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Figure S5. Average expression in populations for the 9 genes which were significant for Race x Latitude interaction in the 2-way ANOVA

Table S1. Allelic frequencies in the four sampled populations for the six intron RFLP markers scored. N is the sample size.

Locus	Allele	Locality			
		AN	AS	MS	MN
CL116-ia	A	0,667	0,679	0,789	0,732
	B	0,333	0,321	0,211	0,268
	N	24	56	19	41
CL13-ia	A	0,958	0,797	0,842	0,922
	B	0,042	0,203	0,158	0,078
	N	24	59	19	45
CL102-ia	A	0,292	0,682	0,611	0,257
	B	0,708	0,318	0,389	0,743
	N	24	55	18	35
CL126-ia	A	0,667	0,745	0,289	0,128
	B	0,333	0,255	0,605	0,802
	C	0,000	0,000	0,105	0,058
	D	0,000	0,000	0,000	0,012
	N	21	51	19	43
TBP	A	0,283	0,202	0,553	0,677
	B	0,717	0,798	0,447	0,290
	C	0,000	0,000	0,000	0,032
	D	-	-	-	-
	N	23	57	19	31
SRP54	A	0,250	0,114	0,368	0,361
	B	0,568	0,737	0,632	0,583
	C	0,091	0,053	0,000	0,028
	D	0,091	0,096	0,000	0,028
	N	22	57	19	36

Table S2. Estimates of F_{ST} between pairs of populations based on intron polymorphisms

	AN	AS	MS
AS	0.0463 ***		
MS	0.0678 ***	0.0847 ***	
MN	0.1283 ***	0.2273 ***	0.0564 **

** $P < 0.01$; *** $P < 0.001$

Figure S1. Results of Bayesian analysis of genetic structure based on allelic frequencies of six intron RFLP genetic markers (Cordero et al, 2014). Data from the four sampled localities for this study (marked above the chart) were analyzed together with data from 11 other localities from a previous study by Cordero et al (2014). The three races described by Cordero et al (2014) are indicated below the chart with colored lines.

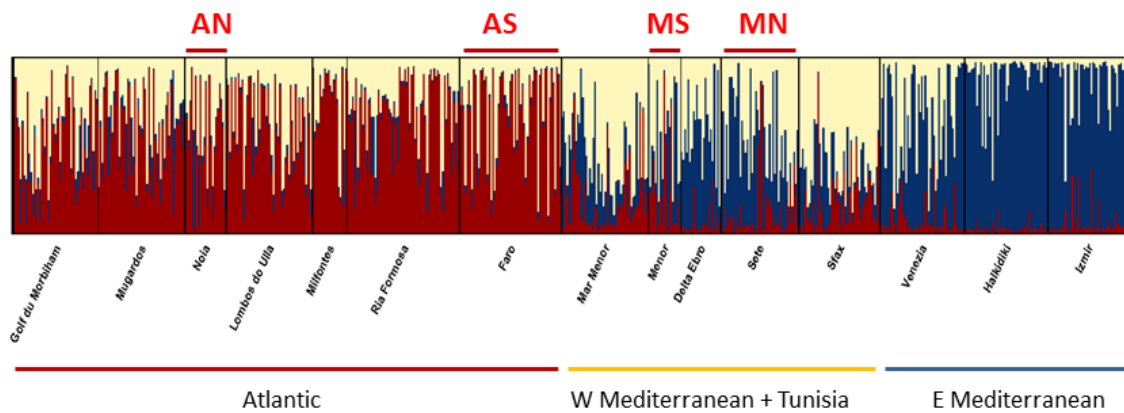


Figure S2. Principal components analysis of expression data from all samples.

