Table S1. Differentially expressed genes in solid and trabecular structures compared to normal breast epithelia (p-value < 0.1)

Gene	Solid structures		Trabecular structures	
	LogFC	P-value	LogFC	P-value
AACS	2.791	0.038	3.038	0.026
AAGAB	3.734	0.032	3.746	0.032
ABCA12	5.171	0.001	5.070	0.001
ABCC11	5.805	0.003	3.742	0.039
ABCF2	3.674	0.008	2.260	0.079
ABCG2	-2.135	0.038	-2.386	0.023
ABHD16A	-2.331	0.025	-3.410	0.002
ABLIM1	-1.969	0.035	-2.498	0.010
ABO	-1.108	0.097	-1.139	0.088
ACAA1	-1.865	0.021	-2.303	0.006
ACOX2	2.906	0.032	3.317	0.017
ACPT	1.542	0.064	1.914	0.025
ACTN4	2.217	0.091	3.592	0.010
ACTR1B	-1.339	0.063	-1.476	0.042
ACTR6	1.723	0.032	1.515	0.055
ADAM15	1.370	0.040	1.268	0.055
ADAMTS16	1.968	0.030	1.849	0.040
ADAMTS19	-1.411	0.059	-1.583	0.037
ADAMTS4	3.073	0.029	2.552	0.065
ADAMTS5	-3.518	0.008	-3.434	0.009
ADCK4	2.323	0.051	3.843	0.003
ADNP2	3.725	0.003	3.363	0.006
ADRB2	-4.990	0.003	-3.719	0.021
AEBP1	2.408	0.042	3.618	0.004
AF111851	-1.967	0.008	-2.339	0.002
AGPAT4	-3.783	0.047	-4.097	0.033
AGT	2.392	0.041	3.241	0.008
AIMP2	3.261	0.012	2.729	0.031
AK027667	-2.933	0.012	-2.304	0.041
AK075182	-1.420	0.029	-1.228	0.055
AK090485	-1.478	0.063	-1.805	0.027
AK124642	-2.601	0.051	-3.026	0.026
AK130224	-1.889	0.039	-1.908	0.037
AK5	-3.467	0.002	-3.213	0.003
AKT1	2.988	0.070	3.147	0.058
ALCAM	2.860	0.042	2.483	0.073
ALDH7A1	-2.031	0.035	-2.932	0.004
ALG11	2.324	0.058	3.300	0.010
ALG5	2.529	0.008	2.014	0.029
ALKBH6	4.223	0.001	2.456	0.036
ALYREF	2.728	0.045	3.047	0.027
AMOTL1	-2.854	0.031	-3.137	0.019
ANKRD29	-2.397	0.009	-1.864	0.036
ANKRD30A	2.178	0.017	2.420	0.009
ANKRD35	-2.879	0.013	-2.186	0.051
ANKRD36	1.893	0.082	2.287	0.040
ANKRD65	-3.559	0.002	-3.411	0.002
ANPEP	-2.315	0.060	-2.435	0.049
ANXA1	-2.595	0.068	-2.957	0.040

ANXA9	4.935	0.002	4.253	0.007
AOC3	2.230	0.097	2.281	0.090
AP1G2	2.144	0.009	2.744	0.002
APC	2.402	0.055	3.118	0.016
APCDD1	-4.793	0.008	-3.816	0.029
APCDD1L	-2.371	0.090	-3.416	0.019
APCDD1L-AS1	-3.901	0.000	-2.502	0.005
APOA1BP	3.700	0.029	3.293	0.049
APOD	-3.832	0.034	-3.609	0.044
APOL2	2.639	0.023	3.033	0.010
ARF1	2.331	0.060	2.225	0.072
ARHGEF10	-1.794	0.050	-1.862	0.043
ARHGEF37	-2.643	0.068	-2.620	0.070
ARHGEF3-AS1	-1.691	0.043	-1.470	0.074
ARIH1	-3.272	0.009	-2.070	0.080
ARL4C	-5.110	0.002	-4.864	0.003
ARL6IP6	1.858	0.068	2.381	0.023
ARMC10	-1.255	0.079	-2.969	0.000
ARRDC3	-2.179	0.075	-2.295	0.062
ARRDC4	-2.008	0.075	-2.027	0.073
ASCC3	3.359	0.037	3.403	0.035
ASPM	3.419	0.042	4.889	0.006
ASPN	4.044	0.000	4.688	0.000
ATAD2	3.859	0.003	5.215	0.000
AURKA	3.052	0.015	4.396	0.001
AW571659	-2.770	0.035	-2.719	0.038
B4GALT3	2.914	0.004	2.957	0.003
B9D2	2.052	0.076	3.151	0.010
BASP1	3.711	0.069	3.376	0.095
BBOX1	-3.328	0.006	-2.900	0.014
BC014063	-1.574	0.092	-2.045	0.033
BC044628	-1.726	0.077	-1.798	0.067
BCAP31	1.459	0.035	1.350	0.048
BCDIN3D	4.293	0.001	4.833	0.001
BCL9	3.353	0.020	2.373	0.086
BF175071	-3.108	0.037	-2.829	0.056
BGN	2.947	0.003	4.852	0.000
BLVRA	1.521	0.018	1.241	0.047
BLVRB	1.728	0.077	1.645	0.091
BMS1	2.990	0.066	3.456	0.037
BNC1	-2.585	0.012	-1.909	0.053
BOP1	-1.824	0.040	-2.742	0.004
BRMS1L	-2.203	0.035	-2.056	0.048
BROX	3.614	0.015	3.312	0.024
BST2	2.086	0.038	2.131	0.035
BU963192	3.430	0.027	3.839	0.015
BUB1B	2.158	0.053	2.964	0.011
BVES	-2.099	0.018	-2.015	0.023
C10orf25	-1.460	0.069	-1.421	0.076
C11orf49	1.892	0.048	1.576	0.093
C15orf26	-1.358	0.065	-1.247	0.087
C15orf40	2.866	0.006	2.195	0.027
C15orf52	-2.964	0.033	-4.544	0.002
C15orf61	-1.644	0.097	-3.364	0.002
C16orf45	3.360	0.017	3.794	0.008

C16orf54	-1.944	0.050	-1.752	0.074
C16orf92	-1.828	0.010	-1.166	0.082
C17orf100	-2.857	0.015	-2.335	0.041
C17orf62	2.058	0.034	3.444	0.001
C18orf32	1.720	0.050	1.954	0.028
C19orf18	-1.623	0.061	-1.651	0.057
C19orf52	3.918	0.003	3.145	0.014
C1orf186	-2.053	0.031	-2.728	0.006
C1orf43	1.124	0.079	1.193	0.064
C1orf53	1.515	0.097	1.584	0.084
C1orf56	1.196	0.061	1.150	0.071
C1QTNF3	1.566	0.066	1.417	0.093
C20orf197	-1.587	0.075	-1.609	0.072
C2orf40	-5.208	0.000	-7.216	0.000
C2orf66	-1.618	0.080	-1.659	0.073
C2orf82	-2.304	0.004	-1.777	0.021
C3	-3.515	0.020	-3.527	0.020
C3orf58	-2.728	0.064	-3.899	0.011
C5orf60	-1.469	0.066	-1.899	0.021
C6orf136	-2.626	0.047	-3.484	0.011
C6orf52	2.064	0.067	2.121	0.060
CA11	-2.161	0.074	-3.613	0.006
CACNA1C	-3.116	0.060	-3.084	0.063
CACNA2D1	-4.364	0.006	-3.503	0.022
CADM3	-4.466	0.001	-4.300	0.002
CALHM2	-1.673	0.077	-3.590	0.001
CALM2	1.106	0.028	0.834	0.088
CAPN13	2.306	0.022	3.108	0.003
CARD6	-2.540	0.070	-2.487	0.076
CAV1	-3.196	0.046	-3.204	0.045
CAV2	-2.383	0.093	-3.017	0.038
CCDC117	1.772	0.015	1.176	0.091
CCDC120	-4.533	0.004	-3.446	0.020
CCDC157	-1.967	0.031	-1.729	0.055
CCDC158	-2.466	0.045	-2.720	0.029
CCDC175	3.297	0.087	3.167	0.099
CCDC47	3.014	0.008	2.493	0.025
CCDC8	-2.114	0.054	-1.850	0.088
CCDC92	3.442	0.014	5.015	0.001
CCL21	-1.442	0.095	-1.483	0.086
CCL28	-2.658	0.069	-4.445	0.005
CCL5	-3.763	0.031	-3.646	0.036
CCNB1	2.788	0.032	2.376	0.062
CCNB2	3.460	0.001	2.746	0.007
CCND1	2.013	0.039	1.722	0.072
CCPG1	1.814	0.042	1.609	0.067
CCT3	2.207	0.047	2.967	0.011
CD109	4.012	0.008	2.585	0.068
CD59	-2.907	0.092	-4.922	0.008
CD97	-2.149	0.022	-2.248	0.017
CDCA4	2.843	0.080	4.196	0.014
CDH3	-1.444	0.043	-3.467	0.000
CDKN2AIPNL	2.373	0.067	2.432	0.061
CDKN3	3.255	0.014	2.676	0.039
CDPF1	-2.620	0.020	-2.475	0.027

CDR1	2.518	0.017	2.077	0.043
CDS2	3.534	0.024	2.778	0.068
CENPF	5.567	0.005	4.958	0.010
CENPW	2.178	0.072	2.836	0.023
CEP19	2.689	0.064	2.404	0.094
CEP55	4.032	0.008	2.666	0.061
CEP78	1.569	0.038	1.564	0.038
CEP85L	-2.333	0.053	-2.307	0.055
CERS4	-3.547	0.001	-3.409	0.001
CFB	1.876	0.007	2.008	0.004
CFP	2.257	0.080	2.834	0.032
CHCHD1	2.692	0.023	1.925	0.091
CHEK1	3.462	0.012	2.165	0.095
CHN1	3.080	0.033	2.376	0.090
CHST2	-2.771	0.011	-2.788	0.011
CHST9	-2.381	0.010	-3.160	0.001
CIC	-1.908	0.074	-2.387	0.029
CKS2	2.635	0.006	2.854	0.004
CLDN11	-3.226	0.034	-4.989	0.002
CLDN8	-3.129	0.029	-2.314	0.095
CLEC19A	1.218	0.071	1.814	0.011
CLGN	2.909	0.021	3.889	0.004
CLPSL2	4.408	0.006	2.842	0.061
CLSTN3	1.498	0.098	1.896	0.041
CLU	-1.795	0.030	-2.051	0.015
CLUAP1	2.909	0.022	3.510	0.008
CMA1	-2.082	0.025	-1.580	0.078
CMPK2	2.827	0.031	2.290	0.073
CMTM4	-2.739	0.048	-2.247	0.098
CNEP1R1	2.404	0.099	2.841	0.055
CNIH4	1.758	0.015	1.384	0.048
CNST	3.014	0.041	3.596	0.017
CNTNAP3B	-2.028	0.019	-2.548	0.005
CNTNAP5	-2.424	0.062	-2.650	0.043
COL10A1	4.653	0.001	6.730	0.000
COL12A1	2.971	0.012	5.315	0.000
COL17A1	-3.030	0.010	-4.892	0.000
COL1A1	4.744	0.000	5.638	0.000
COL1A2	3.501	0.004	5.086	0.000
COL3A1	5.485	0.000	6.466	0.000
COL5A1	3.871	0.006	4.857	0.001
COL5A2	6.433	0.000	7.054	0.000
COL6A3	2.455	0.026	4.127	0.001
COMP	3.793	0.005	4.511	0.002
COPA	3.753	0.003	4.290	0.001
COPB2	1.915	0.013	1.822	0.017
COQ3	-1.448	0.099	-2.526	0.008
COX6C	2.003	0.006	1.826	0.010
COX7A1	-3.167	0.059	-5.240	0.004
CPAMD8	-3.884	0.004	-3.425	0.009
CPS1	-3.726	0.007	-4.821	0.001
CR737597	-2.014	0.017	-1.480	0.067
CRABP2	2.556	0.048	2.974	0.024
CRAT	3.383	0.000	3.348	0.000
CREB3L1	3.051	0.058	4.144	0.014

CRIP1	3.736	0.000	3.832	0.000
CRIP2	1.393	0.079	1.848	0.024
CRYAB	-4.198	0.015	-8.426	0.000
CS	-1.205	0.083	-2.170	0.004
CSN3	-4.110	0.011	-3.130	0.044
CSRP1	-2.375	0.004	-2.877	0.001
CST6	3.001	0.048	2.501	0.093
CST9	-2.570	0.048	-3.134	0.019
CSTA	-3.077	0.013	-3.349	0.008
CTDSPL	-2.126	0.018	-1.834	0.038
CTHRC1	2.298	0.009	4.152	0.000
CTIF	2.482	0.043	2.559	0.038
CTNND1	-2.277	0.020	-2.538	0.011
CTSD	5.419	0.002	5.184	0.002
CTSS	-1.783	0.029	-2.096	0.013
CU692621	-1.068	0.048	-0.891	0.092
CUEDC2	1.978	0.093	2.122	0.073
CXorf21	-2.517	0.080	-2.826	0.052
CXXC5	1.899	0.024	1.381	0.089
CYP7B1	-3.453	0.002	-2.511	0.016
CYR61	-2.964	0.036	-2.596	0.062
CYSLTR2	-1.712	0.037	-1.378	0.085
CYYR1	-5.640	0.000	-5.796	0.000
D21S2088E	-1.920	0.055	-2.267	0.026
DAB2	-1.589	0.091	-2.123	0.029
DAPL1	-3.174	0.005	-2.835	0.011
DARS2	2.760	0.008	2.153	0.031
DCDC2	-2.744	0.058	-4.085	0.008
DDA1	3.798	0.007	4.264	0.003
DDB2	-1.594	0.056	-1.625	0.052
DDI2	-3.700	0.026	-3.541	0.032
DDX39A	1.690	0.093	2.680	0.012
DEFA5	-1.307	0.097	-1.306	0.097
DEGS2	3.417	0.010	3.696	0.006
DENND1B	3.202	0.026	2.757	0.051
DENND6A	2.799	0.022	2.556	0.035
DEPDC1	2.795	0.042	3.886	0.007
DHTKD1	2.265	0.072	2.377	0.060
DLGAP5	2.834	0.026	2.614	0.038
DLL1	1.784	0.085	2.749	0.012
DMD	-4.011	0.002	-5.133	0.000
DNAH1	-1.401	0.048	-1.846	0.012
DNAH14	2.781	0.028	4.116	0.002
DNAH5	2.506	0.073	3.104	0.030
DNAJA1	2.113	0.026	1.776	0.056
DNAJC10	2.748	0.009	1.928	0.055
DNAJC22	2.954	0.008	2.224	0.037
DNALI1	1.570	0.075	2.154	0.019
DNM1P46	-3.170	0.021	-3.453	0.013
DOCK4	-2.306	0.026	-2.418	0.020
DOLPP1	2.833	0.067	3.258	0.038
DPF1	1.736	0.058	1.560	0.086
DPM1	2.872	0.022	2.531	0.040
DPY19L3	2.035	0.095	3.261	0.012
DQ098707	-4.080	0.008	-3.781	0.012

DRD2	-2.439	0.014	-1.735	0.069
DSN1	2.697	0.031	3.451	0.008
DTX3L	1.687	0.061	1.849	0.042
DUPD1	-1.614	0.041	-1.286	0.097
DUSP1	-2.907	0.025	-2.278	0.071
DUSP12	2.632	0.047	2.676	0.043
DUSP2	-2.162	0.049	-2.068	0.058
DZIP3	3.205	0.028	2.635	0.064
EDN3	-5.101	0.000	-5.016	0.000
EED	1.396	0.018	1.691	0.006
EFCAB1	-1.759	0.030	-2.162	0.010
EFHC2	-1.351	0.084	-1.550	0.051
EGFL7	2.144	0.035	2.691	0.011
EGLN3	3.580	0.001	2.862	0.004
EGR1	-2.538	0.001	-2.045	0.007
EGR2	-4.660	0.021	-4.120	0.037
EIF2S2	2.248	0.047	2.126	0.058
EIF3L	-1.771	0.028	-2.168	0.009
EIF4B	-1.326	0.067	-1.265	0.080
ELF5	-2.793	0.024	-3.313	0.009
ELK4	-1.483	0.094	-1.845	0.041
EMC7	0.945	0.098	1.110	0.056
EMP2	1.549	0.024	1.139	0.085
ENPP1	2.363	0.072	2.716	0.041
ENST00000276974	-1.900	0.004	-2.336	0.001
ENST00000299512	-1.620	0.025	-1.898	0.011
ENST00000300992	-2.453	0.014	-3.711	0.001
ENST00000334163	2.033	0.025	2.236	0.015
ENST00000390312	-3.808	0.011	-3.077	0.034
ENST00000390323	-4.153	0.065	-5.225	0.024
ENST00000390399	-2.126	0.010	-1.843	0.022
ENST00000390426	-1.730	0.043	-1.841	0.032
ENST00000390539	-6.486	0.000	-5.151	0.000
ENST00000390547	-6.552	0.001	-7.055	0.001
ENST00000390606	-2.273	0.059	-2.220	0.065
ENST00000397595	-1.753	0.089	-1.777	0.085
ENST00000398190	-0.909	0.094	-1.210	0.031
ENST00000401715	-1.280	0.019	-1.219	0.025
ENST00000401937	-1.344	0.058	-1.251	0.076
ENST00000404609	-1.602	0.009	-1.377	0.021
ENST00000410078	-4.740	0.030	-5.896	0.009
ENST00000412855	2.206	0.053	2.133	0.060
ENST00000413663	-1.547	0.082	-1.640	0.066
ENST00000414915	1.285	0.083	1.422	0.057
ENST00000416350	-1.464	0.072	-1.802	0.030
ENST00000416507	-1.551	0.051	-1.466	0.063
ENST00000416519	1.871	0.074	2.017	0.056
ENST00000416593	-1.467	0.085	-2.071	0.019
ENST00000417039	-1.882	0.069	-1.974	0.058
ENST00000417510	-1.992	0.018	-2.909	0.001
ENST00000417823	-1.628	0.096	-1.986	0.047
ENST00000419614	-1.738	0.014	-1.251	0.066
ENST00000420096	-2.888	0.023	-3.053	0.017
ENST00000420273	-1.527	0.041	-1.331	0.071
ENST00000421481	-1.670	0.042	-1.997	0.017

ENST00000421581	-1.588	0.065	-1.715	0.048
ENST00000422792	-1.427	0.018	-1.693	0.006
ENST00000424565	-1.152	0.041	-0.969	0.080
ENST00000424633	-1.358	0.019	-1.189	0.037
ENST00000424969	-4.348	0.005	-4.264	0.006
ENST00000425181	-1.723	0.030	-1.987	0.014
ENST00000425226	1.780	0.015	1.943	0.009
ENST00000427962	-1.568	0.037	-1.731	0.023
ENST00000429552	-1.202	0.047	-1.193	0.048
ENST00000430152	-1.882	0.036	-1.774	0.046
ENST00000430258	-1.215	0.067	-1.230	0.064
ENST00000431782	-1.379	0.027	-1.407	0.025
ENST00000432629	-1.337	0.020	-1.265	0.027
ENST00000433051	-1.875	0.031	-1.897	0.030
ENST00000434244	2.321	0.013	2.198	0.017
ENST00000434710	-3.955	0.009	-3.563	0.017
ENST00000436077	2.192	0.011	2.366	0.007
ENST00000439423	-0.874	0.084	-0.924	0.069
ENST00000441444	-1.538	0.064	-1.509	0.069
ENST00000441465	-1.619	0.057	-1.672	0.050
ENST00000442083	-0.949	0.084	-1.134	0.042
ENST00000442318	-1.442	0.057	-1.286	0.086
ENST00000443330	-2.054	0.042	-1.795	0.072
ENST00000450820	-2.629	0.008	-2.596	0.009
ENST00000451609	2.492	0.004	2.336	0.006
ENST00000452286	-1.728	0.051	-2.123	0.020
ENST00000452501	-1.682	0.010	-1.841	0.006
ENST00000453166	-2.799	0.046	-3.837	0.009
ENST00000453179	-1.156	0.090	-1.458	0.037
ENST00000453309	-2.409	0.034	-2.906	0.013
ENST00000453678	-1.914	0.046	-1.854	0.053
ENST00000455206	-1.216	0.036	-1.276	0.029
ENST00000456185	-1.217	0.032	-1.192	0.035
ENST00000456555	-1.078	0.091	-1.411	0.032
ENST00000457863	2.409	0.014	2.264	0.019
ENST00000458293	-1.466	0.080	-1.443	0.085
ENST00000461060	-1.065	0.055	-1.197	0.034
ENST00000461513	-1.221	0.031	-1.670	0.005
ENST00000462503	-1.438	0.072	-1.538	0.056
ENST00000462693	-2.321	0.006	-1.547	0.049
ENST00000464118	-1.058	0.058	-1.364	0.018
ENST00000466297	-1.263	0.067	-1.428	0.041
ENST00000469899	-1.222	0.046	-1.198	0.050
ENST00000471205	-1.136	0.071	-1.358	0.034
ENST00000476880	-1.731	0.058	-1.580	0.081
ENST00000481963	-1.193	0.060	-1.038	0.097
ENST00000483158	-3.803	0.014	-4.457	0.005
ENST00000488396	-1.199	0.044	-1.970	0.002
ENST00000492167	-4.072	0.011	-4.151	0.010
ENST00000494861	-1.411	0.022	-1.174	0.051
ENST00000496042	-1.744	0.025	-1.322	0.080
ENST00000496488	3.596	0.004	2.035	0.077
ENST00000497325	-1.450	0.018	-1.539	0.013
ENST00000502684	-1.756	0.022	-1.698	0.026
ENST00000503394	-1.994	0.052	-1.969	0.082

ENST00000506710	-2.078	0.008	-1.494	0.043
ENST00000508156	-2.780	0.024	-2.158	0.071
ENST00000509568	-1.411	0.022	-1.279	0.036
ENST00000510758	-1.404	0.063	-1.287	0.086
ENST00000510975	-1.977	0.027	-2.242	0.014
ENST00000511794	-1.778	0.025	-1.561	0.046
ENST00000511953	-2.049	0.024	-1.536	0.080
ENST00000512898	-2.105	0.021	-1.934	0.033
ENST00000512915	1.891	0.084	2.448	0.030
ENST00000514327	-1.544	0.068	-1.628	0.055
ENST00000515599	3.191	0.003	3.300	0.002
ENST00000521432	2.750	0.077	3.024	0.055
ENST00000524287	-1.316	0.098	-1.530	0.058
ENST00000527434	2.689	0.003	2.114	0.015
ENST00000550042	-2.176	0.061	-2.647	0.026
ENST00000554307	-1.528	0.074	-1.406	0.097
ENST00000559385	-0.852	0.089	-0.915	0.070
ENST00000567054	-1.901	0.092	-2.175	0.057
ENST00000567899	-1.286	0.090	-1.421	0.063
ENST00000575236	-1.526	0.053	-1.664	0.037
ENST00000579793	2.005	0.022	1.465	0.082
ENST00000585065	2.885	0.065	3.034	0.053
ENST00000589177	3.156	0.003	3.004	0.005
ENST00000596267	2.483	0.021	2.502	0.020
ENST00000600588	-1.012	0.071	-1.485	0.012
ENST00000605188	1.080	0.067	1.567	0.012
ENST00000607314	-5.947	0.000	-6.531	0.000
ENST00000607355	2.503	0.046	2.879	0.024
ENST00000608694	3.214	0.004	2.096	0.046
ENST00000609203	-1.479	0.075	-1.372	0.097
ENST00000610439	-3.743	0.028	-5.630	0.002
ENST00000612474	-3.351	0.000	-2.343	0.007
ENST00000612725	-1.835	0.024	-1.294	0.098
ENST00000613254	2.133	0.068	2.643	0.028
ENST00000613594	-3.543	0.024	-4.782	0.004
ENST00000615743	1.236	0.091	1.603	0.033
ENST00000616656	-1.552	0.026	-1.769	0.013
ENST00000618777	-1.938	0.053	-1.940	0.052
ENST00000619495	-2.041	0.063	-1.817	0.095
ENST00000620395	-3.590	0.004	-3.008	0.007
ENST00000621052	2.548	0.011	2.875	0.005
EPB41	-2.728	0.013	-2.057	0.052
EPHB1	-3.636	0.000	-2.528	0.000
EPSTI1	2.152	0.029	1.571	0.099
ERICH5	-2.708	0.000	-2.529	0.001
ERMAP	-2.161	0.035	-2.643	0.012
ERMP1	3.820	0.004	3.925	0.003
ERN2	2.697	0.058	3.504	0.017
ESR1	3.844	0.004	2.379	0.055
ETF1	1.914	0.030	1.695	0.052
ETFDH	2.367	0.048	3.473	0.006
ETNK2	2.178	0.005	1.612	0.028
ETS2	-3.201	0.014	-2.051	0.097
EXOC1	1.947	0.035	3.249	0.001
EZR	1.993	0.036	1.918	0.043

