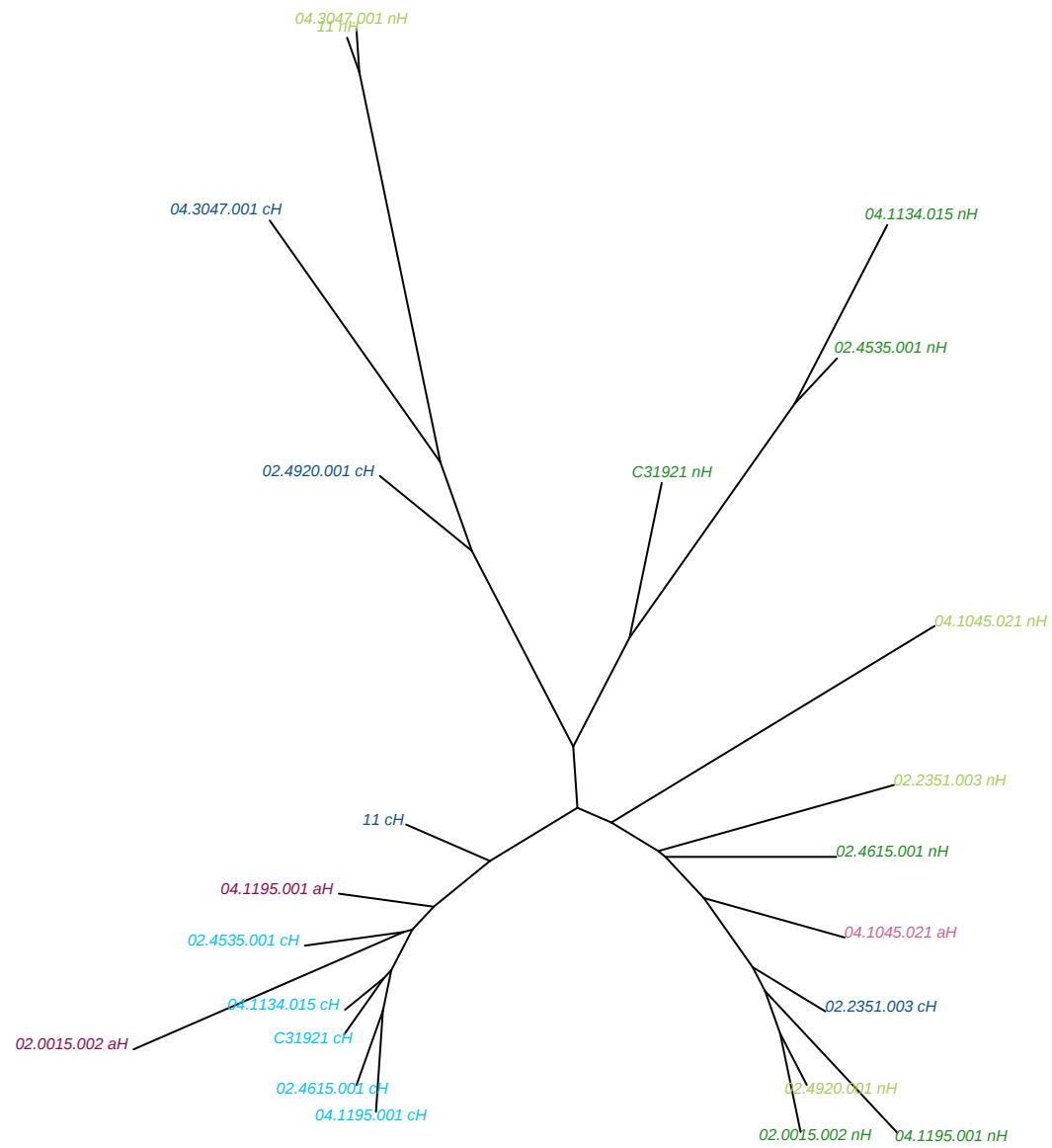
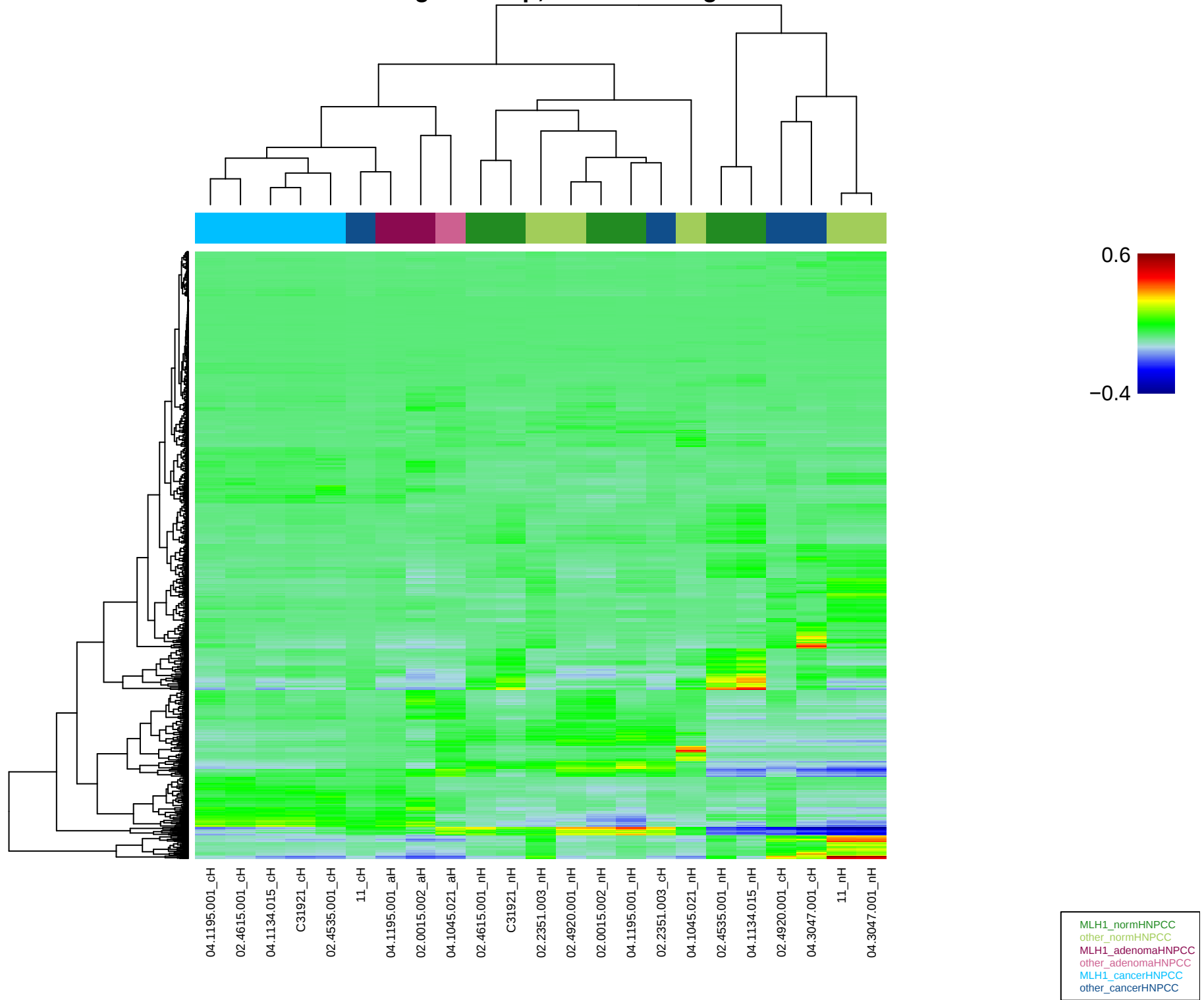


