Supplementary

Contents

Section 1: Supplementary Tables..........2
Supplementary table S1..........2
Supplementary table S2..........3
Supplementary table S3..........4
Supplementary table S4..........4
Section 2: Supplementary Figures..........5
Supplementary fig. S1..........5
Supplementary fig. S2..........6
Supplementary fig. S3..........6
Supplementary fig. S4..........7
Supplementary fig. S5..........8
Supplementary fig. S6..........8
Supplementary fig. S7..........9
Supplementary fig. S8..........9
Supplementary fig. S9..........10
Supplementary fig. S10..........10

Section 1: Supplementary Tables

Supplementary table S1

Supplementary table S1. 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	0.1268	0.2415	0.0594	0.1096	0.2057	0.0490	1.79E-10
btau	0.1218	0.2373	0.0573	0.1024	0.1992	0.0436	1.48E-14
cfam	0.1270	0.2394	0.0576	0.1091	0.2003	0.0454	1.23E-12
cjac	0.1968	0.3655	0.0850	0.1589	0.2945	0.0639	1.73E-16
cpor	0.1145	0.2228	0.0556	0.1025	0.1892	0.0449	9.25E-09
ecab	0.1365	0.2603	0.0618	0.1152	0.2135	0.0482	4.13E-15
itri	0.1167	0.2310	0.0512	0.1026	0.1997	0.0372	1.16E-08
lafr	0.1359	0.2518	0.0654	0.1232	0.2152	0.0571	8.54E-08
mdom	0.0866	0.1567	0.0434	0.0881	0.1565	0.0405	0.363623
mfur	0.1174	0.2277	0.0539	0.1067	0.1995	0.0435	2.19E-07
mluc	0.1415	0.2541	0.0696	0.1271	0.2158	0.0576	1.73E-08
mmul	0.1964	0.3847	0.0758	0.1626	0.3346	0.0581	6.88E-11
mmus	0.1082	0.2052	0.0479	0.0910	0.1742	0.0406	9.50E-10
nleu	0.2219	0.4198	0.0859	0.1968	0.3752	0.0707	5.25E-08
ocun	0.1151	0.2174	0.0555	0.1024	0.1882	0.0433	1.09E-09
ogar	0.1314	0.2490	0.0594	0.1256	0.2299	0.0528	0.000763
pabe	0.2035	0.4078	0.0829	0.1803	0.3584	0.0627	1.18E-07
ptro	0.2412	0.5000	0.0769	0.1760	0.4038	0.0000	3.28E-17
rnor	0.1080	0.2073	0.0485	0.0968	0.1824	0.0434	5.77E-07
shar	0.0840	0.1502	0.0433	0.0869	0.1549	0.0429	0.936342
sscr	0.1267	0.2382	0.0584	0.1083	0.2021	0.0446	1.56E-10

Supplementary table S2

Supplementary table S2. 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	0.8917	0.9519	0.8110	0.9251	0.9691	0.8594	1.01E-38
btau	0.8861	0.9476	0.8000	0.9192	0.9662	0.8503	2.32E-39
cfam	0.8940	0.9531	0.8114	0.9246	0.9694	0.8630	1.14E-37
cjac	0.9420	0.9745	0.8916	0.9605	0.9845	0.9237	2.43E-39
cpor	0.8720	0.9402	0.7727	0.9041	0.9591	0.8235	1.80E-27
ecab	0.9021	0.9577	0.8231	0.9310	0.9718	0.8710	8.24E-38
itri	0.8986	0.9585	0.8170	0.9266	0.9726	0.8612	1.22E-31
lafr	0.8865	0.9459	0.7965	0.9144	0.9613	0.8471	3.92E-30
mdom	0.7910	0.8864	0.6713	0.8269	0.9136	0.7231	4.30E-20
mfur	0.8937	0.9535	0.8084	0.9227	0.9692	0.8560	1.26E-29
mluc	0.8754	0.9370	0.7917	0.9127	0.9592	0.8418	8.02E-39
mmul	0.9685	0.9871	0.9348	0.9774	0.9923	0.9500	1.38E-26
mmus	0.8682	0.9371	0.7752	0.8993	0.9558	0.8185	4.44E-25
nleu	0.9779	0.9915	0.9548	0.9843	0.9947	0.9662	3.70E-24
ocun	0.8870	0.9497	0.8000	0.9169	0.9667	0.8511	1.19E-30
ogar	0.9054	0.9564	0.8284	0.9266	0.9694	0.8643	5.65E-24
pabe	0.9803	0.9924	0.9568	0.9859	0.9952	0.9675	1.19E-21
ptro	0.9920	0.9974	0.9809	0.9954	1.0000	0.9891	7.31E-47
rnor	0.8611	0.9339	0.7556	0.8966	0.9528	0.8119	6.15E-25
shar	0.7878	0.8840	0.6612	0.8330	0.9179	0.7199	1.33E-25
sscr	0.8867	0.9504	0.7962	0.9221	0.9693	0.8527	8.55E-33

