

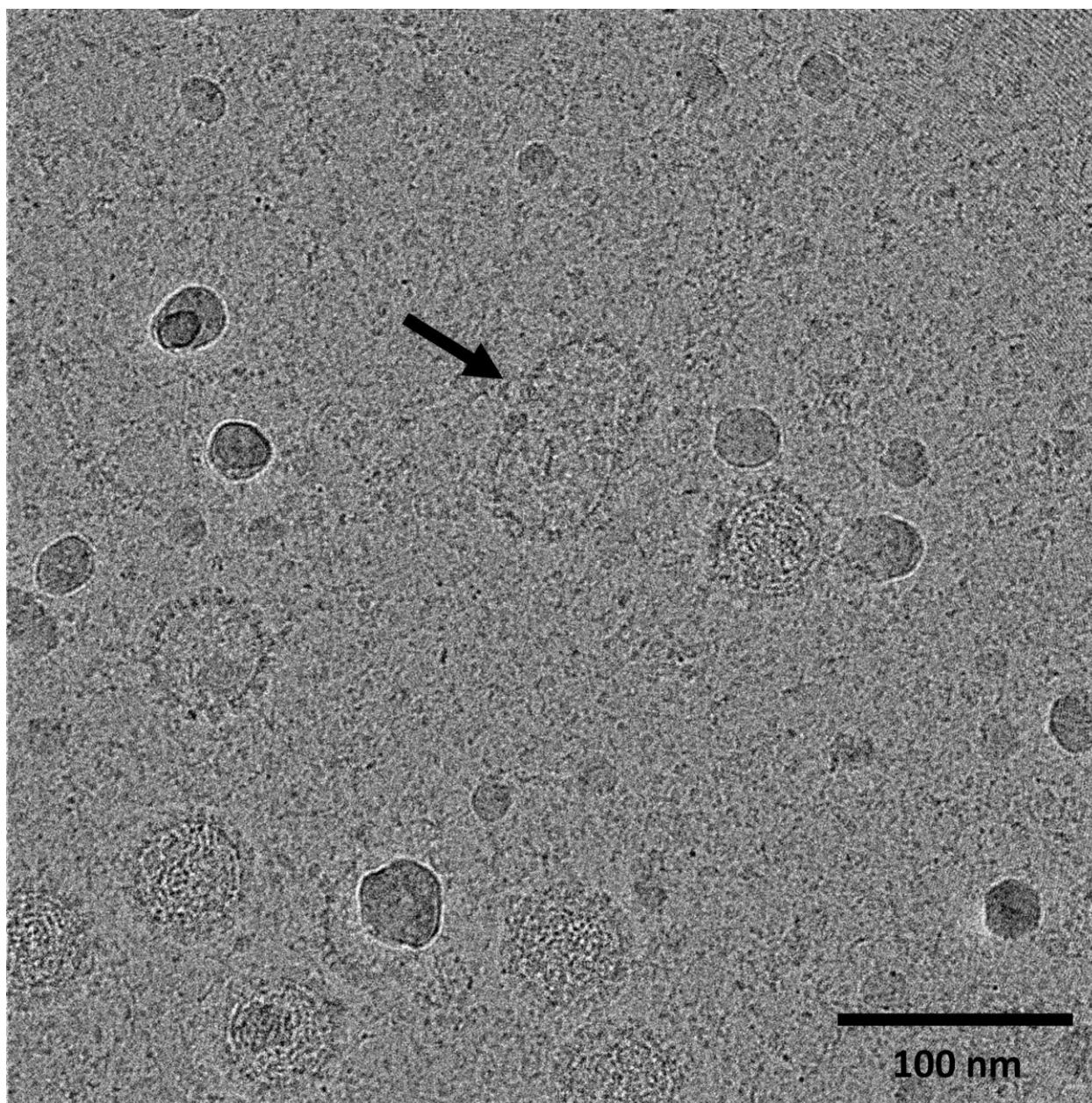
## Supplementary Information

**Supplementary Table S1. Cryo-EM data collection, refinement and validation statistics.**

<b>Data Collection and Processing</b>	<b>Icosahedral</b>	<b>Pentavalent Capsomer</b>	<b>Hexavalent Capsomer</b>
Magnification	59,000	59,000	59,000
Voltage (kV)	300	300	300
Electron Exposure (e-/Å <sup>2</sup> )	45	45	45
Defocus Range (um)	0.5-3.0	0.5-3.0	0.5-3.0
Pixel Size (Å)	1.1	1.1	1.1
Symmetry Imposed	I1	C5	C1
Initial Particle Number	16,978	-	-
Final Particle Number	10,181	-	-
Sub-particles per Particle	-	12	60
Final Sub-particle Number	-	122,172	610,860
Map Resolution	4.41	3.4	3.3
FSC Threshold	0.143	0.143	0.143

<b>Refinement</b>	<b>Recombined Capsid</b>
Model composition	
Non-hydrogen atoms	22959
Protein Residues	2867
B-Factors	
Protein	53.4
Validation	
MolProbity Score	1.71
Clash Score	6.65
Rotamer Outliers (%)	0.04
Ramachandran Plot	
Favored (%)	95.10
Outliers (%)	0.28



**Supplementary Figure S1. Micrograph with rod like structure.** Black arrow points to a rod like structure that is seen within the dataset.

A:F

Level	Count	Std Dev	MeanAbsDif to Mean	MeanAbsDif to Median
HPV16 Quasivirus	43679	0.0407412	0.0289734	0.0289458
MmuPV1 Native Virus	2681	0.0254883	0.0164075	0.0163573

Test	F Ratio	DFNum	DFDen	p-Value
O'Brien[.5]	233.1095	1	46358	<.0001*
Brown-Forsythe	500.3583	1	46358	<.0001*
Levene	501.7482	1	46358	<.0001*
