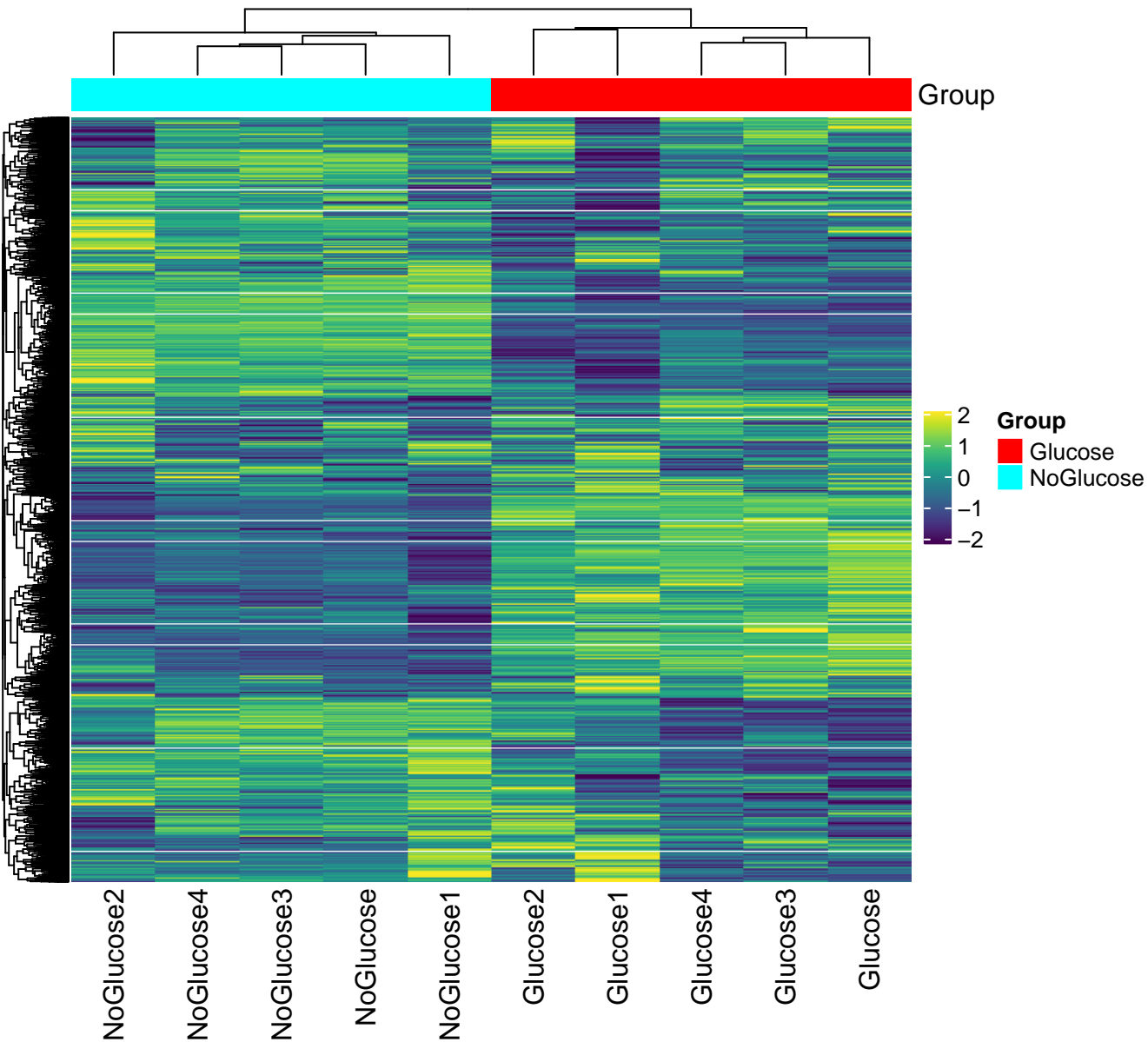
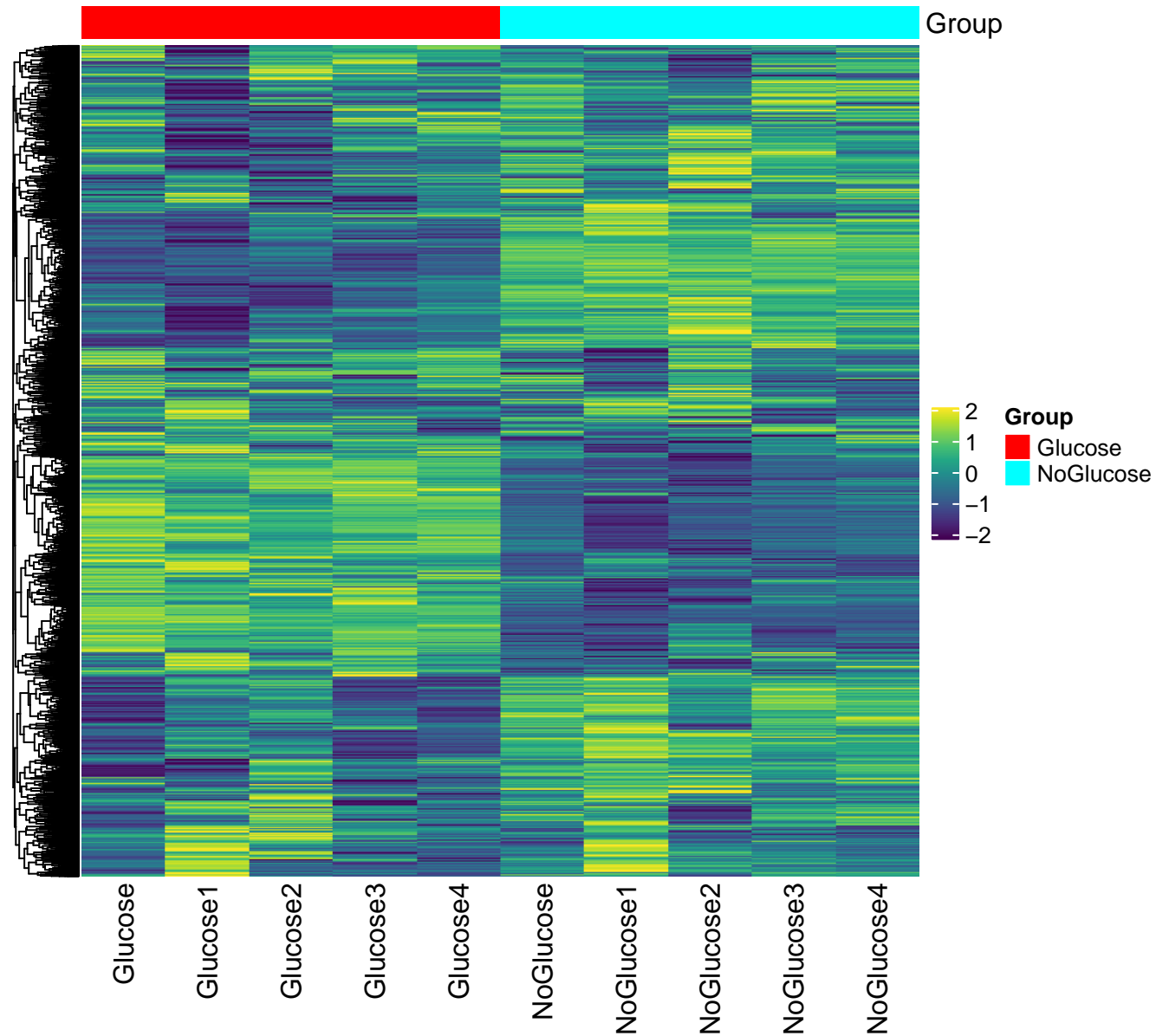


