FeCO3, constructing the network biomarkers using the inter-feature correlation coefficients

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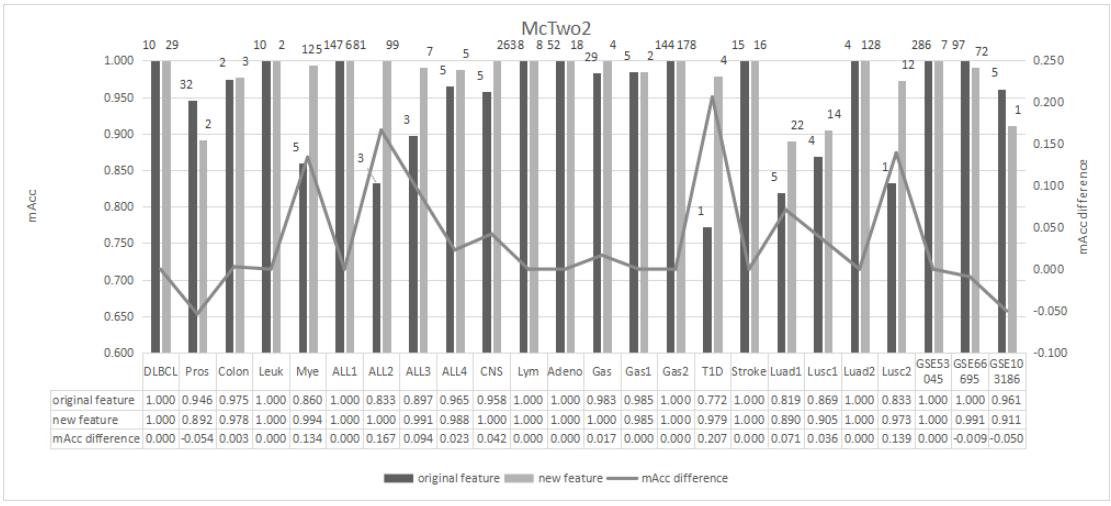
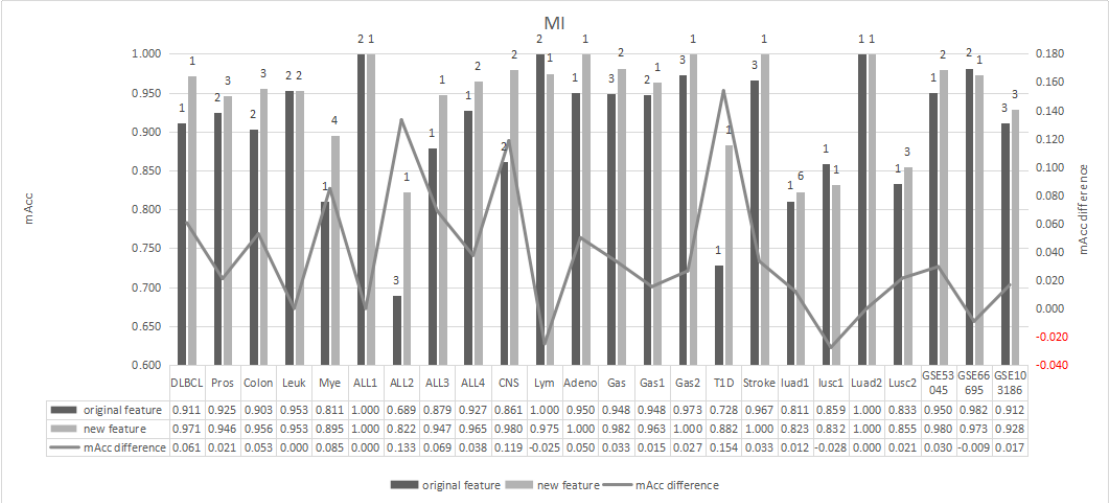
Supplementary Figure S1



