Supplementary information

A spatially resolved single-cell genomic atlas of the adult human breast
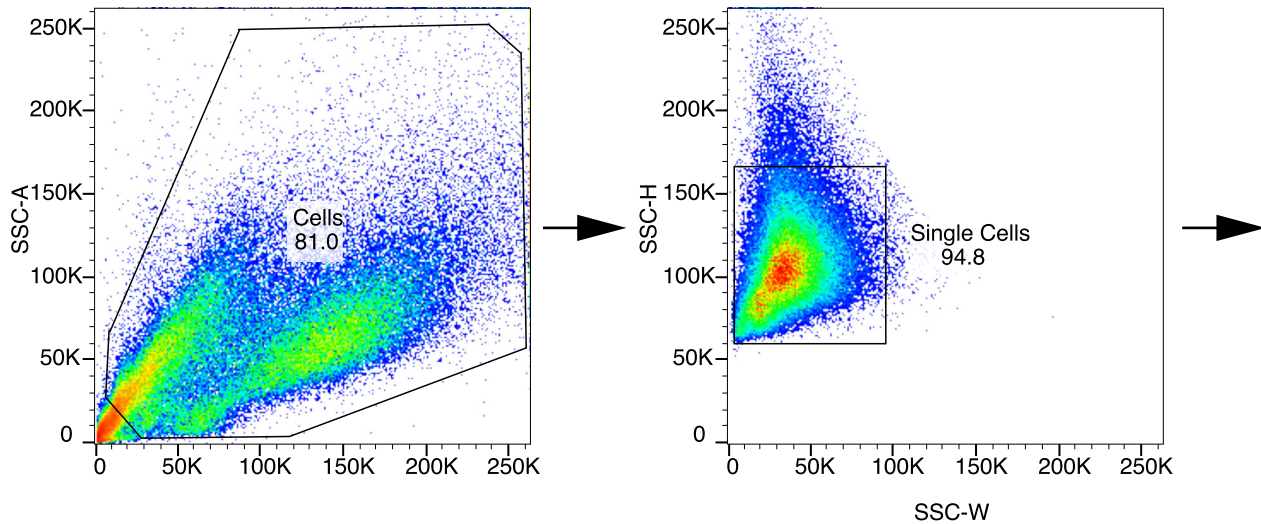
A spatially resolved single cell genomic atlas of the adult human breast

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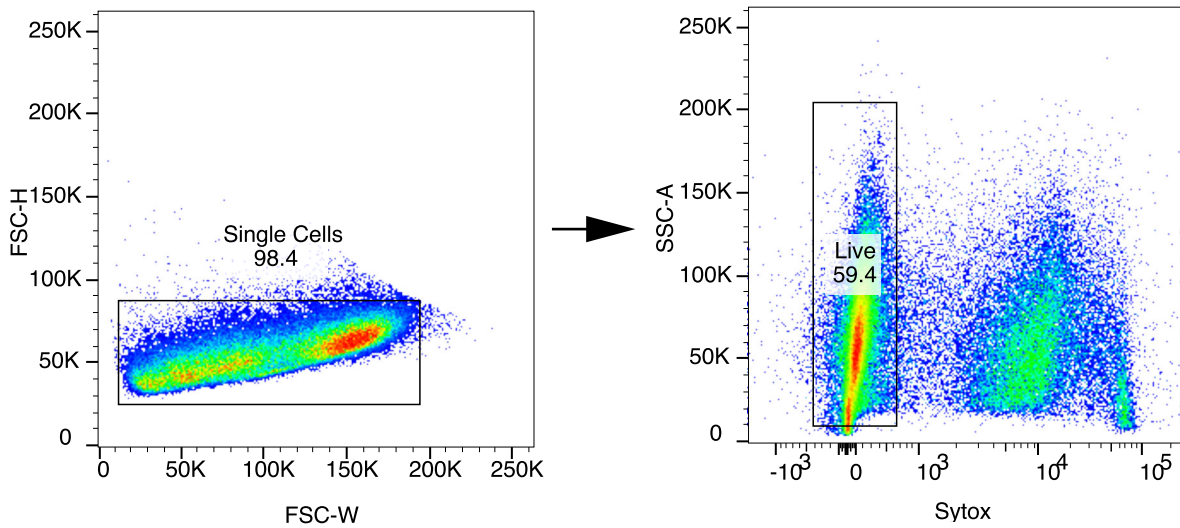# Kumar, Nee, Wei, He, Nguyen et al.

Supplementary Information Figure 1 – FACS Gating strategy for isolating live cells.

A subset of breast tissue samples (HBCA14-24) were FACS sorted to enrich for live cells by staining with Sytox live cell stain and gating positive cells. An example of this gating strategy is shown, in which cells are gated by Side Scatter Area (SSC-A) followed by side-scatter height (SSC-H) and side scatter width (SSC-W) to identify single cell events. The cells were then gated by Forward Scatter Height (FSC-H) and Forward-Scatter Width (FSC-W) to enrich single cell events. Finally live cells were gated from dead cells using Sytox live cell stain.

Supplementary Table 1 – Breast Atlas Tissue Samples and Clinical Metadata

Sample ID	Patient ID	Institution	Tissue Source	Age	Ethnicity	Parity	Menopause	BMI	BMI Group	Digestion Protocol	Prior Treatment
hbca_c01	P01	mda	Cancer Mastectomy	O	caucasian	0	post	27.11	overweight	short	chemotherapy (taxol)
hbca_c02	P02	mda	Cancer Mastectomy	Y	caucasian	1	pre	24.59	Normal	short	unknown
hbca_c03	P03	mda	Cancer Mastectomy	O	caucasian	unknown	post	37.01	obese	short	none
hbca_c04	P04	mda	Cancer Mastectomy	O	caucasian	1	post	24.16	Normal	short	none
hbca_c05	P05	mda	Cancer Mastectomy	Y	caucasian	0	pre	22.89	Normal	short	none
hbca_c06	P06	mda	Cancer Mastectomy	Y	caucasian	1	pre	30.12	obese	short	none
hbca_c07	P07	mda	Cancer Mastectomy	Y	caucasian	0	pre	27.69	overweight	short	targeted therapy (Talazoparib)
hbca_c08	P08	mda	Cancer Mastectomy	O	caucasian	1	post	30.27	obese	short	chemotherapy
hbca_c09	P09	mda	Prophylatic Mastectomy	Y	caucasian	unknown	pre	23.09	Normal	short	none
hbca_c10	P09	mda	Prophylatic Mastectomy	Y	caucasian	unknown	pre	23.09	Normal	long	none
hbca_c11	P10	mda	Cancer Mastectomy	Y	caucasian	1	pre	29.79	overweight	short	chemotherapy (taxol)
hbca_c12	P11	mda	Prophylatic Mastectomy	Y	hispanic	0	pre	22.75	Normal	short	none
hbca_c13	P11	mda	Prophylatic Mastectomy	Y	hispanic	0	pre	22.75	Normal	long	none
hbca_c14	P12	uci	Reduction Mammoplasty	Y	caucasian	unknown	unknown	33.40	obese	long	none
hbca_c15	P12	uci	Reduction Mammoplasty	Y	caucasian	unknown	unknown	33.40	obese	long	none
hbca_c16	P13	uci	Prophylatic Mastectomy	NA	unknown	1	post	unknown	unknown	long	unknown
hbca_c17	P13	uci	Prophylatic Mastectomy	NA	unknown	1	post	unknown	unknown	long	unknown
hbca_c18	P14	uci	Prophylatic Mastectomy	Y	unknown	unknown	unknown	unknown	unknown	long	unknown
hbca_c19	P15	uci	Reduction Mammoplasty	Y	caucasian	unknown	pre	28.70	overweight	long	none
hbca_c20	P16	uci	Reduction Mammoplasty	Y	caucasian	unknown	unknown	27.70	overweight	long	none
hbca_c21	P17	uci	Prophylatic Mastectomy	NA	unknown	0	pre		unknown	long	unknown
hbca_c22	P18	uci	Reduction Mammoplasty	Y	caucasian	unknown	pre	32.40	obese	long	none
hbca_c23	P18	uci	Reduction Mammoplasty	Y	caucasian	unknown	pre	32.40	obese	long	none
hbca_c24	P19	uci	Reduction Mammoplasty	Y	caucasian	unknown	pre	32.20	obese	long	none
hbca_c25	P20	mda	Reduction Mammoplasty	Y	unknown	1	post		unknown	short	none
hbca_c26	P20	mda	Reduction Mammoplasty	Y	unknown	1	post		unknown	long	none
hbca_c27	P21	mda	Cancer Mastectomy	Y	caucasian	1	pre	24.45	Normal	long	chemotherapy (docetaxel, carboplatin, trastuzumab, and pertuzumab)
hbca_c28	P22	mda	Cancer Mastectomy	Y	caucasian	0	pre	29.52	overweight	short	none
hbca_c29	P23	mda	Cancer Mastectomy	Y	caucasian	1	pre	27.92	overweight	short	none
hbca_c30	P23	mda	Cancer Mastectomy	Y	caucasian	1	pre	27.92	overweight	short	none
hbca_c31	P24	mda	Reduction Mammoplasty	NA	unknown	unknown	unknown	unknown	unknown	medium	unknown
hbca_c32	P24	mda	Reduction Mammoplasty	NA	unknown	unknown	unknown	unknown	unknown	long	unknown
hbca_c33	P25	mda	Cancer Mastectomy	O	african-american	unknown	post	25.43	overweight	long	none
hbca_c34	P26	mda	Cancer Mastectomy	Y	caucasian	1	pre	37.07	obese	long	none
hbca_c35	P27	mda	Cancer Mastectomy	O	caucasian	1	post	22.97	Normal	short	none
hbca_c36	P28	mda	Cancer Mastectomy	O	caucasian	unknown	post	32.29	obese	long	none
hbca_c37	P29	mda	Cancer Mastectomy	O	caucasian	unknown	post	38.43	obese	long	hormonal therapy (tamoxifen)
hbca_c38	P30	mda	Prophylatic Mastectomy	Y	caucasian	unknown	post	25.64	overweight	long	none
hbca_c39	P31	mda	Cancer Mastectomy	O	caucasian	0	post	24.19	Normal	long	chemo(ddAC)
hbca_c40	P37	mda	Cancer Mastectomy	O	caucasian	unknown	post	25.45	overweight	short	unknown
hbca_c41	P32	mda	Cancer Mastectomy	Y	caucasian	1	pre	26.98	overweight	long	no previous therapy
hbca_c42	P33	mda	Cancer Mastectomy	Y	caucasian	1	pre	26.76	overweight	long	chemotherapy (docetaxel, carboplatin, trastuzumab, and pertuzumab)
hbca_c43	P34	mda	Cancer Mastectomy	Y	caucasian	1	pre	20.80	Normal	long	chemotherapy (taxol)
hbca_c44	P35	mda	Cancer Mastectomy	Y	caucasian	1	pre	24.71	Normal	long	hormonal therapy (tamoxifen)
hbca_c45	P36	mda	Cancer Mastectomy	Y	african-american	0	pre	33.84	obese	long	chemotherapy (docetaxel, carboplatin, trastuzumab, and pertuzumab)
hbca_c46	P42	mda	Cancer Mastectomy	Y	unknown	1	pre	29.27	overweight	short	chemotherapy (docetaxel, carboplatin, trastuzumab, and pertuzumab)
hbca_c47	P43	mda	Cancer Mastectomy	Y	unknown	1	pre	22.66	Normal	short	none
hbca_c48	P43	mda	Cancer Mastectomy	Y	unknown	1	pre	22.66	Normal	medium	unknown
hbca_c49	P43	mda	Cancer Mastectomy	Y	unknown	1	pre	22.66	Normal	long	unknown
hbca_c50	P44	bcm	Reduction Mammoplasty	O	caucasian	0	post	29.30	overweight	long	none
hbca_c51	P44	bcm	Reduction Mammoplasty	O	caucasian	0	post	29.30	overweight	long	none
hbca_c52	P45	bcm	Reduction Mammoplasty	Y	caucasian	1	pre	25.06	overweight	medium	none
hbca_c53	P46	bcm	Reduction Mammoplasty	Y	caucasian	1	pre	42.51	obese	medium	none
hbca_c54	P46	bcm	Reduction Mammoplasty	Y	caucasian	1	pre	42.51	obese	medium	none
hbca_c55	P47	bcm	Reduction Mammoplasty	Y	african-american	1	pre	29.79	overweight	medium	none
hbca_c56	P47	bcm	Reduction Mammoplasty	Y	african-american	1	pre	29.79	overweight	medium	none
hbca_c57	P48	bcm	Reduction Mammoplasty	Y	african-american	1	pre	34.70	obese	medium	none
hbca_c58	P48	bcm	Reduction Mammoplasty	Y	african-american	1	pre	34.70	obese	medium	none
hbca_c59	P49	bcm	Reduction Mammoplasty	Y	african-american	1	pre	31.37	obese	medium	none
hbca_c60	P49	bcm	Reduction Mammoplasty	Y	african-american	1	pre	31.37	obese	medium	none
hbca_c61	P49	bcm	Reduction Mammoplasty	Y	african-american	1	pre	31.37	obese	medium	none
hbca_c62	P50	bcm	Reduction Mammoplasty	Y	african-american	0	pre	31.18	obese	medium	none
hbca_c63	P50	bcm	Reduction Mammoplasty	Y	african-american	0	pre	31.18	obese	medium	none
hbca_c64	P50	bcm	Reduction Mammoplasty	Y	african-american	0	pre	31.18	obese	medium	none
hbca_c65	P50	bcm	Reduction Mammoplasty	Y	african-american	0	pre	31.18	obese	medium	none

