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 | I 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