

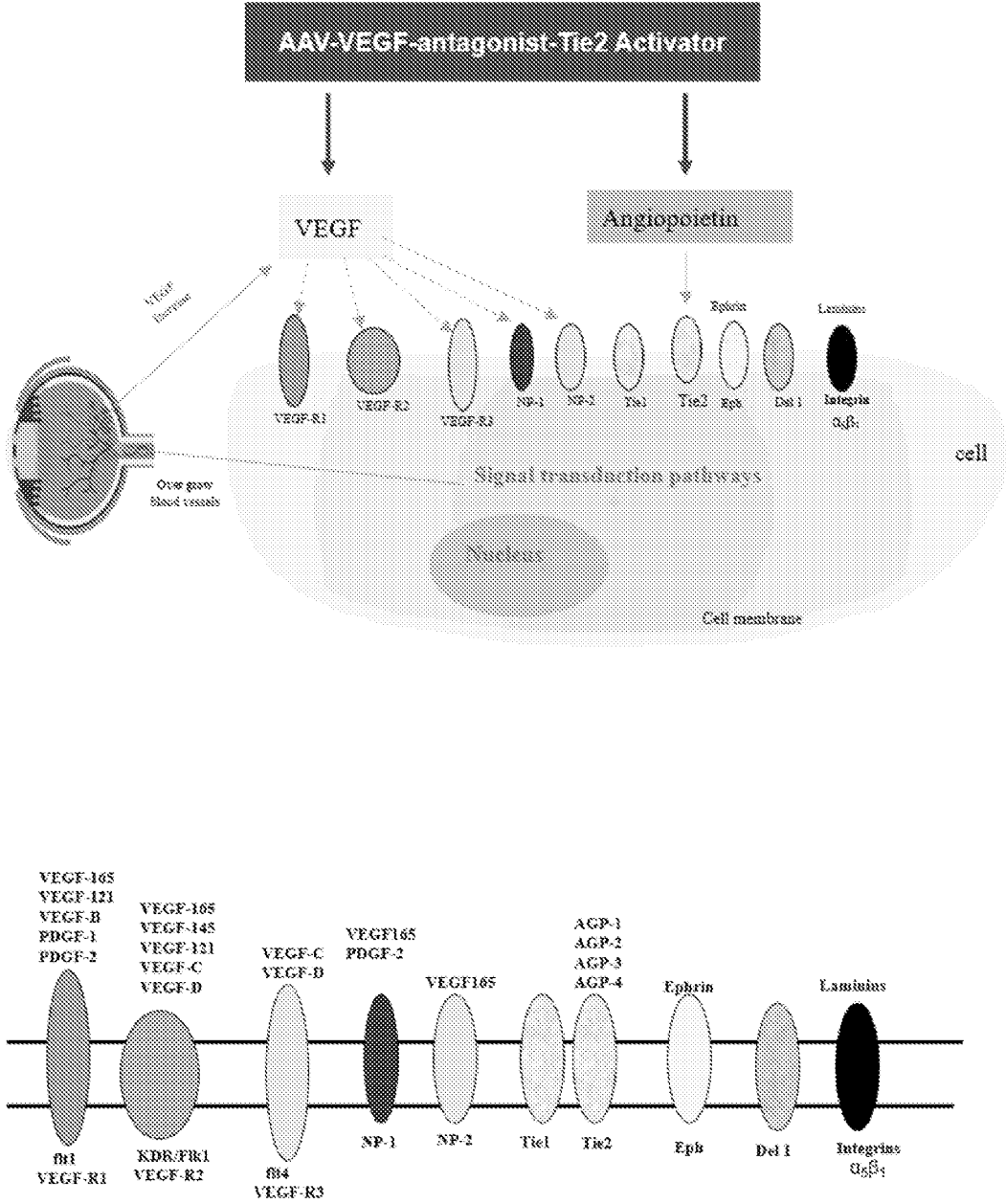
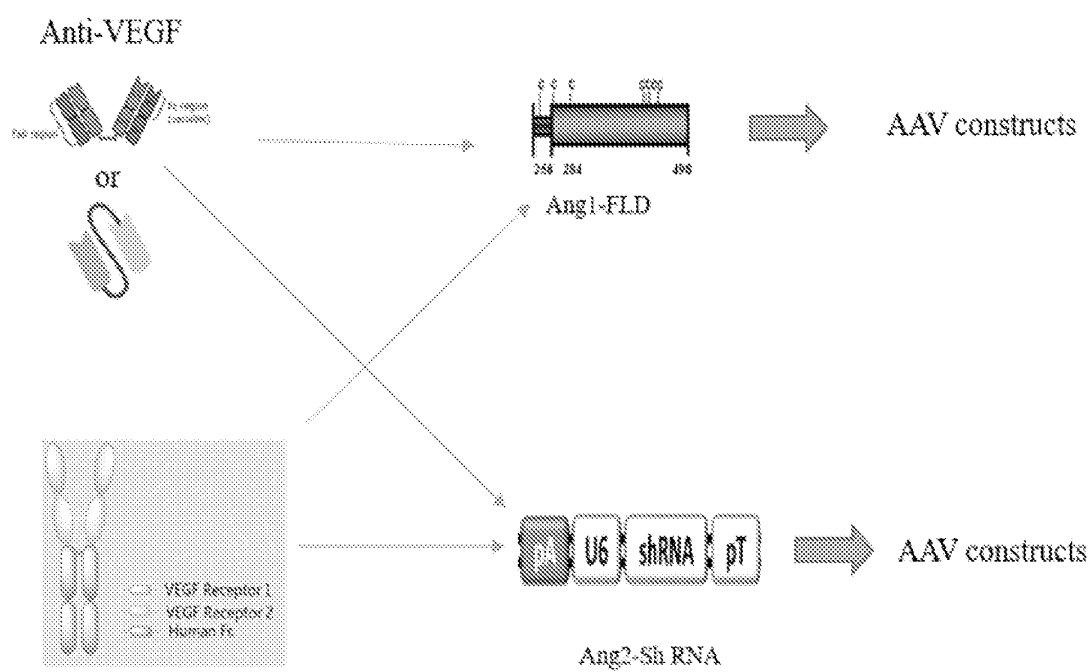


