

**Supplementary Table 1.** Summary of biological samples

Mouse ID	Tissue	Batch num	n cells
m1	Normal mammary fat pad	1	207
m1	Normal mammary fat pad	2	143
m1	Normal mammary fat pad	3	209
m2	Normal mammary fat pad	4	204
m2	Normal mammary fat pad	5	174
m2	Normal mammary fat pad	6	114
m3	Normal mammary fat pad	7	188
m3	Normal mammary fat pad	8	92
m3	Normal mammary fat pad	9	195
m4	Primary tumor, 2 weeks post injection	10	243
m4	Primary tumor, 2 weeks post injection	11	233
m5	Primary tumor, 2 weeks post injection	12	255
m5	Primary tumor, 2 weeks post injection	13	244
m5	Primary tumor, 2 weeks post injection	14	243
m6	Primary tumor, 2 weeks post injection	15	213
m6	Primary tumor, 2 weeks post injection	16	167
m7	Primary tumor, 4 weeks post injection	17	96
m7	Primary tumor, 4 weeks post injection	18	60
m7	Primary tumor, 4 weeks post injection	19	65
m7	Primary tumor, 4 weeks post injection	20	38
m7	Primary tumor, 4 weeks post injection	21	60
m8	Primary tumor, 4 weeks post injection	22	218
m8	Primary tumor, 4 weeks post injection	23	193
m8	Primary tumor, 4 weeks post injection	24	231
m8	Primary tumor, 4 weeks post injection	25	229
m8	Primary tumor, 4 weeks post injection	26	236
m8	Primary tumor, 4 weeks post injection	27	237
m9	Primary tumor, 4 weeks post injection	28	144
m9	Primary tumor, 4 weeks post injection	29	144
m9	Primary tumor, 4 weeks post injection	30	116
m9	Primary tumor, 4 weeks post injection	31	129
m10	Primary tumor, 4 weeks post injection	32	165
m10	Primary tumor, 4 weeks post injection	33	136
m11	Primary tumor, 4 weeks post injection	34	81
m11	Primary tumor, 4 weeks post injection	35	156
m11	Primary tumor, 4 weeks post injection	36	39
m11	Primary tumor, 4 weeks post injection	37	136
m12	Primary tumor, 4 weeks post injection	38	92
m12	Primary tumor, 4 weeks post injection	39	121
m12	Primary tumor, 4 weeks post injection	40	219
m12	Primary tumor, 4 weeks post injection	41	258
m13	Lung metastases	42	128

m13	Lung metastases	43	112
m13	Lung metastases	44	118
m14	Lung metastases	45	217
m14	Lung metastases	46	198
m14	Lung metastases	47	212
m15	Lung metastases	48	200
m15	Lung metastases	49	92
m15	Lung metastases	50	33

**Supplementary Table 5.** Top 40 DE genes between EpCAM-GFP- sCAFs and EpCAM+GFP+ 4T1 cancer cells.

* Gene	**GFP- EpCAM-	**GFP- EpCAM+	**GFP+ EpCAM-	**GFP+ EpCAM+
Ccl3	12.4057137	7.53736747	0	0
Hdc	11.4576988	5.92221425	2.49605844	0
Ccl4	13.1592977	8.0952709	0.94731761	1.74952899
Serpina1b	10.4637127	2.77549865	1.51428295	0
Il13	9.99739237	3.66610358	0	0
Osm	9.88473918	3.37231169	0.94731761	0
Ramp2	11.1172711	5.21925309	3.36216697	1.36456784
Cyp11a1	9.74972947	4.11868813	0	0
Des	10.5811615	3.66610358	1.92023697	0.83793993
Ifitm1	10.4542694	3.66610358	2.2366874	0.83793993
Csf2rb	10.4174865	4.53723893	2.2366874	0.83793993
Cyp4b1	9.51858347	2.77549865	0.94731761	0
Gpx3	11.5223889	11.0727436	1.92023697	2.05310563
Serpingle1	11.5042001	4.67569914	3.36216697	2.05310563
Csf2rb2	10.7807219	4.67569914	1.51428295	1.36456784
Col3a1	11.0819377	4.67569914	2.49605844	1.74952899
Cdh13	9.2649728	5.02567036	2.2366874	0
Meg3	9.24685513	1.73935152	0	0
Cxcl12	9.21738513	4.46268418	0	0
Il4	9.16431816	3.79323816	0	0
Etv4	6.41711128	8.55157789	9.2808219	9.43222119
Krt14	7.75474804	10.9561468	7.87607232	10.7783469
Rhox5	6.39095167	8.97014622	7.20622205	9.44694654
C3	7.71312431	9.88553719	9.87716676	10.7757571
Msln	6.41711128	8.88349371	9.30642962	9.48232149
Mmp13	6.30950041	7.95952768	8.56179708	9.40231178
Tslp	6.22317397	9.24776549	8.36462742	9.34056589
Padi4	6.41711128	9.44461747	9.71453541	9.64157013
Il24	5.96399668	8.49658613	8.3275886	9.19308659
Lad1	6.7199833	9.3978649	9.15726209	9.95142293
Sfn	6.5172496	10.8218544	7.23317612	9.74977814
Cldn4	8.13171734	11.5909493	8.61400156	11.3842299
Kcnn4	6.5648274	9.5085525	8.96698651	9.82810914
Ankrd1	6.0993976	8.76051157	9.22596642	9.3905108
Mmp9	8.52956968	11.4795616	10.8115591	11.8584689
Spp1	10.23835	12.8797319	13.7380379	13.6181744
Tns4	6.33716494	8.93265869	9.96152033	9.79011695
Anxa8	6.03328503	9.38530556	8.7320854	9.49339766
Syt8	6.06671999	8.89771264	9.67248442	9.55057096
Gpa33	6.84086377	9.75884732	9.66425526	10.3350618

