Supplementary Materials

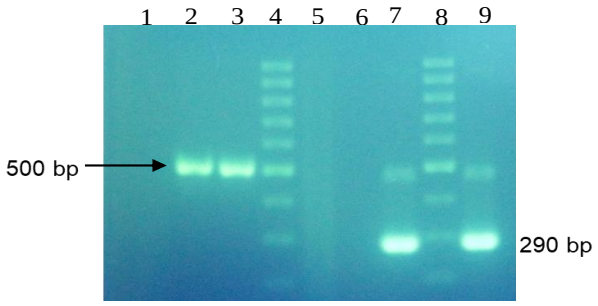


Figure S1. Characterization of DENV RNA isolates amplified by RT-PCR and nested PCR. Lane 1: negative control, Lanes 2 and 3: sequence amplified with primer D1 and D2, lane 4: DNA marker (100bp), lane 5: negative control of RT-PCR, lane 6 negative control of nested PCR, lane 7: sequence target (290 bp), lane 8: DNA marker (100bp), lane 9: positive control DENV 3 (Zymo Bunami).

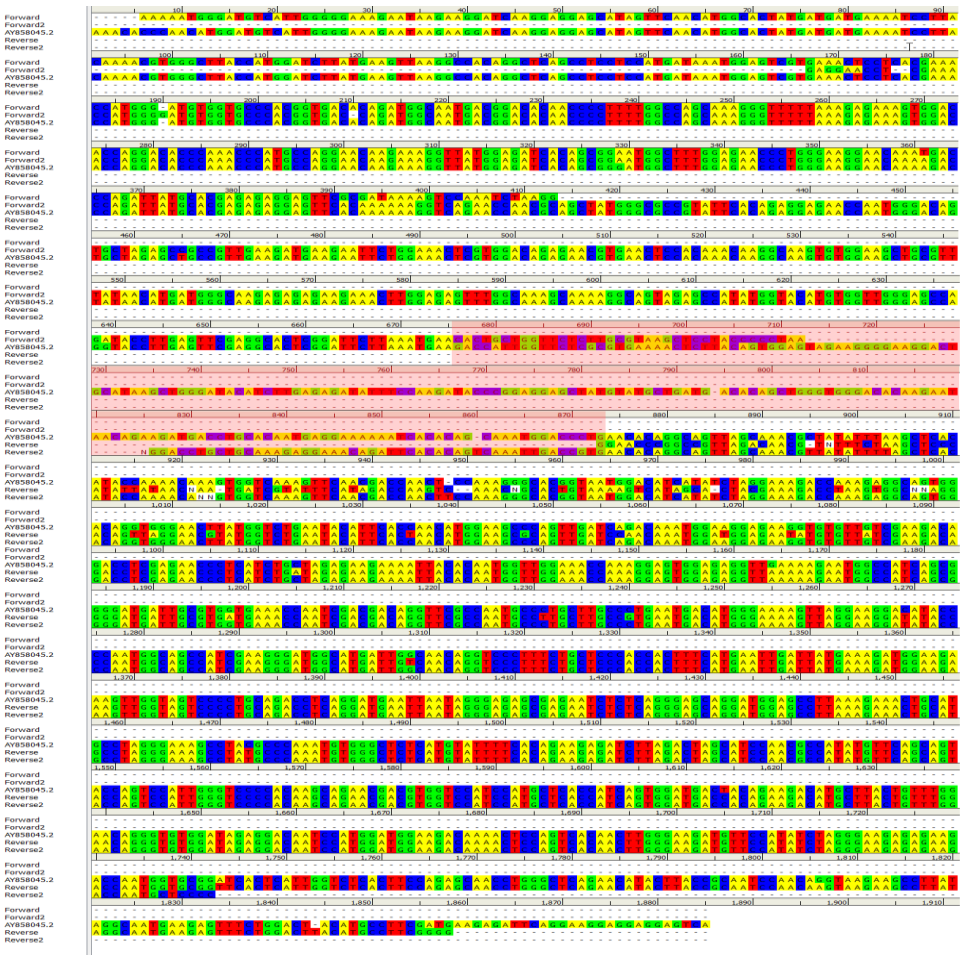


Figure S2. The multiple sequence alignment of reverse and forward to AY858045. The reverse and the forward show high identity, and the missing regions are highlighted in red.

