



Figure S1 Flowchart of selecting blood samples. There were 54 patients with complete US imaging data enrolled in this study. Those who refused breast surgery, breast biopsy, gene detection, or those who had any other cancers were excluded from our study; the remaining 18 patients were included. A further eight blood samples were removed due to unqualified quality, resulting in sample disqualification. In total, 10 blood samples were successfully subjected to WGS for ctDNA. US, ultrasound; WGS, whole-genome sequencing; ctDNA, cell-free tumor DNA.

Table S1 The QC of WGS data

Barcode	Total raw reads (M)	Raw reads Q20 (%)	Raw reads Q30 (%)	Raw data GC (%)	Total clean reads (M)	Clean reads Q20 (%)	Clean reads Q30 (%)	Clean data GC (%)	Percentage of HQ reads (%)	Align rate (%)	Duplication (%)	Usable reads (M)	Usable reads ratio (%)	Usable reads GC (%)	SeqCov	PhyCov	Coverage uniformity (%)
1	96.955	96.12	92.77	49.85	95.196	96.93	93.74	49.60	98.19	98.62	49.43	3.415	3.52	42.36	0.082	0.053	99.67
2	82.099	96.95	93.38	53.68	81.873	97.06	93.54	53.78	99.72	95.46	19.91	32.987	40.18	42.78	0.999	0.614	100
3	83.258	96.72	93.26	43.94	82.788	96.97	93.56	43.65	99.44	94.49	27.42	48.252	57.95	43.34	1.788	1.066	100
4	81.262	96.78	93.34	44.82	80.898	96.97	93.58	44.55	99.55	94.77	24.03	49.413	60.81	44.35	1.787	1.082	100
5	97.281	96.46	93.13	46.07	95.968	97.06	93.85	45.50	98.65	95.84	38.18	32.903	33.82	44.31	0.973	0.58	99.67
6	82.199	96.49	92.87	44.65	81.605	96.81	93.25	44.37	99.28	88.15	27.79	44.023	53.56	43.40	1.732	1.006	100
7	104.009	97.09	93.52	52.92	103.878	97.15	93.63	53.03	99.87	94.74	17.43	6.96	6.69	41.95	0.253	0.16	99.67
8	84.119	96.89	93.42	44.04	83.927	96.99	93.54	43.92	99.77	95.38	20.53	54.139	64.36	43.81	2.297	1.335	100
9	74.311	96.95	93.45	42.90	74.135	97.05	93.58	42.61	99.76	90.50	21.83	24.865	33.46	42.40	1.092	0.653	100
10	82.26	96.86	93.35	44.52	82.105	96.93	93.47	44.19	99.81	97.27	20.85	47.774	58.08	43.68	1.53	1.047	100

QC, quality control; WGS, whole-genome sequencing.

Table S2 SWE values and the expression of α -SMA of 10 patients

Patient	Group	Pathologic results	E _{mean} (kPa)	α -SMA expression
1	1	Breast FAs	31.35	15.90
2	1	Breast FAs	30.46	18.87
3	1	Breast FAs	38.78	16.98
4	2	Breast invasive carcinoma	109.41	20.55
5	2	Breast invasive carcinoma	106.84	19.63
6	2	Breast invasive carcinoma	142.31	22.79
7	3	Breast invasive carcinoma	189.74	20.65
8	3	Breast invasive carcinoma	216.15	24.27
9	3	Breast invasive carcinoma	188.84	25.42
10	3	Breast invasive carcinoma	226.17	19.14

FA, fibroadenoma; SWE, shear wave elastography; α -SMA, alpha-smooth muscle actin.**Table S3** CV of RCs of every 10 k bin across samples and autosomes

Chromosome	1	2	3	4	5	6	7	8	9	10
Chr1	1.614	2.857	2.555	2.566	2.888	2.324	6.955	2.186	3.211	3.492
Chr2	2.971	3.244	3.624	3.385	4.011	3.041	8.661	3.142	3.276	3.393
Chr3	1.125	0.317	0.326	0.345	0.392	0.331	0.86	0.31	0.297	0.31
Chr4	1.325	2.826	3.772	3.189	3.236	2.673	4.335	2.902	3.413	2.475
Chr5	0.989	0.597	0.554	0.491	0.547	0.407	1.11	0.417	0.5	0.427
Chr6	1.048	1.733	2.605	1.786	1.934	1.359	2.844	1.138	3.496	2.266
Chr7	1.104	1.565	1.974	2.022	2.06	1.588	2.923	1.624	2.306	3.071
Chr8	1.348	1.189	1.117	1.116	1.071	1.265	5.073	1.078	1.125	1.228
Chr9	1.15	2.169	1.978	1.961	2.021	1.57	3.346	1.723	2.275	2.374
Chr10	1.492	4.274	5.213	3.677	4.79	4.34	7.298	3.962	4.922	3.719
Chr11	1.148	2.022	1.211	2.214	2.457	1.341	3.322	1.57	1.813	1.806
Chr12	1.098	0.361	0.371	0.367	0.41	0.341	3.699	0.358	0.358	0.347
Chr13	1.188	0.231	0.245	0.267	0.315	0.255	1.081	0.259	0.236	0.252
Chr14	1.085	0.364	0.366	0.393	0.396	0.34	1.654	0.351	0.344	0.369
Chr15	1.239	0.226	0.247	0.284	0.465	0.259	0.932	0.3	0.308	0.267
Chr16	2.169	3.502	3.127	4.565	3.898	3.145	6.638	2.592	4.089	3.199
Chr17	0.995	2.63	2.541	2.285	2.293	2.603	4.809	2.454	2.597	2.986
Chr18	1.505	5.444	5.11	5.457	5.281	4.831	6.479	5.176	5.973	5.324
Chr19	1.408	2.231	2.11	2.038	2.162	2.072	4.454	1.529	2.325	2.648
Chr20	0.897	0.832	1.063	0.825	0.841	0.773	1.279	0.837	1.057	0.735
Chr21	4.254	1.538	1.884	1.537	1.662	1.609	11.182	1.55	1.635	1.434
Chr22	1.07	0.27	0.261	0.256	0.314	0.294	0.882	0.269	0.293	0.321

CV, coefficient of variation; RC, read count.