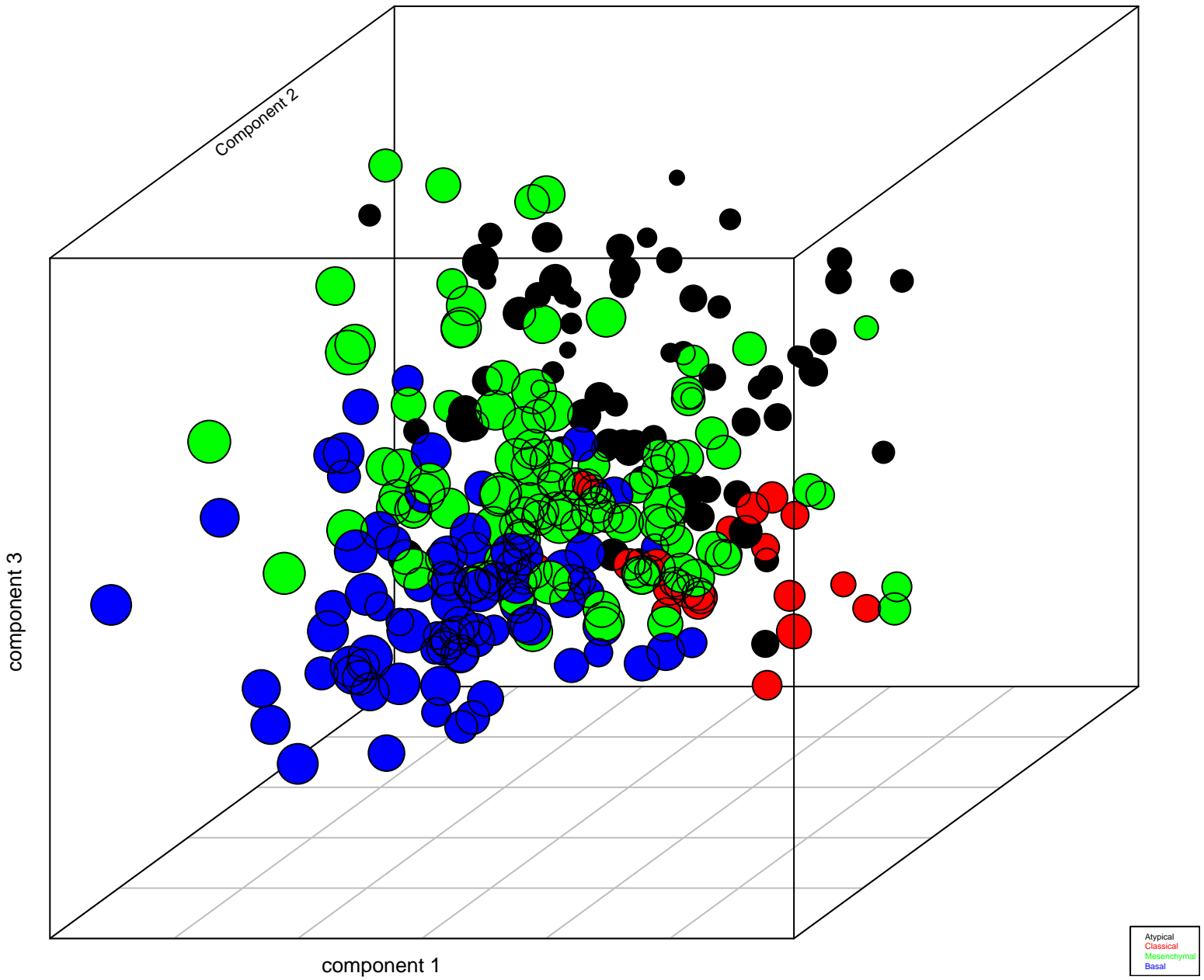
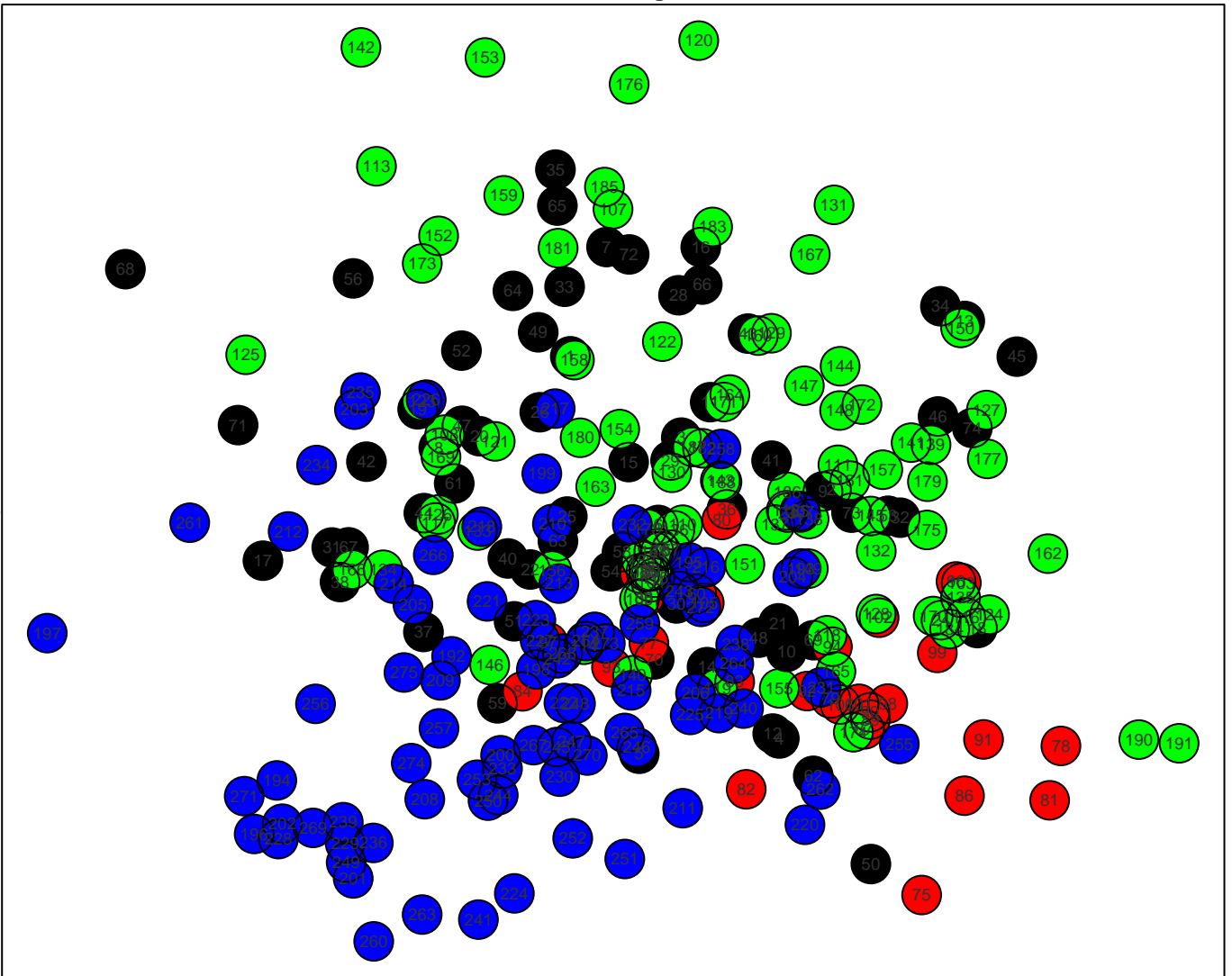