F11R	1.067	0.090	1.093	0.083
F13A1	3.636	0.019	4.639	0.004
FABP5	2.902	0.062	2.610	0.090
FABP7	-2.037	0.060	-2.264	0.039
FADD	2.325	0.045	2.038	0.075
FAHD2A	-2.692	0.032	-2.227	0.071
FAM109A	-3.613	0.015	-3.259	0.026
FAM114A1	3.723	0.004	2.812	0.021
FAM138A	-2.195	0.018	-1.467	0.097
FAM160A1	-2.237	0.015	-3.416	0.001
FAM189B	3.821	0.002	3.570	0.003
FAM212A	-1.366	0.078	-1.704	0.032
FAM3D	-6.058	0.000	-5.426	0.000
FAM53B	-3.044	0.026	-4.832	0.001
FAM53B-AS1	-1.476	0.056	-1.688	0.031
FAM90A27P	-1.387	0.072	-1.563	0.045
FANCI	2.428	0.029	2.807	0.013
FAP	3.294	0.008	5.527	0.000
FARSB	1.978	0.099	2.489	0.043
FASN	2.399	0.001	2.138	0.003
FASTKD3	4.482	0.002	3.124	0.018
FBXO28	2.370	0.015	1.881	0.047
FCER1A	-3.174	0.026	-3.224	0.024
FCGBP	-3.388	0.030	-3.936	0.014
FCGRT	-1.864	0.047	-1.576	0.088
FCRL1	-2.122	0.035	-1.737	0.078
FDCSP	-3.715	0.030	-3.687	0.031
FEM1C	3.637	0.001	2.419	0.012
FERMT1	-2.009	0.058	-1.750	0.094
FGF14	-3.749	0.003	-2.799	0.019
FGF14-AS2	-3.034	0.023	-2.815	0.033
FGF2	-3.750	0.000	-4.080	0.000
FGL2	-2.261	0.011	-2.408	0.007
FIGF	-2.150	0.068	-2.584	0.032
FIGN	-2.064	0.029	-2.534	0.010
FKBP4	2.858	0.017	2.811	0.018
FLJ22447	2.203	0.029	1.923	0.053
FLVCR1	2.168	0.067	3.835	0.003
FLVCR2	-1.997	0.045	-2.031	0.042
FMO2	-3.179	0.022	-2.328	0.083
FN1	6.517	0.000	7.046	0.000
FOLR1	-4.694	0.021	-5.393	0.009
FOLR3	-1.793	0.004	-1.250	0.035
FOSB	-3.058	0.063	-4.067	0.017
FOXN3	-3.435	0.028	-2.852	0.063
FRG2	-1.805	0.057	-1.626	0.084
FSIP1	2.645	0.038	4.276	0.002
FSTL3	2.255	0.041	4.099	0.001
FUT3	3.667	0.007	3.641	0.007
FUT8	3.424	0.001	4.541	0.000
FYB	-2.850	0.013	-4.170	0.001
FZD7	-2.923	0.039	-3.386	0.019
G0S2	-5.023	0.000	-5.655	0.000
GABRG1	-1.618	0.025	-1.274	0.069
GABRP	-3.858	0.007	-4.418	0.002

GALK2	-2.351	0.091	-3.413	0.019
GALNT8	-1.142	0.053	-1.154	0.051
GAPDHS	-1.529	0.058	-1.455	0.069
GAS2L1	-2.426	0.036	-2.230	0.051
GBA	3.187	0.018	2.308	0.075
GBGT1	-2.638	0.030	-2.411	0.045
GCNT2	-1.610	0.014	-1.923	0.004
GFM2	2.799	0.028	2.908	0.023
GGH	4.151	0.001	3.708	0.002
GGTA1P	-2.347	0.022	-3.211	0.003
GINS1	3.975	0.000	2.658	0.004
GJA1	3.344	0.033	2.683	0.080
GJB2	2.889	0.056	3.167	0.038
GLB1L	-2.000	0.070	-2.461	0.030
GLG1	-1.616	0.040	-1.737	0.029
GLIPR2	-2.693	0.088	-3.124	0.051
GLT8D1	2.473	0.048	2.411	0.053
GLTSCR2	-1.288	0.046	-1.406	0.031
GLUL	3.259	0.008	3.150	0.010
GMEB1	2.893	0.034	2.903	0.033
GNB2L1	-1.698	0.027	-1.342	0.072
GPR141	-1.239	0.059	-1.643	0.016
GPR75	-2.847	0.048	-4.330	0.005
GPRC5A	6.217	0.000	5.854	0.000
GPRC5B	-5.398	0.002	-6.709	0.000
GPX8	3.758	0.001	4.538	0.000
GRAMD3	-2.804	0.045	-2.707	0.052
GRB14	6.529	0.011	4.826	0.050
GRB2	4.053	0.009	2.952	0.047
GRIN3A	-1.427	0.070	-1.794	0.027
GSAP	3.861	0.023	2.995	0.070
GSTP1	-2.075	0.014	-2.604	0.007
GTF2A1	2.531	0.075	2.560	0.072
GTF2H2C_2	2.515	0.011	2.293	0.019
GTF3C5	-1.515	0.012	-1.911	0.002
GUK1	1.551	0.079	1.756	0.049
GUSBP5	-1.664	0.045	-1.441	0.079
H2AFV	1.775	0.096	2.215	0.042
H2AFY	1.882	0.004	2.414	0.000
HAGH	3.679	0.004	3.107	0.012
HAX1	1.422	0.036	1.274	0.058
HCLS1	-3.755	0.011	-4.499	0.003
HDAC3	2.046	0.016	1.978	0.020
HDAC5	-2.477	0.075	-2.468	0.076
HEATR5A	2.453	0.009	1.637	0.066
HEPACAM2	-2.735	0.009	-2.483	0.016
HHAT	2.660	0.043	3.659	0.008
HIGD2B	-1.474	0.096	-1.528	0.085
HIST1H1C	2.882	0.038	3.985	0.006
HIST1H2AI	2.846	0.014	2.549	0.026
HIST1H2BC	1.082	0.082	1.290	0.042
HIST1H2BD	1.094	0.052	1.243	0.030
HIST1H2BI	1.471	0.049	1.852	0.016
HIST1H2BJ	1.251	0.030	1.541	0.010
HIST1H2BK	0.994	0.082	1.237	0.035

HIST1H2BL	1.302	0.099	1.880	0.022
HIST1H2BM	1.644	0.038	2.013	0.014
HIST1H3B	2.651	0.027	2.864	0.018
HIST1H3H	1.752	0.035	2.246	0.009
HIST1H3J	2.958	0.045	2.490	0.086
HIST2H2AA4	2.281	0.071	2.834	0.029
HIST2H2AB	1.107	0.048	1.631	0.006
HIST2H2AC	1.291	0.069	1.387	0.053
HIST2H2BF	1.472	0.041	1.640	0.025
HJURP	3.100	0.054	2.748	0.083
HLF	-5.713	0.006	-4.342	0.028
HMGB2	1.748	0.029	1.691	0.034
HMGB3	5.350	0.000	4.831	0.000
HMGB3P1	2.657	0.009	2.486	0.013
HMMR	4.244	0.005	3.891	0.008
HN1L	1.796	0.009	1.933	0.006
HOTAIRM1	-4.547	0.000	-4.162	0.000
HOXA2	-2.734	0.001	-2.466	0.001
HOXA3	-4.818	0.003	-4.609	0.004
HOXA7	-2.130	0.047	-1.933	0.069
HOXC6	4.115	0.012	2.970	0.057
HSD17B3	-1.281	0.075	-1.527	0.037
HSPA13	1.788	0.041	2.064	0.021
HSPA14	3.079	0.014	2.332	0.053
HSPA4	2.495	0.033	2.290	0.048
HSPA8	1.089	0.085	1.233	0.054
HSPB1	1.613	0.018	2.186	0.003
HULC	-2.077	0.035	-2.083	0.035
HYDIN	-2.838	0.042	-3.054	0.030
IARS2	1.963	0.051	1.900	0.058
ID4	-3.515	0.033	-3.183	0.051
IDS	1.964	0.092	2.519	0.035
IFFO2	-5.354	0.001	-4.135	0.008
IFI27	4.121	0.000	3.901	0.000
IFI6	1.903	0.091	2.464	0.033
IGFBP5	3.532	0.002	3.354	0.003
IGFBP6	-2.849	0.026	-2.815	0.028
IGJ	-6.064	0.002	-5.598	0.004
IGLL1	-4.961	0.014	-6.183	0.003
IGLL5	-4.822	0.019	-5.743	0.007
IL10RB-AS1	-3.571	0.006	-3.745	0.004
IL13RA1	1.883	0.037	2.077	0.023
IL17RD	-2.874	0.073	-2.851	0.075
IL22RA1	-1.830	0.050	-1.515	0.098
IMPAD1	2.244	0.004	1.698	0.024
INAFM1	3.515	0.003	4.587	0.000
INAFM2	-2.447	0.078	-2.784	0.048
INHBA	1.685	0.036	3.173	0.001
INTS6	3.364	0.009	2.971	0.018
IPO13	2.522	0.064	2.343	0.083
IPPK	3.776	0.017	3.360	0.031
IQCA1	-2.748	0.007	-2.458	0.013
IQSEC3	-1.683	0.047	-2.189	0.013
IRF3	2.358	0.045	2.426	0.039
IRX1	-4.662	0.001	-7.259	0.000

IRX4	-3.933	0.015	-4.785	0.004
ISM1	-4.617	0.000	-5.717	0.000
ISY1-RAB43	-2.462	0.021	-2.836	0.009
ITGAV	1.765	0.042	1.548	0.070
ITGB1BP1	2.093	0.062	2.096	0.061
ITGB3BP	2.286	0.045	2.110	0.062
ITM2A	-3.462	0.001	-4.521	0.000
ITPA	-2.466	0.023	-1.728	0.097
IWS1	3.510	0.028	4.465	0.007
JMJD7	-1.715	0.012	-1.167	0.074
JPH2	-2.303	0.053	-3.035	0.014
KANK1	-2.877	0.061	-4.627	0.005
KANK2	3.306	0.031	4.005	0.011
KAZALD1	2.383	0.088	4.134	0.006
KBTBD6	-2.913	0.014	-2.251	0.049
KCNH8	-1.672	0.006	-1.847	0.003
KCNIP3	-1.493	0.012	-1.398	0.018
KCNJ8	-4.067	0.000	-4.865	0.000
KCNK1	2.590	0.013	2.286	0.026
KCNK15	3.100	0.004	3.223	0.003
KCNK16	-1.208	0.096	-1.202	0.098
KCNK5	-3.230	0.039	-2.697	0.079
KCNN4	-4.298	0.006	-3.610	0.017
KCTD12	-2.463	0.011	-1.955	0.036
KCTD14	-4.498	0.000	-4.619	0.000
KDM5B	1.658	0.059	1.955	0.029
KHNYN	-2.660	0.067	-3.544	0.019
KIAA0101	4.516	0.001	4.293	0.001
KIAA0196	1.947	0.074	2.167	0.049
KIF14	3.874	0.060	3.422	0.093
KIF25	-2.366	0.053	-2.671	0.031
KIT	-4.153	0.000	-7.598	0.000
KLHL13	-2.410	0.037	-3.886	0.002
KLHL14	1.386	0.034	1.870	0.006
KLHL21	-2.881	0.056	-3.960	0.012
KLHL7	-1.814	0.084	-3.311	0.004
KLK7	-2.966	0.019	-2.802	0.026
KLK8	-2.240	0.034	-4.611	0.000
KLRB1	-3.087	0.006	-3.111	0.006
KLRC3	-2.124	0.025	-2.377	0.014
KPNA2	1.922	0.041	2.760	0.006
KPNB1	1.769	0.032	1.760	0.033
KRT13	-4.652	0.000	-3.281	0.006
KRT14	-3.254	0.011	-4.327	0.002
KRT15	-6.310	0.001	-6.971	0.000
KRT17P5	-1.650	0.077	-1.637	0.079
KRT19	1.532	0.029	1.702	0.017
KRT19P2	1.470	0.099	1.559	0.083
KRT5	-3.557	0.012	-4.124	0.005
KRT8	1.334	0.027	1.728	0.006
KRT8P12	1.483	0.022	2.016	0.003
KRTAP6-3	-1.852	0.098	-2.179	0.055
L3HYPDH	2.652	0.040	2.902	0.027
LAGE3	1.805	0.081	1.698	0.099
LAMA3	-3.169	0.089	-3.579	0.057

LARP1B	3.046	0.031	3.032	0.032
LARP6	-1.648	0.093	-1.928	0.053
LAYN	-2.229	0.039	-2.293	0.034
LBR	3.657	0.015	3.521	0.019
LDHB	-3.603	0.024	-3.647	0.022
LEF1	4.216	0.009	4.025	0.012
LFNG	3.980	0.007	3.003	0.034
LGALS9	3.325	0.003	2.110	0.042
LGR6	-2.889	0.028	-4.666	0.001
LHFPL4	-2.842	0.004	-2.930	0.003
LIMK2	-3.000	0.016	-5.288	0.000
LIN9	4.072	0.033	4.186	0.029
LINC00086	-2.084	0.053	-2.864	0.011
LINC00152	2.110	0.023	2.445	0.010
LINC00240	-2.121	0.029	-2.374	0.016
LINC00298	1.541	0.086	1.830	0.045
LINC00515	-2.597	0.087	-2.558	0.091
LINC00842	-2.034	0.042	-2.119	0.035
LINC00865	-2.723	0.018	-2.708	0.019
LINC01000	-1.260	0.099	-2.195	0.007
LINC01152	-3.773	0.003	-3.239	0.009
LINC01235	-2.532	0.028	-2.998	0.011
LINC01270	2.407	0.056	2.281	0.068
LIPG	-1.589	0.022	-1.625	0.020
LMCD1	5.390	0.000	6.042	0.000
LOC100130152	1.950	0.025	2.156	0.014
LOC100130232	-1.329	0.063	-1.322	0.064
LOC100130540	-1.873	0.029	-1.608	0.056
LOC100130560	-2.452	0.017	-3.060	0.004
LOC100130899	-3.231	0.005	-2.680	0.016
LOC100131907	-2.614	0.016	-2.509	0.020
LOC100134423	-1.654	0.036	-2.033	0.013
LOC100287477	-2.013	0.056	-2.700	0.014
LOC100288619	-1.263	0.048	-1.340	0.037
LOC100505923	-2.511	0.012	-2.568	0.011
LOC100506314	-1.646	0.046	-2.120	0.013
LOC100506411	2.372	0.016	1.905	0.047
LOC100506674	5.205	0.001	3.913	0.010
LOC100506827	-1.602	0.026	-1.662	0.022
LOC100507131	-1.885	0.015	-1.750	0.023
LOC100507291	1.717	0.099	1.731	0.097
LOC100507599	-1.968	0.031	-1.621	0.070
LOC100652768	-2.494	0.021	-2.293	0.032
LOC100996535	-1.937	0.075	-1.813	0.094
LOC101926934	-1.651	0.023	-1.531	0.033
LOC101927322	-1.802	0.046	-2.040	0.026
LOC101927331	-1.871	0.065	-2.164	0.036
LOC101927354	-1.522	0.044	-1.329	0.074
LOC101927389	-1.603	0.057	-1.461	0.080
LOC101927584	-1.293	0.068	-1.205	0.086
LOC101927770	2.588	0.088	3.045	0.048
LOC101928201	-1.581	0.019	-1.495	0.025
LOC101928347	-1.061	0.067	-1.256	0.033
LOC101928413	1.961	0.026	1.734	0.045
LOC101928659	1.926	0.084	2.596	0.024

LOC101928865	1.762	0.060	1.808	0.054
LOC101929128	-1.874	0.078	-2.323	0.033
LOC101929181	-1.693	0.079	-1.717	0.076
LOC101929231	-2.270	0.036	-1.742	0.098
LOC101929998	-2.250	0.072	-3.805	0.005
LOC102723428	2.181	0.009	1.537	0.052
LOC102723505	-6.450	0.000	-6.291	0.000
LOC102723765	-1.788	0.046	-1.941	0.032
LOC102723854	-2.744	0.001	-3.526	0.000
LOC102723882	-1.863	0.035	-1.716	0.050
LOC102723920	-3.106	0.011	-2.595	0.029
LOC102724505	-1.509	0.036	-1.310	0.064
LOC102725242	-1.399	0.084	-1.378	0.088
LOC102725394	-3.038	0.031	-4.622	0.002
LOC102800447	-2.212	0.008	-2.296	0.006
LOC154761	-2.711	0.016	-2.561	0.021
LOC283299	-1.653	0.054	-1.960	0.025
LOC339988	-1.133	0.099	-2.037	0.006
LOC340017	-2.239	0.042	-2.045	0.060
LOC388242	-2.389	0.004	-2.690	0.001
LOC401287	-2.472	0.060	-2.281	0.080
LOC401296	-1.499	0.073	-1.869	0.029
LOC440300	2.189	0.097	2.878	0.034
LOC541473	-2.646	0.044	-2.634	0.045
LOC643454	1.896	0.024	1.664	0.044
LOC643733	-2.994	0.008	-2.813	0.011
LOC644070	-1.788	0.054	-2.139	0.024
LOC644919	-1.833	0.035	-1.895	0.030
LOC645188	-1.713	0.029	-1.274	0.093
LOC728040	-1.271	0.090	-1.435	0.059
LOC729047	-2.165	0.011	-2.208	0.010
LOC93432	-1.738	0.017	-1.830	0.013
LOXL3	2.823	0.051	2.868	0.048
LPCAT1	3.811	0.007	2.632	0.049
LRFN1	-2.556	0.075	-2.659	0.065
LRG1	3.790	0.064	3.703	0.070
LRRC42	2.179	0.058	2.293	0.048
LRRC56	3.013	0.025	3.032	0.025
LRRFIP1	1.868	0.095	2.660	0.022
LRRN2	2.718	0.071	2.985	0.049
LRRN4CL	3.000	0.041	3.525	0.019
LRRTM4	-1.718	0.095	-1.732	0.093
LTB	-3.045	0.011	-2.651	0.023
LTBP1	4.948	0.005	3.402	0.042
LTBP2	-2.676	0.041	-2.126	0.096
LUC7L2	-2.566	0.011	-2.435	0.015
LUM	3.865	0.004	4.755	0.001
LUZP2	-3.344	0.008	-2.436	0.044
LY75	-4.050	0.014	-4.853	0.004
LY9	1.812	0.024	1.518	0.054
LYN	-3.238	0.008	-2.883	0.017
LYPD6	-2.492	0.054	-3.103	0.020
LYRM9	-4.852	0.003	-3.363	0.030
MAB21L1	-1.386	0.040	-1.088	0.099
MAG	-1.763	0.057	-1.646	0.074

MAGI1	-3.338	0.059	-4.007	0.027
MAGI2-AS3	-2.461	0.049	-3.263	0.012
MAL2	2.327	0.019	1.946	0.045
MAML3	-3.152	0.078	-3.328	0.064
MAP2K6	-2.630	0.016	-4.515	0.000
MAP3K12	2.365	0.026	1.966	0.058
MAPK9	2.469	0.046	3.256	0.011
MAPKAPK2	1.478	0.076	1.558	0.063
MAST4	2.228	0.098	3.520	0.013
MASTL	3.283	0.049	3.579	0.034
MATN2	-5.135	0.001	-4.883	0.001
MBNL1-AS1	-1.551	0.062	-1.488	0.073
MED20	1.701	0.061	1.824	0.046
MED27	-1.763	0.050	-2.095	0.023
MEN1	2.291	0.049	2.187	0.059
MESP1	-2.444	0.018	-1.945	0.052
METTL10	1.855	0.042	1.864	0.042
METTL7A	-1.789	0.083	-3.296	0.004
MFI2	-2.873	0.023	-3.043	0.017
MIA	-4.018	0.007	-7.409	0.000
MID1	-2.831	0.018	-2.419	0.038
MIEF1	-2.549	0.033	-2.315	0.050
MIR100HG	-3.264	0.078	-3.329	0.073
MIR31HG	-2.201	0.040	-2.299	0.033
MIR3916	2.218	0.033	2.143	0.039
MIR503HG	1.585	0.040	1.762	0.024
MITD1	3.063	0.005	2.148	0.036
MMD	2.609	0.060	2.589	0.061
MME	-4.328	0.002	-4.214	0.002
MMP1	3.555	0.006	2.363	0.051
MMP11	3.624	0.016	4.978	0.002
MMP7	-5.326	0.010	-7.057	0.001
MOAP1	2.932	0.003	1.727	0.058
MOB3B	-3.320	0.007	-2.399	0.040
MPC2	2.695	0.007	2.794	0.005
MPHOSPH10	2.878	0.029	2.968	0.025
MRAS	-2.697	0.014	-3.013	0.007
MRGBP	2.332	0.022	3.087	0.004
MRPL27	2.202	0.039	2.686	0.014
MRPL28	2.978	0.068	3.103	0.058
MRPL47	3.378	0.015	2.779	0.040
MRPL55	1.307	0.036	1.632	0.011
MRPS30	3.293	0.025	2.589	0.069
MRVI1	1.848	0.089	3.023	0.009
MRVI1-AS1	-2.012	0.086	-1.967	0.093
MSI1	-2.687	0.067	-2.823	0.056
MSL3P1	-2.547	0.007	-1.548	0.082
MSMB	6.000	0.000	4.127	0.004
MSRA	-2.854	0.044	-4.766	0.002
MSRB1	1.745	0.096	2.249	0.036
MST1R	2.434	0.050	3.825	0.004
MSTO1	2.022	0.075	1.898	0.093
MT1A	-1.642	0.034	-1.834	0.019
MT1E	-2.409	0.005	-2.817	0.002
MT1G	-2.193	0.020	-4.823	0.000

