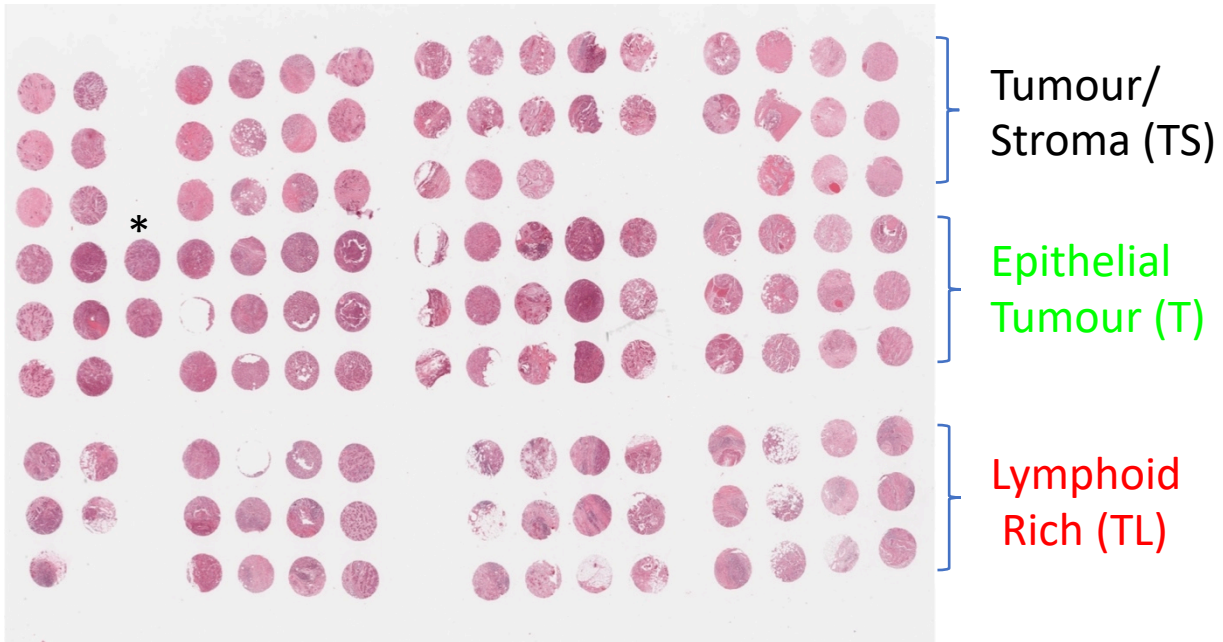
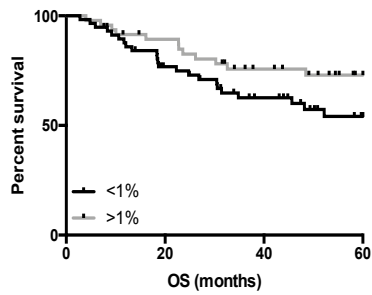


Supp Figure 1

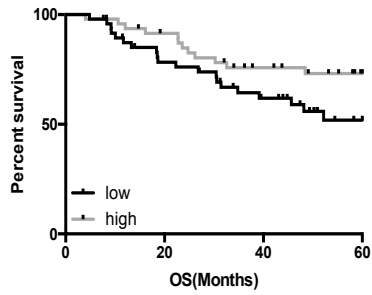
(A)



