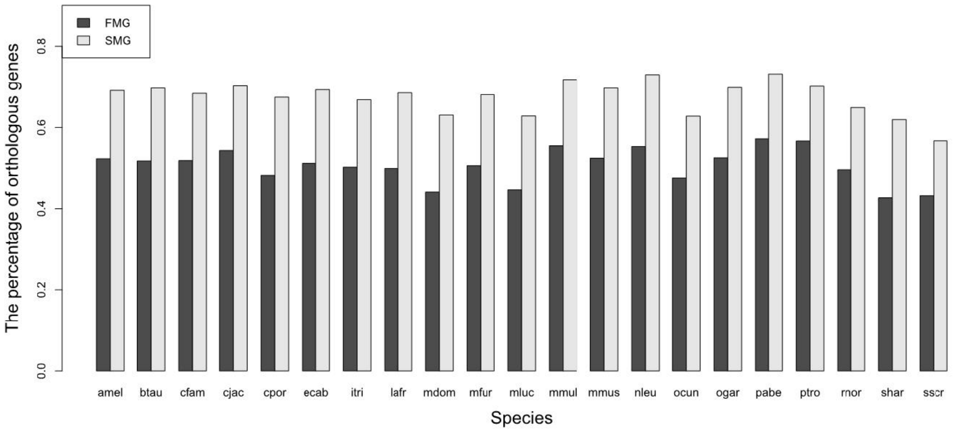
Comparison of evolutionary conservation between SM (top 50%) and FM genes (bottom 50%)

Supplementary File

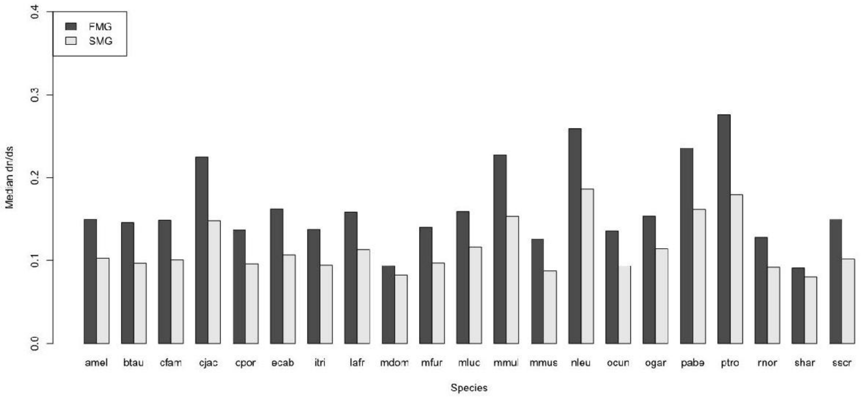
Contents

Supplementary Figure 1. The bar plots of the SM genes against the FM genes in the percentage of orthologous genes for each of the 21 species.



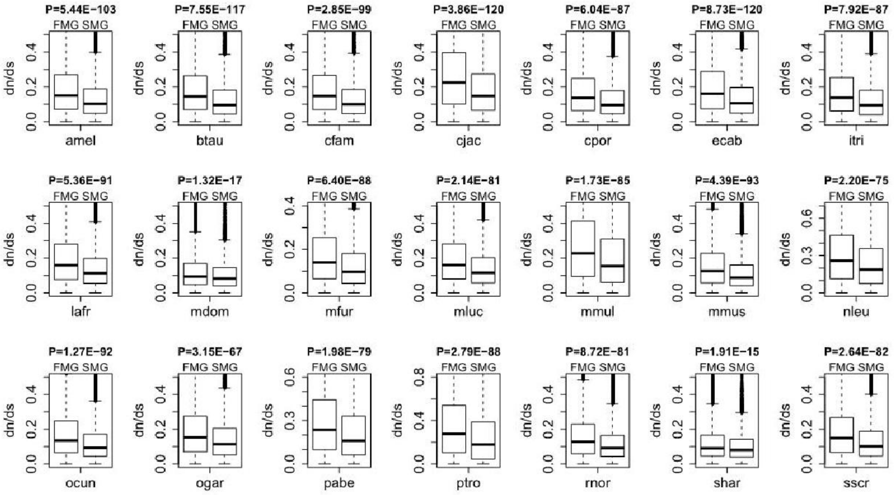
Supplementary Figure 1. The bar plots of the SM genes against the FM genes in the percentage of orthologous genes for each of the 21 species.

