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## Improving the screening of precancerous anal lesions in high-risk subjects with normal cytology: A longitudinal cohort study using simple tests

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1           **Identifying new potential genetic biomarkers for HELLP syndrome**  
2           **using massive parallel sequencing**

3  
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## **Abstract**

**Background:** Preeclampsia (PE) is a frequently occurring multisystemic disease affecting ~5% of pregnancies. PE patients may develop HELLP syndrome (haemolysis, elevated liver enzymes, and low platelet), a mother and foetus life-threatening condition. Research into HELLP's genetic origin has been relatively unsuccessful, mainly because normal placental function and blood pressure regulation involve the fine-regulation of hundreds of genes.

**Objective:** To identify new genes and mutations constituting potential biomarkers for HELLP syndrome.

**Study design:** The present case-control study involved whole-exome sequencing of 79 unrelated HELLP women. Candidate variants were screened in a control population constituted by 176 individuals. Stringent bioinformatics filters were used for selecting potentially etiological sequence variants in a subset of 487 genes. We used robust *in silico* mutation modelling for predicting the potential effect on protein structure.

**Results:** We identified numerous sequence variants in genes related to angiogenesis/coagulation/blood pressure regulation, cell differentiation/communication/adhesion, cell cycle and transcriptional gene regulation, extracellular matrix biology, lipid metabolism and immunological response. Five sequence variants generated premature stop codons in genes playing an essential role in placental physiology (*STOX1*, *PDGFD*, *IGF2*, *MMP1* and *DNAH11*). Six variants (ERAP1- p.Ile915Thr, ERAP2- p.Leu837Ser, COMT-p.His192Gln, CSAD-p.Pro418Ser, CDH1- p.Ala298Thr and CCR2-p.Met249Lys) led to destabilisation of protein structure as they had significant energy and residue interaction-related changes. We identified at

59 least two mutations in 57% of patients, arguing in favour of a polygenic origin for the  
60 HELLP syndrome.

61 **Conclusion:** Our results provide novel evidence regarding PE/HELLP's genetic origin,  
62 leading to new biomarkers, having potential clinical usefulness, being proposed.

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64 **Key words:** Genetic biomarkers; HELLP syndrome; molecular medicine; protein  
65 modelling; whole-exome sequencing (WES).

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84 **Introduction**

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86 Preeclampsia (PE), clinically characterised by pregnancy-induced hypertension and  
87 proteinuria after the 20<sup>th</sup> week of gestation, is a frequently occurring multisystemic  
88 disease affecting ~5% of pregnancies [1,2]. Women affected by PE can suffer foetal  
89 intra-uterine growth restriction (IUGR) and have an increased risk of being affected by  
90 cardiovascular disease later in life [3,4]. It has been seen that ~15% of patients affected  
91 by severe PE may develop HELLP (haemolysis, elevated liver enzymes, and low  
92 platelet) syndrome, a mother and foetus life-threatening condition. Concerning PE *per*  
93 *se*, mechanisms have been described regarding PE, such as defective deep placentation,  
94 anticoagulant factor activation, immune response at the placental–maternal interface,  
95 increased endoplasmic and oxidative stress, having autoantibodies to type-1 angiotensin  
96 II receptor, intravascular inflammation, angiogenesis imbalance and endothelial  
97 dysfunction [5].

98 However, the exact mechanisms triggering PE developing into HELLP syndrome have  
99 not been completely elucidated. Several potentially PE-linked biochemical markers (e.g.  
100 PAPP-A, free CG- $\beta$ , AFP, PP13, ADAM12, PIGF, VEGF, P-Selectin and inhibin A)  
101 have been studied for identifying those underlying possible usefulness in clinical  
102 environments [5]. For the moment, while some of these markers are indeed associated  
103 with preeclampsia, the effectiveness of those for predicting early PE is still disputable.  
104 Regarding genetics of PE, at least 15 PE loci have been mapped to date and candidate  
105 genes have been proposed, such as *ACVR2A*, *TNFSF13B*, *EPAS1* and *STOX1*[6,7]. The  
106 *STOX1* c.457T>C (p.Tyr153His) mutation has been functionally linked to PE aetiology,  
107 while *Stox1* overexpression in mice leads to PE, IUGR and cardiovascular disease [8–12].  
108 The p.Ala356Gly deleterious mutation in Forkhead Box D1 (FOXD1), leading to C3

109 promoter transactivation disturbances, has been identified recently in a woman suffering  
110 PE and IUGR [13,14]. Some sequence variants in other genes (i.e. *VEGF*, *MMP9*,  
111 *SERPINEA8* and *MMP9*) seem to increase the risk of PE.

