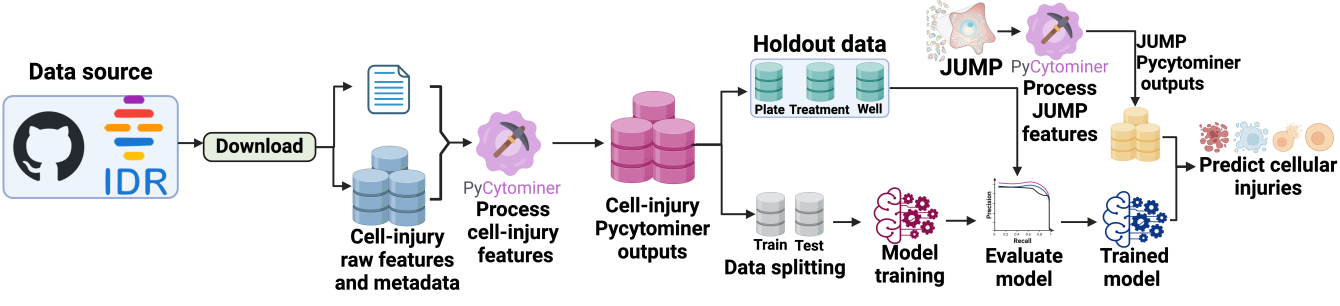
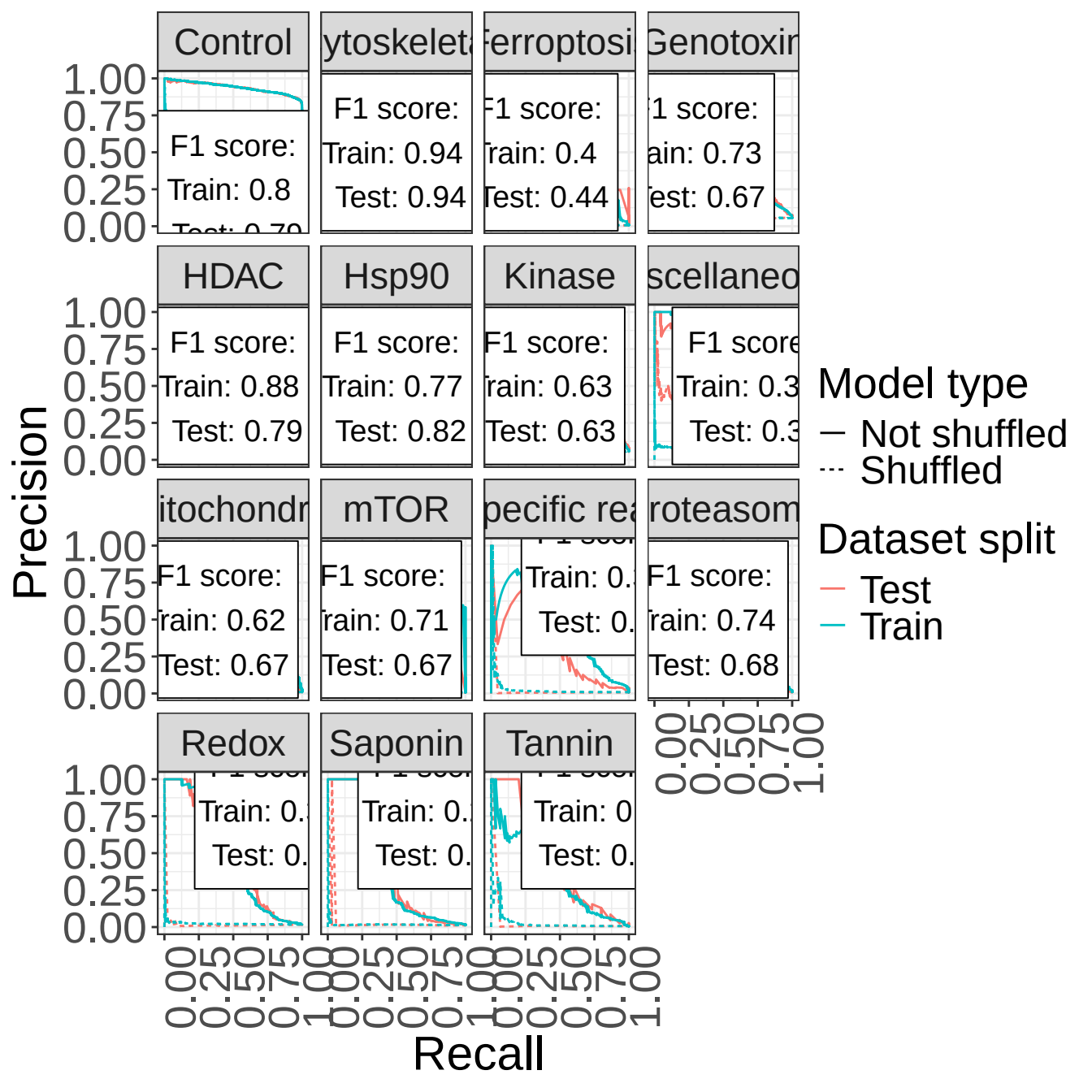
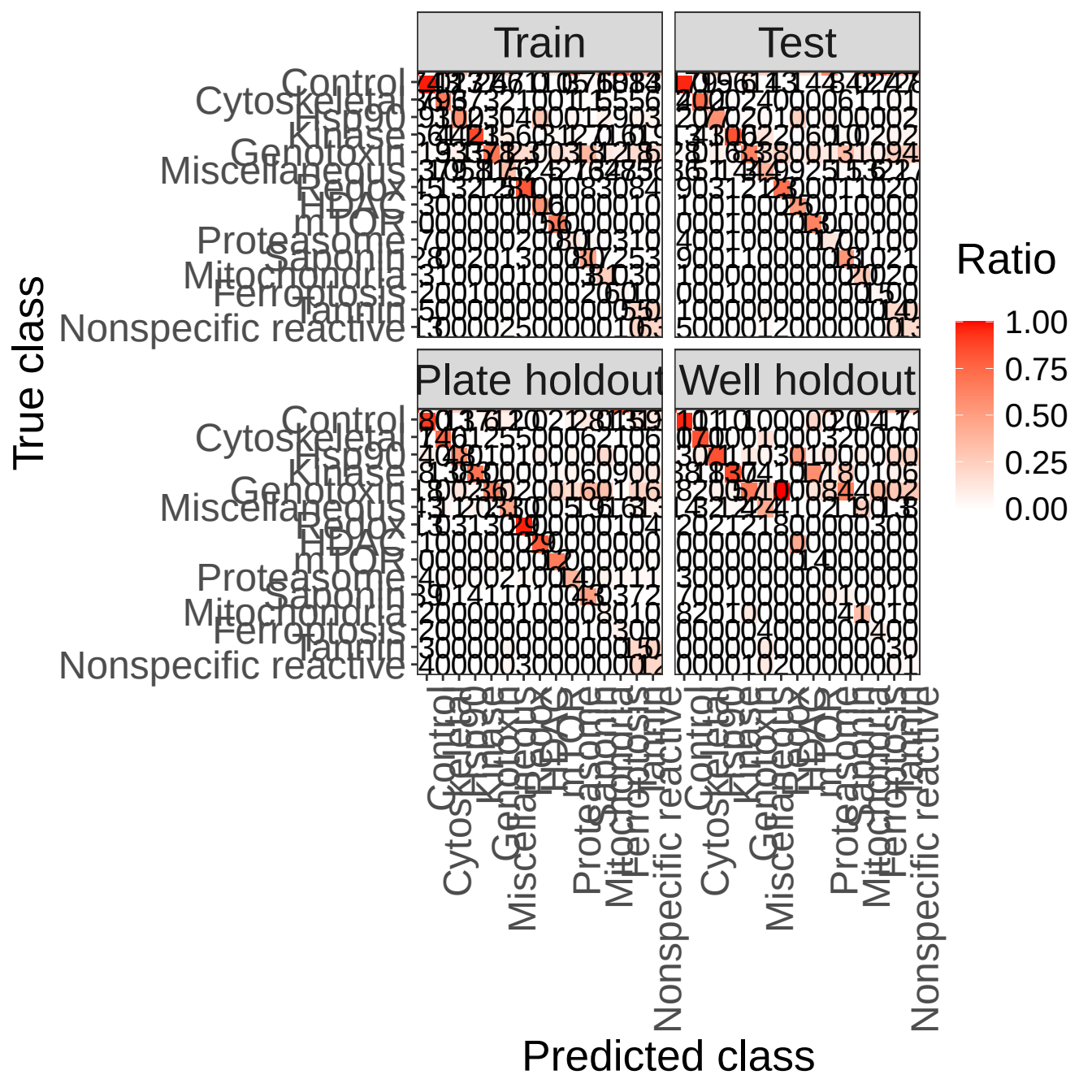
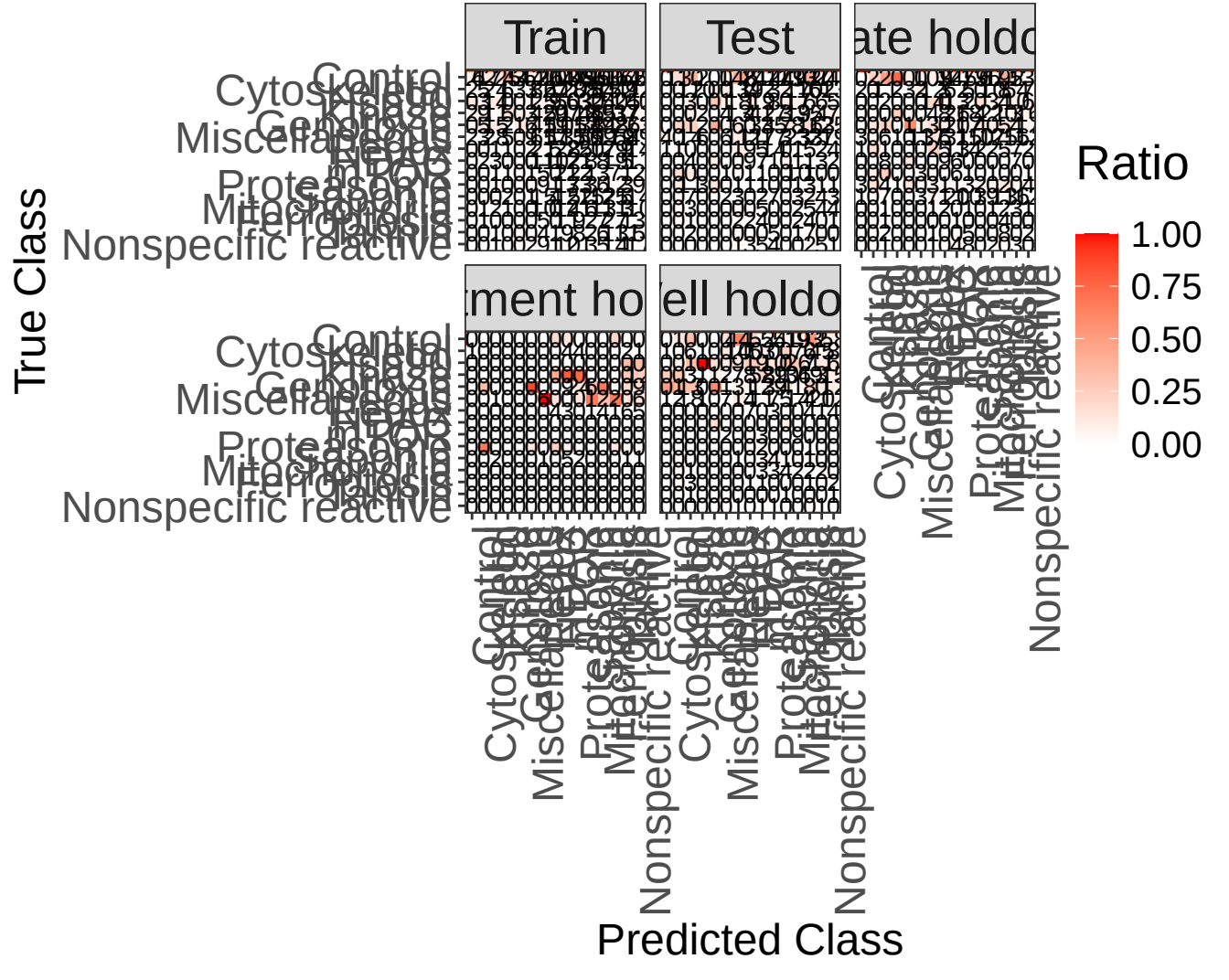
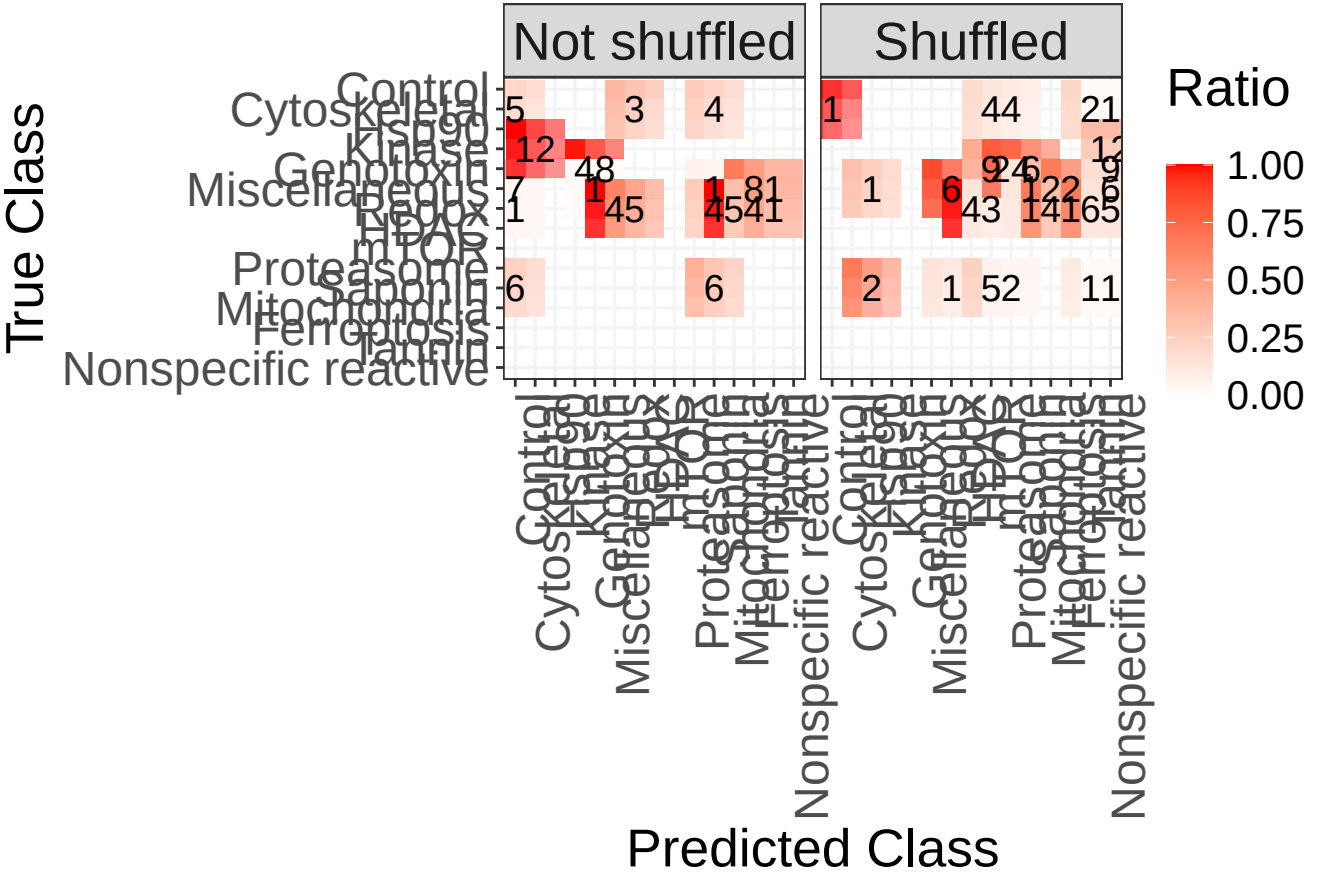
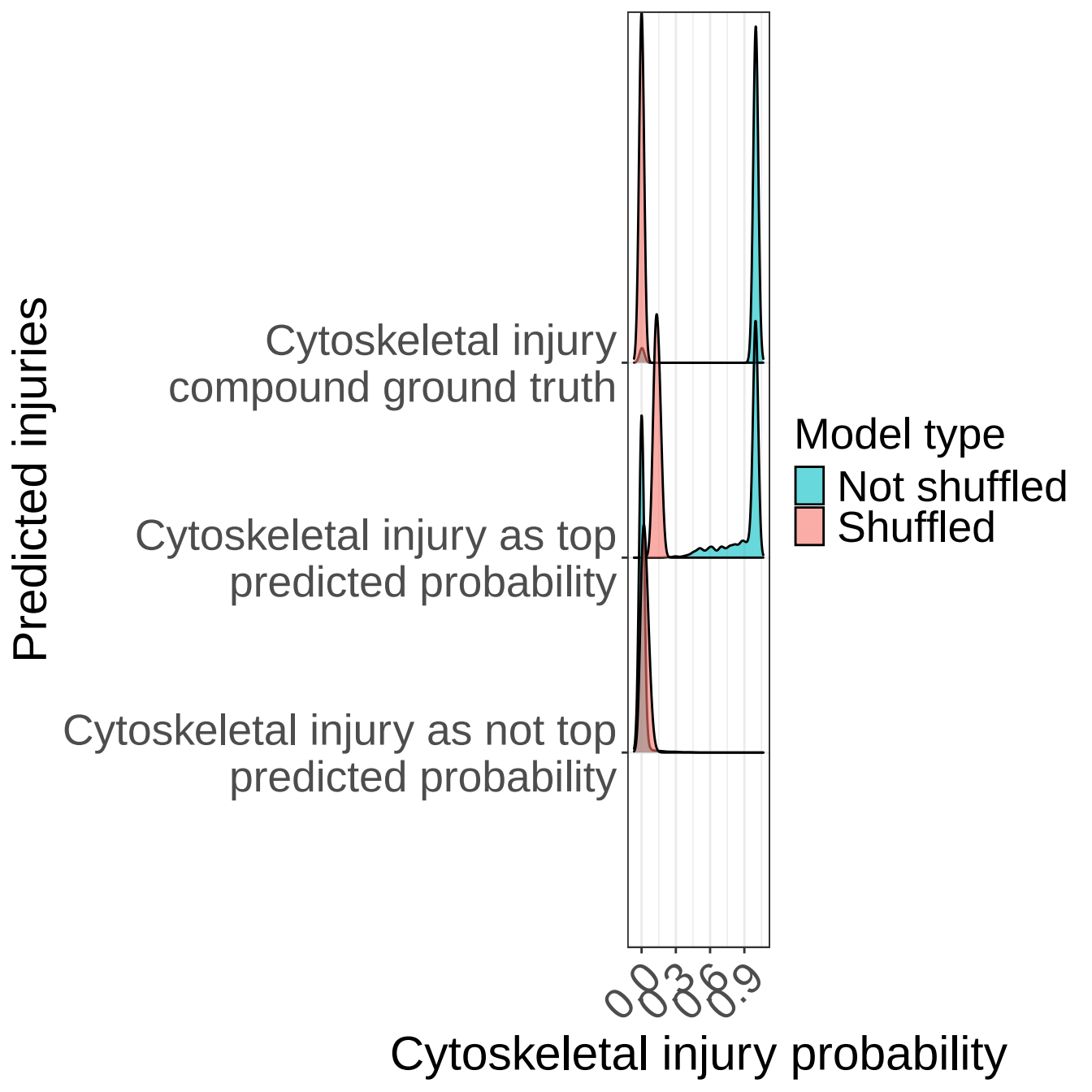

Data source
IDR
Download
Cell-injury raw features and metadata
PyCytominer
Process cell-injury features
Cell-injury Pycytominer outputs
Holdout data
Plate
