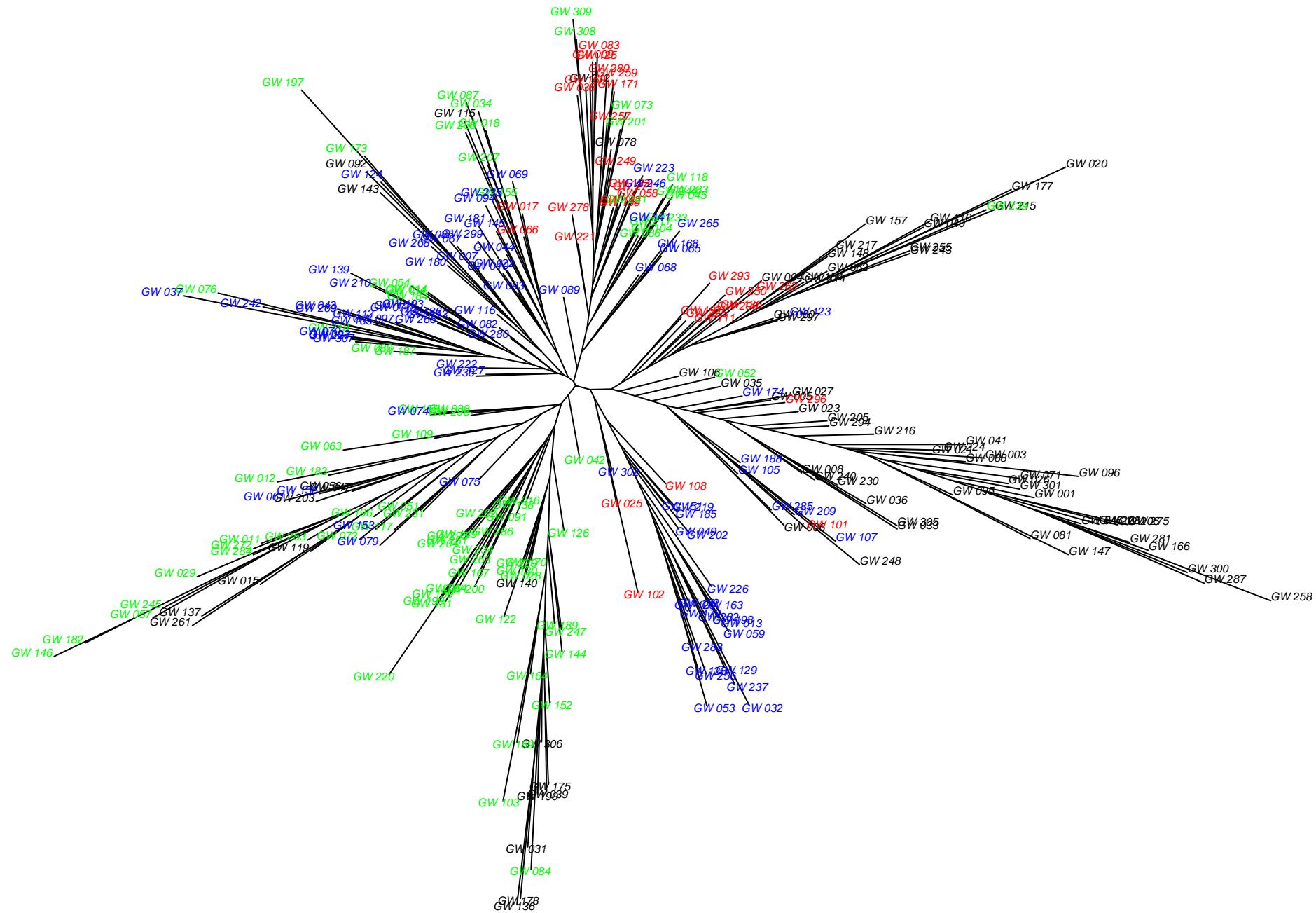
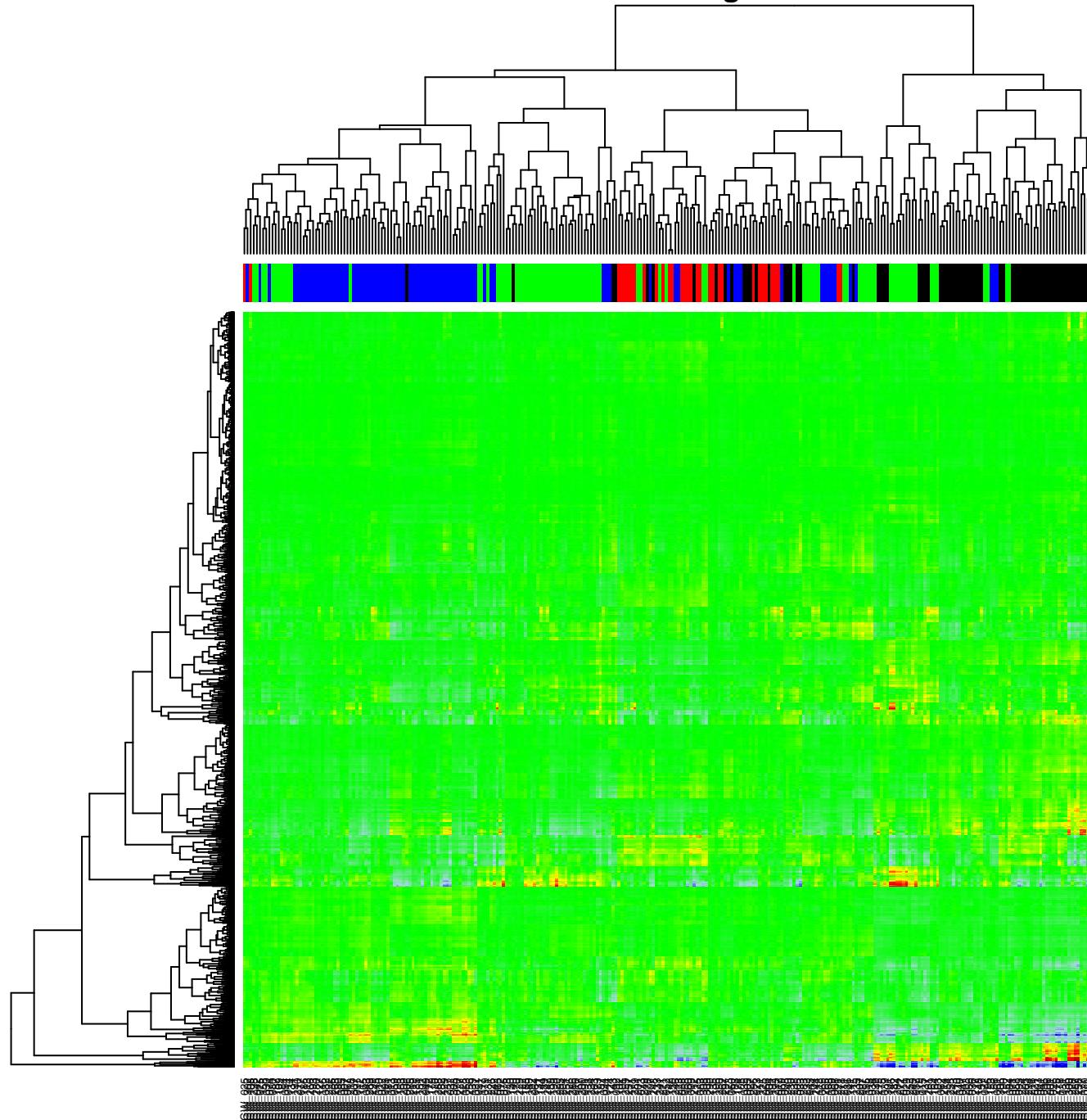


