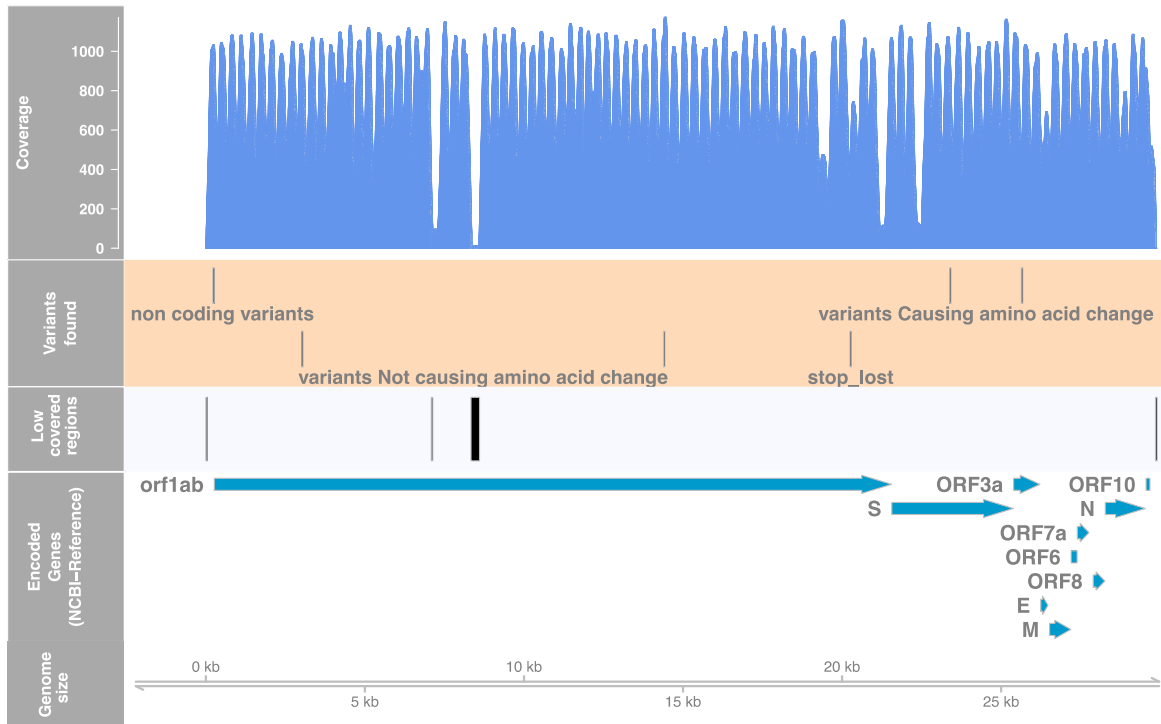**Figure S5. Representative diagnostic output from COVGAP.** This output generated per sample, indicates (from top to bottom): **A**. the coverage –not represented if over 1000x; **B**. which variants were detected in which position of the genome, and their corresponding annotation; **C**. low coverage regions (under 50x); **D**. genome annotation; and **E**. genome size markers as reference. Of note, a report generated in parallel provides further information on the variants, including which amino acids are affected by the variant.