

# Example of RNA-seq analysis on cell lines WT vs. KO

Table: GSEA Results Summary

Dataset	AllGenomeCCM2
Phenotype	NoPhenotypeAvailable
Upregulated in class	na_pos
GeneSet	SASP gene set.grp
Enrichment Score (ES)	0.8189947
Normalized Enrichment Score (NES)	1.9341803
Nominal p-value	0.0
FDR q-value:	0.0
FWER p-Value	0.0

Cell lines was produced by Eva Faurobert and Daphné Vannier (Albiges-Rizo team)

RNA was sequenced by MGX platform (Montpellier)

Bioinformatic and biostatistics was performed by EpiMed (IAB)

Functional analysis was performed by Eva and Daphné

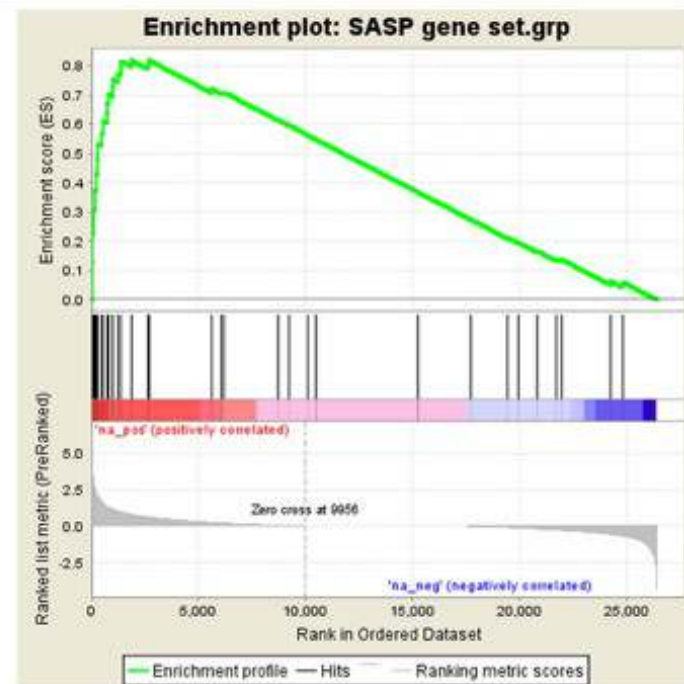


Fig 1: Enrichment plot: SASP gene set.grp  
Profile of the Running ES Score & Positions of GeneSet Members on the Rank Ordered List

[The same image](#) in compressed SVG format