Supplementary Information

**Supplementary Table 1** – TaqMan assay codes

**Supplementary Table 2** – mRNA expression as measure by RT-PCR

**Supplementary Table 3** – Gene copy-number variation associated with figitumumab sensitivity at false discovery rate < 0.25

**Supplementary Table 4** – Single agent activity of figitumumab in 8 cell lines implanted in vivo as subcutaneous xenografts

**Supplementary Figure S1** – Drug combinations

The top panel describes single agent and combination activity of various combinations. Cell lines with area under curve (AUC) over 15% were labeled as synergistic.

The second panel compares the synergy call with the genetic status of major cancer drivers. The red color shows protein-coding mutations as obtained from COSMIC and Oncocarta profiling, green amplification, blue deletions, and yellow indicates likely wild-type status. Note that many deletions are recorded as protein mutations in COSMIC and thus marked red. On the right are the p-values from the Fisher’s exact binomial test.

The third panel compares the synergy call with the mRNA expression of major cancer drivers. The expression data are from U133 Plus 2 arrays (Affymetrix). On the right are the p-values from the Kruskal-Wallis rank test. The bottom panel compares the synergy call with the mRNA expression of key IGF pathway drivers. The expression data are from TaqMan PCR data. On the right are the p-values from the Kruskal-Wallis rank test. All significant associations are highlighted in yellow.

**Supplementary Material** – DLDA expression signature

**Supplementary Material** – DLDA-classifier_IGF-pathway_score