## **Input files**



\*\*\*RUNNING METAANALYSIS USING METAL\*\*\*

MARKERLABEL MARKER

ALLELELABELS EA NEA

**EFFECTLABEL BETA** 

WEIGHTLABEL NS

**PVALUELABEL PVALUE** 

STDERRLABEL SEBETA

FREQLABEL EAF

**GENOMICCONTROL ON** 

**AVERAGEFREQ ON** 

MINMAXFREQ ON

COLUMNCOUNTING LENIENT

**CUSTOMVARIABLE NS** 

LABEL TOTALSAMPLESIZE AS NS

SCHEME STDERR

ADDFILTER EAF > 0

ADDFILTER EAF < 1

PROCESS ADDITION\_PRO\_Glucagon0.txt

PROCESS GDM\_Glucagon0.txt

OUTFILE Glucagon0 TBL

## ANALYZE HETEROGENEITY

CLEAR

## **Output files**

