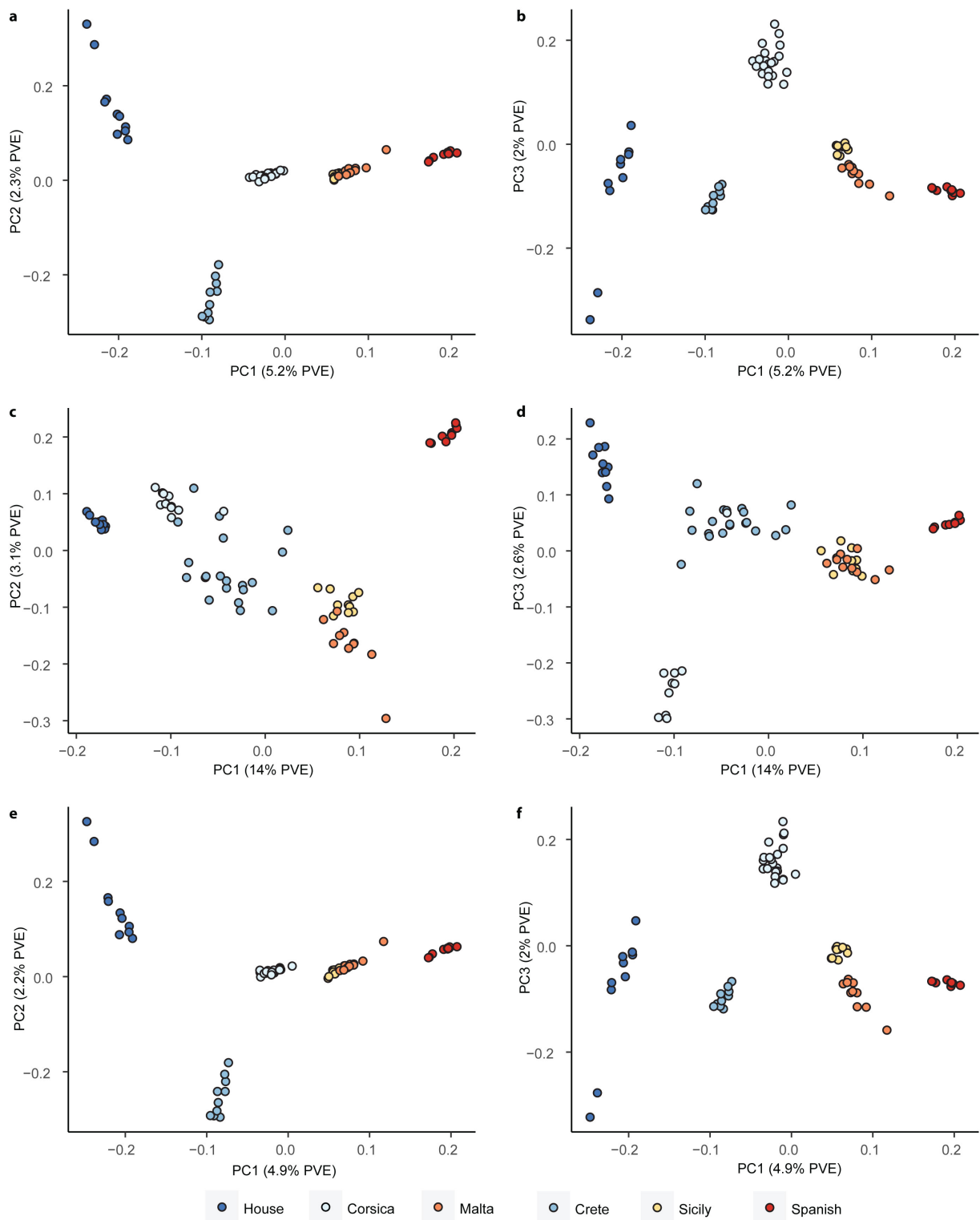
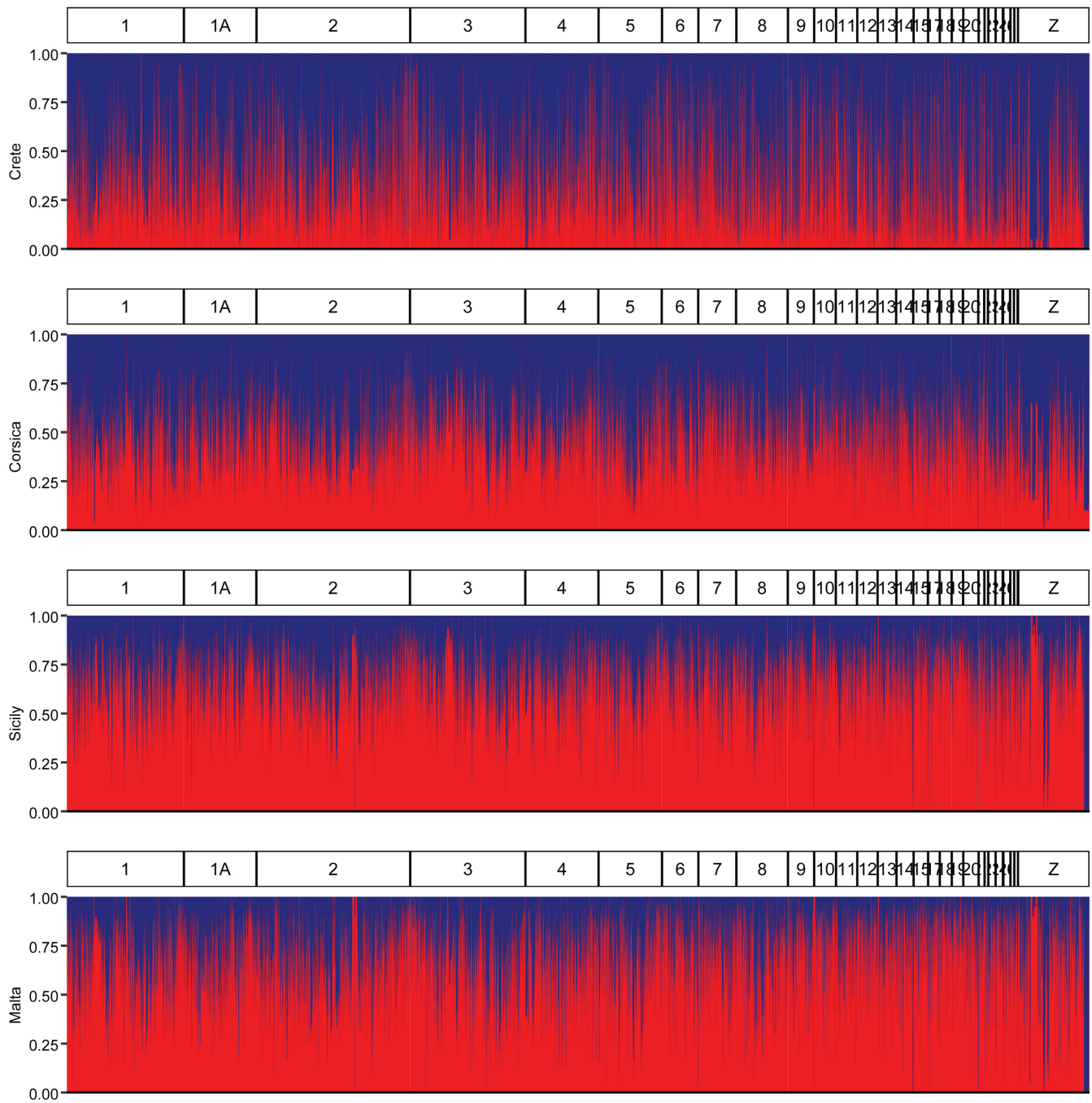


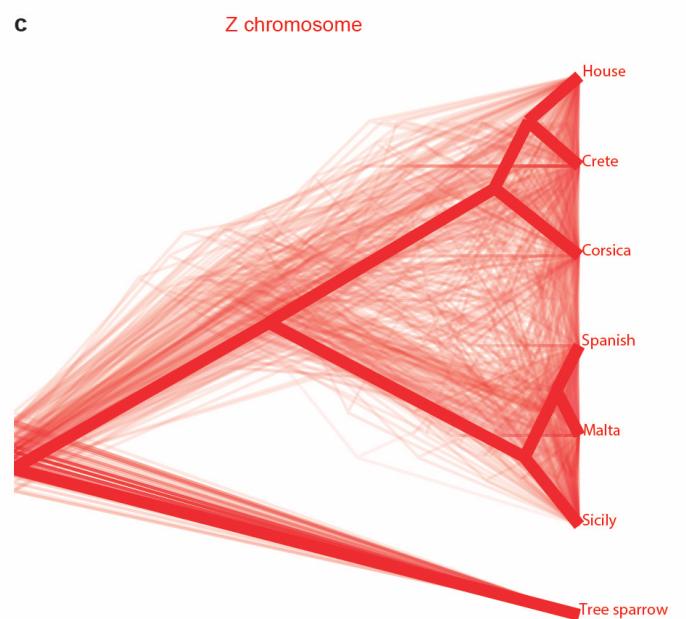
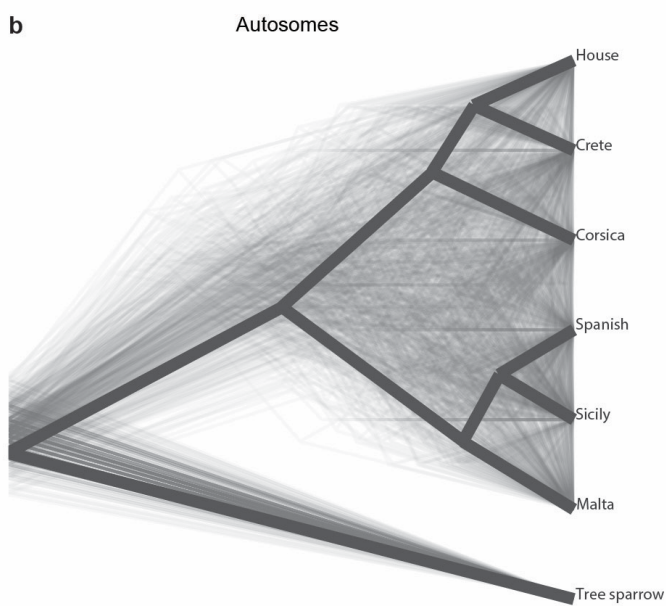
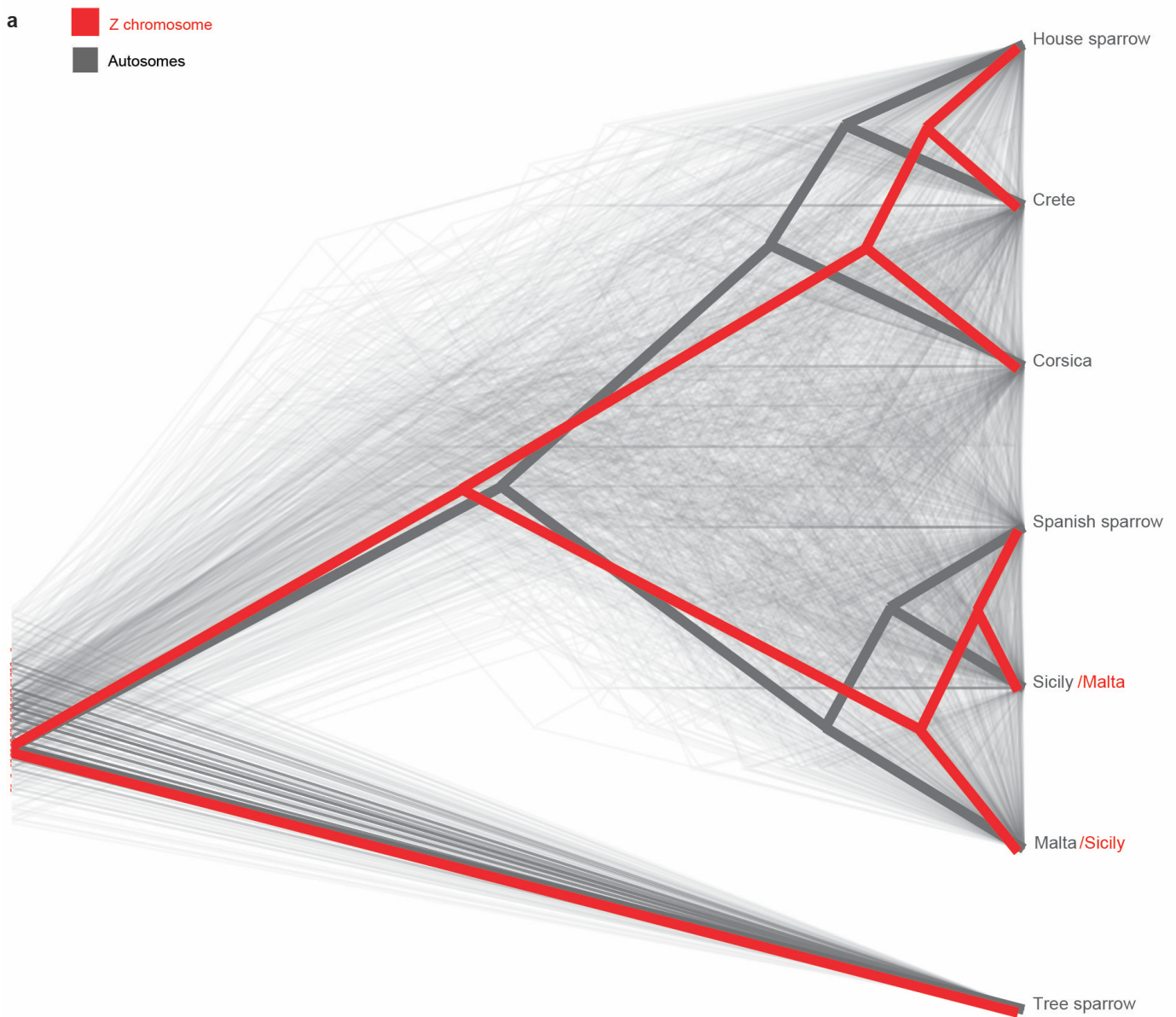
Supplementary Figures



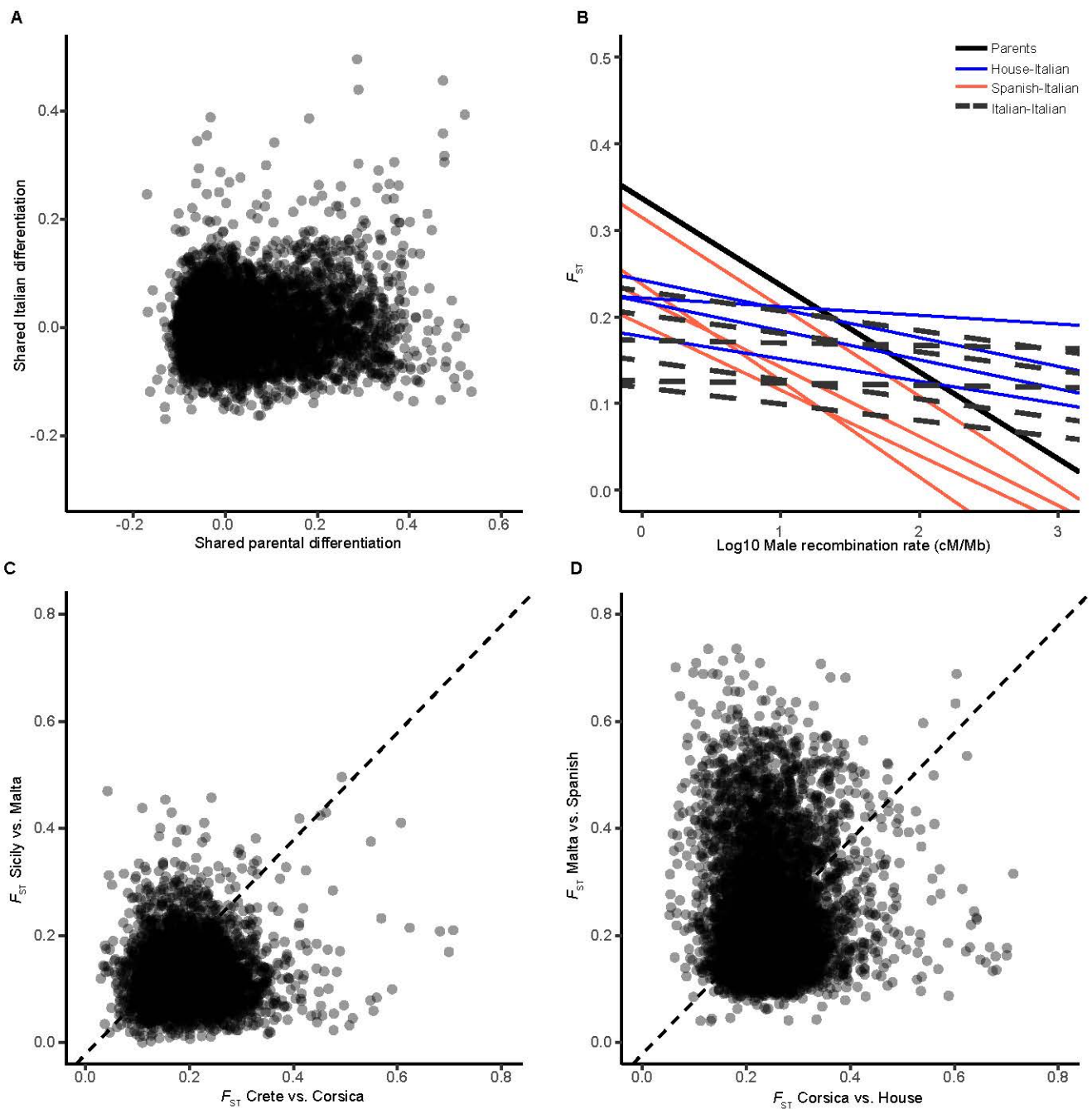
Extended data figure 1. Principal component analysis performed in ANGSD. Data shown for all sites (a-b), the Z chromosome only (c-d) and autosomes only (e-f).