Bartlett	853.3847	1	.	<.0001*
F Test 2-sided	2.5550	43678	2680	<.0001*

B:Null

Level	Count	Std Dev	MeanAbsDif to Mean	MeanAbsDif to Median
HPV16 Quasivirus	87358	0.0358045	0.0255266	0.0255079
MmuPV1 Native Virus	5108	0.0230426	0.0151967	0.0151844

Test	F Ratio	DFNum	DFDen	p-Value
O'Brien[.5]	401.7804	1	92464	<.0001*
Brown-Forsythe	835.8814	1	92464	<.0001*
Levene	841.2870	1	92464	<.0001*
Bartlett	1460.2527	1	.	<.0001*
F Test 2-sided	2.4144	87357	5107	<.0001*

C:D

Level	Count	Std Dev	MeanAbsDif to Mean	MeanAbsDif to Median
HPV16 Quasivirus	87358	0.0375155	0.0262676	0.0262637
MmuPV1 Native Virus	4825	0.0254530	0.0157794	0.0157787

Test	F Ratio	DFNum	DFDen	p-Value
O'Brien[.5]	304.5668	1	92181	<.0001*
Brown-Forsythe	716.1693	1	92181	<.0001*
Levene	717.7739	1	92181	<.0001*
Bartlett	1101.6752	1	.	<.0001*
F Test 2-sided	2.1724	87357	4824	<.0001*

E:E

Level	Count	Std Dev	MeanAbsDif to Mean	MeanAbsDif to Median
HPV16 Quasivirus	43679	0.0392467	0.0282713	0.0282526
MmuPV1 Native Virus	2765	0.0274450	0.0187063	0.0186933

Test	F Ratio	DFNum	DFDen	p-Value
O'Brien[.5]	181.0447	1	46442	<.0001*
Brown-Forsythe	328.5869	1	46442	<.0001*
Levene	330.0078	1	46442	<.0001*
Bartlett	542.9211	1	.	<.0001*
F Test 2-sided	2.0449	43678	2764	<.0001*

Diameter

Level	Count	Std Dev	MeanAbsDif to Mean	MeanAbsDif to Median
HPV16 Quasivirus	50224	0.0090671	0.0072330	0.0072330
MmuPV1 Native Virus	3967	0.0106710	0.0078790	0.0078165