all 2500 Metagenes

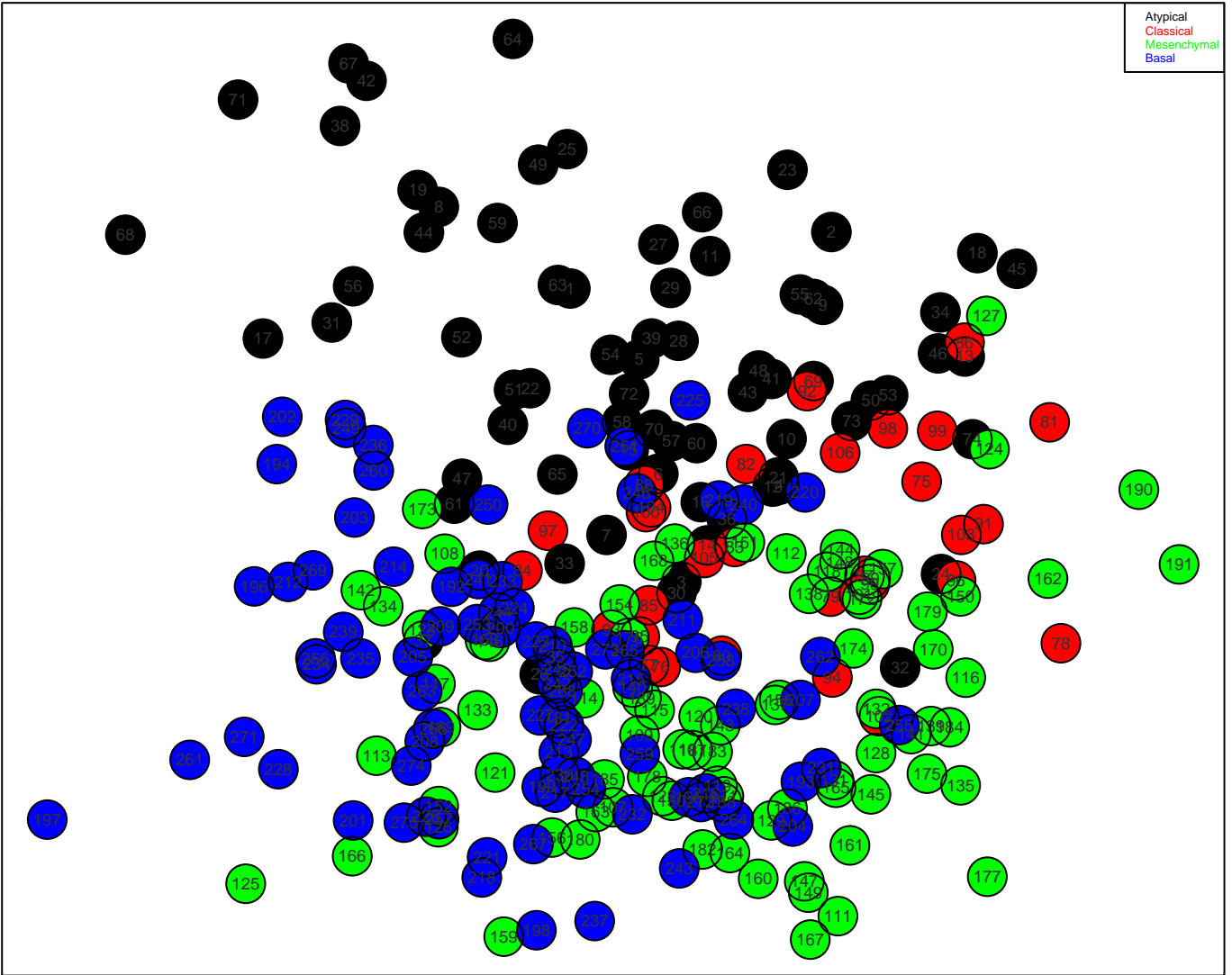


all 2500 Metagenes

component 3



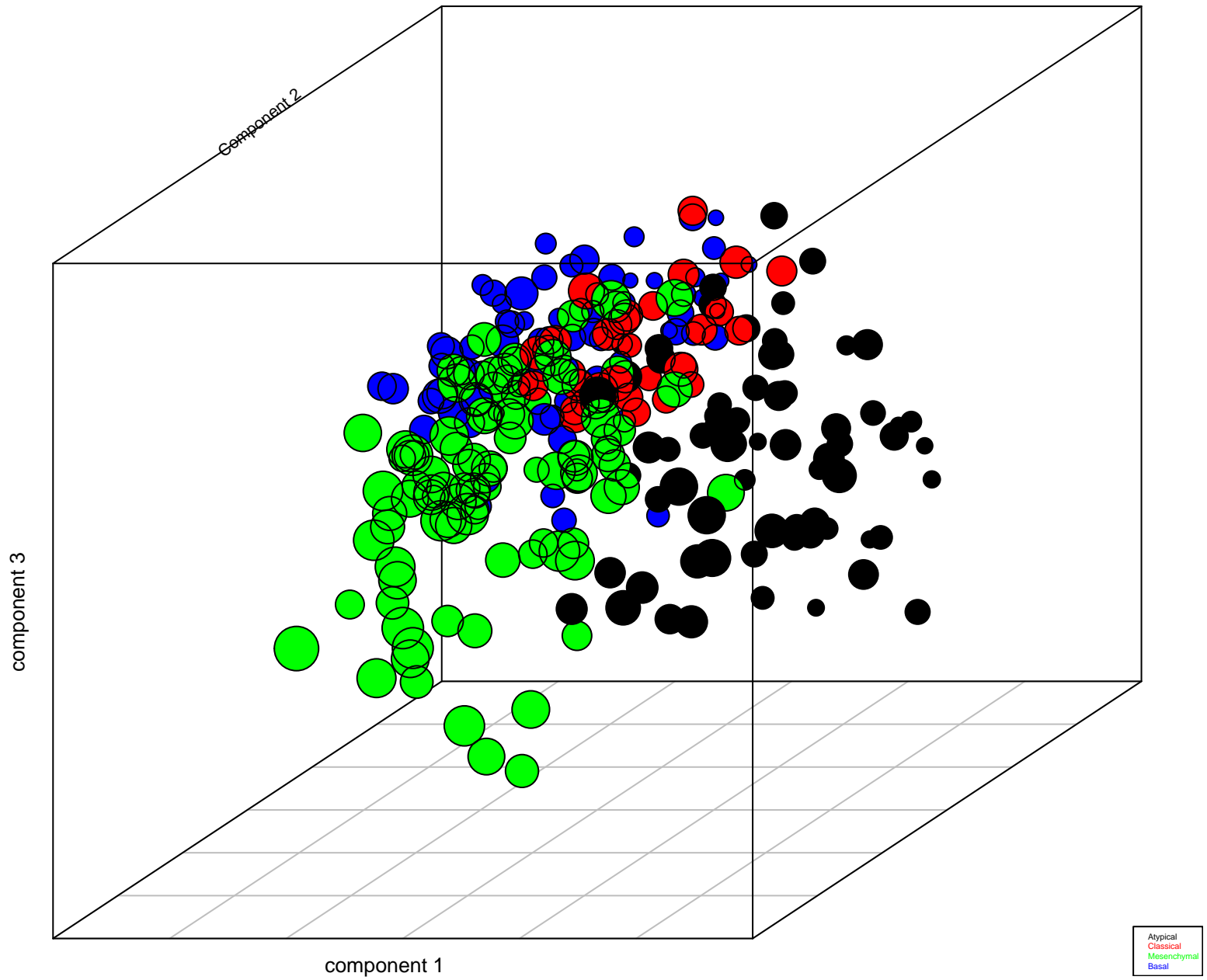