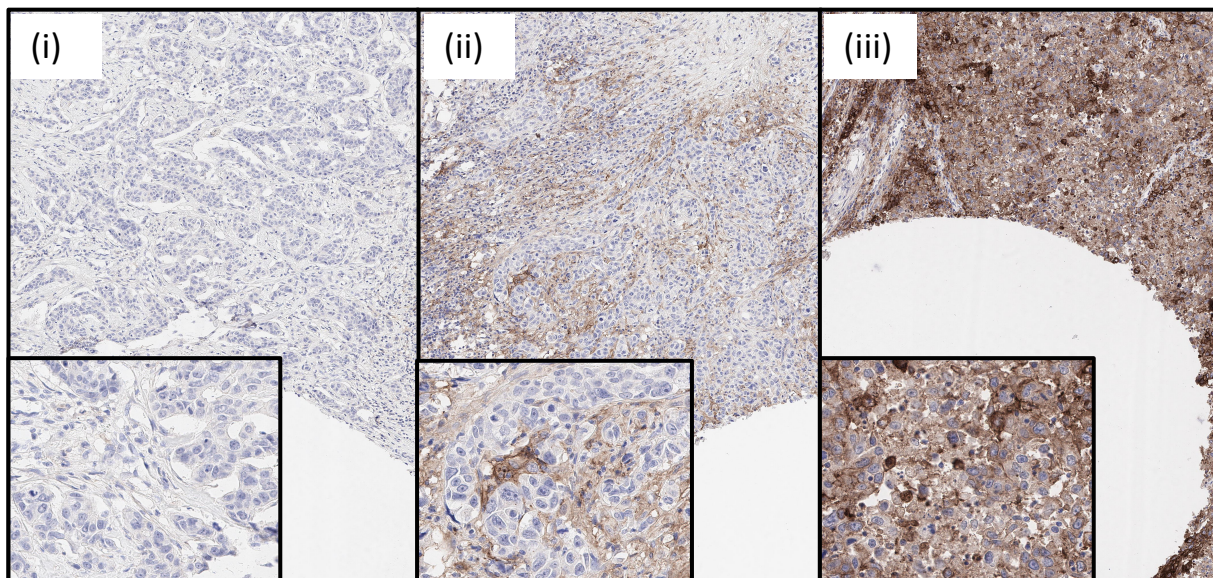
(B)(i)



(ii)

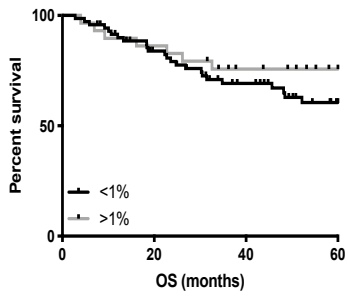


(C)

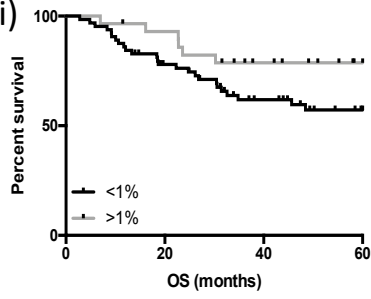


Supp Figure 2

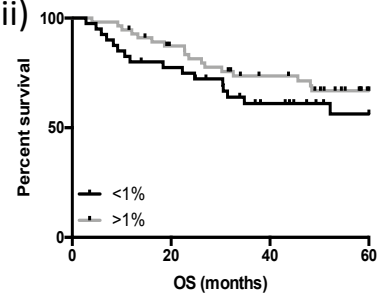
(A)(i)



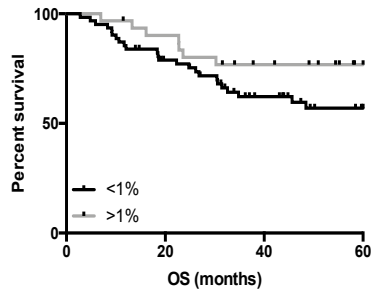
(ii)



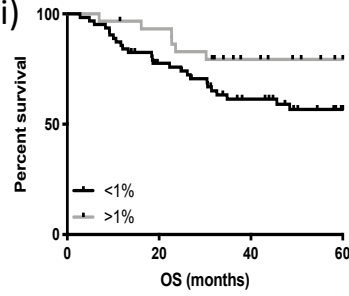
(iii)



