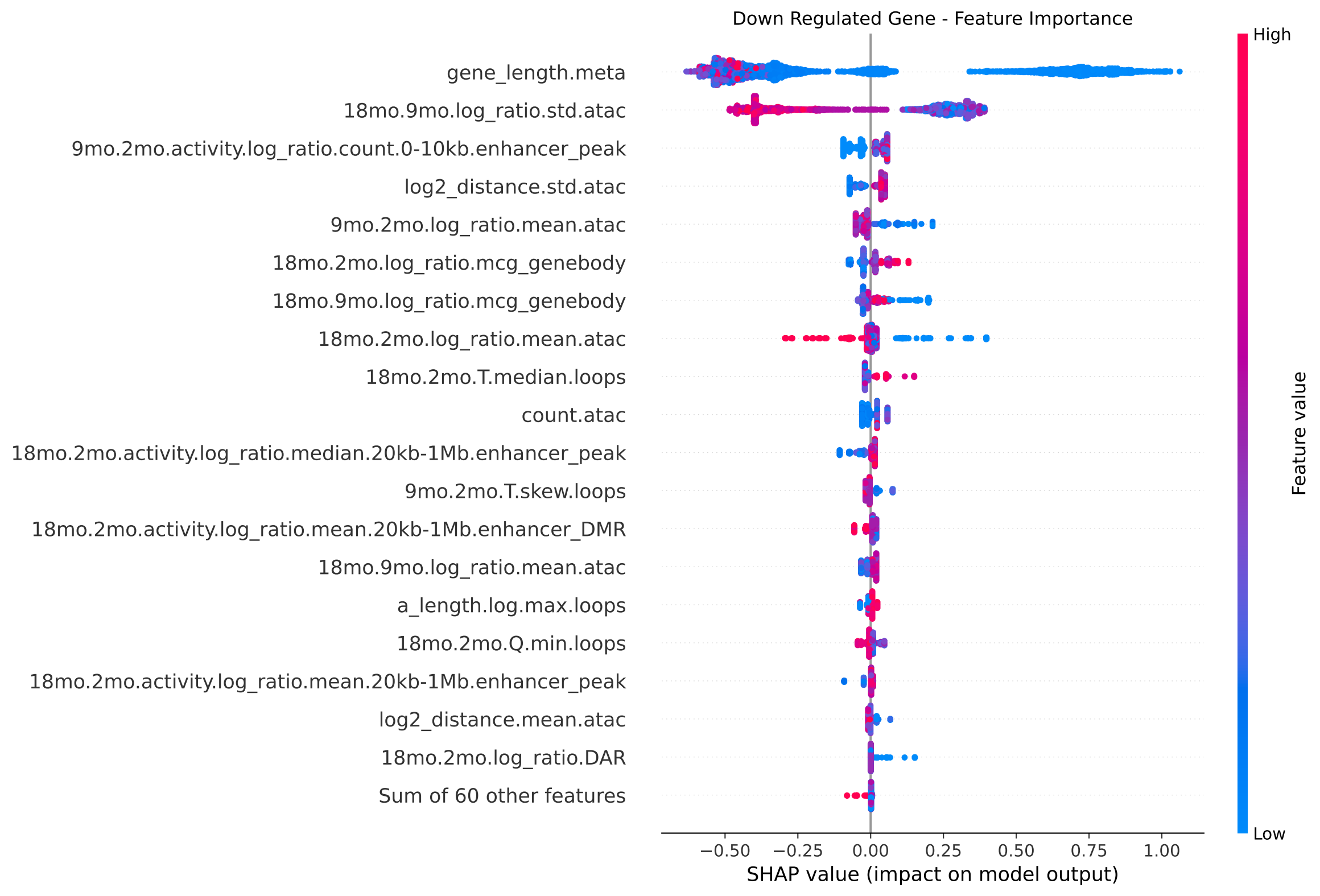
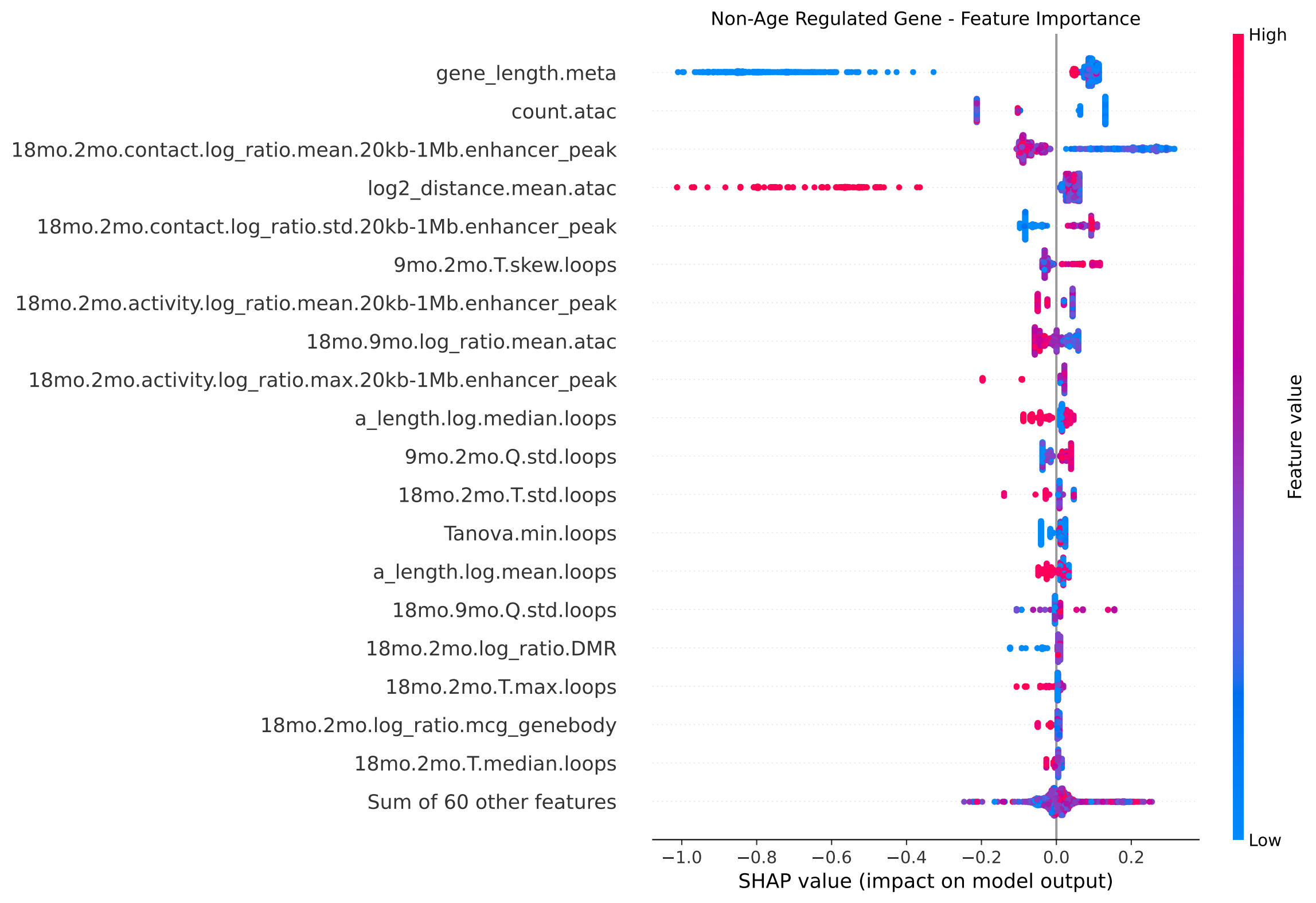
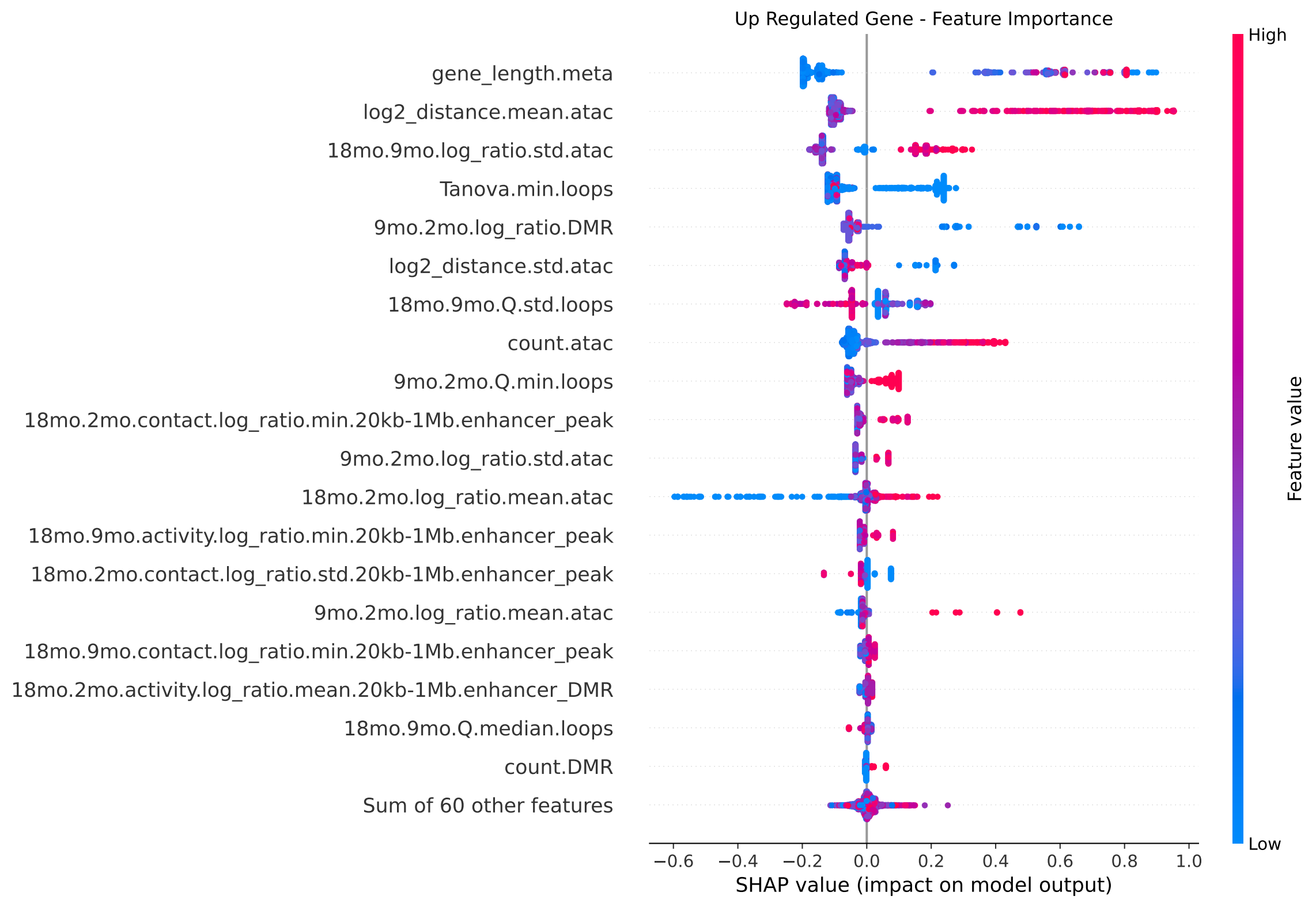

Down Regulated Gene - Feature Importance
gene_length.meta
18mo.9mo.log_ratio.std.atac
9mo.2mo.activity.log_ratio.count.0-10kb.enhancer_peak
log2_distance.std.atac
9mo.2mo.log_ratio.mean.atac
18mo.2mo.log_ratio.mcg_genebody
18mo.9mo.log_ratio.mcg_genebody
18mo.2mo.log_ratio.mean.atac
18mo.2mo.T.median.loops
count.atac
18mo.2mo.activity.log_ratio.median.20kb-1Mb.enhancer_peak
9mo.2mo.T.skew.loops
18mo.2mo.activity.log_ratio.mean.20kb-1Mb.enhancer_DMR
18mo.9mo.log_ratio.mean.atac
a_length.log.max.loops
18mo.2mo.Q.min.loops
18mo.2mo.activity.log_ratio.mean.20kb-1Mb.enhancer_peak
log2_distance.mean.atac
18mo.2mo.log_ratio.DAR
Sum of 60 other features
