Command line of MacSyFinder that we employed

macsyfinder --db-type ordered_replicon -w 1 -d ./CasFinder-2.0.2/DEF-SubTyping-2.0.2/ -p ./CasFinder-2.0.2/CASprofiles-2.0.2/ --sequence-db whole_protein_file_in_a_fasta_format all --out-dir ./out

CasFinder-2.0.2 was obtained from standalone version of CRISPRCasFinder. MacSyFinder has two dependencies makeblastdb from BLAST toolkit and Hmmer. We adopted version 2.7.1+ and 3.1b2, respectively.