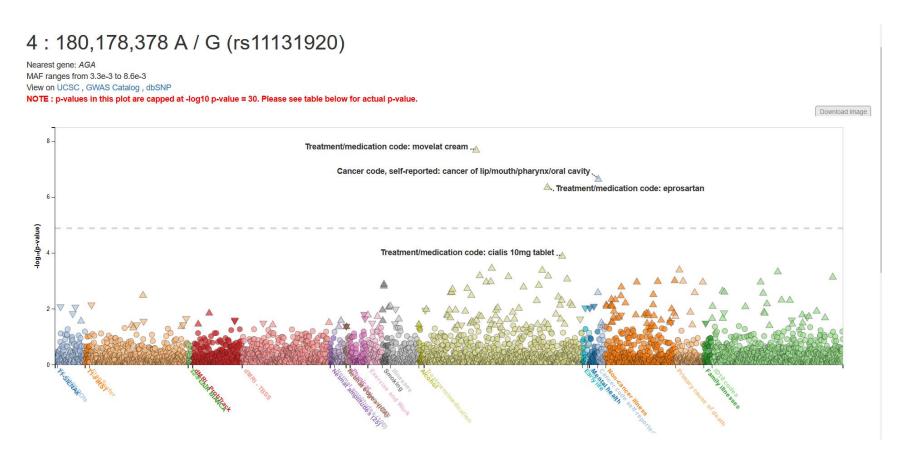
Figure S16: Association of low frequency variants representing the genome-wide significant locus with other phenotypes in the UK Biobank (Images from the Oxford Brain Imaging Genetics (BIG) Server - version 2.0; http://big.stats.ox.ac.uk/)



Source: http://big.stats.ox.ac.uk/variant/4:180178378-A-G

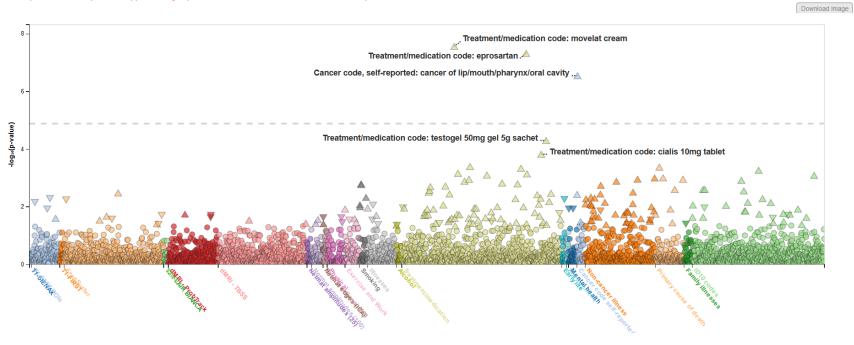
4:180,179,576 C/T (rs11131921)

Nearest gene: AGA

MAF ranges from 3.3e-3 to 8.7e-3

View on UCSC, GWAS Catalog, dbSNP

NOTE: p-values in this plot are capped at -log10 p-value = 30. Please see table below for actual p-value.



Source: http://big.stats.ox.ac.uk/variant/4:180179576-C-T

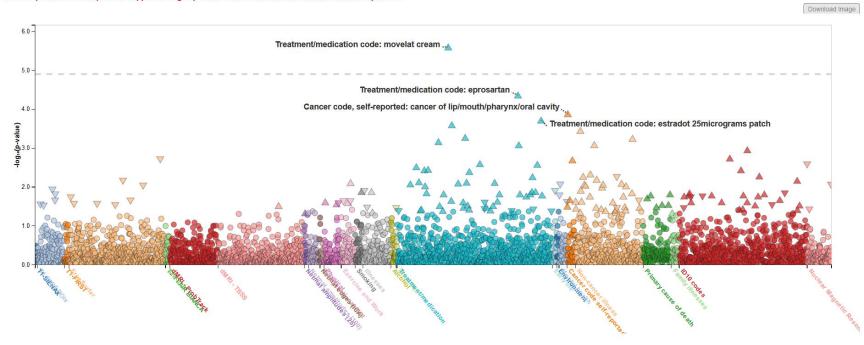
4:180,164,081 A/G (rs969219)

Nearest gene: AGA

MAF ranges from 5.9e-3 to 8.4e-2

View on UCSC, GWAS Catalog, dbSNP

NOTE: p-values in this plot are capped at -log10 p-value = 30. Please see table below for actual p-value.



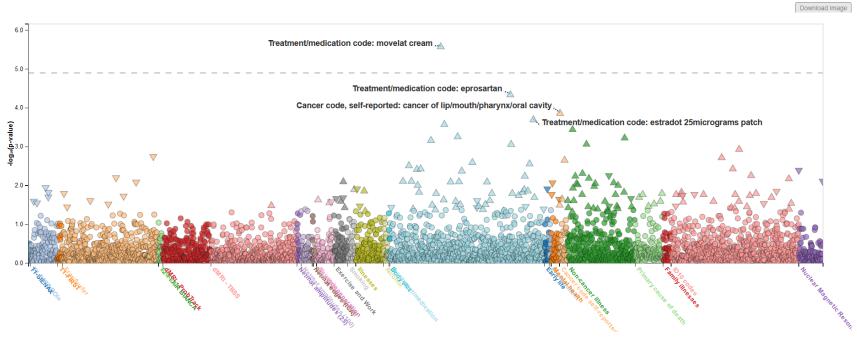
Source: http://big.stats.ox.ac.uk/variant/4:180164081-A-G

4: 180,151,019 G / T (rs4146838)

Nearest gene: *AGA*MAF ranges from 5.9e-3 to 9.3e-2

View on UCSC, GWAS Catalog, dbSNP

NOTE: p-values in this plot are capped at -log10 p-value = 30. Please see table below for actual p-value.



Source: http://big.stats.ox.ac.uk/variant/4:180151019-G-T

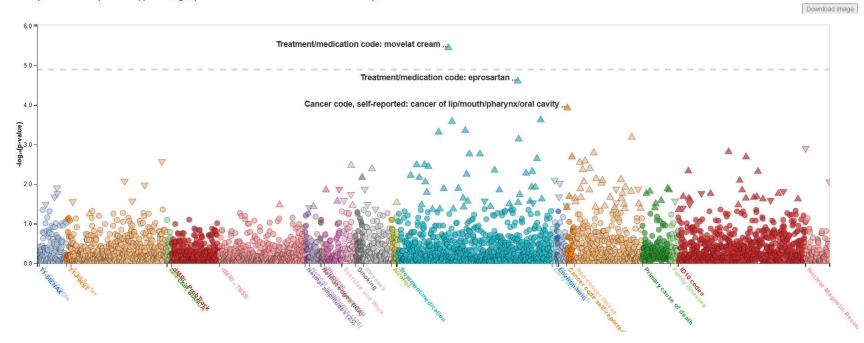
4:180,139,179 T/C (rs10520420)

Nearest gene: AGA

MAF ranges from 5.8e-3 to 8.9e-2

View on UCSC, GWAS Catalog, dbSNP

NOTE: p-values in this plot are capped at -log10 p-value = 30. Please see table below for actual p-value.



Source: http://big.stats.ox.ac.uk/variant/4:180139179-T-C