\* 20 most upregulated and 20 most downregulated genes from all genes with a minimum of 2^8 average normalized reads (between GFP+EpCAM+ and GFP-EpCAM-; 1525 in total). Genes upregulated in EpCAM-GFP- are in orange; Genes upregulated in EpCAM+GFP+ are in blue

\*\* Reads are presented as log2 normalized values.

**Supplementary Table 8.** TNBC cohort univariate analyses  
Two-way Cox proportional hazards model

Variable (n)	Hazard Ratio	95% CI	P-Value
*CK (70)	36514.700		0.028
*Pdpn (70)	14019.614		0.013
S100A4 (70)	0.058	0 - 10075.709	0.644
CD3 (68)	4.539	0.058 - 356.571	0.497
S100A4/Pdpn (70)	0.388	0.199 - 0.758	0.005
Pdpn/CK (70)	0.956	0.861 - 1.065	0.424
S100A4/CK (70)	0.909	0.791 - 1.045	0.180
LN (69)	1.865	0.865 - 3.964	0.105
**Tumor size (69)	T1	1 [Reference]	
	T2	2.100	0.956 - 4.607
	T3	4.475	1.258 - 15.921
BRCA status (45)	WT	1 [Reference]	
	Mut	0.624	0.315 - 1.238
Age (72)	1.022	0.999 - 1.045	0.062

\* CI with wide range, since variance of the markers is big

\*\* T1 = { TS ≤ 2} , T2 = {2 < TS ≤ 5}, T3 = {TS >5}, TS = Tumor Size (cm)

**Supplementary Table 10.** TNBC cohort Multiplicative Multivariate Analysis  
Two-way Cox proportional hazards model

Variable (n)	Hazard Ratio	95% CI	P-Value	Likelihood ratio test
S100A4/Pdpn (45)	0.828	0.421 - 1.631	0.585	< 0.001
BRCA status (45)	37.101	4.000 - 344.491	0.001	
S100A4/Pdpn:BRCA (45)	0.015	0.001 - 0.230	0.002	

Variable (n)	Hazard Ratio	95% CI	P-Value	Likelihood ratio test
Pdpn/Total ROI (45)	5.57E+05	0.6 - 5.058E+11	0.059	0.095
BRCA status (45)	0.143	0.021 - 0.9692	0.046	
Pdpn/Total ROI:BRCA (45)	8.26E+12	2.778 - 2.45E+18	0.039	

**Supplementary Table 12.** Selected genes, priority, and fold change threshold for subset specific gene expression analysis

Group	Gene	Priority	T_fold
Wound healing	Acta2	6	4.1
Immune regulatory E	Cxcl12	9	4.9
ECM	Mfap5	5	8.2
NMF	Gsn	5	18
Inflammatory A	Cxcl1	4	3.5
Immune regulatory L	Saa3	7	15
Inflammatory B	Il6	17	5
Antigen presentation	Spp1	7	3.1
Protein folding	S100a4	13	1.77