Supplementary Data

Supplementary Table S1. SNPs and their chromosome number (Chr.), position on the chromosome, annotated gene name, distance from the gene, raw p-value are listed. ‘match’ indicates that the SNP was included in the gene and ‘-’ indicates that no gene was in 100kd distance of the SNPs.

SNP	Chr	Position	Gene	Distance	p-value
MARC0018001	1	13478198	-	-	2.04E-03
ASGA0001052	1	13677927	CLDN20	85316	8.32E-03
M1GA0000785	1	16529867	ESR1	12501	7.76E-03
ALGA0001232	1	17130048	CCDC170	match	5.20E-04
ASGA0001260	1	17256411	RMND1	match	2.22E-03
ALGA0001244	1	17279855	ZBTB2	16864	1.76E-03
DRGA0001141	1	79571312	-	-	6.11E-03
INRA0002909	1	83308522	SEC63	match	9.40E-03
ALGA0005610	1	1.25E+08	-	-	8.69E-03
H3GA0003313	1	1.86E+08	-	-	5.19E-03
ALGA0007007	1	1.91E+08	-	-	9.84E-03
INRA0005278	1	1.92E+08	LRFN5	51070	3.96E-03
MARC0080275	1	1.92E+08	LRFN5	22518	3.96E-03
ASGA0005303	1	1.92E+08	LRFN5	2176	3.96E-03
MARC0033468	1	1.92E+08	LRFN5	13558	4.74E-03
H3GA0003345	1	1.92E+08	LRFN5	31112	4.81E-03
MARC0002276	1	1.92E+08	LRFN5	48118	6.86E-03
ALGA0007015	1	1.92E+08	LRFN5	63056	2.69E-03
ALGA0115186	1	1.92E+08	-	-	3.79E-03
MARC0036886	1	2.13E+08	NTRK3	match	9.80E-03
ASGA0005512	1	2.14E+08	-	-	6.56E-03
M1GA0001554	1	2.97E+08	SNORD90	44608	2.30E-03
ASGA0008803	2	6896014	GPR137	match	5.42E-03
M1GA0002584	2	9336635	MYRF	4509	7.74E-03
MARC0005659	2	20249153	HSD17B12	37203	5.24E-03
ALGA0112320	2	20842615	-	-	4.44E-03
ALGA0109169	2	22336683	-	-	5.67E-03

ALGA0012462	2	22590108	-	-	7.23E-03
ALGA0012504	2	23230160	-	-	2.98E-03
ASGA0009568	2	23271214	-	-	3.68E-04
ALGA0012515	2	23297131	-	-	7.60E-03
ALGA0113768	2	32333658	DCDC1	72522	3.06E-03
ALGA0012891	2	32621630	MPPED2	match	4.27E-03
ASGA0009858	2	32649983	MPPED2	match	4.42E-03
ALGA0012897	2	32887535	FSHB	22530	8.46E-03
MARC0113797	2	33100405	-	-	6.46E-03
H3GA0006477	2	33751046	-	-	9.35E-03
MARC0061061	2	35054445	-	-	6.69E-03
MARC0049526	2	35068263	-	-	9.62E-03
MARC0057893	2	35069583	-	-	7.40E-03
ALGA0012954	2	35089353	-	-	7.40E-03
MARC0067928	2	65512888	CC2D1A	match	6.55E-03
ALGA0013819	2	65741376	CCDC130	41960	4.27E-03
ALGA0013817	2	65761499	CCDC130	62083	4.52E-03
MARC0097970	2	67524684	OR7G3	94155	4.94E-03
DIAS0000914	2	69067481	PIN1	8231	1.23E-03
ALGA0014210	2	88585407	-	-	9.87E-03
ASGA0010795	2	89804886	HOMER1	39474	7.47E-03
H3GA0007086	2	90190571	CMYA5	3578	9.71E-03
ALGA0123643	2	1.36E+08	CTXN3	66969	3.84E-03
ALGA0015985	2	1.37E+08	-	-	1.71E-03
H3GA0007722	2	1.38E+08	-	-	7.32E-03
DRGA0003625	2	1.38E+08	-	-	7.26E-03
MARC0063459	2	1.39E+08	-	-	7.08E-03
ALGA0118500	3	12373502	-	-	6.27E-03
MARC0113856	3	18690752	ATXN2L	1178	2.09E-03
ASGA0090908	3	18873907	SBK1	6056	7.01E-03
ALGA0102956	3	18876394	SBK1	8543	7.72E-03
ALGA0116808	3	18943557	XPO6	60677	2.51E-03
ALGA0114914	3	32478883	-	-	5.23E-03

