Table III. Continued.

Probe ID	Accession no.	Symbol	Gene name	Fold change (log)	P-value
A_24_P468950	AK021439	N/A		-2.6	1.26E-04
A_24_P683583	N/A	N/A		-2.6	1.26E-04
A_23_P203558	NM_000518	*HBB*	Hemoglobin, β	-2.6	2.33E-04
A_32_P140153	N/A	N/A		-2.6	1.26E-04
A_32_P124461	AK129743	N/A		-2.59	1.26E-04
A_23_P136026	AK128476	N/A		-2.59	1.26E-04
A_23_P28295	NM_004525	*LRP2*	Low density lipoprotein-related protein 2	-2.59	4.43E-04
A_24_P586712	NM_198485	*TPRG1*	Tumor protein p63 regulated 1	-2.58	1.26E-04
A_23_P139500	NM_030762	*BHLHE41*	Basic helix-loop-helix family, member e41	-2.58	1.26E-04
A_23_P121480	NM_001004196	*CD200*	CD200 molecule	-2.58	1.26E-04
A_23_P32577	NM_080759	*DACH1*	Dachshund homolog 1 (*Drosophila*)	-2.58	1.26E-04
A_23_P315815	NM_004495	*NRG1*	Neuregulin 1	-2.58	1.26E-04
A_23_P93772	NM_019102	*HOXA5*	Homeobox A5	-2.58	1.26E-04
A_32_P150748	CR749529	N/A		-2.58	1.26E-04
A_32_P204959	N/A	N/A		-2.58	1.26E-04
A_23_P363149	N/A	N/A		-2.57	4.43E-04
A_23_P41487	NM_015130	*TBC1D9*	TBC1 domain family, member 9 (with GRAM domain)	-2.57	1.26E-04
A_23_P257296	NM_003226	*TFF3*	Trefoil factor 3 (intestinal)	-2.56	3.41E-04
A_23_P250735	NM_175709	*CBX7*	Chromobox homolog 7	-2.56	1.26E-04
A_24_P189516	NM_001609	*ACADSB*	acyl-coenzyme A dehydrogenase, short/ branched chain	-2.56	1.26E-04
A_23_P253012	NM_017577	GRAMD1C	GRAM domain containing 1C	-2.56	1.26E-04
A_24_P179244	XM_001723863	*LOC100128979*	Hypothetical protein LOC100128979	-2.55	1.26E-04
A_32_P117846	N/A	N/A		-2.55	1.26E-04
A_32_P42224	BX097190	N/A		-2.55	2.33E-04
A_24_P119665	NM_001128933	*SYNPO2*	Synaptopodin 2	-2.54	1.26E-04
A_32_P105825	NM_001584	*MPPED2*	Metallophosphoesterase domain containing 2	-2.54	3.41E-04
A_24_P225679	NM_005544	*IRS1*	Insulin receptor substrate 1	-2.54	1.26E-04
A_32_P226907	N/A	N/A		-2.54	1.26E-04
A_23_P356581	NM_022370	*ROBO3*	Roundabout, axon guidance receptor, homolog 3 (*Drosophila*)	-2.53	1.26E-04
A_32_P221096	AW015426	N/A		-2.53	1.26E-04
A_23_P106016	NM_002742	*PRKD1*	Protein kinase D1	-2.52	1.26E-04
A_32_P210193	N/A	N/A		-2.52	1.26E-04
A_32_P38436	N/A	N/A		-2.52	1.26E-04
A_24_P512775	N/A	N/A		-2.52	1.26E-04
A_23_P151529	NR_023938	*C14orf132*	Chromosome 14 open reading frame 132	-2.52	1.26E-04
A_32_P235568	AK125221	N/A		-2.52	1.26E-04
A_23_P71270	NM_001185	*AZGP1*	α-2-glycoprotein 1, zinc-binding	-2.52	4.43E-04
A_24_P650425	N/A	N/A		-2.51	1.26E-04
A_23_P71328	NM_030583	*MATN2*	Matrilin 2	-2.51	2.33E-04
A_24_P153803	NM_020663	*RHOJ*	ras homolog gene family, member J	-2.51	1.26E-04
A_24_P912730	N/A	N/A		-2.51	1.26E-04
A_24_P347624	NM_022804	*SNURF*	SNRPN upstream reading frame	-2.5	1.26E-04
A_32_P52785	NM_015345	*DAAM2*	Dishevelled associated activator of morphogenesis 2	-2.5	3.41E-04
A_23_P61042	N/A	N/A		-2.5	1.26E-04

Table III. Continued.

Probe ID	Accession no.	Symbol	Gene name	Fold change (log)	P-value
A_23_P67661	NM_001864	*COX7A1*	Cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)	-2.49	1.26E-04
A_23_P213486	N/A	*PARP8*	Poly(ADP-ribose) polymerase family, member 8	-2.49	1.26E-04
A_23_P18713	NM_004827	*ABCG2*	ATP-binding cassette, sub-family G (WHITE), member 2	-2.48	4.43E-04
A_23_P76658	NM_052818	*N4BP2L1*	NEDD4 binding protein 2-like 1	-2.48	1.26E-04
A_23_P96590	NM_014710	*GPRASP1*	G protein-coupled receptor associated sorting protein 1	-2.48	1.26E-04
A_24_P460763	AK022443	N/A		-2.48	1.26E-04
A_23_P85672	NM_006610	*MASP2*	Mannan-binding lectin serine peptidase 2	-2.48	1.26E-04
A_24_P416489	N/A	N/A		-2.47	1.26E-04
A_24_P321525	NM_032918	*RERG*	RAS-like, estrogen-regulated, growth inhibitor	-2.47	1.26E-04
A_24_P256526	BC005914	*SP2*	Sp2 transcription factor	-2.47	1.26E-04
A_24_P261417	NM_015881	*DKK3*	Dickkopf homolog 3 (*Xenopus laevis*)	-2.47	1.26E-04
A_23_P98369	NM_000829	*GRIA4*	Glutamate receptor, ionotrophic, AMPA 4	-2.47	1.26E-04
A_23_P6818	NM_020163	*SEMA3G*	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G	-2.46	3.41E-04
A_32_P100379	N/A	N/A		-2.46	1.26E-04
A_23_P30163	NR_026804	*FLJ13197*	Hypothetical FLJ13197	-2.46	1.26E-04
A_24_P206328	NM_005020	*PDE1C*	Phosphodiesterase 1C, calmodulin-dependent 70 kDa	-2.46	1.26E-04
A_24_P93948	AB210045	N/A		-2.46	1.26E-04
A_32_P52414	N/A	N/A		-2.45	1.26E-04
A_23_P123228	NM_000111	*SLC26A3*	Solute carrier family 26, member 3	-2.45	1.26E-04
A_24_P666553	N/A	N/A		-2.45	1.26E-04
A_24_P916816	N/A	N/A		-2.44	1.26E-04
A_23_P134734	NM_017786	*GOLSYN*	Golgi-localized protein	-2.44	1.26E-04
A_24_P296772	NM_033256	*PPP1R14A*	Protein phosphatase 1, regulatory (inhibitor) subunit 14A	-2.43	1.26E-04
A_24_P267523	NM_144613	*COX6B2*	Cytochrome c oxidase subunit VIb polypeptide 2 (testis)	-2.43	1.26E-04
A_23_P133517	NM_002310	*LIFR*	Leukemia inhibitory factor receptor α	-2.43	1.26E-04
A_24_P787680	N/A	N/A		-2.43	1.26E-04
A_32_P52829	N/A	N/A		-2.43	3.41E-04
A_23_P162047	NM_015881	*DKK3*	Dickkopf homolog 3 (*Xenopus laevis*)	-2.43	1.26E-04
A_32_P185140	BX648171	*TPM1*	Tropomyosin 1 (α)	-2.43	1.26E-04
A_24_P319892	NM_198274	*SMYD1*	SET and MYND domain containing 1	-2.43	1.26E-04
A_24_P226322	NM_031469	*SH3BGRL2*	SH3 domain binding glutamic acid-rich protein like 2	-2.42	1.26E-04
A_23_P86012	NM_001017402	*LAMB3*	Laminin, β3	-2.42	1.26E-04
A_23_P62255	NM_005314	*GRPR*	Gastrin-releasing peptide receptor	-2.41	1.26E-04
A_24_P141520	N/A	N/A		-2.41	2.33E-04
A_23_P114883	NM_002023	*FMOD*	Fibromodulin	-2.41	1.26E-04
A_23_P300033	NM_006206	*PDGFRA*	Platelet-derived growth factor receptor, α polypeptide	-2.41	2.33E-04
A_24_P108311	NM_015277	*NEDD4L*	Neural precursor cell expressed, developmentally downregulated 4-like	-2.41	1.26E-04

Table III. Continued.

Probe ID	Accession no.	Symbol	Gene name	Fold change (log)	P-value
A_23_P345746	NM_199261	*TPTE*	Transmembrane phosphatase with tensin homology	-2.41	1.26E-04
A_23_P418083	NM_181714	*LCA5*	Leber congenital amaurosis 5	-2.41	1.26E-04
A_32_P208341	N/A	N/A		-2.41	1.26E-04
A_24_P930337	N/A	N/A		-2.41	1.26E-04
A_24_P915095	NM_017577	*GRAMD1C*	GRAM domain containing 1C	-2.4	1.26E-04
A_32_P4792	AK057820	N/A		-2.4	1.26E-04
A_24_P82032	NM_020663	*RHOJ*	ras homolog gene family, member J	-2.39	2.33E-04
A_23_P204296	NM_032918	*RERG*	RAS-like, estrogen-regulated, growth inhibitor	-2.38	1.26E-04
A_24_P920712	N/A	N/A		-2.38	2.33E-04
A_24_P401185	NM_001042784	*CCDC158*	Coiled-coil domain containing 158	-2.38	1.26E-04
A_32_P109604	XM_001715342	*LOC100132733*	Similar to FLJ00310 protein	-2.37	1.26E-04
A_24_P131173	NM_024709	*C1orf115*	Chromosome 1 open reading frame 115	-2.37	2.33E-04
A_24_P64241	NM_001012421	*ANKRD20A2*	Ankyrin repeat domain 20 family, member A2	-2.37	1.26E-04
A_32_P58437	N/A	N/A		-2.37	1.26E-04
A_24_P602348	N/A	N/A		-2.37	1.26E-04
A_24_P135856	NM_016124	*RHD*	Rh blood group, D antigen	-2.37	1.26E-04
A_23_P333038	NM_025145	*C10orf79*	Chromosome 10 open reading frame 79	-2.37	2.33E-04
A_23_P352266	NM_000633	*BCL2*	B-cell CLL/lymphoma 2	-2.36	1.26E-04
A_23_P207699	NM_016835	*MAPT*	Microtubule-associated protein tau	-2.36	1.26E-04
A_23_P392529	NR_027270	*C21orf81*	Ankyrin repeat domain 20 family, member A3 pseudogene	-2.36	1.26E-04
A_23_P904	NM_024603	*BEND5*	BEN domain containing 5	-2.36	1.26E-04
A_23_P115785	NM_145235	*FANK1*	Fibronectin type III and ankyrin repeat domains 1	-2.35	1.26E-04
A_32_P146844	N/A	N/A		-2.35	1.26E-04
A_23_P26865	NM_002470	*MYH3*	Myosin, heavy chain 3, skeletal muscle, embryonic	-2.35	1.26E-04
A_32_P100641	XM_001714998	*LOC100128139*	Hypothetical LOC100128139	-2.35	2.33E-04
A_24_P930727	AK091677	N/A		-2.35	1.26E-04
A_23_P406341	NM_001001936	*AFAP1L2*	Actin filament associated protein 1-like 2	-2.35	1.26E-04
A_24_P54863	NM_152400	*C4orf32*	Chromosome 4 open reading frame 32	-2.34	1.26E-04
A_23_P133120	NM_018342	*TMEM144*	Transmembrane protein 144	-2.34	1.26E-04
A_32_P86705	BC040577	N/A		-2.34	1.26E-04
A_24_P833256	N/A	N/A		-2.33	1.26E-04
A_23_P401106	NM_002599	*PDE2A*	Phosphodiesterase 2A, cGMP-stimulated	-2.33	1.26E-04
A_24_P102119	AF264623	N/A		-2.33	1.26E-04
A_23_P358714	NM_020775	*KIAA1324*	KIAA1324	-2.32	1.26E-04
A_32_P162494	N/A	N/A		-2.32	3.41E-04
A_23_P326931	NM_145170	*TTC18*	Tetratricopeptide repeat domain 18	-2.32	1.26E-04

