Illustration the additional Tables and Figures referred in the manuscript.

Table S1: The fscore, recall, precision, AUC,AUCPR,HGS, Stability, Recovery and TDC values of 23 methods under the NCG6.0 benchmark. Some values with '\' indicate this attribute is invalid to the corresponding method.

Methods type		cancer_type	Precision	Recall	Fscore	AUC	AUCPR	HGS	Stability	Recovery	TDC
statistical significance method	Activedriver	lung	0.1176	0.1143	0.116	0.5091	0.2121	1.47E-20	0.145	0.16	0.07
		breast	0.1069	0.1022	0.1045	0.6183	0.2017	2.57E-05	0.1167	0.0633	0.06333333
		HNSC	0.1043	0.1032	0.1038	0.531	0.168	9.08E-12	0.087	0.135	0.06
	MuSic	lung	0.1032	0.0998	0.1014	0.669	0.4494	5.80E-19	\	\	\
		breast	0.0937	0.0922	0.0929	0.7749	0.5944	9.74E-21	\	\	\
		HNSC	0.1084	0.1057	0.1071	0.6517	0.3364	3.69E-14	\	\	\
	dndSCV	lung	0.1095	0.1092	0.1094	0.6942	0.5952	2.15E-25	0.192	0.265	0.1966667
		breast	0.1452	0.081	0.104	0.7592	0.7179	6.42E-27	0.222	0.315	0.21
		HNSC	0.115	0.1124	0.1137	0.7631	0.6433	2.11E-22	0.22	0.25	0.2533333
	polyphen-2	lung	0.072	0.067	0.0694	0.6358	0.0666	0.3650259	0.0633	0.035	0.1933
		breast	0.0924	0.0498	0.0647	0.5225	0.0959	0.002079259	0.112	0.056	1
		HNSC	0.0811	0.0604	0.0692	0.6627	0.0884	0.06529098	0.073	0.042	0.13
	SIFT	lung	0.0519	0.0517	0.0518	0.4276	0.0367	0.4759415	0.04	0.045	1
		breast	0.0538	0.0537	0.0538	0.4151	0.044	0.4775766	0.065	0.055	1
		HNSC	0.0465	0.0461	0.0463	0.2174	0.0176	8.45E-01	0.05	0.03	1
	Mutation Assessor	lung	0.0572	0.0568	0.057	0.3617	0.0435	2.07E-01	0.077	0.057	0.1833
		breast	0.0552	0.0531	0.0541	0.5963	0.0578	6.39E-01	0.0533	0.0383	0.1083
		HNSC	0.0646	0.0621	0.0633	0.688	0.2313	4.15E-03	0.09	0.09	0.14
	OncodriveFM	lung	0.0668	0.0648	0.0658	0.5574	0.1791	3.94E-04	0.39	0.2217	0.5183
		breast	0.074	0.0736	0.0738	0.6097	0.15	7.46E-08	0.3433	0.1717	0.3283
		HNSC	0.0588	0.057	0.0579	0.4872	0.158	9.71E-08	0.357	0.28	0.427
	Dots-Finder	lung	0.1471	0.1471	0.1471	0.669	0.4609	1.42E-25	0.25	0.2583	0.76
		breast	0.1335	0.1314	0.1324	0.7101	0.5492	4.84E-33	0.242	0.32	0.41
		HNSC	0.1774	0.146	0.1601	0.6357	0.4372	6.58E-27	0.267	0.265	0.6433
	oncodriveclust	lung	0.0863	0.0859	0.0861	0.4902	0.1786	9.88E-13	\	\	\
		breast	0.1053	0.1035	0.1044	0.7059	0.3351	2.87E-18	\	\	\
		HNSC	0.1028	0.1015	0.1022	0.5742	0.2816	5.48E-22	\	\	\
Machine learning methods	CHASM	lung	0.0704	0.0437	0.0539	0.6107	0.234	2.68E-33	0.097	0.085	0.005
		breast	0.1956	0.136	0.1605	0.7364	0.7292	2.64E-73	0.085	0.013	0.01
		HNSC	0.0493	0.0219	0.0303	0.5937	0.291	3.58E-25	0.0516	0.07	0.0783
Network based methods	MCGfinder	lung	0.1878	0.1005	0.1309	0.6713	0.4195	1.72E-64	0.265	0.25	0.68
		breast	0.1837	0.0464	0.0742	0.7076	0.4704	1.75E-59	0.362	0.283	0.5822011
		HNSC	0.2057	0.1032	0.1374	0.5906	0.3941	1.25E-75	0.286	0.211	0.5719697
	NMFT	lung+breast+hnsc	0.1457	0.0277	0.0465	0.6415	0.2624	9.29E-56	0.1175	0.1175	0.88

Method	Type									
Intdriver	lung	0.2186	0.0291	0.0514	0.6212	0.301	2.91E-77	0.02	0.02	0.127
	breast	0.201	0.0259	0.0459	0.6732	0.3736	9.18E-70	0.083	0.082	0.187
	HNSC	0.1414	0.0235	0.0403	0.6173	0.2708	4.86E-53	0.072	0.071	0.27
Dawnrank	lung	0.0442	0.0102	0.0166	0.6254	0.0895	6.24E-14	/	/	/
	breast(90)	0.0909	0.0046	0.0088	0.8853	0.3951	2.94E-15	/	/	/
	HNSC	0.049	0.0101	0.0167	0.7447	0.1399	2.26E-17	/	/	/
Dendrix_freq	lung	0.0263	0.0015	0.0028	0.7475	0.0192	0.00018434	0.00125	0.00125	0.02
	breast	0.0407	0.0046	0.0083	0.7387	0.4122	7.66E-13	0.0133	0.0133	0.02666667
	HNSC	0.0291	0.0042	0.0073	0.561	0.0575	6.31E-10	0.005	0.005	0.02
Dendrix_weight	lung	0.1628	0.0051	0.0099	0.4394	0.0103	0.00018434	0	0	0.01666667
	breast	0.0851	0.0053	0.01	0.8893	0.4567	1.40E-14	0.015	0.015	0.02666667
	HNSC	0.0526	0.0076	0.0132	0.4828	0.0641	2.52E-17	0.005	0.005	0.01666667
DriverNet	lung	0.2	0.0211	0.0382	0.7366	0.2675	3.47E-60	0	0	0.05555556
	breast	0.2746	0.0352	0.0624	0.558	0.3804	3.60E-96	0	0	0.1809524
	HNSC	0.2476	0.0436	0.0742	0.5976	0.393	1.25E-95	0.0536	0	0.3660714
Diffusion	lung	0.1521	0.1005	0.1211	0.6418	0.2171	2.57E-21	0.102	0.082	0.233
	breast	0.165	0.0776	0.1056	0.4908	0.1348	1.85E-17	0.163	0.083	0.08360544
	HNSC	0.1319	0.1166	0.1238	0.5057	0.2012	5.94E-27	0.102	0.1083	0.32
MaxMIF_HumanNet	lung	0.1529	0.15	0.1515	0.567	0.3598	2.11E-34	0.2683	0.305	0.537
	breast	0.1801	0.1466	0.1617	0.7013	0.5908	4.85E-40	0.355	0.345	0.433
	HNSC	0.1697	0.1695	0.1696	0.6613	0.5073	9.26E-34	0.293	0.3	0.667
MaxMIF_Stringv10	lung	0.1624	0.1617	0.162	0.6077	0.4426	1.57E-38	0.293	0.325	0.473
	breast	0.2019	0.142	0.1667	0.6713	0.6414	5.99E-50	0.325	0.39	0.5
	HNSC	0.1809	0.172	0.1763	0.6922	0.5932	1.68E-45	0.33	0.355	0.657
MaxMIF_Influencegraph	lung	0.1438	0.1435	0.1436	0.6792	0.3994	5.75E-24	0.23	0.25	0.373
	breast	0.1281	0.1062	0.1161	0.745	0.4823	3.53E-17	0.213	0.22	0.317
	HNSC	0.1594	0.1225	0.1385	0.6672	0.4201	4.70E-26	0.2417	0.26	0.457
UniCovEx_PPR	lung	0.1577	0.1552	0.1564	0.5748	0.3945	1.94E-38	0.82	0.2983	0.753
	breast	0.1528	0.1327	0.142	0.6476	0.4478	2.93E-31	0.27	0.275	0.56
	HNSC	0.1577	0.1552	0.1564	0.593	0.373	8.67E-39	0.2783	0.295	0.71
UniCovEx_Influencegraph	lung	0.1897	0.169	0.1787	0.5554	0.4216	7.11E-50	0.3	0.335	0.73
	breast	0.1715	0.1327	0.1496	0.6487	0.4694	4.47E-36	0.282	0.29	0.557
	HNSC	0.1726	0.1711	0.1719	0.5824	0.3781	3.03E-43	0.293	0.305	0.7
Muffinne_max_humannet	lung	0.159	0.1537	0.1563	0.5827	0.3226	7.99E-28	0.285	0.28	1
	breast	0.1573	0.1559	0.1566	0.5938	0.4207	5.04E-23	0.28	0.285	1
	HNSC	0.164	0.1636	0.1638	0.6422	0.3353	2.92E-18	0.227	0.225	1
Muffinne_max_stringv10	lung	0.1432	0.142	0.1426	0.625	0.3738	1.67E-25	0.257	0.265	0.925
	breast	0.1404	0.14	0.1402	0.6315	0.5118	1.58E-26	0.293	0.3	0.998
	HNSC	0.14	0.1393	0.1396	0.6603	0.525	2.07E-26	0.2583	0.27	1
Muffinne_sum_humannet	lung	0.1601	0.1573	0.1587	5.65E-01	0.3305	5.21E-26	0.243	0.27	0.913
	breast	0.1575	0.1526	0.155	0.6415	0.4285	2.43E-26	0.3	0.305	0.66
	HNSC	0.1725	0.1686	0.1706	0.5861	0.3412	1.59E-28	0.283	0.285	0.87
Muffinne_sum_stringv10	lung	0.1663	0.1588	0.1624	0.6465	0.4591	4.24E-39	0.3283	0.335	0.812

	cancer_type	Precision	Recall	Fscore	AUC	AUCPR	HGS	Stability	Recovery	TDC
	breast	0.1616	0.146	0.1534	0.6921	0.4971	2.15E-27	0.293	0.305	0.54
	HNSC	0.1726	0.1636	0.168	0.5964	0.4583	2.10E-43	0.3367	0.355	0.798
Muffinne_max_influencegraph	lung	0.1388	0.1355	0.1371	0.5512	0.2113	3.07E-14	0.182	0.195	0.815
	breast	0.1432	0.1287	0.1356	0.6952	0.5322	9.99E-19	0.325	0.255	0.6183
	HNSC	0.1531	0.125	0.1376	0.7041	0.4607	6.17E-14	0.3183	0.242	0.942
Muffinne_sum_influencegraph	lung	0.1766	0.1639	0.17	0.5543	0.3386	4.81E-36	0.315	0.32	0.93
	breast	0.1707	0.1486	0.1589	0.5533	0.4069	6.63E-36	0.325	0.355	0.795
	HNSC	0.1883	0.1829	0.1855	0.5216	0.3465	1.40E-38	0.3183	0.335	0.8983
RME	lung	0.0458	0.0131	0.0204	0.5548	0.1113	5.41E-29			
	breast									
	HNSC	0.0939	0.0143	0.0248	0.5715	0.1727	5.55E-31			
Subdyquency	lung	0.1418	0.1413	0.1416	0.5733	0.4108	1.44E-64	0.2717	0.2483	0.485
	breast	0.1574	0.1221	0.1375	0.6283	0.4942	5.25E-68	0.28	0.2083	0.3383
	HNSC	0.1677	0.1661	0.1669	0.5977	0.3879	3.65E-51	0.253	0.205	0.452
EntroRank	lung	0.1711	0.1588	0.1647	0.6297	0.4812	9.82E-51	0.335	0.36	0.705
	breast	0.156	0.1427	0.149	0.6606	0.5831	3.20E-54	0.327	0.3683	0.4933
	HNSC	0.2132	0.1653	0.1862	0.6577	0.539	4.35E-56	0.3483	0.375	0.643

Table S2: The fscore, recall, precision, AUC, AUCPR, HGS, Stability, Recovery and TDC values of 23 methods under the CGC benchmark.

