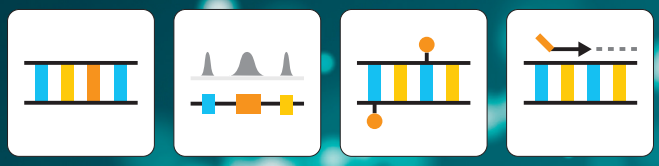
NGS Product Overview.

LIBRARY PREPARATION SOLUTIONS
FOR DNA AND RNA SEQUENCING



DNA-Seq

Tecan offers simple and streamlined workflows for DNA sequencing library preparation on Illumina platforms. Our library preparation kits are optimized for use across a variety of automation platforms and include our proprietary DimerFree® technology – that simplifies the workflow by eliminating adaptor dimers and adaptor dilution steps – and NuQuant® for rapid, integrated library quantification for research purposes.

Celero™ DNA-Seq: short, three-step, addition-only, single-tube library preparation

- Sample input: 10 to 500 ng
- Single-tube workflow with one bead purification following library amplification
- Available with Unique Dual Index (UDI) adaptors for detection of index hopping
- Integrated NuQuant technology for library QC in less than six minutes

Ovation® Ultralow DNA-Seq V2: simple DNA-Seq library preparation workflow for low input and degraded sample types

- Sample input: 10 pg to 100 ng
- Ultralow input range for any sample type – DNA from cell lines, fresh and FFPE tissue, liquid biopsy and cell-free DNA
- Available with UDI adaptors for detection of index hopping, and molecular tags for detection of PCR duplicates
- Unbiased libraries from samples with a broad range of GC content

Celero PCR Workflow with Enzymatic Fragmentation DNA-Seq: short, three-step workflow can be completed in under four hours

- Sample input: 10 to 500 ng
- Consistent, optimization-free enzymatic fragmentation, regardless of input
- Available with UDI adaptors for detection of index hopping
- Integrated NuQuant technology for library QC in less than six minutes

Rapid EZ DNA-Seq: short, add and incubate workflow for PCR-free libraries in 2.5 hours

- Sample input: 200 to 500 ng
- Optimization-free, robust enzymatic fragmentation to generate insert sizes from 200 - 500 bp
- PCR-fee workflow enables high quality data for any sample type, including microbial genomes with a broad range of GC content
- Available with UDI adaptors for detection of index hopping

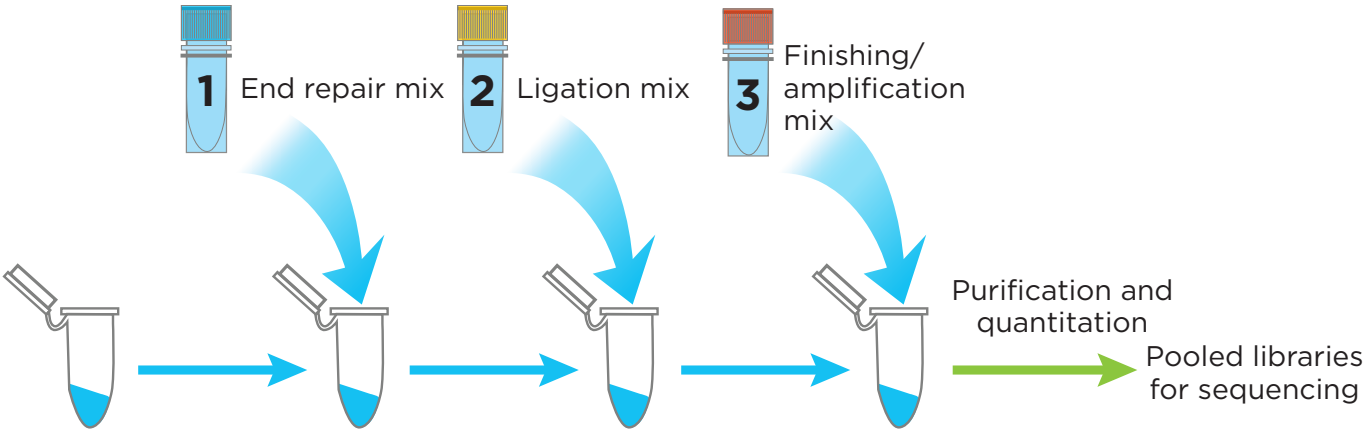


Figure 1: Celero DNA-Seq is a simple, addition-only workflow that produces DNA-Seq libraries in 3 steps.

