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Supplemental information

AAVolve: Concatenated long-read deep sequencing enables whole capsid tracking during shuffled AAV library selection

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Supplemental Material

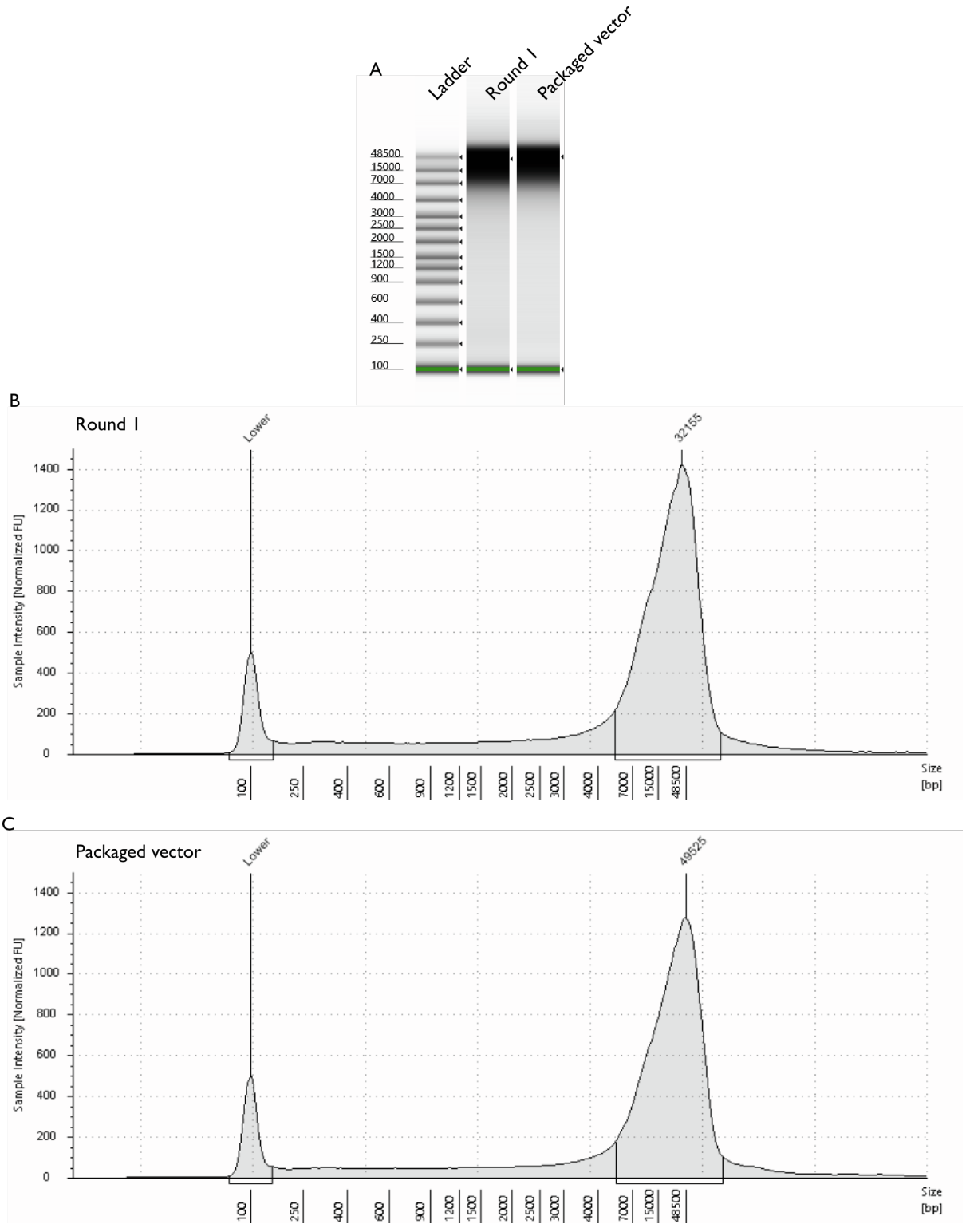

Figure S1: Concatenated sequence sizes after rolling circle amplification. Concatenated sequence sizes were assessed by TapeStation using a gDNA TapeScreen (**A**). A range of fragment sizes were observed, with peaks at 32 kb (**B**) and 50 kb (**C**).

Table S1: Read counts at each stage of processing for nanopore R2C2 sequencing of a shuffled library throughout selection.

Selection round	Raw	Consensus	Filtered consensus	Filtered by reference coverage	Reads with identified parents	Distinct amino acids	Distinct nucleotides
packaged	6608269	4661647	1828943	1304081	911631	790877	835120
round 1	3693976	2562420	1249968	849257	613756	435364	508164
round 5	2249965	1485856	431377	415711	315647	13069	60135

Table S2: Read counts for sequencing technologies used at round 5 of selection (see Table S1 for ONT R2C2

Sequencing technology	Raw	Consensus	Filtered consensus	Filtered by reference coverage	Reads with identified parents	Distinct amino acids	Distinct nucleotides
Nanopore	5274844	NA	NA	2833705	2249	755	2107

Sanger	48	NA	NA	48	44	23	27
PacBio	113581	NA	67971	64926	42412	2094	8749