Supporting Online Material

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Table S1 Frequently recurrent aberrations in 49 primary breast cancer samples

Cytogenetic loci	Start (bp)	End (bp)	Start clone	End clone	Pattern	Gain	Loss
1p36.31-33	5866184	47041895	bA49J3	bA8J9	loss	10%	85%
1p33-q44	48002310	246181016	bA330M19	bA438H8	gain and loss	50%	47%
2p25.3-q37.3	596981	241796109	bA125K7	bA556H17	gain	70%	13%
3p26.3-21.31	768376	46150224	bA86C13	bA91E8	gain and loss	53%	42%
3p21.31-21.1	47384084	52839788	dJ544D10	dJ966M1	loss	23%	72%
3p21.1-q11.2	54007394	96250469	bA122D19	bA12A13	gain and loss	58%	37%
3q11.2-13.13	97022228	110272403	bA12J13	bA93N14	gain	67%	28%
3q13.13-21.1	111576135	124037428	bA286P15	bA457E6	gain and loss	64%	31%
3q21.1-29	124853438	194023814	bA9N20	bA56C4	gain	68%	25%
3q29	195537808	199160165	bA279P10	bA23M2	gain and loss	55%	38%
4p16.3-16.2	1065598	4366937	bA296G16	bA324I10	gain and loss	60%	36%
4p16.2-q35.1	4919317	186822363	bA211H6	bA301L8	gain	70%	23%
4q35.1-35.2	187292771	190668407	bA279K24	bA45F23	gain and loss	64%	31%
5p15.33-q35.3	2570762	180060082	bK2265D9	bA451H23	gain and loss	44%	47%
6p25.3-q27	1241036	170509779	bA13J16	dJ1086L22	gain and loss	42%	49%
7p22.3-q36.3	1080569	157756716	bA449P15	bA518I12	gain and loss	54%	43%
8p23.3-q11.21	477653	49685914	bA338B22	bA567J20	gain and loss	40%	57%
8q11.21-24.3	49937832	146167102	bA22C8	dJ1056B24	gain	91%	7%
9p24.3-q33.2	1340595	125649123	bA66M18	bA417B4	gain and loss	36%	56%
9q33.3-34.3	126127930	139715973	bA101K10	bA417A4	loss	16%	76%
10p15.3-q26.3	1206029	135072261	bA29A19	bA122K13	gain and loss	41%	52%
11p15.5-q12.3	1585438	62271625	bA295K3	bA163K24	gain and loss	55%	40%
11q13.1	63543757	66035373	bA424O11	bA142G8	loss	28%	67%
11q13.1-25	66710945	134156487	bA126P21	bA469N6	gain and loss	46%	50%
12p13.33-q13.13	152534	48970250	bA283I3	dJ405J10	gain and loss	40%	55%
12q13.13-13.3	49019643	56288135	bA112N23	bA181L23	loss	28%	67%
12q13.3-24.22	56286203	116748345	bA571M6	bA110J12	gain and loss	38%	57%
12q24.23-24.33	117108431	132036472	bA68H18	bA46H11	loss	20%	76%
13q12.11-34	19136604	113954546	bA76K19	bA245B11	gain and loss	42%	53%
14q11.2-23.2	19570817	62046831	bA98N22	bA559M6	gain and loss	41%	51%
14q23.2-32.33	63342212	105437086	bA544I20	bA417P24	loss	25%	68%
15q11.2-26.3	20363717	100036168	bA289D12	bA14C10	loss	20%	79%
16p13.3-11.2	11088	29730534	bA344L6	bA74E23	gain and loss	34%	65%
16p11.2-q12.1	30539964	45688066	bA2C24	bA283C7	loss	23%	76%

16q12.1-12.1	46446494	47397787	bA523L20	bA452G23	gain and loss	30%	69%
16q12.1	47238951	47397755	bA452G23	bA452G23	loss	28%	71%
16q12.1-12.2	48210521	53975887	bA305A7	bA7O2	gain and loss	32%	67%
16q12.2-24.3	54425522	88643456	bA165M2	bA533D19	loss	15%	84%
17p13.3-q21.32	801989	43043105	bA216P6	bA416K7	loss	11%	88%
17q21.32-25.1	43957677	69639765	bA361K8	bA155C2	gain and loss	35%	63%
17q25.1-25.3	69779007	78374783	bA478P5	bA567O16	loss	28%	69%
18p11.32-q23	168428	75701174	bA324G2	bA154H12	gain and loss	61%	34%
19p13.3-q13.43	183116	63516696	bK3113P16	bK3138B18	loss	11%	88%
20p13-q13.33	275014	62284676	dJ852M4	bB152O15	gain and loss	40%	59%
21q11.2-22.3	13462479	46607897	bA193B6	bA178H12	gain and loss	51%	48%
22q11.23-13.33	22510132	49521447	bA80O7	bK799F10	loss	14%	85%
Xp22.32-22.2	4616007	10437613	bA62N12	dA1O2	gain and loss	30%	69%
Xp22.2-q21.1	11152967	79447843	dJ27C22	bA217H19	loss	28%	71%
Xq21.1-28	80307294	153862276	bA102P23	bA402H20	gain and loss	31%	68%

