

Supplementary Figure 1

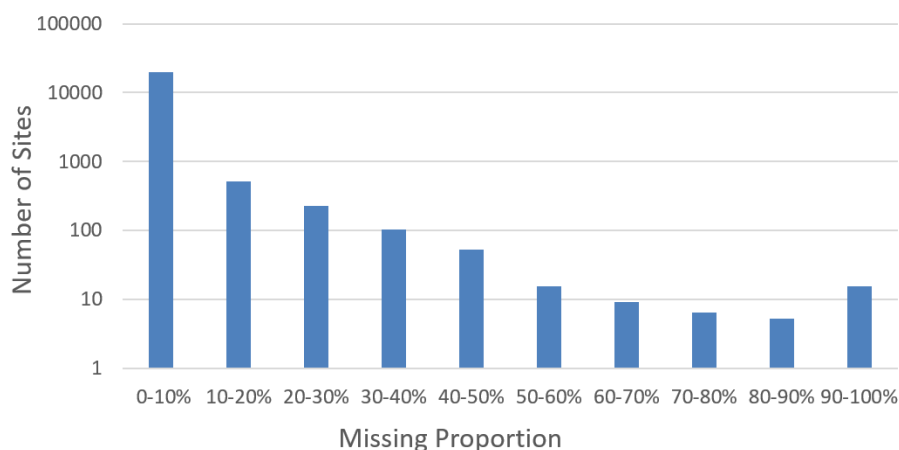


Fig.S1. The average number of sites corresponding to different proportions of missing values on all cancers

Supplementary Figure 2

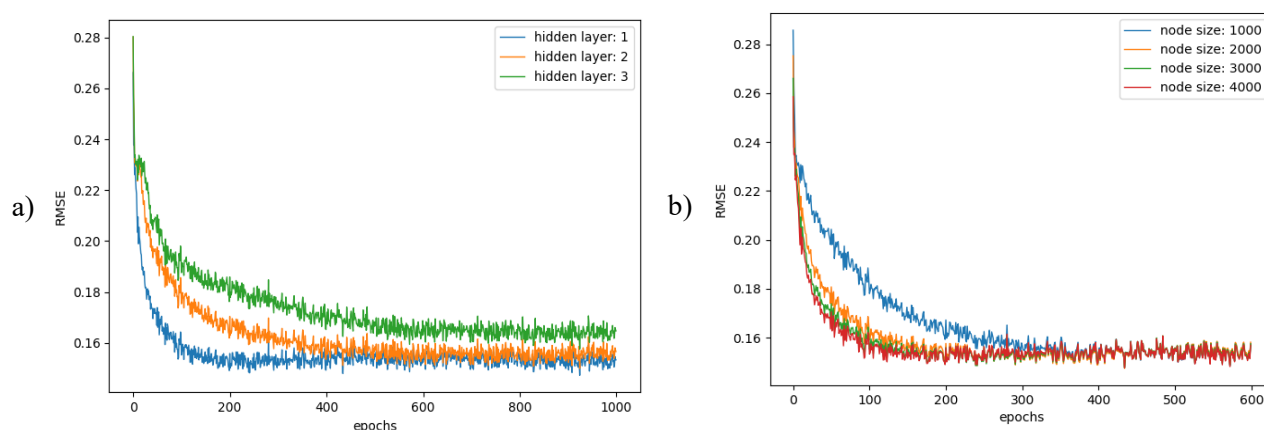


Fig.S2. Selection process of hidden layer and node size. The x coordinate is the training epoch, and the y coordinate is the training loss. (a) Shows that when the hidden layer is 1, the convergence speed is faster. (b) Shows that the RMSE of the node size 3000 and 4000 are close, the value of the node size is determined to be 3000 to reduce some calculations.

Supplementary Figure 3

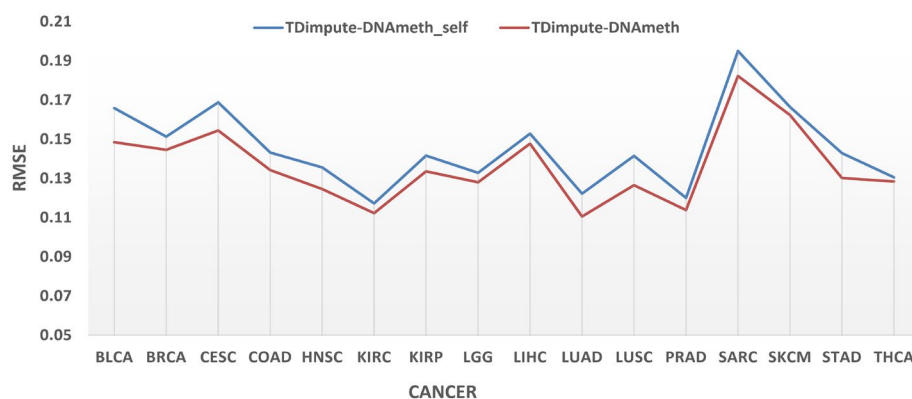


Fig.S3. Comparing the RMSE of TDimpute-DNA meth_self and TDimpute-DNA meth methods on 16 cancers. The results were averaged over four missing rates. Table S3 details the RMSE value at the four missing rates.

Supplementary Figure 4

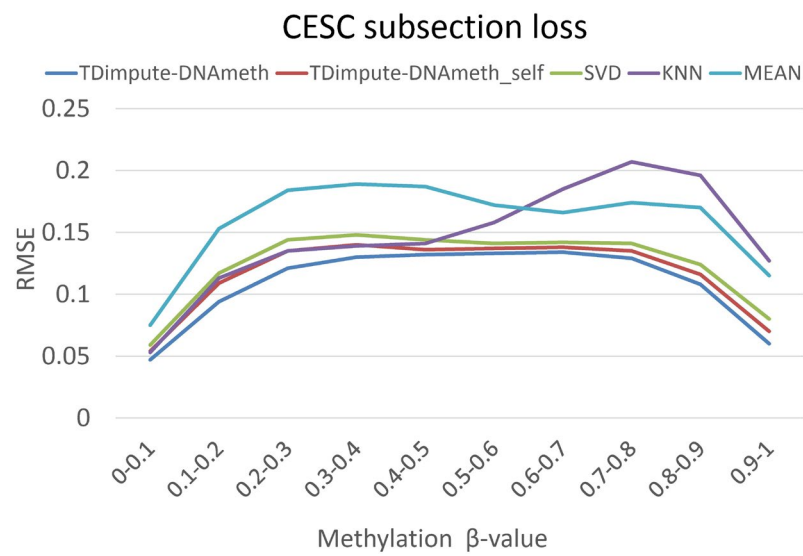


Fig.S4. Subsection RMSE of five methods on CESC cancer datasets. There is no obvious relationship between the β -value of methylation and the RMSE.

