

Sample	HC II Value	Interpretation	VisionArray Results
S26	<1	Neg	42
S27	<1	Neg	55
S28	<1	Neg	42
S29	<1	Neg	Neg
S30	<1	Neg	16+42
S31	<1	Neg	6+11+53
S32	<1	Neg	Neg
S33	<1	Neg	Neg
S34	<1	Neg	Neg
S35	<1	Neg	Neg
S36	<1	Neg	Neg
S37	<1	Neg	Neg
S38	<1	Neg	Neg
S39	352	Pos	16
S40	225	Pos	35
S41	1028	Pos	51
S42	338	Pos	56
S43	2338	Pos	56
S44	2870	Pos	16+39
S45	1.11	Pos	16+52+53
S46	1.69	Pos	16+54+56+66
S47	782	Pos	16+61
S48	2.5	Pos	18+16
S49	394.85	Pos	42+40+44+54
S50	7.8	Pos	6+31

Supplementary Table S1. Results of samples analyzed by HC II and VisionArray. Neg: Negative; Pos: Positive

Display Result **SEQ1** Display Type **Table view**

Database and Query Information
[Download Raw BLAST Results](#)

Results
 Query : SEQ1

Download Sequences [Select All](#) [Deselect All](#)

▼	<input type="checkbox"/>	Locus ID	Description	Score	Query Coverage	E Value	Max Ident
		HPV33REF	Human papillomavirus 33 (HPV33), complete genome	345.0	85.6%	5.0E-96	99.4%

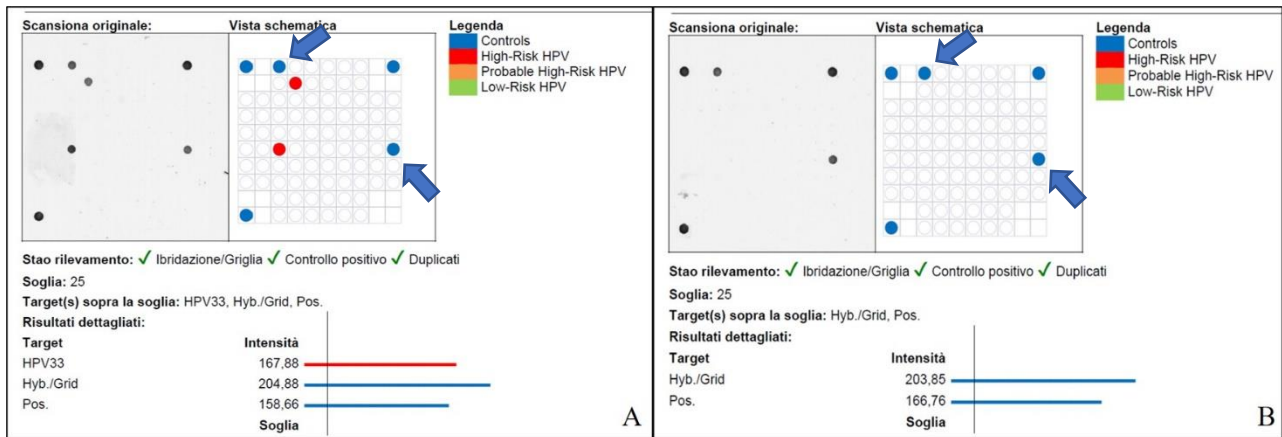
Score = 345, Expect = 5e-96
 Identities = 177/178 (99%)
 Strand = plus / minus

```

Query : 11  ttatcatatgccactgtaccatttcacttaaatcaaatatattatcattaaagctatgttgtaaacagttagtctatctatccattcaggtgtgtac 110
          |||
Sbjct : 1780 ttatcatatgccactgtaccatttcacttaaatcaaatatattatcattaaagctatgttgtaaacagttagtctatctatccattcaggtgtgtac 1879

Query : 111  cttgtacatcactaatgtttgacattgctgttctaaaccaatacaatgcacatgtttggctccgtaattttggaggct 188
          |||
Sbjct : 1880 cttgtacatcactaatgtttgacattgctgttctaaaccaatacaatgcacatgtttggctccgtaattttggaggct 1957
  
```

Supplementary Figure S1. Example of HPV positive sample (S16 Table 1) after NGS sequencing and alignment on PaVe database (<https://pave.niaid.nih.gov/>).



Supplementary Figure S2. Example of HPV positive (A, S16 Table 1) and negative (B, S3 Table 1) specimens obtained by VisionArray®. Blu dots in the three corners are the Hybridization Grid control signals; blu dots pointed by the arrows are the HLA DNA control signals; red dots are the HPV positive signals.