Figure S1. ^{1}H 600 MHz metabolomic spectra of adipose tissue extracts from the twelve BN.GK congenic strains and the BN control.

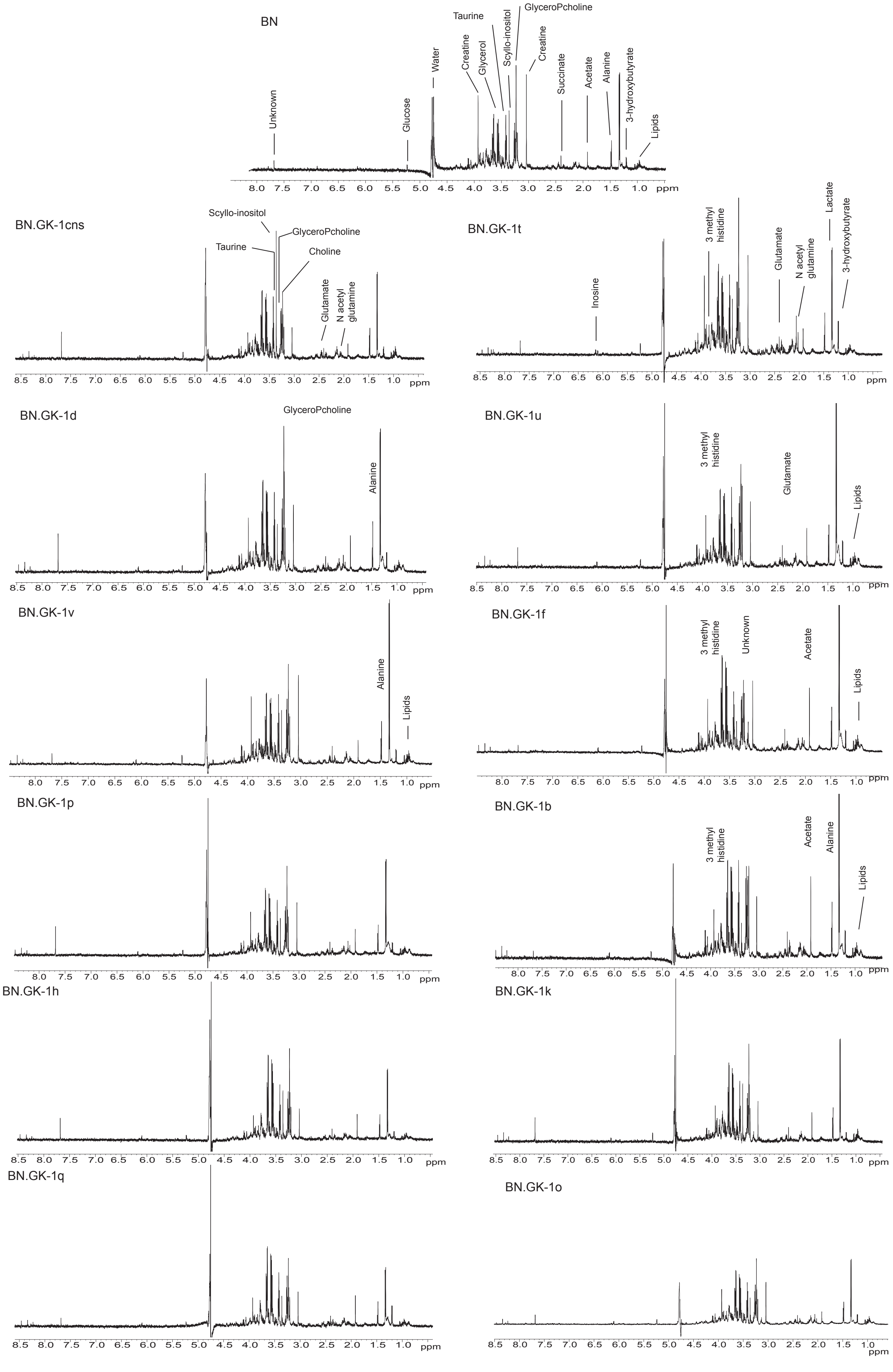


Figure S2. Score plot from O-PLS model of each BN.GK congenic strain against the BN control and corresponding cross-validation with 200 permutations