112 Regarding the HELLP syndrome, a few genetic studies have been undertaken and it has  
113 generally been accepted that, due to common molecular pathways, most PE-related genes  
114 may also contribute towards HELLP's aetiology.

115 However, research into PE/HELLP's genetic origin has been relatively unsuccessful,  
116 mainly because normal placental function and blood pressure regulation involve the fine-  
117 regulation of hundreds of genes. Furthermore, large pedigrees displaying PE/HELLP are  
118 rare, thereby generally hampering the mapping of genomic regions by classic genetic  
119 approaches. Whole-exome sequencing (WES) has been carried out in familial and  
120 isolated cases of PE which led to proposing some possible new genes and sequence  
121 variants related to the phenotype [15–18]. However, no large-scale genomic approaches  
122 have yet been adopted in patients with HELLP syndrome.

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124 Here is presented the first WES study for patients affected by the HELLP syndrome, on a  
125 relatively large cohort (79 unrelated women) of Colombian origin. Stringent  
126 bioinformatics filters were used for selecting potentially etiological non-synonymous  
127 sequence variants in a subset of 487 genes. We used robust *in silico* mutation modelling  
128 for predicting the potential effect on protein structure. We identified 110 variants (87  
129 different) in 67 genes related to several biological processes, such as  
130 angiogenesis/coagulation/blood pressure regulation, cell  
131 differentiation/communication/adhesion, cell cycle and transcriptional gene regulation,  
132 extracellular matrix biology, lipid metabolism and immunological response. Five  
133 sequence variants were particularly drastic as they generated premature stop codons in

134 genes playing an essential role in placental physiology (e.g. STOX1, PDGFD, IGF2,  
135 MMP1 and DNAH11). Six variants (ERAP1-p.Ile915Thr, ERAP2- p.Leu837Ser,  
136 COMT-p.His192Gln, CSAD-p.Pro418Ser, CDH1-p.Ala298Thr and CCR2-p.Met249Lys)  
137 led to potential destabilisation of protein structure as they had significant energy and  
138 residue interaction-related changes. We identified at least two mutations in 57% of  
139 patients, arguing in favour of a polygenic origin for the HELLP syndrome.

140  
141 Taken together, our results provide novel evidence regarding PE/HELLP's genetic origin,  
142 leading to new biomarkers, having potential clinical usefulness, being proposed.

143  
144 **Materials and Methods**

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146 ***Women affected by HELLP syndrome and control population***

147 The study involved selecting 79 unrelated women affected by HELLP syndrome for WES  
148 sequencing. The patients (all from Colombia) are part of the GenPE study (Genetics and  
149 Pre-eclampsia), large, multi-centre, case-control study conducted between December  
150 2000 and February 2012 in eight Colombian cities ([www.genpe.org](http://www.genpe.org)) or the Hospital  
151 Universitario Mayor-Méderi (Bogotá, Colombia). The **Supplementary Table 1** includes  
152 the clinical characteristics of the HELLP patients.

153 To calculate the sample size, we have first explored a Colombian health database (named  
154 SIVIGILA) that records numerous epidemiological events  
155 (<http://www.ins.gov.co/buscador>). We found that 22,915 women were affected by  
156 extreme gestational morbidity, 44.2% of which were suffered severe preeclampsia (PE).  
157 Thereafter, based on the reported frequency of HELLP (~20%) we estimated that 2028  
158 should be affected by the disease. This number was taken as the total population. The

159 final calculation (5% proportion), which was performed considering a precision of 5%  
160 and a confidence interval of 95%, led us to establish a sample size of 70 patients.

