

Supplementary Table S1.

Optimization results of meth-SemiCancer and the machine-learning-based classifiers with the different combination of the parameters. Grid search was adopted for the model tuning, and the hyperparameters showing the best accuracy were selected.

meth-SemiCancer							
# of hidden nodes	Pre-training		Fine-tuning		Dropout	Alpha	Accuracy
	Learning rate	Training epoch	Learning rate	Training epoch			
1000-500	1e-5	1000	1e-3	2000	0.7	0.001	0.8018
1000-500	1e-5	1000	1e-3	2000	0.7	0.005	0.8113
1000-500	1e-5	1000	1e-3	2000	0.7	0.01	0.8113
1000-500	1e-5	1000	1e-3	2000	0.7	0.05	0.8018
1000-500	1e-5	1000	1e-3	2000	0.7	0.1	0.8018
1000-500	1e-5	1000	1e-3	2000	0.7	0.5	0.8018
1000-500	1e-3	1000	1e-3	2000	0.7	0.001	0.8113
1000-500	1e-3	1000	1e-3	2000	0.7	0.005	0.8113
1000-500	1e-3	1000	1e-3	2000	0.7	0.01	0.8207
1000-500	1e-3	1000	1e-3	2000	0.7	0.05	0.8207
1000-500	1e-3	1000	1e-3	2000	0.7	0.1	0.8113
1000-500	1e-3	1000	1e-3	2000	0.7	0.5	0.8113
1000-500	1e-5	1500	1e-3	3000	0.7	0.001	0.8301
1000-500	1e-5	1500	1e-3	3000	0.7	0.005	0.8301
1000-500	1e-5	1500	1e-3	3000	0.7	0.01	0.8301
1000-500	1e-5	1500	1e-3	3000	0.7	0.05	0.8490
1000-500	1e-5	1500	1e-3	3000	0.7	0.1	0.8301
1000-500	1e-5	1500	1e-3	3000	0.7	0.5	0.8207
1000-500	1e-3	1500	1e-3	3000	0.7	0.001	0.8207
1000-500	1e-3	1500	1e-3	3000	0.7	0.005	0.8207
1000-500	1e-3	1500	1e-3	3000	0.7	0.01	0.8301
1000-500	1e-3	1500	1e-3	3000	0.7	0.05	0.8301
1000-500	1e-3	1500	1e-3	3000	0.7	0.1	0.8301
1000-500	1e-3	1500	1e-3	3000	0.7	0.5	0.8207

Support vector machine (SVM)			
Kernel	Penalty parameter (C)	RBF kernel coeff (Gamma)	Accuracy
Linear	2 ⁻⁵	-	0.8066
Linear	2⁻³	-	0.8113
Linear	2 ⁻¹	-	0.7925
Linear	2 ¹	-	0.7925
Linear	2 ³	-	0.7925
Linear	2 ⁵	-	0.7925
RBF	2 ⁻⁵	2 ⁻¹⁵	0.5755
RBF	2 ⁻⁵	2 ⁻¹³	0.5755
RBF	2 ⁻⁵	2 ⁻¹¹	0.5755
RBF	2 ⁻⁵	2 ⁻⁹	0.5755
RBF	2 ⁻⁵	2 ⁻⁷	0.5755
RBF	2 ⁻⁵	2 ⁻⁵	0.5755
RBF	2 ⁻⁵	2 ⁻³	0.5755
RBF	2 ⁻⁵	2 ⁻¹	0.5755
RBF	2 ⁻⁵	2 ¹	0.5755
RBF	2 ⁻⁵	2 ³	0.5755
RBF	2 ⁻³	2 ⁻¹⁵	0.5755
RBF	2 ⁻³	2 ⁻¹³	0.5755
RBF	2 ⁻³	2 ⁻¹¹	0.5755
RBF	2 ⁻³	2 ⁻⁹	0.7547
RBF	2 ⁻³	2 ⁻⁷	0.7547
RBF	2 ⁻³	2 ⁻⁵	0.5991
RBF	2 ⁻³	2 ⁻³	0.5755
RBF	2 ⁻³	2 ⁻¹	0.5755
RBF	2 ⁻³	2 ¹	0.5755
RBF	2 ⁻³	2 ³	0.5755
RBF	2 ⁻¹	2 ⁻¹⁵	0.5755
RBF	2 ⁻¹	2 ⁻¹³	0.5755
RBF	2 ⁻¹	2 ⁻¹¹	0.7547
RBF	2 ⁻¹	2 ⁻⁹	0.7500
RBF	2 ⁻¹	2 ⁻⁷	0.7830
RBF	2 ⁻¹	2 ⁻⁵	0.7170
RBF	2 ⁻¹	2 ⁻³	0.5755
RBF	2 ⁻¹	2 ⁻¹	0.5755
RBF	2 ⁻¹	2 ¹	0.5755
RBF	2 ⁻¹	2 ³	0.5755
RBF	2 ¹	2 ⁻¹⁵	0.5755

