

# Signaling receptor activity (GO:0038023)

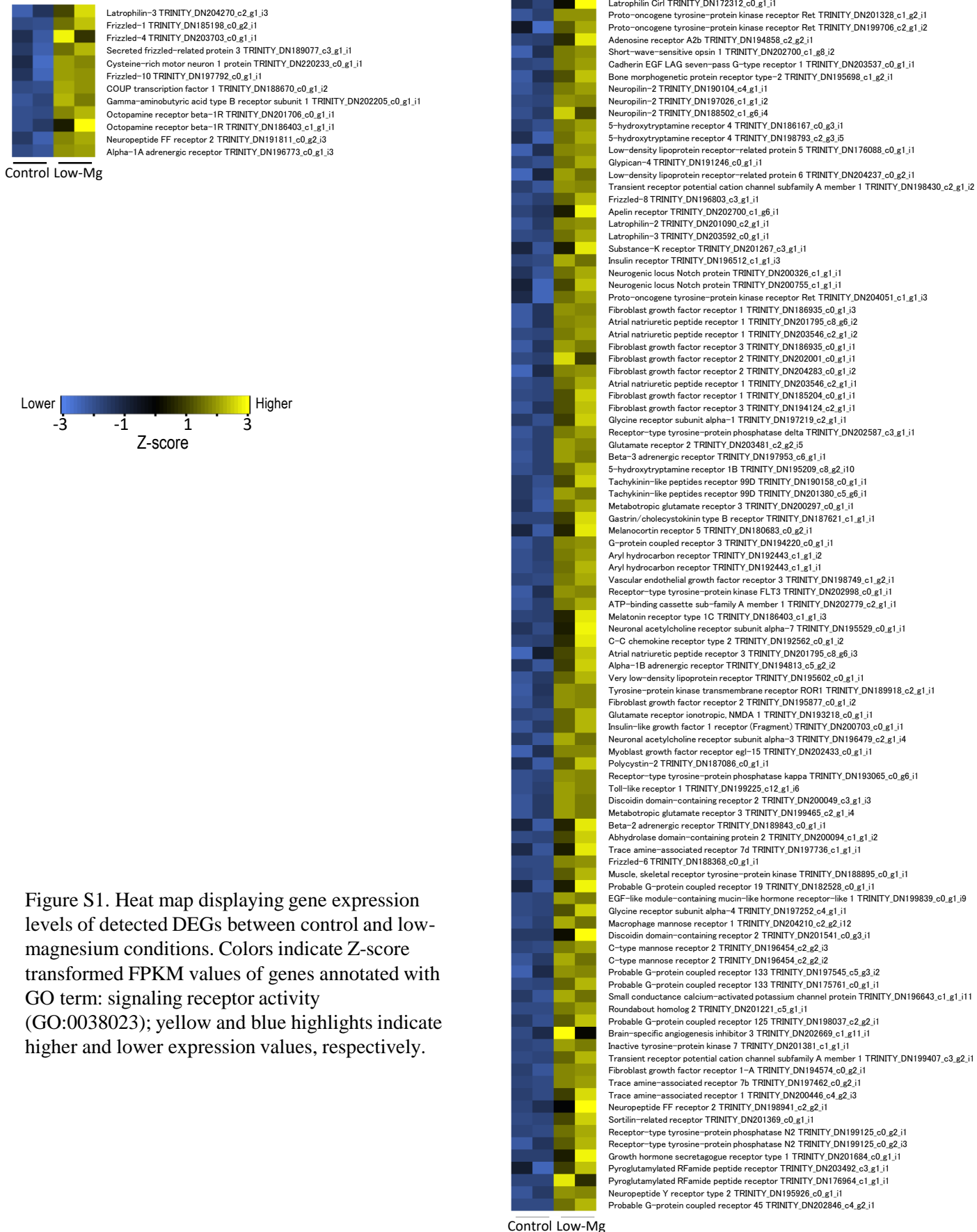


Figure S1. Heat map displaying gene expression levels of detected DEGs between control and low-magnesium conditions. Colors indicate Z-score transformed FPKM values of genes annotated with GO term: signaling receptor activity (GO:0038023); yellow and blue highlights indicate higher and lower expression values, respectively.

