| **Supplementary table 1. List of select WARP workflows** | | | | | |
| --- | --- | --- | --- | --- | --- |
| **Pipeline** | **WARP WDL Code** | **Input Data** | **Overview** | **Terra Workspace** | **Publication (if applicable)** |
| Exome Germline Single Sample | [Exome Germline Single Sample](https://github.com/broadinstitute/warp/blob/master/pipelines/broad/dna_seq/germline/single_sample/exome/ExomeGermlineSingleSample.wdl) | Human exome sequencing data | [Exome Germline Single Sample Overview](https://broadinstitute.github.io/warp/docs/Pipelines/Exome_Germline_Single_Sample_Pipeline/README) | [Exome Germline Single Sample](https://app.terra.bio/#workspaces/warp-pipelines/Exome-Analysis-Pipeline) | [Van der Auwera & O'Connor, 2020](https://www.oreilly.com/library/view/genomics-in-the/9781491975183/) |
| Imputation | [Imputation](https://github.com/broadinstitute/warp/blob/master/pipelines/broad/arrays/imputation/Imputation.wdl) | Multi-sample variants calls from genotyping array data | [Imputation Overview](https://broadinstitute.github.io/warp/docs/Pipelines/Imputation_Pipeline/README) | [Imputation](https://app.terra.bio/#workspaces/warp-pipelines/Imputation) |  |
| MethylC-Seq (CEMBA) | [CEMBA](https://github.com/broadinstitute/warp/blob/master/pipelines/cemba/cemba_methylcseq/CEMBA.wdl) | Multiplexed single-nucleus bisulfite sequencing data | [CEMBA Overview](https://broadinstitute.github.io/warp/docs/Pipelines/CEMBA_MethylC_Seq_Pipeline/README) | [CEMBA](https://app.terra.bio/#workspaces/brain-initiative-bcdc/Methyl-c-seq_Pipeline) | [Luo et al. 2017](https://science.sciencemag.org/content/357/6351/600/tab-pdf) |
| Optimus | [Optimus](https://github.com/broadinstitute/warp/blob/master/pipelines/skylab/optimus/Optimus.wdl) | 10x Genomics V2 and V3 3' single-cell and single-nucleus data | [Optimus Overview](https://broadinstitute.github.io/warp/docs/Pipelines/Optimus_Pipeline/README) | [Optimus](https://app.terra.bio/#workspaces/featured-workspaces-hca/HCA_Optimus_Pipeline) |  |
| Single-Cell ATAC (scATAC) | [scATAC](https://github.com/broadinstitute/warp/blob/master/pipelines/skylab/scATAC/scATAC.wdl) | Single-cell ATAC-seq data from nuclear isolates | [scATAC Overview](https://broadinstitute.github.io/warp/docs/Pipelines/Single_Cell_ATAC_Seq_Pipeline/README) | [scATAC](https://app.terra.bio/#workspaces/brain-initiative-bcdc/scATAC) | [Fang et al. (2021)](https://www.nature.com/articles/s41467-021-21583-9) |
| Slide-seq | [Slide-Seq](https://github.com/broadinstitute/warp/blob/master/pipelines/skylab/slideseq/SlideSeq.wdl) | Spatial transcriptomic data | [Slide-seq Overview](https://broadinstitute.github.io/warp/docs/Pipelines/SlideSeq_Pipeline/README/) | [Slide-seq](https://app.terra.bio/#workspaces/warp-pipelines/Slide-seq) |  |
| Smart-seq2 Single Nucleus Multi-Sample | [Smart-seq2 Single Nucleus Multi-Sample](https://github.com/broadinstitute/warp/blob/master/pipelines/skylab/smartseq2_single_nucleus_multisample/MultiSampleSmartSeq2SingleNucleus.wdl) | Single-cell data generated with Smart-seq2 assays | [Smart-seq2 Single Nucleus Multi-Sample Overview](https://broadinstitute.github.io/warp/docs/Pipelines/Smart-seq2_Single_Nucleus_Multi_Sample_Pipeline/README) | [Smart-seq2 Single Nucleus Multi-Sample](https://app.terra.bio/#workspaces/warp-pipelines/Smart-seq2_Single_Nucleus_Muti-Sample) |  |
| Whole Genome Germline Single Sample | [Whole Genome Germline Single Sample](https://github.com/broadinstitute/warp/blob/master/pipelines/broad/dna_seq/germline/single_sample/wgs/WholeGenomeGermlineSingleSample.wdl) | Human whole-genome paired-end sequencing data | [Whole Genome Germline Single Sample Overview](https://broadinstitute.github.io/warp/docs/Pipelines/Whole_Genome_Germline_Single_Sample_Pipeline/README) | [Whole Genome Germline Single Sample](https://app.terra.bio/#workspaces/warp-pipelines/Whole-Genome-Analysis-Pipeline) | [Van der Auwera & O'Connor, 2020](https://www.oreilly.com/library/view/genomics-in-the/9781491975183/) |