

Supplementary Tables

table S1. IPA localization of breast cancer whole cell lysate citrullinome

Gene	IPA_Location	IPA_Types
ADCK1	Cytoplasm	kinase
ALDH7A1	Cytoplasm	enzyme
ARF5	Cytoplasm	enzyme
ATP2A2	Cytoplasm	transporter
ATP6V1A	Plasma Membrane	transporter
CALD1	Cytoplasm	other
CAPNS1	Cytoplasm	peptidase
CCT2	Cytoplasm	kinase
CEP128	Cytoplasm	other
CLNS1A	Plasma Membrane	ion channel
COL1A1	Extracellular Space	other
CRK	Cytoplasm	other
CTTN	Plasma Membrane	other
DBI	Cytoplasm	other
DNAJC8	Nucleus	other
DPP3	Cytoplasm	peptidase
EIF4G1	Cytoplasm	translation regulator
EPRS	Cytoplasm	enzyme
EZR	Plasma Membrane	other
FKBP4	Nucleus	enzyme
G6PD	Cytoplasm	enzyme
GPI	Extracellular Space	enzyme
GPR161	Plasma Membrane	G-protein coupled receptor
HADHB	Cytoplasm	enzyme
HDLBP	Nucleus	transporter
HSP90AB1	Cytoplasm	enzyme
HSPD1	Cytoplasm	enzyme
IQGAP1	Cytoplasm	other
KRT15	Cytoplasm	other
KRT19	Cytoplasm	other
KRT7	Cytoplasm	other
LONP1	Cytoplasm	peptidase
LRPPRC	Cytoplasm	other
MSN	Plasma Membrane	other
MVP	Nucleus	other

MYH14	Extracellular Space	enzyme
PAWR	Nucleus	transcription regulator
PFN1	Cytoplasm	other
PGAM1	Cytoplasm	phosphatase
PGRMC2	Nucleus	other
PSMA1	Cytoplasm	peptidase
RAB1B	Cytoplasm	other
RCN1	Cytoplasm	other
RHOA	Cytoplasm	enzyme
RPN1	Cytoplasm	enzyme
SERPINH1	Extracellular Space	other
SFN	Cytoplasm	other
SFPQ	Nucleus	transcription regulator
SMARCC2	Nucleus	transcription regulator
SNRPD1	Nucleus	other
SRSF1	Nucleus	other
TAF15	Nucleus	other
UBQLN2	Nucleus	other
VCP	Cytoplasm	enzyme
VIM	Cytoplasm	other
XRCC6	Nucleus	enzyme
YWHAE	Cytoplasm	other

table S2. Breast cancer cell surface MHC binding peptidylcitrullinome

Gene	Sequence	Modification	MDA-MB-468 (TNBC)	HCC1954 (HR- /Her2+)	Net MHCIIpan-2.3 prediction of unmodified form peptides			
					MHC II allele	Affinity(nM)	%Rank	Bind Level
AIMP2	YQVKPYHGGGAPLRVELPT	R14(Cit.)	MHC-II		DRB5_0101	285.5	8.5	Moderate
API5	SGKLSLQTVSGRQQL	R12(Cit.)	MHC-II		DRB1_0101	15.5	1.6	Strong
ARPC2	NRARPDAEKKEMKTITGTFSSR	R4(Cit.)	MHC-II		DRB1_0101	20	2.5	Moderate
ARPC3	VKRQFMNKSLSGPGQ	R3(Cit.)	MHC-II					
ATL3	YVLEQASSHIGNSTQATVRDAVVGRPSMDKKAQ	R19(Cit.); R25(Cit.)	MHC-II		DRB5_0101	282.4	8.5	Moderate
ATL3	YVLEQASSHIGNSTQATVRDAVVGRPSMDKKAQ	R19(Cit.)	MHC-II					
ATP50	LAENGRLSNTQGVVSAFS	R6(Cit.)	MHC-II					
ATP50	LAENGRLSNTQGVVSAFSTM	R6(Cit.)	MHC-II					
ATP6V1E1	IAQQMMPEVRGALFGANANRKF	R10(Cit.)	MHC-II		HLA-DPA10103-DPB10301	852.5	1.9	Strong
					DRB5_0101	62.6	3	Moderate
					HLA-DPA10103-DPB10301	3365.3	7	Moderate
B2M	LLKNGERIEKVEHSDLSFSKDWS	R7(Cit.)	MHC-II					
CALM1	MARKMKDTDSEEEIREA	R3(Cit.)		MHC-II				
CALM1	MIREADIDGGQVNYEE	R3(Cit.)	MHC-II					
CALM1	IREADIDGGQVNYEE	R2(Cit.)	MHC-II					
CALM1	IREADIDGGQVNYE	R2(Cit.)	MHC-II					
CALM1	DKDNGYISAAELRHVM	R14(Cit.)	MHC-II		DRB5_0101	86.9	3.5	Moderate
CALML5	MIREADVDDQGRVNYEE	R12(Cit.)	MHC-II					
CALML5	MIREADVDDQGRVNYEEF	R12(Cit.)	MHC-II					
CALML5	MIREADVDDQGRVNYE	R12(Cit.)	MHC-II					
CALML5	IREADVDDQGRVNYE	R11(Cit.)	MHC-II					
CAP1	EAVSHTSDMHRGYADSPSKAGAAPVYQAF	R11(Cit.)	MHC-II					
CAPZA1	NNDNLLREGAAHFAQY	R7(Cit.)	MHC-II		DRB1_0101	42.7	6	Moderate
					HLA-DPA10103-DPB10301	4810.8	9.5	Moderate
CBR1	LPPDAEGPHGQFVSEKRVE	R17(Cit.)	MHC-II					
CCT8	IPRALAENSGVKANEVSKL	R3(Cit.)	MHC-II					
CCT8	RVDQIIMAKPAGGPKPPSGKKDWDDQND	R1(Cit.)	MHC-II		DRB1_0101	12.9	1.2	Strong
					DRB5_0101	267.6	8	Moderate
					HLA-DPA10103-DPB10301	1974.1	4	Moderate
CHST2	NPDGLGAAAGAAGGSWGRPGPPPA	R19(Cit.)		MHC-II				
COBLL1	VTRRLGAGARAAPRR	R4(Cit.)		MHC-II	HLA-DPA10103-DPB10301	219	0.5	Strong
					HLA-DPA10103-DPB10301	3601.9	7.5	Moderate
COP55	KLEQSEAQLGRGSF	R11(Cit.)	MHC-II					
COX5A	FNKPDIDAWELRKGINTL	R12(Cit.)	MHC-II					
CSTB	FVHLRVFQSLPHENKPLTSLNYQTNKAKHDE	R5(Cit.)	MHC-II		HLA-DPA10103-DPB10301	722	1.6	Strong
					DRB5_0101	345.8	9.5	Moderate
					HLA-DPA10103-DPB10301	4041.2	8	Moderate

