

Figure 3 - figure supplement 2: Distance matrices for whole genome comparisons and gene comparisons

Mean distances of whole genomes (from 10,000 25kb windows)

MEAN	AFG	CAS	CZE	FRA	GER	IRA	KAZ	MAT	SPI	SPR
AFG	0	0.00541086	0.00166811	0.00782105	0.00782785	0.00739552	0.00130151	0.06324006	0.01503435	0.01568621
CAS	0.00541086	0	0.00563758	0.00566411	0.00567391	0.00519473	0.0055197	0.06144667	0.01308614	0.01373323
CZE	0.00166811	0.00563758	0	0.00793853	0.00794452	0.00752934	0.00149276	0.06342217	0.01523522	0.01588459
FRA	0.00782105	0.00566411	0.00793853	0	0.00175979	0.00202539	0.00792647	0.06303092	0.01492818	0.01559957
GER	0.00782785	0.00567391	0.00794452	0.00175979	0	0.00204749	0.00793534	0.06300955	0.01492032	0.0156008
IRA	0.00739552	0.00519473	0.00752934	0.00202539	0.00204749	0	0.00750167	0.06264982	0.01451421	0.01519135
KAZ	0.00130151	0.0055197	0.00149276	0.00792647	0.00793534	0.00750167	0	0.06333035	0.01512862	0.01577962
MAT	0.06324006	0.06144667	0.06342217	0.06303092	0.06300955	0.06264982	0.06333035	0	0.06380344	0.06413239
SPI	0.01503435	0.01308614	0.01523522	0.01492818	0.01492032	0.01451421	0.01512862	0.06380344	0	0.01336037
SPR	0.01568621	0.01373323	0.01588459	0.01559957	0.0156008	0.01519135	0.01577962	0.06413239	0.01336037	0

Expected substitutions for the Gm13030 reading frame

MEAN	AFG	CAS	CZE	FRA	GER	IRA	KAZ	MAT	SPI	SPR
AFG	0	2	1	3	3	3	1	27	6	7
CAS	2	0	2	2	2	2	2	26	6	6
CZE	1	2	0	3	3	3	1	27	7	7
FRA	3	2	3	0	1	1	3	27	6	7
GER	3	2	3	1	0	1	3	27	6	7
IRA	3	2	3	1	1	0	3	27	6	7
KAZ	1	2	1	3	3	3	0	27	7	7
MAT	27	26	27	27	27	27	27	0	27	28
SPI	6	6	7	6	6	6	7	27	0	6
SPR	7	6	7	7	7	7	7	28	6	0