Supplementary Figure 2. The bar plots of the SM genes against the FM genes in the evolutionary rate for each of the 21 species.



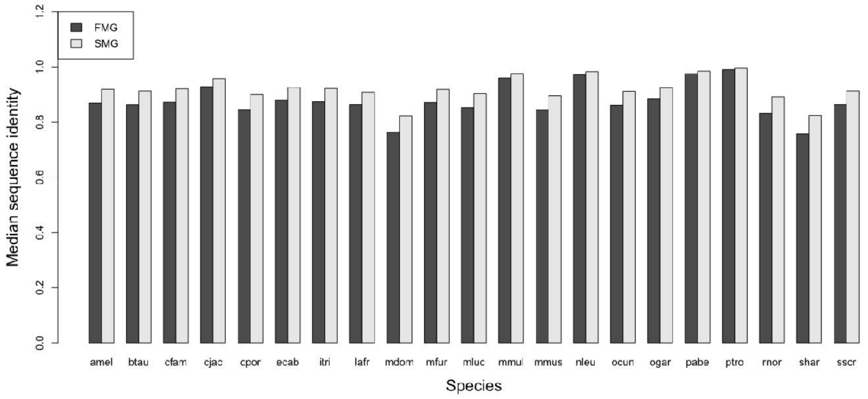
Supplementary Figure 2. The bar plots of the SM genes against the FM genes in the evolutionary rate for each of the 21 species.

Supplementary Figure 3. The box plots of the SM genes against the FM genes in the evolutionary rate for each of the 21 species.



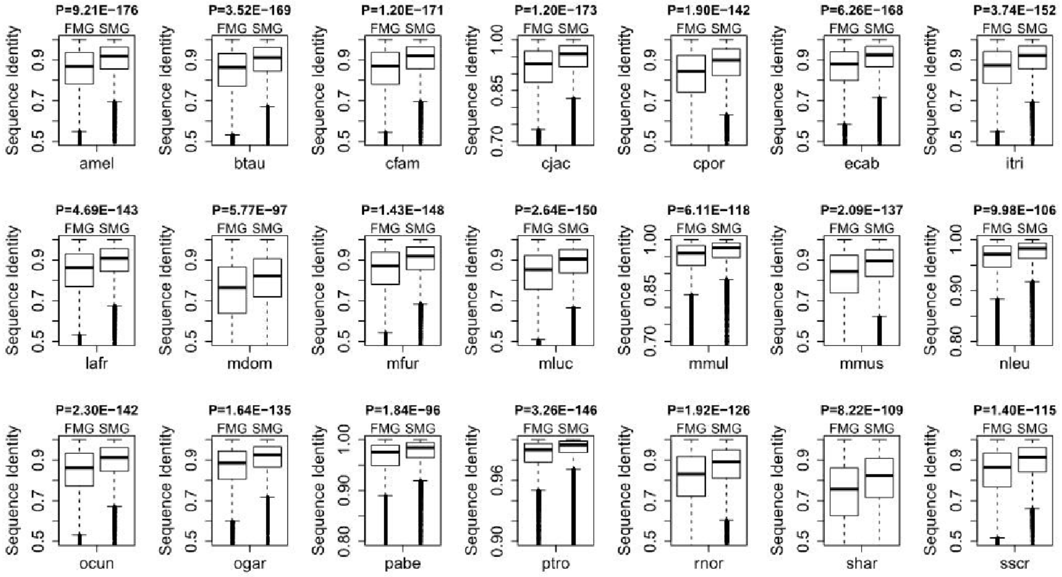
Supplementary Figure 3. The box plots of the SM genes against the FM genes in the evolutionary rate for each of the 21 species.

