

Dear Tim, please find attached herewith the results of our first approach to replicate your findings. We have focused in those SNP pairs that have been detected by you using different InterSNP models (listTEST5.txt, listTEST6.txt, listTEST15.txt, listTEST16.txt) (for details see procedure 1). In meta1.csv you will find a list of SNP pairs (original pairs plus proxy pairs) including chromosomes numbers, SNP1, SNP2, global p-value (meta-analysis of 3 to five studies depending on the availability of the pair), N (number of studies), Escore (is referred to effect direction on each dataset. i.e. +++- = +1, +++++=5, --=2, +++=+3 , and so forth and so on). Individual effect size obtained for each dataset is included at the end of the table (last five columns).

Available Datasets:

- ADMURimpQC2: Spanish GWAS (<http://www.ncbi.nlm.nih.gov/pubmed/21627779>)
- ADNIimpQC2: ADNI GWAS (<http://www.ncbi.nlm.nih.gov/pubmed/17476317?dopt=Abstract&holding=f1000,f1000m,isrctn>)
- GenADA_impQC2: GenADA (<http://www.ncbi.nlm.nih.gov/pubmed/17998437>)
- NIA_AD_impQC2: NIA/NIH GWAS (<http://www.ncbi.nlm.nih.gov/pubmed/21379329?dopt=Abstract&holding=f1000,f1000m,isrctn>)
- TGEN_impQC2: Arizona GWAS (<http://www.ncbi.nlm.nih.gov/pubmed/17553421?dopt=Abstract&holding=f1000,f1000m,isrctn>)

Now we are analyzing snp pairs not present in all your models (listTEST5.txt, listTEST6.txt, listTEST15.txt, listTEST16.txt). If you need the crude genotype of any pair for further research or replication, do not hesitate to get into contact with us. IF you have any question please ask directly to Oscar or me.

BW,

Oscar & Agustín

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