

Figure S1 Phylogenetic tree of GmFNR and other plants FNR genes. The phylogenetic tree was constructed from the amino acid sequences by MEGA-X, using the neighbour-joining method. Full-length sequences of FNR genes were obtained from the NCBI database. A scale of distance is shown below.

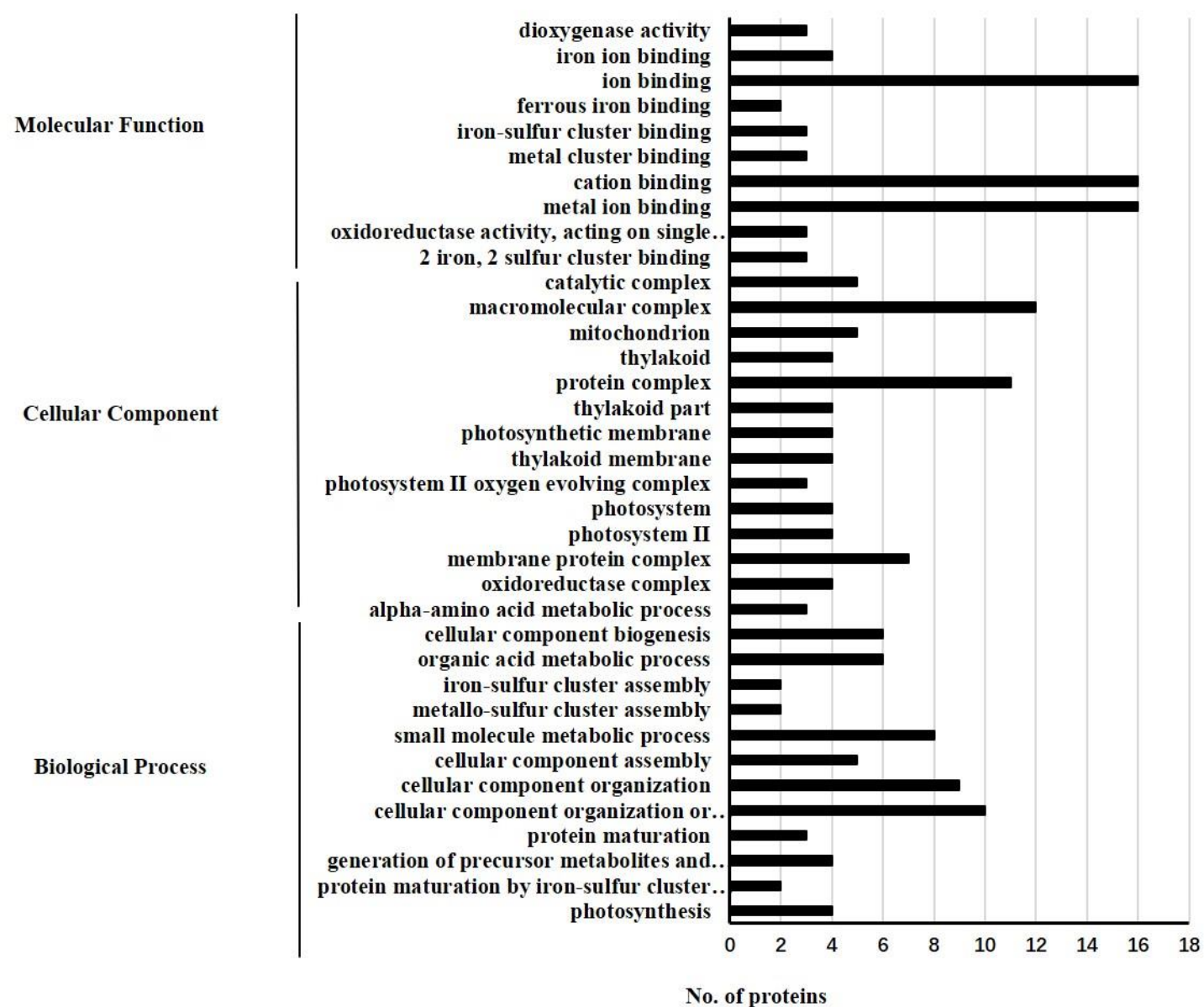


Figure S2 Gene ontology classification of proteins interacted with *GmFNR*. DAVID Bioinformatics Resources 6.8 (<https://david.ncifcrf.gov>) was used for GO analysis.

Table S1 71 proteins interacting with GmFNR.