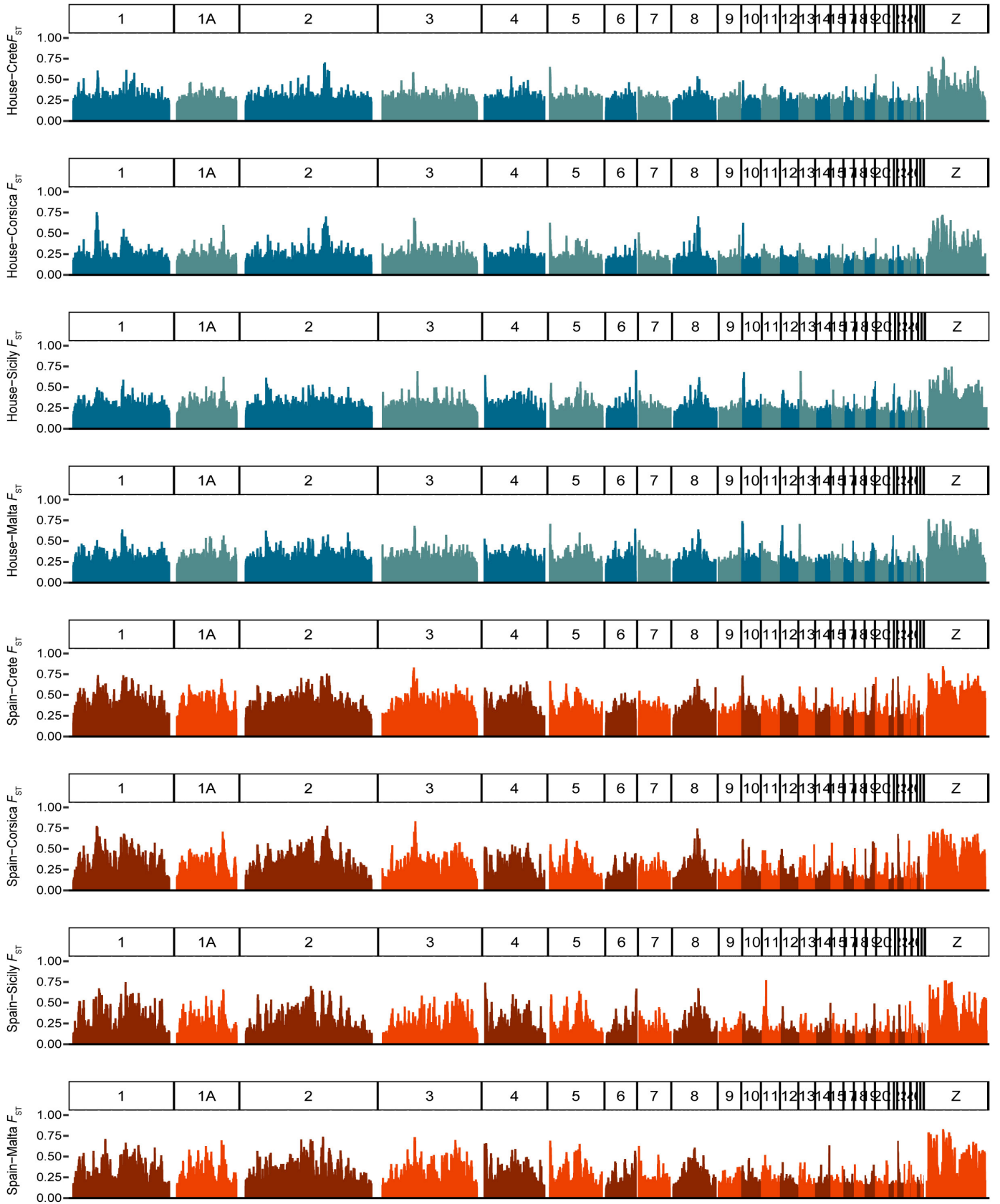
Extended data figure 2. ADMIXTURE analysis of 100 kb non-overlapping windows across the Italian sparrow island populations' genomes. House sparrow ancestry is illustrated in blue and Spanish sparrow ancestry in red.



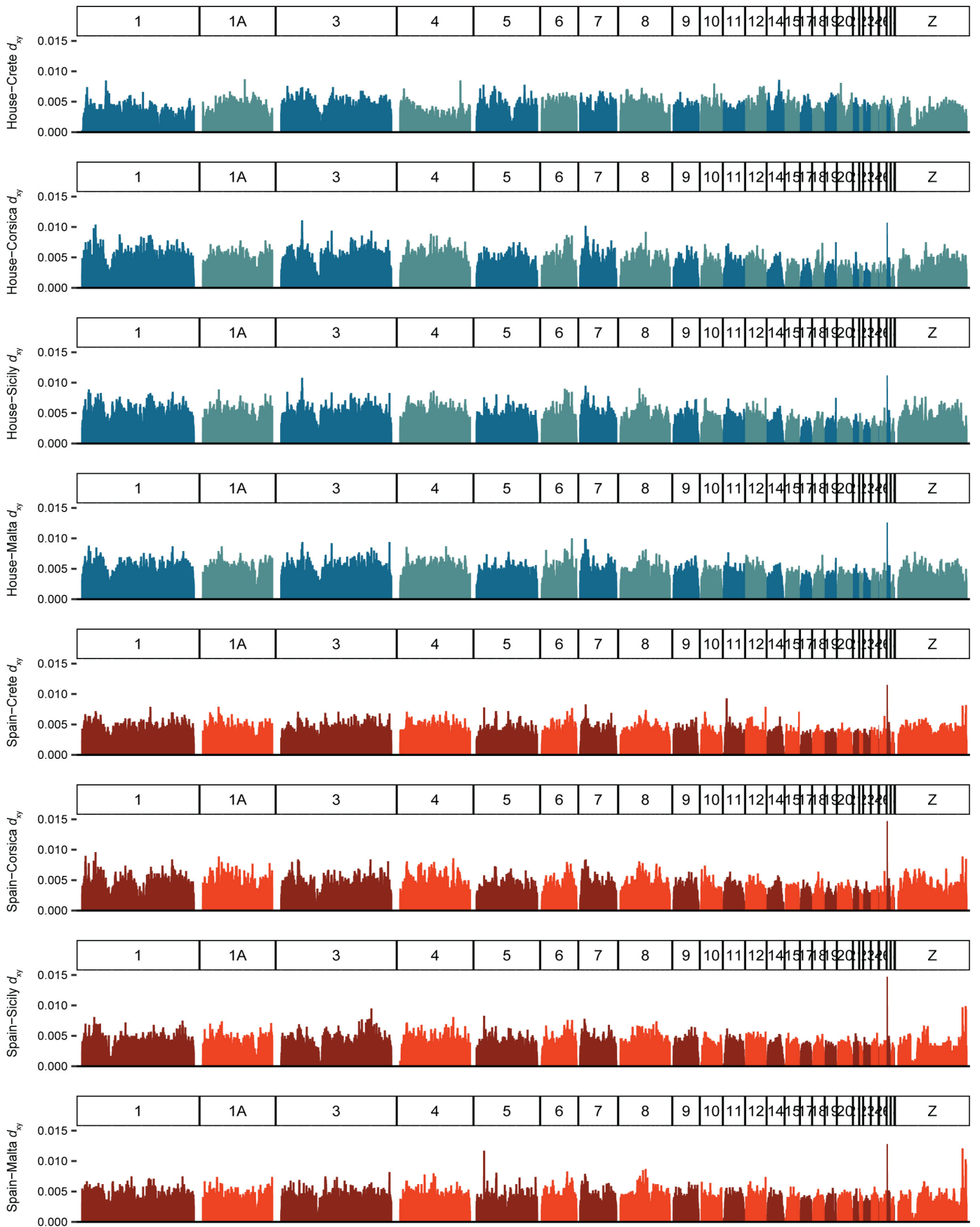
Extended data figure 3. Phylogenetic relationships between different parts of the genome based on BEAST analyses. a, All phylogenetic trees (thin grey lines) with the whole genome consensus tree depicted with thick grey lines and the Z chromosome consensus in thick red lines. b, Autosomal trees depicted with thin grey lines, and the autosomal consensus tree with thick grey lines. c, All Z chromosome trees (thin red lines) as well as the Z consensus in thick red lines.



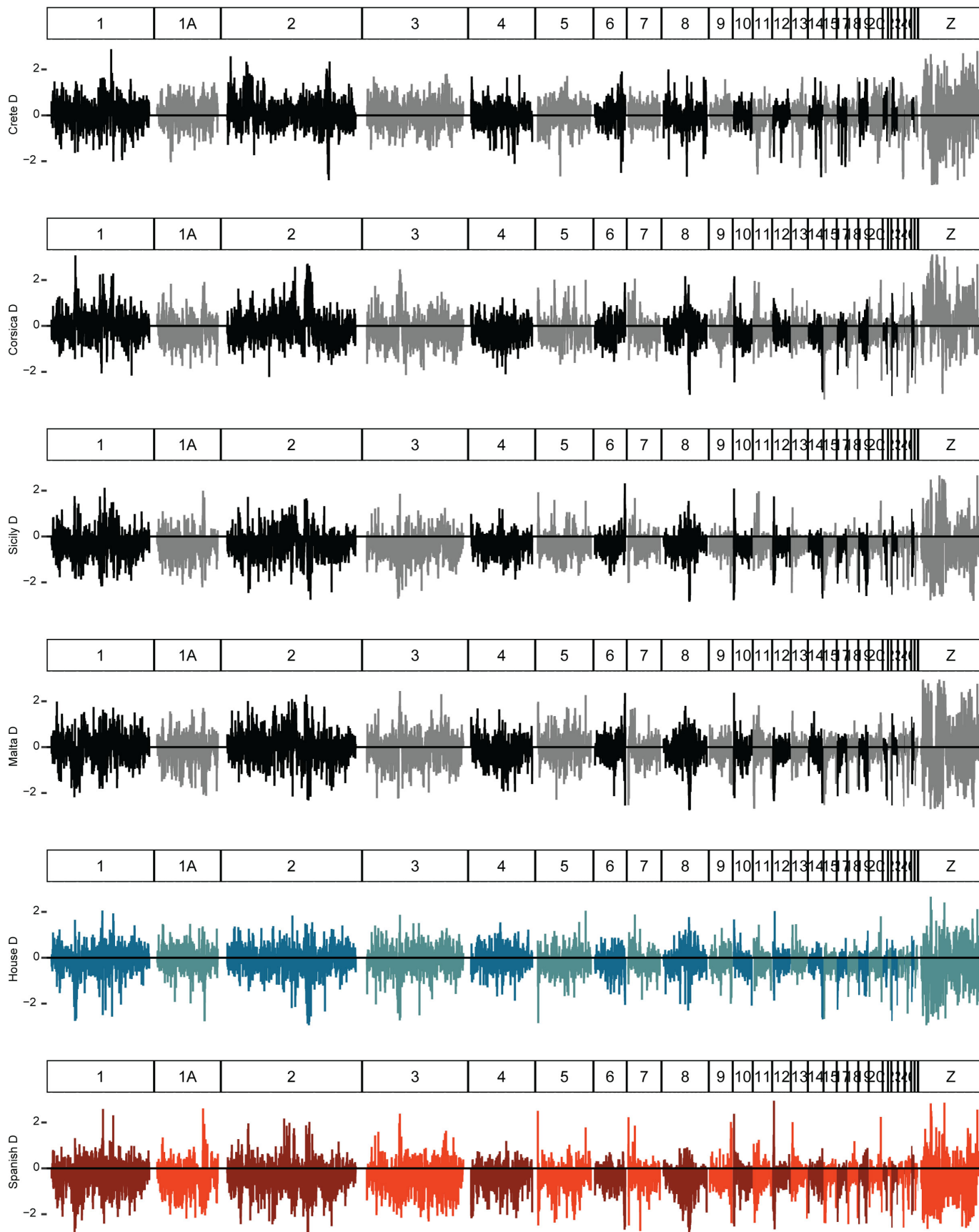
Extended data figure 4. Relationship between parental differentiation, recombination rate and hybrid divergence. a, A regression of the first principal component analysis based on hybrid-hybrid F_{ST} and parent-parent f_{ST} shows that parental differentiation does not predict differentiation within the Italian sparrow. The correlation between the two data sets was calculated using Pearson's product correlation coefficient r . b, Relationship between F_{ST} and recombination rate for parent-parent (black line), Italian sparrow - Spanish sparrow (red lines), Italian sparrow - house sparrow (blue lines) and between different populations of Italian sparrow (grey lines). While parent species F_{ST} is elevated in low recombination regions, F_{ST} between Italian populations is not strongly elevated in low recombination regions. c, F_{ST} between Italian populations is not strongly correlated with that between two other Italian populations. Dashed lines indicate the 1:1 slope. d, differentiation between a parent species and one Italian sparrow population is not correlated with that between the other parent species and another Italian sparrow population, supporting a scenario of unique differentiation from the parent species across Italian populations. Dashed lines indicate a 1:1 slope.



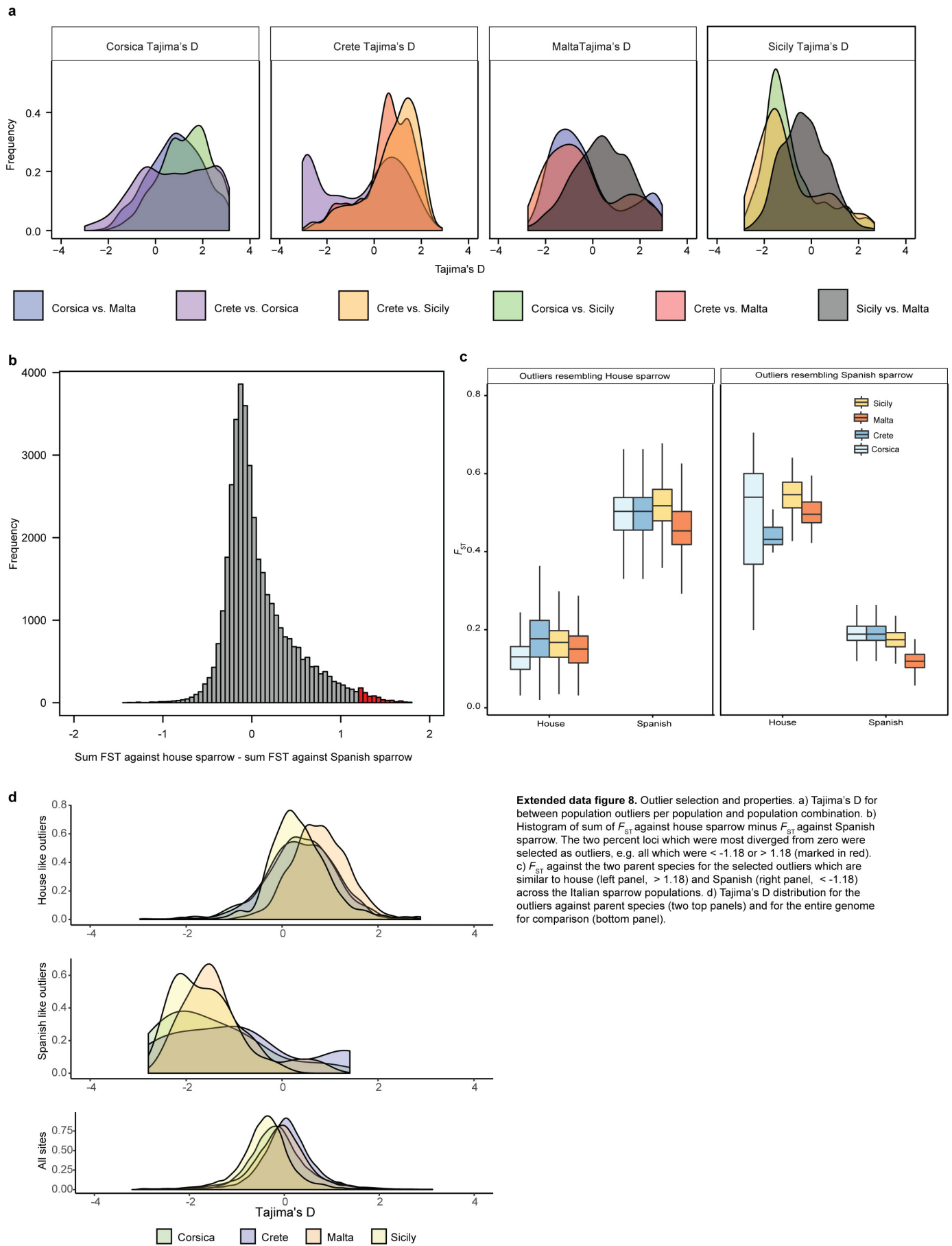
Extended data figure 5. ANGSD estimates of F_{ST} against house sparrow (blue) and Spanish sparrow (red) in 100 kb sliding windows across the genome for Italian sparrow populations.



Extended data figure 6. d_{xy} against house sparrow (blue) and Spanish sparrow (red) in 100 kb sliding windows across the genome for Italian sparrow populations.



