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Supplemental Information

**The 2.8 Å Electron Microscopy Structure
of Adeno-Associated Virus-DJ Bound
by a Heparinoid Pentasaccharide**

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Supplemental Figures

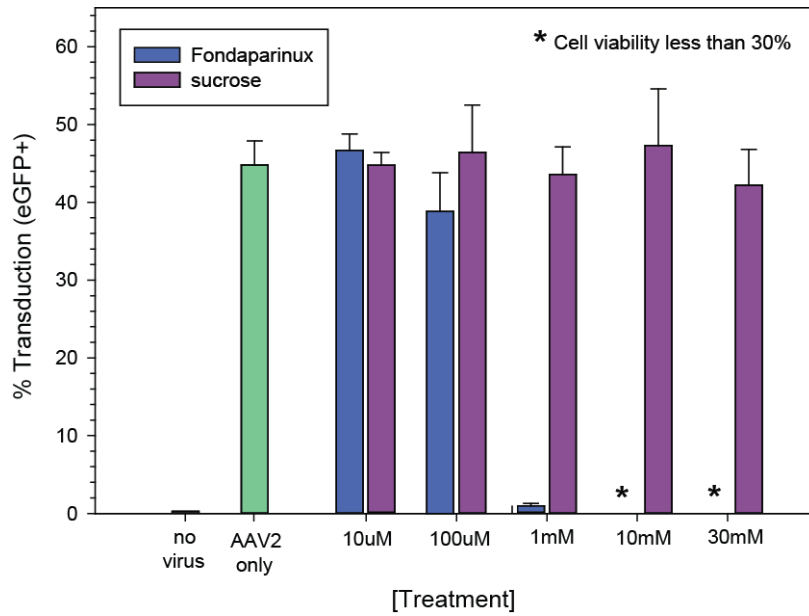


Figure S1: Controls for the transduction inhibition assay (Figure 2). Transduction in HeLa cells was measured using an eGFP-AAV2 vector, but otherwise as in Figure 2. The histogram shows that the inhibition, specific for fondaparinux, is not shared by equimolar treatments with sucrose. Viability was assayed by trypan blue exclusion, counted by hand.