Phylogenetic sample clustering, all 1600 Metagenes

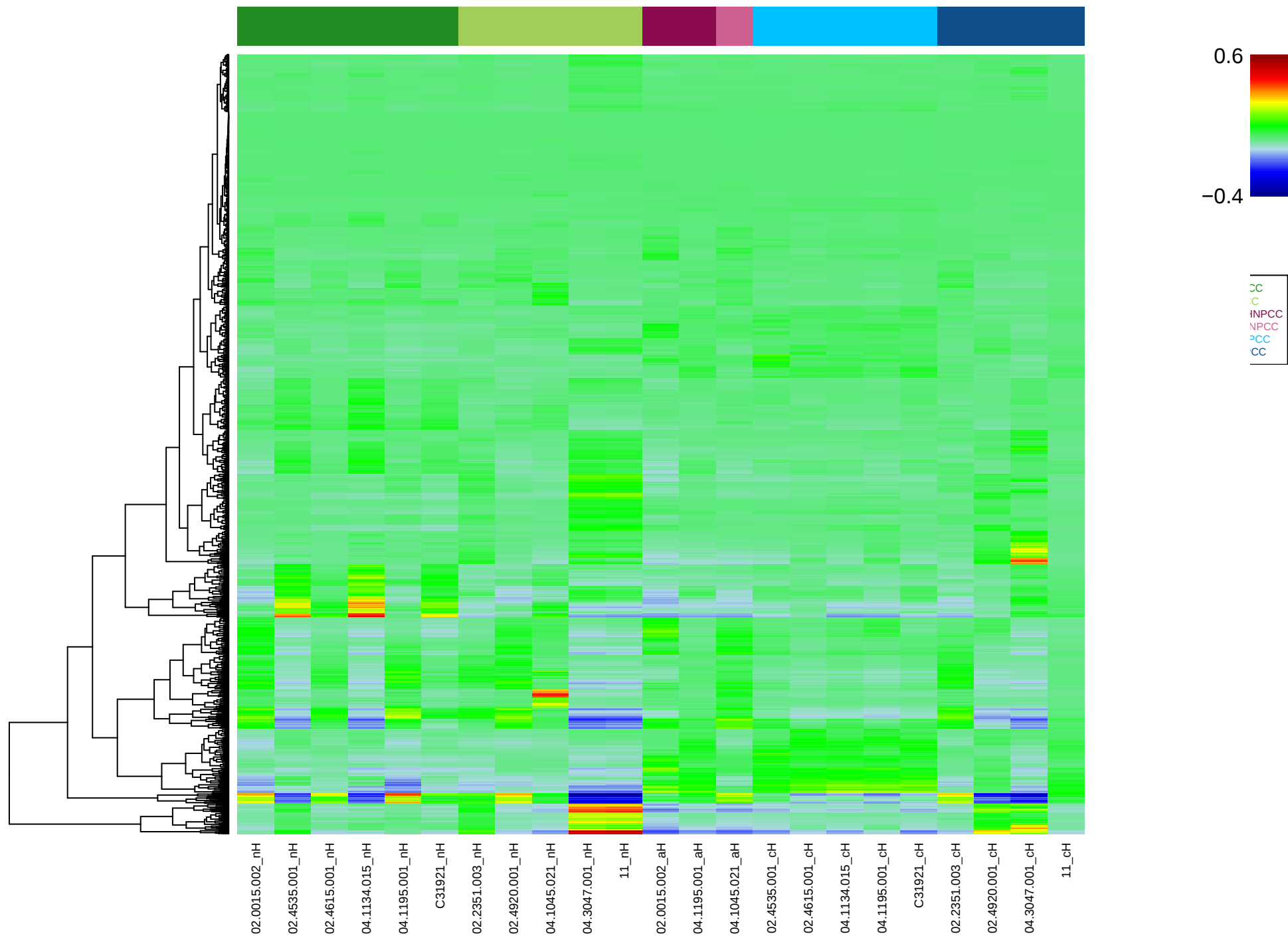


MLH1_normHNPCC
other_normHNPCC
MLH1_adenomaHNPCC
other_adenomaHNPCC
MLH1_cancerHNPCC
other_cancerHNPCC

