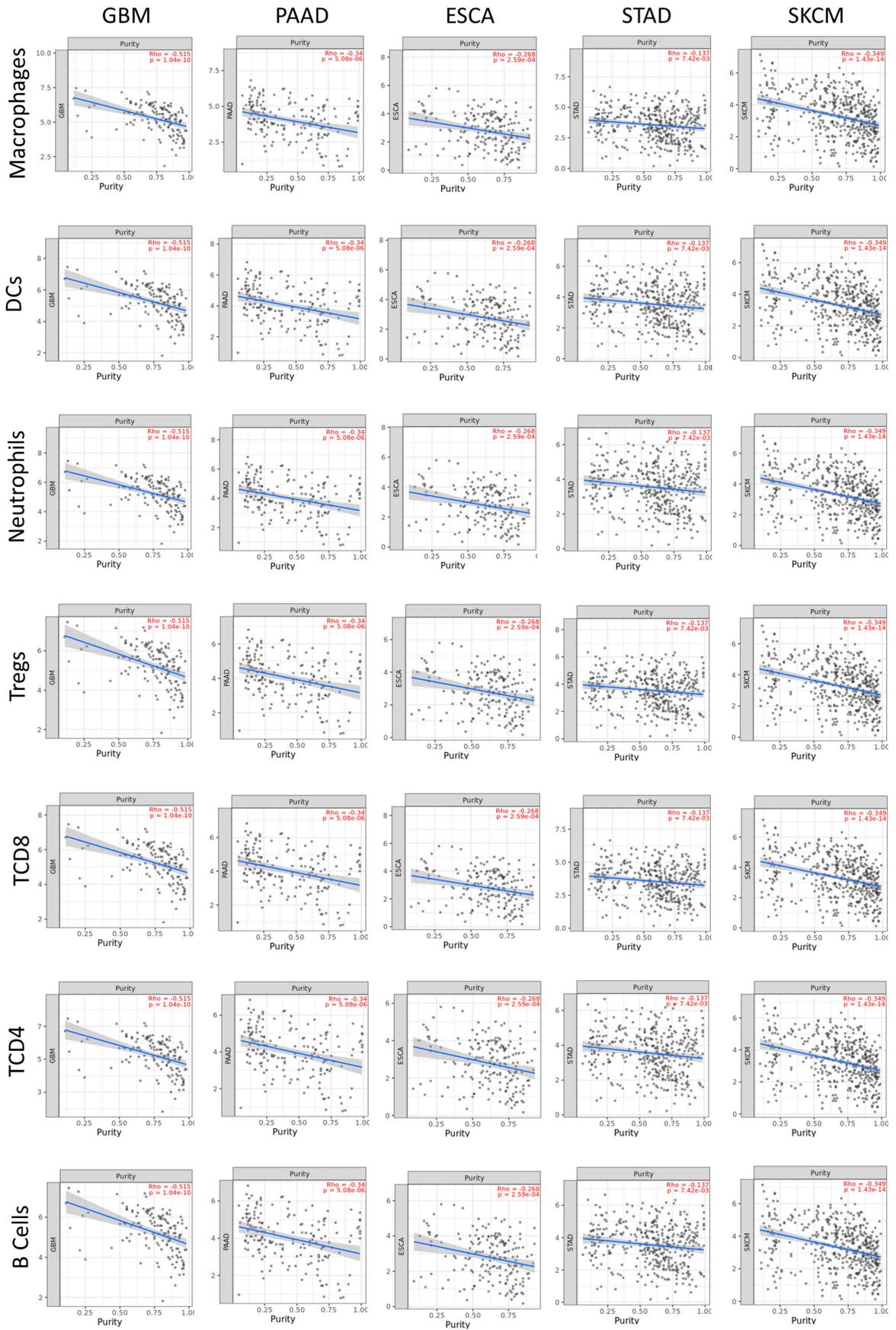
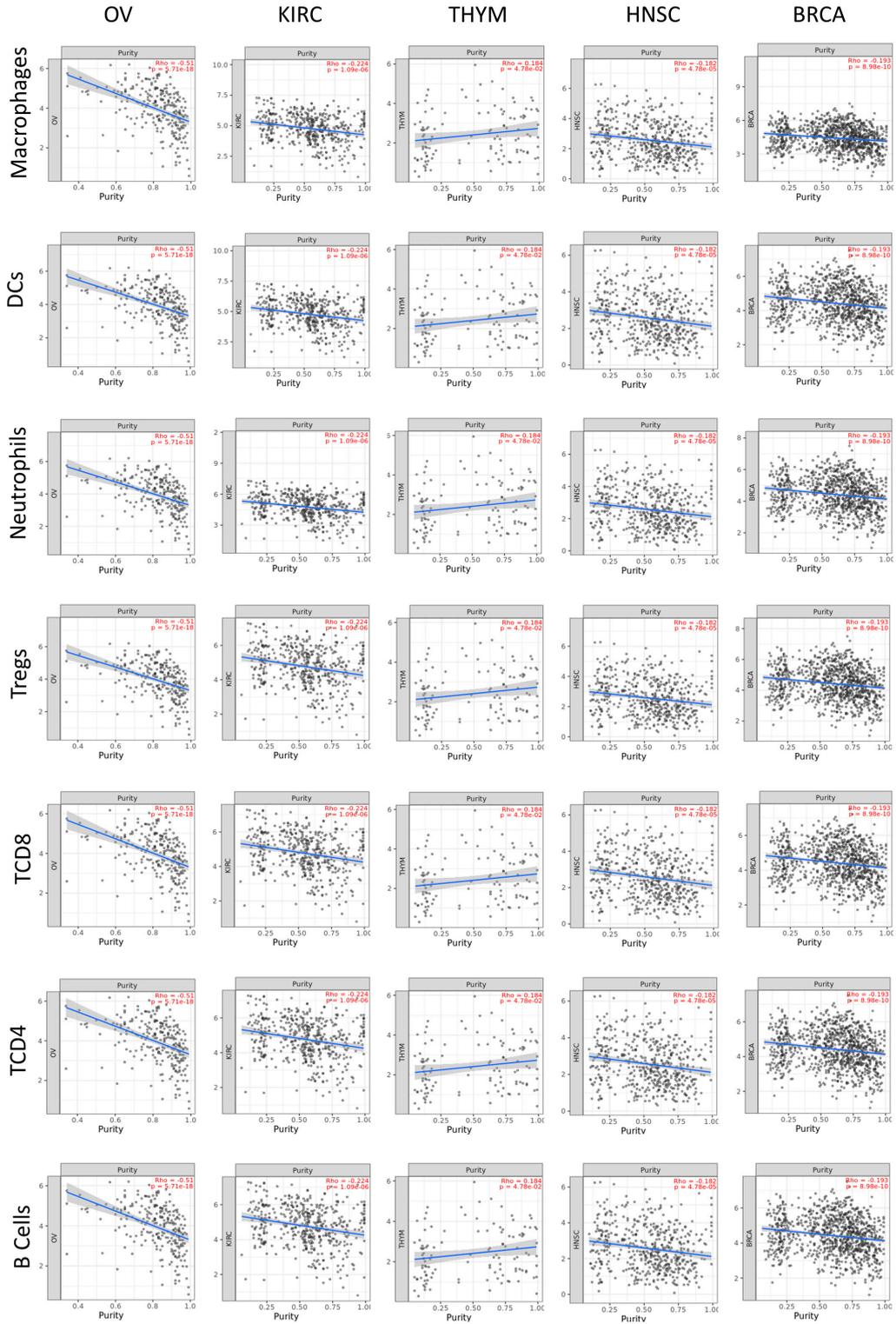


