

Additional data

Supplementary table 1. Association of parous and nulliparous groups with clinicopathological characteristics

Clinicopathological factors	Subgroups	PPBC1 (1 to 5 years)(n=23) n(%)	PPBC2 (6 to 10 years)(n=38) n(%)	PPBC3 (>10 years)(n=72) n(%)	NPBC (Nulliparous) (n=22) n(%)	P value
T size (cm)	>3	06(26)	15(40)	35(49)	11(50)	0.179
	≤3	14(61)	21(55)	30(42)	08(36)	
	Missing	03(13)	02(5)	07(9)	03(14)	
Grade	Low	13(57)	20(53)	31(43)	12(54)	0.228
	High	07(30)	15(39)	35(49)	05(23)	
	Missing	03(13)	03(8)	06(8)	05(23)	
Lymph node status	Positive	15(65)	24(63)	39(54)	14(64)	0.61
	Negative	08(35)	14(37)	33(46)	07(32)	
	Missing	0	0	0	01(4)	
Stage	Early	14(61)	25(66)	43(60)	12(55)	0.98
	Late	07(30)	11(29)	21(29)	7(32)	
	Missing	02(9)	02(5)	08(11)	03(13)	
Lymphovascular invasion (LVI)	Yes	12(52)	16(42)	36(50)	07(32)	0.517
	No	09(39)	19(50)	29(40)	11(50)	
	Missing	02(9)	03(8)	08(10)	04(18)	
Tumor infiltrating Lymphocytes (TILs)	High	09(39)	22(58)	39(54)	08(36)	0.127
	Low	10(44)	12(32)	14(19)	08(36)	

	Missing	04(17)	04(10)	19(27)	06(28)	
Estrogen Receptor (ER) status	Positive	15(65)	22(58)	42(58)	16(73)	0.60
	Negative	08(35)	16(42)	30(42)	06(27)	
Progesterone Receptor (PR) status	Positive	15(65)	22(58)	41(58)	15(68)	0.75
	Negative	08(35)	16(42)	31(42)	07(32)	
Human epidermal growth factor receptor 2 (HER2) status	Positive	04(17)	09(24)	22(30)	06(27)	0.63
	Negative	17(74)	24(63)	40(56)	15(68)	
	Equivocal	02(9)	05(13)	10(14)	01(5)	

P<0.05, considered as statistically significant (represented in bold); PPBC- postpartum breast cancer

Supplementary table 2. Clinicopathological features of the 10 samples used for RNA sequencing

PPBC groups	PPBC category	ER status	Grade	LN status	IHC subtype	PAM50 subtype
PPBC1	Early	Negative	II	Positive	TNBC	Normal
PPBC1	Early	Positive	I	Negative	HR+	LumA
PPBC1	Early	Positive	III	Negative	HR+	Basal
PPBC2	Late	Negative	I	Negative	HER2 amplified	Normal
PPBC2	Late	Positive	II	Negative	HR+	LumA
PPBC2	Late	Negative	II	Positive	HER2 Amplified	Her2
PPBC3	Late	Positive	II	Negative	HR+	Normal
PPBC3	Late	Positive	III	Positive	HER2 amplified	Basal
PPBC3	Late	Negative	III	Positive	TNBC	Her2
PPBC3	Late	Positive	II	Negative	HER2 amplified	LumB

Supplementary table 3. List of the DEGs mapped with the hallmark pathways from molecular signature database

Signature	Genes
EMT Signatures	DST, TIMP1, ITGA5, IGFBP3, TNFAIP3, ECM1, IL32, MATN2, RGS4, MMP1, OXTR, MMP3, SCG2, APLP1, SGCG
Angiogenesis	CD14, DDIT3, ERBB2, HMGB2, HMOX1, IFITM3, IL18, IL1B, IRF1, LEF1, PDCD4, TAP1, TIMP
ECM Remodeling	TIMP1, ADAMTSL3, EGLN3, ADAMDEC1, ADAM19, ADAMTS2, CST3, CTSB, CTSH, HTRA4, HTRA3, F7, MMP1, MMP3, MMP7, SERPINC1, PCSK6
Hypoxia	ALDOC, BCAN, DDIT3, HMOX1, IGFBP3, ILVBL, NCAN, NEDD4L, SIAH2, STC2, TNFAIP3
Stemness	GAL, PON1, CDX2, RBP2, LCAT, SST, ADH4, LPA, CYP19A1

