

Genome in FASTA format (e.g., *Rhizopus oryzae* )



Step 1: Identification of Reverse Transcriptase encoding domains



*383 fragments*



Step 2: Extraction of a fragment for each Reverse Transcriptase hit with 5kb flanking sequences



Step 3: Identification of Tyrosine Recombinase encoding domains within the 10kb extracted fragments



*39 fragments*



Step 4: Identification of Methyltransferase encoding domains within the 10kb extracted fragments



*27 fragments*



Step 5: Filter for the co-orientation and the order of the three coding domains



*25 fragments*



Step 6: Set aside the fragments harboring at least two occurrences of one domain



*23 fragments*