

Supplementary Materials for

The genomic mosaicism of hybrid speciation

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Published 14 June 2017, *Sci. Adv.* **3**, e1602996 (2017)

DOI: 10.1126/sciadv.1602996

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Supplementary Materials

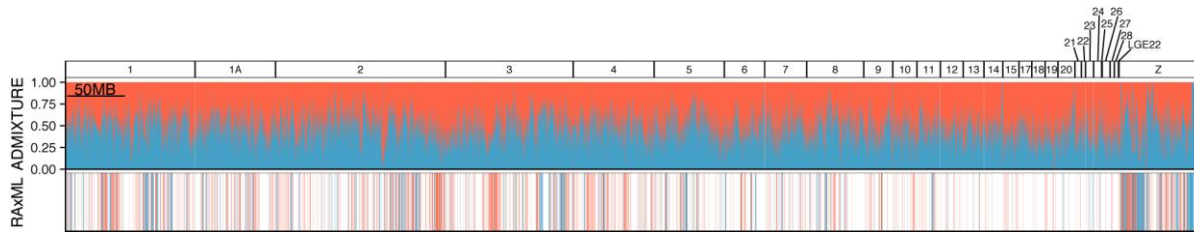


fig. S1. Stepping window ADMIXTURE and RAxML analyses across the Italian sparrow genome. On the top panel, the results from 100kb stepping window ADMIXTURE analysis across the Italian sparrow genome with assignment probabilities to house sparrow ancestry (blue) and Spanish sparrow ancestry (red) on the y-axis. The bottom panel depicts 100kb windows where the Italian sparrow grouped monophyletically with the house (blue), Spanish (red) or in its own clade (green) according to RAxML analysis across the genome.

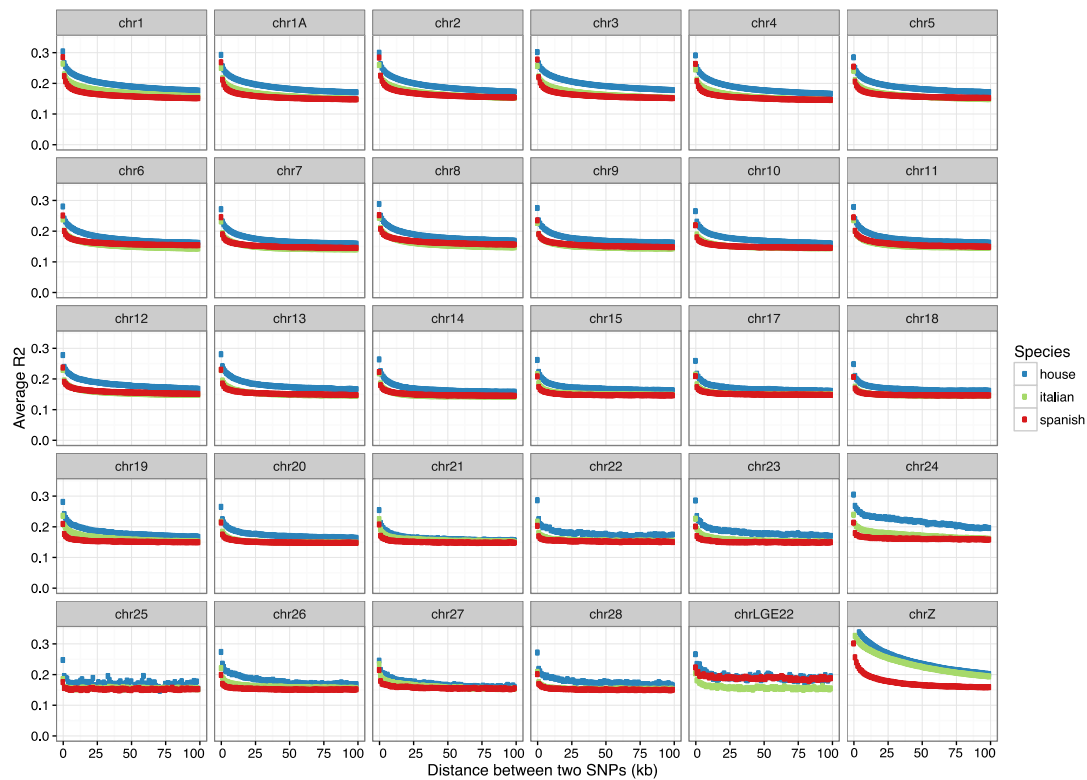


fig. S2. LD decay across all chromosomes. Pairwise r^2 values for all SNPs genotyped in at least 80% of individuals within each population in a 100 kb window binned in 1kb increments. Decay of linkage disequilibrium is plotted by distance between SNPs for the house (blue), Italian (green) and Spanish (red) sparrow populations.

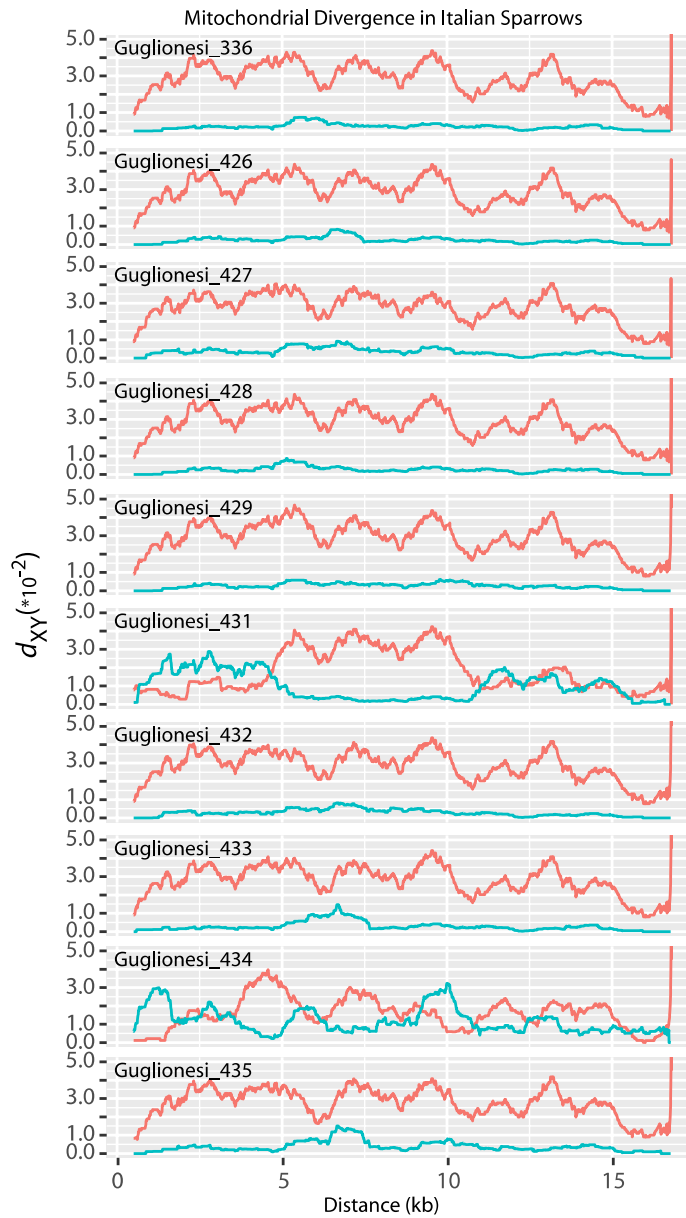


fig. S3. Mitochondrial sequence divergence between each Italian sparrow and the parent populations. Plots of overlapping sliding window (1kb window, 100bp step) d_{XY} estimates along the mitochondria of the house and Italian (blue), and Spanish and Italian (red) sparrows for all ten Italian sparrow individuals.

