

Supplementary Table 1. Patients characteristics in ER+/HER2- and TNBC mBC populations.

Characteristics	TNBC	ER+/HER2-
	(n = 361) n (%)	(n = 565) n (%)
Age median (Q1-Q3)	52 [43-61]	55 [47-64]
Histological grade		
SBR1	3 (0.9)	35 (6.6)
SBR2	60 (17.4)	283 (53.2)
SBR3	276 (80)	207 (38.9)
SBR X (non gradable)	6 (1.7)	7 (1.3)
Missing	16	33
ECOG[†]		
ECOG 0	214 (61.5)	259 (50.3)
ECOG 1	132 (37.9)	254 (49.3)
ECOG 2	2 (0.6)	2 (0.4)
Missing	13	50
Progesteron status		
Negative	361 (100)	135 (24.6)
Positive	0	413 (75.4)
Missing	0	17
IHC subtype (primary diagnosis)		
ER+/HER2-	0	565 (100)
TNBC	361 (100)	0
Number of metastatic sites (at screening) median (Q1-Q3)	2 (2-3)	3 (2-4)
Number of metastatic sites (categorical)		
1-2	191 (53.7)	248 (45.2)
3-4	133 (37.4)	242 (44.1)
>= 5	32 (9)	59 (10.7)
Missing	5	16
Presence of liver metastasis		
No	226 (63.5)	152 (27.7)
Yes	130 (36.5)	397 (72.3)
Missing	5	16
Presence of lung metastasis		
No	208 (58.4)	406 (74)
Yes	148 (41.6)	143 (26)
Missing	5	16
Line of chemotherapy at screening		
First line	353 (99.2)	522 (95.1)
Second line	3 (0.8)	27 (4.9)
Missing	5	16
Previous chemotherapy		
No	104 (29.2)	149 (27.1)
Yes	252 (70.8)	400 (72.9)
Missing	5	16
Previous adjuvant chemotherapy		
Anthracyclin + Other	26 (7.3)	56 (10)
Anthracyclin based	69 (19.4)	190 (33.9)
No	228 (64.0)	276 (49.3)
Other chemo/target	33 (9.3)	38 (6.8)
Missing	5	16
Previous neoadjuvant chemotherapy		
Anthracyclin + Other	39 (11.0)	55 (10)
Anthracyclin based	103 (28.9)	184 (33.5)
No	207 (58.1)	275 (50.1)
Other chemo/target	7 (2)	35 (6.4)
Missing	5	16
Previous hormoneotherapy		
No	349 (98)	12 (2.2)
Yes	7 (2)	537 (97.8)
Missing	5	16
Previous radiotherapy		
No	118 (33.1)	71 (12.9)
Yes	238 (66.9)	478 (87.1)
Missing	5	16
Overall survival		
Alive	111 (31.2)	251 (45.7)
Death	245 (68.8)	298 (54.3)
Missing	5	16
Follow-up (years) median (CI* 95%)	2.1 [2.0-2.4]	2.1 [2.1 - 2.3]

[†] ECOG: Eastern Cooperative Oncology Group
Performance score

* CI: confidence interval

Supplementary Table 2. Patient characteristics in ER+/HER2- and TNBC eBC populations.

Characteristics	Metabric		TCGA		PACS04		Total	
	ER+/HER2- (n = 1314)	TNBC (n = 306)	ER+/HER2- (n = 605)	TNBC (n = 165)	ER+/HER2- (n = 243)	NA	ER+/HER2- (n = 2162)	TNBC (n = 471)
	n (%)	n (%)	n (%)	n (%)	n (%)		n (%)	n (%)
Age (median)	64.0	53.7	59.0	54.0	50.7		61.0	54.0
Menopause								
No	196 (15.3)	104 (40.8)	122 (24.6)	34 (26.8)	0 (NaN)		318 (17.9)	138 (36.1)
Yes	1089 (84.7)	151 (59.2)	373 (75.4)	93 (73.2)	0 (NaN)		1462 (82.1)	244 (63.9)
NA	0	0	39	11	243		282	11
Missing	29	51	71	27	0		100	78
Progesteron status								
Negative	415 (32.3)	255 (100)	71 (13.3)	138 (100)	43 (18.8)		529 (25.9)	393 (100)
Positive	870 (67.7)	0 (0)	461 (86.7)	0 (0)	186 (81.2)		1517 (74.1)	
Missing	29	51	73	27	14		116	78
Histological grade								
1	147 (12)	6 (2.1)	0 (NaN)	0 (NaN)	39 (16.5)		186 (12.7)	6 (2.1)
2	638 (52)	23 (9.1)	0 (NaN)	0 (NaN)	130 (55.1)		768 (52.5)	23 (9.1)
3	442 (36)	230 (90.9)	0 (NaN)	0 (NaN)	67 (28.4)		509 (34.8)	230 (90.9)
Missing	87	53	605	165	7		699	218
T stage								
T1 (T ≤ 2 cm)	586 (46)	94 (37.0)	154 (28.8)	37 (26.8)	125 (51.7)		865 (42.2)	131 (33.4)
T2 (2cm < T ≤ 5 cm)	633 (49.7)	143 (56.3)	293 (54.9)	85 (61.6)	105 (43.4)		1031 (50.3)	228 (58.2)
T3 (T > 5 cm)	55 (4.3)	17 (6.7)	87 (16.3)	16 (11.6)	12 (5)		154 (7.5)	33 (8.6)
NA	11	1	0	0	1		12	1
Missing	29	51	71	27	0		100	78
N stage								
N0 (0)	714 (55.6)	120 (47.1)	214 (46.4)	85 (66.9)	0 (0)		928 (46.7)	205 (53.7)
N1 (1-3)	391 (30.4)	95 (37.3)	167 (36.2)	25 (19.7)	155 (63.8)		713 (35.8)	120 (31.4)
N2 (4-9)	134 (10.4)	21 (8.2)	49 (10.6)	12 (9.4)	65 (26.7)		248 (12.5)	33 (8.6)
N3 (10+)	46 (3.6)	19 (7.5)	31 (6.7)	5 (3.9)	23 (9.5)		100 (5)	24 (6.3)
Missing	29	51	144	38	0		173	89
Previous hormonotherapy								
No	350 (27.2)	195 (76.5)	0 (NaN)	0 (NaN)	2 (0.8)		352 (23.1)	195 (76.5)
Yes	935 (72.8)	60 (23.5)	0 (NaN)	0 (NaN)	237 (99.2)		1172 (76.9)	60 (23.5)
Missing	29	51	605	165	4		638	216
Previous radiotherapy								
No	546 (42.5)	72 (28.2)	194 (39.6)	53 (42.4)	7 (2.9)		747 (37)	125 (32.9)
Yes	739 (57.5)	183 (71.8)	296 (60.4)	72 (57.6)	236 (97.1)		1271 (63)	255 (67.1)
Missing	29	51	115	40	0		144	91
Overall survival								
0	537 (41.8)	117 (45.9)	484 (90.6)	117 (84.8)	204 (84)		1225 (59.4)	234 (59.5)
1	748 (58.2)	138 (54.1)	50 (9.4)	21 (15.2)	39 (16)		837 (40.6)	159 (40.5)
Missing	29	51	71	27	0		100	78