component 2



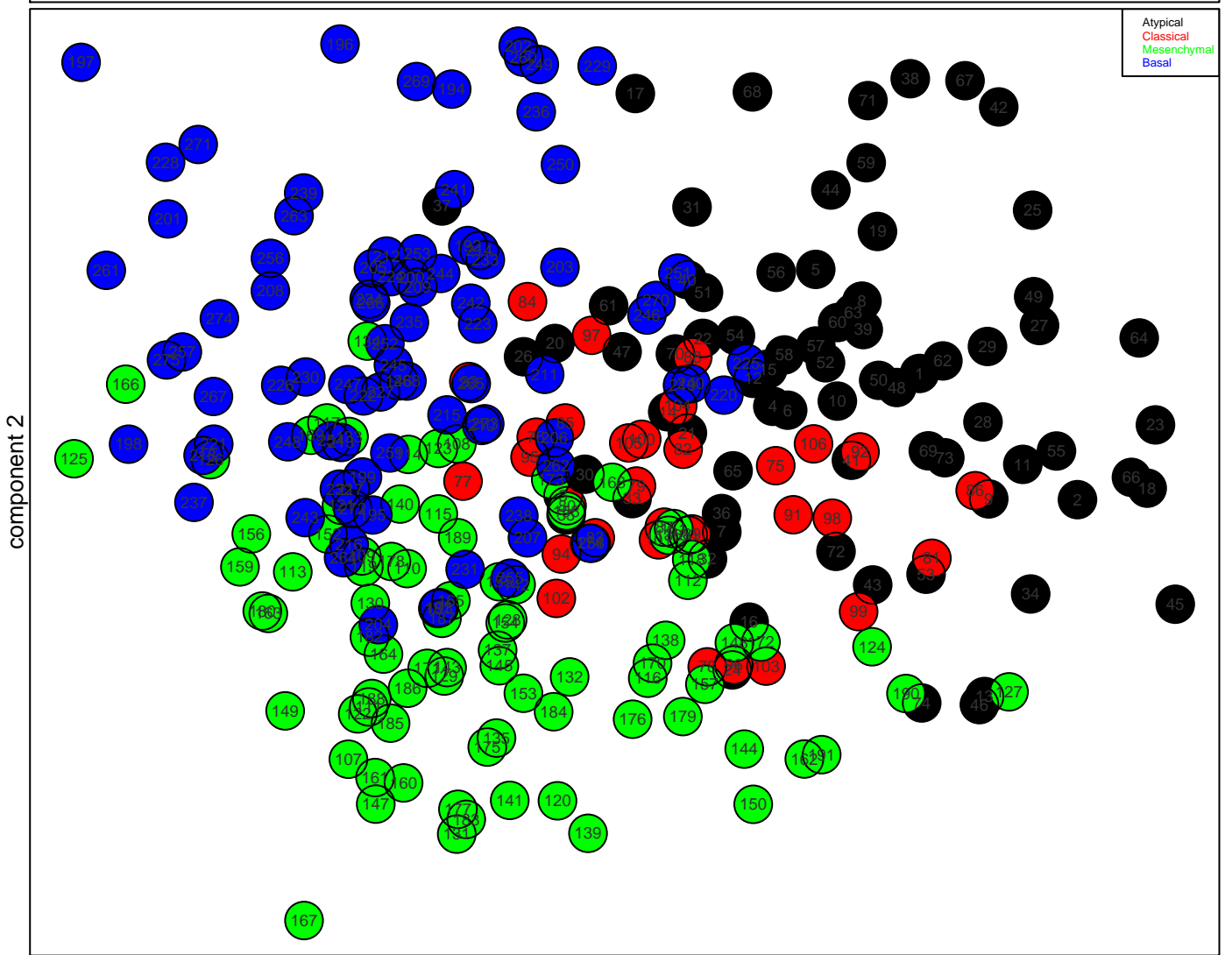
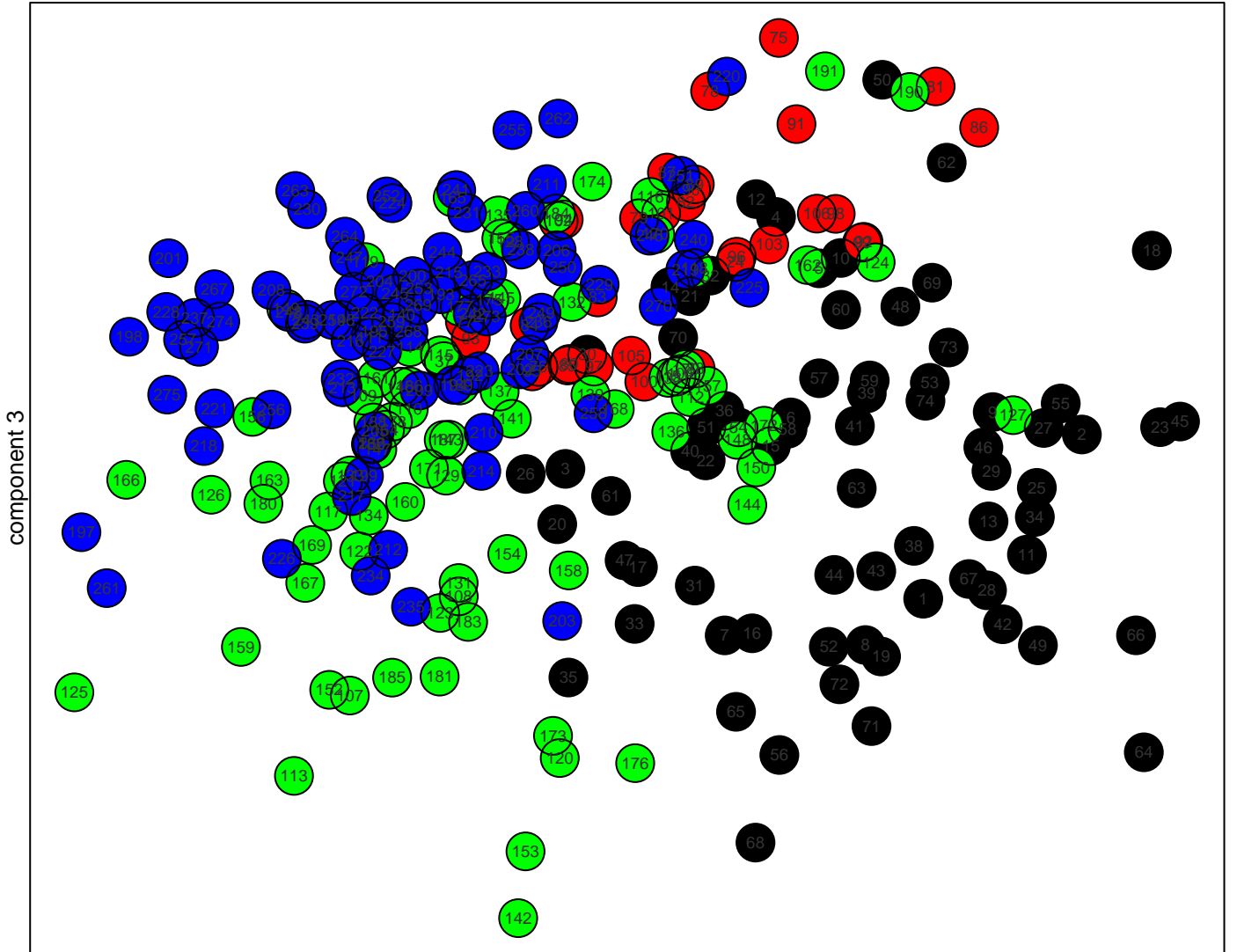
Atypical
Classical
Mesenchymal
Basal

