**Table S1.**

Results of the first and second feature selection steps (first two sub-tables), and of the final classification (last sub-table) for the ER+/ER- classification task.

| Positive/Negative ER marker. Number of patients=80 (P=62.5%,N=37.5%). | | | | | | |
|---|---|---|---|---|---|---|
| **First feature selection step** | | | | | | |
| **Feature type** | **Image modality** | **Algorithm** | **Feature selection algorithm** | **Feature threshold t1** | **accuracy ± variance** | **f1score ± variance** |
| **radiomics from single modalities** | **ADC** | svm | no_alg | all | 0.56 ± 0.02 | 0.53 ± 0.03 |
| | | mlp | fisher | 45 | 0.61 ± 0.03 | 0.58 ± 0.02 |
| | | rf | fisher | 45 | 0.6 ± 0.03 | 0.56 ± 0.03 |
| | **PC** | dt | no_alg | all | 0.64 ± 0.01 | 0.6 ± 0.01 |
| | | dt | reliefF | 20 | 0.65 ± 0.03 | 0.62 ± 0.04 |
| | | svm | reliefF | 5 | 0.61 ± 0.02 | 0.6 ± 0.02 |
| | **SUB** | dt | no_alg | all | 0.53 ± 0.03 | 0.5 ± 0.03 |
| | | mlp | reliefF | 20 | 0.63 ± 0.05 | 0.59 ± 0.06 |
| | | knn | gini_index | 5 | 0.6 ± 0.02 | 0.59 ± 0.02 |
| | **T2** | mlp | no_alg | all | 0.7 ± 0.04 | 0.66 ± 0.05 |
| | | **mlp** | **fisher** | **45** | **0.73 ± 0.02** | **0.69 ± 0.02** |
| | | mlp | fisher | 35 | 0.7 ± 0.04 | 0.67 ± 0.04 |
| **radiomics from single modalities/clinical** | **ADC** | rf | no_alg | all | 0.59 ± 0.03 | 0.54 ± 0.03 |
| | | dt | gini_index | 30 | 0.6 ± 0.03 | 0.58 ± 0.04 |
| | | mlp | chi | 50 | 0.61 ± 0.03 | 0.57 ± 0.03 |
| | **PC** | dt | no_alg | all | 0.58 ± 0.02 | 0.5 ± 0.03 |
| | | dt | chi | 50 | 0.65 ± 0.03 | 0.62 ± 0.04 |
| | | dt | reliefF | 15 | 0.66 ± 0.02 | 0.62 ± 0.02 |
| | **SUB** | rf | no_alg | all | 0.63 ± 0.01 | 0.59 ± 0.01 |
| | | dt | reliefF | 5 | 0.66 ± 0.07 | 0.65 ± 0.07 |
| | | mlp | chi | 25 | 0.63 ± 0.05 | 0.6 ± 0.05 |
| | **T2** | mlp | no_alg | all | 0.69 ± 0.02 | 0.65 ± 0.03 |
| | | **mlp** | **fisher** | **25** | **0.7 ± 0.01** | **0.68 ± 0.01** |
| | | mlp | chi | 35 | 0.7 ± 0.03 | 0.66 ± 0.04 |
| **radiomics/clinical** | **ALL** | mlp | no_alg | all | 0.56 ± 0.04 | 0.51 ± 0.05 |
| | | **mlp** | **chi** | **50** | **0.68 ± 0.04** | **0.65 ± 0.04** |
| | | svm | chi | 50 | 0.61 ± 0.06 | 0.61 ± 0.06 |
| **radiomics** | **ALL** | mlp | no_alg | all | 0.58 ± 0.05 | 0.53 ± 0.06 |
| | | **mlp** | **chi** | **25** | **0.63 ± 0.03** | **0.59 ± 0.04** |
| | | mlp | reliefF | 15 | 0.63 ± 0.02 | 0.59 ± 0.02 |

| Second feature selection step | | | | | | |
|---|---|---|---|---|---|---|
| **Feature type** | **Image modality** | **Algorithm** | **Feature selection algorithm** | **Feature threshold t2** | **accuracy ± variance** | **f1score ± variance** |
| **radiomics from single modalities** | **T2** | **mlp** | **lr** | **11** | **0.74 ± 0.01** | **0.72 ± 0.01** |
| | | mlp | lr | 43 | 0.74 ± 0.03 | 0.71 ± 0.04 |
| **radiomics from single modalities/clinical \*** | **T2** | mlp | lr | 9 | 0.73 ± 0.02 | 0.68 ± 0.03 |

