Table S1. Somatic copy number alterations (SCNAs) in TCGA breast tumors (n=886) that differ significantly by race.

Chromosome number: base pair position start-end*	Length in megabases	SCNA type	Cytoband	Beta Coefficient†	SE	T-statistic	P-value
3:154227886-169450068	15.22	Amp	q25.2-q26.2	0.026	0.016	1.61	0.107
3:169450069-171879450	2.43	Amp	q26.2-q26.31	0.035	0.019	1.91	0.057
4:109489756-109493251	0.00	Del	q25	-0.017	0.009	-1.79	0.074
4:176731730-182822332	6.09	Del	q34.2-q34.3	-0.034	0.018	-1.86	0.064
4:182822333-191154275	8.33	Del	q34.3-q35.2	-0.031	0.013	-2.37	0.018
4:3369932-3431340	0.06	Del	p16.3	-0.032	0.017	-1.89	0.059
5:160562330-165741478	5.18	Del	q34	-0.070	0.019	-3.68	0.000
5:51204966-51924477	0.72	Del	q11.2	-0.055	0.020	-2.76	0.006
5:51924478-88003401	36.08	Del	q11.2-q14.3	-0.083	0.019	-4.34	0.000
5:88003402-114971116	26.97	Del	q14.3-q22.3	-0.087	0.019	-4.67	0.000
6:105142579-105544119	0.40	Amp	q16.3-q21	0.066	0.028	2.34	0.020
6:105544120-107830797	2.29	Amp	q21	0.074	0.031	2.42	0.016
6:107830798-108690475	0.86	Amp	q21	0.061	0.030	2.00	0.046
6:152481982-170769426	18.29	Del	q25.1-q27	0.038	0.022	1.79	0.075
6:170769427-171115066	0.35	Del	q27	0.019	0.009	2.18	0.029
6:21312556:22614340	1.30	Amp	p22.3	0.035	0.021	1.70	0.089
6:2232105-4756175	2.52	Del	p25.3-p25.1	0.050	0.021	2.41	0.016
6:22614341-22817848	0.20	Amp	p22.3	0.036	0.020	1.75	0.080
6:6754109-21312555	14.56	Amp	p25.1-p22.3	0.057	0.019	3.00	0.003
6:69393208-83933646	14.54	Del	q12-q14.2	0.036	0.020	1.86	0.063
6:99929476:152481981	52.55	Del	q16.2-q25.1	0.037	0.021	1.74	0.082
7:151140793-151976410	0.84	Del	q36.1	0.035	0.021	1.71	0.088
7:151981957:153770265	1.79	Del	q36.1-q36.2	0.035	0.020	1.76	0.079
7:32999602-33047676	0.05	Amp	p14.3	-0.034	0.015	-2.28	0.023
8:1-37953889	37.95	Del	p23.3-p11.23	-0.045	0.027	-1.67	0.095
8:61177663-146364021	85.19	Amp	q12.1-q24.3	0.070	0.028	2.51	0.012
9:1-18127677	18.13	Del	p24.3-p22.2	0.035	0.021	1.70	0.090

Table S1. Somatic copy number alterations (SCNAs) in TCGA breast tumors (n=886) that differ significantly by race.

Chromosome number: base pair position start-end*	Length in megabases	SCNA type	Cytoband	Beta Coefficient†	SE	T-statistic	P-value
9:22147714-30113862	7.97	Del	p21.3-p21.1	0.057	0.024	2.45	0.015
10:1-3730104	3.73	Amp	p15.3-p15.2	0.072	0.018	3.99	0.000
10:3730105-6398980	2.67	Amp	p15.2-p15.1	0.081	0.021	3.91	0.000
10:61852107-62575303	0.72	Amp	q21.2	0.053	0.021	2.57	0.011
10:6398981-14643449	8.24	Amp	p15.1-p13	0.086	0.020	4.30	0.000
11:1-766166	0.77	Del	p15.5	-0.021	0.008	-2.64	0.008
11:64592727-65674138	1.08	Del	q13.1	-0.038	0.018	-2.14	0.033
11:65766045-66641072	0.88	Amp	q13.1-q13.2	-0.053	0.022	-2.46	0.014
11:66641073-68027183	1.39	Amp	q13.2	-0.048	0.025	-1.93	0.054
11:68027184-68168228	0.14	Amp	q13.2	-0.075	0.027	-2.77	0.006
11:74235492-135006515	60.77	Del	q13.4-q25	-0.037	0.019	-1.94	0.052
11:766167-11684113	10.92	Del	p15.5-p15.3	-0.047	0.018	-2.65	0.008
12:11703865-12303099	0.60	Amp	p13.2	0.040	0.025	1.62	0.105
12:1-2306551	2.31	Amp	p13.33	0.024	0.013	1.78	0.076
13:30777606-30978054	0.20	Amp	q12.3	-0.050	0.024	-2.11	0.035
13:31949050-38243466	6.29	Del	q12.3-q13.3	-0.044	0.022	-2.03	0.042
13:38243467-52321574	14.08	Del	q13.3-q14.3	-0.051	0.022	-2.34	0.020
13:52321575-59628349	7.31	Del	q14.3-q21.2	-0.048	0.022	-2.23	0.026
14:66905865-67198116	0.29	Del	q23.3	-0.054	0.018	-2.93	0.004
14:67198117-70999022	3.80	Del	q23.3-q24.2	-0.054	0.019	-2.88	0.004
14:70999023-97705236	26.71	Del	q24.2-q32.2	-0.036	0.018	-2.02	0.043
15:1-37513451	37.51	Del	p13-q14	-0.013	0.007	-1.88	0.060
15:37513452-43466475	5.95	Del	q14-q15.2	-0.046	0.018	-2.53	0.012
16:55240635-58196161	2.96	Del	q12.2-q21	0.046	0.025	1.88	0.060
16:58196162-90354752	32.16	Del	q21-q24.3	0.066	0.023	2.83	0.005
17:45603013-45969605	0.37	Amp	q21.32	-0.039	0.023	-1.73	0.084
19:1-4677580	4.68	Del	p13.3	-0.035	0.015	-2.37	0.018

Table S1. Somatic copy number alterations (SCNAs) in TCGA breast tumors (n=886) that differ significantly by race.

Chromosome number: base pair position start-end*	Length in megabases	SCNA type	Cytoband	Beta Coefficient†	SE	T-statistic	P-value
19:29282210-29315606	0.03	Amp	q12	0.046	0.022	2.12	0.035
19:29315607-31229637	1.91	Amp	q12	0.076	0.022	3.49	0.001
19:31229638-36069787	4.84	Amp	q12-q13.12	0.053	0.016	3.20	0.001
19:55573038-58776089	3.20	Amp	q13.42-q13.43	-0.032	0.018	-1.75	0.081

Abbreviations: SCNA=somatic copy number alteration; Del=deletion; Amp=amplification; AA=African American; EA=European American; SE=standard error of the beta coefficient.

*Based on human genome build hg19

† Beta coefficient for the "race" term in the linear model "cnAUC=race+age+tumor pathology"

In amplified regions, a positive beta coefficient signifies a greater degree of amplification among AAs relative to EAs.

In deletion regions, a negative beta coefficient signifies a greater degree of DNA loss among AAs relative to EAs.