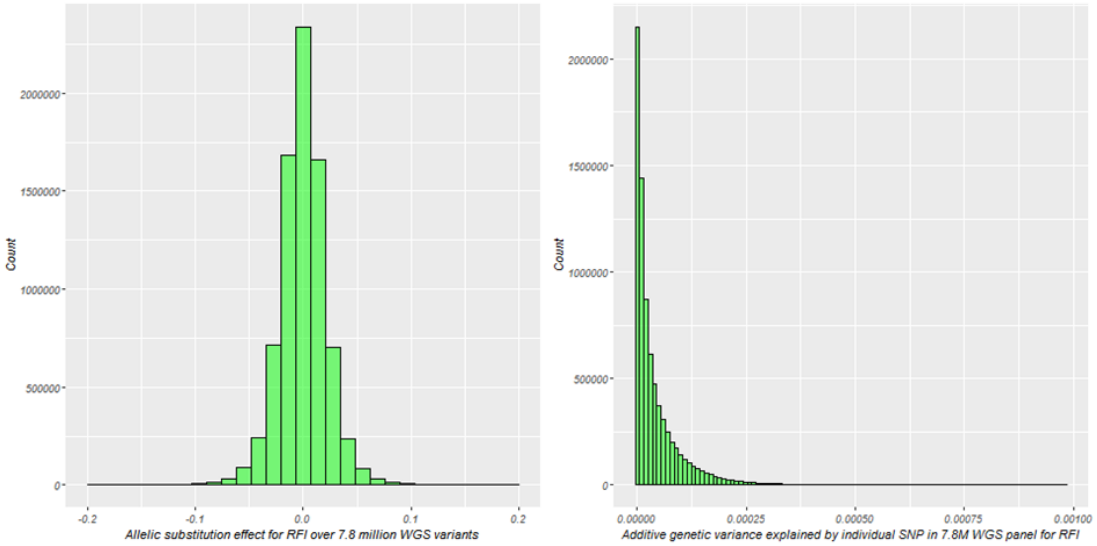
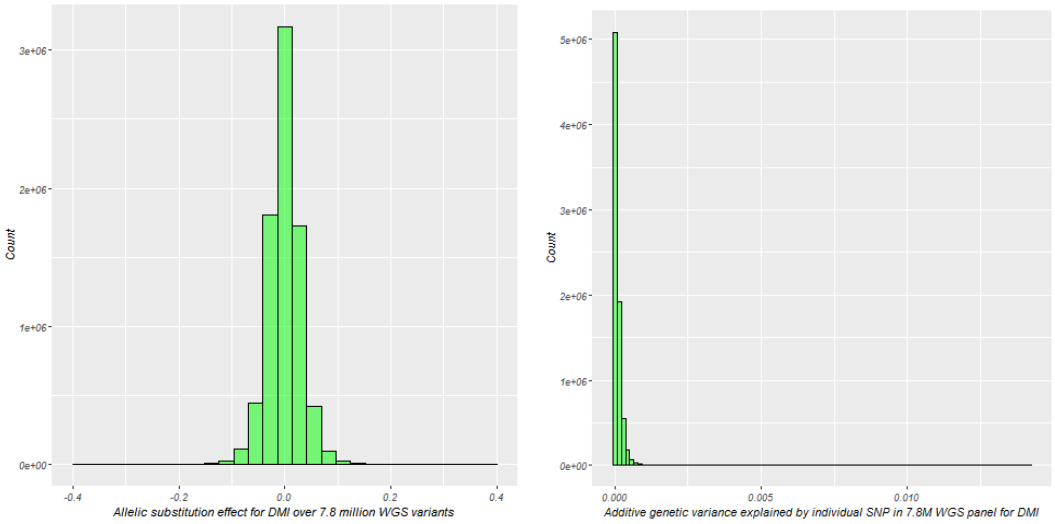
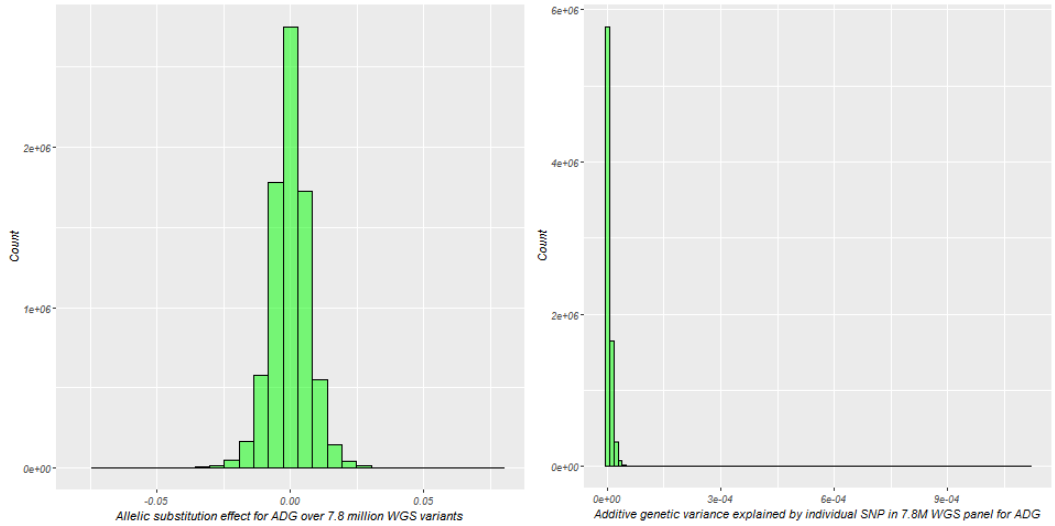


