Next-Generation Sequencing Product Citations

Nucleic Acid Extraction

Product Used	Citation	Notes
Maxwell® 16 MDx Research Instrument Maxwell® 16 LEV simplyRNA Blood Kit	Hermson et. al. (2015) Genomic landscape of rat strain and substrain variation. *BMC Genomics*, **16**:357-369.	Isolated RNA from brain, heart, kidney, liver, lung, muscle, ovary, skin, spleen, testis, thymus and whole blood using TRIzol® first followed by re-purification with the Maxwell® 16 Instrument and Kit.
Maxwell® 16 Instrument One of the Maxwell® 16 LEV simplyRNA Purification Kits	Lozano-Torres et. al. (2014) Apoplastic venom allergen-like proteins of cyst nematodes modulate the activation of basal plant innate immunity by cell surface receptors. *PLOS PATH.*, **10**: e1004569.	Extracted RNA from *Arabidopsis* using the Maxwell® 16 Instrument and one of the simplyRNA Kits and provided the RNA to BGI for RNA-seq on Illumina Instruments.
Maxwell® 16 Instrument and unnamed Kit	Meinel et. al. (2014) Next generation sequencing analysis of nine Corynebacterium ulcerans isolates reveals zoonotic transmission and a novel putative diphtheria toxin-encoding pathogenicity island. *Genome Medicine*, **6**:113-125.	Isolated gDNA from *C. ulcerans* using the Maxwell® Instrument and Kit followed by whole genome NGS using an Illumina MiSeq Instrument.
Maxwell® 16 Instrument Maxwell® 16 FFPE Plus LEV DNA Purification Kit	Heydt et. al. (2014) Comparison of pre-analytical FFPE sample preparation methods and their impact on massively parallel sequencing in routine diagnostics. *PLOS ONE*, **9**: e104566.	Extracted DNA from FFPE samples using the Maxwell® 16 Instrument and FFPE Plus DNA Kit. Side-by-side comparison to other extraction methods with demonstrated the Maxwell® 16 System produced the best quality DNA which was the only DNA used in the downstream NGS using an Illumina MiSeq Instrument.
Maxwell® 16 Instrument Unidentified Maxwell® 16 FFPE DNA Purification Kit	Beltran et. al. (2013) Targeted next-generation sequencing of advanced prostate cancer identifies potential therapeutic targets and disease heterogeneity. *Euro. Urology*, **63**: 920-926.	Extracted DNA from FFPE samples using the Maxwell® 16 Instrument and an unidentified Maxwell® FFPE DNA Kit. Purified DNA subjected to NGS on an Illumina HiSeq 2000 Instrument.
Maxwell® 16 Instrument Maxwell® 16 FFPE Plus LEV DNA Purification Kit	Javle et. al. (2013) Molecular characterization of gallbladder cancer using somatic mutation profiling. *Human Pathology*, **45**: 701-708.	Extracted DNA from gallbladder cancer FFPE samples using the Maxwell® 16 Instrument and the FFPE Plus DNA Kit. Did target enrichment followed by NGS on an Illumina HiSeq 2000 Instrument.
Maxwell® 16 Instrument Maxwell® 16 FFPE Plus LEV DNA Purification Kit	Vaishnavi et. al. (2014) Oncogenic and drug-sensitive *NTRK1* rearrangements in lung cancer. *Nat. Med.*, **19**: 1469-1472.	Extracted DNA from FFPE or frozen lung cancer samples using the Maxwell® 16 Instrument and the FFPE Plus DNA Kit. Did target enrichment followed by NGS on an Illumina HiSeq 2000 Instrument.

