotch*		■		1, 13
34	*Scarb2*		*hi1463*[Dre]			3, 14
35	*Sfxn1*	*flexed tail*				1
36	*Snai2*					1
37	*Sox9**		*b971* (*sox9b*)[Dre]	■		3, 15, 16
38	*Sox10**	*Dominant megacolon*	*colourless* (*sox10b*)[Dre]	■		1, 3, 17
39	*Sox18*	*ragged*	-			1
40	*Tfap2a*	-	*lockjaw*[Dre]			1, 3, 18
41	*Trmp1*	-		■		19

42	*Trmp7*	-	*touchtone*^{Dre}			3, 19
43	*Wnt1*	-	-			1
44	*Wnt3a*	-	-			1
45	*Zic2*	*Kumba*	-	■		1

b) components of melanosomes (FSGD duplicate retention ratio: 6/10 = 60.0%)

46	*Dct*	*slaty*	-			1
47	*Gpnmb*	*iris pigment dispersion*	-			1
48	*Rab38*	*chocolate*	-	■		1
49	*Rab32*	-		■		20
50	*Silv*	*silver*	*fading vision* (*silva*)^{Dre}	■		1, 3, 21
51	*Slc24a4*	-	-	■		22
52	*Slc24a5*	-	*golden*^{Dre}			3, 23
53	*Slc45a2*	*underwhite*	*b*^{Ola}			1, 24
54	*Tyr*	*albino*	*sandy* (*tyra*)^{Dre}; *i* (tyra)^{Ola}	■		1, 3, 25, 26
55	*Tyrp1*	*brown*		■		1

c) melanosome construction (FSGD duplicate retention ratio: 2/22 = 9.1%)

56	*Ap3b1*	*pearl*			◊	1
57	*Ap3d1*	*mocha*				1
58	*Bloc1s3*	*reduced pigmentation*				1
59	*Cno*	*cappuchino*				1
60	*Dtnbp1*	*sandy*		■		1
61	*Fig4*	*pale temor*				1
62	*Gpr143*	*Oa1*				1
63	*Hps1*	*pale ear*				1
64	*Hps3*	*cocoa*				1
65	*Hps4*	*light ear*				1
66	*Hps5*	*Ruby-eye 2*				1
67	*Hps6*	*Ruby-eye*				1
68	*Lyst*	*beige*			◊	1
69	*Nsf*		*hi2869* (*nsfb*)^{Dre}	■		3
70	*Oca2*	*pinkeyed-dilution*	*i-3*^{Ola}			1, 27
71	*Pldn*	*pallid*				1
72	*Rabggta*	*gunmetal*				1
73	*Txndc5*	*muted*				1
74	*Vps33a*	*buff*				1
75	*Vps11*		*pale grey eyes*^{Ola}			28
76	*Vps18**		*vps18*^{Dre}			3, 29
77	*Vps39**		*lbk/vam6*^{Dre}			3, 30

d) melanosome transport (retention ratio : 3/4 = 75.0%)

78	*Mlph*	*leaden*	*j120*^{Dre}	■		1, 3, 31
79	*Myo5a*	*dilute*		■		1
80	*Myo7a*	*shaker-1*		■		1
81	*Rab27a*	*ashen*				1

e) regulation of melanogenesis (FSGD duplicate retention ratio: 3/7 = 42.9%)

82	*Asip*	*nonagouti*				1
83	*Atrn*	*mahogany*				1
4	*Creb1**			■	◊	2
84	*Drd2*					1
85	*Mc1r*	*extension*				1
86	*Mgrn1*	*Mahoganoid*		■		1
87	*Pomc*			■		1

f) systemic effects (FSGD duplicate retention ration: 2/13 = 15.4%)

88	*Atox1*					1
89	*Atp7a*	*mottled*	*calamity*^{Dre}			1, 3
90	*Atp7b*	*toxic milk*				1

