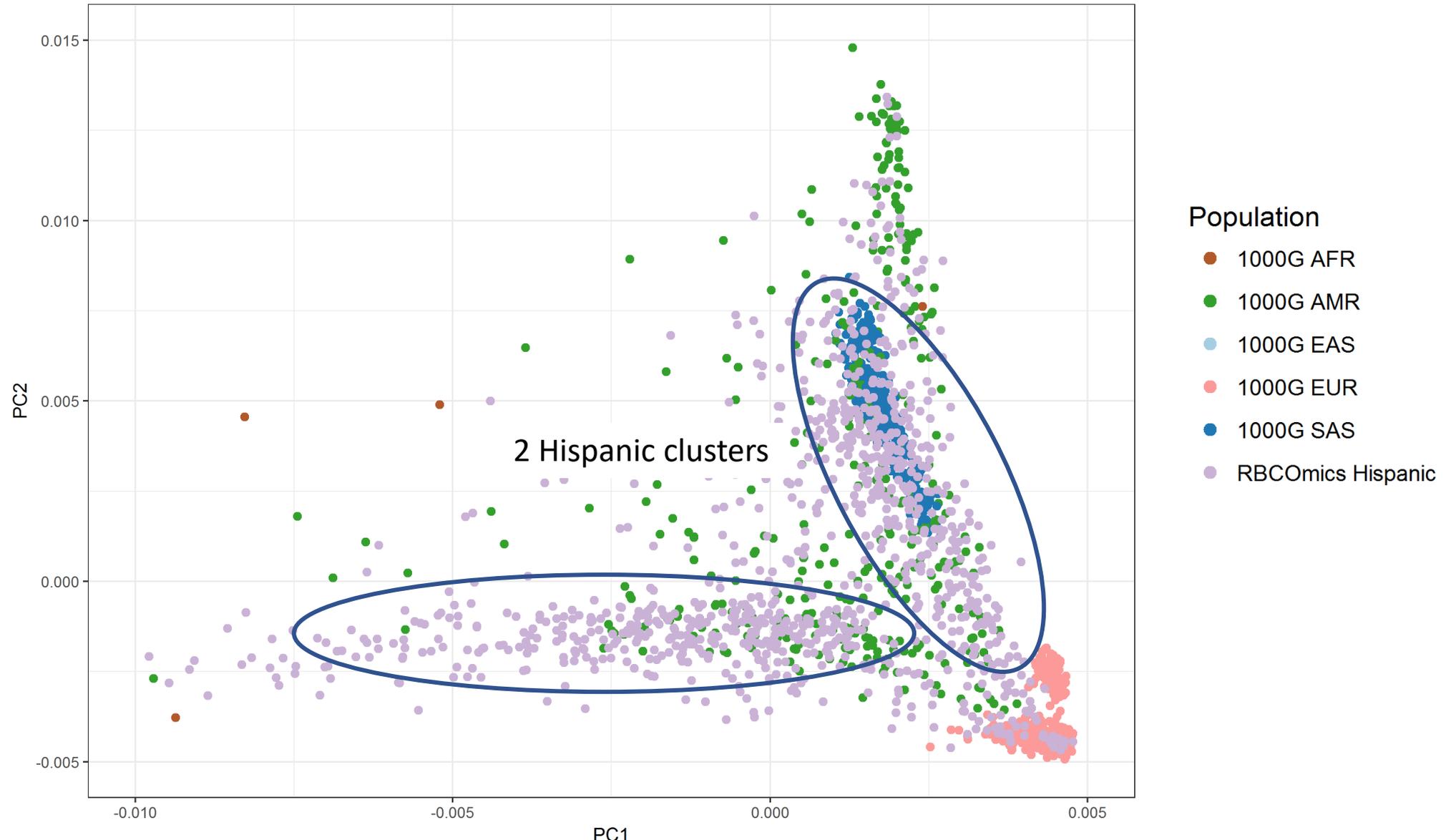


Red Blood Cell (RBC)-Omics Study Group Member

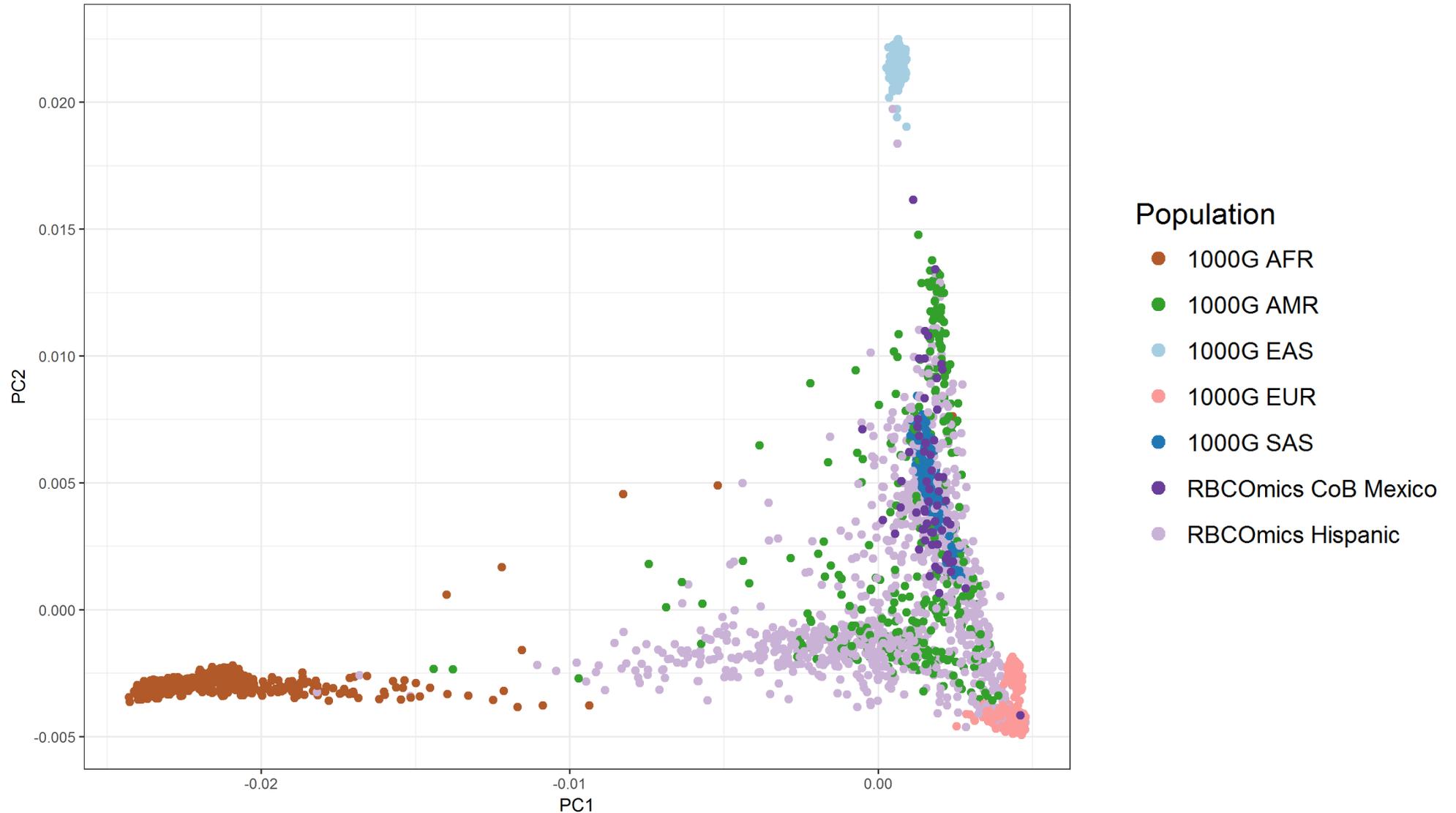
The NHLBI REDS-III, Red Blood Cell (RBC)-Omics Study members are:

- **Hubs:** J. L. Gottschall, W. Bialkowski, L. Anderson, J. Miller, A. Hall, Z. Udee, and V. Johnson, BloodCenter of Wisconsin, Milwaukee, WI; D. J. Triulzi, and P. A. D'Andrea, The Institute for Transfusion Medicine (ITxM), Pittsburgh, PA; E. L. Murphy and A. M. Gultinan, University of California, San Francisco, San Francisco, CA , and S. T. Johnson, American Red Cross Blood Services, Farmington, CT
- **Data coordinating center:** M. T. Sullivan, N. Haywood, D. Ringer, and B. C. Siege, RTI International, Rockville, MD; Central and testing laboratories: M. Stone, and S. Keating, Blood Systems Research Institute, San Francisco, CA
- **NHLBI, National Institutes of Health:** S. A. Glynn, K. B. Malkin, and A. M. Cristman

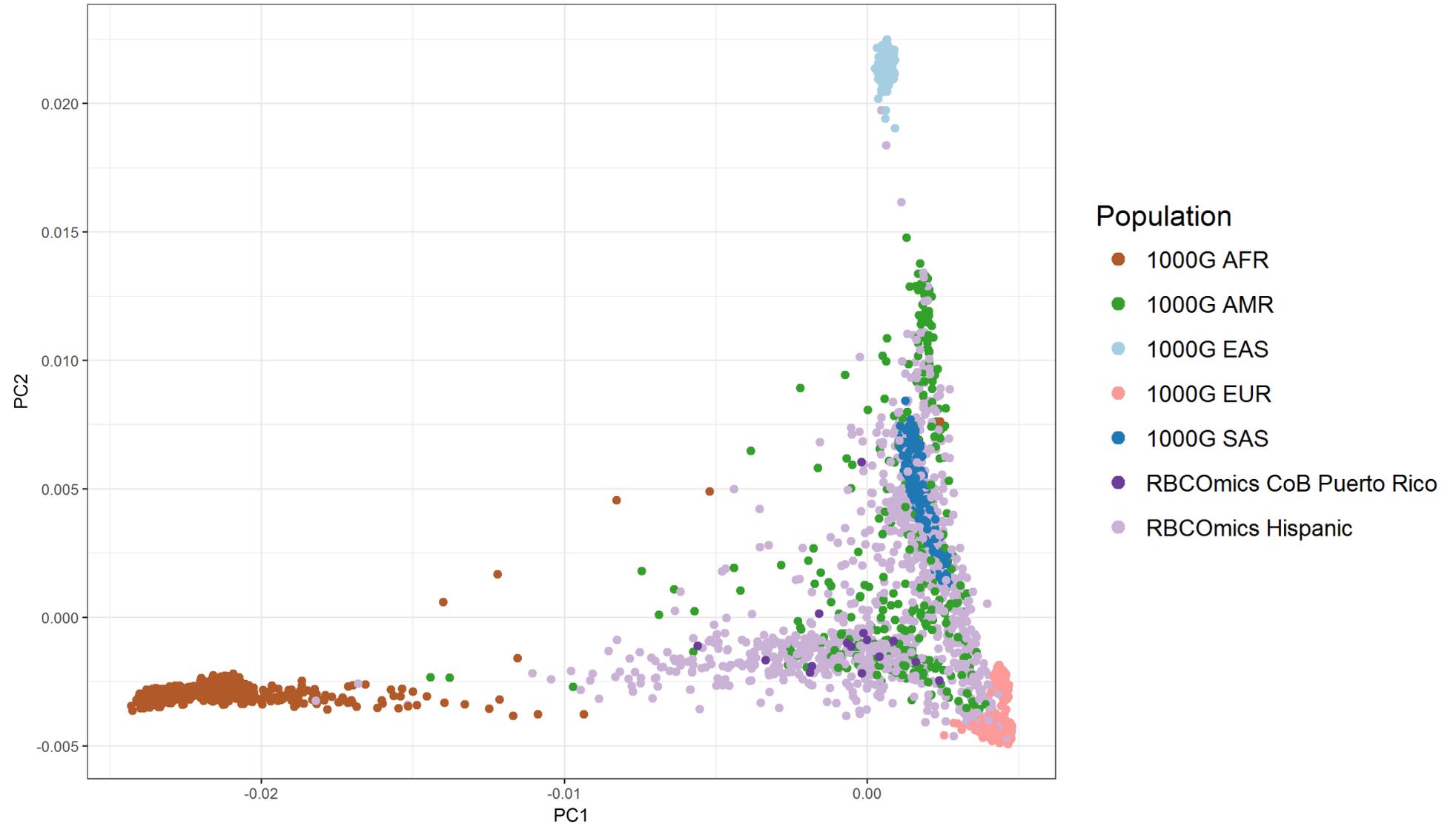
Supplemental Figure 1: Two Hispanic clusters. Self-reported Hispanics and Latinos in lavender. 1000 genomes phase 3 populations in brown, green, light blue, pink, and dark blue for super-populations AFR, AMR, EAS, EUR, and SAS, respectively. 2 Hispanic clusters were identified. This is a zoomed in version of figure 1A with a subset of the subjects.



Supplemental Figure 2: PCA analysis of RBC-Omics population. Self-reported Hispanics and Latinos in lavender. Self-identified RBC-Omics samples country of birth of Mexico in purple. 1000 genomes phase 3 populations in brown, green, light blue, pink, and dark blue for super-population AFR, AMR, EAS, EUR, and SAS, respectively. This cluster of Hispanics is called Mexican and Central American Hispanic (MCAH). This is a zoomed in version of figure 1A with a subset of the subjects.



Supplemental Figure 3: PCA analysis of RBC-Omics population. Self-reported Hispanics and Latinos in lavender. Self-identified RBC-Omics samples 'country of birth' as Puerto Rico in purple. 1000 genomes phase 3 populations in brown, green, light blue, pink, and dark blue for super-population AFR, AMR, EAS, EUR, and SAS, respectively. This cluster of Hispanics are called Caribbean Islands Hispanics (CIH). This is a zoomed in version of figure 1A with a subset of the subjects.



