Supplementary Table 1: Summary of tumor-bearing NIC/ShcA$^{fl/fl}$ transgenic females.

Mouse Number	Parity	Number of Litters	Number of Tumors
2749	**Multiparous**	**10**	**2 (BT1, BT2)**
6262	**Multiparous**	**8**	**1**
8033	**Multiparous**	**6**	**1**
8296	**Multiparous**	**5**	**2 (BT1, BT2)**
9094	**Multiparous**	**9**	**1**
1474	**Multiparous**[1]	**0**	**2 (BT1, BT2)**
5479	**Virgin**[2]	**0**	**2 (BT1, BT2)**
5863	**Virgin**[2]	**0**	**2 (BT1, BT2)**

1. This female was mated with a male from 8 weeks of age but never had a visible pregnancy. She was nonetheless placed into the multiparous cohort to account for the possibility of a failed pregnancy.
2. These females were never mated with a male and thus are part of the virgin cohort.

Supplementary Table 2: Differentially-expressed chemokines and their receptors in NIC/ShcA-null mammary tumors.

Gene[c]	Chemotactic Gene Function	Avg FC[b]	2749BT1[a]	2749BT2[a]	6262[a]	1474BT1[aa]	1474BT2[a]	8296BT1[a]	8296BT2[a]	9094[a]
Ccl2	monocytes, basophils, memory T cells, dendritic cells	1.7 ± 0.7	1.3	1.5	**3.1**	1.3	1.4	2.1	**2.1**	1.0
Ccl3	polymorphonuclear leukocytes	1.8 ± 1	1.8	1.4	**2.6**	1.1	0.7	**3.8**	1.5	1.7
Ccl5	monocytes, eosinophils, memory T cells, dendritic cells	2.7 ± 2.6	1.3	1.7	1.4	1.4	1.3	1.8	**8.9**	**3.4**
Ccl7	monocytes	1.8 ± 1.3	1.2	1.3	**4.9**	1.1	1.0	**2.1**	1.7	0.9
Ccl8	monocytes, T cells, NK cells, mast cells, eosinophils, basophils	2 ± 1.5	0.9	1.7	**5.4**	**2.4**	1.5	1.8	1.7	0.5
Ccl12	monocytes, eosinophils	1.5 ± .7	1.2	1.0	**3.1**	1.0	0.8	1.7	1.7	1.1
Ccl17	T cells	2 ± 1.4	1.0	1.4	**2.3**	1.2	1.7	**5.0**	**2.9**	0.9
Ccl19	B cells and T cells	3.9 ± 4.1	1.3	1.8	**3.2**	2.5	**2.4**	**4.9**	**13.7**	1.6
Ccl22	monocytes, dendritic cells, NK cells, activated T cells	4.8 ±0 8	**3.1**	1.2	**3.5**	3.2	1.4	0.9	**24.3**	**0.4**
Ccl24	resting T cells, eosinophils	1.4 ± 0.9	0.6	0.9	**3.0**	1.6	0.8	**2.4**	1.5	**0.5**
Ccl25	activated macrophages, dendritic cells	0.9 ± 0.7	**0.5**	**0.4**	**0.4**	0.8	0.8	**2.6**	1.4	0.6
Ccl27	memory T cells	0.8 ± 0.2	0.9	0.8	0.8	0.6	0.6	1.2	1.0	0.6
