

Additional file 5. Module Membership (MM) ranking of transcription factor related genes within clusters. Highest rank and p-value is compared after performing rank analysis using three different databases for rice transcription-related entities. Significant top ranked TFs are indicated in bold. n/f, none found; n/s, not significant.

Cluster	# of genes in cluster	Highest rank of TF related gene		
		MapMan (p-value)	PlnTFDB (p-value)	DRTF (p-value)
Module 1	469	24 (0.8852)	24 (0.8796)	24 (0.8062)
Module 2	376	40 (0.8766)	27 (0.6608)	27 (0.6624)
Module 3	743	27 (0.7222)	61 (0.9352)	61 (0.9089)
Module 4	270	10 (0.2474)	19 (0.4688)	44 (0.7022)
Module 5	157	5 (0.3739)	5 (0.3490)	5 (0.3217)
Module 6	2880	123 (0.9562)	52 (0.8822)	52 (0.7790)
Module 7	11861	95 (0.9578)	94 (0.9571)	108 (0.9550)
Module 8	694	9 (0.6725)	9 (0.5442)	9 (0.3335)
Module 9	1343	15 (0.5970)	15 (0.4734)	15 (0.2814)
Module 10	3337	7 (0.1829)	7 (0.1673)	7 (0.1340)
Module 11	610	1 (0.0605)	1 (0.0559)	1 (0.0518)
Module 12	390	41 (0.819)	13 (0.3029)	13 (0.2254)
Module 13	102	n/f	10 (0.2721)	10 (0.2193)
Module 14	604	1 (0.0481)	1 (0.0461)	1 (0.0459)
Module 15	8907	27 (0.9116)	27 (0.8674)	27 (0.7811)
Module 16	431	2 (0.0712)	8 (0.2745)	8 (0.2454)
Module 17	195	10 (0.4050)	14 (0.6617)	14 (0.4793)
Module 18	233	176 (n/s)	176 (n/s)	161 (n/s)