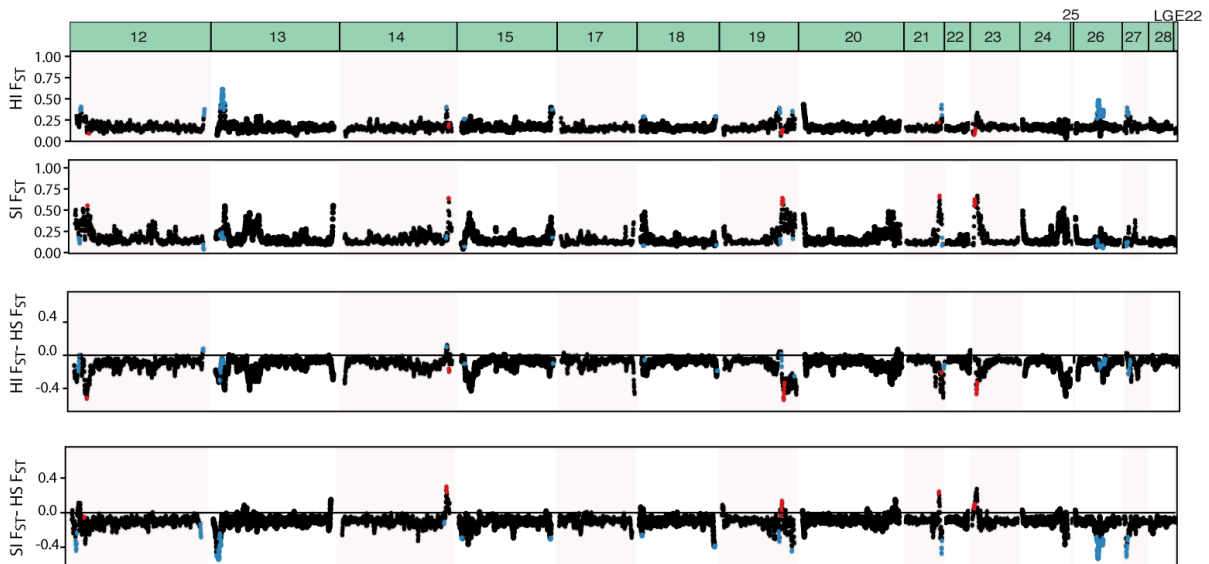


fig. S4. Divergence peaks between the Italian sparrow and either parent taxa on microchromosomes. F_{ST} plot for the HI (top), and SI comparisons (second from top) for 100kb overlapping windows with 25kb steps across the genome. The bottom two panels display the disparities in F_{ST} values between each SI and HI comparison from the parent species comparison for the same 100kb overlapping windows. Windows identified as HI divergence peaks are shown in blue, SI in red, and PI peaks in green.

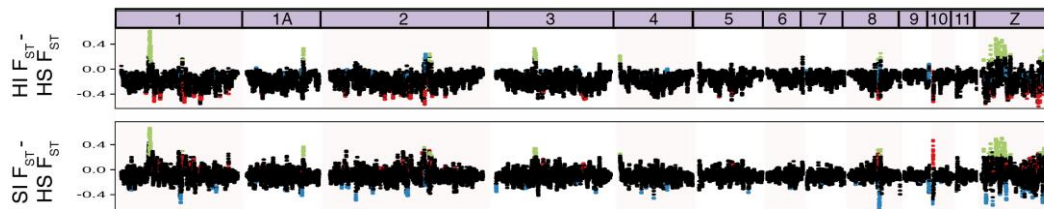


fig. S5. Divergence peaks for PI regions on large chromosomes. F_{ST} disparities between the HI and HS comparisons for 100kb overlapping windows with 25 kb steps across the large chromosomes (top) and disparities between SI and HS comparisons in the bottom panel. HI divergence peaks are shown in blue, SI in red, PI in green.

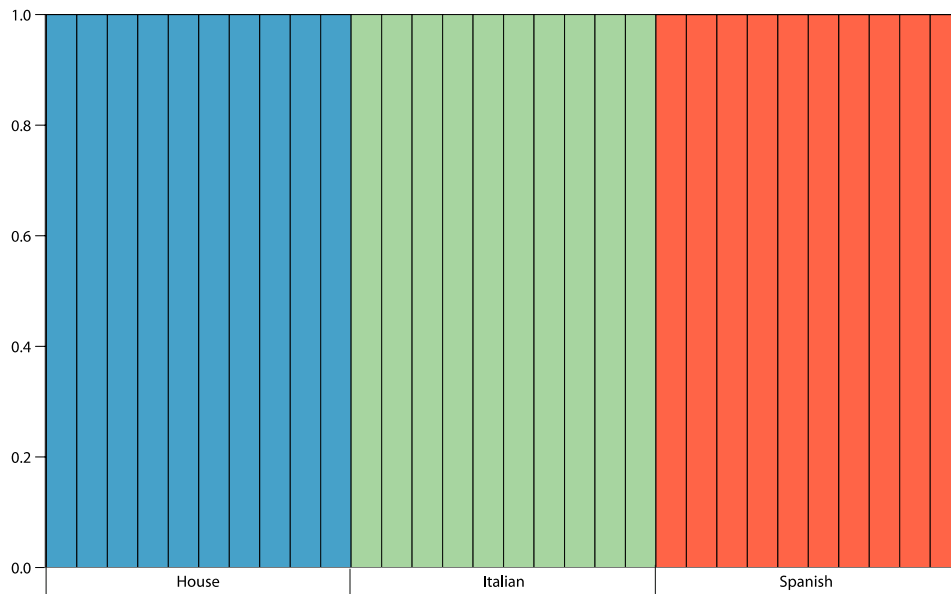


fig. S6. Population structuring analysis of sparrow individuals. Results from NgsAdmix analysis of house, Italian and Spanish sparrows (K=3). Species are labelled along the x-axis while the y-axis is the probability of ancestry to the given assignment group.

table S1. Sequencing scheme for the house sparrow reference genome assembly.

Type	Insert size (bp)	Read length (bp)	# of reads	Coverage*
Paired end	180	100	601,573,350	49.7
Mate Pair	3,000	100	566,727,504	46.8
Mate Pair	8,000	100	245,671,168	20.3
Mate Pair	10,000	100	166,477,940	13.8
Total			1,580,449,962	130.6

*Coverage per library - calculated from the estimated genome size from the ALLPATHS-LG output, i.e. (number of reads x read length)/genome size.

table S2. Final assembly statistics. Descriptive statistics for the scaffolded (including linkage groups) house sparrow reference genome following the Assemblathon parameters (56).

Number of scaffolds	2,301	
Total size of scaffolds	1,042,720,703	
Longest scaffold	147,836,772	
Shortest scaffold	1,000	
Number of scaffolds > 500 nt	2,301	100.0%
Number of scaffolds > 1K nt	2,300	100.0%
Number of scaffolds > 10K nt	748	32.5%
Number of scaffolds > 100K nt	170	7.4%
Number of scaffolds > 1M nt	30	1.3%
Mean scaffold size	453,160	
Median scaffold size	1,756	
N50 scaffold length	68,733,010	
L50 scaffold count	6	
N50 scaffold - NG50 scaffold length difference	68,733,010	
scaffold %A	27.94	
scaffold %C	19.96	
scaffold %G	19.99	
scaffold %T	27.99	
scaffold %N	4.12	
scaffold N nt	42,993,395	
scaffold %non-ACGTN	0	
Number of scaffold non-ACGTN nt	0	
Percentage of assembly in scaffolded contigs	99.8%	
Percentage of assembly in unscaffolded contigs	0.2%	
Average number of contigs per scaffold	19	
Average length of breaks (20 or more Ns) between contigs	1,037	
Number of contigs	43,686	
Number of contigs in scaffolds	42,359	
Number of contigs not in scaffolds	1,327	
Total size of contigs	999,796,755	
Longest contig	681,761	
Shortest contig	217	

Number of contigs > 500 nt	43,578	99.8%
Number of contigs > 1K nt	43,091	98.6%
Number of contigs > 10K nt	19,201	44.0%
Number of contigs > 100K nt	2,091	4.8%
Number of contigs > 1M nt	0	0.00%
Mean contig size	22,886	
Median contig size	7,568	
N50 contig length	65,274	
L50 contig count	4,069	
N50 contig - NG50 contig length difference	65,274	
contig %A	29.14	
contig %C	20.81	
contig %G	20.85	
contig %T	29.19	
contig %N	0.01	
contig N nt	69,447	
contig %non-ACGTN	0	

table S3. Sample information.

