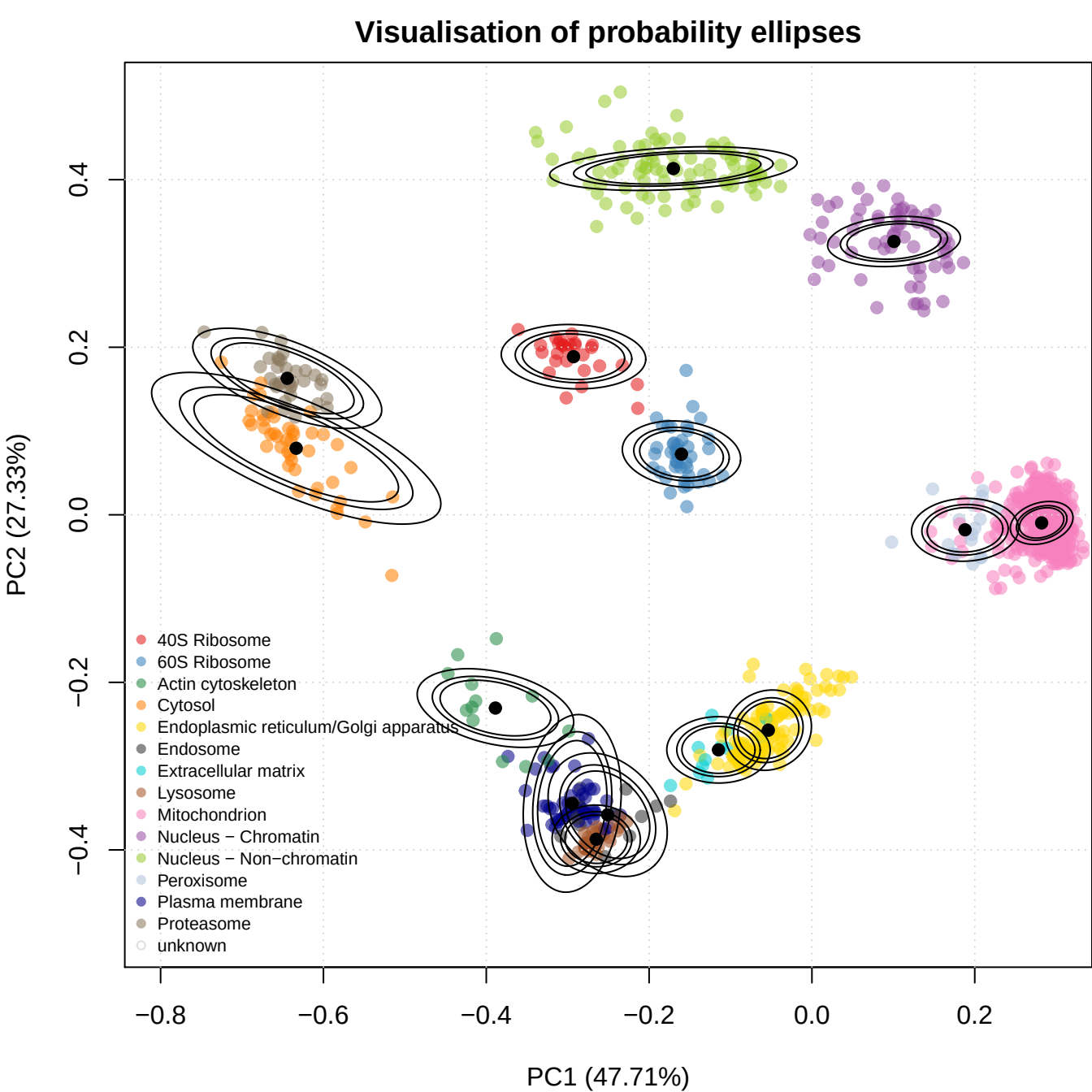
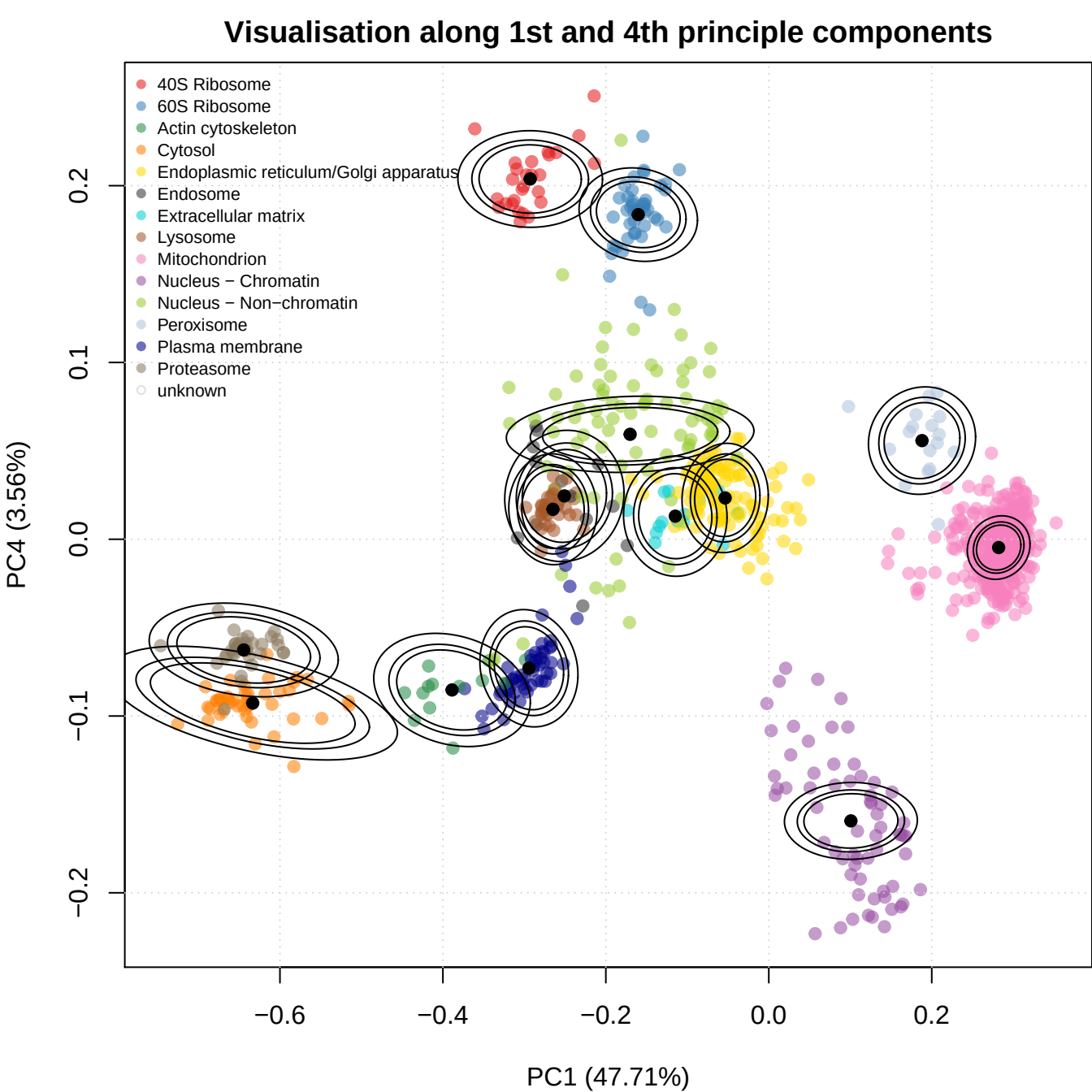
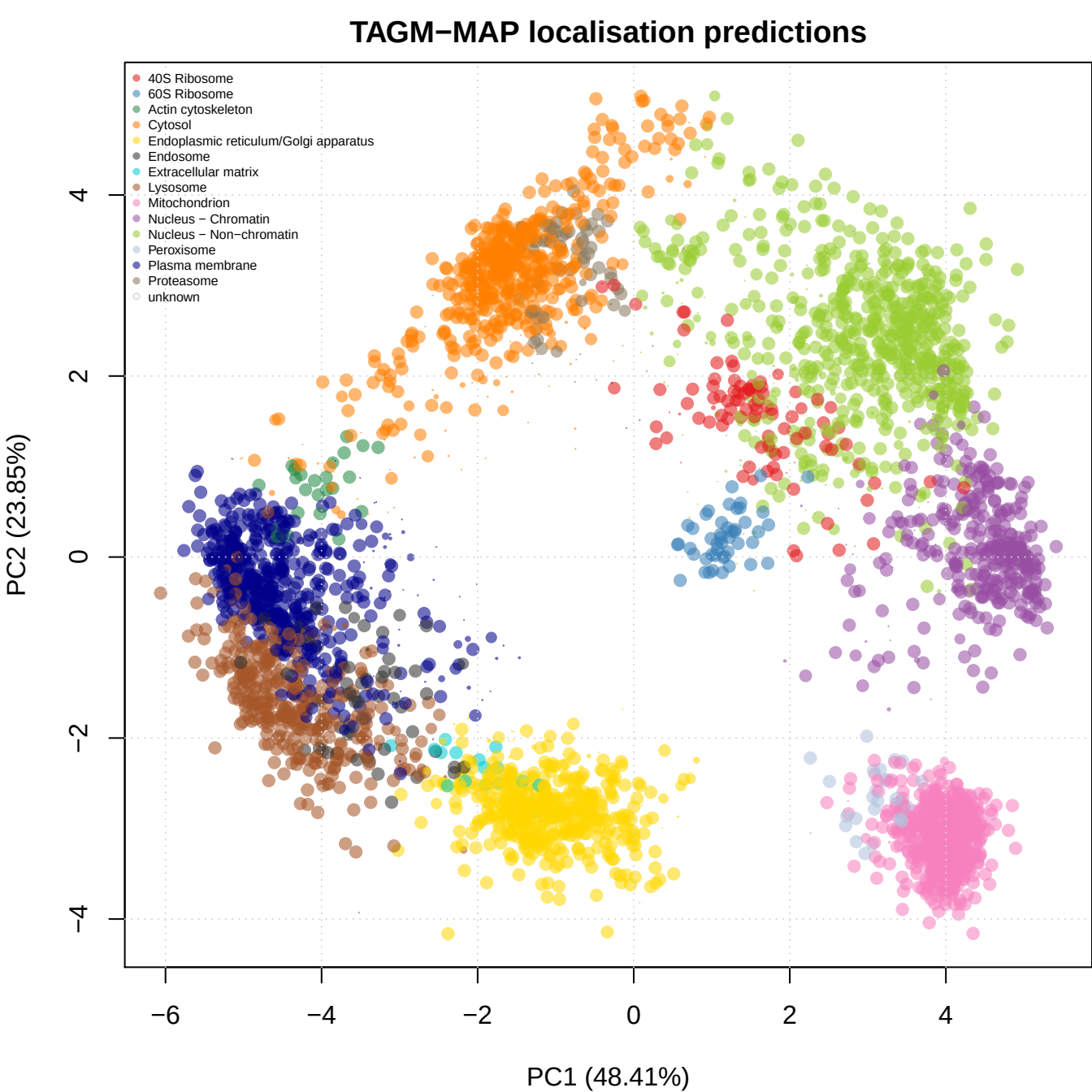
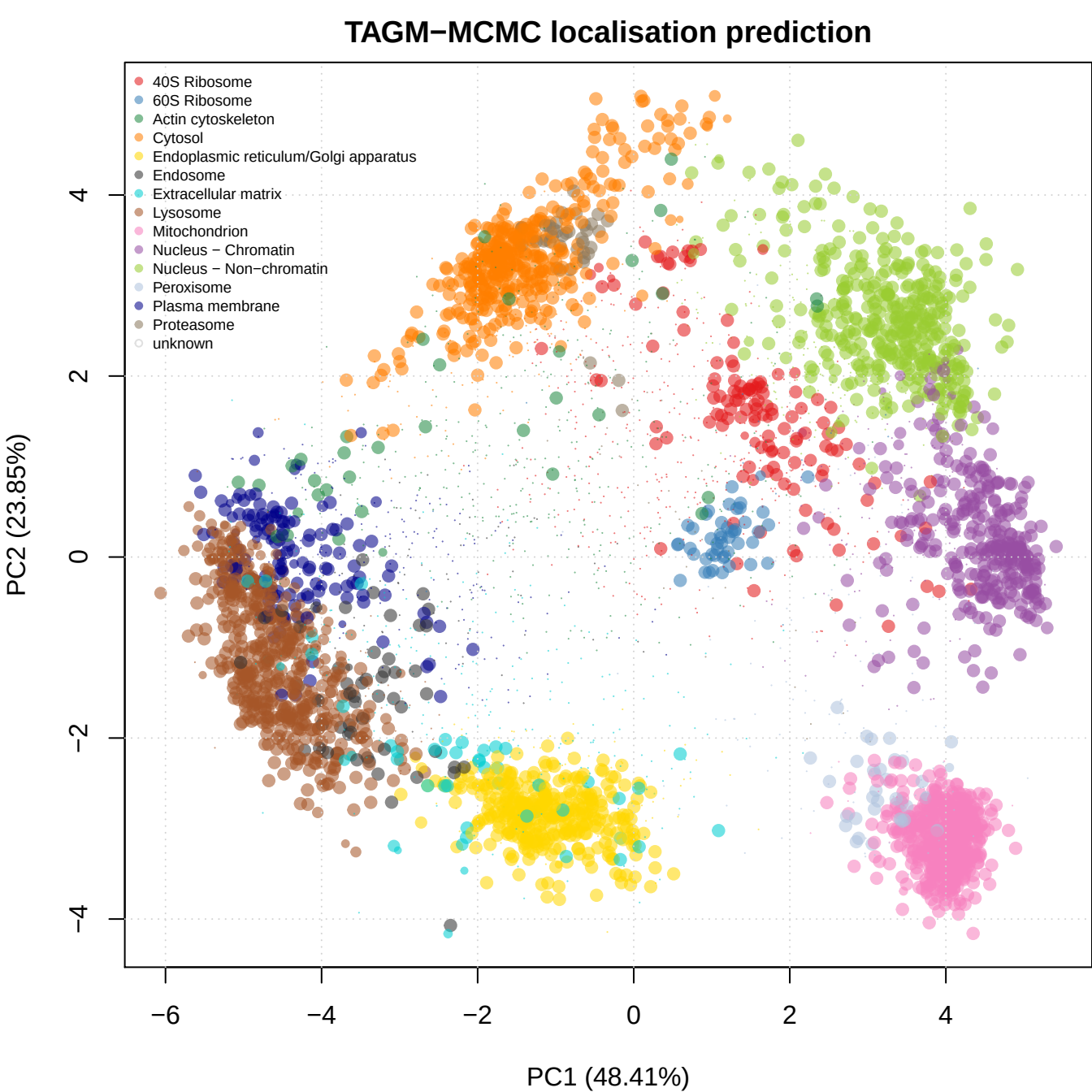
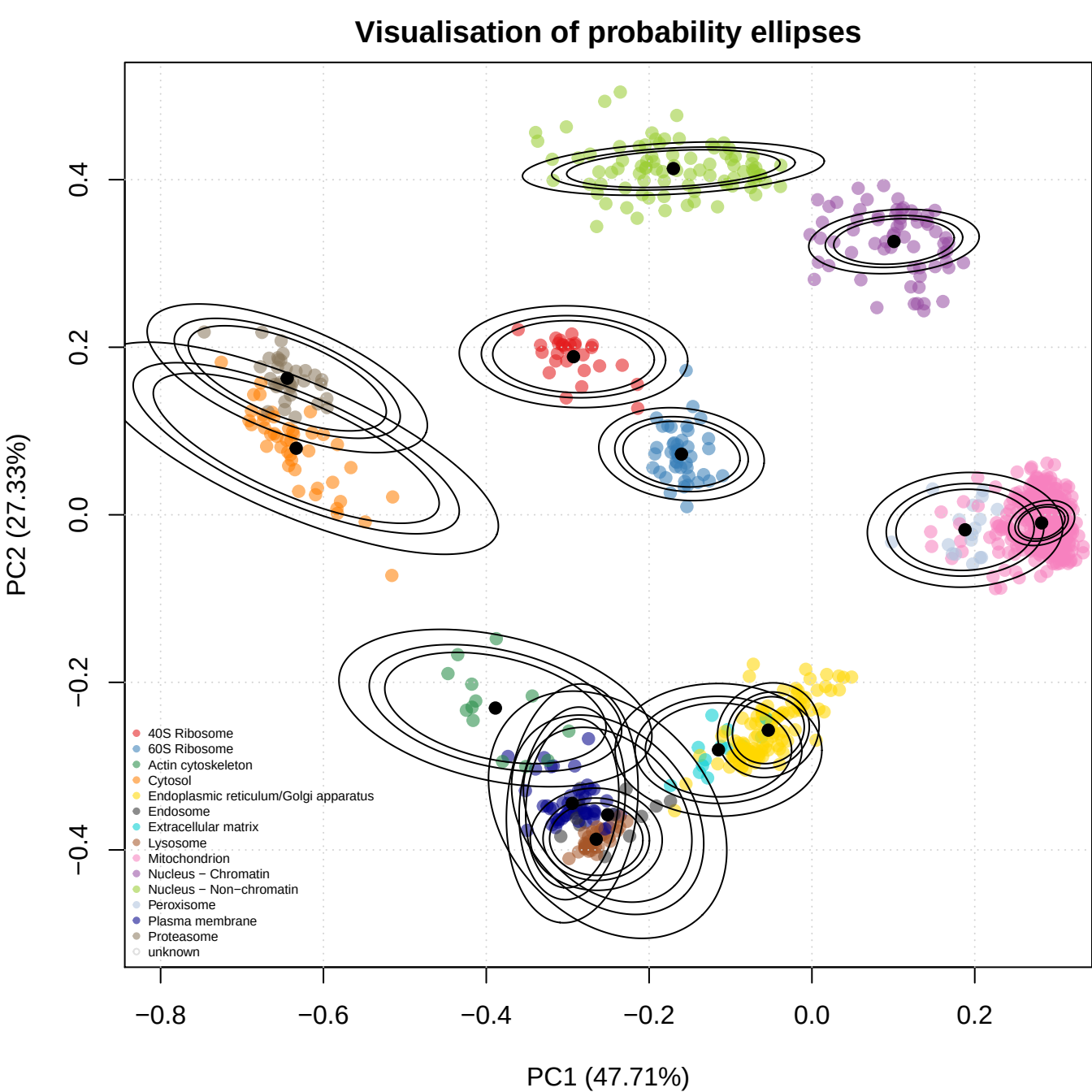
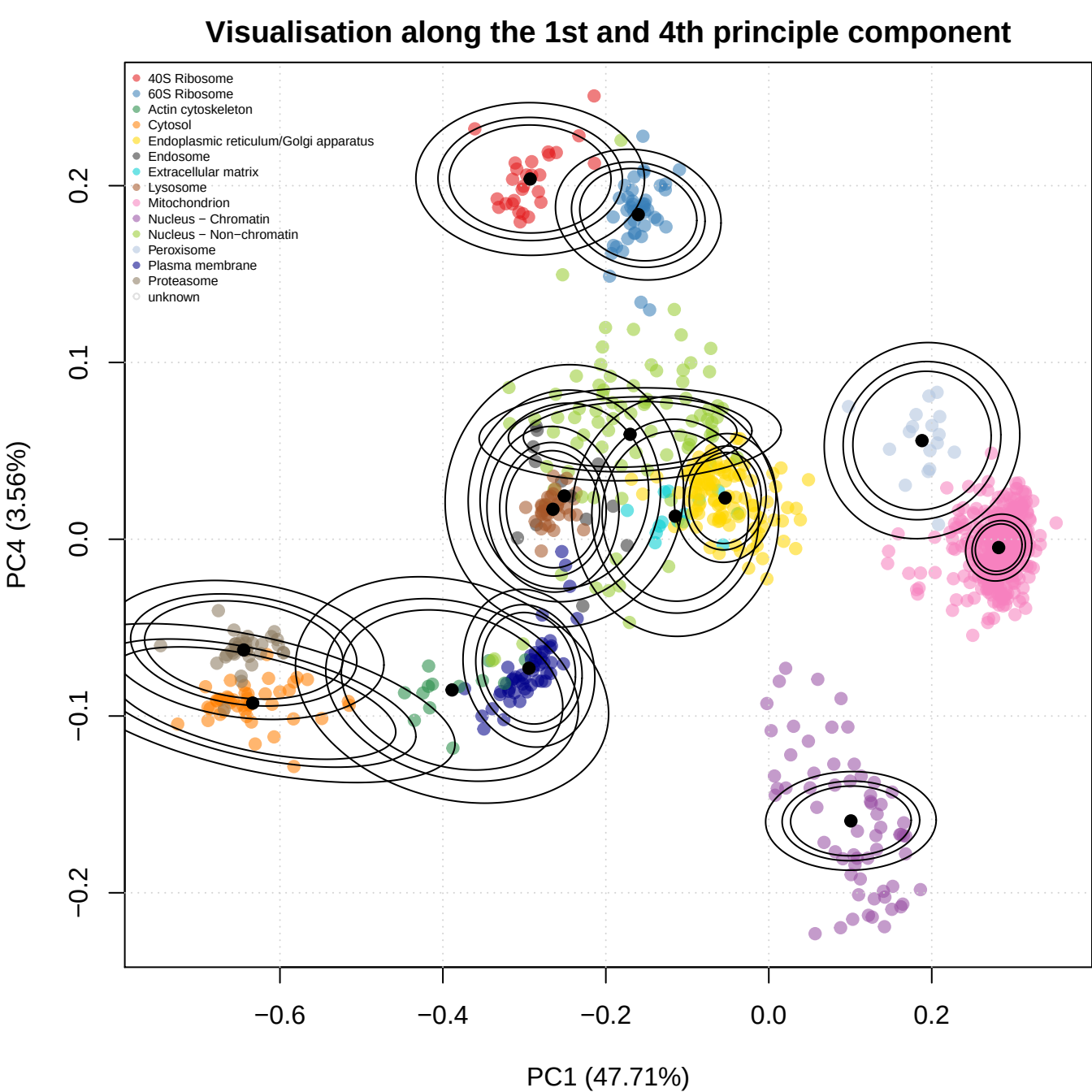