Supplementary Table 3. Genomic alterations in the ER+/HER2- populations.

Gene(s)	Chromosomal band	Location	Status ^a	mBC (n = 565) % ^b	TCGA (n = 605)		Metabric (n = 1314)		PACS04 (n = 243)				
					% ^b	Raw p-value ^c	Corrected p-value ^d	% ^b	Raw p-value ^c	Corrected p-value ^d	% ^b	Raw p-value ^c	Corrected p-value ^d
Know candidate genes (n = 45)													
<i>DLEU2L</i>	1p31.3	64014588	amp	0,2	0,3	1,00E+00	1,00E+00	0,2	1,00E+00	1,00E+00	0,0	1,00E+00	1,00E+00
<i>TRIM46</i>	1q22	155145873	amp	6,5	1,8	8,53E-05	4,68E-03	2,1	3,05E-06	5,98E-05	1,6	6,20E-03	1,17E-01
<i>FASLG (TNFSF18/TNFSF4)</i>	1q24.3	172628154	amp	4,6	1,5	3,15E-03	5,49E-02	1,1	5,74E-06	1,01E-04	0,4	4,72E-03	1,12E-01
<i>KDMSB</i>	1q32.1	202696526	amp	4,2	3,0	3,12E-01	8,49E-01	2,3	2,87E-02	1,09E-01	2,9	4,67E-01	9,54E-01
<i>RAB7L1</i>	1q32.1	205737114	amp	5,5	2,3	7,63E-03	1,05E-01	2,5	1,80E-03	1,25E-02	3,7	3,71E-01	9,02E-01
<i>PFN2</i>	3q25.1	149682691	amp	1,8	0,0	2,99E-03	5,39E-02	0,4	4,79E-03	2,72E-02	0,0	8,19E-02	4,46E-01
<i>PIK3CA</i>	3q26.32	178865902	amp	2,3	1,2	2,00E-01	6,92E-01	0,2	2,56E-05	3,71E-04	0,8	2,53E-01	7,22E-01
<i>EREG</i>	4q13.3	75230860	amp	1,4	1,3	1,00E+00	1,00E+00	0,9	4,66E-01	8,05E-01	1,2	1,00E+00	1,00E+00
<i>AIM1</i>	6q21	106959730	amp	2,5	1,7	4,30E-01	9,56E-01	0,6	1,28E-03	9,62E-03	0,8	2,03E-01	6,75E-01
<i>EGFR</i>	7p11.2	55086714	amp	1,1	0,7	6,70E-01	1,00E+00	0,5	3,34E-01	6,53E-01	1,6	7,33E-01	1,00E+00
<i>ZNF703 (FGFR1)</i>	8p11.23	37553269	amp	24,6	15,7	1,92E-04	7,97E-03	10,8	2,57E-14	5,98E-12	11,5	3,86E-05	1,23E-02
<i>MYC</i>	8q24.21	128747680	amp	13,3	4,3	8,35E-08	3,47E-05	3,1	1,21E-16	6,08E-14	3,3	3,19E-05	1,23E-02
<i>SEPHS1</i>	10p13	13359424	amp	3,2	0,7	3,06E-03	5,41E-02	0,6	3,05E-05	4,30E-04	0,0	1,06E-02	1,43E-01
<i>ZMI21</i>	10q22.3	80828792	amp	2,3	1,7	5,57E-01	1,00E+00	1,2	1,23E-01	3,30E-01	0,8	2,53E-01	7,22E-01
<i>EHF</i>	11p13	34642640	amp	2,8	0,8	1,82E-02	1,79E-01	0,8	9,38E-04	7,42E-03	0,4	5,35E-02	3,59E-01
<i>PLD4</i>	11q13.2	67118248	amp	8,8	5,5	3,18E-02	2,49E-01	4,7	7,73E-04	6,27E-03	2,9	3,87E-03	1,02E-01
<i>CNCD1</i>	11q13.3	69455855	amp	30,1	15,7	6,44E-09	5,24E-06	14,0	4,96E-16	1,80E-13	13,2	5,59E-07	1,43E-03
<i>P2RY2</i>	11q13.4	72929343	amp	5,7	3,8	1,72E-01	6,57E-01	3,4	3,42E-02	1,27E-01	2,9	1,30E-01	5,56E-01
<i>NDUFC2-KCTD14</i>	11q14.1	77728017	amp	13,6	6,0	1,40E-05	1,50E-03	6,7	1,76E-06	3,88E-05	7,8	2,63E-02	2,41E-01
<i>FOXM1</i>	12p13.33	2966847	amp	2,7	2,0	5,69E-01	1,00E+00	1,9	3,89E-01	7,40E-01	0,8	1,63E-01	6,16E-01
<i>MDM2</i>	12q15	69201956	amp	5,8	3,8	1,35E-01	5,72E-01	2,2	9,51E-05	1,13E-03	1,2	6,45E-03	1,17E-01
<i>STOML3</i>	13q13.3	39540062	amp	0,0	0,3	5,09E-01	9,95E-01	0,2	8,76E-01	1,00E+00	0,0	NA	NA
<i>NEMF</i>	14q21.3	50249997	amp	3,0	1,2	4,27E-02	2,92E-01	1,4	3,73E-02	1,34E-01	0,8	1,04E-01	5,01E-01
<i>IGF1R</i>	15q26.3	99192200	amp	1,6	2,1	6,28E-01	1,00E+00	1,8	9,62E-01	1,00E+00	2,5	5,74E-01	1,00E+00
<i>TP53I13</i>	17q11.2	27893070	amp	3,7	2,3	2,17E-01	7,04E-01	0,5	5,27E-07	1,44E-05	0,4	1,59E-02	1,80E-01
<i>ERBB2</i>	17q12	37844167	amp	1,6	0,0	5,41E-03	8,21E-02	0,0	2,42E-05	3,53E-04	0,0	1,07E-01	5,01E-01
