SUPPLEMENTARY MATERIAL

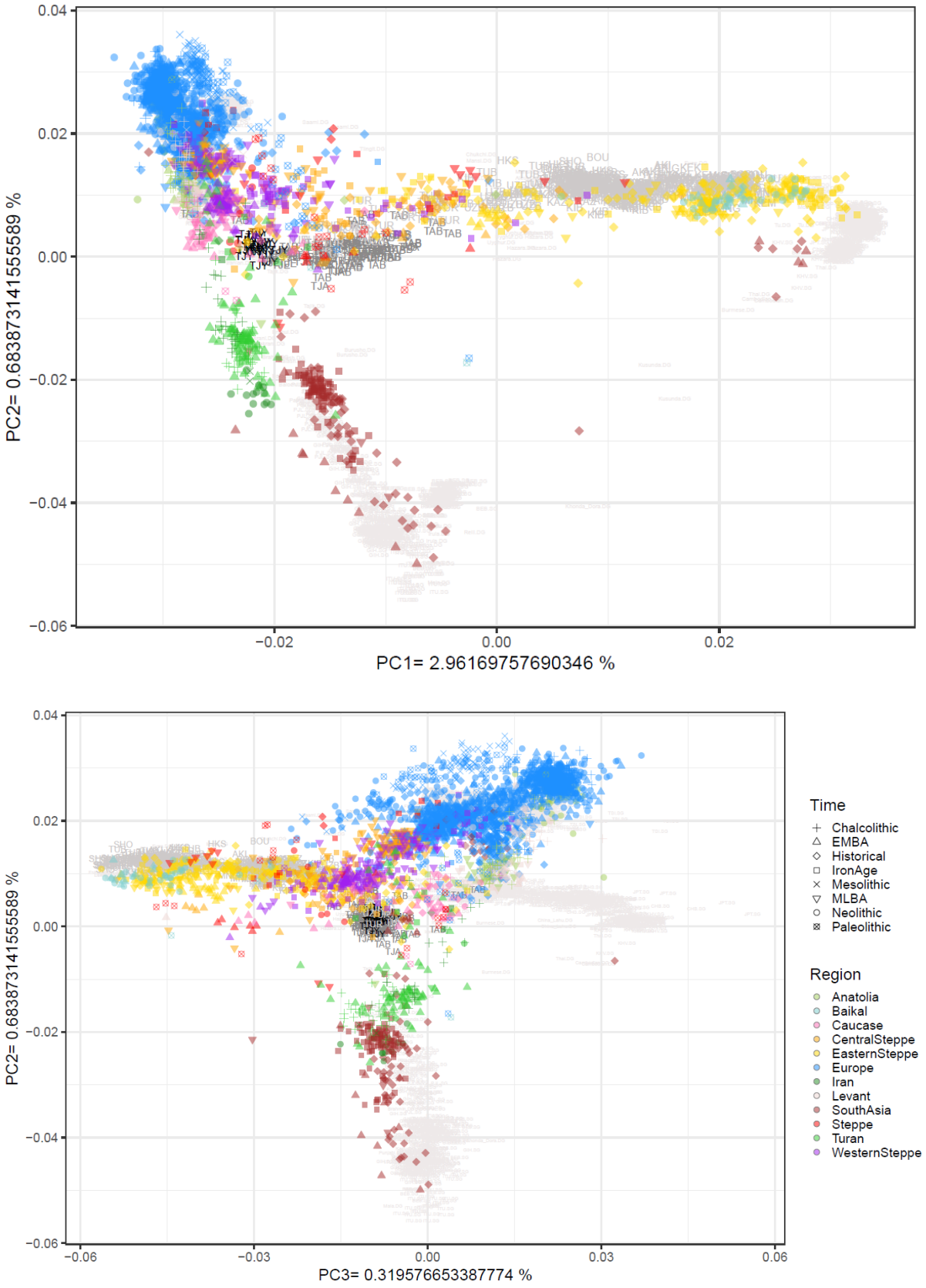

Figure S1. Full PCA computed on 1915 modern genomes, with projection of 3102 ancient genomes

