

1 **The Genome-wide Characterisation of Alternative Splicing and RNA Editing in the**
2 **Development of *Coprinopsis cinerea***

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62 Table S1. Sample collection, sequencing quality and alignment rate.

Stage (Abb.)	Incubation	Sample	Clean reads	Clean bases	Q20 (%)	Q30 (%)	GC (%)	Mapping rate (%)	Mapped reads (deduplicated)
Vegetative mycelia (Myc)	Continuous darkness at 37 °C for 4 d	Myc1	25,085,950	3,762,892,500	97.7	93.7	54.5	93.87	15,936,386
		Myc2	32,513,954	4,877,093,100	97.8	93.9	54.5	94.28	20,024,836
		Myc3	26,208,640	3,931,296,000	97.7	93.7	54.5	94.38	17,280,727
Oidia forming mycelia (Oidia)	Continuous light at 37 °C for 4 d	Oidia1	31,417,198	4,712,579,700	97.5	93.2	54.1	95.01	20,476,670
		Oidia2	30,190,208	4,528,531,200	97.8	93.8	54.3	95.06	19,248,283
		Oidia3	29,196,406	4,379,460,900	97.7	93.7	54.3	94.58	18,912,548
Sclerotia forming mycelia (Scl)	Continuous darkness at 37 °C for 12 d	Scl1	32,972,822	4,945,923,300	94.1	85.7	53.9	92.55	21,480,526
		Scl2	37,357,474	5,603,621,100	95.0	87.6	54.0	92.89	24,696,908
		Scl3	29,848,036	4,477,205,400	94.4	86.1	54.0	93.14	20,434,835
Mycelia with hyphal knots (Knot)	Continuous darkness at 37 °C for 5.5 d, and 12 h:12 h light– dark cycle for 1 d	Knot1	28,412,998	4,261,949,700	97.8	93.8	54.0	94.43	18,137,097
		Knot2	31,571,766	4,735,764,900	97.7	93.7	54.3	93.65	18,237,961
		Knot3	34,713,178	5,206,976,700	97.8	94.0	54.5	93.39	20,334,292
Primordia undergoing meiosis (Pri)	Continuous darkness at 37 °C for 5.5 d, and 12 h:12 h light– dark cycle for 6 d	Pri1	24,910,904	3,736,635,600	97.8	93.9	54.0	94.78	16,965,939
		Pri2	24,551,978	3,682,796,700	97.7	93.8	54.2	94.26	17,247,702
		Pri3	25,494,022	3,824,103,300	97.4	92.8	54.2	94.26	18,233,166
Young fruiting bodies undergoing spore formation (YFB)	Continuous darkness at 37 °C for 5.5 d, and 12 h:12 h light– dark cycle for 6.5 d	YFB1	26,599,914	3,989,987,100	97.7	93.7	54.1	94.92	17,311,918
		YFB2	24,264,552	3,639,682,800	97.7	93.8	54.2	94.56	16,574,052
		YFB3	28,400,844	4,260,126,600	97.8	93.8	54.1	95.31	18,221,676
Mature basidiospores (BS)	Basidiospore discharged from mature cap	BS1	17,064,684	2,546,579,938	96.6	91.1	54.2	93.60	12,093,628
		BS2	17,492,502	2,606,856,924	96.6	90.9	54.0	93.46	10,770,048
		BS3	17,355,936	2,586,947,642	96.7	91.1	54.2	93.78	11,111,413
Half germinating basidiospores (BS12h)	Continuous darkness at 37 °C for 12 h, broth 150 rpm	BS12h1	17,126,036	2,546,749,128	94.3	87.6	45.9	9.28	832,554
		BS12h2	17,158,542	2,552,883,760	95.2	88.9	49.3	27.17	2,431,668
		BS12h3	17,244,842	2,571,283,772	95.6	89.8	49.5	29.61	2,544,746
Fully germinated basidiospores (BS24h)	Continuous darkness at 37 °C for 24 h, broth 150 rpm	BS24h1	17,162,606	2,556,983,164	96.6	91.0	54.5	93.12	11,181,138
		BS24h2	16,525,520	2,461,013,426	96.7	91.3	54.5	93.08	10,628,646
		BS24h3	16,917,964	2,519,857,620	95.9	90.0	52.0	61.54	6,686,954
Genomic DNA	Continuous darkness at 37 °C	DNA	9,213,544	1,382,031,600	98.0	94.4	50.3	98.84	8,068,437

64 Table S2. Primers used in this study.

	Target		Sequence (5' →3')
PCR-Sanger	Hypothetical protein (CC2G_003350, scaffold_11: 1716350T>C)	F	TTCAGCGTCTTCGCTGCAAT
	Spliceosomal U1 snRNP C (CC2G_010208)	R	CTCATCGAACGCAAGTTCCGG
	STE/STE11 protein kinase (CC2G_011916)	F	ACTCACGACTCGGCTTCAG
	RhoGAP (CC2G_009456)	R	TGGGCCGTAAATCCACCTG
		F	GGTGGACTATCTGCCTGGTC
		R	GCCACTTCCCTTACGGAGG
qRT-PCR	18S rRNA	F	CTGGAGCTAGCCAACCTTCG
		R	CAACACAGCACGGGTTGAC
	Adenosine deaminase-like protein (CC2G_001628)	F	GCCTGTTGAGTGTCAATTAAATTCTC
	Guanine deaminase (CC2G_005289)	R	CTGCAACCCCCACATCCA
	adenosine deaminase (CC2G_005434)	F	GAGAGTGCCTGGACATAGCC
	tRNA specific adenosine deaminase (CC2G_010905)	R	CGCAAAGAACGTCTGGAACG
	cytosine deaminase-uracil phosphoribosyltransferase deaminase (CC2G_011103)	F	ACCACGACAACCTCTACGG
	cytidine deaminase (CC2G_012163)	R	TCGATGTTCCGGTTGGTCC
	AMP deaminase (CC2G_012607)	F	GGTCAACGCCAGGTTCTTA
	tRNA specific adenosine deaminase (CC2G_012760)	R	ATACTCGTCGCTGCATGTCC
		F	ATCGATTGCATCCTCAGCGA
		R	TGATGCACGGCTCTACTGTG
		F	AAGTGCTCATCGAACACGGT
		R	TCACTTGAGCGACGGGAAG
		F	CGTATTGCGGGTTCCCTGTG
		R	CAGCGCAGATAGTCCACCA
		F	GTACAGCCTGCTGAACGAGT
		R	TGGACTTGATGAACCGGAGC
		F	TGCTTGGGACTCGGTTCTC
		R	TTCTCCAGGTTCGATGTCGC

66 Table S3. Number of expressed genes in *C. cinerea* development, CPM > 1 in at least two
67 replicates.

Stage	(Abb.)	Number of genes
Vegetative mycelia	(Myc)	11,333
Oidia forming mycelia	(Oidia)	11,269
Sclerotia forming mycelia	(Scl)	11,075
Mycelia with hyphal knots	(Knot)	11,396
Primordia undergoing meiosis	(Pri)	11,392
Young fruiting bodies undergoing spore formation	(YFB)	10,722
Mature basidiospores	(BS)	10,043
Half germinating basidiospores	(BS12h)	10,301
Fully germinated basidiospores	(BS24h)	10,060
Total		12,450

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69 Table S4. Functional enrichment summary of DEGs.

Groups	ID	Description	ONTOLOGY
cluster1	GO:0020037	heme binding	Molecular Function
cluster1	GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	Molecular Function
cluster2	GO:0020037	heme binding	Molecular Function
cluster2	GO:0030248	cellulose binding	Molecular Function
cluster2	GO:0016831	carboxy-lyase activity	Molecular Function
cluster2	GO:0046872	metal ion binding	Molecular Function
cluster5	GO:0051539	4 iron, 4 sulfur cluster binding	Molecular Function
cluster5	GO:0008168	methyltransferase activity	Molecular Function
cluster6	GO:0003723	RNA binding	Molecular Function
cluster1	GO:0016021	integral component of membrane	Cellular Component
cluster2	GO:0016021	integral component of membrane	Cellular Component
cluster2	GO:0005618	cell wall	Cellular Component
cluster2	GO:0009277	fungal-type cell wall	Cellular Component
cluster3	GO:0016021	integral component of membrane	Cellular Component
cluster3	GO:0098803	respiratory chain complex	Cellular Component
cluster3	GO:0098800	inner mitochondrial membrane protein complex	Cellular Component
cluster3	GO:0000323	lytic vacuole	Cellular Component
cluster4	GO:0016021	integral component of membrane	Cellular Component
cluster4	GO:1905369	endopeptidase complex	Cellular Component
cluster4	GO:0005839	proteasome core complex	Cellular Component
cluster5	GO:0005730	nucleolus	Cellular Component
cluster5	GO:0043232	intracellular non-membrane-bounded organelle	Cellular Component
cluster5	GO:0005840	ribosome	Cellular Component
cluster5	GO:0043231	intracellular membrane-bounded organelle	Cellular Component
cluster5	GO:0070013	intracellular organelle lumen	Cellular Component
cluster6	GO:0005840	ribosome	Cellular Component
cluster6	GO:0043232	intracellular non-membrane-bounded organelle	Cellular Component
cluster6	GO:0005739	mitochondrion	Cellular Component

71 Table S4. Functional enrichment summary of DEGs (continued).

Groups	ID	Description	ONTOLOGY
cluster3	GO:0043436	oxoacid metabolic process	Biological Process
cluster3	GO:1901605	alpha-amino acid metabolic process	Biological Process
cluster3	GO:0055086	nucleobase-containing small molecule metabolic process	Biological Process
cluster3	GO:0006520	cellular amino acid metabolic process	Biological Process
cluster3	GO:0072524	pyridine-containing compound metabolic process	Biological Process
cluster3	GO:0006753	nucleoside phosphate metabolic process	Biological Process
cluster4	GO:0007186	G protein-coupled receptor signaling pathway	Biological Process
cluster5	GO:0022613	ribonucleoprotein complex biogenesis	Biological Process
cluster5	GO:1901566	organonitrogen compound biosynthetic process	Biological Process
cluster5	GO:0016053	organic acid biosynthetic process	Biological Process
cluster6	GO:0006518	peptide metabolic process	Biological Process
cluster6	GO:0043603	cellular amide metabolic process	Biological Process
cluster6	GO:1901566	organonitrogen compound biosynthetic process	Biological Process
cluster6	GO:0044267	cellular protein metabolic process	Biological Process
cluster6	GO:0010467	gene expression	Biological Process
cluster6	GO:0019538	protein metabolic process	Biological Process

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73 Table S5. Wilcoxon test on PSI score of nine developmental stages.