Extended data figure 7. ANGSD estimates of Tajima's D for Italian sparrow populations (black/grey) house sparrow (blue) and Spanish sparrow (red) in 100 kb sliding windows across the genome.



Supplementary Tables

Supplementary Table 1. Sampling sites and number of raw reads for all species and populations investigated. Raw read quantity is estimated in gigabases (GB).

Species	Sex	Date	Location	Coordinates	GB
<i>P. domesticus</i>	M	04.07.07	Alta, Norway	69° 58' 23.41" N. 23° 29' 01.67" E	13.4
<i>P. domesticus</i>	M	10.02.09	Leka, Norway	65° 05' 28.05" N. 11° 43' 20.78" E	13.2
<i>P. domesticus</i>	M	21.05.09	Træna, Norway	66° 30' 04.28" N. 12° 06' 02.70" E	12.8
<i>P. domesticus</i>	M	14.02.10	Leka, Norway	65° 05' 53.28" N. 11° 42' 00.49" E	13.5
<i>P. domesticus</i>	M	30.03.11	Løkta, Norway	66° 10' 51.93" N. 12° 43' 16.06" E	13.8
<i>P. domesticus</i>	M	05.07.10	Kvål, Norway	63° 14' 12.36" N. 10° 16' 33.11" E	11.8
<i>P. domesticus</i>	M	20.02.12	Leka, Norway	65° 02' 58.27" N. 11° 36' 12.62" E	12.9
<i>P. domesticus</i>	M	02.04.12	Linesøya, Norway	64° 01' 40.21" N. 09° 55' 15.07" E	11.9
<i>P. domesticus</i>	M	03.06.13	Lauvøya, Norway	63° 55' 36.54" N. 09° 56' 07.74" E	13.1
<i>P. domesticus</i>	M	03.07.13	Lauvøya, Norway	63° 55' 36.54" N. 09° 56' 07.74" E	14.1
<i>P. hispaniolensis</i>	M	04.02.08	Lesina, Italy	41° 51' 30.84" N. 15° 27' 03.23" E	16.9
<i>P. hispaniolensis</i>	M	04.02.08	Lesina, Italy	41° 51' 30.84" N. 15° 27' 03.23" E	13.9
<i>P. hispaniolensis</i>	M	04.02.08	Lesina, Italy	41° 51' 30.84" N. 15° 27' 03.23" E	13.2
<i>P. hispaniolensis</i>	M	04.02.08	Lesina Italy	41° 51' 30.84" N. 15° 27' 03.23" E	12.5
<i>P. hispaniolensis</i>	M	04.02.08	Lesina, Italy	41° 51' 30.84" N. 15° 27' 03.23" E	13.9
<i>P. hispaniolensis</i>	M	04.02.08	Lesina, Italy	41° 51' 30.84" N. 15° 27' 03.23" E	14.5
<i>P. hispaniolensis</i>	M	04.02.08	Lesina, Italy	41° 51' 30.84" N. 15° 27' 03.23" E	13
<i>P. hispaniolensis</i>	M	04.02.08	Lesina, Italy	41° 51' 30.84" N. 15° 27' 03.23" E	13
<i>P. hispaniolensis</i>	M	04.02.08	Lesina, Italy	41° 51' 30.84" N. 15° 27' 03.23" E	15
<i>P. hispaniolensis</i>	M	04.02.08	Lesina, Italy	41° 51' 30.84" N. 15° 27' 03.23" E	13.1
<i>P. montanus</i>	M	17.04.08	GiardinaNaxos Italy	37° 49' 08.91" N. 15° 16' 12.50" E	14.7
<i>P. italiae</i>	M	10.05.13	Perama, Crete	35° 36' 47.31" N. 24° 71' 47.46" E	7.38
<i>P. italiae</i>	M	10.05.13	Perama, Crete	35° 36' 47.31" N. 24° 71' 47.46" E	7.65
<i>P. italiae</i>	M	10.05.13	Perama, Crete	35° 36' 47.31" N. 24° 71' 47.46" E	8.06
<i>P. italiae</i>	M	10.05.13	Perama, Crete	35° 36' 47.31" N. 24° 71' 47.46" E	11.03
<i>P. italiae</i>	M	10.05.13	Perama, Crete	35° 36' 47.31" N. 24° 71' 47.46" E	10.94
<i>P. italiae</i>	M	10.05.13	Perama, Crete	35° 36' 47.31" N. 24° 71' 47.46" E	9.3
<i>P. italiae</i>	M	10.05.13	Perama, Crete	35° 36' 47.31" N. 24° 71' 47.46" E	8.63
<i>P. italiae</i>	M	10.05.13	Perama, Crete	35° 36' 47.31" N. 24° 71' 47.46" E	8.5
<i>P. italiae</i>	M	10.05.13	Perama, Crete	35° 36' 47.31" N. 24° 71' 47.46" E	9.78
<i>P. italiae</i>	M	10.05.13	Perama, Crete	35° 36' 47.31" N. 24° 71' 47.46" E	7.66
<i>P. italiae</i>	M	09.06.13	Muratello, Corsica	41° 58' 44.3" N. 9° 19' 80.6" E	12.35
<i>P. italiae</i>	M	09.06.13	Muratello, Corsica	41° 58' 44.3" N. 9° 19' 80.6" E	13.63
<i>P. italiae</i>	M	09.06.13	Muratello, Corsica	41° 58' 44.3" N. 9° 19' 80.6" E	14.05
<i>P. italiae</i>	M	09.06.13	Muratello, Corsica	41° 58' 44.3" N. 9° 19' 80.6" E	14.03
<i>P. italiae</i>	M	09.06.13	Muratello, Corsica	41° 58' 44.3" N. 9° 19' 80.6" E	14.84
<i>P. italiae</i>	M	09.06.13	Muratello, Corsica	41° 58' 44.3" N. 9° 19' 80.6" E	15.21
<i>P. italiae</i>	M	09.06.13	Muratello, Corsica	41° 58' 44.3" N. 9° 19' 80.6" E	17.38
<i>P. italiae</i>	M	09.06.13	Muratello, Corsica	41° 58' 44.3" N. 9° 19' 80.6" E	13.25
<i>P. italiae</i>	M	09.06.13	Muratello, Corsica	41° 58' 44.3" N. 9° 19' 80.6" E	15.44

<i>P. italiae</i>	M	09.06.13	Muratello, Corsica	41° 58' 44.3" N. 9° 19' 80.6" E	16.01
<i>P. italiae</i>	M	09.06.13	Muratello, Corsica	41° 58' 44.3" N. 9° 19' 80.6" E	8.84
<i>P. italiae</i>	M	09.06.13	Muratello, Corsica	41° 58' 44.3" N. 9° 19' 80.6" E	14.59
<i>P. italiae</i>	M	09.06.13	Muratello, Corsica	41° 58' 44.3" N. 9° 19' 80.6" E	14.83
<i>P. italiae</i>	M	09.06.13	Muratello, Corsica	41° 58' 44.3" N. 9° 19' 80.6" E	16.11
<i>P. italiae</i>	M	09.06.13	Muratello, Corsica	41° 58' 44.3" N. 9° 19' 80.6" E	14.89
<i>P. italiae</i>	M	09.06.13	Muratello, Corsica	41° 58' 44.3" N. 9° 19' 80.6" E	15.23
<i>P. italiae</i>	M	09.06.13	Muratello, Corsica	41° 58' 44.3" N. 9° 19' 80.6" E	12.41
<i>P. italiae</i>	M	09.06.13	Muratello, Corsica	41° 58' 44.3" N. 9° 19' 80.6" E	13.74
<i>P. italiae</i>	M	09.06.13	Muratello, Corsica	41° 58' 44.3" N. 9° 19' 80.6" E	9.45
<i>P. italiae</i>	M	09.06.13	Muratello, Corsica	41° 58' 44.3" N. 9° 19' 80.6" E	15.07
<i>P. italiae</i>	M	09.06.13	Muratello, Corsica	41° 58' 44.3" N. 9° 19' 80.6" E	10.13
<i>P. italiae</i>	M	09.06.13	Muratello, Corsica	41° 58' 44.3" N. 9° 19' 80.6" E	10.05
<i>P. italiae</i>	M	23.04.13	Cos, Sicily	37° 02' 98.8" N. 14° 52' 26.7" E	10.05
<i>P. italiae</i>	M	23.04.13	Cos, Sicily	37° 02' 98.8" N. 14° 52' 26.7" E	9.6
<i>P. italiae</i>	M	23.04.13	Cos, Sicily	37° 02' 98.8" N. 14° 52' 26.7" E	10.76
<i>P. italiae</i>	M	23.04.13	Cos, Sicily	37° 02' 98.8" N. 14° 52' 26.7" E	9.58
<i>P. italiae</i>	M	23.04.13	Cos.,Sicily	37° 02' 98.8" N. 14° 52' 26.7" E	9.39
<i>P. italiae</i>	M	23.04.13	Cos, Sicily	37° 02' 98.8" N. 14° 52' 26.7" E	10.41
<i>P. italiae</i>	M	23.04.13	Cos, Sicily	37° 02' 98.8" N. 14° 52' 26.7" E	9.74
<i>P. italiae</i>	M	23.04.13	Cos, Sicily	37° 02' 98.8" N. 14° 52' 26.7" E	11.51
<i>P. italiae</i>	M	23.04.13	Cos, Sicily	37° 02' 98.8" N. 14° 52' 26.7" E	10.3
<i>P. italiae</i>	M	23.04.13	Cos, Sicily	37° 02' 98.8" N. 14° 52' 26.7" E	9.7
<i>P. italiae</i>	M	09.06.14	Malta	35° 94' 58.39" N. 14° 38' 26.19" E	
<i>P. italiae</i>	M	09.06.14	Malta	35° 94' 58.39" N. 14° 38' 26.19" E	
<i>P. italiae</i>	M	11.06.14	Malta	35° 86' 04.05" N. 14° 39' 81.39" E	
<i>P. italiae</i>	M	12.06.14	Malta	35° 96' 97.83" N. 14° 34' 72.45" E	
<i>P. italiae</i>	M	13.06.14	Malta	35° 94' 58.39" N. 14° 38' 26.19" E	
<i>P. italiae</i>	M	13.06.14	Malta	35° 94' 58.39" N. 14° 38' 26.19" E	
<i>P. italiae</i>	M	14.06.14	Malta	35° 88' 52.84" N. 14° 36' 73.88" E	
<i>P. italiae</i>	M	14.06.14	Malta	35° 88' 52.84" N. 14° 36' 73.88" E	
<i>P. italiae</i>	M	14.06.14	Malta	35° 88' 52.84" N. 14° 36' 73.88" E	
<i>P. italiae</i>	M	14.06.14	Malta	35° 88' 52.84" N. 14° 36' 73.88" E	

Supplementary Table 2. Mean coverage per sample. Mean read depth is mean number of reads per position in the genome per individual after filtering.

Species and population	Individual	Mean read depth
House sparrow	House8L19786	9.30183
House sparrow	House8L64869	8.84489
House sparrow	House8L89915	8.60915
House sparrow	House8M31651	9.00454
House sparrow	House8M71932	9.21965
House sparrow	House8M72455	8.02784
House sparrow	House8N05890	8.91281
House sparrow	House8N06612	8.21378
House sparrow	House8N73248	8.88908
House sparrow	House8N73604	9.60954
Spanish sparrow	Spanish_280	11.6397
Spanish sparrow	Spanish_281	9.57842
Spanish sparrow	Spanish_282	9.1406
Spanish sparrow	Spanish_285	8.35143
Spanish sparrow	Spanish_286	9.20896
Spanish sparrow	Spanish_287	9.71762
Spanish sparrow	Spanish_288	8.71897
Spanish sparrow	Spanish_289	8.6171
Spanish sparrow	Spanish_292	9.75672
Spanish sparrow	Spanish_295	8.88463
Tree sparrow	Naxos2	11.5488
Italian sparrow from Malta	Malta019	15.7987
Italian sparrow from Malta	Malta010	5.98968
Italian sparrow from Malta	Malta012	6.04988
Italian sparrow from Malta	Malta037	7.58559
Italian sparrow from Malta	Malta022	9.2418
Italian sparrow from Malta	Malta028	9.06979
Italian sparrow from Malta	Malta030	9.44683
Italian sparrow from Malta	Malta031	7.21075
Italian sparrow from Malta	Malta033	9.19488
Italian sparrow from Malta	Malta036	12.7716
Italian sparrow from Corsica	Corsica096	7.0319
Italian sparrow from Corsica	Corsica006	7.02024
Italian sparrow from Corsica	Corsica010	7.80143
Italian sparrow from Corsica	Corsica011	7.25636
Italian sparrow from Corsica	Corsica015	7.19225
Italian sparrow from Corsica	Corsica019	7.52628
Italian sparrow from Corsica	Corsica021	7.30475
Italian sparrow from Corsica	Corsica022	6.86698
Italian sparrow from Corsica	Corsica026	6.71987
Italian sparrow from Corsica	Corsica029	7.37389
Italian sparrow from Corsica	Corsica031	7.44812

Italian sparrow from Corsica	Corsica032	7.33279
Italian sparrow from Corsica	Corsica034	7.33798
Italian sparrow from Corsica	Corsica035	7.35358
Italian sparrow from Corsica	Corsica039	7.64138
Italian sparrow from Corsica	Corsica071	7.32424
Italian sparrow from Corsica	Corsica073	7.37707
Italian sparrow from Corsica	Corsica083	6.65694
Italian sparrow from Corsica	Corsica085	6.64172
Italian sparrow from Corsica	Corsica089	7.75849
Italian sparrow from Corsica	Corsica090	7.13215
Italian sparrow from Sicily	Sicily029	7.24013
Italian sparrow from Sicily	Sicily040	7.05358
Italian sparrow from Sicily	Sicily045	6.93798
Italian sparrow from Sicily	Sicily046	6.82374
Italian sparrow from Sicily	Sicily049	7.77132
Italian sparrow from Sicily	Sicily052	7.55605
Italian sparrow from Sicily	Sicily058	7.02391
Italian sparrow from Sicily	Sicily059	7.94485
Italian sparrow from Sicily	Sicily064	7.39739
Italian sparrow from Sicily	Sicily065	6.91349
Italian sparrow from Crete	Crete060	8.23542
Italian sparrow from Crete	Crete065	7.95604
Italian sparrow from Crete	Crete067	6.22187
Italian sparrow from Crete	Crete068	5.68179
Italian sparrow from Crete	Crete080	5.3123
Italian sparrow from Crete	Crete081	6.95272
Italian sparrow from Crete	Crete088	6.36891
Italian sparrow from Crete	Crete090	5.86372
Italian sparrow from Crete	Crete094	5.44188
Italian sparrow from Crete	Crete109	5.33869

Supplementary Table 3. Successive eigenvalues from the principal component analysis. Principal components are denoted PC, and eigenvalues are presented from three different analyses: one including the entire genome, one including the Z-chromosome only and finally one with only autosomal SNP's.

Principal Component	All	Z	Autosomes
PC1	0.052	0.142	0.049
PC2	0.023	0.031	0.022
PC3	0.020	0.026	0.020
PC4	0.020	0.022	0.019
PC5	0.018	0.018	0.018
PC6	0.016	0.017	0.016
PC7	0.016	0.016	0.016
PC8	0.016	0.015	0.016
PC9	0.016	0.015	0.016
PC10	0.016	0.015	0.016
PC11	0.015	0.014	0.016
PC12	0.015	0.014	0.016
PC13	0.015	0.014	0.015
PC14	0.015	0.014	0.015
PC15	0.015	0.014	0.015
PC16	0.015	0.014	0.015
PC17	0.015	0.013	0.015
PC18	0.014	0.013	0.014
PC19	0.014	0.013	0.014
PC20	0.014	0.013	0.014
PC21	0.014	0.013	0.014
PC22	0.014	0.012	0.014
PC23	0.014	0.012	0.014
PC24	0.014	0.012	0.014
PC25	0.014	0.012	0.014
PC26	0.014	0.012	0.014
PC27	0.014	0.012	0.014
PC28	0.013	0.012	0.014
PC29	0.013	0.012	0.013
PC30	0.013	0.012	0.013

Supplementary Table 4. Principal component scores per individual and population. The first three Principal Components (PCs) from three different analyses are presented. First, an analysis based on the whole genome is presented (All), then an analysis for the Z-chromosome only (Z) and lastly an analysis based on autosomes only (auto) are presented. The eigenvalues for the PCs are listed in the first row.