<i>SGCA</i>	17q21.33	48241575	amp	5,8	3,8	1,35E-01	5,72E-01	2,5	5,44E-04	4,96E-03	1,6	1,50E-02	1,74E-01
<i>RPS6KB1</i>	17q23.1	57970447	amp	9,4	6,0	3,56E-02	2,54E-01	3,4	1,87E-07	6,23E-06	2,5	9,15E-04	5,70E-02
<i>BIRC5</i>	17q25.3	76210267	amp	5,1	2,0	5,64E-03	8,50E-02	1,6	2,56E-05	3,71E-04	0,8	6,43E-03	1,17E-01
<i>NOTCH3</i>	19p13.12	15270444	amp	1,2	1,3	1,00E+00	1,00E+00	1,1	9,29E-01	1,00E+00	0,4	4,83E-01	9,60E-01
<i>CNCE1</i>	19q12	30302805	amp	1,9	1,5	7,04E-01	1,00E+00	0,8	6,92E-02	2,09E-01	0,4	1,81E-01	6,16E-01
<i>RCN3</i>	19q13.33	50030875	amp	1,4	0,8	4,95E-01	9,95E-01	1,4	1,00E+00	1,00E+00	0,4	3,78E-01	9,02E-01
<i>SEMG1</i>	20q13.12	43835638	amp	5,0	2,5	3,62E-02	2,55E-01	1,3	4,30E-06	7,93E-05	1,6	4,39E-02	3,25E-01
<i>ZNF217</i>	20q13.2	52183604	amp	10,4	6,6	2,46E-02	2,18E-01	4,3	5,16E-07	1,42E-05	3,7	2,48E-03	8,59E-02
<i>TPD52L2</i>	20q13.33	62496596	amp	7,8	5,0	6,20E-02	3,53E-01	3,0	5,63E-06	1,00E-04	2,9	1,34E-02	1,62E-01
<i>PCNT</i>	21q22.3	47744036	amp	1,8	1,5	8,81E-01	1,00E+00	0,9	1,77E-01	4,17E-01	0,8	4,82E-01	9,60E-01
<i>CDKN2AIP</i>	4q35.1	184365744	del	0,0	0,2	1,00E+00	1,00E+00	0,1	1,00E+00	1,00E+00	0,0	NA	NA
<i>LZTS1</i>	8p21.3	20103676	del	0,4	0,7	7,45E-01	1,00E+00	0,2	1,00E+00	1,00E+00	0,0	8,75E-01	1,00E+00
<i>PPP2R2A</i>	8p21.2	26149007	del	0,4	0,5	1,00E+00	1,00E+00	0,3	1,00E+00	1,00E+00	0,4	1,00E+00	1,00E+00
<i>CDKN2A</i>	9p21.3	21967751	del	6,4	2,0	2,79E-04	8,47E-03	0,8	5,84E-12	2,73E-10	1,2	3,23E-03	1,10E-01
<i>PTEN</i>	10q23.31	89622870	del	4,2	1,5	7,52E-03	1,44E-01	1,4	2,16E-04	3,55E-03	1,2	4,86E-02	7,97E-01
<i>RB1</i>	13q14.2	48877887	del	2,1	0,7	5,73E-02	7,65E-01	0,3	2,50E-04	4,08E-03	0,4	1,42E-01	1,00E+00
<i>CAPN3</i>	15q15.1	42640301	del	0,0	0,2	1,00E+00	1,00E+00	0,0	NA	NA	0,0	NA	NA
<i>CDH1</i>	16q22.1	68771128	del	1,2	0,2	6,12E-02	7,65E-01	0,2	1,57E-02	1,55E-01	0,4	4,83E-01	1,00E+00
<i>MAR2K4</i>	17p12	11924141	del	5,1	2,6	3,95E-02	5,57E-01	1,8	7,97E-05	1,41E-03	3,7	4,85E-01	1,00E+00
New discovered genes													
<i>GJC2</i>	1q42.13	228337553	Amp	5,0	0,5	5,01E-06	7,29E-04	1,0	1,75E-07	5,89E-06	0,4	2,90E-03	9,26E-02
<i>TERT</i>	5p15.33	1253262	Amp	5,8	1,8	5,40E-04	1,55E-02	1,4	2,32E-07	7,31E-06	0,0	2,59E-04	3,47E-02
<i>RAD21</i>	8q24.11	117858174	Amp	14,0	4,5	2,59E-08	1,58E-05	2,2	2,57E-23	1,26E-19	5,3	6,22E-04	4,79E-02
<i>ST3GAL1 (NDRG1/WISP1)</i>	8q24.22	134467091	Amp	9,4	2,5	8,80E-07	1,85E-04	2,0	5,77E-13	1,14E-10	2,5	9,15E-04	5,70E-02
<i>SOC1</i>	16p13.13	11348262	Amp	4,1	1,0	1,39E-03	3,07E-02	1,0	1,83E-05	2,76E-04	0,0	3,07E-03	9,39E-02

^a: Amp : Focal amplification; Del : Homozygous deletion

^b: Percentage of genomic alterations

^c: Chi-squared test : TCGA (or Metabric or PACS04) versus mBC ; genes and p-values in bold are significant

^d: Corrected Chi-squared test : TCGA (or Metabric or PACS04) versus mBC ; genes and p-values in bold are significant

NA: Not Applicable. Frequencies at 0% in both populations (mBC and eBC)

Supplementary Table 4. Prognostic effect of copy number alterations in the ER+/HER2- mBC population.