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Maxwell® 16 Instrument Maxwell® 16 LEV Blood DNA Kit	Knudsen et. al. (2015) Revisiting bovine pyometra—New insights into the disease using a culture-independent deep sequencing approach. *Vet. Micro.*, **175**: 319-324.	Purified DNA from endometrial biopsy samples using a modified protocol and the Maxwell® 16 Instrument and Blood DNA Kit.
Maxwell® 16 Instrument Maxwell® 16 Cell LEV DNA Purification Kit	De Man et. al. (2015) Draft genome sequence of a New Delhi metallo--lactamase-5 (NDM-5)-producing multidrug-resistant *Escherichia coli* isolate. *Genome Announcements*, **3**: e00017-15.	Extracted DNA from *E. coli* using the Maxwell® 16 Instrument and the Cell LEV DNA Kit. Did whole genome sequencing on purified DNA by NGS on an Illumina MiSeq Instrument.
Maxwell® 16 Instrument Maxwell® 16 Cell DNA Purification Kit	Kohlman et. al. (2015) Draft genome sequence of *Hafnia paralvei* strain GTA-HAF03. *Genome Announcements*, **3**: e01592-14.	Extracted DNA from *H. paralvei* using a Maxwell® 16 System followed by whole genome sequencing by NGS on an Illumina MiSeq Instrument.
ReliaPrep™ Blood gDNA Miniprep System	Donáth et.al. (2015) Polymorphisms of CSF1 and TM7SF4 genes in a case of mild juvenile Paget's disease found using next-generation sequencing. *Croat Med J.,* **56**:145-51.	Isolated genomic DNA from blood and used as input for amplicon production followed by NGS.
ReliaPrep™ FFPE gDNA Miniprep System	Yan et.al. (2014) Platform comparison for evaluation of ALK protein immunohistochemical expression, genomic copy number and hotspot mutation status in neuroblastomas. *PLOS ONE,* **9**: e106575.	Isolated genomic DNA from neuroblastoma FFPE samples using the ReliaPrep™ FFPE Kit followed by PCR enrichment and NGS on an Ion Torrent PGM Instrument.
SV Total RNA Isolation System	Breinholt, J.W. and A.Y. Kawahara. (2013) Phylotranscriptomics: saturated third codon positions radically influence the estimation of trees based on next-gen data. *Genome Biol. Evol.*, **5**: 2082–2092.	Extracted RNA from multiple tree species using the SV Total RNA Isolation System and performed RNA-seq on the RNA using an Illumina HiSeq 2000 Instrument.
SV Total RNA Isolation System	Li et. al. (2013) First transcriptome and digital gene expression analysis in Neuroptera with an emphasis on chemoreception genes in *Chrysopa pallens* (Rambur). *PLOS ONE*, **8**: e67151.	RNA was isolated from adult *C. pallens* (insect) tissues using the SV Total RNA Isolation System prior to cDNA library construction and NGS at BGI using Illumina Instruments.
Wizard® Genomic DNA Purification Kit	Chao et. al. (2013) High-resolution definition of the Vibrio cholerae essential gene set with hidden Markov model-based analyses of transposon-insertion sequencing data. *Nuc. Acids Res.*, **41**: 9033-9048.	Isolated initial genomic DNA from *V. cholerae* transposon library followed ultimately by NGS with an Illumina MiSeq Instrument.
Wizard® DNA Clean-Up System	Dong et. al. (2013) Sequencing angiosperm plastid genomes made easy: A complete set of universal primers and a case study on the phylogeny of saxifragales. *Genome Biol. Evol.*, **5**: 989-997.	Extracted chloroplast DNA using a CTAB method and then cleaned up that DNA using the Wizard® DNA Clean-Up System before NGS on an Illumina Genome Analyzer II.
Wizard® SV Gel and PCR Clean-Up System	Davey et. al. (2012) Seasonal trends in the biomass and structure of bryophyte-associated fungal communities explored by 454 pyrosequencing. *New Phytologist*, **195**: 844-856.	Extracted genomic DNA and then used the Wizard® SV Gel and PCR Clean-Up System to clean-up samples before starting library prep.

Nucleic Acid Quantitation Before and During Library Preparation

Product Used	Citation	Notes
QuantiFluor®-ST Fluorometer QuantiFluor® dsDNA System	Heydt et. al. (2014) Comparison of pre-analytical FFPE sample preparation methods and their impact on massively parallel sequencing in routine diagnostics. *PLOS ONE*, **9**: e104566.	Tested various quantitation methods/products and these two products were part of the testing.
QuantiFluor® dsDNA System	Van der Merwe et. al. (2014) Next-gen phyogeography of rainforest trees: Exploring landscape-level cpDNA variation from whole-genome sequencing. *Mol. Ecol. Resour.*, **14**: 199-208.	Extracted genomic DNA from leaf samples, and quantified the DNA with the QuantiFluor™ dsDNA System on the SpectraMax Gemimi XPS dectector before NGS.
QuantiFluor® dsDNA System	Cabeza et. al. (2014) An RNA sequencing transcriptome analysis reveals novel insights into molecular aspects of the nitrate impact on the nodule activity of *Medicago truncatula*. *Plant Physiol.*, **164**: 400-411.	Total RNA purified and converted into cDNA. The cDNA library was quantified using the QuantiFluor® dsDNA System prior to sequencing using the Illumina HiSeq 2000 Instrument.
QuantiFluor® dsDNA System	Brinsmade et. al. (2014) Hierarchical expression of genes controlled by the *Bacillus subtilis* global regulatory protein CodY. *Proc. Natl. Acad. Sci.*, **111**: 8227-8232.	The QuantiFluor® dsDNA System was used to quantify cDNA during construction of an RNA sequencing library and prior to sequencing on an Illumina HiSeq 2500 instrument
QuantiFluor® dsDNA System	De Donato et. al. (2013) Genotyping-by-Sequencing (GBS): A novel, efficient and cost-effective genotyping method for cattle using next-generation sequencing. *PLOS ONE*, **8**: e62137.	Genomic DNA was extracted and then quantitated using the QuantiFluor® dsDNA System on a SpectraFluor Plus plate-format fluorometer before being used for NGS.
QuantiFluor® dsDNA System	Chen et. al. (2013) Mining conifers' mega-genome using rapid and efficient multiplexed high-throughput genotyping-by-sequencing (GBS) SNP discovery platform. *Tree Genetics and Genomes*, **9**: 1537-1544.	DNA was extracted from dormant vegetative buds and DNA was quantitated using QuantiFluor® dsDNA System on a SpectraFluor Plus plate-format fluorometer prior to NGS.
QuantiFluor® dsDNA System	Shin et. al. (2012) Genome-wide ChIP-seq mapping and analysis reveal butyrate-induced acetylation of H3K9 and H3K27 correlated with transcription activity in bovine cells. *Func. Integr. Genomics*, **12**: 119-130.	Performed ChIP and quantitated immunoprecipitated DNA with the QuantiFluor® dsDNA System prior to NGS on an Illumina Instrument.