Group1	Group2	p	p.adj	p.format	p.signif
BS	BS12h	0.858611	1	0.85861	ns
BS	Oidia	8.24E-07	2.90E-05	8.20E-07	****
BS	Scl	4.15E-06	0.00014	4.10E-06	****
BS	BS12h	3.18E-07	1.10E-05	3.20E-07	****
BS	Knot	6.55E-06	0.00022	6.60E-06	****
BS	Myc	0.000219	0.0068	0.00022	***
BS	YFB	0.002648	0.079	0.00265	**
BS	Pri	0.01848	0.5	0.01848	*
BS	BS24h	1.86E-05	6.00E-04	1.90E-05	****
Oidia	Scl	0.723552	1	0.72355	ns
Oidia	BS12h	0.867384	1	0.86738	ns
Oidia	Knot	0.578461	1	0.57846	ns
Oidia	Myc	0.253901	1	0.2539	ns
Oidia	YFB	0.03807	0.89	0.03807	*
Oidia	Pri	0.011542	0.32	0.01154	*
Oidia	BS24h	0.850476	1	0.85048	ns
Scl	BS12h	0.642752	1	0.64275	ns
Scl	Knot	0.854224	1	0.85422	ns
Scl	Myc	0.439598	1	0.4396	ns
Scl	YFB	0.085381	1	0.08538	ns
Scl	Pri	0.028827	0.72	0.02883	*
Scl	BS24h	0.891506	1	0.89151	ns
BS12h	Knot	0.466307	1	0.46631	ns
BS12h	Myc	0.207701	1	0.2077	ns
BS12h	YFB	0.025464	0.66	0.02546	*
BS12h	Pri	0.007177	0.21	0.00718	**
BS12h	BS24h	0.757683	1	0.75768	ns
Knot	Myc	0.524763	1	0.52476	ns
Knot	YFB	0.12103	1	0.12103	ns
Knot	Pri	0.040944	0.9	0.04094	*
Knot	BS24h	0.759005	1	0.759	ns
Myc	YFB	0.387848	1	0.38785	ns
Myc	Pri	0.179955	1	0.17996	ns
Myc	BS24h	0.393579	1	0.39358	ns
YFB	Pri	0.591205	1	0.59121	ns
YFB	BS24h	0.092002	1	0.092	ns
Pri	BS24h	0.036983	0.89	0.03698	*

75 Table S6. Number of RNA editing sites identified during *C. cinerea* development.

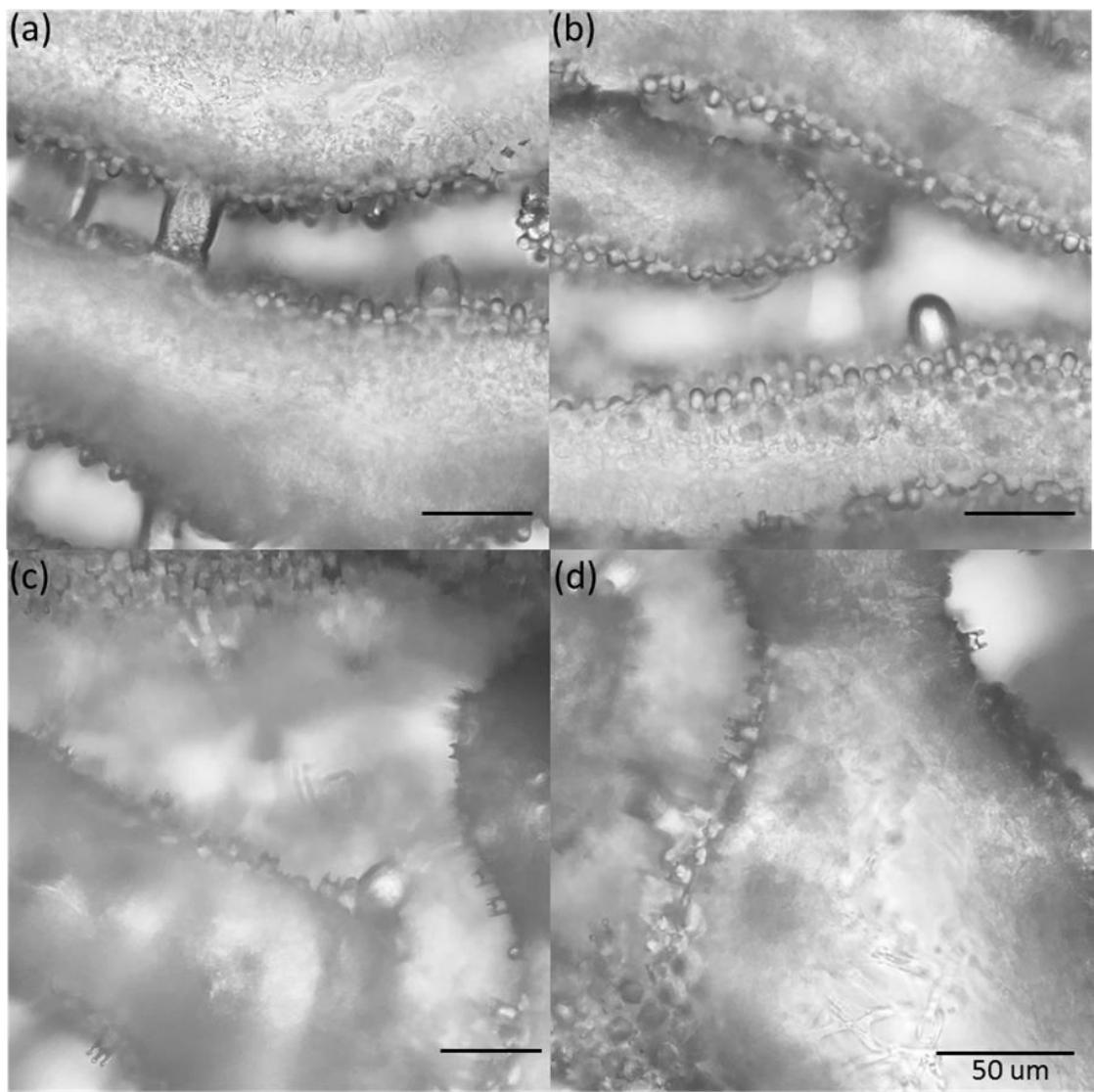
Stage	RE sites	Stage-specific RE sites	Mean editing level	Sample	RE events
BS	24	13	0.143	BS1	13
				BS2	18
				BS3	19
BS12h	7	4	0.0879	BS12h1	2
				BS12h2	6
				BS12h3	6
BS24h	17	4	0.0685	BS24h1	17
				BS24h2	17
				BS24h3	0
Myc	29	12	0.100	Myc1	22
				Myc2	23
				Myc3	19
Oidia	24	6	0.105	Oidia1	18
				Oidia2	19
				Oidia3	17
Scl	141	97	0.0665	Scl1	114
				Scl2	119
				Scl3	100
Knot	33	13	0.0685	Knot1	23
				Knot2	31
				Knot3	23
Pri	21	3	0.0872	Pri1	15
				Pri2	17
				Pri3	18
YFB	22	11	0.0849	YFB1	20
				YFB2	14
				YFB3	15
Total	217	163	0.0810		726

77 Table S7. Wilcoxon test on RNA editing levels of nine developmental stages.

Group1	Group2	p	p.adj	p.format	p.signif
Pri	Scl	0.65	1	0.65	ns
Pri	Oidia	0.76	1	0.76	ns
Pri	YFB	0.77	1	0.77	ns
Pri	BS	0.10	1	0.10	ns
Pri	BS24h	0.12	1	0.12	ns
Pri	Knot	0.56	1	0.56	ns
Pri	Myc	0.52	1	0.52	ns
Pri	BS12h	0.04	1	0.04	*
Scl	Oidia	0.92	1	0.92	ns
Scl	YFB	0.37	1	0.37	ns
Scl	BS	0.07	1	0.07	ns
Scl	BS24h	0.11	1	0.11	ns
Scl	Knot	0.70	1	0.70	ns
Scl	Myc	0.67	1	0.67	ns
Scl	BS12h	0.04	1	0.04	*
Oidia	YFB	0.56	1	0.56	ns
Oidia	BS	0.18	1	0.18	ns
Oidia	BS24h	0.20	1	0.20	ns
Oidia	Knot	0.70	1	0.70	ns
Oidia	Myc	0.76	1	0.76	ns
Oidia	BS12h	0.08	1	0.08	ns
YFB	BS	0.05	1	0.05	ns
YFB	BS24h	0.06	1	0.06	ns
YFB	Knot	0.32	1	0.32	ns
YFB	Myc	0.33	1	0.33	ns
YFB	BS12h	0.02	0.81	0.02	*
BS	BS24h	0.97	1	0.97	ns
BS	Knot	0.21	1	0.22	ns
BS	Myc	0.27	1	0.27	ns
BS	BS12h	0.40	1	0.40	ns
BS24h	Knot	0.24	1	0.24	ns
BS24h	Myc	0.34	1	0.34	ns
BS24h	BS12h	0.34	1	0.34	ns
Knot	Myc	0.93	1	0.93	ns
Knot	BS12h	0.07	1	0.07	ns
Myc	BS12h	0.12	1	0.12	ns