−0.50
−0.25
0.00
0.25
0.50
0.75
1.00
SHAP value (impact on model output)
High
Feature value
Low


Non-Age Regulated Gene - Feature Importance
gene_length.meta
count.atac
18mo.2mo.contact.log_ratio.mean.20kb-1Mb.enhancer_peak
log2_distance.mean.atac
18mo.2mo.contact.log_ratio.std.20kb-1Mb.enhancer_peak
9mo.2mo.T.skew.loops
18mo.2mo.activity.log_ratio.mean.20kb-1Mb.enhancer_peak
18mo.9mo.log_ratio.mean.atac
18mo.2mo.activity.log_ratio.max.20kb-1Mb.enhancer_peak
a_length.log.median.loops
9mo.2mo.Q.std.loops
18mo.2mo.T.std.loops
Tanova.min.loops
a_length.log.mean.loops
18mo.9mo.Q.std.loops
18mo.2mo.log_ratio.DMR
18mo.2mo.T.max.loops
18mo.2mo.log_ratio.mcg_genebody
18mo.2mo.T.median.loops
Sum of 60 other features
−1.0
−0.8
−0.6
−0.4
−0.2
0.0
0.2
SHAP value (impact on model output)
High
Feature value
Low


Up Regulated Gene - Feature Importance
gene_length.meta
log2_distance.mean.atac
18mo.9mo.log_ratio.std.atac
Tanova.min.loops
9mo.2mo.log_ratio.DMR
log2_distance.std.atac
18mo.9mo.Q.std.loops
count.atac
9mo.2mo.Q.min.loops
18mo.2mo.contact.log_ratio.min.20kb-1Mb.enhancer_peak
9mo.2mo.log_ratio.std.atac
18mo.2mo.log_ratio.mean.atac
18mo.9mo.activity.log_ratio.min.20kb-1Mb.enhancer_peak
18mo.2mo.contact.log_ratio.std.20kb-1Mb.enhancer_peak
9mo.2mo.log_ratio.mean.atac
18mo.9mo.contact.log_ratio.min.20kb-1Mb.enhancer_peak
18mo.2mo.activity.log_ratio.mean.20kb-1Mb.enhancer_DMR
18mo.9mo.Q.median.loops
count.DMR
Sum of 60 other features
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
1.0
SHAP value (impact on model output)
High
Low
Feature value