Supplementary Information

Close inbreeding and low genetic diversity in Inner Asian human populations despite geographical exogamy

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#Co-supervised this work

Supplementary Materials and Methods

Geographical exogamy

To infer the geographical distance between the birth places of spouses (collected by the use of questionnaire available at the end of this document), we obtained the geographical coordinates of each location and calculated the pairwise great-circle distances with an own designed python3 code using the Spherical Law of Cosines formula and an Earth radius of 6,367.445 km. Based on the population local minima on Figure 2 (comprised between 2 km and 12 km, with an average 4 km, while Tja, a population that did not have a local minimum, was excluded), we defined exogamous couples as those with spouses born at more than 4 km. We also tested for other definitions of exogamy with arbitrary thresholds at 10, 20, 30, 40, and 50 km. Note that for three out of 16 populations (Kaz, Tur and Uzb), we had no information for the parental generation.

SNP genotyping and quality control

All individuals were genotyped on an Illumina genotyping array (either 660W-Quad, OmniExpress, Omni1-Quad, Omni2.5, or Omni5Exome; see details in Supplementary Table 3). Genotyping was performed by the "Plate-forme Post-Génomique de la Pitié-Salpétrière (P3S)" or by the "Institut Pasteur – Genopole (Génotypage des Eucaryotes)", in Paris, France. For two of the arrays (Illumina Omni1-Quad and Omni2.5), we performed our own genotype-calling quality control whereas for the others, the quality control was done by the sequencing platform. Indeed, for each array separately, we performed a three-stage quality control procedure inspired from [1], restricting our analyses to autosomal SNPs (*i.e.,* excluding CNVs and non-autosomal markers). Briefly, we excluded SNPs with ambiguous genomic position, SNPs that failed genotyping in the sample set, SNPs with a call rate below 90% or a cluster separation below 0.2, SNPs without ID in rs nomenclature, SNPs found to be duplicates, indels and monomorphic SNPs. We removed samples with more than 15% of missing data. Then, we performed a population-genetic quality control following [1]. We first identified pairs of samples more related than first cousins using

Relpair 2.0.1 software [2,3]. We performed this analysis on three non-overlapping subsets of SNPs in Hardy-Weinberg equilibrium (*p-value*>10^{-5} for each population and >10^{-2} for each pair of populations) and bimorphic in every population. For pairs of individuals closer than first cousins, we removed the individual with the lowest genotyping-call or the individual involved in the highest number of relations, resulting in 52 individuals being excluded. Finally, we removed the monomorphic SNPs within each array. At the end, for the five arrays, we obtained data for 526,823 to 2,609,107 SNPs genotyped for the 519 samples of interest.

To generate a joint dataset, we manually merged the five datasets based on SNPs rs. To control that alleles are coded on the same strand between arrays, we removed A-T and C-G polymorphisms, and SNPs that were triallelic on the two arrays, resulting in a dataset of 253,606 SNPs. We found three pairs of relatives within the merged dataset, and as previously described, we excluded three samples, in addition to 13 samples with a call-rate < 95%, leading to a total of 503 individuals. 292 of these individuals genotyped on the Omni1 and Omni2.5 arrays have already been published in [4], while the 211 other individuals were newly published in our present study. Finally, we excluded SNPs in Hardy-Weinberg disequilibrium (plink1.9 [5] function --*hardy*, *p-value*>10^{-5}), leading to a final dataset of 253,532 SNPs. Within this dataset, we generated a subset of 105,858 independent SNPs with $r^2<0.5$ (plink1.9 function --*indep* 50 5 2).

Genetic diversity

We computed the matrix of allele-sharing dissimilarity between all individuals for the independent SNPs dataset, using the software *asd* [6]. We also computed pairwise F_{ST} distances for each pair of populations on the independent SNPs dataset using ArlSumStat [7] (Supplementary Table 2). We present only F_{ST} distances on the independent SNPs as they are highly correlated to those based on the whole SNP dataset (Spearman's *rho*=0.997, *p-value*<$2.2*10^{-16}$). We represented both the ASD and F_{ST} pairwise distance matrices as the two first dimensions of

MultiDimensional Scaling (MDS) performed with R function *cmdscale*[8]. To evaluate whether the first two MDS dimensions represented accurately the whole matrix, we calculated the Spearman's rank-sum correlation *rho* between the MDS distances on dimensions 1 and 2, and their corresponding F_{ST} and ASD distances, respectively.

We calculated the haplotypic heterozygosity of each population based on [1]. We first reconstructed non-overlapping blocks of SNPs in high linkage disequilibrium (LD) using the whole SNPs dataset. We defined blocks of LD as intervals of 5-15 SNPs where the recombination rate is below 0.5cM/Mb between each pair of contiguous SNPs (using the GRCh37 recombination map). We generated 2,267 such blocks of LD, with on average 103 blocks per chromosome (from 24 on chromosome 21 to 222 on chromosome 1). These blocks include 13,340 SNPs, *i.e.,* 5.3% of the total dataset.

Then we phased these blocks with plink1.7 [9] *--hap* function, that uses an expectation-maximization phasing algorithm. For each population, we estimated the frequencies of the haplotypes (plink1.7 *--hap-freq* function), calculated the heterozygosity of each haplotype based on Nei's formula and computed the mean haplotypic heterozygosity along each chromosome:

$$\mathrm{H}_{\text{k-chromosome}}=\frac{\frac{2Npop}{2Npop-1}*\sum_{j=1}^{Nblocks}\left(1-\sum_{i=1}^{Nalleles}{f_{i,j}}^{2}\right)}{Nblocks}.$$

Inbreeding coefficients and parental mating types

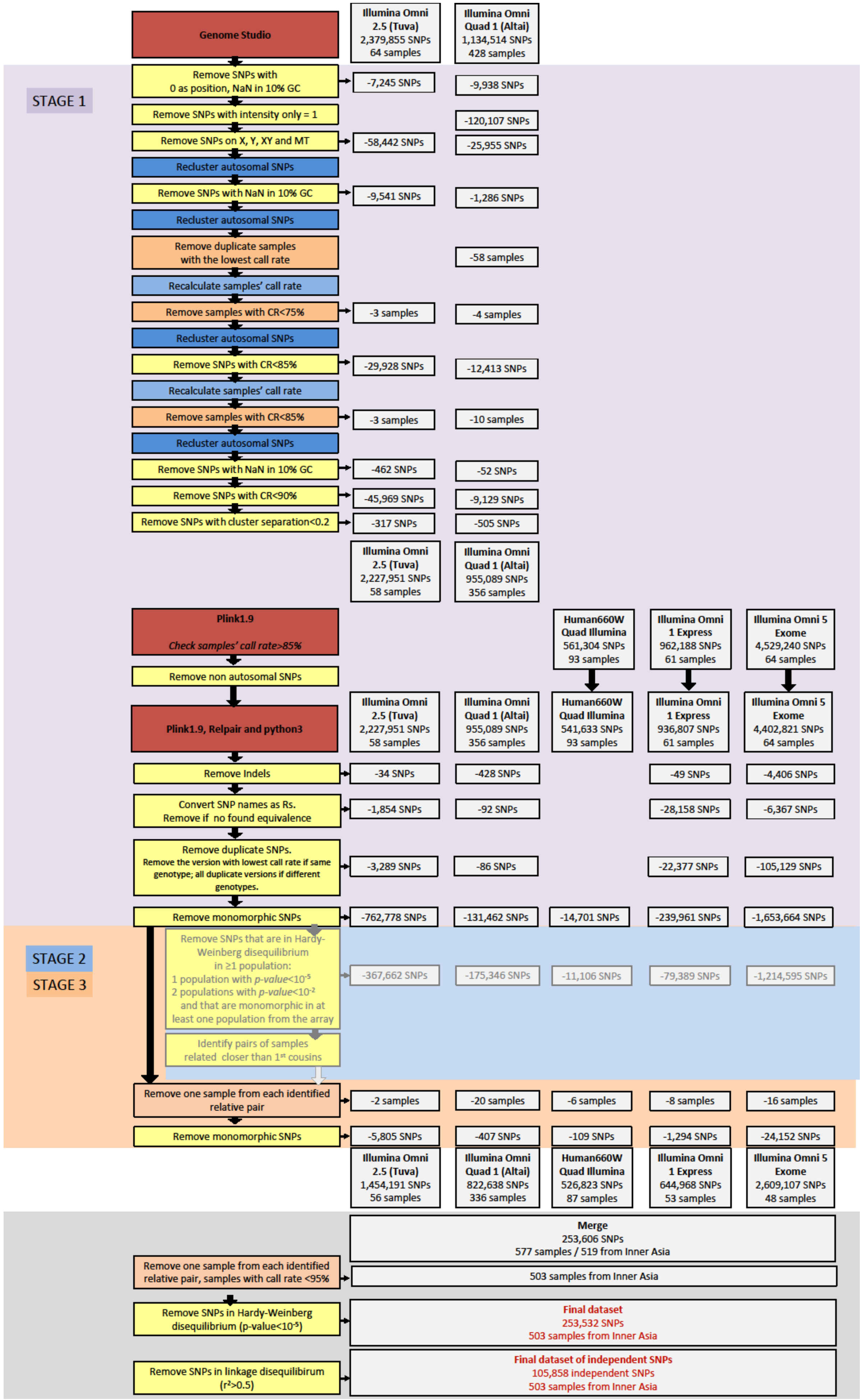
We chose to use FSuite to infer the inbreeding coefficient, as it is efficient to infer distant relationships (1C and 2C type)[10], even in small-sized samples[11]. We used the software's default option that creates 100 random submaps with one marker every 0.5 cM[11].