Fig. 1

**Fig. 2**

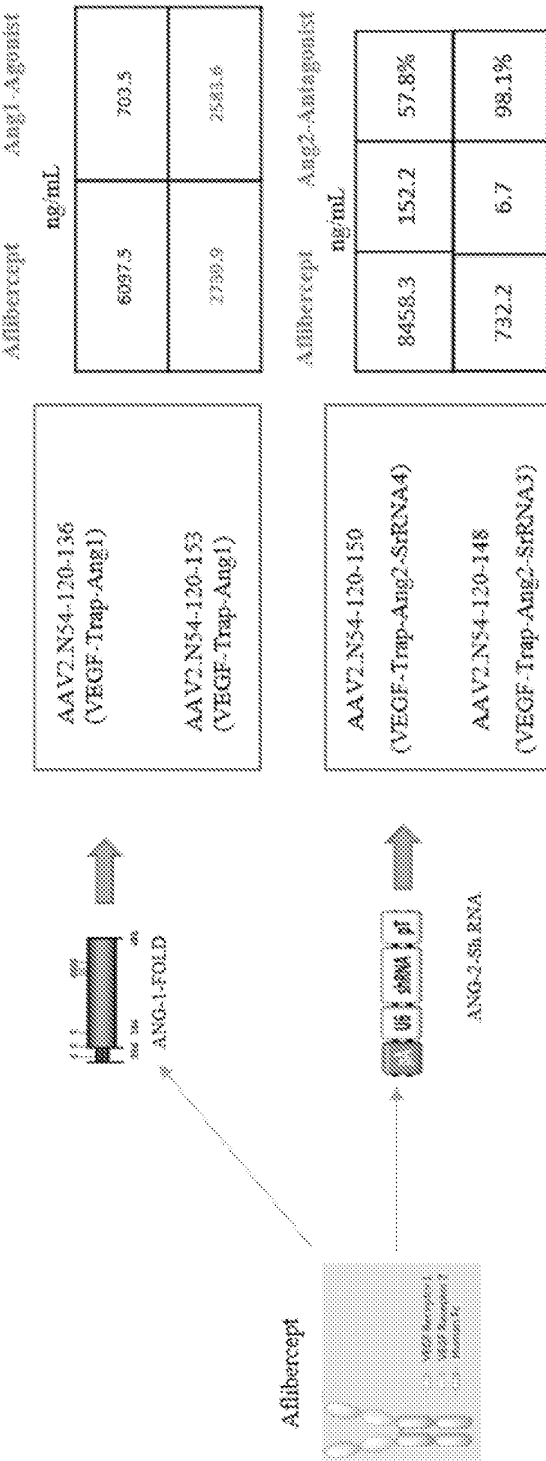


Fig. 3A

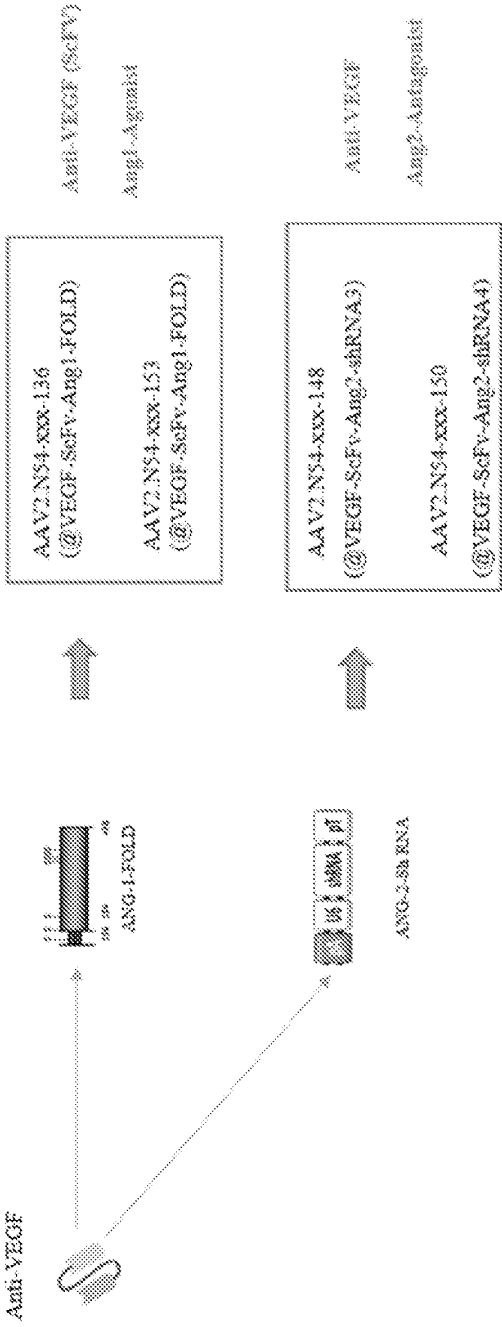


Fig. 3B

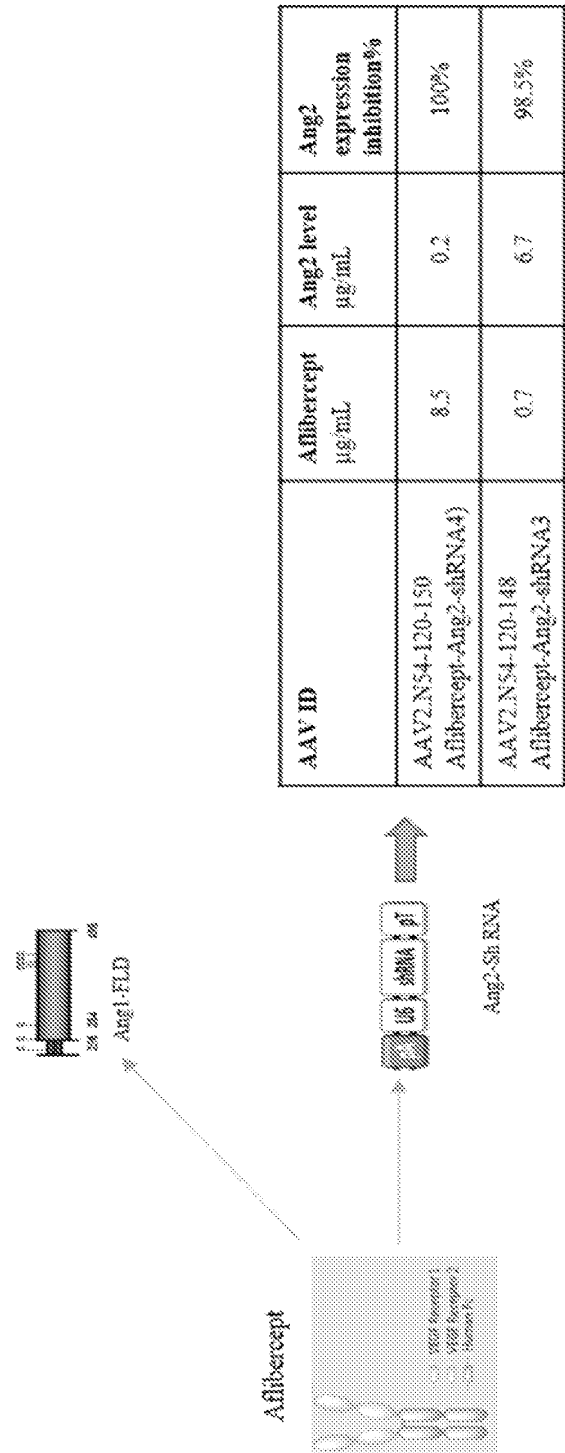


Fig. 4

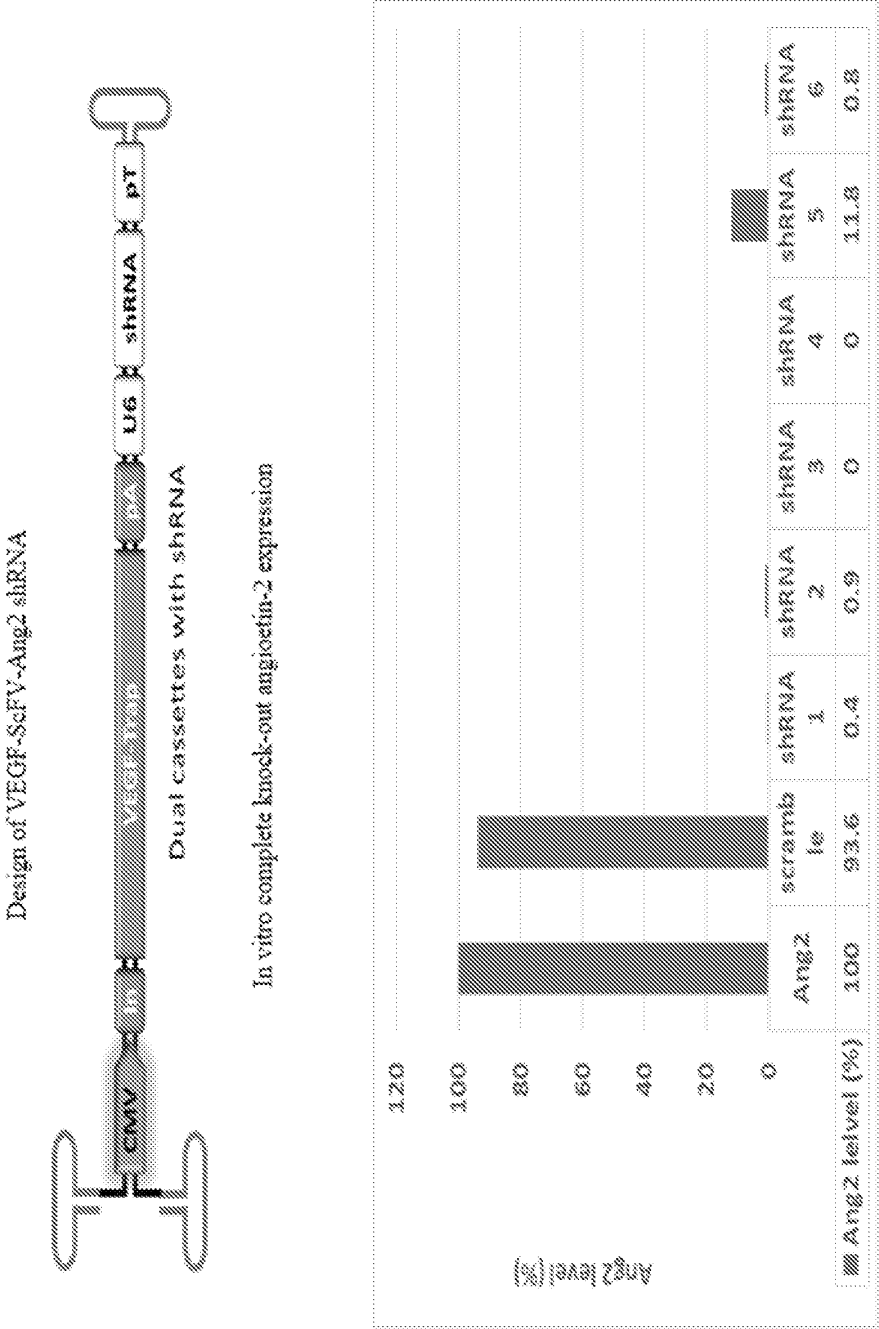


Fig. 5

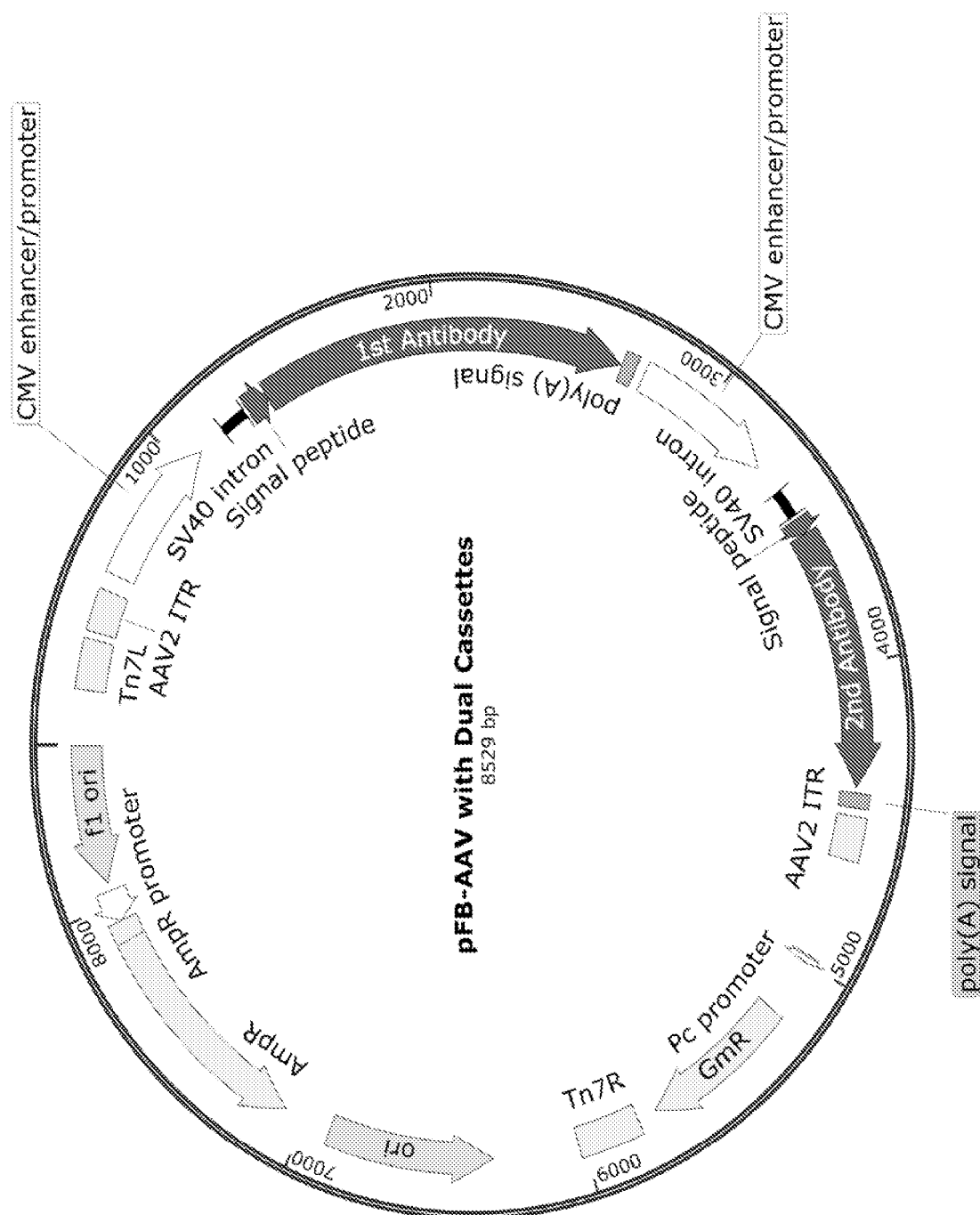


Fig. 6A

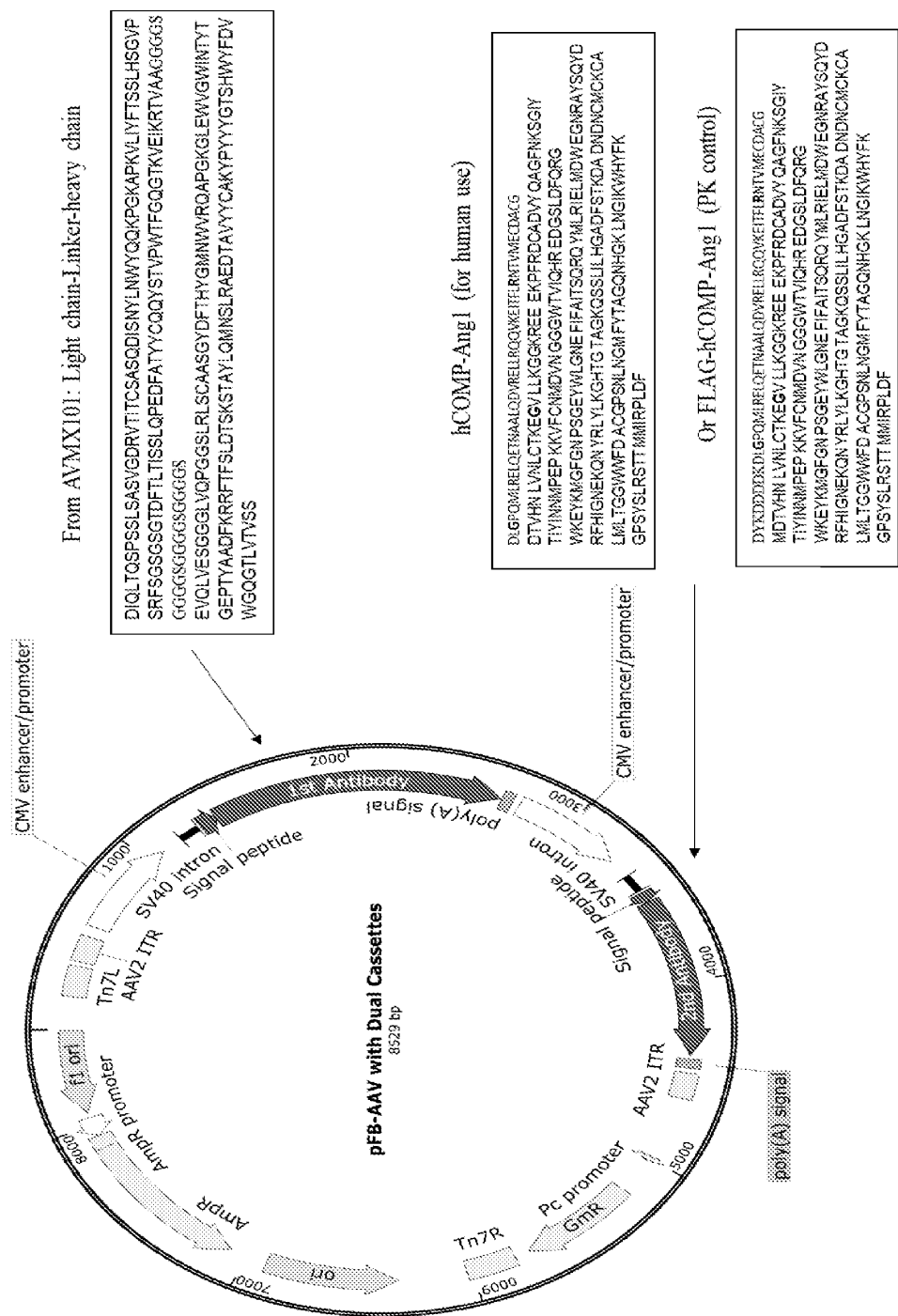


Fig. 6B

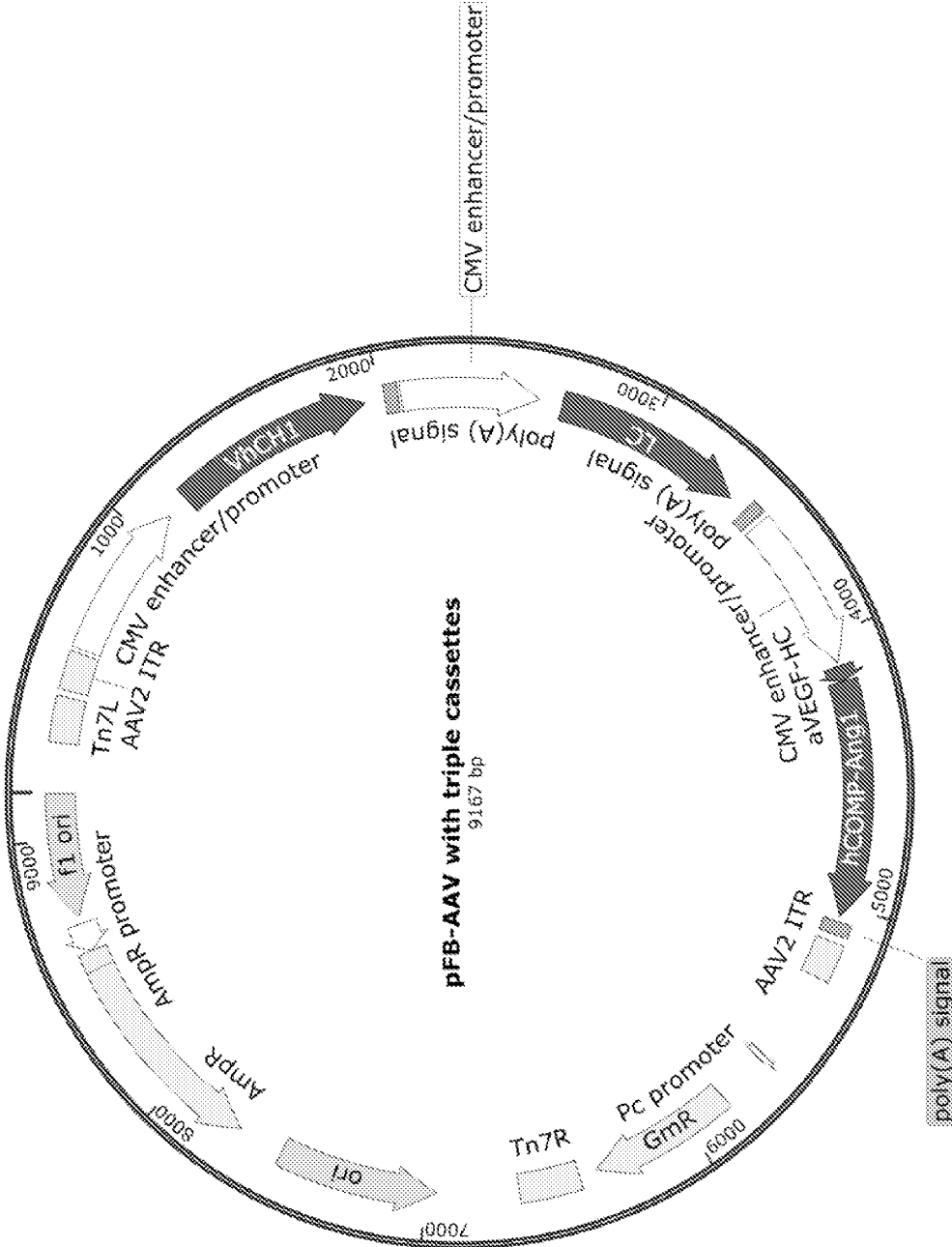


