

S1 Table. Summary of Associations in Each Dataset.

Dataset	Release	New Multivariate SNPs ^a	Univariate p -Value Threshold ^b	New SNPs Below Univariate Threshold ^c	New SNPs Near Previous Association ^d
GlobalLipids	2010	19	5×10^{-8}	0	0
	2013	65	5×10^{-8}	18	11
GIANT	2010	60	5×10^{-8}	6	5
	2014/5	162	5×10^{-8}	41	21
HaemgenRBC	2012	16	1×10^{-8}	4	3
	2016	60	8.31×10^{-9}	0	0
ICBP	2011	22	5×10^{-8}	2	1
MAGIC	2010	1	5×10^{-8}	0	0
GEFOS	2015	13	1.2×10^{-8}	3	1
GIS	2014	5	5×10^{-8}	5	0
SSGAC	2016	1	5×10^{-8}	0	0
CKDGen	2010/1	6	5×10^{-8}	0	0
ENIGMA2	2015	3	7.1×10^{-9}	0	0

^a Number of new multivariate associations discovered by our analysis. Note that we required a multivariate association to be at least 500kb from a previous reported association to be considered “new”.

^b Univariate GWAS significance p -value threshold used by the original study publication.

^c These are new multivariate SNPs that were not reported by the original study despite having a univariate association (in the public summary data) that was genome-wide significant by the original study’s univariate significance threshold.

^d A “previous association” means an association reported by the original GWAS; “near” means within 1Mb (but these are all more than 500kb away from a previous association since our classification of new multivariate SNPs requires this).