MT1HL1	-1.796	0.040	-2.219	0.014
MT1L	-1.799	0.018	-1.890	0.014
MT1M	-3.188	0.010	-5.596	0.000
MT1X	-1.867	0.038	-2.650	0.005
MTA1	3.820	0.009	3.030	0.031
MTF2	2.787	0.033	2.715	0.037
MTX1	1.831	0.054	1.617	0.085
MUC1	2.313	0.003	2.098	0.006
MUC15	-3.744	0.004	-3.086	0.015
MUC7	-2.685	0.045	-2.275	0.084
MUTYH	2.956	0.032	3.573	0.012
MVB12B	-2.918	0.050	-3.041	0.042
MYC	-3.178	0.006	-4.012	0.001
MYCBP	2.809	0.005	2.351	0.015
MYL5	-1.732	0.036	-1.547	0.058
MYLK	-1.545	0.028	-2.371	0.002
NAA10	2.254	0.049	2.996	0.012
NAGK	1.545	0.065	1.394	0.093
NAP1L2	-2.435	0.011	-2.335	0.013
NARF	2.231	0.067	2.647	0.033
NAT1	5.978	0.000	5.657	0.000
NAT2	3.481	0.013	2.360	0.077
NBPF10	1.401	0.012	1.216	0.025
NBPF6	3.111	0.064	4.094	0.019
NBPF9	1.590	0.035	1.331	0.071
NCALD	-4.083	0.006	-4.878	0.002
NCKAP1L	-1.724	0.027	-1.737	0.026
NCMAP	-2.374	0.009	-5.249	0.000
NDFIP1	1.857	0.051	2.421	0.014
NDRG2	-2.820	0.041	-4.245	0.004
NDUFAB1	2.075	0.060	2.871	0.013
NDUFB6	2.949	0.021	3.260	0.012
NEDD4L	-3.474	0.006	-2.434	0.042
NEIL1	-2.997	0.043	-3.746	0.014
NENF	1.173	0.067	1.270	0.049
NES	-3.898	0.013	-3.764	0.016
NEURL3	-4.162	0.005	-4.825	0.002
NFIB	-2.820	0.003	-3.567	0.000
NIPSNAP1	1.523	0.063	2.190	0.011
NOTCH4	-2.151	0.072	-2.749	0.025
NPAT	-2.099	0.043	-2.368	0.025
NPNT	2.452	0.088	3.527	0.019
NPRL3	1.845	0.075	2.630	0.015
NR3C1	-1.222	0.080	-1.546	0.031
NT5DC3	-1.824	0.058	1.652	0.083
NTRK3	-2.014	0.064	-1.876	0.083
NUCKS1	1.510	0.027	1.498	0.029
NUDT5	1.942	0.093	1.978	0.088
NUDT6	-5.234	0.000	-4.603	0.000
NUDT9P1	-4.438	0.004	-3.635	0.013
NUF2	2.650	0.029	2.201	0.064
NUP37	2.224	0.023	2.277	0.020
NUSAP1	3.581	0.006	3.146	0.014
NVL	3.505	0.031	3.812	0.020
OGFRL1	-2.256	0.078	-3.132	0.018

OR10AD1	-1.305	0.097	-1.473	0.064
OR12D2	-1.564	0.028	-1.416	0.044
OR1L3	-1.780	0.048	-1.495	0.092
OXTR	-2.684	0.028	-3.224	0.011
P2RY12	-2.017	0.062	-1.853	0.084
PADI2	-3.253	0.011	-3.584	0.006
PAK7	-2.789	0.006	-2.007	0.038
PALMD	-2.618	0.067	-3.681	0.014
PANK2	3.052	0.024	2.271	0.083
PARD6B	2.962	0.012	2.052	0.069
PARP14	1.657	0.030	1.840	0.018
PBK	2.717	0.055	3.042	0.034
PCDH15	-3.304	0.030	-2.930	0.051
PCDHB4	-2.729	0.040	-2.383	0.069
PDCD5	1.429	0.077	1.467	0.070
PDE8A	3.003	0.013	2.378	0.042
PDGFA	-2.087	0.089	-4.582	0.001
PDGFRA	-3.439	0.003	-3.246	0.005
PDK4	-3.981	0.003	-5.753	0.000
PDLIM3	-3.019	0.038	-2.464	0.084
PDP1	2.148	0.007	1.638	0.033
PER1	-2.469	0.034	-3.249	0.008
PGAM1	2.224	0.011	1.486	0.072
PHF1	-2.060	0.043	-3.575	0.002
PHF13	-2.134	0.055	-2.914	0.012
PHLDA1	-3.000	0.004	-3.334	0.002
PI15	-5.018	0.001	-6.295	0.000
PI4K2A	-2.685	0.053	-2.274	0.095
PICK1	-2.829	0.005	-3.071	0.003
PIGC	2.301	0.042	2.228	0.049
PIGN	2.101	0.029	2.799	0.005
PIGR	-7.006	0.002	-7.964	0.001
PIK3C3	2.996	0.058	3.128	0.048
PIK3CG	-2.533	0.090	-2.523	0.091
PINLYP	-3.862	0.000	-4.034	0.000
PITX1	2.851	0.058	3.699	0.018
PKD1P6	3.863	0.010	2.571	0.070
PKN3	-2.108	0.097	-2.642	0.042
PLA2G6	-1.691	0.096	-2.569	0.016
PLAGL1	-3.288	0.001	-1.741	0.056
PLCD1	-2.173	0.098	-2.821	0.036
PLCH1	-1.734	0.046	-1.762	0.043
PLEKHM3	-2.201	0.090	-4.884	0.001
PLK1	2.831	0.034	2.471	0.089
PLOD2	3.300	0.001	2.716	0.003
PLS3	-2.049	0.048	-1.928	0.062
PMAIP1	2.678	0.038	2.172	0.086
PMF1	2.556	0.044	2.466	0.051
PMPCA	-2.124	0.064	-2.049	0.073
PMS2L2	2.381	0.051	2.240	0.064
PMVK	2.974	0.052	2.521	0.095
PNPLA7	-2.027	0.036	-1.841	0.054
PNRC1	-1.695	0.030	-2.027	0.012
PODXL2	-1.471	0.051	-1.546	0.042
POLD3	3.947	0.016	4.796	0.005

POLQ	2.419	0.005	2.225	0.009
POLR1E	-2.122	0.057	-2.303	0.040
POLR2C	-1.834	0.079	-1.786	0.086
POSTN	3.748	0.004	4.578	0.001
POTEB3	3.955	0.000	3.180	0.002
POTED	2.544	0.032	2.585	0.030
POU5F2	-2.507	0.009	-2.040	0.027
PPARA	-1.905	0.044	-1.691	0.070
PPFIA1	3.176	0.003	4.354	0.000
PPM1F	-2.628	0.027	-2.253	0.054
PPP1R15A	-3.729	0.002	-3.195	0.005
PPP1R1A	-1.856	0.034	-1.714	0.048
PRB3	-1.287	0.086	-2.037	0.010
PRDX2	1.407	0.084	1.380	0.090
PRKCQ	-2.064	0.034	-2.172	0.027
PRKCQ-AS1	-3.662	0.004	-2.553	0.034
PRKX	-2.989	0.023	-3.535	0.009
PRMT5	2.707	0.016	2.572	0.021
PRPF3	3.337	0.027	2.605	0.075
PRR19	2.068	0.023	2.054	0.024
PRR34	-1.330	0.056	-1.540	0.030
PRR34-AS1	-1.920	0.025	-2.343	0.008
PRRT3	3.872	0.002	5.126	0.000
PRSS21	-1.804	0.030	-1.431	0.077
PRSS3	-1.939	0.030	-1.718	0.052
PSCA	2.071	0.045	3.296	0.003
PSEN2	3.610	0.019	3.173	0.035
PSMC1	1.735	0.066	1.677	0.075
PSMC4	1.188	0.089	1.558	0.030
PSMD2	1.657	0.040	1.432	0.071
PSMD4	1.176	0.046	1.450	0.017
PTGS2	-1.910	0.078	-1.975	0.069
PTN	-4.036	0.026	-5.222	0.006
PTPN13	2.124	0.078	2.263	0.062
PTPRO	-1.677	0.099	-1.830	0.074
PTRF	-1.610	0.079	-2.586	0.008
QRFPR	-2.699	0.059	-2.940	0.042
RAB14	-2.637	0.027	-3.677	0.004
RAB30	2.201	0.098	2.224	0.095
RABAC1	1.274	0.045	1.564	0.017
RAD17	-2.498	0.013	-2.049	0.036
RAD21	1.777	0.018	1.323	0.068
RANBP3L	-2.230	0.027	-2.685	0.010
RAPH1	1.755	0.041	1.536	0.070
RARRES1	-3.680	0.012	-3.840	0.009
RASA3	-2.395	0.004	-1.997	0.012
RASAL1	-1.840	0.074	-2.203	0.036
RASAL2	-2.322	0.045	-4.031	0.002
RASGEF1B	-2.179	0.093	-2.336	0.074
RASGRF2-AS1	-1.246	0.095	-1.237	0.097
RBAK	4.520	0.009	2.866	0.078
RBBP8	1.913	0.044	1.925	0.043
RBM24	3.160	0.035	2.468	0.091
RBM25	2.842	0.022	2.126	0.077
RBM34	2.970	0.020	2.401	0.054

RBM6	2.449	0.005	3.974	0.000
RBM8A	1.871	0.019	2.254	0.006
RBMS3	-3.033	0.019	-2.570	0.042
RBSG2	-1.719	0.014	-1.784	0.011
RCBTB1	4.310	0.009	3.084	0.050
RECQL	2.091	0.049	3.304	0.004
REEP2	1.909	0.053	2.025	0.042
REEP4	3.582	0.012	4.068	0.005
RERGL	-3.622	0.006	-3.071	0.016
RFTN1	2.980	0.012	2.530	0.030
RGN	-3.232	0.004	-2.124	0.045
RGS2	-4.400	0.016	-4.384	0.016
RIMS3	-3.602	0.004	-2.649	0.025
RIMS4	3.174	0.056	3.662	0.030
RIPPLY3	2.973	0.021	2.047	0.099
RMI1	3.636	0.001	2.418	0.022
RNF103	1.549	0.024	1.185	0.074
RNF150	-2.919	0.003	-2.625	0.007
RNF170	3.046	0.008	1.771	0.095
RNF213	4.151	0.048	4.071	0.052
RNU11	-1.592	0.043	-2.080	0.011
ROPN1	-4.528	0.000	-5.081	0.000
RP2	2.653	0.002	2.470	0.003
RPAP3	1.790	0.011	1.288	0.054
RPF1	2.410	0.013	1.990	0.034
RPH3AL	3.244	0.013	3.763	0.005
RPL10A	-1.272	0.022	-0.945	0.077
RPL13	-1.348	0.012	-1.200	0.022
RPL13A	-1.153	0.059	-1.082	0.074
RPL18A	-1.408	0.035	-1.276	0.054
RPL21P44	-1.936	0.002	-1.651	0.006
RPL26L1	3.892	0.016	2.836	0.069
RPL7A	-1.081	0.051	-1.150	0.039
RPS18	-1.289	0.045	-1.281	0.046
RPS19	-1.482	0.044	-1.248	0.085
RPS27A	-1.563	0.014	-1.646	0.011
RPS6KC1	1.346	0.082	1.275	0.098
RPUSD2	-2.778	0.088	-3.936	0.020
RRAS	1.846	0.044	2.613	0.007
RRM2	4.440	0.005	4.135	0.008
RUNX3	-3.020	0.059	-3.427	0.035
RUSC1	1.803	0.092	1.929	0.073
S100A10	1.543	0.018	1.700	0.010
S100A14	2.842	0.004	2.788	0.005
S100A4	2.703	0.063	2.782	0.057
S100A7	9.062	0.000	8.425	0.000
S100A9	3.967	0.002	2.526	0.030
S100B	-2.066	0.007	-2.514	0.002
S100P	5.401	0.005	4.982	0.008
S1PR3	2.554	0.027	2.105	0.062
SAA4	-2.274	0.044	-3.304	0.006
SAMD5	-4.546	0.000	-5.010	0.000
SAMD9L	3.144	0.016	2.151	0.086
SAP30BP	2.467	0.068	2.663	0.050
SAR1A	2.258	0.026	1.649	0.092

SARM1	-3.514	0.007	-3.373	0.009
SARS	-1.339	0.052	-1.258	0.067
SASH1	-2.949	0.017	-2.905	0.018
SCAMP1	2.096	0.020	2.172	0.016
SCAMP3	1.588	0.022	1.517	0.027
SCD	4.781	0.000	3.746	0.001
SCG2	1.158	0.094	1.656	0.021
SCGB3A2	-1.924	0.060	-2.132	0.040
SCN2B	-2.844	0.008	-2.784	0.010
SCN3B	-3.020	0.001	-2.878	0.002
SCN4B	-3.419	0.015	-3.742	0.009
SCNN1B	-1.680	0.081	-1.920	0.049
SDF2	2.587	0.078	2.656	0.071
SEC22B	1.317	0.026	0.989	0.084
SEC23A	2.877	0.036	2.434	0.070
SEC62	1.672	0.076	1.698	0.072
SEMA3B	4.449	0.000	4.437	0.000
SEMA3B-AS1	3.257	0.024	2.769	0.051
SEMA5A	-3.198	0.015	-3.471	0.009
SEMA6D	-1.628	0.055	-1.747	0.041
SEPT4	-1.930	0.034	-1.504	0.090
SEPT7	2.562	0.008	2.524	0.008
SERPINA1	2.204	0.044	2.023	0.062
SERPINB5	-2.957	0.050	-5.999	0.001
SERPINH1	1.508	0.052	1.293	0.091
SERTAD2	2.089	0.055	3.422	0.004
SF3B2	1.966	0.023	2.080	0.017
SFRP1	-5.240	0.000	-5.572	0.000
SFRP4	3.417	0.000	4.870	0.000
SFT2D2	-2.760	0.074	-2.750	0.075
SGK1	-2.479	0.018	-2.051	0.044
SGSH	-3.049	0.019	-2.282	0.069
SH3BGRL	1.847	0.012	1.342	0.056
SH3BGRL2	-3.401	0.030	-4.140	0.011
SH3BGRL3	2.408	0.011	1.654	0.065
SIAH2	2.295	0.021	1.661	0.083
SIDT1	3.547	0.020	3.115	0.037
SIGIRR	2.722	0.004	2.527	0.006
SIGLEC8	-2.143	0.028	-2.726	0.007
SKAP2	-4.251	0.003	-3.651	0.009
SLC16A3	2.729	0.043	3.918	0.006
SLC1A1	3.595	0.028	3.484	0.032
SLC22A1	-2.277	0.006	-1.988	0.015
SLC24A1	-2.194	0.053	-2.075	0.065
SLC25A39	1.886	0.044	1.689	0.069
SLC25A44	2.320	0.017	2.485	0.011
SLC27A2	3.922	0.032	3.669	0.043
SLC2A10	3.372	0.021	3.353	0.022
SLC2A4RG	1.511	0.066	1.367	0.093
SLC35F2	2.604	0.030	3.075	0.012
SLC35F5	2.695	0.074	3.236	0.036
SLC39A6	3.660	0.001	2.659	0.007
SLC4A11	-3.117	0.013	-3.617	0.005
SLC5A9	-1.440	0.090	-1.952	0.026
SLC6A14	-5.878	0.004	-6.232	0.003

SLC7A2	3.117	0.004	3.088	0.004
SLFN12	-1.905	0.031	-1.741	0.047
SLITRK6	3.031	0.041	3.200	0.032
SMAD3	-1.849	0.063	-1.934	0.053
SMAD5	1.715	0.068	1.635	0.081
SMARCC2	3.767	0.011	2.758	0.052
SMCO4	-2.615	0.067	-3.691	0.013
SMIM17	3.243	0.027	3.682	0.013
SMOX	-1.712	0.031	-2.385	0.004
SMYD1	-1.877	0.032	-1.782	0.041
SMYD4	-3.940	0.031	-3.906	0.032
SNAPC1	-1.339	0.057	-1.682	0.020
SND1	-1.456	0.027	-1.478	0.025
SNHG8	-1.095	0.095	-1.524	0.025
SNORA37	2.086	0.092	2.041	0.098
SNORD104	4.456	0.011	3.969	0.022
SNORD48	2.015	0.011	2.076	0.009
SNORD6	2.562	0.013	2.552	0.014
SNORD75	2.270	0.031	3.479	0.002
SNORD76	3.971	0.009	2.640	0.068
SNRPB2	1.236	0.058	1.368	0.038
SNRPE	1.253	0.025	0.973	0.073
SNRPG	1.114	0.052	0.939	0.096
SOCS2	-4.446	0.003	-5.053	0.001
SOSTDC1	-4.276	0.000	-3.133	0.005
SOX10	-5.259	0.000	-4.090	0.007
SOX8	-1.853	0.025	-2.445	0.005
SOX9-AS1	-2.505	0.035	-2.775	0.021
SP110	3.109	0.011	1.923	0.097
SPAG4	2.182	0.021	2.413	0.012
SPATA18	-2.714	0.010	-3.020	0.005
SPATA6L	1.858	0.014	1.405	0.053
SPCS2	1.571	0.011	1.468	0.017
SPECC1	2.694	0.007	1.547	0.095
SPESP1	-1.784	0.036	-1.441	0.084
SPPL3	3.077	0.020	2.950	0.025
SPRN	-2.529	0.037	-2.591	0.033
SPRY2	-3.882	0.001	-4.008	0.001
SPTLC3	-3.272	0.041	-3.654	0.024
SPTSSA	1.525	0.034	1.386	0.051
SRCAP	1.462	0.070	2.193	0.010
SREBF1	2.916	0.003	2.690	0.005
SREK1	3.159	0.016	3.243	0.014
SRGAP2	3.088	0.015	4.303	0.002
SRP9	1.050	0.037	0.969	0.052
SRRM2-AS1	1.770	0.060	2.831	0.005
SRSF11	1.220	0.057	1.159	0.069
ST3GAL6	-3.688	0.000	-4.219	0.000
STAC	-1.483	0.045	-1.339	0.067
STAC2	-3.798	0.000	-3.639	0.000
STARD10	3.101	0.005	2.904	0.007
STX2	2.316	0.083	3.670	0.010
STX7	-1.847	0.058	-1.745	0.072
STYK1	2.242	0.083	3.139	0.019
STYXL1	2.754	0.031	2.988	0.021

SUCO	1.700	0.014	1.191	0.071
SUFU	-3.306	0.016	-2.154	0.098
SVIL	-1.926	0.083	-3.709	0.003
SYAP1	3.645	0.029	3.535	0.033
SYNM	-5.387	0.007	-8.543	0.000
SYT13	6.926	0.000	5.584	0.002
TAF1	2.622	0.055	2.580	0.058
TAGLN	-1.540	0.046	-1.931	0.015
TARS2	3.210	0.035	3.080	0.042
TAS2R40	1.272	0.077	1.519	0.038
TBCE	1.834	0.041	2.014	0.027
TBL1Y	-1.916	0.035	-1.732	0.054
TCF4	2.514	0.022	2.315	0.033
TEFM	-1.997	0.094	-3.413	0.008
TERF2IP	-1.620	0.037	-1.634	0.036
TESC	-5.858	0.000	-5.330	0.000
TEX10	-2.273	0.039	-2.312	0.036
TF	-2.813	0.005	-4.064	0.000
TFAP4	-2.896	0.020	-3.408	0.008
TFB1M	-2.403	0.005	-1.694	0.038
TFF1	3.443	0.000	2.974	0.000
TFF3	3.555	0.010	2.816	0.034
TFPI	-4.674	0.002	-4.098	0.005
TFRC	2.801	0.006	1.891	0.051
TGFB1I1	-2.968	0.024	-2.650	0.041
TGFBR2	-4.572	0.004	-6.776	0.000
THBS3	1.952	0.079	3.869	0.002
THC2497493	-2.898	0.043	-2.354	0.093
THC2507047	7.695	0.000	9.125	0.000
THC2537043	-2.171	0.055	-2.158	0.056
THC2538174	4.375	0.001	5.970	0.000
THC2581513	2.679	0.064	3.025	0.039
THC2586088	-3.838	0.006	-3.588	0.009
THC2588995	-1.571	0.074	-1.454	0.097
THC2670954	-1.884	0.005	-1.266	0.046
THC2686816	-1.705	0.036	-1.596	0.048
THC2698991	-2.182	0.035	-1.805	0.074
THC2769306	-1.296	0.051	-1.377	0.039
THC2772172	2.612	0.013	1.896	0.060
THEMIS	-1.695	0.039	-1.683	0.040
THOC2	2.161	0.070	2.677	0.028
THSD4	-3.848	0.010	-2.455	0.081
THY1	1.768	0.063	1.934	0.044
TIFA	-1.538	0.093	-1.626	0.077
TIMM17B	1.341	0.058	1.162	0.096
TIMM8A	-2.609	0.052	-3.880	0.007
TIPRL	1.479	0.064	1.654	0.041
TJP3	3.967	0.033	3.254	0.074
TK1	3.222	0.011	4.367	0.001
TK2	-2.400	0.069	-3.455	0.013
TLR6	-2.105	0.018	-1.508	0.077
TMEM108	-1.367	0.053	-1.356	0.055
TMEM126A	3.323	0.008	2.281	0.054
TMEM126B	2.007	0.019	1.455	0.078
TMEM139	-4.105	0.021	-4.279	0.017

TMEM14A	3.295	0.061	3.701	0.037
TMEM255A	-1.858	0.023	-2.032	0.015
TMEM41A	2.166	0.073	2.701	0.029
TMOD4	1.623	0.097	1.937	0.052
TMPRSS6	1.963	0.095	2.206	0.064
TNFAIP1	1.563	0.047	1.721	0.030
TNPO1	3.473	0.019	2.421	0.089
TNS4	-3.075	0.030	-3.883	0.008
TOP2A	3.758	0.021	4.072	0.013
TOX3	2.108	0.080	2.534	0.039
TP53INP1	5.120	0.002	4.508	0.006
TPBG	1.617	0.055	1.499	0.073
TPK1	-4.476	0.000	-4.733	0.000
TPM3	2.402	0.004	2.288	0.006
TPPP2	-2.198	0.005	-1.471	0.046
TPR	2.560	0.006	2.849	0.003
TPRXL	-2.253	0.017	-3.155	0.002
TRAF3IP2	-2.978	0.027	-2.374	0.070
TRAPPC9	2.049	0.071	2.597	0.026
TRIB3	2.816	0.021	2.205	0.062
TRIM11	1.557	0.099	2.073	0.033
TRIM29	-4.741	0.009	-5.106	0.006
TRIM52-AS1	-1.654	0.055	-1.747	0.044
TRIM67	-1.893	0.023	-1.449	0.072
TRMT1	-2.916	0.095	-4.269	0.019
TSPAN31	-1.977	0.094	-2.079	0.079
TSPAN7	-2.183	0.015	-1.688	0.050
TSTA3	1.877	0.088	2.998	0.011
TTC37	1.481	0.086	1.908	0.031
TTLL11	-3.704	0.001	-4.655	0.000
TTLL4	-2.920	0.023	-3.766	0.005
TTPAL	4.122	0.017	4.200	0.015
TTYH1	-3.869	0.001	-3.710	0.002
TUBB3	3.975	0.007	5.106	0.001
TUBE1	-3.212	0.042	-4.450	0.007
TWSG1	1.524	0.072	1.574	0.064
TXNDC8	1.415	0.016	1.283	0.026
TXNIP	-1.607	0.020	-1.252	0.063
TXNL4A	1.945	0.007	1.173	0.081
TYMS	3.205	0.024	3.707	0.011
UBE2C	3.561	0.015	3.143	0.029
UBE2Q2P1	1.863	0.081	2.893	0.010
UBE2S	2.103	0.087	2.044	0.095
UBE2T	4.658	0.000	3.169	0.006
UBXN4	2.631	0.022	2.902	0.024
UCP3	2.004	0.032	1.878	0.042
UGDH	2.085	0.006	2.250	0.004
UGT2B15	-1.703	0.099	-1.774	0.087
UHMK1	2.880	0.006	3.274	0.002
UHRF1	2.739	0.076	2.719	0.078
ULK4P3	-2.751	0.047	-2.974	0.033
UNC13B	2.589	0.092	2.975	0.056
UNC5B	2.209	0.030	2.390	0.020
USPL1	-2.127	0.095	-2.701	0.039
UTP3	2.093	0.077	2.403	0.045

