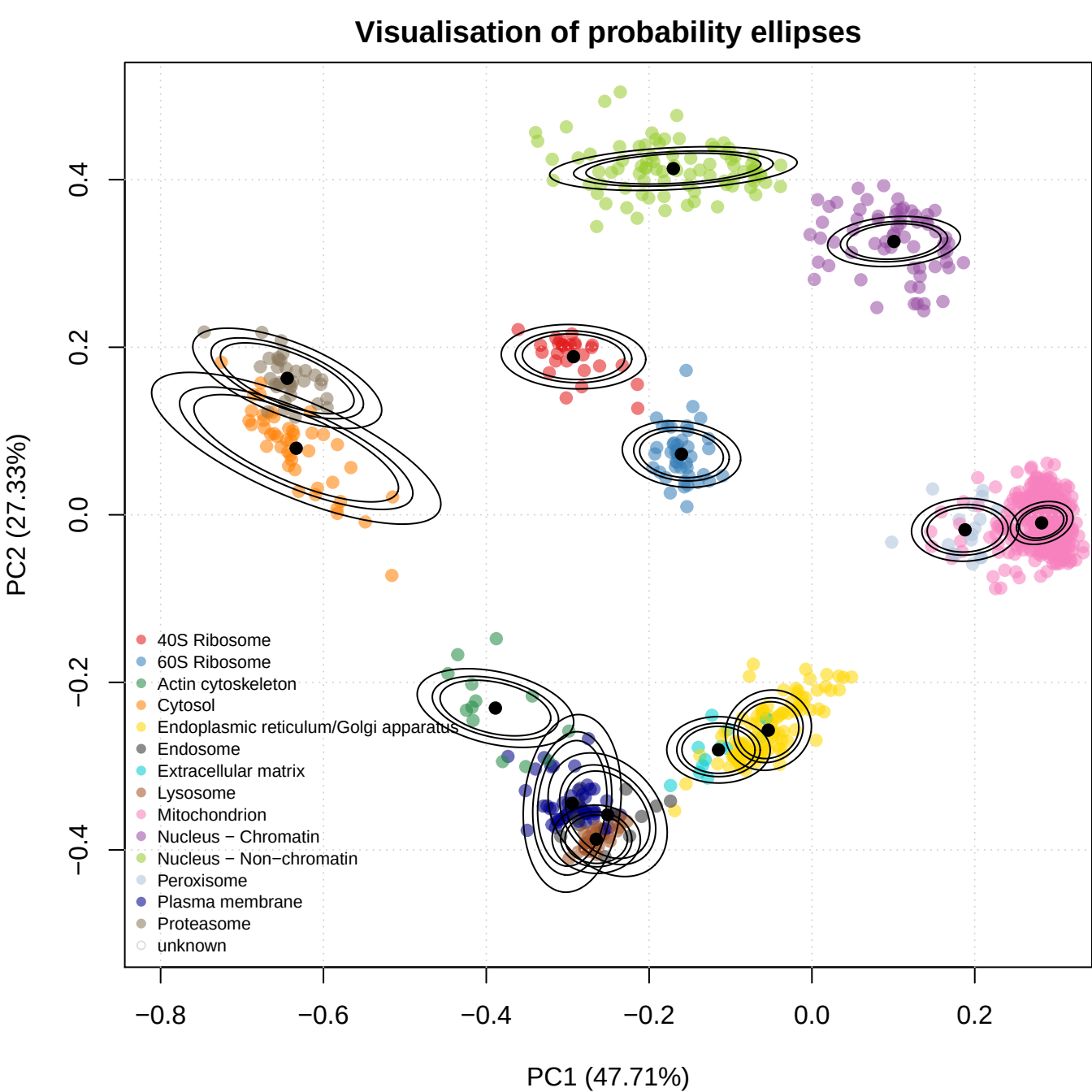
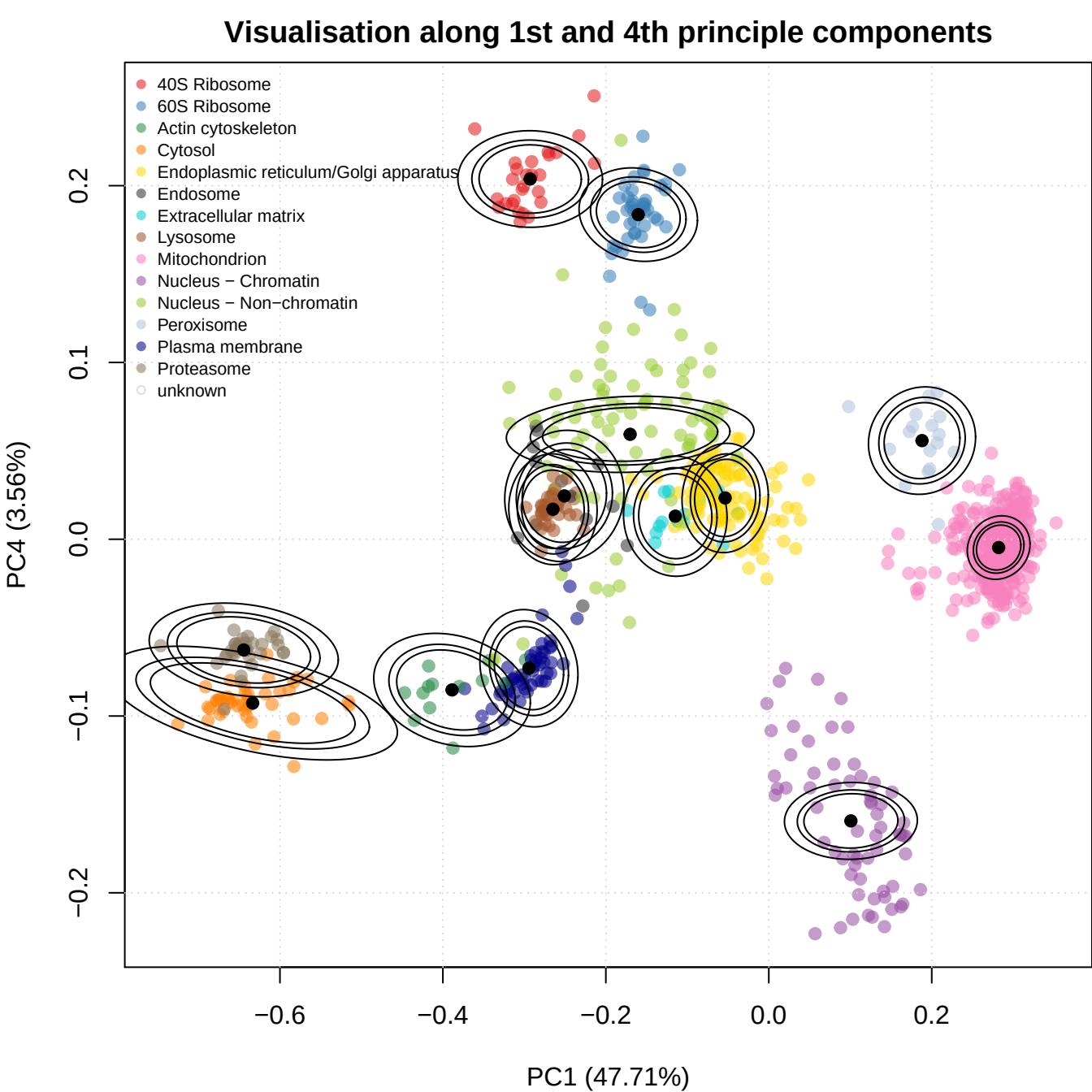
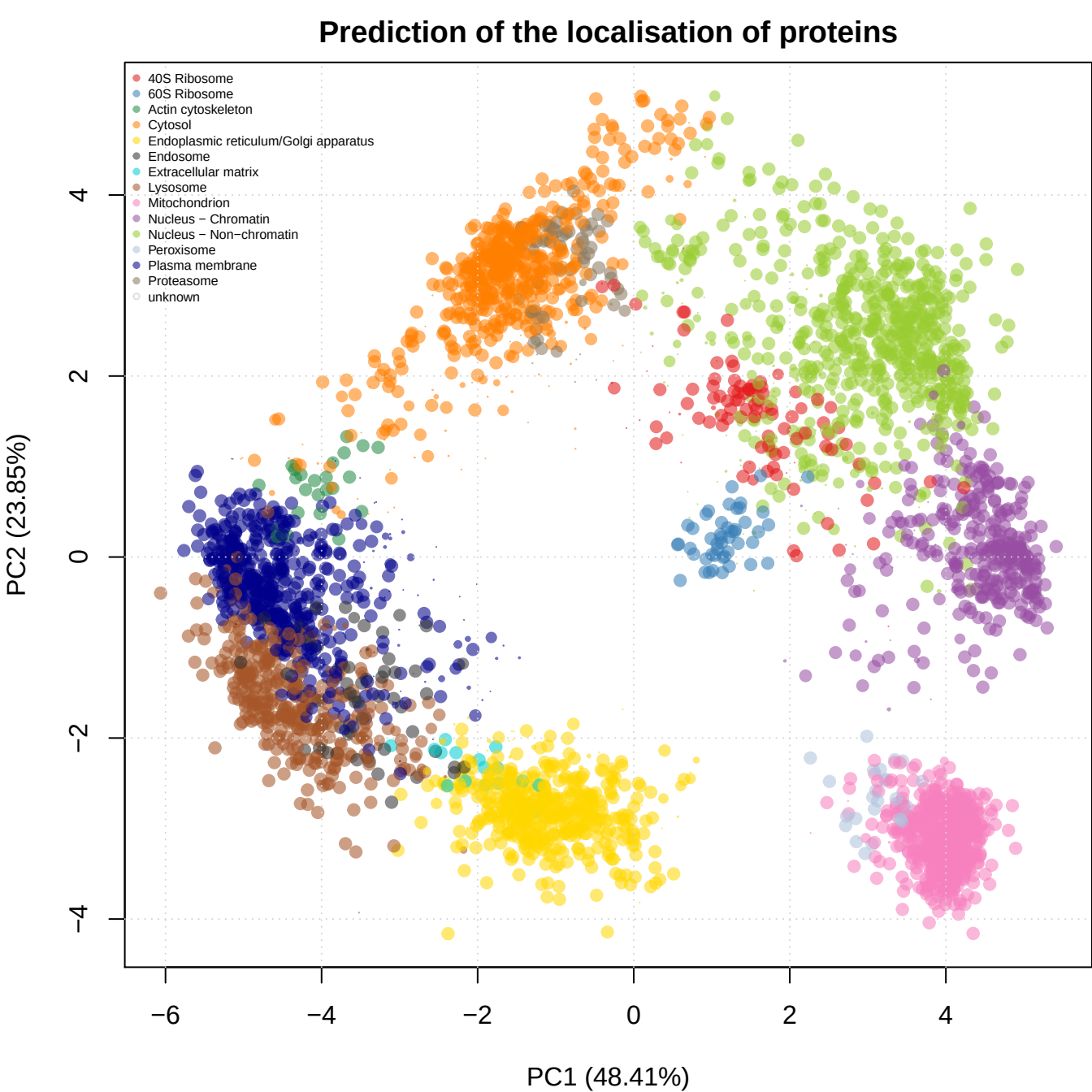
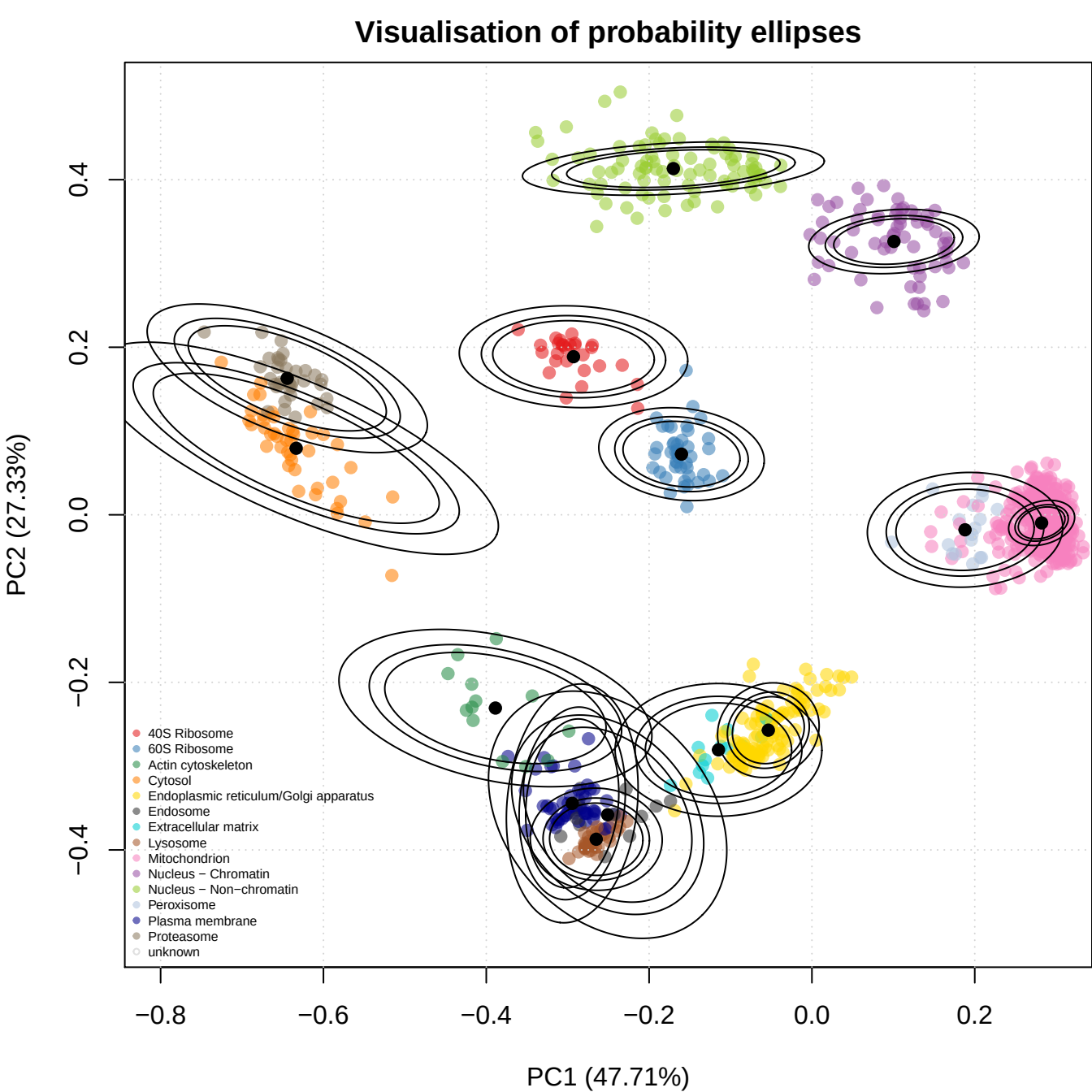
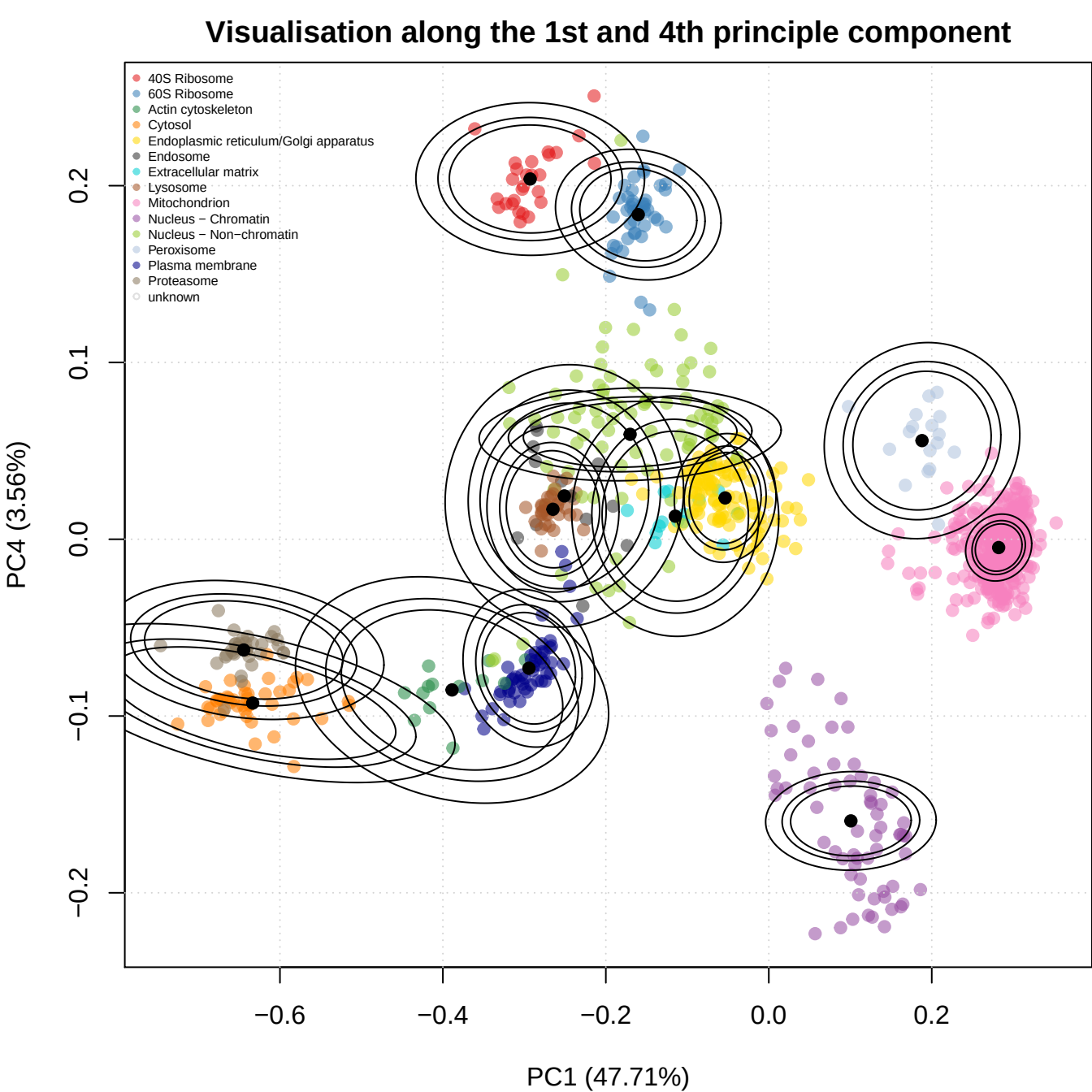
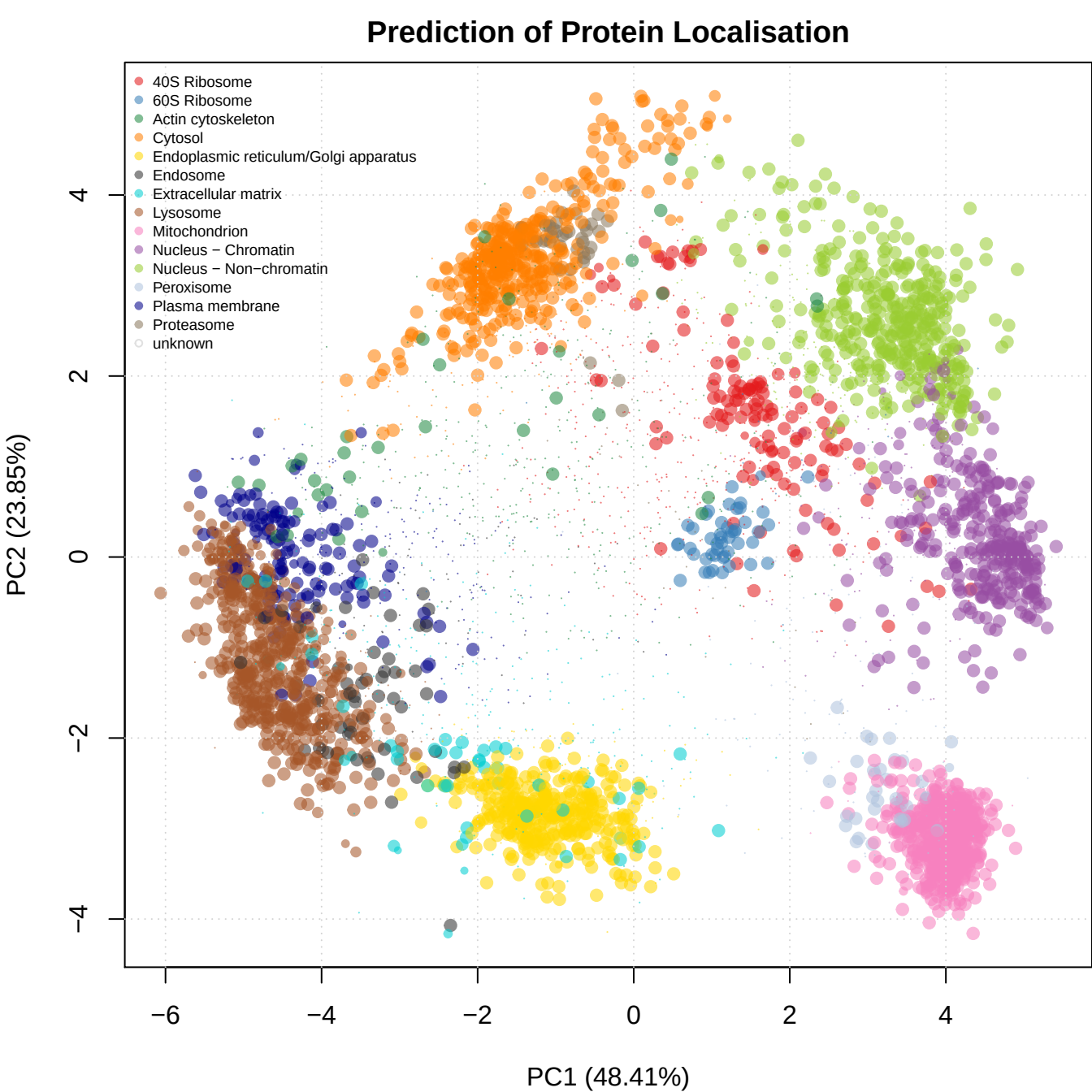