ALGA0107071	3	35759370	-	-	8.58E-03
ALGA0018852	3	49511934	EDAR	91461	1.76E-03
ALGA0018859	3	49555847	EDAR	47548	3.38E-03
H3GA0009479	3	49619062	EDAR	match	1.40E-03
ALGA0018869	3	49634868	CCDC138	match	2.27E-03
MARC0016359	3	49652312	CCDC138	match	4.49E-03
ALGA0018856	3	49698069	CCDC138	12421	2.79E-03
ASGA0014485	3	49720172	CCDC138	34524	2.54E-03
ALGA0104619	3	49867263	GCC2	20143	2.27E-03
CASI0006979	3	49869950	GCC2	17456	2.27E-03
MARC0009789	3	55205882	-	-	8.46E-03
MARC0100326	3	55496229	CREG2	match	9.63E-03
ALGA0019011	3	55561820	RNF149	16604	5.46E-03
MARC0065978	3	55717403	TBC1D8	59678	2.81E-03
ALGA0019168	3	58986683	TMEM131	match	4.92E-03
ASGA0094490	3	1.26E+08	GDF7	15667	5.33E-03
ASGA0103683	3	1.35E+08	ITGB1BP1	match	5.83E-03
H3GA0011795	4	8845519	-	-	1.98E-03
ALGA0023171	4	11921004	-	-	6.29E-03
ASGA0018288	4	11933016	-	-	4.40E-03
ALGA0023189	4	12065855	-	-	9.08E-03
ASGA0018338	4	12257838	-	-	7.63E-03
ASGA0018370	4	12821695	MYC	38214	2.85E-03
ASGA0018384	4	12941813	-	-	4.70E-03
DRGA0004465	4	13201853	-	-	8.34E-03
ALGA0023289	4	13259971	-	-	6.89E-03
ASGA0018422	4	13393209	-	-	6.96E-03
ALGA0023303	4	13453436	-	-	6.17E-03
ASGA0019158	4	33419642	ABRA	57931	9.51E-03
ASGA0019164	4	33447340	ABRA	85629	9.51E-03
M1GA0005832	4	33879367	-	-	8.95E-03
ALGA0026965	4	1.04E+08	KCNN3	match	8.73E-03
INRA0015741	4	1.04E+08	KCNN3	match	8.73E-03

MARC0109265	4	1.19E+08	DDX20	match	1.99E-03
INRA0016754	4	1.23E+08	-	-	2.72E-03
ALGA0123355	4	1.24E+08	-	-	7.76E-03
H3GA0014317	4	1.25E+08	-	-	6.27E-03
ALGA0028566	4	1.28E+08	-	-	4.13E-03
ASGA0022428	4	1.28E+08	-	-	8.52E-03
H3GA0014451	4	1.31E+08	-	-	9.21E-03
MARC0071918	5	6772267	DDX17	match	3.73E-03
ASGA0106044	5	6784209	DDX17	425	4.92E-03
ALGA0105509	5	6793058	KDELR3	match	4.09E-03
M1GA0007422	5	6800467	KDELR3	3641	3.48E-03
ALGA0032587	5	69669256	WASH1	24816	8.91E-03
MARC0019446	6	1829369	JPH3	match	8.52E-03
ASGA0084674	6	1838412	JPH3	match	7.89E-03
ALGA0115499	6	11401848	-	-	9.15E-03
ALGA0119163	6	40937246	COX7A1	14345	6.24E-03
MARC0005493	6	41367001	ZNF260	47542	6.24E-03
MARC0061190	6	41583185	ZNF829	match	6.69E-03
ALGA0115443	6	76356357	-	-	3.82E-03
ALGA0105228	6	76712823	MTFR1L	match	6.78E-03
ASGA0097645	6	77180997	PDIK1L	match	3.98E-03
ASGA0098887	6	77540317	RPS6KA1	60318	5.72E-03
ALGA0105183	6	77561790	RPS6KA1	81791	6.35E-03
ALGA0035761	6	78173716	CD164L2	match	8.02E-03
ASGA0099240	6	78503422	STX12	1399	8.27E-03
MARC0018089	6	79884592	EPB41	8507	9.02E-03
ALGA0103867	6	79924229	TMEM200B	5615	7.62E-03
ASGA0105794	6	1.27E+08	-	-	9.13E-03
M1GA0008912	6	1.27E+08	-	-	9.98E-03
ASGA0029775	6	1.39E+08	-	-	5.94E-03
ASGA0104725	6	1.46E+08	TTC4	26930	6.12E-03
ALGA0116372	6	1.55E+08	ERI3	match	5.26E-03
H3GA0010900	7	5120430	BMP6	41987	8.90E-03

