Supplementary materials:

Capsid structure and its Stability at the Late Stages of Bacteriophage SPP1 Assembly

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Table S1

Data collection statistics and structural features of the SPP1 capsids

Capsid	Imaging detector	Image ##	Defocus range (μm)	Resolu-tion (Å)	Average diameter (Å)	Wall (shell) (Å)	Spike height (Å)	Average inter-DNA distance (Å)
FP	SO163 film	5293	0.7-2.5	8.8	610	27	35	23.5±2.5
EP	SO163 film	1243	0.7-2.5	10.5	610	27	35	n/a
H	CCD	~4000	1.0-3.5	11.7	610	27	35	24.5±2.5
HΔ12	CCD	~3200	1.0-3.5	15.1	600	27	n/a	24.5±2.5

Table S2

Role of capsid auxiliary proteins. Phages that require auxiliary proteins for capsid stability are shaded blue, while those that do not are shaded green.

Phage	Protein name	Location	References
lambda	gpD	3-fold	(6, 9)
T4	Soc	Between hexamers	(3, 4)
phage L	Dec	3-fold axes nearest to the icosahedral 2-fold axes	(7)
epsilon 15	gp10	staples adjacent capsomers at the 2-fold axes	(5)
phage N4	gp17	near quasi-3-fold axes	(1)
T4	Hoc	centre of hexamers	(3)
T5	pb10	centre of hexamers	(2)
SPP1	gp12	centre of hexamers	(8)

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2. **Effantin, G., P. Boulanger, E. Neumann, L. Letellier, and J. F. Conway.** 2006. Bacteriophage T5 structure reveals similarities with HK97 and T4 suggesting evolutionary relationships. Journal of molecular biology **361:**993-1002.
3. **Fokine, A., P. R. Chipman, P. G. Leiman, V. V. Mesyanzhinov, V. B. Rao, and M. G. Rossmann.** 2004. Molecular architecture of the prolate head of bacteriophage

T4. Proceedings of the National Academy of Sciences of the United States of America **101:**6003-6008.

