

nf-core/mag params json:

```
{  
  "input": "samplesheet.csv",  
  "outdir": ".\\results",  
  "save_clipped_reads": true,  
  "reads_minlength": 50,  
  "fastp_cut_mean_quality": 25,  
  "skip_spadeshybrid": true,  
  "skip_spades": true,  
  "skip_prodigal": true,  
  "skip_binning": true,  
  "skip_binqc": true  
}
```

nf-core/funcscan params json:

```
{  
  "input": "samplesheet.csv",  
  "outdir": ".\\results",  
  "run_arg_screening": true,  
  "arg_skip_deeparg": true,  
  "arg_skip_rgi": true,  
  "arg_skip_fargene": true,  
  "arg_hamronization_summarizeformat": "tsv"  
}
```

**Supplementary Figure S2.** Bioinformatics analysis parameters.