Cxcl1	neutrophils	0.9 ± 0.6	**0.4**	1.1	**2.1**	**0.5**	**0.4**	0.9	0.7	1.0
Cxcl5	neutrophils	0.9 ± 0.9	**0.2**	0.8	**2.8**	0.7	**0.2**	1.2	1.0	**0.5**
Cxcl9	NK cells, T cells; IFNγ-inducible	5.1 ± 2.8	**3.9**	**5.3**	**2.3**	**7.7**	**6.9**	**2.6**	**9.8**	**2.2**
Cxcl10	NK cells, T cells; IFNγ-inducible	4.3 ± 1.6	**4.4**	**6.9**	**2.4**	**3.5**	**2.2**	**5.0**	**5.2**	**4.6**
Cxcl11	activated T cells; IFNγ-inducible	3.7 ± 2.7	**2.5**	**9.7**	1.9	**3.6**	1.9	1.3	**5.2**	**3.6**
Cxcl12	endothelial progenitor cells	1.5 ± 0.7	1.5	**2.6**	**2.1**	0.7	**0.4**	1.2	1.8	1.7
Cxcl13	B cells	7.1 ± 5.9	1.2	**3.0**	**2.2**	**6.5**	**4.3**	**12.3**	**18.5**	**8.7**
Cxcl14	monocytes, dendritic cells, NK cells	2.6 ± 1.5	1.6	**2.3**	**5.7**	1.9	1.7	**2.3**	**3.8**	1.4
Cxcl15	neutrophils	1.8 ± 1.1	0.9	1.4	**2.3**	0.8	1.9	1.5	**4.2**	1.0
Cxcl16	T cells, NKT cells; IFNγ-inducible	1.4 ± 0.6	0.8	1.6	**2.7**	1.0	0.8	1.3	1.3	1.5
Cx3cl1	NK and T cells (soluble); endothelial cells (mb bound)	0.5 ± 0.2	**0.4**	0.7	0.8	**0.4**	**0.5**	**0.4**	**0.4**	0.6
Xcl1	T cells	1.0 ± 0.5	1.5	0.6	**0.4**	1.3	1.1	0.7	1.6	0.7
Ccr2	Ccl2, Ccl7, Ccl8, Ccl11, Ccl13 and Ccl16 receptor	3.0 ± 2.3	1.5	1.3	**4.9**	**2.5**	1.1	**7.5**	**4.0**	1.1
Ccr3	Ccl11, Ccl13, Ccl24, Ccl26 and Ccl28 receptor	1,2 ± 0.3	1.3	1.2	1.8	1.2	0.7	1.2	1.1	1.1
Ccr4	Ccl17 and Ccl22 receptor	1.4 ± 0.4	1.6	1.1	1.1	1.4	**2.2**	1.2	1.2	1.2
Ccr5	Ccl4, Ccl5, Ccl8, Ccl11, Ccl13 and Ccl16 receptor	1.6 ± 0.6	1.2	1.7	**2.7**	1.4	1.1	**2.1**	1.6	1.3
Ccr7	Ccl19 receptor	4.5 ± 6.5	**2.2**	1.4	**4.9**	**2.0**	**2.6**	0.9	**20.1**	1.3
Ccr9	Ccl25 receptor	2.0 ±1.4	1.6	1.2	1.5	1.3	1.2	**4.8**	**3.4**	1.0
Cxcr3	Cxcl9, Cxcl10 and Cxcl11 receptor	2.7 ± 2.1	1.4	1.5	**2.2**	**2.0**	1.8	**4.1**	**7.2**	1.1
Cxcr4	Cxcl12 receptor	2.0 ± 0.8	**2.0**	0.6	1.4	**2.4**	**2.6**	**2.9**	**2.4**	1.7
Cxcr6	Cxcl16 receptor	2.8 ± 2.4	1.2	1.2	2.0	**2.5**	**2.2**	**3.0**	**8.5**	1.3
Xcr1	Xcl1 receptor	1.5 ± 0.5	1.8	0.9	1.6	1.8	1.2	1.2	**2.3**	0.8
Cx3cr1	Cx3cl1 receptor	0.6 ± 0.3	**0.4**	1.0	1.1	**0.5**	**0.4**	**0.4**	**0.4**	**0.4**