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6. **Lander, G. C., A. Evilevitch, M. Jeembaeva, C. S. Potter, B. Carragher, and J. E. Johnson.** 2008. Bacteriophage lambda stabilization by auxiliary protein gpD: timing, location, and mechanism of attachment determined by cryo-EM. Structure **16:**1399-1406.
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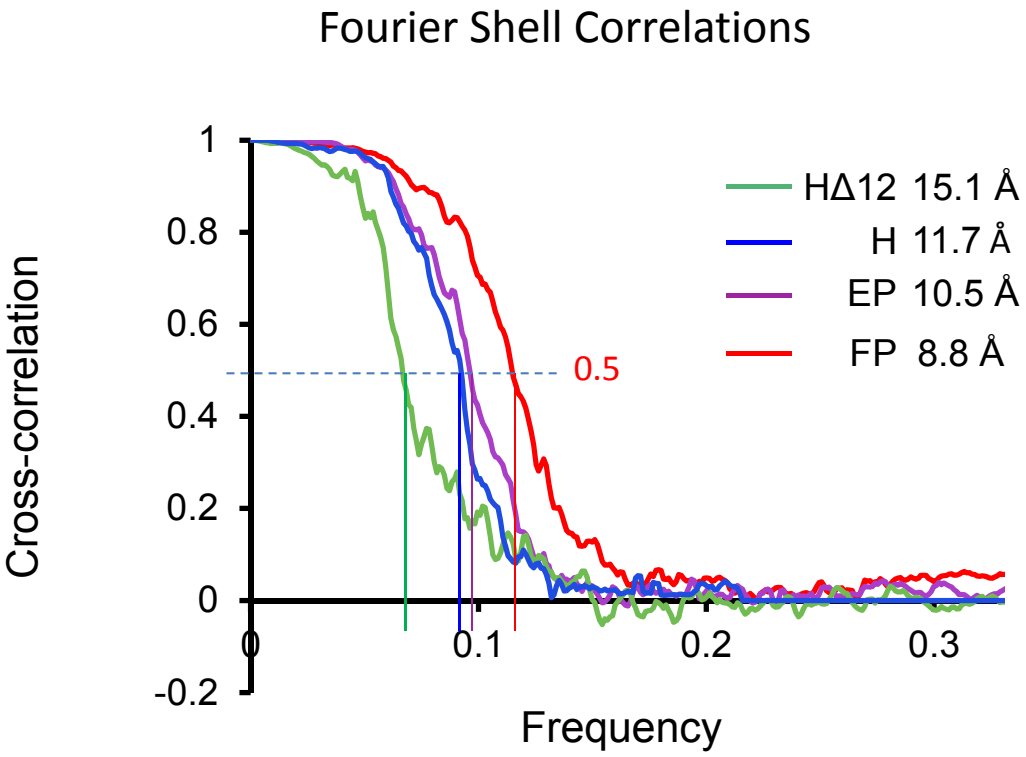
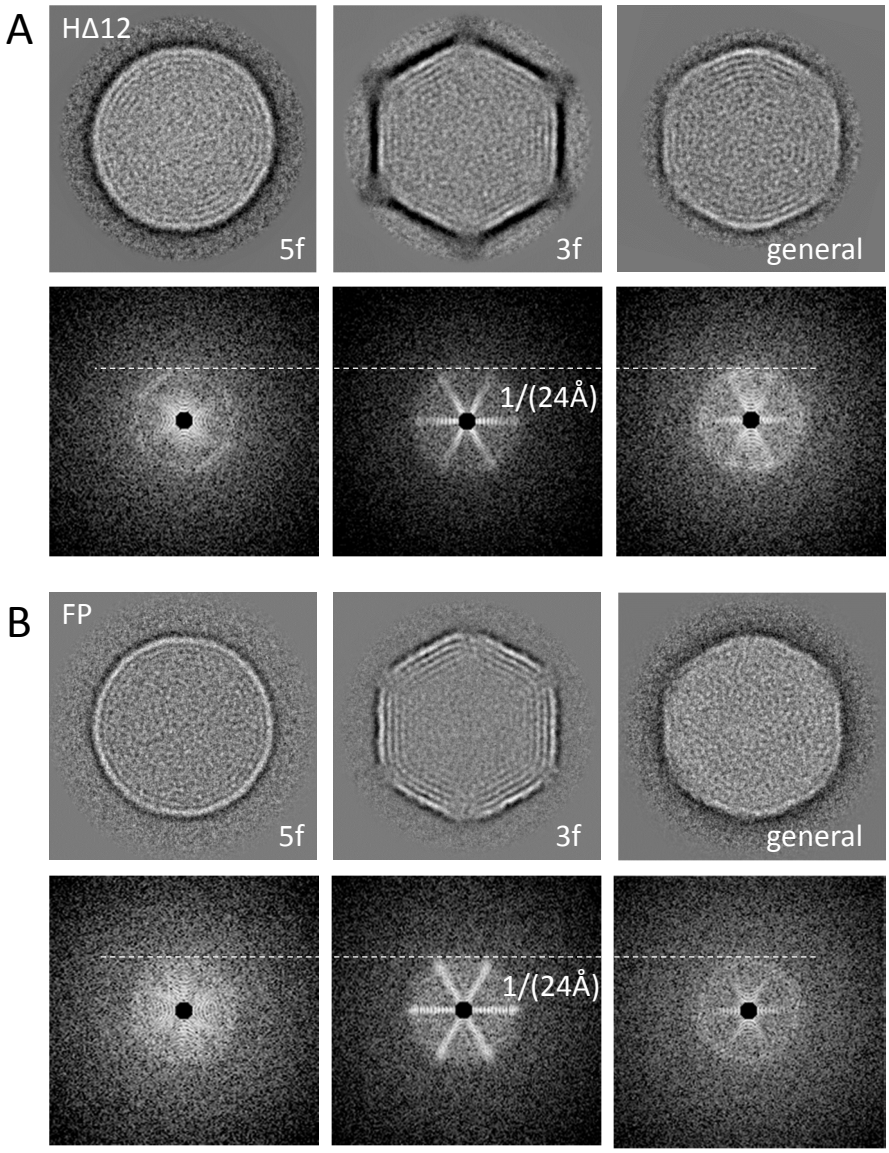