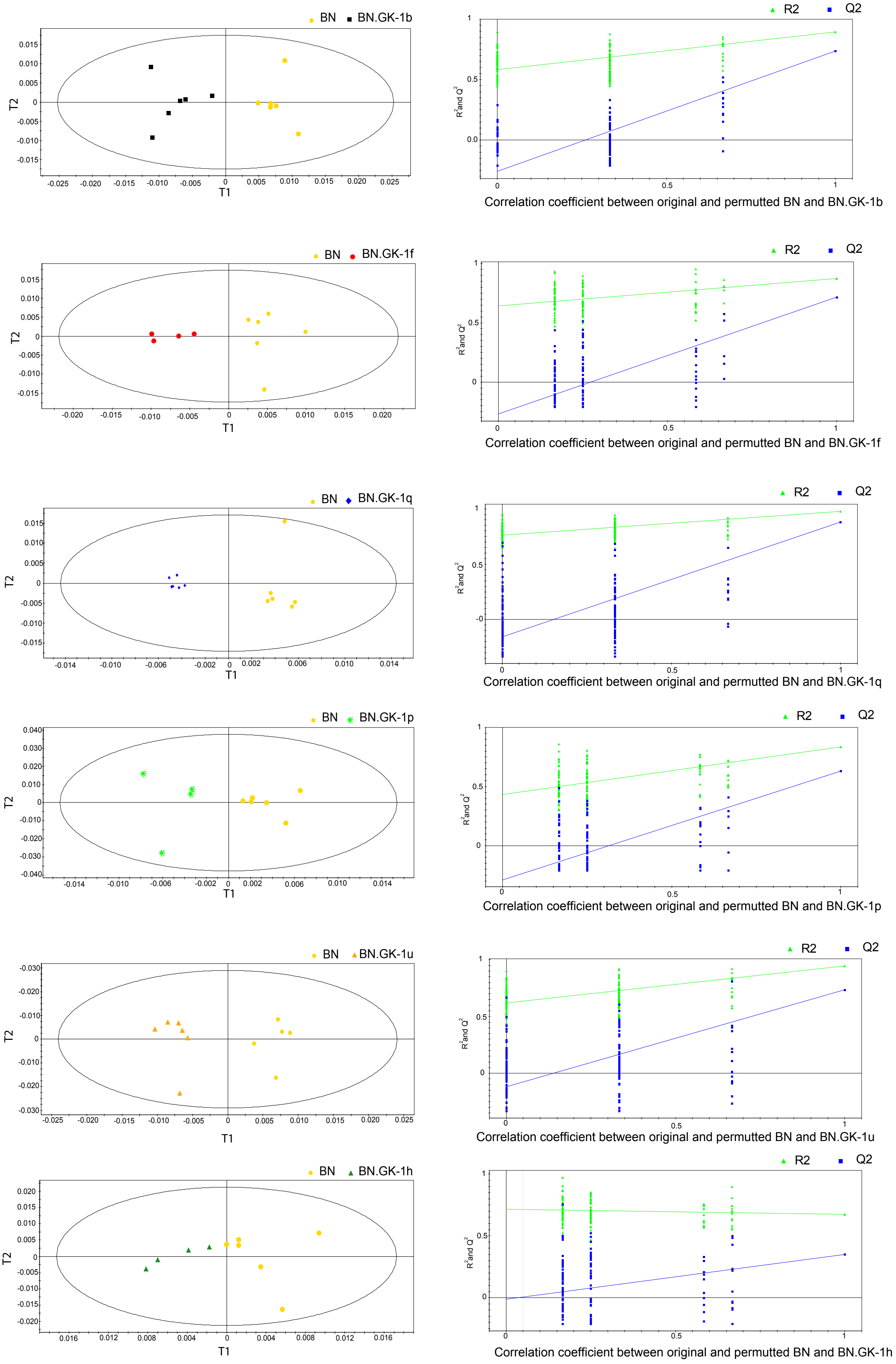


Fig S2 (cntd)

