# 1: SRX23991988: GSM8153964: ovary, H2; Huso dauricus x Acipenser schrenckii; RNA-Seq

Title: ---------------------------------------------------------

SRX23991988: GSM8153964: ovary, H2; Huso dauricus x Acipenser schrenckii; RNA-Seq

SRX23991988: GSM8153964:卵,H2;Huso dauriscus x Acipenser schrencki;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX23991988>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8153964\_r1

GSM8153964\_r1

Study: ---------------------------------------------------------

Critical gene filtration for the caviar yield of hybrid sturgeon

混合螺旋藻鱼子酱产量的关键基因过滤

Library: ---------------------------------------------------------

Library:  
Name: GSM8153964  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA simple extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in ovary tissues. 60 mg fresh tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 4 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragmentation with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that were provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (300±50 bp) was established by amplifying the target sequences.

姓名: 姓名: GSM 8153964 资料库: GSM 8153964 资料库: GSM 8153964 资料库: Illumina NovaSeq 600 战略: RNA-Sequa 来源: TARNA 选择了 TARED 建筑协议: 商业 RNA 简单抽取包(DP419, TIANGEN, 中国) 抽取全部 RNA 。 60毫克新鲜组织由高速同源同源同源(HFFFFSPTPR-32D,中国) 进行1 mLL 透析缓冲RZ, 以获得同源同源, 然后添加三氯甲烷。 在4分钟的室内温度中停留4分钟后, 混合物被离心化为1 000平方 , 以获得与绝对酒精酒精混合的水相混合的液相配相。 RNA 和纯化的DNA总储存在重复离心管中。 当RNA 完完后, RNA 之后, IMA IMO 和 NIS IMO IMO 和 NIS IMO IMO 具体目标以100 基 提供了 。

BioData: SRR28387161

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# 2: SRX24419487: GSM8244989: gut, D14FL1; Huso dauricus; RNA-Seq

Title: ---------------------------------------------------------

SRX24419487: GSM8244989: gut, D14FL1; Huso dauricus; RNA-Seq

SRX244149487: GSM8244989:直肠,D14FL1;Huso dauriscus;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX24419487>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8244989\_r1

GSM8244989\_r1

Study: ---------------------------------------------------------

Multi-omics integration reveals the dynamic impacts of stock enhancement on the intestinal health condition in kaluga sturgeon (Huso dauricus)

多组集成表明,鱼量增强对Kaluga sturgeon(Huso dauriscus)肠胃健康状况的动态影响。

Library: ---------------------------------------------------------

Library:  
Name: GSM8244989  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA sample extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in gut tissues. 90 mg fresh intestine tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 6 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragment with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that was provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (150 bp) was established by amplifying the target sequences.

Name: 姓名: GSM8244989 资料库: GSM 8244989 工具: Illuma NovaSeq 600 战略: RNA-Seq 来源: TRARIPTOMI 选择: CDNA布局: PARED 建筑协议: 商业 RNA 样本提取包(DP419, TIANGEN, 中国) 抽取腹腔组织中的全部RNA。 90毫克新鲜肠组织由高速同源同源同源(DHFFSTPRP-32D,中国劳森) , 1 mLL 透析缓冲RZZ 以获得同源,然后添加三氯甲烷。 在房间温度为6分钟后, 混合温度为1,200平米后, 将混合物离心化为1, 与绝对乙醇酒精混合剂混合剂混合剂混合剂。 RDRA解决方案用于消除RNA样品中的残留蛋白质性。 由RNA II 和NIS IMO 和 IMO IMF IMF 提供 IMF5, 和C IMU IMF IMF IMF IMD IMF IM IM 和 IMF IMF IMF IM IM IMF IM IM IM IM IM IM IM IM IM IM 和 IMF IMF IM IMF IM IM IMF IMF IMF IM IMF IM IM IM IMF 和 IMF IMF IMF IMF IM IM IM IM IM IM IM IM IM IMF IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IMF IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM

BioData: SRR28859445

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# 3: ERX5525572: NextSeq 500 paired end sequencing; Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

Title: ---------------------------------------------------------

ERX5525572: NextSeq 500 paired end sequencing; Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

ERX55255572:下一个Seq 500对齐端序列;

Link:

<https://www.ncbi.nlm.nih.gov/sra/ERX5525572>

Submitted: ---------------------------------------------------------

Friedrich-Loeffler-Institut Federal Research Institute for Animal Health Institute of Diagnostic Virology (Friedrich-Loeffler-Institut Federal Research Insti)

Friedrich-Loeffler研究所 联邦动物卫生研究所

Design: ---------------------------------------------------------

Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

婴儿仓鼠肾细胞的粘附和悬浮性婴儿仓鼠肾细胞有不同的细胞骨质素和表面受体

Study: ---------------------------------------------------------

Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

婴儿仓鼠肾细胞的粘附和悬浮性婴儿仓鼠肾细胞有不同的细胞骨质素和表面受体

Library: ---------------------------------------------------------

Library:  
Name: BHK\_InV\_3\_p  
Instrument: NextSeq 500  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: PolyA  
Layout: PAIRED  
Construction protocol: Batches of each of the cell lines BHK179, BHK-2P and BHK-InV were lysed in three volumes of TRIzol LS Reagent. Culture conditions were 37 °C, 5% CO2, and for suspension cells 320 rpm in TubeSpin bioreactors (TPP Techno Plastic Products AG, Trasadingen, Switzerland) at 80% relative humidity. All adherent cell lines were cultured in Minimum Essential Medium Eagle (MEM) supplemented with Hanks' and Earle's salts (Sigma-Aldrich) with 10% FBS. All suspension cell lines were adapted to grow in CellventoTM BHK200 medium (Merck KGaA). After adding trichloromethane the aqueous phase was collected and mixed with one volume of 100% ethanol. From this, total RNA was extracted using the RNeasy Mini Kit (Qiagen, Hilden, Germany) with on-column DNase digestion with the RNase-Free DNase Set (Qiagen). The ERCC RNA Spike-In Mix 1 (Thermo Fisher Scientific) was added and used as an internal control for all following steps. Next, polyadenylated mRNA was isolated from 1-3 µg of high-quality total RNA using the Dynabeads mRNA DIRECT Micro kit (Thermo Fisher Scientific). The mRNA was subsequently fragmented and used for cDNA synthesis and library preparation using the TruSeq Stranded mRNA LT Sample Prep Kit (Illumina, San Diego, USA) according to the manufacturer's instructions.

图书馆: 名称: BHK\_ InV\_ 3\_ p 工具 : NextSeq 500 战略 来源: TRARIPTOMI 选择 80% 相对湿度 TRARIPTOMI 选择 : PolyA 布局: PAIRED 建设协议: BHK179, BHK-2P 和 BHK-InV 的每条细胞管用三卷TRizol LS 试剂来解析。 文化条件为37 °C, 5% CO2, TubeSpin 生物反应器的悬浮电池 320 rpmm (TPP Techno Flickno 塑料产品AGAG, Trasaden, Strading 80% Nsiden) 。 所有嵌入的细胞系在最低基本中螺旋螺旋螺旋螺旋管(RNA ) 之后, 与SilNSeal-NSeal Q 一起, 使用 RC RC , 用于Silentrial IM , 和 RC RC RC RC 的中子 。

BioData: ERR5882043

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# 4: SRX17532088: GSM6573333: KO1; Mus musculus; RNA-Seq

Title: ---------------------------------------------------------

SRX17532088: GSM6573333: KO1; Mus musculus; RNA-Seq

SRX175532088:GSM65733333:KO1;Mus Musculus;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX17532088>

Submitted: ---------------------------------------------------------

BNU

BNU BNU BNU

Design: ---------------------------------------------------------

GSM6573333\_r1

GSM6573333\_r1

Study: ---------------------------------------------------------

Granulocyte-monocyte progenitor (GMP) RNA-seq in wild type and MST1-deficient mice.

Granulocyte-monocyte progenitor (GMP) RNA-seq(野性)和MST1缺陷小鼠。

Library: ---------------------------------------------------------

Library:  
Name: GSM6573333  
Instrument: Illumina HiSeq 2000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Trizol and 0.2-fold volume of trichloromethane were added to the cells, and isopropanol and absolute ethanol were added to precipitate the extracted RNA. The RNA was dissolved with water and the RNA concentration and purity were detected with nano drop. RNA was enriched with magnetic beads with oligo (DT), then cDNA was synthesized using mRNA as a template, double stranded cDNA was purified and amplified by PCR.

资料库: 名称: GSM657333 工具: Illuma Hiseq 2000 战略: RNA-Seq 来源: TRARIPTOMI 选择: CDNA布局: CDNA 建筑协议: 细胞中添加三氯甲烷的三氯甲烷和0.2倍体积,并添加异丙醇和绝对乙醇来加速提取的RNA。 RNA 与水溶解,RNA 浓度和纯度用纳米液检测出来。 RNA 以磁珠与oligo(DT)相丰富,然后使用 mRNA作为模版对cDNA进行合成,由PCR 净化和放大了双倍受困的cDNA。

BioData: SRR21529728

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# 5: SRX4680921: GSM3389637: Diseased D1; Hylocereus polyrhizus; RNA-Seq

Title: ---------------------------------------------------------

SRX4680921: GSM3389637: Diseased D1; Hylocereus polyrhizus; RNA-Seq

SRX4680921: GSM3389637: 疾病D1; 甲状腺素聚氨酯; RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX4680921>

Submitted: ---------------------------------------------------------

Transcriptomic de novo analysis of pitaya (Hylocereus polyrhizus) canker disease caused by Neoscytalidium dimidiatum  
PRJNA490886 • SRP161778 • All experiments • All runs  
show Abstract

• 全部实验 全部运行显示摘要

Design: ---------------------------------------------------------

NCBI (GEO)

国家协调机构(GEO)

Study: ---------------------------------------------------------

Diseased D1

疾病D1

Library: ---------------------------------------------------------

Library:  
Instrument: Illumina HiSeq 2000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Tissues (100 mg) were placed into a precooled mortar to be ground into a powder with liquid nitrogen. The ground stem powder was collected into a precooled 2 mL Eppendorf tube with 2 mL RNase-free cetyltrimethylammonium bromide (CTAB) extracting solution, which contained 0.1% diethyl pyrocarbonate (DEPC), 2.5% CTAB, 1.4 M NaCl, 20 mM EDTA, 100 mM Tris-HCl (pH 8.0), and 4% polyvinylpyrrolidone (PVP). The tubes were then placed in a water bath at 65 °C for 30 min to induce cell lysis, and centrifuged at 13,000 rpm for 5 min at 25-28 °C. The residue was discarded, and the supernatant solution was transferred into a clean 2 mL Eppendorf tube. Trichloromethane (1 mL) was added to the supernatant solution, blended lightly, and centrifuged at 13 000 rpm for 15 min at 4 °C. The supernatant was transferred into a clean 2 mL Eppendorf tube, and this procedure was repeated once more. Subsequently, 8 M lithium chloride was added with RNase-free water to 0.6 volume of the supernatant and left overnight. The mixture was centrifuged for 30 min at 13 000 rpm and 4 °C to obtain the RNA precipitate. RNase-free ethyl alcohol (75%) was used to wash the RNA precipitate twice. Finally, RNA was dissolved in RNase-free ddH2O and stored at -80 °C until further use. Poly (A) mRNA from the total RNA was enriched by poly-T oligo-attached magnetic beads (Invitrogen), according to the manufacturer's protocol. Purified mRNA was then divided into short fragments by mixing with fragmentation buffer. The first strand cDNA was synthesized using a random hexamer primer. The buffer, dNTPs, RNase H, and DNA polymerase I were then added to the fragmented mRNA templates to synthesize the second-strand cDNA. The double-stranded cDNA was purified using magnetic beads. End repair and the addition of 3′-end single nucleotide A (adenine) were then performed. Finally, sequencing adaptors were ligated to the fragments, which were enriched by PCR amplification. During the quality control step, a 2100 Bioanalyzer (Agilent, Santa Clara, CA, USA) and a StepOnePlus Real-Time PCR System (Applied Biosystems Inc., Foster City, CA, USA) were used to qualify and quantify sequences for the sample libraries. The constructed library products were prepared for sequencing using a HiSeq 2000 system (Illumina, San Diego, CA, USA) at the Beijing Genomics Institute (BGI).

托盘(100毫克)被放置在预冷凝固的迫击炮中,成为含液态氮粉的粉末。 地面干粉被收集到一个2°C的预冷2 mL Eppendorf 水槽中,2 mL Rase-无碳基甲基溴(CTAB)提取溶液中含有0.1% dili-rock-cyrocolate(DEPC),2.5% 碳- 碳- 碳(CTAB), 1.4 MNCl, 20 mMEDTA, 100 mm Tris-Hlors(p 8.0 毫克) 和 4% 聚氨醇(PVP) 。 地面干粉在65 °C 水槽中被收集了30 分钟来诱导细胞分解, 在25- 28 °C 解析时, 离心器被丢弃, 超级液溶液被转移到了2 mmL Eppendrod-nal- demodal O.

BioData: SRR7829958

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# 6: SRX9177112: GSM4799936: active\_ALKBH5\_dox\_minus\_ip2; Homo sapiens; OTHER

Title: ---------------------------------------------------------

SRX9177112: GSM4799936: active\_ALKBH5\_dox\_minus\_ip2; Homo sapiens; OTHER

SRX91777112: GSM47999936: 活性\_ ALKBH5\_dox\_minus\_ip2; 智人; 其他

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX9177112>

Submitted: ---------------------------------------------------------

Targeted RNA N6-Methyladenosine Demethylation Controls Cell Fate Transition in Human Pluripotent Stem Cells  
PRJNA665206 • SRP285100 • All experiments • All runs  
show Abstract

RNA N6-M6-MEVEDEnessine脱甲基化控制细胞在人类多能细胞中发生转变的情况 PRJNA665206 PRJNA665206 PRJNA665206 • SRP285100 • 所有实验 全部运行 显示摘要

Design: ---------------------------------------------------------

NCBI (GEO)

国家协调机构(GEO)

Study: ---------------------------------------------------------

GEO accession GSM4799936 is currently private and is scheduled to be released on Sep 01, 2022.

GSM4799936目前是私营的,定于2022年9月1日发布。

Library: ---------------------------------------------------------

Library:  
Instrument: HiSeq X Ten  
Strategy: OTHER  
Source: TRANSCRIPTOMIC  
Selection: other  
Layout: PAIRED  
Construction protocol: Cells were washed with PBS and lysed with TRIzol (Thermo Fisher Scientific). Then trichloromethane (Guangzhou Chemical Reagent Factory) was used to extract the total RNA from the TRIzol lysate. Isopropanol (Sangon Biotech) was used to precipitates RNA from the mixture. mRNA was separated from the total RNA by using the Dynabeads™ mRNA Purification Kit (Thermo Fisher Scientific) according to the manufacturer's protocol. The m6A immunoprecipitation method was the same as above. Input samples and IP samples were applied for NGS library construction by using the NEBNext® Ultra II Directional RNA Library Prep (NEB) according to the manufacturer's guide. The adaptor ligated DNAs amplified by PCR for 15 cycles were sequenced on the HiSeqX sequencing platform.

资料库:仪器:HiSeq X 10战略:其他来源: TRARIPTOMIC选择:其他布局:PARED建筑协议:细胞用PBS冲洗,用TRIZOL(热水生科学)浸透,然后使用三氯甲烷(广州化学试剂厂)从TRIZOL液酸盐中提取总RNA。使用SOSOPAN醇(桑贡生物科技)从混合物中分离出RNA。MRNA根据制造商协议使用DynabadsTM mRNA净化工具包(热水生科学)与总RNA分离。M6A免疫喷洒方法与上述相同。根据制造商指南,在NEBNBNEXT Ulttra II定向RNA图书馆前p(NEB)对NGS图书馆的建设应用输入样品和IP样品。根据厂商指南,在HISECECECX测序平台上按15个周期放大的调控DNA顺序排列。

BioData: SRR12697489

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# 7: SRX4500787: RNA-seq of Bombyx mori: male fat body

Title: ---------------------------------------------------------

SRX4500787: RNA-seq of Bombyx mori: male fat body

SRX445/000787:RNA-seq of Bombyx Mori: 男性脂肪体

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX4500787>

Submitted: ---------------------------------------------------------

State Key Laboratory of Silkworm Genome Biology

丝虫基因组生物学国家关键实验室

Design: ---------------------------------------------------------

For RNA sequnencing, total RNA was extracted from fat body at different development stage respectively. 1-17mg fat body were dissected in PBS and directly transferred to Trizol (Invitrogen, USA), then grinded with liquid nitrogen. RNA was extracted again trichloromethane, after precipitate by isopropanol and cleared by 75% ethanol, RNA samples were stored in a refrigerator at 80C for sequencing libraries. Each cDNA sample was clustered using Oligo-dT magnetic beads and then sequenced on the HiSeq2000 (Illumina, USA) platform using Single-read techology. All of the Raw data presented in this study have been deposited in the NCBI Short Read Archive (http://www.ncbi.nlm.nih.gov/sra/) under SRA accession number

在RNA后续阶段,在不同的开发阶段分别从脂肪体中提取了全部RNA。 1-17毫克的脂肪体在PBS中解剖,直接转移到Trizol(美国,Invitrogen),然后用液氮研磨。RNA在异丙醇沉淀后再次提取三氯甲烷,并用75%的乙醇清除。RNA样品储存在冰箱中,储存在80C用于测序的图书馆中。每个cDNA样本都使用Oligo-dT磁珠进行集成,然后在Hiseq2000(美国,Illumina)平台上用单读技术学进行测序。本研究中提供的所有原始数据都存放在CBCI短期阅读档案库中(http://www.ncbi.nlm.nih.gov/sra/),根据SRA的加入号。

Study: ---------------------------------------------------------

RNA-seq of Bombyx mori: male fat body

RNA-Seq of Bombyx Mori: 男性脂肪体

Library: ---------------------------------------------------------

Library:  
Name: P0\_rep2  
Instrument: Illumina HiSeq 2000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: PCR  
Layout: SINGLE

图书馆: 名称: P0\_rep2 仪器: Illuma Hiseq 2000 战略: RNA-Seq 来源: TRARIPTOMI 选择: PCR布局: SINGLE

BioData: SRR7637238

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# 8: SRX9177109: GSM4799932: active\_ALKBH5\_dox\_minus\_input1; Homo sapiens; OTHER

Title: ---------------------------------------------------------

SRX9177109: GSM4799932: active\_ALKBH5\_dox\_minus\_input1; Homo sapiens; OTHER

SRX91777109: GSM47999932: 活性 \_ALKBH5\_dox\_minus\_input1; 智人; 其他

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX9177109>

Submitted: ---------------------------------------------------------

Targeted RNA N6-Methyladenosine Demethylation Controls Cell Fate Transition in Human Pluripotent Stem Cells  
PRJNA665206 • SRP285100 • All experiments • All runs  
show Abstract

RNA N6-M6-MEVEDEnessine脱甲基化控制细胞在人类多能细胞中发生转变的情况 PRJNA665206 PRJNA665206 PRJNA665206 • SRP285100 • 所有实验 全部运行 显示摘要

Design: ---------------------------------------------------------

NCBI (GEO)

国家协调机构(GEO)

Study: ---------------------------------------------------------

GEO accession GSM4799932 is currently private and is scheduled to be released on Sep 01, 2022.

GSM4799932目前是私营的,定于2022年9月1日发布。

Library: ---------------------------------------------------------

Library:  
Instrument: HiSeq X Ten  
Strategy: OTHER  
Source: TRANSCRIPTOMIC  
Selection: other  
Layout: PAIRED  
Construction protocol: Cells were washed with PBS and lysed with TRIzol (Thermo Fisher Scientific). Then trichloromethane (Guangzhou Chemical Reagent Factory) was used to extract the total RNA from the TRIzol lysate. Isopropanol (Sangon Biotech) was used to precipitates RNA from the mixture. mRNA was separated from the total RNA by using the Dynabeads™ mRNA Purification Kit (Thermo Fisher Scientific) according to the manufacturer's protocol. The m6A immunoprecipitation method was the same as above. Input samples and IP samples were applied for NGS library construction by using the NEBNext® Ultra II Directional RNA Library Prep (NEB) according to the manufacturer's guide. The adaptor ligated DNAs amplified by PCR for 15 cycles were sequenced on the HiSeqX sequencing platform.

资料库:仪器:HiSeq X 10战略:其他来源: TRARIPTOMIC选择:其他布局:PARED建筑协议:细胞用PBS冲洗,用TRIZOL(热水生科学)浸透,然后使用三氯甲烷(广州化学试剂厂)从TRIZOL液酸盐中提取总RNA。使用SOSOPAN醇(桑贡生物科技)从混合物中分离出RNA。MRNA根据制造商协议使用DynabadsTM mRNA净化工具包(热水生科学)与总RNA分离。M6A免疫喷洒方法与上述相同。根据制造商指南,在NEBNBNEXT Ulttra II定向RNA图书馆前p(NEB)对NGS图书馆的建设应用输入样品和IP样品。根据厂商指南,在HISECECECX测序平台上按15个周期放大的调控DNA顺序排列。

BioData: SRR12697486

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# 9: SRX9177118: GSM4799944: inactive\_ALKBH5\_dox\_minus\_ip1; Homo sapiens; OTHER

Title: ---------------------------------------------------------

SRX9177118: GSM4799944: inactive\_ALKBH5\_dox\_minus\_ip1; Homo sapiens; OTHER

SRX91777118: GSM47999944: 非活动\_ ALKBH5\_dox\_minus\_ip1; 智人; 其他

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX9177118>

Submitted: ---------------------------------------------------------

Targeted RNA N6-Methyladenosine Demethylation Controls Cell Fate Transition in Human Pluripotent Stem Cells  
PRJNA665206 • SRP285100 • All experiments • All runs  
show Abstract

RNA N6-M6-MEVEDEnessine脱甲基化控制细胞在人类多能细胞中发生转变的情况 PRJNA665206 PRJNA665206 PRJNA665206 • SRP285100 • 所有实验 全部运行 显示摘要

Design: ---------------------------------------------------------

NCBI (GEO)

国家协调机构(GEO)

Study: ---------------------------------------------------------

inactive\_ALKBH5\_dox\_minus\_ip1

非活动(\_ALKBH5\_dox\_minus\_ip1)

Library: ---------------------------------------------------------

Library:  
Instrument: HiSeq X Ten  
Strategy: OTHER  
Source: TRANSCRIPTOMIC  
Selection: other  
Layout: PAIRED  
Construction protocol: Cells were washed with PBS and lysed with TRIzol (Thermo Fisher Scientific). Then trichloromethane (Guangzhou Chemical Reagent Factory) was used to extract the total RNA from the TRIzol lysate. Isopropanol (Sangon Biotech) was used to precipitates RNA from the mixture. mRNA was separated from the total RNA by using the Dynabeads™ mRNA Purification Kit (Thermo Fisher Scientific) according to the manufacturer's protocol. The m6A immunoprecipitation method was the same as above. Input samples and IP samples were applied for NGS library construction by using the NEBNext® Ultra II Directional RNA Library Prep (NEB) according to the manufacturer's guide. The adaptor ligated DNAs amplified by PCR for 15 cycles were sequenced on the HiSeqX sequencing platform.

资料库:仪器:HiSeq X 10战略:其他来源: TRARIPTOMIC选择:其他布局:PARED建筑协议:细胞用PBS冲洗,用TRIZOL(热水生科学)浸透,然后使用三氯甲烷(广州化学试剂厂)从TRIZOL液酸盐中提取总RNA。使用SOSOPAN醇(桑贡生物科技)从混合物中分离出RNA。MRNA根据制造商协议使用DynabadsTM mRNA净化工具包(热水生科学)与总RNA分离。M6A免疫喷洒方法与上述相同。根据制造商指南,在NEBNBNEXT Ulttra II定向RNA图书馆前p(NEB)对NGS图书馆的建设应用输入样品和IP样品。根据厂商指南,在HISECECECX测序平台上按15个周期放大的调控DNA顺序排列。

BioData: SRR12697495

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# 10: ERX5525571: NextSeq 500 paired end sequencing; Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

Title: ---------------------------------------------------------

ERX5525571: NextSeq 500 paired end sequencing; Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

ERX5525571: 下一个Seq 500对齐端序列;

Link:

<https://www.ncbi.nlm.nih.gov/sra/ERX5525571>

Submitted: ---------------------------------------------------------

Friedrich-Loeffler-Institut Federal Research Institute for Animal Health Institute of Diagnostic Virology (Friedrich-Loeffler-Institut Federal Research Insti)

Friedrich-Loeffler研究所 联邦动物卫生研究所

Design: ---------------------------------------------------------

Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

婴儿仓鼠肾细胞的粘附和悬浮性婴儿仓鼠肾细胞有不同的细胞骨质素和表面受体

Study: ---------------------------------------------------------

Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

婴儿仓鼠肾细胞的粘附和悬浮性婴儿仓鼠肾细胞有不同的细胞骨质素和表面受体

Library: ---------------------------------------------------------

Library:  
Name: BHK\_InV\_2\_p  
Instrument: NextSeq 500  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: PolyA  
Layout: PAIRED  
Construction protocol: Batches of each of the cell lines BHK179, BHK-2P and BHK-InV were lysed in three volumes of TRIzol LS Reagent. Culture conditions were 37 °C, 5% CO2, and for suspension cells 320 rpm in TubeSpin bioreactors (TPP Techno Plastic Products AG, Trasadingen, Switzerland) at 80% relative humidity. All adherent cell lines were cultured in Minimum Essential Medium Eagle (MEM) supplemented with Hanks' and Earle's salts (Sigma-Aldrich) with 10% FBS. All suspension cell lines were adapted to grow in CellventoTM BHK200 medium (Merck KGaA). After adding trichloromethane the aqueous phase was collected and mixed with one volume of 100% ethanol. From this, total RNA was extracted using the RNeasy Mini Kit (Qiagen, Hilden, Germany) with on-column DNase digestion with the RNase-Free DNase Set (Qiagen). The ERCC RNA Spike-In Mix 1 (Thermo Fisher Scientific) was added and used as an internal control for all following steps. Next, polyadenylated mRNA was isolated from 1-3 µg of high-quality total RNA using the Dynabeads mRNA DIRECT Micro kit (Thermo Fisher Scientific). The mRNA was subsequently fragmented and used for cDNA synthesis and library preparation using the TruSeq Stranded mRNA LT Sample Prep Kit (Illumina, San Diego, USA) according to the manufacturer's instructions.

图书馆: 名称: BHK\_ InV\_ 2\_p 工具: NextSeq 500 战略: NextSeq 500 战略 来源: TRARIPTOMI 选择 80%相对湿度 TRARIPTOMI 选择: PolyA 布局: PAIRED 建设协议: 每一个细胞线 BHK179、 BHK-2P 和 BHK- InV 的电池都用三卷TRizol LS试剂解析。 文化条件为37 °C, 5% CO2 和 TubeSpin 生物反应器中的悬浮电池 320 rpmmm (TPP Techno Florno 塑料产品AGAG, Trasaden, Strading 80% Nsad ; 所有粘固电池线都是在最低基本基本中螺旋螺旋体(RNA ) 使用RSeal NSeal RC 的内置 , 然后用Setrial Q 和 RC RC RC RC RC 的内置 , 用于Sil-Sil-RQ 。

BioData: ERR5882042

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# 11: SRX23991991: GSM8153967: ovary, H5; Huso dauricus x Acipenser schrenckii; RNA-Seq

Title: ---------------------------------------------------------

SRX23991991: GSM8153967: ovary, H5; Huso dauricus x Acipenser schrenckii; RNA-Seq

SRX23991991: GSM8153967:卵,H5;Huso dauriscus x Acipenser schrencki;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX23991991>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8153967\_r1

GSM8153967\_r1

Study: ---------------------------------------------------------

Critical gene filtration for the caviar yield of hybrid sturgeon

混合螺旋藻鱼子酱产量的关键基因过滤

Library: ---------------------------------------------------------

Library:  
Name: GSM8153967  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA simple extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in ovary tissues. 60 mg fresh tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 4 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragmentation with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that were provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (300±50 bp) was established by amplifying the target sequences.

