

Stanford

Shining Ma

Research Scientist

Statistics

Bio

ACADEMIC APPOINTMENTS

- Basic Life Science Research Associate, Statistics

Publications

PUBLICATIONS

- **Integrated functional genomic analyses of Klinefelter and Turner syndromes reveal global network effects of altered X chromosome dosage.** *Proceedings of the National Academy of Sciences of the United States of America*
Zhang, X., Hong, D., Ma, S., Ward, T., Ho, M., Pattni, R., Duren, Z., Stankov, A., Bade Shrestha, S., Hallmayer, J., Wong, W. H., Reiss, A. L., Urban, et al
2020
- **Model-Based Approach to the Joint Analysis of Single-Cell Data on Chromatin Accessibility and Gene Expression** *STATISTICAL SCIENCE*
Lin, Z., Zamanighomi, M., Daley, T., Ma, S., Wong, W.
2020; 35 (1): 2–13
- **Network Effects of the 15q13.3 Microdeletion on the Transcriptome and Epigenome in Human-Induced Neurons.** *Biological psychiatry*
Zhang, S., Zhang, X., Purmann, C., Ma, S., Shrestha, A., Davis, K. N., Ho, M., Huang, Y., Pattni, R., Wong, W. H., Bernstein, J. A., Hallmayer, J., Urban, et al
2020
- **INTEGRATED ANALYSIS OF GENE EXPRESSION, DNA METHYLATION AND CHROMATIN ACCESSIBILITY IN A HUMAN IPSC-TO-INDUCED-NEURON MODEL OF THE 15Q13.3 MICRODELETION**
Zhang, S., Zhang, X., Ma, S., Purmann, C., Davis, K., Wong, W., Bernstein, J., Hallmayer, J., Urban, A.
ELSEVIER.2019: S105
- **ANALYZING THE MOLECULAR NETWORK EFFECTS OF LARGE NEUROPSYCHIATRIC CNVS WITH IPSC BASED NEURONAL TISSUE CULTURE MODELS**
Purmann, C., Ma, S., Zhang, S., Ward, T., Huang, E., Pattni, R., Hallmayer, J., Wong, W., Urban, A.
ELSEVIER.2019: 1060
- **Constructing tissue-specific transcriptional regulatory networks via a Markov random field.** *BMC genomics*
Ma, S., Jiang, T., Jiang, R.
2018; 19 (Suppl 10): 884
- **FreePSI: an alignment-free approach to estimating exon-inclusion ratios without a reference transcriptome** *NUCLEIC ACIDS RESEARCH*
Zhou, J., Ma, S., Wang, D., Zeng, J., Jiang, T.
2018; 46 (2): e11
- **Simultaneous inference of phenotype-associated genes and relevant tissues from GWAS data via Bayesian integration of multiple tissue-specific gene networks** *JOURNAL OF MOLECULAR CELL BIOLOGY*
Wu, M., Lin, Z., Ma, S., Chen, T., Jiang, R., Wong, W.
2017; 9 (6): 436–52
- **Differential regulation enrichment analysis via the integration of transcriptional regulatory network and gene expression data.** *Bioinformatics*
Ma, S., Jiang, T., Jiang, R.

