file: produceType\_avgFiles.R

function: typeAvgFiles()

#read the signature matrix file and put each cell type values in a separate file.

#Then, it calculaes the acerage value (between samples) for each cell type and return each in a separate file.

File: valculateAdjPval.R

Function: pvalCalculation()

#read the separated file for each cell type, number of probes x number of samples, and calculate the pairwise adjusted p-value between cell types and return the ones for each cell type in a separate file (PvalB, PvalG, ...)

File: calculateEffectSize.R

Function: effectSize()

#read the files with the average values for each cell types, and return the effect size matrixes for them

file:

#read the Pvalue, effectSize and average value files.

#check the threshold for Pvalues and effect size apirwise between cell types for each probe

#every probe which passes both threshold will be save in signature matrix with its average (between samples) values (between samples)