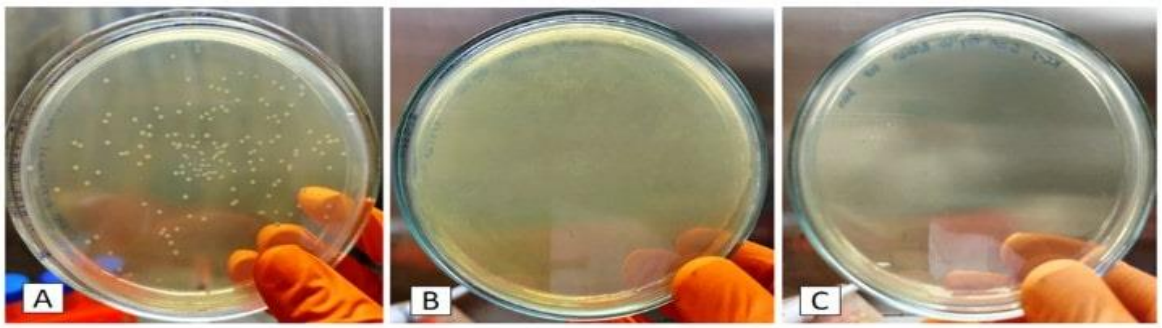


Figure S3. Transformation results (A) positive results of *E. coli* BL21(DE3)-pET28a(+)[NS5-RdRp DENV3] on selection medium 50µg/mL kanamycin; (B) positive control, non-transformant *E. coli* BL21 (DE3); (C) negative control, non-transformant *E. coli* BL21(DE3) on selection media 50µg/mL kanamycin.

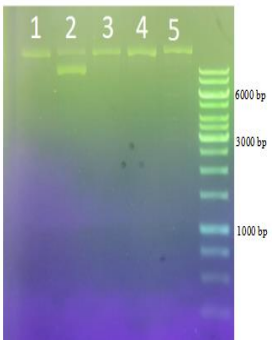


Figure S4. Characterization of pET28a(+)[NS5-RdRp DENV3] plasmid isolates. Lane 1 colony-1 9.8 ng/µL, lane 2 colony-2 15.9 ng/µL, lane 3 colony-3 10.1 ng/µL, lane 4 colony-4 15.8 ng/µL, and lane 5 colony-5 15 ng/µL.