CGC										
	cancer_type	Precision	Recall	Fscore	AUC	AUCPR	HGS	Stability	Recovery	TDC
Activedriver	lung		0.0714	0.0784	0.6907	0.0507	3.21E-04	0.017	0.027	0.07
	breast		0.0833	0.0952	0.89	0.1524	2.75E-03	0.03	0.03	0.06333333
	HNSC						1.00E+00	0	0	0.06
MuSic	lung		0.0714	0.1053	0.7259	0.0971	1.08E-06			
	breast		0.3333	0.3692	0.8563	0.4958	4.17E-19			
	HNSC		0.2222	0.25	0.9848	0.2381	7.14E-03			
dndSCV	lung		0.1429	0.2105	0.92	0.4268	9.46E-07	0.33	0.05	0.1966667
	breast		0.3611	0.4815	0.91	0.6844	6.62E-26	0.137	0.17	0.21
	HNSC		0.2222	0.25	0.8906	0.1588	3.28E-07	0.033	0.04	0.2533333
polyphen-2	lung						1	0	0	0.1933
	breast				0.2727	0.0068	0.2260077	0.01	0.01	1
	HNSC						1	0	0	0.13
SIFT	lung						1	0	0	1
	breast						1	0.01	0	1
	HNSC						1.00E+00	0	0	1
MA	lung				0.3106	0.0071	4.51E-02	0.01	0.01	0.1833
	breast				0.4545	0.009	1.41E-01	0.012	0.01	0.1083
	HNSC				0.9045	0.025	1.11E-01	0.01	0.005	0.14
OncodriveFM	lung		0.0357	0.0606	0.8232	0.0611	2.98E-02	0.072	0.035	0.5183
	breast		0.0357	0.04	0.8342	0.0399	3.70E-03	0.0783	0.057	0.3283
	HNSC				0.1206	0.0028	8.45E-02	0.0983	0.075	0.427

Method	Tissue									
Dots-Finder	lung		0.1071	0.15	0.8958	0.31	2.29E-05	0.025	0.00683	0.76
	breast		0.1944	0.2917	0.7193	0.4448	5.50E-20	0.09	0.13	0.41
	HNSC		0.2222	0.2222	0.8522	0.1362	2.06E-05	0.03	0.03	0.6433
oncodriveclust	lung		0.0357	0.0625	0.6837	0.0749	7.27E-03			
	breast		0.1389	0.1724	0.7509	0.2188	3.00E-13			
	HNSC						1.00E+00			
CHASM	lung		0.0357	0.0435	0.803	0.0259	1.84E-04	0.0083	0.0083	0.005
	breast		0.1944	0.2059	0.7152	0.1888	2.85E-22	0.0067	0.0067	0.01
	HNSC							0	0	0.0783
MCGfinder	lung		0.0714	0.1081	0.5916	0.102	1.63E-09	0.045	0.05	0.68
	breast		0.1389	0.2222	0.7473	0.4226	8.80E-17	0.1306	0.121	0.5822011
	HNSC		0.2222	0.25	0.9347	0.1881	1.50E-06	0.03	0.03	0.5719697
NMFT	pancancer		0.1176	0.1509	0.7716	0.3961	8.10E-28	0.16	0.16	0.88
Intdriver	lung		0.0357	0.0541	0.7245	0.0435	2.73E-04	0.0033	0.00667	0.127
	breast		0.1389	0.2128	0.7589	0.3773	3.41E-18	0.05	0.06	0.187
	HNSC		0.1111	0.1333	0.6529	0.0542	3.77E-07	0.02	0.0233	0.27
Dawnrank	lung						1.00E+00			
	breast(90)		0.0278	0.05	0.7449	0.0779	7.45E-05			
	HNSC						1.00E+00			
Dendrix_freq	lung		0.0357	0.0364	0.7374	0.0185	0.006805499	0	0	0.02
	breast		0.0833	0.1538	1	0.8333	8.14E-07	0.027	0.027	0.02666667
	HNSC						1.00E+00	0	0	0.02
Dendrix_weight	lung						1	0	0	0.01666667
	breast		0.1111	0.186	0.9922	0.7589	7.45E-09	0.0267	0.0267	0.02666667
	HNSC						1.00E+00	0	0	0.01666667
DriverNet	lung		0.0714	0.087	0.8418	0.0581	1.37E-04	0	0	0.05555556
	breast		0.1389	0.2041	0.7644	0.3117	3.84E-20	0	0	0.1809524
	HNSC		0.1111	0.1818	0.8213	0.1322	3.77E-07	0	0	0.3660714
Diffusion	lung						1.00E+00	0	0	0.233
	breast						1.00E+00	0	0	0.08360544
	HNSC				0.8081	0.025	2.89E-02	0.01	0.01	0.32
MaxMIF_HumanNet	lung		0.0714	0.1111			1.00E+00	0	0	0.537
	breast		0.1944	0.2121			1.00E+00	0	0	0.433
	HNSC						1.00E+00	0	0	0.667
MaxMIF_Stringv10	lung		0.0714	0.125			1.00E+00	0	0	0.473
	breast		0.3333	0.4138			1.00E+00	0	0	0.5
	HNSC						1.00E+00	0	0	0.657
MaxMIF_Influencegraph	lung		0.1071	0.1429			1.00E+00	0	0	0.373
	breast		0.2222	0.2963			1.00E+00	0	0	0.317
	HNSC						1.00E+00	0	0	0.457
UniCovEx_PPR	lung		0.0714	0.0909	0.6598	0.2081	1.94E-04	0.033	0.03	0.753
	breast		0.1944	0.2692	0.7579	0.4518	2.17E-15	0.1	0.11	0.56
	HNSC		0.2222	0.25	0.9347	0.175	1.29E-05	0.03	0.03	0.71
UniCovEx_Influencegraph	lung		0.0714	0.0952	0.5885	0.1721	3.45E-06	0.04	0.04	0.73
	breast		0.1944	0.2692	0.7712	0.4634	1.41E-15	0.107	0.11	0.557
	HNSC		0.2222	0.25	0.9416	0.1875	1.29E-05	0.03	0.03	0.7

Method	cancer_type	Precision	Recall	Fscore	AUC	AUCPR	HGS	Stability	Recovery	TDC
Muffinne_max_humannet	lung		0.1071	0.125	0.8542	0.127	2.69E-05	0.0433	0.04	1
	breast		0.0833	0.125	0.8126	0.3802	2.02E-05	0.05	0.05	1
	HNSC						1.00E+00	0	0	1
Muffinne_max_stringv10	lung		0.0714	0.08	0.6797	0.0668	2.29E-05	0.037	0.04	0.925
	breast		0.1944	0.2545	0.8864	0.4619	2.36E-11	0.087	0.09	0.998
	HNSC		0.1111	0.1818	0.7908	0.143	1.44E-03	0.02	0.02	1
Muffinne_sum_humannet	lung		0.1071	0.1538	7.87E-01	0.1904	2.69E-05	0.03	0.03	0.913
	breast		0.1389	0.2222	0.7937	0.4436	3.12E-11	0.1	0.09	0.66
	HNSC		0.2222	0.2667	0.8247	0.1405	3.07E-05	0.03	0.03	0.87
Muffinne_sum_stringv10	lung		0.0714	0.1212	0.633	0.1478	1.36E-08	0.06	0.06	0.812
	breast		0.1944	0.2545	0.7374	0.4015	2.60E-18	0.11	0.13	0.54
	HNSC		0.2222	0.25	0.9072	0.1557	2.06E-05	0.03	0.03	0.798
Muffinne_max_influencegraph	lung		0.0357	0.05	0.6263	0.0132	6.81E-03	0.01	0.01	0.815
	breast		0.2222	0.3019	0.707	0.1681	4.09E-19	0.077	0.077	0.6183
	HNSC						1.00E+00	0	0	0.942
Muffinne_sum_influencegraph	lung		0.0357	0.0571	0.7778	0.0217	6.81E-03	0.01	0.01	0.93
	breast		0.1389	0.2174	0.8337	0.1305	6.75E-11	0.05	0.05	0.795
	HNSC				0.1111	0.0056	7.30E-03	0.033	0.033	0.8983
RME	lung				0.4399	0.0248	1.22E-06			
	breast									
	HNSC				0.3827	0.0154	1.58E-04			
Subdyquency	lung		0.1071	0.1395	0.6255	0.1223	2.47E-10	0.0283	0.0267	0.485
	breast		0.1667	0.2553	0.7776	0.3602	5.92E-26	0.065	0.067	0.3383
	HNSC		0.2222	0.2667	0.9798	0.1833	2.06E-03	0.0133	0.01	0.452
EntroRank	lung		0.0714	0.125	0.6512	0.187	3.67E-07	0.0283	0.03	0.705
	breast		0.2778	0.3846	0.8814	0.4997	3.43E-18	0.067	0.075	0.4933
	HNSC		0.1111	0.1333	0.7258	0.0769	1.49E-06	0.0633	0.02	0.643

Table S3: The fscore, recall, precision, AUC,AUCPR,HGS, Stability, Recovery and TDC values of 23 methods under the CCGs benchmark.

CCGs										
	cancer_type	Precision	Recall	Fscore	AUC	AUCPR	HGS	Stability	Recovery	TDC
Activedriver	lung	0.3265	0.3264	0.3265	0.5077	0.4734	1.53E-25	0.357	0.335	0.07
	breast	0.3309	0.3309	0.3309	0.4889	0.4268	6.06E-14	0.3817	0.273	0.06333333
	HNSC	0.3262	0.3262	0.3262	0.4752	0.463	8.56E-24	0.353	0.407	0.06
Music	lung	0.2158	0.2133	0.2146	0.6508	0.628	4.04E-06			
	breast	0.2193	0.2183	0.2188	0.7166	0.5515	9.30E-01			
	HNSC	0.2348	0.2316	0.2332	0.5814	0.5023	1.06E-03			
dndSCV	lung	0.2491	0.2484	0.2488	0.5412	0.4934	1.66E-04	0.345	0.385	0.1966667
	breast	0.2573	0.2573	0.2573	0.68	0.6637	2.66E-01	0.335	0.4	0.21
	HNSC	0.2621	0.2615	0.2618	0.7036	0.6344	6.29E-03	0.357	0.37	0.2533333
polyphen-2	lung	0.224	0.224	0.224	0.388	0.1884	0.04627518	0.273	0.1783	0.1933
	breast	0.2446	0.2432	0.2439	0.4706	0.2279	0.085123	0.3883	0.115	1
	HNSC	0.2348	0.2348	0.2348	0.5568	0.2574	0.009614871	0.28	0.1883	0.13
SIFT	lung	0.2267	0.2249	0.2258	0.5304	0.1994	0.8501789	0.195	0.19	1

Method	Type									
	breast	0.2208	0.2207	0.2208	0.536	0.2783	0.8940014	0.27	0.23	1
	HNSC	0.2265	0.2262	0.2263	0.4822	0.1664	9.21E-01	0.16	0.18	1
MA	lung	0.1711	0.1711	0.1711	0.48	0.2971	0.2464208	0.252	0.215	0.1833
	breast	0.2086	0.2086	0.2086	0.5695	0.3716	3.37E-02	0.317	0.24	0.1083
	HNSC	0.1898	0.1896	0.1897	0.5129	0.3771	4.10E-03	0.302	0.295	0.14
OncodriveFM	lung	0.2232	0.2217	0.2225	0.5379	0.3257	4.75E-06	0.297	0.22	0.5183333
	breast	0.261	0.261	0.261	0.4327	0.3033	1.82E-14	0.33	0.133	0.3283
	HNSC	0.2334	0.2326	0.233	0.5398	0.4146	1.79E-12	0.305	0.275	0.427
Dots-Finder	lung	0.2934	0.2931	0.2932	0.6548	0.7013	6.90E-21	0.51	0.525	0.76
	breast	0.3025	0.3007	0.3016	0.6564	0.6843	6.59E-11	0.465	0.507	0.41
	HNSC	0.3049	0.3049	0.3049	0.6022	0.6641	1.11E-20	0.512	0.545	0.6433
oncodriveclust	lung	0.2774	0.2773	0.2773	0.5195	0.3324	2.46E-13			
	breast	0.3243	0.2106	0.2554	0.6183	0.4256	7.99E-24			
	HNSC	0.3086	0.2783	0.2927	0.5414	0.4166	2.83E-27			
CHASM	lung	0.2472	0.0536	0.0881	0.5718	0.4203	1.90E-66	0.262	0.2217	0.005
	breast	0.3418	0.3417	0.3418	0.6267	0.8235	3.63E-45	0.22	0.0217	0.01
	HNSC	0.2473	0.0402	0.0692	0.4922	0.3274	5.33E-65	0.207	0.163	0.0783
MCGfinder	lung	0.4532	0.0825	0.1395	0.6309	0.6911	1.34E-126	0.353	0.327	0.68
	breast	0.4734	0.0484	0.0878	0.5795	0.6387	6.15E-135	0.6041	0.4232	0.5822011
	HNSC	0.5083	0.0758	0.1319	0.5842	0.659	2.91E-143	0.557	0.3501	0.5719697
NMFT	pancancer	0.5276	0.0259	0.0494	0.6559	0.7096	3.12E-211	0.405	0.405	0.88
Intdriver	lung	0.441	0.0212	0.0405	0.5313	0.4546	9.58E-171	0.027	0.0268	0.127
	breast	0.5076	0.0247	0.0471	0.5902	0.6257	1.95E-186	0.119	0.1186	0.187
	HNSC	0.402	0.0198	0.0377	0.5108	0.487	1.03E-155	0.165	0.167	0.27
Dawnrank	lung	0.2297	0.0294	0.0521	0.5258	0.3215	1.44E-86			
	breast(90)	0.2346	0.0047	0.0092	0.8508	0.2603	9.31E-41			
	HNSC	0.2284	0.0163	0.0304	0.6542	0.4055	5.12E-88			
Dendrix_freq	lung	0.132	0.0064	0.0122	0.4982	0.1592	9.18E-27	0.027	0.0101	0.02
	breast	0.1005	0.0049	0.0094	0.6696	0.3359	4.67E-13	0.025	0.022	0.02666667
	HNSC	0.195	0.0096	0.0184	0.4928	0.2134	2.89E-40	0.033	0.0133	0.02
Dendrix_weight	lung	0.1759	0.0086	0.0165	0.5445	0.2179	2.59E-36	0.027	0.0133	0.01666667
	breast	0.0909	0.004	0.0076	0.6458	0.201	4.27E-15	0.025	0.025	0.02666667
	HNSC	0.148	0.0072	0.0137	0.601	0.2871	1.98E-29	0.033	0.01	0.01666667
DriverNet	lung	0.5655	0.0202	0.0391	0.7479	0.5799	1.00E-177	0.187	0.0467	0.05555556
	breast	0.5285	0.0252	0.0481	0.6013	0.6216	4.48E-192	0.1	0	0.1809524
	HNSC	0.5667	0.0294	0.0559	0.5336	0.6159	1.45E-226	0.117	0	0.3660714
Diffusion	lung	0.4923	0.1104	0.1803	0.556	0.5115	1.81E-85	0.4583	0.2933	0.233
	breast	0.4979	0.0872	0.1484	0.476	0.3679	3.63E-67	0.583	0.164	0.08360544
	HNSC	0.4677	0.1217	0.1932	0.511	0.4921	1.37E-71	0.475	0.283	0.32
MaxMIF_HumanNet	lung	0.3905	0.3847	0.3876	0.5839	0.6862	8.15E-35	0.65	0.63	0.537
	breast	0.3751	0.3751	0.3751	0.6329	0.8135	3.12E-49	0.7283	0.725	0.433
	HNSC	0.3927	0.3914	0.392	0.5788	0.8036	2.62E-58	0.705	0.76	0.667
MaxMIF_Stringv10	lung	0.3894	0.3894	0.3894	0.562	0.6918	4.86E-34	0.6217	0.625	0.473
	breast	0.3967	0.3896	0.3931	0.6026	0.8013	1.65E-45	0.707	0.703	0.5
	HNSC	0.4203	0.4183	0.4193	0.5963	0.8199	3.29E-55	0.74	0.745	0.657
MaxMIF_Influencegraph	lung	0.2908	0.2906	0.2907	0.6167	0.5968	1.63E-16	0.473	0.49	0.373

