Supplementary Materials

Methodological development of a multi-readout assay for the assessment of antiviral drugs against SARS-CoV-2

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Table S1. Oligonucleotide primers used in this study. The following information is given by the sequence description: translational start or stop codons (capital letters, underlined), restriction sites (capital letters, bold), additional bases (lower case letters) and coding sequences (capital letters).

Primer	Sequence (5' → 3')
5-BamHI-eCFP	tag**GGATCC**ATGGTGAGCAAGGGCGAGGAG
3-XbaI-NotI-eYFP	tag**TCTAGA**ctcga**GCGGCCGC**TTACTTGTACAGCTCGTCCATG
5-3CL pro Cleavage-SpeI-eYFP	GC**GCTAGC**GTGGCCAGACTGCAGAGCGGCTTC**ACTAGT**GGCAGCGTGAGCAAGGGCGAGGAG
3-3CL pro Cleavage-NheI-eCFP	CCACTAGTGAAGCCGCTCTGCAGTCTGGCCAC**GCTAGC**GCTGCCCTTGTACAGCTCGTCCATGC
5-T2A Cleavage-eYFP	GGGCAGCCTGCTGACCTGCGGCGACGTGGAGGAGAACCCCGGCCCCGTGAGCAAGGGCGAGGAG
3-T2A Cleavage-eCFP	GGGGTTCTCCTCCACGTCGCCGCAGGTCAGCAGGCTGCCCCGGCCCTCGCCGCTGCCCTTGTACAGCTCGTCCATG

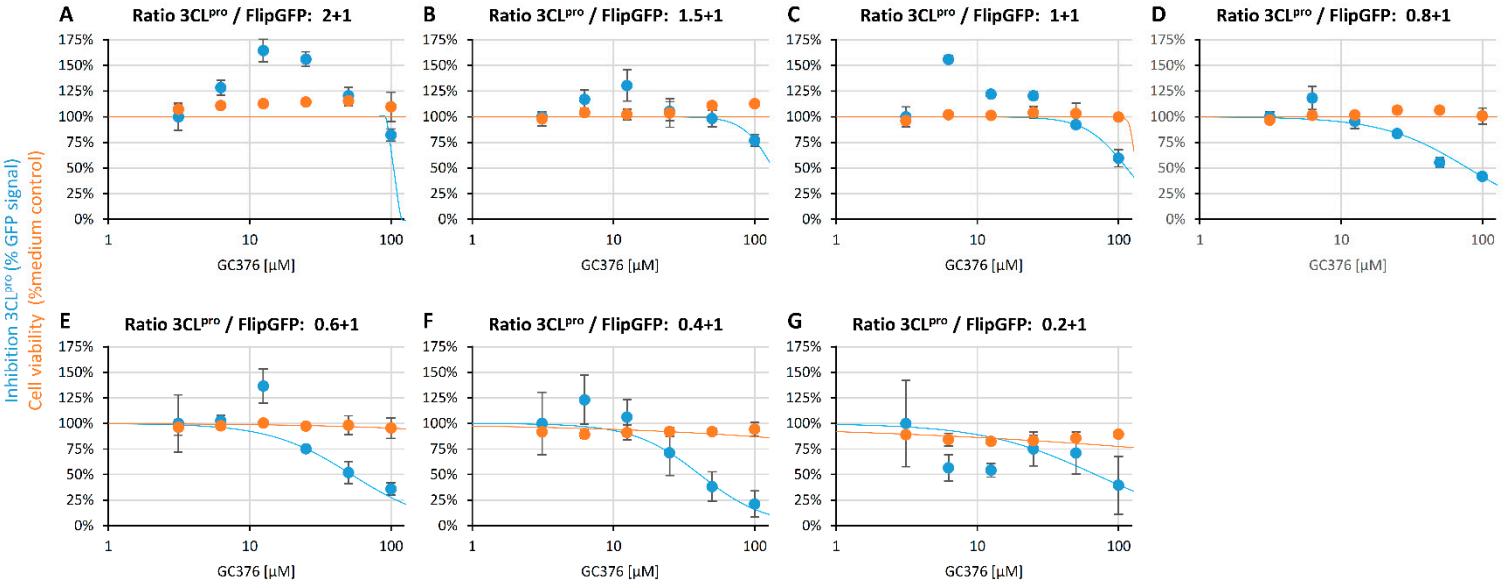

Figure S1: Steps of optimization of the FlipGFP assay: protease/reporter ratios **(A-G)**. Several different ratios of transfected plasmids coding for the protease or reporter protein, respectively, were applied as indicated.