Supplementary table S3

Supplementary table S3. 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	0.0940	0.2080	0.0420	0.1750	0.3375	0.0880	1.29E-80
CEU	0.1710	0.4300	0.0640	0.3270	0.6920	0.1500	5.84E-74
CHB	0.1730	0.4830	0.0560	0.3400	0.7880	0.1455	8.04E-67
CHD	0.1710	0.4920	0.0570	0.3330	0.7785	0.1440	3.43E-65
GIH	0.1710	0.4160	0.0630	0.3100	0.6675	0.1550	1.16E-74
JPT	0.1740	0.5020	0.0590	0.3360	0.7765	0.1470	4.94E-64
LWK	0.0680	0.1730	0.0280	0.1410	0.2915	0.0665	5.19E-80
MEX	0.1800	0.4190	0.0710	0.3210	0.6610	0.1580	3.18E-70
MKK	0.0940	0.2170	0.0350	0.1790	0.3455	0.0880	1.39E-83
TSI	0.1640	0.4320	0.0580	0.3220	0.6760	0.1525	1.01E-76
YRI	0.0660	0.1710	0.0240	0.1390	0.2890	0.0610	2.18E-78

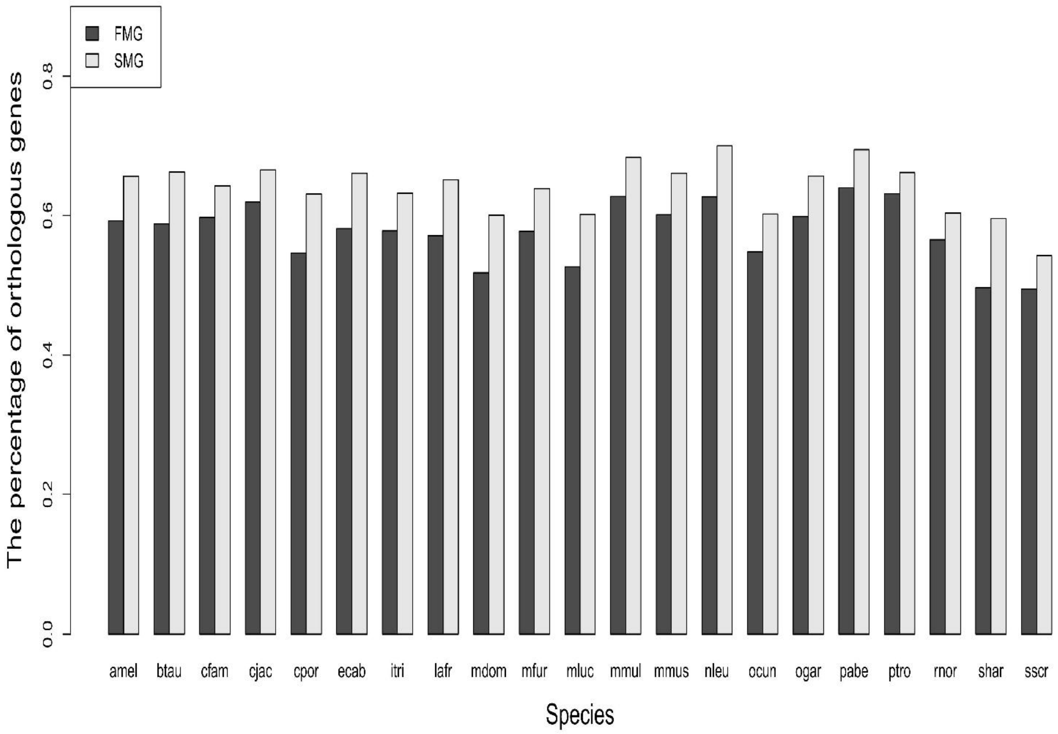
Supplementary table S4

Supplementary table S4. 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	0.2200	0.3340	0.1320	0.2990	0.4100	0.2160	1.23E-87
CEU	0.3240	0.4790	0.2000	0.4160	0.5760	0.3040	6.58E-68
CHB	0.3340	0.5050	0.2090	0.4300	0.5960	0.3100	8.58E-63
CHS	0.3350	0.5080	0.2100	0.4340	0.6010	0.3140	7.76E-63
CLM	0.3080	0.4580	0.1920	0.3980	0.5490	0.2900	4.67E-69
FIN	0.3250	0.4790	0.2030	0.4170	0.5770	0.3010	2.04E-66
GBR	0.3210	0.4750	0.2030	0.4130	0.5730	0.3030	2.23E-69
JPT	0.3350	0.5070	0.2120	0.4330	0.6010	0.3100	7.43E-60
LWK	0.1970	0.2970	0.1140	0.2710	0.3730	0.1920	1.54E-89
MXL	0.3200	0.4700	0.2000	0.4050	0.5690	0.2980	1.63E-67
PUR	0.3040	0.4490	0.1890	0.3890	0.5380	0.2870	9.13E-73
TSI	0.3190	0.4760	0.1990	0.4130	0.5700	0.3020	6.12E-70
YRI	0.1940	0.2990	0.1180	0.2690	0.3710	0.1910	1.81E-87