Method	Cancer								
	breast	0.2825	0.2825	0.2825	0.6111	0.6285	2.14E-12	0.445	0.46	0.317
	HNSC	0.2998	0.2998	0.2998	0.6601	0.6652	6.13E-17	0.463	0.495	0.457
UniCovEx_PPR	lung	0.3612	0.361	0.3611	0.6104	0.6972	1.07E-34	0.543	0.558	0.753
	breast	0.355	0.3548	0.3549	0.5626	0.6654	1.54E-39	0.547	0.58	0.56
	HNSC	0.358	0.358	0.358	0.6218	0.6939	3.25E-41	0.592	0.58	0.71
UniCovEx_Influencegraph	lung	0.4059	0.4059	0.4059	0.6115	0.7383	1.77E-44	0.5683	0.59	0.73
	breast	0.3965	0.3956	0.396	0.6489	0.7173	3.05E-40	0.542	0.56	0.557
	HNSC	0.4	0.3993	0.3997	0.5847	0.7269	1.56E-53	0.615	0.625	0.7
Muffinne_max_humannet	lung	0.4031	0.403	0.403	0.4868	0.2397	6.76E-99	0.237	0.237	1
	breast	0.4028	0.4015	0.4021	0.5231	0.2658	1.67E-93	0.2583	0.2583	1
	HNSC	0.4121	0.4121	0.4121	0.4835	0.2654	3.52E-107	0.272	0.272	1
Muffinne_max_stringv10	lung	0.4259	0.4257	0.4258	0.4897	0.2373	6.16E-93	0.175	0.175	0.925
	breast	0.4518	0.4516	0.4517	0.5296	0.2935	8.50E-103	0.235	0.235	0.998
	HNSC	0.4522	0.444	0.448	0.5185	0.2953	4.06E-113	0.243	0.243	1
Muffinne_sum_humannet	lung	0.3749	0.3719	0.3734	5.71E-01	0.2308	3.31E-75	0.165	0.165	0.913
	breast	0.3749	0.3748	0.3749	0.5111	0.2488	4.04E-86	0.187	0.187	0.66
	HNSC	0.3839	0.3832	0.3835	0.4764	0.2319	1.42E-87	0.197	0.197	0.87
Muffinne_sum_stringv10	lung	0.3561	0.3556	0.3558	0.4802	0.2494	6.87E-101	0.212	0.212	0.812
	breast	0.3676	0.3672	0.3674	0.5473	0.2607	4.04E-86	0.1783	0.1783	0.54
	HNSC	0.3785	0.3773	0.3779	0.4915	0.2493	2.21E-95	0.2083	0.2083	0.798
Muffinne_max_influencegraph	lung	0.435	0.4348	0.4349	0.5788	0.2282	3.00E-73	0.16	0.16	0.815
	breast	0.4319	0.4311	0.4315	0.5337	0.2756	1.67E-93	0.1633	0.1633	0.6183
	HNSC	0.4449	0.4407	0.4428	0.5457	0.2632	2.00E-93	0.18	0.18	0.942
Muffinne_sum_influencegraph	lung	0.4031	0.403	0.403	0.4587	0.2243	6.60E-97	0.237	0.237	0.93
	breast	0.3894	0.3891	0.3893	0.5511	0.265	8.33E-90	0.227	0.227	0.795
	HNSC	0.4051	0.4049	0.405	0.4799	0.2355	2.21E-95	0.235	0.235	0.8983
RME	lung	0.1033	0.0101	0.0184	0.545	0.1992	4.92E-35			
	breast									
	HNSC	0.0687	0.0067	0.0122	0.6295	0.2223	6.01E-42			
Subdyquency	lung	0.4234	0.2123	0.2828	0.6247	0.7074	6.37E-87	0.545	0.457	0.485
	breast	0.4474	0.1711	0.2475	0.6148	0.7337	8.60E-98	0.555	0.355	0.3383
	HNSC	0.413	0.2286	0.2943	0.5971	0.7417	1.34E-100	0.5983	0.4683	0.452
EntroRank	lung	0.3523	0.3511	0.3517	0.5587	0.717	1.65E-50	0.6483	0.67	0.705
	breast	0.3124	0.3123	0.3124	0.5794	0.7782	1.21E-50	0.615	0.65	0.4933
	HNSC	0.3534	0.3516	0.3525	0.6481	0.8137	2.69E-60	0.6817	0.72	0.643

Table S4: The exactly locations of the union of the top 100 genes by each method and whether they belong to driver genes with respect to different benchmarks, for breast cancer. For the last three column the value 'Y' denotes this gene can be found by the corresponding benchmark, the value 'N' otherwise.

Table S5: The exactly locations of the union of the top 100 genes by each method and whether they belong to driver genes with respect to different benchmarks, for HNSC cancer. For the last three column the value 'Y' denotes this gene can be found by the corresponding benchmark, the value 'N' otherwise.

Table S6: The exactly locations of the union of the top 100 genes by each method and whether they belong to driver genes with respect to different benchmarks, for lung cancer. For the last three column the value 'Y' denotes this gene can be found by the corresponding benchmark, the value 'N' otherwise.

Table S7: The count of top 100 genes which is identified by only one method and acknowledged by NCG 6.0 for each cancer. The empty cell means the total number of detected genes by this method has no 100.

Method names	breast(distinct genes) of top 100	breast driver genes of Top100	HNSC(distinct genes) of top 100	HNSC driver genes of Top100	Lung(distinct genes) of top 100	Lung driver genes of Top100
activedriver	58	15	61	16	53	20
Music	34	44	33	27	17	30
dndscv	41	45	52	38	51	39
OncodriveClust	49	28	59	20	78	16
polyphen-2	58	12	71	9	87	6
SIFT	50	3	68	1	60	4
MA	54	5	49	13	58	3
OncodriveFM	30	15	39	9	49	9
dotsfinder	6	46		35		34
CHASM	45	72	76	10	67	18
dendrix_frequency	57	11	80	4	87	2
dendrix_weight	56	9	80	7	86	1
RME				18	17	24
Unicovex_PPR	12	35		33		33
Unicovex_influencegraph	3	33	6	36	5	37
MaxMIF_HumanNet	15	47	11	34	17	33
MaxMIF_STRINGv10	19	48	19	50	22	41
MaxMIF_Influencegraph	30	34	12	34	11	32
Muf_max_HumanNet	40	34	13	31	26	34
Muf_max_STRINGv10	24	35	31	32	18	35
Muf_sum_HumanNet	24	37	29	35	28	32
Muf_sum_STRINGv10	3	43	0	41	5	45
Muf_max_influencegraph	12	34	39	26	27	21
Muf_sum_influencegraph	14	40	29	38	29	37
DawnRank	69	7	84	9	86	6
drivernet	34	29	27	29	39	24
diffusion	71	10	13	15	53	17
Subdyquency	12	42	7	34	5	32
EntroRank	22	50	24	46	24	46
MCGfinder	16	32	7	34	17	36
NMTF	33	24	28	30	0	34
Intdriver	23	28	40	17	38	25

Table S8: The 47 pathways which can be simultaneously enriched by the three best Fscore methods e.g. DotsFinder for statistical significance-based methods, CHASM for machine-learning-based method, MaxMIF_stringV10 for network-based method for breast cancer.

Triple overlapped pathways for breast cancer
Thyroid hormone signaling pathway
Pancreatic cancer
EGFR tyrosine kinase inhibitor resistance
Endometrial cancer
ErbB signaling pathway
Proteoglycans in cancer
Breast cancer
Central carbon metabolism in cancer
Prostate cancer
Melanoma
Endocrine resistance
Platinum drug resistance
Glioma
Gastric cancer
Non-small cell lung cancer
Calcium signaling pathway
PI3K-Akt signaling pathway
Cellular senescence
Focal adhesion
Type II diabetes mellitus
Human papillomavirus infection
Chronic myeloid leukemia
Human T-cell leukemia virus 1 infection
Colorectal cancer
PD-L1 expression and PD-1 checkpoint pathway in cancer
Small cell lung cancer
Hepatitis B
Hepatocellular carcinoma
Acute myeloid leukemia
MAPK signaling pathway
Bladder cancer
cAMP signaling pathway
HIF-1 signaling pathway
Longevity regulating pathway
Rap1 signaling pathway
MicroRNAs in cancer
Longevity regulating pathway - multiple species
Ubiquitin mediated proteolysis
Apoptosis
Apelin signaling pathway
Measles
GnRH secretion

Chagas disease (American trypanosomiasis)
Kaposi sarcoma-associated herpesvirus infection
Toll-like receptor signaling pathway
Fc epsilon RI signaling pathway
Aldosterone-regulated sodium reabsorption

Table S9: The count of enriched pathway by the top 100 genes of each method and the involving distinct genes for breast cancer.

method_name	pathway_count	distinct_counts
activedriver	1	10
CHASM	10	57
diffusion	10	52
dndscv	10	34
dotsfinder	10	24
drivernet	10	63
EntroRank	10	72
Intdriver	10	39
MA	10	37
MaxMIF_HumanNet	10	59
MaxMIF_Influencegraph	10	28
MaxMIF_STRINGv10	10	76
MCGfinder	10	41
Muf_max_HumanNet	10	86
Muf_max_influencegraph	10	83
Muf_max_STRINGv10	10	91
Muf_sum_HumanNet	10	66
Muf_sum_influencegraph	10	91
Muf_sum_STRINGv10	10	56
Music	10	20
NMTF	10	35
OncodriveClust	10	29
Subdyquency	10	62
Unicovex_influnecegraph	10	47
Unicovex_PPR	10	44

Table S10: The count of enriched pathway by the top 100 genes of each method and the involving distinct genes for lung cancer.

method_name	pathway_count	distinct_counts
activedriver	9	33
CHASM	3	15
DawnRank	2	18
diffusion	10	47
dndscv	10	18
dotsfinder	10	32
drivernet	10	55
EntroRank	10	73
Intdriver	10	71
MA	2	11
MaxMIF_HumanNet	10	52
MaxMIF_Influencegraph	10	29
MaxMIF_STRINGv10	10	54
MCGfinder	10	44
Muf_max_HumanNet	10	59
Muf_max_influencegraph	10	67
Muf_max_STRINGv10	10	76
Muf_sum_HumanNet	10	49
Muf_sum_influencegraph	10	88
Muf_sum_STRINGv10	10	48
Music	1	29
NMTF	10	35
OncodriveClust	10	43
OncodriveFM	1	7
RME	10	40
Subdyquency	10	63
Unicovex_influencegraph	10	49
Unicovex_PPR	10	44

Table S11: The count of enriched pathway by the top 100 genes of each method and the involving distinct genes for HNSC cancer.

method_name	pathway_count	distinct_counts
activedriver	10	29
CHASM	1	9
diffusion	10	48
dndscv	10	35
dotsfinder	10	46
drivernet	10	65
EntroRank	10	62
Intdriver	8	33
MA	10	33
MaxMIF_HumanNet	10	61
MaxMIF_Influencegraph	4	25
MaxMIF_STRINGv10	10	55
MCGfinder	10	41
Muf_max_HumanNet	10	82
Muf_max_influencegraph	10	84
Muf_max_STRINGv10	10	82
Muf_sum_HumanNet	10	57
Muf_sum_influencegraph	10	82
Muf_sum_STRINGv10	10	54
Music	8	21
NMTF	10	35
OncodriveClust	10	30
OncodriveFM	1	5
RME	10	10
Subdyquency	10	54
Unicovex_influencegraph	10	44
Unicovex_PPR	10	37

Table S12: the co-citer counts of breast cancer with keywords('breast', 'cancer', 'driver') and whether they can be recognized by the three benchmarks (NCG 6.0, CGC, CCGs) and which category method they are detected by.