# Response to endogenous stimulus (GO:0009719)

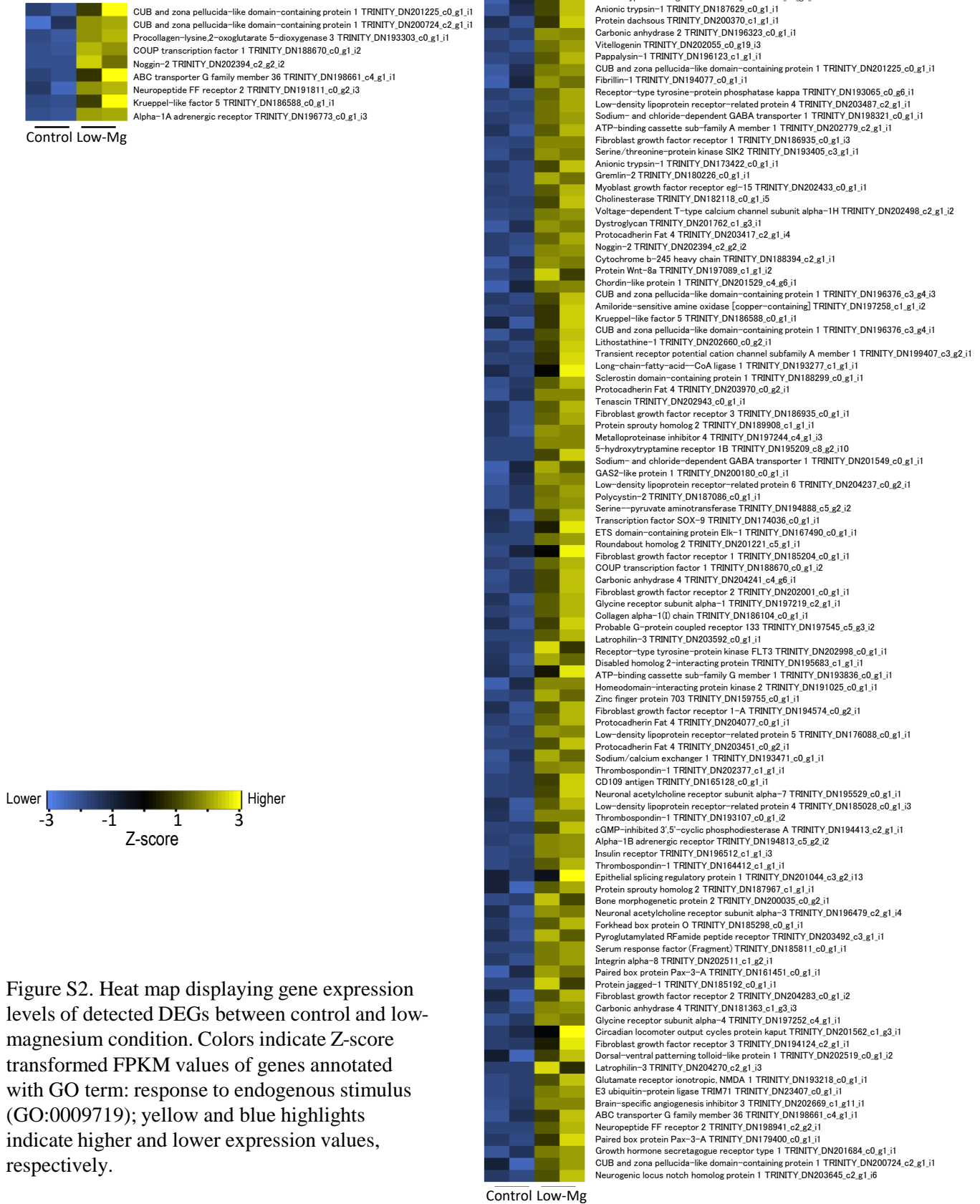


Figure S2. Heat map displaying gene expression levels of detected DEGs between control and low-magnesium condition. Colors indicate Z-score transformed FPKM values of genes annotated with GO term: response to endogenous stimulus (GO:0009719); yellow and blue highlights indicate higher and lower expression values, respectively.