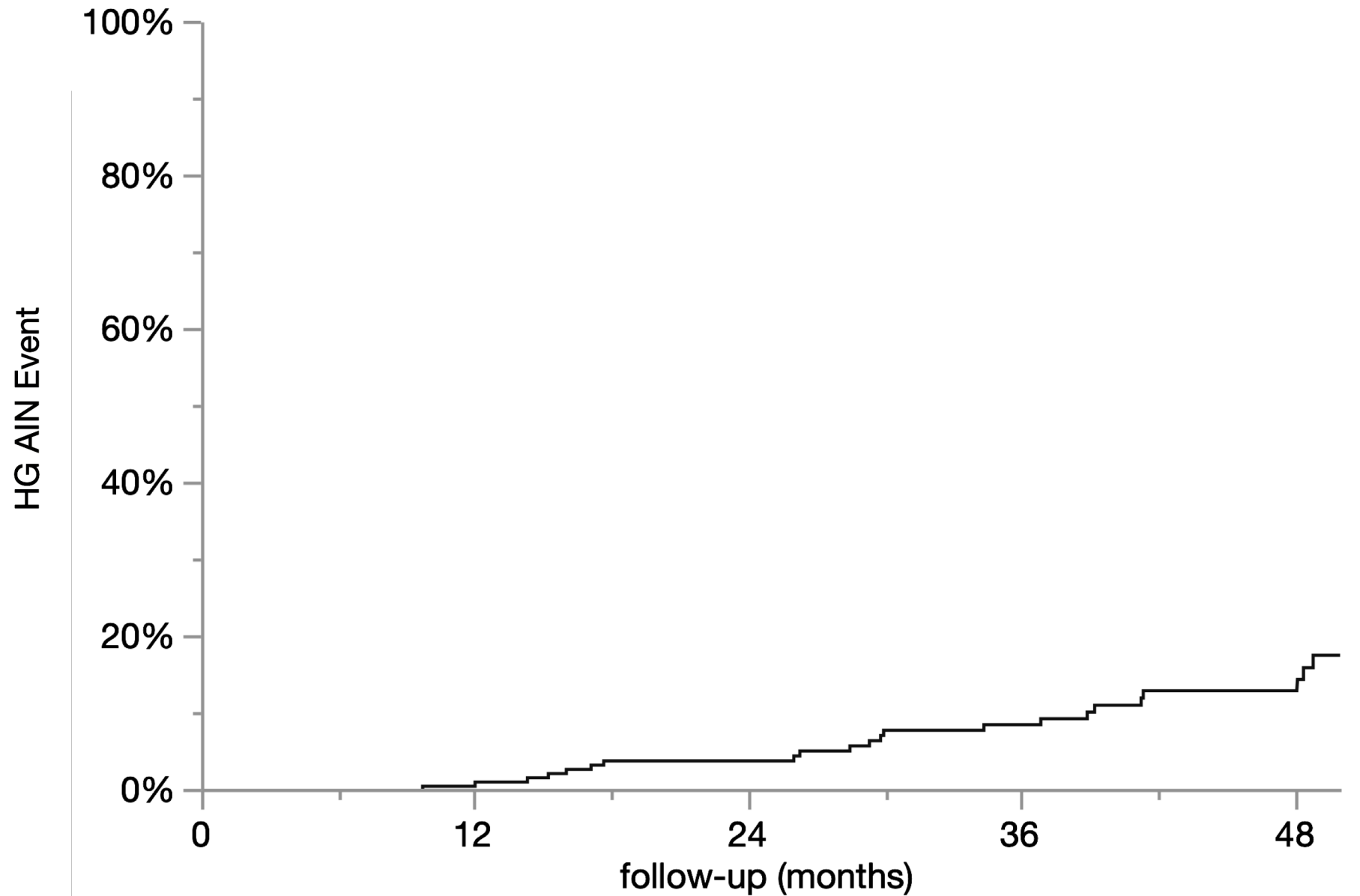
161 The Tennessee Classification System diagnostic criteria for HELLP syndrome [19] were  
162 used for selecting patients. The main diagnostic laboratory criteria were thus:  $\leq$   
163 100,000/L platelets,  $\geq$  70 IU/ AST L and  $\geq$  600 IU/L LDH. This classification system  
164 rates HELLP syndrome as being complete (three criteria) or incomplete (one or two  
165 criteria). Candidate variants were screened using WES data from 176 Colombian women  
166 (control group, C) over 50 years old having at least one child and lacking antecedents of  
167 medical complications during pregnancy. Individuals having antecedents of hypertensive  
168 disorders were excluded as controls. The Universidad del Rosario (Code: DVN-021-1-  
169 063, May 2017) Ethics' Committee approved the clinical study and all experimental  
170 procedures. Clinical investigation followed Declaration of Helsinki guidelines (1975, as  
171 revised in 1996). All individuals had signed informed consent forms.