UTP6	2.630	0.021	2.153	0.053
UTRN	-1.656	0.017	-2.708	0.000
VAC14-AS1	2.465	0.017	2.201	0.031
VAT1L	-1.313	0.089	-1.267	0.099
VCAN	2.566	0.054	3.514	0.012
VCP	1.581	0.021	1.183	0.075
VCPIP1	3.145	0.022	4.462	0.002
VDAC3	4.073	0.006	3.133	0.026
VEGFA	2.816	0.059	2.754	0.064
VEPH1	-1.826	0.029	-1.374	0.089
VGLL1	-3.038	0.007	-1.746	0.098
VPS13D	-2.018	0.017	-1.608	0.051
VPS37A	2.443	0.009	2.784	0.004
VPS37B	-2.630	0.085	-2.930	0.057
VPS51	-1.657	0.082	-2.715	0.008
VPS72	1.146	0.076	1.317	0.044
VSIG10L	-1.954	0.024	-2.356	0.008
VSNL1	-2.467	0.021	-2.081	0.047
WBP1	3.537	0.053	3.729	0.042
WDHD1	3.510	0.015	2.565	0.065
WDR35	-2.463	0.092	-2.845	0.055
WDR86	-2.068	0.069	-2.230	0.051
WDR91	3.224	0.067	2.998	0.086
WIF1	-4.287	0.003	-3.945	0.005
WIPI1	2.957	0.024	3.228	0.015
WNT6	-2.355	0.044	-2.215	0.057
WNT9B	-1.537	0.050	-1.545	0.049
WSB2	1.041	0.072	1.224	0.037
WWP1	2.420	0.013	2.172	0.023
XAB2	3.464	0.071	3.639	0.059
XIRP2	-1.450	0.033	-1.342	0.046
XK	-1.487	0.082	-1.577	0.067
YBX3	-2.204	0.001	-1.316	0.027
YWHAZ	0.876	0.091	0.917	0.078
ZBTB49	-2.534	0.002	-2.482	0.003
ZBTB7C	2.772	0.017	3.213	0.007
ZC3H14	1.648	0.034	1.880	0.018
ZC4H2	-2.284	0.075	-2.917	0.027
ZDHHC16	2.337	0.079	2.517	0.060
ZFP36L2	-2.210	0.066	-2.515	0.039
ZG16B	2.414	0.006	3.100	0.001
ZKSCAN2	2.270	0.045	3.318	0.006
ZNF285	-2.784	0.022	-3.377	0.007
ZNF322	2.353	0.008	2.217	0.011
ZNF350	2.315	0.069	2.277	0.073
ZNF358	-1.183	0.098	-2.066	0.007
ZNF442	-1.604	0.063	-1.586	0.096
ZNF470	2.077	0.068	2.480	0.032
ZNF471	-1.806	0.071	-1.687	0.089
ZNF501	-3.222	0.002	-2.238	0.022
ZNF502	-4.927	0.001	-4.157	0.004
ZNF506	-2.719	0.014	-1.824	0.084
ZNF521	-5.390	0.002	-2.820	0.073
ZNF548	2.158	0.052	2.067	0.061
ZNF567	2.557	0.020	2.136	0.047

ZNF586	-2.931	0.051	-2.469	0.095
ZNF627	2.602	0.019	1.894	0.075
ZNF649	-1.912	0.026	-2.173	0.013
ZNF699	-1.603	0.079	-2.091	0.026
ZNF705G	-1.489	0.051	-1.859	0.018
ZNF721	3.608	0.000	3.452	0.000
ZNF827	-1.386	0.094	-2.069	0.017
ZNF846	-1.320	0.075	-1.397	0.061
ZNFX1	4.348	0.007	3.272	0.035
ZNRF1	-2.437	0.027	-2.529	0.023
ZP1	1.296	0.048	1.098	0.089
ZSCAN9	-2.540	0.005	-3.341	0.001
ZWINT	5.104	0.000	4.458	0.001

Table S2. Gene-set enrichment analysis of cell migration in solid and trabecular structures

Gene Set Name	Overlap	P-value	FDR q-value	Genes
GO_LOCOMOTION	141/1984	2.15E-22	1.62E-19	*AKT1; CAV1; AGT; LYN; PTGS2; DAB2; SPRY2; DRD2; ITGB1BP1; SMAD3; SFRP1; FADD; GJA1; TGFB1I1; MESP1; IGFBP5; KANK1; LGALS9; PDGFRA; FGF2; SEMA5A; COL3A1; APC; TGFBR2; THY1; PRKCQ; ITGAV; GLG1; HMGB2; CTHRC1; SOX10; PTPRO; ANXA1; RPS19; SEMA3B; SEMA6D; VEGFA; CCN1; EDN3; EMP2; KIT; NTRK3; GCNT2; GLIPR2; PTN; P2RY12; S100A9; F11R; ACTN4; CHN1; ASPM; COL1A1; KIF14 ; FN1; NCKAP1L; EPHB1; PRKX; LEF1; HDAC5; SRGAP2; TP53INP1; HOXA7; SOX8; HOXA2; TRIM11; POSTN; MAG; COL5A1; BMERB1; RACK1; CAV2; CCL5; GRB2; FERMT1; GRB14; UNC5B; PDGFA; BST2; PAK5; EZR ; HSPB1; DNAJA1; DUSP1; GSTP1; ARRDC3; SCG2; TNFAIP1; KANK2; APOD; PADI2; CYP7B1; APCDD1; FAP; PLA2G6; CCL21; PIK3CG; TF; SASH1; S100A7; GLUL; BVES; LGR6; DCDC2; PPM1F; RGN; VEGFD; ROPN1; RRAS; GAPDHS; SGK1; MYLK; PKN3; MMP1; VPS37B; ADAM15; PRSS3; DOCK4; SEPTIN7; PARD6B; TUBB3; NFIB; FOLR1; JCHAIN; COL1A2; DNAH5; DNAH1; EGR2; CCL28; LAMA3; PODXL2; MATN2; AMOTL1; S100A14; FUT8; IGLL1; SAA4; CAVIN1; S100P; SLC16A3; ALCAM; ZNF502*
GO_LAMELLIPODIUM	18/194	0.0000184	0.000263	*ITGAV; APC; FAP; AMOTL1; SRGAP2; CTNND1; SLC39A6; HCLS1; STX2; PTPRO; MYLK; TESC; HAX ; TUBB3; ITGB1BP1; PTPN13; RAPH1; ABLIM1*

Table S3. Genes expressed in solid and trabecular structures but not in tubular and alveolar structures of breast cancer (p-value < 0.05)

Gene	Solid structures		Trabecular structures		Association with cell migration	
	LogFC	P-value	LogFC	P-value	Reference	Link
AACS	2.791	0.038	3.038	0.026	No data	
ABLIM1	-1.969	0.035	-2.498	0.010	Narahara et al, J Cell Physiol. 2018	https://doi.org/10.1002/jcp.26605
ADAMTS16	1.968	0.030	1.849	0.040	Surridge et al., Matrix Biol. 2009	https://doi.org/10.1016/j.matbio.2009.07.001
AK130224	-1.889	0.039	-1.908	0.037	No data	
ALDH7A1	-2.031	0.035	-2.932	0.004	Elsalem et al., EJC 2016	https://doi.org/10.1016/S0959-8049(16)61361-8
ALG5	2.529	0.008	2.014	0.029	No data	
ALYREF	2.728	0.045	3.047	0.027	Saito et al., J Cancer Res Clin Oncol. 2013	https://doi.org/10.1007/s00432-012-1361-5
AMOTL1	-2.854	0.031	-3.137	0.019	Couderc et al., Neoplasia 2016	https://doi.org/10.1016/j.neo.2015.11.010
APOA1BP	3.700	0.029	3.293	0.049	No data	
ASCC3	3.359	0.037	3.403	0.035	No data	
BRMS1L	-2.203	0.035	-2.056	0.048	Gong et al., Nat Commun. 2014	https://doi.org/10.1038/ncomms6406
BU963192	3.430	0.027	3.839	0.015	No data	
BVES	-2.099	0.018	-2.015	0.023	Benesh et al., Mol Biol Cell. 2013	https://doi.org/10.1091/mbc.E12-07-0539
CAV1	-3.196	0.046	-3.204	0.045	Grande-García et al., J Cell Biol. 2007	https://doi.org/10.1083/jcb.200701006
CEP78	1.569	0.038	1.564	0.038	No data	
CHST2	-2.771	0.011	-2.788	0.011	No data	
CLUAP1	2.909	0.022	3.510	0.008	Beyer et al., Mol Cell Proteomics. 2018	https://doi.org/10.1074/mcp.RA117.000487
CNIH4	1.758	0.015	1.384	0.048	Mishra et al., Oncogene 2019	https://doi.org/10.1038/s41388-019-0845-z
CTIF	2.482	0.043	2.559	0.038	No data	
CTNND1	-2.277	0.020	-2.538	0.011	Tang et al., J Exp Clin Cancer Res. 2016	https://doi.org/10.1186/s13046-016-0344-9
DDI2	-3.700	0.026	-3.541	0.032	No data	
DNAH1	-1.401	0.048	-1.846	0.012	Milosevic et al., BMC Cancer. 2013	https://doi.org/10.1186/1471-2407-13-473
DNAJC22	2.954	0.008	2.224	0.037	No data	
ENST00000299512	-1.620	0.025	-1.898	0.011	No data	
ENST00000334163	2.033	0.025	2.236	0.015	No data	
ENST00000417510	-1.992	0.018	-2.909	0.001	No data	
ENST00000429552	-1.202	0.047	-1.193	0.048	No data	
ENST00000433051	-1.875	0.031	-1.897	0.030	No data	
ENST00000455206	-1.216	0.036	-1.276	0.029	No data	
ENST00000457863	2.409	0.014	2.264	0.019	No data	
ENST00000502684	-1.756	0.022	-1.698	0.026	No data	

ENST00000506710	-2.078	0.008	-1.494	0.043	No data	
ENST00000527434	2.689	0.003	2.114	0.015	No data	
ENST00000596267	2.483	0.021	2.502	0.020	No data	
ETFDH	2.367	0.048	3.473	0.006	No data	
EXOC1	1.947	0.035	3.249	0.001	Andersen & Yeaman, Mol Biol Cell. 2010	https://doi.org/10.1091/mbc.E09-06-0459
EZR	1.993	0.036	1.918	0.043	Arpin et al., Cell Adh Migr. 2011	https://doi.org/10.4161/cam.5.2.15081
F13A1	3.636	0.019	4.639	0.004	Dardik et al., Cell Physiol Biochem. 2007	https://doi.org/10.1159/000099199
FAM109A	-3.613	0.015	-3.259	0.026	No data	
FBXO28	2.370	0.015	1.881	0.047	No data	
FCER1A	-3.174	0.026	-3.224	0.024	No data	
FDCSP	-3.715	0.030	-3.687	0.031	Wang et al., Oncol Rep. 2010	https://www.ncbi.nlm.nih.gov/pubmed/20811673
GLG1	-1.616	0.040	-1.737	0.029	Planche et al., Cancer Res. 2012	https://doi.org/10.1158/1538-7445.AM2012-3245
GPR75	-2.847	0.048	-4.330	0.005	Fan & Roman, Circ Res. 2017	https://doi.org/10.1161/CIRCRESAHA.117.311022
HDAC3	2.046	0.016	1.978	0.020	He et al., Int J Oncol. 2018	https://doi.org/10.3892/ijo.2018.4284
HMGB3P1	2.657	0.009	2.486	0.013	No data	
IL13RA1	1.883	0.037	2.077	0.023	Moretti et al., Medical Express 2015	https://doi.org/10.5935/MedicalExpress.2015.05.05
IQSEC3	-1.683	0.047	-2.189	0.013	No data	
KBTBD6	-2.913	0.014	-2.251	0.049	No data	
KCNIP3	-1.493	0.012	-1.398	0.018	No data	
KLHL14	1.386	0.034	1.870	0.006	Di Lollo et al., Sci Rep. 2020	https://doi.org/10.1038/s41598-020-61017-y
KPNB1	1.769	0.032	1.760	0.033	Stelma & Leaner, Oncotarget. 2017	https://doi.org/10.18632/oncotarget.15834
L3HYPDH	2.652	0.040	2.902	0.027	No data	
LINC00240	-2.121	0.029	-2.374	0.016	No data	
LINC00865	-2.723	0.018	-2.708	0.019	No data	
LIPG	-1.589	0.022	-1.625	0.020	Lo et al., eLife. 2018	https://doi.org/10.7554/eLife.31334
LOC100506314	-1.646	0.046	-2.120	0.013	No data	
LOC100506411	2.372	0.016	1.905	0.047	No data	
LOC100506827	-1.602	0.026	-1.662	0.022	No data	
LOC101927322	-1.802	0.046	-2.040	0.026	No data	
LOC102723882	-1.863	0.035	-1.716	0.050	No data	
LOC643454	1.896	0.024	1.664	0.044	No data	
LOC643733	-2.994	0.008	-2.813	0.011	No data	
LRRN4CL	3.000	0.041	3.525	0.019	No data	
LUC7L2	-2.566	0.011	-2.435	0.015	No data	
MASTL	3.283	0.049	3.579	0.034	Rogers et al., Oncogene. 2018	https://doi.org/10.1038/s41388-018-0295-z
METTL10	1.855	0.042	1.864	0.042	No data	

MFI2	-2.873	0.023	-3.043	0.017	Yin et al., Oncol Rep. 2016	https://doi.org/10.3892/or.2016.5013
MIR3916	2.218	0.033	2.143	0.039	No data	
MIR503HG	1.585	0.040	1.762	0.024	No data	
MRPL55	1.307	0.036	1.632	0.011	No data	
MTF2	2.787	0.033	2.715	0.037	No data	
MUTYH	2.956	0.032	3.573	0.012	Gao et al., Onco Targets Ther. 2018	https://doi.org/10.2147/OTT.S174223
MVB12B	-2.918	0.050	-3.041	0.042	No data	
NAA10	2.254	0.049	2.996	0.012	No data	
NCKAP1L	-1.724	0.027	-1.737	0.026	Afzal et al., J Am Heart Assoc. 2016	https://doi.org/10.1161/JAHA.116.004629
NEIL1	-2.997	0.043	-3.746	0.014	No data	
PLCH1	-1.734	0.046	-1.762	0.043	No data	
PRR19	2.068	0.023	2.054	0.024	No data	
PSCA	2.071	0.045	3.296	0.003	Wang et al., J Pathol. 2015	https://doi.org/10.1002/path.4582
RAD17	-2.498	0.013	-2.049	0.036	No data	
RBBP8	1.913	0.044	1.925	0.043	No data	
RCBTB1	4.310	0.009	3.084	0.050	No data	
RECQL	2.091	0.049	3.304	0.004	No data	
RFTN1	2.980	0.012	2.530	0.030	No data	
RPS18	-1.289	0.045	-1.281	0.046	No data	
SCAMP3	1.588	0.022	1.517	0.027	No data	
SLC16A3	2.729	0.043	3.918	0.006	No data	
SLC4A11	-3.117	0.013	-3.617	0.005	No data	
SLFN12	-1.905	0.031	-1.741	0.047	No data	
SMIM17	3.243	0.027	3.682	0.013	No data	
SNORD104	4.456	0.011	3.969	0.022	No data	
SPAG4	2.182	0.021	2.413	0.012	Ji et al., Oncol Rep. 2018	https://doi.org/10.3892/or.2018.6473
SPATA18	-2.714	0.010	-3.020	0.005	Okuyama et al., Sci Rep. 2019	https://doi.org/10.1038/s41598-019-39563-x
TARS2	3.210	0.035	3.080	0.042	No data	
TERF2IP	-1.620	0.037	-1.634	0.036	No data	
TFAP4	-2.896	0.020	-3.408	0.008	Huang et al., Dis Markers. 2019	https://doi.org/10.1155/2019/7129214
TFB1M	-2.403	0.005	-1.694	0.038	No data	
TFF3	3.555	0.010	2.816	0.034	Yusufu et al., Int J Oncol. 2019	https://doi.org/10.3892/ijo.2019.4854
TGFB1I1	-2.968	0.024	-2.650	0.041	Gulvady et al., Mol Biol Cell. 2018	https://doi.org/10.1091/mbc.E18-02-0092
THEMIS	-1.695	0.039	-1.683	0.040	No data	
TNFAIP1	1.563	0.047	1.721	0.030	Xiao et al., EBioMedicine. 2020	https://doi.org/10.1016/j.ebiom.2019.102603
TUBE1	-3.212	0.042	-4.450	0.007	No data	

TXNDC8	1.415	0.016	1.283	0.026	No data	
ULK4P3	-2.751	0.047	-2.974	0.033	No data	
UNC5B	2.209	0.030	2.390	0.020	Kong et al., BMC Cancer. 2016	https://doi.org/10.1186/s12885-016-2922-9
WWP1	2.420	0.013	2.172	0.023	Goto et al., Br J Cancer. 2016	https://doi.org/10.1038/bjc.2016.95
ZKSCAN2	2.270	0.045	3.318	0.006	Kawahara et al., Oncotarget. 2016	https://doi.org/10.18632/oncotarget.10679
ZNF285	-2.784	0.022	-3.377	0.007	No data	
ZNF567	2.557	0.020	2.136	0.047	No data	
ZNRF1	-2.437	0.027	-2.529	0.023	No data	

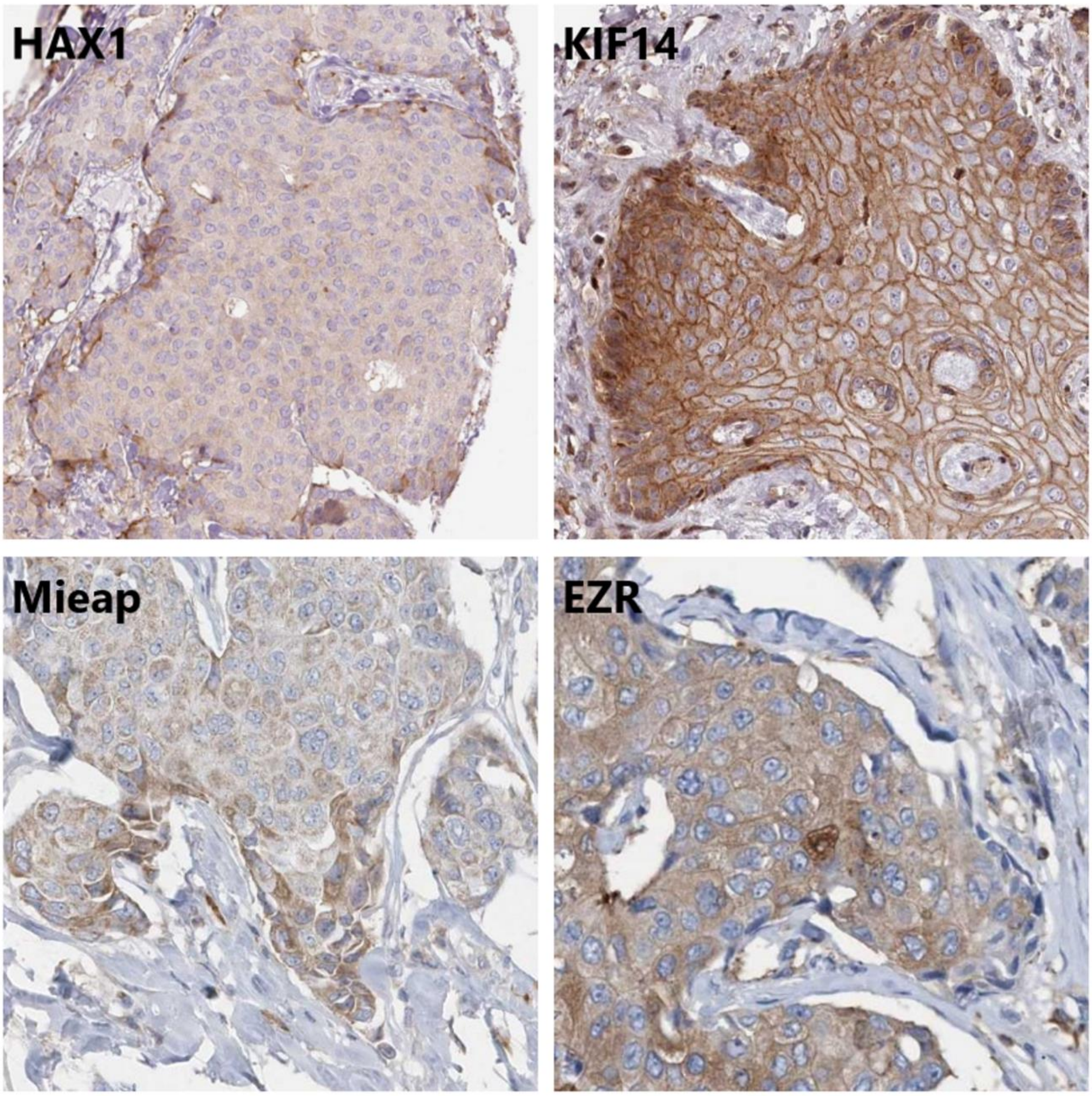

Figure S1. Expression of HAX1, KIF14, Mieap and EZR proteins in breast cancer (according to the Human Protein Atlas). HAX1 is predominantly expressed at the periphery of solid structure. Positive expression of KIF14 and Mieap and negative expression of EZR are observed at the tips of the solid structures.

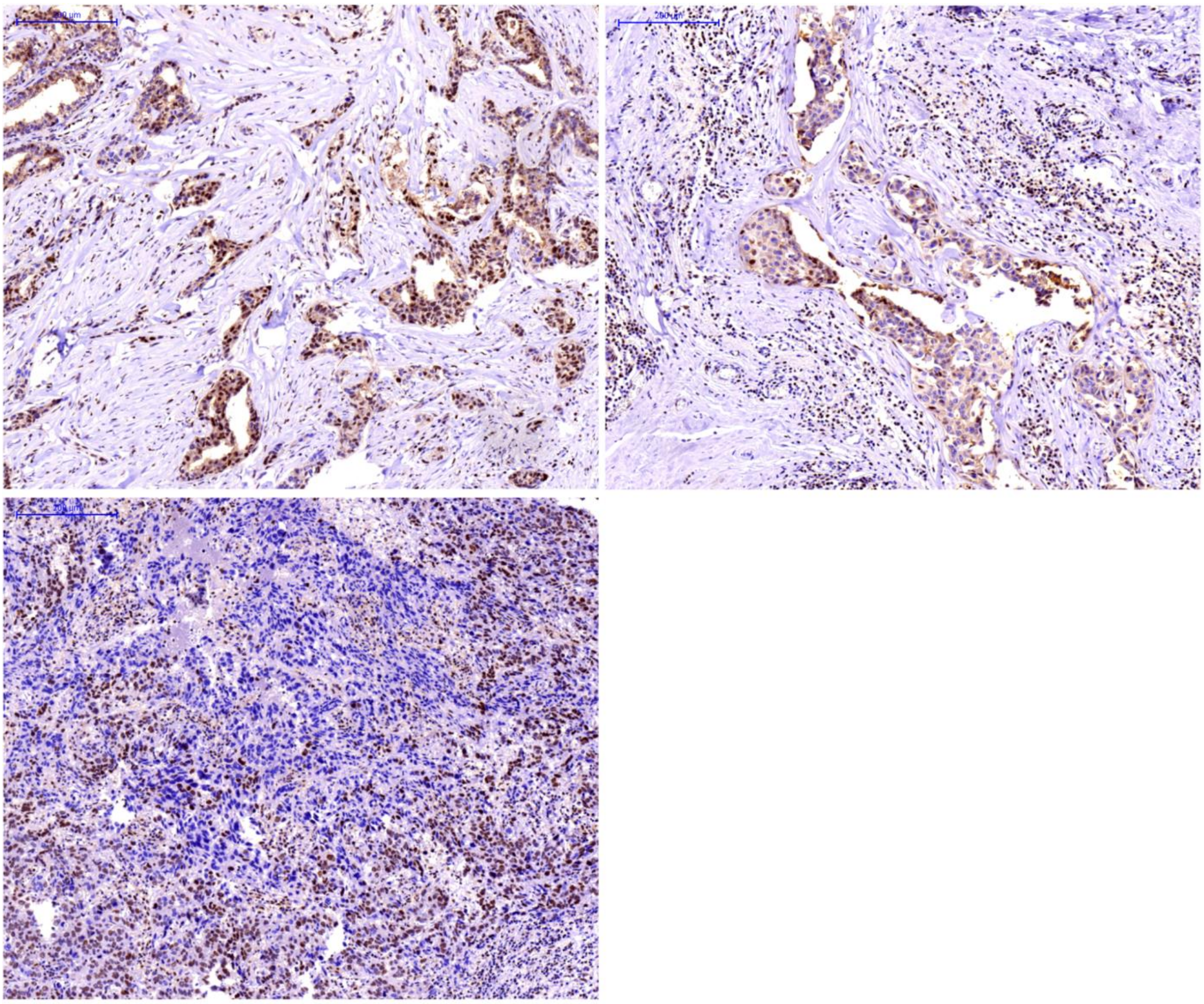

Figure S2. Immunohistochemical staining for KIF14 in breast cancers. 200x magnification.