# Extracellular matrix (GO:0031012)

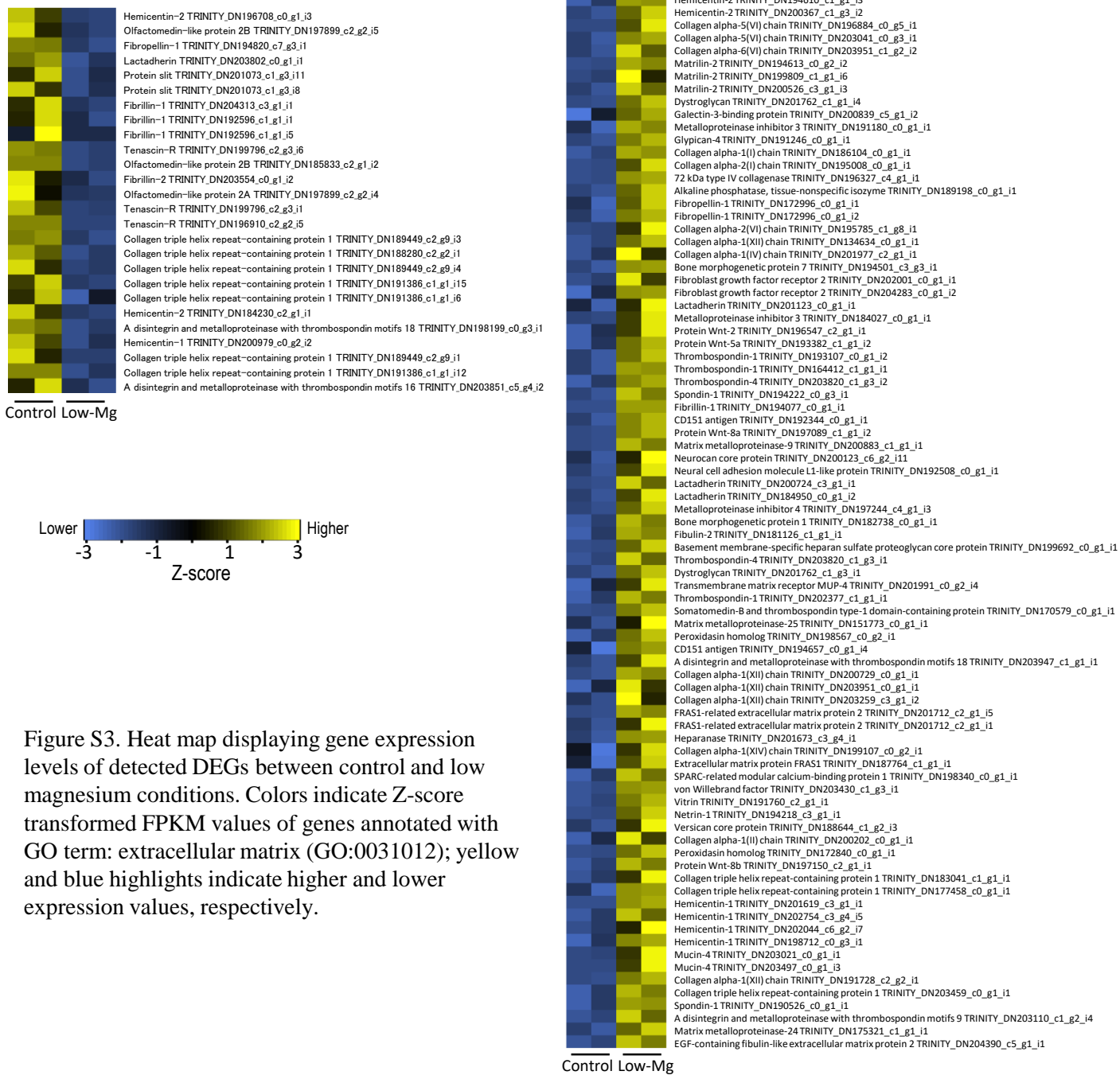


Figure S3. Heat map displaying gene expression levels of detected DEGs between control and low magnesium conditions. Colors indicate Z-score transformed FPKM values of genes annotated with GO term: extracellular matrix (GO:0031012); yellow and blue highlights indicate higher and lower expression values, respectively.

