Annex 2: Duplicates elimination

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UNIX

```
# Keep only chromosome, start, end, window and score
awk '{print $1,$2,$3,$4,$5}' windows_200.bed > windows_200_bedtools.bed

# Sort by chromosome and x1
sort -k1,1 -k2,2n windows_200_bedtools.bed > sorted_windows_200_bedtools.bed

# Tab-separate the file
sed 's/ /\t/g' sorted_windows_200_bedtools.bed > tab_sorted_windows_200_bedtools.bed

# Detection of overlapping with BEDtools (11907 original, 11045 unique, 862 overlapping)
bedtools merge -nms -i tab_sorted_windows_200_bedtools.bed > duplicates.txt

# Save duplicates
cut -f4 duplicates.txt | grep -o ";.*" | awk '{print substr($1,2); }' > my_duplicates_1.txt

cut -f4 duplicates.txt | grep -o ";.*" | awk '{print substr($1,2); }' | grep -o ";.*" |
awk '{print substr($1,2);}' > my_duplicates_2.txt
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```
setwd("~/ProjectX")
# Initial 200-sized DHSs
original <- read.table("windows_200.bed", h = T)</pre>
# Duplicated windows detected with Bedtools
dups_1 <- read.table("my_duplicates_1.txt")</pre>
dups_2 <- read.table("my_duplicates_2.txt")</pre>
# Regex to parse out triplicates
myregex <- "(;.*)"
# Keep only what is before; once (for duplicates)...
dups_1_fixed <- data.frame(gsub(pattern = myregex, "\\2", x = dups_1$V1))</pre>
# ... and again (for triplicates)
dups_2_fixed <- data.frame(gsub(pattern = myregex, "\\2", x = dups_2$V1))</pre>
# 1 quadriplicate left
dups_3_fixed <- data.frame("4:981220-981370")</pre>
colnames(dups_1_fixed) <- "duplicated_windows"</pre>
colnames(dups_2_fixed) <- "duplicated_windows"</pre>
colnames(dups_3_fixed) <- "duplicated_windows"</pre>
```