We calculated the proportion of homozygous sites within each individual genome, relative to an expected baseline of homozygosity per population, using plink1.9 *--het* function on the independent SNPs dataset[9] without any options. Thus our results were obtained without the Nei and Roychoudhury's correction, implemented the *--small-sample* option. For comparison, we also computed it for the 11 populations from the HapMap3 worldwide dataset. First, we removed 236 first-degree relatives, and SNPs that were non-autosomal, monomorphic or deviating from Hardy-Weinberg equilibrium (*p-value*$<10^{-5}$ in at least one population, and $<10^{-2}$ in at least two populations) [12], to eventually generate a dataset of 195,874 independent SNPs ($r^2<0.5$, plink1.9 function *--indep 50 5 2*).

We identified runs of homozygosity, called ROHs [13], within each individual genome based on the whole SNPs dataset, using the plink1.9 *--homozyg* function with by-default options but changing the options *--homozyg-kb 20 --homozyg-snp 50* as done in [14] to be able to detect ROHs contained more than 50 SNPs (rather than 100 by default) for a length larger than 20 kb.

Pipeline for quality control and datasets merging.

The pipeline includes three stages of analysis. Briefly, the first step cleans SNPs and samples with a low quality or in duplicate; the second step estimates the genetic relatedness between samples and the third steps remove relatives closer than 1st cousins as well as monomorphic SNPs. Then the five arrays were merged, quality and relatedness were controlled one more time and other individuals included in these arrays but not from Inner Asia were removed. Moreover, we added a Hardy-Weinberg equilibrium test on the SNPs dataset. An additional step generates a subset of independent SNPs.


Illumina Omni 2.5 (Tuva) 2,379,855 SNPs 64 samples
Illumina Omni Quad 1 (Altai) 1,134,514 SNPs 428 samples
Genome Studio
STAGE 1
Remove SNPs with 0 as position, NaN in 10% GC
-7,245 SNPs
-9,938 SNPs
Remove SNPs with intensity only = 1
-120,107 SNPs
Remove SNPs on X, Y, XY and MT
-58,442 SNPs
-25,955 SNPs
Recluster autosomal SNPs
Remove SNPs with NaN in 10% GC
-9,541 SNPs
-1,286 SNPs
Recluster autosomal SNPs
Remove duplicate samples with the lowest call rate
-58 samples
Recalculate samples' call rate
Remove samples with CR<75%
-3 samples
-4 samples
Recluster autosomal SNPs
Remove SNPs with CR<85%
-29,928 SNPs
-12,413 SNPs
Recalculate samples' call rate
Remove samples with CR<85%
-3 samples
-10 samples
Recluster autosomal SNPs
Remove SNPs with NaN in 10% GC
-462 SNPs
-52 SNPs
Remove SNPs with CR<90%
-45,969 SNPs
-9,129 SNPs
Remove SNPs with cluster separation<0.2
-317 SNPs
-505 SNPs
Illumina Omni 2.5 (Tuva) 2,227,951 SNPs 58 samples
Illumina Omni Quad 1 (Altai) 955,089 SNPs 356 samples
Plink1.9
Check samples' call rate>85%
Human660W Quad Illumina 561,304 SNPs 93 samples
Illumina Omni 1 Express 962,188 SNPs 61 samples
Illumina Omni 5 Exome 4,529,240 SNPs 64 samples
Remove non autosomal SNPs
Plink1.9, Relpair and python3
Illumina Omni 2.5 (Tuva) 2,227,951 SNPs 58 samples
Illumina Omni Quad 1 (Altai) 955,089 SNPs 356 samples
Human660W Quad Illumina 541,633 SNPs 93 samples
Illumina Omni 1 Express 936,807 SNPs 61 samples
Illumina Omni 5 Exome 4,402,821 SNPs 64 samples
Remove Indels
-34 SNPs
-428 SNPs
-49 SNPs
-4,406 SNPs
Convert SNP names as Rs. Remove if no found equivalence
-1,854 SNPs
-92 SNPs
-28,158 SNPs
-6,367 SNPs
Remove duplicate SNPs. Remove the version with lowest call rate if same genotype; all duplicate versions if different genotypes.
-3,289 SNPs
-86 SNPs
-22,377 SNPs
-105,129 SNPs
Remove monomorphic SNPs
-762,778 SNPs
-131,462 SNPs
-14,701 SNPs
-239,961 SNPs
-1,653,664 SNPs
STAGE 2
STAGE 3
Remove SNPs that are in Hardy-Weinberg disequilibrium in ≥1 population: 1 population with p-value<10⁻⁵ 2 populations with p-value<10⁻² and that are monomorphic in at least one population from the array
-367,662 SNPs
-175,346 SNPs
-11,106 SNPs
-79,389 SNPs
-1,214,595 SNPs
Identify pairs of samples related closer than 1st cousins
Remove one sample from each identified relative pair
-2 samples
-20 samples
-6 samples
-8 samples
-16 samples
Remove monomorphic SNPs
-5,805 SNPs
-407 SNPs
-109 SNPs
-1,294 SNPs
-24,152 SNPs
Illumina Omni 2.5 (Tuva) 1,454,191 SNPs 56 samples
Illumina Omni Quad 1 (Altai) 822,638 SNPs 336 samples
Human660W Quad Illumina 526,823 SNPs 87 samples
Illumina Omni 1 Express 644,968 SNPs 53 samples
Illumina Omni 5 Exome 2,609,107 SNPs 48 samples
Merge 253,606 SNPs 577 samples / 519 from Inner Asia
Remove one sample from each identified relative pair, samples with call rate <95%
503 samples from Inner Asia
Remove SNPs in Hardy-Weinberg disequilibrium (p-value<10⁻⁵)
Final dataset 253,532 SNPs 503 samples from Inner Asia
Remove SNPs in linkage disequilibrium (r²>0.5)
Final dataset of independent SNPs 105,858 independent SNPs 503 samples from Inner Asia

№ ....   № ....

Inspection site ....

Date ..../08/2012

M	F
Name..	**Name**..
Date Of Birth… Place of Birth	**DOB …………….** Place of Birth
Child order in the family	Child order in the family ....
Son order	Girl order ....

Your spouse

Alive: ....Yes / No   First marriage : ..... Yes / No   (Который : ....)

Are you related to your spouse ? .... Yes / No

M	Location	F
Place of Birth		Place of Birth ....
Domicile .... , when ?		Domicile .... , when ? ....
Domicile of father		Domicile of father ....
Paternal grandfather		Paternal grandfather ....
Paternal grandmother		Paternal grandmother ....
Domicile of mother...		Domicile of mother...
Maternal grandfather		Maternal grandfather ....
Maternal grandmother		Maternal grandmother ....

M	Language	F
Your language		Your language ....
Father’s language		Father’s language ....
Paternal grandfather		Paternal grandfather ....
Paternal grandmother		Paternal grandmother ....
Mother’s language		Mother’s language ....
Maternal grandfather		Maternal grandfather ....
Maternal grandmother		Maternal grandmother ....

M	Tribe	F
Your tribe		Your tribe ....
Father’s tribe		Father’s tribe ....
Paternal grandfather		Paternal grandfather ....
Paternal grandmother		Paternal grandmother ....
Mother’s tribe		Mother’s tribe ....
Maternal grandfather		Maternal grandfather ....
Maternal grandmother		Maternal grandmother ....

.../...

