## Supplemental Methods

### Aqueous Humor and Cell-Free DNA Extraction Technique

Aqueous humor (AH) was extracted via an anterior chamber paracentesis either at the time of diagnosis or as part of the standard safety-enhanced procedure for intravitreal injection of chemotherapy. Paracentesis was performed by using a 32-gauge needle via the clear cornea at the limbus to extract 0.1 ml of AH, which was then stored at -80$^{o}$C without other preservation. Per the manufacturer's instructions, the QIAamp Circulating Nucleic Acid Kit (Qiagen) was used for cell-free DNA (cfDNA) isolation from AH samples.

### Cell-Free DNA Sequencing

We obtained genome-wide somatic copy number alteration (SCNA) profiles from AH and blood cfDNA by shallow whole-genome sequencing, followed by assigning mapped reads to pre-assigned 'bins' across the genome. DNA libraries for sequencing were constructed with QIAseq Ultralow Input Library Kit (Qiagen) for both AH and blood plasma samples. Each library was constructed with a sample barcode to permit pooling of multiple samples on a single Illumina HiSeq (Illumina, San Diego CA) lane using the single-end 50 base pair (bp) protocol for sequencing. All sample libraries were prepared within 72 hours of extraction and sequenced within one month of extraction.

### Data Analysis

Fragment size distribution of cfDNA was determined with Agilent BioAnalyzer 2100 High-sensitivity DNA Assay (High-sensitivity DNA Assay and Kit, Agilent Technologies). SCNAs were considered positive at 20% deflection from a baseline genome (log2-ratio = 0), meaning losses at log2-ratios <-0.2 (ratio of 0.87 or lower) and gains at log2-ratios >0.2 (ratio of 1.15 or higher). Stata/SE 14.2 (StataCorp, College Station, TX, USA) was used for statistical analyses. Due to the small sample size, Fisher's Exact Test was used to analyze the frequency of events in the blood vs. the AH.