**Supplementary Table Legends**

**Supplementary Table 1: Detailed assessment of each of the 282 patients**. For each of the 282 patients, genomic testing outcome for each modality and each of the eight genomic biomarkers is outlined, as well as *KRAS* and tissue assessed PD-L1 expression. “-“ denotes where mutations in these genes were not assessed.

**Supplementary Table 2: Comparison of tissue versus cfDNA results for biomarkers in newly diagnosed metastatic NSCLC.** For *EGFR*, four patients had baseline *EGFR* tissue results that were “negative”. Upon review, patients received targeted *EGFR* testing that did not assess for the mutation identified in cfDNA. Therefore, they were coded as “not assessed” in these expanded tables but were “negative” for the primary endpoint.

**Supplementary Table 3:** **Detailed results for patients with positive results.** For all 221 patients with a guideline-recommended biomarker detected in cfDNA or tissue, *KRAS* detected in cfDNA or tissue, or PDL-1 over-expression on tissue

**Supplementary Table 4: Co-occurring guideline-recommended biomarker and PD-L1 overexpression.**

**Supplementary Table 5: Tissue versus cfDNA analysis**

**Supplementary Table 6: Sites and Principal Investigators for the NILE (Non-invasive versus Invasive Lung Evaluation)**