

**Table S5 GO enrichment analysis of genes from important modules**

<b>Module</b>	<b>GO ID</b>	<b>Description</b>
<b>MElightyellow</b>	GO:0016469(8.5e-05)	proton-transporting two-sector ATPase complex
<b>MEbrown4</b>	GO:0042254(2.1e-10)	ribosome biogenesis
<b>MEtan</b>	GO:0003700(5.0e-07)	DNA-binding transcription factor activity
<b>MElightpink4</b>	GO:0003700(0.0106)	DNA-binding transcription factor activity
<b>MEcoral1</b>	GO:0016491(6.5e-05)	oxidoreductase activity
<b>MEgreen</b>	GO:0016491(0.00312)	oxidoreductase activity
<b>MEdarkorange</b>	GO:0015979(1.3e-11)	photosynthesis
	GO:0016717(8.2e-05)	oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water
<b>MEbisque4</b>	GO:0016787(1.1e-08)	hydrolase activity
<b>MEyellow</b>	GO:0009055(1.3e-05)	electron transfer activity
<b>MEthistle2</b>	GO:0009117(0.0047)	nucleotide metabolic process