

TABLE S1a

Annotation of sex-linked genetic markers of *Poecilia reticulata*

Marker	Origin	Guppy clone	Genbank Accession	Annotation of possible function (BLAST results)
0009	EST	Tra_Embryo_15_D19	ES375672	Rab interacting lysosomal protein-like 1
0030	EST	Qua_Embryo_U2_N18	ES382008	Fructose-1,6-bisphosphatase 1 [Danio rerio]
0032	EST	Tra_Embryo_8_L19	ES386074	Steroid-sensitive protein 1 [Danio rerio]
0061	EST	Qua_Embryo_B2_E02	ES379217	Ectodermal-neural cortex 1 ENC1
0073	EST	Qua_Embryo_C1_D11	ES379375	Replication factor C (activator 1) 3 [Danio rerio], CAG00421, [Tetraodon nigroviridis] (Medaka Chromosome 14
0090	EST	Blu_Brain_U2-3_E08	ES372993	N-Shc (1E-50)
0148	EST	Blu_Testis_6_H06	ES380905	Calmodulin regulated spectrin-associated protein 1
0155	EST	Oro_Skin_3_K13	ES385036	Splicing factor, arginine/serine-rich 12 (1.2E-31)
0199	EST	Blu_Brain_L2_H11	ES372663	Thyroid hormone receptor-associated protein 2
0210	EST	Blu_Testis_6_K19	ES380974	Heat shock 70kDa protein 5 (glucose-regulated protein 78kDa)
0229	EST	Tra_Embryo_10_F17	ES374479	Cyclin I
0230	BAC	24-K15	FH890169	NS
0244	EST	Oro_Retina_5_C12	ES373878	TGF beta-inducible nuclear protein 1 (CDK105)
0245	EST	Tra_Embryo_15_F16	ES375709	Catenin ARVCF [Danio rerio]; DW618591
0246	EST	Tra_Embryo_2-1_F11	ES371278	NADH dehydrogenase ubiquinone 1 alpha subcomplex, 8, 19kDa
0247	EST	Tra_Embryo_1-4_G05	ES371208	Transcription factor BTF3a
0315	BAC	01-4_H01	FH888831	NS
0380	BAC	03-F10	FH889280	(Medaka Chromosome 15) The start of this sequence is located in Contig scaffold91_contig45820
0398	BAC	03-J09	FH889369	NS
0423	BAC	03-P19	FH889502	Fundulus heteroclitus cDNA similar to PDZ and LIM domain protein (5e-42)
0429	BAC	04-G05	FH889541	Guppy EST Tra_Liver_5_C16 (ES377721.1; 2e-92)
0442	BAC	04-A18	FH889605	Guppy EST Tra_Liver_5_N20; REX2, microsatellite Msd018
0490	BAC	04-B08	FH889775	NS

0517	BAC	05-C08	FH889941	(Medaka Chromosome 03) Contig scaffold312_contig85780,3 coding genes near by: ENSORLG00000015448, ENSORLG00000015460, ENSORLG00000015469
0568	BAC	32-L01	FH890372	RHO GTPASE ACTIVATING RHO TYPE GTPASE ACTIVATING
0603	BAC	33-E18	FH890561	C07125rat cDNA (2e-15)
0666	BAC	34-L18	FH891090	BJ731761 MF015DA cDNA <i>Oryzias latipes</i> cDNA (4e-46)
0691	BAC	01-G08	FH891254	Medaka ENSORLG00000009417; Vitamin K-dependent gamma-glutamyl carboxylase (4e-42)
0987	BAC	33-D15	FH893254	NS
1025	BAC	34-K02	FH893550	NS
1053	EST	Tra_Liver_7-4_H05	ES377437	JanusA / ocnus (8.00E-21); phosphohistidine phosphatase 1 (3e-51)
1075	Homology cloning		FJ200253	aim1 slc45a2 membrane-associated transporter protein B
1079	Homology cloning		FJ236234	phosphodiesterase 6A
1103	EST	Tra_Embryo_3-3_G01	ES371695	Cyclin G2
1104	Consensus	Medaka ZBTB7C ^s	ENSORLG00000005778	ZINC FINGER AND BTB DOMAIN CONTAINING Protein
1105	Consensus	Medaka LIN54 ^s	ENSORLG00000001906	TESMIN METALLOTHIONEIN 5
1106	EST	Qua_Embryo_02_D01	ES383177	BX901878.6 GI:60098192 on Zebrafish linkage group 21
1107	EST	Tra_Liver_4_F16	ES377165	Unnamed protein product [Tetraodon nigroviridis] gi 47210133 emb CAF95582.1
1108	EST	Qua_Embryo_U5_M02	ES378762	Ab012309 <i>Cyprinus carpio</i> mRNA for allograft inflammatory factor-1
1109	EST	Blu_Testis_8_E24	ES380544	TIA1 cytotoxic granule-associated RNA binding protein [Danio rerio]
1110	EST	Blu_Testis_8_P16	ES380724	COP9 signalosome subunit 4
1111	EST	Blu_Testis_6_H23	ES380918	Restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)
1112	EST	Blu_Testis_4_A23	ES379967	Zinc finger FYVE domain-containing endosome-associated FYVE-domain protein
1113	EST	Qua_Embryo_01_C04	ES383103	beta A4-crystallin
1114	EST	Blu_Testis_8_G09	ES380567	Putative alpha-mannosidase C1orf22
1115	EST	Oro_Skin_4_O13	ES384849	Thioredoxin-like 1
0228; 1080_ya	BAC	34-P12	FH893402; FH890782	NS
0231; 1081_ya	BAC	08-M18	FH892752; FH890160	NS