Individual	Popu- lation	PC1 all	PC2 all	PC3 all	PC1 Z	PC2 Z	PC3 Z	PC1 auto	PC2 auto	PC3 auto
Eigenvalue	-	0.052	0.023	0.020	0.142	0.031	0.026	0.049	0.022	0.020
C060	Crete	-0.091	-0.295	-0.126	-0.116	0.111	-0.297	-0.084	-0.295	-0.119
C065	Crete	-0.097	-0.289	-0.120	-0.109	0.102	-0.294	-0.091	-0.292	-0.109
C067	Crete	-0.082	-0.235	-0.099	-0.099	0.058	-0.218	-0.077	-0.241	-0.094
C068	Crete	-0.083	-0.218	-0.091	-0.111	0.080	-0.218	-0.077	-0.220	-0.086
C080	Crete	-0.080	-0.179	-0.077	-0.102	0.096	-0.236	-0.073	-0.181	-0.067
C081	Crete	-0.093	-0.280	-0.126	-0.108	0.100	-0.299	-0.087	-0.282	-0.114
C088	Crete	-0.100	-0.288	-0.126	-0.105	0.082	-0.253	-0.095	-0.292	-0.114
C090	Crete	-0.091	-0.263	-0.114	-0.099	0.078	-0.237	-0.086	-0.265	-0.104
C094	Crete	-0.090	-0.237	-0.099	-0.092	0.071	-0.214	-0.087	-0.241	-0.090
C109	Crete	-0.084	-0.203	-0.081	-0.100	0.076	-0.218	-0.078	-0.205	-0.077
K006	Corsica	-0.017	0.015	0.159	-0.028	-0.092	0.076	-0.018	0.014	0.146
K010	Corsica	-0.010	0.017	0.191	-0.014	-0.057	0.036	-0.010	0.017	0.209
K011	Corsica	-0.027	0.010	0.161	-0.059	-0.087	0.053	-0.023	0.010	0.155
K015	Corsica	-0.031	0.005	0.194	-0.047	-0.045	0.073	-0.028	0.007	0.195
K019	Corsica	-0.043	0.006	0.160	-0.081	-0.021	0.037	-0.035	0.009	0.161
K021	Corsica	-0.011	0.013	0.169	-0.024	-0.062	0.050	-0.010	0.014	0.183
K022	Corsica	-0.011	0.014	0.213	-0.026	-0.106	0.069	-0.009	0.015	0.212
K026	Corsica	-0.028	0.005	0.175	-0.083	-0.048	0.071	-0.017	0.008	0.172
K029	Corsica	-0.024	0.004	0.154	0.018	-0.003	0.038	-0.034	-0.001	0.166
K031	Corsica	-0.035	0.012	0.163	-0.076	0.110	0.120	-0.025	0.013	0.162
K032	Corsica	-0.019	0.015	0.132	-0.063	-0.048	0.031	-0.010	0.019	0.125
K034	Corsica	-0.039	0.007	0.150	-0.063	-0.046	0.026	-0.035	0.013	0.145
K035	Corsica	-0.030	0.009	0.151	-0.041	-0.066	0.046	-0.029	0.007	0.145
K039	Corsica	-0.002	0.020	0.138	-0.023	-0.069	0.051	0.005	0.022	0.135
K071	Corsica	-0.021	0.015	0.156	0.008	-0.106	0.028	-0.027	0.010	0.166
K073	Corsica	-0.031	-0.003	0.136	-0.092	0.050	-0.024	-0.017	0.008	0.140
K083	Corsica	-0.006	0.021	0.115	0.024	0.036	0.082	-0.010	0.016	0.124
K085	Corsica	-0.024	0.006	0.140	-0.044	0.022	0.072	-0.019	0.006	0.139
K089	Corsica	-0.016	0.008	0.231	-0.041	-0.054	0.048	-0.010	0.014	0.234
K090	Corsica	-0.024	0.004	0.130	-0.048	0.061	0.032	-0.020	0.009	0.130
K096	Corsica	-0.025	0.002	0.116	-0.044	0.069	0.068	-0.021	0.004	0.118
S029	Sicily	0.065	0.016	-0.005	0.088	-0.096	0.006	0.058	0.014	-0.006
S040	Sicily	0.062	0.014	-0.004	0.093	-0.081	-0.032	0.055	0.014	-0.005
S045	Sicily	0.058	0.013	-0.002	0.069	-0.068	-0.042	0.056	0.014	-0.001
S046	Sicily	0.059	0.008	-0.003	0.072	-0.115	-0.012	0.056	0.010	-0.007
S049	Sicily	0.068	0.015	0.002	0.056	-0.066	0.000	0.068	0.018	-0.006
S052	Sicily	0.072	0.017	-0.011	0.089	-0.099	-0.036	0.069	0.023	-0.014

S058	Sicily	0.069	0.015	-0.005	0.099	-0.074	-0.045	0.063	0.018	-0.003
S059	Sicily	0.059	0.000	-0.021	0.093	-0.108	-0.016	0.049	-0.003	-0.024
S064	Sicily	0.062	0.008	-0.023	0.077	-0.096	0.018	0.058	0.006	-0.027
S065	Sicily	0.059	0.003	-0.020	0.088	-0.110	-0.018	0.050	0.000	-0.023
M010	Malta	0.072	0.020	-0.039	0.076	-0.107	-0.006	0.070	0.023	-0.063
M012	Malta	0.076	0.025	-0.044	0.072	-0.164	-0.016	0.076	0.026	-0.070
M019	Malta	0.122	0.065	-0.099	0.128	-0.296	-0.034	0.117	0.074	-0.159
M022	Malta	0.085	0.025	-0.075	0.094	-0.163	0.004	0.081	0.026	-0.115
M028	Malta	0.076	0.014	-0.057	0.083	-0.145	-0.015	0.073	0.019	-0.088
M030	Malta	0.084	0.021	-0.057	0.094	-0.165	-0.038	0.081	0.024	-0.089
M031	Malta	0.064	0.009	-0.046	0.062	-0.122	-0.022	0.064	0.013	-0.072
M033	Malta	0.078	0.016	-0.052	0.079	-0.150	-0.029	0.075	0.022	-0.086
M036	Malta	0.097	0.026	-0.077	0.113	-0.183	-0.051	0.092	0.033	-0.116
M037	Malta	0.074	0.012	-0.043	0.088	-0.172	-0.031	0.068	0.014	-0.069
8L19786	House	-0.189	0.086	0.036	-0.169	0.043	0.093	-0.191	0.080	0.047
8L64869	House	-0.215	0.171	-0.089	-0.176	0.051	0.140	-0.221	0.166	-0.083
8L89915	House	-0.192	0.113	-0.015	-0.170	0.038	0.150	-0.195	0.106	-0.017
8M31651	House	-0.238	0.330	-0.338	-0.189	0.069	0.229	-0.247	0.326	-0.322
8M71932	House	-0.202	0.140	-0.038	-0.173	0.053	0.141	-0.206	0.134	-0.032
8M72455	House	-0.202	0.097	-0.029	-0.171	0.046	0.115	-0.207	0.088	-0.020
8N05890	House	-0.199	0.135	-0.064	-0.173	0.037	0.186	-0.204	0.123	-0.058
8N06612	House	-0.192	0.104	-0.020	-0.175	0.046	0.155	-0.195	0.094	-0.012
8N73248	House	-0.229	0.287	-0.286	-0.180	0.050	0.185	-0.238	0.284	-0.277
8N73604	House	-0.217	0.166	-0.075	-0.186	0.062	0.171	-0.221	0.158	-0.069
Lesina_280	Spanish	0.197	0.056	-0.099	0.202	0.221	0.054	0.196	0.058	-0.077
Lesina_281	Spanish	0.178	0.048	-0.089	0.188	0.201	0.046	0.177	0.048	-0.070
Lesina_282	Spanish	0.173	0.041	-0.085	0.176	0.189	0.043	0.173	0.040	-0.067
Lesina_285	Spanish	0.191	0.055	-0.082	0.191	0.192	0.047	0.191	0.057	-0.064
Lesina_286	Spanish	0.197	0.056	-0.090	0.198	0.207	0.051	0.198	0.060	-0.071
Lesina_287	Spanish	0.199	0.062	-0.093	0.203	0.215	0.055	0.198	0.062	-0.071
Lesina_288	Spanish	0.195	0.059	-0.089	0.197	0.204	0.051	0.196	0.060	-0.069
Lesina_289	Spanish	0.196	0.056	-0.088	0.197	0.203	0.049	0.197	0.059	-0.069
Lesina_292	Spanish	0.206	0.058	-0.094	0.202	0.225	0.064	0.207	0.063	-0.074
Lesina_295	Spanish	0.172	0.039	-0.084	0.174	0.190	0.039	0.172	0.040	-0.067

Supplementary Table 5. Average and standard deviation of F_{ST} , D_{xy} , nucleotide diversity (Pi) and Tajima's D for all populations of Italian sparrow.

	Crete	Corsica	Sicily	Malta	House	Spanish
Mean F_{ST} against house	0.222	0.180	0.221	0.245	NA	0.333
Std of F_{ST} against house	0.070	0.080	0.077	0.085	NA	0.105
Mean F_{ST} against Spanish	0.308	0.233	0.1876	0.219	0.333	NA
Std of F_{ST} against Spanish	0.116	0.128	0.109	0.115	0.105	NA
Mean D_{xy} against house	0.00278	0.00306	0.00329	0.00344	NA	0.00418
Std of D_{xy} against house	0.00122	0.00138	0.00132	0.00127	NA	0.00158
Mean D_{xy} against Spanish	0.00291	0.00306	0.00279	0.00295	0.00418	NA
Std of D_{xy} against Spanish	0.00114	0.00127	0.00118	0.00121	0.00158	NA
Mean Pi	0.0067	0.0071	0.0069	0.0063	0.0072	0.0054
Std of Pi	0.0026	0.0026	0.0027	0.0027	0.0029	0.0028
Mean of Tajima's D	0.0344	-0.1099	-0.3950	-0.0731	-0.1494	-0.3993
Std of Tajima's D	0.6128	0.6375	0.5730	0.6558	0.5538	0.6058

Supplementary Table 6. Support for different values of K, representing the number of genetic clusters in the data set of the ADMIXTURE analysis. The lowest cross-validation (CV) error is the preferred model.

K (number of populaltions)	CV error
1	0.64
2	0.64
3	0.74
4	0.78
5	0.81
6	0.86
7	0.99
8	1.07
9	1.22
10	1.37

Supplementary Table 7. Tukey's post hoc comparisons for test for differences in probability of assignment to house sparrow between the island populations of Italian sparrow based on data from an ADMIXTURE analysis.

Comparison	Estimate	Std. Error	t	Pr(> t)
Crete vs. Corsica	-0.138675	0.009045	-15.33	<2e-16
Crete vs. Sicily	-0.382125	0.010529	-36.29	<2e-16
Crete vs. Malta	-0.405122	0.010529	-38.48	<2e-16
Corsica vs. Sicily	-0.24345	0.009045	-26.91	<2e-16
Corsica vs. Malta	-0.266446	0.009045	-29.46	<2e-16
Sicily vs. Malta	-0.022997	0.010529	-2.184	0.034

Supplementary Table 8. Phylogenetic trees from the BEAST analysis and their relative frequencies.

Frequency	Phylogenetic relationship
32	(Naxos1,((K035,(8L19786,C081)),(S059,(Lesina_280,M036))))
28	(Naxos1,((C081,(8L19786,K035)),(S059,(Lesina_280,M036))))
26	(Naxos1,((C081,(8L19786,K035)),(Lesina_280,(M036,S059))))
22	(Naxos1,((8L19786,(C081,K035)),(S059,(Lesina_280,M036))))
20	(Naxos1,((8L19786,(C081,K035)),(M036,(Lesina_280,S059))))
20	(Naxos1,((C081,(8L19786,K035)),(M036,(Lesina_280,S059))))
19	(Naxos1,((K035,(8L19786,C081)),(Lesina_280,(M036,S059))))
18	(Naxos1,((8L19786,C081),(K035,(Lesina_280,(M036,S059))))
15	(Naxos1,((8L19786,(C081,K035)),(Lesina_280,(M036,S059))))
14	(Naxos1,((8L19786,C081),(K035,S059),(Lesina_280,M036))))
14	(Naxos1,((C081,(8L19786,M036)),(K035,(Lesina_280,S059))))
13	(Naxos1,((8L19786,K035),(C081,(M036,(Lesina_280,S059))))
13	(Naxos1,((K035,(8L19786,C081)),(M036,(Lesina_280,S059))))
12	(Naxos1,((8L19786,C081),(K035,(S059,(Lesina_280,M036))))
11	(Naxos1,((K035,(8L19786,M036)),(S059,(C081,Lesina_280))))
10	(Naxos1,((8L19786,C081),(K035,(M036,(Lesina_280,S059))))
9	(Naxos1,((8L19786,C081),(Lesina_280,(M036,(K035,S059))))
9	(Naxos1,((K035,(8L19786,M036)),(C081,(Lesina_280,S059))))
9	(Naxos1,((Lesina_280,S059),(K035,(8L19786,(C081,M036))))
8	(Naxos1,((8L19786,(K035,M036)),(S059,(C081,Lesina_280))))
8	(Naxos1,((8L19786,C081),(K035,M036),(Lesina_280,S059))))
8	(Naxos1,((8L19786,K035),(C081,(S059,(Lesina_280,M036))))
8	(Naxos1,((Lesina_280,M036),(C081,(8L19786,(K035,S059))))
8	(Naxos1,((M036,(8L19786,C081)),(K035,(Lesina_280,S059))))
7	(Naxos1,((8L19786,(C081,M036)),(K035,(Lesina_280,S059))))
7	(Naxos1,((8L19786,K035),(C081,(Lesina_280,(M036,S059))))
7	(Naxos1,((8L19786,M036),(C081,(K035,(Lesina_280,S059))))
7	(Naxos1,((C081,(8L19786,S059)),(K035,(Lesina_280,M036))))
7	(Naxos1,((Lesina_280,M036),(C081,(S059,(8L19786,K035))))
7	(Naxos1,((M036,(8L19786,C081)),(Lesina_280,(K035,S059))))
6	(Naxos1,((8L19786,C081),(K035,Lesina_280),(M036,S059))))
6	(Naxos1,((8L19786,C081),(Lesina_280,(S059,(K035,M036))))
6	(Naxos1,((8L19786,C081),(S059,(Lesina_280,(K035,M036))))
6	(Naxos1,((8L19786,C081),(S059,(M036,(K035,Lesina_280))))
6	(Naxos1,((8L19786,Lesina_280),(C081,M036),(K035,S059))))
6	(Naxos1,((8L19786,Lesina_280),(C081,(M036,(K035,S059))))
6	(Naxos1,((C081,(8L19786,M036)),(S059,(K035,Lesina_280))))
6	(Naxos1,((Lesina_280,S059),(8L19786,C081),(K035,M036))))
6	(Naxos1,((Lesina_280,S059),(8L19786,(K035,(C081,M036))))
6	(Naxos1,((S059,(8L19786,C081)),(K035,(Lesina_280,M036))))

Supplementary Table 9. Patterson's D statistics quantification shows differences in level of introgression of Spanish sparrow genetic material into the Italian sparrow populations. The overall glm is highly significant. Post hoc t-tests show that there is a tendency of a difference between Crete and Corsica, no difference between Sicily and Malta, and all other post hoc comparisons are significant.

Population 1	Population 2	t	P
Crete	Corsica	-1.92	0.057
Crete	Sicily	6.591	1.38e-09
Crete	Malta	6.625	1.17e-09
Corsica	Sicily	4.68	7.77e-06
Corsica	Malta	4.70	7.22e-06
Sicily	Malta	-0.022	0.98
	DF, errorDF	F	P
Overall glm	3,115	22.52	1.53e-11

Supplementary Table 10. Standardized slopes (beta) between differentiation and recombination rate for different population combinations.

Populations	Combination type	Beta (standardized slope)
House, Spanish	Parent vs. Parent	0.486
Crete, Spanish	Italian vs. Spanish	0.457
Corsica, Spanish	Italian vs. Spanish	0.460
Sicily, Spanish	Italian vs. Spanish	0.359
Malta, Spanish	Italian vs. Spanish	0.370
Crete, House	Italian vs. House	0.082
Corsica, House	Italian vs. House	0.192
Sicily, House	Italian vs. House	0.242
Malta, House	Italian vs. House	0.231
Crete, Corsica	Italian vs. Italian	0.028
Crete, Sicily	Italian vs. Italian	0.165
Crete, Malta	Italian vs. Italian	0.162
Corsica, Sicily	Italian vs. Italian	0.179
Corsica, Malta	Italian vs. Italian	0.175
Sicily, Malta	Italian vs. Italian	0.028

Supplementary Table 11. Differences in standardized slopes against recombination rate between different categories of combinations. There is an overall significant difference in slope between categories, whereas 4 of 6 post hoc comparisons (t-tests) are significant after Bonferroni correction for multiple testing.

Comparison 1	Comparison 2	t	P
Parent-Parent	Italian-Spanish	-1.0	0.35
Parent-Parent	Italian-House	-3.9	0.0025
Parent-Parent	Italian-Italian	-4.9	0.0005
Italian-Spanish	Italian-House	-4.6	0.0007
Italian-Spanish	Italian-Italian	-6.5	4.4e-5
Italian-House	Italian-Italian	1.43	0.18
	DF, errorDF	F	P
Overall glm	3,11	19.17	0.0001

Supplementary Table 12. Gene ontology results for outliers with high divergence between islands based on a GOSTAT analysis. Correction for multiple testing was performed using false discovery rate (Benjamini method). Terms significant at $P < 0.001$ are shown.

