

CORRECTION

# Correction: Gene Expression Ratios Lead to Accurate and Translatable Predictors of DR5 Agonism across Multiple Tumor Lineages

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[S1 File](#) includes the incorrect data in the “Data S3 GREP model classifier” tab and in Column F (GREP prediction) of the “Data S4 in-vivo data” tab, which are from another model not discussed in this paper.

Please see the corrected [S1 File](#) here. The authors confirm that all results and figures in the original work remain unaffected by this error and correspond to the updated supplementary data in this correction.

## Supporting Information

**S1 File. Supplementary data tables: In-vitro results.** Excel table showing for each line the  $IC_{50}$ , Amax, experimental sensitivity call, MAS5 gene expression value, 2-gene prediction, and  $GREP^{DR5}$  prediction for all genes used in the GREP model. **All genes.** Excel table showing differential analysis of all genes with DR5Nb1-tetra sensitivity calls. **GREP model classifier.** Excel table showing coefficients for ratios used in the  $GREP^{DR5}$  model. **In-vivo data.** Excel table showing for each primary tumor xenograft model, the T/C, sensitivity call, GREP prediction and gene expression for all genes used in the GREP model. (XLSX)



## Reference

1. Reddy A, Growney JD, Wilson NS, Emery CM, Johnson JA, Ward R, et al. (2015) Gene Expression Ratios Lead to Accurate and Translatable Predictors of DR5 Agonism across Multiple Tumor Lineages. PLoS ONE 10(9): e0138486. doi:[10.1371/journal.pone.0138486](https://doi.org/10.1371/journal.pone.0138486) PMID: [26378449](https://pubmed.ncbi.nlm.nih.gov/26378449/)

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