N/A, not annotated; P-value, Benjamini-Hochberg false discovery rate of random permutation test; log fold change, between groups. Gene symbol, accession number and gene name were exported from GeneSpring (from the NCBI databases).

showing significant knockdown effects. FACS analysis revealed that depleting *ASPM* caused a cell cycle arrest at the G2/M phase in HCC1937 cells (si*EGFP*:si*ASPM*, 24.4:34.0%) at 2 days after transfection, and a subsequent increase in the

Table IV. Genes specifically expressed in TNBC, but not expressed in normal human vital organs.

Probe ID	Accession no.	Symbol	Gene name	Fold change (log)	P-value
A_23_P118834	NM_001067	*TOP2A*	Topoisomerase (DNA) IIα 170 kDa	4.76	1.26E-04
A_32_P119154	BE138567	N/A		4.75	1.26E-04
A_23_P35219	NM_002497	*NEK2*	NIMA (never in mitosis gene a)-related kinase 2	4.67	1.26E-04
A_23_P166360	NM_206956	*PRAME*	Preferentially expressed antigen in melanoma	4.64	1.26E-04
A_24_P332314	NM_198947	*FAM111B*	Family with sequence similarity 111, member B	4.63	1.26E-04
A_24_P413884	NM_001809	*CENPA*	Centromere protein A	4.59	1.26E-04
A_23_P68610	NM_012112	*TPX2*	TPX2, microtubule-associated, homolog (Xenopus laevis)	4.58	1.26E-04
A_23_P401	NM_016343	*CENPF*	Centromere protein F, 350/400 ka (mitosin)	4.44	1.26E-04
A_23_P57379	NM_003504	*CDC45L*	CDC45 cell division cycle 45-like (*S. cerevisiae*)	4.44	1.26E-04
A_23_P356684	NM_018685	*ANLN*	Anillin, actin binding protein	4.29	1.26E-04
A_23_P52017	NM_018136	*ASPM*	asp (abnormal spindle) homolog, microcephaly associated (*Drosophila*)	4.17	1.26E-04
A_32_P199884	NM_032132	*HORMAD1*	HORMA domain containing 1	4.13	2.33E-04
A_23_P259586	NM_003318	*TTK*	TTK protein kinase	4.09	1.26E-04
A_23_P200310	NM_017779	*DEPDC1*	DEP domain containing 1	4.08	1.26E-04
A_23_P115872	NM_018131	*CEP55*	Centrosomal protein 55 kDa	4.03	1.26E-04
A_24_P911179	NM_018136	*ASPM*	asp (abnormal spindle) homolog, microcephaly associated (*Drosophila*)	4.02	1.26E-04
A_24_P96780	NM_016343	*CENPF*	Centromere protein F, 350/400 ka (mitosin)	3.92	1.26E-04
A_24_P14156	NM_006101	*NDC80*	NDC80 homolog, kinetochore complex component (*S. cerevisiae*)	3.86	1.26E-04
A_23_P254733	NM_024629	*MLF1IP*	MLF1 interacting protein	3.85	1.26E-04
A_23_P74115	NM_003579	*RAD54L*	RAD54-like (*S. cerevisiae*)	3.84	1.26E-04
A_23_P50108	NM_006101	*NDC80*	NDC80 homolog, kinetochore complex component (*S. cerevisiae*)	3.84	1.26E-04
A_23_P155815	NM_022346	*NCAPG*	Non-SMC condensin I complex, subunit G	3.82	1.26E-04
A_23_P51085	NM_020675	*SPC25*	SPC25, NDC80 kinetochore complex component, homolog (*S. cerevisiae*)	3.81	1.26E-04
A_32_P62997	NM_018492	*PBK*	PDZ binding kinase	3.8	1.26E-04
A_23_P256956	NM_005733	*KIF20A*	Kinesin family member 20A	3.79	1.26E-04
A_23_P212844	NM_006342	*TACC3*	Transforming, acidic coiled-coil containing protein 3	3.78	1.26E-04
A_24_P254705	NM_020394	*ZNF695*	Zinc finger protein 695	3.76	1.26E-04
A_23_P432352	NM_001017978	*CXorf61*	Chromosome X open reading frame 61	3.73	1.26E-04
A_23_P48669	NM_005192	*CDKN3*	Cyclin-dependent kinase inhibitor 3	3.71	1.26E-04
A_23_P94571	NM_004432	*ELAVL2*	ELAV (embryonic lethal, abnormal vision, *Drosophila*)-like 2 (Hu antigen B)	3.67	1.26E-04
A_23_P150667	NM_031217	*KIF18A*	Kinesin family member 18A	3.64	1.26E-04
A_32_P68525	BC035392	N/A		3.58	1.26E-04
A_24_P319613	NM_002497	*NEK2*	NIMA (never in mitosis gene a)-related kinase 2	3.53	1.26E-04
A_23_P10385	NM_016448	*DTL*	Denticleless homolog (*Drosophila*)	3.53	1.26E-04
A_23_P94422	NM_014791	*MELK*	Maternal embryonic leucine zipper kinase	3.5	1.26E-04
A_23_P340909	BC013418	*SKA3*	Spindle and kinetochore associated complex subunit 3	3.48	1.26E-04
A_23_P124417	NM_004336	*BUB1*	Budding uninhibited by benzimidazoles 1 homolog (yeast)	3.47	1.26E-04
A_24_P257099	NM_018410	*HJURP*	Holliday junction recognition protein	3.43	1.26E-04

Table IV. Continued.

Probe ID	Accession no.	Symbol	Gene name	Fold change (log)	P-value
A_23_P74349	NM_145697	*NUF2*	NUF2, NDC80 kinetochore complex component, homolog (*S. cerevisiae*)	3.36	1.26E-04
A_24_P302584	NM_003108	*SOX11*	SRY (sex determining region Y)-box 11	3.36	4.43E-04
A_24_P68088	NR_002947	*TCAM1*	Testicular cell adhesion molecule 1 homolog (mouse)	3.35	2.33E-04
A_24_P366033	NM_018098	*ECT2*	Epithelial cell transforming sequence 2 oncogene	3.34	1.26E-04
A_23_P93258	NM_003537	*HIST1H3B*	Histone cluster 1, H3b	3.33	1.26E-04
A_23_P149668	NM_014875	*KIF14*	Kinesin family member 14	3.29	1.26E-04
A_23_P34325	NM_033300	*LRP8*	Low density lipoprotein receptor-related protein 8, apolipoprotein E receptor	3.28	1.26E-04
A_32_P56154	N/A	N/A		3.28	1.26E-04
A_23_P138507	NM_001786	*CDC2*	Cell division cycle 2, G1→S and G2→M	3.24	1.26E-04
A_23_P49972	NM_001254	*CDC6*	Cell division cycle 6 homolog (*S. cerevisiae*)	3.22	1.26E-04
A_24_P306896	XR_040656	*LOC283711*	Hypothetical protein LOC283711	3.22	1.26E-04
A_23_P44684	NM_018098	*ECT2*	Epithelial cell transforming sequence 2 oncogene	3.21	1.26E-04
A_23_P100344	NM_014321	*ORC6L*	Origin recognition complex, subunit 6 like (yeast)	3.2	1.26E-04
A_23_P163481	NM_001211	*BUB1B*	Budding uninhibited by benzimidazoles 1 homolog β (yeast)	3.17	1.26E-04
A_32_P87849	N/A	N/A		3.16	1.26E-04
A_24_P397107	NM_001789	*CDC25A*	Cell division cycle 25 homolog A (S. pombe)	3.15	1.26E-04
A_23_P209200	NM_001238	*CCNE1*	Cyclin E1	3.15	1.26E-04
A_32_P16625	N/A	N/A		3.15	1.26E-04
A_24_P37903	N/A	*LOX*	Lysyl oxidase	3.12	1.26E-04
A_24_P313504	NM_005030	*PLK1*	Polo-like kinase 1 (*Drosophila*)	3.07	1.26E-04
A_23_P252292	NM_006733	*CENPI*	Centromere protein I	3.04	1.26E-04
A_23_P161474	NM_182751	*MCM10*	Minichromosome maintenance complex component 10	2.99	1.26E-04
A_23_P253762	N/A	N/A		2.94	1.26E-04
A_24_P225534	NM_017821	*RHBDL2*	Rhomboid, veinlet-like 2 (*Drosophila*)	2.94	1.26E-04
A_24_P412088	NM_182751	*MCM10*	Minichromosome maintenance complex component 10	2.94	1.26E-04
A_32_P109296	NM_152259	*C15orf42*	Chromosome 15 open reading frame 42	2.91	1.26E-04
A_24_P76521	AK056691	*GSG2*	Germ cell associated 2 (haspin)	2.83	1.26E-04
A_23_P126212	NM_022111	*CLSPN*	Claspin homolog (*Xenopus laevis*)	2.83	1.26E-04
A_23_P60120	NM_031415	*GSDMC*	Gasdermin C	2.81	2.33E-04
A_24_P902509	NM_018193	*FANCI*	Fanconi anemia, complementation group I	2.8	1.26E-04
A_23_P155969	NM_014264	*PLK4*	Polo-like kinase 4 (*Drosophila*)	2.79	1.26E-04
A_32_P183218	NM_153695	*ZNF367*	Zinc finger protein 367	2.77	1.26E-04
A_23_P46118	NM_001821	*CHML*	Choroideremia-like (Rab escort protein 2)	2.76	2.33E-04
A_23_P327643	N/A	N/A		2.75	1.26E-04
A_23_P215976	NM_057749	*CCNE2*	Cyclin E2	2.72	2.33E-04
A_32_P151800	NM_207418	*FAM72D*	Family with sequence similarity 72, member D	2.7	1.26E-04
A_23_P34788	NM_006845	*KIF2C*	Kinesin family member 2C	2.7	1.26E-04
A_23_P133956	NM_002263	*KIFC1*	Kinesin family member C1	2.69	1.26E-04
A_23_P88630	NM_000057	*BLM*	Bloom syndrome, RecQ helicase-like	2.68	1.26E-04
A_24_P276102	NM_183404	*RBL1*	Retinoblastoma-like 1 (p107)	2.68	1.26E-04
A_23_P23303	NM_003686	*EXO1*	Exonuclease 1	2.67	1.26E-04
A_23_P88691	NM_000745	*CHRNA5*	Cholinergic receptor, nicotinic, α5	2.67	1.26E-04
A_32_P72341	NM_173084	*TRIM59*	Tripartite motif-containing 59	2.62	1.26E-04

Table IV. Continued.