Treatment
Well
Train
Test
Data splitting
Model training
Evaluate model
Trained model
JUMP
PyCytominer
Process JUMP features
JUMP Pycytominer outputs
Predict cellular injuries

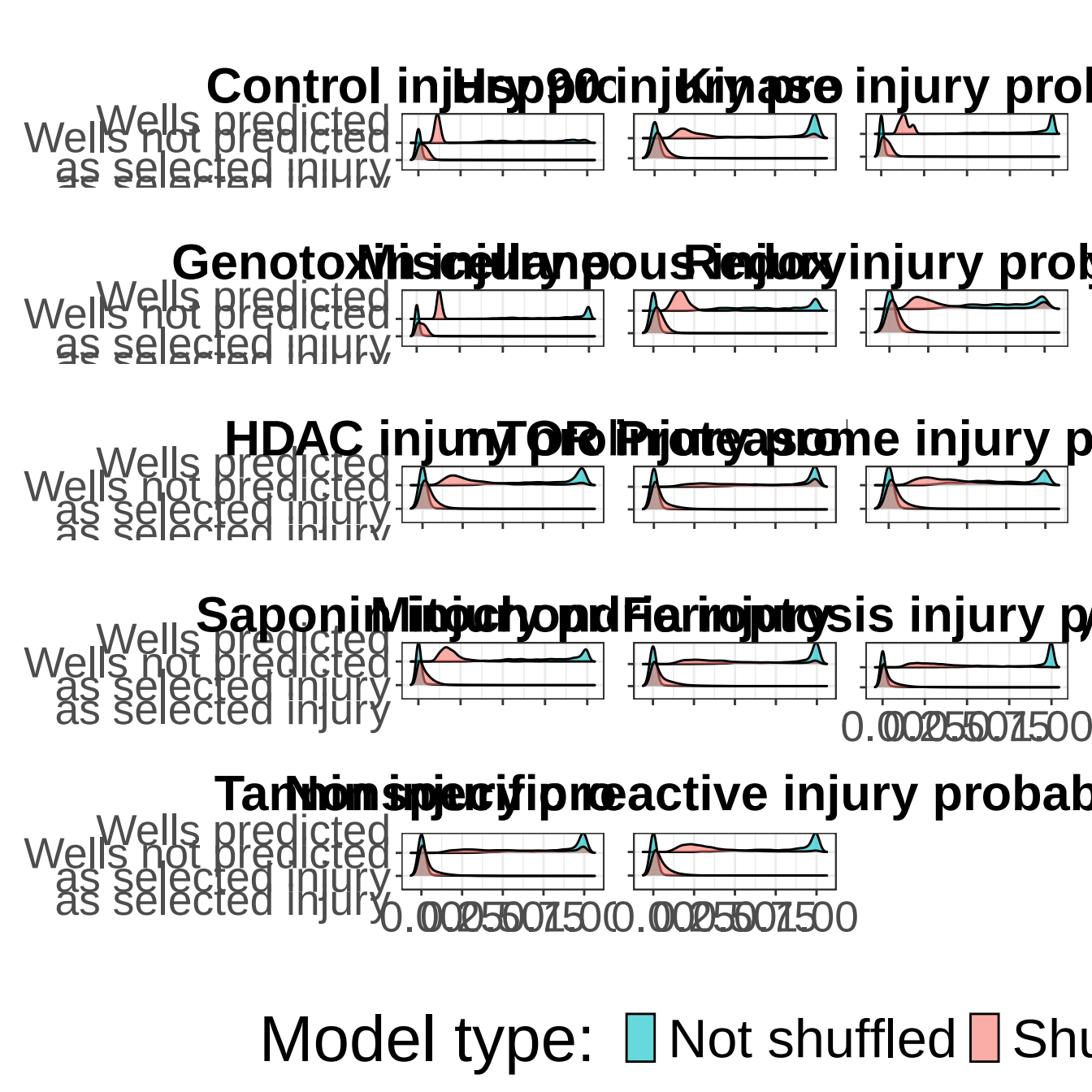

Control
F1 score:
Train: 0.8
ytoskelet
F1 score:
Train: 0.94
Test: 0.94
Ferroptosi
F1 score:
Train: 0.4
Test: 0.44
Genotoxin
1 score:
ain: 0.73
est: 0.67
HDAC
F1 score:
Train: 0.88