Supplementary Figure 4. The bar plots of the SM genes against the FM genes in the sequence identity for each of the 21 species.



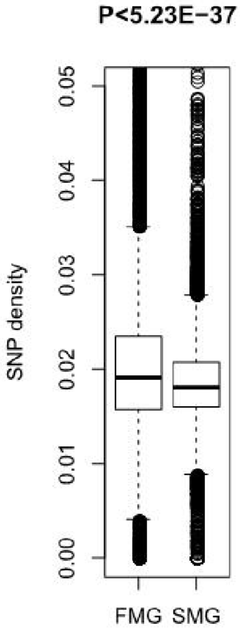
Supplementary Figure 4. The bar plots of the SM genes against the FM genes in the sequence identity for each of the 21 species.

Supplementary Figure 5. The box plots of the SM genes against the FM genes in the sequence identity for each of the 21 species.



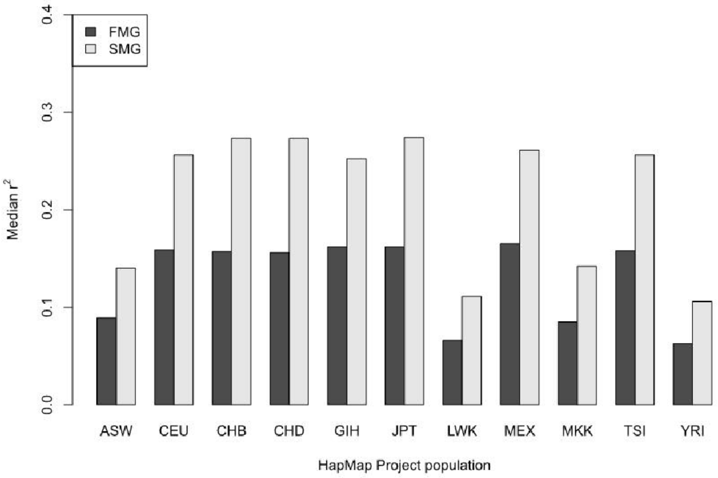
Supplementary Figure 5. The box plots of the SM genes against the FM genes in the sequence identity for each of the 21 species.

Supplementary Figure 6. The box plot of the SM genes against the FM genes in the SNP density.



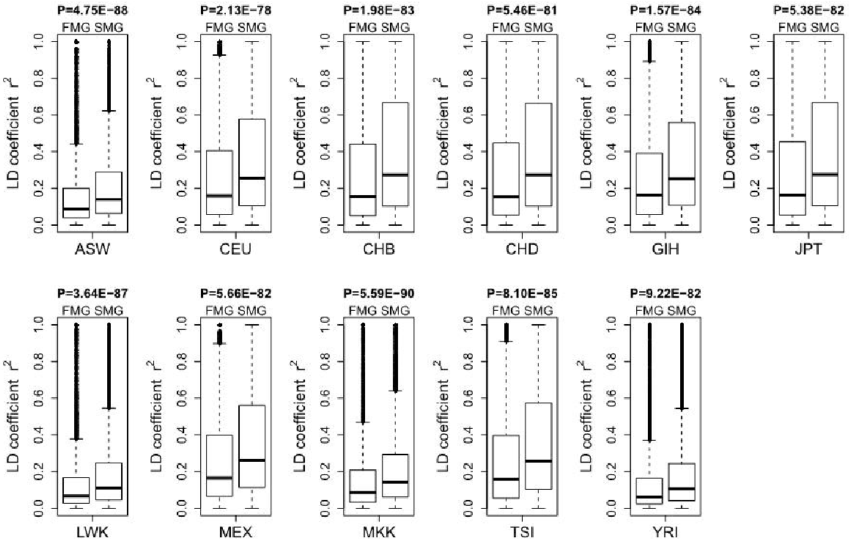
Supplementary Figure 6. The box plot of the SM genes against the FM genes in the SNP density.

Supplementary Figure 7. The bar plots of the SM genes against the FM genes in the LD coefficient r2 for each of the 11 populations of HapMap Project.



