Supplementary information:

A new *mib* allele with a chromosomal deletion covering *foxc1a* exhibits anterior somite specification defect

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Table S1. Percentage of embryos showing nn2002 homozygous phenotype from each clutch.

Clutch no.	no. of embryos showing early segmentation phenotype	no. of embryos showing no segmentation phenotype	ratio of homozygotes
1	21	78	21%
2	16	64	20%
3	14	58	19%
4	19	65	23%
5	44	151	23%
6	11	23	32%
Total	125	439	22%

Table S2. Percentage of embryos showing transheterozygous (ta52b/nn2002) phenotypes from each clutch.

Clutch no.	no. of transheterozygotes from mib^{ta52b} ♀ x mib^{nn2002} ♂	no. of total embryos	ratio of transheterozygotes	no. of transheterozygotes from mib^{nn2002} ♀ x mib^{ta52b} ♂	no. of total embryos	ratio of transheterozygotes
1	45	158	28%			
2	24	118	20%			
3	5	21	24%			
4	17	57	30%			
5				2	6	33%
6	11	59	19%			
7	29	102	28%			
8	41	145	28%			
9	12	35	34%			
10				51	198	26%
11	23	82	28%			
12	24	105	23%			
13	27	115	23%			
14	35	175	20%			
15	36	179	20%			
16	62	274	23%			
17	31	143	22%			
18	14	43	33%			
19				63	205	31%
20				11	37	30%
21				42	177	24%
22				66	268	25%
23				54	219	25%
Total	436	1811	24%	289	1110	26%

Table S3. List of genes in LG2 and their relative expression in wild type embryos (AB) and *mib* mutants (2002).

Feature ID	AB1 Expression values	AB 2 Expression values	AB3 Expression values	2002-1 Expression values	2002-2 Expression values	2002-3 Expression values	Chromosome	Chromosome region start	Chromosome region end
ZNF554 (5 of 5)	0	0.4499938	0	0	0	0	2	19233	21298
CABZ01092286.1	3.6315475	10.712303	6.9913215	0	0	0	2	23916	32332
CABZ01090951.1	2.5127515	2.0062799	1.0365979	0	0	0	2	50561	53808
CABZ01084950.1	6.6380348	13.60351	12.459818	0	0	0	2	60855	62944
CABZ01084952.1	0	0	0	0	0	0	2	73298	80311
zgc:158345	18.337346	15.903438	23.73781	0	0	0	2	81941	87436
cldn1	4.4232592	8.9273643	13.837681	0	0	0	2	88773	91785
CPN2	9.2958934	14.239643	11.632473	0	0	0	2	93928	97276
ANGPTL1 (2 of 2)	0	0	0	0	0	0	2	108647	114343
CABZ01085888.1	11.678024	8.702582	16.861577	0	0	0	2	115939	151915
fggy	7.3862678	6.6346734	7.6177345	0	0	1.4793259	2	154495	158192
znfl2a	69.331429	74.93296	57.75331	0	0	0	2	161051	164976
igfbp1b	0	0.3346374	0	0	0	0	2	167258	170770
adcy1b	0	0	0	0	0	0	2	179198	199691
MOV10L1	0.3377878	0.786634	0.975445	0	0	0	2	200138	211977
zgc:171570	3.0876964	2.4927312	3.8638077	0	0	0	2	221432	246482
zgc:113293	0	0	0	0	0	0	2	250271	255471
DHX30	1.9104279	1.7795878	2.2067315	0	0	0	2	256480	277540
CABZ01064861.1	0	0.3278235	0	0	0	0	2	282825	287502
PHLPP1	0.8673863	0.5386542	1.6698603	0	0	0	2	290248	301002
wu:fi19a06	0	0.4998397	0	0	0	0	2	304364	314202
CU928013.2	2.7183719	2.6728755	3.7069276	0	0	0	2	319490	340465
zgc:113452	5.7539346	5.1781727	4.5060053	0	0	0	2	334714	346967
CU693494.2	0	0	0	0	0	0	2	372564	373196
SHARPIN (2 of 2)	0	0.4013795	0.6221501	0	0	0	2	377851	385099
CU693494.3	0.1015127	0.9456036	1.0259996	0	0	0	2	387136	392836
wrnip1	1.6606899	1.1602152	1.4986402	0	0	0	2	394830	410278
MYLK4 (1 of 2)	1.2608858	0.4698124	0.7282233	0	0	0	2	427011	447851
CABZ01064012.1	0	0	0	0	0	0	2	689562	790847
foxc1a	16.336109	14.216155	18.000801	0	0	0	2	868219	870389
CU856140.1	0.8288701	0	0	0	0	0	2	878904	888438
foxf2a	1.8110757	2.53056	1.7433082	0	0	0	2	895049	897768
foxq1a	2.0006596	3.2613695	2.8886972	0	0	0	2	902565	903497
irf4a	0.2857648	0	0.4126078	0	0	0	2	1038215	1063571
dusp22b	0.3251943	0.9087679	0.4695391	0	0	0	2	1065725	1082670
ripk1l	4.2831927	3.1918786	3.0921919	0	0	0	2	1088190	1104351
si:ch211-241e1.5	1.9021217	1.476542	1.6783684	0	0	0	2	1119723	1128678
si:ch211-241e1.3	0	0	0	0	0	0	2	1128112	1169253
si:ch211-241e1.4	0	0	0	0	0	0	2	1131839	1134018
si:ch211-241e1.2	0.1655388	0	0	0	0	0	2	1185863	1268105
polr2d	149.96869	121.26047	129.70156	0	0	0	2	1308283	1313492
CABZ01084564.1	0	0	0	0	0	0	2	1358788	1372630
OSBPL1A (2 of 2)	0.3535256	0	0.5104459	0	0	0	2	1386360	1401154
ABCF3	24.004828	21.913585	24.261936	0	0	0	2	1402471	1409711
prkacbb (2 1411669	6.349032	6.093422	11.528438	0	0	0	2	1411670	1439425
CU467642.1	5.8150012	7.3126088	9.2357318	0	0	0	2	1522259	1622366
LPHN2 (1 of 4)	8.5346722	6.6678721	9.9378851	0	0	0	2	1626935	1688776
FP102463.1	3.5219158	2.4605319	2.1188321	0	0	0	2	1691997	1695667
exosc4	29.205547	40.808005	26.584857	0	0	0	2	1709545	1713492
FP245444.1	6.8854209	12.413916	11.545164	0	0	0	2	1727339	1743445
BCL10	1.0477774	0.9760179	1.1346426	0	0	0	2	1747679	1756376
MCOLN3 (1 of 2)	1.4349749	2.4060552	3.7294573	0	0	0	2	1760876	1787181
ssx2ip	3.8780098	1.3761582	1.5998147	0	0	0	2	1792049	1810559
zgc:112335	0.5858805	2.7287757	3.8067153	0	0	0	2	1812389	1822105
SLC22A23 (3 of 3)	2.4206828	3.5702531	4.6602094	0	0	0	2	1823446	1897681
5S_rRNA (2 182444	0	0	0	0	0	0	2	1824450	1824564
FP243387.1	0	0	0	0	0	0	2	1856129	1856224
dspa	19.497449	23.782491	26.538543	0	0	0	2	1912379	1964899
hig1	10.291989	15.432922	17.759895	0	0	0	2	1970655	1975857
si:ch211-163f10.4	0	0	0	0	0	0	2	1973479	1974747
CCDC13	0.6076222	0.5660078	0.8773289	0	0	0	2	1983827	2009351

tmie	0	0	0	0	0	0	2	2025945	2081419
pth1ra	0	0.6168789	0	0	0	0	2	2092256	2240623
mir460	0	0	0	0	0	0	2	2103466	2103542
ss18	48.369846	54.92678	48.555349	0	0	0	2	2368246	2384584
FP236168.1	2.1371128	4.5502803	6.8326618	0	0	0	2	2392229	2424395
FP102801.1 (2 2428	0.1011606	0	0	0	0	0	2	2428046	2446159
rpe65a	0.8027302	0	0.7726934	0	0	0	2	2448547	2463377
FP102801.1 (2 2472	3.7877748	8.7032883	6.1982719	0	0	0	2	2472964	2488188
si:ch211-188c16.1	0	0.1610574	0.2496438	0	0.1566048	0	2	2490000	2505953
c8a	9.1500755	9.7410413	11.638739	0	0	0	2	2506994	2523112
c8b	9.3984576	10.467674	11.505147	0	0	0	2	2519755	2533944
dab1b	0	0.504871	0.2608551	0	0	0	2	2542265	2589205
si:ch211-188c16.4	0	0	0	0	0	0	2	2543103	2547948
prkacbb (2 2614676	1.007496	2.6448504	2.6449015	0	0	0	2	2614677	2642068
zgc:66286	197.97436	178.77025	182.30211	0	0	0	2	2654111	2659244
CRHR2	0	0	0	0	0	0	2	2681130	2785846
aqp1a.1	1.9840725	1.4785509	2.291798	0	0	0	2	2888643	2900295
aqp1a.2	0	0	0	0	0	0	2	2912958	2917596
thoc1	61.949203	64.445908	62.67801	0	0	0	2	2923616	2941632
usp14	56.795291	63.368194	61.503865	0	0	0.297108	2	2941647	2964335
rock1	13.554978	13.430877	14.585248	0	0	0	2	2970496	3052905
eif2b5	25.673513	26.494293	27.983669	0	0	0	2	3055167	3068257
wacb	4.9512345	2.3060688	2.6808565	0	0	0	2	3070270	3086434
bambib	3.3529651	3.6745052	5.6955927	0	0	0	2	3091038	3098818
adipoqb	0	0	0	0	0	0	2	3178319	3185111
tmtopsa	0	0	0	0	0	0	2	3255205	3340664
CABZ01063645.2	0	0	0	0	0	0	2	3258302	3258383
CABZ01063645.1	0	0	0	0	0	0	2	3260712	3260802
CABZ01088149.2	0	1.8341518	0	0	0	0	2	3385910	3386762
CABZ01088149.1	2.7482559	2.0480281	4.761757	0	0	0	2	3388619	3392143
SERBP1 (2 of 3)	73.090362	72.972722	81.179351	0	0	0	2	3397407	3409194
IPP (1 of 2)	1.2855478	2.3950081	0.9280835	0	0	0	2	3413431	3421555
guk1a	13.009744	11.064937	13.884129	0	0	0	2	3425900	3444870
C2H1orf35	7.518766	6.2425404	6.1360784	0	0	0.4583061	2	3444090	3461887
arf1	64.72169	55.83353	67.983156	0	0	0	2	3463796	3476115
LRRC52 (2 of 2)	0	0	0	0	0	0	2	3497699	3505613
wu:fi26e04	0	0	0	0	0	0	2	3508171	3530580
pik3r3a	9.1626098	10.321501	10.460645	0	0	0	2	3546016	3567452
ipp	0	0.9501508	1.472762	0	0	0	2	3580312	3589765
wnt3a	1.2750105	0.3958961	2.4546033	0	0	0	2	3599278	3652698
wnt9a	0.4040293	0.7527168	1.7501003	0	0	0	2	3695124	3764786
5S_rRNA (2 375137	0	0	0	0	0	0	2	3751376	3751490
snap47	0.437488	1.1546559	0.9475152	0	0	0	2	3879432	3898088
jmjd4	2.6275555	1.4685607	1.8969274	0	0	0	2	3897559	3908363
iba57	7.6047294	5.4739241	4.4919241	0	0	0	2	3910978	3914185
CU633991.1	0	0	0	0	0	0	2	3922257	3923551
cyp8b1	0	0	0	0	0	0	2	3930186	3932157
CU694226.2	0	0	0	0	0	0	2	3946885	3948851
CU694226.1	0	0	0	0	0	0	2	3962396	3964308
cx47.1	0	0	0	0	0	0	2	3967127	3992746
CU694226.3	0	0	0	0	0	0	2	3990061	3990173
SERP1	108.21668	102.62974	105.34575	0.561183	0	0	2	3996683	4003534
FUZ	1.0089813	0.9398789	1.4568402	0	0	0	2	4011338	4016439
gpt2l	13.245633	14.309711	15.353553	0	0	0	2	4027400	4067295
c1ql3b (2 40896272	0	0.3039818	0	0	0	0	2	4089628	4092270
pter	1.2944628	3.3159734	0.4672598	0	0	0	2	4097884	4110658
mmp16b	0.1511674	0	0.2182665	0	0	0	2	4124602	4172324
egfra	0.3568859	0.6648875	1.0305955	0	0	0	2	4190333	4307017
npc1	13.88407	19.095981	20.85408	0	0	0	2	4310671	4353828
MPP7 (2 of 3)	0	0	0	0	0	0	2	4358228	4380961
phb2	43.882587	47.856217	37.089281	0	0	0	2	4408283	4429954
PEX5L (2 of 2)	0.2709953	0.2524355	0.3912826	0	0	0	2	4440346	4511292
CABZ01087197.1	3.7332308	5.7959196	7.1870785	0	0	0	2	4530979	4541827
MFN1 (4 of 4)	0	0	0	0	0	0	2	4552774	4574576
tnk2b	0.110294	0.2054805	0.3185009	0	0	0	2	4622092	4686262

tfr1a	3.3503353	4.4583997	4.3767465	0	0	0	2	4738019	4763716
dlg1l	2.9761087	1.9658006	3.7502149	0	0	0	2	4788963	4963219
CABZ01055591.1	0	0	0	0	0	0	2	4989926	4999272
FAM132B	1.8985104	0.7073946	1.644724	0	0	0	2	5005145	5032086
si:ch1073-184j22.2	0.3697733	0.4592646	0.1779685	0	0	0	2	5038156	5046905
sft2d3	15.062694	12.951776	10.874304	0	0	0	2	5048645	5050255
wdr33	29.743353	26.312797	27.571588	0	0	0	2	5052822	5086135
DUSP28	1.7879458	0	0	0	0	0	2	5089269	5092304
proc	0.7346566	1.9161573	1.9093506	0	0	0	2	5098931	5118311
PROC (2 of 2)	1.2944628	0	0	0	0	0	2	5110275	5118311
saga	0	0	0	0	0	0	2	5122515	5147484
cldn15la	0	0.4659099	0	0	0	0	2	5150932	5159828
crfb16	0.6436605	0	0	0	0	0	2	5164061	5179317
parla	1.3847295	0.4837099	0.7497648	0	0	0	2	5186291	5203409
mb21d2a	2.9391039	2.2962298	1.9165056	0	0	0	2	5205467	5224162
fgf12a	0	0.1312878	0	0	0	0	2	5229885	5324048
cwc25	25.537072	18.177703	17.04473	0	0	0	2	5351814	5366176
sst2	1.7315542	5.6453762	2.5001433	0	0	0	2	5368743	5371233
NYAP2 (2 of 2)	0	0	0.1398482	0	0	0	2	5377260	5418420
slc35d1b	9.0697613	3.2704248	6.33657	0	0	0	2	5436277	5452716
mier1b	6.319529	4.7324622	8.2300255	0	0	0	2	5453872	5478506
dis3l2	4.6721773	4.6523435	5.350298	0	0	0	2	5483498	5527479
ACAP2 (2 of 2)	0.5247724	0.3666241	1.3259827	0	0	0	2	5530016	5566691
si:ch211-168b3.2	2.9566242	1.8360886	0	0	0	0	2	5569645	5572719
tmem125b	0	0	0	0	0	0	2	5578811	5584297
slc1a7a	0.4652581	0.4333938	0.3358866	0	0	0	2	5590924	5642026
scp2a	10.3311	9.4419743	5.6289775	0	0	0	2	5647589	5682147
C2H1orf123	55.379514	67.897226	54.091232	0	0	0	2	5684429	5694226
uck2b	74.531433	65.132521	66.935093	0	0.2319848	0	2	5694306	5707806
aldh9a1b	15.621889	12.126656	15.904881	0	0	0	2	5709761	5734452
zte38	0	0	0	0	0	0	2	5734448	5746425
prdx1	31.429103	25.457919	21.210037	0	0	0	2	5748881	5758078
CU467854.1	1.7899052	2.1436963	1.476797	0	0	0	2	5769983	5791691
CU467854.2	0	0	0	0	0	0	2	5794512	5823951
si:ch73-344o19.1	0	0.2016206	0.6250358	0	0	0	2	5823773	5839652
rec8a	0	0	0	0	0	0	2	5854588	5874907
gng5	151.18493	160.65882	133.96967	0	0	0	2	5885534	5891553
zp3b	1.0062617	1.6403546	1.0896851	0	1.3671469	0	2	5895636	5901186
arl14	0	1.2673294	0.6547994	0	0	0	2	5903803	5904831
ppm1la	8.2685067	8.0231445	8.9540015	0	0	0	2	5908158	5934900
otol1a	0	0	0	0	0	0	2	5946029	5958557
SMC6	3.4996305	3.8711907	5.5267404	0	0	0	2	5964013	6016219
5S_rRNA (2 601009	0	0	0	0	0	0	2	6010092	6010206
rgs13	0	0	0	0	0	0	2	6179990	6186663
rgs1	0	0	0	0	0	0	2	6216200	6223208
rgs18	0	0	0	0	0	0	2	6240288	6253261
FAM5C (2 of 3)	0.2022774	0	0	0	0	0	2	6439225	6509894
5S_rRNA (2 64708	0	0	0	0	0	0	2	6470817	6470931
si:zfos-986b4.1	0	0	0	0	0	0	2	6580575	6624140
rgs5b	0	0	0	0	0	0	2	6590676	6593943
nos1apb	0	0.2009681	0	0	0	0	2	6630924	6657578
si:ch211-170d12.2	0	0	0	0	0	0	2	6663337	6663958
ddr2b	0	0	0	0	0	0	2	6668120	6701310
XPR1 (1 of 2)	8.7595091	13.636581	10.048789	0	0	0	2	6704193	6762154
cdc14aa	1.0928662	1.3573582	0.7889796	0	0	0	2	6780044	6810356
si:dkey-60b12.6	0	0	0	0	0	0	2	6785126	6785749
VCAM1 (2 of 2)	0	0	0	0	0	0	2	6811661	6818735
extl2	2.4971443	2.6168868	2.7041683	0	0	0	2	6828061	6836515
zgc:110366	5.8186265	5.6911305	2.1003386	0	0	0	2	6837105	6853273
si:dkey-60b12.9	3.7297205	2.6568038	2.8510096	0	0	0	2	6854412	6856538
RC3H1 (1 of 2)	3.4898161	3.5555711	6.7709536	0	0	0	2	6859433	6894418
si:ch211-13f8.1	0	0	0.1654281	0	0	0	2	6897790	6914529
COLGALT2 (2 of 2	1.0387398	0.2418998	0.7499039	0	0	0	2	6918043	6939984
zgc:153115	12.403483	14.898581	17.437756	0	0	0	2	6943373	6951681
si:dkeyp-106c3.3	0	0	0	0	0	0	2	6984470	6991133

si:dkeyp-106c3.2	0	0.8616332	2.0033358	1.5901112	0.8378122	0	2	6992921	6994227
si:dkeyp-106c3.1	0	0.197738	0	0	0	0	2	7000339	7117405
5S_rRNA (2 709961	0	0	0	0	0	0	2	7099614	7099732
CABZ01088691.2	0	0	0	0	0	0	2	7151503	7153771
CABZ01088691.1	0	0	0	0	0	0	2	7155344	7158267
ripk2	1.2510827	0.3329713	1.2902884	0	0	0	2	7264635	7298101
CCDC39	0.3281673	1.3756138	1.421495	0	0	0	2	7362320	7480705
dcun1d1	10.912521	8.8276314	9.9513395	0	0	0	2	7482658	7495864
eif4a2	17.875086	17.536554	21.141696	0	0	0	2	7500004	7511589
SNORD2 (2 750489	0	0	0	0	0	0	2	7504900	7504970
SNORD2 (2 750527	0	0	0	0	0	0	2	7505280	7505350
SNORA81 (2 75055	0	0	0	0	0	0	2	7505553	7505731
SNORA81 (2 75077	0	0	0	0	0	0	2	7507735	7507924
SNORD2 (2 750821	0	0	0	0	0	0	2	7508211	7508282
b3gnt5b	5.6720357	4.082761	1.8612945	0	0	0.3614541	2	7533735	7541614
tbl1xr1b	1.8659934	3.476393	4.4904275	0	0	0	2	7549012	7585043
kcnmb2	0	0	0	0	0	0	2	7602709	7613741
KCNMB3	0	0	0	0	0	0	2	7616255	7629451
si:ch211-38m6.6	0	0	0	0	0	0	2	7631821	7658416
ephb3a	9.948859	7.511543	8.0140926	0	0	0	2	7708305	7801920
pcolce2a	0.5622336	1.3093192	1.2176903	0	0	0	2	7815722	7831598
pls1	0	0.2670931	1.6560089	0	0	0	2	7845116	7895670
chst2a	14.607608	12.136126	11.400823	0	0	0	2	7896790	7899153
5S_rRNA (2 797362	0	0	0	0	0	0	2	7973626	7973741
C2H3orf58 (2 of 2)	2.5794936	4.1503444	4.7402214	0	0	0	2	8045450	8096540
si:ch211-222m2.2	1.4447488	1.0093513	0.5215082	1.6557505	1.635744	0	2	8268735	8272479
si:ch211-222m2.1	0	0	0.2656895	0.2108862	0.5000113	0	2	8274929	8279057
si:ch211-71m22.1	2.0164055	0.8049888	1.2477567	0	0	0	2	8371294	8396016
si:ch211-71m22.5	0	0	0	0	0	0	2	8402160	8416146
si:ch211-71m22.2	0	0	0	0	0	0	2	8418581	8419473
si:ch211-71m22.3	0	0	0	0	0	0	2	8428763	8432781
fubp1	99.016087	86.636676	94.622399	0	0	0.2674701	2	8433634	8447445
SCARNA24	0	0	0	0	0	0	2	8441729	8441863
fam73a	13.59714	14.185817	14.135425	0	0	0	2	8447449	8473100
usp33	4.4192968	6.7868779	7.0707277	0	0	0	2	8501496	8561837
zzz3	11.126238	11.974209	12.477567	0	0	0	2	8563505	8625237
ak5	0	0	0.2633015	0	0	0	2	8630181	8844296
CR450828.1	0	0	0	0	0	0	2	8680562	8680640
pigk	2.204168	3.5197892	4.5464819	0	0	0	2	8846226	8922838
st6galnac5a	0	0.4390848	0.6805946	0	0	0	2	8945288	9044160
st6galnac3	0.5467532	1.5279226	4.3419301	0	0	0	2	9114487	9273952
5S_rRNA (2 919089	0	0	0	0	0	0	2	9190899	9191016
cope	93.83458	89.754625	85.473859	0.7217374	0.5704133	0	2	9297672	9309055
wu:fi34b01	0	0	0.5223168	0	0	0.5071565	2	9313963	9315252
zgc:153615	1.0278719	0.7181068	1.1130869	0	0	0	2	9315715	9334070
CABZ01069745.1	0	0	0	0	0	0	2	9338010	9342344
txndc12	19.632686	25.321979	23.986002	0	0	0	2	9361512	9368564
gipc2	9.5763685	9.1616033	7.1003792	0	0	0	2	9371736	9415099
dnajb4	1.2014775	0.4476766	0.346956	0	0	0	2	9415509	9424697
zgc:136678	0	0	0	0	0	0	2	9432998	9448262
selt1a	33.694727	30.712074	25.633262	0	0	0	2	9473203	9485168
dvl3a	22.177302	22.825406	23.064216	0	0	0	2	9490950	9532978
si:ch1073-170o4.1	0	0	0.9306473	0	1.1676139	0	2	9535335	9536958
SNORA13 (2 95357	0	0	0	0	0	0	2	9535755	9535890
SNORA13 (2 95361	0	0	0	0	0	0	2	9536199	9536328
pcyt1aa	1.4151116	2.0160619	2.4038124	0	0	0.2334042	2	9544319	9572728
ap2m1a	107.01384	96.070221	90.231648	120.53646	119.68119	120.82532	2	9578708	9607608
anxa13l	0.6481303	0.8049888	0.9358175	1.2379801	0.9784172	0	2	9610654	9631137
abi1b	1.1249754	1.7028843	1.5228008	1.1281157	1.0826422	0.8871609	2	9651729	9704711
5S_rRNA (2 966442	0	0	0	0	0	0	2	9664426	9664542
acbd5b	0	0	0	0	0	0	2	9707575	9730294
tsen15	2.0835762	1.6904418	1.6497777	1.6175941	1.6437071	3.2037858	2	9735018	9746702
C2H1orf21	25.925214	26.936165	22.315648	17.426951	21.449916	17.474143	2	9746978	9760625
sec22ba	19.695576	17.857434	16.304395	18.05765	19.504475	20.617325	2	9759839	9772558
imp3	52.191549	34.794583	56.887854	41.635226	44.028775	52.367246	2	9771984	9778860

SLC35A3 (2 of 2)	3.2263937	3.8250884	4.2350007	4.3698908	7.9700109	2.4672479	2	9779386	9829157
FP102157.1	0	0.5066363	0.7853014	0	0	0	2	9845472	9850467
cmpk	56.090983	59.79062	68.46427	60.638014	59.44703	79.853584	2	9852644	9865826
bcl6ab	6.8069443	4.579434	7.3712693	7.1509904	5.4804051	5.3017172	2	9876231	9887088
insl5b	0	0	0	0	0	0	2	9916659	9917958
AHSG	0	0	0	0	0	0	2	9923242	9930638
pfn2l	159.68389	126.88198	154.66349	108.17394	111.5458	107.99577	2	9935926	9940736
nsun4	6.6951772	5.301146	6.283538	5.371093	5.7610105	1.8772795	2	9949381	9958330
dmbx1a	5.2970594	2.8650646	5.9212474	4.1123967	4.3335536	5.9889409	2	9974227	9981384
5S_rRNA (2 999509	0	0	0	0	0	0	2	9995091	9995208
gadd45aa	2.6070047	0.6938451	2.1509613	45.669906	48.575721	49.602578	2	10071950	10075877
gng12a	13.391331	7.399946	7.2098003	7.80361	7.8121095	7.3187421	2	10078443	10130118
wls	70.772148	87.213482	85.687177	68.012632	66.773498	58.395106	2	10133495	10178043
si:ch211-132a5.4	0	0.6201055	1.9223641	0.7629207	0	0	2	10177784	10207577
scinlb	5.2893124	4.6091865	4.6807984	3.5197562	3.2454117	1.4352437	2	10187884	10242089
CCDC18 (2 of 2)	1.7613489	1.3511802	2.6927609	2.4935514	2.1584266	2.1788363	2	10259668	10355322
CCDC18 (1 of 2)	0.4771512	1.3334171	0	0	0	0	2	10259795	10272567
mtf2	10.152675	7.7378278	13.593046	8.2505889	9.6974771	10.351771	2	10398979	10423736
fam69a	0.4502932	0.1398179	0	0.6880764	0.4078574	0	2	10433352	10478531
rpl5a	2201.2228	2122.4278	1832.0046	1378.9692	1511.3015	1392.8402	2	10478581	10494926
EVI5 (2 of 2)	0	0	0	0	0	0	2	10501363	10526503
gfi1aa	8.606321	9.5015075	6.9035718	8.4020289	4.6194125	4.4687971	2	10558049	10576954
rpap2	6.2022043	8.3195018	7.5223609	5.6864158	4.4941653	3.8259175	2	10582838	10612358
glmna	9.9697412	9.7757264	8.839056	9.6217224	8.3964921	11.525075	2	10612459	10649203
cdc7	13.444488	8.2818089	12.523952	8.9465923	6.2851486	3.0401111	2	10655336	10669070
tceanc2	11.608305	5.6229071	12.738292	7.9822001	4.2057338	8.4627012	2	10669711	10671898
cdcp2	0.5529074	0.2575201	0.7983277	0	0.5008012	0.3875781	2	10672547	10698051
mrpl37	44.310425	37.234742	41.161057	39.773193	39.853935	45.613778	2	10705328	10723075
ssbp3a	5.8955297	5.280539	7.5301934	10.134834	12.733687	13.033774	2	10726557	10818715
5S_rRNA (2 107979	0	0	0	0	0	0	2	10797962	10798095
acot11a	1.1503382	0.5357773	0.8304708	0.659171	0.6077925	0.4031832	2	10820443	10857700
fam151a	0	0	0	0.4753844	0.3757122	0	2	10860360	10874219
cryz	5.2828738	8.4751654	5.5089635	9.7543489	8.7725258	11.109598	2	10895509	10910704
tyw3	10.035567	10.224657	11.320373	3.5941358	1.9883963	8.3537675	2	10910620	10917526
lhx8a	0	0	0	0	0	0	2	10997100	11001473
slc44a5a	0	0	0	0	0	0	2	11008119	11259816
5S_rRNA (2 11035	0	0	0	0	0	0	2	11035191	11035312
si:dkey-189n19.4	0	0	2.5047904	0	6.2851486	4.8641777	2	11122029	11122621
si:dkey-189n19.3	0	0	0	0	0	0	2	11128345	11129288
sdr16c5a	32.148017	40.033455	40.065748	50.416942	51.187043	55.982135	2	11274377	11295652
penka	0	0	0	0	0	0	2	11299996	11304124
impad1	21.856658	26.705651	35.656697	38.061111	46.792625	42.580787	2	11424558	11440036
MFF (1 of 2)	1.647983	1.2792642	0.793159	0.6295555	0.7463383	0.3850688	2	11442481	11454228
ftr01	0.2711527	0	0	0	0	0	2	11461586	11468724
greb1l (2 11548228.	5.1671014	11.732225	13.056112	9.9929411	14.040456	18.110226	2	11548229	11568413
si:dkey-203o21.2	0	0	0	0	0	0	2	11552131	11558509
greb1l (2 11555477.	20.305225	20.669535	23.499861	27.409104	21.946742	19.075955	2	11555478	11624584
abhd3	0	0	0	0	0	0	2	11646751	11703651
trove2	3.1027517	3.4683029	3.1359842	3.3781053	2.66983	1.3049838	2	11714916	11737238
cdc73	19.802173	22.329338	24.077315	37.624642	25.252014	28.8578	2	11737859	11789602
CT573433.2	0	0	0	0	0	0	2	11768536	11769702
KCNT2 (2 of 2)	0	0	0.2501071	0	0	0	2	11810785	11853432
KCNT2 (1 of 2)	0	0	0	0	0	0	2	11862531	11868932
GPR158 (1 of 2)	0	0.1125859	0.1745114	0.554061	0.437893	0.6777849	2	11899842	12034000
5S_rRNA (2 120157	0	0	0	0	0	0	2	12015728	12015844
prtfdc1	54.300677	40.200357	40.057555	32.610208	35.867344	28.921837	2	12062931	12087538
arhgap21b	16.261982	17.814333	20.474759	17.295138	17.145078	17.691802	2	12099800	12198630
dpp6b	0.7194047	0.1116891	0.1731214	0.137412	0.2172026	0	2	12198703	12424750
kmt2cb	3.8892322	4.0002512	5.9665272	8.2335206	6.3849114	4.3923429	2	12639649	12829533
prkag2	0	0	0	0	0	0	2	12848791	12941196
5S_rRNA (2 129155	0	0	0	0	0	0	2	12915555	12915671
BCL2 (2 of 2)	0	0	0	0	0	0	2	12979720	13007658
kdsr	7.7288238	6.2265922	6.63534	6.4636526	8.5140693	5.5641925	2	13016280	13046785
vps4b	30.922845	23.895075	27.905402	32.015955	34.055992	32.760859	2	13047975	13060553
si:dkey-185p13.1	0	0	0	0	1.3569061	0	2	13090040	13125921

NMUR1 (2 of 2)	0	0	0	0	0	0	2	13168221	13174684
wdr65	1.4336524	0.8012792	0.8280044	0	0.3895634	0	2	13254294	13461565
5S_rRNA (2 13354(	0	0	0	0	0	0	2	13354085	13354199
LEPROT	4.320869	4.0249442	14.557161	8.2532007	5.2182252	16.153874	2	13523455	13524358
ebna1bp2	165.0095	172.00706	177.74405	183.60554	141.55107	160.34496	2	13526922	13550157
ZBTB41	2.9387805	2.1671964	1.944811	2.6663187	2.1072812	2.5750403	2	13575574	13634443
zgc:66475	14.634567	17.150293	12.269292	12.714187	13.041604	5.2947448	2	13740482	13773947
pde4bb	0	0	0	0	0.1942446	0	2	13915648	14057782
si:dkey-228i19.34	0	0	0	0	0	0	2	13960500	13962401
si:dkey-228i19.32	2.5044035	1.5552557	4.8213854	1.9134433	1.5122585	4.6814447	2	13984724	13986152
tctex1d1	3.4312783	4.7944188	2.477164	1.9662037	0.5179856	0.8017548	2	14241524	14305449
SGIP1	0.7268752	0.2256978	0.6996766	0.8330333	0.6583742	0.3396843	2	14312207	14432336
BX510915.1	0	0	0	0	0	0	2	14318806	14321829
BX510915.3	0	0	0	0	0	0	2	14478533	14480583
U2 (2 14480938..14	0	0	0	0	0	0	2	14480939	14481129
U2 (2 14485750..14	0	0	0	0	0	0	2	14485751	14485936
U2 (2 14491579..14	0	0	0	0	0	0	2	14491580	14491756
U2 (2 14496377..14	0	0	0	0	0	0	2	14496378	14496568
U2 (2 14501190..14	0	0	0	0	0	0	2	14501191	14501376
U2 (2 14529046..14	0	0	0	0	0	0	2	14529047	14529234
U2 (2 14533976..14	0	0	0	0	0	0	2	14533977	14534121
U2 (2 14545542..14	0	0	0	0	0	0	2	14545543	14545729
U2 (2 14588059..14	0	0	0	0	0	0	2	14588060	14588209
ZCCHC3	0	0	0	0	0	0	2	14588404	14588922
si:dkey-48k17.29	0	0	0	0	0	0	2	14599687	14600658
si:ch73-366i20.25	0	1.6219924	0	0	0	0	2	14609366	14609830
si:ch73-366i20.1 (2	0	0	0	0	0	0	2	14611738	14618878
si:dkey-10f21.16	0	0	0	0	0	0	2	14790590	14791602
hccsal	0	0	0	0	0	0	2	14802966	14807865
si:dkey-10f21.3	0	0	0.4871935	0	0	0	2	14813462	14815633
hccsa	8.1732534	7.9760361	11.801135	6.6906681	9.8706712	12.004255	2	14819195	14853746
si:dkey-10f21.4	0	0.1980383	0	0	0.1925632	0.2980555	2	14855673	14862429
cnn3b	47.234732	44.785461	41.712173	33.108276	33.997456	28.97186	2	14868993	14895878
f3b	2.4143215	2.5702526	0.995992	0.3952752	0	1.4506251	2	14921325	14927551
si:dkey-61d19.4	0	0	0	0	0	0	2	14922686	14928299
abcd3b	4.2973565	7.0963017	9.5892896	6.2681487	7.0770405	6.5724427	2	14930111	14946095
arhgap29b	3.8809961	4.0168856	6.1225209	5.1891062	4.3615137	4.8364594	2	14949001	15018503
5S_rRNA (2 149938	0	0	0	0	0	0	2	14993850	14993966
abca4b	0	0	0.1824749	0	0	0	2	15030259	15115218
tecrl2	0	0	0	0	0	0	2	15120671	15145420
olfm3b	0	0	0	0	0	0	2	15164217	15169961
col11a1b	3.0754591	2.6309655	4.4405705	2.0140696	2.046583	1.2319094	2	15210524	15383469
amy2a	2.3130302	0.8079814	0.4174651	0	0	0.4053481	2	15433338	15447555
vav3b (2 15610726..	0	0	0	0	0	0	2	15610727	15720770
si:dkey-94a14.1	0	0.770734	0	0	0	0	2	15654136	15664619
5S_rRNA (2 15689(	0	0	0	0	0	0	2	15689008	15689123
5S_rRNA (2 157063	0	0	0	0	0	0	2	15706358	15706472
vav3b (2 15813971..	0	0.1254166	0.388799	0	0	0	2	15813972	15979786
selj	9.3437556	7.211742	3.4691633	2.4476311	1.6926394	2.2456473	2	15981489	15992851
sh3glb1	4.6585066	7.7810969	8.3498761	8.468551	8.729974	7.6571031	2	15994629	16031206
arhgef4	1.6997326	0.9715842	1.8406477	0.6198099	0.279918	0.1083165	2	16019126	16179625
si:dkey-231j24.3	0	0	0	0	0	3.3266029	2	16186657	16197001
atr	3.0915196	2.8797897	3.5869499	1.5184405	2.2001366	1.4705319	2	16204868	16270087
GEN1	10.591181	11.36064	14.82891	11.402359	9.8837636	8.0991569	2	16270210	16279055
agfg1b	4.8827757	7.6347595	5.0357893	5.9955987	5.5282767	6.8454758	2	16280904	16299874
fbxo36b	1.9283217	0	2.0881878	0.552487	0	0	2	16302921	16305991
CR377211.1	0	0	0.7665399	0	0	0	2	16308194	16309072
si:dkeyp-13a3.6	0	0.574992	0.4456274	0	0	0	2	16324266	16327378
si:dkeyp-13a3.7	0	0	0	0	0	0	2	16329407	16333005
si:dkeyp-13a3.8	0	0	0	0	0	0	2	16333444	16339963
si:dkeyp-13a3.9	0	0	0	0	0	0	2	16347781	16349263
grk7a	0	0.1374309	0	0.1690823	0	0	2	16357036	16364710
atp1b3a	45.750377	43.856825	55.008054	82.747385	68.562456	75.102557	2	16368289	16386273
si:dkeyp-13a3.10	5.0084174	5.2739352	5.9738608	8.7346053	5.1281299	3.3581665	2	16406132	16416179
xrn1	5.6145303	8.3143687	10.497092	8.496863	8.7364826	6.6603895	2	16417594	16467843

