

Table SII. Gene Ontology enrichment analysis results of the brown module.

ID	Description	Gene ratio	Bg ratio	P-value	p.adjust	q-value	geneID	Count
GO:0005201	extracellular matrix structural constituent	18/320	155/176 32	4.47x10 ⁻¹⁰	1.95x10 ⁻⁷	1.73x10 ⁻⁷	1300/115908/1301/1277/1281/7058/1311/1290/1278/2202/ 1289/10516/25878/4237/1296/1285/80781/8483	18
GO:0030020	extracellular matrix structural constituent conferring tensile strength	10/320	37/1763 2	7.60x10 ⁻¹⁰	1.95x10 ⁻⁷	1.73x10 ⁻⁷	1300/1301/1277/1281/1290/1278/1289/1296/1285/80781	10
GO:0016538	cyclin-dependent protein serine/threonine kinase regulator activity	9/320	48/1763 2	1.72x10 ⁻⁷	2.94x10 ⁻⁵	2.61x10 ⁻⁵	9133/891/890/1163/898/1029/9134/1031/1164	9
GO:0140097	catalytic activity, acting on DNA	16/320	185/176 32	2.77x10 ⁻⁷	3.55x10 ⁻⁵	3.16x10 ⁻⁵	7153/4830/9837/2237/4173/5111/5427/8318/9156/92667/1 763/4175/8438/1663/25788/641	16
GO:0003688	DNA replication origin binding	6/320	17/1763 2	3.57x10 ⁻⁷	3.61x10 ⁻⁵	3.21x10 ⁻⁵	4171/23594/8318/55388/990/1663	6
GO:0008017	microtubule binding	18/320	240/176 32	4.23x10 ⁻⁷	3.61x10 ⁻⁵	3.21x10 ⁻⁵	51203/10112/332/9928/3832/24137/11004/9055/10615/12 0892/146909/56992/9493/29127/1062/5347/81610/81930	18
GO:0016887	ATPase activity	24/320	445/176 32	2.19x10 ⁻⁶	0.0001	0.0001	7153/10112/9928/3832/24137/11004/4173/21/26154/5984/ 29028/146909/56992/1763/9493/1062/4175/6596/1663/25 788/641/81930/5985/5983	24
GO:0015631	tubulin binding	20/320	325/176 32	2.19x10 ⁻⁶	0.0001	0.0001	4830/51203/10112/332/9928/3832/24137/11004/9055/106 15/120892/146909/56992/9493/29127/1062/5347/81610/6 72/81930	20
GO:0003777	microtubule motor activity	10/320	84/1763 2	2.84x10 ⁻⁶	0.0002	0.0001	10112/9928/3832/24137/11004/146909/56992/9493/1062/ 81930	10
GO:0003678	DNA helicase activity	8/320	50/1763 2	2.98x10 ⁻⁶	0.0002	0.0001	9837/4173/8318/1763/4175/1663/25788/641	8
GO:0004386	helicase activity	13/320	151/176 32	3.86x10 ⁻⁶	0.0002	0.0001	9837/4171/4173/8318/3070/1763/4175/6596/8438/1663/25 788/84515/641	13
GO:0008094	DNA-dependent ATPase activity	10/320	87/1763 2	3.92x10 ⁻⁶	0.0002	0.0001	7153/4173/5984/1763/4175/1663/25788/641/5985/5983	10

GO:0035173	histone kinase activity	5/320	17/1763 2	9.87x10 ⁻⁶	0.0004	0.0003	891/6790/983/9212/1111	5
GO:0048407	platelet-derived growth factor binding	4/320	11/1763 2	3.18x10 ⁻⁵	0.0012	0.0010	1277/1281/1278/1289	4
GO:0097472	cyclin-dependent protein kinase activity	6/320	37/1763 2	4.93x10 ⁻⁵	0.0017	0.0015	9133/891/983/890/898/9134	6
GO:0043142	single-stranded DNA-dependent ATPase activity	4/320	14/1763 2	9.23x10 ⁻⁵	0.0030	0.0026	5984/1763/5985/5983	4
GO:0003697	single-stranded DNA binding	9/320	105/176 32	0.0001	0.0038	0.0033	4830/4173/8318/6119/55388/10635/4175/1663/641	9
GO:0003774	motor activity	10/320	137/176 32	0.0002	0.0058	0.0051	10112/9928/3832/24137/11004/146909/56992/9493/1062/81930	10
GO:0004674	protein serine/threonine kinase activity	20/320	455/176 32	0.0003	0.0070	0.0062	701/9133/891/9833/4751/6790/699/7272/120892/983/9212/898/1111/1612/55872/203447/9134/5347/115701/130399	20
GO:0004693	cyclin-dependent protein serine/threonine kinase activity	5/320	36/1763 2	0.0005	0.0113	0.0100	9133/891/983/898/9134	5
GO:0019887	protein kinase regulator activity	11/320	180/176 32	0.0005	0.0113	0.0100	9133/891/26585/890/1163/898/1029/9134/1031/10926/1164	11
GO:0008297	single-stranded DNA exodeoxyribonuclease activity	3/320	10/1763 2	0.0006	0.0151	0.0134	2237/9156/92667	3
GO:0042623	ATPase activity, coupled	16/320	357/176 32	0.0009	0.0187	0.0167	7153/9928/3832/4173/21/26154/5984/146909/1763/4175/1663/25788/641/81930/5985/5983	16
GO:0004523	RNA-DNA hybrid ribonuclease activity	3/320	11/1763 2	0.0009	0.0187	0.0167	2237/10535/9156	3
GO:0008574	ATP-dependent microtubule motor activity, plus-end-directed	4/320	26/1763 2	0.0012	0.0238	0.0212	9928/3832/146909/81930	4
GO:0016893	endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters	5/320	46/1763 2	0.0014	0.0281	0.0249	2237/10535/9156/10799/1763	5

GO:0019207	kinase regulator activity	11/320	208/176 32	0.0015	0.0287	0.0255	9133/891/26585/890/1163/898/1029/9134/1031/10926/116 4	11
GO:0003684	damaged DNA binding	6/320	69/1763 2	0.0016	0.0287	0.0255	79000/2237/5111/6119/672/641	6
GO:0043138	3'-5' DNA helicase activity	3/320	14/1763 2	0.0019	0.0329	0.0292	9837/8318/641	3
GO:0005178	integrin binding	8/320	126/176 32	0.0021	0.0364	0.0323	1281/1289/4323/10516/7070/2191/1285/6423	8
GO:0016888	endodeoxyribonuclease activity, producing 5'-phosphomonoesters	3/320	16/1763 2	0.0028	0.0460	0.0409	2237/9156/1763	3
