

Supplementary Material

Comprehensive Analysis of Differentially Expressed Profiles of lncRNAs/mRNAs and miRNAs with Associated ceRNA Networks in Triple-Negative Breast Cancer

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Fig. S1

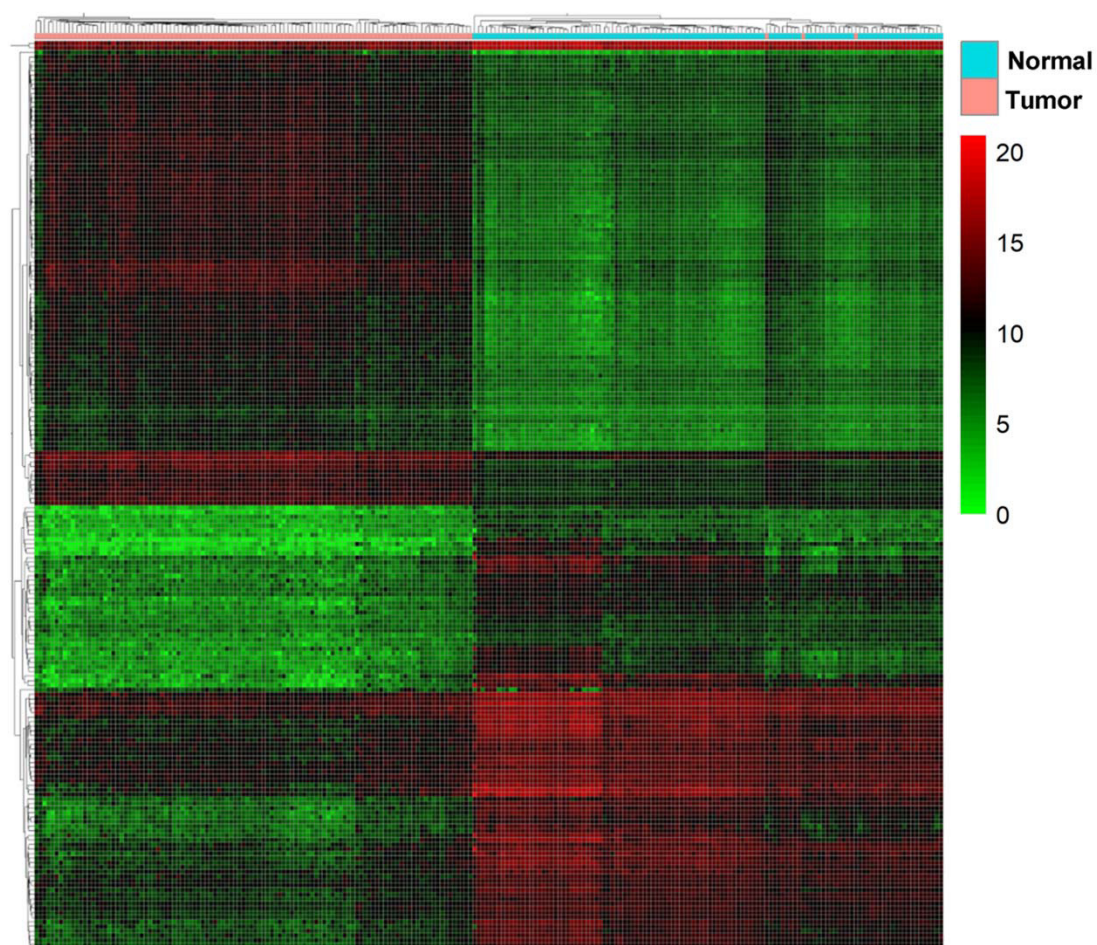


Fig. S1 Heat map with bidirectional hierarchical clustering of DEmRNAs in TNBC. The top 100 up-regulated and 100 down-regulated DEmRNAs were displayed by heat map.

