

Supplementary table 1. The custom NanoString gene expression panel used in the study.

HUGO Gene	Accession	NSID	Target Sequence	Reference
ACTB	NM_001101.2	NM_001101.2:1685	CCAACCTTGAGATGTATGAAGGCTTTTGGTCTCCCTGGGAGTGGGTG GAGGCAGCCAGGGCTTACCTGTACACTGACTTGAGACCAGTTGAAT AAAAGTGC	HK
ACTR3B	NM_001040135.1	NM_001040135.1:905	CCAGAAGAAGTTTGTTATAGACGTTGGTTACGAAAGATTCTGCGA CCTGAAATATTCTTTACCCGGAGTTTGCCAACCCAGACTTTATGGA GTCCATC	
ANLN	NM_018685.2	NM_018685.2:240	CGTGCCAGGCGAGAGAATCTTCAGAGAAAAATGGCTGAGAGGCCC ACAGCAGCTCCAAGGTCTATGACTCATGCTAAGCGAGCTAGACAGC CACTTTCAG	
AURKA	NM_003600.2	NM_003600.2:405	AGCTCCAGTTGGAGGTCCAAAACGTGTTCTCGTGACTCAGCAATTT CCTTGTCAGAATCCATTACCTGTAAATAGTGGCCAGGCTCAGCGGG TCTTGTGT	
AZGP1	NM_001185.2	NM_001185.2:123	GTTACTCTCTGACCTATATCTACACTGGGCTGTCCAAGCATGTTGAA GACGTCCCCGCGTTTCAGGCCCTTGGCTCACTCAATGACCTCCAGT TCTTTAG	
BAG1	NM_004323.3	NM_004323.3:540	CTTCATGTTACCTCCCAGCAGGGCAGCAGTGAACCAGTTGTCCAAG ACCTGGCCCAGGTTGTTGAAGAGGTCATAGGGGTTCCACAGTCTTT TCAGAAAC	
BCL2	NM_000633.2	NM_000633.2:1525	CCAAGCACCGCTTCGTGTGGCTCCACCTGGATGTTCTGTGCCTGTA AACATAGATTTCGCTTTCCATGTTGTTGGCCGGATCACCATCTGAAGA GCAGACG	
BIRC5	NM_001168.2	NM_001168.2:1215	CCATTCTAAGTCATTGGGGAAACGGGGTGAACCTCAGGTGGATGAG GAGACAGAATAGAGTGATAGGAAGCGTCTGGCAGATACTCCTTTTG CCTCTGCT	
BLVRA	NM_000712.3	NM_000712.3:485	TTCCTGAAAAAAGAAGTGGTGGGGAAAGACCTGCTGAAAGGGTCG CTCCTCTTCACAGCTGGCCCGTTGGAAGAAGAGCGGTTTGGCTTCC CTGCATTCA	
BUB1B	NM_001211.4	NM_001211.4:835	GAGTCTTCTGTACCACAACGAAGCACACTAGCTGAACTAAAGAGCA AAGGGAAAAAGACAGCAAGAGCTCCAATCATCCGTGTAGGAGGTG CTCTCAAGG	