Proteomics:  
All features, row z score

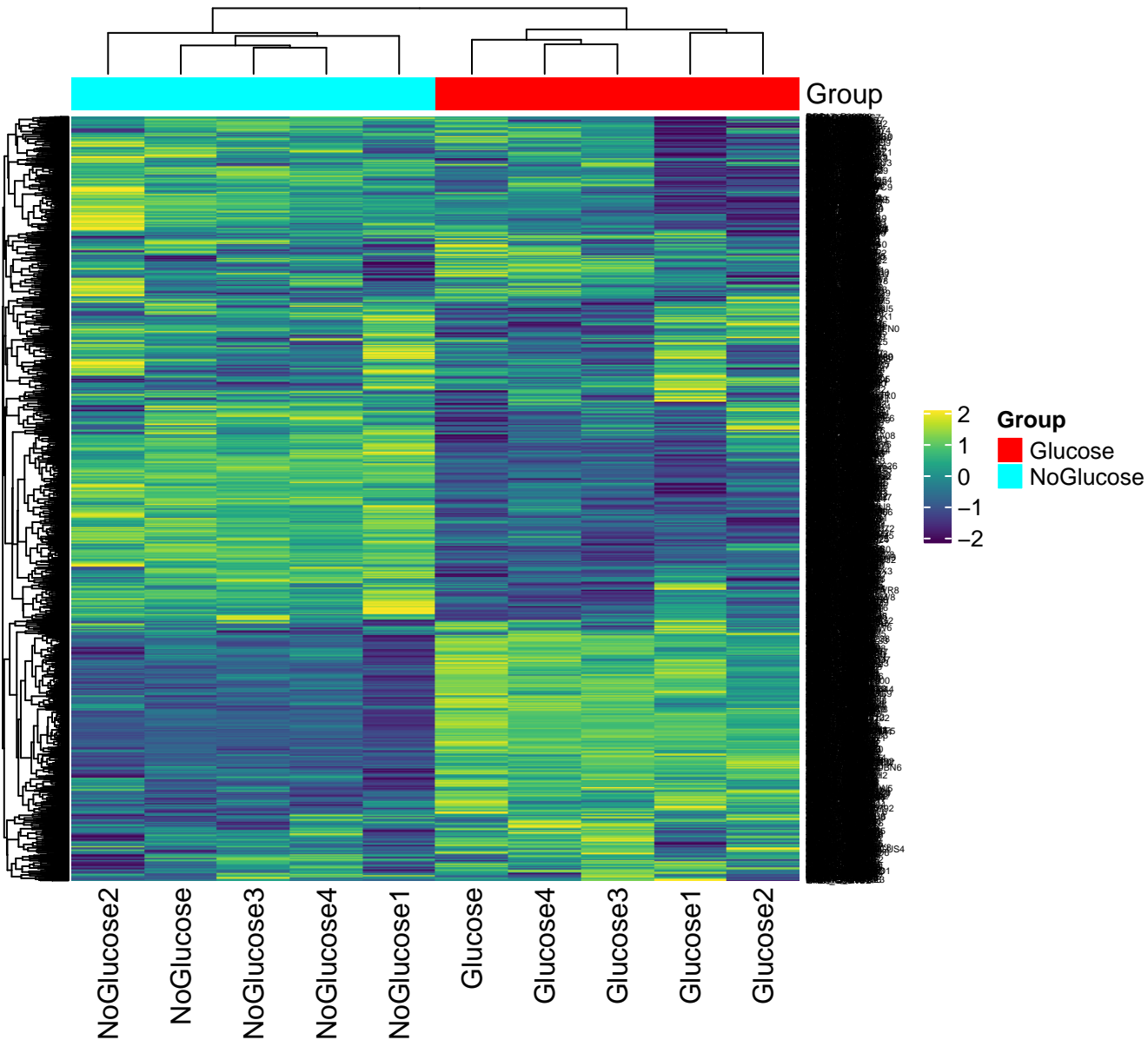


Proteomics:  
All features, row z score



# Proteomics: human1\_gene1\_expanded

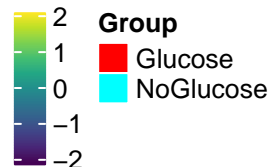
Subset, row z score



# Proteomics: human1\_gene1\_expanded

Subset, row z score

Group



Glucose

Glucose1

Glucose2

Glucose3

Glucose4

NoGlucose

NoGlucose1

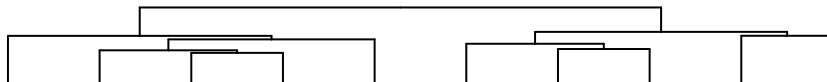
NoGlucose2

NoGlucose3