姓名: 姓名: GSM 8153967 资料库: GSM 8153967 资料库: GSM 8153967 资料库: Illumina NovaSeq 600 战略: RNA-Sequa 来源: TRA 选择 TRA 建筑协议: 商业 RNA 简单抽取包(DP 419, TIANGEN, 中国) 抽取全部 RNA 。 60毫克新鲜组织由高速同源同源同源(DHFFSTPR-32D,中国) 进行1 mLL 透析缓冲RZ, 以获得同源同源,然后添加三氯甲烷。 在4分钟的室内温度中停留4分钟后, 将混合物调离心化为1 000 ,以获得与绝对乙醇混合的水分相混合的水相接合阶段。 RRMNA 使用RNA 样本中残留的蛋白质(DNETP ) 以双倍的RNIS 和NIS IMO IMO 和 IMIS 具体的DNA 提供 。

BioData: SRR28387158

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# 12: SRX10761843: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

Title: ---------------------------------------------------------

SRX10761843: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

SRX10761843: 16S RNDNA V4区域肌肉肌肉细胞顺序:成年男性累积含量

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX10761843>

Submitted: ---------------------------------------------------------

China Pharmaceutical University

中国制药大学

Design: ---------------------------------------------------------

DNA extracted via phenol-Trichloromethane method, and V4 region amplified with primer of 515F and 806R, then Illumina NovaSeq 6000 used for sequencing

通过酚-三氯甲烷方法提取的DNA,以及V4区域,以515F和806R的基质放大515F和806R,然后用Illuma NovaSeq 6000来测序

Study: ---------------------------------------------------------

16S sequencing of amlodipine treated NAFLD & hypertension mice

NAFLD和高血压小鼠

Library: ---------------------------------------------------------

Library:  
Name: Cont1  
Instrument: Illumina NovaSeq 6000  
Strategy: AMPLICON  
Source: GENOMIC  
Selection: PCR  
Layout: SINGLE

图书馆: 名称: Cont1 仪器: Illuma NovaSeq 6000战略: AMPLICON 资料来源: GENMIC 选择: PCR布局: SINGLE

BioData: SRR14410430

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# 13: SRX23450327: GSM8046385: liver,CW2; Hipposideros armiger; RNA-Seq

Title: ---------------------------------------------------------

SRX23450327: GSM8046385: liver,CW2; Hipposideros armiger; RNA-Seq

SRX234500327:GSM8046385:肝脏、CW2;Hipposideros 武装武装;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX23450327>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8046385\_r1

GSM8046385\_r1

Study: ---------------------------------------------------------

Excessive heavy metals enrichment disturbs the liver function through gut microbe in great Himalayan leaf-nosed bat (Hipposideros armiger)

大喜马拉雅山叶鼻蝙蝠(Hipposideros Afriger)通过肠道微生物,过度重金属浓缩会扰乱肝脏功能。

Library: ---------------------------------------------------------

Library:  
Name: GSM8046385  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA simple extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in liver tissues. 60 mg fresh tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 4 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragmentation with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that were provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (300±50 bp) was established by amplifying the target sequences.

资料库: 姓名: GSM8046385 工具: Illuma NovaSeq 600 战略: RNA-Seq 来源: TRARIPTOMI 选择: CDNA布局: PARED 建筑协议: 商业 RNA 简单抽取包(DP419, TIANGEN, 中国) 以提取肝脏组织中的全部RNA。 60毫克新鲜组织是高速同质器(DHFFSTPRP-32D, 中国Lawson) 的地面。 1 mLL 透析缓冲RZ 以获得同质体, 然后添加三氯甲烷 。 在房间温度为4分钟后, 混合物被离心机在12000 rpm: 调离心, 以获得与绝对乙醇混合的排水阶段。 RDRNA 被选用RNA样本中残留的蛋白质不精度。 当RNA 之后, A260/280 和 A260/280 NS 变色的送信器被IM(MNA) 和 IMIS IMIS IMU 基的DNA 制成一个固定的DNA 。

BioData: SRR27785531

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# 14: SRX24419489: GSM8244991: gut, D14FL3; Huso dauricus; RNA-Seq

Title: ---------------------------------------------------------

SRX24419489: GSM8244991: gut, D14FL3; Huso dauricus; RNA-Seq

SRX244149489:GSM8244991:直肠,D14FL3;Huso dauriscus;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX24419489>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8244991\_r1

GSM8244991\_r1

Study: ---------------------------------------------------------

Multi-omics integration reveals the dynamic impacts of stock enhancement on the intestinal health condition in kaluga sturgeon (Huso dauricus)

多组集成表明,鱼量增强对Kaluga sturgeon(Huso dauriscus)肠胃健康状况的动态影响。

Library: ---------------------------------------------------------

Library:  
Name: GSM8244991  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA sample extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in gut tissues. 90 mg fresh intestine tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 6 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragment with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that was provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (150 bp) was established by amplifying the target sequences.

Name: 姓名: GSM8244991 工具: GSM 824991 工具: Illuma NovaSeq 600 战略: RNA-Seq 来源: TRARIPTOMI 选择: CDNA布局: PARED 建筑协议: 商业RNA样本提取包(DP 419, TIANGEN, 中国) 抽取腹腔组织中的全部RNA。 90毫克新鲜肠组织由高速同源同源同源(DHFFSTPRP-32D, 中国劳森) 使用 1 mLL 透析缓冲RZ, 以获得同源, 然后添加三氯甲烷。 在房间温度为6分钟的温度为6分钟后, 调离心的混合物在12000 rpmbm:

BioData: SRR28859444

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# 15: SRX4500782: RNA-seq of Bombyx mori: male fat body

Title: ---------------------------------------------------------

SRX4500782: RNA-seq of Bombyx mori: male fat body

SRX445/000782:RNA-seq of Bombyx Mori: 男性脂肪体

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX4500782>

Submitted: ---------------------------------------------------------

State Key Laboratory of Silkworm Genome Biology

丝虫基因组生物学国家关键实验室

Design: ---------------------------------------------------------

For RNA sequnencing, total RNA was extracted from fat body at different development stage respectively. 1-12mg fat body were dissected in PBS and directly transferred to Trizol (Invitrogen, USA), then grinded with liquid nitrogen. RNA was extracted again trichloromethane, after precipitate by isopropanol and cleared by 75% ethanol, RNA samples were stored in a refrigerator at 80C for sequencing libraries. Each cDNA sample was clustered using Oligo-dT magnetic beads and then sequenced on the HiSeq2000 (Illumina, USA) platform using Single-read techology. All of the Raw data presented in this study have been deposited in the NCBI Short Read Archive (http://www.ncbi.nlm.nih.gov/sra/) under SRA accession number

在RNA后续阶段,在不同的开发阶段分别从脂肪体中提取了全部RNA。1,12毫克脂肪体在PBS中解剖,直接转移到Trizol(美国,Invitrogen),然后用液氮研磨。RNA在异丙醇沉淀后再次提取三氯甲烷,并用75%的乙醇清除。RNA样品储存在冰箱中,储存在80C的图书馆排序中。每个cDNA样本都使用Oligo-dT磁珠进行分组,然后在Hiseq 2000(美国,Illuma)平台上用单读技术学进行排序。本研究中提供的所有原始数据都存放在CBCI短期阅读档案库中(http://www.ncbi.nlm.nih.gov/sra/),根据SRA的加入号。

Study: ---------------------------------------------------------

RNA-seq of Bombyx mori: male fat body

RNA-Seq of Bombyx Mori: 男性脂肪体

Library: ---------------------------------------------------------

Library:  
Name: W0\_rep1  
Instrument: Illumina HiSeq 2000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: PCR  
Layout: SINGLE

图书馆: 名称: W0\_rep1 仪器: Illuma Hiseq 2000 战略: RNA-Seq 来源: TRARIPTOMI 选择: PCR布局: SINGLE

BioData: SRR7637243

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# 16: SRX10761851: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

Title: ---------------------------------------------------------

SRX10761851: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

SRX10761851: 16S RNDNA V4区域肌肉肌肉细胞顺序:成年男性累积含量

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX10761851>

Submitted: ---------------------------------------------------------

China Pharmaceutical University

中国制药大学

Design: ---------------------------------------------------------

DNA extracted via phenol-Trichloromethane method, and V4 region amplified with primer of 515F and 806R, then Illumina NovaSeq 6000 used for sequencing

通过酚-三氯甲烷方法提取的DNA,以及V4区域,以515F和806R的基质放大515F和806R,然后用Illuma NovaSeq 6000来测序

Study: ---------------------------------------------------------

16S sequencing of amlodipine treated NAFLD & hypertension mice

NAFLD和高血压小鼠

Library: ---------------------------------------------------------

Library:  
Name: AB12  
Instrument: Illumina NovaSeq 6000  
Strategy: AMPLICON  
Source: GENOMIC  
Selection: PCR  
Layout: SINGLE

图书馆:名称:AB12仪器:Illuma NovaSeq 6000战略:AMPLICON 资料来源:GENMIC选择:PCR布局: SINGLE

BioData: SRR14410422

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# 17: SRX4500781: RNA-seq of Bombyx mori: male fat body

Title: ---------------------------------------------------------

SRX4500781: RNA-seq of Bombyx mori: male fat body

SRX445/000781:RNA-seq of Bombyx Mori: 男性脂肪体

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX4500781>

Submitted: ---------------------------------------------------------

State Key Laboratory of Silkworm Genome Biology

丝虫基因组生物学国家关键实验室

Design: ---------------------------------------------------------

For RNA sequnencing, total RNA was extracted from fat body at different development stage respectively. 1-11mg fat body were dissected in PBS and directly transferred to Trizol (Invitrogen, USA), then grinded with liquid nitrogen. RNA was extracted again trichloromethane, after precipitate by isopropanol and cleared by 75% ethanol, RNA samples were stored in a refrigerator at 80C for sequencing libraries. Each cDNA sample was clustered using Oligo-dT magnetic beads and then sequenced on the HiSeq2000 (Illumina, USA) platform using Single-read techology. All of the Raw data presented in this study have been deposited in the NCBI Short Read Archive (http://www.ncbi.nlm.nih.gov/sra/) under SRA accession number

在RNA后续阶段,在不同的开发阶段分别从脂肪体中提取了全部RNA。1-1-11毫克的脂肪体在PBS中解剖,直接转移到Trizol(美国,Invitrogen),然后用液氮研磨。RNA在异丙醇沉淀后再次提取三氯甲烷,并用75%的乙醇清除。RNA样品储存在冰箱中,储存在80C用于测序的图书馆中。每个cDNA样本都使用Oligo-dT磁珠集中,然后在Hiseq2000(美国,Illumina)平台上用单读技术学进行排序。本研究中提供的所有原始数据都存放在CBCI短期阅读档案库中(http://www.ncbi.nlm.nih.gov/sra/),根据SRA的加入号。

Study: ---------------------------------------------------------

RNA-seq of Bombyx mori: male fat body

RNA-Seq of Bombyx Mori: 男性脂肪体

Library: ---------------------------------------------------------

Library:  
Name: L5D3\_rep2  
Instrument: Illumina HiSeq 2000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: PCR  
Layout: SINGLE

图书馆: 名称: L5D3\_rep2 仪器: Illuma Hiseq 2000 战略: RNA-Seq 来源: TRARIPTOMI 选择: PCR布局: SINGLE

BioData: SRR7637244

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# 18: SRX10761844: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

Title: ---------------------------------------------------------

SRX10761844: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

SRX10761844: 16S RNDNA V4区域Mus muscululus测序:成年男性累积含量

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX10761844>

Submitted: ---------------------------------------------------------

China Pharmaceutical University

中国制药大学

Design: ---------------------------------------------------------

DNA extracted via phenol-Trichloromethane method, and V4 region amplified with primer of 515F and 806R, then Illumina NovaSeq 6000 used for sequencing

通过酚-三氯甲烷方法提取的DNA,以及V4区域,以515F和806R的基质放大515F和806R,然后用Illuma NovaSeq 6000来测序

Study: ---------------------------------------------------------

16S sequencing of amlodipine treated NAFLD & hypertension mice

NAFLD和高血压小鼠

Library: ---------------------------------------------------------

Library:  
Name: Cont2  
Instrument: Illumina NovaSeq 6000  
Strategy: AMPLICON  
Source: GENOMIC  
Selection: PCR  
Layout: SINGLE

图书馆: 名称: Cont2 仪器: Illuma NovaSeq 6000战略: AMPLICON 资料来源: GENMIC 选择: PCR布局: SINGLE

BioData: SRR14410429

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# 19: SRX6432725: GSM3938244: CR; Musa acuminata AAA Group; RNA-Seq

Title: ---------------------------------------------------------

SRX6432725: GSM3938244: CR; Musa acuminata AAA Group; RNA-Seq

SRX6432725: GSM3938244: CR; Musa acuminata AAAA集团; RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX6432725>

Submitted: ---------------------------------------------------------

Transcriptome analysis of banana (Musa acuminata) in response to low-nitrogen stress  
PRJNA554129 • SRP214312 • All experiments • All runs  
show Abstract

应对低氮压力PPRJNA554129 PRJNA554129 • SRRP214312 • 所有实验 • 所有运行情况显示摘要

Design: ---------------------------------------------------------

NCBI (GEO)

国家协调机构(GEO)

Study: ---------------------------------------------------------

CR

CR 公司

Library: ---------------------------------------------------------

Library:  
Instrument: Illumina HiSeq 2000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: SINGLE  
Construction protocol: Tissues (100 mg) were placed into a precooled mortar to be ground into a powder with liquid nitrogen. The powder was collected into a precooled 2 mL Eppendorf tube with 2 mL RNase-free cetyltrimethylammonium bromide (CTAB) extracting solution, which contained 0.1% diethyl pyrocarbonate (DEPC), 2.5% CTAB, 1.4 M NaCl, 20 mM EDTA, 100 mM Tris-HCl (pH 8.0), and 4% polyvinylpyrrolidone (PVP). The tubes were then placed in a water bath at 65 °C for 30 min to induce cell lysis, and centrifuged at 13,000 rpm for 5 min at 25-28 °C. The residue was discarded, and the supernatant solution was transferred into a clean 2 mL Eppendorf tube. Trichloromethane (1 mL) was added to the supernatant solution, blended lightly, and centrifuged at 13 000 rpm for 15 min at 4 °C. The supernatant was transferred into a clean 2 mL Eppendorf tube, and this procedure was repeated once more. Subsequently, 8 M lithium chloride was added with RNase-free water to 0.6 volume of the supernatant and left overnight. The mixture was centrifuged for 30 min at 13 000 rpm and 4 °C to obtain the RNA precipitate. RNase-free ethyl alcohol (75%) was used to wash the RNA precipitate twice. Finally, RNA was dissolved in RNase-free ddH2O and stored at -80 °C until further use. Poly (A) mRNA from the total RNA was enriched by poly-T oligo-attached magnetic beads (Invitrogen), according to the manufacturer's protocol. Purified mRNA was then divided into short fragments by mixing with fragmentation buffer. The first strand cDNA was synthesized using a random hexamer primer. The buffer, dNTPs, RNase H, and DNA polymerase I were then added to the fragmented mRNA templates to synthesize the second-strand cDNA. The double-stranded cDNA was purified using magnetic beads. End repair and the addition of 3′-end single nucleotide A (adenine) were then performed. Finally, sequencing adaptors were ligated to the fragments, which were enriched by PCR amplification. During the quality control step, a 2100 Bioanalyzer (Agilent, Santa Clara, CA, USA) and a StepOnePlus Real-Time PCR System (Applied Biosystems Inc., Foster City, CA, USA) were used to qualify and quantify sequences for the sample libraries. The constructed library products were prepared for sequencing using a HiSeq 2000 system (Illumina, San Diego, CA, USA) at the Beijing Genomics Institute (BGI).

托盘(100毫克)被放置在预冷凝固的迫击炮中,成为含液态氮粉的粉末。 粉末被收集到一个2°C的预冷的2 mL Eppendorf 水槽中,2 mL Rase-无丙基甲基溴(CTAB)提取溶液中含有0.1%的二乙基丙基丙烯基丙烷(DEPC)、2.5%的丙基乙基氨基氨基氨基氢(CTB)、1.4 MCl、20 mM EDTA、100 mM Tris-Hl(PH 8.0)和4% 聚丙基醇酮(PVP)中含有1 mcion 30 mm(RS-28°C)的离心解液中含有0.13 rmtmd 。

BioData: SRR9672273

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# 20: SRX23991989: GSM8153965: ovary, H3; Huso dauricus x Acipenser schrenckii; RNA-Seq

Title: ---------------------------------------------------------

SRX23991989: GSM8153965: ovary, H3; Huso dauricus x Acipenser schrenckii; RNA-Seq

SRX23991989: GSM8153965:卵,H3;Huso dauriscus x Acipenser schrencki;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX23991989>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8153965\_r1

GSM8153965\_r1

Study: ---------------------------------------------------------

Critical gene filtration for the caviar yield of hybrid sturgeon

混合螺旋藻鱼子酱产量的关键基因过滤

Library: ---------------------------------------------------------

Library:  
Name: GSM8153965  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA simple extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in ovary tissues. 60 mg fresh tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 4 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragmentation with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that were provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (300±50 bp) was established by amplifying the target sequences.

姓名: 姓名: GSM 8153965 资料库: GSM 8153965 资料库: GSM 8153965 资料库: Illumina NovaSeq 600 战略: RNA-Sequa 来源: TARNA 选择了 TARED 建筑协议: 商业 RNA 简单抽取包(DP419, TIANGEN, 中国) 抽取全部 RNA 。 60 毫克新鲜组织由高速同源同源同源(ILawson,中国) 进行1 mLL 透析缓冲RZ, 以获得同源同源,然后添加三氯甲烷。 在4分钟的室温度保持4分后,该混合物被离心于12000 rmbmm: 获得与乙醇完全混合的水相接合的水相相接的气相相相。 RNA 在重复离心后被RNA 储存在无色管里(DNETP ) 之后, 以 INA 7 0 and A280 droudy RNA (Mell delly, lad) 和 Annex RNA (后, lax lax the the the the broild the the brequelates broild the broild the bromod)

BioData: SRR28387160

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# 21: SRX4500789: RNA-seq of Bombyx mori: male fat body

Title: ---------------------------------------------------------

SRX4500789: RNA-seq of Bombyx mori: male fat body

SRX445/000789:RNA-seq of Bombyx Mori: 男性脂肪体

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX4500789>

Submitted: ---------------------------------------------------------

State Key Laboratory of Silkworm Genome Biology

丝虫基因组生物学国家关键实验室

Design: ---------------------------------------------------------

For RNA sequnencing, total RNA was extracted from fat body at different development stage respectively. 1-19mg fat body were dissected in PBS and directly transferred to Trizol (Invitrogen, USA), then grinded with liquid nitrogen. RNA was extracted again trichloromethane, after precipitate by isopropanol and cleared by 75% ethanol, RNA samples were stored in a refrigerator at 80C for sequencing libraries. Each cDNA sample was clustered using Oligo-dT magnetic beads and then sequenced on the HiSeq2000 (Illumina, USA) platform using Single-read techology. All of the Raw data presented in this study have been deposited in the NCBI Short Read Archive (http://www.ncbi.nlm.nih.gov/sra/) under SRA accession number

在RNA后续阶段,在不同的开发阶段分别从脂肪体中提取了全部RNA。 1-19毫克的脂肪体在PBS中解剖,直接转移到Trizol(美国,Invitrogen),然后用液氮研磨。RNA在异丙醇沉淀后再次提取三氯甲烷,并用75%的乙醇清除。RNA样品储存在冰箱中,储存在80C用于测序的图书馆。每个cDNA样本都使用Oligo-dT磁珠进行组装,然后在Hiseq2000(美国,Illumina)平台上用单读技术学进行排序。本研究中提供的所有原始数据都存放在CBCI短期阅读档案库中(http://www.ncbi.nlm.nih.gov/sra/),根据SRA的加入号。

Study: ---------------------------------------------------------

RNA-seq of Bombyx mori: male fat body

RNA-Seq of Bombyx Mori: 男性脂肪体

Library: ---------------------------------------------------------

Library:  
Name: P3\_rep2  
Instrument: Illumina HiSeq 2000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: PCR  
Layout: SINGLE

图书馆: 名称: P3\_rep2 仪器: Illuma Hiseq 2000 战略: RNA-Seq 来源: TRARIPTOMI 选择: PCR布局: SINGLE

BioData: SRR7637236

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# 22: ERX5525566: NextSeq 500 paired end sequencing; Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

Title: ---------------------------------------------------------

ERX5525566: NextSeq 500 paired end sequencing; Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

ERX55255566: 下一个Seq 500对齐端序列; 适应和悬浮婴儿仓鼠肾细胞的细胞骨质素和表面受体细胞素不同

Link:

<https://www.ncbi.nlm.nih.gov/sra/ERX5525566>

Submitted: ---------------------------------------------------------

Friedrich-Loeffler-Institut Federal Research Institute for Animal Health Institute of Diagnostic Virology (Friedrich-Loeffler-Institut Federal Research Insti)

Friedrich-Loeffler研究所 联邦动物卫生研究所

Design: ---------------------------------------------------------

Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

婴儿仓鼠肾细胞的粘附和悬浮性婴儿仓鼠肾细胞有不同的细胞骨质素和表面受体

Study: ---------------------------------------------------------

Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

婴儿仓鼠肾细胞的粘附和悬浮性婴儿仓鼠肾细胞有不同的细胞骨质素和表面受体

Library: ---------------------------------------------------------

Library:  
Name: BHK\_179\_3\_p  
Instrument: NextSeq 500  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: PolyA  
Layout: PAIRED  
Construction protocol: Batches of each of the cell lines BHK179, BHK-2P and BHK-InV were lysed in three volumes of TRIzol LS Reagent. Culture conditions were 37 °C, 5% CO2, and for suspension cells 320 rpm in TubeSpin bioreactors (TPP Techno Plastic Products AG, Trasadingen, Switzerland) at 80% relative humidity. All adherent cell lines were cultured in Minimum Essential Medium Eagle (MEM) supplemented with Hanks' and Earle's salts (Sigma-Aldrich) with 10% FBS. All suspension cell lines were adapted to grow in CellventoTM BHK200 medium (Merck KGaA). After adding trichloromethane the aqueous phase was collected and mixed with one volume of 100% ethanol. From this, total RNA was extracted using the RNeasy Mini Kit (Qiagen, Hilden, Germany) with on-column DNase digestion with the RNase-Free DNase Set (Qiagen). The ERCC RNA Spike-In Mix 1 (Thermo Fisher Scientific) was added and used as an internal control for all following steps. Next, polyadenylated mRNA was isolated from 1-3 µg of high-quality total RNA using the Dynabeads mRNA DIRECT Micro kit (Thermo Fisher Scientific). The mRNA was subsequently fragmented and used for cDNA synthesis and library preparation using the TruSeq Stranded mRNA LT Sample Prep Kit (Illumina, San Diego, USA) according to the manufacturer's instructions.

图书馆: 名称: BHK\_ 179\_ 379\_ 3\_ p 工具: NextSeq 500 战略 来源: TRARIPTOMI 选择 80% 相对湿度 TRARIPTOMI 选择: PolyA 布局: PAIRED 建设协议: 每一个细胞线 BHK179、 BHK-2P 和 BHK- InV 的棒用三卷TRizol LS 试剂解析。 文化条件为37 °C, 5% CO2, TubeSpin生物反应器的悬浮电池 320 Rpmmm (TP Techno Flickno 塑料产品AGAG, Trasaden, Strading 80% Nsiden) 。 所有粘固电池线都是在最低基本中 Hanks 和厄尔尼氏 盐(Seral Q) 中, 用于Silental- RC RC 的中程 。

BioData: ERR5882038

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# 23: SRX25145395: GSM8367751: gut, Q1; Acipenser schrenckii; RNA-Seq

Title: ---------------------------------------------------------

SRX25145395: GSM8367751: gut, Q1; Acipenser schrenckii; RNA-Seq

SRX25145395:GSM8367751:直肠,Q1;Acipenserschrenckii;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX25145395>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8367751\_r1

GSM8367751\_r1

Study: ---------------------------------------------------------

Dynamic impacts of stock enhancement on wild Amur sturgeon (Acipenser schrenkii): New protection insight into intestinal microbe and gene expression mode

种群增强对野生亚穆尔外科动物(Acipenserschrenkii):对肠微生物和基因表达模式的新的保护洞见

Library: ---------------------------------------------------------

Library:  
Name: GSM8367751  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA sample extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in gut tissues. 100 mg fresh intestine tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 7 min, the mixture was centrifuged at 12500 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragment with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that was provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (150 bp) was established by amplifying the target sequences.

Name: 姓名: GSM8367751 工具: GSM8367751 工具: Illumina NovaSeq 600 战略: RNA-Seq 来源: TRARIPTOMI 选择: CDNA布局: PARED 建筑协议: 商业RNA样本提取包(DP419, TIANGEN, 中国) 以抽取腹腔组织中的全部RNA。 100毫克新鲜肠组织被高速同质同质器(DHFFSTPRP-32D,中国劳森) 地面 1 mLL 透析缓冲RZ 以获得同质,然后添加三氯甲烷。在7分钟的室内温度保持7分钟后,该混合物以12500 平米调离心机离心,以获得与绝对乙醇混合的水相相吸附的水阶段。 RDA解决方案用于消除RNA样本中的残留蛋白性。 由RNA IMA 和 IMIS IMO 和 IMO IMF IMO IMF 提供 IMF IMF 和 IMF IMF IMO IMF IMD IMF IM IMO 和 C IMO IMF IMF IMO IMD IMS IMD IMF IMF IMS IMS IM IMF IMF IM IMF IMF IM IM IM IMF IM IM IM IM IM IM IMF 和 IMF IMF IMF IMF IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IMS IMS IMS IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM

BioData: SRR29640993

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# 24: ERX5525569: NextSeq 500 paired end sequencing; Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

Title: ---------------------------------------------------------

ERX5525569: NextSeq 500 paired end sequencing; Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

ERX55255669: 下一个Seq 500对齐端序列; 适应和悬浮婴儿仓鼠肾细胞的细胞骨质素和表面受体细胞素不同

Link:

<https://www.ncbi.nlm.nih.gov/sra/ERX5525569>

Submitted: ---------------------------------------------------------

Friedrich-Loeffler-Institut Federal Research Institute for Animal Health Institute of Diagnostic Virology (Friedrich-Loeffler-Institut Federal Research Insti)

Friedrich-Loeffler研究所 联邦动物卫生研究所

Design: ---------------------------------------------------------

Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

婴儿仓鼠肾细胞的粘附和悬浮性婴儿仓鼠肾细胞有不同的细胞骨质素和表面受体

Study: ---------------------------------------------------------

Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

婴儿仓鼠肾细胞的粘附和悬浮性婴儿仓鼠肾细胞有不同的细胞骨质素和表面受体

Library: ---------------------------------------------------------

Library:  
Name: BHK\_2P\_3\_p  
Instrument: NextSeq 500  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: PolyA  
Layout: PAIRED  
Construction protocol: Batches of each of the cell lines BHK179, BHK-2P and BHK-InV were lysed in three volumes of TRIzol LS Reagent. Culture conditions were 37 °C, 5% CO2, and for suspension cells 320 rpm in TubeSpin bioreactors (TPP Techno Plastic Products AG, Trasadingen, Switzerland) at 80% relative humidity. All adherent cell lines were cultured in Minimum Essential Medium Eagle (MEM) supplemented with Hanks' and Earle's salts (Sigma-Aldrich) with 10% FBS. All suspension cell lines were adapted to grow in CellventoTM BHK200 medium (Merck KGaA). After adding trichloromethane the aqueous phase was collected and mixed with one volume of 100% ethanol. From this, total RNA was extracted using the RNeasy Mini Kit (Qiagen, Hilden, Germany) with on-column DNase digestion with the RNase-Free DNase Set (Qiagen). The ERCC RNA Spike-In Mix 1 (Thermo Fisher Scientific) was added and used as an internal control for all following steps. Next, polyadenylated mRNA was isolated from 1-3 µg of high-quality total RNA using the Dynabeads mRNA DIRECT Micro kit (Thermo Fisher Scientific). The mRNA was subsequently fragmented and used for cDNA synthesis and library preparation using the TruSeq Stranded mRNA LT Sample Prep Kit (Illumina, San Diego, USA) according to the manufacturer's instructions.