1082_za; 1082_ya	BAC	24-K15	FH892762; FH890169	NS
1083_za; 1083_ya	BAC	18-N08	FH892760; FH890167	NS
1084_za; 1084_ya	BAC	01-H04	FH891124; FH888484	NS
1085_za; 1085_ya	BAC	02-P16	FH891473; FH888843	NS
1086_za; 1086_ya	BAC	10-H16	FH892753; FH890161	NS
1087_za; 1087_ya	BAC	17-F23	FH892756; FH890164	NS
1088_za; 1088_ya	BAC	02-J05	FH891472; FH888842	NS
1089_za; 1089_ya	BAC	18-C03	FH892759; FH890166	NS
1090_za; 1090_ya	BAC	20-M10	FH892761; FH890168	NS
1091_za; 1091_ya	BAC	40-A10	FH893709; FH891119	AM145618 <i>Oryzias latipes</i> ; Similar to vertebrate Ca ⁺⁺ transporting ATPase (2e-53), FM022709 cDN32 <i>Dicentrarchus labrax</i> cDNA (2e-40)
1092_za; 1092_ya	BAC	44-N22	FH893711; FH891121	Nasal embryonic LHRH factor (3e-06)
1093_za	BAC	37-F13	FH893708	CH211-231O6 in linkage group 21 (1e-24)
1094_za	BAC	04-F13	FH892222;	NS
1095_za; 1095_ya	BAC	05-E09	FH892431; FH889837	NS
1096_za; 1096_ya	BAC	13-L11	FH892755; FH890163	NS
1097_za; 1097_ya	BAC	33-I09	FH893056; FH890448	NS
1098_za; 1098_ya	BAC	36-H23	FH893706; FH891117	NS
1099_za; 1099_ya	BAC	45-I12	FH893712; FH891122	Tra_Liver_8_O01 similar to 60S ribosomal protein L7a (<i>Surfeit</i> locus protein 3)
1100_za; 1100_ya	BAC	12-E10	FH892754; FH890162	Fugu rubripes LSFR2 gene
1101_za; 1101_ya	BAC	42-N13	FH893710; FH891120	Alpha 2,6 sialyltransferase 3 [<i>Salmo salar</i>] (4e-17)
1102_za; 1102_ya	BAC	05-J04	FH892432; FH889838	NS

NS: No significant hits for Blast Results

Annotations in boldface are based on e-values lower than 1e-100.

Markers 0009 to 1079 represent SNP markers that were used for genotyping in multiplexed MALDI TOF assays (Sequenom).

Markers 1080 to 1102 resulted from a genomic walk using the Cumaná genomic BAC library spotted on filters.

Markers with the same number with suffixes ya or za were derived from opposite ends of the same BAC.

Markers 1103 to 1115 were generated by synteny-based candidate gene approaches.