CALM2	NM_001743.3	NM_001743.3:868	TGGAGTTGTA ACTCTGCGTGGACTATGGACAGTCAACAATATGTACT TAAAAGTTGCACTATTGCAAACGGGTGTATTATCCAGGTACTCGTA CACTAT	HK
CCNB1	NM_031966.2	NM_031966.2:710	GAGACA ACTTGAGGAAGAGCAAGCAGTCAGACCAAAATACCTACTG GGTCGGGAAGTCACTGGAAACATGAGAGCCATCCTAATTGACTGGC TAGTACAG	
CCNE1	NM_001238.1	NM_001238.1:1155	GAGAACTGTGTCAAGTGGATGGTTCCATTTGCCATGGTTATAAGGG AGACGGGGAGCTCAAACTGAAGCACTTCAGGGGCGTCGCTGATG AAGATGCAC	
CD68	NM_001251.2	NM_001251.2:1140	ACCGGTCCATCTTGCTGCCTCTCATCATCGGCCTGATCCTTCTTGG CCTCCTCGCCCTGGTGCTTATTGCTTTCTGCATCATCCGGAGACGC CCATCCGC	
CDC20	NM_001255.1	NM_001255.1:915	CCCGAGTGGGCTCCCTAAGCTGGAACAGCTATATCCTGTCCAGTGG TTCACGTTCTGGCCACATCCACCACCATGATGTTTCGGGTAGCAGAA CACCATGT	
CDC6	NM_001254.3	NM_001254.3:1655	GGGGAAGTTATATGAAGCCTACAGTAAAGTCTGTGCGAAACAGCAG GTGGCGGCTGTGGACCAGTCAGAGTGTTTGTCACCTTTCAGGGCTCT TGGAAGCC	
CDH3	NM_001793.3	NM_001793.3:2005	CCCTCGACCGTGAGGATGAGCAGTTTGTGAGGAACAACATCTATGA AGTCATGGTCTTGGCCATGGACAATGGAAGCCCTCCCACCACTGGC ACGGGAAC	
CENPA	NM_001042426.1	NM_001042426.1:979	CACTTTGAGCAGTTGCCTGGAAGGCTGGGCATTTCCATCATATAGA CCTCTGCCCTTCAGAGTAGCCTCACCATTAGTGGCAGCATCATGTA ACTGAGTG	
CENPF	NM_016343.3	NM_016343.3:9260	AGAAAATCTTGCAGAGTCCTCCAAACCAACAGCTGGTGGCAGCAGA TCACAAAAGGTCAAAGTTGCTCAGCGGAGCCCAGTAGATTCAGGCA CCATCCTC	
CEP55	NM_018131.3	NM_018131.3:570	GTA CTACCGCATTGCTTGAACAGCTGGAAGAGACAACGAGAGAAGG AGAAAGGAGGGAGCAGGTGTTGAAAGCCTTATCTGAAGAGAAAGAC GTATTGAA	
CTSV	NM_001333.3	NM_001333.3:2820	GTGAAATTTAATCGAAAGGTGATCCATTGTGAATGCAATGGGAGGG AAGGGGCATGTGGGACTGTGTATCCCCAAAACCCCTTTGATAGCCTA TGTCACA	

CXXC5	NM_016463.5	NM_016463.5:1630	AGCTGCCCTCTCCGTGCAATGTCACTGCTCGTGTGGTCTCCAGCAA GGGATTCGGGCGAAGACAAACGGATGCACCCGTCTTTAGAACCAAA AATATTCT	
DHCR7	NM_001360.2	NM_001360.2:780	CCCACCATCATCTTCGACAACTGGATCCCCTGCTGTGGTGCGCCA ACATCCTTGGCTATGCCGTCTCCACCTTCGCCATGGTCAAGGGCTA CTTCTTCC	
EGFR	NM_005228.3	NM_005228.3:2760	GCAGCCAGGAACGTAAGTGGTGAAAACACCGCAGCATGTCAAGATCA CAGATTTTGGGCTGGCCAACTGCTGGGTGCGGAAGAGAAAGAATA CCATGCAG	
ERBB2	NM_004448.2	NM_004448.2:2405	TGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCAT CTGGATCCCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAA GTGTTGAG	
ESR1	NM_000125.2	NM_000125.2:1595	AGGAACCAGGGAAAATGTGTAGAGGGCATGGTGGAGATCTTCGAC ATGCTGCTGGCTACATCATCTCGGTTCCGCATGATGAATCTGCAGG GAGAGGAGT	
EXO1	NM_006027.3	NM_006027.3:820	TGGCCCACAAAGTAATTAAGCTGCCCGGTCTCAGGGGGTAGATTG CCTCGTGGCTCCCTATGAAGCTGATGCGCAGTTGGCCTATCTTAAC AAAGCGGG	
FGFR4	NM_002011.3	NM_002011.3:1002	CCCACATCCAGTGGCTGAAGCACATCGTCATCAACGGCAGCAGCTT CGGAGCCGACGGTTTCCCCTATGTGCAAGTCCTAAAGACTGCAGAC ATCAATAG	
FOXA1	NM_004496.2	NM_004496.2:280	TGGATGGTTGTATTGGGCAGGGTGGCTCCAGGATGTTAGGAACTGT GAAGATGGAAGGGCATGAAACCAGCGACTGGAACAGCTACTACGC AGACACGCA	
FOXC1	NM_001453.1	NM_001453.1:1530	TTCGAGTCACAGAGGATCGGCTTGAACAACTCTCCAGTGAACGGGA ATAGTAGCTGTCAAATGGCCTTCCCTTCCAGCCAGTCTCTGTACCG CACGTCCG	
GAPDH	NM_002046.3	NM_002046.3:972	CACTCCTCCACCTTTGACGCTGGGGCTGGCATTGCCCTCAACGACC ACTTTGTCAAGCTCATTTCTGCTATGACAACGAATTTGGCTACAGC AACAGGG	HK
GPR160	NM_014373.1	NM_014373.1:760	GGATTTCAAGTCCTTGCTTATGTTTTGGGAGACCCAGCCATCTACCAA AGCCTGAAGGCACAGAATGCTTATTCTCGTCACTGTCCTTTCTATGT CAGCAT	