H3GA0020119	7	17178315	CDKAL1	match	9.43E-03
MARC0024047	7	18074254	-	-	5.79E-03
H3GA0021382	7	49132338	-	-	3.14E-03
ASGA0033396	7	49191515	-	-	4.06E-03
ALGA0041186	7	49212847	-	-	2.86E-03
ASGA0033431	7	49785873	-	-	1.57E-03
H3GA0021402	7	50260219	CRISP1	15588	6.28E-03
H3GA0021406	7	50518152	-	-	9.02E-03
ALGA0041468	7	52319155	-	-	3.51E-03
H3GA0021745	7	56152592	-	-	8.15E-04
ASGA0034040	7	56199606	-	-	6.76E-03
MARC0001031	7	57317276	TM6SF1	match	4.43E-03
ALGA0042134	7	58188114	PDE8A	98766	5.61E-03
ALGA0042187	7	59301837	-	-	9.27E-03
H3GA0021903	7	62283996	LINGO1	93788	4.09E-03
M1GA0010442	7	62310234	LINGO1	67550	5.84E-03
H3GA0021941	7	63940639	ISLR	27268	3.03E-03
ASGA0034428	7	70929327	NPAS3	match	5.46E-03
M1GA0010466	7	71050476	NPAS3	79545	2.53E-03
MARC0006751	7	71727031	-	-	4.90E-03
ASGA0034705	7	88646106	-	-	7.80E-03
ALGA0043433	7	91741766	RGMA	73267	7.33E-03
ALGA0043428	7	91766941	RGMA	48092	2.95E-03
ALGA0043424	7	91780068	RGMA	34965	4.17E-03
ALGA0043415	7	91825127	RGMA	match	4.17E-03
ALGA0043406	7	91890551	CHD2	match	1.60E-03
ALGA0043404	7	91922539	CHD2	match	1.60E-03
DRGA0007977	7	92008579	CHD2	5988	1.60E-03
ALGA0043403	7	92021174	CHD2	18583	2.39E-03
ALGA0043398	7	92050130	CHD2	47539	2.84E-03
ALGA0043393	7	92089815	CHD2	87224	1.45E-03
ALGA0043388	7	92162122	FAM174B	49639	2.39E-03
H3GA0022349	7	92212775	FAM174B	match	3.85E-03

M1GA0010535	7	92231886	FAM174B	match	1.80E-03
MARC0095879	7	95409946	RAB15	7121	5.13E-03
MARC0098820	7	1.2E+08	SLC24A4	1550	7.88E-03
H3GA0023236	7	1.21E+08	TMEM251	48069	9.42E-03
ALGA0045073	7	1.22E+08	-	-	6.11E-03
MARC0044680	7	1.23E+08	GSC	26063	2.37E-03
ALGA0120902	9	11173743	MOGAT2	40781	9.37E-03
ALGA0119045	9	15055605	ssc-mir-708	64872	1.68E-03
ASGA0106225	9	22588132	ME3	1498	7.76E-04
ASGA0099198	9	22748344	ME3	56081	4.19E-03
ALGA0118782	9	22793075	-	-	2.20E-03
MARC0019308	9	25110616	TYR	54202	4.53E-03
H3GA0026870	9	30522282	PIWIL4	17025	4.76E-03
ALGA0052237	9	32169995	-	-	5.64E-03
MARC0018577	9	36364394	TRPC6	255	1.25E-03
ALGA0114399	9	36476161	ANGPTL5	82952	3.32E-03
ASGA0096889	9	37305665	MMP27	6788	6.09E-03
MARC0086124	9	37323349	MMP27	match	6.90E-03
ALGA0102606	9	37337886	MMP8	match	6.08E-03
ASGA0042475	9	37614741	DCUN1D5	5328	3.93E-03
DIAS0004102	9	37622654	DCUN1D5	match	3.36E-03
ASGA0042913	9	49127680	BUD13	81254	9.20E-03
H3GA0027281	9	51825334	PVRL1	55932	5.33E-03
ASGA0043018	9	52486044	OAF	53775	3.61E-03
MARC0057714	9	1.32E+08	-	-	9.38E-03
ALGA0055453	9	1.42E+08	SMYD2	50732	7.71E-04
ALGA0055456	9	1.42E+08	SMYD2	69072	9.58E-03
ALGA0056924	10	11062696	LYPLAL1	1973	7.47E-03
ASGA0046818	10	17948351	AKT3	17715	9.55E-03
ASGA0046812	10	18176414	AKT3	match	9.23E-03
MARC0064247	10	19258175	ZBTB18	97827	6.37E-03
ALGA0058975	10	50080838	PTER	match	2.86E-03
H3GA0030974	11	2923443	-	-	1.06E-03

