

# Allele-specific ChIPseq analysis. Explore peaksets

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## 3.4.1. Explore DEX

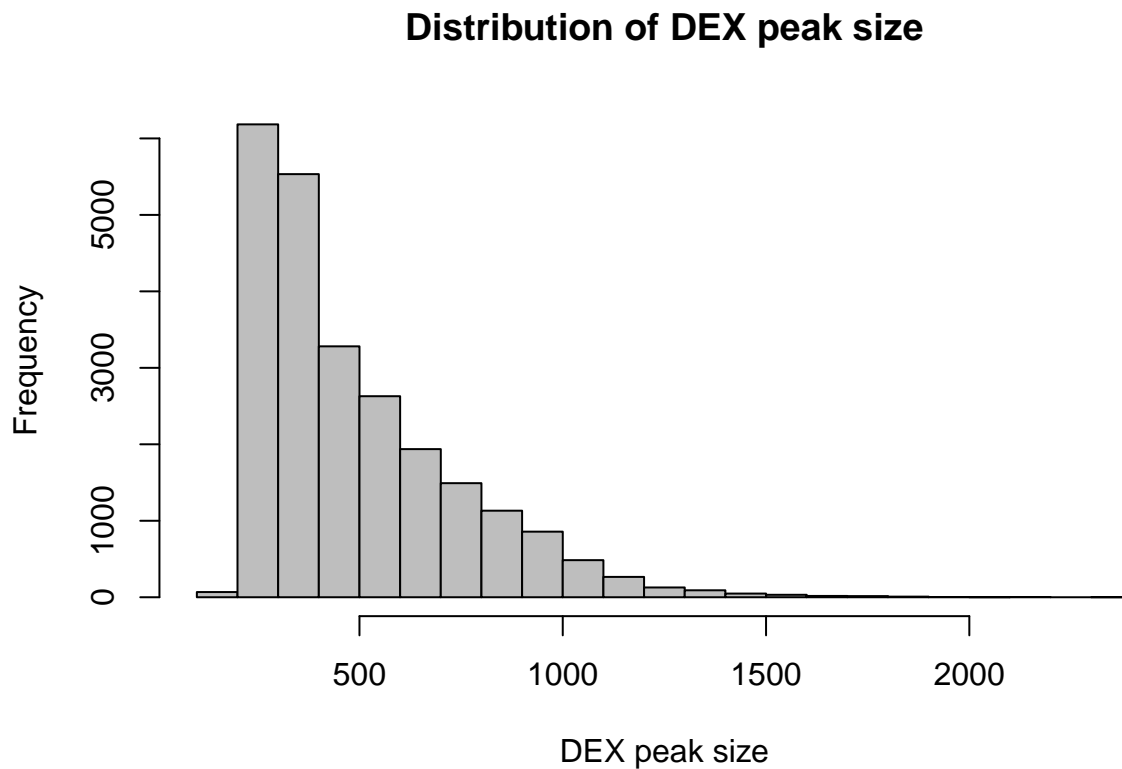
### 3.4.1.1. Mean, median, and max size of the peaks

```
summary(width(grange.dex))
```