Probe ID	Accession no.	Symbol	Gene name	Fold change (log)	P-value
A_24_P227091	NM_004523	*KIF11*	Kinesin family member 11	2.61	1.26E-04
A_23_P136805	NM_014783	*ARHGAP11A*	Rho GTPase activating protein 11A	2.6	1.26E-04
A_23_P63402	NM_013296	*GPSM2*	G-protein signaling modulator 2 (AGS3-like, *C. elegans*)	2.6	1.26E-04
A_23_P35871	NM_024680	*E2F8*	E2F transcription factor 8	2.58	1.26E-04
A_23_P207307	N/A	N/A		2.58	1.26E-04
A_24_P399888	NM_001002876	*CENPM*	Centromere protein M	2.58	1.26E-04
A_23_P155989	NM_022145	*CENPK*	Centromere protein K	2.57	1.26E-04
A_23_P411335	NM_152524	*SGOL2*	Shugoshin-like 2 (S. pombe)	2.54	1.26E-04
A_23_P43484	NM_058197	*CDKN2A*	Cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	2.52	1.26E-04
A_32_P28704	N/A	N/A		2.52	1.26E-04
A_24_P351466	NM_020890	*KIAA1524*	KIAA1524	2.5	1.26E-04
A_24_P334248	NM_014996	*PLCH1*	Phospholipase C, eta 1	2.48	1.26E-04
A_23_P88331	NM_014750	*DLGAP5*	Discs, large (*Drosophila*) homolog-associated protein 5	2.47	1.26E-04
A_32_P31021	N/A	N/A		2.46	1.26E-04
A_23_P361419	NM_018369	*DEPDC1B*	DEP domain containing 1B	2.45	1.26E-04
A_23_P397341	NM_152341	*PAQR4*	Progestin and adipoQ receptor family member IV	2.42	1.26E-04
A_23_P140316	NM_001099652	*GPR137C*	G protein-coupled receptor 137C	2.42	1.26E-04
A_23_P217049	NM_014286	*FREQ*	Frequenin homolog (*Drosophila*)	2.41	2.33E-04
A_32_P35839	N/A	N/A		2.4	1.26E-04
A_24_P857404	NM_001093725	*MEX3A*	mex-3 homolog A (*C. elegans*)	2.4	1.26E-04
A_24_P323598	NM_001017420	*ESCO2*	Establishment of cohesion 1 homolog 2 (*S. cerevisiae*)	2.36	1.26E-04
A_23_P112673	NM_017975	*ZWILCH*	Zwilch, kinetochore associated, homolog (*Drosophila*)	2.33	1.26E-04
A_24_P296254	NM_014783	*ARHGAP11A*	Rho GTPase activating protein 11A	2.32	1.26E-04

N/A, not annotated; P-value, Benjamini-Hochberg false discovery rate of random permutation test; log fold change, between groups. Gene symbol, accession number and gene name were exported from GeneSpring (from the NCBI databases).

sub-G1 population (si*EGFP*:si*ASPM*, 9.86:43.68%) at 6 days (Fig. 5A). On the other hand, reduced *CENPK* expression resulted in an increase in the proportion of G0/G1 phase cells (si*EGFP*:si*CENPK*, 56.49:72.2%) in MDA-MB-231 after 2 days of transfection, and a subsequent increase in the sub-G1 population (si*EGFP*:si*CENPK*, 12.73:30.96%) at 6 days (Fig. 5B). Interestingly, we observed an enlarged size of HCC1937 cells, which was likely due to abnormal tubulin formation due to decreased *ASPM* expression (Fig. 5C, arrowheads). In addition, we observed a disruption in the structural integrity of tubulin in *CENPK*-depleted MDA-MB-231 cells (Fig. 5D, arrowheads), compared with those in si*EGFP*-transfected cells.

These results suggest that the absence of *ASPM* and *CENPK* caused an arrest in the G2/M and G0/G1 phases, respectively, and then induced cell death. Taken together, these findings strongly suggest that *ASPM* and *CENPK* have indispensable roles in cell proliferation and mitosis, especially in the G2/M and G0/G1 phases, in TNBC cells.

Discussion

TNBC patients do not benefit from endocrine therapy and trastuzumab. Conventional chemotherapy is currently the mainstay of systemic medical treatment, although TNBC patients have a worse outcome after chemotherapy than patients with other breast subtypes. In particular, because cytotoxic drugs often cause severe adverse effects, it is obvious that thoughtful selection of novel target molecules based on the detailed molecular mechanisms of TNBC carcinogenesis

Table V. Genes listed in cluster 1 and cluster 2.

No. of genes	Genes
Cluster 1 (enrichment score, 29.90)	
87	*BLM, CKS1B, CKS2, CHEK1, E2F1, E2F2, E2F8, FANCA, FANCI, H2AFX, HORMAD1, HJURP, MAD2L1, NDC80, NEK2, NUF2, OIP5, PBK, RAD51, RAD54L, SPC25, TPX2, TTK, ZWINT ZWILCH, ANLN, ASPM, AURKA, BIRC5, BUB1, BUB1B, CASC5, CDC25A, CDC6, CDCA2, CDCA5, CDCA8, CENPA, CENPF, CEP55, CHAF1B, SKA3, C13orf34, CIT, CLSPN, CCNA2, CCNB1, CCNE1, CCNE2, CDKN2A, CDKN2C, CDKN3, DSCC1, DLGAP5, ESCO2, EXO1, FAM83D, GSG2, INHBA, KIF11, KIF14, KIF18A, KIF18B, KIF20A, KIF23, KIF2C, KIFC1, LMNB1, MND1, NCAPG, NUSAP1, PTTG1, PLK1, PLK4, PKMYT1, PRC1, RBL1, SGOL2 SPAG5, STMN1, SMC4, TMSB15A, TOP2A, TACC3, TUBB3, UBE2C, UHRF1*
Cluster 2 (enrichment score, 6.43)	
45	*ADAMTS5, MAMDC2, SPARCL1, WIF1, AZGP1, APOD, FIGF, CHL1, CCL28, CXCL2, COL4A6, COL14A1, COL17A1, CNTNAP3, DKK3, DST, FGF1, FMOD, HS3ST4, IGJ, IL33, LAMA3, LAMAB, LTBP2, LIFR, LRP2, MASP2, MATN2, MGP, NTN4, NRG1, PTHLH, PI15, PLAT, PDGFA, PTN, PIGR, PIP, SCGB1D1, SCGB1D2, SCGB3A1, SEMA3G, STC2, THSD4, TFF3*

Genes enriched in cluster 1 and cluster 2 according to DAVID.

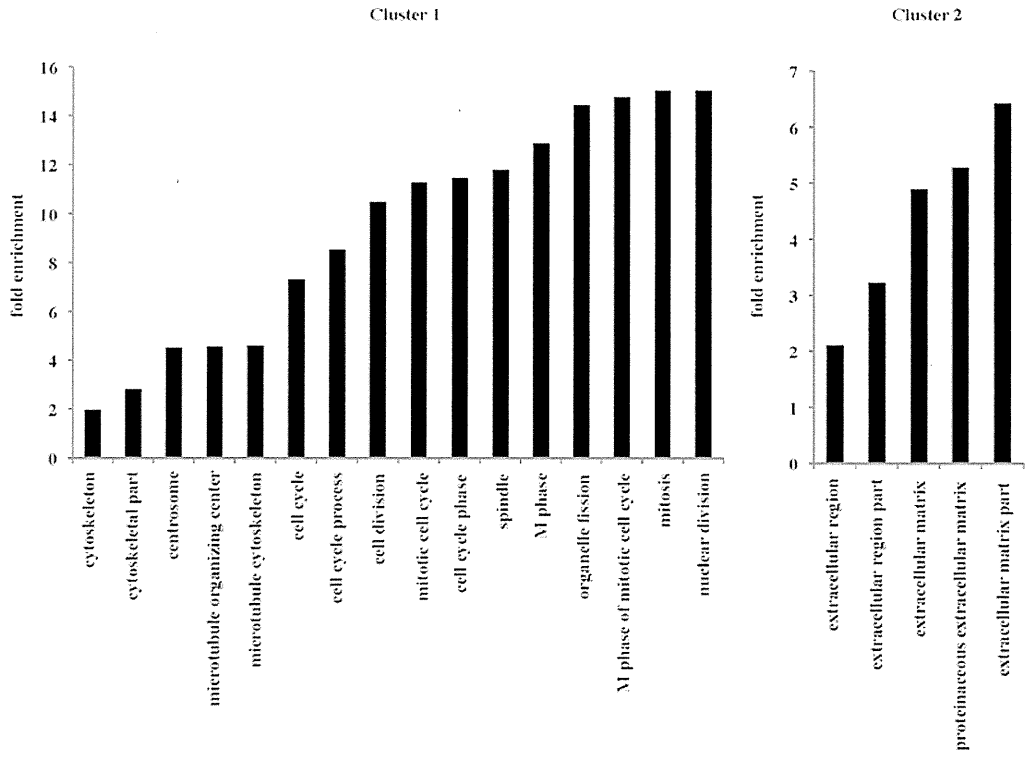

Figure 2. Gene annotation enrichment analysis based on DAVID was performed to elucidate the biological processes and pathways characterized in TNBC. Functional annotation terms are shown in bar plots; the value of the vertical axis represents the fold enrichment score of each term.

should be very helpful to develop effective anticancer drugs with a minimum risk of side effects. To this end, we performed DNA microarray using the microdissected TNBC and normal ductal cells, and normal human vital organs including the