图书馆: 名称: BHK\_ 2P\_ 3\_ p 工具: NextSeq 500 战略 来源: TRARIPTOMI 选择 80% 相对湿度 TRARIPTOMI 选择 : PolyA 布局: PAIRED 建设协议: 每一个细胞线 BHK179 、 BHK-2P 和 BHK- InV 都用三卷TRizol LS 试剂解析。 文化条件为37 °C, 5% CO2, TubeSpin 生物反应器( TPP Terno FlickRNA AG, Trassaden,瑞士) 320 RPMM) 的悬浮细胞细胞 320 Rpmmation 。 所有恒定的细胞线都是在最低基本基本中螺旋螺旋形 , 之后, RNA 和 RSentRRC 的内序 使用 RSeal Q 程序 。

BioData: ERR5882040

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# 25: SRX4500788: RNA-seq of Bombyx mori: male fat body

Title: ---------------------------------------------------------

SRX4500788: RNA-seq of Bombyx mori: male fat body

SRX445/000788:RNA-seq of Bombyx Mori: 男性脂肪体

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX4500788>

Submitted: ---------------------------------------------------------

State Key Laboratory of Silkworm Genome Biology

丝虫基因组生物学国家关键实验室

Design: ---------------------------------------------------------

For RNA sequnencing, total RNA was extracted from fat body at different development stage respectively. 1-18mg fat body were dissected in PBS and directly transferred to Trizol (Invitrogen, USA), then grinded with liquid nitrogen. RNA was extracted again trichloromethane, after precipitate by isopropanol and cleared by 75% ethanol, RNA samples were stored in a refrigerator at 80C for sequencing libraries. Each cDNA sample was clustered using Oligo-dT magnetic beads and then sequenced on the HiSeq2000 (Illumina, USA) platform using Single-read techology. All of the Raw data presented in this study have been deposited in the NCBI Short Read Archive (http://www.ncbi.nlm.nih.gov/sra/) under SRA accession number

在RNA后续阶段,在不同的开发阶段分别从脂肪体中提取了全部RNA。 1-18毫克的脂肪体在PBS中解剖,直接转移到Trizol(美国,Invitrogen),然后用液氮研磨。RNA在异丙醇沉淀后再次提取三氯甲烷,并用75%的乙醇清除。RNA样品储存在冰箱中,储存在80C的图书馆排序。每个cDNA样本都使用Oligo-dT磁珠进行组装,然后在Hiseq2000(美国,Illuma)平台上用单读技术学进行顺序排列。本研究中提供的所有原始数据都存放在CBCI短期阅读档案库中(http://www.ncbi.nlm.nih.gov/sra/),根据SRA的加入号。

Study: ---------------------------------------------------------

RNA-seq of Bombyx mori: male fat body

RNA-Seq of Bombyx Mori: 男性脂肪体

Library: ---------------------------------------------------------

Library:  
Name: P3\_rep1  
Instrument: Illumina HiSeq 2000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: PCR  
Layout: SINGLE

图书馆: 名称: P3\_rep1 仪器: Illuma Hiseq 2000 战略: RNA-Seq 来源: TRARIPTOMI 选择: PCR布局: SINGLE

BioData: SRR7637237

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# 26: SRX17532086: GSM6573331: WT1; Mus musculus; RNA-Seq

Title: ---------------------------------------------------------

SRX17532086: GSM6573331: WT1; Mus musculus; RNA-Seq

SRX175532086:GSM6573331:WT1;Mus 肌肉囊肿;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX17532086>

Submitted: ---------------------------------------------------------

BNU

BNU BNU BNU

Design: ---------------------------------------------------------

GSM6573331\_r1

GSM6573331\_r1

Study: ---------------------------------------------------------

Granulocyte-monocyte progenitor (GMP) RNA-seq in wild type and MST1-deficient mice.

Granulocyte-monocyte progenitor (GMP) RNA-seq(野性)和MST1缺陷小鼠。

Library: ---------------------------------------------------------

Library:  
Name: GSM6573331  
Instrument: Illumina HiSeq 2000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Trizol and 0.2-fold volume of trichloromethane were added to the cells, and isopropanol and absolute ethanol were added to precipitate the extracted RNA. The RNA was dissolved with water and the RNA concentration and purity were detected with nano drop. RNA was enriched with magnetic beads with oligo (DT), then cDNA was synthesized using mRNA as a template, double stranded cDNA was purified and amplified by PCR.

资料库: 名称: GSM6573331 工具: Illuma Hiseq 2000 战略: RNA-Seq 来源: TRARIPTOMI 选择: CDNA布局: CDNA 建筑协议: 将三氯甲烷的三分之一和0.2倍体积添加到细胞中,并在提取的RNA中添加了异丙醇和绝对乙醇。 RNA 与水溶解,RNA 浓度和纯度检测到纳米下降。 RNA 以磁珠添加了oligo(DT),然后用 mRNA作为模版对cDNA进行了合成,并用PCRR来净化和放大了双倍受困的cDNA。

BioData: SRR21529730

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# 27: SRX9177119: GSM4799945: inactive\_ALKBH5\_dox\_plus\_input1; Homo sapiens; OTHER

Title: ---------------------------------------------------------

SRX9177119: GSM4799945: inactive\_ALKBH5\_dox\_plus\_input1; Homo sapiens; OTHER

SRX91777119: GSM47999945: 非活动\_ ALKBH5\_dox\_plus\_input1; 智人; 其他

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX9177119>

Submitted: ---------------------------------------------------------

Targeted RNA N6-Methyladenosine Demethylation Controls Cell Fate Transition in Human Pluripotent Stem Cells  
PRJNA665206 • SRP285100 • All experiments • All runs  
show Abstract

RNA N6-M6-MEVEDEnessine脱甲基化控制细胞在人类多能细胞中发生转变的情况 PRJNA665206 PRJNA665206 PRJNA665206 • SRP285100 • 所有实验 全部运行 显示摘要

Design: ---------------------------------------------------------

NCBI (GEO)

国家协调机构(GEO)

Study: ---------------------------------------------------------

GEO accession GSM4799945 is currently private and is scheduled to be released on Sep 01, 2022.

GSM4799945目前是私营的,定于2022年9月1日发布。

Library: ---------------------------------------------------------

Library:  
Instrument: HiSeq X Ten  
Strategy: OTHER  
Source: TRANSCRIPTOMIC  
Selection: other  
Layout: PAIRED  
Construction protocol: Cells were washed with PBS and lysed with TRIzol (Thermo Fisher Scientific). Then trichloromethane (Guangzhou Chemical Reagent Factory) was used to extract the total RNA from the TRIzol lysate. Isopropanol (Sangon Biotech) was used to precipitates RNA from the mixture. mRNA was separated from the total RNA by using the Dynabeads™ mRNA Purification Kit (Thermo Fisher Scientific) according to the manufacturer's protocol. The m6A immunoprecipitation method was the same as above. Input samples and IP samples were applied for NGS library construction by using the NEBNext® Ultra II Directional RNA Library Prep (NEB) according to the manufacturer's guide. The adaptor ligated DNAs amplified by PCR for 15 cycles were sequenced on the HiSeqX sequencing platform.

资料库:仪器:HiSeq X 10战略:其他来源: TRARIPTOMIC选择:其他布局:PARED建筑协议:细胞用PBS冲洗,用TRIZOL(热水生科学)浸透,然后使用三氯甲烷(广州化学试剂厂)从TRIZOL液酸盐中提取总RNA。使用SOSOPAN醇(桑贡生物科技)从混合物中分离出RNA。MRNA根据制造商协议使用DynabadsTM mRNA净化工具包(热水生科学)与总RNA分离。M6A免疫喷洒方法与上述相同。根据制造商指南,在NEBNBNEXT Ulttra II定向RNA图书馆前p(NEB)对NGS图书馆的建设应用输入样品和IP样品。根据厂商指南,在HISECECECX测序平台上按15个周期放大的调控DNA顺序排列。

BioData: SRR12697496

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# 28: SRX23991999: GSM8153975: ovary, L5; Huso dauricus x Acipenser schrenckii; RNA-Seq

Title: ---------------------------------------------------------

SRX23991999: GSM8153975: ovary, L5; Huso dauricus x Acipenser schrenckii; RNA-Seq

SRX23991999: GSM8153975:卵,L5;Huso dauriscus x Acipenser schrencki;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX23991999>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8153975\_r1

GSM8153975\_r1

Study: ---------------------------------------------------------

Critical gene filtration for the caviar yield of hybrid sturgeon

混合螺旋藻鱼子酱产量的关键基因过滤

Library: ---------------------------------------------------------

Library:  
Name: GSM8153975  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA simple extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in ovary tissues. 60 mg fresh tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 4 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragmentation with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that were provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (300±50 bp) was established by amplifying the target sequences.

姓名: 姓名: GSM 8153975 资料库: GSM 8153975 资料库: GSM 8153975 资料库: Illumina NovaSeq 600 战略: RNA-Sequa 来源: TARNA 选择了 TARED 建筑协议: 商业 RNA 简单抽取包(DP419, TIANGEN, 中国) 抽取全部 RNA 。 60 毫克新鲜组织由高速同源同源同源(ILawson,中国) 进行1 mLL 透析缓冲RZ,以获得同源同源,然后添加三氯甲烷。 在4分钟的室温度保持4分后,混合物被离心于12000 rpmmm: 以获得与绝对乙醇混合的水相相接合的水相相接的气相相相。 RED解决方案用于消除RNA样本中的残留蛋白性蛋白性。 精密的RNA在重复离裂后被RNNE, II 和A IMO 和NEODRNIS IMO 数据基底的血基 。

BioData: SRR28387150

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# 29: SRX24419485: GSM8244987: gut, Ori2; Huso dauricus; RNA-Seq

Title: ---------------------------------------------------------

SRX24419485: GSM8244987: gut, Ori2; Huso dauricus; RNA-Seq

SRX244149485: GSM8244987:直肠,Ori2;Huso dauriscus;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX24419485>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8244987\_r1

GSM8244987\_r1

Study: ---------------------------------------------------------

Multi-omics integration reveals the dynamic impacts of stock enhancement on the intestinal health condition in kaluga sturgeon (Huso dauricus)

多组集成表明,鱼量增强对Kaluga sturgeon(Huso dauriscus)肠胃健康状况的动态影响。

Library: ---------------------------------------------------------

Library:  
Name: GSM8244987  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA sample extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in gut tissues. 90 mg fresh intestine tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 6 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragment with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that was provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (150 bp) was established by amplifying the target sequences.

Name: 姓名: GSM8244987 资料库: GSM 8244987 工具: Illuma NovaSeq 600 战略: RNA-Seq 来源: TRARIPTOMI 选择: CDNA布局: PARED 建筑协议: 商业 RNA 样本提取包(DP 419, TIANGEN, 中国) 抽取腹腔组织中的全部RNA。 90毫克新鲜肠组织由高速同源同源同源(DHFFSTPRP-32D, 中国劳森) , 1 mLL 透析缓冲RZ, 以获得同源, 然后添加三氯甲烷。 在房间温度为6分钟后, 混合温度为1, 2000 平米, 将混合物离心化,以获得与绝对乙醇酒精混合的水相混合的水相。 RDA解决方案用于去除残留蛋白质。 在RNA之后, 由INA II 和A IMO 以 IMO IMF IMO 和 IMU IMU IMU IMF 提供 IMF IMF IMD IMF IMF IM 和 IMF IMF IMF IM IM IM IM IM IM IMF IM IM IM IM IM IM IM IMF IMF IM IMF IM IM IM IM IM IM IM IM IM IM IM IM IMF 和 IMF IMF IMF IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IMF IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM

BioData: SRR28859449

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# 30: SRX4680923: GSM3389639: Normal N2; Hylocereus polyrhizus; RNA-Seq

Title: ---------------------------------------------------------

SRX4680923: GSM3389639: Normal N2; Hylocereus polyrhizus; RNA-Seq

SRX4680923: GSM3389639: 正常N2; Hylocerephenus 聚极体; RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX4680923>

Submitted: ---------------------------------------------------------

Transcriptomic de novo analysis of pitaya (Hylocereus polyrhizus) canker disease caused by Neoscytalidium dimidiatum  
PRJNA490886 • SRP161778 • All experiments • All runs  
show Abstract

• 全部实验 全部运行显示摘要

Design: ---------------------------------------------------------

NCBI (GEO)

国家协调机构(GEO)

Study: ---------------------------------------------------------

Normal N2

正常 N2

Library: ---------------------------------------------------------

Library:  
Instrument: Illumina HiSeq 2000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Tissues (100 mg) were placed into a precooled mortar to be ground into a powder with liquid nitrogen. The ground stem powder was collected into a precooled 2 mL Eppendorf tube with 2 mL RNase-free cetyltrimethylammonium bromide (CTAB) extracting solution, which contained 0.1% diethyl pyrocarbonate (DEPC), 2.5% CTAB, 1.4 M NaCl, 20 mM EDTA, 100 mM Tris-HCl (pH 8.0), and 4% polyvinylpyrrolidone (PVP). The tubes were then placed in a water bath at 65 °C for 30 min to induce cell lysis, and centrifuged at 13,000 rpm for 5 min at 25-28 °C. The residue was discarded, and the supernatant solution was transferred into a clean 2 mL Eppendorf tube. Trichloromethane (1 mL) was added to the supernatant solution, blended lightly, and centrifuged at 13 000 rpm for 15 min at 4 °C. The supernatant was transferred into a clean 2 mL Eppendorf tube, and this procedure was repeated once more. Subsequently, 8 M lithium chloride was added with RNase-free water to 0.6 volume of the supernatant and left overnight. The mixture was centrifuged for 30 min at 13 000 rpm and 4 °C to obtain the RNA precipitate. RNase-free ethyl alcohol (75%) was used to wash the RNA precipitate twice. Finally, RNA was dissolved in RNase-free ddH2O and stored at -80 °C until further use. Poly (A) mRNA from the total RNA was enriched by poly-T oligo-attached magnetic beads (Invitrogen), according to the manufacturer's protocol. Purified mRNA was then divided into short fragments by mixing with fragmentation buffer. The first strand cDNA was synthesized using a random hexamer primer. The buffer, dNTPs, RNase H, and DNA polymerase I were then added to the fragmented mRNA templates to synthesize the second-strand cDNA. The double-stranded cDNA was purified using magnetic beads. End repair and the addition of 3′-end single nucleotide A (adenine) were then performed. Finally, sequencing adaptors were ligated to the fragments, which were enriched by PCR amplification. During the quality control step, a 2100 Bioanalyzer (Agilent, Santa Clara, CA, USA) and a StepOnePlus Real-Time PCR System (Applied Biosystems Inc., Foster City, CA, USA) were used to qualify and quantify sequences for the sample libraries. The constructed library products were prepared for sequencing using a HiSeq 2000 system (Illumina, San Diego, CA, USA) at the Beijing Genomics Institute (BGI).

托盘(100毫克)被放置在预冷凝固的迫击炮中,成为含液态氮粉的粉末。 地面干粉被收集到一个2°C的预冷2 mL Eppendorf 水槽中,2 mL Rase-无碳基甲基溴(CTAB)提取溶液中含有0.1% dili-rock-cyrocolate(DEPC),2.5% 碳- 碳- 碳(CTAB), 1.4 MNCl, 20 mMEDTA, 100 mm Tris-Hlors(p 8.0 毫克) 和 4% 聚氨醇(PVP) 。 地面干粉在65 °C 水槽中被收集了30 分钟来诱导细胞分解, 在25- 28 °C 解析时, 离心器被丢弃, 超级液溶液被转移到了2 mmL Eppendrod-nal- demodal O.

BioData: SRR7829960

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# 31: SRX23991992: GSM8153968: ovary, H6; Huso dauricus x Acipenser schrenckii; RNA-Seq

Title: ---------------------------------------------------------

SRX23991992: GSM8153968: ovary, H6; Huso dauricus x Acipenser schrenckii; RNA-Seq

SRX23991992: GSM8153968:卵,H6;Huso dauriscus x Acipenser schrencki;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX23991992>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8153968\_r1

GSM8153968\_r1

Study: ---------------------------------------------------------

Critical gene filtration for the caviar yield of hybrid sturgeon

混合螺旋藻鱼子酱产量的关键基因过滤

Library: ---------------------------------------------------------

Library:  
Name: GSM8153968  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA simple extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in ovary tissues. 60 mg fresh tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 4 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragmentation with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that were provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (300±50 bp) was established by amplifying the target sequences.

姓名: 姓名: GSM 8153968 资料库: GSM 8153968 资料库: GSM 8153968 资料库: Illumina NovaSeq 600 战略: RNA-Sequa 来源: TARNA 选择了 TARED 建筑协议: 商业 RNA 简单抽取包(DP419, TIANGEN, 中国) 抽取全部 RNA 。 60毫克新鲜组织由高速同源同源(DHFFSTPRP-32D,中国劳森) 使用 1 mLL 透析缓冲RZ, 以获得同源, 然后添加三氯甲烷。 在4分钟的室内温度中停留4分后, 将混合物调离心于12000 平点, 以获得与绝对乙醇混合的水分相混合的液相配制阶段。 RNA 使用RNA 样本中残留的蛋白质(DHR) 以RNA 和NIS IMO IMO 基 提供 。

BioData: SRR28387157

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# 32: SRX23366459: GSM8031811: liver,CW1; Hipposideros armiger; RNA-Seq

Title: ---------------------------------------------------------

SRX23366459: GSM8031811: liver,CW1; Hipposideros armiger; RNA-Seq

SRX23366459:GSM8031811:肝脏、CW1;Hipposideros 冷冻船;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX23366459>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8031811\_r1

GSM8031811\_r1

Study: ---------------------------------------------------------

Excessive heavy metals enrichment disturbs the liver function through gut microbe in great Himalayan leaf-nosed bat (Hipposideros armiger)

大喜马拉雅山叶鼻蝙蝠(Hipposideros Afriger)通过肠道微生物,过度重金属浓缩会扰乱肝脏功能。

Library: ---------------------------------------------------------

Library:  
Name: GSM8031811  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA simple extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in liver tissues. 60 mg fresh tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 4 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragmentation with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that were provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (300±50 bp) was established by amplifying the target sequences.

资料库: 名称: GSM8031811 工具: Illuma NovaSeq 600 战略: RNA-Seq 来源: TRARIPTOMI 选择: CDNA布局: PARED 建筑协议: 商业 RNA 简单抽取包(DP419, TIANGEN, 中国) 提取肝脏组织中的全RNA。 60毫克新鲜组织由高速同质同质体(DHFFSTPRP-32D,中国Lawson) 制成。 当RNA 的完整度 > 7.0 和 A260/280 RED 后, 添加了50 类同质的RNA 。在室内温度为4分钟后, 混合物在12000 调离心后被离心, 以获得与绝对乙醇酒精混合的液相配制的液相配制阶段 。 RDRNA 和 IMIS 的精密性精制的DNA , 和 IMIS 的精制的精制成型 。

BioData: SRR27699634

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# 33: SRX23991996: GSM8153972: ovary, L2; Huso dauricus x Acipenser schrenckii; RNA-Seq

Title: ---------------------------------------------------------

SRX23991996: GSM8153972: ovary, L2; Huso dauricus x Acipenser schrenckii; RNA-Seq

SRX23991996: GSM8153972:卵巢,L2;Huso dauriscus x Acipenser schrencki;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX23991996>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8153972\_r1

GSM88535972\_r1

Study: ---------------------------------------------------------

Critical gene filtration for the caviar yield of hybrid sturgeon

混合螺旋藻鱼子酱产量的关键基因过滤

Library: ---------------------------------------------------------

Library:  
Name: GSM8153972  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA simple extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in ovary tissues. 60 mg fresh tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 4 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragmentation with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that were provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (300±50 bp) was established by amplifying the target sequences.

姓名: 姓名: GSM 8153972 工具: 姓名: GSM 8153972 工具: Ilmluma NovaSeq 600 战略: RNA-Seq 来源: TRARIP 选择 TDNA 选择: PARED 建筑协议: 商业 RNA 简单抽取包(DP 419, TIANGEN, 中国) 抽取全部 RNA 。 60 毫克新鲜组织由高速同源同源同源(DHFFSTPRP-32D, 中国) 使用 1 mLL 透析缓冲RZ, 以获得同源同值同值同值同值,然后加上三氯甲烷。 在室内温度4分钟保持4分后, 将混合物调离心于12000 rpm: 获得与乙醇完全混合的水相接的水相相相相接的水相接的阶段。 RED溶液溶液在重复离心后被储存在RNase-trotrotrod 。 当RNA 之后, RNA 和AICFSIS IMF5, 和NIS 具体的血解解解解解解解解解解解解解解解解解解解解解解解解解解解解解解解解解解解解解到中国。

BioData: SRR28387153

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# 34: SRX24419484: GSM8244986: gut, Ori1; Huso dauricus; RNA-Seq

Title: ---------------------------------------------------------

SRX24419484: GSM8244986: gut, Ori1; Huso dauricus; RNA-Seq

SRX244149484: GSM8244986:直肠,Ori1;Huso dauriscus;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX24419484>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8244986\_r1

GSM8244986\_r1

Study: ---------------------------------------------------------

Multi-omics integration reveals the dynamic impacts of stock enhancement on the intestinal health condition in kaluga sturgeon (Huso dauricus)

多组集成表明,鱼量增强对Kaluga sturgeon(Huso dauriscus)肠胃健康状况的动态影响。

Library: ---------------------------------------------------------

Library:  
Name: GSM8244986  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA sample extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in gut tissues. 90 mg fresh intestine tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 6 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragment with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that was provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (150 bp) was established by amplifying the target sequences.

Name: 姓名: GSM 8244986 资料库: GSM 8244986 资料库: GSM 8244986 资料库: Illumina NovaSeq 600 战略: RNA-Seq 来源: TRARIP 选择: TARED 选择 PARED 建筑协议: 商业 RNA 样本提取包( DP 419, TIANGEN, 中国) 在肠组织中提取全部 RNA 。 90 毫克新鲜肠组织在高速度同质器( DHFFSTPRP-32D, 中国劳森) 下方 1 mLL 透析缓冲RZZ 以获得同质,然后添加三氯甲烷。 在房间温度为6分钟的室内温度为6: Cro温后, 调离心的混合物在12000 rpmbm: 获得与乙级酒精混合酒精混合的水相相混合的水相。 RDUNA 的精度序列和精度为RNA 。

BioData: SRR28859450

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# 35: SRX25145400: GSM8367756: gut, H3; Acipenser schrenckii; RNA-Seq

Title: ---------------------------------------------------------

SRX25145400: GSM8367756: gut, H3; Acipenser schrenckii; RNA-Seq

SRX251454400:GSM8367756:直肠,H3;Acipenserschrenckii;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX25145400>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8367756\_r1

GSM8367756\_r1

Study: ---------------------------------------------------------

Dynamic impacts of stock enhancement on wild Amur sturgeon (Acipenser schrenkii): New protection insight into intestinal microbe and gene expression mode

种群增强对野生亚穆尔外科动物(Acipenserschrenkii):对肠微生物和基因表达模式的新的保护洞见

Library: ---------------------------------------------------------

Library:  
Name: GSM8367756  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA sample extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in gut tissues. 100 mg fresh intestine tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 7 min, the mixture was centrifuged at 12500 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragment with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that was provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (150 bp) was established by amplifying the target sequences.

Name: 姓名: GSM 8367756 工具: 姓名: GSM 8367756 工具: Illuma NovaSeq 600 战略: RNA-Seq 来源: TRARIPTOMI 选择: CDNA布局: PARED 建筑协议: 商业 RNA 样本提取包(DP 419, TIANGEN, 中国) 抽取胃组织中的全部 RNA 。 100毫克新鲜肠组织被高速同质同素(DHFFSTPRP-32D, 中国劳森) , 1 mLL 透析缓冲RZZ 以获得同质,然后添加三氯甲烷。 在7分钟的室内温度为7m: TRA 选择: CLDM: 12500 调试样之后,该混合物被离心化为12500 rPMMM: 以获得与绝对乙醇混合的水相混合阶段。 RDRA 样本用于消除RNA 的蛋白质性。 在重复离心管中,然后由IMIS IMER IMER 和C IMIS IMER 和C IMER IMF 提供 IMF IMF IMD IMF IMF 和 IMD IMD IMD IMF IMF IMF IMF IMD 和 C IMF IMF IMF IMF IMF IMF IMF IMF IMF IM IM IM IMF 和 IMF IMF IMF IMD IMF IMF IMF IMD IMF IMF IMD IMF IM IMF IMF IMF IM IM IM IM IM IMF IMS IM IMS IM IMF IMF IMF IMF IMF IMF IM IMF IMF IMS IMD IM IM IMF IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM

BioData: SRR29640988

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# 36: ERX5525567: NextSeq 500 sequencing; Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

Title: ---------------------------------------------------------

ERX5525567: NextSeq 500 sequencing; Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

ERX55255567: 下等Seq 500排序; 婴儿仓鼠肾细胞的粘附和悬浮细胞有不同的细胞素和地表受体

Link:

<https://www.ncbi.nlm.nih.gov/sra/ERX5525567>

Submitted: ---------------------------------------------------------

Friedrich-Loeffler-Institut Federal Research Institute for Animal Health Institute of Diagnostic Virology (Friedrich-Loeffler-Institut Federal Research Insti)

Friedrich-Loeffler研究所 联邦动物卫生研究所

Design: ---------------------------------------------------------

Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

婴儿仓鼠肾细胞的粘附和悬浮性婴儿仓鼠肾细胞有不同的细胞骨质素和表面受体

Study: ---------------------------------------------------------

Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

婴儿仓鼠肾细胞的粘附和悬浮性婴儿仓鼠肾细胞有不同的细胞骨质素和表面受体

Library: ---------------------------------------------------------

Library:  
Name: BHK\_2P\_1\_s  
Instrument: NextSeq 500  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: PolyA  
Layout: SINGLE  
Construction protocol: Batches of each of the cell lines BHK179, BHK-2P and BHK-InV were lysed in three volumes of TRIzol LS Reagent. Culture conditions were 37 °C, 5% CO2, and for suspension cells 320 rpm in TubeSpin bioreactors (TPP Techno Plastic Products AG, Trasadingen, Switzerland) at 80% relative humidity. All adherent cell lines were cultured in Minimum Essential Medium Eagle (MEM) supplemented with Hanks' and Earle's salts (Sigma-Aldrich) with 10% FBS. All suspension cell lines were adapted to grow in CellventoTM BHK200 medium (Merck KGaA). After adding trichloromethane the aqueous phase was collected and mixed with one volume of 100% ethanol. From this, total RNA was extracted using the RNeasy Mini Kit (Qiagen, Hilden, Germany) with on-column DNase digestion with the RNase-Free DNase Set (Qiagen). The ERCC RNA Spike-In Mix 1 (Thermo Fisher Scientific) was added and used as an internal control for all following steps. Next, polyadenylated mRNA was isolated from 1-3 µg of high-quality total RNA using the Dynabeads mRNA DIRECT Micro kit (Thermo Fisher Scientific). The mRNA was subsequently fragmented and used for cDNA synthesis and library preparation using the TruSeq Stranded mRNA LT Sample Prep Kit (Illumina, San Diego, USA) according to the manufacturer's instructions.