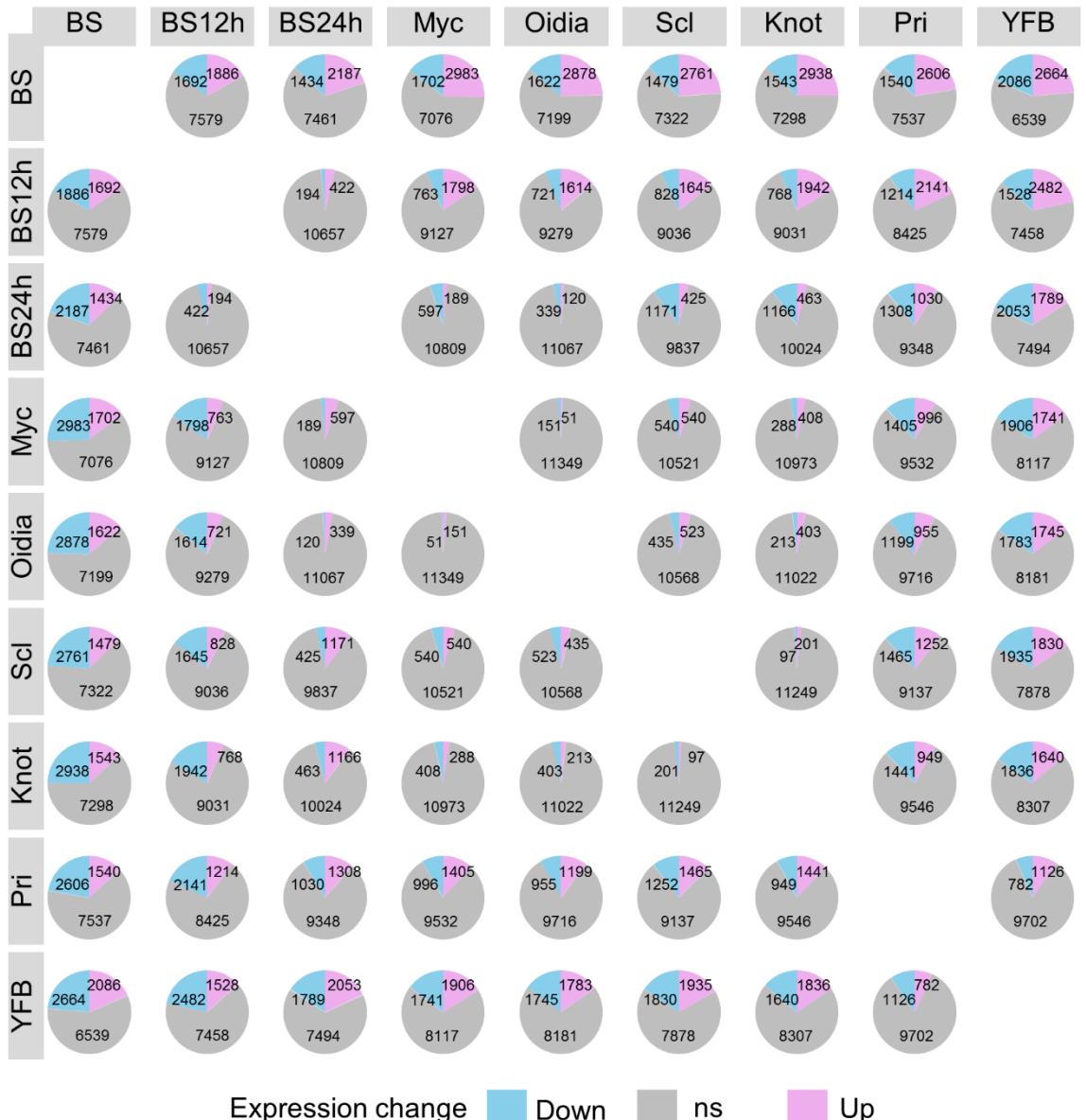
79 Table S8. Wilcoxon test on RNA editing levels of twelve editing types.

Group	Group	P	P	P	P	Group	Group	P	P	P	P	P
1	2		adj	format	signif	1	2		adj	format	signif	
TC	AG	0.24	1	0.24	ns	CT	TG	0.85	1	0.85	ns	
TC	CG	0.02	1	0.02	*	CT	AC	0.05	1	0.05	ns	
TC	CT	0.47	1	0.47	ns	CT	GC	0.07	1	0.07	ns	
TC	GA	0.29	1	0.29	ns	CT	TA	0.93	1	0.93	ns	
TC	GT	0.05	1	0.05	ns	CT	CA	0.72	1	0.72	ns	
TC	AT	0.01	0.33	0.01	**	GA	GT	0.14	1	0.14	ns	
TC	TG	0.87	1	0.87	ns	GA	AT	0.01	0.5	0.01	**	
TC	AC	0.06	1	0.06	ns	GA	TG	0.84	1	0.84	ns	
TC	GC	0.03	1	0.03	*	GA	AC	0.15	1	0.15	ns	
TC	TA	0.82	1	0.82	ns	GA	GC	0.01	0.5	0.01	**	
TC	CA	0.96	1	0.96	ns	GA	TA	0.68	1	0.68	ns	
AG	CG	0.03	1	0.03	*	GA	CA	0.75	1	0.75	ns	
AG	CT	0.09	1	0.09	ns	GT	AT	0.15	1	0.15	ns	
AG	GA	0.92	1	0.92	ns	GT	TG	0.39	1	0.39	ns	
AG	GT	0.13	1	0.13	ns	GT	AC	0.65	1	0.65	ns	
AG	AT	0.00	0.24	0.00	**	GT	GC	0.01	0.41	0.01	**	
AG	TG	0.78	1	0.78	ns	GT	TA	0.32	1	0.32	ns	
AG	AC	0.07	1	0.07	ns	GT	CA	0.24	1	0.24	ns	
AG	GC	0.01	0.42	0.01	**	AT	TG	0.07	1	0.07	ns	
AG	TA	0.69	1	0.69	ns	AT	AC	0.65	1	0.65	ns	
AG	CA	0.69	1	0.69	ns	AT	GC	0.00	0.2	0.00	**	
CG	CT	0.01	0.46	0.01	**	AT	TA	0.07	1	0.07	ns	
CG	GA	0.04	1	0.04	*	AT	CA	0.03	1	0.03	*	
CG	GT	0.52	1	0.52	ns	TG	AC	0.17	1	0.17	ns	
CG	AT	0.33	1	0.33	ns	TG	GC	0.64	1	0.64	ns	
CG	TG	0.23	1	0.23	ns	TG	TA	0.70	1	0.70	ns	
CG	AC	0.84	1	0.84	ns	TG	CA	1.00	1	1.00	ns	
CG	GC	0.01	0.38	0.01	**	AC	GC	0.02	1	0.02	*	
CG	TA	0.21	1	0.21	ns	AC	TA	0.19	1	0.19	ns	
CG	CA	0.10	1	0.10	ns	AC	CA	0.17	1	0.17	ns	
CT	GA	0.13	1	0.13	ns	GC	TA	0.53	1	0.53	ns	
CT	GT	0.02	1	0.02	*	GC	CA	0.22	1	0.22	ns	
CT	AT	0.00	0.16	0.00	**	TA	CA	1.00	1	1.00	ns	



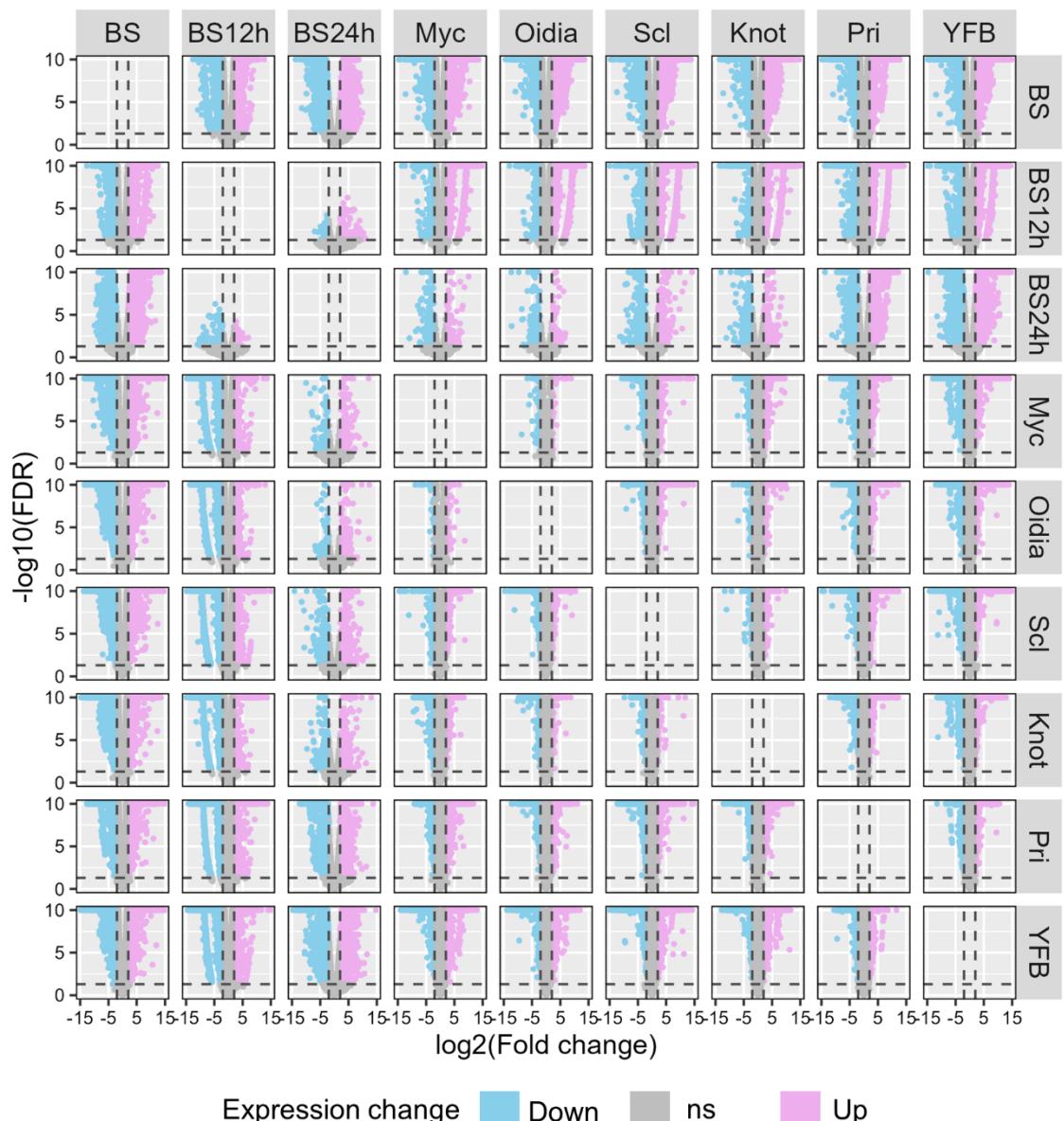
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82 Figure S1. Cross dissection of pileus under high power microscope (400 ×). (a) and (b)
83 Primordium contains the meiosis tissue. (c) and (d) Young fruiting body contains the tissue
84 undergoing basidiospore formation.