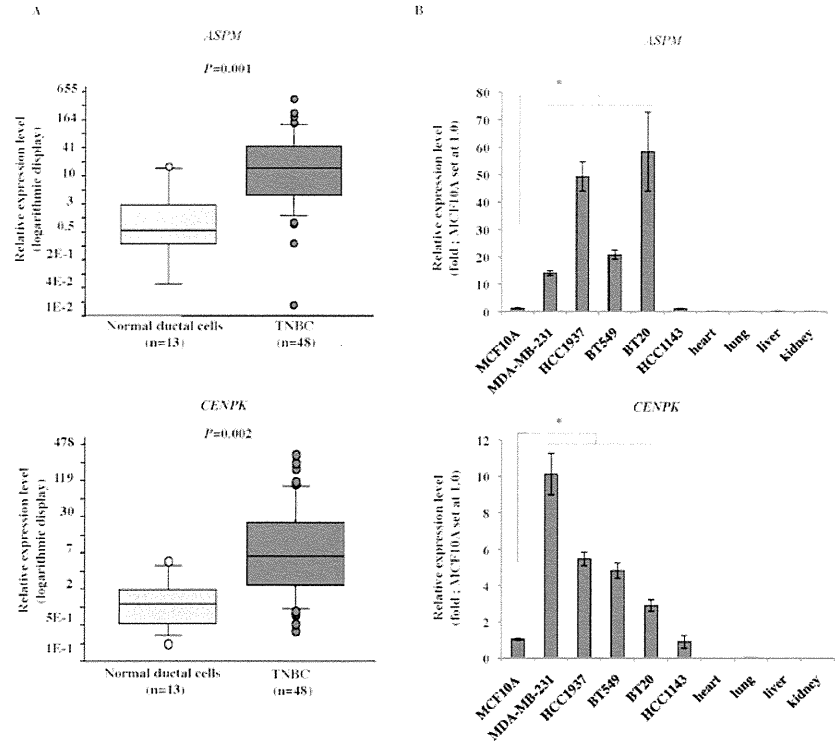

Figure 3. *ASPM* and *CENPK* expression profiles. (A) qRT-PCR results of *ASPM* and *CENPK* in microdissected tumor cells from 48 TNBC tissues and 13 normal ductal cells (Mann-Whitney t-test). (B) qRT-PCR results of *ASPM* and *CENPK* in five TNBC cell lines, MCF10A cells (human normal mammary epithelial cell line) and various normal organs (Student's two-sided t-test: *P<0.05).

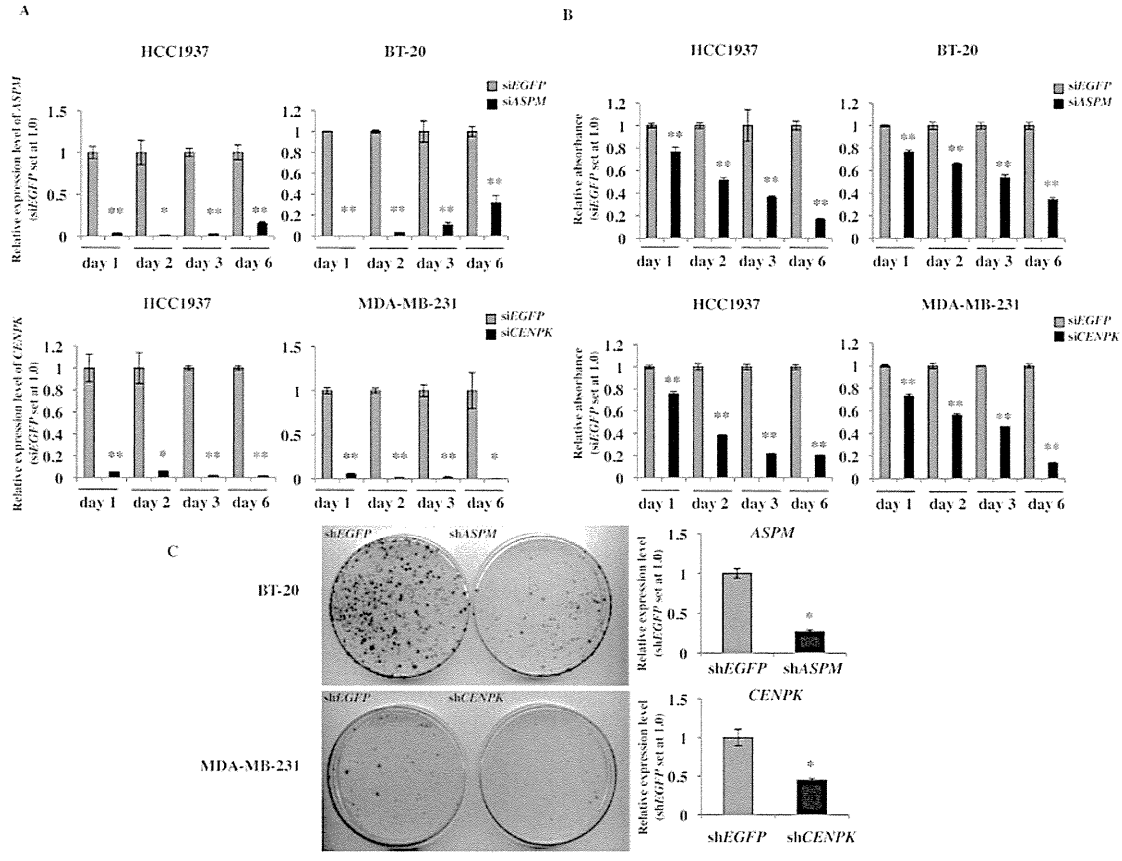

Figure 4. siRNA-mediated growth inhibitory effects in TNBC cells. (A) siRNA-mediated knockdown of *ASPM* in HCC1937 and BT-20 cells, and *CENPK* in HCC1937 and MDA-MB-231 cells was validated by qRT-PCR analysis (Student's two-sided t-test: *P<0.05, **P<0.01). (B) The MTT assay showing a decrease in the number of cells upon *ASPM* knockdown in HCC1937 and BT-20 cells and *CENPK* knockdown in HCC1937 and MDA-MB-231 cells (Student's two-sided t-test: *P<0.05, **P<0.01). (C) Colony formation assay (left) demonstrating a decrease in the number of colonies upon *ASPM* and *CENPK* knockdown (right) (Student's two-sided t-test: *P<0.05).

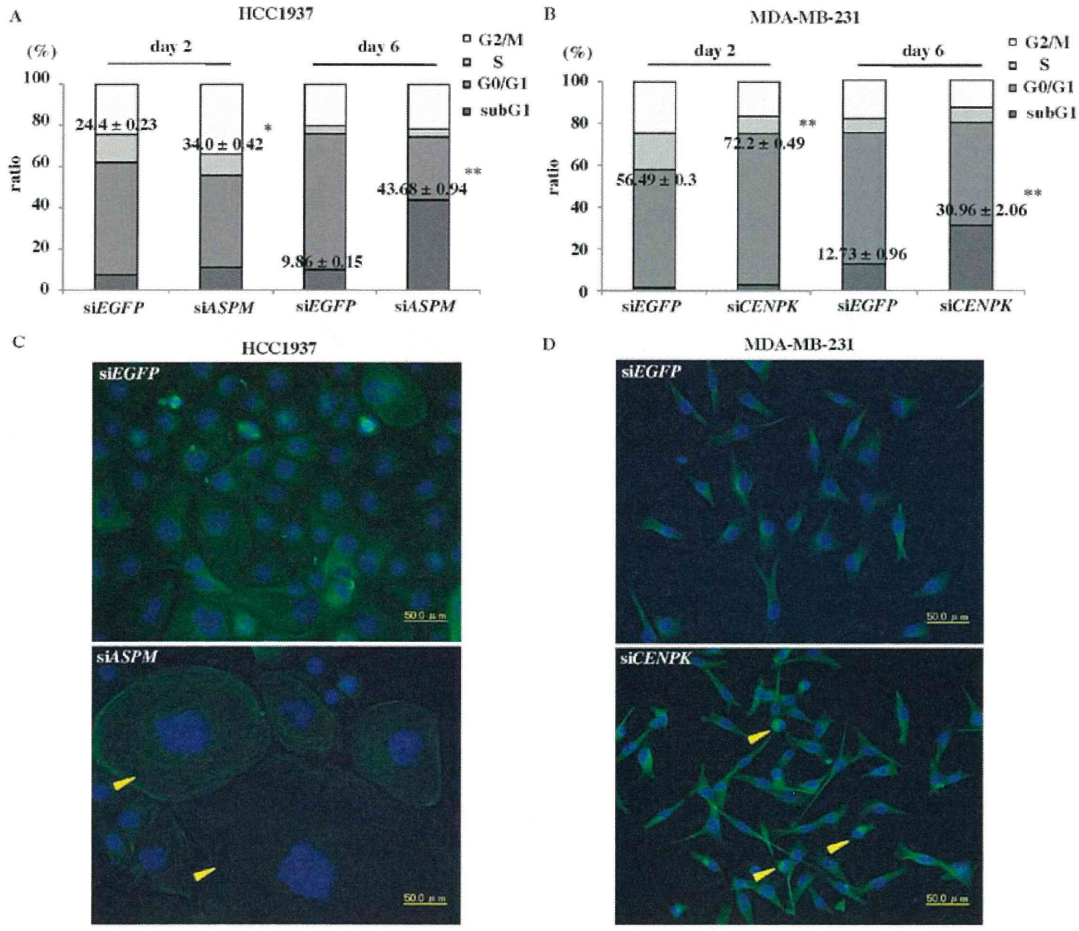

Figure 5. Alteration of the cell cycle and changes in cancer cell morphology upon *ASPM* and *CENPK* knockdown in TNBC cells. (A) FACS analysis at each time-point. The proportion of cells at the G2/M phase was elevated 2 days after si*ASPM* transfection followed by sub-G1 induction at 6 days in HCC1937 cells. (B) Upon *CENPK* knockdown, the proportion of cells at the G0/G1 phase was elevated in MDA-MB-231 cells at 2 days after si*CENPK* transfection, followed by sub-G1 induction at 6 days after transfection. A total of 10,000 cells were counted (Student's two-sided t-test: $^{*}P<0.05$, $^{**}P<0.01$). (C) Immunocytochemical staining analysis of α/β-tubulin at 48 h after siRNA transfection. Enlarged si*ASPM*-treated HCC1937 cells (arrowhead). Control cells that entered metaphase are indicated by the arrow. (D) Disruption of the structural integrity of tubulin in si*CENPK*-treated MDA-MB-231 cells (arrowhead). α/β-tubulin and nuclei staining are shown as green and blue, respectively. Scale bars, 50 μm.

heart, lung, liver and kidney and identified 104 genes that were significantly upregulated in TNBC compared to normal duct cells, but not expressed in normal human vital organs. They included cancer specific kinases, such as *NEK2*, *PBK*, and *MELK*, which might serve as druggable targets for new therapeutic agents against TNBC.

NEK2, a member of the NIMA-related serine/threonine kinase family, is involved in cell division and the mitotic regulation by centrosome splitting, and is upregulated in a wide variety of human cancers including breast cancer (40). siRNA-mediated depletion of *NEK2* expression results in growth suppression of breast and colorectal cancers (29,30). *PBK*, a mitotic serine/threonine kinase, is significantly upregulated in the majority of breast cancers. siRNA-mediated knockdown of PBK expression also results in significant suppression of cell growth due to cytokinetic failure (31). *MELK*, a member of the snf1/AMPK serine-threonine kinase family, is involved in mammalian embryonic development and is also frequently upregulated in breast cancers and brain tumors (33,41). Suppression of *MELK* expression by siRNA significantly inhibits the growth of human breast cancer cells (33). These findings strongly suggest that these cancer-specific kinases, *NEK2, PBK* and *MELK*, are promising therapeutic targets for TNBC.