Visualisation of probability ellipses
PC1 (47.71%)
PC2 (27.33%)
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus − Chromatin
Nucleus − Non−chromatin
Peroxisome
Plasma membrane
Proteasome
unknown

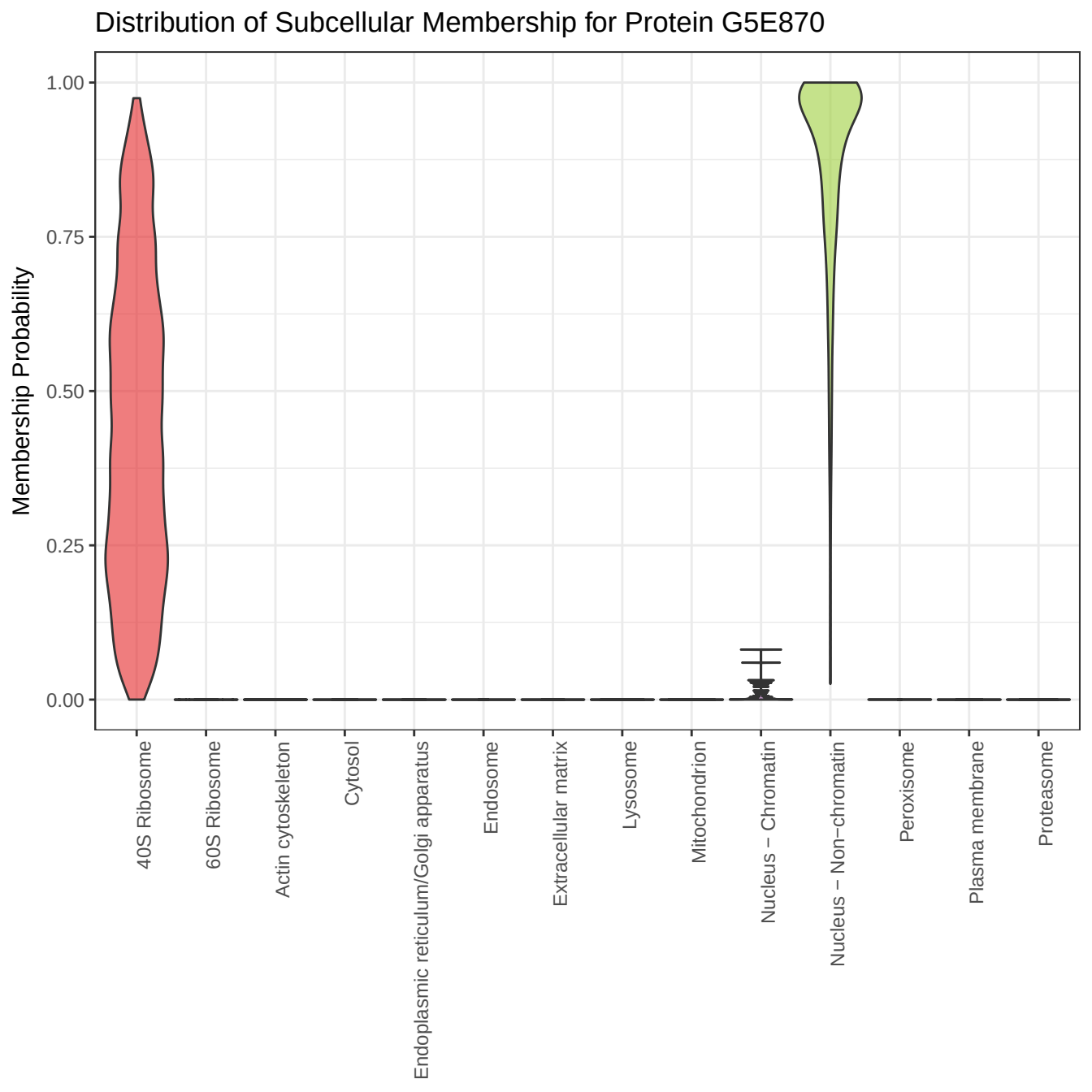

Visualisation along 1st and 4th principle components
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus − Chromatin
Nucleus − Non−chromatin
Peroxisome
Plasma membrane
Proteasome
unknown
PC4 (3.56%)
0.2
0.1
0.0
−0.1
−0.2
−0.6
−0.4
−0.2
0.0
0.2
PC1 (47.71%)