Visualisation of probability ellipses
PC1 (47.71%)
PC2 (27.33%)
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus − Chromatin
Nucleus − Non−chromatin
Peroxisome
Plasma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

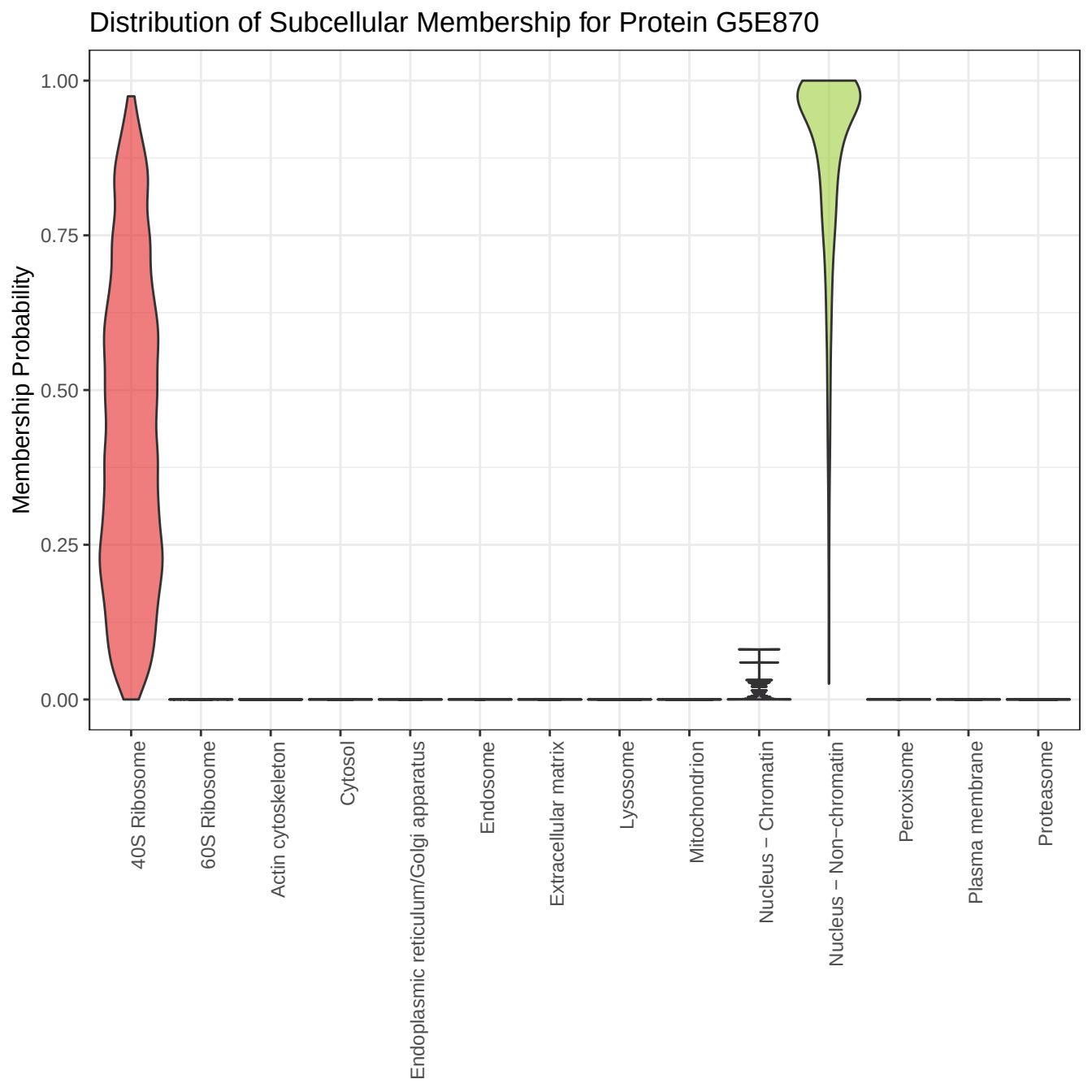

Visualisation along 1st and 4th principle components
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus − Chromatin
Nucleus − Non−chromatin
Peroxisome
Plasma membrane
Proteasome
unknown
PC4 (3.56%)
0.2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