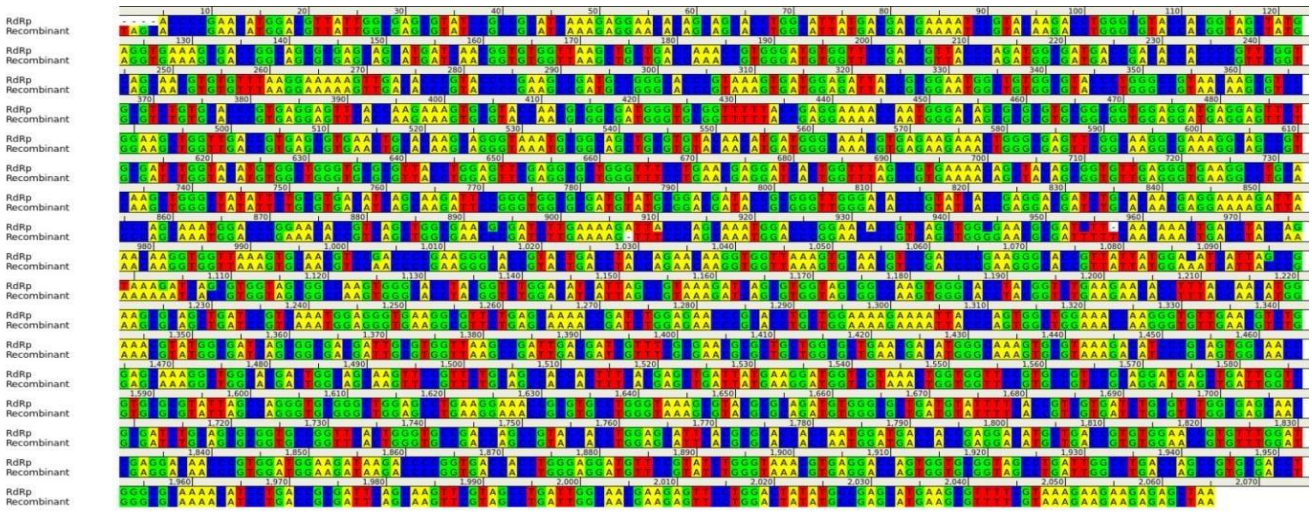


Figure S5. Alignment of NS5-RdRp DENV3 gene sequence with RdRp Contig1 sequence and RdRp sequence result with primer T7 terminator reverse.

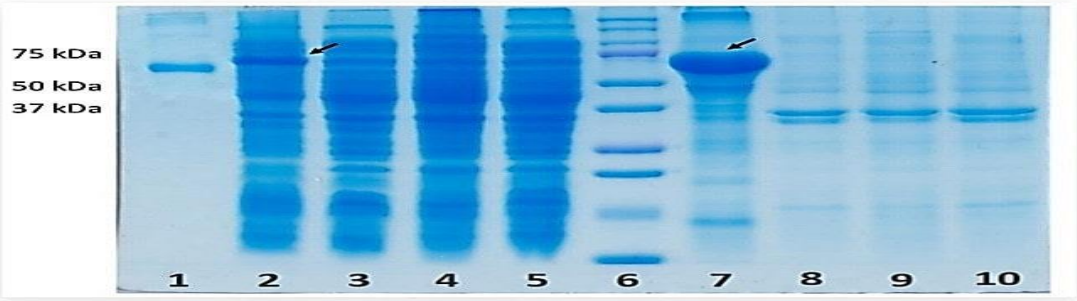
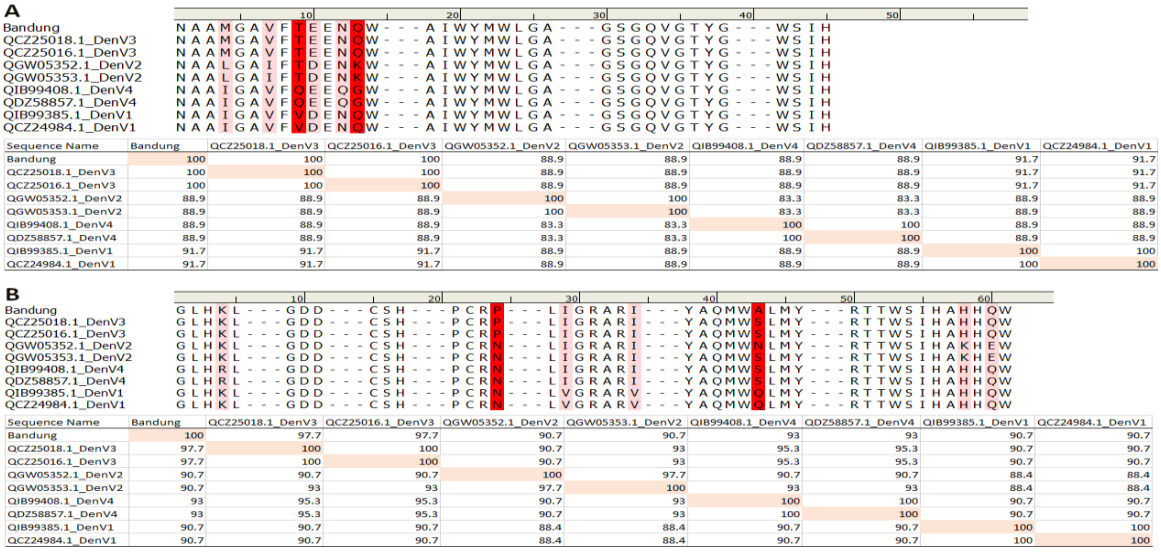


