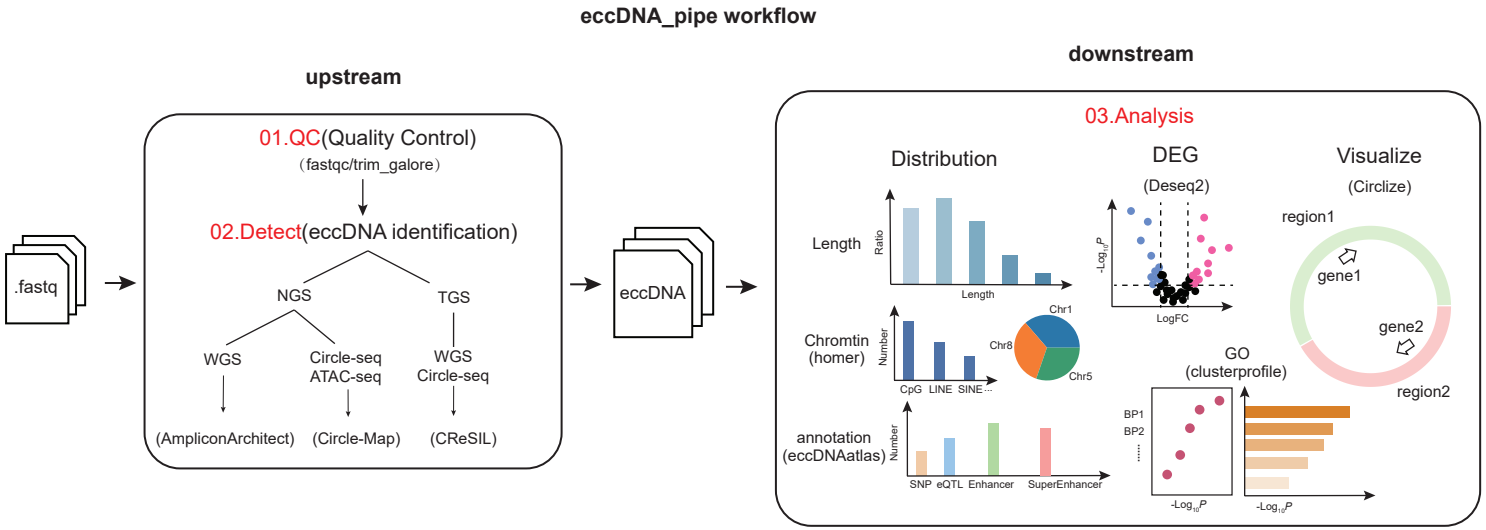
eccDNA_pipe workflow
upstream
downstream
.fastq
01.QC(Quality Control)
(fastqc/trim_galore)
02.Detect(eccDNA identification)
NGS
TGS
WGS
Circle-seq
ATAC-seq
WGS
Circle-seq
(AmpliconArchitect)
(Circle-Map)
(CReSIL)
eccDNA
03.Analysis
Distribution
DEG
(Deseq2)
Visualize
(Circlize)
Length
Ratio
Length
-Log10P
LogFC
region1
gene1
gene2
region2
Chromtin
(homer)
Number
CpG
LINE
SINE
Chr1
Chr8
Chr5
GO
(clusterprofile)
annotation
(eccDNAatlas)
Number
SNP
eQTL
Enhancer
SuperEnhancer
BP1
BP2
-Log10P
-Log10P