gk5	9.0152512	7.8284768	7.5012485	8.5807344	8.4424528	8.3546313	2	16472899	16515517
ppp1r7	27.209541	26.870605	27.176042	26.259724	27.610153	22.945441	2	16517108	16528856
zgc:158450	71.311328	82.514769	93.3018	105.47705	92.030664	90.291064	2	16534447	16574921
SNORD66 (2 16543	0	0	0	0	0	0	2	16543809	16543884
SNORD66 (2 16548	0	0	0	0	0	0	2	16548754	16548814
tfa	983.20151	1083.5453	893.58213	2024.1956	2017.8582	1751.7505	2	16581396	16592930
ubxn7	16.144172	27.841549	18.900101	19.502093	25.688598	24.162842	2	16636583	16663153
clcn2	0	0	0.1600828	0	0	0	2	16726157	16825889
5S_rRNA (2 16768(	0	0	0	0	0	0	2	16768660	16768779
fam131a	0	0	0	0	0	0	2	16837577	16863572
thpo	0	0	0	0	0	0	2	16876364	16893854
pif1	5.6786796	6.6899931	6.5111999	2.105541	3.0255994	2.8098722	2	16918145	16936147
si:ch211-234e14.2	0	0	2.6527111	0	0	0	2	17003072	17007080
artnb	0	0	0	0	0	0	2	17021615	17022236
st3gal3b	1.5121641	2.8172001	2.9111627	2.4262164	1.3696573	1.5546664	2	17085994	17214190
kdm4ab	4.9298655	6.0483057	6.4236482	6.201065	5.3365462	4.7200446	2	17271981	17313945
si:dkey-183g16.1	0	0	0	0	0	0	2	17328080	17330598
si:dkey-183g16.2	0	0	0.2502929	0	0	0	2	17341146	17347082
ptprfb	17.303643	22.092576	25.508398	29.260823	24.879426	23.326043	2	17349918	17599781
si:dkey-21k10.2	0.7253687	2.2523004	2.0946796	0.8313068	1.0950162	0.6779605	2	17382949	17385372
5S_rRNA (2 17429(	0	0	0	0	0	0	2	17429460	17429578
si:dkey-21k10.3	0	0	0	0	0	0	2	17478994	17486322
dpydb	1.3871993	3.1012649	2.4035266	5.8822455	5.5284645	5.2509695	2	17988789	18244676
ptbp2b	18.181319	20.410206	23.110299	19.590015	13.79363	14.596582	2	18274456	18292829
5S_rRNA (2 18375(	0	0	0	0	0	0	2	18375814	18375928
rwdd3	3.2227476	2.1014211	2.3266181	1.8467107	1.4595174	1.8072704	2	18420634	18429023
si:dkey-1p9.2 (2 184	0	0	0	0	0	0	2	18434321	18436482
BX088713.1	0	0	0	0	0	0	2	18434884	18434981
si:dkey-236a14.10 (2	0	0	0	0	0	0	2	18439678	18441841
si:dkey-1p9.4	0	0.5645376	0	0	0	0	2	18448331	18468279
si:dkey-1p9.5	0	0	0	0	0	0	2	18453186	18455022
si:dkey-236a14.4	0	0	0	0	0	0	2	18489887	18491896
BX664750.2	0	0	0	0	0	0	2	18490296	18490393
si:dkey-236a14.5	0	0	0	0	0	0	2	18493335	18495479
si:dkey-236a14.6	3.7407122	0.2903767	2.7005556	1.4290111	0.5646977	0.4370287	2	18506556	18510928
si:dkey-236a14.7	0	0.4724934	0	0	0	0	2	18510804	18530295
si:dkey-236a14.10 (2	0	0	0	0	0	0	2	18545728	18547893
BX664750.3	0	0	0	0	0	0	2	18546292	18546389
si:dkey-1p9.2 (2 185	0	0	0	0	0	0	2	18549285	18551455
BX664750.1	0	0	0	0	0	0	2	18550793	18550890
si:dkey-236a14.12	0	0	0	0	0	0	2	18556679	18563664
si:dkey-236a14.13	2.4641787	1.1477068	2.2237248	1.0590246	0.8369827	2.1591812	2	18561839	18564712
mir137-1	0	0	0	0	0	0	2	18658781	18658865
lppr5a	0	0.3008263	0	0	0	0	2	18777292	18837198
lppr4a	0	0.3846849	0	0.3549607	0.2805373	0.4342247	2	18845341	18884569
palmda	0.3761821	1.2264642	2.1726356	2.1556123	1.3629222	0.7910906	2	18919836	18933712
frrs1a (2 18957773..	0	0	0	0	0	0	2	18957774	18983437
si:ch211-153l6.3	0	0.3219955	0.4991027	0	0.3130935	0.4846162	2	18966911	18976220
si:ch211-153l6.4	0	2.420345	3.0012856	4.1688773	3.2948037	2.18563	2	18971244	18972306
si:ch211-153l6.1	0	0	6.5735474	0	2.0618353	3.1913751	2	18985447	18986613
zfyve9a	5.2580715	5.1805348	5.839988	7.996037	6.5027114	4.961672	2	19131620	19171555
cc2d1b	1.8937593	2.6460911	2.2786223	1.6277533	1.7152908	1.3274912	2	19180207	19205166
cdc20	53.380286	51.697603	60.558395	43.211856	39.332106	40.091378	2	19218016	19234798
elovl1a	8.4529733	7.4108721	6.1025074	7.9779474	9.0074852	8.3652454	2	19237376	19288419
si:dkey-225f23.4	0	0.5269018	0	0	0	0	2	19270815	19299800
KNCN	0	0	0	1.4338	0	0	2	19323999	19332537
glula	193.86722	185.18443	163.49283	124.85393	122.95683	145.21783	2	19460034	19463977
PBX1A	0	0	0	0	0	0	2	19615653	19618709
pbx1a	1.7445004	0	0.629709	0.49982	0.7900491	0	2	19717559	19749261
5S_rRNA (2 19881(	0	0	0	0	0	0	2	19881796	19881912
5S_rRNA (2 19950(	0	0	0	0	0	0	2	19950258	19950374
frrs1a (2 20213892..	0	0	0	0	0	0	2	20213893	20239553
agla	3.7372711	4.1399426	6.2711927	3.0097386	3.7510229	3.3986073	2	20242651	20295817
5S_rRNA (2 20255(	0	0	0	0	0	0	2	20255652	20255766
si:ch211-267e7.2	0	0	0	0	0	0	2	20308866	20325163

si:ch211-267e7.3	22.338279	22.016619	16.647032	23.453567	23.496517	17.174092	2	20325257	20368685
olfml2bb	1.7492231	0.1810471	1.9643983	1.113718	1.2322923	2.4523478	2	20374342	20384758
si:ch211-267e7.11	0	0	0	0	0	0	2	20401639	20402945
dusp12	5.5283034	3.9379941	5.1649301	1.4907523	2.3563832	1.8236429	2	20430282	20436382
si:ch211-267e7.22	0	0.9460152	0	0.5819449	0.4599306	0	2	20468899	20473941
rxrga (2 20495130..2	7.374911	4.5009185	5.8749961	0.8743445	2.9944366	2.4957075	2	20495131	20546256
rxrga (2 20495130..2	0	0	0	0	0	0	2	20495131	20495229
5S_rRNA (2 20527	0	0	0	0	0	0	2	20527154	20527271
prg4a	1.4006619	0	1.6853142	0.5350749	0.4228877	0.6545592	2	20566497	20584574
tpra	14.810575	17.695175	16.270876	25.091438	26.319297	19.522573	2	20584192	20662758
C2H1orf27	3.6479255	7.0575689	8.1032906	4.1806953	8.387442	9.4417111	2	20662898	20675820
pdca	0	0	0	0	0	0	2	20678954	20686429
ptgs2a	12.978995	10.258265	12.493341	18.029748	17.277537	13.509213	2	20712497	20719864
cpla2	5.4031708	5.033122	4.1607942	4.128193	3.099517	4.7975323	2	20721899	20753362
arpc5a	36.157857	28.36337	33.16932	36.45352	38.41392	42.878584	2	20763673	20771677
lyrm4	26.414369	22.261955	20.885631	7.207647	15.380402	18.515997	2	20775956	20777907
nrn1b	0	0.5734749	0	0	0	0	2	20788259	20790126
si:ch211-279l9.7	3.8205578	4.575726	8.6686254	4.3785402	2.9661491	3.060734	2	20796355	20829158
rreb1b	10.350152	11.24818	13.449869	14.155039	11.812185	9.9639044	2	20840352	20858154
riok1	19.334507	20.678537	21.712881	9.3009984	10.810134	13.051173	2	20859660	20872570
nebl	0	0	0	0	0	0	2	20873367	20878695
pip4k2ab	0	0	0	0	0.2732232	0.4229036	2	20886317	20951844
bmi1b	11.347206	10.570066	8.1919588	7.663328	4.955388	4.5452498	2	20960930	20966517
dnajc1	36.260961	40.686588	39.564629	39.903952	51.318308	50.258874	2	20970998	20978561
si:dkey-29d8.3	2.9083243	0.4925711	1.1452498	0	0.4789532	0.7413393	2	20981903	21039018
si:dkey-29d8.2	0	0	0	0	0	0	2	21002878	21004102
vipr1a	0.705448	0	0	0	0.3194832	0	2	21026266	21094983
zbtb47a	0	0.2137138	0	0	0	0	2	21105860	21116657
klhl40a	8.5951518	12.49794	12.712993	2.402549	3.0381042	1.7634283	2	21123259	21131131
hhatla	2.4918409	3.5872803	3.2708185	2.076922	1.6414611	1.2703532	2	21133813	21148101
ctdsplb	31.830226	39.180699	33.648396	33.221897	34.236261	40.640471	2	21152242	21177506
dre-mir-26a-2	0	0	0	0	0	0	2	21171567	21171694
plcd1b	11.772163	9.3641558	8.2122762	6.5183442	6.2299219	5.1923167	2	21184002	21235078
si:ch211-12e1.5	0.5379295	0.7516322	0	0	0	0	2	21228248	21231672
afg3l2	10.167514	9.7977604	12.149457	15.067827	13.02008	15.729091	2	21249272	21265553
inhbab	0	0	0	0	0	0	2	21283052	21300265
si:ch211-12e1.3	0	1.0325272	0	0	0	0	2	21337905	21339602
mplkip	19.060509	20.510208	18.505462	21.467621	14.585307	20.271974	2	21402070	21404307
ralab	7.4626509	5.7683106	8.25328	5.0951369	5.8964702	4.8972786	2	21404875	21415152
C2H7orf25	1.0492498	0.4886947	1.8937285	1.2024899	0.9503682	0.3677526	2	21416700	21422016
FBXL7	0	0.9166891	0.5683582	0	0.1782692	0.2759308	2	21430651	21531256
5S_rRNA (2 214518	0	0	0	0	0	0	2	21451846	21451960
chd7	33.377344	43.082707	47.950452	50.313896	48.955852	44.324814	2	21562193	21617220
rab2a	97.407452	76.117653	81.781842	102.74421	108.9776	108.23782	2	21618206	21644458
ca8	10.732609	10.597415	9.6078413	6.8880439	7.9713551	5.7177581	2	21651559	21675050
CR847864.1	0	0	0	0	0	0	2	21685669	21685775
tox	17.8247	17.202273	18.317034	17.299345	17.599389	16.884856	2	21779436	21901069
cyp7a1a	0	0	0	0	0	0	2	21946657	21949389
fam110b	1.9607305	1.4943643	2.0589415	1.0214045	1.9374007	2.2490783	2	22001581	22023508
sept2	92.078821	87.465468	81.34445	97.889889	101.32524	103.04648	2	22049350	22073010
stk25b	29.590317	23.948836	20.661917	16.400019	22.407992	19.38213	2	22075319	22094365
bokb	1.2369883	0.8642027	0.8930267	0.7088236	0.2801035	1.3006598	2	22097859	22108079
thap4	5.3168274	7.2385499	4.1336725	2.8123089	4.0748805	5.160462	2	22110767	22117094
FBXO15 (1 of 2)	1.2216069	1.8207077	3.1749202	0	0.4425929	1.0275894	2	22117431	22134663
5S_rRNA (2 221303	0	0	0	0	0	0	2	22130366	22130480
agxtb	0	0	0	0	0	0	2	22134387	22146295
kif1ab	0.0830641	0.7737522	0.7196034	0.4759767	0.5266525	0.2329056	2	22152026	22216234
5S_rRNA (2 221593	0	0	0	0	0	0	2	22159306	22159420
espnl	0	0.3668304	0	0.9026285	0	0	2	22223136	22246097
rab6bb	4.4714219	1.1359598	4.695391	3.2610208	6.9955127	5.1289957	2	22253138	22259454
aire	0	0	0.2914311	0.6939542	0	0	2	22266590	22304197
amotl2b	11.724971	8.8831933	10.834792	15.229022	10.195206	11.397005	2	22309476	22318822
myo7bb	0	0.0678044	0	0.5005217	0.1318597	0.5102417	2	22338706	22385207
5S_rRNA (2 223549	0	0	0	0	0	0	2	22354929	22355045
sap130b	7.3434246	11.228734	10.202856	12.862055	13.05176	10.295217	2	22391020	22423741

MLLT1 (2 of 2)	7.2162966	8.5673463	7.9677853	9.8918289	6.7925533	6.3479141	2	22427784	22451277
zgc:136639os	0	0	0	0	0	0	2	22443926	22449165
ZNF414	7.3577927	4.7449918	7.7634831	7.7837342	6.9207147	5.1576802	2	22451602	22461949
mknk2a	1.0478754	1.4099355	1.0086656	0.26687	0.738207	0.326463	2	22464436	22482596
csnk1g2a	21.145705	19.697492	24.258063	20.582284	19.808849	25.178385	2	22496685	22536392
mfsd12a	2.1144998	1.2121128	2.1136624	0.932045	1.031277	0	2	22538891	22557288
si:dkey-218h11.6	0	0	0	0	0	0	2	22588033	22589778
prrx1a	14.430072	20.048778	27.544817	5.886245	5.7597392	6.5148879	2	22622894	22630352
kifap3b	5.2415695	3.733744	7.3455647	1.0600741	2.9323426	2.5935853	2	22680583	22750209
fam129ab	0	1.2127771	0.5370973	0.2131556	0	0	2	22753914	22806760
rnf2	60.183532	60.589784	59.825477	64.728674	52.624869	63.281359	2	22809088	22819674
ivns1abpb	58.669598	59.390897	80.579149	24.599318	23.90605	24.073951	2	22837433	22849650
si:ch73-129a22.11 (2	0	0	0.3043309	0.9662284	0.7636427	0.5909954	2	22861058	22870500
FP016152.1	0	0	1.6158	1.9237676	1.5204181	3.1378029	2	22890713	22896737
si:ch73-129a22.11 (2	1.6548009	0	0	0.6321601	0.4996173	0	2	22929932	22931788
CLDN18	0	0	0	0	0	1.6127327	2	22977987	22981393
hfm1	0.1207696	0.1124984	0.5231278	0.2768154	0.1093883	0	2	22984098	23009022
znf644a	6.1360062	4.828838	6.8738353	4.8497611	5.2702773	3.1146837	2	23014596	23039201
lrrc8da	1.8031447	2.5194782	3.3845641	1.8598403	1.4698942	2.527944	2	23046115	23050291
gtf2b	34.22525	41.029788	40.822652	50.138194	50.678019	50.068768	2	23053276	23065450
pkn2	4.4607676	4.6914243	6.4407792	6.4315414	4.9527281	5.6486257	2	23068424	23128679
5S_rRNA (2 23111(	0	0	0	0	0	0	2	23111019	23111135
zgc:56628	0.3277064	0	0.4731662	0	0	0	2	23132627	23136270
hs2st1a	9.4178375	11.185364	15.297925	13.49161	15.567793	11.222949	2	23149705	23181558
sep15	159.41591	139.94806	129.7357	119.03063	133.45368	135.45174	2	23182115	23192145
si:dkey-43b14.6	0	0.3104957	0	0.7640106	0	0	2	23194397	23196918
si:dkey-43b14.7	0.9150075	0.2841137	0	0	0	0	2	23195649	23238279
si:dkey-43b14.8	0.7291466	2.037628	1.0527947	0	1.3208633	0	2	23230502	23231814
si:dkey-43b14.9	0	0	0	0	0.3001962	0.4646533	2	23235660	23238142
si:dkey-43b14.3	0	0	0	0	0	0	2	23258737	23258827
crsp7	4.2848016	3.991347	5.9054928	5.8034193	7.585592	7.0993445	2	23298624	23304670
cnn2	71.558665	63.8213	67.598694	44.49458	36.716982	37.087371	2	23309714	23315897
angptl4	6.475501	13.815251	15.985137	14.842462	12.676503	8.1998627	2	23321879	23327384
rps28	1140.0902	1050.5332	907.13715	970.78805	1036.8984	1011.1604	2	23354448	23356528
5S_rRNA (2 23358(	0	0	0	0	0	0	2	23358056	23358171
si:rp71-39b20.4	0	0	0	0	0	0.8076937	2	23359248	23366668
si:rp71-39b20.6	0	0	0	0	0	0	2	23366305	23379871
insl3	0	0	0	0	0	0	2	23375494	23376826
kcnn1a	0.5236577	0.3484241	0.6480814	0.6001366	0.4065498	0.2097569	2	23401945	23453652
OCEL1	0	0	0	0	0.253555	0	2	23456213	23461254
zgc:154006	0.679593	0.422033	0.3270819	0	0	0	2	23461785	23477693
nr2f6a	24.639804	26.451114	25.380962	31.509902	28.577595	24.64428	2	23477764	23489841
si:dkey-208k22.3	0	0	0	0	0	0	2	23495059	23498314
si:dkey-208k22.2	1.3725113	1.9177675	0.4954328	1.572963	0.6215827	0	2	23508686	23511649
si:dkey-208k22.1	0	0	1.2641437	0	0	0	2	23513106	23515557
ano8a	0.1779763	0.0828936	0.1284875	0.815877	1.0478244	0.2495164	2	23515198	23544177
mrpl34	71.21825	62.165413	61.841858	53.081205	74.430715	53.0647	2	23543963	23546681
C2H6orf52	28.696626	27.974585	38.543503	39.771162	35.210427	35.085729	2	23546710	23553511
fitm1	13.342043	8.2855215	8.2560892	0	2.8773059	0.8907174	2	23555464	23559292
vmhcl	0	0.0642373	0.0995698	0.1580634	0	0.0966798	2	23574503	23589822
vmhc	2.259259	4.4267666	3.8245097	0.0892834	0.0705636	0.1092207	2	23594235	23607626
mir736	0	0	0	0	0	0	2	23602850	23602929
MAP4 (1 of 3)	0.2083586	0.2587849	0.2005622	0	0	0.1947409	2	23611810	23687140
kcnh2	0	0.3466459	0	0.1421604	0.1123541	0	2	23695890	23783096
si:dkeyp-99c4.5	0	0	0	0	0	0	2	23758671	23788133
si:dkeyp-99c4.4	2.5710956	2.3950081	9.2808349	13.259688	17.46596	28.836668	2	23795298	23796544
slc12a7a	2.4033675	5.3481661	5.0124475	14.99603	11.247179	8.9851591	2	23802571	23832951
si:dkeyp-99c4.2	0	0	0	0	0	0	2	23849203	23850896
col15a1b	19.686526	18.940914	21.618886	16.418132	19.756703	15.67876	2	23850967	23927192
tgfbr1a	2.4661683	4.594534	2.7695363	4.7105761	7.942243	11.909095	2	23932610	24008101
VOPP1 (2 of 2)	0	0	0	0	0	0	2	24026726	24040524
gorasp1	9.5125592	4.8485097	9.9772545	17.586936	14.305965	10.694175	2	24043868	24055506
csrnp1a	2.6836324	5.2774348	4.7358944	6.8345994	4.3212907	2.9262769	2	24060404	24073222
si:dkey-24c2.7	2.9818137	0	0	0	0	0	2	24080107	24091068
xirp1	6.7123071	7.0825901	11.235528	7.0799351	5.8645253	6.2458493	2	24106798	24114653

si:dkey-24c2.6	0	0	0	1.0351111	0	0	2	24123890	24132952
oxsr1a	5.0149452	8.3594994	10.67086	15.72963	11.475373	11.841301	2	24142810	24162533
5S_rRNA (2 24184	0	0	0	0	0	0	2	24184157	24184273
cdyl	3.7417834	4.7303467	3.087233	5.207174	7.7466436	7.4940653	2	24187298	24239708
rpp40	9.3783518	6.6273509	9.3387195	4.4474628	9.9591076	4.9872148	2	24243923	24251106
si:dkey-58b18.8	0	0	0	0	1.0755121	0.8323561	2	24255064	24259492
si:dkey-58b18.9	0	0	0	0	0	0	2	24261085	24261683
si:dkey-58b18.10 (2	0	0	0	0	0	0	2	24263325	24264250
si:dkey-58b18.5	0	0	0	0	0.5418926	0.8387588	2	24286474	24290464
si:dkey-58b18.6	0.7302877	0	0	0	0	0	2	24292042	24292916
si:dkey-58b18.10 (2	0	0	0	0	0	0	2	24294313	24295239
si:dkey-58b18.2	0	0	0	0	0.5418926	0.8387588	2	24317519	24321510
si:dkey-58b18.3	0	0	0	0	0.6165955	1.4315796	2	24317628	24325424
si:dkey-58b18.10 (2	0	0	0	0	0	0	2	24325352	24326278
CRTC1 (1 of 2)	0	0.9790405	1.8969274	0.9033909	0.2379934	0	2	24347533	24372807
MAST3 (2 of 2)	2.2822196	5.3707363	4.3358341	6.4699995	5.4398487	5.5571822	2	24410684	24452847
pik3r2	4.9064073	4.7396539	8.9208773	11.454208	9.7110196	8.1524224	2	24470404	24517964
ifi30	90.653248	84.800955	88.36572	198.14176	226.23573	205.92217	2	24532156	24537113
mpv17l2	23.885034	20.858636	19.829991	31.137219	31.910299	36.834553	2	24540024	24548501
pde4ca	0.3104816	0.1446088	0	0.3558266	0.5624434	0	2	24550615	24632413
U3 (2 24598592..24	0	0	0	0	0	0	2	24598593	24598798
rab3aa	0.9689656	1.0831245	2.5183129	1.1104805	1.93083	1.3584549	2	24637599	24648248
si:dkey-149i17.7	0	0	0	0	0	0	2	24655576	24656341
si:dkey-149i17.9	0	0	0	0	0	0	2	24666576	24668529
si:dkey-149i17.8	0	0	0	0	0	0	2	24666576	24671484
agtr1a	0	0	0	0	0	0	2	24701266	24702342
gyg1a	3.5568129	4.6385027	5.9059215	4.076276	5.3156692	3.7398927	2	24706355	24714408
hltf	6.0416766	6.7290088	8.9130495	6.3219564	5.1154175	6.8129975	2	24713629	24731591
nck1a	1.0789684	1.256341	1.5578927	1.8548234	0.9772861	1.8908436	2	24733456	24750945
slc35g2a	0.193552	0.1802961	0	0	0	0	2	24759987	24766030
stag1a	2.6248566	3.2955522	6.9207928	1.5695008	1.6539056	0.6399921	2	24788976	24875072
pccb	16.907748	22.469688	21.808617	28.161356	27.565842	26.864595	2	24878158	24889628
msl2a	4.2516373	5.4626952	5.5037713	7.0568366	5.3116713	7.1938789	2	24894944	24898998
nceh1a	2.9913708	2.0898749	2.1595789	1.1427509	2.0320973	2.7958628	2	24901206	24909611
5S_rRNA (2 249254	0	0	0	0	0	0	2	24925431	24925547
si:dkey-223d7.6	0	0	0	0	0	0	2	24927931	24928898
si:dkeyp-7b3.1	8.9914036	6.7004851	6.4912198	4.1218297	2.8504178	4.4119685	2	24990341	24995543
si:dkey-5n7.1	0	0	0	0	0	0	2	25219747	25346191
si:dkey-5n7.2	0	0	0	1.4092422	1.1137714	0	2	25230338	25231382
ppp2r3a	0	0.7028197	0.9078262	0	0.569491	0.5288859	2	25393831	25437998
fndc3ba	0.9973604	1.7548795	3.0401291	3.6830717	2.1078606	4.3501527	2	25463828	25688438
ghsra	0	0	0	0	0	0	2	25699627	25701802
pld1a	2.08607	1.7488805	2.7108169	2.7493452	0.6613173	0.4386892	2	25708726	25780260
tnika	1.582548	2.3955157	3.4274961	4.0807687	3.4043445	2.634677	2	25806282	25963360
si:dkey-153n9.5	2.2195189	2.06751	0	1.2718369	3.5181138	2.3337642	2	25962722	25965002
slc2a2	10.886628	17.815327	15.718902	42.319249	37.443892	30.31907	2	25965013	25986156
eif5a2	308.34261	296.48041	313.94054	214.45435	244.18627	267.21821	2	25987363	25993197
si:dkey-153n9.4	0	0	0	0	5.196839	0	2	26000849	26001969
5S_rRNA (2 260037	0	0	0	0	0	0	2	26003798	26003915
slc7a14a	0.0787203	0.2933158	0.2273241	0.541303	0.7130166	0.772541	2	26016574	26139598
cldn11a	0	0	0.5119974	0	0	0	2	26145596	26149343
si:ch211-253d24.1	0	0	0	0	0	0	2	26182345	26187776
si:ch211-253d24.2	0	0.4242987	0	0	0	0	2	26202283	26206082
grin3b	0	0.1294888	0.2007115	0.3186222	0	0.1948859	2	26208810	26304333
5S_rRNA (2 262333	0	0	0	0	0	0	2	26233332	26233449
lppr3a	12.706833	18.183726	18.347046	17.728422	17.681011	12.392712	2	26327266	26356309
palm1b	17.265378	15.627741	12.464501	15.120209	18.736434	21.236847	2	26385492	26432415
si:dkey-57i11.4	0	0	0	0	0	0	2	26434635	26435675
ptbp1a	47.807894	39.057362	46.766407	36.611489	35.867701	39.033089	2	26436471	26448682
efna2	4.9232509	4.5860705	3.554273	2.6196293	4.6185422	3.4511102	2	26451797	26592673
si:dkey-15h14.4	0	0	0	0	0	0	2	26583106	26584283
rabggtb	14.324962	20.355077	12.970957	16.417085	21.331735	27.912079	2	26611284	26617263
acadm	12.981258	16.470419	14.86536	13.08162	12.974235	18.199257	2	26618240	26624320
hectd3	10.370086	16.137658	14.796926	16.638453	15.581007	17.959307	2	26627846	26643214
rps8a	1660.9713	1758.8465	1616.1476	1366.5564	1413.5321	1558.5326	2	26646616	26650038

SNORD46	0	0	0	0	0	0	2	26647819	26647924
SNORD38	0	0	0	0	0	0	2	26649203	26649273
SNORA47	0	0	0	0	0	0	2	26649938	26650070
best4	0	0	0	0	0	0	2	26653135	26657227
si:ch211-106k21.5	7.6230813	7.1009967	7.1293764	9.2327991	12.004727	9.958607	2	26662307	26675900
glis1a	0	0	0	0	0	0.3839389	2	26677617	26712148
ndc1	29.540473	23.263439	29.259322	24.3689	25.463982	26.20929	2	26725023	26738798
zgc:113691	1.4027671	3.0489557	3.3756945	0.5358792	2.1176164	0.655543	2	26740138	26744964
yipf1	4.7723604	4.4455141	3.2955423	8.0851275	4.6984909	4.0725863	2	26746971	26752488
lrrc42	3.0361343	5.0907557	3.5070325	2.783643	1.9250057	5.1078613	2	26752943	26759203
tmem59	16.101607	14.453438	14.371903	16.104614	17.766191	20.932137	2	26760744	26769072
u2surp	21.611756	20.87724	29.55358	30.272117	22.785781	20.359581	2	26771547	26791114
mir124-1	0	0	0	0	0	0	2	26793487	26793568
ttpa	0	0	0	0	0.2198004	0	2	26795642	26801318
asph	90.00596	80.909522	86.63808	98.52902	95.779292	74.056183	2	26804453	26830352
si:dkey-181m9.5	0	0	0	0	0	0	2	26815850	26821017
impa1	17.046716	14.555962	18.972739	14.652258	8.3634568	14.936801	2	26831083	26837078
si:dkey-181m9.8	0.9865832	1.9215763	1.0360002	1.850189	1.8684516	1.1316716	2	26838033	26869024
si:dkey-148a12.2	0	3.4961981	14.45123	2.8676	6.7990816	7.0158917	2	27148712	27158515
cdh7	5.3208954	8.4365642	8.8269251	4.670807	3.7940371	5.0789473	2	27158567	27244127
5S_rRNA (2 271878	0	0	0	0	0	0	2	27187858	27187974
5S_rRNA (2 273818	0	0	0	0	0	0	2	27381836	27381951
dsel	0.3914881	0.1215587	0	0	0.2363961	0	2	27460033	27463608
tmx3	0	0	0	0	0	0	2	27466576	27478351
si:dkey-40i22.5	0	0	0	0	0	0	2	27469184	27472351
tesk2	3.0753692	3.8611785	2.702877	2.9115589	2.5433241	3.1868029	2	27478631	27527497
toe1	10.218697	5.892619	11.944115	12.268783	15.205767	11.256336	2	27526657	27534104
si:ch73-382f3.1	5.1191819	3.5136926	5.0573048	8.0282867	8.0533002	4.5327845	2	27534787	27539728
sepp1b	49.029297	49.477362	42.559506	120.07246	114.72263	69.964762	2	27542968	27549275
zgc:153394	0	0.9805127	0.506608	2.412665	1.5890084	0	2	27551470	27557876
si:ch73-176g19.2	0	0	0	0	0	0	2	27632729	27633479
zswim5	17.083667	18.07735	18.608163	26.362536	22.735475	20.168999	2	27639236	27692112
urod	39.369404	50.131116	36.505575	26.905945	31.733433	36.458744	2	27704338	27723973
lyn	0	0	0.2041784	0	0	0	2	27725640	27757359
tgs1	6.2386878	2.8226881	3.8605153	3.8813372	2.5832009	1.9991807	2	27761944	27799950
tmem68 (2 2780337	1.8741118	1.7457589	1.3529892	4.2956418	0.8487475	3.941156	2	27803371	27804687
tmem68 (2 2782390	0.9314448	0	0	0	4.2183258	3.9175563	2	27823907	27827694
CABZ01085085.1	1.7283476	4.0249442	3.7432701	3.4663443	0.3913669	0	2	27829274	27849933
dhcr7	2.0966476	2.5110691	2.8110565	1.029796	3.9337648	3.9892189	2	27967560	27989080
nadsyn1	0.7777564	2.4149665	2.245962	1.4855761	0.9392805	2.5442352	2	27990088	28011192
CU693487.1	2.1874399	4.075256	4.2111788	4.7352739	2.2014388	0.6814916	2	28011847	28021904
buc	0	0	0	0	0	0	2	28022981	28027100
rnf152	2.3568376	2.9272321	4.5372971	0.9003492	7.1157617	5.5070025	2	28037861	28038454
zgc:163121	1.8079572	0	0.8701532	0.6906682	0	0	2	28045787	28068414
mc4r	0	0	0	0	0	0	2	28100596	28101736
C2H5orf22	2.0220918	3.7672082	0.3244047	0	1.4245227	0.6299778	2	28125521	28143409
5S_rRNA (2 28173	0	0	0	0	0	0	2	28173131	28173245
cdh6	23.517786	30.629393	27.511201	29.697658	29.7826	28.086484	2	28216925	28270171
cdh10	0	0	0.2444806	0	0	0	2	28604768	28649116
CDH12 (2 of 2)	0	0	0	0	0	0	2	28710608	28831724
cdh18	1.9884052	1.1576404	0.7177509	0.712127	0.5628179	0.8711477	2	28964393	29067510
cahz	23.101676	26.729488	30.195842	33.442881	40.087064	45.001882	2	29192215	29200240
5S_rRNA (2 292156	0	0	0	0	0	0	2	29215697	29215811
dlgap1a	0	0	0	0	0.2812217	0	2	29324946	29407657
5S_rRNA (2 293927	0	0	0	0	0	0	2	29392742	29392860
ptf1a	0	1.6341879	0.8443466	0	0	0	2	29425689	29426593
si:ch211-142h2.1	0	0	0	0	0	0	2	29427529	29441760
C2H10orf67	0	0	0	0	0	0	2	29441590	29476797
si:dkey-188g12.2	0	0	0	1.2389361	0	0	2	29479227	29482122
si:ch211-207d6.4	0	0.8049888	0	0.9903841	0	1.2115406	2	29557420	29614710
si:ch211-207d6.2	0.1642569	0.5355258	1.422996	1.6000926	2.1572705	0.921129	2	29557670	29608149
paxip1	16.147192	17.586767	23.493827	16.085504	13.725446	9.5775231	2	29617508	29638235
htr5a	0	0.9525799	0.4921758	0.781311	0.9262445	0.4778904	2	29640509	29653812
eng2b	19.177555	10.718481	11.445176	7.9122191	4.8636718	5.0187653	2	29691251	29694788
cnpy1	20.209419	22.248117	27.057653	14.738787	18.304877	20.090586	2	29701087	29710868

RBM33	0	0	1.3784546	0	0	0.535378	2	29710422	29762469
shhb	3.6980989	3.4448259	5.3395829	3.7084218	2.5121916	1.620188	2	29765373	29770264
dnajb6a	24.229499	23.742557	29.532205	23.801274	19.09596	24.704644	2	29818117	29833015
5S_rRNA (2 298284	0	0	0	0	0	0	2	29828467	29828581
trpa1a	0	0.4096056	0.1587252	0	0.1991408	0	2	29831318	29850278
kcnb2	0.1965272	0.3661352	0	0.450459	0.1780064	0.4132861	2	29859811	29892301
rpl7	2475.6458	2763.3818	2308.6501	2093.4184	2163.4189	2201.972	2	29892308	29897185
SNORD12 (2 29895	0	0	0	0	0	0	2	29895962	29896051
rdh10b	23.55269	16.876638	16.816687	21.356702	36.102131	44.994318	2	29897263	29901139
ube2w	1.3964704	1.7344398	2.3523792	3.734316	1.8972998	2.9367018	2	29908579	29915038
tceb1b	31.935808	24.284579	38.112345	26.14282	22.727703	26.498219	2	29960685	29964617
tmem70	10.467002	11.781425	15.113016	9.4965801	20.541275	12.228634	2	29964809	29967179
si:dkey-82k12.7	16.824332	14.022386	21.735117	11.162963	7.2183798	7.4485605	2	29984138	29984995
si:dkey-82k12.8	0.906124	1.6881319	2.6166548	0	0	0	2	29991049	29991894
jph1b	1.2403676	2.1824564	2.785895	1.5794666	1.1234749	2.3186009	2	30005551	30039129
CR788254.1	0	0	0	0	0	0	2	30061436	30062203
5S_rRNA (2 300758	0	0	0	0	0	0	2	30075845	30075960
pi15b	0	0	0	0	0	0	2	30083902	30087881
crispld1b	0	0	0	0	0	0	2	30094482	30111291
socs6b	9.3117059	9.9537382	10.579605	11.721327	10.093348	11.984621	2	30138260	30145177
cbln2a	0	0	0	0	0	0	2	30173538	30175125
neto1	0.2559813	0	0	0	0	0	2	30178657	30191780
fam173b	10.251231	11.209873	7.7225056	10.215996	8.477747	9.3729498	2	30195739	30198041
march6	4.3163274	8.5897063	8.215207	14.502871	10.840131	9.6271249	2	30204678	30241553
ankrd33bb	0	0	0	0.3906555	0.9262445	0	2	30246558	30264097
ctnnd2b	7.2879078	6.4351962	9.426683	7.4822575	5.6384337	5.8537098	2	30269088	30408574
GPR141 (1 of 2)	0	0	0	0	0	0	2	30428700	30436334
si:dkey-94e7.2	0	0	0	0	0	0	2	30435902	30441252
rp1	0	0	0	0	0	0	2	30441997	30448963
tcea1	55.248659	46.639998	63.390261	75.189625	63.222715	81.260305	2	30454512	30462842
5S_rRNA (2 304668	0	0	0	0	0	0	2	30466809	30466941
rgs20	0.4210157	0.0784363	0	0.1930016	0.1525356	0	2	30467360	30499334
atp6v1h	24.512945	24.948389	23.267992	29.653718	28.987038	32.45703	2	30501605	30561705
oprk1	0	0	0	0	0	0	2	30593696	30601399
chmp5a	0.8991404	2.0939016	3.2456099	0.5152287	0.4072025	1.2605624	2	30609427	30615952
bag1	32.716102	24.112454	22.840292	30.077766	28.656016	21.169291	2	30618901	30623132
myl12.2	106.7374	115.27796	92.320208	80.959795	72.859109	79.519899	2	30624964	30627754
myom1a	0.7817957	1.4565052	1.3545759	0.8063774	0.5664952	1.2056544	2	30631020	30674745
lipin2	4.1707839	3.6202423	3.2847708	13.470672	11.590756	9.8340769	2	30675183	30699340
emilin2a	4.8490926	3.4541697	3.2948098	3.9227927	2.8419552	3.199178	2	30701828	30732894
si:ch211-209l5.1	0	0	0	0	3.0083718	0	2	30816810	30817295
si:ch211-209l5.2	0	0	0	0	0	0	2	30823651	30824136
yes1	24.003228	23.445593	30.869116	26.506489	27.022409	25.340927	2	30986804	31079129
adcyap1b	0.142056	0.3969808	1.2306641	0.1628029	0.6433428	0	2	31012872	31018341
clul1	0.6714444	0.4169726	1.29264	0	0	0	2	31079008	31092329
colec12	10.264484	9.8270938	11.664365	6.971013	7.4032906	5.0633019	2	31098312	31150880
stam	15.818775	18.711605	17.402127	19.136235	18.421725	18.129106	2	31153269	31168328
si:dkey-32m20.1	0	0	0	0	0.7692015	0	2	31170284	31173582
cacnb2b	0.1353797	0.7566475	0	0	0.245243	0.1897975	2	31191494	31229079
mrc1b	0	0.0712613	0	0	0	0	2	31231575	31256560
CR293515.1	0	0.2634509	0	0	0	0	2	31289455	31295411
si:ch211-106h4.4	0	0.2943087	0	1.8104516	0.2861721	0	2	31316383	31322411
si:ch211-106h4.5	0	0.5971071	0.9255338	0.7346256	0	0	2	31326756	31330113
PLXDC2 (2 of 2)	0.432621	0.5373226	0.2082165	0	0	0.202173	2	31330255	31341931
MYRIP (2 of 2)	0	0	0	0.1235406	0	0	2	31342538	31377331
si:ch211-106h4.12	0	0	0	0	0	0	2	31381558	31384833
ccrl1a	0	0	0	0	0.3557881	0.5507003	2	31387229	31390125
e2f5	0.5699589	1.1945788	1.0286849	1.4696997	0.1290614	1.5981237	2	31392512	31402125
lrrcc1	1.6907748	2.4937154	3.8653332	2.906562	3.3181106	3.7531419	2	31403044	31426473
CABZ01071757.1	0	0	0	0	0	0	2	31436090	31451928
and2	0	0	0	0.2670032	0	0	2	31480049	31484497
BX323064.1	3.0367929	1.2572494	2.4359675	0.7734019	1.2224909	0.4730527	2	31499718	31518539
zgc:153414	0	0	0	0	0.8263465	0	2	31522457	31523479
ranbp9	20.926182	23.976394	21.452463	24.941691	23.503074	28.164243	2	31524535	31544786
nol7	85.507723	92.785555	87.999682	85.485784	95.98788	85.445492	2	31548060	31551114