Sample ID	Patient ID	Institution	Tissue Source	Age	Ethnicity	Parity	Menopause	BMI	BMI Group	Digestion Protocol	Prior Treatment
hbca_c66	P51	bcm	Reduction Mammoplasty	Y	african-american	unknown	pre	30.61	obese	medium	none
hbca_c67	P51	bcm	Reduction Mammoplasty	Y	african-american	unknown	pre	30.61	obese	medium	none
hbca_c68	P51	bcm	Reduction Mammoplasty	Y	african-american	unknown	pre	30.61	obese	medium	none
hbca_c69	P51	bcm	Reduction Mammoplasty	Y	african-american	unknown	pre	30.61	obese	medium	none
hbca_c70	P52	bcm	Reduction Mammoplasty	Y	african-american	1	pre	39.89	obese	medium	none
hbca_c71	P52	bcm	Reduction Mammoplasty	Y	african-american	1	pre	39.89	obese	medium	none
hbca_c72	P53	bcm	Reduction Mammoplasty	O	african-american	1	pre	24.93	normal	medium	none
hbca_c73	P53	bcm	Reduction Mammoplasty	O	african-american	1	pre	24.93	normal	medium	none
hbca_c74	P54	bcm	Reduction Mammoplasty	Y	african-american	1	pre	35.92	obese	medium	none
hbca_c75	P54	bcm	Reduction Mammoplasty	Y	african-american	1	pre	35.92	obese	medium	none
hbca_c76	P55	bcm	Reduction Mammoplasty	Y	caucasian	0	pre	28.13	overweight	medium	none
hbca_c77	P55	bcm	Reduction Mammoplasty	Y	caucasian	0	pre	28.13	overweight	medium	none
hbca_c78	P56	bcm	Reduction Mammoplasty	Y	african-american	0	pre	34.00	obese	medium	none
hbca_c79	P56	bcm	Reduction Mammoplasty	Y	african-american	0	pre	34.00	obese	medium	none
hbca_c80	P57	bcm	Reduction Mammoplasty	Y	african-american	1	pre	43.95	obese	medium	none
hbca_c81	P57	bcm	Reduction Mammoplasty	Y	african-american	1	pre	43.95	obese	medium	none
hbca_c82	P38	bcm	Reduction Mammoplasty	O	caucasian	1	post	27.64	overweight	medium	none
hbca_c83	P38	bcm	Reduction Mammoplasty	O	caucasian	1	post	27.64	overweight	medium	none
hbca_c84	P39	bcm	Reduction Mammoplasty	Y	african-american	unknown	pre	30.79	obese	medium	none
hbca_c85	P39	bcm	Reduction Mammoplasty	Y	african-american	unknown	pre	30.79	obese	medium	none
hbca_c86	P40	bcm	Reduction Mammoplasty	Y	african-american	0	pre	38.09	obese	medium	none
hbca_c87	P40	bcm	Reduction Mammoplasty	Y	african-american	0	pre	38.09	obese	medium	none
hbca_c88	P58	bcm	Reduction Mammoplasty	Y	african-american	0	pre	35.19	obese	medium	none
hbca_c89	P58	bcm	Reduction Mammoplasty	Y	african-american	0	pre	35.19	obese	medium	none
hbca_c90	P41	bcm	Reduction Mammoplasty	Y	african-american	1	pre	34.41	obese	medium	none
hbca_c91	P41	bcm	Reduction Mammoplasty	Y	african-american	1	pre	34.41	obese	medium	none
hbca_c92	P59	bcm	Reduction Mammoplasty	O	hispanic	unknown	post	31.50	obese	medium	none
hbca_c93	P59	bcm	Reduction Mammoplasty	O	hispanic	unknown	post	31.50	obese	medium	none
hbca_c94	P60	bcm	Reduction Mammoplasty	O	hispanic	unknown	unknown	39.00	obese	medium	none
hbca_c95	P60	bcm	Reduction Mammoplasty	O	hispanic	unknown	unknown	39.00	obese	medium	none
hbca_c96	P61	bcm	Reduction Mammoplasty	O	african-american	unknown	unknown	42.16	obese	medium	none
hbca_c97	P61	bcm	Reduction Mammoplasty	O	african-american	unknown	unknown	42.16	obese	medium	none
hbca_c98	P62	bcm	Reduction Mammoplasty	Y	african-american	unknown	pre	38.04	obese	medium	none
hbca_c99	P62	bcm	Reduction Mammoplasty	Y	african-american	unknown	pre	38.04	obese	medium	none
hbca_c100	P59	bcm	Reduction Mammoplasty	O	hispanic	unknown	post	31.50	obese	medium	none
hbca_c101	P63	bcm	Reduction Mammoplasty	Y	african-american	1	pre	44.10	obese	medium	none
hbca_c102	P63	bcm	Reduction Mammoplasty	Y	african-american	1	pre	44.10	obese	medium	none
hbca_c103	P64	bcm	Reduction Mammoplasty	Y	african-american	1	pre	34.80	obese	medium	none
hbca_c104	P64	bcm	Reduction Mammoplasty	Y	african-american	1	pre	34.80	obese	medium	none
hbca_c105	P65	bcm	Reduction Mammoplasty	Y	african-american	1	pre	41.46	obese	medium	none
hbca_c106	P65	bcm	Reduction Mammoplasty	Y	african-american	1	pre	41.46	obese	medium	none
hbca_c107	P66	bcm	Reduction Mammoplasty	Y	african-american	0	pre	26.34	overweight	medium	none
hbca_c108	P67	bcm	Reduction Mammoplasty	Y	caucasian	0	pre	25.89	overweight	medium	none
hbca_c111	P70	bcm	Reduction Mammoplasty	O	african-american	1	post	33.23	obese	medium	none
hbca_c109	P68	bcm	Reduction Mammoplasty	Y	african-american	1	pre	39.20	obese	medium	none
hbca_c110	P69	bcm	Reduction Mammoplasty	Y	african-american	1	pre	40.97	obese	medium	none
hbca_c112	P71	bcm	prophylatic Mastectomy	Y	caucasian	1	unknown	37.01	obese	medium	unknown
hbca_c113	P72	bcm	Reduction Mammoplasty	Y	caucasian	0	pre	33.11	obese	medium	none
hbca_c114	P73	bcm	Reduction Mammoplasty	Y	hispanic	1	pre	34.88	obese	medium	none
hbca_c115	P74	bcm	Reduction Mammoplasty	O	caucasian	0	post	40.76	obese	medium	none
hbca_c116	P75	bcm	prophylatic Mastectomy	Y	asian	1	pre	16.64	underweight	medium	unknown
hbca_c117	P76	bcm	prophylatic Mastectomy	Y	caucasian	0	pre	19.44	normal	medium	unknown
hbca_c118	P77	bcm	Reduction Mammoplasty	Y	african-american	1	pre	35.94	obese	medium	none
hbca_c119	P78	bcm	Reduction Mammoplasty	Y	african-american	1	pre	35.28	obese	medium	none
hbca_c120	P79	bcm	prophylatic Mastectomy	Y	hispanic	1	pre	30.61	obese	medium	unknown
hbca_c121	P80	bcm	Reduction Mammoplasty	Y	african-american	0	pre	33.52	obese	medium	none
hbca_c122	P81	bcm	Reduction Mammoplasty	Y	caucasian	0	pre	31.53	obese	medium	none
hbca_c123	P82	bcm	Reduction Mammoplasty	Y	african-american	1	pre	45.46	obese	medium	none
hbca_c124	P83	bcm	Reduction Mammoplasty	Y	african-american	1	pre	41.43	obese	medium	none
hbca_c125	P84	bcm	Reduction Mammoplasty	O	caucasian	0	post	26.48	overweight	medium	none
hbca_c126	P85	bcm	Reduction Mammoplasty	Y	hispanic	1	pre	30.90	obese	medium	none
hbca_c127	P86	bcm	Reduction Mammoplasty	Y	african-american	1	pre	30.36	obese	medium	none
hbca_c128	P87	bcm	Reduction Mammoplasty	Y	african-american	1	pre	46.95	obese	medium	none
hbca_c129	P88	bcm	Reduction Mammoplasty	Y	african-american	1	pre	39.31	obese	medium	none
hbca_c130	P89	bcm	Reduction Mammoplasty	Y	african-american	1	pre	43.24	obese	medium	none
hbca_c131	P90	bcm	Reduction Mammoplasty	Y	african-american	1	pre	26.62	overweight	medium	none
hbca_c132	P91	bcm	Reduction Mammoplasty	Y	african-american	1	pre	42.77	obese	medium	none
hbca_c133	P92	bcm	Reduction Mammoplasty	Y	african-american	1	pre	39.39	obese	medium	none
hbca_c134	P93	bcm	Reduction Mammoplasty	Y	african-american	1	pre	38.78	obese	medium	none
hbca_c135	P94	bcm	Reduction Mammoplasty	Y	african-american	1	pre	32.28	obese	medium	none
hbca_c136	P95	bcm	Reduction Mammoplasty	Y	african-american	1	pre	42.80	obese	medium	none
hbca_c137	P96	bcm	Reduction Mammoplasty	Y	african-american	0	pre	47.44	obese	medium	none
hbca_c138	P97	bcm	Reduction Mammoplasty	Y	hispanic	1	pre	35.48	obese	medium	none
hbca_c139	P98	bcm	Reduction Mammoplasty	Y	african-american	1	pre	35.63	obese	medium	none
hbca_c140	P99	bcm	Reduction Mammoplasty	Y	african-american	0	pre	28.85	overweight	medium	none
hbca_c141	P100	bcm	Reduction Mammoplasty	Y	caucasian	1	pre	25.14	overweight	medium	none

Sample ID	Patient ID	Institution	Tissue Source	Age	Ethnicity	Parity	Menopause	BMI	BMI Group	Digestion Protocol	Prior Treatment
hbca_c142	P101	bcm	Reduction Mammoplasty	Y	african-american	1	pre	39.72	obese	medium	none
hbca_c143	P102	bcm	Reduction Mammoplasty	Y	african-american	1	pre	32.97	obese	medium	none
hbca_c144	P103	bcm	Reduction Mammoplasty	Y	african-american	1	pre	26.63	overweight	medium	none
hbca_c145	P104	bcm	Reduction Mammoplasty	Y	african-american	1	pre	36.95	obese	medium	none
hbca_c146	P105	bcm	Reduction Mammoplasty	Y	african-american	1	pre	34.19	obese	medium	none
hbca_c147	P106	bcm	Reduction Mammoplasty	Y	african-american	1	pre	27.66	overweight	medium	none
hbca_c148	P107	bcm	Reduction Mammoplasty	Y	african-american	0	pre	27.02	overweight	medium	none
hbca_c149	P108	bcm	Reduction Mammoplasty	Y	caucasian	0	pre	27.13	overweight	medium	none
hbca_c150	P109	bcm	Reduction Mammoplasty	O	caucasian	0	post	32.95	obese	medium	none
hbca_c151	P110	bcm	Reduction Mammoplasty	O	caucasian	0	post	26.73	overweight	medium	none
hbca_c152	P111	bcm	Reduction Mammoplasty	Y	african-american	0	pre	41.15	obese	medium	none
hbca_c153	P112	bcm	Reduction Mammoplasty	Y	caucasian	1	pre	34.00	obese	medium	none
hbca_c154	P113	uci	Cancer Mastectomy	Y	caucasian	1	unknown	23.72	Normal	medium	(Perjeta/Xeloda/Kajinta)
hbca_c155	P114	uci	Cancer Mastectomy	Y	caucasian	1	pre	25.32	overweight	medium	hormonal therapy (aromatase)
hbca_c156	P115	uci	Cancer Mastectomy	O	caucasian	1	post	23.08	Normal	medium	hormonal therapy (aromatase)
hbca_c157	P116	uci	Cancer Mastectomy	O	caucasian	1	post	35.21	obese	medium	chemo
hbca_c158	P117	uci	Cancer Mastectomy	Y	hispanic	1	pre	30.34	obese	medium	none
hbca_c159	P118	uci	Prophylatic Mastectomy	O	caucasian	1	post	23.41	Normal	medium	unknown
hbca_c160	P119	uci	Cancer Mastectomy	Y	caucasian	1	pre	22.31	Normal	medium	hormonal therapy (tamoxifen)
hbca_c161	P120	uci	Cancer Mastectomy	O	hispanic	1	post	30.14	obese	medium	chemotherapy
hbca_c162	P121	uci	Prophylatic Mastectomy	Y	caucasian	unknown	unknown	29.28	overweight	medium	unknown
hbca_c163	P122	uci	Cancer Mastectomy	Y	caucasian	1	pre	21.54	normal	medium	chemotherapy (docetaxel, carboplatin, trastuzumab, and pertuzumab)
hbca_c164	P123	uci	prophylatic Mastectomy	Y	caucasian	1	pre	18.17	normal	medium	hormonal therapy (tamoxifen)
hbca_c165	P124	uci	Cancer Mastectomy	O	caucasian	0	pre	25.40	overweight	medium	none
hbca_c166	P125	uci	prophylatic Mastectomy	Y	caucasian	1	unknown	33.72	obese	medium	none
hbca_c167	P126	uci	prophylatic Mastectomy	O	caucasian	1	pre	23.76	normal	medium	unknown

Supplementary Table 1 – Breast Atlas Tissue Samples and Clinical Metadata

This table lists the n =167 tissue samples and clinical metadata for the 126 women included in the breast atlas project. The columns list from left to right the sample identifier (Sample ID), the patient identifier (Patient ID), the institution where the tissue sample was collected from MD Anderson (MDA), UC Irvine (UCI) or Baylor College of Medicine (BCM), the procedure from which the tissue source was collected reduction mammoplasties (RM=111), prophylactic mastectomies (PM=18), and contralateral mastectomies (CM=38), the age of the women as < 50 (Y), >= 50 (O), the ethnicity the women self-identifies as, the parity status as positive (1), negative (0) or unknown, the menopause status (pre/post), the Body Mass Index (BMI), the BMI Group classification and digestion protocol time use during sample dissociation (short, medium, or long) and whether the woman received any prior treatment before the tissue was collected.

Supplementary Table 2 – Single Cell RNA-seq Quality Control Metrics

Sample ID	Number of Cells	Mean Reads per Cell	Median Genes per Cell	Number of Reads	Fraction Reads in Cells	Genes Detected	Median UMI Counts per Cell
hbca_c01	4,091	79,318	353	324,492,736	75.1%	20,828	1,981
hbca_c02	9,577	36,403	923	348,639,606	72.3%	23,775	2,336
hbca_c03	5,450	65,569	1,032	357,352,385	70.6%	22,024	2,564
hbca_c04	8,924	39,111	800	349,034,669	69.8%	23,140	1,705
hbca_c05	5,786	57,183	709	330,866,587	70.1%	22,209	1,604
hbca_c06	3,593	89,184	1,178	320,441,257	83.5%	22,069	2,948
hbca_c07	5,250	60,928	953	319,872,861	76.8%	22,364	2,250
hbca_c08	2,533	137,485	1,055	348,249,946	69.5%	20,626	2,570
hbca_c09	7,894	42,387	823	334,609,974	71.8%	23,308	1,922
hbca_c10	5,682	63,430	771	360,412,188	87.9%	21,623	1,645
hbca_c11	4,052	84,470	787	342,274,452	76.6%	21,264	1,729
hbca_c12	2,322	141,601	872	328,799,276	55.0%	20,459	2,177
hbca_c13	4,127	83,670	1,099	345,309,344	86.8%	21,564	2,690
hbca_c14	9,969	41,530	2,106	414,015,762	95.6%	22,850	8,247
hbca_c15	9,921	42,668	1,955	423,315,895	96.1%	22,609	7,829
hbca_c16	10,603	38,889	1,197	412,348,361	95.0%	22,866	4,501
hbca_c17	10,362	40,884	1,234	423,649,081	94.4%	22,849	4,428
hbca_c18	5,955	56,256	2,024	335,010,009	97.4%	21,296	7,468
hbca_c19	7,580	48,118	1,812	364,736,800	95.6%	22,342	7,183
hbca_c20	11,999	39,924	2,573	479,054,503	97.0%	23,811	10,611
hbca_c21	10,537	33,038	1,645	348,128,564	96.2%	23,356	6,257
hbca_c22	8,554	40,097	1,476	342,994,984	95.8%	22,282	5,158
hbca_c23	10,030	36,670	1,427	367,801,885	95.8%	22,526	4,877
hbca_c24	2,345	148,555	770	348,361,547	65.7%	24,166	1,162
hbca_c25	6,401	59,231	2,582	379,140,265	84.7%	24,813	7,353
hbca_c26	7,845	50,538	2,020	396,476,992	90.1%	25,280	6,664
hbca_c27	5,944	59,127	1,755	351,455,269	78.1%	23,853	5,445
hbca_c28	2,526	154,806	1,449	391,041,072	70.4%	22,713	4,255
hbca_c29	6,425	59,692	1,509	383,526,635	74.7%	24,811	4,744
hbca_c30	12,399	30,024	1,654	372,270,308	78.7%	25,997	4,849
hbca_c31	7,134	44,541	2,003	317,759,854	85.3%	24,105	6,488
hbca_c32	11,034	32,093	1,506	354,120,495	81.5%	25,021	4,758
hbca_c33	6,839	58,653	2,054	401,131,543	88.3%	24,780	7,035
hbca_c34	8,930	55,014	1,918	491,282,666	87.3%	25,091	6,060
hbca_c35	5,694	76,943	1,203	438,114,228	55.1%	23,846	3,606
hbca_c36	7,582	58,284	2,382	441,911,150	92.1%	23,845	7,912
hbca_c37	10,318	44,250	1,460	456,573,803	85.5%	25,256	5,031
hbca_c38	8,639	43,128	2,012	372,584,898	88.2%	24,854	5,860
hbca_c39	5,917	66,216	2,055	391,801,107	85.9%	24,007	7,619
hbca_c41	8,420	47,239	1,529	397,758,089	85.6%	25,743	4,501
hbca_c42	6,864	56,666	2,001	388,956,766	86.0%	25,564	5,956
hbca_c43	10,061	39,595	2,277	398,365,868	90.4%	25,700	7,654
hbca_c44	12,386	37,439	1,850	463,722,721	87.8%	25,490	6,745
hbca_c45	16,520	25,592	1,183	422,790,667	74.8%	25,474	2,830
hbca_c40	4,570	90,273	1,377	412,548,145	78.4%	23,685	3,944
hbca_c82	7,533	42,551	1,564	320,540,361	77.1%	24,934	4,602
hbca_c83	9,969	36,167	1,336	360,555,401	75.7%	25,155	3,819
hbca_c84	12,466	38,226	1,372	476,527,092	72.8%	25,280	3,941
hbca_c85	11,774	41,479	1,700	488,380,226	78.7%	25,568	5,555
hbca_c86	11,983	30,404	1,467	364,335,501	78.7%	25,618	4,308
hbca_c87	10,890	36,260	1,478	394,879,939	81.8%	25,572	4,509
hbca_c90	9,161	44,766	1,635	410,105,314	87.9%	24,367	4,604
hbca_c91	9,469	28,450	1,403	269,397,441	87.6%	24,043	3,557
hbca_c46	11,913	34,346	1,207	409,172,629	71.5%	25,136	2,945
hbca_c47	9,126	39,254	1,125	358,234,249	70.8%	24,276	2,895
hbca_c48	8,627	46,106	1,391	397,758,601	87.0%	25,214	4,322
hbca_c49	8,126	58,187	2,040	472,831,839	89.7%	24,266	6,953
hbca_c50	5,018	87,632	1,703	439,739,114	89.7%	26,109	5,064
hbca_c51	6,129	76,466	2,255	468,665,048	90.6%	25,517	7,893
hbca_c52	5,805	82,968	808	481,631,031	59.3%	23,909	2,252
hbca_c53	10,090	44,704	1,337	451,065,448	86.7%	25,902	3,777
hbca_c54	8,900	53,864	1,946	479,396,431	87.5%	26,149	5,733
hbca_c55	11,025	33,129	1,976	365,251,856	88.4%	25,648	6,164
hbca_c56	13,292	27,174	1,745	361,197,190	86.4%	25,562	5,157