all 2500 Metagenes

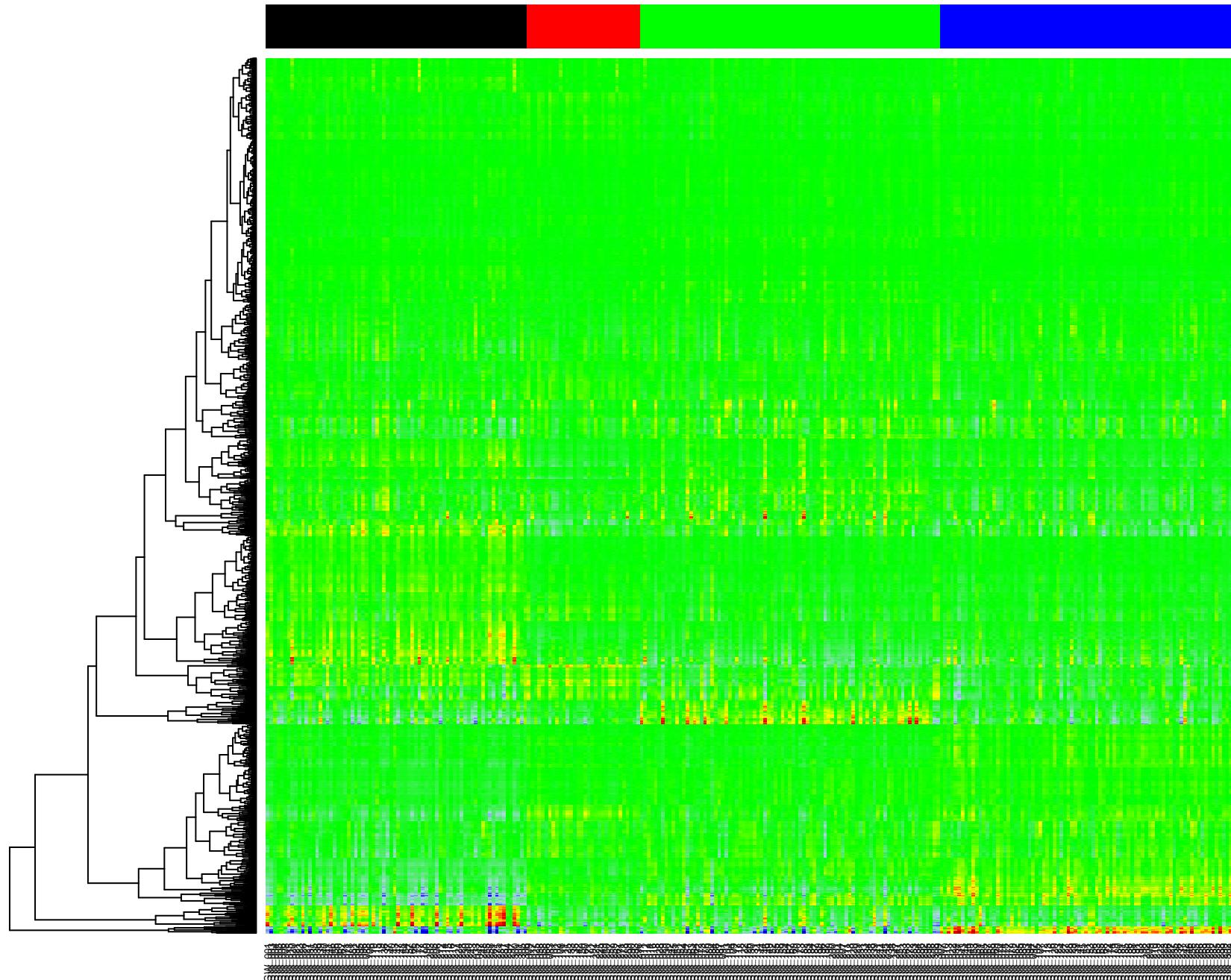


all 2500 Metagenes



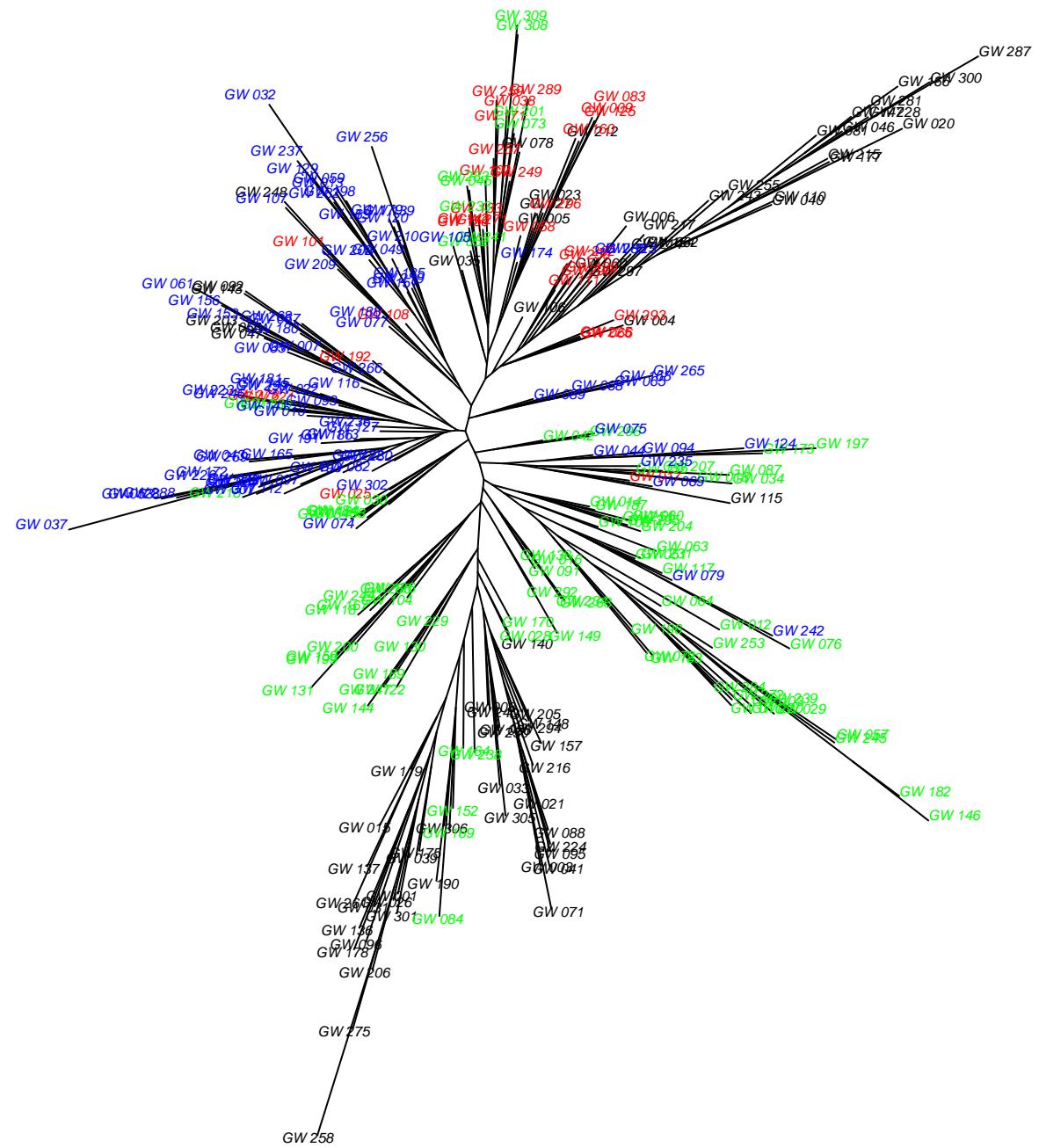
Atypical
Classical
Mesenchymal
Basal

all 2500 Metagenes

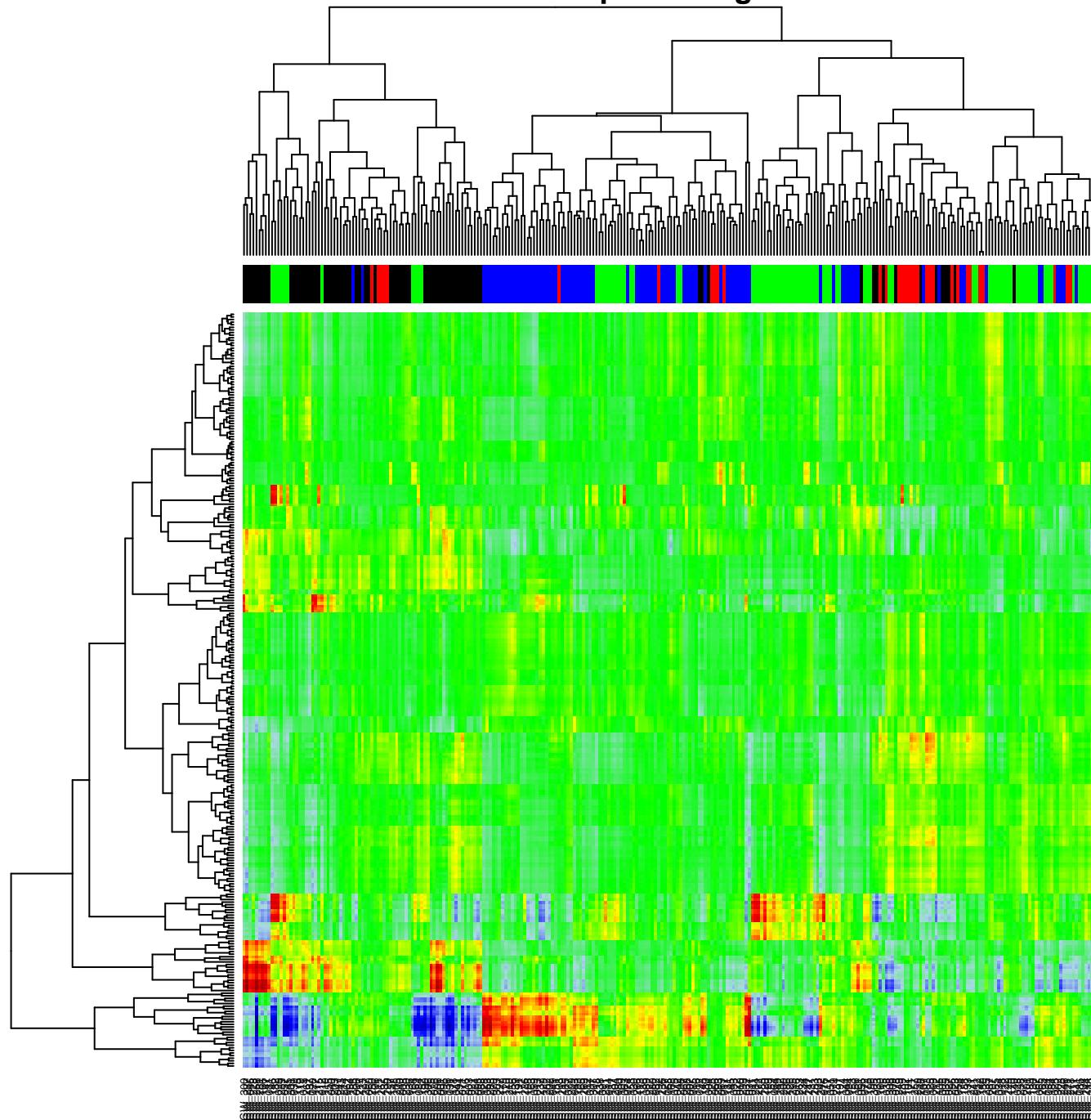


Atypical
