

Figure S1. Correlation between SLC7A5 mRNA expression and expression of genes related to breast cancer, hypoxia and cell metabolism in the Örebro cohort (n=80). Correlation between SLC7A5 expression and expression of (A) ESR1, (B) ERBB2, (C) MKI67, (D) MYC, (E) MTOR, (F) CCND1, (G) HIF1A, (H) VEGFA, (I) EPAS1, (J) LDHA, (K) SLC2A1, (L) CA9 and (M) NDUFA4L2. SLC7A5, solute carrier family 7 member 5; ESR1, estrogen receptor 1; ERBB2, Erb-B2 receptor tyrosine kinase 2; MYC, MYC proto-oncogene, BHLH transcription factor; MTOR, mechanistic target of rapamycin; MKI67, marker of proliferation Ki-67; CCND1, cyclin D1; HIF1A, hypoxia inducible factor 1 subunit alpha; EPAS1, endothelial PAS domain-containing protein 1; VEGFA, vascular endothelial growth factor A; LDHA, lactate dehydrogenase A; SLC2A1, solute carrier family 2, facilitated glucose transporter member 1; CAIX, carbonic anhydrase IX; NDUFA4L2, NDUFA4 mitochondrial complex associated like 2.

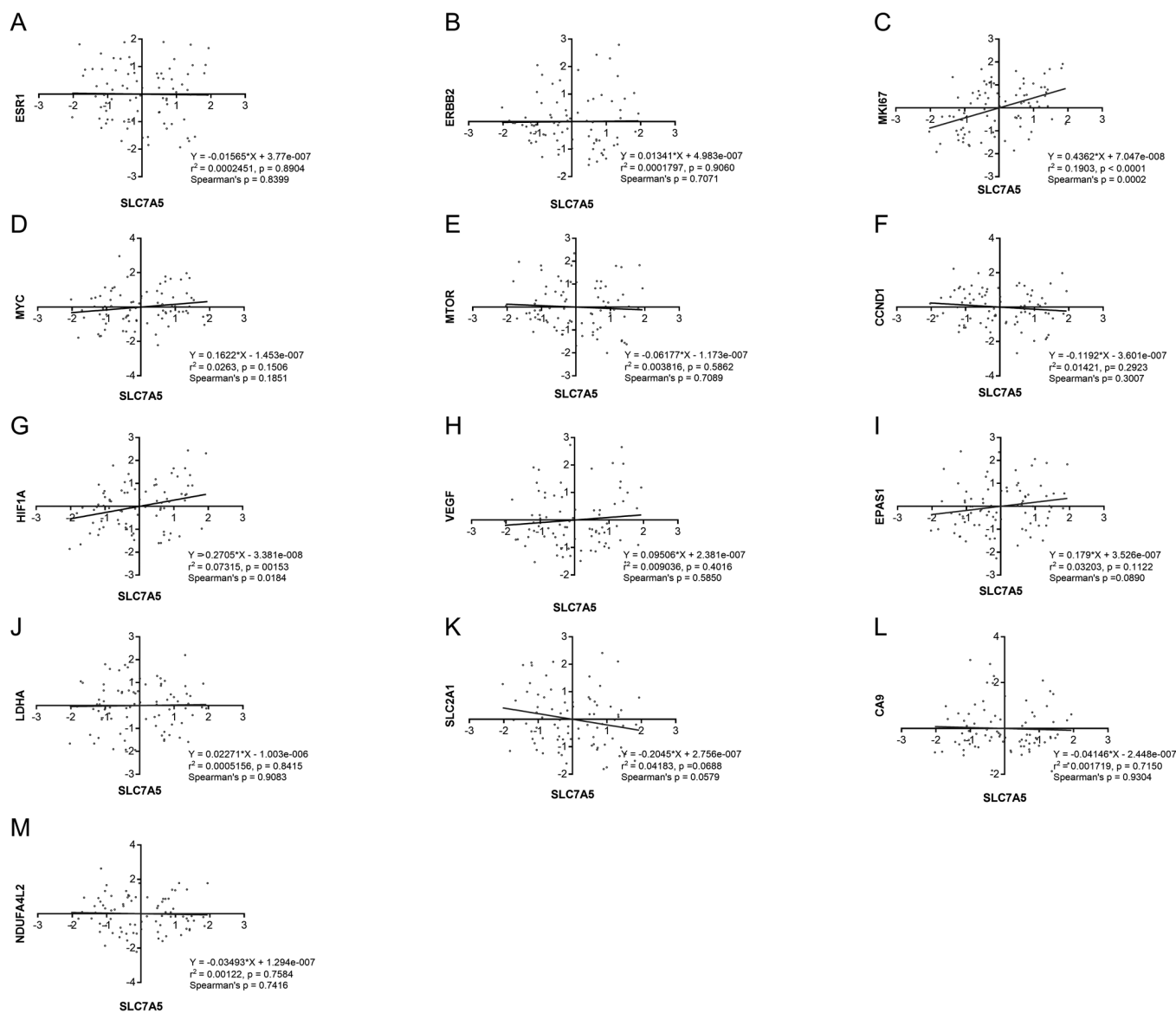


