SUPPLEMENTARY MATERIALS

Supplementary Table 1. Patient demographics and somatic gene alteration patterns by race and ethnicity.

	NH White N=611	**Hispanic** N=159	**NH Asian** N=154	**NH Black** N=95	**P-value***
Sex: Male	59.7% (365/611)	54.1% (86/159)	50.6% (78/154)	55.8% (53/95)	0.17
Sequencing age: Years, median [IQR]	64 [54;72]	58 [47;67]	59 [51;71]	62 [52;71]	**<0.001**
Early-onset**	16.4% (100/611)	32.1% (51/159)	23.4% (36/154)	17.9% (17/95)	**<0.001**
Genes:					
ΔTP53	54.2% (324/598)	47.8% (76/159)	59.7% (92/154)	57.8% (52/90)	0.150
ΔARID1A	20.2% (119/588)	20.7% (23/111)	17.6% (27/153)	19.0% (16/84)	0.346
ΔCDH1	21.6% (127/587)	16.7% (19/114)	19.5% (30/154)	24.4% (21/86)	0.497
ΔKMT2D	12.9% (75/583)	18.2% (20/110)	11.8% (18/153)	16.0% (13/81)	0.333
ΔPIK3CA	11.0% (66/598)	12.6% (20/159)	5.2% (8/154)	14.4% (13/90)	0.051
ΔKRAS	11.2% (67/598)	10.1% (16/158)	5.8% (9/154)	5.6% (5/90)	0.086
***ERBB2*:AMP**	**9.8% (53/543)**	**13.9% (14/101)**	**8.1% (11/136)**	**11.0% (9/82)**	**<0.001**
ΔAPC	9.0% (53/591)	3.4% (4/116)	6.5% (10/154)	10.3% (9/87)	0.173
***CCNE1*:AMP**	8.4% (46/543)	4.0% (4/101)	3.7% (5/136)	15.9% (13/82)	**<0.001**
ΔATM	7.6% (45/591)	9.6% (11/115)	6.5% (10/154)	7.9% (7/89)	0.830
ΔERBB4	7.1% (42/593)	5.2% (6/115)	5.8% (9/154)	5.6% (5/89)	0.882
ΔERBB3	7.3% (43/589)	4.5% (7/155)	5.2% (8/153)	4.8% (4/84)	0.658†
ΔNOTCH1	7.4% (44/595)	5.2% (6/116)	5.8% (9/154)	5.6% (5/90)	0.795
ΔBRCA2	7.2% (42/587)	4.5% (5/111)	8.5% (13/153)	10.7% (9/84)	0.383
ΔSMARCA4	7.0% (41/583)	9.0% (10/111)	5.2% (8/153)	8.4% (7/83)	0.602

ΔARID1B	7.4% (42/569)	7.5% (8/107)	4.0% (6/151)	4.2% (3/72)	0.420†
ΔSMAD4	5.7% (34/597)	8.5% (10/117)	6.5% (10/154)	3.3% (3/90)	0.468†
ΔGNAS	4.8% (29/598)	2.5% (4/157)	2.6% (4/154)	3.3% (3/90)	0.471†
ΔCDKN2A	4.2% (25/598)	2.5% (4/158)	1.3% (2/154)	1.1% (1/90)	0.196†
ΔPBRM1	6.0% (34/568)	0.9% (1/110)	6.5% (10/153)	5.1% (4/79)	0.110†
Sequencing Center*: **MSK**	59.4% (349/588)	13.6% (80/588)	19.0%(112/588)	8.0% (47/588)	**<0.001**
DFCI	74.5% (196/263)	7.6% (20/263)	9.9% (26/263)	8.0% (21/263)	
Other	39.3% (66/168)	35.1% (59/168)	9.5% (16/168)	16.1% (27/168)	

NH, non-Hispanic; N, number; AMP, amplification; Δ, non-silent mutation; MSK, Memorial Sloan Kettering; DFCI, Dana Farber Cancer Institute.

*Bold indicates P-value < 0.05.

**Early-onset gastric cancer is defined as individuals age < 50 years at sequencing.

***Other sequencing centers include: Herbert Irving Comprehensive Cancer Center, Columbia University (n=5), Duke Cancer Institute (n=27), Johns Hopkins Sidney Kimmel Comprehensive Cancer Center (n=12), The University of Texas MD Anderson Cancer Center (n=5), Providence Health & Services Cancer Institute (n=1), Swedish Cancer Institute (n=2), University of California-San Francisco (UCSF Helen Diller Family Comprehensive Cancer Center) (n=22), Vall D'Hebron Institute of Oncology (n=50), Vanderbilt-Ingram Cancer Center (n=24), Wake Forest University Health Sciences, Wake Forest Baptist Medical Center (n=12), and Yale (n=8).