Genes	breast	cancer	driver	ncg_6	cgc	ccgs	statistical significance-based method	machine-learning-based method	network-based method
TP53	1177	5942	55	Y	Y	Y	1	1	1
PIK3CA	170	576	13	Y	Y	Y	1	1	1
GATA3	84	114	4	Y	Y	Y	1	1	1
NCOR1	16	58	2	Y	Y	Y	1	1	1
PTEN	595	2597	35	Y	N	Y	1	1	1
CDH1	291	1143	13	Y	Y	Y	1	0	1
MAP2K4	10	66	2	Y	Y	Y	1	1	1
TTN	2	8	1	N	N	Y	1	0	1
AKT1	477	1863	13	Y	Y	Y	1	0	1
PIK3R1	14	97	6	Y	N	Y	1	1	1
MAP3K1	59	129	2	Y	Y	Y	1	1	1
BRCA1	3565	4068	11	Y	N	Y	1	1	1
RYR2	2	3	2	Y	N	Y	1	0	1
MUC16	17	239	1	N	N	Y	1	0	1
NEB	1	4	1	N	N	N	1	0	1
NF1	19	137	8	Y	N	Y	1	1	1
CTCF	18	50	3	Y	Y	Y	1	1	1
BRCA2	2433	2829	12	Y	Y	Y	1	1	1
SPTA1	0	3	1	Y	N	Y	1	0	1
APOB	1	23	1	Y	N	N	1	0	1
MUC12	0	2	0	N	N	N	1	0	1
ERBB2	3631	4422	36	Y	Y	Y	1	1	1
ATM	370	1222	5	Y	N	Y	1	1	1
RUNX1	14	110	6	Y	N	Y	1	1	1
FLG	2	7	0	Y	N	N	1	0	1
LRP2	0	9	1	N	N	Y	1	0	1
DMD	1	19	3	Y	N	Y	1	0	1
SPEN	1	8	1	Y	N	Y	1	0	1
RYR3	1	3	1	N	N	Y	1	0	1
TBX3	22	43	2	Y	Y	N	1	0	1
OBSCN	1	4	0	N	N	Y	1	0	1
MED12	2	13	2	Y	N	Y	1	1	1
RB1	116	604	7	Y	Y	Y	1	1	1
MUC5B	6	26	2	N	N	Y	1	0	1
FOXA1	82	128	5	Y	Y	Y	1	0	1
SYNE1	0	2	1	Y	N	Y	1	0	1
CBFB	5	18	2	Y	N	Y	1	0	1
MTOR	321	1896	21	Y	N	Y	0	1	1
CREBBP	38	95	2	Y	N	Y	0	1	1
DNAH5	0	2	1	N	N	N	1	0	1
MUC17	0	7	0	Y	N	Y	1	0	1
RELN	2	9	2	N	N	Y	1	0	1

Table S13: the co-citer counts of lung cancer with keywords('lung', 'cancer', 'driver') and whether they can be recognized by the three benchmarks (NCG 6.0, CGC, CCGs) and which category method they are detected by. For the last six column, the value '1' or 'Y' denote this gene can be found by the corresponding category method or benchmark, the value '0' or 'N', otherwise.

Genes	lung	cancer	driver	ncg_6	cgc	ccgs	statistical significance-based method	machine-learning-based method	network-based method
TP53	854	5942	55	Y	Y	Y	1	1	1
TTN	1	8	1	N	N	Y	1	0	1
KRAS	867	2538	95	Y	Y	Y	1	0	1
MUC16	22	239	1	Y	N	Y	1	0	1
RYR2	3	3	2	N	N	Y	1	0	1
EGFR	2262	4091	94	Y	N	Y	1	0	1
ANK2	1	4	0	N	N	Y	1	0	1
LRP1B	8	15	2	Y	N	Y	1	0	1
SPTA1	2	3	1	Y	N	Y	1	0	1
DMD	14	19	3	Y	N	Y	1	0	1
APOB	3	23	1	Y	N	N	1	0	1
RYR3	2	3	1	N	N	Y	1	0	1
OBSCN	0	4	0	N	N	Y	1	0	1
RYR1	0	3	1	N	N	Y	1	0	1
CDH10	2	0	1	Y	N	Y	1	1	1
ACTN2	3	5	1	N	N	N	0	0	1
TSHZ3	1	3	1	Y	N	N	1	0	1
PTPRD	7	16	1	Y	Y	Y	1	1	1
MYH2	4	3	1	N	N	Y	1	0	1
MUC17	0	7	0	Y	N	Y	1	0	1
FLG	3	7	0	Y	N	N	1	0	1
RIMS2	0	1	1	Y	N	Y	1	0	1
CACNA1E	0	1	1	N	N	Y	1	0	1
PEG3	1	13	2	N	N	Y	1	0	1
SYNE1	1	2	1	N	N	Y	1	0	1
KEAP1	63	173	3	Y	N	Y	1	0	1
CSMD3	0	3	1	Y	Y	Y	1	0	1
FAT3	1	0	1	N	N	Y	1	0	1
COL11A1	7	14	1	Y	N	Y	1	0	1
MYH1	1	14	1	N	N	Y	1	0	1
PAPPA2	1	4	1	N	N	Y	1	0	1
NLRP3	57	31	1	Y	N	Y	1	0	1
NAV3	2	5	2	Y	N	Y	1	0	1
FAT1	7	15	2	Y	N	Y	1	0	1
NEB	0	4	1	N	N	N	0	0	1
USH2A	2	4	1	N	N	Y	1	0	1
VCAN	8	30	1	Y	N	Y	0	0	1
ZFHX4	1	3	1	Y	N	Y	1	0	1

Table S14: the co-citer counts of HNSC cancer with keywords('Head', 'Neck', 'Head-Neck squamous cell carcinoma' 'cancer', 'driver') and whether they can be recognized by the three benchmarks (NCG 6.0, CGC, CCGs) and which category method they are detected by. For the last six column, the value '1' or 'Y' denote this gene can be found by the corresponding category method or benchmark, the value '0' or 'N', otherwise.

Genes	Head	Neck	Head-Neck Squamous Cell Carcinoma	cancer	driver	ncg_6	cgc	ccgs	statistical significance-based method	machine-learning-based method	network-based method
TP53	203	192	72	5942	55	Y	N	Y	1	0	1
CDKN2A	72	69	24	1073	13	Y	N	Y	1	1	1
TTN	10	2	0	8	1	N	N	Y	1	0	1
NOTCH1	51	14	6	486	23	Y	Y	Y	1	0	1
EP300	1	0	0	145	2	Y	N	Y	1	0	1
PIK3CA	27	18	12	576	13	Y	N	Y	1	0	1
FAT1	2	2	0	15	2	Y	Y	Y	1	0	1
RYR2	2	3	0	3	2	N	N	Y	1	0	1
CREBBP	4	0	0	95	2	Y	N	Y	0	0	1
MUC16	1	1	0	239	1	N	N	Y	1	0	1
DMD	2	0	0	19	3	Y	N	Y	1	0	1
CASP8	24	20	8	694	1	Y	N	Y	1	0	1
SYNE1	1	0	0	2	1	Y	N	Y	1	0	1
DNAH5	1	0	0	2	1	N	N	N	1	1	1
PCDH15	6	0	0	4	1	Y	N	Y	1	0	1
ANK2	1	0	0	4	0	N	N	Y	1	0	1
LRP2	1	0	0	9	1	N	N	Y	1	0	1
LRP1B	0	0	0	15	2	N	N	Y	1	0	1
NSD1	7	1	0	16	2	Y	N	Y	1	0	1
CTNND2	1	0	0	19	1	N	N	N	1	1	1
COL11A1	3	1	0	14	1	N	N	Y	1	0	1
APOB	6	2	0	23	1	Y	N	N	1	0	1
FBXW7	3	2	1	144	8	Y	N	Y	1	0	1
RELN	3	1	0	9	2	N	N	Y	1	0	1
PLEC	5	1	1	25	1	N	N	Y	1	0	1
HRAS	19	17	1	699	8	Y	N	Y	1	1	1
HUWE1	0	0	0	22	2	Y	N	Y	1	0	1
DNAH7	1	0	0	0	1	N	N	N	1	0	1
FLG	0	1	0	7	0	Y	N	N	1	0	1
MUC17	0	0	0	7	0	Y	N	Y	1	0	1
CUBN	1	0	0	8	2	N	N	N	1	0	1
FAT4	8	1	0	29	1	N	Y	Y	1	0	1
NEB	2	1	0	4	1	N	N	N	1	0	1
CDH10	0	0	0	0	1	Y	N	Y	1	0	1
COL1A2	4	9	1	23	1	Y	N	Y	0	0	1
PCLO	0	0	0	2	1	N	N	N	1	0	1
AHNAK	2	2	0	13	1	N	N	N	1	0	1
PEG3	3	0	0	13	2	N	N	Y	1	0	1