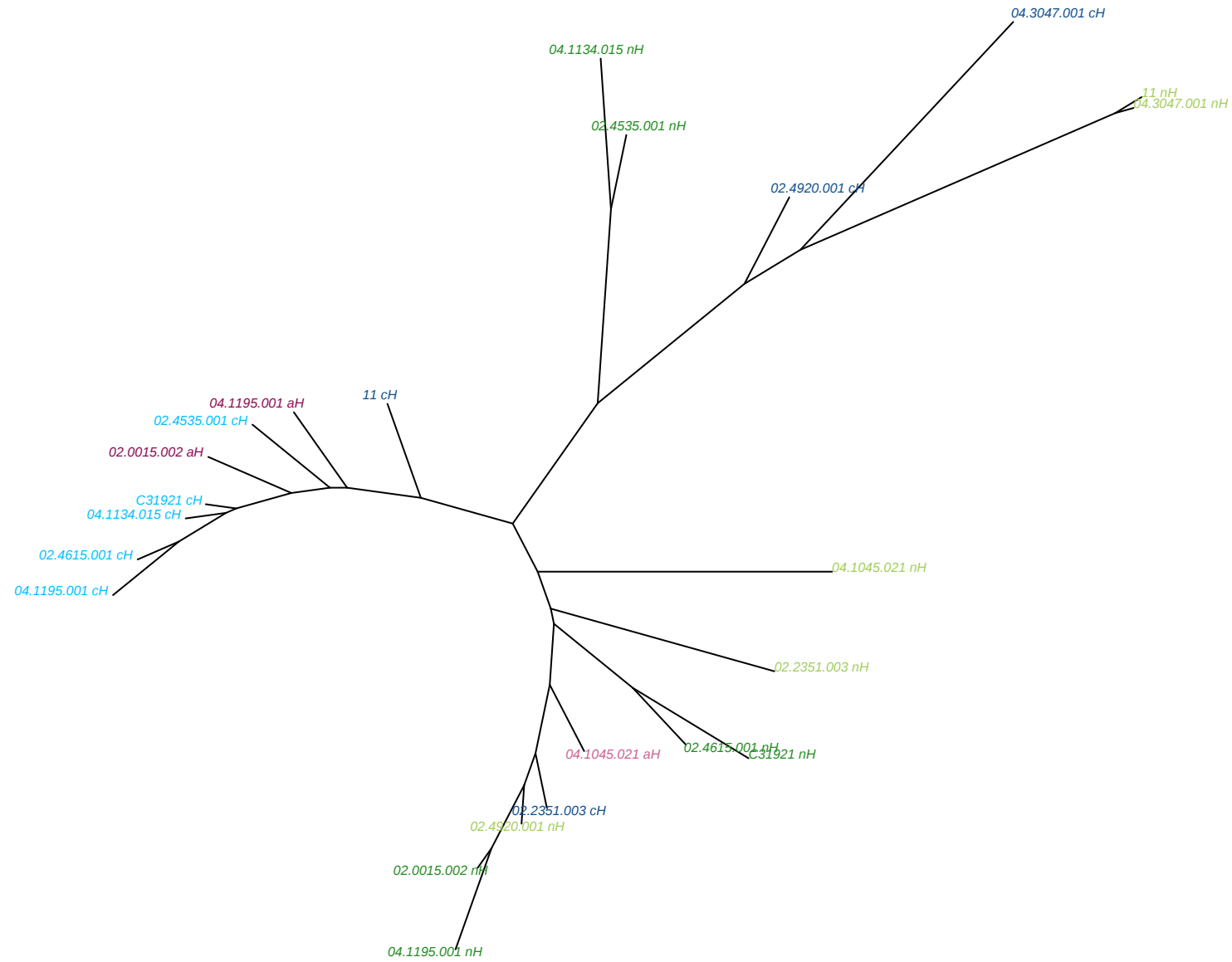
Clustering heatmap, all 1600 Metagenes



Clustering heatmap, all 1600 Metagenes

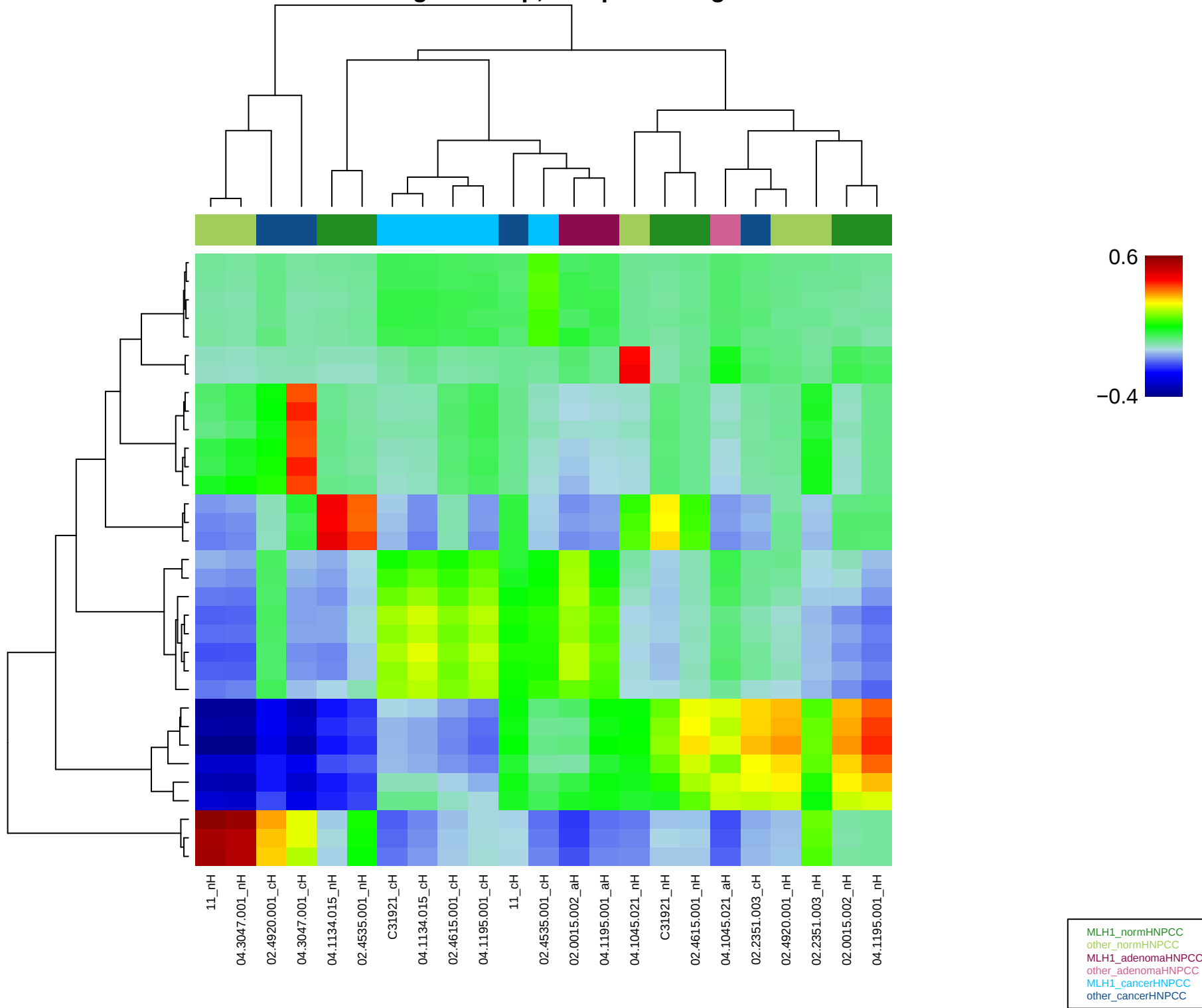