图书馆: 名称: BHK\_ 2P\_ 1\_\_s 工具 : NextSeq 500 战略 来源: TRARIPTOMI 选择 80% 相对湿度 TRARIPTOMI 选择 : PolyA 布局: SINGLE 建设协议 : BHK-P 和 BHK-InV 的每条电池用三卷TRizol LS 试剂解析。 文化条件为 37 °C, 5% CO2 , TubeSpin 生物反应器中的悬浮细胞320 rpmm (TPP Terno FlickRTRTFIGA AG, Trasaden, Stradingendencial湿度 。所有粘固电池线都是在最低基本基本中型鹰鹰(MIQ) , 用于SilNSeral-NSeral RQ 的内置 , 用于Silental-NC 和 RC RC RC 的内置 , 用于Sental-ral-ral-ral-ral-ral-Q 。

BioData: ERR5882035

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# 37: SRX10761862: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

Title: ---------------------------------------------------------

SRX10761862: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

SRX10761862: 16S RNDNA V4区域肌肉肌肉细胞顺序:成年男性累积含量

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX10761862>

Submitted: ---------------------------------------------------------

China Pharmaceutical University

中国制药大学

Design: ---------------------------------------------------------

DNA extracted via phenol-Trichloromethane method, and V4 region amplified with primer of 515F and 806R, then Illumina NovaSeq 6000 used for sequencing

通过酚-三氯甲烷方法提取的DNA,以及V4区域,以515F和806R的基质放大515F和806R,然后用Illuma NovaSeq 6000来测序

Study: ---------------------------------------------------------

16S sequencing of amlodipine treated NAFLD & hypertension mice

NAFLD和高血压小鼠

Library: ---------------------------------------------------------

Library:  
Name: AA16  
Instrument: Illumina NovaSeq 6000  
Strategy: AMPLICON  
Source: GENOMIC  
Selection: PCR  
Layout: SINGLE

图书馆:名称:AA16仪器:Illuma NovaSeq 6000战略:AMPLICON 资料来源:GENMIC选择:PCR布局: SINGLE

BioData: SRR14410411

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# 38: SRX23991998: GSM8153974: ovary, L4; Huso dauricus x Acipenser schrenckii; RNA-Seq

Title: ---------------------------------------------------------

SRX23991998: GSM8153974: ovary, L4; Huso dauricus x Acipenser schrenckii; RNA-Seq

SRX23991998: GSM8153974:卵,L4;Huso dauriscus x Acipenser schrencki;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX23991998>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8153974\_r1

GSM8153974\_r1

Study: ---------------------------------------------------------

Critical gene filtration for the caviar yield of hybrid sturgeon

混合螺旋藻鱼子酱产量的关键基因过滤

Library: ---------------------------------------------------------

Library:  
Name: GSM8153974  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA simple extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in ovary tissues. 60 mg fresh tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 4 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragmentation with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that were provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (300±50 bp) was established by amplifying the target sequences.

姓名: 姓名: GSM 8153974 资料库: GSM 8153974 资料库: GSM 8153974 资料库: Illumina NovaSeq 600 战略: RNA-Sequa 来源: TARNA 选择了 TARED 建筑协议: 商业 RNA 简单抽取包(DP419, TIANGEN, 中国) 抽取全部 RNA 。 60 毫克新鲜组织由高速同源同源同源同源的1 mLLL透析缓冲RZ, 以获得同源同源, 然后添加三氯甲烷 来源: 资料来源: TRANS 选择 TRA 选择 : TRAD 选择 选择 : CRAD: PARED 建筑布局: PARE: PARE: 1 2000 ROMMM: 获得与绝对酒精酒精混合的水分相接合的水相接合阶段 : SA 样本中残留的蛋白。 DNA总在重复离心后由RNA II II ODRNA 提供 IMO 和血解 IMIS IMIS IMLD IMF IMF IMF IMF IMF IMF 和 IMF IMD IMF IMF IMF IMF 和 IM IM IM IMF IMF IMF IM IM IMF IMF IM IM IM IMF IM IM 和 IMF IMF IM IM IMF IM IM IMF IM IM IM IM IM IMF IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IMS IMF IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM

BioData: SRR28387151

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# 39: ERX5525568: NextSeq 500 paired end sequencing; Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

Title: ---------------------------------------------------------

ERX5525568: NextSeq 500 paired end sequencing; Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

ERX55255568:下一个Seq 500对齐端序列;

Link:

<https://www.ncbi.nlm.nih.gov/sra/ERX5525568>

Submitted: ---------------------------------------------------------

Friedrich-Loeffler-Institut Federal Research Institute for Animal Health Institute of Diagnostic Virology (Friedrich-Loeffler-Institut Federal Research Insti)

Friedrich-Loeffler研究所 联邦动物卫生研究所

Design: ---------------------------------------------------------

Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

婴儿仓鼠肾细胞的粘附和悬浮性婴儿仓鼠肾细胞有不同的细胞骨质素和表面受体

Study: ---------------------------------------------------------

Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

婴儿仓鼠肾细胞的粘附和悬浮性婴儿仓鼠肾细胞有不同的细胞骨质素和表面受体

Library: ---------------------------------------------------------

Library:  
Name: BHK\_2P\_2\_p  
Instrument: NextSeq 500  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: PolyA  
Layout: PAIRED  
Construction protocol: Batches of each of the cell lines BHK179, BHK-2P and BHK-InV were lysed in three volumes of TRIzol LS Reagent. Culture conditions were 37 °C, 5% CO2, and for suspension cells 320 rpm in TubeSpin bioreactors (TPP Techno Plastic Products AG, Trasadingen, Switzerland) at 80% relative humidity. All adherent cell lines were cultured in Minimum Essential Medium Eagle (MEM) supplemented with Hanks' and Earle's salts (Sigma-Aldrich) with 10% FBS. All suspension cell lines were adapted to grow in CellventoTM BHK200 medium (Merck KGaA). After adding trichloromethane the aqueous phase was collected and mixed with one volume of 100% ethanol. From this, total RNA was extracted using the RNeasy Mini Kit (Qiagen, Hilden, Germany) with on-column DNase digestion with the RNase-Free DNase Set (Qiagen). The ERCC RNA Spike-In Mix 1 (Thermo Fisher Scientific) was added and used as an internal control for all following steps. Next, polyadenylated mRNA was isolated from 1-3 µg of high-quality total RNA using the Dynabeads mRNA DIRECT Micro kit (Thermo Fisher Scientific). The mRNA was subsequently fragmented and used for cDNA synthesis and library preparation using the TruSeq Stranded mRNA LT Sample Prep Kit (Illumina, San Diego, USA) according to the manufacturer's instructions.

图书馆: 名称: BHK\_ 2P\_ 2\_p 工具 : NextSeq 500 战略 来源: TRARIPTOMI 选择 80% 相对湿度 TRARIPTOMI 选择 : PolyA 布局: PAIRED 建设协议: 每一个细胞线 BHK179 、 BHK-2P 和 BHK- InV 的棒用三卷TRizol LS 试剂解。 文化条件为 37 °C, 5% CO2 , TubeSpin 生物反应器的悬浮电池 320 rpm( TP Techno Flickr NAT 塑料产品AGAG, Trasaden, 瑞士,瑞士, Trasad Nsad Rad) 。 所有粘固的电池线都是在最低基本中精度的中型中雄鹰( RAS Q) , 之后, 使用Sil- RC 的内质 , ROQ , , 和 RC RC 的内质 , 做了 的 , 的 的 , 和 RC ROQ 的中 的 的 , 的 的 , , 的 和 的 的 的 的 , 和 RC- RC 做了 的 的 的 的 的 的 , 的 , , , 和 R. RC 的 的 和 R- RC 的 的 的 的 的 的 的 的 的 的 的 的 的 和 RC ROQ 的 的 的 的 RC 的 的 的 的 的 的 的 的 的 的 的 的 和 R- RC 的 的 的 的 的 的 的 的 的 的 和 RC 和 RC 和 RC 的 的 和 RC 和 RC 的 的 的 和 RC 的 的 的 的 的 的 和 RC 的 和 RC 的 的 的 的 的 的

BioData: ERR5882039

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# 40: SRX10761855: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

Title: ---------------------------------------------------------

SRX10761855: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

SRX10761855: 16S RNDNA V4区域肌肉肌肉细胞顺序:成年男性累积含量

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX10761855>

Submitted: ---------------------------------------------------------

China Pharmaceutical University

中国制药大学

Design: ---------------------------------------------------------

DNA extracted via phenol-Trichloromethane method, and V4 region amplified with primer of 515F and 806R, then Illumina NovaSeq 6000 used for sequencing

通过酚-三氯甲烷方法提取的DNA,以及V4区域,以515F和806R的基质放大515F和806R,然后用Illuma NovaSeq 6000来测序

Study: ---------------------------------------------------------

16S sequencing of amlodipine treated NAFLD & hypertension mice

NAFLD和高血压小鼠

Library: ---------------------------------------------------------

Library:  
Name: Cont3  
Instrument: Illumina NovaSeq 6000  
Strategy: AMPLICON  
Source: GENOMIC  
Selection: PCR  
Layout: SINGLE

图书馆: 名称: Cont3 仪器: Illuma NovaSeq 6000 战略: AMPLICON 资料来源: GENMIC 选择: PCR布局: SINGLE

BioData: SRR14410418

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# 41: ERX5525570: NextSeq 500 paired end sequencing; Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

Title: ---------------------------------------------------------

ERX5525570: NextSeq 500 paired end sequencing; Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

ERX5525570: 下一个Seq 500对齐端序列; 适应和悬浮婴儿仓鼠肾细胞的细胞骨质素和表面受体细胞素不同

Link:

<https://www.ncbi.nlm.nih.gov/sra/ERX5525570>

Submitted: ---------------------------------------------------------

Friedrich-Loeffler-Institut Federal Research Institute for Animal Health Institute of Diagnostic Virology (Friedrich-Loeffler-Institut Federal Research Insti)

Friedrich-Loeffler研究所 联邦动物卫生研究所

Design: ---------------------------------------------------------

Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

婴儿仓鼠肾细胞的粘附和悬浮性婴儿仓鼠肾细胞有不同的细胞骨质素和表面受体

Study: ---------------------------------------------------------

Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

婴儿仓鼠肾细胞的粘附和悬浮性婴儿仓鼠肾细胞有不同的细胞骨质素和表面受体

Library: ---------------------------------------------------------

Library:  
Name: BHK\_InV\_1\_p  
Instrument: NextSeq 500  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: PolyA  
Layout: PAIRED  
Construction protocol: Batches of each of the cell lines BHK179, BHK-2P and BHK-InV were lysed in three volumes of TRIzol LS Reagent. Culture conditions were 37 °C, 5% CO2, and for suspension cells 320 rpm in TubeSpin bioreactors (TPP Techno Plastic Products AG, Trasadingen, Switzerland) at 80% relative humidity. All adherent cell lines were cultured in Minimum Essential Medium Eagle (MEM) supplemented with Hanks' and Earle's salts (Sigma-Aldrich) with 10% FBS. All suspension cell lines were adapted to grow in CellventoTM BHK200 medium (Merck KGaA). After adding trichloromethane the aqueous phase was collected and mixed with one volume of 100% ethanol. From this, total RNA was extracted using the RNeasy Mini Kit (Qiagen, Hilden, Germany) with on-column DNase digestion with the RNase-Free DNase Set (Qiagen). The ERCC RNA Spike-In Mix 1 (Thermo Fisher Scientific) was added and used as an internal control for all following steps. Next, polyadenylated mRNA was isolated from 1-3 µg of high-quality total RNA using the Dynabeads mRNA DIRECT Micro kit (Thermo Fisher Scientific). The mRNA was subsequently fragmented and used for cDNA synthesis and library preparation using the TruSeq Stranded mRNA LT Sample Prep Kit (Illumina, San Diego, USA) according to the manufacturer's instructions.

图书馆: 名称: BHK\_ InV\_ 1\_p 工具: NextSeq 500 战略: NextSeq 500 战略 来源: TRARIPTOMI 选择 80%相对湿度 TRARIPTOMI 选择: PolyA 布局: PAIRED 建设协议: 每一个细胞线 BHK179、 BHK-2P 和 BHK- InV 的电池都用三卷TRizol LS试剂解析。 文化条件为37 °C, 5% CO2 和 TubeSpin 生物反应器中的悬浮电池 320 rpmm: RNA 生物反应器 (TPP Techno Flickno 塑料产品AGAGAG, Trassaden, Stradingenning 80% NSeralNADR) 所有粘固的细胞线都是在最低基本中型中型中型中型中型中型中型钢铁(RNA) 之后, 用于Silent RC 和Silmacial Kinial 。

BioData: ERR5882041

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# 42: SRX25145396: GSM8367752: gut, Q2; Acipenser schrenckii; RNA-Seq

Title: ---------------------------------------------------------

SRX25145396: GSM8367752: gut, Q2; Acipenser schrenckii; RNA-Seq

SRX25145396:GSM8367752:肠道,Q2;Acipenserschrenckii;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX25145396>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8367752\_r1

GSM8367752\_r1

Study: ---------------------------------------------------------

Dynamic impacts of stock enhancement on wild Amur sturgeon (Acipenser schrenkii): New protection insight into intestinal microbe and gene expression mode

种群增强对野生亚穆尔外科动物(Acipenserschrenkii):对肠微生物和基因表达模式的新的保护洞见

Library: ---------------------------------------------------------

Library:  
Name: GSM8367752  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA sample extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in gut tissues. 100 mg fresh intestine tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 7 min, the mixture was centrifuged at 12500 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragment with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that was provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (150 bp) was established by amplifying the target sequences.

Name: 姓名: GSM8367752 工具: GSM8367752 工具: Ilmluma NovaSeq 600 战略: RNA-Seq 来源: TRARIPTOMI 选择: CDNA布局: PARED 建筑协议: 商业RNA采样袋(DP419, TIANGEN, 中国) 以提取腹腔组织中的全部RNA。 100毫克新鲜肠组织由高速同源同源同源(DHFFSTPRP-32D,中国劳森) 以 1 mLL 透析缓冲RZ 来获取同源,然后添加三氯甲烷。在7分钟的室内温度为7分钟后,该混合物被离心为12500 rpmm: 以获得与绝对乙醇混合的水相相吸附的水相。 RDRNA 样本在重复离心后被储存在无色管中。 当RNA 完完后, P0 and A260proud REN RNA (MIN) 和混凝解的RNISODER IMO, 然后被提供。

BioData: SRR29640992

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# 43: SRX10761845: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

Title: ---------------------------------------------------------

SRX10761845: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

SRX10761845: 16S RNDNA V4区域肌肉肌肉细胞顺序:成年男性累积含量

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX10761845>

Submitted: ---------------------------------------------------------

China Pharmaceutical University

中国制药大学

Design: ---------------------------------------------------------

DNA extracted via phenol-Trichloromethane method, and V4 region amplified with primer of 515F and 806R, then Illumina NovaSeq 6000 used for sequencing

通过酚-三氯甲烷方法提取的DNA,以及V4区域,以515F和806R的基质放大515F和806R,然后用Illuma NovaSeq 6000来测序

Study: ---------------------------------------------------------

16S sequencing of amlodipine treated NAFLD & hypertension mice

NAFLD和高血压小鼠

Library: ---------------------------------------------------------

Library:  
Name: AA18  
Instrument: Illumina NovaSeq 6000  
Strategy: AMPLICON  
Source: GENOMIC  
Selection: PCR  
Layout: SINGLE

图书馆:名称:AA18仪器:Illuma NovaSeq 6000战略:AMPLICON 资料来源:GENMIC选择:PCR布局: SINGLE

BioData: SRR14410428

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# 44: ERX645737: Illumina Genome Analyzer II sequencing; Deregulation of PPAR-beta/delta target genes in tumor-associated macrophages by fatty acid ligands in the ovarian cancer microenvironment - RNAseq

Title: ---------------------------------------------------------

ERX645737: Illumina Genome Analyzer II sequencing; Deregulation of PPAR-beta/delta target genes in tumor-associated macrophages by fatty acid ligands in the ovarian cancer microenvironment - RNAseq

ERX645737: IRX645737: II 光素基因组分析分析仪的排序; 对卵巢癌微环境中脂肪酸皮条动物在肿瘤相关巨形中的PPPAR-beta/delta目标基因进行调控-RNAseq

Link:

<https://www.ncbi.nlm.nih.gov/sra/ERX645737>

Submitted: ---------------------------------------------------------

Institute for molecular and tumor biology Philipps University Marburg Germany (Institute for molecular and tumor biology Philipps)

德国马尔堡大学分子和肿瘤生物学研究所(分子和肿瘤生物学研究所)

Design: ---------------------------------------------------------

Deregulation of PPAR-beta/delta target genes in tumor-associated macrophages by fatty acid ligands in the ovarian cancer microenvironment - RNAseq

在卵巢癌微环境中,脂肪酸皮条动物在肿瘤相关大型基因中解管PPAR-beta/delta目标基因 -- -- RNAseq

Study: ---------------------------------------------------------

Deregulation of PPAR-beta/delta target genes in tumor-associated macrophages by fatty acid ligands in the ovarian cancer microenvironment - RNAseq

在卵巢癌微环境中,脂肪酸皮条动物在肿瘤相关大型基因中解管PPAR-beta/delta目标基因 -- -- RNAseq

Library: ---------------------------------------------------------

Library:  
Name: ST004  
Instrument: Illumina Genome Analyzer II  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: RANDOM  
Layout: SINGLE  
Construction protocol: Ascites was collected from 30 patients with high-grade serous ovarian carcinoma undergoing primary surgery at the University Hospital in Marburg. Informed consent was obtained from all patients according to the protocols approved by the local ethical committe Cells were isolated on June 06th 2013 from healthy human donor blood of unknown gender via LSM1077 gradient centrifugation. Adherent cells were positively selected on primaria 6 well dishes (3x10^6 monocytes per well in 2 ml PBS (PAA)) followed by 6 washing steps with PBS. Finally the monocytes were cultured for 6d in humidified incubator at 37 degrees C, 5 % CO2 in 2ml RPMI medium supplemented with 10 % FCS (both PAA). Cells were treated with control (DMSO), L165 1 uM final concentration or ST247 300 nM final concentration for 1d. Cells were washed with PBS, supernatant was removed completly, then 1 ml of peqGOLD TriFast (PEQLAB) was added to each well and transfered to a 1,5 ml Eppi. Following 5 min of incubation at RT 200 ul trichloromethane were added to the solution. The probes were mixed thoroughly every 3 minutes during a 10 minute incubation at RT. Probes were centrifuged at 13.000 g for 15 min at 4 degrees C then the aquouse top phase was transfered to a new eppi containing 600 ul of ice cold 2-propanol. Probes were mixed and centrifuged for 10 min at 13.000 g, 4 degrees C. The supernatant was removed and the pelleted RNA was washed twice with 75 % Ethanol for 5 minutes at 13.000 g, 4 degrees C. The pellet was dried and dissolved in 15 ul of RNase free water following quality control using Xcalibur (Thermo scientific). Libraries were created using the Illumina Truseq mRNA kit used according to the manufacturer's instructions.

图书馆: 姓名: ST004 工具: ST004 根据当地道德承诺小组批准的协议, 于2013年6月从健康的人体捐赠者血液中分离出 通过 LSM 1077 梯度离心法, 施用细胞是积极的。 在原始6 盘(3x10+6) 中选择了活性细胞: RANDOM布局: SINGLE 建设协议: 30名在马尔堡大学医院接受初级外科手术的高等级雌性卵巢癌病人采集了Ascites。 根据当地道德承诺小组批准的协议, 于2013年6月6日得到了所有病人的知情同意。 由LSMSM 10 降压到 不明性别: 13.2 000 梯度离心体 选择了Adrial 6 盘(3x10+6) 硬盘盘: 2 mBSl PBS 盘(PBA) 之后, 以 15 磁盘 QL 进行15 磁盘 的磁带 , 5-LL 3 进行磁带 。

BioData: ERR701473

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# 45: ERX645736: Illumina Genome Analyzer II sequencing; Deregulation of PPAR-beta/delta target genes in tumor-associated macrophages by fatty acid ligands in the ovarian cancer microenvironment - RNAseq

Title: ---------------------------------------------------------

ERX645736: Illumina Genome Analyzer II sequencing; Deregulation of PPAR-beta/delta target genes in tumor-associated macrophages by fatty acid ligands in the ovarian cancer microenvironment - RNAseq

ERX645736: IRX645736: II光素基因组分析分析仪的排序; 对卵巢癌微环境中脂肪酸皮条动物在肿瘤相关巨形中的PPPAR-beta/delta目标基因进行调控-RNAseq

Link:

<https://www.ncbi.nlm.nih.gov/sra/ERX645736>

Submitted: ---------------------------------------------------------

Institute for molecular and tumor biology Philipps University Marburg Germany (Institute for molecular and tumor biology Philipps)

德国马尔堡大学分子和肿瘤生物学研究所(分子和肿瘤生物学研究所)

Design: ---------------------------------------------------------

Deregulation of PPAR-beta/delta target genes in tumor-associated macrophages by fatty acid ligands in the ovarian cancer microenvironment - RNAseq

在卵巢癌微环境中,脂肪酸皮条动物在肿瘤相关大型基因中解管PPAR-beta/delta目标基因 -- -- RNAseq

Study: ---------------------------------------------------------

Deregulation of PPAR-beta/delta target genes in tumor-associated macrophages by fatty acid ligands in the ovarian cancer microenvironment - RNAseq

在卵巢癌微环境中,脂肪酸皮条动物在肿瘤相关大型基因中解管PPAR-beta/delta目标基因 -- -- RNAseq

Library: ---------------------------------------------------------

Library:  
Name: ST005  
Instrument: Illumina Genome Analyzer II  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: RANDOM  
Layout: SINGLE  
Construction protocol: Ascites was collected from 30 patients with high-grade serous ovarian carcinoma undergoing primary surgery at the University Hospital in Marburg. Informed consent was obtained from all patients according to the protocols approved by the local ethical committe Cells were isolated on June 06th 2013 from healthy human donor blood of unknown gender via LSM1077 gradient centrifugation. Adherent cells were positively selected on primaria 6 well dishes (3x10^6 monocytes per well in 2 ml PBS (PAA)) followed by 6 washing steps with PBS. Finally the monocytes were cultured for 6d in humidified incubator at 37 degrees C, 5 % CO2 in 2ml RPMI medium supplemented with 10 % FCS (both PAA). Cells were treated with control (DMSO), L165 1 uM final concentration or ST247 300 nM final concentration for 1d. Cells were washed with PBS, supernatant was removed completly, then 1 ml of peqGOLD TriFast (PEQLAB) was added to each well and transfered to a 1,5 ml Eppi. Following 5 min of incubation at RT 200 ul trichloromethane were added to the solution. The probes were mixed thoroughly every 3 minutes during a 10 minute incubation at RT. Probes were centrifuged at 13.000 g for 15 min at 4 degrees C then the aquouse top phase was transfered to a new eppi containing 600 ul of ice cold 2-propanol. Probes were mixed and centrifuged for 10 min at 13.000 g, 4 degrees C. The supernatant was removed and the pelleted RNA was washed twice with 75 % Ethanol for 5 minutes at 13.000 g, 4 degrees C. The pellet was dried and dissolved in 15 ul of RNase free water following quality control using Xcalibur (Thermo scientific). Libraries were created using the Illumina Truseq mRNA kit used according to the manufacturer's instructions.

图书馆: 姓名: ST 005 仪器: ST 005 仪器: 3300 基因组60 000 Analyzer II 战略: RNA-Sequ 来源: TRARIPTOMI 选择: RANDOM 布局: SINGLE 建筑协议: 收集了30名在马尔堡大学医院接受初级手术的高等级雌性卵巢癌病人的Ascites。 根据当地道德承诺细胞的规程,所有病人在2013年6月得到知情同意,通过LSM1077 梯度离心法将未知性别的健康血液从人体捐赠者血液中分离出来。 在灵敏性6 盘(3x10+6) 盘盘(3x10+6) 精液: 2 mBS (PAA) 之后, 以PBBS 的精度为6 。最后浓度在37摄氏度 C, 5ml RPA 中,以 4 CO2+RM 补充了10% 。

BioData: ERR701471

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# 46: SRX4500785: RNA-seq of Bombyx mori: male fat body

Title: ---------------------------------------------------------

SRX4500785: RNA-seq of Bombyx mori: male fat body

SRX445/000785:RNA-seq of Bombyx Mori: 男性脂肪体

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX4500785>

Submitted: ---------------------------------------------------------

State Key Laboratory of Silkworm Genome Biology

丝虫基因组生物学国家关键实验室

Design: ---------------------------------------------------------

For RNA sequnencing, total RNA was extracted from fat body at different development stage respectively. 1-15mg fat body were dissected in PBS and directly transferred to Trizol (Invitrogen, USA), then grinded with liquid nitrogen. RNA was extracted again trichloromethane, after precipitate by isopropanol and cleared by 75% ethanol, RNA samples were stored in a refrigerator at 80C for sequencing libraries. Each cDNA sample was clustered using Oligo-dT magnetic beads and then sequenced on the HiSeq2000 (Illumina, USA) platform using Single-read techology. All of the Raw data presented in this study have been deposited in the NCBI Short Read Archive (http://www.ncbi.nlm.nih.gov/sra/) under SRA accession number

在RNA后续阶段,在不同的开发阶段分别从脂肪体中提取了全部RNA。 1-15毫克的脂肪体在PBS中解剖,直接转移到Trizol(美国,Invitrogen),然后用液氮研磨。RNA在异丙醇沉淀后再次提取三氯甲烷,并用75%的乙醇清除。RNA样品储存在冰箱中,储存在80C用于测序的图书馆中。每个cDNA样本都使用Oligo-dT磁珠进行集成,然后在Hiseq2000(美国,Illuma)平台上用单读技术学进行测序。本研究中提供的所有原始数据都存放在CBCI短期阅读档案库中(http://www.ncbi.nlm.nih.gov/sra/),根据SRA的加入号。

Study: ---------------------------------------------------------

RNA-seq of Bombyx mori: male fat body

RNA-Seq of Bombyx Mori: 男性脂肪体

Library: ---------------------------------------------------------

Library:  
Name: W2\_rep2  
Instrument: Illumina HiSeq 2000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: PCR  
Layout: SINGLE

图书馆: 名称: W2\_rep2 仪器: Illuma Hiseq 2000 战略: RNA-Seq 来源: TRARIPTOMI 选择: PCR布局: SINGLE

BioData: SRR7637240

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# 47: SRX17532089: GSM6573334: KO2; Mus musculus; RNA-Seq

Title: ---------------------------------------------------------

SRX17532089: GSM6573334: KO2; Mus musculus; RNA-Seq

SRX175532089:GSM6573334:KO2;Mus Musculus;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX17532089>

Submitted: ---------------------------------------------------------

BNU

BNU BNU BNU

Design: ---------------------------------------------------------

GSM6573334\_r1

GSM6573334\_r1

Study: ---------------------------------------------------------

Granulocyte-monocyte progenitor (GMP) RNA-seq in wild type and MST1-deficient mice.

Granulocyte-monocyte progenitor (GMP) RNA-seq(野性)和MST1缺陷小鼠。

Library: ---------------------------------------------------------

Library:  
Name: GSM6573334  
Instrument: Illumina HiSeq 2000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Trizol and 0.2-fold volume of trichloromethane were added to the cells, and isopropanol and absolute ethanol were added to precipitate the extracted RNA. The RNA was dissolved with water and the RNA concentration and purity were detected with nano drop. RNA was enriched with magnetic beads with oligo (DT), then cDNA was synthesized using mRNA as a template, double stranded cDNA was purified and amplified by PCR.

资料库: 名称: GSM6573334 工具: Illuma Hiseq 2000 战略: RNA-Seq 来源: TRARIPTOMI 选择: CDNA布局: PARED 建筑协议: 细胞中添加三氯甲烷的三氯甲烷和0.2倍体积,在提取的RNA中添加异丙醇和绝对乙醇。 RNA 与水溶解,RNA 浓度和纯度与纳米液溶解。 RNA 以磁珠与oligo(DT)相丰富,然后使用 mRNA作为模版对cDNA 合成。

BioData: SRR21529727

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# 48: SRX23991990: GSM8153966: ovary, H4; Huso dauricus x Acipenser schrenckii; RNA-Seq

Title: ---------------------------------------------------------

SRX23991990: GSM8153966: ovary, H4; Huso dauricus x Acipenser schrenckii; RNA-Seq

SRX23991990: GSM8153966:卵,H4;Huso dauriscus x Acipenser schrencki;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX23991990>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8153966\_r1

GSM8153966\_r1

Study: ---------------------------------------------------------

Critical gene filtration for the caviar yield of hybrid sturgeon

混合螺旋藻鱼子酱产量的关键基因过滤

Library: ---------------------------------------------------------

Library:  
Name: GSM8153966  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA simple extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in ovary tissues. 60 mg fresh tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 4 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragmentation with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that were provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (300±50 bp) was established by amplifying the target sequences.

