Sup. Table S1. Genetic polymorphisms associated with HPV-induced cancers susceptibility

| Type of study (GWAS or target SNP) | Type of cancer/ N0 of individuals/ Ethnicity | Main findings | Ref. |
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| Target SNP<br>-318 C/T, +49 A/G and CT60 A/G SNP in CTL-4 gene | Cases: women with cervical squamous cell carcinoma (n=144) and Controls (n= 378)<br>Taiwanese | The -318 C/T variant in the promoter region of the CTLA-4 gene is associated with HPV-16-associated CSCC | [1] |
| Target SNP<br>Inflammasome genes (NLRP1, NLRP3, NLRP6, CARD8, IL1B, IL18, TNFAIP3) | HPV+ case (n=246)<br>Controls (n =310)<br><br>Brazilians | SNPs rs1143643 (L1B gene) was associated with protection against HPV infection.<br>SNPs rs11651270 and rs10754558 (NLRP1) were associated with protection against HPV persistence and/or oncogenesis.<br><br>SNP rs10754558 (NLRP3) was associated with significantly lower risk to be infected with a high-risk HPV | [2] |
| | | SNP rs2844511 (CHR6) and cervix cancer risk. | [3] |
| Target SNP<br>SNPs rs25164488, rs3117027 and rs9272143 | Cases: cervical cancer (n=790) and Controls (n=717) from Algeria, Morocco, India and Thailand | Borderline associations between rs2665390 (TIPARP) and rs13117307 (EXOC1) with cervical cancer risk.<br><br>Also confirmed the association between rs2844511 and cervical cancer risk as previously reported in a Swedish population. | |
| SNP array<br>genotyped 92 SNPs from 49 candidate immune response and DNA repair genes | Women with CIN3 or cancer (n=469),<br>Women with persistent HPV infections (n=390), and<br>Controls (n=452)<br><br>Costa Rica | SNP G501S (FANCA gene) was associated with increased risk of CIN3 or cancer.<br><br>The FANCA haplotype that included G501S also conferred increased risk of CIN3 or cancer.<br><br>A SNP in the innate immune gene IRF3 (S427T) was associated with increased risk for HPV persistence | [4] |
| Target SNP rs1049174<br>NKG2D gene | 153 women with HPV+cervical cancer | LNK was significantly associated with increased cancer susceptibility to HPV+ cancers | [5] |

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| | 123 patients with HPV+ anogenital cancers<br><br>Cervical and anogenitalcancers<br><br>Vietnamese | LNK was significantly associated with lower NKG2D expression in NK cells and lower<br>cytotoxicity | |
| Target SNP<br>p73 cytosine thymine | Cases:<br>HSIL (n=38)<br>Invasive cervical cancer (n=141)<br>Controls (n=176) from Portugal | Twofold increased susceptibility to the development of HSIL in women carrying the p73 AT allele (OR=2.39; p=0.022) which was specially evident in women with high parity. | [6] |
| Array genotype<br>SNPs at the HLA class II *DQB1* typed using a linear array of immobilized sequence-specific oligonucleotide probes | Cases: cervical cancer (n=1306)<br><br>Controls (n=288)<br><br>Sweden | *DQB1*was strongly associated; alleles **0301*, **0402* and **0602*increased cancer susceptibility, whereas **0501* and **0603*decreased susceptibility. | [7] |
| HLA-DRB1*1501 and DQB1*0602 by PCR-SSP analysis | Cases invasive cervical cancer (n=287) (192 Chinese Uighurs and 95 Hans)<br>Healthy controls (n=312 Chinese 218 Uighurs and 94 Hans) | The HLA-DQB1*0602 allele frequency was significantly lower among Uighur women with invasive cervical cancer. Similar tendencies were observed for DQB1*0602 with HPV16-positive invasive cervical cancer. | [8] |
| HLA-DRB1*13 allele | 86 women with CIN1 Low-Grade Cervical Intraepithelial Neoplasia<br><br>France | HLA-DRB1*13 allele and HPV16/18 negative status were independently associated with an increased probability for regression | [9] |