† The Fisher's exact test was conducted; otherwise, the chi-square test was performed.

Supplementary Table 2. Driver alteration patterns by race and ethnicity*.

Genes:	NH White N=611	NH Asian N=154	Hispanic N=159	NH Black N=95	P-value
ΔTP53	54.4% (322/592)	59.7% (92/154)	47.2% (75/159)	58% (51/88)	0.135
ΔARID1A	19.3% (109/564)	13.7% (21/153)	15.1% (23/152)	18.8% (15/80)	0.330
ΔCDH1	12.2% (70/572)	9.2% (14/153)	10.1% (11/109)	15.9% (13/82)	0.434
ΔKMT2D	8.5% (47/555)	6.8% (10/147)	11.7% (12/103)	10.4% (8/77)	0.552
ΔPIK3CA	10.7% (61/570)	4.6% (7/153)	11.6% (17/147)	14% (12/86)	0.069
ΔKRAS	11.7% (67/571)	5.8% (9/154)	11% (16/146)	5.8% (5/86)	0.086
ΔAPC	8% (43/538)	5.2% (7/134)	3% (3/100)	5.6% (4/72)	0.278†
ΔATM	4.8% (26/546)	5% (7/140)	3.7% (4/107)	5.3% (4/75)	0.945†
ΔERBB4	1.1% (6/566)	1.3% (2/152)	0% (0/103)	0% (0/76)	0.714†
ΔERBB3	4.1% (23/559)	4.2% (6/144)	3.5% (5/142)	1.4% (1/71)	0.809†
ΔNOTCH1	1.5% (8/531)	0% (0/140)	0% (0/100)	4.2% (3/71)	0.051†
ΔBRCA2	4.1% (22/539)	2.9% (4/140)	2% (2/100)	4% (3/75)	0.801†
ΔSMARCA4	3.4% (18/535)	2.1% (3/140)	8% (8/100)	4.1% (3/73)	0.124†
ΔARID1B	3% (17/558)	2.1% (3/145)	5.9% (6/101)	2.8% (2/71)	0.392†
ΔSMAD4	5.6% (31/556)	6% (9/150)	8.8% (9/102)	4.1% (3/73)	0.562†
ΔGNAS	4.3% (24/552)	2% (3/147)	2.7% (4/146)	1.3% (1/76)	0.433†
ΔCDKN2A	6.2% (20/324)	1.3% (1/78)	2.8% (3/107)	2.3% (1/44)	0.209†
ΔPBRM1	4% (21/530)	5.7% (8/140)	1% (1/100)	2.8% (2/71)	0.300†

NH, non-Hispanic; N, number; AMP, amplification; Δ, non-silent mutation.

*Driver alterations were included as oncogenic/likely oncogenic/resistance in OncoKB, or pathogenic/likely pathogenic in ClinVar.

† The Fisher's exact test was conducted; otherwise, the chi-square test was performed.

Supplementary Table 3. Stratified analyses by sequencing age of *ERBB2* amplification patterns by race/ethnicity: GENIE v15.

Sequencing age	NH White	NH Asian	Hispanic	NH Black	P-value*
Early-onset (< 50 years)	6.5% (6/93)	6.3% (2/32)	8.3% (3/36)	7.7% (1/13)	**0.013**†
Late-onset (50+ years)	10.4% (47/450)	8.7% (9/104)	16.9% (11/65)	11.6% (8/69)	**<0.001**

NH, non-Hispanic; N, number; AMP, amplification.

*Fisher's exact test. Bold indicates P-value < 0.05.

† The Fisher's exact test was conducted; otherwise, the chi-square test was performed.

Supplementary Table 4. Multivariate logistic regression models for *ERBB2* amplification: GENIE v15.

	Gastric adenocarcinoma patients (n=1019)	
Race/Ethnicity	**OR (95% CI)**	***P****
NH White	Ref	
Hispanic	**2.52 (1.20-5.33)**	**0.02**
NH Black	0.84 (0.34-2.11)	0.72
NH Asian	0.86 (0.39-1.88)	0.70

NH, non-Hispanic; N, number; AMP, amplification.

Multivariable logistic regression analyses were adjusted for age, sex, histological subtype, and sequencing center.

*Bold indicates P-value < 0.05