On the Y-axis, the residuals of log$_2$ transformed expression levels for probe ILMN_1741881 mapping to \textit{C9orf72} after regression of covariates in the replication data. On the X-axis SNP genotype bins, according to an additive model; on the left homozygotes for the major allele and homozygotes for the minor allele on the right. A regression line is plotted for each linear model. P values and R$^2$ (variance explained) for GWAS and eQTL associations in both discovery and replication cohorts are shown below each plot. Disc, Discovery; Repl, Replication; eQTL, expression quantitative trait locus; GWAS, genome-wide association study.