[a] Fold change (log2) from the Agilent array for each individual NIC/ShcA$^{fl/fl}$ tumor relative to a pool of five NIC/ShcA$^{+/+}$ tumors.

[b] Average fold change for each gene over all eight NIC/ShcA$^{fl/fl}$ tumors.

[c] Genes that are differentially regulated, at least two fold, in at least 50% of the NIC/ShcA-null tumors are highlighted

Supplementary Table 3: A 43 gene ShcA-regulated immune signature (SRIS) that is differentially regulated in NIC/ShcA$^{fl/fl}$ mammary tumors^{a}

Mouse Gene	Human Gene	Entrez ID	Gene Function	# DE tumors^{b}	Avg. FC^{c}	Avg FC (DE)^{d}	Avg. P Value^{e}	Ref
CD247	CD247	NM198053	Zeta chain of the TCR;	6/8	3.1 ± 4.2	3.7 ± 4.7	0.0008	(1)
CD3e	CD3E	NM000733	Epsilon subunit of the TCR-CD3 complex	Validated by IHC†	2.4 ± 1.6	N/A	N/A	(2)
CD4	CD4	NM000616	expressed by Th cells; binds MHC class II	7/8	3 ± 3.8	3.2 ± 4	0.0006	(3)
CD28	CD28	NM006139	Co-stimulatory molecule in T cells	qRT-PCR†	3.5± 4.4	6.9± 6.1	0.001	(4)
Ctla4	CTLA4	NM005214	T cell co-inhibitory molecule	6/8	3 ± 2.7	3.5 ± 2.8	<0.0001	(4)
Cxcl11	CXCL11	NM005409	Chemotactic for T cells; induced by IFNγ signaling	7/8	3.7 ± 2.8	4.1 ± 2.8	0.0001	(5)
Cxcl13	CXCL13	NM006419	Chemotactic for B cells	7/8	7.1 ± 6	7.9 ± 5.8	0.0002	(5)
Cxcl9	CXCL9	NM002416	Chemotactic for T cells; induced by IFNγ signaling	8/8	5 ± 2.8	5 ± 2.8	0.0005	(5)
Cxcr3	CXCR3	NM001142797	Receptor for CXCL9, CXCL10 and CXCL11	7/8	2.7 ± 2.1	2.9 ± 2.1	0.005	(5)
H2-Aa	HLA-DQA1	NM002122	MHC class II molecule	8/8	2.5 ± 1.3	2.5 ± 1.3	0.0005	(6)
IL1b	IL1B	NM00576	Mediator of the inflammatory immune response	8/8	3.6 ± 3.5	3.6 ± 3.5	<0.0001	(7)
Itk	ITK	NM005546	IL2-inducible kinase expressed in T cells	7/8	4.6 ± 7.3	5.1 ± 7.1	0.005	(8)
Lag3	LAG3	NM002286	MHC class II binding CD4 homologue	6/8	3 ± 2.4	3.5 ± 2.6	0.007	(9)
Lck	LCK	NM001042771	T cell specific Src family member	7/8	3.7 ± 3.6	4 ± 3.8	0.002	(10)
Nfatc2	NFATC2	NM01136021	NFAT family member expressed in B and T cells	7/8	0.4 ± 0.2	0.3 ± 0.1	0.001	(11)
Ppia	PPIA	NM021130	cyclosporine A-mediated immunosuppression	8/8	3.5 ± 2.1	3.5 ± 2.1	<0.0001	(12)
Ptprc	PTPRC	NM002838	Hematopoeitic-specific protein tyrosine phosphatase	8/8	1.8 ± 0.9	1.8 ± 0.9	0.004	(13)
Slamf6	SLAMF6	NM052931	Expressed on NK, B and T cells	7/8	2.1 ± 2.3	2.2 ± 2.5	0.01	(14)