*only radiomics were selected

| Predictor building with the Leave-One-Out approach | | | | | | |
|---|---|---|---|---|---|---|
| **Feature type** | **Image modality** | **Algorithm** | **Feature selection algorithm** | **Feature number** | **accuracy** | **f1score** |
| **radiomics from single modalities** | **T2** | **svm** | no_alg | **11** | **0,81** | **0,85** |
| | | mlp | no_alg | 11 | 0,8 | 0,84 |

in **bold** = best result (F1score) for each "Feature type" section
in **red** = best result (F1score) among ALL the "Feature type" sections

**Table S2.**

Results of the first and second feature selection steps (first two sub-tables), and of the final classification (last sub-table) for the HER2+/HER2- classification task.

| | | | | | | |
|---|---|---|---|---|---|---|
| **Positive/Negative HER2 marker. Number of patients=80 (P=29%,N=71%)** <br> **First feature selection step** | | | | | | |
| **Feature type** | **Image modality** | **Algorithm** | **Feature selection algorithm** | **Feature threshold t1** | **accuracy ± variance** | **f1score ± variance** |
| radiomics from single modalities | ADC | dt | no_alg | all | 0.64 ± 0.02 | 0.56 ± 0.02 |
| | | **rf** | **reliefF** | **30** | **0.76 ± 0.01** | **0.7 ± 0.03** |
| | | mlp | gini_index | 5 | 0.71 ± 0.03 | 0.65 ± 0.05 |
| | PC | nb | no_alg | all | 0.66 ± 0.02 | 0.52 ± 0.03 |
| | | svm | reliefF | 5 | 0.66 ± 0.03 | 0.62 ± 0.04 |
| | | mlp | fisher | 15 | 0.64 ± 0.04 | 0.58 ± 0.06 |
| | SUB | nb | no_alg | all | 0.71 ± 0.03 | 0.58 ± 0.07 |
| | | knn | fisher | 5 | 0.7 ± 0.04 | 0.67 ± 0.04 |
| | | dt | fisher | 15 | 0.69 ± 0.02 | 0.62 ± 0.03 |
| | T2 | mlp | no_alg | all | 0.68 ± 0.03 | 0.59 ± 0.03 |
| | | dt | gini_index | 40 | 0.7 ± 0.01 | 0.63 ± 0.01 |
| | | dt | reliefF | 15 | 0.71 ± 0.02 | 0.63 ± 0.03 |
| radiomics from single modalities/clinical | ADC | dt | no_alg | all | 0.74 ± 0.02 | 0.67 ± 0.03 |
| | | **nb** | **reliefF** | **10** | **0.73 ± 0.02** | **0.69 ± 0.03** |
| | | svm | reliefF | 25 | 0.75 ± 0.02 | 0.67 ± 0.03 |
| | PC | nb | no_alg | all | 0.68 ± 0.02 | 0.54 ± 0.04 |
| | | mlp | gini_index | 20 | 0.66 ± 0.01 | 0.56 ± 0.02 |
| | | dt | chi | 5 | 0.66 ± 0.02 | 0.55 ± 0.04 |
| | SUB | nb | no_alg | all | 0.71 ± 0.03 | 0.58 ± 0.07 |
| | | nb | reliefF | 5 | 0.64 ± 0.02 | 0.62 ± 0.02 |
| | | mlp | chi | 30 | 0.69 ± 0.03 | 0.62 ± 0.04 |
| | T2 | nb | no_alg | all | 0.68 ± 0.04 | 0.57 ± 0.05 |
| | | nb | fisher | 50 | 0.68 ± 0.03 | 0.64 ± 0.02 |
| | | dt | reliefF | 50 | 0.71 ± 0.02 | 0.63 ± 0.03 |
| radiomics/clinical | ALL | nb | no_alg | all | 0.7 ± 0.02 | 0.59 ± 0.04 |
| | | **mlp** | **gini_index** | **10** | **0.73 ± 0.02** | **0.68 ± 0.02** |
| | | dt | reliefF | 50 | 0.71 ± 0.02 | 0.64 ± 0.02 |
| radiomics | ALL | dt | no_alg | all | 0.66 ± 0.02 | 0.6 ± 0.02 |
| | | **rf** | **reliefF** | **30** | **0.7 ± 0.01** | **0.62 ± 0.02** |
| | | knn | chi | 5 | 0.64 ± 0.04 | 0.6 ± 0.04 |