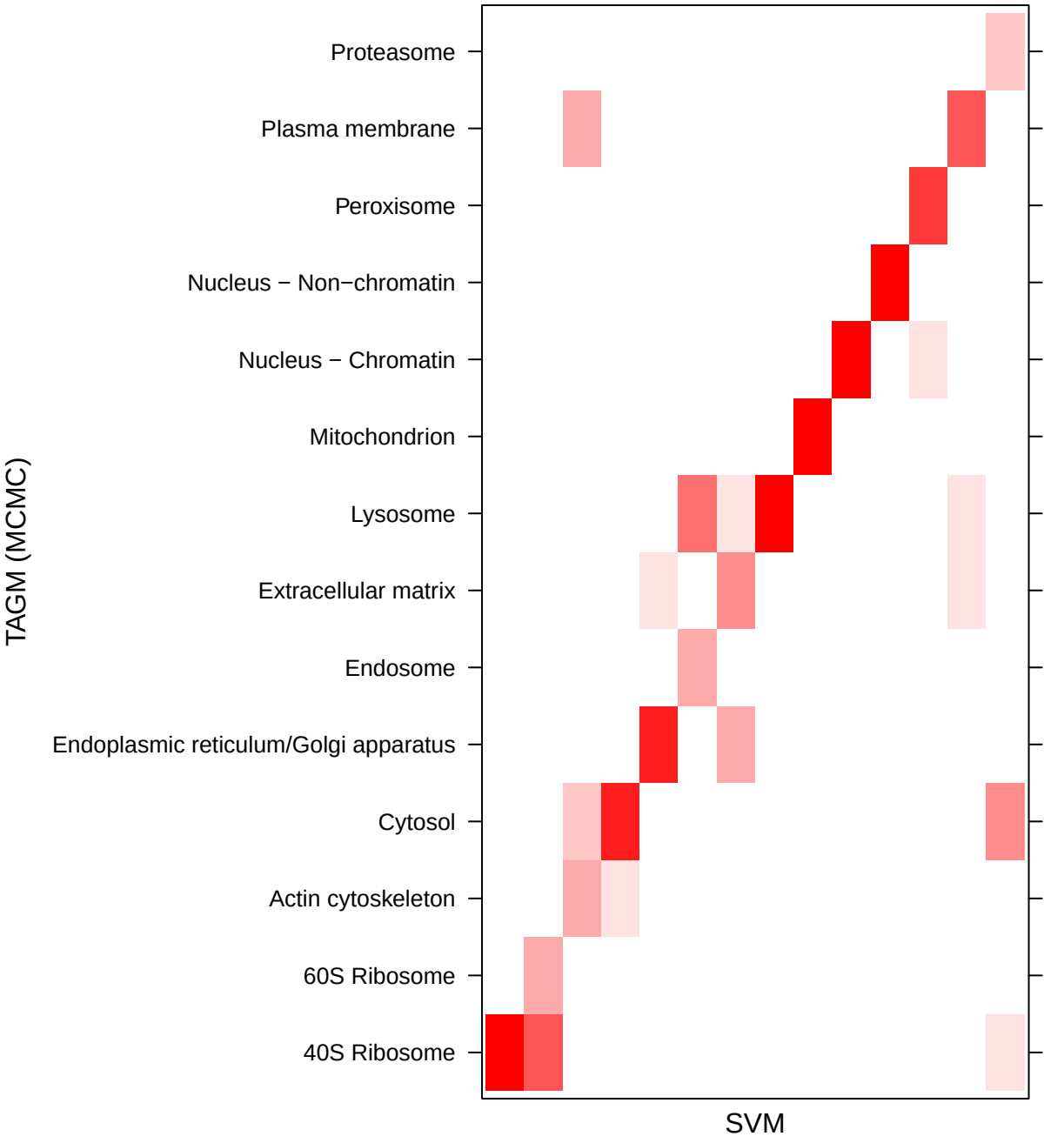

Prediction of the localisation of proteins
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus − Chromatin
Nucleus − Non−chromatin
Peroxisome
Plasma membrane
Proteasome
unknown
PC2 (23.85%)
PC1 (48.41%)
−6
−4
−2
0
2
4
−4
−2
0
2
4

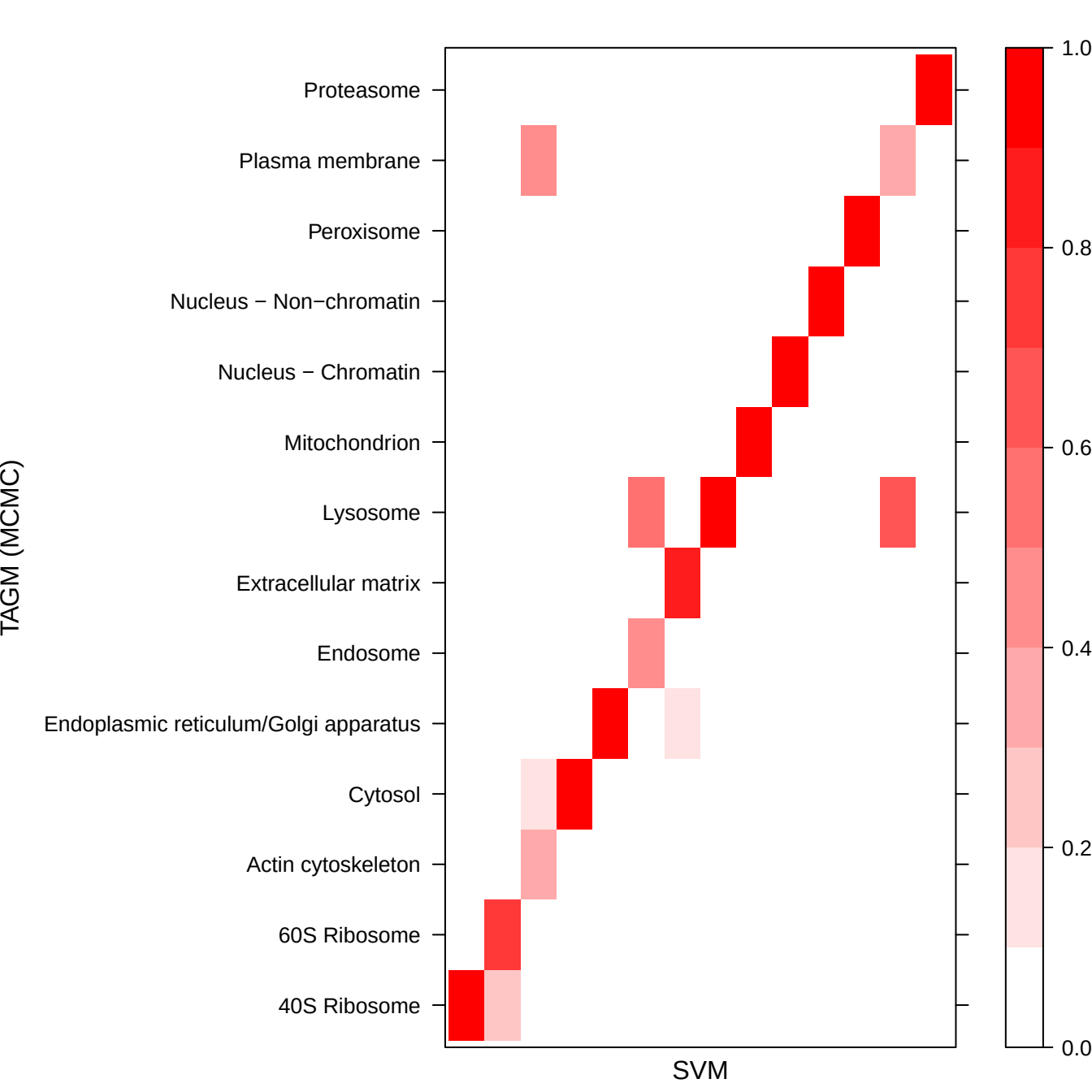

Visualisation of probability ellipses
PC2 (27.33%)
PC1 (47.71%)
0.4
0.2
0.0
−0.2
−0.4
−0.8
−0.6
−0.4
−0.2
0.0
0.2
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus − Chromatin
Nucleus − Non−chromatin
Peroxisome
Plasma membrane
Proteasome
unknown

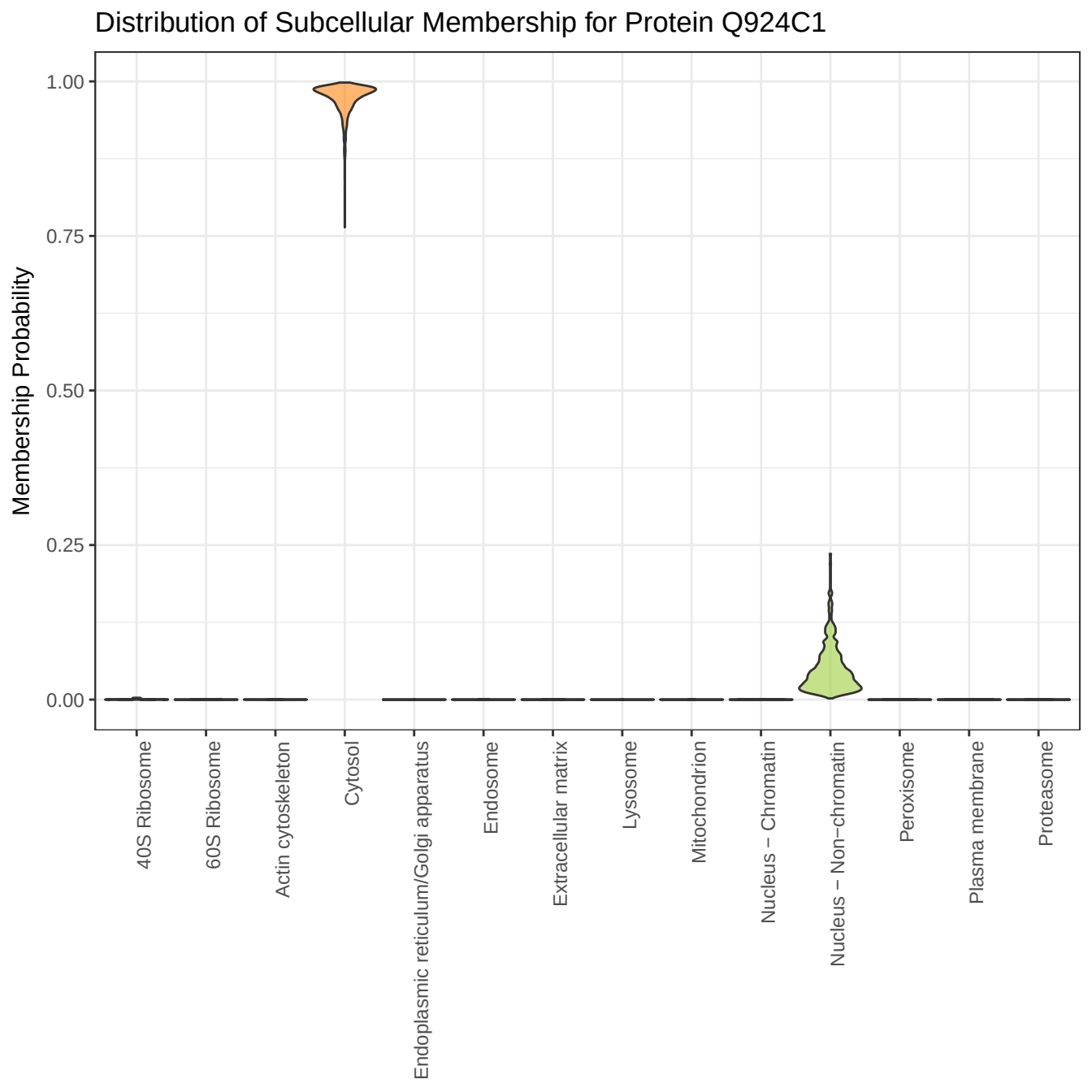

Visualisation along the 1st and 4th principle component
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus − Chromatin
Nucleus − Non−chromatin
Peroxisome
Plasma membrane
Proteasome
unknown
PC4 (3.56%)
0.2
0.1
0.0
−0.1
−0.2
−0.6
−0.4
−0.2
0.0
0.2
PC1 (47.71%)