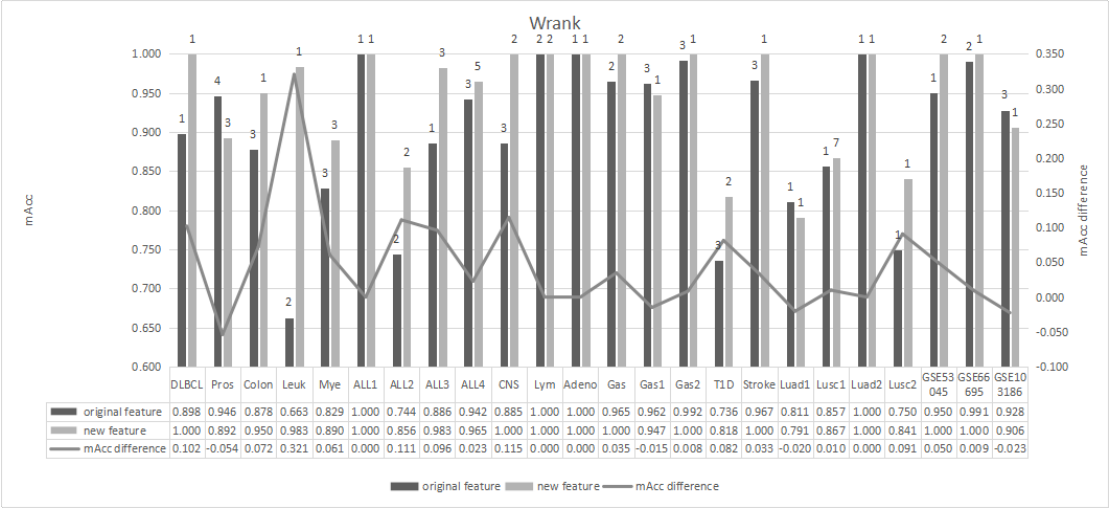
	DLBCL	Pros	Colon	Leuk	Mye	ALL1	ALL2	ALL3	ALL4	CNS	Lym	Adeno	Gas	Gas1	Gas2	T1D	Stroke	Luad1	Lusc1	Luad2	Lusc2	GSE5345	GSE6695	GSE103186
original feature	1.000	0.946	0.975	1.000	0.860	1.000	0.833	0.897	0.965	0.958	1.000	1.000	0.983	0.985	1.000	0.772	1.000	0.819	0.869	1.000	0.833	1.000	1.000	0.961
new feature	1.000	0.892	0.978	1.000	0.994	1.000	1.000	0.991	0.988	1.000	1.000	1.000	1.000	0.985	1.000	0.979	1.000	0.890	0.905	1.000	0.973	1.000	0.991	0.911
mAcc difference	0.000	-0.054	0.003	0.000	0.134	0.000	0.167	0.094	0.023	0.042	0.000	0.000	0.017	0.000	0.000	0.207	0.000	0.071	0.036	0.000	0.139	0.000	-0.009	-0.050

Comparison of the classification metric mAcc and the number of features between the original features and the FeCO3 features using the feature selection algorithm McTwo2. The series “original” gives the data of the original features, and the series “FeCO3” illustrates the status of the FeCO3 features. The series “Improvement” is the mAcc value of the FeCO3 features minus the mAcc value of the original features. The classification accuracy is calculated using the 5-fold cross validation strategy. The data was calculated using the feature selection algorithms



