# 1: SRX24052351: GSM8168282: Plate13\_E17; Homo sapiens; RNA-Seq

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

SRX24052351: GSM8168282: Plate13\_E17; Homo sapiens; RNA-Seq

SRX24052351:GSM8168282:Plate13\_E17;智人;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX24052351>

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

Department of Veterinary Integrative Biosciences, Texas A&M University

得克萨斯A&M大学兽医综合生物科学系

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

GSM8168282\_r1

GSM8168282\_r1

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

Informing Hazard Identification and Risk Characterization of Environmental Chemicals by Combining Transcriptomic and Functional Data from Human Induced Pluripotent Stem Cell-Derived Cardiomyocytes

通过将人类诱导多功能细胞细胞-多基因心肺细胞的中转体和功能数据结合起来,为环境化学品的危险识别和风险定性提供信息

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

Library:  
Name: GSM8168282  
Instrument: Illumina HiSeq 2500  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: SINGLE  
Construction protocol: The media and chemicals from the 384-well plates was fully aspirated and replaced with 10 μL/well of 2X lysis buffer. The plates were then shaken using an orbital plate shaker for 10 minutes. The plates were then checked to ensure that the cells were lysed, and if not placed back on the plate shaker for an additional five minutes. Once the cells were lysed, adhesive seals were placed on the plates and the lysates were frozen in the 384-well plates and stored at −80 °C until further processing. The Templated Oligonucleotide Sequencing Assay (TempO-Seq™, BioSpyder Technologies, Carlsbad, CA) was used as an RNA sequencing technology of choice. Detailed protocols for TempO-seq are provided by the manufacturer and were previously reported detailed elsewhere (Grimm et al., 2016; House et al., 2022). TempO-seq libraries were prepared using the human whole transcriptome panel consisting of 22,537 protein-coding transcripts.

资料库: 名称: GSM8168282 工具: Illuma Hiseq 2500 战略: RNA-Seq 来源: TRARIPTOMI 选择: cDNA布局: SINGLE 建筑协议: 384 well 板块的介质和化学品完全喷洒,代之以10 μL/well 2X 透析缓冲。然后用轨道板摇动器对板块进行了10分钟的摇动。然后对板块进行了检查,以确保细胞被解析,如果不再放在盘子摇动器上5分钟。一旦细胞被解析,粘贴印在板上和胶合物被冻结在384-well板上,并储存在-80 °C 进一步处理之前。模版的Oligonucleocleotide Sequment Assay (TemO-Secepyder Techno, Carlsbad, CA) 被用作RNA 排序技术选择。 详细协议由制造商提供,TEMO-sequal-chemalreports, 20 etal-reportalal-al-al-als, 和al-reports。

BioData: SRR28449004

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# 2: SRX24052631: GSM8168232: Plate13\_C17; Homo sapiens; RNA-Seq

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

SRX24052631: GSM8168232: Plate13\_C17; Homo sapiens; RNA-Seq

SRX240526311:GSM8168232:Plate13\_C17;智人;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX24052631>

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

Department of Veterinary Integrative Biosciences, Texas A&M University

得克萨斯A&M大学兽医综合生物科学系

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

GSM8168232\_r1

GSM8168232\_r1

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

Informing Hazard Identification and Risk Characterization of Environmental Chemicals by Combining Transcriptomic and Functional Data from Human Induced Pluripotent Stem Cell-Derived Cardiomyocytes

通过将人类诱导多功能细胞细胞-多基因心肺细胞的中转体和功能数据结合起来,为环境化学品的危险识别和风险定性提供信息

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

Library:  
Name: GSM8168232  
Instrument: Illumina HiSeq 2500  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: SINGLE  
Construction protocol: The media and chemicals from the 384-well plates was fully aspirated and replaced with 10 μL/well of 2X lysis buffer. The plates were then shaken using an orbital plate shaker for 10 minutes. The plates were then checked to ensure that the cells were lysed, and if not placed back on the plate shaker for an additional five minutes. Once the cells were lysed, adhesive seals were placed on the plates and the lysates were frozen in the 384-well plates and stored at −80 °C until further processing. The Templated Oligonucleotide Sequencing Assay (TempO-Seq™, BioSpyder Technologies, Carlsbad, CA) was used as an RNA sequencing technology of choice. Detailed protocols for TempO-seq are provided by the manufacturer and were previously reported detailed elsewhere (Grimm et al., 2016; House et al., 2022). TempO-seq libraries were prepared using the human whole transcriptome panel consisting of 22,537 protein-coding transcripts.