Classical
Mesenchymal
Basal

290 Spot-Metagenes

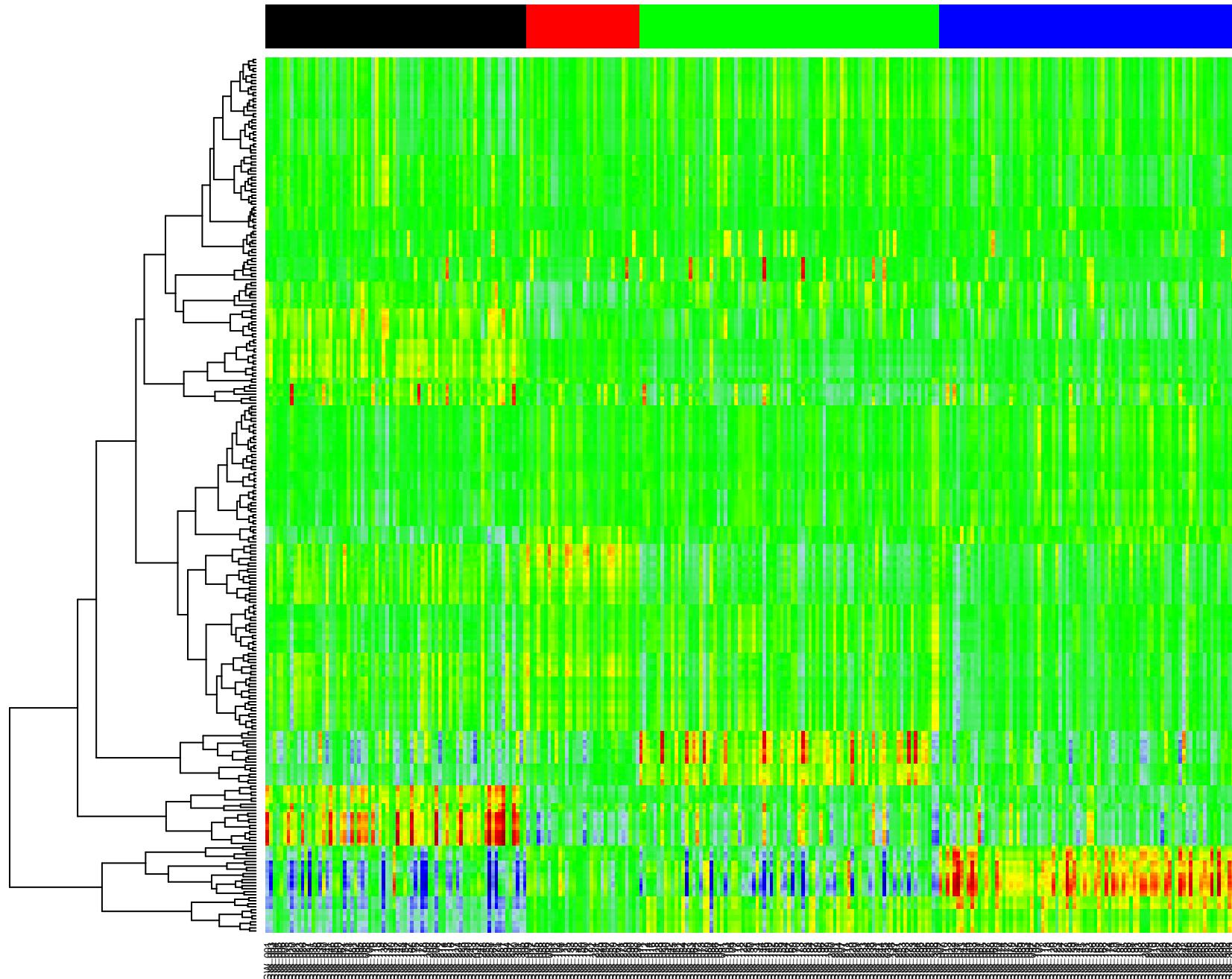


290 Spot-Metagenes



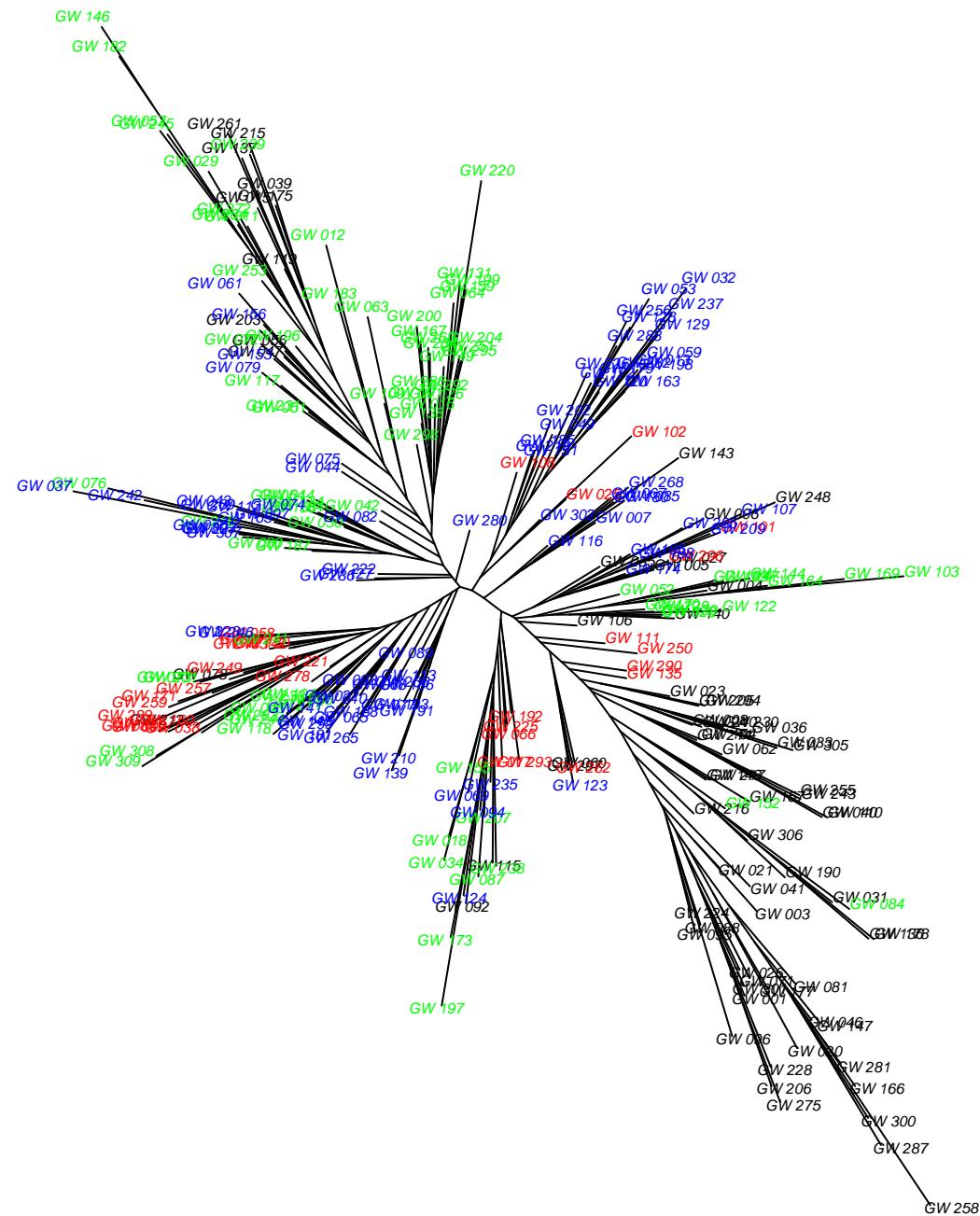
Atypical
Classical
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Basal

