

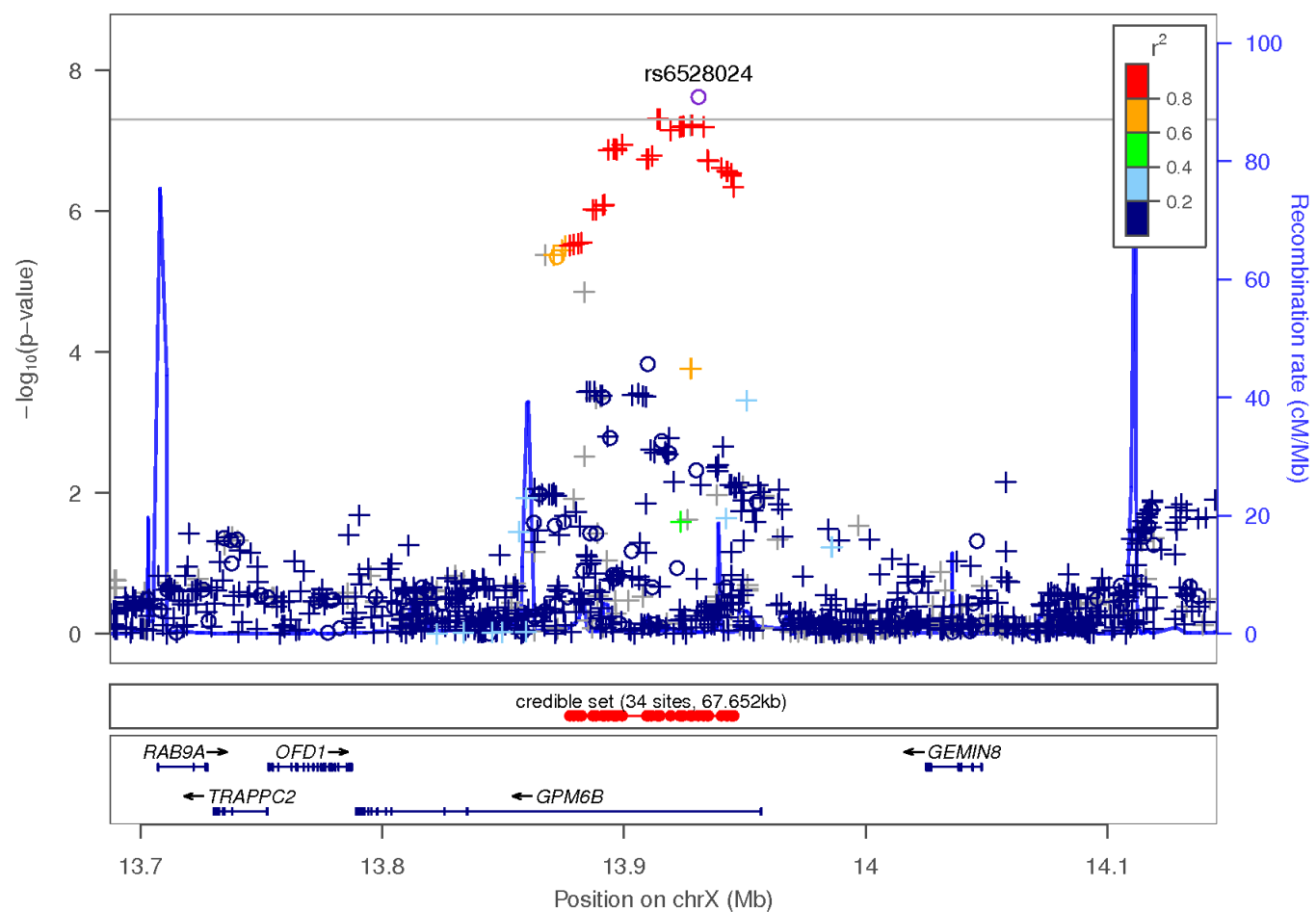
In the format provided by the authors and unedited.

Genome-wide association study of delay discounting in 23,217 adult research participants of European ancestry

Sandra Sanchez-Roige¹, Pierre Fontanillas², Sarah L. Elson², the 23andMe Research Team³, Anita Pandit⁴, Ellen M. Schmidt⁴, Johanna R. Foerster⁵, Gonçalo R. Abecasis⁴, Joshua C. Gray⁶, Harriet de Wit⁷, Lea K. Davis⁸, James MacKillop⁹ and Abraham A. Palmer^{1,10*}

¹Department of Psychiatry, University of California San Diego, La Jolla, CA, USA. ²23andMe, Inc., Mountain View, CA, USA. ³A full list of members appears in the Supplementary Note. ⁴Department of Biostatistics and Center for Statistical Genetics, University of Michigan, Ann Arbor, MI, USA. ⁵K.G. Jebsen Center for Genetic Epidemiology, Department of Public Health and Nursing, NTNU, Norwegian University of Science and Technology, Trondheim, Norway. ⁶Center for Deployment Psychology, Uniformed Services University, Bethesda, MD, USA. ⁷Department of Psychiatry and Behavioral Neuroscience, University of Chicago, Chicago, IL, USA. ⁸Vanderbilt Genetics Institute, Division of Genetic Medicine, Department of Medicine, Vanderbilt University, Nashville, TN, USA. ⁹Peter Boris Centre for Addictions Research, McMaster University/St. Joseph's Healthcare Hamilton, Hamilton, Ontario, Canada. ¹⁰Institute for Genomic Medicine, University of California San Diego, La Jolla, CA, USA. *e-mail: aap@ucsd.edu

