CURRICULUM VITAE

Name: Lothar Hennighausen

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Position: Chief, Laboratory of Genetics and Physiology

Institution: National Institutes of Health

Location: Bethesda, MD, USA

Education: Harvard Medical School, Post-doctoral fellow, 1985

University of Köln (Germany), Doctorate, 1982 University of Köln (Germany), Diploma, 1979

University of Edinburgh (Scotland), Honors Program, Molecular Biology, 1978

University of Marburg (Germany), BSc, 1977

Representative Careers:

FASEB Conference, Growth Hormone, Keynote lecture (2019)

Mammary Gland Biology Gordon Conference, Keynote Speaker, (2016)

Distinguished Lecture Series, Lady Davis Institute, McGill, Montreal, Speaker (2012)

Korean Society for Molecular and Cellular Biology, Annual meeting, Plenary speaker, Seoul (2009)

Member and Chair, Scientific Advisory Board, Georg-Speyer Haus, Frankfurt, Germany (2009-present)

Korean Society of Science and Engineering, Distinguished World Class Scholar (2008)

Deutsche Forschungsgemeinschaft, Mercator Professorship (2007)

Alexander von Humboldt Foundation, Humboldt Research Prize (2002)

Alexander von Humboldt Foundation, Humboldt Fellow (1992)

Specialty & Present Interest:

Genetics, gene regulation, super-enhancers controlling cell lineages, genome engineering

Representative papers:

- 1. Willi M, Smith HE, Wang C, Liu C, Hennighausen L (2018) Mutation frequency is not increased in CRISPR-Cas9-edited mice. **Nature Methods**, doi: 10.1038/s41592-018-0148-2.
- 2. Lee HK, Willi M, Miller SM, Kim S, Liu C, Liu DR, Hennighausen L (2018) Targeting fidelity of adenine and cytosine base editors in mice. **Nature Commun**, in press.
- 3. Lee HK, Willi M, Shin HY, Liu C, Hennighausen L (2018) Progressing super-enhancer landscape during mammary differentiation controls tissue-specific gene regulation. **Nucleic Acids Res**, doi.1093/nar/gky891
- **4.** Shin HY, Wang C, Lee HK, Yoo KH, Zeng X, Kuhns T, Yang CM, Mohr T, Liu C, Hennighausen L (2017) CRISPR/Cas9 targeting events cause complex deletions and insertions at 17 sites in the mouse genome. **Nature Commun** 8: 15464
- 5. Shin HY, Willi M, Yoo HK, Zeng X, Wang C, Metser G, Hennighausen L (2016) Hierarchy within the mammary STAT5-driven Wap super-enhancer. **Nature Genetics** 48: 904-911