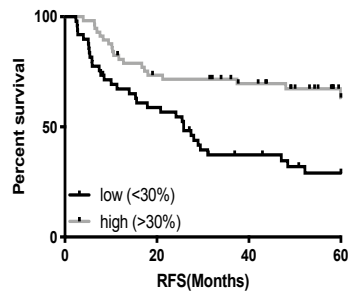
(B)(i)



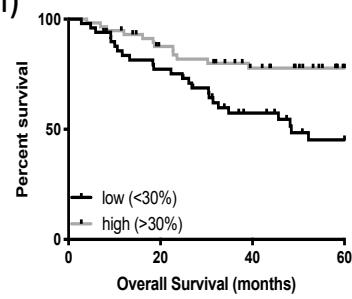
(ii)



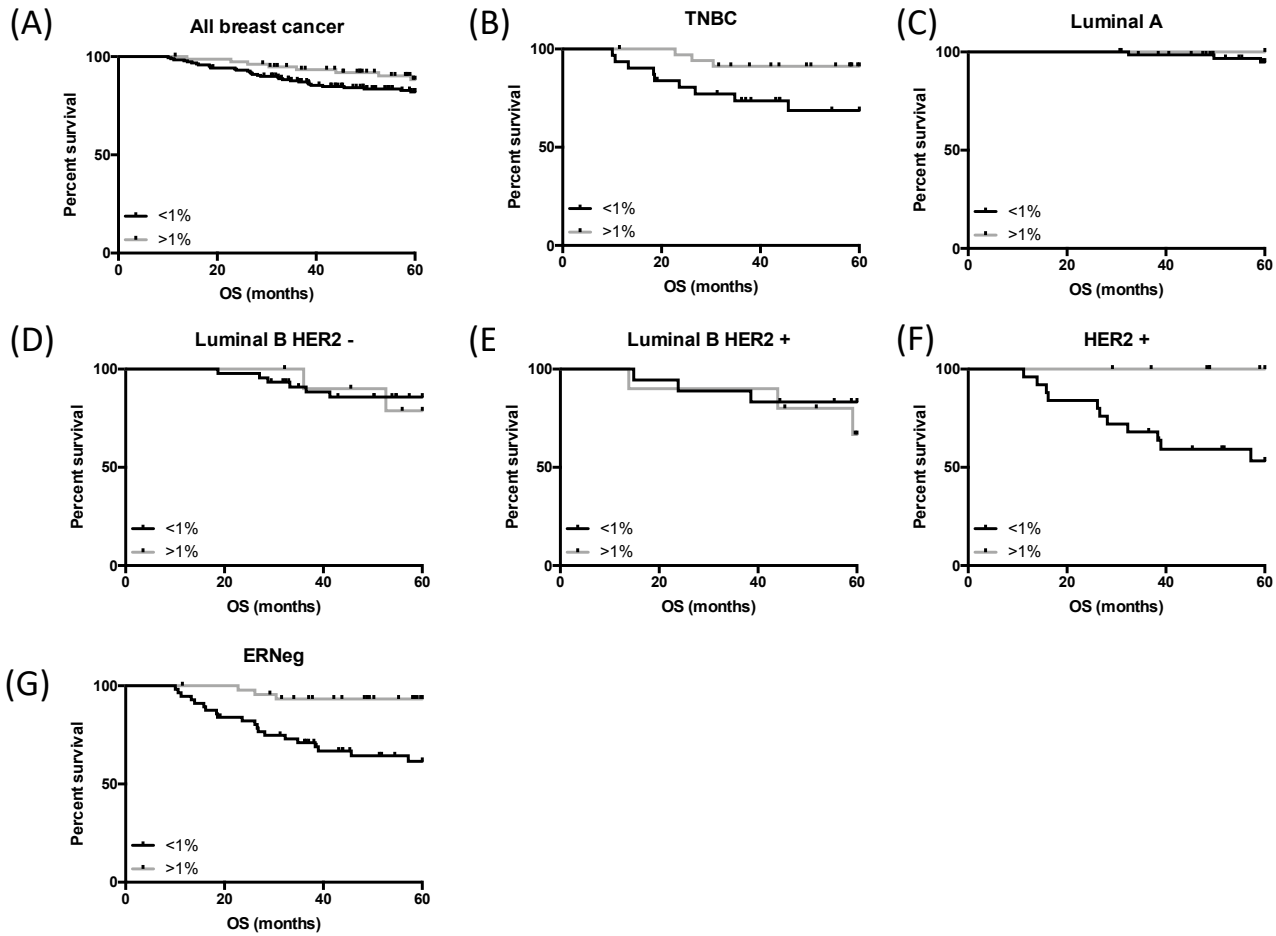
(C)(i)