CSTB	RVFQSLPHENKPLTLSNYQTNKAKHDE	R1(Cit.)	MHC-II						
DUT	EVQALDDTERGSGGFGSTGKN	R10(Cit.)	MHC-II						
DYNC1I2	INANRADAEAAAATRIPA	R5(Cit.)	MHC-II						
DYNLRB1	LRIRSKNEIMVAPDKDYFL	R2(Cit.)	MHC-II						
EEF1A1	WKVTRKDGNASGTLL	R5(Cit.)	MHC-II	MHC-II					
EEF1A1	WKVTRKDGNASGTLL	R5(Cit.)	MHC-II						
EEF1A1	WKVTRKDGNASGTTLE	R5(Cit.)	MHC-II						
EEF1A1	YVTIIDAPGHRDFIKNM	R11(Cit.)		MHC-II	DRB5_0101	159.9	5.5	Moderate	
EEF1A1	RQTVAVGVKAVDKKAAGAGKVTKSAQKAQKAK	R1(Cit.)	MHC-II		DRB5_0101	39.5	1.8	Strong	
EEF1G	YVSNEELRGSTPEAAAQVVQ	R8(Cit.)	MHC-II		HLA-DPA10103-DPB10301	665	1.5	Strong	
					HLA-DPA10103-DPB10301	1127	2.5	Moderate	
EEF1G	YVSNEELRGSTPEAAAQVVQWVS	R8(Cit.)	MHC-II						
ENO1	FKSPDDPSRYISPDQLADL	R9(Cit.)	MHC-II	MHC-II					
ENO1	FTSKGLFRAAVPSGASTGIYE	R8(Cit.)	MHC-II		DRB1_0101	14.9	1.5	Strong	
ENO1	GVMVSHRSGETEDTF	R7(Cit.)		MHC-II					
ENO1	LAQANGWGMVSHRSGETEDTF	R14(Cit.)		MHC-II	DRB5_0101	335.2	9.5	Moderate	
ENO1	AVEKGVPLYRHIADLAGNS	R10(Cit.)		MHC-II	HLA-DPA10103-DPB10301	694.5	1.5	Strong	
					HLA-DPA10103-DPB10301	3609.6	7.5	Moderate	
FUBP1	YRQQAAYYATQSPQMPQHPPAPQGG	R2(Cit.)	MHC-II		DRB1_0101	53	7.5	Moderate	
					HLA-DPA10103-DPB10301	3361.9	7	Moderate	
GAPDH	TVHAITATQKTVDGSPGKLWR	R21(Cit.)		MHC-II	DRB5_0101	24.8	1.1	Strong	
					DRB5_0101	100	4	Moderate	
GAPDH	ISWYDNEFGYSNRVVDL	R13(Cit.)	MHC-II						
GAPDH	ISWYDNEFGYSNRVVD	R13(Cit.)	MHC-II						
GAPDH	WYDNEFGYSNRVVD	R11(Cit.)	MHC-II						
GAR1	GGGNFRGGGRGGFGRGGGRGGFNKGQ	R19(Cit.)		MHC-II					
GBA	SLTGLLLLQAVSWASGARP	R18(Cit.)	MHC-II		DRB5_0101	345.3	9.5	Moderate	
HDDC2	ELEAERSTNIAAAASEPHS	R6(Cit.)	MHC-II		HLA-DPA10103-DPB10301	611.3	1.4	Strong	
					HLA-DPA10103-DPB10301	4782.3	9.5	Moderate	
HIBADH	MDAPVSGGVGAARSGLNLF	R13(Cit.)	MHC-II						
HIST1H2BO	VRLLLPGLAKHAVSEGTKAVTKYTSSK	R2(Cit.)	MHC-II		DRB1_0101	10.4	0.8	Strong	
					HLA-DPA10103-DPB10301	2641.4	5.5	Moderate	
HMGCS1	YSPQQLAGKRIGVFSYSGGLAA	R10(Cit.)	MHC-II		DRB1_0101	69.7	9.5	Moderate	
					HLA-DPA10103-DPB10301	4136.3	8.5	Moderate	
HMG1	PKRKVSSAEGAAKEPKRRSARLS	R19(Cit.)	MHC-II		DRB5_0101	277.3	8.5	Moderate	
					HLA-DPA10103-DPB10301	2799.1	6	Moderate	
HNRNPA1	FAKPRNQGGYGGSSSSSYGSGRRF	R5(Cit.); R23(Cit.)	MHC-II						
HSPB1	SRAQLGGPEAAKSDETAAK	R2(Cit.)	MHC-II						
IL16	GIYVKTFAGGAAAADGRLQEGDE	R18(Cit.)	MHC-II		DRB1_0101	71.5	9.5	Moderate	
					HLA-DPA10103-DPB10301	4419	9	Moderate	
IPO4	QIRQFAAVLRRRLNTRWRRLAAEQRESLKSL	R3(Cit.); R11(Cit.)		MHC-II	DRB5_0101	23.6	1	Strong	
					HLA-DPA10103-DPB10301	28.1	0.04	Strong	
					DRB5_0101	80.8	3.5	Moderate	