component 1

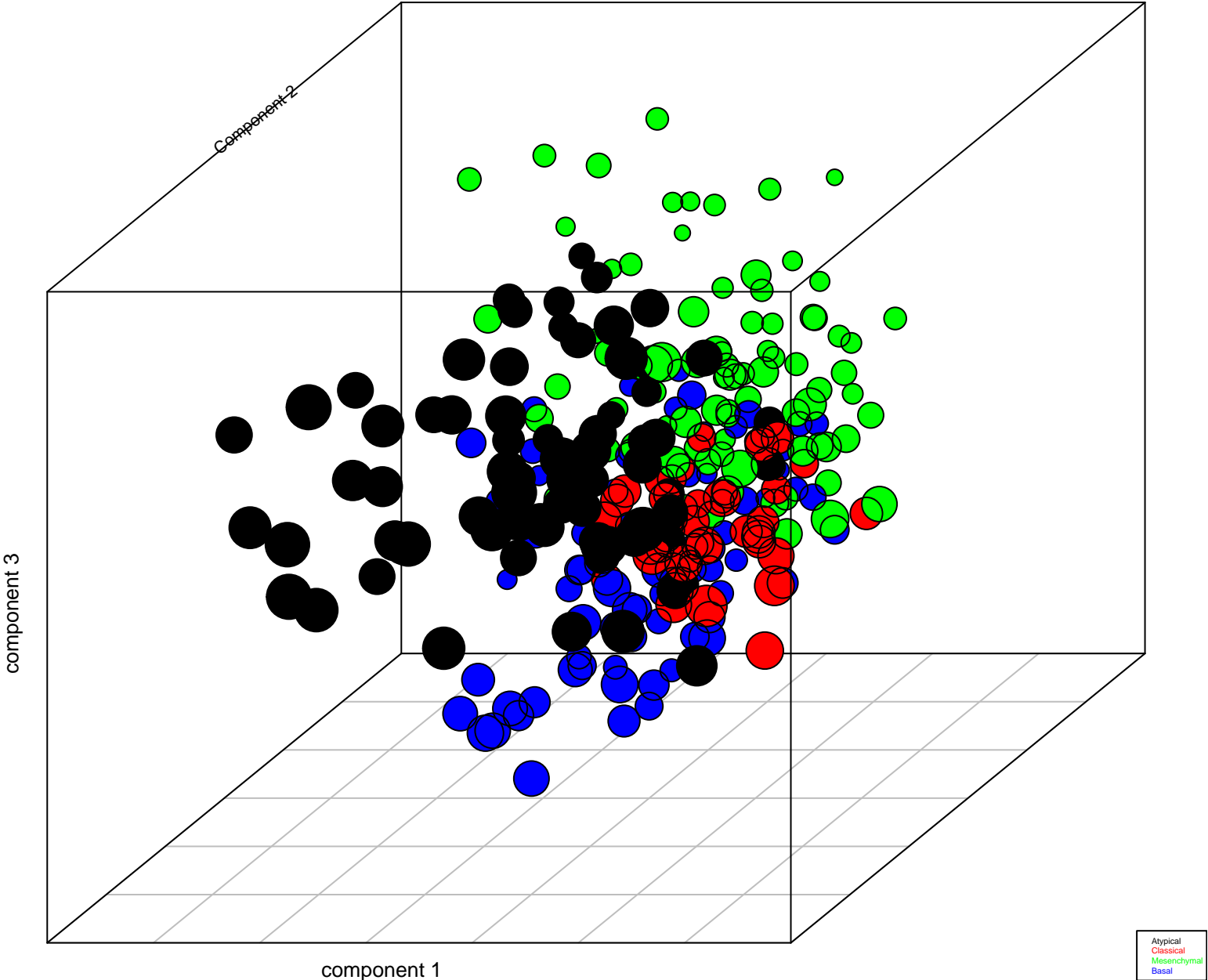
290 Spot-Metagenes



290 Spot-Metagenes