290 Spot-Metagenes

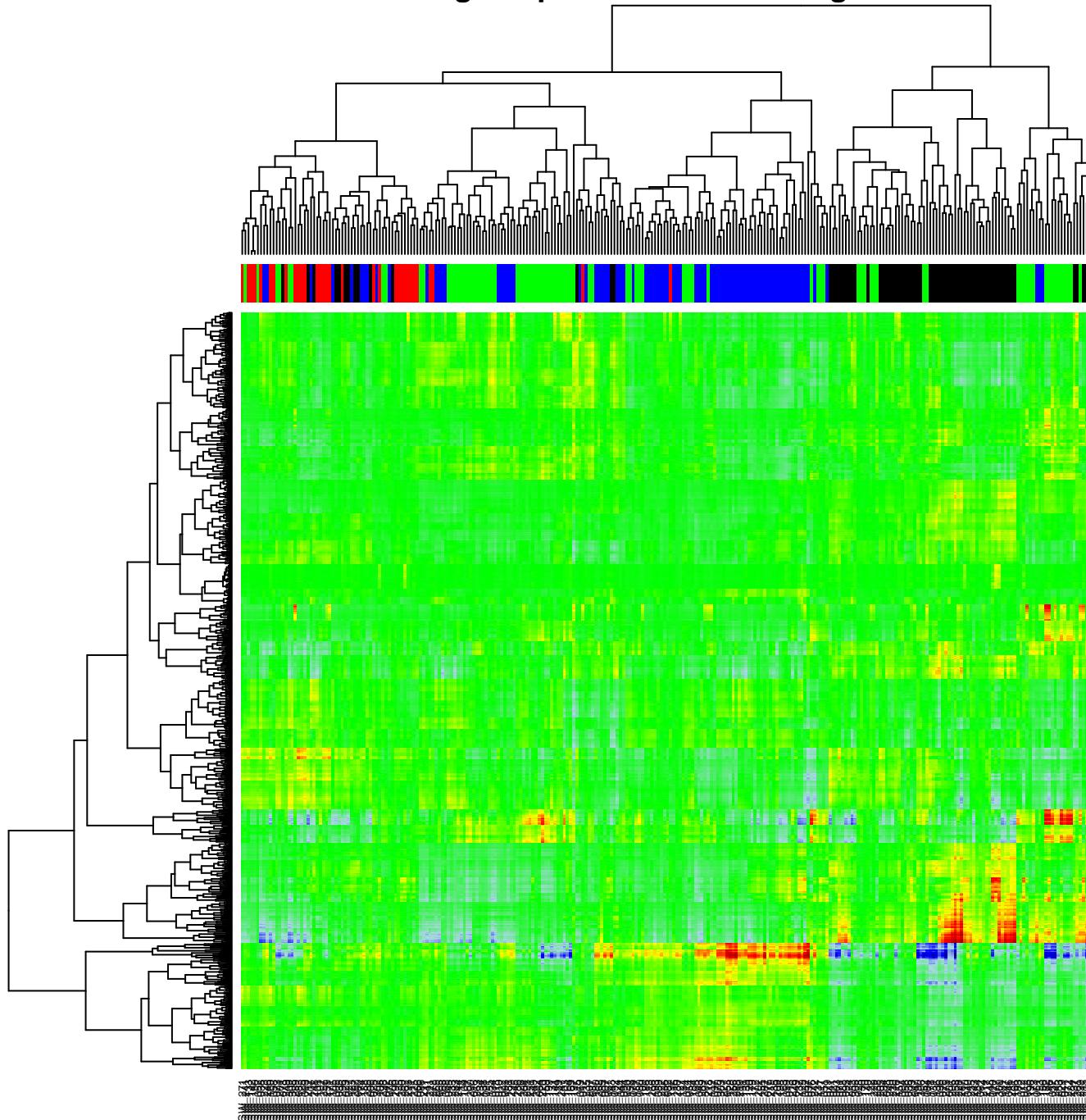


Atypical
Classical
Mesenchymal
Basal

High Expression: 1000 Metagenes

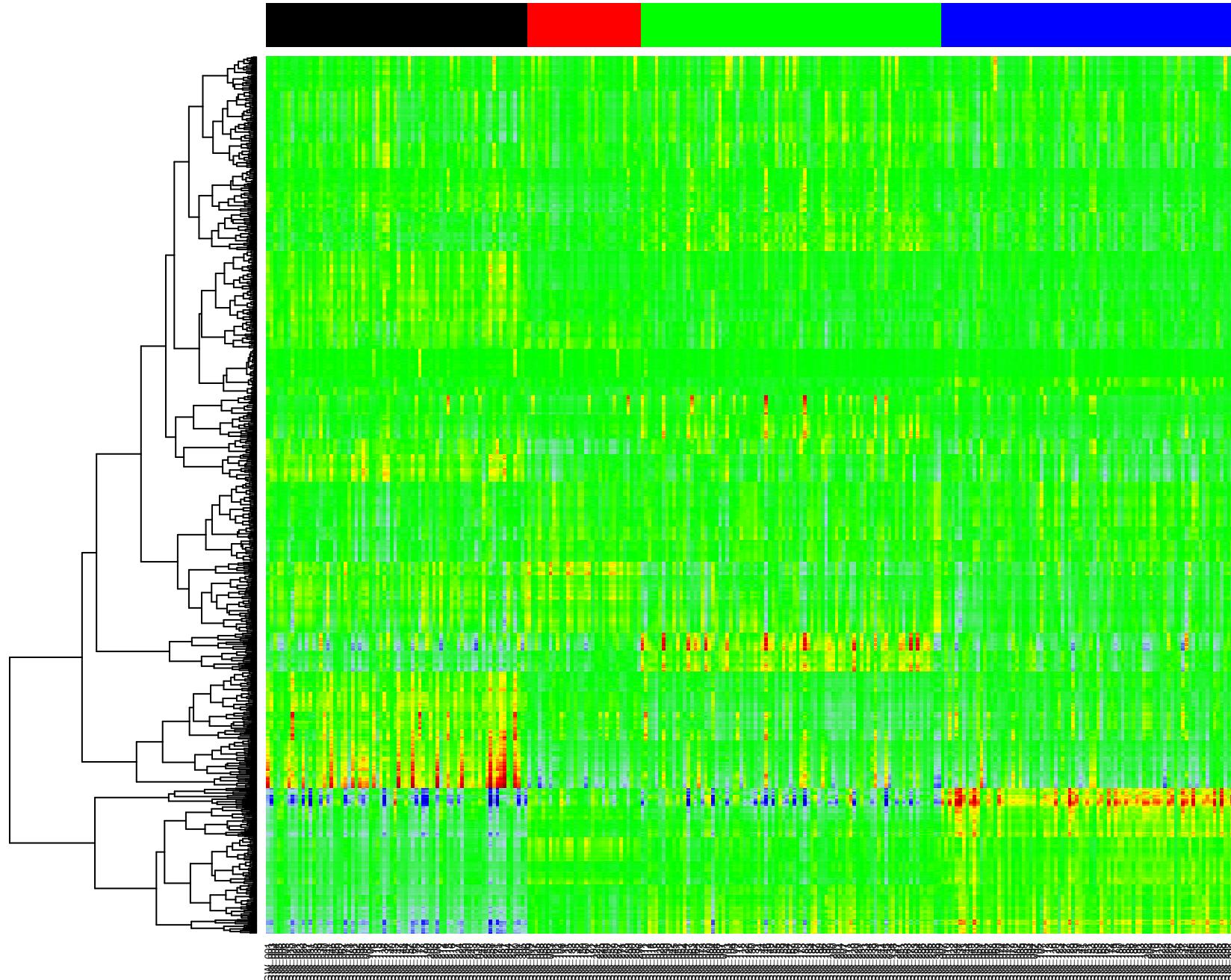


High Expression: 1000 Metagenes



