fromSynapse workflow:

location: source('/Users/fredcommo/Documents/Projet Safir/Safir RSources/CGHObjects/fromSynapse/fromSynapse.R')

buildAgilent(synId) :

- load synId using loadEntity(synId)

- build an Agilent object using:

info = c(fileName = propertyValue(entity, 'name'), sampleId = propertyValue(entity, 'id'), platform = 'Agilent'))

- Read the first lines of the file to complete the information

- Add the CBS presettings

- Read the file by skipping the first lines to get the values

- curate the matrix :

- suppress unmapped probes

- rename ChrX & Y

- get #Chr & probeStart : from chr4:40513326-40513385 returns 4, 40513326

- Suppress Flagged probes using appropriate QC columns and coding values (0/1)

- Suppress Duplicated probes

- returns an AgilentObj.

Adjust the Signal :

- Adjust Cy3/Cy5

- Adjust GC% : needs to sort by ProbeName

Add genomic positions : needs to sort by Chr and start postions

Suppress outliers : needs to sort by genomic postions.