Name and abbreviation of soybean proteins	Accession number	Identity(%)
Glycine max protein LSD1 (LOC100776644), transcript variant X1, mRNA	XM_003533780.3	99%
Glycine max putative light-regulated protein 1 (LOC100305960), mRNA	NM_001248611.2	99%
Glycine max TATA binding protein associated factor 21kDa subunit (LOC100527659)	NM_001248657.2	99%
Glycine max superoxide dismutase [Cu-Zn] (LOC100305732), mRNA	NM_001249007.2	99%
Glycine max nuclear transcription factor Y subunit A-7-like (LOC100784325), transcript variant X2, mRNA	XM_003535034.3	99%
Glycine max E3 ubiquitin-protein ligase MBR2-like (LOC100819874), mRNA	XM_003526408.3	99%
Glycine max elongation factor 1-alpha (LOC100785429), mRNA	XM_003553244.3	100%
Glycine max miraculin-like (LOC100776726), mRNA	XM_003540468.3	100%
Glycine max BEL1-like homeodomain protein 1 (LOC100810851), transcript variant X5, mRNA	XM_014768419.1	99%
Glycine max mitochondrial adenine nucleotide transporter ADNT1-like (LOC100787927), mRNA	XM_003554710.3	99%
Glycine max vacuolar protein sorting-associated protein 35B-like (LOC100778365), mRNA	XM_003544979.3	99%
Glycine max chaperone protein dnaJ 20, chloroplastic-like (LOC100819682), mRNA	XM_003524885.3	100%
Glycine max 5'-3' exoribonuclease 4-like (LOC100793385), transcript variant X2, mRNA	XM_003554638.3	100%
Glycine max peroxisomal fatty acid beta-oxidation multifunctional protein MFP2-like (LOC100777319), mRNA	XM_003529513.3	99%
Glycine max desumoylating isopeptidase 1 (LOC100787486), mRNA	XM_003532248.3	97%
Glycine max SNAP25 homologous protein SNAP33-like (LOC100806698), transcript variant X2, mRNA	XM_014776588.1	99%
Glycine max eukaryotic translation initiation factor 3 subunit I-like (LOC100793485), mRNA	XM_003517657.3	99%
Glycine max histone H3.3 (LOC100783277), mRNA	XM_003551977.3	100%
Glycine max putative 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase 2 (LOC100812492), transcript variant X1, mRNA	XM_003536462.3	99%
Glycine max linoleate 13S-lipoxygenase 3-1, chloroplastic-like (LOC100791000), transcript variant X2, misc_RNA	XR_001385508.1	99%
Glycine max triose phosphate/phosphate translocator, chloroplastic (LOC732611), mRNA	XM_003542673.2	100%
Glycine max SNF1-related protein kinase regulatory subunit gamma-1-like (LOC100776754), transcript variant X2, mRNA	XM_003526913.3	98%
Glycine max protein PHLOEM PROTEIN 2-LIKE A1-like (LOC100799048), mRNA	NM_001255241.1	99%
Glycine max psbP-like protein 1, chloroplastic (LOC100305918), mRNA	XM_003552627.3	99%
Glycine max OPA3-like protein (LOC100817281), mRNA	XM_003535354.3	99%
Glycine max probable ribose-5-phosphate isomerase 3, chloroplastic (LOC100792666), mRNA	NM_001317524.1	97%
Glycine max iron-sulfur cluster assembly protein 1-like (LOC100776408), transcript variant X1, mRNA	XM_003542526.3	99%
Glycine max dual specificity protein kinase zakA-like (LOC100807921), mRNA	XM_003525287.3	99%
Glycine max protein EARLY RESPONSIVE TO DEHYDRATION 15-like (LOC100796671), mRNA	XM_003519368.3	100%

