

HPV Type-specific Distribution in a Group of Women Attending at Hospital Fernando Fonseca, Lisbon

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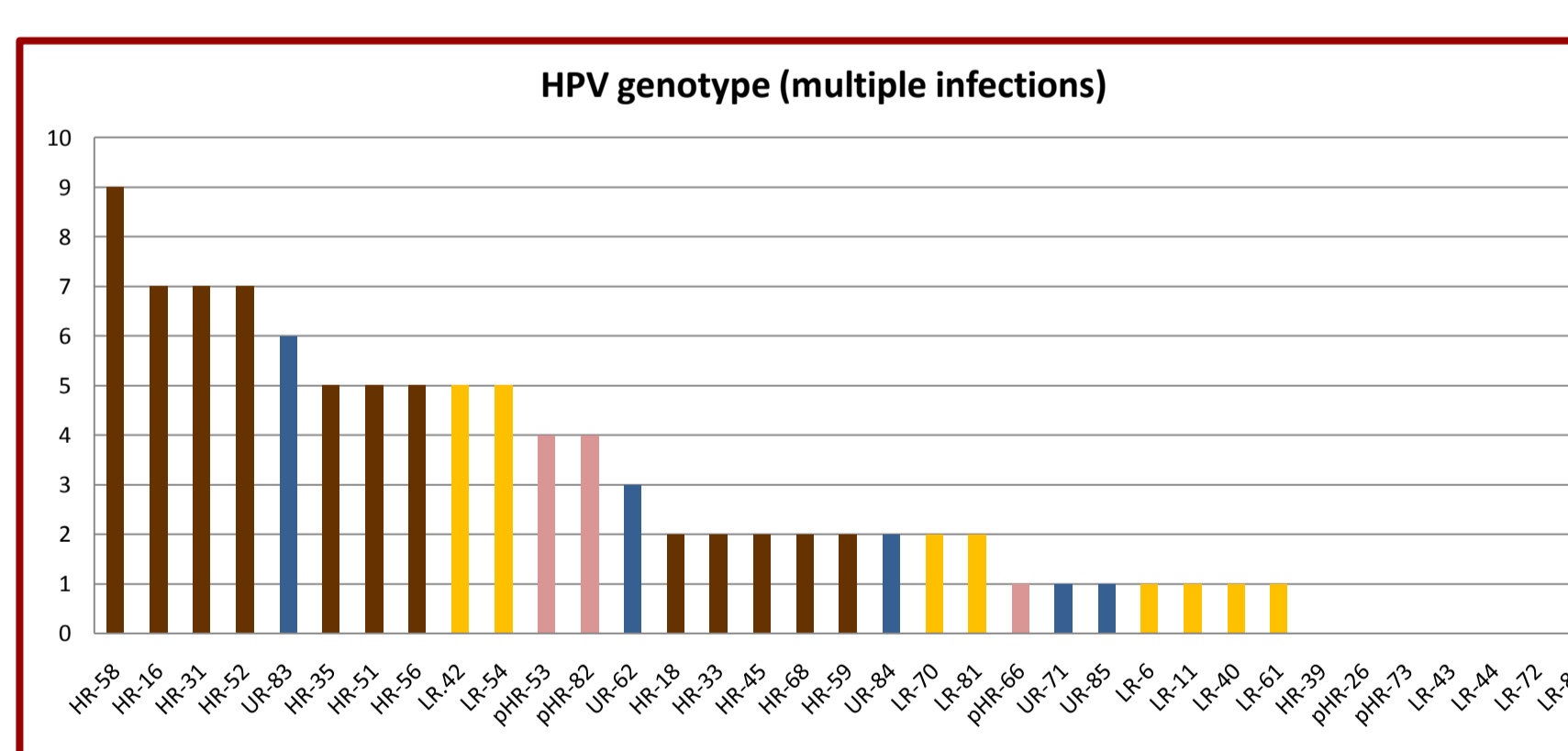
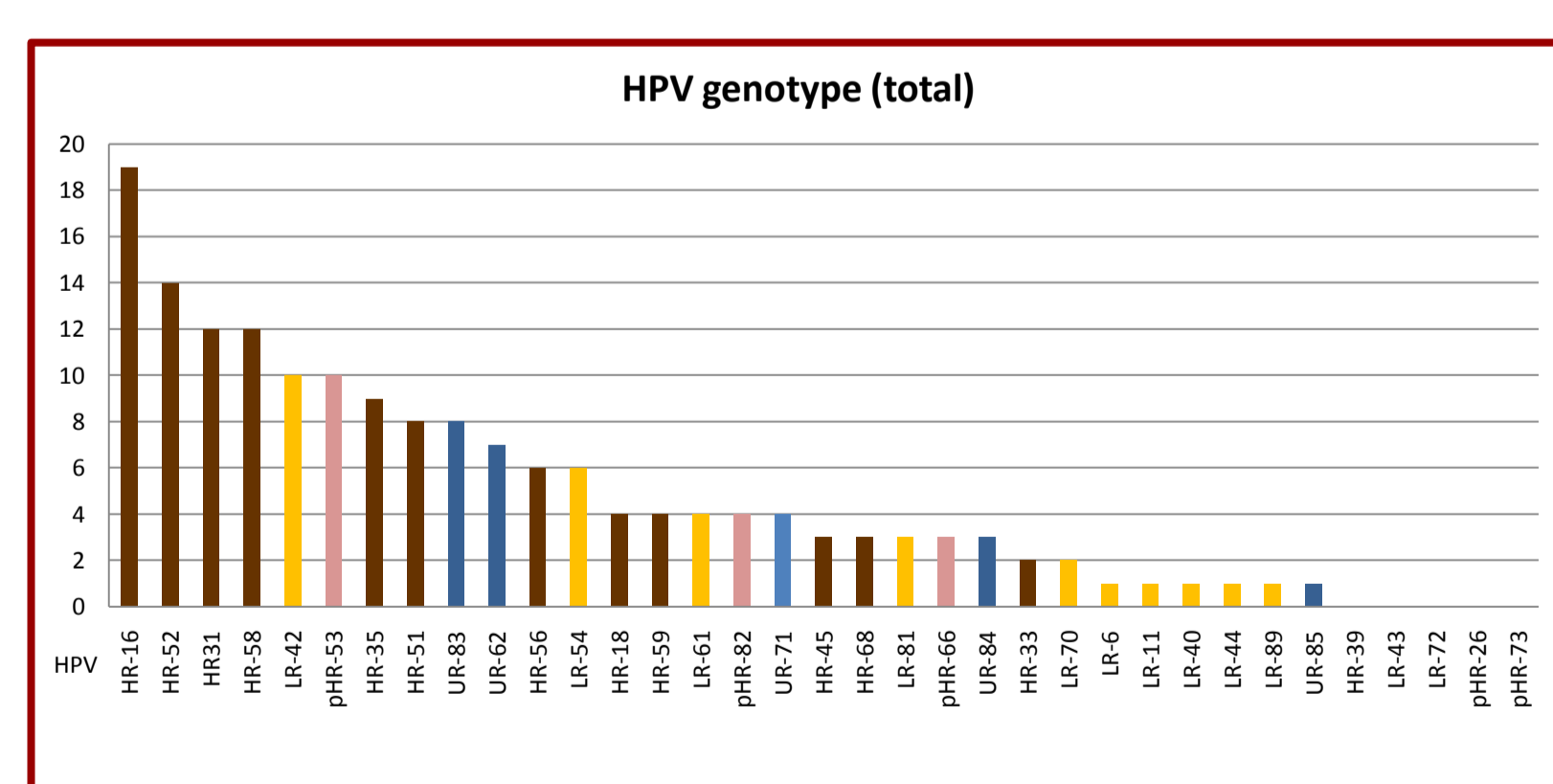
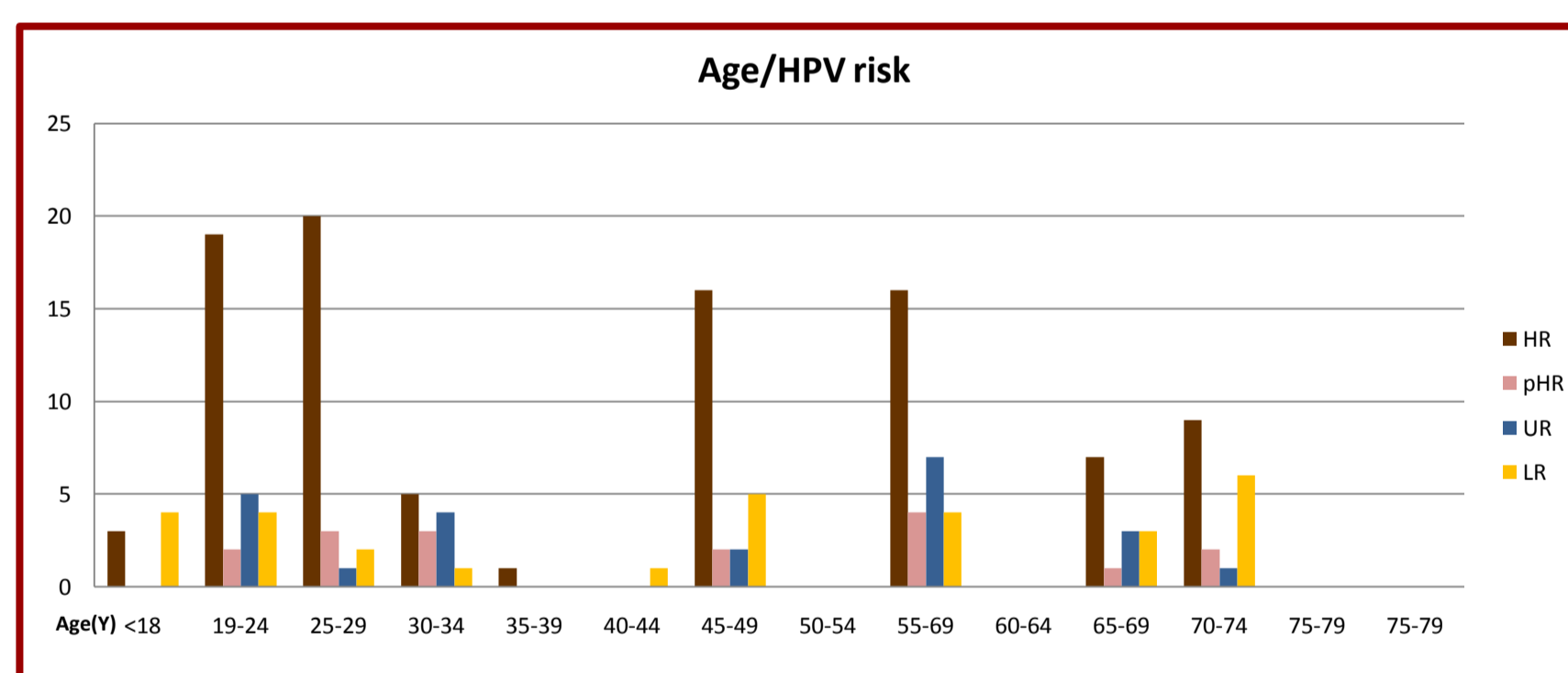
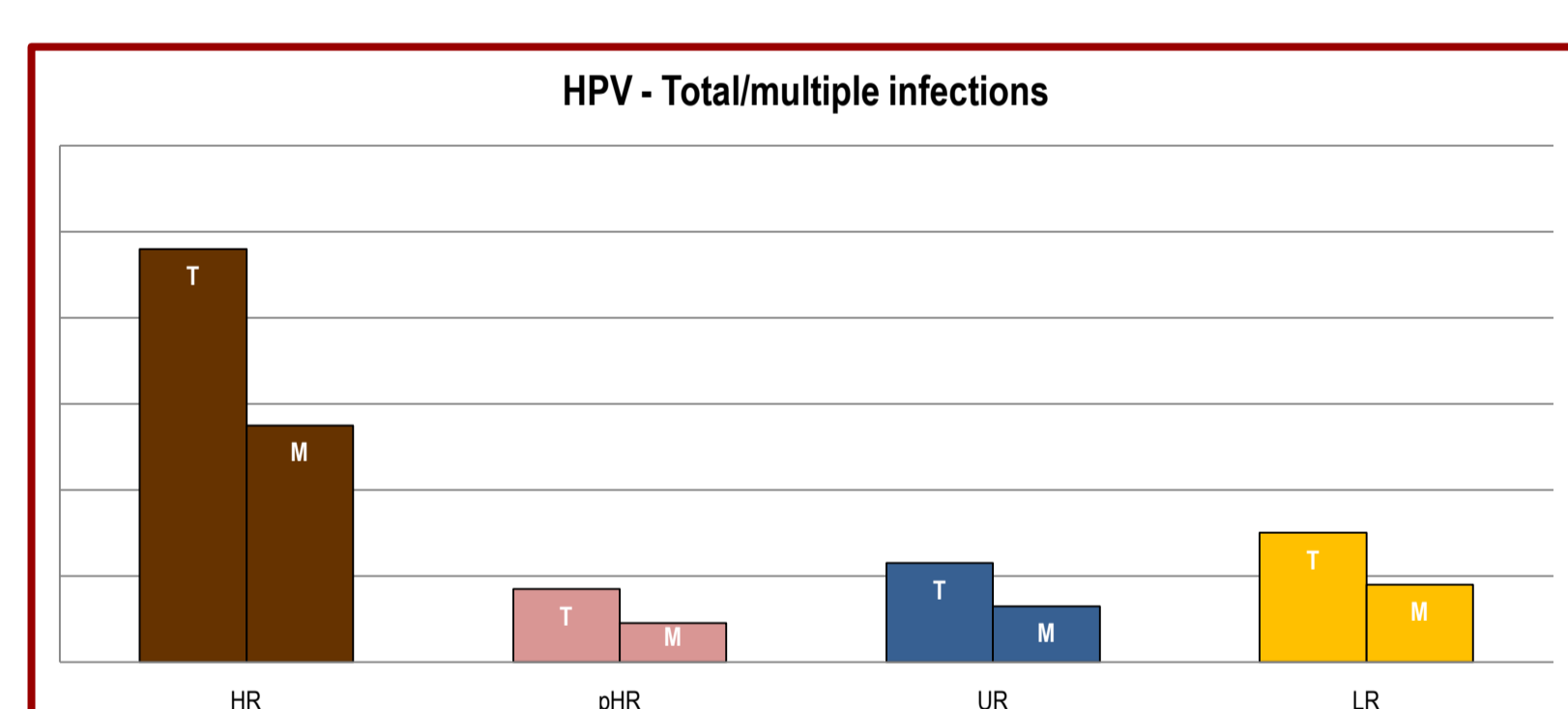