Supplementary table 4. Short listed nine genes used as invasion signature

SYMBOL	log2FoldChange	P value
MMP1	3.1247609	0.001432168
MMP3	2.5384273	0.026407387
RGS4	2.4842818	0.009062749
CCR1	1.920523	0.000500629
HLA-DQA1	1.8653139	0.0000016
SLAMF8	1.7226503	0.000236575
TMEM158	1.6739826	0.020415247
IGFBP3	1.5845726	0.022743236
CCL5	1.5465715	0.011148845
HLA-DQB1	1.5132629	0.019533088

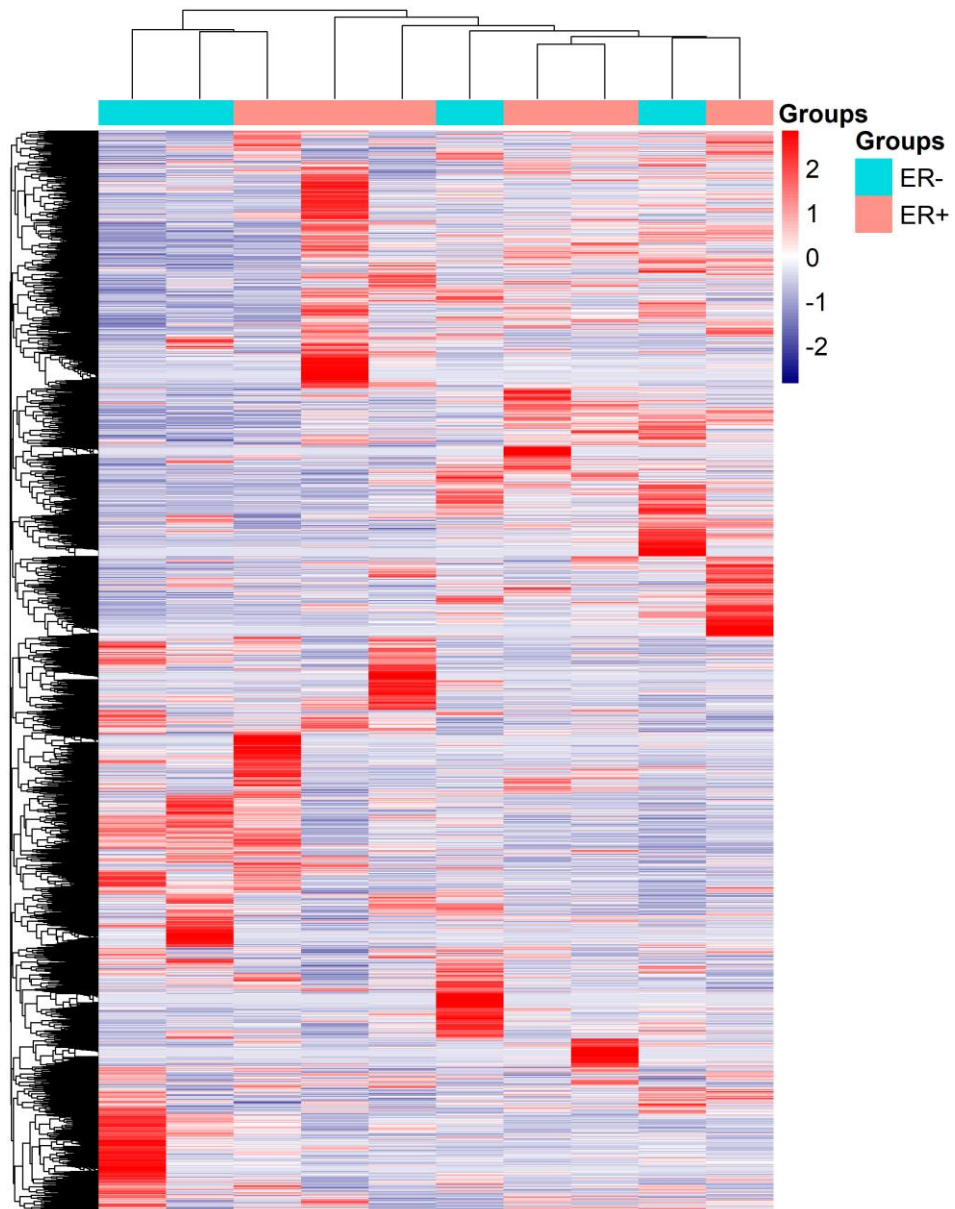


Figure S1. Unsupervised hierarchical clustering of 10 samples across ER positive and negative status.