Married sons and daughters

Total amount of children (including died)	Amount of daughters (including died)	Amount of sons (including died) ......
Total amount of married sons and daughters	Amount of married daughters	Amount of married sons ....
Is last child married ? Yes / No		Age of last child ....

Eldest child :	Sex: M / F	DOB	Domicile ....
Spouse :	Date of birth	Language	Tribe ....
Are the spouse related ? Yes / No			

Second child :	Sex: M / F	DOB	Domicile ....
Spouse :	Date of birth	Language	Tribe ....
Are the spouse related ? Yes / No			

Third child :	Sex: M / F	DOB	Domicile ....
Spouse :	Date of birth	Language	Tribe ....
Are the spouse related ? Yes / No			

Fourth child :	Sex: M / F	DOB	Domicile ....
Spouse :	Date of birth	Language	Tribe ....
Are the spouse related ? Yes / No			

Fifth child :	Sex: M / F	DOB	Domicile ....
Spouse :	Date of birth	Language	Tribe ....
Are the spouse related ? Yes / No			

Sixth child :	Sex: M / F	DOB	Domicile ....
Spouse :	Date of birth	Language	Tribe ....
Are the spouse related ? Yes / No			

Seventh child :	Sex: M / F	DOB	Domicile ....
Spouse :	Date of birth	Language	Tribe ....
Are the spouse related ? Yes / No			

Eighth child :	Sex: M / F	DOB	Domicile ....
Spouse :	Date of birth	Language	Tribe ....
Are the spouse related ? Yes / No			

Ninth child :	Sex: M / F	DOB	Domicile ....
Spouse :	Date of birth	Language	Tribe ....
Are the spouse related ? Yes / No			

.../...

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relatedness among individuals in HapMap phase III. *Am. J. Hum. Genet.* **87,** 457–464 (2010).

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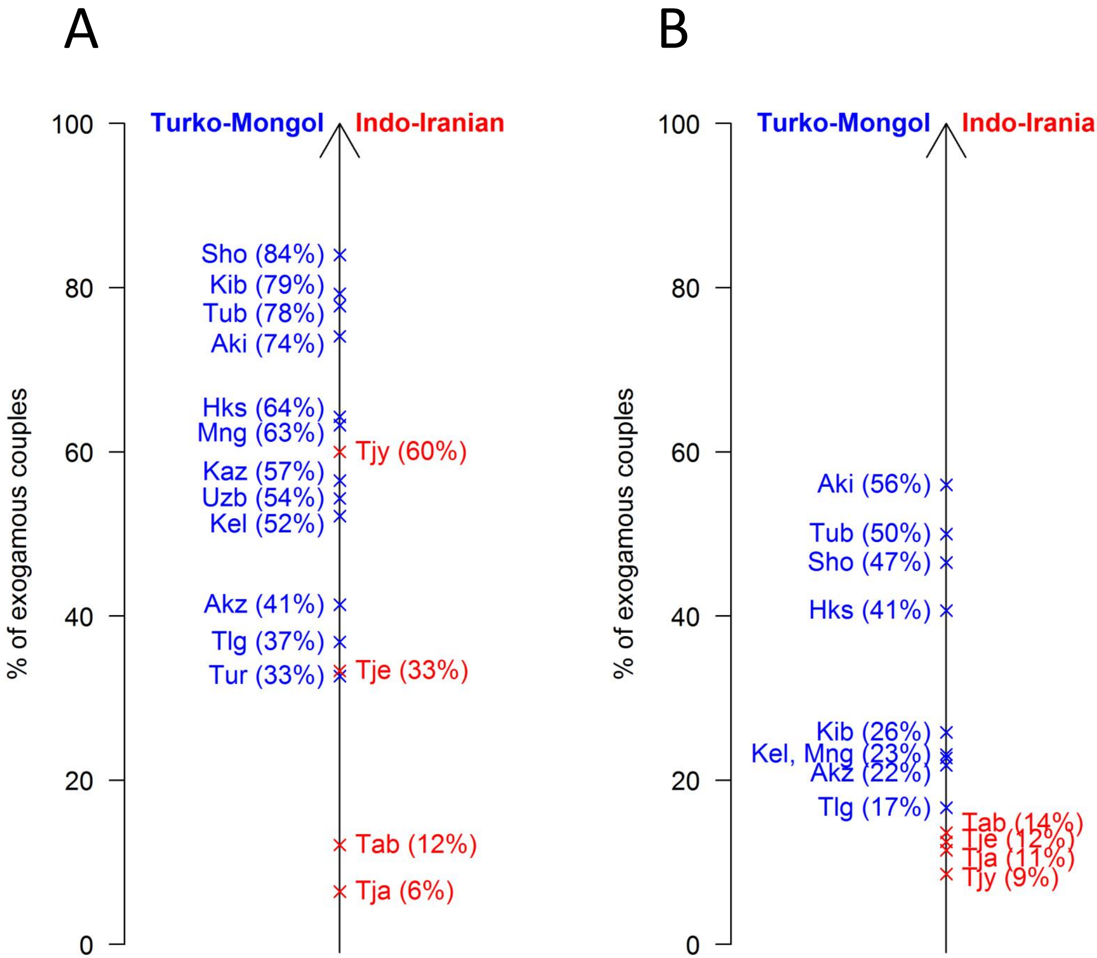

Figure S1 – Population exogamy rate.
Percentage of exogamous couples with a distance between the mates' birth places >4 km for the sampled couples (A), or their parents (B).

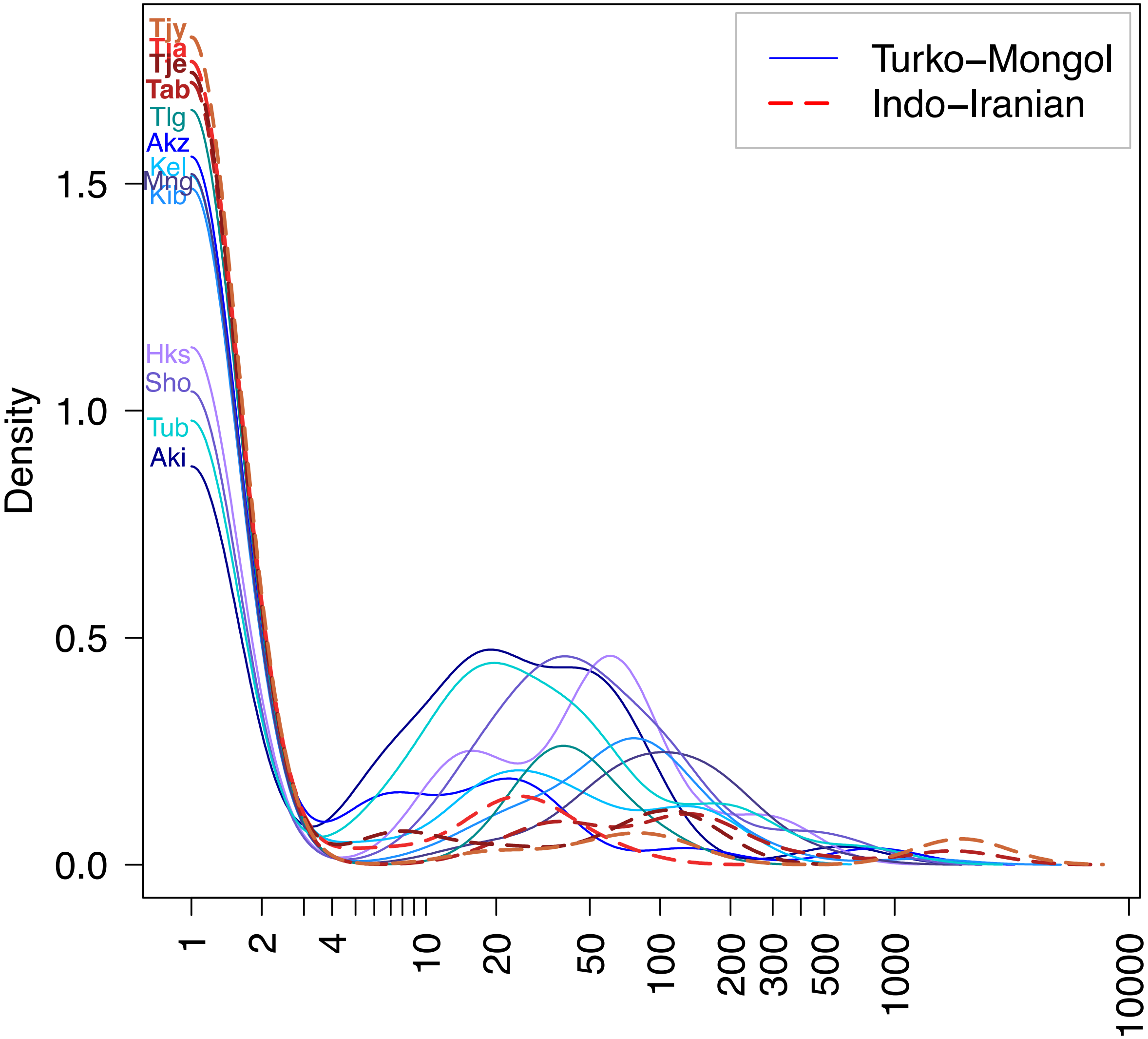

Figure S2 – Geographical distances between parents' birth places.
The distances are plotted in log scale (km).