资料库: 名称: GSM8168232 工具: Illuma Hiseq 2500 战略: RNA-Seq 来源: TRARIPTOMI 选择: cDNA布局: SINGLE 建筑协议: 384 well 板块的介质和化学品完全喷洒,代之以10 μL/well 2X 透析缓冲。然后用轨道板摇动器对板块进行了10分钟的摇动。然后对板块进行了检查,以确保细胞被解析,如果不再放在盘子摇动器上5分钟。一旦细胞被解析,粘贴印在板上和胶合物被冻结在384-well板上,并储存在-80 °C 进一步处理之前。模版Oligonucleocleotide Sequmentalsay (TemOspypyder Techno, Carlsbad, CA) 用作RNA 排序技术的选择。制造商提供了TemO-seqecon-secontal 详细的规程协议,此前报告了20-remaqal-alal-al-al-al-al-als, 2022。

BioData: SRR28449068

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# 3: SRX24052291: GSM8168326: Plate13\_F17; Homo sapiens; RNA-Seq

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

SRX24052291: GSM8168326: Plate13\_F17; Homo sapiens; RNA-Seq

SRX24052291:GSM8168326:Plate13\_F17;智人;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX24052291>

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

Department of Veterinary Integrative Biosciences, Texas A&M University

得克萨斯A&M大学兽医综合生物科学系

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

GSM8168326\_r1

GSM8168326\_r1

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

Informing Hazard Identification and Risk Characterization of Environmental Chemicals by Combining Transcriptomic and Functional Data from Human Induced Pluripotent Stem Cell-Derived Cardiomyocytes

通过将人类诱导多功能细胞细胞-多基因心肺细胞的中转体和功能数据结合起来,为环境化学品的危险识别和风险定性提供信息

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

Library:  
Name: GSM8168326  
Instrument: Illumina HiSeq 2500  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: SINGLE  
Construction protocol: The media and chemicals from the 384-well plates was fully aspirated and replaced with 10 μL/well of 2X lysis buffer. The plates were then shaken using an orbital plate shaker for 10 minutes. The plates were then checked to ensure that the cells were lysed, and if not placed back on the plate shaker for an additional five minutes. Once the cells were lysed, adhesive seals were placed on the plates and the lysates were frozen in the 384-well plates and stored at −80 °C until further processing. The Templated Oligonucleotide Sequencing Assay (TempO-Seq™, BioSpyder Technologies, Carlsbad, CA) was used as an RNA sequencing technology of choice. Detailed protocols for TempO-seq are provided by the manufacturer and were previously reported detailed elsewhere (Grimm et al., 2016; House et al., 2022). TempO-seq libraries were prepared using the human whole transcriptome panel consisting of 22,537 protein-coding transcripts.

资料库: 名称: GSM8168326 工具: Illuma Hiseq 2500 战略: RNA-Seq 来源: TRARIPTOMI 选择: cDNA布局: SINGLE 建筑协议: 384 well 板块的介质和化学品完全喷洒,代之以10 μL/well 2X 透析缓冲。然后用轨道板摇动器对板块进行了10分钟的摇动。然后对板块进行了检查,以确保细胞被解析,如果不再放在盘子摇动器上5分钟。一旦细胞被解析,粘贴印在板上和胶合物被冻结在384-well板上,并储存在-80 °C 进一步处理之前。模版的Oligonucleocleotide Sequmentalsay(TemOSpyder Techno, Carlsbad, CA) 用作RNA 排序技术选择。制造商提供了Temlodro-seqeetro-sremed 详细的规程规程协议,此前报告了20-real-qal-al-al-al-al-al-al-als。

BioData: SRR28448720

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# 4: SRX24052655: GSM8168304: Plate13\_G17; Homo sapiens; RNA-Seq

