Abstract

MM-201a compares favorably with competitor death receptor agonists

Two-gene biomarker predicts MM-201a sensitivity in CRC cell lines

Two-gene biomarker predicts MM-201a sensitivity in CRC PDX models

Figure 1. Engineering MM-201a for improved thermal stability and pharmacodynamics. (A) Format of the Fc engineering strategy. The thermally unstable native scTRAIL (scTRAIL, red) was grafted with a thermally stable Fc backbone containing ar-1 and ar-2 domains. (B, C) Thermal stability assay. (B) Heat stability of wild-type scTRAIL and MM-201a at 50°C for 30 minutes. (C) Comparative analysis of ar-1 domain design with the ar-2 domain of MM-201a and wild-type scTRAIL. Two-way ANOVA with Tukey's multiple comparison test was used. *p < 0.05, **p < 0.01. 

Figure 2. Computational logic gate model analyses of public and private protein data from the cloud-based Cancer Genome Atlas (TCGA) and Cancer Cell Line Encyclopedia (CCLE) databases to identify potential drug targets for CRC. The model was trained using two CRC datasets and validated in the TCGA. The model was then used to predict drug sensitivity in the CCLE dataset. The model was compared with the MM-201a activity in CRC cell lines. The model was validated in the TCGA dataset. The model was then used to predict drug sensitivity in the CCLE dataset. The model was compared with the MM-201a activity in CRC cell lines. The model was validated in the TCGA dataset. The model was then used to predict drug sensitivity in the CCLE dataset. The model was compared with the MM-201a activity in CRC cell lines.