

NGS

Next-Generation Sequencing Unit

The Next-Generation Sequencing (NGS) unit, established in 2015, is part of the DNA Sequencing Facility (DSF) at the Institute of Molecular and Cell Biology (IMCB). We support IMCB researchers with their diverse NGS projects, all the way from initially planning a project together to finally receiving sequencing data. Our mission is to provide high quality NGS service and cost- and time-efficient solutions to every project.

Current standard protocols include:

- RNA-Seq (rRNA-depletion/mRNA enrichment)
- Low-input and single cell RNA-Seq
- Chromatin-IP (ChIP)-Seq
- ATAC-Seq
- 16S rDNA-Seq

Furthermore, we develop customized solutions and methods for individual applications.

Contact

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Heike obtained her PhD from the University of Tuebingen, Germany, studying miRNAs and post-transcriptional regulation in plants at the nearby Max Planck Institute for Developmental Biology. She moved to Singapore in 2009 to join Temasek Life Sciences Laboratory, shifting her research towards epigenetic regulatory mechanisms and the role of histone variants in plant chromatin architecture. After a brief interval at the Genome Institute of Singapore,

focusing on single cell RNA-Sequencing, Heike started at IMCB in 2015 to establish and manage the NGS Unit, under the umbrella of the DNA Sequencing Facility.

Recent Publications

The KRAB-zinc-finger protein ZFP708 mediates epigenetic repression at RMER19B retrotransposons.

Seah MKY, Wang Y, Goy PA, Loh HM, Peh WJ, Low DHP, Han BY, Wong E, Leong EL, Wolf G, Mzoughi S, Wollmann H, Macfarlan TS, Guccione E, Messerschmidt DM.

Development. 2019

MBNL1 alternative splicing isoforms play opposing roles in cancer.

Tabaglio T, Low DH, Teo WKL, Goy PA, Cywoniuk P, Wollmann H, Ho J, Tan D, Aw J, Pavesi A, Sobczak K, Wee DKB, Guccione E.

Life Sci Alliance. 2018

PRDM15 safeguards naive pluripotency by transcriptionally regulating WNT and MAPK-ERK signalling.

Mzoughi S, Zhang J, Hequet D, Teo SX, Fang H, Xing QR, Bezzi M, Seah MKY, Ong SLM, Shin EM, Wollmann H, Wong ESM, Al-Haddawi M, Stewart CL, Tergaonkar V, Loh YH, Dunn NR, Messerschmidt DM, Guccione E.

Nat Genet. 2017

Loss of maternal Trim28 causes male-predominant early embryonic lethality.

Sampath Kumar A, Seah MK, Ling KY, Wang Y, Tan JH, Nitsch S, Lim SL, Lorthongpanich C, Wollmann H, Low DH, Guccione E, Messerschmidt DM.

Genes Dev. 2017