Supplementary Figure 5

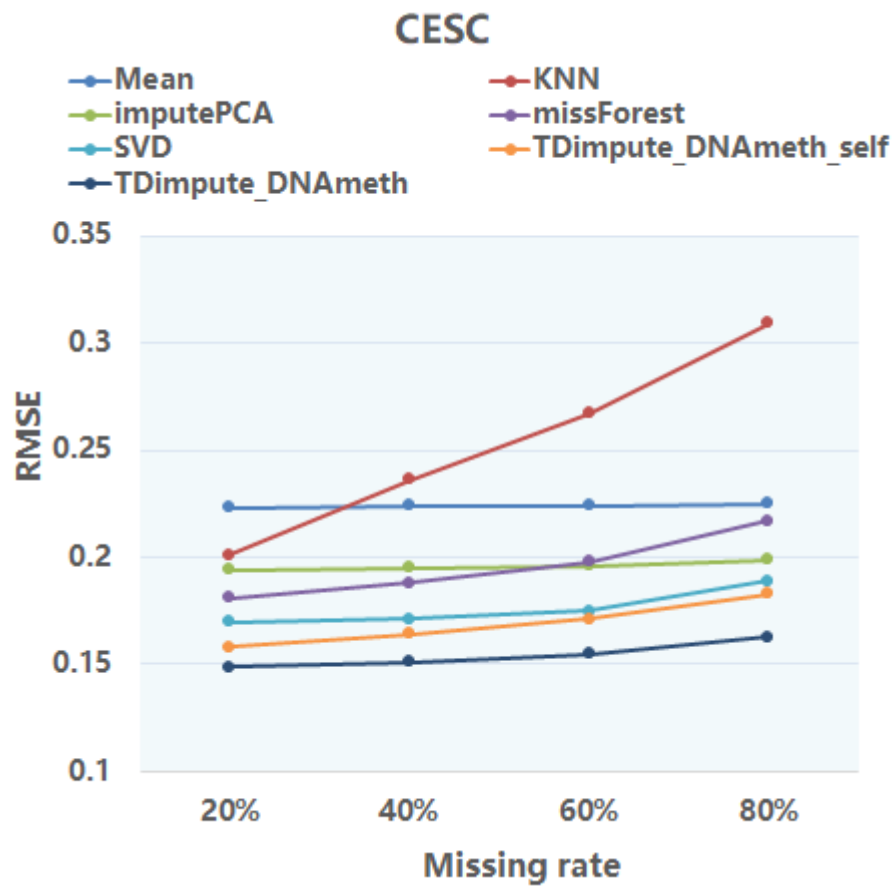


Fig.S5. The comparison of seven methods by RMSE on the CESC dataset. The missForest is not as effective as the SVD method, and the time taken by this method is unacceptable. Therefore, the missForest is not in the manuscript.