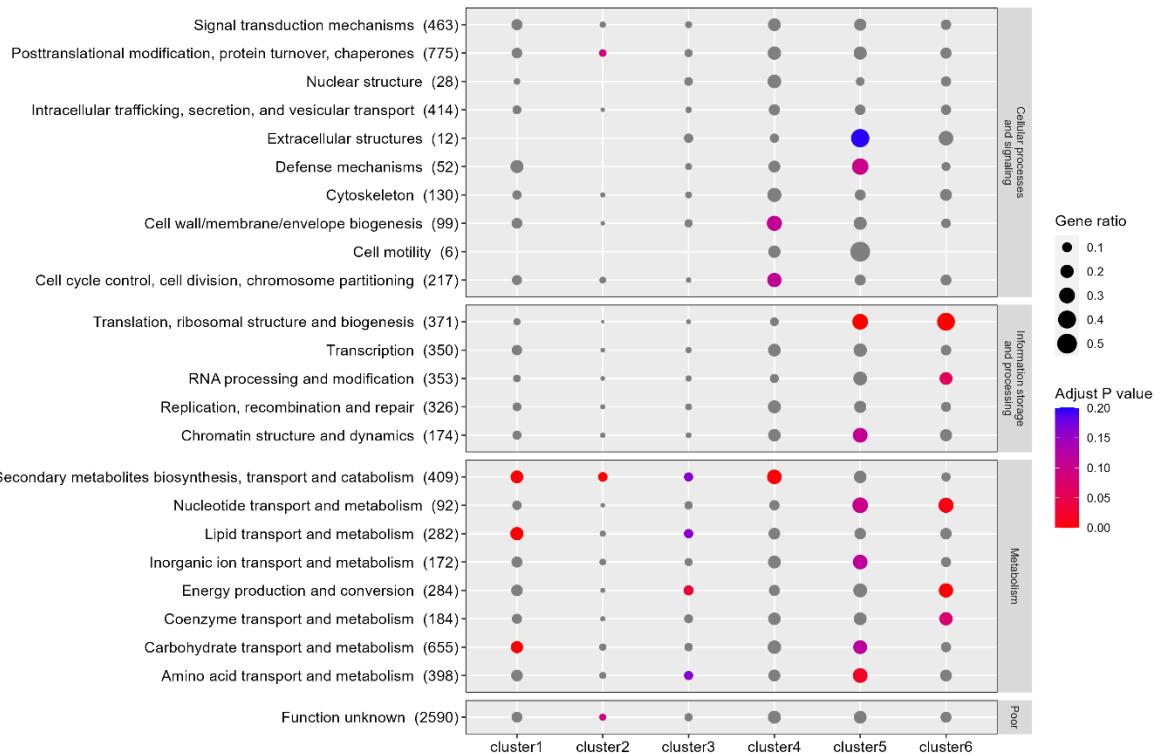
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86 Figure S2. Pie chart showing the summary of gene expression levels. Sample of each column
 87 were compared against sample of each row, for example, compare to BS, 1,886 genes were
 88 up-regulated, and 1,692 genes were down-regulated in BS12h.



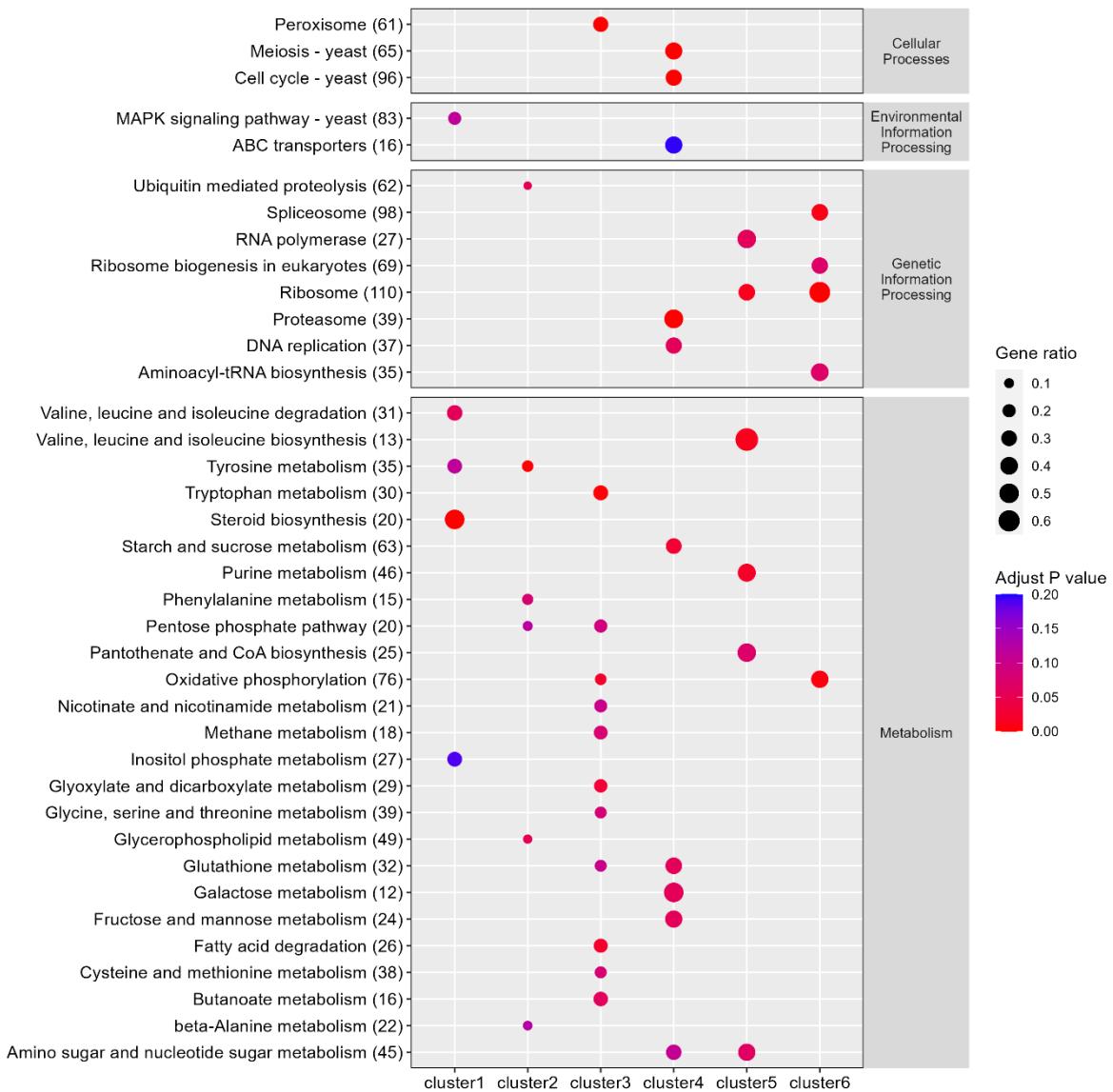
89

90 Figure S3. Volcano plot showing the distribution of gene expression changes. Sample of each
 91 column were compared against sample of each row, for example, compare to BS, 1,886 genes
 92 were up-regulated, and 1,692 genes were down-regulated in BS12h.



