**Samples QC**

Initial Total **1161**

Cord blood sample failure **4**

3 yo sample failure **1**

7 yo sample failure **5**

Carried to QC **129**

Carried to QC **549**

Carried to QC **473**

* Replicates **42**
* Low quality **10**
* Genotype Mismatch **6**
* Sex mismatch **6**
* Replicates **0**
* Low quality **3**
* Genotype Mismatch **3**
* Sex mismatch **3**
* Replicates **0**
* Low quality **6**
* Genotype Mismatch **4**
* Sex mismatch **3**

Removed

QC **64**

Removed

QC **9**

Removed

QC **13**

Total Failed N=**10**

Total Carried to QC N=**1151**

Total Removed QC N=**86**

Total Removed QC N=**86**

After QC **485**

After QC **120**

After QC **460**

Total After QC N=**1065**

**Probes QC**

On 450K arrays **485,577**

Quality detection>75 Median<0.05

**459**

Non Cg

**2,994**

On sex chromosome **11,648**

Actual SNPs

**65**

Total probes after standard QC **470,411**

Normalization with BMIQ

Include main exposure/outcome of interest in [mode]

Other co-variates may be included in [mode] depending on the analysis

**Analysis**

**Batch Effect Adjustment = Combat**

Cell count estimated using Housman blood cells reference. Using 5out 6-leaving out granulocytes

Additional co-variables that will be in your final regression model for the plan analysis

**Cell Count Correction**

**Regression Analysis**

**`**

* Robust regression
* Methylation levels using betas (values 0-1)
* Guidelines for co-variables
* Sex, race, age at sampling (gestational age for cord blood), maternal age at enrollment, education (marker SES)
* Cord blood = maternal smoking during pregnancy, parity

**Interpretation**

Annotation bioconductor package R

**Multiple Test Correction**

**FDR**