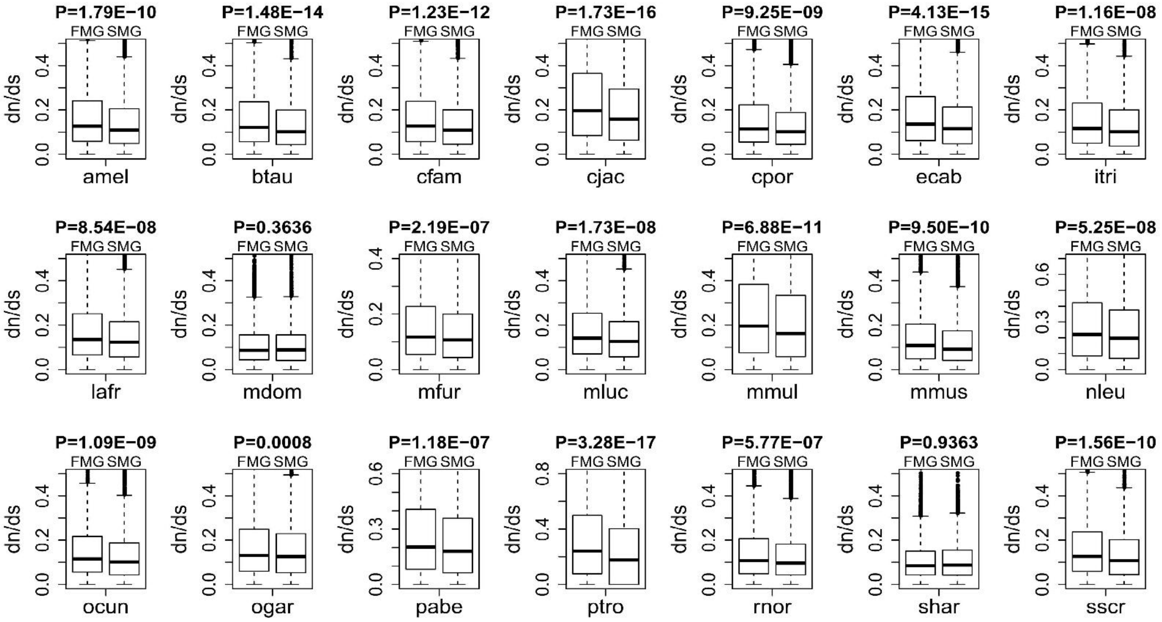
Section 2: Supplementary Figures

Supplementary fig. S1



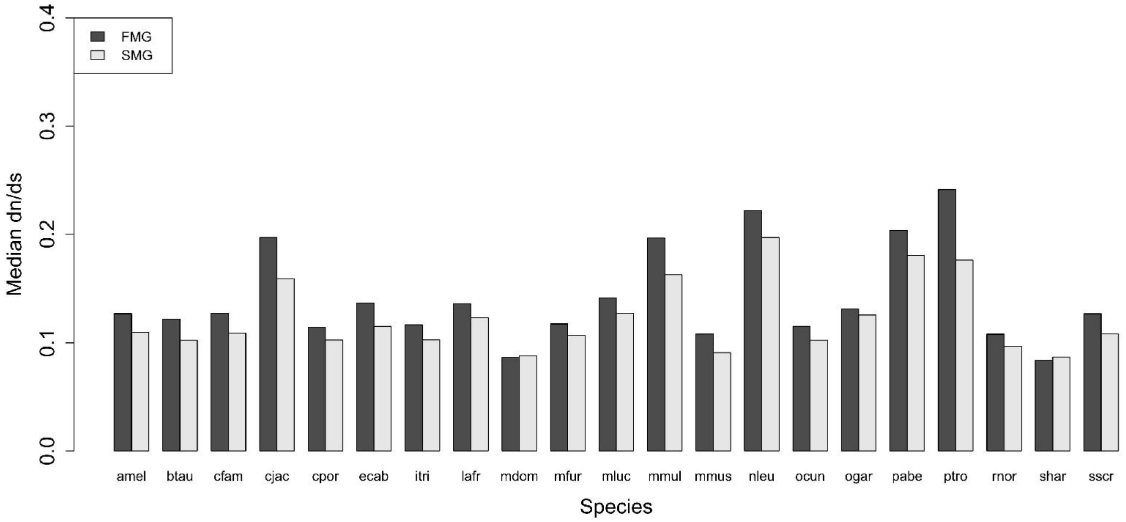
Supplementary fig. S1. The bar plots of the SM genes against the FM genes in the percentage of orthologous genes for each of the 21 species.