Supplementary Figure 6

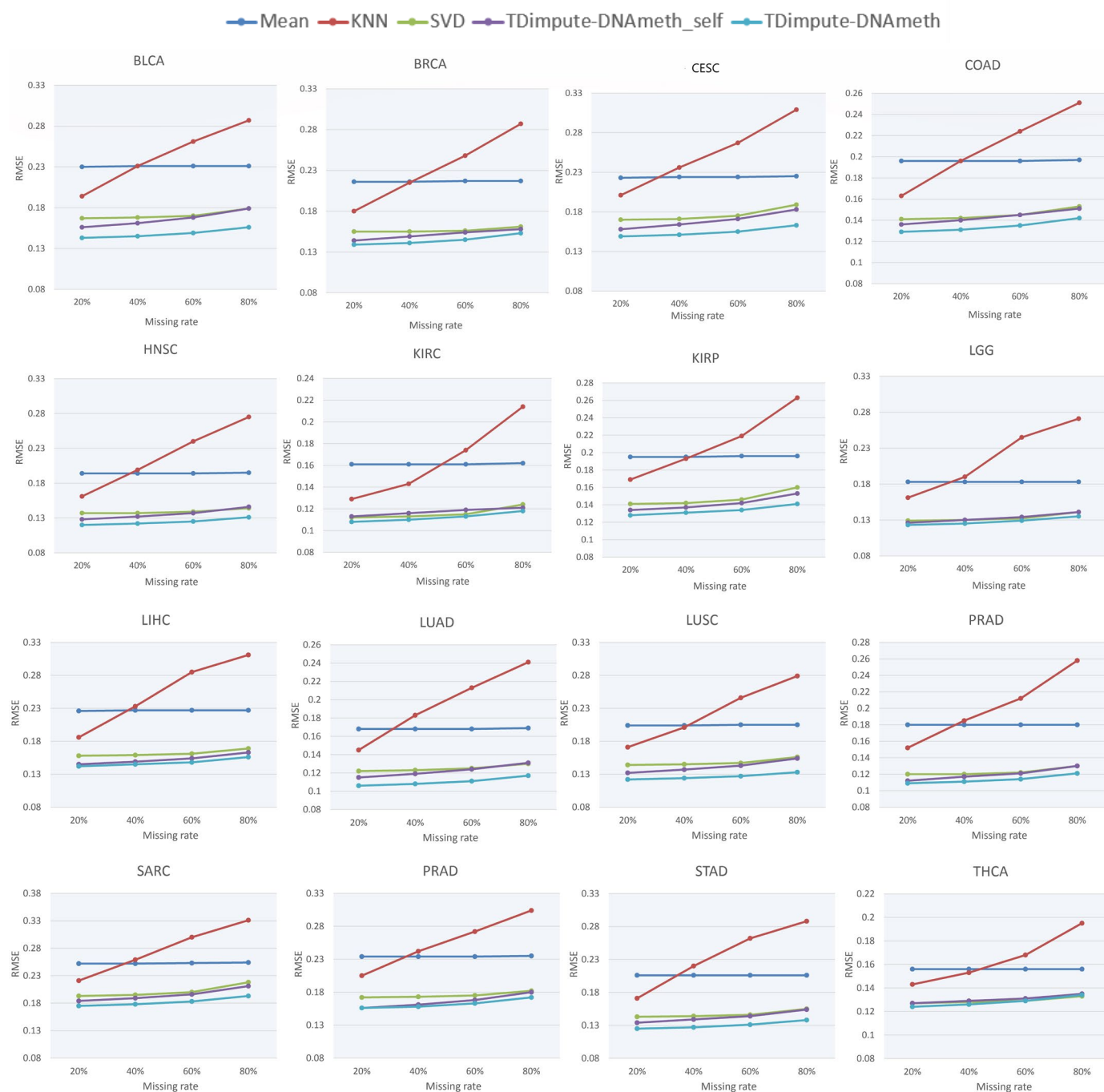


Fig.S6. RMSE of five methods on 16 imputed cancer datasets with different missing rates. The results were averaged over 5 random replicas.

Supplementary Figure 7

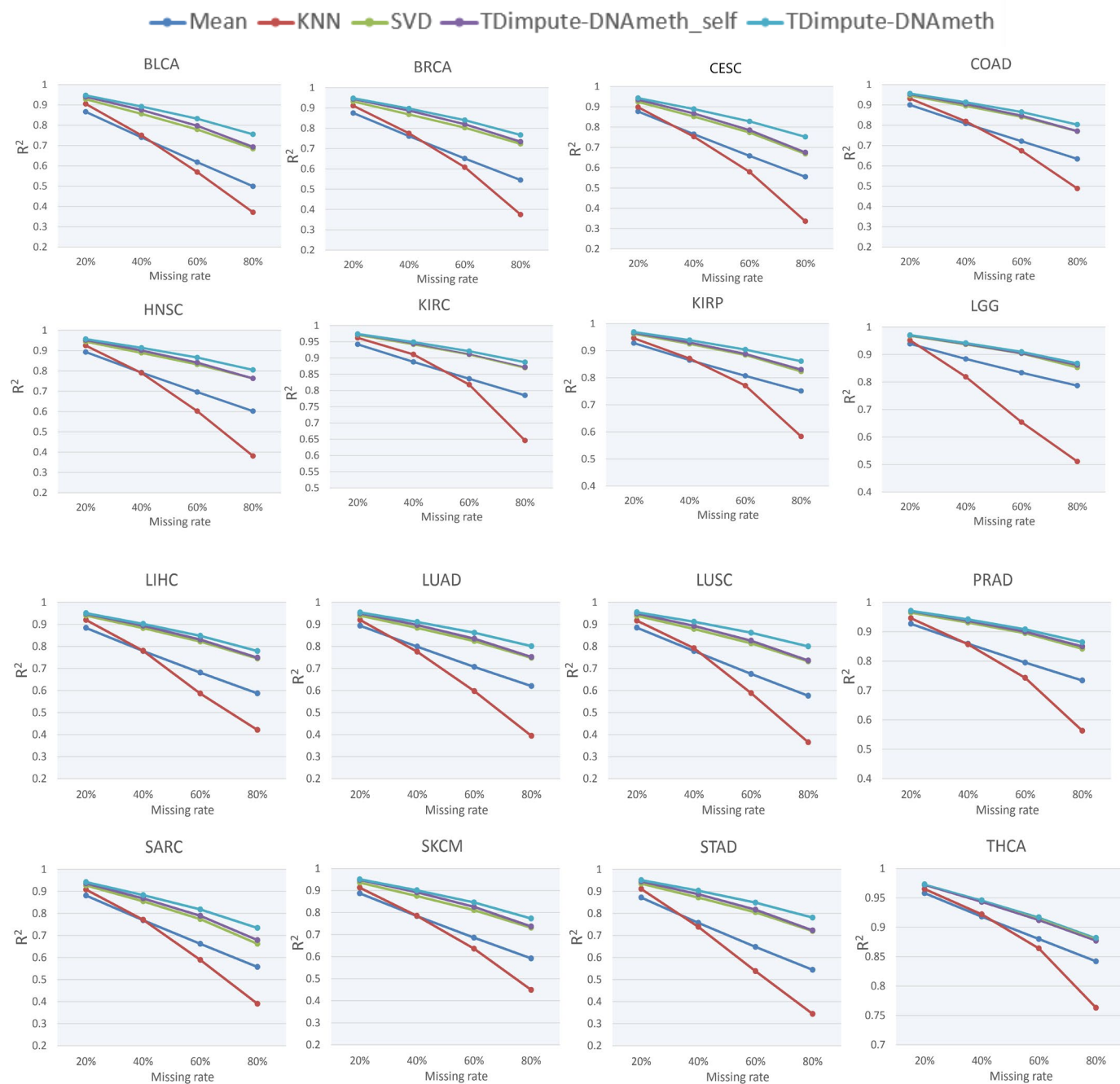


Fig.S7. R^2 of five methods on 16 imputed cancer datasets with different missing rates. The results were averaged over 5 random replicas.

Supplementary Figure 8A

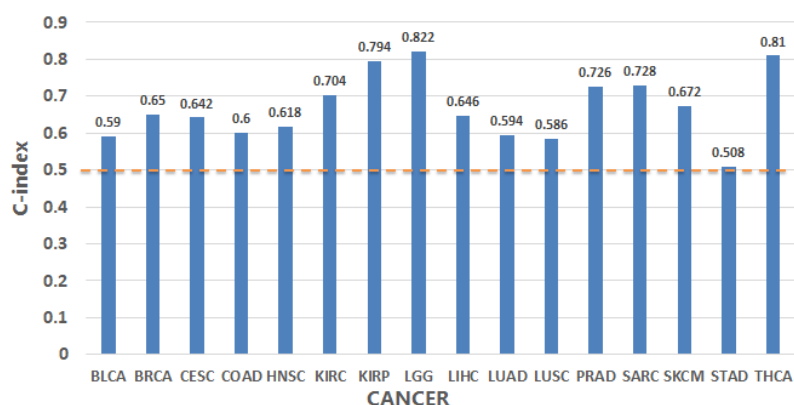


Fig.S8A. The C-index of the survival prediction of 16 cancers on the TCGA dataset without simulation missing values.