Sample ID	Number of Cells	Mean Reads per Cell	Median Genes per Cell	Number of Reads	Fraction Reads in Cells	Genes Detected	Median UMI Counts per Cell
hbca_c57	12,807	28,873	1,244	369,783,072	82.1%	25,986	3,855
hbca_c58	12,035	37,459	1,444	450,819,388	85.1%	25,941	4,758
hbca_c59	9,448	42,433	1,160	400,915,804	71.4%	24,937	3,589
hbca_c60	18,664	21,815	1,582	407,158,167	87.6%	26,701	4,431
hbca_c61	12,740	29,815	1,730	379,843,424	87.2%	26,172	5,275
hbca_c62	11,795	29,324	1,706	345,879,461	85.1%	25,732	4,892
hbca_c63	11,648	32,884	1,715	383,040,911	84.0%	25,098	5,211
hbca_c64	10,615	46,004	2,228	488,341,054	84.7%	25,395	7,493
hbca_c65	13,521	31,221	1,864	422,151,595	82.8%	25,085	6,331
hbca_c66	10,884	44,418	1,747	483,454,528	83.7%	25,936	5,098
hbca_c67	13,547	31,444	1,608	425,972,057	81.8%	25,651	4,667
hbca_c68	10,582	42,935	1,566	454,341,839	78.7%	26,038	4,470
hbca_c69	15,150	31,424	1,619	476,074,866	81.4%	25,869	4,586
hbca_c70	9,916	39,706	2,072	393,728,950	87.3%	25,873	6,800
hbca_c71	11,964	32,298	1,887	386,422,651	86.1%	25,966	5,908
hbca_c72	11,502	32,651	1,974	375,557,112	83.2%	26,308	5,548
hbca_c73	11,647	32,187	2,044	374,889,239	85.4%	26,033	6,289
hbca_c74	13,610	29,180	1,643	397,144,206	85.5%	25,747	4,829
hbca_c75	16,502	21,757	1,373	359,038,086	83.9%	25,739	3,648
hbca_c76	11,679	36,674	2,152	428,317,510	85.7%	26,425	6,040
hbca_c77	11,403	36,082	2,210	411,454,267	87.8%	26,681	6,083
hbca_c78	12,214	28,491	1,775	347,997,546	80.3%	25,107	5,101
hbca_c79	12,305	29,823	1,654	366,983,410	76.0%	25,296	4,695
hbca_c80	13,289	28,285	1,563	375,892,640	81.7%	25,546	4,511
hbca_c81	13,122	28,146	1,645	369,333,714	83.4%	25,945	4,718
hbca_c88	7,041	58,303	1,985	410,512,392	86.4%	24,851	6,021
hbca_c89	6,718	57,121	2,108	383,742,211	87.9%	24,654	6,480
hbca_c100	8,927	50,041	2,485	446,716,152	84.2%	25,675	8,324
hbca_c92	8,476	51,364	2,060	435,365,199	84.0%	26,145	6,471
hbca_c93	6,618	62,898	2,086	416,264,504	84.3%	25,696	6,561
hbca_c94	8,431	44,139	2,135	372,138,533	84.1%	24,879	6,451
hbca_c95	8,086	42,646	1,720	344,840,516	76.8%	24,895	5,008
hbca_c96	10,184	27,403	1,499	279,075,635	84.6%	24,581	4,325
hbca_c97	8,411	38,493	1,855	323,768,135	86.0%	25,019	5,764
hbca_c98	7,145	55,077	2,082	393,531,047	86.3%	25,265	6,755
hbca_c99	7,950	50,287	2,220	399,788,791	87.6%	25,471	7,480
hbca_c101	11,847	28,648	1,702	339,399,886	82.1%	25,507	4,848
hbca_c102	7,981	46,193	1,896	368,671,215	87.4%	25,386	5,979
hbca_c103	6,575	59,460	1,883	390,955,869	82.8%	24,818	6,455
hbca_c104	8,231	44,503	1,689	366,310,737	82.7%	24,799	5,523
hbca_c105	9,672	39,087	1,754	378,051,031	80.2%	25,719	5,232
hbca_c106	6,905	50,595	1,799	349,364,118	79.5%	25,122	5,266
hbca_c107	16,373	23,899	1,404	391,303,086	82.8%	25,054	4,313
hbca_c108	7,522	50,855	1,284	382,532,558	84.7%	23,666	3,532
hbca_c109	10,893	35,130	1,501	382,674,799	78.2%	25,276	4,143
hbca_c110	9,996	36,836	1,973	368,221,340	80.4%	26,131	5,686
hbca_c111	13,195	31,551	1,667	416,327,108	86.3%	25,852	4,971
hbca_c112	9,200	43,586	1,357	400,991,623	79.0%	24,709	4,364
hbca_c113	12,361	32,006	1,454	395,636,808	81.1%	25,480	4,022
hbca_c114	6,942	57,555	1,637	399,549,786	76.0%	24,498	4,711
hbca_c115	10,538	37,439	1,978	394,541,850	89.9%	25,304	6,054
hbca_c116	10,804	42,673	1,278	461,041,111	72.8%	24,826	3,624
hbca_c117	14,842	32,039	1,747	475,529,139	85.7%	26,165	5,293
hbca_c118	13,505	33,511	1,341	452,569,153	82.0%	25,891	3,657
hbca_c119	14,000	21,599	1,311	302,388,805	78.8%	25,801	3,507
hbca_c120	14,895	24,107	1,633	359,083,871	82.6%	25,638	4,496
hbca_c121	14,372	24,150	1,654	347,090,147	81.4%	26,049	4,335
hbca_c122	9,182	45,153	2,061	414,603,688	86.4%	26,155	6,163
hbca_c123	7,915	52,654	1,459	416,758,293	81.5%	25,024	4,669
hbca_c124	11,118	30,853	1,418	343,027,485	84.0%	25,252	3,980

Sample ID	Number of Cells	Mean Reads per Cell	Median Genes per Cell	Number of Reads	Fraction Reads in Cells	Genes Detected	Median UMI Counts per Cell
hbca_c125	11,846	29,921	1,630	354,452,553	80.0%	25,290	4,845
hbca_c126	13,775	28,931	1,529	398,533,174	84.5%	25,967	4,386
hbca_c127	15,262	23,761	1,479	362,643,192	89.3%	25,860	4,269
hbca_c128	11,606	29,845	1,236	346,390,571	84.4%	24,230	2,776
hbca_c129	13,665	25,641	1,398	350,385,998	83.7%	25,781	3,754
hbca_c130	12,946	27,950	1,616	361,852,867	84.2%	26,059	4,459
hbca_c131	10,004	39,896	1,461	399,123,293	77.7%	25,154	4,185
hbca_c132	11,895	18,060	1,726	214,835,483	84.9%	24,574	4,741
hbca_c133	11,820	23,403	1,565	276,623,881	81.1%	25,851	4,179
hbca_c134	11,735	36,751	1,690	431,277,850	75.7%	26,152	4,780
hbca_c135	3,025	135,406	1,986	409,604,334	86.7%	24,779	6,867
hbca_c136	15,721	25,999	1,832	408,737,174	86.3%	26,111	5,724
hbca_c137	15,523	26,608	1,544	413,049,215	87.3%	26,070	4,342
hbca_c138	13,432	33,324	2,074	447,616,500	85.2%	26,380	5,930
hbca_c139	13,461	28,347	1,406	381,590,819	82.9%	26,185	3,909
hbca_c140	13,719	28,310	1,440	388,386,621	79.4%	25,702	4,386
hbca_c141	8,643	50,086	1,804	432,898,337	76.3%	25,749	5,456
hbca_c142	14,040	32,229	1,819	452,499,084	84.0%	26,384	5,369
hbca_c143	11,377	36,111	1,886	410,842,800	79.9%	25,902	6,072
hbca_c144	14,623	28,942	1,368	423,224,604	80.8%	26,247	3,911
hbca_c145	7,779	51,558	1,924	401,069,920	83.7%	26,191	5,740
hbca_c146	10,420	41,819	2,246	435,762,558	87.6%	26,590	7,428
hbca_c147	16,396	27,843	1,823	456,518,118	86.1%	26,602	5,523
hbca_c148	12,133	35,379	1,981	429,254,174	84.1%	26,238	5,549
hbca_c149	15,047	28,209	1,653	424,470,724	86.6%	25,315	4,938
hbca_c150	11,377	33,789	1,917	384,419,538	85.7%	26,167	5,802
hbca_c151	11,573	35,975	1,930	416,343,438	84.7%	25,467	6,096
hbca_c152	10,921	37,854	1,979	413,405,270	81.3%	25,501	6,532
hbca_c153	13,262	33,068	1,834	438,549,472	82.0%	26,101	5,593
hbca_c154	9,473	46,895	1,672	444,236,569	91.4%	25,798	5,613
hbca_c155	13,146	45,395	1,522	596,766,041	86.9%	26,009	4,901
hbca_c156	11,052	56,779	1,591	627,526,390	87.4%	26,396	4,740
hbca_c157	7,219	46,745	2,441	337,456,663	87.8%	25,875	8,255
hbca_c158	9,460	44,674	1,754	422,618,255	78.6%	25,371	5,368
hbca_c159	7,262	63,461	2,021	460,857,056	90.7%	25,728	6,736
hbca_c160	7,091	56,563	1,789	401,089,051	90.1%	25,372	5,509
hbca_c161	7,291	45,513	2,108	331,836,547	91.7%	24,847	6,949
hbca_c162	9,054	57,130	1,980	517,263,400	91.5%	26,008	6,515
hbca_c163	10,161	41,428	1,496	420,957,053	92.6%	25,836	4,356
hbca_c164	9,297	53,506	1,774	497,447,029	91.0%	25,713	5,818
hbca_c165	7,339	99,427	1,723	729,696,394	73.2%	25,658	6,325
hbca_c166	9,116	38,452	1,871	350,528,531	90.7%	25,478	5,551
hbca_c167	8,053	48,291	2,392	388,888,979	79.0%	25,689	7,740

Supplementary Table 2 – Single Cell RNA-seq Quality Control Metrics

This table lists the quality control metrics for the fresh breast tissue samples sequenced with single cell RNA sequencing using the 10X Genomics Chromium Platform before any filtering was applied. The columns listed from left to right indicate the Sample ID, Number of Cells, Mean Reads per Cell, Median Genes per Cell, Number of Reads, Fraction Reads in Cells, Total Genes Detected, Median UMI Counts per Cell.

Supplementary Table 3 – Top Marker Genes Expressed in Major Breast Cell Types

Cell Type	Gene	Average LogFC	pct1	pct2	Cell Type	Gene	Average LogFC	pct1	pct2
Basal	KRT14	3.614	0.946	0.144	Vascular	SELE	2.617	0.405	0.022
	KRT17	3.491	0.977	0.191		ACKR1	2.537	0.511	0.021
	DST	2.752	0.966	0.455		FABP4	2.406	0.674	0.142
	KRT5	2.407	0.929	0.076		STC1	2.125	0.519	0.058
	SAA1	2.306	0.796	0.184		CLDN5	2.125	0.746	0.035
	ACTA2	2.204	0.902	0.164		ANGPT2	2.077	0.729	0.082
	SFN	2.043	0.871	0.150		CSF3	2.016	0.402	0.041
	MYLK	2.033	0.832	0.118		IFI27	1.987	0.921	0.293
	TAGLN	1.999	0.958	0.301		ADGRL4	1.872	0.820	0.013
	ACTG2	1.891	0.665	0.031		ADAMTS9	1.866	0.741	0.082
	MT1X	1.790	0.898	0.466		AQP1	1.861	0.588	0.062
	TPM2	1.723	0.968	0.360		C2CD4B	1.807	0.534	0.037
	C2orf40	1.640	0.717	0.070		GNG11	1.751	0.876	0.197
	CNN1	1.631	0.735	0.076		TM4SF1	1.750	0.968	0.520
	FBXO32	1.477	0.679	0.148		SPARCL1	1.750	0.917	0.471
	OXTR	1.455	0.527	0.014		CD93	1.713	0.773	0.040
	TPM1	1.443	0.944	0.492		VWF	1.702	0.654	0.018
	CRYAB	1.406	0.837	0.253		RBP7	1.702	0.564	0.068
	MT2A	1.382	0.986	0.820		PECAM1	1.700	0.766	0.037
	MT1E	1.303	0.778	0.387		SPRY1	1.668	0.736	0.192
LumHR	AREG	3.142	0.860	0.291	Perivascular cells	RGS5	2.573	0.567	0.018
	MUCL1	3.075	0.425	0.151		C11orf96	2.414	0.914	0.321
	AZGP1	2.887	0.983	0.220		MT1A	2.199	0.779	0.264
	PIP	2.679	0.411	0.086		IGFBP5	1.942	0.700	0.218
	KRT18	2.440	0.989	0.274		STEAP4	1.895	0.485	0.074
	AGR2	2.111	0.728	0.036		MYL9	1.696	0.738	0.351
	ANKRD30A	2.069	0.810	0.023		IGFBP7	1.639	0.974	0.463
	TFF1	1.998	0.386	0.030		ADIRF	1.623	0.848	0.498
	S100A14	1.987	0.931	0.145		ADAMTS4	1.584	0.591	0.205
	KRT19	1.954	0.915	0.206		TAGLN	1.481	0.808	0.362
	KRT8	1.952	0.978	0.299		PDK4	1.475	0.542	0.217
	TCIM	1.844	0.808	0.133		NDUFA4L2	1.472	0.446	0.015
	AGR3	1.607	0.619	0.019		GADD45B	1.442	0.774	0.601
	CD24	1.596	0.931	0.211		RGS16	1.416	0.502	0.178
	STC2	1.571	0.739	0.078		ADAMTS1	1.392	0.745	0.304
	SYTL2	1.544	0.784	0.079		MYH11	1.391	0.388	0.094
	TFF3	1.540	0.540	0.052		NR2F2	1.389	0.657	0.227
	SPINT2	1.453	0.977	0.280		CCL2	1.385	0.641	0.394
	MGP	1.425	0.967	0.774		NOTCH3	1.367	0.550	0.073
	PTHLH	1.368	0.380	0.052		MCAM	1.341	0.592	0.121
LumSec	SCGB2A2	2.624	0.523	0.132	B cells	IGKC	5.936	0.835	0.385
	SLPI	2.260	0.835	0.090		IGLC2	5.501	0.509	0.139
	WFDC2	2.180	0.672	0.210		IGHA1	5.324	0.663	0.255
	LTF	2.168	0.675	0.068		IGLC3	5.116	0.397	0.086
	KRT15	2.159	0.806	0.097		JCHAIN	5.060	0.568	0.088
	MMP7	2.042	0.600	0.067		IGHA2	4.555	0.446	0.085
	SCGB3A1	1.908	0.442	0.120		IGHG1	3.879	0.219	0.013
	PI3	1.895	0.285	0.019		IGHM	3.711	0.408	0.026
	FDCSP	1.853	0.116	0.030		IGHG3	2.953	0.207	0.008
	KRT23	1.826	0.671	0.063		IGLL5	2.864	0.148	0.002
	CLDN4	1.811	0.890	0.217		IGHG2	2.837	0.125	0.005
	S100A9	1.758	0.494	0.054		IGHG4	2.168	0.120	0.004
	KRT7	1.738	0.953	0.324		MZB1	2.104	0.519	0.015
	CCL28	1.680	0.793	0.046		IGHD	1.994	0.192	0.002
	TACSTD2	1.587	0.938	0.370		SSR4	1.894	0.755	0.677
	KRT19	1.558	0.868	0.224		CD79A	1.835	0.782	0.004
	ALDH1A3	1.558	0.755	0.107		CD37	1.654	0.556	0.086
	PIGR	1.523	0.645	0.034		DERL3	1.431	0.475	0.007
	CD24	1.511	0.930	0.224		HLA-DRA	1.406	0.540	0.226
	CLDN3	1.482	0.697	0.089		HERPUD1	1.372	0.850	0.575

Cell Type	Gene	Average LogFC	pct1	pct2
	DCN	3.847	0.991	0.251
	APOD	3.458	0.962	0.289
	CFD	3.454	0.789	0.236
	TNFAIP6	2.918	0.823	0.085
	LUM	2.886	0.939	0.077
	COL1A2	2.622	0.839	0.095
	COL1A1	2.481	0.693	0.083
	COL3A1	2.481	0.613	0.074
	MMP3	2.427	0.203	0.044
Fibroblasts	GSN	2.287	0.966	0.539
	FBLN1	2.166	0.855	0.064
	CCDC80	2.151	0.820	0.114
	MEG3	2.107	0.861	0.111
	SFRP2	2.107	0.698	0.037
	COL6A2	1.980	0.943	0.217
	IGFBP6	1.899	0.684	0.094
	IGF1	1.896	0.669	0.040
	C1S	1.894	0.895	0.098
	COL6A3	1.872	0.847	0.056
	C1R	1.868	0.871	0.152
	CCL21	4.375	0.909	0.016
	TFF3	2.945	0.893	0.093
	MMRN1	2.928	0.910	0.010
	CAVIN2	2.259	0.758	0.094
	CLDN5	2.109	0.874	0.108
	LYVE1	2.108	0.689	0.019
	TFPI	2.027	0.971	0.404
	PPFIBP1	1.915	0.893	0.278
	GNG11	1.879	0.904	0.269
Lymphatic	ECSCR	1.774	0.759	0.075
	ANGPT2	1.717	0.647	0.151
	PROX1	1.679	0.636	0.039
	CD9	1.667	0.933	0.506
	FABP4	1.656	0.804	0.197
	FABP5	1.635	0.809	0.229
	AKAP12	1.503	0.838	0.319
	RAMP2	1.440	0.668	0.152
	CAV1	1.425	0.914	0.460
	EFEMP1	1.412	0.695	0.227
	S100A10	1.316	0.984	0.796

Cell Type	Gene	Average LogFC	pct1	pct2
	IL7R	3.143	0.780	0.023
	CCL5	2.796	0.659	0.014
	PTPRC	2.674	0.940	0.051
	CXCR4	2.559	0.913	0.098
	GNLY	2.408	0.180	0.007
	CD2	1.995	0.700	0.003
	SRGN	1.985	0.961	0.279
	NKG7	1.970	0.323	0.005
	KLRB1	1.890	0.442	0.002
T cells	ARHGDIB	1.816	0.829	0.204
	CD3D	1.803	0.671	0.003
	CREM	1.787	0.744	0.322
	TRBC2	1.785	0.593	0.006
	LEPROTL1	1.736	0.712	0.143
	CD7	1.731	0.570	0.014
	SARAF	1.724	0.905	0.594
	CD52	1.688	0.594	0.024
	SYTL3	1.680	0.591	0.020
	CNOT6L	1.680	0.710	0.161
	CST7	1.669	0.505	0.011
	HLA-DRA	3.553	0.933	0.200
	IL1B	3.125	0.524	0.020
	HLA-DPA1	3.112	0.870	0.149
	HLA-DPB1	3.014	0.855	0.212
	HLA-DRB1	2.935	0.894	0.195
	CD74	2.828	0.941	0.331
	CCL3	2.733	0.461	0.033
	HLA-DQA1	2.686	0.743	0.052
	C1QB	2.611	0.710	0.012
Myeloid	C1QA	2.570	0.724	0.013
	RNASE1	2.539	0.466	0.077
	FCER1G	2.528	0.921	0.024
	TYROBP	2.528	0.943	0.021
	LYZ	2.527	0.696	0.011
	CCL4	2.425	0.431	0.051
	HLA-DQB1	2.374	0.769	0.102
	GPR183	2.232	0.808	0.070
	CTSB	2.205	0.874	0.338
	CD163	2.203	0.646	0.009
	C1QC	2.197	0.682	0.006

Supplementary Table 3 – Top Marker Genes Expressed in Major Breast Cell Types

This table lists the top 20 marker genes expressed in the scRNA-seq data for each major cell type cluster based on average log fold-change and specificity of the gene expressed in the indicated cell type (pct1) compared to the other cell types (pct2). The columns listed (from left to right) indicate the name of the major cell type, the gene names, the average log-fold change (Average LogFC), the pct1 value indicating the fraction of cells within the cluster expressing the gene, the pct2 value indicating the fraction of cells in other clusters expressing the gene.