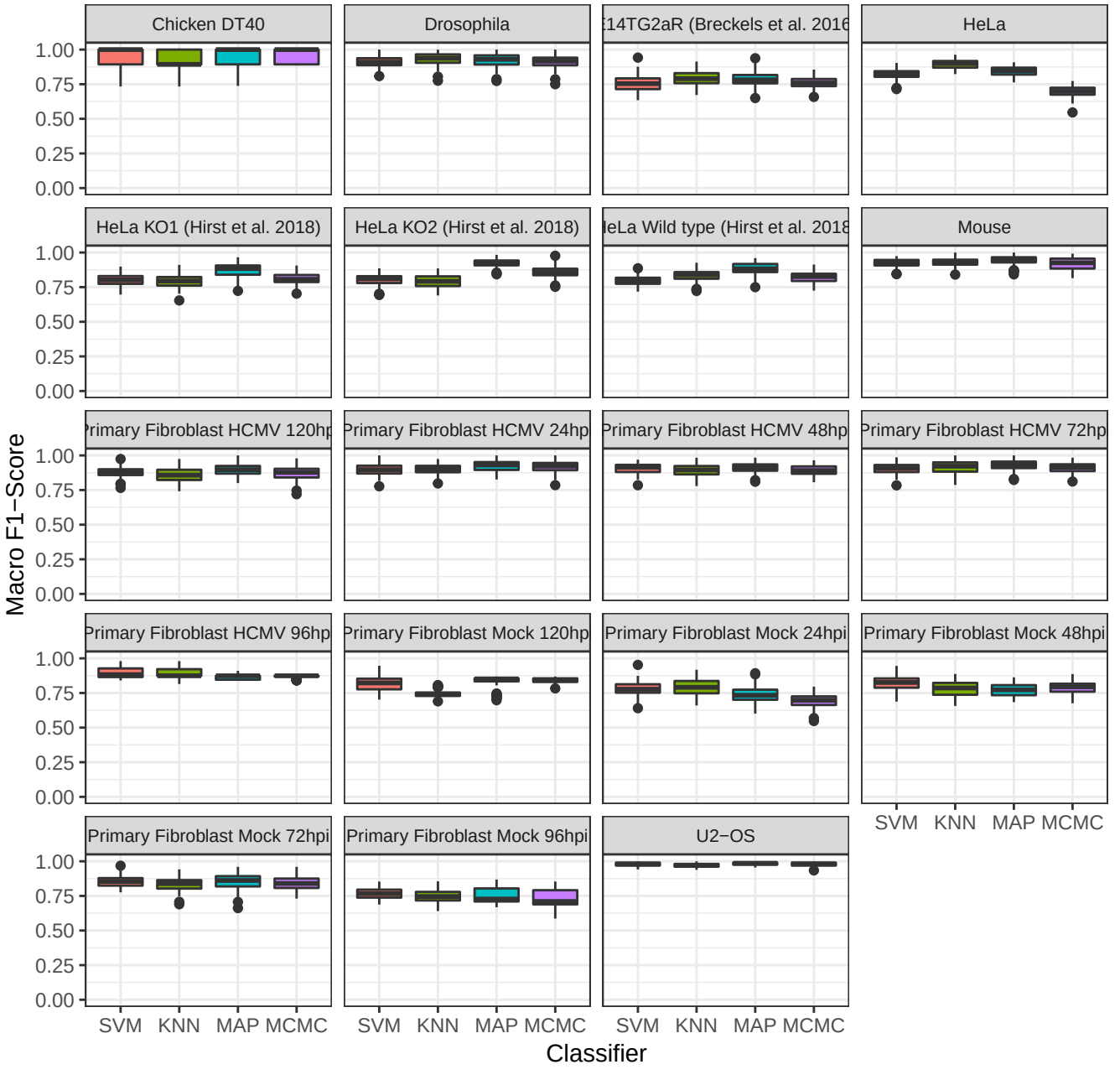

TAGM−MAP localisation predictions
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus − Chromatin
Nucleus − Non−chromatin
Peroxisome
Plasma membrane
Proteasome
unknown
PC2 (23.85%)
PC1 (48.41%)
−6
−4
−2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

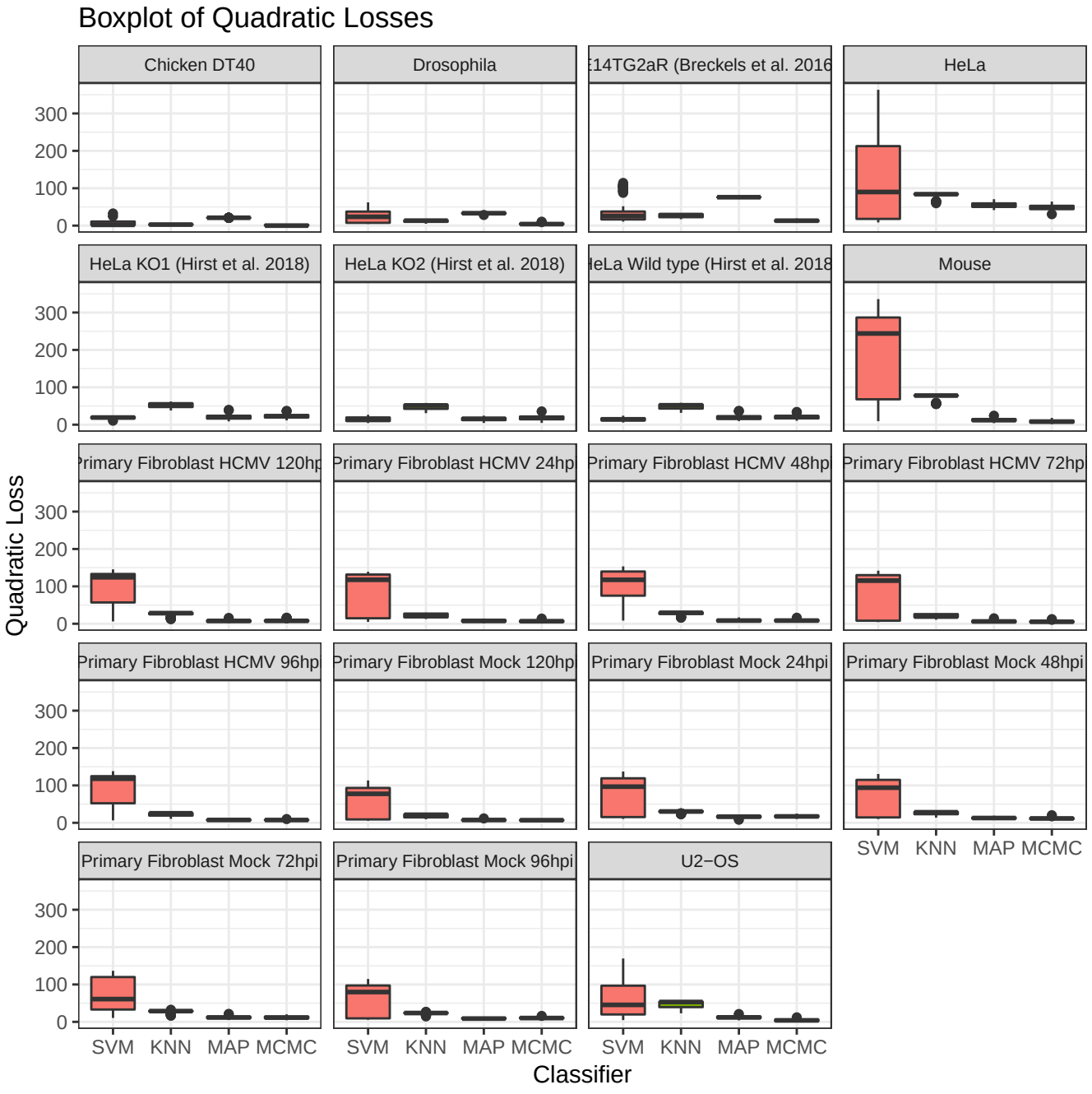

TAGM−MCMC localisation prediction
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus − Chromatin
Nucleus − Non−chromatin
Peroxisome
Plasma membrane
Proteasome
unknown
PC2 (23.85%)
PC1 (48.41%)
−6
−4
−2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

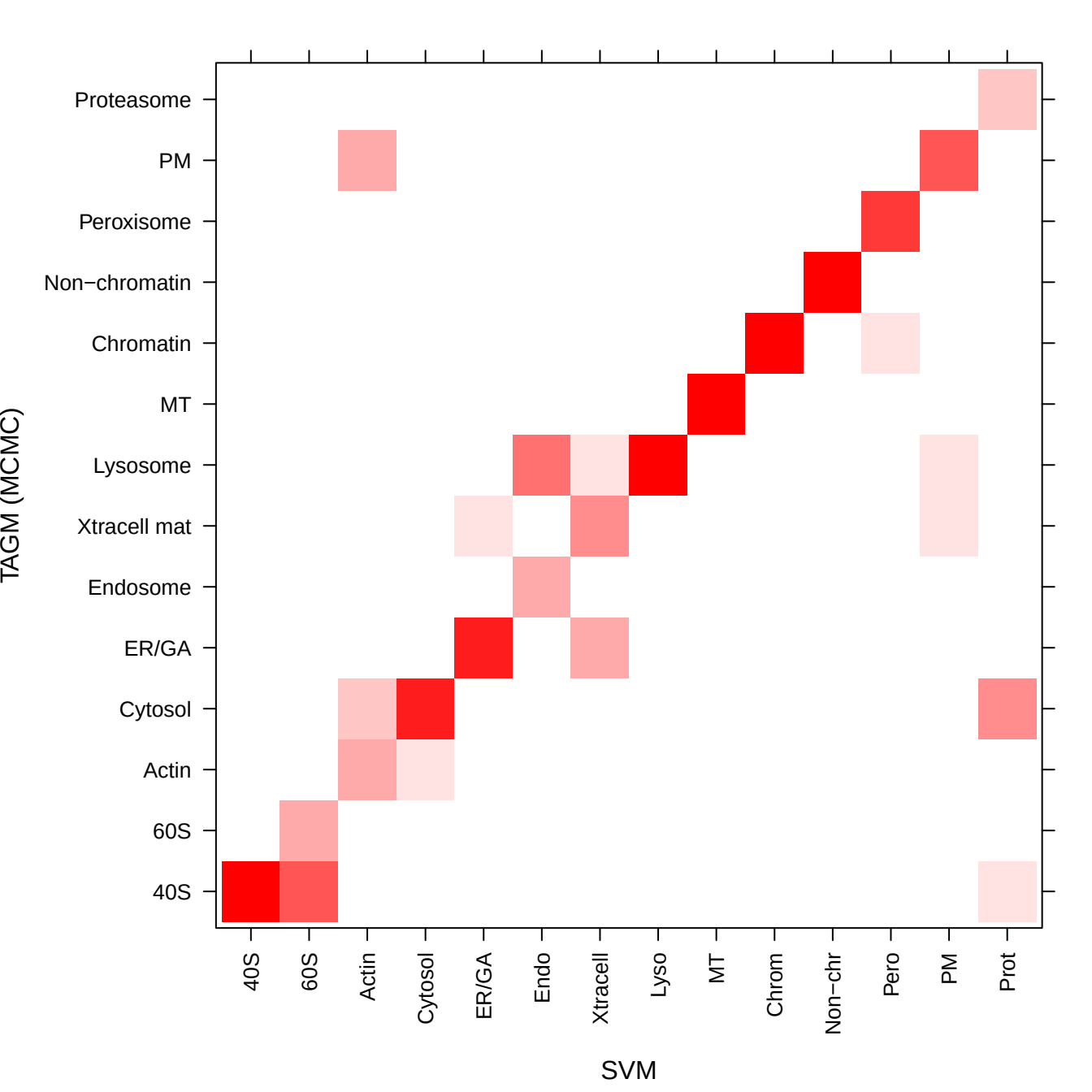

Visualisation of probability ellipses
PC2 (27.33%)
PC1 (47.71%)
0.4
0.2
0.0
−0.2
−0.4
−0.8
−0.6
−0.4
−0.2
0.0
0.2
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus − Chromatin
Nucleus − Non−chromatin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

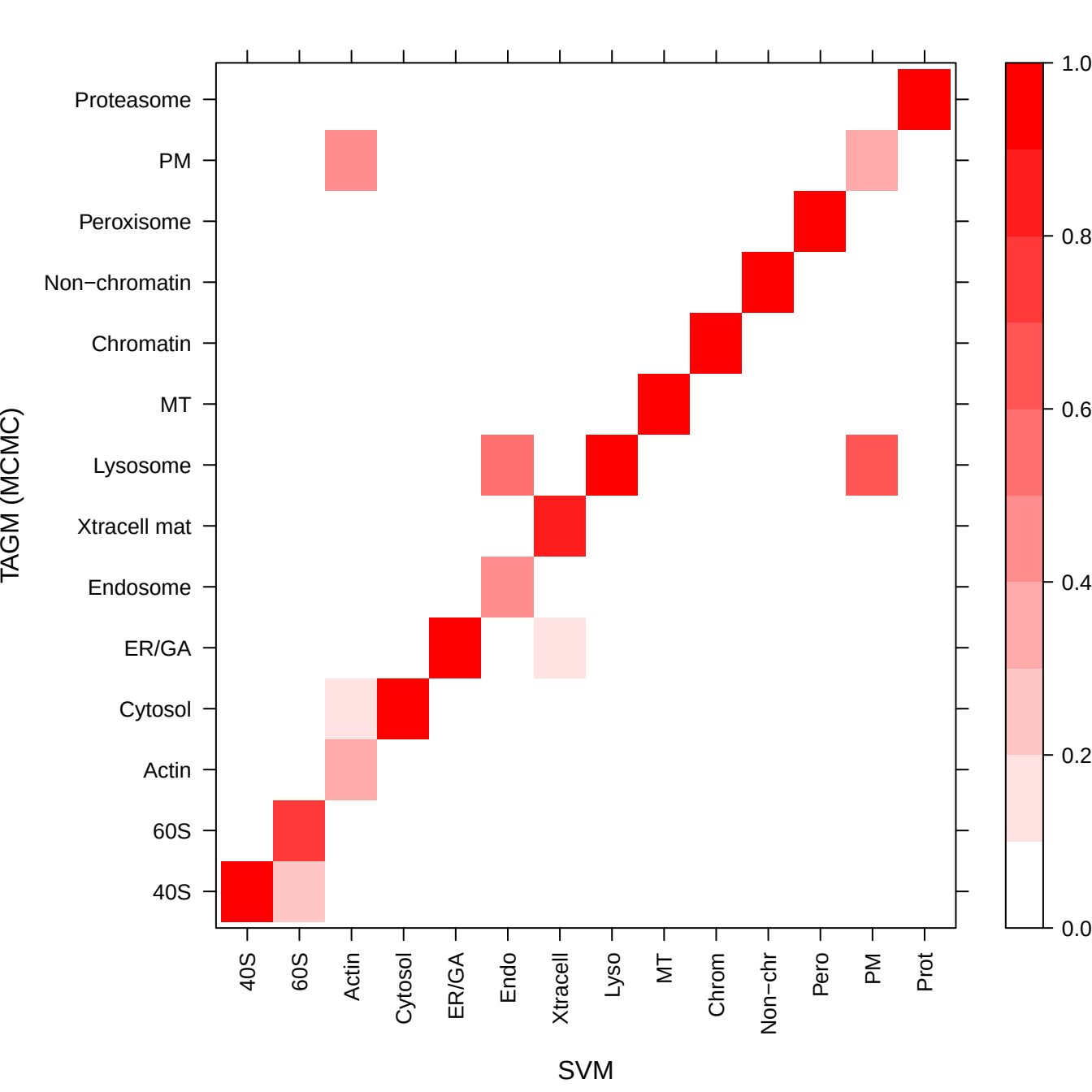

Visualisation along the 1st and 4th principle component
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus − Chromatin
Nucleus − Non−chromatin
Peroxisome
Plasma membrane
Proteasome
unknown
PC4 (3.56%)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