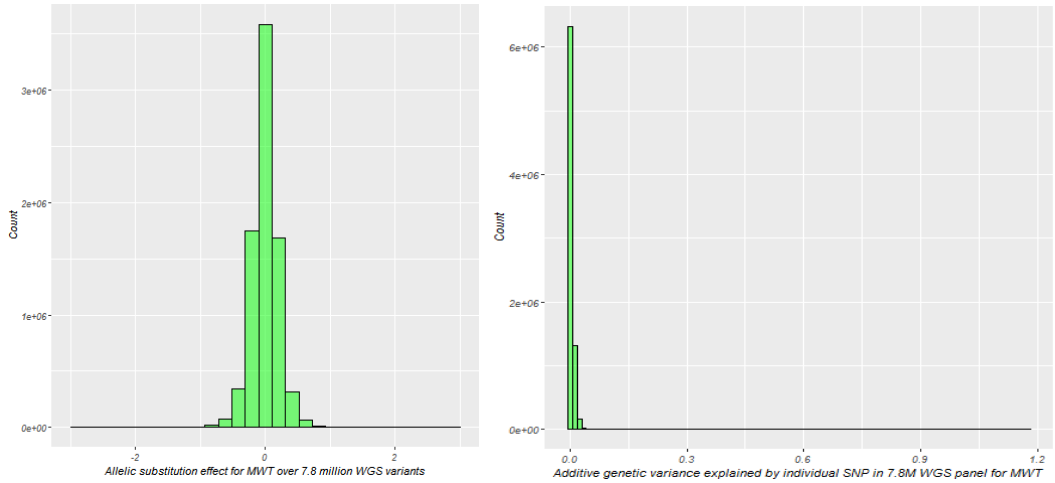
RFI_7.8M GWAS



DMI_7.8M GWAS

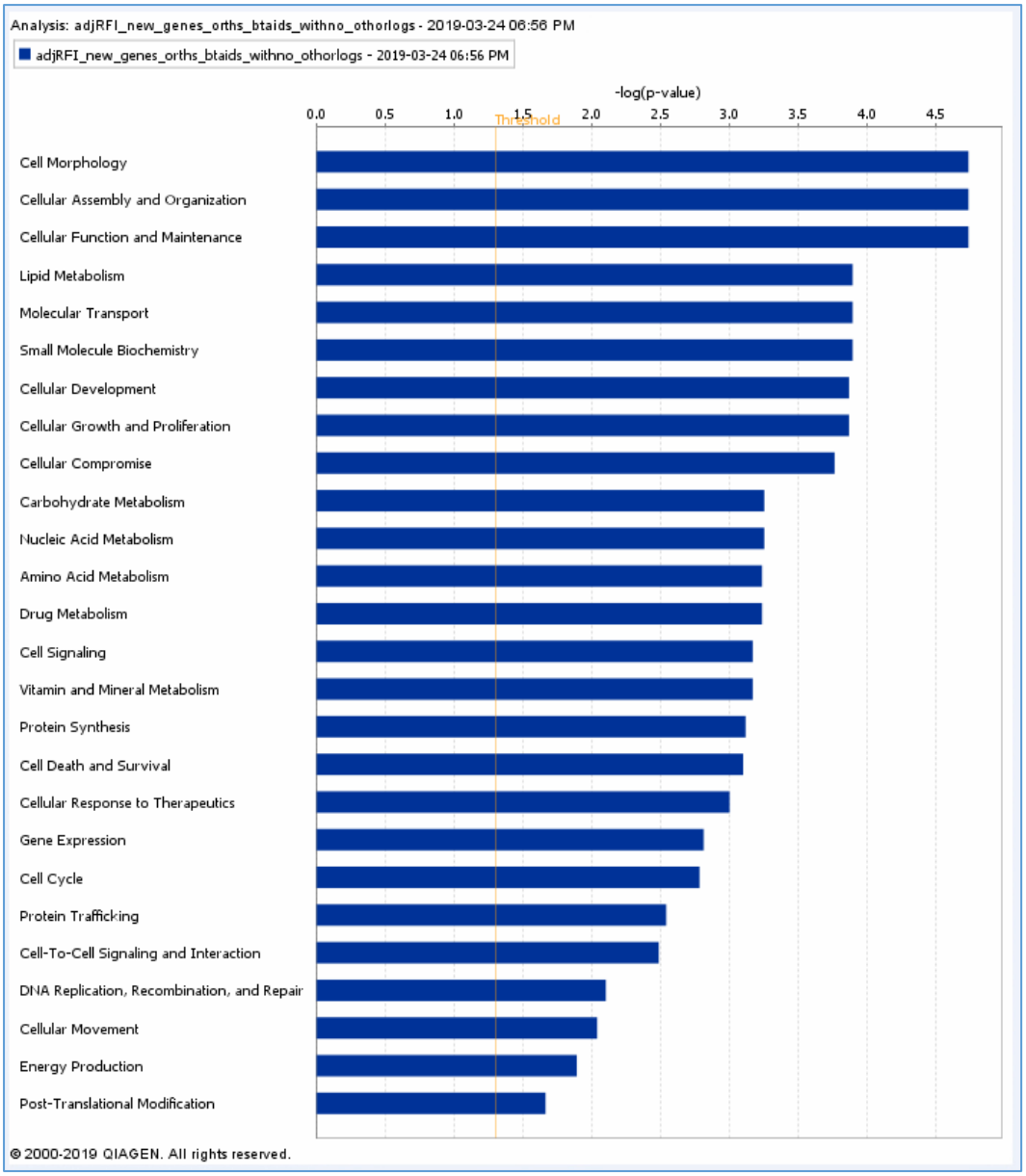


ADG_7.8M GWAS



MWT_7.8M GWAS

Figure S1. Distribution of SNP allele substitution effects (left) and additive genetic variances explained by single SNPs (right) for RFI, DMI, ADG, and MWT based on 7.8 M whole genome sequence (WGS) variants.


Analysis: adjRFI_new_genes_orths_btaids_withno_othorlogs - 2019-03-24 06:56 PM
adjRFI_new_genes_orths_btaids_withno_othorlogs - 2019-03-24 06:56 PM
-log(p-value)
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
4.0
4.5
Threshold
Cell Morphology
Cellular Assembly and Organization
Cellular Function and Maintenance
Lipid Metabolism
Molecular Transport
Small Molecule Biochemistry
Cellular Development
Cellular Growth and Proliferation
Cellular Compromise
Carbohydrate Metabolism
Nucleic Acid Metabolism
Amino Acid Metabolism
Drug Metabolism
Cell Signaling
Vitamin and Mineral Metabolism
Protein Synthesis
Cell Death and Survival
Cellular Response to Therapeutics
Gene Expression
Cell Cycle
Protein Trafficking
Cell-To-Cell Signaling and Interaction
DNA Replication, Recombination, and Repair
Cellular Movement
Energy Production
Post-Translational Modification
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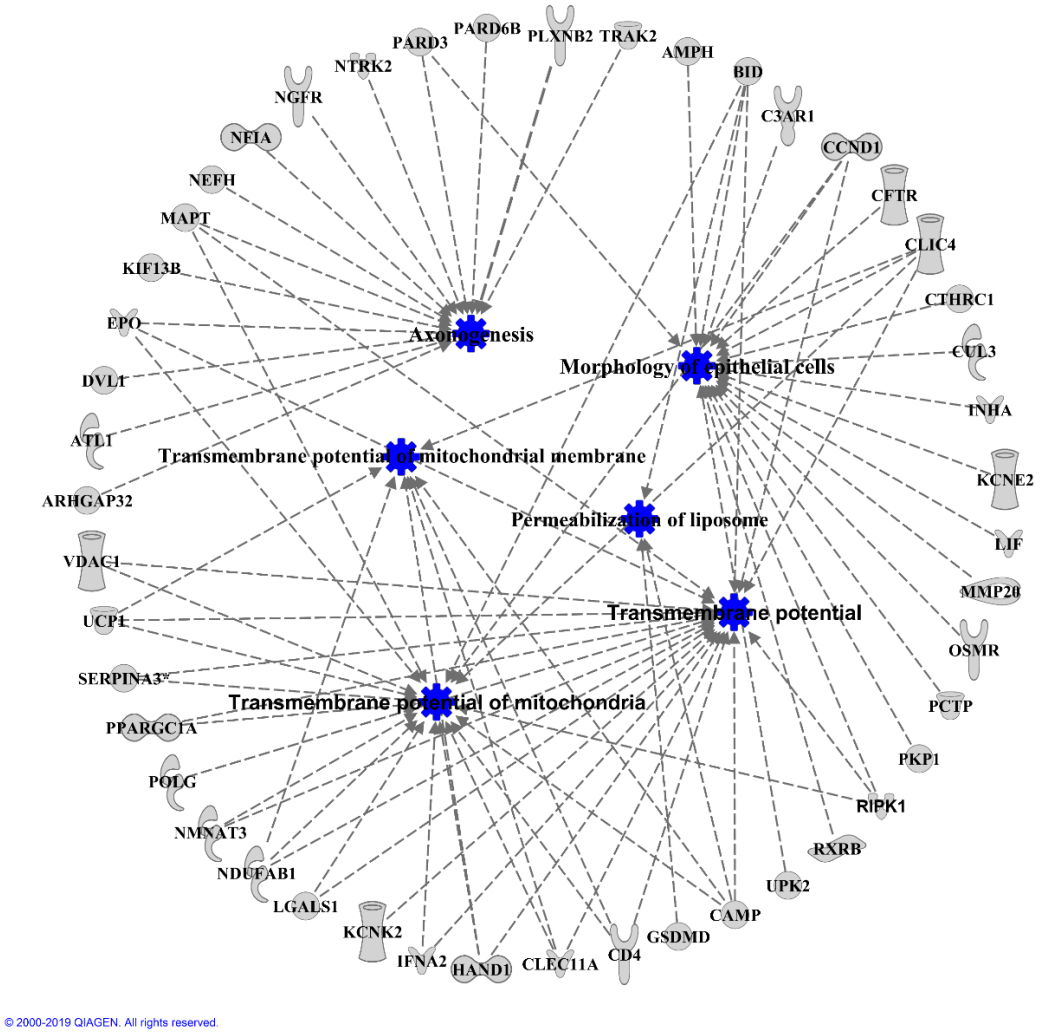