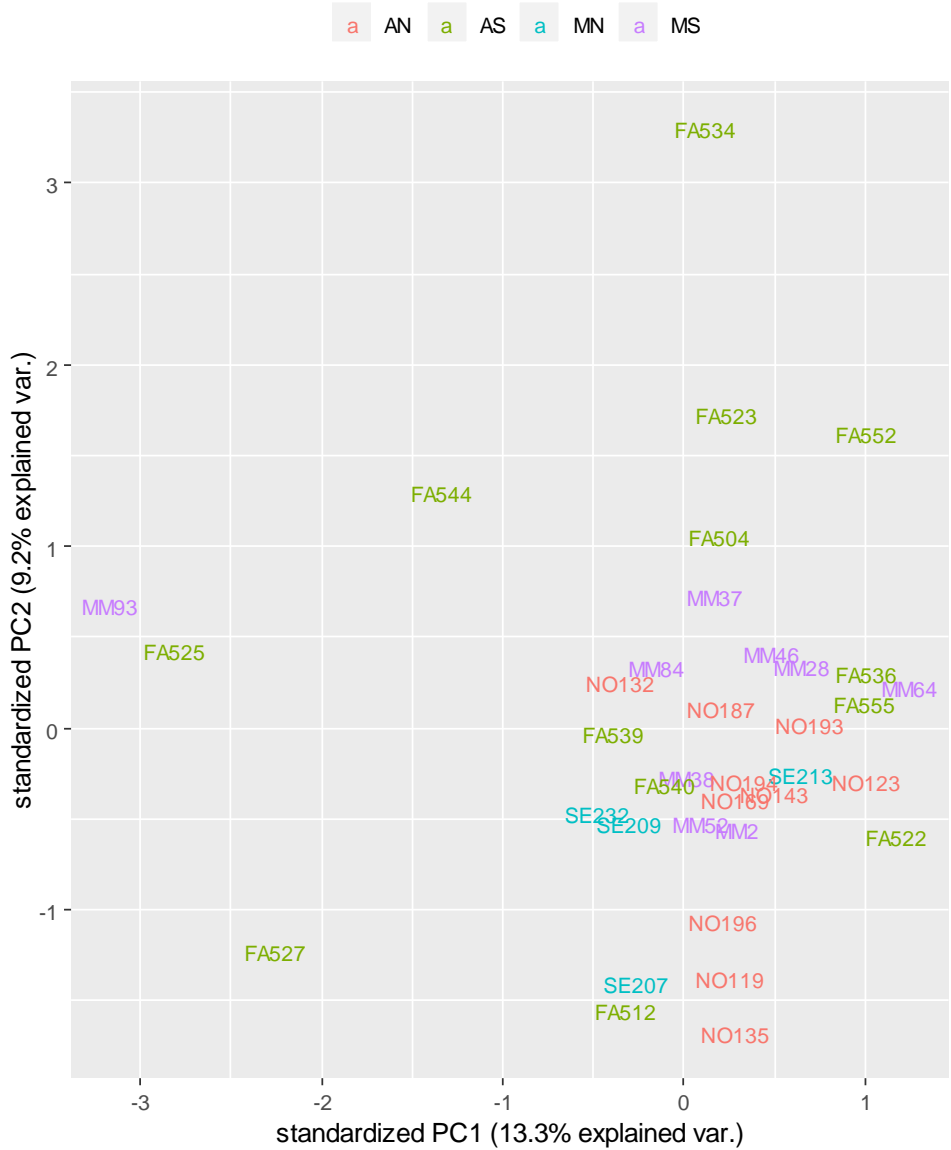


Figure S3. Heatmap showing gene expression variation across samples for the 105 genes which were significant for the Race factor in the 2-way ANOVA and contributed to the associated enriched GO terms.