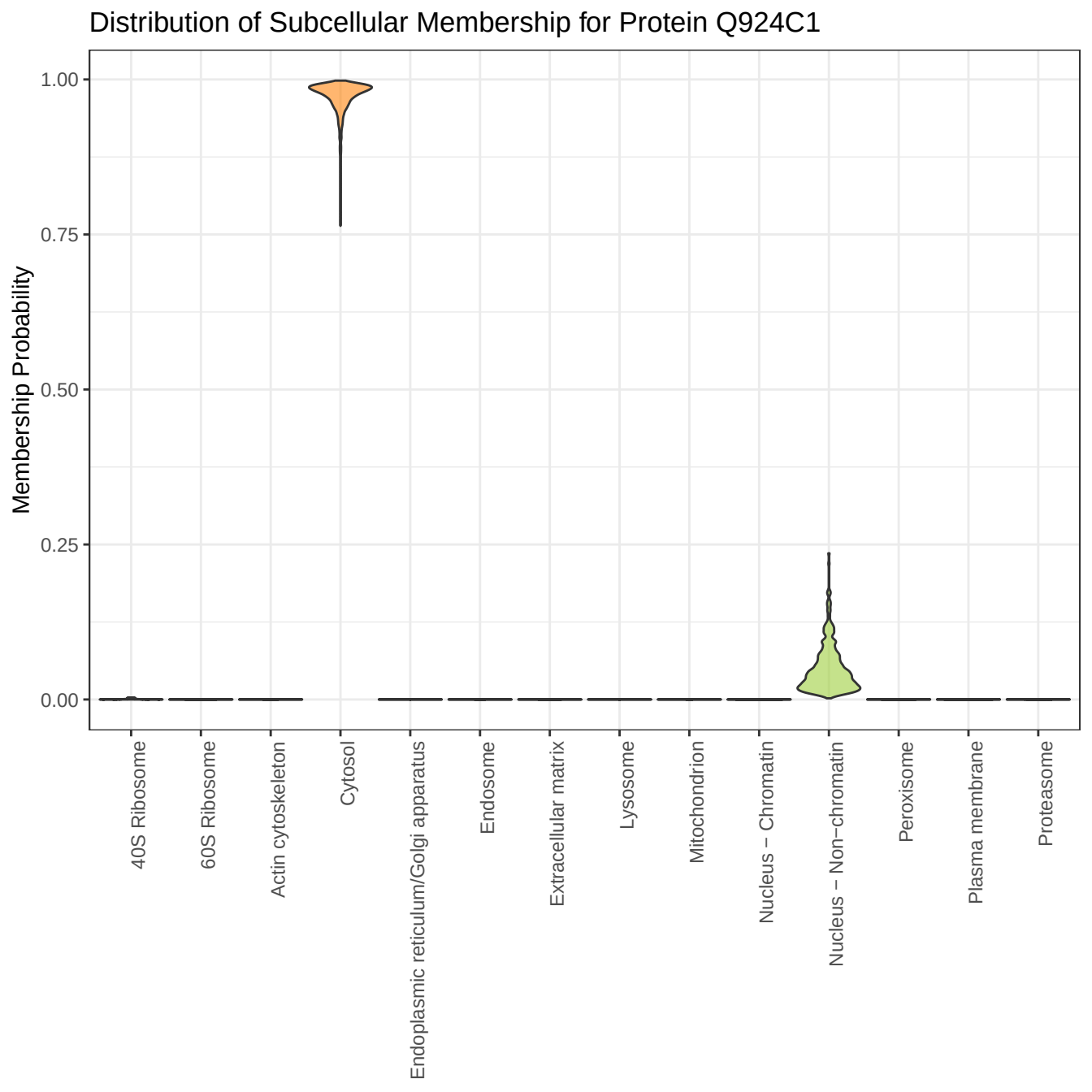

Distribution of Subcellular Membership for Protein G5E870
Membership Probability
1.00
0.75
0.50
0.25
0.00
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus – Chromatin
Nucleus – Non−chromatin
Peroxisome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


Boxplot of Macro F1 scores
Chicken DT40
Drosophila
E14TG2aR (Breckels et al. 2016
HeLa
HeLa KO1 (Hirst et al. 2018)
HeLa KO2 (Hirst et al. 2018)
HeLa Wild type (Hirst et al. 2018
Mouse
Primary Fibroblast HCMV 120hpi
Primary Fibroblast HCMV 24hpi
Primary Fibroblast HCMV 48hpi
Primary Fibroblast HCMV 72hpi
Primary Fibroblast HCMV 96hpi
Primary Fibroblast Mock 120hpi
Primary Fibroblast Mock 24hpi
Primary Fibroblast Mock 48hpi
Primary Fibroblast Mock 72hpi
Primary Fibroblast Mock 96hpi
U2−OS
Macro F1−Score
1.00
0.75
0.50
0.25
0.00
SVM
KNN
MAP
MCMC
Classifier

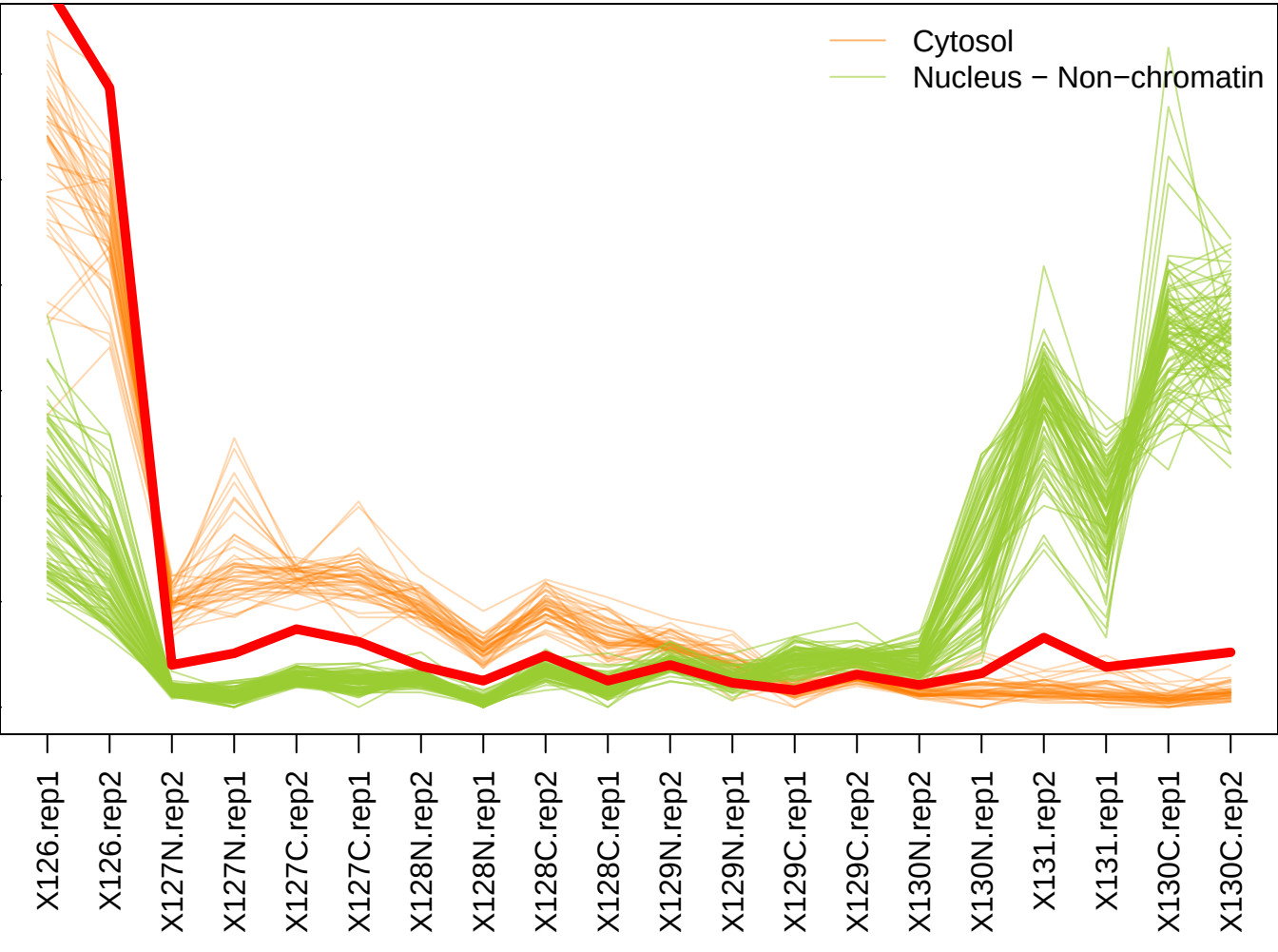

Boxplot of Quadratic Losses
Chicken DT40
Drosophila
E14TG2aR (Breckels et al. 2016
HeLa
HeLa KO1 (Hirst et al. 2018)
HeLa KO2 (Hirst et al. 2018)
HeLa Wild type (Hirst et al. 2018
Mouse
Primary Fibroblast HCMV 120hpi
Primary Fibroblast HCMV 24hpi
Primary Fibroblast HCMV 48hpi
Primary Fibroblast HCMV 72hpi
Primary Fibroblast HCMV 96hpi
Primary Fibroblast Mock 120hpi
Primary Fibroblast Mock 24hpi
Primary Fibroblast Mock 48hpi
Primary Fibroblast Mock 72hpi
Primary Fibroblast Mock 96hpi
U2−OS
Quadratic Loss
0
100
200
300
SVM
KNN
MAP
MCMC
Classifier

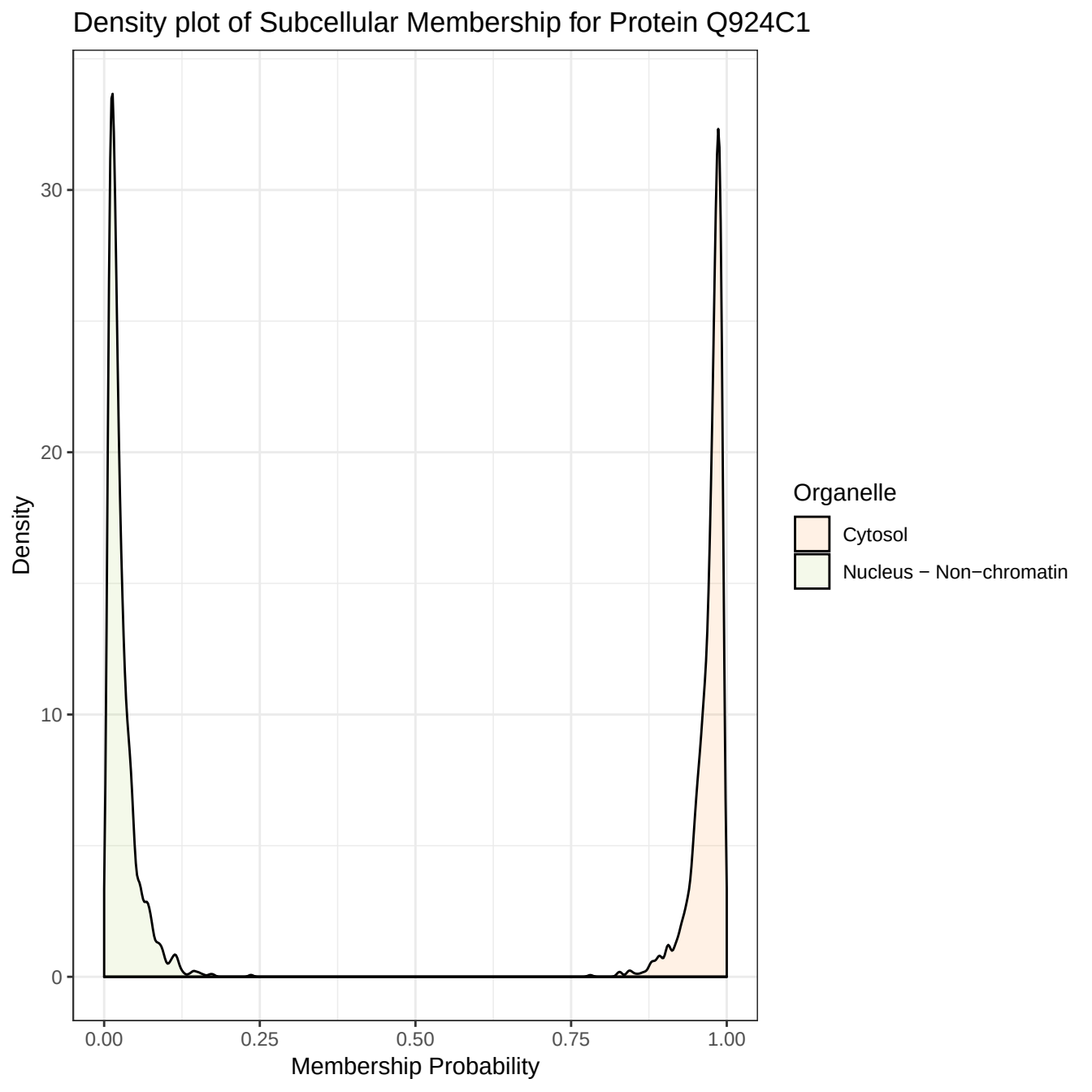

TAGM (MCMC)
Proteasome
PM
Peroxisome
Non−chromatin
Chromatin
MT
Lysosome
Xtracell mat
Endosome
ER/GA
Cytosol
Actin
60S
40S
SVM
40S
60S
Actin
Cytosol
ER/GA
Endo
Xtracell
Lyso
MT
Chrom
Non−chr
Pero
PM
Prot