		498	33972	
multicellular organismal development	cull1 tle1 fkbp4 hlx kcnj8 hus1 col6a3 tead4 vldlr angptl2 scube1 cdh6 aldh5a1 ror2 syk cep290 cer1 kif2a lox lrmp ntf3 ptch1 acsbgl col8a1 dbx1 crabp1 ghr apba1 gbx2 grin3a tssk2 efna5 tlx3 kras phgdh col12a1 pak3 till1 map1b gli3 gnaq sh3gl2 nf2 rasa1 dgkd aicda jak2 frem1 htatip2 cript2 ntrk2 phc1 tgfb2 hmgcr wnt7a t col11a1 gpr98 kazald1 bpnt1 cenpf isl2 slitrk1 shroom4 cdh11 fut10 lif sepp1 spry3 nrg1 cfc1 nefh fst cd9 prrx1 ugt8 notch2 fgf10 ush2a ephb2 alx1 dll1 sirt1 disp1 ptger4 trim14 inhba gal3st1	88	2299	6.67e-19
system development	cull1 tle1 kcnj8 col6a3 tead4 vldlr scube1 cdh6 aldh5a1 syk ror2 cep290 kif2a lox lrmp ntf3 ptch1 col8a1 acsbgl ghr apba1 gbx2 grin3a efna5 tlx3 phgdh kras col12a1 till1 map1b gli3 gnaq sh3gl2 rasa1 nf2 aicda jak2 htatip2 cript2 ntrk2 tgfb2 hmgcr wnt7a col11a1 t gpr98 kazald1 bpnt1 cenpf slitrk1 cdh11 shroom4 fut10 lif sepp1 fst nefh cd9 ugt8 fgf10 notch2 ush2a ephb2 alx1 sirt1 dll1 ptger4 gal3st1 inhba	69	1605	8.79e-19
anatomical structure development	cull1 myoc tle1 kcnj8 col6a3 tead4 vldlr scube1 cdh6 enox2 aldh5a1 pes1 ror2 syk cep290 cer1 kif2a lox lrmp ntf3 ptch1 acsbgl col8a1 ghr apba1 gbx2 grin3a efna5 tlx3 phgdh kras col12a1 till1 map1b gli3 igfbp1 gnaq sh3gl2 nf2 rasa1 dgkd aicda jak2 htatip2 cript2 ntrk2 tgfb2 hmgcr erbb2ip wnt7a t col11a1 gpr98 kazald1 bpnt1 cenpf slitrk1 shroom4 cdh11 fut10 lif sepp1 cfc1 cda nefh fst cd9 ugt8 notch2 fgf10 ush2a ephb2 palm2 alx1 dll1 sirt1 ptger4 inhba gal3st1	79	2005	2.77e-18
Cellular component organization and biogenesis	nup155 slu7 paip1 fkbp4 mtrf11 vldlr scube1 lysmd3 enox2 vwf aldh5a1 pes1 syk cep290 kif2a lox lrmp srp19 rsf1 dnm3 ipo11 tekt1 myo7a pdpk1 stk381 akap6 cklf rnf20 ghr apba1 necap1 gbx2 grin3a epb41 kras slc25a14 col12a1 a2m vps13a hook3 sf3a1 map1b camk4 pacsin2 prex1 sncaip gli3 nrm1 tgfb1 igfbp1 slc9a3 arfgef2 sh3gl2 nf2 rasa1 dgkd jak2 etf1 snx2 htatip2 utp14a cetn3 hdac8 vamp4 tgfb2 ezh2 erbb2ip rab3gap2 kif27 col11a1 wnt7a kazald1 apc m6pr clen5 wdr36 cenpf gtf2i gnptg slitrk1 tubgcp4 shroom4 fut10 clta ddx19b pak1 tnp01 col4a6 chrnb4 nbn scamp1 tspo nrg1 cda mark1 cd9 aifm1 notch2 fgf10 acr bcor11 palm2 ttk sec61g sirt1 inhba uhmk1	107	3277	1.45e-16
multicellular organismal process	cull1 myoc tle1 fkbp4 hlx kcnj8 hus1 col6a3 tead4 vldlr galr1 angptl2 scube1 cdh6 vwf aldh5a1 ror2 syk cep290 cer1 kif2a lox lrmp ntf3 ptch1 mia3 acsbgl col8a1 dbx1 c1qc crabp1 myo7a slc6a1 ghr apba1 gbx2 fxn grin3a efna5 tssk2 tlx3 epb41 kras phgdh col12a1 chrna5 pak3 till1 map1b camk4 sncaip gli3 gnaq sh3gl2 nf2 rasa1 dgkd aicda jak2 mmp27 frem1 htatip2 pde6b f2r11 cript2 ntrk2	119	3822	1.45e-16

developmental process	<p>phc1 elovl4 tgfb2 hmger coll1a1 mmp3 npy5r t wnt7a kazald1 gpr98 clen5 kenv2 bpnt1 sspn wdr36 isl2 cenpf slitrk1 cdh11 shroom4 fut10 lif gabrg1 c3ar1 chrnb4 sepp1 spry3 cfc1 nrg1 mmp1 fst nefh cd9 kcnip1 prrx1 ugt8 fgf10 f2r12 notch2 htr6 ush2a ephb2 alx1 lpl clns1a dll1 sirt1 disp1 ptger4 trim14 inhba gal3st1 cull1 myoc tle1 fkbp4 hlx kcnj8 hus1 col6a3 tead4 vldlr angptl2 scube1 cdh6 enox2 aldh5a1 pes1 ror2 syk cep290 cer1 kif2a lox lrmp ntf3 ptch1 acsbg1 col8a1 dbx1 crabp1 stk17a ghr apba1 gbx2 grin3a efna5 tssk2 tlx3 kras phgdh coll2a1 casp9 pak3 tll1 map1b gli3 npm1 igfbp1 gnaq sh3gl2 nf2 rasa1 dgkd prune2 aicda jak2 mrps30 frem1 htatip2 cript2 phc1 ntrk2 tgfb2 hmger erbb2ip coll1a1 t wnt7a kazald1 gpr98 bpnt1 thoc5 pacs2 isl2 cenpf dapk2 slitrk1 cdh11 shroom4 fut10 lif pak1 sepp1 spry3 tspo cfc1 nrg1 jmy cda fst dapk1 nefh cd9 aifm1 prrx1 ugt8 fgf10 notch2 ush2a ephb2 palm2 alx1 dll1 sirt1 disp1 ptger4 trim14 inhba gal3st1</p>	108	3347	2.34e-16
negative regulation of cellular process	<p>cull1 jak2 tle1 rgs5 rgs4 htatip2 hus1 hdac8 rgs18 tgfb2 cer1 rgs1 apc gpr98 reck ntf3 ptch1 rsf1 nbl1 mcc mia3 rgs2 cenpf lif nbn nr0b2 rgs17 nrg1 cda jmy fst dapk1 tlx3 kras notch2 fgf10 map1b ush2a ephb2 rgs21 dll1 gli3 sirt1 npm1 rgs13 inhba uhmk1 nf2 rasa1</p>	49	1137	2.99e-13
localization	<p>nup155 tcn2 fkbp4 kcnj8 slc44a1 col6a3 vldlr galr1 golga4 snx30 enox2 rhobtb3 pitpnm3 syk cep290 cer1 kif2a lrmp osbp2 srp19 ntf3 dnm3 slc28a3 ipo11 mia3 col8a1 c1qc crabp1 myo7a slc26a1 akap6 rasef slc25a46 slc6a1 cklf ghr trpm8 apba1 necap1 sft2d1 gbx2 fxn sv2c nnt ryr3 clic2 grin3a slc30a10 tlx3 phgdh slc25a14 coll2a1 a2m abcc9 slc13a5 vps13a hook3 chrna5 col4a3bp camk4 slc6a11 hiatl1 pacsin2 sncaip gli3 npm1 sec14l2 slc9a3 arfgef2 sh3gl2 nf2 jak2 snx24 slc2a3 htatip2 snx2 vamp4 tgfb2 hmger gpr119 erbb2ip rab3gap2 kif27 coll1a1 wnt7a atp1b1 m6pr clen5 kenv2 slc17a6 cenpf gnptg tspan3 fut10 clta ddx19b lif slc46a2 stard4 tnpol gabrg1 col4a6 c3ar1 chrnb4 kenn2 scamp1 tspo fmo1 aqp11 fst gabrp cd9 kcnip1 chrna3 fgf10 etfa acr rab33a slc13a4 clns1a sec61g vps13c inhba uhmk1 itpr2 slc3a1</p>	126	4481	2.99e-13
organ development	<p>aicda cull1 jak2 tle1 kcnj8 htatip2 col6a3 tead4 cript2 scube1 cdh6 tgfb2 hmger ror2 syk cep290 coll1a1 lox lrmp t wnt7a gpr98 kazald1 ptch1 col8a1 cenpf cdh11 shroom4 fut10 lif ghr sepp1 gbx2 fst kras phgdh coll2a1 notch2 fgf10 tll1 ush2a alx1 gli3 dll1 sirt1 ptger4 gnaq inhba</p>	49	1141	3.07e-13

negative regulation of biological process	rasa1 cull1 jak2 tle1 rgs5 rgs4 htatip2 hus1 hdac8 rgs18 tgfb2 cer1 rgs1 apc gpr98 reck ntf3 ptch1 rsf1 nbl1 mcc mia3 rgs2 cenpf lif nbn nr0b2 rgs17 nrg1 cda jmy fst dapk1 tlx3 kras notch2 fgf10 map1b ush2a ephb2 rgs21 dll1 gli3 sirt1 npm1 rgs13 inhba uhmk1 nf2 rasa1	49	1182	2.61e-12
nervous system development	vldlr ntrk2 tgfb2 aldh5a1 kif2a cep290 wnt7a t gpr98 ntf3 bpnt1 acsbg1 slitrk1 shroom4 fut10 apba1 sepp1 gbx2 grin3a efna5 nefh cd9 tlx3 phgdh ugt8 notch2 map1b ephb2 alx1 gli3 gnaq gal3st1 inhba sh3gl2 nf2	35	716	6.75e-12
cell-cell signaling	slc6a1 gabrg1 chrnb4 apba1 fxn galr1 efna5 fst cd9 tgfb2 knip1 aldh5a1 gpr119 kras syk fgf10 npy5r wnt7a chrna5 htr6 lnpep ntf3 xcl1 camk4 pcsk5 sncaip acsbg1 gnaq gal3st1 inhba lif	31	640	3.19e-10
establishment of localization	nup155 tcn2 fkbp4 kcnj8 slc44a1 col6a3 vldlr galr1 golga4 snx30 enox2 pitpnm3 syk cep290 kif2a lrmp osbp2 srp19 dnm3 slc28a3 ipo11 col8a1 c1qc crabp1 myo7a slc26a1 akap6 rasef slc25a46 slc6a1 cklf trpm8 ghr apba1 necap1 sft2d1 fxn sv2c nnt ryr3 clic2 grin3a slc30a10 phgdh slc25a14 col12a1 a2m abcc9 slc13a5 vps13a chrna5 col4a3bp camk4 slc6a11 hiatl1 pacsin2 sncaip gli3 npm1 sec1412 slc9a3 arfgef2 sh3gl2 snx24 jak2 slc2a3 htatip2 snx2 vamp4 gpr119 rab3gap2 kif27 col11a1 wnt7a atp1b1 m6pr clcn5 kcnv2 slc17a6 cenpf gnptg fut10 clta lif ddx19b slc46a2 stard4 tnpol gabrg1 col4a6 chrnb4 kenn2 scamp1 tspo fmo1 aqp11 fst gabrp knip1 chrna3 fgf10 acr etfa rab33a slc13a4 clns1a sec61g inhba uhmk1 itpr2 slc3a1	111	4135	7.11e-10
transport	nup155 tcn2 fkbp4 kcnj8 slc44a1 col6a3 vldlr galr1 golga4 snx30 enox2 pitpnm3 syk cep290 kif2a lrmp osbp2 srp19 dnm3 slc28a3 ipo11 col8a1 c1qc crabp1 myo7a slc26a1 akap6 rasef slc25a46 slc6a1 cklf trpm8 ghr apba1 necap1 sft2d1 fxn sv2c nnt ryr3 clic2 grin3a slc30a10 phgdh slc25a14 col12a1 a2m abcc9 slc13a5 vps13a chrna5 col4a3bp camk4 slc6a11 hiatl1 pacsin2 sncaip gli3 npm1 sec1412 slc9a3 arfgef2 sh3gl2 snx24 jak2 slc2a3 htatip2 snx2 vamp4 gpr119 rab3gap2 kif27 col11a1 wnt7a atp1b1 m6pr clcn5 kcnv2 slc17a6 gnptg fut10 clta ddx19b slc46a2 stard4 tnpol gabrg1 col4a6 chrnb4 kenn2 scamp1 tspo fmo1 aqp11 gabrp knip1 chrna3 fgf10 acr etfa rab33a slc13a4 clns1a sec61g uhmk1 itpr2 slc3a1	107	4035	4.56e-09
regulation of progression through cell cycle	cull1 nbn htatip2 hus1 jmy tgfb2 notch2 apc reck ephb2 ptch1 ttk nbl1 mcc cenpf fboxo5 inhba uhmk1 nf2 ccnh	20	353	1.96e-08
Regulation of cell cycle	cull1 nbn htatip2 hus1 jmy tgfb2 notch2	20	359	3.33e-08

cell communication	apc reck ephb2 ptch1 ttk nbl1 mcc cenpf fbxo5 inhba uhmk1 nf2 ccnh rgs4 tulp3 vldlr snx30 dusp10 cer1 lrrfip2 acsbg1 epha7 crabp1 stk17a pdpk1 rasef tbc1d10a cntnap4 mta1 slc6a1 klrg1 apba1 rgs17 clic2 efna5 fer chrna5 ddr2 prex1 ocl1 gli3 ncoa3 gnaq csnk1g3 sh3gl2 arfgef2 nf2 rasa1 snx24 snx2 garnl3 aplp2 gpr119 erbb2ip rgs1 apc iqgap2 dapk2 pak1 c3ar1 plk2 spry3 arntl2 cda fst mark1 cd9 psd3 chrna3 aifm1 fgf10 iqgap1 rab33a ephb2 rgs21 rabgap11 dll1 asb18 inhba gal3st1 tle1 rgs5 ank2 galr1 angptl2 aldh5a1 ror2 syk lox ntf3 ptch1 pcsk5 itfg2 stk381 prkab2 dgkb fbwx11 fxn kras casp9 nsmce1 xcl1 camk4 sncaip tle4 nrm1 rgs13 tgfr1 igfbp1 ralgs1 dgkd jak2 fnta ncf1 pde10a f2r11 pde6b ntrk2 rassf8 rgs18 tgfb2 wnt7a npy5r t gpr98 ppic tbc1d2b mcc rgs2 gtf2i lif gabrg1 capn5 chrnb4 ptprd dapk1 kcnp1 pink1 f2r12 notch2 acr htr6 lnpep ptger4 clec4a itpr2	133	5560	4.69e-08
biological regulation	cull1 habp4 hlx rgs4 tulp3 tead4 cer1 phf10 mia3 acsbg1 c1qc stk17a tsc22d3 tbc1d10a mta1 nr0b2 rgs17 ryr3 znf367 foxb2 map1b ddr2 prex1 adnp2 gli3 sec14l2 ncoa3 slc9a3 gnaq arfgef2 rasa1 nf2 ccnh etf1 garnl3 hdac8 bnc2 erbb2ip foxj2 rgs1 kazald1 apc iqgap2 snapc3 cenpf zbtb43 dapk2 prdm10 pak1 c3ar1 plk2 smarca2 spry3 arntl2 nrg1 jmy cda fst cd9 psd3 ube2i aifm1 fgf10 iqgap1 ephb2 palm2 alx1 ttk rgs21 clns1a txnde17 dll1 rabgap11 sirt1 inhba gal3st1 tp53bp1 tle1 rgs5 paip1 knj8 hus1 galr1 scube1 enox2 vwf aldh5a1 syk irx2 ntf3 reck ptch1 rsf1 l3mbtl3 dbx1 stk381 zfhx4 psip1 dgkb gbx2 fxn med21 tlx3 kras casp9 xcl1 sncaip tle4 tgfr1 nrm1 rgs13 igfbp1 dgkd prune2 jak2 htatip2 foxm1 znf131 f2r11 cript2 rgs18 tgfb2 med31 ezh2 med18 rab3gap2 wnt7a t gpr98 nbl1 tbc1d2b rgs2 mcc isl2 gtf2i lif taf1a chrnb4 nbn tspo dapk1 prrx1 znf366 notch2 f2r12 acr ireb2 ush2a bcor11 ptger4 ascc2 fbxo5 hnf4g uhmk1	154	6731	4.8e-08
biological adhesion	cdh5 frem1 pcdh7 col6a3 cdh6 pcdh9 vwf ror2 syk erbb2ip col11a1 parvb t gpr98 apc gne sspn mia3 pcdh17 col8a1 selp cdh11 cntnap4 col4a6 apba1 dpt thbs2 parvg cd9 col12a1 fer ddr2 alx1 dll1 rasa1 nf2 clec4a	37	960	8.13e-08
cell adhesion	cdh5 frem1 pcdh7 col6a3 cdh6 pcdh9 vwf ror2 syk erbb2ip col11a1 parvb t gpr98 apc gne sspn mia3 pcdh17 col8a1 selp cdh11 cntnap4 col4a6 apba1 dpt thbs2 parvg cd9 col12a1 fer ddr2 alx1 dll1 rasa1 nf2 clec4a	37	960	8.13e-08
cellular localization	jak2 nup155 htatip2 snx2 syk rab3gap2	40	1126	5.19e-07

