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Cell

Corrections

Comprehensive Characterization of Cancer Driver Genes and Mutations

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It has come to our attention that we made two errors in preparation of this manuscript. First, in the STAR Methods, under the subheading of "Hypermutators and Immune Infiltrates" within the "Quantification and Statistical Analysis" section, we inadvertently referred to Figures S7A–S7C for data corresponding to sample stratification by hypermutator status alone in the last sentence. It should have referred to Figure S6A–S6C. Second, the lists of highly frequent missense mutations for COAD (colon adenocarcinoma) and READ (rectum adenocarcinoma) displayed in Figure S7 were incorrect because when we ordered the mutations in the initial analysis, we mistakenly combined the two cancer types COAD and READ for analysis, despite the fact that they were listed as two separate cancer types in the x-axis of the figure. After re-ordering the mutations by frequency for COAD and READ independently, information on highly frequent missense mutations for each of these cancer types is different and updated now in the revised Figure S7. These errors don't change the major conclusions of the paper and have been corrected online. We apologize for any confusion they may have caused.

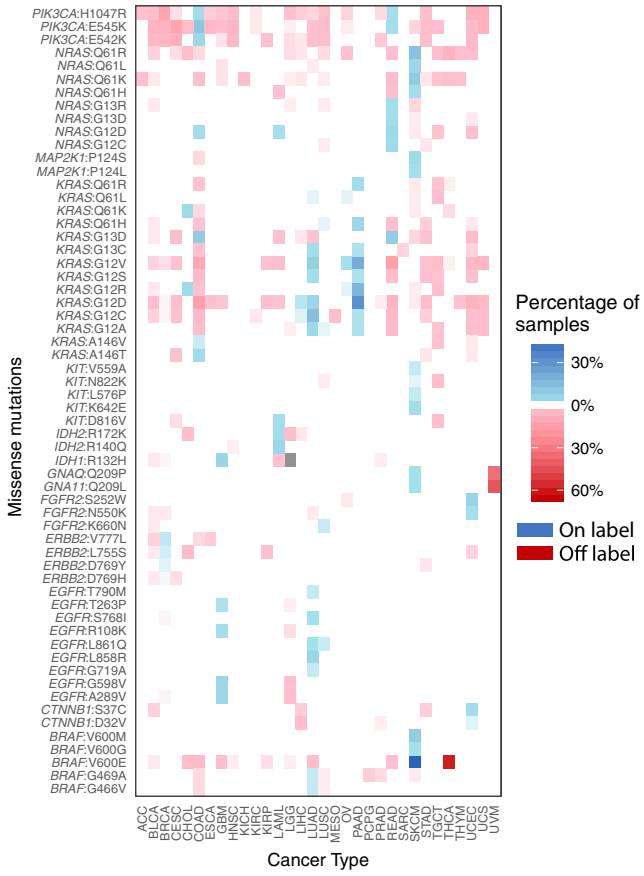

Figure S7. On-Label/Off-Label Calculations for Druggable Mutations in Cancer (corrected)

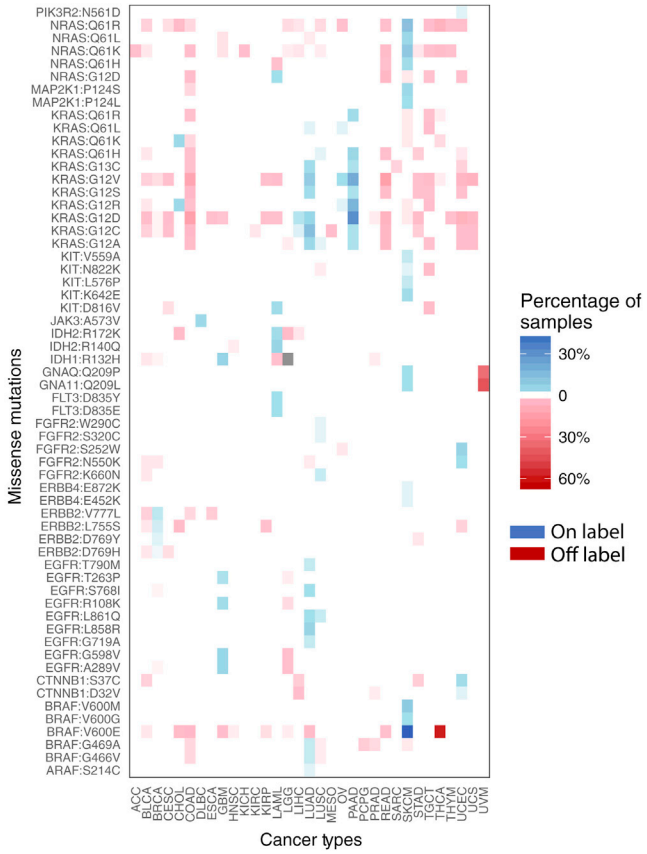

Figure S7. On-Label/Off-Label Calculations for Druggable Mutations in Cancer (original)

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