Publications

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1. Gao, A.W., Alam, G.E., Zhu, Y., Li, W., Sulc, J., Li, X., Katsyuba, E., Li, T.Y., Overmyer, K.A., Lalou, A., Mouchiroud, L., Bou Sleiman, M., Cornaglia, M., Morel, J.-D., Houtkooper, R.H., Coon, J.J., and Auwerx, J. (2024). High-content phenotypic analysis of a C. Elegans recombinant inbred population identifies genetic and molecular regulators of lifespan. *Cell Reports* 43 https://doi.org/10.1016/j.celrep.2024.114836.

2. Li, X., Morel, J.-D., Sulc, J., Masi, A.D., Lalou, A., Benegiamo, G., Poisson, J., Liu, Y., Alvensleben, G.V.G.V., Gao, A.W., Bou Sleiman, M., and Auwerx, J. (2024). Systems genetics of metabolic health in the BXD mouse genetic reference population. *Cell Systems* 15, 497–509.e3 https://doi.org/10.1016/j.cels.2024.05.006.

3. Choi, S., Kang, J.-G., Tran, Y.T.H., Jeong, S.-H., Park, K.-Y., Shin, H., Kim, Y.H., Park, M., Nahmgoong, H., Seol, T., Jeon, H., Kim, Y., Park, S., Kim, H., Kim, M.-S., Li, X., Bou Sleiman, M., Lee, E., Choi, J., Eisenbarth, D., Lee, S.H., Cho, S., Moore, D.D., Auwerx, J., Kim, I.-Y., Kim, J.B., Park, J.-E., Lim, D.-S., and Suh, J.M. (2024). Hippo–YAP/TAZ signalling coordinates adipose plasticity and energy balance by uncoupling leptin expression from fat mass. *Nature Metabolism* 6, 847–860 https://doi.org/10.1038/s42255-024-01045-4.

4. Park, A., Kim, K., Park, I., Lee, S.H., Park, K.-Y., Jung, M., Li, X., Bou Sleiman, M., Lee, S.J., Kim, D.-S., Kim, J., Lim, D.-S., Woo, E.-J., Lee, E.W., Han, B.S., Oh, K.-J., Lee, S.C., Auwerx, J., Mun, J.Y., Rhee, H.-W., Kim, W.K., Bae, K.-H., and Suh, J.M. (2023). Mitochondrial matrix protein LETMD1 maintains thermogenic capacity of brown adipose tissue in male mice. *Nature Communications* 14, 3746 https://doi.org/10.1038/s41467-023-39106-z.

5. Li, X., Morel, J.-D., Benegiamo, G., Poisson, J., Bachmann, B., Rapin, A., Willams, E., Perino, A., Schoonjans, K., Bou Sleiman, M., and Auwerx, J. (2023). Genetic and dietary modulators of the inflammatory response in the gastro-intestinal tract of the BXD mouse genetic reference population. *eLife* 12 https://doi.org/10.7554/eLife.87569.

6. Morel, J.-D., Bou Sleiman, M., Li, T.Y., Alvensleben, G. von, Bachmann, A.M., Hofer, D., Broeckx, E., Ma, J.Y., Carreira, V., Chen, T., Azhar, N., Gonzalez-Villalobos, R.A., Breyer, M., Reilly, D., Mullican, S., and Auwerx, J. (2023). Mitochondrial and NAD^+ metabolism predict recovery from acute kidney injury in a diverse mouse population. *JCI Insight* 8 https://doi.org/10.1172/jci.insight.164626.

7. Benegiamo, G., Alvensleben, G.V.G. von, Rodríguez-López, S., Goeminne, L.J.E., Bachmann, A.M., Morel, J.-D., Broeckx, E., Ma, J.Y., Carreira, V., Youssef, S.A., Azhar, N., Reilly, D.F., D'Aquino, K., Mullican, S., Bou Sleiman, M., and Auwerx, J. (2023). The genetic background shapes the susceptibility to mitochondrial dysfunction and NASH progression. *Journal of Experimental Medicine* 220, e20221738 https://doi.org/10.1084/jem.20221738.

8. Liu, Y., Scantlebery, A.M.L., Strotjohann, K., Rodriguez-Lopez, S., Li, X., Homicsko, K., Smith, K., Ciavarri, J., Bou Sleiman, M., Houtkooper, R.H., and Auwerx, J. eds. (2023). INHIBITING SARM1 IS MORE EFFICACIOUS THAN NICOTINAMIDE RIBOSIDE SUPPLEMENTATION FOR THE TREATMENT OF A MOUSE MODEL WITH NAFLD/NASH. *Hepatology*.

9. Benegiamo, G., Bou Sleiman, M., Wohlwend, M., Rodríguez-López, S., Goeminne, L.J.E., Laurila, P.-P., Klevjer, M., Salonen, M.K., Lahti, J., Jha, P., Cogliati, S., Enriquez, J.A., Brumpton, B.M., Bye, A., Eriksson, J.G., and Auwerx, J. (2022). COX7A2L genetic variants determine cardiorespiratory fitness in mice and human. *Nature Metabolism* 4, 1336–1351 https://doi.org/10.1038/s42255-022-00655-0.

