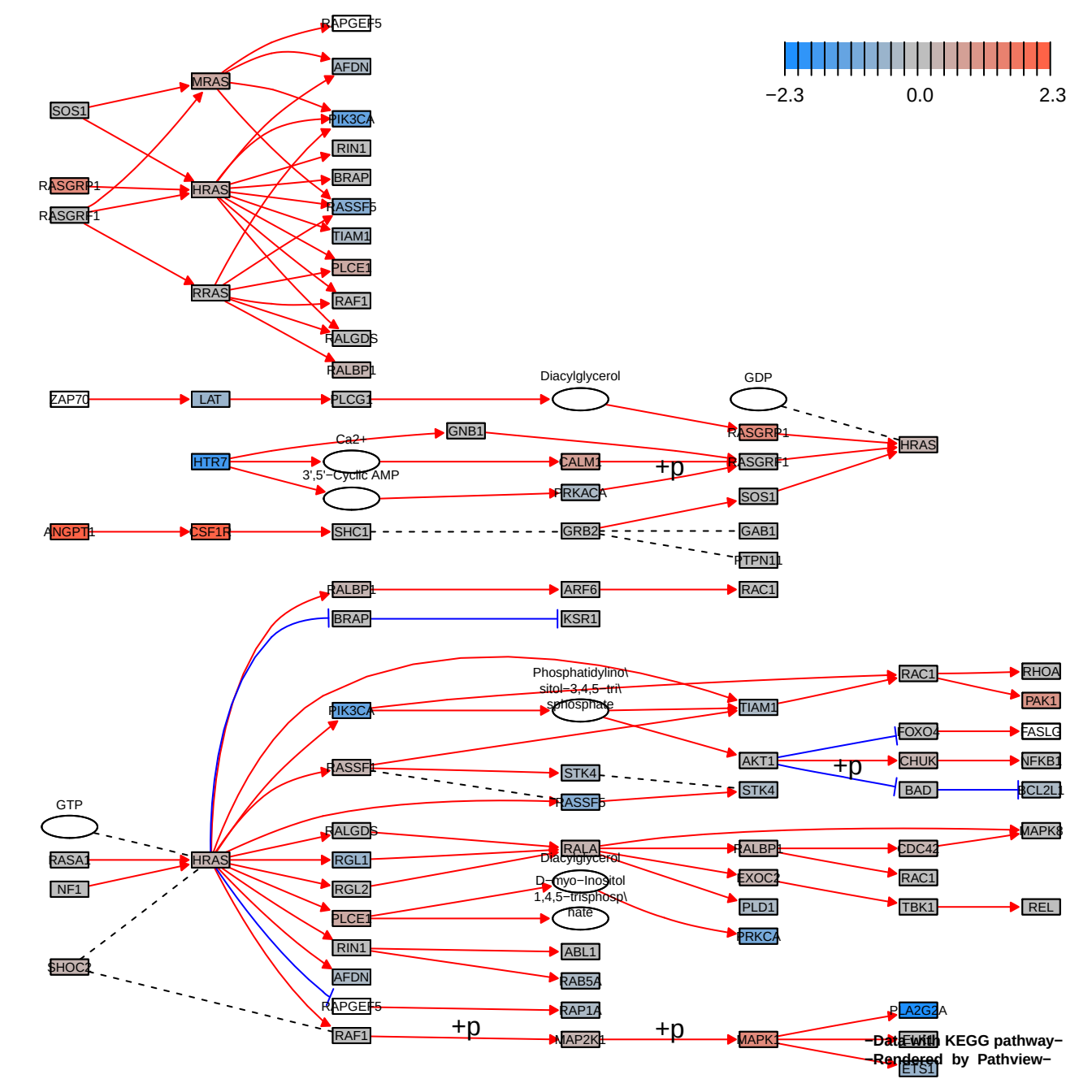
−2.3
0.0
2.3
RAPGEF5
AFDN
MRAS
SOS1
PIK3CA
RIN1
BRAP
RASGRP1
HRAS
RASSF5
RASGRF1
TIAM1
PLCE1
RRAS
RAF1
RALGDS
RALBP1
ZAP70
LAT
PLCG1
Diacylglycerol
GDP
GNB1
RASGRP1
Ca2+
HRAS
HTR7
CALM1
RASGRF1
3',5'−Cyclic AMP
+p
PRKACA
SOS1
ANGPT1
CSF1R
SHC1
GRB2
GAB1
PTPN11
RALBP1
ARF6
RAC1
BRAP
KSR1
Phosphatidylinol\
sitol−3,4,5−tri\
sphosphate
RAC1
RHOA
PIK3CA
TIAM1
PAK1
FOXO4
FASLG
RASSF1
AKT1
+p
CHUK
NFKB1
STK4
BAD
BCL2L1
STK4
RASSF5
GTP
RALGDS
MAPK8
RASA1
HRAS
RGL1
RALA
RALBP1
CDC42
NF1
Diacylglycerol
EXOC2
RAC1
RGL2
D−myo−Inositol
1,4,5−trisphosp\
hate
PLD1
TBK1
REL
PLCE1
PRKCA
RIN1
ABL1
SHOC2
AFDN
RAB5A
RAPGEF5
RAP1A
+p
+p
RAF1
MAP2K1
MAPK1
PLA2G4A
ETS1
−Data with KEGG pathway−
−Rendered by Pathview−

KEGG diagram legend

Edge Types

compound

hidden compound

activation

inhibition

expression

repression

indirect effect

state change

binding/association

dissociation

phosphorylation +p

dephosphorylation −p

glycosylation +g

ubiquitination +u

methylation +m

others/unknown ?

Node Types

gene (protein/enzyme)

group (complex)

compound (metabolite/glycan)

map (pathway) Pathway name