Supplemental Figure 4: Q-Q plots of the GWA analysis of the full dataset for osmotic hemolysis (A), oxidative hemolysis (B), and storage hemolysis (C). These data correspond to the p-values for figures 1B-1D.

Lambda = 1.003

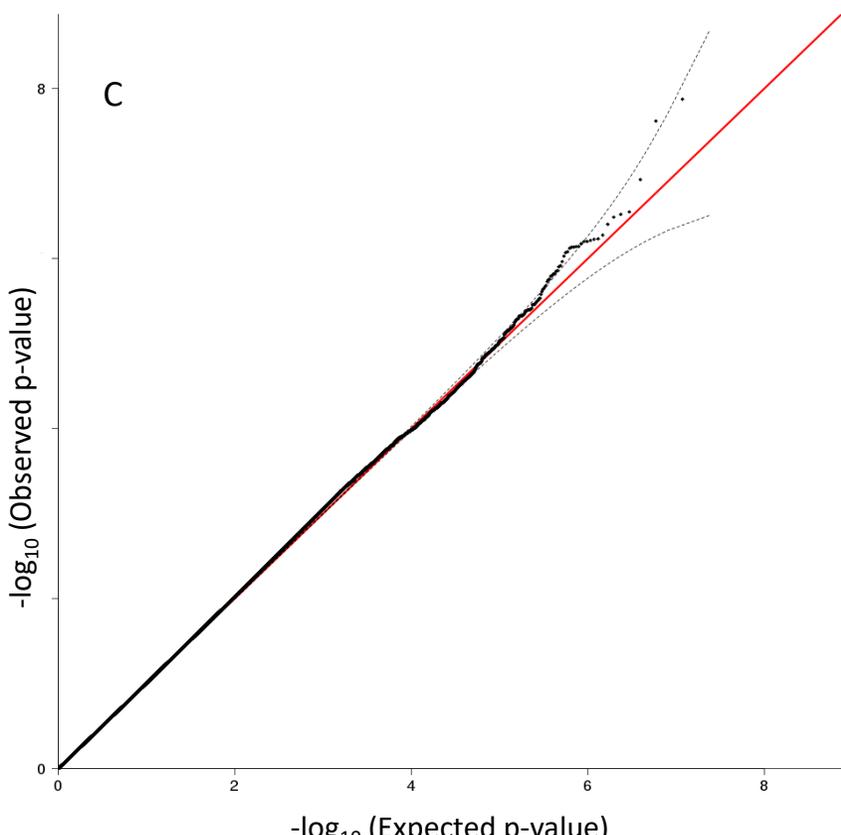
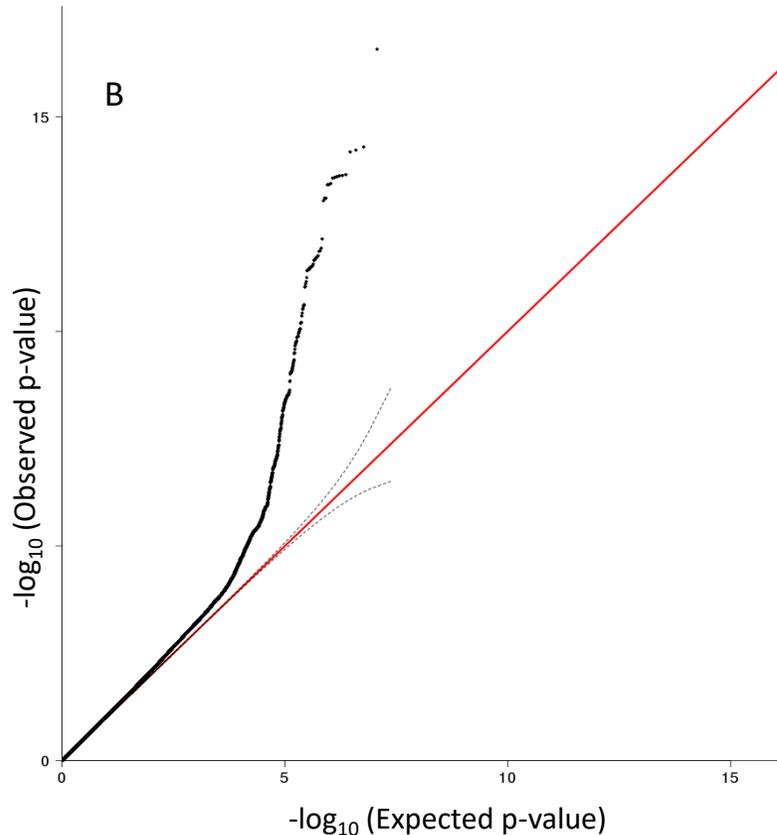
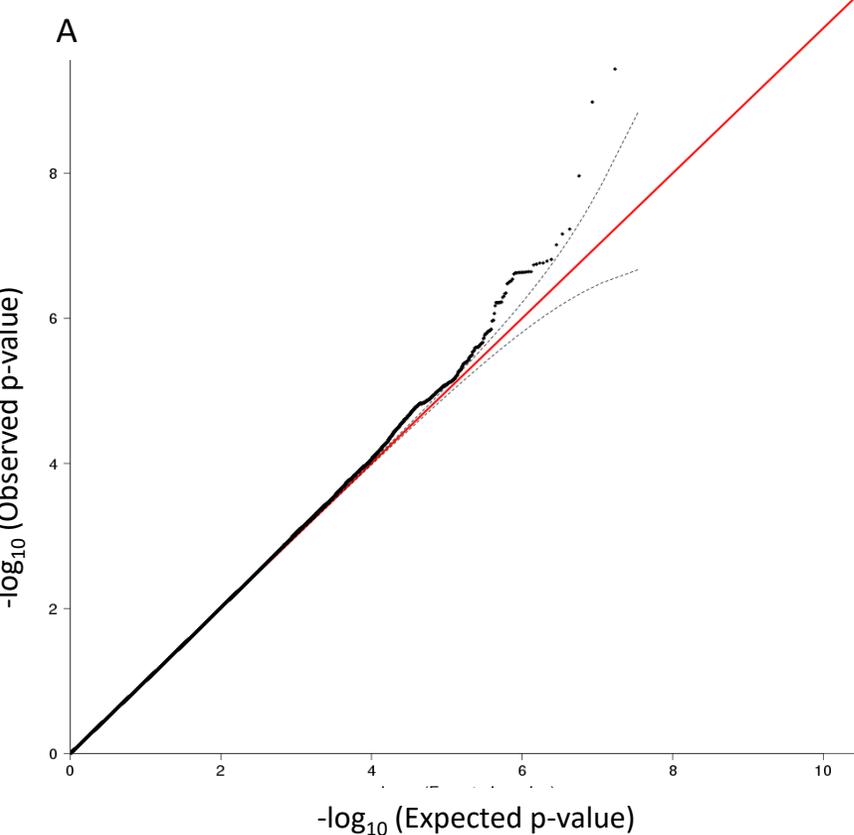
Lambda = 1.048