10. Li, H., Perino, A., Huang, Q., Von Alvensleben, G.V.G., Banaei-Esfahani, A., Velazquez-Villegas, L.A., Gariani, K., Korbelius, M., Bou Sleiman, M., Imbach, J., Sun, Y., Li, X., Bachmann, A., Goeminne, L.J.E., Gallart-Ayala, H., Williams, E.G., Ivanisevic, J., Auwerx, J., and Schoonjans, K. (2022). Integrative systems analysis identifies genetic and dietary modulators of bile acid homeostasis. *Cell Metabolism* https://doi.org/10.1016/j.cmet.2022.08.015.

11. Bou Sleiman, M., Roy, S., Gao, A.W., Sadler, M.C., Alvensleben, G.V.G. von, Li, H., Sen, S., Harrison, D.E., Nelson, J.F., Strong, R., Miller, R.A., Kutalik, Z., Williams, R.W., and Auwerx, J. (2022). Sex- and age-dependent genetics of longevity in a heterogeneous mouse population. *Science* 377, eabo3191 https://doi.org/10.1126/science.abo3191.

12. Bachmann, A.M., Morel, J.-D., El Alam, G., Rodríguez-López, S., Imamura de lima, T., Goeminne, L.J.E., Benegiamo, G., Loric, S., Conti, M., Bou Sleiman, M., and Auwerx, J. (2022). Genetic background and sex control the outcome of high-fat diet feeding in mice. *iScience* 25, 104468 https://doi.org/10.1016/j.isci.2022.104468.

13. Gao, A.W., El Alam, G., Lalou, A., Li, T.Y., Molenaars, M., Zhu, Y., Overmyer, K.A., Shishkova, E., Hof, K., Bou Sleiman, M., Houtkooper, R.H., Coon, J.J., and Auwerx, J. (2022). Multi-omics analysis identifies essential regulators of mitochondrial stress response in two wild-type C. Elegans strains. *iScience* 25, 103734 https://doi.org/10.1016/j.isci.2022.103734.

14. Roy, S., Bou Sleiman, M., Jha, P., Ingels, J.F., Chapman, C.J., McCarty, M.S., Ziebarth, J.D., Hook, M., Sun, A., Zhao, W., Huang, J., Neuner, S.M., Wilmott, L.A., Shapaker, T.M., Centeno, A.G., Ashbrook, D.G., Mulligan, M.K., Kaczorowski, C.C., Makowski, L., Cui, Y., Read, R.W., Miller, R.A., Mozhui, K., Williams, E.G., Sen, S., Lu, L., Auwerx, J., and Williams, R.W. (2021). Gene-by-environment modulation of lifespan and weight gain in the murine BXD family. *Nature Metabolism* 3, 1217–1227 https://doi.org/10.1038/s42255-021-00449-w.

15. Porcu, E., Sadler, M.C., Lepik, K., Auwerx, C., Wood, A.R., Weihs, A., Bou Sleiman, M., Ribeiro, D.M., Bandinelli, S., Tanaka, T., Nauck, M., Völker, U., Delaneau, O., Metspalu, A., Teumer, A., Frayling, T., Santoni, F.A., Reymond, A., and Kutalik, Z. (2021). Differentially expressed genes reflect disease-induced rather than disease-causing changes in the transcriptome. *Nature Communications* 12, 5647 https://doi.org/10.1038/s41467-021-25805-y.

16. Sorrentino, G., Perino, A., Yildiz, E., El Alam, G., Bou Sleiman, M., Gioiello, A., Pellicciari, R., and Schoonjans, K. (2020). Bile Acids Signal via TGR5 to Activate Intestinal Stem Cells and Epithelial Regeneration. *Gastroenterology* 159, 956–968.e8 https://doi.org/10.1053/j.gastro.2020.05.067.

17. Bou Sleiman, M., Jha, P., Houtkooper, R., Williams, R.W., Wang, X., and Auwerx, J. (2020). The Gene-Regulatory Footprint of Aging Highlights Conserved Central Regulators. *Cell Reports* 32 https://doi.org/10.1016/j.celrep.2020.108203.

18. Frochaux, M.V., Bou Sleiman, M., Gardeux, V., Dainese, R., Hollis, B., Litovchenko, M., Braman, V.S., Andreani, T., Osman, D., and Deplancke, B. (2020). Cis-regulatory variation modulates susceptibility to enteric infection in the Drosophila genetic reference panel. *Genome Biology* 21, 6 https://doi.org/10.1186/s13059-019-1912-z.

19. Bou Sleiman, M., Frochaux, M.V., Andreani, T., Osman, D., Guigo, R., and Deplancke, B. (2020). Enteric infection induces Lark-mediated intron retention at the 5' end of Drosophila genes. *Genome Biology* 21, 4 https://doi.org/10.1186/s13059-019-1918-6.