姓名: 姓名: GSM 8153966 资料库: GSM 8153966 资料库: GSM 8153966 资料库: Illumina NovaSeq 600 战略: RNA-Sequa 来源: TRA 选择 TRA 建筑协议: 商业 RNA 简单抽取包(DP419, TIANGEN, 中国) 抽取全部 RNA 。 60 毫克新鲜组织由高速同源同源同源(DHFFSTPRP-32D, 中国) 使用 1 mLL 透析缓冲RZ, 以获得同源同值同值同值同值,然后添加三氯甲烷。 在室内温度4分钟保持4分后, 将混合物调离心于12000 rmpm: 获得与乙醇完全混合的水相相相交的液相配相接的液相接相接的气相接相接相接相接合的 。

BioData: SRR28387159

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# 49: SRX10761854: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

Title: ---------------------------------------------------------

SRX10761854: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

SRX10761854: 16S RNDNA V4区域肌肉肌肉细胞顺序:成年男性累积含量

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX10761854>

Submitted: ---------------------------------------------------------

China Pharmaceutical University

中国制药大学

Design: ---------------------------------------------------------

DNA extracted via phenol-Trichloromethane method, and V4 region amplified with primer of 515F and 806R, then Illumina NovaSeq 6000 used for sequencing

通过酚-三氯甲烷方法提取的DNA,以及V4区域,以515F和806R的基质放大515F和806R,然后用Illuma NovaSeq 6000来测序

Study: ---------------------------------------------------------

16S sequencing of amlodipine treated NAFLD & hypertension mice

NAFLD和高血压小鼠

Library: ---------------------------------------------------------

Library:  
Name: AB8  
Instrument: Illumina NovaSeq 6000  
Strategy: AMPLICON  
Source: GENOMIC  
Selection: PCR  
Layout: SINGLE

图书馆:名称:AB8仪器:Illuma NovaSeq 6000战略:AMPLICON 资料来源:GENMIC选择:PCR布局: SINGLE

BioData: SRR14410419

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# 50: SRX9177110: GSM4799933: active\_ALKBH5\_dox\_minus\_input2; Homo sapiens; OTHER

Title: ---------------------------------------------------------

SRX9177110: GSM4799933: active\_ALKBH5\_dox\_minus\_input2; Homo sapiens; OTHER

SRX91777110: GSM4799933: 活性 \_ALKBH5\_dox\_minus\_input2; 智人; 其他

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX9177110>

Submitted: ---------------------------------------------------------

Targeted RNA N6-Methyladenosine Demethylation Controls Cell Fate Transition in Human Pluripotent Stem Cells  
PRJNA665206 • SRP285100 • All experiments • All runs  
show Abstract

RNA N6-M6-MEVEDEnessine脱甲基化控制细胞在人类多能细胞中发生转变的情况 PRJNA665206 PRJNA665206 PRJNA665206 • SRP285100 • 所有实验 全部运行 显示摘要

Design: ---------------------------------------------------------

NCBI (GEO)

国家协调机构(GEO)

Study: ---------------------------------------------------------

GEO accession GSM4799933 is currently private and is scheduled to be released on Sep 01, 2022.

GSM4799933目前是私营的,定于2022年9月1日发布。

Library: ---------------------------------------------------------

Library:  
Instrument: HiSeq X Ten  
Strategy: OTHER  
Source: TRANSCRIPTOMIC  
Selection: other  
Layout: PAIRED  
Construction protocol: Cells were washed with PBS and lysed with TRIzol (Thermo Fisher Scientific). Then trichloromethane (Guangzhou Chemical Reagent Factory) was used to extract the total RNA from the TRIzol lysate. Isopropanol (Sangon Biotech) was used to precipitates RNA from the mixture. mRNA was separated from the total RNA by using the Dynabeads™ mRNA Purification Kit (Thermo Fisher Scientific) according to the manufacturer's protocol. The m6A immunoprecipitation method was the same as above. Input samples and IP samples were applied for NGS library construction by using the NEBNext® Ultra II Directional RNA Library Prep (NEB) according to the manufacturer's guide. The adaptor ligated DNAs amplified by PCR for 15 cycles were sequenced on the HiSeqX sequencing platform.

资料库:仪器:HiSeq X 10战略:其他来源: TRARIPTOMIC选择:其他布局:PARED建筑协议:细胞用PBS冲洗,用TRIZOL(热水生科学)浸透,然后使用三氯甲烷(广州化学试剂厂)从TRIZOL液酸盐中提取总RNA。使用SOSOPAN醇(桑贡生物科技)从混合物中分离出RNA。MRNA根据制造商协议使用DynabadsTM mRNA净化工具包(热水生科学)与总RNA分离。M6A免疫喷洒方法与上述相同。根据制造商指南,在NEBNBNEXT Ulttra II定向RNA图书馆前p(NEB)对NGS图书馆的建设应用输入样品和IP样品。根据厂商指南,在HISECECECX测序平台上按15个周期放大的调控DNA顺序排列。

BioData: SRR12697487

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# 51: SRX4500783: RNA-seq of Bombyx mori: male fat body

Title: ---------------------------------------------------------

SRX4500783: RNA-seq of Bombyx mori: male fat body

SRX445/000783:RNA-seq of Bombyx Mori: 男性脂肪体

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX4500783>

Submitted: ---------------------------------------------------------

State Key Laboratory of Silkworm Genome Biology

丝虫基因组生物学国家关键实验室

Design: ---------------------------------------------------------

For RNA sequnencing, total RNA was extracted from fat body at different development stage respectively. 1-13mg fat body were dissected in PBS and directly transferred to Trizol (Invitrogen, USA), then grinded with liquid nitrogen. RNA was extracted again trichloromethane, after precipitate by isopropanol and cleared by 75% ethanol, RNA samples were stored in a refrigerator at 80C for sequencing libraries. Each cDNA sample was clustered using Oligo-dT magnetic beads and then sequenced on the HiSeq2000 (Illumina, USA) platform using Single-read techology. All of the Raw data presented in this study have been deposited in the NCBI Short Read Archive (http://www.ncbi.nlm.nih.gov/sra/) under SRA accession number

在RNA后续阶段,在不同的开发阶段分别从脂肪体中提取了全部RNA。 1-13毫克的脂肪体在PBS中解剖,直接转移到Trizol(美国,Invitrogen),然后用液氮研磨。RNA在异丙醇沉淀后再次提取三氯甲烷,并用75%的乙醇清除。RNA样品储存在冰箱中,储存在80C用于测序的图书馆中。每个cDNA样本都使用Oligo-dT磁珠集中,然后在Hiseq2000(美国,Illumina)平台上用单读技术学进行排序。本研究中提供的所有原始数据都存放在CBCI短期阅读档案库中(http://www.ncbi.nlm.nih.gov/sra/),根据SRA的加入号。

Study: ---------------------------------------------------------

RNA-seq of Bombyx mori: male fat body

RNA-Seq of Bombyx Mori: 男性脂肪体

Library: ---------------------------------------------------------

Library:  
Name: W0\_rep2  
Instrument: Illumina HiSeq 2000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: PCR  
Layout: SINGLE

图书馆: 名称: W0\_rep2 仪器: Illuma Hiseq 2000 战略: RNA-Seq 来源: TRARIPTOMI 选择: PCR布局: SINGLE

BioData: SRR7637242

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# 52: SRX23992002: GSM8153978: ovary, L8; Huso dauricus x Acipenser schrenckii; RNA-Seq

Title: ---------------------------------------------------------

SRX23992002: GSM8153978: ovary, L8; Huso dauricus x Acipenser schrenckii; RNA-Seq

SRX23992002: GSM8153978:卵,L8;Huso dauriscus x Acipenser schrencki;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX23992002>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8153978\_r1

GSM8153978\_r1

Study: ---------------------------------------------------------

Critical gene filtration for the caviar yield of hybrid sturgeon

混合螺旋藻鱼子酱产量的关键基因过滤

Library: ---------------------------------------------------------

Library:  
Name: GSM8153978  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA simple extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in ovary tissues. 60 mg fresh tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 4 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragmentation with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that were provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (300±50 bp) was established by amplifying the target sequences.

姓名: 姓名: GSM 8153978 资料库: GSM 8153978 资料库: GSM 8153978 资料库: Illumina NovaSeq 600 战略: RNA-Sequa 来源: TARNA 选择了 TARED 建筑协议: 商业 RNA 简单抽取包(DP419, TIANGEN, 中国) 抽取全部 RNA 。 60毫克新鲜组织由高速同源同源(DHFFSTPRP-32D,中国劳森) 使用 1 mLL 透析缓冲RZ, 以获得同源, 然后添加三氯甲烷。 在4分钟的室内温度中停留4分后, 将混合物调离心于12000 平点, 以获得与绝对乙醇混合的水分相混合的液相配制阶段。 RNA 使用RNA 样本中残留的蛋白质(DIS ) , 和 NIS DNA 的血解解解解解(由IO 提供) 和血解解到中国。

BioData: SRR28387147

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# 53: SRX10761846: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

Title: ---------------------------------------------------------

SRX10761846: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

SRX10761846: 16S RNDNA V4区域肌肉肌肉细胞顺序:成年男性累积含量

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX10761846>

Submitted: ---------------------------------------------------------

China Pharmaceutical University

中国制药大学

Design: ---------------------------------------------------------

DNA extracted via phenol-Trichloromethane method, and V4 region amplified with primer of 515F and 806R, then Illumina NovaSeq 6000 used for sequencing

通过酚-三氯甲烷方法提取的DNA,以及V4区域,以515F和806R的基质放大515F和806R,然后用Illuma NovaSeq 6000来测序

Study: ---------------------------------------------------------

16S sequencing of amlodipine treated NAFLD & hypertension mice

NAFLD和高血压小鼠

Library: ---------------------------------------------------------

Library:  
Name: AA19  
Instrument: Illumina NovaSeq 6000  
Strategy: AMPLICON  
Source: GENOMIC  
Selection: PCR  
Layout: SINGLE

图书馆:名称:AA19仪器:Illuma NovaSeq 6000战略:AMPLICON 资料来源:GENMIC选择:PCR布局: SINGLE

BioData: SRR14410427

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# 54: SRX25145398: GSM8367754: gut, H1; Acipenser schrenckii; RNA-Seq

Title: ---------------------------------------------------------

SRX25145398: GSM8367754: gut, H1; Acipenser schrenckii; RNA-Seq

SRX25145398:GSM8367754:直肠,H1;Acipenserschrenckii;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX25145398>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8367754\_r1

GSM8367754\_r1

Study: ---------------------------------------------------------

Dynamic impacts of stock enhancement on wild Amur sturgeon (Acipenser schrenkii): New protection insight into intestinal microbe and gene expression mode

种群增强对野生亚穆尔外科动物(Acipenserschrenkii):对肠微生物和基因表达模式的新的保护洞见

Library: ---------------------------------------------------------

Library:  
Name: GSM8367754  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA sample extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in gut tissues. 100 mg fresh intestine tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 7 min, the mixture was centrifuged at 12500 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragment with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that was provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (150 bp) was established by amplifying the target sequences.

Name: 姓名: GSM8367754 工具: GSM8367754 工具: Ilmluma NovaSeq 600 战略: RNA-Seq 来源: TRARIPTOMI 选择: CDNA布局: PARED 建筑协议: 商业RNA采样袋(DP419, TIANGEN, 中国) 以提取腹腔组织中的全部RNA。 100毫克新鲜肠组织由高速同源同源同源(DHFFSTPRP-32D,中国劳森) 以 1 mLL 透析缓冲RZ 来获取同源,然后添加三氯甲烷。在7分钟的室内温度为7分钟后,该混合物被离心为12500 rpmm: 以获得与绝对乙醇混合的水相相吸附的水相。 RDRNA 样本在重复离心后被存储在无色管中。 当RNA 完完整后, P0 and A260proud REN RNA (MNA) 和混凝解的RISODER IMO,然后被存储到美国(255, 和CDNE) 具体的DNA IMO 和C 和C IMER IMUDNU 的DNA IMF 的DNA 和C IMFD IMF5, IMU IMO IMO 。

BioData: SRR29640989

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# 55: SRX4680924: GSM3389640: Normal N3; Hylocereus polyrhizus; RNA-Seq

Title: ---------------------------------------------------------

SRX4680924: GSM3389640: Normal N3; Hylocereus polyrhizus; RNA-Seq

SRX4680924: GSM3389640: 正常N3; Hylocerephenus 聚极体; RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX4680924>

Submitted: ---------------------------------------------------------

Transcriptomic de novo analysis of pitaya (Hylocereus polyrhizus) canker disease caused by Neoscytalidium dimidiatum  
PRJNA490886 • SRP161778 • All experiments • All runs  
show Abstract

• 全部实验 全部运行显示摘要

Design: ---------------------------------------------------------

NCBI (GEO)

国家协调机构(GEO)

Study: ---------------------------------------------------------

Normal N3

正常 N3

Library: ---------------------------------------------------------

Library:  
Instrument: Illumina HiSeq 2000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Tissues (100 mg) were placed into a precooled mortar to be ground into a powder with liquid nitrogen. The ground stem powder was collected into a precooled 2 mL Eppendorf tube with 2 mL RNase-free cetyltrimethylammonium bromide (CTAB) extracting solution, which contained 0.1% diethyl pyrocarbonate (DEPC), 2.5% CTAB, 1.4 M NaCl, 20 mM EDTA, 100 mM Tris-HCl (pH 8.0), and 4% polyvinylpyrrolidone (PVP). The tubes were then placed in a water bath at 65 °C for 30 min to induce cell lysis, and centrifuged at 13,000 rpm for 5 min at 25-28 °C. The residue was discarded, and the supernatant solution was transferred into a clean 2 mL Eppendorf tube. Trichloromethane (1 mL) was added to the supernatant solution, blended lightly, and centrifuged at 13 000 rpm for 15 min at 4 °C. The supernatant was transferred into a clean 2 mL Eppendorf tube, and this procedure was repeated once more. Subsequently, 8 M lithium chloride was added with RNase-free water to 0.6 volume of the supernatant and left overnight. The mixture was centrifuged for 30 min at 13 000 rpm and 4 °C to obtain the RNA precipitate. RNase-free ethyl alcohol (75%) was used to wash the RNA precipitate twice. Finally, RNA was dissolved in RNase-free ddH2O and stored at -80 °C until further use. Poly (A) mRNA from the total RNA was enriched by poly-T oligo-attached magnetic beads (Invitrogen), according to the manufacturer's protocol. Purified mRNA was then divided into short fragments by mixing with fragmentation buffer. The first strand cDNA was synthesized using a random hexamer primer. The buffer, dNTPs, RNase H, and DNA polymerase I were then added to the fragmented mRNA templates to synthesize the second-strand cDNA. The double-stranded cDNA was purified using magnetic beads. End repair and the addition of 3′-end single nucleotide A (adenine) were then performed. Finally, sequencing adaptors were ligated to the fragments, which were enriched by PCR amplification. During the quality control step, a 2100 Bioanalyzer (Agilent, Santa Clara, CA, USA) and a StepOnePlus Real-Time PCR System (Applied Biosystems Inc., Foster City, CA, USA) were used to qualify and quantify sequences for the sample libraries. The constructed library products were prepared for sequencing using a HiSeq 2000 system (Illumina, San Diego, CA, USA) at the Beijing Genomics Institute (BGI).

托盘(100毫克)被放置在预冷凝固的迫击炮中,成为含液态氮粉的粉末。 地面干粉被收集到一个2°C的预冷2 mL Eppendorf 水槽中,2 mL Rase-无碳基甲基溴(CTAB)提取溶液中含有0.1% dili-rock-cyrocolate(DEPC),2.5% 碳- 碳- 碳(CTAB), 1.4 MNCl, 20 mMEDTA, 100 mm Tris-Hlors(p 8.0 毫克) 和 4% 聚氨醇(PVP) 。 地面干粉在65 °C 水槽中被收集了30 分钟来诱导细胞分解, 在25- 28 °C 解析时, 离心器被丢弃, 超级液溶液被转移到了2 mmL Eppendrod-nal- demodal O.

BioData: SRR7829961

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# 56: SRX23992001: GSM8153977: ovary, L7; Huso dauricus x Acipenser schrenckii; RNA-Seq

Title: ---------------------------------------------------------

SRX23992001: GSM8153977: ovary, L7; Huso dauricus x Acipenser schrenckii; RNA-Seq

SRX23992001: GSM8153977:卵,L7;Huso dauriscus x Acipenser schrencki;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX23992001>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8153977\_r1

GSM8153977\_r1

Study: ---------------------------------------------------------

Critical gene filtration for the caviar yield of hybrid sturgeon

混合螺旋藻鱼子酱产量的关键基因过滤

Library: ---------------------------------------------------------

Library:  
Name: GSM8153977  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA simple extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in ovary tissues. 60 mg fresh tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 4 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragmentation with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that were provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (300±50 bp) was established by amplifying the target sequences.

姓名: 姓名: GSM 8153977 工具: 姓名: GSM 8153977 工具: Illuma NovaSeq 600 战略: RNA-Seq 来源: TRARIP 选择 TRA 选择 PARED 建筑协议: 商业 RNA 简单抽取包(DP419, TIANGEN, 中国) 抽取全部 RNA 。 60毫克新鲜组织由高速同源同源同源(DHFFSTPR-32D,中国劳森) 制1 mLLL透析缓冲RZ, 以获得同源同源,然后添加三氯甲烷。 在4分钟的室温度保持4分后,混合物被离心化为12000 rmbm:

BioData: SRR28387148

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# 57: SRX10761850: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

Title: ---------------------------------------------------------

SRX10761850: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

SRX10761850: 16S RNDNA V4区域Mus muscululus测序:成年男性累积含量

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX10761850>

Submitted: ---------------------------------------------------------

China Pharmaceutical University

中国制药大学

Design: ---------------------------------------------------------

DNA extracted via phenol-Trichloromethane method, and V4 region amplified with primer of 515F and 806R, then Illumina NovaSeq 6000 used for sequencing

通过酚-三氯甲烷方法提取的DNA,以及V4区域,以515F和806R的基质放大515F和806R,然后用Illuma NovaSeq 6000来测序

Study: ---------------------------------------------------------

16S sequencing of amlodipine treated NAFLD & hypertension mice

NAFLD和高血压小鼠

Library: ---------------------------------------------------------

Library:  
Name: AB11  
Instrument: Illumina NovaSeq 6000  
Strategy: AMPLICON  
Source: GENOMIC  
Selection: PCR  
Layout: SINGLE

图书馆:名称:AB11仪器:Illuma NovaSeq 6000战略:AMPLICON 资料来源:GENMIC选择:PCR布局: SINGLE

BioData: SRR14410423

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# 58: SRX10761859: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

Title: ---------------------------------------------------------

SRX10761859: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

SRX10761859: 16S RNDNA V4区域肌肉肌肉细胞顺序:成年男性累积含量

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX10761859>

Submitted: ---------------------------------------------------------

China Pharmaceutical University

中国制药大学

Design: ---------------------------------------------------------

DNA extracted via phenol-Trichloromethane method, and V4 region amplified with primer of 515F and 806R, then Illumina NovaSeq 6000 used for sequencing

通过酚-三氯甲烷方法提取的DNA,以及V4区域,以515F和806R的基质放大515F和806R,然后用Illuma NovaSeq 6000来测序

Study: ---------------------------------------------------------

16S sequencing of amlodipine treated NAFLD & hypertension mice

NAFLD和高血压小鼠

Library: ---------------------------------------------------------

Library:  
Name: Cont6  
Instrument: Illumina NovaSeq 6000  
Strategy: AMPLICON  
Source: GENOMIC  
Selection: PCR  
Layout: SINGLE

图书馆: 名称: Cont6 仪器: Illuma NovaSeq 6000 战略: AMPLICON 资料来源: GENMIC 选择: PCR布局: SINGLE

BioData: SRR14410414

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# 59: SRX23991997: GSM8153973: ovary, L3; Huso dauricus x Acipenser schrenckii; RNA-Seq

Title: ---------------------------------------------------------

SRX23991997: GSM8153973: ovary, L3; Huso dauricus x Acipenser schrenckii; RNA-Seq

SRX23991997: GSM8153973:卵,L3;Huso dauriscus x Acipenser schrencki;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX23991997>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8153973\_r1

GSM8153973\_r1

Study: ---------------------------------------------------------

Critical gene filtration for the caviar yield of hybrid sturgeon

混合螺旋藻鱼子酱产量的关键基因过滤

Library: ---------------------------------------------------------

Library:  
Name: GSM8153973  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA simple extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in ovary tissues. 60 mg fresh tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 4 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragmentation with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that were provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (300±50 bp) was established by amplifying the target sequences.

姓名: 姓名: GSM 8153973 工具: 姓名: GSM 8153973 工具: Illuma NovaSeq 600 战略: RNA-Seq 来源: TRARIP 选择 TDNA 选择: PARED 建筑协议: 商业 RNA 简单抽取包(DP419, TIANGEN, 中国) 抽取全部 RNA 。 60毫克新鲜组织由高速同源同源同源(DHFFSTPR-32D,中国劳森) 制1 mLL 透析缓冲RZ,以获得同源同源,然后添加三氯甲烷。 在4分钟的室温度保持4分后,混合物被离心化为12000 rmbm:

BioData: SRR28387152

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# 60: SRX23991987: GSM8153963: ovary, H1; Huso dauricus x Acipenser schrenckii; RNA-Seq

Title: ---------------------------------------------------------

SRX23991987: GSM8153963: ovary, H1; Huso dauricus x Acipenser schrenckii; RNA-Seq

SRX23991987: GSM8153963:卵,H1;Huso dauriscus x Acipenser schrencki;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX23991987>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8153963\_r1

GSM8153663\_r1

Study: ---------------------------------------------------------

Critical gene filtration for the caviar yield of hybrid sturgeon

混合螺旋藻鱼子酱产量的关键基因过滤

Library: ---------------------------------------------------------

Library:  
Name: GSM8153963  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA simple extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in ovary tissues. 60 mg fresh tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 4 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragmentation with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that were provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (300±50 bp) was established by amplifying the target sequences.

姓名: 姓名: GSM 8153963 工具: 姓名: GSM 8153963 工具: Illuma NovaSeq 600 战略: RNA-Seq 来源: TRARIP 选择 TRA 选择 PARED 建筑协议: 商业 RNA 简单抽取包(DP419, TIANGEN, 中国) 抽取全部 RNA 。 60 毫克新鲜组织由高速同源同源同源(DHFFSTPR-32D,中国劳森) 制1 mLL 透析缓冲RZ, 以获得同源同源,然后添加三氯甲烷。 在4分钟的室温度保持4分后,该混合物被离心于12000 rpmm: 获得与绝对乙醇混合的水相相接合的水相相接的阶段。 RNA 被选用RNA 样本(DNETP ) 在重复离动后, RNEA 的完整号为 7.0 和 A 260 Roderemode, NA 和 Annex IMA (MER 和 NIS 具体的DNA 提供了 NIS5, 和 NIS IMT) 和 NIS 的DNA 提供了 。

BioData: SRR28387162

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# 61: SRX10761858: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

Title: ---------------------------------------------------------

SRX10761858: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

SRX10761858: 16S RNDNA V4区域肌肉肌肉细胞顺序:成年男性累积含量

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX10761858>

Submitted: ---------------------------------------------------------

China Pharmaceutical University

中国制药大学

Design: ---------------------------------------------------------

DNA extracted via phenol-Trichloromethane method, and V4 region amplified with primer of 515F and 806R, then Illumina NovaSeq 6000 used for sequencing

通过酚-三氯甲烷方法提取的DNA,以及V4区域,以515F和806R的基质放大515F和806R,然后用Illuma NovaSeq 6000来测序

Study: ---------------------------------------------------------

16S sequencing of amlodipine treated NAFLD & hypertension mice

NAFLD和高血压小鼠

Library: ---------------------------------------------------------

Library:  
Name: Cont5  
Instrument: Illumina NovaSeq 6000  
Strategy: AMPLICON  
Source: GENOMIC  
Selection: PCR  
Layout: SINGLE

图书馆: 名称: Cont5 仪器: Illuma NovaSeq 6000战略: AMPLICON 资料来源: GENMIC 选择: PCR布局: SINGLE

BioData: SRR14410415

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# 62: SRX6432726: GSM3938245: NR; Musa acuminata AAA Group; RNA-Seq

Title: ---------------------------------------------------------

SRX6432726: GSM3938245: NR; Musa acuminata AAA Group; RNA-Seq

SRX6432726:GSM3938245:NR;Musa ancuminata AAAA集团;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX6432726>

Submitted: ---------------------------------------------------------

Transcriptome analysis of banana (Musa acuminata) in response to low-nitrogen stress  
PRJNA554129 • SRP214312 • All experiments • All runs  
show Abstract

应对低氮压力PPRJNA554129 PRJNA554129 • SRRP214312 • 所有实验 • 所有运行情况显示摘要

Design: ---------------------------------------------------------

NCBI (GEO)

国家协调机构(GEO)

Study: ---------------------------------------------------------

NR

NR NR NR

Library: ---------------------------------------------------------

Library:  
Instrument: Illumina HiSeq 2000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: SINGLE  
Construction protocol: Tissues (100 mg) were placed into a precooled mortar to be ground into a powder with liquid nitrogen. The powder was collected into a precooled 2 mL Eppendorf tube with 2 mL RNase-free cetyltrimethylammonium bromide (CTAB) extracting solution, which contained 0.1% diethyl pyrocarbonate (DEPC), 2.5% CTAB, 1.4 M NaCl, 20 mM EDTA, 100 mM Tris-HCl (pH 8.0), and 4% polyvinylpyrrolidone (PVP). The tubes were then placed in a water bath at 65 °C for 30 min to induce cell lysis, and centrifuged at 13,000 rpm for 5 min at 25-28 °C. The residue was discarded, and the supernatant solution was transferred into a clean 2 mL Eppendorf tube. Trichloromethane (1 mL) was added to the supernatant solution, blended lightly, and centrifuged at 13 000 rpm for 15 min at 4 °C. The supernatant was transferred into a clean 2 mL Eppendorf tube, and this procedure was repeated once more. Subsequently, 8 M lithium chloride was added with RNase-free water to 0.6 volume of the supernatant and left overnight. The mixture was centrifuged for 30 min at 13 000 rpm and 4 °C to obtain the RNA precipitate. RNase-free ethyl alcohol (75%) was used to wash the RNA precipitate twice. Finally, RNA was dissolved in RNase-free ddH2O and stored at -80 °C until further use. Poly (A) mRNA from the total RNA was enriched by poly-T oligo-attached magnetic beads (Invitrogen), according to the manufacturer's protocol. Purified mRNA was then divided into short fragments by mixing with fragmentation buffer. The first strand cDNA was synthesized using a random hexamer primer. The buffer, dNTPs, RNase H, and DNA polymerase I were then added to the fragmented mRNA templates to synthesize the second-strand cDNA. The double-stranded cDNA was purified using magnetic beads. End repair and the addition of 3′-end single nucleotide A (adenine) were then performed. Finally, sequencing adaptors were ligated to the fragments, which were enriched by PCR amplification. During the quality control step, a 2100 Bioanalyzer (Agilent, Santa Clara, CA, USA) and a StepOnePlus Real-Time PCR System (Applied Biosystems Inc., Foster City, CA, USA) were used to qualify and quantify sequences for the sample libraries. The constructed library products were prepared for sequencing using a HiSeq 2000 system (Illumina, San Diego, CA, USA) at the Beijing Genomics Institute (BGI).