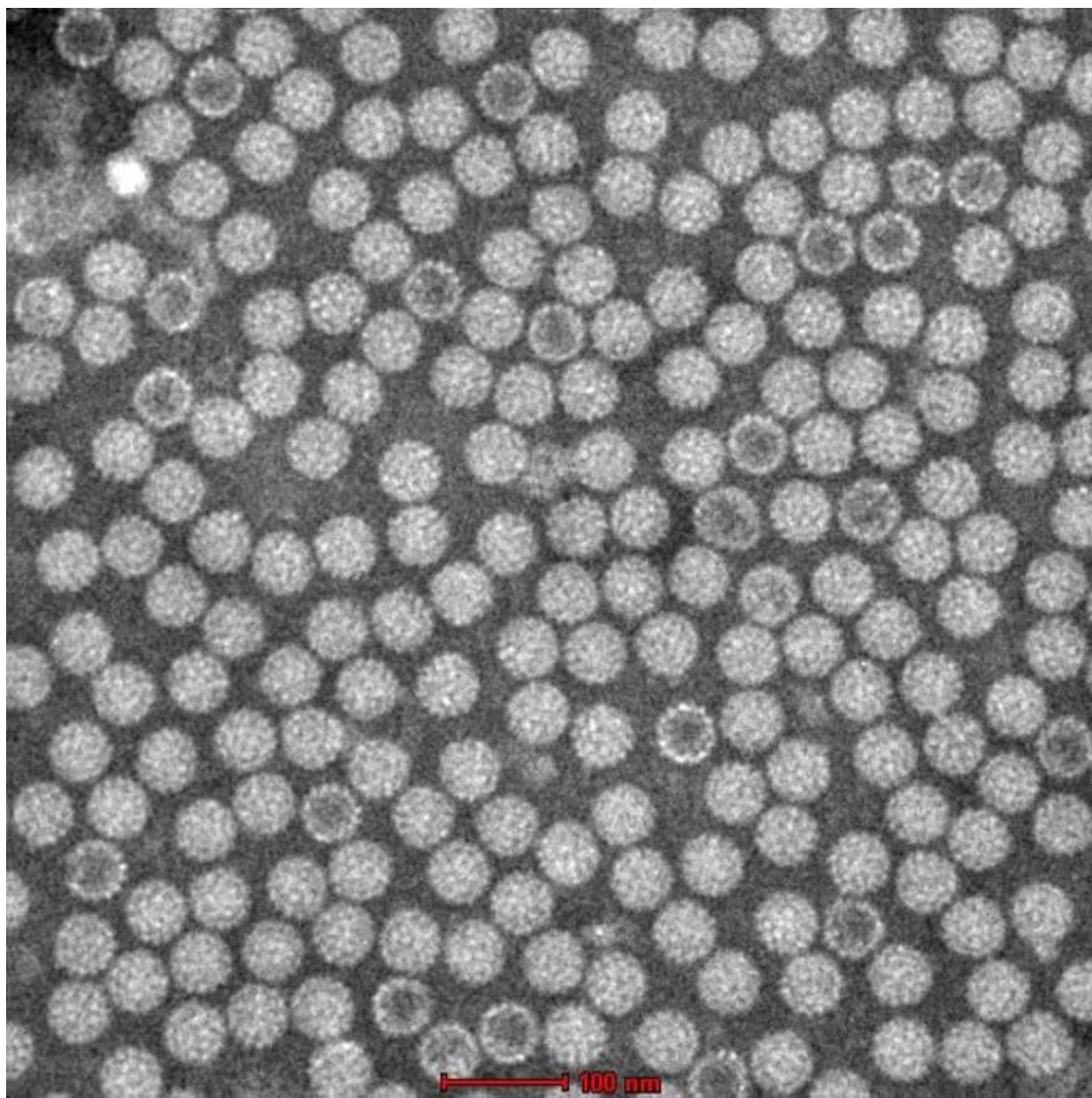
Test	F Ratio	DFNum	DFDen	p-Value
O'Brien[.5]	181.3232	1	54189	<.0001*
Brown-Forsythe	39.5270	1	54189	<.0001*
Levene	48.7183	1	54189	<.0001*
Bartlett	214.1058	1	.	<.0001*
F Test 2-sided	1.3851	3966	50223	<.0001*

**Supplementary Figure S2. Statistical Tests of Unequal Variances.** Comparison of HPV16 QV and MmuPV1 for intercapsomere distances and diameter compared through unequal variances.