Gene(s)	Chromosomal band	Location	Status ^a	Univariate (OS)		Multivariate (OS)	
				p-value ^b	HR (95% CI)	Raw p-value ^b	Corrected p-value ^b
<i>TRIM46</i>	1q22	155145873	Amp	0,38	1.0 [0.5 ; 1.7]	0,16	1.00
<i>FASLG (TNFSF18/TNFSF4)</i>	1q24.3	172628154	Amp	0,49	0.7 [0.3 ; 1.4]	0,3	1.00
<i>ZNF703 (FGFR1)</i>	8p11.23	37553269	Amp	0,09	1.3 [1.0 ; 1.7]	0,09	1.00
<i>MYC</i>	8q24.21	128747680	Amp	0,02	1.5 [1.0 ; 2.3]	0,03	0,53
<i>SEPHS1</i>	10p13	13359424	Amp	0,55	0.8 [0.4 ; 1.6]	0,46	1.00
<i>POLD4</i>	11q13.2	67118248	Amp	0,96	1.1 [0.7 ; 1.7]	0,98	1.00
<i>CCND1</i>	11q13.3	69455855	Amp	0,57	1.1 [0.8 ; 1.4]	0,75	1.00
<i>NDUFC2-KCTD14</i>	11q14.1	77728017	Amp	0,85	0.8 [0.4 ; 1.3]	0,84	1.00
<i>RPS6KB1</i>	17q23.1	57970447	Amp	0,38	0.8 [0.5 ; 1.2]	0,25	1.00
<i>BIRC5</i>	17q25.3	76210267	Amp	0,86	1.2 [0.6 ; 2.1]	0,72	1.00
<i>SEMG1</i>	20q13.12	43835638	Amp	0,64	1.0 [0.5 ; 1.9]	0,92	1.00
<i>ZNF217</i>	20q13.2	52183604	Amp	0,84	1.2 [0.8 ; 1.8]	0,79	1.00
<i>CDKN2A</i>	9p21.3	21967751	Del	0,22	1.2 [0.8 ; 1.9]	0,17	1.00
<i>PTEN</i>	10q23.31	89622870	Del	0,22	1.5 [0.9 ; 2.5]	0,13	1.00
<i>GJC2</i>	1q42.13	228337553	Amp	0,34	0.8 [0.4 ; 1.5]	0,18	1.00
<i>TERT</i>	5p15.33	1253262	Amp	<0.0001	2.6 [1.6 ; 4.0]	<0.001	0.01
<i>RAD21</i>	8q24.11	117858174	Amp	0,03	1.4 [0.9 ; 2.0]	0,07	1.00
<i>ST3GAL1 (NDRG1/WISP1)</i>	8q24.22	134467091	Amp	0,67	0.6 [0.4 ; 1.0]	0,52	1.00
<i>SOCS1</i>	16p13.13	11348262	Amp	0,58	0.8 [0.4 ; 1.6]	0,26	1.00

^a : Amp : Focal amplification; Del : Homozygous deletion

^b : p-values in bold are significant

Supplementary Table 5. Genomic regions with prognostic effect of copy number alterations in the ER+/HER2- eBC population.

Gene(s)	Chromosomal band	Location	Status ^a	Univariate (OS)		Multivariate (OS)	
				p-value ^b	HR (95% CI)	Raw p-value ^b	Corrected p-value
<i>TRIM46</i>	1q22	155145873	Amp	0,38	1.1 [0.7 ; 1.8]	0,38	1,00
<i>FASLG (TNFSF18/TNFSF4)</i>	1q24.3	172628154	Amp	0,47	1.2 [0.6 ; 2.2]	0,39	1,00
<i>ZNF703 (FGFR1)</i>	8p11.23	37553269	Amp	0,20	1.1 [0.9 ; 1.4]	0,35	1,00
<i>MYC</i>	8q24.21	128747680	Amp	0,28	1.2 [0.8 ; 1.9]	0,61	1,00
<i>SEPHS1</i>	10p13	13359424	Amp	0,65	1.0 [0.4 ; 2.5]	0,21	1,00
<i>POLD4</i>	11q13.2	67118248	Amp	0,74	0.9 [0.6 ; 1.3]	0,49	1,00
<i>CCND1</i>	11q13.3	69455855	Amp	0,37	1.2 [0.9 ; 1.5]	0,58	1,00
<i>NDUFC2-KCTD14</i>	11q14.1	77728017	Amp	0,81	0.8 [0.5 ; 1.2]	0,88	1,00
<i>RPS6KB1</i>	17q23.1	57970447	Amp	0,45	0.7 [0.4 ; 1.0]	0,05	1,00
<i>BIRC5</i>	17q25.3	76210267	Amp	0,33	1.3 [0.7 ; 2.2]	0,65	1,00
<i>SEMG1</i>	20q13.12	43835638	Amp	0,51	0.8 [0.4 ; 1.8]	<0.01	0,20
<i>ZNF217</i>	20q13.2	52183604	Amp	0,49	1.0 [0.7 ; 1.6]	0,11	1,00
<i>CDKN2A</i>	9p21.3	21967751	Del	<0.01	2.0 [1.1 ; 3.6]	0,02	0,42
<i>PTEN</i>	10q23.31	89622870	Del	0,02	1.5 [0.9 ; 2.6]	0,03	0,63
<i>GJC2</i>	1q42.13	228337553	Amp	<0.01	2.7 [1.4 ; 5.2]	0,02	0,42
<i>TERT</i>	5p15.33	1253262	Amp	0,13	1.5 [0.8 ; 2.6]	0,46	1,00
<i>RAD21</i>	8q24.11	117858174	Amp	0,70	1.0 [0.6 ; 1.6]	0,14	1,00
<i>ST3GAL1 (NDRG1/WISP1)</i>	8q24.22	134467091	Amp	0,27	NA	0,09	1,00
<i>SOCS1</i>	16p13.13	11348262	Amp	0,29	0.6 [0.3 ; 1.5]	0,03	0,53

^a : Amp : Focal amplification; Del : Homozygous deletion

^b : p-values in bold are significant

NA: Not Applicable.