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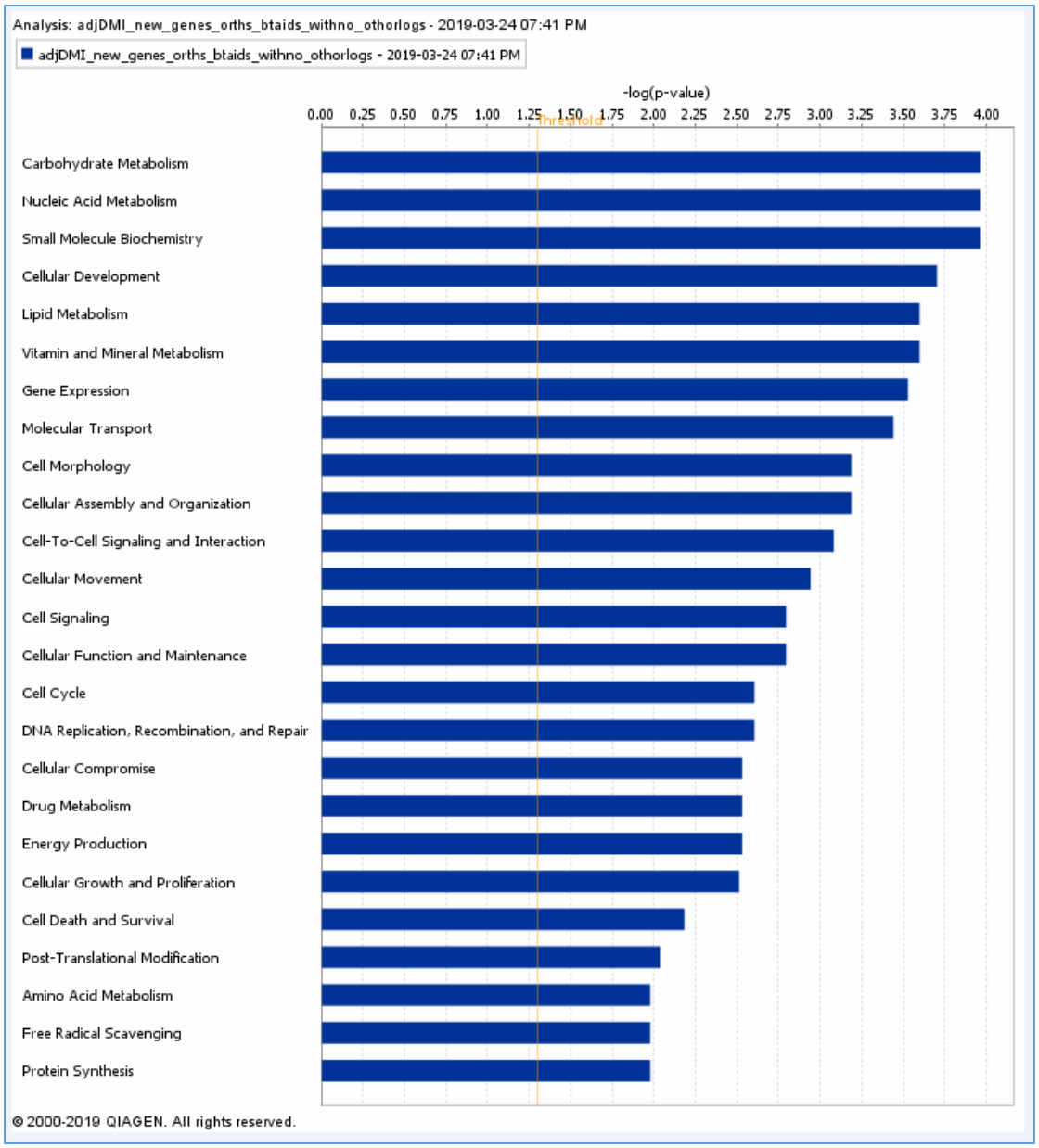
Figure S2. The enriched cellular and molecular functions (top) and cell morphology network (bottom) for RFI. The images were generated through the use of Ingenuity Pathway Analysis (IPA) and written permission was granted by QIAGEN Silicon Valley to use and adapt the figure generated by IPA under the terms of the Creative Commons Attribution License (CC BY) 4.0.


Analysis: adjDMI_new_genes_orths_btaids_withno_othorlogs - 2019-03-24 07:41 PM
adjDMI_new_genes_orths_btaids_withno_othorlogs - 2019-03-24 07:41 PM
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0.00 0.25 0.50 0.75 1.00 1.25 1.50 1.75 2.00 2.25 2.50 2.75 3.00 3.25 3.50 3.75 4.00