Fig. S2

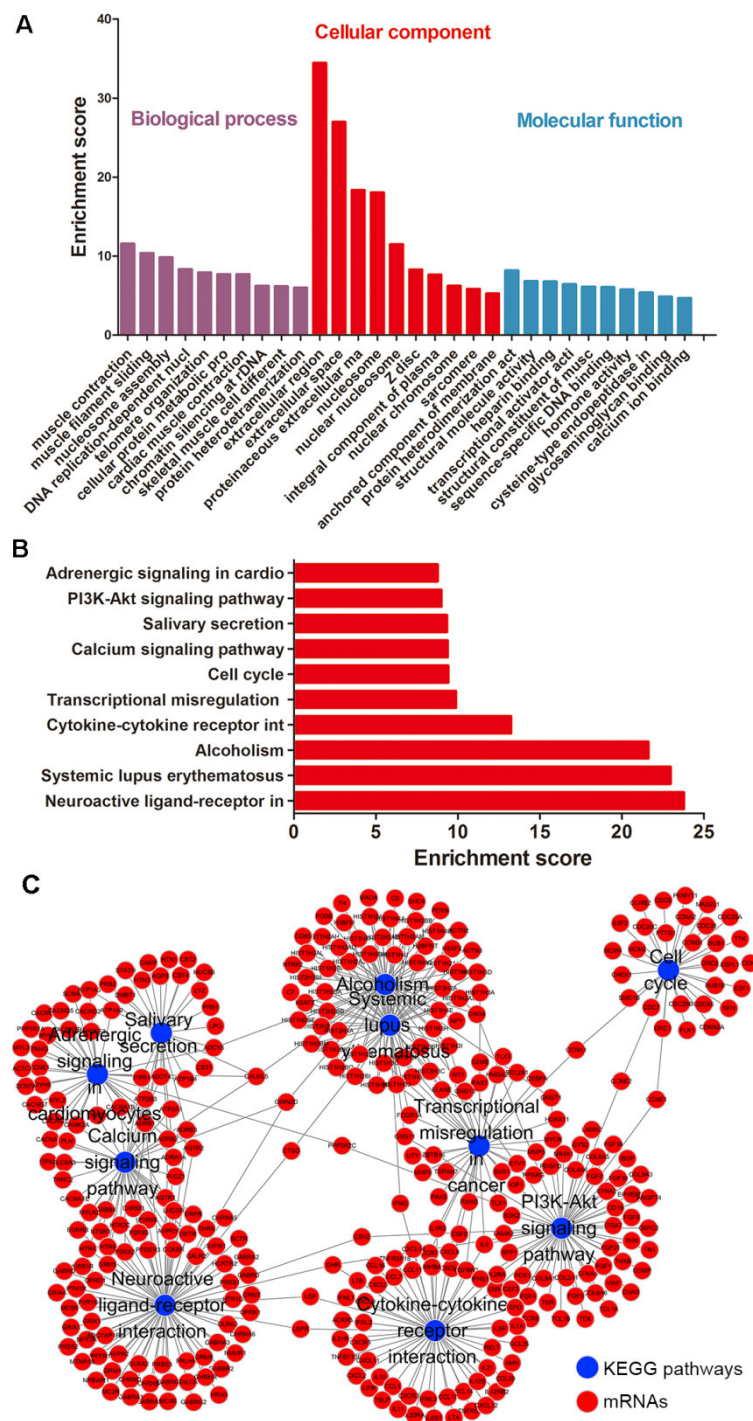


Fig. S2 Significantly enriched GO terms and KEGG pathways for DEmRNAs in TNBC. (A) GO terms with top 30 enrichment score. Each column represents a GO term, including biological process, cellular component and molecular function. (B) KEGG pathways with top 10 enrichment score. (C) The linkage and overlap of molecules among the significantly enriched pathways.