NoGlucose4

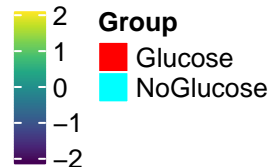
# Proteomics: human1\_gene1\_expanded

Subset, row z score



Group

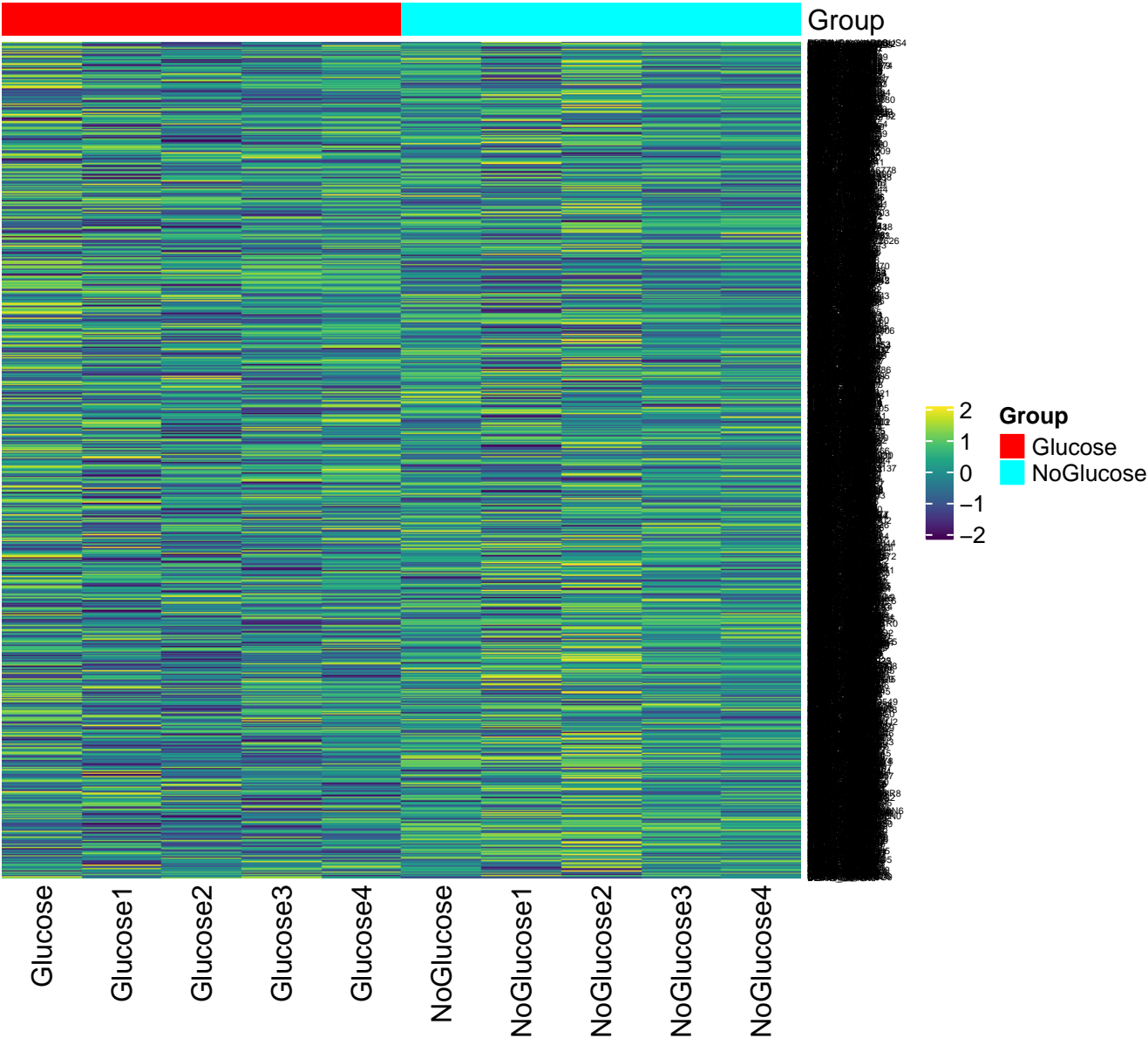
US4  
9  
2  
27  
10  
42  
6  
10  
109  
1  
168  
18  
14  
53  
38  
18  
26  
170  
19  
43  
19  
106  
17  
36  
35  
1  
15  
12  
2  
139  
137  
13  
1  
11  
112  
14  
12  
1  
15  
16  
10  
16  
16  
15  
19  
12  
16  
16  
17  
58  
16  
16  
15