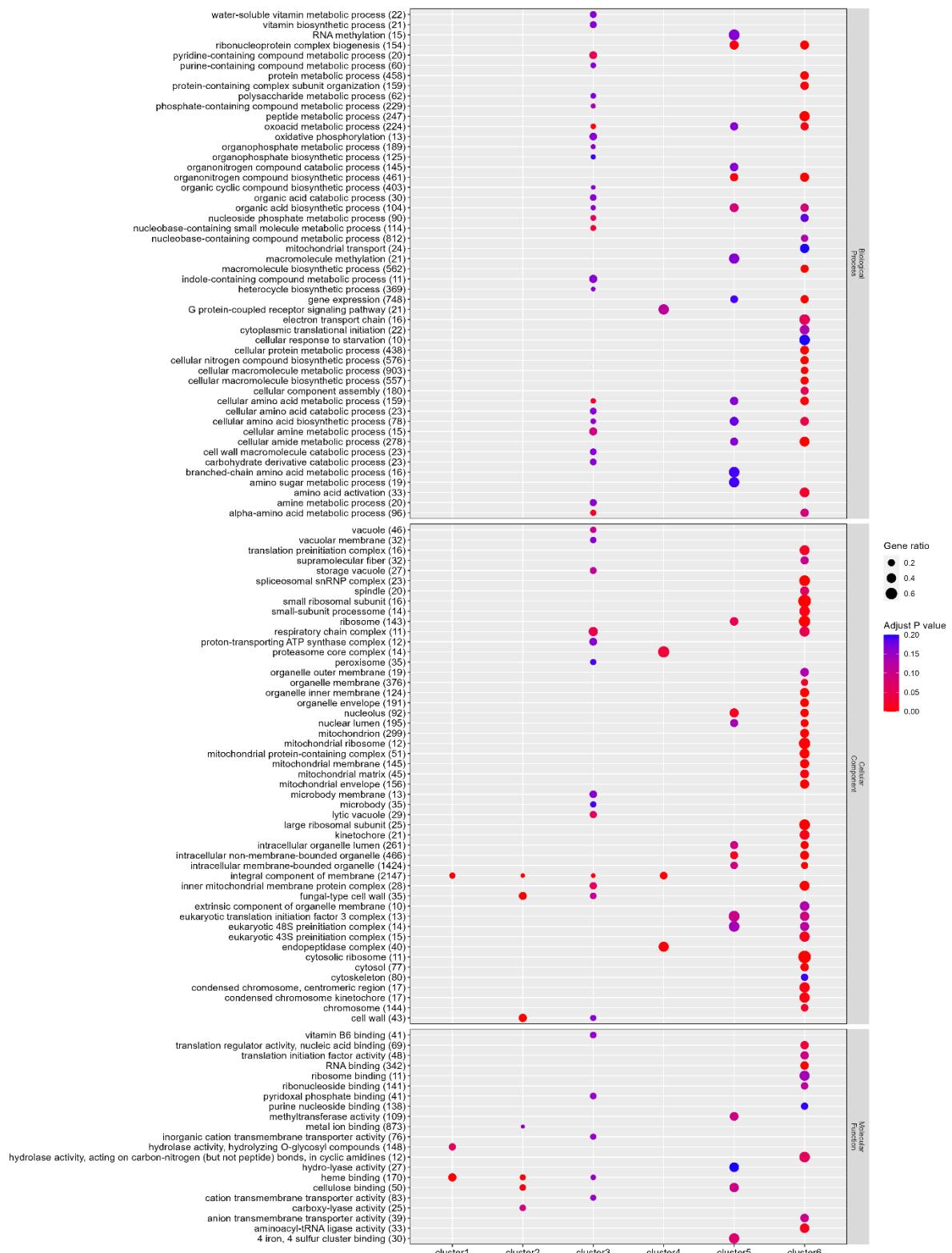
93

94 Figure S4. KOG enrichment analysis on gene clusters. Numbers of genes annotated to
 95 specific KOG term are listed beside the term. Gene ratio is calculated by annotated genes of
 96 specific KOG term in each cluster over annotated genes of specific KOG term in the genome
 97 background. Enriched groups with Benjamini and Hochberg method (BH) adjusted p value \leq
 98 0.20 are coloured red to blue, others are in grey.



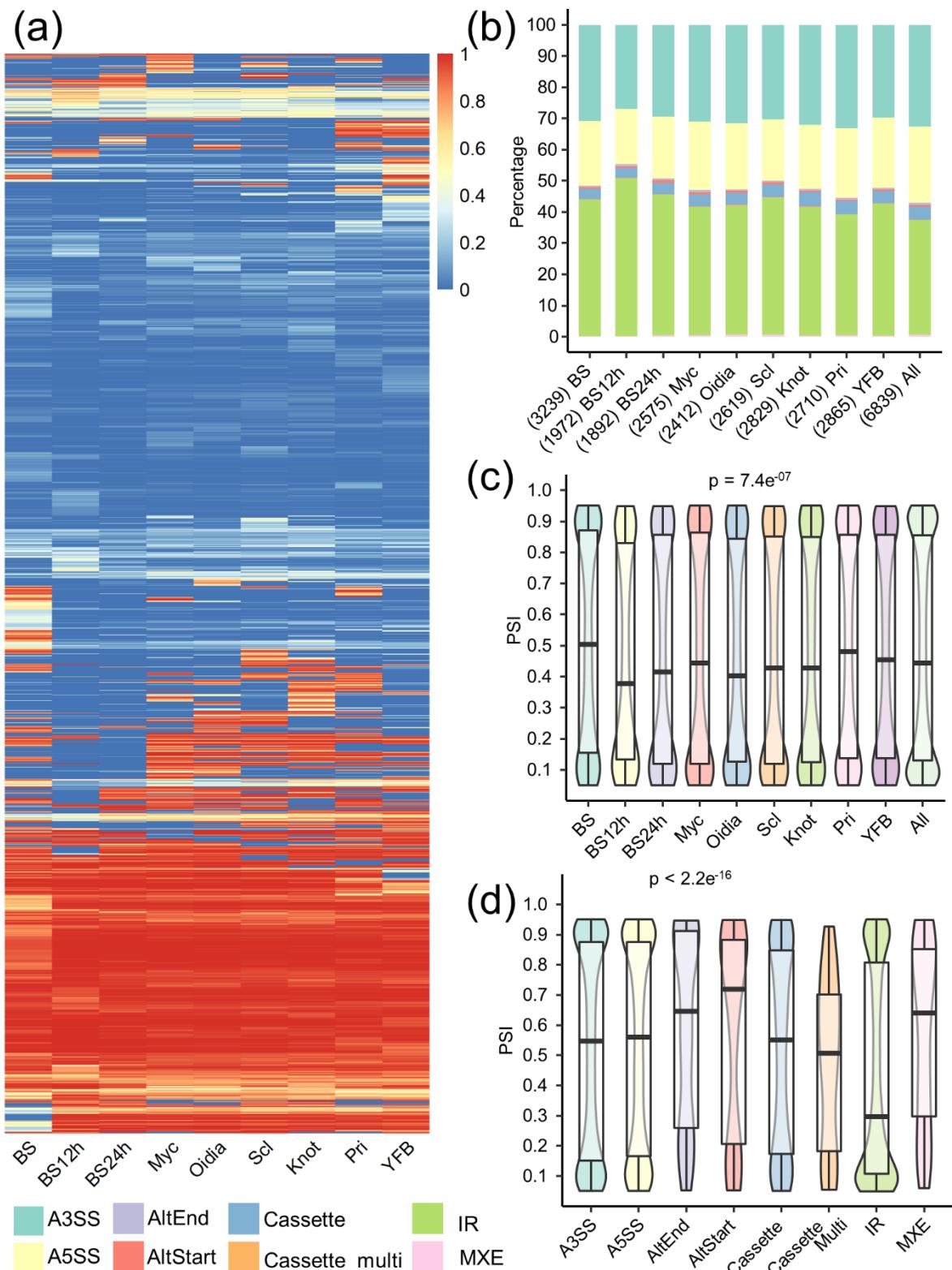
99

100 Figure S5. KEGG enrichment analysis on gene clusters. Numbers of genes annotated to
 101 specific KEGG pathway are listed beside the term. Gene ratio is calculated by annotated
 102 genes of specific KEGG pathway in each cluster over annotated genes of specific KEGG
 103 pathway in the genome background. Enriched groups with Benjamini and Hochberg method
 104 (BH) adjusted p value ≤ 0.20 are coloured red to blue.



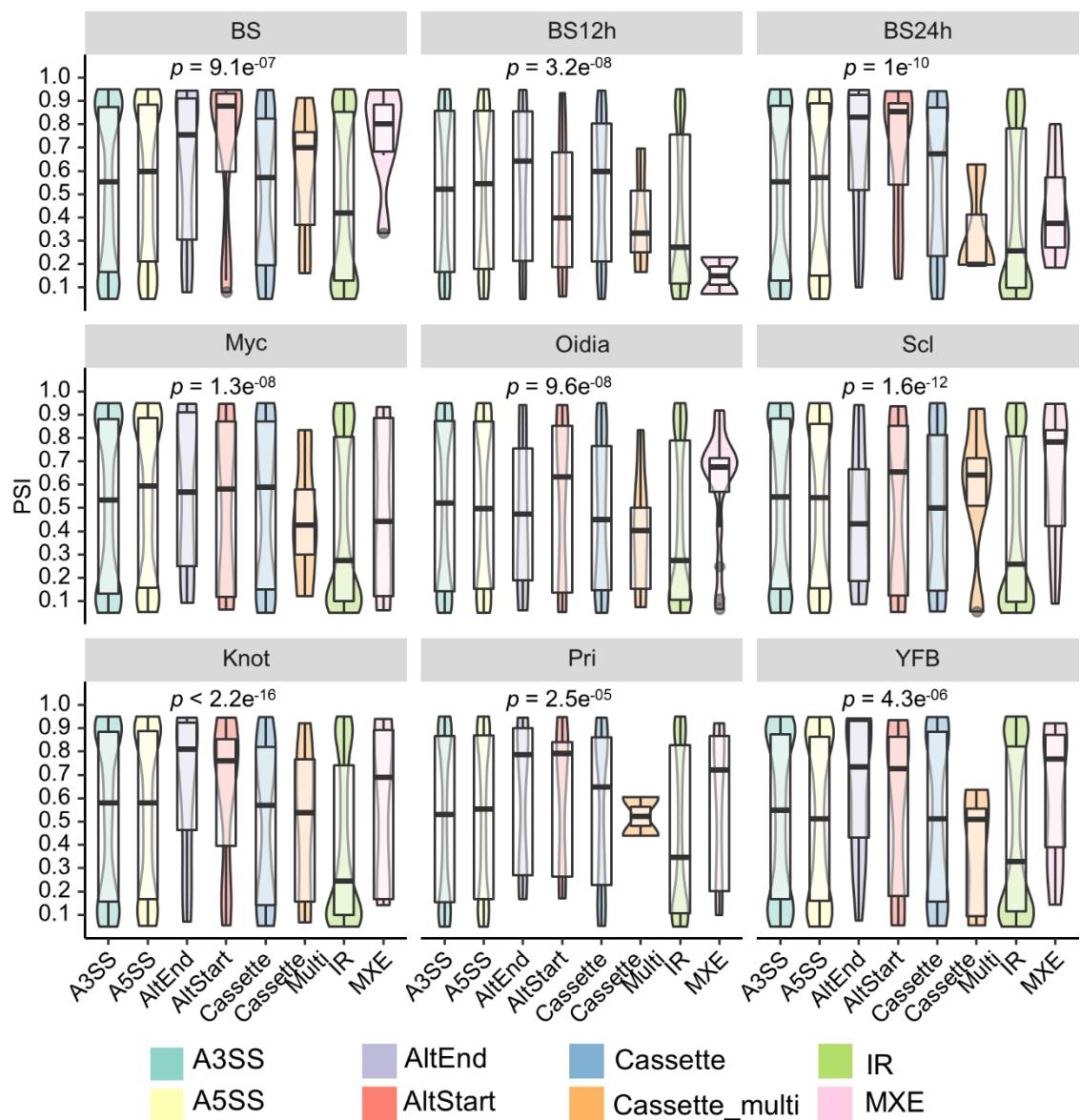
105

106 Figure S6. GO enrichment analysis on gene clusters. Numbers of genes annotated to specific
 107 GO term are listed beside the term. Gene ratio is calculated by annotated genes of specific
 108 GO term in each cluster over annotated genes of specific GO term in the genome background.
 109 Terms are filtered to GO level 5. Enriched groups with Benjamini and Hochberg method
 110 (BH) adjusted p value ≤ 0.20 are coloured red to blue.