172

### 173 *WES, bioinformatics filtering of variants, Sanger sequencing and interactome analysis*

174 Genomic DNA was extracted from all patients' blood samples, using standard  
175 procedures. Details regarding NGS experiments and primary bioinformatics analysis have  
176 been included as **Supplementary methods**. The detected sequence variants were filtered  
177 in parallel using R (v3.5.1; www.r-project.org), Excel (Microsoft Office 365) and VarSeq  
178 (Golden Helix Inc., Bozeman, USA) software. A subset of 487 candidate genes (named  
179 HELLP-487) was created by screening several databases and used to filter rare (MAF  
180  $<0.005$ ) variants evoking potentially harmful effects (**Supplementary methods,**  
181 **Supplementary Table 2**). **Figure 1** illustrates the bioinformatics pipeline used for  
182 candidate variants' filtering. We screened these variants in the C group of women. All  
183 selected variants were verified (n=118) by Sanger sequencing. The primer sequences and





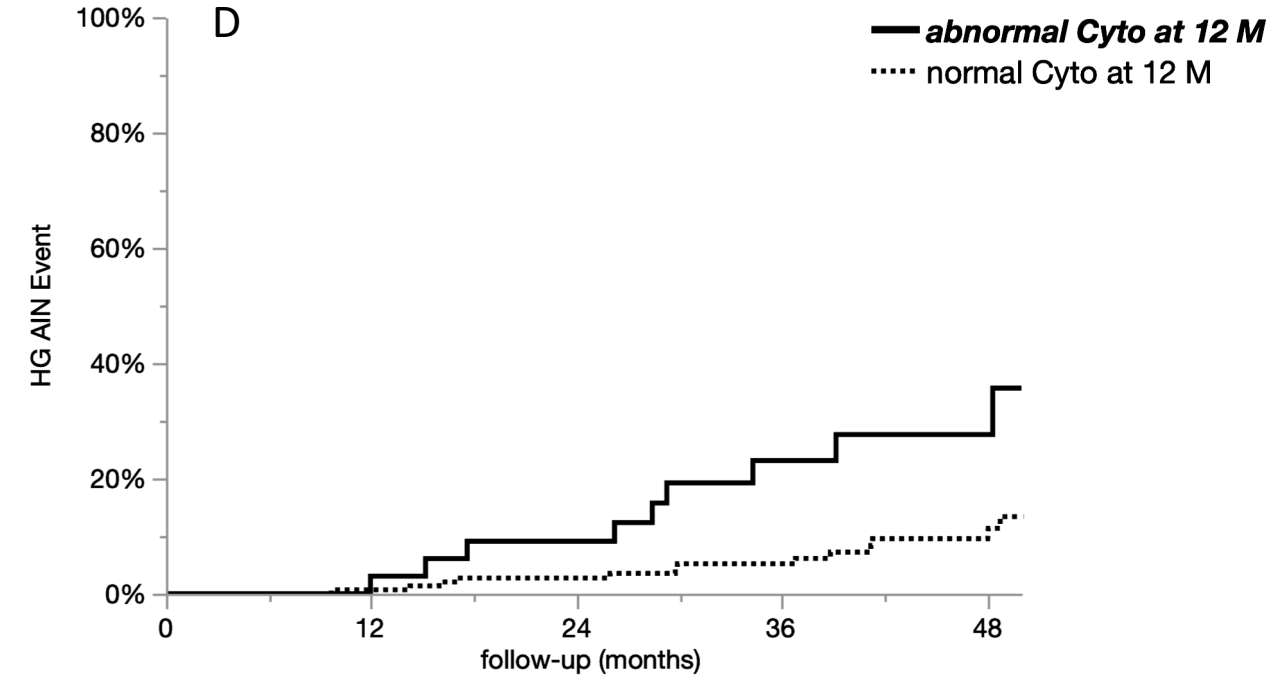
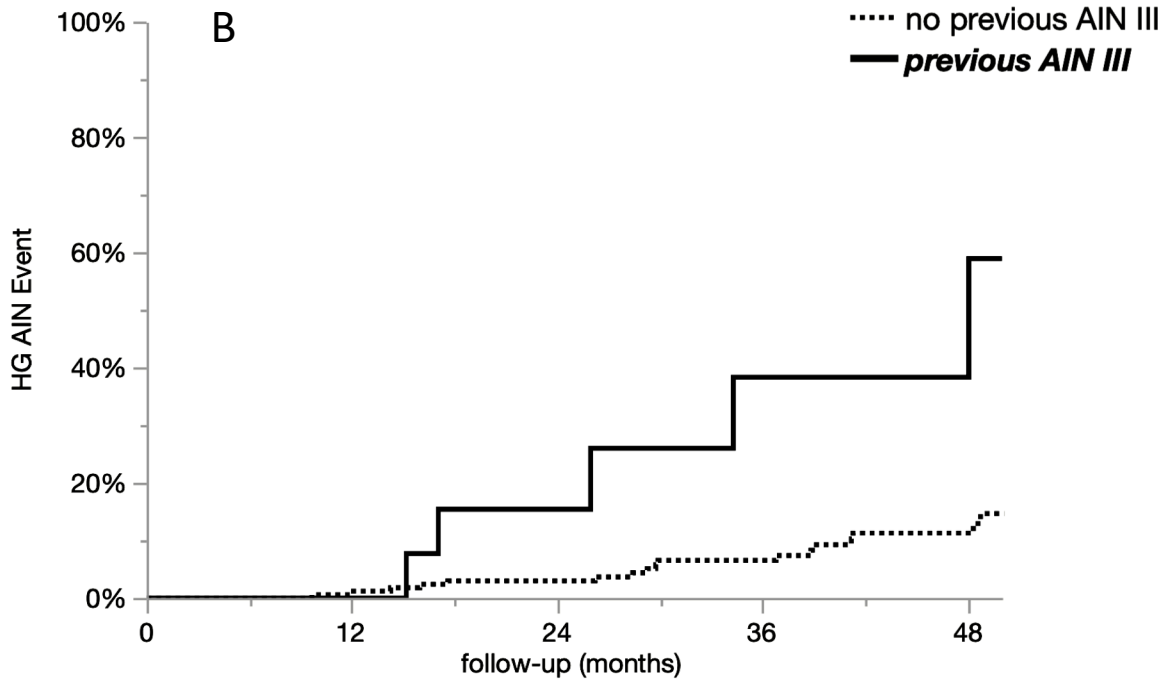
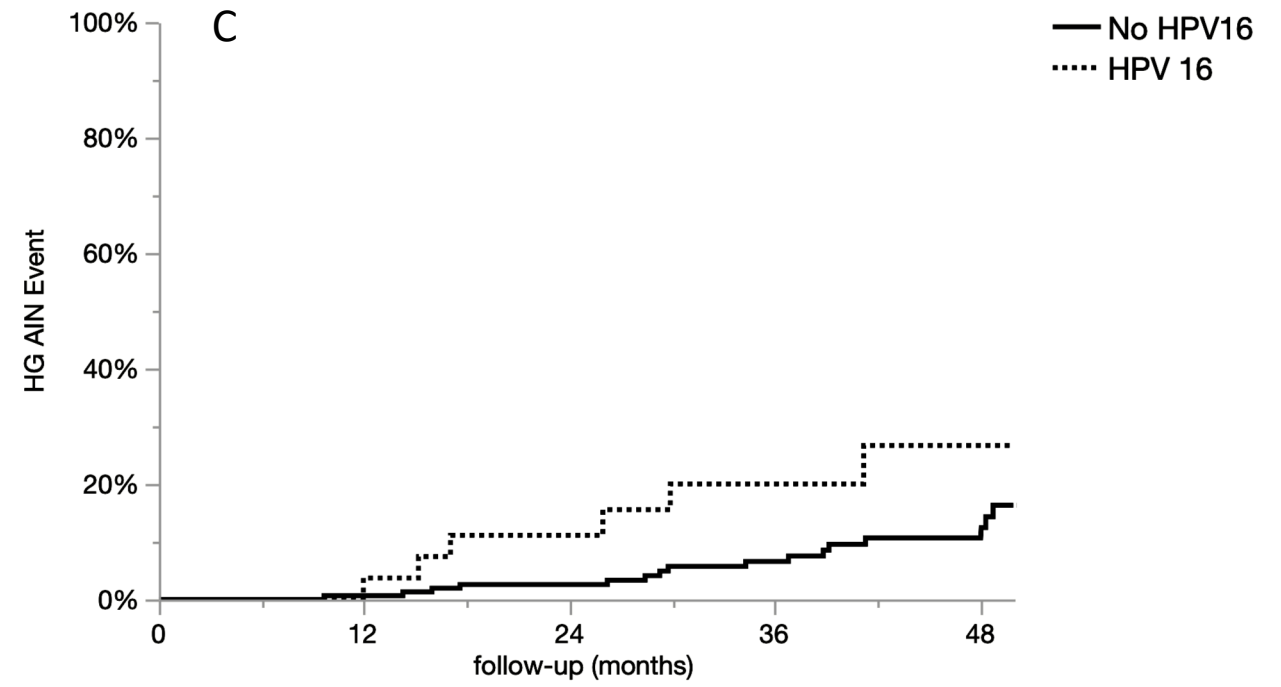
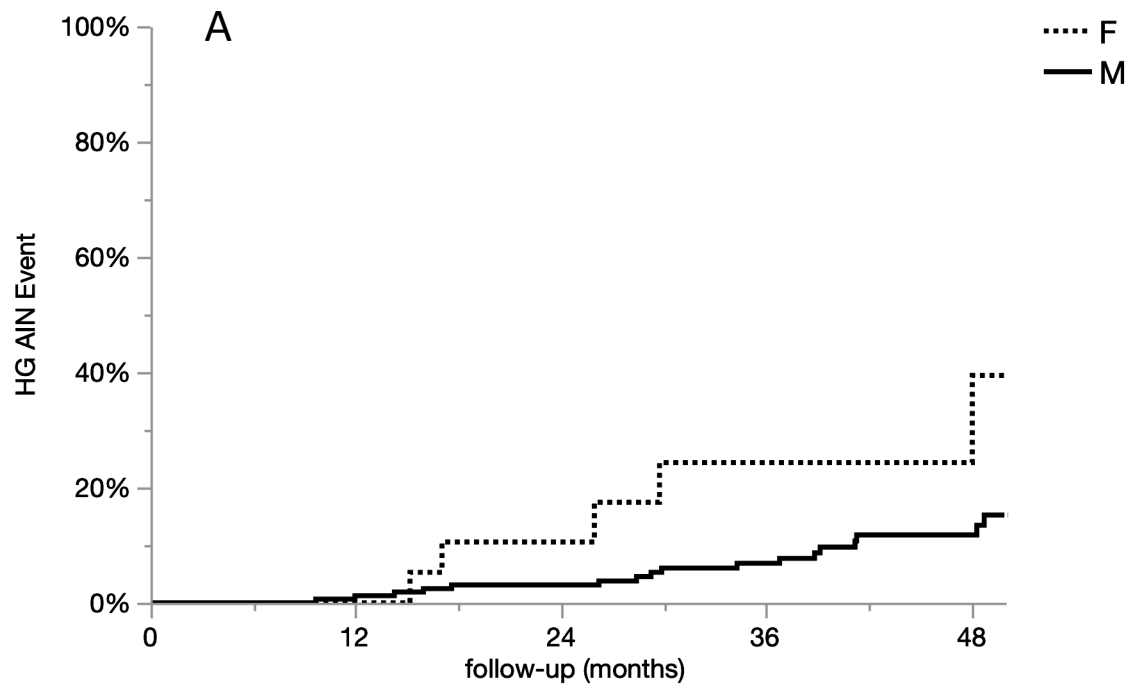
N at risk: 182