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

SRX24052655: GSM8168304: Plate13\_G17; Homo sapiens; RNA-Seq

SRX240052655: GSM8168304: Plate13\_G17; 智人; RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX24052655>

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

Department of Veterinary Integrative Biosciences, Texas A&M University

得克萨斯A&M大学兽医综合生物科学系

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

GSM8168304\_r1

GSM8168304\_r1

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

Informing Hazard Identification and Risk Characterization of Environmental Chemicals by Combining Transcriptomic and Functional Data from Human Induced Pluripotent Stem Cell-Derived Cardiomyocytes

通过将人类诱导多功能细胞细胞-多基因心肺细胞的中转体和功能数据结合起来,为环境化学品的危险识别和风险定性提供信息

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

Library:  
Name: GSM8168304  
Instrument: Illumina HiSeq 2500  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: SINGLE  
Construction protocol: The media and chemicals from the 384-well plates was fully aspirated and replaced with 10 μL/well of 2X lysis buffer. The plates were then shaken using an orbital plate shaker for 10 minutes. The plates were then checked to ensure that the cells were lysed, and if not placed back on the plate shaker for an additional five minutes. Once the cells were lysed, adhesive seals were placed on the plates and the lysates were frozen in the 384-well plates and stored at −80 °C until further processing. The Templated Oligonucleotide Sequencing Assay (TempO-Seq™, BioSpyder Technologies, Carlsbad, CA) was used as an RNA sequencing technology of choice. Detailed protocols for TempO-seq are provided by the manufacturer and were previously reported detailed elsewhere (Grimm et al., 2016; House et al., 2022). TempO-seq libraries were prepared using the human whole transcriptome panel consisting of 22,537 protein-coding transcripts.

资料库: 名称: GSM8168304 工具: Illuma Hiseq 2500 战略: RNA-Seq 来源: TRARIPTOMI 选择: cDNA布局: SINGLE 建筑协议: 384 well 板块的介质和化学品完全喷洒,代之以10 μL/well 2X 透析缓冲。然后用轨道板摇动器对板块进行了10分钟的摇动。然后对板块进行了检查,以确保细胞被解析,如果不再放在盘子摇动器上5分钟。一旦细胞被解析,粘贴印在板上和胶合物被冻结在384-well板上,并储存在-80 °C 进一步处理之前。模版Oligonucleocleotide Sequmentalsay (TemO-Spyder Techno, Carlsbad, CA) 用作RNA 排序技术的选择。制造商提供了Temlodro-seqef 的详细协议。制造商提供了Temlos-se-se-seal-reportalalalal, 2022。

BioData: SRR28449044

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# 5: SRX24052370: GSM8168349: Plate13\_H17; Homo sapiens; RNA-Seq

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

SRX24052370: GSM8168349: Plate13\_H17; Homo sapiens; RNA-Seq

SRX240052370:GSM8168349:Plate13\_H17;智人;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX24052370>

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

Department of Veterinary Integrative Biosciences, Texas A&M University

得克萨斯A&M大学兽医综合生物科学系

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

GSM8168349\_r1

GSM8168349\_r1

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

Informing Hazard Identification and Risk Characterization of Environmental Chemicals by Combining Transcriptomic and Functional Data from Human Induced Pluripotent Stem Cell-Derived Cardiomyocytes

通过将人类诱导多功能细胞细胞-多基因心肺细胞的中转体和功能数据结合起来,为环境化学品的危险识别和风险定性提供信息

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

Library:  
Name: GSM8168349  
Instrument: Illumina HiSeq 2500  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: SINGLE  
Construction protocol: The media and chemicals from the 384-well plates was fully aspirated and replaced with 10 μL/well of 2X lysis buffer. The plates were then shaken using an orbital plate shaker for 10 minutes. The plates were then checked to ensure that the cells were lysed, and if not placed back on the plate shaker for an additional five minutes. Once the cells were lysed, adhesive seals were placed on the plates and the lysates were frozen in the 384-well plates and stored at −80 °C until further processing. The Templated Oligonucleotide Sequencing Assay (TempO-Seq™, BioSpyder Technologies, Carlsbad, CA) was used as an RNA sequencing technology of choice. Detailed protocols for TempO-seq are provided by the manufacturer and were previously reported detailed elsewhere (Grimm et al., 2016; House et al., 2022). TempO-seq libraries were prepared using the human whole transcriptome panel consisting of 22,537 protein-coding transcripts.