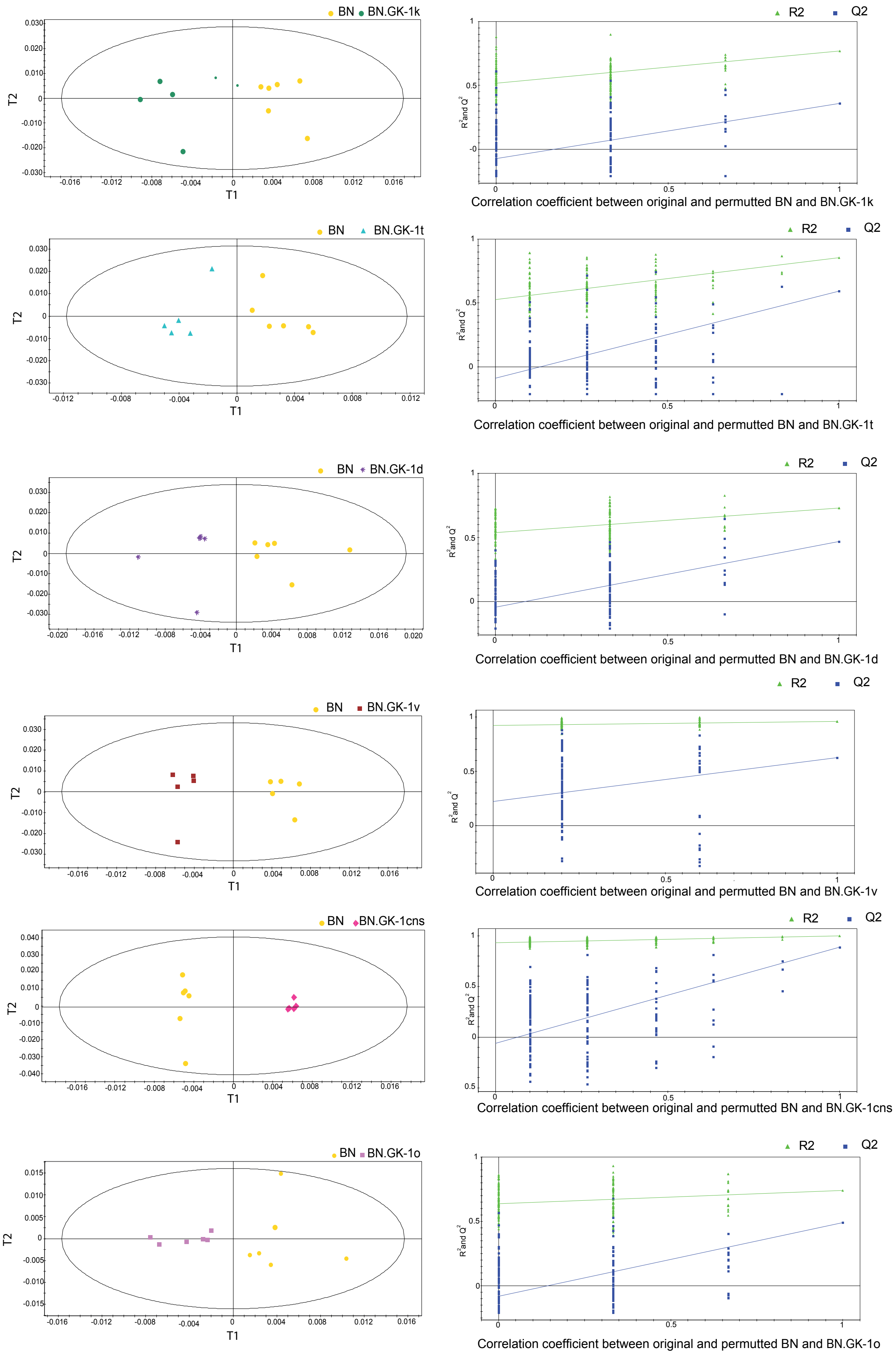

BN ● BN.GK-1k
T2
T1
0.030
0.020
0.010
0
-0.010
-0.020
-0.030
-0.016
-0.012
-0.008
-0.004
0
0.004
0.008
0.012
0.016
▲ R2 ■ Q2
$R^2$and Q^2
1
0.5
-0
0
0.5
1
Correlation coefficient between original and permutted BN and BN.GK-1k
BN ▲ BN.GK-1t
-0.012
-0.008
-0.004
0
0.004
0.008
0.012
Correlation coefficient between original and permutted BN and BN.GK-1t
BN ✱ BN.GK-1d
-0.020
-0.016
-0.012
-0.008
-0.004
0
0.004
0.008
0.012
0.016
0.020
Correlation coefficient between original and permutted BN and BN.GK-1d
BN ■ BN.GK-1v
Correlation coefficient between original and permutted BN and BN.GK-1v
BN ◆BN.GK-1cns
0.040
-0.040
Correlation coefficient between original and permutted BN and BN.GK-1cns
BN ■ BN.GK-1o
0.015
0.010
0.005
0
-0.005
-0.010
-0.015
Correlation coefficient between original and permutted BN and BN.GK-1o

