

# Loop Report (08/15/2022)

All loops were called using SIP with the following parameters (example given is a merged .hic file for all control replicates (3) and with `-isDroso true`):

```
java -jar /proj/phanstiel_lab/Software/SIP/SIP_HiCv1.6.2.jar  
  
hic /proj/phanstiel_lab/Data/processed/YAPP/hic/hg38/220716_dietJuicerMerge_condition/outp  
  
/proj/phanstiel_lab/References/chromSizes/hg38_chromSizes.txt  
  
/proj/phanstiel_lab/Data/processed/YAPP/hic/hg38/220719_sip-loops/isDroso/cont  
  
/proj/phanstiel_lab/Software/juicer/scripts/juicer_tools.jar  
  
-norm SCALE -g 1.0 -min 2.0 -max 2.0 -mat 2000 -d 6 -res 5000 -sat 0.01 -t 2000 -nbZero 6
```

## Load libraries

```
library(hictoolsr)  
library(glue)  
library(dbscan)  
library(tidyverse)  
library(GenomeInfoDb)
```

## Load .hic files

```
cond <- c("cont", "sorb", "omega")  
hic_files <- list.files(path = glue("~/Phanstiel Lab Dropbox/JP Flores/projects/YAPP/YAPP/
```

#### **-isDroso true loops by condition**

```
isDroso_loops <- list.files(path = glue("~/Phanstiel Lab Dropbox/JP Flores/projects/YAPP/YAPP/da",
                                     full.names = T,
                                     pattern = "5kb")
```

```
cont_isDroso_loops <- mergeBedpe("~/Phanstiel Lab Dropbox/JP Flores/projects/YAPP/YAPP/da
```

```
sorb_isDroso_loops <- mergeBedpe("~/Phanstiel Lab Dropbox/JP Flores/projects/YAPP/YAPP/da
```

```
omega_isDroso_loops <- mergeBedpe("~/Phanstiel Lab Dropbox/JP Flores/projects/YAPP/YAPP/da
```

```
isDroso_total_loops <- mergeBedpe(isDroso_loops, res = 10e3)
```

```
## control loops (~-isDroso true~)
nrow(cont_isDroso_loops)
```

[1] 8062

```
## sorbitol loops (~-isDroso true~)
nrow(sorb_isDroso_loops)
```

[1] 7552

```
## omega loops (~-isDroso true~)
nrow(omega_isDroso_loops)
```

[1] 25588

```
## total # of loops (~-isDroso true~)
nrow(isDroso_total_loops)
```

[1] 33593

#### **-isDroso false loops by condition**

```
noDroso_loops <- list.files(path = glue("~/Phanstiel Lab Dropbox/JP Flores/projects/YAPP/YAPP/"),
                           full.names = T,
                           pattern = "5kb")
```

```
cont_noDroso_loops <- mergeBedpe("~/Phanstiel Lab Dropbox/JP Flores/projects/YAPP/YAPP/data/cont_noDroso_loops.bedpe")
```

```
sorb_noDroso_loops <- mergeBedpe("~/Phanstiel Lab Dropbox/JP Flores/projects/YAPP/YAPP/data/sorb_noDroso_loops.bedpe")
```

```
omega_noDroso_loops <- mergeBedpe("~/Phanstiel Lab Dropbox/JP Flores/projects/YAPP/YAPP/data/omega_noDroso_loops.bedpe")
```

```
noDroso_total_loops <- mergeBedpe(noDroso_loops, res = 10e3)
```

```
## control loops (~isDroso false~)
nrow(cont_noDroso_loops)
```

[1] 18959

```
## sorbitol loops (~isDroso false~)
nrow(sorb_noDroso_loops)
```

[1] 5576

```
## omega loops (~isDroso false~)
nrow(omega_noDroso_loops)
```

[1] 22164

```
## total # of loops (~isDroso false~)
nrow(noDroso_total_loops)
```

[1] 30679

**Combining -isDroso true and -isDroso false loops**

```
noDroso_loops <- list.files(path = glue("~/Phanstiel Lab Dropbox/JP Flores/projects/YAPP/Y"),
                           full.names = T,
                           pattern = "5kb")

isDroso_loops <- list.files(path = glue("~/Phanstiel Lab Dropbox/JP Flores/projects/YAPP/Y"),
                           full.names = T,
                           pattern = "5kb")

bothDroso_loops <- c(isDroso_loops, noDroso_loops)

bothDroso_total_loops <- mergeBedpe(bothDroso_loops, res = 10e3)

## combining ALL loops (~isDroso true & false`)
nrow(bothDroso_total_loops)
```

[1] 40114

**i** Note

This report was created because we mentioned that these loop numbers were pretty high.