Slamf7	SLAMF7	NM021181	Expressed on NK, B and T cells	7/8	2.5 ± 1.8	2.6 ± 1.9	0.01	(14)
Slamf9	SLAMF9	NM033438	Expressed on NK, B and T cells	7/8	1.6 ± 0.5	1.7 ± 0.4	0.007	(14)
Tcra	TCRA	NC000014.8	T cell receptor, alpha chain	8/8	4.7 ± 8.1	4.7 ± 8.1	0.004	(15)
Tnfrsf19l	RELT	NM032871	Hematopoietic TNFR family member	7/8	1.6 ± 0.9	1.7 ± 1	0.008	(16)
Tnfrsf7	CD27	NM001242	TNFR family member required for T cell immunity	6/8	2.5 ± 2.5	3 ± 2.7	0.003	(17)
Vtcn1	VTCN1	NM024626	Co-stimulatory molecule on APCs	7/8	2.1 ± 1.4	2.2 ± 1.4	0.01	(18)
Atrn	ATRN	NM139322	Cytokine/receptor interactions in activated T cells	8/8	1.4 ± 0.4	1.4 ± 0.4	0.003	(19)
CD69	CD69	NM001781	Induced in T cells following antigen activation	6/8	2.4 ± 2.2	2.8 ± 2.5	0.0005	(20)
Icos	ICOS	NM012092	Induced in T cells following antigen activation	8/8	3.8 ± 4.8	3.8 ± 4.8	0.003	(21)
IL7r	IL7R	NM002185	Blocks apoptosis of antigen-activated T cells	6/8	3.6 ± 2.8	4.3 ± 2.8	0.01	(22)
B2m	B2M	NM004048	Beta chain of MHC class I molecules	7/8	3.1 ± 1.8	3.3 ± 1.7	0.007	(23)
CD8b1	CD8B	NM172099	expressed by CTLs; binds MHC class I	6/8	3.1 ± 4.4	3.8 ± 4.9	0.01	(3)
Gzmb	GZMB	NM004131	Serine protease expressed by CTL and NK cells	7/8	0.6 ± 0.2	0.6 ± 0.2	0.004	(24)
Ifng	IFNG	NM000619	Th1 cytokine	8/8	2 ± 1	2 ± 1	0.007	(25)
Il12b	IL12B	NM002187	Cytokine that sustains a Th1 response	6/8	1.9 ± 0.7	2.1 ± 0.7	0.002	(26)
Lilrb3	LILRB3	NM001081450	Binds MHC class I; inhibits immune response	6/8	1.9 ± 1.4	2.2 ± 1.5	0.002	(27)
Tia1	TIA1	NM022037	Nucleolytic activity against CTL target cells	8/8	0.8 ± 1.5	0.8 ± 1.5	0.0007	(28)
CD72	CD72	NM001782	Regulates B cell signaling	7/8	2 ± 0.6	2.1 ± 0.5	0.01	(29)
Igh-4	IGHG1	NC000014.8	Ig heavy chain constant gamma 1 region	8/8	7.4 ± 4.9	7.4 ± 4.9	0.005	(30)
Igh-6	IGHM	NC000014.8	Ig heavy chain constant mu region	8/8	2.8 ± 2.9	2.8 ± 2.9	0.001	(30)
Igh-1a	IGHG2	NC000014.8	Ig heavy chain constant gamma 2 region	qRT-PCR†	1.9 ± 0.8	2.5 ± 0.7	0.008	(30)
IgJ	IGJ	NC000004.11	Linker protein Ig alpha and mu polypeptides	8/8	13.8 ± 11.7	13.8 ± 11.7	<0.0001	(31)
IL4	IL4	NM00589	Important for Th2 cell differentiation	7/8	1.7 ± 0.5	1.6 ± 0.5	0.002	(32)
C1s	C1S	NM001734	Serine protease; initiates complement cascade	7/8	2 ± 1	2.3 ± 1.3	0.01	(33)
C3	C3	NM000064	Activation of the complement system	7/8	3 ± 2.2	3.3 ± 2.1	0.0008	(33)

