

Dataset pertaining to the publication “Loci Associated with N-Glycosylation of Human Immunoglobulin G Show Pleiotropy with Autoimmune Diseases and Haematological Cancers”. PLOS Genetics, Jan 31 2013;9(1):e1003225. doi:10.1371/journal.pgen.1003225 . URL: <http://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1003225>. If you use this dataset, please cite the manuscript in order to fairly acknowledge the contribution of all participating studies and their sponsors.

The files are comma separated and contain genome wide association meta-analysis data for the discovery studies. Summary data are given for the meta-analyses of over 2 million directly genotyped or imputed single variant polymorphisms corresponding to the HAPMAP2 release 22 reference panel. allele2 and effallele is allele for which effect (beta) is reported, allele1 is alternate allele, chromosome and position are position of the SNP on NCBI36/hg18 build. Meta-analysis mean effect size (beta) is the inverse-variance weighted estimate derived from individual discovery study; sebeta is its standard error. p is meta-analysis P-value; npops is the number of populations used for meta-analysis at that locus; n is the total number of samples used in meta-analysis. Meta-analysis estimates are corrected for inflation of test statistics using genomic control at the individual study level.

The archive **IgGGlycans_GWAMA_2013.tar.gz** contains seventy-seven gzipped files corresponding to genome-wide association meta-analysis (GWAMA) of seventy-seven IgG glycans traits.

Caroline Hayward, on behalf of all co-authors in the corresponding manuscript.

Variable Name	Definition
effallele	allele for which effect (beta) is reported
allele2	allele for which effect (beta) is reported
allele1	Alternate allele
chromosome	chromosome on which the SNP is found on the NCBI36/hg18 build
position	position of the SNP on NCBI36/hg18 build
Meta-analysis mean effect size (beta)	the inverse-variance weighted estimate derived from individual discovery study
sebeta	Standard error of the pooled effect size
p	Meta-analysis P-value
npops	the number of populations used for meta-analysis at the given locus
n	the total number of samples used in meta-analysis