RBF	2 ¹	2 ⁻¹³	0.7547
RBF	2 ¹	2 ⁻¹¹	0.7594
RBF	2 ¹	2 ⁻⁹	0.8019
RBF	2 ¹	2 ⁻⁷	0.7972
RBF	2 ¹	2 ⁻⁵	0.7311
RBF	2 ¹	2 ⁻³	0.5708
RBF	2 ¹	2 ⁻¹	0.5755
RBF	2 ¹	2 ¹	0.5755
RBF	2 ¹	2 ³	0.5755
RBF	2 ³	2 ⁻¹⁵	0.7547
RBF	2 ³	2 ⁻¹³	0.7642
RBF	2 ³	2 ⁻¹¹	0.7972
RBF	2 ³	2 ⁻⁹	0.8019
RBF	2 ³	2 ⁻⁷	0.8066
RBF	2 ³	2 ⁻⁵	0.7264
RBF	2 ³	2 ⁻³	0.5708
RBF	2 ³	2 ⁻¹	0.5755
RBF	2 ³	2 ¹	0.5755
RBF	2 ³	2 ³	0.5755
RBF	2 ⁵	2 ⁻¹⁵	0.7642
RBF	2 ⁵	2 ⁻¹³	0.7972
RBF	2 ⁵	2 ⁻¹¹	0.7972
RBF	2 ⁵	2 ⁻⁹	0.8066
RBF	2 ⁵	2 ⁻⁷	0.8066
RBF	2 ⁵	2 ⁻⁵	0.7264
RBF	2 ⁵	2 ⁻³	0.5708
RBF	2 ⁵	2 ⁻¹	0.5755
RBF	2 ⁵	2 ¹	0.5755
RBF	2 ⁵	2 ³	0.5755

Random Forest (RF)			
Split criteria (criterion)	# of trees (estimators)	The minimum # of samples in a leaf node (min_samples_leaf)	Accruacy
Gini impurity	100	1	0.7689
Gini impurity	100	2	0.7736
Gini impurity	100	3	0.8019
Gini impurity	100	4	0.7547
Gini impurity	100	5	0.7830
Gini impurity	300	1	0.7500
Gini impurity	300	2	0.7783
Gini impurity	300	3	0.7736
Gini impurity	300	4	0.7736
Gini impurity	300	5	0.7594
Gini impurity	500	1	0.7783
Gini impurity	500	2	0.7736
Gini impurity	500	3	0.7547
Gini impurity	500	4	0.7547
Gini impurity	500	5	0.7736
Gini impurity	700	1	0.7642
Gini impurity	700	2	0.7547
Gini impurity	700	3	0.7736
Gini impurity	700	4	0.7689
Gini impurity	700	5	0.7736
Gini impurity	900	1	0.7736
Gini impurity	900	2	0.7689
Gini impurity	900	3	0.7689
Gini impurity	900	4	0.7783
Gini impurity	900	5	0.7689
Information gain	100	1	0.7830
Information gain	100	2	0.7689
Information gain	100	3	0.7830
Information gain	100	4	0.7783
Information gain	100	5	0.7689
Information gain	300	1	0.7783
Information gain	300	2	0.7736
Information gain	300	3	0.7642
Information gain	300	4	0.7736
Information gain	300	5	0.7830

Information gain	500	1	0.7830
Information gain	500	2	0.7689
Information gain	500	3	0.7972
Information gain	500	4	0.8019
Information gain	500	5	0.7736
Information gain	700	1	0.7877
Information gain	700	2	0.7783
Information gain	700	3	0.7783
Information gain	700	4	0.7736
Information gain	700	5	0.7689
Information gain	900	1	0.7783
Information gain	900	2	0.7736
Information gain	900	3	0.7830
Information gain	900	4	0.7783
Information gain	900	5	0.7736

Logistic Regression (LR)

max_iter (Maximum number of iterations to converge)	Penalty parameter (C)	Accuracy
100	2 ⁻⁵	0.7925
100	2 ⁻³	0.8113
100	2⁻¹	0.8302
100	2 ¹	0.8255
100	2 ³	0.8302
100	2 ⁵	0.8255
200	2 ⁻⁵	0.7925
200	2 ⁻³	0.8113
200	2 ⁻¹	0.8302
200	2 ¹	0.8255
200	2 ³	0.8302
200	2 ⁵	0.8255
300	2 ⁻⁵	0.7925
300	2 ⁻³	0.8113
300	2 ⁻¹	0.8302
300	2 ¹	0.8255
300	2 ³	0.8302
300	2 ⁵	0.8255
400	2 ⁻⁵	0.7925
400	2 ⁻³	0.8113
400	2 ⁻¹	0.8302
400	2 ¹	0.8255
400	2 ³	0.8302
400	2 ⁵	0.8255
500	2 ⁻⁵	0.7925
500	2 ⁻³	0.8113
500	2 ⁻¹	0.8302
500	2 ¹	0.8255
500	2 ³	0.8302
500	2 ⁵	0.8255

Supplementary Table S2.

Average breast cancer subtype classification performance results of BCtypeFinder with other methods for 87 samples of GSE72245 dataset.

Metric	BCtypeFinder	meth-SemiCancer	SVM	RF	LR
Accuracy	0.816	0.736	0.655	0.545	0.667
F1-score	0.822	0.748	0.668	0.505	0.673
MCC	0.752	0.664	0.603	0.522	0.623
AUC	0.883	0.848	0.811	0.747	0.825

Supplementary Table S3.

Average classification performance results of BCtypeFinder with other comparison methods based on the 10-fold cross validation on TCGA-BRCA dataset.

Metric	BCtypeFinder	meth-SemiCancer	SVM	RF	LR
Accuracy	0.849	0.814	0.811	0.764	0.821
F1-score	0.843	0.803	0.807	0.734	0.814
MCC	0.763	0.707	0.703	0.621	0.716
AUC	0.845	0.819	0.83	0.745	0.825

Supplementary Table S4.

Performance improvement results of BCtypeFinder testing GSE72245 dataset by measuring the prediction performance on each training phase.

Metric	Pre-training	SSL	SSL + Subtype alignment
Accuracy	0.720	0.730	0.816
F1-score	0.723	0.731	0.822
MCC	0.673	0.678	0.752
AUC	0.856	0.857	0.883