



**TITLE: Whole Genome Sequencing**

SOP Number:           D-DEZ-PRO-027          

Revision Number:                           0                          

Effective Date:                   8 Aug 2015                  

---

G. BIOINFORMATIC ANALYSIS

6. Download fastq files from NYGC according to emailed instructions.
7. Place files in /Shared/IVR/NGS/raw\_data/<YYYYMMDD>\_DTVR\_genome/.
8. Create analysis directory  
/Shared/IVR/NGS/analysis/genome/DTVR/<sampleID>/<date>\_<pipeline\_version>/
9. Create symbolic links to the fastq files named  
sample.file<1...n>\_<read>.fastq.gz
10. Copy the following files into the analysis directory  
/Shared/IVR/NGS/214/process\_NGS.v214.pl  
/Shared/IVR/NGS/214/config.genome.v214
11. Run the following command in the analysis directory:  
  
qsub -N <SampleID> process\_NGS.v214.pl config.genome.v214 <SampleID> RESEARCH
12. Transfer resulting .xlsx file to DTVR shared folder on WIVR-file1.eng.uiowa.edu.

I. HISTORY

Effective Date	Revision	Change
8 Aug 2015	0	Initial issue of SOP