KCTD8	QWIPPPDKRRNSSELFQ	R9(Cit.)	MHC-II	MHC-II	HLA-DPA10103-DPB10301	4493.6	9	Moderate
KRT8	RGGLGGYGGASGMGGITA	R1(Cit.); M14(Oxi.)						
LDHA	L RTPKIVSGKDYNTVANSKL	R2(Cit.)	MHC-II		DRB5_0101	300.9	9	Moderate
MAGEF1	ALADEADRARAKA	R8(Cit.)						
MIF	VNTNVPRASVPDGFSELE	R7(Cit.)	MHC-II					
MKI67	LALRKRTPSAGKAMDTPKPAVSDEKNIINTF	R6(Cit.)	MHC-II		DRB5_0101	324.4	9	Moderate
					HLA-DPA10103-DPB10301	2418.7	5	Moderate
NDUFA4	WDRNNPEPWNLGPNDDQYK	R3(Cit.)	MHC-II					
NME2	NVVKTRVMLGETNPADSKPGTIRGD	R7(Cit.); R24(Cit.)	MHC-II					
NME2	NVVKTRVMLGETNPADSKPGTIRGDF	R7(Cit.)	MHC-II					
NME2	NVVKTRVMLGETNPADSKPGTIRGD	R7(Cit.)	MHC-II					
NME2	NVVKTRVMLGETNPAD	R7(Cit.)	MHC-II					
NUMB	WAALENKSKQRTNPSPTNPFSSDLQK	R11(Cit.)	MHC-II		DRB5_0101	95.6	4	Moderate
NUMB	WAALENKSKQRTNPSPTNPFSSDLQKT	R11(Cit.)	MHC-II					
PA2G4	LMPNGPMRITSGPFEPDL	R8(Cit.)	MHC-II	MHC-II	HLA-DPA10103-DPB10301	4557.1	9	Moderate
PCBP1	YSIQGQHTISPLDLAKLNQVARQQSH	R22(Cit.)	MHC-II		DRB1_0101	60.1	8	Moderate
PCBP1	SIQGQHTISPLDLAKLNQVARQQSHF	R21(Cit.)	MHC-II					
PCSK5	AEKWTTVPRQHVCVESTDRQIKTIRPN	R9(Cit.); R19(Cit.)	MHC-II					
PEX7	LLVTGAVDCSLRGWDLRN	R17(Cit.)	MHC-II					
PFN1	RTKSTGGAPTFNVTVTKDCTL	R1(Cit.)	MHC-II	MHC-II				
PGK1	HLGRPDGVPMPDKYSLEPVAVELK	R4(Cit.)	MHC-II					
PGLS	LARELPAAVAPAGASLARWTLG	R3(Cit.); R19(Cit.)	MHC-II		HLA-DPA10103-DPB10301	473.3	1.1	Strong
					DRB1_0101	48.4	7	Moderate
PGLS	LARELPAAVAPAGASLARWTLG	R19(Cit.)	MHC-II					
PGLS	RLVPFDHAESTYGLYRTHL	R16(Cit.)	MHC-II					
PHGDH	QVVGRAAGTVDNVDL	R5(Cit.)	MHC-II					
PLIN3	DVASVQQQRQEQSY	R9(Cit.)		MHC-II				
PPIA	GGDFTRHNGTGKSIYGEKFEDEF	R6(Cit.)	MHC-II					
PPIA	GGDFTRHNGTGKSIYGEKFEDEF	R6(Cit.)	MHC-II					
PPIA	GGDFTRHNGTGKSIYGEKFEDE	R6(Cit.)	MHC-II					
PPIA	FTRHNGTGKSIYGEKF	R3(Cit.)	MHC-II					
PPIAL4E	ENLRKHTGSGILSMANAGPNTNGSQF	R5(Cit.)	MHC-II					
PPIAL4E	LIRKHTGSGILSMANAGPNTN	R3(Cit.); M13(Oxi.)		MHC-II				
PPIAL4E	LIRKHTGSGILSMANAGPNTNGSQFF	R3(Cit.); M13(Oxi.)	MHC-II					
PPIAL4E	LIRKHTGSGILSMANAGPNTNGSQF	R3(Cit.); M13(Oxi.)	MHC-II					
PPIAL4E	LIRKHTGSGILSMANAGPNTN	R3(Cit.)	MHC-II	MHC-II				
PPIAL4E	LIRKHTGSGILSMANAGPN	R3(Cit.)	MHC-II					
PPIAL4E	LIRKHTGSGILSMANAGPNTNGSQF	R3(Cit.)	MHC-II					
PPIAL4E	LIRKHTGSGILSMANAGPNTNGSQFF	R3(Cit.)	MHC-II					
PPP1R2P3	LETADGESMNTESNQGSTPSDQQQNKLR	R29(Cit.)	MHC-II					
PPP1R2P3	LETADGESMNTESNQGSTPSDQQQNKLRSS	R29(Cit.)	MHC-II					
PPP1R7	WSDLDELKGARSET	R11(Cit.)	MHC-II		DRB1_0101	70.6	9.5	Moderate