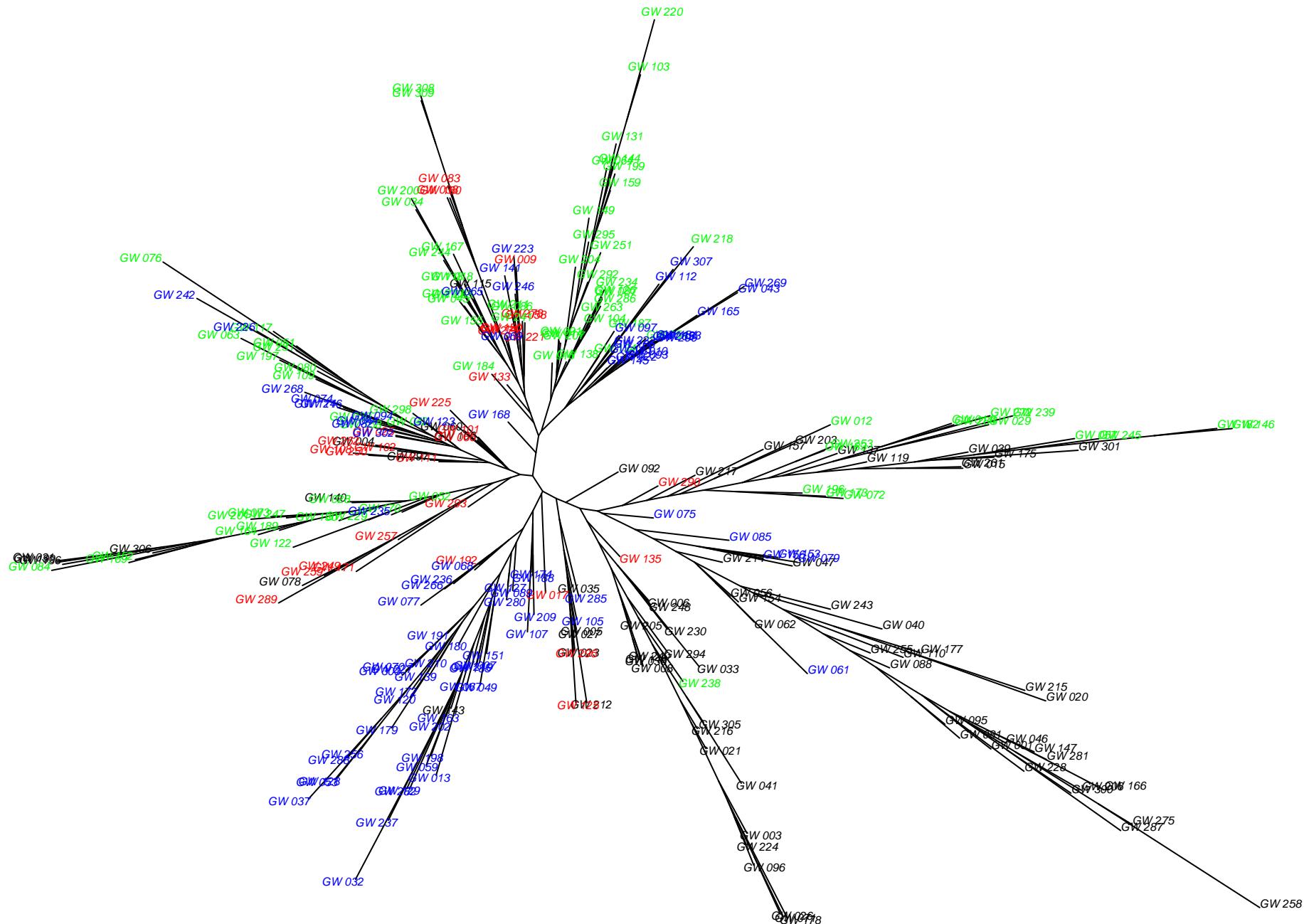
Atypical
Classical
Mesenchymal
Basal

High Expression: 1000 Metagenes

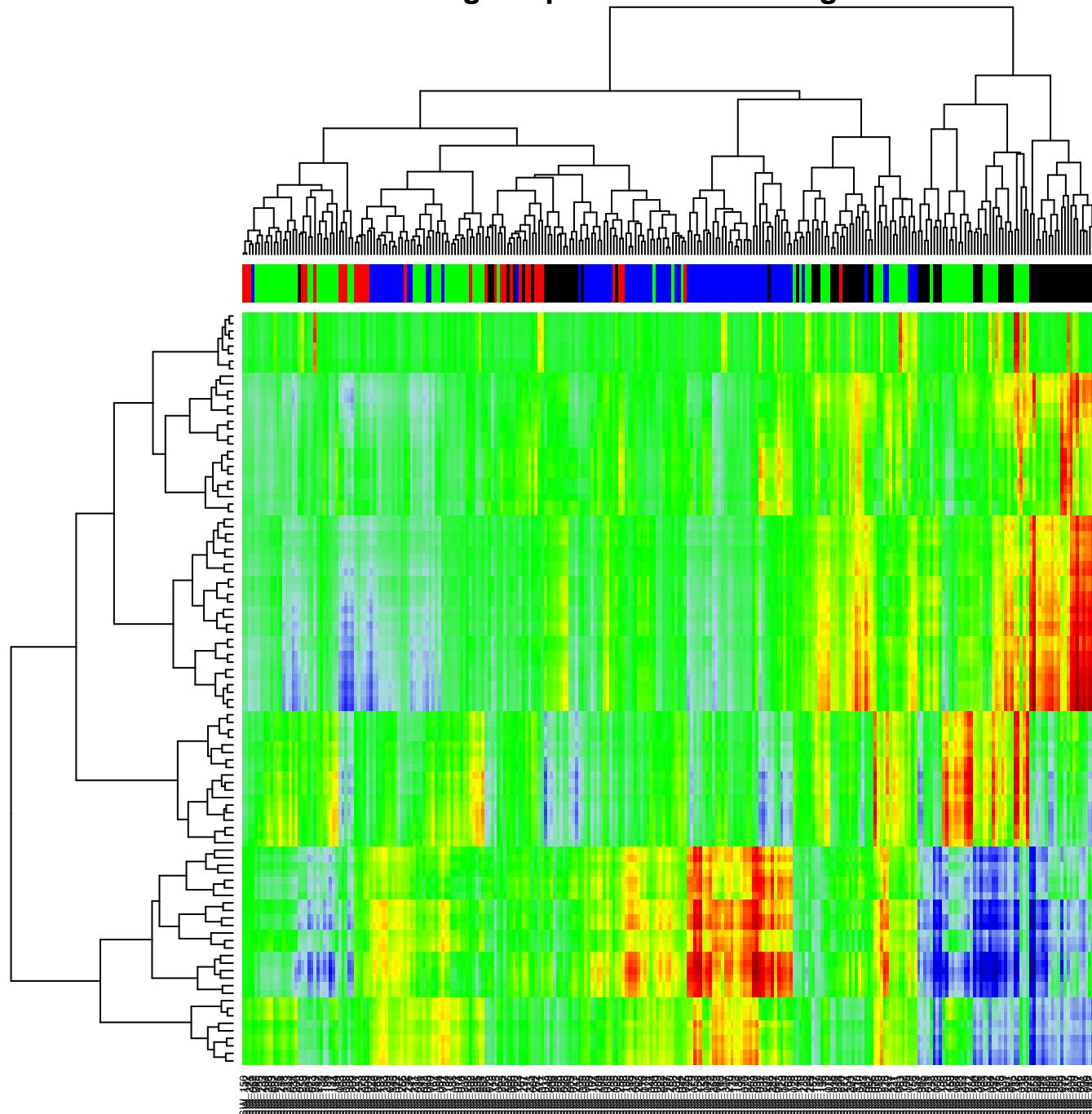


Atypical
Classical
Mesenchymal
Basal

High Expression: 100 Metagenes

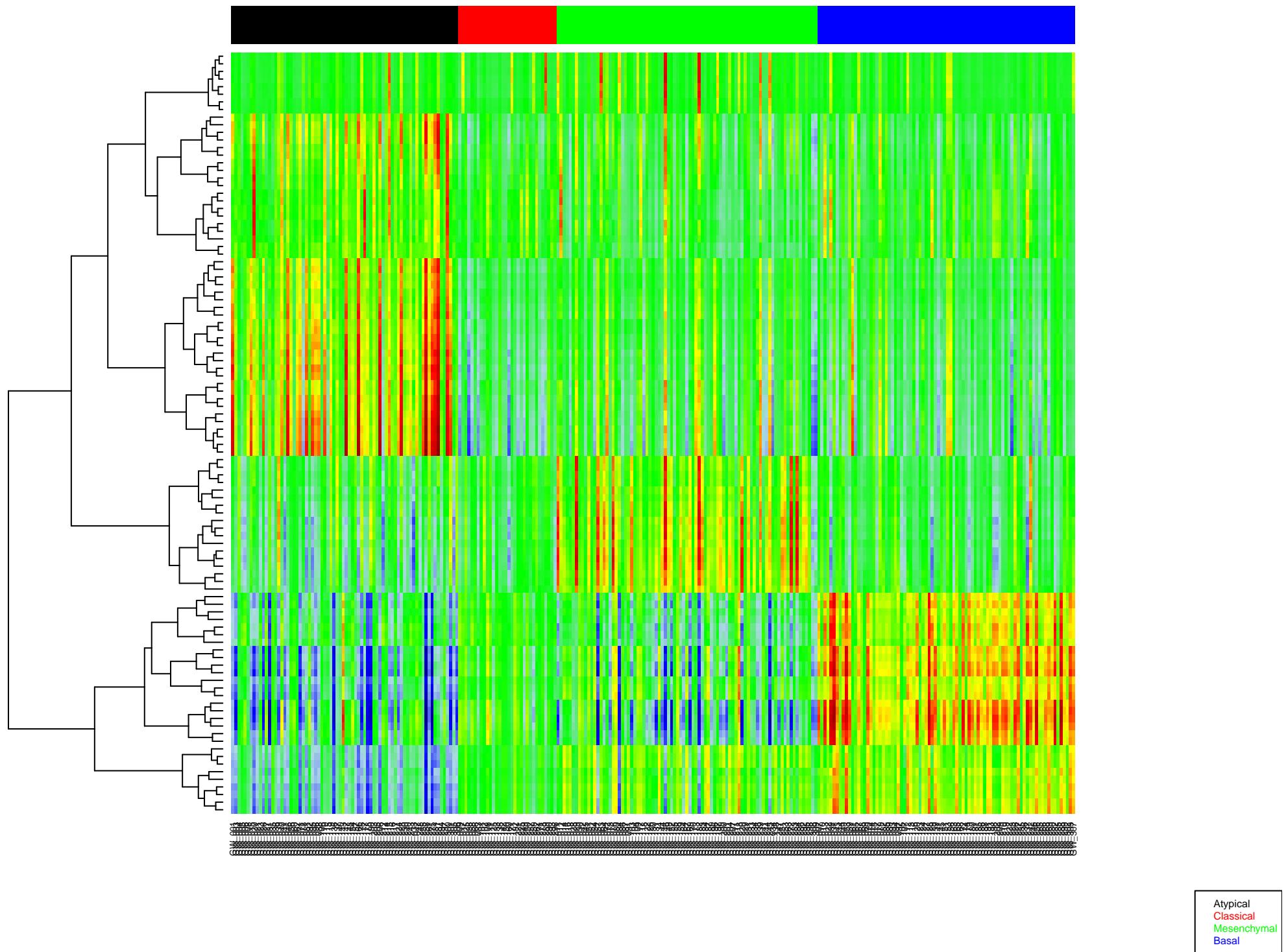