Prediction of Protein Localisation
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus − Chromatin
Nucleus − Non−chromatin
Peroxisome
Plasma membrane
Proteasome
unknown
PC2 (23.85%)
PC1 (48.41%)
−6
−4
−2
0
2
4
−4
−2
0
2
4

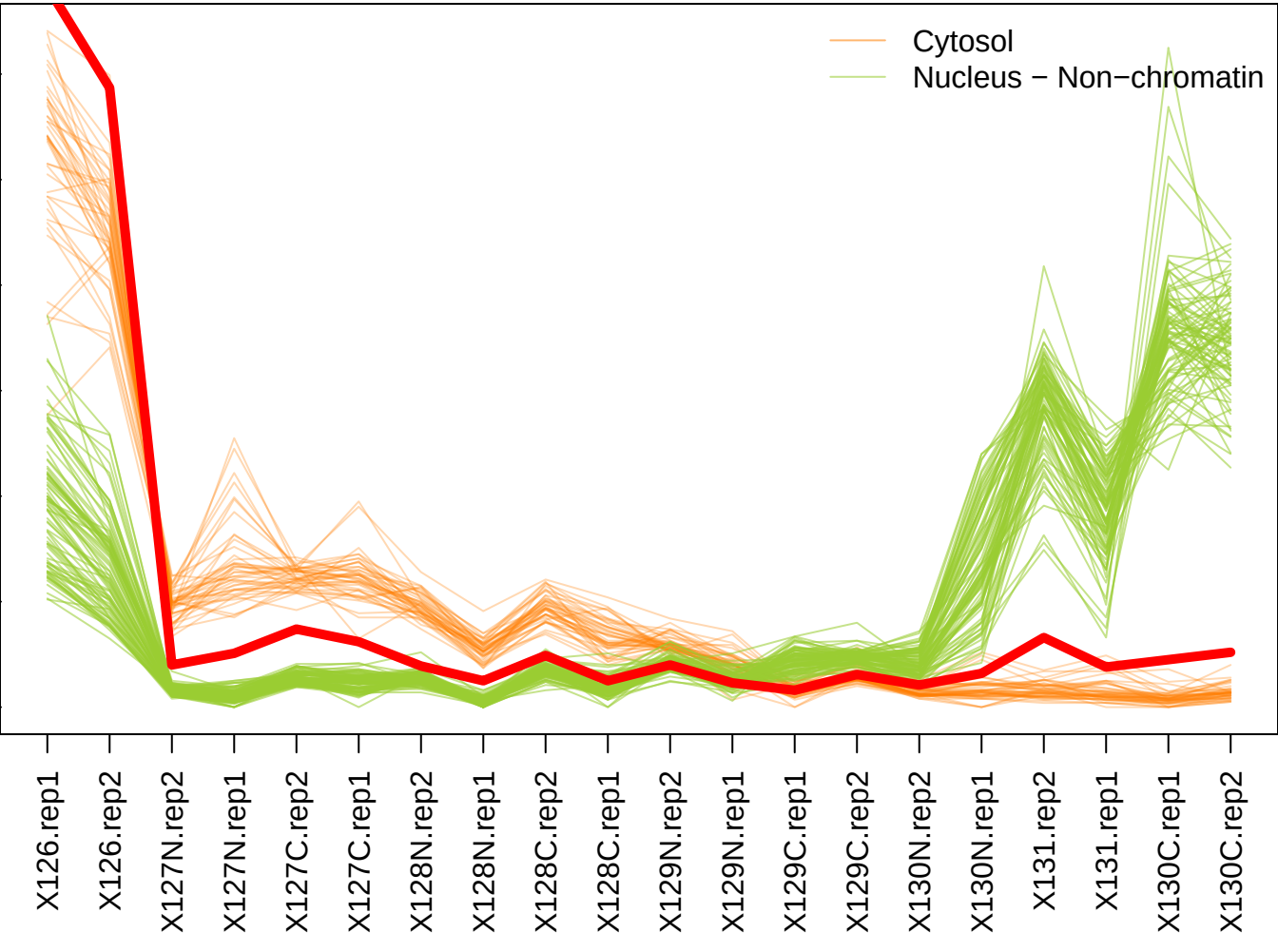

Distribution of Subcellular Membership for Protein G5E870
Membership Probability
1.00
0.75
0.50
0.25
0.00
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus – Chromatin
Nucleus – Non−chromatin
Peroxisome
Plasma membrane
Proteasome

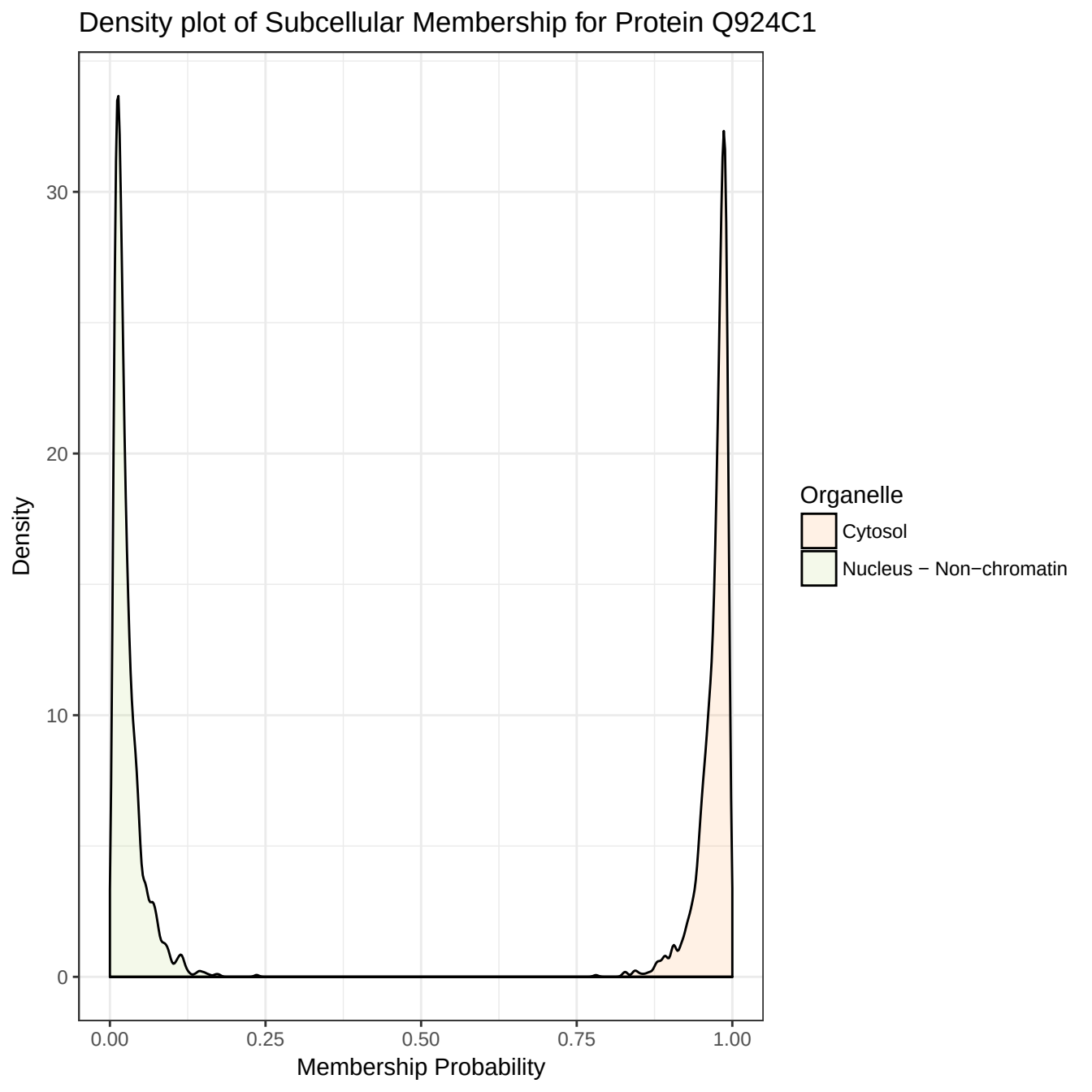

Proteasome
Plasma membrane
Peroxisome
Nucleus − Non−chromatin
Nucleus − Chromatin
Mitochondrion
Lysosome
Extracellular matrix
Endosome
Endoplasmic reticulum/Golgi apparatus
Cytosol
Actin cytoskeleton
60S Ribosome
40S Ribosome
TAGM (MCMC)
SVM

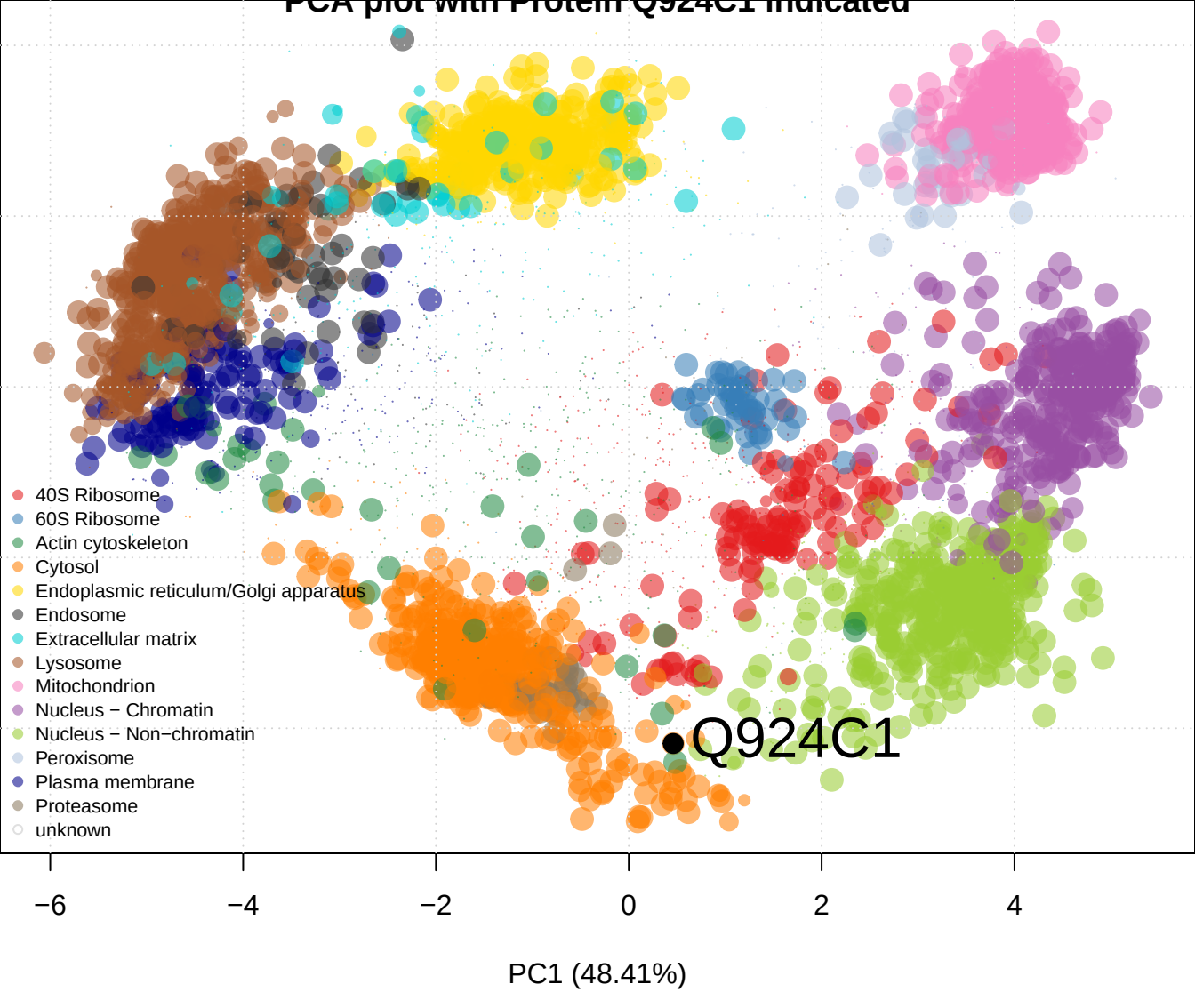

Proteasome
Plasma membrane
Peroxisome
Nucleus − Non−chromatin
Nucleus − Chromatin
Mitochondrion
Lysosome
Extracellular matrix
Endosome
Endoplasmic reticulum/Golgi apparatus
Cytosol
Actin cytoskeleton
60S Ribosome
40S Ribosome
TAGM (MCMC)
SVM
1.0
0.8
0.6
0.4
0.2
0.0