Supplementary Figure 8B

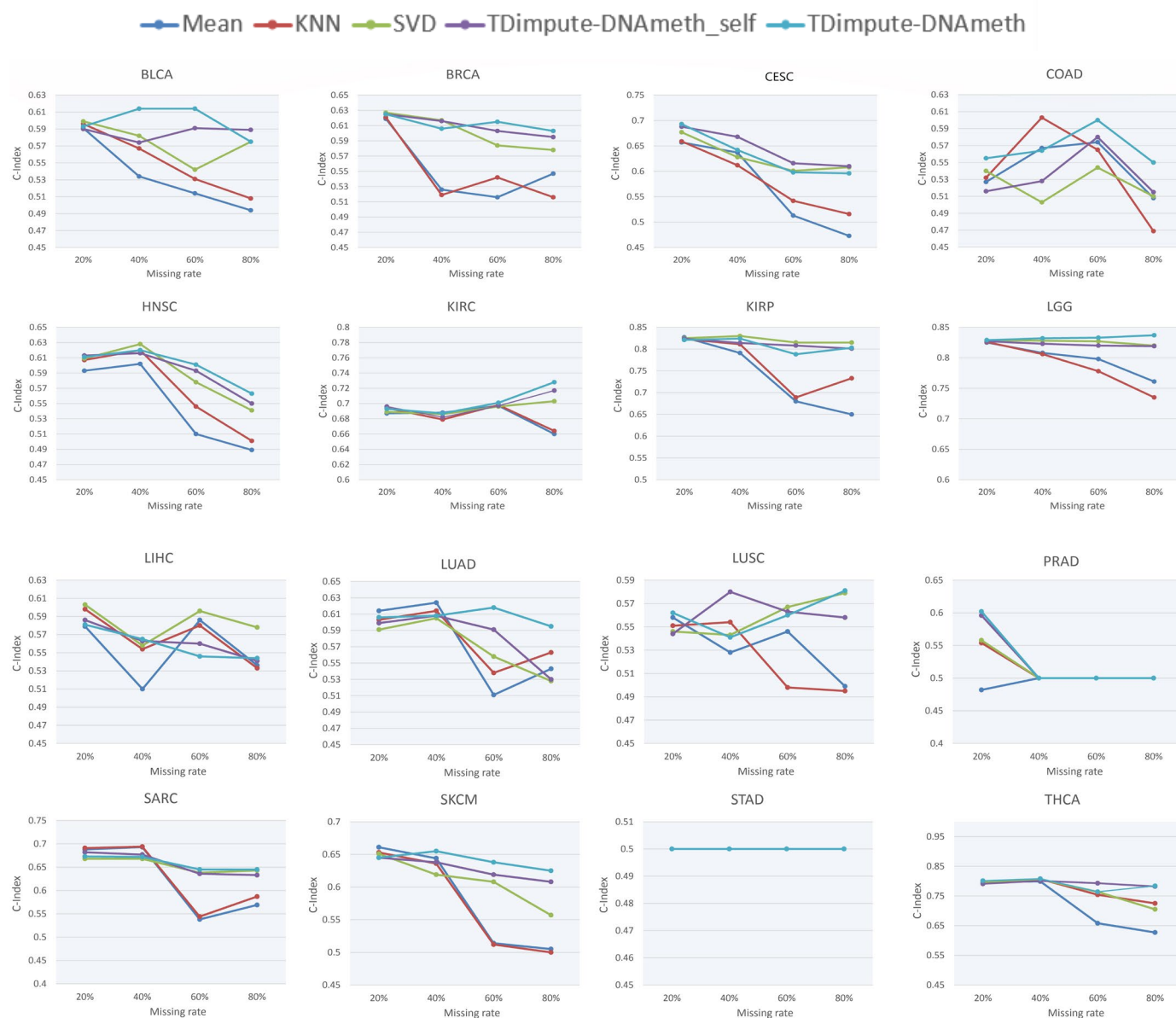


Fig.S8B. C-index of five methods on 16 imputed cancer datasets with different missing rates. The results were averaged over 5 random replicas. If the predicted value of all methods is less than 0.5, use 0.5 instead.

Supplementary Table

Table S1: The RMSE of CV(5 fold) and test on 16 cancer datasets.