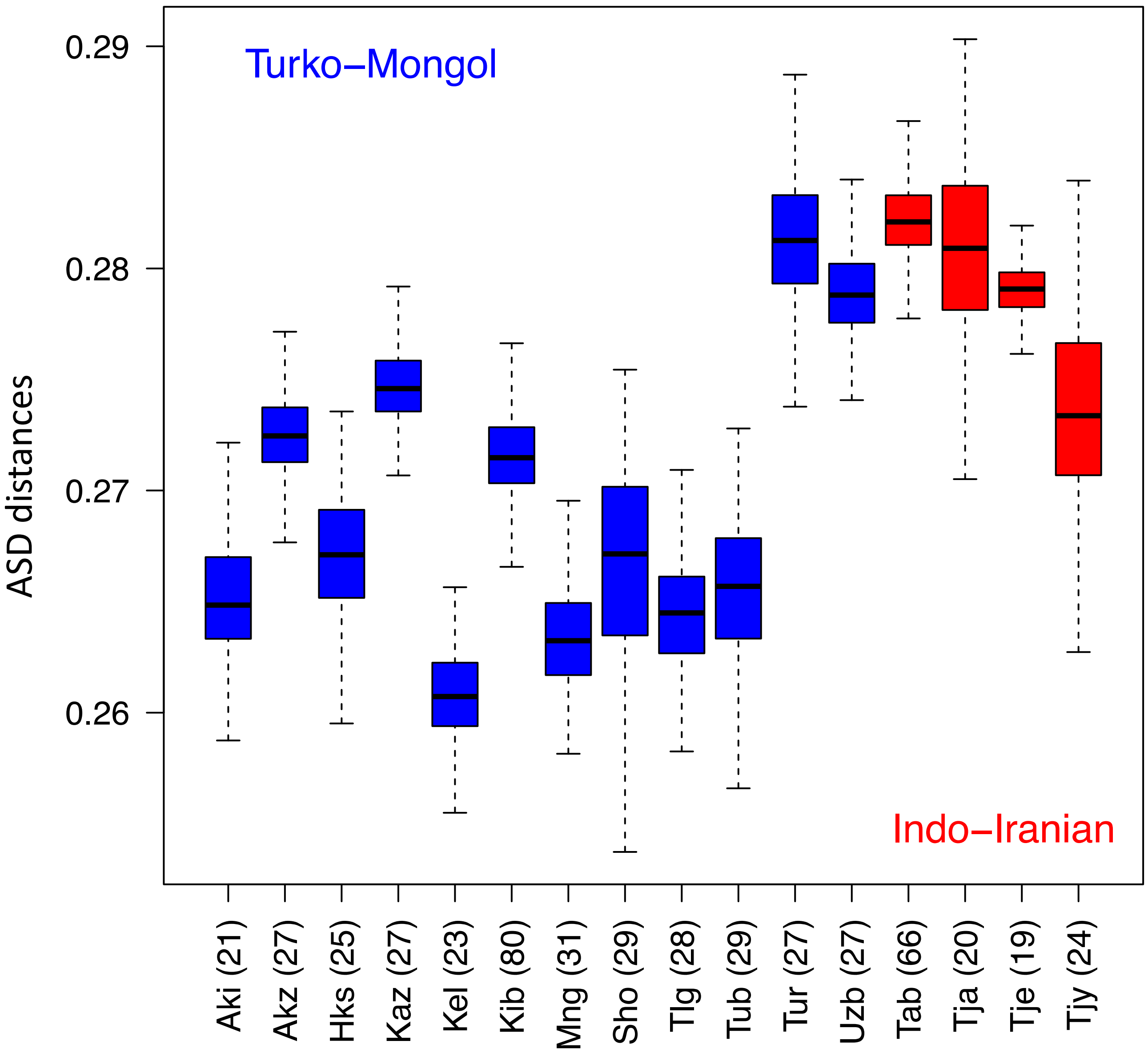

Figure S3 – ASD distances computed for pairs of individuals within population.
The number of samples by population is indicated after their name.

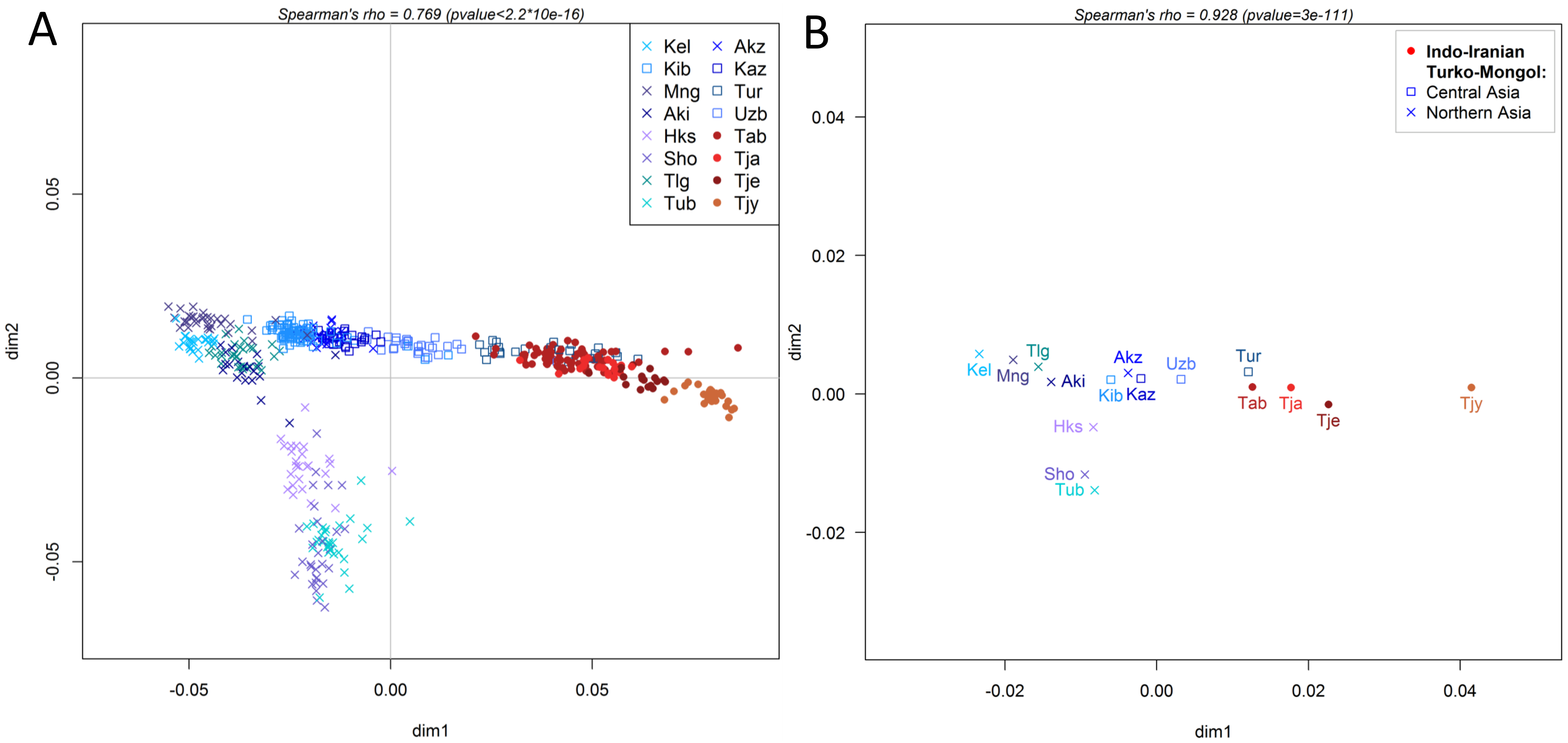

Figure S4 – Multidimensional Scaling (MDS) plot over individuals pairwise ASD distances (A), and populations pairwise F_{ST} distances (B). Only the two first dimensions are represented. Each Spearman's coefficient of correlation (*rho*) was calculated between the MDS matrix and the pairwise genetic distances matrix.