PRDX1	IIDDKGILRQITVNDLPVGRSVDET	R9(Cit.)	MHC-II	HLA-DPA10103-DPB10301	4343.5	9	Moderate
PRDX1	VNTPKKQGGGLPMMNIPLVSDPKRTIAQDYG	R23(Cit.)	MHC-II				
PRDX2	IIDGKGVLRQITVNDLPVGRSVDEAL	R9(Cit.)	MHC-II				
PRDX2	RRLSEYGVLTDEGIAYRG	R1(Cit.); R2(Cit.)	MHC-II	DRB5_0101	346.5	9.5	Moderate
PSMA5	QFGEEDADPGAMSRPFQVAL	R14(Cit.)	MHC-II				
RAD23A	GQENPQLLQIQISRHQEQF	R13(Cit.)	MHC-II				
RAD23B	LQIQIGRENPLLQIQISHQEH	R6(Cit.)	MHC-II				
RPS21	NVAEVDKVTGRFNGQFKTY	R11(Cit.)	MHC-II				
RPS25	LSKGLIKLVSKHRAQVIYTRNTKGGDAPAAGEDA	R13(Cit.)	MHC-II	DRB5_0101	4.3	0.05	Strong
				DRB5_0101	5.2	0.08	Strong
				DRB1_0101	48.9	7	Moderate
				HLA-DPA10103-DPB10301	3255.9	6.5	Moderate
RPS25	KGLIKLVSKHRAQVIYTRNTKGGDAPAAGEDA	R11(Cit.)	MHC-II				
S100A6	MEDLDRNKDQEVNFQE	R6(Cit.)	MHC-II				
S100A6	MEDLDRNKDQEVNF	M1(Oxi.); R6(Cit.)	MHC-II				
S100A9	MARLTWASHEKMHGDEGPGHHHKPGLGEG	R3(Cit.)	MHC-II				
S100A9	MARLTWASHEKMHGDEGPGHHHKPGLGEGTP	R3(Cit.)	MHC-II				
S100A9	MARLTWASHEKMHGDEGPGHHHKPGLGEGTP	M1(Oxi.); R3(Cit.)	MHC-II				
SERBP1	PGHLQEGFGCVTNRNF	R15(Cit.)	MHC-II				
SERBP1	PGHLQEGFGCVTNRFDQL	R15(Cit.)	MHC-II				
SFN	GLLDSHLIKEAGDAESR	R17(Cit.)	MHC-II				
SLC9A3R1	LRAQEAPGQAEPPAAAEVQAGAGN	R2(Cit.)	MHC-II				
SRF	GGTRGANGGRVPGNGAGLGPGR	R4(Cit.); R10(Cit.); R22(Cit.)	MHC-II				
SRP14	LRATDGKKKISTVSSKEVNFQMA	R2(Cit.)	MHC-II	DRB5_0101	259.3	8	Moderate
				HLA-DPA10103-DPB10301	4255.9	8.5	Moderate
SRP9	MVAKEARNVTMETE	R7(Cit.)					
TAGLN2	LGGLAVARDDGL	R8(Cit.)	MHC-II				
TAGLN2	VIGLQMGTRNGASQAGMTGYGMPRQ	R24(Cit.)	MHC-II				
TAGLN2	TNRGASQAGMTGYGMPRQIL	R17(Cit.)	MHC-II	MHC-II			
TAGLN2	QLQEGKNVIGLQMGTRNGASQAGMTGYGMPRQIL	R17(Cit.)	MHC-II				
TAGLN2	VIGLQMGTRNGASQAGMTGYGMPRQIL	R10(Cit.); M17(Oxi.)	MHC-II				
TECR	FTKTHPQWYPARQSL	R12(Cit.)	MHC-II				
TIMM9	HIQQNEALAAKAGLLGQPR	R19(Cit.)	MHC-II	HLA-DPA10103-DPB10301	2249.1	4.5	Moderate
TIPRL	IFPERIDPNPADSQKSTQVE	R5(Cit.)	MHC-II				
UBA7	RAEASQELLAQ	R1(Cit.)	MHC-I				
UBE2L3	WQGLIVPDNPPYDKGAFR	R18(Cit.)	MHC-II				
YWHAZ	KSVTEQGAELSNEERNLL	R15(Cit.)	MHC-II				
ZBED1	MLVSNRVSWWGSTLAMLQRLKEQFVIAGVL	M1(Oxi.); R6(Cit.)	MHC-II				

#Oxi. Oxidized Met.