Test: 0.79
Hsp90
F1 score:
Train: 0.77
Test: 0.82
Kinase
F1 score:
rain: 0.63
Test: 0.63
scellaneo
F1 score
Train: 0.3
Test: 0.3
itochondr
F1 score:
rain: 0.62
Test: 0.67
mTOR
F1 score:
rain: 0.71
Test: 0.67
pecific rea
Train: 0.
Test: 0.
roteasom
F1 score:
rain: 0.74
Test: 0.68
Redox
Train: 0.
Test: 0.
Saponin
Train: 0.
Test: 0.
Tannin
Train: 0
Test: 0.
Precision
Recall
0.00
0.25
0.50
0.75
1.00
Model type
Not shuffled
Shuffled
Dataset split
Test
Train

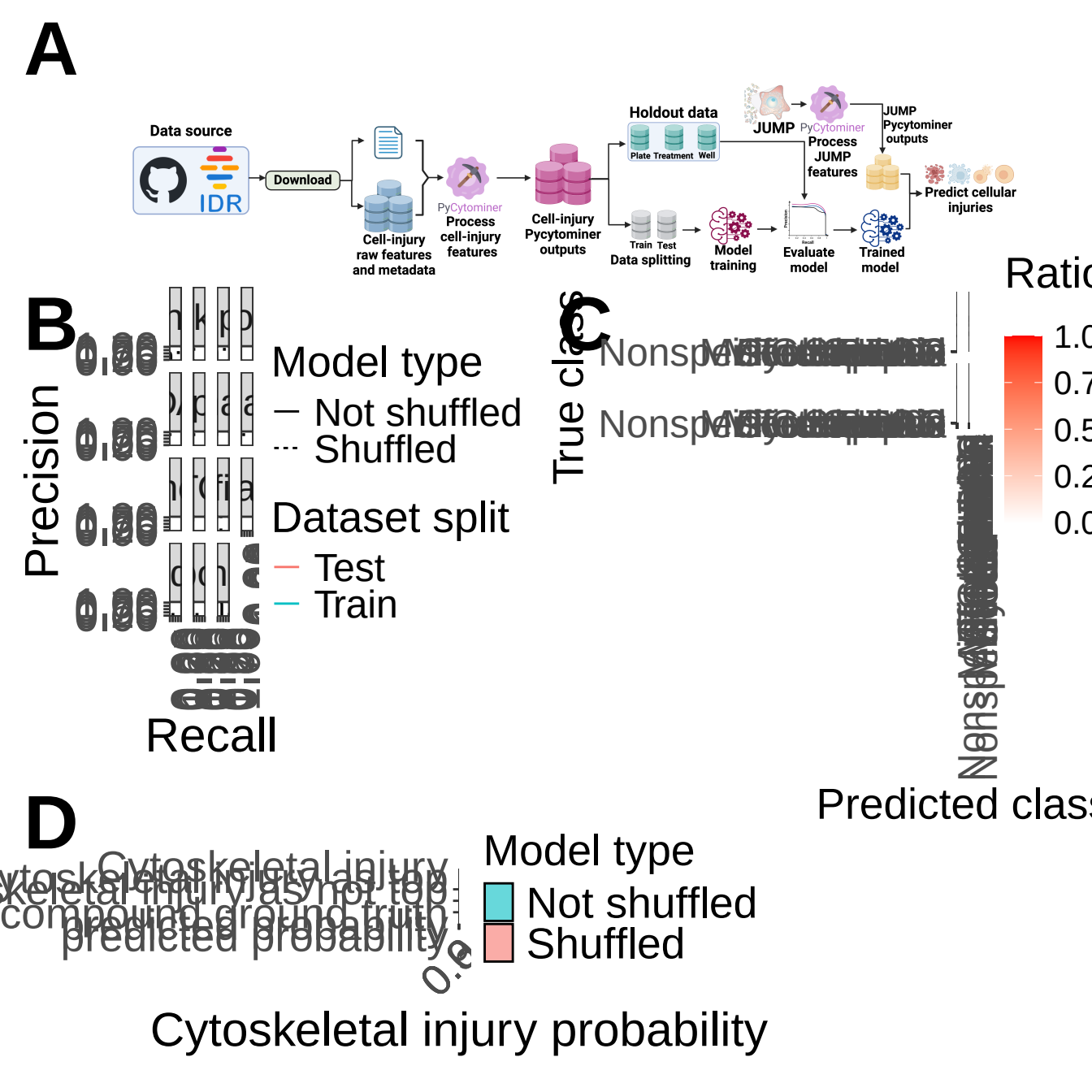

Train
Test
Plate holdout
Well holdout
True class
Predicted class
Ratio
1.00
0.75
0.50
0.25
0.00
Control
Cytoskeletal
Hsp90
Kinase
Genotoxin
Miscellaneous
Redox
HDAC
mTOR
Proteasome
Saponin
Mitochondria
Ferroptosis
Tannin
Nonspecific reactive


Train
Test
ate holdo
ment ho
ell holdo
True Class