establishment of cellular localizaiton	kif2a kif27 wnt7a lrmp srp19 m6pr ipo11 cenpf gnptg myo7a akap6 fut10 clta ddx19b tnpo1 cklf chrnb4 apba1 scamp1 tspo slc25a14 vps13a a2m fgf10 hook3 acr camk4 pacsin2 sncaip sec61g gli3 npm1 uhmk1 arfgef2	39	1098	7.94e-07
transmission of nerve impulse	slc6a1 gabrg1 chrnb4 apba1 fxn galr1 tgfb2 cd9 kcnip1 aldh5a1 kras npy5r wnt7a chrna5 htr6 ntf3 camk4 sncaip acsbgl gnaq gal3st1	21	330	1.75e-06
cell cycle process	cull1 nbn htatip2 hus1 cetn3 jmy tgfb2 pes1 ube2i notch2 apc reck ptch1 ephb2 ccnb3 ttk nbl1 mcc cenpf npm1 fbxo5 inhba uhmk1 nf2 ccnh prune2	26	625	2.75e-06
embryonic development	hus1 gbx2 cfc1 nrg1 tgfb2 ror2 cep290 cer1 fgf10 t wnt7a ptch1 gli3 dll1 gnaq fut10 rasal	17	235	5.58e-06
cell cycle	cull1 plk2 nbn htatip2 hus1 cetn3 gak jmy tgfb2 pes1 ube2i erbb2ip notch2 apc reck ephb2 ptch1 ccnb3 ttk nbl1 mcc rgs2 cenpf npm1 nipbl fbxo5 inhba uhmk1 nf2 ccnh prune2	31	839	7.49e-06
protein localization	jak2 snx24 nup155 fkbp4 snx2 snx30 rhobtb3 erbb2ip rab3gap2 cep290 srp19 ipo11 gnptg rasef akap6 clta fut10 ddx19b tnpo1 apba1 necap1 scamp1 sft2d1 tspo vps13a a2m fgf10 rab33a pacsin2 sec61g gli3 npm1 vps13c uhmk1	34	961	7.55e-06
anatomical structure morphogenesis	cull1 myoc tle1 kcnj8 htatip2 enox2 tgfb2 pes1 ror2 syk cer1 cep290 erbb2ip t wnt7a kazald1 ptch1 col8a1 slitrk1 lif gbx2 cfc1 cda grin3a cd9 fgf10 notch2 map1b palm2 gli3 dll1 igfbp1 gnaq inhba rasal dgkd	36	1047	8.21e-06
negative regulation of cell transduction	rgs1 tle1 rgs5 rgs4 rgs17 rgs21 rgs2 rgs18 rgs13 nf2 cer1	11	104	2.21e-05
regulation of biological quality	c3ar1 paip1 kcnj8 f2rl1 fxn ryr3 cda scubel enox2 cd9 vwf tgfb2 kras aifm1 erbb2ip notch2 f2rl2 ireb2 kazald1 gpr98 ush2a xcl1 ntf3 txndc17 clns1a acsbgl slc9a3 igfbp1 gnaq gal3st1 inhba rasal dgkd	33	953	2.21e-05
signal transduction	tle1 rgs5 ank2 rgs4 tulp3 vldlr galr1 angptl2 dusp10 ror2 syk cer1 lox ntf3 lrrfip2 ptch1 crabp1 itfg2 epha7 pdpk1 stk17a stk38l rasef cntnap4 tbc1d10a mta1 prkab2 klr1 dgkb rgs17 fbwx11 clie2 kras casp9 nsmce1 chrna5 fer ddr2 xcl1 camk4 prex1 ocl1 gli3 tle4 ncoa3 npm1 rgs13 tgfb1 igfbp1 csnk1g3 gnaq ralgps1 arfgef2 sh3gl2 nf2 rasal dgkd fnta jak2 pde10a pde6b f2rl1 garnl3 ntrk2 rgs18 rassf8 gpr119 aplp2 erbb2ip npy5r t	116	5142	2.28e-05

	wnt7a gpr98 apc rgs1 iqgap2 ppic tbc1d2b mcc rgs2 gtf2i dapk2 lif pak1 gabrg1 capn5 c3ar1 chrnb4 plk2 spry3 arntl2 cda ptpd dapk1 mark1 knip1 chrna3 pink1 psd3 aifm1 notch2 fgf10 f2rl2 acr htr6 iqgap1 ephb2 rab33a rgs21 dll1 rabgap11 ptger4 asb18 inhba itpr2 clec4a			
regulation of signal transduction	tle1 rgs5 plk2 rgs4 rgs17 spry3 garnl3 rgs18 psd3 kras syk cer1 fgf10 notch2 rgs1 iqgap1 iqgap2 ptch1 prex1 rgs21 tbc1d2b rgs2 rabgap11 rgs13 inhba arfgef2 rasa1 nf2 tbc1d10a	29	800	3.02e-05
protein modification process	cull1 hus1 gak here4 syk ror2 dusp10 st3gal6 lox ptch1 pcsk5 cdc14b fbxo22 fbxl22 epha7 ptpn20a pdpk1 stk381 stk17a ttl1 rnf20 pigg fbwx11 here1 tssk2 st8sia1 sf3a1 pak3 fer col4a3bp ddr2 camk4 hecw1 ttl12 tgfbr1 gnaq esnk1g3 styk1 nf2 fnta jak2 hdac8 ntrk2 fbwx2 prkx hace1 dapk2 gnptg ptpn14 fut10 pak1 ubqln1 plk2 ptpd dapk1 mark1 pink1 ube2i fbxo39 ctdp1 ephb2 aga gcnt1 ttk sirt1 asb18 usp3 fbxo5 gal3st1 uhmk1	70	2704	3.13e-05
macromolecule localization	jak2 snx24 nup155 fkbp4 snx2 snx30 rhobtb3 erbb2ip rab3gap2 cep290 srp19 ipo11 gnptg rasef akap6 clta fut10 ddx19b tnpo1 apba1 necap1 scamp1 sft2d1 tspo vps13a a2m fgf10 rab33a pacsin2 sec61g gli3 npm1 vps13c uhmk1	34	1012	3.44e-05
cellular lipid metabolic process	pigg nr0b2 pip5k1b nans tspo vldlr elov14 pitpnm3 hmger aldh5a1 syk ugt8 st3gal6 st8sia1 osbp2 gne sptlc1 lpl hsd17b7 acsbg1 sec14l2 mcat hmgcs2 gal3st1 emas dgkd prkab2 stard4	28	768	3.78e-05
regulation of biological process	cull1 habp4 hlx rgs4 tulp3 tead4 cer1 phf10 mia3 clqc stk17a tsc22d3 tbc1d10a mta1 nr0b2 rgs17 znf367 foxb2 map1b ddr2 prex1 adnp2 gli3 sec14l2 ncoa3 slc9a3 gnaq arfgef2 rasa1 nf2 ccnh etf1 garnl3 hdac8 bnc2 foxj2 rgs1 apc kazald1 iqgap2 snapc3 cenpf zbtb43 dapk2 prdm10 plk2 smarca2 spry3 arntl2 nrg1 cda jmy fst psd3 ube2i aifm1 fgf10 iqgap1 ephb2 palm2 ttk alx1 rgs21 dll1 rabgap11 sirt1 inhba tp53bp1 tle1 rgs5 paip1 hus1 enox2 aldh5a1 syk irx2 ntf3 reck ptch1 rsf1 l3mbtl3 dbx1 stk381 zfhx4 psip1 gbx2 med21 tlx3 kras casp9 sncaip tle4 npm1 rgs13 tgfbr1 igfbp1 prune2 jak2 htatip2 foxm1 znf131 cript2 rgs18 med31 tgfb2 med18 ezh2 t wnt7a gpr98 nbl1 tbc1d2b mcc rgs2 isl2 gtf2i lif taf1a chrnb4 nbn tspo dapk1 znf366 prrx1 notch2 ush2a bcorl1 ascc2 ptger4 fbxo5 uhmk1 hnf4g	132	6140	5.11e-05
cellular development process	aicda cull1 jak2 mrps30 hlx htatip2 scube1 ntrk2 tgfb2 ror2 syk cep290 kif2a lrmp t wnt7a gpr98 kazald1 ntf3 thoc5 pacs2	51	1810	6.05e-05

	dapk2 slitrk1 stk17a pak1 tspo gbx2 nrg1 jmy grin3a efna5 tssk2 dapk1 tlx3 kras aifm1 casp9 notch2 fgf10 tll1 map1b ush2a dll1 gli3 sirt1 npml gnaq inhba nf2 rasa1 prune2			
cell differentiation	aicda cull1 jak2 mrps30 hlx htatip2 scube1 ntrk2 tgfb2 ror2 syk cep290 kif2a lrmp t wnt7a gpr98 kazald1 ntf3 thoc5 pacs2 dapk2 slitrk1 stk17a pak1 tspo gbx2 nrg1 jmy grin3a efna5 tssk2 dapk1 tlx3 kras aifm1 casp9 notch2 fgf10 tll1 map1b ush2a dll1 gli3 sirt1 npml gnaq inhba nf2 rasa1 prune2	51	1810	6.05e-05
regulation of cellular process	cull1 tle1 rgs5 paip1 habp4 hlx rgs4 tulp3 hus1 tead4 enox2 syk cer1 irx2 reck ntf3 ptch1 rsf1 l3mbtl3 mia3 phf10 dbx1 stk17a stk381 psip1 zfhx4 tbc1d10a tsc22d3 mta1 nr0b2 rgs17 gbx2 med21 znf367 tlx3 foxb2 kras casp9 ddr2 map1b prex1 adnp2 gli3 tle4 ncoa3 npml rgs13 sec14l2 tgfbr1 igfbp1 slc9a3 gnaq arfgef2 nf2 rasa1 ccnh prune2 jak2 etf1 foxm1 htatip2 znf131 cript2 garnl3 hdac8 rgs18 med31 bnc2 tgfb2 med18 ezh2 foxj2 t kazald1 gpr98 apc rgs1 iqgap2 nbl1 snapc3 tbc1d2b mcc rgs2 isl2 cenpf gtf2i dapk2 zbtb43 prdm10 lif taf1a plk2 nbn smarca2 spry3 arntl2 tspo nrg1 jmy cda dapk1 fst psd3 aifm1 prrx1 znf366 fgf10 notch2 iqgap1 ush2a ephb2 bcorl1 alx1 ttk rgs21 dll1 rabgap1 sirt1 ascc2 fbxo5 inhba hnf4g uhmk1 tp53bp1	124	5704	6.05e-05
protein transport	jak2 snx24 tnpol1 nup155 apba1 necap1 scamp1 sft2d1 snx2 tspo snx30 cep290 a2m rab3gap2 vps13a fgf10 srp19 rab33a pacsin2 ipo11 sec61g gli3 npml gnptg akap6 rasef uhmk1 clta fut10 ddx19b	30	866	6.05e-05
synaptic transmission	slc6a1 gabrg1 chrnb4 apba1 fxn galr1 tgfb2 kcnip1 aldh5a1 kras npy5r wnt7a chrna5 htr6 ntf3 camk4 sncaip	17	290	6.52e-05
biopolymer modificationn	cull1 hus1 gak herc4 syk ror2 dusp10 st3gal6 lox ptch1 pesk5 cdc14b fbxo22 fbxl22 epha7 ptpn20a pdpk1 stk381 stk17a tll1 rnf20 pigg fbwx11 herc1 tssk2 st8sia1 sf3a1 pak3 fer col4a3bp ddr2 camk4 hecw1 tll12 tgfbr1 gnaq csnk1g3 styk1 nf2 fnta jak2 hdac8 ntrk2 fbwx2 apobec1 prkx hace1 dapk2 gnptg ptpn14 fut10 pak1 ubqln1 plk2 ptpnd1 dapk1 mark1 pink1 ube2i fbxo39 ctdp1 ephb2 aga gent1 ttk sirt1 asb18 usp3 fbxo5 gal3st1 uhmk1	71	2815	6.56e-05
response to external stimulus	cklf klrg1 c3ar1 arntl2 f2r1l1 pde6b scube1 cmtm3 cd9 vwf tgfb2 aldob syk a2m f2r12 fgf10 fer xcl1 mia3 clqc gnaq inhba hmgcs2 fut10	24	633	7.8e-05
pattern specification process	ptch1 gbx2 cfc1 dll1 gli3 trim14 ror2 cer1 t fgf10 wnt7a	11	124	8.5e-05
regulation of developmental process	gpr98 ntf3 ush2a palm2 dll1 gli3 fst tgfb2 gnaq inhba tlx3 rasa1 notch2 fgf10 wnt7a	15	236	9.02e-05

enzyme linked protein receptor pathway	fnta jak2 ptprd ntrk2 syk cer1 erbb2ip lox fgf10 ddr2 ephb2 rgs2 epha7 tgfr1 pdpk1 inhba dgkd	17	300	9.2e-05
intracellular protein transport	jak2 tnpo1 nup155 apba1 snx2 tspo rab3gap2 a2m fgf10 srp19 pacsin2 ipo11 sec61g gli3 npm1 gnptg uhmk1 akap6 clta fut10 ddx19b	21	529	0.000117
protein complex assembly	tnpo1 apba1 fkbp4 scube1 cda vamp4 vwf cd9 aldh5a1 syk a2m apc ipo11 cenpf tgfr1 tubgcp4 clta dgkd	18	340	0.000117
negative regulation of cell differentiation	gpr98 ush2a gli3 dll1 tlx3 inhba notch2 fgf10	8	65	0.000163
regionalization	ptch1 dll1 gli3 trim14 ror2 cer1 t wnt7a fgf10	9	87	0.000177
intracellular transport	jak2 tnpo1 nup155 apba1 htatip2 scamp1 snx2 tspo slc25a14 a2m kif2a rab3gap2 vps13a fgf10 kif27 srp19 m6pr camk4 pacsin2 ipo11 sec61g gli3 npm1 gnptg myo7a akap6 uhmk1 clta fut10 ddx19b	30	910	0.000199
negative regulation of progression through cell cycle	apc cul1 reck ephb2 ptch1 nbn htatip2 nbl1 mcc jmy inhba uhmk1 nf2 notch2	14	225	0.000214
cell proliferation	cull1 jak2 cklf tspo cript2 tgfb2 kras syk pes1 cer1 fgf10 notch2 t apc ddr2 ptch1 ttk gli3 col8a1 cenpf npm1 tgfr1 tspan3 nf2 lif cript1	26	745	0.000215
organ morphogenesis	cull1 tle1 htatip2 gbx2 tgfb2 syk ror2 cep290 fgf10 notch2 t ptch1 gli3 col8a1 lif rasa1	16	362	0.000223
generation of a signal involved in cell-cell signaling	fst chrnb4 inhba gpr119 sncaip syk lif wnt7a	8	70	0.000254
establishment of protein localization	jak2 snx24 tnpo1 nup155 apba1 necap1 scamp1 sft2d1 snx2 tspo snx30 cep290 a2m rab3gap2 vps13a fgf10 srp19 rab33a pacsin2 ipo11 sec61g gli3 npm1 gnptg akap6 rasef uhmk1 clta fut10 ddx19b	30	922	0.000261
embryonic morphogenesis	ptch1 gbx2 gli3 gnaq ror2 cep290 t wnt7a fgf10	9	93	0.000269
regulation of cell differentiation	gpr98 ntf3 ush2a dll1 gli3 gnaq tgfb2 tlx3 inhba notch2 fgf10	11	144	0.000274
positive regulation of biological process	cull1 htatip2 cript2 tgfb2 syk wnt7a t ntf3 rsf1 mia3 c1qc dapk2 stk17a lif plk2 med21 jmy dapk1 fst aifm1 kras fgf10 notch2 ddr2 ttk ncoa3 sec14l2 tgfr1 inhba nf2 tp53bp1 ccnh prune2	33	1062	0.00031
skeletal development	kazald1 tll1 ghr alx1 tead4 ptger4 tgfb2 gnaq inhba cdh11 ror2 col12a1 col11a1	13	209	0.000395
post-translational protein modification	cull1 jak2 hus1 gak herc4 hdac8 ntrk2 fbw2 dusp10 ror2 syk prkx st3gal6 hace1 ptch1 pcsk5 cdc14b fbxo22 fbx122 epha7 dapk2 ptpn20a pdpk1 ptpn14 stk17a stk38l pak1 rnf20 plk2 fbw11 herc1 ptprd dapk1 tssk2 mark1 pink1 fbxo39 ctdp1 ube2i fer pak3 col4a3bp ddr2 camk4 ephb2 hecw1 ttk sirt1 tgfr1 asb18 usp3 gnaq fbxo5 csnk1g3 styk1 uhmk1 nf2	57	2235	0.000412
negative regulation of developmental process	gpr98 ush2a gli3 dll1 tlx3 inhba notch2 fgf10	8	77	0.00046

