

**BIOINFORMATICS POSTDOC IN FUNCTIONAL EVOLUTIONARY GENOMICS** Center for Molecular Biology of the University of Heidelberg (ZMBH), Heidelberg, Germany A postdoctoral position (2 years with possible extensions) is available immediately in the evolutionary genomics group of Henrik Kaessmann. We are seeking highly qualified and enthusiastic applicants with strong skills in computational biology/bioinformatics, preferably also with experience in data mining and comparative or evolutionary genome analyses. We have been interested in a range of topics related to the functional evolution of genomes across mammals. In the framework of our research, we are generating comprehensive sets of RNA-seq data for a large collection of germline and somatic tissues from representatives of all major mammalian lineages (placental mammals, marsupials, and the egg-laying monotremes) and evolutionary outgroups (e.g., birds). In conjunction with various high-throughput genomic and epigenomic datasets, we are using these transcriptome data to study the functional (expression) evolution of mammalian genomes across gene types, lineages, tissues, developmental stages, chromosomes and sexes. The postdoctoral fellow will perform integrated evolutionary/bioinformatics analyses based on data produced in our lab and available genomic data. The specific project will be developed together with the candidate. The language of the institute is English, and its members form a highly international group. The ZMBH is located in Heidelberg, a beautiful international city next to the Odenwald forest and Neckar river. For more information on the group and our institute more generally, please refer to our website at the ZMBH (<http://www.zmbh.uni-heidelberg.de/Kaessmann/>) and also our website at the University of Lausanne (Switzerland, <http://www.unil.ch/cig/kaessmann>), where our lab is currently located (before moving to Heidelberg October 1, 2015). Please submit a CV, statement of research interest, and names of three references to: Henrik Kaessmann ([h.kaessmann@zmbh.uni-heidelberg.de](mailto:h.kaessmann@zmbh.uni-heidelberg.de)) or [Henrik.Kaessmann@unil.ch](mailto:Henrik.Kaessmann@unil.ch)). -- Henrik Kaessmann, Ph.D. Full Professor ZMBH Im Neuenheimer Feld 282 69120 Heidelberg, Germany Selected recent publications: Cortez, D., Marin, R., Toledo-Flores, D., Froidevaux, L., Liechti, A., Waters, P.D., Grd'z'znier, F., and Kaessmann, H. (2014) Origins and functional evolution of Y chromosomes across mammals. *Nature* 508: 488-493. Necsulea, A., Soumillon, M., Warnefors, M., Liechti, A., Daish, T., Zeller, U., Baker, J.C., Grd'z'znier, F., and Kaessmann, H. (2014) The evolution of lncRNA repertoires and expression patterns in tetrapods. *Nature* 505: 635-640. Necsulea, A. and Kaessmann, H. (2014) Evolutionary dynamics of coding and noncoding transcriptomes. *Nat. Rev. Genet.* 5: 734-48. Meunier, J., Lemoine, F., Soumillon, M., Liechti, A., Weier, M., Guschanski, K., Hu, H., Khaitovich, P., and Kaessmann, H. (2013) Birth and expression evolution of mammalian microRNA genes. *Genome Res.* 23: 34-45. Julien, P., Brawand, D., Soumillon, M., Necsulea, A., Liechti, A., Schd'z'tz, F., Daish, T., Grd'z'znier, F., and Kaessmann, H. (2012) Mechanisms and evolutionary patterns of mammalian and avian dosage compensation *PLoS Biol.* 5:e1001328. Brawand, D., Soumillon, M., Necsulea, A., Julien, P., Csd'z'rdi, G., Harrigan, P., Weier, M., Liechti, A., Aximu-Petri, A., Kircher, M., Albert, F.W., Zeller, U., Khaitovich, P., Grd'z'znier, F., Bergmann, S., Nielsen, R., Pd'z'd'z'bo, S., and Kaessmann, H. (2011) The evolution of gene expression levels in mammalian organs. *Nature* 478: 343-348.