托盘(100毫克)被放置在预冷凝固的迫击炮中,成为含液态氮粉的粉末。 粉末被收集到一个2°C的预冷的2 mL Eppendorf 水槽中,2 mL Rase-无丙基甲基溴(CTAB)提取溶液中含有0.1%的二乙基丙基丙烯基丙烷(DEPC)、2.5%的丙基乙基氨基氨基氨基氢(CTB)、1.4 MCl、20 mM EDTA、100 mM Tris-Hl(PH 8.0)和4% 聚丙基醇酮(PVP)中含有1 mcion 30 mm(RS-28°C)的离心解液中含有0.13 rmtmd 。

BioData: SRR9672274

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# 63: SRX24419492: GSM8244994: gut, D30FL3; Huso dauricus; RNA-Seq

Title: ---------------------------------------------------------

SRX24419492: GSM8244994: gut, D30FL3; Huso dauricus; RNA-Seq

SRX244149492: GSM8244994:直肠,D30FL3;Huso dauriscus;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX24419492>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8244994\_r1

GSM8244994\_r1

Study: ---------------------------------------------------------

Multi-omics integration reveals the dynamic impacts of stock enhancement on the intestinal health condition in kaluga sturgeon (Huso dauricus)

多组集成表明,鱼量增强对Kaluga sturgeon(Huso dauriscus)肠胃健康状况的动态影响。

Library: ---------------------------------------------------------

Library:  
Name: GSM8244994  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA sample extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in gut tissues. 90 mg fresh intestine tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 6 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragment with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that was provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (150 bp) was established by amplifying the target sequences.

Name: 姓名: GSM8244994 资料库: GSM8244994 工具: Illumina NovaSeq 600 战略: RNA-Seq 来源: TRARIPTOMI 选择: CDNA布局: PARED 建筑协议: 商业RNA采样袋(DP419, TIANGEN, 中国) 选用腹腔组织总RNA。 90毫克新鲜肠组织由高速度同质同质器(DHFFSTPRP-32D,中国劳森) 地面 1 mLL 透析缓冲RZ, 以获得同质同质,然后添加三氯甲烷。 在房间温度为6分钟后, 混合温度为1, 2000 平米调, 以获得与绝对乙醇混合的水分相混合阶段。 RDUA 样本中的残留蛋白质杂质在RNA中被储存在RNET管中。 当RNA的完整后, 由IMO 和DNA IMO IMO IMO 和C IMO IMU IMO 和 IMO IMF IMO IMF5, 和 C IMO IMO IMF5, 然后 和 C IMO IMO IMO 提供 和 IMF IMS IMO 和 IMO IMF IMO IMF 的 的 IM IM IMF IM IM IM IM IM IM IM 的 的 IMF IM IM IMS IM IM 和 IM IM IM IM IM IMS IMS IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM 的 的 IMS IMS IMS IMS 的 IM IM IM IM IM IM IM IM IM 的 IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM IM 和

BioData: SRR28859442

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# 64: SRX4500780: RNA-seq of Bombyx mori: male fat body

Title: ---------------------------------------------------------

SRX4500780: RNA-seq of Bombyx mori: male fat body

SRX445/000780:RNA-seq of Bombyx Mori: 男性脂肪体

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX4500780>

Submitted: ---------------------------------------------------------

State Key Laboratory of Silkworm Genome Biology

丝虫基因组生物学国家关键实验室

Design: ---------------------------------------------------------

For RNA sequnencing, total RNA was extracted from fat body at different development stage respectively. 1-10mg fat body were dissected in PBS and directly transferred to Trizol (Invitrogen, USA), then grinded with liquid nitrogen. RNA was extracted again by trichloromethane, after precipitate by isopropanol and cleared by 75% ethanol, RNA samples were stored in a refrigerator at 80C for sequencing libraries. Each cDNA sample was clustered using Oligo-dT magnetic beads and then sequenced on the HiSeq2000 (Illumina, USA) platform using Single-read techology. All of the Raw data presented in this study have been deposited in the NCBI Short Read Archive (http://www.ncbi.nlm.nih.gov/sra/) under SRA accession number

在RNA后续阶段,在不同的开发阶段分别从脂肪体中提取了全部RNA。1至10毫克的脂肪体在PBS中解剖,直接转移到Trizol(美国,Invitrogen),然后用液氮研磨。RNA再次由三氯甲烷提取,经过异丙醇的沉淀并用75%的乙醇清除后,RNA样品被储存在冰箱中,储存在80C用于测序的图书馆中。每一份cDNA样本都使用Oligo-dT磁珠进行集成,然后在Hiseq2000(美国,Illuma)平台上用单读技术学进行测序。本研究中提供的所有原始数据都存放在CBCI短期阅读档案馆(http://www.ncbi.nlm.nih.gov/sra/)的加入号之下。

Study: ---------------------------------------------------------

RNA-seq of Bombyx mori: male fat body

RNA-Seq of Bombyx Mori: 男性脂肪体

Library: ---------------------------------------------------------

Library:  
Name: L5D3\_rep1  
Instrument: Illumina HiSeq 2000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: PCR  
Layout: SINGLE

图书馆: 名称: L5D3\_rep1 仪器: Illuma Hiseq 2000 战略: RNA-Seq 来源: TRARIPTOMI 选择: PCR布局: SINGLE

BioData: SRR7637245

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# 65: SRX10761861: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

Title: ---------------------------------------------------------

SRX10761861: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

SRX10761861: 16S RNDNA V4区域肌肉肌肉细胞顺序:成年男性累积含量

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX10761861>

Submitted: ---------------------------------------------------------

China Pharmaceutical University

中国制药大学

Design: ---------------------------------------------------------

DNA extracted via phenol-Trichloromethane method, and V4 region amplified with primer of 515F and 806R, then Illumina NovaSeq 6000 used for sequencing

通过酚-三氯甲烷方法提取的DNA,以及V4区域,以515F和806R的基质放大515F和806R,然后用Illuma NovaSeq 6000来测序

Study: ---------------------------------------------------------

16S sequencing of amlodipine treated NAFLD & hypertension mice

NAFLD和高血压小鼠

Library: ---------------------------------------------------------

Library:  
Name: AA15  
Instrument: Illumina NovaSeq 6000  
Strategy: AMPLICON  
Source: GENOMIC  
Selection: PCR  
Layout: SINGLE

图书馆:名称:AA15仪器:Illuma NovaSeq 6000战略:AMPLICON 资料来源:GENMIC选择:PCR布局: SINGLE

BioData: SRR14410412

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# 66: SRX24419486: GSM8244988: gut, Ori3; Huso dauricus; RNA-Seq

Title: ---------------------------------------------------------

SRX24419486: GSM8244988: gut, Ori3; Huso dauricus; RNA-Seq

SRX244149486: GSM8244988:直肠,Ori3;Huso dauriscus;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX24419486>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8244988\_r1

GSM8244988\_r1

Study: ---------------------------------------------------------

Multi-omics integration reveals the dynamic impacts of stock enhancement on the intestinal health condition in kaluga sturgeon (Huso dauricus)

多组集成表明,鱼量增强对Kaluga sturgeon(Huso dauriscus)肠胃健康状况的动态影响。

Library: ---------------------------------------------------------

Library:  
Name: GSM8244988  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA sample extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in gut tissues. 90 mg fresh intestine tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 6 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragment with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that was provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (150 bp) was established by amplifying the target sequences.

Name: 姓名: GSM8244988 资料库: GSM 8244988 工具: Illuma NovaSeq 600 战略: RNA-Seq 来源: TRARIPTOMI 选择: CDNA布局: PARED 建筑协议: 商业 RNA 样本提取包(DP419, TIANGEN, 中国) 抽取腹腔组织中的全部RNA。 90毫克新鲜肠组织由高速同源同源同源(DHFFSTPRP-32D, 中国劳森) , 1 mLL 透析缓冲RZ 以获得同源,然后添加三氯甲烷。 在室内温度为6分钟后,调离心的混合物在1200平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平。

BioData: SRR28859446

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# 67: SRX10761847: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

Title: ---------------------------------------------------------

SRX10761847: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

SRX10761847: 16S RNDNA V4区域肌肉肌肉细胞顺序:成年男性累积含量

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX10761847>

Submitted: ---------------------------------------------------------

China Pharmaceutical University

中国制药大学

Design: ---------------------------------------------------------

DNA extracted via phenol-Trichloromethane method, and V4 region amplified with primer of 515F and 806R, then Illumina NovaSeq 6000 used for sequencing

通过酚-三氯甲烷方法提取的DNA,以及V4区域,以515F和806R的基质放大515F和806R,然后用Illuma NovaSeq 6000来测序

Study: ---------------------------------------------------------

16S sequencing of amlodipine treated NAFLD & hypertension mice

NAFLD和高血压小鼠

Library: ---------------------------------------------------------

Library:  
Name: AA20  
Instrument: Illumina NovaSeq 6000  
Strategy: AMPLICON  
Source: GENOMIC  
Selection: PCR  
Layout: SINGLE

图书馆:名称:AA20仪器:Illuma NovaSeq 6000战略:AMPLICON 资料来源:GENMIC选择:PCR布局: SINGLE

BioData: SRR14410426

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# 68: SRX10761849: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

Title: ---------------------------------------------------------

SRX10761849: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

SRX10761849: 16S RNDNA V4区域肌肉肌肉细胞顺序:成年男性累积含量

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX10761849>

Submitted: ---------------------------------------------------------

China Pharmaceutical University

中国制药大学

Design: ---------------------------------------------------------

DNA extracted via phenol-Trichloromethane method, and V4 region amplified with primer of 515F and 806R, then Illumina NovaSeq 6000 used for sequencing

通过酚-三氯甲烷方法提取的DNA,以及V4区域,以515F和806R的基质放大515F和806R,然后用Illuma NovaSeq 6000来测序

Study: ---------------------------------------------------------

16S sequencing of amlodipine treated NAFLD & hypertension mice

NAFLD和高血压小鼠

Library: ---------------------------------------------------------

Library:  
Name: AB10  
Instrument: Illumina NovaSeq 6000  
Strategy: AMPLICON  
Source: GENOMIC  
Selection: PCR  
Layout: SINGLE

图书馆:名称:AB10仪器:Illuma NovaSeq 6000战略:AMPLICON 资料来源:GENMIC选择:PCR布局: SINGLE

BioData: SRR14410424

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# 69: ERX645742: Illumina Genome Analyzer II sequencing; Deregulation of PPAR-beta/delta target genes in tumor-associated macrophages by fatty acid ligands in the ovarian cancer microenvironment - RNAseq

Title: ---------------------------------------------------------

ERX645742: Illumina Genome Analyzer II sequencing; Deregulation of PPAR-beta/delta target genes in tumor-associated macrophages by fatty acid ligands in the ovarian cancer microenvironment - RNAseq

ERX645742: IRX645742: II 光素基因组分析分析仪的排序; 对卵巢癌微环境中脂肪酸皮条动物在肿瘤相关巨形中的PPPAR-beta/delta目标基因进行调控-RNAseq

Link:

<https://www.ncbi.nlm.nih.gov/sra/ERX645742>

Submitted: ---------------------------------------------------------

Institute for molecular and tumor biology Philipps University Marburg Germany (Institute for molecular and tumor biology Philipps)

德国马尔堡大学分子和肿瘤生物学研究所(分子和肿瘤生物学研究所)

Design: ---------------------------------------------------------

Deregulation of PPAR-beta/delta target genes in tumor-associated macrophages by fatty acid ligands in the ovarian cancer microenvironment - RNAseq

在卵巢癌微环境中,脂肪酸皮条动物在肿瘤相关大型基因中解管PPAR-beta/delta目标基因 -- -- RNAseq

Study: ---------------------------------------------------------

Deregulation of PPAR-beta/delta target genes in tumor-associated macrophages by fatty acid ligands in the ovarian cancer microenvironment - RNAseq

在卵巢癌微环境中,脂肪酸皮条动物在肿瘤相关大型基因中解管PPAR-beta/delta目标基因 -- -- RNAseq

Library: ---------------------------------------------------------

Library:  
Name: ST003  
Instrument: Illumina Genome Analyzer II  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: RANDOM  
Layout: SINGLE  
Construction protocol: Ascites was collected from 30 patients with high-grade serous ovarian carcinoma undergoing primary surgery at the University Hospital in Marburg. Informed consent was obtained from all patients according to the protocols approved by the local ethical committe Cells were isolated on June 06th 2013 from healthy human donor blood of unknown gender via LSM1077 gradient centrifugation. Adherent cells were positively selected on primaria 6 well dishes (3x10^6 monocytes per well in 2 ml PBS (PAA)) followed by 6 washing steps with PBS. Finally the monocytes were cultured for 6d in humidified incubator at 37 degrees C, 5 % CO2 in 2ml RPMI medium supplemented with 10 % FCS (both PAA). Cells were treated with control (DMSO), L165 1 uM final concentration or ST247 300 nM final concentration for 1d. Cells were washed with PBS, supernatant was removed completly, then 1 ml of peqGOLD TriFast (PEQLAB) was added to each well and transfered to a 1,5 ml Eppi. Following 5 min of incubation at RT 200 ul trichloromethane were added to the solution. The probes were mixed thoroughly every 3 minutes during a 10 minute incubation at RT. Probes were centrifuged at 13.000 g for 15 min at 4 degrees C then the aquouse top phase was transfered to a new eppi containing 600 ul of ice cold 2-propanol. Probes were mixed and centrifuged for 10 min at 13.000 g, 4 degrees C. The supernatant was removed and the pelleted RNA was washed twice with 75 % Ethanol for 5 minutes at 13.000 g, 4 degrees C. The pellet was dried and dissolved in 15 ul of RNase free water following quality control using Xcalibur (Thermo scientific). Libraries were created using the Illumina Truseq mRNA kit used according to the manufacturer's instructions.

图书馆: 姓名: ST003 工具: ST003 所有病人根据当地道德承诺小组批准的协议于2013年6月从通过 LSM 1077 梯度离心机进行的健康人体捐赠者血液中分离出。 来源: TRANSRIPTOMI 选择: RANDOM 配置: SINGLE 构建协议: 30名在马尔堡大学医院进行初级手术的高等级雌性卵巢癌患者收集了Ascites。 根据当地道德承诺小组批准的协议,所有病人均于2013年6月通过 LSMPO 1077 梯度离心机法,从健康的人体捐献者血液中分离出未知性别。 在灵敏6 盘( 3x10+6) 盘中积极选择了适应细胞; 在 2 mBBS (PA) 上方2 m) 盘中,在2 mBS(PBA) 上层温度2 0; 在1 电离心机中,在1 将1 的电解离心器中,在1 5 5-LL 流中,在5 流电流中将1 和1 流电流流中将1 流电解一个15 。

BioData: ERR701478

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# 70: SRX23991995: GSM8153971: ovary, L1; Huso dauricus x Acipenser schrenckii; RNA-Seq

Title: ---------------------------------------------------------

SRX23991995: GSM8153971: ovary, L1; Huso dauricus x Acipenser schrenckii; RNA-Seq

SRX23991995: GSM8153971:卵,L1;Huso dauriscus x Acipenser schrencki;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX23991995>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8153971\_r1

GSM81535971\_r1

Study: ---------------------------------------------------------

Critical gene filtration for the caviar yield of hybrid sturgeon

混合螺旋藻鱼子酱产量的关键基因过滤

Library: ---------------------------------------------------------

Library:  
Name: GSM8153971  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA simple extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in ovary tissues. 60 mg fresh tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 4 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragmentation with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that were provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (300±50 bp) was established by amplifying the target sequences.

姓名: 姓名: GSM 8153971 工具: GSM 8153971 工具: GSM 8153971 工具: Illumina NovaSeq 600 战略: RNA-Sequa 来源: TATNA 选择了 TARED 建筑协议: 商业 RNA 简单提取包(DP 419, TIANGEN, 中国) 抽取全部 RNA 。 60毫克新鲜组织由高速同源同源同源(DHFFSTPRP-32D, 中国) 使用 1 mLL 透析缓冲RZ, 以获得同源同值同值同值同值,然后添加三氯甲烷。 在室内温度4分钟保持4分后, 将混合物调离心于12000 平点, 以获得与乙醇绝对酒精混合的水相混合的水相相接的水相接合的阶段。 RDU方案用于消除RNA 样本中的残留的蛋白质。

BioData: SRR28387154

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# 71: SRX9177116: GSM4799941: active\_ALKBH5\_dox\_plus\_ip2; Homo sapiens; OTHER

Title: ---------------------------------------------------------

SRX9177116: GSM4799941: active\_ALKBH5\_dox\_plus\_ip2; Homo sapiens; OTHER

SRX91777116: GSM47999941: 活性 \_ALKBH5\_dox\_plus\_ip2; 智人; 其他

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX9177116>

Submitted: ---------------------------------------------------------

Targeted RNA N6-Methyladenosine Demethylation Controls Cell Fate Transition in Human Pluripotent Stem Cells  
PRJNA665206 • SRP285100 • All experiments • All runs  
show Abstract

RNA N6-M6-MEVEDEnessine脱甲基化控制细胞在人类多能细胞中发生转变的情况 PRJNA665206 PRJNA665206 PRJNA665206 • SRP285100 • 所有实验 全部运行 显示摘要

Design: ---------------------------------------------------------

NCBI (GEO)

国家协调机构(GEO)

Study: ---------------------------------------------------------

active\_ALKBH5\_dox\_plus\_ip2

活动(\_ALKBH5\_dox\_plus\_ip2)

Library: ---------------------------------------------------------

Library:  
Instrument: HiSeq X Ten  
Strategy: OTHER  
Source: TRANSCRIPTOMIC  
Selection: other  
Layout: PAIRED  
Construction protocol: Cells were washed with PBS and lysed with TRIzol (Thermo Fisher Scientific). Then trichloromethane (Guangzhou Chemical Reagent Factory) was used to extract the total RNA from the TRIzol lysate. Isopropanol (Sangon Biotech) was used to precipitates RNA from the mixture. mRNA was separated from the total RNA by using the Dynabeads™ mRNA Purification Kit (Thermo Fisher Scientific) according to the manufacturer's protocol. The m6A immunoprecipitation method was the same as above. Input samples and IP samples were applied for NGS library construction by using the NEBNext® Ultra II Directional RNA Library Prep (NEB) according to the manufacturer's guide. The adaptor ligated DNAs amplified by PCR for 15 cycles were sequenced on the HiSeqX sequencing platform.

资料库:仪器:HiSeq X 10战略:其他来源: TRARIPTOMIC选择:其他布局:PARED建筑协议:细胞用PBS冲洗,用TRIZOL(热水生科学)浸透,然后使用三氯甲烷(广州化学试剂厂)从TRIZOL液酸盐中提取总RNA。使用SOSOPAN醇(桑贡生物科技)从混合物中分离出RNA。MRNA根据制造商协议使用DynabadsTM mRNA净化工具包(热水生科学)与总RNA分离。M6A免疫喷洒方法与上述相同。根据制造商指南,在NEBNBNEXT Ulttra II定向RNA图书馆前p(NEB)对NGS图书馆的建设应用输入样品和IP样品。根据厂商指南,在HISECECECX测序平台上按15个周期放大的调控DNA顺序排列。

BioData: SRR12697493

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# 72: SRX4500786: RNA-seq of Bombyx mori: male fat body

Title: ---------------------------------------------------------

SRX4500786: RNA-seq of Bombyx mori: male fat body

SRX4450000786:RNA-seq of Bombyx Mori: 男性脂肪体

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX4500786>

Submitted: ---------------------------------------------------------

State Key Laboratory of Silkworm Genome Biology

丝虫基因组生物学国家关键实验室

Design: ---------------------------------------------------------

For RNA sequnencing, total RNA was extracted from fat body at different development stage respectively. 1-16mg fat body were dissected in PBS and directly transferred to Trizol (Invitrogen, USA), then grinded with liquid nitrogen. RNA was extracted again trichloromethane, after precipitate by isopropanol and cleared by 75% ethanol, RNA samples were stored in a refrigerator at 80C for sequencing libraries. Each cDNA sample was clustered using Oligo-dT magnetic beads and then sequenced on the HiSeq2000 (Illumina, USA) platform using Single-read techology. All of the Raw data presented in this study have been deposited in the NCBI Short Read Archive (http://www.ncbi.nlm.nih.gov/sra/) under SRA accession number

在RNA后续阶段,在不同的开发阶段分别从脂肪体中提取了全部RNA。 1-16毫克的脂肪体在PBS中解剖,直接转移到Trizol(美国,Invitrogen),然后用液氮研磨。RNA在异丙醇沉淀后再次提取三氯甲烷,并用75%的乙醇清除。RNA样品储存在冰箱中,储存在80C用于测序的图书馆中。每个cDNA样本都使用Oligo-dT磁珠进行集成,然后在Hiseq2000(美国,Illumina)平台上用单读技术学进行测序。本研究中提供的所有原始数据都存放在CBCI短期阅读档案库中(http://www.ncbi.nlm.nih.gov/sra/),根据SRA的加入号。

Study: ---------------------------------------------------------

RNA-seq of Bombyx mori: male fat body

RNA-Seq of Bombyx Mori: 男性脂肪体

Library: ---------------------------------------------------------

Library:  
Name: P0\_rep1  
Instrument: Illumina HiSeq 2000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: PCR  
Layout: SINGLE

图书馆: 名称: P0\_rep1 仪器: Illuma Hiseq 2000 战略: RNA-Seq 来源: TRARIPTOMI 选择: PCR布局: SINGLE

BioData: SRR7637239

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# 73: SRX24419490: GSM8244992: gut, D30FL1; Huso dauricus; RNA-Seq

Title: ---------------------------------------------------------

SRX24419490: GSM8244992: gut, D30FL1; Huso dauricus; RNA-Seq

SRX244149490:GSM8244992:肠道,D30FL1;Huso dauriscus;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX24419490>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8244992\_r1

GSM8244992\_r1

Study: ---------------------------------------------------------

Multi-omics integration reveals the dynamic impacts of stock enhancement on the intestinal health condition in kaluga sturgeon (Huso dauricus)

多组集成表明,鱼量增强对Kaluga sturgeon(Huso dauriscus)肠胃健康状况的动态影响。

Library: ---------------------------------------------------------

Library:  
Name: GSM8244992  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA sample extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in gut tissues. 90 mg fresh intestine tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 6 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragment with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that was provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (150 bp) was established by amplifying the target sequences.

Name: 姓名: GSM8244992 工具: GSM 824992 工具: Illuma NovaSeq 600 战略: RNA-Seq 来源: TRARIPTOMI 选择: CDNA布局: PARED 建筑协议: 商业RNA样本提取包(DP 419, TIANGEN, 中国) 抽取胃组织中的全部RNA。 90毫克新鲜肠组织由高速同源同源同源(DHFFSTPRP-32D,中国劳森) 使用 1 mLL 透析缓冲RZ, 以获得同源, 然后添加三氯甲烷。 在室内温度为6分钟的温度为6分之一后, 将混合物调离心于1 2000 rpmbm: 获得与乙醇完全混合的水相吸附的水阶段。 RDA 用于消除RNA 样本中的残留蛋白质杂质性。 RNA 在RNA 之后, 以 INA II 和 NEO IMO IMO IMO 和 NEX IMO 向 提供了 和 NSA 基 的DNA IMO 的DNA 的DNA 的DNA , 的 和 和 和 NFER 基 提供了 的 和 NFER 的DNA 和 NF 基 的 的 。

BioData: SRR28859448

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# 74: SRX9177114: GSM4799938: active\_ALKBH5\_dox\_plus\_input2; Homo sapiens; OTHER

Title: ---------------------------------------------------------

SRX9177114: GSM4799938: active\_ALKBH5\_dox\_plus\_input2; Homo sapiens; OTHER

SRX91777114: GSM4799938: 活性\_ ALKBH5\_dox\_plus\_input2; 智人; 其他

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX9177114>

Submitted: ---------------------------------------------------------

Targeted RNA N6-Methyladenosine Demethylation Controls Cell Fate Transition in Human Pluripotent Stem Cells  
PRJNA665206 • SRP285100 • All experiments • All runs  
show Abstract

RNA N6-M6-MEVEDEnessine脱甲基化控制细胞在人类多能细胞中发生转变的情况 PRJNA665206 PRJNA665206 PRJNA665206 • SRP285100 • 所有实验 全部运行 显示摘要

Design: ---------------------------------------------------------

NCBI (GEO)

国家协调机构(GEO)

Study: ---------------------------------------------------------

GEO accession GSM4799938 is currently private and is scheduled to be released on Sep 01, 2022.

GSM4799938目前是私营的,定于2022年9月1日发布。

Library: ---------------------------------------------------------

Library:  
Instrument: HiSeq X Ten  
Strategy: OTHER  
Source: TRANSCRIPTOMIC  
Selection: other  
Layout: PAIRED  
Construction protocol: Cells were washed with PBS and lysed with TRIzol (Thermo Fisher Scientific). Then trichloromethane (Guangzhou Chemical Reagent Factory) was used to extract the total RNA from the TRIzol lysate. Isopropanol (Sangon Biotech) was used to precipitates RNA from the mixture. mRNA was separated from the total RNA by using the Dynabeads™ mRNA Purification Kit (Thermo Fisher Scientific) according to the manufacturer's protocol. The m6A immunoprecipitation method was the same as above. Input samples and IP samples were applied for NGS library construction by using the NEBNext® Ultra II Directional RNA Library Prep (NEB) according to the manufacturer's guide. The adaptor ligated DNAs amplified by PCR for 15 cycles were sequenced on the HiSeqX sequencing platform.