Figure S2. Correlation between SLC7A5 mRNA expression and expression of genes related to breast cancer, hypoxia and cell metabolism in ER⁺ tumors as assessed with immunohistochemistry (METABRIC, n=1,445). Correlation between SLC7A5 expression and expression of (A) ESR1, (B) ERBB2, (C) MKI67, (D) MYC, (E) MTOR, (F) CCND1, (G) HIF1A, (H) VEGFA, (I) EPAS1, (J) LDHA, (K) SLC2A1, (L) CA9 and (M) NDUFA4L2. SLC7A5, solute carrier family 7 member 5; ESR1, estrogen receptor 1; ERBB2, Erb-B2 receptor tyrosine kinase 2; MYC, MYC proto-oncogene, BHLH transcription factor; MTOR, mechanistic target of rapamycin; MKI67, marker of proliferation Ki-67; CCND1, cyclin D1; HIF1A, hypoxia inducible factor 1 subunit alpha; EPAS1, endothelial PAS domain-containing protein 1; VEGFA, vascular endothelial growth factor A; LDHA, lactate dehydrogenase A; SLC2A1, solute carrier family 2, facilitated glucose transporter member 1; CAIX, carbonic anhydrase IX; NDUFA4L2, NDUFA4 mitochondrial complex associated like 2.