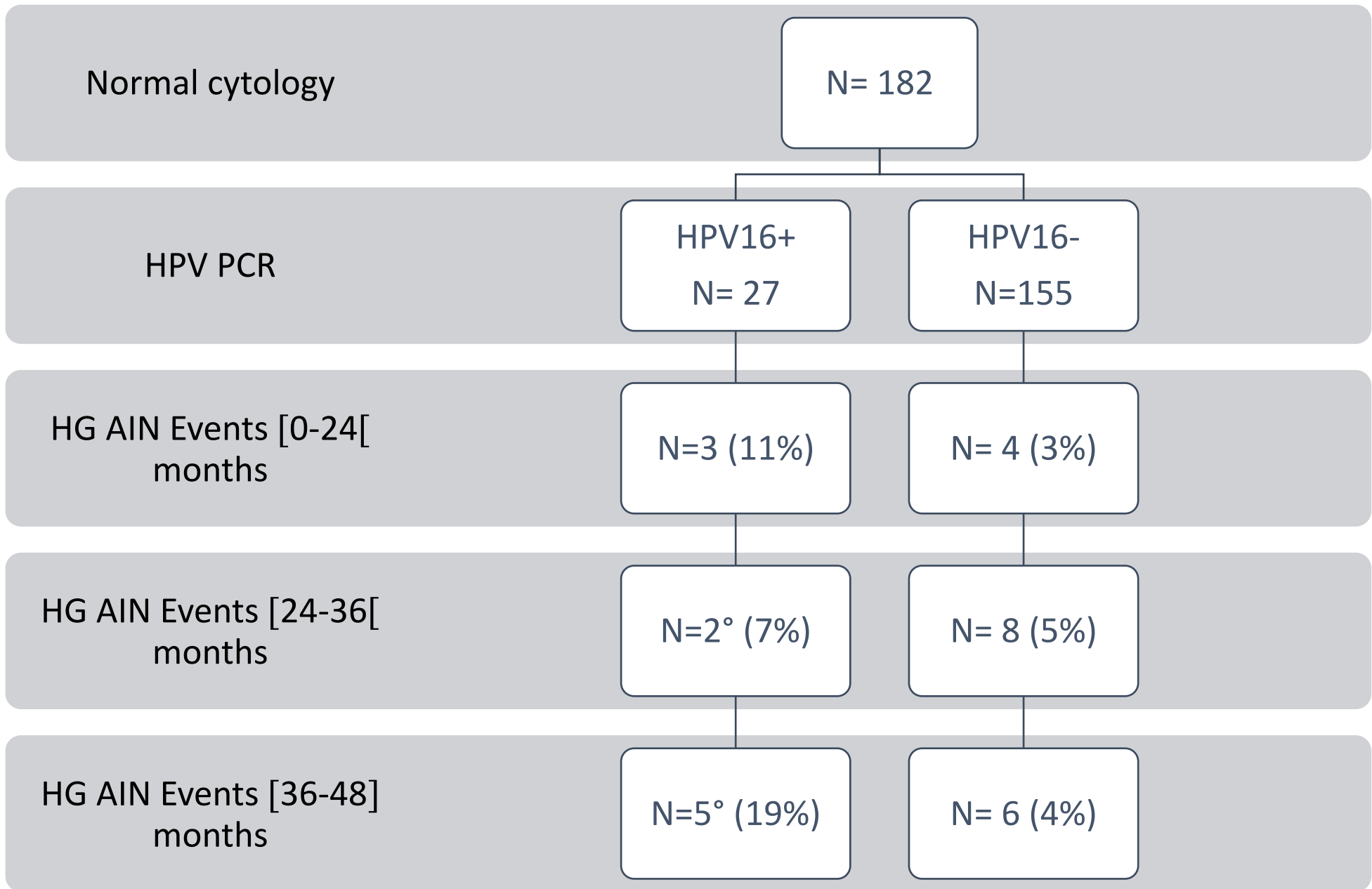
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° one invasive cancer