资料库:仪器:HiSeq X 10战略:其他来源: TRARIPTOMIC选择:其他布局:PARED建筑协议:细胞用PBS冲洗,用TRIZOL(热水生科学)浸透,然后使用三氯甲烷(广州化学试剂厂)从TRIZOL液酸盐中提取总RNA。使用SOSOPAN醇(桑贡生物科技)从混合物中分离出RNA。MRNA根据制造商协议使用DynabadsTM mRNA净化工具包(热水生科学)与总RNA分离。M6A免疫喷洒方法与上述相同。根据制造商指南,在NEBNBNEXT Ulttra II定向RNA图书馆前p(NEB)对NGS图书馆的建设应用输入样品和IP样品。根据厂商指南,在HISECECECX测序平台上按15个周期放大的调控DNA顺序排列。

BioData: SRR12697491

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# 75: SRX10761848: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

Title: ---------------------------------------------------------

SRX10761848: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

SRX10761848: 16S RNDNA V4区域肌肉肌肉细胞顺序:成年男性累积含量

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX10761848>

Submitted: ---------------------------------------------------------

China Pharmaceutical University

中国制药大学

Design: ---------------------------------------------------------

DNA extracted via phenol-Trichloromethane method, and V4 region amplified with primer of 515F and 806R, then Illumina NovaSeq 6000 used for sequencing

通过酚-三氯甲烷方法提取的DNA,以及V4区域,以515F和806R的基质放大515F和806R,然后用Illuma NovaSeq 6000来测序

Study: ---------------------------------------------------------

16S sequencing of amlodipine treated NAFLD & hypertension mice

NAFLD和高血压小鼠

Library: ---------------------------------------------------------

Library:  
Name: AA21  
Instrument: Illumina NovaSeq 6000  
Strategy: AMPLICON  
Source: GENOMIC  
Selection: PCR  
Layout: SINGLE

图书馆:名称:AA21仪器:Illuma NovaSeq 6000战略:AMPLICON 资料来源:GENMIC选择:PCR布局: SINGLE

BioData: SRR14410425

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# 76: SRX10761856: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

Title: ---------------------------------------------------------

SRX10761856: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

SRX10761856: 16S RNDNA V4区域肌肉肌肉细胞顺序:成年男性累积含量

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX10761856>

Submitted: ---------------------------------------------------------

China Pharmaceutical University

中国制药大学

Design: ---------------------------------------------------------

DNA extracted via phenol-Trichloromethane method, and V4 region amplified with primer of 515F and 806R, then Illumina NovaSeq 6000 used for sequencing

通过酚-三氯甲烷方法提取的DNA,以及V4区域,以515F和806R的基质放大515F和806R,然后用Illuma NovaSeq 6000来测序

Study: ---------------------------------------------------------

16S sequencing of amlodipine treated NAFLD & hypertension mice

NAFLD和高血压小鼠

Library: ---------------------------------------------------------

Library:  
Name: AB9  
Instrument: Illumina NovaSeq 6000  
Strategy: AMPLICON  
Source: GENOMIC  
Selection: PCR  
Layout: SINGLE

图书馆:名称:AB9仪器:Illuma NovaSeq 6000战略:AMPLICON 资料来源:GENMIC选择:PCR布局: SINGLE

BioData: SRR14410417

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# 77: SRX6432724: GSM3938243: NL; Musa acuminata AAA Group; RNA-Seq

Title: ---------------------------------------------------------

SRX6432724: GSM3938243: NL; Musa acuminata AAA Group; RNA-Seq

SRX6432724: GSM3938243: NL; Musa acuminata AAAA集团; RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX6432724>

Submitted: ---------------------------------------------------------

Transcriptome analysis of banana (Musa acuminata) in response to low-nitrogen stress  
PRJNA554129 • SRP214312 • All experiments • All runs  
show Abstract

应对低氮压力PPRJNA554129 PRJNA554129 • SRRP214312 • 所有实验 • 所有运行情况显示摘要

Design: ---------------------------------------------------------

NCBI (GEO)

国家协调机构(GEO)

Study: ---------------------------------------------------------

NL

无

Library: ---------------------------------------------------------

Library:  
Instrument: Illumina HiSeq 2000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: SINGLE  
Construction protocol: Tissues (100 mg) were placed into a precooled mortar to be ground into a powder with liquid nitrogen. The powder was collected into a precooled 2 mL Eppendorf tube with 2 mL RNase-free cetyltrimethylammonium bromide (CTAB) extracting solution, which contained 0.1% diethyl pyrocarbonate (DEPC), 2.5% CTAB, 1.4 M NaCl, 20 mM EDTA, 100 mM Tris-HCl (pH 8.0), and 4% polyvinylpyrrolidone (PVP). The tubes were then placed in a water bath at 65 °C for 30 min to induce cell lysis, and centrifuged at 13,000 rpm for 5 min at 25-28 °C. The residue was discarded, and the supernatant solution was transferred into a clean 2 mL Eppendorf tube. Trichloromethane (1 mL) was added to the supernatant solution, blended lightly, and centrifuged at 13 000 rpm for 15 min at 4 °C. The supernatant was transferred into a clean 2 mL Eppendorf tube, and this procedure was repeated once more. Subsequently, 8 M lithium chloride was added with RNase-free water to 0.6 volume of the supernatant and left overnight. The mixture was centrifuged for 30 min at 13 000 rpm and 4 °C to obtain the RNA precipitate. RNase-free ethyl alcohol (75%) was used to wash the RNA precipitate twice. Finally, RNA was dissolved in RNase-free ddH2O and stored at -80 °C until further use. Poly (A) mRNA from the total RNA was enriched by poly-T oligo-attached magnetic beads (Invitrogen), according to the manufacturer's protocol. Purified mRNA was then divided into short fragments by mixing with fragmentation buffer. The first strand cDNA was synthesized using a random hexamer primer. The buffer, dNTPs, RNase H, and DNA polymerase I were then added to the fragmented mRNA templates to synthesize the second-strand cDNA. The double-stranded cDNA was purified using magnetic beads. End repair and the addition of 3′-end single nucleotide A (adenine) were then performed. Finally, sequencing adaptors were ligated to the fragments, which were enriched by PCR amplification. During the quality control step, a 2100 Bioanalyzer (Agilent, Santa Clara, CA, USA) and a StepOnePlus Real-Time PCR System (Applied Biosystems Inc., Foster City, CA, USA) were used to qualify and quantify sequences for the sample libraries. The constructed library products were prepared for sequencing using a HiSeq 2000 system (Illumina, San Diego, CA, USA) at the Beijing Genomics Institute (BGI).

托盘(100毫克)被放置在预冷凝固的迫击炮中,成为含液态氮粉的粉末。 粉末被收集到一个2°C的预冷的2 mL Eppendorf 水槽中,2 mL Rase-无丙基甲基溴(CTAB)提取溶液中含有0.1%的二乙基丙基丙烯基丙烷(DEPC)、2.5%的丙基乙基氨基氨基氨基氢(CTB)、1.4 MCl、20 mM EDTA、100 mM Tris-Hl(PH 8.0)和4% 聚丙基醇酮(PVP)中含有1 mcion 30 mm(RS-28°C)的离心解液中含有0.13 rmtmd 。

BioData: SRR9672272

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# 78: SRX9177111: GSM4799935: active\_ALKBH5\_dox\_minus\_ip1; Homo sapiens; OTHER

Title: ---------------------------------------------------------

SRX9177111: GSM4799935: active\_ALKBH5\_dox\_minus\_ip1; Homo sapiens; OTHER

SRX91777111: GSM47999935: 活性\_ ALKBH5\_dox\_minus\_ip1; 智人; 其他

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX9177111>

Submitted: ---------------------------------------------------------

Targeted RNA N6-Methyladenosine Demethylation Controls Cell Fate Transition in Human Pluripotent Stem Cells  
PRJNA665206 • SRP285100 • All experiments • All runs  
show Abstract

RNA N6-M6-MEVEDEnessine脱甲基化控制细胞在人类多能细胞中发生转变的情况 PRJNA665206 PRJNA665206 PRJNA665206 • SRP285100 • 所有实验 全部运行 显示摘要

Design: ---------------------------------------------------------

NCBI (GEO)

国家协调机构(GEO)

Study: ---------------------------------------------------------

GEO accession GSM4799935 is currently private and is scheduled to be released on Sep 01, 2022.

GSM4799935目前是私营的,定于2022年9月1日发布。

Library: ---------------------------------------------------------

Library:  
Instrument: HiSeq X Ten  
Strategy: OTHER  
Source: TRANSCRIPTOMIC  
Selection: other  
Layout: PAIRED  
Construction protocol: Cells were washed with PBS and lysed with TRIzol (Thermo Fisher Scientific). Then trichloromethane (Guangzhou Chemical Reagent Factory) was used to extract the total RNA from the TRIzol lysate. Isopropanol (Sangon Biotech) was used to precipitates RNA from the mixture. mRNA was separated from the total RNA by using the Dynabeads™ mRNA Purification Kit (Thermo Fisher Scientific) according to the manufacturer's protocol. The m6A immunoprecipitation method was the same as above. Input samples and IP samples were applied for NGS library construction by using the NEBNext® Ultra II Directional RNA Library Prep (NEB) according to the manufacturer's guide. The adaptor ligated DNAs amplified by PCR for 15 cycles were sequenced on the HiSeqX sequencing platform.

资料库:仪器:HiSeq X 10战略:其他来源: TRARIPTOMIC选择:其他布局:PARED建筑协议:细胞用PBS冲洗,用TRIZOL(热水生科学)浸透,然后使用三氯甲烷(广州化学试剂厂)从TRIZOL液酸盐中提取总RNA。使用SOSOPAN醇(桑贡生物科技)从混合物中分离出RNA。MRNA根据制造商协议使用DynabadsTM mRNA净化工具包(热水生科学)与总RNA分离。M6A免疫喷洒方法与上述相同。根据制造商指南,在NEBNBNEXT Ulttra II定向RNA图书馆前p(NEB)对NGS图书馆的建设应用输入样品和IP样品。根据厂商指南,在HISECECECX测序平台上按15个周期放大的调控DNA顺序排列。

BioData: SRR12697488

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# 79: SRX4680922: GSM3389638: Diseased D3; Hylocereus polyrhizus; RNA-Seq

Title: ---------------------------------------------------------

SRX4680922: GSM3389638: Diseased D3; Hylocereus polyrhizus; RNA-Seq

SRX4680922: GSM3389638: 疾病D3; Hylocerephenus 聚氨酯; RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX4680922>

Submitted: ---------------------------------------------------------

Transcriptomic de novo analysis of pitaya (Hylocereus polyrhizus) canker disease caused by Neoscytalidium dimidiatum  
PRJNA490886 • SRP161778 • All experiments • All runs  
show Abstract

• 全部实验 全部运行显示摘要

Design: ---------------------------------------------------------

NCBI (GEO)

国家协调机构(GEO)

Study: ---------------------------------------------------------

Diseased D3

疾病D3

Library: ---------------------------------------------------------

Library:  
Instrument: Illumina HiSeq 2000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Tissues (100 mg) were placed into a precooled mortar to be ground into a powder with liquid nitrogen. The ground stem powder was collected into a precooled 2 mL Eppendorf tube with 2 mL RNase-free cetyltrimethylammonium bromide (CTAB) extracting solution, which contained 0.1% diethyl pyrocarbonate (DEPC), 2.5% CTAB, 1.4 M NaCl, 20 mM EDTA, 100 mM Tris-HCl (pH 8.0), and 4% polyvinylpyrrolidone (PVP). The tubes were then placed in a water bath at 65 °C for 30 min to induce cell lysis, and centrifuged at 13,000 rpm for 5 min at 25-28 °C. The residue was discarded, and the supernatant solution was transferred into a clean 2 mL Eppendorf tube. Trichloromethane (1 mL) was added to the supernatant solution, blended lightly, and centrifuged at 13 000 rpm for 15 min at 4 °C. The supernatant was transferred into a clean 2 mL Eppendorf tube, and this procedure was repeated once more. Subsequently, 8 M lithium chloride was added with RNase-free water to 0.6 volume of the supernatant and left overnight. The mixture was centrifuged for 30 min at 13 000 rpm and 4 °C to obtain the RNA precipitate. RNase-free ethyl alcohol (75%) was used to wash the RNA precipitate twice. Finally, RNA was dissolved in RNase-free ddH2O and stored at -80 °C until further use. Poly (A) mRNA from the total RNA was enriched by poly-T oligo-attached magnetic beads (Invitrogen), according to the manufacturer's protocol. Purified mRNA was then divided into short fragments by mixing with fragmentation buffer. The first strand cDNA was synthesized using a random hexamer primer. The buffer, dNTPs, RNase H, and DNA polymerase I were then added to the fragmented mRNA templates to synthesize the second-strand cDNA. The double-stranded cDNA was purified using magnetic beads. End repair and the addition of 3′-end single nucleotide A (adenine) were then performed. Finally, sequencing adaptors were ligated to the fragments, which were enriched by PCR amplification. During the quality control step, a 2100 Bioanalyzer (Agilent, Santa Clara, CA, USA) and a StepOnePlus Real-Time PCR System (Applied Biosystems Inc., Foster City, CA, USA) were used to qualify and quantify sequences for the sample libraries. The constructed library products were prepared for sequencing using a HiSeq 2000 system (Illumina, San Diego, CA, USA) at the Beijing Genomics Institute (BGI).

托盘(100毫克)被放置在预冷凝固的迫击炮中,成为含液态氮粉的粉末。 地面干粉被收集到一个2°C的预冷2 mL Eppendorf 水槽中,2 mL Rase-无碳基甲基溴(CTAB)提取溶液中含有0.1% dili-rock-cyrocolate(DEPC),2.5% 碳- 碳- 碳(CTAB), 1.4 MNCl, 20 mMEDTA, 100 mm Tris-Hlors(p 8.0 毫克) 和 4% 聚氨醇(PVP) 。 地面干粉在65 °C 水槽中被收集了30 分钟来诱导细胞分解, 在25- 28 °C 解析时, 离心器被丢弃, 超级液溶液被转移到了2 mmL Eppendrod-nal- demodal O.

BioData: SRR7829959

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# 80: SRX24419488: GSM8244990: gut, D14FL2; Huso dauricus; RNA-Seq

Title: ---------------------------------------------------------

SRX24419488: GSM8244990: gut, D14FL2; Huso dauricus; RNA-Seq

SRX244149488: GSM8244990:肠道,D14FL2;Huso dauriscus;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX24419488>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8244990\_r1

GSM8244990\_r1

Study: ---------------------------------------------------------

Multi-omics integration reveals the dynamic impacts of stock enhancement on the intestinal health condition in kaluga sturgeon (Huso dauricus)

多组集成表明,鱼量增强对Kaluga sturgeon(Huso dauriscus)肠胃健康状况的动态影响。

Library: ---------------------------------------------------------

Library:  
Name: GSM8244990  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA sample extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in gut tissues. 90 mg fresh intestine tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 6 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragment with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that was provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (150 bp) was established by amplifying the target sequences.

Name: 姓名: GSM8244990 工具: GSM 8244990 工具: Illumina NovaSeq 600 战略: RNA-Seq 来源: TRARIPTOMI 选择: CDNA布局: PARED 建筑协议: 商业 RNA 样本提取包(DP419, TIANGEN, 中国) 抽取胃组织中的全部RNA。 90毫克新鲜肠组织由高速同源同源同源(DHFFSTPRP-32D, 中国劳森) , 1 mLL 透析缓冲RZ 以获得同源,然后添加三氯甲烷。 在室内温度为6分钟后,调离心的混合物在1200平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平方平。

BioData: SRR28859447

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# 81: SRX10761852: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

Title: ---------------------------------------------------------

SRX10761852: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

SRX10761852: 16S RNDNA V4区域肌肉肌肉细胞顺序:成年男性累积含量

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX10761852>

Submitted: ---------------------------------------------------------

China Pharmaceutical University

中国制药大学

Design: ---------------------------------------------------------

DNA extracted via phenol-Trichloromethane method, and V4 region amplified with primer of 515F and 806R, then Illumina NovaSeq 6000 used for sequencing

通过酚-三氯甲烷方法提取的DNA,以及V4区域,以515F和806R的基质放大515F和806R,然后用Illuma NovaSeq 6000来测序

Study: ---------------------------------------------------------

16S sequencing of amlodipine treated NAFLD & hypertension mice

NAFLD和高血压小鼠

Library: ---------------------------------------------------------

Library:  
Name: AB13  
Instrument: Illumina NovaSeq 6000  
Strategy: AMPLICON  
Source: GENOMIC  
Selection: PCR  
Layout: SINGLE

图书馆:名称:AB13仪器:Illuma NovaSeq 6000战略:AMPLICON 资料来源:GENMIC选择:PCR布局: SINGLE

BioData: SRR14410421

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# 82: ERX5525564: NextSeq 500 sequencing; Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

Title: ---------------------------------------------------------

ERX5525564: NextSeq 500 sequencing; Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

ERX55255564: 下等Seq 500测序;

Link:

<https://www.ncbi.nlm.nih.gov/sra/ERX5525564>

Submitted: ---------------------------------------------------------

Friedrich-Loeffler-Institut Federal Research Institute for Animal Health Institute of Diagnostic Virology (Friedrich-Loeffler-Institut Federal Research Insti)

Friedrich-Loeffler研究所 联邦动物卫生研究所

Design: ---------------------------------------------------------

Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

婴儿仓鼠肾细胞的粘附和悬浮性婴儿仓鼠肾细胞有不同的细胞骨质素和表面受体

Study: ---------------------------------------------------------

Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

婴儿仓鼠肾细胞的粘附和悬浮性婴儿仓鼠肾细胞有不同的细胞骨质素和表面受体

Library: ---------------------------------------------------------

Library:  
Name: BHK\_179\_1\_s  
Instrument: NextSeq 500  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: PolyA  
Layout: SINGLE  
Construction protocol: Batches of each of the cell lines BHK179, BHK-2P and BHK-InV were lysed in three volumes of TRIzol LS Reagent. Culture conditions were 37 °C, 5% CO2, and for suspension cells 320 rpm in TubeSpin bioreactors (TPP Techno Plastic Products AG, Trasadingen, Switzerland) at 80% relative humidity. All adherent cell lines were cultured in Minimum Essential Medium Eagle (MEM) supplemented with Hanks' and Earle's salts (Sigma-Aldrich) with 10% FBS. All suspension cell lines were adapted to grow in CellventoTM BHK200 medium (Merck KGaA). After adding trichloromethane the aqueous phase was collected and mixed with one volume of 100% ethanol. From this, total RNA was extracted using the RNeasy Mini Kit (Qiagen, Hilden, Germany) with on-column DNase digestion with the RNase-Free DNase Set (Qiagen). The ERCC RNA Spike-In Mix 1 (Thermo Fisher Scientific) was added and used as an internal control for all following steps. Next, polyadenylated mRNA was isolated from 1-3 µg of high-quality total RNA using the Dynabeads mRNA DIRECT Micro kit (Thermo Fisher Scientific). The mRNA was subsequently fragmented and used for cDNA synthesis and library preparation using the TruSeq Stranded mRNA LT Sample Prep Kit (Illumina, San Diego, USA) according to the manufacturer's instructions.

图书馆: 名称: BHK\_ 179\_ 1\_\_ 1\_\_s 工具 : NextSeq 500 战略 来源: TRARIPTOMI 选择 80% 相对湿度 : PolyA 布局: SINGLE 建设协议 : BHK179, BHK-2P 和 BHK-InV 的每条细胞管线都用三卷TRizol LS 试剂来解析。 文化条件为37 °C, 5% CO2, TubeSpin生物反应器中的悬浮细胞320 rpmm( TPP Techno Flickral Nation AGAG, Trasaden, Stradingencial Rad) 。所有粘固细胞管线都是在最低基本中 HankSeral-NSyal HINC 上培养的,然后用 RSilental-NC RC 和 RC RC RC 用于科学。

BioData: ERR5882033

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# 83: SRX23992000: GSM8153976: ovary, L6; Huso dauricus x Acipenser schrenckii; RNA-Seq

Title: ---------------------------------------------------------

SRX23992000: GSM8153976: ovary, L6; Huso dauricus x Acipenser schrenckii; RNA-Seq

SRX23992000: GSM8153976:卵,L6;Huso dauriscus x Acipenser schrencki;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX23992000>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8153976\_r1

GSM8153976\_r1

Study: ---------------------------------------------------------

Critical gene filtration for the caviar yield of hybrid sturgeon

混合螺旋藻鱼子酱产量的关键基因过滤

Library: ---------------------------------------------------------

Library:  
Name: GSM8153976  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA simple extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in ovary tissues. 60 mg fresh tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 4 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragmentation with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that were provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (300±50 bp) was established by amplifying the target sequences.

姓名: 姓名: GSM 8153976 资料库: GSM 8153976 资料库: GSM 8153976 资料库: Illumina NovaSeq 600 战略: RNA-Sequa 来源: TARNA 选择了 TARED 建筑协议: 商业 RNA 简单抽取包(DP419, TIANGEN, 中国) 抽取全部 RNA 。 60 毫克新鲜组织由高速同源同源同源同源的1 mLLL透析缓冲RZ, 以获得同源同源, 然后添加三氯甲烷 来源: 资料来源: TRANS 选择 TRAD 选择 : TRAD 选择 : CRAD: PARED: PARE: PARED: 1 2000 ROMM:

BioData: SRR28387149

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# 84: SRX10761860: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

Title: ---------------------------------------------------------

SRX10761860: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

SRX10761860: 16S RNDNA V4 肌肉肌肉细胞序列区域:成年男性累积含量

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX10761860>

Submitted: ---------------------------------------------------------

China Pharmaceutical University

中国制药大学

Design: ---------------------------------------------------------

DNA extracted via phenol-Trichloromethane method, and V4 region amplified with primer of 515F and 806R, then Illumina NovaSeq 6000 used for sequencing

通过酚-三氯甲烷方法提取的DNA,以及V4区域,以515F和806R的基质放大515F和806R,然后用Illuma NovaSeq 6000来测序

Study: ---------------------------------------------------------

16S sequencing of amlodipine treated NAFLD & hypertension mice

NAFLD和高血压小鼠

Library: ---------------------------------------------------------

Library:  
Name: Cont7  
Instrument: Illumina NovaSeq 6000  
Strategy: AMPLICON  
Source: GENOMIC  
Selection: PCR  
Layout: SINGLE

图书馆: 名称: Cont7 仪器: Illuma NovaSeq 6000战略: AMPLICON 资料来源: GENMIC 选择: PCR布局: SINGLE

BioData: SRR14410413

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# 85: SRX10761863: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

Title: ---------------------------------------------------------

SRX10761863: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

SRX10761863: 16S RNDNA V4区域肌肉肌肉细胞顺序:成年男性累积含量

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX10761863>

Submitted: ---------------------------------------------------------

China Pharmaceutical University

中国制药大学

Design: ---------------------------------------------------------

DNA extracted via phenol-Trichloromethane method, and V4 region amplified with primer of 515F and 806R, then Illumina NovaSeq 6000 used for sequencing

通过酚-三氯甲烷方法提取的DNA,以及V4区域,以515F和806R的基质放大515F和806R,然后用Illuma NovaSeq 6000来测序

Study: ---------------------------------------------------------

16S sequencing of amlodipine treated NAFLD & hypertension mice

NAFLD和高血压小鼠

Library: ---------------------------------------------------------

Library:  
Name: AA17  
Instrument: Illumina NovaSeq 6000  
Strategy: AMPLICON  
Source: GENOMIC  
Selection: PCR  
Layout: SINGLE

图书馆:名称:AA17仪器:Illuma NovaSeq 6000战略:AMPLICON 资料来源:GENMIC选择:PCR布局: SINGLE

BioData: SRR14410410

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# 86: SRX9177120: GSM4799947: inactive\_ALKBH5\_dox\_plus\_ip1; Homo sapiens; OTHER

Title: ---------------------------------------------------------

SRX9177120: GSM4799947: inactive\_ALKBH5\_dox\_plus\_ip1; Homo sapiens; OTHER

SRX91777120: GSM47999947: 非活动\_ALKBH5\_dox\_plus\_ip1; 智人; 其他

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX9177120>

Submitted: ---------------------------------------------------------

Targeted RNA N6-Methyladenosine Demethylation Controls Cell Fate Transition in Human Pluripotent Stem Cells  
PRJNA665206 • SRP285100 • All experiments • All runs  
show Abstract

RNA N6-M6-MEVEDEnessine脱甲基化控制细胞在人类多能细胞中发生转变的情况 PRJNA665206 PRJNA665206 PRJNA665206 • SRP285100 • 所有实验 全部运行 显示摘要

Design: ---------------------------------------------------------

NCBI (GEO)

国家协调机构(GEO)

Study: ---------------------------------------------------------

inactive\_ALKBH5\_dox\_plus\_ip1

非活动(\_ALKBH5\_dox\_plus\_ip1)

Library: ---------------------------------------------------------

Library:  
Instrument: HiSeq X Ten  
Strategy: OTHER  
Source: TRANSCRIPTOMIC  
Selection: other  
Layout: PAIRED  
Construction protocol: Cells were washed with PBS and lysed with TRIzol (Thermo Fisher Scientific). Then trichloromethane (Guangzhou Chemical Reagent Factory) was used to extract the total RNA from the TRIzol lysate. Isopropanol (Sangon Biotech) was used to precipitates RNA from the mixture. mRNA was separated from the total RNA by using the Dynabeads™ mRNA Purification Kit (Thermo Fisher Scientific) according to the manufacturer's protocol. The m6A immunoprecipitation method was the same as above. Input samples and IP samples were applied for NGS library construction by using the NEBNext® Ultra II Directional RNA Library Prep (NEB) according to the manufacturer's guide. The adaptor ligated DNAs amplified by PCR for 15 cycles were sequenced on the HiSeqX sequencing platform.

资料库:仪器:HiSeq X 10战略:其他来源: TRARIPTOMIC选择:其他布局:PARED建筑协议:细胞用PBS冲洗,用TRIZOL(热水生科学)浸透,然后使用三氯甲烷(广州化学试剂厂)从TRIZOL液酸盐中提取总RNA。使用SOSOPAN醇(桑贡生物科技)从混合物中分离出RNA。MRNA根据制造商协议使用DynabadsTM mRNA净化工具包(热水生科学)与总RNA分离。M6A免疫喷洒方法与上述相同。根据制造商指南,在NEBNBNEXT Ulttra II定向RNA图书馆前p(NEB)对NGS图书馆的建设应用输入样品和IP样品。根据厂商指南,在HISECECECX测序平台上按15个周期放大的调控DNA顺序排列。

BioData: SRR12697497

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# 87: ERX5525565: NextSeq 500 paired end sequencing; Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

Title: ---------------------------------------------------------

ERX5525565: NextSeq 500 paired end sequencing; Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

ERX55255565:下一个Seq 500对齐端序列;

Link:

<https://www.ncbi.nlm.nih.gov/sra/ERX5525565>

Submitted: ---------------------------------------------------------

Friedrich-Loeffler-Institut Federal Research Institute for Animal Health Institute of Diagnostic Virology (Friedrich-Loeffler-Institut Federal Research Insti)

Friedrich-Loeffler研究所 联邦动物卫生研究所

Design: ---------------------------------------------------------

Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

婴儿仓鼠肾细胞的粘附和悬浮性婴儿仓鼠肾细胞有不同的细胞骨质素和表面受体

Study: ---------------------------------------------------------

Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire

婴儿仓鼠肾细胞的粘附和悬浮性婴儿仓鼠肾细胞有不同的细胞骨质素和表面受体

Library: ---------------------------------------------------------

Library:  
Name: BHK\_179\_2\_p  
Instrument: NextSeq 500  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: PolyA  
Layout: PAIRED  
Construction protocol: Batches of each of the cell lines BHK179, BHK-2P and BHK-InV were lysed in three volumes of TRIzol LS Reagent. Culture conditions were 37 °C, 5% CO2, and for suspension cells 320 rpm in TubeSpin bioreactors (TPP Techno Plastic Products AG, Trasadingen, Switzerland) at 80% relative humidity. All adherent cell lines were cultured in Minimum Essential Medium Eagle (MEM) supplemented with Hanks' and Earle's salts (Sigma-Aldrich) with 10% FBS. All suspension cell lines were adapted to grow in CellventoTM BHK200 medium (Merck KGaA). After adding trichloromethane the aqueous phase was collected and mixed with one volume of 100% ethanol. From this, total RNA was extracted using the RNeasy Mini Kit (Qiagen, Hilden, Germany) with on-column DNase digestion with the RNase-Free DNase Set (Qiagen). The ERCC RNA Spike-In Mix 1 (Thermo Fisher Scientific) was added and used as an internal control for all following steps. Next, polyadenylated mRNA was isolated from 1-3 µg of high-quality total RNA using the Dynabeads mRNA DIRECT Micro kit (Thermo Fisher Scientific). The mRNA was subsequently fragmented and used for cDNA synthesis and library preparation using the TruSeq Stranded mRNA LT Sample Prep Kit (Illumina, San Diego, USA) according to the manufacturer's instructions.

图书馆: 名称: BHK\_ 179\_ 279\_ 2\_ p 工具: NextSeq 500 战略 来源: TRARIPTOMI 选择 80% 相对湿度 TRARIPTOMI 选择: PolyA 布局: PAIRED 建设协议: 每一个细胞线 BHK179、 BHK-2P 和 BHK- InV 的棒用三卷TRizol LS 试剂解析三卷。 文化条件为37 °C, 5% CO2, TubeSpin生物反应器的悬浮电池 320 Rpmmm (TP Techno Frealno Floral NAT AG, Trassaden, Tresiding Nsal-NAD) 。 所有嵌入的细胞线都是在最低基本基本中 HankSeral-NSyal Hindal Helfile 中, 用于Sil-Silal-NC 和 RC Rdeal- Rdeal- Rdeal 。 用于Sental- RC 和 RC 的中文本 和RQ 用于Silal-Seral-Q 和R-Sental-Seral-R-Seral 。

BioData: ERR5882037

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# 88: SRX23991994: GSM8153970: ovary, H8; Huso dauricus x Acipenser schrenckii; RNA-Seq

Title: ---------------------------------------------------------

SRX23991994: GSM8153970: ovary, H8; Huso dauricus x Acipenser schrenckii; RNA-Seq

SRX23991994: GSM8153970:卵,H8;Huso dauriscus x Acipenser schrencki;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX23991994>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8153970\_r1

GSM8153970\_r1

Study: ---------------------------------------------------------

Critical gene filtration for the caviar yield of hybrid sturgeon

混合螺旋藻鱼子酱产量的关键基因过滤

Library: ---------------------------------------------------------

Library:  
Name: GSM8153970  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA simple extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in ovary tissues. 60 mg fresh tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 4 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragmentation with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that were provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (300±50 bp) was established by amplifying the target sequences.

