Setting up a portable metagenome assembly pipeline for CBIO - Issues

#	Tracker	Status	Priority	Subject	Assignee	Updated
60	Support	New	Normal	Setup Nextflow metagenomics pipeline YAMP on hex		07/24/2018 12:13 PM
50	Support	New	Normal	Validate binning using single copy core genes		05/16/2018 02:41 PM
45	Support	New	Normal	Quality trimming with Trimmomatic		04/26/2018 05:17 PM
38	Support	New	Normal	How to download SRA files to hex		04/20/2018 03:35 PM
27	Support	New	Normal	What we already know and have setup	Katie Lennard	04/26/2018 01:13 PM