

# Molekulare Grundlagen der Epigenetik

Datum	Seminarthema
24.10.2019	Fragen zur 1. Vorlesung, Organisatorisches, Themenvergabe
07.11.2019	[PC-Pool] Sequenz-Übungen zur Methylierungsanalyse
21.11.2019	<p><b>Nicola Schmidt und Jasmin Noack:</b> Now and then: Comparison of two Arabidopsis methylome studies from 2008 and 2017</p> <p>Lister et al., Cell (2008): „Highly Integrated Single-Base Resolution Maps of the Epigenome in Arabidopsis“</p> <p>Kawakatsu et al., Genome Biol (2017): „Dynamic DNA methylation reconfiguration during seed development and germination“</p>
05.12.2019	<p><b>Vivien Quitzke:</b> Hiraoka et al., Nat Comm (2016): “Metaepigenomic analysis reveals the unexplored diversity of DNA methylation in an environmental prokaryotic community”</p> <p><b>Frances Morgenstern:</b> Stajic et al, Nat Ecol Evol (2019): “Epigenetic gene silencing alters the mechanisms and rate of evolutionary adaptation” oder Colicchio et al., BMC Genomics (2018): “Parental experience modifies the <i>Mimulus</i> methylome”</p>
19.12.2019	<p><b>Nicole Rüsing:</b> Elsner et al., PNAS (2018): „Longevity and transposon defense, the case of termite reproductives “</p> <p><b>Christoph Hinze:</b> Wittmeyer et al., Plant Cell (2018): “The dominant and poorly penetrant phenotypes of maize unstable factor for orange1 are caused by DNA methylation changes at a linked transposon”</p> <p><b>Sofie Lobert:</b> De Mendoza et al., Genome Res (2019): „Capture of a functionally active methyl-CpG binding domain by an arthropod retrotransposon family“</p>
09.01.2020	<p><b>Sophie Richter:</b> Lehretz et al., Curr Biol (2019): „Post-transcriptional regulation of FLOWERING LOCUS T modulates heat-dependent source-sink development in potato“</p> <p><b>Theresa Fischer:</b> Mutzel et al., Nature Struct Mol Biol (2019): „A symmetric toggle switch explains the onset of random X inactivation in different mammals“</p>
23.01.2020	Auswertung des Fragenkatalogs