Supplementary Table 6. Known candidate genomic alterations in the TNBC populations.

Gene(s)	Chromosomal band	Location	Status ^a	mBC (n = 361)	TCGA (n = 165)		Metabric (n = 306)	
				% ^b	% ^b	Raw p-value ^c	% ^b	Raw p-value ^c
<i>DLEU2L</i>	1p31.3	64014588	amp	0,8	0,0	5,82E-01	1,6	5,54E-01
<i>TRIM46</i>	1q22	155145873	amp	15,2	13,3	6,60E-01	8,2	7,38E-03
<i>FASLG (TNFSF18/TNFSF4)</i>	1q24.3	172628154	amp	5,0	3,0	4,31E-01	3,3	3,63E-01
<i>KDM5B</i>	1q32.1	202696526	amp	4,2	2,4	4,62E-01	2,0	1,63E-01
<i>RAB7L1</i>	1q32.1	205737114	amp	5,3	3,6	5,53E-01	3,6	3,96E-01
<i>PFN2</i>	3q25.1	149682691	amp	3,0	0,6	1,54E-01	2,3	7,16E-01
<i>PIK3CA</i>	3q26.32	178865902	amp	3,0	2,4	9,08E-01	2,9	1,00E+00
<i>EREG</i>	4q13.3	75230860	amp	1,7	0,0	2,21E-01	1,3	9,55E-01
<i>AIM1</i>	6q21	106959730	amp	6,9	3,6	1,98E-01	3,6	8,46E-02
<i>EGFR</i>	7p11.2	55086714	amp	3,0	3,0	1,00E+00	3,3	1,00E+00
<i>ZNF703 (FGFR1)</i>	8p11.23	37553269	amp	4,7	9,1	7,94E-02	5,2	8,97E-01
<i>MYC</i>	8q24.21	128747680	amp	16,3	12,1	2,60E-01	6,9	2,77E-04
<i>SEPHS1</i>	10p13	13359424	amp	5,0	2,4	2,60E-01	5,2	1,00E+00
<i>ZMIZ1</i>	10q22.3	80828792	amp	6,4	2,4	9,09E-02	3,9	2,15E-01
<i>EHF</i>	11p13	34642640	amp	7,5	3,6	1,36E-01	5,2	3,07E-01
<i>POLD4</i>	11q13.2	67118248	amp	1,7	2,4	8,03E-01	2,3	7,63E-01
<i>CCND1</i>	11q13.3	69455855	amp	7,5	4,2	2,26E-01	4,2	1,12E-01
<i>P2RY2</i>	11q13.4	72929343	amp	0,8	3,0	1,26E-01	2,0	3,56E-01
<i>NDUFC2-KCTD14</i>	11q14.1	77728017	amp	3,0	1,8	6,03E-01	2,9	1,00E+00
<i>FOXM1</i>	12p13.33	2966847	amp	7,8	7,3	9,87E-01	8,8	7,20E-01
<i>MDM2</i>	12q15	69201956	amp	1,1	1,8	8,03E-01	2,3	3,75E-01
<i>STOML3</i>	13q13.3	39540062	amp	0,8	0,0	5,82E-01	0,7	1,00E+00
<i>NEMF</i>	14q21.3	50249997	amp	1,1	0,6	9,47E-01	1,0	1,00E+00
<i>IGF1R</i>	15q26.3	99192200	amp	1,9	1,2	8,15E-01	1,6	9,98E-01
<i>TP53I13</i>	17q11.2	27893070	amp	1,1	0,6	9,47E-01	1,6	8,03E-01
<i>ERBB2</i>	17q12	37844167	amp	0,6	0,0	8,46E-01	0,0	5,53E-01
<i>SGCA</i>	17q21.33	48241575	amp	0,8	0,6	1,00E+00	1,0	1,00E+00
<i>RPS6KB1</i>	17q23.1	57970447	amp	1,7	3,0	4,91E-01	2,0	1,00E+00
<i>BIRC5</i>	17q25.3	76210267	amp	3,0	3,0	1,00E+00	2,0	5,22E-01
<i>NOTCH3</i>	19p13.12	15270444	amp	2,5	3,6	6,54E-01	3,6	5,46E-01
<i>CCNE1</i>	19q12	30302805	amp	10,8	9,1	6,56E-01	5,9	3,35E-02
<i>RCN3</i>	19q13.33	50030875	amp	0,8	1,2	1,00E+00	1,0	1,00E+00
<i>SEMG1</i>	20q13.12	43835638	amp	2,8	1,2	4,26E-01	0,7	7,89E-02
<i>ZNF217</i>	20q13.2	52183604	amp	3,9	1,8	3,30E-01	2,6	4,88E-01
<i>TPD52L2</i>	20q13.33	62496596	amp	4,7	3,6	7,43E-01	4,6	1,00E+00
<i>PCNT</i>	21q22.3	47744036	amp	5,0	4,2	8,80E-01	2,6	1,69E-01
<i>CDKN2AIP</i>	4q35.1	184365744	del	0,0	1,2	1,83E-01	0,0	NA
<i>LZTS1</i>	8p21.3	20103676	del	0,6	1,8	3,67E-01	1,0	8,53E-01
<i>PPP2R2A</i>	8p21.2	26149007	del	1,9	1,2	8,15E-01	1,3	7,39E-01
<i>CDKN2A</i>	9p21.3	21967751	del	7,2	4,2	2,69E-01	2,6	1,22E-02
<i>PTEN</i>	10q23.31	89622870	del	9,7	7,9	6,11E-01	2,9	8,22E-04
<i>RB1</i>	13q14.2	48877887	del	6,4	3,6	2,85E-01	1,6	4,42E-03
<i>CAPN3</i>	15q15.1	42640301	del	0,6	1,2	7,91E-01	0,3	1,00E+00
<i>CDH1</i>	16q22.1	68771128	del	0,3	0,6	1,00E+00	0,7	8,86E-01
<i>MAP2K4</i>	17p12	11924141	del	0,8	2,4	2,85E-01	1,6	5,54E-01

