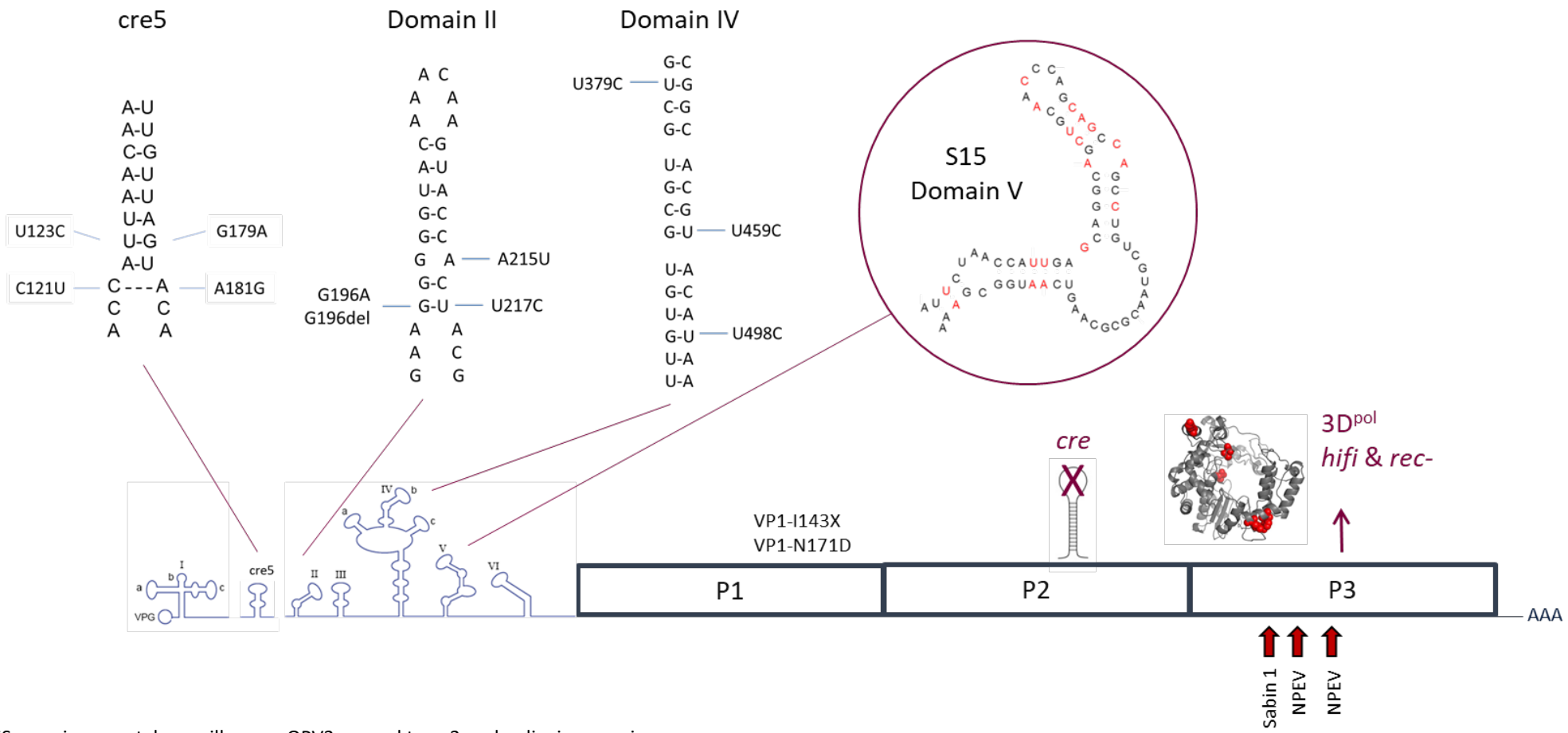
SUPPLEMENTARY FIGURE. Genomic structure of nOPV2-c1 vaccine strain with genetic modifications* responsible for attenuation, increased genetic stability and reduced potential for recombination engineered in nOPV2 and location of key mutations† and recombination junctions§ identified in nOPV2 isolates¶



Abbreviations: ES = environmental surveillance; nOPV2 = novel type 2 oral poliovirus vaccine.

* Modifications include stabilized domain V, knock-out of wild-type cis-acting replication element (cre) originally present in the P2 coding region, new cre5 introduced in the 5'NCR, and hifi and rec- 3D polymerase mutations.

† Mutations that have been shown or inferred to decrease attenuation identified in nOPV2 isolates are indicated.

§ The location of recombinant crossover points identified in 6 recombinant nOPV2 isolates is shown with red arrows. One nOPV2 isolate from an AFP contact case from Sierra Leone showed recombination with a species C enterovirus at nucleotide position 5837, three nOPV2 isolates from an ES sample from Tajikistan had recombined with Sabin 1 poliovirus between nucleotides 5525-5554 and two nOPV2 isolates from an ES sample from Congo Brazzaville recombined with another species C enterovirus at nucleotide position 6076.

¶ Whole genome sequences were generated for 251 nOPV2 isolates. Of the 128 nOPV2 isolates from stools, corresponding to 99 distinct AFP cases and 1 healthy child, 9 were from Benin, 4 from Liberia, 17 from Niger, 88 from Nigeria, 4 from Sierra Leone and 6 from Tajikistan. Of the 123 nOPV2 isolates corresponding to 39 distinct ES samples, 2 were from Benin, 11 from Congo Brazzaville, 8 from Liberia, 11 from Nigeria, 17 from Sierra Leone, 2 from Togo, and 72 from Tajikistan.