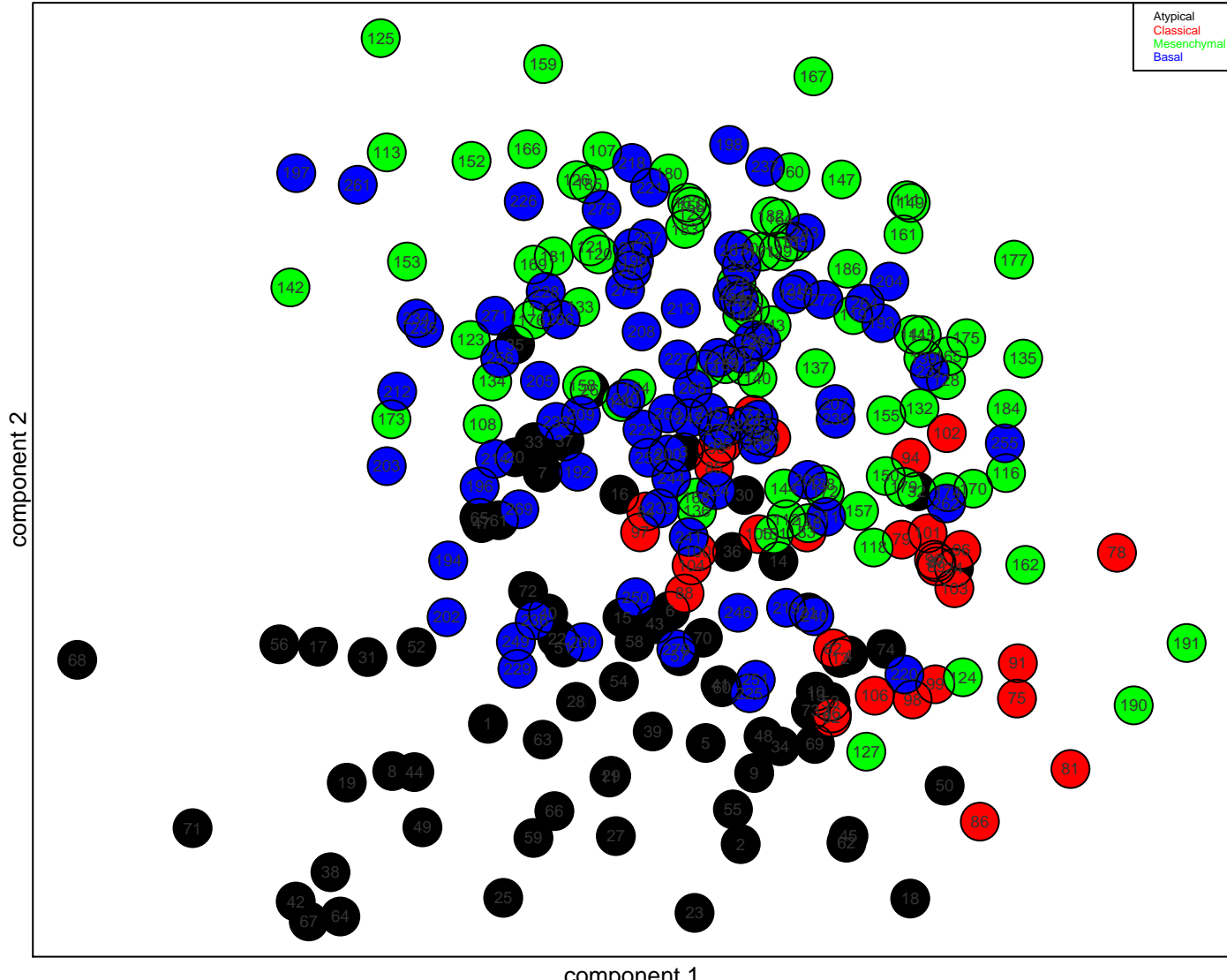
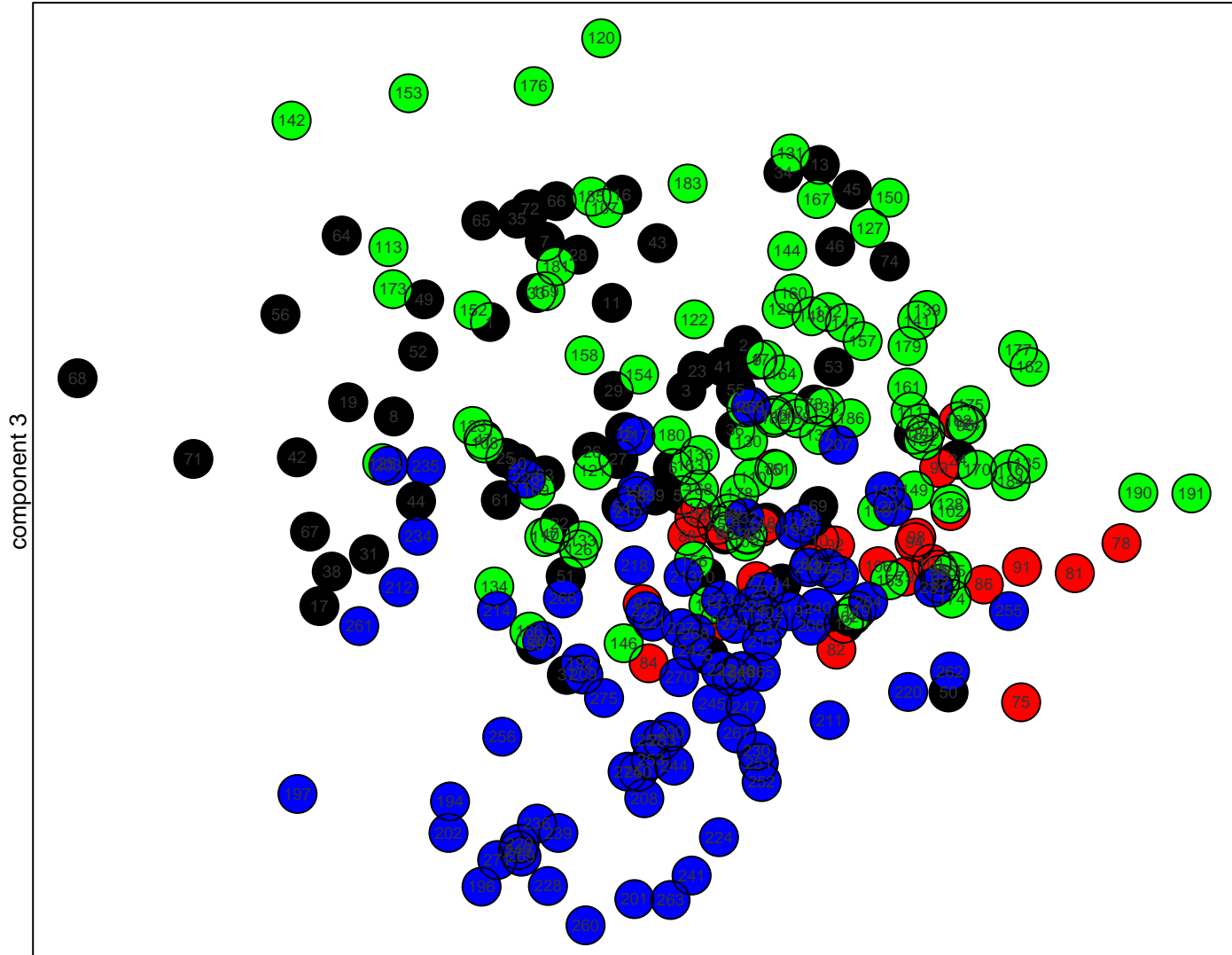