GRB7	NM_005310.2	NM_005310.2:1010	GCCGATCTGGCCTCTATTACTCCACCAAGGGGCACCTCTAAGGATCC GAGGCACCTGCAGTACGTGGCAGATGTGAACGAGTCCAACGTGTA CGTGGTGAC	
GSTM1	NM_000561.2	NM_000561.2:335	GATTCGTGTGGACATTTTGGAGAACCAGACCATGGACAACCATATG CAGCTGGGCATGATCTGCTACAATCCAGAATTTGAGAACTGAAGC CAAAGTAC	
GUSB	NM_000181.1	NM_000181.1:1350	CGGTCGTGATGTGGTCTGTGGCCAACGAGCCTGCGTCCCACCTAG AATCTGCTGGCTACTACTTGAAGATGGTGATCGCTCACACCAAATC CTTGGACCC	HK
HMBS	NM_000190.3	NM_000190.3:315	CATTGCTATGTCCACCACAGGGGACAAGATTCTTGATACTGCACTCT CTAAGATTGGAGAGAAAAGCCTGTTTACCAAGGAGCTTGAACATGC CCTGGAG	HK
HOXB13	NM_006361.5	NM_006361.5:1220	CCACCAGGGTTCCCAAAGAACCTGGCCCAGTCATAATCATTTCATCC TGACAGTGGCAATAATCACGATAACCAGTACTAGCTGCCATGATCG TTAGCCTC	
IL17RB	NM_018725.3	NM_018725.3:688	TCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAACAAACGCG AGCTTCAGTGGTGATTCCAGTGACTGGGGATAGTGAAGGTGCTACG GTGCAGCT	
IL6ST	NM_002184.2	NM_002184.2:2505	CAAAACACTTCGAGCACTGTCCAGTATTCTACCGTGGTACACAGTG GCTACAGACACCAAGTTCCGTCAGTCCAAGTCTTCTCAAGATCCGA GTCTACCC	
KIF2C	NM_006845.2	NM_006845.2:1020	GTTGTCTACAGGTTACAGCAAGGCCACTGGTACAGACAATCTTTG AAGGTGGAAAAGCAACTTGTTTTGCATATGGCCAGACAGGAAGTGG CAAGACAC	
KRT14	NM_000526.3	NM_000526.3:1365	GCAGTCATCCAGAGATGTGACCTCCTCCAGCCGCCAAATCCGCACC AAGGTCATGGATGTGCACGATGGCAAGGTGGTGTCCACCCACGAG CAGGTCCTT	
KRT17	NM_000422.1	NM_000422.1:1230	CTGACTCAGTACAAGAAAGAACCGGTGACCACCCGTCAGGTGCGTA CCATTGTGGAAGAGGTCCAGGATGGCAAGGTCATCTCCTCCCGCG AGCAGGTCC	
KRT5	NM_000424.2	NM_000424.2:130	CTGGTTCTCTTGCTCCACCAGGAACAAGCCACCATGTCTCGCCAGT CAAGTGTGTCCTTCCGGAGCGGGGGCAGTCGTAGCTTCAGCACCG CCTCTGCCA	