**Supplementary Figure S3. Lesions virus sample was purified from.** Virus sample was purified from mouse wart homogenate from the muzzle and tail of infected mice.





**Supplementary Figure S4. TEM negative stain image of virus before vitrification.**

# Sequence Alignment

AYV61481.1 L1 [Human papillomavirus type 16]

ATU83344.1 viral protein L1 [Mus musculus papillomavirus type 1]

AYV61481.1	1	MQVTFIYILVITCYENDVNVYHIFQMSIWLSEATVYLP-VPVSKVSTDEYVARTNI
ATU83344.1	1	-----MAWTFQTGKLYLPPTTPVAKVSTDEYVYPTSL
AYV61481.1	60	YYHAGTSRLLA VGHPYFPKKENNNKILVPKVSGLOYRVFRIHLPDPNKFQFPDTSFYNP
ATU83344.1	35	ECHAHTDRLLTVGHPEFSVI--DNDKVTVPKVSGNQYRVFRLKFPDPNKFALPQKDFYDP
AYV61481.1	120	LTQRLVWACVGVGVGRGQPLGVGISGHPLLNKLLDTENASAYAANAGVDNRECI SMDYKQ
ATU83344.1	93	EKERLVWRLRGLEITGRGGPLGIGTTGHPLFNKLGDTENPNKYQQG-SKDNRRQNTSMDPKQ
AYV61481.1	180	TQLCLIGCKPPIGEHWGKESPTCNVAVNP GDCPPELNNVVIQDGMVDTGFGAMDFTTL
ATU83344.1	152	TQLFIVGCEPPTGEHWDVVKPCG--ALEK GDCPPIQLVNSVIEDGDMCDIGFGNMNFKEI
AYV61481.1	240	QANKSEVPLDICTSICKYPDYIKMVSEPYGDSLFFYLRRQMFVRHLEFNRAVGENVPD
ATU83344.1	210	QQDRSGVPLDIVSTRCKNPDFIKMTNEAYGDKVFFFGRRQVYARHFTTRNGSVGEPIPN
AYV61481.1	300	D-----LYIKG--SGSTANLASSNYFPTPSGSMVTSDAQIFNKPYPWLQRAQCHNNGICWG
ATU83344.1	270	SVSPSDFYYAPDSIQDQKTLAPSVYFGTPSGSLVSSDQIFNRPFWLQRAQGNNGVCWH
AYV61481.1	353	NQLFVTVVDITRSTNMSLCAAISTSE-TTYKNTNFKEYLRHGEEYDLQFIFQLCKITLTA
ATU83344.1	330	NELFVTVVDNTRNTNFTISQQTNTPNPDYDSTNFKNYLRHVEQFELSILIAQLCKVPLDP
AYV61481.1	412	DVMYTIHSMNSTILEDWNEGLQPPPGGTLEBDTYRFVTSCAIACQKHTPPAPKEDPLKKYT
ATU83344.1	390	GVLAHINTMNPITILENWNLGFVPPPQQSISLDYRYITSSATRCPDQNPPKEDDPYKGLI
AYV61481.1	472	FWEVNLKEKFSADLDQFPLGRKFLLQAGLKAKPKFTLGKRKAIPPTSSISTAKRKKRKL
ATU83344.1	450	FWEVDLTERFSQDLDQFALGRKFLYQAGIRTAVTGRGVKRAASTTSASSRRVVKRKRGSK

**Supplementary Figure S5. Sequence alignment of HPV16 and MmuPV1 L1, major capsid protein.**