Lambda = 1.002

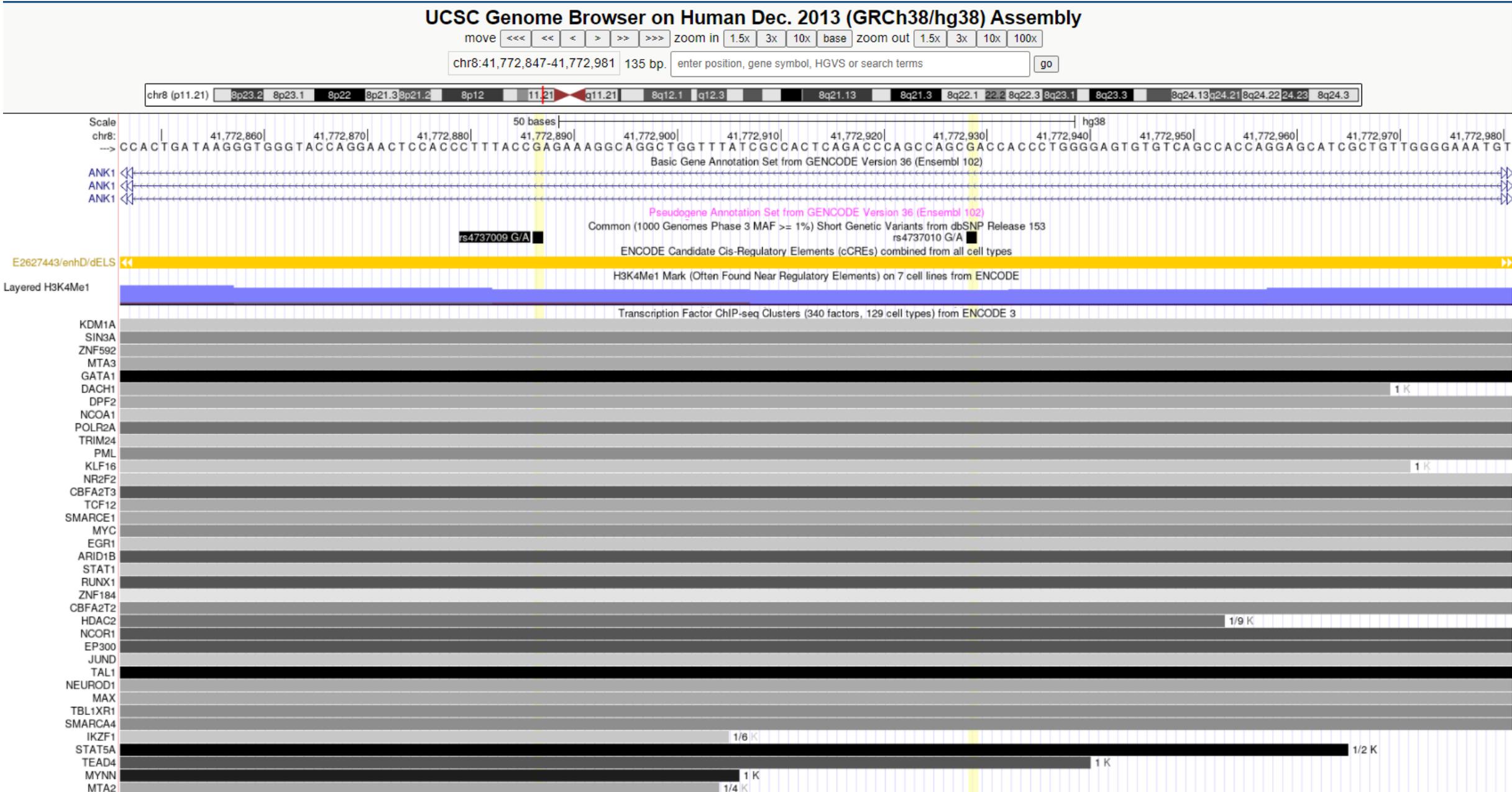
A

B

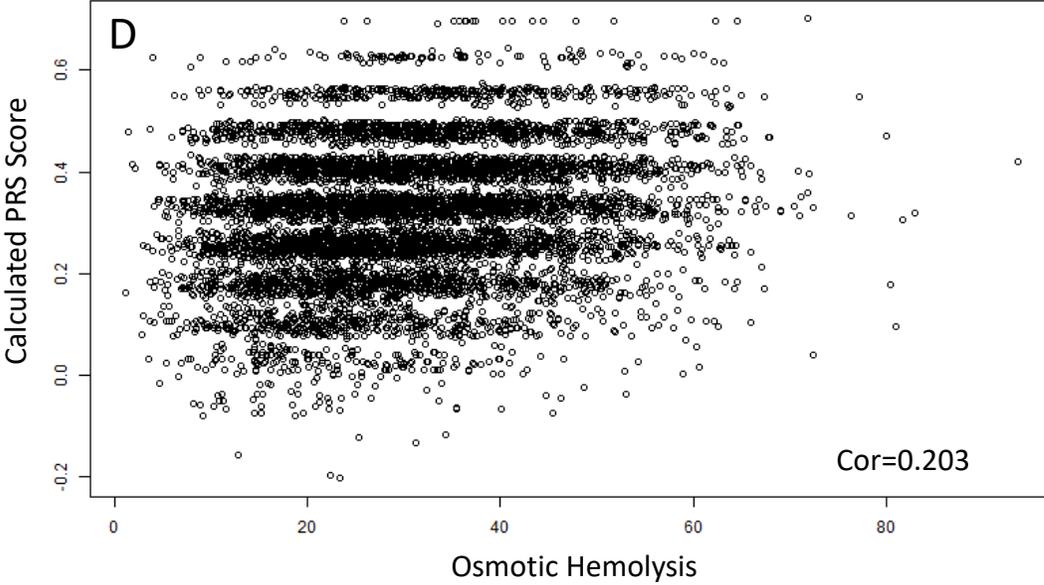
