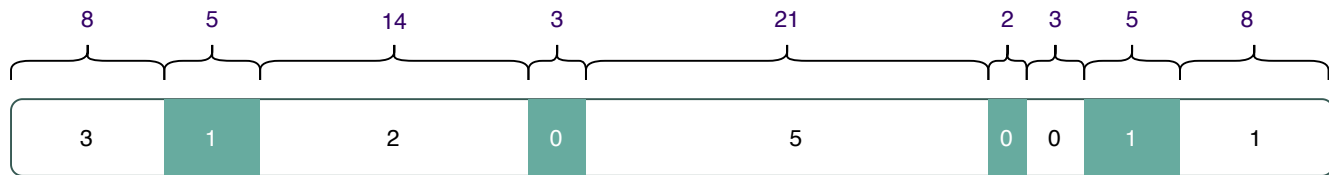


sequence
length



open chromatin
mutation counts

closed chromatin
mutation counts

	mutated	non-mutated	total
closed	11	43	54
open	2	13	15

G-test (*G*-statistic, *p*-value)

- H_0 : closed=open
- H_a : reject H_0

Odds ratio (*OR*)

measures the
mutation bias
towards closed
chromatin region