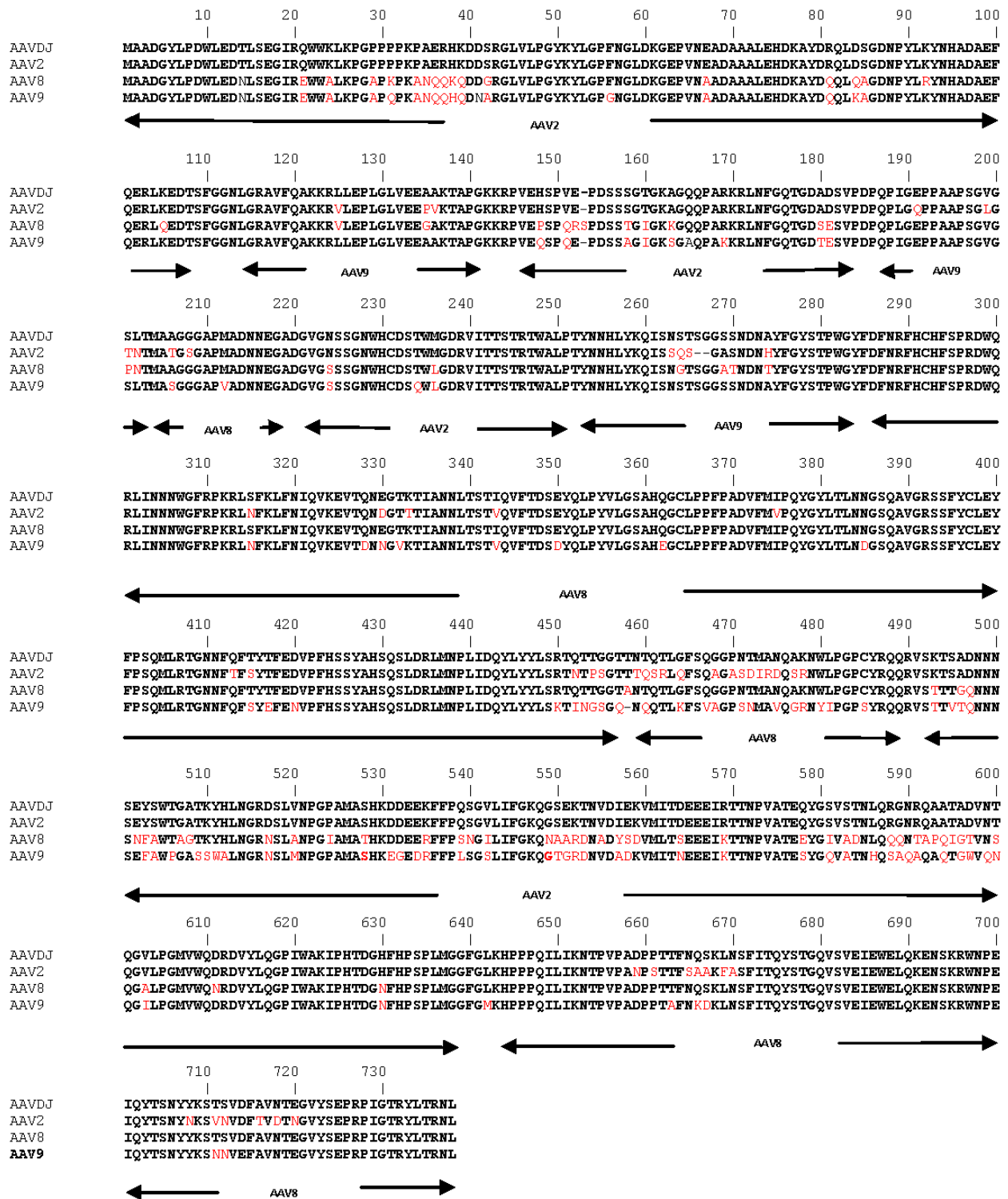


Figure S2: Sequence and structural alignment of AAV-DJ with its parental strains. Residues differing in amino acid type from AAV-DJ are shown in red. In places, the absence of sequence

differences uniquely defines the parental origin, but in other regions of higher serotype sequence identity, the designation (shown with arrows under the sequences) is ambiguous, so a parsimonious choice has been made that minimizes the number of sequence cross-overs, and gives have closest C_{α} alignment, in the 3D structures.

Supplemental Table

Serotype	Antibody	Neutralizing	Mapping	Resolution	Citation
AAV-1	ADK1a	Yes	<i>Cryo-EM</i>	11 Å	(1)
	ADK1b	Yes	<i>Cryo-EM</i>	11 Å	(1)
	4E4	Yes	<i>Cryo-EM</i>	12 Å	(2)
	5H7	Yes	<i>Cryo-EM</i>	23 Å	(2)
AAV-2	A20	Yes	<i>Cryo-EM</i>	8.5 Å	(3)
			Site-directed mutagenesis		(4)
			Peptide insertion		(5)
			Peptide scanning		(6)
	C37B	Yes	<i>Cryo-EM</i>	11 Å	(2)
			Peptide insertion		(5)
	D3	No	Peptide scanning		(6)
C24B	Yes	Peptide scanning		(6)	
AAV-5	ADK5a	No	<i>Cryo-EM</i>	11 Å	(1)
	ADK5b	Yes	<i>Cryo-EM</i>	12 Å	(1)
	3C5(B)	No	<i>Cryo-EM</i>	15 Å	(2)
AAV-6	5H7	Yes	<i>Cryo-EM</i>	15 Å	(2)
AAV-8	ADK8	Yes	<i>Cryo-EM</i>	19 Å	(7)
			Site-directed mutagenesis		(7)
			Peptide insertion		(7)

References

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