epdr1	0.3328487	2.4804221	0.480591	0.7629207	0.9044427	0.9332837	2	31551907	31554777
stard3nl	2.5182649	2.7066872	3.6360531	2.6640469	2.6318571	3.5305167	2	31556322	31570969
5S_rRNA (2 316052	0	0	0	0	0	0	2	31605285	31605399
amph	1.6031624	0.9955774	0.7715873	1.6841917	0.36302	0.561894	2	31609102	31654841
5S_rRNA (2 316338	0	0	0	0	0	0	2	31633882	31633998
fam105bb	7.2237438	8.2991109	5.9104264	3.5874594	4.7981823	4.3885525	2	31660265	31669876
ankhb	3.5126372	3.7628759	3.2966699	3.6230837	2.7043644	5.1708204	2	31675429	31724187
mycb	21.001984	30.776906	31.0638	48.138537	30.853974	31.239394	2	31734131	31736246
si:ch211-139k8.2	1.3117466	0.9164314	1.8939947	0	0.2970318	0	2	31737582	31807885
si:ch211-139k8.3	0	0	1.6275087	0	0	0	2	31807106	31809856
si:ch211-139k8.4	0.3451582	0.3215192	0	0.3955676	0.3126304	0	2	31833726	31837071
fam49ba	10.233637	9.151452	8.274597	9.1480214	11.123059	10.043034	2	31933330	31980162
asap1a	6.6610972	8.5463667	9.6177744	9.6504433	8.0824167	8.2814164	2	31985773	32070919
5S_rRNA (2 320112	0	0	0	0	0	0	2	32011276	32011391
si:ch211-160i2.4	0	2.1734698	0	0	0	3.2711595	2	32073303	32073925
ubtfl	15.118375	14.787106	16.553662	12.99478	11.069005	8.8314241	2	32075481	32105316
slc4a2a	1.3753429	1.4733217	2.4822746	5.2014867	5.4189262	6.6522253	2	32109772	32175798
ttc19	2.9457371	2.0579935	4.6077075	0.562659	2.6681299	3.097363	2	32193669	32203955
faim2a	2.6132616	3.1297966	3.2341853	3.8506133	3.3814099	4.7104697	2	32212087	32223025
abcf2a	87.836172	87.046927	89.391524	70.287706	73.249863	69.437548	2	32223429	32231413
SNORD89	0	0	0	0	0	0	2	32226018	32226140
smarcd3a	0.6307838	1.8802659	2.5501597	2.7470507	2.0568187	1.2380706	2	32232503	32276670
tmub1	9.7638344	11.235167	7.4635046	19.417623	20.028351	19.727608	2	32279058	32292819
fastk	2.4067381	3.8938385	3.6579186	5.9519825	5.5071823	5.5052087	2	32296892	32312652
si:dkeyp-73d8.4	0	0	0.8206926	0.6514098	0	1.593744	2	32322722	32325902
si:dkeyp-73d8.5	0	1.6947133	1.3134281	0	0	1.2753058	2	32328753	32329517
si:dkeyp-73d8.6	0	0	0	0	0	0	2	32339552	32342452
si:dkeyp-73d8.8	0	0	0	0	0	0	2	32354383	32355467
si:dkeyp-73d8.9	0	0	0	0	0	0	2	32360213	32361613
puf60a	35.620475	39.148715	36.631012	36.711107	34.584712	37.36415	2	32371845	32389729
SNORA57 (2 32384	0	0	0	0	0	0	2	32384199	32384334
SNORA57 (2 32385	0	0	0	0	0	0	2	32385007	32385140
nrbp2	3.4080093	3.0234322	3.6319678	4.2777153	4.9242407	3.7540693	2	32391243	32456410
si:dkeyp-73d8.12	0.4980297	0	0	0	0	0	2	32419695	32437349
klhl18	4.3920362	2.6593043	2.8536929	4.5301333	4.5748487	2.7708645	2	32461682	32474581
si:dkeyp-73d8.13	0	0	0	0	0	0	2	32476538	32478207
bfsp2	0	0.5016664	0	0	0	0	2	32479005	32486826
zgc:136930	0	0	0	0	0	0	2	32498013	32508762
ccr9a	0	0	0	0	0	0	2	32514748	32516958
prpf4ba	6.20445	9.4685815	12.008114	13.010873	10.522068	13.14016	2	32528356	32543983
si:dkey-154p10.3	7.5391467	4.1416575	6.4196927	5.0955138	3.8520619	4.3362512	2	32544110	32552316
pxdc1a	0	0	0	0	0	0	2	32553506	32556769
opn4.1	0.4395484	0	0	0	0	0	2	32561008	32564192
tmem53	4.5578513	6.2052482	4.5560462	6.0271308	9.2093246	4.423807	2	32564477	32568496
rnf220a	20.52681	17.73317	19.599385	11.762348	11.545254	7.658621	2	32770235	32934615
si:ch211-236l6.2	0	2.4698521	2.5522296	2.0257856	3.2020927	1.2390756	2	32990439	32999457
klf4b	26.419787	28.355422	36.488245	27.645429	18.727809	16.10417	2	33044397	33046563
slc6a9	2.2183403	2.462108	3.4074472	2.0014033	2.778796	1.0587347	2	33064484	33140673
ccdc24	0.1916443	0.5355573	0.2767099	0.6589003	0.1735837	0.8060352	2	33140286	33173149
zgc:113531	0	0.778324	0	1.4363672	0	2.9285224	2	33175185	33184246
b4galt2	0.841323	0.7837031	0.404921	0.3213987	0.5080243	0.3931682	2	33194963	33394369
5S_rRNA (2 332877	0	0	0	0	0	0	2	33287797	33287914
atp6v0b	22.954069	23.586336	21.184023	24.136845	21.433887	30.190214	2	33399057	33405089
si:dkey-31m5.2	0	0	0	0	0	0	2	33410040	33413629
si:dkey-31m5.3	0	0	0	0	0	0	2	33415215	33417186
si:dkey-31m5.4	0	0	0	0	0	0	2	33440422	33443203
si:dkey-31m5.5	0	0	0.5032028	0	0.3156656	0	2	33440493	33446769
si:dkey-31m5.6	0	0	0	0	0	0	2	33465384	33468165
si:dkey-31m5.7	0	0	0	0	0	0	2	33468967	33475440
si:dkey-31m5.8	0	0	0	0	0	0	2	33474253	33475443
kiss1ra	0	0	0	0	0	0	2	33514082	33539327
mir23a-3	0	0	0	0	0	0	2	33618310	33618387
mir27a	0	0	0	0	0	0	2	33620200	33620330
BX664751.1	0	0	0	0	0	0	2	33623632	33623729
kif2c	30.895703	27.430688	28.810272	25.818289	22.882817	20.754943	2	33644786	33668083

ptch2	15.101153	16.301846	22.211692	20.218033	16.745981	13.355709	2	33685224	33711408
eif2b3	26.08624	23.808761	17.88146	29.292105	29.833162	28.444865	2	33726830	33789927
klhl20	6.3082123	6.7361083	7.1088808	6.8768509	7.2466748	9.7067047	2	33829975	33844754
cenpl	3.5319118	4.9350309	6.3745375	2.78282	3.5989462	3.7137099	2	33846613	33856275
dars2	3.0020619	2.0196646	4.3345944	2.4848092	2.2659556	2.8058552	2	33852924	33891364
si:dkey-21n10.3	0	0.3508426	0	0	0	0	2	33935518	33937106
fam5b	0	0.1837253	0.2847796	0.2260386	0.1786459	0	2	34098857	34201502
astn1	1.1805482	1.0996956	0.2435087	0.966403	1.1456711	2.0097474	2	34291015	34703231
pappa2	0.2774811	0.5169543	0.600971	1.0335211	0.7539936	1.5560741	2	34707034	34823902
rfwd2	7.2759636	8.4720653	13.609479	10.802276	10.933865	11.823468	2	34837460	34858050
5S_rRNA (2 349593	0	0	0	0	0	0	2	34959385	34959501
tnr	0	0.1719517	0	0.5288839	0	0.1293971	2	34961597	35194948
5S_rRNA (2 351387	0	0	0	0	0	0	2	35138792	35138906
si:dkey-4i23.7	0	0.4216236	0	0.5187269	0	0	2	35202989	35217751
tnw	1.9288198	2.9196702	2.0887273	0.967102	0.5459523	1.1830595	2	35230251	35287808
mrps14	32.050402	32.243783	31.468149	40.404406	29.029962	33.250797	2	35312256	35315017
cacybp	31.777734	33.656343	38.340583	36.917675	29.571565	32.955711	2	35316287	35322203
plk3	16.959442	15.045652	20.017372	28.074689	28.527903	23.210419	2	35324470	35332623
si:dkey-4i23.5	0.8158284	0	0	0	0	3.4312862	2	35333454	35335126
si:ch73-27j14.1	0	0	0	1.6060282	0	0	2	35336228	35342700
ankrd45	1.4158187	1.3188531	0.4088523	0.3245191	0.7694349	1.5879415	2	35336380	35452609
5S_rRNA (2 354073	0	0	0	0	0	0	2	35407362	35407476
si:ch73-27j14.2	0.4584026	0.4270078	0.6618749	0	0	1.2853279	2	35449422	35454585
rasal2	15.91265	17.852917	18.279118	18.23665	18.951949	17.378805	2	35454168	35572494
5S_rRNA (2 355521	0	0	0	0	0	0	2	35552162	35552278
dhx9	39.495323	44.268814	49.698072	70.221894	68.621158	71.283721	2	35575075	35595362
lamc1	41.468506	49.756264	58.447015	95.398549	79.80745	72.111652	2	35601433	35700011
LAMC2	0.1189533	0.221613	0	1.090609	0.5387156	0.8338413	2	35714224	35742453
nmnat2	0.5299873	1.4810697	0.7652341	0.3036953	0.4800412	1.4860463	2	35747016	35761653
smg7	13.667357	13.902012	14.97056	24.935474	18.426721	16.408105	2	35767100	35799340
CT867973.1	0	0	0	0	0	0	2	35872701	35876576
CR352230.1 (2 360	0	0	0	0	0	0	2	36037394	36037848
CR352230.1 (2 360	0	0	0	0	0	0	2	36045319	36045832
CU571384.1	0	0	0	0	0	0	2	36059920	36060430
CU571384.2	0	0	0	0	0	0	2	36070267	36070808
CU693370.1	0	0	0	0	0	0	2	36120139	36120656
BX901889.1 (2 362	0	0	0	0	0	0	2	36203683	36204156
BX901889.4	0	0	0	0	0	0	2	36210938	36211403
BX901889.5 (2 362	0	0	0	0	0	0	2	36214682	36215141
BX901889.1 (2 362	0	0	0	0	0	0	2	36217469	36217946
BX901889.3	0	0	0	0	0	0	2	36220719	36221180
BX901889.2	0	0	0	0	0	0	2	36229918	36230386
BX901889.5 (2 363	0	0	0	0	0	0	2	36318046	36319659
ing5b	39.88861	35.159071	37.776751	47.188889	46.230214	40.288178	2	36326839	36329489
pak2a	40.207773	44.263877	48.756058	41.890919	40.359984	25.378634	2	36337663	36357699
klhl6	0	0.1747162	0	0	0	0	2	36367284	36379989
ccnl1b	28.68973	20.23237	32.999025	44.211241	37.143831	31.132258	2	36385006	36394838
ptx3b	0	0	1.0185769	0.8084768	1.2779327	0	2	36406835	36415977
golim4b	1.3129329	1.3977298	1.6248922	4.0841402	1.8687454	0.2629549	2	36422155	36442122
pdcd10b	28.349874	33.010333	34.470401	33.77281	37.165777	26.148357	2	36442190	36452796
dre-mir-2198	0	0	0	0	0	0	2	36474482	36474591
slitrk3b	0	0	0	0	0	0	2	36535521	36540457
NRD1 (2 of 2)	16.867007	19.92219	18.623498	20.46747	22.26714	20.246723	2	36549076	36575333
FAM163A (2 of 2)	0	0	0	0	0	0	2	36583306	36613716
si:dkey-193b15.7	0	0	0	0	0	0	2	36615858	36619973
si:dkey-193b15.6	7.8994695	11.719022	10.983388	9.3884686	7.4200218	12.305302	2	36619815	36626028
si:dkey-193b15.5	0	0	0	0	0	0	2	36627969	36635114
zgc:153654	0	0	0	0	0	0	2	36634957	36639542
MAP1S (1 of 2)	0	0.0976621	0	0.2403089	0.1899242	0.1469854	2	36641517	36653086
gadd45bb	4.7136752	6.4399107	7.2596753	13.325168	13.377632	16.741288	2	36660582	36662821
gng7	2.4326004	7.1756607	2.9269705	2.7878753	5.5083785	3.4104182	2	36710857	36764738
diras1b	0	0	0	0	0	0	2	36780137	36781749
zgc:101744	30.197618	26.254166	26.160904	56.756955	66.738354	67.737556	2	36810195	36824455
slc1a8b	0	0	0	0	0.1637645	0	2	36831337	36843995
elavl1	119.97777	118.92338	117.14734	53.784608	51.27351	51.855312	2	36844171	36855031

pex19	12.00328	18.243023	15.202812	19.548466	20.981221	24.208942	2	36855114	36867405
si:dkey-52k20.13	2.3843627	2.8556538	3.4427155	1.5614815	1.542614	2.8652492	2	36857495	36861256
copa	67.202455	76.522164	76.38341	92.913545	91.839561	98.436274	2	36897647	36926913
APOD (2 of 3)	0	0	0	0	0.3818214	0	2	36928294	36936822
apod	0	0	0	0	0	0	2	36928632	36931230
samd7	0	0	0.3090773	0.2453245	0.7755527	0.3001064	2	36947844	36963370
sec62	25.883168	23.405514	26.881609	31.918444	33.452158	31.19432	2	36966215	36986736
nadkb	10.736185	8.1041716	9.8890038	18.456265	20.45478	17.387361	2	36988074	37002581
gpr160	1.3059343	1.2164943	3.7712049	2.993325	1.5771502	1.8308729	2	37015921	37016992
skila	0.4615765	2.1498218	1.3329152	2.9094369	2.717503	1.6177841	2	37028246	37073405
prkci	29.520982	26.348576	27.643524	34.11556	33.67537	31.689899	2	37086384	37122433
si:dkey-31b10.2	0	0	0.9092964	0	0	0	2	37126184	37129990
phc3	0	0	0.4334439	0.1720191	0	0	2	37145094	37168609
MUM1	2.2569624	4.3048919	4.1898417	4.6804886	4.0885311	2.1094534	2	37170127	37182556
si:dkey-57k2.7	3.7299153	0	2.3935652	4.7496217	1.8768927	2.324092	2	37181473	37183295
si:dkey-57k2.6	0	0	0	0	0	0	2	37184249	37186350
dapk3	5.4373649	8.0443709	9.2363072	18.327875	13.90573	17.039625	2	37190409	37199251
sppl2	7.2019535	5.1840038	7.090024	4.6896475	7.2645163	3.6715926	2	37201502	37223842
GIN1	0	0	0	0	0	0	2	37206978	37210544
arhgef18a	6.377456	6.9649364	7.4618437	5.5446574	6.4735994	7.8618819	2	37225077	37258737
5S_rRNA (2 37229	0	0	0	0	0	0	2	37229108	37229223
insra	4.6372879	4.9842605	4.4294313	5.8868878	6.5911904	5.9011897	2	37265784	37353729
hiat1a	5.5853243	5.3328704	6.4515965	5.9209677	7.3354943	3.9152118	2	37376911	37405474
myo9b	2.1000644	2.0017305	2.9617082	3.5262027	3.8927796	4.0397365	2	37405755	37465784
MYADM (1 of 2)	0	0.4911796	0.7613431	0	0	0	2	37475050	37475934
ftr66	0	0	0	0	0	0	2	37483787	37490982
NFATC4	2.3350655	2.0078243	2.5934897	0.6175605	0.6507717	0.2518214	2	37496754	37517505
si:dkeyp-66d1.2	0	0	0	0	0	0	2	37528039	37532476
sdr39u1	7.4334241	9.4888949	2.7826078	4.4172883	5.9847964	3.4737977	2	37536607	37561848
RNaseP_nuc (2 375	0	0	0	0	0	0	2	37551528	37551830
mettl17	9.1112381	7.3802032	8.8656396	7.2639376	7.3555713	8.886002	2	37552359	37575883
rpph1	0	0	0	0	0	4.3183624	2	37565147	37565449
RNaseP_nuc (2 375	0	0	0	0	0	0	2	37575030	37575331
parp2	32.837947	35.549336	32.548936	15.867241	17.202875	18.415048	2	37575232	37585260
si:ch211-284o19.8	0	0	0	0	0	0	2	37589535	37603076
zgc:66427	9.9080699	11.49904	15.009562	15.450405	12.652334	9.3364107	2	37605291	37613058
cbln13	4.8864277	5.3103975	5.2915336	5.1334044	3.6882744	0	2	37613182	37616715
hbl4	2.9375692	7.0364132	7.8770251	8.6569544	8.3622998	5.8833804	2	37618223	37621667
hbl3	0.8871746	0.4132072	0	0.5083721	0.4017835	0	2	37625688	37627563
hbl2	0	0.4911796	0.7613431	0.6043022	0	1.4784902	2	37631017	37632321
hbl1	8.7011022	4.6924766	7.934704	7.3476974	5.8071319	3.8521996	2	37633260	37635376
TEP1	5.2945284	10.137836	7.0075714	17.866242	20.114753	16.082599	2	37635490	37657771
cbln10	8.0181074	4.4813811	2.3154248	7.3513045	5.8099827	2.2482196	2	37658833	37659476
cbln14	0	0	0	0	0	0	2	37662058	37663345
cbln9	1.140963	0	0	0	0	0	2	37666026	37670126
apol1	0	0.3347662	0	0.4118655	0.4882667	0	2	37670743	37677483
APOLD1 (3 of 4)	0.8995737	0.6284732	0.9741522	0	0.2036994	0.3152925	2	37679785	37693261
pcp4l1	1.8444816	1.1454387	0	0	2.2275428	0	2	37697938	37703032
DCAF8	1.6774042	2.6042054	3.2292768	3.7166103	2.8360735	1.4109962	2	37704438	37725422
hnrnpc	100.49925	69.175697	76.443889	59.60203	65.777929	66.999652	2	37727933	37736951
cbln5	0	0	0.6854411	2.7202818	1.289958	0	2	37736781	37738032
casq1a	0	0	0	0	0	0	2	37742615	37756145
si:rp71-1g18.1	15.871263	11.538952	14.532148	11.756446	12.973058	12.482234	2	37758249	37768934
tox4	11.954131	15.672079	13.85081	17.928395	20.719424	19.242115	2	37770447	37783417
chd8	13.492262	14.541734	16.663589	13.737586	14.341703	13.913175	2	37790283	37818491
cbln12	0.8430964	0.3926775	0	0	0	0.5909954	2	37824173	37828415
trim110	0	0	0	0	0	0	2	37830744	37844755
SALL2	0.9643269	0.5239982	1.0442737	1.2893583	0.3639368	0.3379879	2	37850519	37859580
mmp14b	5.3206676	6.1224503	7.6823651	5.1412292	3.968791	1.9014117	2	37864076	37886399
acin1a	26.429622	25.488452	45.254459	44.899875	35.542205	27.637462	2	37900578	37928232
C2H14orf119	22.627889	13.821748	16.068091	29.758759	14.783589	23.402572	2	37928185	37932766
si:ch211-14a17.10	0	0	0	0	0	0.5657814	2	37936319	37964030
dhrs1	9.7582582	7.1420966	7.0448399	13.180466	7.2603089	6.8403634	2	37964506	37972433
homez	29.096981	30.389564	36.283374	51.535527	46.121026	51.300187	2	37974150	37978416
C2H14orf164	0	0	0	1.2643201	0	0	2	37980033	37984837

si:ch211-14a17.7	0	0.744339	0.5768738	2.2894153	1.8094017	2.2405202	2	37985405	37987509
si:ch211-14a17.6	0	0.2959115	0	0.7281244	0	0.8907174	2	37988172	37990782
ap1g2	5.8027554	6.451535	5.6757163	6.2211852	5.2559019	2.8867031	2	37992902	38014304
SLC7A8 (2 of 2)	0	0	0	1.4204712	0	0.4344169	2	38020758	38039853
prmt5	28.339303	32.206071	37.372081	30.746013	27.89321	37.611712	2	38045045	38065775
PSMB11 (1 of 2)	0	0	0	0	0	0	2	38073355	38074482
psmb5	146.63206	180.79015	163.29586	245.73337	257.22499	272.09645	2	38076030	38095333
FP015916.1	0	0	0	0	0	0	2	38081665	38081773
CDH24 (2 of 2)	0	0	0.1327662	0.1053808	0.083286	0.1289127	2	38257744	38413397
5S_rRNA (2 38342	0	0	0	0	0	0	2	38342118	38342235
gig2q	0	0	0	0	0	0	2	38425302	38426037
CABZ01011032.1	0	0	0	0	0	0	2	38435909	38442464
LRRC16B	0	0.0555804	0.0861512	0	0	0	2	38446369	38594873
si:ch211-119o8.4	0	0	0	0	0	0	2	38596827	38613597
rem2	0	0.2770516	0	0.3408588	0	0	2	38629171	38681494
si:ch211-119o8.6	0	0.7361456	0	0	0	0.8309465	2	38689685	38696509
copb2	68.651747	73.070875	67.314599	78.168083	85.462435	86.263767	2	38701553	38719326
rbp2b	2.9287898	7.5783467	6.5781315	3.3565318	5.6003128	4.1060579	2	38720262	38740708
RBP1	0	0	0	0	0	0	2	38725478	38732248
rbp1b	0	0	0	0.552487	0	0.6758594	2	38732533	38740800
si:ch211-119o8.8	0	0	0	0	1.5890084	0	2	38740928	38749816
NMNAT3	0.7142661	0.8871305	1.3750788	0.8185828	2.5878137	1.3351671	2	38766950	38794482
clstn2	0	0.2978376	0	0	0.4344052	0	2	38812535	39253455
cbln7	1.0286271	0	0	0	0	0	2	39253572	39262839
BX322588.1	0	0.6383171	0	0	0	0	2	39264719	39267386
spsb4a	16.311004	13.896866	15.221993	12.994042	13.873005	17.011145	2	39288262	39380025
si:dkeyp-55c8.4	0	0.6062677	0.9397331	0	0	0	2	39314517	39316660
zgc:136870	0.3220523	1.799975	1.3950075	1.4763489	0	1.8060232	2	39323147	39325299
slc25a36a	0	0.3455437	1.6068091	1.4879379	0.3359907	0.9101	2	39435480	39463255
si:ch211-16k18.1	0	0	0	0	0	0	2	39631157	39730818
5S_rRNA (2 39761(	0	0	0	0	0	0	2	39761095	39761212
epha4a	22.419818	22.382377	25.26878	31.00647	26.990273	22.546001	2	39772017	39840214
si:ch211-122l24.4 (2	0	0	0	0	0	0	2	39903198	39903976
si:ch211-122l24.6	0	0	0	0	0	0	2	39969460	39976808
si:ch211-122l24.5	0	0	0	0	0	0	2	39979678	39982185
si:ch211-122l24.4 (2	0	0	0	0	0	0	2	39984417	39985381
si:ch211-122l24.3	0	0	0	0	0	0	2	39998824	39999929
si:ch211-122l24.2	0	0	0	0	0	0	2	40009077	40009724
epha4b	2.8515359	4.2499869	6.175881	0.653599	1.8079644	0	2	40081937	40266727
5S_rRNA (2 403479	0	0	0	0	0	0	2	40347951	40348070
uggt1	3.963651	4.1844833	5.9137732	4.9210761	4.2483031	3.8898273	2	40583387	40642628
HS6ST1 (1 of 3)	0	3.6224497	0	1.4855761	0	0	2	40654960	40655805
si:dkeyp-82d1.2	0	0	0	0	0	0	2	40814872	40816884
5S_rRNA (2 40867(	0	0	0	0	0	0	2	40867655	40867770
hs6st1a	0.6331803	2.3592617	4.5711575	3.6282728	1.1470183	0	2	40954856	40955592
5S_rRNA (2 410488	0	0	0	0	0	0	2	41048843	41048959
5S_rRNA (2 413062	0	0	0	0	0	0	2	41306249	41306365
SSBP4 (2 of 2)	3.2077222	2.273504	4.0274274	3.0368621	2.4632955	2.2485555	2	41487546	41530151
znf622	28.24835	20.719446	22.802189	23.451993	30.018475	31.495435	2	41536204	41544585
d2hgdh	2.2912628	3.3200849	5.5138184	4.0847265	3.9200743	1.4276746	2	41544790	41561387
acvr1l	16.246309	19.11618	20.062419	23.886268	16.74828	23.076434	2	41563236	41583420
otomp	1.7974149	2.0928934	1.9464283	0	0	0	2	41589199	41603527
efr3a (2 41686644..4	0.6714444	0.4690942	1.45422	1.9237676	0.7602091	1.8826817	2	41686645	41714376
CR848728.2	17.83845	19.773923	22.408108	9.4041057	10.825424	5.2518616	2	41720884	41787554
5S_rRNA (2 417895	0	0	0	0	0	0	2	41789553	41789669
5S_rRNA (2 418354	0	0	0	0	0	0	2	41835429	41835546
KCNQ3 (2 of 2)	0	0	0	0	0	0	2	41838136	41842617
CABZ01046038.1	0	0	0	0	0	0	2	41845658	41874524
keap1a	5.3694481	2.7282048	3.523999	3.5430058	4.5686763	4.5622866	2	41936143	41962158
crlf1a	2.9381909	4.0249442	4.7414754	1.9807682	1.7220143	3.1500054	2	41977713	42021750
ODF3L2 (1 of 2)	4.4137509	1.8688477	4.6348314	3.6788128	3.9977976	2.8126909	2	42027825	42035137
ebi3	0.4504381	0	1.3007502	8.2595738	6.5278184	0.631498	2	42037721	42043784
si:dkey-97a13.5	0	0	0	1.1354722	0	0	2	42047093	42048014
HELZ2 (2 of 2)	0.1086631	0	0.1568957	0.1245331	0.0984227	0.2285127	2	42050304	42076835
gbp2	0.5794543	0.359846	1.3944301	6.1980991	4.0238218	4.0618702	2	42106335	42118400

gbp1	10.246586	10.030155	9.5288304	12.340178	13.528157	11.200099	2	42122033	42136425
si:dkey-97a13.9	4.6346751	3.3728582	4.6006671	4.6476125	3.4107953	2.6396694	2	42140154	42172676
vcpip1	1.6494019	1.4182511	1.2823601	0.8724427	1.1492013	1.4230166	2	42173798	42184631
si:dkey-97a13.12	0	0	0	0	0	0	2	42189574	42193044
adhfe1	10.033169	7.6845088	5.7946465	8.4322238	4.8467414	9.3774281	2	42196605	42212732
crha	0	0	0	0	0	0	2	42213621	42215154
trim55a	3.0124368	1.7857147	1.5816634	0.9415623	1.4882966	1.9196945	2	42215428	42229832
cyp7c1	2.4603894	2.8011914	3.5524883	3.7596303	6.437951	7.2820188	2	42236837	42253253
slc39a6	17.642868	19.392774	17.577094	20.421757	15.980198	17.808959	2	42257404	42275102
tmeff1a	0	0.3027117	1.4076364	0.7448571	1.7660567	0	2	42278040	42288236
murca	2.8872628	1.3447609	1.0422098	0.4136175	0	0.5059798	2	42292710	42299718
ift57	13.879328	11.49224	10.687989	7.7764461	10.895158	11.242584	2	42301508	42311644
TMEM71	1.03242	1.6349109	1.639751	0.8282416	1.4961991	0.2894831	2	42314066	42328692
apom	75.093723	54.961306	57.310756	75.610702	71.903545	78.207032	2	42329859	42335679
ftr02	1.0463091	0.8354144	0.8632782	0.5139085	0.1353864	0	2	42337236	42343872
ftr03	0	0	0	0	0	0	2	42348696	42351372
ftr04	0	0	0	0	0	0	2	42361094	42362671
ftr05	0	0	0	0	0	0	2	42372948	42374493
ftr06	0	0	0	0	0	0	2	42396062	42405281
ftr07	0	0	0.4143841	0	0	0	2	42410874	42415336
ftr08	0	0	0	0	0	0	2	42419130	42422784
ftr09	0	0	0	0.6161376	0	0	2	42431946	42434347
ftr10	0	0	0	0	0	0	2	42445422	42446689
si:dkey-7l6.3	2.4537248	2.077887	3.8649442	1.5338645	2.4245291	0.9381911	2	42455761	42461532
gtpbp4	142.93009	148.83744	128.23165	130.40758	136.82213	150.35661	2	42462491	42476393
si:dkey-7l6.4	0.3021391	0.8443392	1.0906258	0.8656643	1.2314944	0.4235882	2	42486295	42517020
esyt2a	1.8802902	3.5030283	2.7148992	8.5216565	5.341513	4.9127304	2	42520959	42593563
5S_rRNA (2 42524	0	0	0	0	0	0	2	42524802	42524917
si:dkey-7l6.7	0.9911232	0.5385589	0.4770185	0.8519056	0.2992398	0.9263461	2	42596779	42680096
RNaseP_nuc (2 426	0	0	0	0	0	0	2	42687856	42688153
march11	0	0	0	0	0	0	2	42693690	42701231
myo10	6.7726288	5.757536	6.7407343	4.5967665	4.4072202	4.148293	2	42705883	42806051
ftr11	0	0	0	0	0	0	2	42809792	42816259
ftr12	0	0	0	0	0	0	2	42817113	42819940
basp1	1.9047096	0.3548522	1.100063	0.8731549	2.070251	2.1362674	2	42825522	42849775
adcy8	0	0	0	0.3923752	0.1550536	0	2	42877342	42966373
efr3a (2 42973772..4	0.5847793	1.9065525	1.0554333	0.8377309	1.1917563	1.0247993	2	42973773	43027438
oc90	17.038072	17.130797	23.624579	10.383105	7.2262817	8.3414093	2	43043670	43061471
5S_rRNA (2 430633	0	0	0	0	0	0	2	43063346	43063462
HHLA1	0	0	0	0	0	0	2	43081596	43082550
5S_rRNA (2 430999	0	0	0	0	0	0	2	43099920	43100037
kcnq3	0	0	0	0.1452886	0	0	2	43102630	43184873
lrrc6	1.0410571	1.2121973	2.2547304	0.2982752	1.1786844	0	2	43199355	43225067
ftr13	0	0	0	0	0	0	2	43229480	43232048
ftr14	0.1874112	0.5237277	0.5411957	1.5034746	0.339499	0.2627437	2	43232265	43236818
ftr15	2.3885034	1.6686909	0.8621735	0.6843345	0.5408525	0	2	43245068	43252476
CREM (1 of 2)	0.2584863	0.4013054	0.9952564	1.5799333	0.6243371	1.3287575	2	43256633	43297713
pard3	5.0894929	7.0296505	6.9684794	8.8497653	7.3121877	5.6590198	2	43306095	43490366
5S_rRNA (2 433235	0	0	0	0	0	0	2	43323563	43323677
nrp1b	4.3278381	4.1190759	4.4828678	2.91125	3.6643303	3.1656382	2	43570359	43633838
itgb1b.2	0.8222975	0	0	0.235598	0.186201	0	2	43670284	43684517
itgb1b.1	4.5750377	5.9008231	5.3354302	2.8232668	3.8251244	4.440488	2	43687135	43704034
EPC1 (1 of 2)	7.5327498	7.952432	7.2508863	6.0430215	4.0937166	5.1043113	2	43717977	43737245
CU693495.1	0.3716877	0	0	0	0.1683298	0.2605464	2	43739588	43750519
CABZ01071036.1	0	0	0	1.048642	1.6575539	0	2	43757513	43758022
kif5ba	37.16173	33.576231	39.143072	45.265466	48.558106	49.964186	2	43765423	43801060
ftr16	0	0	0	0.3112965	0	0	2	43804075	43806647
arhgap12a	3.4226003	3.5180089	2.7265093	4.4634912	4.2759357	4.6329017	2	43810722	43858719
zeb1a	3.7017066	2.4471001	5.8620299	1.779042	2.8120733	0.8370418	2	43868731	43913416
nlrb5	0	0	0	0	0	0	2	43926076	43934272
gbp3	3.8519272	3.9867989	3.9137828	1.961996	2.842824	2.2001073	2	43955869	43980375
si:ch211-195h23.3	4.5900379	5.4633668	8.4683815	0.2922445	0	1.0725113	2	43981962	44016911
si:ch211-195h23.4	0	0	0	0	0	0	2	44002426	44004096
kirrelb	1.651872	1.2090098	1.36291	0.1352231	0.6412282	0	2	44023127	44100277
cadm3	0.9024844	0.8406756	0.902127	1.2729721	1.2575907	0.5839618	2	44105656	44245114

sdhc	56.522995	58.970112	62.67801	63.223356	52.83453	57.055107	2	44254153	44261341
atp1a2a	3.702654	3.0040279	4.4838761	0.4106532	0.5409217	0	2	44264576	44317038
mpz	7.0906568	6.1922218	7.465211	0.5078893	0.8028039	0.8284038	2	44320983	44344410
LIG1	44.555549	41.992341	58.845341	37.245784	34.065735	26.639603	2	44362777	44405822
zgc:152670	0.3229438	0.6016526	0.2331448	0.5551634	0	0	2	44409991	44424444
ETV3L	0.5782576	0	0.8349301	0	0	0	2	44427193	44432915
TMEM55B (1 of 2)	2.2566615	0.8850984	2.4008757	2.1778871	1.6136787	1.8316495	2	44444676	44460112
pih1d3	3.8393361	5.2020221	4.5356002	4.8000665	3.161378	5.382611	2	44462271	44467626
KCNAB1 (1 of 3)	1.6067767	0.8552759	2.3199805	1.0522526	2.4948917	2.252643	2	44488199	44572252
pask	2.9086825	5.4189492	4.382365	2.4638824	3.092753	2.1275834	2	44574233	44606763
MTERFD2	12.467851	10.507869	12.001324	17.010414	8.6040965	16.647122	2	44612299	44618774
BX323035.1 (2 446	0	0	0	0	0	0	2	44623829	44625766
5S_rRNA (2 44625	0	0	0	0	0	0	2	44625879	44625995
BX323035.1 (2 446	0	0	0	0	0	0	2	44627715	44628827
klhl24	1.030596	0.5760079	1.7856589	1.6535565	0.1866945	0.2889717	2	44632701	44665956
YEATS2	4.3920362	3.5497501	4.569639	4.4413072	3.7441217	3.9842496	2	44677192	44756745
MAP6D1	0	0	0	0	0	0	2	44759069	44782214
acsm3	0.738766	1.3763397	1.0666838	1.8344317	1.6728611	2.0714466	2	44787051	44808224
ncapd2	37.344653	49.449314	47.830673	40.794392	37.086672	47.307774	2	44811404	44839093
snoU85 (2 4482458	0	0	0	0	0	0	2	44824583	44824876
snoU85 (2 4483577	0	0	0	0	0	0	2	44835776	44836096
si:ch211-224b1.4	6.3367157	5.4811073	13.070584	5.7059956	1.639869	6.3456052	2	44842735	44984354
si:ch211-224b1.5	4.1480342	0.6439911	1.9964107	0.7923073	1.8785611	0	2	44985300	44986177
camk2n1a	1.5372127	1.4319331	0.634154	2.2650667	0.9945323	0.9236215	2	45004897	45007595
mul1a	0.9625036	0.5977229	1.3897324	0.6434603	0.9444467	0.899597	2	45022377	45033052
alg3	9.6322929	8.9726028	13.31598	8.2205794	7.239514	7.4703686	2	45034221	45042845
vwa5b2	0.2486169	0.1157949	0	0.5698534	0.2251871	0	2	45046044	45083205
PRSS56	0	0	0	0	2.3560549	0	2	45110791	45119741
si:dkey-76d14.2	0.6554127	0	0	0	0.5936464	2.7565951	2	45129867	45131943
5S_rRNA (2 451352	0	0	0	0	0	0	2	45135295	45135411
chrng	4.6004076	8.0350087	13.284803	5.272285	1.5625739	2.4186022	2	45143065	45158422
eif4e2	5.4395234	6.9337688	6.6138759	13.452211	12.446908	12.041078	2	45178320	45197119
capn10	2.847493	1.2482239	1.4510882	0.5758874	1.3654294	0.7044852	2	45200971	45216123
CU929150.1	0	0	0	0	0	0	2	45221499	45222824
zgc:195195	0	0	0	0	0	0	2	45241704	45243634
mir181b-1	0	0	0	0	0	0	2	45252630	45252738
CU571393.1	0	0	0	0	0	0	2	45255036	45255102
CAMSAP2 (1 of 2)	0.5523838	1.6465681	1.9141722	0.8862812	0.1000654	1.5488445	2	45346799	45431744
5S_rRNA (2 453859	0	0	0	0	0	0	2	45385914	45386046
si:ch211-141h20.6	0	0	0	0	0	0	2	45387428	45392266
wdr47a	0.497423	0.1985811	1.3338285	0.6515089	0.6436367	0.1992483	2	45437773	45478472
si:ch211-66k16.20	0.271074	0.3787633	0.1956981	0.4659954	0.8593476	1.1401079	2	45487179	45503631
si:ch211-66k16.27	0	0	0	0	0	0	2	45496903	45503631
si:ch211-66k16.2	0	0	0	0	0	0	2	45509755	45512232
si:ch211-66k16.24	0	0	0	0	0	0	2	45516473	45517314
si:ch211-66k16.28	0.1186207	0.1104967	0.1712732	0	0.1074419	0	2	45535181	45543193
gpsm2	4.7350724	6.8483162	6.4770067	7.2830915	4.6274302	5.240843	2	45546372	45566044
si:dkeyp-51f11.3	0	0	0.4291647	0	0	0.4167082	2	45566799	45593275
fndc7	0	0	0	0	0	0	2	45604230	45623042
FNDC7 (4 of 4)	0	0	0	0	0	0	2	45649123	45653991
FNDC7 (1 of 4)	0	0	0	1.084802	0	0	2	45675289	45682103
si:dkeyp-51f11.9	0	0	0	0	0	0	2	45691374	45694499
si:dkeyp-51f11.8	0	0.3253697	1.0086656	0	0	0	2	45698462	45707715
prpf38b	35.576206	36.13636	34.427155	30.145267	31.537887	20.693466	2	45710634	45719285
fam102ba	1.5562539	1.0354787	2.2470321	1.0191661	0.6041109	0.6233748	2	45720833	45746468
CU467828.1	0.2974212	0	0	0	0	0	2	45752083	45931456
si:ch211-170p16.1	0	0	0	0	0	0	2	46050492	46053459
itgb1b	26.528126	41.840699	50.49062	58.732079	53.2441	47.757238	2	46095866	46102453
5S_rRNA (2 463194	0	0	0	0	0	0	2	46319414	46319550
GPC6 (4 of 4)	1.0301409	0	0	0	0	0	2	46421273	46423420
gpc1b	0.496969	0.4629329	3.5877988	2.8477498	0.4501344	0.6967326	2	46430883	46442745
EPHB1	0	0.2934148	0	0.1804952	0	0	2	46498776	46805910
CABZ01044741.1	0	0	0	0	0	0	2	46965059	46987692
5S_rRNA (2 470393	0	0	0	0	0	0	2	47039302	47039418
si:ch211-226f6.1	0	0	0	0	0	0	2	47181435	47182794