Figure S1: The number of the top 100 genes that were predicted by one, two or more methods for breast cancer. The red bar on the left indicates the scale of identified genes for each method.
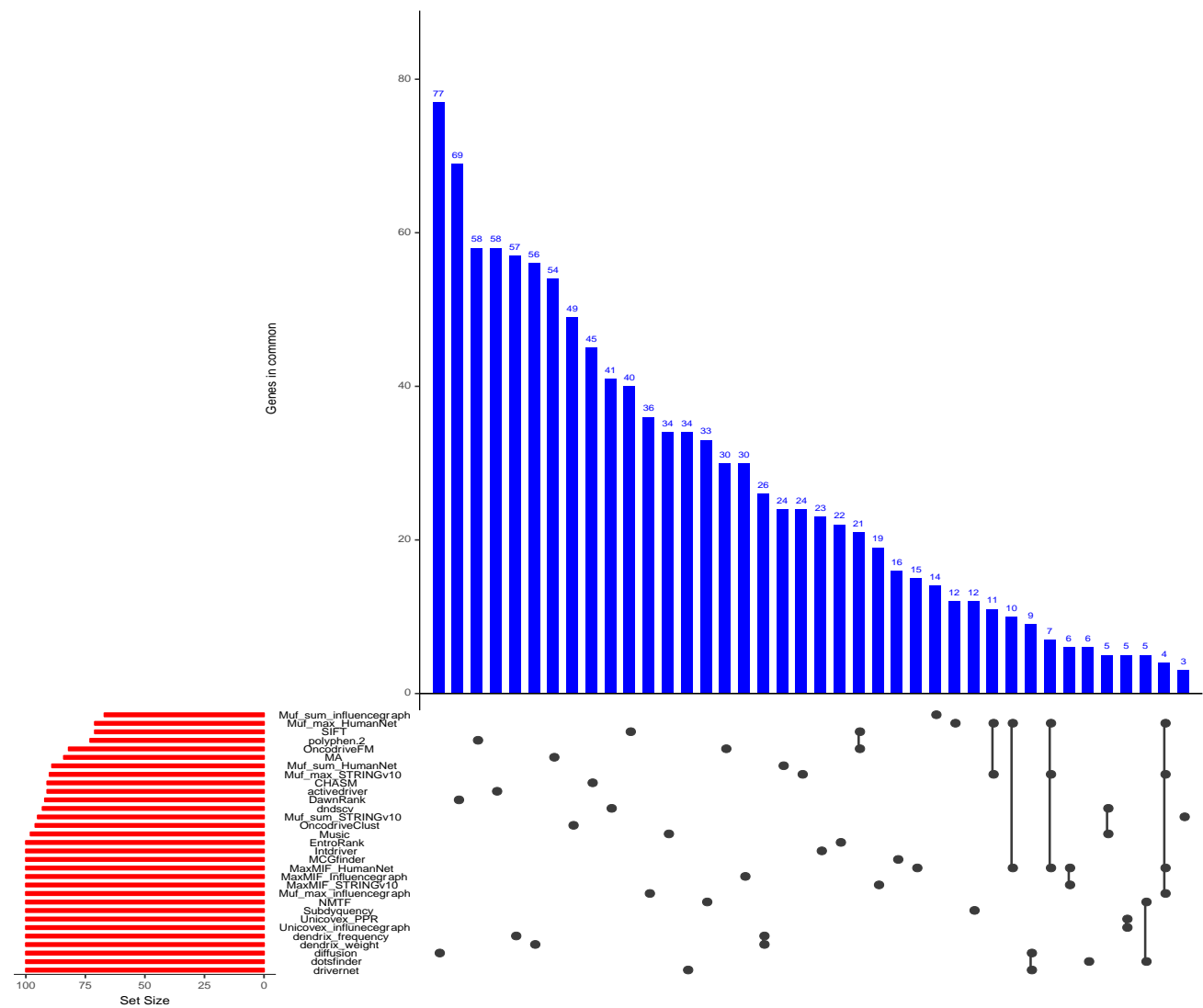
Figure S2: The number of the top 100 genes that were predicted by one, two or more methods for lung cancer. The red bar on the left indicates the scale of identified genes for each method.
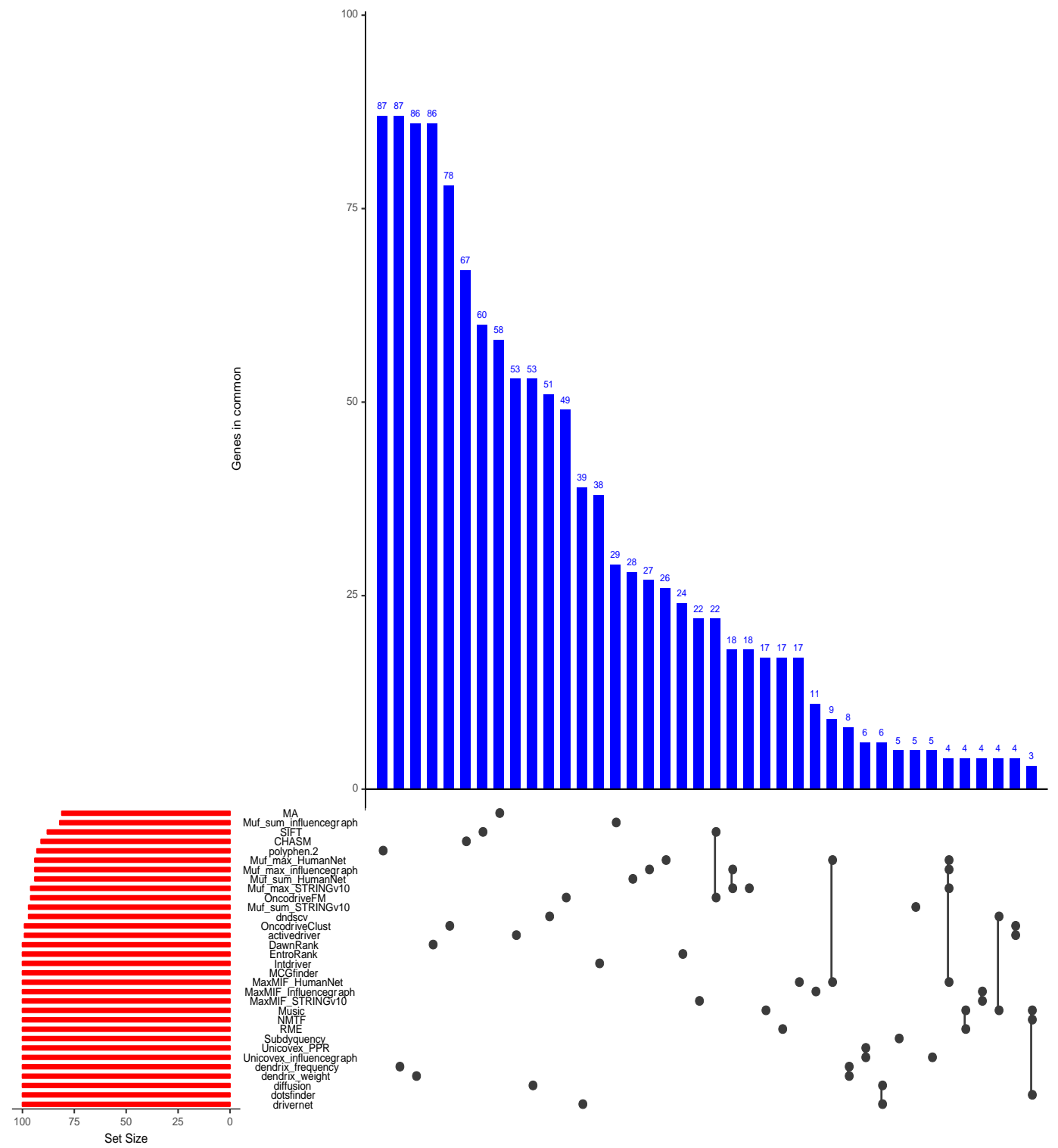
Figure S3: The number of the top 100 genes that were predicted by one, two or more methods for HNSC cancer. The red bar on the left indicates the scale of identified genes for each method.
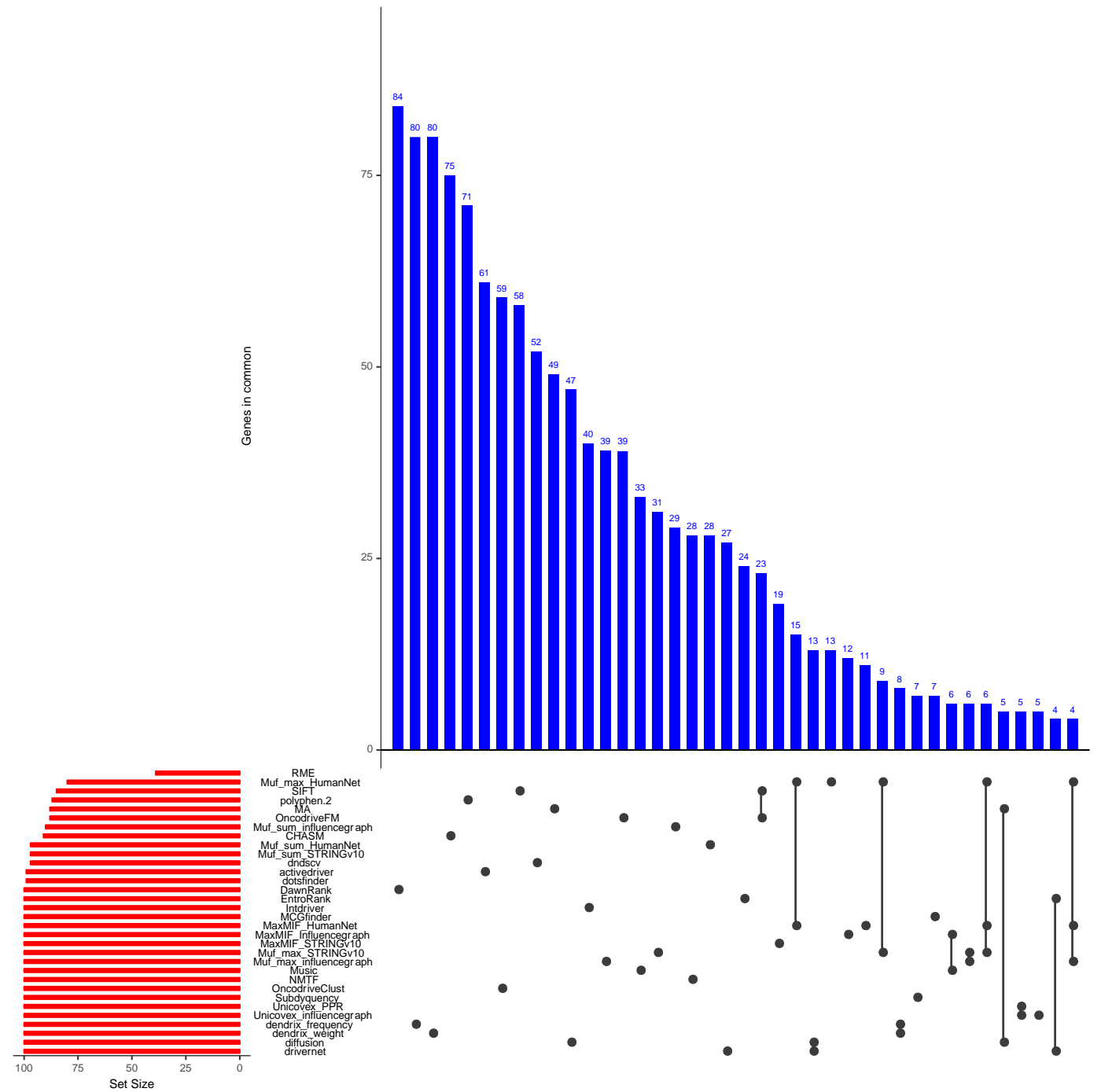
Figure S4: The number of distinct genes and real driver genes identified by each method from its top 100 gene list for breast cancer.
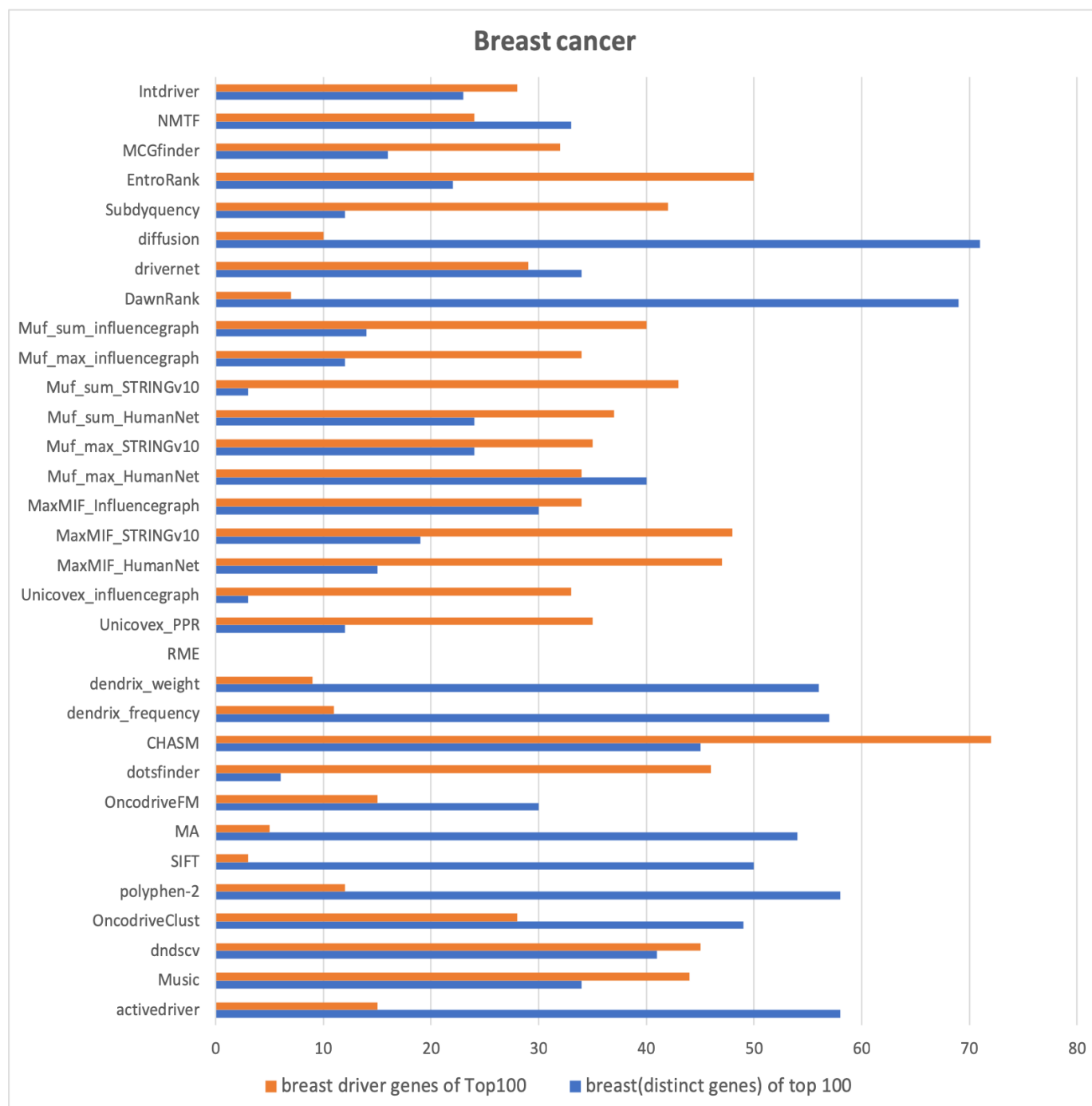
Lung cancer

■ Lung driver genes of Top100   ■ Lung(distinct genes) of top 100

Figure S6: The number of distinct genes and real driver genes identified by each method from its top 100 gene list for HNSC cancer.