Phylogenetic sample clustering, 33 Spot-Metagenes

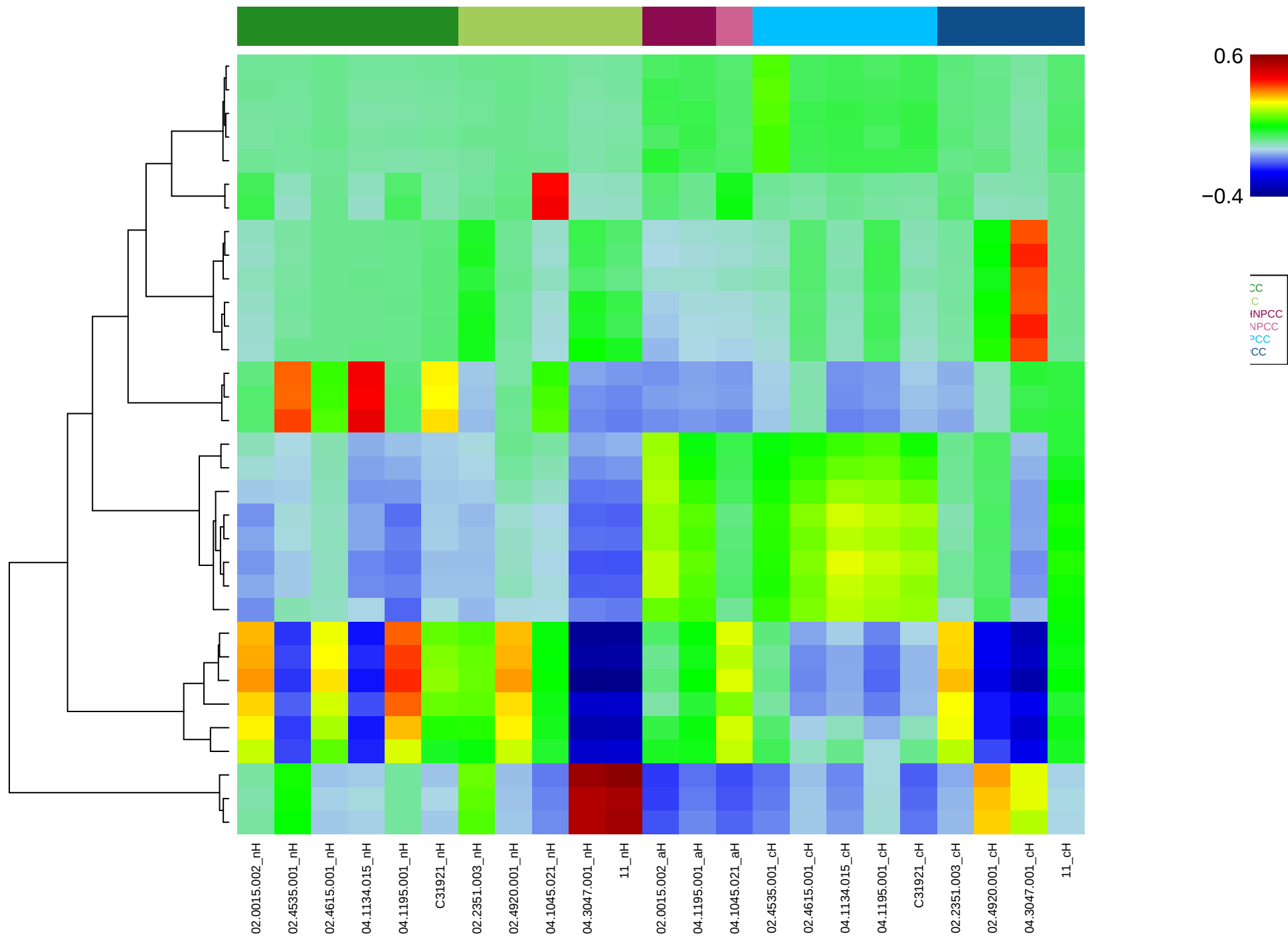


MLH1_normHNPCC
other_normHNPCC
MLH1_adenomaHNPCC
other_adenomaHNPCC
MLH1_cancerHNPCC
other_cancerHNPCC