si:ch211-284d12.1	0	0	0	0	0	0	2	47255728	47256686
si:ch211-284d12.2	0	0	0	0	0	0	2	47291965	47292601
5S_rRNA (2 473032	0	0	0	0	0	0	2	47303227	47303341
si:ch211-284d12.3	0	0	0	0	0	0.6379638	2	47392211	47413529
CU633981.2	0	0	0	0	0	1.204847	2	47419289	47422014
CU633981.1	0	0	0	0	0	0	2	47425941	47432044
wu:fb63a08	0	0	0	0.4818085	0	0.8840972	2	47429190	47435272
CABZ01078499.2	0	0	0	0	0	0	2	47440933	47444779
CABZ01078499.1	0	0	0	0	0	0	2	47441887	47444778
si:dkey-20f20.6	0	0	0	0	0	0	2	47466663	47470565
acsl3b	15.982569	18.263725	19.454271	18.529767	13.298058	16.153874	2	47496912	47540359
si:dkey-20f20.4	0.529086	0	0	0	0	0	2	47547466	47580215
pax3a	8.9525918	7.2970211	9.233143	8.0615025	8.3985002	6.7238633	2	47581097	47641979
si:dkey-20f20.3	0	0	0	0	0	0	2	47663520	47667261
BX085193.1	0	0	0	0	0	0	2	47682925	47685999
scg2b	0	0.3218763	0.2494589	0.5940104	0.1564888	0.2422184	2	47704725	47707925
ap1s3b	10.822214	17.33937	15.00086	19.844431	19.996742	21.241295	2	47709967	47743534
CU467824.1	0	0.8889447	0.6889454	0	0	0	2	47745990	47756677
cul3a	37.597703	31.049569	32.617391	31.320813	30.90659	32.33509	2	47766773	47804182
mbnl1	0	0.1640974	0.5087117	0.2018903	0	0	2	47877473	47943654
ftr19 (2 47957087..4	0	0	0	0	0	0	2	47957088	47958388
5S_rRNA (2 47967	0	0	0	0	0	0	2	47967141	47967256
CU929191.1	0	0	0	0	0	0	2	47967748	47968739
CU929191.2	0	0	0	1.4732986	0.5821987	1.8022917	2	47983693	47984626
ftr19 (2 47990291..4	0	0	0	0	0	0	2	47990292	47991634
ftr22	0	0	0	0.2209948	0	0	2	48011265	48018262
ftr23	1.6692705	1.2094029	1.3390076	1.0628128	0.6719813	0.7800857	2	48020412	48047591
ftr24	1.4643949	6.1384609	4.9335986	6.7130637	7.5162093	5.8169154	2	48030376	48037975
ftr26 (2 48041197..4	0	0	0	0.6295555	0	0	2	48041198	48047579
ftr26 (2 48049647..4	0	0	0	0	0	0	2	48049648	48052583
ftr26 (2 48056362..4	0	0	0	0	0	0	2	48056363	48057664
ftr27	0.5732848	0	1.6555003	0	2.0770331	0	2	48059139	48060047
fzd8b	2.414047	1.729781	3.2174546	2.7666121	3.0275258	6.5084749	2	48069333	48071845
BX548047.2	0	0	0	0	0	0	2	48096548	48098223
si:ch211-77g15.32	0	0	0	0	0	0	2	48100834	48102714
BX548047.1	0	0	0	0	0	0	2	48108982	48110499
klf6b	0	0	0.5926021	0	0	0	2	48188415	48196354
pitrm1	12.74016	15.936518	15.767284	19.467768	17.474135	13.438461	2	48203229	48233581
pfkpb	0	0	0	0.5028276	0.1589606	0	2	48233666	48286440
si:dkeyp-12a9.5	0	0.4730076	0	1.7458348	0	1.4237909	2	48296776	48310264
gigfy2	15.104639	18.235671	21.378727	25.852062	22.141899	17.553922	2	48317450	48370015
si:ch211-195j11.8	0	0	0	0	0	0	2	48377202	48379013
5S_rRNA (2 48391(	0	0	0	0	0	0	2	48391058	48391172
lpar5a	0	0.2766989	0	0	0	0	2	48396762	48398332
itm2cb	27.005961	18.121132	22.470635	45.638297	40.837283	41.711695	2	48398577	48420960
hes6	39.90093	51.977435	47.259722	56.088686	33.599514	36.273379	2	48402633	48418868
per2	1.033182	1.4436331	1.3674677	2.4668238	2.2615518	0.9656559	2	48423772	48489514
si:ch211-195j11.24	0	0	0	0	0	0	2	48519216	48520377
si:ch211-195j11.27	0	0	0	0	0	0	2	48528118	48529568
CR381673.2	0	0	0	0	0	0	2	48574935	48582050
CR381673.1 (2 4859	0	0	0	0	0	0	2	48595934	48629072
CR381673.1 (2 487	0	0	0	0	0	0.6333319	2	48710962	48717469
CR381673.3	0	0	0	1.2252174	0.4841652	0	2	48732060	48735452
CR391991.2	0	0	0	0	0	0	2	48853842	48854551
CR391991.1	0	0	1.7144748	0	0	0	2	48911934	48912326
wu:fj40e01	0	0	0	2.9821974	0.7856436	1.2160444	2	48937401	48943912
BX005223.4	0	0	0	0	0	0	2	48983386	48993667
BX005223.3	0	0	0	0	0	0	2	48999689	49001537
BX005223.5 (2 490(	0	0	0	0	0	0	2	49009151	49012479
BX005223.2	0	0	0	0	0	0	2	49041004	49045324
BX005223.1	0	0	0	0	0	0	2	49095879	49097256
BX005223.5 (2 491	0	0	0	0	0	0	2	49119527	49186410
zgc:123035	0	0	0	1.5637643	3.0897386	1.9129588	2	49286037	49286720
CABZ01044732.1	0	0	0	0	0	0	2	49295576	49298552
5S_rRNA (2 493095	0	0	0	0	0	0	2	49309547	49309676

svilb (2 49311117..4	6.5169309	5.9414419	7.1072636	13.745607	14.882524	9.5252899	2	49311118	49391635
svilb (2 49462106..4	0	0	0.1449943	0	0	0	2	49462107	49467357
KCNJ9	0	0	0	0.3537086	0	0	2	49512969	49528843
cdc34b	18.75803	13.015857	17.964011	22.15568	20.804409	24.151301	2	49569956	49594175
ABHD17A (2 of 2)	17.820438	13.2237	12.647165	13.153839	13.405266	20.749102	2	49601523	49626268
SEMA6B (1 of 2)	1.069081	1.4937937	1.5436165	0.8168116	0.3227768	0.7494065	2	49802577	49912504
GPR35 (3 of 3)	0	0	0	0	0	0	2	49936705	49937559
rorcb	0	0.408739	1.9006731	0.7543123	0.5961583	2.1530904	2	49987900	50017464
sh3gl1a	23.806391	17.65025	19.992687	21.43684	27.723689	27.586041	2	50027864	50081696
stap2a	3.4506809	2.4580346	1.465395	4.1872698	3.4931921	2.8457238	2	50092416	50139542
si:ch211-209f23.3	0.4557166	0	0	0	0	0	2	50126006	50128170
sema4e	4.4811131	7.0529816	8.255026	4.0730365	4.1987706	1.7330646	2	50139218	50173919
cactin	23.755843	25.448199	24.867795	25.523739	34.6963	30.182509	2	50179034	50197341
BX323861.1	0	0	0	0	0	0	2	50201281	50203389
BX284666.1	0	0	0	0	0	0	2	50313783	50315978
si:ch211-190k17.13	0	0	0	0	0	0	2	50337816	50339790
si:ch211-190k17.17	0	0	0	0	0	0	2	50362746	50363555
si:ch211-190k17.19	0	0	0	0	0	0	2	50369708	50371249
wdr48	10.076665	10.5194	8.7798218	8.3625879	8.9696745	7.5507032	2	50376130	50404290
blvra	13.702723	8.154944	13.739572	7.8519847	8.6190098	4.8026812	2	50414868	50430961
si:ch211-190k17.31	0.5690901	0	0	0	0.5154588	0	2	50425984	50427031
rpl37 (2 50430959..5	5.1927357	5.4820456	3.4989023	3.1739312	4.3898126	1.9413409	2	50430960	50437026
hecw1	0	0.2763471	0.1427821	0.2266613	0.1791381	0	2	50454934	50548465
ccr12.3	0	0	0	0	0	0	2	50554397	50555589
si:ch211-106n13.3	0	0	0	0.127822	0.2020441	0.1563652	2	50557326	50623244
ZCCHC2	3.4881503	2.6841682	3.5036132	3.3023532	5.4946538	3.6145409	2	50632528	50670220
exoc3	9.0037953	10.543845	11.143141	10.466187	7.805763	6.6721555	2	50675049	50696575
ahrrb	0	0	0	0	0	0	2	50703832	50768566
mcm6l	0.3610475	1.177121	0.5213065	1.0344437	1.7986223	2.5308778	2	50769976	50795733
si:ch211-120f16.3	0	0	1.871635	0	0	0	2	50772876	50773533
cul1a	21.503047	26.824284	27.234786	26.805222	25.513198	26.796887	2	50799421	50842315
cntnap2b	0	0	0.3441208	1.0925585	0	0	2	50849183	50870460
viml	0	0.2621797	0	0.3225618	0	0	2	50896948	50915380
CNTNAP2 (4 of 4)	0	0.1140031	0.7068331	0.7012948	0	0	2	50964823	51035413
CNTNAP2 (2 of 4)	0	0	0	0	1.1007194	0	2	51134319	51138378
CABZ01053212.1	0	0	0	0	0	0	2	51171499	51189739
5S_rRNA (2 511969	0	0	0	0	0	0	2	51196969	51197085
neurod6b	0	0.271514	0	0	0	0	2	51233146	51235788
CABZ01053219.1	0	0	0	0	0	0	2	51304861	51308734
CABZ01053221.1	0	0	0	0	0	0	2	51313236	51314231
5S_rRNA (2 513161	0	0	0	0	0	0	2	51316103	51316219
XCR1 (4 of 4)	0	0	0	0	0	0	2	51324849	51325907
FYCO1 (1 of 2)	0.1133756	0.6336647	0.6547994	0.9095364	1.2322923	0.7947423	2	51329179	51371813
scn12aa (2 5147041	0	0	0	0.1734136	0	0	2	51470415	51506531
ACVR2B (2 of 2)	5.3844675	6.9662495	19.004294	17.141263	17.340564	13.000762	2	51541542	51569913
5S_rRNA (2 515447	0	0	0	0	0	0	2	51544760	51544891
crygn1	0	0	0	2.0055278	2.6417265	0	2	51587030	51598133
CABZ01040054.1	0	0	0	0	0	0	2	51627068	51627372
CABZ01040055.1	0	0	0	0	0	0	2	51633350	51641977
si:ch211-9d9.1	0.7055547	1.4459128	2.6487003	1.9406377	2.3006267	2.9674867	2	51648981	51671212
tgm1l1	0.1095946	0.1020888	0	0	0.794131	0	2	51686652	51738436
abhd4	1.1942517	0.5562303	1.2932603	2.3951707	0.8112788	0.8371489	2	51748981	51760936
dad1	152.05575	144.57238	169.58275	210.31752	167.17083	132.31656	2	51762047	51765500
pigr	0	0	0	0	0	0	2	51771670	51792638
si:ch211-9d9.8	0	0	0	0	0	0	2	51794747	51795507
si:ch211-9d9.7	0	0	0	0	0	0	2	51812256	51813699
CABZ01040076.1	0	0	0	0	0	0	2	51905766	51907213
si:dkeyp-104b3.1	0	0	0	0	0	0	2	51949325	51956701
si:dkeyp-104b3.2	0	0	0	0	0	0	2	51963213	51966978
5S_rRNA (2 519904	0	0	0	0	0	0	2	51990489	51990603
si:dkeyp-104b3.18	0	0	0	0	0	0	2	52033367	52034083
si:dkeyp-104b3.21	0	0	0	0	0	0	2	52087439	52096308
si:ch211-215e19.2	0	0	0	0	0	0	2	52101894	52103230
si:ch211-215e19.8	0	0	0	0	0	0	2	52114144	52117464
si:ch211-215e19.3	0	0	0	0	0	0	2	52127474	52136302

si:ch211-215e19.4	0	0	0	0	0	0	2	52142208	52144286
si:ch211-215e19.6	0	0	0	0	0	0	2	52158710	52160911
si:ch211-215e19.7	0	0	0	0	0	0	2	52196883	52197526
lrrc24	0	0.0588219	0	0	0	0	2	52212554	52234826
5S_rRNA (2 52244	0	0	0	0	0	0	2	52244131	52244247
5S_rRNA (2 52267	0	0	0	0	0	0	2	52267095	52267209
THEM6 (2 of 2)	14.3724	17.571845	14.266939	26.251374	23.188206	25.816658	2	52308605	52319443
THEM6 (1 of 2)	0.7436715	1.0391091	0	1.2784241	0	0.5213003	2	52321434	52327464
ftr67	17.032991	13.066485	11.211727	18.085275	17.015952	16.856216	2	52331004	52352304
eef1da	59.059578	55.7896	54.047215	52.114328	57.260953	64.140382	2	52386821	52418406
BX255896.2	0	0	0	0	0	0	2	52443979	52445580
BX255896.1	0	0	0	0	0	0	2	52446230	52447144
ghrhra	0	0	0	0	0	0	2	52451957	52511984
adcyap1r1a	0	0	0	0	0	0	2	52526137	52556894
CU929148.1	0.3686049	0.3433602	0	0	0	0	2	52560070	52636980
THEG	0	0	0	0.4848662	0	0	2	52669981	52687014
shda	2.8877095	1.344969	1.6677936	1.3237807	1.0462283	0.8096929	2	52716172	52743793
ccdc94	23.902327	15.190359	16.449602	23.041008	19.424088	23.801639	2	52746237	52760438
scn12aa (2 52789	0	0	0	0	0	0	2	52789628	52789894
CABZ01040021.1	0	0.579592	1.7967696	0	1.1271366	0.8723092	2	52814258	52828309
PPAP2C (1 of 2)	0	0.503118	0.7798479	0.6189901	0	0.7572128	2	52861686	52935538
TLE1	0.2439382	1.5906209	0.7044314	0.2795648	0.4418988	0	2	52954905	53014572
chico	0.3703602	5.86491865	7.4865401	10.186808	12.747379	8.3077067	2	53035303	53084360
gna11b	3.3615885	2.7834331	2.8987404	5.3507494	3.2139464	3.4037077	2	53090568	53178564
C2CD4C (2 of 2)	0.3677335	0.3425484	0	0	0	0	2	53375472	53376740
RAB31	3.174516	0.7392755	2.291798	0	0.7188371	7.788475	2	53411307	53432629
ralbp1	0.8539665	0.867797	1.4572038	2.0463434	2.5314165	1.3060693	2	53435983	53470581
zgc:165603	0	0	0	0	0	0	2	53510777	53543519
sirt6	15.147316	17.90874	16.403094	19.362565	27.175813	19.602454	2	53554287	53645654
si:ch211-155i14.1 (2	0	0	0	0	0	0	2	53588514	53590833
CR384061.1	0	0	0	0	0	0	2	53626191	53626272
rxfp3.2a	0	0	0	0	0	0	2	53781623	53782819
5S_rRNA (2 53795	0	0	0	0	0	0	2	53795271	53795385
CREB3L3 (1 of 2)	2.8435238	3.2373958	5.0180601	7.6038968	9.1575083	9.7448218	2	53806113	53854173
CELF5 (1 of 2)	0	0	0	0	0	0	2	53876129	53912269
CABZ01117637.1	0	0	0	0	0	0	2	54003041	54008440
HSD11B1L (2 of 2)	0	1.0132727	0	2.4932746	3.9410372	4.5750482	2	54045004	54068709
admp	0	0.4676643	1.4497872	1.1507421	0.2273675	1.4077072	2	54071703	54087723
im:7138239	0	0	0	0	0	0	2	54088548	54112518
CU694222.2	0	0	0	0	0	0	2	54130893	54144217
CU693369.1	0	0	0	0	0	0	2	54170996	54179310
RANBP3 (1 of 2)	63.522267	66.079009	66.736478	82.713857	60.67016	66.878579	2	54206171	54261877
5S_rRNA (2 54273	0	0	0	0	0	0	2	54273252	54273369
ctnnbl1	57.348937	54.713711	49.749506	52.47367	54.248338	56.410481	2	54307209	54402862
capsla	6.3061331	4.0667835	2.1012119	0	1.3181172	0.6800747	2	54479382	54485838
abhd8	0	0	0	0	0	0	2	54597840	54609170
5S_rRNA (2 54624	0	0	0	0	0	0	2	54624264	54624380
CABZ01050249.1	0	3.2931361	8.7505015	2.3151836	0.9148836	0	2	54634186	54644845
CU179656.1	0.1888675	0.0351865	0.0545401	0	0	0.0529571	2	54798988	54950572
napg	0.4974988	0	0.7183247	4.5612572	0	0	2	54956218	54979500
rab12	6.3312972	5.8976835	9.1415853	5.5486802	8.7706164	12.009045	2	54979658	55010979
SOGA2	0.3499466	0.1629899	0.7579174	0.6015831	0.3169676	0.2453063	2	55022580	55094860
SOGA1	1.3115623	0.2443474	0.7574914	0.9018675	0	0.3677526	2	55139956	55151816
CABZ01087853.1	0.6029119	0.8424302	1.7410558	1.3819313	2.1843733	4.2263043	2	55186164	55226184
ndufv2	63.735383	82.085916	68.01904	92.098662	96.382231	91.685706	2	55227956	55277424
ankrd12	2.4989114	3.2588746	4.329731	4.5821932	4.2681505	2.202127	2	55283371	55388809
CU570683.1	2.1755424	7.0929086	6.2824113	12.466373	8.8673338	1.5250161	2	55398717	55415486
twsg1a	0.3658117	1.249447	0.1760618	1.1179669	1.3253501	2.2223712	2	55427608	55462812
rnf126	0	0.8676526	2.6897749	2.1349597	3.3746606	3.9175563	2	55472895	55479329
HCN2 (2 of 2)	0	0	0	0	0.1553386	0	2	55503950	55663728
CABZ01112877.1	0.9150075	3.4093645	0	0	0	1.2828076	2	55803426	55814829
calrl	67.04605	60.279221	57.634051	40.139226	51.26095	53.934772	2	55840231	55854933
EPS15L1 (1 of 2)	1.3826781	1.5026458	1.6636756	0.2641024	1.043645	1.9384649	2	55859792	55896981
CABZ01118627.1	0	0	0	0	0	0	2	55936475	55962017
rab8a	2.2824332	2.5126819	10.785411	4.5181595	3.1949738	5.5270814	2	55967916	55993632

tpm4b	22.810524	18.432253	20.237467	24.567125	29.124335	24.273622	2	55995983	56012592
rx2	1.7986658	2.0478088	4.6169669	1.3742374	2.172212	1.6811098	2	56045666	56074438
cplx4c	0	0.2343364	0	0	0	0	2	56106356	56216886
atcayb	0	0	0	0	0	0	2	56129980	56169710
nmrk2	0.4668873	0.2174557	0	1.0701499	0.2114438	0	2	56196027	56203416
lox15b	9.7473389	9.0797696	12.314674	14.801458	18.319649	15.715231	2	56225103	56254977
jund	0.467589	1.3066953	0	1.6076375	1.2705699	0.655543	2	56343402	56344399
pgpep1	4.5638518	3.1884643	4.9422148	4.7945244	7.2340677	7.997945	2	56353059	56375691
upf1	17.081161	17.93052	21.533192	24.246192	24.895646	19.084803	2	56382690	56448130
uba52	3241.1744	3609.888	3124.423	3129.0546	3032.8725	3321.2821	2	56552145	56561814
CERS4 (1 of 2)	0	0	1.1146214	0	0	0	2	56569739	56598459
CTXN1	0	0	0	0	0	0	2	56644028	56644297
rab11bb (2 5667394	0	0	0	0	0	0.5544338	2	56673949	56688176
ftr28l	0	0	0	0	0	0	2	56697521	56704428
si:ch211-117a23.3	0	0	0	0	0	0	2	56708560	56718784
pip5k1cb	0	0	0.334885	0	0	0	2	56725357	56798009
si:ch1073-382c16.2	0	0	0	0	1.40424	0	2	56859963	56863678
slc25a42	0.610005	0.4261706	0.6605771	1.1360288	1.3122302	0.5345032	2	56873542	56912362
ARMC6	2.8924825	0.598752	0.9280835	0.7366493	1.746596	2.7034376	2	56921908	56945353
eef2b	1799.6928	2107.0052	1872.635	1809.886	1706.1561	1791.6066	2	56950887	56976839
BTBD2 (1 of 2)	2.3930967	3.2199553	3.8392514	2.4378685	1.445047	1.8639085	2	57008133	57029578
CABZ01117751.1	0	0	0	0	0	0	2	57034232	57068290
CABZ01117755.1	0	0	0	1.1247264	0.888909	0	2	57118915	57130311
CABZ01117756.1	0	0	0	0	0	0	2	57136132	57140954
rab11bb (2 5719002	2.3829133	1.4798093	1.7203114	0.4551552	1.4388978	1.1135862	2	57190023	57203845
CU469531.1	0	0	0	0	0	0	2	57214524	57220517
CU469531.2	0	0	0	0	0	0	2	57223990	57231924
gpx4b	201.78156	206.20099	167.2692	339.08535	351.24494	342.36611	2	57368919	57382529
POLR2E (1 of 2)	0	0	0	0	0	0	2	57385084	57398104
HMHA1 (1 of 2)	0	0	0	0.4853062	0.1278513	0	2	57410229	57483531
GBGT1 (4 of 10)	0	0	0	0	0	0	2	57491838	57501211
CABZ01024428.1	0.57399	2.4060552	1.6575366	2.6312787	2.0795879	1.6094266	2	57537989	57551652
ncana	0.4741346	0.4416624	0.6845899	1.2075128	0.3817351	0.1477155	2	57606632	57707460
si:ch1073-325m22.2	141.97141	117.29837	110.51559	94.793905	105.10997	152.30796	2	57733064	57733441
mbd3a	54.959773	56.597108	56.058048	78.877591	84.489578	72.810249	2	57737888	57762598
tcf3a	6.5725894	4.6291697	13.193387	8.4510961	7.4051832	5.3938734	2	57776875	57853745
map2k2b	1.2525218	2.3334799	2.3251908	2.6658345	1.7827602	1.0034232	2	57891760	57918126
pias4b	1.5624571	0.2425748	0.3759981	0.2984416	0.4717369	0	2	57922021	57948907
ONECUT3 (1 of 2)	0	0	0	0	0	0	2	57978989	58038804
5S_rRNA (2 580744	0	0	0	0	0	0	2	58074471	58074585
LINGO3 (1 of 2)	0	0	0	0	0	0	2	58084207	58099551
ncstn	4.899253	3.9932517	5.3054221	8.4221639	5.5469323	2.5757161	2	58109732	58124624
pvrl4 (2 58153474..5	1.2114586	1.2789542	1.1661277	1.2032704	1.3167484	0.4529124	2	58153475	58191051
CU984580.1	8.792029	6.9299039	8.7885471	5.4255824	1.2251485	3.7926487	2	58192923	58201113
CU915267.1 (2 5822	0	0	0	0	0	0	2	58222375	58233774
CU984580.4 (2 5825	0	0	0	0	0	0	2	58253742	58258254
CR774186.2	3.8657715	2.0577229	1.5947659	0.6329082	2.5010429	1.5484779	2	58303299	58311045
CR774186.1	0.3002921	0.5594517	0.8671668	0.6882978	0.5439849	0	2	58313646	58339136
si:dkeyp-68b7.5 (2 5	0.2464504	0	0.1779215	0.4236658	0.1116124	0	2	58340428	58353694
arhgap30	0	0	0	0	0	0	2	58361519	58399320
si:ch211-155e24.5	0	0	0	0	0	0	2	58369801	58370736
si:ch211-155e24.6	0	0	0	0	0	0	2	58378004	58382083
si:ch211-155e24.3	3.8483977	3.7176027	4.3217962	4.7371456	4.0021269	2.5977443	2	58414089	58434168
si:ch211-155e24.2	0.8562456	1.5952072	0	0	1.5511055	0	2	58431639	58433101
pvrl4 (2 58439049..5	0	0.8781696	0	1.080419	1.2808371	0	2	58439050	58448431
si:dkeyp-68b7.10	0	0	0	0	0	0	2	58620785	58637964
5S_rRNA (2 586233	0	0	0	0	0	0	2	58623333	58623447
sf3a2	96.099281	80.838696	52.273389	128.74428	136.71274	162.71826	2	58644257	58656663
plekhj1	0.6833843	0.7275213	1.2686396	1.5663815	0.530556	0	2	58667669	58690078
TPGS1 (1 of 2)	2.4668926	4.5958834	7.7174026	5.6543514	4.8412257	5.7641577	2	58698172	58710329
si:dkeyp-68b7.7	1.2868772	1.498428	2.5548689	1.4748222	2.1855028	2.029675	2	58711491	58719262
si:dkeyp-68b7.6	1.0159373	0.3154528	2.9337675	0.3881041	0.920195	1.8990766	2	58732315	58737139
si:dkeyp-68b7.5 (2 5	0.8717846	1.3921344	0.8991041	1.5700244	0.7896274	1.2222106	2	58738265	58760688
CU984580.4 (2 587	0	0	0	0	0	0	2	58773987	58790437
CU915267.1 (2 5879	0	0	0	0	0	0	2	58791605	58794724

KCNJ10 (2 of 2)	0	0	0	0	0	0	2	58822161	58829594
si:ch1073-185p12.3	0	0	0	0	0	0	2	58838190	58838833
pnp5b	1.6189206	1.8850562	1.753136	2.3191995	1.0997647	2.2696683	2	58850206	58864548
si:ch1073-185p12.2	0	0	0.2941024	0.9337537	0.1844942	0.5711322	2	58868462	58904922
CABZ01052486.1	4.7136752	6.8999043	5.8336676	6.1738229	3.6595346	3.7762303	2	58908628	58919029
CABZ01081294.1	0	0	0	1.9066218	1.5068672	0	2	58958976	58966658
epb41l3b	17.077229	15.734746	15.008816	32.547945	24.210572	27.584957	2	58969930	59038058
FOXL2 (2 of 2)	1.0839811	2.0194842	0	0.6211468	0.9818263	0	2	59124201	59125061
AL954696.1	19.026107	17.962561	20.046603	19.742202	21.89067	25.232084	2	59216223	59239826
vapal	42.986714	48.898259	47.147299	55.896611	62.521641	51.57364	2	59246438	59296669
LRRC30 (1 of 2)	0	0	0	0	0	0	2	59394955	59398361
zgc:112425	1082.3593	919.87647	1042.1773	536.32244	590.01053	766.35946	2	59487737	59495440
CABZ01088877.1	0	0	0	0	0	0	2	59505728	59505816
fem1a	1.0877712	3.7153331	4.7118085	2.4932746	2.9557779	3.0500322	2	59522037	59523994
CABZ01085657.1	4.1480342	0.7727893	1.7967696	1.9015374	3.3814099	0	2	59530550	59532984
CABZ01092973.1	0.831825	0.3874278	0	0.4766554	0.3767168	0	2	59550923	59562634
sugp1	19.648583	23.086617	21.922309	34.033199	31.346803	26.607517	2	59583003	59597403
mau2	14.336524	16.025584	26.910144	18.073369	18.179623	24.119148	2	59600501	59615379
PRKAB2	5.1850428	2.1466369	1.6636756	1.3205121	3.6527576	0	2	59619446	59623198
ndufa13	0	0	0	0	0	0	2	59673089	59676041
GATAD2A	0	0.1037208	0	0	0.1008533	0	2	59673268	59681384
ptprsb	0.6877728	0.3203345	0.6206601	0.4926376	0.6229569	0.2410582	2	59697319	59715893
CABZ01100278.1	0	1.4205685	0	0	0	0	2	59810152	59822032
si:ch1073-391i24.1	0	0.4819224	1.4939881	0	0	0	2	59848058	59864896
5S_rRNA (2 598703	0	0	0	0	0	0	2	59870375	59870492
stk11	16.304242	12.109039	16.860622	26.260609	19.15813	25.0202	2	59873261	59895753
C2H19orf26 (2 of 2)	0	0	0.7107475	0	0	0	2	59908055	59915834
CABZ01030469.1	0	0	0	0	0	0	2	59926861	59928467
mir9-7	0	0	0	0	0	0	2	59942577	59942660
ftr65	4.5416433	2.9085363	3.2787767	4.8796296	2.313921	1.5918051	2	59976754	59984723
si:ch211-150h8.1	0	0	0	0	0	0	2	59989683	59990633
si:ch211-150h8.2	0	0	0	0	0	0	2	59997251	59997921
si:ch211-150h8.3	0	0.5519923	0	0	0	0.4153853	2	60000855	60004784
ftr30	0	0	0	0	0.5415455	0	2	60016649	60031424
ftr29	0.8888645	0	1.2834069	2.3769218	0	1.246156	2	60047931	60057000
ftr37	0.1823579	0.3397374	0.2633015	0.6269723	0.1651724	1.0226368	2	60071068	60171903
ftr32	1.0057195	0	0	0	0	0	2	60071223	60073794
ftr33	0	0	0	0.6782592	0	0	2	60081176	60091504
ftr34	0	0.2528761	0.3919655	0	0	0	2	60104663	60111068
ftr35	0	0.2582852	0	0.3177703	0.2511445	0.3887296	2	60119016	60129389
ftr36	0	0.25391	0.3935681	0.3123875	0	0	2	60138604	60153282
si:dkey-264b2.2	0	0	0	0	0	0	2	60148113	60150671
si:dkey-264b2.3	1.9203862	0	0.9242642	0	0	0	2	60161764	60162946
ftr38	0.3277064	0	0	0.375567	0.2968232	0	2	60193412	60202382
ftr39p	1.6656294	1.8101474	0.8016521	1.5907418	1.50866	2.7243446	2	60205149	60216447
BX537288.1	0	0	0	1.0674799	0.8436652	1.3058521	2	60234130	60235990

Zv9_scaffold3504

PTCHD3 (1 of 3)	0	0.9790405	0	0	0	0	Zv9_scaffold	554	997
rab18b	9.8242916	13.218764	12.214881	0	0	0	Zv9_scaffold	8949	22048
mib	18.719097	19.726793	23.205848	0	0	0	Zv9_scaffold	38978	65722
yme1l1b	6.1890431	7.686896	8.3404426	0	0	0	Zv9_scaffold	69385	82038

Zv9_scaffold3540

WAC	0	0	6.3564963	0	0	0	Zv9_scaffold	3299	7062
cables1	1.0548233	0.786065	0.8122828	0	0	0	Zv9_scaffold	23857	79366
gata6	10.104709	11.808616	9.815031	0	0	0	Zv9_scaffold	164734	175324
MIB1	13.837895	13.666691	20.70233	0	0	0	Zv9_scaffold	221356	278892
mir133a-1	0	0	0	0	0	0	Zv9_scaffold	268599	268697

Table S4. Summarized results of genomic PCR for the deleted genes in nn2002 allele.

predicted position by synteny	Feature ID	AB - AB1_S1_L001_R1_001 (paired) RNA-Seq - Expression values	AB - AB2_S2_L001_R1_001 (paired) RNA-Seq - Expression values	AB - AB3_S3_L001_R1_001 (paired) RNA-Seq - Expression values	1207 - 1207-1_S1_L001_R1_001 (paired) RNA-Seq - Expression values	1207 - 1207-2_S2_L001_R1_001 (paired) RNA-Seq - Expression values	1207 - 1207-3_S3_L001_R1_001 (paired) RNA-Seq - Expression values	contig	scaffold	LG	Chromosome region start	Chromosome region end	amplified in mibnn2002 or not (in black means results shown in Fig. 7; in red means results shown in supplementary Fig. 10)
	cldn1	4.42325923	8.9273643	13.837681	0	0	0			LG2	88773	91785	not amplified in nn2002 gPCR
	znfl2a	69.331429	74.932960	57.753310	0	0	0			LG2	161051	164976	not amplified in nn2002 gPCR
	genes not shown												
	foxc1a	16.336109	14.216155	18.000801	0	0	0			LG2	868215	870389	not amplified in nn2002 gPCR
	genes not show												
1	pth1ra	0	0.6168789	0	0	0	0			LG2	2092256	2240623	not amplified in nn2002 gPCR
2	crhr2	0	0	0	0	0	0			LG2	2681130	2785846	not amplified in nn2002 gPCR
3	aqp1a.1	1.98407249	1.4785509	2.291798	0	0	0			LG2	2888643	2900295	not amplified in nn2002 gPCR
4	thoc1	61.949203	64.445908	62.678010	0	0	0			LG2	2923616	2941632	not amplified in nn2003 gPCR
5	usp14	56.795291	63.368194	61.503865	0	0	0.29710804			LG2	2941647	2964335	not amplified in nn2002 gPCR
6	rock1	13.554978	13.430877	14.585248	0	0	0			LG2	2970496	3052905	not amplified in nn2002 gPCR
7	wacb	4.95123447	2.3060688	2.6808565	0	0	0	cabz0165389, cabz0165390		LG2	3070270	3086434	not amplified in nn2002 gPCR
8	mkxb	0	0	0	0	0	0		Zv9_NA916	no	(1686)	(9444)	not amplified in nn2002 gPCR
9	rab18b	9.82429156	13.218764	12.214881	0	0	0	cu694527	scaffold 3504	no	(8949)	(22048)	not amplified in nn2002 gPCR
10	PTCHD3 (3 of 3)	0	0	0	0	0	0		scaffold 3504	no	(61359675)	(61362524)	not amplified in nn2002 gPCR
11	yme1l1b	6.18904309	7.686896	8.3404426	0	0	0	cu681854	scaffold 3504	no	(69385)	(82038)	not amplified in nn2002 gPCR
12	mib	18.719097	19.726793	23.205848	0	0	0	cu681854, cabz01065400	scaffold 3504	no	(38978)	(65722)	not amplified in nn2002 gPCR
12	MIB1	13.837895	13.666691	20.702330	0	0	0	cabz01065398, BX842700	scaffold 3540	no	(221356)	(278892)	not amplified in nn2002 gPCR
13	gata6	10.104709	11.808616	9.815031	0	0	0	BX842700	scaffold 3540	no	(164734)	(175324)	not amplified in nn2002 gPCR
14	cables1	1.05482335	0.786065	0.8122828	0	0	0	BX842700, cabz0165391	scaffold 3540	no	(23857)	(79366)	not amplified in nn2002 gPCR
15	npc1^	13.884070	19.095981	20.854080	0	0	0			LG2	4310671	4353828	not amplified in nn2002 gPCR
16	egfra^	0.35688593	0.6648875	1.0305955	0	0	0			LG2	4190333	4307017	not amplified in nn2002 gPCR
	genes not shown												
	selt1a	33.694727	30.712074	25.633262	0	0	0			LG2	9473203	9485168	not amplified in nn2002 gPCR
	dvl3a	22.177302	22.825406	23.064216	0	0	0			LG2	9490950	9532978	not amplified in nn2002 gPCR
	ap2m1a	107.013837	96.070221	90.231648	120.536461	119.681194	120.825322			LG2	9578708	9607608	amplifiable by gPCR
	genes not shown												
20	anxa13l	0.648130	0.8049888	0.9358175	1.2379801	0.97841723	0			LG2	9610654	9631137	amplifiable by gPCR
19	apbb1ip	2.12954297	1.586957	2.2548448	0.65081522	2.18603472	0.99518086			LG24*	(6123408)	(6161601)	amplifiable by gPCR
18	abi1b	1.12497538	1.7028843	1.5228008	1.12811567	1.08264218	0.88716093			LG2	9651729	9704711	amplifiable by gPCR
17	acbd5b	0	0	0	0	0	0			LG2	9707575	9730294	amplifiable by gPCR
	genes not shown												
21	greb1l (2 1154822	5.16710144	11.732225	13.056112	9.99294113	14.0404565	18.1102256			LG2	11548229	11568413	amplifiable by gPCR
	greb1l (2 1155547	20.305225	20.669535	23.499861	27.4091044	21.9467422	19.0759553			LG2	11555478	11624584	amplifiable by gPCR
22	abhd3	0	0	0	0	0	0			LG2	11646751	11703651	amplifiable by gPCR

^ The relative position of npc1 and egfra is reverse according to Zv9.

* The position of this gene is located on LG24 according to Zv9.

Table S5. DAVID functional annotation results.