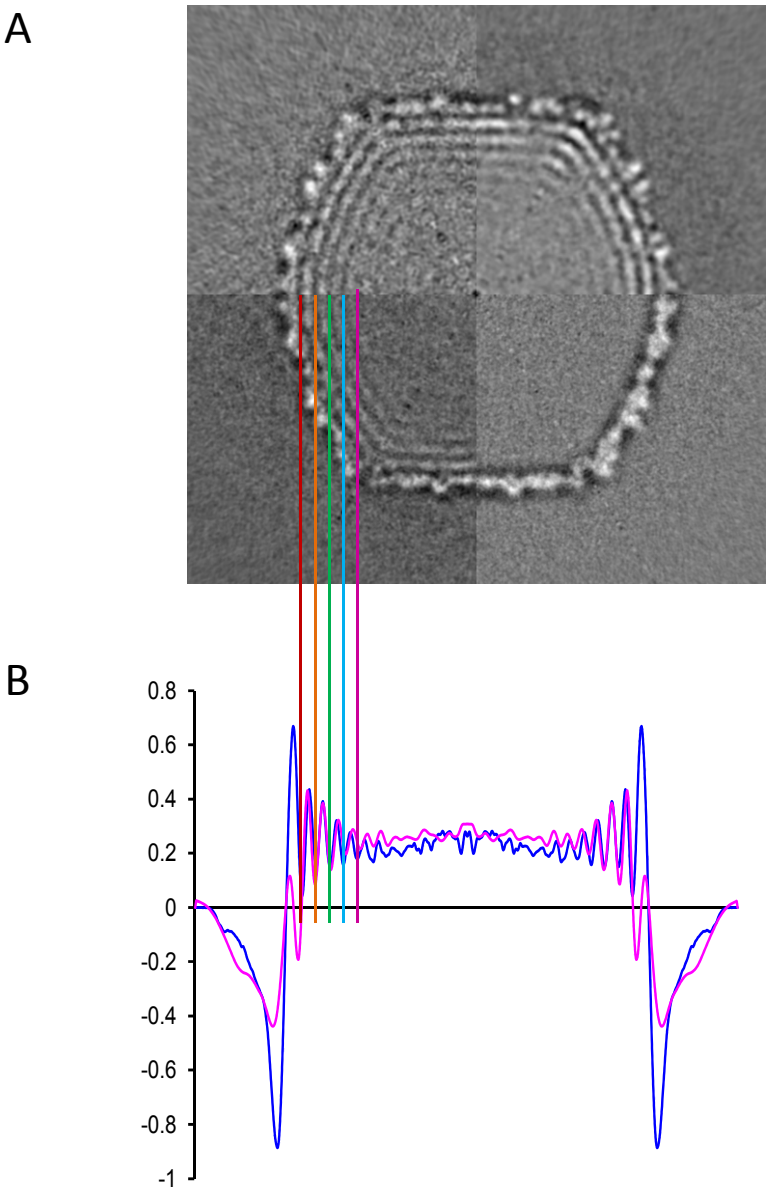
Supplementary Fig1. Fourier shell correlations for HΔ12 (green), H (blue), EP (purple) and FP (red) capsid reconstructions.