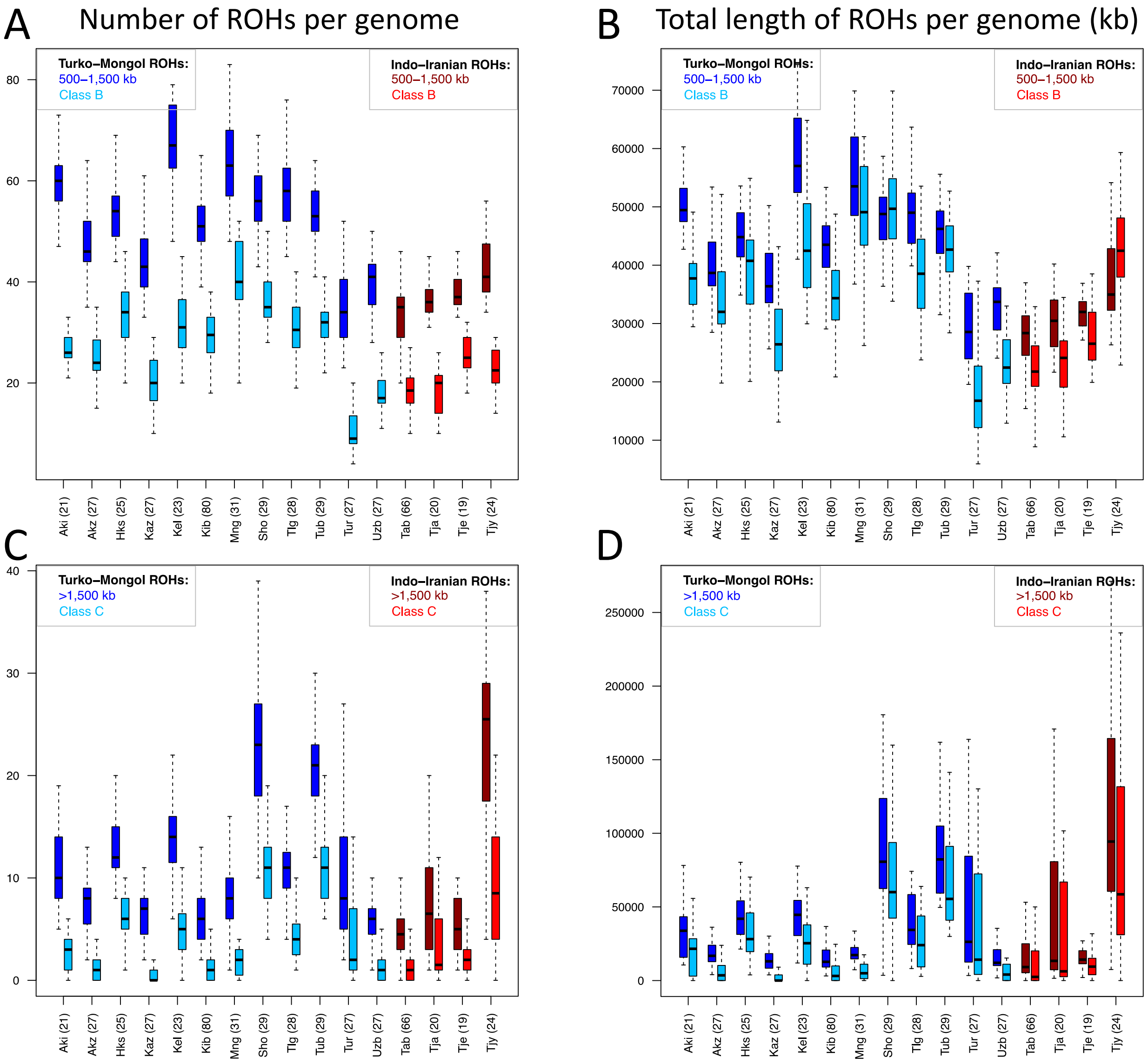

Figure S5 – Populations pattern of intermediate sized ROHs (length between 500 and 1500 kb, or class B) (top) and long sized ROHs (larger than 1500 kb or class C) (bottom).
Information is summarized by the number of segments per individual genome (A and C), or their total length by genome (B and D, in kb), and represented for each population. The number of genomes by population is indicated after their name.

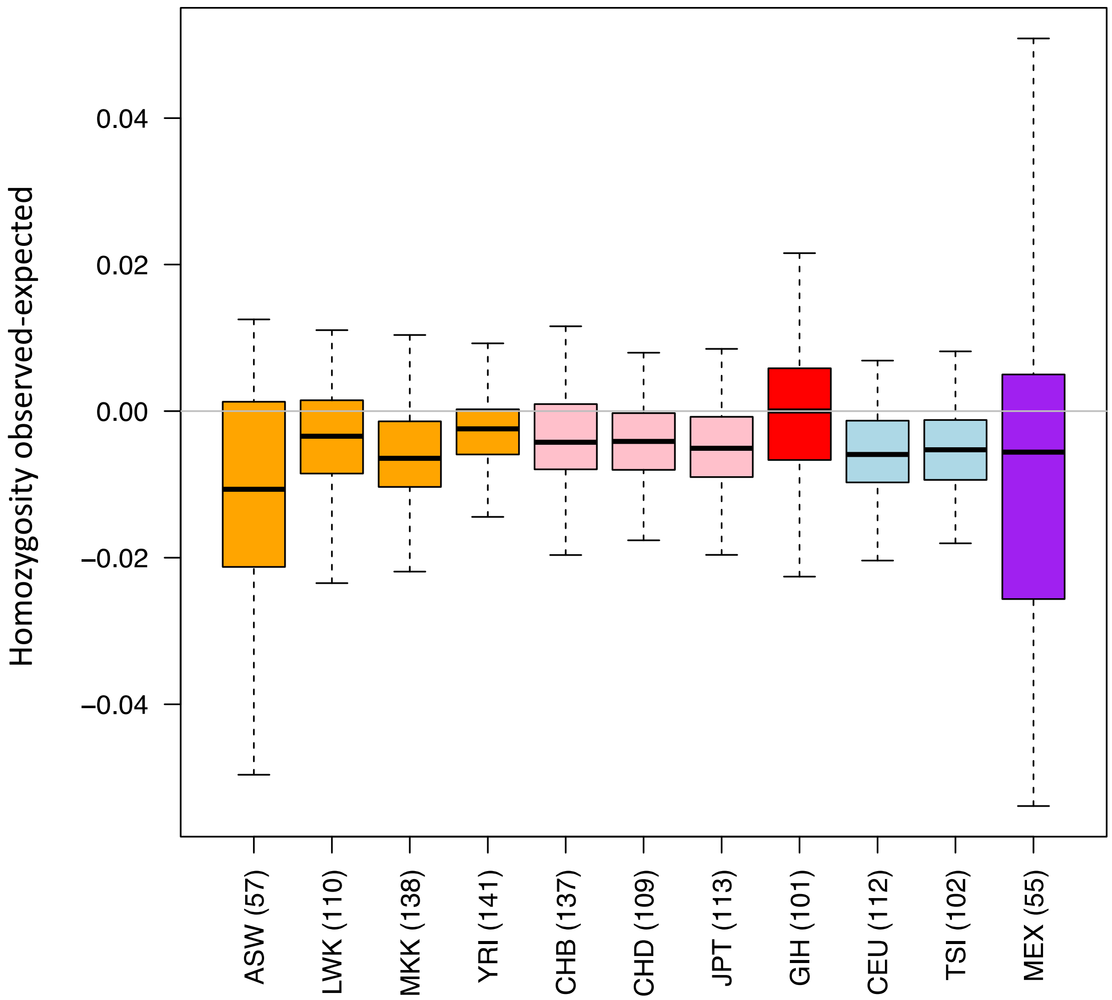

Figure S6 – Inbreeding avoidance within HapMap3 populations
Differences between the observed homozygosity within individual genomes and the population baseline, expected under panmixia. Number of samples by population is indicated after their name.