lipid metabolic process	pigg nr0b2 pip5k1b nans tspo vldlr elov14 pitpnm3 hmger apobec1 aldh5a1 syk ugt8 st3gal6 st8sia1 osbp2 gne sptlc1 lpl ocr1 hsd17b7 acsbg1 sec1412 mcat hmges2 gal3st1 cmas dgkd prkab2 stard4	30	946	0.000464
nucleocytoplasmic transport	jak2 tnp01 nup155 camk4 htatip2 ipo11 gli3 npm1 uhmk1 ddx19b fgf10	11	154	0.000469
nuclear transport	jak2 tnp01 nup155 camk4 htatip2 ipo11 gli3 npm1 uhmk1 ddx19b fgf10	11	156	0.00052
positive regulation of cellular process	cull1 plk2 htatip2 cript2 med21 jmy dapk1 tgfb2 aifm1 kras syk fgf10 notch2 t ntf3 ddr2 rsf1 ttk mia3 ncoa3 sec1412 tgfr1 dapk2 stk17a inhba nf2 lif ccnh prune2 tp53bp1	30	954	0.000553
protein homooligomerization	cda scube1 vwf aldh5a1 a2m dgkd	6	41	0.000681
protein metabolic process	cull1 paip1 fkbp4 hus1 mtrf11 prepl gak herc4 scube1 vwf aldh5a1 dusp10 ror2 syk st3gal6 lox psma4 ptch1 psck5 cdc14b fbxo22 ipo11 fbxl22 c1qc epha7 dnajc12 ptpn20a pdpk1 stk17a stk381 capn8 tll1 psmb1 rnf20 pigg apba1 mrpl32 fbwx11 herc1 tssk2 casp9 a2m st8sia1 sf3a1 dnajc16 fer pak3 col4a3bp iars2 tll1 ddr2 map1b camk4 hecw1 prex1 tll12 tgfr1 csnk1g3 gnaq styk1 nf2 rasa1 dgkd jak2 fnta etf1 mrps30 mmp27 hdac8 ntrk2 vamp4 fbwx2 pin4 apobec1 prkx mmp3 psma2 apc agtpbp1 hace1 ppic cenpf gnptg dapk2 ptpn14 tubgcp4 fut10 clta mars2 pak1 tnp01 capn5 ubqln1 plk2 nrg1 cda mmp1 ptpn14 dapk1 mark1 cd9 pink1 fbxo39 ctdp1 ube2i acr lnpep ephb2 aga gcnt1 ttk ctsc sirt1 asb18 usp3 fbxo5 xpnpep2 inhba gal3st1 uhmk1 dnaja4	121	5858	0.000839
lipid biosynthetic process	pigg nans elov14 hmger ugt8 syk st8sia1 gne hsd17b7 sec1412 mcat hmges2 gal3st1 cmas prkab2 stard4	16	333	0.000917
regulation of cell proliferation	cull1 jak2 cript2 tgfb2 syk kras cer1 fgf10 notch2 t apc ddr2 ttk gli3 npm1 tgfr1 nf2 lif	18	469	0.000918
glycolipid metabolic process	gal3st1 aldh5a1 ugt8 st3gal6 st8sia1	5	29	0.00135
cellular component assembly	tnp01 slu7 paip1 apba1 fkbp4 scube1 cda vamp4 cd9 vwf aldh5a1 syk a2m lox sf3a1 apc rsf1 ipo11 cenpf sirt1 npm1 gtf2i tgfr1 tubgcp4 clta dgkd	26	813	0.00136
vesicle-mediated transport	ghr necap1 scamp1 snx2 vldlr fxn golga4 vamp4 syk vps13a fgf10 lrmp acr m6pr clcn5 pacsin2 dnm3 slc9a3 sh3gl2 arfgef2 clta	21	606	0.00166
primary metabolic process	cull1 idua habp4 tyrp1 hlx tulp3 prepl tead4 vldlr herc4 dusp10 phka1 ipo11 phf10 acsbg1 epha7 c1qc pdpk1 stk17a tsc22d3 mta1 pigg nr0b2 apba1 nans herc1 nnt tssk2 znf367 phgdh foxb2 st8sia1 fer dnajc16 ddr2 map1b sptlc1 prex1 adnp2 hsd17b7 ocr1 tll12 gli3 tmlhe ncoa3 sec1412 csnk1g3 gnaq nf2 rasa1 ccnh aicda etf1 mrps30 hdac8	230	12764	0.00171

	vamp4 fbxw2 bnc2 hmgcr aldob polk apobec1 foxj2 apc agtpbp1 hace1 gne snapc3 wdr36 cenpf dapk2 gnptg zbtb43 mars2 prdm10 pak1 tnpo1 dcp2 ubqln1 plk2 smarca2 arntl2 nrg1 cda jmy mmp1 trip13 fst cd9 mark1 ctdp1 aifm1 ube2i fgf10 ephb2 alx1 gent1 nme7 ttk ctsc lpl sirt1 asb18 ldhb gal3st1 inhba slc3a1 tp53bp1 uap1 tle1 slu7 paip1 fkbp4 hus1 mtrf11 gak scube1 idh3a vwf pitpnm3 syk ror2 aldh5a1 st3gal6 lox psma4 osbp2 rnaset2 irx2 ptch1 pcsk5 rsf1 l3mbtl3 fbxo22 cdc14b fbxl22 dbx1 dnajc12 ptpn20a stk381 mcat hmgs2 capn8 psip1 ttl1 zfhx4 prkab2 mgat4c psmb1 rnf20 mrpl32 neil3 gbx2 fbxw11 zmat5 med21 tlx3 a2m casp9 nsmce1 sf3a1 pak3 iars2 col4a3bp tll1 camk4 agmat hecw1 sncaip tle4 npml tgfbr1 styk1 dgkd jak2 fnta slc2a3 mmp27 htatip2 gys1 foxm1 pip5k1b znf131 utp14a ntrk2 elovl4 pin4 med31 tgfb2 med18 ezh2 prkx mmp3 psma2 t bpnt1 ppic isl2 gtf2i ptpn14 tubgcp4 fut10 clta cmas stard4 taf1a capn5 nbn tspo ptpnd dapk1 pink1 fbxo39 prrx1 ugt8 znf366 itpa notch2 acr lnpep tk2 bcor1l1 aga ascc2 usp3 fbxo5 xpnpep2 hnf4g uhmk1 dnaja4			
locomotory behavior	fer cklf c3ar1 xcl1 chrb4 sepp1 cmtm3 tgfb2 syk calb1 fgf10	11	181	0.00176
protein targeting	jak2 tnpo1 srp19 ipo11 tspo sec61g gli3 gnptg uhmk1 akap6 fut10 fgf10	12	218	0.00215
biopolymer metabolic process	cull1 habp4 hlx tulp3 tead4 herc4 dusp10 phka1 phf10 epha7 stk17a pdpk1 tsc22d3 mta1 pigg nr0b2 nans herc1 tssk2 znf367 foxb2 st8sia1 fer ddr2 adnp2 ttl12 gli3 sec14l2 ncoa3 gnaq csnk1g3 nf2 rasal ccnh aicda hdac8 fbxw2 bnc2 polk apobec1 foxj2 hace1 gne snapc3 wdr36 zbtb43 dapk2 gnptg prdm10 mars2 pak1 dcp2 ubqln1 plk2 smarca2 arntl2 trip13 mmp1 jmy fst mark1 ube2i ctdp1 aifm1 ephb2 gent1 alx1 ttk sirt1 asb18 inhba gal3st1 tp53bp1 tle1 slu7 paip1 hus1 gak ror2 syk st3gal6 lox psma4 irx2 rnaset2 ptch1 pesk5 rsf1 cdc14b fbxo22 fbxl22 dbx1 ptpn20a stk381 zfhx4 ttl1 psip1 psmb1 rnf20 zmat5 fbxw11 gbx2 neil3 med21 tlx3 nsmce1 sf3a1 pak3 col4a3bp iars2 camk4 hecw1 tle4 tgfbr1 styk1 fnta jak2 htatip2 gys1 foxm1 mmp27 znf131 utp14a ntrk2 med31 ezh2 med18 prkx t psma2 mmp3 isl2 gtf2i ptpn14 fut10 cmas taf1a nbn ptpnd dapk1 pink1 prrx1 fbxo39 znf366 notch2 tk2 aga bcor1l1 ascc2 usp3 fbxo5 hnf4g uhmk1	153	7940	0.00248
cellular macromolecule metabolic process	cull1 paip1 fkbp4 hus1 mtrf11 prepl gak herc4 dusp10 ror2 syk st3gal6 lox psma4 ptch1 pesk5 phka1 cdc14b fbxo22 ipo11 fbxl22 c1qc epha7 dnajc12 ptpn20a	115	5656	0.0027

	pdpk1 stk17a stk38l capn8 tll1 rnf20 psmb1 pigg mrpl32 fbxw11 nans herc1 tssk2 casp9 st8sia1 sf3a1 dnajc16 fer pak3 col4a3bp iars2 tll1 ddr2 map1b camk4 hecw1 prex1 tll12 tgfbr1 csnk1g3 gnaq styk1 nf2 rasa1 fnta jak2 etf1 mrps30 mmp27 gys1 hdac8 ntrk2 fbxw2 pin4 apobec1 prkx mmp3 psma2 apc agtpbp1 hace1 gne ppic cenpf gnptg dapk2 ptpn14 mars2 fut10 pak1 cmas tnp01 capn5 ubqln1 plk2 nrg1 mmp1 ptrd dapk1 mark1 pink1 ctdp1 fbxo39 ube2i acr lnpep ephb2 aga gcnt1 ttk ctsc sirt1 asb18 usp3 fbxo5 xpnpep2 inhba gal3st1 uhmk1 dnaja4			
hemopoiesis	aicda jak2 cript2 dll1 tgfb2 inhba syk fut10 notch2 lrmp	10	161	0.00289
wound healing	f2r1l mia3 scube1 vwf cd9 gnaq tgfb2 fut10 f2r12	9	131	0.00289
macromolecular complex assembly	tnp01 slu7 paip1 apba1 fkbp4 scube1 cda vamp4 cd9 vwf aldh5a1 syk a2m sf3a1 apc rsf1 ipo11 cenpf npm1 gtf2i tgfbr1 tubgcp4 clta dgkd	24	756	0.00291
secretion	acr cklf srp19 chrnb4 clen5 scamp1 sncaip fst inhba gpr119 arfgef2 syk lif vps13a wnt7a	15	384	0.00298
anterior/posterior pattern formation	dll1 gli3 trim14 ror2 cer1 t	6	55	0.00298
cell-cell adhesion	gpr98 cdh5 alx1 pcdh7 pcdh17 cdh6 pcdh9 cdh11 ror2 syk nf2 rasa1 coll1a1 t	14	347	0.00307
membrane invagination	ghr m6pr clen5 pacsin2 dnm3 necap1 snx2 vldlr slc9a3 sh3gl2 fgf10	11	197	0.00318
endocytosis	ghr m6pr clen5 pacsin2 dnm3 necap1 snx2 vldlr slc9a3 sh3gl2 fgf10	11	197	0.00318
response to chemical stimulus	cklf c3ar1 chrnb4 sepp1 cpox tgfb2 cmtm3 aldob kenip1 syk a2m fgf10 fer xcl1 hiat1 hspb3 cenpf hmgs2 slc46a2 dgkd	20	589	0.00318
Regulation of G-protein coupled receptor protein signaling pathway	rgs13 rgs18 rgs5 rgs4 rgs2	5	36	0.00318
embryonic organ development	gli3 ror2 fgf10 t	4	20	0.00336
central nervous system development	sepp1 alx1 gbx2 gli3 tlx3 shroom4 sh3gl2 phgdh ugt8 aldh5a1 cep290 wnt7a	12	235	0.00363
cellular metabolic process	cull1 idua habp4 tyrp1 hlx tulp3 prepl tead4 vldlr herc4 dusp10 phka1 ipo11 phf10 acsbg1 epha7 c1qc pdpk1 stk17a tsc22d3 mta1 pigg nr0b2 nans herc1 nnt tssk2 znf367 phgdh foxb2 st8sia1 fer dnajc16 ddr2 map1b sptlc1 prex1 adnp2 hsd17b7 tll12 gli3 tmlhe ncoa3 sec1412 csnk1g3 gnaq nf2 rasa1 ccnh aicda etf1 mrps30 cpox hdac8 fbxw2 bnc2 hmger aldob polk apobec1 rfk foxj2 apc agtpbp1 hace1 ca12 gne snapc3 wdr36 cenpf dapk2 gnptg zbtb43 mars2 prdm10 pak1 tnp01 dcp2 ubqln1 plk2 smarca2 arntl2 nrg1 cda jmy mmp1 trip13 fst mark1 aifm1 ctdp1 ube2i fgf10 ephb2 alx1 gcnt1	226	12668	0.00363

	nme7 ttk ctsc lpl sirt1 asb18 ldhb gal3st1 inhba slc3a1 tp53bp1 uap1 tle1 slu7 paip1 fkbp4 hus1 mtrf11 gak idh3a lysmd3 pitpnm3 syk ror2 aldh5a1 st3gal6 lox psma4 osbp2 maset2 irx2 ptch1 rsf1 pcsk5 l3mbtl3 fbxo22 cdc14b fbxl22 dbx1 dnajc12 ptpn20a stk381 mcat hmgcs2 capn8 psip1 tll1 zfhx4 prkab2 psmb1 rnf20 mrpl32 neil3 gbx2 fbwx11 zmat5 med21 tlx3 casp9 nsmce1 sf3a1 pak3 iars2 col4a3bp tll1 camk4 agmat hecw1 sncaip tle4 npm1 tgfbr1 styk1 dgkd jak2 fnta nef1 gdpd4 mmp27 htatip2 gys1 foxm1 pip5k1b znf131 utp14a ntrk2 elov14 pin4 med31 tgfb2 med18 ezh2 prkx mmp3 psma2 t bpnt1 ppic isl2 gtf2i ptpn14 fut10 cmas stard4 taf1a capn5 nbn sepp1 tspo ptpnd dapk1 pink1 fbxo39 prrx1 ugt8 znf366 itpa notch2 acr lnpep tk2 aga bcorl1 ascc2 usp3 fbxo5 xpnpep2 hnf4g uhmk1 dnaja4			
regulation of hair follicle development	fst tgfb2	2	2	0.00376
positive regulation of hair follicle development	fst tgfb2	2	2	0.00376
transcription from RNA polymerase II promoter	taf1a hlx nr0b2 smarca2 htatip2 tead4 med21 hdac8 jmy trip13 fst znf367 ctdp1 t alx1 snapc3 gli3 gtf2i inhba hnf4g ccnh	21	640	0.00386
cytoskeleton organization and biogenesis	apba1 mark1 epb41 kras erbb2ip kif2a kif27 lrmp hook3 apc map1b pacsin2 ttk prex1 tekt1 pdpk1 myo7a tubgcp4 shroom4 pak1 nf2 rasal	22	686	0.00411
macromolecule metabolic process	cull1 idua habp4 hlx tulp3 prepl tead4 herc4 dusp10 phka1 ipo11 phf10 epha7 c1qc stk17a pdpk1 tsc22d3 mta1 pigg nr0b2 apba1 nans herc1 nnt tssk2 znf367 foxb2 st8sia1 fer dnajc16 map1b ddr2 prex1 adnp2 tll12 gli3 ncoa3 sec14l2 csnk1g3 gnaq nf2 rasal ccnh aicda etf1 mrps30 hdac8 vamp4 fbwx2 bnc2 aldob polk apobec1 foxj2 apc agtpbp1 hace1 gne snapc3 wdr36 cenpf zbtb43 gnptg dapk2 mars2 prdm10 pak1 tnpo1 dcp2 ubqln1 plk2 smarca2 arntl2 nrg1 cda jmy mmp1 trip13 fst cd9 mark1 aifm1 ctdp1 ube2i ephb2 alx1 gent1 ttk ctsc sirt1 asb18 ldhb gal3st1 inhba slc3a1 tp53bp1 uap1 tle1 slu7 paip1 fkbp4 hus1 mtrf11 gak scube1 idh3a vwf syk ror2 aldh5a1 st3gal6 lox psma4 maset2 irx2 ptch1 rsf1 pcsk5 cdc14b fbxo22 fbxl22 dbx1 ptpn20a dnajc12 stk381 capn8 zfhx4 tll1 psip1 mgat4c psmb1 rnf20 mrpl32 neil3 gbx2 fbwx11 zmat5 med21 tlx3 nsmce1 a2m casp9 sf3a1 pak3 iars2 col4a3bp tll1 camk4 hecw1 tle4 npm1 tgfbr1 styk1 dgkd jak2 fnta slc2a3 mmp27 htatip2 gys1 foxm1 znf131 utp14a ntrk2 pin4 med31 med18 ezh2 prkx mmp3 psma2 t ppic isl2 gtf2i ptpn14 tubgcp4 clta fut10	202	11144	0.00416

	emas taf1a capn5 nbn ptpd dapk1 pink1 fbxo39 prrx1 znf366 notch2 acr lnpep tk2 aga bcor1l ascc2 usp3 fbxo5 xpnpep2 hnf4g uhmk1 dnaja4			
hemopoietic or lymphoid organ development	aicda jak2 cript2 dll1 tgfb2 inhba syk fut10 notch2 lrmp	10	173	0.00426
protein import into nucleus, translocation	gli3 jak2 tnpo1 fgf10	4	22	0.00446
cell morphogenesis	gbx2 cda enox2 grin3a tgfb2 cep290 erbb2ip wnt7a notch2 kazald1 map1b palm2 igfbp1 slitrk1 inhba rasa1 dgkd	17	478	0.00446
cellular structure morphogenesis	gbx2 cda enox2 grin3a tgfb2 cep290 erbb2ip wnt7a notch2 kazald1 map1b palm2 igfbp1 slitrk1 inhba rasa1 dgkd	17	478	0.00446
sensory organ development	col8a1 dll1 gli3 tgfb2 cep290 gbx2 fgf10	7	86	0.00446
regulation of action potential	acsbgl1 ntf3 cd9 gnaq gal3st1	5	40	0.00457
protein oligomerization	cda scube1 vwf aldh5a1 a2m dgkd	6	62	0.00467
wnt receptor signaling pathway	apc tle1 lrrfip2 fbxw11 tle4 csnk1g3 ror2 wnt7a fgf10	9	145	0.00476
membrane organization and biogenesis	ghr m6pr clcn5 pacsin2 dnm3 necap1 snx2 vldlr slc9a3 cd9 sh3g12 lrmp fgf10	13	284	0.00502
immune system development	aicda jak2 cript2 dll1 tgfb2 inhba syk fut10 notch2 lrmp	10	182	0.00584
behavior	fer cklf c3ar1 xcl1 chrnb4 sepp1 vldlr cmtm3 tgfb2 syk kras calb1 fgf10	13	294	0.00684
negative regulation of hormone secretion	fst inhba lif	3	11	0.00707
cartilage condensation	alx1 ror2 coll1a1	3	11	0.00707
inorganic anion transport	col4a6 gabrg1 clcn5 slc13a4 col6a3 clns1a col8a1 clic2 clqc slc26a1 coll2a1 coll1a1	12	260	0.00747
myelination	acsbgl1 ntf3 cd9 gal3st1	4	26	0.00775
system process	myoc kenj8 pde6b galr1 elov14 tgfb2 aldh5a1 coll1a1 npy5r wnt7a gpr98 ntf3 clcn5 kcnv2 sspn wdr36 acsbgl1 myo7a shroom4 slc6a1 gabrg1 c3ar1 chrnb4 apba1 fxn cd9 kcnip1 epb41 kras chrna5 htr6 ush2a camk4 sncaip lpl clns1a gnaq gal3st1 nf2	39	1539	0.00786
Extracellular matrix organization and biogenesis	col4a6 tgfb2 coll2a1 coll1a1 lox	5	46	0.00799
cell development	cull1 jak2 mrps30 htatip2 tgfb2 cep290 wnt7a lrmp ntf3 pacs2 dapk2 stk17a slitrk1 pak1 gbx2 tspo jmy grin3a dapk1 tlx3 aifm1 kras casp9 notch2 map1b gli3 sirt1 npm1 gnaq inhba nf2 rasa1 prune2	33	1242	0.00837
mitotic cell cycle checkpoint	cenpf nbn hus1 ttk	4	27	0.00866
cell fate commitment	dll1 gli3 tgfb2 tlx3 fgf10 notch2	6	71	0.00866
neutrophil chemotaxis	cklf tgfb2 syk	3	12	0.00869

Supplementary Table 13. Gene ontology results for private Italian outliers based on a GOSTAT analysis. Correction for Multiple testing was performed using false discovery rate (Benjamini method).