Species	Sample ID	Sex	Date	Location	Latitude	Longitude
<i>P. domesticus</i> BIOSAMPLE: SAMN02929199	8887266	<i>F</i>	08/08/02	Aldra, Norway	~ 66° 24' 03" N	~ 13° 06' 29" E
<i>P. domesticus</i>	8L19786	<i>M</i>	7/4/07	Alta, Norway	~ 69° 58' 23." N	~ 23° 29' 01" E
<i>P. domesticus</i>	8L64869	<i>M</i>	2/10/09	Leka, Norway	~ 65° 05' 28" N	~ 11° 43' 20" E
<i>P. domesticus</i>	8L89915	<i>M</i>	5/21/09	Træna, Norway	~ 66° 30' 04" N	~ 12° 06' 02" E
<i>P. domesticus</i>	8M31651	<i>M</i>	2/14/10	Leka, Norway	~ 65° 05' 53" N	~ 11° 42' 00" E
<i>P. domesticus</i>	8M71932	<i>M</i>	3/30/11	Løkta, Norway	~ 66° 10' 51" N	~ 12° 43' 16" E
<i>P. domesticus</i>	8M72455	<i>M</i>	7/5/10	Kvål, Norway	~ 63° 14' 12" N	~ 10° 16' 33" E
<i>P. domesticus</i>	8N05890	<i>M</i>	2/20/12	Leka, Norway	~ 65° 02' 58" N	~ 11° 36' 12" E
<i>P. domesticus</i>	8N06612	<i>M</i>	2/4/12	Linesøya, Norway	~ 64° 01' 40" N	~ 09° 55' 15" E
<i>P. domesticus</i>	8N73248	<i>M</i>	3/6/13	Lauvøya, Norway	~ 63° 55' 36" N	~ 09° 56' 07" E
<i>P. domesticus</i>	8N73604	<i>M</i>	3/7/13	Lauvøya, Norway	~ 63° 55' 36" N	~ 09° 56' 07" E
<i>P. hispaniolensis</i>	Phisp_11_Lesina_280	<i>M</i>	4/2/08	Lesina, Italy	~ 41° 51' 30.84" N	~ 15° 27' 03" E
<i>P. hispaniolensis</i>	Phisp_12_Lesina_281	<i>M</i>	4/2/08	Lesina, Italy	~ 41° 51' 30.84" N	~ 15° 27' 03" E
<i>P. hispaniolensis</i>	Phisp_13_Lesina_282	<i>M</i>	4/2/08	Lesina, Italy	~ 41° 51' 30.84" N	~ 15° 27' 03" E
<i>P. hispaniolensis</i>	Phisp_14_Lesina_285	<i>M</i>	4/2/08	Lesina, Italy	~ 41° 51' 30.84" N	~ 15° 27' 03" E
<i>P. hispaniolensis</i>	Phisp_15_Lesina_286	<i>M</i>	4/2/08	Lesina, Italy	~ 41° 51' 30.84" N	~ 15° 27' 03" E
<i>P. hispaniolensis</i>	Phisp_16_Lesina_287	<i>M</i>	4/2/08	Lesina, Italy	~ 41° 51' 30.84" N	~ 15° 27' 03" E
<i>P. hispaniolensis</i>	Phisp_17_Lesina_288	<i>M</i>	4/2/08	Lesina, Italy	~ 41° 51' 30.84" N	~ 15° 27' 03" E
<i>P. hispaniolensis</i>	Phisp_18_Lesina_289	<i>M</i>	4/2/08	Lesina, Italy	~ 41° 51' 30.84" N	~ 15° 27' 03" E
<i>P. hispaniolensis</i>	Phisp_19_Lesina_292	<i>M</i>	4/2/08	Lesina, Italy	~ 41° 51' 30.84" N	~ 15° 27' 03" E
<i>P. hispaniolensis</i>	Phisp_20_Lesina_295	<i>M</i>	4/2/08	Lesina, Italy	~ 41° 51' 30.84" N	~ 15° 27' 03" E
<i>P. italiae</i>	Pitaliae_21_Guglionesi_426	<i>M</i>	4/15/08	Guglionesi, Italy	~ 41° 54' 48.25" N	~ 14° 54' 50" E
<i>P. italiae</i>	Pitaliae_22_Guglionesi_427	<i>M</i>	4/15/08	Guglionesi, Italy	~ 41° 54' 48.25" N	~ 14° 54' 50" E
<i>P. italiae</i>	Pitaliae_23_Guglionesi_428	<i>M</i>	4/15/08	Guglionesi, Italy	~ 41° 54' 48.25" N	~ 14° 54' 50" E
<i>P. itallae</i>	Pitaliae_24_Guglionesi_429	<i>M</i>	4/15/08	Guglionesi, Italy	~ 41° 54' 48.25" N	~ 14° 54' 50" E
<i>P. italiae</i>	Pitaliae_25_Guglionesi_431	<i>M</i>	4/15/08	Guglionesi, Italy	~ 41° 54' 48.25" N	~ 14° 54' 50" E

<i>P. italiae</i>	Pitaliae_26_Guglionesi_432	<i>M</i>	4/15/08	Guglionesi, Italy	~ 41° 54' 48.25" N	~ 14° 54' 50" E
<i>P. italiae</i>	Pitaliae_27_Guglionesi_433	<i>M</i>	4/15/08	Guglionesi, Italy	~ 41° 54' 48.25" N	~ 14° 54' 50" E
<i>P. italiae</i>	Pitaliae_28_Guglionesi_434	<i>M</i>	4/15/08	Guglionesi, Italy	~ 41° 54' 48.25" N	~ 14° 54' 50" E
<i>P. italiae</i>	Pitaliae_29_Guglionesi_435	<i>M</i>	4/15/08	Guglionesi, Italy	~ 41° 54' 48.25" N	~ 14° 54' 50" E
<i>P. italiae</i>	Pitaliae_30_Guglionesi_336	<i>M</i>	4/15/08	Guglionesi, Italy	~ 41° 54' 48.25" N	~ 14° 54' 50." E
<i>P. montanus</i>	Pmontanus_1_Naxos_2	<i>M</i>	4/17/08	Giardina Naxos, Italy	~ 37° 49' 08.91" N	~ 15° 16' 12." E

table S4. Results from genome-wide RAxML analysis.

Chromosome	HI Resolved Phylogenies (%)	PI Resolved Phylogenies (%)	SI Resolved Phylogenies (%)	Unresolved Phylogenies (%)
1	13.8	0.3	16.6	69.4
1A	7.7	0.7	13.9	77.7
2	10.3	1.1	17.0	71.6
3	10.1	1.6	17.3	71.0
4	5.1	0.6	19.2	75.1
5	8.3	1.5	10.8	79.4
6	6.6	0.3	9.1	84.0
7	4.1	0.5	9.3	86.1
8	8.5	0.4	9.1	82.1
9	3.2	1.6	9.5	85.8
10	1.9	0.0	9.5	88.6
11	4.9	0.0	10.2	84.9
12	1.5	0.0	6.1	92.4
13	2.8	0.0	3.3	93.9
14	1.2	0.0	1.8	97.0
15	0.7	0.7	11.3	87.2
17	0.0	0.0	2.6	97.4
18	0.0	0.0	4.3	95.7
19	0.0	0.0	12.4	87.6
20	5.4	0.0	3.4	91.3
21	0.0	0.0	6.8	93.2
22	0.0	0.0	0.0	100.0
23	7.0	0.0	7.0	85.9
24	2.8	0.0	9.9	87.3
25	0.0	0.0	0.0	100.0
26	1.4	0.0	1.4	97.1
27	0.0	0.0	7.9	92.1
28	0.0	0.0	0.0	100.0
LGE22	0.0	0.0	0.0	100.0
Z	34.2	0.0	26.7	39.1
Whole genome	9.4	0.7	13.9	76.1

table S5. Comparison of resolved RAxML phylogenies at variable window sizes.

Window Size	Region	HI Resolved Phylogenies (%)	PI Resolved Phylogenies (%)	SI Resolved Phylogenies (%)	Unresolved Phylogenies (%)
100kb	Chr. Z	34.2	0.0	26.7	39.1
	Whole genome	9.4	0.7	13.9	76.1
50kb	Chr. Z	34.6	0.4	24.1	40.9
	Whole genome	9.9	0.8	12.7	76.6
10kb	Chr. Z	31.3	0.6	19.0	49.1
	Whole genome	9.4	0.8	10.2	79.6

table S6. ENSEMBLE gene IDs for genes within top divergence windows.

