Downloading significant associations from genome wide association studies

Standard operating procedure 9

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Study eligibility

Accept the following studies:

- Genome wide studies designed to detect the associations between single-nucleotide polymorphisms (SNPs) and relevant cardiovascular traits.
- The studies are based on microarrays or next generation sequencing
- The study has significant SNPs with p-values less than 0.001 or q-values below 0.05
- The study must have Pubmed ID

Record eligibility

Record the following associations:

- The association originates from an eligible study
- The association is significant with a p-value below 0.001 or the q-value less than 0.05
- The SNP id (rs******) is provided
- P-value must be available

Columns to be included in the resulting table

- SNP_ID: rs identifiers for associations
- RISK_ALLELE: allele associated with the trait, insert “NA” if the risk allele was not provided
- RISK_ALLELE_FREQUENCY: the frequency of the allele associated with the trait, substitute with NA if not available
- BETA_OR: beta value or odds ratio
- PVALUE: p-value or qvalue
- CI: confidence intervals, substitute with NA if not available
- DISEASE_TRAIT: Name of the trait, I.e Stroke, Coronary hear disease, etc.