[a] The 43 gene SRIS is composed of genes that are differentially expressed in NIC/ShcA$^{fl/fl}$ tumors and are associated with pan T cells (yellow), activated T cells (blue), the Th1/CTL response (green) and the Th2/humoral immune response (red).

[b] Number of NIC/ShcA$^{fl/fl}$ tumors in which each gene is differentially expressed by Agilent arrays.

[c] Average fold change (log2 values) on Agilent arrays over all 8 individual NIC/ShcA$^{fl/fl}$ tumors relative to a pool of 5 NIC/ShcA$^{+/+}$ tumors.
[d] Average fold change (log2 values) on Agilent arrays NIC/ShcA$^{fl/fl}$ tumors that are differentially expressed ($p \leq 0.01$) relative to a pool of 5 NIC/ShcA$^{+/+}$ tumors.
[e] Average p value in NIC/ShcA$^{fl/fl}$ tumors in which the gene is differentially expressed.
[f] Three genes were not differentially expressed in 6/8 of of NIC/ShcA$^{fl/fl}$ tumors based on Agilent arrays but validated as being differentially expressed by qRT-PCR or IHC analyses and thus are included within the SRIS.

References

1. Weissman AM, Hou D, Orloff DG, Modi WS, Seuanez H, O'Brien SJ, et al. Molecular cloning and chromosomal localization of the human T-cell receptor zeta chain: distinction from the molecular CD3 complex. Proc Natl Acad Sci U S A. 1988;85:9709-13.
2. Frank SJ, Samelson LE, Klausner RD. The structure and signalling functions of the invariant T cell receptor components. Semin Immunol. 1990;2:89-97.
3. Miceli MC, Parnes JR. Role of CD4 and CD8 in T cell activation and differentiation. Adv Immunol. 1993;53:59-122.
4. Rudd CE, Taylor A, Schneider H. CD28 and CTLA-4 coreceptor expression and signal transduction. Immunol Rev. 2009;229:12-26.
5. Vandercappellen J, Van Damme J, Struyf S. The role of CXC chemokines and their receptors in cancer. Cancer Lett. 2008;267:226-44.
6. Mach B, Steimle V, Martinez-Soria E, Reith W. Regulation of MHC class II genes: lessons from a disease. Annu Rev Immunol. 1996;14:301-31.
7. Roy D, Sarkar S, Felty Q. Levels of IL-1 beta control stimulatory/inhibitory growth of cancer cells. Front Biosci. 2006;11:889-98.
8. Readinger JA, Mueller KL, Venegas AM, Horai R, Schwartzberg PL. Tec kinases regulate T-lymphocyte development and function: new insights into the roles of Itk and Rlk/Txk. Immunol Rev. 2009;228:93-114.
9. Triebel F. LAG-3: a regulator of T-cell and DC responses and its use in therapeutic vaccination. Trends Immunol. 2003;24:619-22.
10. Salmond RJ, Filby A, Qureshi I, Caserta S, Zamoyska R. T-cell receptor proximal signaling via the Src-family kinases, Lck and Fyn, influences T-cell activation, differentiation, and tolerance. Immunol Rev. 2009;228:9-22.
11. Peng SL, Gerth AJ, Ranger AM, Glimcher LH. NFATc1 and NFATc2 together control both T and B cell activation and differentiation. Immunity. 2001;14:13-20.
12. Colgan J, Asmal M, Yu B, Luban J. Cyclophilin A-deficient mice are resistant to immunosuppression by cyclosporine. J Immunol. 2005;174:6030-8.
13. Hermiston ML, Zikherman J, Zhu JW. CD45, CD148, and Lyp/Pep: critical phosphatases regulating Src family kinase signaling networks in immune cells. Immunol Rev. 2009;228:288-311.
14. Ma CS, Nichols KE, Tangye SG. Regulation of cellular and humoral immune responses by the SLAM and SAP families of molecules. Annu Rev Immunol. 2007;25:337-79.
15. Minden MD, Mak TW. The structure of the T cell antigen receptor genes in normal and malignant T cells. Blood. 1986;68:327-36.
16. Sica GL, Zhu G, Tamada K, Liu D, Ni J, Chen L. RELT, a new member of the tumor necrosis factor receptor superfamily, is selectively expressed in hematopoietic tissues and activates transcription factor NF-kappaB. Blood. 2001;97:2702-7.
17. Croft M. The role of TNF superfamily members in T-cell function and diseases. Nat Rev Immunol. 2009;9:271-85.
18. Yi KH, Chen L. Fine tuning the immune response through B7-H3 and B7-H4. Immunol Rev. 2009;229:145-51.
19. Duke-Cohan JS, Tang W, Schlossman SF. Attractin: a cub-family protease involved in T cell-monocyte/macrophage interactions. Adv Exp Med Biol. 2000;477:173-85.
20. Ziegler SF, Ramsdell F, Hjerrild KA, Armitage RJ, Grabstein KH, Hennen KB, et al. Molecular characterization of the early activation antigen CD69: a type II membrane glycoprotein related to a family of natural killer cell activation antigens. Eur J Immunol. 1993;23:1643-8.
21. van Berkel ME, Oosterwegel MA. CD28 and ICOS: similar or separate costimulators of T cells? Immunol Lett. 2006;105:115-22.

