Supplementary

Table S1 The targets of MA-regulated autophagy in breast cancer

Gene name	Uniprot ID	Degree score
TP53	P04637	44
AKT1	P31749	44
BCL2	P10415	44
HSP90AA1	P07900	40
TNF	P01375	40
EGFR	P00533	39
MTOR	P42345	39
IL6	P05231	39
BCL2L1	Q07817	38
MAPK3	Q16644	37
GSK3B	P49841	36
SIRT1	Q99500	36
MAPK8	P45983	35
MAPK1	P28482	34
TGFB1	P01137	33
MDM2	Q00987	32
PIK3CA	P42336	31
BECN1	Q14457	31
FN1	P02751	30
MCL1	Q07820	30
ABL1	P00519	28
MAPK14	Q16539	28
APP	P05067	28
RELA	Q04206	28
RPS6KB1	P23443	27
KDR	P35968	24
MAP2K1	Q02750	24
ATG5	Q9H1Y0	24
AKT2	P31751	24
IKBKB	O14920	24
HDAC6	Q9UBN7	23
LC3B	Q9GZQ8	23
PRKCD	Q05655	20
NOS3	P29474	20
HMGB1	P09429	20

Table S1 (*continued*)

https://dx.doi.org/10.21037/tcr-2026-1-0145

Table S1 (*continued*)

Gene name	Uniprot ID	Degree score
AKT3	Q9Y243	20
BAX	Q07812	19
MET	P08581	19
AURKA	O14965	18
PIK3CB	P42338	18
PLG	P00747	16
XPO1	O14980	15
NOS2	P35228	15
TP73	O15350	11
CTSL	P07711	10
ULK1	O75385	10
CXCR3	P49682	5
EPHB2	P29323	4
S1PR3	Q99500	3

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Table S2 The targets of MA-regulated ferroptosis in breast cancer

Gene name	Uniprot ID	Degree score
EGFR	P00533	36
IL6	P05231	35
RELA	Q04206	33
PTGS2	P35354	32
PPARG	P37231	32
MAPK3	P27361	32
SRC	P12931	32
IL1B	P01584	31
TGFB1	P01137	29
MTOR	P42345	29
PARP1	P09874	29
CDH1	P12830	28
CREB1	P16220	28
MAPK8	P45983	27
SIRT1	Q96EB6	27
GSK3B	P49841	27
BECN1	Q14457	27
MAPK14	Q16539	25
AR	P10275	24
MAPK1	P28482	24
MDM2	Q00987	24
PIK3CA	P42336	24
HMOX1	P09601	24
PPARA	Q07869	18
TERT	O14746	17
MUC1	P15941	15
YAP1	P46937	15
HMGB1	P09429	15
PPARD	Q03181	15
MAPK9	P45984	13
GPX4	P36969	13
CTSB	P07858	12
TGFBR1	P36897	12
NOS2	P35228	11
FLT3	P36888	10

Table S2 (*continued*)

https://dx.doi.org/10.21037/tcr-2026-1-0145

Table S2 (*continued*)

Gene name	Uniprot ID	Degree score
SLC7A11	Q9UPY5	9
ALOX5	P09917	8
FTH1	P02794	8
NCOA4	Q13772	7
CDC25A	P30304	7
PEBP1	P30086	7
ALOX12	P18054	6
PTPN6	P29350	6
CA9	Q16790	5
AKR1C3	P42330	2