Gene	Outlier Type	Human ID	Chicken ID	Zebra finch ID
ABCC9	SI	ENSG00000069431	ENSGALG00000013244	NA
ALDOB	SI	ENSG00000136872	ENSGALG00000015544	ENSTGUG00000000650
APTX	SI	ENSG00000137074	ENSGALG00000001954	ENSTGUG00000001441
ATP9B	SI	ENSG00000166377	ENSGALG00000012656	ENSTGUG00000006549
CALN1	SI	ENSG00000183166	ENSGALG00000001122	NA
CHRNA3	SI	ENSG00000080644	ENSGALG00000003014	ENSTGUG00000003469
CHRNA5	SI	ENSG00000169684	ENSGALG00000003021	ENSTGUG00000003451
CHRNB4	SI	ENSG00000117971	ENSGALG00000003005	NA
CKMT2	SI	ENSG00000131730	ENSGALG00000015602	NA
CMAS	SI	ENSG00000111726	ENSGALG00000013229	ENSTGUG00000012063
CORO2A	SI	ENSG00000106789	ENSGALG00000001933	ENSTGUG00000001408
CRABP1	SI	ENSG00000166426	ENSGALG00000003193	ENSTGUG00000003323
CTDP1	SI	ENSG00000060069	ENSGALG00000012653	ENSTGUG00000006649
DNAJA1	SI	ENSG00000086061	ENSGALG00000023066	ENSTGUG00000001446
DNAJC25	SI	ENSG00000059769	ENSGALG00000015684	NA
ECM29 (=KIAA0368)	SI	ENSG00000136813	ENSGALG00000015689	ENSTGUG00000001279
EPHB2	SI	ENSG00000133216	ENSGALG00000004741	ENSTGUG00000017194
ETFA	SI	ENSG00000140374	ENSGALG00000002925	
FAM78B	SI	ENSG00000188859	ENSGALG00000003035	ENSTGUG00000017258
FASLG	SI	ENSG00000117560	ENSGALG00000003076	ENSTGUG00000017264
FBXO22	SI	ENSG00000167196	ENSGALG00000028035	ENSTGUG00000003514
FMO5	SI	ENSG00000131781	NA	NA
FOCAD	SI	ENSG00000188352	ENSGALG00000015071	ENSTGUG00000004262
FXN	SI	ENSG00000165060	ENSGALG00000015108	ENSTGUG00000004200
GEMIN8	SI	ENSG00000046647	ENSGALG00000016574	
GHR	SI	ENSG00000112964	ENSGALG00000014855	ENSTGUG00000002265
GLI3	SI	ENSG00000106571	ENSGALG00000012329	ENSTGUG00000001834
GNG10	SI	ENSG00000242616	ENSGALG00000015683	ENSTGUG00000001275
GREM2	SI	ENSG00000180875	ENSGALG00000010773	ENSTGUG00000010595
HMGCS2	SI	ENSG00000134240	ENSGALG00000002960	ENSTGUG00000017243
HSDL2	SI	ENSG00000119471	ENSGALG00000015663	NA
HYKK	SI	ENSG00000188266	ENSGALG00000003063	ENSTGUG00000003420
IKBKAP	SI	ENSG00000070061	ENSGALG00000001947	ENSTGUG00000001421
INHBA	SI	ENSG00000122641	ENSGALG00000012327	ENSTGUG00000001843
IREB2	SI	ENSG00000136381	ENSGALG00000003171	ENSTGUG00000003332
ISL2	SI	ENSG00000159556	NA	NA
KCNJ8	SI	ENSG00000121361	ENSGALG00000026373	ENSTGUG00000012087
L3MBTL3	SI	ENSG00000198945	ENSGALG00000014009	ENSTGUG00000011709
LPPR1 (=PLPPR1)	SI	ENSG00000148123	ENSGALG00000015542	ENSTGUG00000000645
MECR	SI	ENSG00000116353	ENSGALG00000001426	ENSTGUG00000000771
N (=NOTCH1)	SI	ENSG00000148400	ENSGALG00000002375	ENSTGUG00000006073
NFATC1	SI	ENSG00000131196	ENSGALG00000012654	ENSTGUG00000006621
NOTCH2	SI	ENSG00000134250	ENSGALG00000002922	ENSTGUG000000017231
NRG1	SI	ENSG00000157168	ENSGALG00000015422	ENSTGUG00000000280
NTN3	SI	ENSG00000162068	ENSGALG00000029072	ENSTGUG00000003265
PCDH9	SI	ENSG00000184226	ENSGALG00000016908	ENSTGUG00000012486
PDE4DIP	SI	ENSG00000178104	ENSGALG00000011777	NA
PHGDH	SI	ENSG00000092621	ENSGALG00000002988	NA
PIP5K1B	SI	ENSG00000107242	ENSGALG00000015107	ENSTGUG00000004178
PPAPDC2 (=PLPP6)	SI	ENSG00000205808	NA	NA

PRDX6	SI	ENSG00000117592	ENSGALG00000003053	NA
PRKAB2	SI	ENSG00000131791	ENSGALG00000001678	ENSTGUG000000017249
PSMA4	SI	ENSG00000041357	ENSGALG00000003046	ENSTGUG00000003425
PTBP3	SI	ENSG00000119314	ENSGALG00000015669	ENSTGUG00000001262
PTCH1	SI	ENSG00000185920	ENSGALG00000012620	ENSTGUG00000000532
PTPLAD2 (=HACD4)	SI	ENSG00000188921	ENSGALG00000028142	NA
PTPRU	SI	ENSG00000060656	ENSGALG00000001443	ENSTGUG00000000777
RCN2	SI	ENSG00000117906	ENSGALG00000002844	ENSTGUG00000003639
REG4	SI	ENSG00000134193	ENSGALG00000002931	ENSTGUG00000017242
RFK	SI	ENSG00000135002	ENSGALG00000000004	ENSTGUG00000003505
RGS7	SI	ENSG00000182901	ENSGALG00000010772	ENSTGUG00000010596
RNF20	SI	ENSG00000155827	ENSGALG00000015548	ENSTGUG00000017517
SCAPER	SI	ENSG00000140386	ENSGALG00000002883	ENSTGUG00000003573
SEPP1	SI	ENSG00000250722	ENSGALG00000014857	NA
SLC10A2	SI	ENSG00000125255	ENSGALG00000016858	ENSTGUG00000010806
SMU1	SI	ENSG00000122692	ENSGALG00000002014	ENSTGUG00000001458
SRSF4	SI	ENSG00000116350	ENSGALG00000001411	ENSTGUG00000000765
SUCO	SI	ENSG00000094975	ENSGALG00000003081	ENSTGUG00000017265
SUSD1	SI	ENSG00000106868	ENSGALG00000015677	ENSTGUG00000001267
TADA1	SI	ENSG00000152382	ENSGALG00000003064	ENSTGUG00000017261
TBC1D2	SI	ENSG00000095383	ENSGALG00000001944	ENSTGUG00000001416
TBC1D24	SI	ENSG00000162065	NA	NA
TJP2	SI	ENSG00000119139	ENSGALG00000015109	NA
TMEM246	SI	ENSG00000165152	ENSGALG00000015545	ENSTGUG00000000659
WBCR17	SI	ENSG00000185274	ENSGALG00000001130	ENSTGUG00000003475
ZCCHC9	SI	ENSG00000131732	ENSGALG00000015603	ENSTGUG00000006994
ACR	HI	ENSG00000100312	ENSGALG00000023986	NA
ADORA1	HI	ENSG00000163485	ENSGALG00000000168	ENSTGUG00000001381
AGXT2	HI	ENSG00000113492	ENSGALG00000003432	ENSTGUG00000001974
ANKRD55	HI	ENSG00000164512	ENSGALG00000014717	ENSTGUG00000002579
ANXA10	HI	ENSG00000109511	ENSGALG00000009573	ENSTGUG00000006030
ASXL3	HI	ENSG00000141431	ENSGALG00000015196	ENSTGUG00000010779
ATG7	HI	ENSG00000197548	ENSGALG00000004932	ENSTGUG00000004145
ABCA1	HI	ENSG00000165029	ENSGALG00000015433	ENSTGUG00000000310
BMP15	HI	ENSG00000130385	ENSGALG00000004742	ENSTGUG00000004869
BRD9	HI	ENSG00000028310	ENSGALG00000012514	ENSTGUG00000006776
C16ORF59	HI	ENSG00000162062	NA	NA
C6	HI	ENSG00000039537	ENSGALG00000014840	ENSTGUG00000002207
C7	HI	ENSG00000112936	ENSGALG00000014835	ENSTGUG00000002197
CA12	HI	ENSG00000074410	ENSGALG00000003456	NA
CAB39	HI	ENSG00000135932	ENSGALG00000027262	ENSTGUG00000005413
CANT1	HI	ENSG00000171302	ENSGALG00000011822	ENSTGUG00000003205
CCNB3	HI	ENSG00000147082	ENSGALG00000025810	NA
CLDN4	HI	ENSG00000189143	ENSGALG00000027569	ENSTGUG00000003355
CLIC2	HI	ENSG00000155962	ENSGALG00000004730	ENSTGUG00000004925
CMTM3	HI	ENSG00000140931	ENSGALG00000000424	ENSTGUG00000009792
COL4A6	HI	ENSG00000197565	ENSGALG00000008266	ENSTGUG00000004100
COPB2	HI	ENSG00000184432	ENSGALG00000005357	ENSTGUG00000005180
CRHR1	HI	ENSG00000263715	ENSGALG00000000371	NA
CRIP1	HI	ENSG00000213145	NA	NA
CSRP1	HI	ENSG00000159176	ENSGALG00000000318	ENSTGUG00000001313
CYTH1	HI	ENSG00000108669	ENSGALG00000007093	NA
CDC42	HI	ENSG00000070831	ENSGALG00000004796	ENSTGUG00000017253
CIB2	HI	ENSG00000136425	ENSGALG00000026674	ENSTGUG00000003241
CKLF	HI	ENSG00000217555	ENSGALG00000005254	NA
CLDN3	HI	ENSG00000165215	ENSGALG00000022557	NA
CRIP2	HI	ENSG00000182809	ENSGALG00000026471	ENSTGUG00000017183