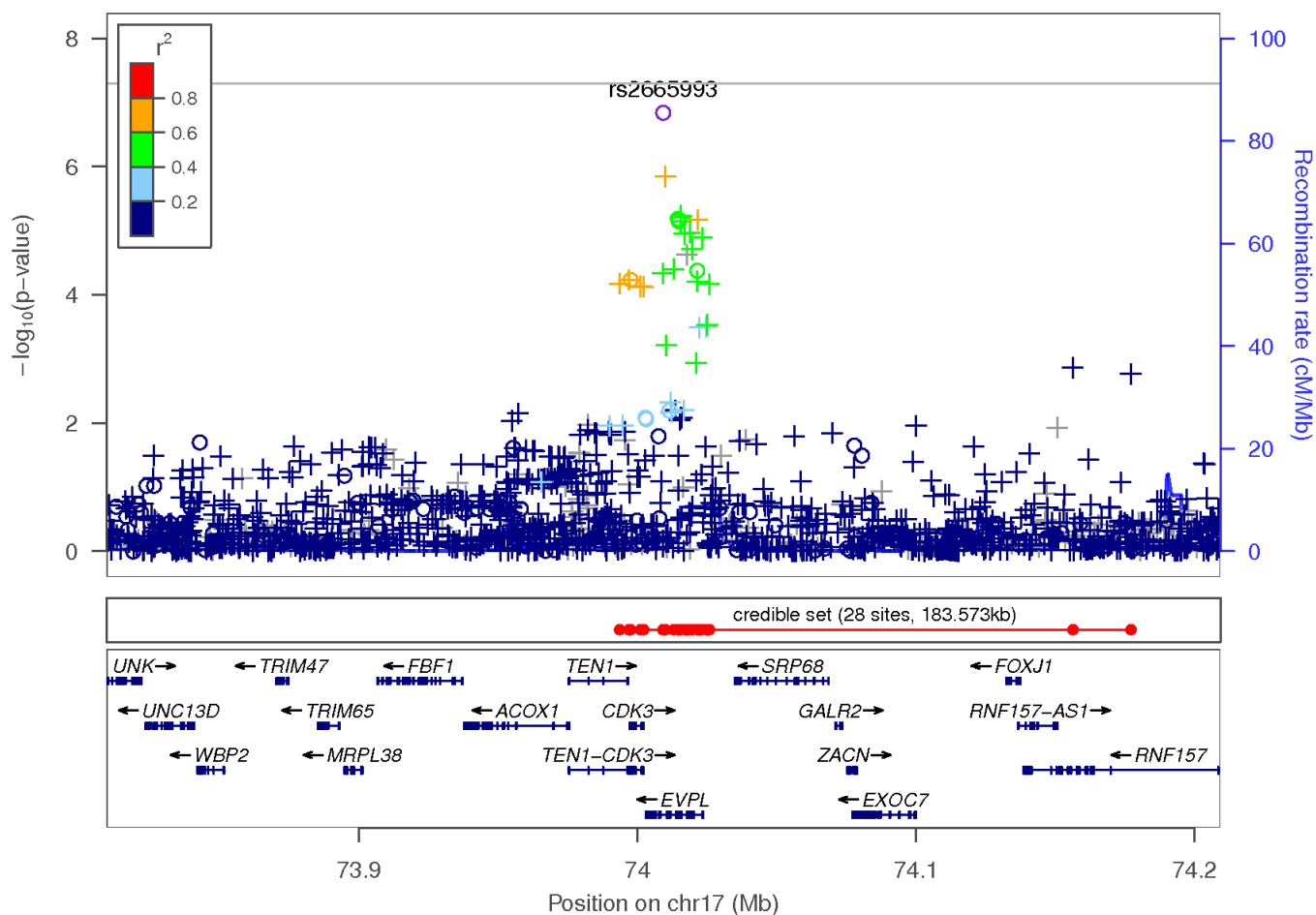
I



Supplementary Figure 1

Regional association plot focusing on top SNP rs6528025 at 3' of *GPM6B* gene on chromosome X at position 13.9 Mb.

This plot was generated using LocusZoom1. The $-\log_{10}(P \text{ value})$ is shown on the left y-axis; position in Mb is on the x-axis. Recombination rates (expressed in centiMorgans cM per Mb; NCBI Build GRCh37; highlighted in blue) are shown on the right y-axis. Pairwise linkage disequilibrium (r^2) of each SNP with the top SNP in the region is indicated by its color. Crossed points represent imputed SNPs, circles represent directly genotyped SNPs. The statistical tests used were two-sided; sample size = 23,217.



Supplementary Figure 2

Regional association plot showing the second index SNP rs2665993, located in the *EVPL* gene on chromosome 17.

This plot was generated using LocusZoom1. The $-\log_{10}(P\text{ value})$ is shown on the left y-axis; position in Mb is on the x-axis. Recombination rates (expressed in centiMorgans cM per Mb; NCBI Build GRCh37; highlighted in blue) are shown on the right y-axis. Pairwise linkage disequilibrium (r^2) of each SNP with the top SNP in the region is indicated by its color. Crossed points represent imputed SNPs, circles represent directly genotyped SNPs. The statistical tests used were two-sided; sample size = 23,217.