Miss- ing rate	BLCA					BRCA			
	TDim- pute-DNAmeth_self		TDim- pute-DNAmeth			TDimpute-DNAmeth_self		TDim- pute-DNAmeth	
	cv(5fold)	test	cv(5fold)	test		cv(5fold)	test	cv(5fold)	test
20%	0.1584± 0.0052	0.1581	0.1481 ±0.0029	0.1488		0.1443 ± 0.0029	0.1425	0.1404± 0.0029	0.1392
40%	0.1647± 0.0051	0.1647	0.1518 ±0.0029	0.1524		0.1523 ± 0.0029	0.1511	0.1447 ± 0.0027	0.1436
60%	0.1735± 0.0051	0.1733	0.1572 ±0.0030	0.1574		0.1627 ± 0.0030	0.1619	0.1502 ± 0.0026	0.1490
80%	0.1889± 0.0054	0.1881	0.1677± 0.0032	0.1676		0.1768 ± 0.0032	0.1758	0.1591 ± 0.0027	0.1578
Miss- ing rate	CESC					COAD			
	TDim- pute-DNAmeth_self		TDim- pute-DNAmeth			TDimpute-DNAmeth_self		TDim- pute-DNAmeth	
	cv(5fold)	test	cv(5fold)	test		cv(5fold)	test	cv(5fold)	test
20%	0.1653± 0.0047	0.1646	0.1514± 0.0040	0.1516		0.1387 ± 0.0053	0.1374	0.1333± 0.0047	0.1324
40%	0.1725± 0.0047	0.1710	0.1559± 0.0039	0.1558		0.1451 ± 0.0051	0.1449	0.1373± 0.0048	0.1366
60%	0.1839± 0.0052	0.1796	0.1619± 0.0040	0.1616		0.1542± 0.0051	0.1553	0.1421± 0.0048	0.1416
80%	0.2059± 0.0058	0.1986	0.1737± 0.0043	0.1736		0.1701± 0.0051	0.1706	0.1514± 0.0048	0.1510
Miss- ing rate	HNSC					KIRC			
	TDim- pute-DNAmeth_self		TDim- pute-DNAmeth			TDimpute-DNAmeth_self		TDim- pute-DNAmeth	
	cv(5fold)	test	cv(5fold)	test		cv(5fold)	test	cv(5fold)	test
20%	0.1312± 0.0036	0.1277	0.1236± 0.0031	0.1208		0.1122± 0.0047	0.1100	0.1073± 0.0037	0.1060
40%	0.1374± 0.0036	0.1353	0.1271± 0.0032	0.1242		0.1168± 0.0048	0.1178	0.1104± 0.0037	0.1092
60%	0.1468± 0.0037	0.1460	0.1322± 0.0032	0.1294		0.1246± 0.0050	0.1302	0.1141± 0.0036	0.1128
80%	0.1634± 0.0039	0.1608	0.1416± 0.0035	0.1380		0.1363± 0.0050	0.1412	0.1209± 0.0040	0.1190
Miss- ing rate	KIRP					LGG			
	TDim- pute-DNAmeth_self		TDim- pute-DNAmeth			TDimpute-DNAmeth_self		TDim- pute-DNAmeth	
	cv(5fold)	test	cv(5fold)	test		cv(5fold)	test	cv(5fold)	test
20%	0.1405± 0.0071	0.1369	0.1319± 0.0052	0.1314		0.1284± 0.0026	0.1263	0.1275± 0.0024	0.1260
40%	0.1460± 0.0076	0.1424	0.1355± 0.0053	0.1346		0.1339± 0.0026	0.1320	0.1315± 0.0023	0.1296
60%	0.1539± 0.0081	0.1510	0.1403± 0.0055	0.1400		0.1421± 0.0028	0.1398	0.1359± 0.0022	0.1346
80%	0.1705± 0.0082	0.1678	0.1504± 0.0061	0.1484		0.1606± 0.0031	0.1581	0.1435± 0.0026	0.1418
Miss- ing	LIHC					LUAD			
	TDim-		TDim-			TDimpute-DNAmeth self		TDim-	

rate	pute-DNA _{meth} _self		pute-DNA _{meth}					pute-DNA _{meth}	
	cv(5fold)	test	cv(5fold)	test		cv(5fold)	test	cv(5fold)	test
20%	0.1533	0.1517	0.1485	0.1472		0.1179	0.1189	0.1103	0.1122
40%	0.1598	0.1581	0.1526	0.1510		0.1295	0.1298	0.1138	0.1158
60%	0.1679	0.1666	0.1579	0.1564		0.1440	0.1438	0.1184	0.1206
80%	0.1814	0.1797	0.1674	0.1656		0.1573	0.1568	0.1270	0.1286
Miss- ing rate	LUSC					PRAD			
	TDim- pute-DNA _{meth} _self		TDim- pute-DNA _{meth}			TDimpute-DNA _{meth} _self		TDim- pute-DNA _{meth}	
	cv(5fold)	test	cv(5fold)	test		cv(5fold)	test	cv(5fold)	test
20%	0.1385± 0.0056	0.1370	0.1268± 0.0050	0.1264		0.1168± 0.0028	0.1124	0.1153± 0.0025	0.1118
40%	0.1454± 0.0057	0.1441	0.1303± 0.0048	0.1300		0.1246± 0.0028	0.1199	0.1197± 0.0024	0.1162
60%	0.1570± 0.0059	0.1555	0.1355± 0.0050	0.1352		0.1374± 0.0030	0.1320	0.1251± 0.0025	0.1214
80%	0.1733± 0.0063	0.1714	0.1456± 0.0054	0.1450		0.1531± 0.0037	0.1476	0.1335± 0.0028	0.1296
Miss- ing rate	SARC					SKCM			
	TDim- pute-DNA _{meth} _self		TDim- pute-DNA _{meth}			TDimpute-DNA _{meth} _self		TDim- pute-DNA _{meth}	
	cv(5fold)	test	cv(5fold)	test		cv(5fold)	test	cv(5fold)	test
20%	0.1900± 0.0066	0.1849	0.1790± 0.0063	0.1768		0.1638± 0.0037	0.1637	0.1582± 0.0035	0.1590
40%	0.1953± 0.0066	0.1906	0.1832± 0.0063	0.1810		0.1702± 0.0039	0.1704	0.1627± 0.0036	0.1634
60%	0.2036± 0.0069	0.1984	0.1895± 0.0062	0.1872		0.1780± 0.0043	0.1783	0.1682± 0.0037	0.1692
80%	0.2236± 0.0081	0.2168	0.2029± 0.0071	0.1992		0.1935± 0.0050	0.1923	0.1790± 0.0040	0.1790
Miss- ing rate	STAD					THCA			
	TDim- pute-DNA _{meth} _self		TDim- pute-DNA _{meth}			TDimpute-DNA _{meth} _self		TDim- pute-DNA _{meth}	
	cv(5fold)	test	cv(5fold)	test		cv(5fold)	test	cv(5fold)	test
20%	0.1379± 0.0031	0.1376	0.1278± 0.0028	0.1290		0.1278± 0.0036	0.1277	0.1267± 0.0031	0.1262
40%	0.1441± 0.0030	0.1442	0.1316± 0.0030	0.1328		0.1309± 0.0036	0.1326	0.1293± 0.0032	0.1286
60%	0.1527± 0.0034	0.1533	0.1370± 0.0028	0.1380		0.1362± 0.0036	0.1416	0.1324± 0.0032	0.1318
80%	0.1699± 0.0043	0.1694	0.1475± 0.0031	0.1478		0.1482± 0.0037	0.1532	0.1374± 0.0035	0.1364

Table S2: The RMSE of five methods on 16 cancer datasets. Optimal results are highlighted in bold.

