**MINI PROJECT BIOINFORMATICS**

2,3,7,8-tetrachlorodibenzo-p-dioxin (TCDD)

organism : Mus Musculus

experiment type : Expression profiling by high throughput sequencing

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| --- | --- | --- | --- | --- | --- |
|  | What do they do? | # samples | link | PubMed | title |
| GSE109863 | hepatic ChIP-seq analyses were integrated with RNA-seq time course data | 42 | [https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE104551)109863 | <https://omictools.com/b9ea7515613b950a2ff041e66f070720-dataset> | RNA-Seq Analysis of Dose-Dependent TCDD-Elicited Femoral Gene Expression in Male Mice |
| GSE104551 | These data were used to examine the effect of repeated TCDD exposure on gene expression in the femur of C57BL/6 male mice | 27 | <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE104551> | <https://www.omicsdi.org/dataset/geo/GSE87519> | RNA-Seq Analysis of Dose-Dependent TCDD-Elicited Femoral Gene Expression in Male Mice |
| GSE90097 | Dose-dependent jejunal gene expression was examined following repeated exposure (every 4 days for 28 days) to 2,3,7,8-tetrachlorodibenzo-p-dioxin (TCDD). These data were used to examine the effect of repeated TCDD exposure on gene expression in the intestinal epithelium of C57BL/6 male mice. | 27 | <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi>[?acc](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE104551)=GSE90097 | <https://www.omicsdi.org/dataset/geo/GSE90097> | RNA-Seq Analysis of Dose-Dependent TCDD-Elicited Jejunal Gene Expression in Male Mice |
| GSE89430 | These data were used to examine the effect of repeated TCDD exposure on gene expression in the intestinal epithelium of C57BL/6 male mice. | 28 | <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE89430> | <https://www.omicsdi.org/dataset/geo/GSE89430> | RNA-Seq Analysis of Dose-Dependent TCDD-Elicited Ileal Gene Expression in Male Mice |
| GSE87519 | Dose-dependent hepatic gene expression was examined following repeated exposure (every 4 days for 28 days) | 27 | <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi>[?acc=](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE89430)GSE87519 | <https://www.omicsdi.org/dataset/geo/GSE87519> | RNA-Seq Analysis of Dose-Dependent TCDD-Elicited Hepatic Gene Expression in Male Mice |
| GSE87542 | Dose-dependent duodenal gene expression was examined following repeated exposure (every 4 days for 28 days) to 2,3,7,8-tetrachlorodibenzo-p-dioxin (TCDD). These data were used to examine the effect of repeated TCDD exposure on gene expression in the intestinal epithelium of C57BL/6 male mice. | 27 | <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi>[?acc=](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE89430)GSE87542 | <https://www.omicsdi.org/dataset/geo/GSE87542> | RNA-Seq Analysis of Dose-Dependent TCDD-Elicited Duodenal Gene Expression in Male Mice |
| GSE81990 | In addition to metabolic reprogramming in support of NADPH production for ROS defense, we demonstrate that glycogen, ascorbic acid, and amino acid metabolism are also reorganized to support remodeling of the extracellular matrix, progressing to hepatic fibrosis in response to chronic injury from TCDD. | 27 | <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE81990> | <https://www.ncbi.nlm.nih.gov/pubmed/27562557> | Dose-dependent metabolic reprogramming and differential gene expression in TCDD-elicited hepatic fibrosis |
| GSE80953 | RNA-Seq was used to analyze and compare temporal TCDD-induced gene expression changes in primary human, mouse and rat B cells. Most of the differentially expressed genes exibited species-specific expression. Cross-species comparison identified 28 orthologs commonly deregulated in all 3 species. The study provides new insight into mechanisms of TCDD-indu12ced suppression of B cell effector function. | 30 | <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi>[?acc=](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE89430)GSE80953 |  |  |
| GSE73787 | we investigated whether Ahr ablation or TCDD exposure in utero resulted in cardiac abnormalities in adult mice long after removal of the agent | 72 | <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE73787> | <https://www.ncbi.nlm.nih.gov/pubmed/26555816> | Disruption of Ah Receptor Signaling during Mouse Development Leads to Abnormal Cardiac Structure and Function in the Adult |
|  | | | | | |
| GSE60114 | Combining genome-wide approaches, we demonstrate that developmental activation alters DNA methylation and gene expression patterns in isolated CD8+ T cells prior to and during infection. | 8 | <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi>[?acc=](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE89430)GSE60114 | <https://www.ncbi.nlm.nih.gov/pubmed/25810390> | Linking the aryl hydrocarbon receptor with altered DNA methylation patterns and developmentally induced aberrant antiviral T cell responses [RNA-Seq] |
| GSE62902 | Dose-dependent hepatic gene expression was examined following repeated exposure (every 4 days for 28 days) | 45 | <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi>[?acc=](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE89430)GSE62902 | <https://www.ncbi.nlm.nih.gov/pubmed/25958198> | RNA-Seq Versus Oligonucleotide Array Assessment of Dose-Dependent TCDD-elicited Hepatic Gene Expression in Mice [RNA-Seq] |
| 4GSE47964 | We generated an AHR-positive cardiomyocyte lineage differentiated from mouse ES cells that expresses puromycin resistance and enhanced green fluorescent protein (eGFP) under the control of the Cyp1a1 (cytochrome P450 1a1) promoter. We used RNA sequencing (RNA.Seq) to analyze temporal trajectories of TCDD-dependent global gene expression in these cells during differentiation. | 24 | https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE47964 | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3855521/ | Activation of the aryl hydrocarbon receptor by dioxin during embryonic stem cell differentiation disrupts the expression of homeobox transcription factors that control cardiomyogenesis |

