

Dr. Chongyuan Luo received his B.Sc. degree in Biology (Honors Program in Life Sciences) from China Agricultural University, in 2006. Dr. Luo received his Ph.D. degree in Plant Biology from Rutgers University in 2012. During his Ph.D. study, he studied histone modifications of the model plant species *Arabidopsis thaliana* using high-throughput sequencing approaches. After completing his postdoctoral training at the Salk Institute for Biological Studies, Dr. Luo joined the Department of Human Genetics at UCLA as an Assistant Professor in 2019.

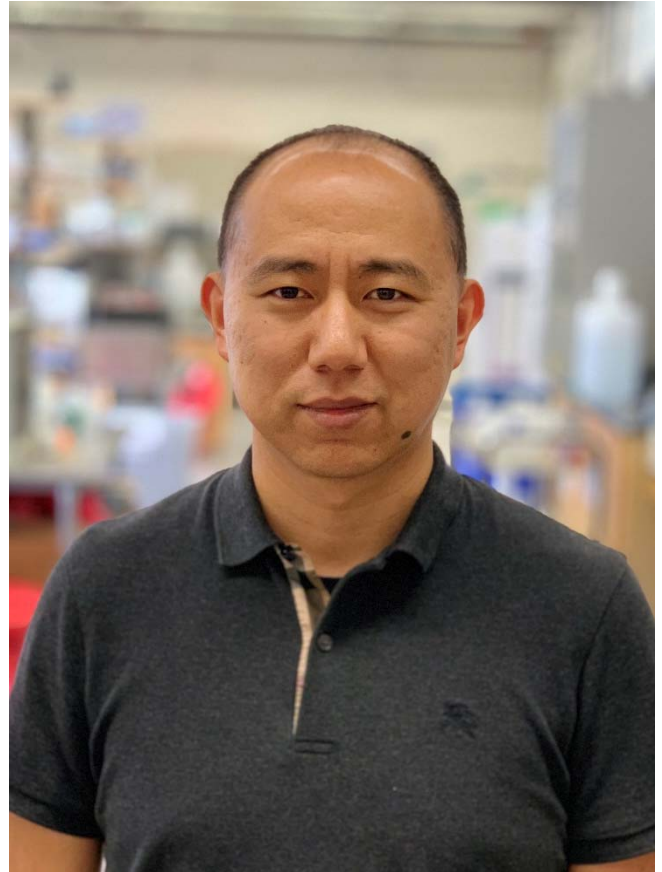
Dr. Luo is interested in developing and applying new genomic and genetic technologies to address long-standing questions in human diseases including the causal cell type(s) of diseases and the functions of non-coding genetic variants. Two major areas of his research are described below.

Developing new epigenomic technologies

Genomic profiling of epigenomic signatures (e.g. DNA methylation, histone modifications) enables the study of gene regulatory events at a global scale. In previous works, they have developed single-cell epigenomic and multi-omic technologies, and use these methods to study the gene regulatory diversity in the brain. His group developed a high-throughput single-cell methylome profiling method snmC-seq and its major update snmC-seq2 that have enabled cell-type classification and the identification of cell-type-specific regulatory elements across cortical neuron subtypes in mouse and human. More recently they have developed two single-cell multi-omic methods (snmCT-seq and sn-m3C-seq) that allow the multi-modal integration of transcriptome, DNA methylome, chromatin accessibility and chromatin conformation, providing a near-comprehensive epigenomic characterization of individual brain cells.

Genetic basis of neurodevelopmental disorders

Psychiatric neurodevelopmental disorders such as schizophrenia and autism spectrum disorders (ASD) are highly heritable. Regulatory mechanisms play an important role in both diseases and schizophrenia risk variants are enriched in bulk brain tissue enhancers and immune cell types. Importantly, ASD can be contributed by epigenetic regulation by 5mC. Rett's syndrome is a type of ASD and is caused by mutations in MECP2 (methyl-CpG binding protein 2) that recognize 5mC. Neurodevelopmental disorders are likely contributed by multiple cell types in developing and adult brains. His group will use a combination of single-cell multi-epigenomics and population genetics approaches to address the contribution of aberrant gene regulations in neurodevelopmental disorders.