Missi ng rate	BLCA					BRCA				
	Me an	KN N	SV D	TDim- pute-DNA _{meth} _s elf	TDim- pute-DNA _{met} h	Me an	KN N	SV D	TDim- pute-DNA _{meth} _s elf	TDim- pute-DNA _{met} h
20%	0.23 0	0.1 94	0.1 67	0.156	0.143	0.21 6	0.1 80	0.1 55	0.144	0.139
40%	0.23 1	0.2 31	0.1 68	0.161	0.145	0.21 6	0.2 15	0.1 55	0.149	0.141

To impute DNA methylation by transferred learning

60%	0.23 1	0.2 61	0.1 70	0.168	0.149		0.21 7	0.2 48	0.1 56	0.154	0.145
80%	0.23 1	0.2 87	0.1 79	0.179	0.156		0.21 7	0.2 87	0.1 61	0.158	0.153
Missi ng rate	CESC						COAD				
	Me an	KN N	SV D	TDim- pute-DNAmeth_s elf	TDim- pute-DNAmet h		Me an	KN N	SV D	TDim- pute-DNAmeth_s elf	TDim- pute-DNAmet h
20%	0.22 3	0.2 01	0.1 70	0.158	0.149		0.19 6	0.1 63	0.1 41	0.136	0.129
40%	0.22 4	0.2 36	0.1 71	0.164	0.151		0.19 6	0.1 96	0.1 42	0.140	0.131
60%	0.22 4	0.2 67	0.1 75	0.171	0.155		0.19 6	0.2 24	0.1 45	0.145	0.135
80%	0.22 5	0.3 09	0.1 89	0.183	0.163		0.19 7	0.2 51	0.1 53	0.151	0.142
Missi ng rate	HNSC						KIRC				
	Me an	KN N	SV D	TDim- pute-DNAmeth_s elf	TDim- pute-DNAmet h		Me an	KN N	SV D	TDim- pute-DNAmeth_s elf	TDim- pute-DNAmet h
20%	0.19 4	0.1 61	0.1 37	0.128	0.120		0.16 1	0.1 29	0.1 12	0.113	0.108
40%	0.19 4	0.1 99	0.1 37	0.132	0.122		0.16 1	0.1 43	0.1 13	0.116	0.110
60%	0.19 4	0.2 40	0.1 39	0.137	0.125		0.16 1	0.1 74	0.1 15	0.119	0.113
80%	0.19 5	0.2 75	0.1 44	0.146	0.131		0.16 2	0.2 14	0.1 24	0.121	0.118
Missi ng rate	KIRP						LGG				
	Me an	KN N	SV D	TDim- pute-DNAmeth_s elf	TDim- pute-DNAmet h		Me an	KN N	SV D	TDim- pute-DNAmeth_s elf	TDim- pute-DNAmet h
20%	0.19 5	0.1 69	0.1 41	0.134	0.128		0.18 3	0.1 61	0.1 29	0.126	0.123
40%	0.19 5	0.1 93	0.1 42	0.137	0.131		0.18 3	0.1 90	0.1 30	0.130	0.125
60%	0.19 6	0.2 19	0.1 46	0.142	0.134		0.18 3	0.2 45	0.1 32	0.134	0.129
80%	0.19 6	0.2 63	0.1 60	0.153	0.141		0.18 3	0.2 71	0.1 41	0.141	0.135
Missi ng rate	LIHC						LUAD				
	Me an	KN N	SV D	TDim- pute-DNAmeth_s elf	TDim- pute-DNAmet h		Me an	KN N	SV D	TDim- pute-DNAmeth_s elf	TDim- pute-DNAmet h
20%	0.22 6	0.1 86	0.1 58	0.145	0.142		0.16 8	0.1 45	0.1 22	0.115	0.106
40%	0.22 7	0.2 33	0.1 59	0.149	0.145		0.16 8	0.1 83	0.1 23	0.119	0.108
60%	0.22 7	0.2 85	0.1 61	0.154	0.148		0.16 8	0.2 13	0.1 25	0.124	0.111
80%	0.22 7	0.3 11	0.1 69	0.163	0.156		0.16 9	0.2 41	0.1 30	0.131	0.117
Missi ng rate	LUSC						PRAD				
	Me an	KN N	SV D	TDim- pute-DNAmeth_s elf	TDim- pute-DNAmet h		Me an	KN N	SV D	TDim- pute-DNAmeth_s elf	TDim- pute-DNAmet h

20%	0.20 4	0.1 71	0.1 44	0.132	0.122	0.18 0	0.1 52	0.1 20	0.112	0.109
40%	0.20 4	0.2 01	0.1 45	0.137	0.124	0.18 0	0.1 85	0.1 20	0.117	0.111
60%	0.20 5	0.2 46	0.1 47	0.143	0.127	0.18 0	0.2 12	0.1 22	0.121	0.114
80%	0.20 5	0.2 79	0.1 56	0.154	0.133	0.18 0	0.2 58	0.1 30	0.130	0.121
Missi ng rate	SARC					SKCM				
	Me an	KN N	SV D	TDim- pute-DNAmeth_ self	TDim- pute-DNAmet h	Me an	KN N	SV D	TDim- pute-DNAmeth_ self	TDim- pute-DNAmet h
20%	0.25 2	0.2 21	0.1 93	0.184	0.175	0.23 4	0.2 05	0.1 72	0.156	0.156
40%	0.25 2	0.2 59	0.1 95	0.189	0.178	0.23 4	0.2 42	0.1 73	0.161	0.158
60%	0.25 3	0.3 00	0.2 00	0.196	0.183	0.23 4	0.2 72	0.1 75	0.168	0.163
80%	0.25 4	0.3 31	0.2 18	0.211	0.193	0.23 5	0.3 04	0.1 82	0.180	0.172
Missi ng rate	STAD					THCA				
	Me an	KN N	SV D	TDim- pute-DNAmeth_ self	TDim- pute-DNAmet h	Me an	KN N	SV D	TDim- pute-DNAmeth_ self	TDim- pute-DNAmet h
20%	0.20 6	0.1 71	0.1 43	0.134	0.125	0.15 6	0.1 43	0.1 27	0.127	0.124
40%	0.20 6	0.2 20	0.1 44	0.139	0.127	0.15 6	0.1 53	0.1 28	0.129	0.126
60%	0.20 6	0.2 62	0.1 46	0.144	0.131	0.15 6	0.1 68	0.1 29	0.131	0.129
80%	0.20 6	0.2 88	0.1 55	0.154	0.138	0.15 6	0.1 95	0.1 33	0.135	0.134

Table S3: The R^2 of five methods on 16 cancer datasets. Optimal results are highlighted in bold.