^a : Amp : Focal amplification; Del : Homozygous deletion

^b : Percentage of genomic alterations

^c : Chi-squared test : TCGA (or Metabric) versus mBC ; genes and p-values in bold are significant

NA: Not Applicable. Frequencies at 0% in both populations (mBC and Metabric)

Supplementary Table 7. Genomic regions with prognostic effect of copy number alterations in the TNBC mBC population.

Gene(s)	Chromosomal band	Location	Status ^a	mBC (n = 361) % ^b	TCGA (n = 165)		Metabric (n = 306)		Univariate (OS)		Multivariate (OS)	
					% ^b	Raw p-value ^c	% ^b	Raw p-value ^c	P-value	HR (95% CI)	Raw p-value	Corrected p-value
<i>NFIB (LINCO0583)</i>	9p23	14081842	Amp	9,1	4,2	7,35E-02	5	4,99E-02	0,93	0.9 [0.4 ; 1.9]	6,20E-01	1,00
<i>GPC5</i>	13q31.3	92050929	Del	5,3	0,6	1,90E-02	0,3	5,00E-04	0,45	1.9 [0.4 ; 7.9]	4,10E-01	0,82

^a: Amp : Focal amplification; Del : Homozygous deletion

^b: Percentage of genomic alterations

^c: Chi-squared test: TCGA (or Metabric) *versus* mBC; p-values in bold are significant

Supplementary Table 8. Known candidate genomic alterations in ER+/HER2- mBC in comparison with mTNBC.

Gene(s)	Chromosomal band	Location	Status ^a	ER+/HER2- mBC (n = 565)	mTNBC (n = 361)	Raw p-value ^c	Corrected p-value
				% ^b	% ^b		
<i>DLEU2L</i>	1p31.3	64014588	amp	0,2	0,8	3,34E-01	7,64E-01
<i>TRIM46</i>	1q22	155145873	amp	6,5	15,2	2,70E-05	1,28E-03
<i>FASLG (TNFSF18/TNFSF4)</i>	1q24.3	172628154	amp	4,6	5,0	9,13E-01	1,00E+00
<i>KDM5B</i>	1q32.1	202696526	amp	4,2	4,2	1,00E+00	1,00E+00
<i>RAB7L1</i>	1q32.1	205737114	amp	5,5	5,3	1,00E+00	1,00E+00
<i>PFN2</i>	3q25.1	149682691	amp	1,8	3,0	2,95E-01	7,58E-01
<i>PIK3CA</i>	3q26.32	178865902	amp	2,3	3,0	6,28E-01	1,00E+00
<i>EREG</i>	4q13.3	75230860	amp	1,4	1,7	9,81E-01	1,00E+00
<i>AIM1</i>	6q21	106959730	amp	2,5	6,9	1,82E-03	2,78E-02
<i>EGFR</i>	7p11.2	55086714	amp	1,1	3,0	5,19E-02	2,69E-01
<i>ZNF703 (FGFR1)</i>	8p11.23	37553269	amp	24,6	4,7	6,29E-15	2,06E-11
<i>MYC</i>	8q24.21	128747680	amp	13,3	16,3	2,31E-01	6,86E-01
<i>SEPHS1</i>	10p13	13359424	amp	3,2	5,0	2,27E-01	6,76E-01
<i>ZMIZ1</i>	10q22.3	80828792	amp	2,3	6,4	3,17E-03	4,24E-02
<i>EHF</i>	11p13	34642640	amp	2,8	7,5	1,82E-03	2,78E-02
<i>POLD4</i>	11q13.2	67118248	amp	8,8	1,7	1,47E-05	8,55E-04
<i>CCND1</i>	11q13.3	69455855	amp	30,1	7,5	4,78E-16	4,70E-12
<i>P2RY2</i>	11q13.4	72929343	amp	5,7	0,8	3,38E-04	8,68E-03
<i>NDUFC2-KCTD14</i>	11q14.1	77728017	amp	13,6	3,0	1,61E-07	2,98E-05
<i>FOXO1</i>	12p13.33	2966847	amp	2,7	7,8	5,86E-04	1,31E-02
<i>MDM2</i>	12q15	69201956	amp	5,8	1,1	6,40E-04	1,40E-02
<i>STOML3</i>	13q13.3	39540062	amp	0,0	0,8	1,15E-01	4,44E-01
<i>NEMF</i>	14q21.3	50249997	amp	3,0	1,1	9,52E-02	3,91E-01
<i>IGF1R</i>	15q26.3	99192200	amp	1,6	1,9	8,92E-01	1,00E+00
<i>TP53I13</i>	17q11.2	27893070	amp	3,7	1,1	2,92E-02	1,89E-01
<i>ERBB2</i>	17q12	37844167	amp	1,6	0,6	2,66E-01	7,58E-01
<i>SGCA</i>	17q21.33	48241575	amp	5,8	0,8	2,41E-04	6,71E-03
<i>RPS6KB1</i>	17q23.1	57970447	amp	9,4	1,7	5,31E-06	3,89E-04
<i>BIRC5</i>	17q25.3	76210267	amp	5,1	3,0	1,75E-01	5,54E-01
<i>NOTCH3</i>	19p13.12	15270444	amp	1,2	2,5	2,42E-01	7,06E-01
<i>CCNE1</i>	19q12	30302805	amp	1,9	10,8	1,46E-08	5,02E-06
<i>RCN3</i>	19q13.33	50030875	amp	1,4	0,8	6,24E-01	1,00E+00
<i>SEMG1</i>	20q13.12	43835638	amp	5,0	2,8	1,43E-01	5,28E-01
<i>ZNF217</i>	20q13.2	52183604	amp	10,4	3,9	4,83E-04	1,15E-02
<i>TPD52L2</i>	20q13.33	62496596	amp	7,8	4,7	8,80E-02	3,83E-01
<i>PCNT</i>	21q22.3	47744036	amp	1,8	5,0	9,58E-03	8,77E-02
<i>CDKN2AIP</i>	4q35.1	184365744	del	0,0	0,0	2,76E-01	7,58E-01
<i>LZTS1</i>	8p21.3	20103676	del	0,4	0,6	1,00E+00	1,00E+00
<i>PPP2R2A</i>	8p21.2	26149007	del	0,4	1,9	8,21E-01	1,00E+00
<i>CDKN2A</i>	9p21.3	21967751	del	6,4	7,2	5,37E-03	6,11E-02
<i>PTEN</i>	10q23.31	89622870	del	4,2	9,7	2,96E-01	7,58E-01
<i>RB1</i>	13q14.2	48877887	del	2,1	6,4	8,21E-01	1,00E+00
<i>CAPN3</i>	15q15.1	42640301	del	0,0	0,6	9,51E-01	1,00E+00
<i>CDH1</i>	16q22.1	68771128	del	1,2	0,3	6,95E-01	1,00E+00
<i>MAP2K4</i>	17p12	11924141	del	5,1	0,8	1,00E+00	1,00E+00