(ii)



Supplementary Figure 3



Supp Table 1:
(a) 9 core TNBC TMA

Variable (N=109)	N (%)
Age (mean (range))	56.69 (28-90)
Grade N(%)	
G2	13 (11.9)
G3	96 (88.1)
T code N(%)	
T1	31 (28.5)
T2	53 (48.6)
T3	19 (17.4)
T4	6 (5.5)
N code N(%)	
N0	63 (57.8)
N1	29 (26.6)
N2	8 (7.35)
N3	8 (7.35)
Unknown	1 (0.9)
Chemotherapy	
None	18 (16.5)
FEC	81 (74.3)
FEC-D	9 (8.3)
AC	1 (0.9)

(b) 300 breast cohort

Variable (<i>N</i> = 293)	<i>N</i> (%)
Tumour grade	
G1	5 (2)
G2	119 (41)
G3	169 (58)
pN stage (nodal involvement)	
N0	127 (43)
N1mi	4 (1)
N1	95 (32)
N2	38 (13)
N3	29 (10)
pT stage	
T1	65 (22)
T2	181 (62)
T3	41 (14)
T4	6 (2)
Histological type	
Ductal (no special type)	230 (78)
Lobular (no special type)	31 (11)
Mixed ductal and lobular	25 (9)
Other	7 (2)
ER status (at diagnosis)	
Positive	175 (60)
Negative	115 (39)
Unknown	3 (1)
PR status (at diagnosis)	
Positive	115 (39)
Negative	139 (47)
Unknown	39 (13)
HER2 status (at diagnosis)	
Positive	75 (26)
Negative	192 (66)
Unknown	26 (9)

Supp Table 2:

Antibody	Company/Clone	Platform/pre-treatment/dilution	Detection chemistry	Mono-/polyclonal	Epitope
ER	Ventana/SP1	BenchMark/CC1 60mins	Ultraview	Rabbit Monoclonal	synthetic peptide corresponding to the C-terminal
PR	Ventana/1E2	BenchMark/CC1 60mins	Ultraview	Rabbit Monoclonal	Synthetic peptide identified as an area of potential high antigenicity common to progesterone receptor A and B forms
HER2	Ventana/4B5	BenchMark/CC1 30mins	Ultraview	Rabbit Monoclonal	Internal domain of HER2
PDL1	Ventana /SP142 (originally sourced from Spring Bioscience)	BenchMark/CC1 56mins/1:40	Optiview with amplification	Rabbit Monoclonal	Synthetic peptide derived from C-terminus
PDL1	Abcam/28-8	BenchMark/CC1 56mins/1:800	Optiview with amplification	Rabbit Monoclonal	extracellular domain of PDL1 (Phe19-Thr239)
PDL1	Cell Signalling /405.9A11	BenchMark/CC1 56mins/1:20	Optiview with amplification	Mouse Monoclonal	Synthetic peptide derived from C-terminus

Supp Table 3:

	PDL1 Abcam Benchmark	PDL1 Abcam Bondmax	PDL1 SP142 Benchmark	PDL1 SP142 Bondmax	PDL1 Cell Signalling Benchmark	PDL1 Cell Signalling Bondmax
PDL1 Abcam Benchmark		0.7707 (95%CI 0.4066-0.9233)	0.8254 (95%CI 0.5775-0.9541)	0.8285 95%CI 0.5215-0.9456	0.7718 (95% CI 0.4089 - 0.9239)	0.8571 (95%CI 0.5843 - 0.9558)
PDL1 Abcam Bondmax	0.7707 (95%CI 0.4066-0.9233)		0.9826 95%CI 0.9407-0.0049	0.9908 95%CI 0.9683-0.9973	0.9992 (95%CI 0.9971-0.9997)	0.9774 95%CI 0.9238-0.9934
PDL1 SP142 Benchmark	0.8254 (95%CI 0.5775-0.9541)	0.9826 95%CI 0.9407-0.0049		0.9973 95%CI 0.9905-0.9992)	0.9823 95%CI 0.9501-0.9949	0.9985 95%CI 0.9947-0.9995
PDL1 SP142 Bondmax	0.8285 95%CI 0.5215-0.9456	0.9908 95%CI 0.9683-0.9973	0.9973 95%CI 0.9905-0.9992)		0.9908 95%CI 0.9680-0.9974	0.9961 95%CI 0.9864-0.9989
PDL1 Cell Signalling Benchmark	0.7718 (95% CI 0.4089 - 0.9239)	0.9992 (95%CI 0.9971-0.9997)	0.9823 95%CI 0.9501-0.9949	0.9908 95%CI 0.9680-0.9974		0.9772 95% CI 0.9226-0.9934)
PDL1 Cell Signalling Bondmax	0.8571 (95%CI 0.5843 - 0.9558)	0.9774 95%CI 0.9238-0.9934	0.9985 95%CI 0.9947-0.9995	0.9961 95%CI 0.9864-0.9989	0.9772 95% CI 0.9226-0.9934)	

Supp Table 4a

Relapse Free Survival			Univariate		
All core types - Overall core score			HR	95% CI	p-value
SP142		N(n)104 (52)			
PDL1	>1%	46 (18)	1		
	<1%	58 (34)	0.536	0.316-0.94	0.0294*
RNAScope		N (n) 96 (45)			
PDL1	high	48 (19)	1		
	low	48 (26)	0.632	0.352- 1.136	0.1258

Supp Table 4b

Overall Survival			Univariate		
All core types - Overall core score			HR	95% CI	p-value
SP142		N(n)104 ()			
PDL1	>1%	46 (12)	1		
	<1%	58 (23)	0.548	0.288- 1.084	0.0858
RNAScope		N (n) 96 (32)			
PDL1	high	48 (12)	1		
	low	48 (20)	0.519	0.260-1.045	0.0669

Supp Table 5

Relapse Free Survival			Univariate		
9 core TMA SP142			HR	95% CI	p-value
TS Cores		100 (47)			
PDL1	>1%	29 (11)	1		
	<1%	71 (38)	0.640	0.360-1.225	0.1914
T cores		93 (45)			
PDL1	>1%	29 (9)	1		
	<1%	64 (36)	0.445	0.271-0.917	0.0255*
TL cores		96 (49)			
PDL1	>1%	56 (24)	1		
	<1%	40 (25)	0.562	0.305-0.972	0.0405*
T cores tumour region		93 (45)			
PDL1	>1%	31 (10)	1		
	<1%	62 (35)	0.455	0.274-0.909	0.0237*
T cores stroma region		93 (45)			
PDL1	>1%	30 (9)	1		
	<1%	63 (36)	0.421	0.260-0.872	0.0164*

Supp Table 5b

Overall Survival			Univariate		
9 core TMA SP142		N(n)	HR	95% CI	p-value
TS Cores		100(31)			
PDL1	>1%	29 (7)	1		
	<1%	71 (24)	0.631	0.308-1.402	0.2785
T cores		93 (31)			
PDL1	>1%	29 (6)	1		
	<1%	64 (25)	0.457	0.244-1.074	0.0767
TL cores		96 (33)			
PDL1	>1%	56 (17)	1		
	<1%	40 (16)	0.668	0.326-1.326	0.2426
T cores tumour region		93 (31)			
PDL1	>1%	31 (7)	1		
	<1%	62 (24)	0.505	0.262-1.133	0.1040
T cores stroma region		93 (31)			
PDL1	>1%	30 (6)	1		
	<1%	63 (25)	0.434	0.236-1.026	0.0586

