

# Reproductive Health Research Analysis Software (RHAS) v1.0

## Features

- Perform copy number analysis for CytoScan HTCMA array plates.
- Perform genotyping and variant analysis for CytoScan HTCMA and CarrierScan array plates.
- Perform SMN analysis for CytoScan HTCMA and CarrierScan array plates.
- Create customer's own copy number reference model file for future copy number analysis
- View Sample QC data and analysis summaries in tables and graphs.
- View chromosomal aberration results for CytoScan HTCMA, and CytoScan family of arrays, OncoScan arrays, and ReproSeq data.
- View variant data in Cluster Plots.
- View variant data in tables and summary matrix.
- View SMN results in table and graphs.
- Link out to external databases including ClinVar, NCBI, Ensembl, UCSC genome browser, DGV, Taqman
- Synchronize with ChAS software
- Export Data in various formats for use in 3<sup>rd</sup> party software, including VCF export.

## 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	16 GB	8 GB

## Library file packages

**Table 2** Available RHAS Library file packages

Array name	hg38
CytoScan HTCMA (96 format)	CytoScan_HTCMA_96.r1.zip

**Table 3** Available MSV Library file packages

MSV Files	hg19/hg38
MSV Files	MSV_RHAS_Files.r1.zip