Fig. S3

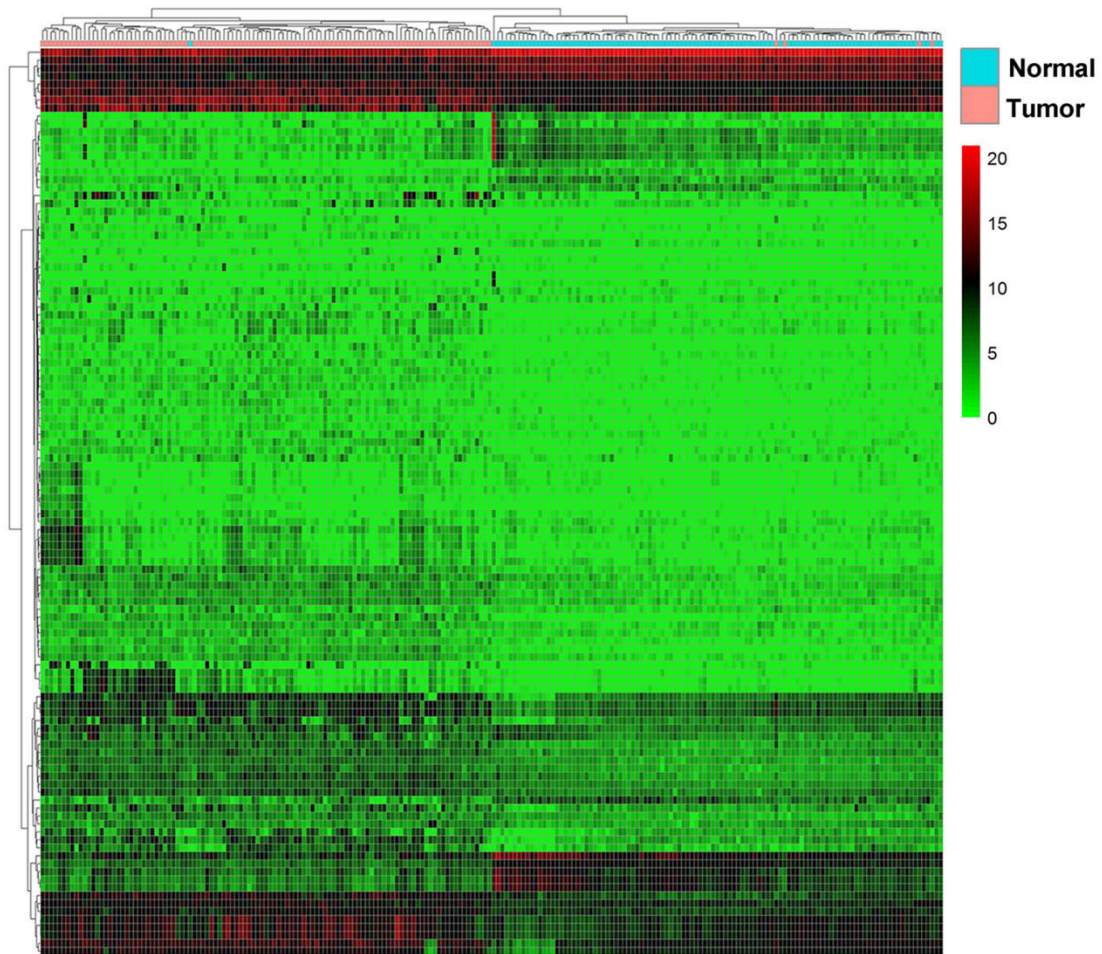


Fig. S3 Heat map with bidirectional hierarchical clustering of DE miRNAs in TNBC.

Fig. S4

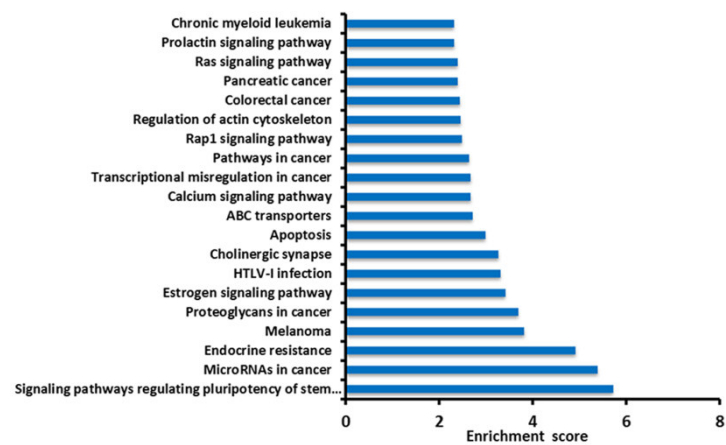


Fig. S4 Significantly enriched KEGG pathways for DE miRNAs in the ceRNA network. The pathways with top 20 enrichment score were displayed.

Table S1. The list of DEmRNAs which were associated with patients' overall survival in TNBC

