Gene	Coding Mutations Detected
AKT1	E17K
ALK	C1156Y, L1196M
BRAF	D594G/V, G469S/E/A/V, L597Q/V, V600E/K/M
DDR2	C580Y, D125Y, G253C, G505S, G774E/V, I120M, I638F, L239R, L63V, T765P
EGFR	R108K, T263P, A289V, G598V, E709K/H, E709A/G/V, G719S/C/A/D, G719S/C/A/D, M766_A767insAI, D761Y/N, S768I, R776C/H, V769_D770insASV, V769_D770insCV, D770_N771>AGG/V769_D770insASV/V769_D770insASV, D770_N771insG, N771_P772>SVDNR, P772_H773insV, H773>NPY, H773_V774insNPH/PH/H, V774L, V774_C775insHV, T790M, L858R/M, L861Q, E746_T751del, E746_A750del, E746_T751del, E746_T751del, S752D, L747_E749del, L747_T750del, L747_S752del, L747_T751del, L747_S752del, P753S, A750P, T751A, T751P, T751I, S752I/F, S752_I759del, L747_Q ins, E746_T751del, I ins (combined), E746_A750del, T751A (combined), L747_E749del, A750P (combined), L747_T750del, P ins (combined), L747_S752del, Q ins (combined), T854A
EPHA3	A435S, D446Y, S449F, D806N, G187R, G518L, K761N, G766E, M269I, N379K, N85S, S229Y, T166N, T37K, T393K, W250R
EPHA5	D493Y, G582E, M1034I, N1032S, R1007Q, S566Y, S810I, T856I
ERBB2	M774_A775insAYVM, A775_G776insAYVM
FGFR4	P672T, H192fs*19
JAK2	L609S, P503L, R1122P, Y931C
KRAS	G12S/V/F/R/A/C/D, G13C/S/A/V/D, Q61L/R/P/H/E/K
MAP2K1	D67N, K57N, Q56P
STK11	A347fs*13, A43_L50del6, D327fs*10, E120*, E165*, E223*, E70*, E70fs*26, F354L, G163C, G188fs*99, G196V, G56fs*4, G56W, G91L, H174R, I26fs*25, K191*, K78E, L285Q, L50_D53del4, M51fs*14, P179L, Q123R, Q137*, Q159*, Q170*,Q220*, Q37L, R426W, R86G, V197fs*69, V236fs*30, Y272Y
MET	N375S, 982_1028del47
NOTCH1	H2276fs*79, D1643H, R2328W, T1997M, V1671I, V2444fs*35
NRAS	Q61E/K/H/L/R/P
NRF2	D29H, D77N/A, E79Q/K/G, G31A, G81D, R34Q
NTRK1	Q80*, R119H, S326R
NTRK2	Q666R, C45F, G261R, L138F, L670M, L755L
NTRK3	I769N, L152I, L248M, L270M, L336Q, S184C, T283K, V307L, R271F
PIK3CA	E542Q/K, E545Q/K, H1047Y/R/L
PTCH1	R1308G, R682L, S1326fs*46
PTEN	R233*
PTPN11	E76V
PTPRD	S1703R, T337A, V483E
TP53	G245C/S, G245D/V, R158C/G/L/P, R175L/H, R248G/L/Q/W, R249S/W/M, R273C/H/L/P, R282G/W, V157F, Y163C, R175L/H, Y220C

Supplementary Table 1. List of gene-specific coding mutations analyzed. Abbreviations: fs, frame shift; ins, insertion; del, deletion; *, nonsense. Amino Acids: A, Alanine; R, Arginine; N, Asparagine; D, Aspartate; C, Cysteine; E, Glutamate; Q, Glutamine; G, Glycine; H, Histidine; I, Isoleucine; L, Leucine; M, Methionine; F, Phenylalanine; P, proline; S, Serine; T, Threonine; W, Tryptophan; Y, Tyrosine; V, Valine.

Supplementary Table 2. Logistic regression for odds ratio of having 1 or more mutations by race, adjusted for covariates.

Variable	Odds ratio	Lower 95% CI	Upper 95% CI	P value
Race Black	0.582	0.363	0.933	0.025
Gender Female	1.815	1.200	2.747	0.005
Age	1.008	0.989	1.028	0.411
StageII	1.379	0.827	2.299	0.218
StageIII,IV	0.986	0.586	1.658	0.957
Histology NSCLC	0.574	0.302	1.091	0.090
Histology Squamous	0.583	0.374	0.909	0.017
Smoke Never	1.083	0.517	2.268	0.834
Smoke Unknown	1.303	0.665	2.553	0.440

Reference groups: stageI, adenocarcinoma or smoker.

Supplementary Table 3. SNP allele frequency in NSCLC compared to NHLBI ESP population database.

	Gene variant	Allele Frequency NHLBI ESP	Allele Frequency NSCLC Current Study	P value
Blacks:	*MET* (N375S)	26/3854(1%)	1/274(0%)	1.000
	NOTCH1 (V1671I)	56/3128(2%)	12/274(4%)	0.010
	STK11 (Y272Y)	293/3938(7%)	21/274(8%)	0.905
Whites:	*MET* (N375S)	151/8278(2%)	19/670(3%)	0.076
	NOTCH1 (V1671I)	2/6752(0%)	0/670(0%)	1.000
	STK11 (Y272Y)	6/8258(0%)	1/670(0%)	0.421

Abbreviations: SNP, single nucleotide polymorphism; NSCLC, non-small cell lung cancer; NHLBI ESP, National Institutes of Health Heart, Lung and Blood Institute (NHLBI) Grand Opportunity (GO) Exome Sequencing 6,500 Project

Supplementary Table 4. Frequency of specific mutations identified in tumor tissue among 472 patients by histology.

gene	variant	Adeno	Squamous	NSCLC	P value
KRAS	G12C	22 (9%)	1 (1%)	2 (4%)	<0.001
KRAS	G12V	10 (4%)	0 (0%)	1 (2%)	0.016
TP53	R249S	0 (0%)	4 (2%)	0 (0%)	0.029
PIK3CA	E545K	0 (0%)	4 (2%)	0 (0%)	0.029
EGFR	E746-A750del	11 (4%)	1 (1%)	0 (0%)	0.036