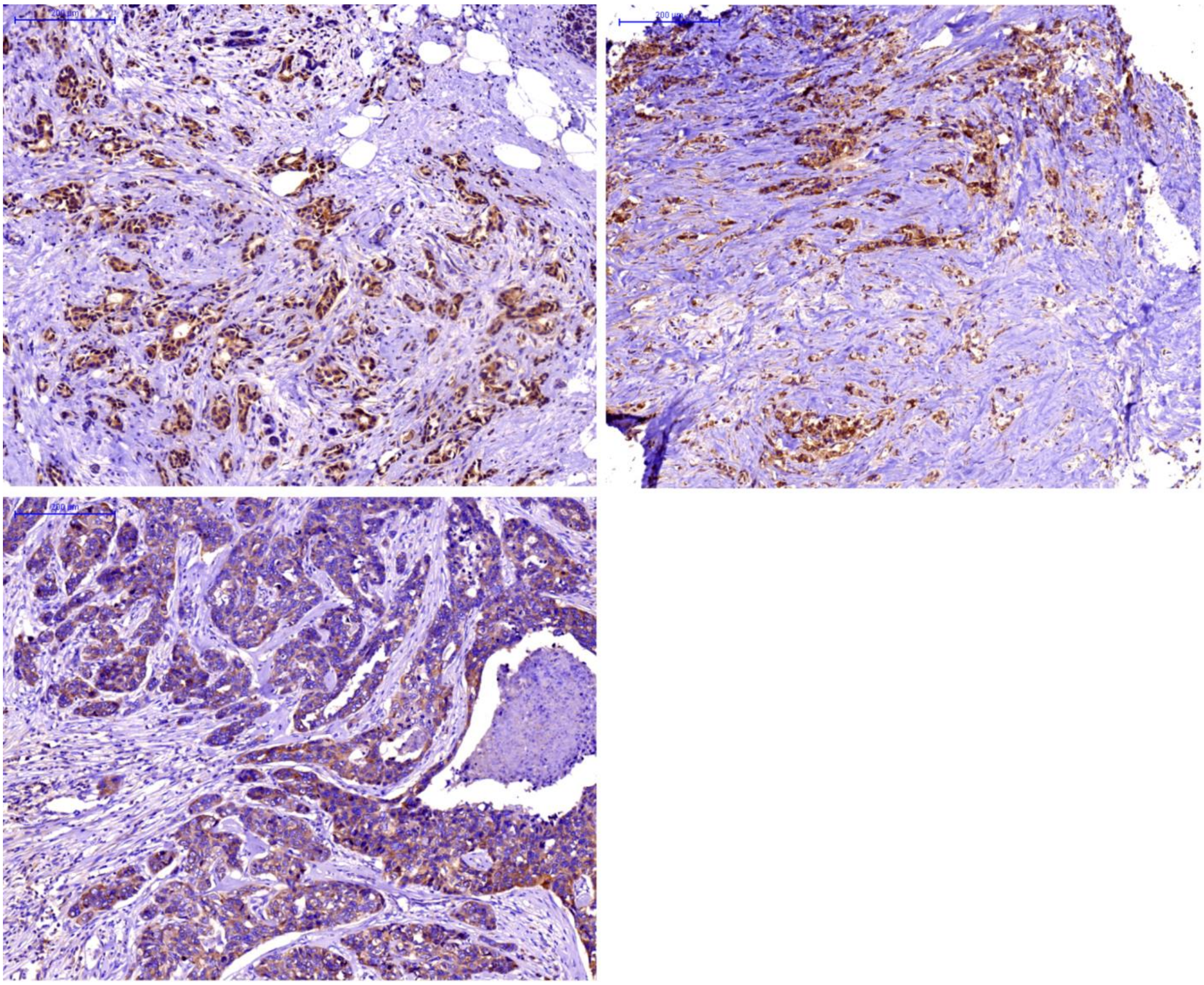

Figure S3. Immunohistochemical staining for Mieap in breast cancers. 200x magnification.

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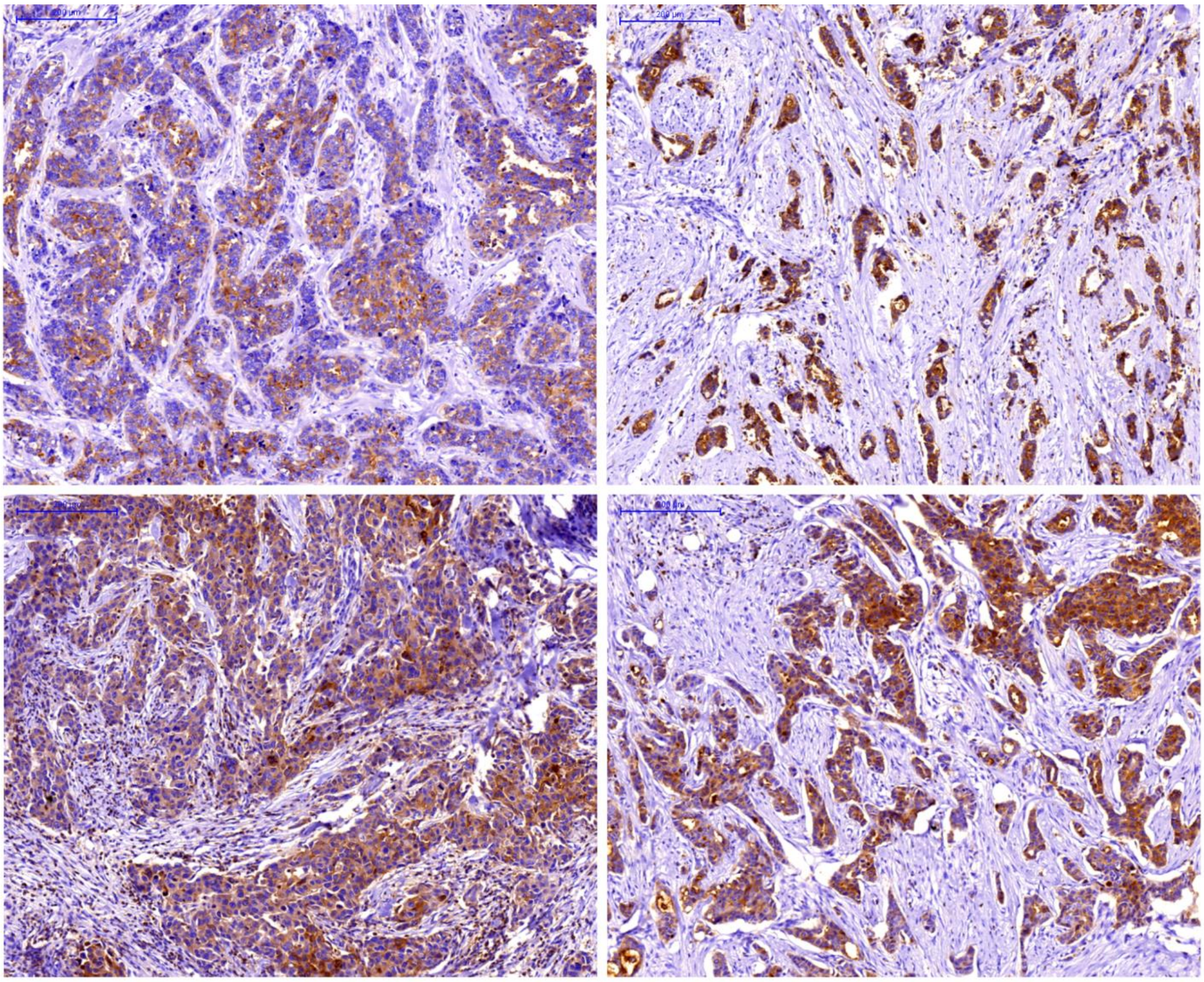

Figure S4. Immunohistochemical staining for EZR in breast cancers. 200x magnification.

Table S4. The frequency of nuclear expression of KIF14 in different morphological structures of breast tumors

	Morphological structures	Number of cases (%)
1	Single tumor cells	27/69 (39.1) p_2=0.05 p_3=0.02
2	At the tips of torpedo-like sprouts associated with solid structures	26/48 (54.2)
3	At the tips of torpedo-like structures (separated from solid structures)	21/35 (60.0)
4	At the periphery of solid structures	37/71 (52.1)
5	At the periphery of alveolar structures	35/67 (52.2)
6	At the periphery of trabecular structures	33/36 (91.7) p_1=0.0000 p_2=0.0001 p_3=0.0008 p_4=0.0000 p_5=0.0000
7	At the periphery of tubular structures	14/16 (87.5) p_1=0.0002 p_2=0.007 p_3=0.02 p_4=0.004 p_5=0.004

$p_{1\text{-}5,}$ comparison between different structures (1-5); Chi-square test

Table S5. The frequency of cytoplasmic expression of Mieap in different morphological structures of breast tumors

	Morphological structures	Number of cases (%)
1	Single tumor cells	30/70 (42.8)
2	At the tips of torpedo-like sprouts associated with solid structures	24/49 (48.9)
3	At the tips of torpedo-like structures (separated from solid structures)	20/36 (55.5)
4	At the periphery of solid structures	29/72 (40.2)
5	At the periphery of alveolar structures	30/68 (44.1)
6	At the periphery of trabecular structures	29/39 (74.3) p_1=0.0009 p_2=0.008 p_3=0.05 p_4=0.003 p_5=0.01
7	At the periphery of tubular structures	10/16 (62.5) p_4=0.04

$p_{1\text{-}5,}$ comparison between different structures (1-5); Chi-square test

Table S6. The frequency of negative cytoplasmic expression of EZR in different morphological structures of breast tumors

	Morphological structures	Number of cases (%)
1	Single tumor cells	33/66 (50.0)
2	At the tips of torpedo-like sprouts associated with solid structures	25/45 (55.5)
3	At the tips of torpedo-like structures (separated from solid structures)	19/34 (55.9)
4	At the periphery of solid structures	36/69 (52.2)
5	At the periphery of alveolar structures	19/35 (54.3)
6	At the periphery of trabecular structures	28/34 (82.3) $p_1=0.0009$ $p_2=0.007$ $p_3=0.01$ $p_4=0.002$ $p_5=0.006$
7	Tubular structures	15/17 (88.2) $p_1=0.002$ $p_2=0.009$ $p_3=0.01$ $p_4=0.003$ $p_5=0.007$

$p_{1-5,}$ comparison between different structures (1-5); Chi-square test

Table S7. Differentially expressed genes between KIF14-positive and KIF14-negative cells located in torpedo-like structures ($p < 0.05$)

Gene	P-value	LogFC
SLITRK6	0.000	-22.277
NHS	0.000	8.725
CNOT2-DT	0.000	7.941
CLIP4	0.001	7.223
LOC101928728	0.001	8.473
THBS4	0.002	6.420
DDHD1	0.002	-5.906
LUM	0.002	-5.989
GPRIN1	0.002	5.594
HIF1A-AS3	0.002	7.172
PIK3CB	0.003	-4.657
UGT8	0.003	6.986
ARL13A	0.003	6.792
ATPAF2	0.003	-5.752
LRRC26	0.004	5.290
GPR87	0.004	6.137
RBM12B	0.004	-4.698
PRICKLE2	0.004	-5.305
DENND5B	0.004	-5.869
CROT	0.004	-5.644
ZNF761	0.004	-4.858
TMEM175	0.005	-5.734
DCHS2	0.005	5.624
GTF2E1	0.005	-5.567
EYA1	0.005	-6.392
KIF21A	0.005	-5.652
RALB	0.005	-5.550
NEURL1	0.005	7.024
ARPC5L	0.005	-5.536
C2orf66	0.006	7.442
ADGRG7	0.006	7.442
EPHB1	0.006	7.442
CPN1	0.006	7.442
MYADM	0.006	-5.601
PLA2G7	0.006	6.576
CALD1	0.006	-3.831
DPT	0.008	6.774
PLCL1	0.008	-6.319
PSAPL1	0.008	6.957
TRIM38	0.008	-5.336
PLA2G4F	0.008	4.146
LOC105369779	0.010	6.630
FAM102B	0.010	4.540
XKR5	0.010	7.064
PITRM1-AS1	0.010	7.064
BCL2A1	0.010	7.064
MAMDC2-AS1	0.010	6.423

PLCB4	0.010	-5.201
ZNF460	0.011	-4.177
NAPB	0.011	-5.202
MSANTD1	0.011	6.262
LEPROT	0.011	-4.477
METTL6	0.012	-5.210
THBS2	0.012	-4.013
CYP4F8	0.012	-5.747
C17orf58	0.013	-5.114
ADAMTS7	0.013	6.692
DTNA	0.013	-5.138
RBM48	0.013	-5.334
DDX20	0.013	-5.159
INPP5J	0.013	-4.556
DLC1	0.013	5.076
USP46	0.014	-4.618
LINC00635	0.014	6.831
TRPC7	0.014	6.831
LTA	0.014	6.831
KRTAP13-4	0.014	6.831
EPHB6	0.014	5.616
C1orf105	0.015	6.228
BMP2K	0.015	-4.558
POT1	0.015	-5.083
QDPR	0.015	-5.517
VPS29	0.015	-4.826
SNAPC1	0.015	-5.149
PGAM5	0.015	-5.070
SAP30L	0.015	-4.447
IL1RN	0.015	6.171
CXorf56	0.016	-5.047
DGAT1	0.016	3.952
ANTKMT	0.016	-5.028
LIMD1	0.016	-3.737
SEC61A2	0.016	-5.088
ERCC4	0.017	-5.131
TLL2	0.017	6.538
FCGBP	0.017	-4.525
PVT1	0.017	-5.537
SLC26A2	0.017	-5.081
CINP	0.018	-4.998
ASTN2	0.018	-5.407
ST7L	0.018	-4.985
LAP3	0.018	-3.951
AIP	0.019	3.591
ZNF273	0.019	-4.026
CDH6	0.019	6.472
ZNF726	0.019	-5.149
CYP2U1	0.020	6.307
KIAA0930	0.020	-4.112

B4GALT6	0.020	6.091
AKR7A3	0.021	-5.242
NFATC1	0.021	-4.878
CAMP	0.021	6.402
EDN2	0.021	6.555
IVL	0.021	6.555
GAL3ST4	0.021	6.555
AGAP4	0.021	6.555
CCDC196	0.021	6.555
ADGRG3	0.021	6.555
B4GAT1	0.022	5.163
CDAN1	0.022	3.286
MIR3136	0.022	6.519
RAD51B	0.022	-4.903
SLC49A3	0.022	-4.943
CSGALNACT1	0.022	-4.510
ASCC2	0.023	-4.195
HMGN4	0.023	-4.903
SNHG3	0.023	-4.976
N4BP3	0.023	3.499
ATP6AP1L	0.023	-3.818
MGAT5	0.023	-3.534
STAM	0.023	-4.845
CRY1	0.023	-4.861
EEF1A2	0.024	-5.047
CCDC61	0.024	-4.833
MAB21L2	0.024	-4.899
ATF3	0.024	-4.911
TBC1D8B	0.024	-5.028
NOS1AP	0.024	-4.506
TMEM169	0.024	4.867
KIF1A	0.025	6.318
RGP1	0.025	-4.088
NAPRT	0.026	5.682
NEDD1	0.027	-5.206
MMP13	0.027	-5.336
ALDH1A1	0.027	5.857
ZNF519	0.028	-4.868
LCP1	0.028	-4.780
SLC15A2	0.028	-4.819
PARP12	0.029	-4.126
EIF2B3	0.029	-4.728
CREBL2	0.029	-4.290
TMEM170B	0.029	4.354
GLI4	0.029	4.170
EIF4ENIF1	0.029	-4.416
BET1	0.030	-4.024
TMEM41B	0.030	-3.824
TSBP1	0.030	5.596
RAB18	0.030	-3.087

ASB7	0.031	-4.715
CLCA2	0.031	6.189
ACYP2	0.031	5.729
ZFHX4	0.031	-4.859
NDUFAF1	0.031	-4.700
SDHAF1	0.031	-4.702
NAA10	0.031	5.233
RPL22L1	0.032	-4.795
ZSCAN9	0.032	-4.680
TLE6	0.033	4.771
VCX	0.033	5.545
ZRANB3	0.033	-4.768
ENC1	0.033	-3.147
VPS9D1	0.034	4.028
FGFR1	0.034	3.521
ZNF571-AS1	0.034	-4.529
VRK1	0.034	-4.665
GMPS	0.034	-3.475
TUBGCP5	0.034	-3.967
SCNM1	0.035	-4.745
CRIPT	0.035	-4.412
LY6G5B	0.035	5.756
CLDN19	0.035	6.216
PRR9	0.035	6.216
OTOL1	0.035	6.216
LINC02015	0.035	6.216
PDE6A	0.035	6.216
RS1	0.035	6.216
MROH5	0.035	6.216
SH2D4B	0.035	6.216
SLC10A2	0.035	6.216
KCNH5	0.035	6.216
GCNT3	0.035	6.216
LINC01255	0.035	6.216
PLA2G4C	0.035	6.216
TGIF2LY	0.035	6.216
TOP3B	0.035	6.216
ZSCAN22	0.035	-4.682
B3GALT2	0.035	-4.650
DFFA	0.036	-4.141
IFT27	0.036	-4.658
EDARADD	0.036	-5.528
LINS1	0.037	-4.166
SIRPA	0.037	-4.636
IPMK	0.037	-4.631
USP45	0.037	-4.046
PLEKHG6	0.037	3.310
LINC01608	0.037	6.069
FAM86DP	0.039	-4.769
RAB11FIP5	0.039	-4.597

COL2A1	0.039	5.579
ARVCF	0.039	-3.402
SSH2	0.039	-4.155
UNKL	0.039	2.608
LOC100129484	0.039	-4.687
RGS1	0.040	-4.659
FAM200A	0.040	-4.575
NETO2	0.040	6.023
CAMK1D	0.040	4.303
CYP20A1	0.041	-3.263
BBS5	0.041	-4.579
KCNK5	0.041	6.011
ANXA3	0.041	-4.977
PPA1	0.041	-4.042
SCUBE3	0.041	-4.977
PROS1	0.042	4.855
CTTNBP2	0.042	-4.909
PPRC1	0.042	-3.940
CSRNP2	0.042	-3.233
SOCS6	0.042	-3.746
GET1	0.042	4.264
KLK14	0.043	-5.400
SLC9A2	0.043	-5.031
NRAS	0.043	-3.599
GALNT3	0.043	-4.461
CSF1R	0.043	-4.652
YPEL5	0.043	-3.124
ZBTB26	0.043	-4.509
ASNS	0.044	4.668
PDE5A	0.044	-4.546
RNVU1-7	0.044	5.410
S1PR3	0.044	-4.874
FAM71F2	0.044	4.839
KIAA0319	0.044	5.468
EEF1E1	0.044	3.848
PCNP	0.044	-3.357
PDZD11	0.044	-4.201
ZNF639	0.044	-4.543
FBLIM1	0.045	-4.511
TXNDC15	0.045	-4.554
ZNF876P	0.045	4.421
MAPK14	0.045	-3.050
QTRT1	0.046	-4.499
PKDREJ	0.046	5.320
TRIM44	0.046	-2.630
PPA2	0.046	-2.867
DNAJC14	0.046	-4.575
DNAJC22	0.047	-4.868
PCSK1	0.047	5.155
KANK1	0.047	-4.188

ZFR	0.047	-2.608
PSMG3	0.048	-4.489
PTPRC	0.048	-4.515
ARV1	0.048	-3.930
DYNLT3	0.048	-3.983
TBX3	0.048	-5.302
ZNF438	0.048	-4.617
GSTCD-AS1	0.049	5.983
CCDC87	0.049	5.983
C12orf71	0.049	5.983
ZNF136	0.049	-4.276
TBP	0.049	-4.831
POLR1E	0.049	3.419

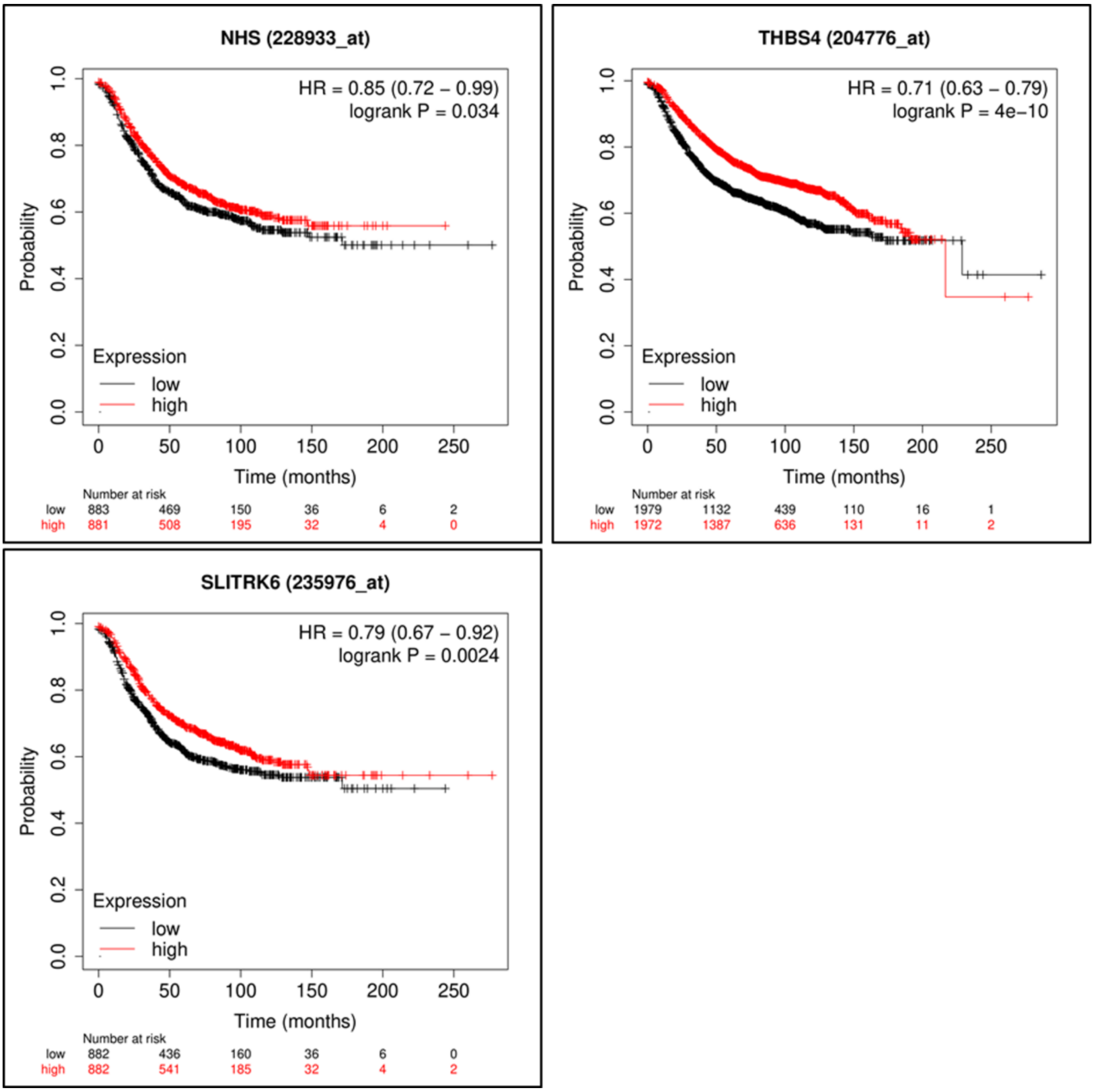

Figure S5. Association of DEGs (*NHC*, *THBS4* and *SLITRK6*) in KIF14-positive cells with relapse-free survival of breast cancer patients according to Kaplan-Meyer Plotter database.