High Expression: 1000 Metagenes

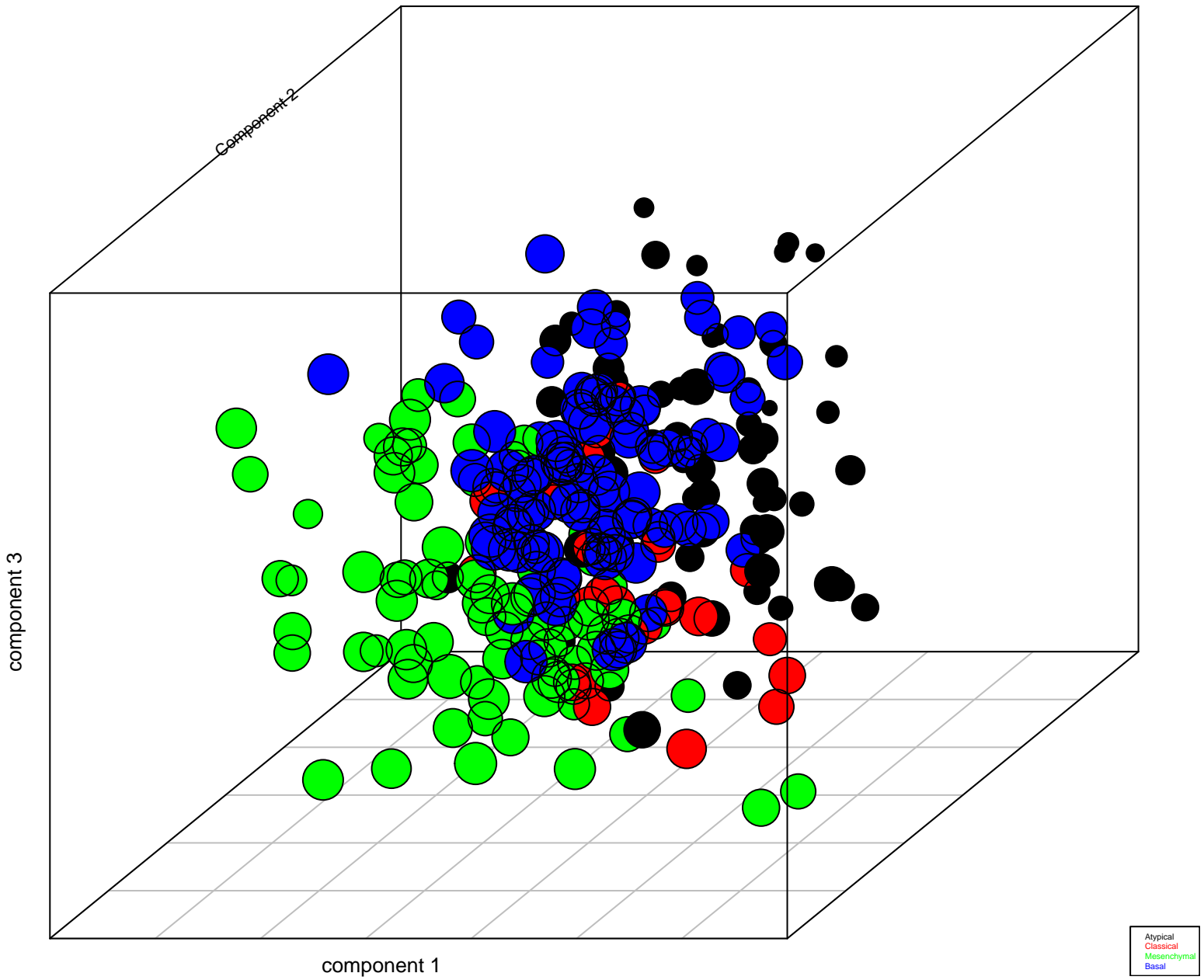


Atypical
Classical
Mesenchymal
Basal

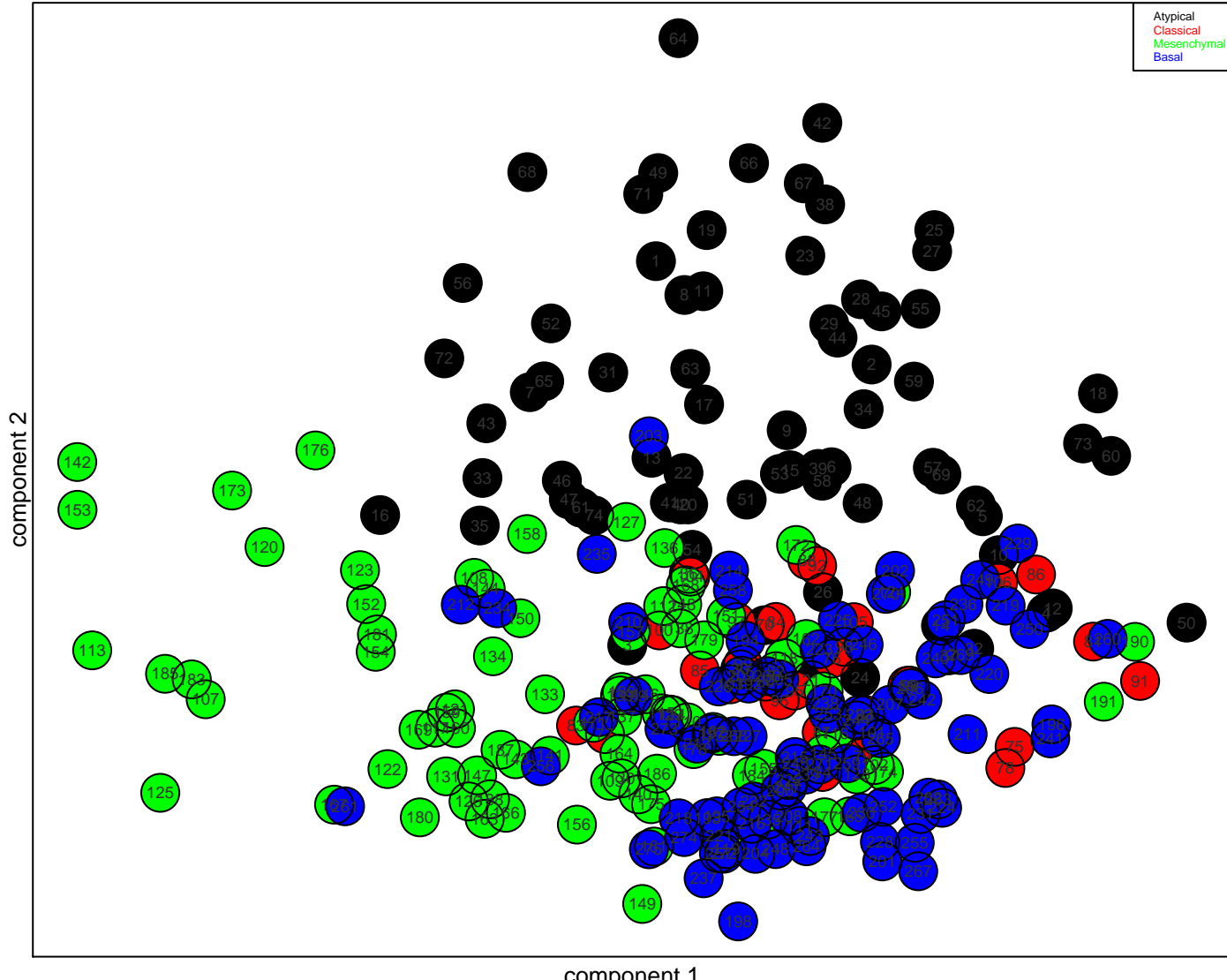
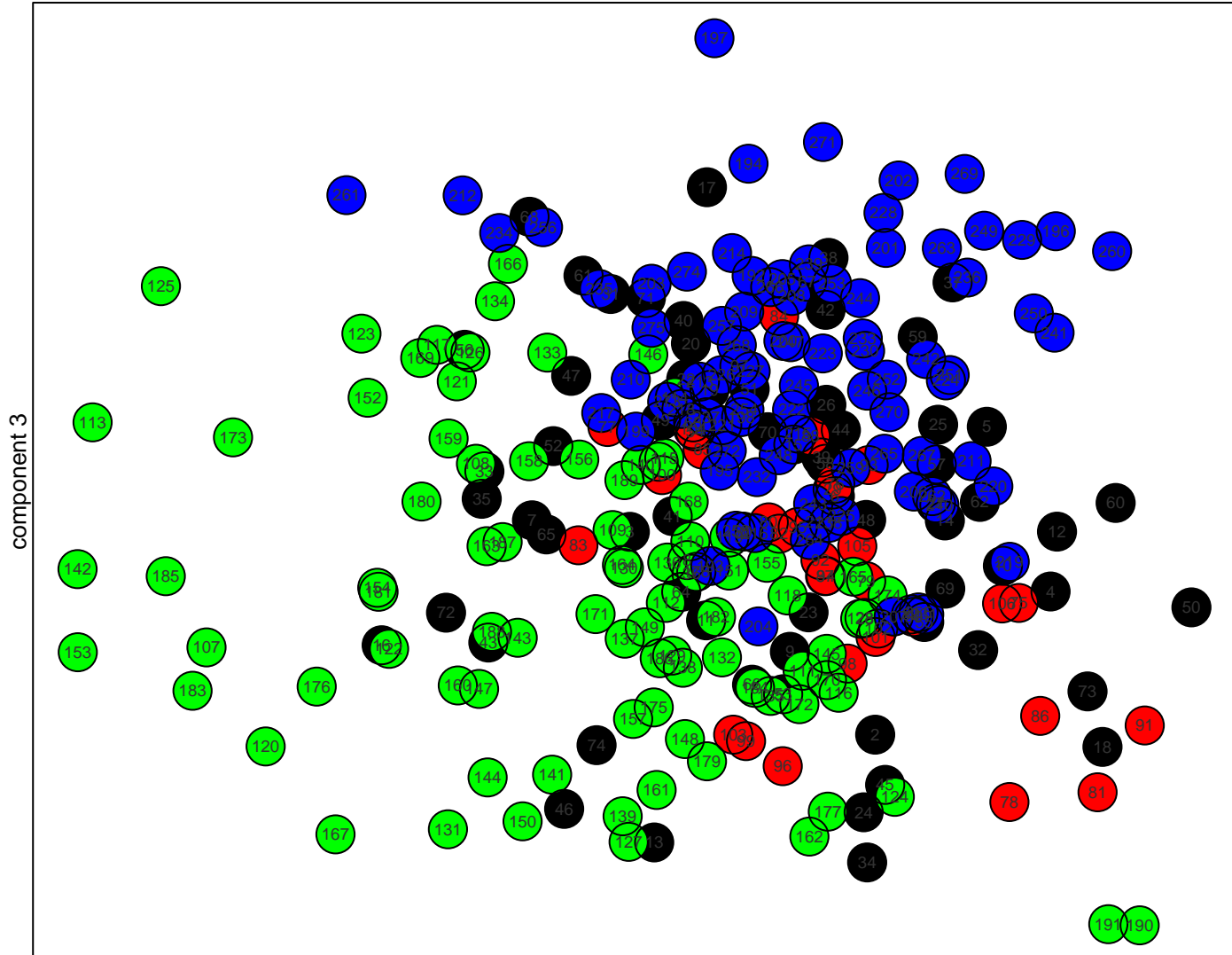
High Expression: 1000 Metagenes