Gene symbol	P	H_5year	H_lower 95% CI	H_upper 95% CI	L_5year	L_lower 95% CI	L_upper 95% CI	positive or negative	High n	Low n
ELFN2	0.010	0.455	0.265	0.782	0.925	0.845	1.000	negative	55	55
SMPX	0.001	0.979	0.940	1.000	0.471	0.296	0.748	positive	55	55
NEB	0.001	0.908	0.793	1.000	0.580	0.408	0.826	positive	55	55
SLC22A16	0.002	0.907	0.792	1.000	0.573	0.403	0.814	positive	55	55
IL12RB2	0.003	0.891	0.780	1.000	0.526	0.335	0.826	positive	55	55
ART3	0.005	0.855	0.732	0.999	0.598	0.417	0.858	positive	55	55
GPR19	0.005	0.886	0.766	1.000	0.583	0.408	0.833	positive	55	55
NMUR1	0.006	0.805	0.663	0.977	0.648	0.460	0.914	positive	55	55
LHX1	0.006	0.567	0.400	0.804	0.932	0.840	1.000	negative	55	55
PRB2	0.006	0.583	0.393	0.863	0.841	0.704	1.000	negative	55	55
C8orf46	0.007	0.890	0.777	1.000	0.548	0.366	0.819	positive	55	55
SIGLEC12	0.007	0.523	0.345	0.791	0.912	0.797	1.000	negative	55	55
TRH	0.007	0.557	0.381	0.814	0.917	0.809	1.000	negative	55	55
ZBTB8B	0.008	0.865	0.732	1.000	0.610	0.439	0.847	positive	55	55
CADPS	0.008	0.604	0.425	0.857	0.851	0.721	1.000	negative	55	55
ETV7	0.008	0.859	0.734	1.000	0.591	0.408	0.858	positive	55	55
SORBS1	0.008	0.850	0.705	1.000	0.612	0.445	0.843	positive	55	55
DAND5	0.009	0.873	0.741	1.000	0.600	0.430	0.838	positive	55	55
TMPRSS15	0.010	0.879	0.752	1.000	0.600	0.430	0.837	positive	55	55
OTX1	0.010	0.866	0.734	1.000	0.628	0.464	0.850	positive	55	55
AKAP12	0.010	0.575	0.395	0.839	0.880	0.759	1.000	negative	55	55
AQP5	0.010	0.861	0.727	1.000	0.613	0.446	0.843	positive	55	55
OFCC1	0.011	0.879	0.753	1.000	0.607	0.442	0.834	positive	55	55
NUF2	0.011	0.890	0.778	1.000	0.545	0.358	0.831	positive	55	55
C12orf56	0.012	0.909	0.796	1.000	0.598	0.433	0.826	positive	55	55
ZNF716	0.012	0.917	0.827	1.000	0.479	0.286	0.803	positive	55	55
MIA-RAB4B	0.012	0.826	0.682	1.000	0.642	0.474	0.870	positive	55	55
SALL4	0.012	0.863	0.727	1.000	0.603	0.431	0.846	positive	55	55
FAM216B	0.013	0.600	0.420	0.856	0.860	0.734	1.000	negative	55	55
RLBP1	0.013	0.851	0.722	1.000	0.600	0.416	0.865	positive	55	55
PLAC9	0.013	0.584	0.408	0.836	0.879	0.757	1.000	negative	55	55
C1orf64	0.014	0.551	0.385	0.788	0.977	0.934	1.000	negative	55	55
PODN	0.014	0.565	0.388	0.823	0.896	0.786	1.000	negative	55	55
SGOL2	0.014	0.920	0.819	1.000	0.586	0.418	0.821	positive	55	55
ZNF695	0.015	0.903	0.801	1.000	0.523	0.338	0.810	positive	55	55
FOXE3	0.015	0.862	0.728	1.000	0.613	0.442	0.850	positive	55	55
ABCC9	0.015	0.544	0.354	0.835	0.876	0.765	1.000	negative	55	55
CHRNA5	0.016	0.941	0.861	1.000	0.536	0.360	0.797	positive	55	55
NFE2L3	0.016	0.828	0.697	0.983	0.608	0.415	0.890	positive	55	55

COCH	0.017	0.851	0.707	1.000	0.641	0.480	0.855	positive	55	55
ABRACL	0.017	0.899	0.792	1.000	0.569	0.392	0.826	positive	55	55
ANKRD62	0.017	0.870	0.753	1.000	0.600	0.422	0.852	positive	55	55
BTNL9	0.017	0.595	0.434	0.815	0.953	0.891	1.000	negative	55	55
RAD51AP1	0.018	0.892	0.777	1.000	0.565	0.386	0.828	positive	55	55
HES2	0.018	0.565	0.380	0.839	0.867	0.737	1.000	negative	55	55
OLIG1	0.019	0.590	0.407	0.856	0.852	0.721	1.000	negative	55	55
MOCS1	0.019	0.547	0.365	0.819	0.890	0.774	1.000	negative	55	55
TRIM59	0.019	0.908	0.780	1.000	0.611	0.452	0.827	positive	55	55
STATH	0.019	0.670	0.510	0.882	0.801	0.641	1.000	negative	55	55
TREH	0.020	0.577	0.402	0.828	0.903	0.794	1.000	negative	55	55
RIPPLY3	0.020	0.852	0.724	1.000	0.596	0.412	0.864	positive	55	55
FABP7	0.022	0.883	0.762	1.000	0.592	0.419	0.836	positive	55	55
LAMP3	0.023	0.833	0.694	1.000	0.626	0.449	0.872	positive	55	55
ASPM	0.023	0.876	0.765	1.000	0.537	0.346	0.833	positive	55	55
CHAF1B	0.023	0.912	0.817	1.000	0.607	0.440	0.836	positive	55	55
BPI	0.024	0.869	0.752	1.000	0.571	0.386	0.844	positive	55	55
SDS	0.025	0.658	0.494	0.875	0.809	0.651	1.000	negative	55	55
GSTA2	0.026	0.875	0.760	1.000	0.566	0.383	0.836	positive	55	55
CNTN5	0.026	0.868	0.748	1.000	0.632	0.466	0.858	positive	55	55
PNPLA2	0.026	0.581	0.407	0.830	0.891	0.775	1.000	negative	55	55
LHX5	0.027	0.579	0.404	0.831	0.886	0.763	1.000	negative	55	55
LRRC39	0.027	0.885	0.779	1.000	0.592	0.417	0.841	positive	55	55
HOXD13	0.027	0.609	0.429	0.865	0.842	0.705	1.000	negative	55	55
C4orf26	0.027	0.832	0.677	1.000	0.636	0.472	0.857	positive	55	55
MTHFD2	0.029	0.929	0.840	1.000	0.562	0.389	0.811	positive	55	55
KRTDAP	0.029	0.649	0.482	0.874	0.821	0.670	1.000	negative	55	55
GPIHBP1	0.029	0.597	0.435	0.819	0.921	0.822	1.000	negative	55	55
ADM2	0.029	0.856	0.729	1.000	0.618	0.444	0.860	positive	55	55
ZNF730	0.031	0.816	0.677	0.984	0.643	0.466	0.886	positive	55	55
CABP7	0.031	0.648	0.484	0.866	0.835	0.686	1.000	negative	55	55
NAT8L	0.031	0.849	0.722	0.998	0.583	0.391	0.869	positive	55	55
KRT6A	0.032	0.615	0.428	0.885	0.825	0.690	0.987	negative	55	55
GPR34	0.032	0.638	0.469	0.866	0.826	0.674	1.000	negative	55	55
ZFP36	0.032	0.641	0.482	0.852	0.869	0.732	1.000	negative	55	55
BMP8A	0.032	0.607	0.428	0.861	0.854	0.727	1.000	negative	55	55
PPM1E	0.032	0.848	0.699	1.000	0.636	0.475	0.853	positive	55	55
TMEM26	0.033	0.615	0.432	0.876	0.839	0.706	0.998	negative	55	55
FDCSP	0.033	0.811	0.661	0.993	0.654	0.484	0.882	positive	55	55
ACTA1	0.034	0.832	0.693	0.998	0.621	0.434	0.888	positive	55	55
SLITRK1	0.034	0.884	0.763	1.000	0.613	0.446	0.842	positive	55	55
PLSCR5	0.035	0.902	0.798	1.000	0.601	0.433	0.834	positive	55	55
DBNDD1	0.035	0.895	0.784	1.000	0.561	0.379	0.829	positive	55	55
S1PR1	0.036	0.572	0.403	0.811	0.938	0.853	1.000	negative	55	55