Supplementary Table 4 – Top Marker Genes Expressed in Major Breast Nuclei Cell Types

Nuclei Type	Gene	Average LogFC	pct1	pct2	Nuclei Type	Gene	Average LogFC	pct1	pct2
Basal	AC044810.3	2.572	0.723	0.031	Vascular	MECOM	2.854	0.773	0.035
	CARMN	2.289	0.705	0.083		BTNL9	2.744	0.547	0.018
	LINC01060	2.283	0.64	0.054		MCTP1	2.610	0.759	0.105
	ACTA2	2.274	0.699	0.094		PTPRB	2.343	0.685	0.031
	KLHL29	2.156	0.733	0.139		VWF	2.206	0.669	0.058
	DST	1.993	0.919	0.515		ADGRL4	2.160	0.571	0.009
	IL1RAPL2	1.842	0.336	0.054		LDB2	2.125	0.833	0.155
	NRG1	1.837	0.452	0.06		ANO2	2.084	0.589	0.034
	SEMA3C	1.830	0.688	0.177		EPAS1	2.063	0.689	0.127
	PTPRT	1.801	0.64	0.113		CD36	2.010	0.694	0.221
	SAMD5	1.777	0.546	0.064		ABLIM3	2.007	0.538	0.072
	FBXO32	1.772	0.563	0.123		ENPP2	1.974	0.42	0.049
	TP63	1.766	0.475	0.035		PTPRM	1.956	0.879	0.348
	GRIA4	1.739	0.48	0.063		EMCN	1.955	0.562	0.041
	MYLK	1.737	0.547	0.078		PECAM1	1.924	0.605	0.052
	RBBP8	1.728	0.543	0.105		FLT1	1.885	0.466	0.013
	FHOD3	1.712	0.483	0.055		PREX2	1.854	0.61	0.078
	TMEFF2	1.696	0.395	0.036		SPARCL1	1.827	0.756	0.199
	KLHL13	1.674	0.523	0.101		ZNF385D	1.776	0.55	0.165
	CACNA1C	1.673	0.662	0.144		PLCB4	1.765	0.627	0.161
LumHR	ANKRD30A	3.788	0.862	0.191	Perivascular cells	RGS6	2.247	0.531	0.081
	AFF3	2.949	0.991	0.243		KCNAB1	2.191	0.504	0.11
	ERBB4	2.948	0.983	0.207		COL25A1	2.154	0.375	0.042
	TTC6	2.412	0.855	0.03		ADGRL3	2.021	0.404	0.065
	MYBPC1	2.173	0.43	0.036		PRKG1	1.915	0.83	0.327
	NEK10	2.140	0.624	0.057		NR2F2-AS1	1.740	0.576	0.13
	THSD4	2.081	0.948	0.248		AC012409.2	1.717	0.455	0.105
	ESR1	2.062	0.675	0.167		IGFBP7	1.711	0.602	0.128
	INPP4B	1.991	0.881	0.122		ITGA8	1.656	0.191	0.022
	PRLR	1.864	0.803	0.091		TEX41	1.646	0.317	0.023
	LINC01194	1.811	0.112	0.017		EBF2	1.584	0.411	0.054
	XBP1	1.755	0.851	0.185		GUCY1A2	1.563	0.293	0.03
	AC093001.1	1.714	0.331	0.016		PDE3A	1.513	0.375	0.055
	SERHL2	1.687	0.338	0.085		RCAN2	1.475	0.406	0.105
	DIO2	1.658	0.257	0.07		FHL5	1.457	0.254	0.001
	ALCAM	1.651	0.73	0.129		DLC1	1.401	0.706	0.306
	PI15	1.611	0.282	0.034		RYR2	1.391	0.33	0.073
	ST8SIA6	1.597	0.627	0.03		STEAP4	1.385	0.255	0.023
	CADPS2	1.593	0.736	0.221		PDGFRB	1.376	0.358	0.045
	EFHD1	1.584	0.708	0.089		CHSY3	1.373	0.315	0.094
LumSec	AC011247.1	2.246	0.724	0.079	Adipocytes	PDE3B	3.073	0.927	0.072
	COBL	2.024	0.773	0.129		ACACB	2.750	0.966	0.201
	GABRP	1.922	0.606	0.032		WDPCP	2.255	0.884	0.379
	ELF5	1.919	0.619	0.023		PCDH9	2.158	0.776	0.068
	CCL28	1.869	0.654	0.063		CLSTN2	2.156	0.739	0.086
	KRT15	1.804	0.619	0.152		ADIPOQ	1.921	0.687	0.022
	KIT	1.773	0.626	0.038		TRHDE	1.851	0.616	0.021
	BARX2	1.729	0.501	0.048		SOX5	1.845	0.948	0.267
	EHF	1.703	0.582	0.095		GPAM	1.837	0.652	0.039
	LINC01152	1.697	0.581	0.072		AQP7	1.836	0.783	0.038
	HS3ST4	1.627	0.499	0.068		KCNIP2-AS1	1.828	0.589	0.02
	NEBL	1.514	0.797	0.244		LINC02237	1.798	0.693	0.016
	SLC12A2	1.479	0.538	0.135		CPM	1.793	0.885	0.137
	TFCP2L1	1.444	0.388	0.049		PLIN1	1.776	0.743	0.042
	SORBS2	1.439	0.798	0.26		SLC19A3	1.772	0.706	0.01
	SHANK2	1.433	0.704	0.2		CAV2	1.755	0.721	0.099
	PDE4B	1.395	0.664	0.173		GHR	1.661	0.897	0.258
	AC078923.1	1.389	0.288	0.019		DIRC3	1.659	0.663	0.062
	DTNB	1.365	0.725	0.217		LINC02456	1.657	0.613	0.059
	CX3CL1	1.357	0.358	0.042		MARC1	1.640	0.662	0.031

Nuclei Type	Gene	Average LogFC	pct1	pct2
Fibroblasts	LAMA2	2.896	0.857	0.132
	DCLK1	2.655	0.832	0.101
	NEGR1	2.501	0.681	0.079
	LINC02511	2.265	0.558	0.031
	ANK2	2.242	0.69	0.113
	KAZN	2.226	0.857	0.324
	SLIT2	2.043	0.552	0.053
	COL6A3	2.028	0.609	0.047
	BICC1	2.026	0.731	0.142
	NOVA1	1.967	0.744	0.172
	COL5A2	1.925	0.676	0.112
	DLC1	1.924	0.848	0.217
	HPSE2	1.906	0.327	0.049
	ABCA9	1.891	0.608	0.074
	ABCA9-AS1	1.878	0.472	0.057
	DCN	1.868	0.646	0.134
	SLIT3	1.839	0.663	0.146
	ABCA10	1.818	0.591	0.128
	ABCA6	1.800	0.692	0.116
	ROBO2	1.793	0.377	0.081
Lymphatic	AL357507.1	3.310	0.766	0.07
	PKHD1L1	3.210	0.875	0.014
	KLHL4	2.498	0.629	0.023
	LINC02147	2.453	0.647	0.018
	RHOJ	2.447	0.767	0.069
	ST6GALNAC3	2.358	0.84	0.108
	MMRN1	2.345	0.623	0.011
	GPM6A	2.316	0.602	0.022
	STOX2	2.255	0.807	0.129
	AKAP12	2.202	0.688	0.113
	NRG3	2.191	0.604	0.054
	PDE1A	2.134	0.597	0.054
	PPFIBP1	2.094	0.884	0.292
	RELN	2.093	0.527	0.038
	KALRN	2.013	0.832	0.233
	HECW2	1.938	0.607	0.065
	ZDHHC14	1.906	0.714	0.134
	CNKSR3	1.870	0.66	0.137
	STK32B	1.866	0.571	0.074
	AL356277.3	1.841	0.36	0.023
Mast	NTM	3.209	0.938	0.144
	IL18R1	3.027	0.808	0.017
	SYTL3	2.989	0.932	0.101
	SLC24A3	2.613	0.894	0.175
	HPGD	2.474	0.742	0.053
	TPSB2	2.467	0.408	0.002
	HDC	2.452	0.683	0.005
	KIAA1549	2.442	0.745	0.065
	RAB27B	2.424	0.724	0.09
	TNFAIP3	2.416	0.54	0.06
	SLC18A2	2.318	0.65	0.039
	CPA3	2.281	0.556	0.002
	TNIK	2.271	0.867	0.182
	CPM	2.262	0.893	0.194
	CD69	2.254	0.538	0.02
	SRGN	2.231	0.755	0.085
	SLC8A3	2.143	0.56	0.003
	GPAT3	2.128	0.489	0.024
	RHOH	2.093	0.683	0.092
	RGS13	2.071	0.558	0.006
T cells	SKAP1	2.577	0.765	0.077
	ARHGAP15	2.442	0.779	0.098
	PTPRC	2.384	0.744	0.056
	THEMIS	2.373	0.509	0.013
	IKZF1	2.370	0.662	0.033
	PARP8	2.273	0.678	0.146
	CD247	2.230	0.497	0.015
	STAT4	2.080	0.507	0.022
	AC022075.1	2.073	0.392	0.028
	CD96	2.071	0.521	0.038
	ITK	2.067	0.45	0.006
	IL7R	2.041	0.366	0.006
	ANKRD44	2.031	0.772	0.191
	AOAH	1.995	0.503	0.055
	CAMK4	1.961	0.407	0.012
	SYTL3	1.947	0.545	0.081
	AC010609.1	1.934	0.369	0.005
	BCL11B	1.919	0.422	0.01
	CARD11	1.905	0.433	0.019
	LINC01934	1.863	0.367	0.017
Myeloid	F13A1	2.999	0.564	0.032
	MRC1	2.817	0.596	0.049
	RBPJ	2.589	0.714	0.254
	TBXAS1	2.360	0.676	0.041
	FRMD4B	2.208	0.747	0.176
	CD163	2.153	0.521	0.01
	RAB31	2.148	0.655	0.09
	SLC8A1	2.133	0.594	0.071
	MS4A6A	2.120	0.54	0.011
	MERTK	1.934	0.547	0.062
	SLCO2B1	1.918	0.495	0.028
	LGMN	1.904	0.433	0.055
	COLEC12	1.895	0.457	0.094
	FMN1	1.883	0.631	0.158
	SLC1A3	1.859	0.498	0.074
	PDK4	1.831	0.641	0.275
	HDAC9	1.826	0.591	0.111
	SLC9A9	1.822	0.61	0.153
	P2RY14	1.816	0.362	0.021
	LYVE1	1.803	0.357	0.022

Supplementary Table 4 – Top Marker Genes Expressed in Major Breast Cell Types in Nuclei data

This table lists the top 20 marker genes expressed in the snRNA-seq data for each major cell type cluster based on average log fold-change and specificity of the gene expressed in the indicated cell type (pct1) compared to the other cell types (pct2). The columns listed (from left to right) indicate the name of the major cell type, the gene names, the average log-fold change (Average LogFC), the pct1 value indicating the fraction of cells within the cluster expressing the gene, the pct2 value indicating the fraction of cells in other clusters expressing the gene.

Patient ID	Number of spots under tissue	Number of reads	Median UMI per spot	Median Genes per spot	Total genes detected	Reads mapped to exonic regions	Reads mapped to intergenic regions	Reads mapped to intronic regions	Reads mapped to transcriptome
P10	2741	461115960	3031	1546	23050	0.836	0.022	0.032	0.816
P35	1896	478182981	2223	1184	22295	0.878	0.019	0.026	0.855
P46	3129	404340693	2348	1315	22442	0.823	0.026	0.052	0.803
P47	3449	362966308	1108	797	22121	0.837	0.027	0.06	0.817
P65	3226	404107425	2284	1035	23915	0.896	0.02	0.027	0.875
P67	3655	452452634	2666	1343	23688	0.899	0.018	0.026	0.879
P79	3571	438705200	2379	1279	24489	0.816	0.027	0.047	0.798
P82	3631	376273215	1512	841	23688	0.82	0.03	0.05	0.801
P85	3669	404861379	3570	1545	24788	0.845	0.027	0.038	0.826
P127	2854	423500797	2000	1024	23038	0.75	0.04	0.064	0.732

Supplementary Table 5 – Quality Control Metrics for Spatial Transcriptomics Data

This table lists the quality control metrics for breast tissue samples sequenced with the Spatial Transcriptomics platform (Visium, 10X Genomics). The columns listed (from left to right) indicate the Patient ID, Number of spots under tissue, Number of reads, Median UMI per spot, Median Genes per spot, Total genes detected, Reads mapping rate (exonic, intergenic, intronic regions and transcriptome).

Cell Type	Gene	Cell Annotation (module score)
Basal	KRT5	1
	ACTG2	1
	TUBB2B	0
	COL17A1	1
	KRT6B	0
	LAMA3	1
LumHR	AR	1
	ESR1	1
	PGR	1
	AREG	1
	OXTR	0
	ANKRD30A	1
	AGR3	1
	AGR2	1
	TMC5	1
	DNAJC12	1
	RASEF	1
LumSec	SLPI	1
	LTF	1
	KRT15	1
	MMP7	1
	CCL28	1
	ALDH1A3	1
	PIGR	1
Fibroblasts	LUM	1
	TNFAIP6	0
	COL1A2	1
	COL1A1	1
	FBLN1	1
	MMP2	1
	SERPINF1	1
Pericytes	MCAM	0
	RGS5	1
	GJA4	1
	NDUFA4L2	1
	SSTR2	1
	AVPR1A	0
	PLN	1
	EDNRA	1
Lymphatic	CCL21	1
	MMRN1	0
	PROX1	1
	SCN3B	1
	PKHD1L1	0
	TBX1	1
	PGM5	1
Vascular	VWF	0
	SELE	0
	ACKR1	1
	CSF3	0
	ADGRL4	0
	RBP7	1
	PGF	1
	AQP1	1

Cell Type	Gene	Cell Annotation (module score)
Myeloid	CD14	1
	CD68	1
	C1QA	1
	C1QB	1
	FCER1G	0
	C1QC	1
	LYZ	1
	CD163	1
	MSR1	1
Mast	IL18R1	0
	HPGD	0
	HDC	0
	SLC18A2	0
	CPA3	0
	CD69	0
	HPGDS	0
T cells	CD3D	0
	CD3E	0
	CD4	1
	CD8A	1
	IL7R	1
	CCL5	1
	NKG7	1
	GZMB	1
	CD2	1
B cells	CD27	0
	DERL3	0
	JCHAIN	1
	IGHM	1
	TNFRSF17	0
	MZB1	1
	CD79A	0
Adipocytes	PLIN1	0
	ADIPOQ	0
	PLIN4	0
	GPD1	0
	LPL	0
	LIPE	0
Epithelial	EPCAM	0
Endothelial	PECAM1	0
Proliferation	MKI67	0
Immune	PTPRC	0
Immune	TRAC	0
Mis	TP63	0
Luminal	KRT19	0
B cells	IGHA2	Did not work

Supplementary Table 6 – Custom Targeted Gene Panel for smFISH (Resolve)

This table lists the top expressed genes selected for each breast cell type from the scRNA-seq data to generate a custom 100-gene panel for smFISH analysis (Resolve Biosciences). The entire panel of 100 genes was used to profile each of the breast tissue samples, to determine the spatial distribution of the breast cell types in the tissue sections. The table shows the cell type, the genes used for classification and cell annotation module score with values of 1 (Yes) or 0 (No).

Section ID	Patient ID	Total Counts (raw)	Total Counts (post filter)	Total Cells (raw)	Filtered Cells (post filter)
P46-S1	P46	1491813	1301494	11929	9879
P35-S1	P35	913325	702059	7604	6683
P47-S1	P47	667314	615735	6872	6050
P69-S1	P69	491862	330047	4276	3390
P69-S2	P69	580993	157526	4754	4018
P46-S2	P46	460881	319725	5847	3961
P128-S1	P128	113031	75978	1244	868
P69-S3	P69	1549406	853581	5441	4591
P46-S3	P46	1991213	1018173	11788	8989
P46-S4	P46	703202	343803	3635	2906
P128-S2	P128	208133	95192	1290	928
P128-S3	P128	1019583	545389	4597	3372

Supplementary Table 7 – Quality Control Metrics for smFISH Data

The table lists the quality control metrics for the 12 breast tissue samples profiled with the custom 100-gene panel for smFISH analysis (Resolve Biosciences). The columns listed (from left to right) indicate the Section ID, Patient ID, the number of transcripts captured under tissue, the number of transcripts after filtering, the number of cells detected and the number of cells after filtering.

Sample	Patient ID	Cells profiled
P129_s1	P129	78219
P130_s1	P130	62302
P131_s1	P131	40781
P132_s1	P132	49985
P123_s1	P123	21585
P125_s1	P125	5557
P119_s1	P119	18144
P114_s1	P114	10468

Supplementary Table 8 - Breast Tissue Samples for CODEX

This table lists the 8 breast tissue samples that were used for CODEX analysis, along with the clinical metadata for each woman, and total number of cells that were profiled and analyzed. Columns from left to right are Sample Section, Patient ID, number of cells profiled.