Annotation Cluster 1	Enrichment Score: 1.11	Count	P_Value	Bonferroni	
GOTERM_BP_FAT	somitogenesis	3	2.80E-02	1.00E+00	
GOTERM_BP_FAT	segmentation	3	3.30E-02	1.00E+00	
GOTERM_BP_FAT	anterior/posterior pattern formation	3	7.00E-02	1.00E+00	
GOTERM_BP_FAT	embryonic development ending in birth or egg hatching	3	8.60E-02	1.00E+00	
GOTERM_BP_FAT	chordate embryonic development	3	8.60E-02	1.00E+00	
GOTERM_BP_FAT	regionalization	3	1.50E-01	1.00E+00	
GOTERM_BP_FAT	pattern specification process	3	2.30E-01	1.00E+00	
Annotation Cluster 2	Enrichment Score: 1.03	Count	P_Value	Bonferroni	
KEGG_PATHWAY	Hedgehog signaling pathway	3	3.50E-02	8.30E-01	
KEGG_PATHWAY	Melanogenesis	3	1.20E-01	1.00E+00	
KEGG_PATHWAY	Wnt signaling pathway	3	1.90E-01	1.00E+00	
Annotation Cluster 3	Enrichment Score: 0.99	Count	P_Value	Bonferroni	
INTERPRO	Zinc finger, C2H2-type/integrase, DNA-binding	5	4.90E-02	1.00E+00	
SMART	ZnF_C2H2	5	1.20E-01	9.90E-01	
INTERPRO	Zinc finger, C2H2-like	5	1.30E-01	1.00E+00	
INTERPRO	Zinc finger, C2H2-type	5	1.40E-01	1.00E+00	
Annotation Cluster 4	Enrichment Score: 0.96	Count	P_Value	Bonferroni	
GOTERM_BP_FAT	protein amino acid phosphorylation	5	8.80E-02	1.00E+00	
SP_PIR_KEYWORDS	kinase	5	1.00E-01	1.00E+00	
GOTERM_MF_FAT	protein kinase activity	5	1.10E-01	1.00E+00	
INTERPRO	Protein kinase, core	5	1.10E-01	1.00E+00	
GOTERM_BP_FAT	phosphorylation	5	1.30E-01	1.00E+00	
Annotation Cluster 5	Enrichment Score: 0.85	Count	P_Value	Bonferroni	
INTERPRO	Serine/threonine protein kinase, active site	4	1.20E-01	1.00E+00	
GOTERM_MF_FAT	protein serine/threonine kinase activity	4	1.30E-01	1.00E+00	
INTERPRO	Serine/threonine protein kinase-related	4	1.90E-01	1.00E+00	
Annotation Cluster 6	Enrichment Score: 0.84	Count	P_Value	Bonferroni	
SMART	EGF	3	1.20E-01	9.90E-01	
INTERPRO	EGF-like	3	1.20E-01	1.00E+00	
INTERPRO	EGF-like region, conserved site	3	2.10E-01	1.00E+00	
Annotation Cluster 7	Enrichment Score: 0.74	Count	P_Value	Bonferroni	
GOTERM_MF_FAT	ribonucleotide binding	9	1.70E-01	1.00E+00	
GOTERM_MF_FAT	purine ribonucleotide binding	9	1.70E-01	1.00E+00	
GOTERM_MF_FAT	purine nucleotide binding	9	2.00E-01	1.00E+00	

Cluster 1	
1517339	hypothetical protein LOC100148408
1537586	mind bomb
1526949	wingless-type MMTV integration site family, member 3 like
Cluster2	
1546713	protein kinase, cAMP-dependent, catalytic, beta
1526949	wingless-type MMTV integration site family, member 3 like
1526580	wingless-type MMTV integration site family, member 9A
Cluster 3	
1538660	si:ch211-241e1.5
1521138	zgc:113452
1533153	zgc:153115
1533539	zgc:171570
1539599	zinc finger-like gene 2a
Cluster 4	
1521068	epidermal growth factor receptor
1518006	myosin light chain kinase family, member 4
1546713	protein kinase, cAMP-dependent, catalytic, beta
1519322	receptor (TNFRSF)-interacting serine-threonine kinase 1, like
1518369	receptor-interacting serine-threonine kinase 2
Cluster 5	
1518006	myosin light chain kinase family, member 4
1546713	protein kinase, cAMP-dependent, catalytic, beta
1519322	receptor (TNFRSF)-interacting serine-threonine kinase 1, like
1518369	receptor-interacting serine-threonine kinase 2
Cluster 6	
1525846	complement component 8, alpha polypeptide
1523183	complement component 8, beta polypeptide
1532880	protein C (inactivator of coagulation factors Va and VIIIa)
Cluster 7	
1546722	ADP-ribosylation factor 1
1532072	RAB18B, member RAS oncogene family
1521068	epidermal growth factor receptor
1547472	eukaryotic translation initiation factor 4A, isoform 2
1518006	myosin light chain kinase family, member 4
1546713	protein kinase, cAMP-dependent, catalytic, beta

Annotation Cluster 8	Enrichment Score: 0.41	Count	P_Value	Bonferroni
SP_PIR_KEYWORDS	gtp-binding	3	3.00E-01	1.00E+00
GOTERM_MF_FAT	GTP binding	3	4.30E-01	1.00E+00
GOTERM_MF_FAT	guanyl ribonucleotide binding	3	4.30E-01	1.00E+00
GOTERM_MF_FAT	guanyl nucleotide binding	3	4.30E-01	1.00E+00

Annotation Cluster 9	Enrichment Score: 0.36	Count	P_Value	Bonferroni
GOTERM_MF_FAT	ATP binding	6	4.00E-01	1.00E+00
GOTERM_MF_FAT	adenyl ribonucleotide binding	6	4.10E-01	1.00E+00
GOTERM_MF_FAT	adenyl nucleotide binding	6	4.50E-01	1.00E+00
GOTERM_MF_FAT	purine nucleoside binding	6	4.50E-01	1.00E+00
GOTERM_MF_FAT	nucleoside binding	6	4.50E-01	1.00E+00

Annotation Cluster 10	Enrichment Score: 0.26	Count	P_Value	Bonferroni
GOTERM_MF_FAT	metal ion binding	11	5.30E-01	1.00E+00
GOTERM_MF_FAT	cation binding	11	5.50E-01	1.00E+00
GOTERM_MF_FAT	ion binding	11	5.50E-01	1.00E+00

1519322	receptor (TNFRSF)-interacting serine-threonine kinase 1, like
1518369	receptor-interacting serine-threonine kinase 2
1538421	zgc:112335

Cluster 8

1546722	ADP-ribosylation factor 1
1532072	RAB18B, member RAS oncogene family
1538421	zgc:112335

Cluster 9

1521068	epidermal growth factor receptor
1547472	eukaryotic translation initiation factor 4A, isoform 2
1518006	myosin light chain kinase family, member 4
1546713	protein kinase, cAMP-dependent, catalytic, beta
1519322	receptor (TNFRSF)-interacting serine-threonine kinase 1, like
1518369	receptor-interacting serine-threonine kinase 2

Cluster 10

1537586	mind bomb
1523243	phosphotriesterase related
1532880	protein C (inactivator of coagulation factors Va and VIIIa)
1516098	ring finger and CCCH-type zinc finger domains 1
1538660	si:ch211-241e1.5
1516089	ubiquitin specific peptidase 33
1521138	zgc:113452
1533153	zgc:153115
1533539	zgc:171570
1540346	zgc:66286
1539599	zinc finger-like gene 2a

Table S6. List of primers used in this article.

primers for probe synthesis		
dystrophin (dmd)	sense	GACCACCCAAAGATGGCAGA
dystrophin (dmd)	T7 antisense	TAATACGACTCACTATAGGGCTCCTTGGCTGTGAGGGAAG
fgf8a	sense	GGACTTTACACATTTGAGCTGG
fgf8a	T7 antisense	TAATACGACTCACTATAGGAATCAAAGCAGAACGAGAGAGG
foxc1a	Sp6 sense	GATTTAGGTGACACTATAGCAGTCTTCTTGACGACTGTTCTTC
foxc1a	T7 antisense	TAATACGACTCACTATAGGTAATCGAAATACTGGTTTGGTC
p53	Sp6 sense	GATTTAGGTGACACTATAGATGGCGCAAAACGACAGCCA
p53	T7 antisense	TAATACGACTCACTATAGGGTTAATCAGAGTCGCTTCTTCC
papc	sense	GATCACTCGCCGCAATTCAC
papc	T7 antisense	TAATACGACTCACTATAGGGCAGCAACAGCACACAACCTC
tcf15	sense	GCTAGTGCTTGACGACAA
tcf15	T7 antisense	TAATACGACTCACTATAGGGCTCTCCCTGAGTGTCACT
primers for real-time RT-PCR		
mib/herc2	sense	TGACCACCGGCAGGAATAAC
mib/herc2	antisense	TGATTCCTGTAGGCGCACTG
mib zinc finger	sense	CAGTGCGCCTACAGGAATCA
mib zinc finger	antisense	TTCGACTTGCGACGAGACTC
mib/her2 -2	sense	GAGTCTCGTCGCAAGTCGAA
mib/her2 -2	antisense	CCTCCTTTGGCATCTTGCAC
mib ank	sense	AGACGCAGGAGTCTGGAGAC
mib ank	antisense	CTTGTTGACAGCGATGTGCA
mib ring finger 2,3	sense	GCAAGGAACAGGTTCAGTCC
mib ring finger 2,3	antisense	GTAAAGCAGGATTCGGCGCT
Primers for genomic PCR		
fih	sense	TGTAGGAGCCTGTTGTACTGA
fih	antisense	GAGTTTGTGGACAAGATGCA
vhl	sense	TAAGGGCTTAGCGCATGTTC
vhl	antisense	CGAGTTAAACGCGTAGATAG
mib exon1 GTP2F GTP4R	sense	TAGCCTAGACTCGCTAACTG
mib exon1 GTP2F GTP4R	antisense	GGTTCAGCCAGCTTTGAGAA
mib exon2 GTP5F GTP1R	sense	GGGACCTTTAAAGAGCCAAC
mib exon2 GTP5F GTP1R	antisense	GAGCAGACTTATCCACAAGG
mib exon8 and 9	sense	GCATTCTTGCCCTTTCTGAG
mib exon8 and 9	antisense	CTTGAAACATCCAGGCAGGT

mib exon 20 and 21	sense	TGGGGTAAGCGAAAACATTC
mib exon 20 and 21	antisense	TCCCATCTGCACACTGTCAT
mib exon 22 (ta52b)	sense	GGTGTGTCTGGATCGTCTGA
mib exon 22 (ta52b)	antisense	GACAAGGAGAGCCTTGCAGA
nn2000 genotyping	sense	CTGATGAAAAAGTGTGTGCAGAG
nn2000 genotyping	antisense	AAGGCGGAGAGAGAGGAAAG
tfi91 genotyping (tfi91)	sense	GCTCGTAAATGACCACCGGC
tfi91 genotyping (tfi91)	antisense	CAACTGCAGTATTAGAAACGCG
foxc1a	sense	TATCAGTTCATCATGGAGCG
foxc1a	antisense	TCATGGCGTCCTTCTTTTTA
pth1ra	sense	TCCATGTTTATTTTCTACAG
pth1ra	antisense	CTGGACTGAGTTAAAGAG
crhr2	sense	TTCTTGTGTTTGTGTGTTTG
crhr2	antisense	CTGAAAAGACTGAAGAAAC
aqp1a.1	sense	TGCTTTTATTTGTGTGCAG
aqp1a.1	antisense	GGCTGTCAGATGTCC
thoc1	sense	TTGCTGAAAGAAATCCCTC
thoc1	antisense	CCTCTGTGTTCAGGATGTG
usp14	sense	TGCATATGTCTGCGTC
usp14	antisense	CCAGGCTTCTTATTCGG
rock1	sense	CTTTATTTTATTTGTGTCTTCCAG
rock1	antisense	CTGTGAATGAAGCCCATG
wacb	sense	GTTTGTGTTGTTTTGTTTTCTAG
wacb	antisense	GCCTTGAACATGCTTAATGA
mkxb	sense	ATGAACACGGCAGTC
mkxb	antisense	GATGGAGCTCAAAACGTAC
ptchd3ex	sense	TGGCTCTGAATGGCAGAAGG
ptchd3ex	antisense	CCCTCCAACACAGCAGAGAG
gata6	sense	TTCTGCGTGTGTCAG
gata6	antisense	ATGCGCTTCTGAGGTT
cables1	sense	TCTGTCAATCTCTTTGCAG
cables1	antisense	CTGTGTCAAGGCTACTC
npc1	sense	TCTGATGGCACAGATTTAATAG
npc1	antisense	GGAAAAAAGCACACACGA
egfra	sense	TGATCATGAAGTGTTGGTGCT
egfra	antisense	TGAGAAATGCCTTGCTCTGTT

acbd5b	sense	GCATGGAAAGACTTGGGAAA
acbd5b	antisense	AATGGGTCAAGAGCATCCAA
apbb1ip	sense	ATTTGTGGTTTGTTGTGATAG
apbb1ip	antisense	CAGTCTGTAAGTCAGGGT
anxa13l	sense	GCAAAAAGTTCTGGGACTGC
anxa13l	antisense	TCCTCCAACTCCTCCAACAA
greb1la	sense	ATCATGGGAAATTCATACGC
greb1la	antisense	GGACAAATAGCCTTGCTTAC
greb1l1b	sense	TCAAGTCATCTGTGCACA
greb1l1b	antisense	GAAAATGTATTGGAACACCAAC
abhd3	sense	CGAAACCCTGGGTCAACTAC
abhd3	antisense	GCACGATCTGGCACTGTGTA
cldn1	sense	GTCTTTCGTGGGCATGAAGT
cldn1	antisense	GAGCGCTGTCATGTGTGTTT
znfl2a	sense	GGAGAATGAAGAGCCGAGTG
znfl2a	antisense	TGTGATCTCGAAGGCTTCCT
selt1a	sense	GGGCCTTATGTCTTCACAGC
selt1a	antisense	TGTGCTCCACTAAAGGCAGTT
dvl3a	sense	GTCACCCTTTTGGACCTGAA
dvl3a	antisense	GGAAGATCATGGCAGTCGAT
ap2m1a	sense	TCAACGCTGCTATGGTGTTC
ap2m1a	antisense	TCGCTGGGTCACTGGTATAA
abi1b	sense	CAAAGCCTACACCACCCAGT
abi1b	antisense	AATTTGCCCCTGCATTTTT
rab18b	sense	TCGTCATTTCACCTTTGCAC
rab18b	antisense	ATGGTTCTGGATGCTGCTTT
mib	sense	AACCGAGTGATGATGGAAGG
mib	antisense	TTAGCTCTGCAGCCTCACCT
yme1l1b	sense	CCAGCTGAGTCACCTCATCA
yme1l1b	antisense	AAGTGGCCGGAGAGTGTAAA

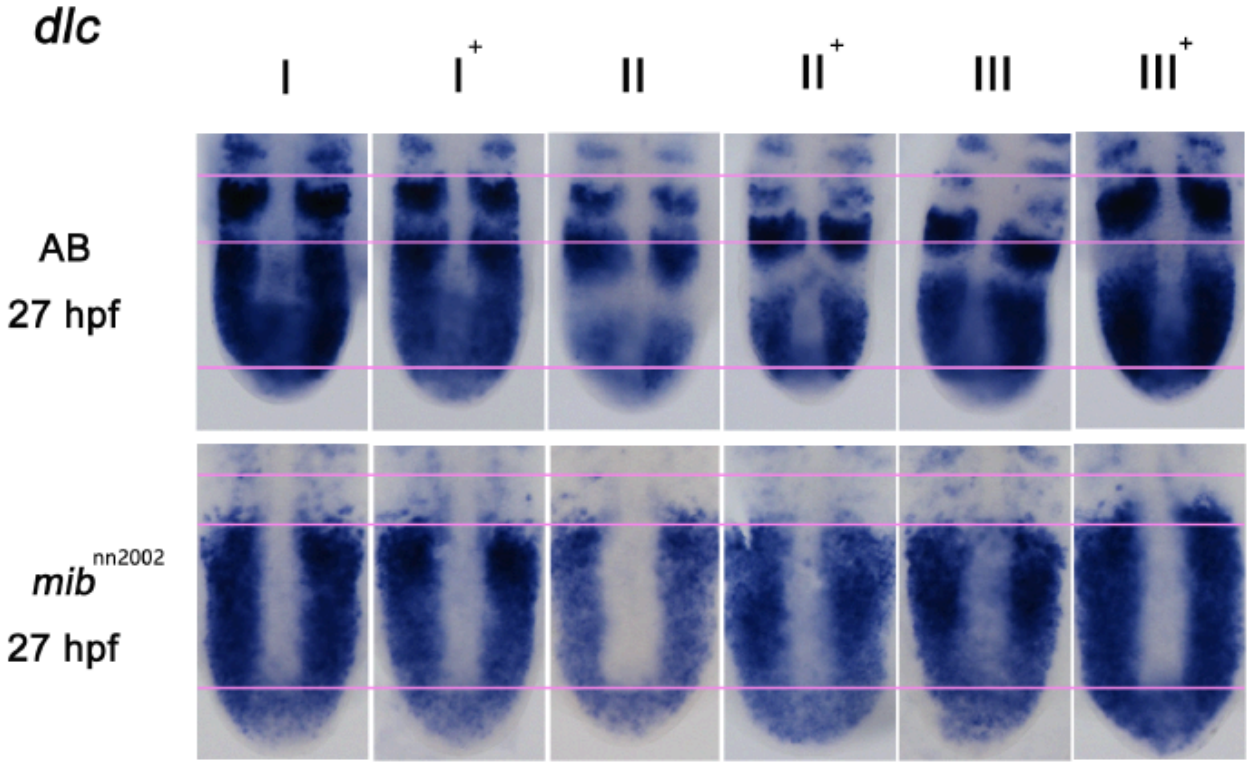

Figure S1. Cold-sensitive *dlc* cycling expression pattern in *mib*^{nn2002} mutants.
Embryos were raised at 22 °C before the desired stage (siblings are with 16 somites or at 27 hpf). Typical salt-and-pepper pattern shown in previous Notch-related mutants was observed in *mib*^{nn2002} mutants. Although *dlc* was still cyclically expressed in the PSM of *mib*^{nn2002} mutants, the sharp-striped pattern of *dlc* was not maintained in the region where somites are about to form.

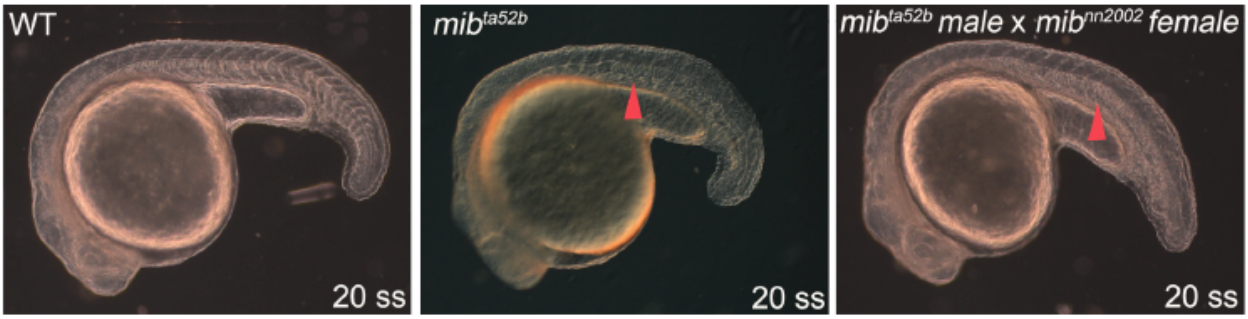

Figure S2. Somite phenotypes of homozygotes (*mib*^{ta52b}/*mib*^{ta52b}) and transheterozygotes (*mib*^{ta52b}/ *mib*^{nn2002}). Embryos are in lateral view with head to left. While 22 visible somites were observed in the WT embryos (left panel) at 22 ss, only 3 and 7 visible somites were observed in *mib*^{ta52b} homozygotes (middle panel) and transheterozygotes (*mib*^{ta52b}♂ x *mib*^{nn2002}♀, right panel), respectively.

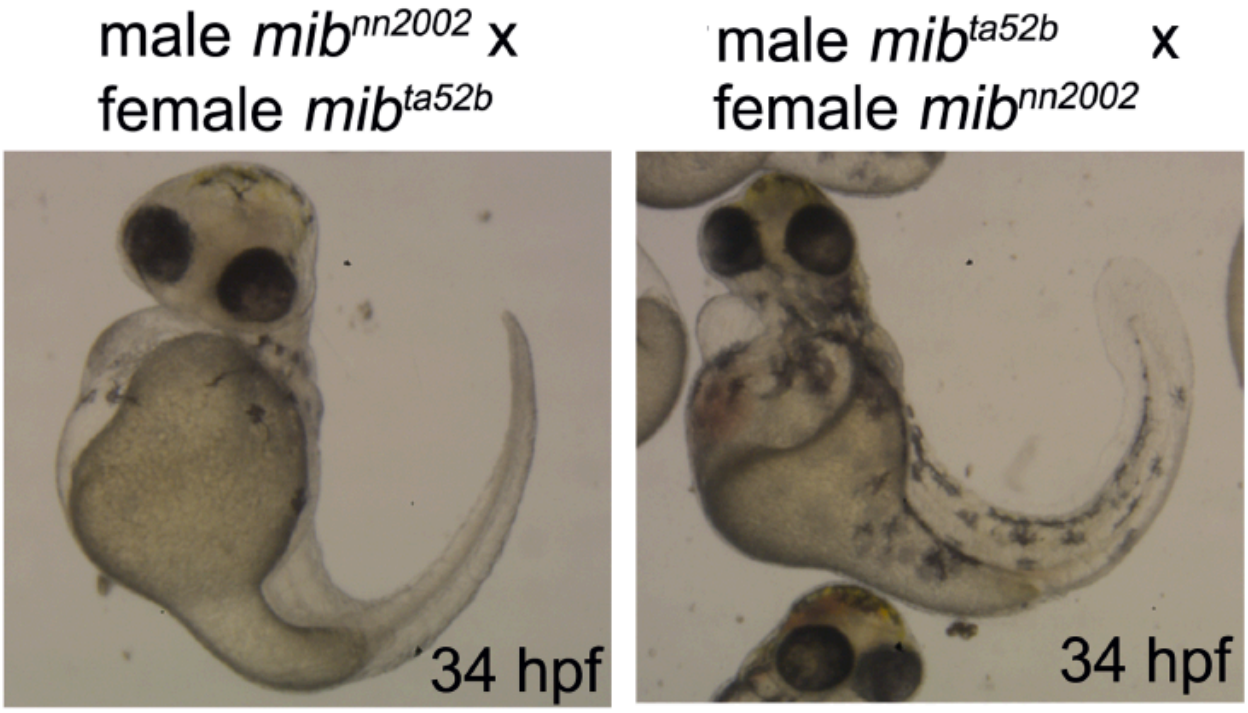

Figure S3. The maternal effect on phenotypes of transheterozygotes (*mib*^{ta52b}/*mib*^{nn2002}) at 34 hpf. The transheterozygotes have typical *mib* phenotype at 34 hpf, including less pigmentation and curly tail. Note that the transheterozygous embryos from incrosses of male *mib*^{nn2002} carrier and female *mib*^{ta52b} carrier (left) showed a more severe pigmentation phenotype (typical white tail phenotype of *ta52b* allele[17]) than those from incrosses of male *mib*^{ta52b} carrier and female *mib*^{nn2002} carrier (right).

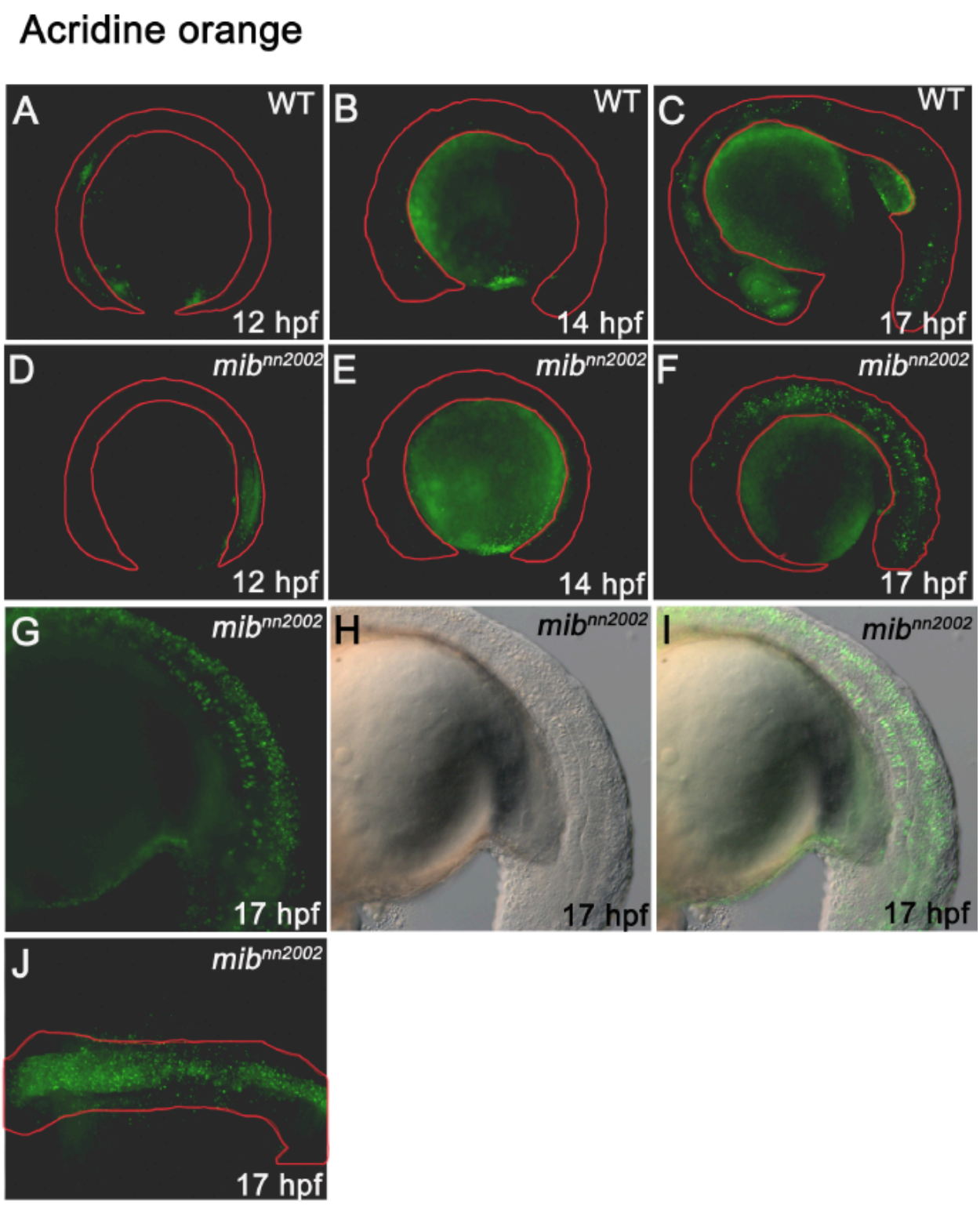

Figure S4. Cell death in *mib*^{nn2002} mutants.
All the embryos are treated with acridine orange. A–C are wt embryos; D–J are *mib*^{nn2002} homozygotes. A and D are at 12 hpf; B and E are at 14 hpf; C and F–J are at 17 hpf. A–I are lateral views with head toward left; J is dorsal view with head toward left. The contours of embryos are outlined by the red lines.
(F) The amount of cell death is highly increased in 17 hpf *mib*^{nn2002} homozygotes. Cell death was mainly located around (G–I) neural tube and notochord.

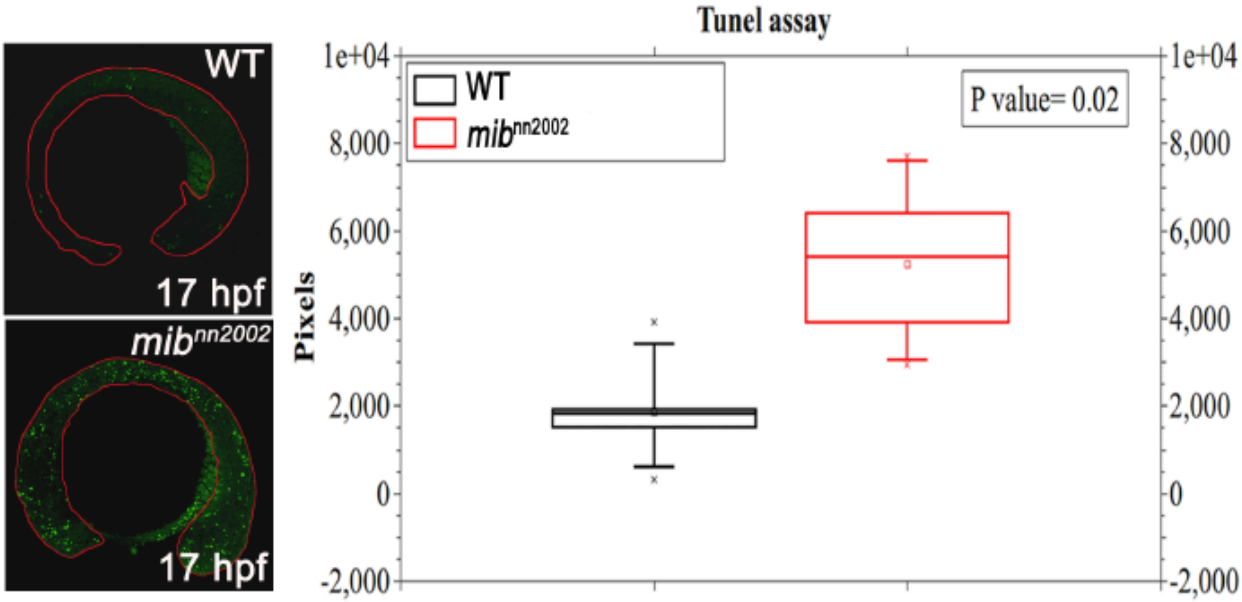

Figure S5. Apoptosis is highly increased in *mib*^{nn2002} mutants.
TUNEL assay was employed to study the apoptosis in wt embryos and *mib*^{nn2002} homozygotes. The lateral view of embryos is shown with head to the left. Apoptosis is increased in *mib*^{nn2002} homozygotes at 17 hpf. Analyzed and calculated by Image J, the fluorescent signal increases by 2~3-fold in *mib*^{nn2002} homozygous embryos.

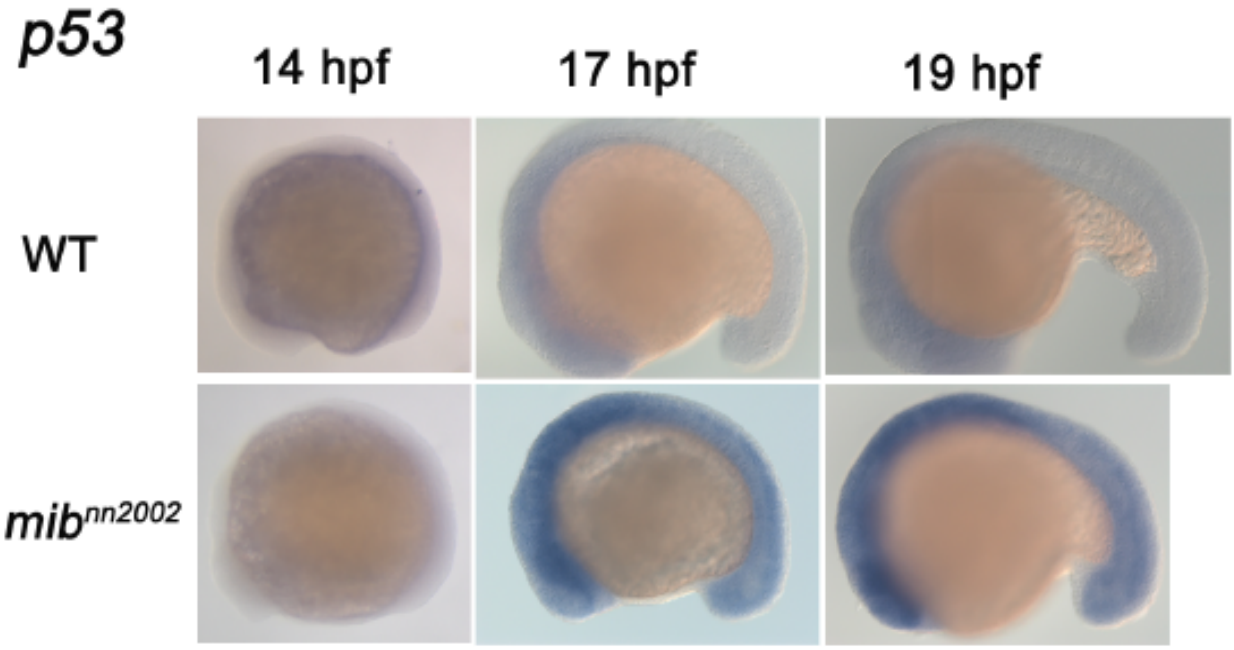

Figure S6. *p53* is highly up-regulated in *mib*^{nn2002} mutants.
p53 WISH was performed in the wt embryos and *mib*^{nn2002} homozygotes. Embryos are shown in lateral views with head to the left. The staining of *p53* was highly up-regulated in *mib*^{nn2002} mutants compared to wt embryos.

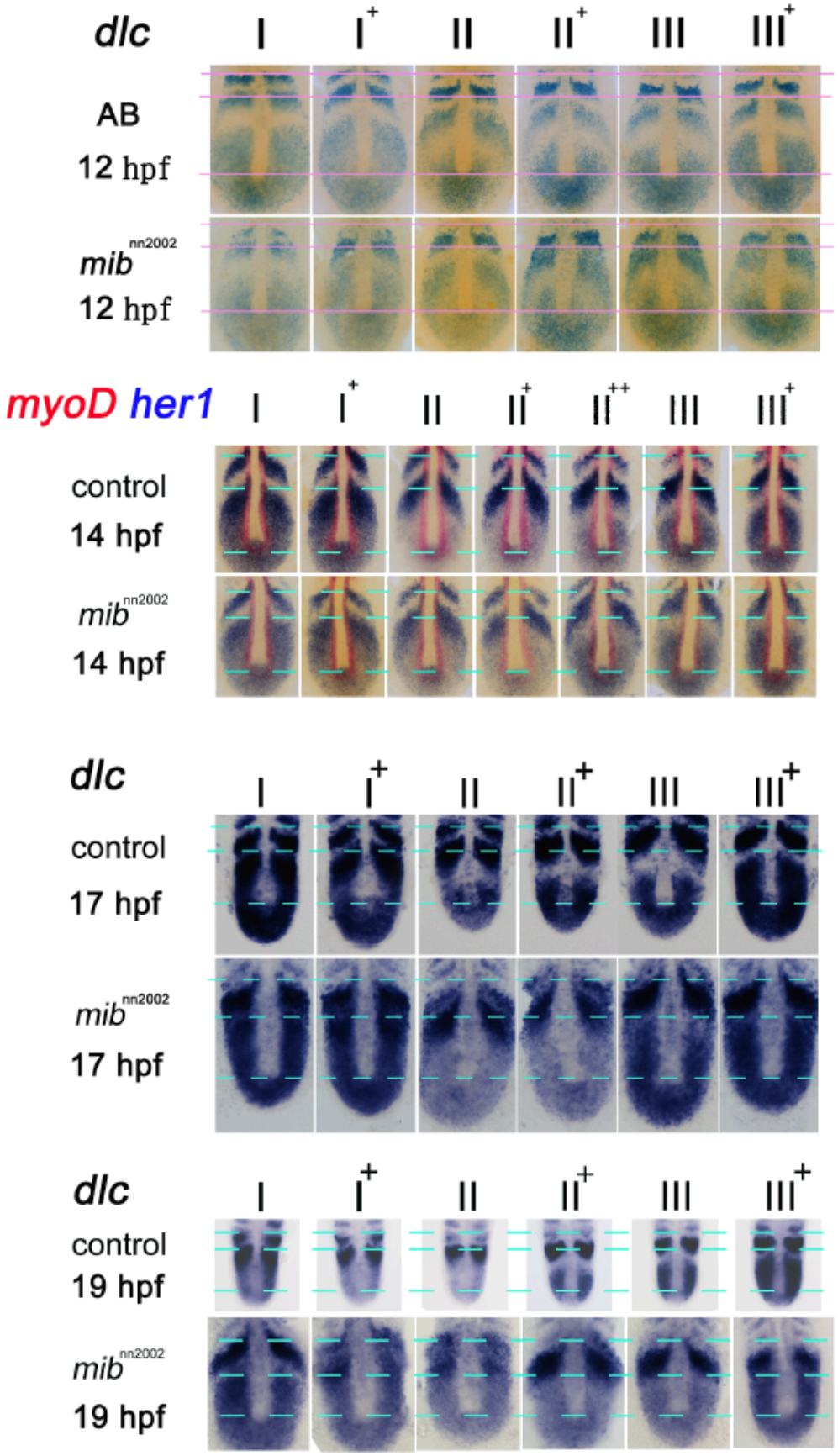

Figure S7. The expression of *dlc* in *mib*^{nn2002} mutants during the stages of 12 hpf, 14 hpf, 17 hpf and 19 hpf at 28.5 °C.
dlc WISH was performed in the wt embryos and *mib*^{nn2002} homozygotes. Embryos are flat-mounted with head to the top. The cyclically *dlc* expression was detected in both wt embryos and mutants. No salt-and-pepper pattern was observed.

