

Supplementary Table S1: Consistency evaluation for DEGs identified by RankCompV2 in signal dataset.

Disease	Dataset1	Dataset2	Overlap ^a	DEGs_con ^b	Consistency	POG1 ^c	POG2 ^d
COAD	GSE37364	GSE23878	2480	2440	98.39%	48.15%	63.25%
	GSE37364	GSE20916	2306	2234	96.88%	44.09%	59.86%
	GSE23878	GSE20916	2167	2148	99.12%	55.68%	57.56%
ESCC	GSE29001	GSE20347	471	471	100.00%	82.78%	19.01%
	GSE29001	GSE38129	457	457	100.00%	80.32%	22.29%
	GSE20347	GSE38129	1743	1734	100.00%	69.98%	84.59%
BRCA	Batch 96	Batch109	3482	3482	100.00%	80.03%	60.04%
	Batch 93	Batch109	4869	4869	100.00%	78.52%	83.96%
	Batch 93	Batch96	3655	3655	100.00%	58.94%	84.00%

Note: ^a the number of the overlapping DEGs from the two datasets, ^b the number of the consistent DEGs from the two datasets. ^{c, d} POG1 (or POG2) denotes the percentage of the consistent DEGs identified from the two datasets in all DEGs identified in dataset1 (or dataset2).

Supplementary Table S2: The enriched biological pathways by the DEGs in RD groups.

GOid	Name	Ref num	Interest num	pvalue	adjustp
The enriched biological pathways of ER negative breast cancer					
GO:0000278	mitotic cell cycle	760	89	<1.0E-16	<1.0E-16
GO:0006260	DNA replication	249	37	3.86E-14	8.22E-11
GO:0006261	DNA-dependent DNA replication	105	22	6.71E-12	7.79E-09
GO:0006281	DNA repair	326	36	5.69E-10	4.03E-07
GO:0000075	cell cycle checkpoint	213	26	1.99E-08	9.78E-06
GO:0071103	DNA conformation change	160	22	2.91E-08	1.38E-05
GO:0006312	mitotic recombination	35	9	2.02E-06	0.0005
GO:0008608	attachment of spindle microtubules to kinetochore	17	6	1.46E-05	0.0030
GO:0034622	cellular macromolecular complex assembly	528	37	3.17E-05	0.0059
GO:0051983	regulation of chromosome segregation	22	6	7.61E-05	0.0131
GO:0071824	protein-DNA complex subunit organization	124	14	9.31E-05	0.0158
GO:0051254	positive regulation of RNA metabolic process	1026	56	0.0004	0.0470
GO:0006284	base-excision repair	40	7	0.0004	0.0498
GO:0051383	kinetochore organization	12	4	0.0006	0.0663
GO:0006298	mismatch repair	21	5	0.0006	0.0702
GO:0061640	cytoskeleton-dependent cytokinesis	21	5	0.0006	0.0702
GO:0010557	positive regulation of macromolecule biosynthetic process	1152	60	0.0007	0.0820
GO:0006396	RNA processing	534	33	0.0008	0.0906
The enriched biological pathways of ER positive breast cancer					
GO:0000278	mitotic cell cycle	760	60	<1.0E-16	<1.0E-16
GO:0007017	microtubule-based process	385	32	1.35E-13	1.56E-10
GO:0007059	chromosome segregation	130	19	9.39E-13	9.99E-10
GO:0006271	DNA strand elongation involved in DNA replication	32	6	1.65E-05	0.0031
GO:0051983	regulation of chromosome segregation	22	5	3.22E-05	0.0050
GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	175	12	5.69E-05	0.0083
GO:0050870	positive regulation of T cell activation	162	11	0.0001	0.0153
GO:0002449	lymphocyte mediated immunity	164	11	0.0001	0.0167
GO:0051607	defense response to virus	166	11	0.0002	0.0181
GO:0006310	DNA recombination	178	11	0.0003	0.0286
GO:0006909	phagocytosis	154	10	0.0004	0.0334
GO:0051782	negative regulation of cell division	9	3	0.0004	0.0362
GO:0031497	chromatin assembly	81	7	0.0005	0.0438
GO:0001895	retina homeostasis	39	5	0.0006	0.0458
GO:0006268	DNA unwinding involved in DNA replication	10	3	0.0006	0.0476
GO:0034728	nucleosome organization	92	7	0.0011	0.0835
GO:0006270	DNA replication initiation	27	4	0.0012	0.0843

Supplementary Table S3: The enriched molecular functions by the DEGs in RD groups.

