SUPPLEMENTARY TABLES

Supplementary Table 1. The list of 62 cancer susceptibility genes included in the gene panel.

Major associated tumor types	Gene list
Breast and/or ovarian tumors	ATM,BARD1,BRAC1,BRAC2,BRIP1,CDK12,CHEK2,NBN,NF1,PALB2,PPP2R2A,PTEN,RAD51B,STK11,TP53
Gatrointestinal tumors	APC,BMPR1A,CDH1,CHEK1,CHEK2,EPCAM,GREM1,KIT,MLH1,MSH2,MSH3,MSH6,MUTYH,NF1,NTHL1,PDGFRA,PMS2,POLD1,POLE,PPP2R2A,PTEN,SDHA,SDHAF2,SDHB,SDHC,SDHD,SMAD4,STK11,TP53
Melanoma	CDK4,CDKN2A,CHEK1,PTEN
Renal tumors	FH,FLCN,MET,PTEN,TP53,VHL,WT1
Hematologic tumors	FANCA,FANCI,FANCL,NBN,PPP2R2A,TP53
Thyroid tumors	MEN1,NF1,PTEN,RET
Lung tumors	EGFR,PPP2R2A
Prostate cancer	CHEK2,HOXB13,NBN
Pancreatic cancer	NBN
Schwannoma/Meningioma	NF1,NF2
Carney complex	PRKAR1A
Gorlin syndrome	PTCH1
Retinoblastoma	RB1
Familial Paraganglioma syndrome	SDHA,SDHAF2,SDHB,SDHC,SDHD
Li-Fraumeni syndrome	TP53
Tuberous Sclerosis	TSC1,TSC2
Wilms Tumor	WT1

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Supplementary Table 2. Variants of unknown significance identified in study cohort.

Supplementary Table 3. Distribution of LP/P germline mutations according to breast cancer molecular subtype.

	Molecular subtype				
Cancer susceptibility genes	**HR-/HER2-**	**HR-/HER2+**	**HR+/HER2-**	**HR+/HER2+**	**Unknown**
BRCA1 (n=11)	4 (36.4%)	3 (27.3%)	3 (27.3%)	1 (9.1%)	0 (0%)
BRCA2 (n=18)	0 (0%)	1 (5.6%)	14 (77.8%)*	1 (5.6%)	2 (11.1%)
PALB2 (n=4)	2 (50%)	0 (0%)	1 (25%)	1 (25%)	0 (0%)
MUTYH (n=4)	1 (25%)	0 (0%)	2 (50%)	1 (25%)	0 (0%)
ATM (n=3)	0 (0%)	1 (33.3%)	1 (33.3%)	1 (33.3%)	0 (0%)
BRIP1 (n=3)	0 (0%)	0 (0%)	1 (33.3%)	1 (33.3%)	1 (33.3%)
CDH1 (n=3)	1 (33.3%)	0 (0%)	2 (66.7%)	0 (0%)	0 (0%)
RAD51C (n=3)	1 (33.3%)	0 (0%)	1 (33.3%)	0 (0%)	1 (33.3%)
CHEK2 (n=2)	0 (0%)	0 (0%)	2 (100%)	0 (0%)	0 (0%)
FANCA (n=2)	0 (0%)	0 (0%)	2 (100%)	0 (0%)	0 (0%)
PMS2 (n=2)	0 (0%)	0 (0%)	1 (50%)	1 (50%)#	0 (0%)
TP53 (n=2)	0 (0%)	0 (0%)	1 (50%)	1 (50%)#	0 (0%)
FANCI (n=1)	0 (0%)	0 (0%)	1 (100%)*	0 (0%)	0 (0%)
FANCL (n=1)	0 (0%)	0 (0%)	1 (100%)	0 (0%)	0 (0%)
PTEN (n=1)	0 (0%)	0 (0%)	1 (100%)	0 (0%)	0 (0%)

Note: Asterisk (*) denotes the detection of concurrent germline mutation in *BRCA2* and *FANCI* in a patient with HR+/HER2- tumor; Sharp sign (#) denotes the detection of concurrent germline mutation in *TP53* and *PMS2* in a patient with HR+/HER2+ tumor.

Supplementary Table 4. Germline mutation detection rates according to breast cancer molecular subtype.

	Molecular subtype				
	HR-/HER2- (n=61)	**HR-/HER2+ (n=59)**	**HR+/HER2- (n=267)**	**HR+/HER2+ (n=82)**	**Unknown (n=55)**
Overall	9 (14.8%)	5 (8.5%)	33 (12.4%)	7 (8.5%)	4 (7.3%)
BRCA1/2	4 (6.6%)	4 (6.8%)	17 (6.4%)	2 (2.4%)	2 (3.6%)
Non-BRCA1/2	5 (8.2%)	1 (1.7%)	16 (6.0%)	5 (6.1%)	2 (3.6%)

Supplementary Table 5. The difference of somatic mutations among Germline-BRCA1/2 group, Germline- others group and Others group.