Publications

Luo, C.*, Lee, Q.Y.* , Wapinski, O., Castanon, R., Nery, J.R., Mall, M., Kareta, M.S., Cullen, S.M., Goodell, M.A., Chang, H.Y., Wernig, M., Ecker, J.R. [Global DNA methylation remodeling during direct reprogramming of fibroblasts to neurons](#). (2019) *Elife*. 8. DOI: 10.7554/eLife.40197 * Co-first author

Lee, D.* , **Luo, C.***, Zhou, J., Chandran, S., Rivkin, A., Bartlett, A., Nery J.R., Fitzpatrick, C., O'Conner, C., Dixon, J.R. and Ecker, J.R. [Single-cell multi-omic profiling of chromatin conformation and DNA methylome](#). (2018) *bioRxiv*. <https://doi.org/10.1101/503235> *Co-first author.

Luo, C.*, Liu, H.* , Wang, B., Rivkin, A., Bartlett, A., Nery, J.R., and Ecker, J.R. [Multi-omic profiling of transcriptome and DNA methylome in single nuclei with molecular partitioning](#). (2018) *bioRxiv*. <https://doi.org/10.1101/434845> *Co-first author.

Luo, C.*, Hajkova, P.* , Ecker, J.R. [Dynamic DNA methylation: In the right place at the right time](#). (2018) *Science*. 361(6409):1336-1340. DOI: 10.1126/science.aat6806 * Co-first author

Sabbagh, M.F., Heng, J.S., **Luo, C.**, Castanon, R.G., Nery, J.R., Rattner, A., Goff, L.A., Ecker, J.R., Nathans, J. [Transcriptional and epigenomic landscapes of CNS and non-CNS vascular endothelial cells](#). (2018) *Elife*. 7. DOI: 10.7554/eLife.36187

Luo, C., Rivkin, A., Zhou, J., Sandoval, J.P., Kurihara, L., Lucero, J., Castanon, R., Nery, J.R., Pinto-Duarte, A., Bui, B., Fitzpatrick, C., Connor, C., Ruga, S., Van Eden, M.E., Davis, D.A., Mash, D.C., Behrens, M.M., Ecker, J.R. [Robust single-cell DNA methylome profiling with snmC-seq2](#). (2018) *Nature Communications*. 9(1):3824. DOI: 10.1038/s41467-018-06355-2

Luo, C.*, Keown, C.L.* , Kurihara, L., Zhou, J., He, Y., Li, J., Castanon, R., Lucero, J., Nery, J.R., Sandoval, J.P., Bui, B., Sejnowski, T.J., Harkins, T.T., Mukamel, E.A., Behrens, M.M., Ecker, J.R. [Single-cell methylomes identify neuronal subtypes and regulatory elements in mammalian cortex](#). (2017)*Science*. 357(6351):600-604. DOI: 10.1126/science.aan3351 * Co-first author

Luo, C.*, Lancaster, M.A.* , Castanon, R., Nery, J.R., Knoblich, J.A., Ecker, J.R. [Cerebral Organoids Recapitulate Epigenomic Signatures of the Human Fetal Brain](#). (2016) *Cell Reports*. 17(12):3369-3384. DOI: 10.1016/j.celrep.2016.12.001 * Co-first author

Chin, C.S., Peluso, P., Sedlazeck, F.J., Nattestad, M., Concepcion, G.T., Clum, A., Dunn, C., O'Malley, R., Figueroa-Balderas, R., Morales-Cruz, A., Cramer, G.R., Delledonne, M., **Luo, C.**, Ecker, J.R., Cantu, D., Rank, D.R., Schatz, M.C. [Phased diploid genome assembly with single-molecule real-time sequencing](#). (2016) *Nature Methods*. 13(12):1050-1054. DOI: 10.1038/nmeth.4035

Mo, A., **Luo, C.**, Davis, F.P., Mukamel, E.A., Henry, G.L., Nery, J.R., Urich, M.A., Picard, S., Lister, R., Eddy, S.R., Beer, M.A., Ecker, J.R., Nathans, J. [Epigenomic landscapes of retinal rods and cones](#). (2016) *Elife*. 5:e11613. DOI: 10.7554/eLife.11613

