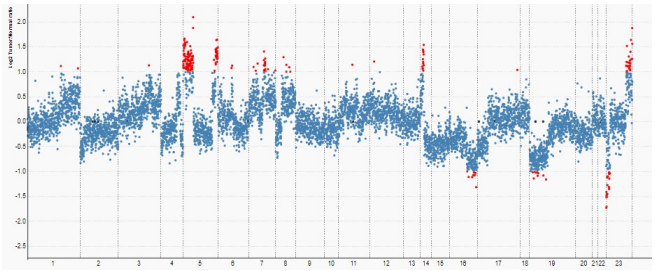
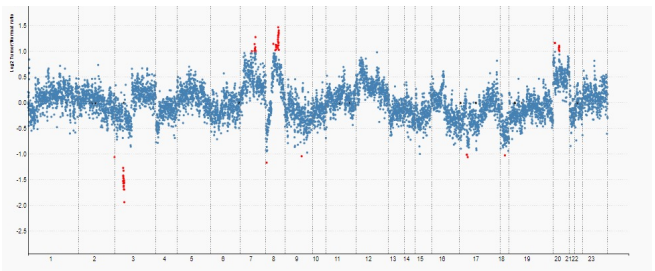
A



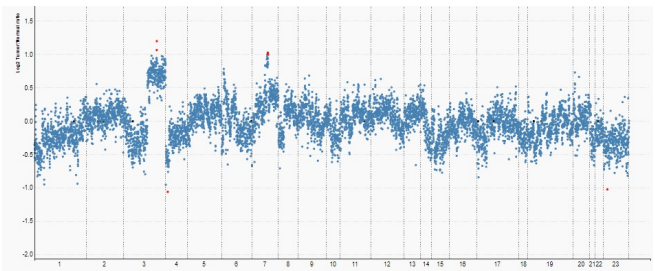
P-0009789 – Lung adenocarcinoma

B



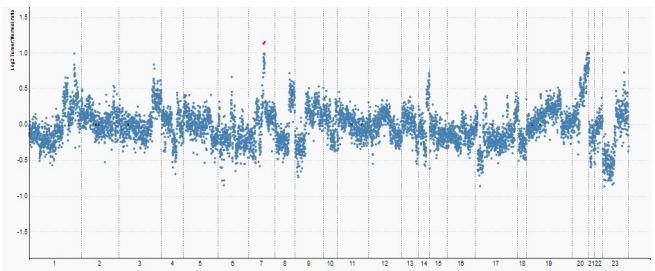
P-0026365 – Renal clear cell carcinoma

C



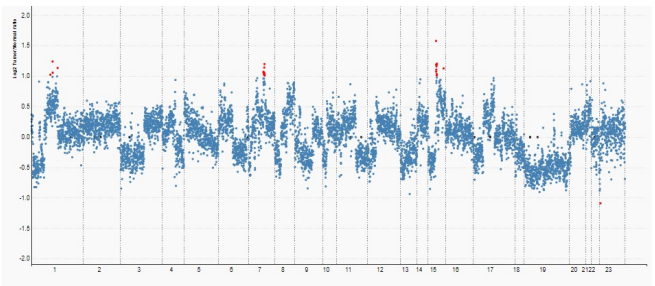
P-0018267 – Pancreatic adenocarcinoma

D



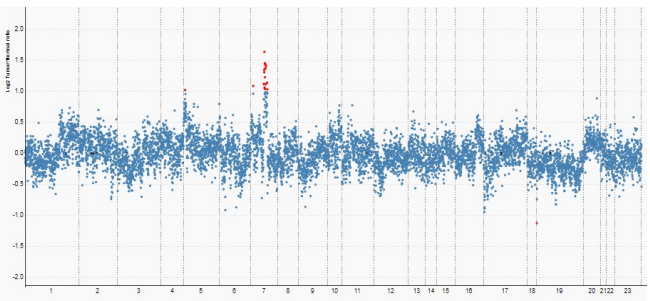
P-0031751 – High grade serous ovarian carcinoma

E



P-0035786 – Lung adenocarcinoma

F



P-0044127 – Lung adenocarcinoma

Supplementary Figure 2. Cases that demonstrated a discrepancy between *MET* amplification calls by NGS and FISH. a-b Two false positive cases (P-0009789 and P-0026365) exhibited copy number gain and a fragmented copy number profile of chromosome 7; manual review of the copy number plot could easily determine that a biologically relevant focal amplification of *MET* was not present. c-e In three other cases (one case of a pancreatic adenocarcinoma, P-0018267, c, one case of a high grade serous ovarian carcinoma, P-0031751, d, and one case of lung adenocarcinoma, P-0035786, e) review of the copy number plot appears to support the presence of a true focal amplification of *MET*, highlighting the sensitivity of the FACETS algorithm for detecting focal amplifications. However, these focal amplifications appear to be low amplitude and in the background of a number of other copy number changes, and none of them met the read-depth criteria of a fold-change greater than 2 for calling amplification. Additionally, in the case of the pancreatic adenocarcinoma, a KRAS p.Q61H is also present, which is a driver alteration usually mutually exclusive with other MAPK-pathway drivers. f. In addition, there was a false negative case where FISH demonstrated amplification that was not detected by FACETS (lung adenocarcinoma, P-0044127). This case was called amplified by the FACETS algorithm, but the size of the amplified region was 31 megabases. While FISH demonstrated low-level amplification (*MET:CEP7* ratio of 2.55 and *MET* signal count of 6.91), the read count method of determining amplification was also negative (fold change of 1.74).