Fig. 7A

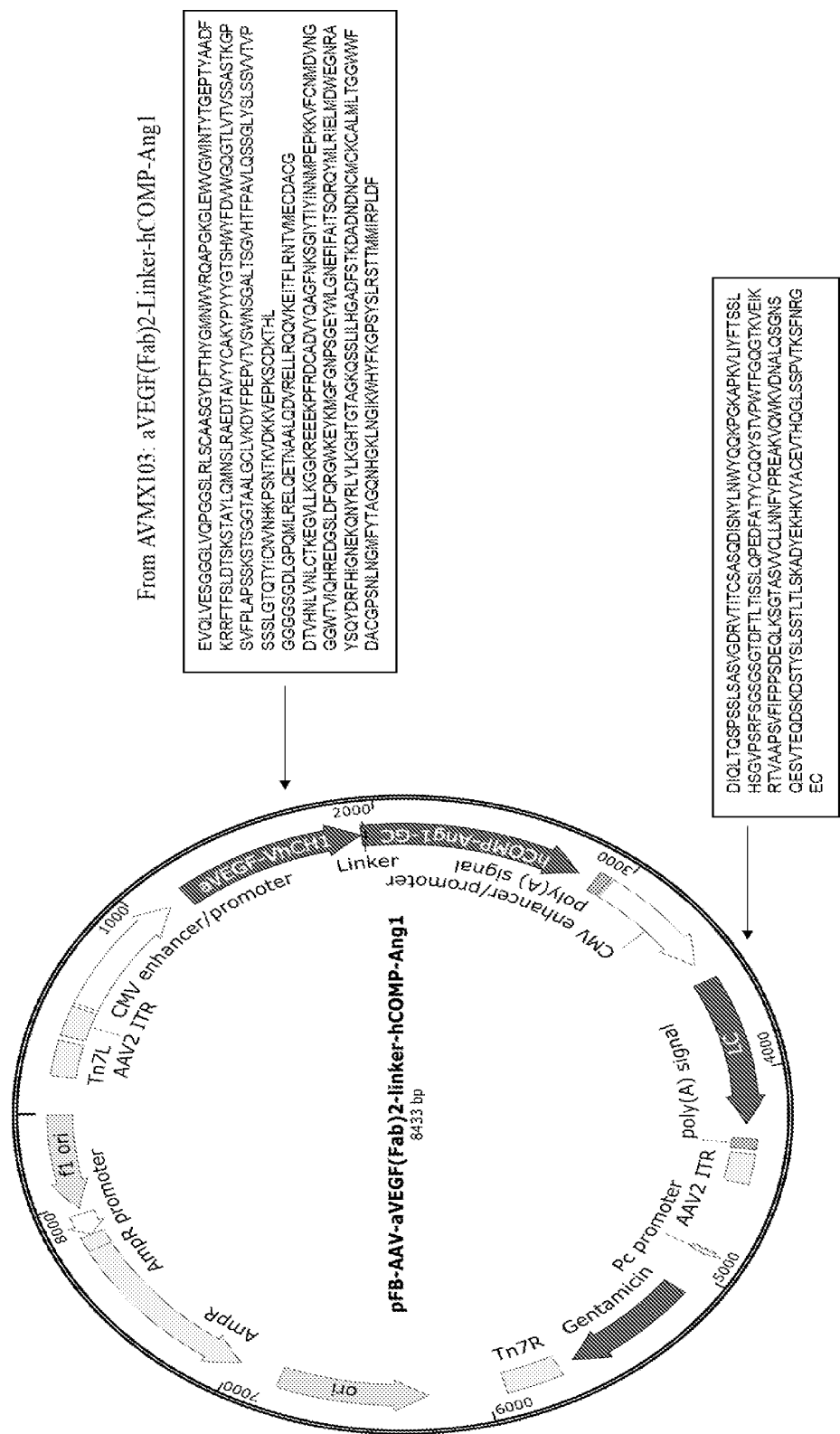


Fig. 7B

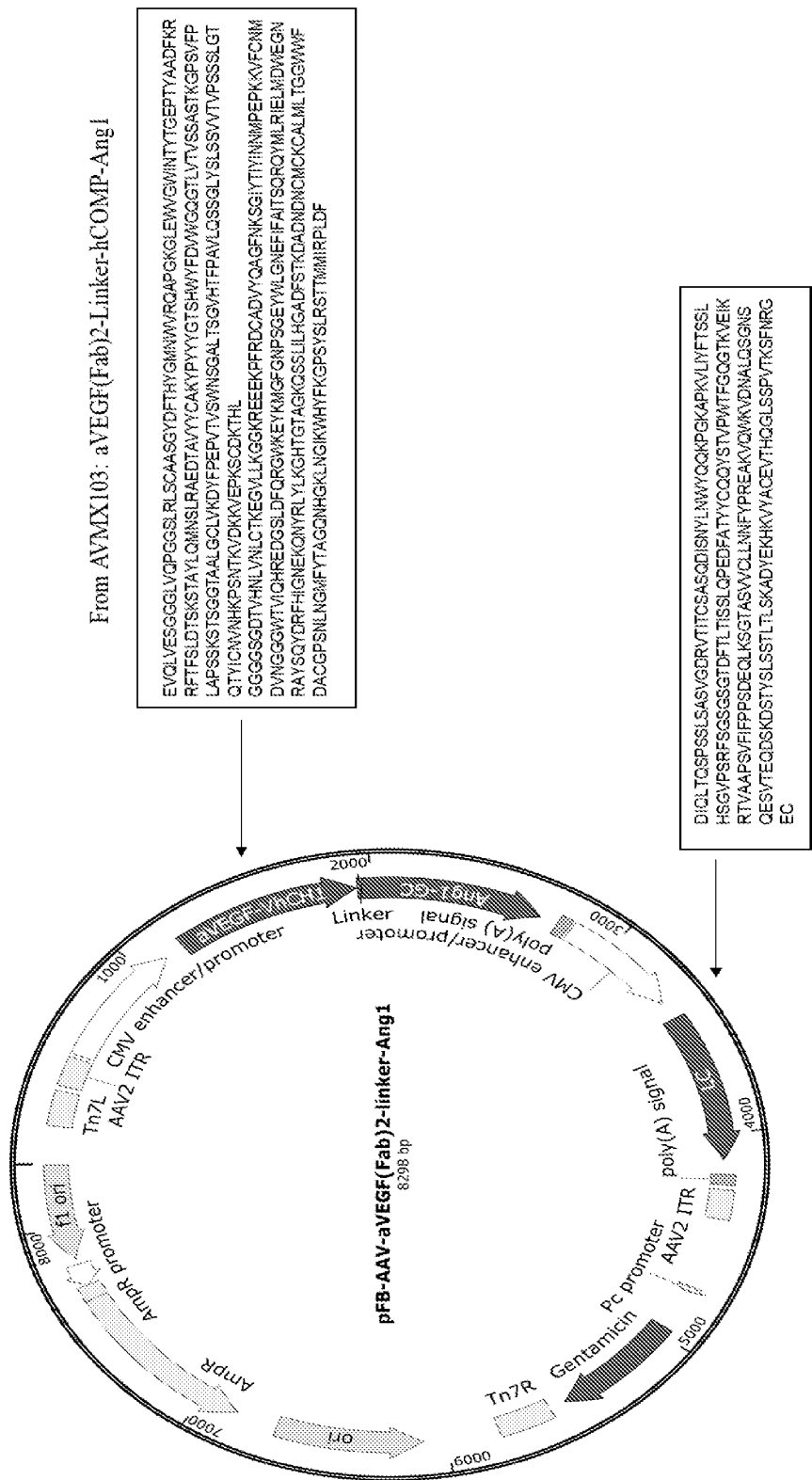


Fig. 7C

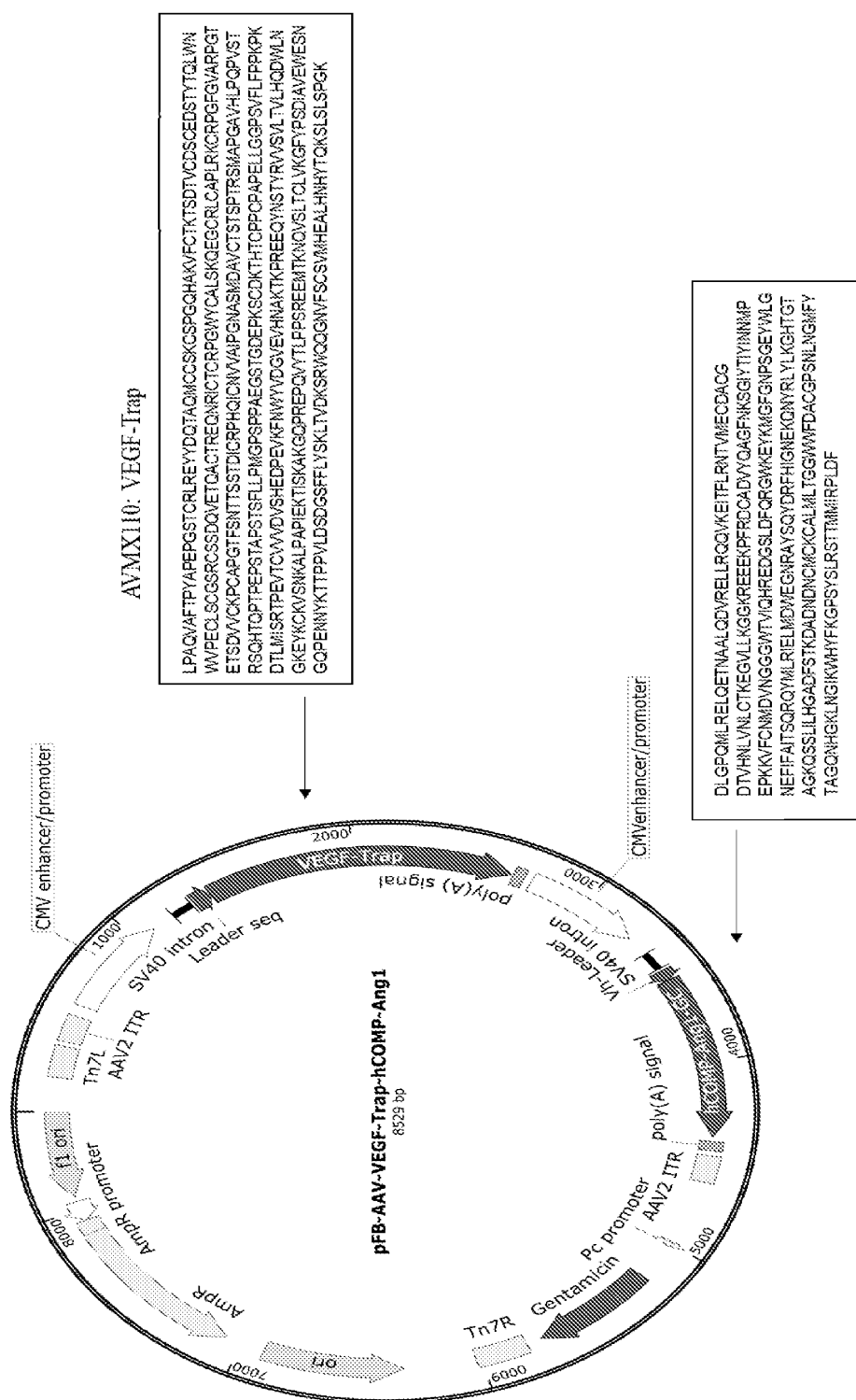


Fig. 7D

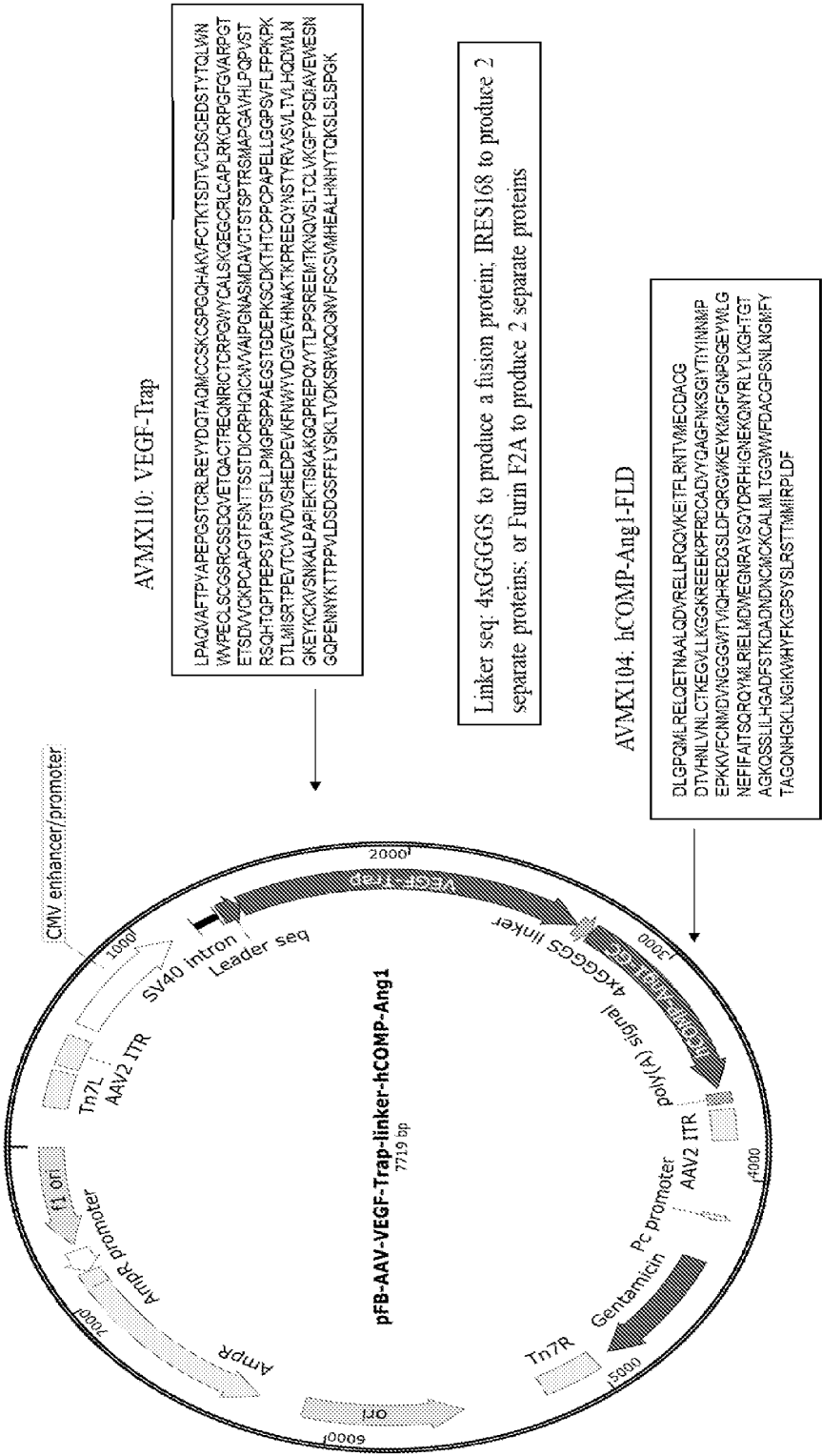


Fig. 8A

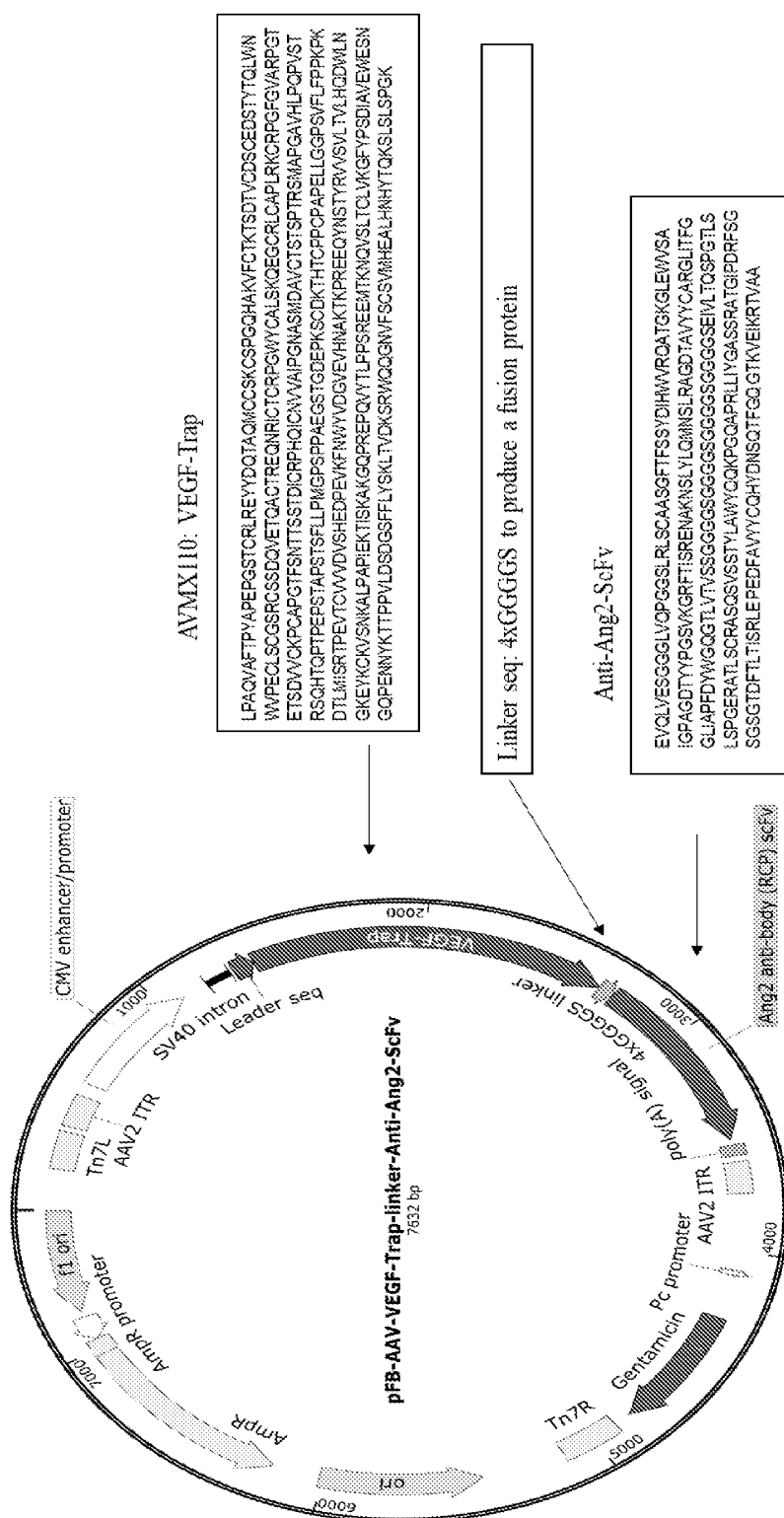


Fig. 8B

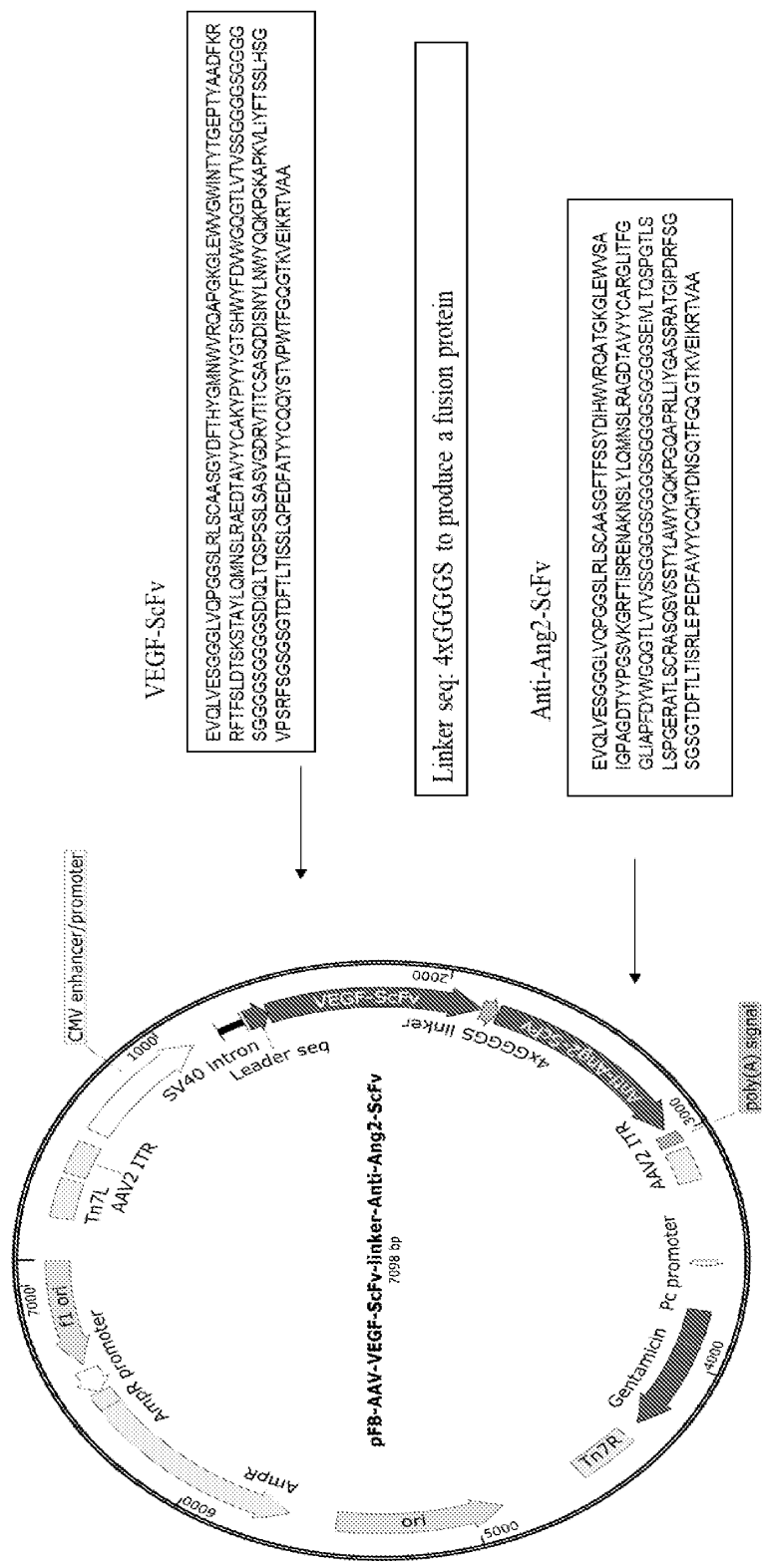


Fig. 8C

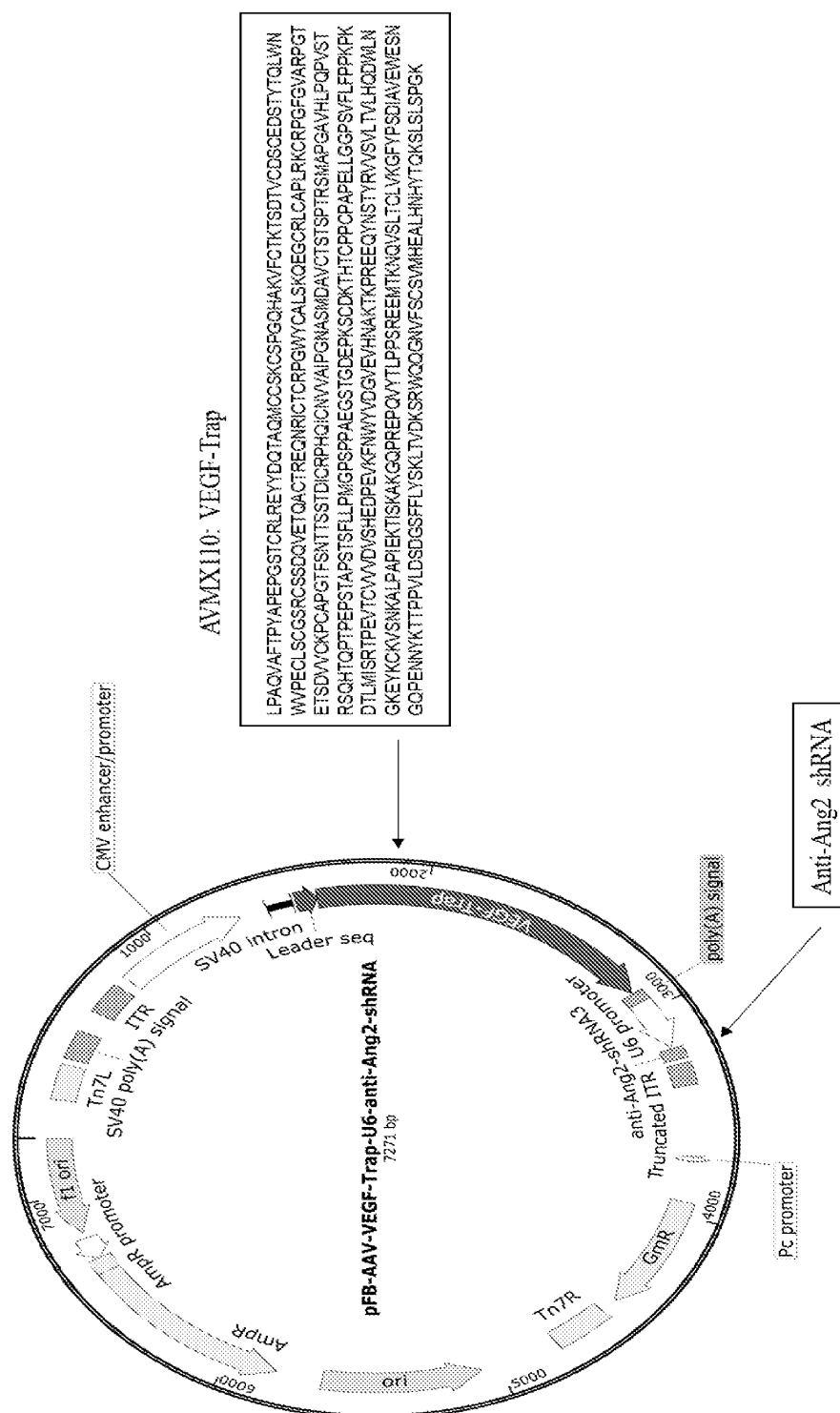