Table S8. KEGG enrichment analysis of up- and down-regulated genes in KIF14-positive cells located in torpedo-like structures ($p < 0.05$)

Term	P-value	Adjusted P-value	Genes
VEGF signaling pathway	0.001	0.311	*PLA2G4F; NRAS; PLA2G4C; PIK3CB; MAPK14*
Fc epsilon RI signaling pathway	0.002	0.294	*PLA2G4F; NRAS; PLA2G4C; PIK3CB; MAPK14*
Ether lipid metabolism	0.003	0.330	*UGT8; PLA2G4F; PLA2G4C; PLA2G7*
GnRH signaling pathway	0.007	0.565	*PLA2G4F; NRAS; PLCB4; PLA2G4C; MAPK14*
Long-term depression	0.008	0.474	*PLA2G4F; NRAS; PLCB4; PLA2G4C*
Arachidonic acid metabolism	0.009	0.468	*PLA2G4F; CYP2U1; PLA2G4C; CYP4F8*
AGE-RAGE signaling pathway in diabetic complications	0.010	0.435	*NRAS; PLCB4; NFATC1; PIK3CB; MAPK14*
Inflammatory mediator regulation of TRP channels	0.010	0.381	*PLA2G4F; PLCB4; PLA2G4C; PIK3CB; MAPK14*
T cell receptor signaling pathway	0.010	0.352	*NRAS; PTPRC; NFATC1; PIK3CB; MAPK14*
Acute myeloid leukemia	0.011	0.330	*CSF1R; NRAS; BCL2A1; PIK3CB*
Phospholipase D signaling pathway	0.013	0.363	*PLA2G4F; NRAS; PLCB4; RALB; PLA2G4C; PIK3CB*
Prolactin signaling pathway	0.013	0.336	*NRAS; PIK3CB; SOCS6; MAPK14*
Oxytocin signaling pathway	0.015	0.357	*PLA2G4F; NRAS; CAMK1D; PLCB4; PLA2G4C; NFATC1*
Inositol phosphate metabolism	0.016	0.347	*PLCB4; IPMK; INPP5J; PIK3CB*
Rap1 signaling pathway	0.018	0.379	*CSF1R; NRAS; PLCB4; RALB; PIK3CB; MAPK14; FGFR1*
Sphingolipid signaling pathway	0.020	0.379	*NRAS; PLCB4; S1PR3; PIK3CB; MAPK14*
Platelet activation	0.023	0.418	*PLA2G4F; PLCB4; PLA2G4C; PIK3CB; MAPK14*
Osteoclast differentiation	0.025	0.432	*CSF1R; SIRPA; NFATC1; PIK3CB; MAPK14*
Relaxin signaling pathway	0.028	0.447	*NRAS; MMP13; PLCB4; PIK3CB; MAPK14*
Vascular smooth muscle contraction	0.029	0.450	*PLA2G4F; EDN2; PLCB4; CALD1; PLA2G4C*
Fc gamma R-mediated phagocytosis	0.031	0.454	*PLA2G4F; PTPRC; ARPC5L; PIK3CB*
Ras signaling pathway	0.032	0.454	*CSF1R; NRAS; PLA2G4F; RALB; PLA2G4C; PIK3CB; FGFR1*
Signaling pathways regulating pluripotency of stem cells	0.035	0.473	*NRAS; PIK3CB; MAPK14; TBX3; FGFR1*

Choline metabolism in cancer	0.040	0.517	*PLA2G4F; NRAS; PLA2G4C; PIK3CB*
Phosphatidylinositol signaling system	0.040	0.496	*PLCB4; IPMK; INPP5J; PIK3CB*
alpha-Linolenic acid metabolism	0.042	0.492	*PLA2G4F; PLA2G4C*
C-type lectin receptor signaling pathway	0.047	0.535	*NRAS; NFATC1; PIK3CB; MAPK14*

A total of 105 upregulated and 155 downregulated genes have been analyzed

Table S9. GO enrichment analysis of up- and down-regulated genes in KIF14-positive cells located in torpedo-like structures ($p < 0.05$)

Term	P-value	Adjusted P-value	Genes
phosphate-containing compound metabolic process (GO:0006796)	0.001	1.000	*PLA2G4F; PTPRC; PLCB4; IPMK; PLA2G4C; INPP5J; ACYP2; PIK3CB; LIMD1*
negative regulation of signal transduction (GO:0009968)	0.001	1.000	*EPHB6; KANK1; CSF1R; LEPROT; PTPRC; NEURL1; CRY1; KLK14; NFATC1; EPHB1; FGFR1*
negative regulation of DNA metabolic process (GO:0051053)	0.002	1.000	*ZRANB3; DFFA; CDAN1; ERCC4*
phosphatidylinositol metabolic process (GO:0046488)	0.003	1.000	*CSF1R; PLA2G4F; PLA2G4C; C2ORF66; INPP5J; PIK3CB*
positive regulation of kinase activity (GO:0033674)	0.004	1.000	*EPHB6; CSF1R; PTPRC; EEF1A2; EPHB1; FGFR1*
regulation of cellular protein localization (GO:1903827)	0.004	1.000	*RALB; LCP1; RAB11FIP5*
positive regulation of voltage-gated potassium channel activity (GO:1903818)	0.006	1.000	*LRRC26; NOS1AP*
negative regulation of heterotypic cell-cell adhesion (GO:0034115)	0.006	1.000	*IL1RN; MYADM*
regulation of cell-cell adhesion involved in gastrulation (GO:0070587)	0.006	1.000	*IL1RN; MYADM*
collagen fibril organization (GO:0030199)	0.006	1.000	*COL2A1; LUM; DPT*
keratan sulfate biosynthetic process (GO:0018146)	0.006	1.000	*B4GAT1; LUM; B4GALT6*
keratan sulfate metabolic process (GO:0042339)	0.010	1.000	*B4GAT1; LUM; B4GALT6*
PERK-mediated unfolded protein response (GO:0036499)	0.010	1.000	*ASNS; ATF3*
extracellular matrix organization (GO:0030198)	0.010	1.000	*CSGALNACT1; SCUBE3; COL2A1; MMP13; LUM; DPT; TLL2; LCP1*
regulation of execution phase of apoptosis (GO:1900117)	0.012	1.000	*DFFA; DLC1*

negative regulation of Rho protein signal transduction (GO:0035024)	0.014	1.000	*KANK1; DLC1*
inositol lipid-mediated signaling (GO:0048017)	0.014	1.000	*CSF1R; PIK3CB; FGFR1*
tRNA aminoacylation (GO:0043039)	0.015	1.000	*PPA2; PPA1; EEF1E1*
regulation of clathrin-dependent endocytosis (GO:2000369)	0.016	1.000	*BMP2K; PIK3CB*
protein O-linked glycosylation (GO:0006493)	0.017	1.000	*B4GAT1; GALNT3; B3GALT2; GCNT3; ADAMTS7*
phosphatidylinositol acyl-chain remodeling (GO:0036149)	0.018	1.000	*PLA2G4F; PLA2G4C*
regulation of reactive oxygen species biosynthetic process (GO:1903426)	0.018	1.000	*GPRIN1; NOS1AP*
response to ionizing radiation (GO:0010212)	0.018	1.000	*RAD51B; EYA1; ERCC4; MAPK14*
negative regulation of cell communication (GO:0010648)	0.019	1.000	*EPHB6; CSF1R; EPHB1; FGFR1*
extracellular matrix disassembly (GO:0022617)	0.019	1.000	*SCUBE3; MMP13; TLL2; LCP1*
regulation of telomere maintenance via telomere lengthening (GO:1904356)	0.020	1.000	*ERCC4; POT1*
DNA packaging (GO:0006323)	0.020	1.000	*CDAN1; NAA10*
detection of mechanical stimulus (GO:0050982)	0.020	1.000	*DENND5B; PKDREJ*
protein complex subunit organization (GO:0071822)	0.021	1.000	*COL2A1; LUM; DPT*
sulfur compound biosynthetic process (GO:0044272)	0.022	1.000	*CSGALNACT1; SLC26A2; B4GAT1; LUM; B4GALT6*
tRNA aminoacylation for protein translation (GO:0006418)	0.022	1.000	*PPA2; PPA1; EEF1E1*
DNA conformation change (GO:0071103)	0.022	1.000	*TOP3B; NAA10*
negative regulation of signaling (GO:0023057)	0.023	1.000	*EPHB6; CSF1R; EPHB1; FGFR1*
polyol metabolic process (GO:0019751)	0.023	1.000	*PLCB4; IPMK; INPP5J*
inositol phosphate metabolic process (GO:0043647)	0.023	1.000	*PLCB4; IPMK; INPP5J*

neutrophil degranulation (GO:0043312)	0.023	1.000	*ADGRG3; NRAS; PTPRC; DGAT1; ANXA3; DLC1; NAPRT; RAB18; SIRPA; YPEL5; MAPK14; CAMP*
neutrophil activation involved in immune response (GO:0002283)	0.025	1.000	*ADGRG3; NRAS; PTPRC; DGAT1; ANXA3; DLC1; NAPRT; RAB18; SIRPA; YPEL5; MAPK14; CAMP*
regulation of heterotypic cell-cell adhesion (GO:0034114)	0.025	1.000	*IL1RN; MYADM*
osteoclast differentiation (GO:0030316)	0.025	1.000	*CSF1R; MAPK14*
neutrophil mediated immunity (GO:0002446)	0.026	1.000	*ADGRG3; NRAS; PTPRC; DGAT1; ANXA3; DLC1; NAPRT; RAB18; SIRPA; YPEL5; MAPK14; CAMP*
proteoglycan metabolic process (GO:0006029)	0.027	1.000	*CSGALNACT1; GAL3ST4*
inositol phosphate-mediated signaling (GO:0048016)	0.027	1.000	*EDN2; NFATC1*
positive regulation of lipid metabolic process (GO:0045834)	0.030	1.000	*EEF1A2; CREBL2*
negative regulation of G-protein coupled receptor protein signaling pathway (GO:0045744)	0.030	1.000	*CRY1; KLK14*
negative regulation of protein polymerization (GO:0032272)	0.033	1.000	*KANK1; MYADM*
positive regulation of biosynthetic process (GO:0009891)	0.033	1.000	*GPRIN1; CREBL2*
negative regulation of actin filament polymerization (GO:0030837)	0.033	1.000	*KANK1; MYADM*
positive regulation of transferase activity (GO:0051347)	0.033	1.000	*EPHB6; CSF1R; POT1; EPHB1; FGFR1*
phosphatidylinositol-mediated signaling (GO:0048015)	0.036	1.000	*CSF1R; PIK3CB; FGFR1*
positive regulation of neutrophil chemotaxis (GO:0090023)	0.039	1.000	*CAMK1D; THBS4*
negative regulation of cytoskeleton organization (GO:0051494)	0.039	1.000	*KANK1; MYADM*
DNA geometric change (GO:0032392)	0.039	1.000	*ZRANB3; POT1*

proteoglycan biosynthetic process (GO:0030166)	0.039	1.000	*CSGALNACT1; GAL3ST4*
cellular senescence (GO:0090398)	0.039	1.000	*MAPK14; TBX3*
glycosaminoglycan biosynthetic process (GO:0006024)	0.040	1.000	*CSGALNACT1; B4GAT1; LUM; B4GALT6*
positive regulation of neutrophil migration (GO:1902624)	0.042	1.000	*CAMK1D; THBS4*
prostaglandin metabolic process (GO:0006693)	0.042	1.000	*EDN2; CYP4F8*
regulation of kinase activity (GO:0043549)	0.043	1.000	*EPHB6; CSF1R; EPHB1; FGFR1*
phosphatidylethanolamine acyl-chain remodeling (GO:0036152)	0.045	1.000	*PLA2G4F; PLA2G4C*
positive regulation of granulocyte chemotaxis (GO:0071624)	0.045	1.000	*CAMK1D; THBS4*
negative regulation of telomere maintenance via telomere lengthening (GO:1904357)	0.045	1.000	*ERCC4; POT1*
peptide metabolic process (GO:0006518)	0.047	1.000	*PCSK1; PROS1; EEF1E1; CPN1*
phosphatidylcholine acyl-chain remodeling (GO:0036151)	0.048	1.000	*PLA2G4F; PLA2G4C*
peptidyl-glutamic acid modification (GO:0018200)	0.048	1.000	*NAA10; PROS1*
transcription from RNA polymerase III promoter (GO:0006383)	0.048	1.000	*TBP; SNAPC1*
regulation of protein localization to cell surface (GO:2000008)	0.048	1.000	*LEPROT; RAB11FIP5*
oligosaccharide metabolic process (GO:0009311)	0.049	1.000	*GALNT3; B3GALT2; GAL3ST4*

A total of 105 upregulated and 155 downregulated genes have been analyzed

Table S10. Differentially expressed genes between Mieap-positive and Mieap-negative cells located in torpedo-like structures ($p < 0.05$)

Genes	P-value	LogFC
FOSB	0.000	-8.642
CCDC18	0.001	4.732
GPR153	0.001	-7.251
ZNF337	0.001	-7.229
MYH4	0.001	-8.198
IER5	0.001	-4.042
MTG1	0.001	-6.903
SAMD9	0.001	7.136
OLFML2B	0.001	-7.023
KDR	0.002	-7.390
COL4A1	0.002	-4.392
MYH3	0.002	-5.666
SLIT2	0.002	-6.863
RRAS2	0.002	6.386
FOPNL	0.002	5.779
DGKI	0.002	-7.395
MED10	0.002	-6.759
TACC1	0.002	-3.804
KLHL7	0.002	5.690
KDM4C	0.003	4.068
LIAS	0.003	6.305
B4GALT6	0.003	-7.148
MFSD8	0.003	6.289
NOTCH4	0.003	-7.197
BIN2	0.003	-7.121
TCF4	0.003	-6.239
PRPF18	0.004	6.746
ACTG2	0.004	-7.096
RASD1	0.004	-5.307
DHFR2	0.004	5.975
TOE1	0.004	6.024
FAM110B	0.005	-6.496
RMI2	0.005	6.043
LTB4R2	0.005	-6.939
RSAD1	0.005	6.041
MXRA7	0.005	-6.586
STK32B	0.005	-6.910
LACTB2	0.005	6.003
CAPN9	0.006	-6.896
NPR2	0.006	-6.273
MBIP	0.006	6.541
C17orf58	0.006	6.491
CDO1	0.006	-6.833
SLC2A13	0.007	6.359
BICDL1	0.007	5.241
MMP11	0.007	-6.834
KIF26B	0.007	-4.854

ADAMTS6	0.007	-6.756
CENPL	0.008	5.946
THY1	0.008	-6.283
APEX2	0.008	5.242
PLEK2	0.008	-6.383
SYNPO2	0.008	-6.323
DUSP22	0.009	-5.930
SLC26A8	0.009	-6.691
TEKT2	0.010	-6.663
H3C7	0.010	5.700
ACTA1	0.010	-5.537
SUSD4	0.010	-6.651
PDCD1LG2	0.010	-6.053
MRVI1	0.011	-6.120
ISOC1	0.011	3.816
ZNF17	0.011	5.715
RNF181	0.011	5.035
ZNF423	0.012	-5.243
FSCN2	0.012	-6.534
KXD1	0.013	4.521
SYT11	0.013	-6.548
ZNF470	0.013	-5.880
BCYRN1	0.014	4.066
BOC	0.014	-5.814
VAV1	0.014	-6.492
H2BC11	0.014	5.046
SCAMP5	0.015	6.045
PHF11	0.016	3.318
SLC10A5	0.016	-6.449
M1AP	0.016	-6.523
C19orf18	0.016	5.950
H1-6	0.017	-5.919
MED7	0.017	5.438
PKNOX1	0.017	-4.008
SDAD1P1	0.017	5.940
GLI2	0.017	-6.544
WRAP73	0.018	5.444
ZNF624	0.018	-3.533
ATP8A2	0.018	-6.378
ZEB2	0.018	-3.619
PALB2	0.019	2.613
PGAM5	0.019	5.881
MRPL23	0.019	5.500
LOC441666	0.020	-5.324
CSGALNACT1	0.020	3.520
RPH3A	0.021	-6.315
PCGF1	0.021	5.384
DOK4	0.021	-6.280
P3H3	0.022	-6.288
CSTF1	0.022	2.818

C9orf43	0.022	-4.995
LINC00536	0.022	5.554
CTSC	0.023	-4.773
DBP	0.023	5.847
USP49	0.023	4.744
SPARCL1	0.023	-3.782
C3	0.023	-3.234
EIF6	0.023	4.055
ACTR10	0.024	2.868
CCDC192	0.024	-6.232
SPAG6	0.024	-5.620
NCS1	0.024	-4.655
ZSWIM5	0.025	5.783
SCN3A	0.025	-6.288
HTRA1	0.025	-4.905
MRPL22	0.026	-6.204
A2M	0.026	-3.680
IL15RA	0.026	-6.258
IFIT1	0.026	4.646
PIP4K2A	0.026	-3.162
LSM5	0.026	2.546
ZNF256	0.026	5.286
SUFU	0.027	-2.885
CRLF3	0.027	-3.588
SLC7A6	0.027	5.255
FBXL6	0.027	4.603
ZNF837	0.027	5.248
TMEM75	0.027	4.870
DPM1	0.028	3.254
PRKAB1	0.028	4.163
EIF4A1	0.028	-4.955
RTCB	0.028	3.101
STPG3-AS1	0.029	-6.143
SGO1-AS1	0.029	5.304
NEURL1B	0.029	5.706
CPXM2	0.029	-6.129
ADCY10	0.029	-5.768
DNAJC4	0.029	4.135
WNT4	0.029	5.319
MPZL3	0.030	3.347
ZNF573	0.030	3.455
C11orf1	0.030	5.331
MAGI1-AS1	0.031	5.248
FNDC1	0.031	-3.688
MRPS15	0.031	2.897
TRAF3IP3	0.031	-4.871
POMK	0.032	-3.259
AXDND1	0.032	5.638
MAP2K6	0.032	-2.863
BMPR1A	0.032	3.064

RNF225	0.033	5.685
GNRHR	0.033	5.618
TCEANC	0.033	5.218
CPVL	0.033	-5.128
TRIM59	0.033	5.201
HSPA13	0.033	5.184
SLC39A14	0.033	-3.540
MMD	0.033	-6.072
FH	0.034	3.467
MOCS3	0.034	3.806
STK16	0.035	-4.559
CD248	0.035	-6.029
CDK8	0.035	3.180
PDE12	0.035	-2.416
KBTBD8	0.035	-6.059
ZMYM4-AS1	0.035	-6.022
URM1	0.036	4.547
RBP5	0.037	-5.315
MPZL2	0.037	-3.372
JMJD4	0.037	-4.479
CTDNEP1	0.038	2.824
CX3CL1	0.038	-3.549
NMD3	0.038	-2.116
DIPK1B	0.038	-5.972
FLJ37453	0.038	-5.985
CPAMD8	0.038	-2.362
CDKN2AIPNL	0.038	5.207
EDDM13	0.038	4.080
ZNF763	0.038	5.095
IER2	0.039	-3.345
C8orf58	0.039	4.436
KRT81	0.039	-5.969
TAP1	0.039	5.467
SPI1	0.040	-5.940
TMEM44	0.040	-5.253
MALRD1	0.041	5.496
ILK	0.041	-5.576
PKD2	0.041	-4.585
DENND4B	0.041	-2.554
HABP4	0.041	-6.034
LOC102724788	0.042	5.494
USP18	0.042	4.959
NOC4L	0.042	-3.707
ZNF284	0.042	-5.239
COX10	0.043	5.417
ZNF200	0.043	3.615
EXOSC2	0.043	3.617
MX2	0.044	3.849
ETS1	0.044	-4.910
SLC29A4	0.044	5.070

RPL39	0.044	-3.729
RBAK	0.044	2.460
PRC1-AS1	0.045	5.022
TMEM70	0.045	-4.425
HEIH	0.045	-5.893
CARD9	0.045	3.534
LINC01811	0.045	-5.877
HMCN1	0.046	-4.058
MAP3K21	0.046	5.433
ZC2HC1C	0.046	5.017
ST7	0.047	-3.950
COA3	0.047	5.019
NINJ2-AS1	0.047	5.057
ADAMTS16	0.048	-5.848
CAVIN3	0.048	-5.855
PROSER1	0.048	2.218
TMEM69	0.048	4.343
EOGT	0.049	-4.266
CCDC122	0.049	3.098
COL4A2	0.049	-3.012
BNIP3	0.049	2.278
KIAA1671-AS1	0.049	-4.611
ZNF517	0.049	5.382
BCL7B	0.049	2.836
TFPI2	0.049	3.871
H2AC16	0.049	5.319
BTN2A3P	0.049	5.401
TIGD7	0.049	5.320
SYT14	0.049	-5.841

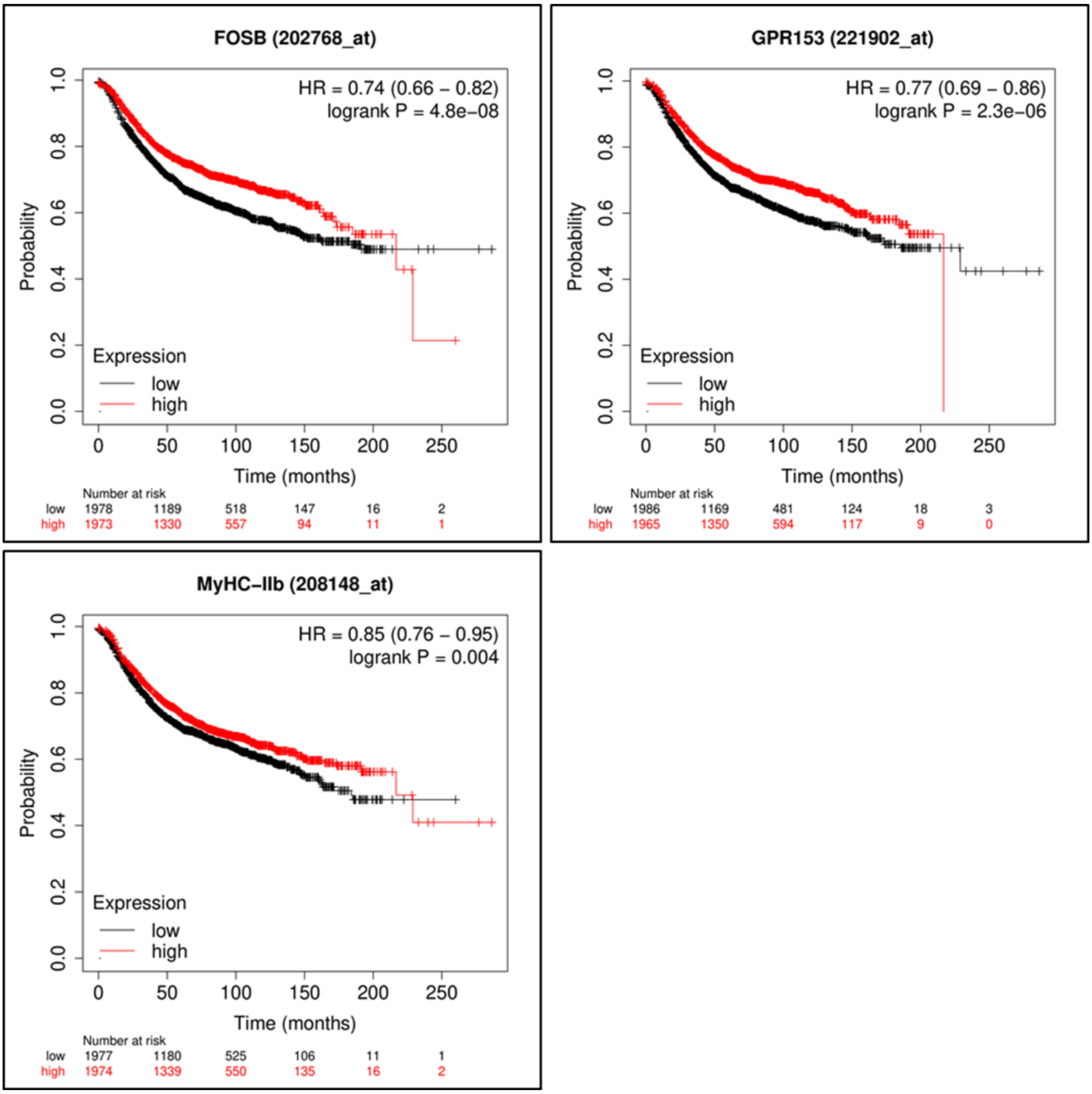

Figure S6. Association of DEGs (*FOSB*, *GPR153* and *MYH4*) in Mieap-positive cells with relapse-free survival of breast cancer patients according to Kaplan-Meyer Plotter database.