Threshold
Carbohydrate Metabolism
Nucleic Acid Metabolism
Small Molecule Biochemistry
Cellular Development
Lipid Metabolism
Vitamin and Mineral Metabolism
Gene Expression
Molecular Transport
Cell Morphology
Cellular Assembly and Organization
Cell-To-Cell Signaling and Interaction
Cellular Movement
Cell Signaling
Cellular Function and Maintenance
Cell Cycle
DNA Replication, Recombination, and Repair
Cellular Compromise
Drug Metabolism
Energy Production
Cellular Growth and Proliferation
Cell Death and Survival
Post-Translational Modification
Amino Acid Metabolism
Free Radical Scavenging
Protein Synthesis
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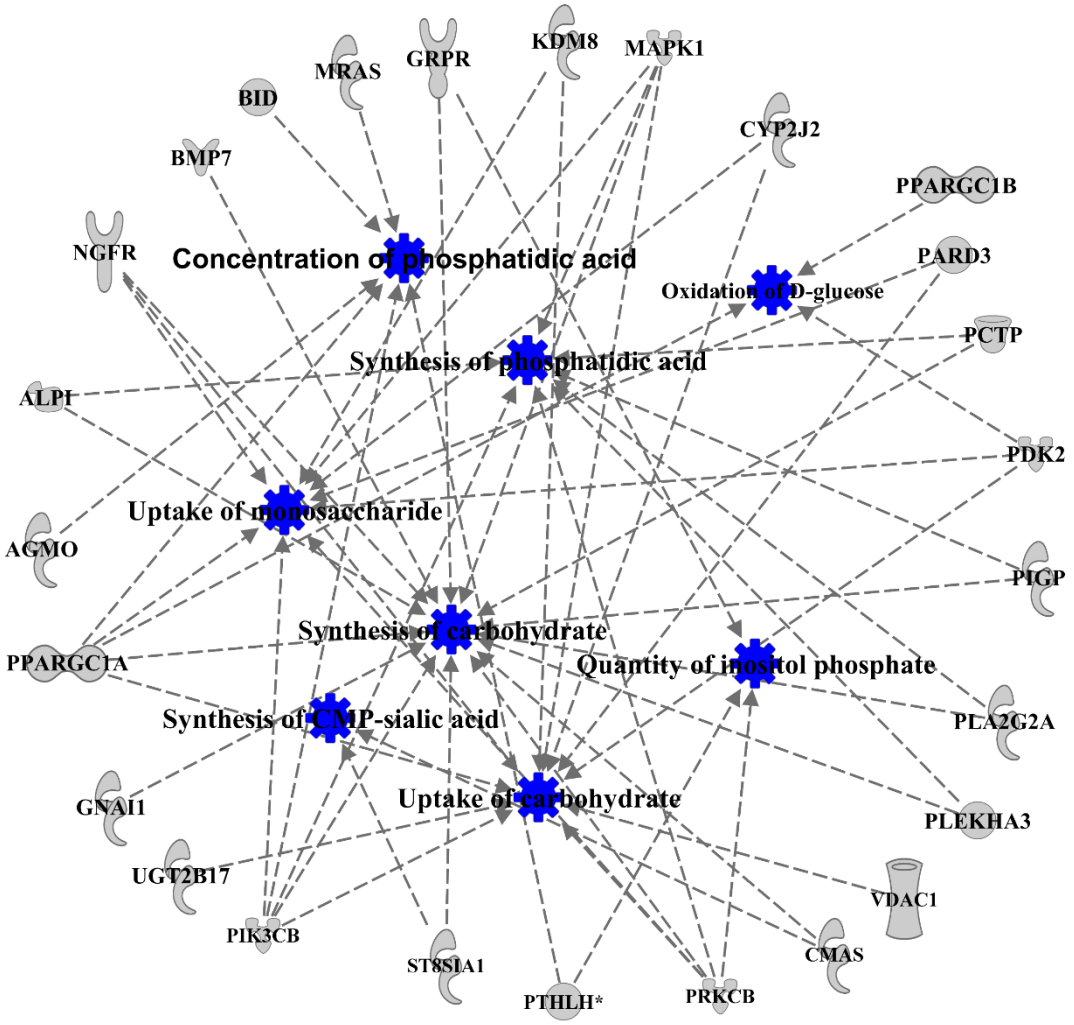
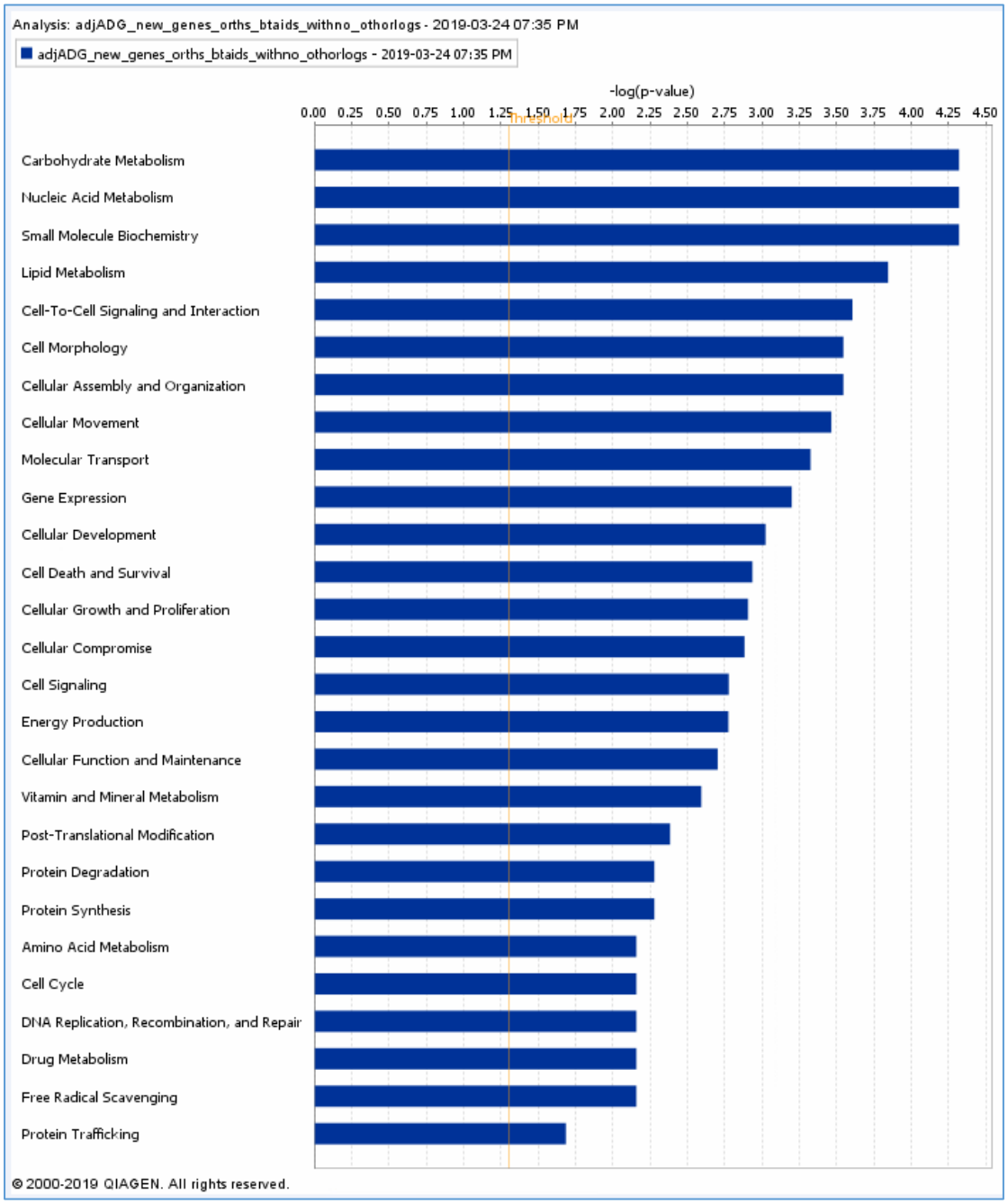


