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| CAVIAR\_example.script.sh | Example of CAVIAR script |
| **STRgenotype.hipstr** | Script for generating STR genotypes from cram files using HipSTR |
| **ExtractingFilteredSTRGenotypesFromVCF.sh** | Script for extracting STR genotypes from VCF file generated by HipSTR |
| QualityControl.DNAmetylation.R | Script for performing quality control of DNA methylation measurements |
| computingLD\_perSTR.R | Script for computing LD structure between STR and SNV genotypes |
| computingVst.R | Script for computing Vst metric |
| extractingresiduals.DNAmethylation.R | Script for extracting residuals obtained from adjusting DNA methylation measurements for covariates |
| mappingMethylationSTRs.R | Script for DNA methylation QTL mapping using STR genotypes |
| mappingMethylationSTRs.filtering.R | Script for filtering step of identified mSTRs |
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