ALGA0060411	11	4117930	USP12	46528	2.25E-04
ALGA0060892	11	12388831	CCNA1	24088	2.99E-03
MARC0031054	11	15537141	FOXO1	7719	8.32E-03
MARC0065987	11	16153984	NEK5	match	4.06E-03
ASGA0091162	11	18394930	ARL11	18017	1.53E-03
ALGA0061166	11	18613210	SETDB2	14124	4.01E-03
INRA0035578	11	19434517	CYSLTR2	31003	8.76E-04
H3GA0031500	11	19458211	CYSLTR2	7309	6.58E-03
DRGA0010995	11	28499617	-	-	2.04E-03
DRGA0011044	11	30843049	-	-	2.90E-04
ALGA0111608	11	33518592	-	-	6.97E-03
MARC0058247	11	40557571	-	-	8.83E-03
MARC0038885	11	42076772	-	-	9.26E-03
DRGA0011147	11	42683281	-	-	7.20E-04
ALGA0061971	11	43178260	-	-	5.91E-03
ALGA0062095	11	48231247	-	-	4.59E-03
ASGA0050759	11	49418020	RPS3A	60162	7.71E-03
DRGA0011263	11	51624925	-	-	7.89E-03
MARC0064023	11	52484631	UCHL3	7498	1.34E-03
MARC0057778	11	52507508	UCHL3	30375	2.14E-03
H3GA0031956	11	53021827	-	-	5.27E-03
ALGA0062282	11	53081698	-	-	3.95E-03
INRA0036447	11	53204913	-	-	1.28E-03
MARC0112524	11	53343454	-	-	5.63E-04
DRGA0011285	11	53365158	-	-	1.46E-03
INRA0036471	11	54041663	MYCBP2	7359	2.48E-03
INRA0036473	11	54059956	MYCBP2	25652	3.99E-03
ALGA0062309	11	54125788	MYCBP2	91484	7.84E-03
ASGA0102962	11	75272010	-	-	2.09E-03
ALGA0063437	11	76088356	ZIC5	match	3.77E-03
M1GA0015266	11	76187291	ZIC2	79290	2.13E-03
MARC0021953	11	76512208	GGACT	37247	1.01E-03
ASGA0051686	11	76688874	TMTC4	match	5.72E-03

ASGA0051750	11	77617889	-	-	8.06E-03
ASGA0098350	12	8826038	-	-	2.58E-03
ASGA0052986	12	8952780	SOX9	74859	9.47E-03
ALGA0065691	12	24829127	HOXB9	13910	6.16E-03
MARC0013292	12	24901251	HOXB13	2806	9.43E-03
MARC0065078	12	42958510	-	-	7.96E-03
ALGA0066582	12	44523799	RHOT1	23380	9.54E-03
MARC0110796	12	48693970	GOSR1	10842	1.48E-03
H3GA0034708	12	54636449	BCL6B	71720	7.59E-03
M1GA0017107	12	59863471	-	-	9.96E-03
MARC0093419	12	60329152	-	-	1.84E-03
ASGA0100802	12	60335124	-	-	7.49E-04
ASGA0101283	12	60445578	-	-	2.12E-04
H3GA0052996	12	60451706	-	-	4.63E-05
ALGA0120651	12	60466957	-	-	5.28E-05
H3GA0034965	12	60524116	-	-	9.13E-04
M1GA0017119	12	60549103	-	-	2.07E-04
M1GA0017151	12	60577246	-	-	1.61E-03
MARC0030180	12	61535474	U6atac	30049	5.75E-03
MARC0050410	12	61605585	-	-	5.69E-03
ASGA0055602	13	2180354	-	-	4.49E-03
ALGA0067480	13	3433598	GALNT15	86918	7.86E-03
MARC0015921	13	4575905	TBC1D5	match	8.01E-03
ASGA0089913	13	5308771	-	-	7.47E-03
ALGA0067602	13	6000731	SATB1	16413	1.97E-03
MARC0037054	13	7650575	EFHB	77580	6.36E-04
ASGA0055807	13	7699209	EFHB	28946	2.55E-03
M1GA0025009	13	25577420	SCN5A	match	7.19E-03
MARC0004520	13	1.41E+08	-	-	7.37E-03
MARC0093228	13	1.41E+08	-	-	5.62E-03
H3GA0037291	13	1.41E+08	-	-	6.88E-03
MARC0093203	13	1.44E+08	TNK2	8716	6.88E-03
ALGA0073790	13	2.1E+08	-	-	3.90E-03