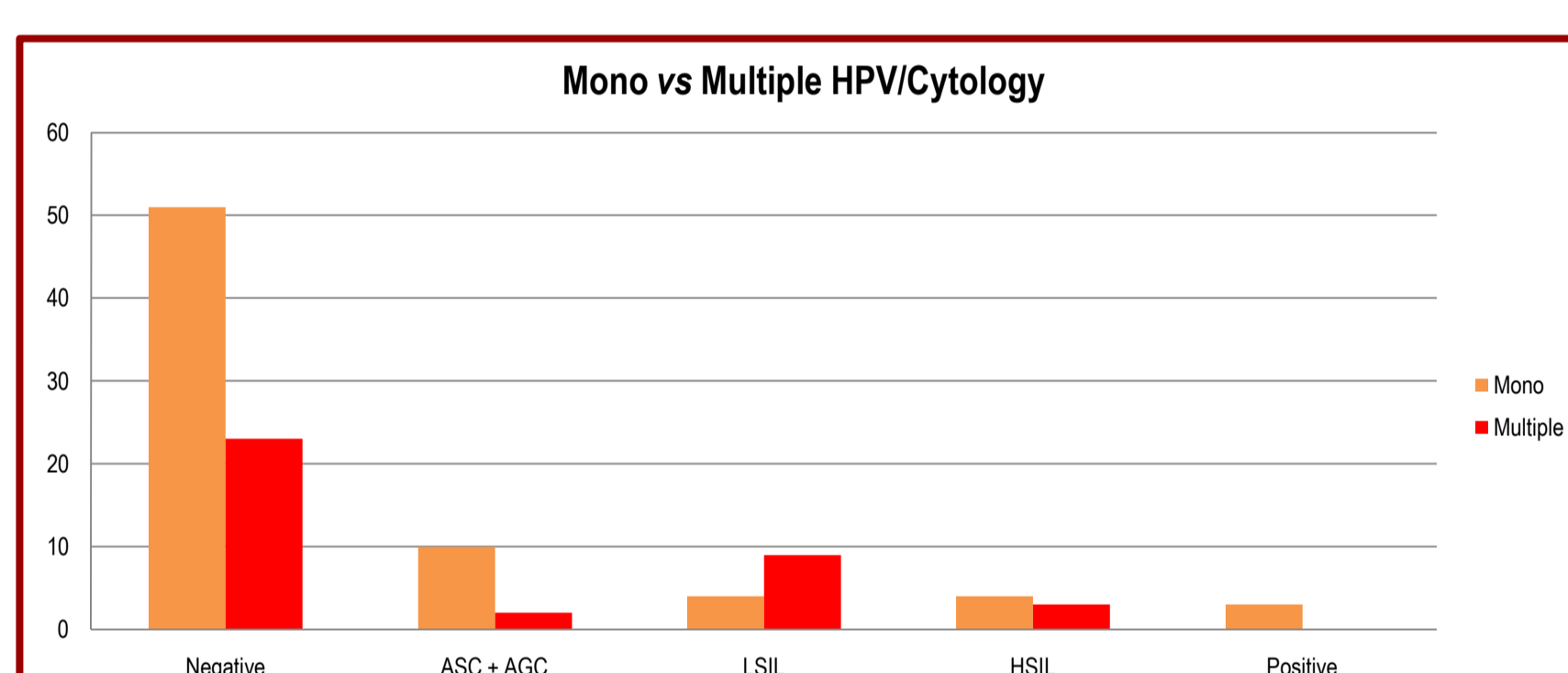
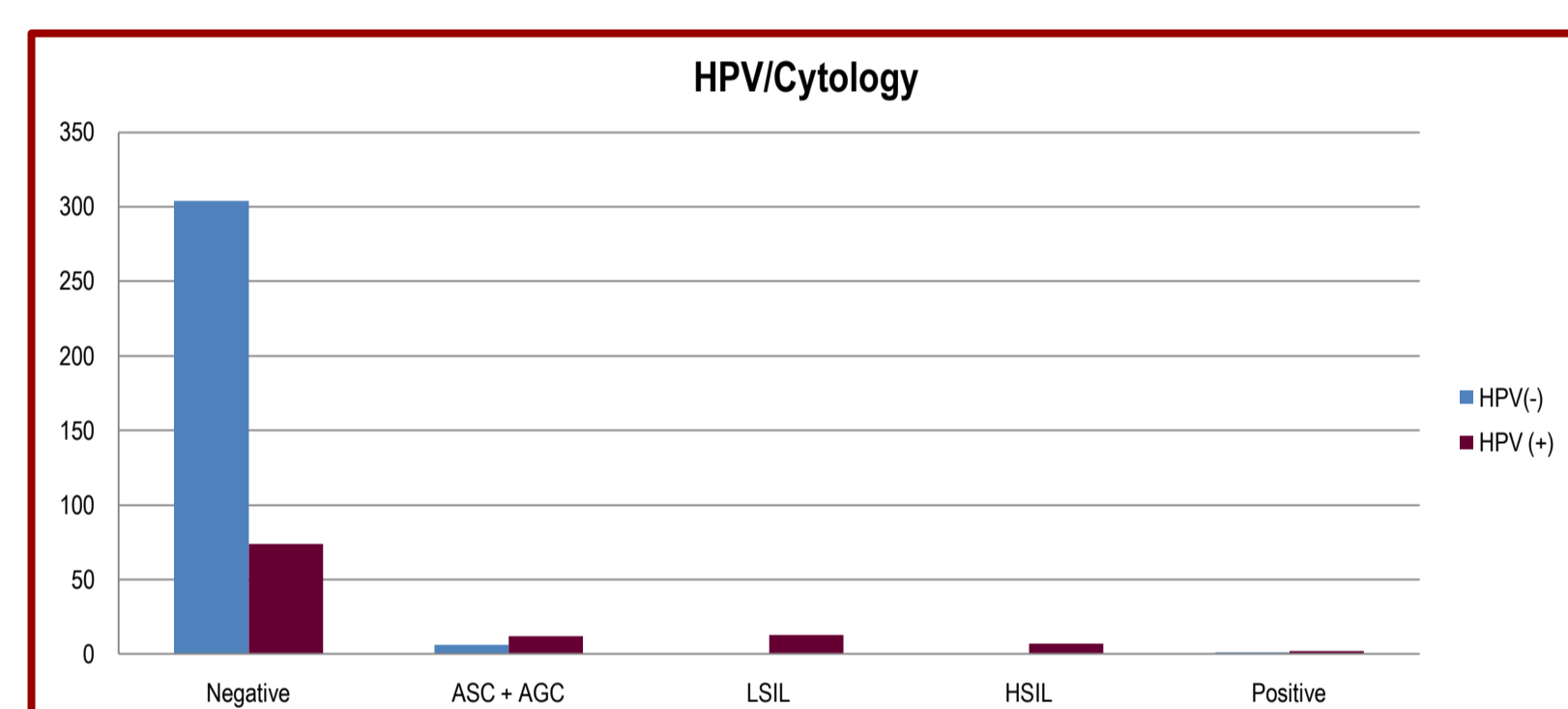
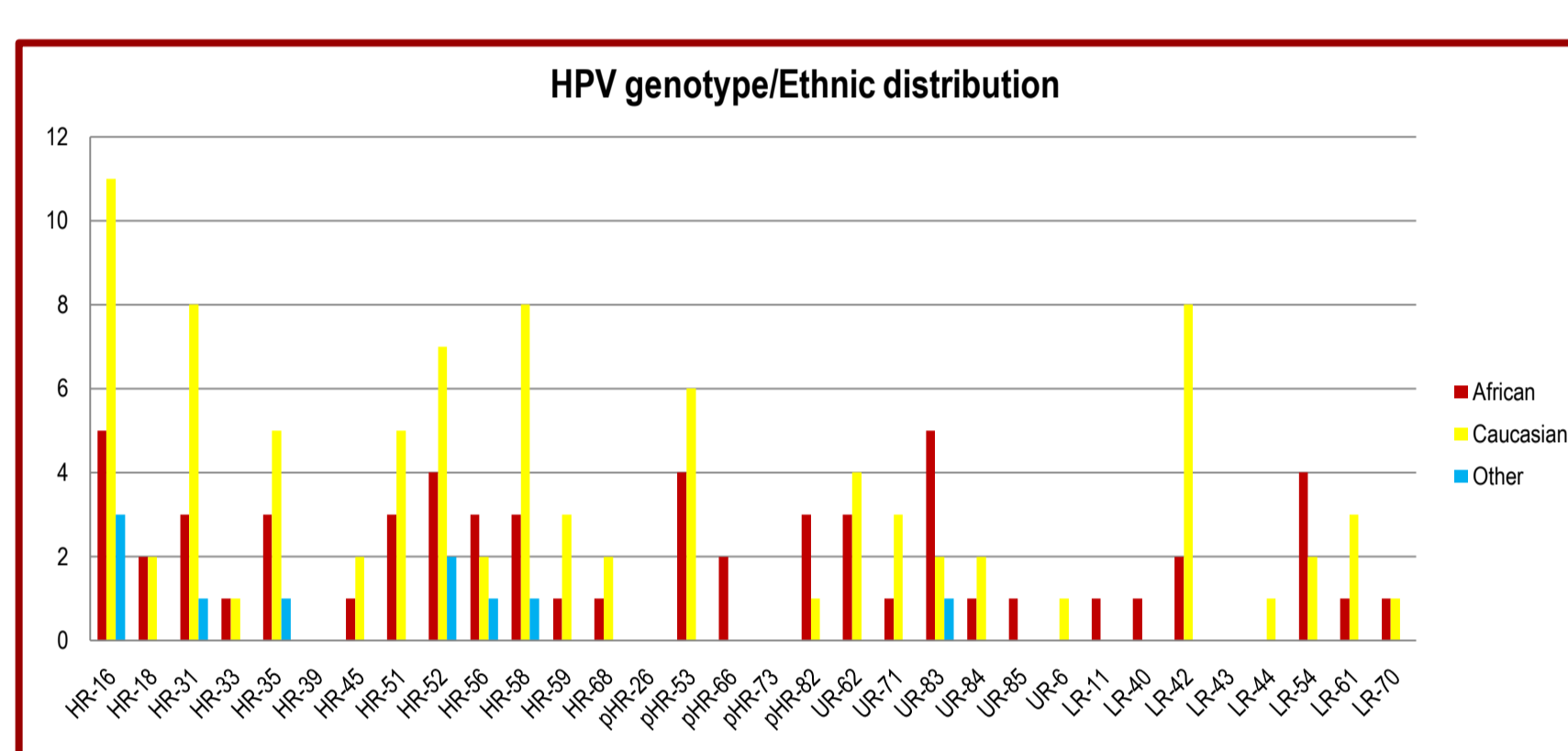
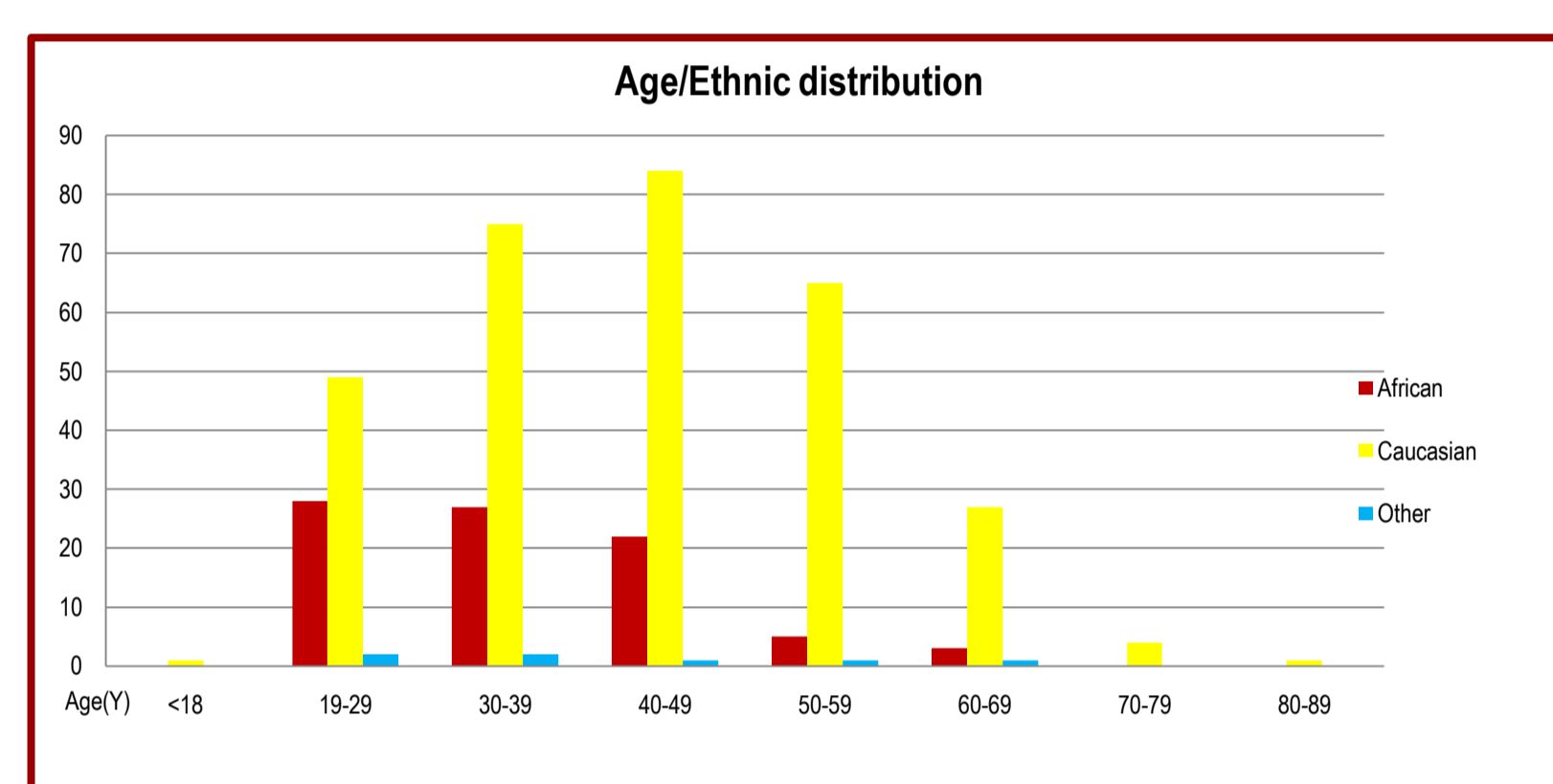
Introduction: Genital HPV infection is very frequent. Nevertheless, type-specific distribution can vary greatly in different populations.