Supplementary fig. S2



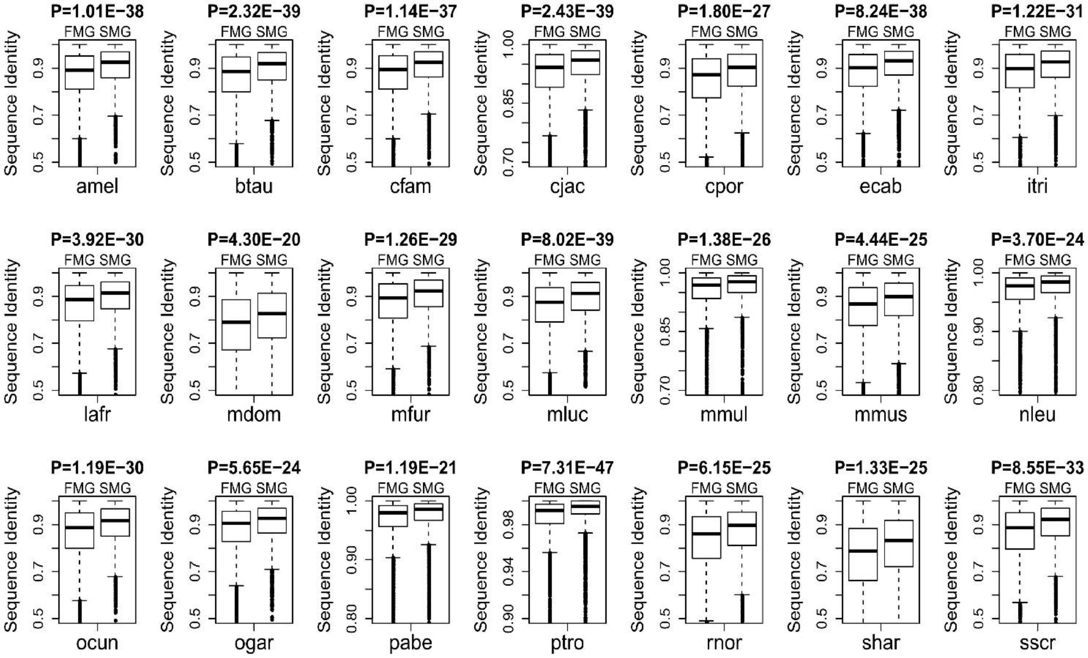
Supplementary fig. S2. The box plots of the SM genes against the FM genes in the evolutionary rate for each of the 21 species.

Supplementary fig. S3



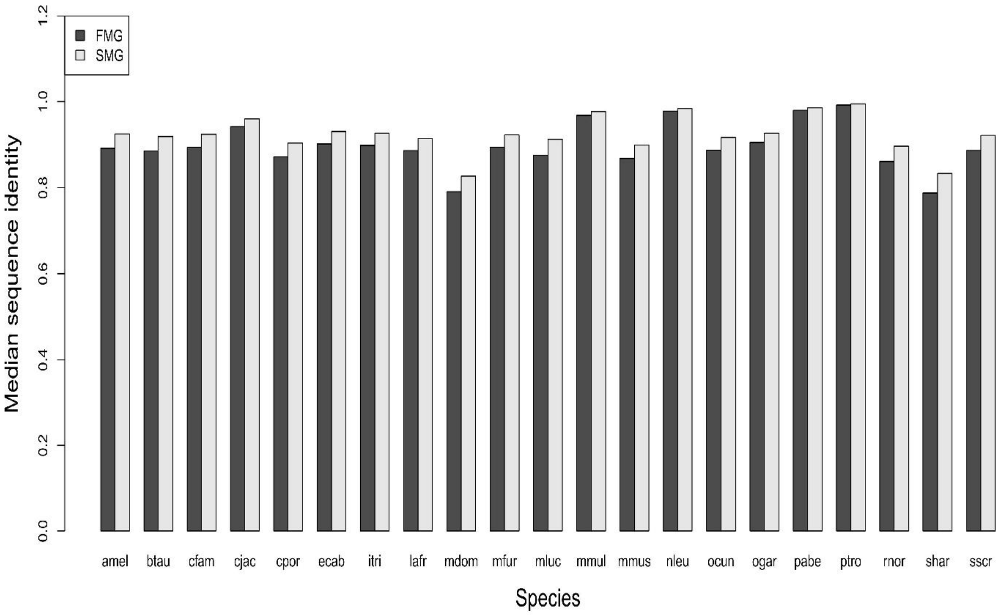
Supplementary fig. S3. The bar plots of the SM genes against the FM genes in the evolutionary rate for each of the 21 species.

Supplementary fig. S4



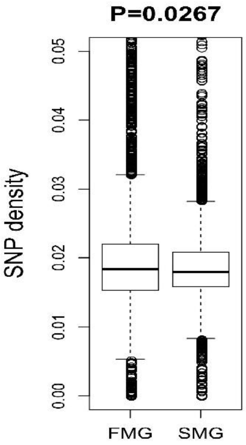
Supplementary fig. S4. The box plots of the SM genes against the FM genes in the sequence identity for each of the 21 species.