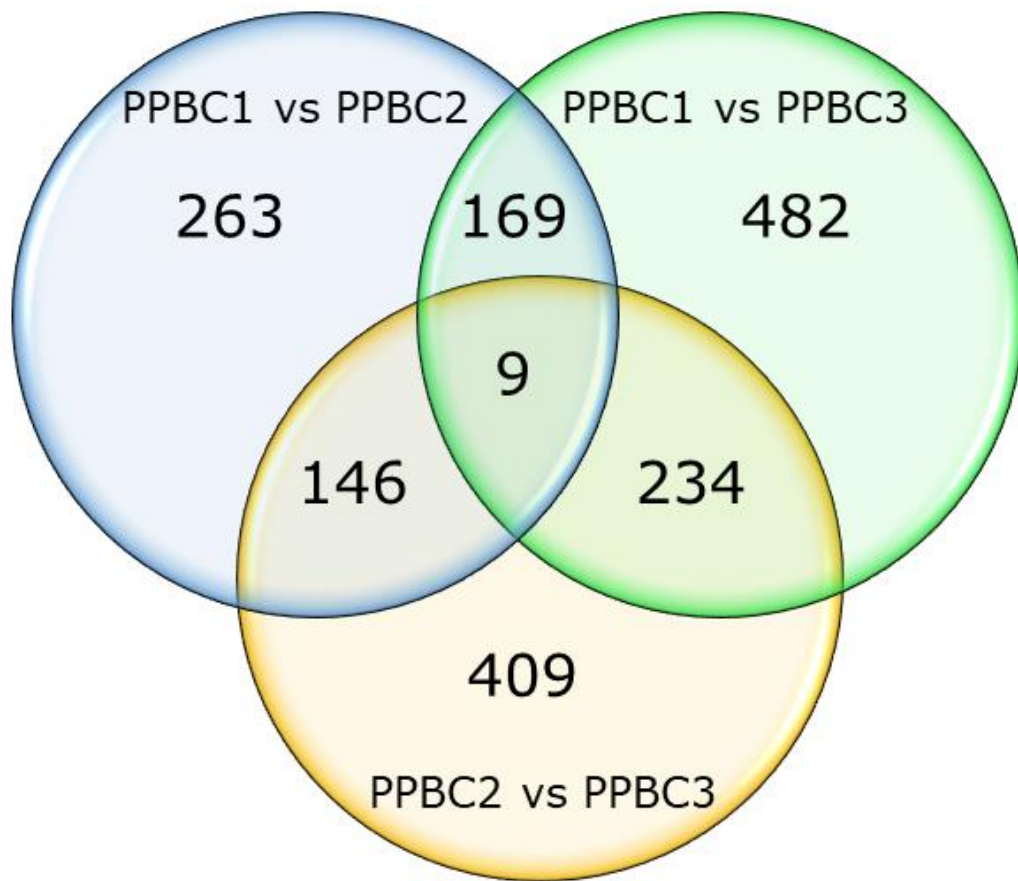


Figure S2. Venn diagram showing unique and common DEGs within PPBC subgroups.