Figure S3. The enriched cellular and molecular functions (top) and carbohydrate metabolism network (bottom) for DMI. The images were generated through the use of Ingenuity Pathway Analysis (IPA) and written permission was granted by QIAGEN Silicon Valley to use and adapt the figure generated by IPA under the terms of the Creative Commons Attribution License (CC BY) 4.0.


Analysis: adjADG_new_genes_orths_btaids_withno_othorlogs - 2019-03-24 07:35 PM
adjADG_new_genes_orths_btaids_withno_othorlogs - 2019-03-24 07:35 PM
-log(p-value)
0.00 0.25 0.50 0.75 1.00 1.25 1.50 1.75 2.00 2.25 2.50 2.75 3.00 3.25 3.50 3.75 4.00 4.25 4.50
Threshold
Carbohydrate Metabolism
Nucleic Acid Metabolism
Small Molecule Biochemistry
Lipid Metabolism
Cell-To-Cell Signaling and Interaction
Cell Morphology
Cellular Assembly and Organization
Cellular Movement
Molecular Transport
Gene Expression
Cellular Development
Cell Death and Survival
Cellular Growth and Proliferation
Cellular Compromise
Cell Signaling
Energy Production
Cellular Function and Maintenance
Vitamin and Mineral Metabolism
Post-Translational Modification
Protein Degradation
Protein Synthesis
Amino Acid Metabolism
Cell Cycle
DNA Replication, Recombination, and Repair
Drug Metabolism
Free Radical Scavenging
Protein Trafficking
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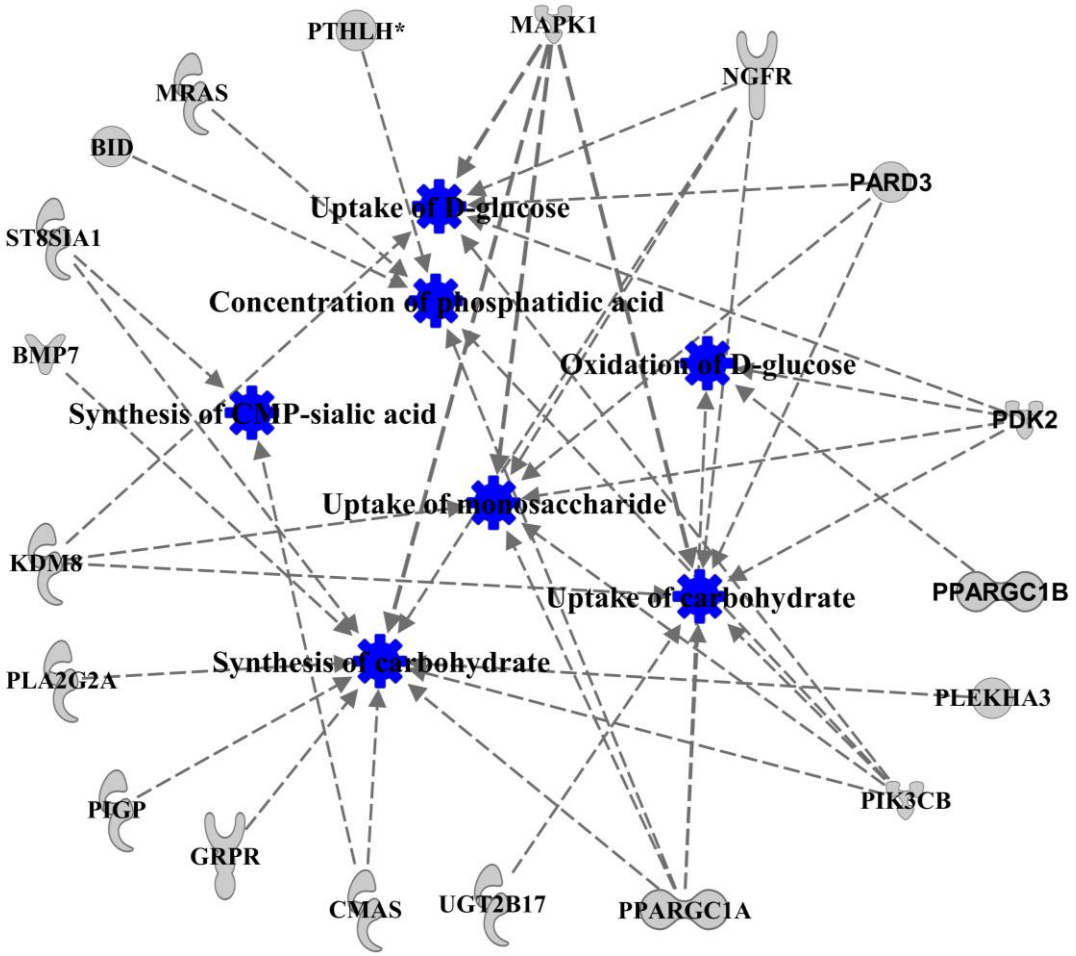
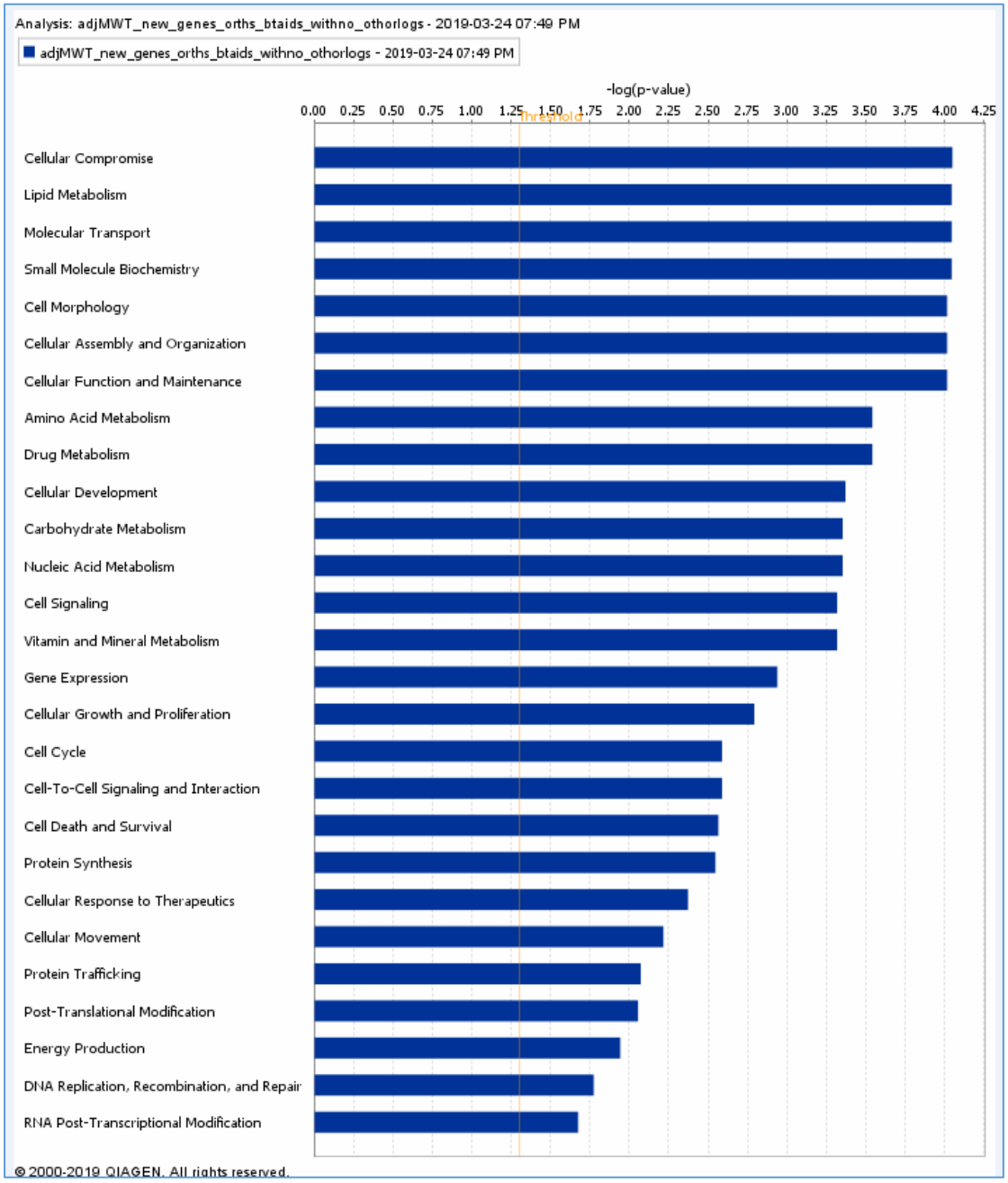