High Expression: 100 Metagenes

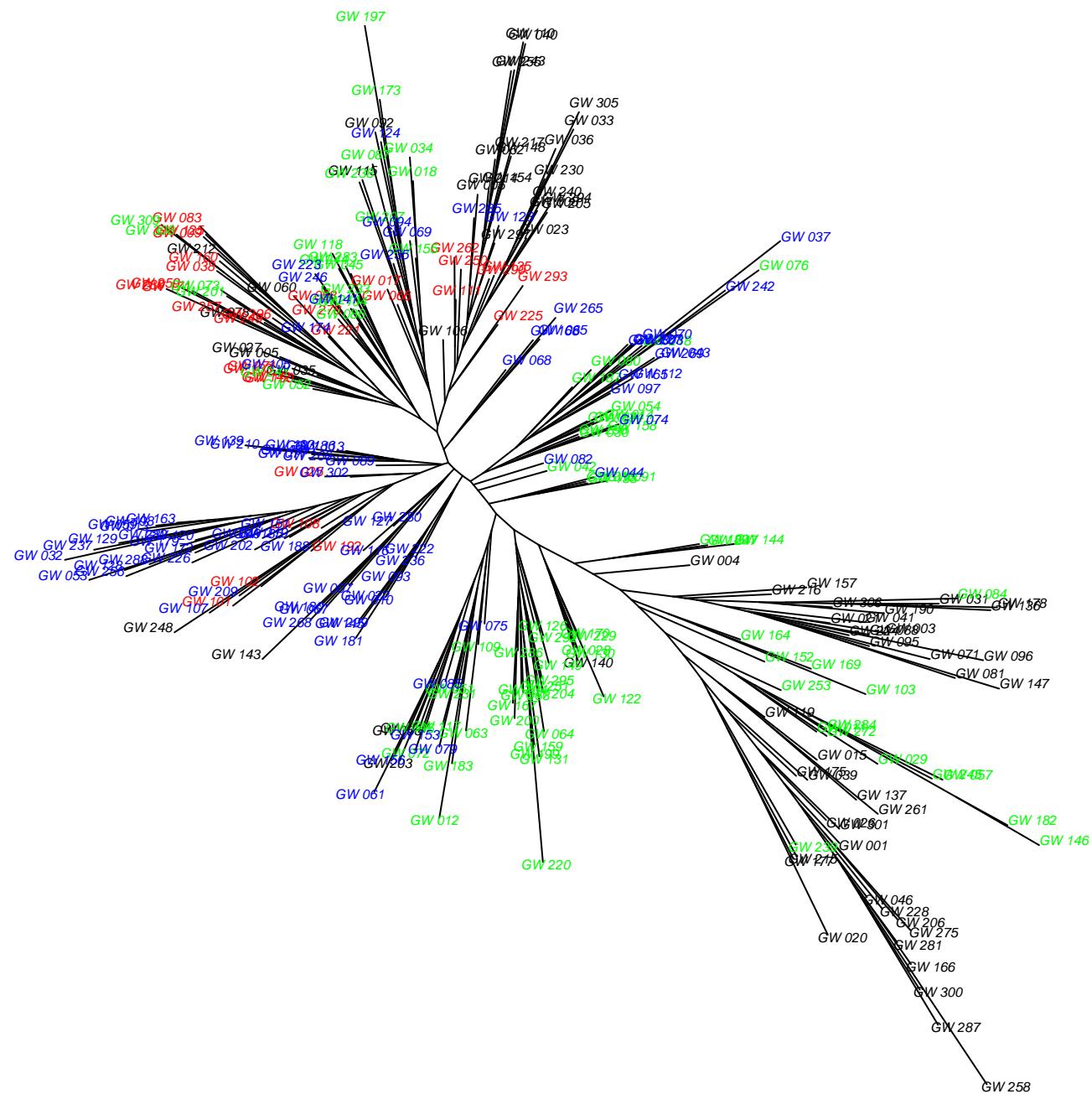


Atypical
Classical
Mesenchymal
Basal

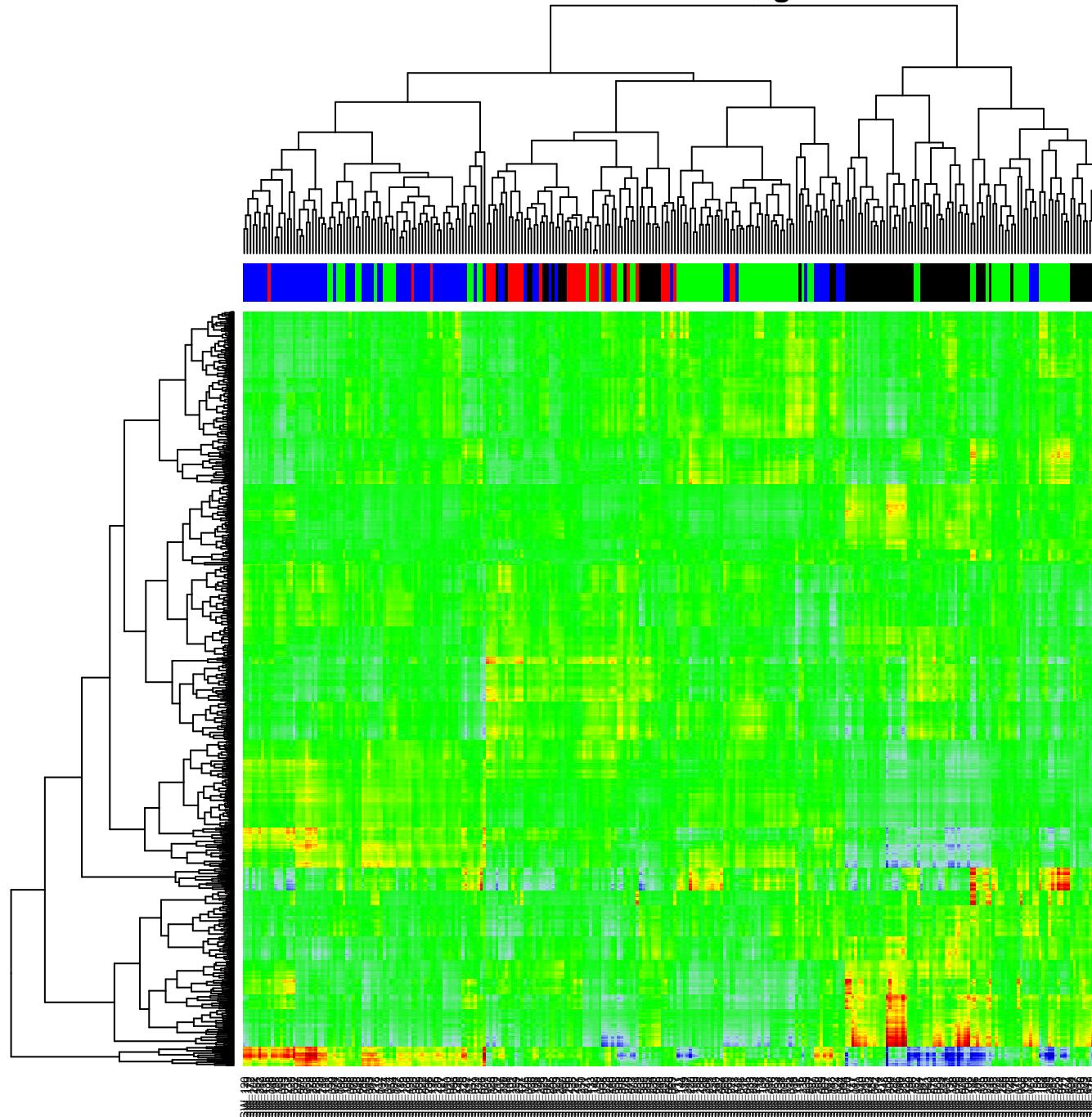
High Expression: 100 Metagenes



Variance: 1000 Metagenes