^a : Amp : Focal amplification; Del : Homozygous deletion

^b : Percentage of genomic alterations; values in bold correspond to genes statistically more amplified with corrected pvalue

^c : Chi-squared test : mTNBC versus ER+/HER2- mBC; p-values in bold are significant

Supplementary Table 9. New specific genomic alterations in the ER-/HER2- mBC or mTNBC population

Gene(s)	Chromosomal band	Location	Status ^a	ER+/HER2- mBC (n = 565) % ^b	mTNBC (n = 361) % ^b	Raw p-value ^c
New specific genomic alterations in the mTNBC						
<i>ANGPTL1 (ABL2)</i>	1q25.2	178818840	Amp	3,2	8,8	3,49E-04
<i>TFEB (APOBEC2)</i>	6p21.1	41651716	Amp	0,7	4,7	1,68E-04
<i>NFKBIE (VEGFA)</i>	6p21.1	44225903	Amp	0,5	4,4	1,20E-04
<i>RAB23 (BMP5)</i>	6p11.2	57053607	Amp	0,9	4,2	1,89E-03
<i>CYP3A4</i>	7q22.1	99354604	Amp	0,4	3,6	3,84E-04
<i>AKR1B10</i>	7q33	134212344	Amp	0,4	3,9	1,73E-04
<i>ASB13</i>	10p15.1	5680830	Amp	3,2	8,9	3,44E-04
New specific genomic alterations in the ER+/HER2- mBC						
<i>NFKBIA</i>	14q13.2	35870717	Amp	4,2	0,3	6,08E-04
<i>TRAF7 (NAGPA)</i>	16p13.3	2205699	Amp	5,3	0,6	2,33E-04

^a: Amp : Focal amplification

^b: Percentage of genomic alterations

^c: Chi-squared test : mTNBC versus ER+/HER2- mBC ; p-values in bold are significant

Supplementary Table 10. Known candidates genomic alterations in the ER+/HER2- population by CDK4 inhibitor before biopsies collection.

Gene(s)	Chromosomal band	Location	Status ^a	non pre-treated mBC (n = 323)	pre-treated mBC (n = 102)	Raw p-value ^c
				% ^b	% ^b	
DLEU2L	1p31.3	64014588	amp	0.3	0.0	1.00E+00
TRIM46	1q22	155145873	amp	8.7	4.9	3.04E-01
FASLG (TNFSF18/TNFSF4)	1q24.3	172628154	amp	5.9	5.9	1.00E+00
KDM5B	1q32.1	202696526	amp	5.3	3.9	7.77E-01
RAB7L1	1q32.1	205737114	amp	5.9	8.8	4.15E-01
PFN2	3q25.1	149682691	amp	2.5	1.0	6.03E-01
PIK3CA	3q26.32	178865902	amp	2.2	2.9	9.40E-01
EREG	4q13.3	75230860	amp	1.5	2.0	1.00E+00
AIM1	6q21	106959730	amp	1.9	4.9	1.83E-01
EGFR	7p11.2	55086714	amp	1.2	1.0	1.00E+00
ZNF703 (FGFR1)	8p11.23	37553269	amp	25.1	31.4	2.60E-01
MYC	8q24.21	128747680	amp	13.0	16.7	4.42E-01
SEPHS1	10p13	13359424	amp	3.7	3.9	1.00E+00
ZMI21	10q22.3	80828792	amp	1.5	6.9	1.31E-02
EHF	11p13	34642640	amp	2.8	3.9	8.02E-01
POLD4	11q13.2	67118248	amp	10.5	8.8	7.57E-01
CCND1	11q13.3	69455855	amp	30.0	29.4	1.00E+00
P2RY2	11q13.4	72929343	amp	4.6	8.8	1.78E-01
NDUFC2-KCTD14	11q14.1	77728017	amp	13.6	12.7	9.52E-01
FOXM1	12p13.33	2966847	amp	1.2	6.9	5.76E-03
MDM2	12q15	69201956	amp	5.3	10.8	8.35E-02
STOML3	13q13.3	39540062	amp	0.0	0.0	NA
NEMF	14q21.3	50249997	amp	4.0	2.0	4.98E-01
IGF1R	15q26.3	99192200	amp	1.2	2.0	9.54E-01
TP53I13	17q11.2	27893070	amp	3.1	3.9	9.29E-01
ERBB2	17q12	37844167	amp	2.2	2.0	1.00E+00
SGCA	17q21.33	48241575	amp	6.2	6.9	9.93E-01
RPS6KB1	17q23.1	57970447	amp	9.3	10.8	8.00E-01
BIRC5	17q25.3	76210267	amp	4.6	7.8	3.20E-01
NOTCH3	19p13.12	15270444	amp	1.9	0.0	3.65E-01
CCNE1	19q12	30302805	amp	2.2	1.0	7.26E-01
RCN3	19q13.33	50030875	amp	1.9	0.0	3.65E-01
SEMG1	20q13.12	43835638	amp	5.0	8.8	2.28E-01
ZNF217	20q13.2	52183604	amp	10.8	11.8	9.36E-01
TPD52L2	20q13.33	62496596	amp	8.7	9.8	8.80E-01
PCNT	21q22.3	47744036	amp	1.9	2.9	7.89E-01
CDKN2AIP	4q35.1	184365744	del	0.0	0.0	NA
LZTS1	8p21.3	20103676	del	n	0.0	NA
PPP2R2A	8p21.2	26149007	del	0.0	0.0	NA
CDKN2A	9p21.3	21967751	del	6.5	2.9	2.66E-01
PTEN	10q23.31	89622870	del	3.7	4.9	8.08E-01
RB1	13q14.2	48877887	del	1.9	3.9	4.10E-01
CAPN3	15q15.1	42640301	del	0.0	0.0	NA
CDH1	16q22.1	68771128	del	1.9	1.0	8.72E-01
MAP2K4	17p12	11924141	del	4.3	5.9	7.07E-01