Supplementary Table 9 – CODEX 34-Antibody Panel Design

Cycle #	Antibody	Clone		Reporter	Ratio	Ab vendor	Ab Catalog number
Cycle1	blank						
	blank						
	blank						
Cycle2	Keratin19	A53-B/A2	BX025	RX025-A750	1:50	Biolegend	628502
	CD8	C8/144B	BX026	BX026-ATTO	1:200	Akoya	4250012
	PCNA	PC10	BX020	RX020-Cy5	1:50	Biolegend	307902
Cycle3	Vimentin	RV202	BX034	RX034-A750	1:50	BD	550513
	CD31	EP3095	BX001	RX001-ATTO	1:200	Akoya	(custom, ab226157 from abcam)
	CD3e	EP449E	BX045	RX045-Cy5	1:150	Akoya	(custom, ab271850 from abcam)
Cycle4	Keratin7	W16155A	BX019	RX019-A750	1:50	Biolegend	601602
	Ki67	B56	BX047	RX047-ATTO	1:200	Akoya	4250019
	CD4	EPR6855	BX003	RX003-Cy5	1:200	Akoya	(custom, ab181724 from abcam)
Cycle5	CD227	HMPV	BX004	BX004-A750	1:50	BD	555925
	Perlecan	5D7-2E4	BX017	RX017-ATTO	1:50	BD	565781
	CD45	2D1	BX021	RX021-Cy5	1:100	Akoya	from Novus
Cycle6	Keratin17	W16131A	BX022	RX022-A750	1:50	Biolegend	W16131A
	Podoplanin	NC-08	BX023	BX023-ATTO	1:200	Akoya	4250004
	CD68	KP1	BX015	RX015-Cy5	1:200	Akoya	(custom; MA5-13324 frm ThermoFisher
Cycle7	Empty						
	CD14	EPR3653	BX037	RX037-ATTO	1:50	Abcam	ab226121
	CollagenIV	EPR20966	BX042	RX042-Cy5	1:50	Abcam	ab226485
Cycle8	Keratin18	DA-7	BX049	RX049-A750	1:50	Biolegend	628402
	HLA-DPB1	EPR11226	BX035	RX035-ATTO	1:50	Abcam	ab157210
	CD11c	118/A5	BX024	RX024-Cy5	1:200	Akoya	Biological NBP2-
Cycle9	Empty						
	E-Cadherin	4A2C7	BX014	RX014-ATTO	1:200	Akoya	4250021
	PR	KMC912	BX007	RX007-Cy5	1:50	ThermoFis	14-9764-82
Cycle10	Keratin8	1E8	BX040	RX040-A750	1:50	Biolegend	697902
	Keratin14	Poly19053	BX032	BX032-ATTO	1:300	Akoya	(custom; 905304 from Biolegend)
	TP63	W15093A	BX033	RX033-Cy5	1:50	Biolegend	W15093A
Cycle11	Empty						
	Empty						
	SMA	1A4	BX030	RX030-Cy5	1:50	Abcam	ab7817
Cycle12	Empty						
	Empty						
	Runx3	R3-5G4	BX036	RX036-Cy5	1:50	Biolegend	R3-5G4

Cycle #	Antibody	Clone		Reporter	Ratio	Ab vendor	Ab Catalog number
Cycle13	Empty						
	Empty						
	CD66e	BSB-13	BX016	RX016-Cy5	1:50	Biolegend	847002
Cycle14	Empty						
	Empty						
	BCL6	K112-91	BX041	RX041-Cy5	1:50	BD	561520
Cycle15	Empty						
	Empty						
	Foxp3	259D/C7	BX027	RX027-Cy5	1:40	BD	560044
Cycle16	Empty						
	Empty						
	LIF	M1506B09	BX006	RX006-Cy5	1:200	Akoya	(custom; 674702 from Biolegend)
Cycle17	Empty						
	Empty						
	GranzymeB	D6E9W	BX046	RX046-Cy5	1:50	CST	79903SF
Cycle18	Empty						
	Empty						
	BCL2	N46-467	BX029	RX029-Cy5	1:50	BD	N46-467
Cycle19	Empty						
	Empty						
	Keratin5	Poly19055	BX005	RX005-Cy5	1:50	Biolegend	905504
Cycle20	blank						
	blank						
	blank						

Supplementary Table 9 – CODEX 34-Antibody Panel Design

This table lists the cycle order and description of the 34 antibodies run in the CODEX panel. The columns listed (from left to right) indicate, the cycle, the antibody, the clone, the reporter, the dilution ratio use, antibody vendor and antibody catalog number.

Supplementary Table 10 – Top Gene Markers Expressed for Breast Cell States

Cell state	Gene	Average LogFC	pct1	pct2	Cell state	Gene	Average LogFC	pct1	pct2
		Epithelial					**Epithelial**		
Basal	TAGLN	3.071	0.958	0.182	LumSec-major	SCGB3A1	1.248	0.696	0.304
	KRT14	3.012	0.946	0.281		CYP24A1	0.617	0.354	0.118
	ACTA2	2.899	0.902	0.089		MSMO1	0.562	0.510	0.284
	TPM2	2.686	0.968	0.128		MMP7	0.520	0.659	0.568
	KRT17	2.595	0.977	0.389		TM4SF1	0.494	0.979	0.924
	MT2A	2.546	0.986	0.797		HMGCS1	0.492	0.477	0.277
	DST	2.465	0.966	0.656		PDCD4	0.450	0.830	0.597
	MYLK	2.282	0.832	0.046		CALML5	0.449	0.373	0.108
	MT1X	2.242	0.898	0.474		JUND	0.430	0.937	0.823
	CXCL14	2.095	0.586	0.055		RPS18	0.424	0.999	0.997
	KRT5	2.095	0.929	0.212		RACK1	0.422	0.993	0.978
	APOE	1.965	0.710	0.164		IDI1	0.409	0.597	0.377
	SPARCL1	1.937	0.795	0.129		RPLP0	0.401	0.996	0.984
	ACTG2	1.909	0.665	0.031		RPS21	0.400	0.984	0.973
	C2orf40	1.863	0.717	0.031		FAM3B	0.400	0.535	0.121
	CALD1	1.787	0.965	0.443		DBI	0.399	0.940	0.821
	CNN1	1.771	0.735	0.032		PIGR	0.397	0.751	0.588
	MT1E	1.752	0.778	0.380		RPS8	0.396	0.997	0.995
	MYL9	1.677	0.802	0.189		RPS28	0.394	0.996	0.991
	NNMT	1.668	0.921	0.398		MT-ND6	0.386	0.792	0.575
LumHR-major	S100A6	0.77	0.976	0.906	LumSec-KIT	PLCG2	4.012	0.933	0.535
	TNFRSF11B	0.65	0.319	0.130		MAFB	1.930	0.551	0.128
	AC097059.1	0.61	0.322	0.143		SOX4	1.693	0.767	0.594
	FAM107B	0.58	0.811	0.670		JUN	1.649	0.928	0.857
	ITGA2	0.52	0.750	0.599		HES1	1.591	0.602	0.292
	C15orf48	0.48	0.629	0.442		HEXIM1	1.513	0.503	0.227
	SYTL4	0.48	0.508	0.318		CSKMT	1.486	0.448	0.160
	TUBA1C	0.48	0.902	0.813		FOSB	1.454	0.800	0.626
	IER5	0.46	0.747	0.615		HIST1H4C	1.391	0.550	0.473
	NFKBIA	0.46	0.865	0.805		GOLGA8A	1.391	0.504	0.197
	RBP1	0.45	0.629	0.452		FOS	1.333	0.850	0.638
	SYTL2	0.45	0.837	0.691		SLC38A2	1.262	0.634	0.564
	KRT8	0.42	0.981	0.973		IER5L	1.253	0.430	0.192
	ATP1B1	0.42	0.879	0.777		AL355075.4	1.242	0.318	0.093
	SPINK1	0.39	0.194	0.100		HSPA2	1.224	0.331	0.075
	PAWR	0.39	0.876	0.794		NR4A1	1.207	0.467	0.226
	HMGA1	0.38	0.718	0.568		HSPA1B	1.172	0.482	0.459
	ARID5B	0.38	0.824	0.753		XIST	1.164	0.818	0.819
	TNFRSF12A	0.38	0.954	0.896		IGKC	1.153	0.474	0.328
	S100A14	0.37	0.961	0.880		AC023157.3	1.123	0.266	0.046
LumHR-active	CXCL13	1.753	0.456	0.039	LumSec-HLA	CCL20	2.771	0.422	0.080
	DIO2	1.344	0.473	0.134		PI3	1.999	0.579	0.278
	TFF3	1.025	0.853	0.490		SAT1	1.702	0.975	0.790
	MYBPC1	0.889	0.683	0.207		CD74	1.613	0.898	0.489
	EREG	0.851	0.500	0.208		TMSB4X	1.530	0.991	0.762
	SLC26A3	0.820	0.394	0.154		HSPB1	1.481	0.735	0.181
	PTHLH	0.726	0.739	0.323		RBP1	1.465	0.931	0.192
	FASN	0.689	0.815	0.473		SLPI	1.361	0.982	0.831
	MS4A7	0.651	0.332	0.135		CRABP2	1.354	0.955	0.504
	TFF1	0.621	0.590	0.353		IER3	1.273	0.919	0.691
	PLCG2	0.567	0.474	0.419		HIST1H1C	1.221	0.755	0.291
	PNMT	0.552	0.367	0.066		SPARCL1	1.184	0.671	0.167
	CA2	0.545	0.398	0.145		HLA-DRB1	1.182	0.720	0.259
	C2CD4A	0.510	0.422	0.150		NFKBIA	1.177	0.949	0.804
	GSTM3	0.506	0.825	0.664		SELENOM	1.159	0.958	0.603
	KCNMA1	0.479	0.530	0.243		HLA-DRA	1.097	0.721	0.283
	NNMT	0.441	0.559	0.356		SNCG	1.029	0.547	0.124
	ANKRD30A	0.439	0.941	0.789		IFI27	1.007	0.420	0.055
	EFHD1	0.434	0.885	0.748		SERPINB1	1.000	0.861	0.475
	RGS1	0.406	0.101	0.020		ANXA1	0.986	0.999	0.877

Cell state	Gene	Average LogFC	pct1	pct2
LumHR-SCGB	SCGB2A2	3.390	0.411	0.189
	PIP	3.166	0.816	0.291
	SCGB1D2	2.886	0.224	0.068
	MUCL1	2.463	0.684	0.348
	SCGB3A1	2.070	0.545	0.264
	SERPINA1	1.431	0.551	0.220
	TFPI2	1.413	0.330	0.035
	APOD	1.043	0.404	0.282
	CP	1.033	0.282	0.061
	KRT23	0.835	0.433	0.196
	HMGB3	0.771	0.382	0.201
	SAA1	0.770	0.237	0.149
	MGP	0.707	0.978	0.964
	CA2	0.688	0.221	0.167
	TAT	0.648	0.202	0.059
	SOD2	0.618	0.652	0.560
	CITED1	0.595	0.329	0.198
	CYP4X1	0.589	0.346	0.040
	TNFSF10	0.585	0.535	0.301
	CCL2	0.577	0.192	0.146
LumSec-prol	HMGB2	1.645	0.706	0.350
	TUBA1B	1.471	0.940	0.885
	HMGN2	1.429	0.797	0.721
	TOP2A	1.427	0.435	0.005
	PTTG1	1.400	0.481	0.091
	UBE2C	1.398	0.471	0.011
	HIST1H4C	1.389	0.527	0.477
	TYMS	1.376	0.550	0.019
	NUSAP1	1.375	0.487	0.029
	PCLAF	1.357	0.536	0.010
	HMGB1	1.321	0.952	0.939
	PCNA	1.314	0.502	0.150
	TUBB	1.310	0.830	0.678
	IGKC	1.301	0.491	0.333
	H2AFZ	1.294	0.890	0.841
	DUT	1.140	0.677	0.571
	CDK1	1.094	0.405	0.004
	CENPW	1.053	0.476	0.141
	TK1	1.049	0.421	0.014

Cell state	Gene	Average LogFC	pct1	pct2
LumSec-lac	LALBA	5.632	0.757	0.017
	CSN1S1	4.658	0.935	0.018
	CSN2	4.538	0.618	0.006
	CSN3	4.296	0.921	0.016
	LYZ	3.320	0.306	0.013
	SPP1	2.869	0.462	0.039
	IGKC	2.030	0.632	0.331
	LTF	1.879	0.827	0.673
	FDCSP	1.859	0.495	0.109
	IGHA1	1.707	0.540	0.221
	FABP3	1.680	0.465	0.039
	ZG16B	1.628	0.485	0.278
	CLU	1.483	0.845	0.749
	PLIN2	1.467	0.569	0.314
	XDH	1.298	0.333	0.089
	S100A1	1.170	0.766	0.659
	PIGR	1.155	0.720	0.644
	HLA-DRA	1.143	0.554	0.288
	CEL	1.106	0.205	0.002
	NUPR1	1.053	0.673	0.593
LumSec-basal	PTN	2.235	0.667	0.127
	WFDC2	1.879	0.918	0.414
	MGP	1.547	0.993	0.953
	RARRES1	1.380	0.683	0.283
	SCGB2A2	1.331	0.692	0.346
	KRT6B	1.219	0.659	0.237
	CXCL8	1.197	0.394	0.198
	S100A8	1.084	0.238	0.086
	CCL2	1.049	0.317	0.196
	S100A6	1.005	0.996	0.920
	S100A9	0.977	0.615	0.367
	KRT14	0.960	0.590	0.273
	KRT17	0.959	0.629	0.313
	KRT81	0.927	0.221	0.104
	S100A10	0.889	0.950	0.735
	LCN2	0.855	0.592	0.314
	PI3	0.835	0.408	0.156
	KRT23	0.826	0.818	0.518
	ADIRF	0.792	0.716	0.288
	LTF	0.771	0.813	0.531
LumSec-myo	ACTA2	2.068	0.863	0.076
	TAGLN	1.915	0.932	0.216
	DST	1.858	0.948	0.675
	TPM2	1.853	0.929	0.128
	MT2A	1.722	0.972	0.720
	MYLK	1.498	0.770	0.038
	KRT14	1.447	0.911	0.421
	CXCL14	1.418	0.575	0.046
	KRT17	1.338	0.954	0.460
	APOE	1.320	0.694	0.229
	SPARCL1	1.238	0.788	0.159
	C2orf40	1.179	0.661	0.029
	CNN1	1.091	0.660	0.020
	ACTG2	1.040	0.578	0.028
	MYL9	1.005	0.735	0.173
	MT1E	0.963	0.718	0.331
	NNMT	0.956	0.859	0.402
	IGFBP2	0.945	0.527	0.040
	THBS1	0.897	0.731	0.297
	POSTN	0.889	0.460	0.022

Cell state	Gene	Average LogFC	pct1	pct2
		Fibroblasts		
	COL3A1	1.625	0.943	0.552
	POSTN	1.482	0.688	0.220
	COL1A1	1.345	0.943	0.646
	IGF1	1.306	0.931	0.620
	IGFBP2	1.158	0.591	0.133
	ADAM12	1.086	0.740	0.199
	TNC	1.016	0.391	0.072
	DLK1	0.952	0.573	0.176
	COL5A2	0.914	0.779	0.415
	PENK	0.900	0.145	0.049
Fibro-matrix	ECEL1	0.831	0.324	0.008
	COL15A1	0.830	0.788	0.427
	TAC1	0.815	0.606	0.217
	COL1A2	0.790	0.973	0.814
	HGF	0.782	0.586	0.290
	MXRA5	0.782	0.768	0.388
	SPARC	0.773	0.932	0.711
	APOE	0.739	0.902	0.531
	TGFBI	0.736	0.610	0.198
	HSPA6	0.714	0.140	0.063
	MMP3	1.529	0.251	0.135
	CXCL1	0.890	0.508	0.338
	GEM	0.612	0.922	0.737
	KDM6B	0.593	0.811	0.626
	CEBPB	0.587	0.972	0.899
	TNFAIP6	0.574	0.893	0.724
	CXCL2	0.537	0.559	0.415
	SAT1	0.523	0.893	0.842
	TNFRSF12A	0.510	0.723	0.552
Fibro-major	IGKC	0.500	0.497	0.356
	GPRC5A	0.499	0.674	0.533
	SERPINE2	0.493	0.497	0.418
	MEG3	0.491	0.883	0.830
	THBS1	0.477	0.620	0.462
	H2AFZ	0.476	0.865	0.763
	PLAUR	0.471	0.522	0.369
	CTSL	0.462	0.881	0.813
	ADPRHL1	0.461	0.209	0.085
	CXCL3	0.459	0.353	0.251
	CREM	0.433	0.349	0.250
	CFD	1.536	0.951	0.737
	FOS	1.525	0.703	0.464
	GPX3	1.469	0.760	0.236
	PLA2G2A	1.446	0.308	0.024
	WISP2	1.423	0.742	0.199
	MGST1	1.323	0.675	0.200
	MFAP5	1.312	0.590	0.186
	ADH1B	1.310	0.660	0.149
	JUN	1.224	0.852	0.628
Fibro-prematrix	GSN	1.188	0.985	0.960
	GPC3	1.174	0.888	0.529
	IGFBP6	1.053	0.854	0.630
	CXCL14	1.045	0.646	0.457
	PCOLCE2	1.045	0.444	0.044
	FBLN2	1.012	0.742	0.390
	C3	0.966	0.879	0.504
	TXNIP	0.930	0.738	0.487
	S100A4	0.892	0.908	0.777
	S100A10	0.887	0.951	0.859
	C7	0.872	0.267	0.083
	SFRP4	3.597	0.901	0.194
	CLU	2.332	0.993	0.416
	G0S2	1.909	0.317	0.088
	MGP	1.693	0.993	0.956
	OGN	1.475	0.931	0.577
	ADIRF	1.387	0.891	0.614
	IGFBP5	1.339	0.771	0.379
	BGN	1.241	0.793	0.339
	IGFBP6	1.170	0.965	0.681
	CD9	1.143	0.855	0.261
Fibro-SFRP4	RRAD	1.137	0.406	0.052
	LTBP1	1.133	0.732	0.157
	CRYAB	1.115	0.644	0.257
	PDK4	1.098	0.598	0.255
	PRG4	1.095	0.168	0.033
	ABI3BP	1.085	0.894	0.477
	KCNMA1	1.048	0.436	0.012
	COL14A1	0.997	0.900	0.620
	GREM1	0.915	0.434	0.052
	ASPN	0.907	0.624	0.210

