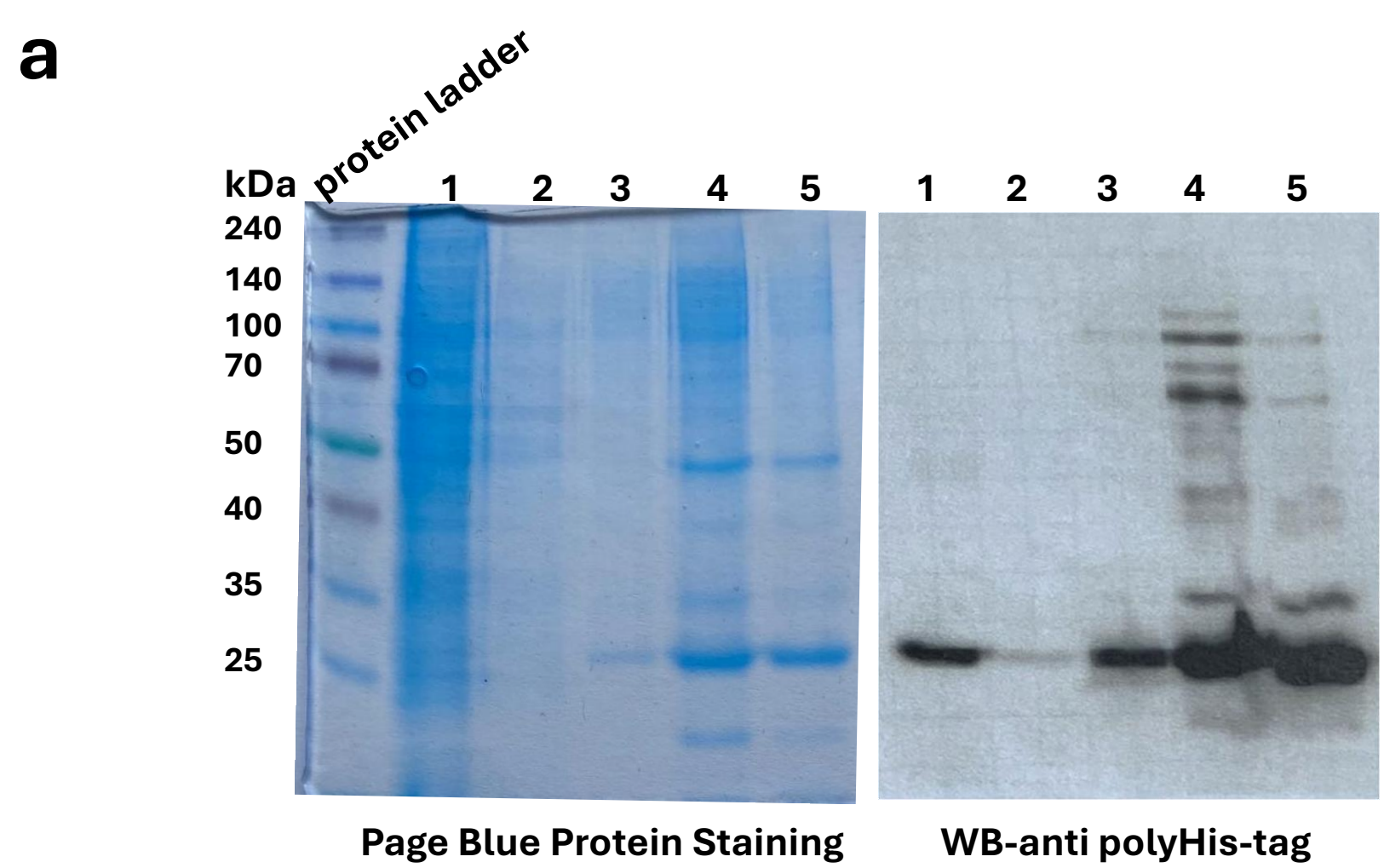
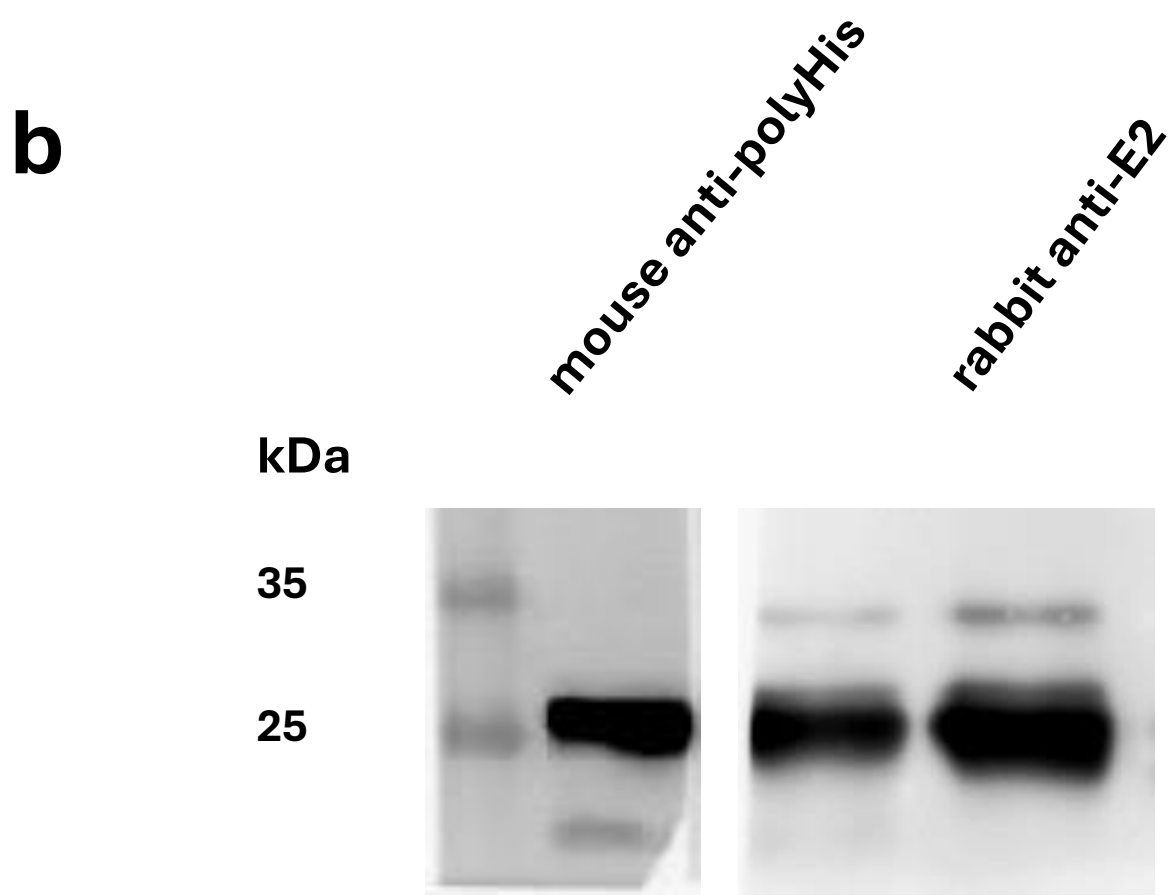
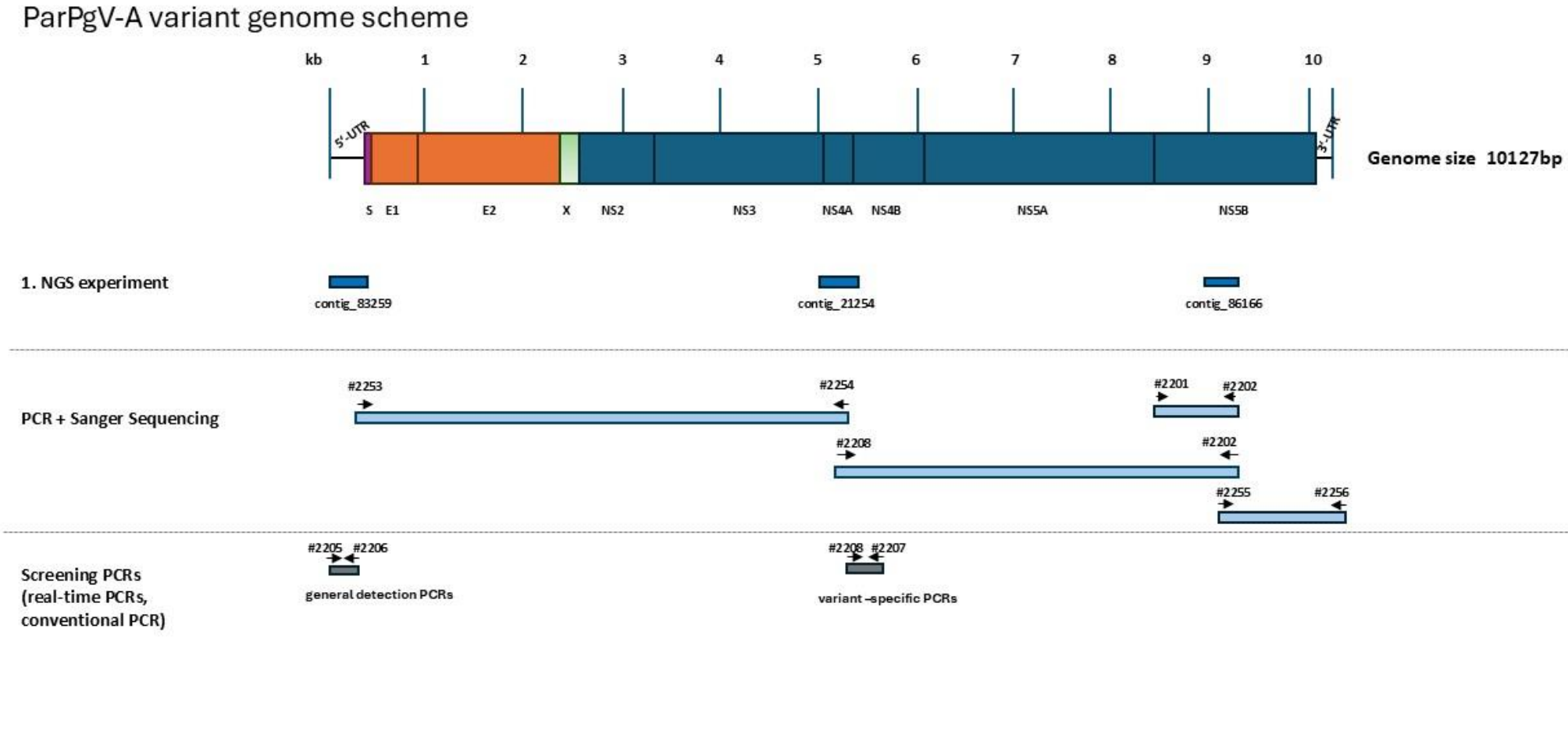


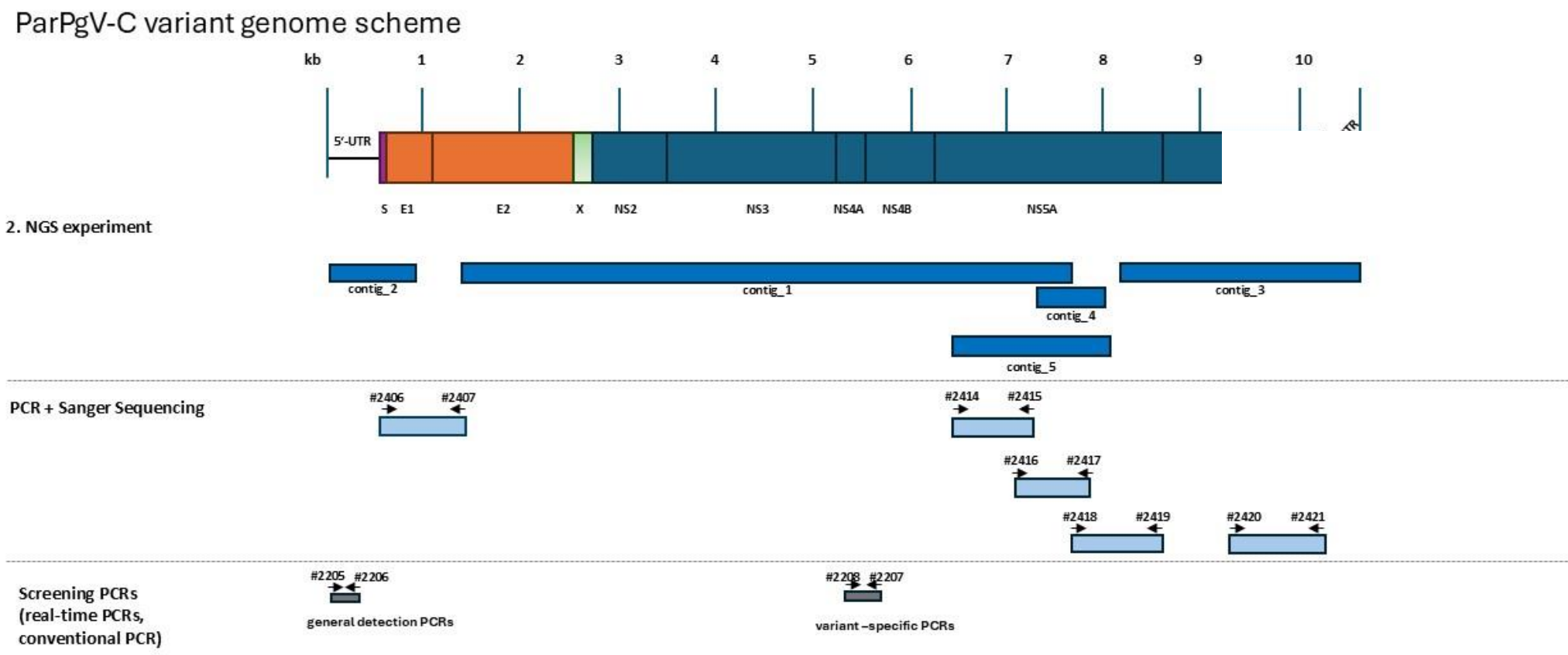


Supplementary Fig. 1. Expression, purification, and detection of recombinant partial ParPgV E2 protein.
(a) Two identical 12% SDS-PAGE gels were run in parallel with the following samples: unpurified E2 protein (lane 1), wash fraction (lane 2), and three elution fractions (lanes 3–5). The left panel shows SDS-PAGE stained with PageBlue Protein Staining Solution (Thermo