| | | | | | | |
|---|---|---|---|---|---|---|
| **Second feature selection step** | | | | | | |
| **Feature type** | **Image modality** | **Algorithm** | **Feature selection algorithm** | **Feature threshold t2** | **accuracy ± variance** | **f1score ± variance** |
| radiomics from single modalities | ADC | **knn** | **mi** | **27** | **0.74 ± 0.03** | **0.69 ± 0.05** |
| | | svm | mi | 42 | 0.73 ± 0.03 | 0.68 ± 0.04 |
| radiomics/clinical * | ALL | dt | cfs | 5 | 0.8 ± 0.02 | 0.75 ± 0.04 |

*only radiomics were selected

| | | | | | | |
|---|---|---|---|---|---|---|
| **Predictor building with the Leave-One-Out approach** | | | | | | |
| **Feature type** | **Image modality** | **Algorithm** | **Feature selection algorithm** | **Feature number** | **accuracy** | **f1score** |
| cliniche/radiomiche * | ALL | rf | no_alg | 5 | 0,8 | 0,64 |
| | | svm | no_alg | 5 | 0,74 | 0,64 |

in **bold** = best result (F1score) for each "Feature type" section
in **red** = best result (F1score) among ALL the "Feature type" sections

**Table S3.**

Results of the first and second feature selection steps (first two sub-tables), and of the final classification (last sub-table) for the KI67+/KI67- classification task.

| Feature type | Image modality | Algorithm | Feature selection algorithm | Feature threshold t1 | accuracy ± variance | f1score ± variance |
|---|---|---|---|---|---|---|
| **Positive/Negative  KI67 marker. Number of patients=78  (P=14%,N=86%)** | | | | | | |
| **First feature selection step** | | | | | | |
| radiomics from single modalities | ADC | svm | no_alg | all | 0.78 ± 0.03 | 0.61 ± 0.06 |
| | | nb | chi | 10 | 0.86 ± 0.01 | 0.69 ± 0.05 |
| | | rf | reliefF | 45 | 0.82 ± 0.03 | 0.68 ± 0.06 |
| | PC | svm | no_alg | all | 0.9 ± 0.01 | 0.69 ± 0.06 |
| | | **svm** | **chi** | **10** | **0.89 ± 0.01** | **0.77 ± 0.06** |
| | | rf | fisher | 5 | 0.86 ± 0.02 | 0.77 ± 0.05 |
| | SUB | dt | no_alg | all | 0.82 ± 0.01 | 0.64 ± 0.05 |
| | | rf | fisher | 30 | 0.88 ± 0 | 0.72 ± 0.03 |
| | | dt | reliefF | 50 | 0.9 ± 0.01 | 0.7 ± 0.07 |
| | T2 | svm | no_alg | all | 0.76 ± 0.03 | 0.57 ± 0.06 |
| | | nb | chi | 25 | 0.81 ± 0.02 | 0.67 ± 0.06 |
| | | dt | reliefF | 40 | 0.85 ± 0.02 | 0.66 ± 0.06 |
| radiomics from single modalities/clinical | ADC | svm | no_alg | all | 0.79 ± 0.03 | 0.64 ± 0.07 |
| | | dt | chi | 20 | 0.81 ± 0.02 | 0.68 ± 0.04 |
| | | nb | reliefF | 15 | 0.82 ± 0.02 | 0.67 ± 0.06 |
| | PC | svm | no_alg | all | 0.87 ± 0.01 | 0.67 ± 0.05 |
| | | **mlp** | **gini_index** | **5** | **0.85 ± 0.02** | **0.75 ± 0.05** |
| | | nb | fisher | 10 | 0.86 ± 0.02 | 0.74 ± 0.06 |
| | SUB | rf | no_alg | all | 0.82 ± 0.02 | 0.63 ± 0.07 |
| | | rf | fisher | 30 | 0.85 ± 0.01 | 0.69 ± 0.03 |
| | | dt | fisher | 5 | 0.81 ± 0.01 | 0.68 ± 0.04 |
| | T2 | dt | no_alg | all | 0.79 ± 0 | 0.59 ± 0.03 |
| | | rf | chi | 5 | 0.8 ± 0.02 | 0.71 ± 0.05 |
| | | dt | fisher | 30 | 0.8 ± 0.02 | 0.67 ± 0.05 |
| radiomics/clinical | ALL | dt | no_alg | all | 0.82 ± 0.01 | 0.57 ± 0.03 |
| | | **dt** | **chi** | **50** | **0.85 ± 0.01** | **0.72 ± 0.03** |
| | | dt | chi | 35 | 0.86 ± 0.02 | 0.71 ± 0.07 |
| radiomics | ALL | dt | no_alg | all | 0.77 ± 0.02 | 0.53 ± 0.04 |
| | | <span style="color:red">**dt**</span> | <span style="color:red">**fisher**</span> | <span style="color:red">**20**</span> | <span style="color:red">**0.87 ± 0.02**</span> | <span style="color:red">**0.79 ± 0.05**</span> |
| | | dt | fisher | 40 | 0.85 ± 0.01 | 0.7 ± 0.05 |