Table 1: Patient characteristics and anal events

Item	N	N (%) or mean (SD)
Age (years)	182	48.1 (11)
Sex (F/M)	182	19/163 (10/90)
<u>Past history and comorbidities</u>		
HPV-related conditions	182	77 (42)
Treatment of high-grade anal intraepithelial lesions	182	13 (7)
Cervical high-grade lesion or invasive cancer	19	2 (11)
Sexually transmitted diseases (other than HPV)	182	47(28)
HIV infection	182	147 (81)
HAART	147	124 (84)
Nadir CD4 count (cell/mm <sup>3</sup> )	82	302 (214)
MSM	163	126 (77)
Tobacco consumption (yes/ex/no)	181	29/36/116 (16/20/64)
Tobacco exposure (months)	60	331(128)
Body mass index (kg/m <sup>2</sup> )	177	23.5 (4)
BMI>30	177	12 (7)
Diabetes mellitus	182	1 (1)
Immunocompromised host (HIV exclusion)	180	2 (1)
Hysterectomy for cancer	19	1 (5)
Crohn's disease	182	1 (1)
<u>HPV genotypes at baseline</u>		
Number of HPV genotypes per patient	182	1.4 (1.6)
HPV16	182	27 (15)
High-risk HPV	182	81 (45)
<u>Events within the study period</u>		
Follow-up duration (months)	182	41.2 (10.7)
High-grade AIN/invasive cancer during the follow-up	182	28/2 (15/1)
AIN treatments during follow-up	182	19 (10)

Table 2: Events within the study period

Follow-up (months)	[0-12[	[12-24[	[24-36[	[36-48]
Pathology	182	166	120	79
Abnormal cytology	30 (17%)	54 (33%)	34 (28%)	35 (44%)
New HSIL	3 (2%)	4 (2%)	3 (3%)	8 (10%)
New HG AIN	2 (1%)	5 (3%)	10 (8%)	11 (14%)
Virology	182	161	114	73
New HPV16	27 (15%)	6 (4%)	5 (4%)	8 (11%)
HPV16+	34 (19%)	33 (21%)	28 (25%)	26 (36%)
HR HPV+	87 (48%)	80 (48%)	66 (58%)	48 (66%)

Table 3: Factors associated with the occurrence of high-grade lesions (univariate and multivariate analyses)

	Univariate analysis			Multivariate analysis		
	HR	IC95%	p	HR	IC95%	p
Female status	<b>2.6</b>	<b>0.9-6.4</b>	<b>0.0046</b>	1.6	0.4-6.0	0.59
Previously treated HR-AIN	<b>4.2</b>	<b>1.4-10.3</b>	<b>0.0008</b>	3.9	0.9-15.0	0.05
Age>44 years	<b>2.0</b>	<b>0.8-6.1</b>	<b>0.14</b>	1.4	0.5-4.4	0.53
HIV-positive status	0.8	0.3-2.4	0.66			
Tobacco consumption	1.1	0.3-4.1	0.75			
Obesity	0.9	0.1-3.1	0.89			
Previous HPV disease	1.6	0.8-3.4	0.21			
Anal sex	1.2	0.5-3.0	0.70			
Positive HPV16 at baseline	<b>3.0</b>	<b>1.3-6.4</b>	<b>0.0005</b>	<b>2.9</b>	<b>1.2-6.4</b>	<b>0.02</b>
Abnormal cytology at 1 year	<b>3.0</b>	<b>1.4-6.4</b>	<b>0.01</b>	2.4	1.0-5.3	0.08
HPV 16 & abnormal cytology	6.7	2.0-19.8	0.0001			