Cell state	Gene	Average LogFC	pct1	pct2
		Vascular cells		
	IGFBP3	2.191	0.660	0.155
	CXCL12	1.517	0.565	0.147
	FOS	1.437	0.661	0.407
	CXCL3	1.367	0.362	0.181
	HEY1	1.353	0.582	0.110
	FN1	1.240	0.467	0.123
	TCIM	1.114	0.371	0.180
	BTG2	1.086	0.642	0.426
	DUSP1	1.085	0.775	0.572
	EGR1	1.083	0.535	0.321
Vas-arterial	GADD45B	1.083	0.721	0.597
	RHOB	1.069	0.790	0.527
	JUN	1.046	0.845	0.748
	SEMA3G	1.042	0.405	0.040
	ZFP36	1.041	0.809	0.678
	FOSB	1.007	0.578	0.363
	HES1	0.989	0.482	0.357
	PLPP1	0.980	0.546	0.263
	RASD1	0.974	0.343	0.117
	IER2	0.939	0.750	0.661
	RBP7	1.328	0.737	0.471
	FABP4	1.319	0.769	0.623
	RGCC	1.197	0.618	0.170
	ESM1	1.196	0.216	0.027
	CD36	1.126	0.658	0.415
	CA4	1.112	0.324	0.040
	C11orf96	1.098	0.533	0.328
	BTNL9	1.052	0.472	0.104
	COL4A1	0.968	0.743	0.483
Vas-capillary	SPP1	0.946	0.160	0.036
	APOD	0.891	0.566	0.370
	ADGRF5	0.867	0.701	0.309
	MT1M	0.839	0.395	0.249
	CD300LG	0.802	0.337	0.064
	KDR	0.767	0.544	0.294
	ITGA1	0.765	0.481	0.234
	COL4A2	0.759	0.630	0.397
	MLEC	0.759	0.479	0.169
	SPARC	0.748	0.853	0.677
	MT1A	0.730	0.447	0.328
	SELE	2.554	0.712	0.104
	ACKR1	2.123	0.832	0.197
	CSF3	1.981	0.655	0.154
	IL6	1.753	0.601	0.187
	G0S2	1.504	0.399	0.114
	CLU	1.167	0.810	0.360
	MMP1	1.152	0.169	0.067
	ADIRF	1.063	0.850	0.530
	CYP1B1	1.049	0.328	0.119
Vas-venous	SELP	0.965	0.511	0.027
	CXCL1	0.922	0.219	0.147
	VCAM1	0.905	0.327	0.050
	IL1R1	0.837	0.630	0.259
	CNKSR3	0.830	0.599	0.193
	TFPI	0.786	0.816	0.325
	MED24	0.784	0.397	0.111
	CXCL8	0.766	0.419	0.259
	PMP22	0.724	0.609	0.237
	VCAN	0.719	0.377	0.032
	CST3	0.701	0.910	0.674

Cell state	Gene	Average LogFC	pct1	pct2
		Lymphatic cells		
Lymph-major	FABP4	2.083	0.855	0.267
	LYVE1	2.039	0.746	0.085
	CCL21	2.037	0.945	0.529
	FABP5	1.359	0.842	0.453
	PRSS23	1.214	0.654	0.221
	CYR61	1.200	0.552	0.250
	MMRN1	1.107	0.930	0.698
	NRP2	1.065	0.700	0.361
	PLCG2	1.012	0.459	0.417
	IGF1	0.997	0.461	0.152
	RGS16	0.904	0.630	0.403
	EFEMP1	0.804	0.714	0.497
	TM4SF18	0.800	0.491	0.192
	LOX	0.786	0.381	0.086
	FN1	0.785	0.524	0.284
	RELN	0.765	0.390	0.079
	GNG11	0.741	0.910	0.840
	SOD2	0.738	0.525	0.526
	CTGF	0.738	0.393	0.267
	ANXA1	0.733	0.701	0.488
Lymph-valve1	SCG3	2.849	0.798	0.049
	GJA4	1.428	0.577	0.032
	HGF	1.389	0.548	0.019
	ADM	1.077	0.783	0.407
	CLDN11	1.074	0.480	0.032
	FOXC2	1.019	0.645	0.235
	SOCS2	0.938	0.788	0.380
	NUDT9	0.927	0.528	0.126
	EDNRB	0.907	0.776	0.418
	MYLIP	0.896	0.602	0.180
	ODC1	0.886	0.755	0.428
	OAZ1	0.879	0.967	0.829
	DSEL	0.872	0.480	0.090
	DEGS2	0.828	0.370	0.013
	C17orf58	0.825	0.538	0.156
	CLDN5	0.812	0.985	0.869
	NAV1	0.803	0.482	0.096
	CDC42EP5	0.780	0.724	0.442
	CFH	0.776	0.559	0.210
	PPP1R14B	0.772	0.763	0.466
Lymph-immune	NTS	2.824	0.747	0.095
	CXCL2	2.267	0.753	0.280
	CXCL1	2.253	0.487	0.145
	CXCL8	2.212	0.565	0.241
	CLU	2.021	0.916	0.523
	IGFBP5	2.009	0.318	0.098
	PTGS2	1.809	0.597	0.031
	CXCL3	1.751	0.396	0.117
	CSF3	1.742	0.442	0.055
	CCL2	1.628	0.649	0.357
	PLAT	1.544	0.565	0.072
	TGM2	1.477	0.662	0.061
	AKR1C2	1.441	0.558	0.219
	SERPINB1	1.395	0.643	0.165
	MT1X	1.279	0.773	0.313
	IL6	1.244	0.286	0.051
	AKR1C1	1.204	0.695	0.440
	SAT1	1.189	0.864	0.635
	SRGN	1.185	0.565	0.091
	MED24	1.140	0.422	0.085
Lymph-valve2	CD24	2.275	0.725	0.119
	SLC41A1	1.594	0.799	0.276
	ADAMTS1	1.485	0.633	0.114
	CALM1	1.461	0.987	0.786
	NEO1	1.456	0.703	0.125
	TRDC	1.320	0.581	0.040
	ODC1	1.263	0.860	0.432
	TTN	1.123	0.598	0.199
	MDK	1.111	0.734	0.290
	GSTM3	1.074	0.664	0.177
	SLC5A3	1.038	0.699	0.321
	SBSPON	1.033	0.568	0.067
	ALCAM	1.013	0.415	0.037
	KCNJ2	1.007	0.415	0.007
	ISYNA1	0.994	0.611	0.110
	MRPS6	0.921	0.738	0.391
	IRX3	0.881	0.424	0.027
	DPP4	0.872	0.638	0.200
	SOX4	0.870	0.956	0.679
	NPPC	0.852	0.341	0.059

Cell state	Gene	Average LogFC	pct1	pct2
		Perivascular cells		
Pericyte	COL6A3	1.489	0.584	0.044
	SERPINE1	1.472	0.311	0.098
	CXCL3	1.464	0.223	0.104
	CTSC	1.423	0.563	0.078
	CFD	1.295	0.421	0.159
	CD36	1.271	0.414	0.063
	CCL19	1.212	0.102	0.013
	CYP1B1	1.194	0.312	0.044
	STEAP4	1.158	0.685	0.309
	EMP1	1.154	0.581	0.23
	MARCKS	1.142	0.613	0.174
	CCL2	1.126	0.73	0.563
	C1R	1.087	0.559	0.127
	TFPI	1.072	0.704	0.301
	CXCL8	1.063	0.274	0.193
	EDNRB	1.057	0.632	0.302
	S100A10	1.051	0.56	0.176
	FGF7	1.048	0.397	0.1
	GUCY1A2	1.033	0.44	0.094
	GGT5	1.028	0.437	0.051
VSMC	MYH11	1.821	0.656	0.085
	RERGL	1.491	0.472	0.008
	DSTN	1.340	0.928	0.678
	CREM	1.334	0.523	0.281
	CRYAB	1.330	0.718	0.282
	PLN	1.286	0.528	0.036
	SORBS2	1.155	0.587	0.134
	TSC22D1	1.109	0.809	0.373
	NDUFA4	1.103	0.742	0.311
	TPM2	1.098	0.927	0.7
	ADIRF	1.095	0.938	0.746
	NET1	1.083	0.436	0.026
	GADD45B	1.076	0.908	0.622
	GADD45G	1.070	0.385	0.061
	BCAM	1.054	0.523	0.087
	MCAM	1.034	0.793	0.365
	ZNF331	0.999	0.478	0.234
	CMSS1	0.977	0.325	0.23
	MYL9	0.964	0.833	0.63
	CYCS	0.927	0.802	0.661

Cell state	Gene	Average LogFC	pct1	pct2
		B cells		
	YBX3	1.602	0.621	0.206
	CD37	1.133	0.938	0.471
	TCL1A	1.082	0.304	0.003
	PLCG2	1.058	0.515	0.444
	KLF2	1.053	0.656	0.408
	CD79B	1.051	0.583	0.289
	CD74	1.041	0.987	0.868
	HLA-DRA	1.033	0.980	0.441
	HLA-DRB1	1.010	0.945	0.412
Bnaive	LAPTM5	1.001	0.865	0.407
	BTG1	1.000	0.982	0.884
	HLA-DQA2	0.993	0.390	0.108
	HLA-DPB1	0.990	0.936	0.392
	CD69	0.971	0.461	0.190
	HLA-DQB1	0.967	0.831	0.370
	HLA-DMB	0.963	0.559	0.163
	LINC00926	0.961	0.551	0.172
	RCSD1	0.960	0.565	0.241
	STK17A	0.954	0.666	0.403
	HLA-DPA1	0.915	0.894	0.434
	LTB	1.117	0.800	0.222
	HLA-DPB1	1.016	0.939	0.318
	HLA-DRA	1.005	0.980	0.369
	HLA-DPA1	0.922	0.895	0.372
	MTRNR2L8	0.921	0.427	0.402
	GPR183	0.904	0.551	0.141
	HLA-DRB1	0.897	0.929	0.348
	CD52	0.892	0.787	0.293
	BANK1	0.883	0.707	0.207
Bmem-switched	SMCHD1	0.877	0.757	0.465
	RPL27A	0.876	0.988	0.965
	MS4A1	0.872	0.749	0.219
	CD74	0.869	0.982	0.854
	HLA-A	0.867	0.946	0.827
	RPS20	0.858	0.985	0.948
	RPS12	0.858	0.996	0.990
	RPL13A	0.851	0.997	0.985
	RPL30	0.847	0.996	0.983
	ATP1B3	0.831	0.565	0.430
	TNFRSF13C	0.821	0.720	0.352
	BCL2A1	1.898	0.790	0.098
	DUSP2	1.733	0.748	0.156
	MYC	1.628	0.693	0.153
	MIR155HG	1.622	0.719	0.258
	CD83	1.620	0.962	0.299
	EGR3	1.464	0.536	0.041
	REL	1.383	0.964	0.414
	CD69	1.357	0.783	0.221
	NFKBID	1.345	0.750	0.214
Bmem-unswitched	CCR7	1.344	0.779	0.249
	PLEK	1.316	0.524	0.089
	FABP5	1.288	0.469	0.104
	ZFP36L1	1.253	0.898	0.454
	HLA-DQA1	1.236	0.921	0.384
	NR4A1	1.219	0.579	0.192
	DDX21	1.212	0.845	0.478
	NFKB1	1.200	0.790	0.324
	HSP90AB1	1.164	0.979	0.874
	CD70	1.126	0.498	0.068
	PIKFYVE	1.121	0.633	0.132

Cell state	Gene	Average LogFC	pct1	pct2
		B cells		
	IGHA2	5.091	0.851	0.154
	IGHA1	4.812	0.958	0.452
	JCHAIN	3.597	0.952	0.292
	IGHM	2.222	0.220	0.543
	IGLC2	2.105	0.650	0.408
	IGLL5	1.910	0.285	0.049
	IGLC3	1.818	0.504	0.320
	SSR4	1.550	0.997	0.582
	IGKC	1.496	0.885	0.799
	DERL3	1.421	0.935	0.144
Bplasma-IgA	ANKRD28	1.413	0.923	0.152
	VIM	1.408	0.990	0.714
	GADD45A	1.362	0.659	0.159
	MZB1	1.314	0.966	0.197
	ERN1	1.291	0.770	0.099
	IGHD	1.252	0.046	0.297
	HSPA5	1.196	0.891	0.354
	SEC11C	1.192	0.962	0.317
	NEAT1	1.187	0.980	0.748
	CYTOR	1.166	0.862	0.148
	IGHG1	4.581	0.919	0.153
	IGHG4	4.160	0.792	0.056
	IGHG3	3.895	0.888	0.143
	IGHG2	3.843	0.618	0.078
	IGHGP	2.609	0.388	0.008
	IGLC7	1.812	0.112	0.079
	IGKC	1.116	0.879	0.831
	MZB1	0.954	0.912	0.482
	PRDX4	0.853	0.787	0.446
Bplasma-IgG	DNAAF1	0.843	0.327	0.134
	IGLV3-1	0.802	0.281	0.107
	JSRP1	0.739	0.508	0.210
	FKBP11	0.707	0.847	0.478
	SSR4	0.702	0.986	0.733
	IGKV3-20	0.692	0.139	0.053
	XBP1	0.672	0.792	0.501
	ITM2C	0.642	0.638	0.381
	IGKV4-1	0.602	0.138	0.062
	PSAP	0.556	0.700	0.459
	NPC2	0.555	0.730	0.490

Cell state	Gene	Average LogFC	pct1	pct2
		T cells		
CD4-Th	CCL20	1.498	0.294	0.032
	KLRB1	0.808	0.776	0.402
	CCR6	0.759	0.488	0.143
	IL7R	0.669	0.990	0.754
	RORA	0.639	0.792	0.494
	MYBL1	0.595	0.443	0.190
	PTPN13	0.583	0.207	0.017
	CEBPD	0.575	0.366	0.163
	FURIN	0.552	0.308	0.089
	LTB	0.545	0.566	0.311
	RBMS1	0.542	0.493	0.247
	IL4I1	0.529	0.183	0.012
	ODF2L	0.528	0.525	0.296
	TNFRSF25	0.526	0.308	0.093
	MCAM	0.515	0.213	0.032
	ERN1	0.514	0.439	0.205
	IL18R1	0.508	0.307	0.101
	NFKBIA	0.505	0.654	0.473
	MAP3K4	0.500	0.262	0.072
	TNFSF13B	0.484	0.149	0.014
CD4-Thlike	MAF	0.968	0.508	0.214
	PGAP1	0.665	0.247	0.072
	SOCS3	0.649	0.430	0.188
	CMSS1	0.612	0.278	0.147
	GPR183	0.586	0.650	0.421
	DDIT4	0.585	0.770	0.563
	ARID5B	0.582	0.618	0.339
	CRYBG1	0.582	0.644	0.433
	CH25H	0.579	0.118	0.022
	FTH1	0.567	0.996	0.982
	SESN3	0.546	0.288	0.136
	NR3C1	0.513	0.705	0.477
	ZFP36	0.507	0.829	0.663
	SRGN	0.500	0.996	0.952
	AP3M2	0.497	0.327	0.139
	SLC2A3	0.495	0.564	0.354
	FRMD4B	0.472	0.214	0.063
	GLIPR1	0.462	0.650	0.439
	ANXA1	0.442	0.849	0.710
	UGP2	0.435	0.431	0.265
CD4-naive	MTRNR2L8	1.155	0.486	0.251
	LTB	1.038	0.816	0.304
	KLF2	1.006	0.730	0.222
	SELL	0.926	0.474	0.048
	CCR7	0.860	0.542	0.129
	SESN3	0.725	0.473	0.146
	LDHB	0.637	0.804	0.400
	TSHZ2	0.624	0.284	0.031
	LEF1	0.623	0.357	0.038
	PASK	0.579	0.327	0.075
	RPL23	0.566	0.984	0.892
	RIPOR2	0.522	0.472	0.146
	RPS8	0.475	1.000	0.993
	S1PR1	0.447	0.287	0.039
	RPS6	0.441	0.999	0.994
	TXNIP	0.430	0.855	0.581
	EIF3E	0.424	0.841	0.543
	RPS12	0.415	1.000	0.997
	GIMAP7	0.410	0.756	0.450
	RPL22	0.406	0.994	0.942

Cell state	Gene	Average LogFC	pct1	pct2
		T cells		
CD4-Tem	HSPA1A	1.455	0.534	0.210
	KLF6	1.371	0.898	0.621
	FOS	1.251	0.569	0.396
	HSP90AA1	1.083	0.955	0.895
	FOSB	1.033	0.522	0.277
	HSPA1B	1.015	0.290	0.090
	DNAJA1	1.003	0.786	0.560
	IFNG	0.980	0.240	0.073
	UBE2S	0.975	0.565	0.268
	GADD45B	0.959	0.533	0.335
	NFKBIA	0.924	0.670	0.481
	JUN	0.920	0.704	0.489
	HSP90AB1	0.919	0.928	0.829
	LMNA	0.911	0.553	0.379
	TUBB4B	0.898	0.764	0.444
	PPP1R15A	0.898	0.556	0.319
	XCL1	0.890	0.250	0.123
	DNAJB1	0.880	0.550	0.360
	HSPH1	0.845	0.477	0.286
	TNFAIP3	0.845	0.785	0.644
CD4-Treg	TIGIT	1.416	0.669	0.134
	TBC1D4	1.235	0.539	0.072
	BATF	1.195	0.608	0.179
	CARD16	1.192	0.510	0.111
	CTLA4	1.162	0.498	0.056
	MTRNR2L8	1.141	0.462	0.261
	RTKN2	1.104	0.332	0.020
	IKZF2	1.012	0.404	0.036
	PMAIP1	1.008	0.436	0.114
	STAM	0.926	0.453	0.071
	HPGD	0.924	0.219	0.057
	LTB	0.860	0.651	0.329
	TNFRSF9	0.846	0.348	0.059
	TNFRSF4	0.818	0.299	0.085
	SELL	0.792	0.354	0.068
	GK	0.780	0.254	0.024
	TNFRSF18	0.779	0.358	0.100
	LAYN	0.771	0.221	0.007
	SESN3	0.766	0.418	0.160
	ARID5B	0.756	0.741	0.388
CD4-activated	HSPA1A	3.043	0.533	0.222
	HSPA1B	2.798	0.493	0.091
	DNAJB1	2.521	0.528	0.367
	PLCG2	2.404	0.816	0.352
	HSPA6	2.284	0.168	0.018
	HSP90AA1	1.654	0.825	0.901
	HSPH1	1.525	0.388	0.296
	HSPD1	1.260	0.468	0.532
	HSPE1	1.193	0.553	0.537
	HIST1H4C	0.868	0.428	0.455
	HSPB1	0.858	0.323	0.166
	TRAF3IP3	0.826	0.373	0.144
	RMRP	0.717	0.157	0.018
	TECR	0.680	0.277	0.199
	TXNIP	0.662	0.840	0.593
	CACYBP	0.661	0.345	0.289
	DNAJA1	0.630	0.428	0.579
	CHORDC1	0.628	0.283	0.199
	CD52	0.624	0.726	0.590
	TRAC	0.622	0.592	0.454

