The first project year is characterised by start of the generation of large scale and high-throughput data in Pillar 1 and the work packages (WPs) therein:

- 12 rat strains have been sequenced with more than 20X coverage (WP 1.1 – Genome Sequencing).
- 362 mature miRNAs have been quantified and revealed novel dandidate miRNAs for the rat (WP 1.2 – transcriptome).
- ChIP protocols have been set up and single base resolution methylation profiles of the left ventricle of the Brown Norway (BN-Lx/Cub) and spontaneously hypertensive rat (SHR/Ola) were generated (WP 1.3 - epigenetics).
- A large-scale quantiative analysis of two liver proteomes (one BN-Lx and one SHR rat) and one heart proteome (left ventrical from BN-Lx rat) to a depth of 6,808 unique proteins was derived through in vitro super SILAC rat mix (WP 1.4 – proteomics).
- MESA, statistical tools and analytical systems for metabolic patterns have been developed (WP 1.5 – metabonomics).

Ontologies and the rat interime tool enable data integration and standards for data submission, description and analysis have been developed (WP 1.6 – data infrastructure). Mapping of different kinds of QTLs results in a transcriptional network that is published (Heinig et al (2010) A trans-acting locus regulates an anti-viral expression network and type 1 diabetes risk. Nature 467 (7314):460-464) (WP 2.1 – regulatory networks).

Rat genome modification technology has advanced through EC cells (Meek et. al, Efficient Gene Targeting by Homologous Recombination in Rat Embryonic Stem Cells, Plos ONE 5(12): e14225); ZNF technology has knocked out the first gene (WP 2.2 – functional validation).

Phenotypic and funcational imputation (WP 3.1 – comparative analysis) and tissue collection for translation of the results (WP 3.3 – validation in human tissues) has started. Orthologous regions of interest identified are accessible via Ensembl and RGD (WP 3.2 – integration with hGWAS).

(31.03.2011)