Furthermore, we performed a gene-annotation enrichment analysis using DAVID based on gene expression profiling to elucidate the biological processes and pathways associated with each gene cluster. We found that the vast majority of genes upregulated in TNBC are functionally responsible for cell cycle progression involved in nuclear division, microtubule organization, kinetochore, and chromosome segregation, and that most inactivated functions closely related to TNBC progression are involved in cell-cell or cell-matrix interactions, which is consistent with epithelial mesenchymal transition (EMT) features as a phenotype of TNBC (42).

To further the development of novel anticancer drugs with minimum adverse effects, we focused on the cancer-specific cell-cycle associated genes *ASPM* and *CEPNK* as novel molecular targets for TNBC therapy. *ASPM* has been reported to play an essential role in nucleating microtubules at centrosomes, to localize to the spindle poles during mitosis (39) and to contribute to glioblastoma cell growth (43), but has not been associated with breast carcinogenesis, especially

TNBC. Here, we confirmed that *ASPM* is upregulated in clinical samples and TNBC cell lines (Fig. 3) and that siRNA-mediated knockdown of endogenous *ASPM* results in the loss of nucleating microtubules through mitosis by impeding centrosome function, resulting in G2/M cell cycle arrest and subsequent apoptosis. These results suggest that aberrant *ASPM* expression might be involved in the carcinogenesis of TNBC and that *ASPM* targeting might be an attractive therapeutic option with less adverse effects. *CENPK* is known to be a subunit of the *CENPH-I* complex, and essential for proper kinetochore assembly (39), but little is known about the roles of *CENPK* in human cancer growth, progression, and carcinogenesis. We also confirmed that *CENPK* is upregulated in clinical samples and TNBC cell lines, and that siRNA-mediated knockdown also causes cell growth inhibition through G0/G1 cell cycle arrest due to a loss of correct tubulin structures (Figs. 3-5). Interestingly, we determined that other centromere or kinetochore-associated proteins, *CENPA, CENPF, CENPI, CENPM, NDC80* and *HJURP*, were also significantly overexpressed in TNBC cases, but not expressed in normal vital organs (Fig. 1C and Table IV). Human *CENPA* was first identified based on autoantibodies found in patients suffering from scleroderma (44) and is overexpressed in colorectal cancers (45). *CENPF* is also reportedly upregulated in head and neck squamous cell carcinomas and pancreatic ductal carcinomas (46,47). *NDC80* and *HJURP* are reportedly overexpressed in breast cancers and associated with tumor grade and poor prognosis (48,49). These findings suggest that aberrant regulation of kinetochore assembly and centromere function through mitosis might contribute to the carcinogenesis of TNBC and that destroying one component of the kinetochore, such as targeting *CENPK*, might be a novel molecular target for TNBC treatment.

TNBC is a heterogeneous subgroup of breast cancers; therefore oncologists, pathologists, and geneticists had tried to clarify TNBC by means of gene expression profiling and immunohistochemical analyses. We also applied unsupervised 2-dimensional hierarchical clustering analysis to groups of genes based on similarities in the expression pattern, but there is no clustering for TNBC based on gene expression patterns, probably due to the small sample size (data not shown). However, the information provided in this study will facilitate the development of novel and attractive molecular drug targets without adverse events.

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ORIGINAL ARTICLE

A genome-wide association study identifies a genetic variant in the *SIAH2* locus associated with hormonal receptor-positive breast cancer in Japanese

Seham Elgazzar[1], Hitoshi Zembutsu[1], Atsushi Takahashi[2], Michiaki Kubo[3], Fuminori Aki[4], Koichi Hirata[5], Yuichi Takatsuka[6], Minoru Okazaki[7], Shozo Ohsumi[8], Takashi Yamakawa[9], Mitsunori Sasa[10], Toyomasa Katagiri[11], Yoshio Miki[12] and Yusuke Nakamura[1]

In Japan, breast cancer is the most common cancer among women and the second leading cause of cancer death among women worldwide. To identify genetic variants associated with the disease susceptibility, we performed a genome-wide association study (GWAS) using a total of 1086 Japanese female patients with hormonal receptor-positive (HRP) breast cancer and 1816 female controls. We selected 33 single-nucleotide polymorphisms (SNPs) with suggestive associations in GWAS (*P*-value of $< 1 \times 10^{-4}$) as well as 4 SNPs that were previously implicated their association with breast cancer for further replication by an independent set of 1653 cases and 2797 controls. We identified significant association of the disease with a SNP rs6788895 ($P_{combined}$ of 9.43×10^{-8} with odds ratio (OR) of 1.22) in the *SIAH2* (*intron of seven in absentia homolog 2*) gene on chromosome 3q25.1 where the involvement in estrogen-dependent diseases was suggested. In addition, rs3750817 in intron 2 of the *fibroblast growth factor receptor 2* gene, which was reported to be associated with breast cancer susceptibility, was significantly replicated with $P_{combined}$ of 8.47×10^{-8} with OR = 1.22. Our results suggest a novel susceptibility locus on chromosome 3q25.1 for a HRP breast cancer.
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Keywords: breast cancer in the Japanese population; *FGFR2* gene; GWAS; hormonal receptor-positive breast cancer; *SIAH2* gene; 3q25.1 locus; 10q26 locus

INTRODUCTION

Nearly 70% of breast cancer is known to be hormone dependent, as estrogen and progesterone have key roles both in the development and progression of the disease.[1,2] The exposures to higher level and/or for longer period of estrogen such as early menarche, late menopause, late age at first pregnancy, nulliparity, postmenopausal obesity and high serum estrogen level in postmenopausal women is considered to be risk factors for breast cancer.[3–5] Furthermore, progestin, synthetic progesterone, was shown to markedly increase the risk of breast cancer in postmenopausal women when this hormonal therapy was provided for >10 years.[6] In Japan, breast cancer is the most common cancer among women and its incidence has been doubled in both pre- and postmenopausal women in the last 20 years, mainly as an estrogen receptor-positive subgroup.[7] Although hormone therapy and radiotherapy are effective, cancer cells often become resistant to these treatments; nearly half of estrogen receptor-positive breast cancer patients at an advanced stage suffer from recurrence[8–10] and only one-third of hormonal receptor-positive (HRP) patients with metastatic disease respond to radiotherapy.[11] Therefore, new therapeutic options for the disease are eagerly awaited.

The aim of this study is to identify the genetic factors susceptible to HRP breast cancer in the Japanese population and should facilitate the development of novel approaches to prevent and/or treat breast cancer.

MATERIALS AND METHODS

Samples

Characteristics of study subjects are shown in Table 1. Most of the breast cancer cases and all the controls in this study were registered in the BioBank Japan, which begun in 2003 with the goal of collecting DNA and serum

[1]Laboratory of Molecular Medicine, Human Genome Center, Institute of Medical Science, The University of Tokyo, Tokyo, Japan; [2]Laboratory for Statistical Analysis, RIKEN Center for Genomic Medicine, Yokohama, Japan; [3]Laboratory for Genotyping Development, RIKEN Center for Genomic Medicine, Yokohama, Japan; [4]Department of Surgery, Itoh Surgery and Breast Clinic, Kochi, Japan; [5]First Department of Surgery, Sapporo Medical University, Sapporo, Japan; [6]Department of Breast Surgery, Kansai Rosai Hospital, Hyogo, Japan; [7]Department of Surgery, Sapporo Breast Surgical Clinic, Sapporo, Japan; [8]Department of Breast Oncology, Shikoku Cancer Center, Ehime, Japan; [9]Department of Surgery, Yamakawa Breast Clinic, Kochi, Japan; [10]Department of Surgery, Tokushima Breast Care Clinic, Tokushima, Japan; [11]Division of Genome Medicine, Institute for Genome Research, The University of Tokushima, Tokushima, Japan and [12]Genome Center, The Cancer Institute, Japanese Foundation for Cancer Research, Tokyo, Japan
Correspondence: Dr Y Nakamura, Laboratory of Molecular Medicine, Human Genome Center, Institute of Medical Science, The University of Tokyo, 4-6-1 Shirokanedai, Minato-ku, Tokyo 108-8639, Japan.
E-mail: yusuke@ims.u-tokyo.ac.jp
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Table 1 Characterization of samples used in hormonal receptor-positive breast cancer

	GWAS	*Replication*
Case		
Number of subjects	1086	1653
Mean age at interview (±s.d.)	66.7 (18.5)	60.7 (9.3)
Mean age of menarche	12.4	12.2
Mean age of menopause	48.3	47.9
Cases with DCIS	52	207
Cases with invasion	1034	1446
Body mass index prime	1.08	1.03
Platform	Illumina HumanHap 610K	Invader assay
Source	BioBank Japan Collaborative hospitals[a]	BioBank Japan Collaborative hospitals[a]
Control		
Number of subjects	1816	2797
Mean age at interview (±s.d.)	61.3 (12.6)	65.9 (13.2)
Body mass index prime	1.06	1.02
Platform	Illumina HumanHap 610K	Illumina HumanHap 610K
Source	BioBank Japan	BioBank Japan
Diseases in control[b]	MRC healthy volunteer Hepatitis B Keloid Drug eruption Pulmonary tuberculosis Peripheral artery disease Arrhythmias Stroke Myocardial infarction	Rheumatoid arthritis Amyotrophic lateral sclerosis Liver cirrhosis

Abbreviations: DCIS, ductal carcinoma in situ; GWAS, genome-wide association study.
[a]Tokushima Breast Care Clinic, Yamakawa Breast Clinic, Shikoku Cancer Center, and Itoh Surgery and Breast Clinic, Kansai Rosai Hospital, Sapporo Breast Surgical Clinic and Sapporo Medical University Hospital.
[b]The control groups from BioBank Japan consisted of female individuals without cancer also without any disease related to breast cancer.

samples, along with clinical information from 300 000 individuals who were diagnosed to have any of 47 different diseases from a collaborative network of 66 hospitals in Japan. All cases were diagnosed to have a HRP breast cancer by the following examinations: examination of breast tissue (biopsy or cytology), estrogen receptor and progesterone receptor positivities were evaluated by immunohistochemistry. For the genome-wide association study (GWAS) study, 1086 subjects with HRP breast cancer had been selected as cases (Table 1); 846 samples were collected from the BioBank Japan and the remaining 240 samples were collected from collaborative hospitals. Controls for the GWAS consisted of 1816 females including 231 healthy volunteers from the Midosuji Rotary Club, Osaka, Japan. In addition, we also used genome-wide screening data of 1585 female samples for 8 diseases registered in the BioBank Japan (Table 1). In the replication stage, 1547 cases were obtained from BioBank Japan and 105 cases from the collaborative hospitals. In all, 2797 female controls were registered in BioBank Japan and were genotyped in GWAS for other diseases (Table 1).