Glycine max apoptosis inhibitor 5 (LOC100800145), mRNA	XM_003529311.3	99%
Glycine max probable 2-oxoglutarate/Fe(II)-dependent dioxygenase (LOC100806800), mRNA	XM_006591214.2	99%
Glycine max C2 domain-containing protein At1g53590 (LOC100779958), transcript variant X5, mRNA	XM_006594636.2	99%
Glycine max chlorophyllide a oxygenase, chloroplastic (LOC100806298), mRNA	XM_003523394.3	99%
Glycine max calvin cycle protein CP12-2, chloroplastic (LOC100814289), mRNA	XM_003535887.3	100%
Glycine max E3 ubiquitin-protein ligase RING1-like (LOC100804867), mRNA	XM_003537934.3	98%
Glycine max GTP-binding protein SAR1A (LOC100499682), misc_RNA	XR_418354.2	99%
Glycine max homocysteine S-methyltransferase 3-like (LOC100811127), mRNA	NM_001255423.1	99%
Glycine max chlorophyll a-b binding protein CP29.2, chloroplastic-like (LOC100785180), mRNA	XM_003516902.3	98%
Glycine max sucrose transport protein SUC8 (LOC100784153), mRNA	XM_003518300.3	99%
Glycine max expansin-like B1 (LOC100777265), mRNA	XM_003524109.3	99%
Glycine max probable aquaporin PIP-type 7a (LOC100775766), mRNA	XM_003519335.3	99%
Glycine max 60S ribosomal protein L35 (LOC100801539), mRNA	XM_003556495.3	96%
Glycine max arginine/serine-rich-splicing factor RSP40-like (LOC100796509), transcript variant X1, mRNA	XM_006588396.2	99%
Glycine max syntaxin-51 (LOC100782666), mRNA	XM_006595646.2	99%
Glycine max oxygen-evolving enhancer protein 1, chloroplastic (LOC100792252), mRNA	XM_003547960.2	99%
Glycine max probable mitochondrial-processing peptidase subunit beta (LOC100777553), mRNA	XM_003552046.3	99%
Glycine max protein MEI2-like 2 (LOC100812324), transcript variant X3, mRNA	XM_006602183.2	99%
Glycine max ATP-dependent RNA helicase DHX36-like (LOC100806141), mRNA	XM_003524302.3	94%
Glycine max cytosolic malate dehydrogenase (LOC547963), mRNA	NM_001249732.1	99%
Glycine max stem-specific protein TSJT1-like (LOC100814871), mRNA	XM_003540043.3	99%
Glycine max methionine synthase (LOC547643), mRNA	NM_001248865.1	99%
Glycine max pathogenesis-related protein 1-like (LOC100805116), mRNA	XM_003545722.3	100%
Glycine max probable protein phosphatase 2C 58 (LOC100819846), mRNA	XM_003539891.3	98%
Glycine max exo-poly-alpha-D-galacturonosidase-like (LOC100794954), mRNA	XM_003554139.3	97%
Glycine max thaumatin-like protein 1b (LOC100780217), mRNA	XM_003535166.3	99%
Glycine max dynamin-related protein 3A-like (LOC100807752), transcript variant X1, mRNA	XM_003543087.3	99%
Glycine max pleckstrin homology domain-containing protein 1-like (LOC100779324), mRNA	XM_003519341.3	92%
Glycine max probable protein phosphatase 2C 46 (LOC100777920), mRNA	XM_003520084.3	99%
Glycine max probable caffeoyl-CoA O-methyltransferase At4g26220 (LOC100800911), transcript variant X2, mRNA	XM_003517889.2	98%
Glycine max protein SUPPRESSOR OF K(+) TRANSPORT GROWTH DEFECT 1-like (LOC100806836), mRNA	XM_003540192.3	99%
Glycine max ferric leghemoglobin reductase-2 precursor (LOC547523), mRNA	NM_001250835.1	99%
Glycine max phospholipase A1-Ibeta2, chloroplastic (LOC100806573), mRNA	XM_003517357.3	99%
Glycine max iron-sulfur assembly protein IscA, chloroplastic-like (LOC100811312), mRNA	XM_003525036.3	99%

Glycine max FRIGIDA-like protein 4a (LOC100805780), mRNA	XM_003556002.3	100%
Glycine max peptidyl-prolyl cis-trans isomerase 1-like (LOC106795232), mRNA	XM_014764426.1	100%
Glycine max chaperone protein dnaJ 8, chloroplastic-like (LOC100804784), mRNA	NM_001254267.2	99%
Glycine max uncharacterized LOC100526959 (LOC100526959), transcript variant X4, mRNA	XM_006590209.2	97%
Glycine max uncharacterized LOC100527715 (LOC100527715), transcript variant X2, mRNA	XM_006576145.2	100%
Glycine max uncharacterized LOC100499745 (LOC100499745), mRNA	NM_001248513.2	100%
Glycine max uncharacterized LOC100800943 (LOC100800943), transcript variant X1, mRNA	XM_014771267.1	93%
Glycine max uncharacterized LOC100787547 (LOC100787547), transcript variant X2, mRNA	XM_003537119.3	99%