Mo, A.* , Mukamel, E.A.* , Davis, F.P.* , **Luo, C.***, Henry, G.L., Picard, S., Urich, M.A., Nery, J.R., Sejnowski, T.J., Lister, R., Eddy, S.R., Ecker, J.R. and Nathans, J. [Epigenomic Signatures of Neuronal Diversity in the Mammalian Brain](#). (2015) *Neuron*. 86: 1369-1384. *Co-first author.

Wu, J., Okamura, D., Li, M., Suzuki, K., **Luo, C.**, Ma, L., He, Y., Li, Z., Benner, C., Tamura, I., Krause, M.N., Nery, J.R., Du, T., Zhang, Z., Hishida, T., Takahashi, Y., Aizawa, E., Kim, N.Y., Lajara, J., Guillen, P., Campistol, J.M., Esteban, C.R., Ross, P.J., Saghatelian, A., Ren, B., Ecker, J.R., Izpisua Belmonte, J.C. (2015). [An alternative pluripotent state confers interspecies chimaeric competency](#). *Nature*. 521: 316-321.

Luo, C., Ecker, J.R. [Exceptional epigenetics in the brain](#). (2015) *Science*. 348: 1094-1095.

Widiez, T., Symeonidi, A., **Luo, C.**, Lam, E., Lawton, M. and Rensing, S.A. [The chromatin landscape of the moss *Physcomitrella patens* and its dynamics during development and drought stress.](#) (2014) *Plant J.* 79: 67-81.

Luo, C.*, Dong, J.*, Zhang, Y. and Lam, E. [Decoding the role of chromatin architecture in development: coming closer to the end of the tunnel.](#) (2014) *Front. Plant Sci.* 5:374. *Co-first author.

Luo, C. and Lam, E. [Quantitatively profiling genome-wide patterns of histone modifications in *Arabidopsis thaliana* using ChIP-seq.](#) (2014) *Methods Mol Biol.* 1112: 177-193.

Luo, C., Sidote, D.J., Zhang, Y., Kerstetter, R.A., Michael, T.P. and Lam, E. [Integrative analysis of chromatin states in *Arabidopsis* identified potential regulatory mechanisms for Natural Antisense Transcript production.](#) (2012) *Plant J.* 73: 77-90.

Vaquero-Sedas, M.I., **Luo, C.** and Vega-Palas, M.A. [Analysis of the epigenetic status of telomeres by using ChIP-seq data.](#) (2012) *Nucleic Acids Res.* 40: e163.

Amini, A., **Luo, C.** and Lam, E. [Chromatin Beacons: Global sampling of chromatin physical properties using chromatin charting lines.](#) (2011) *Methods Mol Biol.* 701: 301-14.

Luo, C., and Lam, E. [ANCORP: a high resolution approach that generated distinct chromatin state model from multiple genome-wide datasets.](#) (2010) *Plant J.* 63: 339-351.

Lam, E., **Luo, C.** and Watanabe, N. [Charting functional and physical properties of chromatin in living cells.](#) (2009) *Curr Opin Genet Dev.* 19, 135-141.

Luo, C.*, Durgin, B.G.*, Watanabe, N.*, and Lam, E. [Defining the Functional Network of Epigenetic Regulators in *Arabidopsis thaliana*.](#) (2009) *Mol. Plant.* 2, 661-674. *Co-first author.

Luo, C. and Lam, E. [Chromatin Charting: Global mapping of epigenetic effects.](#) (2009) *Methods Mol Biol.* 553, 127-139.

Rotter, D., Bharti, A.K., Li, H.M., **Luo, C.**, Bonos, S.A., Bughrara, S., Jung, G., Messing, J., Meyer, W.A., Rudd, S., Warnke, S.E., and Belanger, F.C. [Analysis of EST sequences suggests recent origin of allotetraploid colonial and creeping bentgrasses.](#) (2007) *Mol Genet Genomics.* 278, 197-209.