DAPK2	HI	ENSG0000035664	ENSGALG0000003336	ENSTGUG0000003221
DDR2	HI	ENSG00000162733	NA	ENSTGUG00000017090
DGKD	HI	ENSG00000077044	ENSGALG00000001730	ENSTGUG00000007464
DNAJC21	HI	ENSG00000168724	ENSGALG00000003387	ENSTGUG00000001971
DENND2D	HI	ENSG00000162777	ENSGALG00000000154	ENSTGUG00000001388
DNAH17	HI	ENSG00000187775	ENSGALG00000007106	NA
EIF3E	HI	ENSG00000104408	ENSGALG00000016093	NA
EMC2	HI	ENSG00000104412	ENSGALG00000016097	NA
ENGASE	HI	ENSG00000167280	ENSGALG00000011816	ENSTGUG00000003184
ERBB2IP	HI	NA	ENSGALG00000014773	NA
EVA1C	HI	ENSG00000166979	ENSGALG00000015888	ENSTGUG00000013443
FBXL22	HI	ENSG00000197361	ENSGALG00000003401	ENSTGUG00000003187
FCGBP	HI	ENSG00000275395	ENSGALG00000007208	NA
FGD5	HI	ENSG00000154783	ENSGALG00000008546	ENSTGUG00000010607
FOXL2	HI	ENSG00000183770	ENSGALG00000021009	ENSTGUG00000005285
GABRP	HI	ENSG00000094755	ENSGALG00000002152	ENSTGUG00000014916
GNAI1	HI	ENSG00000127955	ENSGALG00000008382	ENSTGUG00000002652
GNPDA2	HI	ENSG00000163281	ENSGALG00000014210	ENSTGUG00000008441
GPR35	HI	ENSG00000178623	ENSGALG00000005546	NA
GUF1	HI	ENSG00000151806	ENSGALG00000014217	ENSTGUG00000008453
GOLGA4	HI	ENSG00000144674	ENSGALG00000012258	ENSTGUG00000001889
GPR55	HI	ENSG00000135898	ENSGALG00000005544	ENSTGUG00000005448
HDAC11	HI	ENSG00000163517	ENSGALG00000005092	ENSTGUG00000003803
HERC1	HI	ENSG00000103657	ENSGALG00000003381	ENSTGUG00000003191
HRH1	HI	ENSG00000196639	ENSGALG00000004930	ENSTGUG00000004180
HTATIP2	HI	ENSG00000109854	ENSGALG00000002581	ENSTGUG00000017027
HDAC8	HI	ENSG00000147099	ENSGALG00000004825	ENSTGUG00000004801
HSD17B7	HI	ENSG00000132196	ENSGALG00000002681	ENSTGUG00000017081
IGFBP1	HI	ENSG00000146678	ENSGALG00000012437	ENSTGUG00000007176
IL6ST	HI	ENSG00000134352	ENSGALG00000014716	ENSTGUG00000002569
ITM2B	HI	ENSG00000136156	ENSGALG00000016996	ENSTGUG00000012223
IGFN1	HI	ENSG00000163395	ENSGALG00000000295	NA
ITM2C	HI	ENSG00000135916	ENSGALG00000005539	ENSTGUG00000005426
JAG1	HI	ENSG00000101384	ENSGALG00000009020	ENSTGUG00000006079
KCNMB1	HI	ENSG00000145936	ENSGALG00000002118	ENSTGUG00000014898
KLHL12	HI	ENSG00000117153	ENSGALG00000000518	ENSTGUG00000001234
KAZALD1	HI	ENSG00000107821	ENSGALG00000007837	ENSTGUG00000010037
KCNIP1	HI	ENSG00000182132	ENSGALG00000002132	ENSTGUG00000014900
KCNV2	HI	ENSG00000168263	ENSGALG00000010173	ENSTGUG00000005377
LOX	HI	ENSG00000113083	ENSGALG000000028063	ENSTGUG00000001145
LPL	HI	ENSG00000175445	ENSGALG00000015425	ENSTGUG00000000287
MCAT	HI	ENSG00000100294	ENSGALG00000014165	ENSTGUG00000012035
MGAT4C	HI	ENSG00000182050	ENSGALG000000028360	ENSTGUG00000007933
MRPS25	HI	ENSG00000131368	ENSGALG00000008506	ENSTGUG00000010579
MYBPH	HI	ENSG00000133055	ENSGALG00000000164	NA
MYOG	HI	ENSG00000122180	ENSGALG00000000172	ENSTGUG00000001380
MRPS22	HI	ENSG00000175110	ENSGALG00000005367	ENSTGUG00000005274
MTA1	HI	ENSG00000182979	ENSGALG00000002803	ENSTGUG00000017196
NIPSNAP3A	HI	ENSG00000136783	NA	NA
NMNAT1	HI	ENSG00000173614	ENSGALG000000026695	NA
NPM1	HI	ENSG00000181163	ENSGALG00000002197	ENSTGUG00000014970
NR2C2	HI	ENSG00000177463	ENSGALG00000008519	ENSTGUG00000010590
NTRK2	HI	ENSG00000148053	ENSGALG00000012594	ENSTGUG00000003077
NUP155	HI	ENSG00000113569	ENSGALG00000003688	ENSTGUG00000002069
NOS1AP	HI	ENSG00000198929	NA	NA
OLFML2B	HI	ENSG00000162745	ENSGALG00000002667	ENSTGUG00000017073
PACS2	HI	ENSG00000179364	ENSGALG00000002894	ENSTGUG00000017216
PCDH17	HI	ENSG00000118946	ENSGALG00000016941	ENSTGUG00000012457

PER2	HI	ENSG00000132326	ENSGALG00000005521	NA
PGS1	HI	ENSG00000087157	ENSGALG00000007181	ENSTGUG00000003319
PHKA1	HI	ENSG00000067177	ENSGALG00000004801	ENSTGUG00000004827
PHLDA3	HI	ENSG00000174307	ENSGALG00000019802	NA
PIK3CB	HI	ENSG00000051382	ENSGALG00000005505	NA
PRKAA1	HI	ENSG00000132356	ENSGALG00000014832	ENSTGUG00000002173
PRLR	HI	ENSG00000113494	ENSGALG00000003446	ENSTGUG00000001979
PSD3	HI	ENSG00000156011	ENSGALG00000015428	NA
PKP1	HI	ENSG00000081277	ENSGALG00000000299	ENSTGUG00000001339
PPFIA4	HI	ENSG00000143847	ENSGALG00000000217	ENSTGUG00000001363
PUMILIO DOMAIN- CONTAININ G PROTEIN KIAA0020 HOMOLOG	HI	NA	NA	NA
RABIF	HI	ENSG00000183155	ENSGALG00000000436	NA
RAPGEF6	HI	ENSG00000158987	NA	NA
RBSN	HI	ENSG00000131381	ENSGALG00000008500	ENSTGUG00000010568
RGS13	HI	ENSG00000127074	ENSGALG00000026810	NA
RGS18	HI	ENSG00000150681	ENSGALG00000021143	NA
RGS2	HI	ENSG00000116741	ENSGALG00000002540	ENSTGUG00000016954
RGS21	HI	ENSG00000253148	ENSGALG00000023897	NA
RGS4	HI	ENSG00000117152	ENSGALG00000002564	ENSTGUG00000016967
RGS5	HI	ENSG00000143248	ENSGALG00000026572	ENSTGUG00000016990
RPGRIP1L	HI	ENSG00000103494	ENSGALG00000003602	NA
RPS4 (=RPS4X)	HI	ENSG00000198034	ENSGALG00000004831	NA
RBP1	HI	ENSG00000114115	ENSGALG00000027820	ENSTGUG00000005153
RBP2	HI	ENSG00000114113	ENSGALG00000005327	ENSTGUG00000005160
RGS1	HI	ENSG00000090104	ENSGALG00000002549	NA
RPL37	HI	ENSG00000145592	ENSGALG00000014833	ENSTGUG00000002186
SCUBE1	HI	ENSG00000159307	ENSGALG00000014178	ENSTGUG00000012016
SELP	HI	ENSG00000174175	ENSGALG00000002643	ENSTGUG00000017040
SFSWAP	HI	ENSG00000061936	ENSGALG00000002487	ENSTGUG00000004623
SLC9A3	HI	ENSG00000066230	ENSGALG00000012517	ENSTGUG00000006804
SNCAIP	HI	ENSG00000064692	ENSGALG00000005330	ENSTGUG00000001137
SPP2	HI	ENSG00000072080	ENSGALG00000004129	ENSTGUG00000003884
SREK1	HI	ENSG00000153914	ENSGALG00000014775	ENSTGUG00000002935
SRFBP1	HI	ENSG00000151304	ENSGALG00000005316	NA
SH3BP4	HI	ENSG00000130147	ENSGALG00000004140	ENSTGUG00000003098
SHROOM4	HI	ENSG00000158352	NA	NA
SLC12A7	HI	ENSG00000113504	ENSGALG00000012497	ENSTGUG00000006931
SYNAPTO- BREVIN	HI	NA	NA	NA
TBC1D2B	HI	ENSG00000167202	ENSGALG00000003322	ENSTGUG00000003235
TIMP2	HI	ENSG00000035862	ENSGALG00000027070	
TK2	HI	ENSG00000166548		
TLX3	HI	ENSG00000164438	ENSGALG00000002191	ENSTGUG00000014966
TMEM121	HI	ENSG00000184986	ENSGALG00000002756	ENSTGUG00000017172
TMEM183 (=TMEM183 A)	HI	ENSG00000163444	NA	NA
TNNT2	HI	ENSG00000118194	ENSGALG00000000302	ENSTGUG00000001330
TRH	HI	ENSG00000170893	ENSGALG00000008490	
TRIP13	HI	ENSG00000071539	ENSGALG00000012508	ENSTGUG00000006756
TRPM8	HI	ENSG00000144481	ENSGALG00000004116	ENSTGUG00000003521
TSPO	HI	ENSG00000100300	ENSGALG00000014166	ENSTGUG00000012033
TTLL1	HI	ENSG00000100271	ENSGALG00000014163	ENSTGUG00000012037