ALGA0109869	13	2.1E+08	SIM2	24130	8.40E-03
ALGA0073982	13	2.14E+08	-	-	1.13E-03
ALGA0073987	13	2.14E+08	-	-	7.95E-04
M1GA0017861	13	2.14E+08	-	-	7.25E-04
H3GA0038523	14	5972387	GFRA2	92072	4.20E-03
ALGA0074628	14	6363534	-	-	8.00E-03
ASGA0061144	14	10777706	CDCA2	46175	1.36E-03
ALGA0075064	14	10905579	-	-	3.09E-03
MARC0025520	14	30477143	-	-	6.00E-03
MARC0080850	14	41317882	RPH3A	match	8.00E-03
MARC0016119	14	44298981	UNG	12724	6.56E-03
ALGA0077164	14	44313339	UNG	match	3.07E-03
ALGA0077178	14	44528915	SSH1	match	3.10E-03
INRA0043787	14	44548710	SSH1	match	2.19E-03
ASGA0063107	14	46665998	-	-	7.46E-03
ASGA0063110	14	46685558	-	-	8.05E-03
ASGA0063368	14	53273094	MIF	9458	4.02E-03
ALGA0077597	14	54540355	SLC25A1	1209	3.65E-03
ASGA0063385	14	54569925	SLC25A1	25470	2.77E-03
ALGA0077602	14	54595487	HIRA	617	5.78E-03
ALGA0077603	14	54680716	UFD1L	42	4.44E-03
H3GA0040220	14	54744216	UFD1L	match	2.77E-03
ASGA0063388	14	54791586	CLDN5	12252	2.77E-03
ASGA0063392	14	54837568	U3	25135	5.78E-03
MARC0059175	14	54867497	SEPT5	24594	3.65E-03
ASGA0063418	14	56633326	-	-	7.32E-03
ALGA0077635	14	56741944	-	-	6.38E-03
MARC0066981	14	56894113	-	-	7.70E-03
ASGA0063487	14	58847222	LGALS8	match	9.39E-03
ASGA0063736	14	62108085	MAP10	13196	3.47E-03
MARC0008126	14	65033626	URB2	6270	9.33E-03
ASGA0063956	14	65870468	ZNF37A	24351	8.90E-03
MARC0059823	14	65951741	-	-	9.87E-03

ASGA0063978	14	66119152	RET	42564	1.56E-03
MARC0097527	14	66239886	CSGALNACT2	match	9.08E-03
H3GA0040656	14	66437562	FXYD4	27335	3.18E-03
ALGA0078253	14	66455930	FXYD4	8967	8.41E-03
ASGA0064014	14	66708189	BICC1	match	4.02E-03
H3GA0040682	14	67337783	-	-	5.75E-03
MARC0009517	14	67360532	-	-	3.82E-03
ALGA0078315	14	67556695	FAM13C	match	4.79E-03
ASGA0064046	14	67586214	FAM13C	match	4.59E-03
ASGA0064057	14	67938907	SLC16A9	61736	4.09E-03
ALGA0078325	14	67973979	SLC16A9	26664	3.65E-03
H3GA0040698	14	68241945	CCDC6	match	8.48E-03
ALGA0078353	14	68492083	ANK3	match	8.69E-03
MARC0047133	14	68911064	-	-	8.13E-03
DRGA0013970	14	69219663	PSMA5	35898	7.51E-03
DRGA0013984	14	70168690	-	-	3.25E-03
ALGA0078438	14	70180492	-	-	4.19E-03
ALGA0078447	14	70318427	-	-	8.01E-03
ASGA0064171	14	70424031	-	-	5.89E-03
M1GA0018867	14	81218454	DNAJB12	224	1.23E-03
H3GA0042409	14	1.35E+08	-	-	4.89E-03
ASGA0066628	14	1.35E+08	ADRB1	96737	4.06E-03
ASGA0066777	14	1.37E+08	ATRNL1	28528	3.48E-03
ASGA0068236	14	1.52E+08	-	-	9.40E-03
ASGA0092166	15	2613630	-	-	3.24E-03
MARC0083940	15	4198197	-	-	9.19E-03
DRGA0014803	15	5072478	-	-	7.10E-03
ASGA0068402	15	7398646	-	-	4.63E-03
MARC0035392	15	53557172	-	-	3.16E-03
DRGA0015125	15	53593754	-	-	7.49E-03
ALGA0090697	16	52371543	MAP1B	20273	3.25E-03
H3GA0046642	16	55928776	-	-	8.26E-03
ALGA0090781	16	57686358	-	-	3.61E-03