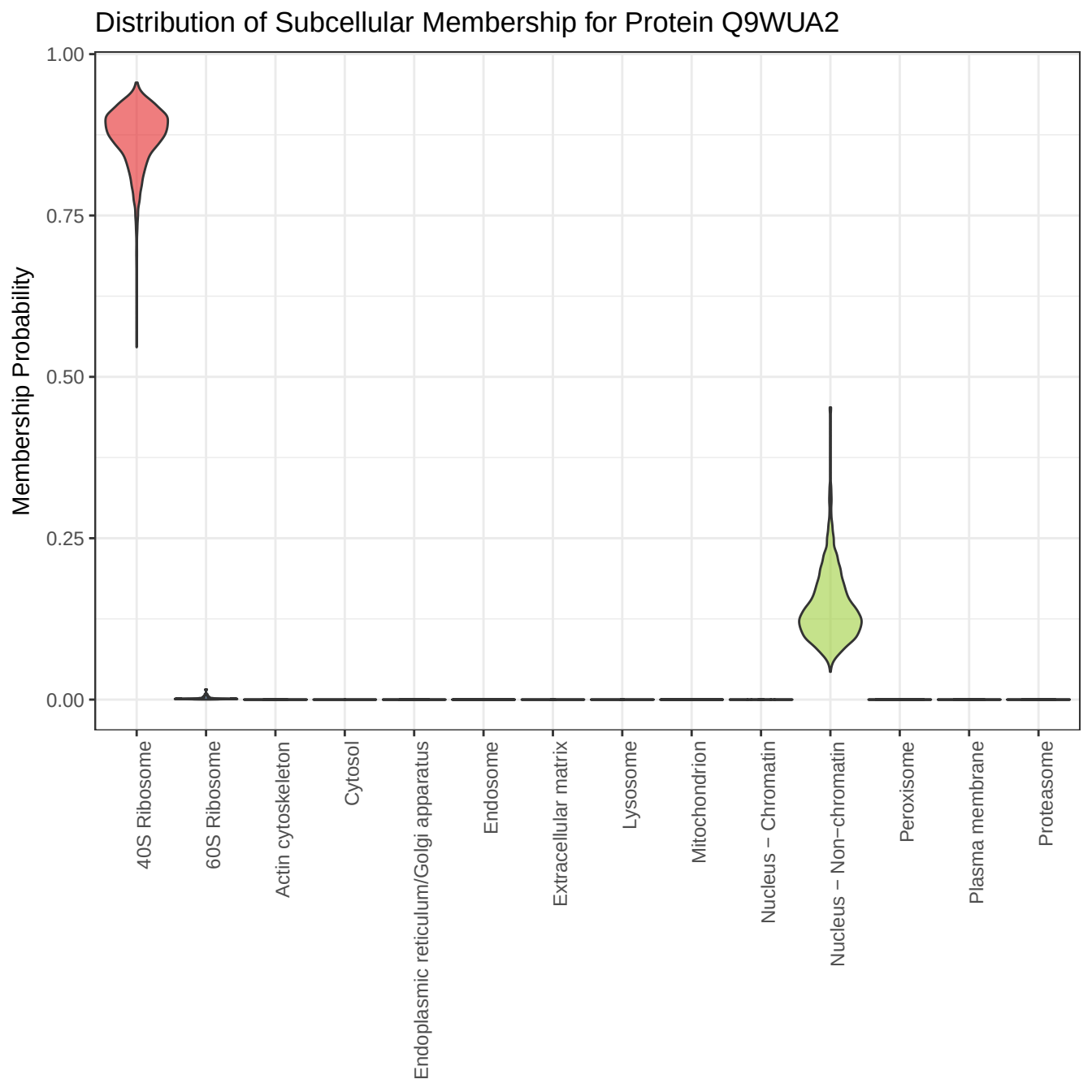

Distribution of Subcellular Membership for Protein Q924C1
Membership Probability
1.00
0.75
0.50
0.25
0.00
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus – Chromatin
Nucleus – Non−chromatin
Peroxisome
Plasma membrane
Proteasome

Profile of Protein Q924C1 with marker distributions

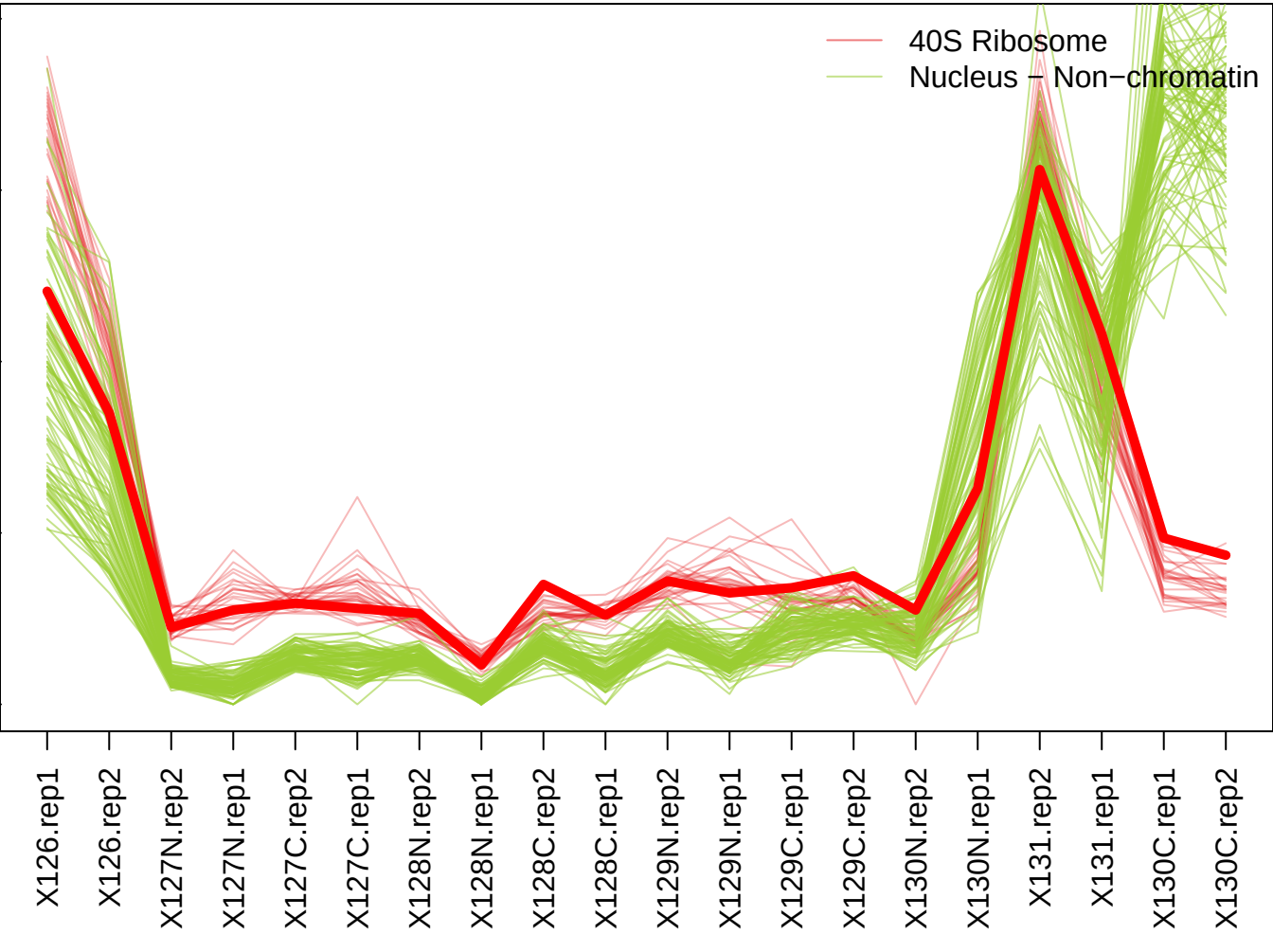


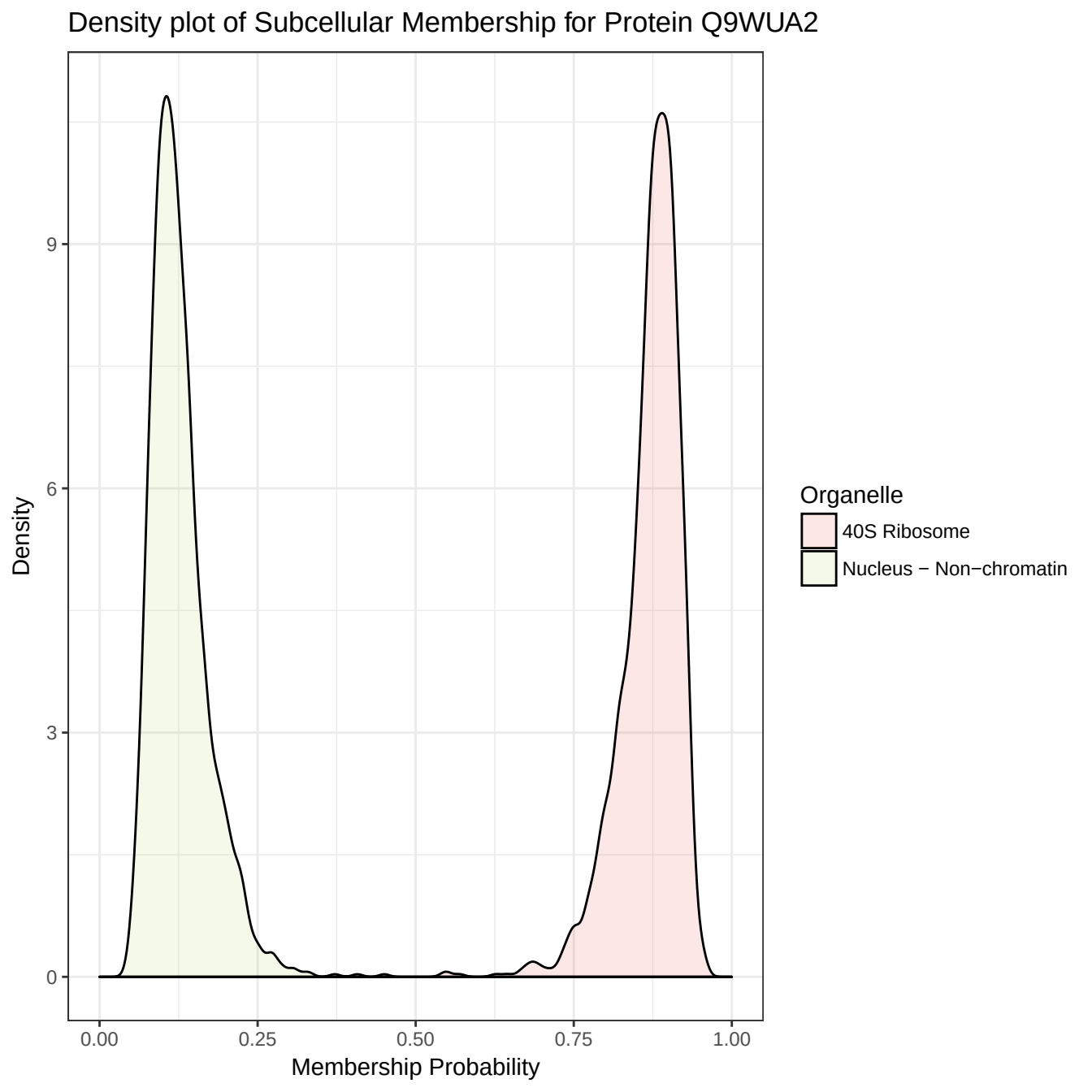

Density plot of Subcellular Membership for Protein Q924C1
Density
30
20
10
0
0.00
0.25
0.50
0.75
1.00
Membership Probability
Organelle
Cytosol
Nucleus − Non−chromatin

