

COHORTS

Newly diagnosed RA
patients (N=11)

MTX treated RA
patients (N=18)

Controls (N=9)

CELL TYPES

CD4⁺ naive T cells

CD4⁺ memory
T cells

mRRBS

Genomic
DNA

MspI
digestion

End repair,
A-tailing
and adapter
ligation

Bisulfite
conversion

PCR and
library
preparation

Sequencing
on Hiseq
2500 or
3000

Bioinformatic pipeline and statistical analyses

Annotation
of DMP
•CpGs and
genes
•RA risk
genes
•Gene
ontology

Statistical
comparison
of
methylation
values
(coverage
≥10 and
group size
≥5)

Filtering out
SNPs, sex
chromo-
somes and
outlier
samples

Quality
control,
alignment
of reads,
calling
methylation
values