ASGA0073900	16	71043011	-	-	8.27E-03
ALGA0091318	16	71070479	-	-	9.07E-03
ASGA0074891	17	15174	-	-	5.08E-03
H3GA0052370	17	439303	RPS19	13887	3.25E-03
ASGA0106200	17	494222	RPS19	68806	8.38E-03
ASGA0097925	17	536580	-	-	8.11E-03
ASGA0075356	17	11848326	SFRP1	match	1.59E-03
MARC0096794	17	13254722	PLAT	57497	2.32E-03
ALGA0095128	17	46668799	KIAA1755	12352	1.66E-03
ASGA0077339	17	53943853	CD40	519	5.52E-03
INRA0054309	17	58229635	-	-	4.60E-04
INRA0054308	17	58236218	-	-	7.96E-04
INRA0054314	17	58294982	PTPN1	60151	6.44E-03
H3GA0050343	18	9979868	-	-	4.04E-03
MARC0069211	18	10393660	TBXAS1	match	3.38E-03
ALGA0103897	18	10395342	TBXAS1	1259	3.51E-03
ALGA0102027	18	10404529	TBXAS1	10446	3.38E-03
ALGA0114284	18	10521082	-	-	3.62E-03
INRA0055202	18	13299138	ssc-mir-490-1	62842	2.33E-03
ALGA0097246	18	17876779	-	-	9.88E-03
ASGA0079081	18	18911412	-	-	5.24E-03
ASGA0090721	18	19225959	TSGA13	match	7.22E-03
ASGA0079728	18	43556023	BMPER	93939	5.49E-03
ASGA0079726	18	43567691	-	-	7.29E-03
H3GA0050905	18	47853853	-	-	2.42E-03
ALGA0098358	18	48005642	CPVL	match	2.36E-03
MARC0061468	18	48297065	-	-	6.70E-03
MARC0103241	18	48620026	-	-	2.00E-03
DBWU0000577	18	49563919	-	-	3.13E-04
ASGA0080057	18	49673542	-	-	3.07E-04
M1GA0023271	18	50032307	ssc-mir-196b-1	5195	1.31E-03
MARC0033103	18	50615451	-	-	2.39E-03
ALGA0111601	23	1182388	-	-	8.24E-03

ASGA0102465	23	2108185	CH242-227G12.1	17804	7.74E-03
ASGA0096921	23	2174682	CH242-227G12.1	34046	1.78E-03
ALGA0103241	23	3024536	NLGN4X	match	3.00E-03
ALGA0105315	23	3059017	NLGN4X	match	2.41E-04
ASGA0101131	23	3744915	-	-	3.62E-03
MARC0114252	23	3766084	-	-	6.24E-03
ALGA0124535	23	3876374	-	-	1.58E-03
ASGA0093054	23	4325817	STS	70802	6.87E-03

Supplementary Table S2. Gene ontologies with p <0.05, count >3 and the genes involved in the ontology. Count is the number of genes involved the ontology and % is (involved genes)/(total genes).

GO ID	GO term name	Count	%	p-value	Genes
GO:0043408	regulation of MAPK cascade	10	8.93	0.0018	BMPER, GDF7, FOXO1, EDAR, RNF149, CD40, PTPN1, MYC, MIF, BMP6
GO:0006355	regulation of transcription, DNA-templated	22	19.64	0.0050	SATB1, GSC, GDF7, ESR1, HIRA, FOXO1, HOXB13, CD40, SMYD2, SOX9, RGMA, DDX17, BMPER, RPS6KA1, MYRF, BCL6B, CHD2, ABRA, HOXB9, MYC, BMP6, SIM2
GO:2001141	regulation of RNA biosynthetic process	22	19.64	0.0054	SATB1, GSC, GDF7, ESR1, HIRA, FOXO1, HOXB13, CD40, SMYD2, SOX9, RGMA, DDX17, BMPER, RPS6KA1, MYRF, BCL6B, CHD2, ABRA, HOXB9, MYC, BMP6, SIM2
GO:1902531	regulation of intracellular signal transduction	15	13.39	0.0058	GDF7, ESR1, FOXO1, SMYD2, CD40, EDAR, SOX9, MIF, BMPER, ADRB1, ABRA, PTPN1, RNF149, MYC, BMP6
GO:0000165	MAPK cascade	9	8.04	0.0062	BMPER, FOXO1, EDAR, RNF149, CD40, PTPN1, SOX9, MYC, MIF
GO:0023014	signal transduction by protein phosphorylation	9	8.04	0.0065	BMPER, FOXO1, EDAR, RNF149, CD40, PTPN1, SOX9, MYC, MIF
GO:0045935	positive regulation of nucleobase-containing compound metabolic process	14	12.5	0.0072	DDX17, ADRB1, RPS6KA1, GDF7, UNG, MYRF, ESR1, ABRA, FOXO1, HOXB9, CD40, SOX9, MYC, BMP6
GO:0019220	regulation of phosphate metabolic process	15	13.39	0.0072	WASH1, GDF7, FOXO1, EDAR, CD40, SOX9, MIF, BMPER, ADRB1, CDCA2, RNF149, TNK2, PTPN1, MYC, BMP6
GO:0031399	regulation of protein modification process	15	13.39	0.0076	WASH1, GDF7, FOXO1, EDAR, CD40, SOX9, MIF, BMPER, CDCA2, RNF149,