Ovation Rapid DR Multiplex System: fast, PCR-free DNA-Seq library preparation workflow that can be easily completed in under two hours

- Sample input: 100 to 500 ng
- Single tube workflow with one bead purification
- Useful for applications sensitive to PCR bias or PCR artifacts, such as the sequencing of GC- or AT-rich regions of the human genome, microbiome and prokaryotic samples

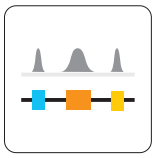
Ovation Low Complexity Sequencing System: single solution for PCR and PCR-free library preparation for amplicons and other low sequence diversity samples

- Sample input: 40 to 60 ng (depending on amplicon size)
- Libraries from PCR amplicons as small as 100 to 450 bp in length, or other low diversity samples, without the need for PhiX spike-in
- Dual index adaptors for flexible multiplexing

ORDERING INFORMATION

Description	Part No.	No. of reactions	No. of barcodes	Automation fill (A01) availability
Celero DNA-Seq	0360	24, 96	Up to 384	Yes
Celero DNA-Seq	0360A-UDI, 0360B-UDI*	96	Up to 192	–
Celero PCR Workflow with Enzymatic Fragmentation	9363	24, 96	Up to 192	Yes
Celero PCR Workflow with Enzymatic Fragmentation	9363A-UDI, 9363B-UDI*	96	Up to 192	Yes
Rapid EZ DNA-Seq	0567	24, 96	96	Yes
Ovation Rapid DR Multiplex System	0319, 0320	32	Up to 16	–
Ovation Rapid DR Multiplex System 1-96	0328	96	96	–
Ovation Rapid + UDI	9154	96	96	–
Ovation Ultralow System V2	0344NB	8, 32, 96	Up to 96	Yes
Ovation Ultralow DNA-Seq V2 + UDI	9149	96	96	Yes
Ovation Low Complexity Sequencing System	9092	32, 96	Up to 96	–

*This Celero kit does not include NuQuant for library quantitation.



RNA-Seq

Tecan RNA-Seq kits offer faster, simpler, more sensitive RNA sequencing on Illumina platforms. These kits feature novel, proprietary technologies including AnyDeplete® targeted transcript depletion – to remove unwanted transcripts – Single Primer Isothermal Amplification (SPIA®) – for detection of rare transcripts – DimerFree adaptor ligation, and NuQuant for rapid, integrated library quantification for research purposes.

Universal Plus mRNA-Seq with NuQuant: streamlined library preparation solution for mRNA sequencing

- Sample input: 10 to 1,000 ng total RNA
- Available with up to 192 UDI adaptors for detection of index hopping, and molecular tags for detection of PCR duplicates
- Integrated NuQuant technology for library QC in less than six minutes
- Optional integration of AnyDeplete technology for customizable post-library depletion of unwanted reads

Universal RNA-Seq with NuQuant: first end-to-end solution for whole transcriptome RNA-Seq libraries combining library preparation, targeted depletion and library quantification

- Sample input: 10 to 250 ng total RNA
- Compatible with any RNA sample type and all levels of sample quality, from high quality RNA to degraded FFPE samples
- Available with UDI adaptors for detection of index hopping
- Integrated AnyDeplete technology for customizable post-library depletion of unwanted reads
- Integrated NuQuant technology for library QC in less than six minutes

Trio RNA-Seq: complete solution for library preparation, incorporating SPIA for sensitive detection of rare transcripts

- Sample input: 500 pg to 50 ng total RNA
- Robust up-front cDNA amplification improves the detection of low expression transcripts
- Available with UDI adaptors for detection of index hopping
- Integrated AnyDeplete technology for customizable post-library depletion of unwanted reads
- Sample types include fragmented RNA, cell-free RNA, FFPE samples and samples for viral detection

Universal Prokaryotic RNA-Seq: simple library preparation solution for metatranscriptomic studies

- Sample input: 100 to 500 ng total RNA
- Strand-specific RNA sequencing for prokaryotic transcriptomics
- Available with UDI adaptors for detection of index hopping
- Integrated AnyDeplete technology for customizable post-library depletion of unwanted prokaryotic rRNA
- Sample types include purified RNA from bacterial cell lines, environmental samples and samples from human microbiome studies

Ovation SoLo RNA-Seq: robust library preparation workflow for whole transcriptome RNA-Seq from single cells or ultralow, degraded inputs

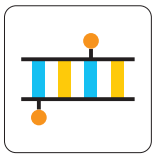
- Sample input 10 pg to 10 ng, 1 to 500 cells
- Whole transcriptome analysis starting from isolated RNA or cell lysate
- Integrated AnyDeplete and molecular tags to provide high quality data
- Sample types include purified RNA or lysates from cell lines including single cells, fresh or FFPE tissues, liquid biopsies, cell-free RNA and other ultra low input RNA samples

Ovation RNA-Seq System V2: rapid and sensitive workflow for generating micrograms of cDNA for multiple downstream applications

