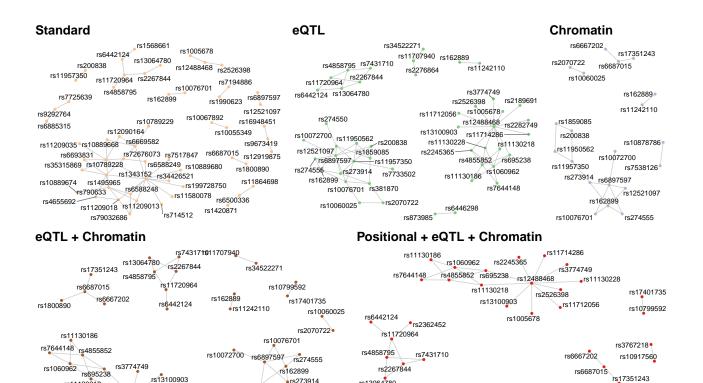
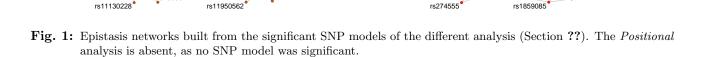
Supplementary materials

 Table 1: eQTL enriched Pathways

GO hyaluronoglycosaminidase activity GO hexosaminidase activity KEGG glycosaminoglycan degradation GO hydrolase activity hydrolyzing o glycosyl compounds GO hydrolase activity acting on glycosyl bonds NABA ecm regulators GO response to UV B GO hyaloronan catabolic process **REACTOME** hyaluronan metabolism GO hyaluronan metabolic process $\operatorname{REACTOME}$ chondoitrin sulfate dermatan sulfate GO aminoglycan catabolic process NABA matrisome associated GO cellular response to UV B **REACTOME CS DS** degradation REACTOME hyaluronan uptake and degradation





rs13064780

rs10076701

s273914

rs11957350

rs200838

rs11130218

rs2245365

rs11712056

rs12488468

___rs11714286

rs1005678

rs2526398

rs12521097

rs1859085

rs17351243

rs11950562

rs200838

rs273914

rs11957350 rs12521097

rs6897597

rs162899

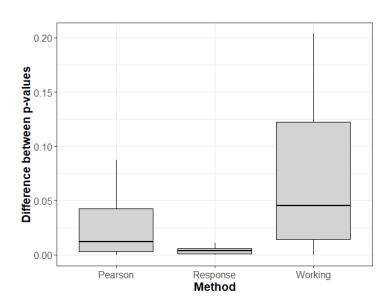


Fig. 2: To choose the best way of computing residuals in order to obtain the phenotype adjusted for population structure, we randomly extracted five SNPs in the dataset (rs12488468, rs1005678, rs11714286, rs2267844, rs11720964) and compared the associated outputs of epistasis detection. First, we computed the different residuals: we ran a logistic regression model with binary phenotypes as response variable and 7 PCs as independent variables. We derived three vectors of adjusted phenotypes from response, working and Pearson residuals. Then, we looked for statistical epistasis: we computed three linear models using the different residuals as response variable and SNP interactions as dependent variables. Finally, we performed logistic regressions with the binary phenotype as dependent variable, two SNPs and their interaction as explanatory variables, in addition to 7 PCs as covariates. We aimed at identifying the residuals leading to P-values as close as possible to the P-values from the logistic regression. P-values obtained with response residuals as phenotypes are the closest to the ones obtained with the logistic regression and are therefore selected as adjusted phenotypes in our analysis.