Figure S6. Characterization of recombinant RdRp expression. Lane 1: 0,4 mg/mL BSA Standard, Lane 2: soluble fraction of induced *E. coli* BL21(DE3)-pET28a(+)[NS5-RdRp DENV3], Lane 3: soluble fraction of uninduced *E. coli* E. coli BL21(DE3)-pET28a(+)[NS5-RdRp DENV3], Lane 4: soluble fraction of induced *E. coli* BL21 (DE3) non-transformed, lane 5:soluble fraction of non-induced *E. coli* BL21 (DE3) non-transformed, lane 6: Protein marker Lane 7: insoluble fraction of induced *E. coli* BL21(DE3)-pET28a(+)[NS5-RdRp DENV3], Lane 8: insoluble fraction of uninduced *E. coli* BL21 *E. coli* BL21(DE3)-pET28a(+)[NS5-RdRp DENV3], Lane 9: insoluble fraction of induced *E. coli* BL21 (DE3) non-transformed, Lane 10: insoluble fraction of uninduced *E. coli* BL21 (DE3) non-transformed.



Sequence Name	Bandung	QCZ25018.1_DenV3	QCZ25016.1_DenV3	QGW05352.1_DenV2	QGW05353.1_DenV2	QIB99408.1_DenV4	QDZ58857.1_DenV4	QIB99385.1_DenV1	QCZ24984.1_DenV1
Bandung	100	100	100	88.9	88.9	88.9	88.9	91.7	91.7
QCZ25018.1_DenV3	100	100	100	88.9	88.9	88.9	88.9	91.7	91.7
QCZ25016.1_DenV3	100	100	100	88.9	88.9	88.9	88.9	91.7	91.7
QGW05352.1_DenV2	88.9	88.9	88.9	100	100	83.3	83.3	88.9	88.9
QGW05353.1_DenV2	88.9	88.9	88.9	100	100	83.3	83.3	88.9	88.9
QIB99408.1_DenV4	88.9	88.9	88.9	83.3	83.3	100	100	88.9	88.9
QDZ58857.1_DenV4	88.9	88.9	88.9	83.3	83.3	100	100	88.9	88.9
QIB99385.1_DenV1	91.7	91.7	91.7	88.9	88.9	88.9	88.9	100	100
QCZ24984.1_DenV1	91.7	91.7	91.7	88.9	88.9	88.9	88.9	100	100

Sequence Name	Bandung	QCZ25018.1_DenV3	QCZ25016.1_DenV3	QGW05352.1_DenV2	QGW05353.1_DenV2	QIB99408.1_DenV4	QDZ58857.1_DenV4	QIB99385.1_DenV1	QCZ24984.1_DenV1
Bandung	100	97.7	97.7	90.7	90.7	93	93	90.7	90.7
QCZ25018.1_DenV3	97.7	100	100	90.7	93	95.3	95.3	90.7	90.7
QCZ25016.1_DenV3	97.7	100	100	90.7	93	95.3	95.3	90.7	90.7
QGW05352.1_DenV2	90.7	90.7	90.7	100	97.7	90.7	90.7	88.4	88.4
QGW05353.1_DenV2	90.7	93	93	97.7	100	93	93	88.4	88.4
QIB99408.1_DenV4	93	95.3	95.3	90.7	93	100	100	90.7	90.7
QDZ58857.1_DenV4	93	95.3	95.3	90.7	93	100	100	90.7	90.7
QIB99385.1_DenV1	90.7	90.7	90.7	88.4	88.4	90.7	90.7	100	100
QCZ24984.1_DenV1	90.7	90.7	90.7	88.4	88.4	90.7	90.7	100	100

Figure S7. The sequence alignment of two inhibitor pocket of NS5 RdRp. (A) The binding pocket near finger subdomain, (B) The binding pocket near thumb subdomain. The color gradient from Red to White represent the non-matching to identical.