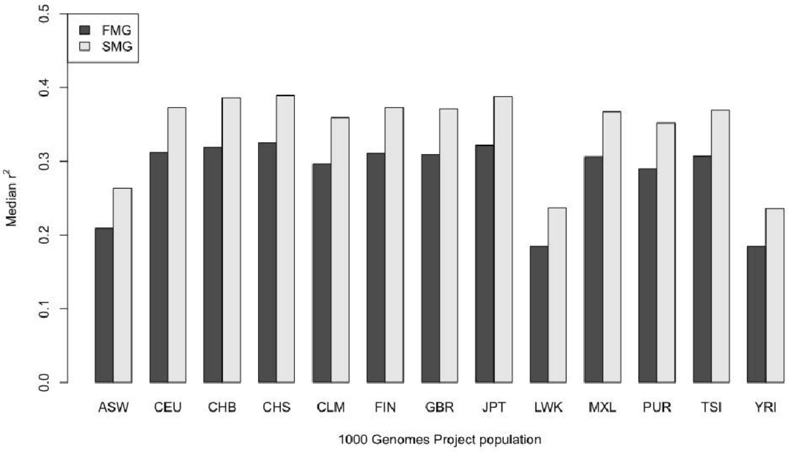
Supplementary Figure 7. The bar plots of the SM genes against the FM genes in the LD coefficient r2 for each of the 11 populations of HapMap Project.

Supplementary Figure 8. The box plots of the SM genes against the FM genes in the LD coefficient r2 for each of the 11 populations of HapMap Project.



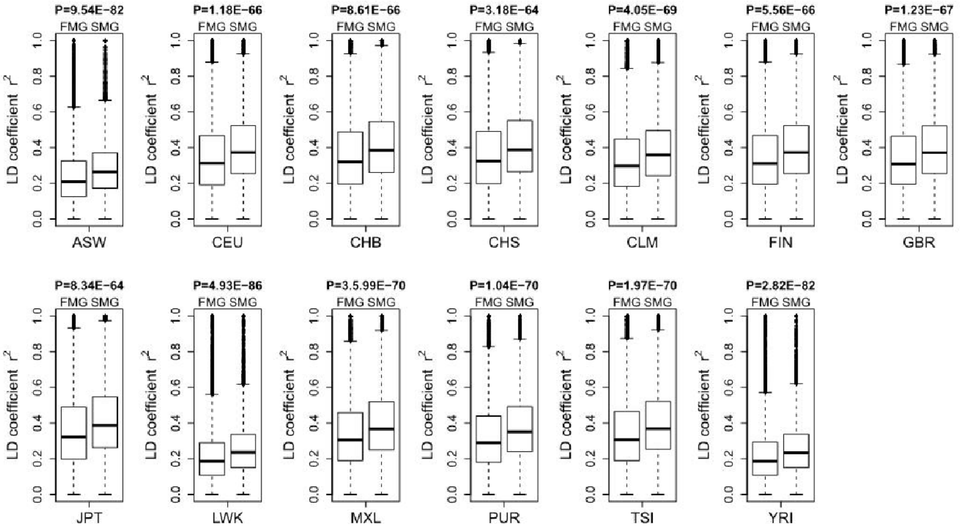
Supplementary Figure 8. The box plots of the SM genes against the FM genes in the LD coefficient r2 for each of the 11 populations of HapMap Project.

Supplementary Figure 9. The bar plots of the SM genes against the FM genes in the LD coefficient r2 for each of the 13 populations of 1000 Genomes Project.



Supplementary Figure 9. The bar plots of the SM genes against the FM genes in the LD coefficient r2 for each of the 13 populations of 1000 Genomes Project.

Supplementary Figure 10. The box plots of the SM genes against the FM genes in the LD coefficient r2 for each of the 13 populations of 1000 Genomes Project.



Supplementary Figure 10. The box plots of the SM genes against the FM genes in the LD coefficient r2 for each of the 13 populations of 1000 Genomes Project.

Supplementary Table 1. Summary statistics for the comparisons of dn/ds in 21 species.

Supplementary Table 1. Summary statistics for the comparisons of dn/ds in 21 species.