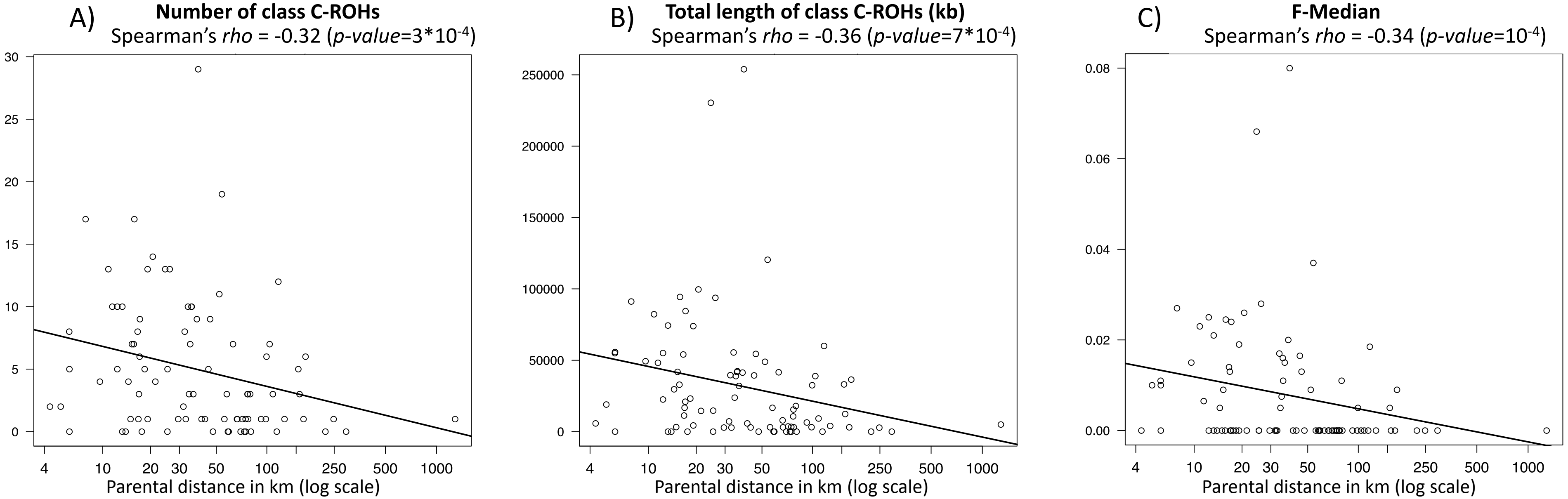

Figure S7 – Inbreeding and parental couple distance for the offspring of exogamous Turko-Mongol couples.
Three estimators of inbreeding are plotted against the distances between parents' birth places of exogamous couples. These two variables were correlated based on Spearman's correlation test (illustrated as a regression line on the plot).

Table S1 A - Genetic diversity, inbreeding and exogamy pattern within populations.

Population:		**Aki**	**Akz**	**Hks**	**Kaz**	**Kel**	**Kib**	**Mng**	**Sho**	**Tlg**	**Tub**	**Tur**	**Uzb**	**Tab**	**Tja**	**Tje**	**Tjy**
Genetic dataset sample size (N)	Females	9	11	15	0	11	40	15	12	13	11	0	0	35	0	0	0
	Males	12	16	10	27	12	40	16	17	15	18	27	27	31	20	19	24
	Couples	4	4	2	0	8	38	14	5	12	4	0	0	24	0	0	0
ASD between individuals	Mean distance	0.228	0.236	0.230	0.238	0.224	0.235	0.227	0.229	0.223	0.228	0.247	0.243	0.249	0.247	0.246	0.240
	s.d.	*0.005*	*0.003*	*0.003*	*0.002*	*0.004*	*0.002*	*0.003*	*0.005*	*0.004*	*0.005*	*0.004*	*0.002*	*0.002*	*0.005*	*0.005*	*0.007*
Haplotypic heterozygosity	Mean	0.673	0.691	0.681	0.699	0.663	0.692	0.670	0.676	0.673	0.678	0.712	0.710	0.721	0.709	0.709	0.691
	s.d.	*0.017*	*0.013*	*0.018*	*0.015*	*0.019*	*0.015*	*0.016*	*0.020*	*0.018*	*0.019*	*0.013*	*0.013*	*0.014*	*0.014*	*0.011*	*0.017*
ROH limits	Limit A-B (kb)	931	863	791	946	928	808	773	859	847	870	1107	889	813	858	709	1117
	Limit B-C (kb)	2748	2768	2239	2896	2569	2596	2410	2641	2461	2546	3243	2604	2400	2490	2119	3642
Individual F-Median	Median	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.019	0.000	0.015	0.000	0.000	0.000	0.000	0.000	0.022
	s.d.	*0.0066*	*0.0040*	*0.0089*	*0.0129*	*0.0067*	*0.0080*	*0.0030*	*0.0178*	*0.0073*	*0.0134*	*0.0232*	*0.0137*	*0.0122*	*0.0171*	*0.0014*	*0.0263*
	Positive F-Median (%)	33%	22%	48%	15%	43%	14%	10%	83%	46%	90%	48%	19%	29%	35%	11%	79%
Type of parental relatedness	Outbred (%)	76	85	60	85	61	89	90	21	57	17	52	81	74	65	95	21
	2C-type (%)	24	15	40	7	39	10	10	69	43	76	30	15	20	30	5	54
	1C-type (%)	0	0	0	7	0	1	0	10	0	7	19	4	6	5	0	21
	2x1C-type (%)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4
Individuals with a deficit in homozygosity		100% (21/21)	100% (27/27)	96% (24/25)	89% (24/27)	91% (21/23)	76% (61/80)	90% (28/31)	79% (23/29)	93% (26/28)	90% (26/29)	70% (19/27)	89% (24/27)	68% (45/66)	85% (17/20)	100% (19/19)	75% (18/24)
Distances between partners' birth places	Couples in the ethnological dataset (N)	27	29	28	46	23	82	49	25	19	27	52	46	66	31	27	35
	Median (km)	15	0	22	40	13	48	58	46	0	23	0	12	0	0	0	18
	0-95% (km)	0-67	0-26	0-123	0-607	0-149	0-261	0-180	0-252	0-74	0-576	0-163	0-264	0-43	0-3	0-137	0-111
	Exogamous couples (%)	74	41	64	57	52	79	63	84	37	78	33	54	12	6	33	60

Table S1 B – Geographical and ethnological information about the populations under study.

Population:	**Aki**	**Akz**	**Hks**	**Kaz**	**Kel**	**Kib**	**Mng**	**Sho**	**Tlg**	**Tub**	**Tur**	**Uzb**	**Tab**	**Tja**	**Tje**	**Tjy**
Cultural group	Turko-Mongol	Turko-Mongol	Turko-Mongol	Turko-Mongol	Turko-Mongol	Turko-Mongol	Turko-Mongol	Turko-Mongol	Turko-Mongol	Turko-Mongol	Turko-Mongol	Turko-Mongol	Indo-Iranian	Indo-Iranian	Indo-Iranian	Indo-Iranian
Ethnic Group	Altai-Kizhi	Kazakh	Khakas	Kazakh	Kyrgyz	Kyrgyz	Mongol	Shor	Telengit	Tubalar	Turkmen	Uzbek	Tajik	Tajik	Tajik	Tajik-Yagnob
Location	Kulady, Russia	Kosh-Agach, Russia	Kazanovka, Russia	Qongirat area, UZB	Erzin & Chagonar area, Russia	Bishkek, KYR.	Khovd, Mongolia	Mezhdurechensk, Russia	Kokorja, Russia	Kebezen, Russia	Tortkul area, UZB	Qongirat area, UZB	Bukhara, UZB.	Agalyk, UZB	Nimich, TAJ	Dughoba, TAJ
Altitude (m)	1150	1784	473	59	1028	755	1916	261	1857	420	101	59	229	825	2064	825
Ecosystem	Steppe	Steppe	Steppe	Desert	Steppe	Plain	Steppe	Forest	Steppe	Forest	Desert	Desert	Plain	Mountain	Mountain	Mountain
Lifestyle	Rural	Rural	Rural	Rural	Rural	Urban	Urban	Rural	Rural	Rural	Rural	Rural	Urban	Rural	Rural	Rural
	Traditionally; Turko-Mongol are semi-nomadic herders.												Traditionally; Indo-Iranians are sedentary agriculturists			

UZB: Uzbekistan, KYR: Kyrgyzstan, TAJ: Tajikistan.