- Sample input: 500 pg to 100 ng
- Whole transcriptome amplification using SPIA for preparing cDNA from total RNA or poly(A) selected mRNA
- Sample types include total RNA from laser capture microdissection (LCM) tissue, fine needle aspirates, sorted cells, liquid biopsies, prokaryotes, viruses, and other challenging sample types
- Micrograms of DNA obtained for downstream applications such as RNA-Seq, qPCR, microarrays and sample archiving

ORDERING INFORMATION

Description	Part No.	No. of reactions	No. of barcodes	Automation fill (AO1) availability
Universal RNA-Seq with NuQuant, Human AnyDeplete	0530	32, 96	Up to 96	Yes
Universal RNA-Seq with NuQuant, Mouse AnyDeplete	0531	32, 96	Up to 96	Yes
Universal RNA-Seq with NuQuant, *Drosophila* AnyDeplete	0532	32, 96	Up to 96	Yes
Universal RNA-Seq with NuQuant, Custom AnyDeplete	0533	32, 96	Up to 96	Yes
Universal RNA-Seq with NuQuant+ UDI, Human AnyDeplete	0537	96	96	Yes
Universal RNA-Seq with NuQuant + UDI, Mouse AnyDeplete	0538	96	96	Yes
Universal RNA-Seq with NuQuant + UDI, *Drosophila* AnyDeplete	0539	96	96	Yes
Universal RNA-Seq with NuQuant + UDI, Custom AnyDeplete	0540	96	96	Yes
Universal Plus mRNA-Seq with NuQuant + UDI	0520	24, 96	Up to 192	Yes
Universal Plus mRNA-Seq with NuQuant + UDI, Human Globin AnyDeplete	0521	24, 96	Up to 192	Yes
Trio RNA-Seq, Human rRNA AnyDeplete	0506	8, 32, 96	Up to 96	Yes
Trio RNA-Seq + UDI, Human rRNA AnyDeplete	9143	96	96	Yes
Trio RNA-Seq + UDI, Mouse rRNA AnyDeplete	0507	8, 32, 96	Up to 96	Yes
Universal Prokaryotic RNA-Seq	0363	32	32	–
Ovation SoLo RNA-Seq System, Human rRNA AnyDeplete	0500	32, 96	Up to 96	–
Ovation SoLo RNA-Seq System, Mouse rRNA AnyDeplete	0501	32, 96	Up to 96	–
Ovation SoLo RNA-Seq System, *Drosophila* rRNA AnyDeplete	0502	32, 96	Up to 96	–
Ovation RNA-Seq System V2	7102	8, 32, 96	-	Yes



Methyl-Seq

Tecan Methyl-Seq kits combine library preparation and bisulfite sequencing conversion tools for a broad range of research applications, including NGS and methylation arrays. With the integration of TrueMethyl® oxBS chemistry, users can gain new insight into epigenetic modifications, with the ability to interrogate both 5-methylcytosine (5mC) and 5-hydroxymethylcytosine (5hmC) in a single protocol. Methyl-Seq products feature our DimerFree ligation technology to enable streamlined, simple workflows for a variety of input quantities and sample types.

TrueMethyl oxBS Module: robust solution for bisulfite conversion of 5mC and 5hmC

- Sample input: 100 ng to 1 µg gDNA
- Accurate differentiation of 5mc and 5hmC in the same workflow
- Streamlined protocol enables processing of 32 oxBS reactions and 32 BS-only reactions in less than five hours

Ovation Ultralow Methyl-Seq with TrueMethyl oxBS: all-in-one NGS library preparation kit for whole genome methylation studies with integrated bisulfite conversion

- Sample input: 10 to 300 ng total DNA (100 ng minimum input for TrueMethyl oxBS conversion)
- Streamlined solution for whole genome Methyl-Seq library preparation that can be completed in approximately six hours
- Integrated TrueMethyl oxBS technology allows accurate differentiation between 5mC and 5hmC
- DimerFree technology eliminates adaptor artifacts without the need for adaptor titration

Ovation RRBS Methyl-Seq with TrueMethyl oxBS: cost-effective, fast solution for assessing methylation state of regions with high CpG density through a Reduced Representation Bisulfite Sequencing (RRBS) with integrated bisulfite conversion

- Sample input: 100 ng total DNA
- Built-in sequence diversity eliminates the need for PhiX spike-in, and produces more informative reads with improved quality
- Integrated molecular tag enables removal of non-unique reads from the dataset
- Integrated TrueMethyl oxBS technology allows accurate differentiation between 5mC and 5hmC

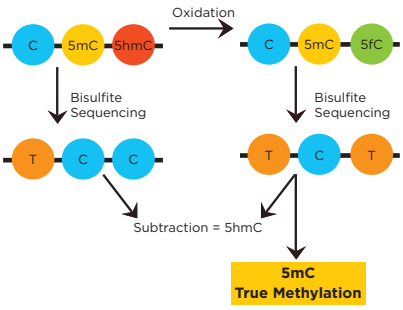
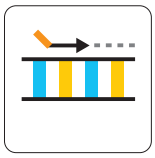


Figure 2: Achieve complete measurements of methyl-ation with oxBS. The schematic (Left) shows classic bisulfite conversion, which creates a library that detects both 5mC and 5hmC. Processing with the oxidation of 5hmV (Right) generates a bisulfite-con-vertible base that leads to detection of only 5hmC. Differences between the liabraries can be used to deduce the sites of 5hmC modifications.