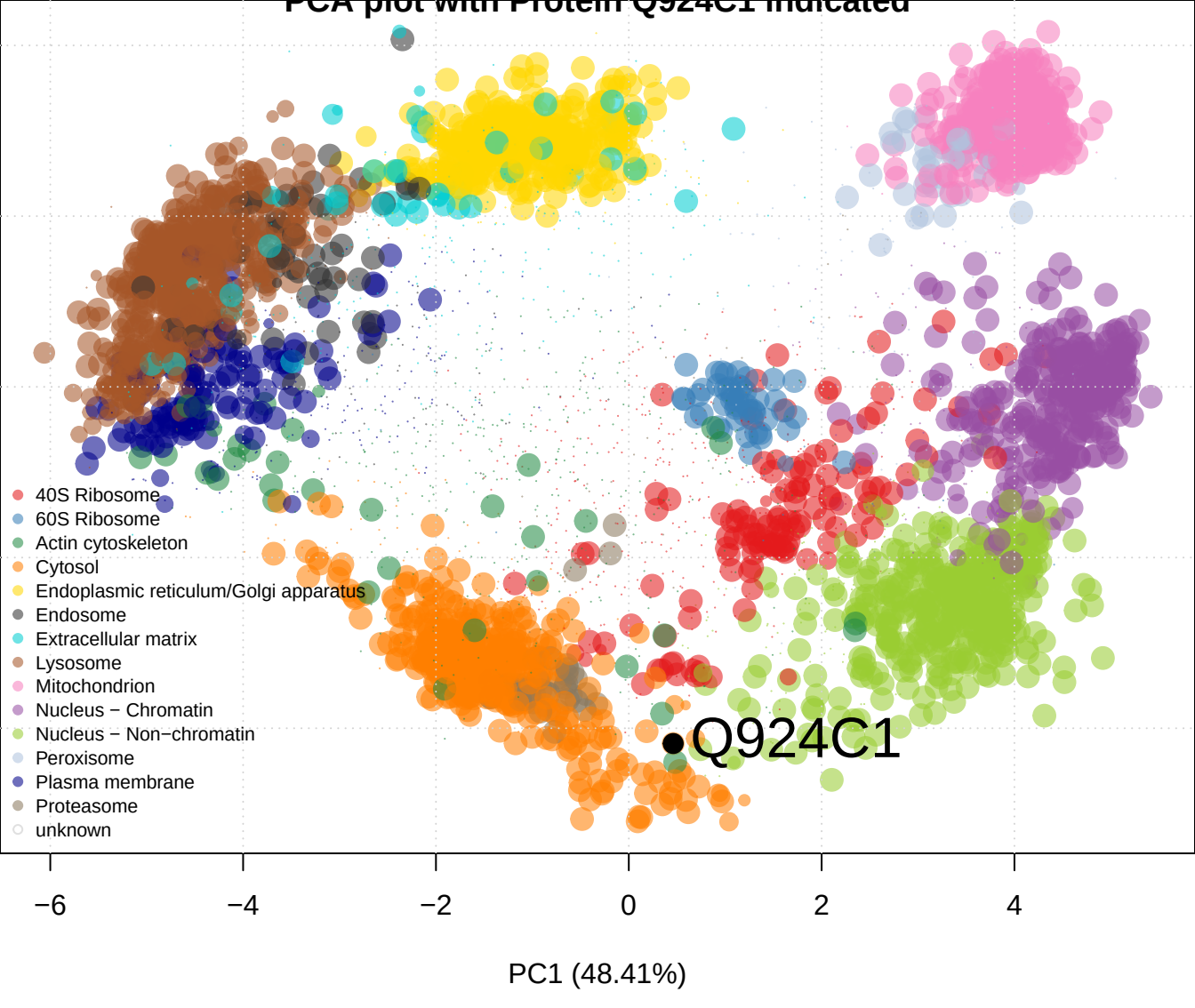

TAGM (MCMC)
Proteasome
PM
Peroxisome
Non−chromatin
Chromatin
MT
Lysosome
Xtracell mat
Endosome
ER/GA
Cytosol
Actin
60S
40S
SVM
40S
60S
Actin
Cytosol
ER/GA
Endo
Xtracell
Lyso
MT
Chrom
Non−chr
Pero
PM
Prot
1.0
0.8
0.6
0.4
0.2
0.0

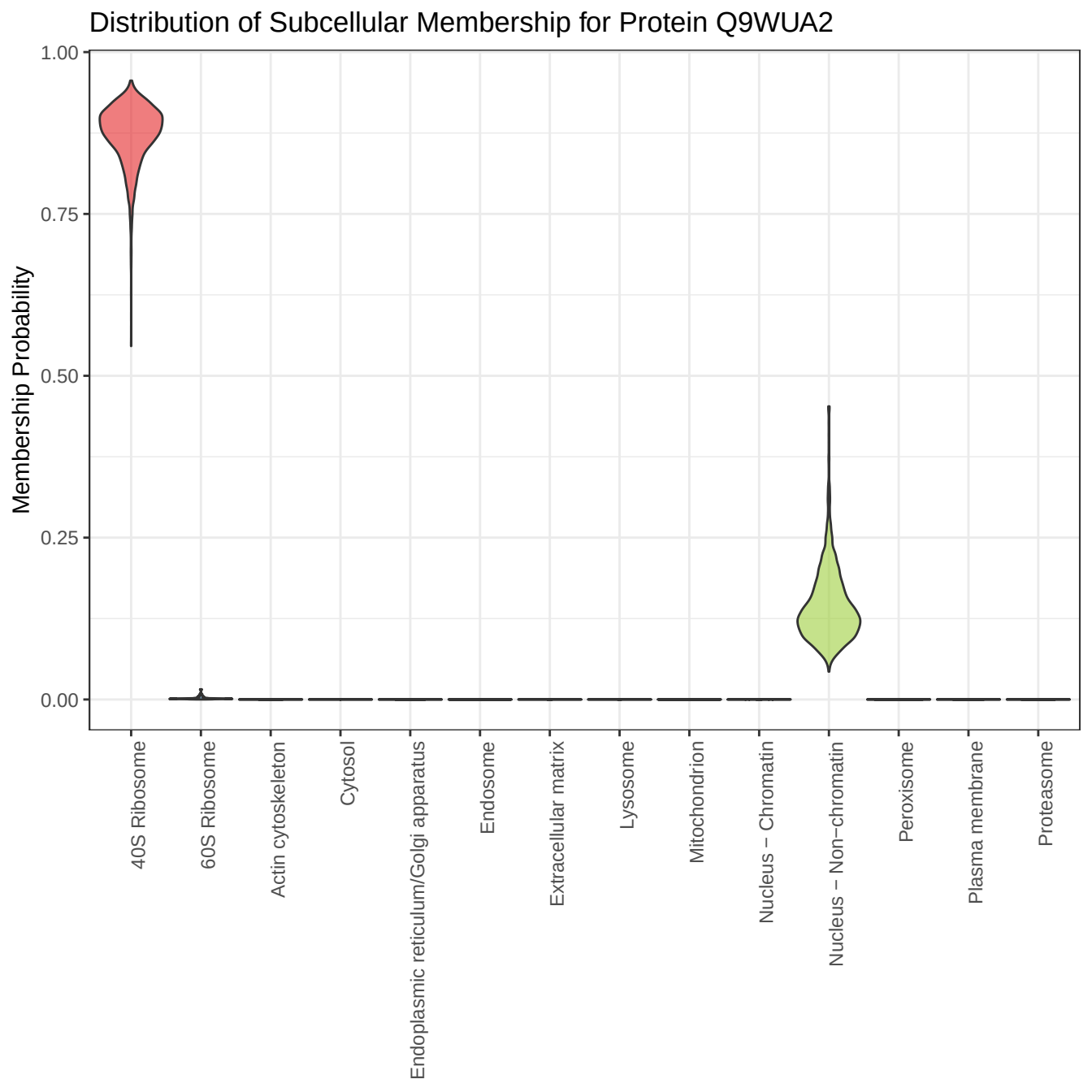

Distribution of Subcellular Membership for Protein Q924C1
Membership Probability
1.00
0.75
0.50
0.25
0.00
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus – Chromatin
Nucleus – Non−chromatin
Peroxisome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

