

Table S1. Phenotypes in congenic and BN and GK progenitor strains. Values are means \pm SE. Number of observations is reported in parentheses. ***P<0.001; **P<0.01; *P<0.05, significantly different to BN controls. Details of GK genomic regions in the congenics are given in Table 1.

strain	Body weight (g)	Adiposity	CumG (mg/dL)	CumI (μ g/L)
BN	243.4 \pm 3.5 (62)	0.376 \pm 0.031 (40)	5104 \pm 83 (39)	43.45 \pm 3.23 (29)
GK	284.9 \pm 5.4 (16)***	1.246 \pm 0.087 (25)***	12181 \pm 849 (8)***	76.05 \pm 6.76 (18)***
BN.GK1b	243.4 \pm 3.3 (44)	0.342 \pm 0.022 (31)	4695 \pm 59 (20)***	50.15 \pm 4.51 (16)
BN.GK1cns	270.0 \pm 5.7 (21)***	0.416 \pm 0.028 (29)*	5504 \pm 135 (14)***	70.21 \pm 11.50 (14)*
BN.GK1f	253.5 \pm 2.3 (36)*	0.375 \pm 0.026 (30)	5048 \pm 154 (7)	48.99 \pm 3.06 (15)
BN.GK1d	249.0 \pm 7.5 (20)	0.327 \pm 0.025 (10)	4934 \pm 129 (6)	40.07 \pm 3.82 (12)
BN.GK1h	253.4 \pm 8.1 (7)	0.457 \pm 0.059 (11)	4849 \pm 78 (6)*	67.82 \pm 7.17 (10)**
BN.GK1k	258.0 \pm 5.2 (22)*	0.330 \pm 0.021 (15)	5074 \pm 89 (11)	57.52 \pm 5.18 (8)*
BN.GK1o	264.3 \pm 3.9 (20)***	0.419 \pm 0.032 (22)	5356 \pm 65 (11)*	32.01 \pm 2.85 (14)*
BN.GK1p	265.6 \pm 9.5 (16)*	0.596 \pm 0.044 (6)*	4977 \pm 156 (7)	40.54 \pm 5.01 (7)
BN.GK1q	251.6 \pm 5.3 (17)	0.357 \pm 0.042 (18)	4520 \pm 128 (9)**	69.24 \pm 6.87 (10)**
BN.GK1t	216.5 \pm 5.7 (22)***	0.442 \pm 0.044 (12)	4883 \pm 205 (8)	47.78 \pm 3.42 (11)
BN.GK1u	260.3 \pm 3.7 (19)**	0.452 \pm 0.038 (13)*	5018 \pm 87 (11)	57.30 \pm 9.80 (6)
BN.GK1v	231.6 \pm 5.7 (19)	0.325 \pm 0.040 (6)	5105 \pm 88 (10)	50.65 \pm 3.85 (11)

Table S2. Parameter values for cross-validations performed to assess the validity of the O-PLS models designed to compare metabolomic data in each BN.GK congenic strain against BN controls.

O-PLS model	R ² X	Q ² Y
1b/BN	0.542	0.737
1f/BN	0.683	0.718
1q/BN	0.753	0.879
1p/BN	0.717	0.631
1u/BN	0.870	0.735
1k/BN	0.647	0.358
1t/BN	0.758	0.592
1v/BN	0.935	0.625
1cons/BN	0.815	0.887
1d/BN	0.843	0.468
1h/BN	0.688	0.351
1o/BN	0.616	0.489

Table S3. Parameter values for cross-validations performed to assess the validity of the O-PLS models designed to compare metabolomic data attached to each chromosomal region.

O-PLS model	R ²	Q ² Y
R2/Others	0.653	0.474
R3/Others	0.650	0.242
R4/Others	0.654	0.256
R5/Others	0.540	0.136
R6/Others	0.653	0.464
R7/Others	0.653	0.477
R8/Others	0.648	0.300
R9/Others	0.579	0.005
R10/Others	0.540	-0.091
R11/Others	0.513	-0.005
R12/Others	0.633	0.027
R13/Others	0.635	0.091
R14/Others	0.645	0.060
R15/Others	0.564	0.207
R16/Others	0.568	0.257