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| HLA-DRB1*1302 allele | Cases: CIN1 (n=505)<br>CIN2/3 (n=96)<br>Invasive cervical cancer (n=311)<br>Controls (n=341)<br>Japanese | Protective effect of HLA-DRB1*1302 allele against progression from CIN 1 to CIN2/3 | [10] |
| Array genotype including 205 SNPs in and around 32 candidate gene regions | Cases<br>Cervical cancer (n=876)<br>Vulvar cancer (n=517)<br>Controls (n=1100)<br>United States | The TNF region was significantly associated with the risks of cervical cancer and vulvar cancer.<br>The allele A of the SNP rs2239704 LTA gene associated with increased risk of cervical cancer and of vulvar cancer.<br>SNP rs2239704 in TLR gene was no associated with these cancers | [11] |
| Systematic review and m*eta-analysis* to establish the associations between cancers and *LTA* variants (rs1041981, rs2239704, rs2229094 and rs746868) | A total of 30 case-control studies involving 58,649 participants | rs1041981 increased the risk of several types of cancer, such as adenocarcinoma, squamous carcinoma, hematological malignancy in Asians, Europeans. | [12] |
| Target SNP rs3087404 and rs2029167 in SMUG1 gene | Cases<br>cervical squamous cell carcinoma (n=400)<br>CIN III (n=400)<br>Chinese | The homozygous GG of rs3087404 and rs2029167 had a significantly increased risk of CIN III and cervical squamous cell carcinoma<br>Individuals with G allele or G carrier at rs3087404 were at higher risk for cervical squamous cell carcinoma, and at rs2029167 were at higher risk for CIN III | [13] |
| Target Ser326Cys polymorphism in hOGG1( | Cases CIN grade III (n=400) | The genotype hOGG1 Cys326Cys (GG) was associated with increased risk of CIN | [14] |

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| human 8-oxoguanine glycosylase 1) | Cervical squamous cell carcinoma (n=400)<br>Chinese | III and cervical squamous cell carcinoma and also in HR-HPV infected. | |
| Target SNP rs11637235 of the DUT gene | Cases<br>Cervical squamous cell carcinoma (n=400)<br>CIN<br>(n=400)<br>Chinese | GG genotype of rs3784619 and the TT genotype of rs11637235 in the DUT gene significantly increased the risk of CIN III and cervical squamous cell carcinoma<br>The TT genotype of rs11637235 was enriched in the HR-HPV–positive cases | [15] |
| Target 3DS1 and 2DS1 in KIR gene | Cases:<br>RRP patients (n=66)<br>United States<br>(Caucasians, African Americans, Hispanics) | Individuals lacking activating KIR genes 3DS1 and 2DS1 are more likely to develop a more severe form of RRP (caused by HPV-6/11) than those harboring these receptors | [16] |
| Systematic review and m*eta-analysis* | Meta –analysis<br>Cervical cancer<br>Indian | rs1048943 A>G, in exon 7 of CYP1A1 to be associated with cervical cancer | [17] |
| Target SNP rs1982073 of TGF-β1 gene | Cases: squamous cell carcinoma of the oropharynx (n=200)<br>HPV16+ patients (n = 147) HPV16- patients (n = 53)<br>United States | *Patients with rs1982073 CT/CC genotypes* were significantly associated with HPV16-positive tumor status among patients with squamous cell carcinoma compared with TT genotype | [18] |
| GWAS | Cervical cancer<br>1075 Cases and 4014 controls<br>Sweden | Three loci: rs2516448 in MICA gene; rs9272143 between HLA-DRB1 and HLA-DQA1 genes and rs3117027 at HLA-DPB2 gene were associated with susceptibility to cervical cancer.<br>The study also confirmed previously reported associations of B*0702 and DRB1*1501-DQB1*0602 with susceptibility to and DRB1*1301-DQA1*0103- | [19] |

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| | | DQB1*0603 with protection against cervical cancer | [20] |
| SNP array including 7140 tag SNPs from 305 candidate genes/regions using custom-designed iSelect Infinium assay | Cases 1 (n=416), (CIN3)/cancer<br>Cases 2 (n=356), Persistent HPV women (median: 25 months),<br>Control (n=425) random controls<br>Costa Rica | SNPs rs12302655 (OAS3), rs4737999 (SULF1), rs3784621 (DUT), and rs2894054 (GTF2H4) were associated with HPV persistence<br>SNPs rs11177074 (IFNG) and rs9893818 (EVER1/EVER2) were associated with progression to CIN3/cancer. | |
| *Target SNP*<br>rs2910164(G>C) on the passenger strand of the precursor of miR-146a | Chinese Cervical cancer cases (n=447) and Controls (n=443) | Subjects carrying GG homozygote had a 1.496-fold increased risk than those carrying CG/CC genotypes.<br>Carriers of GG genotype had lower miR-146a expression level compared with the carriers of CC genotype. | [21] |
| Target SNP<br>TP53, rs1042522<br>*MDM2* (SNP309)<br>and *NQO1* (SNP609, SNP465) | Patients with cervical cancer (n=577) and their biological parents and/or siblings | No association between *MDM2* SNP309 or *NQO1* SNP465 and cervical cancer.<br>*TP53* codon 72 and *NQO1* SNP609 associate with higher risk of cervical cancer especially in women infected with HPVs 16–and/or 18. | [22] |

Foot notes:

GWAS study: genome-wide association study; SNP: single nucleotide polymorphism

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