**Table SI: List of antibodies used for immunoblotting (IB) experiments.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **S. No.** | **Antibodies****(Mol. Wt.)** | **Source and Cat. No.** | **Origin and type** | **Dilution in IB** |
|  | Alix (1A12)(95 kDa) | Santa Cruz(sc-53540) | Mu monoclonal IgG1 | 1:3000 |
|  | HSP 70(70 kDa) | Abcam(47455) | Mu monoclonal IgG1 | 1:3000 |
|  | Flotillin-2 (B-6)(42 kDa) | Santa Cruz(sc-28320) | Mu monoclonal IgG1 | 1:3000 |
|  | β-actin(42 kDa) | Sigma(A1978) | Mu monoclonal IgG1 | 1:5000 |
|  | Anti-mouse-HRP | Santa Cruz(sc-2031) | Goat anti-mouse IgG | 1:5000 |
|  | Anti- Rabbit-HRP | Santa Cruz(sc-2030) | Goat anti-rabbit IgG | 1:5000 |

**Table SII: List of primers used in the study along with their sequence and amplicon size.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Primers** | **Sequence** | **Amplicon size** | **Annealing temp.** | **References** |
| **R-HPV16E6** | F- 5’-AATGTTTCAGGACCCTACGG-3’R- 5’-TCAGGACACAGTGGCTTTTG-3’ | 157 bp | 57.3 | **(**[**Chang *et al.* 2010**](#_ENREF_1)**)** |
| **R-HPV16E7** | F- 5’-TTTGCAACCAGAGACAACTGA-3’R- 5’-GCCCATTAACAGGTCTTCCA-3’ | 214 bp | 57 | **(**[**Chang *et al.* 2010**](#_ENREF_1)**)** |
| **R-HPV18E6** | F-5’-GCGACCCTACAAGCTACCTG-3’R- 5’-GTTGGAGTCGTTCCTGTCGT-3’ | 245 bp428 bp | 62 | **(**[**Chang *et al.* 2010**](#_ENREF_1)**)** |
| **R-HPV18E7** | F-5’-GCATGGACCTAAGGCAACAT-3’R-5’-TGTTGCTTACTGCTGGGATG-3’ | 322 bp | 58 | **(**[**Chang *et al.* 2010**](#_ENREF_1)**)** |
|  |
| **Beta-actin** | F-ATCCACGAAACTACCTTCAACTCCATCR- CATACTCCTGCTTGCTGATCCACATC | 268 bp | 61 | **(**[**Raff *et al.* 1997**](#_ENREF_2)**)** |

**References:**

**Chang, J. T., Kuo, T. F., Chen, Y. J., Chiu, C. C., Lu, Y. C., Li, H. F., Shen, C. R. and Cheng, A. J. (2010)**. Highly potent and specific siRNAs against E6 or E7 genes of HPV16- or HPV18-infected cervical cancers. Cancer Gene Ther **17**(12): 827-36.

**Raff, T., van der Giet, M., Endemann, D., Wiederholt, T. and Paul, M. (1997)**. Design and testing of beta-actin primers for RT-PCR that do not co-amplify processed pseudogenes. Biotechniques **23**(3): 456-60.

**Table SIII: Summary of raw sequence data and quality.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Sample- ID** | **Number of Reads** | **Read Length** | **GC%** | **% Bases > Q20** | **% Bases > Q30** |
| SiHa-Exo | 41861174 | 151 | 44 | 98.80 | 84.97 |
| HeLa-Exo | 41604974 | 151 | 51 | 98.81 | 83.98 |
| C33a-Exo | 32186130 | 151 | 44.5 | 99.01 | 89.30 |

**Table SIV:** Read alignment statistics with Combined Genome (GRCh38.p7, HPV16 & HPV18)

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Sample- ID** | **Reads after QC** | **Mapped reads** | **Mapped reads %** | **Uniquely mapped reads** | **Uniquely mapped reads %** | **Unmapped Reads** | **Unmapped Reads %** |
| SiHa-Exo | 37166256 | 36707542 | 98.77 | 32842616 | 88.37 | 458714 | 1.23 |
| HeLa-Exo | 35736678 | 33110372 | 92.65 | 20282718 | 56.76 | 2626306 | 7.35 |
| C33a-Exo | 29970450 | 29739990 | 99.23 | 26953750 | 89.93 | 230460 | 0.77 |