Scientific), and the right panel shows the corresponding western blot probed with mouse anti-polyHis-tag antibody (1:3000) followed by anti-mouse HRP-conjugated secondary antibody (1:1000).
(b) Western blot of purified E2 protein separated on a 12% SDS-PAGE gel. The left panel shows detection using mouse anti-polyHis-tag antibody (1:3000) with anti-mouse HRP-conjugated secondary antibody (1:1000). The right panel shows detection using rabbit anti-E2 antibody (1:5000) with anti-rabbit HRP-conjugated secondary antibody (1:20,000). Spectra™ Multicolor Broad Range Protein Ladder (Thermo Scientific) was used in all gels.

a



b



Supplementary Fig. 2. Genome organization and sequencing strategy for two partridge pegivirus (ParPgV) strains.
(a) ParPgV-A variant genome scheme showing the genome structure (10,127 bp) and the regions obtained through next-generation sequencing (NGS), PCR, and Sanger sequencing. Three contigs were assembled from NGS data (contig_83259, contig_21354, contig_86166), and additional regions were confirmed or completed using specific PCRs and sequencing primers. General detection and variant-specific PCRs are also indicated.
(b) ParPgV-C variant genome scheme (10,687 bp), assembled from total RNA extracted from infected partridge embryos. NGS yielded four contigs (contig_1–contig_4), and gap-filling was completed using PCR and Sanger sequencing. General detection and variant-specific PCR targets are indicated, aligning with those used for ParPgV-A.
Notably, ParPgV-C displayed longer 5' and 3' untranslated regions (UTRs), suggesting the ParPgV-A genome may be slightly incomplete.