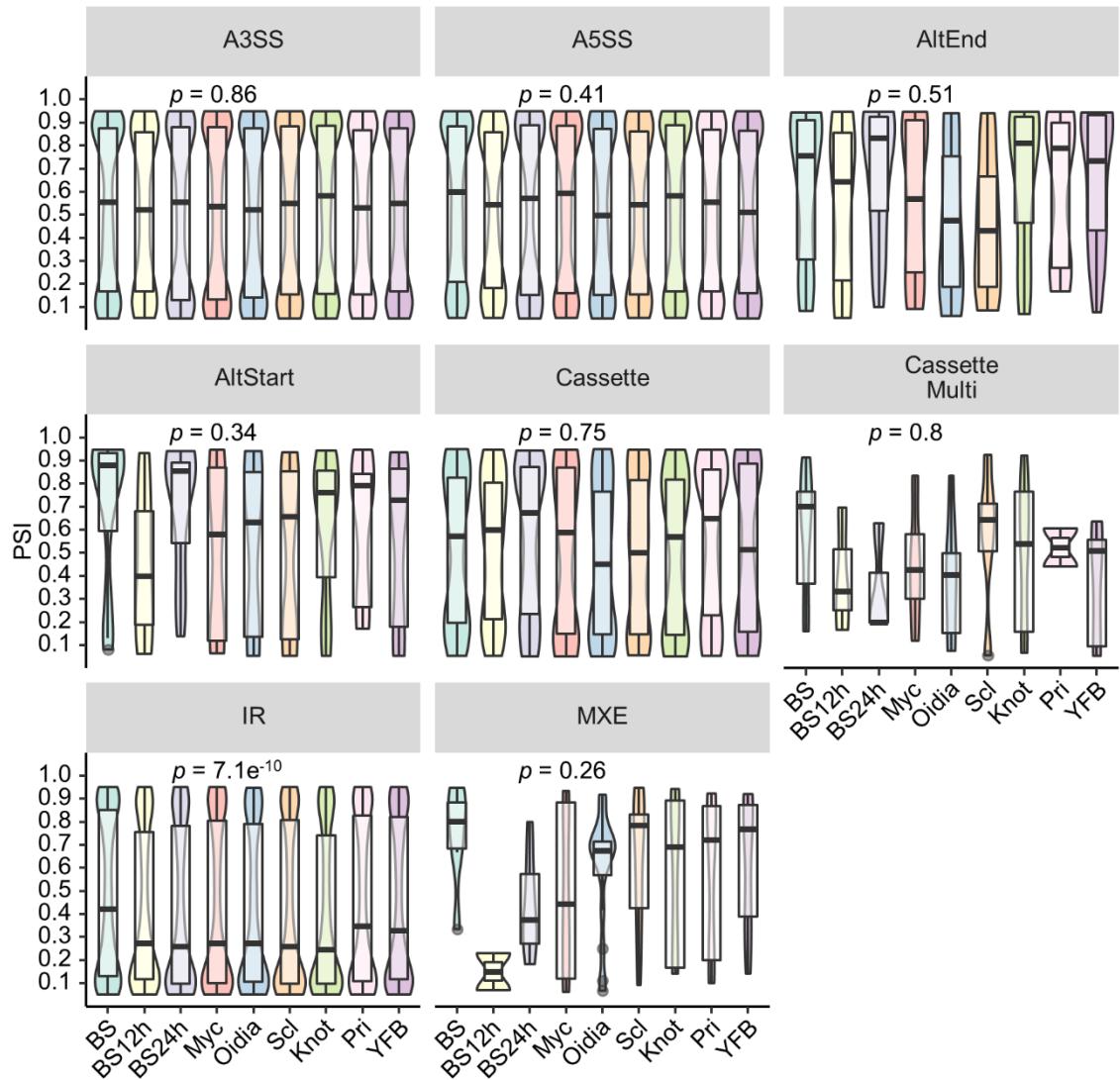
111

112 Figure S7. PSI score of AS events identified in nine developmental stages. (a) Heatmap
 113 showing the PSI score; (b) Distribution of eight AS types in nine stages; (c) PSI score of
 114 different stages, statistical results were detailed in table S5; (d) Violin plot summarising the
 115 PSI score of each AS types.