High Expression: 100 Metagenes



High Expression: 100 Metagenes



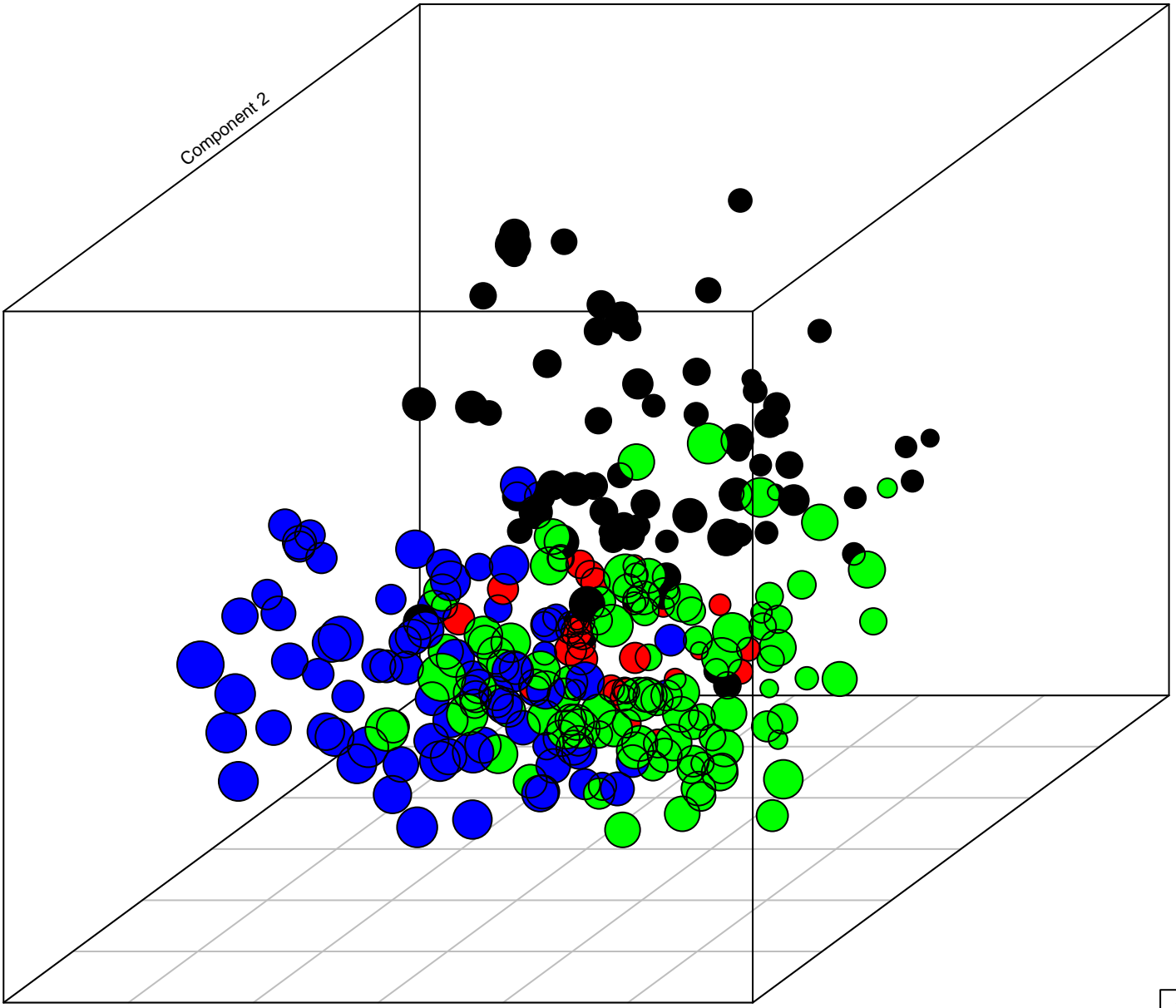
Variance: 1000 Metagenes

Component 2

component 3

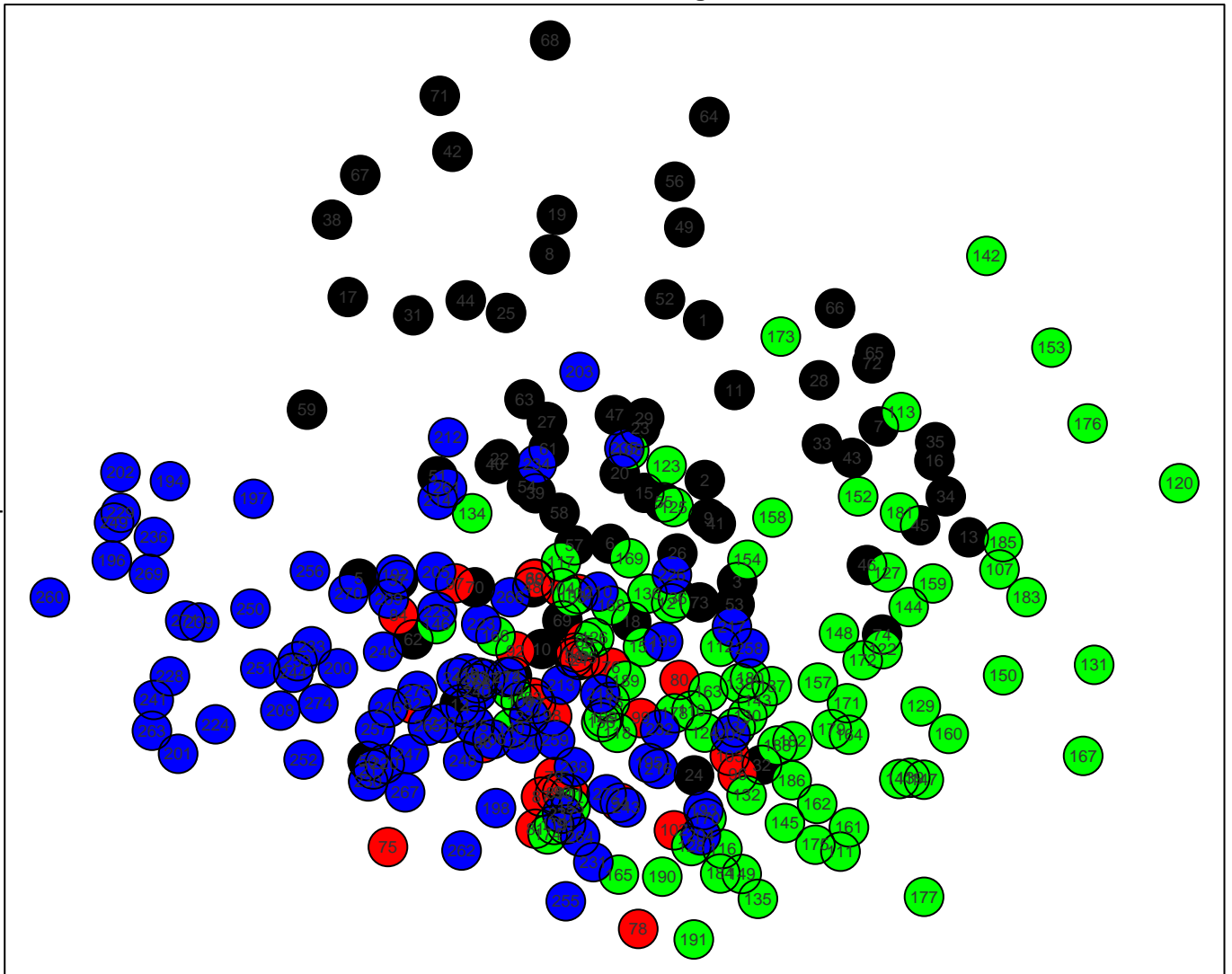
component 1

Atypical
Classical
Mesenchymal
Basal

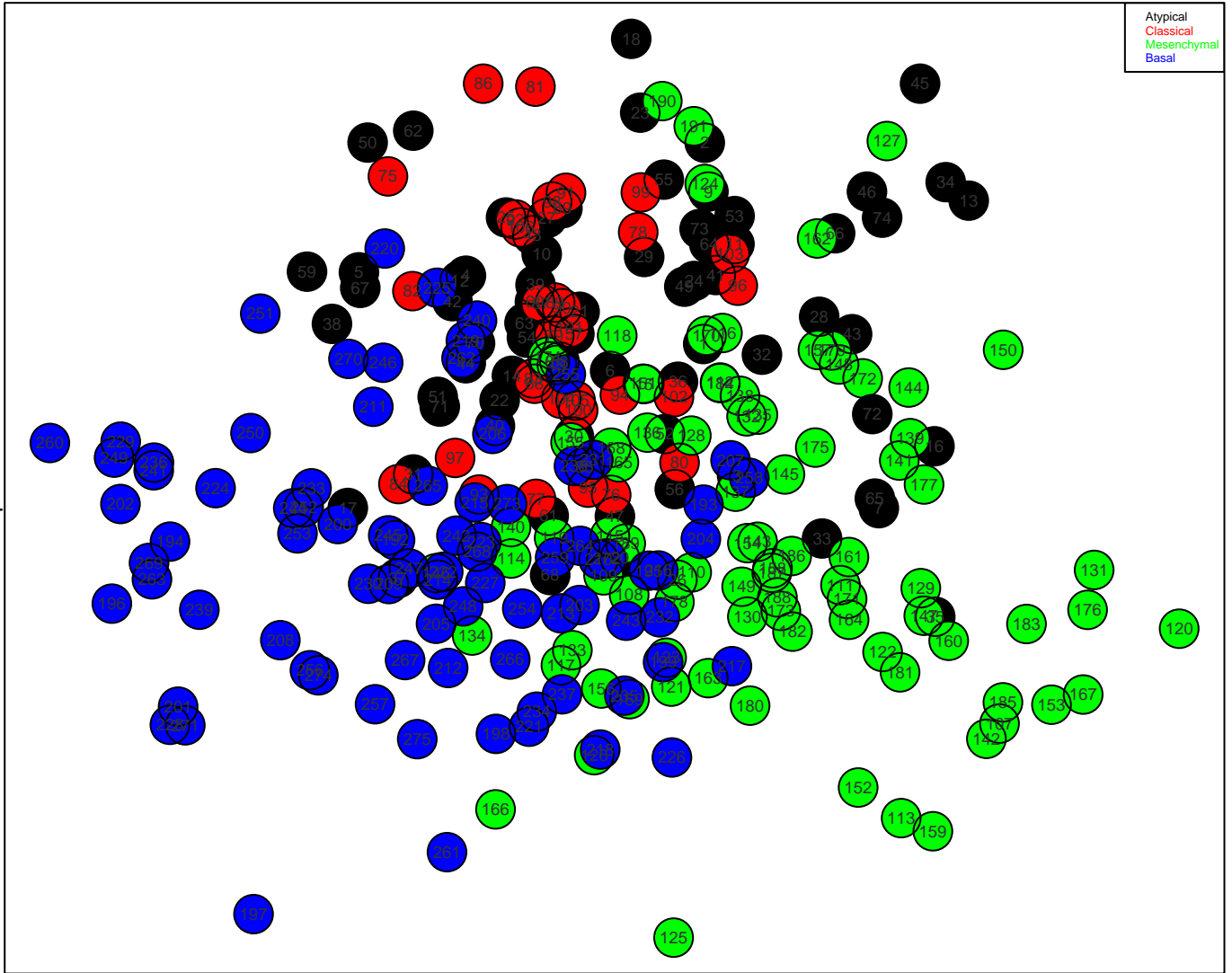