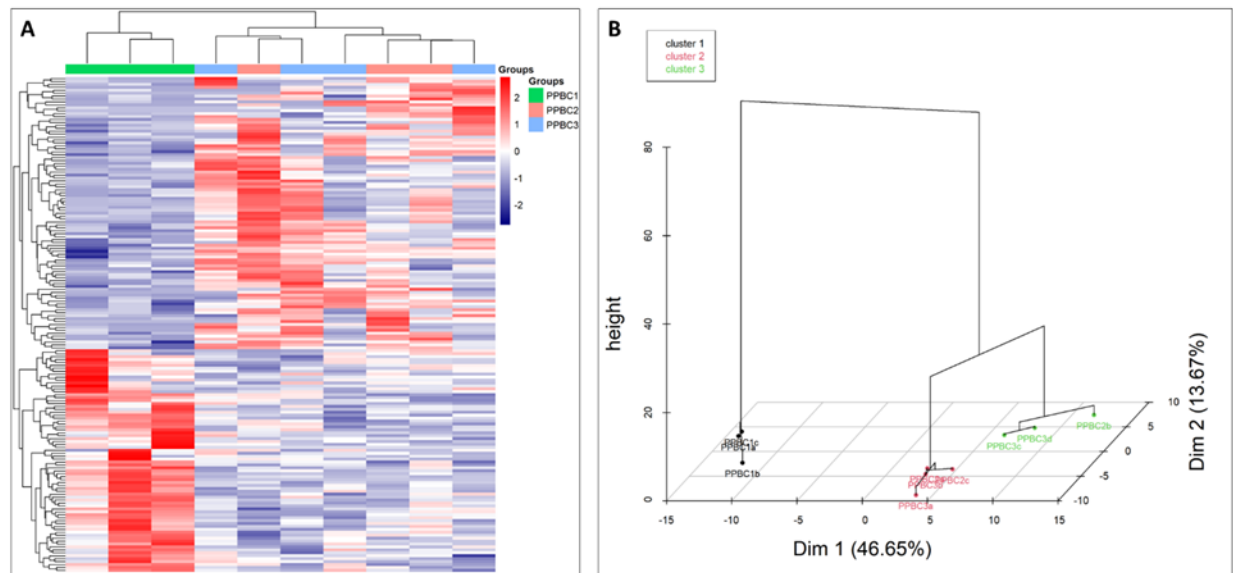
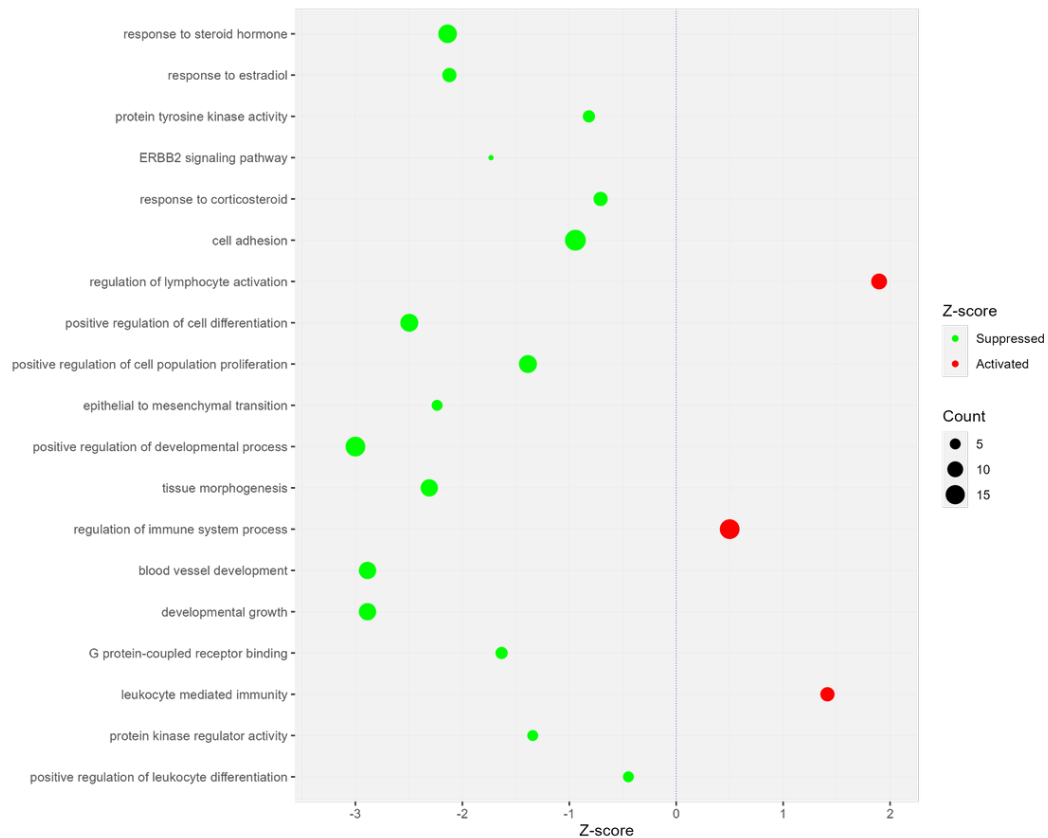


Figure S3. A. Heat map showing unsupervised hierarchical clustering of overlapping differentially expressed genes (n=178) between PPBC1 vs PPBC2 and PPBC1 vs PPBC3 across three parous groups (PPBC1, PPBC2 and PPBC3). B. PCA plot showing clustering of 3 PPBC group sample.



Supplementary figure 4. Gene Ontologies from enrichment analysis in normal early postpartum breast tissue (n=30) compared to late postpartum breast tissue (n=49) showing major differentially regulated biological processes using data from Pereira et al 2019 BCR.