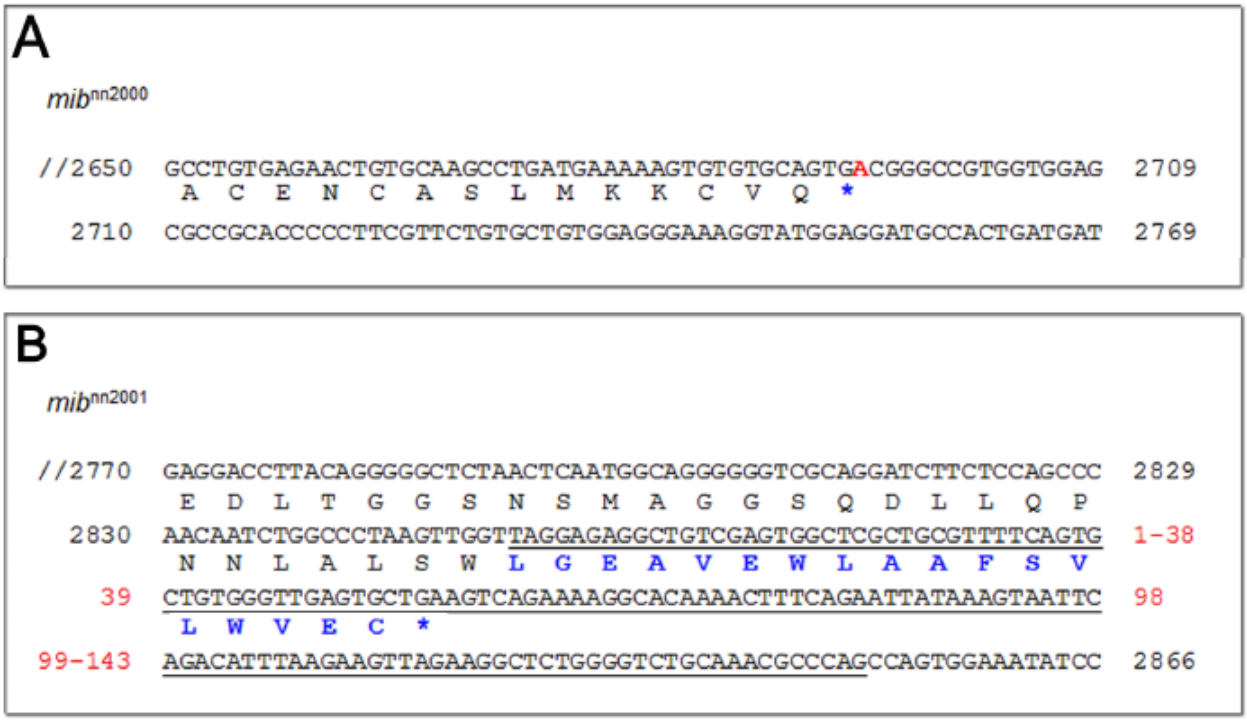

Figure S8. The mutations of *mib*^{nn2000} *and mib*^{nn2001} alleles.
This panel shows the mutations of *mib*^{nn2000} and *mib*^{nn2001} in nucleotide sequences and amino acids. *mib*^{nn2000} mutation is a nonsense point mutation that leads to a truncated protein without ring finger domain 3 (RF3). *mib*^{nn2001} is a nonsense mutation caused by a failure to splice a 143 bp long intron (the underlined nucleotides) out from *mib* mRNA. The stop coden is marked by blue asterisks.

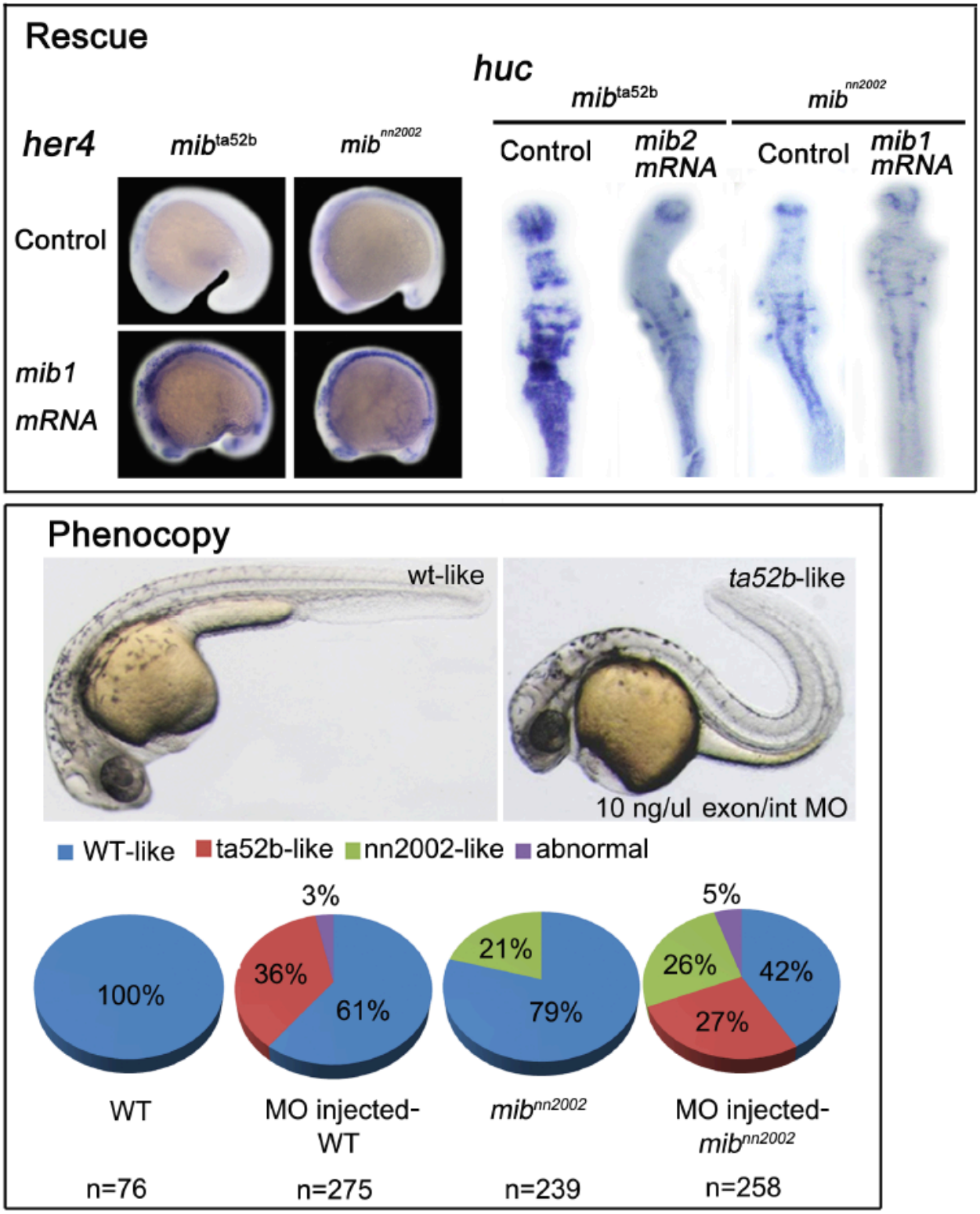

Figure S9. The rescue and phenocopy of *mib*^{nn2002} phenotypes.
In rescue experiments, *her4* WISH was carried out in the *mib* mRNA (1 ng/μl) injected *mib*^{ta52b} and *mib*^{nn2002} embryos. 19 hpf embryos in lateral views with head toward left were shown. The expression of *her4* was rescued (increased) by *mib* mRNA in *mib*^{ta52b} and *mib*^{nn2002} homozygotes. *huc* WISH was carried out in the *mib2* mRNA (1 ng/μl) injected *mib*^{ta52b} and *mib* mRNA (1 ng/μl) injected *mib*^{nn2002} embryos. 19 hpf embryos in flat mount with head toward top were shown. *huc* was rescued (decreased) by *mib2* mRNA in *mib*^{ta52b} and *mib* mRNA in *mib*^{nn2002} homozygotes.
In phenocopy experiments, *mib* morpholino injected-wt and -*mib*^{nn2002} embryos were examined. Morpholino can successfully convert 36% of wt and 27% *mib*^{nn2002} siblings into embryos that exhibit typical *mib* phenotypes (ta52b-like). However, the morpholino failed to convert the *mib*^{nn2002} homozygous embryos into embryos having typical *mib* phenotypes. The ratio of embryos carried *mib*^{nn2002} phenotype is 21% without injection and 26% with injection. The ratio of embryos that exhibited *mib*^{nn2002} phenotypes was not reduced with the injection of *mib* morpholino.

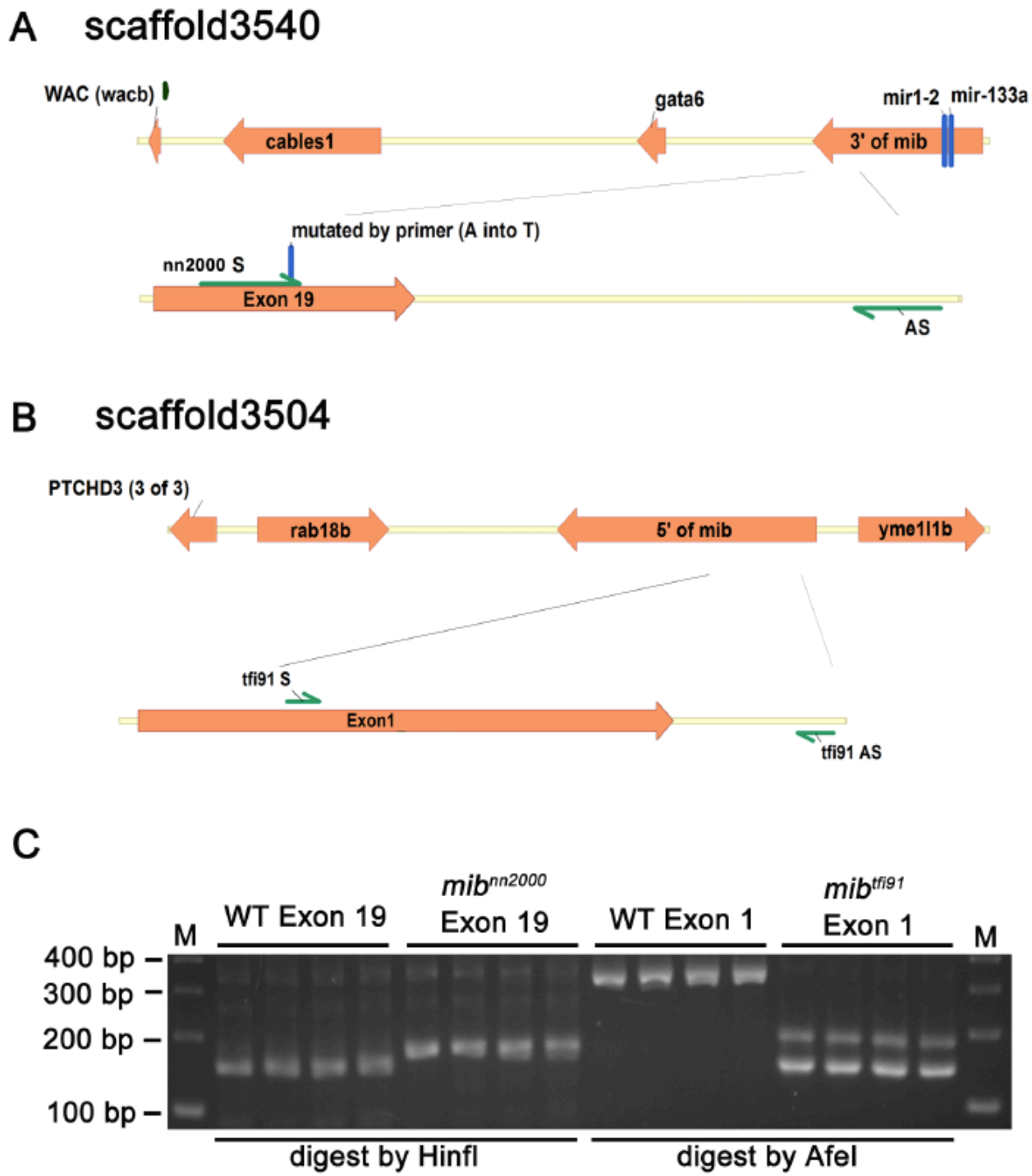

Figure S10. The continuity test of scaffold 3504 and scaffold 3540.
Panels A and B illustrate the design of (A) *mib*^{nn2000} and (B) *mib*^{tfi91} genotyping primers related to scaffolds 3540 and 3504, respectively. The *mib*^{nn2000} genotyping PCR products of wt and *mib*^{nn2000} are 173 bp long. Hinf1 cutting site was created by using CTGATGAAAAAGTGTGTGCAG**A**G instead of CTGATGAAAAAGTGTGTGCAG**T**G. Only the wt PCR products will be recognized and digested into fragments of 152 bp and 21 bp long. The *mib*^{tfi91} genotyping PCR products of wt and *mib*^{tf91} are 335 bp long. Only the *mib*^{tfi91} PCR products will be recognized and digested by AfeI into fragments of 189 bp and 146 bp long. The genotyping results were shown in panel C. The digested PCR products were analyzed on 3% agarose gel. The digested PCR products of *mib*^{nn2000} and *mib*^{tfi91} can be easily distinguished from those of wt with the expected size mentioned above.

Supplementary File 11

>Zv9_scaffold3504 dna:scaffold scaffold:Zv9:Zv9_scaffold3504:1:82506:1 (encode 5' of mib genomic sequence)

Loci (4 total)

PTCHD3 (3 of 3) Start: 18 End: 4706 (Complementary)

rab18b Start: 8883 End: 22055

5' of *mib* Start: 38977 End: 65063 (Complementary)

yme1l1b Start: 69307 End: 82031

#Genomic sequence was compared with mib mRNA sequence (NM_173286.3)

Yellow color: Indicate the site of CpG islet

Red color: Indicate the site of Exons

Blue color: Indicate the site of introns

Green color: Indicate the site of polymorphism

ATG: indicate translation start site

A← : The variation on mRNA is A

→G: The variation on chromosome is G

CpG islet CTGCTGTTTACAGACCCGAGCGTGCGTTTGTTTCGAGCATGAAGGACTGCGCTTTCTTCACCTACCGCCA

TTCATTCAGGAATTATATCTGAACTCGAGTAAACCAGAAGGTTTTAATCAAAGTGCTTCAGCTGGACTGT

TTTTGCAAACGCTTTTCCTGCACAGACATTCTGAACCGCGTCGCGCGAAGTTGGACCATCTGTTGAACGT

TTGCGAGCGCACCGCAAAGTTCTCAACGCGTTTATTTTTTTAACATTTAATCGCAAAACAACTGTTGTTG

TTTCCTAAAGCGAACGTTTTTGTTGCGTTTATGCTAACGCCAAGCAACTTTGGAGAGGTTAGCTATAGCT

GGTTAGCCTAGACTCGCTAACTGGCCTCTGCTAAAAGGGCCGTTAGTGACCTAAACGTATTGTTTTTCTA

CATTTATTCATAACGTGTAATAATAACAACTACAAAGTTTGTTTTCTAATAATCTCTGTACGTTATATTT

CACTAAAACAGTTGCATTTATGAGTCGACAACTTGAGCAGTTGTGAAAAGCATTAGCACTCCAAAAAAAC

TTCAGTTAAACATTTTCCTTAAGGAATTAACGTAAGCATTCTCTCTGTGTTTTGCTATACAGCAAGAGTG

Mib **Exon 1** ACCTCCATCATTGGCCATATGTAAGACGAACCAGTCCTTTTAAAACCCAATATTCTCAAAGCTGGCTGAA

CCGCCAGCTAAAAGTAACTTAAATCGCAACTTTTGCTCGTAA**ATG**ACCACCGGCAGGAATAACCGAGTGA

TGATGGAAGGAGTGGGTGCTCGAGTTATCCGCGGGCCTGACTGGAAGTGGGGGAAGCAGGACGGCGGAGA

AGGGCATGTGGGCACCGTCAGGAGCTTCGAGAGCCCGGAGGAGGTGGTGGTGGTGTGGGATAACGGCACC

GCCGCCAATTACCGCTGCTCCGGGGCTTATGATGTGAGGATATTGGACAGTGCGCCTACAGGTGAGGCTG A←→G

CAGAGCTAATTGACTTCATCTCTCACCTTATCTAAACATCAGCTAACTAATTTATTAGAATAAAACACGC

GTTTCTAATACTGCAGTTGAGGTGTATTTGTATTTTGTGAACTGTATAATGTATAATAAAGTGCTAGTTC

ACACTTTAATAATAATTGCAAATTTAATCCATTGCCATTGTCATTCATTCAGTCATTTTTAAAGTCCCTT

TATTAATCTGGGGTCGCCACAGCGAAATGAACCGCCAACTTATCCAGCAAGTTTTTACGCAGCGGATGCC

CTTCCAGCCGCAACCCATCTCTGGGAAACATCCACACACACACTCATACACTATGGACAATTTAGCCTAC

CCAATTCACTTATACCGCATGTCTTTGGACTATGGGGGAAACCAGAGGAAACCCACACGAAGGCAGGGAG

AACATGCAAACTCCACACAGAAACGCCAACTGAGCCGAGGTTCGAACCAGCGACCTTCTTGCTGTGAGGC

GACAACCTACTGCGCCACTGCCATCCATCTGCGGTCCATCAAATATAAATTTTACATAACATAATTAAAT

GTAATTTGAGGATCCTTCCACTGAAATTTTCTTCACGCAAAATGTTTGCTTCAAATGCGATCTTAAATCA

GTATGAATGGTTTCATCCAAGTCCACCACTTTTCTGATGTGAATATTGCATTTTATGCTTTATGTAATGC

TTAGAGTGCTAGTTCATCCTAAAATCACATGTAATTGAGCGTCACATGAAATGTTTGAAATAAATGTCTT

ATGCATTCGTAATGACATGGGGTAAGTAAATGTTAACTTATGTTTATCTCAAATATTTCATGTGATGCTC

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TTCTTGCTCATGATTGAGTTAAAGTCTAATATTTTACAGTCTATCAAAGTCTATTAATGAAATATGAGCT

CAACTCTTCAGAATACTTTGATTAAACTGCACAATTCATATAGATTTAGTTTTTTTTTTTATCTCTTTAA

AAAGTTTTGGATGAACTGACTATGCAACAAATATTAGATTTCTCACACACTCACGCACAAAAAGTCTGCA

TTGTGATATGATATATGTACAGTAAGAATAATGTTTTGTTTACCCCCACACACACACACACACACACACA

TACAAAATAAGAAAACTCTCATTATTATTCCTCTGTTTCCAAACCTGATTGAGTTTCTTTTTTCCATTGA

CTTAAATTGATATTTTGAAGAATGTTGAAAACTGCTAGCAATTGGCTTTATTTTTTTCTCTACCATGAAT

TTCTGTGGGTACCATTTTCCAAAATTCTTCAAAACTTCTATTTTTTTTTAATGTTCAATGTGACAAAATAG

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TGCTCCAAACCCGTGGCGAAATTCGCGTTTAGAAGATATAAAACCGATATCAACATGTCATTTTATTCAC

GTCACCTCATACTACAGTTTCTCATCAAATCATAACCAATCGAATGCTCTCTAGTATCTGACATGCCCCG

CCACCTTCAAGATGCTTCTCTTTGGCTGCGTCCAAAACCGCCTACTACTCAGTACAGCATTTGAATTTAA

ACGTACTACTCGGTCTAGAGCTGCACGATTCTGGCTAAAATGAGAATCGCGATTTTTTTTTTTTGCTTAA

AATAAAGATCACGATATTCTCACGATTCTGTAGATGTAAATTAAAGGTATGGTAAAAACAAACATATGGC

ACAACATCGATAATAATATTATGTGTAGGTCTACTGGTGTCTATAAATAATTCTATTCTACTTATAATAA

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CGCATGCGCCCTCGCTGTGATAACAGCTCATGGTAAGTAGCTCATGTCACGTGTCATTTCCCGTTCGCGA

AAACATAATTATATTAAGAGAAAAATGACATTTTTAGGTGAATTATACCTTATAAATACAGGTGTCAATG

TCACTGAGCAACGTGTGTGAAACAATGAAAAGACTTGTGCAGCCGCCTTTTCTTCTCTCCTGAACATGAA

AATATGATTGATAGAATCGTAGAAATGCTGGATTAAGATCGTCTGGGGGGTCGAATCGAGATCGCAATCT

TTTAACGATTAATTGTGCAGCTCTAACTCGGCCGTTAGAAAAGTACAATCTATACAGTATGAATGTGAAA

AGTATGAATGGAATTTGGACGAACTACATCCTGACCTACCTGCGTCAGTTGCGTCGCGTCAGTCCCATTC

ATGTTTTGGTTGAGATCGCGTCAAACATCGAATAAAAATGCACATTTCAAAGCACTTAATGGGACCTTTA

Mib **exon 2** AAGAGCCAACTTAAGTTTAAACAGGTGGAAGTCAACCCATTAAATATGAATCTAATTGCAATGTTCCAGG

AATCAAGCATGATGGCACCATGTGTGACACCTGTCGGCAGCAGCCCATCATTGGAATCCGATGGAAATGT

GCAGAGTGCACCAACTACGACCTCTGTACCACCTGTTACCATGGCGACAAGCACCACCTGCGCCACAGGT

TTTACCGCATCACCACCCCTGGCAGTGAAAGGTGAGTGTGGCGTTTCTCCATGTGCTCTTCACTCCTTGT

GGATAAGTCTGCTCTGGCCGGTTTCACACAGCTATGGACCCTTTTCACATTTCTGGGGTTTTCTGAAGTC

GTGTTAGTTTGGTAAACTTAAATGTTTGTGCACACCGGGACGCTTTTTGCTTGCGTTTACCGTCAACGTT

TAACACCTCGTGACTAAATAAAGGGCGCCAATGTGACCGTACACACCAACGCGCAAAACGGCAAGCGCAA

AAGCGTCATTTTTTTAAGAAACGCTTCATGCTCGTTTTTTTGTTTTGATACACTGCGTCAAAATCTTCTC

CACCAATCAGATTGGCACTTTTGTTCACGTGCACGGAGCTGTTAAAGTTACAGTGAACAACACTTGGAGG

CGCTCAAGCGCAGCTGTCAATGCAAGCGCACATAGAAGAAGACGCCCAGAGGCGATATGAACATTCAGCT

GCTTATTGCTCTCTAAACAATAATCATTTCTTCATCGCTAGAGCTGGAGTTGCTGCTTGAACCATCCATG

CTTGTTCGAGTCACCAGTAACTTTAACAACAGGCATATGAACTTCCTCTCTTCCTCTTCTTTTGTGTTAT

AAGCGGGGTGTCAGAAGCTTACAGTTGTTTAGCGCCATCTAACATCAAGGAGTGATTTTGCATACTCTTC

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CGCAAACGAAAGCGTCCTGGTGTGTACGAGCACTAGGCCCGGTTTTCTTGAACTATCCTCAGGCACAATT

GTGCCCTTTCCCCTTGACCTGCACTCACACTGCATTATTTACCTTCCGAGCCTGAGCGCGCTTGCGTCGT

TGATAATGCGACTGTTCAGTTTAACAGAAGAGAAGATTGGAGTAGAGATTGCTTTAGTTGTATTGTTTTG

TATTATTTTAAAATGTTTGTGATGCTATGACAAACAGTCAAATATTTTGCTGAACAGATCCTAAACTTTT

GACGCTCATAAATGTTCATGAAAGTCATTGTGCTGCTCGTATTAAGAGGGATCCTGGGATTTTTAACGAC

TACAGAGAGTCAGGACCTCGGTTTAACCTCTCACACCCCATTCACACGGGGTGTCAGCGTCAACGCTTAC

TATTCACTTTGAATGGGTGACGTCAGGCGTTGCCGAACTGCATAGTGGATCCGTCGGCTCCGCTTCAGAG

GCGTTGCTCAGTGCAGAAGTTGGGACTAGCTCAACTTTTCAAGTGCCGACAGATCGCTATATGCAAATAC

ACCAGCTAGACAGTGGCCTATTGCTGACTGAATTTCATTGGCTGACGCTGCTATGATGATCGCTTTAGCC

CCAACTTCAGACACGACTTCAGTCAAGCGTTGACGCTGAAGCCCGTGTGAATGGGGCGTCATCCGAAAGA

CTTCGCTCACTGAGAAGTATAGAGTCCCCGTCACTATACTGGGGCATTAGGACCAACACAGACCACAGGT

TGGACGCCCCCTGCTGGCCTCACAAACACCACTTCCAGCAGCAACCTAGCTTTCCCATGTGGTCTCCCAT

CCAGGTACTGACCAGGCACAGCCCTGCTTAGCTTCAGTGGGTGACCATGTGAGAGTTGCAGAGAGCTAGC

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GTGGTTTCCAGCTGCTTTAAGACACATGTGATCTTAATACAACCAGAATAAAATTCTCTAGTGCTTTTAT

TTAATTTTTTCTTGTCCTGAAGTTTTTTAATTTTTTTTAATTTTGCTATTTAAAGGCAAAATTGTCTTTT

TAAAATACAAAAAAACCCACCTGAACAGTGTTATATATTTTACTGGCTTATACATTTGCATTATCCTAAA

TGTTTTGAAGAATGTTCAAGTCAAGAGAAAAAGCTTTCCTCCTTACTGACGGCTGTTGCAATTTCAAGCC

Mib **exon 3** AATAATTTTAGTTTTGTACGTTTCATATTTCCTTTTTTTGCTACTTCAATGTGTTTGCTCAGAGTTCTTC

TGGAGTCTCGTCGCAAGTCGAAGAAGATCACAGCCCGCGGCATCTTTGCAGGAGGACGAGTGGTGCGAGG

GGTGGATTGGCAATGGGAGGATCAGGATGGCGGGAATGGAAGAAGAGGGAAGGTAATGCCTCGACACGTC

TGACTATGCTCACCTTCCTGTGCTCATCTTTTATTACATGAAAAACATTCCTCTTATCACGTGCATGCAG

TGTTTTGTGCTCAATTTAATTTCAACGTTGTTTTTATTGTTTTTAATTATGATACAAAACCCAGAAAACA

ATACAAAATATTAACTTGTATAATATTTCAGAATTTACTTTCCCACAGCAACATTATTTAAACAGAAATA

GCATTTAAAATAAGTTTAAAATAAAACACAATGCTATTATATAAAAATAAAATTAAGAGTAAATAAATAC

CTAAAGAGCCCCTATTATGTTTTTTTTTTTTTTTATATTTCCTTTCATTCAGTGTGTAACACAGCTGTAA

GTGAATGAAAACATCCAGCTGAGGGTTAACTCTGAAAGTGCACCTTGCTTAAAAATGCAGATTTTTTAAA

ATAAAAGATTTGACTTAGTCAAATCTTTTAAATGTCGTTTAAATGATTTGTTGTTCACTCGGATATTTTG

CCTGTTTGTATTGACGTCAACACAAAACAATACCAAATATGTTTTGTGCCGGATTCGGCAAAACGTGAAC

GTGCCTTTCCCTTCAAACACTTGCTTCGTGCAGGTGTGGGACTGATCATGACTGAAGATGAGTGAACATT

AATAAGTAAATGTTCTGGTGATTAATGAAATAATCTACCCTGCAACGGGGGATTCGTCGGCTGTTTGTTT

GAATTCTAGTGTATGGGACTTTGTCAGAGCTTGACGGGTACTTTACAGTATACAGTTCATGGATCAGTTT

CTTCCTCCATTCACAAATGTAAGTAAGTGCGAATAAAATTGCTGCCTCATTTTCTCTAGCTTGCAAAATG

TGTATTTAGTCGGCGCAATAGCCTAGTAGTTAGCGCGCCGACATATGTTGCAATAGCACGTCAGGGCGTC

GCGAGTTCGAATCCCGGCTCGACGACATTTCCCTACCCCCTCTCTCTCTCCCACTTCGCTTCCTGTCTCA

ATACTGTCCTATCTAATAAAGGCAAAAAGGCCAAAAATAAAATCTAAAAAAAAAAAAAAATGTGTATTTAA

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TTTGAGGTTGTAAACATGCTCGAAAACTGACAAAACTTTGCACACACATTAGAAGTGGCTAAAATTTTGA

TATGGTTTCGGAAGAGGGTGTGGCAAAACACACAATAAACATGTCAATACTTGCAAAAAGTCTCTGAGGC

CATGTCTACGCTAATCACGTCCACTTCACGTCCACACTGTCGTTTCTATTCATTTTCCAAAACATTGTCA

TTCCCACTGAAACGACTATAAATGCTTTCAACCTGTACTGTGCATGCATGAAACTTAAGACGCTTCGGCA

CGCGTCATTTCCGCCTGACGTTTATTTTCTTTCCGGCTCTTTGAAACGTTACGGCAAAATGTCAAGGAAA

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GCTTACCCTCACAGTAAGGACGACATCACTAAAATCAGAATCACAACAAAATTAAAGTAAACGAATTAGT

AACATGACTGTCACATGACAAAAACGCGTCCGTGTCTACAGTCTACACTACGACACGAAAATGGCGTTTT

CAAAATTATCCACTTTGGAGAGCGTTTTCAAAAAGATACGTTTTTGTTTCCTAAAAACACGTCTCAGTGT

GGACGGATGAACACGCATTAAGGCTGATTTATACTTCTGCGTCAAACGCCGGCGTATGCTACGGCGCTGA

CGCATAGCCATGGCCGTCGGCGTCGCTGACATGCACCTCTCAAAAAATGTAACTACACGTCGCAACGACG

CGTAGCGCAAGCTCTGTGATTGGTCGGCTTGGTAGCACTGACGAGTCTGGGCGGGACCGAGAGCCGCGCG

AGCTGGACGCGAGCCCAATGGAGCGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATACAAGTGTGG

AGTCCCGTGAAAGAGCTCCGGATGGAAAGTTTTGTTTTGTGTTTACCTCATAGTTAATGTTGTTGCACGT

CCGCCGGTTCCTGCCTCAAAATGAGTGAGTTTGAGCCACTTGTACTTCCAGGAAGTGTTCAGGAAAAGCA

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GGACATGGCCTGAGTTAAATTCAAACCTGAACCGGAAGTTGGAAATTTTTAACTTTCCTTTCGAAAAAAG

AGCAGCTTAAATTTTTTTTCTTGTAATTTTGATGCAAGATGATAAAATCCGTGCATAAATACATAAATAC

ATAAATAAATGTTTTTTTTATTTAATAAAATCTAAATATTAAATACTTTAAAGGATTTAAGATGCTAATG

ACCATTAAACGTGTCTTATGAAAATGTCCATAGTGCATCATTTGGGACACTAAATCAAGAGGTTCATTAA

CTCTTTTGAAGGTTTTGTTTAGTCAGTAATCACTACAGCTACTTTTCTTTTCTCTCATAAACTGTCCATT

Mib **exon 4** TCAGGTGACGGAGATCCAGGACTGGAGTGCTGCCAGCCCCCACAGCGCAGCCTACGTCCTTTGGGACAAC

GGGGCCAAGAACCTCTACCGAGTGGGATTCGAGGGCATGGTGAGCCACCCCCATTCCTACACACACACAC

ACAAAAGACTGCAGTTAACAGGCCTTTGTGTTATTACCCACCCCCCCGTCCTACCCAACACTGCACCACA

CGCAGGCCAGGCGTCCCATAAGCTGGCCTTCTTTATAAGGGGCAGCCATTGTGAAGGGCAGCTGGATGAG

CTATCTGCATGATAAAAGAAGTCTGTTGGCTTTACAAGAGAGCGAGACTCGACACCAAGACCAAAAGCGT

GCCTCAGTTGTTGAAGGCCGCCCTTTGATTGGCTGATCCACTTTCTGCAACATCTGAATTCCAGCCAATG

GCTCTGCAGATGCGCTCCGGCTTTTGTCTGTGATTGCAGTGTGTCCGGAGGGTGTGCGCAGCCATCTGCC

ACTGGAATTATTAATTAGATCTGGATATAGAGGAAGATATATAAGGAGGAATAGAGACGTTCAAGTCATC

TGGTGAATTAGTACTCATGTCGCAGAAACACTAAATATCACAATATCAGATTTGTCCAATGCCATGCAGC

Mib **exon 5** CATAATCAGCTGTCTGTTTCTGTTTTTTCAGTCTGATTTGAAATGTGTGCAAGATGCCAAAGGAGGGACT

TTTTACAGAGACCACTGTCCAGTATTGGGTAAGATTTAAAATATCTGATATTACCAAAATATACCATGCC

GGTTCAATGAATATACAGTGGGGGAAATAAGTATTGAGCACGTCACCATTTTTCTCAGAAAACAAATTTC

TAAAGGTGCTGTTGACTTGACTTTTCACCAGATGTTGGTAACAACCAAAGAAATCCATATATGCCAAAAA

AACAATATTAATTCATTTACTAATGAACTTCTGTGTTATAAAATGAAATGACAAAGGGAAAAAGTATTGA

ACACATGAAGGAAGGAAGCTGTAGAAAGACATGGAACGCCCAGACAGCAGCAGAGGTCTTTCTTATTGTA

AAGTAGTATTAGCTGCTTTTGTGCAACATCTACATAAATCAGGAGGATGAAGATGAAACCAGGGTGGACA

TTTCAGCAAGACAATGATCCAAAACACAGCCAATGAAACTCTCAAATGCTTTCAGAGAAAATAATCTAGC

TGTAGAATGGCCCAGCCTATCACCTGACCTGAACCCAATAGAAAATGCAAAACAAAAAGCTCAGATTTTA

TAGACAAGACCTACATAACTGTCAAGGTTTTTACACTGTTGAAGTCTGTGAAAAAAAATCACACCTGAGC

AATGTATGTGACTATATTCTCCATATGAGAGGCGTCTTTAAGCTGACAGCATCAAAAAAGCCTTTTATAT

AAAGTATTAAATACATTTCTGTAGTTCAGCACCTTCTCCTTGTGTCTATTGTTATTATTAAACAACACAT

TTTTTCAGATTTTTTTGGTTTGGTTTTATTTTTATGTTTGTAATGTTTGGGTTTTTACTAAAATTTGGTT

TAATCCCATGTCAACAGCTCCTTTAGAATATTATTCCCAGAAAAAAAACATGACTAGTTGAGTACTTTTC

CCCCACTCTAGTTATCTTTGTCAAGTAAATGTCCTCCAGTATATGTTAATGTTGTATGTGATGCCTCCAC

TAGGTGTCAGCATTGGATGCCTAATATAGCTGATCTTCAAACATTCATCGCTACAGTGAAACATTCCTGT

TTAAAAGCTATTTTGGCCCCAGTCCATAATTTACTCTTTGCCGTCCAAACCAATAACATAAAGCTGTTTG

CAATGATGGTCAGCTCAGATTAATTACACTTGAGGCCTTAAAAAAAAAAAAAAAGGTCCAATCATTTTTAA

AGATGTTAAGCTACATGCCACTTCACAGGATGTTCACTAAGTTTTCTACACTATACTGAAACGAATAAAG

ACATGTCTGTTTAGTAAAAAATGTATTTTTGAAGAAATGTTTATTAAATTTTTTATTTTTGTTTATTAAT

TAATTAATTTATTTATTTGTTTATATATTTATTAATTTATTTATCTATTTACTAATCTATCTATTTATTT

TATTTATTTATTTATTTACATATTTATCTATTTAGTAATTTATCTATTTATTTATTTATTTATTTATCTA

TTTACATATTTATCTATTTGCTTATTTATATATTTATTTATTTATCTATTTACGTATTTATCTATTTTCT

TACCTATTTATTTATCTATCTGTTTATTTATTTATCTATTGATTTAATTATTTATCTATTATTTATTAAT

TAGTCCATTTATTTGTTTATCTATTTATTTAGCTATATATTTGTTTATATATTTGTTTATCTAATTTATT

TATTTATATATTTATTTAATTATTTATTTATCTATTTATTTATCTATGTATTTATTTATAAATTTATTTA

TCAAATTTATTTATTTATTTACTTATCTAATTTATTTATCTATGTATTTATTTATTTATCTATTTATTTA

TTTTAATCTATTTTATTTATATATCTATCTATTTATTTATCAACTTAGAACCGAAGTACCGCTTCTTTTG

ATAACACCAGTTAGCTCCAACACATTACATAGAACATAAATACCAAATTCGCTAGAGACTGCAAATACAT

CGAAATAGGCTATATTTTACCTCCCATAATGATAGTCAGACAGGCAGGGTGGATTAATTTTTGGTAGCCC

AACTGGAAAACGTAATGACGTTGGCCTAGCAGTATTTCGAGCCCTGGTTCAGCTGAATTTTCCTAGTTTT

Mib **exon 6** GTTTAGCCTTAGATGATAATGATCATCATATTCGTCCTGTTGTTGGTTTTCTGTAGGTGAGCAGAACGGC

AACAGGAACCCAGGAGGCCTGCAGATCGGAGACTTGGTCAACATTGATTTGGACCTGGAGATCGTTCAGT

CACTGCAGCATGGGCATGGAGGATGGACCGACGGCATGTTCGAGACGCTCACCACCACAGGCACTGTCTG

CGGCATCGATGAAGACCACGACATTGTTGTGCAGTATCCTAGCGGAAACAGGTCAGGCACACAGCATTGC

ACTTATTCATGGGACATTATTTATTATTAGGGTTGCACAGTTTACCGGTACTATGGCAGTATCGCAATAC

TATGGCTAGAAAATACTGGCAGTGCCAATGTAGTTTGTAAACGGTAGAATCGTCATTAATGGTTTATCTA

TAATAGATGTTGTTGCATGTGGAAAAGTCTCTAAAATGCTTATACATTTGTTCAATAATAGACAATTTAT

TTTAATAGTCTGTAGAGCCCTTTAACGTTGCAAAACTGTTTGCCGGCAGCTAGCTCTCTGCAACTCTCAC

ATGGTCGCCCCCTGAAGCTAAGCAGGGCTGCGCCCGGTCAGTACCTGGATGGGAGACCACATGGGAAAGC

TAGGTTGCTGCCGGAAATTGTGTTAGTGAGGCCAGCAGGGGGCGCCCAACCTGCGGTCTGTGTGGGTCCT

AATGCCCCAGTATAATGACGGGGATGCTATACTGCTCAGTGAGCGCCATCTTTCGGATGAGACGTTAAAC

CGAGGTCCCGACTCTCTGTGGTCGTTAAAAATCCCAGGATGTCCTTTAAAAAGAGTAGGGGTTTAACCCC

GGCATCCTGCCCAAATCTGCCCACTGGCCTCTGTCCATCATGGCCTCCTAACCATCCCCATATTCAATTG

GCTTCATCACTCTGTCTCCTCTCCACCAATCAGCTGGTGTGTGGTGTGCGGTCTGGCGCAAAATGGCTGC

CGTCGCGTCATCCAGGTGGATGCTGCACACTGGTGGGGGTTAAGGAGATCCCCCCCCATTGTGTAAAGTG

CTTTGAGTGCCCAGAAAAGCACTATATAAATGTAAGTAATTATTATTATTAATTATTAGAATTCACACCT

TTTATGGTAGCCTATTGCACGTTTTCTGAGGCTTTAGTTCAAACGCACATCTGAATCAGTTCATTTCTGT

TCCTGTTAATATGATTTAGTAGCTACAACAACCGTGTCGATCTCTTTAAAAGAACGACTCACAAAGAGAC

TTTTATTTGGATTGTTACCTGATAAGACCAAGAAAAAGAATAAATGGAAAACCCAAAATAGCAACACGAA

ACATTGAATCAATGTTTGACCACTTCATATAGGCTAATTTTGTTGGAAAAATTTTGTAAATAAATTTATT

TTCATGTATTTTTGTTGGTCAGTTATCTTCATGTATTTTTGTTGGTCAGTTATCTACAAAATAAACAAAA

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TAAACCAAAGTGATGGAATTATCGGTTTCACAGCATGGCTGTATCTATTGTCTTCTCTGTCTCCAGAACA