资料库: 名称: GSM8168349 工具: Illuma Hiseq 2500 战略: RNA-Seq 来源: TRARIPTOMI 选择: cDNA 版图: SINGLE 建筑协议: 384 well 板块的介质和化学物质完全被喷洒,代之以10 微克/升 2X 透析缓冲。然后用轨道板摇动器对板块进行了10分钟的摇动。然后对板块进行了检查,以确保细胞被解析,如果不在盘子摇动器上再加5分钟。一旦细胞被解析,粘合印印在板上和胶合物被冷冻,并储存在-80 °C 进一步处理之前。模版Oligonucleocleotide Sequmentalsayal(TemOspyder Techno, Carlsbad, CA)被作为RNA 的排序技术选择。制造商提供了TEMO-seqeconn 的详细协议,此前报告在其他地方有2022号的Oremal-reportal-reportal-al-al-al-al;

BioData: SRR28448985

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# 6: SRX24052383: GSM8168400: Plate13\_I17; Homo sapiens; RNA-Seq

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

SRX24052383: GSM8168400: Plate13\_I17; Homo sapiens; RNA-Seq

SRX240052383:GSM8168400:Plate13\_I17;智人;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX24052383>

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

Department of Veterinary Integrative Biosciences, Texas A&M University

得克萨斯A&M大学兽医综合生物科学系

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

GSM8168400\_r1

GSM8168400\_r1

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

Informing Hazard Identification and Risk Characterization of Environmental Chemicals by Combining Transcriptomic and Functional Data from Human Induced Pluripotent Stem Cell-Derived Cardiomyocytes

通过将人类诱导多功能细胞细胞-多基因心肺细胞的中转体和功能数据结合起来,为环境化学品的危险识别和风险定性提供信息

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

Library:  
Name: GSM8168400  
Instrument: Illumina HiSeq 2500  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: SINGLE  
Construction protocol: The media and chemicals from the 384-well plates was fully aspirated and replaced with 10 μL/well of 2X lysis buffer. The plates were then shaken using an orbital plate shaker for 10 minutes. The plates were then checked to ensure that the cells were lysed, and if not placed back on the plate shaker for an additional five minutes. Once the cells were lysed, adhesive seals were placed on the plates and the lysates were frozen in the 384-well plates and stored at −80 °C until further processing. The Templated Oligonucleotide Sequencing Assay (TempO-Seq™, BioSpyder Technologies, Carlsbad, CA) was used as an RNA sequencing technology of choice. Detailed protocols for TempO-seq are provided by the manufacturer and were previously reported detailed elsewhere (Grimm et al., 2016; House et al., 2022). TempO-seq libraries were prepared using the human whole transcriptome panel consisting of 22,537 protein-coding transcripts.

资料库: 名称: GSM8168400 资料库: GSM8168400 资料库: Illuma Hiseq 2500 战略: RNA-Seq 资料来源: TRARIPTOMI 选择: cDNA布局: SINGLE 建筑协议: 384 well 板块的介质和化学物质完全被喷洒,代之以10 微克/ well 2X 透析缓冲。然后用轨道板摇动器对板块进行了10分钟的摇动。然后对板块进行了检查,以确保细胞被解析,如果不是再放在盘子摇动器上5分钟。一旦细胞被解析,粘合印印在板上,粘合剂被冻结在384 4 well 牌盘上,然后储存在- 80 °C 进一步处理之前。模版的Oligonucleocleotide Sequment Asssay (Tem-Shoal-Creportyls, etal and AL) 20-Crimeal-Creductionalsal-qal-alsal-al- 2022, Creportyals.

