

#File options.bpp

#Run with maffilter param=options.bpp

input.file=chr1.maf.gz		Describes the input file
input.file.compression=gzip		
input.format=Maf		
output.log=chr1.maffilter.log		
maf.filter=		Specifies the list of filters to apply
SequenceStatistics (		
statistics=(		
BlockSize(),		
BlockLength()),		Compute block statistics
ref_species=hg19,		
file=chr1.statistics.csv),		
MinBlockLength(min_length=100),		Filter by block size
Subset (		
species=(hg19,panTro2,gorGor1,ponAbe2,rheMac2),		
strict=yes,		
remove_duplicates=yes,		Extract Primate sequences
verbose=no,		
keep=no),		
Merge (		
species=(hg19,panTro2,gorGor1,ponAbe2,rheMac2),		Merge syntenic blocks
max_dist=20),		
XFullGap (		
species=(hg19,panTro2,gorGor1,ponAbe2,rheMac2),		Remove gap columns
verbose=no),		
MinBlockLength(min_length=1000),		
WindowSplit (		
preferred_size=1000,		Split blocks in 1kb windows
align=center),		
DistanceEstimation (		
method=ml,		
model=K80(kappa=2.0),		
rate=Constant,		
parameter_estimation=pairwise,		Compute distance with a Kimura
max_freq_gaps=0.3,		(1980) model of substitution and
gaps_as_unresolved=yes,		constant rate across sites
verbose=no,		
profiler=profile.txt,		
message_handler=messages.txt),		
DistanceBasedPhylogeny (		
method=bionj,		Build a BioNJ tree from the
dist_mat=MLDistance),		previously built distance matrices
NewOutgroup (		
tree_input=BioNJ,		Root the trees, setting
tree_output=BioNJ_rerooted,		Macaque as outgroup
outgroup=rheMac2),		
OutputTrees (		
tree=BioNJ_rerooted,		
file=chr1.window1k.dnd,		Write the trees in Newick format.
compression=none)		