22. Colpitts SL, Dalton NM, Scott P. IL-7 receptor expression provides the potential for long-term survival of both CD62Lhigh central memory T cells and Th1 effector cells during Leishmania major infection. J Immunol. 2009;182:5702-11.
23. Cresswell P, Ackerman AL, Giodini A, Peaper DR, Wearsch PA. Mechanisms of MHC class I-restricted antigen processing and cross-presentation. Immunol Rev. 2005;207:145-57.
24. Chowdhury D, Lieberman J. Death by a thousand cuts: granzyme pathways of programmed cell death. Annu Rev Immunol. 2008;26:389-420.
25. Schroder K, Hertzog PJ, Ravasi T, Hume DA. Interferon-gamma: an overview of signals, mechanisms and functions. J Leukoc Biol. 2004;75:163-89.
26. Del Vecchio M, Bajetta E, Canova S, Lotze MT, Wesa A, Parmiani G, et al. Interleukin-12: biological properties and clinical application. Clin Cancer Res. 2007;13:4677-85.
27. Anderson KJ, Allen RL. Regulation of T-cell immunity by leucocyte immunoglobulin-like receptors: innate immune receptors for self on antigen-presenting cells. Immunology. 2009;127:8-17.
28. Anderson P. TIA-1: structural and functional studies on a new class of cytolytic effector molecule. Curr Top Microbiol Immunol. 1995;198:131-43.
29. Wu HJ, Bondada S. Positive and negative roles of CD72 in B cell function. Immunol Res. 2002;25:155-66.
30. Berman JE, Mellis SJ, Pollock R, Smith CL, Suh H, Heinke B, et al. Content and organization of the human Ig VH locus: definition of three new VH families and linkage to the Ig CH locus. EMBO J. 1988;7:727-38.
31. Niles MJ, Matsuuchi L, Koshland ME. Polymer IgM assembly and secretion in lymphoid and nonlymphoid cell lines: evidence that J chain is required for pentamer IgM synthesis. Proc Natl Acad Sci U S A. 1995;92:2884-8.
32. Li-Weber M, Krammer PH. Regulation of IL4 gene expression by T cells and therapeutic perspectives. Nat Rev Immunol. 2003;3:534-43.
33. Duncan RC, Wijeyewickrema LC, Pike RN. The initiating proteases of the complement system: controlling the cleavage. Biochimie. 2008;90:387-95.

Supplementary Table 4: The SRIS functions as an independent prognostic marker within the HER2 and basal subtypes among 12 publically available datasets.

	Variable	Hazard Ratio	Standard Error	P-Value
Luminal A	Grade II	1.732	0.287	0.056
	Grade III	2.617	0.392	0.014*
	LN +ve	1.717	0.246	0.028*
	Her2+	2.505	0.530	0.083
	ER+	0.853	0.531	0.76
	SRIS-Low	**0.751**	**0.386**	**0.46**
Luminal B	Grade II	1.999	0.328	0.034*
	Grade III	2.556	0.339	0.0056**
	LN +ve	1.893	0.187	0.0007**
	Her2+	0.979	0.601	0.97
	ER+	0.524	0.394	0.1
	SRIS-Low	**1.394**	**0.284**	**0.24**
Normal	Grade II	2.075	0.463	0.12
	Grade III	1.917	0.621	0.29
	LN +ve	2.252	0.361	0.025*
	Her2+	0.541	0.643	0.34
	ER+	0.430	0.417	0.043*
	SRIS-Low	**2.246**	**0.647**	**0.21**
Her2	Grade II	1.627	1.007	0.31
	Grade III	1.609	0.979	0.33
	LN +ve	1.240	1.017	0.31
	Her2+	1.043	0.180	0.86
	ER+	0.768	-1.184	0.24
	SRIS-Low	**2.088**	**3.068**	**0.002****
Basal	Grade II	1.044	0.614	0.94
	Grade III	1.000	0.599	1.0
	LN +ve	1.373	0.205	0.12
	Her2+	0.515	0.460	0.15
	ER+	0.840	0.209	0.4
	SRIS-Low	**2.551**	**0.210**	**0.000009****

*p<0.05 **p<0.01

Supplementary Table 5: Published datasets used to interrogate the relationship between expression of the SRIS and patient outcome.

Dataset	Luminal A[a]	Luminal B[a]	Normal[a]	HER2[a]	Basal[a]	Total[a]	Reference
Anders	16	21	10	9	22	78	(1)
Bild	26	35	21	37	39	158	(2)
Chin	28	31	10	20	29	118	(3)
Desmedt	59	46	18	28	47	198	(4)
Ivshina	66	61	35	38	49	249	(5)
Loi	98	111	66	48	91	414	(6)
Van de Vijver	97	66	18	56	58	295	(7)
Parker	53	54	18	34	66	225	(8)
Pawitan	35	34	32	29	29	159	(9)
Schmidt	63	34	35	30	38	200	(10)
Sotiriou	16	32	19	13	21	101	(11)
Wang	72	72	29	48	65	286	(12)
	629	**597**	**311**	**390**	**554**	**2481**	