# Cell surface receptor signaling pathway (GO:0007166)



Control Low-Mg

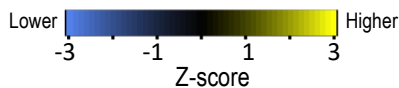


Figure S3 Continued

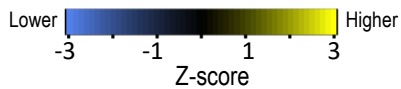


Control Low-Mg



Control Low-Mg

Figure S3 Continued



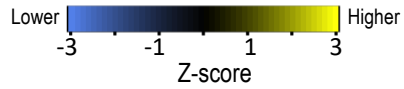
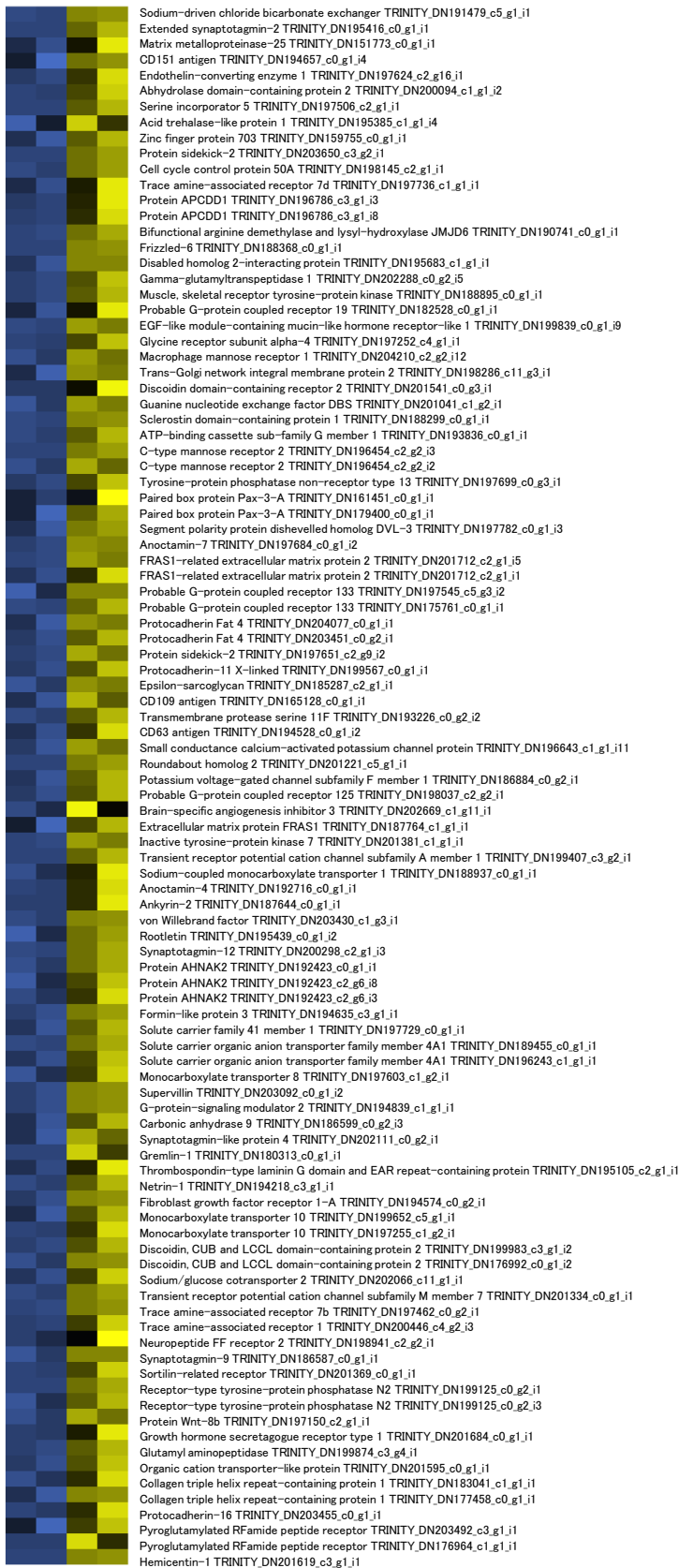
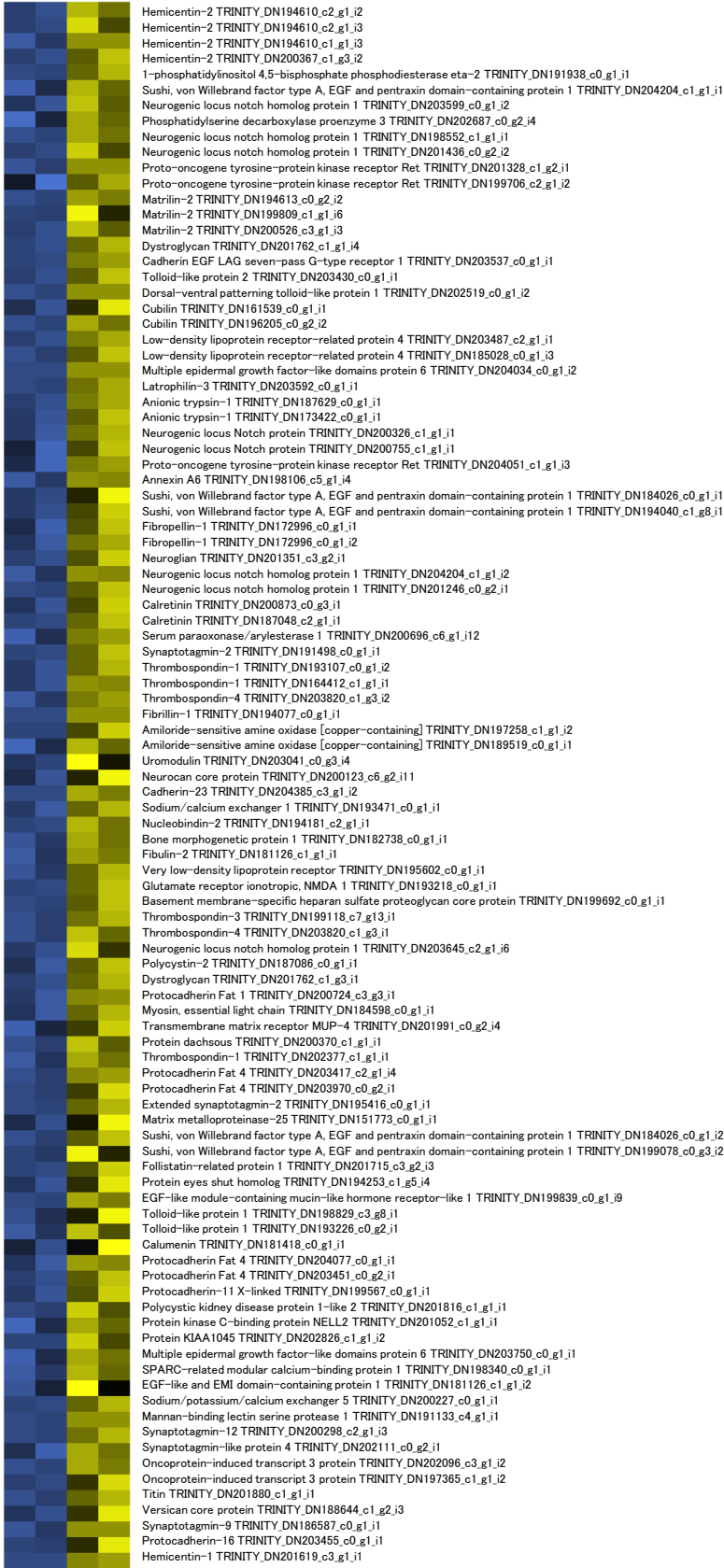