NoGlucose2  
NoGlucose  
NoGlucose3  
NoGlucose4  
NoGlucose1  
Glucose  
Glucose4  
Glucose3  
Glucose1  
Glucose2

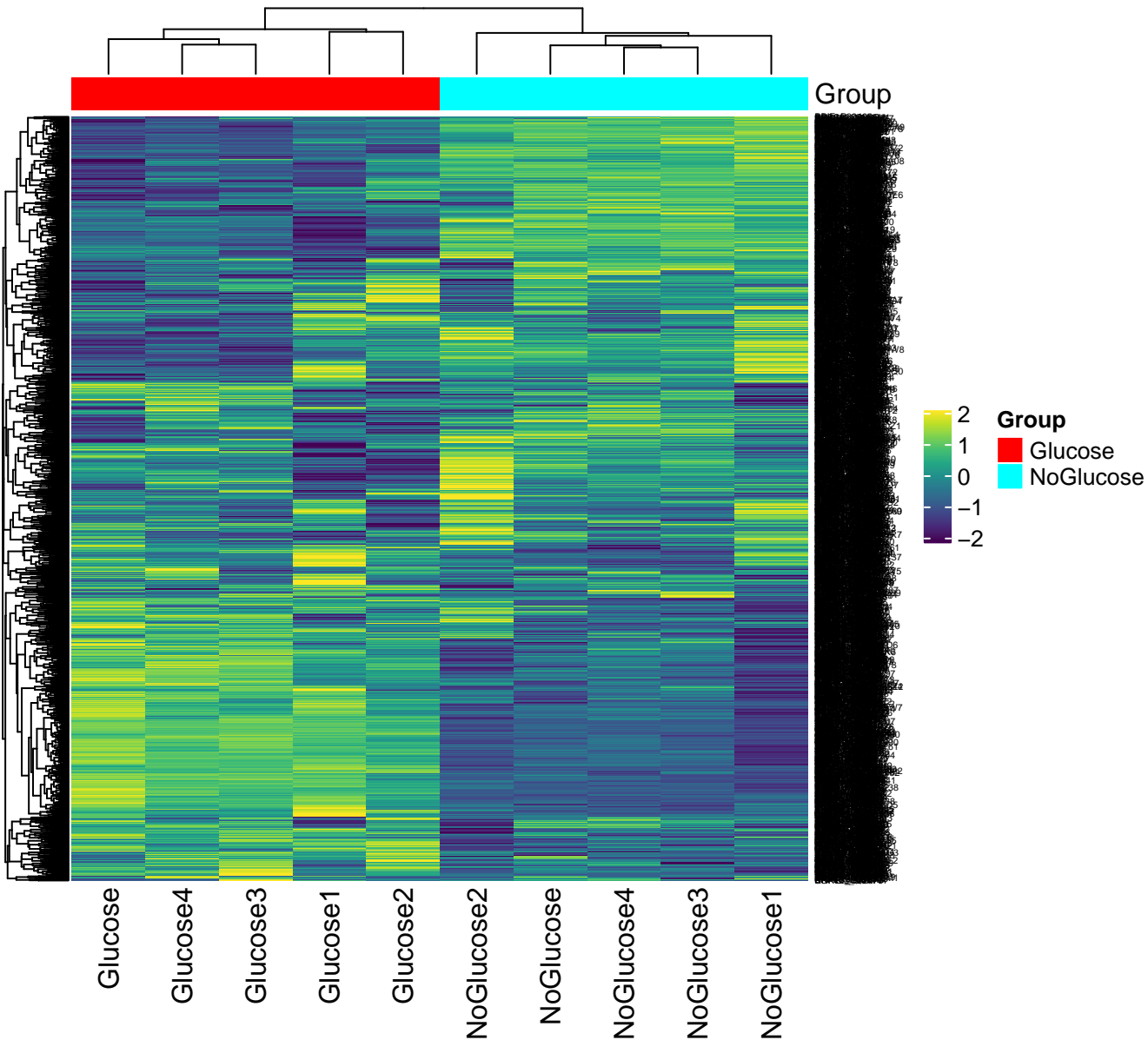