| Feature type | Image modality | Algorithm | Feature selection algorithm | Feature threshold t2 | accuracy ± variance | f1score ± variance |
|---|---|---|---|---|---|---|
| **Second feature selection step** | | | | | | |
| radiomics | ALL | **svm** | **lr** | **21** | **0.84 ± 0.02** | **0.7 ± 0.06** |
| | | mlp | cfs | 7 | 0.82 ± 0.02 | 0.7 ± 0.06 |
| radiomics from single modalities | PC | <span style="color:red">**mlp**</span> | <span style="color:red">**cfs**</span> | <span style="color:red">**1**</span> | <span style="color:red">**0.87 ± 0.02**</span> | <span style="color:red">**0.79 ± 0.05**</span> |
| | | mlp | cfs | 2 | 0.86 ± 0.03 | 0.78 ± 0.06 |

| Feature type | Image modality | Algorithm | Feature selection algorithm | Feature number | accuracy | f1score |
|---|---|---|---|---|---|---|
| **Predictor building with the Leave-One-Out approach** | | | | | | |
| radiomics from single modalities | PC | knn/svm * | no_alg | 1 | 0,88 | 0,93 |
| | | mlp | no_alg | 1 | 0,82 | 0,89 |
| | | svm * | no_alg | 2 | 0,88 | 0,93 |
| | | <span style="color:red">**mlp**</span> | <span style="color:red">**no_alg**</span> | <span style="color:red">**2**</span> | <span style="color:red">**0,85**</span> | <span style="color:red">**0,9**</span> |

\* predicts only a single class
in **bold** = best result (F1score) for each "Feature type" section
in <span style="color:red">red</span> = best result (F1score) among ALL the "Feature type" sections

**Table S4.**

Results of the first and second feature selection steps (first two sub-tables), and of the final classification (last sub-table) for the PR+/PR- classification task.