##	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
##	168	298	409	492	622	2391

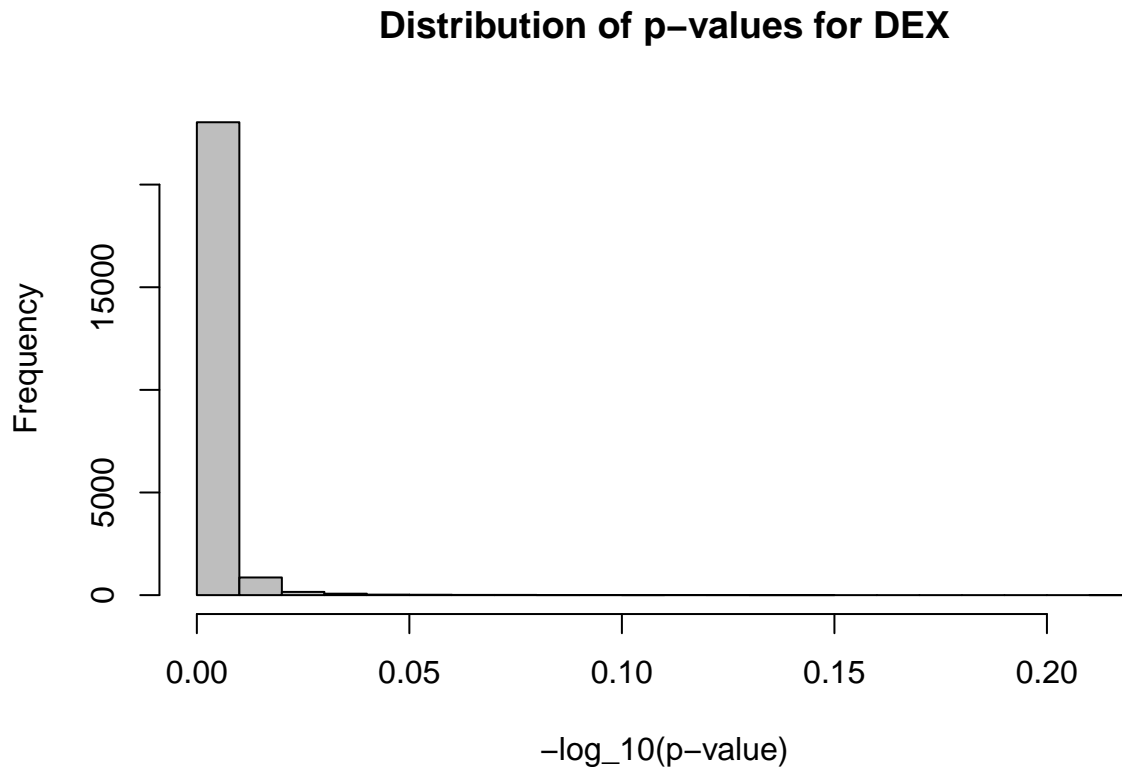
### 3.4.1.2. Distribution of peak sizes

```
hist(width(grange.dex), xlab = "DEX peak size", col = "gray", main = "Distribution of DEX peak size")
```



### 3.4.1.3 Distribution of peak p-values

```
p.values <- score(grange.dex)
hist(p.values, xlab = "-log10(p-value)", col = "gray", main = "Distribution of p-values for DEX")
```



### 3.4.2. Explore VEH

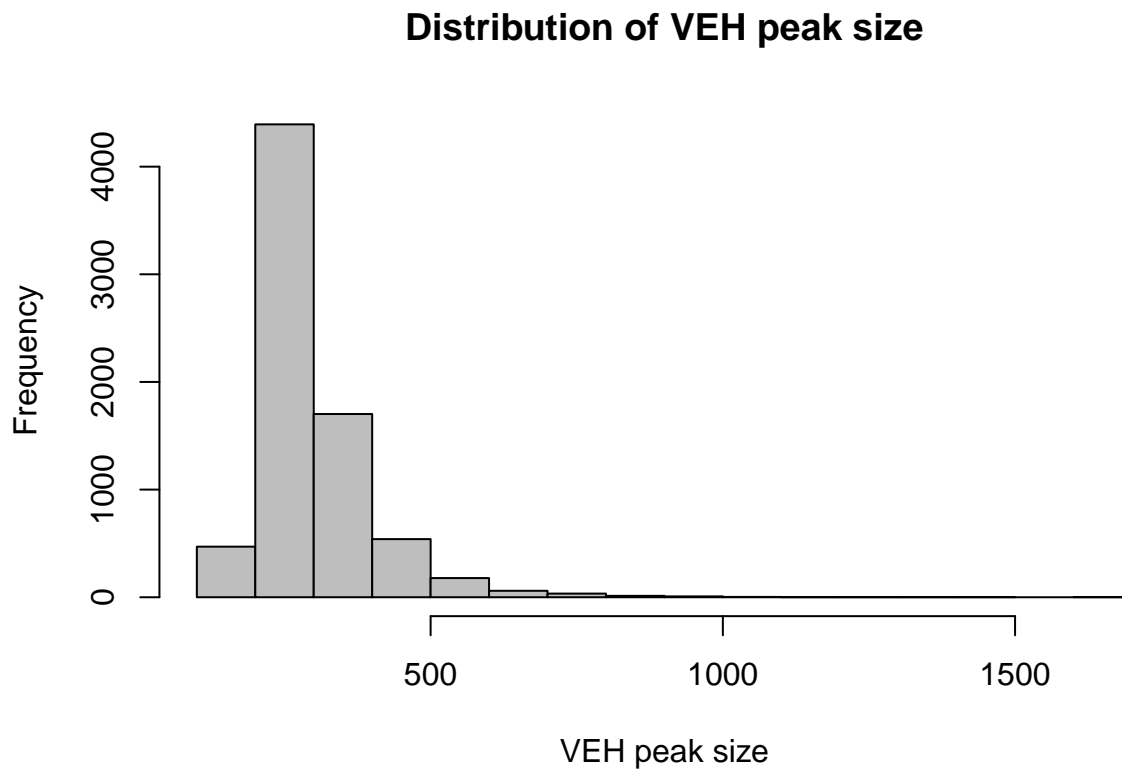
#### 3.4.2.1. Mean, median, and max size of the peaks

```
summary(width(grange.veh))
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    172.0   232.0   270.0   295.7   327.8  1643.0
```