Figure S4. Heat map displaying gene expression levels of detected DEGs between control and low magnesium conditions. Colors indicate Z-score transformed FPKM values of genes annotated with GO term: cell surface receptor signaling pathway (GO:0007166); yellow and blue highlights indicate higher and lower expression values, respectively.

Control Low-Mg

# Calcium ion binding (GO:0005509)



Control Low-Mg

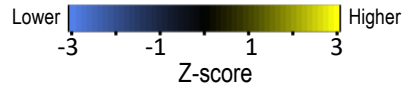


Figure S5. Heat map displaying gene expression levels of detected DEGs between control and low magnesium conditions. Colors indicate Z-score transformed FPKM values of genes annotated with GO term: calcium ion binding (GO:0005509); yellow and blue highlights indicate higher and lower expression values, respectively.

## Calcium ion binding (GO:0005509)

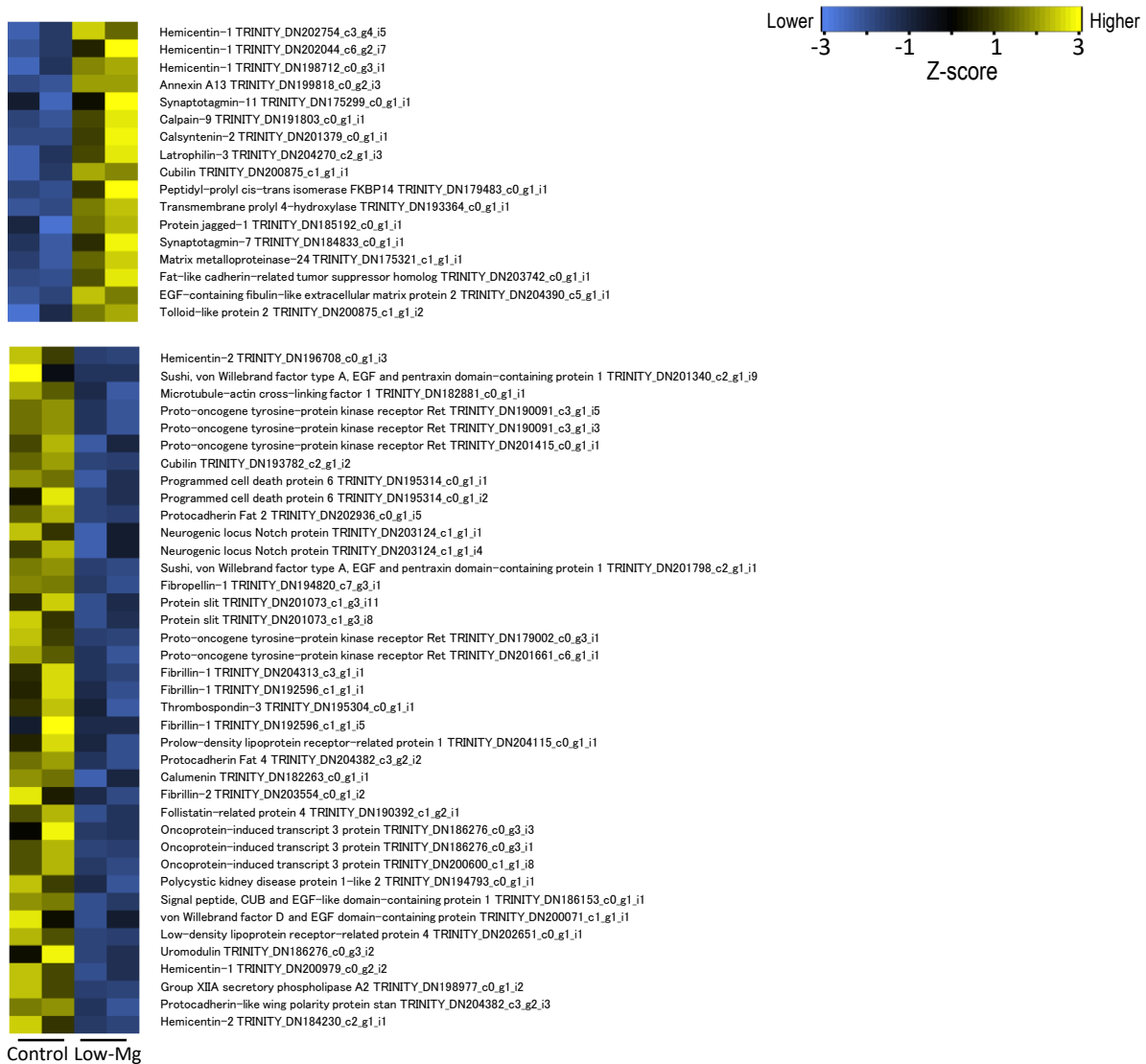
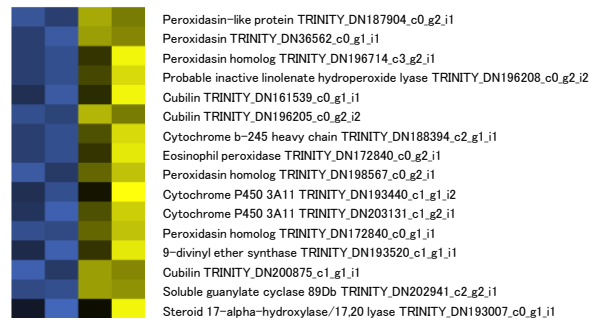


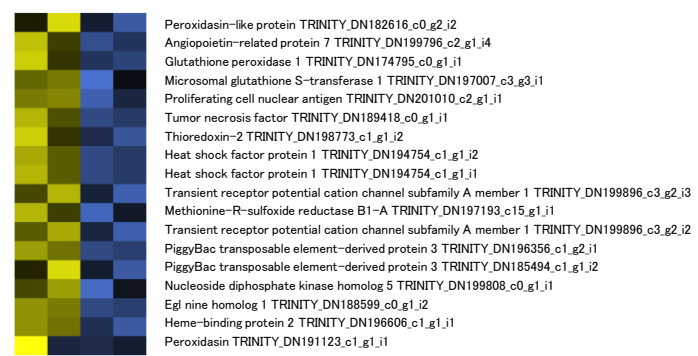
Figure S5 Continued



### Tetrapyrrole binding (GO:0046906)

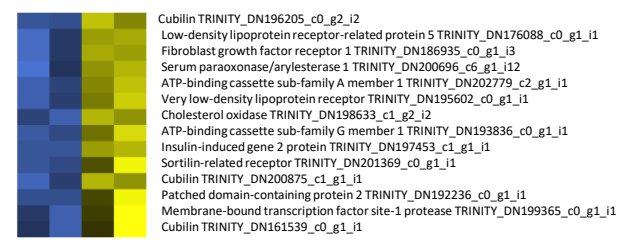


### Response to oxidative stress (GO:0006979)



Control Low-Mg

### Secondary alcohol metabolic process (GO:1902652)



Control Low-Mg

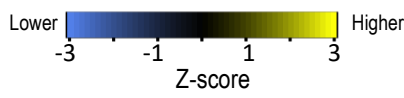
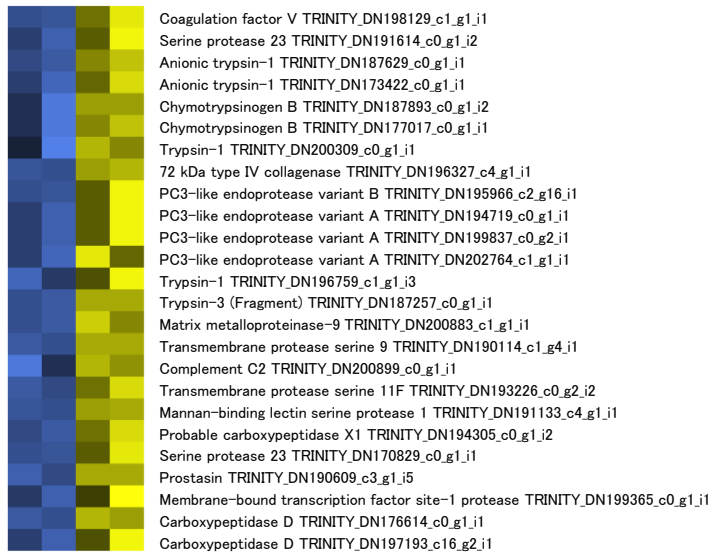
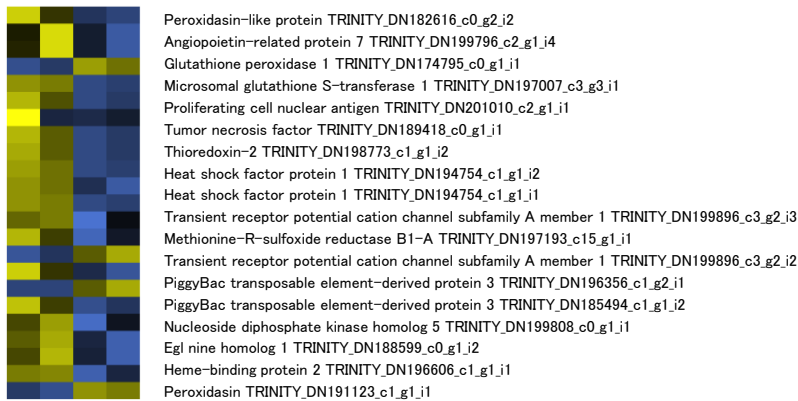


