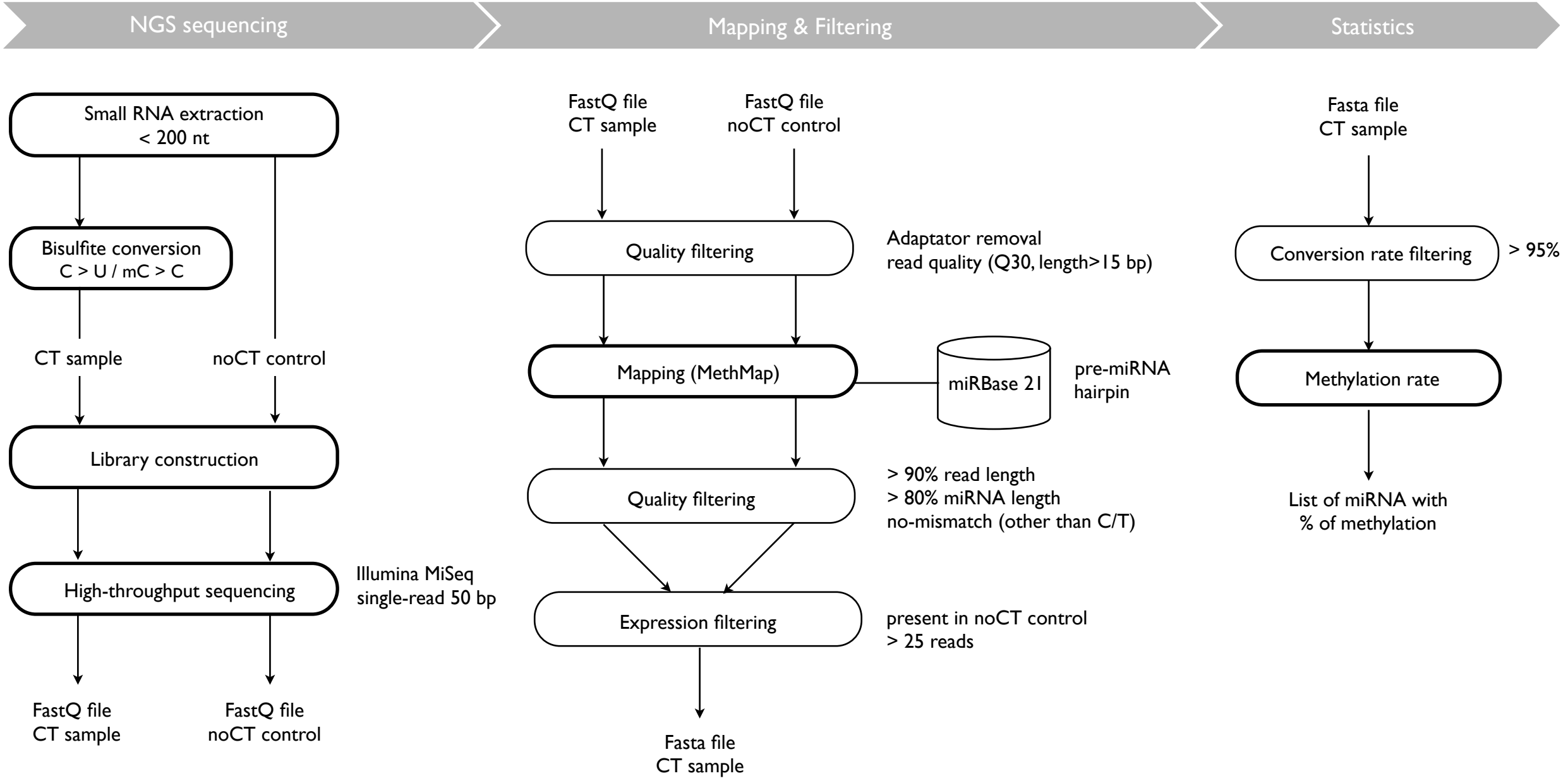
NGS sequencing
Mapping & Filtering
Statistics
Small RNA extraction
< 200 nt
Bisulfite conversion
C > U / mC > C
CT sample
noCT control
Library construction
High-throughput sequencing
Illumina MiSeq
single-read 50 bp
FastQ file
CT sample
FastQ file
noCT control
FastQ file
CT sample
FastQ file
noCT control
Quality filtering
Adaptator removal
read quality (Q30, length>15 bp)
Mapping (MethMap)
miRBase 21
pre-miRNA
hairpin
Quality filtering
> 90% read length
> 80% miRNA length
no-mismatch (other than C/T)
Expression filtering
present in noCT control
> 25 reads
Fasta file
CT sample
Fasta file
CT sample
Conversion rate filtering
> 95%
Methylation rate
List of miRNA with
% of methylation