#Cit. citrullinated Arg.

Affinity prediction was based on unmodified sequence.

table S3. TCGA breast cancer PADI2 and immune gene signature correlation

Variable	PADI2-All BrCa Cases		
	Spearman Coefficient	95% CI	p-value
CTAG1B	0.1704	0.1072 to 0.2323	<0.0001
MAGEA4	0.245	0.1835 to 0.3047	<0.0001
SAGE1	0.03806	-0.02644 to 0.1022	0.2336
CD274	0.2517	0.1904 to 0.3111	<0.0001
PDCD1	0.2967	0.2368 to 0.3544	<0.0001
CD247	0.3139	0.2546 to 0.3708	<0.0001
PDCD1LG2	0.3675	0.3104 to 0.4219	<0.0001
CTLA4	0.3411	0.2829 to 0.3968	<0.0001
TNFRSF9	0.3346	0.2761 to 0.3906	<0.0001
TNFRSF4	0.1612	0.09782 to 0.2234	<0.0001
TLR9	0.3782	0.3216 to 0.4321	<0.0001
aDC	0.3114	0.2520 to 0.3685	<0.0001
APM1	0.2642	0.2032 to 0.3232	<0.0001
APM2	0.2918	0.2318 to 0.3497	<0.0001
B cells	0.486	0.4352 to 0.5337	<0.0001
CD8 T cells	0.1252	0.06123 to 0.1881	<0.0001
Cytotoxic cells	0.2694	0.2085 to 0.3281	<0.0001
DC	0.3383	0.2800 to 0.3942	<0.0001
Eosinophils	-0.1217	-0.1847 to -0.05776	0.0001
iDC	0.1669	0.1035 to 0.2288	<0.0001
Lymph vessels	0.1338	0.06994 to 0.1965	<0.0001
Macrophages	0.2762	0.2156 to 0.3347	<0.0001
Mast cells	-0.01705	-0.08140 to 0.04743	0.5937
Neutrophils	0.3029	0.2432 to 0.3603	<0.0001
NK CD56bright cells	-0.3105	-0.3676 to -0.2511	<0.0001
NK CD56dim cells	0.3071	0.2476 to 0.3643	<0.0001
NK cells	0.1169	0.05284 to 0.1800	0.0002
pDC	0.1232	0.05924 to 0.1862	0.0001
T cells	0.3392	0.2810 to 0.3950	<0.0001
T helper cells	0.1393	0.07557 to 0.2020	<0.0001
Tcm cells	0.02992	-0.03458 to 0.09418	0.3491
Tem cells	0.1854	0.1224 to 0.2469	<0.0001
Tfh cells	0.1892	0.1263 to 0.2505	<0.0001
Tgd cells	0.221	0.1588 to 0.2814	<0.0001
Th1 cells	0.3935	0.3376 to 0.4466	<0.0001
Th17 cells	0.06732	0.002898 to 0.1312	0.035
Th2 cells	0.2154	0.1530 to 0.2760	<0.0001

Treg cells	0.3411	0.2829 to 0.3968	<0.0001
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Variable	PADI2-HR+ Subtype		
	Spearman Coefficient	95% CI	p-value
CTAG1B	0.1246	0.04860 to 0.1992	0.001
MAGEA4	0.08475	0.008303 to 0.1602	0.0254
SAGE1	0.04367	-0.03295 to 0.1198	0.2499
CD274	0.2083	0.1339 to 0.2803	<0.0001
PDCD1	0.2792	0.2071 to 0.3483	<0.0001
CD247	0.3044	0.2333 to 0.3722	<0.0001
PDCD1LG2	0.3125	0.2418 to 0.3800	<0.0001
CTLA4	0.2688	0.1963 to 0.3383	<0.0001
TNFRSF9	0.2568	0.1839 to 0.3269	<0.0001
TNFRSF4	0.1028	0.02651 to 0.1779	0.0066
TLR9	0.2685	0.1960 to 0.3380	<0.0001
aDC	0.2119	0.1377 to 0.2838	<0.0001
APM1	0.1085	0.03228 to 0.1835	0.0042
APM2	0.3795	0.3121 to 0.4432	<0.0001
B cells	0.4207	0.3556 to 0.4817	<0.0001
CD8 T cells	0.3185	0.2480 to 0.3856	<0.0001
Cytotoxic cells	0.3399	0.2704 to 0.4059	<0.0001
DC	0.3592	0.2907 to 0.4240	<0.0001
Eosinophils	0.1901	0.1153 to 0.2628	<0.0001
iDC	0.3555	0.2868 to 0.4206	<0.0001
Lymph vessels	0.3399	0.2705 to 0.4059	<0.0001
Macrophages	0.3057	0.2347 to 0.3735	<0.0001
Mast cells	0.3276	0.2575 to 0.3942	<0.0001
Neutrophils	0.3796	0.3121 to 0.4432	<0.0001
NK CD56bright cells	-0.06905	-0.1448 to 0.007496	0.0687
NK CD56dim cells	0.3367	0.2671 to 0.4028	<0.0001
NK cells	0.3522	0.2833 to 0.4174	<0.0001
pDC	0.1882	0.1133 to 0.2609	<0.0001
T cells	0.3668	0.2986 to 0.4312	<0.0001
T helper cells	0.02243	-0.05416 to 0.09877	0.5546
Tcm cells	0.1575	0.08197 to 0.2312	<0.0001
Tem cells	0.1771	0.1020 to 0.2502	<0.0001
Tfh cells	0.3347	0.2649 to 0.4009	<0.0001
Tgd cells	0.2918	0.2202 to 0.3603	<0.0001