Profile of Protein Q924C1 with marker distributions

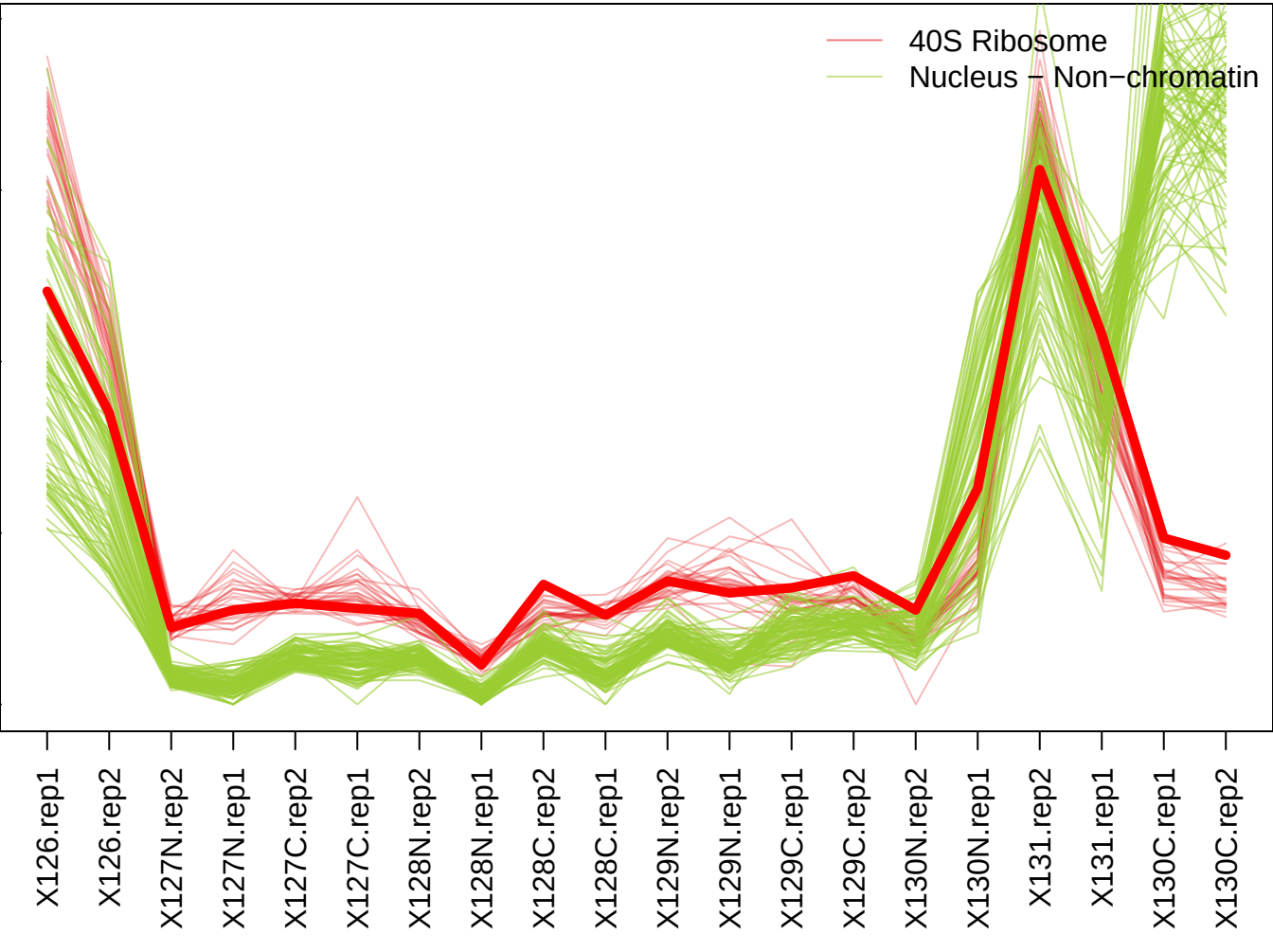


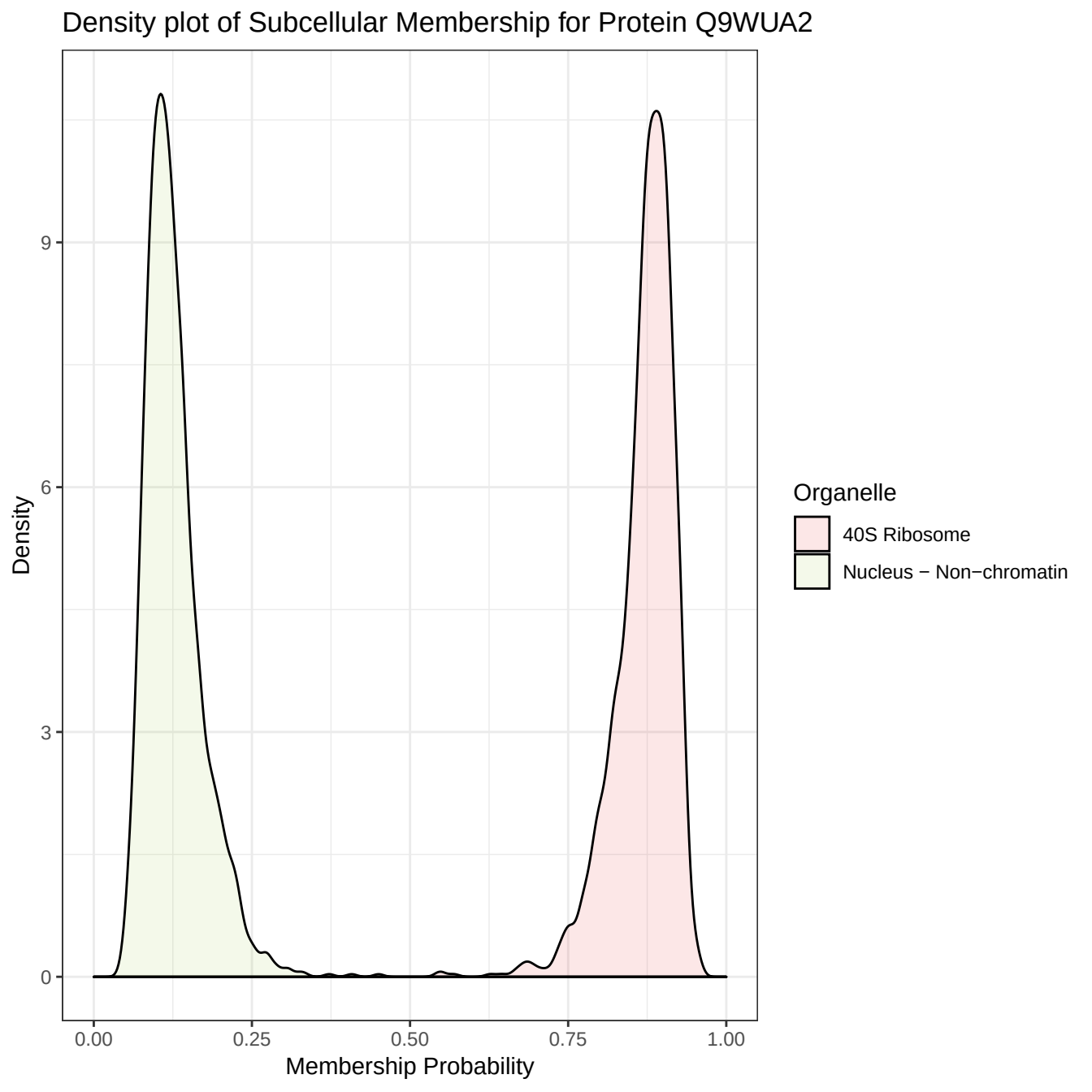

Density plot of Subcellular Membership for Protein Q924C1
Density
30
20
10
0
0.00
0.25
0.50
0.75
1.00
Membership Probability
Organelle
Cytosol
Nucleus − Non−chromatin

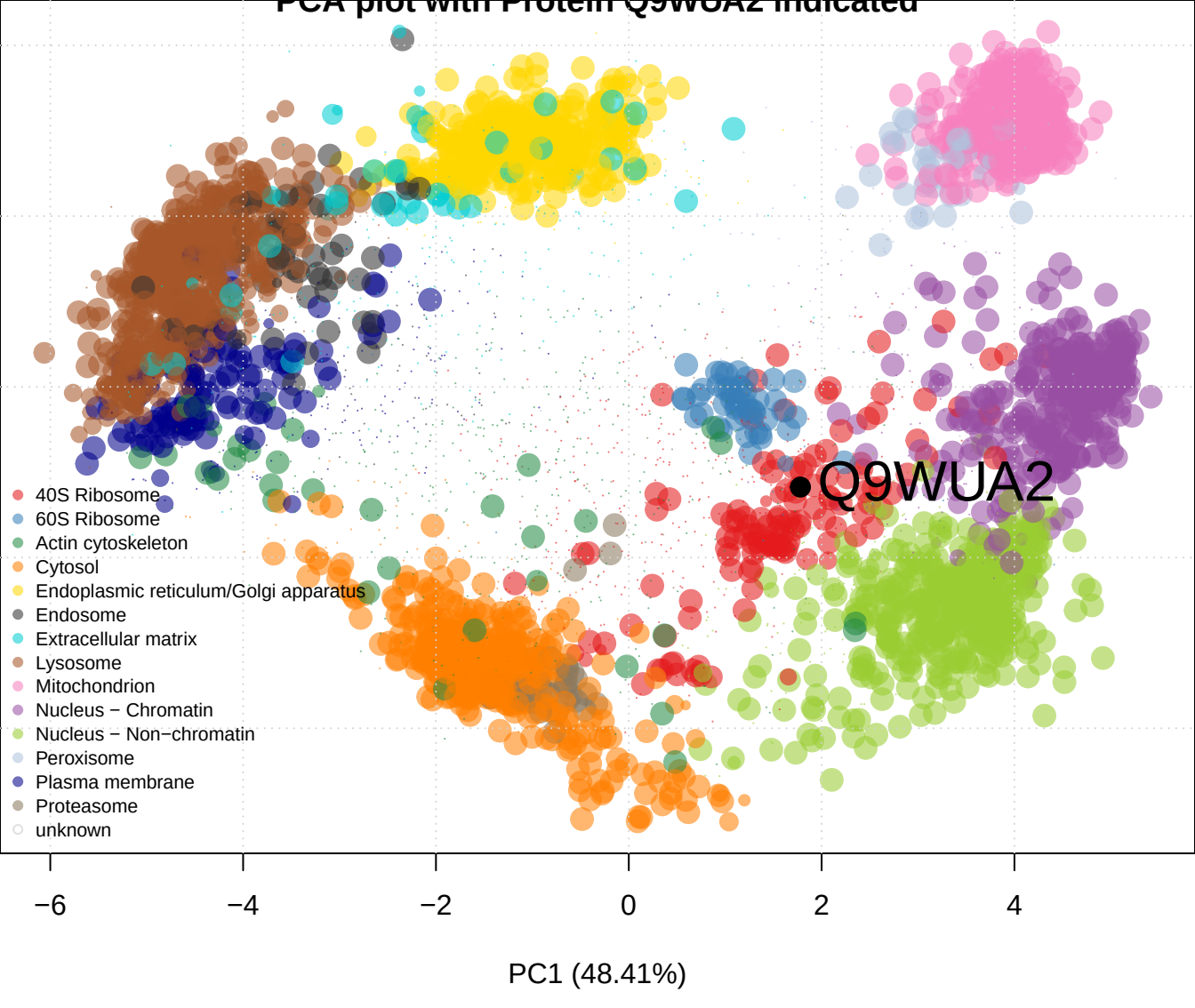

PCA plot with Protein Q924C1 indicated
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus − Chromatin
Nucleus − Non−chromatin
Peroxisome
Plasma membrane
Proteasome
unknown
Q924C1
−6
−4
−2
0
2
4
PC1 (48.41%)

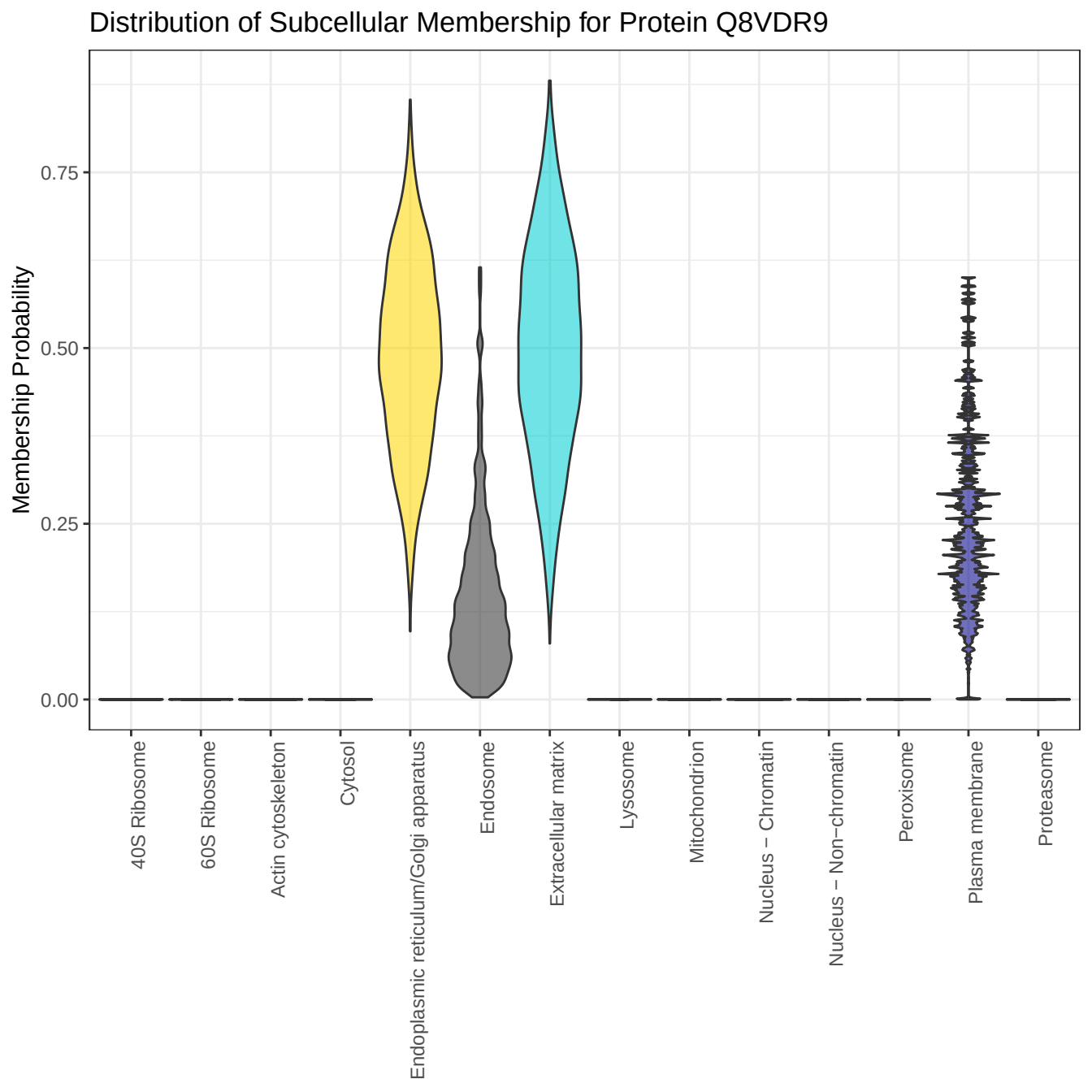

Distribution of Subcellular Membership for Protein Q9WUA2
Membership Probability
1.00
0.75
0.50
0.25
0.00
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus – Chromatin
Nucleus – Non−chromatin
Peroxisome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

