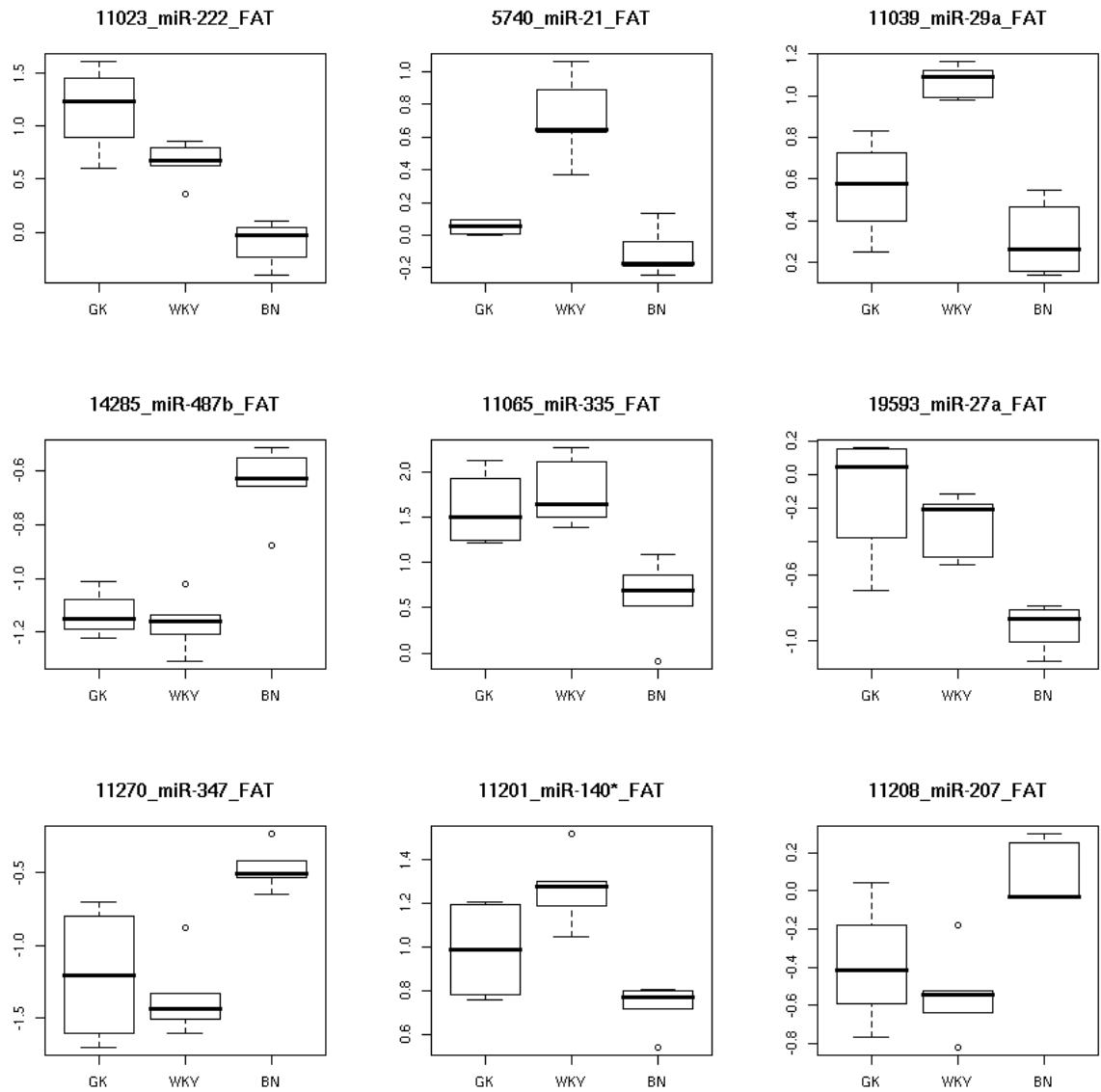


Electronic supplementary material

**ESM Fig. 2** Box plots of expression in GK, WKY and BN rats (relative to a common reference) for 29 microRNAs with significant differential expression across strains. Expression patterns of miR-222 and miR-27a in adipose tissue (a), miR-195 and miR-103 in liver (b) and miR-10b in skeletal muscle (c) correlated to fasting glucose phenotypes (GK>WKY>BN or GK<WKY<BN) (see ESM Fig. 1). Measured expression levels for: miR-29a, miR-21, miR-347, miR-140\*, miR-207 in adipose tissue. MiR-let-7e in skeletal muscle, and miR-290, miR-146, miR15b, miR-296, miR-422b, miR-140\* in liver levels which correlated with HDL cholesterol and total cholesterol phenotypes (the order BN<GK<WKY or BN>GK>WKY). In