Supplemental Digital Content 2. *FLT1* rs9582036 and *KRAS* rs10505980 genotype calls from squamous NSCLC genotyped samples from The Cancer Genome Atlas[1]. Out of the five SNPs passing false discovery rate (FDR) for association with relapse-free survival (RFS) in the initial cohort and genotyped in both patient cohorts, *FLT1* rs9582036 and *KRAS* rs10505980 were genotyped in matching tumor/germline paired DNAs. Data were then available from 288 and 282 patients with squamous NSCLC, respectively, genotyped using the Affymetrix 6.0 SNP chip. Of the 288 patients with genotype data for *FLT1* rs9582036, 183 were White (self-reported), 14 were African American, 5 were Asian, and the race was not available for 86; of the 282 patients with genotype data for *KRAS* rs10505980, 179 were White, 13 were African American, 5 were Asian and the race was not available for 85. The concordance between genotype calls in the germline and tumor DNA for *FLT1* rs9582036 was 94% (93% in Whites only) and for *KRAS* rs10505980 was 95% (95% in White only). In White patients only, the alleles are in Hardy-Weinberg equilibrium (HWE, $p<0.01$) for both tumor and germline for *FLT1* rs9582036 (tumor: p 0.042; germline: p 0.84) and for *KRAS* rs10505980 (tumor: p 0.052; germline: p 0.23). Discordance between genotype call in the tumor and germline included 18 (7 AC→CC, 9 AC→AA, 2 AA→AC) and 15 (3 GA→GG, 9 GA→AA, 1 GG→AA, 1 GG→GA, 1 AA→GA) changes between germline and tumor at *FLT1* rs9582036 and *KRAS* rs10505980, respectively. Of the 18 samples with discordant rs9582036 genotype calls, no germline samples displayed a DNA copy number imbalance at the rs9582036 locus. Recurrent deletion of the proximal end of chromosome 13q (encompassing rs9582036) has been previously observed in NSCLC[2-4], and here 5 (31%, 2 AC→CC and 3 AC→AA) of the 18 tumor samples with discordant genotype calls display heterozygous deletion at the rs9582036 locus. Of the 15 samples with discordant rs10505980 genotype calls, no germline samples displayed DNA copy number imbalance at the rs10505980 locus. Gain of chromosome 12p and the *KRAS* locus has been previously reported in NSCLC[2, 4], and here 6 (50%, 6 GA→AA) of the 15 discordant tumor samples displayed copy number gain (3-4 copies) at the rs10505980 locus. Discordant genotype calls can be ascribed, in part, to the presence of tumor DNA copy number imbalance.

***FLT1* - rs9582036**								
	AA	AC	CC	Total	%AA	%AC	%CC	Total
Tumor	164	88	36	288	0.57	0.31	0.12	1
Germline	157	102	29	288	0.55	0.35	0.10	1
Concordance				270				0.94
***KRAS* - rs10505980**								
	GG	GA	AA	Total	%GG	%GA	%AA	Total
Tumor	104	121	57	282	0.37	0.43	0.20	1
Germline	103	131	48	282	0.37	0.46	0.17	1
Concordance				267				0.95
***FLT1* - rs9582036, Whites only**								
	AA	AC	CC	Total	%AA	%AC	%CC	Total
Tumor	111	56	16	183	0.60	0.31	0.09	1
Germline	108	64	11	183	0.59	0.35	0.06	1
Concordance				171				0.93
***KRAS* - rs10505980, Whites only**								
	GG	GA	AA	Total	%GG	%GA	%AA	Total
Tumor	70	73	36	179	0.39	0.41	0.20	1
Germline	70	77	32	179	0.39	0.43	0.18	1
Concordance				170				0.95

[1]Network CGAR: Comprehensive genomic characterization of squamous cell lung cancers. *Nature* 2012; 489:519-25.
[2]Weir BA, Woo MS, Getz G, et al. Characterizing the cancer genome in lung adenocarcinoma. *Nature* 2007;450(7171): 893-8.
[3]Tonon G, Wong KK, Maulik G, et al. High-resolution genomic profiles of human lung cancer. *Proc Natl Acad Sci U S A* 2005;102(27): 9625-30.
[4]Newnham GM, Conron M, McLachlan S, et al. Integrated mutation, copy number and expression profiling in resectable non-small cell lung cancer. *BMC Cancer* 2011;11:93.