Table S1. The general information of each cervical sample.

Patient no.	Histology	HPV Genotype	Cytology	Age
1	CIN1	HPV16	ASC-US	48
2	CIN1	HPV16	LSIL	41
3	CIN1	HPV16	HSIL	38
4	CIN1	HPV16	LSIL	40
5	CIN1	HPV16	LSIL	48
6	CIN1	HPV16	HSIL	41
7	CIN1	HPV16	ASC-H	48
8	CIN1	HPV16	LSIL	50
9	CIN1	HPV16	LSIL	26
10	CIN1	HPV16 and other hrHPVs	LSIL	36
11	CIN1	HPV16 and other hrHPVs	LSIL	23
12	CIN2	HPV16 and other hrHPVs	HSIL	46
13	CIN1	HPV16 and other hrHPVs	LSIL	45
14	CIN1	HPV16 and other hrHPVs	LSIL	44
15	CIN3	HPV16	HSIL	27
16	CIN2	HPV16	ASC-US	34
17	CIN3	HPV16	ASC-H	35
18	CIN3	HPV16	LSIL	34
19	CIN2	HPV16 and other hrHPVs	LSIL	36
20	CIN2	HPV16 and other hrHPVs	ASC-US	23
21	CIN3	HPV16 and other hrHPVs	ASC-US	32
22	CIN1	HPV16 and other hrHPVs	NILM/LSIL	28
23	CIN1	HPV16 and other hrHPVs	LSIL	49
24	CIN1	HPV16 and other hrHPVs	ASC-US	36
25	CIN1	HPV16 and other hrHPVs	LSIL	32
26	CIN1	Other hrHPVs	LSIL	39
27	CIN1	Other hrHPVs	LSIL	44
28	CIN1	Other hrHPVs	ASC-US	23
29	CIN1	Other hrHPVs	ASC-US	36
30	CIN3	HPV16	HSIL	49
31	CIN2	HPV16 and other hrHPVs	ASC-H	42
32	CIN3	Other hrHPVs	LSIL	24
33	CIN3	Other hrHPVs	ASC-H	49
34	CIN2	Other hrHPVs	LSIL	34
35	CIN3	HPV16 and other hrHPVs	LSIL	49

Supplementary Method S1. The scripts for Virus Identification Pipeline

1. Copy local files into docker
   docker cp /mnt/[PATH]/[FILE NAME_R1&2].fastq.gz [CONTAINER ID]:/
2. Go to the container
   sudo docker exec -it [CONTAINER ID] bash
3. Extract the FASTQ files

$ gunzip *.gz

4. Merge the read1 and read2 files
   $ cat [FILE NAME_R1.fastq] [FILE NAME_R2.fastq] >[FILE NAME.fastq]
5. Run the VIP (Using sense mode)
   $ VIP.sh -z -i [FILE NAME.fastq] -p illumina -f fastq -r /VIPDB
   $ /VIP/VIP.sh -c [FILE NAME.fastq].conf -i [FILE NAME.fastq]
6. Export the outputs
   docker cp [CONTAINER ID]:/[FILE NAME] /mnt/[PATH]