WISP1	0.036	0.559	0.364	0.859	0.850	0.734	0.986	negative	55	55
SCN9A	0.036	0.584	0.413	0.826	0.901	0.789	1.000	negative	55	55
CWH43	0.036	0.690	0.540	0.882	0.781	0.611	0.999	negative	55	55
ASPA	0.036	0.648	0.490	0.857	0.854	0.709	1.000	negative	55	55
OVOS2	0.037	0.893	0.780	1.000	0.579	0.404	0.829	positive	55	55
HMCN2	0.037	0.557	0.391	0.792	0.976	0.930	1.000	negative	55	55
CD24	0.038	0.890	0.790	1.000	0.505	0.312	0.816	positive	55	55
TCF24	0.038	0.861	0.722	1.000	0.648	0.492	0.853	positive	55	55
SNX22	0.038	0.814	0.665	0.998	0.658	0.491	0.882	positive	55	55
NEFH	0.038	0.643	0.478	0.865	0.841	0.703	1.000	negative	55	55
SMC4	0.039	0.866	0.731	1.000	0.619	0.453	0.847	positive	55	55
RTBDN	0.039	0.893	0.785	1.000	0.588	0.416	0.831	positive	55	55
THRB	0.039	0.830	0.686	1.000	0.623	0.446	0.868	positive	55	55
COL9A3	0.040	0.803	0.658	0.982	0.661	0.484	0.903	positive	55	55
NPFFR1	0.040	0.794	0.642	0.981	0.669	0.496	0.901	positive	55	55
KCNQ2	0.041	0.615	0.452	0.837	0.875	0.735	1.000	negative	55	55
CLSTN2	0.041	0.576	0.392	0.847	0.869	0.753	1.000	negative	55	55
TFPI2	0.041	0.602	0.431	0.841	0.885	0.765	1.000	negative	55	55
CCL7	0.041	0.859	0.730	1.000	0.611	0.436	0.854	positive	55	55
CT83	0.041	0.855	0.714	1.000	0.642	0.480	0.858	positive	55	55
CEL	0.042	0.865	0.746	1.000	0.573	0.384	0.856	positive	55	55
SFN	0.043	0.882	0.772	1.000	0.569	0.387	0.837	positive	55	55
PEAR1	0.043	0.564	0.380	0.836	0.889	0.789	1.000	negative	55	55
ARTN	0.043	0.619	0.433	0.886	0.823	0.688	0.985	negative	55	55
HIST1H2BB	0.043	0.834	0.703	0.990	0.581	0.391	0.864	positive	55	55
BRINP3	0.045	0.660	0.498	0.876	0.821	0.667	1.000	negative	55	55
GPLD1	0.045	0.796	0.635	0.999	0.666	0.501	0.885	positive	55	55
RFC4	0.045	0.875	0.742	1.000	0.618	0.452	0.846	positive	55	55
FAM72A	0.045	0.895	0.787	1.000	0.514	0.324	0.817	positive	55	55
OBP2B	0.045	0.842	0.707	1.000	0.601	0.419	0.863	positive	55	55
GJB6	0.045	0.616	0.435	0.874	0.818	0.676	0.990	negative	55	55
SCRG1	0.047	0.849	0.722	0.998	0.587	0.395	0.872	positive	55	55
NPBWR1	0.048	0.630	0.461	0.862	0.838	0.693	1.000	negative	55	55
LAMP5	0.048	0.613	0.445	0.847	0.864	0.730	1.000	negative	55	55
ART1	0.048	0.606	0.442	0.831	0.920	0.834	1.000	negative	55	55
CDC7	0.049	0.898	0.772	1.000	0.606	0.443	0.828	positive	55	55
LRRC14B	0.049	0.887	0.773	1.000	0.561	0.380	0.829	positive	55	55
RHOXF1	0.049	0.514	0.322	0.820	0.896	0.801	1.000	negative	55	55
IQGAP3	0.049	0.868	0.737	1.000	0.586	0.410	0.837	positive	55	55
LSR	0.049	0.895	0.776	1.000	0.614	0.450	0.837	positive	55	55
GLDC	0.050	0.839	0.701	1.000	0.622	0.446	0.868	positive	55	55