Figure S6. Heat map displaying gene expression levels of detected DEGs between control and low magnesium conditions. Colors indicate Z-score transformed FPKM values of genes annotated with GO terms: tetrapyrrole binding (GO:0046906), regulation of tumor necrosis factor biosynthetic process (GO: 0042534 ), response to oxidative stress (GO:0006979), sterol metabolic process (GO:0016125), Notch signaling pathway (GO:0007219), and secondary alcohol metabolic process (GO:1902652); yellow and blue highlights indicate higher and lower expression values, respectively.

## Serine hydrolase activity (GO:0017171)



## Response to oxidative stress (GO:0006979)



Control Low-Mg

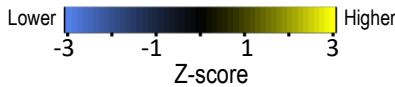
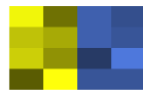


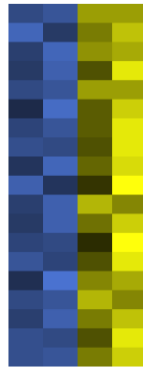
Figure S7. Heat map displaying gene expression levels of detected DEGs between control and low magnesium conditions. Colors indicate Z-score transformed FPKM value of genes annotated with GO terms: serine hydrolase activity (GO:0017171), regulation of tumor necrosis factor biosynthetic process GO:0042534), response to oxidative stress (GO: 0006979), and regulation of MAPK cascade (GO:0043408); yellow and blue highlights indicate higher and lower expression values, respectively.

## Necrotic cell death (GO:0070265)



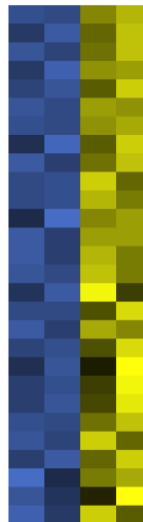
Tumor necrosis factor TRINITY\_DN189418\_c0.g1.i1  
Heme-binding protein 2 TRINITY\_DN196606\_c1.g2.i1  
Heme-binding protein 2 TRINITY\_DN196606\_c1.g1.i1  
Ubiquitin carboxyl-terminal hydrolase CYLD TRINITY\_DN190797\_c3.g3.i2

## Potassium ion transport (GO:0006813)



Solute carrier family 12 member 8 TRINITY\_DN201789\_c0.g1.i1  
Ankyrin-3 TRINITY\_DN203333\_c0.g1.i3  
Potassium channel subfamily K member 3 TRINITY\_DN201544\_c0.g1.i2  
Potassium voltage-gated channel subfamily H member 6 TRINITY\_DN190442\_c0.g1.i2  
Potassium voltage-gated channel subfamily C member 1 TRINITY\_DN200352\_c0.g3.i1  
Potassium voltage-gated channel subfamily C member 1 TRINITY\_DN200850\_c5.g1.i3  
Sodium/potassium-transporting ATPase subunit alpha-1 TRINITY\_DN200268\_c0.g1.i1  
Ankyrin-3 TRINITY\_DN202268\_c1.g1.i1  
Polycystin-2 TRINITY\_DN187086\_c0.g1.i1  
Sodium/hydrogen exchanger 8 TRINITY\_DN193838\_c4.g3.i1  
Small conductance calcium-activated potassium channel protein TRINITY\_DN196643\_c1.g1.i11  
Potassium voltage-gated channel subfamily F member 1 TRINITY\_DN186884\_c0.g2.i1  
Ankyrin-2 TRINITY\_DN187644\_c0.g1.i1  
Calcium-activated potassium channel subunit beta-4 TRINITY\_DN188532\_c4.g4.i6  
Potassium channel subfamily K member 10 TRINITY\_DN200472\_c0.g4.i1  
Potassium channel subfamily K member 9 TRINITY\_DN184978\_c0.g1.i1  
Potassium channel subfamily K member 9 TRINITY\_DN197211\_c2.g1.i1  
Four and a half LIM domains protein 1 TRINITY\_DN190125\_c0.g1.i2  
Sodium/potassium/calcium exchanger 5 TRINITY\_DN200227\_c0.g1.i1