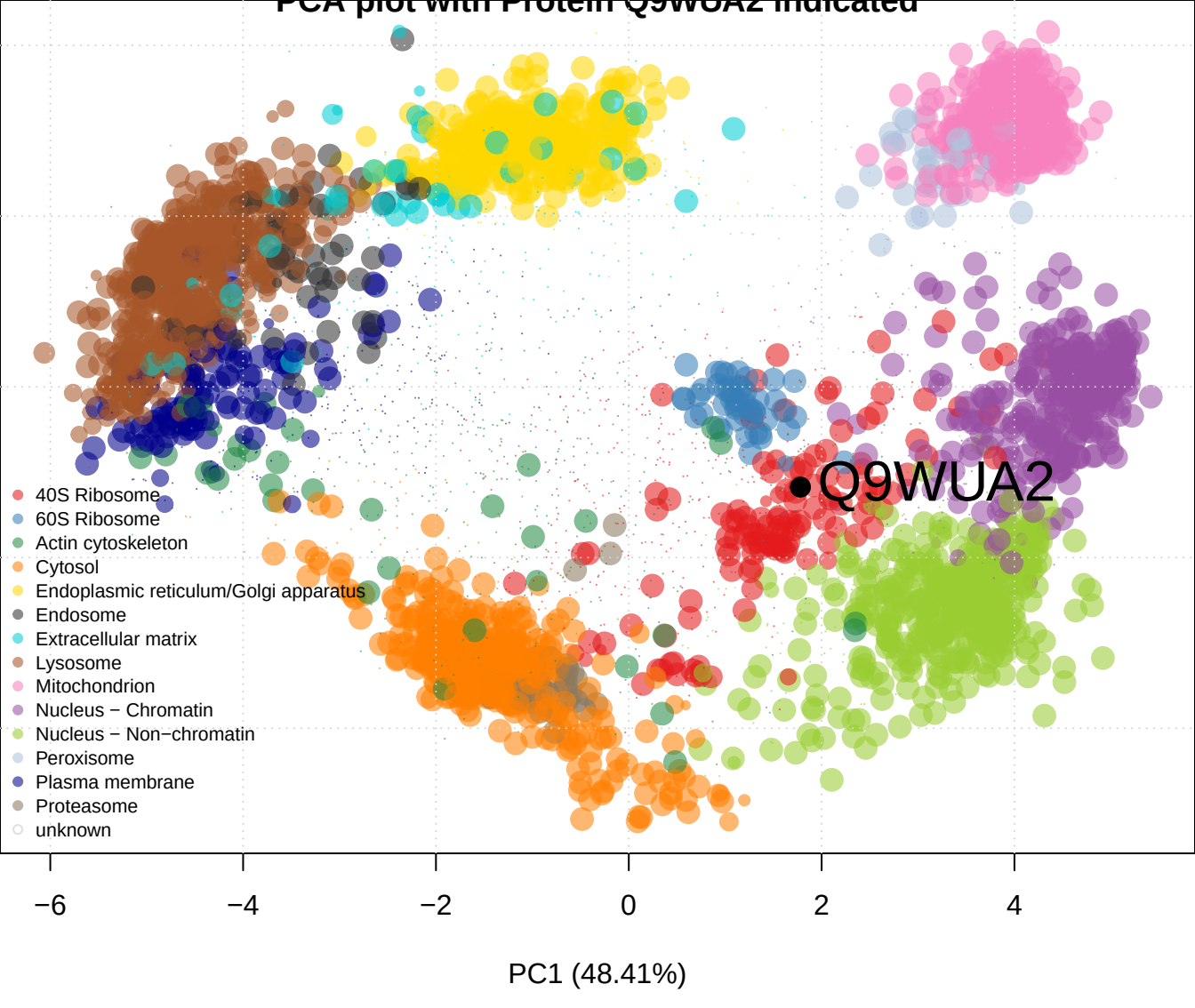

PCA plot with Protein Q924C1 indicated
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus − Chromatin
Nucleus − Non−chromatin
Peroxisome
Plasma membrane
Proteasome
unknown
Q924C1
−6
−4
−2
0
2
4
PC1 (48.41%)

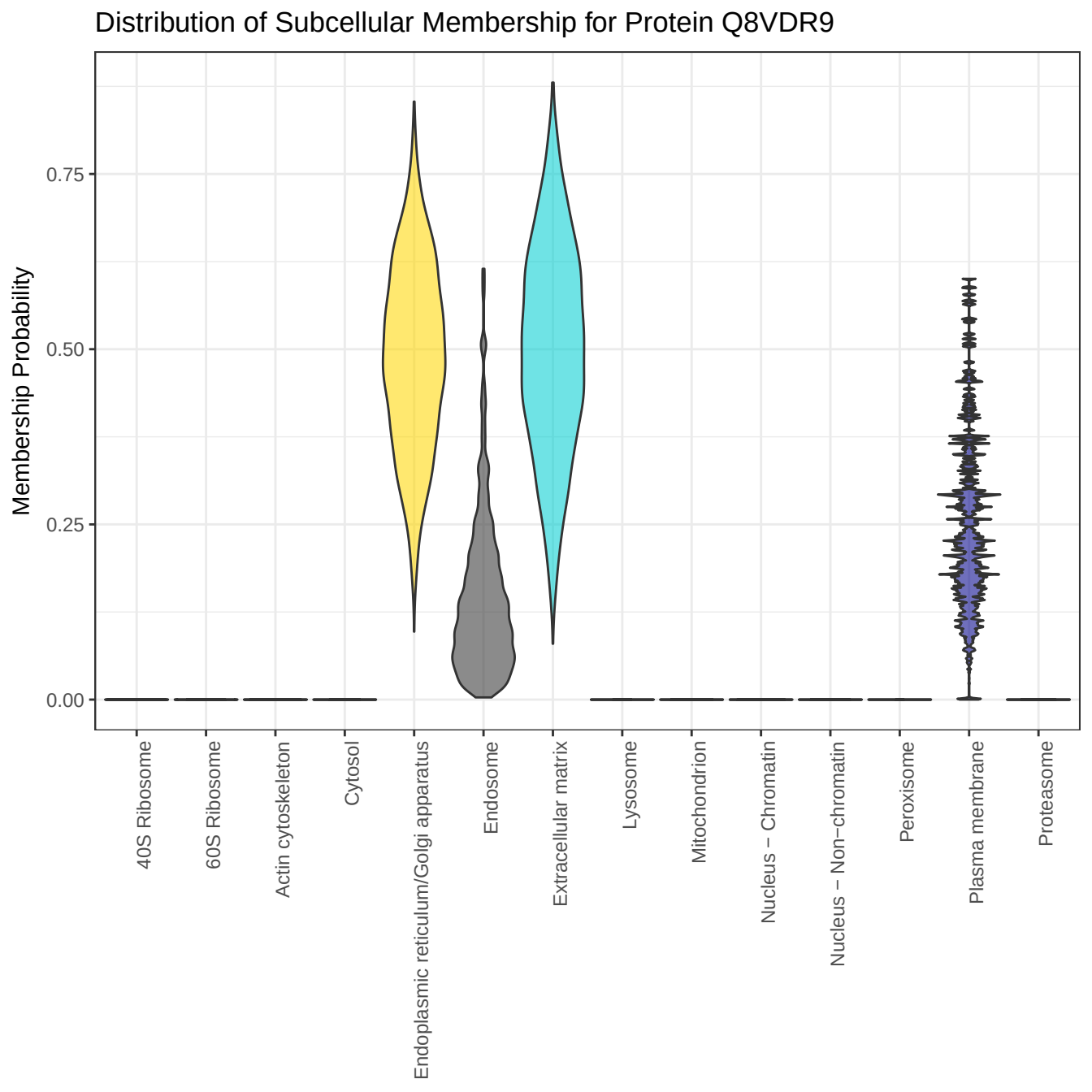

Distribution of Subcellular Membership for Protein Q9WUA2
Membership Probability
1.00
0.75
0.50
0.25
0.00
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus – Chromatin
Nucleus – Non−chromatin
Peroxisome
Plasma membrane
Proteasome

Profile of Protein Q9WUA2 with marker distributions

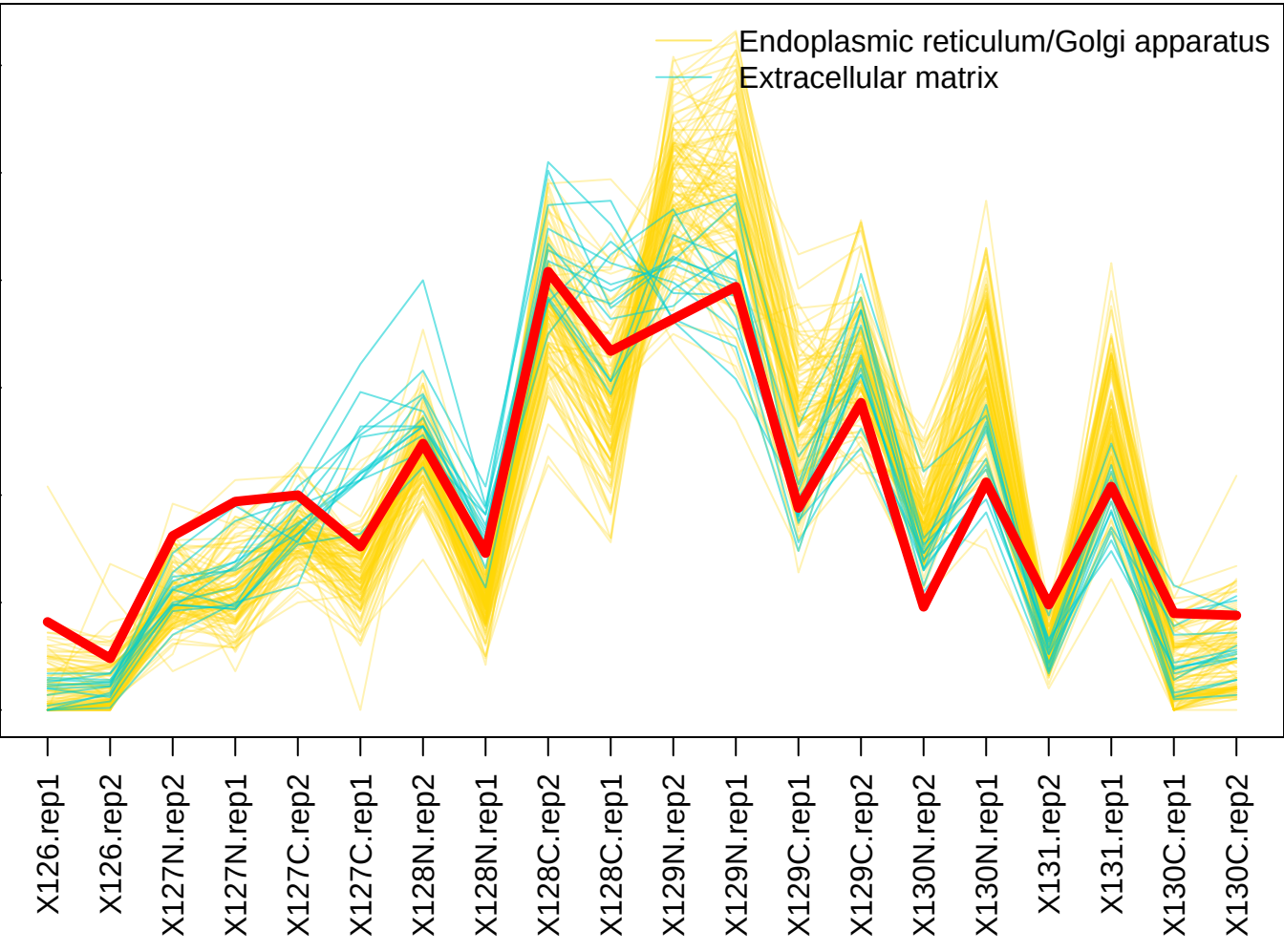


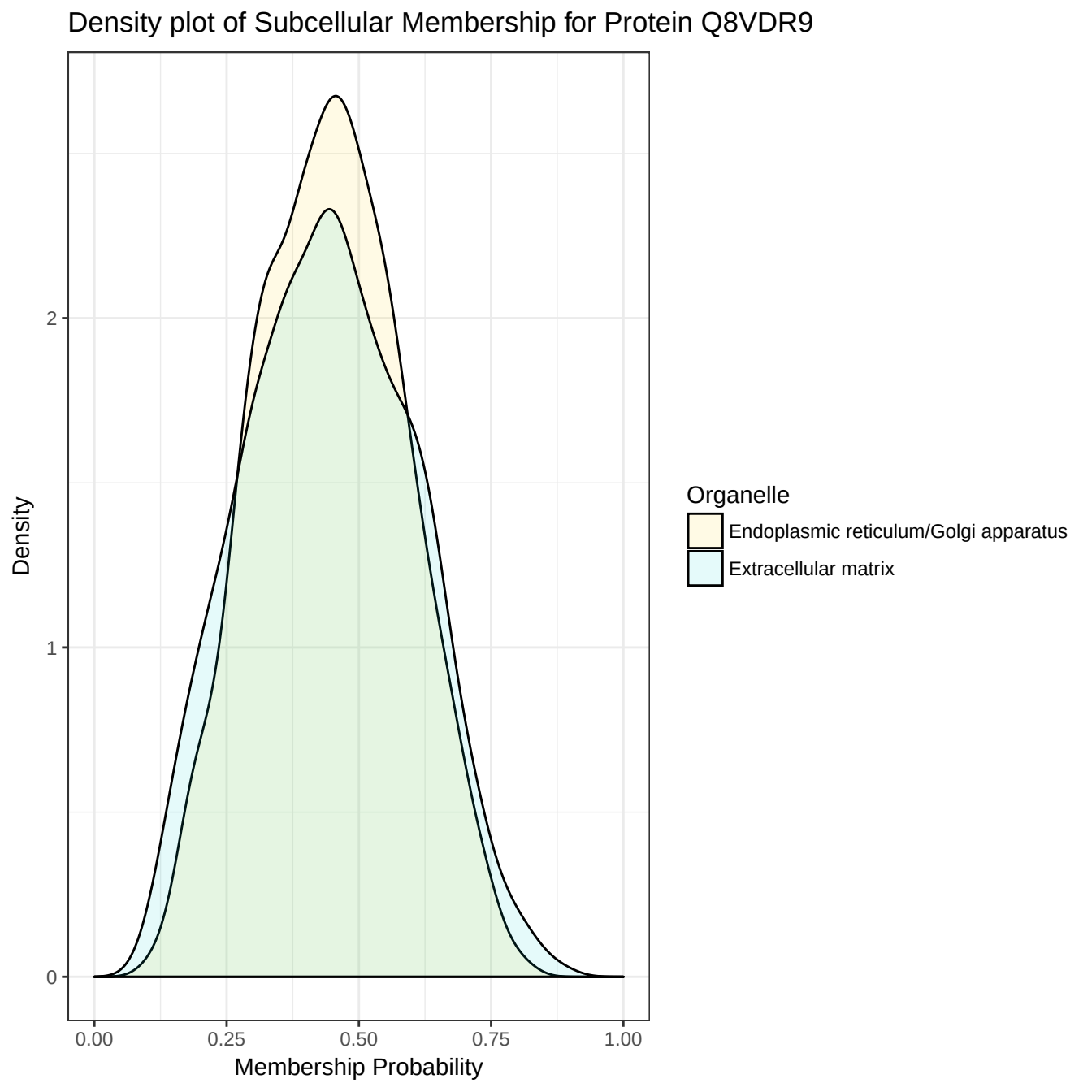

Density plot of Subcellular Membership for Protein Q9WUA2
Density
9
6
3
0
0.00
0.25
0.50
0.75
1.00
Membership Probability
Organelle
40S Ribosome
Nucleus − Non−chromatin

