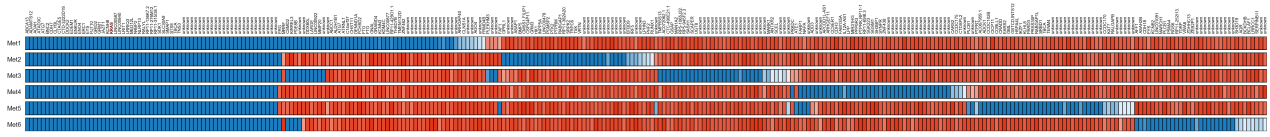
Treeomics analysis report of patient example

Input data

Sample	Median coverage (mean)	Median MAF (mean)	Purity	No variants present	absent
Met1	143.0 (147.2)	34.6% (30.7%)	69.8%	115	195
Met2	147.5 (147.6)	34.3% (30.1%)	71.4%	102	208
Met3	146.0 (148.6)	33.6% (29.9%)	67.5%	109	201
Met4	144.0 (148.3)	35.1% (31.0%)	71.9%	106	204
Met5	147.0 (148.1)	33.3% (29.9%)	70.5%	112	198
Met6	145.0 (148.6)	35.0% (31.2%)	70.8%	101	209

Samples that passed the filtering: 6/6
Median coverage in the passed samples: 146.0 (mean: 148.08)

Total number of passed somatic variants: 310
Variants removed due to common variants filter: 1
Variants classified as present in at least one of the samples that passed the filtering: 310
Founders (variants present in all samples): 63 (20.3%)
Mean number of unique (private) variants per sample: 38.8 (35.7%)
Total number of likely driver gene mutations: 1 in 1 genes (**KRAS**; more red colored gene names correspond to better supported driver genes. Bold names are also present in the Cancer Gene Census list)
Other mutations in likely driver genes: IncompleteTranscript (1), Intronic (1)



Probabilistic variant classification across 6 samples of patient example. Blue rectangles correspond to present variants, red to absent variants, and white to unknown mutation status. Brighter colors denote higher probability. Reddish colored gene names correspond to likely cancer drivers with increasing support. Bold names are also present in the Cancer Gene Census list.

Genetic similarity

Probabilistic Jaccard similarity coefficient between all pairs of samples (median: 0.46; mean: 0.46; classification threshold: 90%).

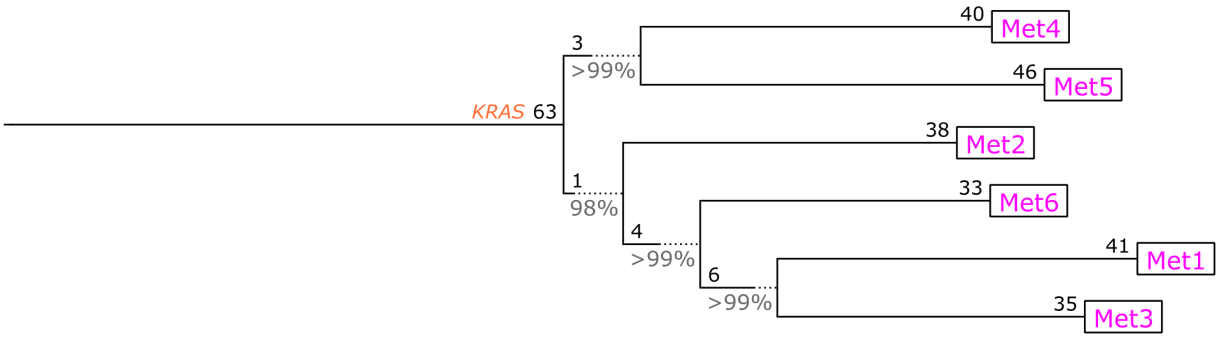
Sample	Met1	Met2	Met3	Met4	Met5	Met6
Met1	1.00					
Met2	0.44	1.00				
Met3	0.52	0.46	1.00			
Met4	0.41	0.45	0.43	1.00		

Met5	0.41	0.44	0.43	0.46	1.00	
Met6	0.50	0.50	0.52	0.47	0.46	1.00

Genetic distance between all pairs of samples (median: 78; mean: 77.7; classification threshold: 90%).