					TNK2, PTPN1, MYC, DCUN1D5, BMP6
GO:0035556	intracellular signal transduction	20	17.86	0.0081	GDF7, ESR1, FOXO1, EDAR, CD40, SMYD2, SOX9, MIF, ARL11, BMPER, ADRB1, RPS6KA1, RHOT1, ABRA, RAB15, RNF149, PTPN1, MYC, GFRA2, BMP6
GO:0045893	positive regulation of transcription, DNA-templated	12	10.71	0.0091	DDX17, RPS6KA1, GDF7, MYRF, ESR1, ABRA, FOXO1, HOXB9, CD40, SOX9, MYC, BMP6
GO:0051252	regulation of RNA metabolic process	22	19.64	0.0092	SATB1, GSC, GDF7, ESR1, HIRA, FOXO1, HOXB13, CD40, SMYD2, SOX9, RGMA, DDX17, BMPER, RPS6KA1, MYRF, BCL6B, CHD2, ABRA, HOXB9, MYC, BMP6, SIM2
GO:0010604	positive regulation of macromolecule metabolic process	20	17.86	0.0095	GDF7, UNG, ESR1, FOXO1, EDAR, CD40, SOX9, MIF, DDX17, BMPER, RPS6KA1, MYRF, CDCA2, ABRA, HOXB9, TNK2, PTPN1, MYC, DCUN1D5, BMP6
GO:1902680	positive regulation of RNA biosynthetic process	12	10.71	0.0096	DDX17, RPS6KA1, GDF7, MYRF, ESR1, ABRA, FOXO1, HOXB9, CD40, SOX9, MYC, BMP6
GO:0045937	positive regulation of phosphate metabolic process	11	9.82	0.0112	ADRB1, BMPER, GDF7, CDCA2, EDAR, CD40, PTPN1, TNK2, SOX9, MIF, BMP6
GO:0010562	positive regulation of phosphorus metabolic process	11	9.82	0.0112	ADRB1, BMPER, GDF7, CDCA2, EDAR, CD40, PTPN1, TNK2, SOX9, MIF, BMP6
GO:0006351	transcription, DNA-templated	20	17.86	0.0115	SATB1, GSC, GDF7, ESR1, HIRA, FOXO1, SMYD2, CD40, SOX9, RGMA, DDX17, BMPER, RPS6KA1, MYRF, BCL6B, ABRA, HOXB9, MYC, BMP6, SIM2

GO:0051254	positive regulation of RNA metabolic process	12	10.71	0.0127	DDX17, RPS6KA1, GDF7, MYRF, ESR1, ABRA, FOXO1, HOXB9, CD40, SOX9, MYC, BMP6
GO:0022612	gland morphogenesis	4	3.57	0.0140	GDF7, HOXB13, EDAR, SOX9
GO:0032774	RNA biosynthetic process	22	19.64	0.0140	SATB1, GSC, GDF7, ESR1, HIRA, FOXO1, HOXB13, CD40, SMYD2, SOX9, RGMA, DDX17, BMPER, RPS6KA1, MYRF, BCL6B, CHD2, ABRA, HOXB9, MYC, BMP6, SIM2
GO:0031401	positive regulation of protein modification process	11	9.82	0.0141	BMPER, GDF7, CDCA2, EDAR, CD40, PTPN1, TNK2, SOX9, DCUN1D5, MIF, BMP6
GO:0051247	positive regulation of protein metabolic process	13	11.61	0.0145	BMPER, GDF7, CDCA2, FOXO1, EDAR, CD40, PTPN1, TNK2, SOX9, MYC, DCUN1D5, MIF, BMP6
GO:0007167	enzyme linked receptor protein signaling pathway	9	8.04	0.0161	PLAT, RGMA, BMPER, GDF7, FOXO1, PTPN1, TNK2, SOX9, BMP6
GO:0010468	regulation of gene expression	24	21.43	0.0163	SATB1, GSC, GDF7, ESR1, HIRA, FOXO1, HOXB13, EDAR, CD40, SMYD2, SOX9, MIF, RGMA, DDX17, BMPER, RPS6KA1, MYRF, BCL6B, CHD2, ABRA, HOXB9, MYC, SIM2, BMP6
GO:0010628	positive regulation of gene expression	13	11.61	0.0175	DDX17, RPS6KA1, GDF7, MYRF, ESR1, ABRA, FOXO1, HOXB9, EDAR, CD40, SOX9, MYC, BMP6
GO:0048732	gland development	6	5.36	0.0207	TYR, GDF7, HOXB13, HOXB9, EDAR, SOX9
GO:2000112	regulation of cellular macromolecule biosynthetic process	22	19.64	0.0208	SATB1, GSC, GDF7, ESR1, HIRA, FOXO1, HOXB13, CD40, SMYD2, SOX9, RGMA, DDX17, BMPER, RPS6KA1, MYRF, BCL6B, CHD2, ABRA, HOXB9, MYC, BMP6, SIM2