TGFBR1	HI	ENSG00000106799	ENSGALG00000012617	ENSTGUG00000006726
TMEM9	HI	ENSG00000116857	ENSGALG00000000226	ENSTGUG00000001345
TNNI1	HI	ENSG00000159173	ENSGALG00000000313	ENSTGUG00000001319
TTL12	HI	ENSG00000100304	ENSGALG00000014167	ENSTGUG00000012025
UAP1	HI	ENSG00000117143	ENSGALG00000002725	ENSTGUG00000017130
UGT1A1	HI	ENSG00000241635	NA	ENSTGUG00000003102
UHK1	HI	ENSG00000152332	ENSGALG00000002734	ENSTGUG00000017148
UNC13A	HI	ENSG00000130477	ENSGALG00000026462	NA
UNCHARACTERIZED PROTEIN C1ORF50 HOMOLOG	HI	ENSG00000164008	ENSGALG00000004800	ENSTGUG00000017254
USP3	HI	ENSG00000140455	ENSGALG00000003427	ENSTGUG00000003160
USP36	HI	ENSG00000055483	ENSGALG00000028462	NA
VGLL4	HI	ENSG00000144560	ENSGALG00000004937	ENSTGUG00000004136
WBSR27	HI	ENSG00000165171	ENSGALG00000026762	NA
WDR72	HI	ENSG00000166415	ENSGALG00000004545	ENSTGUG00000006614
WNT4	HI	ENSG00000162552	ENSGALG00000004790	ENSTGUG00000017251
ZNF474	HI	ENSG00000164185	NA	NA
ABHD11	HI	ENSG00000106077	ENSGALG00000001056	NA
GAG polyprotein	HI	NA	NA	NA
MTMR4	HI	ENSG00000108389	ENSGALG00000001042	ENSTGUG00000003314
TAMM41	HI	ENSG00000144559	ENSGALG00000004940	ENSTGUG00000004121
A2M	PI	ENSG00000175899	ENSGALG00000022964	NA
A2ML1	PI	ENSG00000166535	NA	NA
ALDH1A1	PI	ENSG00000165092	ENSGALG00000015147	ENSTGUG00000000800
AOPEP=(C9orf3)	PI	ENSG00000148120	ENSGALG00000012615	ENSTGUG00000000565
APC	PI	ENSG00000134982	NA	
APOBEC1	PI	ENSG00000111701	NA	
ASUN	PI	ENSG00000064102	ENSGALG00000014083	ENSTGUG00000012188
ACER3	PI	ENSG00000078124	ENSGALG00000000755	ENSTGUG00000013058
AIDA	PI	ENSG00000186063	ENSGALG00000009426	NA
AIFM1	PI	ENSG00000156709	ENSGALG00000004003	NA
BROX	PI	ENSG00000162819	ENSGALG00000009413	NA
BCORL1	PI	ENSG00000085185	ENSGALG00000003976	NA
BHLHE41	PI	ENSG00000123095	NA	NA
BNC2	PI	ENSG00000173068	ENSGALG00000015101	ENSTGUG00000004482
CEP120	PI	ENSG00000168944	ENSGALG00000005368	ENSTGUG00000001104
CLCN1	PI	ENSG00000188037	ENSGALG00000014695	ENSTGUG00000013222
CLCN5	PI	ENSG00000171365	ENSGALG00000007234	ENSTGUG00000005324
CP37	PI	NA	NA	NA
CAPN5	PI	ENSG00000149260	ENSGALG00000000750	ENSTGUG00000013052
CLEC4A	PI	ENSG00000111729	NA	NA
DCP2	PI	ENSG00000172795	ENSGALG00000000215	ENSTGUG00000001035
DISP1	PI	ENSG00000154309	ENSGALG00000009404	ENSTGUG00000002654
DPT	PI	ENSG00000143196	ENSGALG00000019229	ENSTGUG00000013432
DUSP10	PI	ENSG00000143507	ENSGALG00000009450	ENSTGUG00000002705
ENOX2	PI	ENSG00000165675	ENSGALG00000004079	ENSTGUG00000005267
EPHA1	PI	ENSG00000146904	ENSGALG00000014687	ENSTGUG00000013242
FAM115C (=TCAF2)	PI	ENSG00000170379	NA	NA
FGFR1OP2	PI	ENSG00000111790	ENSGALG00000014084	NA
FKBP4	PI	ENSG00000004478	ENSGALG00000014331	ENSTGUG00000013147
FAM131B	PI	ENSG00000159784	ENSGALG00000014689	ENSTGUG00000013232
FMO1	PI	ENSG00000010932	NA	NA

FOXJ2	PI	ENSG00000065970	ENSGALG00000014329	ENSTGUG00000013133
FOXM1	PI	ENSG00000111206	ENSGALG00000013420	NA
GPR119	PI	ENSG00000147262	ENSGALG00000004069	ENSTGUG00000018290
GORAB	PI	ENSG00000120370	ENSGALG00000003329	NA
ITFG2	PI	ENSG00000111203	ENSGALG00000014335	ENSTGUG00000013150
ITPR2	PI	ENSG00000123104	ENSGALG00000014071	ENSTGUG00000012196
KDM4C	PI	ENSG00000107077	NA	NA
KLRG1	PI	ENSG00000139187	NA	NA
KCNN2	PI	ENSG00000080709	ENSGALG00000002539	ENSTGUG00000001344
LRRC32	PI	ENSG00000137507	ENSGALG00000000818	NA
M6PR	PI	ENSG00000003056	ENSGALG00000014256	ENSTGUG00000013099
MARS2	PI	ENSG00000247626	ENSGALG00000004019	ENSTGUG00000005225
MCC	PI	ENSG00000171444	ENSGALG00000000208	ENSTGUG00000001036
MIA3	PI	ENSG00000154305	ENSGALG00000009434	NA
MUG2	PI	NA	NA	NA
NDST4	PI	ENSG00000138653	ENSGALG00000012015	NA
NECAP1	PI	ENSG00000089818	ENSGALG00000014330	ENSTGUG00000013138
OR10K2	PI	ENSG00000180708	NA	NA
OVO-STATIN (=OVST)	PI	NA	ENSGALG00000022962	NA
PARP11	PI	ENSG00000111224	ENSGALG00000014347	ENSTGUG00000013169
PDE10A	PI	ENSG00000112541	ENSGALG00000011537	ENSTGUG00000009390
PHC1	PI	ENSG00000111752	ENSGALG00000014263	NA
PRRX1	PI	ENSG00000116132	ENSGALG00000003324	NA
PRMT8	PI	ENSG00000111218	ENSGALG00000013272	ENSTGUG00000013173
PTPRD	PI	ENSG00000153707	ENSGALG00000015058	ENSTGUG00000004740
REEP5	PI	ENSG00000129625	ENSGALG00000023157	ENSTGUG00000001029
RIMKLB	PI	ENSG00000166532	ENSGALG00000014274	ENSTGUG00000013112
RORB	PI	ENSG00000198963	ENSGALG00000015150	ENSTGUG00000000785
RAB33A	PI	ENSG00000134594	ENSGALG00000024049	ENSTGUG00000005228
RBMX2	PI	ENSG00000134597	ENSGALG00000004025	NA
SECISBP2	PI	ENSG00000187742	ENSGALG00000010694	NA
SLC25A14	PI	ENSG00000102078	ENSGALG00000004063	NA
SLC2A3	PI	ENSG00000059804	ENSGALG00000014324	NA
SRP19	PI	ENSG00000153037	NA	NA
SSPN	PI	ENSG00000123096	ENSGALG00000014042	ENSTGUG00000012229
SUSD4	PI	ENSG00000143502	ENSGALG00000009388	ENSTGUG00000002646
SHC3	PI	ENSG00000148082	ENSGALG00000010688	ENSTGUG00000000448
T	PI	ENSG00000164458	ENSGALG00000011489	ENSTGUG00000009448
TAF1A	PI	ENSG00000143498	ENSGALG00000009441	ENSTGUG00000002690
TEAD4	PI	ENSG00000197905	ENSGALG00000014342	ENSTGUG00000013161
TMC1	PI	ENSG00000165091	ENSGALG00000015145	ENSTGUG00000000808
TMEM2	PI	ENSG00000135048	ENSGALG00000015138	ENSTGUG00000000841
TMLHE	PI	ENSG00000185973	ENSGALG00000007443	ENSTGUG00000005397
TRPM6	PI	ENSG00000119121	ENSGALG00000015154	ENSTGUG00000000774
TSPAN9	PI	ENSG00000011105	ENSGALG00000014346	ENSTGUG00000013167
TULP3	PI	ENSG00000078246	ENSGALG00000013424	ENSTGUG00000013157
UGT8	PI	ENSG00000174607	ENSGALG00000012018	ENSTGUG00000001840
XCL1	PI	ENSG00000143184	ENSGALG00000015235	NA
ZCCHC6	PI	ENSG00000083223	ENSGALG00000012607	ENSTGUG00000000624
ZFAND5	PI	ENSG00000107372	ENSGALG00000015144	ENSTGUG00000000824
ZYX	PI	ENSG00000159840	ENSGALG00000014688	ENSTGUG00000013238
C3AR1	PI	ENSG00000171860	ENSGALG00000013218	NA

table S7. Significantly enriched GO pathways from ClueGo analysis in HI outlier windows.