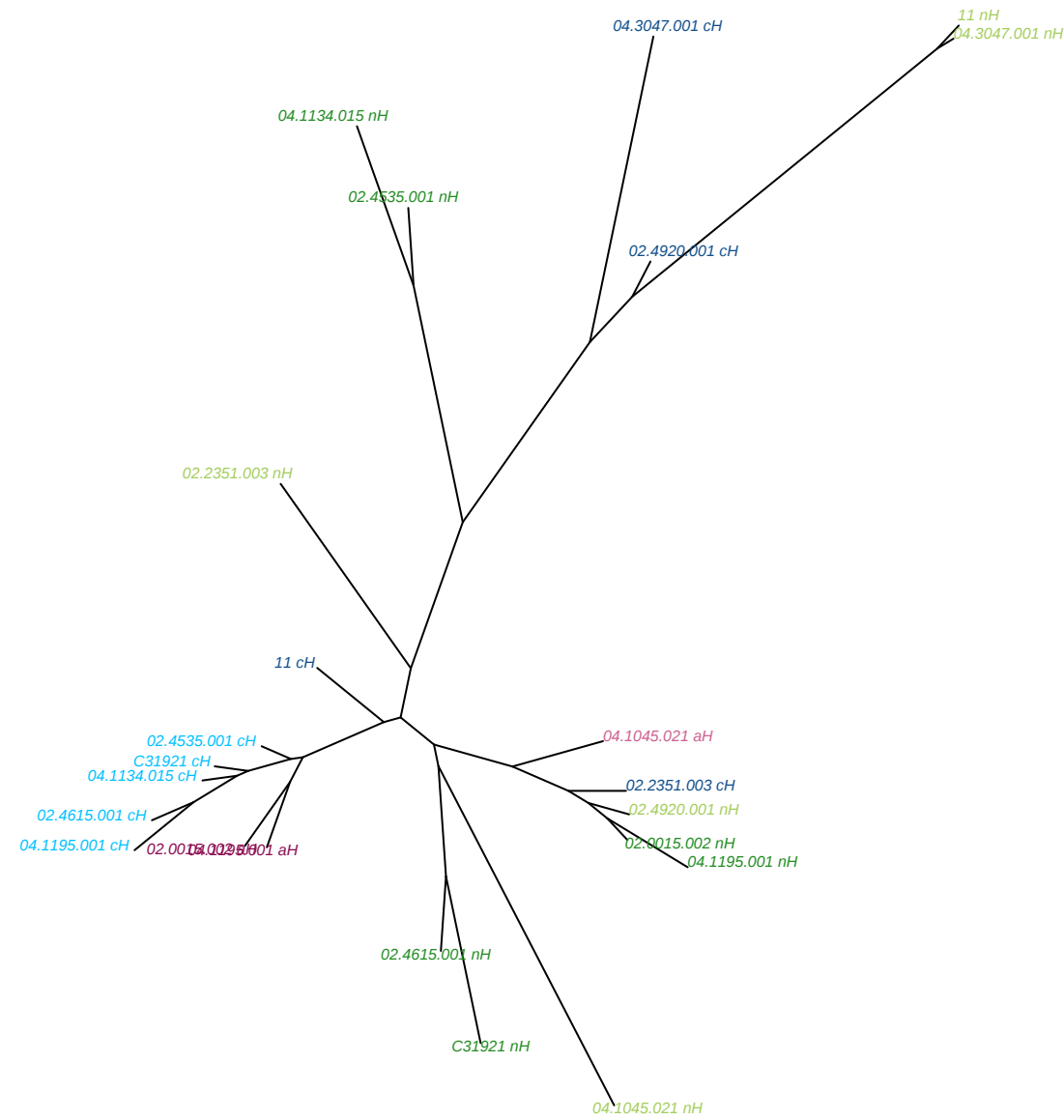
Clustering heatmap, 33 Spot-Metagenes



Clustering heatmap, 33 Spot-Metagenes

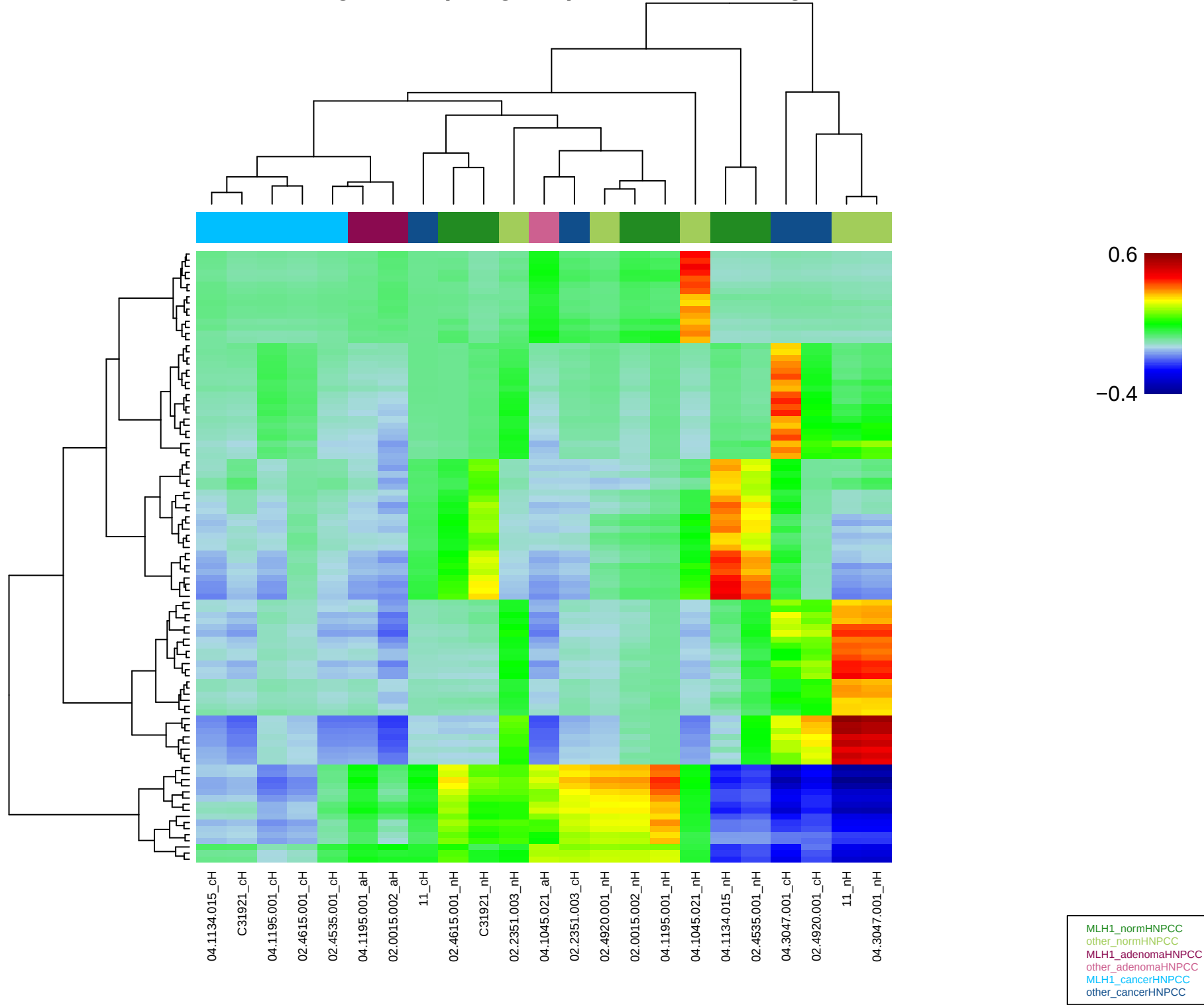