Miss- ing rate	BLCA					BRCA				
	Me an	KN N	SV D	TDim- pute-DNAmeth_ self	TDim- pute-DNAmet h	Me an	KN N	SV D	TDim- pute-DNAmeth_ self	TDim- pute-DNAmet h
20%	0.8 66	0.9 05	0.92 8	0.940	0.947	0.8 75	0.9 11	0.9 32	0.944	0.948
40%	0.7 40	0.7 50	0.85 6	0.875	0.892	0.7 61	0.7 75	0.8 68	0.887	0.897
60%	0.6 18	0.5 69	0.77 9	0.797	0.832	0.6 51	0.6 08	0.8 03	0.820	0.840
80%	0.4 99	0.3 71	0.68 4	0.693	0.755	0.5 45	0.3 75	0.7 23	0.734	0.767
Miss- ing rate	CESC					COAD				
	Me an	KN N	SV D	TDim- pute-DNAmeth_ self	TDim- pute-DNAmet h	Me an	KN N	SV D	TDim- pute-DNAmeth_ self	TDim- pute-DNAmet h
20%	0.8 77	0.8 98	0.92 4	0.935	0.943	0.9 00	0.9 31	0.9 46	0.953	0.956
40%	0.7 65	0.7 53	0.85 2	0.867	0.889	0.8 08	0.8 19	0.8 95	0.904	0.913

60%	0.658	0.579	0.773	0.785	0.828	0.721	0.674	0.841	0.847	0.865
80%	0.555	0.336	0.668	0.675	0.752	0.634	0.488	0.770	0.771	0.803
Missing rate	HNSC					KIRC				
	Me an	KN N	SV D	TDim-pute-DNAmeth_self	TDim-pute-DNAmet_h	Me an	KN N	SV D	TDim-pute-DNAmeth_self	TDim-pute-DNAmet_h
20%	0.893	0.925	0.944	0.952	0.957	0.942	0.962	0.971	0.972	0.974
40%	0.792	0.790	0.889	0.901	0.914	0.888	0.911	0.942	0.944	0.949
60%	0.696	0.602	0.832	0.841	0.866	0.836	0.818	0.911	0.912	0.921
80%	0.602	0.381	0.763	0.763	0.805	0.785	0.646	0.870	0.872	0.887
Missing rate	KIRP					LGG				
	Me an	KN N	SV D	TDim-pute-DNAmeth_self	TDim-pute-DNAmet_h	Me an	KN N	SV D	TDim-pute-DNAmeth_self	TDim-pute-DNAmet_h
20%	0.928	0.946	0.962	0.966	0.969	0.939	0.952	0.968	0.970	0.971
40%	0.865	0.871	0.925	0.930	0.939	0.884	0.819	0.937	0.939	0.942
60%	0.807	0.771	0.884	0.888	0.904	0.834	0.654	0.904	0.905	0.910
80%	0.751	0.583	0.823	0.830	0.861	0.787	0.511	0.953	0.862	0.868
Missing rate	LIHC					LUAD				
	Me an	KN N	SV D	TDim-pute-DNAmeth_self	TDim-pute-DNAmet_h	Me an	KN N	SV D	TDim-pute-DNAmeth_self	TDim-pute-DNAmet_h
20%	0.884	0.920	0.940	0.948	0.951	0.894	0.920	0.940	0.950	0.954
40%	0.779	0.780	0.883	0.894	0.902	0.799	0.776	0.884	0.897	0.911
60%	0.681	0.586	0.822	0.831	0.848	0.707	0.597	0.824	0.835	0.862
80%	0.587	0.421	0.745	0.749	0.779	0.620	0.394	0.748	0.752	0.801
Missing rate	LUSC					PRAD				
	Me an	KN N	SV D	TDim-pute-DNAmeth_self	TDim-pute-DNAmet_h	Me an	KN N	SV D	TDim-pute-DNAmeth_self	TDim-pute-DNAmet_h
20%	0.885	0.917	0.939	0.949	0.955	0.927	0.946	0.965	0.970	0.971
40%	0.779	0.792	0.879	0.893	0.912	0.859	0.857	0.931	0.937	0.942
60%	0.675	0.588	0.814	0.826	0.862	0.795	0.743	0.95	0.900	0.908
80%	0.576	0.365	0.732	0.736	0.800	0.734	0.563	0.842	0.850	0.864
Missing rate	SARC					SKCM				
	Me an	KN N	SV D	TDim-pute-DNAmeth_self	TDim-pute-DNAmet_h	Me an	KN N	SV D	TDim-pute-DNAmeth_self	TDim-pute-DNAmet_h

20%	0.8 81	0.9 08	0.92 7	0.936	0.942	0.8 87	0.9 13	0.9 36	0.948	0.951
40%	0.7 69	0.7 71	0.85 5	0.868	0.883	0.7 84	0.7 85	0.8 75	0.892	0.901
60%	0.6 62	0.5 89	0.77 4	0.789	0.818	0.6 86	0.6 36	0.8 11	0.826	0.846
80%	0.5 57	0.3 90	0.66 2	0.679	0.734	0.5 92	0.4 49	0.7 31	0.737	0.773
Miss- ing rate	STAD					THCA				
	Me an	KN N	SV D	TDim- pute-DNAmeth_ self	TDim- pute-DNAmet h	Me an	KN N	SV D	TDim- pute-DNAmeth_ self	TDim- pute-DNAmet h
20%	0.8 72	0.9 11	0.93 5	0.945	0.951	0.9 58	0.9 65	0.9 72	0.972	0.973
40%	0.7 57	0.7 39	0.87 2	0.887	0.903	0.9 18	0.9 22	0.9 44	0.943	0.946
60%	0.6 48	0.5 38	0.80 5	0.817	0.849	0.8 80	0.8 64	0.9 15	0.912	0.917
80%	0.5 44	0.3 44	0.72 0	0.723	0.781	0.8 42	0.7 63	0.8 80	0.877	0.882

Table S4: The C-index of five methods on 16 cancer datasets. Optimal results are highlighted in bold.