GO ID	GO Term	Term Corrected P Value	Group Corrected P Value	Genes Associated
GO:0003015	heart process	0.04151716	Group2=1.475865E-5	ADORA1, CDC42, CLIC2, KCNIP1, NOS1AP, NUP155, RGS2, TNNI1, TNNT2
GO:0006865	amino acid transport	0.0354880	Group0=9.09950E-4	ADORA1, NTRK2, PER2, PPFIA4, SH3BP4, TRH, XK
GO:0006937	regulation of muscle contraction	0.02525859	Group2=1.475865E-5	ADORA1, CLIC2, MYBPH, NOS1AP, RGS2, TNNI1, TNNT2
GO:0006941	striated muscle contraction	0.00531038	Group2=1.475865E-5	ADORA1, CLIC2, MYBPH, NOS1AP, NUP155, RGS2, TNNI1, TNNT2
GO:0006942	regulation of striated muscle contraction	0.00536288	Group2=1.475865E-5	ADORA1, CLIC2, MYBPH, NOS1AP, RGS2, TNNI1
GO:0008277	regulation of G-protein coupled receptor protein signaling pathway	0.01400887	Group1=6.75126E-4	RGS1, RGS13, RGS18, RGS2, RGS4, RGS5, RPGRIP1L
GO:0010506	regulation of autophagy	0.0329784	Group3=0.00123669	ATG7, DAPK2, HERC1, PIK3CB, PRKAA1, SH3BP4, TSPO, USP36
GO:0043087	regulation of GTPase activity	2.769808E-4	Group4=1.55607E-5	CYTH1, DENND2D, FGD5, HERC1, NTRK2, PSD3, RABIF, RAPGEF6, RGS1, RGS13, RGS18, RGS2, RGS21, RGS4, RGS5, SH3BP4, TBC1D2B, WNT4
GO:0043502	regulation of muscle adaptation	0.025065	Group2=1.475865E-5	IL6ST, MTMR4, MYOG, RGS2, TNNI1
GO:0045727	positive regulation of translation	0.04927559	Group5=0.04927559	NPM1, RPS4X, UHMK1
GO:0045744	negative regulation of G-protein coupled receptor protein signaling pathway	0.003844289	Group1=6.75126E-4	RGS13, RGS18, RGS2, RGS4, RPGRIP1L
GO:0060047	heart contraction	0.0398800	Group2=1.475865E-5	ADORA1, CDC42, CLIC2, KCNIP1, NOS1AP, NUP155, RGS2, TNNI1, TNNT2
GO:0060048	cardiac muscle contraction	0.006473059	Group2=1.475865E-5	ADORA1, CLIC2, NOS1AP, NUP155, RGS2, TNNI1, TNNT2
GO:0090257	regulation of muscle system process	8.31039E-4	Group2=1.475865E-5	ADORA1, CLIC2, IL6ST, MTMR4, MYBPH, MYOG, NOS1AP, RGS2, TNNI1, TNNT2
GO:1903522	regulation of blood circulation	0.0352360	Group2=1.475865E-5	ADORA1, CLIC2, CSRP1, HRH1, KCNIP1, NOS1AP, NUP155, PER2, RGS2, TNNT2

table S8. Significantly enriched GO pathways from ClueGo analysis in SI outlier windows.

GO ID	GO Term	Corrected Term PValue	Corrected Group PValue	Associated Genes Found
GO:0001708	cell fate specification	0.01439245	Group1=1.107587E-4, Group4=0.00215771	GLI3, ISL2, NOTCH1, PTCH1
GO:0007271	synaptic transmission, cholinergic	0.01822650	Group5=0.0354636	CHRNA3, CHRNA5, CHRN4
GO:0007274	neuromuscular synaptic transmission	0.00632436	Group5=0.0354636	CHRNA3, CHRNA5, CHRN4
GO:0016202	regulation of striated muscle tissue development	0.01907224	Group1=1.107587E-4	CTDP1, FBXO22, NOTCH1, NRG1
GO:0016525	negative regulation of angiogenesis	0.03022749	Group1=1.107587E-4	FASLG, NOTCH1, NRG1
GO:0021510	spinal cord development	0.003122994	Group1=1.107587E-4, Group4=0.00215771	GLI3, ISL2, NOTCH1, PHGDH, PTCH1
GO:0021515	cell differentiation in spinal cord	0.002658011	Group1=1.107587E-4, Group4=0.00215771	GLI3, ISL2, NOTCH1, PTCH1
GO:0021517	ventral spinal cord development	0.0205499	Group1=1.107587E-4, Group4=0.00215771	GLI3, ISL2, PTCH1
GO:0021522	spinal cord motor neuron differentiation	0.01195684	Group1=1.107587E-4, Group4=0.00215771	GLI3, ISL2, PTCH1
GO:0030510	regulation of BMP signaling pathway	0.02574682	Group7=0.01716454	GREM2, NOTCH1, NOTCH2
GO:0034101	erythrocyte homeostasis	0.02056678	Group0=0.005412310	INHBA, IREB2, L3MBTL3, PTBP3
GO:0035094	response to nicotine	0.02776161	Group5=0.035463	CHRNA3, CHRNA5, CHRN4
GO:0035095	behavioral response to nicotine	1.152215E-4	Group5=0.0354636	CHRNA3, CHRNA5, CHRN4
GO:0040014	regulation of multicellular organism growth	0.0290452	Group2=0.001484056	FXN, GHR, PTCH1
GO:0045667	regulation of osteoblast differentiation	0.02217046	Group1=1.107587E-4, Group4=0.00215771	GLI3, NOTCH1, PTCH1, SUCO
GO:0045682	regulation of epidermis development	0.02951283	Group4=0.00215771	INHBA, NOTCH1, PTCH1
GO:0046620	regulation of organ growth	0.01157895	Group1=1.107587E-4, Group2=0.001484056	CTDP1, FXN, NOTCH1, NRG1
GO:0048521	negative regulation of behavior	0.0311752	Group1=1.107587E-4, Group4=0.00215771	NOTCH1, NRG1, PTPRU
GO:0048634	regulation of muscle organ development	0.01865057	Group1=1.107587E-4	CTDP1, FBXO22, NOTCH1, NRG1
GO:0048640	negative regulation of developmental growth	0.01355532	Group1=1.107587E-4, Group2=0.001484056	CTDP1, FXN, PTCH1
GO:0048663	neuron fate commitment	0.00733350	Group1=1.107587E-4, Group4=0.00215771	GLI3, ISL2, NOTCH1, NRG1
GO:0048709	oligodendrocyte differentiation	0.0244387	Group1=1.107587E-4, Group4=0.00215771	GLI3, NOTCH1, NRG1
GO:0050684	regulation of mRNA processing	0.006968076	Group6=0.015522	PTBP3, RNF20, SRSF4
GO:0050686	negative regulation of mRNA processing	0.0079974	Group6=0.015522	PTBP3, RNF20, SRSF4
GO:0050922	negative regulation of	0.02129803	Group1=1.107587E-4,	NOTCH1, NRG1,