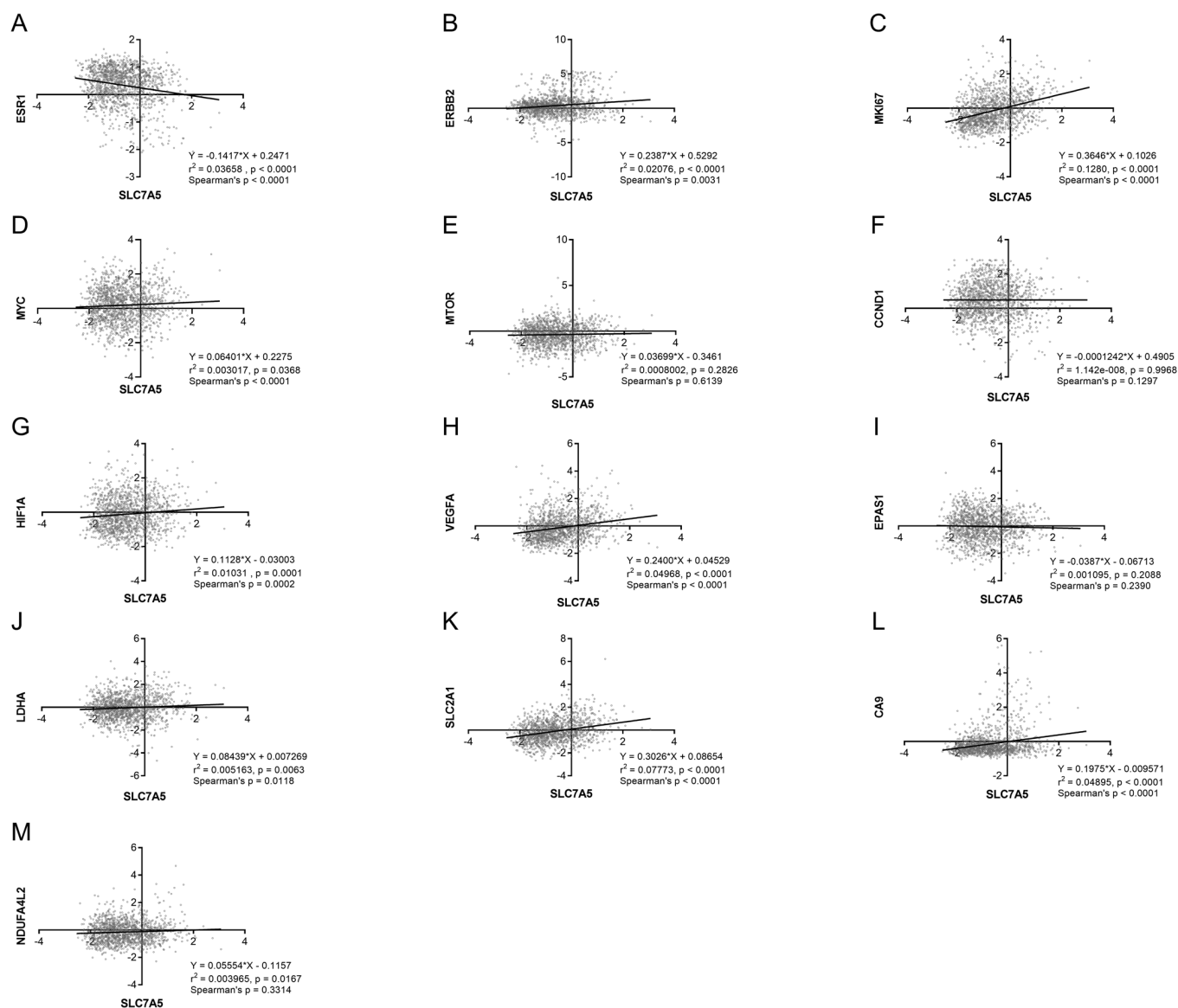


Figure S3. Correlation between SLC7A5 mRNA expression and expression of genes related to breast cancer, hypoxia and cell metabolism in all tumors regardless of ER-status (METABRIC, n=1,903). Correlation between SLC7A5 expression and expression of (A) ESR1, (B) ERBB2, (C) MKI67, (D) MYC, (E) MTOR, (F) CCND1, (G) HIF1A, (H) VEGFA, (I) EPAS1, (J) LDHA, (K) SLC2A1, (L) CA9 and (M) NDUFA4L2. SLC7A5, solute carrier family 7 member 5; ESR1, estrogen receptor 1; ERBB2, Erb-B2 receptor tyrosine kinase 2; MYC, MYC proto-oncogene, BHLH transcription factor; MTOR, mechanistic target of rapamycin; MKI67, marker of proliferation Ki-67; CCND1, cyclin D1; HIF1A, hypoxia inducible factor 1 subunit alpha; EPAS1, endothelial PAS domain-containing protein 1; VEGFA, vascular endothelial growth factor A; LDHA, lactate dehydrogenase A; SLC2A1, solute carrier family 2, facilitated glucose transporter member 1; CAIX, carbonic anhydrase IX; NDUFA4L2, NDUFA4 mitochondrial complex associated like 2.

