

	Trecode	OTP	HTS-Flow	QuickNGS	Closha	Terra
Data type	WGS, WXS, RNA-Seq, Methylation Array	WGS, WXS, WGBS, RNA-Seq, ChIP-Seq	BS-seq, RNA-Seq, ChIP-Seq, DNaseI-Seq	WGS, RNA-Seq, ChIP-Seq,miRNA	WGS,WXS, RNA-Seq, ChIP-Seq	WGS,WXS,RNA-Seq,WGBS
Meta data	+++	++	+	++		+
GUI	+++	++	+	+	++	++
Data provenance	+++	++	+	+		+
Reproducibility	+++	++	+	+	++	++
EGA/SRA compatibility	+++	++	+			
Automation	+++	+++	++	++	+	+
Flexibility	+++	++	++	+	++	++
Workflow specification	WDL	Java/Groovy	R	bash/perl	Closha canvas	WDL
Workflow execution	Cromwell	Roddy/PBS/SGE/LSF	R BatchJob/SGE	Slurm, Torque	Hadoop	Cromwell
Execution environment	HPC Cluster, Cloud	HPC cluster	HPC cluster	HPC cluster	HPC cluster	Cloud
Major genomics softwares	GATK4, BWA, Samtools, STAR, MultiQC	BWA, Picard, Samtools, Platypus, ACSeq, STAR	BWA, TopHat, Bismark, MACS, Cufflinks, Cuffdiff	BWA, MACS, Samtools, Cufflinks	GATK, BWA, Samtools, STAR, TopHat, Cufflinks, Cuffdiff	GATK4, BWA, Samtools,STAR
Access control	*	+		+		
Availability	open source	open source	open source	open source	service	service/open source**
Re-use	+++	+			+	+
unified QC	yes (MultiQC)	no (custom)	no (custom)	no (custom)	no	no
Result visualization	+***	++		++	+	
Version control	yes	yes	yes	yes		yes
Multiuser	yes	yes	no	no	yes	yes
Institution	Princess Máxima Center for Pediatric Oncology	German Cancer Research Center (DKFZ)	Fondazione Istituto Italiano di Tecnologia	CECAD Research Center, University of Cologne	Korea Research Institute of Bioscience and Biotechnology	Broad Institute / Verily Life Sciences
Latest development	2020	2020	2016	2016	2020	2020

*=waiting for implementation in Molgenis

**=no documentation yet for spinning up a Terra instance

***=trecode includes exports to visualization platforms cBioportal and R2