



Figure 2. Gene flow from EAFR goats into SWA goat populations.

(a) F -branch (f_b) summary of introgression among the eight goat populations. The ML tree was used as a basis for the branch statistic. Each cell shows the f_b statistic between tree nodes (rows) and terminal nodes (column). The tree nodes in the rows represent terminal nodes or (dotted lines) internal nodes within the tree. Grey cells in the matrix correspond to tests that are not consistent with the phylogeny. (b) Inferred goat tree of mixture events deduced by TreeMix. The branch length is proportional to the drift of each population and the scale bar shows 10 times the average standard error (S.E.) of the entries in the sample covariance matrix. Argali was used as the outgroup to root the tree. (c and d) The distribution of introgressed segments from EAFR, serving as proxy of the source of introgression from Levant, into the IRQ and IRN goat populations.