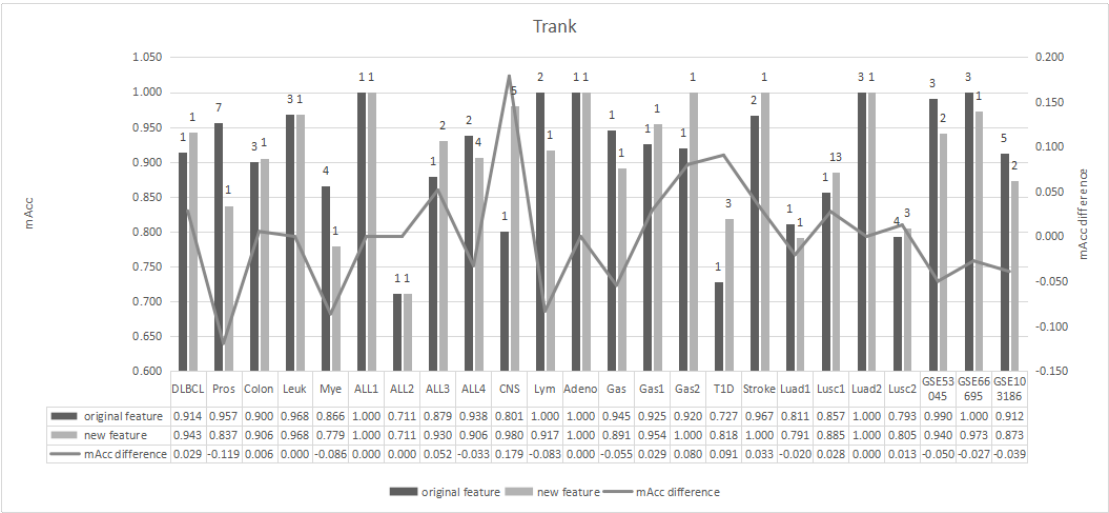
	DLBCL	Pros	Colon	Leuk	Mye	ALL1	ALL2	ALL3	ALL4	CNS	Lym	Adeno	Gas	Gas1	Gas2	T1D	Stroke	luad1	lusc1	Luad2	Lusc2	GSE5345	GSE6695	GSE103186
original feature	0.911	0.925	0.903	0.953	0.811	1.000	0.689	0.879	0.927	0.861	1.000	0.950	0.948	0.948	0.973	0.728	0.967	0.811	0.859	1.000	0.833	0.950	0.982	0.912
new feature	0.971	0.946	0.956	0.953	0.895	1.000	0.822	0.947	0.965	0.980	0.975	1.000	0.982	0.963	1.000	0.882	1.000	0.823	0.832	1.000	0.855	0.980	0.973	0.928
mAcc difference	0.061	0.021	0.053	0.000	0.085	0.000	0.133	0.069	0.038	0.119	-0.025	0.050	0.033	0.015	0.027	0.154	0.033	0.012	-0.028	0.000	0.021	0.030	-0.009	0.017

Comparison of the classification metric mAcc and the number of features between the original features and the FeCO3 features using the feature selection algorithm MI. The series “original” gives the data of the original features, and the series “FeCO3” illustrates the status of the FeCO3 features. The series “Improvement” is the mAcc value of the FeCO3 features minus the mAcc value of the original features. The classification accuracy is calculated using the 5-fold cross validation strategy. The data was calculated using the feature selection algorithms



