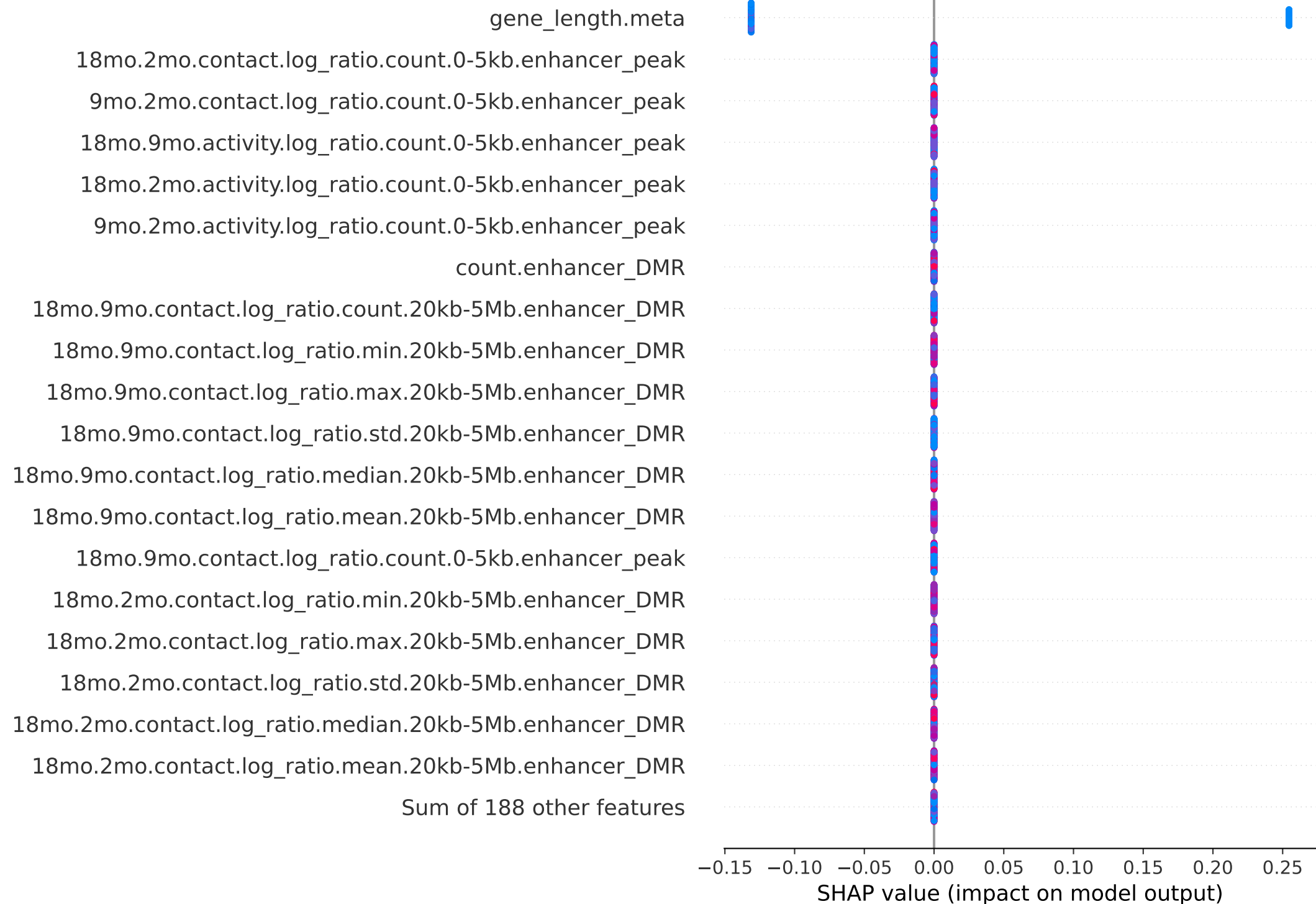


Down Regulated Gene - Feature Importance

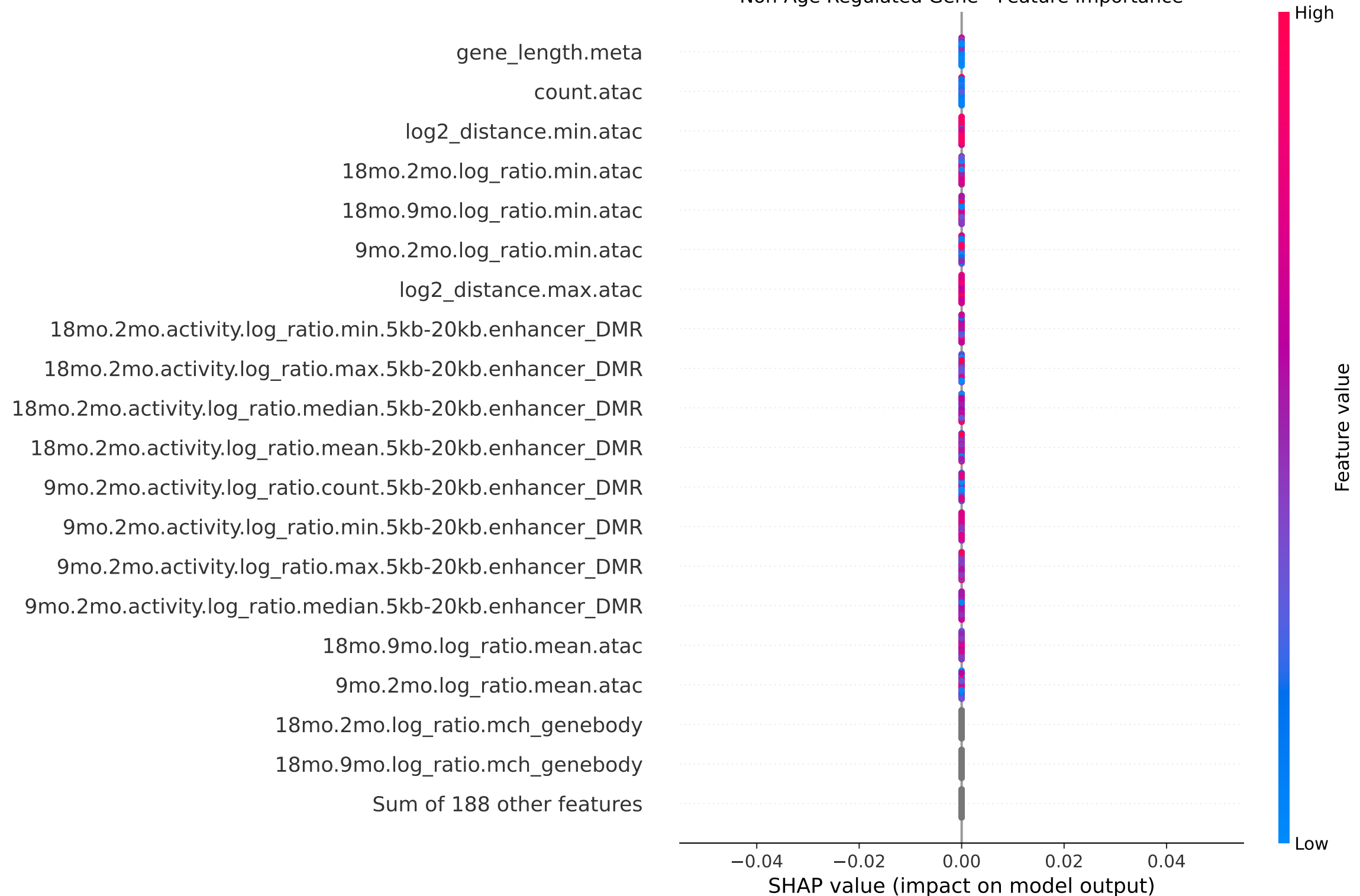
High

Feature value

Low



Non-Age Regulated Gene - Feature Importance



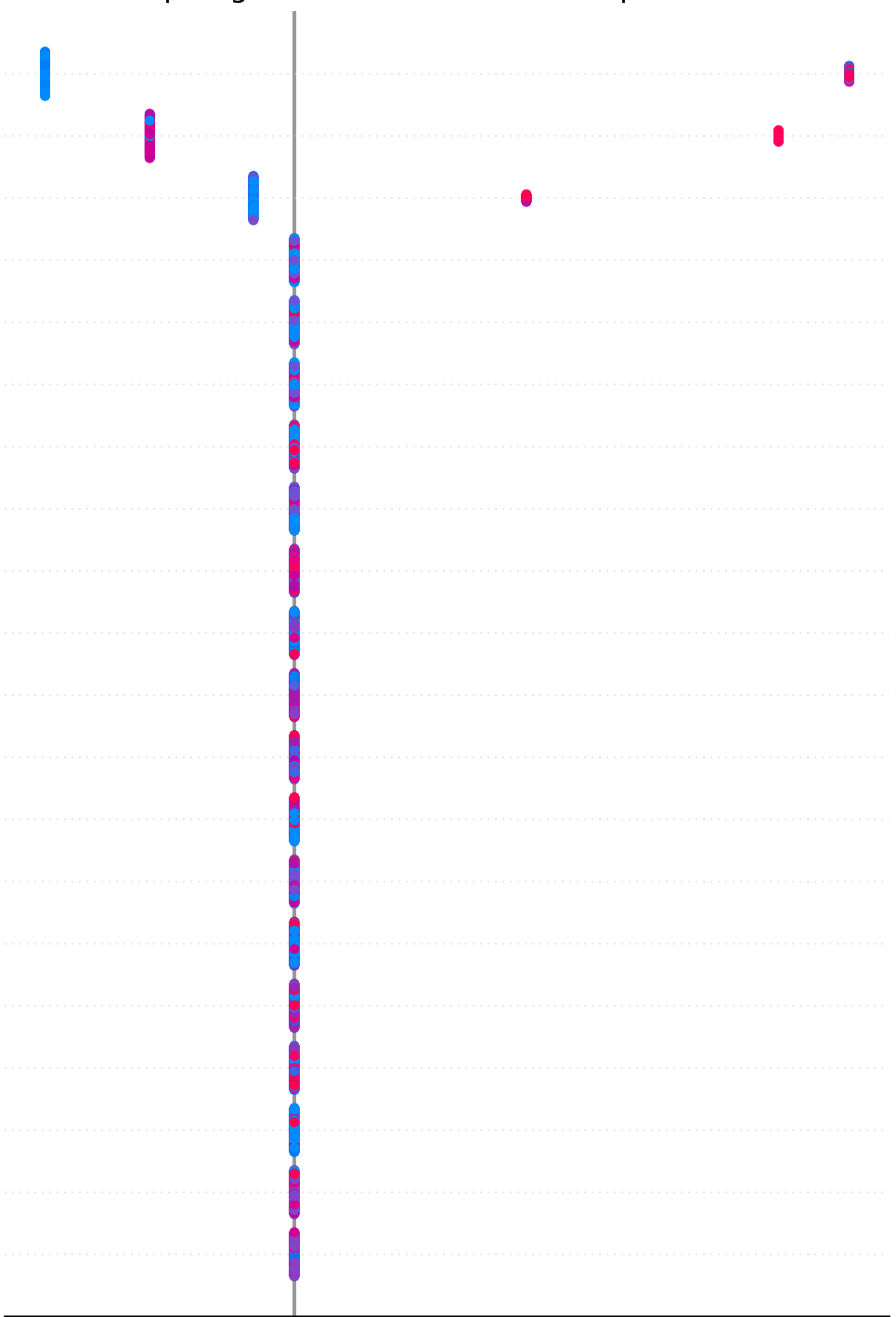
Up Regulated Gene - Feature Importance

High

Feature value

Low

- gene_length.meta
- log2_distance.max.atac
- min_distance.log.std.loops
- 18mo.2mo.contact.log_ratio.count.0-5kb.enhancer_peak