Missi ng rate	BLCA					BRCA				
	Me an	KN N	SV D	TDim- pute-DNAmeth_ self	TDim- pute-DNAmet h	Me an	KN N	SV D	TDim- pute-DNAmeth_ self	TDim- pute-DNAmet h
20%	0.59 1	0.5 96	0.5 99	0.59	0.593	0.61 9	0.6 21	0.6 27	0.625	0.625
40%	0.53 4	0.5 67	0.5 82	0.574	0.614	0.52 6	0.5 19	0.6 17	0.616	0.606
60%	0.51 4	0.5 31	0.5 42	0.591	0.614	0.51 6	0.5 42	0.5 84	0.603	0.615
80%	0.49 4	0.5 08	0.5 75	0.589	0.575	0.54 7	0.5 16	0.5 78	0.595	0.603
Missi ng rate	CESC					COAD				
	Me an	KN N	SV D	TDim- pute-DNAmeth_ self	TDim- pute-DNAmet h	Me an	KN N	SV D	TDim- pute-DNAmeth_ self	TDim- pute-DNAmet h
20%	0.65 7	0.6 59	0.6 77	0.688	0.693	0.52 7	0.5 32	0.5 4	0.516	0.555
40%	0.63 7	0.6 12	0.6 28	0.668	0.642	0.56 7	0.6 03	0.5 03	0.528	0.564
60%	0.51 3	0.5 42	0.6 01	0.616	0.598	0.57 4	0.5 65	0.5 44	0.58	0.6
80%	0.47 3	0.5 16	0.6 08	0.61	0.596	0.50 8	0.4 69	0.5 1	0.515	0.55
Missi ng rate	HNSC					KIRC				
	Me an	KN N	SV D	TDim- pute-DNAmeth_ self	TDim- pute-DNAmet h	Me an	KN N	SV D	TDim- pute-DNAmeth_ self	TDim- pute-DNAmet h
20%	0.59 3	0.6 07	0.6 09	0.613	0.611	0.68 7	0.6 94	0.6 89	0.696	0.693
40%	0.60	0.6	0.6	0.616	0.62	0.68	0.6	0.6	0.682	0.687

To impute DNA methylation by transferred learning

	2	2	28				8	79	86		
60%	0.51	0.5 46	0.5 78	0.593	0.601		0.69 7	0.6 98	0.6 96	0.697	0.701
80%	0.48 9	0.5 01	0.5 41	0.55	0.563		0.66	0.6 64	0.7 03	0.717	0.728
Missi ng rate	Me an	KN N	SV D	TDim- pute-DNAmeth_s elf	TDim- pute-DNAmet h		Me an	KN N	SV D	TDim- pute-DNAmeth_s elf	TDim- pute-DNAmet h
20%	0.82 7	0.8 23	0.8 25	0.824	0.821		0.82 5	0.8 26	0.8 29	0.827	0.829
40%	0.79 1	0.8 11	0.8 3	0.814	0.824		0.80 8	0.8 06	0.8 28	0.823	0.832
60%	0.68	0.6 89	0.8 15	0.808	0.788		0.79 8	0.7 78	0.8 27	0.82	0.833
80%	0.65	0.7 33	0.8 15	0.801	0.803		0.76 1	0.7 35	0.8 2	0.819	0.837
Missi ng rate	Me an	KN N	SV D	TDim- pute-DNAmeth_s elf	TDim- pute-DNAmet h		Me an	KN N	SV D	TDim- pute-DNAmeth_s elf	TDim- pute-DNAmet h
20%	0.57 9	0.5 98	0.6 03	0.586	0.581		0.61 4	0.6 03	0.5 91	0.599	0.606
40%	0.51	0.5 54	0.5 58	0.563	0.565		0.62 4	0.6 14	0.6 05	0.608	0.608
60%	0.58 6	0.5 8	0.5 96	0.56	0.546		0.51 1	0.5 38	0.5 58	0.591	0.618
80%	0.53 6	0.5 33	0.5 78	0.541	0.544		0.54 3	0.5 63	0.5 28	0.53	0.595
Missi ng rate	Me an	KN N	SV D	TDim- pute-DNAmeth_s elf	TDim- pute-DNAmet h		Me an	KN N	SV D	TDim- pute-DNAmeth_s elf	TDim- pute-DNAmet h
20%	0.55 8	0.5 51	0.5 46	0.544	0.562		0.48 2	0.5 54	0.5 58	0.596	0.602
40%	0.52 8	0.5 54	0.5 43	0.58	0.541		0.5	0.5	0.5	0.5	0.5
60%	0.54 6	0.4 98	0.5 67	0.563	0.56		0.5	0.5	0.5	0.5	0.5
80%	0.49 9	0.4 95	0.5 79	0.558	0.581		0.5	0.5	0.5	0.5	0.5
Missi ng rate	Me an	KN N	SV D	TDim- pute-DNAmeth_s elf	TDim- pute-DNAmet h		Me an	KN N	SV D	TDim- pute-DNAmeth_s elf	TDim- pute-DNAmet h
20%	0.68 8	0.6 91	0.6 68	0.682	0.673		0.6 61	0.6 53	0.6 51	0.645	0.645
40%	0.69 3	0.6 94	0.6 68	0.677	0.672		0.64 4	0.6 36	0.6 19	0.638	0.655
60%	0.53 8	0.5 44	0.6 38	0.636	0.645		0.51 4	0.5 12	0.6 08	0.619	0.638
80%	0.56 9	0.5 87	0.6 43	0.633	0.645		0.50 5	0.5	0.5 57	0.608	0.625
Missi	STAD						THCA				

To impute DNA methylation by transferred learning

ng rate	Me an	KN N	SV D	TDim- pute-DNAmeth_s elf	TDim- pute-DNAmet h		Me an	KN N	SV D	TDim- pute-DNAmeth_s elf	TDim- pute-DNAmet h
20%	0.5	0.5	0.5	0.5	0.5		0.79 7	0.7 96	0.7 95	0.791	0.801
40%	0.5	0.5	0.5	0.5	0.5		0.79 9	0.8 07	0.8 06	0.801	0.808
60%	0.5	0.5	0.5	0.5	0.5		0.65 8	0.7 54	0.7 64	0.793	0.764
80%	0.5	0.5	0.5	0.5	0.5		0.62 7	0.7 25	0.7 05	0.782	0.784