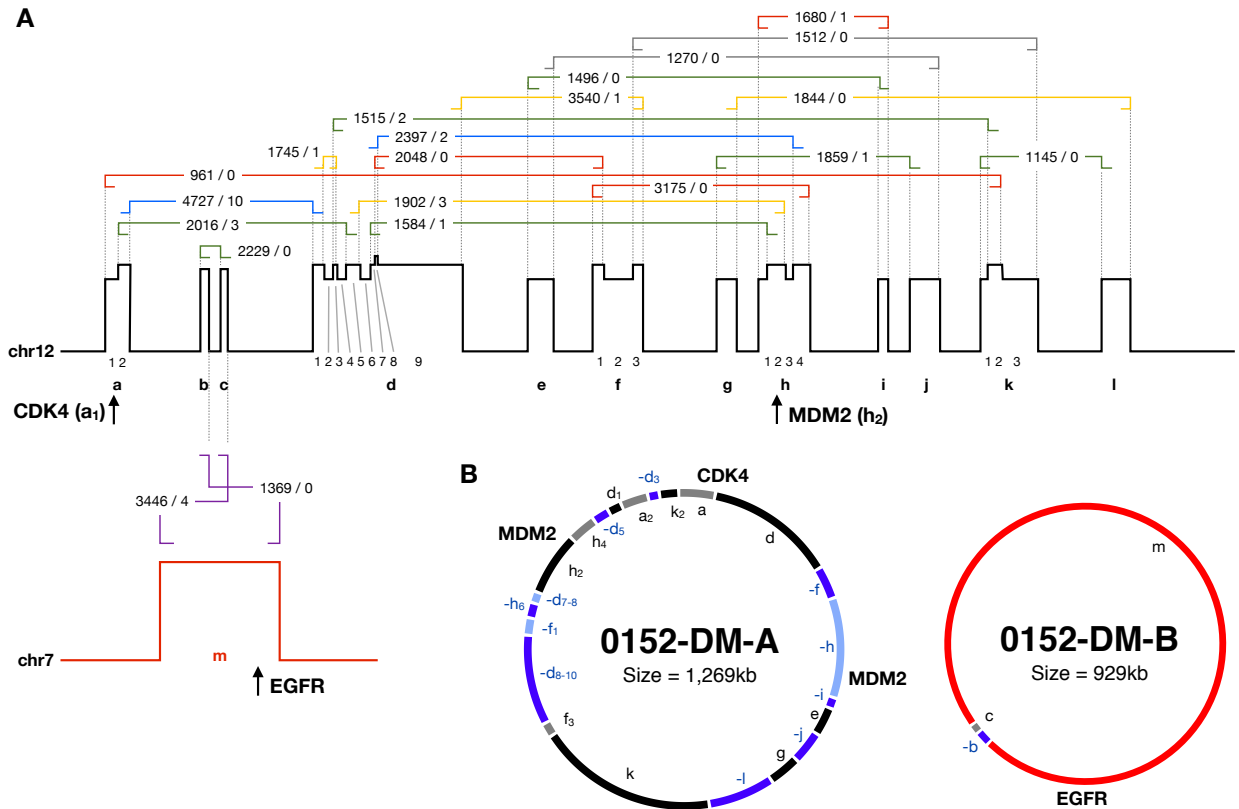
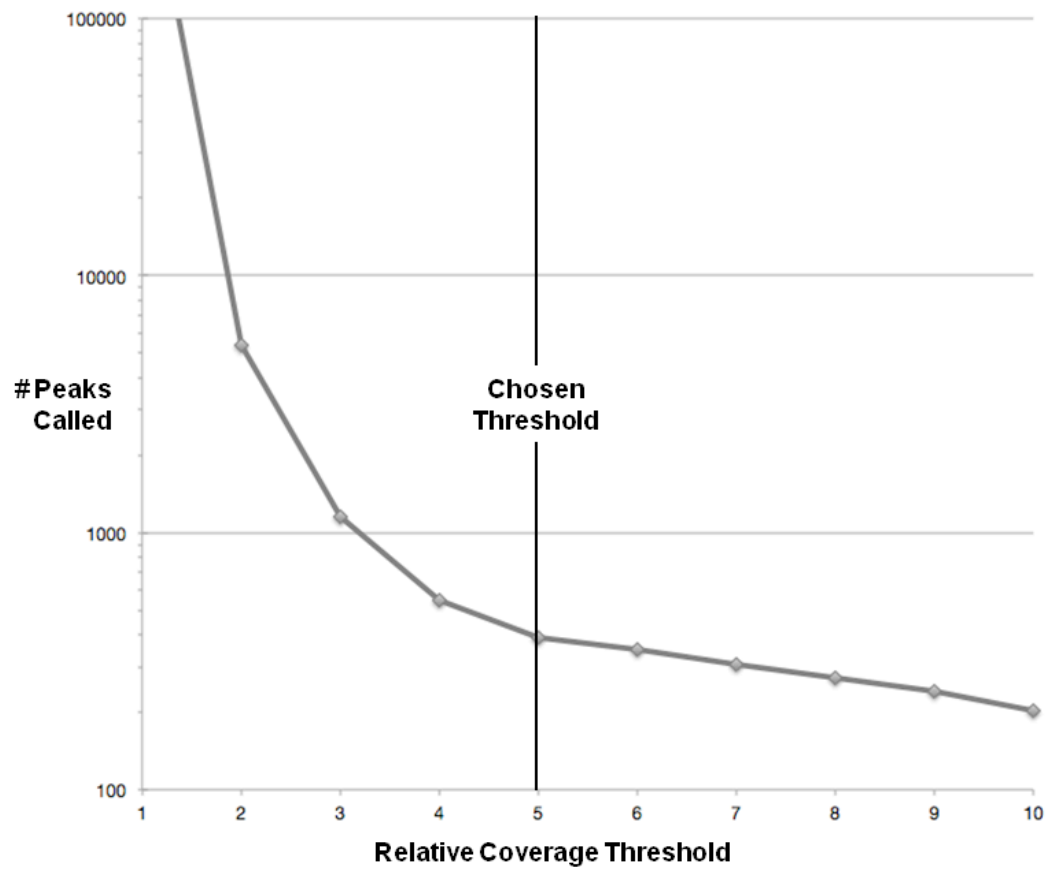