20. Li, H., Rukina, D., David, F.P.A., Li, T.Y., Oh, C.-M., Gao, A.W., Katsyuba, E., Bou Sleiman, M., Komljenovic, A., Huang, Q., Williams, R.W., Robinson-Rechavi, M., Schoonjans, K., Morgenthaler, S., and Auwerx, J. (2019). Identifying gene function and module connections by the integration of multispecies expression compendia. *Genome Research* https://doi.org/10.1101/gr.251983.119.

21. Ma, D., Bou Sleiman, M., Joncour, P., Indelicato, C.-E., Frochaux, M., Braman, V., Litovchenko, M., Storelli, G., Deplancke, B., and Leulier, F. (2019). Commensal Gut Bacteria Buffer the Impact of Host Genetic Variants on Drosophila Developmental Traits under Nutritional Stress. *iScience* 19, 436–447 https://doi.org/10.1016/j.isci.2019.07.048.

22. Hook, M., Roy, S., Williams, E.G., Bou Sleiman, M., Mozhui, K., Nelson, J.F., Lu, L., Auwerx, J., and Williams, R.W. (2018). Genetic cartography of longevity in humans and mice: Current landscape and horizons. *Biochimica et Biophysica Acta (BBA) - Molecular Basis of Disease* https://doi.org/https://doi.org/10.1016/j.bbadis.2018.01.026.

23. Jha, P., McDevitt, M.T., Gupta, R., Quiros, P.M., Williams, E.G., Gariani, K., Bou Sleiman, M., Diserens, L., Jochem, A., Ulbrich, A., Coon, J.J., Auwerx, J., and Pagliarini, D.J. (2018). Systems Analyses Reveal Physiological Roles and Genetic Regulators of Liver Lipid Species. *Cell Systems* 6, 722–733.e6 https://doi.org/10.1016/j.cels.2018.05.016.

24. Jha, P., McDevitt, M.T., Halilbasic, E., Williams, E.G., Quiros, P.M., Gariani, K., Bou Sleiman, M., Gupta, R., Ulbrich, A., Jochem, A., Coon, J.J., Trauner, M., Pagliarini, D.J., and Auwerx, J. (2018). Genetic Regulation of Plasma Lipid Species and Their Association with Metabolic Phenotypes. *Cell Systems* 6, 709–721.e6 https://doi.org/10.1016/j.cels.2018.05.009.

25. Letizia, M.C., Cornaglia, M., Trouillon, R., Sorrentino, V., Mouchiroud, L., Bou Sleiman, M., Auwerx, J., and Gijs, M.A.M. (2018). Microfluidics-enabled phenotyping of a whole population of C. Elegans worms over their embryonic and post-embryonic development at single-organism resolution. *Microsystems & Nanoengineering* 4, 6 https://doi.org/10.1038/s41378-018-0003-8.

26. Li, H., Wang, X., Rukina, D., Huang, Q., Lin, T., Sorrentino, V., Zhang, H., Bou Sleiman, M., Arends, D., McDaid, A., Luan, P., Ziari, N., Velázquez-Villegas, L.A., Gariani, K., Kutalik, Z., Schoonjans, K., Radcliffe, R.A., Prins, P., Morgenthaler, S., Williams, R.W., and Auwerx, J. (2018). An Integrated Systems Genetics and Omics Toolkit to Probe Gene Function. *Cell Systems* 6, 90–102.e4 https://doi.org/10.1016/j.cels.2017.10.016.

27. Bou Sleiman, M., Bou Sleiman, M., Abbas, O., Btadini, W., Najjar, T., Tofaili, M., Chedraoui, A., Khalil, S., Kibbi, A.G., and Kurban, M. (2015). Novel mutation in LIPH in a Lebanese patient with autosomal recessive woolly hair/hypotrichosis. *The Journal of Dermatology* 42, 822–824 https://doi.org/10.1111/1346-8138.12939.

28. Bou Sleiman, M., Osman, D., Massouras, A., Hoffmann, A.A., Lemaitre, B., and Deplancke, B. (2015). Genetic, molecular and physiological basis of variation in Drosophila gut immunocompetence. *Nat Commun* 6 https://doi.org/10.1038/ncomms8829.

29. Neyen, C., Binggeli, O., Roversi, P., Bertin, L., Bou Sleiman, M., and Lemaitre, B. (2014). The Black cells phenotype is caused by a point mutation in the Drosophila pro-phenoloxidase 1 gene that triggers melanization and hematopoietic defects1. *Developmental & Comparative Immunology* 50, 166–174 https://doi.org/http://dx.doi.org/10.1016/j.dci.2014.12.011.

30. Chng, W.A., Bou Sleiman, M., Schüpfer, F., and Lemaitre, B. (2014). Transforming Growth Factor β/Activin Signaling Functions as a Sugar-Sensing Feedback Loop to Regulate Digestive Enzyme Expression. *Cell Reports* 9, 336–348 https://doi.org/http://dx.doi.org/10.1016/j.celrep.2014.08.064.

31. Possik, E.J., Bou Sleiman, M., Ghattas, I.R., and Smith, C.A. (2013). Randomized codon mutagenesis reveals that the HIV Rev arginine-rich motif is robust to substitutions and that double substitution of two critical residues alters specificity. *Journal of Molecular Recognition* 26, 286–296 https://doi.org/10.1002/jmr.2272.