**Uitdehaag *et al*. (2018) Supplementary Figure S1**. Workflow for filtering cell line genomic data and subsequent identification of predictive drug response biomarkers. Mutation selection is based on Chang *et al.* Nat Biotechnol. 2016;34:155-163. Copy number variation gene selection is based on Vogelstein *et al.* Science 2013;339:1546-58 and Zack *et al.* Nat Genet. 2013;45:1134-40.