Cell state	Gene	Average LogFC	pct1	pct2	Cell state	Gene	Average LogFC	pct1	pct2
		T cells					**T cells**		
CD8-activated	PLCG2	2.493	0.868	0.358	NKT	GZMH	1.866	0.870	0.133
	IGKC	1.311	0.560	0.404		NKG7	1.800	0.986	0.297
	CCL5	1.277	0.984	0.654		FGFBP2	1.642	0.721	0.049
	ZNF683	1.106	0.297	0.029		GNLY	1.568	0.854	0.154
	TRAF3IP3	1.051	0.479	0.145		CCL4	1.327	0.798	0.252
	TRG-AS1	1.016	0.346	0.076		GZMB	1.116	0.776	0.160
	CCL4L2	0.998	0.303	0.093		GZMA	1.048	0.731	0.242
	ITGA1	0.975	0.410	0.159		ZEB2	1.034	0.645	0.171
	TRAC	0.960	0.699	0.455		KLRD1	1.018	0.727	0.225
	RMRP	0.932	0.242	0.019		CD52	1.005	0.851	0.584
	EVL	0.929	0.648	0.367		C12orf75	0.915	0.548	0.143
	TRGC2	0.884	0.386	0.158		KLRG1	0.901	0.413	0.058
	IGHA1	0.875	0.353	0.270		TRGC2	0.894	0.494	0.149
	CKLF	0.865	0.402	0.169		KLF2	0.889	0.692	0.239
	LINC00324	0.863	0.177	0.043		ACTB	0.888	0.928	0.850
	CD8B	0.861	0.458	0.191		FCGR3A	0.878	0.397	0.051
	JCHAIN	0.853	0.133	0.096		CTSW	0.833	0.630	0.221
	HSPA1B	0.849	0.225	0.101		PRF1	0.805	0.615	0.186
	KLRC1	0.839	0.290	0.144		HCST	0.803	0.790	0.518
	GPR174	0.813	0.328	0.112		PLEK	0.800	0.358	0.046
CD8-Trm	CD8A	1.117	0.741	0.180	NK/ILCs	XCL2	1.762	0.613	0.111
	KLRC1	0.958	0.378	0.069		TYROBP	1.599	0.762	0.075
	LDLRAD4	0.824	0.383	0.123		XCL1	1.532	0.623	0.121
	AUTS2	0.797	0.490	0.168		AREG	1.527	0.743	0.347
	ITGA1	0.789	0.392	0.085		TNFRSF18	1.389	0.592	0.097
	CD8B	0.788	0.459	0.105		FCER1G	1.380	0.661	0.052
	LINC01871	0.781	0.566	0.229		GNLY	1.355	0.507	0.173
	SYTL3	0.752	0.812	0.517		CMC1	1.164	0.466	0.138
	PGK1	0.726	0.722	0.474		NFKB1	1.094	0.636	0.265
	CD7	0.707	0.818	0.486		REL	1.047	0.764	0.482
	PARD6G	0.625	0.264	0.045		CSF2	1.023	0.144	0.004
	CCL5	0.617	0.946	0.563		CTSW	1.002	0.633	0.227
	GABARAPL1	0.595	0.622	0.357		CCL3	0.954	0.164	0.061
	SPRY1	0.583	0.294	0.097		CD83	0.913	0.235	0.036
	PARP8	0.575	0.613	0.371		KIT	0.887	0.239	0.017
	METRNL	0.573	0.702	0.398		KLRD1	0.887	0.590	0.236
	SLA2	0.572	0.286	0.085		NFKBIA	0.866	0.732	0.487
	SYTL2	0.536	0.377	0.179		TRDC	0.858	0.346	0.038
	NKAP	0.535	0.295	0.125		KLRC1	0.849	0.477	0.139
	RGS1	0.534	0.674	0.397		KLRB1	0.821	0.817	0.434
CD8-Tem	GZMK	1.919	0.833	0.119	NK	GNLY	2.602	0.968	0.133
	HLA-DRB1	1.292	0.501	0.128		NKG7	2.368	0.994	0.282
	CRTAM	1.191	0.409	0.075		FGFBP2	2.168	0.778	0.032
	TNFRSF9	1.144	0.311	0.042		CCL3	2.165	0.429	0.041
	CST7	0.996	0.866	0.467		GZMB	2.117	0.924	0.138
	CD74	0.920	0.611	0.315		TYROBP	2.053	0.824	0.045
	SH2D1A	0.915	0.461	0.164		FCGR3A	2.008	0.769	0.021
	CMC1	0.903	0.391	0.119		FCER1G	1.939	0.690	0.028
	DUSP2	0.891	0.830	0.520		SPON2	1.894	0.694	0.075
	HLA-DPB1	0.889	0.504	0.178		CCL4	1.837	0.822	0.240
	HLA-DRA	0.857	0.317	0.108		PRF1	1.813	0.823	0.165
	TUBA4A	0.794	0.697	0.478		KLRD1	1.794	0.915	0.203
	LYST	0.740	0.396	0.147		KLRF1	1.752	0.636	0.014
	HLA-DPA1	0.733	0.386	0.143		CTSW	1.567	0.778	0.203
	CEMIP2	0.717	0.695	0.474		CMC1	1.564	0.618	0.117
	DUSP4	0.691	0.369	0.174		GZMA	1.504	0.820	0.227
	HLA-DQB1	0.686	0.264	0.069		CLIC3	1.470	0.579	0.082
	GZMA	0.672	0.562	0.229		ITGB2	1.299	0.648	0.172
	CCL4L2	0.635	0.206	0.085		CD247	1.291	0.771	0.282
	EOMES	0.606	0.208	0.031		CCL4L2	1.289	0.324	0.083

Supplementary Table 10: Top Gene Markers Expressed for Breast Cell States

Cell state	Gene	Average LogFC	pct1	pct2
		T cells		
	XCL1	1.122	0.395	0.130
	CEMIP2	0.980	0.796	0.493
	SMC4	0.913	0.308	0.129
	GPCPD1	0.894	0.526	0.159
	LITAF	0.877	0.802	0.411
	METRNL	0.849	0.836	0.471
	REL	0.845	0.824	0.486
	CCDC57	0.839	0.365	0.091
	TRGC2	0.807	0.497	0.159
	IKZF2	0.790	0.327	0.046
GD-T	GNLY	0.767	0.382	0.179
	PIK3R1	0.740	0.837	0.576
	CD7	0.737	0.902	0.567
	KLRC2	0.737	0.250	0.051
	CD55	0.717	0.656	0.360
	CHPT1	0.710	0.335	0.109
	TRDC	0.699	0.240	0.043
	SOX4	0.672	0.178	0.076
	NR4A2	0.665	0.567	0.288
	AREG	0.664	0.595	0.354
	STMN11	2.393	0.973	0.257
	TUBB	2.105	0.942	0.227
	MKI67	1.975	0.830	0.003
	HIST1H4C1	1.918	0.861	0.452
	HMGN23	1.876	0.969	0.327
	TOP2A	1.835	0.710	0.009
	CENPF	1.826	0.730	0.032
	TUBA1B1	1.812	0.981	0.543
	HMGB21	1.803	0.954	0.419
T-prol	ASPM	1.663	0.687	0.004
	PCLAF	1.641	0.784	0.004
	TYMS	1.556	0.745	0.008
	NUSAP1	1.553	0.776	0.034
	DUT	1.527	0.846	0.163
	ACTB4	1.509	0.992	0.852
	PCNA	1.364	0.730	0.090
	CKS1B	1.351	0.768	0.079
	SMC42	1.346	0.799	0.128
	GZMA5	1.283	0.757	0.259
	HIST1H1B	1.223	0.417	0.010

Cell state	Gene	Average LogFC	pct1	pct2
		Myeloid cells		
	CPVL	2.041	0.961	0.546
	DNASE1L3	1.995	0.871	0.024
	CPNE3	1.780	0.963	0.197
	IDO1	1.775	0.815	0.060
	C1orf54	1.683	0.954	0.253
	TACSTD2	1.681	0.854	0.147
	S100B	1.571	0.580	0.052
	LGALS2	1.428	0.902	0.167
	SNX3	1.319	0.974	0.707
cDC1	CLEC9A	1.315	0.854	0.040
	CST3	1.315	0.991	0.936
	WDFY4	1.305	0.889	0.098
	HLA-DPB1	1.217	0.996	0.853
	RAB11FIP1	1.216	0.911	0.251
	DAPP1	1.139	0.852	0.132
	HLA-DPA1	1.026	0.994	0.868
	EEF1B2	1.021	0.991	0.899
	PPA1	0.990	0.943	0.404
	GPR157	0.982	0.662	0.116
	C12orf45	0.976	0.787	0.221
	FCER1A	1.796	0.829	0.146
	CD1C	1.527	0.723	0.052
	IL1R2	1.479	0.839	0.212
	CLEC10A	1.278	0.783	0.165
	CST3	1.192	0.984	0.931
	AREG	1.149	0.736	0.391
	LYZ	0.906	0.973	0.661
	HLA-DQA1	0.902	0.991	0.712
	HLA-DPB1	0.838	0.997	0.837
cDC2	LGALS2	0.836	0.633	0.123
	HLA-DQB1	0.804	0.990	0.741
	TIMP1	0.803	0.945	0.663
	CST7	0.779	0.570	0.138
	CPVL	0.754	0.841	0.518
	CFP	0.732	0.625	0.149
	CD1E	0.730	0.401	0.030
	CCL22	0.725	0.328	0.064
	HLA-DRA	0.714	0.999	0.925
	S100A10	0.712	0.985	0.841
	AC020656.1	0.707	0.671	0.280
	CCL22	2.995	0.791	0.083
	BIRC3	2.555	0.965	0.484
	CCR7	2.451	0.965	0.211
	IDO1	2.167	0.659	0.064
	CCL17	2.070	0.404	0.026
	LAMP3	1.866	0.921	0.044
	TXN	1.839	0.969	0.800
	IL7R	1.806	0.954	0.247
	DAPP1	1.729	0.901	0.133
	CST7	1.720	0.818	0.177
mDC	NUB1	1.699	0.774	0.188
	MARCKSL1	1.633	0.884	0.299
	FSCN1	1.593	0.741	0.147
	RAMP1	1.526	0.629	0.087
	GADD45A	1.525	0.677	0.183
	RAB9A	1.430	0.864	0.289
	CRIP1	1.424	0.778	0.280
	EBI3	1.376	0.580	0.203
	GPR157	1.362	0.796	0.115
	CCL19	1.361	0.297	0.008

Supplementary Table 10: Top Gene Markers Expressed for Breast Cell States

Cell state	Gene	Average LogFC	pct1	pct2	Cell state	Gene	Average LogFC	pct1	pct2
		Myeloid cells					**Myeloid cells**		
pDC	GZMB	2.825	0.399	0.011	Mono-classical	CXCL5	2.360	0.336	0.073
	IGKC	2.557	0.696	0.409		SERPINB2	2.124	0.227	0.014
	PTGDS	2.161	0.196	0.031		EREG	1.745	0.709	0.178
	JCHAIN	2.059	0.459	0.110		VCAN	1.745	0.686	0.149
	IRF8	1.633	0.608	0.236		THBS1	1.623	0.820	0.354
	DNASE1L3	1.622	0.446	0.037		S100A9	1.473	0.627	0.284
	LGALS2	1.549	0.372	0.179		FCN1	1.346	0.606	0.102
	C1orf54	1.394	0.338	0.265		LYZ	1.322	0.915	0.661
	CLIC3	1.377	0.318	0.007		S100A8	1.265	0.436	0.146
	IRF4	1.353	0.331	0.110		TIMP1	1.085	0.937	0.657
	PLAC8	1.344	0.311	0.055		AC020656.1	1.002	0.606	0.280
	SNX3	1.341	0.791	0.712		CXCL3	0.963	0.814	0.419
	S100B	1.323	0.216	0.061		S100A12	0.876	0.251	0.018
	CLEC9A	1.273	0.223	0.053		CXCL1	0.840	0.359	0.195
	CPNE3	1.263	0.392	0.209		CD300E	0.837	0.561	0.189
	ITM2C	1.261	0.399	0.160		CYP1B1	0.817	0.444	0.200
	TSPAN13	1.244	0.345	0.030		CCL20	0.816	0.421	0.182
	BCL11A	1.178	0.338	0.051		MT1X	0.798	0.370	0.324
	C12orf75	1.167	0.318	0.099		CXCL2	0.781	0.865	0.514
	IRF7	1.135	0.378	0.218		IL1RN	0.778	0.436	0.196
Mast	TPSB2	3.829	0.843	0.007	Macro-lipo	FABP4	3.578	0.605	0.193
	TPSAB1	3.647	0.816	0.007		APOC1	2.573	0.786	0.259
	HPGD	3.504	0.827	0.073		SPP1	2.017	0.476	0.116
	CTSG	3.464	0.755	0.002		APOE	1.835	0.875	0.461
	CPA3	3.192	0.837	0.001		GPNMB	1.568	0.900	0.359
	IL1RL1	2.281	0.687	0.013		ACP5	1.545	0.817	0.178
	CMA1	2.278	0.488	0.001		LIPA	1.534	0.824	0.362
	HDC	2.135	0.556	0.001		CCL18	1.409	0.379	0.083
	ADCYAP1	2.117	0.270	0.001		CSTB	1.405	0.984	0.804
	GATA2	2.105	0.511	0.003		CTSD	1.382	0.964	0.710
	HPGDS	2.001	0.630	0.125		FABP5	1.349	0.896	0.567
	MS4A2	1.895	0.530	0.001		CHIT1	1.294	0.224	0.005
	GCSAML	1.846	0.461	0.001		MMP9	1.263	0.508	0.232
	KIT	1.798	0.491	0.012		LGALS3	1.186	0.953	0.757
	FAM107B	1.734	0.702	0.510		CD36	1.118	0.646	0.250
	LGALS3	1.577	0.818	0.763		CHI3L1	1.100	0.159	0.022
	ANXA1	1.498	0.860	0.866		CD52	1.095	0.530	0.191
	BATF	1.493	0.455	0.117		CYP27A1	1.094	0.584	0.048
	SELENOK	1.474	0.702	0.663		LPL	1.086	0.520	0.121
	LEO1	1.473	0.423	0.110		PLD3	1.043	0.835	0.508
Mono-nonclassical	LST1	2.082	0.985	0.570	Macro-m1	C3	1.679	0.861	0.163
	CD52	1.839	0.861	0.182		FCGBP	1.381	0.509	0.119
	FCGR3A	1.602	0.942	0.345		SDS	1.367	0.714	0.219
	COTL1	1.581	0.986	0.672		APOE	1.155	0.836	0.365
	FCN1	1.550	0.805	0.149		RGS1	1.049	0.915	0.499
	SMIM25	1.520	0.843	0.169		OLR1	0.945	0.695	0.259
	SERPINA1	1.489	0.946	0.397		CXCR4	0.904	0.865	0.538
	STXBP2	1.405	0.872	0.275		YWHAH	0.846	0.773	0.433
	IFITM2	1.303	0.947	0.577		RGS2	0.845	0.875	0.539
	CORO1A	1.266	0.882	0.341		CD81	0.829	0.924	0.664
	S100A4	1.253	0.991	0.733		CREM	0.818	0.904	0.629
	LILRA5	1.248	0.723	0.078		TFRC	0.802	0.684	0.416
	CDKN1C	1.186	0.592	0.118		HLA-DPA1	0.790	0.985	0.834
	LILRB2	1.185	0.865	0.350		AXL	0.769	0.725	0.237
	CD48	1.183	0.884	0.343		PLXDC2	0.745	0.810	0.369
	LYPD2	1.182	0.226	0.000		ZNF331	0.744	0.591	0.265
	SPN	1.161	0.710	0.103		ALOX5AP	0.743	0.865	0.510
	PLAC8	1.146	0.519	0.041		ATP1B3	0.741	0.926	0.785
	IFITM3	1.144	0.918	0.641		SAT1	0.727	1.000	0.979
	AIF1	1.140	0.987	0.808		CD9	0.724	0.770	0.344

Cell state	Gene	Average LogFC	pct1	pct2
Myeloid cells				
Macro-m1-CCL	CCL4L2	1.910	0.860	0.290
	CCL20	1.884	0.569	0.195
	IL1B	1.770	0.975	0.499
	CCL3L1	1.607	0.805	0.278
	CCL4	1.488	0.919	0.405
	G0S2	1.412	0.728	0.368
	IL23A	1.335	0.150	0.016
	TCHH	1.310	0.516	0.107
	OLR1	1.297	0.801	0.339
	IL1A	1.249	0.574	0.120
	INHBA	1.244	0.413	0.120
	CCL3	1.179	0.871	0.439
	CD83	1.084	0.943	0.633
	C3	1.074	0.869	0.299
	RGS1	1.031	0.937	0.579
	CCR7	1.026	0.597	0.202
	REL	1.022	0.978	0.809
	PLAUR	1.004	0.967	0.813
	BCL2A1	0.982	0.932	0.550
	IL6	0.942	0.349	0.099
Macro-m2	RNASE1	2.061	0.982	0.299
	HMOX1	1.862	0.840	0.553
	LYVE1	1.828	0.809	0.112
	SELENOP	1.824	0.922	0.300
	F13A1	1.539	0.785	0.244
	EMP1	1.521	0.772	0.330
	MRC1	1.437	0.920	0.338
	CD163	1.350	0.962	0.544
	PLTP	1.304	0.736	0.232
	FOLR2	1.234	0.789	0.279
	PDK4	1.199	0.469	0.193
	LGMN	1.179	0.849	0.467
	MAN1A1	1.159	0.788	0.344
	CCL18	1.156	0.273	0.036
	STAB1	1.152	0.806	0.312
	LILRB5	1.135	0.665	0.089
	DAB2	1.099	0.867	0.440
	MARCO	1.078	0.390	0.138
	CD36	1.074	0.577	0.163
	MAFB	1.017	0.933	0.616
Macro-m2-CXCL	CCL3L1	2.290	0.868	0.275
	CCL4	2.181	0.911	0.406
	CCL3	2.158	0.954	0.436
	CCL4L2	2.042	0.809	0.294
	CXCL3	1.945	0.959	0.447
	CXCL1	1.735	0.590	0.198
	CXCL8	1.684	0.998	0.723
	CXCL2	1.563	0.960	0.541
	TNF	1.544	0.574	0.167
	IL1A	1.353	0.472	0.126
	IL1B	1.347	0.851	0.507
	CCL2	1.215	0.612	0.258
	GCLM	1.104	0.830	0.386
	EIF4E	1.064	0.772	0.510
	ICAM1	1.020	0.859	0.493
	TXNRD1	1.018	0.802	0.502
	MMP9	0.988	0.489	0.230
	HMOX1	0.980	0.901	0.609
	LUCAT1	0.954	0.701	0.327
	JAG1	0.896	0.450	0.134

