**HPV serotyping done in QMH report generation logic**:

Description by default: ‘HPV serotyping’.

Operation by default: ‘liquid base cytology for HPV typing

HPV choose either +ve or –ve

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**If choose ‘-ve’**, hide the three boxes and ‘hybridization’ and ‘sequencing’

Microscopic examination printed as: ‘*HPV specific PCR performed on the extracted DNA did not yield any specific amplification product indicating the absence of human papilloma virus in the specimen.*’

If also choose weak control, append a sentence: ‘*There is, however, weak signal in the control PCR limiting interpretation.*’

Diagnosis would be: ‘*- Genome of HPV not detected.*’

M-code: ‘no malignancy’

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**If choose ‘+ve’,**

microscopic starts as: ‘*PCR reveals the presence of HPV genome.*’

If choose ‘hybridization’ but not ‘sequencing’, Add this sentence: ‘*The following HPV serotype(s) is/are detected by hybridization:*’.

If choose ‘sequencing’ but not ‘hybridization’, Add this sentence: ‘*The following HPV serotype(s) is/are detected by sequencing:*’.

If choose both ‘hybridization’ and ‘sequencing’, Add this sentence: ‘*The following HPV serotype(s) is/are detected by hybridization and sequencing:*’.

Then followed by a table with two columns (please refer to the excel file):

Serotype Risk of developing high grade lesion or carcinoma

( ) **If h**: ‘*High risk*’; **if p**: *Probable high risk (data inadequate for firm conclusion, but currently considered high risk)*; **if l**: ‘Low risk’. **For all other numbers**: ‘*Uncertain risk (only limited data at present)*’

If also choose weak control, append a sentence: ‘*There is, however, weak signal in the control PCR limiting interpretation.*’

For diagnosis:

‘- Genomes of ( ), ( ), ( ) detected.’

‘- See above for details of risk.’

M-code: ‘condyloma nos & planum’

The generated report would overwrite previous ‘description’ ‘microscopic’ ‘operation’ ‘diagnosis’ and M-code