ORDERING INFORMATION

Description	Part No.	No. of reactions	No. of barcodes	Automation fill (A01) availability
TrueMethyl oxBS Module	0414	32	–	–
Ultralow Methyl-Seq with TrueMethyl oxBS	0541, 9513	32, 96	Up to 96	Yes
Ovation RRBS Methyl-Seq System with TrueMethyl oxBS	0553, 9522	32, 96	Up to 96	Yes



Allegro® Targeted Genotyping

Allegro Targeted Genotyping provides a fast, scalable, cost-effective approach for targeted genotyping-by-sequencing on a wide variety of organisms using NGS. This workflow combines three core technologies to enable efficient SNP interrogation:

1. **Enzymatic fragmentation** – integrated for ease of use and automation
2. **DimerFree ligation** – eliminates adaptor dimer formation
3. **Single Primer Enrichment Technology (SPET)** – for targeted SNP interrogation

Allegro offers high sample multiplexing capabilities, the ability to interrogate over 100,000 SNPs in a single assay, and flexible design possibilities for targeting new markers.

- Sample input: 10 to 100 ng total DNA
- Simple, single-tube assay that can be completed in less than 24 hours
- Optimal probe placement for more efficient sequencing
- Independent probes provide validation of each SNP
- Ability to multiplex up to 3,072 libraries with the Allegro Metaplex Module
- Flexible panel designs for any sequenced genome
- Automation-friendly on a variety of platforms

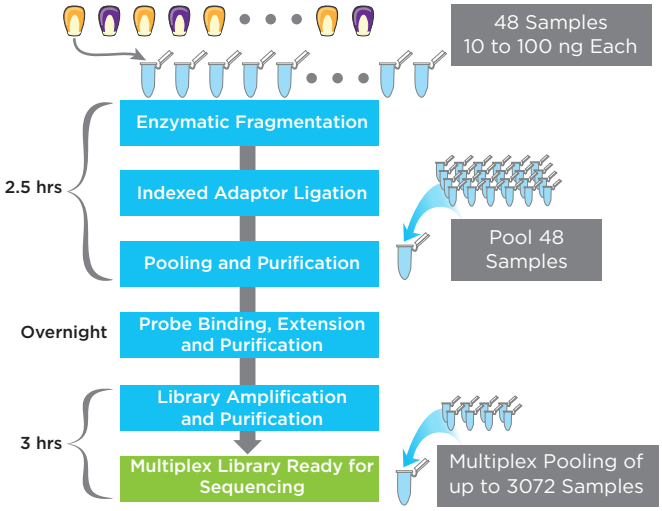


Figure 3: Allegro Targeted Genotyping V2 is a simple add and incubate workflow that can be easily automated.

ORDERING INFORMATION

Description	Part No.	No. of reactions	No. of barcodes	Automation fill (A01) availability
Allegro Targeted Genotyping (<5k probes, <2.5k SNPs)	10036	96, 192, 384	Up to 192	Yes
Allegro Targeted Genotyping (5-10k probes, 2.5-5k SNPs)	10030	96, 192, 384	Up to 192	Yes
Allegro Targeted Genotyping (10-50k probes, 5-25k SNPs)	10031	96, 192, 384	Up to 192	Yes
Allegro Targeted Genotyping (50-100k probes, 25-50k SNPs)	10032	96, 192, 384	Up to 192	Yes
Allegro Targeted Genotyping (>100k probes, >50k SNPs)	*	96, 192, 384	Up to 192	Yes
Allegro Targeted Genotyping V2 (<5k probes, <2.5k SNPs)	10050	192, 384, 768	Up to 192	Yes
Allegro Targeted Genotyping V2 (5-10k probes, 2.5-5k SNPs)	10051	192, 384, 768	Up to 192	Yes
Allegro Targeted Genotyping V2 (10-50k probes, 5-25k SNPs)	10052	192, 384, 768	Up to 192	Yes
Allegro Targeted Genotyping V2 (50-100k probes, 25-50k SNPs)	10053	192, 384, 768	Up to 192	Yes
Allegro Targeted Genotyping V2 (>100k probes, >50k SNPs)	*	192, 384, 768	Up to 192	Yes
Allegro Metaplex Module	0413-16	–	–	–

*Contact your local Tecan sales representative

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