HNSC Cancer
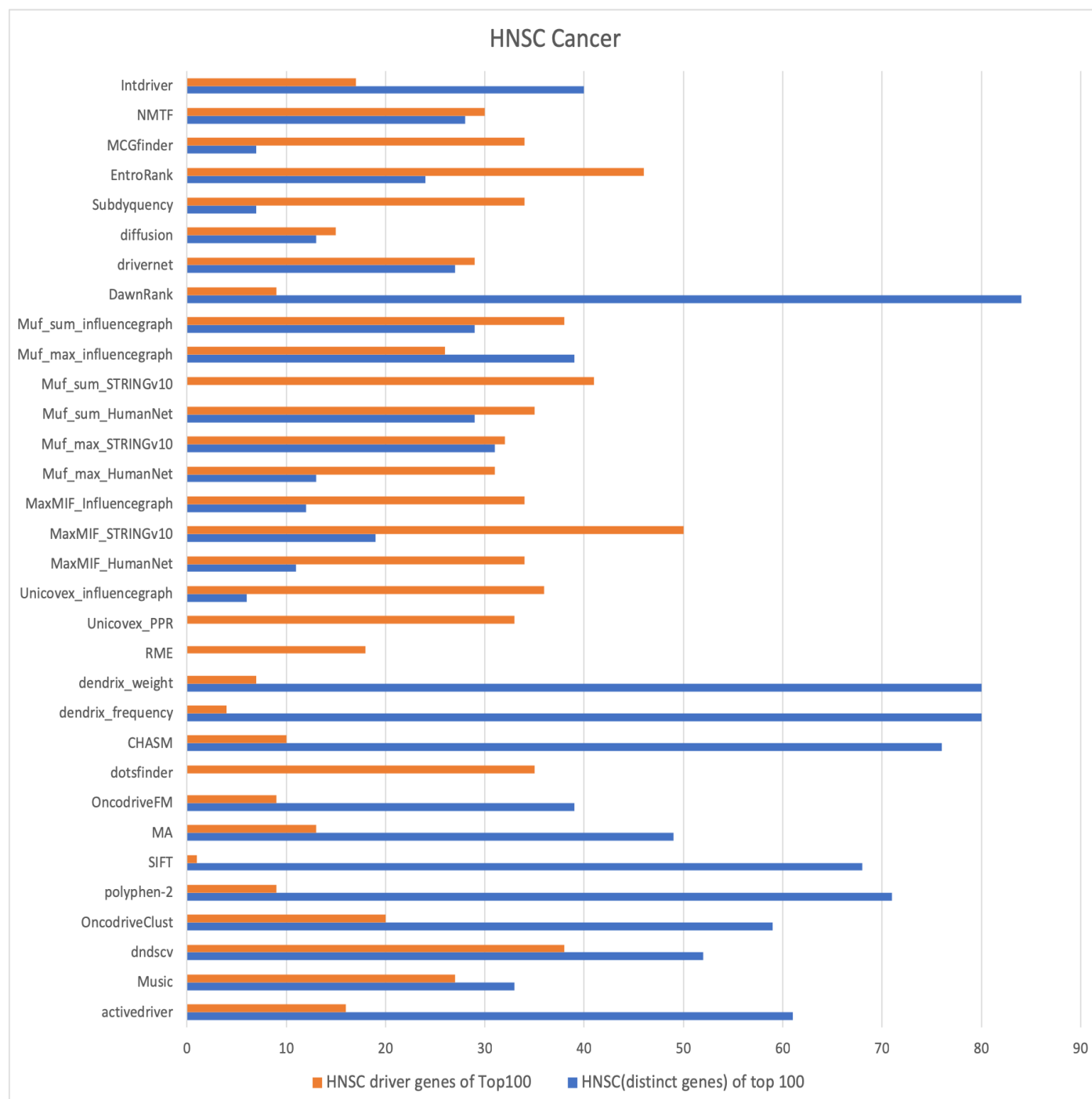
Figure S7: the overlap of enriched pathways for the three big category methods(e.g. statistical significance-based method, machine-learning-based method and network-based method) with best Fscore.
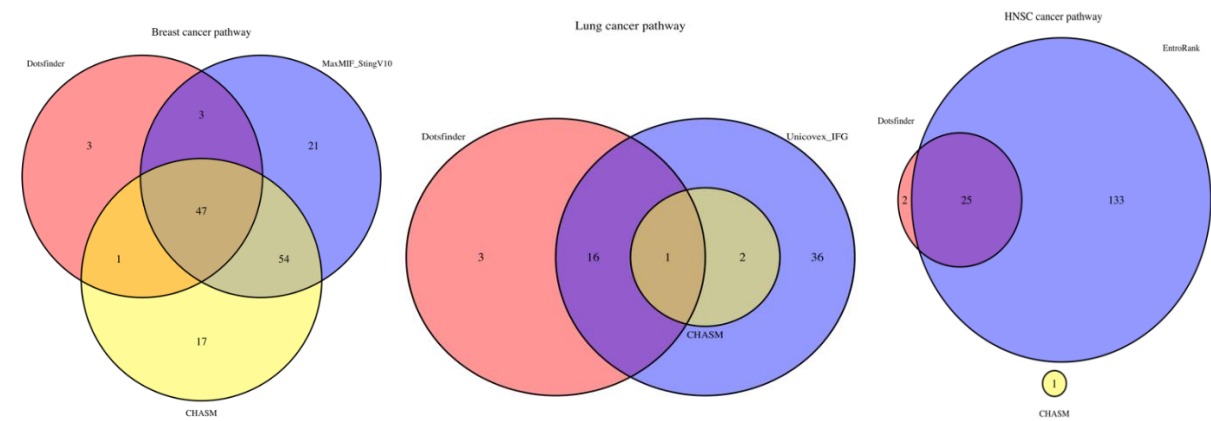
Figure S8: the overlap of enriched GO terms(e.g. biological process, molecular function and cellular component) for the three big category methods(e.g. statistical significance-based method, machine-learning-based method and network-based method) with best Fscore for breast cancer.
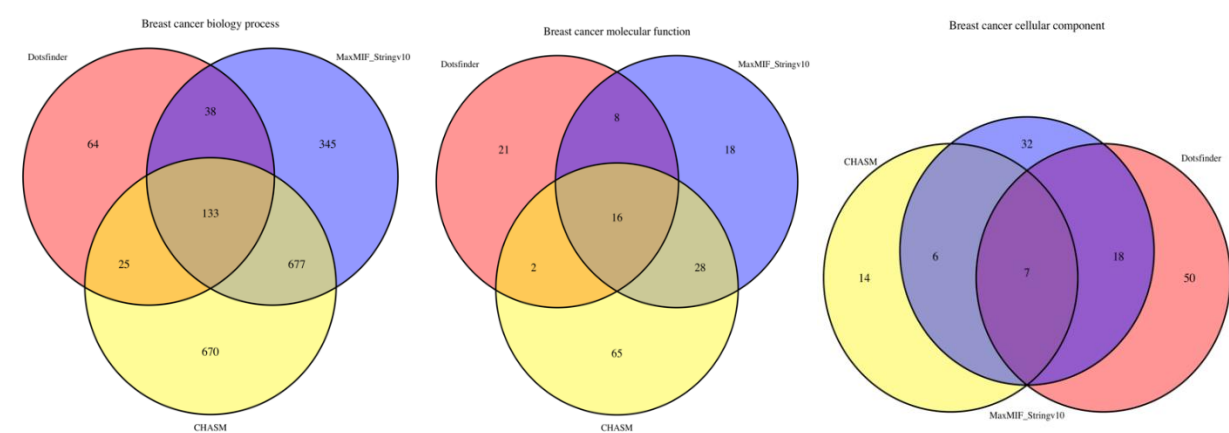
Figure S9: the overlap of enriched GO terms(e.g. biological process, molecular function and cellular component) for the three big category methods(e.g. statistical significance-based method, machine-learning-based method and network-based method) with best Fscore for lung cancer.
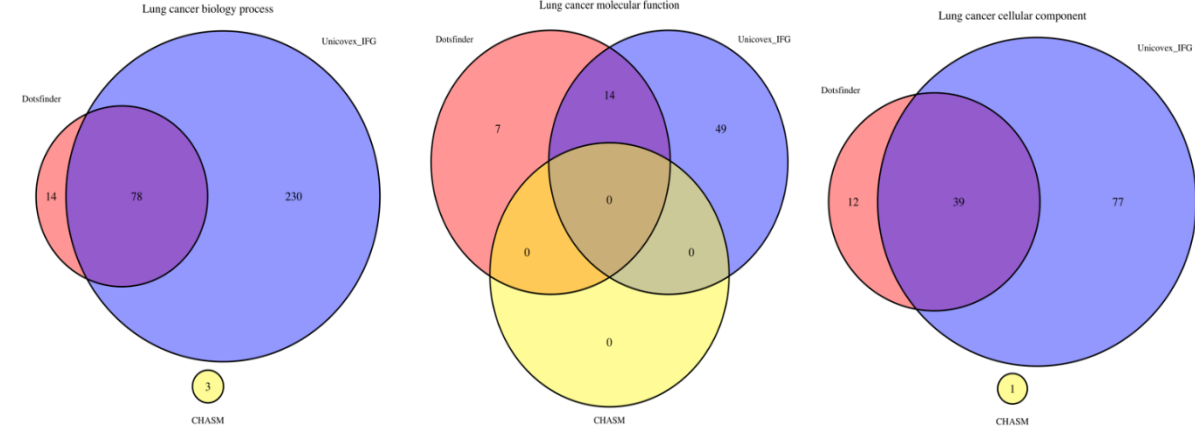
Figure S10: the overlap of enriched GO terms(e.g. biological process, molecular function and cellular component) for the three big category methods(e.g. statistical significance-based method, machine-learning-based method and network-based method) with best Fscore for HNSC cancer.
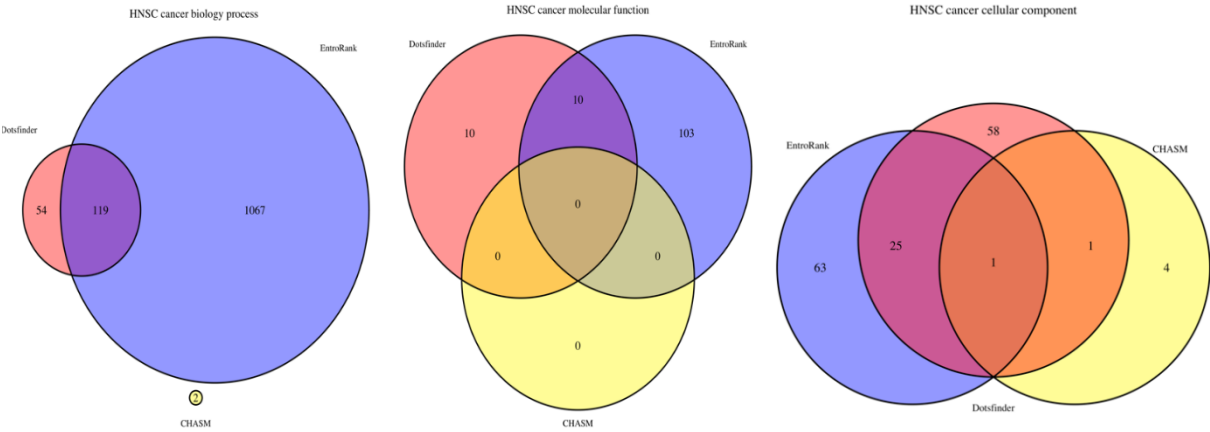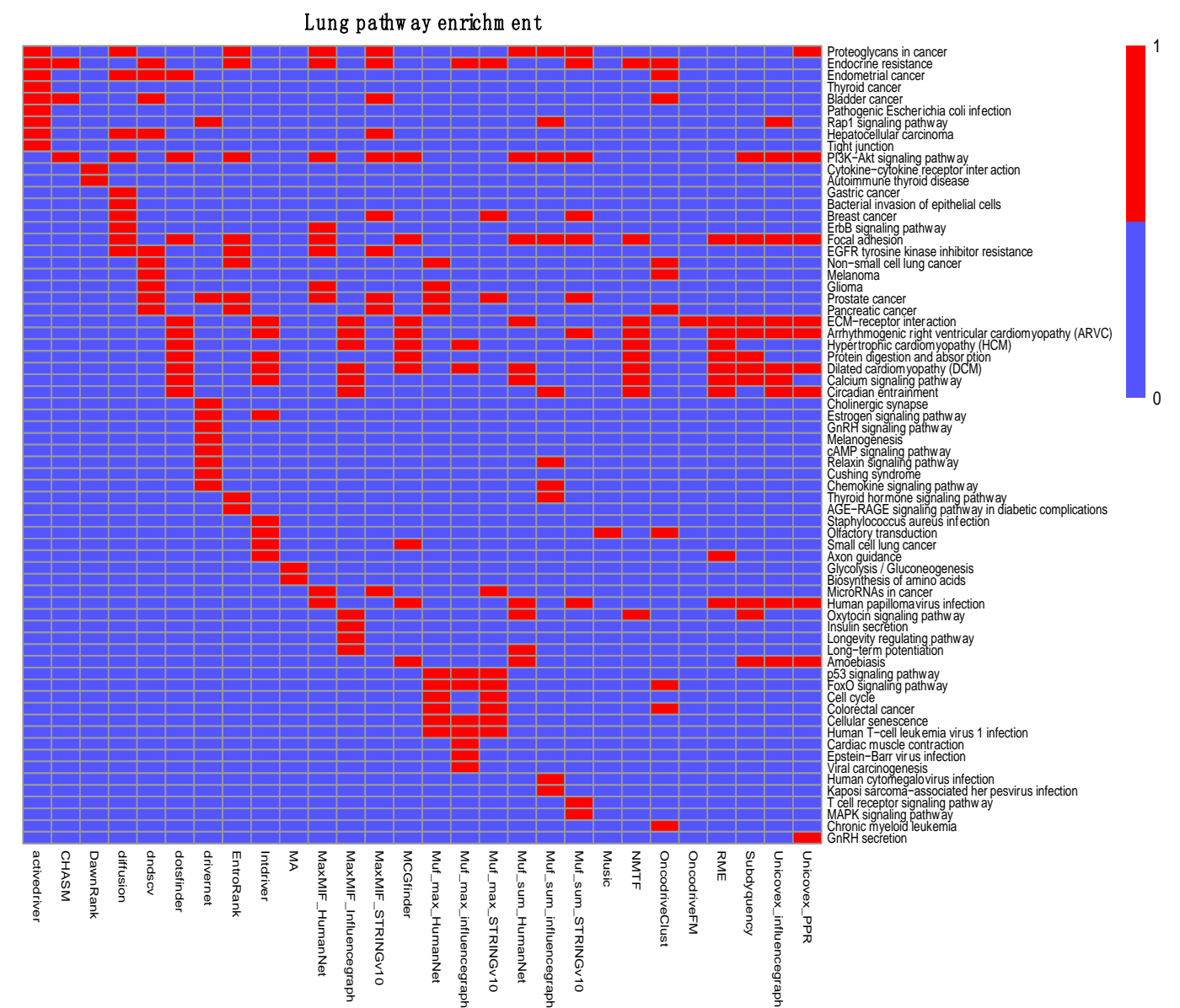