姓名: 姓名: GSM 8153970 资料库: GSM 8153970 资料库: GSM 8153970 资料库: Illumina NovaSeq 600 战略: RNA-Sequa 来源: TRA 选择了 TARED 建筑协议: 商业 RNA 简单抽取包(DP419, TIANGEN, 中国) 抽取全部 RNA 。 60 毫克新鲜组织由高速同源同源(DHFFSTPRP-32D,中国劳森) 使用 1 mLL 透析缓冲RZ, 以获得同源, 然后添加三氯甲烷。 在4分钟的室内温度中停留4分后, 将混合物调离心于12000 平点, 以获得与绝对乙醇混合的水分相混合的液相配制阶段。 RNA 使用RNA 样本中残留的蛋白质(DHR) 以RNA 和NIS IMO IMO 基 提供 。

BioData: SRR28387155

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# 89: SRX24419491: GSM8244993: gut, D30FL2; Huso dauricus; RNA-Seq

Title: ---------------------------------------------------------

SRX24419491: GSM8244993: gut, D30FL2; Huso dauricus; RNA-Seq

SRX244149491: GSM8244993:直肠,D30FL2;Huso dauriscus;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX24419491>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8244993\_r1

GSM8244993\_r1

Study: ---------------------------------------------------------

Multi-omics integration reveals the dynamic impacts of stock enhancement on the intestinal health condition in kaluga sturgeon (Huso dauricus)

多组集成表明,鱼量增强对Kaluga sturgeon(Huso dauriscus)肠胃健康状况的动态影响。

Library: ---------------------------------------------------------

Library:  
Name: GSM8244993  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA sample extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in gut tissues. 90 mg fresh intestine tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 6 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragment with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that was provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (150 bp) was established by amplifying the target sequences.

Name: 姓名: GSM8244993 资料库: GSM8244993 工具: Illumina NovaSeq 600 战略: RNA-Seq 来源: TRARIPTOMI 选择: CDNA布局: PARED 建筑协议: 商业RNA采样袋(DP419, TIANGEN, 中国) 选用腹腔组织总RNA。 90毫克新鲜肠组织由高速度同质同质器(DHFFSTPRP-32D, 中国劳森) 地面 1 mLL 透析缓冲RZ, 以获得同质同质的RZZ, 然后添加三氯甲烷。 在房间温度为6分钟后, 将配对质的混合的RNA(MNA) 离子在1200升后, 并使用粉碎的EOLGO, 和 具体的 RISO IMO 的DNA 的DNA 和 DNA 的DNA 的DNA , 和 DNA 基底的DNA 。

BioData: SRR28859443

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# 90: SRX4500784: RNA-seq of Bombyx mori: male fat body

Title: ---------------------------------------------------------

SRX4500784: RNA-seq of Bombyx mori: male fat body

SRX445000784:RNA-seq of Bombyx Mori: 男性脂肪体

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX4500784>

Submitted: ---------------------------------------------------------

State Key Laboratory of Silkworm Genome Biology

丝虫基因组生物学国家关键实验室

Design: ---------------------------------------------------------

For RNA sequnencing, total RNA was extracted from fat body at different development stage respectively. 1-14mg fat body were dissected in PBS and directly transferred to Trizol (Invitrogen, USA), then grinded with liquid nitrogen. RNA was extracted again trichloromethane, after precipitate by isopropanol and cleared by 75% ethanol, RNA samples were stored in a refrigerator at 80C for sequencing libraries. Each cDNA sample was clustered using Oligo-dT magnetic beads and then sequenced on the HiSeq2000 (Illumina, USA) platform using Single-read techology. All of the Raw data presented in this study have been deposited in the NCBI Short Read Archive (http://www.ncbi.nlm.nih.gov/sra/) under SRA accession number

在RNA后续阶段,在不同的开发阶段分别从脂肪体中提取了全部RNA。1-14毫克的脂肪体在PBS中解剖,直接转移到Trizol(美国,Invitrogen),然后用液氮研磨。RNA在异丙醇沉淀后再次提取三氯甲烷,并用75%的乙醇清除。RNA样品储存在冰箱中,储存在80C用于测序的图书馆中。每个cDNA样本都使用Oligo-dT磁珠进行集成,然后在Hiseq2000(美国,Illuma)平台上用单读技术学进行测序。本研究中提供的所有原始数据都存放在CBCI短期阅读档案库中(http://www.ncbi.nlm.nih.gov/sra/),根据SRA的加入号。

Study: ---------------------------------------------------------

RNA-seq of Bombyx mori: male fat body

RNA-Seq of Bombyx Mori: 男性脂肪体

Library: ---------------------------------------------------------

Library:  
Name: W2\_rep1  
Instrument: Illumina HiSeq 2000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: PCR  
Layout: SINGLE

图书馆: 名称: W2\_rep1 仪器: Illuma Hiseq 2000 战略: RNA-Seq 来源: TRARIPTOMI 选择: PCR布局: SINGLE

BioData: SRR7637241

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# 91: SRX17532087: GSM6573332: WT2; Mus musculus; RNA-Seq

Title: ---------------------------------------------------------

SRX17532087: GSM6573332: WT2; Mus musculus; RNA-Seq

SRX175532087:GSM6573332:WT2;Mus musculus;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX17532087>

Submitted: ---------------------------------------------------------

BNU

BNU BNU BNU

Design: ---------------------------------------------------------

GSM6573332\_r1

GSM6573332\_r1

Study: ---------------------------------------------------------

Granulocyte-monocyte progenitor (GMP) RNA-seq in wild type and MST1-deficient mice.

Granulocyte-monocyte progenitor (GMP) RNA-seq(野性)和MST1缺陷小鼠。

Library: ---------------------------------------------------------

Library:  
Name: GSM6573332  
Instrument: Illumina HiSeq 2000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Trizol and 0.2-fold volume of trichloromethane were added to the cells, and isopropanol and absolute ethanol were added to precipitate the extracted RNA. The RNA was dissolved with water and the RNA concentration and purity were detected with nano drop. RNA was enriched with magnetic beads with oligo (DT), then cDNA was synthesized using mRNA as a template, double stranded cDNA was purified and amplified by PCR.

资料库: 名称: GSM6573332 工具: Illuma Hiseq 2000 战略: RNA-Seq 来源: TRARIPTOMI 选择: CDNA布局: CDNA 建筑协议: 将三氯甲烷的三分之一和0.2倍体积添加到细胞中,并在提取的RNA中添加了异丙醇和绝对乙醇。 RNA 与水溶解,RNA 浓度和纯度检测到纳米下降。 RNA 以磁珠添加了oligo(DT),然后用 mRNA作为模版对cDNA进行了合成,并用PCRR来净化和放大了双倍受困的cDNA。

BioData: SRR21529729

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# 92: SRX6432723: GSM3938242: CL; Musa acuminata AAA Group; RNA-Seq

Title: ---------------------------------------------------------

SRX6432723: GSM3938242: CL; Musa acuminata AAA Group; RNA-Seq

SRX6432723:GSM3938242:CL;Musa ancuminata AAAA集团;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX6432723>

Submitted: ---------------------------------------------------------

Transcriptome analysis of banana (Musa acuminata) in response to low-nitrogen stress  
PRJNA554129 • SRP214312 • All experiments • All runs  
show Abstract

应对低氮压力PPRJNA554129 PRJNA554129 • SRRP214312 • 所有实验 • 所有运行情况显示摘要

Design: ---------------------------------------------------------

NCBI (GEO)

国家协调机构(GEO)

Study: ---------------------------------------------------------

CL

CL 中转

Library: ---------------------------------------------------------

Library:  
Instrument: Illumina HiSeq 2000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: SINGLE  
Construction protocol: Tissues (100 mg) were placed into a precooled mortar to be ground into a powder with liquid nitrogen. The powder was collected into a precooled 2 mL Eppendorf tube with 2 mL RNase-free cetyltrimethylammonium bromide (CTAB) extracting solution, which contained 0.1% diethyl pyrocarbonate (DEPC), 2.5% CTAB, 1.4 M NaCl, 20 mM EDTA, 100 mM Tris-HCl (pH 8.0), and 4% polyvinylpyrrolidone (PVP). The tubes were then placed in a water bath at 65 °C for 30 min to induce cell lysis, and centrifuged at 13,000 rpm for 5 min at 25-28 °C. The residue was discarded, and the supernatant solution was transferred into a clean 2 mL Eppendorf tube. Trichloromethane (1 mL) was added to the supernatant solution, blended lightly, and centrifuged at 13 000 rpm for 15 min at 4 °C. The supernatant was transferred into a clean 2 mL Eppendorf tube, and this procedure was repeated once more. Subsequently, 8 M lithium chloride was added with RNase-free water to 0.6 volume of the supernatant and left overnight. The mixture was centrifuged for 30 min at 13 000 rpm and 4 °C to obtain the RNA precipitate. RNase-free ethyl alcohol (75%) was used to wash the RNA precipitate twice. Finally, RNA was dissolved in RNase-free ddH2O and stored at -80 °C until further use. Poly (A) mRNA from the total RNA was enriched by poly-T oligo-attached magnetic beads (Invitrogen), according to the manufacturer's protocol. Purified mRNA was then divided into short fragments by mixing with fragmentation buffer. The first strand cDNA was synthesized using a random hexamer primer. The buffer, dNTPs, RNase H, and DNA polymerase I were then added to the fragmented mRNA templates to synthesize the second-strand cDNA. The double-stranded cDNA was purified using magnetic beads. End repair and the addition of 3′-end single nucleotide A (adenine) were then performed. Finally, sequencing adaptors were ligated to the fragments, which were enriched by PCR amplification. During the quality control step, a 2100 Bioanalyzer (Agilent, Santa Clara, CA, USA) and a StepOnePlus Real-Time PCR System (Applied Biosystems Inc., Foster City, CA, USA) were used to qualify and quantify sequences for the sample libraries. The constructed library products were prepared for sequencing using a HiSeq 2000 system (Illumina, San Diego, CA, USA) at the Beijing Genomics Institute (BGI).

托盘(100毫克)被放置在预冷凝固的迫击炮中,成为含液态氮粉的粉末。 粉末被收集到一个2°C的预冷的2 mL Eppendorf 水槽中,2 mL Rase-无丙基甲基溴(CTAB)提取溶液中含有0.1%的二乙基丙基丙烯基丙烷(DEPC)、2.5%的丙基乙基氨基氨基氨基氢(CTB)、1.4 MCl、20 mM EDTA、100 mM Tris-Hl(PH 8.0)和4% 聚丙基醇酮(PVP)中含有1 mcion 30 mm(RS-28°C)的离心解液中含有0.13 rmtmd 。

BioData: SRR9672271

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# 93: SRX9177113: GSM4799937: active\_ALKBH5\_dox\_plus\_input1; Homo sapiens; OTHER

Title: ---------------------------------------------------------

SRX9177113: GSM4799937: active\_ALKBH5\_dox\_plus\_input1; Homo sapiens; OTHER

SRX91777113: GSM4799937: 活性 \_ALKBH5\_dox\_plus\_input1; 智人; 其他

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX9177113>

Submitted: ---------------------------------------------------------

Targeted RNA N6-Methyladenosine Demethylation Controls Cell Fate Transition in Human Pluripotent Stem Cells  
PRJNA665206 • SRP285100 • All experiments • All runs  
show Abstract

RNA N6-M6-MEVEDEnessine脱甲基化控制细胞在人类多能细胞中发生转变的情况 PRJNA665206 PRJNA665206 PRJNA665206 • SRP285100 • 所有实验 全部运行 显示摘要

Design: ---------------------------------------------------------

NCBI (GEO)

国家协调机构(GEO)

Study: ---------------------------------------------------------

active\_ALKBH5\_dox\_plus\_input1

活动(\_ALKBH5\_dox\_plus\_ input1)

Library: ---------------------------------------------------------

Library:  
Instrument: HiSeq X Ten  
Strategy: OTHER  
Source: TRANSCRIPTOMIC  
Selection: other  
Layout: PAIRED  
Construction protocol: Cells were washed with PBS and lysed with TRIzol (Thermo Fisher Scientific). Then trichloromethane (Guangzhou Chemical Reagent Factory) was used to extract the total RNA from the TRIzol lysate. Isopropanol (Sangon Biotech) was used to precipitates RNA from the mixture. mRNA was separated from the total RNA by using the Dynabeads™ mRNA Purification Kit (Thermo Fisher Scientific) according to the manufacturer's protocol. The m6A immunoprecipitation method was the same as above. Input samples and IP samples were applied for NGS library construction by using the NEBNext® Ultra II Directional RNA Library Prep (NEB) according to the manufacturer's guide. The adaptor ligated DNAs amplified by PCR for 15 cycles were sequenced on the HiSeqX sequencing platform.

资料库:仪器:HiSeq X 10战略:其他来源: TRARIPTOMIC选择:其他布局:PARED建筑协议:细胞用PBS冲洗,用TRIZOL(热水生科学)浸透,然后使用三氯甲烷(广州化学试剂厂)从TRIZOL液酸盐中提取总RNA。使用SOSOPAN醇(桑贡生物科技)从混合物中分离出RNA。MRNA根据制造商协议使用DynabadsTM mRNA净化工具包(热水生科学)与总RNA分离。M6A免疫喷洒方法与上述相同。根据制造商指南,在NEBNBNEXT Ulttra II定向RNA图书馆前p(NEB)对NGS图书馆的建设应用输入样品和IP样品。根据厂商指南,在HISECECECX测序平台上按15个周期放大的调控DNA顺序排列。

BioData: SRR12697490

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# 94: SRX10761857: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

Title: ---------------------------------------------------------

SRX10761857: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

SRX10761857: 16S RNDNA V4区域肌肉肌肉细胞顺序:成年男性累积含量

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX10761857>

Submitted: ---------------------------------------------------------

China Pharmaceutical University

中国制药大学

Design: ---------------------------------------------------------

DNA extracted via phenol-Trichloromethane method, and V4 region amplified with primer of 515F and 806R, then Illumina NovaSeq 6000 used for sequencing

通过酚-三氯甲烷方法提取的DNA,以及V4区域,以515F和806R的基质放大515F和806R,然后用Illuma NovaSeq 6000来测序

Study: ---------------------------------------------------------

16S sequencing of amlodipine treated NAFLD & hypertension mice

NAFLD和高血压小鼠

Library: ---------------------------------------------------------

Library:  
Name: Cont4  
Instrument: Illumina NovaSeq 6000  
Strategy: AMPLICON  
Source: GENOMIC  
Selection: PCR  
Layout: SINGLE

图书馆: 名称: Cont4 仪器: Illuma NovaSeq 6000 战略: AMPLICON 资料来源: GENMIC 选择: PCR布局: SINGLE

BioData: SRR14410416

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# 95: SRX10761853: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

Title: ---------------------------------------------------------

SRX10761853: 16S rDNA V4 region sequencing of mus musculus: adult male cecum content

SRX10761853: 16S RNDNA V4区域肌肉肌肉细胞顺序:成年男性累积含量

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX10761853>

Submitted: ---------------------------------------------------------

China Pharmaceutical University

中国制药大学

Design: ---------------------------------------------------------

DNA extracted via phenol-Trichloromethane method, and V4 region amplified with primer of 515F and 806R, then Illumina NovaSeq 6000 used for sequencing

通过酚-三氯甲烷方法提取的DNA,以及V4区域,以515F和806R的基质放大515F和806R,然后用Illuma NovaSeq 6000来测序

Study: ---------------------------------------------------------

16S sequencing of amlodipine treated NAFLD & hypertension mice

NAFLD和高血压小鼠

Library: ---------------------------------------------------------

Library:  
Name: AB14  
Instrument: Illumina NovaSeq 6000  
Strategy: AMPLICON  
Source: GENOMIC  
Selection: PCR  
Layout: SINGLE

图书馆:名称:AB14仪器:Illuma NovaSeq 6000战略:AMPLICON 资料来源:GENMIC选择:PCR布局: SINGLE

BioData: SRR14410420

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# 96: SRX23991993: GSM8153969: ovary, H7; Huso dauricus x Acipenser schrenckii; RNA-Seq

Title: ---------------------------------------------------------

SRX23991993: GSM8153969: ovary, H7; Huso dauricus x Acipenser schrenckii; RNA-Seq

SRX23991993: GSM8153969:卵,H7;Huso dauriscus x Acipenser schrencki;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX23991993>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8153969\_r1

GSM8153969\_r1

Study: ---------------------------------------------------------

Critical gene filtration for the caviar yield of hybrid sturgeon

混合螺旋藻鱼子酱产量的关键基因过滤

Library: ---------------------------------------------------------

Library:  
Name: GSM8153969  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA simple extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in ovary tissues. 60 mg fresh tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 4 min, the mixture was centrifuged at 12000 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragmentation with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that were provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (300±50 bp) was established by amplifying the target sequences.

姓名: 姓名: GSM 8153969 资料库: GSM 8153969 资料库: GSM 8153969 资料库: Illumina NovaSeq 600 战略: RNA-Sequa 来源: TRA 选择了 TARED 建筑协议: 商业 RNA 简单抽取包(DP 419, TIANGEN, 中国) 抽取全部 RNA 。 60毫克新鲜组织被高速同质体(DHFSTPRP-32D,中国劳森) 和 1 mLL透析缓冲RZ 以获得同质,然后添加三氯甲烷。 在4分钟的室内温度中停留后, 4分钟后, 将混合物调离心器调离心, 以获得与绝对乙醇混合的水分相接合的水相接合阶段。 RRNA 使用RNA 样本中残留的蛋白的蛋白质(DHR) 以双倍的RNA 和RIS IMO IMO 和NIS IMO IMO 基 提供 。

BioData: SRR28387156

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# 97: SRX25145397: GSM8367753: gut, Q3; Acipenser schrenckii; RNA-Seq

Title: ---------------------------------------------------------

SRX25145397: GSM8367753: gut, Q3; Acipenser schrenckii; RNA-Seq

SRX25145397: GSM8367753:直肠,Q3;Acipenserschrenckii;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX25145397>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8367753\_r1

GSM8367753\_r1

Study: ---------------------------------------------------------

Dynamic impacts of stock enhancement on wild Amur sturgeon (Acipenser schrenkii): New protection insight into intestinal microbe and gene expression mode

种群增强对野生亚穆尔外科动物(Acipenserschrenkii):对肠微生物和基因表达模式的新的保护洞见

Library: ---------------------------------------------------------

Library:  
Name: GSM8367753  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA sample extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in gut tissues. 100 mg fresh intestine tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 7 min, the mixture was centrifuged at 12500 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragment with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that was provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (150 bp) was established by amplifying the target sequences.

Name: 姓名: GSM8367753 工具: GSM8367753 工具: Illumina NovaSeq 600 战略: RNA-Seq 来源: TRARIPTOMI 选择: CDNA布局: PARED 建筑协议: 商业RNA样本提取包(DP419, TIANGEN, 中国) 以抽取腹腔组织中的全部RNA。 100毫克新鲜肠组织由高速同质同质同质(DHFFSTPRP-32D,中国劳森) 以 1 mLL 透析缓冲RZ 来获取同质,然后添加三氯甲烷。在7分钟的室温室温度为7分钟后,该混合物被离心为12500 rpmm: 以获得与绝对乙醇混合的水相吸附阶段。 RDRNA 被选用RNA样本中残留的蛋白性。 由RNA II 和 IMIS IMO 和 IMO IMO 提供 IMF IMF 和 CEN IMF5, 然后 IMV 和 NY IMO 和 IMO 。

BioData: SRR29640990

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# 98: SRX25145399: GSM8367755: gut, H2; Acipenser schrenckii; RNA-Seq

Title: ---------------------------------------------------------

SRX25145399: GSM8367755: gut, H2; Acipenser schrenckii; RNA-Seq

SRX25145399: GSM 8367755: 肠道, H2; Acipenser schrenckii; RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX25145399>

Submitted: ---------------------------------------------------------

Northeast Normal University

东北师范大学

Design: ---------------------------------------------------------

GSM8367755\_r1

GSM8367755\_r1

Study: ---------------------------------------------------------

Dynamic impacts of stock enhancement on wild Amur sturgeon (Acipenser schrenkii): New protection insight into intestinal microbe and gene expression mode

种群增强对野生亚穆尔外科动物(Acipenserschrenkii):对肠微生物和基因表达模式的新的保护洞见

Library: ---------------------------------------------------------

Library:  
Name: GSM8367755  
Instrument: Illumina NovaSeq 6000  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: PAIRED  
Construction protocol: Commercial RNA sample extraction kit (DP419, TIANGEN, China) was selected to extract the total RNA in gut tissues. 100 mg fresh intestine tissue was ground by high-speed homogenizer (DHFSTPRP-32D, LAWSON, China) with 1 mL lysis buffer RZ to obtain homogenate and then trichloromethane was added. After staying at room temperature for 7 min, the mixture was centrifuged at 12500 rpm to obtain the aqueous phase that was mixed with absolute ethyl alcohol. RD solution was used to remove residual protein impurity in RNA samples and the purified total RNA was stored at RNase-free tubes after repeated centrifugation. When RNA integrity number > 7.0 and A260/280 > 1.8, messenger RNA (mRNA) with poly A was caught using oligo(dT) dynabeads (25-61005, THERMO FISHER, USA) and then broken into fragment with the specific kit (E6150S, NEBNEST, USA). Double-strands complementary DNA was synthesized based on the reverse transcriptase and E. coli DNA polymerase I that was provided by LIANCHUAN BIO TECHNOLOGIES Co., LTD (Hangzhou, China). Paired-ends of the complementary DNA were added with a “A” base, which could combine with the adapter sequence. After the second strand was digested, the sequencing library (150 bp) was established by amplifying the target sequences.

Name: 姓名: GSM 8367755 工具: 姓名: GSM 8367755 工具: Illuma NovaSeq 600 战略: RNA-Seq 来源: TRARIPTOMI 选择: CDNA 布局: PARED 建筑协议: 商业 RNA 样本提取包(DP 419, TIANGEN, 中国) 抽取胃组织中的全部 RNA 。 100毫克新鲜肠组织被高速同质同素(DHFFSTPRP-32D, 中国劳森) , 1 mLL 透析缓冲RZZ 以获得同质, 然后添加三氯甲烷。 在7分钟的室内温度为7m: TRA 选择: CLDM: 12500 调试样之后,该混合物被离心化为12500 rPMMM: 以获得与乙醇混合的水相吸附阶段。 RDRNA 样本中,在重复离心管中存储了RNA。

BioData: SRR29640991

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# 99: SRX9177117: GSM4799943: inactive\_ALKBH5\_dox\_minus\_input1; Homo sapiens; OTHER

Title: ---------------------------------------------------------

SRX9177117: GSM4799943: inactive\_ALKBH5\_dox\_minus\_input1; Homo sapiens; OTHER

SRX91777117: GSM47999943: 非活动\_ALKBH5\_dox\_minus\_input1; 智人; 其他

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX9177117>

Submitted: ---------------------------------------------------------

Targeted RNA N6-Methyladenosine Demethylation Controls Cell Fate Transition in Human Pluripotent Stem Cells  
PRJNA665206 • SRP285100 • All experiments • All runs  
show Abstract

RNA N6-M6-MEVEDEnessine脱甲基化控制细胞在人类多能细胞中发生转变的情况 PRJNA665206 PRJNA665206 PRJNA665206 • SRP285100 • 所有实验 全部运行 显示摘要

Design: ---------------------------------------------------------

NCBI (GEO)

国家协调机构(GEO)

Study: ---------------------------------------------------------

inactive\_ALKBH5\_dox\_minus\_input1

非活动(\_ALKBH5)\_dox\_minus\_input1

Library: ---------------------------------------------------------

Library:  
Instrument: HiSeq X Ten  
Strategy: OTHER  
Source: TRANSCRIPTOMIC  
Selection: other  
Layout: PAIRED  
Construction protocol: Cells were washed with PBS and lysed with TRIzol (Thermo Fisher Scientific). Then trichloromethane (Guangzhou Chemical Reagent Factory) was used to extract the total RNA from the TRIzol lysate. Isopropanol (Sangon Biotech) was used to precipitates RNA from the mixture. mRNA was separated from the total RNA by using the Dynabeads™ mRNA Purification Kit (Thermo Fisher Scientific) according to the manufacturer's protocol. The m6A immunoprecipitation method was the same as above. Input samples and IP samples were applied for NGS library construction by using the NEBNext® Ultra II Directional RNA Library Prep (NEB) according to the manufacturer's guide. The adaptor ligated DNAs amplified by PCR for 15 cycles were sequenced on the HiSeqX sequencing platform.

资料库:仪器:HiSeq X 10战略:其他来源: TRARIPTOMIC选择:其他布局:PARED建筑协议:细胞用PBS冲洗,用TRIZOL(热水生科学)浸透,然后使用三氯甲烷(广州化学试剂厂)从TRIZOL液酸盐中提取总RNA。使用SOSOPAN醇(桑贡生物科技)从混合物中分离出RNA。MRNA根据制造商协议使用DynabadsTM mRNA净化工具包(热水生科学)与总RNA分离。M6A免疫喷洒方法与上述相同。根据制造商指南,在NEBNBNEXT Ulttra II定向RNA图书馆前p(NEB)对NGS图书馆的建设应用输入样品和IP样品。根据厂商指南,在HISECECECX测序平台上按15个周期放大的调控DNA顺序排列。

BioData: SRR12697494

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# 100: SRX9177115: GSM4799940: active\_ALKBH5\_dox\_plus\_ip1; Homo sapiens; OTHER

Title: ---------------------------------------------------------

SRX9177115: GSM4799940: active\_ALKBH5\_dox\_plus\_ip1; Homo sapiens; OTHER

SRX91777115: GSM47999940: 活性 \_ALKBH5\_dox\_plus\_ip1; 智人; 其他

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX9177115>

Submitted: ---------------------------------------------------------

Targeted RNA N6-Methyladenosine Demethylation Controls Cell Fate Transition in Human Pluripotent Stem Cells  
PRJNA665206 • SRP285100 • All experiments • All runs  
show Abstract

RNA N6-M6-MEVEDEnessine脱甲基化控制细胞在人类多能细胞中发生转变的情况 PRJNA665206 PRJNA665206 PRJNA665206 • SRP285100 • 所有实验 全部运行 显示摘要

Design: ---------------------------------------------------------

NCBI (GEO)

国家协调机构(GEO)

Study: ---------------------------------------------------------

active\_ALKBH5\_dox\_plus\_ip1

活动(\_ALKBH5\_dox\_plus\_ip1)

Library: ---------------------------------------------------------

Library:  
Instrument: HiSeq X Ten  
Strategy: OTHER  
Source: TRANSCRIPTOMIC  
Selection: other  
Layout: PAIRED  
Construction protocol: Cells were washed with PBS and lysed with TRIzol (Thermo Fisher Scientific). Then trichloromethane (Guangzhou Chemical Reagent Factory) was used to extract the total RNA from the TRIzol lysate. Isopropanol (Sangon Biotech) was used to precipitates RNA from the mixture. mRNA was separated from the total RNA by using the Dynabeads™ mRNA Purification Kit (Thermo Fisher Scientific) according to the manufacturer's protocol. The m6A immunoprecipitation method was the same as above. Input samples and IP samples were applied for NGS library construction by using the NEBNext® Ultra II Directional RNA Library Prep (NEB) according to the manufacturer's guide. The adaptor ligated DNAs amplified by PCR for 15 cycles were sequenced on the HiSeqX sequencing platform.

资料库:仪器:HiSeq X 10战略:其他来源: TRARIPTOMIC选择:其他布局:PARED建筑协议:细胞用PBS冲洗,用TRIZOL(热水生科学)浸透,然后使用三氯甲烷(广州化学试剂厂)从TRIZOL液酸盐中提取总RNA。使用SOSOPAN醇(桑贡生物科技)从混合物中分离出RNA。MRNA根据制造商协议使用DynabadsTM mRNA净化工具包(热水生科学)与总RNA分离。M6A免疫喷洒方法与上述相同。根据制造商指南,在NEBNBNEXT Ulttra II定向RNA图书馆前p(NEB)对NGS图书馆的建设应用输入样品和IP样品。根据厂商指南,在HISECECECX测序平台上按15个周期放大的调控DNA顺序排列。

BioData: SRR12697492

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