MAARS_all_Fri_Apr_04_14h_CEST_2014.csv

= Clinical and technical features common to all samples (Atopic Dermatitis - AD / Psoriasis = PSO / CTRL)

Please be careful that several duplicated lines exist for a same MAARS_identifier (unique patient id), this only changes the sample_id

<u>Most interesting variables for sample identification</u>
- sample_id : unique sample's identification.
    - Common with transcriptomic data's column names
    - Common with MAARS_AD_full.../involved skin biopsy#involved skin biopsy#MAARS Sample identifier (MAARS_Sample_identifier) for lesional skin
    - Commun with MAARS_AD_full.../uninvolved skin biopsy#uninvolved skin biopsy#MAARS Sample identifier (MAARS_Sample_identifier) for non lesional skin
- clinical_group : AD = Atopic dermatitis / PSO = Psoriasis / CTRL = Control
- lesional : LES = lesional / NON_LES = Non lesional

<u>The other variables</u> can be useful to identify potential confounding factor of interesting clinical features

MAARS_AD_full_20190131_12-34-49.csv

= Clinical and technical features specific to AD samples (only AD Lesional and AD Non_lesional)

Please be careful that clinical and technical features are common for a same MAARS_identifier and sample_id. Thus, for the severity stratification (SCORAD_Score) it is recommended to analyse separately lesional and non lesional skin.

<u>Most interested variables for sample identification</u>
- involved skin biopsy#involved skin biopsy#MAARS Sample identifier (MAARS_Sample_identifier) : lesional sample_id
- uninvolved skin biopsy#uninvolved skin biopsy#MAARS Sample identifier (MAARS_Sample_identifier) : non lesional sample_id

<u>Most interesting variable for severity stratification and prediction</u>
- patient#SCORAD index#SCORAD#SCORAD Score (SCORAD_Score)

<u>The others variables</u> can be useful to identify potential confounding factor of interesting clinical features