Supplementary Materials and Methods

1. Next generation sequencing

DNA was extracted from the tissues using the RecoverAll Multi-Sample Isolation Kit (Thermo Fisher Scientific, Waltham, MA, USA), according to the manufacturer's instructions. Next-generation sequencing library (prepared using, 5–40 ng of DNA) was purified using Agencourt AmpureXP beads (Beckman Coulter, Brea, CA, USA). Quantification was carried out by quantitative polymerase chain reaction using the Ion Universal Quantitation Kit (Thermo Fisher Scientific, Waltham, MA, USA). Sequencing runs were planned on Torrent Suite Software v5.10 (Thermo Fisher Scientific). Libraries were diluted to 50 pM (in batches of five libraries) and loaded onto an Ion 540™ chip using the Ion Chef instrument and then sequenced on an Ion S5XL™ platform (Thermo Fisher Scientific). Raw data were processed automatically on the Torrent Server and aligned with the hg19 reference genome. Sequenced data were subsequently uploaded in BAM format, and variant detection was performed on Ion Reporter Analysis Software v5.20 using the Oncomine Comprehensive Assay Plus (Thermo Fisher Scientific) workflow. The deamination score, which reflects the potential deamination artifacts, was automatically calculated using this workflow. The default limit of detection was set at 5% allelic frequency and adjusted to 10% depending on the deamination score. Variants, including missense or nonsense single nucleotide variants, and indels in exonic locations were listed as detected mutations.