**#MassiveSeq Flow Diagram for Iron Hack**

**Quality Control (QC)**

**Prepare input**

Get meta-data

Take text file and put into format that BCBio can parse out

1. Get control samples
2. Get affected samples (cases)

**SnakeMake (Hisat2)**

**Multiply by n**

**Differential Expression (DE)**

**Analyses of differences between cases and controls:**

**PCA**

**TSNE**

**Docker**

**Megablast**

**Variants**

**Transcript (Count info)**

**RNA**