D Ren, et al. Brain adaptive CSCs in TNBC brain metastases

Supplementary Table 1. Seventeen differentially expressed genes between the tumorspheres relative to Br cell lines.

Gene symbol	Mean difference (tumorsphere-MB231-Br)	P value	Mean difference (tumorsphere-CN34-Br)	P value	Description
ADAMTS1	4.877	0.002	3.153	5×10^{-5}	ADAM metallopeptidase with thrombospondin type 1 motif, 1
ARHGAP29	1.565	0.002	1.746	0.0015	Rho GTPase activating protein 29
COL12A1	1.482	0.004	1.648	0.0016	collagen, type XII, alpha 1
DUSP1	1.45	0.008	2.044	0.0009	dual specificity phosphatase 1
FGF5	3.486	0.008	1.684	0.0022	fibroblast growth factor 5
FRAS1	4.52	0.001	2.013	0.0014	Fraser syndrome 1
HSPG2	2.061	5×10^{-5}	1.474	0.0075	heparan sulfate proteoglycan 2
IL18	3.111	0.0001	2.131	0.0011	interleukin 18 (interferon-gamma-inducing factor)
LPAR1	3.241	0.0015	2.809	0.0003	lysophosphatidic acid receptor 1
LPHN2	1.855	0.0035	1.966	0.0013	latrophilin 2
MMP1	8.35	5×10^{-5}	1.416	0.0093	matrix metallopeptidase 1 (interstitial collagenase)
NMNAT2	3.032	0.0019	2.209	0.0067	nicotinamide nucleotide adenylyltransferase 2
PCDH7	5.859	0.0008	1.781	0.007	protocadherin 7
PTGFRN	3.99	0.0011	4.929	0.0032	prostaglandin F2 receptor negative regulator
SDPR	1.757	0.0018	3.471	0.001	serum deprivation response
TIE1	4.810	0.0081	2.105	0.0013	tyrosine kinase with immunoglobulin-like and EGF-like domains 1
STC1	-1.385	0.0087	-1.597	0.0053	stanniocalcin 1

Supplementary Table 2. Expression of PCDH7 in brain metastases tissues of breast cancer patient.

H score	Negative (0-9)	Low (10-100)	Medium (101-200)	High (201-300)
Primary breast tumors	25 (73%)	6 (18%)	3 (9%)	0 (0%)
Brain metastatic tumors of breast cancer	0 (0%)	0 (0%)	2 (7%)	27 (93%)

Supplementary Table 3. Pairwise sequence comparison of PCDH7 EC1-EC2 domain to diverse cadherins with structures available in Protein Data bank.

Protein	PDB code	Sequence Identity	Sequence Similarity	Residues	Description	Subfamily	Resolution (Å)
E cadherin	2O72 (14)	19.40%	32.40%	1-213	EC1 and EC2; strand exchange trans dimer	TYPE I	2.00
C cadherin	1L3W (10)	20.80%	35.50%	1-540	EC1 - EC5; strand exchange trans dimer	TYPE I	3.08
N cadherin	2QVI	20.60%	35.50%	1-215	EC1 and EC2; strand exchange trans dimer	TYPE I	3.01
Desmoglein-2	2YQG	10.40%	15.00%	1-123	EC1, monomer	Desmoglein	Null*
Cadherin-6	3LND (15)	22.90%	36.90%	1-207	EC1 and EC2; X dimer, W4A mutation	TYPE II	2.82
VE-Cadherin	3PPE (16)	20.90%	36.10%	1-203	EC1 and EC2; strand exchange trans dimer	TYPE II	2.1
Cadherin-8	2A62 (17)	20.80%	37.40%	1-322	EC1 - EC3; strand exchange trans dimer	TYPE II	4.5
Cadherin-11	2A4E (17)	20.90%	34.80%	0-207	EC1 and EC2; strand exchange trans dimer	TYPE II	3.2
MN-cadherin	1ZVN (17)	19.60%	45.10%	0-98	EC1; strand exchange trans dimer	TYPE II	2.16
T-cadherin	3K6D (18)	9.20%	14.30%	1-99	EC1, X dimer	nonclassical	1.8
Cadherin-23 Protocadherin 15	3MVS (19)	19.00%	36.20%	1-210	EC1 and EC2	nonclassical	1.1
Protocadherin 4	1WUZ (20)	28.90%	44.70%	1-103	EC1, monomer	nonclassical	Null*
Protocadherin 7	2YST	10.80%	17.30%	302-413	EC3, monomer	nonclassical	Null*
E cadherin	1EDH (21)	16.10%	32.60%	3-213	EC1 and EC2, X dimer; DW residues in N terminus were removed	TYPE I	2