Table S2. The list of DElncRNAs which were associated with patients' overall survival in TNBC

Gene symbol	P	H_5year	H_lower 95% CI	H_upper 95% CI	L_5year	L_lower 95% CI	L_upper 95% CI	positive or negative	High n	Low n
RP11-61I13.3	0.007	0.444	0.247	0.799	0.915	0.826	1.000	negative	55	55
RP11-44F21.2	0.000	0.540	0.365	0.798	0.922	0.824	1.000	negative	55	55
RP11-17A4.3	0.013	0.602	0.428	0.846	0.877	0.754	1.000	negative	55	55
RP11-277P12.10	0.001	0.546	0.357	0.835	0.871	0.745	1.000	negative	55	55
RP3-333A15.2	0.009	0.590	0.419	0.830	0.912	0.820	1.000	negative	55	55
MIR7-3HG	0.018	0.607	0.441	0.835	0.886	0.755	1.000	negative	55	55
LINC01460	0.020	0.896	0.781	1.000	0.580	0.408	0.824	positive	55	55
RP11-548L20.1	0.040	0.674	0.505	0.901	0.800	0.655	0.976	negative	55	55
TMEM246-AS1	0.038	0.690	0.526	0.906	0.790	0.642	0.973	negative	55	55
CTD-2541J13.1	0.043	0.615	0.429	0.883	0.830	0.699	0.985	negative	55	55
C10orf71-AS1	0.004	0.615	0.447	0.845	0.866	0.735	1.000	negative	55	55
LINC00200	0.006	0.557	0.377	0.823	0.885	0.763	1.000	negative	55	55
RP1-251M9.2	0.047	0.691	0.526	0.908	0.791	0.643	0.974	negative	55	55
C8orf31	0.001	0.532	0.356	0.796	0.936	0.850	1.000	negative	55	55
RP11-15I11.3	0.039	0.878	0.769	1.000	0.523	0.328	0.833	positive	55	55
CTA-929C8.5	0.045	0.705	0.549	0.907	0.766	0.600	0.977	negative	55	55
LINC01267	0.034	0.538	0.357	0.812	0.912	0.821	1.000	negative	55	55
RP11-838N2.5	0.022	0.870	0.734	1.000	0.623	0.456	0.851	positive	55	55
RP11-595B24.2	0.023	0.871	0.757	1.000	0.551	0.360	0.843	positive	55	55
RP11-1041F24.1	0.026	0.662	0.499	0.878	0.818	0.670	0.999	negative	55	55
AC144833.1	0.007	0.612	0.443	0.846	0.867	0.728	1.000	negative	55	55
AC011286.1	0.038	0.659	0.487	0.893	0.795	0.643	0.983	negative	55	55
AC108676.1	0.010	0.884	0.764	1.000	0.563	0.378	0.839	positive	55	55
RP11-119K6.6	0.029	0.890	0.791	1.000	0.513	0.320	0.821	positive	55	55
RP11-107I14.2	0.041	0.681	0.525	0.884	0.804	0.647	0.999	negative	55	55
LINC00702	0.024	0.608	0.424	0.872	0.844	0.712	1.000	negative	55	55
CTD-2507G9.1	0.004	0.641	0.480	0.855	0.849	0.705	1.000	negative	55	55
LINC00906	0.011	0.602	0.430	0.843	0.870	0.742	1.000	negative	55	55
CTD-2587H24.5	0.026	0.649	0.486	0.868	0.833	0.690	1.000	negative	55	55
AC019172.2	0.017	0.609	0.433	0.855	0.837	0.695	1.000	negative	55	55
ELFN1-AS1	0.009	0.898	0.791	1.000	0.554	0.372	0.825	positive	55	55
RP11-280H21.1	0.011	0.649	0.479	0.881	0.825	0.682	0.998	negative	55	55
RP11-6O2.4	0.006	0.899	0.776	1.000	0.607	0.444	0.829	positive	55	55
LINC00452	0.048	0.616	0.426	0.888	0.824	0.689	0.986	negative	55	55
RP11-676J12.6	0.012	0.561	0.370	0.851	0.859	0.734	1.000	negative	55	55
RP11-734K21.5	0.026	0.847	0.714	1.000	0.615	0.437	0.865	positive	55	55
RP5-978I12.1	0.049	0.634	0.471	0.854	0.865	0.734	1.000	negative	55	55
RP11-128B16.3	0.005	0.592	0.413	0.847	0.865	0.732	1.000	negative	55	55
RP11-3J1.1	0.001	0.944	0.844	1.000	0.574	0.413	0.798	positive	55	55
RP11-654C22.2	0.026	0.801	0.650	0.987	0.659	0.488	0.889	positive	55	55