Figure S4. The enriched cellular and molecular functions (top) and carbohydrate metabolism network (bottom) for ADG. The images were generated through the use of Ingenuity Pathway Analysis (IPA) and written permission was granted by QIAGEN Silicon Valley to use and adapt the figure generated by IPA under the terms of the Creative Commons Attribution License (CC BY) 4.0.


Analysis: adjMWT_new_genes_orths_btaids_withno_othorlogs - 2019-03-24 07:49 PM
adjMWT_new_genes_orths_btaids_withno_othorlogs - 2019-03-24 07:49 PM
-log(p-value)
0.00 0.25 0.50 0.75 1.00 1.25 1.50 1.75 2.00 2.25 2.50 2.75 3.00 3.25 3.50 3.75 4.00 4.25
Threshold
Cellular Compromise
Lipid Metabolism
Molecular Transport
Small Molecule Biochemistry
Cell Morphology
Cellular Assembly and Organization
Cellular Function and Maintenance
Amino Acid Metabolism
Drug Metabolism
Cellular Development
Carbohydrate Metabolism
Nucleic Acid Metabolism
Cell Signaling
Vitamin and Mineral Metabolism
Gene Expression
Cellular Growth and Proliferation
Cell Cycle
Cell-To-Cell Signaling and Interaction
Cell Death and Survival
Protein Synthesis
Cellular Response to Therapeutics
Cellular Movement
Protein Trafficking
Post-Translational Modification
Energy Production
DNA Replication, Recombination, and Repair
RNA Post-Transcriptional Modification
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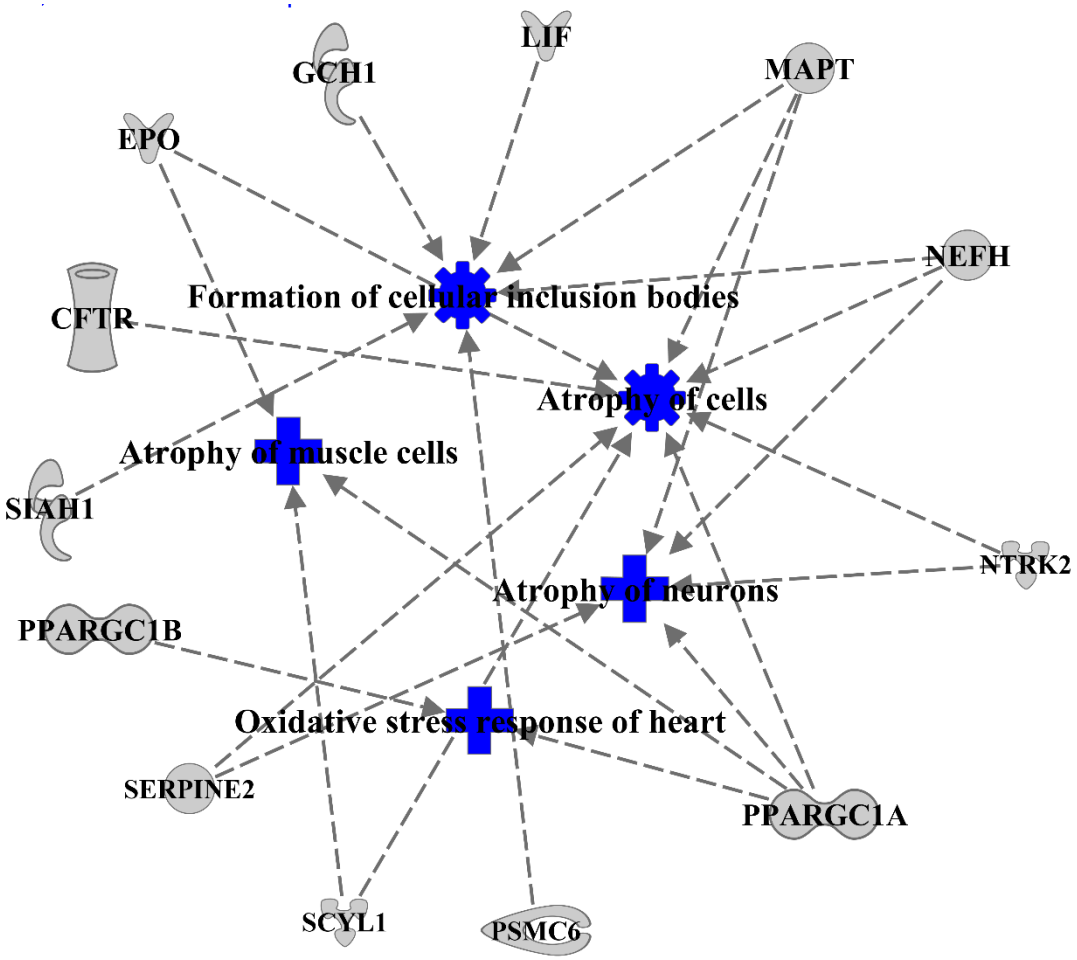
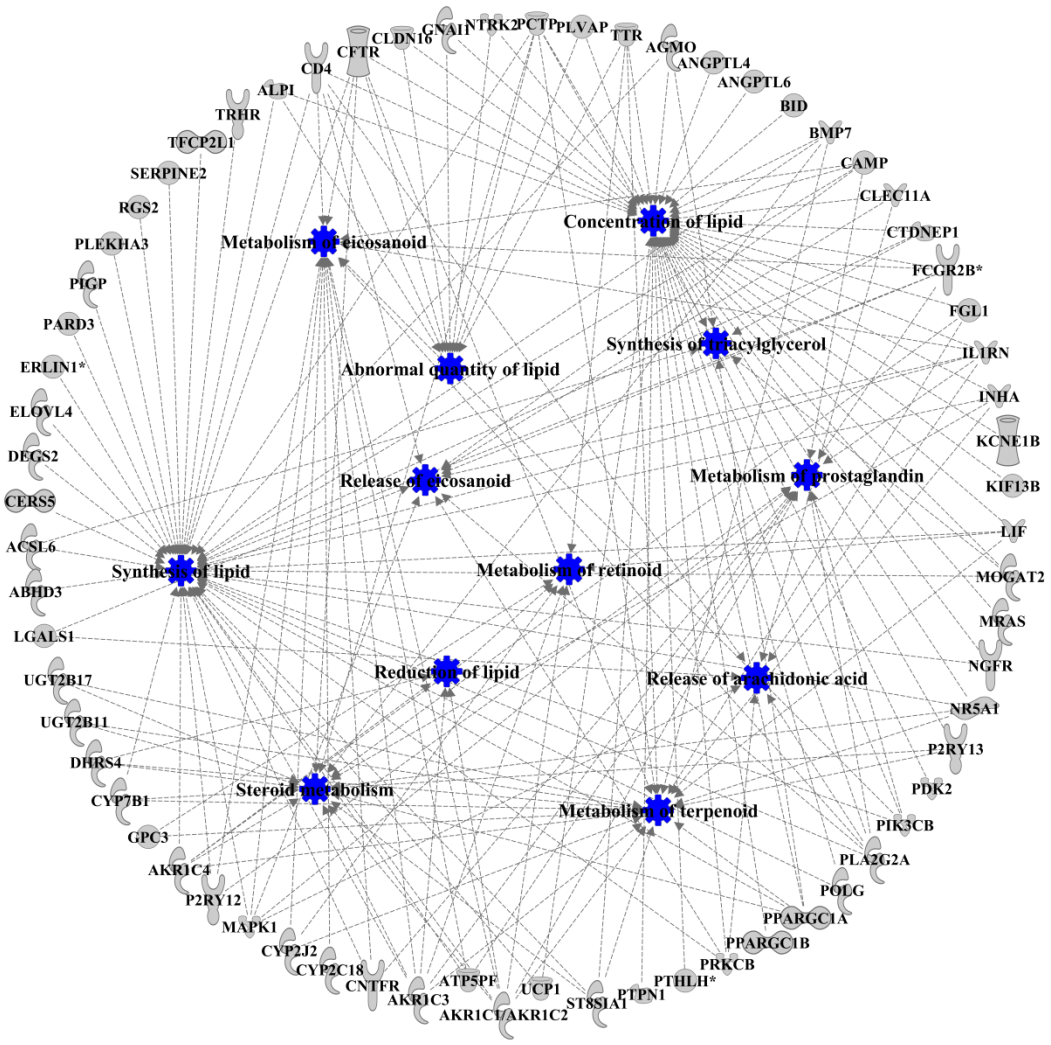
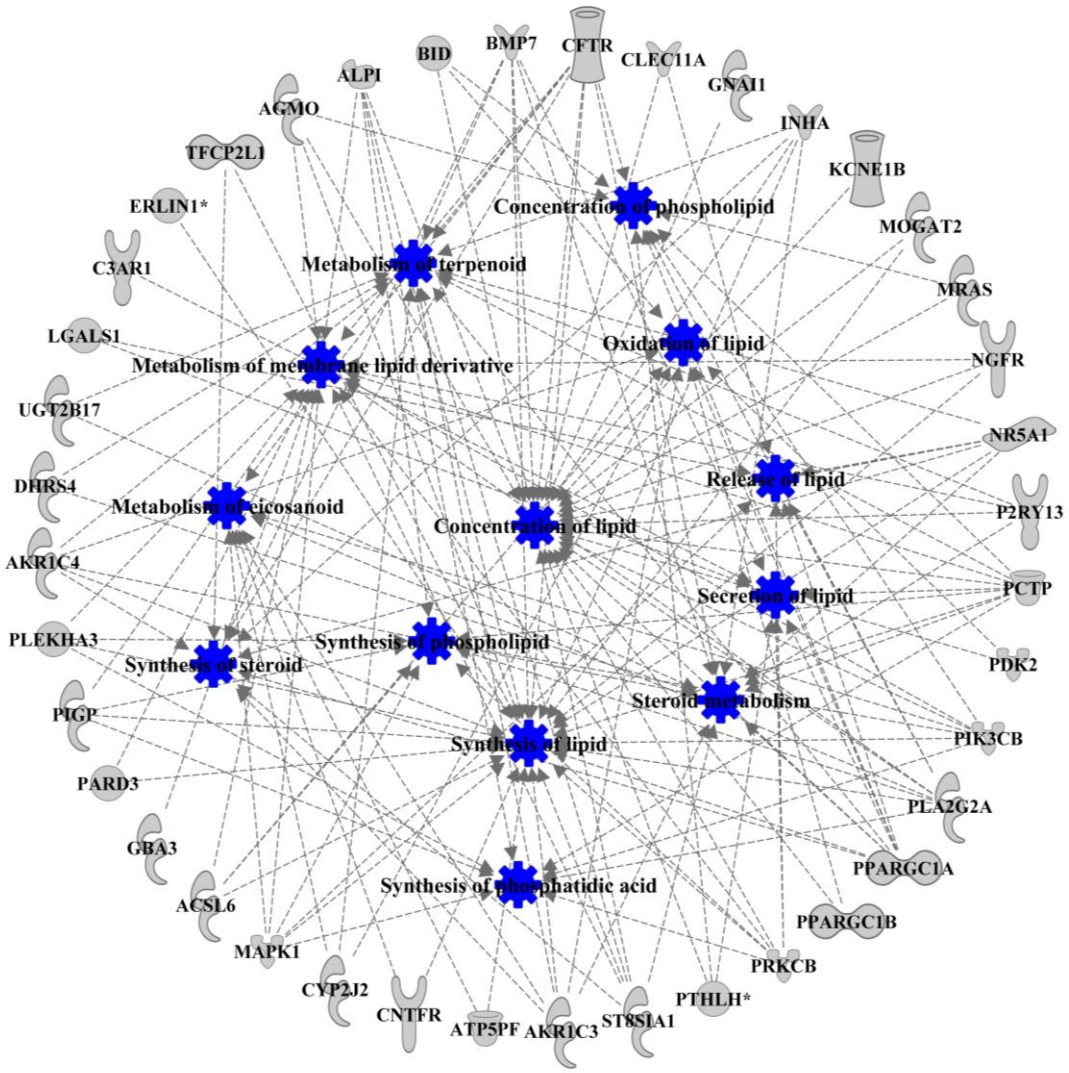