Phylogenetic sample clustering, High Expression: 100 Metagenes

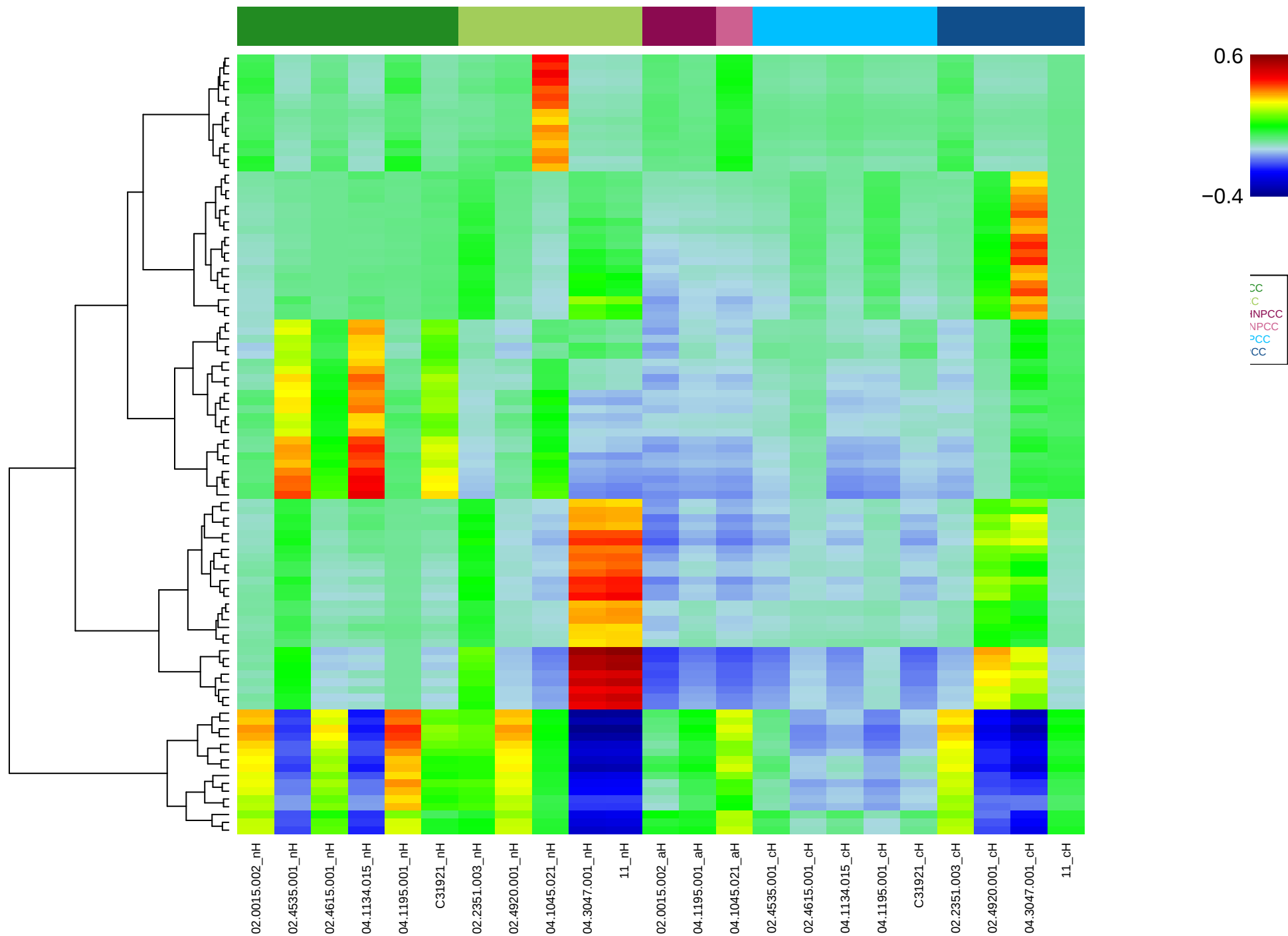


MLH1_normHNPCC
other_normHNPCC
MLH1_adenomaHNPCC