Supp Table 5b

Relapse Free Survival			Univariate		
		N(n)	HR	95% CI	p-value
TILs	>30%	57 (19)	1		
	<30%	49 (33)	0.3787	0.2173-0.66	0.0004
Overall Survival		N(n)	HR	95% CI	p-value
TILs	>30%	58 (23)	1		
	<30%	50 (24)	0.3712	0.192-0.719	0.0034

Supp Table 6a

Relapse Free Survival			Univariate		
Breast 300 TMA SP142		N(n)	HR	95% CI	p-value
All breast		268 (65)			
PDL1	>1%	78 (13)	1		
	<1%	190 (53)	0.547	0.350-0.994	0.0477*
Luminal A		78 (10)			
PDL1	>1%	10 (0)	1		
	<1%	68 (10)	0.314 [†]	0.051-1.928	0.2112
Luminal B HER2-		66 (14)			
PDL1	>1%	11 (2)	1		
	<1%	55 (12)	0.620	0.183-2.381	0.5272
Luminal B HER2 +		28 (9)			
PDL1	>1%	10 (2)	1		
	<1%	18 (7)	0.484	0.136-2.041	0.3550
HER2 +		36 (12)			
PDL1	>1%	11 (2)	1		
	<1%	25 (10)	0.350	0.131-1.378	0.1553
TNBC		67 (21)			
PDL1	>1%	35 (7)	1		
	<1%	32 (14)	0.355	0.148-0.841	0.0190*
ER -		103 (33)			
PDL1	>1%	46 (9)	1		
	<1%	57 (24)	0.360	0.195-0.761	0.0063**

[†] Mantel-Haenszel HR reported

Supp Table 6b

Overall Survival			Univariate		
Breast 300 TMA SP142	N(n)	HR	95% CI	p-value	
All breast	268 (40)				
PDL1	>1%	78 (8)	1		
	<1%	190 (32)	0.584	0.316-1.224	0.1695
Luminal A	78 (3)				
PDL1	>1%	10 (0)	1		
	<1%	68 (3)	0.314†	0.0115-8.576	0.4714
Luminal B HER2-	66 (8)				
PDL1	>1%	11 (2)	1		
	<1%	55 (6)	1.297	0.237-7.38	0.7493
Luminal B HER2 +	28 (6)				
PDL1	>1%	10 (3)	1		
	<1%	18 (3)	1.85	0.360-10.30	0.4437
HER2 +	36 (11)				
PDL1	>1%	11 (0)	1		
	<1%	25 (11)	0.215†	0.062-0.745	0.0153*
TNBC	67 (12)				
PDL1	>1%	35 (3)	1		
	<1%	32 (9)	0.255	0.087-0.861	0.0269*
ER -	103 (23)				
PDL1	>1%	46 (3)	1		
	<1%	57 (20)	0.154	0.103-0.526	0.0005***

† Mantel-Haenszel HR reported

Supp Table 6c

Relapse Free Survival			Multivariate- Stepwise regression		
ER Neg SP142	N(n)	103 (33)	HR	95% CI	p-value
PDL1	>1%	57 (24)	1		
	<1%	46 (9)	0.386	0.179-0.833	0.0153*
Lymph node	no	54 (10)	1		
	yes	49 (23)	0.308	0.146-0.651	0.0020**

Supp Table 6d

Overall Survival			Multivariate- Stepwise Regression		
ER Neg SP142	N(n)	103 (23)	HR	95% CI	p-value
PDL1	>1%	57 (20)	1		
	<1%	46 (3)	0.185	0.055-0.942	0.00656**
Lymph node	no	54 (4)	1		
	yes	49 (19)	0.189	0.064-0.56	0.00263**