Table S2 - Fst pairwise differences

	Aki	**Akz**	**Bou**	**Hks**	**Kaz**	**Kel**	**Kib**	**Mng**	**Sho**	**Tab**	**Tja**	**Tje**	**Tjy**	**Tlg**	**Tub**	**Tur**	**Uzb**
Aki	0	0.00784	0.0141	0.01318	0.00759	0.00832	0.00581	0.00694	0.01977	0.0297	0.03801	0.04463	0.06432	0.00674	0.01975	0.02978	0.01233
Akz	0.00784	0	0.01418	0.01083	0.00194	0.01096	0.00194	0.00609	0.01739	0.01716	0.02459	0.02993	0.04887	0.00876	0.01941	0.01772	0.00428
Bou	0.0141	0.01418	0	0.02251	0.01487	0.01218	0.01095	0.00784	0.03033	0.04484	0.05491	0.06336	0.0837	0.01456	0.03369	0.04465	0.02233
Hks	0.01318	0.01083	0.02251	0	0.01016	0.01591	0.00986	0.01458	0.00971	0.02488	0.03199	0.03702	0.05602	0.01436	0.01964	0.02582	0.01225
Kaz	0.00759	0.00194	0.01487	0.01016	0	0.01094	0.00151	0.00639	0.01625	0.01426	0.02113	0.02637	0.04483	0.0087	0.0179	0.01499	0.00221
Kel	0.00832	0.01096	0.01218	0.01591	0.01094	0	0.00767	0.00559	0.02376	0.03876	0.04828	0.0559	0.07631	0.00803	0.0272	0.03847	0.0179
Kib	0.00581	0.00194	0.01095	0.00986	0.00151	0.00767	0	0.00327	0.01628	0.01979	0.02728	0.03317	0.05199	0.00648	0.0184	0.02008	0.00487
Mng	0.00694	0.00609	0.00784	0.01458	0.00639	0.00559	0.00327	0	0.0221	0.03462	0.04399	0.05191	0.07216	0.00739	0.02504	0.0343	0.0134
Sho	0.01977	0.01739	0.03033	0.00971	0.01625	0.02376	0.01628	0.0221	0	0.02865	0.03565	0.04011	0.05865	0.02127	0.02091	0.02996	0.01759
Tab	0.0297	0.01716	0.04484	0.02488	0.01426	0.03876	0.01979	0.03462	0.02865	0	0.00429	0.00472	0.01918	0.03131	0.02869	0.00383	0.00651
Tja	0.03801	0.02459	0.05491	0.03199	0.02113	0.04828	0.02728	0.04399	0.03565	0.00429	0	0.00676	0.02183	0.04004	0.03537	0.00817	0.01245
Tje	0.04463	0.02993	0.06336	0.03702	0.02637	0.0559	0.03317	0.05191	0.04011	0.00472	0.00676	0	0.01975	0.04686	0.03994	0.00932	0.01615
Tjy	0.06432	0.04887	0.0837	0.05602	0.04483	0.07631	0.05199	0.07216	0.05865	0.01918	0.02183	0.01975	0	0.06654	0.05766	0.02475	0.03336
Tlg	0.00674	0.00876	0.01456	0.01436	0.0087	0.00803	0.00648	0.00739	0.02127	0.03131	0.04004	0.04686	0.06654	0	0.02297	0.03143	0.01354
Tub	0.01975	0.01941	0.03369	0.01964	0.0179	0.0272	0.0184	0.02504	0.02091	0.02869	0.03537	0.03994	0.05766	0.02297	0	0.02998	0.01869
Tur	0.02978	0.01772	0.04465	0.02582	0.01499	0.03847	0.02008	0.0343	0.02996	0.00383	0.00817	0.00932	0.02475	0.03143	0.02998	0	0.00801
Uzb	0.01233	0.00428	0.02233	0.01225	0.00221	0.0179	0.00487	0.0134	0.01759	0.00651	0.01245	0.01615	0.03336	0.01354	0.01869	0.00801	0

All pairwise distances were significant with *p-values* = 0.00000 (+-0.0000) for 1023 permutations.

Table S3 - Description of the genotyped dataset

SampleID	Sex	Array
AKI001	2	Omni1Quad
AKI002	1	Omni1Quad
AKI009	2	Omni1Quad
AKI010	1	Omni1Quad
AKI011	1	Omni1Quad
AKI014	2	Omni1Quad
AKI016	2	Omni1Quad
AKI022	1	Omni1Quad
AKI024	2	Omni1Quad
AKI026	1	Omni1Quad
AKI027	1	Omni1Quad
AKI028	2	Omni1Quad
AKI031	1	Omni1Quad
AKI032	2	Omni1Quad
AKI036	1	Omni1Quad
AKI037	2	Omni1Quad
AKI038	1	Omni1Quad
AKI039	1	Omni1Quad
AKI042	2	Omni1Quad
AKI043	1	Omni1Quad
AKI045	1	Omni1Quad
AKZ002	1	Omni1Quad
AKZ003	1	Omni1Quad
AKZ004	2	Omni1Quad
AKZ005	2	Omni1Quad
AKZ006	1	Omni1Quad
AKZ009	1	Omni1Quad
AKZ010	2	Omni1Quad
AKZ012	2	Omni1Quad
AKZ013	2	Omni1Quad
AKZ014	1	Omni1Quad
AKZ015	2	Omni1Quad
AKZ016	1	Omni1Quad
AKZ017	2	Omni1Quad
AKZ018	1	Omni1Quad
AKZ019	2	Omni1Quad
AKZ020	1	Omni1Quad
AKZ021	1	Omni1Quad
AKZ022	1	Omni1Quad
AKZ026	1	Omni1Quad
AKZ028	2	Omni1Quad
AKZ029	1	Omni1Quad
AKZ030	2	Omni1Quad

AKZ035	1	Omni1Quad
AKZ038	1	Omni1Quad
AKZ040	2	Omni1Quad
AKZ043	1	Omni1Quad
AKZ044	1	Omni1Quad
HKS003	2	Omni1Quad
HKS004	2	Omni1Quad
HKS007	2	Omni1Quad
HKS008	2	Omni1Quad
HKS009	1	Omni1Quad
HKS010	2	Omni1Quad
HKS011	2	Omni1Quad
HKS013	2	Omni1Quad
HKS014	2	Omni1Quad
HKS016	2	Omni1Quad
HKS017	2	Omni1Quad
HKS019	1	Omni1Quad
HKS020	2	Omni1Quad
HKS021	2	Omni1Quad
HKS023	2	Omni1Quad
HKS024	2	Omni1Quad
HKS026	1	Omni1Quad
HKS027	2	Omni1Quad
HKS028	1	Omni1Quad
HKS034	1	Omni1Quad
HKS035	1	Omni1Quad
HKS038	1	Omni1Quad
HKS039	1	Omni1Quad
HKS042	1	Omni1Quad
HKS043	1	Omni1Quad
KAZ001	1	Omni1Quad
KAZ002	1	Omni1Quad
KAZ003	1	Omni1Quad
KAZ004	1	Omni1Quad
KAZ005	1	Omni1Quad
KAZ006	1	Omni1Quad
KAZ007	1	Omni1Quad
KAZ008	1	Omni1Quad
KAZ013	1	Omni1Quad
KAZ015	1	Omni1Quad
KAZ016	1	Omni1Quad
KAZ017	1	Omni1Quad
KAZ018	1	Omni1Quad
KAZ019	1	Omni1Quad
KAZ021	1	Omni1Quad
KAZ022	1	Omni1Quad

KAZ025	1	Omni1Quad
KAZ026	1	Omni1Quad
KAZ028	1	Omni1Quad
KAZ030	1	Omni1Quad
KAZ032	1	Omni1Quad
KAZ033	1	Omni1Quad
KAZ036	1	Omni1Quad
KAZ038	1	Omni1Quad
KAZ039	1	Omni1Quad
KAZ040	1	Omni1Quad
KAZ042	1	Omni1Quad
KEK001	2	Omni2.5
KEK002	1	Omni2.5
KEK003	2	Omni2.5
KEK006	1	Omni2.5
KEK007	1	Omni2.5
KEK008	2	Omni2.5
KEK009	2	Omni2.5
KEK010	1	Omni2.5
KEK014	1	Omni2.5
KEK015	2	Omni2.5
KEK018	1	Omni2.5
KEK019	2	Omni2.5
KEM001	2	Omni2.5
KEM002	1	Omni2.5
KEM007	1	Omni2.5
KEM008	2	Omni2.5
KEM009	2	Omni2.5
KEM010	1	Omni2.5
KEM013	2	Omni2.5
KEM016	1	Omni2.5
KEM017	1	Omni2.5
KEM019	2	Omni2.5
KEM020	1	Omni2.5
KIB001	2	660W-Quad
KIB003	2	Omni1Quad
KIB004	1	Omni1Quad
KIB005	1	Omni1Quad
KIB006	2	Omni1Quad
KIB007	2	660W-Quad
KIB008	1	660W-Quad
KIB010	1	Omni1Quad
KIB011	2	Omni1Quad
KIB012	2	660W-Quad
KIB013	1	660W-Quad
KIB015	2	Omni1Quad