Bisphenol A

organism : Mus Musculus

experiment type : Expression profiling by high throughput sequencing

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| --- | --- | --- | --- | --- | --- |
|  | What do they do? | # samples | link | PubMed | Title |
| GSE119012 | The goals of this study are to define the putatitve impacts of FXRalpha deficiency in testicular physiology following environmental exposure (bisphenol-A and stigmasterol) | 21 | https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE119012 |  |  |
| GSE121603 | Here, we leveraged systems biology approaches to assess the target tissues, molecular pathways, and gene regulatory networks associated with prenatal exposure to the model EDC Bisphenol A (BPA) | 18 | <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi>[?acc=](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE89430)GSE121603 | <https://academic.oup.com/endo/article/160/2/409/5250673> | **Prenatal Bisphenol A Exposure in Mice Induces Multitissue Multiomics Disruptions Linking to Cardiometabolic Disorders** |
| GSE102849 | We report here hippocampal RNA-seq data from adult (20 weeks) male offspring exposed to 0 mg (control) or 50 mg BPA/kg diet during gestation and lactation. | 8 | https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE102849 |  |  |
| GSE46815 | our study for the first time shows that pubertal BPA exposure altered MaSC gene expression and function such that they induced early neoplastic transformation | 4 | https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE46815 |  |  |

<https://watermark.silverchair.com/en.2018-00817.pdf?token=AQECAHi208BE49Ooan9kkhW_Ercy7Dm3ZL_9Cf3qfKAc485ysgAAAkcwggJDBgkqhkiG9w0BBwagggI0MIICMAIBADCCAikGCSqGSIb3DQEHATAeBglghkgBZQMEAS4wEQQMZ2Vvm8AX0GbMbrIkAgEQgIIB-rViLvze4V7hr9V9DwblwHHnpmiztikHzXdQThyO7GyzSHc8A8hO26OPOVNah_1taX2GdxUIi0wsqv8XK66q07are4P1mQWhitDCr-0nk21igaxYQbMAkjBshb448BIX1hNYBjqmxxxxfu4vnMLTYOFqFzHn3p-H7VyFEZ8tWa8TzkU-9QM4_yHY6STF6UkXrgUHWGsX1FuQ1qKJnP7gkcLNAHlIN4CM-5TtL_wQ2mzgsIVDsUr-7beLDa9DU3Mwza_gaV43A-dp3M6caixN7hBvEliVg6AhvW5QuR8Zx8maHP4Qoqmyn1cuGD9sI3cU3tJwfighVgfozuDk1RM39E1LG8Vs_Pc1UE0_bGJwqHk8pI7XTKB7CtKK_l8UD-uIsY8b4hdviAeh6WRmVvC-YgyY1PJ0IWsgAfzwx_9zjmJaa4J2qegNNBLdilW5npNL_72gecWug-ZeCWwwSi1wEKtFJaBoEj9bcaYh3PKwQ2mmtx--bfPEgOdsnYVFk6pJlfcBiwiNxwYR888-vEOWEVwPyRss0cH1f8KNBChTbNgKg3G7SO_dxEUl3VTP_dcV38Wc1R9R8SdFuUBZwg0s59iSLDBgfOhwCA1VCjuT-XyXhu0dp3t6nJA6ZYU0OuPMb04jJcEELta0yjf0pTUewXQ8VVmiui0EeAd_>

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GSM3439948 WT rep1 adipose RNA-Seq

GSM3439949 WT rep2 adipose RNA-Seq

GSM3439950 WT rep3 adipose RNA-Seq

GSM3439951 BPA rep1 adipose RNA-Seq

GSM3439952 BPA rep2 adipose RNA-Seq

GSM3439953 BPA rep3 adipose RNA-Seq

GSM3439954 WT rep1 hypothalamus RNA-Seq

GSM3439955 WT rep2 hypothalamus RNA-Seq

GSM3439956 WT rep3 hypothalamus RNA-Seq

GSM3439957 BPA rep1 hypothalamus RNA-Seq

GSM3439958 BPA rep2 hypothalamus RNA-Seq

GSM3439959 BPA rep3 hypothalamus RNA-Seq

GSM3439960 WT rep1 liver RNA-Seq

GSM3439961 WT rep2 liver RNA-Seq

GSM3439962 WT rep3 liver RNA-Seq

GSM3439963 BPA rep1 liver RNA-Seq

GSM3439964 BPA rep2 liver RNA-Seq

GSM3439965 BPA rep3 liver RNA-Seq

<https://edwards.sdsu.edu/research/fastq-dump/>

<https://www.cyberciti.biz/faq/howto-open-a-tar-gz-file-in-linux-unix/>

<https://ncbi.github.io/sra-tools/install_config.html>

<https://www.ncbi.nlm.nih.gov/books/NBK158899/>