Table S2 Recurrent aberrations and correspondingly localized oncogenes or tumor suppressor genes in "normal" tissues, primary tumors, and lymph node metastases*

Cytogenetic loci	Start clone	End clone	N46 N47 N48 N49	T46 T47 T48 T49	M47 M49	No. of clones	30% primary tumors	Oncogenes or tumor suppressor genes in the regions
1p36.32-34.1	dJ37J18	bA420M12	loss	loss	loss	47	47	*PLEKHG5, TNFRSF9, TNFRSF8, TNFRSF1B, NBL1, FABP3*
1p13.3-12	dJ1077K16	bA418J17	no change	gain	gain	16	0	*RAP1A, WNT2B, BCAS2*
1q21.1-22	bA326G21	bA172I6	loss	loss	no change	12	0	*LASS2, TNFAIP8L2, EFNA1*
1q23.3-44	bA541J2	bA438H8	no change	gain	gain	86	86	*RASAL2, RABIF, RAB7L1, RASSF5, TGFB2, RAB3GAP2, WNT9A, WNT3A*
3p25.3	bA439F4	bA438J1	loss	loss	loss	4	0	*CIDEC, VHL*
3p25.3-25.1	bA94A14	bA163D23	loss	no change	loss	3	0	
3p22.1-21.1	bA437N10	dJ966M1	loss	loss	loss	16	10	*RBM5, TUSC2, TUSC4, CYB561D2*
3q26.33-27.3	bA416O18	bA119E13	loss	no change	loss	7	0	
3q29	bA279P10	bA23M2	loss	loss	loss	7	0	*PAK2*
4p16.3	bA296G16	bA572O17	loss	loss	loss	3	0	
5q35.2-35.3	bK1087L24	bA451H23	loss	no change	loss	8	0	
8p23.3-23.2	bA338B22	bA104F14	no change	gain	gain	5	0	
8q11.21-24.3	bA22C8	dJ1056B24	no change	gain	gain	106	105	
9q33.3-34.3	bA101K10	bA417A4	loss	loss	loss	15	13	*MAPKAP1, PTGES, TRAF2*
10q21.3-22.2	bA297N15	bA345K20	loss	loss	no change	7	0	*CCAR1, AMID, UNC5B*
11p15.4-13	bA309J20	dJ85M6	no change	gain	gain	31	0	

11q12.2-13.1	bA286N22	bA142G8	loss	loss	loss	9	7	*DDB1, BRMS1*
11q13.1	bA126P21	bA126P21	loss	loss	no change	1	1	
11q13.2-14.1	bA569N5	bA7H7	no change	gain	gain	16	0	
12q13.11-13.3	bA89H19	bA571M6	loss	loss	loss	16	0	*DDIT3*
12q24.23-24.31	bA144B2	bA338K17	loss	loss	loss	6	0	*CDK2AP1*
12q24.31	bA214K3	bA158L12	no change	loss	loss	2	0	
16p13.3	bA344L6	bA127I20	loss	loss	loss	8	7	*C1QTNF8, TNFRSF12A, Q8NFX8_HUMAN, TRAP1*
16p13.3-11.2	bA518I8	bA274A17	loss	loss	no change	34	2	*TNFRSF17, ERCC4, BFAR*
16q11.2-q12.1	bA5L1	bA283C7	loss	loss	loss	3	3	*DNAJA2*
16q21-24.3	bA63M22	bA533D19	loss	loss	loss	33	33	*TRADD, GAS8*
17p13.3-q25.3	bA216P6	bA567O16	loss	loss	loss	119	110	*TUSC5, TP53, TNFRSF13B, TNFAIP1, TP53I13, BRCA1, RAD51C*
19p13.3-q13.43	bK3113P16	bK3138B18	loss	loss	loss	71	71	*VGLL3, GLTSCR1*
20p13-12.3	dJ852M4	dJ764O22	loss	no change	loss	7	0	
20p11.21	dJ234M6	dJ234M6	loss	no change	loss	1	0	
20p11.21-q11.23	dJ1025A1	dJ469A13	loss	loss	loss	15	0	*PDRG1, TP53INP2*
20q11.23-13.33	dJ633O20	bB152O15	loss	no change	loss	38	0	*NA*
22q11.23-13.33	bA80O7	bK799F10	loss	loss	loss	41	41	*FAM10A6, TNFRSF13C*
Xp22.32-q28	bA62N12	bA402H20	no change	loss	loss	142	72	*NA*