GO:0043409	negative regulation of MAPK cascade	4	3.57	0.0211	FOXO1, RNF149, PTPN1, MYC
GO:0031328	positive regulation of cellular biosynthetic process	13	11.61	0.0218	DDX17, ADRB1, RPS6KA1, GDF7, MYRF, ESR1, ABRA, FOXO1, HOXB9, CD40, SOX9, MYC, BMP6
GO:0032270	positive regulation of cellular protein metabolic process	12	10.71	0.0233	BMPER, GDF7, CDCA2, EDAR, CD40, PTPN1, TNK2, SOX9, MYC, DCUN1D5, MIF, BMP6
GO:0030509	BMP signaling pathway	4	3.57	0.0253	RGMA, BMPER, GDF7, BMP6
GO:0010556	regulation of macromolecule biosynthetic process	22	19.64	0.0272	SATB1, GSC, GDF7, ESR1, HIRA, FOXO1, HOXB13, CD40, SMYD2, SOX9, RGMA, DDX17, BMPER, RPS6KA1, MYRF, BCL6B, CHD2, ABRA, HOXB9, MYC, BMP6, SIM2
GO:0034654	nucleobase-containing compound biosynthetic process	23	20.56	0.0282	SATB1, GSC, GDF7, ESR1, HIRA, FOXO1, HOXB13, CD40, SMYD2, SOX9, RGMA, DDX17, BMPER, ADRB1, RPS6KA1, MYRF, BCL6B, CHD2, ABRA, HOXB9, MYC, SIM2, BMP6
GO:0035148	tube formation	4	3.57	0.0284	RGMA, GDF7, EDAR, SOX9
GO:0071772	response to BMP	4	3.57	0.0292	RGMA, BMPER, GDF7, BMP6
GO:0060627	regulation of vesicle-mediated transport	6	5.36	0.0300	SEPT5, TBC1D8, RAB15, GOSR1, PTPN1, TNK2
GO:0010557	positive regulation of macromolecule biosynthetic process	12	10.71	0.0313	DDX17, RPS6KA1, GDF7, MYRF, ESR1, ABRA, FOXO1, HOXB9, CD40, SOX9, MYC, BMP6
GO:0015031	protein transport	12	10.71	0.037	KDELR3, STX12, TBC1D8, XPO6, ABRA, EDAR, GOSR1, CD40, PTPN1, GCC2, MIF, BMP6
GO:0032268	regulation of cellular protein metabolic process	16	14.29	0.042	PLAT, WASH1, GDF7, FOXO1, EDAR, CD40, SOX9, MIF, BMPER, CDCA2, RNF149, TNK2,

					PTPN1, MYC, DCUN1D5, BMP6
GO:1902532	negative regulation of intracellular signal transduction	6	5.36	0.0451	ESR1, FOXO1, RNF149, PTPN1, MYC, MIF
GO:0032872	regulation of stress-activated MAPK cascade	4	3.57	0.0463	FOXO1, EDAR, PTPN1, MYC
GO:0036211	protein modification process	21	18.75	0.0473	SATB1, WASH1, GDF7, FOXO1, EDAR, CD40, SMYD2, SOX9, MIF, BMPER, USP12, GALNT15, CDCA2, UCHL3, RNF149, LYPLAL1, PTPN1, TNK2, MYC, DCUN1D5, BMP6
GO:0006464	cellular protein modification process	21	18.75	0.0473	SATB1, WASH1, GDF7, FOXO1, EDAR, CD40, SMYD2, SOX9, MIF, BMPER, USP12, GALNT15, CDCA2, UCHL3, RNF149, LYPLAL1, PTPN1, TNK2, MYC, DCUN1D5, BMP6
GO:0070302	regulation of stress-activated protein kinase signaling cascade	4	3.57	0.0476	FOXO1, EDAR, PTPN1, MYC