| Feature type | Image modality | Algorithm | Feature selection algorithm | Feature threshold t1 | accuracy ± variance | f1score ± variance |
|---|---|---|---|---|---|---|
| **Positive/Negative PR marker. Number of patients=80 (P=50%,N=50%)** <br> **First feature selection step** | | | | | | |
| **radiomics from single modalities** | **ADC** | svm | no_alg | all | 0.6 ± 0.03 | 0.59 ± 0.03 |
| | | mlp | fisher | 25 | 0.65 ± 0.02 | 0.64 ± 0.02 |
| | | svm | fisher | 30 | 0.64 ± 0.03 | 0.62 ± 0.03 |
| | **PC** | nb | no_alg | all | 0.61 ± 0.04 | 0.59 ± 0.05 |
| | | **knn** | **fisher** | **5** | **0.74 ± 0.03** | **0.73 ± 0.03** |
| | | knn | fisher | 25 | 0.7 ± 0.03 | 0.67 ± 0.04 |
| | **SUB** | mlp | no_alg | all | 0.54 ± 0.05 | 0.53 ± 0.06 |
| | | knn | fisher | 5 | 0.63 ± 0.04 | 0.61 ± 0.05 |
| | | svm | fisher | 15 | 0.61 ± 0.04 | 0.6 ± 0.04 |
| | **T2** | mlp | no_alg | all | 0.56 ± 0.02 | 0.55 ± 0.02 |
| | | mlp | fisher | 50 | 0.7 ± 0.02 | 0.68 ± 0.03 |
| | | mlp | gini_index | 35 | 0.69 ± 0.03 | 0.67 ± 0.04 |
| **radiomics from single modalities/clinical** | **ADC** | svm | no_alg | all | 0.61 ± 0.04 | 0.6 ± 0.04 |
| | | mlp | fisher | 25 | 0.65 ± 0.02 | 0.64 ± 0.02 |
| | | svm | fisher | 30 | 0.64 ± 0.03 | 0.62 ± 0.03 |
| | **PC** | nb | no_alg | all | 0.61 ± 0.04 | 0.59 ± 0.05 |
| | | **knn** | **fisher** | **5** | **0.74 ± 0.03** | **0.73 ± 0.03** |
| | | dt | chi | 5 | 0.66 ± 0.01 | 0.65 ± 0.01 |
| | **SUB** | mlp | no_alg | all | 0.5 ± 0.05 | 0.49 ± 0.05 |
| | | knn | fisher | 5 | 0.63 ± 0.04 | 0.61 ± 0.05 |
| | | mlp | reliefF | 5 | 0.61 ± 0.03 | 0.6 ± 0.03 |
| | **T2** | mlp | no_alg | all | 0.56 ± 0.02 | 0.54 ± 0.02 |
| | | mlp | fisher | 50 | 0.7 ± 0.02 | 0.68 ± 0.03 |
| | | mlp | gini_index | 25 | 0.66 ± 0.03 | 0.65 ± 0.03 |
| **radiomics/clinical** | **ALL** | mlp | no_alg | all | 0.64 ± 0.02 | 0.62 ± 0.03 |
| | | **mlp** | **reliefF** | **15** | **0.69 ± 0.06** | **0.67 ± 0.07** |
| | | mlp | fisher | 50 | 0.64 ± 0.04 | 0.61 ± 0.05 |
| **radiomics** | **ALL** | nb | no_alg | all | 0.59 ± 0.02 | 0.53 ± 0.04 |
| | | **mlp** | **reliefF** | **15** | **0.69 ± 0.06** | **0.67 ± 0.07** |
| | | mlp | fisher | 50 | 0.64 ± 0.04 | 0.61 ± 0.05 |

| Feature type | Image modality | Algorithm | Feature selection algorithm | Feature threshold t2 | accuracy ± variance | f1score ± variance |
|---|---|---|---|---|---|---|
| **Second feature selection step** | | | | | | |
| **radiomics from single modalities** | **PC** | **knn** | **lr** | **3** | **0.75 ± 0.02** | **0.74 ± 0.03** |
| | | nb | cfs | 6 | 0.73 ± 0.04 | 0.71 ± 0.04 |
| **radiomics** | **ALL** | **rf** | **lr** | **9** | **0.75 ± 0.02** | **0.73 ± 0.02** |

| Feature type | Image modality | Algorithm | Feature selection algorithm | Feature number | accuracy | f1score |
|---|---|---|---|---|---|---|
| **Predictor building with the Leave-One-Out approach** | | | | | | |
| **radiomics from single modalities** | **PC** | **mlp*** | **no_alg** | **3** | **0,73** | **0,73** |
| | | knn | no_alg | 3 | 0,74 | 0,72 |
| | | **nb** | **no_alg** | **6** | **0,73** | **0,74** |
| | | rf | no_alg | 6 | 0,68 | 0,68 |

*the method with the lowest feature number was selected as the best
in **bold** = best result (F1score) for each "Feature type" section
in **red** = best result (F1score) among ALL the "Feature type" sections

**Table S5**. Retrospective studies on predicting BC molecular subtypes. MORPH = morphology, IS = intensity-based statistics, LoG = Laplacian of Gaussian, WL = wavelet, ICCs = intra and inter correlations, PCCs = Pearson correlation coefficients, ANOVA = analysis of variance, mRMR = maximum relevance–minimum redundancy.