^a: Amp : Focal amplification; Del : Homozygous deletion

^b: Percentage of genomic alterations

^c: Chi-squared test : CDK4i pretreated mBC versus CDK4i unpretreated mBC ; p-values in bold are significant

NA: Not Applicable. Frequencies at 0% in mBC population

Supplementary Table 11. Genomic regions with prognostic effect of copy number alterations in the not treated and treated by CDK4 inhibitor population before biopsies collection.

Gene(s)	Chromosomal band	Location	Status ^a	Non pre-treated				Pre-treated			
				Univariate (OS)		Multivariate (OS)		Univariate (OS)		Multivariate (OS)	
				P-value ^b	Overall survival (OS) HR (95% CI)	Raw p-value ^b	Corrected p-value	P-value ^b	Overall survival (OS) HR (95% CI)	Raw p-value ^b	Corrected p-value
Candidate											
ZMIZ1	10q22.3	80828792	Amp	0.84	1.2 [0.5 ; 2.8]	0.22	1	0.68	1.2 [0.3 ; 4.3]	0.96	1
FOXM1	12p13.33	2966847	Amp	0.11	3.0 [0.9 ; 9.6]	0.11	1	0.09	1.9 [0.5 ; 7.5]	0.04	0.5
Discovery											
AGR2	7p21.1	16831435	Amp	0.44	0.6 [0.1 ; 5.1]	0.51	1	0.09	0.2 [0.0 ; 1.7]	0.37	1
CPNE3 (MMP16)	8q21.3	87497059	Amp	0.66	0.8 [0.4 ; 1.8]	0.75	1	0.98	0.7 [0.2 ; 2.1]	0.73	1
CDK4	12q14.1	58141510	Amp	0.48	1.6 [0.5 ; 5.2]	0.71	1	0.51	1.5 [0.3 ; 7.1]	0.29	1
LGR5	12q21.1	71833550	Amp	0.82	0.9 [0.4 ; 2.0]	0.83	1	0.27	1.7 [0.5 ; 5.4]	0.51	1
NFKBIA	14q13.2	35870717	Amp	0.62	1.3 [0.5 ; 3.5]	0.68	1	0.43	0.5 [0.1 ; 2.0]	0.27	1
CCL1	17q12	32687347	Amp	0.72	0.9 [0.2 ; 4.0]	0.27	1	0.07	2.0 [0.7 ; 6.1]	0.19	1
KCNG1	20q13.13	49620193	Amp	0.87	0.9 [0.4 ; 1.8]	0.74	1	0.84	1.7 [0.5 ; 5.8]	0.83	1

^a : Amp : Focal amplification

^b : p-values in bold are significant

Supplementary Table 12. Genomic regions with prognostic effect of copy number alterations in the not treated and treated by CDK4 inhibitor in ER+/HER2- eBC population before biopsies collection.

Gene(s)	Chromosomal band	Location	Status ^a	Univariate (OS)		Multivariate (OS)	
				P-value ^b	Overall survival (OS) HR (95% CI)	Raw p-value ^b	Corrected p-value
Candidate							
ZMIZ1	10q22.3	80828792	Amp	0.68	0.8 [0.4 ; 1.6]	0.92	1
FOXM1	12p13.33	2966847	Amp	0.51	0.9 [0.5 ; 1.5]	0.97	1
Discovery							
NSL1 (ATF3)	1q32.3	212899495	Amp	<0.01	2.1 [1.2 ; 3.6]	0.55	1
AGR2	7p21.1	16831435	Amp	0.36	0.6 [0.1 ; 2.5]	0.49	1
CPNE3 (MMP16)	8q21.3	87497059	Amp	0.24	1.3 [0.8 ; 2.1]	0.33	1
CDK4	12q14.1	58141510	Amp	<0.01	2.0 [1.0 ; 4.2]	0.03	0.4
LGR5	12q21.1	71833550	Amp	0.07	1.4 [0.7 ; 2.5]	0.24	1
NFKBIA	14q13.2	35870717	Amp	1	1.0 [0.4 ; 2.1]	0.82	1
CCL1	17q12	32687347	Amp	0.88	0.7 [0.3 ; 1.9]	1.00	1
KCNG1	20q13.13	49620193	Amp	0.63	0.9 [0.6 ; 1.5]	0.05	0.71

^a : Amp : Focal amplification; Del : Homozygous deletion

^b : p-values in bold are significant