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

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

Cervical and anogenital cancers

Vietnamese

Target SNP

p73 cytosine thymine

Cases: HSIL (n=38)

Invasive cervical cancer (n=141)

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.

Array genotype

SNPs at the HLA class II DQB1 typed using a linear array of immobilized sequence-specific oligonucleotide probes

Cases: cervical cancer (n=1306)

Controls (n=288)

Sweden

DQB1 was strongly associated; alleles *0301, *0402 and *0602 increased cancer susceptibility, whereas *0501 and *0603 decreased susceptibility.

HLA-DRB1*1501 and DQB1*0602 by PCR-SSP analysis

Cases invasive cervical cancer (n=287) (192 Chinese Uighurs and 95 Hans)

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.

HLA-DRB1*13 allele

86 women with CIN1 Low-Grade Cervical Intraepithelial Neoplasia

France

HLA-DRB1*13 allele and HPV16/18 negative status were independently associated with an increased probability for regression
<table>
<thead>
<tr>
<th><strong>HLA-DRB1*1302 allele</strong></th>
<th><strong>Cases: CIN1 (n=505)</strong></th>
<th><strong>CIN2/3 (n=96)</strong></th>
<th><strong>Invasive cervical cancer (n=311)</strong></th>
<th><strong>Controls (n=341)</strong></th>
<th><strong>Japanese</strong></th>
<th><strong>Protective effect of HLA-DRB1*1302 allele against progression from CIN 1 to CIN2/3</strong></th>
<th>[10]</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Array genotype including 205 SNPs in and around 32 candidate gene regions</strong></td>
<td><strong>Cases</strong></td>
<td><strong>Cervical cancer (n=876)</strong></td>
<td><strong>Vulvar cancer (n=517)</strong></td>
<td><strong>Controls (n=1100)</strong></td>
<td><strong>United States</strong></td>
<td><strong>The TNF region was significantly associated with the risks of cervical cancer and vulvar cancer.</strong></td>
<td>[11]</td>
</tr>
<tr>
<td></td>
<td><strong>The allele A of the SNP rs2239704 LTA gene associated with increased risk of cervical cancer and of vulvar cancer.</strong></td>
<td><strong>SNP rs2239704 in TLR gene was no associated with these cancers</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Systematic review and meta-analysis to establish the associations between cancers and LTA variants (rs1041981, rs2239704, rs2229094 and rs746868)</strong></td>
<td><strong>A total of 30 case-control studies involving 58,649 participants</strong></td>
<td><strong>The homozygous GG of rs3087404 and rs2029167 had a significantly increased risk of CIN III and cervical squamous cell carcinoma</strong></td>
<td><strong>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</strong></td>
<td></td>
<td></td>
<td></td>
<td>[12]</td>
</tr>
<tr>
<td><strong>Target SNP rs3087404 and rs2029167 in SMUG1 gene</strong></td>
<td><strong>Cases cervical squamous cell carcinoma (n=400)</strong></td>
<td><strong>CIN III (n=400)</strong></td>
<td><strong>Chinese</strong></td>
<td><strong>The homzygous GG of rs3087404 and rs2029167 had a significantly increased risk of CIN III and cervical squamous cell carcinoma</strong></td>
<td><strong>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</strong></td>
<td></td>
<td>[13]</td>
</tr>
<tr>
<td><strong>Target Ser326Cys polymorphism in hOGG1</strong></td>
<td><strong>Cases CIN grade III (n=400)</strong></td>
<td><strong>The genotype hOGG1 Cys326Cys (GG) was associated with increased risk of CIN</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>[14]</td>
</tr>
<tr>
<td><strong>Target SNP rs11637235 of the DUT gene</strong></td>
<td><strong>Cervical squamous cell carcinoma (n=400)</strong></td>
<td><strong>CIN (n=400)</strong></td>
<td><strong>Chinese</strong></td>
<td><strong>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 and was enriched in the HR-HPV–positive cases</strong></td>
<td>[15]</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Target 3DS1 and 2DS1 in KIR gene</strong></td>
<td><strong>RRP patients (n=66)</strong></td>
<td><strong>United States (Caucasians, African Americans, Hispanics)</strong></td>
<td><strong>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</strong></td>
<td>[16]</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Systematic review and meta-analysis</strong></td>
<td><strong>Cervical cancer</strong></td>
<td><strong>rs1048943 A&gt;G, in exon 7 of CYP1A1 to be associated with cervical cancer</strong></td>
<td>[17]</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Target SNP rs1982073 of TGF-β1 gene</strong></td>
<td><strong>squamous cell carcinoma of the oropharynx (n=200)</strong></td>
<td><strong>HPV16+ patients (n = 147)</strong></td>
<td><strong>HPV16- patients (n = 53)</strong></td>
<td><strong>Patients with rs1982073 CT/CC genotypes were significantly associated with HPV16-positive tumor status among patients with squamous cell carcinoma compared with TT genotype</strong></td>
<td>[18]</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>GWAS</strong></td>
<td><strong>Cervical cancer</strong></td>
<td><strong>Sweden</strong></td>
<td><strong>1075 Cases and 4014 controls</strong></td>
<td><strong>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. The study also confirmed previously reported associations of B<em>0702 and DRB1</em>1501-DQB1*0602 with susceptibility to</strong></td>
<td>[19]</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
DQB1*0603 with protection against cervical cancer

SNPs rs12302655 (OAS3), rs4737999 (SULF1), rs3784621 (DUT), and rs2894054 (GTF2H4) were associated with HPV persistence

SNPs rs11177074 (IFNG) and rs9893818 (EVER1/EVER2) were associated with progression to CIN3/cancer.

Cases 1 (n=416), (CIN3)/cancer

Cases 2 (n=356), Persistent HPV women (median: 25 months),

Control (n=425) random controls

Costa Rica

Target SNP

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.

Carriers of GG genotype had lower miR-146a expression level compared with the carriers of CC genotype.

Target SNP

TP53, rs1042522

MDM2 (SNP309) 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. TP53 codon 72 and NQO1 SNP609 associate with higher risk of cervical cancer especially in women infected with HPVs 16–and/or 18.

Foot notes:

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

REFERENCES