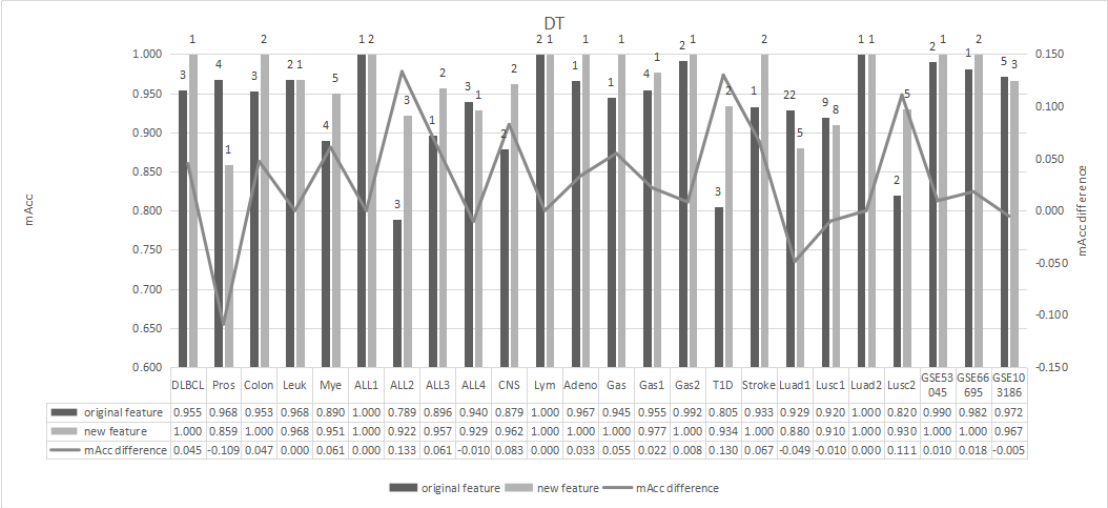
	DLBCL	Pros	Colon	Leuk	Mye	ALL1	ALL2	ALL3	ALL4	CNS	Lym	Adeno	Gas	Gas1	Gas2	T1D	Stroke	Luad1	Lusc1	Luad2	Lusc2	GSE53045	GSE6695	GSE103186
original feature	0.898	0.946	0.878	0.663	0.829	1.000	0.744	0.886	0.942	0.885	1.000	1.000	0.965	0.962	0.992	0.736	0.967	0.811	0.857	1.000	0.750	0.950	0.991	0.928
new feature	1.000	0.892	0.950	0.983	0.890	1.000	0.856	0.983	0.965	1.000	1.000	1.000	1.000	0.947	1.000	0.818	1.000	0.791	0.867	1.000	0.841	1.000	1.000	0.906
mAcc difference	0.102	-0.054	0.072	0.321	0.061	0.000	0.111	0.096	0.023	0.115	0.000	0.000	0.035	-0.015	0.008	0.082	0.033	-0.020	0.010	0.000	0.091	0.050	0.009	-0.023

Comparison of the classification metric mAcc and the number of features between the original features and the FeCO3 features using the feature selection algorithm Wrank. The series “original” gives the data of the original features, and the series “FeCO3” illustrates the status of the FeCO3 features. The series “Improvement” is the mAcc value of the FeCO3 features minus the mAcc value of the original features. The classification accuracy is calculated using the 5-fold cross validation strategy. The data was calculated using the feature selection algorithms



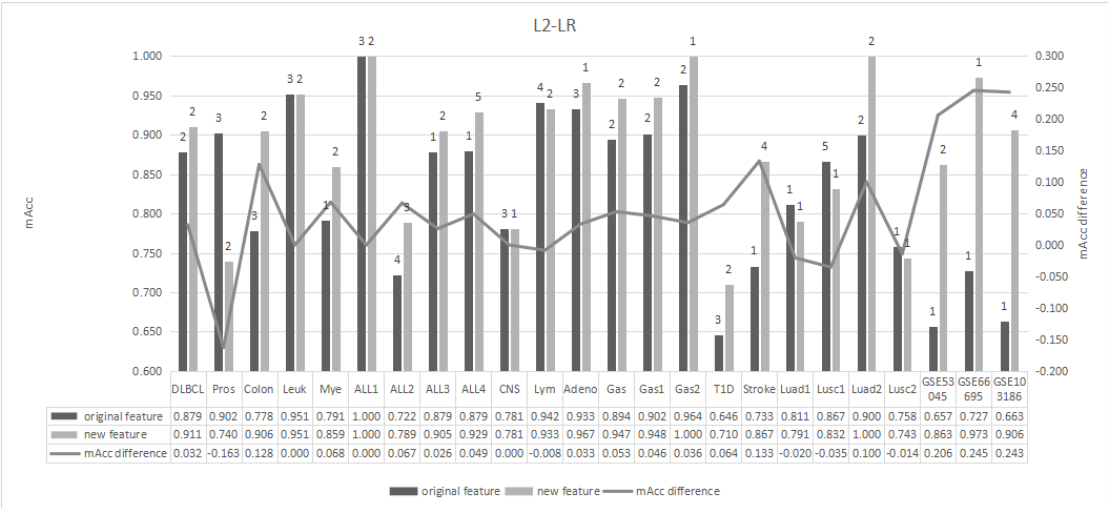
	DLBCL	Pros	Colon	Leuk	Mye	ALL1	ALL2	ALL3	ALL4	CNS	Lym	Adeno	Gas	Gas1	Gas2	T1D	Stroke	Luad1	Lusc1	Luad2	Lusc2	GSE53045	GSE6695	GSE103186
original feature	0.914	0.957	0.900	0.968	0.866	1.000	0.711	0.879	0.938	0.801	1.000	1.000	0.945	0.925	0.920	0.727	0.967	0.811	0.857	1.000	0.793	0.990	1.000	0.912
new feature	0.943	0.837	0.906	0.968	0.779	1.000	0.711	0.930	0.906	0.980	0.917	1.000	0.891	0.954	1.000	0.818	1.000	0.791	0.885	1.000	0.805	0.940	0.973	0.873
mAcc difference	0.029	-0.119	0.006	0.000	-0.086	0.000	0.000	0.052	-0.033	0.179	-0.083	0.000	-0.055	0.029	0.080	0.091	0.033	-0.020	0.028	0.000	0.013	-0.050	-0.027	-0.039