Supplementary Figure S1. Expression data obtained from GENT2. This web tool implies expression levels with the MAS5 algorithm which allows the comparison between independent datasets. a) *MSR1* expression data on breast cancer subtypes. B) *MSR1* expression data on ovarian cancer subtypes.





Supplementary Figure S2. Dot plots for the purity in relation to the immune populations in the ten selected tumor types. *MSR1* expression is represented in the y axes as log₂ (TPM) and purity level in the x axis.

Web Tool	GEPIA2	GENT2	CBIOPORTAL	KM PLOTTER	TIMER2.0	ROC PLOTTER
Data sets contained	TCGA and GTEx	GEO	Several data sets	GEO, EGA andTCGA	TCGA	GEO, EGA andTCGA
Link	https://www.cancer.gov/about-nci/organization/cg/research/structural-genomics/tcga https://gtexportal.org/home/	https://www.ncbi.nlm.nih.gov/geo/	https://www.cbioportal.org/datasets	https://www.ncbi.nlm.nih.gov/geo/ https://ega-archive.org/ https://www.cancer.gov/about-nci/organization/cg/research/structural-genomics/tcga	https://www.cancer.gov/about-nci/organization/cg/research/structural-genomics/tcga	https://www.ncbi.nlm.nih.gov/geo/ https://ega-archive.org/ https://www.cancer.gov/about-nci/organization/cg/research/structural-genomics/tcga

Supplementary Table S1. Table containing information about the data sets used and original source.