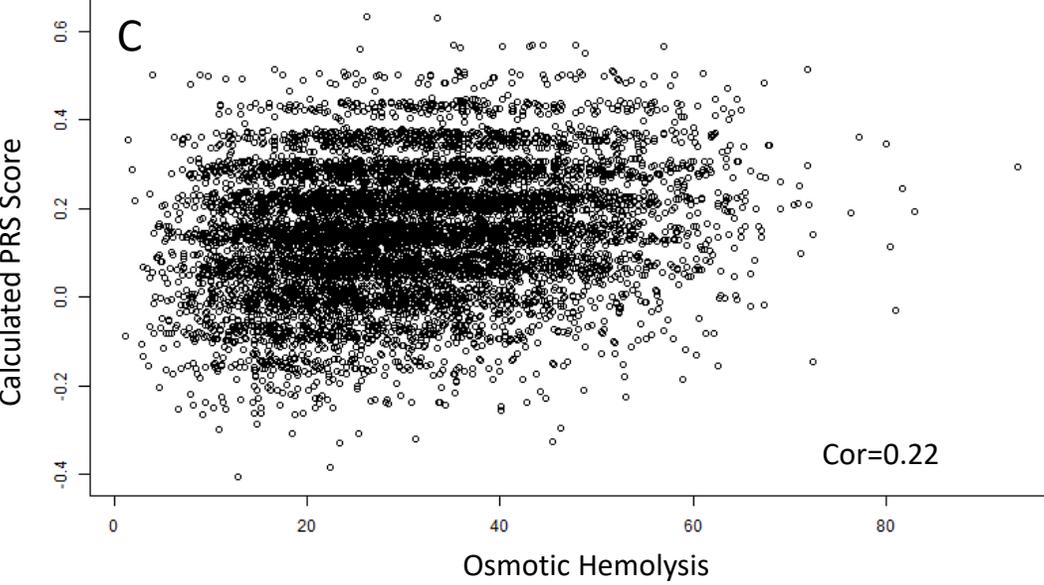
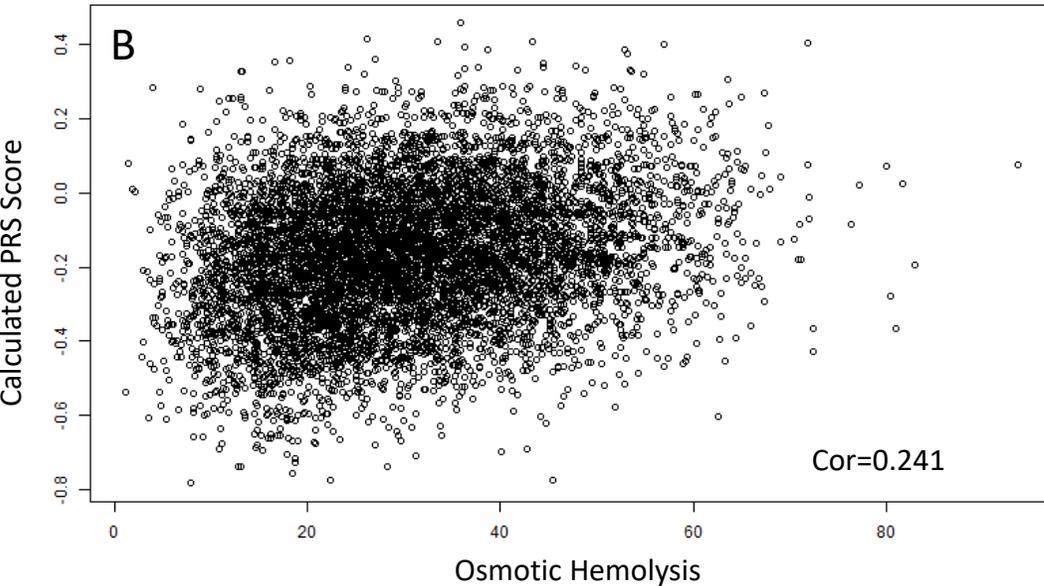
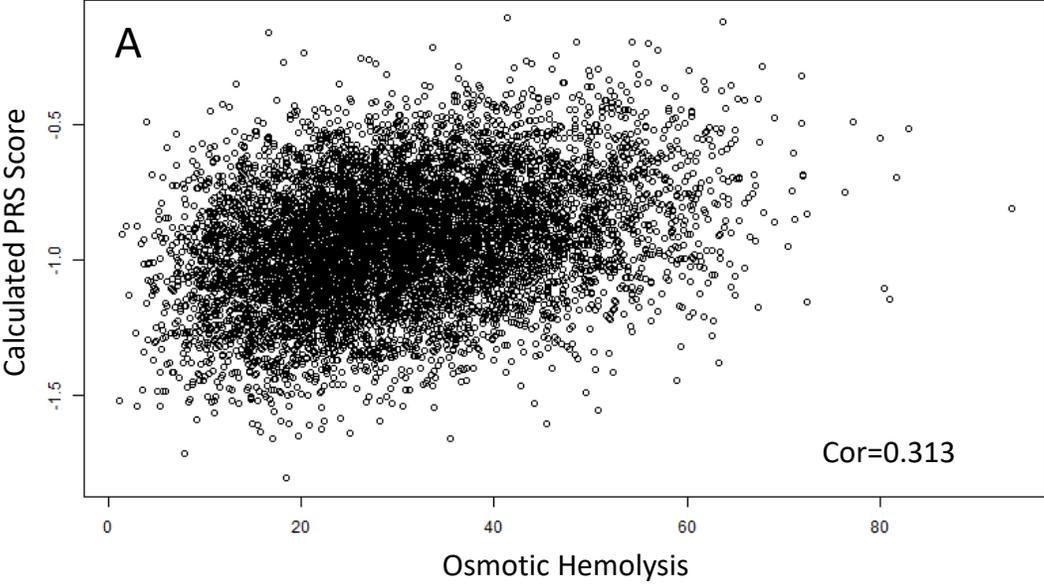
C