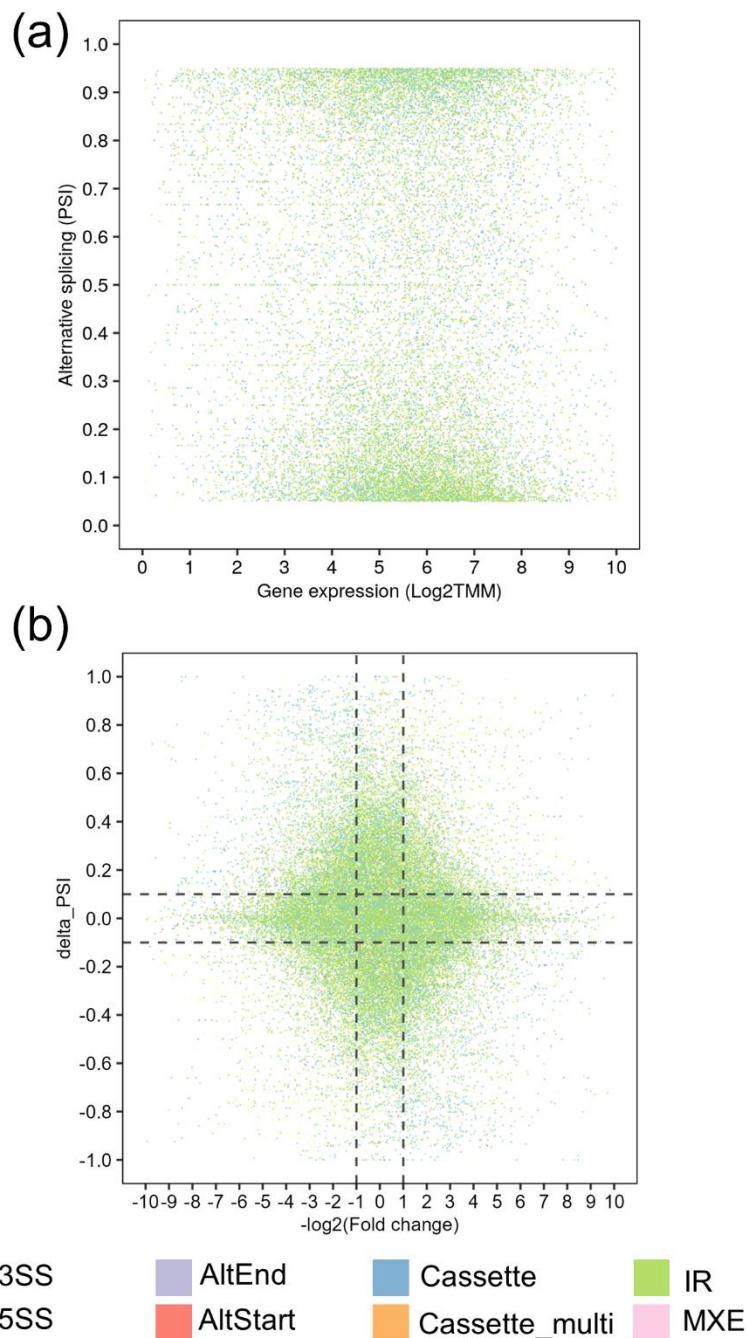
116

117 Figure S8. PSI score of eight AS types in nine developmental stages.



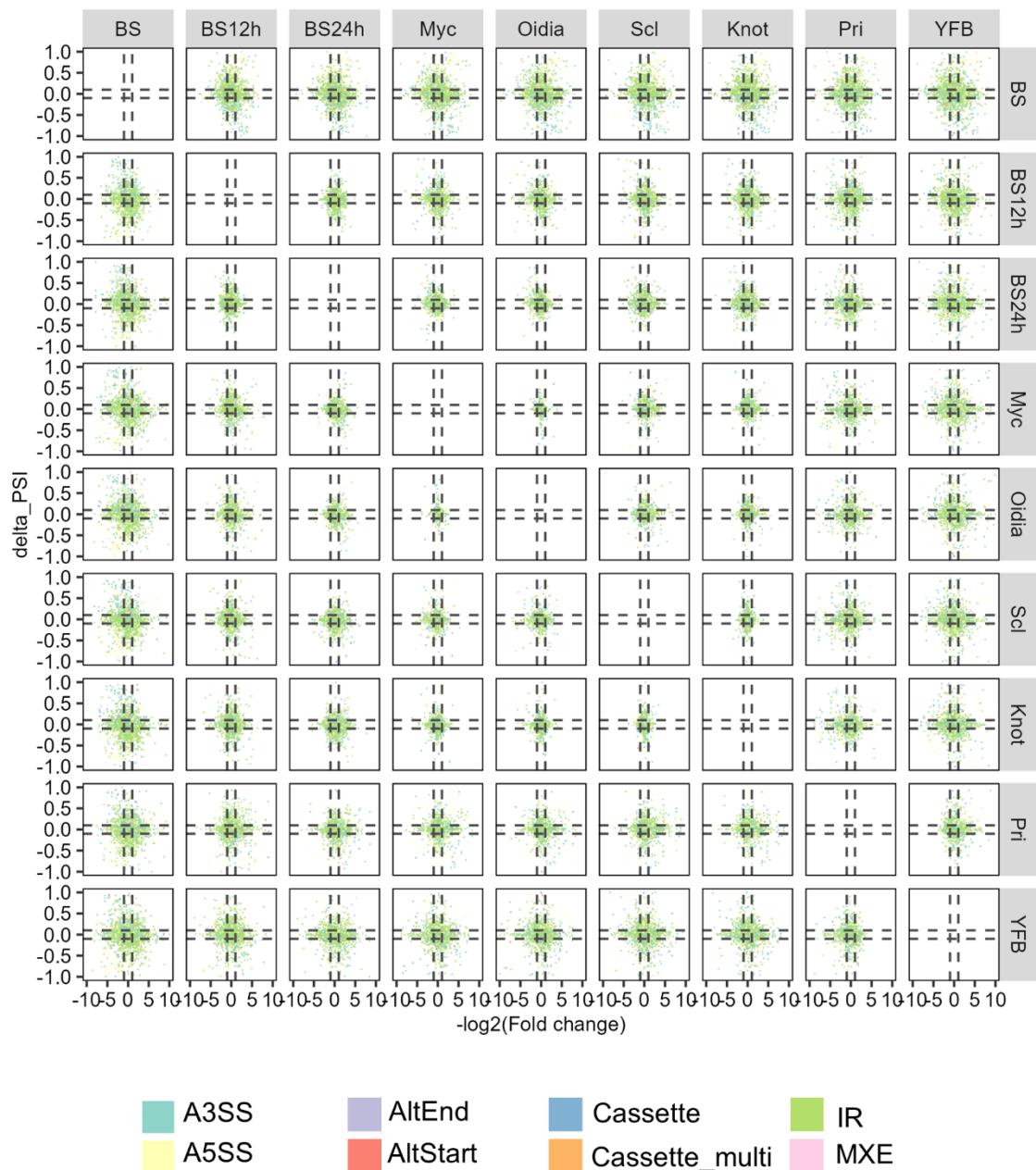
118

119 Figure S9. PSI score of nine developmental stages in eight AS types.



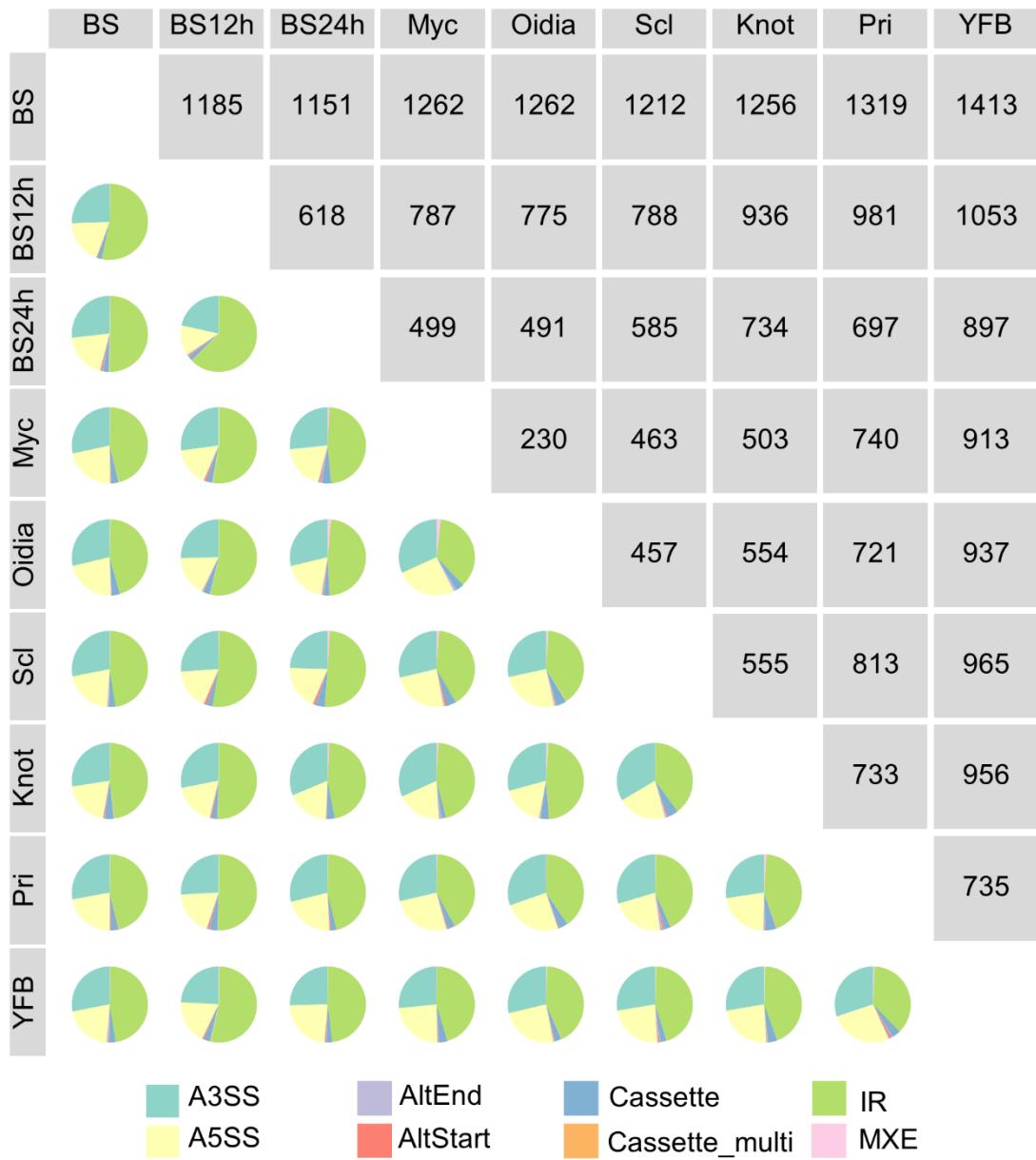
120

121 Figure S10. Quantitative relation of gene expression and PSI value of alternatively spliced
 122 genes. (a) Scatter plot on gene expression levels and PSI scores; (b) Scatter plot on changes
 123 of gene expression levels and PSI scores.



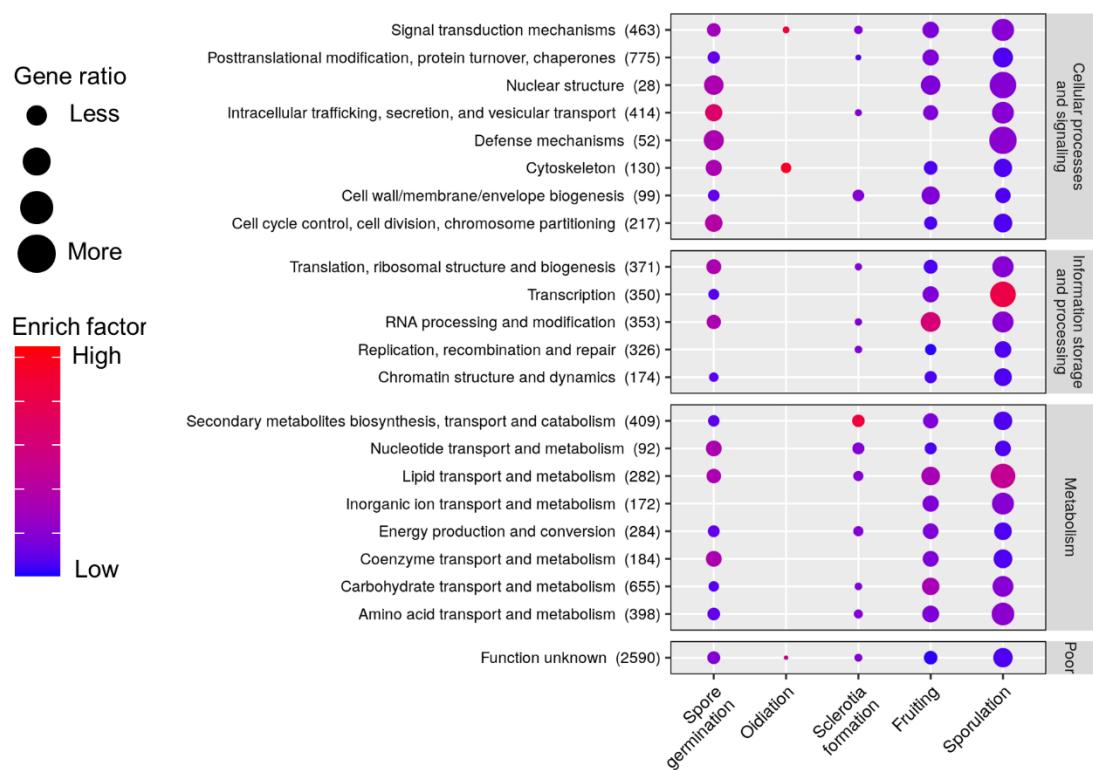
124

125 Figure S11. Scatter plots showing the changes on expression levels of alternative spliced
 126 genes and their PSI scores. Sample of each column were compared against sample of each
 127 row.