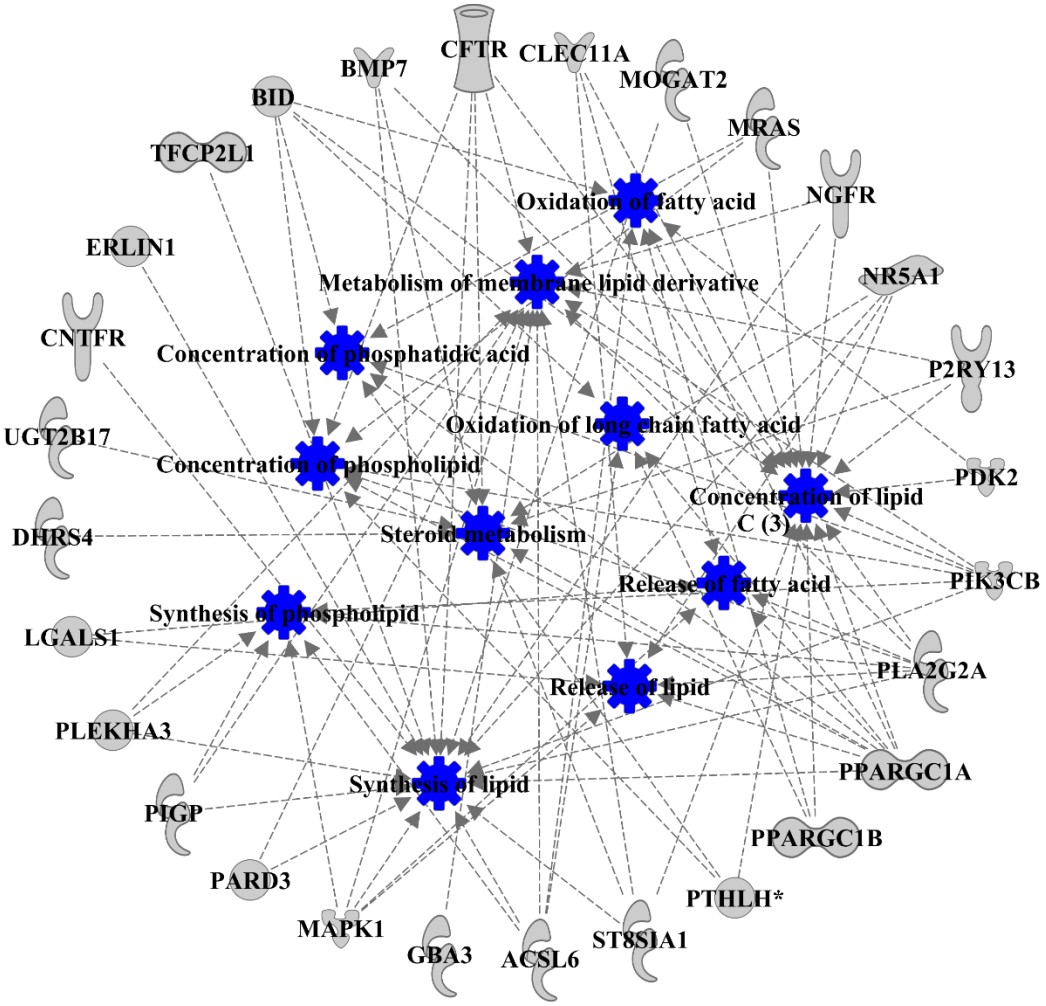
Figure S5. The enriched cellular and molecular functions (top) and cellular compromise network (bottom) for MWT. The images were generated through the use of Ingenuity Pathway Analysis (IPA) and written permission was granted by QIAGEN Silicon Valley to use and adapt the figure generated by IPA under the terms of the Creative Commons Attribution License (CC BY) 4.0.


GNAI1
NTRK2
CTP
PLVAP
TTR
AGMO
ANGPTL4
ANGPTL6
BID
BMP7
CAMP
CLEC11A
CTDNEP1
FCGR2B*
FGL1
IL1RN
INHA
KCNE1B
KIF13B
LIF
MOGAT2
MRAS
NGFR
NR5A1
P2RY13
PDK2
PIK3CB
PLA2G2A
POLG
PPARGC1A
PPARGC1B
PRKCB
PTHLH*
PTPN1
ST8SIA1
UCP1
ATP5PF
AKR1C1/AKR1C2
AKR1C3
CNTFR
CYP2C18
CYP2J2
MAPK1
P2RY12
AKR1C4
GPC3
CYP7B1
DHRS4
UGT2B11
UGT2B17
LGALS1
ABHD3
ACSL6
CERS5
DEGS2
ELOVL4
ERLIN1*
PARD3
PIGP
PLEKHA3
RGS2
SERPINE2
TFCP2L1
TRHR
ALPI
CD4
CFTR
CLDN16
Concentration of lipid
Metabolism of eicosanoid
Synthesis of triacylglycerol
Abnormal quantity of lipid
Metabolism of prostaglandin
Release of eicosanoid
Synthesis of lipid
Metabolism of retinoid
Release of arachidonic acid
Reduction of lipid
Metabolism of terpenoid
Steroid metabolism

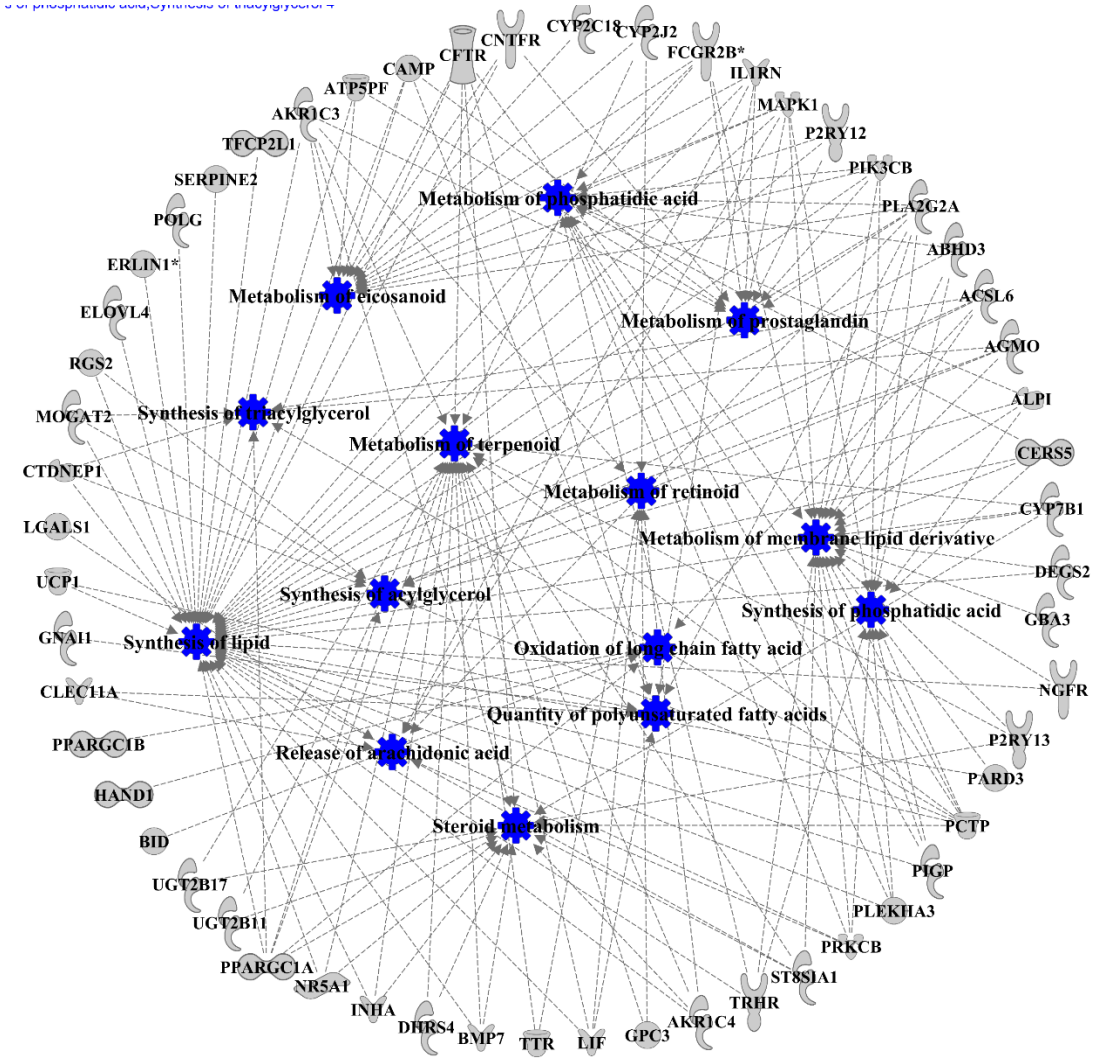
RFI


BID
BMP7
CFTR
CLEC11A
ALPI
GNAI1
AGMO
INHA
TFCP2L1
KCNE1B
ERLIN1*
Concentration of phospholipid
MOGAT2
C3AR1
Metabolism of terpenoid
MRAS
LGALS1
Oxidation of lipid
Metabolism of membrane lipid derivative
NGFR
UGT2B17
NR5A1
Release of lipid
DHRS4
Metabolism of eicosanoid
Concentration of lipid
P2RY13
AKR1C4
Secretion of lipid
PCTP
PLEKHA3
Synthesis of phospholipid
Synthesis of steroid
PDK2
Steroid metabolism
PIGP
Synthesis of lipid
PIK3CB
PARD3
PLA2G2A
GBA3
PPARGC1A
Synthesis of phosphatidic acid
ACSL6
PPARGC1B
MAPK1
PRKCB
CYP2J2
PTHLH*
CNTFR
ATP5PF
AKR1C3
ST8SIA1

