All mammals are colonized by a multitude of microorganisms, constantly co-evolving with these diverse microbial communities and thus establishing symbiotic and mutualistic relationships. Both, the host and the microbiome rely on or are affected by the other in some way. While microbiota depend on the host for a sustainable living environment and access to nutrients, their effects on the hosts organism seem to be far more complex than anyone anticipated. Majority of microbes reside in the intestine, it is no wonder then that the largest impact of microbial activity is most likely coming from the gut. The composition and abundance of microbes making up the gut community is shaped by a number of factors like host genetics, immunological and physiological status of the host, environmental factors and colonization history. Once established, the host-gut microbiota interactions profoundly influence the health and wellbeing of the host. For instance, gut microbes are crucial in priming the innate and adaptive immune responses and promoting gut maturation and cell proliferation in mammals, but can even affect brain chemistry and individual behavior. Intestinal microbiota can also profoundly influence the hosts energy homeostasis and nutrition. For instance, mammals are limited in their ability to digest polysaccharides, thus a large portion of ingested carbohydrates remains inaccessible. With microbial assistance, the end products of fermentation of polysaccharides become available for the host. These are predominantly short chain fatty acids (SCFA) that can be absorbed by the host. Some studies have linked low microbial diversity and shifts in the microflora towards the high energy harvest microbiome to obesity. Other changes in gut microbiome affect the hosts energy expenditure by decreasing the resting metabolic rate and leading to weight gain in the affected subjects. The microbiota-muscle axis hypothesis states that gut microbiota can even affect muscle function, for instance low microbial diversity and low SCFA concentrations (both plasma and fecal) were linked with lower muscle mass, impaired muscle function and decreased running performance in mice.

In this project we focus on **how the genetically determined metabolic landscape of the host shapes the gut microbiome diversity and how the microbial functional diversity affects the host in return.** We will work with a unique model, mice from a long term selection experiment designed to produce two line types with divergent levels of basal metabolic rate, the high BMR (H-BMR) and low BMR (L-BMR) line type. These animals differ not only in their genetically determined basal costs of maintenance (BMR; 50% difference) but also a number of other traits associated with energy acquisition, physical activity and susceptibility to obesity. We aim to (**1) establish the baseline microbial community structure and functional diversity under standard housing conditions in a line of mice selected for high (H-BMR) and low BMR level (L-BMR).** This will be done by analyzing the microbiome of unmanipulated animals and the microbiome of an antibiotic treated group, while we also assess a number of physiological parameters that might be affected. Further, we want to study **(2) how exposure to different diet types affects the microbial community structure and function in both selected line types, and impact physiological performance.**