Fig. S3. Loadings plots from O-PLS models performed on adipose tissue extracts from each congenic BN.GK strain against the BN control

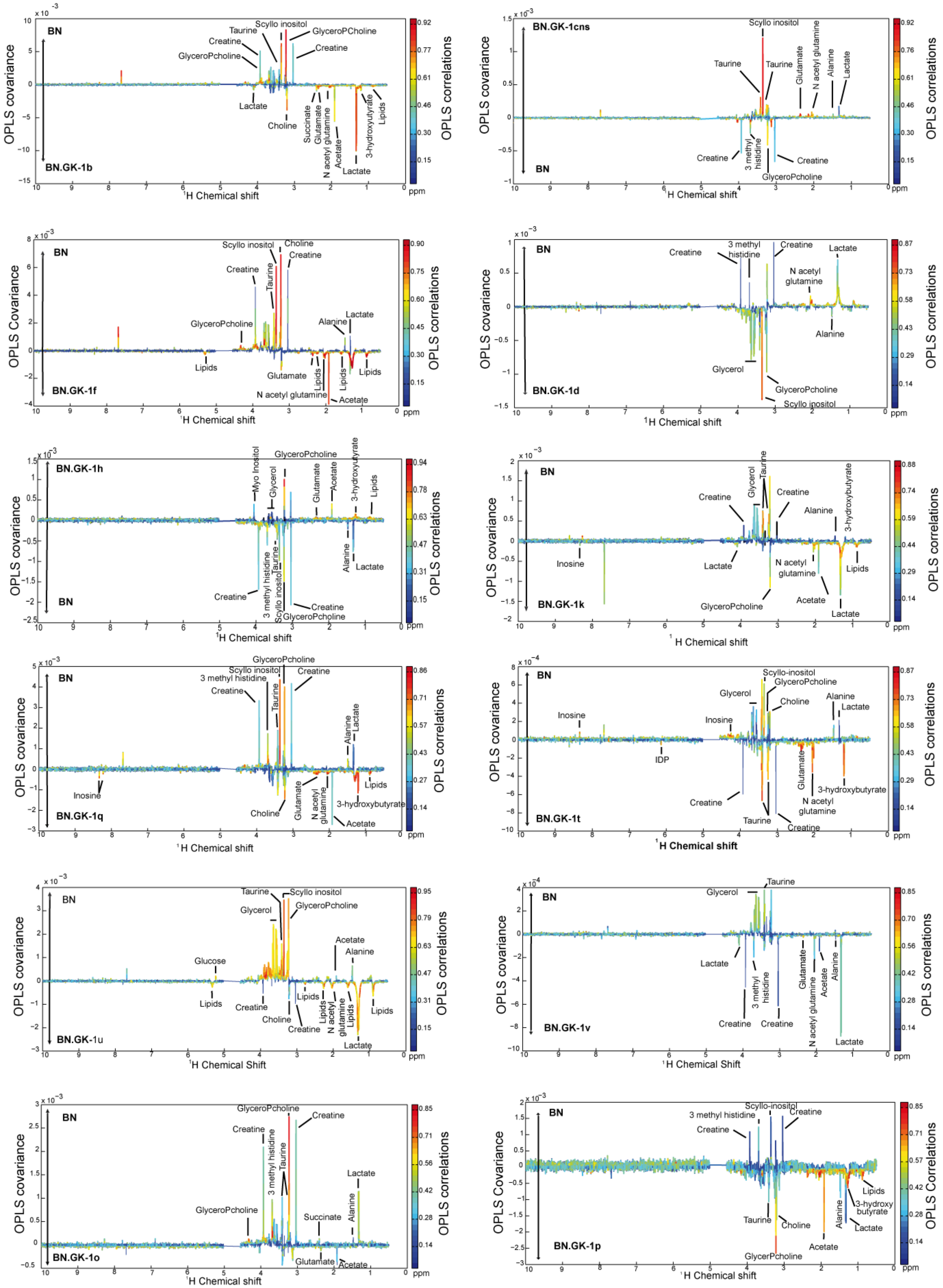


Fig. S4. Score plot from O-PLS model of each region of chromsome 1 against other regions and corresponding cross-validation with 200 permutations.

