

Table S1. Amino acid identity (%) of L1 sequences corresponding to the virus-like particles used in this study. Phylogenetic groups are clustered together as described in the Discussion. Black solid boxes represent self-homology of 100%. The table is symmetric.

	HPV6	HPV11	HPV16	HPV31	HPV33	HPV52	HPV58	HPV18	HPV45
HPV6	100	92	68	69	69	69	70	64	64
HPV11	92	100	69	70	68	69	68	62	63
HPV16	68	69	100	83	79	79	78	65	65
HPV31	69	70	83	100	78	79	77	64	64
HPV33	69	68	79	78	100	85	90	64	64
HPV52	69	69	79	79	85	100	84	64	64
HPV58	70	68	78	77	90	84	100	64	64
HPV18	64	62	65	64	64	64	64	100	88
HPV45	64	63	65	64	64	64	64	88	100