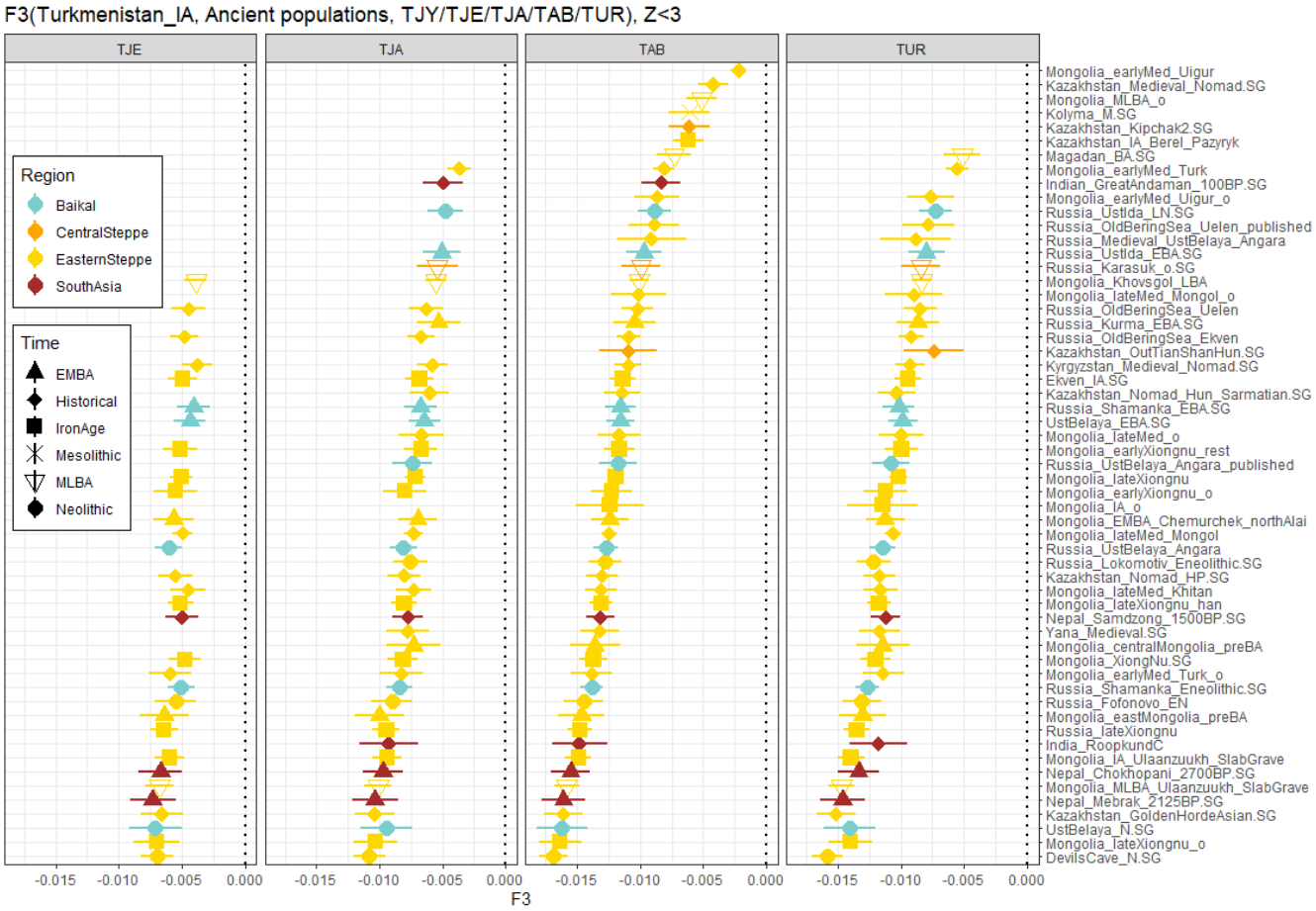

Figure S2. All the significatively negative admixture f3-statistics in the form f3(*Turkmenistan_IA*, *Ancient population*, TJY/TJE/TJA/TAB/TUR) calculated on the first dataset. We did not obtain significative f3 for TJY.

Figure S3 – Full ADMIXTURE analysis for all ancient individuals

Figure S4 – Full ADMIXTURE analysis for all present-day individuals

Table S1 – Contextual information for published ancient genome-wide data

Table S2 – Contextual information for published modern genomes from all Eurasia

Table S3 – Contextual information for modern genome-wide data from Central Asia (300k SNPs array)

Table S4 – Contextual information for modern genome from Central Asia (Shotgun)

Table S5 – All D-stat of the form D(Mbuti, Ancient pop; Iron Age Turan, TAB/TJA/TJE/TJY/TUR)

Table S6 – All f3-admixture of the form f3(Ancient pop, Iron Age Turan; TAB/TJA/TJE/TJY/TUR)

Table S7 - Significantly negative f3-admixture of the form f3(Ancient Pop1, Ancient Pop2; TJY/TJE/TJA/TAB)

Table S8 – All f3-outgroup of the form f3(Ancient pop, Central Asia pop; Outgroup)