201009_NanoNOMe_chm13_mappability

G$

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```r
#genome coverage as sliding window
cov.average <-cov %>%
  group_by(chr) %>%
  summarise(
  window.start = rollapply(start, width=1000, by=1000, FUN=min, align="left", partial=TRUE),
  window.end = rollapply(end, width=1000, by=1000, FUN=max, align="left", partial=TRUE),
  coverage = rollapply(cov, width=1000, by=1000, FUN=mean, align="left", partial=TRUE)
) %>%
  ungroup()
```

```
## `summarise()` regrouping output by 'chr' (override with `.groups` argument)
```

```r
p <- ggplot(cov.average, aes( x = window.start, y = coverage))+geom_smooth(method = "loess", span = 0.0
p
```

```
## `geom_smooth()` using formula 'y ~ x'
```
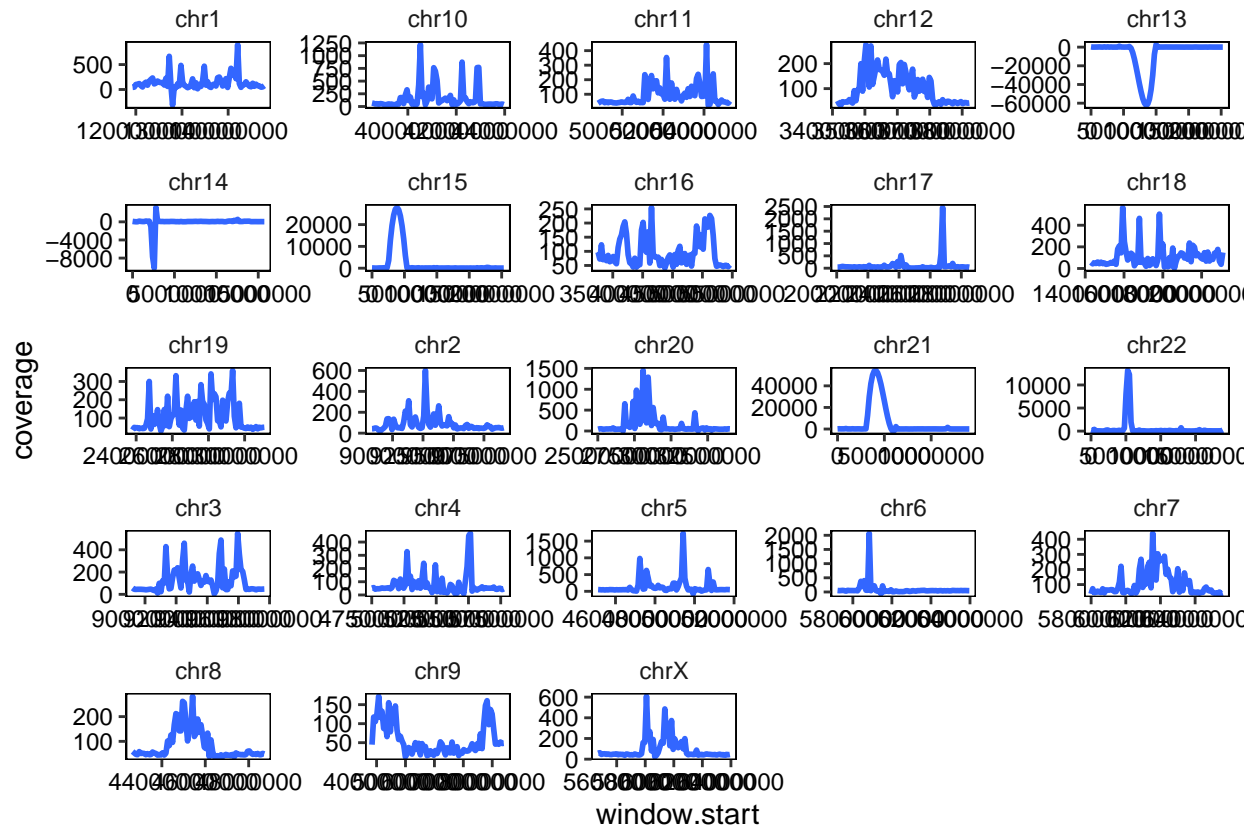
```
ggsave(
  paste0(figs, "/","GM12878_cen_coverage.pdf"),
  plot = p,
  scale = 1,
  width = 10,
  height = 10,
)
```

```
## `geom_smooth()` using formula 'y ~ x'
```