Supplementary Figure 1 (related to Figure 4)



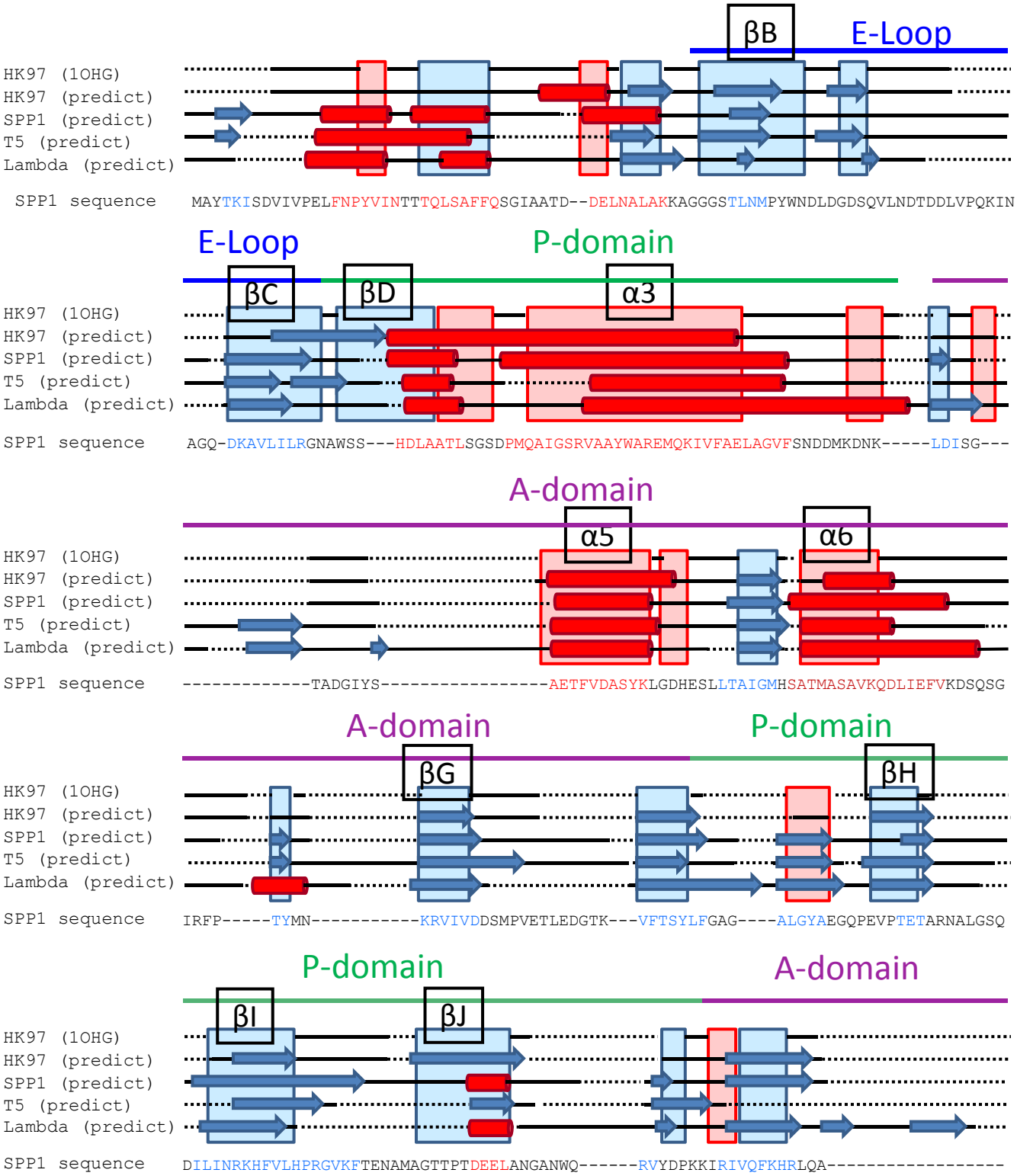
Supplementary Fig 2. Class averages for the 5-fold, 3-fold and a general view (top) of HΔ12 (A) and FP (B) capsids and their corresponding diffraction patterns (bottom). All diffractions (Fourier transforms) demonstrate the same distances for DNA packing in decorated and non-decorated capsids.