Fig. 8D

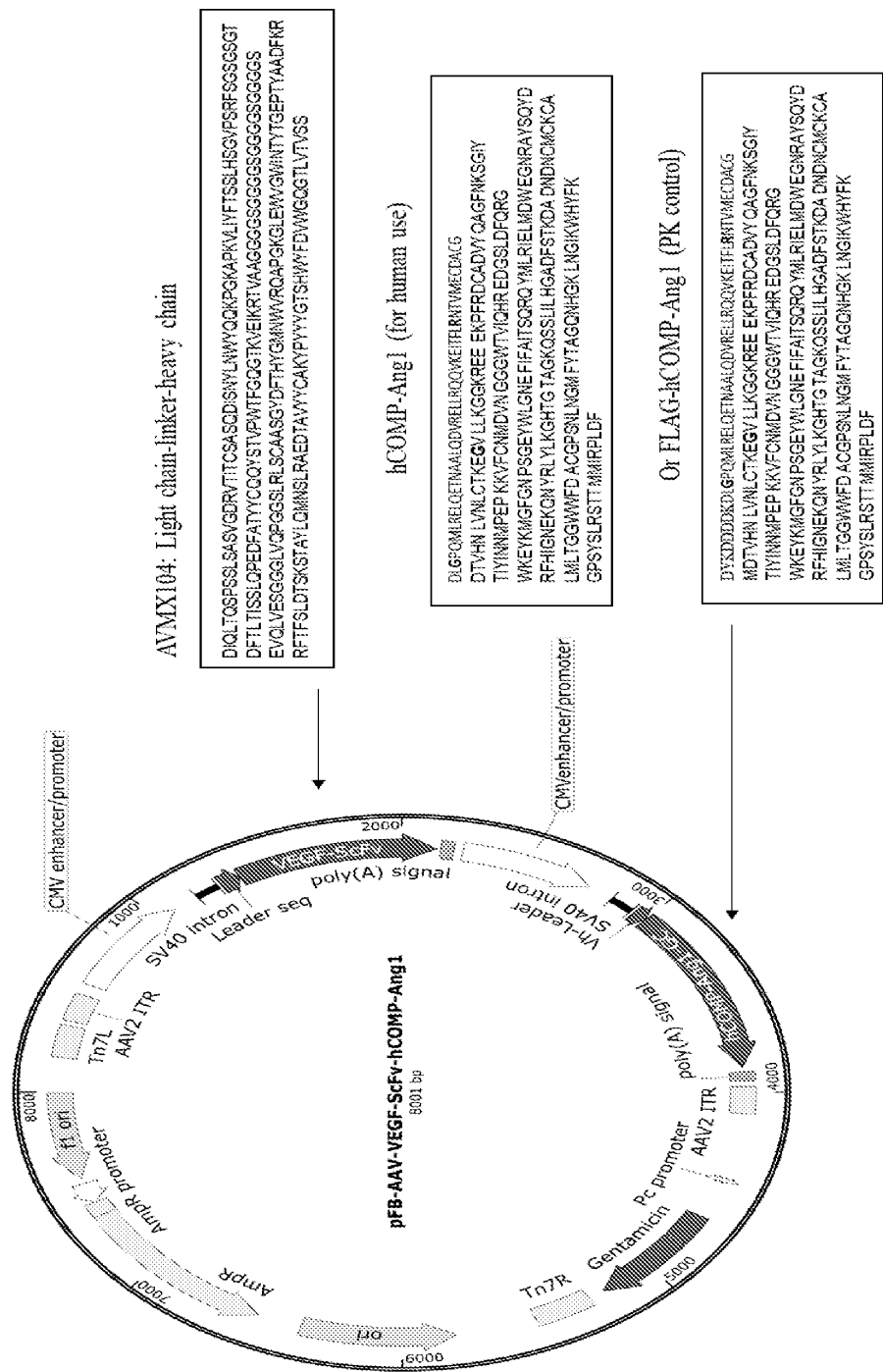


Fig. 9A

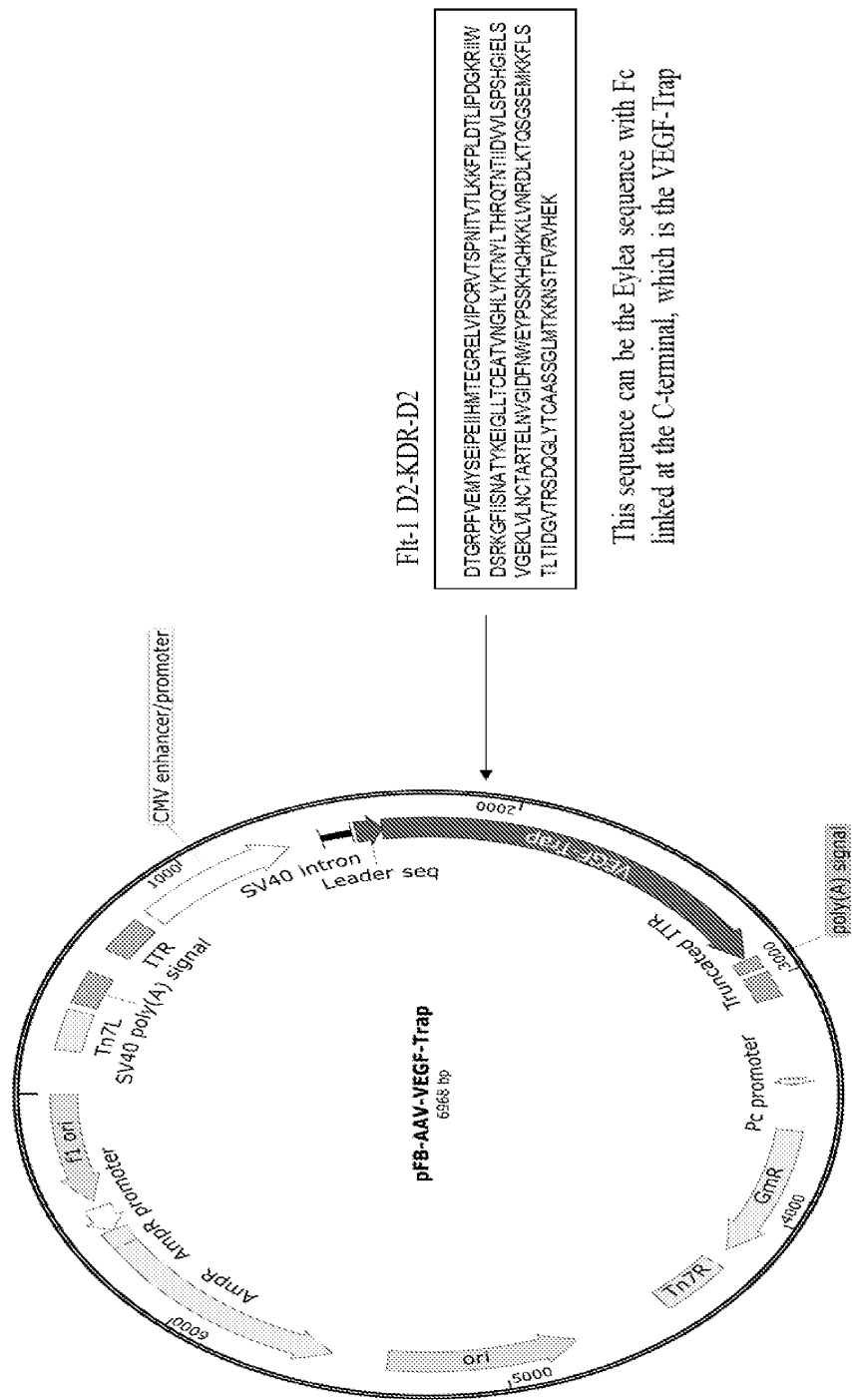


Fig. 9B

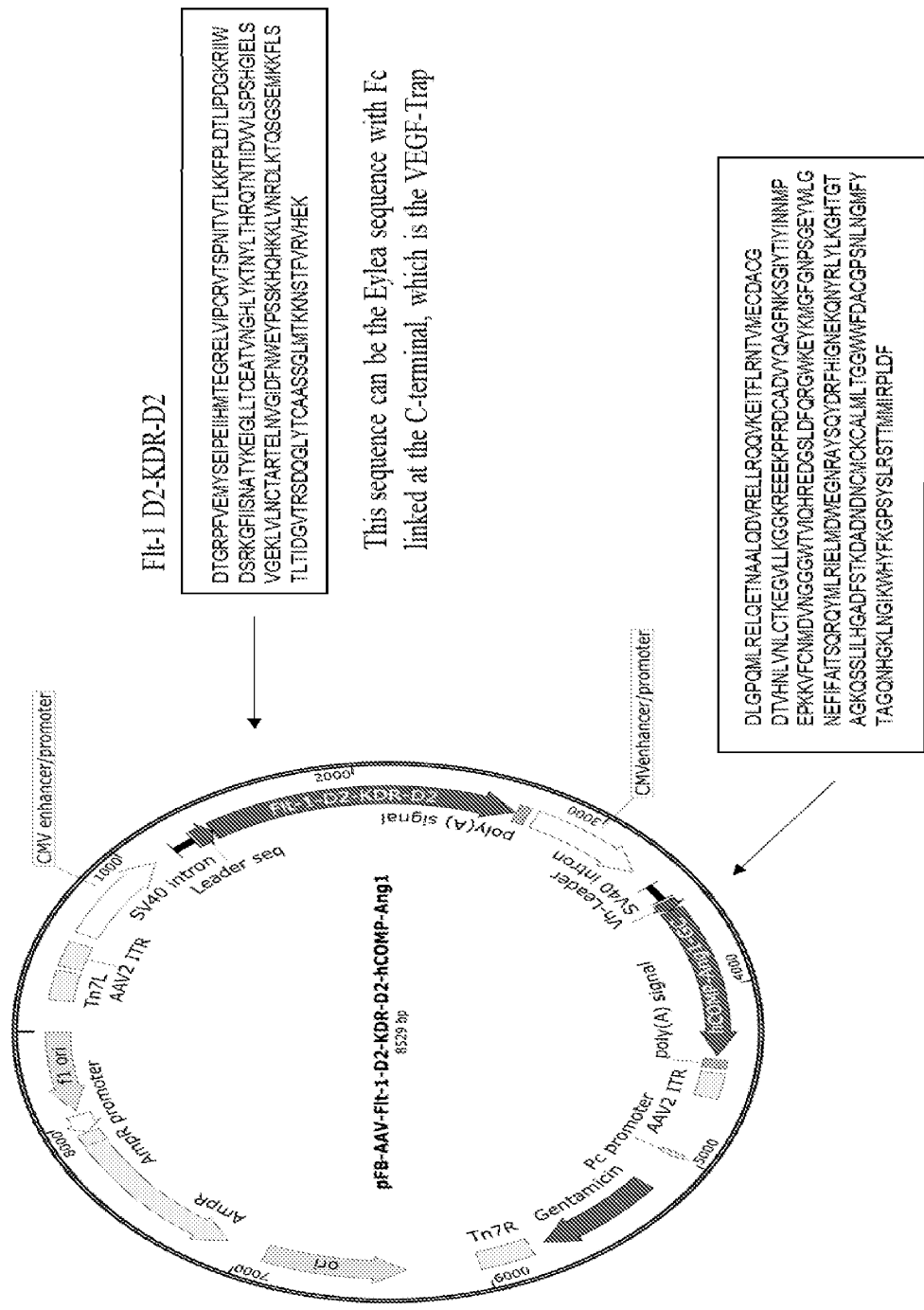


Fig. 9C

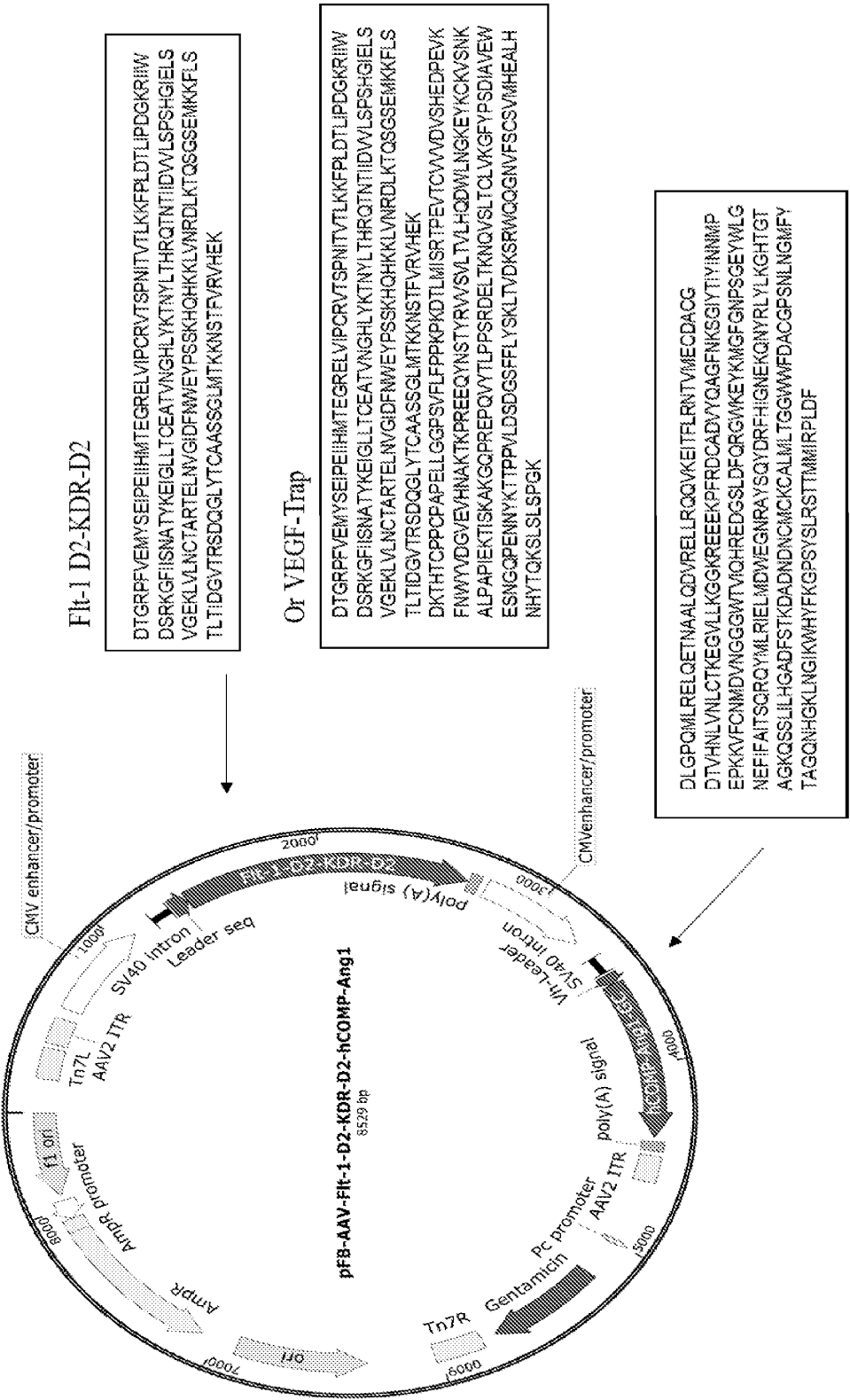


Fig. 9D

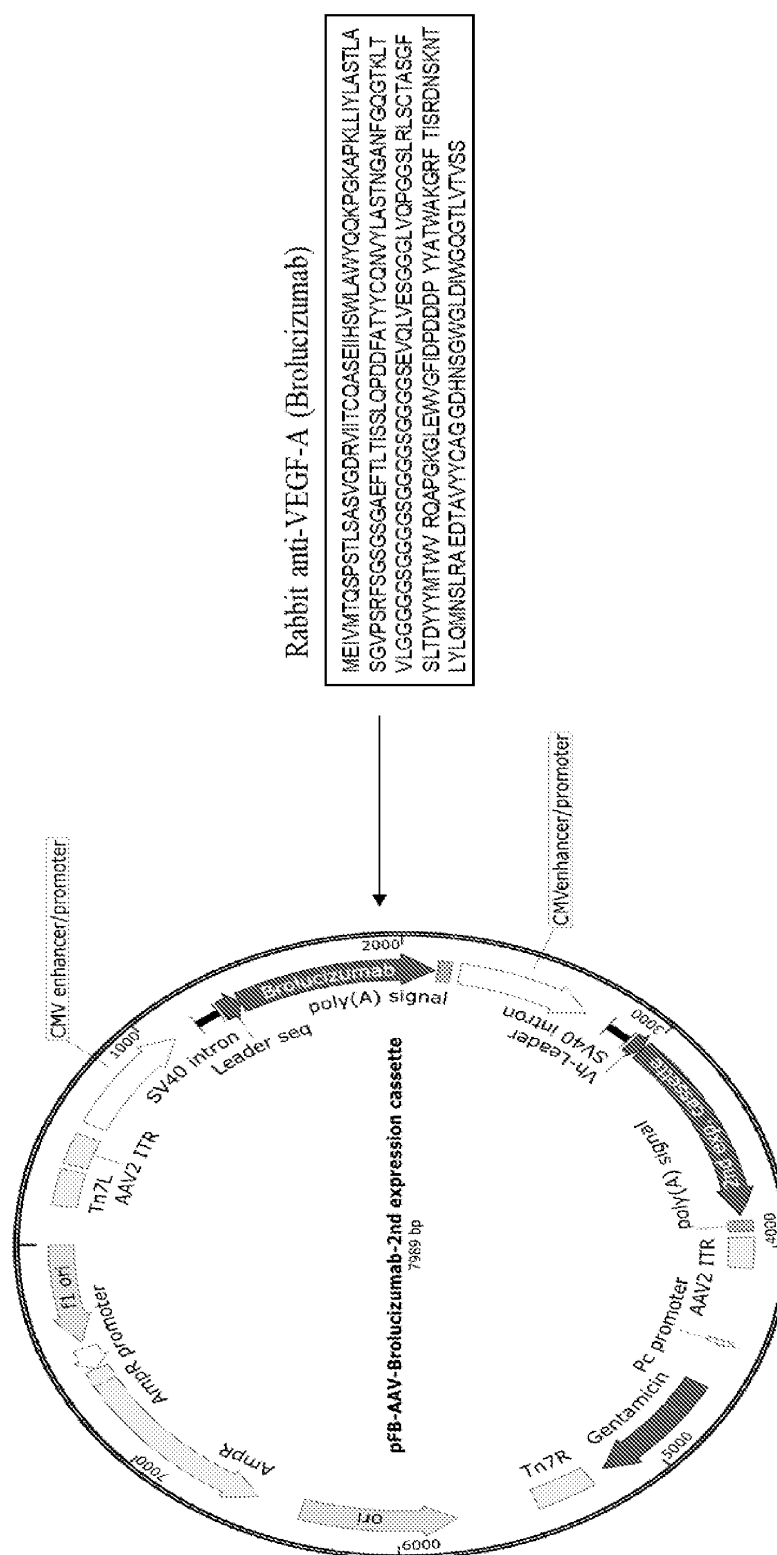


Fig. 9E

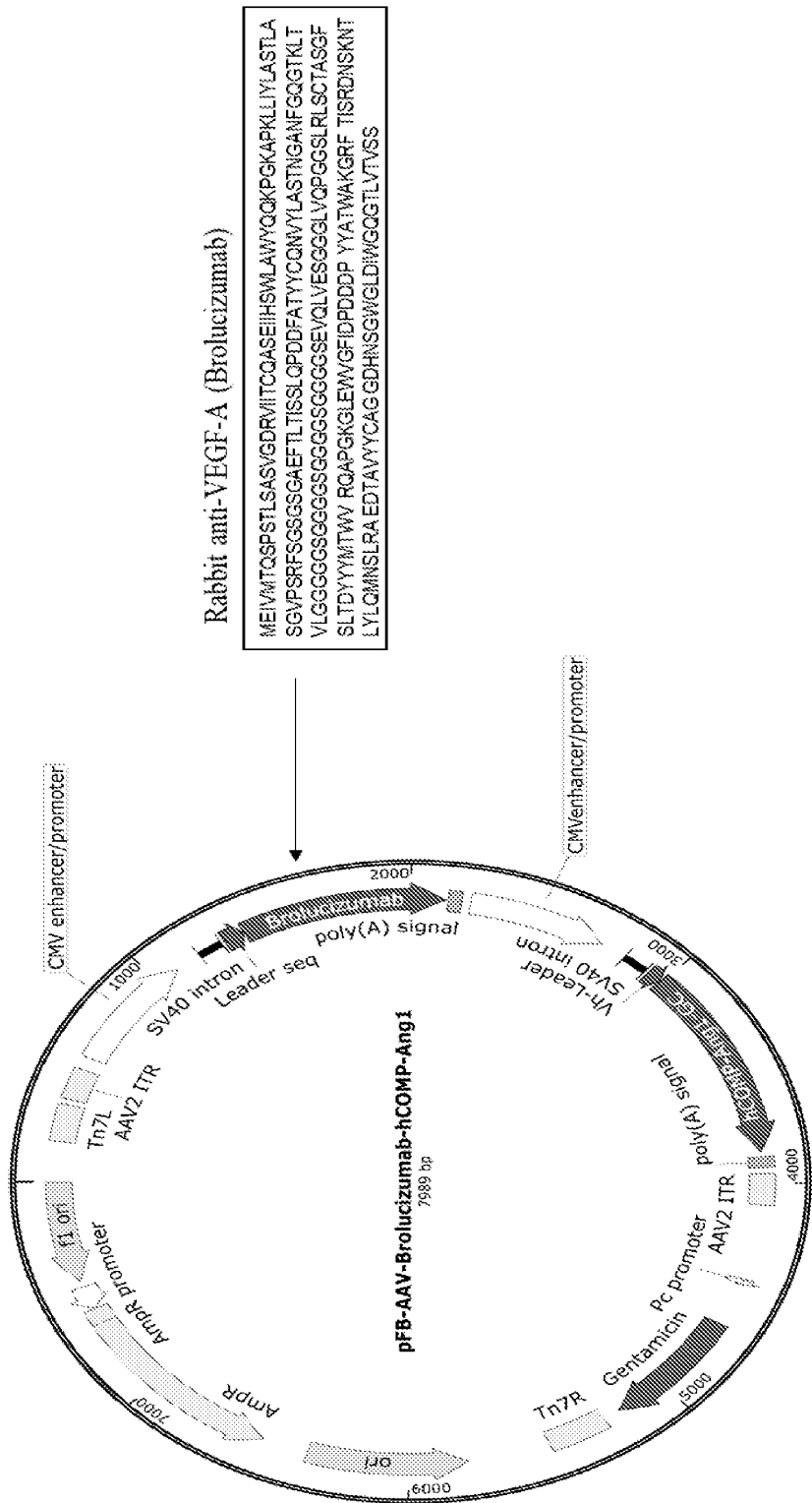


Fig. 9F

- **Ang I structure**
 - AA 1–19: the secretory signal sequence (S)
 - AA 20–158: the super clustering domain (SCD)
 - AA159–255: the coiled-coil oligomeric domain (CCOD)
 - AA 256–283: the linker (L)
 - AA 284–498: the fibrinogen-like domain (FLD), the Tie2 binding domain
 - Cysteines (C) at amino acids 41, 54, 265, 286, 315, 435, 437, 439, and 452
 - **Disadvantages of full length Ang I**
 - High Aggregation
 - Insoluble that cannot be purified
 - Unstable in solution
 - Caused by SCD and CCOD regions
-
- The diagram illustrates the structure of Angiotensin I (Ang I) and its domains. The top part shows a schematic of the full-length protein with domains N, SCD, CCOD, L, and FLD. The bottom part shows a detailed domain structure with residues 1-498. The SCD domain (residues 1-158) is shown as a coiled-coil structure. The CCOD domain (residues 159-255) is shown as a coiled-coil structure. The L domain (residues 256-283) is shown as a linker. The FLD domain (residues 284-498) is shown as a fibrinogen-like domain. The diagram also includes a legend for Native Ang I and COMP-Ang I, showing the difference in the SCD domain structure.