## Metalloendopeptidase activity (GO:0004222)



Metalloprotease TIK1 TRINITY\_DN186203\_c0.g1.i1  
Disintegrin and metalloproteinase domain-containing protein 10 TRINITY\_DN201463\_c2.g1.i1  
Disintegrin and metalloproteinase domain-containing protein 12 TRINITY\_DN202170\_c0.g5.i1  
Disintegrin and metalloproteinase domain-containing protein 12 TRINITY\_DN202170\_c0.g5.i2  
Tolloid-like protein 2 TRINITY\_DN203430\_c0.g1.i1  
Dorsal-ventral patterning tolloid-like protein 1 TRINITY\_DN202519\_c0.g1.i2  
72 kDa type IV collagenase TRINITY\_DN196327\_c4.g1.i1  
Low choriolytic enzyme TRINITY\_DN197257\_c1.g1.i1  
High choriolytic enzyme 2 TRINITY\_DN198857\_c3.g1.i4  
Endothelin-converting enzyme 1 TRINITY\_DN199871\_c1.g1.i1  
Matrix metalloproteinase-9 TRINITY\_DN200883\_c1.g1.i1  
Zinc metalloproteinase nas-4 TRINITY\_DN194185\_c0.g1.i1  
Zinc metalloproteinase nas-15 TRINITY\_DN174384\_c0.g1.i1  
Bone morphogenetic protein 1 TRINITY\_DN182738\_c0.g1.i1  
Pappalysin-1 TRINITY\_DN196123\_c1.g1.i1  
Zinc metalloproteinase nas-14 TRINITY\_DN197190\_c3.g2.i2  
Zinc metalloproteinase nas-13 TRINITY\_DN195501\_c4.g1.i1  
Zinc metalloproteinase nas-13 TRINITY\_DN192569\_c0.g1.i1  
Zinc metalloproteinase nas-13 TRINITY\_DN194740\_c0.g1.i1  
Matrix metalloproteinase-25 TRINITY\_DN151773\_c0.g1.i1  
Endothelin-converting enzyme 1 TRINITY\_DN197624\_c2.g1.i1  
A disintegrin and metalloproteinase with thrombospondin motifs 18 TRINITY\_DN203947\_c1.g1.i1  
Endothelin-converting enzyme 2 TRINITY\_DN196198\_c3.g1.i1  
A disintegrin and metalloproteinase with thrombospondin motifs 9 TRINITY\_DN203110\_c1.g2.i4  
Matrix metalloproteinase-24 TRINITY\_DN175321\_c1.g1.i1  
Tolloid-like protein 2 TRINITY\_DN200875\_c1.g1.i2  
Tolloid-like protein 1 TRINITY\_DN198829\_c3.g8.i1  
Tolloid-like protein 1 TRINITY\_DN193226\_c0.g2.i1

Control Low-Mg

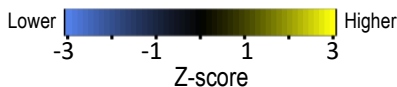
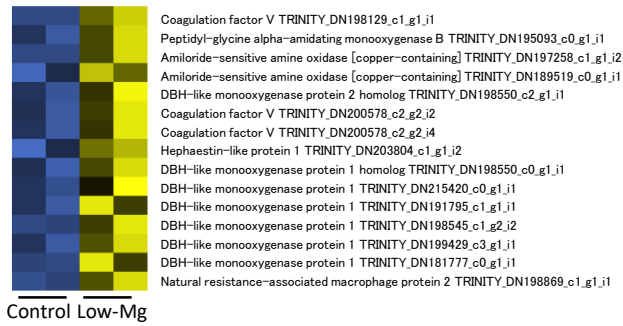
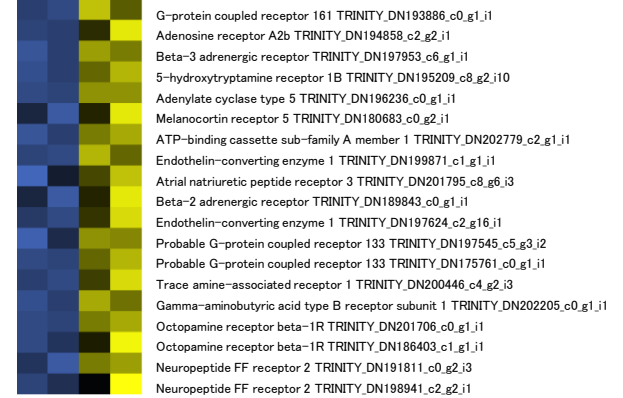


Figure S8. Heat map displaying gene expression levels of detected DEGs between control and low magnesium conditions. Colors indicate Z-score transformed FPKM value of genes annotated with GO terms: positive regulation of nitrogen compound metabolic process (GO:0051173), necrotic cell death (GO:0070265), potassium ion transport (GO:0006813), and metalloendopeptidase activity (GO:0004222); yellow and blue highlights indicate higher and lower expression values, respectively.

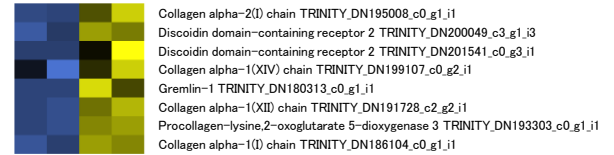
## Copper ion binding (GO:0005507)



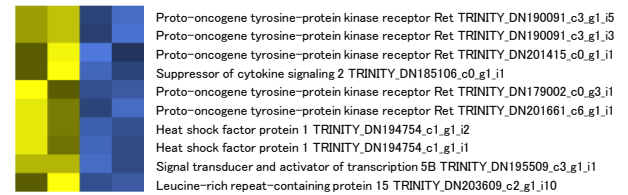
## cAMP biosynthetic process (GO:0006171)