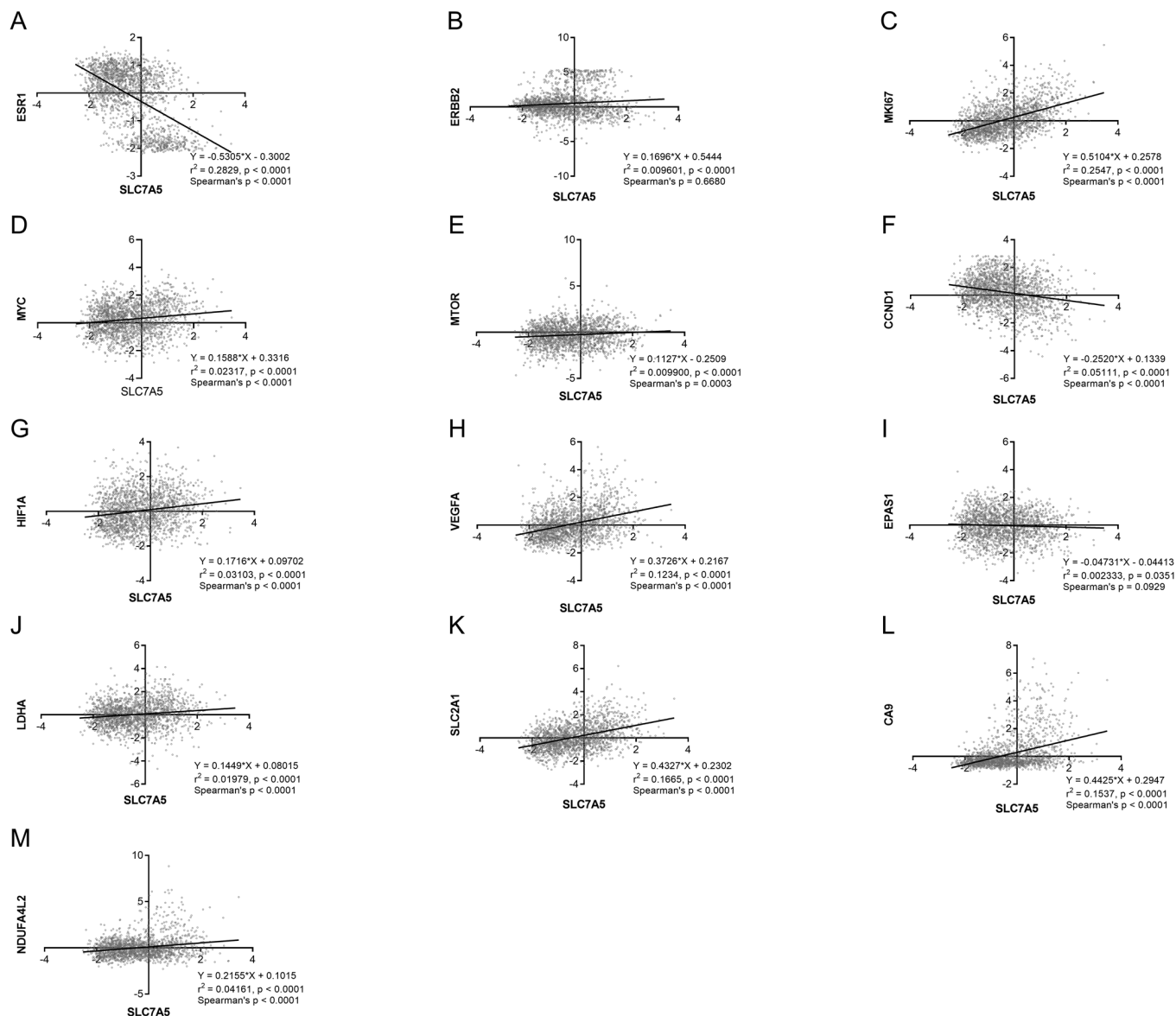


Figure S4. Correlation between SLC7A5 mRNA expression and expression of genes related to breast cancer and hypoxia related in all breast cancer tumors (METABRIC, n=1903). Color coded according to ER-status. Correlation between SLC7A5 expression and expression of (A) ESR1, (B) ERBB2, (C) MKI67, (D) MYC, (E) MTOR, (F) CCND1, (G) HIF1A, (H) VEGFA, (I) EPAS1, (J) LDHA, (K) SLC2A1, (L) CA9 and (M) NDUFA4L2. SLC7A5, solute carrier family 7 member 5; ESR1, estrogen receptor 1; ERBB2, Erb-B2 receptor tyrosine kinase 2; MYC, MYC proto-oncogene, BHLH transcription factor; MTOR, mechanistic target of rapamycin; MKI67, marker of proliferation Ki-67; CCND1, cyclin D1; HIF1A, hypoxia inducible factor 1 subunit alpha; EPAS1, endothelial PAS domain-containing protein 1; VEGFA, vascular endothelial growth factor A; LDHA, lactate dehydrogenase A; SLC2A1, solute carrier family 2, facilitated glucose transporter member 1; CAIX, carbonic anhydrase IX; NDUFA4L2, NDUFA4 mitochondrial complex associated like 2.