Comparison of the classification metric mAcc and the number of features between the original features and the FeCO3 features using the feature selection algorithm Trank. The series “original” gives the data of the original features, and the series “FeCO3” illustrates the status of the FeCO3 features. The series “Improvement” is the mAcc value of the FeCO3 features minus the mAcc value of the original features. The classification accuracy is calculated using the 5-fold cross validation strategy. The data was calculated using the feature selection algorithms



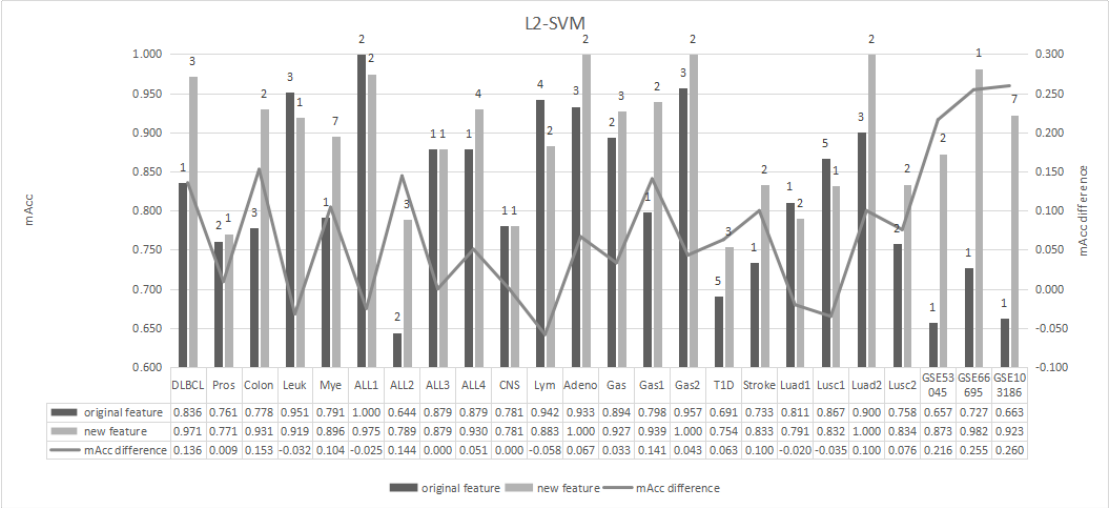
	DLBCL	Pros	Colon	Leuk	Mye	ALL1	ALL2	ALL3	ALL4	CNS	Lym	Adeno	Gas	Gas1	Gas2	T1D	Stroke	Luad1	Lusc1	Luad2	Lusc2	GSE53045	GSE6695	GSE103186
original feature	0.955	0.968	0.953	0.968	0.890	1.000	0.789	0.896	0.940	0.879	1.000	0.967	0.945	0.955	0.992	0.805	0.933	0.929	0.920	1.000	0.820	0.990	0.982	0.972
new feature	1.000	0.859	1.000	0.968	0.951	1.000	0.922	0.957	0.929	0.962	1.000	1.000	1.000	0.977	1.000	0.934	1.000	0.880	0.910	1.000	0.930	1.000	1.000	0.967
mAcc difference	0.045	-0.109	0.047	0.000	0.061	0.000	0.133	0.061	-0.010	0.083	0.000	0.033	0.055	0.022	0.008	0.130	0.067	-0.049	-0.010	0.000	0.111	0.010	0.018	-0.005