TCATTTGTACACTGTAGTACTTATATACTGATGAGATCTGGAGAAGGCATGGCACCCTGCAGACAACCAG

ACTTCATTTGCATGCTTTGTTTGACCGTCCCCACCATGACAGACCCCACCTACATGCTGTAAAATGTACA

AATGTATAATGTTTGCTGTGGAGTTTAGAGTTTGCTTTCGATGACGCCACAGCCACGCTGAGTTCTTCTT

ATTAAAAAGGATTCTGCTTTGAAGACAACCGAAAGATTCTCCCTGGTTTTTGGGGCTCTTAGAAGTTTAC

AACAGGAATTATAAATTACATTCAAGTAGGCCTATTATAACATAAAATATTAATTAAATTACATATTTCT

TTATTATTTGAGTTATGAATTACAGTATCGCTATACTACTTGGTATTTTGATACTTCAGCTGGTTGAGTA

TTGTAAGATTAATATATGGTATTGCGACAATCCTATTTATTATCGTAATTTTTTGCCATTATTTCTCGGT

GAGTGACAAAAGCAAACATTATAACCAGGGCCAGATAGAATCTACAAACATTTATTGGTATTTCTGCACA

AAATGTTGTCAGTATTATAACTTAACACATAAAGTGTTTTTTTATTATATATTTATTTTTTTACCGTCAT

CTGGGAAACGGTTAGGATTTCAGTTCGGTAAAAAAACTATTAGTGTTCCAATTGGGATGACTTTAAATTC

ATATGCGTGTAAATGCATAAGCAGGGCTTAATTTATGCCGGAACAAGCCTGATCCGGATCCGGTACCTCT

AAAATCTGATCCGACACCTCATTTTACCCATCCCCCTCCTCATACGTACCCCCACCCCTAACTTTCTTCC

GCAACTCCCCAAACCTCTTCACTTTCGTACGCGATCGTATATTAAATCTACTGAAAGTATTACTTCCACT

Mib **exon 7** CTGTGGCCTTCTAATAATCGCAGAGCTCTGTATGTGTTCTAGGTGGACGTTTAACCCAGCGGTGCTGACC

AAGGCAAATGTTGTCCGCAGTGGAGAAGTGGCAGCTGGCGCTGAGGGCGGCAGCTCGCAGTTCATGGTGG C←→T

GAGATTTAGTCCAGATCTGCTACGACATCGACCGCATCAAACTGCTCCAGAGAGGACACGGAGAGTGGGC G←→A

CGAAGCCATGCTGCCAGTGAGCATCCCTAGTTTAATGCAGTAGTGCTTGTCCGGTCTGAAACCCACTTTA

TATCATATATCAATCAGGCATCAGAGATCACTGAGTTTTAAAGTTATCAGATCTTAAAAGTGGCGATTTT

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CTCCATTGTGCCACCTCGATTTGACGATAACCCCAATCCAACGTTGGCCAATGCAGACCGAAGGCCTGAC

GTCTACCGACCCTTTAAAGGTGCAATATGTAAGTTTATAACAACACAGATCACTGCCTATTCACGAGTCC

CGCAGAAAAAGTGATTGACAGGTGGTAATTATGTGTGTATCTTGCCTTTATTCATTTACTGTATGATTTG

TTTATGGGTGAAACAAAGACCATGCAGGTCAGGTAGTTTAAACGGTAGGCTACAAATAATTAATTGGTCA

TTAATTATTTAATTATTCATAATCGTAAATCGAATCGTGCCTTTAGAATCGAAAATGTAATAGAATCGAG

AATTTGGAGGATCGTGACACCCTTAGTCCGTATTATGGTATTATCATGCGTTAGAAGAGTCATAAACTTA

CATACAGCACCTATAATGAGCATTAAACTGCATCTGCTGGCCTCCTCTACAAGTAGCACACTTGTTTTAT

CTGCTTACTGTTTAAGCGGCTCAGCCTCCTGAAGCACTGGATGTTATCCCGCCAGTGCGCTCCTGGGCTG

GGTTTCTATATTTTTGGATCGCCTCCCTTTTGTTGCCCTCGATGGACAAAGCTTAACAGAATTCCAATAG

CTTCGGTTATGAGCAGTATAGATGAGAAATGGTCCTGCAAGAGCCTTTGGGTGTTTTCCGTTTAAATGAG

CCAATCTCAATTTTAAAAAGCCAGACCTTACACTTATTGATTTTTCTCCACGTCTCTCTTCACAGGGCTC

TCAGAGGGGCGTTTTGTACCTGTGTGTAACAGGCAGTGTGCACACACAAACACACAGTTGAAGTTTTCTG

TTGAACAGATTTCTTCCATCACATTTCTAAACAATAGTGTTACTAACTAATTCCTAATAACAGATTTGTT

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GTGTCTAGCATTCTTGCCCTTTCTGAGTGTTTGCGAAAAGGCTTGTGGGTTTAAATGCAACCGCTCTCGT

Mib **exon 8** ACTCAGATATTCATGTGTGTCTTTTTTTTTTTGCAGACCCTTGGAAAGGTGGGCAGAGTGCAGCAGATTT

ACTCTGACAGTGACCTGAAAGTGGAGGTGTGCGGGACGTCCTGGACATACAATCCCGCTGCTGTCACTAA T←→C A←→T

AGTGGCCCCTGCTGGATCTGCGGTTACTAATGCTTCTGGAGGTAATGCACGCGTGCGCATTTTGTGTGAA

ATAATCACAAAAGCACAATATAAAAAAGCATTATATTTTATTGTAGTTTTTAAATTGTTGTTAATGTGCT

GCACTTTCTTTTCAAAGTTTAAAAACAATCTAACCTATAATTTCCAAGTCATATTGTGTTCTTGATTGTA

TTCTGGCAAGTTTTGCAGCCCTAATTCCAATGTATTCTGTCATTTAATGTATATGTCAAATGCAGAAAAT

GCCCTTTAATGCCTGTGTGAGTCGAGCACAGTCAGACAAGCATCAATCCGTTTCTCATCCGTCATTGTGT

Mib **exon 9** GCTCTGTGTGACACTGCAGCAGTGTTGACAGAGAGTCCTTCTGTGCCCGCAGAGCGCCTGTCTCAGCTCC

TCAAGAAACTTTTCGAGACGCAGGAGTCTGGAGACATTAACGAAGAGCTGGTGAAGGCCGCAGCCAACGG

TGACCTGGCCAAAGTAGAGGACATCCTGAAGAGACCCGATGTGGATGTAAGAACCCGTCTCTAACACACA

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ATTACCAAAAAATCCATAAATGCATTTCAGTAGTTCGACATTCATTAATGATAAACATGACTGCTTTTTT

CAGAAATGTTTTGTTTTATTTGTGTTGGGGTTTTTACCCAAGTCAATTTCATGCCAACACATCCTTTAGA

TATATCATGACGTCTTAAATGCCTGATGATGTATTAAATACTTAATATTTTACCTTCTGTGTTCACACAC

ACATCACTGAAAGAAGGACATGCAATCAGAGATGTTCATAGCACAACGTGATCAGCTATATCTTTTTATT

Mib **exon 10** TTCCTGCAGGTGAACGGGCAGTGTGCAGGACACACTGCCATGCAGGCGGCGAGTCAAAATGGCCATGTGG

ACGTCCTCAAACTGCTGCTGAAACATAGCGTGGATTTGGAGGCGGAGGTATGTGTCCTGCTCCTCAAACA

CCTCGGTTTTCCCTGAAGTTAATTGCATTTAGAGCGTTCACGTTTTGATCCTCAAGCCAGCAAATGCAGT

GTATATATATCACTTTCACCATGTAACAAACTGATTTATTATGTAATTAATAAACTTAAAAGTTCATTAT

AATTATTAAAATTAGGGTGCTTCATAAAAGTTATTAATTACTGACCATCTCATTAAATATTTAATTTAAA

TACATTTTTAAAATCTTTTGATAATTACTCCATAAATAATTTAATTACATGTAGGCCTGGCATGATTATT

GCACAACACGTGGACATGTCTTTATGTGGCCATAAAAAACAATTCTTGCCACATTTCAGCTGACTGTGTA

GCTTCTCTATCTCTATTGTGTCAATATGTCAGTGTCAGTATGGTTAAAGAAACACTGTAGTATTTACTAT

AAATTACTAAAGTGTATTTTCATGTGGGTGCCTGATGACTGAAAATAAATCTGTTACTTTTTTTCTGGTT

CTTTTTACTTTAGATGTTATTGTTAACATCATATAATATTTATTATTTAGAATAGCCGTTTTCACATTCT

GATTCCAATACCGTACTATTAAATAGTTAAAGTGACTATTATTAGACGAAATGGTCTTTAGTATAAAATA

TGATGTTTTTTGGAAGGGTGCACTTGCATTATGATGCTGTTATAGTGTCAAAATAGTCTTAAAGTGACAA

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AATTTCAGTTTTTCTTTTTTGGAGTTCAGCAATAAAAACAAAAACAAAAGGTTGTTTTAAATTAGAAATG

TTGATCTCTATATTGGCATTCACCCCAACCCTCTCCATCATACTCACTTATCCTCTCAGATGGGATAGTG

GGTAATATCAAAGGTTACAATGGGCTATTTTGAGCTTCTCTGGTGTATATAACTATGTATGTATTTATGT

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ACGCCGTAGCATACGTGTGCGTTTGATGCAGAAGTATGAATCAACCTTTACACACATATTTTACTTAAAG

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ACGAACTAAGTTTAAAAGCAAAAAGTCAACACGAAATAAAAACTAAAACTAATGAAAAGTCCCAAACTAT

TATAACCTTGTACCAGAATAAGTATCTGTCACTGTGATGACTTGTTTTAATCTGGAGCTCAGTTTTACAG

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CATTTTCAATGACAGCAAAATGTTTGTTAAAATCAAAAGACTTTGAAGGTGAAAATGATGTCTGATGTCA

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ACGTCATAACTATTAGTCCTTCTGAATTATTGGCCGCTCCAGGCAGTGAGTGACATGTGGCTCTTTTCCA

Mib **exon 11** GGATAAGGATGGAGATCGAGCTGTCCATCACGCATCCTTCGGGGACGAGGGTTCGGTCATCGAGGTGCTT

CATCGAGGCGGTGCTGACCTGAACGCCAGAAACAAGCGCAGACAGACGCCGCTGCACATCGCTGTCAACA

AGGGCCATCTGCAGGTGGTCAAGACTTTGCTTGACTTTGGCTGCCACCCCAGTCTGCAGGTGAACTATCT

>Zv9_scaffold3540 dna:scaffold scaffold:Zv9:Zv9_scaffold3540:1:281342:1

Loci (6 total)

WAC (*wacb*) Start: 3350 End: 7247 (Complementary)

cables1 Start: 27985 End: 79954 (Complementary)

gata6 Start: 164736 End: 174290 (Complementary)

3' of *mib* Start: 222692 End: 278952 (Complementary)

mir1 -2 Start: 266415 End: 266501

mir-133a Start: 268599 End: 268697

#Genomic sequence was compared with *mib* mRNA sequence (NM_173286.3)

Yellow color: Indicate the site of mir

Red color: Indicate the site of Exons

Blue color: Indicate the site of introns

Green color: Indicate the site of polymorphism

A← ：The variation on mRNA is A

→G: The variation on chromosome is G

Mib **exon 12** CTGTATACATTACAAAGTGTGCAACTCTTTGCCGCCCCCTGCAGGACTCTGAGGGAGACACACCTCTGCA

TGATGCCATCAGCAAGAAGCGGGATGACATGCTCTCTGTGCTCCTGGAAGCAGGCGCAGACGTCACAATC

ACCAACAACAACGGTTTCAATGCGCTCCACCATGCAGCACTGCGAGGGAACCCGAGGTATGGCTGACTTC

AGATCTGACACAACTTGGCCTTACAGTTGAAGTCAGAATTATTCAATCCTTCTGTATTTTTTTTGTTAAA

TTTTTGCCCAACACATTTCCAAACAATAGTTTTAATAGCTAATTTTAAAAATACTAATATTCAGCTTGAT

GTGACATTTAGAGGCTTAACAAGGGTGAAAAATCAAAAAACAATATTGCTTAGGGGCTAATAATATTGAC

CTTAAAATGTTTTTTTTTAAATTAAAAGCTGCTTTCATTCTAGCCGAAATAAAACAAATGAGACTTTCTC

CAAAAGAAAAAAAAAATATTATAGGAAATACTGTGAAAAAGTCCTTGCTCTGATAAACATCATTTGGGAA

ATATTTAAAGGAAATTCACAGAAGGGTGAATAATTTTGACTTCAACTCTCCATTGGGTTATTTAAAGGTA

TGCTTCGTTGACTTTCTTAAACCAATTTCAGCTCATGTTTGGAGCTTGGCAATTTTCTGGTGTCTGACAA

ATCTACAAAGTATGGTATTTCATCTTGCGTTTGCACTGTAATAAAAAAAAAAAAAGACTGAACAGTAGAT

AAATAATAGATCAGGACTGCTGAGGTGTATGGGATTATTTTTTATTGTCTTTATCTGTCTTTAACGTTGC

TTTGGATCTGTAGTGCGTATATCATAATAGTGCTTGTAAGTTTTAGGATGAGACTGAAAATGTGCAAATC

AAGGTAGTTTAGAATGGAGTTTGTTTTTGTAAGTGCTGCTTTTCCATTGTACGATGTTGTCGTAATCTGT

CATAATATTATGCCAAAGCTGATATATCGGCCGATATTTGTCACATTTTATTTTACACATTTATTTTTTG

TACATTTTTCAAATCATTTAAAATTTAATTCAGTTTTAATTTATTTTATTATAAAATAATTATATTGGCT

AAATATCGGCCACCCTACTTTCCAATATATTAGCGTCAGCTTTCAAAAAACCCTTATCGGTCAGCTGCTA

TTGTTACACATATTTTACACAATTTTTTTGTCAAATAATTTTACAGTTAATTCAGTTTTTAATTTAGTTA

TTAAATAAAATAATGATATTGGCTGAATACTGGTTATTGGCCACTCTGCTTTCCAAGATATCAGCCTTAG

CTTCAAAAAAAAAAAAAAAAACATATCGGTTGACCACTAATGTTAAACACAGATATTTAACACTTATTTT

TTGTCAAATCATTTTAAGCTTGATTCAGAATTAATTTAGTTATTGAATAAAATAATATCGGCTAAATATC

GGCCACTCTGCTTCCCAACATATCAGCATCAGCTTTCAAAAAACTCACATCAGTCGACCACTAATGTTAA

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ATAAAATAATAATATTGGCTAAATATCGGTTATCGGCCAGCCTGCTTTCCAAGATATCAGCCTCCGCTTT

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TAATTTAATTATTAAATAAAATATTTATATCAGCCATCGGCCACTCTGCTTTCCAAGATAGCATCAGCTT

TAAAAAAAAAAATATATATATATATATATTATTTCCTAATAAAATCAAAACATTTTTGCTGCATTTTTGT

GCTTTACAGAATAACGGTGTCCAGTTTAGTCACAAATCCCTCAGTGAAACGCTCAATCTTAGCTTCAATC

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TGTTCAAGCTACTTATTTAAAATGAGCTAAAACAATACAATCCTTCAGGATTTTCTGCAACAACCAATTT

GTTTTATGTACAAGCTAGTTACATTTTTAAAAACTAATACATCAACTTAATTCCTTCATGTTGTCCCAAC

TCAAATCGGTTGTGTGGAAATCAGCATATGCGTGTGTAAACGCATATAAAAAATAACTTTTGCTGTCTGA

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CCTGCGGCAGCCGGTCTCTCAGTTCCTCAGCATTGTTCCCGTCAGCCCCATTGTGGCTGGACCTCTGCTG

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GCAGATCTGAGCAGGTGCTAGAAAACGATTTGTCGATCCCTGTAGATTTGTGGTTTTATATCAATTTATC

ATACTCGTTTGATTCTCGGTGCCATTCACAGAAATATGCAGATTTCTATGCTTGCAGTTTCCATGTACTC

TTACTTATAACATGTTCATTGGGTCATTTTTTTCTGTCCATTGCTAAAACTTTGTATTCTGATCTTTGTT

Mib **exon 13** CTGCAGTGCCATGCGTGTGCTGCTTTCCAAACTGCCACGGCCATGGATAGTGGACGAGAAGAAGGACGAT

GGCTACACCGCTCTTCATCTGGCTGCGCTCAACAACCATGTGGAGGTGGCCGAGCTACTAGTTCACCAGG

TCAGCAGCTCTAACACTCACACATTTTACTGTATCAACACCCCATATTAAATAGGAAAGTTGAAAACTTC

TTATTCATACGTCTTAAACTCAAAGTCAAGGTGTTCAAAAGAGTCATGAACACCGTCATTAGTTGCATCA

GCTGTGTTTGATCAGGATTGGAGCTAAACTGTGCAGAGCCATCCAGGAATTGAGTTTGAGACCTATGATC

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GCTTTACTTTTTACACATTTGTTTATGTTGCAGCCTTATTCCAAAATGGATTATATTCATTTATTTCCTC

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CCAACAAAAAACCTGAAGTCACATGACATCAGTATTCACAGCCTTTCCTCAATACTTTGTTGATGCGCTT

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GACACTGAATTTCAGTGAATGTAGCATGTAACACACACTAAAACAAGTGCATTTATATACATAAGAATGA

Mib **exon 14** GTTTAAAGGACAACCCTATTGATTTGCTCTTCCTCCATAGGGAAATGCCAATTTGGACGTCCAGAATGTT

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GTTCTGTTTGTTTTCTTTCCTTTTTTTTTCAATGTTTGACGTCTGCACCCCTCACCCCAGCGCTCAGTCT

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GCACTTTGTATAAGAACGAAATGCAAATTTGAGTGTTTAAAGTGTACGCTACCTGAAAAAGGTCTTGTTG

CCTATCTAAGCTTTTAGGAACAACAAATAGTAGTAATTATAAATTAAAAGAATAGTAATAGTAACTTCTA

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GAGTAAATGATGACAGAATATTTCATTTCGGTTGAACTATCCCTTTGAAAGCTTGTTCTATTTGAAAATA

Mib **exon 15** TGAGCGTTACAATCAGCACTGCTAACAACACAAGGTTTAAGTTGAGTCCTGTGTGCTTGTTTCCAGCTTT

TGGTAAGAGCCGAGGCAAAGTTAGACGTTCAAGACAAGGACGGAGACACGCCACTGCACGAGGCCCTGCG A←→G

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CCCTCCAAAAACACAGTACGTACAGAGAAGTGTCTAAAGGTTAGAGGTGTTCAGTAAATGAATAGAATGT

GAGTTTGATGCACACTTTCACTGCTGTGCACTTGATTAGAAATGGTGTTTTCATGAAATTTTTCGCAATT

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CCCGCAGCCTTTCTTTATCTTCATTAGCACTTTTCTCTATCAATGCACTGTGGATCCGCTGTCAGAAAGT

CACACTATAATGTCTGACACCAGACAGACTGACGATGCTCAACCCTATCTGTTACAGCTTTTGTAGCTCC

TTTTACGCCTGACCCCAGCCCTGCCAGTTCACATCATCGCCTCTCCATGACTGTCGTAAATCAAGCGTTG

TGTGACAGGAGGCTGCTTCCAGGCCAGCCGTCTGCCATTTATTAACACAAACAGTGTGACAAATCTCTCC

ACCCTATCAAACCATCACACTTACCACATGCAGCAGATGGAGAGGCGAGCCATCCATTCAAAACACTCCA

CCGAAGCCATCAGTATTCAGAAACCTGCCCACTTCTTCAGCTCAATGTGCTCCATAGCATTTCATCACTT

CTGTGGCCTGTTGCACAAAACCAGTTGAGGGATGTAGAGTAAGGCTGGGACACACCAAGCTGATGCCAAA

GAACTAGCACCAACTGTGTTTTTACCTTGTGTCGGATGTGTCTAGATTTGTCTGGACCAAAAAGATGAAC

GTGAACACACTAAGGCCCAATCCCAATTCTATTTTTGTACCCGTACCTCTTCCCTTTGGCCCTTGAAACA

GAGTGTGAAGGGCTTCAATATTTACGCCTGAAAATTGGAACAGCATTGCAGCTGCACACATAGTCATATG

TCATCGCAGGCTCTAGCTTCATATGAGATCAGATGACCGCGTCTGCTGTAGTTATTCCAGTTATGTTATT

TTTTGGTAATTATCTTCAGCAAATCACTGAAGGCAGATATCATGACGATATAATGTGGCAATAAGAGCGT

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AAACATGTGCTCGTCTGTTGTAAAAATTTGCAATATTGACAAATAAATAGTAATTTGTGGCTCTCCTTAT

GGGTGCAGCGATCCTGCTGTTATGGCTAGTGTATTCTGGGAAATTTTCTTACCCCTGGGTTTCGAATGTG

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GCCATTGCCGAACTGCATTGTGTATTTGTCGGCGCCGCTTCGGAGGCGTTGTTCGCTGCAGAAGTTGGGA

CTAGCTCAACTTTTCAAGCGCCGATGGAAGCGTCAGCCAATCAGATCGCTGTATGCAAATACACCAGCTA

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TGGGCCTAACCAGGGGTGGCCAAACTCAGTCATGAAGAACCGGTACCCTGCAGAGTTTAGCTCAAACCAC

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GACGACCTGCACTCACACTGCATTTTGCTTGGCACAATGAAGATTGCTTTAGTTATATTGATTTAGTCTT

TTGGGATGCAGTGACACAGTCAAATATTTTACCAGATCCACCACCTTTGATGCTTGGAAATTATCAAAAA

AGTCCTCGTGCTGCATGTGTTAGGAGGTTTGATAAAGGTGCAGCTGTCGTGCAATGAGGGGTTTGCGTCT

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CGTTGCGTCTTCAGTTTCAGGCTTGGGCACACTTTGCACTCACACTACAAGCGTACCACCAAAGCCCAAT

CAAACCGCGCTTTGGCACACCTCTTCCAACCGGGCCAGGACCGGCCAACTGAAGCATGCCTGGGCCTGAT

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CACCCAAACCAGCAAATCAAGTTCTTACTAGGTGCACTAGAAACTTCCTGCCAGGTGTATTGGAGCAAGT

TGGAGCTAAACTCTGCAGTACACCAGTCCTCCAGGATGGAGTTTTGGCACTCCTGACCCTTTAGTACCAT

TATCACTGTAATTGTCACTCACCACAGAGGGGTTTGATCATACAAATATGCCTGATCTATTAATCCATAT

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CACATTAGTCGATCAAACAACTAATCAAACAGCCAATCACGCTACACATCATCGCAGCAAACAGCCAATC

TCAAGACACTCAAGTGCAGTAAACAACCAAGCACACGTCACAACAACACAGCAAACAGCCAATCACACAA

CACCTGAGAGCATCAGTTTGAGTTATTTCTGGCGAGAGAGTCAACAATTTACTTCTCTGTTGAAAATTAA

GTGATACCGTTATGAGAAATATAATGTGTTTGCATGAATTTAATAAACACTGCTAGTGCTGTAATGTTTA

AGGCAACCTAGACAATATATTATATCAGTACAAATCTGTAATTTTAATAATGTAGGTTAACCAACTCTTT

AAAAGACAGTCTTTTAAAATGCTTTATTAAACAGAAGTCTACATAAATATTTAAATGTATGTTTTAATTT

TAAAATACAAACATTAATTGGCAAATTGAAGCTGTTAATGATGATGTTAATCCACAGTATTTGACTGAGT

Mib **exon 16** GTTTGTGTTGTACCTTCACAGTTGATCATGGGACTGGGCACTCAGGGGGCTGAGAAGAAGAGCGCTGCCT

CTATTGCTTGCTTCCTGGCAGCCAACGGAGCTGACCTTACCATCCGTAATAAGAAGGGCCAGTCCCCTCT

GGACCTGTGTCCTGACCCCAGCCTCTGCAAGGCCCTAGCTAAATGCCACAAAGAGAAGACAAGGTTTGTC

TATCCATTCCTAGCTCTACTAGGTGATCTAGTTAAGCTTTTGCTACTGATTAATATCTCCTCTCCTTCTG

TGCTTTACACTTTTTTTATATTAAAGTGTGTACCAAAGTGTTTTTGTTCTCTCTCATTCTCTCTGACCCG

Mib **exon 17** CAGCGGGCAGGTTGGCTCTCGAAGCCCGTCTCTAAACAGTAATAATGAGACTCTGGAGGAATGCATGGTG A↔G

TGCTCGGATATGAAAAGAGACACTCTTTTTGGCCCCTGTGGTCATATCGCCACCTGCTCTCTCTGCTCGC

CTCGTGTCAAGAAGTGTCTTATTTGCAAGGAACAGGTTCAGTCCAGAACTAAGGTACAGAATGCCAGTGG

TTTCTGTGGTTTTTCATTCATGTATTCTAATGTGTCATATGTGATCCTGAACTTCAAAGCCAGAGGTGTA

TTGTTGGCAATCGATTTTTCTTTTATGCCAAAATGTATTGAAATGTTAAGTAAAGTTTAGAGTTGTAAAA

ACTCTACTGACTACTGACATTTTAAAAGCGTCCACATCTGCATTGAGCGTGTTCTTAAATATCGCCAGTT

GGCCATTGTCTTCACGTTTTCAGCAGAAATGACTGTGATTGACAAATAACATCAGTTTCAAAGCAGTGTC

TATCAATGGATTGCTCATATGTCAGCTCATTGACAGATCAGCTGATCGACACGACTTTGAAACACTTTTT

ACATTTGTAAAATTTCTCTACCAACTAATACCAAAGTCAATACTTTTGACCCAGTGTGCTCAAATGTTAG

CTTGAAATGGACAAATGTTAATTCATTCATTTTCTTGCCGGCTTAGTCCAGGGGTGTCAATCTCAATTCC

TGGAACTAAACTGTGCAGGGCTTCGGCCCTTTTGGAACTGAGTTTGACACCTGTGGCTTAGTCCCATTAT

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TAACCCATTGTGCTCATCAGCATTGTTTAAAAGTTATCATGAAATGGGTGTTTGTAACATTTTTGTGCAA

ATTGATACCGAAGTCAATACTTTTGACCTAATTTGCTCATCACCGCTCAAACGTTAATGTGAAATTGACG

TTTGTAAAATTTCAGTACCAACAGAGACCAAAGTCGATACTTTTGACCCATTGTGCTAATCAGCATTGTT

TAAATTATACTGTGAAATGGGTGCTTGTAAAATTTTTGTACAAATTGATACCAAAGTCAATACTTTTGAC

CCAATGTGCTCATCAGCGCTCAAATGTTAGTGTGAAGTGGACGATCGTAAAATTTCAGTACCAATGATAC

CGAAGTCGATTTGAACCAATGTGCTCACCAGCAGTGGTCAAATCTTAGCATGAAATGGACGATTGTAAAA

TTTTACTACCGATTGATACAAAAGTCAATACATTTGACCCAGTGTGCTCATCAGTGCTCAAATGTTAGTG

TGAAATTGACGTTTGTAAAATTTCAGTATCAACTGATACCAAAGTTGATACTTTTGACCCAATGTGCTCA

TCAGCAGCACTCAAATGTTAGCGTGAAACGGACAATTGTAATTTTTAGTACTAATTGGTAACATAGTTGA

TGTTTTTGACCCAACATGCTCATCAGCATTGCTCAAATGTTTGCGTGAAATAGGCGATTGTAAATTCAGT

ACCAATTGATACCAAAGCCAATAGACCCAATGTGCTCATCAGCAGTGCTGAAATGTTTGCATGAAATAGG

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AAATGTTAGCAAGAAATTAACGATTGTAAAATTTCAGTACCAATTCATGTGTCTTGGCCGATTCGTCCTA

CTCTTAACAAAACCAAACATCAATGGAAAATGTATTTATTCAGCTTTCATCTGATGTATAAGTCTCAATG

TCAAAAACTTGACGCCTAAGACTGGTTTTGTGGTCCAGGGTCACACATTTAACCTTTTTTCTATTGCTCA

Mib **exon 18** CCCCTAGATCGAGGAGTGTGTAGTTTGCTCTGATAAAAAGGCAGCGGTGCTCTTCCAGCCCTGTGGTCAC

ATGTGCGCCTGTGAGAGTAAGTCGGTTTTCTCCACACCTCTTCCCTTGTCATCCCATATGAAAAACAGCT

CTTTCTGTCATCTGGCTTGTCAGAATATCACACTTCACATGACTCTGATACAGAGACATGCTTCTAGATG

GATAAGAATAGGATACGGATGAATCAGACATAGTTTGAGGACATCTGTTCATTTGTCATTAGGTTATCAA

AAGAAAAGCCACATTTTTCTGATCATCTTATTATTAGTGACTGTATTTGATGTCTCTGTTAATAGGAAGG

GATGAGTTTGACAGATTTGAGATTTTTTCCTTACCTTACACAACCTGACAAAAGTCTTGTCGCCTATCCA

AGTTTTAGGAACAACAAATAATAACTTGACTTCTAGTTGATCATTTGGTATCAGAAGTGGCTCATATGAA

AGGCAAAGGCCTCTGCTTTTTTTGGGTTCATCTTCAATGCCTCCTCCATCTTACCCCAGACATTCTCAAT

AATGTTCATCTCTGGTGACTGGGCTGGCCAATCCTGGAGCACCTTGACCTTCTATGTTTTCAGGAGCTTT

GATGTGGAGGCTGAAGTATGAGAAGGAGCGCTATCCTGCTGGAGAATTTGACTTCTTCTGTTGTTTGTAA

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CTCCTCCATGCTGAATGAAACCCCAAACCATGATTTTTGCTTCACCAAACTTGACTGATTTCTGTGAGAA

TCGTGGGTCCATGCGGGCCCCAATAGGTCTTCTGCAGTATTTGTGATGATTGGGATGCAGCTCAACAGAA

AAATCCACCTTCTCAACTTTTCCAAATGATCAACTAGAAGTCAAGTTATTATTTGTTGCTCTTACAACTG

GAATTAACAAGACTTTTGTCAGGTAGTCTACATTGGGAAAATCCTGCATTTATTGAAGCTCAGAGCTGAT

GTAAATGTCTTAGAGGTGAGGAATAGTTTGCTCTGAGCTTACATCCCTCCTGTCTGATCCCCTGAGCTTC

ATTCTCTTTAAATACATTCTTCACTTGTCAGCAAGACCCTCTTTTTTCGTTTTATTCTGGCTTTACCTCA

GGCTGCATCCTACTGTTCTGTGGCAATTGACTATTTCTTTTTATGTTTAACAAGTTGGCTTGACAGGATA

ATGTTAGGTAATATACAGGAAATTTCCCAGGTGATATTAAACAGAGCAAGGACATTTTTCACAGTATTTC

ATATCATATTTTTGTTCTGTAGAAAGTTTTTTTTTTTTCTTTGTTTGGAATAATAATATATTTAGAAAAA

TATTTTTGAATATAATTAGCCCCTTAAAGGGATGGTTCAAGTGGTTACAAACCTTTATAAGTATTTTGTT

GAACACTAAATAAGATTATTTAAAGAATGCTGAAAATCTGTAACAATTAACTTTATTACTGTTGTGTTTG

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AATGAAAACAGTTGACTGATTTGAAACAAACAGACGGCCAACCAAAAAAGTTACTCATGGATATACAAAA

GGTGGCCAACACAAAATACATACATTCCTAATATAAGAGTTCCATCTTACACTCAATACACTACATTCAC

TATAGTATAAATACAGCACTGCAACATATAAAAGAGAGATCGACTTAGAATGTCACTTACCTGTTTAATA

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GTCAAACGTCGGCGTATGCTAGGGCGCTGACGCATAGCCCTTCACCGTGGCCGTCGCCGTCACTGACGTG

CACCTCTCGAAAAATATAACTACACGTCGCAACGACGCATAGCGTAAGCTCTGTGATTGGTCGGCTTGGT

ATCGCTGACGAGTCTGGGCGGGATCGAGAGCCACGCGAATGGCGCGAGCGATTGTTTACAAGTGTGGAGT

CCCGTGAAGGAGCTCCGGATGGAAAGTTTTGTTTTGTGTTTACCTCATAGTTAAAGTTGTTGCACGTCCG

CCGGTTCCTGCCTCAAAATGAGCGAGTTTGAGCCACTTGTACATCCTGGAAGTGTTCAAGAAAAGCAAAA

AAGCAGCGAAGAAACTCGACACAGAGGAACATTTACACCTCACTGCCCACTAGCGTTTTGGAAGTGTTAA

TGCAGACCGACAGAGACAGCGCGCAGAAGTATAAATGCACAGCTACGCGCGTTGCATGCGCCGTGGGTTA

CGCCGGTCACCTGATGCAGAAGTATAAATCAGGCTTAAGGGCTTATTATGCGGTCTCTGTCGCCATCTTG

AGAACTCTGGTCTATAGACATCAGCATTCCTTTAAAGAGTATTTATTTAATTAAAATGACTGGAAAATTA

TAATAGAACAAGCTTTTGATCATGCTGATAATTCCCTATCATAATGATAAGTCCCAAAATTAAATGTCAT

ACAGTGAGGTTATAGGGATAAGGGAGCTAATCCTTTGCTTTCTGTGCGTGTACGCGTGTGTCTGTGTGTG

Mib **exon 19** TGTGTCCTGCAGACTGTGCGAGTCTGATGAAAAAGTGTGTGCAGTGTCGGGCCGTGGTGGAGCGCCGCAC A←→G C→T

CCCCTTCGTTCTGTGCTGTGGAGGGAAAGGTATGGAGGATGCCACTGATGATGAGGACCTTAGTGAGTGA

ACTTCCACACGTTCCCGTTTTTTTGTTTTCATTTCTCTTTCCTCTCTCTCCGCCTTCGTTCTCATGTCTC

TCATCTTCAATATTTACGTTGGCTTTGTGTTTAACGCTTTCTCCGTTCCTCCTGCCCACACACATCTCTC

TCTCTCTCTCCCCATTGTTATGACTAATCTGTTATTTCCCAAATGTGCTTTCATGACTAAAATCATAGCC

CCTCCCCTTAATGCATAATATCAACACCCTGGAATGAGCTTTGTAATGCCTTTGGAATGTCTTCATAACA

CTAAATATAAGGATTTTTAGGAGGCCAGTCTTAGGGACAGGGTGTTCACAGAGTCCTAAAAATATCTTAA

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ATTTTAATGTCCATATAAAGTCAATTATTGTTTCCAATGGAGGCACGTGGATTACGGCGCATTTTGGGAG

TGACGCGCTCGCACCTTCCAGGCGCACCCACTTGAAATTTTCTTAACTTTTAAGAATGCTGCGAGCGTAC

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ATCCACAGAAGTTGCAATTGATAATCATATTCTAGAACAATTTGCGTCATGGTAAACCTTCATAACATTA

CATTAAATTATTCTTTATCATTCAATCACAAAGGCGTTAGGGTTCATAAGTTCACAATACACGCTTTAAT

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TTGAAAATACACACAAGCGAACACATATTAGTTCTTCATTACTTTTTTGAGCTCAAAAATCATTGGTCTC

TTCAATTTATGGAATGGTAATACTGAAAGAAACAACGTTTTTAGCTATTAGCAACATAAAGTGTGTTGCA

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ATGTTAAAACGTTAACGTTTTAGTTATCTATACAACCAGCATATAGGGATGCAACAGTTAGAGATTTTGG

TTGTACGATTATAGTCTGAGGAATAATCACAGTTATCACGATTATTACGTGTTCTTTCATTTCAAAATAC

TACTAGTTTAGGAAAATCACATGAAAACTTCTTACATTTTAAAGTGTTATTAGTAACCAATGAATACATC

CCAAAATAACAATAAAAAAGAAAGAATATTATCCATTAATTTTTAGACTTAAAATAAATGAAAAATGTTT

TTAGCATTTAAACATAAGTAATAATTTTACATTAAAAATAAATGACAGAACAAAAATAAATAAATAGTTT

TTGTCTAATAGAAATTTAAGCATCGTATTAGTTAAGTATTTCCCTTTTAAATAGAACAAATGTAGTCGAA

GACTGTTGAACTCCTGTCTGAAAGGCACTAATATGCACGCAAACCACATGCCTCCATTGGAAATAACAAA

CTTGTGCACGTCAAAGATGTGATATGTGAATGGCCTTAGTTAAAACCCTTCTCAGCCATAGTTAAAATTA

GCCTTTGATCCAATGTGCGTGCGTATTGTTTACAGGCTCAGAACTTTAACTAGTGCACATTGGCATAACT

TTAGGTTGCAGCAGTTTTGTTCCATGCGGAAATACGGTGTTGAGAAGCCTTTATGATTAATTAACCGTGA

CAAATTAAACTGCTGTTAATAGTGAAATCGGTTAATTGTTGCATCCCTACCAGCATAGCCTTGTTCTTAT

AGGCTTTGGCTGAATGCGTGTTGCGATAATGTCATATGACGCATCTAAAACAAGCCACACACTAACTTGA

AGTATCGTACACTAGATGACCAGTTTCTGTACGCAAATATAATGCCATTTAATATAAAGCAATGAAGATG

ACGTAGAAGGAATTTGAACTGGTCCAAGGCATATCTGTGATAGAAATATGGCTCAAATGTTAGTGGGAAA

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TGCCCATGTTCTTTATGTTGGTTTAGTTTGAGTTCAAAGGGATACTGGTGTAAGTTCACTTTTTCTTTTT

