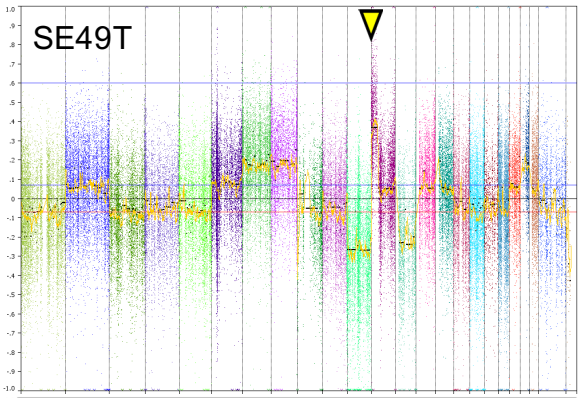
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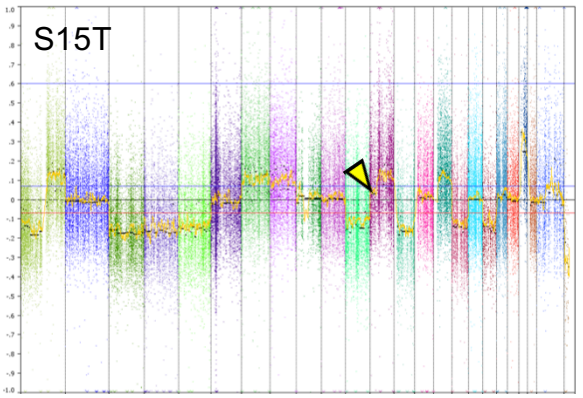
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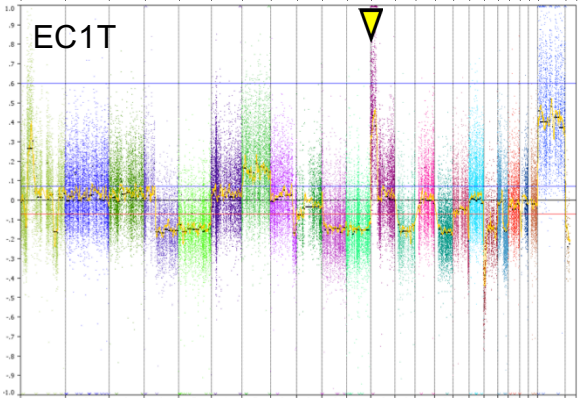
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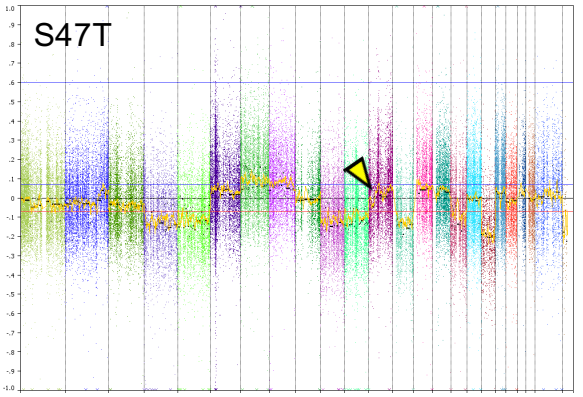
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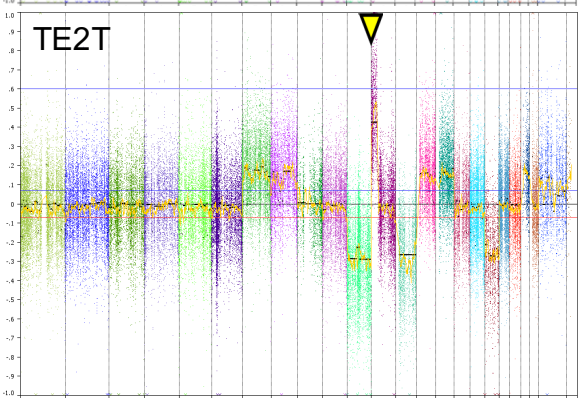
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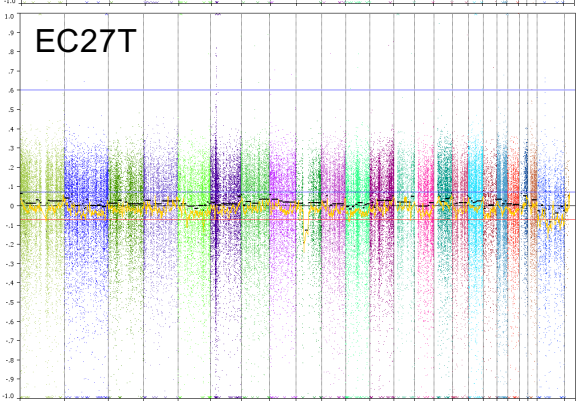
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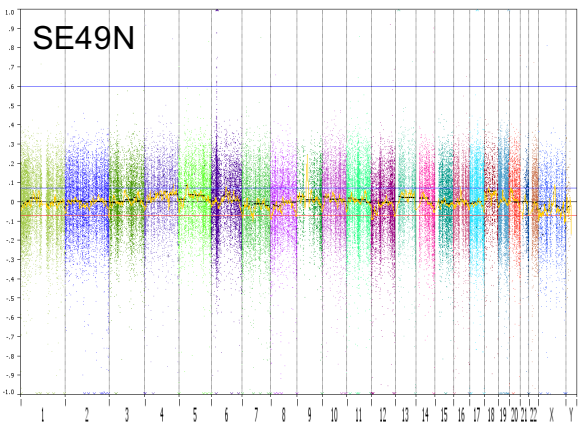
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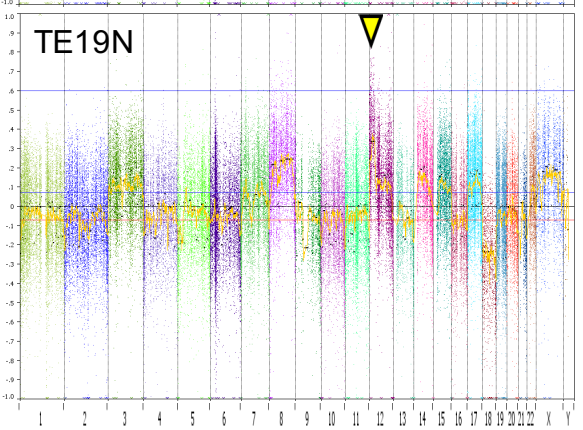
TE19N

Supplemental Fig. S2. Somatic copy number aberration (SCNA) analysis from 450K methylation array data. Shown are representative genome-wide SCNA plots for TGCT and BNT specimens. Left column: representative 12p+ TGCT (upper 3 panels) and flat BNT (lower left). Right column: representative TGCT without 12p gain (upper 3 panels) and BNT with 12p gain (lower right). Rare TGCT adequate for SCNA detection lack 12p gain (right upper 2 panels). In our series, 5/113 (4%) of TGCT adequate for SCNA detection lacked 12p+. 17 TGCT without 12p gain had "flat" genomes, consistent with an inadequate tumor fraction for aberration detection. Among the 128 total BNT, 15 array profiles demonstrated 12p+ gain and other SCNA, consistent with contamination by tumor (example TE19N). Tumor samples with 12p+ and normal without 12p+ met inclusion criteria for further analysis. Recurrent TGCT subtype SCNA are discussed in the main text.