Supplementary 1

GenBank accession number from HPV-45 L1 sequence to build phylogenetic tree

Isolate	Lineage	Sub lineage	GenBank Accession Number
Reference	A	A1	X74479
Qv20214	A	A1	EF202156
Z79	A	A1	KC470250
Z5	A	A1	KC470251
RW632	A	A1	KC470252
Qv02356	A	A2	KC470253
Qv27648	A	A2	KC470254
BF208	A	A2	KC470255
Qv27565	A	A2	EF202157
Qv30004	A	A2	EF202160
Qv33330	A	A2	EF202158
Qv34178	A	A2	EF202159
BF134	A	A3	KC470256
Qv00550	B	B1	EF202161
Qv06560	B	B1	EF202163
Qv35960	B	B1	EF202162
RW894	B	B1	KC470257
RW46	B	B2	KC470258
Qv30712	B	B2	KC470259
Qv25000	B	B2	EF202164
Qv34163	B	B2	KC470260
Qv31748	B	B2	EF202167
Qv26351	B	B2	EF202165
Qv31035	B	B2	EF202166

Supplementary 2

Predicted Linear B-cell Epitopes from Reference and HPV 45 L1 Indonesian Isolates.

The prediction were made using Ellipro (http://tools.immuneepitope.org/tools/ElliPro)

Isolate	Amino Acid Chain Sequence	Number of residues	Amino Acid Sequence	Score
Ref X74479.1	370-395	26	NLTLCASTQNPVPSTYDPTKFKQYSR	0.834
	433-469	37	NFGVPPPPTTSLVDTYRFVQSVAVTCQKDTTPPEKQD	0.833
	286-317	36	HFWNRAGVMGDTVPTDLYIKGTSANMRETPGSCVYS	0.783
	198-216	19	KGTLCKPAQLQPGDCPPLE	0.769
	152-173	22	KLDDTESAHAATAVITQDVRDN	0.703
	482-501	20	KEKFSSDLDQYPLGRKFLVQ	0.67
	77-90	14	RVVPNGAGNKQAVP	0.653
	108-124	17	NKFGLPDSTIYNPETQR	0.651
	46-62	17	RVVSTDDYVSRTSIFYH	0.591
	326-334	9	GSIITSDSQ	0.547
BDG08	432-467	36	WNFGVPPPPTTSLVDTYRFVQSVAVTCQKDTTPPEK	0.848
	370-395	26	NLTLCASTQTPVPNTYDPTKFKHYSR	0.821
	287-315	34	FWNRAGVMGDTVPTDLYIKGTSANMRETPGSCVY	0.792
	198-216	19	KGTLCKPAQLQPGDCPPLE	0.786
	77-89	13	RVVPSGAGNKQAV	0.716
	152-172	21	KLDDTESAHAATAVITQDVRD	0.696
	482-501	20	KEKFSSDLDQYPLGRKFLVQ	0.661
	110-123	14	FGLPDSTIYNPETQ	0.657

	46-60	15	RVVNTDDYVSRTSIF	0.606
	326-334	9	GSITTSDSQ	0.565
BDG22	432-468	37	WNFGVPPPPTTSLVDTYRFVQSVAVTCQKDTTPPEKQ	0.837
	370-395	26	NLTLCASTQNPVPNTYDPTKFKHYSR	0.824
	286-320	35	HFWNRAGVMGDTVPTDLYIKGTSANMRETPGSCVY	0.789
	198-216	19	KGTLCKPAQLQPGDCPPLE	0.772
	77-90	14	RVVPSGAGNKQAVP	0.695
	152-173	22	KLDDTESAHAATAVITQDVRDN	0.694
	482-501	20	KEKFSSDLDQYPLGRKFLVQ	0.665
	109-124	16	KFGLPDSTIYNPETQR	0.648
	46-61	16	RVVNTDDYVSRTSIFY	0.596
	326-334	9	GSITTSDSQ	0.555
BDG163	432-468	37	WNFGVPPPPTTSLVDTYRFVQSVAVTCQKDTTPPEKQ	0.84
	370-395	26	NLTLCASTQNPVPGTYDPTKFKHYSR	0.822
	286-320	35	HFWNRAGVMGDTVPTDLYIKGTSANMRETPGSCVY	0.792
	198-216	19	KGTLCKPAQLQPGDCPPLE	0.768
	77-90	14	RVVPNGAGNKQAVP	0.7
	152-173	22	KLDDTESAHAATAVITQDVRDN	0.694
	482-501	20	KEKFSSDLDQYPLGRKFLVQ	0.661
	109-124	16	KFGLPDSTIYNPETQR	0.653
	46-61	16	RVVNTDDYVSRTSIFY	0.599
	326-334	9	GSIITSDSQ	0.546
	337-345	9	NKPYWLHKA	0.503