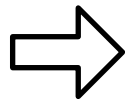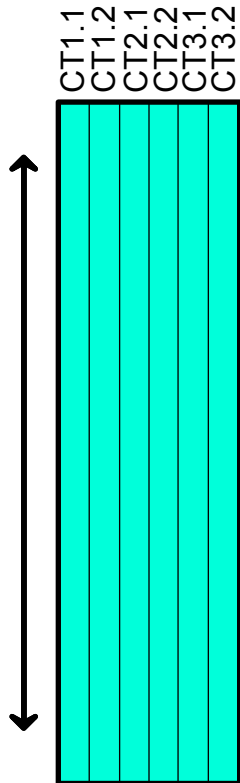# Reference data set

Target data set

1. rank rows by variance

2. rank rows by association with the cell type factor (ANOVA F-statistics),
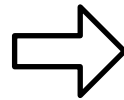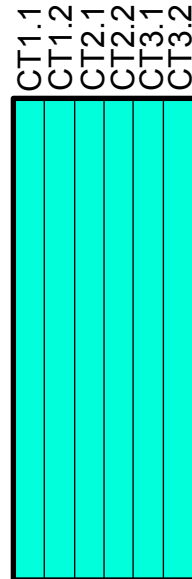3. extract the coefficients

4. constrained projection

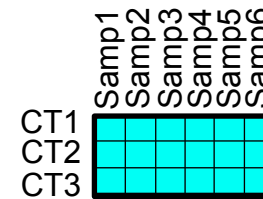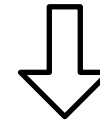5. correction of the differential methylation analysis

CT1.1 CT1.2 CT2.1 CT2.2 CT3.1 CT3.2

CT1.1 CT1.2 CT2.1 CT2.2 CT3.1 CT3.2

CT1 CT2 CT3

Samp1 Samp2 Samp3 Samp4 Samp5 Samp6

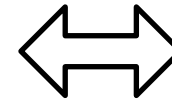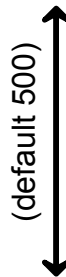Samp1 Samp2 Samp3 Samp4 Samp5 Samp6

m input CpG sites

m input CpG sites
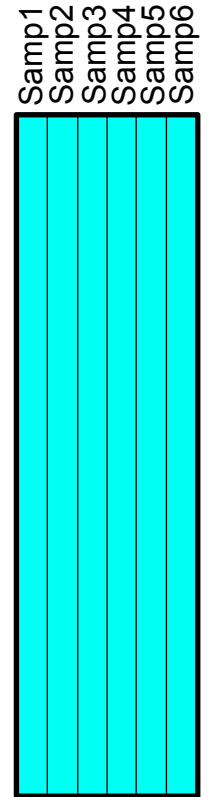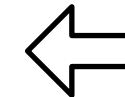
`inference.max.cell.type.markers = 10000`
(default 10,000)
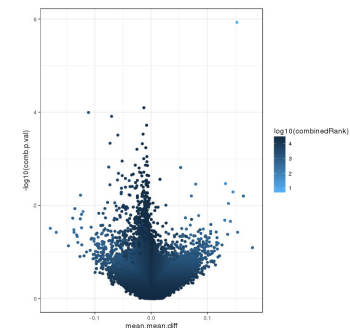
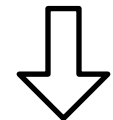`inference.top.cell.type.markers = 500`
(default 500)

Cell type proportion estimates

Samp1 Samp2 Samp3 Samp4 Samp5 Samp6

CT1
CT2
CT3

`rnb.set@inferred.covariates`

Sample annotation sheet

`inference.reference.methylome.column = "Cell_type"`

SampleID	Group	Cell_type
Samp1	Case	NA
Samp2	Control	NA
Samp3	Case	NA
Samp4	Control	NA
Samp5	Case	NA
Samp6	Control	NA
CT1.1	NA	CT1
CT1.2	NA	CT1
CT2.1	NA	CT2
CT2.2	NA	CT2
CT3.1	NA	CT3
CT3.2	NA	CT3

`differential.adjustment.celltype = TRUE`