BioData: SRR28448972

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# 7: SRX24052131: GSM8168250: Plate13\_D17; Homo sapiens; RNA-Seq

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

SRX24052131: GSM8168250: Plate13\_D17; Homo sapiens; RNA-Seq

SRX24052131: GSM8168250: Plate13\_D17; 智人; RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX24052131>

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

Department of Veterinary Integrative Biosciences, Texas A&M University

得克萨斯A&M大学兽医综合生物科学系

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

GSM8168250\_r1

GSM8168250\_r1

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

Informing Hazard Identification and Risk Characterization of Environmental Chemicals by Combining Transcriptomic and Functional Data from Human Induced Pluripotent Stem Cell-Derived Cardiomyocytes

通过将人类诱导多功能细胞细胞-多基因心肺细胞的中转体和功能数据结合起来,为环境化学品的危险识别和风险定性提供信息

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

Library:  
Name: GSM8168250  
Instrument: Illumina HiSeq 2500  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: SINGLE  
Construction protocol: The media and chemicals from the 384-well plates was fully aspirated and replaced with 10 μL/well of 2X lysis buffer. The plates were then shaken using an orbital plate shaker for 10 minutes. The plates were then checked to ensure that the cells were lysed, and if not placed back on the plate shaker for an additional five minutes. Once the cells were lysed, adhesive seals were placed on the plates and the lysates were frozen in the 384-well plates and stored at −80 °C until further processing. The Templated Oligonucleotide Sequencing Assay (TempO-Seq™, BioSpyder Technologies, Carlsbad, CA) was used as an RNA sequencing technology of choice. Detailed protocols for TempO-seq are provided by the manufacturer and were previously reported detailed elsewhere (Grimm et al., 2016; House et al., 2022). TempO-seq libraries were prepared using the human whole transcriptome panel consisting of 22,537 protein-coding transcripts.

资料库: 名称: GSM8168250 工具: Illuma Hiseq 2500 战略: RNA-Seq 来源: TRARIPTOMI 选择: cDNA布局: SINGLE 建筑协议: 384 well 板块的介质和化学物质完全喷洒,代之以10 μL/well 2X 透析缓冲。然后用轨道板摇动器对板块进行了10分钟的摇动。然后对板块进行了检查,以确保细胞被解析,如果不再放在盘子摇动器上5分钟。一旦细胞被解析,粘贴印在板上和胶合物被冻结在384-well板上,然后储存在-80°C,直到进一步处理为止。模版Oligonucleocleot Sequment Assay(Temmoto-Seqretech,Bs,Carlsbad, CA)被使用作为RNA 排序技术选择。制造商提供了TempOseqeet的详尽协议,此前报告是使用Semal-reportal-reportalalalalalalal, 2022, 和Sheal-reportal-al。

BioData: SRR28448536

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# 8: SRX24052501: GSM8168426: Plate13\_K17; Homo sapiens; RNA-Seq

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

SRX24052501: GSM8168426: Plate13\_K17; Homo sapiens; RNA-Seq

SRX240052501: GSM8168426: Plate13\_K17; 智人; RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX24052501>

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

Department of Veterinary Integrative Biosciences, Texas A&M University

得克萨斯A&M大学兽医综合生物科学系

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

GSM8168426\_r1

GSM8168426\_r1

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

Informing Hazard Identification and Risk Characterization of Environmental Chemicals by Combining Transcriptomic and Functional Data from Human Induced Pluripotent Stem Cell-Derived Cardiomyocytes

通过将人类诱导多功能细胞细胞-多基因心肺细胞的中转体和功能数据结合起来,为环境化学品的危险识别和风险定性提供信息

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

Library:  
Name: GSM8168426  
Instrument: Illumina HiSeq 2500  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: SINGLE  
Construction protocol: The media and chemicals from the 384-well plates was fully aspirated and replaced with 10 μL/well of 2X lysis buffer. The plates were then shaken using an orbital plate shaker for 10 minutes. The plates were then checked to ensure that the cells were lysed, and if not placed back on the plate shaker for an additional five minutes. Once the cells were lysed, adhesive seals were placed on the plates and the lysates were frozen in the 384-well plates and stored at −80 °C until further processing. The Templated Oligonucleotide Sequencing Assay (TempO-Seq™, BioSpyder Technologies, Carlsbad, CA) was used as an RNA sequencing technology of choice. Detailed protocols for TempO-seq are provided by the manufacturer and were previously reported detailed elsewhere (Grimm et al., 2016; House et al., 2022). TempO-seq libraries were prepared using the human whole transcriptome panel consisting of 22,537 protein-coding transcripts.