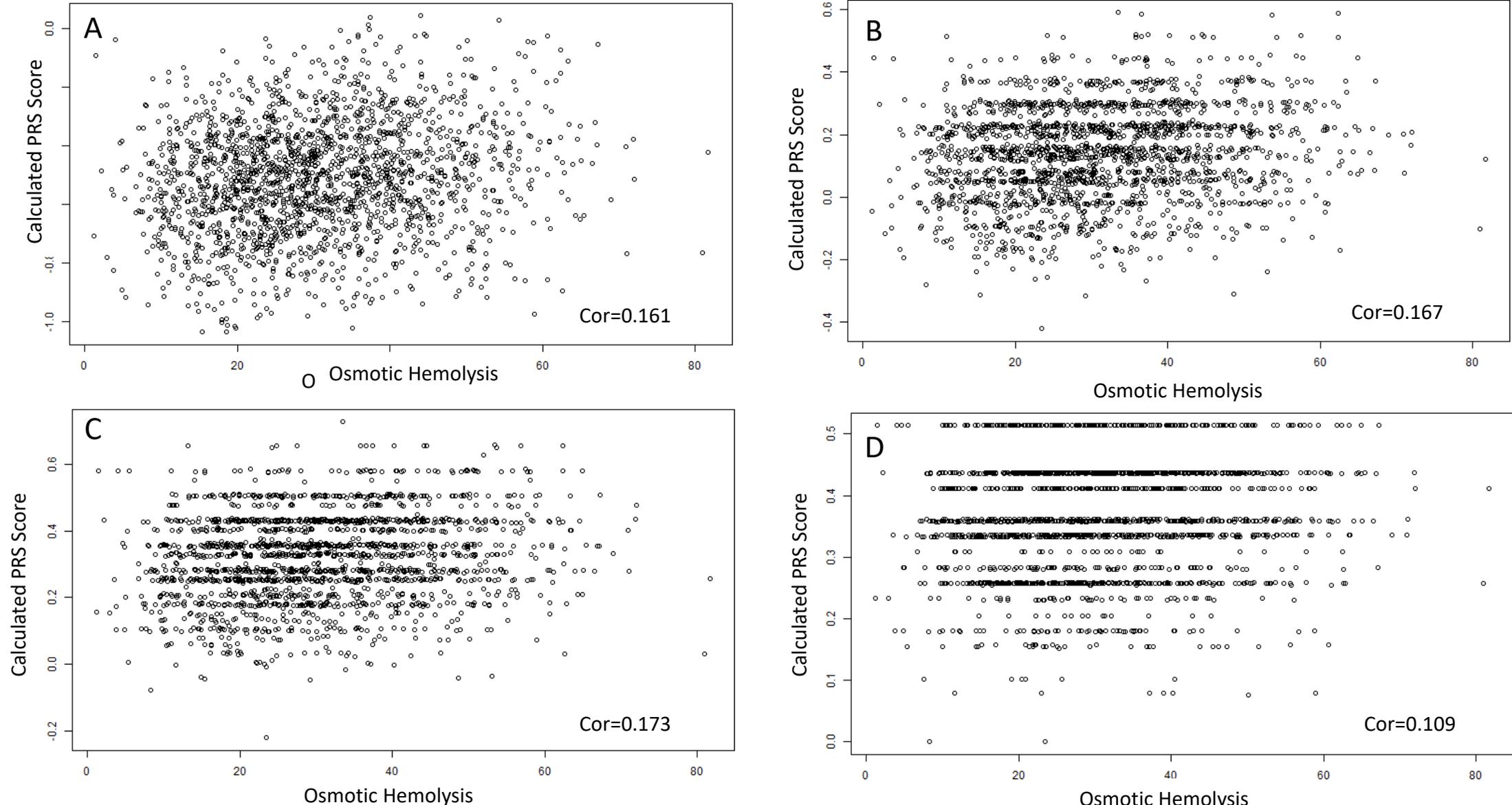
Supplemental Figure 5: Genome browser view of region around rs4737009 and rs4737010 in ANK1. The grey and black boxes are transcription factor binding sites from ENCODE 3.



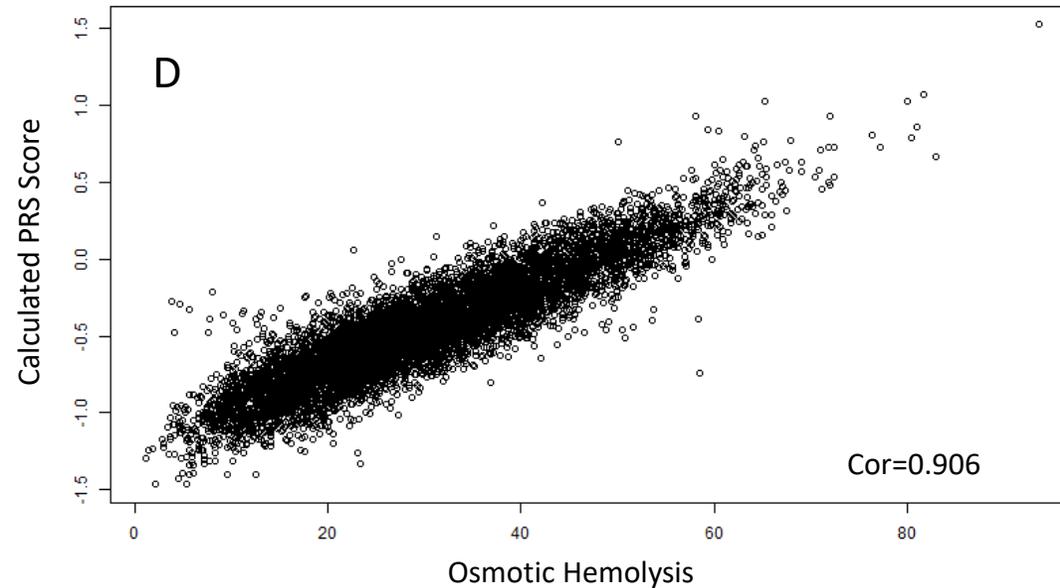
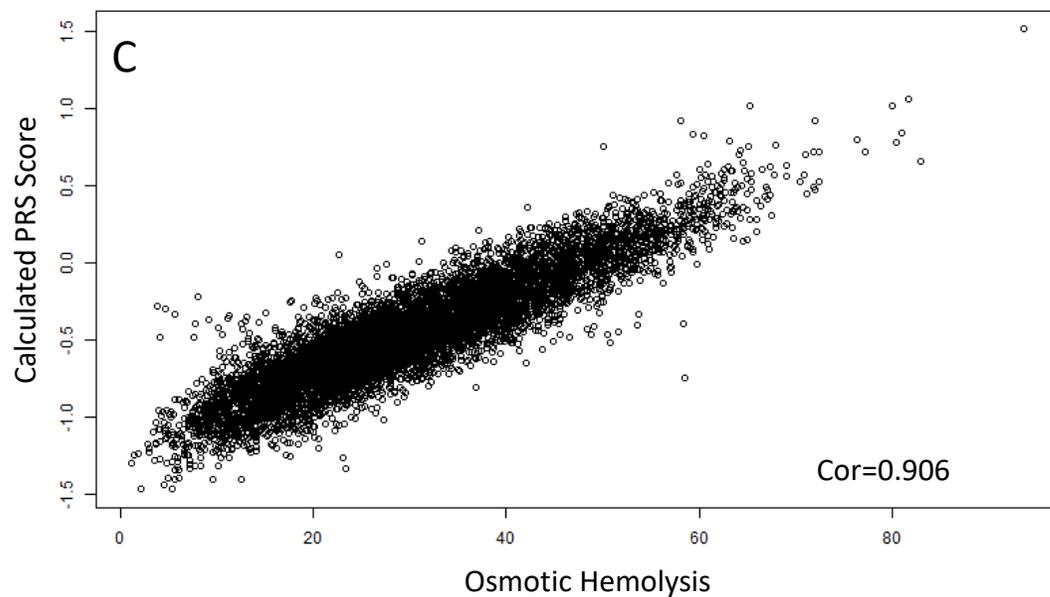
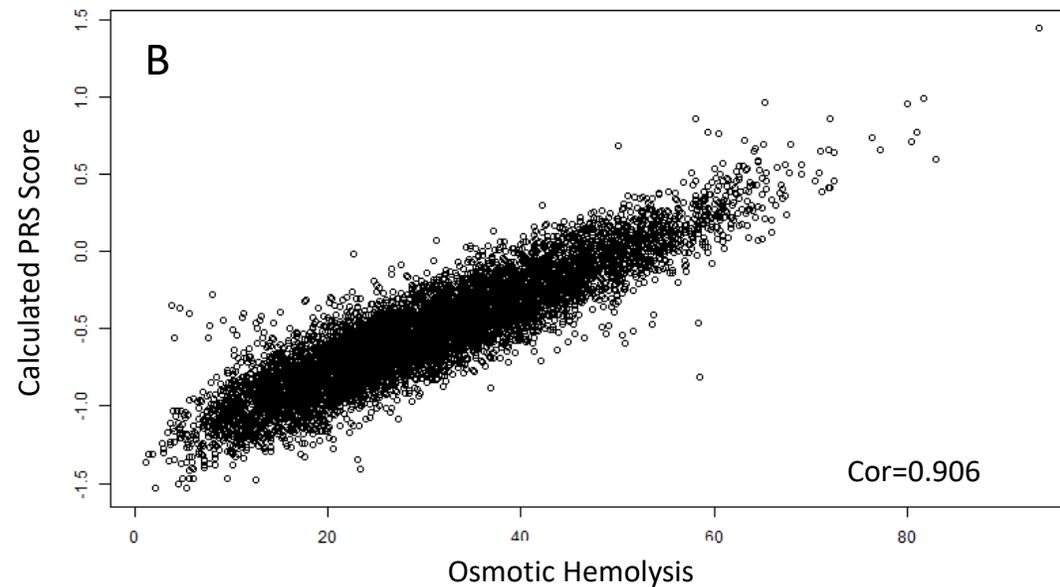
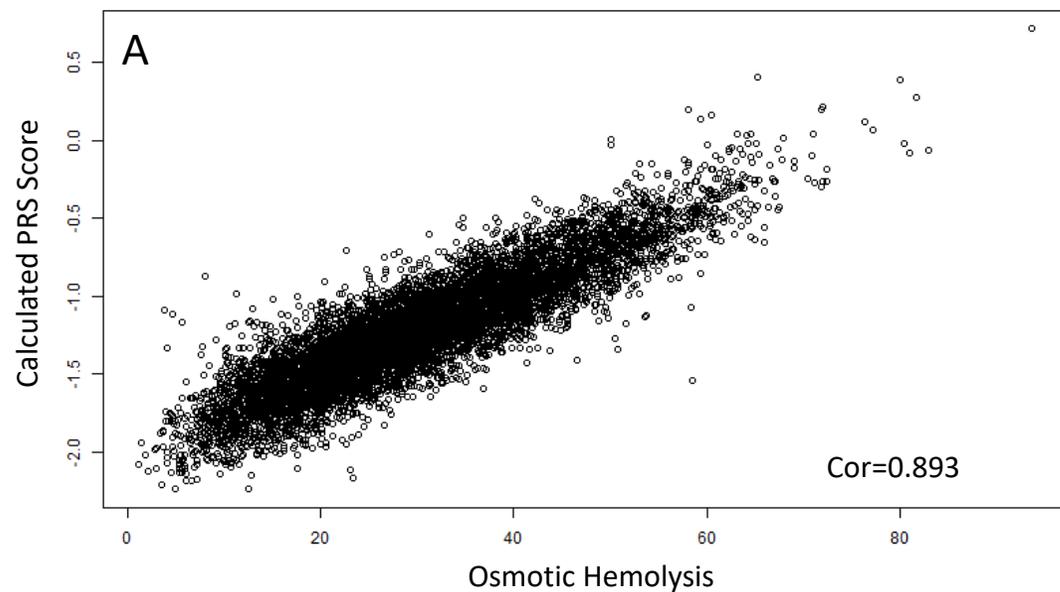
Supplemental Figure 6: Correlation with various cutoffs of the LD-Pruning and thresholding method using the Caucasian osmotic PGS score with the osmotic hemolysis measure derived from the entire Caucasian ancestry group. A: $P < 10^{-5}$ and $r^2 < 0.2$; B: $P < 10^{-6}$ and $r^2 < 0.2$; C: $P < 10^{-7}$ and $r^2 < 0.2$; D: $P < 10^{-8}$ and $r^2 < 0.2$.