Th1 cells	0.3608	0.2924 to 0.4256	<0.0001
Th17 cells	0.09174	0.01535 to 0.1671	0.0155
Th2 cells	0.1035	0.02717 to 0.1786	0.0063
Treg cells	0.2707	0.1983 to 0.3402	<0.0001

Variable	PADI2-ER-/Her2+ Subtype		
	Spearman Coefficient	95% CI	p-value
CTAG1B	0.01529	-0.2143 to 0.2433	0.8943
MAGEA4	0.1571	-0.07444 to 0.3726	0.1695
SAGE1	-0.07675	-0.3004 to 0.1549	0.5042
CD274	0.1726	-0.05860 to 0.3862	0.1308
PDCD1	-0.0246	-0.2521 to 0.2054	0.8307
CD247	0.07358	-0.1580 to 0.2975	0.522
PDCD1LG2	0.06453	-0.1668 to 0.2891	0.5746
CTLA4	0.02055	-0.2093 to 0.2483	0.8583
TNFRSF9	0.09164	-0.1402 to 0.3139	0.4249
TNFRSF4	-0.1274	-0.3462 to 0.1045	0.2662
TLR9	0.09926	-0.1326 to 0.3208	0.3873
aDC	0.07836	-0.1533 to 0.3018	0.4953
APM1	-0.1234	-0.3426 to 0.1085	0.2816
APM2	0.05323	-0.1778 to 0.2787	0.6435
B cells	0.1194	-0.1125 to 0.3390	0.2976
CD8 T cells	-0.1327	-0.3509 to 0.09918	0.2467
Cytotoxic cells	0.01734	-0.2124 to 0.2452	0.8802
DC	-0.0247	-0.2522 to 0.2053	0.8301
Eosinophils	-0.08739	-0.3101 to 0.1444	0.4468
iDC	-0.007119	-0.2356 to 0.2221	0.9507
Lymph vessels	-0.153	-0.3690 to 0.07858	0.181
Macrophages	-0.03674	-0.2634 to 0.1938	0.7495
Mast cells	-0.1678	-0.3820 to 0.06347	0.1419
Neutrophils	0.008763	-0.2206 to 0.2372	0.9393
NK CD56bright cells	-0.06645	-0.2909 to 0.1649	0.5632
NK CD56dim cells	-0.0487	-0.2745 to 0.1822	0.672
NK cells	-0.2642	-0.4649 to -0.03754	0.0194
pDC	0.03975	-0.1909 to 0.2662	0.7297
T cells	0.07293	-0.1586 to 0.2969	0.5257
T helper cells	0.113	-0.1189 to 0.3333	0.3245
Tcm cells	-0.1296	-0.3481 to 0.1023	0.2582

Tem cells	-0.01463	-0.2427 to 0.2150	0.8988
Tfh cells	-0.01703	-0.2450 to 0.2127	0.8823
Tgd cells	0.02561	-0.2045 to 0.2530	0.8239
Th1 cells	0.02227	-0.2077 to 0.2499	0.8466
Th17 cells	-0.02159	-0.2492 to 0.2083	0.8512
Th2 cells	0.0376	-0.1929 to 0.2642	0.7438
Treg cells	0.1085	-0.1235 to 0.3292	0.3444

Variable	PADI2-TNBC (Basal) Subtype		
	Spearman Coefficient	95% CI	p-value
CTAG1B	0.061	-0.09396 to 0.2138	0.425
MAGEA4	0.067	-0.08793 to 0.2196	0.381
SAGE1	0.037	-0.1178 to 0.1906	0.628
CD274	0.124	-0.03114 to 0.2731	0.106
PDCD1	0.069	-0.08621 to 0.2212	0.369
CD247	0.071	-0.08394 to 0.2234	0.353
PDCD1LG2	0.206	0.05357 to 0.3496	0.007
CTLA4	0.055	-0.1005 to 0.2075	0.476
TNFRSF9	0.196	0.04248 to 0.3398	0.010
TNFRSF4	0.001	-0.1533 to 0.1556	0.988
TLR9	0.026	-0.1286 to 0.1800	0.733
aDC	0.098	-0.05704 to 0.2489	0.201
APM1	0.059	-0.09588 to 0.2119	0.440
APM2	0.075	-0.08026 to 0.2269	0.329
B cells	0.186	0.03233 to 0.3308	0.015
CD8 T cells	-0.072	-0.2236 to 0.08375	0.352
Cytotoxic cells	0.075	-0.08084 to 0.2264	0.333
DC	0.085	-0.07074 to 0.2360	0.271
Eosinophils	0.092	-0.06369 to 0.2427	0.233
iDC	0.018	-0.1364 to 0.1724	0.811
Lymph vessels	0.003	-0.1519 to 0.1570	0.973
Macrophages	0.088	-0.06765 to 0.2389	0.254
Mast cells	0.027	-0.1277 to 0.1810	0.723
Neutrophils	0.070	-0.08540 to 0.2220	0.363
NK CD56bright cells	-0.138	-0.2866 to 0.01646	0.071
NK CD56dim cells	-0.040	-0.1930 to 0.1154	0.606
NK cells	-0.034	-0.1876 to 0.1209	0.657
pDC	0.002	-0.1521 to 0.1568	0.975