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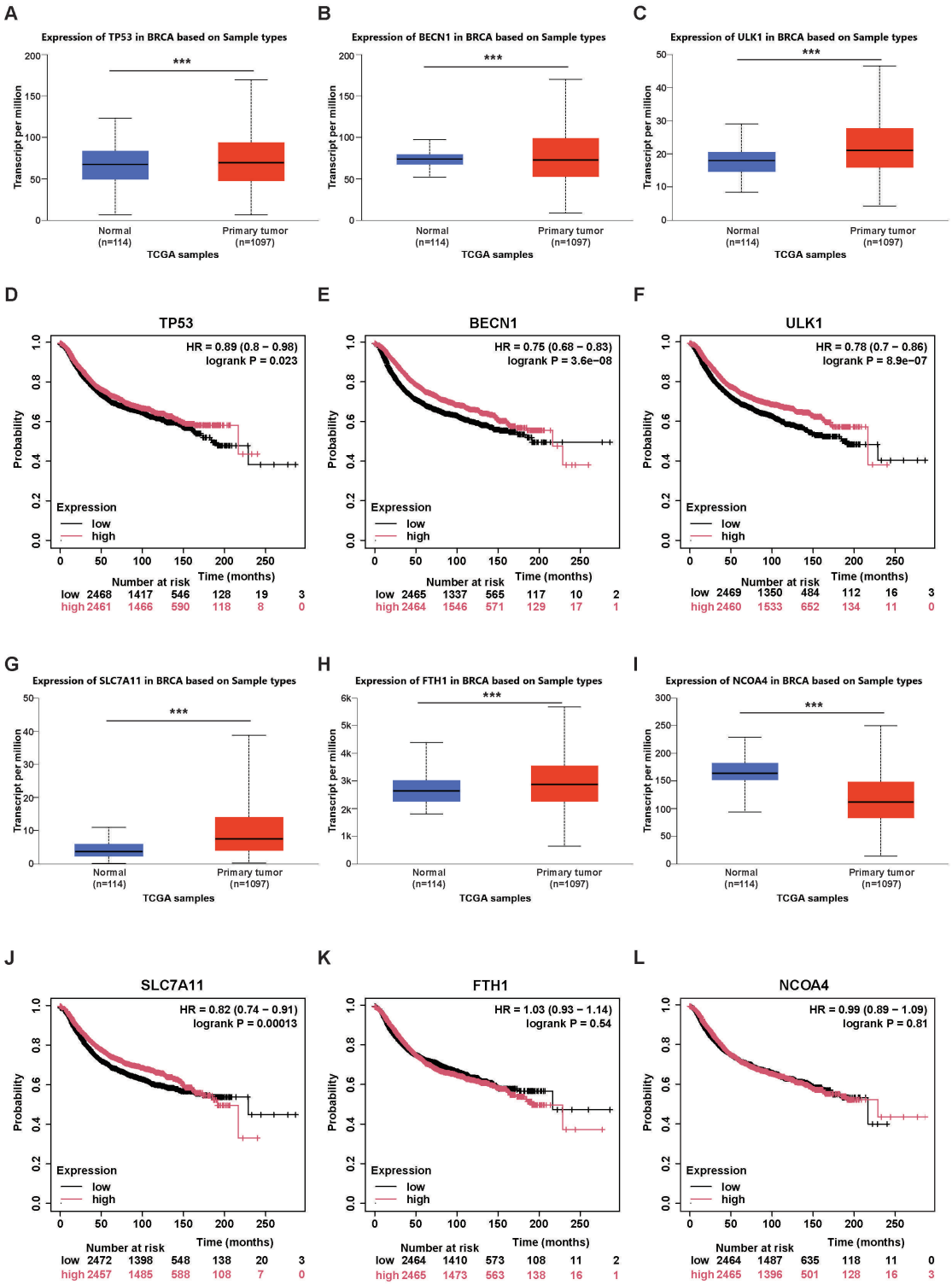

Figure S1 Expression and survival analysis of genes. mRNA expression levels of *TP53* (A), *BECN1* (B), *ULK1* (C), *SLC7A11* (G), *FTH1* (H) and *NCOA4* (I) genes from The Cancer Genome Atlas (TCGA) database analyzed by UALCAN. Correlation between *TP53* (D), *BECN1* (E), *ULK1* (F), *SLC7A11* (J), *FTH1* (K) and *NCOA4* (L) genes mRNA expression levels and overall survival evaluated by the Kaplan-Meier Plotter database. ***, P<0.001 *vs.* the control.

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