Supplementary fig. S5



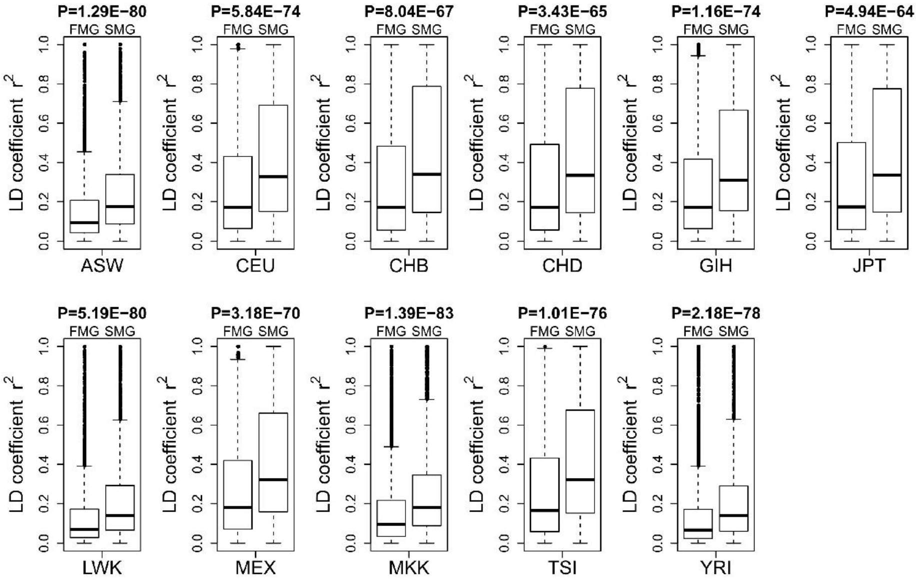
Supplementary fig. S5. The bar plots of the SM genes against the FM genes in the sequence identity for each of the 21 species

Supplementary fig. S6



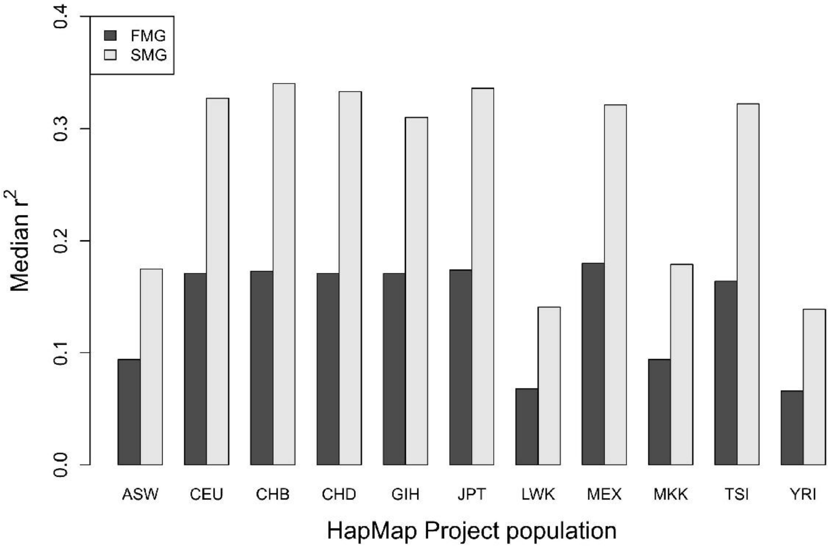
Supplementary fig. S6. The box plot of the SM genes against the FM genes in the SNP density.