Next-Generation Sequencing Product Citations

Library Preparation

Product Used	Citation	Notes
GoTaq® Green Master Mix	Quigley et. al. (2012) High-throughput sequencing for detection of subpopulations of bacteria not previously associated with artisanal cheeses. *App. Env. Micro.*, **78**: 5717-5723.	Used GoTaq® Green Master mixes to amplify 16S bacterial genes from samples and then input those into NGS reactions using the 454 Genome Sequencer FLX Instrument.
One of the GoTaq® Master Mixes	Harris et. al. (2010) Comparison of normalization methods for construction of large, multiplex amplicon pools for next-generation sequencing. *App. Env. Micro.*, **76**: 3863-3868.	Created amplicons for sequencing using one of the GoTaq® Master Mix products. NGS was performed on a 454 Genome Sequencer FLX.
RQ1 RNase-Free DNase Wizard® SV Gel and PCR Clean-Up System	Schapire et. al. (2013) Construction of Specific Parallel Amplification of RNA Ends (SPARE) libraries for the systematic identification of plant microRNA processing intermediates. *Methods*, **6**: 283-291.	Developed a complete method for making cDNA libraries containing miRNA processing-intermediates that used the Promega products listed.
Recombinant RNasin® Ribonuclease Inhibitor	Fehniger et. al. (2010) Next-generation sequencing identifies the natural killer cell microRNA transcriptome. *Genome Res.*, **20**:1590-1604.	Used RNasin during miRNA library prep to protect the RNA from degradation.
LigaFast™ Rapid DNA Ligation System	Matkovich et. al. (2010) Deep mRNA sequencing for in vivo functional analysis of cardiac transcriptional regulators - Application to Gαq. *Circ. Res.*, **106**: 1459-1467.	Used LigaFast™ System for ligating Illumina compatible adaptors to cDNA. Library was sequenced on an Illumina Genome Analyzer II.
Wizard® SV Gel and PCR Clean-Up System	Davey et. al. (2012) Seasonal trends in the biomass and structure of bryophyte-associated fungal communities explored by 454 pyrosequencing. *New Phytologist*, **195**: 844-856.	Used the Wizard® SV Gel and PCR Clean-Up System during amplicon library prep followed by 454 sequencing.
Wizard® SV Gel and PCR Clean-Up System	Tamaki et. al. (2011) Analysis of 16S rRNA amplicon sequencing options on the Roche/454 next-generation titanium sequencing platform. *PLOS ONE*, **6**:e25263.	Used the Wizard® SV Gel and PCR Clean-Up System to purify amplicons before NGS on a 454 Titanium Platform.
Wizard® SV Gel and PCR Clean-Up System	Schutze et. al. (2011) Probing the SELEX process with next-generation sequencing. *PLOS ONE*, **6**:e29604.	Amplified SELEX pools and then purified PCR products using the Wizard® SV Gel and PCR Clean-Up System followed by NGS on an Illumina Genome Analyzer II.
Wizard® SV Gel and PCR Clean-Up System	Jex et. al. (2009) An integrated pipeline for next-generation sequencing and annotation of mitochondrial genomes. *Genome Res.*, **38**:522-533.	Wizard® SV Gel and PCR Clean-Up System was also used to clean-up amplicons generated by long-PCR of mt genomes before input into NGS on a 454 Genome Sequencer FLX.
Wizard® SV Gel and PCR Clean-Up System	Ando, K and R. Grumet. (2010) Transcriptional profiling of rapidly growing cucumber fruit by 454-pyrosequencing analysis. *J. Amer. Hort. Sci.*, **135**: 291-302.	Amplified library cDNA pool and purified the amplified material using the Wizard® SV Gel and PCR Clean-Up System before NGS.