	chemotaxis		Group4=0.00215771	PTPRU
GO:0051147	regulation of muscle cell differentiation	0.01205801	Group1=1.107587E-4	CTDP1, FBXO22, NOTCH1, NRG1, NTN3
GO:0051153	regulation of striated muscle cell differentiation	0.0122296	Group1=1.107587E-4	CTDP1, FBXO22, NOTCH1, NRG1
GO:0055017	cardiac muscle tissue growth	0.0269513	Group1=1.107587E-4	CTDP1, NOTCH1, NRG1
GO:0055021	regulation of cardiac muscle tissue growth	0.0145185	Group1=1.107587E-4	CTDP1, NOTCH1, NRG1
GO:0055024	regulation of cardiac muscle tissue development	0.02176260	Group1=1.107587E-4	CTDP1, NOTCH1, NRG1
GO:0060021	palate development	0.02017733	Group3=0.01513299	EPHB2, GLI3, INHBA
GO:0060419	heart growth	0.03176145	Group1=1.107587E-4	CTDP1, NOTCH1, NRG1
GO:0060420	regulation of heart growth	0.0189312	Group1=1.107587E-4	CTDP1, NOTCH1, NRG1
GO:0061005	cell differentiation involved in kidney development	0.001643586	Group1=1.107587E-4, Group4=0.00215771	GLI3, NOTCH1, PTCH1, PTPRU
GO:0072009	nephron epithelium development	0.02142071	Group1=1.107587E-4, Group4=0.00215771	GLI3, NOTCH1, PTCH1, PTPRU
GO:0099565	chemical synaptic transmission, postsynaptic	0.01921880	Group5=0.0354636	CHRNA3, CHRNA5, CHRNB4
GO:1901343	negative regulation of vasculature development	0.02574682	Group1=1.107587E-4	FASLG, NOTCH1, NRG1
GO:1901861	regulation of muscle tissue development	0.01865057	Group1=1.107587E-4	CTDP1, FBXO22, NOTCH1, NRG1
GO:1903312	negative regulation of mRNA metabolic process	0.01195684	Group6=0.015522	PTBP3, RNF20, SRSF4
GO:2000181	negative regulation of blood vessel morphogenesis	0.0299293	Group1=1.107587E-4	FASLG, NOTCH1, NRG1

table S9. Significantly enriched GO pathways from ClueGo analysis in PI outlier windows.

GO ID	GO Term	Corrected Term PValue	Corrected Group PValue	Associated Genes Found
GO:0002698	negative regulation of immune effector process	0.006649979	Group1=0.00816441	A2M, DUSP10, SUSP4, XCL1
GO:0008589	regulation of smoothened signaling pathway	0.0082550	Group0=0.00270858	DISP1, PRRX1, TULP3
GO:0009953	dorsal/ventral pattern formation	0.006972630	Group0=0.002708588	AIDA, APC, DISP1, TULP3
GO:0032873	negative regulation of stress-activated MAPK cascade	0.00546576	Group2=0.002732883	AIDA, DUSP10, FOXM1
GO:0045824	negative regulation of innate immune response	0.00512626	Group1=0.00816441	A2M, DUSP10, SUSP4
GO:0050777	negative regulation of immune response	0.00800225	Group1=0.00816441	A2M, DUSP10, SUSP4, XCL1
GO:0070303	negative regulation of stress-activated protein kinase signaling cascade	0.00546576	Group2=0.002732883	AIDA, DUSP10, FOXM1
GO:0071300	cellular response to retinoic acid	0.00429302	Group3=0.00429302	PHC1, RORB, T
GO:1903959	regulation of anion transmembrane transport	0.002680228	Group4=0.001675142	CLCN1, CLCN5, TCAF2

table S10. Genes among outlier windows identified as candidates for the involvement in melanogenesis and RI in sparrows.

Gene	Candidate Type	Outlier Type
APC	Melanogenesis	PI
BNC2	Melanogenesis	PI
KCNN2	Melanogenesis	PI
A2M	RI	PI
MIA3	RI	PI
REEP5	RI	PI
SECISBP2	RI	PI
ZCCHC6	RI	PI
ZFAND5	RI	PI
CRHR1	Melanogenesis	HI
GNAI1	Melanogenesis	HI
PRKAA1	Melanogenesis	HI
RBP1	Melanogenesis	HI
TIMP2	Melanogenesis	HI
WNT4	Melanogenesis	HI
RPS4	RI	HI
GLI3	Melanogenesis	SI
NOTCH1	Melanogenesis	SI
NOTCH2	Melanogenesis	SI
ETFA	RI	SI
HSDL2	RI	SI
LPPR1	RI	SI
TJP2	RI	SI

table S11. Significantly enriched GO pathways from ClueGo analysis HI outlier windows with chickens as the reference genome.

GO ID	GO Term	Corrected Term PValue	Corrected Group PValue	Associated Genes Found
GO:0008277	regulation of G-protein coupled receptor protein signaling pathway	0.022938837	Group0=6.37189914E-4	RGS1, RGS13, RGS18, RGS2, RPGRIP1L
GO:0043085	positive regulation of catalytic activity	0.014007527	Group1=7.92328152E-4	CDC42, CRHR1, DENND2D, FGD5, FOXL2, GPR55, PRLR, PSD3, RABIF, RCJMB04_2m10, RGS1, RGS13, RGS18, RGS2, RGS21, RGS4, RGS5, TIMP2, TNNT2, WNT4
GO:0043087	regulation of GTPase activity	3.8067453212E-4	Group1=7.92328152E-4	DENND2D, FGD5, NTRK2, PSD3, RABIF, RCJMB04_2m10, RGS1, RGS13, RGS18, RGS2, RGS21, RGS4, RGS5, WNT4
GO:0043547	positive regulation of GTPase activity	6.118372717E-4	Group1=7.92328152E-4	DENND2D, FGD5, PSD3, RABIF, RCJMB04_2m10, RGS1, RGS13, RGS18, RGS2, RGS21, RGS4, RGS5, WNT4
GO:0051336	regulation of hydrolase activity	0.005203648	Group1=7.92328152E-4	DENND2D, FGD5, FOXL2, GPR55, NPM1, NTRK2, PSD3, RABIF, RCJMB04_2m10, RGS1, RGS13, RGS18, RGS2, RGS21, RGS4, RGS5, TIMP2, TNNT2, WNT4
GO:0051345	positive regulation of hydrolase activity	0.001198228	Group1=7.92328152E-4	DENND2D, FGD5, FOXL2, GPR55, PSD3, RABIF, RCJMB04_2m10, RGS1, RGS13, RGS18, RGS2, RGS21, RGS4, RGS5, TNNT2, WNT4

table S12. Significantly enriched GO pathways from ClueGo analysis in SI outlier windows with chickens as the reference genome.

GO ID	GO Term	Corrected Term PValue	Corrected Group PValue	Associated Genes Found
GO:0003205	cardiac chamber development	0.03598059	Group0=0.01907287	NOTCH1, NOTCH2, NRG1
GO:0007271	synaptic transmission, cholinergic	0.012704136	Group1=0.02006942	CHRNA3, CHRNA5, CHRNB4
GO:0007274	neuromuscular synaptic transmission	0.002935472	Group1=0.02006942	CHRNA3, CHRNA5, CHRNB4
GO:0030326	embryonic limb morphogenesis	0.042476859	Group0=0.01907287	GLI3, NOTCH1, NOTCH2, PTCH1
GO:0030336	negative regulation of cell migration	0.018474666	Group0=0.01907287	NOTCH1, NRG1, RCJMB04_5a23
GO:0030534	adult behavior	0.048262751	Group1=0.02006942	CHRNA3, CHRNA5, CHRNB4, FXN
GO:0035094	response to nicotine	0.002467081	Group1=0.02006942	CHRNA3, CHRNA5, CHRNB4
GO:0035095	behavioral response to nicotine	1.156799262E-4	Group1=0.02006942	CHRNA3, CHRNA5, CHRNB4
GO:0035113	embryonic appendage morphogenesis	0.042689473	Group0=0.01907287	GLI3, NOTCH1, NOTCH2, PTCH1
GO:0035264	multicellular organism growth	0.018474666	Group2=0.01847467	FXN, NOTCH2, PTCH1
GO:0043279	response to alkaloid	0.039772867	Group1=0.02006942	CHRNA3, CHRNA5, CHRNB4
GO:0048663	neuron fate commitment	0.041401127	Group0=0.01907287	GLI3, NOTCH1, NRG1
GO:0061005	cell differentiation involved in kidney development	0.013790996	Group0=0.01907287	GLI3, NOTCH1, PTCH1
GO:0099565	chemical synaptic transmission, postsynaptic	0.041401127	Group1=0.02006942	CHRNA3, CHRNA5, CHRNB4

table S13. Significantly enriched GO pathways from ClueGo analysis in PI outlier windows with chickens as the reference genome.

GO ID	GO Term	Corrected Term PValue	Corrected Group PValue	Associated Genes Found
GO:0030336	negative regulation of cell migration	0.024126799	Group0=0.024126799	EPHA1, MCC, MIA3
GO:0032873	negative regulation of stress-activated MAPK cascade	0.001261716	Group1=0.003575856	AIDA, DUSP10, RCJMB04_8e18
GO:0043409	negative regulation of MAPK cascade	0.003575856	Group1=0.003575856	AIDA, APC, DUSP10, RCJMB04_8e18
GO:0070303	negative regulation of stress-activated protein kinase signaling cascade	0.001261716	Group1=0.003575856	AIDA, DUSP10, RCJMB04_8e18