

DNA Methylation Analysis with Nextflow

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1 Intro

Learn how to read a comma-separated sample metadata file containing semicolon-separated FASTQ file lists, and inspect parsed outputs using channels in Nextflow DSL2.

```
Channel.fromPath(params.metatab) .splitCsv(header:true, sep:',')
```

2 Nextflow notes

3 Test 2

Test 2

4 Test 3

Test3