GOid	Name	Ref num	Interest num	<i>p</i> value	adjust <i>p</i>
The enriched molecular functions of ER negative breast cancer					
GO:0003677	DNA binding	1617	84	3.71E-05	0.0179
GO:0003777	microtubule motor activity	53	10	1.02E-05	0.0066
GO:0005515	protein binding	6670	265	2.91E-05	0.0160
GO:0017056	structural constituent of nuclear pore	9	4	1.48E-04	0.0571
GO:0043566	structure-specific DNA binding	207	18	2.64E-04	0.0923
GO:0044822	poly(A) RNA binding	902	56	7.86E-06	6.06E-03
The enriched molecular functions of ER positive breast cancer					
GO:0003823	antigen binding	65	7	1.01E-04	0.0444
GO:0004748	ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor	2	2	2.79E-04	0.0716
GO:0005524	ATP binding	1130	36	1.04E-04	0.0444
GO:0008017	microtubule binding	134	13	3.57E-07	7.21E-04
GO:0019901	protein kinase binding	365	18	3.96E-05	0.0305
GO:0043548	phosphatidylinositol 3-kinase binding	17	4	1.52E-04	0.0495

Supplementary Table S4: The enriched cellular components by the DEGs in RD groups.

GOid	Name	Ref num	Interest num	<i>p</i> value	adjust <i>p</i>
The enriched cellular components of ER negative breast cancer					
GO:0000228	nuclear chromosome	293	30	8.85E-08	5.90E-06
GO:0000779	condensed chromosome, centromeric region	74	11	4.17E-05	1.57E-03
GO:0000796	condensin complex	6	3	7.50E-04	0.0200
GO:0005643	nuclear pore	61	8	1.10E-03	0.0282
GO:0005654	nucleoplasm	1236	96	5.11E-15	9.35E-13
GO:0005657	replication fork	45	10	2.27E-06	1.27E-04
GO:0005730	nucleolus	544	36	1.26E-04	4.02E-03
GO:0005762	mitochondrial large ribosomal subunit	8	4	8.69E-05	2.83E-03
GO:0005813	centrosome	312	22	1.17E-03	0.0289
GO:0005819	spindle	208	35	4.00E-15	8.36E-13
GO:0031464	Cul4A-RING E3 ubiquitin ligase complex	8	3	2.00E-03	0.0450
GO:0034399	nuclear periphery	97	11	4.89E-04	0.0141
GO:0045120	pronucleus	16	4	1.81E-03	0.0422
GO:1990234	transferase complex	449	33	3.25E-05	1.25E-03
The enriched cellular components of ER positive breast cancer					
GO:0000779	condensed chromosome, centromeric region	74	11	5.10E-08	1.25E-05
GO:0000796	condensin complex	6	3	9.83E-05	5.14E-03
GO:0005615	extracellular space	943	33	7.23E-05	4.07E-03
GO:0005654	nucleoplasm	1236	44	2.16E-06	2.11E-04
GO:0005680	anaphase-promoting complex	14	3	1.61E-03	0.0591
GO:0005813	centrosome	312	19	1.93E-06	2.02E-04
GO:0005819	spindle	208	23	1.17E-12	8.59E-10
GO:0005871	kinesin complex	37	5	4.10E-04	0.0177
GO:0042105	alpha-beta T cell receptor complex	5	2	2.88E-03	0.0886
GO:0044815	DNA packaging complex	49	6	1.87E-04	9.47E-03
GO:0045120	pronucleus	16	3	2.42E-03	0.0788
GO:0071756	pentameric IgM immunoglobulin complex	2	2	2.98E-04	0.0132