Table S11. KEGG enrichment analysis of up- and down-regulated genes in Mieap-positive cells located in torpedo-like structures ($p < 0.05$)

Term	P-value	Adjusted P-value	Genes
Sulfur relay system	0.003	1.000	*MOCS3; URM1*
Herpes simplex virus 1 infection	0.004	0.629	*ZNF17; ZNF284; ZNF470; CARD9; TAP1; C3; ZNF517; ZNF624; ZNF337; RBAK; ZNF763; ZNF256; ZNF200*
Hedgehog signaling pathway	0.016	1.000	*SUFU; BOC; GLI2*
Basal cell carcinoma	0.034	1.000	*SUFU; GLI2; WNT4*
Mitophagy	0.037	1.000	*BNIP3; RRAS2; PGAM5*

A total of 106 upregulated and 120 downregulated genes have been analyzed

Table S12. GO enrichment analysis of up- and down-regulated genes in Mieap-positive cells located in torpedo-like structures ($p < 0.05$)

Term	P-value	Adjusted P-value	Genes
branching morphogenesis of an epithelial tube (GO:0048754)	0.000	0.610	*COL4A1; NOTCH4; SLIT2; PKD2; GLI2*
epithelial tube morphogenesis (GO:0060562)	0.001	1.000	*COL4A1; SLIT2; PKD2; GLI2*
heterocycle biosynthetic process (GO:0018130)	0.001	1.000	*MOCS3; MBIP; LIAS*
mammary gland development (GO:0030879)	0.002	1.000	*NOTCH4; GLI2; WNT4*
pri-miRNA transcription from RNA polymerase II promoter (GO:0061614)	0.003	1.000	*SPI1; ETS1*
molybdopterin cofactor biosynthetic process (GO:0032324)	0.003	1.000	*MOCS3; MBIP*
molybdopterin cofactor metabolic process (GO:0043545)	0.003	1.000	*MOCS3; MBIP*
regulation of calcium ion-dependent exocytosis (GO:0017158)	0.003	1.000	*SCAMP5; RPH3A; SYT11; SYT14*
RNA phosphodiester bond hydrolysis (GO:0090501)	0.004	1.000	*TOE1; LACTB2; PDE12*
vesicle fusion (GO:0006906)	0.004	1.000	*RPH3A; SAMD9; SYT11; TAP1; SYT14*
tRNA wobble uridine modification (GO:0002098)	0.004	1.000	*MOCS3; URM1*
tRNA wobble base modification (GO:0002097)	0.005	1.000	*MOCS3; URM1*
central nervous system projection neuron axonogenesis (GO:0021952)	0.005	1.000	*SLIT2; GLI2*
nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay (GO:0000288)	0.006	1.000	*EIF4A1; PDE12; LSM5; EXOSC2*
metanephric mesenchyme development (GO:0072075)	0.007	1.000	*PKD2; WNT4*
spinal cord development (GO:0021510)	0.007	1.000	*PKD2; GLI2*
ribosomal subunit export from nucleus (GO:0000054)	0.008	1.000	*EIF6; NMD3*
regulation of regulated secretory pathway (GO:1903305)	0.008	1.000	*RPH3A; SYT11; SYT14*
organic cyclic compound biosynthetic process (GO:1901362)	0.008	1.000	*MOCS3; MBIP; LIAS*

actin-myosin filament sliding (GO:0033275)	0.009	1.000	*ACTA1; MYH3; MYH4*
muscle filament sliding (GO:0030049)	0.009	1.000	*ACTA1; MYH3; MYH4*
regulation of triglyceride biosynthetic process (GO:0010866)	0.009	1.000	*C3; CTDNEP1*
positive regulation of cellular biosynthetic process (GO:0031328)	0.010	1.000	*CTDNEP1; ZEB2; EIF6; NMD3; PKD2; GLI2*
gland development (GO:0048732)	0.010	1.000	*NOTCH4; PKD2; GLI2; WNT4*
branching involved in blood vessel morphogenesis (GO:0001569)	0.011	1.000	*COL4A1; NOTCH4*
negative regulation of smooth muscle cell migration (GO:0014912)	0.011	1.000	*SLIT2; BMPR1A*
positive regulation of mitochondrial fission (GO:0090141)	0.011	1.000	*BNIP3; KDR*
cell migration involved in sprouting angiogenesis (GO:0002042)	0.011	1.000	*KDR; SLIT2*
regulation of mitochondrial translation (GO:0070129)	0.012	1.000	*COA3; MTG1*
cytoplasmic sequestering of protein (GO:0051220)	0.012	1.000	*SUFU; PKD2*
positive regulation of macroautophagy (GO:0016239)	0.013	1.000	*BNIP3; KDR; PIP4K2A*
cellular response to dsRNA (GO:0071359)	0.014	1.000	*PDE12; IFIT1*
cytoplasmic sequestering of transcription factor (GO:0042994)	0.014	1.000	*SUFU; PKD2*
positive regulation of focal adhesion assembly (GO:0051894)	0.015	1.000	*KDR; THY1*
response to interferon-alpha (GO:0035455)	0.015	1.000	*PDE12; MX2*
ureteric bud development (GO:0001657)	0.015	1.000	*SLIT2; PKD2*
mesonephric tubule development (GO:0072164)	0.015	1.000	*SLIT2; PKD2*
extracellular matrix organization (GO:0030198)	0.016	1.000	*CSGALNACT1; MMP11; COL4A2; COL4A1; KDR; HTRA1; A2M*
blood vessel endothelial cell migration (GO:0043534)	0.017	1.000	*KDR; SLIT2*
regulation of smooth muscle cell migration (GO:0014910)	0.017	1.000	*SLIT2; BMPR1A*
positive regulation of adherens junction organization (GO:1903393)	0.019	1.000	*KDR; THY1*

regulation of mitochondrial fission (GO:0090140)	0.019	1.000	*BNIP3; KDR*
inactivation of MAPK activity (GO:0000188)	0.021	1.000	*DUSP22; MBIP*
positive regulation of macromolecule biosynthetic process (GO:0010557)	0.023	1.000	*EIF6; KDR; NMD3; WNT4; GLI2*
GTP metabolic process (GO:0046039)	0.023	1.000	*MOCS3; MBIP*
positive regulation of leukocyte cell-cell adhesion (GO:1903039)	0.023	1.000	*THY1; ETS1*
hepaticobiliary system development (GO:0061008)	0.023	1.000	*PKD2; WNT4*
regulation of axonogenesis (GO:0050770)	0.024	1.000	*THY1; SLIT2; ZSWIM5*
cellular response to transforming growth factor beta stimulus (GO:0071560)	0.027	1.000	*DUSP22; STK16; WNT4; BMPR1A*
negative regulation of transcription factor import into nucleus (GO:0042992)	0.028	1.000	*SUFU; PKD2*
positive regulation of cell junction assembly (GO:1901890)	0.028	1.000	*KDR; THY1*
respiratory chain complex IV assembly (GO:0008535)	0.032	1.000	*COA3; COX10*
cellular protein catabolic process (GO:0044257)	0.033	1.000	*BNIP3; CPVL; CTSC*
strand displacement (GO:0000732)	0.035	1.000	*RMI2; PALB2*
endocrine system development (GO:0035270)	0.035	1.000	*GLI2; WNT4*
snRNA 3'-end processing (GO:0034472)	0.035	1.000	*TOE1; EXOSC2*
transcription initiation from RNA polymerase II promoter (GO:0006367)	0.035	1.000	*CDK8; NOTCH4; MED10; TCF4; MED7*
regulation of lipid biosynthetic process (GO:0046890)	0.040	1.000	*C3; EIF6*
coenzyme biosynthetic process (GO:0009108)	0.042	1.000	*MOCS3; LIAS*
regulation of cellular biosynthetic process (GO:0031326)	0.042	1.000	*C3; EIF6*
regulation of endothelial cell migration (GO:0010594)	0.043	1.000	*KDR; SLIT2; ETS1*
regulation of osteoblast differentiation (GO:0045667)	0.043	1.000	*SUFU; WNT4; BMPR1A*
artery morphogenesis (GO:0048844)	0.045	1.000	*PKD2; BMPR1A*
cyclic purine nucleotide metabolic process (GO:0052652)	0.045	1.000	*ADCY10; NPR2*

organelle membrane fusion (GO:0090174)	0.046	1.000	*RPH3A; SYT11; SYT14*
regulation of gene expression (GO:0010468)	0.047	1.000	*ZNF17; ZNF573; EIF4A1; ZNF284; ZNF470; PRKAB1; ETS1; ACTG2; ACTA1; ZNF837; SUFU; KDR; PCGF1; ZNF624; RBAK; ZNF256; ZNF200; WNT4*
positive regulation of release of sequestered calcium ion into cytosol (GO:0051281)	0.048	1.000	*THY1; PKD2*
liver development (GO:0001889)	0.048	1.000	*PKD2; WNT4*
positive regulation of bone mineralization (GO:0030501)	0.048	1.000	*WNT4; BMPR1A*
positive regulation of viral genome replication (GO:0045070)	0.048	1.000	*PDE12; IFIT1*
cofactor biosynthetic process (GO:0051188)	0.048	1.000	*MOCS3; MBIP*
proteolysis (GO:0006508)	0.048	1.000	*CAPN9; CPXM2; SUFU; HTRA1; CPVL; CTSC; FBXL6*
negative regulation of cell migration (GO:0030336)	0.049	1.000	*THY1; SLIT2; CX3CL1; BMPR1A*
sulfur compound biosynthetic process (GO:0044272)	0.049	1.000	*CSGALNACT1; LIAS; B4GALT6; CDO1*

A total of 106 upregulated and 120 downregulated genes have been analyzed

Table S13. Differentially expressed genes between EZR-negative and EZR-positive cells located in torpedo-like structures ($p < 0.05$)

Gene	P-value	LogFC
CD109	0.000	7.836
ID4	0.000	7.848
CA5B	0.000	7.536
GCNT7	0.000	7.273
ST8SIA1	0.000	5.093
NR4A1	0.001	4.957
SYCP3	0.001	-5.976
MAP2	0.001	6.998
LINC00539	0.001	7.450
SLC5A4	0.001	7.426
ZNF416	0.001	7.004
CGRRF1	0.001	5.424
ADAMTS6	0.001	7.398
TMEM72-AS1	0.001	7.008
ZBTB42	0.001	4.585
DCAF8L1	0.001	7.244
FAM174C	0.002	-6.202
TECTA	0.002	6.910
TCHH	0.002	3.354
DKK2	0.002	4.907
FCGR2B	0.002	5.947
SHCBP1	0.003	5.146
ERG	0.003	6.681
EHHADH	0.003	-6.538
NR4A3	0.003	6.266
SPTB	0.004	6.095
SCNN1D	0.004	-5.931
FBXO44	0.004	5.561
JAG1	0.004	3.777
ZNF48	0.005	-5.777
MYH11	0.005	4.037
ADAMTS10	0.005	6.698
ALMS1P1	0.005	-5.905
MFSD13A	0.006	-5.718
SLC26A8	0.006	5.865
EME1	0.006	3.973
C12orf57	0.006	6.438
ACOX2	0.006	3.914
RAD51B	0.006	-3.888
P3H2	0.006	6.412
SLC34A2	0.007	5.464
PRELID1	0.007	-3.957
MIR4697HG	0.007	5.486
SLFNL1	0.007	6.381
VCPKMT	0.007	5.681
CARNS1	0.007	-5.299
RAD51D	0.007	-4.984

ITGA5	0.008	3.486
IMP3	0.008	-5.644
GUCY1B1	0.008	6.040
SYNC	0.008	3.844
TLR2	0.008	5.146
MUC3A	0.009	4.191
CFAP61	0.009	-5.627
NUDT15	0.009	4.080
LOC105371485	0.009	-5.580
KCNN3	0.009	4.484
NUP37	0.010	-6.027
UBL7-AS1	0.011	6.257
FAM184A	0.012	-4.310
EIF4A1	0.012	-5.455
ADAM20	0.012	-5.073
STX18-AS1	0.013	4.411
ITGA4	0.013	4.204
LOC105374580	0.013	5.416
SLC19A1	0.013	-3.405
OVCH2	0.014	6.113
LINC00847	0.014	-5.371
MRPS23	0.014	2.894
RAPGEF3	0.015	-3.509
CHCHD5	0.015	-5.500
LRGUK	0.015	-4.259
NAV3	0.016	3.105
AMN1	0.016	-5.358
FIGNL1	0.019	3.754
FAM98B	0.019	3.018
TRIM65	0.020	-4.667
DBF4B	0.020	3.371
LINC01535	0.020	-4.520
FANCC	0.020	2.817
SPARCL1	0.020	3.049
ARL6IP6	0.020	-4.673
ASIC3	0.020	4.473
CREB5	0.021	5.930
ETNK2	0.022	-5.302
CD302	0.022	-5.304
TUBG1	0.022	2.652
EGLN2	0.023	-2.727
CYCS	0.023	3.001
MAD2L1	0.024	4.139
PAXIP1-AS1	0.024	-4.606
ALG8	0.024	2.422
LRRC75B	0.025	-5.165
NFS1	0.025	-3.365
ASB8	0.027	-4.029
TRMT44	0.027	-2.701
SLIT3	0.028	3.826

TGFB1I1	0.028	3.824
FAM3B	0.028	4.786
DNAAF4	0.028	-5.141
BICD1	0.028	3.248
ILDR2	0.029	4.499
SNAPIN	0.029	3.865
DNAJC9	0.029	-3.352
ANGPTL2	0.030	-4.200
ZNF79	0.031	-4.439
LOC101927787	0.032	-4.530
RYR2	0.032	3.510
ALKBH2	0.032	3.463
CDK8	0.032	2.825
CA5BP1	0.033	-4.149
NMNAT3	0.033	-4.367
PLCG2	0.033	2.432
TTC31	0.033	2.377
ZNF324	0.034	-3.089
MARK1	0.034	4.325
SLC25A11	0.035	-3.017
ANO9	0.035	-3.112
MAGI2	0.035	4.634
ZNF75D	0.035	-2.504
TRIM17	0.036	-4.980
TFCP2L1	0.038	3.603
SYT8	0.038	-3.476
CYSTM1	0.039	3.133
WDR75	0.040	2.052
HCK	0.041	3.710
AIF1	0.042	4.875
TG	0.042	-2.689
LMF2	0.042	-3.196
TP73-AS1	0.042	-2.345
MIR9-3HG	0.042	-4.915
INTS7	0.042	-2.765
PTPRB	0.042	3.566
GET4	0.042	-2.946
KCNK3	0.042	4.386
TMEM220	0.042	4.324
DOCK2	0.042	2.552
AKAP12	0.043	2.878
FAM221B	0.043	-4.488
VTCN1	0.045	3.018
MORC3	0.045	1.853
RGS1	0.045	2.784
ALKBH4	0.045	4.282
PINK1-AS	0.045	3.708
WWTR1	0.045	3.267
DNAH17	0.046	3.619
ZHX2	0.046	2.280

IFI6	0.046	2.704
GID4	0.047	-3.549
ZNF580	0.047	-3.036
COL7A1	0.047	-3.204
SLIT2	0.047	3.219
HMCN2	0.047	3.813
TOPORS	0.048	2.009
ALG1	0.048	-3.476
FUT1	0.048	-4.827
PPP5D1	0.048	-4.171
ST20	0.049	-4.546
SLPI	0.049	-2.857
ZRSR2	0.049	2.013
LRP3	0.049	-3.068
LINC00216	0.049	4.110

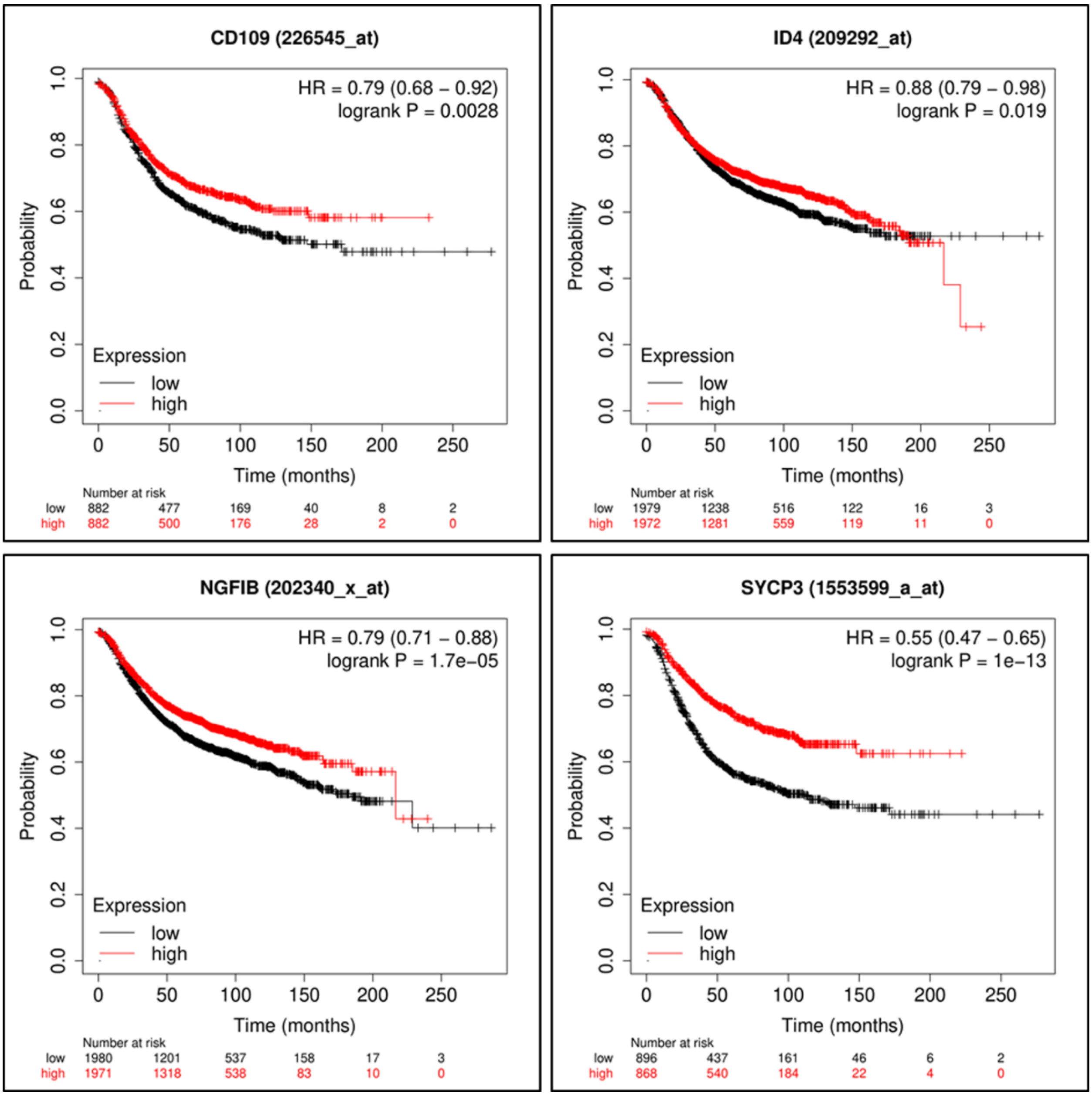

Figure S7. Association of DEGs (*CD109*, *ID4*, *NR4A1* and *SYCP3*) in EZR-negative cells with relapse-free survival of breast cancer patients according to Kaplan-Meyer Plotter database.