KIB016	1	660W-Quad
KIB017	1	660W-Quad
KIB018	2	660W-Quad
KIB021	1	660W-Quad
KIB022	1	660W-Quad
KIB024	2	660W-Quad
KIB025	1	Omni1Quad
KIB026	2	Omni1Quad
KIB027	1	660W-Quad
KIB028	1	660W-Quad
KIB029	1	660W-Quad
KIB030	1	660W-Quad
KIB031	2	660W-Quad
KIB032	2	660W-Quad
KIB033	1	660W-Quad
KIB034	2	Omni1Quad
KIB035	1	660W-Quad
KIB036	2	660W-Quad
KIB037	2	Omni1Quad
KIB038	1	660W-Quad
KIB039	1	Omni1Quad
KIB040	2	660W-Quad
KIB041	1	660W-Quad
KIB042	1	660W-Quad
KIB043	1	Omni1Quad
KIB044	2	660W-Quad
KIB045	2	Omni1Quad
KIB046	2	Omni1Quad
KIB047	1	Omni1Quad
KIB049	2	660W-Quad
KIB050	2	Omni1Quad
KIB051	2	Omni1Quad
KIB052	1	Omni1Quad
KIB053	2	Omni1Quad
KIB054	1	660W-Quad
KIB057	2	Omni1Quad
KIB058	1	Omni1Quad
KIB060	1	Omni1Quad
KIB061	2	Omni1Quad
KIB064	1	Omni1Quad
KIB065	2	Omni1Quad
KIB066	1	Omni1Quad
KIB067	2	Omni1Quad
KIB068	1	Omni1Quad
KIB070	2	660W-Quad
KIB071	1	660W-Quad

KIB072	2	660W-Quad
KIB074	1	660W-Quad
KIB077	2	660W-Quad
KIB083	2	660W-Quad
KIB084	1	660W-Quad
KIB092	2	660W-Quad
KIB093	1	660W-Quad
KIB103	1	660W-Quad
KIB104	2	660W-Quad
KIB105	1	Omni1Quad
KIB106	2	Omni1Quad
KIB107	1	660W-Quad
KIB109	2	660W-Quad
KIB110	1	Omni1Quad
KIB126	1	Omni1Quad
KIB127	2	660W-Quad
KIB128	1	660W-Quad
KIB136	2	660W-Quad
KIB138	2	660W-Quad
KIB149	2	660W-Quad
KIB152	1	660W-Quad
KIB153	2	Omni1Quad
MNG014	2	Omni2.5
MNG015	1	Omni2.5
MNG048	1	Omni2.5
MNG054	2	Omni2.5
MNG055	1	Omni2.5
MNG057	2	Omni2.5
MNG058	1	Omni2.5
MNG059	2	Omni2.5
MNG060	2	Omni2.5
MNG061	1	Omni2.5
MNG062	2	Omni2.5
MNG063	1	Omni2.5
MNG066	2	Omni2.5
MNG067	1	Omni2.5
MNG070	1	Omni2.5
MNG071	2	Omni2.5
MNG072	1	Omni2.5
MNG073	2	Omni2.5
MNG074	1	Omni2.5
MNG075	2	Omni2.5
MNG076	1	Omni2.5
MNG077	2	Omni2.5
MNG078	1	Omni2.5
MNG079	1	Omni2.5

MNG080	1	Omni2.5
MNG081	2	Omni2.5
MNG082	1	Omni2.5
MNG083	2	Omni2.5
MNG088	2	Omni2.5
MNG089	1	Omni2.5
MNG090	1	Omni2.5
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SHO003	2	Omni1Quad
SHO004	2	Omni1Quad
SHO006	2	Omni1Quad
SHO007	1	Omni1Quad
SHO008	1	Omni1Quad
SHO011	1	Omni1Quad
SHO013	2	Omni1Quad
SHO014	1	Omni1Quad
SHO015	1	Omni1Quad
SHO016	2	Omni1Quad
SHO019	1	Omni1Quad
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SHO021	2	Omni1Quad
SHO022	2	Omni1Quad
SHO023	1	Omni1Quad
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SHO034	2	Omni1Quad
SHO035	1	Omni1Quad
SHO036	2	Omni1Quad
SHO038	1	Omni1Quad
SHO039	1	Omni1Quad
SHO040	1	Omni1Quad
SHO041	1	Omni1Quad
SHO042	1	Omni1Quad
TAB001	2	660W-Quad
TAB002	1	660W-Quad
TAB005	1	Omni1Quad
TAB006	1	660W-Quad
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TAB011	2	660W-Quad
TAB012	2	660W-Quad
TAB013	1	Omni1Quad
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TAB015	1	660W-Quad

TAB017	2	660W-Quad
TAB018	1	660W-Quad
TAB019	2	Omni1Quad
TAB020	1	660W-Quad
TAB021	2	660W-Quad
TAB022	1	660W-Quad
TAB023	2	660W-Quad
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TAB036	2	660W-Quad
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TAB057	2	Omni1Quad
TAB058	1	660W-Quad
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TAB060	2	Omni1Quad
TAB061	1	Omni1Quad
TAB062	2	Omni1Quad
TAB063	1	660W-Quad
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TAB066	2	660W-Quad
TAB074	2	Omni1Quad
TAB075	1	660W-Quad
TAB076	2	660W-Quad
TAB077	2	Omni1Quad
TAB078	1	Omni1Quad
TAB079	1	Omni1Quad
TAB080	2	Omni1Quad
TAB081	1	660W-Quad
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TAB087	1	Omni1Quad
TAB088	2	660W-Quad
TAB092	2	660W-Quad
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TAB104	1	Omni1Quad
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TAB112	2	Omni1Quad
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TJA02	1	OmniExpress
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TJA17	1	OmniExpress
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TJA19	1	OmniExpress
TJA20	1	OmniExpress
TJA21	1	OmniExpress
TJA_31	1	Omni5Exome
TJE_1	1	OmniExpress
TJE_10	1	OmniExpress
TJE_11	1	OmniExpress
TJE_12	1	OmniExpress
TJE_13	1	OmniExpress
TJE_14	1	OmniExpress
TJE_15	1	OmniExpress
TJE_16	1	OmniExpress
TJE_17	1	OmniExpress
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TJE_19	1	OmniExpress
TJE_21	1	OmniExpress
TJE_22	1	OmniExpress
TJE_4	1	OmniExpress
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TJE_7	1	OmniExpress
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TJE_9	1	OmniExpress
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TLG001	1	Omni1Quad
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TLG020	1	Omni1Quad
TLG021	1	Omni1Quad
TLG022	2	Omni1Quad
TLG023	1	Omni1Quad

TLG024	2	Omni1Quad
TLG025	2	Omni1Quad
TLG026	1	Omni1Quad
TLG029	2	Omni1Quad
TLG030	1	Omni1Quad
TLG031	2	Omni1Quad
TLG032	1	Omni1Quad
TLG034	1	Omni1Quad
TLG036	1	Omni1Quad
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TUB003	2	Omni1Quad
TUB004	1	Omni1Quad
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TUR012	1	Omni1Quad
TUR013	1	Omni1Quad
TUR016	1	Omni1Quad
TUR018	1	Omni1Quad

TUR025	1	Omni1Quad
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TUR027	1	Omni1Quad
TUR028	1	Omni1Quad
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TUR043	1	Omni1Quad
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TUR050	1	Omni1Quad
TUR051	1	Omni1Quad
TUR054	1	Omni1Quad
UZB002	1	Omni1Quad
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UZB005	1	Omni1Quad
UZB013	1	Omni1Quad
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UZB019	1	Omni1Quad
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UZB023	1	Omni1Quad
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UZB029	1	Omni1Quad
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UZB036	1	Omni1Quad
UZB038	1	Omni1Quad
UZB039	1	Omni1Quad
UZB040	1	Omni1Quad
UZB041	1	Omni1Quad
UZB046	1	Omni1Quad
UZB048	1	Omni1Quad
UZB049	1	Omni1Quad
UZB050	1	Omni1Quad