| First Author Year | # Patients | MRI Modality | Magnetic Field | Radiomic Feature Family | Feature Selection Algorithm | Validation on external dataset | Aim | Outcomes |
|---|---|---|---|---|---|---|---|---|
| *Huang et al[48] (2021)* | 162 | DCE T1, T2w fat sat, ADC maps | 3 T | MORPH, IS, GLCM, GLSZM, GLRLM, NGTDM, NGLDM, LoG and WL | ICCs, LASSO-RFE, mRMR, Boruta method and PCCs. | No | To predict molecular subtypes (ER, PR, HER2) and androgen receptor (AR) expression. | The MLP classifiers showed the best diagnostic performance in three molecular subtype classification tasks and in discriminating AR expression (AUC =0.907; accuracy = 85.8%). |
| *Kayadibi et al[50] (2022)* | 154 | DCE T1w fat sat FLASH, ADC maps | 1.5 T | MORPH, IS, GLCM, GLSZM, GLRLM, NGTDM, NGLDM, LoG and WL | ICC, LASSO | No | To investigate the value of MRI-based radioproteomics in predicting Ki67 expression levels. | The best model performance was achieved with 15 selected features from the ADC sequence based on the Ki67 cut-off value of 14%. |
| *Fan et al[51] (2019)* | 144 | DCE T1w fat sat, ADC maps | 3 T | MORPH, IS, GLCM | Multi task feature selection | No | To improve prediction accuracy of histological grade and Ki67 status based on tumor radiomic analysis. | Multi task learning models improve the prediction of Ki67 status and tumor grade. |
| *Zhong et al[52] (2022)* | 443 | DCE-MRI, | 3 T | IS, GLCM, Gabor and Law | Two-sample t-test, LASSO, Stepwise | No | To establish and validate the multiregional radiomic signatures for the preoperative identification of the ER and PR status. | Multiregional radiomic signatures achieved the best AUCs for evaluating the ER (0.851 and 0.833) and PR (0.848 and 0.763) status. |
| *Park et al[54] (2018)* | 294 | DCE T1w, T2w, PC T1w, SUB DCE T1w | 1.5 T | MORPH, IH, GLCM, GLSZM | ICC value of Rad-score | No | To establish a radiomics nomogram that incorporates the radiomics signature for disease free survival (DFS), MRI and | Higher Rad-scores were significantly associated with worse DFS in both the training and validation sets (P=0.002 and 0.036, respectively). The radiomics nomogram estimated DFS |

| Study | N | Sequences | Field | Features | Methods | Yes/No | Objective | Results |
|---|---|---|---|---|---|---|---|---|
| | | | | | | | clinicopathological findings. | better than the clinicopathological or Rad-score–only nomograms. |
| *Xie et al[55] (2019)* | 134 | T2w, T1w, DCE T1w, DWI | 3 T | MORPH, IS and texture features | ANOVA, CV, t-test, LASSO and ridge regression and elastic net, PCC | No | To classify immunohistochemical subtypes with ML analysis of mpMRI radiomics. | For 4-IHC classification task, the best accuracy of 72.4% was achieved based on linear discriminant analysis. For comparing TN to non-TN cancers, the highest accuracy of 91.0% was obtained with SVM and medium KNN. |
| *Liu et al[56] (2019)* | 586 | DCE T1w, T2w, DWI | | MORPH, IH, texture, Gabor and Law | Univariate analysis with the Mann-Whitney U test, PCC, Boruta method | Yes | To evaluate radiomics of mpMRI for pretreatment prediction of pathologic complete response to neoadjuvant chemotherapy. | Radiomic signature combining multiparametric MRI achieved an AUC of 0.79. |
| *Ni et al[57] (2020)* | 112 | DWI, T2w fat sat, T1w, T1w pre contrast fat sat, DCE T1w fat sat | 3 T | MORPH, IH, texture, GLSZM, GLCM and RLM | Remove outlier, PCC, mean center and standard deviation scale and noise processing | No | To investigate the feasibility of using a Fisher discriminant analysis model based on radiomic features of DWI for predicting the clinicopathological subtypes. | The overall accuracy for predicting the clinicopathological subtypes was 96.4% by Fisher discriminant analysis, and the weighted accuracy was 96.6%. |
| *Saha et al[58] (2018)* | 922 | T1w, T1w fat sat pre contrast, T1w post contrast, DCE | 1.5 – 3 T | MORPH, IS, texture (using spatial and no-spatial information) | -- | Yes | To investigate the associations of MRI-based imaging phenotypes with molecular, genomic, and proliferation markers (ER, PR, HER2 and Ki67). | Luminal A subtype with AUC = 0.697 (95% CI: 0.647–0.746, p < .0001), triple negative breast cancer with AUC = 0.654 (95% CI: 0.589–0.727, p < .0001), ER status with AUC = 0.649 (95% CI: 0.591–0.705, p < .001), and PR status with AUC = 0.622 (95% CI: 0.569–0.674, p < .0001). |