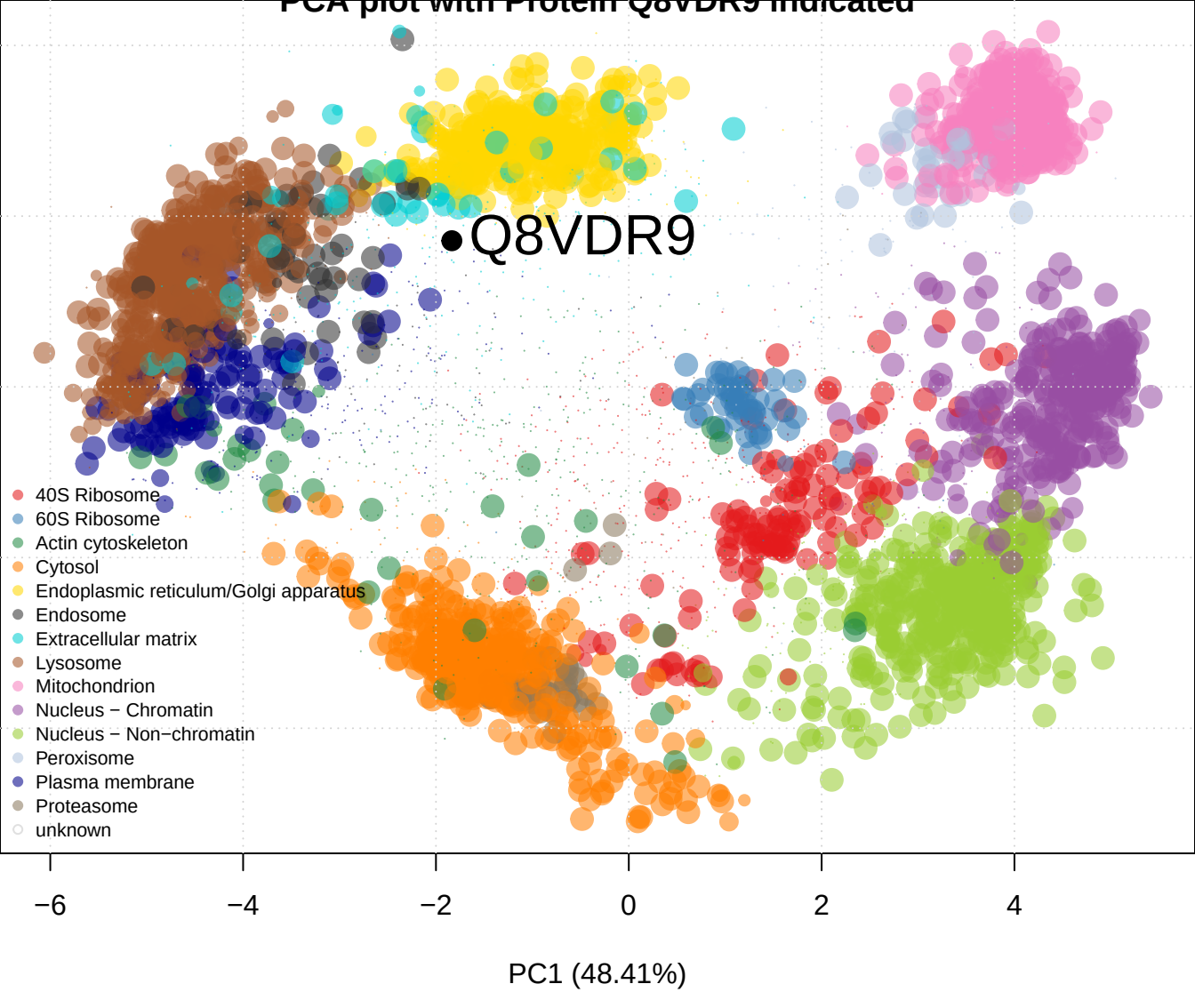

PCA plot with Protein Q9WUA2 indicated
Q9WUA2
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus − Chromatin
Nucleus − Non−chromatin
Peroxisome
Plasma membrane
Proteasome
unknown
−6
−4
−2
0
2
4
PC1 (48.41%)

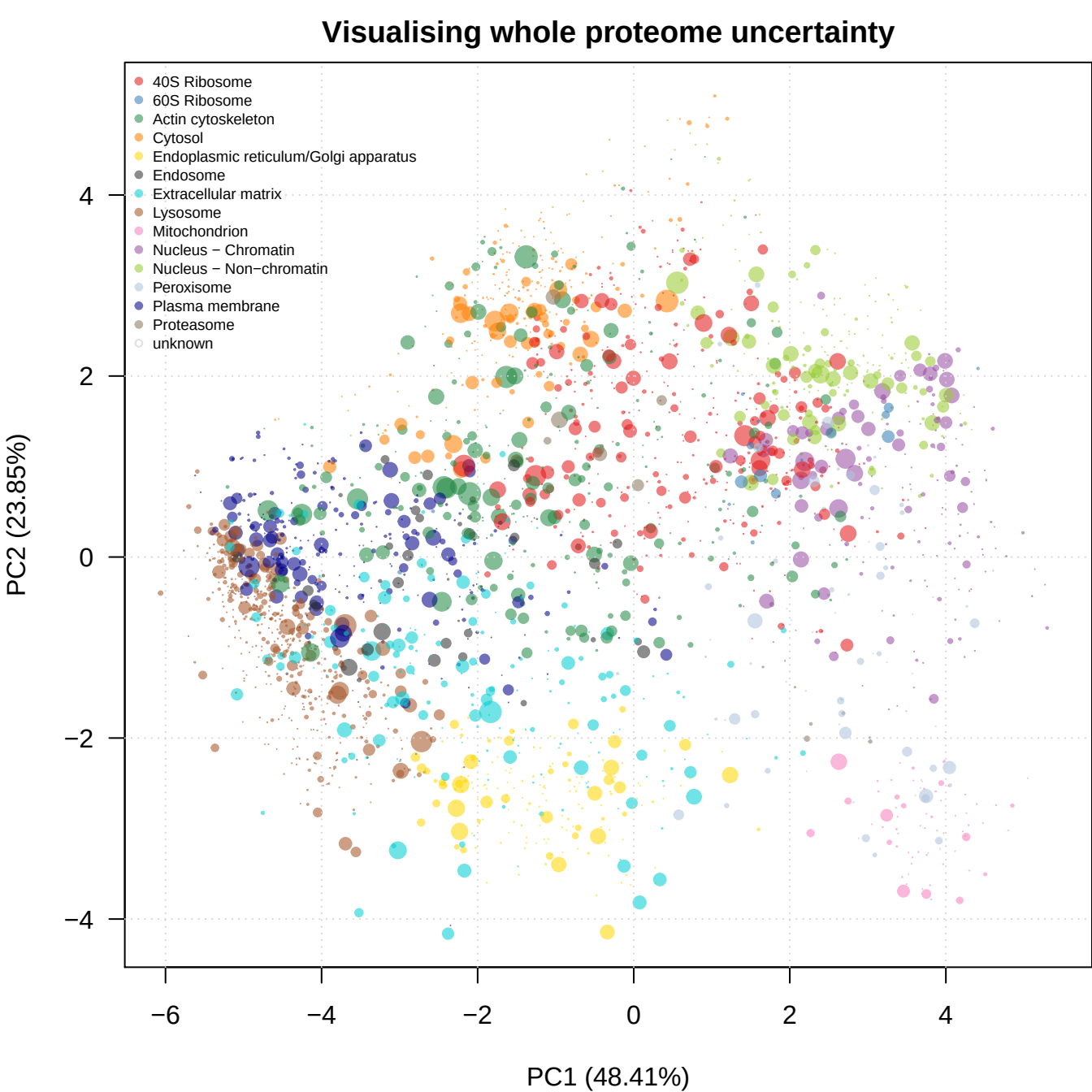

Distribution of Subcellular Membership for Protein Q8VDR9
Membership Probability
0.00
0.25
0.50
0.75
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus – Chromatin
Nucleus – Non−chromatin
Peroxisome
Plasma membrane
Proteasome

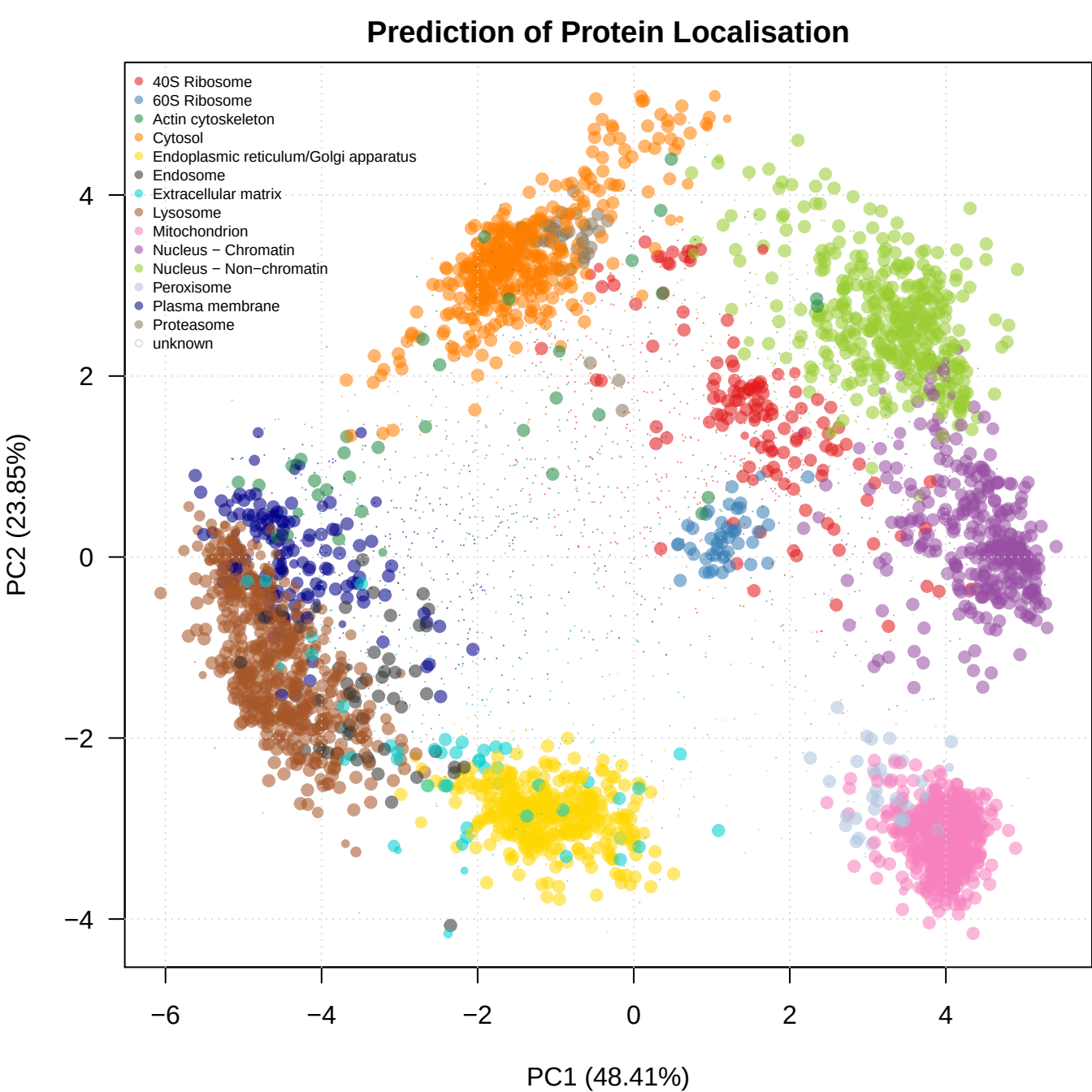
Profile of Protein Q8VDR9 with marker distributions