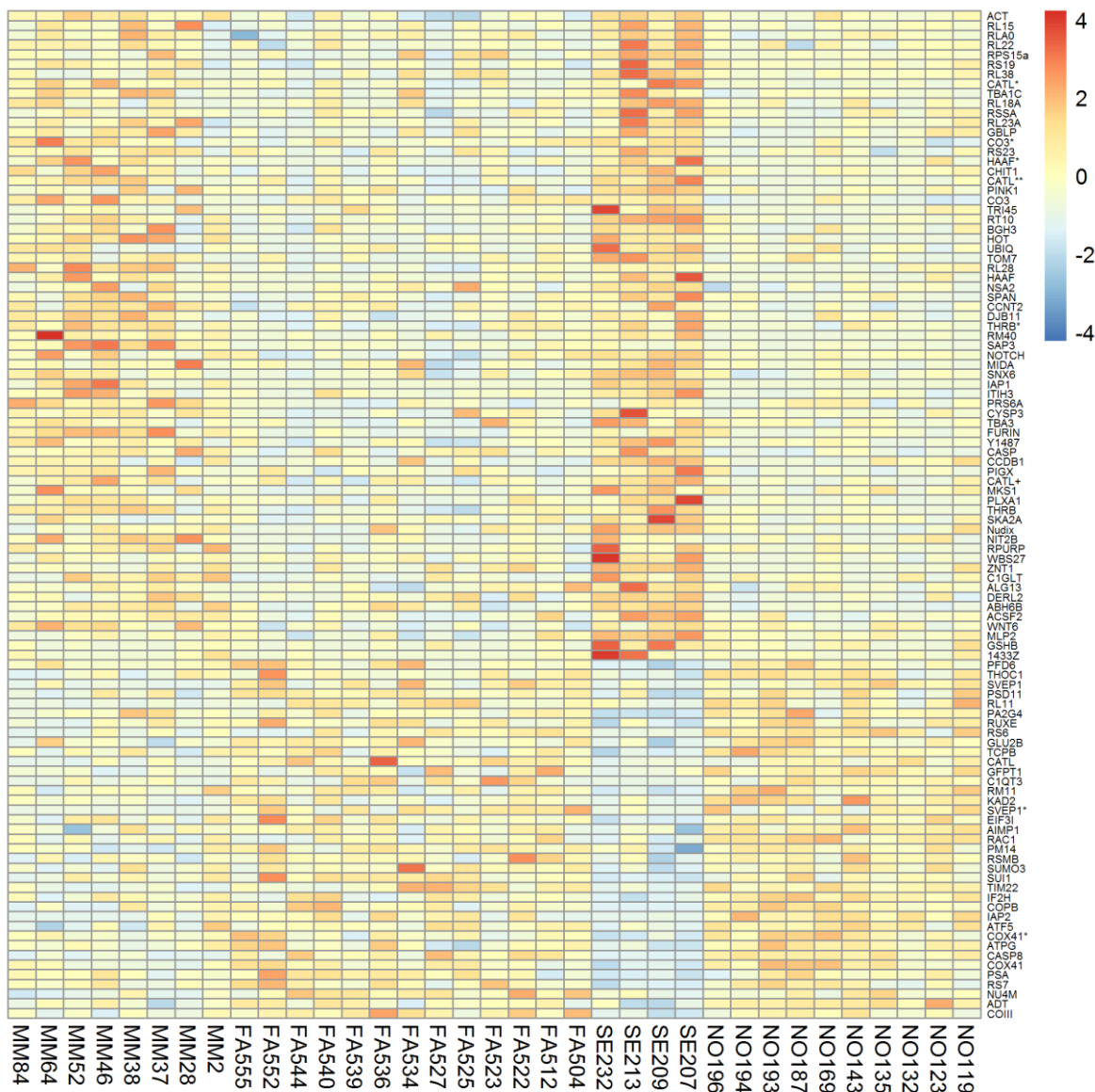
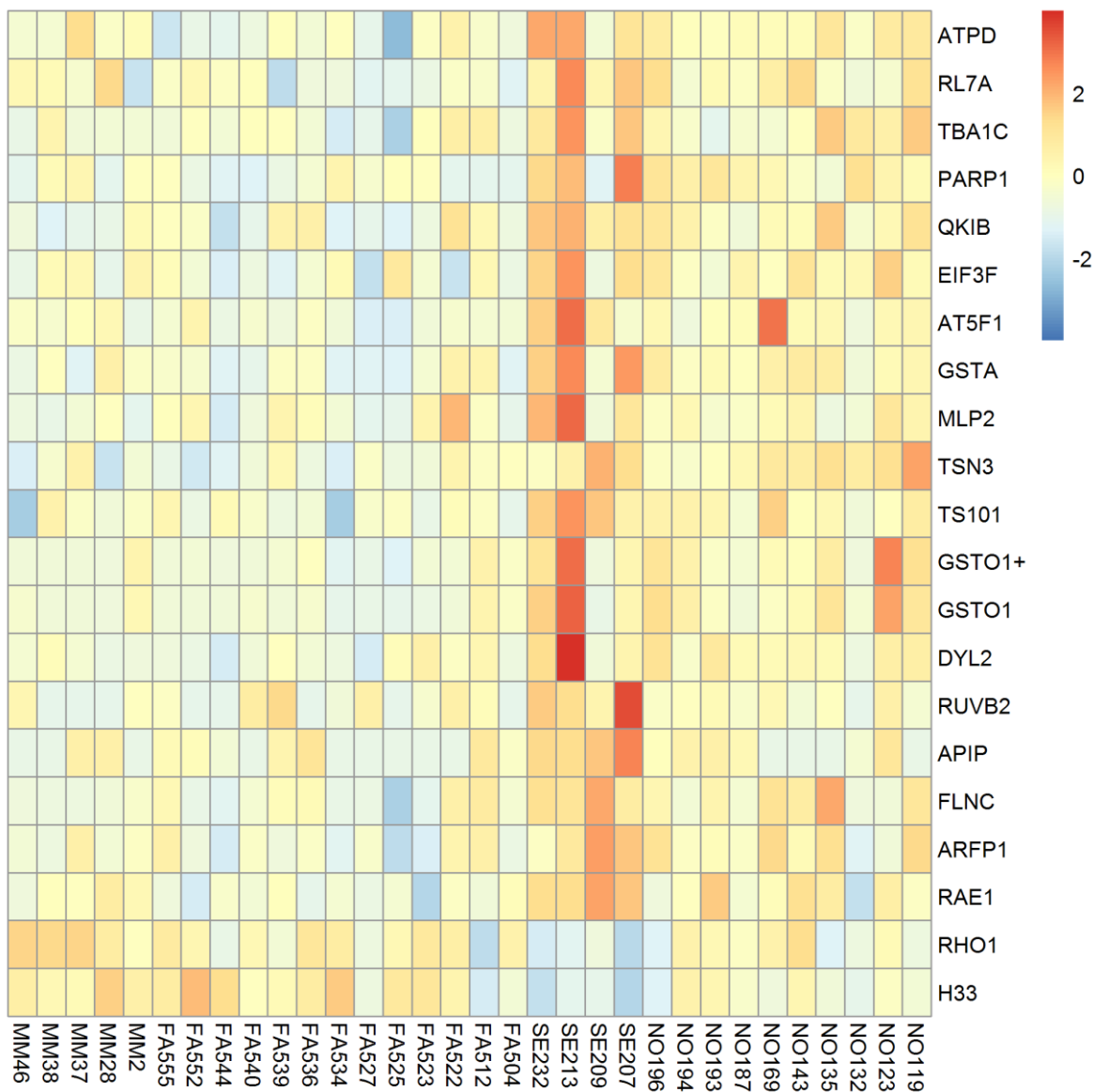


Figure S4. Heatmap showing gene expression variation across samples for the genes which were significant for Latitude only in the 2-way ANOVA and contributed to the enriched GO terms.



FigureS5.- Average expression in populations for the 9 genes which were significant for Race x Latitude interaction in the 2-way ANOVA. Note that the normalized signal intensity is in logarithmic scale. Gene numbers (#) as in supplementary file 1.

