***Idotea baltica* RNA-seq Preprocessing**

FASTQC 0.11.2

**RUNNING**

Connect to Taito with X11 flag and open fastqc

ssh –X ketaya@taito.csc.fi

xterm &

module load biokit

fastqc

\*\*\* ~50min/file, file~300M reads(17GB compressed) (~2hrs/file on my laptop)