Profile of Protein Q9WUA2 with marker distributions

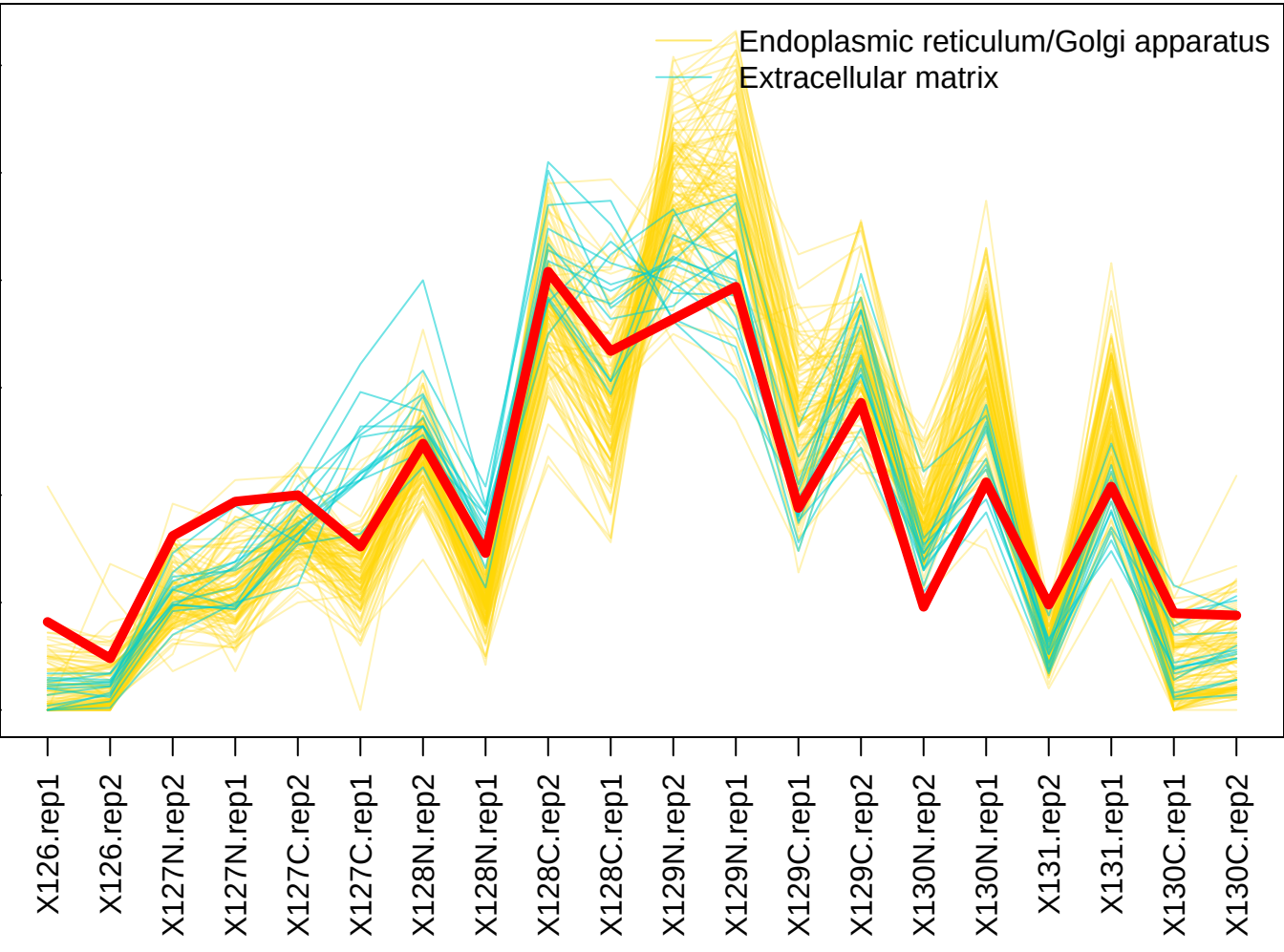


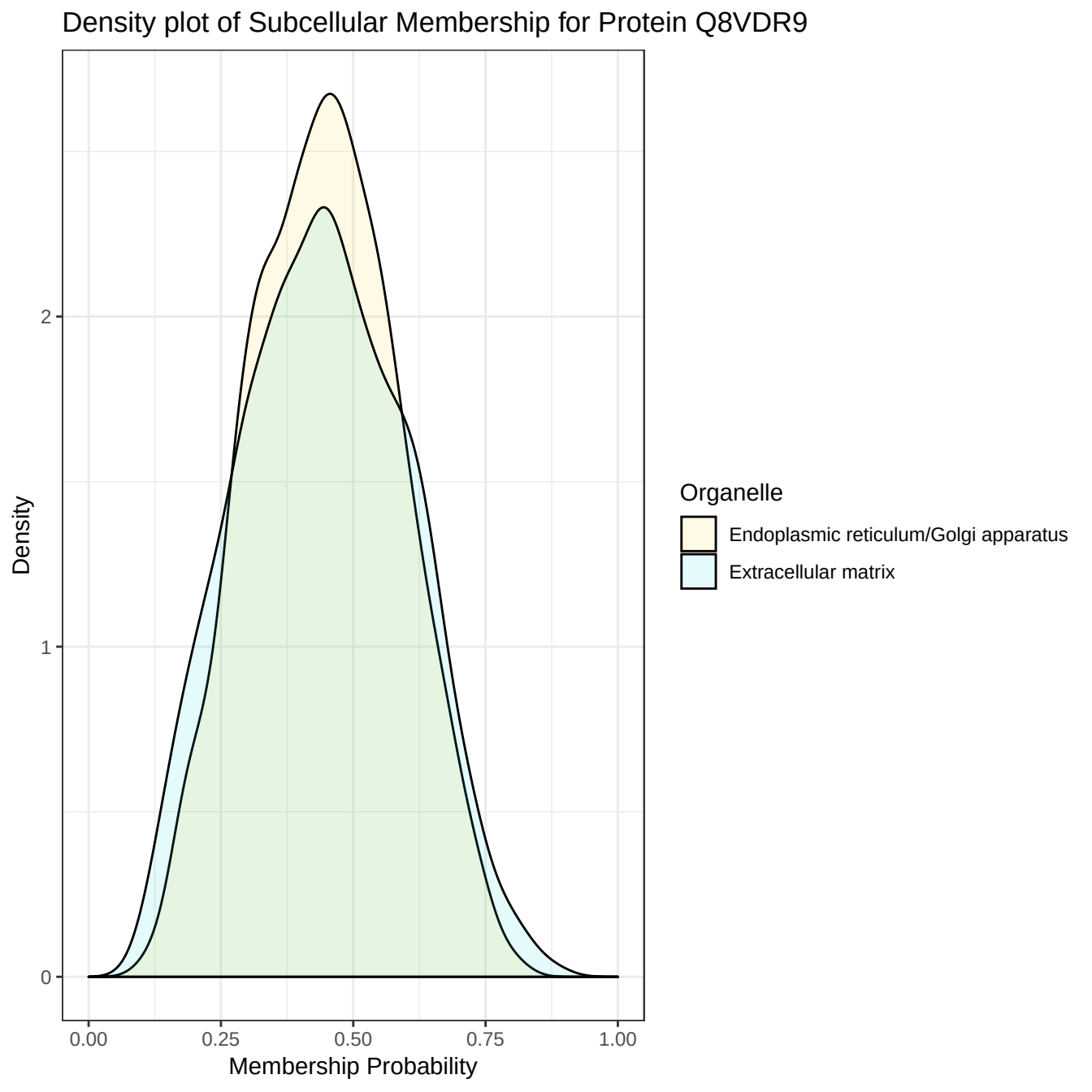

Density plot of Subcellular Membership for Protein Q9WUA2
Density
9
6
3
0
0.00
0.25
0.50
0.75
1.00
Membership Probability
Organelle
40S Ribosome
Nucleus − Non−chromatin

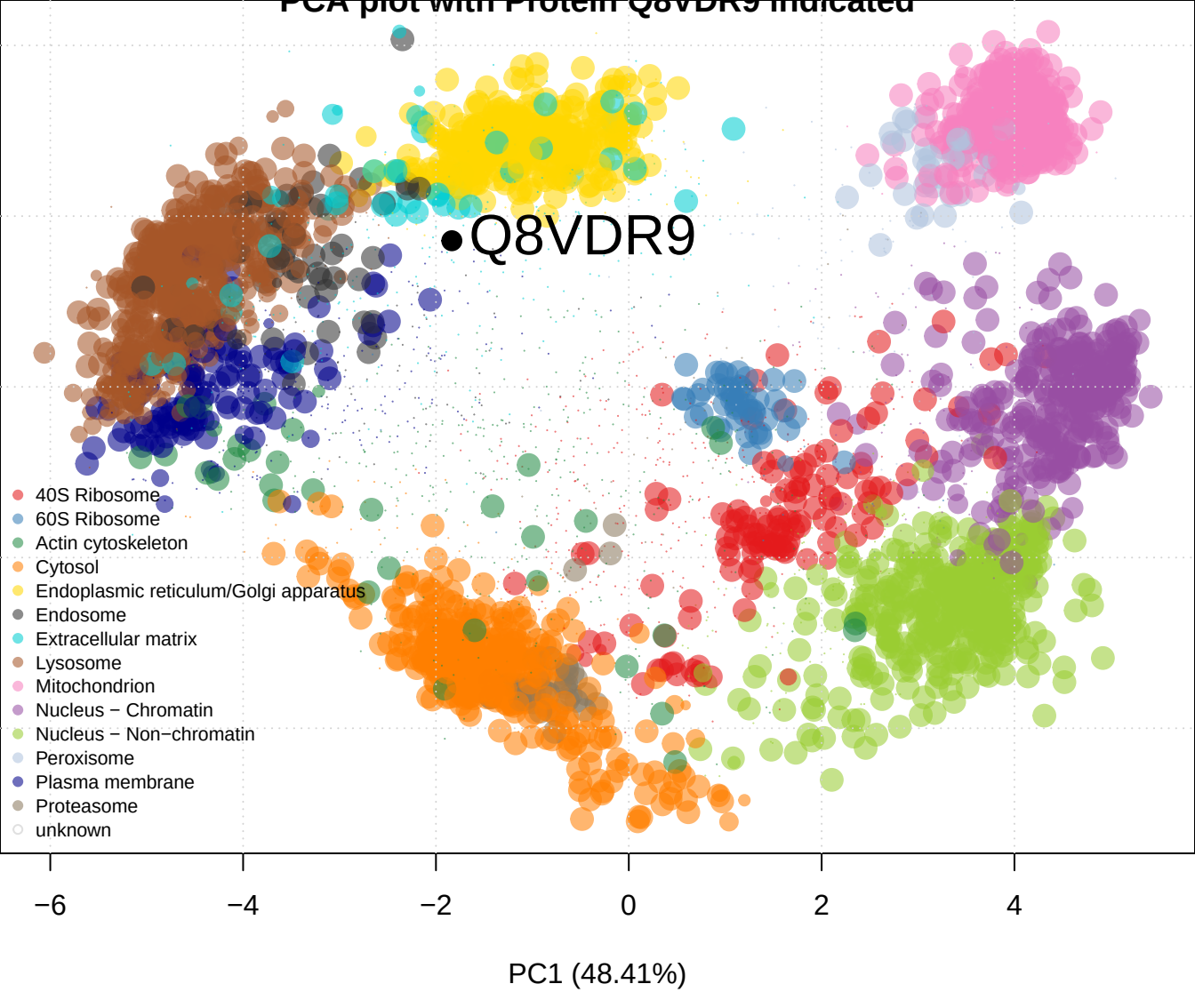

PCA plot with Protein Q9WUA2 indicated
Q9WUA2
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus − Chromatin
Nucleus − Non−chromatin
Peroxisome
Plasma membrane
Proteasome
unknown
−6
−4
−2
0
2
4
PC1 (48.41%)

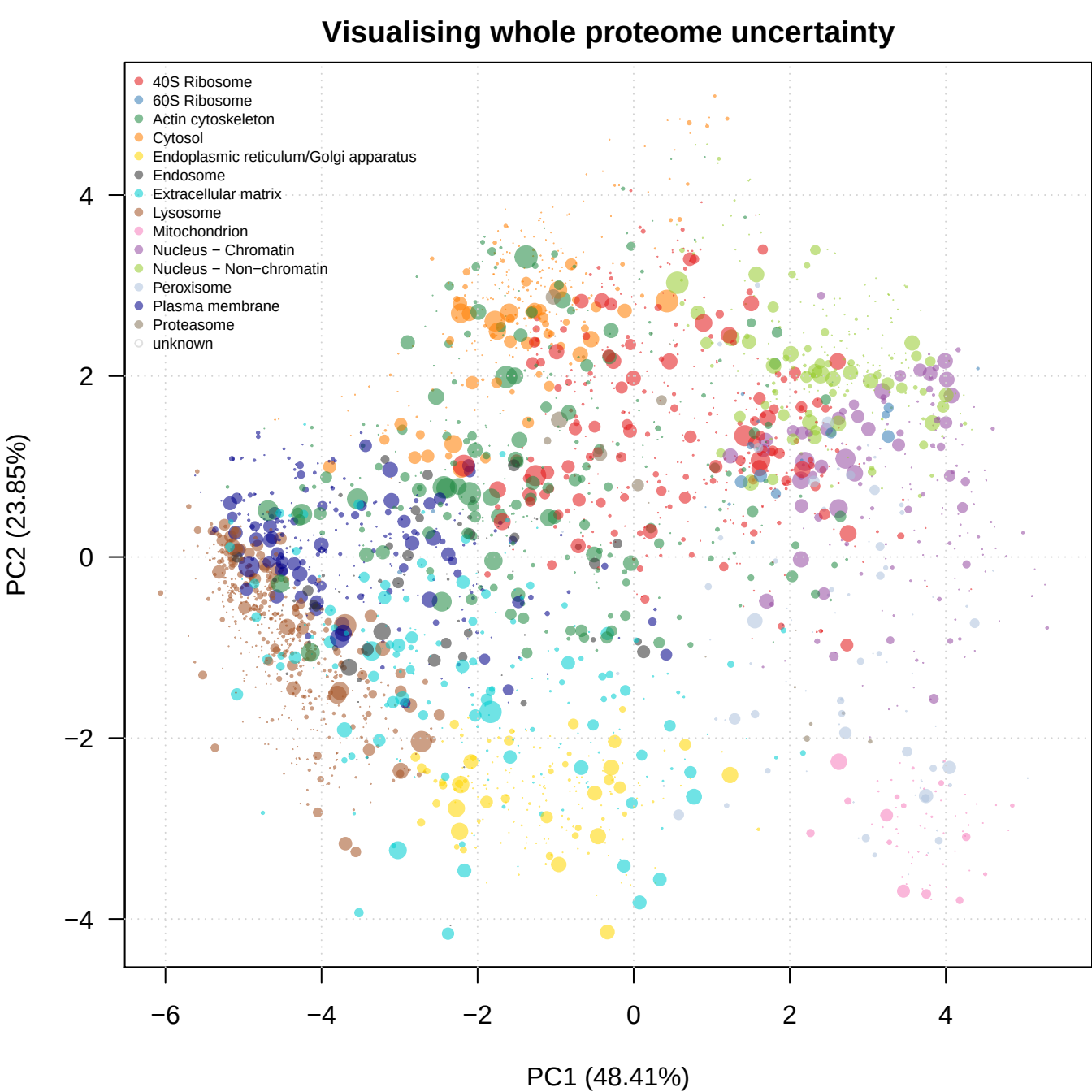

Distribution of Subcellular Membership for Protein Q8VDR9
Membership Probability
0.00
0.25
0.50
0.75
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus – Chromatin
Nucleus – Non−chromatin
Peroxisome
Plasma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

