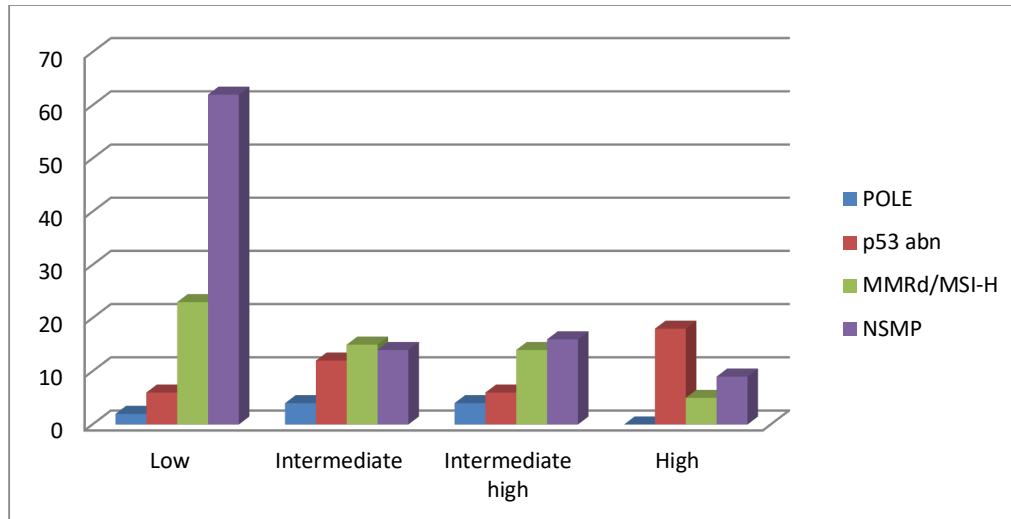


1 **Supplemental material 1: Correlation between molecular and pathological uterine risk factors\***

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6 Abbreviation: dMMR/MSI-H, mismatch repair deficient/microsatellite instability high; p53 abn; p53 abnormal; *POLE*, Polymerase-epsilon;

7 NSMP, non-specific mutational profile. \* Classes of risk based on uterine risk factors according to the ESGO/ESTRO/ESP guidelines.

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15 **Supplemental material 2: Details about nodal disease according to histological uterine risk factors and molecular features**

	Nodal disease (n=41)	Macrometastases (n=21)	Micrometastases (n=8)	Isolate tumor cells (n=12)
<b>Histological classes*</b>				
Low risk (n=93)	2 (2.2%)	0	1 (1.1%)	1 (1.1%)
Intermediate risk (n=45)	7 (15.6%)	1 (2.2%)	4 (8.9%)	2 (4.4%)
Intermediate-high risk (n=40)	22 (55%)	10 (25%)	3 (7.5%)	9 (22.5%)
High risk (n=32)	10 (31.3%)	10 (31.3%)	0	0
<b>Molecular classes</b>				
<i>POLE</i> mutated (n=10)	2 (20%)	0	1 (10%)	1 (10%)
dMMR/MSI-H (n=57)	12 (21%)	2 (3.5%)	3 (5.3%)	7 (12.3%)
p53 abnormal (n=42)	7 (16.6%)	5 (11.9%)	2 (4.8%)	0
NSMP (n=101)	20 (19.8%)	14 (13.9%)	2 (1.9%)	4 (3.9%)

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Data are reported as number (%); Abbreviation: dMMR/MSI-H, mismatch repair deficient/microsatellite instability high; p53 abn; p53 abnormal; *POLE*, Polymerase-epsilon; NSMP, non-specific mutational profile. \* Classes of risk based on uterine risk factors according to the ESGO/ESTRO/ESP guidelines.

23 **Supplemental material 3: Patients with positive nodes according to histological and molecular features**

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	POLE mutated (n=2)	dMMR/MSI-H (n=12)	p53 abnormal (n=7)	NSMP (n=20)
Low risk (n=2)	0	1	0	1
Intermediate risk (n=7)	2	3	2	0
Intermediate-high risk (n=22)	0	8	3	11
High risk (n=10)	0	0	2	8

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