



LEGEND	Branch Length	Nodes	Genes	Collapsed nodes	Collapsed Alignments	Expanded Alignments
	x1 branch length	gene node	Gene ID	collapsed sub-tree	0 - 33% aligned seq	gap
	x10 branch length	speciation node	gene of interest	collapsed (this gene)	33 - 66% aligned seq	aligned seq
	x100 branch length	duplication node	Gene ID	collapsed (paralog)	66 - 100% aligned seq	
		ambiguous node		(x10 branch length)		
		gene split event		(x100 branch length)		