Comparison of the classification metric mAcc and the number of features between the original features and the FeCO3 features using the feature selection algorithm DT. The series “original” gives the data of the original features, and the series “FeCO3” illustrates the status of the FeCO3 features. The series “Improvement” is the mAcc value of the FeCO3 features minus the mAcc value of the original features. The classification accuracy is calculated using the 5-fold cross validation strategy. The data was calculated using the feature selection algorithms



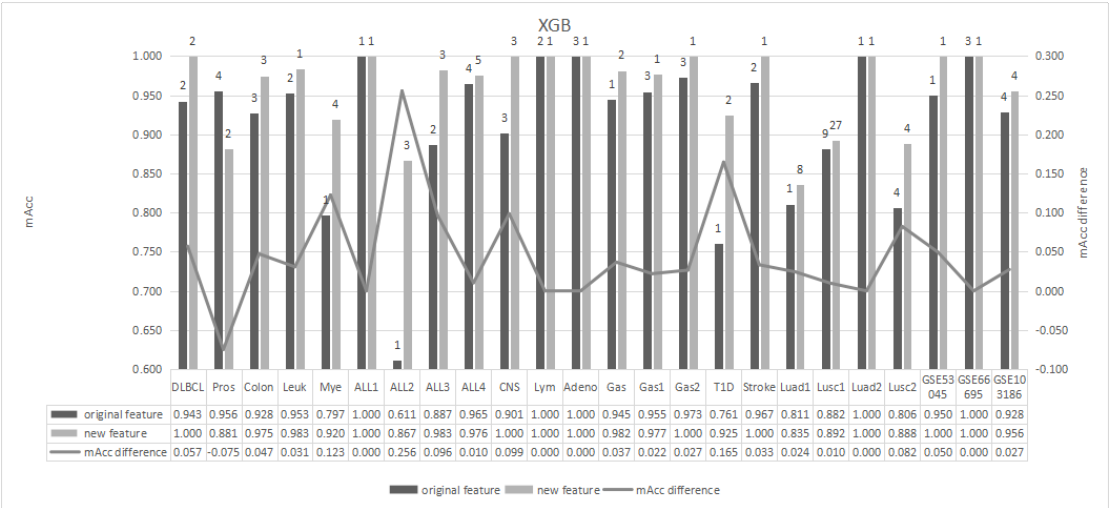
	DLBCL	Pros	Colon	Leuk	Mye	ALL1	ALL2	ALL3	ALL4	CNS	Lym	Adeno	Gas	Gas1	Gas2	T1D	Stroke	Luad1	Lusc1	Luad2	Lusc2	GSE53045	GSE6695	GSE103186
original feature	0.879	0.902	0.778	0.951	0.791	1.000	0.722	0.879	0.879	0.781	0.942	0.933	0.894	0.902	0.964	0.646	0.733	0.811	0.867	0.900	0.758	0.657	0.727	0.663
new feature	0.911	0.740	0.906	0.951	0.859	1.000	0.789	0.905	0.929	0.781	0.933	0.967	0.947	0.948	1.000	0.710	0.867	0.791	0.832	1.000	0.743	0.863	0.973	0.906
mAcc difference	0.032	-0.163	0.128	0.000	0.068	0.000	0.067	0.026	0.049	0.000	-0.008	0.033	0.053	0.046	0.036	0.064	0.133	-0.020	-0.035	0.100	-0.014	0.206	0.245	0.243