*Four “normal” breast tissues were obtained from patients No.46–49 (N46–N49), four primary tumor samples from patients No.46–49 (T46–T49), and two axillary lymph node metastases from patients No.47 and 49 (M47 and M49).

Table S3 Summary of the performance of classification with respect to different clinicopathological parameters

Classifier	No. of clones	Recurrent clones*[1]	Accuracy*[2]	*P* value*[3]	Sensitivity	Specificity
ALN metastases vs primary tumors	18	0				
ALN$^+$ vs ALN$^-$	17	0				
Ductal vs Lobular	42	bA303E16_1, bA123C5, bA354N7, bA298C15, bA229O3, bA148F12, bA303E16, bA467L24, bA370P15, bA298C15_1, bA76H6, bA281J9, bA200H5, dJ991G20, bA70E3, bA24I3, bA556H2, bA328J14, bA77K12, bA285K4, bA467O15	94.4%	0.2083	100%	30%
IDC ER$^-$ vs IDC ER$^+$ vs ILC ER$^+$	13	0				
ER$^+$ vs ER$^-$	144	bA388F14, bA292F22, bA534N5, bA432I13, bA488L1, bA471L13, bA38B21, dJ27J12, bA124O11, bA560C7, bA13E1, bA463P17, bA23F10, bA368O18, bA557N21, bA532F4, bA47O13, bA541M12, bA556E13, bA548F5, bA313B15, bA430K23, bA183D3, bA557N21_1, bA35P15	85.7%	1.398×10^{-4}	46.2%	86.1%

PgR^{+} vs PgR^{-}	91	bA564A8, bA469A15, bA572A16, bA480I12, bA739N20, bA563I16, bA430C7, bA383G10, bA534L20, bA286E7, bA354K1, dJ879K22, bA385M4, bA59A2, bA323K10, bA434B7, dJ799G3, bA46A10, bA12M5, bA538D16, bA163L4, dJ1045J21, dJ990P15, bA71D4	45.8%	0.7676	57.7%	72.7%
ER^{-}PgR^{-} vs ER^{+}PgR^{-} vs ER^{+}PgR^{+}	46	dJ986F12, bA445F12, bA474K4, bA534N5, bA432I13, bA292F22	66.7%	0.036		
HER2/neu+ vs HER2/neu^{-}	72	dJ1112G21, bA115K3, bA58O9, bA94L15, dJ906A24, dJ986F12, bA390P24, bA432I21, bK58E17, dJ1110E20, dJ466A11, bK250D10, dJ437M21, dJ979N1, dJ355C18, bA422A16, bA12M9, bK229A8, dJ85F18	90.0%	5.079×10^{-7}	82.4%	66.7%
Size (small vs moderate vs large)	6	0				
Size (small vs large)	48	0				
Grade 1 vs 2 vs 3	107	bA23F10, bA557N21, bA560C7, bA368O18, bA9O10, bA535E19, bA142A12, bA343N14, bA419E14, bA245N4	61.9%	0.04		
Grade (1+2) vs 3	14	0				
Grade 1 vs (2+3)	47	bA329J7, bK57G9, dJ76B20, dJ539M6, dJ353E16	66.7%	1	12.5%	100%

High grade vs Low grade[#]	52	bA15G16, bA430G6, bK29F11, bA206M24, bA393K10, bA190A12, bA137A12, bA5K23, cN75H12, dJ398C22, bK268H5, dJ925J7, bK299D3, bK397C4, dJ388M5, bK722E9	73.9%	0.0393	75.0%	73.3%

*[1] The recurrent clones in each classifier in at least 70% of samples.

*[2] The performance of LOOCV absolute errors for each clinicopathological parameter based on the recurrent clones was calculated. Accuracy was calculated based on the corresponding LOOCV.

*[3] Fisher exact test was applied for estimation of statistical significance of each classifier for two class prediction. Chi square test was used for the result of three class prediction. The corresponding *P* values are presented.

[#] All the clones of this classifier were used since limiting it for clones recurring in more than 70% of high- and low-grade tumors does not give as satisfactory performance.