MAPT	NM_016835.3	NM_016835.3:1425	GCCGGGTCCCTCAACTCAAAGCTCGCATGGTCAGTAAAAGCAAAGA CGGGACTGGAAGCGATGACAAAAAGCCAAGACATCCACACGTTCC TCTGCTAA	HK
MDM2	NM_006878.2	NM_006878.2:280	GGTGAGGAGCAGGCAAATGTGCAATACCAACATGTCTGTACCTACT GATGGTGCTGTAACCACCTCACAGATTCCAGCTTCGGAACAAGAGA CCCTGGTT	
MELK	NM_014791.2	NM_014791.2:365	AGAGACAGCCAACAAAATATTCATGGTTCTTGAGTACTGCCCTGGA GGAGAGCTGTTTGACTATATAATTTCCCAGGATCGCCTGTCAGAAG AGGAGACC	
MGP	NM_000900.2	NM_000900.2:305	TCAATAGGGAAGCCTGTGATGACTACAGACTTTGCGAACGCTACGC CATGGTTTATGGATACAATGCTGCCTATAATCGCTACTTCAGGAAGC GCCGAGG	
MIA	NM_006533.1	NM_006533.1:265	CCGGGGCCAAGTGGTGTATGTCTTCTCCAAGCTGAAGGGCCGTGG GCGGCTCTTCTGGGGAGGCAGCGTTCAGGGAGATTACTATGGAGA TCTGGCTGCT	
MKI67	NM_002417.2	NM_002417.2:2005	GCTTCCAGCAGCAAATCTCAGACAGAGGTTCTTAAGAGAGGAGGA GAAAGAGTGGCAACCTGCCTTCAAAGAGAGTGTCTATCAGCCGAA GTCAACATG	
MLPH	NM_024101.4	NM_024101.4:1695	GAGGAAGTCAAACCTCCCGATATTTCTCCCTCGAGTGGCTGGGAAA CTTGGCAAGAGACCAGAGGACCCAAATGCAGACCCTTCAAGTGAG GCCAAGGCA	
MMP11	NM_005940.3	NM_005940.3:702	AGCAGCCAAGGCCCTGATGTCCGCCTTCTACACCTTTTCGCTACCCA CTGAGTCTCAGCCCAGATGACTGCAGGGGCGTTCAACACCTATATG GCCAGCCC	
MRPL19	NM_014763.3	NM_014763.3:385	ACAGCTGACCCATATGCCAGTGGAAAAATCAGCCAGTTTCTGGGGA TTTGCATTCAGAGATCAGGAAGAGGACTTGGAGCTACTTTCATCCTT AGGAATG	
MYBL2	NM_002466.2	NM_002466.2:675	GCAACCGCTGGGCCGAGATCGCCAAGATGTTGCCAGGGAGGACAG ACAATGCTGTGAAGAATCACTGGAACCTCTACCATCAAAGGAAGGT GGACACAGG	
MYC	NM_002467.3	NM_002467.3:1615	CACCGAGGAGAATGTCAAGAGGCGAACACACAACGTCTTGGAGCG CCAGAGGAGGAACGAGCTAAACGGAGCTTTTTTGGCCTGCGTGAC CAGATCCCC	