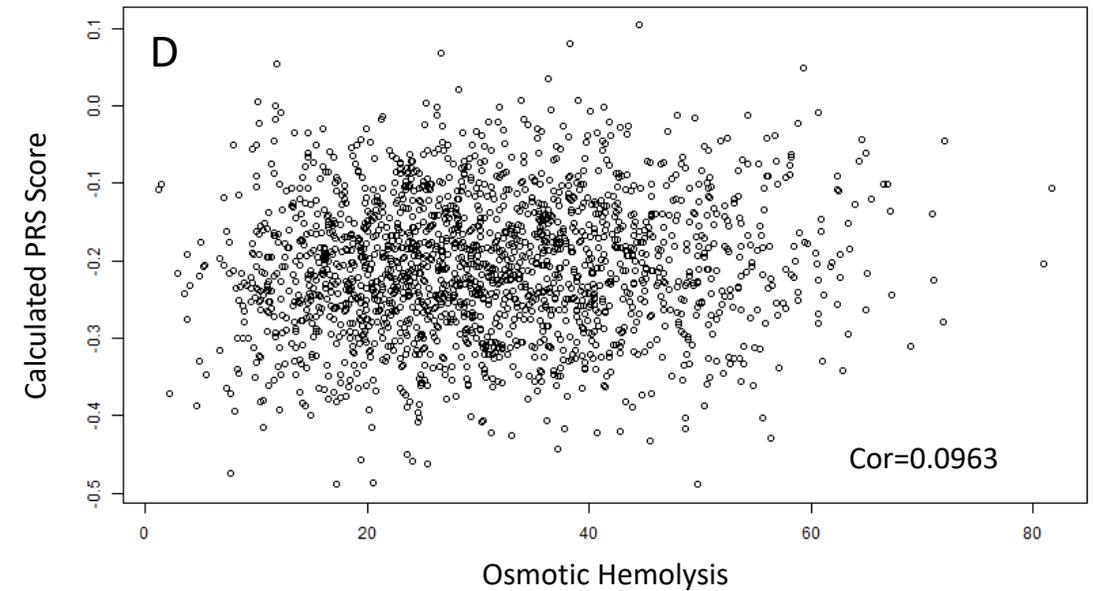
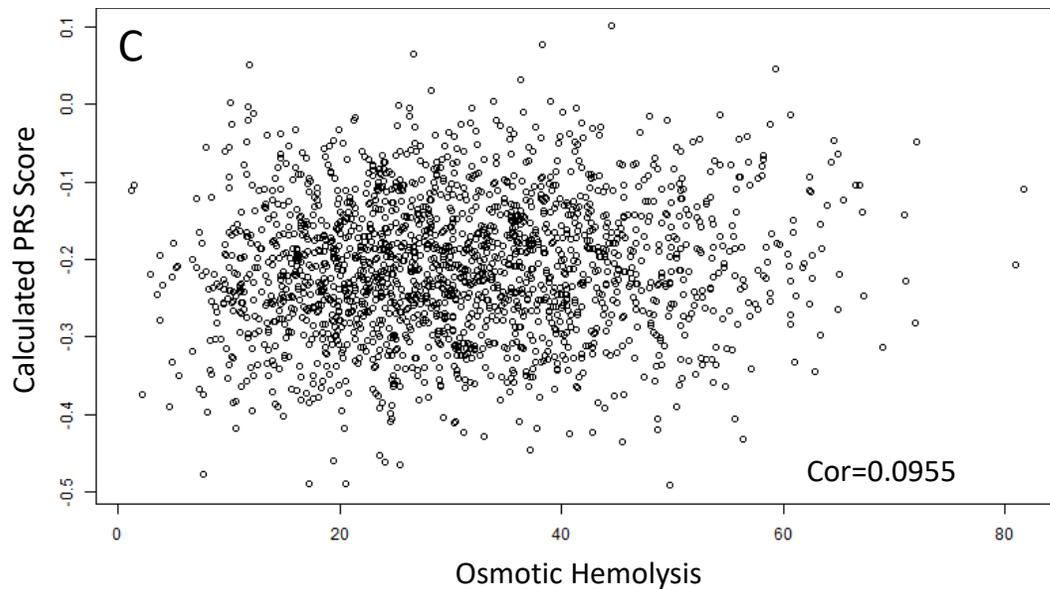
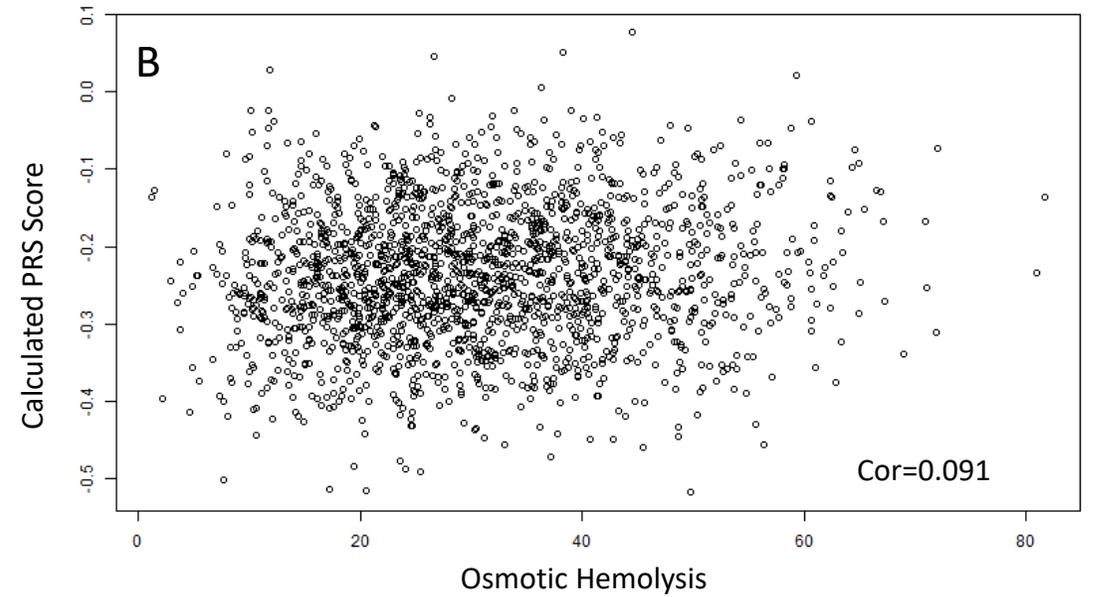
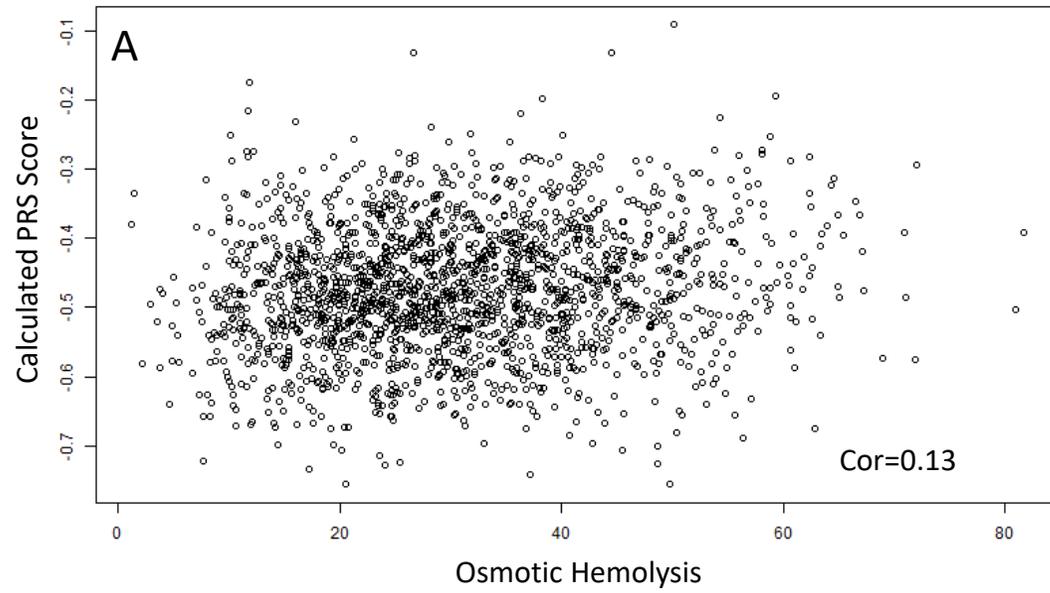
Supplemental Figure 7: Correlation with various cutoffs of the LD-Pruning and thresholding method using the Caucasian osmotic PGS score with the osmotic hemolysis measure derived from the first 2/3 of the Caucasian sample and data and correlation displayed for the remaining 1/3 of the samples. A: $P < 10^{-5}$ and $r^2 < 0.2$; B: $P < 10^{-6}$ and $r^2 < 0.2$; C: $P < 10^{-7}$ and $r^2 < 0.2$; D: $P < 10^{-8}$ and $r^2 < 0.2$.



Supplemental Figure 8: Correlation of Caucasian osmotic hemolysis LDPRED PGS score with Caucasian osmotic hemolysis score in entire data set. The data show various cutoffs of the LD-Pred Score A: $P = 10^{-3}$; B: $P = 10^{-2}$; C: $P = 10^{-1}$; D: $P = 10^0$.



Supplemental Figure 9: Correlation of Caucasian osmotic hemolysis LDPRED PGS score with Caucasian osmotic hemolysis score in validation. PRS score calculated in first 2/3 of the Caucasian samples, and display is the correlation of the PRS prediction in the final 1/3 of the Caucasian Samples. The data show various cutoffs of the LD-Pred Score A: P = 10⁻³; B: P = 10⁻²; C: P = 10⁻¹; D: P = 10⁻⁰.



Supplemental figure 10: Histograms for osmotic (n=12,215), oxidative (n=10,007) and storage hemolysis (n= 12,177). The distribution of storage hemolysis is skewed, thus log-transformed values for storage hemolysis (n= 12,177) was used in analysis.