Figure S11: the heat map of enriched pathways by each method for breast cancer. The red cell indicates this pathway is significant enriched by its corresponding method, 0 otherwise.
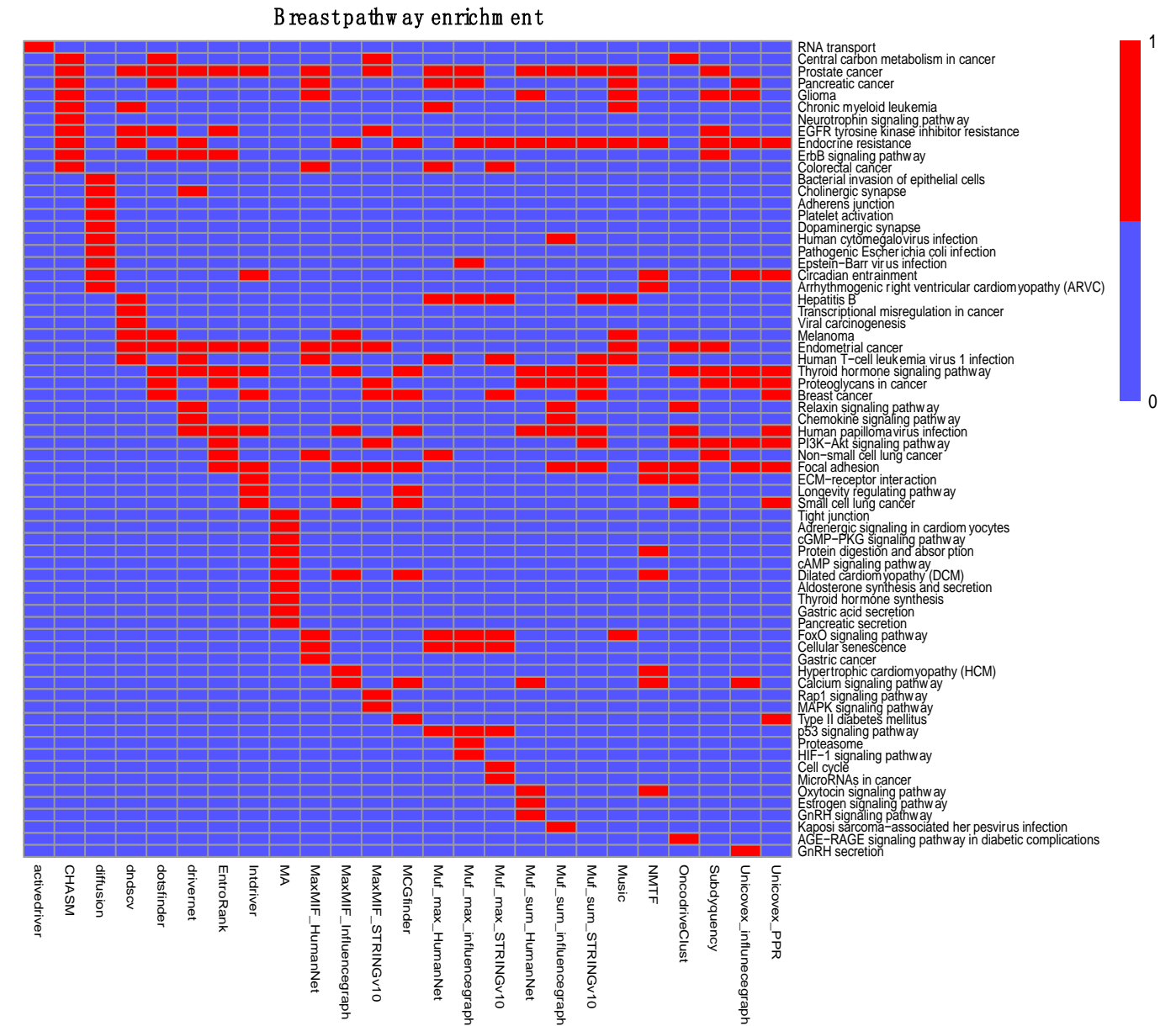
Figure S12: the heat map of enriched pathways by each method for lung cancer.

Figure S13: the heat map of enriched pathways by each method for HNSC cancer. The red cell indicates this pathway is significant enriched by its corresponding method, 0 otherwise.
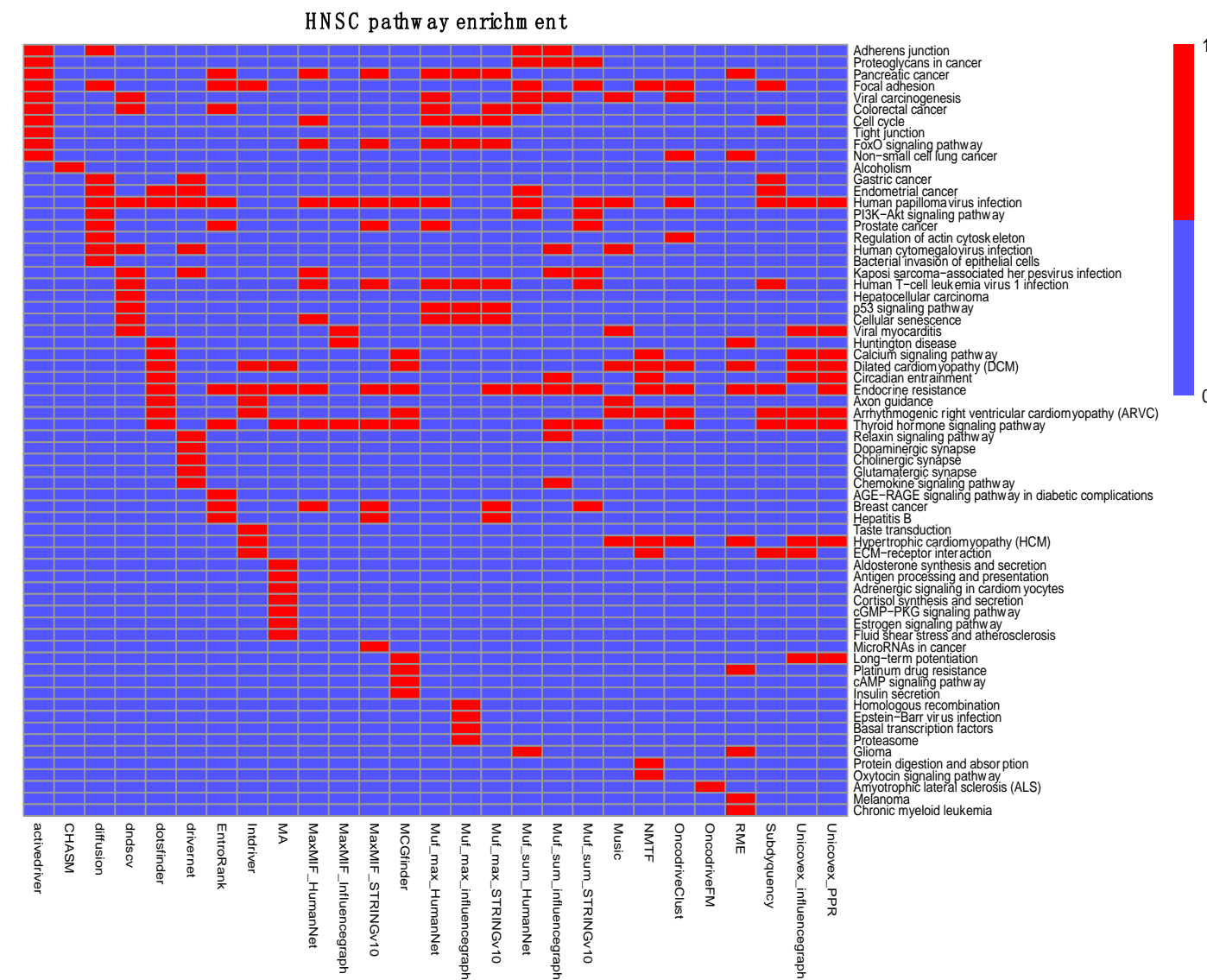

HNSC pathway enrichment

Figure S14: the heat map of enriched GO terms in cellular component(CC) process by each method for breast cancer. The red cell indicates this GO term is significant enriched by its corresponding method, 0 otherwise.
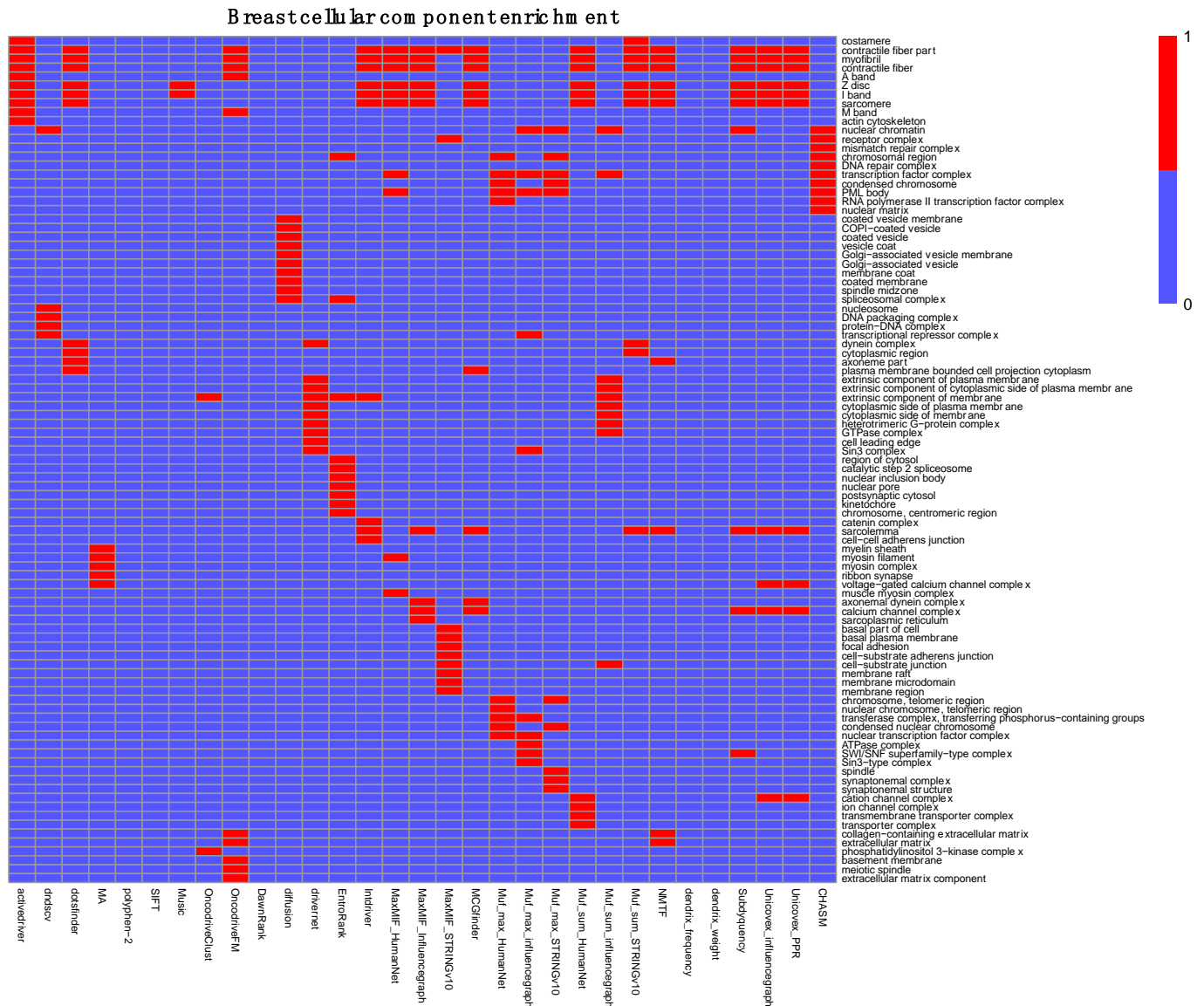

