```
Settings used
alignment          : ./chloro_all_spp_PARTITIONFINDER.nex
branchlengths      : linked
models             : HKY+G, GTR+I, GTR+G, HKY+I, GTR, HKY, JC+G, JC+I, JC
model_selection    : bic
search             : greedy
Best partitioning scheme
Scheme Name        : step_5
Scheme lnL         : -15786.16616
Scheme BIC         : 33758.9182389
Number of params : 252
Number of sites    : 5866
Number of subsets : 3

Subset | Best Model | Subset Partitions                                              | Subset Sites
1        | GTR+I        | accD_fasta, matK_fasta, rpoB_fasta, rpoC1_fasta, trnV_fasta | 1-910, 911-2290, 3640-3982, 3983-4365, 4366-4847
2        | HKY+I        | rbcL_fasta, rpl20_fasta                                        | 2291-3544, 3545-3639
3        | GTR+G        | ycf1_fasta                                                     | 4848-5866

Scheme Description in PartitionFinder format
Scheme_step_5 = (accD_fasta, matK_fasta, rpoB_fasta, rpoC1_fasta, trnV_fasta) (rbcL_fasta, rpl20_fasta) (ycf1_fasta);
RaxML-style partition definitions
DNA, p1 = 1-910, 911-2290, 3640-3982, 3983-4365, 4366-4847
DNA, p2 = 2291-3544, 3545-3639
DNA, p3 = 4848-5866
```