

Tumor sample
with mixed clone
structures

scATAC-seq

Fragments.tsv

scRNA-seq

Mode 1: RNA Gene

Cells

1	0	3	0	...	1
0	2	0	3	...	0
⋮	⋮	⋮	⋮	⋮	⋮
2	0	2	7	...	0

Genes

Chr	Start.bp	End.bp	Barcode	# of reads
Chr5	42679	43200	TGGCAATGTTGAAGCG-1	5
Chr7	39548	39698	ACATGGTGTAGACGCA-1	2
Chr8	28300	28521	CTAGGCATGTTGAAGC-1	3

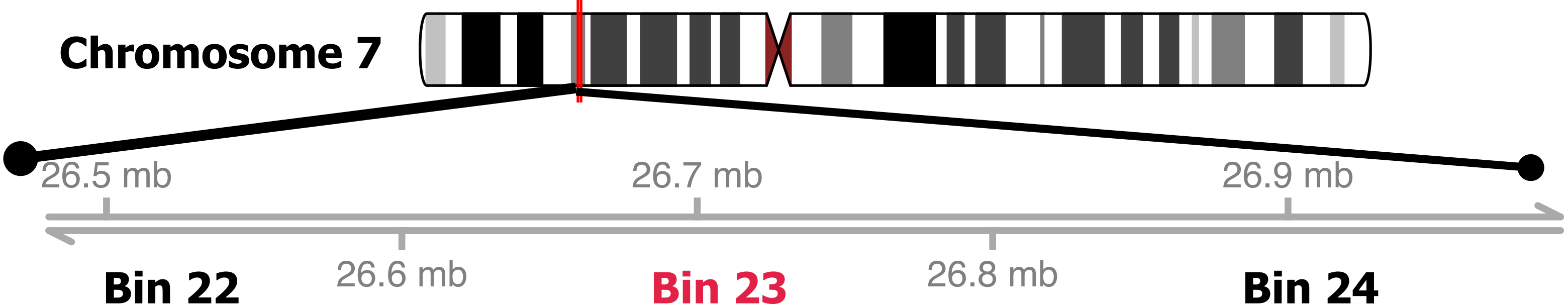
Cell by Peak

Cells

1	0	1	0	0	1	0	...	0
0	1	0	1	0	1	1	...	0
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
0	2	0	0	1	1	2	...	1

Peaks

Chromosome 7



Mode 2: RNA Bin

Mode 4: Combined Bin

Mode 3: ATAC Bin

Cells

4	...	1
5	...	0
⋮	⋮	⋮
11	...	0

Bins

Cells

4	...	1
⋮	⋮	⋮
11	...	0
3	...	0
⋮	⋮	⋮
6	...	1

Bins

Cells

3	...	0
4	...	0
⋮	⋮	⋮
6	...	1

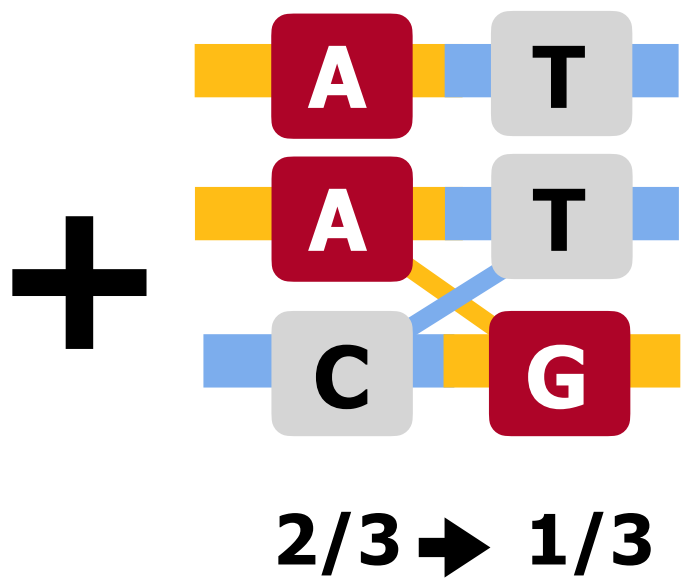
Bins



Numbat-Multitome

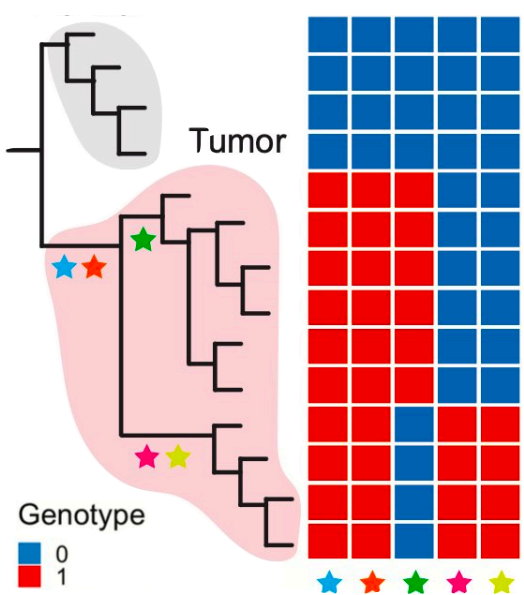
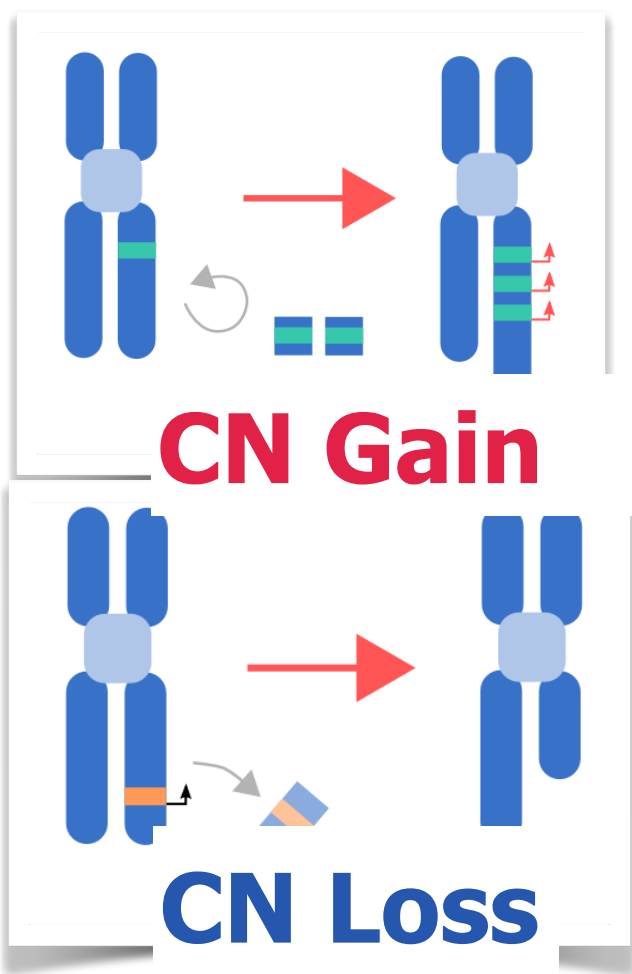


Differential
Molecule
Abundance



paternal Haplotype Frequency

Haplotype-enhanced
Allelic Imbalance



CNV-based
Phylogeny