Breast cellular component enrichment

Figure S15: the heat map of enriched GO term in biology process(BP) by each method for breast cancer. The red cell indicates this GO term is significant enriched by its corresponding method, 0 otherwise.
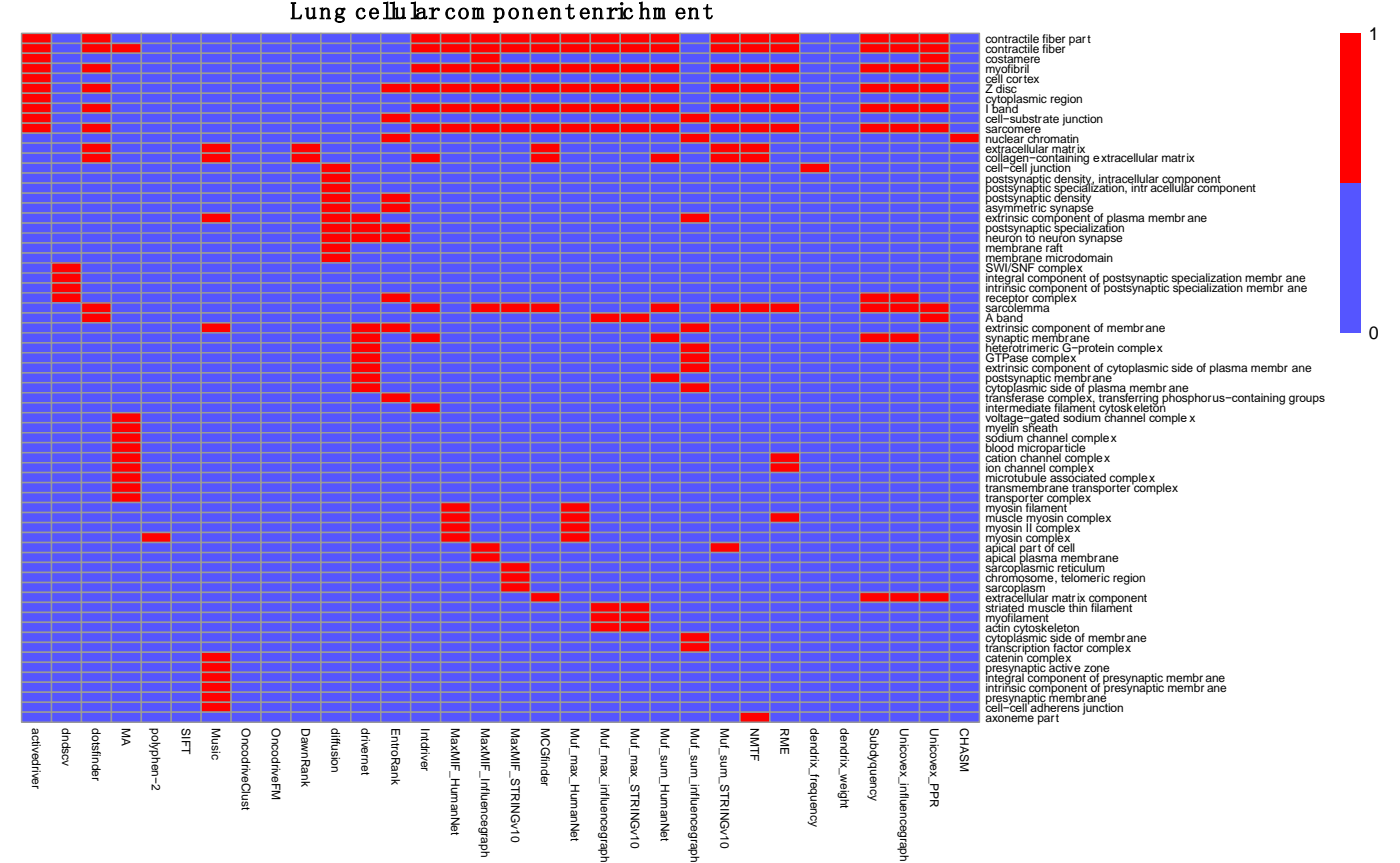
Figure S16: the heat map of enriched GO term in molecular function(MF) by each method for breast cancer. The red cell indicates this GO term is significant enriched by its corresponding method, 0 otherwise.

Breast molecular function enrichment

Figure S17: the heat map of enriched GO term in cellular component(CC) by each method for lung cancer. The red cell indicates this GO term is significant enriched by its corresponding method, 0 otherwise.

Lung biology process enrichment

Figure S19: the heat map of enriched GO term in molecular function(MF) by each method for lung cancer. The red cell indicates this GO term is significant enriched by its corresponding method, 0 otherwise.
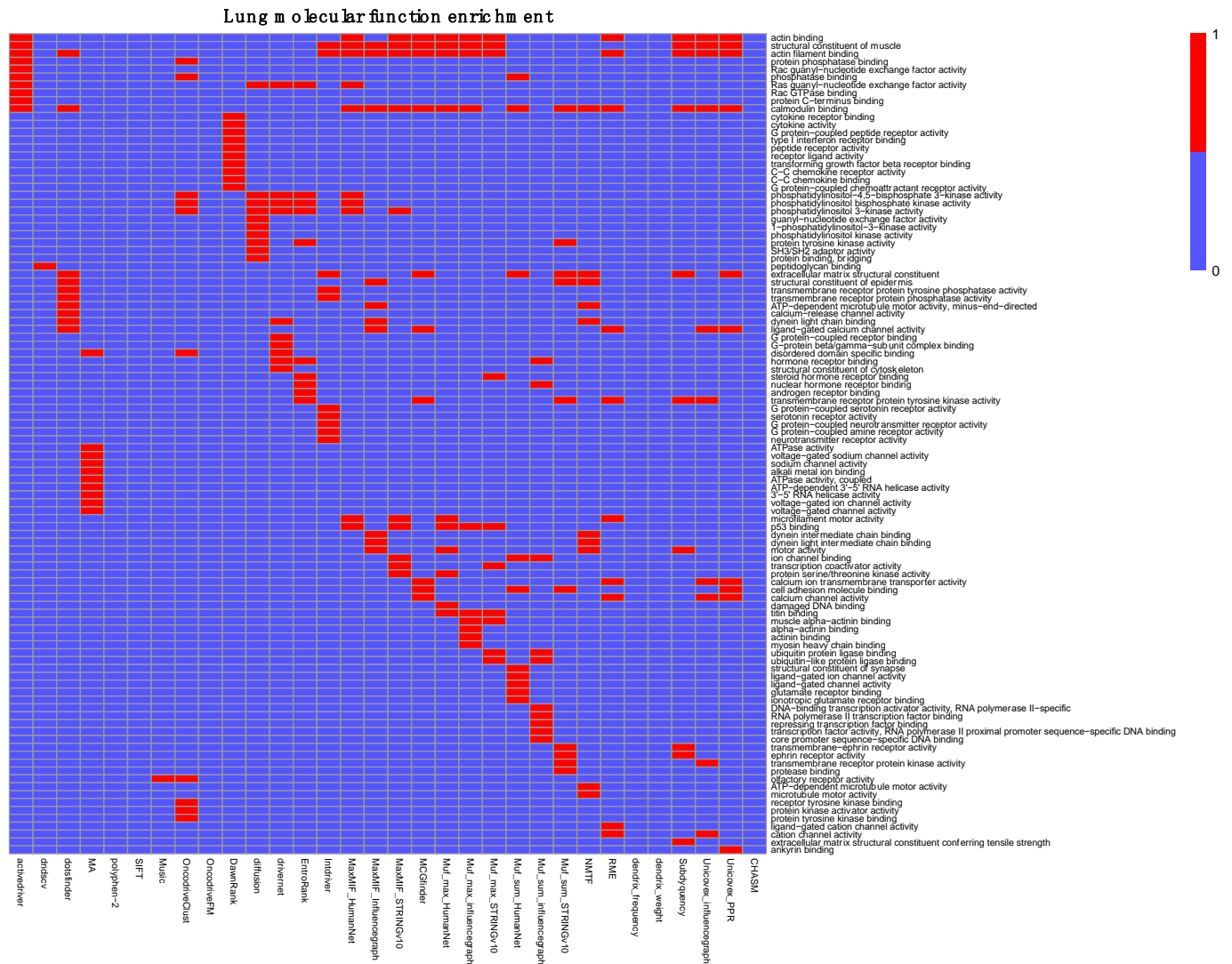
Figure S20: the heat map of enriched GO term in cellular component(CC) by each method for HNSC cancer. The red cell indicates this GO term is significant enriched by its corresponding method, 0 otherwise.
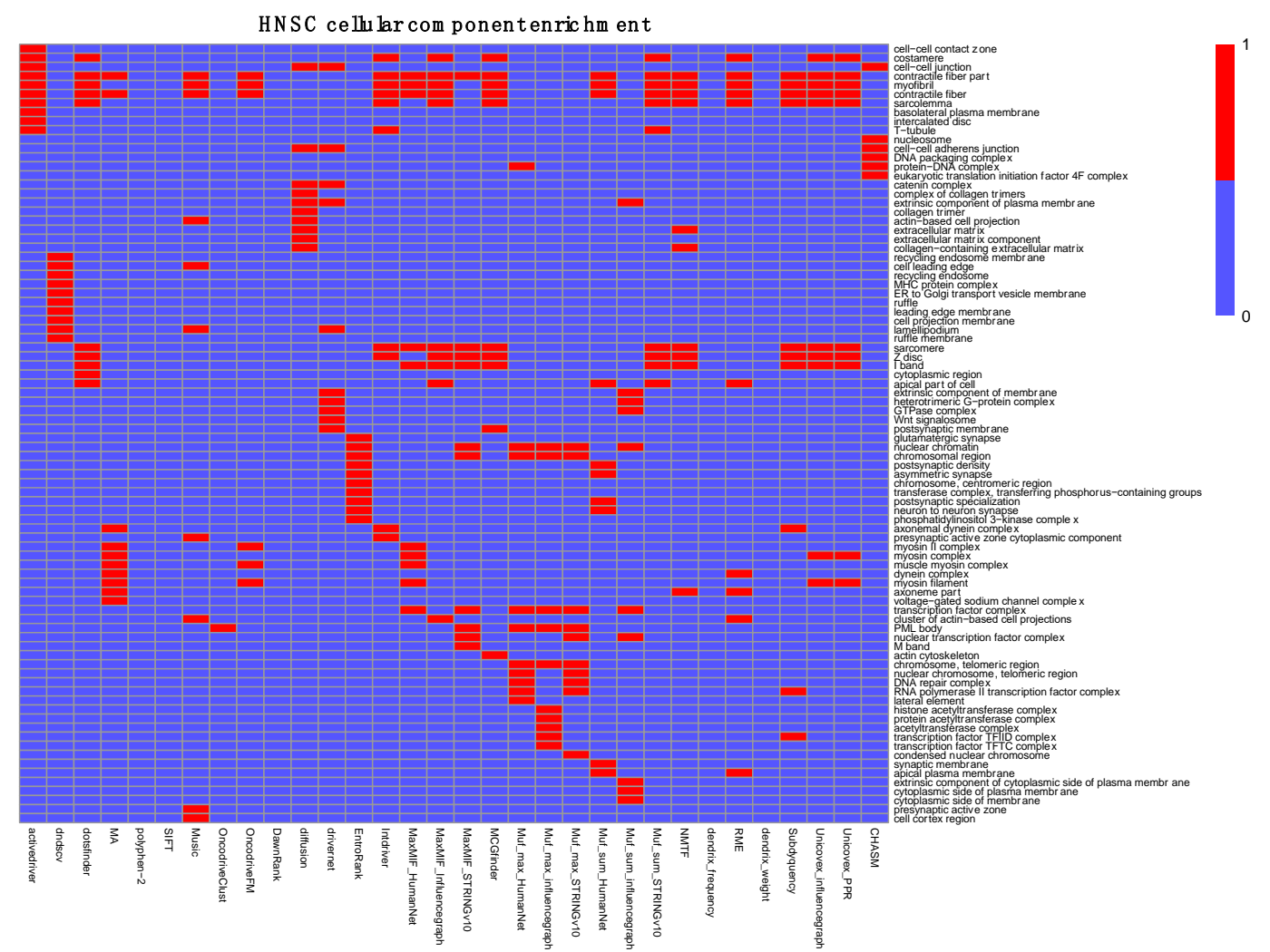

HNSC cellular component enrichment

Figure S21: the heat map of enriched GO term in biology process(BP) by each method for HNSC cancer. The red cell indicates this GO term is significant enriched by its corresponding method, 0 otherwise.

HNSC biology process enrichment

HNSC molecular function enrichment