For re-sequencing analysis, we selected 2266 cases with HRP breast cancer from the BioBank Japan. We used 497 female controls with 4 diseases (hepatitis B, keloid, drug eruption and pulmonary tuberculosis) from the BioBank Japan as well as 231 healthy volunteers from the Midosuji Rotary Club, Osaka, Japan. All participating subjects provided written informed consent to participate in the study in accordance with the process approved by Ethical Committee at each of the Institute of Medical Science of the University of Tokyo and the Center for Genomic Medicine of RIKEN.

SNP genotyping

For the first stage, we genotyped 1086 female individuals with HRP breast cancer and 1816 female controls using the Illumina HumanHap 610 Genotyping BeadChip (Illumina, San Diego, CA, USA). We applied our single-nucleotide polymorphism (SNP) quality control standard (call rate of $\geqslant 0.99$ in both cases and controls, and Hardy–Weinberg equilibrium test of $P < 1.0 \times 10^{-6}$ in controls). A total of 453 627 SNPs on autosomal chromosomes and 10 525 SNPs on X chromosome passed the quality control filters and were further analyzed. All control samples for the replication stage were genotyped using the Illumina HumanHap 610 BeadChip (female samples of three diseases as controls). All cluster plots were checked by visual inspection by trained personnel, and SNPs with ambiguous calls were excluded. For cases in the replication study, we used the multiplex PCR-based Invader assay (Third Wave Technologies).[12] In addition, 22 variations resulted from re-sequencing analysis were selected and genotyped in 2266 cases and 728 female controls also using the multiplex PCR-based Invader assay (Third Wave Technologies, Madison, WI, USA).

Statistical analysis

Associations of SNPs were tested by employing the Cochran–Armitage trend test in both the GWA and replication stages. For the combined study, the simple combined method was applied. In the replication analyses, significance level was applied to be *P*-value of $< 1.35 \times 10^{-3}$ (calculated as 0.05/37) by Bonferroni correction. Odds ratios (ORs) and confidence intervals were calculated using the non-susceptible allele as a reference. Heterogeneity between the GWAS and replication sets was examined using the Breslow–Day test. The genomic inflation factor (λGC) was calculated from the median of the Cochran–Armitage trend test statistics. The quantile–quantile plot of the logarithms of the genome-wide *P*-values was generated by the 'snpMatrix' package in R program v2.10.0 (see URLs), and the Manhattan plot was generated using Haploview v4.1 (see URLs). Haplotype analysis was performed by the use of Haploview v4.1 by considering genotyped SNPs located within 500 kb upstream or downstream of the marker SNP. *In silico* prediction of functional consequences of SNP was done by the use of the SNP info web server (see URLs). (Haploview software was used to analyze linkage disequilibrium (LD) values, visualize haplotype.)

Imputation

Imputation was performed by referring to the genotype data of Japanese (JPT) individuals as deposited in the Phase II HapMap database using MACH v1.0 (see URLs). Genotypes of SNPs that are located in the genomic region within 500 kb upstream or downstream of the marker SNP (the SNP that showed the strongest association with HRP breast cancer) were imputed. In the process of imputation, 50 Markov chain iterations were implemented. Imputed SNPs with an imputation quality score of $r^2 < 0.3$ were excluded from the subsequent analysis.

Re-sequencing analysis

Initially, we carried out SNP discovery by using DNA samples of 96 cases with HRP breast cancer. We designed 98 sets of primers (Supplementary Table 1) using the genomic sequence information from UCSC Genome Bioinformatics data base (NM_005067) to amplify the 22 353 bps (two exons, one intron, 5′-UTR and 3′-UTR) of the genomic region corresponding to the *SIAH2* (*intron of seven in absentia homolog 2*) gene. For each of the 96 DNA samples, PCRs were performed by using GeneAmp PCR system 9700 (Applied Biosystems, Foster City, CA, USA). We performed direct sequencing of the PCR products with the 96-capillary 3730 × l DNA Analyzer (Applied Biosystems) with Big Dye Terminators (Applied Biosystems) according to standard protocols. All amplified fragments were sequenced by two pairs of sequencing primers. Then SNPs were detected by Sequecher software v4.8 (Gene Codes, Ann Arbor, MI, USA).

RESULTS

To identify genetic variants susceptible to HRP breast cancer in the Japanese population, we performed a GWAS using 1086 female patients and 1816 female controls with Illumina HumanHap 610k BeadChip (Table 1). After the quality check of SNP genotyping data, a total of 453 627 SNPs were selected for further analysis. Principal component analysis revealed that all the subjects participating in this study were clustered in the Hapmap Asian population (Supplementary Figure 1S). A quantile–quantile plot for this GWAS is shown in Supplementary Figure 2S. The genomic inflation factor (λGC) of the test statistic in this study was 1.053 indicating a very low possibility of false-positive associations resulted from the population stratification. Although no SNP achieved genome-wide significance level, 46 SNPs in various chromosomes showed suggestive association (*P*-values $< 1 \times 10^{-4}$) as illustrated in Figure 1.

Among these 46 SNPs, we excluded SNPs possessing strong LD ($r^2 > 0.8$) and selected 33 SNPs for replication analysis as well as 4 additional SNPs that were previously reported their association with breast cancer and showed *P*-value of $< 1.0 \times 10^{-2}$ in GWAS analysis, using an independent set of 1653 female patients and 2797 female controls. Among 37 SNPs analyzed in the replication study, an SNP rs6788895 was successfully replicated with the *P*-value of $< 1.35 \times 10^{-3}$ even after the Bonferroni correction (0.05/37) as shown in Table 2 and Supplementary Table 2S. Combined analysis of the results of the GWAS and the replication study suggested strong association of the locus of the *SIAH2* gene on chromosome 3q25.1 (rs6788895, $P_{combined}$ of 9.43×10^{-8} with OR of 1.22, 95% confidence interval 1.13–1.31) without any significant heterogeneity between the two studies ($P_{heterogeneity} = 2.33 \times 10^{-01}$).

The SNP rs6788895 was further examined its association with the subgroups of breast cancer, an invasive papilloductal breast cancer group and a HER2-negative breast cancer group, and found significant associations with them ($P_{combined} = 3.61 \times 10^{-07}$, 6.78×10^{-06}, OR = 1.23, 1.21, respectively) although they did not reach to the genome-wide significant level (Supplementary Table 3S). Imputation analysis of this locus identified nine additional SNPs in strong LD (r^2 of > 0.8) that showed similar levels of association with rs6788895 (Figure 2a). The subsequent logistic regression analysis revealed no significant association of these nine SNPs when we accounted the effect of SNP rs6788895. The haplotype analysis found no haplotype revealing stronger association than the single SNP (Supplementary Table 4S). Although *in silico* prediction of the functional effect of rs6788895 identified no possible biological effect, one SNP rs2018246 showing strong LD with rs6788895 ($r^2 = 0.94$), which was located about 0.7 kb upstream from the transcription initiation site of *SIAH2*, was indicated to be present within the binding site of multiple transcription factors such as STAT1, LEF1, PAX2, which were reported to have some implication to breast cancer.[13–16] The re-sequencing of 22 353 bps corresponding to the *SIAH2* gene identified 10 novel genetic variations in addition to 37 genetic variations reported previously. We further genotyped 22 of the 47 variations after the exclusion of SNPs showing strong LD with the marker SNP (r^2 of > 0.8). As a result, we identified no genetic variant showing significant association in HRP breast cancer (Supplementary Table 5S and Supplementary Table 6S)

Furthermore, we examined the association of 37 previously reported SNPs with the HRP breast cancer[17–26] using our sample sets (Supplementary Table 7S) and found very moderate association of four genetic variants, rs1292011, rs3803662, rs2981579 and rs3750817, with HRP breast cancer in the GWAS phase ($P_{GWAS} = 5.89 \times 10^{-02}$, 6.95×10^{-03}, 8.68×10^{-04} and 5.03×10^{-04}, respectively). Further analysis of these four SNPs identified significant

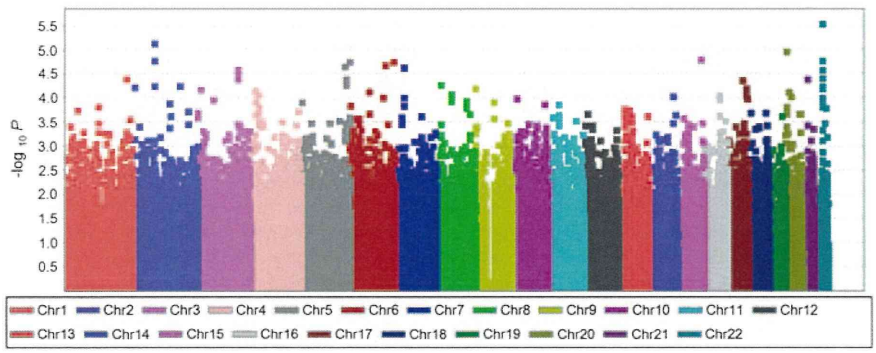

Figure 1 Manhattan plot for the genome-wide association study (GWAS) of hormonal receptor-positive breast cancer indicating −log10*P* of the Cochran–Armitage trend test for 453 627 single-nucleotide polymorphisms (SNPs) plotted against their respective positions on each chromosome.

Table 2 Association of SNP rs6788895 on chromosome 3q25.1 with hormonal receptor-positive breast cancer

					Case				*Control*							
Chr.	*Chrloc.*	*SNP*	*RA*	*Stage*	*11*	*12*	*22*	*RAF*	*11*	*12*	*22*	*RAF*	P_{assoc}[a]	*OR*	*(95% CI)*	*Phet*[b]
3	151950498	rs6788895	G	GWAS	106	456	524	0.69	242	832	742	0.64	2.34E–05	1.28	(1.14–1.43)	
				Rep	164	694	786	0.69	337	1265	1195	0.65	5.77E–04	1.18	(1.07–1.29)	2.33E–01
				Combined	270	1150	1310	0.69	579	2097	1937	0.65	9.43E–08	1.22	(1.13–1.31)	

Abbreviations: Chr., chromosome; chrloc., chromosomal location (bp); CI, confidence interval; GWAS, genome-wide association study; OR, odds ratio (calculated based on the risk allele); RA, risk allele; RAF, risk allele frequency; Rep, replication; SNP, single-nucleotide polymorphism; 11, homozygous non-risk genotype; 12, heterozygous genotype; 22, homozygous risk genotype.
[a]Passoc, *P*-value for the GWAS and replication study obtained from the Cochran–Armitage trend test and *P*-value for the combined study obtained from the simple combined test.
[b]Phet, *P*-value for heterogeneity test obtained from the Breslow–Day test.

