Input
- Event matrix
- Pie sizes: Proportion of cells having each genomic profile.
- Heatmap

Identifying genetic alterations that may cause contradictions in the phylogeny

Create an empty phylo object
- **edge:** Indicates which edges are connected.
- **tip.label:** The subclone names that will be placed at the tips of the phylogeny.
- **Nnode:** The number of nodes in the phylogeny.
- **edge.length:** The length of the branches connecting the edges indicated in "edge".

Create the tip labels. Same as the unique subclones in the EM.

Create a matrix indicating which subclones have been allocated and which are remaining.

Event matrix

	Stem	A	B	C	Normal	Type
3+	1	1	1	1	0	W
5+	0	1	1	0	0	W
7+	0	0	0	1	0	W
8+	0	0	1	1	0	W

Genetic alterations in each subclone
W = whole chromosome alteration

Pie sizes

Stem	P1	P2
100	100	100
A	P1	P2
80	80	0
B	P2	0
70	70	0
C	P1	P2
60	60	60

The proportion of cells in each sample that have a particular genotype

Heatmap

	P1	P2
3+	100	100
5+	80	0
7+	0	70
8+	60	60

The mutated clone fraction for each alteration across samples