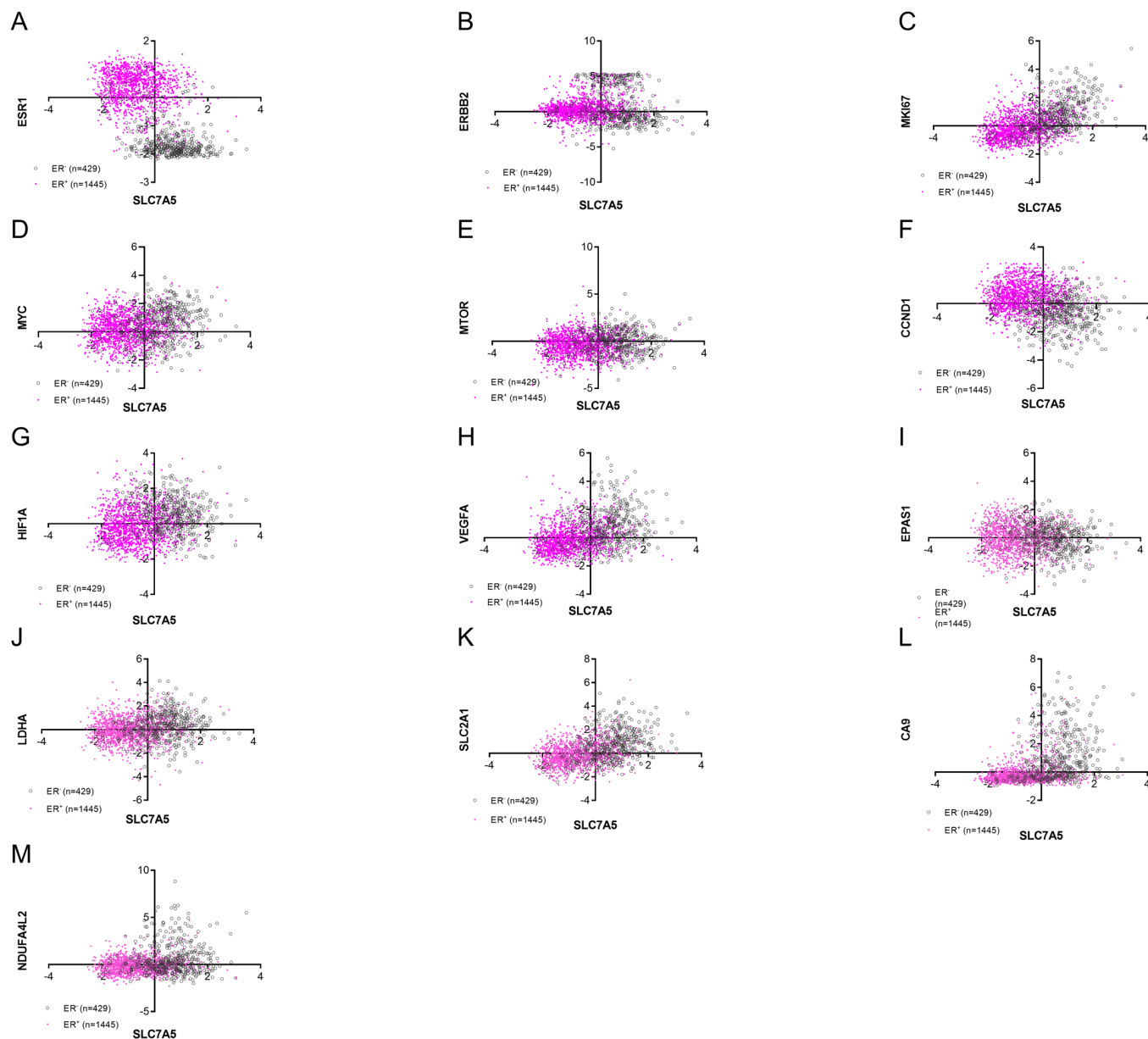


Table SI. Associations between SLC7A5 protein expression and clinicopathological characteristics in patients with ER⁺ breast cancer (n=152).

	SLC7A5 negative expression (n, %)	SLC7A5 positive expression (n, %)	
	SLC7A5 protein score		P-value
Variables	0 (106, 69.7) 1+ (23, 15.1) Median (LQ, UQ)	2+ (17, 11.2) 3+ (6, 4.0) Median (LQ, UQ)	
Age of diagnosis, years	62.1 (52.3, 77.3)	60.1 (52.5, 77.8)	0.90
Age range, years	35.8-92.8	41.0-86.1	
Tumour size, mm	24 (17, 35)	28 (17, 35)	0.37
	Case number (n, %)	Case number (n, %)	
Menopausal status			
Premenopausal	29 (85.3)	5 (14.7)	1.00
Postmenopausal	97 (84.3)	18 (15.7)	
Unknown	3 (100)	0 (0)	
Lymph node infiltration			
No	43 (79.6)	11 (20.4)	0.24
Yes	85 (87.6)	12 (12.4)	
Distant recurrence			
No	99 (87.6)	14 (12.4)	0.10
Yes	30 (76.9)	9 (23.1)	
Nottingham Histologic Score			
1	17 (100)	0 (0)	0.014 ^a
2	84 (87.5)	12 (12.5)	
3	28 (71.8)	11 (28.2)	
Histological type			
Ductal carcinoma	110 (83.3)	22 (16.7)	0.58
Lobular carcinoma	17 (94.4)	1 (5.6)	
Miscellaneous	2 (100)	0 (0)	
PR-status			
Negative	17 (70.8)	7 (29.2)	0.058
Positive	111 (87.4)	16 (12.6)	
HER2-status			
Negative	85 (82.5)	18 (17.5)	0.30
Positive	10 (71.4)	4 (28.6)	

^aP<0.05. LQ, lower quadrant ; UQ, upper quadrant.