Species	dn/ds of FM genes			dn/ds of SM genes			Wilcoxon test P-value
	median	upper quartile	lower quartile	median	upper quartile	lower quartile	
amel	0.1030	0.1885	0.0481	0.1497	0.2701	0.0712	5.44E-103
btau	0.0968	0.1814	0.0437	0.1457	0.2639	0.0684	7.55E-117
cfam	0.1004	0.1850	0.0460	0.1482	0.2670	0.0684	2.85E-99
cjac	0.1477	0.2737	0.0647	0.2248	0.3968	0.1010	3.86E-120
cpor	0.0960	0.1775	0.0454	0.1368	0.2486	0.0639	6.04E-87
ecab	0.1066	0.1961	0.0488	0.1620	0.2888	0.0743	8.73E-120
itri	0.0946	0.1802	0.0396	0.1374	0.2533	0.0619	7.92E-87
lafr	0.1132	0.1968	0.0551	0.1586	0.2793	0.0757	5.36E-91
mdom	0.0823	0.1454	0.0398	0.0936	0.1689	0.0474	1.32E-17
mfur	0.0970	0.1807	0.0435	0.1398	0.2544	0.0646	6.40E-88
mluc	0.1160	0.2020	0.0571	0.1592	0.2813	0.0795	2.14E-81
mmul	0.1533	0.3092	0.0600	0.2273	0.4121	0.0950	1.73E-85
mmus	0.0877	0.1603	0.0406	0.1258	0.2273	0.0574	4.39E-93
nleu	0.1861	0.3564	0.0743	0.2587	0.4630	0.1132	2.20E-75
ocun	0.0935	0.1718	0.0439	0.1358	0.2476	0.0661	1.27E-92
ogar	0.1140	0.2059	0.0515	0.1535	0.2755	0.0702	3.15E-67
pabe	0.1615	0.3310	0.0617	0.2356	0.4428	0.0989	1.98E-79
ptro	0.1791	0.3864	0.0458	0.2762	0.5393	0.1058	2.79E-88
rnor	0.0918	0.1642	0.0426	0.1281	0.2289	0.0587	8.72E-81
shar	0.0803	0.1428	0.0398	0.0908	0.1655	0.0456	1.91E-15
sscr	0.1020	0.1881	0.0460	0.1495	0.2664	0.0674	2.64E-82

Supplementary Table 2. Summary statistics for the comparisons of sequence identity in 21 species.

Supplementary Table 2. Summary statistics for the comparisons of sequence identity in 21 species.

Species	**Sequence identity of FM genes**			**Sequence identity of SM genes**			**Wilcoxon test P-value**
	median	**upper quartile**	**lower quartile**	**median**	**upper quartile**	**lower quartile**	
amel	0.8692	0.9364	0.7812	0.9195	0.9642	0.8561	9.21E-176
btau	0.8639	0.9310	0.7709	0.9130	0.9614	0.8453	3.52E-169
cfam	0.8720	0.9381	0.7806	0.9211	0.9656	0.8576	1.20E-171
cjac	0.9286	0.9665	0.8739	0.9583	0.9825	0.9200	1.20E-173
cpor	0.8449	0.9234	0.7430	0.8996	0.9543	0.8241	1.90E-142
ecab	0.8802	0.9419	0.7984	0.9259	0.9673	0.8663	6.26E-168
itri	0.8741	0.9422	0.7849	0.9225	0.9684	0.8583	3.74E-152
lafr	0.8642	0.9296	0.7702	0.9092	0.9559	0.8433	4.69E-143
mdom	0.7634	0.8660	0.6369	0.8224	0.9063	0.7192	5.77E-97
mfur	0.8710	0.9380	0.7802	0.9187	0.9651	0.8527	1.43E-148
mluc	0.8521	0.9226	0.7563	0.9049	0.9528	0.8376	2.64E-150
mmul	0.9604	0.9828	0.9245	0.9758	0.9910	0.9477	6.11E-118
mmus	0.8440	0.9235	0.7382	0.8955	0.9510	0.8190	2.09E-137
nleu	0.9716	0.9878	0.9459	0.9828	0.9936	0.9630	9.98E-106
ocun	0.8621	0.9331	0.7725	0.9118	0.9614	0.8453	2.30E-142
ogar	0.8853	0.9441	0.8062	0.9244	0.9652	0.8662	1.64E-135
pabe	0.9751	0.9892	0.9494	0.9845	0.9943	0.9642	1.84E-96
ptro	0.9901	0.9962	0.9779	0.9948	0.9986	0.9876	3.26E-146
rnor	0.8311	0.9167	0.7218	0.8916	0.9489	0.8111	1.92E-126
shar	0.7574	0.8606	0.6266	0.8237	0.9082	0.7152	8.22E-109
sscr	0.8643	0.9348	0.7683	0.9135	0.9622	0.8419	1.40E-115

