Author Correction: Massively parallel phenotyping of coding variants in cancer with Perturb-seq

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In the version of this article initially published, the KRAS variant "H166Y" was incorrectly annotated as "Y166H" in Figs. 3 and 4 and Extended Data Figs. 5, 6 and 10, resulting in the following changes: Fig. 3c,d,f: "Y166H" on the *x*-axis is now replaced with "H166Y"; in Fig. 3e, the value for variant H166Y recorded in GILA experiments is added, it was shown as "missing data" originally; in Fig, 4b, the GILA measurement for H166Y had been missing and now appears, causing a slight change in correlation statistics in the same panel (from 0.73 to 0.72, and from *P* value = 1.33×10^{-16} to 1.41×10^{-16}); in Fig. 4f, the GILA value for variant H166Y has been added to the calculation, leading to a slight change in the *P* value reported in the text from $P = 1.8 \times 10^{-20}$ to 1.5×10^{-20}; Fig. 4g was amended to follow the same variant ordering as Fig. 3; in Extended Data Figs. 5a, 6g and 10a–e, "Y166H" is now replaced with "H166Y"; and in Extended Data Fig. 10b, the middle and bottom plots now include the values recorded for H166Y for GILA (middle) and COSMIC (bottom).

Further, the KRAS variant G13V was annotated as involving a single base change, while it in fact involves multiple changes. Therefore, Fig. 5c has been amended to show G13V highlighted in magenta to indicate that it involves multiple base changes compared with the wild-type allele. Also, the text in the Results now reading "First, the low occurrence of seven Impactful IV variants is explained by their lower mutability due to multiple base substitutions (Fig. 5c, magenta text)" originally said "six Impactful IV variants."

Finally, the original Supplementary Table 1 reported the changes that variants produced in the genomic sequence on the positive strand. However, both of the genes we studied are coded on the negative strand, causing confusion for readers. We also want to better identify the changes induced by the variants and include more extensive annotations of which bases are modified by each variant in the ORF sequences and in which way. Thus, to clarify annotations and nomenclature for base changes from each variant, in Supplementary Table 1 we have replaced the columns "From," "To," and "Position" with "Position: base(s)," "From ORF base(s)," "To ORF base(s)," "Position: amino acid(s)," "From amino acid(s)," "To amino acid(s)," "From ORF codon(s)," "To ORF codon(s)" and "Insert sequence." These new columns are also described in the revised Supplementary Table 1 legend online. The changes have been made to the HTML and PDF versions of the article online.