

Supplementary Figure 1. KEGG pathways to which the DEGs were enriched in susceptible (XL19) and tolerant (ZYM1288) hulless barley.

3.00	5.00	5.00	4.00	ko00250	Alanine, aspartate and glutamate metabolism
21.00	18.00	31.00	30.00	ko00520	Amino sugar and nucleotide sugar metabolism
6.00	6.00	8.00	13.00	ko00330	Arginine and proline metabolism
250.00	190.00	298.00	300.00	ko01110	Biosynthesis of secondary metabolites
3.00	5.00	6.00	9.00	ko00905	Brassinosteroid biosynthesis
13.00	8.00	17.00	11.00	ko00710	Carbon fixation in photosynthetic organisms
9.00	7.00	13.00	15.00	ko00906	Carotenoid biosynthesis
12.00	5.00	14.00	15.00	ko04712	Circadian rhythm - plant
5.00	2.00	4.00	3.00	ko00020	Citrate cycle (TCA cycle)
10.00	2.00	9.00	4.00	ko00904	Diterpenoid biosynthesis
9.00	7.00	11.00	12.00	ko00071	Fatty acid degradation
6.00	2.00	4.00	3.00	ko00062	Fatty acid elongation
22.00	23.00	23.00	24.00	ko00941	Flavonoid biosynthesis
11.00	13.00	16.00	17.00	ko00052	Galactose metabolism
4.00	3.00	4.00	3.00	ko00966	Glucosinolate biosynthesis
23.00	16.00	28.00	34.00	ko00480	Glutathione metabolism
12.00	10.00	18.00	19.00	ko00260	Glycine, serine and threonine metabolism
15.00	9.00	19.00	16.00	ko00562	Inositol phosphate metabolism
3.00	2.00	3.00	3.00	ko00943	Isoflavonoid biosynthesis
2.00	2.00	3.00	2.00	ko00540	Lipopolysaccharide biosynthesis
6.00	2.00	3.00	3.00	ko00300	Lysine biosynthesis
40.00	21.00	54.00	51.00	ko04016	MAPK signaling pathway - plant
8.00	7.00	8.00	10.00	ko00902	Monoterpenoid biosynthesis
4.00	4.00	5.00	6.00	ko00910	Nitrogen metabolism
12.00	4.00	9.00	6.00	ko00030	Pentose phosphate pathway
15.00	10.00	14.00	12.00	ko00360	Phenylalanine metabolism
14.00	12.00	17.00	15.00	ko00400	Phenylalanine, tyrosine and tryptophan biosynthesis
8.00	1.00	2.00	5.00	ko00195	Photosynthesis
2.00	1.00	6.00	3.00	ko00196	Photosynthesis - antenna proteins
46.00	22.00	63.00	64.00	ko04075	Plant hormone signal transduction
124.00	80.00	119.00	134.00	ko04626	Plant-pathogen interaction
10.00	8.00	9.00	18.00	ko00230	Purine metabolism
11.00	9.00	10.00	15.00	ko00240	Pyrimidine metabolism
2.00	2.00	2.00	3.00	ko00909	Sesquiterpenoid and triterpenoid biosynthesis
43.00	29.00	51.00	64.00	ko00500	Starch and sucrose metabolism
12.00	13.00	20.00	13.00	ko00945	Stilbenoid, diarylheptanoid and gingerol biosynthesis
5.00	5.00	8.00	10.00	ko00900	Terpenoid backbone biosynthesis
195.00	153.00	231.00	270.00	ko04620	Toll-like receptor signaling pathway
8.00	10.00	16.00	13.00	ko02020	Two-component system
17.00	7.00	11.00	9.00	ko00350	Tyrosine metabolism
2.00	3.00	4.00	2.00	ko00290	Valine, leucine and isoleucine biosynthesis
9.00	5.00	14.00	11.00	ko00908	Zeatin biosynthesis
5 hr	12 hr	24 hr	36 hr		