T cells	0.136	-0.01861 to 0.2847	0.076
T helper cells	0.092	-0.06290 to 0.2434	0.229
Tcm cells	0.124	-0.03085 to 0.2734	0.106
Tem cells	0.232	0.08086 to 0.3734	0.002
Tfh cells	0.120	-0.03499 to 0.2695	0.118
Tgd cells	-0.100	-0.2506 to 0.05524	0.193
Th1 cells	0.131	-0.02373 to 0.2800	0.087
Th17 cells	0.139	-0.01551 to 0.2875	0.069
Th2 cells	0.047	-0.1081 to 0.2001	0.540
Treg cells	0.155	0.001025 to 0.3026	0.042

Variable	PADI2-Normal like Subtype		
	Spearman Coefficient	95% CI	p-value
CTAG1B	0.1842	-0.1635 to 0.4912	0.2822
MAGEA4	0.06258	-0.2809 to 0.3918	0.7169
SAGE1	0.2133	-0.1338 to 0.5138	0.2116
CD274	-0.2136	-0.5141 to 0.1335	0.2109
PDCD1	-0.3761	-0.6332 to -0.04416	0.0238
CD247	-0.1843	-0.4912 to 0.1634	0.2819
PDCD1LG2	-0.2288	-0.5257 to 0.1178	0.1795
CTLA4	-0.3562	-0.6193 to -0.02130	0.033
TNFRSF9	-0.1292	-0.4472 to 0.2178	0.4526
TNFRSF4	-0.3737	-0.6316 to -0.04147	0.0247
TLR9	-0.07207	-0.3998 to 0.2720	0.6762
aDC	-0.312	-0.5876 to 0.02854	0.064
APM1	-0.2468	-0.5394 to 0.09890	0.1467
APM2	-0.1846	-0.4914 to 0.1631	0.2812
B cells	0.182	-0.1657 to 0.4894	0.2881
CD8 T cells	-0.3264	-0.5980 to 0.01250	0.052
Cytotoxic cells	-0.2252	-0.5230 to 0.1215	0.1866
DC	-0.2427	-0.5363 to 0.1032	0.1538
Eosinophils	-0.1395	-0.4556 to 0.2078	0.4171
iDC	-0.2775	-0.5623 to 0.06623	0.1013
Lymph vessels	-0.1297	-0.4476 to 0.2173	0.4508
Macrophages	-0.1681	-0.4784 to 0.1796	0.3271
Mast cells	-0.1851	-0.4919 to 0.1626	0.2799
Neutrophils	-0.2607	-0.5499 to 0.08416	0.1245
NK CD56bright cells	-0.294	-0.5745 to 0.04835	0.0818

NK CD56dim cells	-0.3668	-0.6267 to -0.03343	0.0278
NK cells	-0.3346	-0.6039 to 0.003250	0.0461
pDC	-0.1871	-0.4935 to 0.1605	0.2745
T cells	-0.1444	-0.4595 to 0.2030	0.4008
T helper cells	0.3264	-0.01250 to 0.5980	0.052
Tcm cells	0.1421	-0.2053 to 0.4576	0.4084
Tem cells	-0.4739	-0.6995 to -0.1623	0.0035
Tfh cells	-0.03552	-0.3686 to 0.3056	0.837
Tgd cells	-0.1951	-0.4997 to 0.1524	0.2541
Th1 cells	-0.201	-0.5043 to 0.1464	0.2397
Th17 cells	0.425	0.1021 to 0.6668	0.0098
Th2 cells	-0.1804	-0.4882 to 0.1673	0.2923
Treg cells	-0.1743	-0.4833 to 0.1734	0.3094

table S4. Newly diagnosed breast cancer cohort of the plasma Ig bound citrullinome