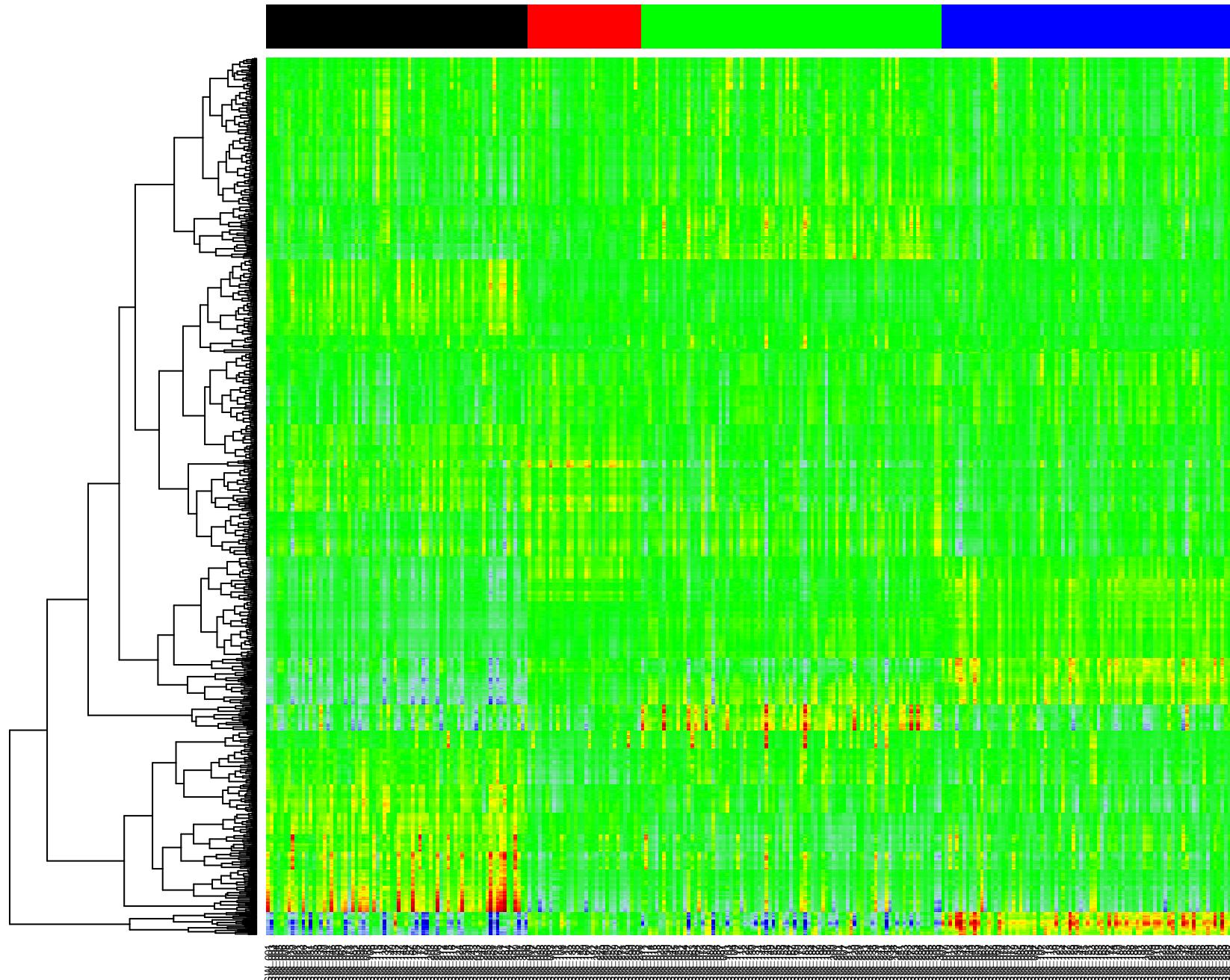


Variance: 1000 Metagenes



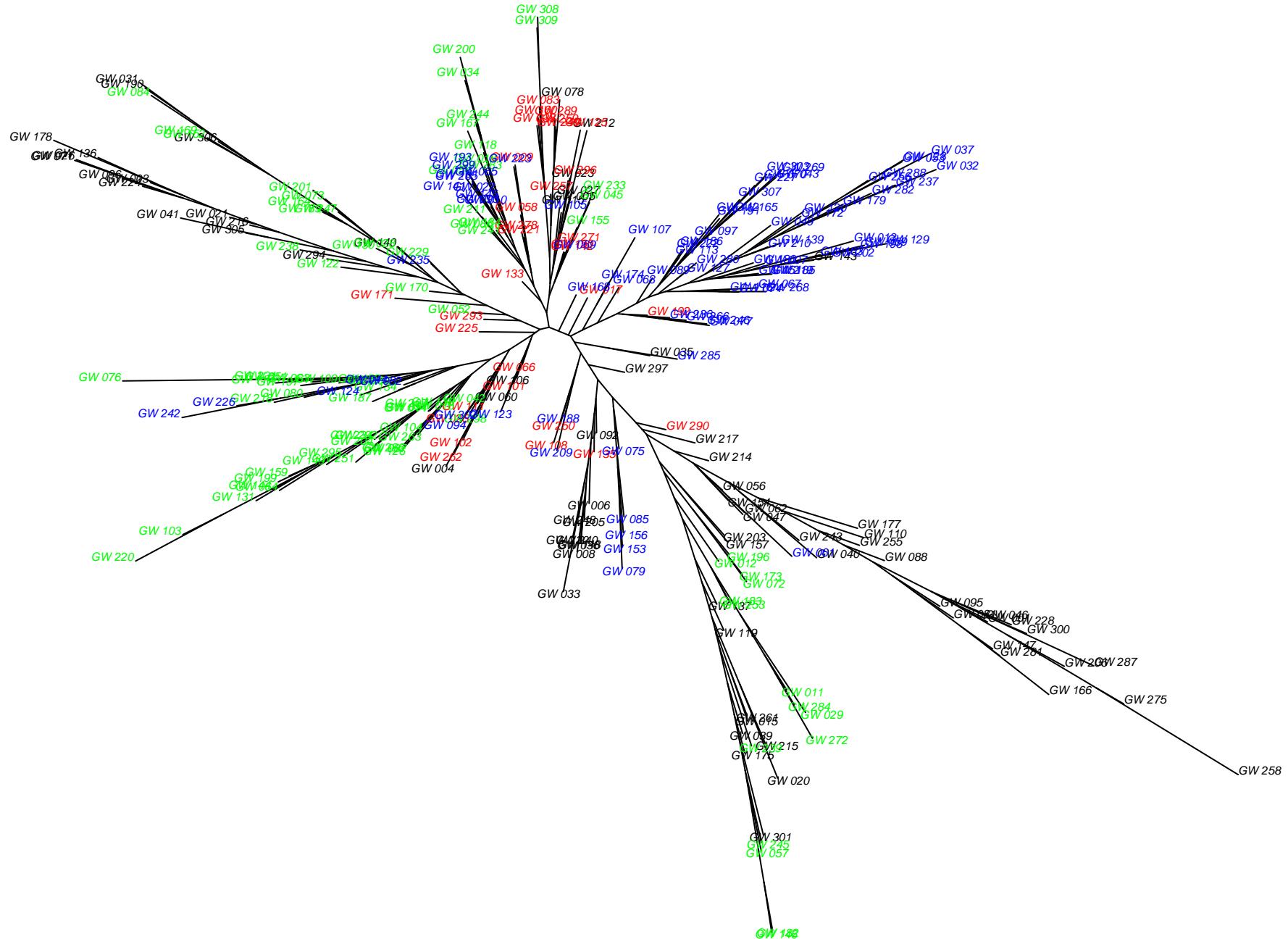
Atypical
Classical
Mesenchymal
Basal

Variance: 1000 Metagenes

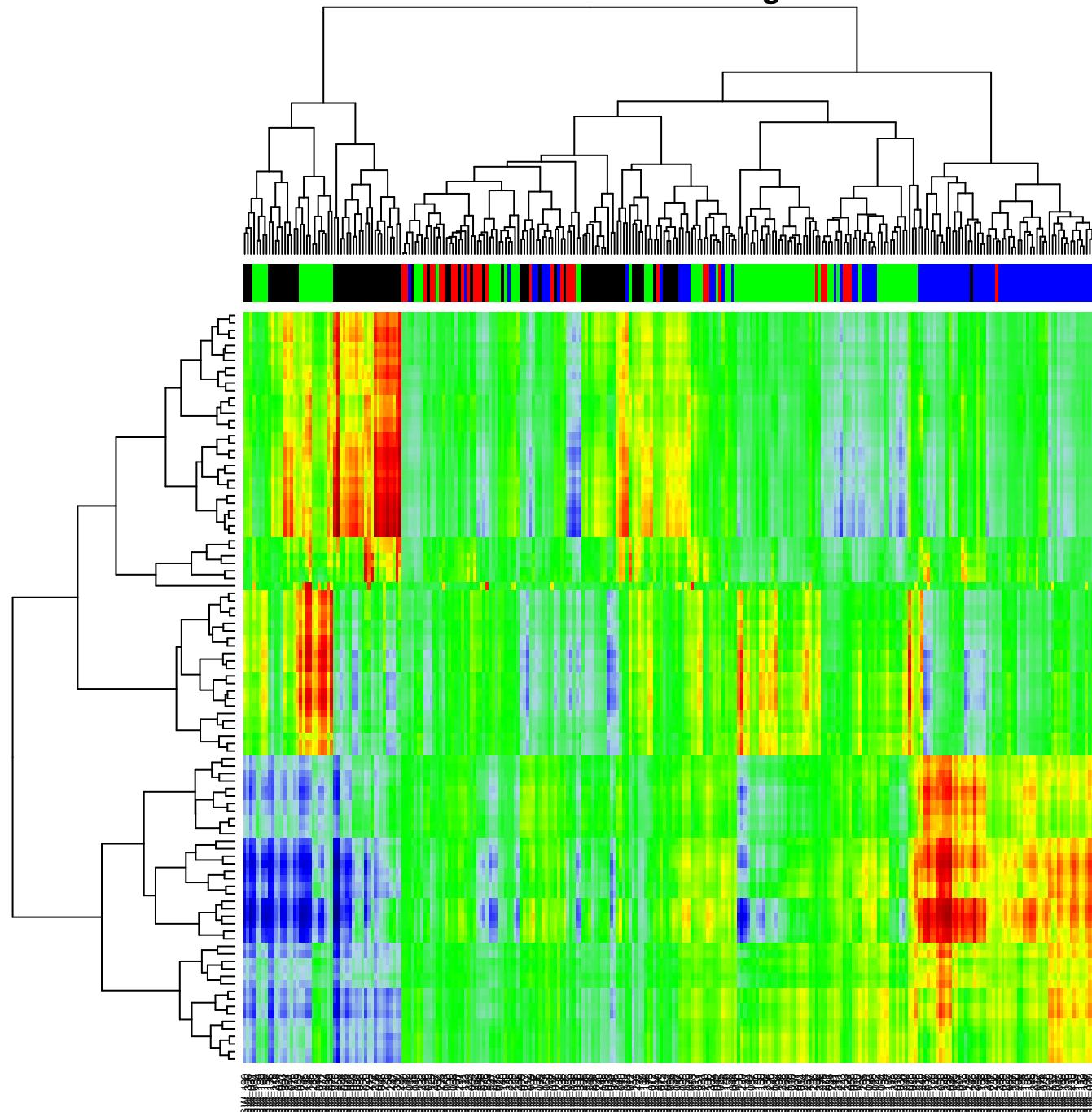


Atypical