- 9mo.2mo.contact.log_ratio.count.0-5kb.enhancer_peak
- 18mo.9mo.activity.log_ratio.count.0-5kb.enhancer_peak
- 18mo.2mo.activity.log_ratio.count.0-5kb.enhancer_peak
- 9mo.2mo.activity.log_ratio.count.0-5kb.enhancer_peak
- count.enhancer_DMR
- 18mo.9mo.contact.log_ratio.count.20kb-5Mb.enhancer_DMR
- 18mo.9mo.contact.log_ratio.min.20kb-5Mb.enhancer_DMR
- 18mo.9mo.contact.log_ratio.max.20kb-5Mb.enhancer_DMR
- 18mo.9mo.contact.log_ratio.std.20kb-5Mb.enhancer_DMR
- 18mo.9mo.contact.log_ratio.median.20kb-5Mb.enhancer_DMR
- 18mo.2mo.contact.log_ratio.count.20kb-5Mb.enhancer_DMR
- 18mo.2mo.contact.log_ratio.min.20kb-5Mb.enhancer_DMR
- 18mo.2mo.contact.log_ratio.max.20kb-5Mb.enhancer_DMR
- 18mo.2mo.contact.log_ratio.std.20kb-5Mb.enhancer_DMR
- 18mo.2mo.contact.log_ratio.median.20kb-5Mb.enhancer_DMR
- Sum of 188 other features



SHAP value (impact on model output)