







Figure 5S.

REMARK diagram detailing patient cohorts with evaluable baseline cfDNA used in the survival analysis for the $\bf A$, squamous and $\bf B$, non-squamous populations. $\bf C$, Whole-genome CNV landscape of 12 baseline cfDNA samples from non-squamous NSCLC patients with tumor fraction $\geq 10\%$. Top track shows CNV regions of significantly high frequency (q-value <0.05%). Bottom tracks show the CNV pattern of each sample. Heatmap density represents CNV log2 ratios between cfDNA sample and the normal reference, ranging between -0.5 to 0.5. $\bf D$, Tumor fraction of all baseline cfDNA of squamous (n = 152) and non-squamous (n = 73) NSCLC patients. $\bf E$, CNV frequency in squamous baseline cfDNA of genes know to be associated with NSCLC.