other_adenomaHNPCC
MLH1_cancerHNPCC
other_cancerHNPCC

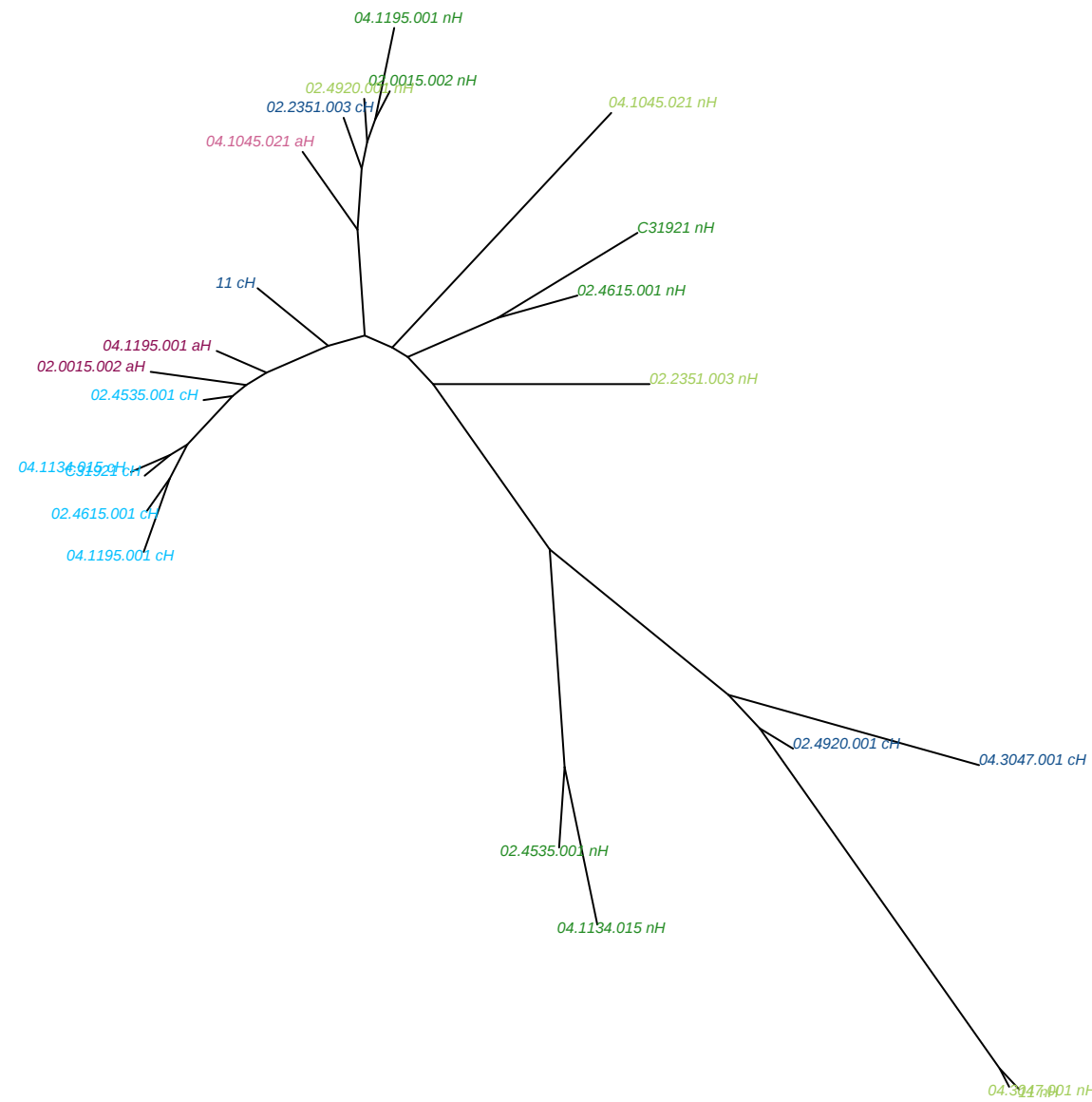
Clustering heatmap, High Expression: 100 Metagenes



