

1 Validation

Chromatin boundaries validation table

```
> library(xtable)
> options(xtable.floating = FALSE)
> options(xtable.timestamp = "")
>
>
> # knitr::opts_chunk$set(echo = TRUE)
>
```

Chromatin boundaries validation plot(ly)s

```
> cyto_ref_hcb = data.frame()
> hcb_validation_df = data.frame()
```

Chromatin boundaries validation shift ggplot

```
>
>
>
```