资料库: 名称: GSM8168426 工具: Illuma Hiseq 2500 战略: RNA-Seq 来源: TRARIPTOMI 选择: CDNA 版图: SINGLE 建筑协议: 384 号板块的介质和化学物质完全被喷洒,代之以10 微克/升 2X 透析缓冲。然后用轨道板摇动器对板块进行了10分钟的摇动。然后对板块进行了检查,以确保细胞被解析,如果不再放在盘子摇动器上5分钟。一旦细胞被解析,粘贴印在板上和胶合物被冻结在384 号板上,并储存在- 80 °C 进一步处理之前。模版的Oligonucleocleotide Squmentalsays(TemO-Spyder Technology, Carlsbad, CA)被作为RNA 的排序技术选择。制造商提供了Temto-seqreal-semberdrodeals, 20 etal-chal-rememberdal-als, 和al-al-al-s。

BioData: SRR28449198

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# 9: SRX24052305: GSM8168376: Plate13\_J17; Homo sapiens; RNA-Seq

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

SRX24052305: GSM8168376: Plate13\_J17; Homo sapiens; RNA-Seq

SRX240052305:GSM8168376:Plate13\_J17;智人;RNA-Seq

Link:

<https://www.ncbi.nlm.nih.gov/sra/SRX24052305>

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

Department of Veterinary Integrative Biosciences, Texas A&M University

得克萨斯A&M大学兽医综合生物科学系

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

GSM8168376\_r1

GSM8168376\_r1

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

Informing Hazard Identification and Risk Characterization of Environmental Chemicals by Combining Transcriptomic and Functional Data from Human Induced Pluripotent Stem Cell-Derived Cardiomyocytes

通过将人类诱导多功能细胞细胞-多基因心肺细胞的中转体和功能数据结合起来,为环境化学品的危险识别和风险定性提供信息

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

Library:  
Name: GSM8168376  
Instrument: Illumina HiSeq 2500  
Strategy: RNA-Seq  
Source: TRANSCRIPTOMIC  
Selection: cDNA  
Layout: SINGLE  
Construction protocol: The media and chemicals from the 384-well plates was fully aspirated and replaced with 10 μL/well of 2X lysis buffer. The plates were then shaken using an orbital plate shaker for 10 minutes. The plates were then checked to ensure that the cells were lysed, and if not placed back on the plate shaker for an additional five minutes. Once the cells were lysed, adhesive seals were placed on the plates and the lysates were frozen in the 384-well plates and stored at −80 °C until further processing. The Templated Oligonucleotide Sequencing Assay (TempO-Seq™, BioSpyder Technologies, Carlsbad, CA) was used as an RNA sequencing technology of choice. Detailed protocols for TempO-seq are provided by the manufacturer and were previously reported detailed elsewhere (Grimm et al., 2016; House et al., 2022). TempO-seq libraries were prepared using the human whole transcriptome panel consisting of 22,537 protein-coding transcripts.

资料库: 名称: GSM8168376 工具: Illuma Hiseq 2500 战略: RNA-Seq 来源: TRARIPTOMI 选择: cDNA布局: SINGLE 建筑协议: 384 well 板块的介质和化学品完全喷洒,代之以10 μL/well 2X 透析缓冲。然后用轨道板摇动器对板块进行了10分钟的摇动。然后对板块进行了检查,以确保细胞被解析,如果不再放在盘子摇动器上5分钟。一旦细胞被解析,粘贴印在板上和胶合物被冻结在384-well板上,并储存在-80 °C 进一步处理之前。模版的Oligonucleocleotide Sequment Assay (TemO-Secepyder Techno, Carlsbad, CA) 被用作RNA 排序技术选择。 详细协议由制造商提供,TEMO-sequal-chemalreports, 20 etal-reportalal-al-al-als, 和al-reports.

BioData: SRR28448706

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