07/03/2017

Rate of aneuploidy for gene conversion lines:

93 lines total

39 whole-chromosome CNVs

2100 generations

aneuploidy events:

39/93/2100 = 1.9969 x 10^-4 events/genome/generation

3n mutations:

38/93/2100 = 1.94 x 10^-4 events/genome/generation

1n mutations:

1/93/2100 = 5.12 x 10^-6 events/genome/generation

two different 3n mutations:

5/93/2100 = 2.56 x 10^-5

07/05/2017

Question: GC lines are hybrids of distant relatives of same species. Is there a higher rate of aneuploidy in them compared to MA lines?

rate of aneuploidy in MA lines: 9.7 +/- 1.8 x 10^-5 events/genome/generation

\*Looks like YES, there is a higher rate of aneuploidy in GC lines

This may be expected:

Marinoni G, Manuel M, Petersen RF, Hvidtfeldt J, Sulo P, et al (1999) Horizontal transfer of genetic material among Saccharomyces yeasts. J Bacteriol 181: 6488-6496.

Dosage Compensation workflow April 2017

Reference genome from SGD – latest update (31-Jan-2015) (S288C)

1. Need to build an index using bowtie

use bowtie2-build (code #1 in text file)

2. Need to use Cufflinks to change .gff transcript file into a .gtf file

http://cole-trapnell-lab.github.io/cufflinks/file\_formats/#the-gffread-utility

3. Need to use Tophat to make a transcriptome index from the .gtf file given from Cufflinks

https://ccb.jhu.edu/software/tophat/manual.shtml

4. Then run Tophat with the transcriptome index and parameters needed and reference sequence from bowtie (#1)

Update 11/15/17

* RNA was extracted using the MasterPure Yeast RNA Purification Kit
* Libraries were prepared using the Illumina Stranded RNAseq Kit.
* They were sequenced at the Georgia Genomics Facility on the Illumina NextSeq (75 cycles) SE75 High Output flow cell. Samples were multiplexed and split across two runs.
* reference genome and GTF file obtained from: https://support.illumina.com/sequencing/sequencing\_software/igenome.html
* FastQC (version jdk1.8.0\_20 ) used to perform quality control on sequenced RNA from all samples
* TrimGalore (version 0.4.4) used to trim sequences below a quality threshold of 20
  + adapters were removed by GGF
* Bowtie (version 2.2.9) was used to map reads to the reference genome
  + Because yeast has so few introns, it wasn’t completely necessary to use a splice-aware mapper like Tophat.
* Samtools (version 1.3.1) was used to view .sam files as .bam files and sort .bam files