## Collagen fibril organization (GO:0030199)



## JAK-STAT cascade (GO:0007259)



## DNA-dependent DNA replication (GO:0006261)

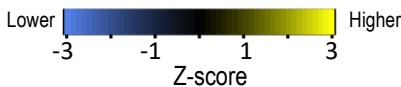
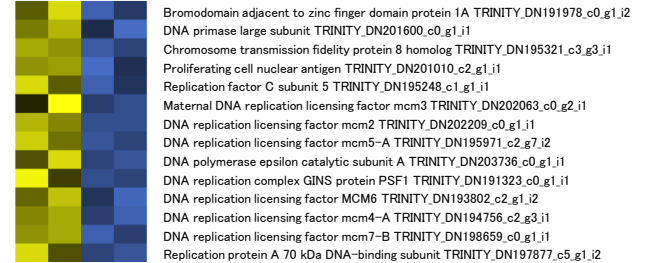
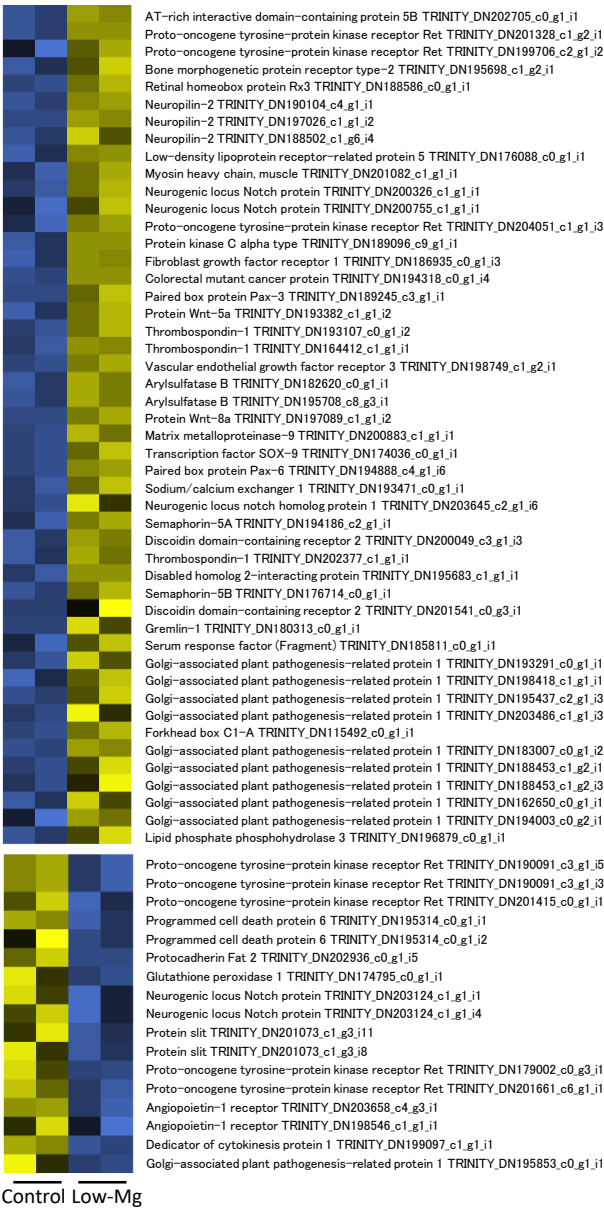


Figure S9, Heat map displaying gene expression levels of detected DEGs between control and low-magnesium condition. Colors indicate Z-score transformed FPKM value of genes annotated with GO terms: macrophage activation (GO:0042116), fibroblast growth factor-activated receptor activity (O:0005007), copper ion binding (GO:0005507), collagen metabolic process (GO:0032963), cAMP biosynthetic process (GO:0006171), collagen fibril organization (GO: 0030199), JAK-STAT cascade (GO:0007259), and DNA-dependent DNA replication (GO:0006261); yellow and blue highlights indicate higher and lower expression values, respectively.

## ameboidal-type cell migration (GO:0001667)



## Wnt signaling pathway (GO:0016055)

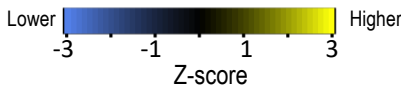
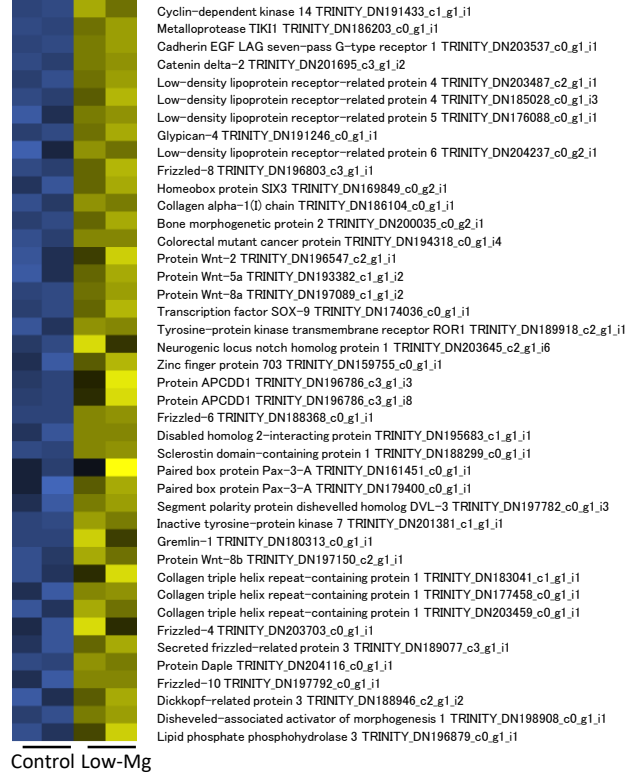


Figure S10. Heat map displaying gene expression levels of detected DEGs between control and low-magnesium conditions. Colors indicate Z-score transformed FPKM value of genes annotated with GO terms: ameboidal type cell migration (GO:0001667) and Wnt signaling pathway (GO: 0016055); yellow and blue highlights indicate higher and lower expression values, respectively.