# Proteomics: human1\_gene1\_expanded

## Subset, row z score



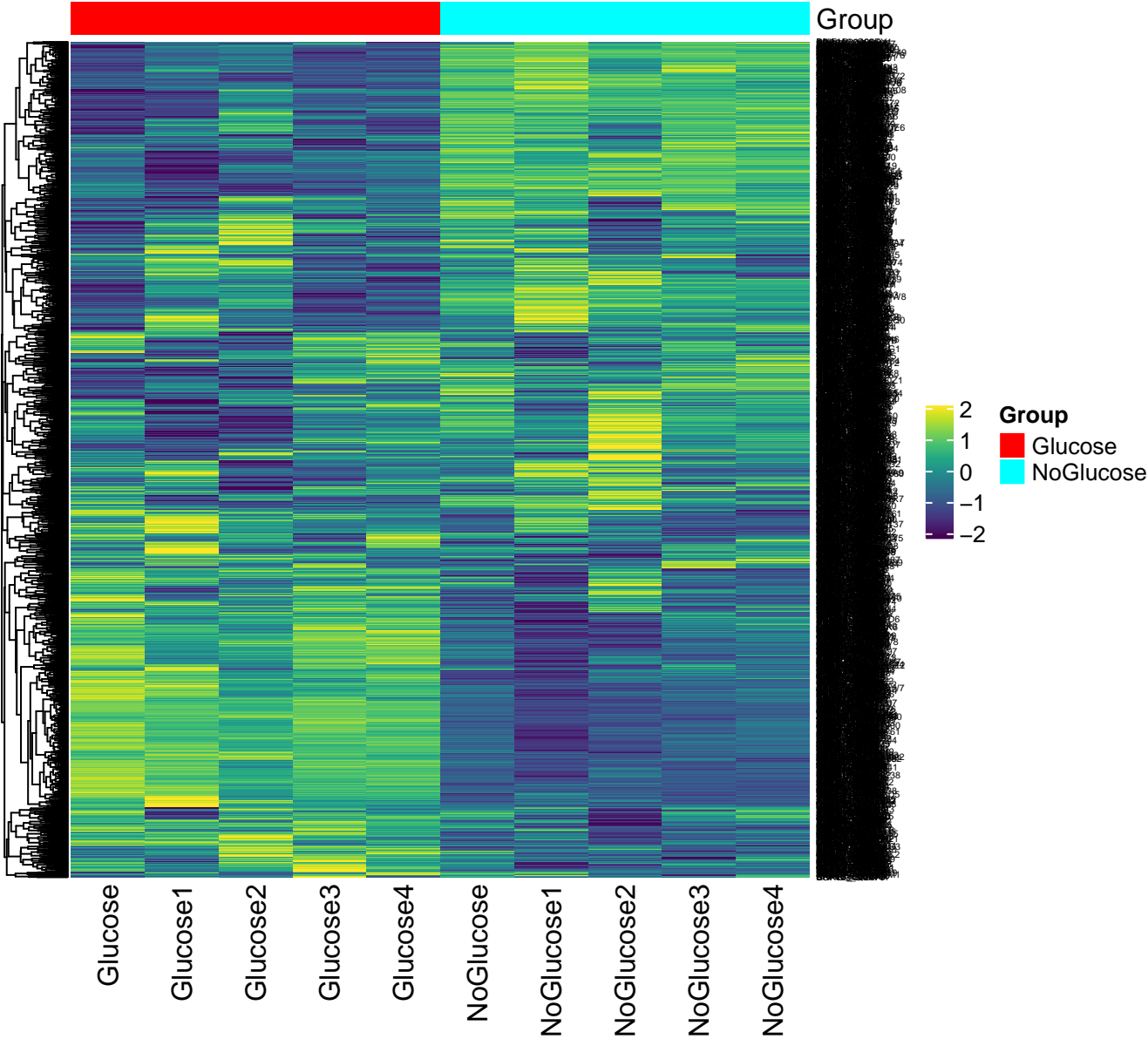
# Proteomics: human2\_gene1\_expanded

Subset, row z score



Proteomics: human2\_gene1\_expanded