Supplementary fig. S7



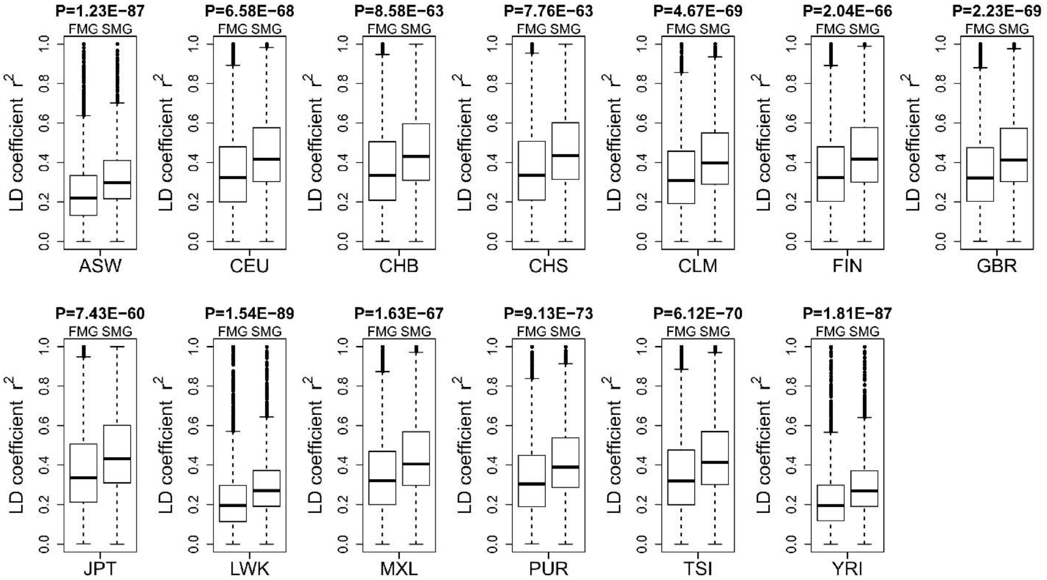
Supplementary fig. S7. The box plots of the SM genes against the FM genes in the LD coefficient r^2 for each of the 11 populations of HapMap Project.

Supplementary fig. S8



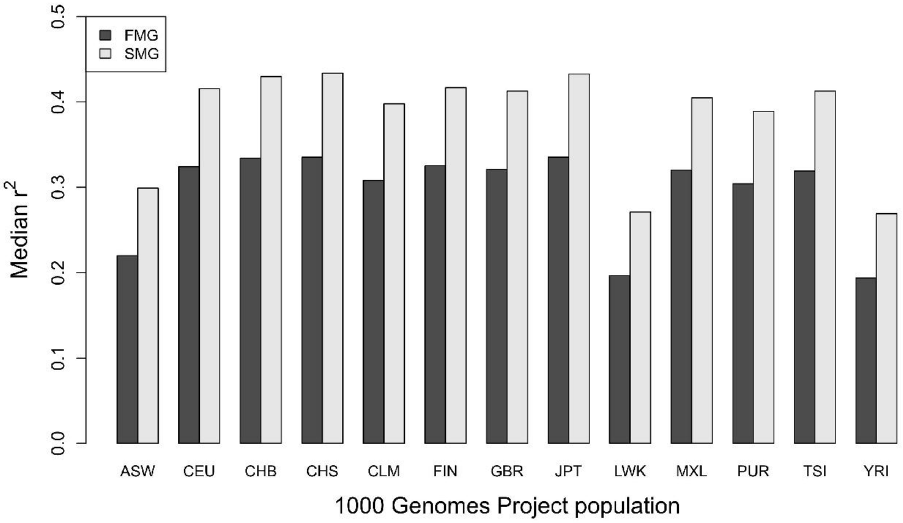
Supplementary fig. S8. The bar plots of the SM genes against the FM genes in the LD coefficient r^2 for each of the 11 populations of HapMap Project.

Supplementary fig. S9



Supplementary fig. S9. The box plots of the SM genes against the FM genes in the LD coefficient r^2 for each of the 13 populations of 1000 Genomes Project.

Supplementary fig. S10



Supplementary fig. S10. The bar plots of the SM genes against the FM genes in the LD coefficient r^2 for each of the 13 populations of 1000 Genomes Project.