Subtype	Stage	Sample pooled	Age at diagnosis	
			Median	Mean
ER/PR+ and HER2-	I	(n=3/group)	63 ± 5.9	61 ± 5.9
ER/PR+ and HER2-	I	(n=9/group)	63 ± 5.3	62 ± 5.3
ER/PR+ and HER2-	II	(n=3/group)	54 ± 4.7	56 ± 4.7
ER/PR+ and HER2-	II	(n=3/group)	40 ± 5.9	38 ± 5.9
ER/PR+ and HER2-	II	(n=9/group)	56 ± 7.9	58 ± 7.9
ER/PR+ and HER2-	II	(n=9/group)	39 ± 2.9	39 ± 2.9
ER/PR+ and HER2-	III	(n=3/group)	52 ± 5.8	55 ± 5.8
ER/PR+ and HER2-	III	(n=3/group)	43 ± 2.5	43 ± 2.5
ER/PR+ and HER2-	III	(n=9/group)	60 ± 6.0	59 ± 6.0
ER/PR+ and HER2-	III	(n=9/group)	44 ± 3.8	44 ± 3.8
HR-/HER2+ enriched	II	(n=3/group)	63 ± 7.6	60 ± 7.6
HR-/HER2+ enriched	II	(n=3/group)	44 ± 11.0	40 ± 11.0
HR-/HER2+ enriched	II	(n=9/group)	57 ± 4.0	58 ± 4.0
HR-/HER2+ enriched	II	(n=9/group)	42 ± 7.3	41 ± 7.3
HR-/HER2+ enriched	III	(n=3/group)	52 ± 14.3	49 ± 14.3
HR-/HER2+ enriched	III	(n=3/group)	36 ± 3.8	38 ± 3.8
HR-/HER2+ enriched	III	(n=9/group)	51 ± 6.6	52 ± 6.6
HR-/HER2+ enriched	III	(n=9/group)	39 ± 2.5	38 ± 2.5
TNBC	II	(n=3/group)	60 ± 6.5	60 ± 6.5

TNBC	II	(n=3/group)	45 ± 6.6	46 ± 6.6
TNBC	II	(n=9/group)	64 ± 7.4	64 ± 7.4
TNBC	II	(n=9/group)	42 ± 3.3	43 ± 3.3
TNBC	III	(n=3/group)	56 ± 8.1	52 ± 8.1
TNBC	III	(n=3/group)	37 ± 4.5	37 ± 4.5
TNBC	III	(n=9/group)	58 ± 5.6	58 ± 5.6
TNBC	III	(n=9/group)	39 ± 7.3	39 ± 7.3
Healthy control		(n=10/group)	52 ± 8.4	54 ± 8.4
Healthy control		(n=10/group)	44 ± 4.7	44 ± 4.7
DCIS (ER/PR+) control		(n=10/group)	58 ± 6.1	59 ± 6.1
DCIS (ER/PR+) control		(n=10/group)	43 ± 6.2	43 ± 6.2
Healthy control		(n=10/group)	70 ± 2.5	70 ± 2.5
Healthy control		(n=20/group)	56 ± 8.7	59 ± 8.7
Healthy control		(n=20/group)	54 ± 4.2	54 ± 4.2
Healthy control		(n=20/group)	63 ± 9.9	64 ± 9.9
Healthy control		(n=1/group)	67	67
Healthy control		(n=1/group)	61	61
Healthy control		(n=1/group)	69	69

table S5. IPA interaction networks of plasma Ig bound citrullinome in breast cancer patients

Luminal A			
ID	Score	Focus Molecules	Top Diseases and Functions
1	60	25	[Cell Morphology, Embryonic Development, Hair and Skin Development and Function]
2	28	14	[Drug Metabolism, Endocrine System Development and Function, Energy Production]
TNBC			
ID	Score	Focus Molecules	Top Diseases and Functions
1	44	17	[Cell Morphology, Embryonic Development, Hair and Skin Development and Function]
2	26	11	[Cancer, Gene Expression, Organismal Injury and Abnormalities]
HR-/Her2			
ID	Score	Focus Molecules	Top Diseases and Functions
1	72	30	[Cell Morphology, Embryonic Development, Hair and Skin Development and Function]
2	47	22	[Cellular Compromise, Cellular Function and Maintenance, Inflammatory Response]

table S6. TNBC stage II cohort used for the plasma citrullinated Vimentin ELISA assay

Menopausal Status	Trigger Event	Histology	Clin T	Clin N	Clin M	Clin STAGE	T_Size Baseline_Neoadj.	Age at DX
PRE	ABNORMAL MAMMOGRAM	INVASIVE DUCTAL, NOS	T2	N0	M0	IIA	3.4	46
PRE	LUMP IN BREAST (PT)	INVASIVE DUCTAL, NOS	T3	N0	M0	IIB	6	45
PRE	LUMP IN BREAST (PT)	INVASIVE DUCTAL, NOS	T2	N1	M0	IIB	3.8	50
PRE	ABNORMAL MAMMOGRAM	INVASIVE DUCTAL, NOS	T2	N0	M0	IIA	3.3	44
POST	LUMP IN BREAST (PT)	INVASIVE DUCTAL, NOS	T2	N0	M0	IIA	4.4	64
POST	LUMP IN BREAST (PT)	INVASIVE DUCTAL, NOS	T2	N1	M0	IIB	4.5	62
POST	LUMP IN BREAST (PT)	INVASIVE DUCTAL, NOS	T2	N0	M0	IIA	2.1	65
POST	LUMP IN BREAST (PT)	INVASIVE DUCTAL, NOS	T2	N0	M0	IIA	4	64
POST	ABNORMAL MAMMOGRAM	INVASIVE DUCTAL, NOS	T1c	N1	M0	IIA		54
POST	ABNORMAL MAMMOGRAM	INVASIVE DUCTAL, NOS	T1c	N1	M0	IIA		54
POST	ABNORMAL MAMMOGRAM	INVASIVE DUCTAL, NOS	T2	N0	M0	IIA	2.1	68