RP11-806L2.5	0.046	0.855	0.731	1.000	0.608	0.428	0.863	positive	55	55
RP11-77A13.1	0.004	0.890	0.773	1.000	0.590	0.417	0.836	positive	55	55
RP11-343H5.6	0.004	0.933	0.843	1.000	0.489	0.304	0.786	positive	55	55
HAGLROS	0.008	0.560	0.403	0.778	1.000	1.000	1.000	negative	55	55
RP11-368I23.3	0.010	0.641	0.469	0.875	0.833	0.695	0.998	negative	55	55
RP11-342D14.1	0.044	0.558	0.364	0.854	0.851	0.734	0.987	negative	55	55
RP11-115D19.3	0.017	0.618	0.447	0.854	0.863	0.730	1.000	negative	55	55
RP11-298O21.6	0.036	0.664	0.502	0.879	0.815	0.666	0.998	negative	55	55
LINC01276	0.029	0.841	0.705	1.000	0.632	0.462	0.865	positive	55	55
RP11-132A1.3	0.013	0.623	0.456	0.850	0.844	0.693	1.000	negative	55	55
RP11-1038A11.3	0.028	0.903	0.801	1.000	0.514	0.323	0.817	positive	55	55
RP4-555D20.3	0.027	0.576	0.398	0.834	0.896	0.802	1.000	negative	55	55
LINC01419	0.021	0.678	0.507	0.906	0.803	0.661	0.975	negative	55	55
CTC-458G6.2	0.043	0.650	0.483	0.874	0.822	0.677	0.999	negative	55	55
LINC00670	0.020	0.596	0.425	0.837	0.888	0.770	1.000	negative	55	55
RP11-434I12.3	0.018	0.667	0.506	0.880	0.815	0.666	0.998	negative	55	55
RP11-717H13.1	0.019	0.649	0.480	0.877	0.827	0.686	0.998	negative	55	55
RP4-663N10.1	0.040	0.576	0.402	0.824	0.910	0.817	1.000	negative	55	55
FOXP4-AS1	0.044	0.828	0.697	0.983	0.625	0.442	0.885	positive	55	55
AC147651.1	0.046	0.637	0.461	0.882	0.829	0.689	0.998	negative	55	55
RP11-626H12.1	0.014	0.582	0.404	0.837	0.878	0.756	1.000	negative	55	55
U91324.1	0.035	0.682	0.526	0.884	0.799	0.639	0.999	negative	55	55
RP11-209K10.2	0.023	0.644	0.484	0.858	0.847	0.701	1.000	negative	55	55
RP11-496D24.2	0.000	0.921	0.823	1.000	0.480	0.294	0.782	positive	55	55
RP11-542B15.1	0.020	0.637	0.466	0.869	0.831	0.686	1.000	negative	55	55
CTC-264K15.6	0.046	0.689	0.523	0.908	0.798	0.652	0.976	negative	55	55
CTA-992D9.6	0.038	0.690	0.525	0.906	0.790	0.642	0.973	negative	55	55
RP11-881M11.8	0.043	0.871	0.737	1.000	0.598	0.428	0.838	positive	55	55
CTD-3010D24.3	0.036	0.919	0.831	1.000	0.584	0.413	0.826	positive	55	55
RP11-61J19.2	0.006	0.909	0.811	1.000	0.494	0.305	0.799	positive	55	55
RP13-379L11.2	0.021	0.929	0.837	1.000	0.521	0.339	0.799	positive	55	55
RP11-830F9.6	0.041	0.571	0.388	0.839	0.883	0.773	1.000	negative	55	55
CTD-2587H19.2	0.038	0.841	0.691	1.000	0.647	0.489	0.856	positive	55	55
RP11-344F13.1	0.037	0.658	0.489	0.884	0.812	0.662	0.997	negative	55	55
LINC01322	0.020	0.636	0.474	0.853	0.855	0.716	1.000	negative	55	55
RP11-461O7.1	0.011	0.542	0.373	0.788	0.955	0.896	1.000	negative	55	55
RP5-1027O11.1	0.002	0.915	0.805	1.000	0.554	0.383	0.800	positive	55	55
RP11-133L19.3	0.034	0.647	0.476	0.879	0.833	0.695	0.998	negative	55	55
LINC00626	0.017	0.627	0.444	0.886	0.804	0.661	0.979	negative	55	55
MIR133A1HG	0.031	0.896	0.789	1.000	0.600	0.429	0.838	positive	55	55
AC010745.4	0.037	0.671	0.511	0.880	0.815	0.664	0.999	negative	55	55
RP11-144L1.4	0.018	0.661	0.496	0.881	0.825	0.681	0.998	negative	55	55
RP11-350D17.2	0.050	0.858	0.711	1.000	0.641	0.480	0.855	positive	55	55
RP11-473L15.3	0.043	0.648	0.467	0.899	0.821	0.686	0.981	negative	55	55