Comparison of the classification metric mAcc and the number of features between the original features and the FeCO3 features using the feature selection algorithm L2-LR. The series “original” gives the data of the original features, and the series “FeCO3” illustrates the status of the FeCO3 features. The series “Improvement” is the mAcc value of the FeCO3 features minus the mAcc value of the original features. The classification accuracy is calculated using the 5-fold cross validation strategy. The data was calculated using the feature selection algorithms



	DLBCL	Pros	Colon	Leuk	Mye	ALL1	ALL2	ALL3	ALL4	CNS	Lym	Adeno	Gas	Gas1	Gas2	T1D	Stroke	Luad1	Lusc1	Luad2	Lusc2	GSE53045	GSE6695	GSE103186
original feature	0.836	0.761	0.778	0.951	0.791	1.000	0.644	0.879	0.879	0.781	0.942	0.933	0.894	0.798	0.957	0.691	0.733	0.811	0.867	0.900	0.758	0.657	0.727	0.663
new feature	0.971	0.771	0.931	0.919	0.896	0.975	0.789	0.879	0.930	0.781	0.883	1.000	0.927	0.939	1.000	0.754	0.833	0.791	0.832	1.000	0.834	0.873	0.982	0.923
mAcc difference	0.136	0.009	0.153	-0.032	0.104	-0.025	0.144	0.000	0.051	0.000	-0.058	0.067	0.033	0.141	0.043	0.063	0.100	-0.020	-0.035	0.100	0.076	0.216	0.255	0.260

Comparison of the classification metric mAcc and the number of features between the original features and the FeCO3 features using the feature selection algorithm L2-SVM. The series “original” gives the data of the original features, and the series “FeCO3” illustrates the status of the FeCO3 features. The series “Improvement” is the mAcc value of the FeCO3 features minus the mAcc value of the original features. The classification accuracy is calculated using the 5-fold cross validation strategy. The data was calculated using the feature selection algorithms



	DLBCL	Pros	Colon	Leuk	Mye	ALL1	ALL2	ALL3	ALL4	CNS	Lym	Adeno	Gas	Gas1	Gas2	T1D	Stroke	Luad1	Lusc1	Luad2	Lusc2	GSE53045	GSE6695	GSE103186
original feature	0.943	0.956	0.928	0.953	0.797	1.000	0.611	0.887	0.965	0.901	1.000	1.000	0.945	0.955	0.973	0.761	0.967	0.811	0.882	1.000	0.806	0.950	1.000	0.928
new feature	1.000	0.881	0.975	0.983	0.920	1.000	0.867	0.983	0.976	1.000	1.000	1.000	0.982	0.977	1.000	0.925	1.000	0.835	0.892	1.000	0.888	1.000	1.000	0.956
mAcc difference	0.057	-0.075	0.047	0.031	0.123	0.000	0.256	0.096	0.010	0.099	0.000	0.000	0.037	0.022	0.027	0.165	0.033	0.024	0.010	0.000	0.082	0.050	0.000	0.027

Comparison of the classification metric mAcc and the number of features between the original features and the FeCO3 features using the feature selection algorithm XGB. The series “original” gives the data of the original features, and the series “FeCO3” illustrates the status of the FeCO3 features. The series “Improvement” is the mAcc value of the FeCO3 features minus the mAcc value of the original features. The classification accuracy is calculated using the 5-fold cross validation strategy. The data was calculated using the feature selection algorithms

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