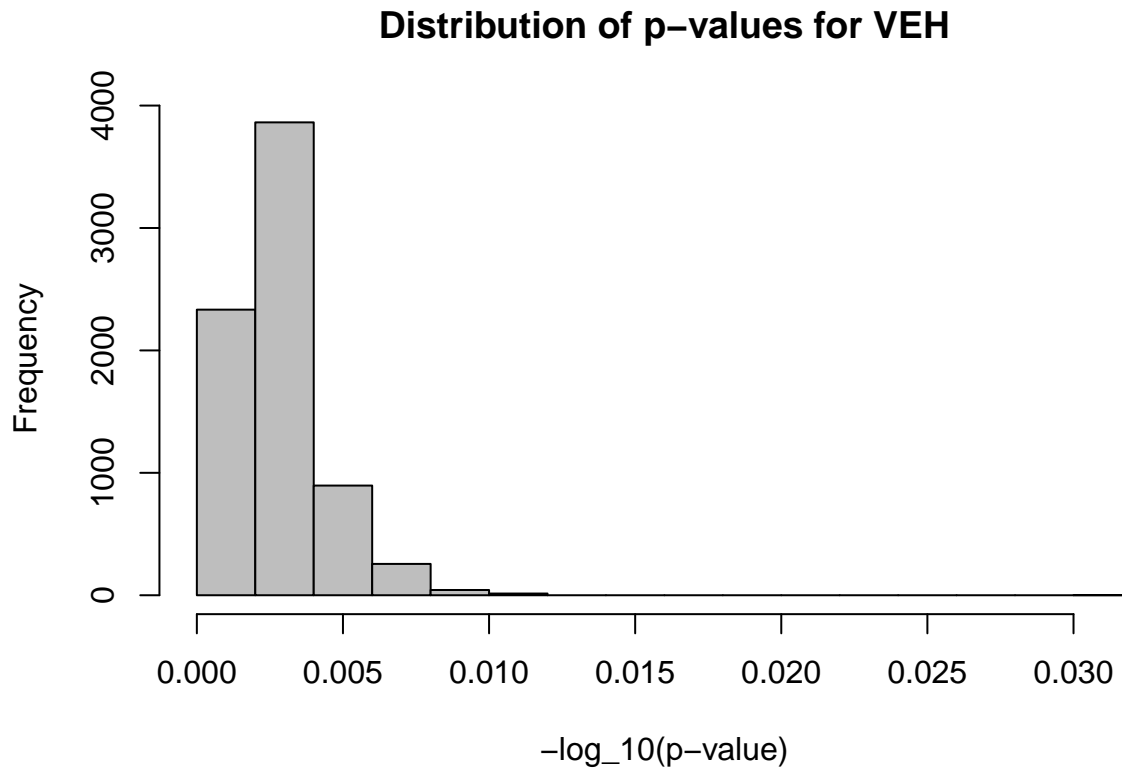
#### 3.4.2.2. Distribution of peak sizes

```
hist(width(grange.veh), xlab = "VEH peak size", col = "gray", main = "Distribution of VEH peak size")
```



#### 3.4.1.3 Distribution of peak p-values

```
p.values <- score(grange.veh)
hist(p.values, xlab = "-log10(p-value)", col = "gray", main = "Distribution of p-values for VEH")
```



### 3.4.1. Explore OVERLAPs

#### 3.4.1.1. Mean, median, and max size of the peaks

```
summary(width(grange.olap))
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  208.0   623.0   842.0   900.8  1099.0  5127.0
```

#### 3.4.1.2. Distribution of peak sizes

```
hist(width(grange.olap), xlab = "Peak size", col = "gray", main = "Distribution of overlapped peak size")
```

**Distribution of overlapped peak size**