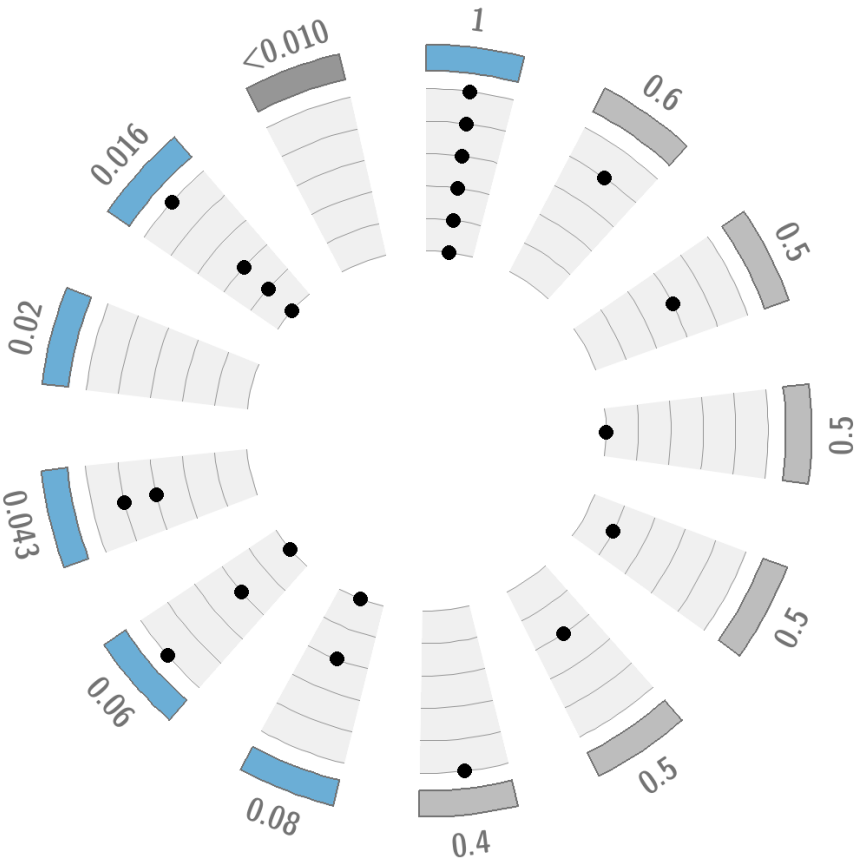
Sample	Met1	Met2	Met3	Met4	Met5	Met6
Met1	0					
Met2	83	0				
Met3	69	76	0			
Met4	91	78	84	0		
Met5	93	80	86	80	0	
Met6	70	65	63	73	75	0

Inferred cancer phylogeny



Phylogenetic tree illustrating the evolutionary history of the cancer in example. Numbers on top of each branch indicate the number of acquired variants (including likely driver gene mutations reported separately in orange). Numbers on bottom of each branch indicate the estimated support values.

Evolutionary conflict graph



Evolutionary conflict graph of 6 samples in patient example. Treeomics considered 65 distinct mutation patterns (MPs). Each circular line represents a distinct sample. Inner to outer lines denote: Met1, Met2, Met3, Met4, Met5, Met6. Marks on these lines denote present variants. Labels denote the MP reliability scores. Only nodes with the highest reliability score are depicted. Blue colored nodes (MPs) are evolutionarily compatible and red colored nodes are evolutionarily incompatible indicated by edges among the nodes. Minimum reliability score value to be considered as a potential subclone: 0.018.

Treeomics settings: sequencing error rate e: 0.01, prior absent probability c0: 0.5, max absent VAF: 0.05, LOH frequency: 0.0, false discovery rate: 0.05, false-positive rate: 0.005. absent classification minimum coverage: 100.