# Appendix Ⅰ

Table1. HistoQC pipeline sequence

|  |
| --- |
| ClassificationModule.byExampleWithFeatures:pen\_markings  ClassificationModule.byExampleWithFeatures:coverslip\_edge  LightDarkModule.getIntensityThresholdPercent:tissue  LightDarkModule.getIntensityThresholdPercent:darktissue  BubbleRegionByRegion.detectSmoothness  MorphologyModule.removeFatlikeTissue  MorphologyModule.fillSmallHoles  MorphologyModule.removeSmallObjects  BlurDetectionModule.identifyBlurryRegions  BasicModule.finalProcessingSpur  BasicModule.finalProcessingArea  HistogramModule.compareToTemplates  HistogramModule.getHistogram  BrightContrastModule.getContrast  BrightContrastModule.getBrightnessGray  BrightContrastModule.getBrightnessByChannelinColorSpace:RGB  DeconvolutionModule.separateStains  SaveModule.saveFinalMask  SaveModule.saveThumbnails  BasicModule.finalComputations |

# Appendix Ⅱ

'wsi\_composite' is calculated as follows.

All the elements in the formula are generated by HistoQC. michelson\_contrast refers to Michelson contrast, while rms\_contrast represents root-mean-square contrast. Similarly, grayscale\_brightness corresponds to grayscale intensity, and chani\_brightness represents intensities of the individual red, green, and blue channels. Additionally, spur\_pixels represents the percentage of pixels that contain small holes.