Supplementary Figure 2 (related to Figure 2)



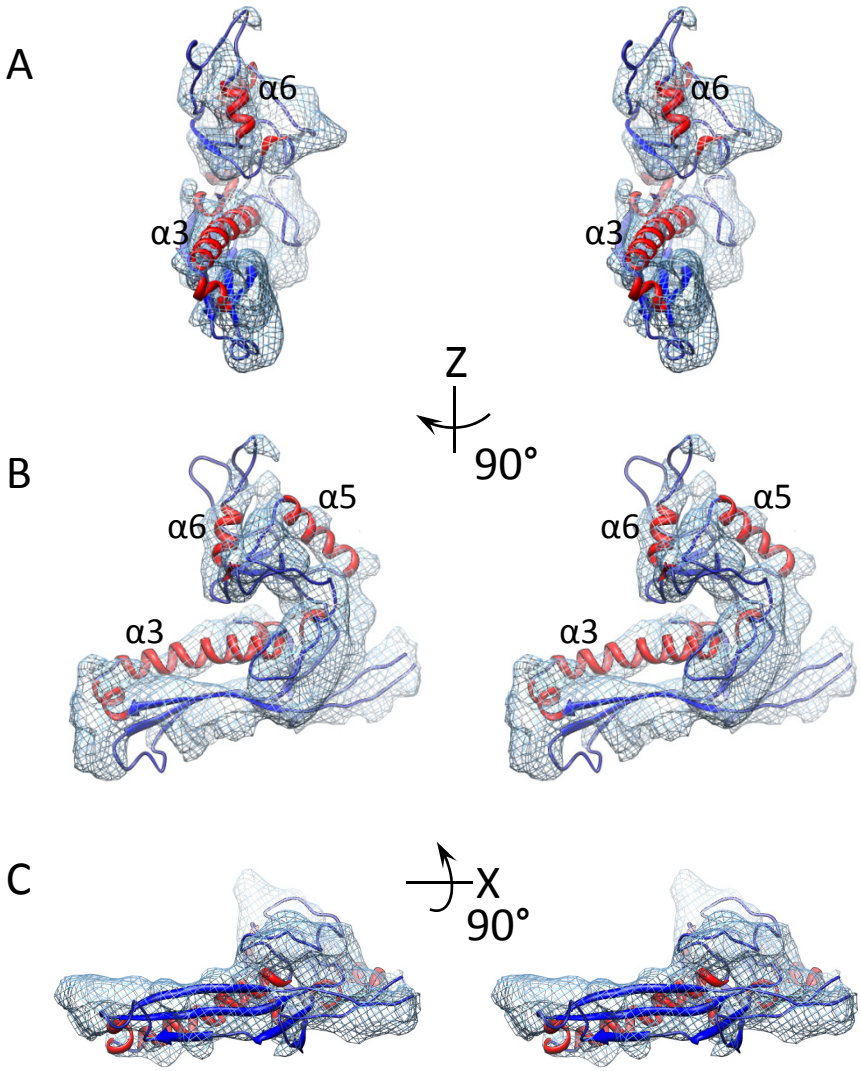
Supplementary Fig 3. DNA organization in 3D reconstructions of SPP1 capsids. A- Sections through the central plane of the reconstructions highlighting the concentric layers of DNA. B - Profile across a rotationally averaged central section showing the position of DNA rings in HΔ12 (magenta) and FP (blue) 3D capsid reconstructions.

Supplementary Figure 3 (related to Figures 2 and 5)



Supplementary Fig 4. Secondary structure alignment of major capsid proteins. The predicted secondary structures for HK97, SPP1, T5 and Lambda proteins are aligned to the secondary structure elements found in the crystallographic structure of gp5 from HK97 (1ohg). Predicted helices are shown as red cylinders and predicted β-strands as blue arrows. Helices in 1ohg are shown as red rectangles and β-strands as blue rectangles. The domain to which the sequence belongs is shown above the alignment. The SPP1 sequence, colored according to the secondary structure prediction, is shown below.

Supplementary Figure 4 (related to Figure 6)



Supplementary Figure 5. Different views of the refined fit of the gp13 model into the EM map.
A) Stereo view of one subunit of FP with helices 3, 5, and 6 coloured red. B) Rotated by 90° around Z axis C) Rotated by 80° around X axis.