DMI


CFTR
CLEC11A
BMP7
MOGAT2
BID
MRAS
TFCP2L1
Oxidation of fatty acid
NGFR
ERLIN1
Metabolism of membrane lipid derivative
NR5A1
CNTFR
Concentration of phosphatidic acid
P2RY13
Oxidation of long chain fatty acid
UGT2B17
Concentration of phospholipid
PDK2
Concentration of lipid C (3)
DHRS4
Steroid metabolism
Release of fatty acid
PIK3CB
Synthesis of phospholipid
LGALS1
PLA2G2A
Release of lipid
PLEKHA3
PPARGC1A
Synthesis of lipid
PIGP
PPARGC1B
PARD3
PTHLH*
MAPK1
ST8SIA1
GBA3
ACSL6

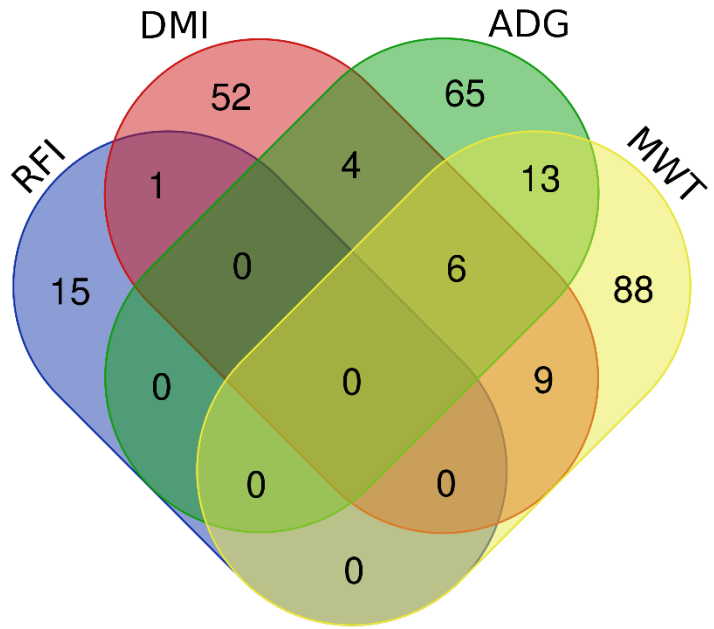
ADG



MWT

Figure S6. Lipid metabolism network for RFI and its component traits DMI, ADG, and MWT. The images were generated through the use of Ingenuity Pathway Analysis (IPA) and written permission was granted by QIAGEN Silicon Valley to use and adapt the figure generated by IPA under the terms of the Creative Commons Attribution License (CC BY) 4.0.

a



b

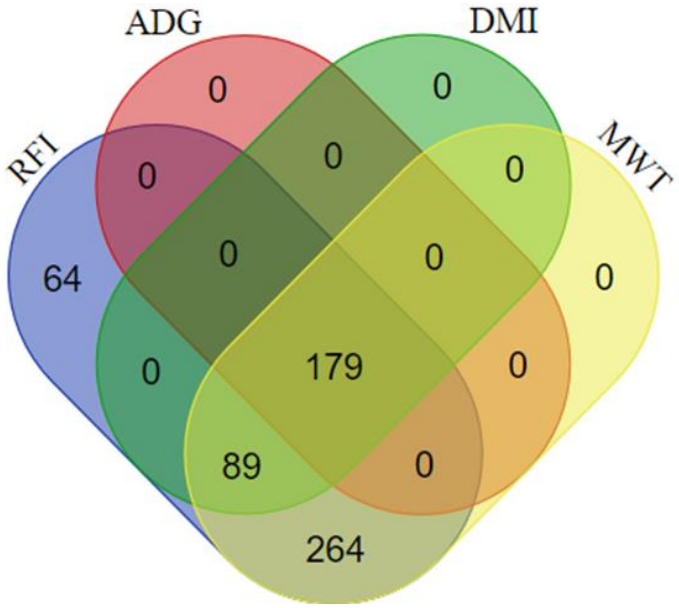
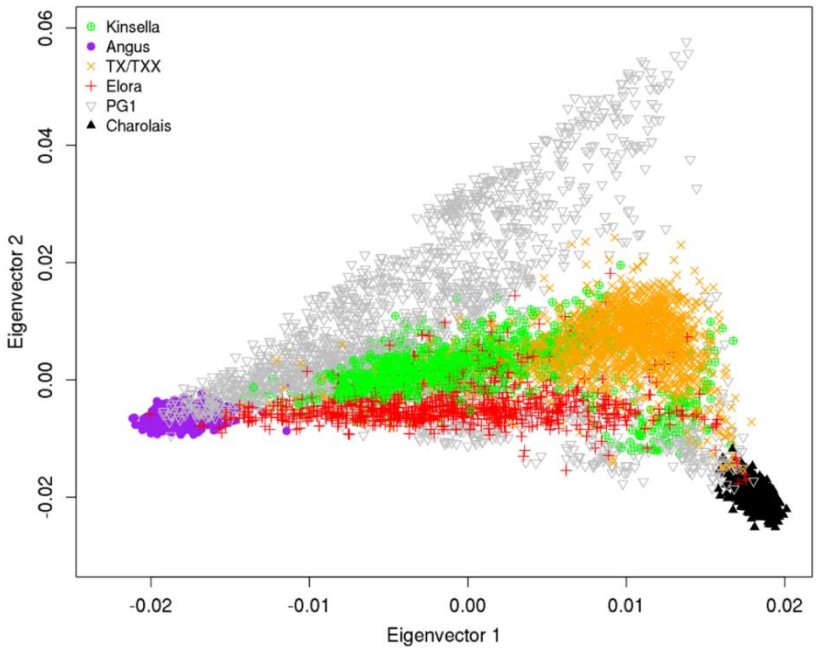


Figure S7. Common lead significant SNPs with the same IDs (a) and candidate genes (b) among RFI and its three component traits at thresholds P-value < 1.00E-05 and FDR < 0.10 based on the imputed 7.8M DNA variant GWAS.

a



b

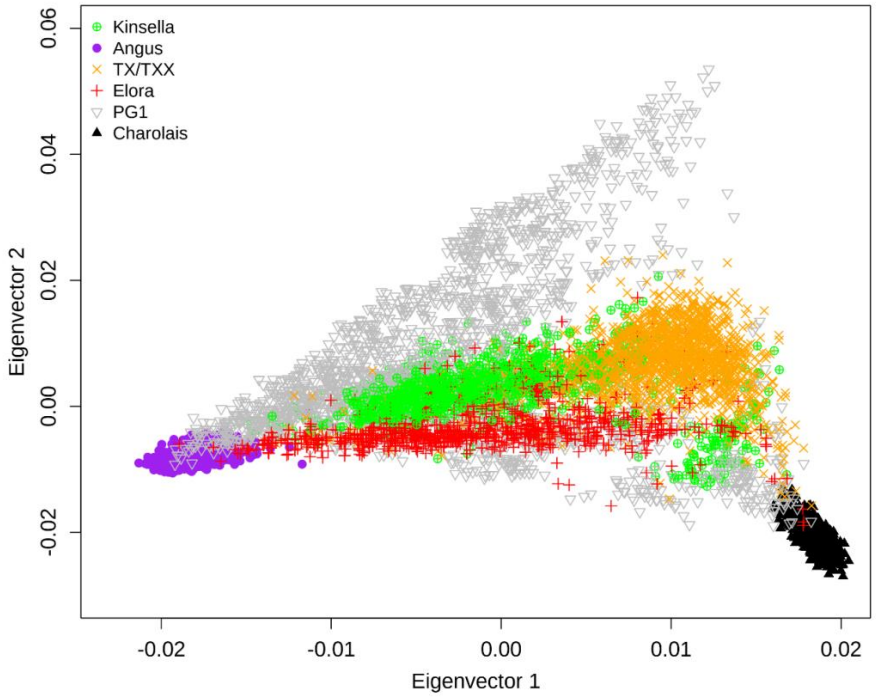


Figure S8. Principal component analyses of Canadian beef cattle populations (N=7573) based on the 50K SNP (a) and 7.8M GWS variant (b) panels.