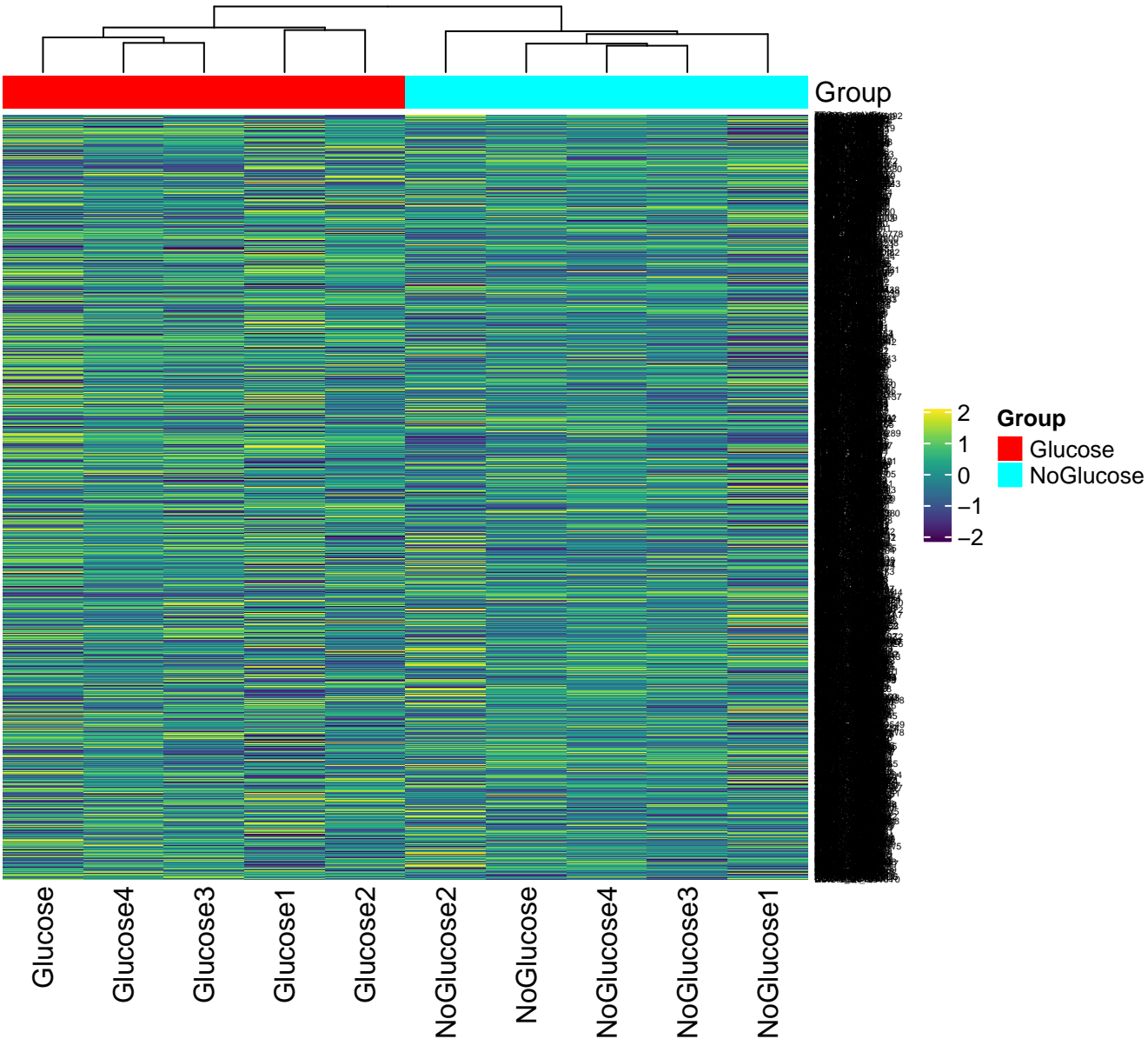
Subset, row z score





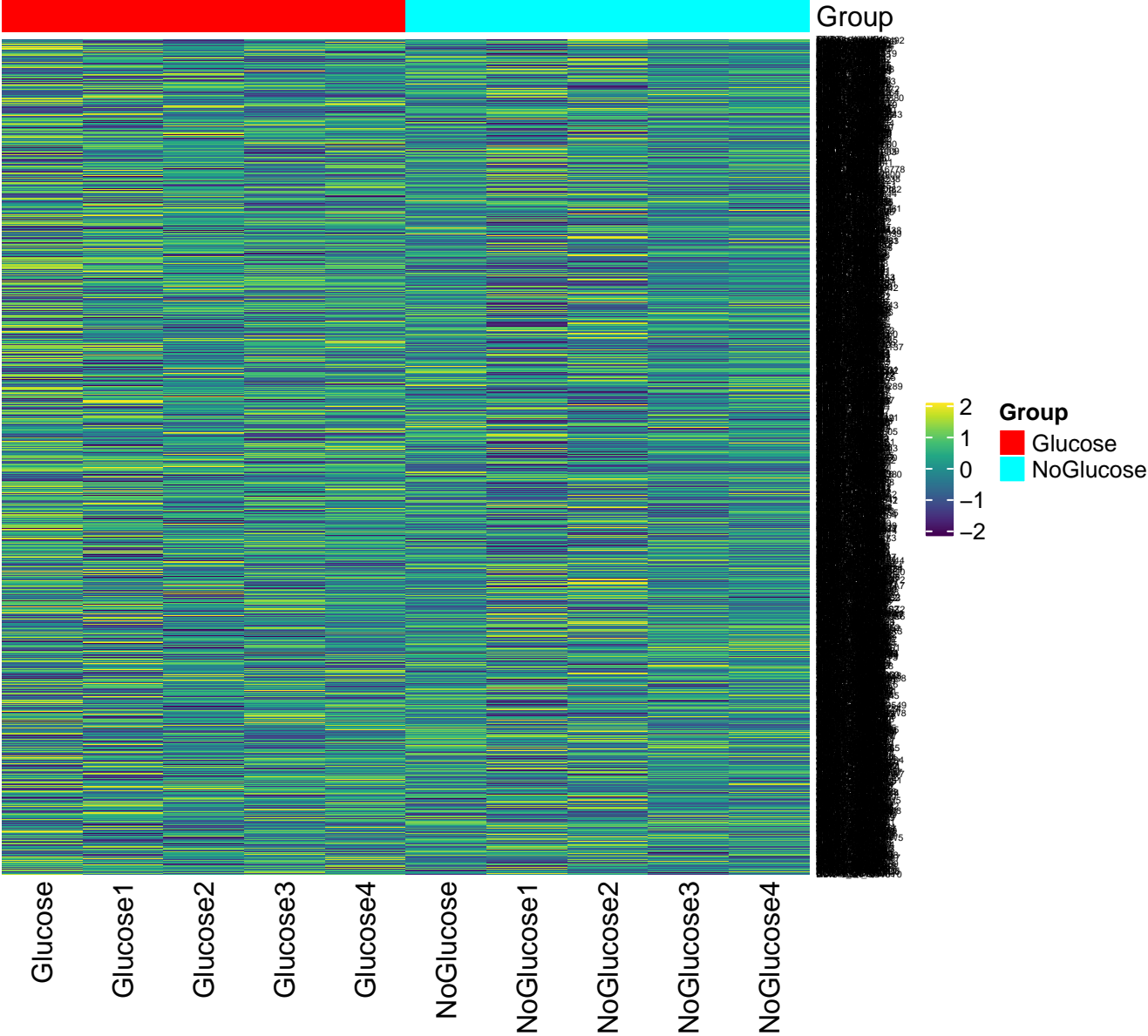
# Proteomics: human2\_gene1\_expanded

Subset, row z score