Supplemental Figure 1. Reconstructing circular amplicons. Toy example demonstrating walking the breakpoint graph to reconstruct a rearranged sequence. Starting with segment “a”, we follow the exiting breakpoint 1 to the right, which enters the left-hand side of segment “b.” Continuing to the right, we follow the exiting breakpoint 2 that enters the right-hand side of segment “c.” This breakpoint points to the left, indicating that segment “c” is found in an inverted orientation in the rearranged sequence. The final breakpoint 3 is followed back to the left-hand side of segment “a,” accounting for all extra copies in the copy number. The final solution found is thus “a b –c”.



Supplemental Figure 2. TCGA-GBM-06-0152 harbors 2 circular amplicons. (A) The breakpoint graph of the structural rearrangements and copy number of the double minutes predicted in GBM-06-0152. The numbers correspond to the read support of each breakpoint. (B) The circular structure of the solutions to the breakpoint graph presented in (A), including the gene content and sizes of the two independent double minutes of GBM-06-0152. The structure of 0152-DM-A contains a single copy of CDK4 and two functional copies of MDM2, while the structure of 0152-DM-B features a single copy of EGFR. Note that segment h₃, located within an intron of MDM2, is deleted in the second copy of MDM2.



Supplemental Figure 3: Cumulative number of peaks called in 264 GBM exomes as a function of the tumor vs. matched normal relative coverage threshold used to define a peak.