NAT1	NM_000662.4	NM_000662.4:0	AGCACTTCCTCATAGACCTTGGATGTGGGAGGATTGCATTCAAGCCAGGAAGA AGTTCTGTTGCCGGCTGAAATAACCTGAATTCAAGCCAGGAAGA AGCAGCAA	
NDC80	NM_006101.1	NM_006101.1:90	AAAAGGTCATAAGCATGAAGCGCAGTTTCAAGTTTCCAGCGGTGGTGC TGGCCGCCTCTCCATGCAGGAGTTAAGATCCCAGGATGTAAATAAA CAAGGCCT	
NEK2	NM_002497.3	NM_002497.3:480	AGAGTTTGTCTTCGAGTGATGACTCAGTTGACTCTGGCCCTGAAG GAATGCCACAGACGAAGTGATGGTGGTCATACCGTATTGCATCGGG ATCTGAAA	
NUF2	NM_145697.1	NM_145697.1:215	GCCTGGCGGTGTTTTTCGTCGTGCTCAGCGGTGGGAGGAGGCGGAA GAAACCAGAGCCTGGGAGATTAACAGGAACTTCCAAGATGGAAAC TTTGTCTTT	
OAZ1	NM_004152.2	NM_004152.2:313	GGTGGGCGAGGGAATAGTCAGAGGGATCACAATCTTTCAGCTAACT TATTCTACTCCGATGATCGGCTGAATGTAACAGAGGAACTAACGTC CAACGACA	HK
ORC6	NM_014321.2	NM_014321.2:580	GACTGTGTAAACAACACTAGAGAAGATTGGACAGCAGGTCGACAGAGA ACCTGGAGATGTAGCTACTCCACCACGGAAGAGAAAGAAGATAGTG GTTGAAGC	
PGR	NM_000926.2	NM_000926.2:3165	GGGATGAAGCATCAGGCTGTCATTATGGTGTCTTACCTGTGGGAG CTGTAAGGTCTTCTTTAAGAGGGCAATGGAAGGGCAGCACAACTAC TTATGTGC	
PHGDH	NM_006623.2	NM_006623.2:505	GCGACGGCTTCGATGAAGGACGGCAAATGGGAGCGGAAGAAGTTC ATGGGAACAGAGCTGAATGGAAAGACCCTGGGAATTCTTGGCCTG GGCAGGATTG	
PSMC4	NM_006503.2	NM_006503.2:300	CATCGGACAATTTCTGGAGGCTGTGGATCAGAATACAGCCATCGTG GGCTCTACCACAGGCTCCAACCTATTATGTGCGCATCCTGAGCACCA TCGATCGG	HK
PTTG1	NM_004219.2	NM_004219.2:202	CACCAGCCTTACCTAAAGCTACTAGAAAGGCTTTGGGAACTGTCAA CAGAGCTACAGAAAAGTCTGTAAAGACCAAGGGACCCCTCAAACAA AAACAGCC	
PUM1	NM_001020658.1	NM_001020658.1:640	CTGGGGAACATCAGATCATTCAAGTTTCCCAGCCAATCATGGTGCAG AGAAGACCTGGTCAGAGTTTCCATGTGAACAGTGAGGTCAATTCTG TACTGTCC	

RACGAP1	NM_013277.3	NM_013277.3:1850	CAGTGACAATGTTACAGGACATCAAGCGTCAACCCAAGGTGGTTGAGCGCCTGCTTTCCTTGCCTCTGGAGTATTGGAGTCAGTTCATGATGTGGAGCA	
RBBP8	NM_002894.2	NM_002894.2:760	AATGATCAACAGCATCAAGCAGCTGAGCTTGAATGTGAGGAAGACGTTATTCCAGATTCACCGATAACAGCCTTCTCATTTTCTGGCGTTAACCGGCTAC	
RPL37A	NM_000998.4	NM_000998.4:298	CTTCCGCTGTACGGTAAAGTCCGCCATCAGAAGACTGAAGGAGTTGAAAGACCAGTAGACGCTCCTCTACTCTTTGAGACATCACTGGCCTATAATAAA	HK
RPLP0	NM_001002.3	NM_001002.3:250	CGAAATGTTTTATTGTGGGAGCAGACAATGTGGGCTCCAAGCAGATGCAGCAGATCCGCATGTCCCTTCGCGGGAAGGCTGTGGTGCTGATGGGCAAGAA	HK
RRM2	NM_001034.1	NM_001034.1:490	TTCCTTTTGGACCGCCGAGGAGGTTGACCTCTCCAAGGACATTTCAGCACTGGGAATCCCTGAAACCCGAGGAGAGATATTTTATATCCCATGTTCTGGCT	
SCUBE2	NM_020974.1	NM_020974.1:1835	CGTAAAGCCATCCGCACGCTCAGAAAGGCCGTCCACAGGGAGCAGTTTCACCTCCAGCTCTCAGGCATGAACCTCGACGTGGCTAAAAAGCCTCCCAGAA	
SDHA	NM_004168.1	NM_004168.1:230	TGGAGGGGGCAGGCTTGCGAGCTGCATTTGGCCTTTCTGAGGCAGGGTTTAATACAGCATGTGTTACCAAGCTGTTTCCTACCAGGTCACACA CTGTTGCA	HK
SF3A1	NM_005877.4	NM_005877.4:1485	GATGATGAGGTGTACGCACCAGGTCTGGATATTGAGAGCAGCTTGAGCAGTTGGCTGAGCGGCGTACTGACATCTTCGGTGTAGAGGAAACAGCCATTG	HK
SFRP1	NM_003012.3	NM_003012.3:1320	GTGGGTACACACACGCACTGCGCCTGTCAGTAGTGGACATTGTAA TCCAGTCGGCTTGTTCTTGCAGCATTCCCGCTCCCTTCCCTCCATAGCCACGCT	
SLC39A6	NM_012319.2	NM_012319.2:1580	GATCGAACTGAAGGCTATTTACGAGCAGACTCACAAGAGCCCTCCC ACTTTGATTCTCAGCAGCCTGCAGTCTTGGAAGAAGAAGAGGTCATGATAGCTC	
STC2	NM_003714.2	NM_003714.2:2825	ATTTCTATGTGTAATTTCTGAGCCATTGTACTGTCTGGGCTGGGGG GGACACTGTCCAAGGGAGTGGCCCCTATGAGTTTATATTTTAACCA CTGCTTCA	