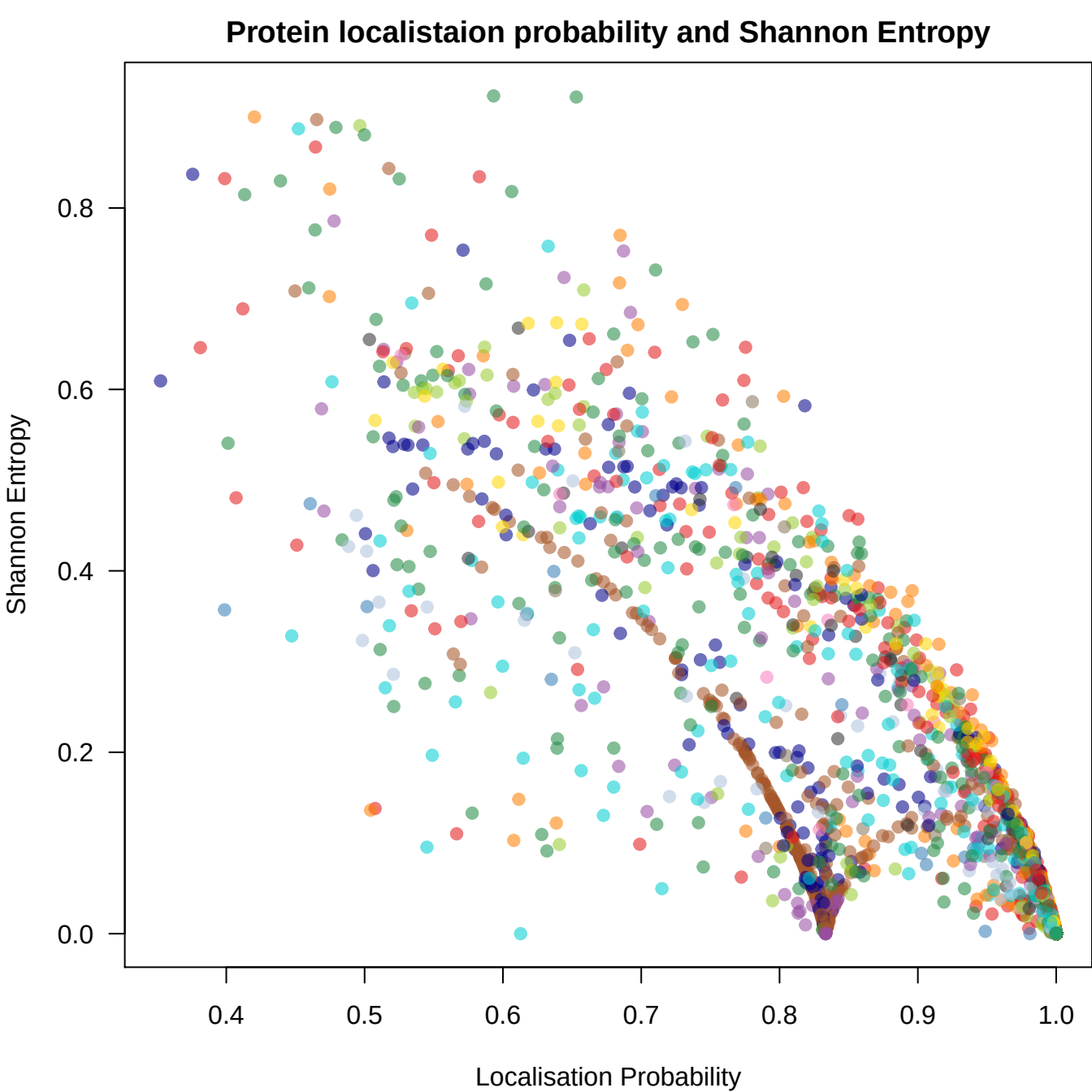


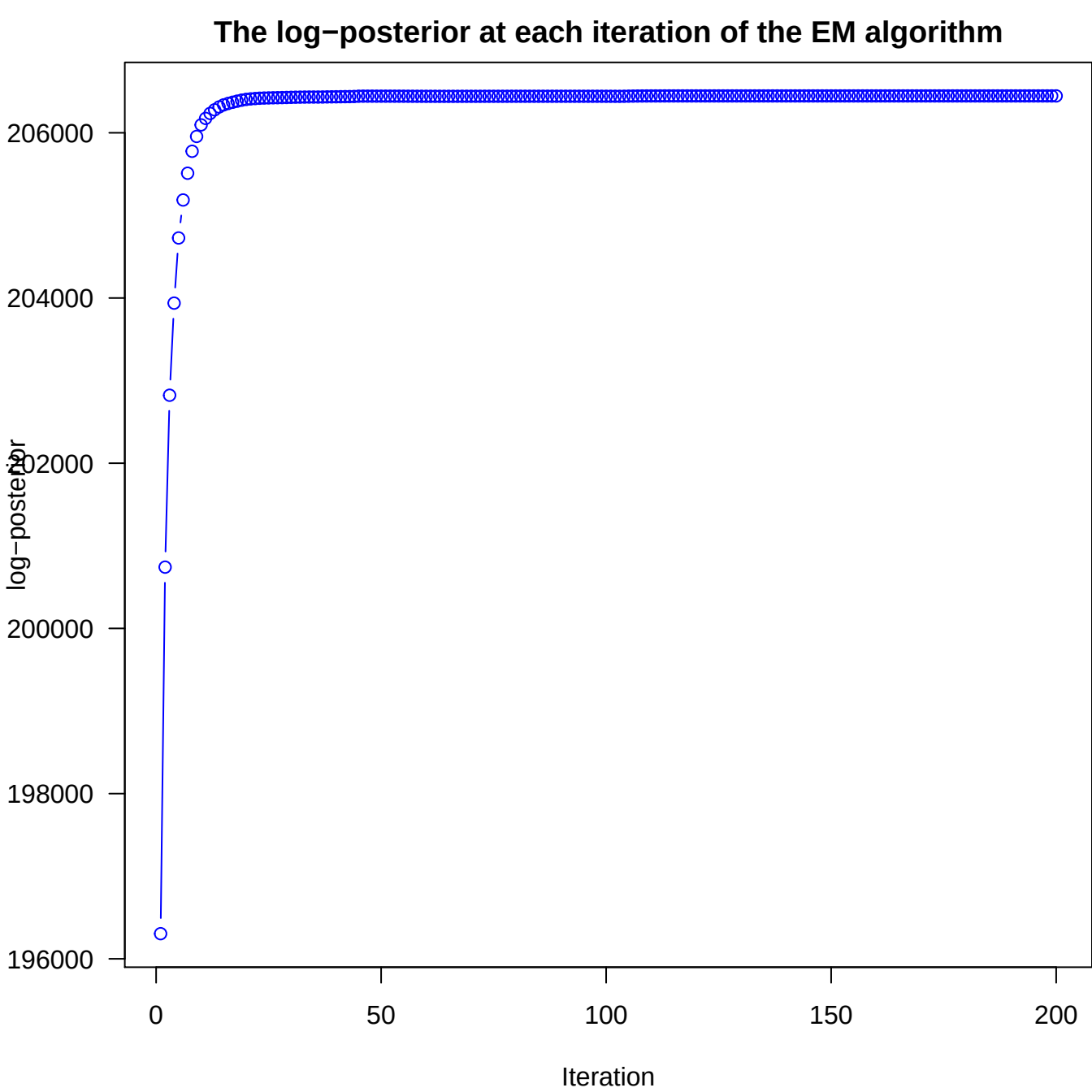

Density plot of Subcellular Membership for Protein Q8VDR9
Density
2
1
0
0.00
0.25
0.50
0.75
1.00
Membership Probability
Organelle
Endoplasmic reticulum/Golgi apparatus
Extracellular matrix

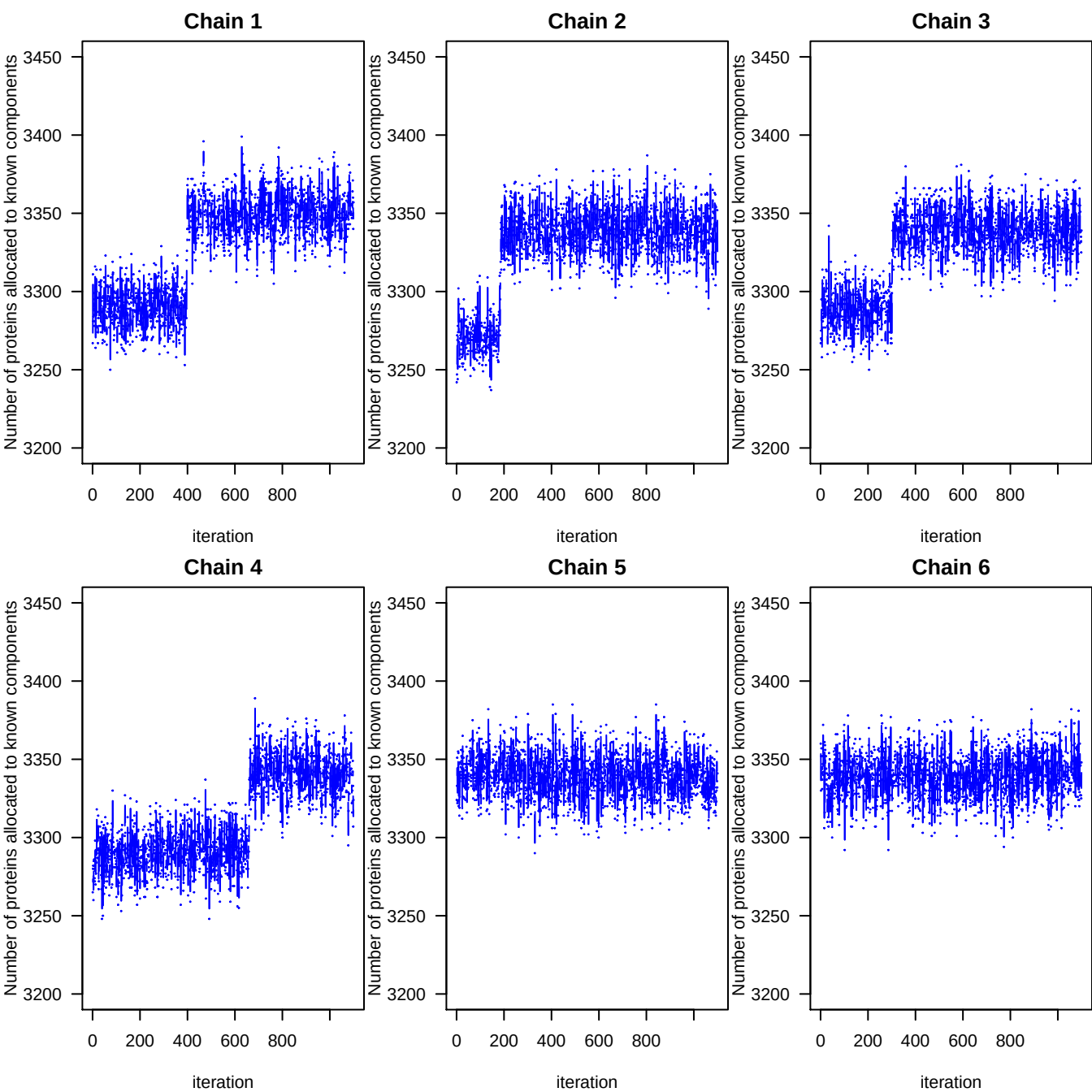

PCA plot with Protein Q8VDR9 indicated
Q8VDR9
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus − Chromatin
Nucleus − Non−chromatin
Peroxisome
Plasma membrane
Proteasome
unknown
−6
−4
−2
0
2
4
PC1 (48.41%)


Visualising whole proteome uncertainty
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus − Chromatin
Nucleus − Non−chromatin
Peroxisome
Plasma membrane
Proteasome
unknown
PC2 (23.85%)
PC1 (48.41%)
4
2
0
−2
−4
−6
−4
−2
0
2
4


Prediction of Protein Localisation
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus − Chromatin
Nucleus − Non−chromatin
Peroxisome
Plasma membrane
Proteasome
unknown
PC2 (23.85%)
PC1 (48.41%)
4
2
0
−2
−4
−6
−4
−2
0
2
4


Protein localistaion probability and Shannon Entropy
Shannon Entropy
0.0
0.2
0.4
0.6
0.8
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Localisation Probability


The log−posterior at each iteration of the EM algorithm
log−posterior
196000
198000
200000
202000
204000
206000
0
50
100
150
200
Iteration


Chain 1
Chain 2
Chain 3
Chain 4
Chain 5
Chain 6
Number of proteins allocated to known components
3200
3250
3300
3350
3400
3450
0
200
400
600
800
iteration