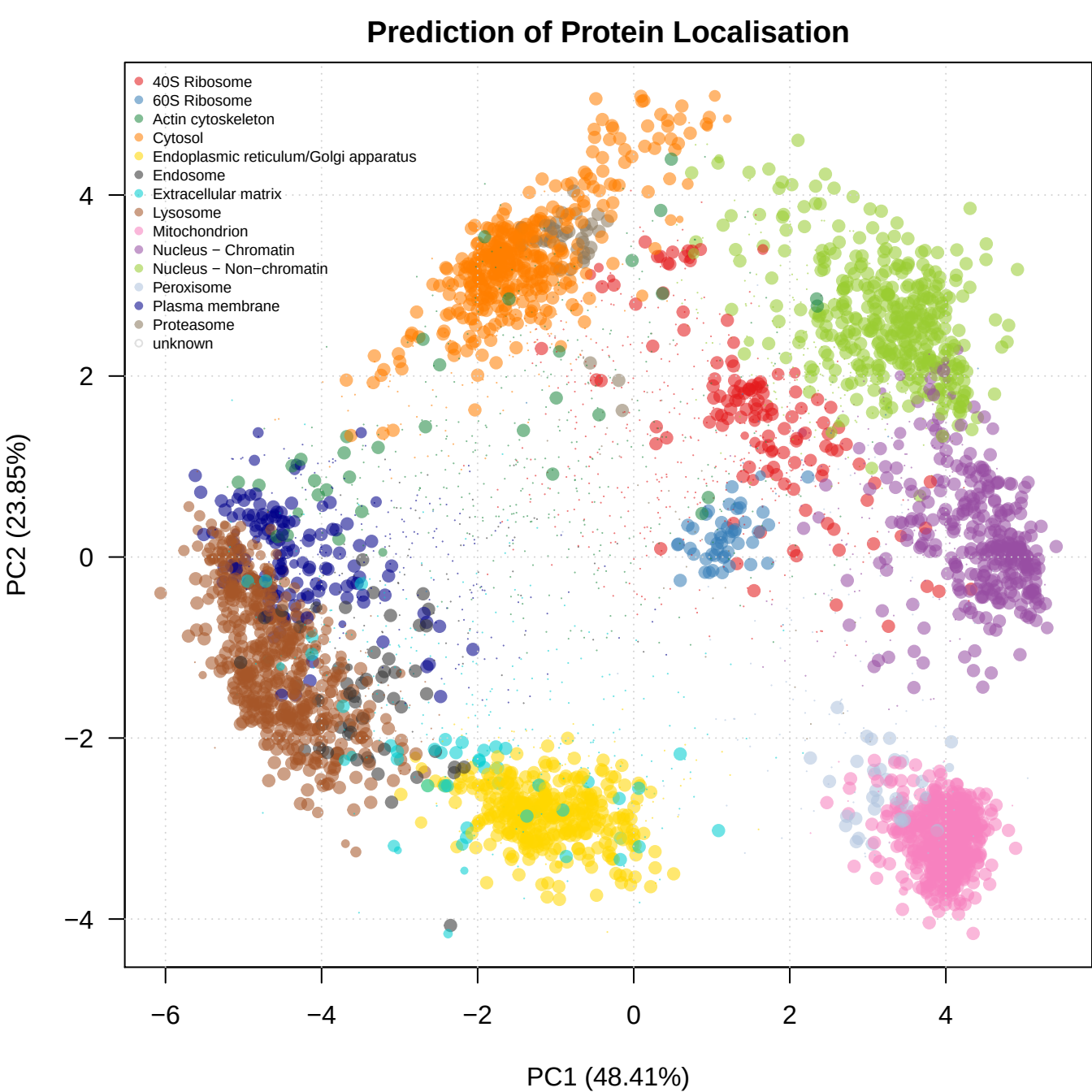
Profile of Protein Q8VDR9 with marker distributions

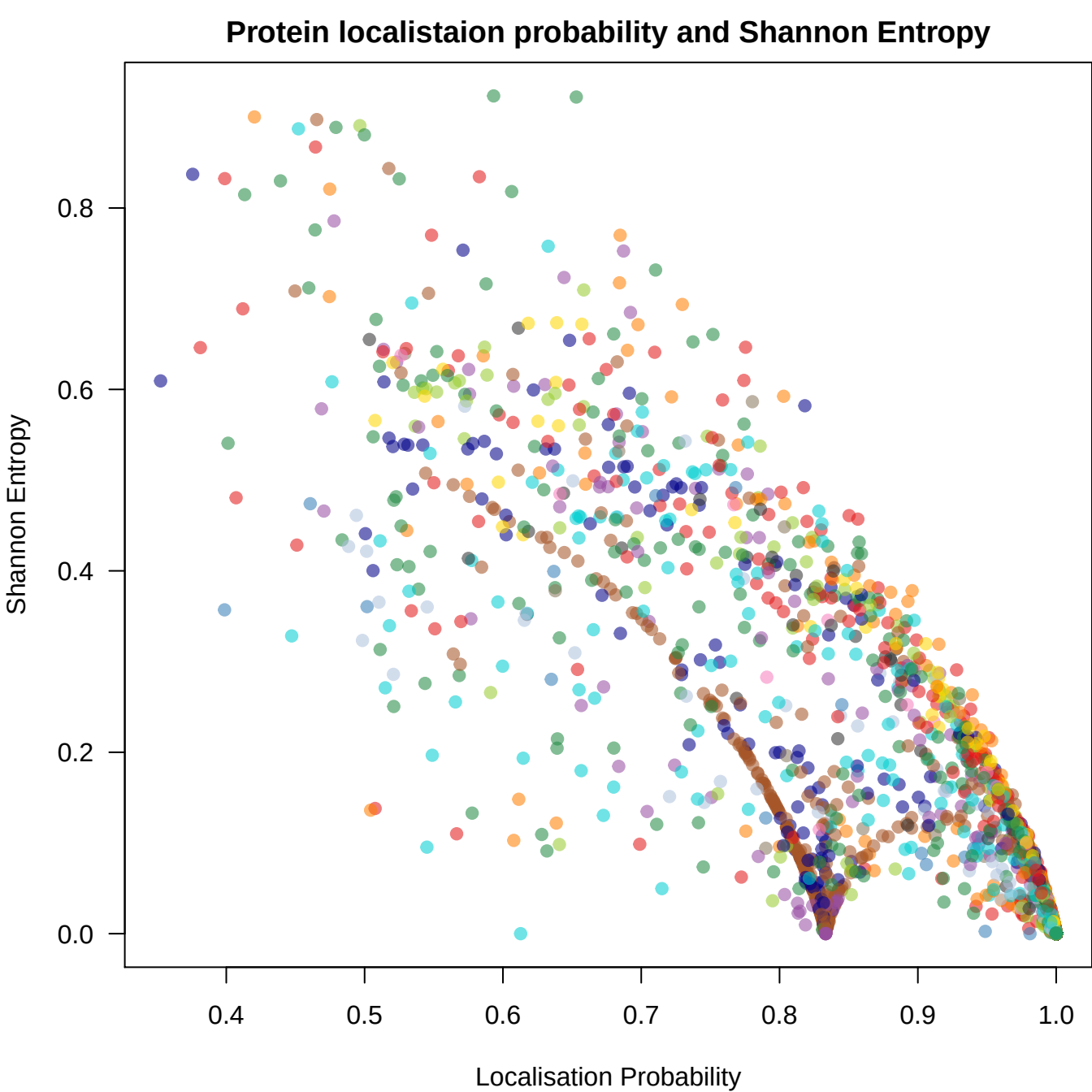


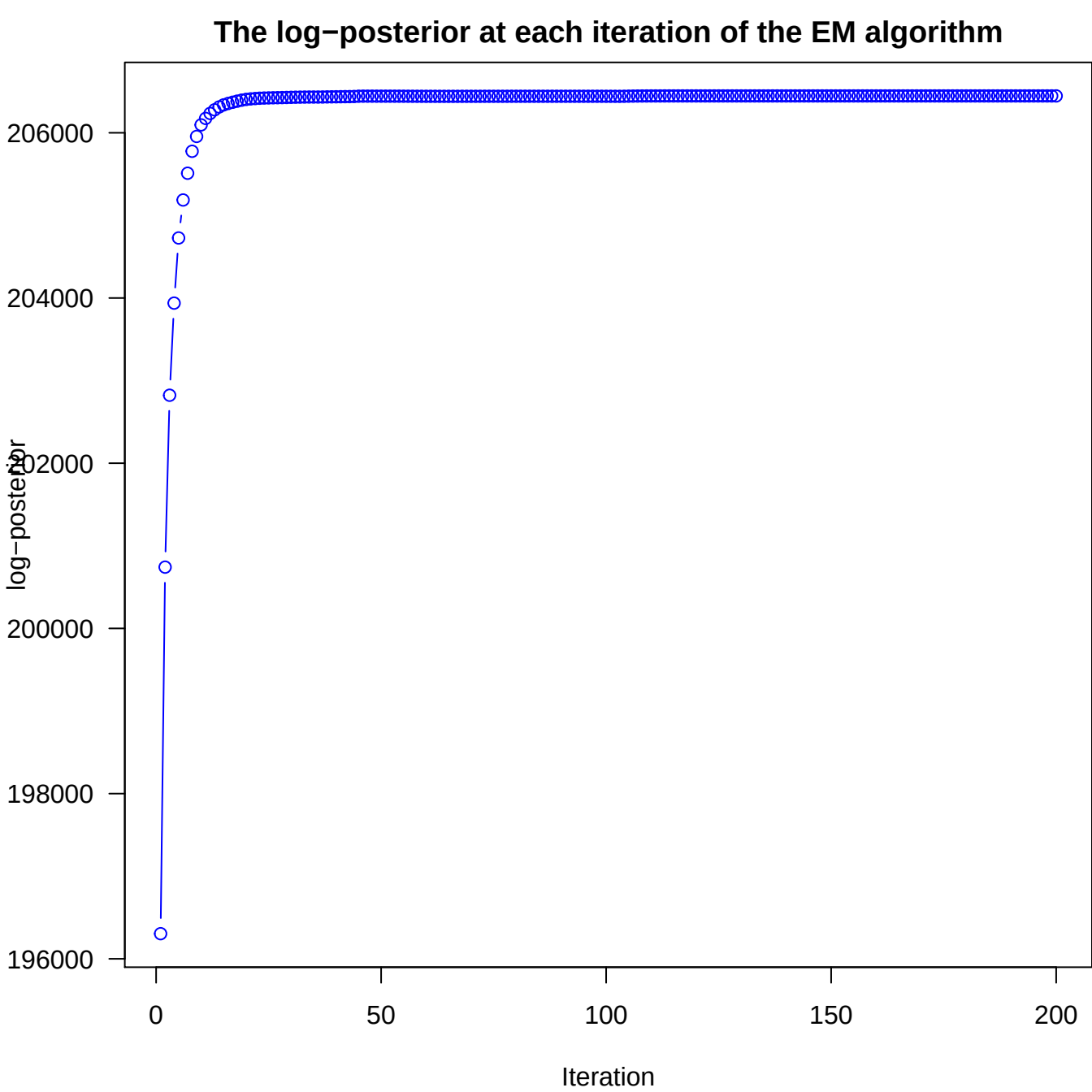

Density plot of Subcellular Membership for Protein Q8VDR9
Density
2
1
0
0.00
0.25
0.50
0.75
1.00
Membership Probability
Organelle
Endoplasmic reticulum/Golgi apparatus
Extracellular matrix

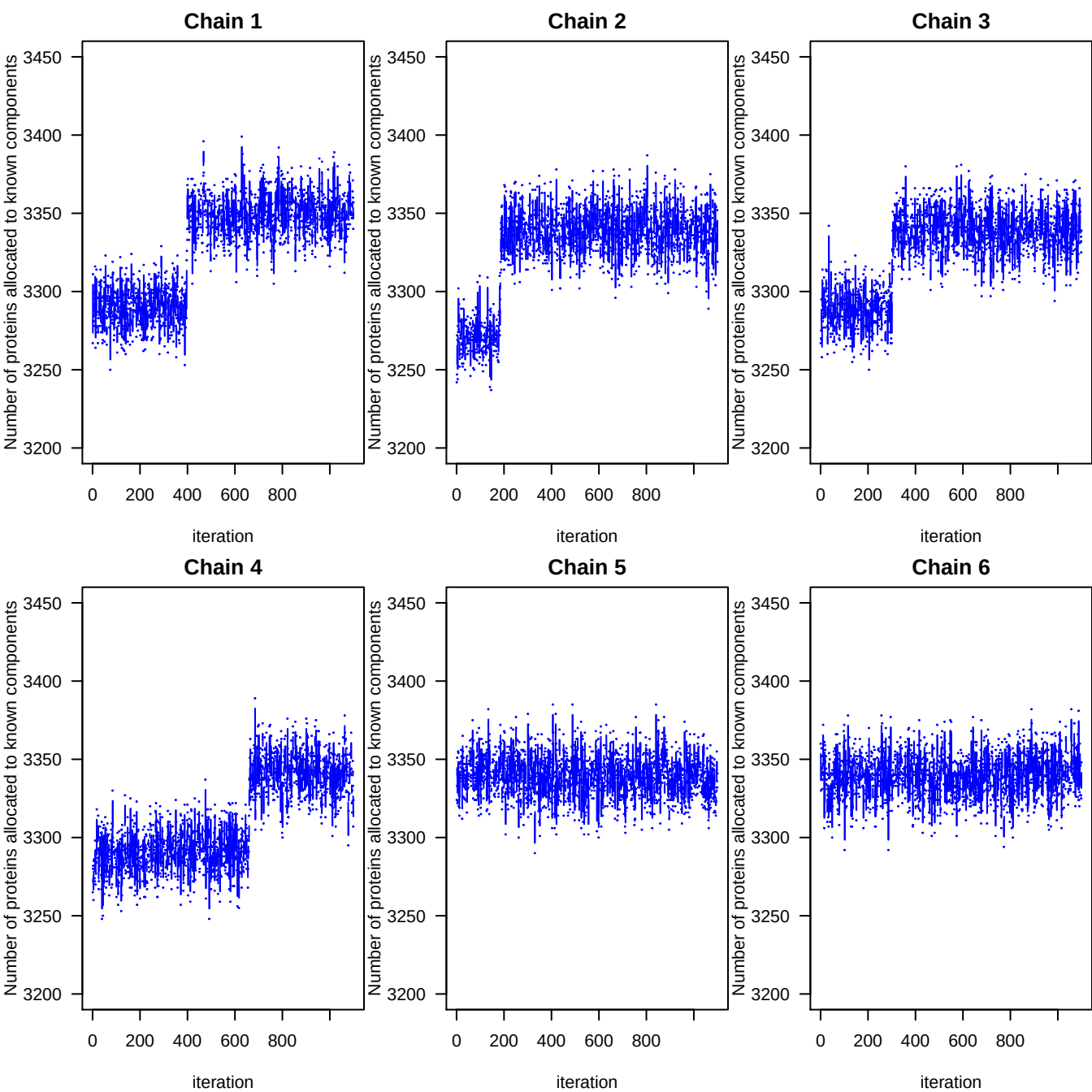

PCA plot with Protein Q8VDR9 indicated
Q8VDR9
40S Ribosome
60S Ribosome
Actin cytoskeleton
Cytosol
Endoplasmic reticulum/Golgi apparatus
Endosome
Extracellular matrix
Lysosome
Mitochondrion
Nucleus − Chromatin
Nucleus − Non−chromatin
Peroxisome
Plasma membrane
Proteasome
unknown
−6
−4
−2
0
2
4
PC1 (48.41%)


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