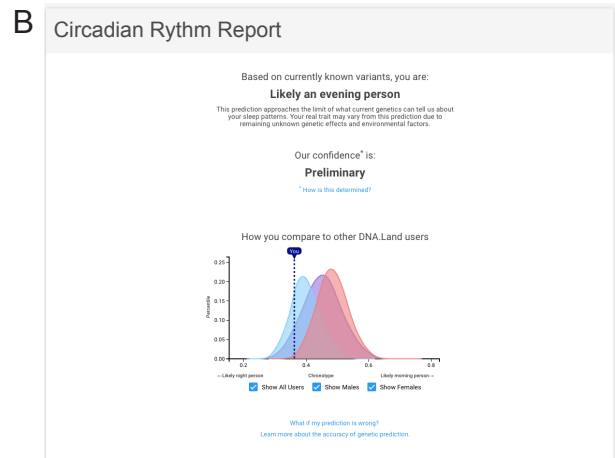
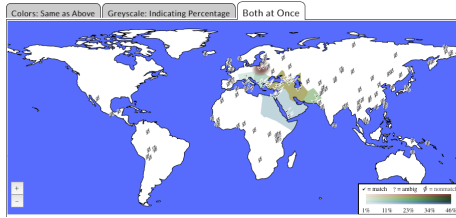
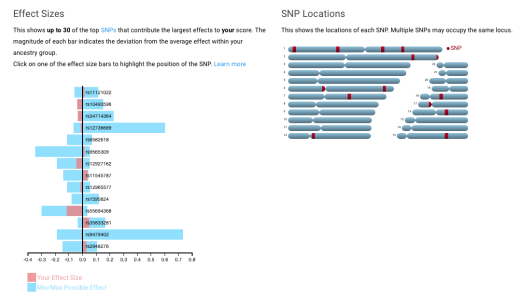


Ancestry Map



Genotype Summary



C Matching Relatives

Showing up to 50 matches (why?).
[Learn more about the report.](#)

High Certainty Matches

Matching Relative	Relationship Degree	# Shared Segments	Total Shared Length (cM)	Total Recomb Shared Length (cM)	Longest Recomb Shared Segment (cM)	Relationship Likelihood	Long Shared Segments
Name: Maya Anand Email: may2112@icloud.com	0 1/2	28	3493.87	3493.78	243.82		
Name: Sam Dzhurayev Email: samdzurayev@icloud.com	2 1/4	30	138.84	46.62	13.28		
Name: Charis Petropoulos Email: rianvgenov@textsys.com	7 1/8	24	112.93	36.93	14.83		

Supplemental Figure 1: A sampling of reports viewable from users' profiles on the DNA.Land website after submission of genotype data. **(A)** Ancestry Report based on a STRUCTURE-like algorithm and a specialized reference of world-wide populations **(B)** Trait Prediction Report. Predictions are calculated from published GWAS summary statistics and users' imputed genomes. The report also displays the distribution of DNA.Land predicted scores and the effect sizes and locations of relevant SNPs. **(C)** Relative Matching report. Relative matching is based on finding shared IBD segments and calculating the most likely genealogical relationship. Each row of the report indicates a matching user and statistics relevant to the match such as degree of relatedness, total length of matching segments, the likelihood distribution on the degree of relatedness, and a display of the location of matching segments on the chromosomes.