Supplemental Material

Supplemental Table Legends (see Excel files):

Table S1. Whole genome sequencing of SHR-A3 and SHR-B2 was performed and aligned to the rat reference genome. Annovar software was used to interrogate sequence differs between the rat reference genome and the genomes of SHR-A3 and SHR-B2 to determine coding sequence differences compare to the reference. This table lists all detected variants by chromosome and position. SHR-A3 variants are indicted in red font and SHR-B2 variants are indicated in green font.

Table S2. Single nucleotide polymorphisms in SHR-A3 and SHR-B2 were obtained by the STAR Consortium[1]. Here available SNP genotypes for Rnor Chr1 are presented with chromosomal position indicated. For each SNP and each SHR line, the presence of rat reference genome allele (BN) and the existence of alleles derived from Wistar rat genetic background (W) are indicated.

Table S3. HuProt Array. The supplementary Excel file includes worksheets indicating the HupProt 3.1 array data Z scores 1) detected by fluorescent anti-IgM, 2) detected by fluorescent anti-IgG and 3) a worksheet examining the signals with high Z scores in SHR-A3, comparing IgM and IgG signals and showing signals for the same array features in SHR-B2 and SHR-A3(*Stim1*-B2).

Supplemental Reference:

1. STAR Consortium, Saar K, Beck A, Bihoreau MT, Birney E, Brocklebank D, Chen Y, Cuppen E, Demonchy S, Dopazo J, Flicek P, Foglio M, Fujiyama A, Gut IG, Gauguier D, Guigo R, Guryev V, Heinig M, Hummel O, Jahn N, Klages S, Kren V, Kube M, Kuhl H, Kuramoto T, Kuroki Y, Lechner D, Lee YA, Lopez-Bigas N, Lathrop GM, Mashimo T, Medina I, Mott R, Patone G, Perrier-Cornet JA, Platzer M, Pravenec M, Reinhardt R, Sakaki Y, Schilhabel M, Schulz H, Serikawa T, Shikhagaie M, Tatsumoto S, Taudien S, Toyoda A, Voigt B, Zelenika D, Zimdahl H, Hubner N. SNP and haplotype mapping for genetic analysis in the rat. *Nat Genet.* 2008;40:560-6.