Cell state	Gene	Average LogFC	pct1	pct2
Myeloid cells				
Macro-ifn	CXCL10	2.991	0.479	0.037
	ISG15	2.395	0.916	0.249
	IFIT3	2.036	0.679	0.033
	RSAD2	1.982	0.666	0.027
	IFIT2	1.966	0.612	0.036
	IFIT1	1.895	0.652	0.019
	MX1	1.799	0.860	0.143
	CCL8	1.750	0.293	0.046
	IFI44L	1.492	0.772	0.061
	IFI6	1.452	0.790	0.204
	PARP14	1.397	0.932	0.381
	GBP1	1.395	0.607	0.110
	RNF213	1.256	0.898	0.432
	EIF2AK2	1.221	0.795	0.190
	MX2	1.211	0.745	0.191
	SAMD9L	1.196	0.648	0.076
	XAF1	1.147	0.688	0.079
	EPSTI1	1.131	0.788	0.171
	LY6E	1.106	0.695	0.196
	CXCL11	1.099	0.214	0.005
Neutrophil	IFITM2	3.24614363	0.964	0.583
	S100A8	2.92206456	0.805	0.176
	S100A9	2.436769	0.889	0.322
	CSF3R	2.41872518	0.633	0.249
	FCGR3B	2.4004261	0.439	0.003
	AQP9	2.39023977	0.597	0.134
	SMCHD1	2.36911565	0.674	0.424
	SLC25A37	2.29825404	0.624	0.32
	PI3	2.22099347	0.156	0.01
	KIAA1551	2.17056387	0.509	0.277
	MNDA	2.12892812	0.486	0.299
	RIPOR2	2.03875218	0.378	0.057
	FPR1	2.00448696	0.606	0.357
	CXCR2	1.97998162	0.308	0.001
	S100A12	1.97440576	0.265	0.046
	VNN2	1.96970848	0.333	0.038
	PROK2	1.96439666	0.269	0.005
	IVNS1ABP	1.95687179	0.606	0.484
	TMEM154	1.94791064	0.36	0.058
	S100P	1.93535019	0.292	0.006
Myeloid-prol	STMN1	2.038	0.943	0.327
	HIST1H4C	1.980	0.734	0.361
	HMGN2	1.808	0.943	0.576
	TUBA1B	1.567	0.970	0.841
	HMGB2	1.542	0.818	0.346
	PCLAF	1.469	0.687	0.012
	MKI67	1.422	0.621	0.006
	TOP2A	1.419	0.599	0.013
	HMGB1	1.406	0.985	0.886
	TUBB	1.371	0.894	0.633
	TYMS	1.345	0.638	0.019
	H2AFZ	1.333	0.938	0.772
	CKS1B	1.291	0.727	0.126
	CENPF	1.247	0.534	0.016
	NUSAP1	1.234	0.601	0.036
	CDK1	1.118	0.562	0.025
	DUT	1.069	0.643	0.251
	PTTG1	1.064	0.623	0.136
	TK1	1.041	0.571	0.020
	UBE2C	1.039	0.421	0.002

Supplementary Table 10 – Top Gene Markers Expressed for Breast Cell States

This table lists the top marker genes expressed for each major cell state cluster based on the average log fold-change within the respective cell type and specificity of the gene expressed in the indicated cell state (pct1) compared to the other cell states of the same cell type (pc2). The columns listed (from left to right) indicate the cell state name, the gene names, the average log- fold change, the pct1 value indicating the fraction of cells within the cluster expressing the gene, the pct2 value indicating the fraction of cells in other clusters expressing the gene, and the Bonferroni adjusted p-value.

Patient ID	Total Counts (raw)	Total Counts (post filter)	Total Cells (raw)	Filtered Cells (post filter)
P91	18962267	17504490	230073	93859
P96	18597651	18187226	218464	93687
P101	12129915	11587548	175447	73242

Supplementary Table 11 - Quality Control Metrics for smFISH (MERFISH) Data

The table lists the quality control metrics for the 3 breast tissue samples profiled with the custom 300-gene panel for smFISH analysis (Merscope). The columns listed (from left to right) indicate the Patient ID, the number of transcripts captured under tissue, the number of transcripts after filtering, the number of cells detected and the number of cells after filtering.

Supplementary Table 12 – Custom Targeted Gene Panel for smFISH (MERFISH)

CellType	CellState	Gene	Cell Type Annotation	Cell State Annotation
adipocytes	adipocytes	ADIPOQ	0	0
adipocytes	adipocytes	GPD1	1	0
adipocytes	adipocytes	LPL	1	0
adipocytes	adipocytes	PDE3B	1	0
adipocytes	adipocytes	PLIN1	1	0
B-cells	b_naive	CD37	0	1
B-cells	b_naive	CD52	0	0
B-cells	b_naive	LTB	0	1
B-cells	B-cells	CREB3	0	0
B-cells	B-cells	TFEB	0	0
B-cells	bmem_unswitched	BCL2A1	0	0
B-cells	bmem_unswitched	CD27	0	0
B-cells	bmem_unswitched	EGR3	0	0
B-cells	bmem_unswitched	IGHD	0	1
B-cells	bmem_unswitched	MYC	0	0
B-cells	cannonical	CD79A	1	0
B-cells	cannonical	IGHM	1	1
B-cells	cannonical	MZB1	1	1
B-cells	plasma_IgA	IGHA2	0	0
B-cells	plasma_IgA	JCHAIN	1	1
B-cells	plasma_IgG	IGHG1	0	0
B-cells	plasma_IgG	IGHG3	1	1
B-cells	plasma_IgG	IGHG4	1	1
basal	basal	CARMN	0	0
basal	basal	COL17A1	1	0
basal	basal	KLF16	0	0
basal	basal	LINC01060	0	0
basal	basal	SOX9	0	0
basal	basal	TEAD3	0	0
basal	basal	TFAP2C	1	0
basal	cannonical	ACTG2	1	1
basal	cannonical	KRT14	1	0
basal	cannonical	KRT5	1	0
basal	cannonical	LAMA3	0	0
basal	cannonical	TUBB2B	0	0
epithelial	cannonical	EPCAM	0	0
epithelial	cannonical	KRT19	0	0
epithelial	cannonical	KRT8	0	0
epithelial	cannonical	TP63	1	0
fibro	cannonical	COL1A1	1	0
fibro	cannonical	FBLN1	1	0
fibro	cannonical	LUM	0	0
fibro	cannonical	TNFAIP6	0	0

CellType	CellState	Gene	Cell Type	Cell State
fibro	fibro	CREB3L1	0	0
fibro	fibro	LAMA2	1	0
fibro	fibro	LINC02511	0	0
fibro	fibro	NEGR1	0	0
fibro	fibro	PLAGL1	1	0
fibro	fibro	TWIST2	0	0
fibro	fibro_col1a1	POSTN	0	0
fibro	fibro_col1a1	TAC1	0	0
fibro	fibro_col1a1	TGFBI	0	0
fibro	fibro_col1a1	WNT2	0	0
fibro	fibro_pcolce2	CCN5	0	0
fibro	fibro_pcolce2	PCOLCE2	0	0
fibro	fibro_pcolce2	PDK4	0	0
fibro	fibro_pcolce2	RAMP2	0	0
fibro	fibro_pcolce2	SVEP1	0	0
fibro	fibro_pdpn	CXCL1	0	0
fibro	fibro_pdpn	CXCL2	0	0
fibro	fibro_pdpn	CXCL3	0	0
fibro	fibro_pdpn	CXCL8	0	0
fibro	fibro_pdpn	IL6	0	0
Immune	cannonical	PTPRC	0	0
lumhr	cannonical	AGR2	0	0
lumhr	cannonical	AGR3	0	0
lumhr	cannonical	ANKRD30A	1	0
lumhr	cannonical	AREG	1	0
lumhr	cannonical	DNAJC12	1	0
lumhr	cannonical	RASEF	1	0
lumhr	cannonical	TMC5	0	0
lumhr	lumhr	AR	0	0
lumhr	lumhr	BATF	1	0
lumhr	lumhr	ESR1	0	0
lumhr	lumhr	GATA3	1	0
lumhr	lumhr	PGR	0	0
lumhr	lumhr	TBX3	0	0
lumhr	lumhr	TTC6	0	0
lumhr	lumhr_egln3	EGLN3	0	0
lumhr	lumhr_fasn	CA2	0	0
lumhr	lumhr_fasn	FASN	0	0
lumhr	lumhr_fasn	MYBPC1	0	0
lumhr	lumhr_pip	SERPINA1	0	1
lumhr	lumhr_pip	TFPI2	0	1

CellType	CellState	Gene	Cell Type	Cell State
lumsec	cannonical	ALDH1A3	1	1
lumsec	cannonical	CCL28	1	0
lumsec	cannonical	KRT15	1	0
lumsec	cannonical	LTF	1	1
lumsec	cannonical	MMP7	0	0
lumsec	cannonical	PIGR	1	0
lumsec	cannonical	SLPI	1	1
lumsec	lumsec	EHF	0	0
lumsec	lumsec	ELF5	1	1
lumsec	lumsec	GABRP	1	1
lumsec	lumsec	GRHL1	0	0
lumsec	lumsec	NR2F6	0	0
lumsec	lumsec_hla	AQP3	0	1
lumsec	lumsec_hla	CCL20	0	1
lumsec	lumsec_hla	RBP1	0	1
lumsec	lumsec_KIT	HES1	0	0
lumsec	lumsec_KIT	KIT	0	0
lumsec	lumsec_krt23	KRT23	0	1
lumsec	lumsec_lactation	CSN1S1	0	0
lumsec	lumsec_lactation	CSN3	0	0
lumsec	lumsec_lactation	LALBA	0	0
lumsec	lumsec_prol	STMN1	0	1
lumsec	lumsec_prol	TYMS	0	1
lymph	cannonical	MMRN1	1	0
lymph	cannonical	PECAM1	0	0
lymph	cannonical	PGM5	1	0
lymph	cannonical	PROX1	1	0
lymph	cannonical	SCN3B	1	0
lymph	cannonical	TBX1	1	0
lymph	lymph	HMGB3	0	0
lymph	lymph	KLHL4	0	0
lymph	lymph	LINC02147	0	0
lymph	lymph	NR2F2	0	0
lymph	lymph	PKHD1L1	0	0
lymph	lymph	RHOJ	0	0
lymph	lymph-immune	ACKR4	0	0
lymph	lymph-immune	PTGS2	0	0
lymph	lymph-immune	TGM2	0	0
lymph	lymph-major	FABP4	0	0
lymph	lymph-major	LYVE1	0	0
lymph	lymph-valve	CLDN11	0	1
lymph	lymph-valve	MYLIP	0	1
lymph	lymph-valve	SCG3	0	1

CellType	CellState	Gene	Cell Type	Cell State
mast	cannonical	CD69	0	0
mast	cannonical	CPA3	0	0
mast	cannonical	HPGD	0	0
mast	cannonical	HPGDS	0	0
mast	cannonical	TPSB2	0	0
myeloid	cannonical	C1QA	1	0
myeloid	cannonical	C1QB	1	0
myeloid	cannonical	C1QC	1	0
myeloid	cannonical	CD14	1	0
myeloid	cannonical	CD163	1	0
myeloid	cannonical	CD68	0	0
myeloid	cannonical	LYZ	1	0
myeloid	cannonical	MSR1	0	0
myeloid	cDC1	CLEC9A	0	0
myeloid	cDC1	WDFY4	0	0
myeloid	cDC1	XCR1	0	0
myeloid	cDC2	CCL21	0	0
myeloid	cDC2	CD1C	0	1
myeloid	cDC2	CLEC10A	0	1
myeloid	cDC2	FCER1A	0	1
myeloid	macro_ifn_m2	IFIT1	0	0
myeloid	macro_ifn_m2	STAT1	0	0
myeloid	macro_ifn_m2	XAF1	0	0
myeloid	macro_lipo	APOC1	0	1
myeloid	macro_lipo	SPP1	0	0
myeloid	macro_lipo	TREM2	0	1
myeloid	macro_m1	APOE	0	0
myeloid	macro_m1	C3	0	1
myeloid	macro_m1	RGS1	0	1
myeloid	macro_m2	MRC1	0	1
myeloid	macro_m2	RNASE1	0	1
myeloid	macro_m2	SELENOP	0	1
myeloid	mast	HDC	0	0
myeloid	mast	IL18R1	0	0
myeloid	mast	NTM	0	0
myeloid	mast	SYTL3	0	0
myeloid	mDC	CCL19	0	0
myeloid	mDC	CCL22	0	0
myeloid	mDC	LAMP3	0	0
myeloid	mono_active	CXCL5	0	0
myeloid	mono_active	SERPINB2	0	0
myeloid	mono_naive	TESC	0	0

CellType	CellState	Gene	Cell Type	Cell State
myeloid	Myeloid	ARID3A	0	0
myeloid	Myeloid	MAF	0	0
myeloid	Myeloid	MAFB	1	0
myeloid	pDC	SPIB	0	0
myeloid	pDC	TPM2	0	0
myeloid	pDC	TSPAN13	0	0
peri	cannonical	AVPR1A	1	0
peri	cannonical	EDNRA	1	0
peri	cannonical	MCAM	1	1
peri	cannonical	PLN	0	0
peri	cannonical	RGS5	1	1
peri	cannonical	SSTR2	0	0
peri	peri	ADGRL3	0	0
peri	peri	COL25A1	1	1
peri	peri	RGS6	1	1
peri	peri	SOX5	0	0
peri	peri	TBX2	1	0
peri	peri_CREM	CREM	0	0
peri	peri_CREM	SLC25A4	0	0
peri	peri_CREM	SYNM	0	1
peri	peri_CREM	ZNF331	0	0
peri	peri_imm	EMP3	0	0
peri	peri_imm	GYPC	0	0
peri	peri_imm	PSME2	0	0
peri	peri_imm	SERPINE2	0	0
peri	peri_myo	EGR1	0	0
peri	peri_myo	PLAC9	0	0
peri	peri_myo	RGS16	0	0
prol	prol	MKI67	0	1
prol	prol	PCNA	0	1
prol	prol	TOP2A	0	1
T-cells	cannonical	CCL5	1	1
T-cells	cannonical	CD2	1	1
T-cells	cannonical	CD3D	1	1
T-cells	cannonical	CD3G	0	0
T-cells	cannonical	CD4	1	1
T-cells	cannonical	CD8A	1	1
T-cells	cannonical	CD8B	0	0
T-cells	cannonical	GZMB	0	0
T-cells	cannonical	IL7R	1	0
T-cells	cannonical	NKG7	1	0
T-cells	cannonical	TRBC1	0	0

CellType	CellState	Gene	Cell Type	Cell State
T-cells	CD4_naive	CCR7	0	1
T-cells	CD4_naive	SELL	0	1
T-cells	CD4_PLCG2	CD40LG	0	0
T-cells	CD4_PLCG2	PLCG2	0	0
T-cells	CD4_Th1	CCR6	0	0
T-cells	CD4_Th1like	PGAP1	0	0
T-cells	CD4_Treg	CTLA4	0	0
T-cells	CD4_Treg	FOXP3	0	0
T-cells	CD4_Treg	TBC1D4	0	0
T-cells	CD8_TEM	CRTAM	0	0
T-cells	CD8_TEM	EOMES	0	1
T-cells	CD8_TEM	GZMK	0	1
T-cells	CD8_TEM	TNFRSF9	0	1
T-cells	CD8_TRM	AUTS2	0	0
T-cells	CD8_TRM	ITGA1	0	1
T-cells	CD8_TRM	KLRC1	0	1
T-cells	CD8_ZNF683	ZNF683	0	1
T-cells	GD	CCDC57	0	0
T-cells	GD	GPCPD1	0	0
T-cells	NK	FCER1G	0	1
T-cells	NK	KLRF1	0	1
T-cells	NK/ILCs	TNFRSF18	0	0
T-cells	NK/ILCs	TRDC	0	0
T-cells	NKT	GNLY	0	0
T-cells	NKT	KLRG1	0	0
T-cells	t_prol	CENPF	0	0
T-cells	t_prol	ZWINT	0	0
T-cells	T-cells	ARHGAP15	0	0
T-cells	T-cells	ELF1	0	0
T-cells	T-cells	IKZF1	0	0
T-cells	T-cells	PRDM1	0	0
T-cells	T-cells	PTPRC	0	0
T-cells	T-cells	RUNX2	0	0
T-cells	T-cells	SKAP1	0	0
T-cells	T-cells	TCF7L2	0	0
T-cells	T-cells	THEMIS	0	0
T-cells	T-cells	ZNF831	0	0
vas	cannonical	AQP1	1	0
vas	cannonical	CSF3	0	0
vas	cannonical	PGF	0	0
vas	vas	BTNL9	1	0
vas	vas	IRF7	1	0
vas	vas	MECOM	0	0
vas	vas	PTPRB	0	0
vas	vas	SMAD1	0	0

CellType	CellState	Gene	Cell Type	Cell State
vas	vas-arterial	GJA4	0	1
vas	vas-arterial	HEY1	1	1
vas	vas-arterial	IGFBP3	0	0
vas	vas-arterial	SOX17	1	1
vas	vas-capillary	CA4	0	1
vas	vas-capillary	RGCC	1	1
vas	vas-veinous	ACKR1	1	1
vas	vas-veinous	RAMP3	0	1
vas	vas-veinous	SELE	0	0
vas	vas-veinous	SELP	1	1

Supplementary Table 12 – Custom Targeted Gene Panel for smFISH (MERFISH)

This table lists the custom panel of 266 genes that were selected to distinguish a subset of cell types and cell states identified by top marker genes expressed in the scRNA-seq data. The table lists the cell types, cell state and gene name, and also shows which markers were used to identify cell types and cell states in the final annotation analysis after cell segmentation.