Aim: To assess the HPV frequency and type-specific distribution in a highly ethnically diverse region and its association with gynecological cytology.

Material and Methods: From March to July 2009, 419 LBC samples (ThinPrep) were collected from women 16-79 years old, attending at Hospital Fernando Fonseca and associated Primary Health Care Centers. HPV genotyping was performed using CLINICAL ARRAY HPV 2. Statistical analysis was performed using χ^2 .

Results:

1. Out of 419 women (median age: 41 years), 74.0% were Caucasian and 21.0% African (Fig 1).
2. Overall, 90.2% of the women had a normal cytology, 4.3% had ASCUS, 3.1% LSIL, 1.7% HSIL, and 0.7% had invasive carcinoma (Fig 3).
3. HPV infection was detected in 25.8% of the cases, whereas 75.0% in women between 20-45 years (Fig 3/6).
4. HR-HPV genotypes were identified in 57.8% of the infected women (Fig 6).
5. The most frequent HR-HPV types were HPV16 (11.4%), HPV52 (8.5%), HPV31 and 58 (7.2% each) (Fig 7).
6. Multiple infections (2-6 genotypes) were observed in 34.2%. HPV58, 16, 31, and 52 (9.5%, 7.4%, 7.4%, 7.4%, respectively) were the most frequent genotypes (Fig 5/8).
7. HPV DNA was detected in 19.6% of the women with normal cytology, of which 31.0% had multiple infections (Fig 4/5).
8. In ASCUS, LSIL, HSIL and invasive carcinoma, HPV was detected in 66.7%, 100%, 100%, and 66.7%, respectively (Fig 3/4).
9. HPV16, 31, 52, 58 and 42 were most frequent among Caucasian, and HPV16, 83, 52, 53 and 54 among African women (Fig 2).
10. HPV16 and 18 were found in 4.5% and 1.0% of the women, respectively (Fig 2/5/7).
11. Infection by multiple HPV was related to lesion grade ($p=0.042$).



Conclusion: Our results are consistent with data observed in the literature. Our findings can help for a better understanding of the wide spectrum of HPV infection and can contribute to a baseline for future assessment of screening and immunization strategies.

We are grateful to our colleagues who helped with all LBC samples and to our sponsors.