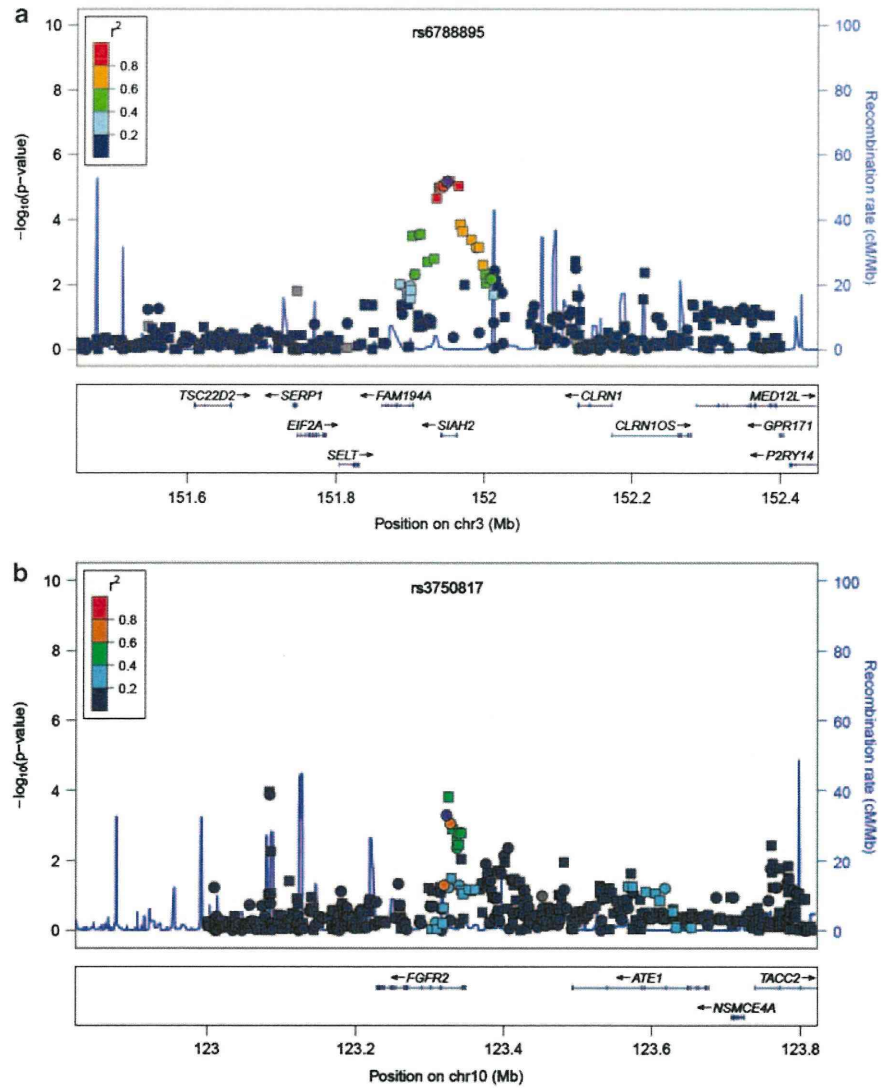

Figure 2 (**a**) Regional association plots of the locus associated with hormonal receptor-positive breast cancer on chromosomes 3q25.1 (*intron of seven in absentia homolog 2* (*SIAH2*)). (**b**) Regional association plots of the locus associated with hormonal receptor-positive breast cancer on chromosomes 10q26 (*fibroblast growth factor receptor 2* (*FGFR2*)). For each plot, $-\log_{10}P$ of the Cochran–Armitage trend test of single-nucleotide polymorphisms (SNPs) in the genome-wide association study (GWAS) was plotted against relative chromosomal locations. The square and rounded signs represent imputed and genotyped SNPs, respectively. All SNPs are color coded as red ($r^2 = 0.8$–1.0), orange ($r^2 = 0.6$–0.8), green ($r^2 = 0.4$–0.6), light blue ($r^2 = 0.4$–0.6), and dark blue ($r^2 < 0.2$) according to their pair wise r^2 to the marker SNP. The marker SNP is represented in purple color. SNP positions followed NCBI build 36 coordinates. Estimated recombination rates (cM/Mb) are plotted as a blue line.

replication of two SNPs, rs3750817 ($P_{\text{replication}} = 5.39 \times 10^{-5}$, OR $= 1.22$) and rs2981579 ($P_{\text{replication}} = 1.21 \times 10^{-3}$, OR $= 1.20$). Both SNPs are located within intron 2 of the fibroblast growth factor receptor 2 *(FGFR2)* genes. The combined analysis of the GWAS and replication phases of rs3750817 revealed strong association with $P_{\text{combined}} = 8.47 \times 10^{-08}$ (OR $= 1.22$) and that of rs2981579 was 1.77×10^{-06} (OR $= 1.20$) (Table 3). Imputation analysis of this locus identified three additional SNPs, rs9420318, rs11199914 and rs10736303 that showed similar levels of association with rs3750817 (Figure 2b).

DISCUSSION

We reported here GWA and replication studies using a total of 2730 female breast cancer cases and 4613 female controls in the Japanese population to identify common genetic variants susceptible to the HRP breast cancer. The SNP rs6788895 located in the intronic region of the *SIAH2* gene on chromosome 3q25.1 revealed a significant association with the HRP breast cancer (P_{combined} of 9.43×10^{-08} with OR of 1.22, 95% confidence interval of 1.13–1.31). We further examined the association of rs6788895 with the subgroups of breast cancer. The analysis of two histological subgroups, an invasive papilloductal breast cancer group and a HER2-negative breast cancer group, indicated suggestive associations with P_{combined} of 3.61×10^{-07} (OR $= 1.24$) and with P_{combined} of 6.78×10^{-06} (OR $= 1.21$), respectively (Supplementary Table 3S). However, rs6788895 showed no association in the GWAS with the hormonal receptor-negative group (P_{trend} of 1.03×10^{-01}) or with the HER2-positive breast cancer group (P_{trend} of 1.15×10^{-01}).

For further characterization of the chromosome 3q25.1 locus, we imputed genotypes of SNPs that were not genotyped in the GWAS

Table 3 rs2981579 and rs3750817 in different population

SNPs	Minor/major allele	MAF	OR	P-trend	Population
rs2981579 (FGFR2)	A/G	0.42	1.43	3.60×10^{-31}	UK[20]
rs2981579	A/G	0.44	1.31	2.60×10^{-09}	American[25]
rs2981579	A/G	0.47	1.20	1.77×0^{-06}	Japanese
rs3750817 (FGFR2)	T/C	0.49	1.22	8.47×10^{-08}	Japanese
rs3750817	T/C	0.37	0.78	8.20×10^{-08}	American[25]

Abbreviations: FGFR2, fibroblast growth factor receptor 2; MAF, minor allele frequency; OR, odds ratio (calculated based on the non susceptible allele) except rs3750817 in American population OR, calculated based on the susceptible allele); SNP, single-nucleotide polymorphism.

and then examined their associations with HRP breast cancer, but found no SNP showing stronger association than the marker SNP rs6788895 although several SNPs having strong LD with rs6788895 ($r^2 > 0.8$) showed similar levels of associations (Figure 2a). Previous reports implicated possible roles of *SIAH2* in breast carcinogenesis and described that SIAH2 expression was highly associated with estrogen receptor levels.[9,27–29] In addition, SIAH2 protein was indicated to have an essential role in the hypoxic response by regulating the hypoxia-inducible factor-α.[30]

Moreover, *SIAH2* was known to induce ubiquitin-mediated degradation of many substrates, including proteins involved in transcriptional regulation (POU2AF1, PML and NCOR1), a cell surface receptor (DCC) and an anti-apoptotic protein (BAG1). These proteins were reported to have some relations to breast cancer by different mechanisms.[31–35] Recent genetic studies showed that the chromosome 3q25.1 region might have a critical role in some estrogen-dependent diseases such as development of peritoneal leioyomatosis.[36,37]

We also examined the association of previously reported loci with the breast cancer[17–26] using our sample sets and found very moderate association of four genetic variants in our GWAS. Further analysis of these four SNPs identified significant replication of two SNPs, rs3750817 and rs2981579 ($P_{combined} = 8.47 \times 10^{-8}$ and 1.77×10^{-06} with OR = 1.22 and OR = 1.20, respectively). A T allele for rs3750817 is a protective allele for both Japanese and American populations with comparable ORs (Table 3).

For characterization of the chromosome 10q26 locus, we imputed genotypes of SNPs that were not genotyped in the GWAS, and examined the associations of these SNPs with HRP breast cancer. As a result, three additional SNPs, rs9420318, rs11199914 and rs10736303 were found to have similar levels of association with rs3750817 (Figure 2b). The most strongly associated SNPs are located in intron 2 of the *FGFR* gene. The intron 2 region contains a highly conserved region and possess the transcription factor binding sites possibly related to the estrogen receptor signaling pathway.[38] FGFR2 encodes a receptor tyrosine kinase and has an important role in human mammary epithelial-cell transformation,[39,40] suggesting that FGFR2 is a good candidate for breast cancer susceptibility. Subsequent functional analyses are thus essential to pinpoint the causal variants and genes associated with HRP breast cancer. In addition, because breast cancer is multi factorial disease, we could not exclude the possibility that some subjects with undiagnosed early stage of cancers or undiagnosed hormonal-dependent diseases or subject have diseases related to breast cancer might have been included as controls. Hence, this study might not have sufficient power to detect SNPs having very modest effects on susceptibility to HRP breast cancer. In conclusion, our findings, the verification of the association of the FGFR2 to the risk of breast cancer in the Japanese population and the novel identification of significant association of genetic variations in the *SIAH2* gene, should contribute to the better understanding of the susceptibility to HRP breast cancer.

URLS

The Leading Project for Personalized Medicine, http://biobankjp.org/;
EIGENSTRATsoftwarev2.0, http://genepath.med.harvard.edu/~reich/Software.htm;
R project v2.10.0, http://www.r-project.org/;
Haploview v4.1, http://www.broadinstitute.org/haploview/haploview;
MACH v1.0, http://www.sph.umich.edu/csg/yli/mach/index.html;
PLINK statistical software v1.06, http://pngu.mgh.harvard.edu/~purcell/plink/;
SNP info web server, http://manticore.niehs.nih.gov/index.html.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

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ORIGINAL ARTICLE

Biological characteristics of luminal subtypes in pre- and postmenopausal estrogen receptor-positive and HER2-negative breast cancers

Keiko Murase · Ayako Yanai · Masaru Saito · Michiko Imamura · Yoshimasa Miyagawa · Yuichi Takatsuka · Natsuko Inoue · Takashi Ito · Seiichi Hirota · Mitsunori Sasa · Toyomasa Katagiri · Yasuhisa Fujimoto · Takuya Hatada · Shigetoshi Ichii · Tomoyuki Nishizaki · Naohiro Tomita · Yasuo Miyoshi

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Abstract
Background Estrogen receptor (ER)-positive and human epidermal growth factor receptor 2 (HER2)-negetive breast cancers can be divided into luminal A and luminal B subtypes based on Ki67 expression levels. However, the biological differences in ER and progesterone receptor (PR) expression levels between these luminal subtypes are not clear.
Methods We examined immunohistochemical expression levels of ER, PR, and Ki67 in 180 ER-positive/HER2-negative breast cancers while taking menopausal status into account. Breast cancers were divided according to ER and PR levels (H: >50%, L: ≤50%), and luminal A and B were classified by the Ki67 labeling index (A: Ki67 <14%, B: Ki67 ≥14%).
Results When breast cancers were classified based on ER and PR levels, the distribution of pre- and postmenopausals was significantly different for luminal A ($P < 0.0001$), but not for luminal B cancers. As for luminal A, ER-H/PR-L cancers were rare among premenopausals (8%), but frequent among postmenopausals (54%). Correlation between ER and PR levels among luminal A cancers was strong in premenopausals but weak in postmenopausals. Since crosstalk with growth factor signaling is unlikely in luminal A, we speculate that intratumoral estrogen insufficiency contributed to the characteristics of postmenopausal ER-H/PR-L cancers.
Conclusion We speculate that the biological characteristics of luminal A cancers are influenced by the estrogen environment, but its influence on luminal B cancers may be