91	*Atp6ap1*		*bleached blond*^{Dre}		◊	3, 14
92	*Atp6ap2*		*hi3681*^{Dre}			3
93	*Atp6v0c*		*hi1207* (*atp6v0c a*)^{Dre}	■		3, 14
94	*Atp6v0d1*		*hi2188b*^{Dre}			3
95	*Atp6v1e1**		*hi577a* (*atp6v1e1a*)^{Dre}	■		3, 14
96	*Atp6v1f*		*hi1988*^{Dre}		◊	3
97	*Atp6v1h**		*hi923*			3, 14
98	*Rpl24*	*belly spot and tail*				1
99	*Rps19*	*dark skin 3*				1
100	*Rps20*	*dark skin 4*				1

g) xanthophore development (retention rate: 9/11 = 81.8%)

95	*Atp6v1e1**		*hi577a* (*atp6v1e1a*)^{Dre}	■		3, 14
97	*Atp6v1h**		*hi923*			3, 14
101	*Csf1r*		*panther* (*csf1ra*)^{Dre}	■		3, 32
6	*Edn3**	*lethal spotting*		■		1
7	*Ednrb1**	*piebald spotting*	*rose* (*ednrb1a*)^{Dre}	■		1, 3, 444
14	*Foxd3**		*mother superior*^{Dre}			3, 8
102	*Ghr*			■		33
33	*Pax3**	*splotch*		■		1, 13
103	*Pax7*			■		1, 13
104	*Smtl*		*color interfere*^{Ola}	■		34
38	*Sox10**	*Dominant megacolon*	*colourless* (*sox10b*)^{Dre}	■		1, 3, 17

h) pteridine synthesis (FSGD duplicate retention rate: 2/11 = 18.2%)

105	*GchIa*					35
106	*GchIb*					3, 35, 36
107	*Gchfr*					35
108	*Mycbp2*		*esrom*^{Dre}			3, 37
109	*Paics*		*hi2688*^{Dre}			3
110	*Pcbd1*					35
111	*Pcbd2*					35
112	*Pts*					35
113	*Qdpr*			■	◊	35
114	*Spr*			■		35
115	*Xdh*					3, 35

i) iridophore development (FSGD duplicate retention rate: 4/11 = 36.4%)

97	*Atp6v1h**		*hi923*			3, 14
116	*Dac*		*hagoromo*^{Dre}			38
6	*Edn3**	*lethal spotting*		■		1
7	*Ednrb1**	*piebald spotting*	*rose* (*ednrb1a*)^{Dre}	■		1, 3, 4
14	*Foxd3**		*mother superior*^{Dre}			3, 8
117	*Ltk*		*shady*^{Dre}			39
37	*Sox9**		*b971* (*sox9b*)^{Dre}	■		3, 15, 16
38	*Sox10**	*Dominant megacolon*	*colourless* (*sox10b*)^{Dre}	■		1, 3, 17
118	*Trim33*		*moonshine*^{Dre}			3
76	*Vps18**		*vps18*^{Dre}			3, 29
77	*Vps39**		*lbk/vam6*^{Dre}			3, 30

j) uncategorized function (FSGD duplicate retention rate: 3/10 = 30.0%)

119	*Abhd11*		*hi3305*^{Dre}			3
120	*Atoh7*		*lakritz*^{Dre}			3, 40
121	*Ebna1bp2*		*hi3625a*^{Dre}			3
122	*Gfpt1*		*eartha*^{Dre}			3
123	*Gja5*		*leopard*^{Dre}	■		3, 41
124	*Irf4*			■	◊	42
125	*Kcnj13*		*jaguar*^{Dre}			3, 43
126	*Pabpc1*		*hi3202b* (*pabpc1a*)^{Dre}	■		3
127	*Skiv2l2*		*julie*^{Dre}			3
128	*Tpcn2*					44

* gene belongs to more than one category

[Dre] *Danio rerio* (zebrafish); [Ola] *Oryzias latipes* (medaka)

[1] ■ indicates that a FSGD duplicate has been retained in teleosts

[2] ◊ indicates that a lineage-specific gene duplication (LSGD) has occurred in one or more teleosts

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