**Supplemental Methods**: DNA Sequencing at Washington University#

Manual dual indexed libraries were constructed with 150-250ng of FFPE derived genomic DNA utilizing the KAPA HTP Library Kit (KAPA Biosystems). Samples were fragmented on the Covaris LE220 instrument targeted 250bp inserts (Duty Factor - 30%; Peak Incident Power (W) – 450; Cycles Per Burst – 200; Treatment Time - 190 seconds).  PCR cycle optimization was performed to prevent over amplification of the libraries. Nine libraries were pooled pre-capture generating a 4.5µg library pool.  The library pool was hybridized with an IDT Gene Pool including the aforementioned 10 genes. The concentration of the captured library pool was accurately determined through qPCR according to the manufacturer's protocol (KAPA Biosystems) to produce cluster counts appropriate for the Illumina MiSeq platform. The libraries were sequenced on a v2 300 cycle flow cell generating 2x150 paired end reads.  Approximately 350Mb of sequence data was generated per sample resulting in greater than 100x mean depth of coverage.

# The McDonnell Genome Institute at Washington University routinely performs sequencing on FFPE-derived DNA for tumor sequencing and a study published from this same institute validated FFPE-derived DNA for Next-Generation Sequencing.13