Clustering heatmap, High Expression: 100 Metagenes

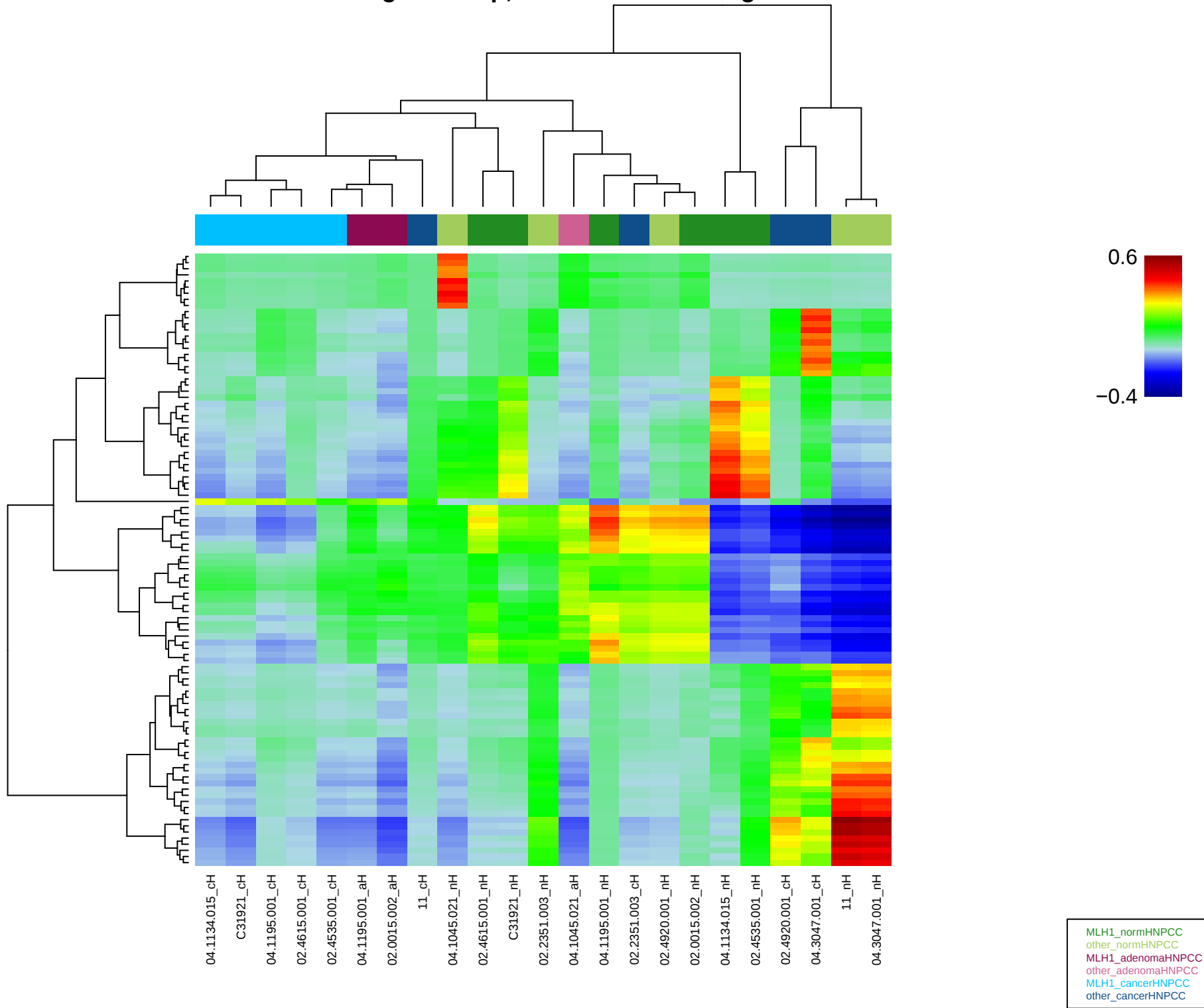


Phylogenetic sample clustering, Variance: 100 Metagenes



MLH1_normHNPCC
other_normHNPCC
MLH1_adenomaHNPCC
other_adenomaHNPCC
MLH1_cancerHNPCC
other_cancerHNPCC

Clustering heatmap, Variance: 100 Metagenes



Clustering heatmap, Variance: 100 Metagenes