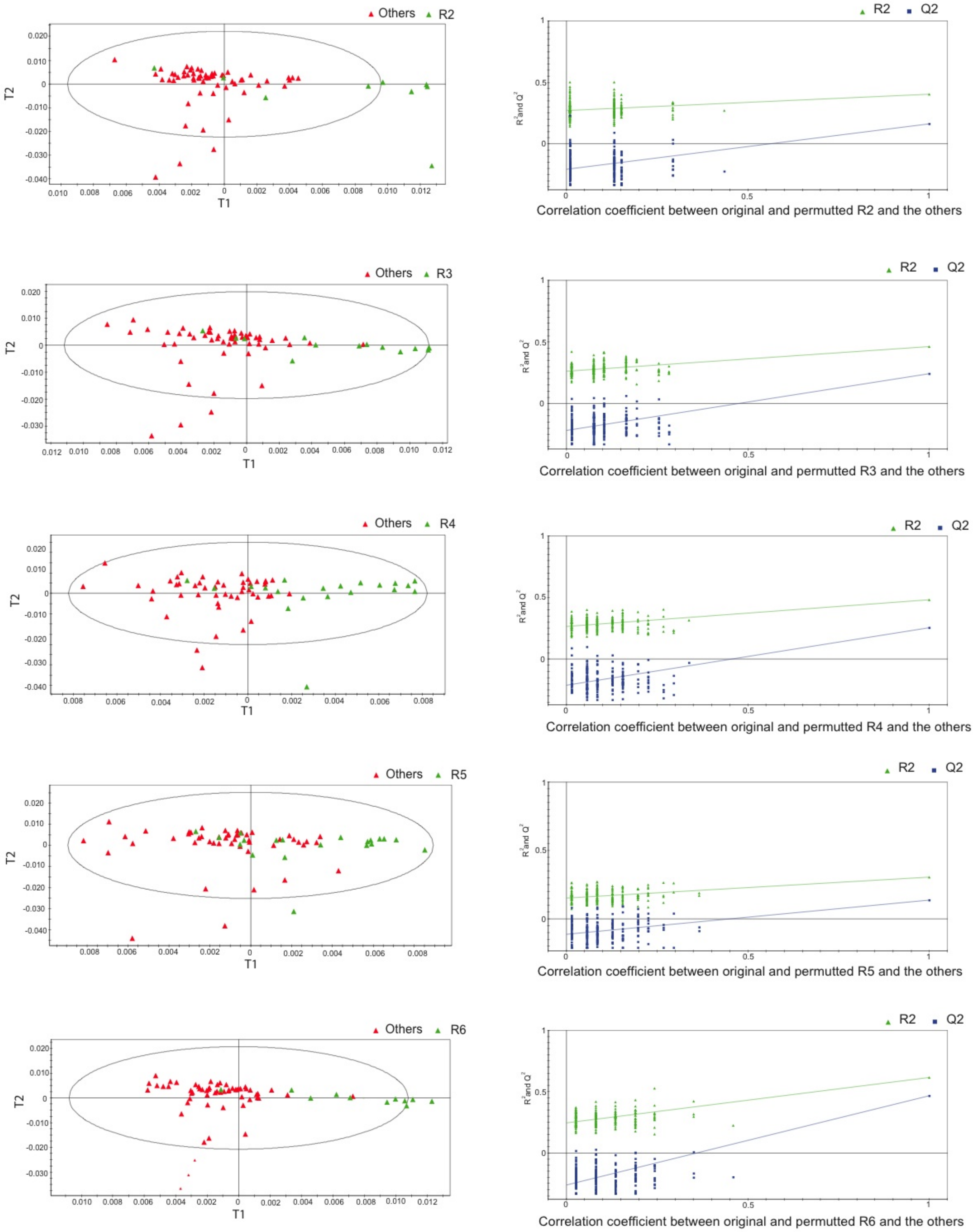
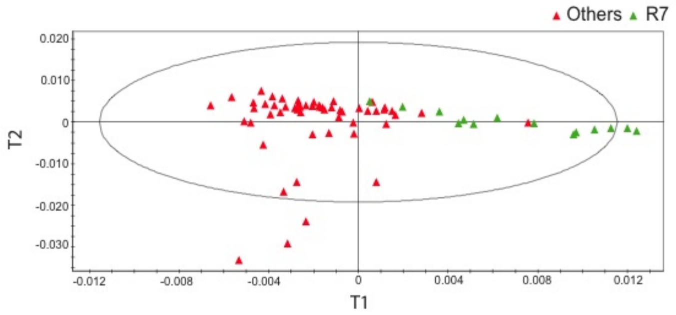
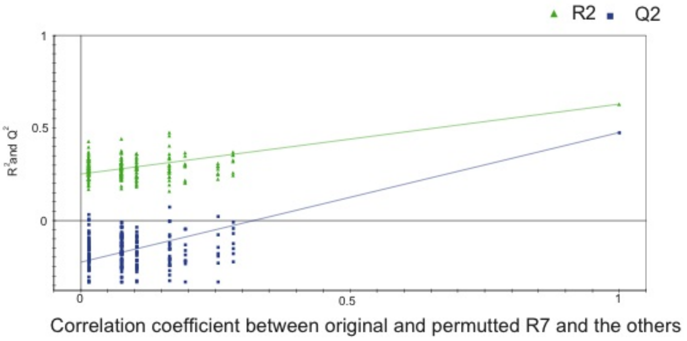
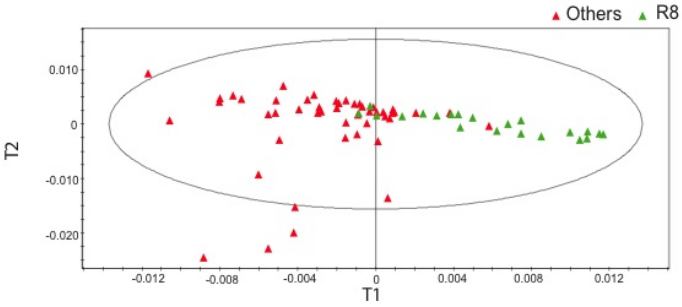
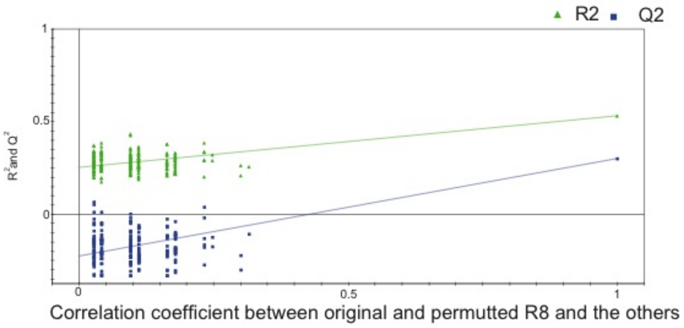