Classical
Mesenchymal
Basal

Variance: 100 Metagenes

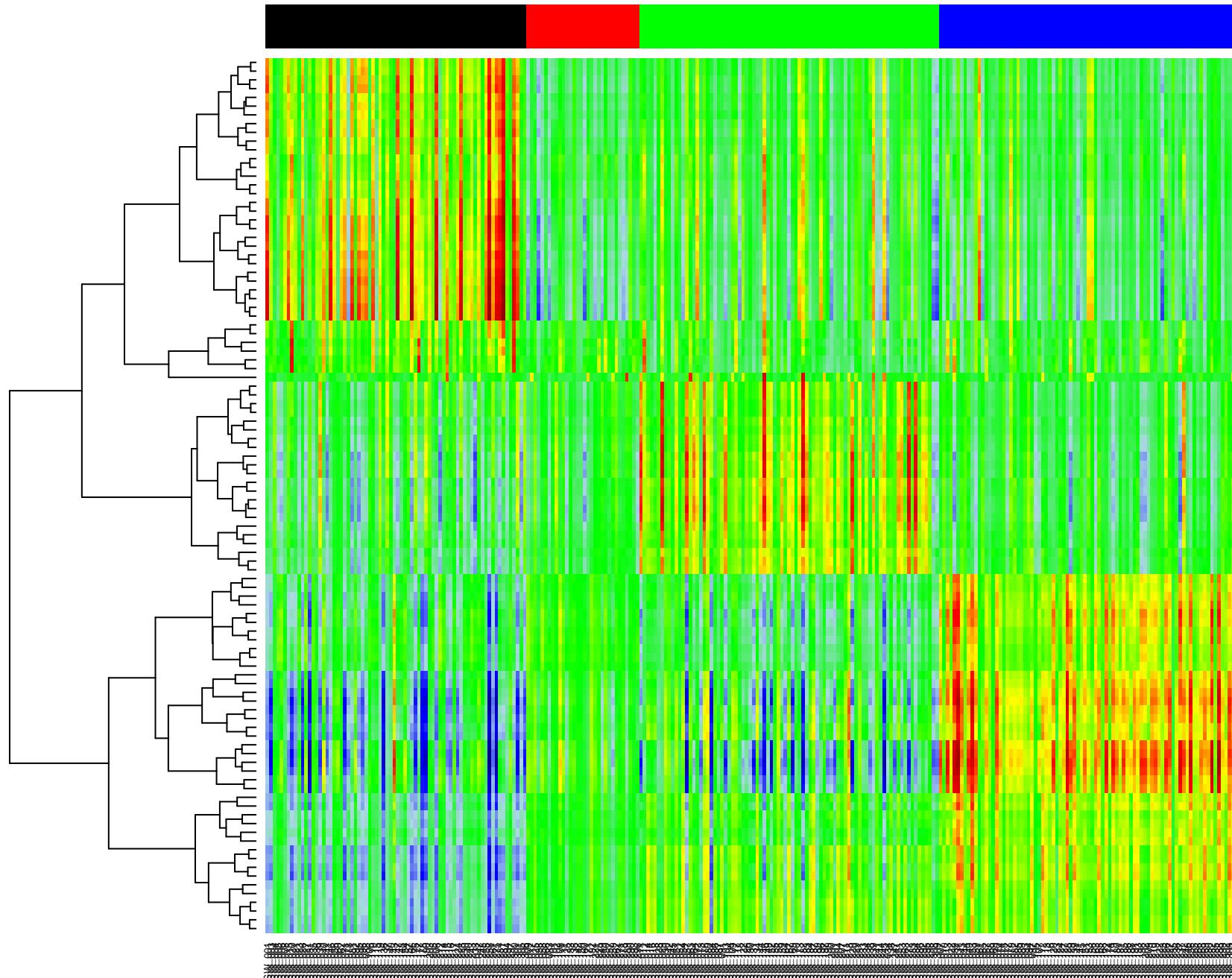


Variance: 100 Metagenes



Atypical
Classical
Mesenchymal
Basal

Variance: 100 Metagenes



Atypical
Classical
Mesenchymal
Basal