K. Murase · A. Yanai · M. Saito · M. Imamura · Y. Miyagawa · Y. Takatsuka · N. Inoue · Y. Miyoshi (✉)
Division of Breast and Endocrine, Department of Surgery, Hyogo College of Medicine, Mukogawa-cho 1-1, Nishinomiya, Hyogo 663-8501, Japan
e-mail: ymiyoshi@hyo-med.ac.jp

T. Ito · S. Hirota
Surgical Pathology, Hyogo College of Medicine, Mukogawa-cho 1-1, Nishinomiya, Hyogo 663-8501, Japan

M. Sasa
Tokushima Breast Care Clinic, Nakashimada-cho 4-7-7, Tokushima, Tokushima 770-0052, Japan

T. Katagiri
Division of Genome Medicine, Institute of Genome Research, Tokushima University, Kuramoto-cho 3-18-15, Tokushima, Tokushima 770-8503, Japan

Y. Fujimoto
Tachibana Hospital, Tachibana-cho 4-3-18, Amagasaki, Hyogo 661-0025, Japan

T. Hatada
Uminosato Clinic, Fukura-ko 1528-6, Minamiawaji, Hyogo 656-0501, Japan

S. Ichii
Department of Surgery, Rokko Island Hospital, Koyocho-naka 2-11, Higashinada-ku, Kobe, Hyogo 658-0032, Japan

T. Nishizaki
Division of Bioinformation, Department of Physiology, Hyogo College of Medicine, Mukogawa-cho 1-1, Nishinomiya, Hyogo 663-8501, Japan

N. Tomita
Division of Lower GI, Department of Surgery, Hyogo College of Medicine, Mukogawa-cho 1-1, Nishinomiya, Hyogo 663-8501, Japan

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limited. We believe these considerations constitute useful information for a better understanding of the biology of ER-positive-HER2-negetive breast cancers.

Keywords Breast cancer · Luminal subtype · Ki67

Introduction

In clinical settings, breast cancer subtypes have been classified according to estrogen receptor (ER), progesterone receptor (PR), and human epidermal growth factor receptor 2 (HER2) status. This classification is essentially useful for determining indications for endocrine therapies and/or anti-HER2 therapies. Recently, gene expression profiling of breast cancers has resulted in classification into five distinct types, i.e., luminal A, luminal B, HER2-overexpressing, basal-like, and normal-like [1]. This classification of intrinsic subtypes enables us to further classify the ER-positive/HER2-negative group into luminal A and luminal B subtypes. Since it is not always feasible to obtain gene expression data in daily clinical practice, Cheang et al. [2] have developed a simple classification method of luminal subtypes similar to the intrinsic subtypes by immunohistochemical staining to determine the expression levels of Ki67, a marker of cell proliferation. They identified the optimal cutoff point for the Ki67 labeling index as 13.25% for distinguishing luminal B from luminal A with a sensitivity of 72% [95% confidence interval (CI) 59–82%] and specificity of 77% (95% CI 67–85%). On the basis of this finding, the 12th St. Gallen International Breast Cancer Conference (2011) Expert Panel adopted a new immunohistochemical classification of intrinsic subtypes, essentially by dividing ER-positive/HER2-negative cancers into luminal A and luminal B following the application of the Ki67 labeling index using 14% as the cutoff value [3]. Although luminal subtypes divided by Ki67 are essentially useful, there is no doubt that evaluation of ER and PR expression levels would provide important additional information for understanding the characteristics of estrogen-dependent breast cancers.

Estrogen dependency can be determined basically from ER and PR expression levels, and tumors with high values for both ER and PR seem to show higher responsiveness to endocrine therapies [4]. However, it is not clear whether tumors with low ER expression levels are dependent on estrogen or if PR expression levels can be low even though ER levels are high. It is conceivable that PR is downregulated not only as a result of estradiol deficiency, but also of crosstalk with growth factor signaling [5]. Although it has been speculated that there are two mechanisms of PR downregulation in ER-positive tumors and that sensitivity to endocrine therapy may differ as a result, identifying and distinguishing these two mechanisms clinically seems to be difficult. If cancers are involved in crosstalk with growth factor signaling preferentially occurring in the luminal B subset, PR may be downregulated irrespective of the amount of estrogen. On the other hand, it is speculated that among cancers without growth factor signaling, insufficient estrogen environment possibly recognized in postmenopausal status induces PR downregulation.

The purpose of our study was to clarify how the estrogen environment influences ER and PR expression levels in breast cancers while taking both luminal subtypes and menopausal status into consideration.

Patients and methods

Tumor samples

Consecutive breast cancer patients who underwent mastectomy or breast-conserving surgery at the Hyogo College of Medicine during the period from August 1999 to July 2011 were recruited. From among these patients, formalin-fixed and paraffin-embedded tumor samples were obtained from 180 cases with ER-positive (nuclear staining more than 1%) and HER2-negative (score 0, 1, 2, and FISH-negative). All breast cancers were histologically diagnosed as invasive ductal carcinomas ($n = 159$), invasive lobular carcinomas ($n = 7$), or other types ($n = 14$), and patients with non-invasive carcinoma or those who had received chemotherapy or hormonal therapy before surgery were excluded. Nuclear grade was determined according to the Japanese Breast Cancer Society classification [6]. Informed consent was obtained from all patients, and the study protocol was approved by the Ethics Committee of the Hyogo College of Medicine.

Immunohistochemistry

Formalin-fixed, paraffin-embedded tissues were cut from tumor samples and used for further immunohistochemical staining. Expression levels of ER (1D5; Dako, Glostrup, Denmark), PR (PgR636; Dako), HER2 (Hercep Test; Dako), and Ki67 (MIB1; Dako) were determined immunohistochemically in terms of the percentage of positive cancer cells in the nuclei for ER, PR, and Ki67, and membrane staining for HER2 used automated immunostainers (BOND-MAX, Leica Microsystems, Tokyo, Japan, for ER and PR, and Autostainer, Dako, for HER2 and Ki67).

Different areas of densely stained lesions were selected microscopically, and nearly 1,000 cancer cells were counted. We determined the percentage of positive cancer cells with moderate or intense nuclear staining for ER, PR,

and Ki67. The slides were examined by two observers who were blinded to the clinicopathological features of the patients and re-checked when the evaluations differed. Using a cutoff value of 50%, the tumors were classified into ER-high (H) (>50%) and -low (L) (≤50%), and PR-high (H) (>50%) and -low (L) (≤50%). Luminal A was characterized as Ki67 <14% and luminal B as Ki67 ≥14% according to the criteria defined by Cheang et al. [2].

Statistical analysis

The relationship between luminal subtypes and various clinicopathological characteristics was evaluated using the chi-squared, Mann-Whitney, or Kruskal-Wallis test. Expression levels of ER, PR, and Ki67 were calculated with the Mann-Whitney or Kruskal-Wallis test, or with Pearson's correlation. Differences were considered statistically significant if $P < 0.05$. Ki67 expression levels were compared among subgroups by means of the Mann-Whitney test with Bonferroni correction for multiple comparisons, and significance was set at $P < 0.0083$.

Results

Relationship of luminal subtypes with clinicopathological characteristics

There were 106 luminal A (59%) and 74 luminal B (41%) cancers. As shown in Table 1, there were significantly more tumors with nuclear grade 3 among luminal B (86%) than luminal A (14%) cancers, and PR expression levels of luminal B (24.8%, 5.0–60.0%, median, 25–75 percentile) were significantly lower than those of luminal A (55.2%, 9.4–84.7%). There was no significant difference between luminal subtypes and other clinicopathological factors, that is, menopausal status, tumor size, histological type, lymph node metastasis, and ER expression levels (Table 1).

Correlation of ER and PR expression levels with menopausal status or Ki67 labeling index

Since PR expression levels of luminal A and B are different, we determined the Ki67 labeling index for ER and PR expression levels and taking menopausal status into consideration. The results are shown in Fig. 1. Using the cutoff value described in Patients and Methods, we divided ER and PR expression levels into four subgroups, i.e., ER-H/PR-H, ER-H/PR-L, PR-L/ER-H, and ER-L/PR-L. Among the premenopausal patients, Ki67 expression of the ER-H/PR-L group (23.1%, 14.0–29.5%) was significantly higher ($P = 0.003$) than that of the ER-H/PR-H subgroup (9.5%, 5.2–18.8%). Among the postmenopausals, on the other hand, Ki67 of the ER-L/PR-L subgroup (22.5%, 12.9–47.9%) was significantly higher ($P = 0.002$) than that of the ER-H/PR-H subgroup (10.0%, 5.0-18.1%).

The distribution of cancers classified according to ER and PR expression levels in pre- and postmenopausals is shown in Table 2. As for luminal A, the distribution between pre- and postmenopausals was significantly different ($P = 0.0001$), with nearly 70% of the cancers recognized in the ER-H/PR-H subgroup among the premenopausals, while ER-H/PR-H accounted for 39%, and ER-H/PR-L (54%) was the most frequent type among the postmenopausals. However, luminal B subtype showed no significant difference of ER and PR expression levels between pre- and postmenopausals.

Correlation between ER and PR expression levels in luminal A subtype

In order to exclude the influence of growth factor signaling in which PR may be downregulated through transcriptional suppression in luminal B, we examined correlations between ER and PR expression levels for the luminal A subtype divided into pre- and postmenopausals. The results are shown in Fig. 2. ER and PR expression levels showed significant correlation (correlation coefficient 0.69, $P < 0.0001$) for premenopausals ($n = 36$), but correlation was weak (correlation coefficient 0.26, $P = 0.02$) for postmenopausals ($n = 70$).

Discussion

The most prominent finding of this study is that the biological characteristics of luminal A and luminal B cancers are different. As shown in Table 2, ER and PR expression levels are more significant in luminal A than in luminal B cancers. Our findings indicate that among premenopausals, nearly 70% of luminal A cancers possessed ER-H/PR-H, but that this was rarely detected in ER-H/PR-L. On the other hand, more than 50% of the postmenopausal luminal A cancers were accounted for by the ER-H/PR-L subgroup. PR, a downstream target molecule of estrogen signaling, may be suppressed during activation of growth factor signaling [5]. However, since PR is induced by estrogen signaling, even if tumors express sufficient ER, estradiol deficiency makes it impossible for much PR to be produced, thus resulting in lower expression levels of PR. Since crosstalk with growth factor signaling is unlikely in luminal A cancers, we hypothesize that low PR expression levels indicate an insufficient supply of intratumoral estradiol. Among premenopausals, estrogen deficiency is unlikely because of high levels of circulating estradiole in the blood produced by menstruation. In the postmenopausal estrogen