tissue: Tissue of which the association between TR length and
                   expression TPM count is significant
gene_id: GENCODE/Ensembl gene ID
gene_name: GENCODE gene name
chr: Chromosome (gene)
start: Gene start position
end: Gene end position
num_var: Number of TRs in cis-window (100kbp)
TR_chr: Chromosome (TR)
TR_start: TR start position
TR_end: TR end position
TR_locus: TR index in our database
eTR: Is an eTR after controlling gene-level FDR from
                   lead_TRs at 5%
lead_TR: Is a lead_TR in the cis-window
lead_p_nominal: Nominal P value of the lead TR in this cis-window
p_nominal: Nominal P value of this TR
slope: Regression slope
slope_se: Standard error of the regression slope
qval: Benjamini-Hochberg q-value dereived from Bonferroni-
                   adjusted P value