Table S14. KEGG enrichment analysis of up- and down-regulated genes in EZR-negative cells located in torpedo-like structures ($p < 0.05$)

Term	P-value	Adjusted P-value	Genes
Homologous recombination	0.000	0.102	*RAD51B; RAD51D; EME1; SYCP3*
Fc gamma R-mediated phagocytosis	0.006	0.989	*HCK; PLCG2; DOCK2; FCGR2B*
Cortisol synthesis and secretion	0.016	1.000	*NR4A1; KCNK3; CREB5*
Arrhythmogenic right ventricular cardio	0.021	1.000	*RYR2; ITGA4; ITGA5*
beta-Alanine metabolism	0.026	1.000	*EHHADH; CARNS1*
Hypertrophic cardiomyopathy (HCM)	0.032	1.000	*RYR2; ITGA4; ITGA5*
Insulin secretion	0.033	1.000	*RYR2; KCNN3; CREB5*
Dilated cardiomyopathy (DCM)	0.038	1.000	*RYR2; ITGA4; ITGA5*
Aldosterone synthesis and secretion	0.045	1.000	*NR4A1; KCNK3; CREB5*

A total of 98 upregulated and 64 downregulated genes have been analyzed

Table S15. GO enrichment analysis of up- and down-regulated genes in EZR-negative cells located in torpedo-like structures ($p < 0.05$)

Term	P-value	Adjusted P-value	Genes
regulation of phagocytosis (GO:0050764)	0.000	1.000	*HCK; FCGR2B; DOCK2; TLR2*
peptidyl-proline hydroxylation (GO:0019511)	0.001	1.000	*EGLN2; P3H2*
regulation of chemokine-mediated signaling pathway (GO:0070099)	0.001	1.000	*SLIT3; SLIT2*
strand invasion (GO:0042148)	0.001	1.000	*RAD51B; RAD51D*
neuron projection extension involved in neuron projection guidance (GO:1902284)	0.002	1.000	*SLIT3; SLIT2*
DNA recombinase assembly (GO:0000730)	0.002	1.000	*RAD51B; RAD51D*
glomerular visceral epithelial cell development (GO:0072015)	0.002	1.000	*JAG1; MAGI2*
glomerular epithelial cell development (GO:0072310)	0.002	1.000	*JAG1; MAGI2*
DNA repair complex assembly (GO:0090735)	0.002	1.000	*RAD51B; RAD51D*
axon extension involved in axon guidance (GO:0048846)	0.002	0.902	*SLIT3; SLIT2*
double-strand break repair via synthesis-dependent strand annealing (GO:0045003)	0.002	0.820	*RAD51B; RAD51D*
endodermal cell differentiation (GO:0035987)	0.002	0.926	*ITGA4; COL7A1; ITGA5*
negative regulation of phagocytosis (GO:0050765)	0.002	0.888	*FCGR2B; TLR2*
central nervous system projection neuron axonogenesis (GO:0021952)	0.003	1.000	*C12ORF57; SLIT2*
endoderm formation (GO:0001706)	0.003	1.000	*ITGA4; COL7A1; ITGA5*
negative regulation of chemotaxis (GO:0050922)	0.003	1.000	*SLIT2; AIF1*
response to ionizing radiation (GO:0010212)	0.004	1.000	*RAD51B; RAD51D; FIGNL1; INTS7*
positive regulation of mitotic cell cycle phase transition (GO:1901992)	0.004	1.000	*RAD51B; DBF4B; AIF1*
glomerular visceral epithelial cell differentiation (GO:0072112)	0.005	1.000	*JAG1; MAGI2*
inorganic anion transport (GO:0015698)	0.005	1.000	*SLC34A2; SLC26A8; ANO9*

oligosaccharide-lipid intermediate biosynthetic process (GO:0006490)	0.006	1.000	*ALG8; ALG1*
negative regulation of smooth muscle cell migration (GO:0014912)	0.006	1.000	*SLIT2; AIF1*
cell migration involved in sprouting angiogenesis (GO:0002042)	0.006	1.000	*NR4A1; SLIT2*
smooth muscle contraction (GO:0006939)	0.006	1.000	*HMCN2; MYH11*
fatty acid beta-oxidation using acyl-CoA oxidase (GO:0033540)	0.006	1.000	*ACOX2; EHHADH*
maintenance of protein location in nucleus (GO:0051457)	0.006	1.000	*MORC3; TOPORS*
positive regulation of G2/M transition of mitotic cell cycle (GO:0010971)	0.007	1.000	*RAD51B; DBF4B*
cilium movement (GO:0003341)	0.007	1.000	*CFAP61; DNAH17; DNAAF4*
negative regulation of cell motility (GO:2000146)	0.008	1.000	*JAG1; NAV3; MAGI2; SLIT2*
positive regulation of cell cycle G2/M phase transition (GO:1902751)	0.008	1.000	*RAD51B; DBF4B*
mitotic recombination (GO:0006312)	0.009	1.000	*RAD51B; RAD51D*
dolichol-linked oligosaccharide biosynthetic process (GO:0006488)	0.009	1.000	*ALG8; ALG1*
maintenance of protein localization in organelle (GO:0072595)	0.009	1.000	*MORC3; TOPORS*
blood vessel endothelial cell migration (GO:0043534)	0.009	1.000	*NR4A1; SLIT2*
negative regulation of lymphocyte activation (GO:0051250)	0.010	1.000	*VTCN1; FCGR2B*
cellular respiration (GO:0045333)	0.011	1.000	*CHCHD5; NR4A3; CYCS*
axon extension (GO:0048675)	0.011	1.000	*SLIT3; SLIT2*
regulation of monocyte chemotaxis (GO:0090025)	0.014	1.000	*SLIT2; AIF1*
cellular response to catecholamine stimulus (GO:0071870)	0.015	1.000	*RYR2; NR4A3*
regulation of proteolysis involved in cellular protein catabolic process (GO:1903050)	0.015	1.000	*DNAAF4; NUDT15*
positive regulation of endocytosis (GO:0045807)	0.015	1.000	*DOCK2; FCGR2B; BICD1*
response to glucocorticoid (GO:0051384)	0.016	1.000	*SLIT3; SLIT2*

receptor clustering (GO:0043113)	0.016	1.000	*ITGA4; MAGI2*
negative regulation of sequestering of calcium ion (GO:0051283)	0.016	1.000	*RYR2; PLCG2*
negative regulation of cell migration (GO:0030336)	0.017	1.000	*JAG1; NAV3; MAGI2; SLIT2*
heterotypic cell-cell adhesion (GO:0034113)	0.017	1.000	*ITGA4; ITGA5*
strand displacement (GO:0000732)	0.019	1.000	*RAD51B; RAD51D*
response to ketone (GO:1901654)	0.019	1.000	*SLIT3; SLIT2*
negative chemotaxis (GO:0050919)	0.019	1.000	*SLIT3; SLIT2*
release of sequestered calcium ion into cytosol (GO:0051209)	0.020	1.000	*RYR2; PLCG2*
negative regulation of endocytosis (GO:0045806)	0.021	1.000	*FCGR2B; TLR2*
regulation of defense response to virus by virus (GO:0050690)	0.021	1.000	*HCK; DOCK2*
regulation of striated muscle contraction (GO:0006942)	0.023	1.000	*C12ORF57; RYR2*
dicarboxylic acid transport (GO:0006835)	0.023	1.000	*SLC26A8; SLC19A1*
protein alkylation (GO:0008213)	0.023	1.000	*VCPKMT; FAM98B*
lysosome localization (GO:0032418)	0.023	1.000	*SNAPIN; NR4A3*
negative regulation of lymphocyte proliferation (GO:0050672)	0.023	1.000	*VTCN1; FCGR2B*
Fc receptor mediated stimulatory signaling pathway (GO:0002431)	0.024	1.000	*HCK; NR4A3; PLCG2; FCGR2B*
regulation of actin cytoskeleton reorganization (GO:2000249)	0.024	1.000	*HCK; RAPGEF3*
regulation of leukocyte chemotaxis (GO:0002688)	0.024	1.000	*ZNF580; SLIT2*
negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway (GO:0090101)	0.025	1.000	*TGFB1I1; CD109; MAGI2*
cellular response to hormone stimulus (GO:0032870)	0.027	1.000	*NR4A3; SLIT3; SLIT2*
ion transport (GO:0006811)	0.031	1.000	*RYR2; SCNN1D; SLC26A8; ANO9; ASIC3; KCNK3*
epithelial tube morphogenesis (GO:0060562)	0.031	1.000	*RYR2; SLIT2*

regulation of interleukin-8 production (GO:0032677)	0.031	1.000	*ZNF580; TLR2*
negative regulation of T cell activation (GO:0050868)	0.031	1.000	*VTCN1; FCGR2B*
regulation of microtubule polymerization (GO:0031113)	0.033	1.000	*NAV3; MAP2*
positive regulation of ATPase activity (GO:0032781)	0.033	1.000	*RYR2; DNAJC9*
ion transmembrane transport (GO:0034220)	0.033	1.000	*RYR2; SCNN1D; ANO9; ASIC3; KCNK3*
calcium ion transmembrane import into cytosol (GO:0097553)	0.034	1.000	*RYR2; PLCG2*
vesicle-mediated transport in synapse (GO:0099003)	0.034	1.000	*SNAPIN; SYT8*
positive regulation of smooth muscle cell proliferation (GO:0048661)	0.036	1.000	*NR4A3; AIF1*
organic cyclic compound biosynthetic process (GO:1901362)	0.036	1.000	*NFS1; TFCP2L1*
regulation of cell proliferation (GO:0042127)	0.039	1.000	*WWTR1; HCK; JAG1; NR4A3; TGFB1I1; MAGI2; P3H2; FAM98B; DBF4B; CGRRF1; SHCBP1*
regulation of proteasomal protein catabolic process (GO:0061136)	0.040	1.000	*DNAAF4; NUDT15*
positive regulation of phagocytosis (GO:0050766)	0.040	1.000	*FCGR2B; DOCK2*
DNA biosynthetic process (GO:0071897)	0.040	1.000	*RAD51B; RAD51D*
transcription initiation from RNA polymerase II promoter (GO:0006367)	0.041	1.000	*WWTR1; NR4A1; CDK8; NR4A3*
negative regulation of cytokine-mediated signaling pathway (GO:0001960)	0.042	1.000	*SLIT3; SLIT2*
neuron migration (GO:0001764)	0.042	1.000	*DNAAF4; MARK1*
positive regulation of epithelial to mesenchymal transition (GO:0010718)	0.042	1.000	*WWTR1; TGFB1I1*
regulation of ATPase activity (GO:0043462)	0.042	1.000	*VCPKMT; DNAJC9*
bicarbonate transport (GO:0015701)	0.044	1.000	*CA5B; SLC26A8*

positive regulation of receptor-mediated endocytosis (GO:0048260)	0.044	1.000	*MAGI2; BICD1*
negative regulation of apoptotic process (GO:0043066)	0.044	1.000	*HCK; PRELID1; FIGNL1; IFI6; VTCN1; ITGA5; TOPORS; MAD2L1*
cell morphogenesis involved in neuron differentiation (GO:0048667)	0.044	1.000	*MAP2; SLIT3; SLIT2*
protein localization to organelle (GO:0033365)	0.044	1.000	*BICD1; TOPORS; GET4*
cellular response to radiation (GO:0071478)	0.045	1.000	*FIGNL1; INTS7*
cellular response to lipoteichoic acid (GO:0071223)	0.048	1.000	*TLR2*
negative regulation of membrane potential (GO:0045837)	0.048	1.000	*PRELID1*
macropinocytosis (GO:0044351)	0.048	1.000	*DOCK2*
release of sequestered calcium ion into cytosol by sarcoplasmic reticulum (GO:0014808)	0.048	1.000	*RYR2*
response to heparin (GO:0071503)	0.048	1.000	*SLIT2*
striated muscle hypertrophy (GO:0014897)	0.048	1.000	*RYR2*
regulation of nuclear cell cycle DNA replication (GO:0033262)	0.048	1.000	*DBF4B*
negative regulation of acute inflammatory response (GO:0002674)	0.048	1.000	*FCGR2B*
cellular response to monoamine stimulus (GO:0071868)	0.048	1.000	*NR4A3*
response to lipoteichoic acid (GO:0070391)	0.048	1.000	*TLR2*
positive regulation of humoral immune response (GO:0002922)	0.048	1.000	*FCGR2B*
cellular response to bacterial lipopeptide (GO:0071221)	0.048	1.000	*TLR2*
response to DNA damage checkpoint signaling (GO:0072423)	0.048	1.000	*EME1*
positive regulation of phospholipid transport (GO:2001140)	0.048	1.000	*PRELID1*
negative regulation of phospholipase activity (GO:0010519)	0.048	1.000	*BICD1*

regulation of skeletal muscle contraction (GO:0014819)	0.048	1.000	*C12ORF57*
positive regulation of protein acetylation (GO:1901985)	0.048	1.000	*RAPGEF3*
retinal ganglion cell axon guidance (GO:0031290)	0.048	1.000	*SLIT2*
response to catecholamine (GO:0071869)	0.048	1.000	*NR4A3*
negative regulation of mononuclear cell migration (GO:0071676)	0.048	1.000	*SLIT2*
nucleoside phosphate catabolic process (GO:1901292)	0.048	1.000	*NUDT15*
negative regulation of leukocyte degranulation (GO:0043301)	0.048	1.000	*FCGR2B*
positive regulation of myeloid leukocyte cytokine production involved in immune response (GO:0061081)	0.048	1.000	*NR4A3*
positive regulation of protein localization to centrosome (GO:1904781)	0.048	1.000	*BICD1*
metal ion transport (GO:0030001)	0.049	1.000	*SCNN1D; SLC5A4; KCNK3*
sprouting angiogenesis (GO:0002040)	0.049	1.000	*NR4A1; SLIT2*
positive regulation of interleukin-8 production (GO:0032757)	0.049	1.000	*ZNF580; TLR2*
regulation of T cell activation (GO:0050863)	0.049	1.000	*PRELID1; VTCN1*
regulation of smooth muscle cell proliferation (GO:0048660)	0.049	1.000	*NR4A3; AIF1*

A total of 98 upregulated and 64 downregulated genes have been analyzed

Table S16. Breast cancer patients with distant metastasis and positive expression of KIF14 and Mieap and negative expression of EZR at the tips of torpedo-like structures

Patients	KIF14 expression	Mieap expression	EZR loss
1	No	No	No
2	Yes	Yes	Yes
3	Yes	Yes	Yes
4	No	Yes	Yes
5	No	No	No
6	Yes	Yes	No
7	Yes	Yes	No data
8	Yes	Yes	Yes
9	Yes	Yes	Yes
10	Yes	Yes	Yes
11	Yes	Yes	Yes
12	No data	No data	Yes
13	Yes	Yes	Yes
14	Yes	Yes	Yes
15	Yes	Yes	Yes
16	Yes	No data	No data
17	Yes	Yes	Yes
18	No data	No	Yes
19	Yes	Yes	Yes

Orange color indicates the simultaneous expression of all three markers. Blue color indicates the simultaneous expression of any two markers.

Table S17. Expression of *MKI67, PLAU, PLAUR, MMP2, MMP9* and *MMP13* genes in KIF14-positive, Mieap-positive, EZR-negative cells located in torpedo-like structures

Markers	KIF14-positive*		Mieap-positive**		EZR-negative***	
	logFC	p-value	logFC	p-value	logFC	p-value
MKI67	-0.425	0.802	0.470	0.677	1.736	0.126
PLAU	-	-	0.483	0.823	-	-
PLAUR	0.004	0.999	1.255	0.435	-0.306	0.759
MMP2	1.228	0.506	0.495	0.669	0.789	0.461
MMP9	-1.295	0.615	3.203	0.252	-0.380	0.785
MMP13	-5.336	0.027	-1.182	0.626	-0.493	0.798

*, compared to KIF14-negative cells; **, compared to Mieap-negative cells; ***, compared to EZR-positive cells.

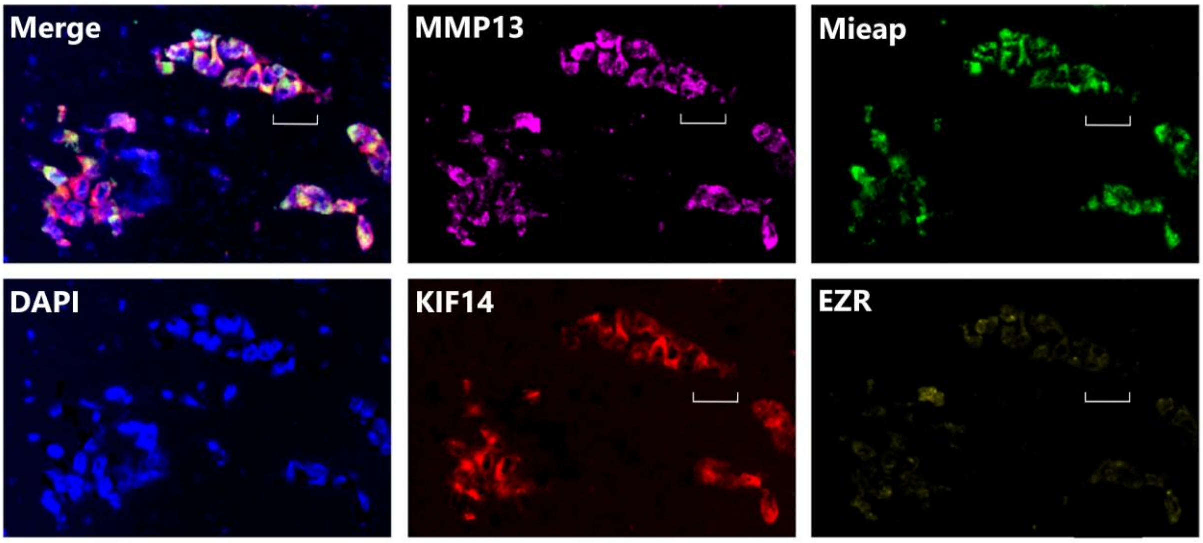

Figure S8. Expression of KIF14, Mieap, EZR and MMP13 in the torpedo-like structures.

Table S18. Clinicopathological parameters of breast cancer patients

Parameter		Number of cases, %
Age	≤ 50	45 (53.5)
	> 50	35 (41.7)
	No data	4 (4.8)
Menopause	Premenopausal	44 (52.4)
	Postmenopausal	35 (41.6)
	No data	5 (6.0)
Tumor size	T1	32 (38.1)
	T2	38 (45.2)
	T3	3 (3.6)
	T4	7 (8.3)
	No data	4 (4.8)
Grade	1	4 (4.7)
	2	58 (69.1)
	3	9 (10.7)
	No data	13 (15.5)
Lymph node metastases	N0	33 (39.2)
	N1	33 (39.2)
	N2	9 (10.7)
	N3	6 (7.4)
	No data	3 (3.6)
Distant metastases	M0	45 (53.6)
	M1	39 (46.4)
Estrogen receptors	Yes	53 (63.1)
	No	26 (31.0)
	No data	5 (5.9)
Progesterone receptors	Yes	46 (54.8)
	No	31 (36.9)
	No data	7 (8.33)
HER2	Yes	39 (46.4)
	No	39 (46.4)
	No data	6 (7.2)
Molecular subtype	Luminal A	14 (16.7)
	Luminal B	39 (46.4)
	Triple-negative	17 (20.2)
	HER2-positive	9 (10.7)
	No data	5 (6.0)
NAC	Yes	34 (40.5)
	No	50 (59.5)

NAC, neoadjuvant chemotherapy

Table S19. Protocol of the assessment of immunohistochemical staining in breast tumors

Parameter	Value
Diffuse staining within the tumor section	Yes, No; Weak, Moderate
Tumor cells with positive staining in comparison with background staining (regardless of morphological structures)	Up to 10%, Up to 50% More than 50% Totally
Tumor cells with negative staining compared to background staining (regardless of morphological structures)	
Tumor cells with negative staining at the tips (up to 3 rows) of:	
torpedo-like sprouts associated with solid structures	Yes, No; Single, Many; No structures
torpedo-like structures (separated from solid structures)	
Negative staining in single tumor cells	Yes, No; Single, Many; No single tumor cells
Tumor cells with positive staining at the tips (up to 3 rows) of:	
torpedo-like sprouts associated with solid structures	Yes, No; Single, Many; No structures
torpedo-like structures (separated from solid structures)	
Tumor cells with positive focal or diffuse staining in torpedo-like structures (except for the tips)	Yes, No
Positive staining in single tumor cells	Yes, No; Single, Many; No structures
Negative segmental staining at the periphery (up to 2 layers) of structures in the cells with	
solid alveolar trabecular tubular	Yes, No; Single, Many; No structures
Negative segmental staining at the periphery (up to 2 layers) of structures in the cells with	
solid alveolar trabecular tubular	Yes, No; Single, Many; No structures
Positive segmental staining at the periphery (up to 2 layers) of structures in the cells with	
solid alveolar trabecular tubular	Yes, No; Single, Many; No structures
Positive segmental staining at the periphery (up to 2 layers) of structures in the cells with	
solid alveolar trabecular tubular	Yes, No; Single, Many; No structures
Atypical positive staining with nonspecific localization in tumor cells	Yes, No

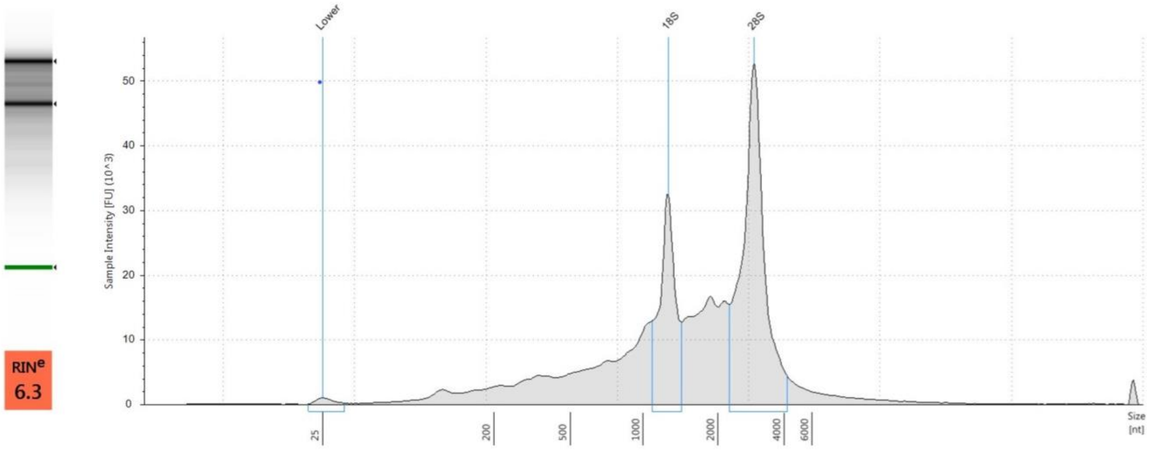

Figure S9. RNA integrity (RIN) of tumor tissue section following RNA-preserving immunolabeling.

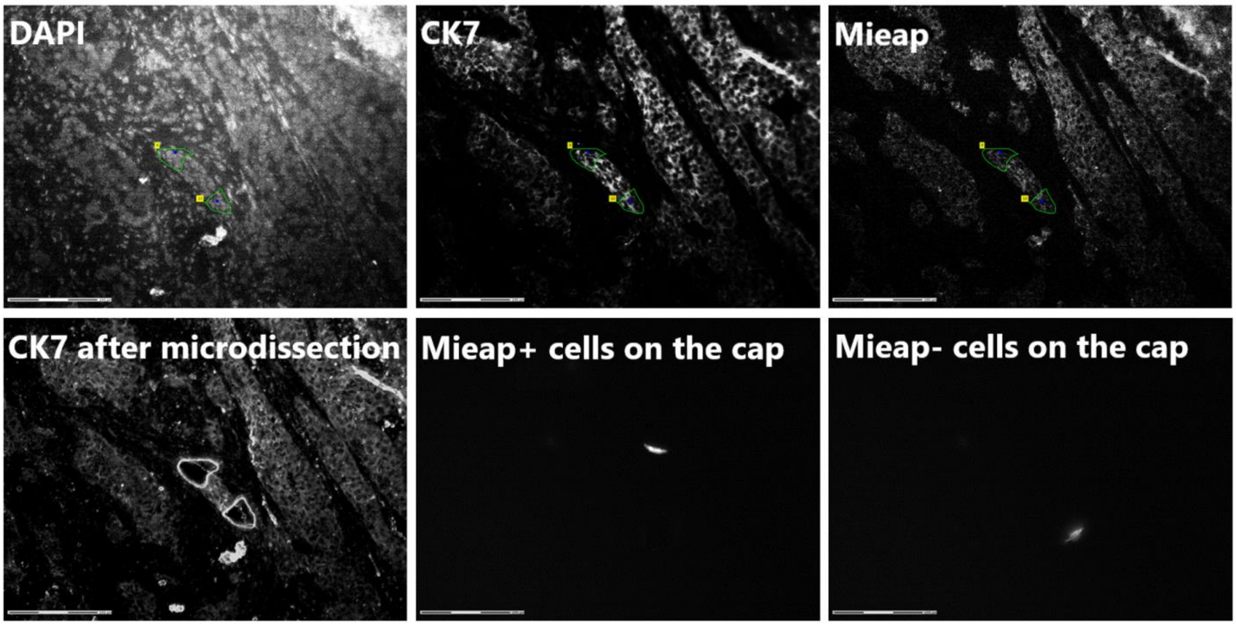

Figure S10. Fluorescence-guided laser microdissection on the example of CK7-positive Mieap-positive and Mieap-negative cells of the torpedo-like structure in breast tumor.