CTD-2540B15.12	0.012	0.608	0.439	0.843	0.877	0.754	1.000	negative	55	55
RP11-61J19.3	0.020	0.890	0.788	1.000	0.523	0.334	0.819	positive	55	55
RBMS3-AS3	0.049	0.561	0.364	0.864	0.856	0.731	1.000	negative	55	55
RP11-297P16.4	0.045	0.688	0.522	0.906	0.797	0.651	0.975	negative	55	55
RP13-16H11.2	0.036	0.878	0.751	1.000	0.615	0.444	0.850	positive	55	55
LINC00844	0.046	0.900	0.791	1.000	0.599	0.428	0.837	positive	55	55
RP11-88I18.3	0.002	0.579	0.410	0.817	0.904	0.786	1.000	negative	55	55
RP11-83M16.5	0.040	0.686	0.520	0.905	0.793	0.646	0.975	negative	55	55
CTD-2263F21.1	0.019	0.623	0.457	0.851	0.860	0.723	1.000	negative	55	55
RP1-90K10.4	0.018	0.863	0.729	1.000	0.612	0.442	0.847	positive	55	55
NRG1-IT1	0.020	0.662	0.499	0.879	0.819	0.673	0.998	negative	55	55
RORB-AS1	0.043	0.640	0.458	0.894	0.812	0.670	0.983	negative	55	55
RP11-100L22.1	0.006	0.598	0.438	0.815	0.950	0.884	1.000	negative	55	55
RP11-98G7.1	0.027	0.874	0.749	1.000	0.615	0.446	0.847	positive	55	55
XXyac-YM21GA2.7	0.029	0.655	0.492	0.872	0.808	0.650	1.000	negative	55	55
LINC01593	0.021	0.655	0.499	0.859	0.849	0.702	1.000	negative	55	55
RP6-191P20.4	0.019	0.878	0.751	1.000	0.622	0.458	0.845	positive	55	55
RP11-510C10.4	0.049	0.697	0.534	0.911	0.786	0.635	0.972	negative	55	55
RP5-1054A22.4	0.019	0.869	0.752	1.000	0.559	0.369	0.846	positive	55	55
RP11-83A16.1	0.000	0.939	0.860	1.000	0.500	0.319	0.783	positive	55	55
CH17-125A10.2	0.023	0.668	0.507	0.880	0.812	0.662	0.997	negative	55	55
RP11-397C12.1	0.043	0.657	0.493	0.876	0.821	0.675	0.998	negative	55	55
LINC01574	0.018	0.633	0.473	0.847	0.860	0.712	1.000	negative	55	55
RP11-202K23.1	0.040	0.613	0.445	0.845	0.870	0.742	1.000	negative	55	55
LINC01044	0.032	0.645	0.469	0.885	0.821	0.676	0.998	negative	55	55

Table S3. The list of DEmiRNAs which were associated with patients' overall survival in TNBC

miRNA	P	H_5year	H_lower 95% CI	H_upper 95% CI	L_5year	L_lower 95% CI	L_upper 95% CI	positive or negative	High n	Low n
hsa-mir-216a	0.035	0.831	0.700	0.987	0.641	0.469	0.878	positive	54	54
hsa-mir-135b	0.015	0.871	0.737	1.000	0.596	0.425	0.836	positive	54	54
hsa-mir-7706	0.023	0.604	0.433	0.842	0.854	0.717	1.000	negative	54	54
hsa-mir-3610	0.005	0.612	0.446	0.839	0.868	0.731	1.000	negative	54	54