TFRC	NM_003234.1	NM_003234.1:1220	CAGTTTCCACCATCTCGGTCATCAGGATTGCCTAATATACCTGTCCA GACAATCTCCAGAGCTGCTGCAGAAAAGCTGTTTGGGAATATGGAA GGAGACT	HK
TMEM45B	NM_138788.3	NM_138788.3:730	CTGGCTGCCCTCAGCATTGTGGCCGTCAACTATTCTTGTCTTACTG CCTTTTGACTCGGATGAAGAGACACGGAAGGGGAGAAATCATTGGA ATTCAGA	
TYMS	NM_001071.1	NM_001071.1:395	TGCTAAAGAGCTGTCTTCCAAGGGAGTGAAAATCTGGGATGCCAAT GGATCCCGAGACTTTTTGGACAGCCTGGGATTCTCCACCAGAGAAG AAGGGGAC	
UBC	NM_021009.3	NM_021009.3:1875	TGCAGATCTTCGTGAAGACCCTGACTGGTAAGACCATCACTCTCGA AGTGGAGCCGAGTGACACCATTGAGAATGTCAAGGCAAAGATCCAA GACAAGGA	HK
UBE2C	NM_007019.2	NM_007019.2:445	GTCTGCCCTGTATGATGTCAGGACCATTCTGCTCTCCATCCAGAGC CTTCTAGGAGAACCCAACATTGATAGTCCCTTGAACACACATGCTG CCGAGCTC	
UBE2T	NM_014176.1	NM_014176.1:50	GTGTCAGCTCAGTGCATCCCAGGCAGCTCTTAGTGTGGAGCAGTGA ACTGTGTGTGGTTCCTTCTACTTGGGGATCATGCAGAGAGCTTCAC GTCTGAAG	
HK housekeeping gene				

Supplementary table 2. Demographic data of breast cancer patients in the study.

MenCER (M) or Vietnamese (V) study	Age in years	Number of positive lymph nodes	Tumour grade	Tumour size	Tumour type	PgR status
V	44	0	2	20	IDC	+
V	47	1	1	20	IDC	-
V	49	0	2	30	IDC	+
V	33	2	2	30	IDC	+
V	36	1	2	12	IDC	+
V	36	1	2	15	IDC	+
V	39	0	2	15	IDC	+
V	41	0	1	41	IDC	+
M	40	0	3	50	IDC	+
M	40	0	3	38	IDC	+
M	43	0	1	25	IDC	+
M	37	0	3	11	IDC	+
M	34	0	2	10	IDC	+
M	49	2	1	17	IDC	+
M	49	1	2	41	IDC	+
M	43	0	2	10	IDC	+
M	45	0	2	32	IDC	+
M	42	0	3	35	IDC	+
M	48	0	3	30	IDC	+
M	46	0	3	53	IDC	+
M	49	1	2	50	IDC	+
M	44	0	2	58	lobular	+
M	49	0	2	15	IDC	-
M	49	0	1	9	IDC	+

M	44	0	1	15	IDC	+
M	44	0	3	10	lobular	+
M	43	0	2	32	IDC	-
M	43	0	2	25	IDC	+
M	41	1	3	34	IDC	+
M	47	0	2	24	IDC	+

IDC intraductal carcinoma, *PgR* progesterone receptor