[a] Total number of patients classified within each group

References

1. Anders CK, Acharya CR, Hsu DS, Broadwater G, Garman K, Foekens JA, et al. Age-specific differences in oncogenic pathway deregulation seen in human breast tumors. PLoS One. 2008;3:e1373.
2. Bild AH, Yao G, Chang JT, Wang Q, Potti A, Chasse D, et al. Oncogenic pathway signatures in human cancers as a guide to targeted therapies. Nature. 2006;439:353-7.
3. Chin K, DeVries S, Fridlyand J, Spellman PT, Roydasgupta R, Kuo WL, et al. Genomic and transcriptional aberrations linked to breast cancer pathophysiologies. Cancer Cell. 2006;10:529-41.
4. Desmedt C, Piette F, Loi S, Wang Y, Lallemand F, Haibe-Kains B, et al. Strong time dependence of the 76-gene prognostic signature for node-negative breast cancer patients in the TRANSBIG multicenter independent validation series. Clin Cancer Res. 2007;13:3207-14.
5. Ivshina AV, George J, Senko O, Mow B, Putti TC, Smeds J, et al. Genetic reclassification of histologic grade delineates new clinical subtypes of breast cancer. Cancer Res. 2006;66:10292-301.
6. Loi S, Haibe-Kains B, Desmedt C, Wirapati P, Lallemand F, Tutt AM, et al. Predicting prognosis using molecular profiling in estrogen receptor-positive breast cancer treated with tamoxifen. BMC Genomics. 2008;9:239.
7. van de Vijver MJ, He YD, van't Veer LJ, Dai H, Hart AA, Voskuil DW, et al. A gene-expression signature as a predictor of survival in breast cancer. N Engl J Med. 2002;347:1999-2009.
8. Parker JS, Mullins M, Cheang MC, Leung S, Voduc D, Vickery T, et al. Supervised risk predictor of breast cancer based on intrinsic subtypes. J Clin Oncol. 2009;27:1160-7.
9. Pawitan Y, Bjohle J, Amler L, Borg AL, Egyhazi S, Hall P, et al. Gene expression profiling spares early breast cancer patients from adjuvant therapy: derived and validated in two population-based cohorts. Breast Cancer Res. 2005;7:R953-64.
10. Schmidt M, Bohm D, von Torne C, Steiner E, Puhl A, Pilch H, et al. The humoral immune system has a key prognostic impact in node-negative breast cancer. Cancer Res. 2008;68:5405-13.
11. Sotiriou C, Wirapati P, Loi S, Harris A, Fox S, Smeds J, et al. Gene expression profiling in breast cancer: understanding the molecular basis of histologic grade to improve prognosis. J Natl Cancer Inst. 2006;98:262-72.
12. Wang Y, Klijn JG, Zhang Y, Sieuwerts AM, Look MP, Yang F, et al. Gene-expression profiles to predict distant metastasis of lymph-node-negative primary breast cancer. Lancet. 2005;365:671-9.

Supplementary Table 6: Primer sequences and conditions used for quantitative real-time polymerase chain reactions.

Gene	Forward Primer Sequence	Reverse Primer Sequence	Input RNA (ng)	Detection Temp (°C)
CD28	GTTTTCACTTGCCAGCACAT	ACCCCAAACACCAACTTAGC	25	72
CXCR3	ATGCCTTTGTGGGAGTGAAG	AGGAGGCCTCAGTTGTCTCA	25	80
GAPDH	CATCAAGAAGGTGGTGAAGC	GGGAGTTGCTGTTGAAGTCG	25	77
ICOS	ACAGGGCACCTGACTTGATT	GGGTCTTCCTTAAGAAGGGG	25	72
IgHM	GGATTGGACGGGTTTATCCT	TAGACCGCAGAGTCCTCGAT	40	78
IgHG1	CGACACCCCCATCTGTCTAT	GACAGGGATCCAGAGTTCCA	40	77
IgHG2a	CACCTAACCTCTTGGGTGGA	CCACGTTGTTCACAAACCAG	40	79
IgJ	CCCTTTGAACAACAGGGAGA	AGGTCTCAGGAACACCATCG	25	77
ShcA	TTGTCAATAAGCCCACACGA	TCCGGGTATTGAAGTCAAGG	25	78
ShcB	AGATCCTGAAGCCACGAGAA	GAGGCTTGACCCTGACTCTG	50	80
ShcC	AGCAACCAGTGGAGAGGAAA	CCCATTTCCATAGGCTGAGA	25	80
ShcD	CATTGAAGCCTGGCATTTTT	GATGGAGGAAAAGCAATGGA	12.5	72