# HPV type and viral load distribution in Norwegian LSIL and ASCUS triage samples

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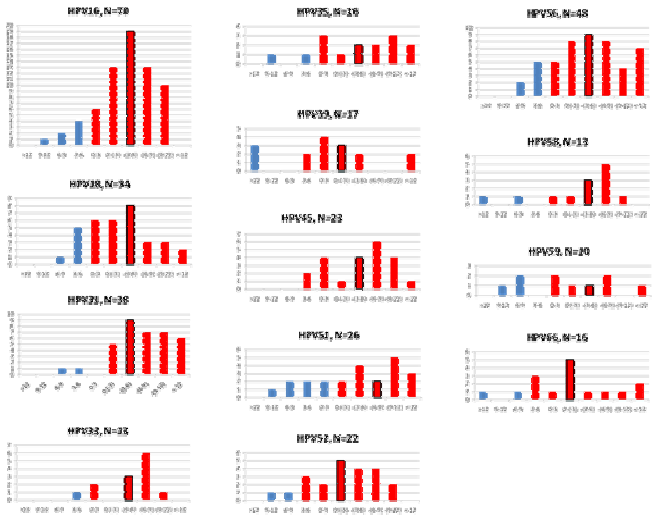
## Abstract
Viral loads of thirteen HR HPV types were determined by quantitative PCR in 512 LSIL/ASCUS triage samples. Viral load distributions differed according to type. Epidemiological studies based on tests with suboptimal sensitivity will give biased prevalence estimates. Several of distributions are apparently multimodal, suggesting that they incorporate different biological entities.

## Introduction
Differences in HPV viral load distribution potentially impact prevalence estimates. Viral load may also be a prognostic factor. We have used quantitative PCR to determine viral load distributions for thirteen HR HPV types in LSIL/ASCUS triage samples.

## Materials and methods
**Material**: 512 cervical cytobrush samples (PreserveCyt) from Norwegian women undergoing LSIL/ASCUS triage.

**Viral load** distributions were obtained for HPV types 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59 and 66 using consensus multiplex real time PCR (PapType13 RT test). Viral load was expressed as relative Cq referenced to a parallel positive control.



Viral load distributions. An interval of 3 Cq units corresponds to a factor of ca. six range of viral load. Blue columns indicate viral loads below 50 000 copies per sample, the cutoff of the HC2 test. The column corresponding to $10^6$ copies per sample is outlined.
Cq is the PCR cycle where amplicon concentration reaches a set threshold. Cq is negatively proportional to the log of HPV viral load.

## Results
**Prevalences:** HPV16: 14%; HPV56: 9%; HPV31, HPV18: 7%; HPV51: 5%; HPV45, HPV52: 4%; HPV66,, HPV33, HPV35, HPV39, HPV58: 3%; HPV59: 2%. 46% of samples were HPV positive, 31% for single HPV types and 15% for multiple types.
**Viral Load distributions**.
**HPV16**: unimodal distribution with peak at ca. $10^6$ copies/sample. **HPV58** similar.
**HPV18:** skewed toward lower viral loads.
**HPV31:** skewed toward higher viral loads.
**HPV51, HPV35:** broad and rather flat distributions.
Several distributions, particularly **HPV45**, **HPV52**, **HPV56** are suggestive of multimodality.

## Conclusions
Viral load distributions for the various types differ in mean, mode and spread. As a result, test sensitivity will differentially affect type specific prevalence estimates. Most distributions appear irregular or multimodal, suggesting different types of infection with different viral loads. Larger studies will be required to confirm this.

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