Supplemental Table 5: Rare variants contributing to *GOLGA8B* association. Abbreviations: CHR = chromosome, POS = base pair position on GRCh38 reference genome, REF = reference allele, ALT = alternate allele, N = sample size, AAC = alternate allele count, DP = mean read depth, AACmax = maximum alternate allele count, AAF_{max} = maximum alternate allele frequency, POP_{max} = population with AACmax, Consequence = most severe consequence in *GOLGA8B*, NA: not applicable. Max values are from gnomAD v3, which includes samples from the Women's Health Initiative study.

CHR:POS:REF:ALT	$N_{control}$	$AAC_{control}$	N_{case}	AAC_{case}	DP	AAC_{max}	AAF_{max}	POP_{max}	Consequence
chr15:34527704:CTCCTGGTGG:C	9422	0	1598	1	18	1	4.20E-05	African	Inframe deletion
chr15:34527750:G:A	9422	0	1598	1	19	1	2.00E-05	Non-Finnish European	Missense
chr15:34528007:G:GA	9421	1	1599	0	9	1	2.85E-05	Non-Finnish European	Frameshift
chr15:34531667:TTC:T	9422	0	1598	1	8	1	7.86E-04	Ashkenazi Jewish	Frameshift
chr15:34532861:GTCAT:G	9422	0	1597	2	23	3	7.76E-05	African	Frameshift
chr15:34533008:G:T	9422	0	1598	1	8	0	NA	NA	Missense
chr15:34533118:C:A	9421	1	1599	0	4	2	6.33E-04	Non-Finnish European	Missense
chr15:34574916:T:C	9421	1	1598	1	34	2	6.38E-04	East Asian	Splice acceptor