RELEASE NOTES

Reproductive Health Research Analysis Software (RHAS) v1.1

Defect Fixes for RHAS 1.1

- Autosomal Loss of Heterozygosity (LOH) calculation has been corrected and Chromosome X is no longer included in the calculation
- If the analysis uses HMM model for Copy Number Analysis, the y-gender will be used by the software for the gender of the samples
- Cache issue for *chp files with genotyping cluster plots when a no step2 run is performed has been resolved.

New Features of RHAS 1.1

- Mendelian Error Checking for HT-CMA Arrays
  - Duo or Trio Analysis
  - Report Generation
    - Export of results as pdf or text file
    - Print results to pdf
- Mosaicism
  - Mosaic gains displayed
    - CN segments
    - Whole Genome View Track
  - Mosaic losses displayed
    - CN segments
    - Whole Genome View Track

Recommended and minimum requirements

Table 1 Software

System Properties	Recommended System Requirements	Minimum System Requirements
Processor	Intel Pentium 4x2.83 GHz Quad Core Processor	Intel Pentium 4x2.83 GHz Quad Core Processor
64-bit Windows Operating System and Web Browser	Microsoft Windows 10 (64-bit) Professional Internet Explorer 11.0 (or above) or Microsoft Edge	Windows 7 Professional SP1 and Windows 10 Internet Explorer 11.0 (or above) or Microsoft Edge
Available Disk Space	250 GB HD + data storage	150 GB HD + data storage
Free Disk Space Required at Installation	≥ 5 GB	≥ 5 GB
RAM	32 GB	16 GB

Library file packages

Table 2 Available RHAS Library file packages (updated for RHAS 1.1)

Array name	hg38
CytoScan HTCMA (96 format)	CytoScan_HTCMA_96.r3.zip

Table 3 Available MSV Library file packages (updated for RHAS 1.1)

MSV Files	hg19/hg38
MSV Files	MSV_RHAS_Files.r2.zip