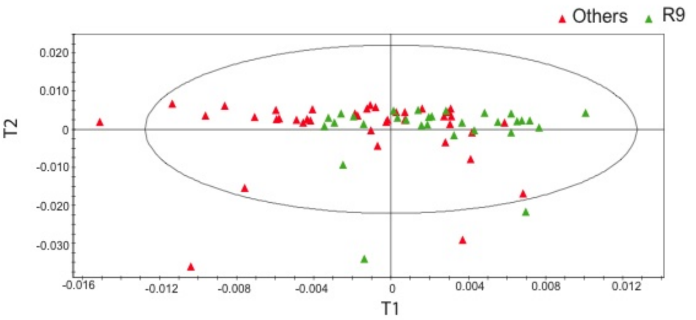
Fig. S4 (Cntd)

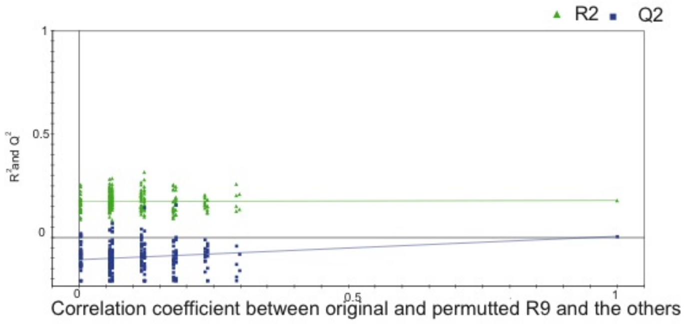

▲ Others ▲ R7
T2
0.020
0.010
0
-0.010
-0.020
-0.030
-0.012
-0.008
-0.004
0
0.004
0.008
0.012
T1