AAACGGTGTTTATTTATAGAGAGGAGGATCTGTTTCTTTTTAGCCTCGCTTAGATGTCCAGCACATCCAT

CCACACTGACGTCTCTGCTGACCTACAGACATGCTGATCCACACACACACACACACACACACAGTTCA

GCCGACAGAGGAATGTAGCCGCTCGCTCTTATCTTGGTCTGTCTTTAGTGCCTGAGATCTGTTTGTTGTA

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CTTTTCTCCACGAACACCGAGCAATGAGAGAGAAGTGCCACCATAGATGGGATTCTCTACTGCTTCGGTC

ACTTTGAAGATTCCACATATTAAAGAGGATAGACGGGTAAACCGGCTAGAGTTACGTGAAGACTTGAATA

TGAACATGGTAAACATCCGCTGTCAGATTTGACATCATTTTGGCGGAAATAAGTGTGTTAAATGACCCAA

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TTGGTGAAAATACATCTAATCTCACACACAAACACGCTTGTCAAGCTTAAAATTAACCAGTCTGTCTTCT

TCTTTCACACTAATCCATCATATAAAATCTCCCTTTTAACACCCATGGCTTCTAAAACCTTTGTTGTAAA

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AAAATTCTTACTTTAAATGCAAAAATAAATCGCAAAAAAAATGTAATCGCAAAAAAAATTAATCATCCTAT

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CTTACATTGTATACGCAGCGCACATGATGTATTTGAGTGTCACTCGAAAAATGACGTCTCACATGCACCC

TCACAATCAATTACATTTCATGAAAGTGGGGGAAAATAATTTAGCAGCCTGTGTAATATATACCAAACCC

CCTAGTTTTTCGTGATTTTGCAATCAATAAATCCAAGGCAAAATCAACAAATGTCCCAATTTTTACACAA

AATTGAATCGCAAAAATATTAAATAATCTTGTAAAACATCCAATTCTAAACCGTTGAATCAAATTTTATT

TATTTCAGTTTGAAATGAATTGTTTCACGTGAACAATTGACCTTATTCTAAAATGCAGAAGTGCGCCTGT

TTTCGCAATTGTTTTAGAACTTCCGATTCTGTCGCCTATGGAAGAAATGACTAGGAATGATAAACGGCAG

AAAACGGTCAAACTACTTGCTCTACAAACAAATGTTTGCATAACTATACAGACCAAGTAGGATAATATAA

TAAGAAAATGTCAGTTTGCAACATCAAACAGCGAAACGAGCAGTGTTTAATGTCTAAAAATGGATGGAAG

ACAATCAGACCGGAAGTCTCGAGCCACAAACATTCAAATGACTGCGTCCGCTTGTCGGCAAAGAATCAGG

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CCCCCTAGATTTTCGTGATTTTGCGATTGCTGATTCCAACGCAAAATCAACAAAATGTCACAATTTTTTT

GCGATTCTGCAAAATTCTTCATTTAAACTCAAATTAATCGCAATAAAACTTAATCATCTCATAAAACATT

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TTCATGATTTTGGGATCGCTTAAACCAATGCAAAATCAACATATTTAGCAATTTTTTGCGATCGTGCAAA

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ATAATCAAATTATATTTATTTCAGTTTGCAATGAATTGTTTTACGTGACTTATAGACGTTGCTCGAAAAT

TGATGTCTCACCTGCGCCCTCACAATCATTACATTACATGAAAGTAATGAAAAAATAATTGAAATCAATA

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CTGTGTAAAACGTATGCTGGATAAGATGGCGGTTCATTCCGTTGTGGCAACCCCTGATAAAGGGACTTAG

CTGAAAGAAAATGAATGAATAAATGAAAGATCATGCCTCAGCCGGCTCAGAAAAAGTAACTCAAAAGTAA

CGTAACGCATTACTTACCATAAAAAGTAACTAAGGGTGTTTTCACATCTGTAGTTTGCTTCATTTGGTCC

GGACCAAGGGCAATAAATGATACATTGTTGCATTTTCTGCCGTCTTTGAGTCGTTTTCACACCACGCTGC

TGGCTTTGGTCCGAACCAGTTGAAACGAACCAAAATGCAGTCATCTGGCAAAATCCACATCTCTCATTGG

CCAGATGTTGTTGAACATTTCCTAAACTGCTTATTGATTGGTCAGAATTTACGTGCGAGAAAATGCCAGT

GAACTCCCGCACGTAAACAAAACCGGCAGACACAAAATGTCGTTTTTACACTGGAGGGACGACTGCGCTG

CTGATTGTATCCCTGCTTTAGACAAACTCTACATTTCGAGAATGCAGGTCTTTTTGGTCCACTTTTGGTG

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GGGGAGTAACTCAATATTGTAATACACTACTTTCTAAAGTAACTTTCCCAACACTGGCCATAGTGATGGC

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AAAACTAAGTGAGCTTTCCCATAATATAAGCTAAATAATCTGCCATTGGGGTAAGCGAAAACATTCTTTT

GTCAATAGTATATATTTCGGATTTATTGATTAGTGACACTAAATTTTAAAAAACAAACAAAAAGACCCTG

AAACATTAGCTCGAGTTTAAATATTGCTGCATCCCTACATCAAATCCTTCTATTTTTGAAGGTGGCTGTC

ATCCCTTGTGCTGTGAAGGATAGTCCTGCAGCCATAAATGATGTATACCTTAATCTACACCGAAGCCTCC

CATCCATAACAGCTTGTGTCAAAAACTTGCTCTCCCCCTTTGCTCCCTCTACTGACTATTTATAAGTAGT

ATATGCCAAAGGCCAGGCTGGATTGTCTCCGGATCCAGCAGCCAGGGGTTGCATGCATTACGTAACACTG

Mib **exon 20** TGACTGGTTGCTTCTCAGCAGGGGGCTCTAACTCAATGGCAGGGGGGTCGCAGGATCTTCTCCAGCCCAA

CAATCTGGCCCTAAGTTGGTGTAAGTATTCAATTCCTCACCCCAACTTCTTCCTGCCTCAACTTCTTCCT

GCTCCTTTGGGCTCAAGAGTCCGCATCTTCACCCCTGCATTGGTCATTCTCTCCAGTTGGAGAGGCTGTC

GAGTGGCTCGCTGCGTTTTCAGTGCTGTGGGTTGAGTGCTGAAGTCAGAAAAGGCACAAAACTTTCAGAA

TTATAAAGTAATTCAGACATTTAAGAAGTTAGAAGGCTCTGGGGGTCTGCAAACGCCCAGGCATGAACCTT

TATAAGCTACATGATTGGCTGTGGGCCTGGTGTGTATATTTTGTTCTCAACGCATTTTGCTTTGCATTTC

Mib **exon 21** AGCCAGTGGAAATATCCCAGCCTTGCAGAGGGACAAAGACAACACTAATGTCAACGCAGATGTACAGAAG

CTGCAACAGCAACTGCAGGATATCAAAGAGCAGGTGAGTATGACAGTGTGCAGATGGGATGGACAATTTT G←→A

AATTCCTTTATTTTTTGTAGAATAATAATCAACTGTATTTTATAGTTCTTTTACAAGTAGGGGTGGGTAC

CGAAACCAGGTACCTATGTAGCCAGTATGCGCCAGATTGCATCAGCATATGCATTTCAGTGCCACTTGTG

CTGCGATATGAACATAAAAGCATCAAAAGCATCTGTCACACGATCTCTAAACATTTAATCCGAAACAACT

TTGAGGGATACAGACACCGTTGGTGATGTTAGGCATTTGTTCTTGTTGCTTAGGGAAGGCACGTAGGAAA

CAAGCGCAGTATAGCGCATCCGGTGATCGACTCTCTTCAGATTCATCAACACGCAGGATCGCGTTCATCA

AATTTGCTTAAGCTAAGCGTTCTAAAGTATGCAAGGATTCTGACAGGGCAACGTGAAGCACATGCGTTAC

AAAAGTTGCGTGTGGGGGGAAACACGTCAGTCAGTCAGCATGTCACCTTAAAGGGTTAAATGAATAAGGC

TCAGCACTACTACCGTTAAAGTTTGCGCTGTTATAATTCACTTACCTTTTAATCAGATTATAATCTGCTA

TTTAAATATAATGCTAATATTCGGCACAAATCCATCAGTTTCCCTTTCCGGCTGTTCTATCTATGAATAA

ACTATGTAAAAGCACTGTCATGCGTGTTTCCTCGTCGGTTAGTAACGCTATATTTCATTGCACAACAATT

AATCTATCAGGCTTTTTGGCAAAAAAATAGAGAAATCACAGTTTCATTTATTGTTATTAGATTATGTTTA

AATTTCACCTCTCCTGCTGAGCTAAGCTGTTGAATGGTTAGCGTATGAGGCGGCTAGGCTAAGCTAGCTT

TCATTTTGATTGAATTATTCTCTAATCGGTTGCCTATTATGTAGTGAATATACCCCTGTACTGCACACTG

CAGTCCTTTTTTTGTCTGGCTTTCTCGGATATCTCACCTGTTCGCCAAAAATGACATTATATCCCTGGCG

ATGTCTGAAACCGGCGCACACACATTGAAAAAGCCGTGCCAGGCACGAAAGCTTGACAGGCGTAGCAACA

GTAACTAAGGAGGGCGGGGCTTAGCGAAGGGTCCACTGCTGTAAGATAGTGTTAGATTTAGCTGAAAGTG

ATGCAGTTTAAACAGTGAATTGAATCTATTTACCGTCTGTCTACCCACAGATTTGCACCTCTAGATCTTC

Mib **exon 22** AGGATGTTTTGTTTTATTGCCGTTATGGCTCATTGAACATGTTTCTCTTCCTCTCAGACTATGTGCCCGG

TGTGTCTGGATCGTCTGAAGAACATGATCTTCATGTGTGGCCACGGCACCTGTCAGCTGTGTGGAGACCG

CATGAGCGAGTGCCCGATCTGCCGCAAGGCCATCGAGCGCCGAATCCTGCTTTACTAGAGCGCCGCGTCT

GTGTGGTTCTCATAAGCACCTTCCCCGGATCTGCAAGGCTCTCCTTGTCTCACGCTAAGCTAAGAGTCAT

CAGTGTTACCACATCCATCTTTGGTTTCATCTTCAATATTAACGTTTTAATTATGTTCGAGGAGACAGAA

Figure S11. The assembled *mib* genomic nucleotide sequence from scaffolds 3504 and 3540.

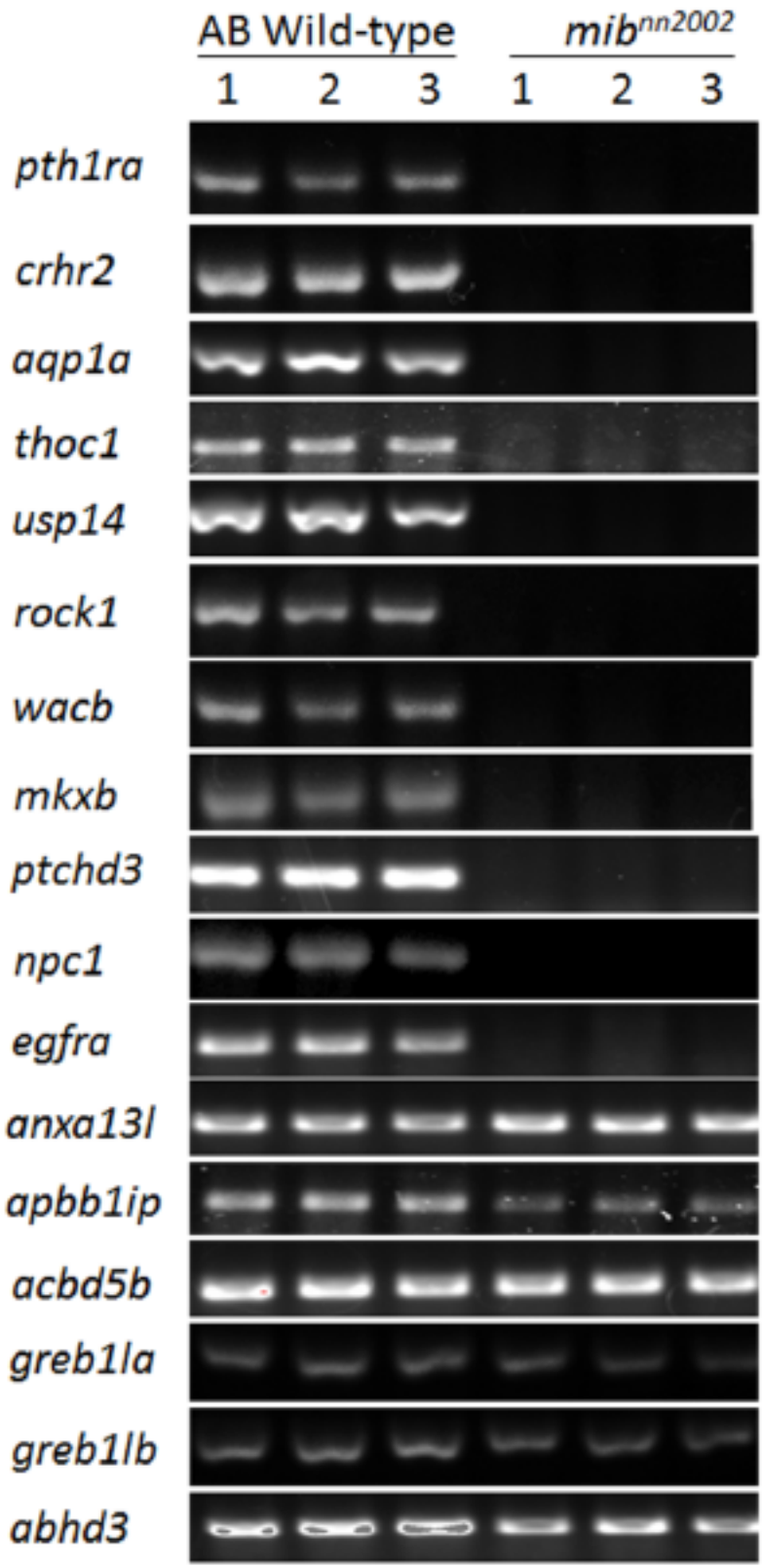
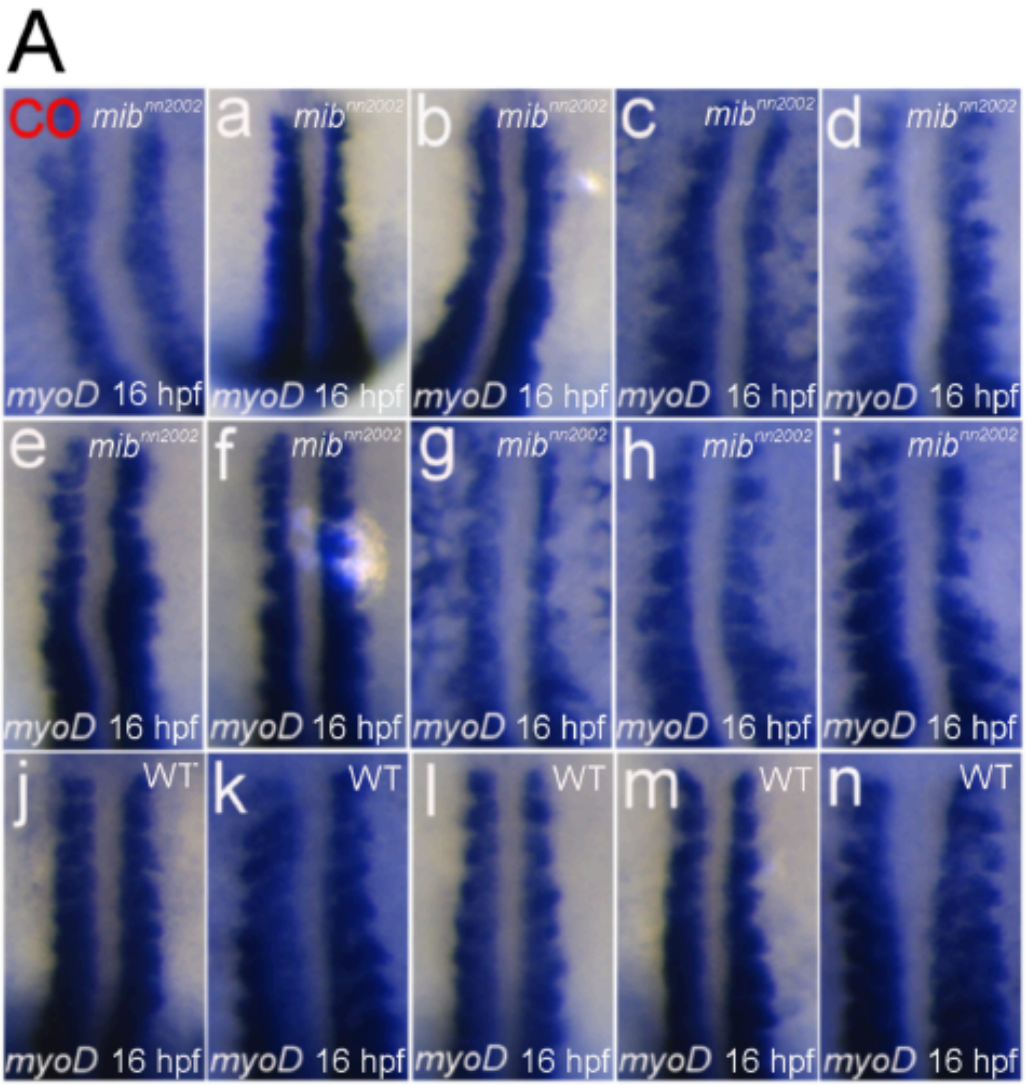


Figure S12. Genomic PCR of genes around *mib* locus on LG2 in wt embryos and *mib*^{nn2002} mutants. Genes listed in the LG2 hypothetical genomic sequences were examined by PCR. The genomic sequence located much close to the terminal (*cldn1* end) of LG2 than *ap2m1a* were not amplified. The not-amplified genes include genes not assembled in LG2, such as *mkxb*, *rab18b* (in Fig. 7), *ptchd3*, *yme1l1b* (in Fig. 7), *mib* (in Fig. 7), *gata6* (in Fig. 7) and *cables1* (in Fig. 7).



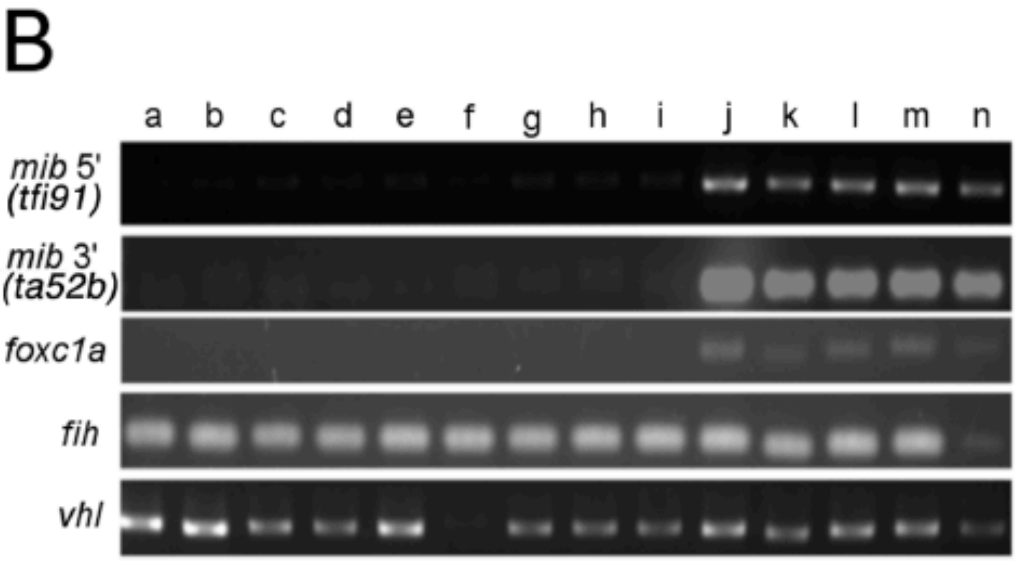


Figure S13. (A) The *myoD* WISH results from 20 pg *foxc1a* mRNA-injected (a–i) *mib*^{nn2002} homozygotes, and (j–n) WT (siblings) and (co) non-injected *mib*^{nn2002} homozygotes and (B) the corresponding genotyping results were shown.

Two major rescued features of *myoD* expression in the anterior somites are segmental and laterally-extended *myoD* pattern, compared (a–n) to (co). The *myoD* expression pattern in the anterior somites was asymmetrically (c, d, h, i) and symmetrically (a, e, f) rescued in *myoD*-overexpressed *mib*^{nn2002} homozygotes, while (b, g) *myoD*-overexpressed *mib*^{nn2002} homozygotes were still indistinguishable from control (co). The genomic fragments of *mib* 5' (amplified with tfi91 primers), *mib* 3' (amplified with ta52b primers), and *foxc1a* (amplified with *foxc1a* primers) were not detected in the homozygous mutants, while the control fragments, *fih* (amplified with *fih* primers) and *vhl* (amplified with *vhl* primers), were detected in the embryos except for *vhl* PCR sample f and *fih* PCR sample n, which might be due to the DNA damage or cross-links that are generated by paraformaldehyde fixation during the WISH procedure[1].

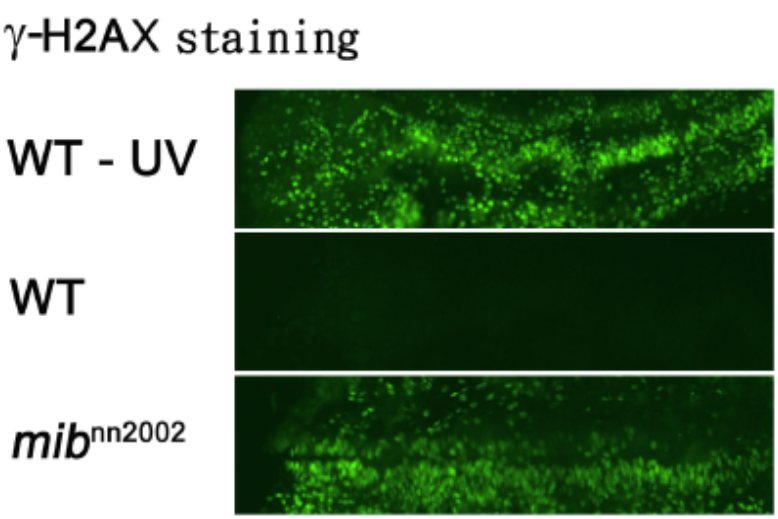


Figure S14. γ-H2AX staining is highly increased in *mib*^{nn2002} mutants.
γ-H2AX, representing the event of DNA damage, was only detected in *mib*^{nn2002} mutants and UV exposed wt embryos (WT-UV).

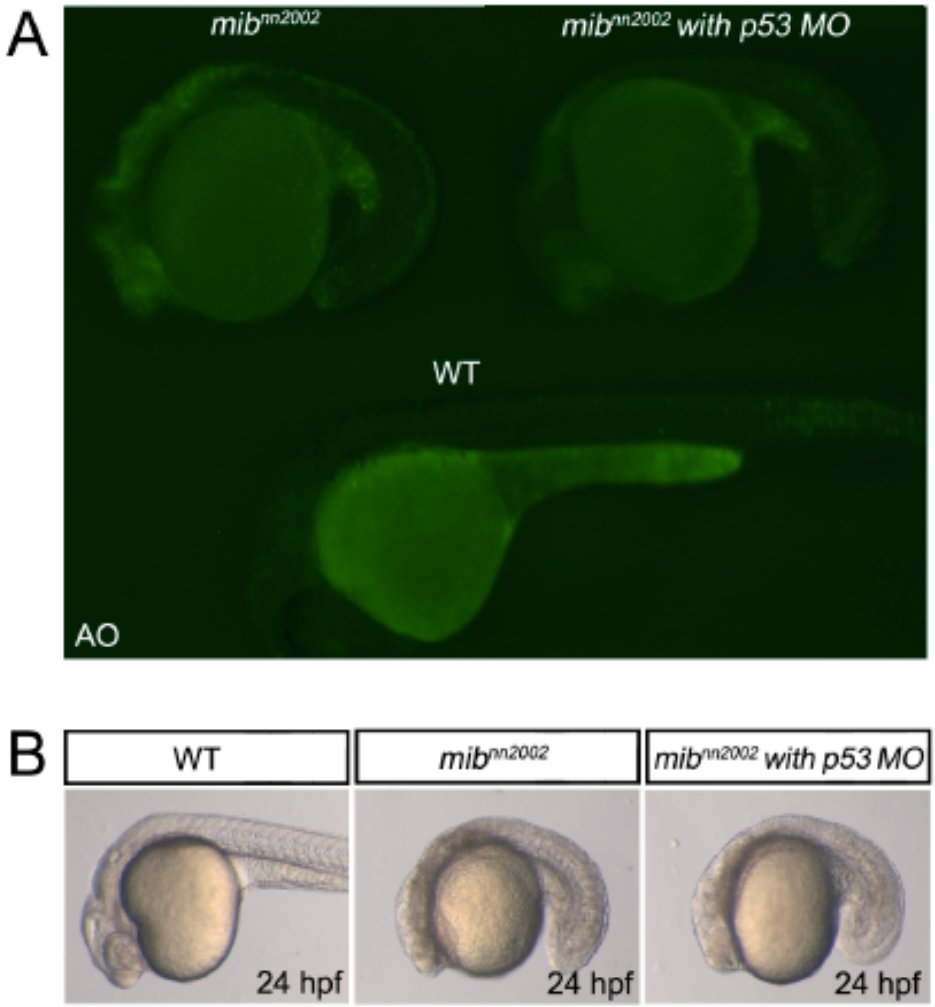


Figure S15. Cell death in *mib*^{nn2002} mutants is *p53*-dependent.
(A) Acridine orange (AO) staining in *mib*^{nn2002}, *mib*^{nn2002} injected with *p53* morpholino and WT. AO staining was partially reduced in *mib*^{nn2002} mutants with *p53* morpholino injection. (B) Nomarski images of WT, *mib*^{nn2002} and *mib*^{nn2002} injected with *p53* morpholino. The deposition of dark granules in *mib*^{nn2002} mutants was suppressed by *p53* down-regulation. This result suggests that the cell death in *mib*^{nn2002} mutants is *p53*-dependent.

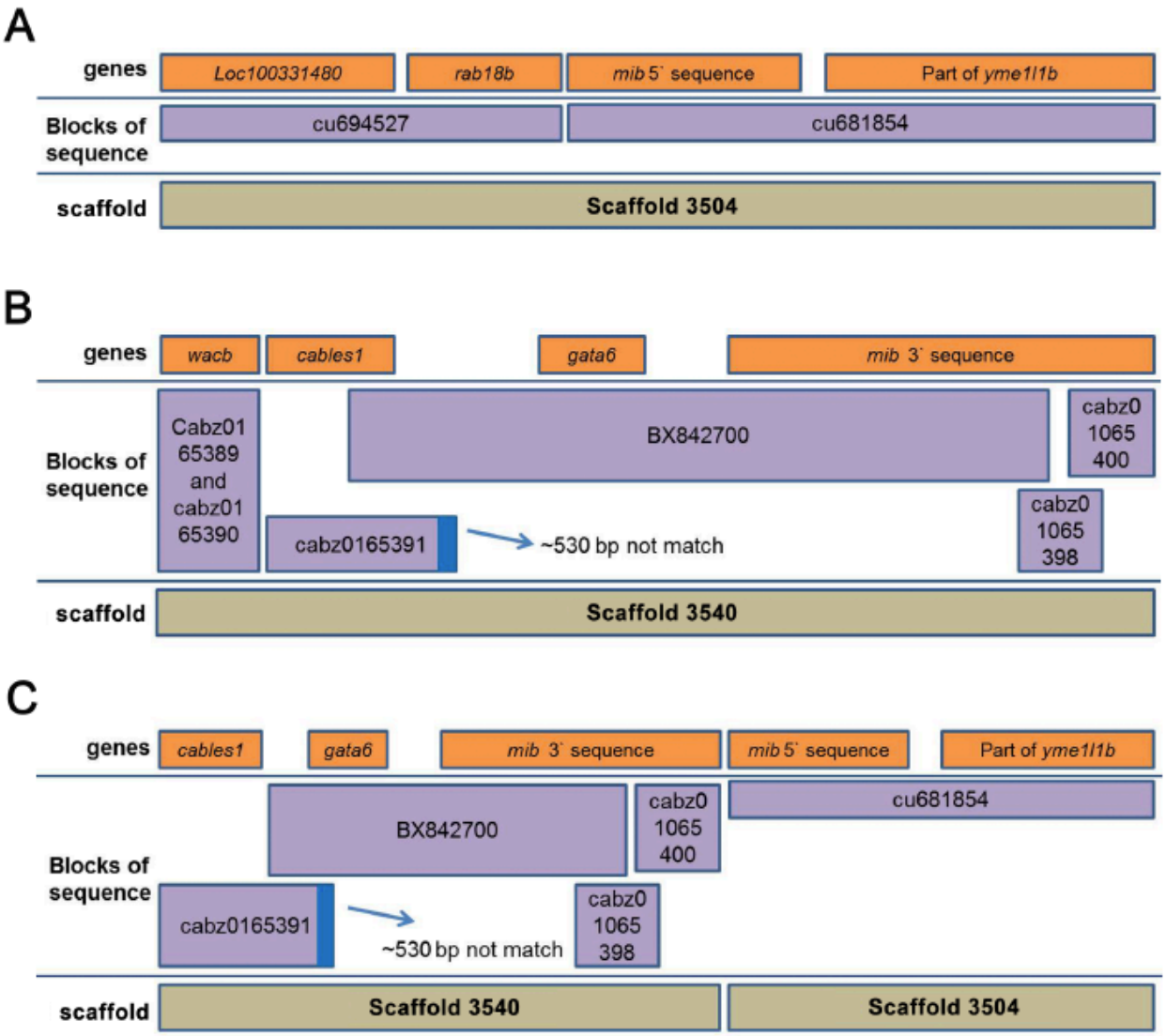


Figure S16. The assembly of *mib* genomic sequence.
(A) Scaffold 3504 of assembling 5' *mib* genomic sequence is illustrated. Scaffold 3504 contains cu694527 and cu681854 sequences. There is no overlap between these two sequences. (B) Scaffold 3540 of assembling of 3' *mib* genomic sequence is illustrated. Scaffold 3540 contains cabz0165389, cabz0165390, cabz0165391, BX842700, cabz01065398 and cabz01065400 sequences. There is no overlap between sequences coding for *wacb* and *cables1*. There is a 530 bp mismatch between cabz0165391 and BX842700. (C) Hypothetical assembly of *mib* genomic sequence is illustrated. In the hypothetical map, the *mib* is located between genes *gata6* and *yme1l1b*.

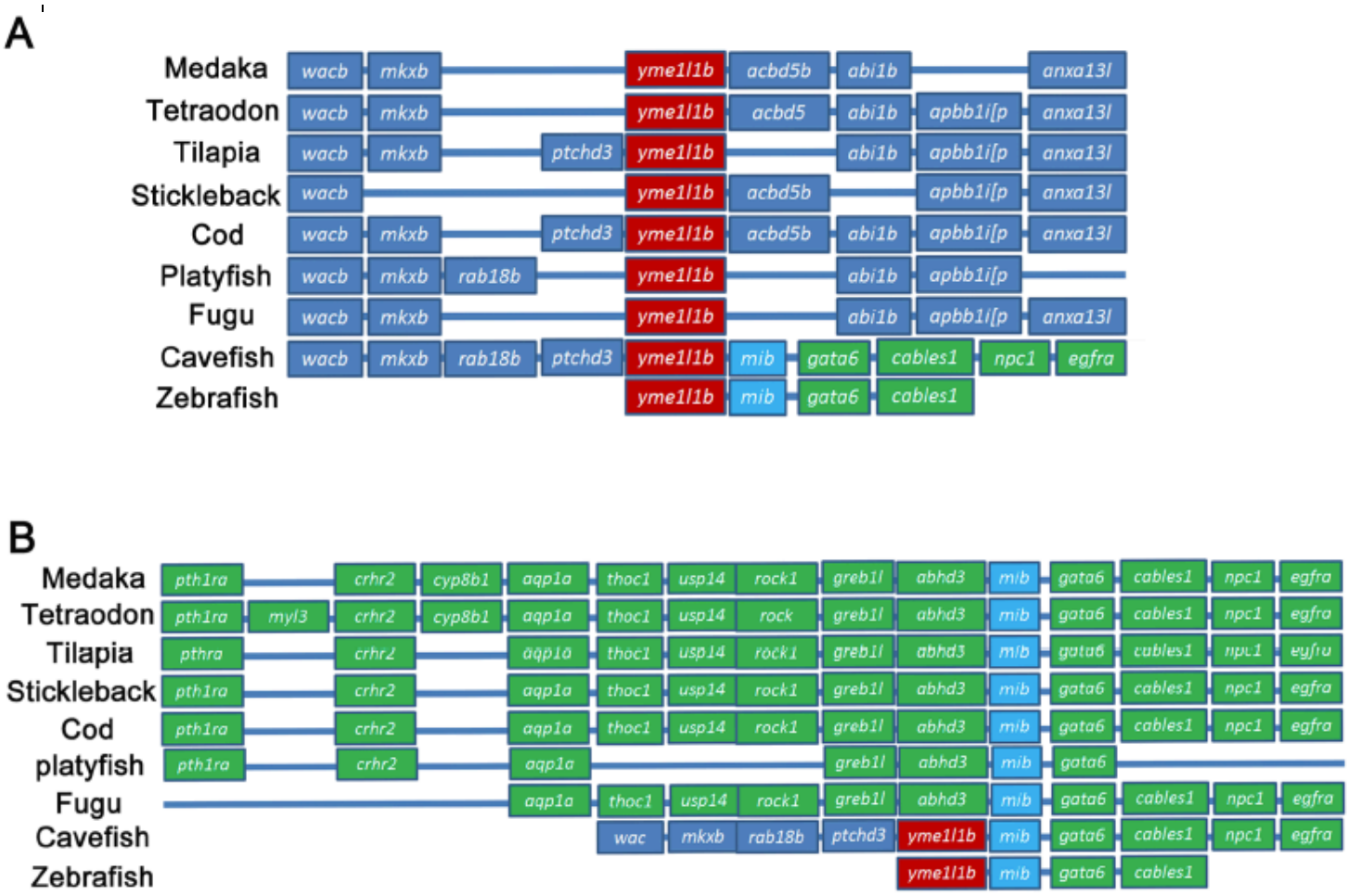


Figure S17. The synteny of genes near *mib* in different fish species.
The synteny in (A) is arranged by aligning the gene *yme1l1b*. The synteny in (B) is arranged by aligning the gene *mib*. The synteny of genes nearby *mib* in zebrafish is much more similar to that of cavefish.

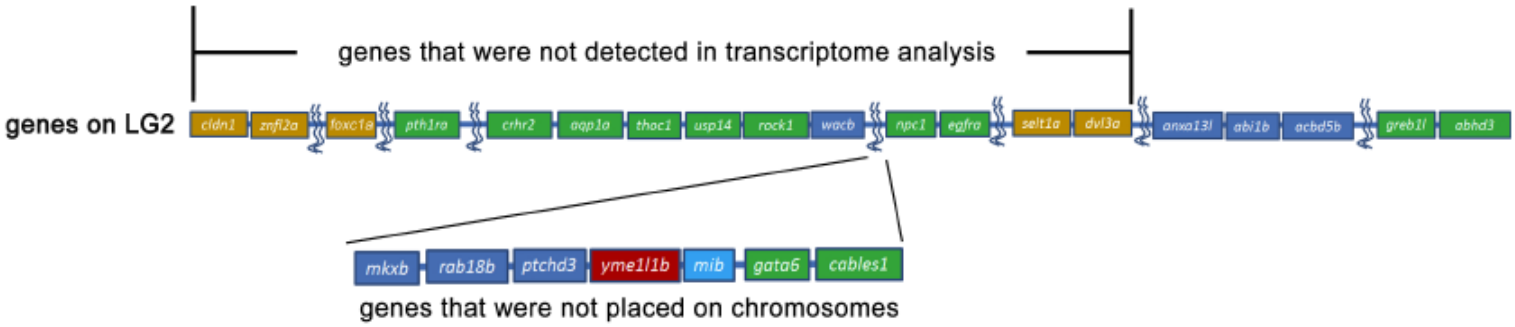


Figure S18. The hypothetical genomic sequence of zebrafish LG2 around *mib* locus.
The location of genes, *cldn1*, *znfl2a* and *foxc1a*, near the chromosome terminal are based on Zv9 zebrafish Ensembl sequence. The gene positions, such as *pth1a*, *crhr2*, *aqp1a*, *thoc1*, *usp14*, *rock1* and *wacb*, are based on the LG2 Ensembl sequence (supplementary Table 4), which match the gene syntenies left to *greb1l* in Medaka, Tetarodon, Tilapia, Stickleback, Cod and Platyfish (supplementary Fig. 17B). This also suggests there is a recombination happened between *wacb* and *rock1* in zebrafish while it was compared with fishes like Medaka. Based on the synteny of cavefish in supplementary Fig. 17, genes, such as *mkxb*, *rab18b*, *ptchd3*, *yme1l1b*, *mib*, *gata6* and *cables1* were placed on the right hand side of *wacb* (these genes are not assembled in any LGs and their genomic DNA is not PCR-amplifiable in mib^{nn2002} mutants). *npc1* and *egfra* were placed on the right hand side of the *mib* scaffold based on the synteny of Cavefish, although *egfra* is much closer to chromosome terminal than *npc1* in Zv9 Ensembl sequence. The location of *selt1a*, *dvl3a*, *anxa13l*, *abi1b*, *acbd5b*, *greb1l* and *abhd3* were based on the Zv9 Ensembl sequence. *anxa13l*, *abi1b* and *acbd5b* were still located near each other as expected (synteny from Medaka to *Fugu*, though *apbb1ip* is located in chromosome 24 in Zv9 Ensembl sequence). *greb1l* and *abhd3* are also located nearby position as expected in synteny. The genes much closer to chromosome terminal than *dvl3a* in the reconsitituted hypothetical map are not detected by RNA-seq and genomic PCR.

References

1. Clingenpeel, S., Schwientek, P., Hugenholtz, P. & Woyke, T. Effects of sample treatments on genome recovery via single-cell genomics. *ISME J.* **8,** 2546–2549 (2014).