Predicted Class
Control
Cytoskeletal
Kinase
Cell cycle
Miscellaneous
Receptor
DNA
Protease
Mitochondrial
Ferroptosis
Nonspecific reactive
Ratio
1.00
0.75
0.50
0.25
0.00


Not shuffled
Shuffled
True Class
Predicted Class
Ratio
1.00
0.75
0.50
0.25
0.00
Control
Cytoskeletal
Kinase
Genotoxin
Miscellaneous
Redox
HDAC
mTOR
Proteasome
Saponin
Mitochondria
Ferroptosis
Tannin
Nonspecific reactive


Predicted injuries
Cytoskeletal injury compound ground truth
Cytoskeletal injury as top predicted probability
Cytoskeletal injury as not top predicted probability
Model type
Not shuffled
Shuffled
0
0.3
0.6
0.9
Cytoskeletal injury probability


Control injury
Hsp90 injury
Kinase injury
Genotoxic injury
Microtubule injury
Ribosome injury
HDAC injury
mTOR injury
Proteasome injury
Saponin injury
Mitochondrial injury
Ferroptosis injury
Tannin injury
Nonspecific reactive injury
Wells predicted as selected injury
Wells not predicted as selected injury
0.00
0.25
0.50
0.75
1.00
Model type:
Not shuffled
Shu


A
Data source
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Cell-injury raw features and metadata
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Process cell-injury features
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Predict cellular injuries
Train Test
Data splitting
Model training
Evaluate model
Trained model
B
Precision
Recall
Model type
Not shuffled
Shuffled
Dataset split
Test
Train
C
True class
Predicted class
Ratio
1.0
0.7
0.5
0.2
0.0
D
Cytoskeletal injury
compound ground truth
predicted probability
Model type
Not shuffled
Shuffled
Cytoskeletal injury probability