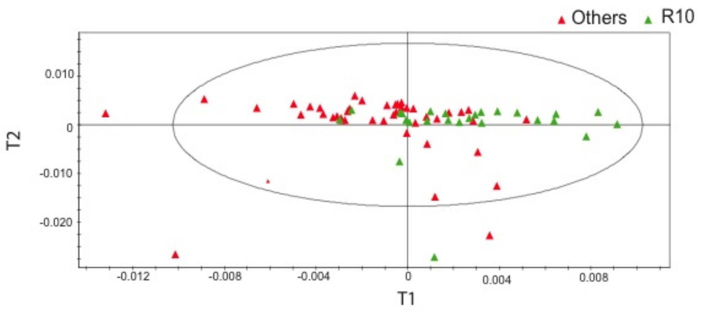

▲ R2 ■ Q2
R²and Q²
1
0.5
0
0
0.5
1
Correlation coefficient between original and permutted R7 and the others

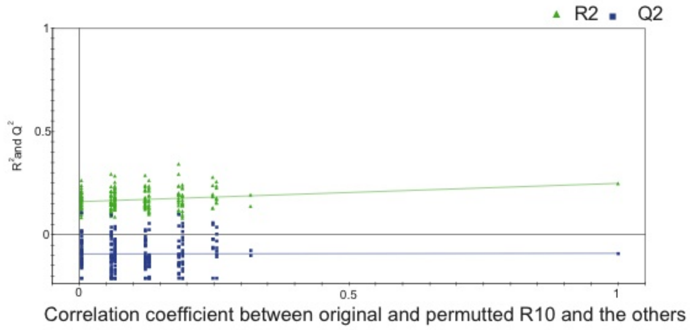

▲ Others ▲ R8
T2
0.010
0
-0.010
-0.020
-0.012
-0.008
-0.004
0
0.004
0.008
0.012
T1

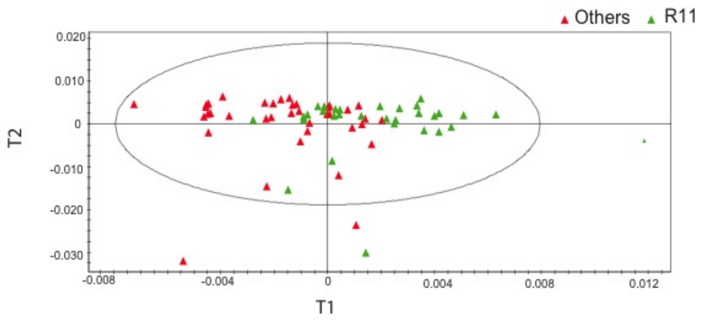

▲ R2 ■ Q2
R²and Q²
1
0.5
0
0
0.5
1
Correlation coefficient between original and permutted R8 and the others


▲ Others ▲ R9
T2
0.020
0.010
0
-0.010
-0.020
-0.030
-0.016
-0.012
-0.008
-0.004
0
0.004
0.008
0.012
T1


▲ R2 ■ Q2
R²and Q²
1
0.5
0
0
0.5
1
Correlation coefficient between original and permutted R9 and the others


▲ Others ▲ R10
T2
0.010
0
-0.010
-0.020
-0.012
-0.008
-0.004
0
0.004
0.008
T1


▲ R2 ■ Q2
R²and Q²
1
0.5
0
0
0.5
1
Correlation coefficient between original and permutted R10 and the others


▲ Others ▲ R11
T2
0.020
0.010
0
-0.010
-0.020
-0.030
-0.008
-0.004
0
0.004
0.008
0.012
T1

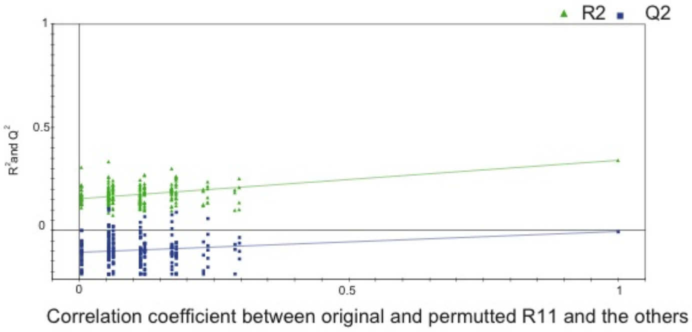

▲ R2 ■ Q2
R²and Q²
1
0.5
0
0
0.5
1
Correlation coefficient between original and permutted R11 and the others

Fig . S5. Loadings plots from O-PLS models performed for each region of chromosome 1 that can be dissected in the BN.GK congenic series against the other regions.