contrast, , miR-100, miR-335 and miR-292-5p displayed the WKY>(GK~BN) or WKY<(GK~BN) pattern in liver, suggesting that strain effects and not phenotypic effects control both HDL and total cholesterol levels (see ESM Fig. 1). MiR-125b and miR-193 expression in the liver corresponded approximately to a linear relationship between plasma triacylglycerol levels across the three strains (GK>BN>WKY or GK<BN<WKY), while the expression of miR-487b and miR-335 (in adipose tissue) and of miR-27b and miR-126 (in the liver) followed a BN>(GK~WKY) or a BN<(GK~WKY) expression pattern, suggesting a strain effect regulating plasma triacylglycerol levels

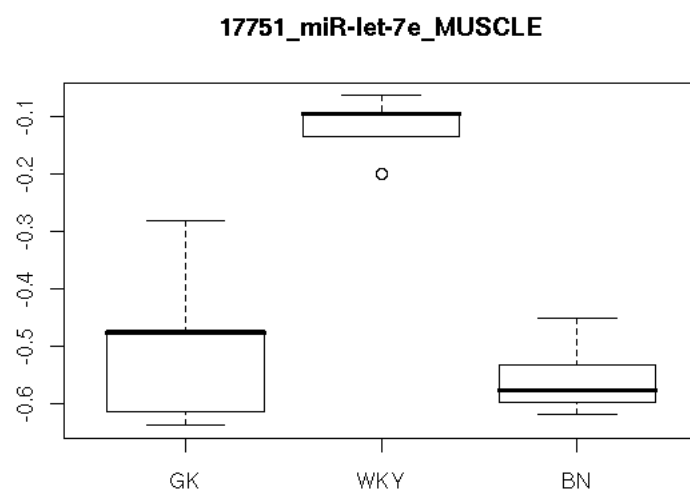
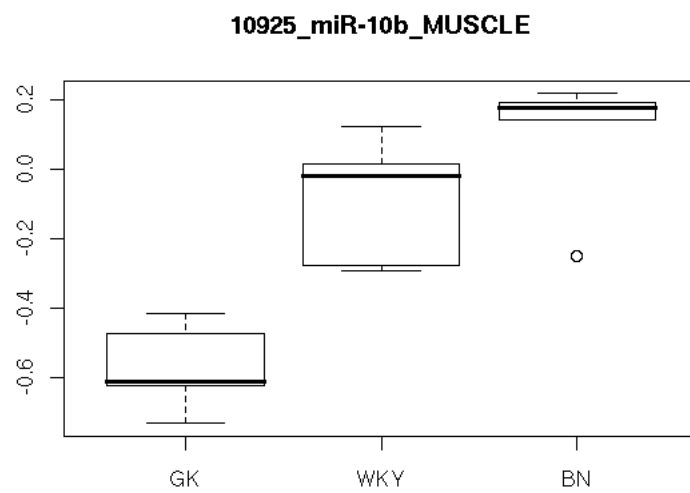
a

Adipose tissue



**b**

Skeletal muscle



**c**

Liver

