

# Association between Mutation and Expression of *TP53* as a Potential Prognostic Marker of Triple-Negative Breast Cancer

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## Supplementary Data

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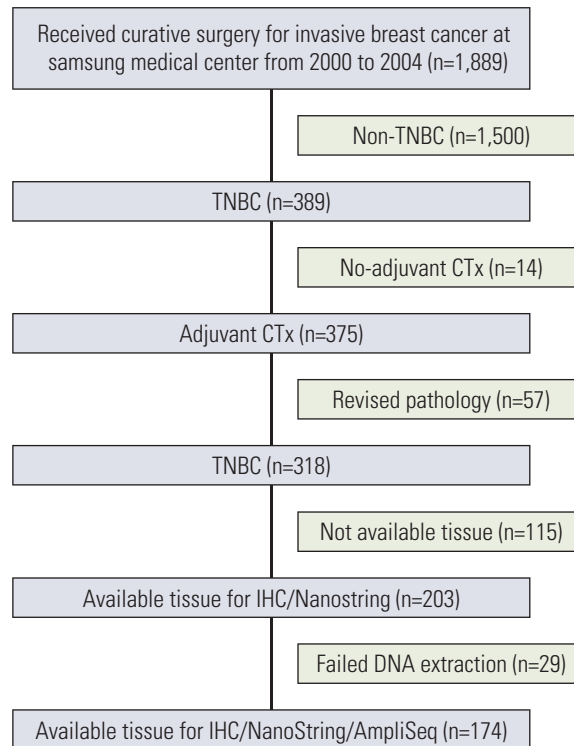
**Supplementary Table 1.** List of sequenced genes

<i>ABL1</i>	<i>CDH1</i>	<i>ERBB4</i>	<i>FLT3</i>	<i>IDH1</i>	<i>KRAS</i>	<i>NRAS</i>	<i>RET</i>	<i>TP53</i>
<i>AKT1</i>	<i>CDKN2A</i>	<i>EZH2</i>	<i>GNA11</i>	<i>IDH2</i>	<i>MET</i>	<i>PDGFRA</i>	<i>SMAD4</i>	<i>VHL</i>
<i>ALK</i>	<i>CSF1R</i>	<i>FBXW7</i>	<i>GNAQ</i>	<i>JAK2</i>	<i>MLH1</i>	<i>PIK3CA</i>	<i>SMARCB1</i>	
<i>APC</i>	<i>CTNNB1</i>	<i>FGFR1</i>	<i>GNAS</i>	<i>JAK3</i>	<i>MPL</i>	<i>PTEN</i>	<i>SMO</i>	
<i>ATM</i>	<i>EGFR</i>	<i>FGFR2</i>	<i>HRAS</i>	<i>KDR</i>	<i>NOTCH1</i>	<i>PTPN11</i>	<i>SRC</i>	
<i>BRAF</i>	<i>ERBB2</i>	<i>FGFR3</i>	<i>HNF1A</i>	<i>KIT</i>	<i>NPM1</i>	<i>RB1</i>	<i>STK11</i>	

**Supplementary Table 2.** Effect of *TP53* status and stage on DRFS (multivariate analysis, Cox-regression)

Clinical variable	Hazard ratio	95% Confidence interval	p-value
<b>Stage</b>			
I	1.0	NA	< 0.001
IIA	1.02	0.32-3.24	
IIB	2.59	0.81-8.27	
IIIA	7.11	1.89-26.68	
IIIC	21.91	5.08-94.54	
<b><i>TP53</i> status</b>			
Wild type, high mRNA expression	1.0	NA	0.057
Wild type, low mRNA expression	1.63	0.57-4.66	
Missense, high mRNA expression	6.73	1.67-27.10	
Missense, low mRNA expression	0.69	0.22-2.20	
Deletion, high mRNA expression	0.94	0.18-4.84	
Deletion, low mRNA expression	2.45	0.28-21.50	

DRFS, distant recurrence-free survival.



**Supplementary Fig. S1.** Patient cohort (n=174). TNBC, triple-negative breast cancer; CTx, chemotherapy; IHC, immunohistochemistry.