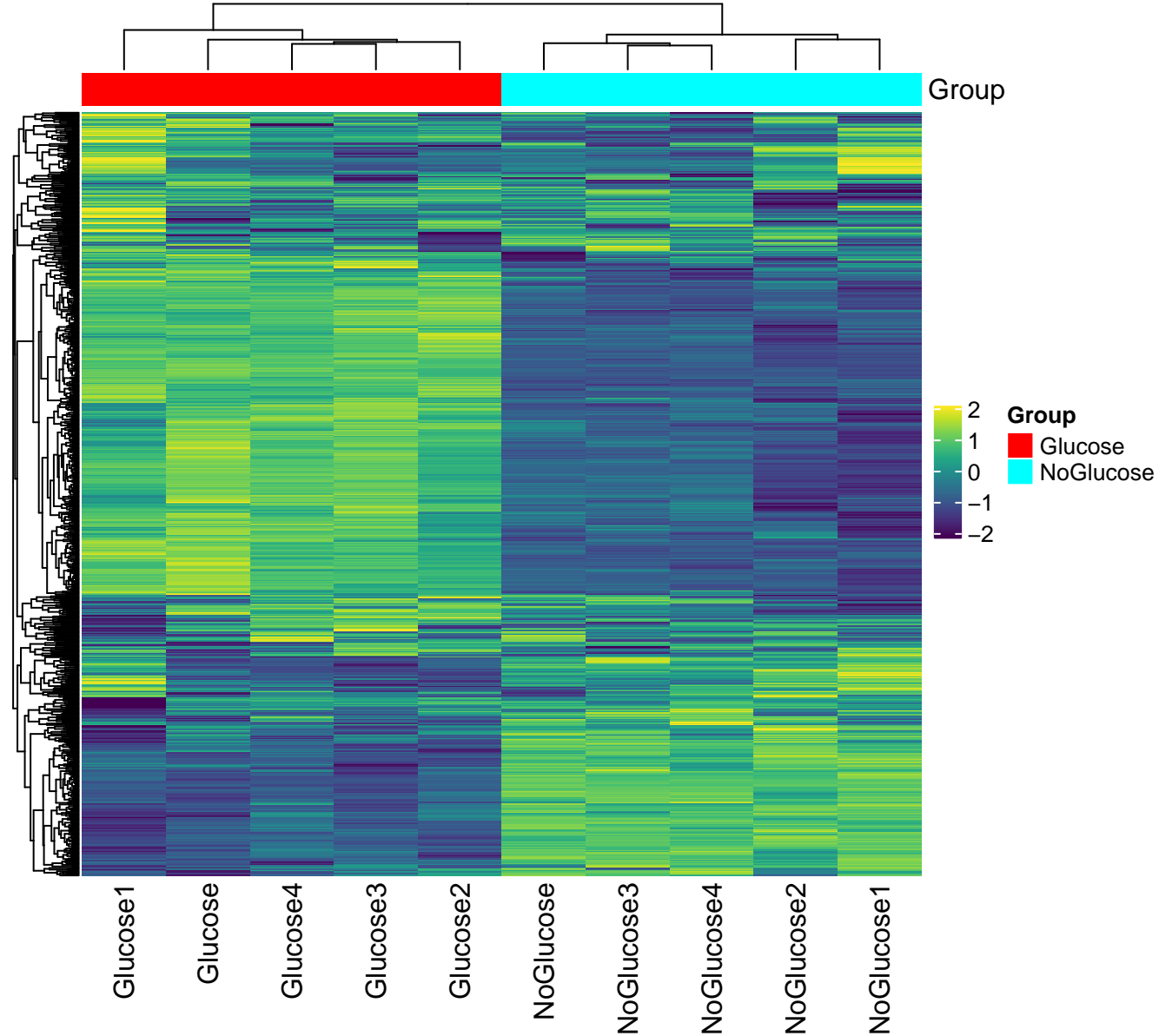
Proteomics: human2\_gene1\_expanded

Subset, row z score

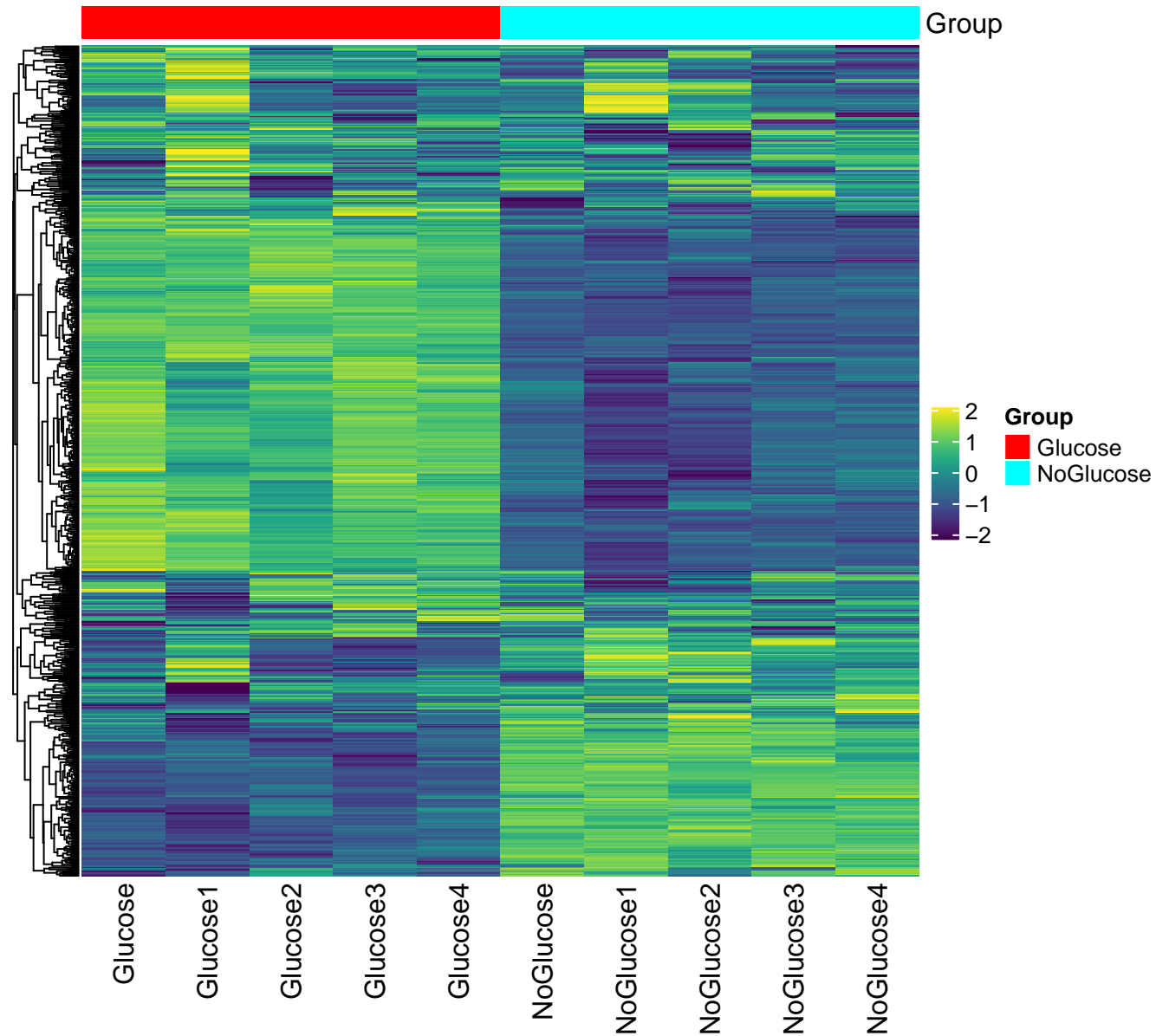


Proteomics:

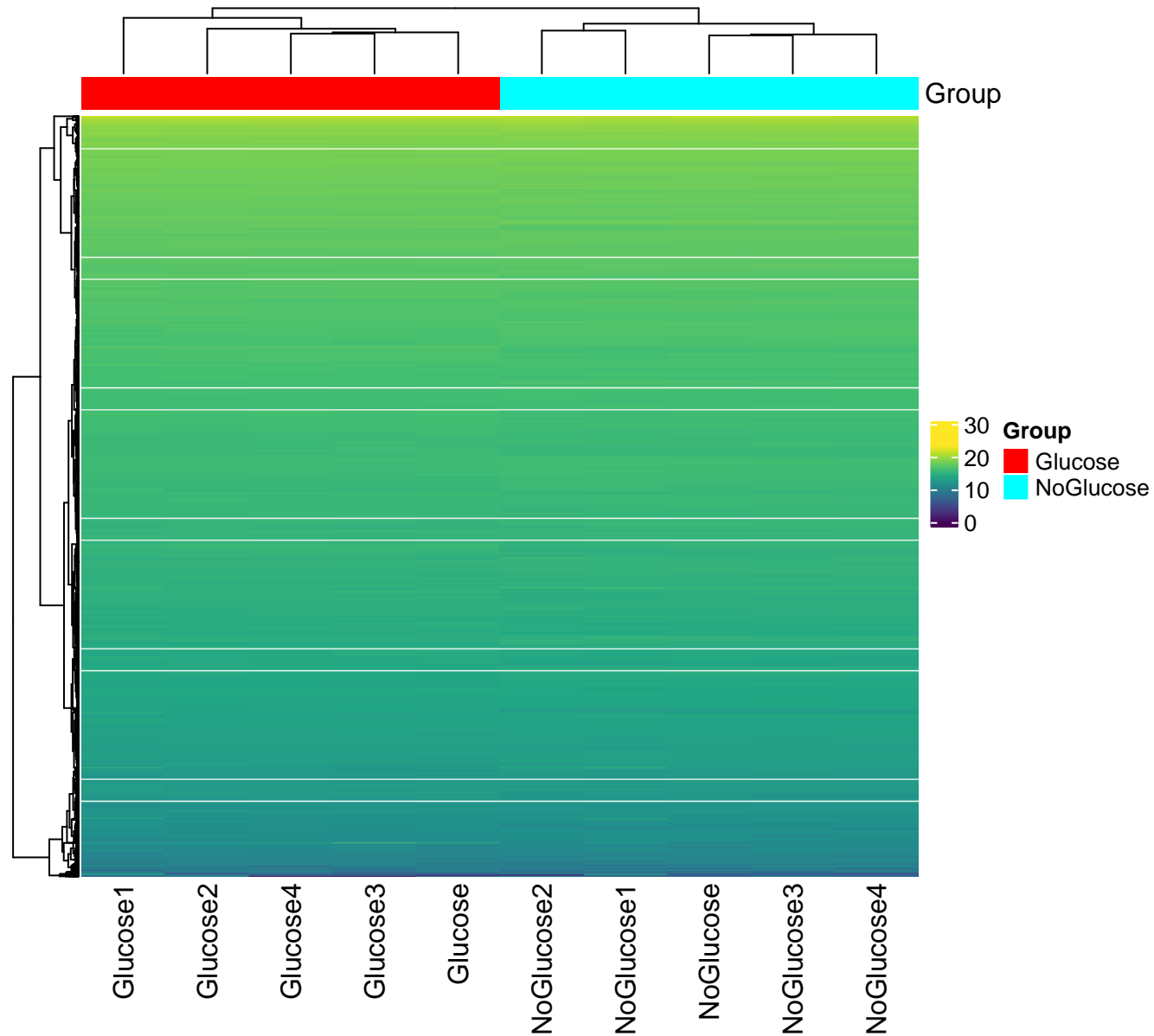
Highest variation, row z score



Proteomics:  
Highest variation, row z score



Proteomics:  
All features, log2 Intensity



Proteomics:  
All features, log2 Intensity