GO (Biological process)	Genes	Count 148	Total 33972	P- Value
cellular component and biogenesis	fkbp4 utp14a enox2 aldh5a1 prmt8 rab3gap2 apc srp19 rbl1 m6pr clcn5 txnl4a wdr36 tekt1 stk38l sema4d myo7a clta apba1 necap1 chd6 kras epb41 aifm1 slc25a14 a2m acr camk4 bcor1l sirt1 slc9a3 igfbp1 rasal	33	3277	0.000 247
transport	slc2a3 fkbp4 golga4 enox2 pitpnm3 gpr119 rab3gap2 srp19 m6pr clcn5 rbp3 myo7a clta clcn1 slc25a46 stard4 abcg2 apba1 kcnn2 necap1 sft2d1 fmo1 slc30a10 keng2 slc25a14 a2m slc13a5 acr col4a3bp pkd21l rab33a camk4 hiatl1 slc9a3 itpr2	35	4035	0.005 52
establishment of localization	slc2a3 fkbp4 golga4 enox2 pitpnm3 gpr119 rab3gap2 srp19 m6pr clcn5 rbp3 myo7a clta clcn1 slc25a46 stard4 abcg2 apba1 kcnn2 necap1 sft2d1 fmo1 slc30a10 keng2 slc25a14 a2m slc13a5 acr col4a3bp pkd21l rab33a camk4 hiatl1 slc9a3 itpr2	35	4135	0.006 01
localization	slc2a3 fkbp4 golga4 enox2 pitpnm3 gpr119 rab3gap2 srp19 m6pr clcn5 mia3 rbp3 myo7a clta clcn1 slc25a46 stard4 c3ar1 abcg2 apba1 kcnn2 necap1 sft2d1 fmo1 slc30a10 keng2 slc25a14 a2m slc13a5 acr col4a3bp camk4 rab33a pkd21l hiatl1 slc9a3 itpr2	37	4481	0.006 01
biological adhesion	apc fer zyx gne apba1 alx1 sspn mia3 sema4d cntnap4 ppfibp1 rasal t clec4a	14	960	0.009 35
cell adhesion	apc fer zyx gne apba1 alx1 sspn mia3 sema4d cntnap4 ppfibp1 rasal t clec4a	14	960	0.009 35
multicellular organismal process	c3ar1 apba1 fkbp4 spry3 tead4 chd6 phc1 efna5 keng2 shc3 prrx1 ugt8 epb41 kras aldh5a1 atoh7 t camk4 clcn5 alx1 sspn bpnt1 wdr36 mia3 sirt1 disp1 trim14 sema4d rbp3 myo7a clcn1 rasal	32	3822	0.010 4
entrainment of circadian clock	arntl2 atoh7	2	5	0.015 7
Circadian rythm	slc9a3 arntl2 atoh7	3	29	0.020 3
nervous system development	apba1 alx1 bpnt1 chd6 efna5 sema4d shc3 aldh5a1 ugt8 atoh7 t	11	716	0.021 4
organelle organization and biogenesis	apc rbl1 bcor1l apba1 wdr36 utp14a sirt1 chd6 tekt1 myo7a slc25a14 prmt8 kras epb41 aifm1 rasal	16	1526	0.026 3
multicellular organismal development	fkbp4 apba1 spry3 tead4 phc1 chd6 efna5 aldh5a1 kras ugt8 prrx1 shc3 atoh7 t alx1 bpnt1 sirt1 disp1 sema4d trim14 rasal	21	2299	0.032 8

Supplementary Table 14. Linkage Disequilibrium (LD) decay in outlier windows and randomly chosen windows based on a plink LD analysis. LD was higher in outlier windows than in windows randomly chosen throughout the genome, but decayed faster in outlier windows. Degrees of freedom are denoted DF.

Model	DF	Error DF	F	P
Outliers vs. Random loci	1	12434	2091.4	< 2.2e-16

Category	Type	Mean intercept	Mean slope
Between	Outlier	0.51	-1.13 e-06
Private	Outlier	0.56	-7.90e-07
House	Outlier	0.41	-1.01e-06
Spanish	Outlier	0.58	-2.07e-06
Random	Random	0.36	-8.10e-07

Supplementary table 15. Overrepresentation of the Z-chromosome in outlier categories. There is a significant overrepresentation of the Z-chromosome compared to the expectation based on the number of genes located on this chromosome in comparison to the rest of the genome for private outliers, house-like outliers and outliers that are divergent between islands as shown by chi-squared tests. For Spanish sparrow-like outliers, none are found on the Z-chromosome, however. Due to the low total number of outliers this is not a significant underrepresentation either, though.

	Between islands	Private	Spanishlike	Houselike	Total
Number on Z	1349	314	0	332	712
Number on autosomes	3364	883	28	372	13066
Percent on Z	0.286	0.262	0	0.472	0.052
Chi-Square value	2084.27	821.11	1.44	1870.66	NA
<i>P</i>	< 0.001	< 0.001	0.22	< 0.001	NA

Supplementary table 16. DN/DS for fixed differences for autosomes and the Z-chromosome. There is a significantly higher proportion non-synonymous substitutions on the Z-chromosome than expected based on the genome wide level for fixed differences against both house sparrow and Spanish sparrow. A goodness of fit test was used to test this, and the test statistics is reported in the final lines of the table.

Parent	Population	ChromosomeType	ObsSynonymous	ObsNonsynonymous
House	Corsica	Autosome	47	29
House	Crete	Autosome	100	60
House	Malta	Autosome	108	72
House	Sicily	Autosome	86	49
House	Corsica	chrZ	1	0
House	Crete	chrZ	4	3
House	Malta	chrZ	38	33
House	Sicily	chrZ	37	28
Spanish	Corsica	Autosome	32	16
Spanish	Crete	Autosome	194	119
Spanish	Malta	Autosome	24	22
Spanish	Sicily	Autosome	33	29
Spanish	Corsica	chrZ	26	10
Spanish	Crete	chrZ	236	128
Spanish	Malta	chrZ	64	37
Spanish	Sicily	chrZ	63	32
Test	Goodness of fit Z		X2=299.6	P<0.001
Test	Goodness of fit Z Spanish		X2=1809.0	P<0.001

Supplementary Table 17. Gene ontology results for outliers against Spanish sparrow based on a GOSTAT analysis. Correction for multiple testing was performed using false discovery rate (Benjamini method).

GO (Biological process)	Genes	Count	Total	P-Value
Protein-N terminus binding	<u>ercc5 gtf2h2 aptx tdrd7</u>	4	39	0.00354
anatomical structure development multicellular organismal process	<u>myt11 foxg1 cdh6 grin3a klf4 dcbl2 barx2 nrsn1 lrmp prl slitrk4 ugcg fbn2 dc2c2 msh3 fktn phf3 cntnap2 myt11 foxg1 grin3a cdh6 klf4 marveld2 barx2 or10k2 nrsn1 cyb5r3 kcna1 lrmp prl ptp4a1 slitrk4 ugcg fbn2 dc2c2 ercc5 ckmt2 msh3 fktn</u>	16	2005	0.00359
plasma membrane part	<u>rgs7 faslg slc10a2 gng10 ptp4a1 ptp4a1 lrmp megf10 grin3a marveld2 dcbl2 slc12a2 kcna1 lrmp parvb zyx kcna6 epha1</u>	17	2285	0.00359
multicellular organismal development developmental process	<u>phf3 myt11 foxg1 grin3a cdh6 klf4 barx2 nrsn1 lrmp prl ptp4a1 slitrk4 ugcg fbn2 dc2c2 msh3 fktn faslg phf3 myt11 foxg1 grin3a cdh6 klf4 aptx dcbl2 nrsn1 barx2 lrmp prl ptp4a1 slitrk4 ugcg fbn2 dc2c2 ercc5 msh3 fktn</u>	17	2299	0.00359
response to endogenous stimulus DNA repair system development	<u>rad17 ercc5 xrcc4 gtf2h2 msh3 aptx aldob rad23b rad17 ercc5 xrcc4 gtf2h2 aptx msh3 rad23b slitrk4 ugcg myt11 foxg1 cdh6 dc2c2 grin3a klf4 fktn msh3 barx2 nrsn1 lrmp prl</u>	8	529	0.0105
response to stress	<u>rad17 xrcc4 gtf2h2 dnaja1 rad23b ercc5 aptx msh3 aldob prdx6 dcbl2 tmod1 lrmp prl</u>	7	392	0.0105
hemocyte development holo TFIIH complex hemocyte differentiation response to DNA damage stimulus plasma membrane	<u>rad17 xrcc4 gtf2h2 dnaja1 rad23b ercc5 aptx msh3 aldob prdx6 dcbl2 tmod1 lrmp prl</u>	14	1605	0.0105
hemocyte development holo TFIIH complex hemocyte differentiation response to DNA damage stimulus plasma membrane	<u>rad17 xrcc4 gtf2h2 dnaja1 rad23b ercc5 aptx msh3 aldob prdx6 dcbl2 tmod1 lrmp prl</u>	12	1222	0.0105
hemocyte development holo TFIIH complex hemocyte differentiation response to DNA damage stimulus plasma membrane	<u>rad17 xrcc4 gtf2h2 dnaja1 rad23b ercc5 aptx msh3 aldob prdx6 dcbl2 tmod1 lrmp prl</u>	2	7	0.0126
hemocyte development holo TFIIH complex hemocyte differentiation response to DNA damage stimulus plasma membrane	<u>ercc5 gtf2h2 lrmp prl</u>	2	8	0.0137
hemocyte development holo TFIIH complex hemocyte differentiation response to DNA damage stimulus plasma membrane	<u>ercc5 gtf2h2 lrmp prl</u>	2	8	0.0137
hemocyte development holo TFIIH complex hemocyte differentiation response to DNA damage stimulus plasma membrane	<u>rad17 ercc5 xrcc4 gtf2h2 aptx msh3 rad23b</u>	7	448	0.0137
hemocyte development holo TFIIH complex hemocyte differentiation response to DNA damage stimulus plasma membrane	<u>rgs7 faslg slc10a2 gng10 ptp4a1 ptp4a1 lrmp megf10 rasgrf2 grin3a cdh6 marveld2 dcbl2 or10k2 slc12a2 kcna1 lrmp parvb ptp4a1 zyx kcna6 epha1 pnpla2</u>	22	3816	0.0137
protein complex	<u>rgs7 xrcc4 rps23 fbxo4 smc2 gtf2h2 slc10a2 gng10 kcna6 ikkbp rad23b ndufa9 ercc5 msh3 gemin8 barx2 kcna1 cyb5r3</u>	18	2883	0.0162
glycosphingolipid biosynthetic complex intracellular membrane-bound organelle	<u>a4galt ugcg</u>	2	10	0.0174
glycosphingolipid biosynthetic complex intracellular membrane-bound organelle	<u>a4galt rad17 xrcc4 gtf2h2 foxg1 ndufa9 rasgrf2 klf4 aptx aldob nrsn1 cyb5r3 zfyve16 lrmp ptp4a1 smc2 l3mbtl3 ugcg rad23b ercc5 smu1 msh3 gemin8 fmo5 cmas samm50 mecr rnf20 slc10a2 myt11 bdp1 tdrd7 prdx6 barx2 znf462 ikkbp ckmt2 fktn fut9</u>	39	8824	0.0247
membrane-bound organelle	<u>a4galt rad17 xrcc4 gtf2h2 foxg1 ndufa9 rasgrf2 klf4 aptx aldob nrsn1 cyb5r3 zfyve16 lrmp ptp4a1 smc2 l3mbtl3 ugcg rad23b ercc5 smu1 msh3 gemin8 fmo5 cmas samm50 mecr rnf20 slc10a2 myt11 bdp1 tdrd7 prdx6 barx2 znf462 ikkbp ckmt2 fktn fut9</u>	39	8827	0.0247
single stranded DNA	<u>ercc5 msh3 rad23b</u>	3	61	0.0284

binding				
cytoplasmic part	<u>a4galt samm50 xrcc4 mecr ndufa9 rasgrf2 tdrd7</u> <u>aldob prdx6 nrsn1 cyb5r3 zfyve16 lrmp ptp4a1</u> <u>rps23 ugcg rad23b pnpla2 ckmt2 fktm fmo5</u> <u>pcsk1 fut9 sult4a1</u>	24	4592	0.0307
glycolipid	<u>a4galt ugcg</u>	2	15	0.0307
biosynthetic process				
cytoplasm	<u>a4galt xrcc4 ndufa9 rasgrf2 aldob nrsn1 zfyve16</u> <u>cyb5r3 lrmp parvb ptp4a1 tmod1 mtap smc2 zyx</u> <u>ugcg rad23b smu1 pnpla2 fmo5 gemin8 txn</u> <u>sult4a1 samm50 mecr tdrd7 prdx6 rps23 ikbkap</u> <u>ckmt2 ldhb fktm pcsk1 fut9</u>	34	7482	0.0307
cytosol	<u>xrcc4 rps23 aldob prdx6 cyb5r3 rad23b sult4a1</u>	7	568	0.0307
integral to plasma membrane	<u>faslg slc10a2 ptpru zyx kcna6 ptprm epha1</u> <u>dcbl2 slc12a2 kcna1 lrmp</u>	11	1330	0.0307
structure-specific	<u>ercc5 aptx msh3 rad23b</u>	4	159	0.0307
DNA binding				
intracellular organelle part	<u>a4galt samm50 xrcc4 gtf2h2 ndufa9 tdrd7 aptx</u> <u>barx2 zfyve16 cyb5r3 lrmp ptp4a1 smc2 rps23</u> <u>ugcg ikbkap ercc5 ckmt2 msh3 fktm fmo5</u> <u>gemin8</u>	22	4120	0.0307
organelle part	<u>a4galt samm50 xrcc4 gtf2h2 ndufa9 tdrd7 aptx</u> <u>barx2 zfyve16 cyb5r3 lrmp ptp4a1 smc2 rps23</u> <u>ugcg ikbkap ercc5 ckmt2 msh3 fktm fmo5</u> <u>gemin8</u>	22	4130	0.0307
transferase activity	<u>a4galt mtap gys1 ugcg fut9</u>	5	281	0.0307
intrinsic to plasma membrane	<u>faslg slc10a2 ptpru zyx kcna6 ptprm epha1</u> <u>dcbl2 slc12a2 kcna1 lrmp</u>	11	1346	0.0307

Supplementary Table 18. Mito-nuclear genes identified among outliers against Spanish sparrow (e.g. outliers for which all Italian populations are similar to house sparrow) and their chromosomal locations.

Chr	Start	End	Gene ID
chrZ	29260942	29262308	TDRD7: Tudor domain-containing protein 7 (Gallus gallus)
chr1A	54111423	54129191	CYB5R3: NADH-cytochrome b5 reductase 3 (Bos taurus)
chrZ	67893905	67913372	CKMT2: Creatine kinase S-type%2C mitochondrial (Gallus gallus)
chrZ	68178097	68183584	DHFR: Dihydrofolate reductase (Gallus gallus)
chrZ	24614001	24634099	HSDL2: Hydroxysteroid dehydrogenase-like protein 2 (Bos taurus)
chr1A	53940119	53949127	LDHB: L-lactate dehydrogenase B chain (Gallus gallus)
chrZ	28978063	28985567	DNAJA1: DnaJ homolog subfamily A member 1 (Pongo abelii)
chrZ	25102516	25104160	TXN: Thioredoxin (Gallus gallus)
chrZ	67893905	67913372	CKMT2: Creatine kinase S-type%2C mitochondrial (Gallus gallus)
chr1A	52489767	52501934	NDUFA9: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9%2C mitochondrial (Bos taurus)
chr23	333846	338663	MECR: Trans-2-enoyl-CoA reductase%2C mitochondrial (Homo sapiens)