Variance: 1000 Metagenes

component 3



component 2



Atypical
Classical
Mesenchymal
Basal

component 1

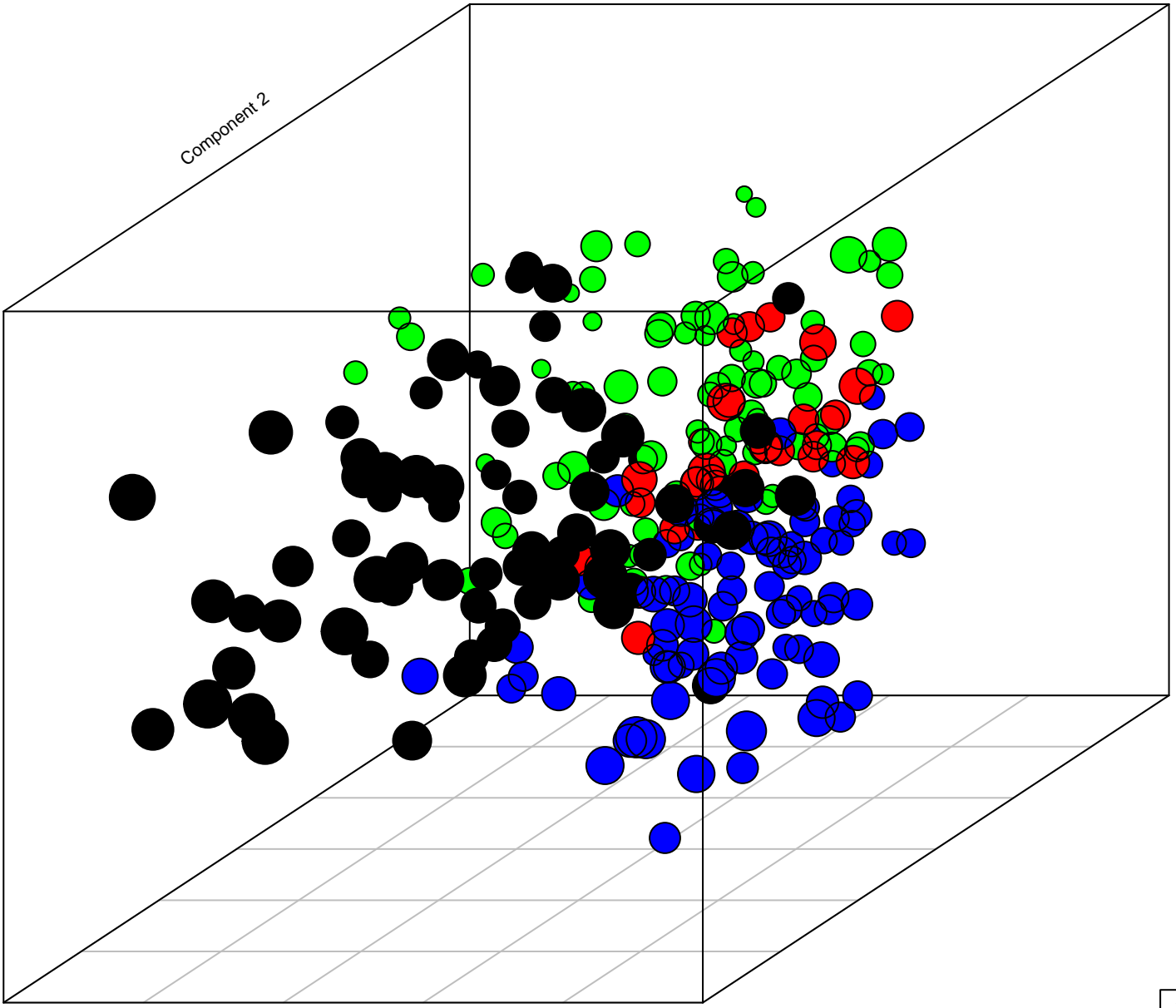
Variance: 100 Metagenes

Component 2

component 3

component 1

Atypical
Classical
Mesenchymal
Basal



Variance: 100 Metagenes