Fig. 10A

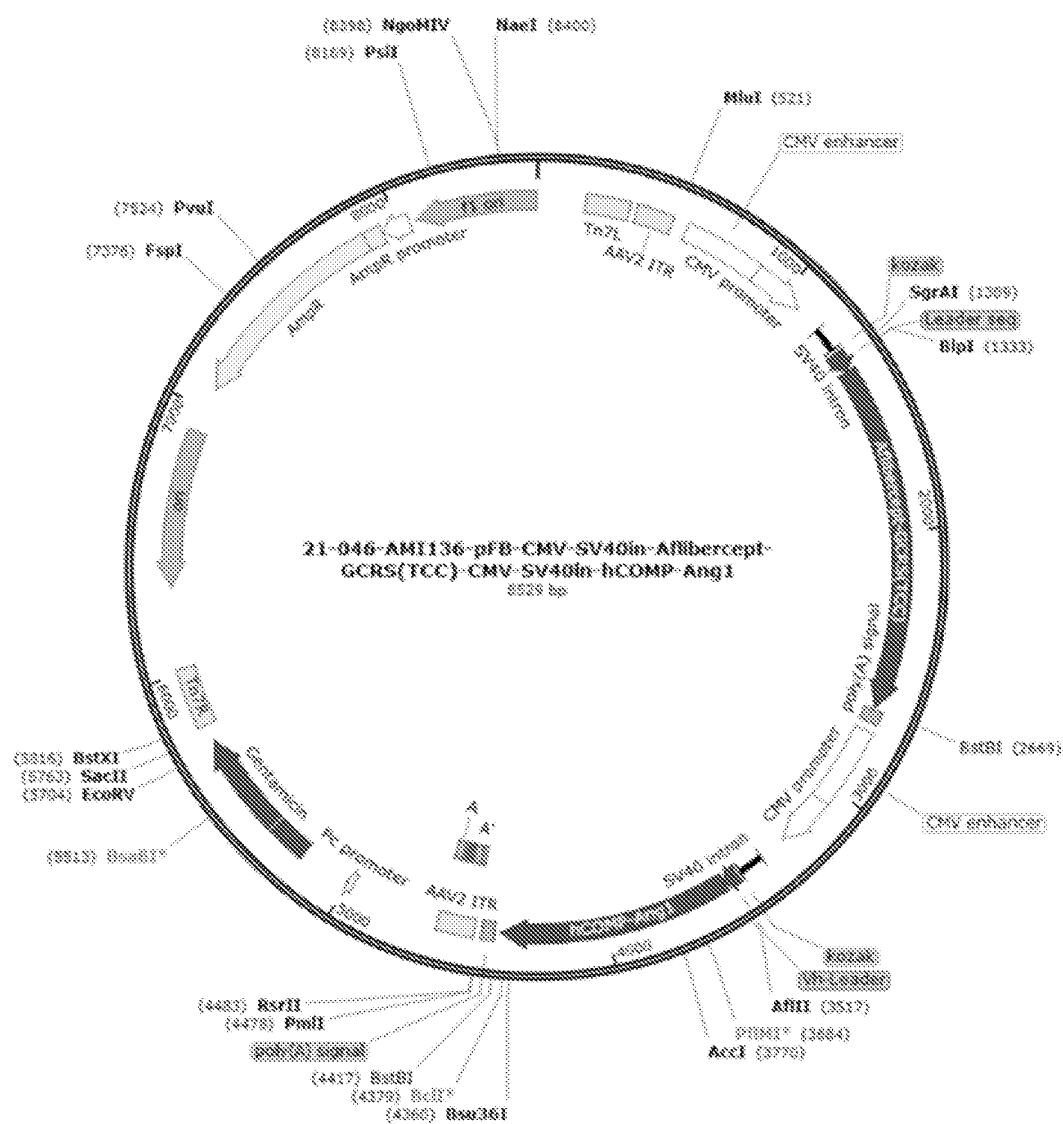


Fig. 10B

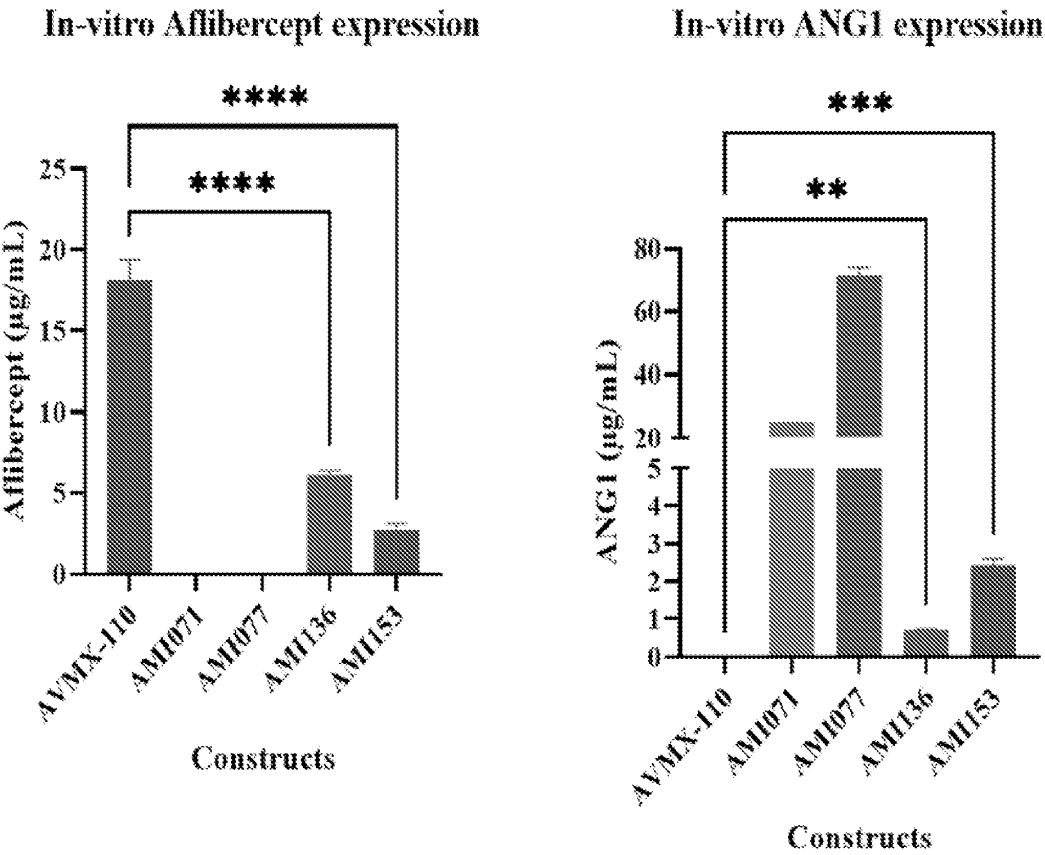


Fig. 11

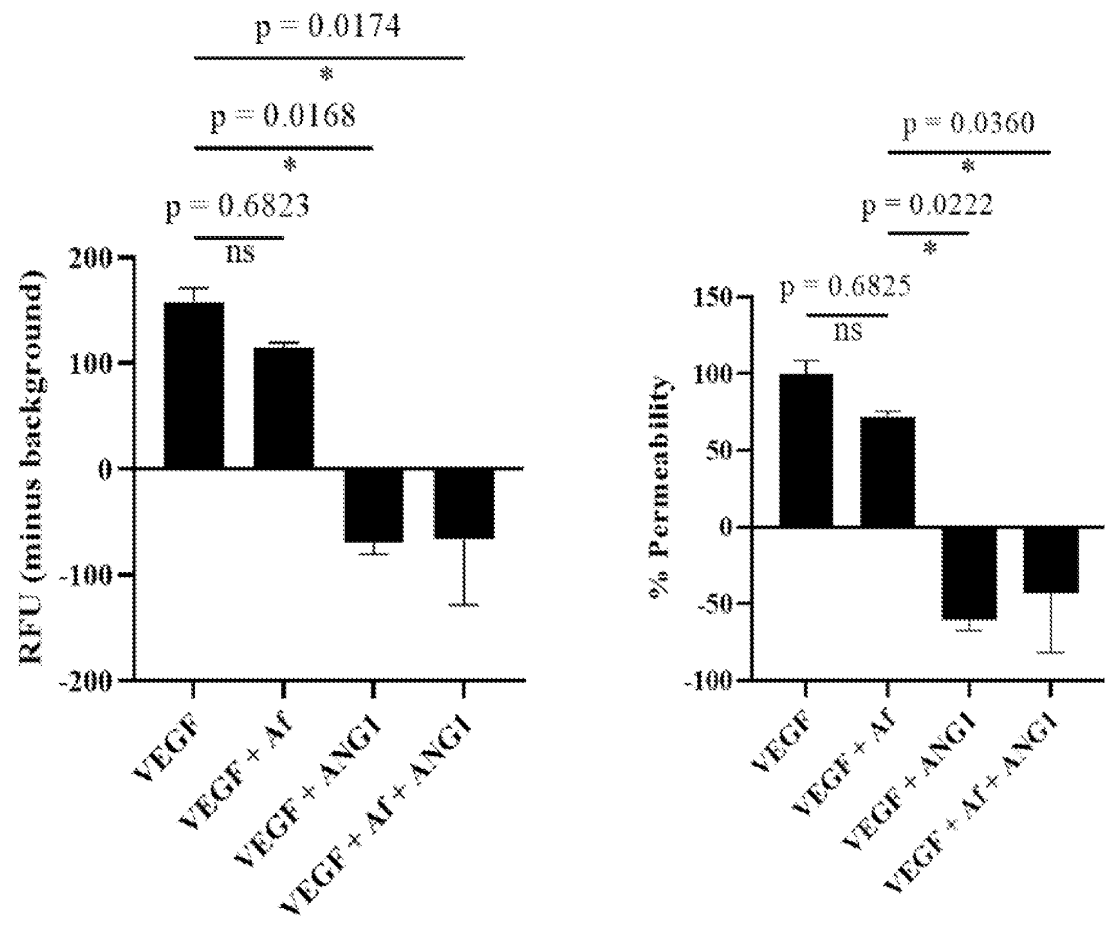


Fig. 12

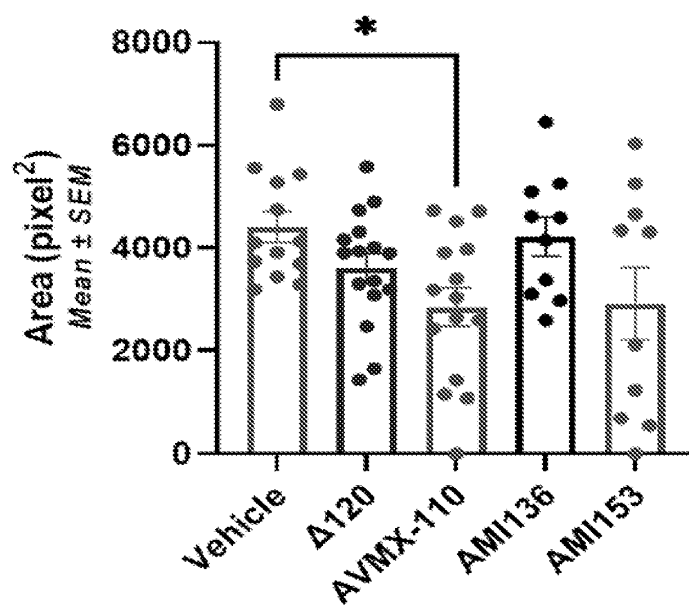


Fig. 13A

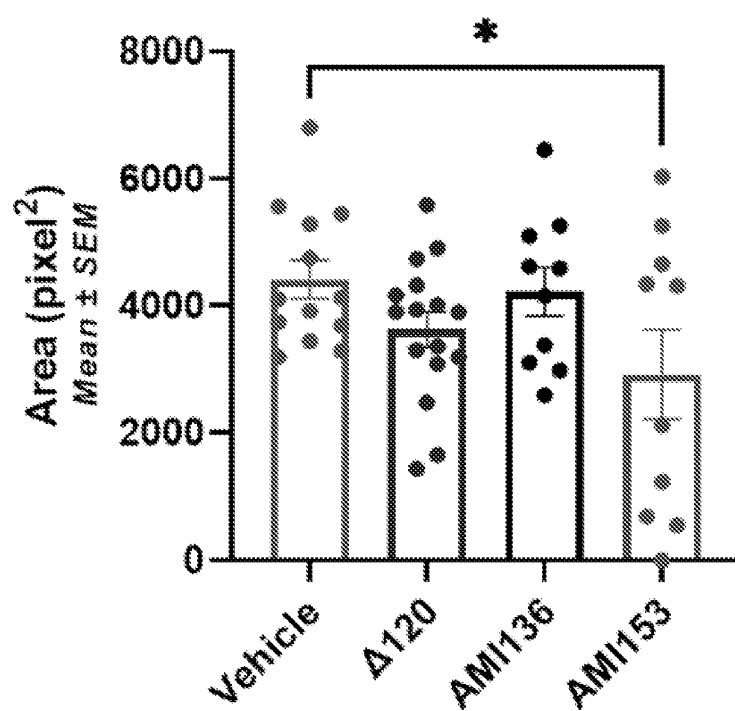
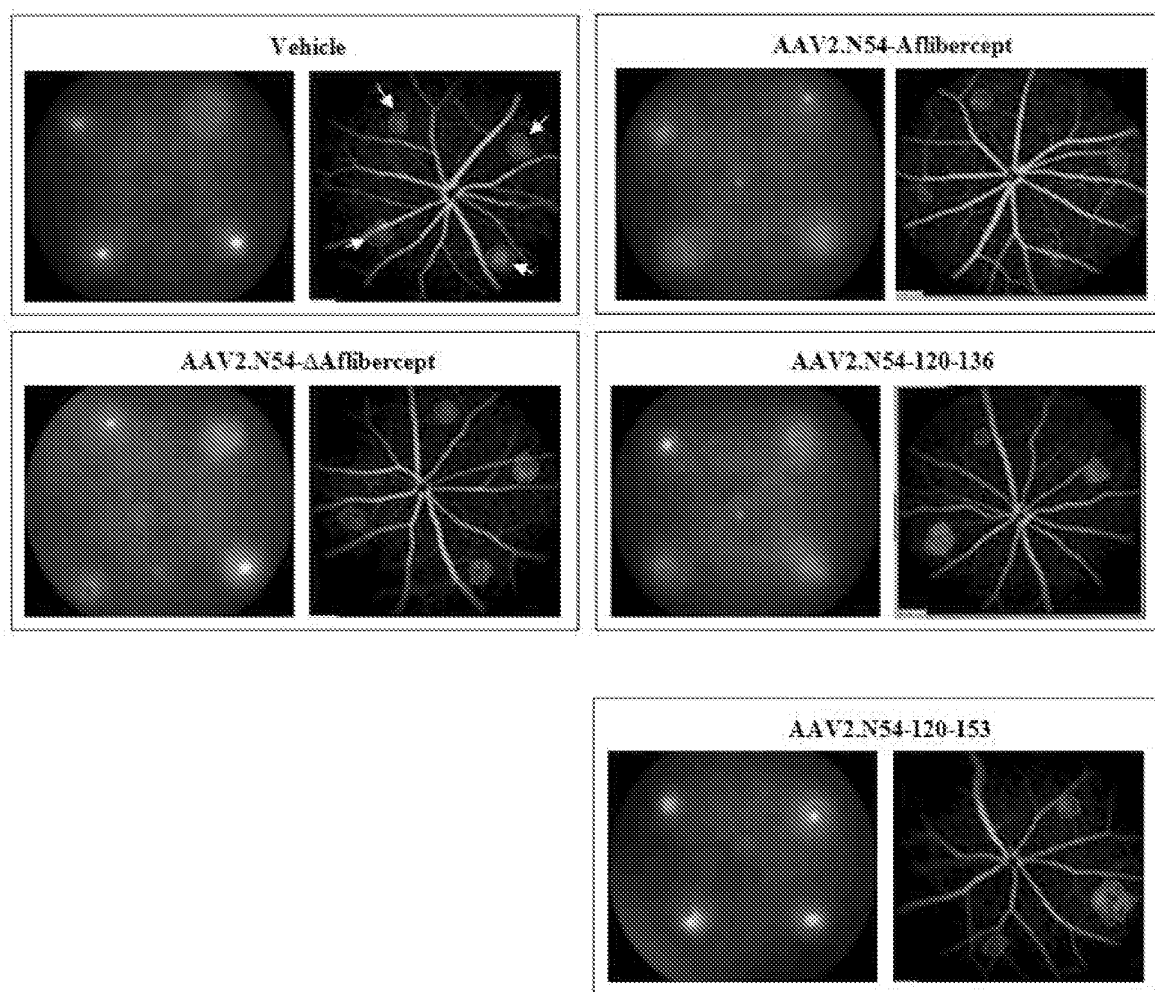


Fig. 13B

**Fig. 14**

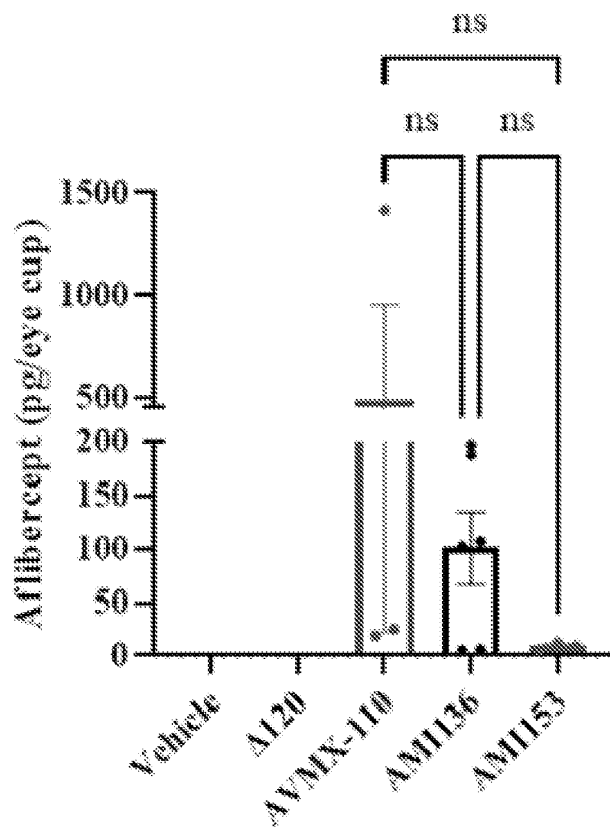


Fig. 15