Supplementary Table 3. Summary statistics for the comparisons of r^2 in HapMap population.

Supplementary Table 3. Summary statistics for the comparisons of r^2 in HapMap population.

HapMap Population	**r^2 of FM genes**			**r^2 of SM genes**			**Wilcoxon test P-value**
	median	**upper quartile**	**lower quartile**	**median**	**upper quartile**	**lower quartile**	
ASW	0.0890	0.2000	0.0390	0.1400	0.2880	0.0640	4.75E-88
CEU	0.1590	0.4050	0.0570	0.2560	0.5770	0.1050	2.13E-78
CHB	0.1570	0.4400	0.0510	0.2730	0.6685	0.1030	1.98E-83
CHD	0.1560	0.4483	0.0530	0.2730	0.6635	0.1035	5.46E-81
GIH	0.1620	0.3910	0.0570	0.2520	0.5590	0.1080	1.57E-84
JPT	0.1620	0.4540	0.0540	0.2740	0.6690	0.1040	5.38E-82
LWK	0.0660	0.1670	0.0260	0.1110	0.2460	0.0460	3.64E-87
MEX	0.1650	0.3980	0.0650	0.2610	0.5610	0.1140	5.66E-82
MKK	0.0850	0.2080	0.0338	0.1420	0.2930	0.0610	5.59E-90
TSI	0.1580	0.3970	0.0550	0.2560	0.5745	0.1050	8.10E-85
YRI	0.0630	0.1630	0.0240	0.1060	0.2430	0.0420	9.22E-82

Supplementary Table 4. Summary statistics for the comparisons of r^2 in 1000 genomes populations.

Supplementary Table 4. Summary statistics for the comparisons of r^2 in 1000 genomes populations.

HapMap Population	**r^2 of FM genes**			**r^2 of SM genes**			**Wilcoxon test P-value**
	median	**upper quartile**	**lower quartile**	**median**	**upper quartile**	**lower quartile**	
ASW	0.2090	0.3260	0.1250	0.2630	0.3700	0.1730	9.54E-82
CEU	0.3120	0.4670	0.1910	0.3730	0.5230	0.2540	1.18E-66
CHB	0.3190	0.4883	0.1950	0.3860	0.5460	0.2620	8.61E-66
CHS	0.3250	0.4923	0.1980	0.3890	0.5520	0.2640	3.18E-64
CLM	0.2965	0.4470	0.1830	0.3590	0.4960	0.2420	4.05E-69
FIN	0.3110	0.4690	0.1930	0.3730	0.5230	0.2540	5.56E-66
GBR	0.3090	0.4630	0.1930	0.3710	0.5220	0.2540	1.23E-67
JPT	0.3215	0.4913	0.1970	0.3880	0.5480	0.2630	8.34E-64
LWK	0.1850	0.2900	0.1090	0.2370	0.3380	0.1510	4.93E-86
MXL	0.3060	0.4580	0.1900	0.3670	0.5180	0.2500	5.99E-70
PUR	0.2900	0.4400	0.1800	0.3520	0.4930	0.2400	1.04E-70
TSI	0.3070	0.4640	0.1890	0.3690	0.5210	0.2530	1.97E-70
YRI	0.1850	0.2940	0.1080	0.2360	0.3390	0.1510	2.82E-82