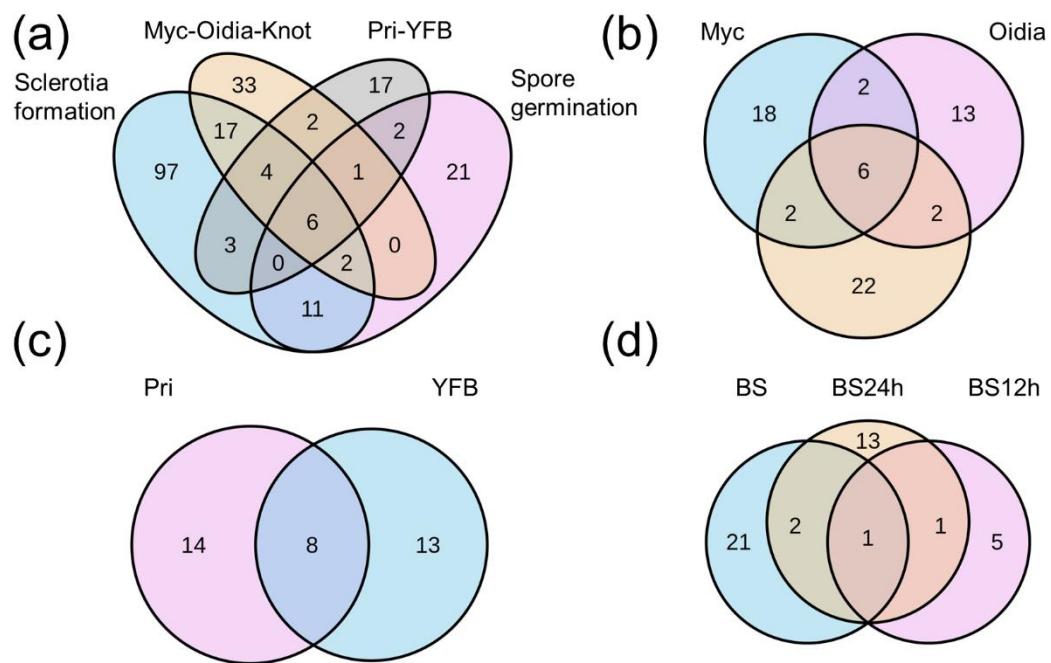
128

129 Figure S12. Summary on differentially spliced events between stages. Right upper triangle
 130 indicated the number of differentially spliced regions, left lower triangle showed the
 131 proportion of AS types.



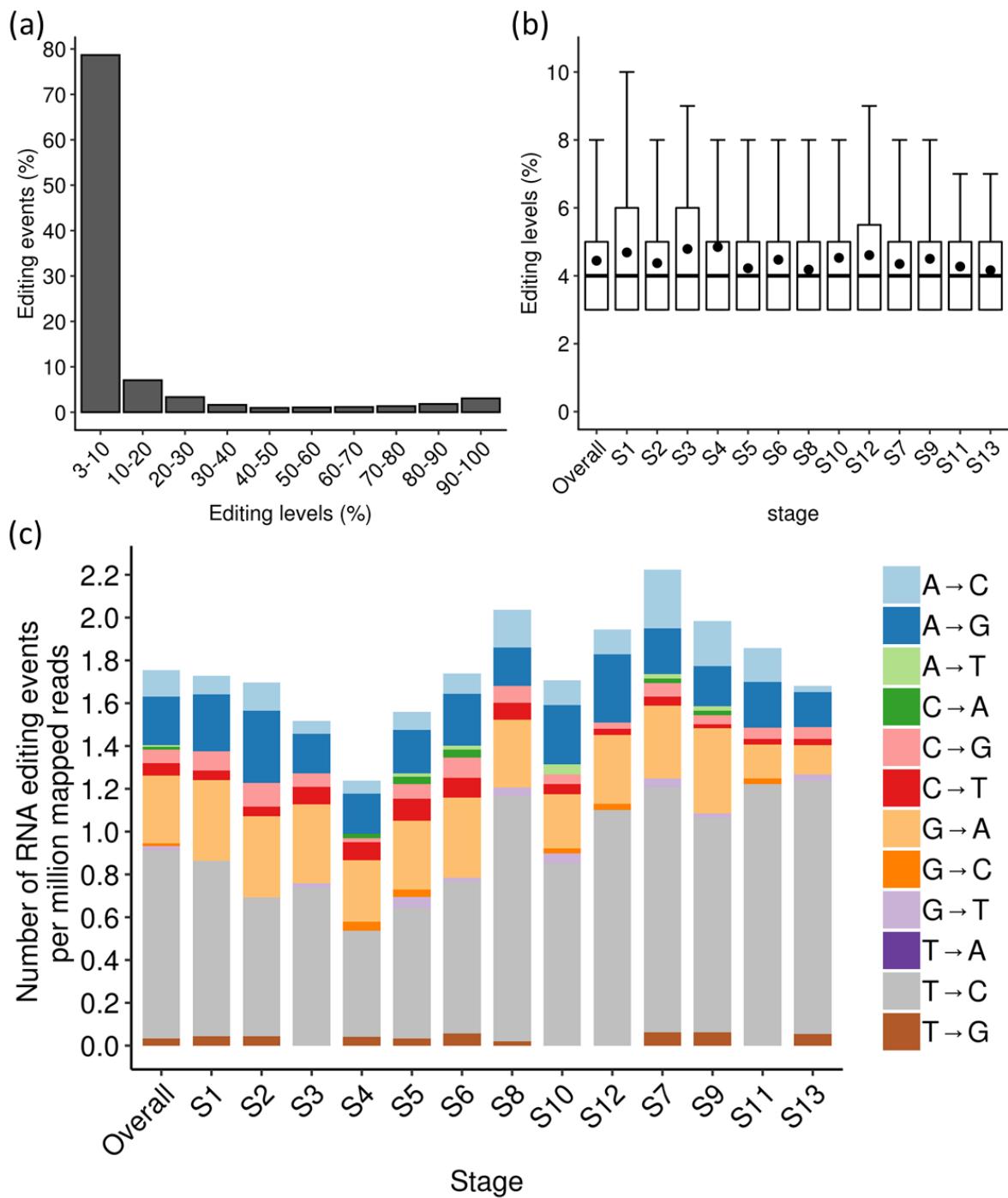
132

133 Figure S13. KOG annotation on developmentally regulated alternative splicing specific to the
134 developmental process.



135

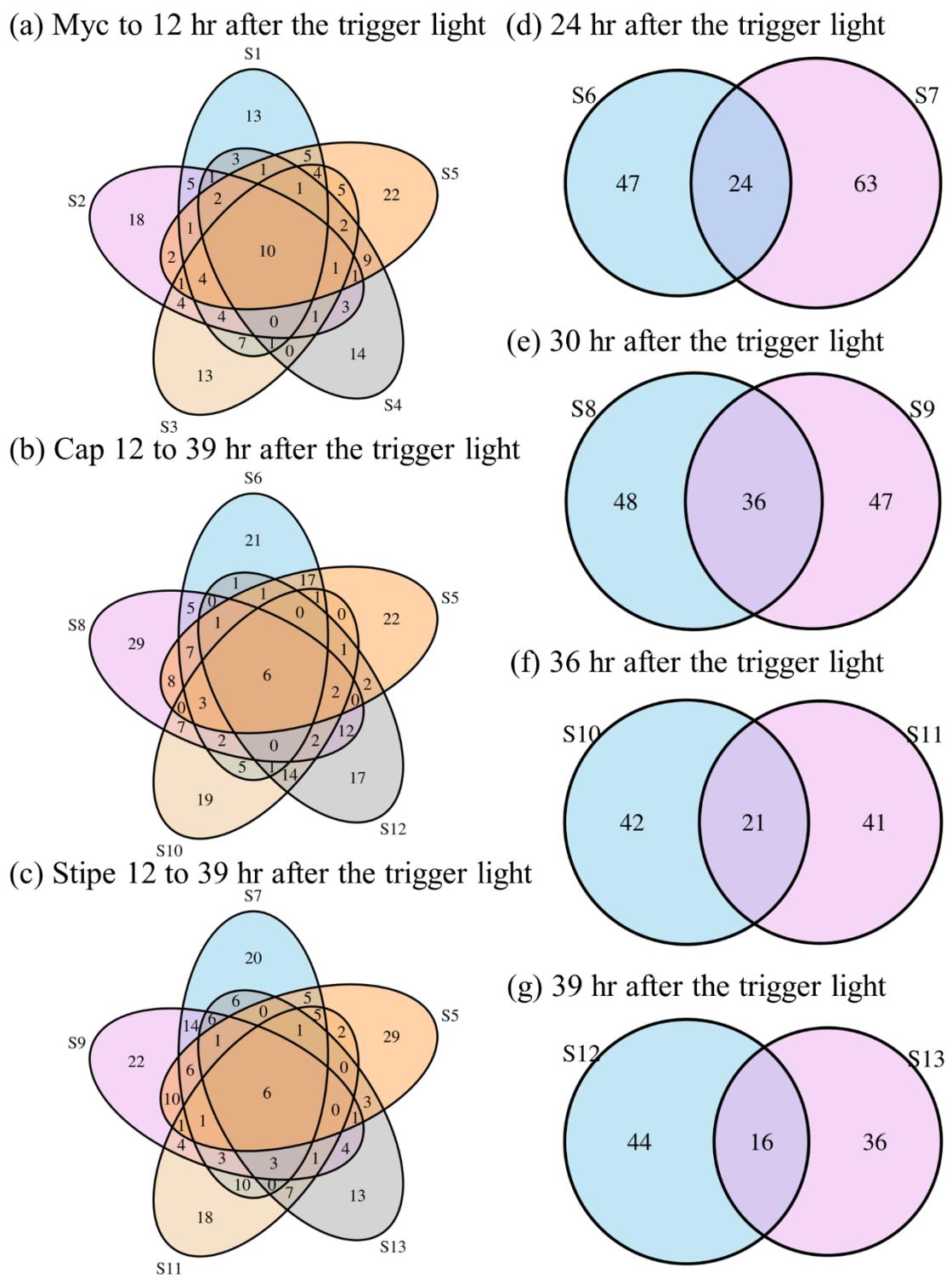
136 Figure S14. Common RNA editing sites among different stages. (a) Shared RNA editing sites
 137 among four major clades; (b) Vegetative mycelia, oidia forming mycelia, mycelia with
 138 hyphal knots; (c) Primordia and young fruiting bodies; (d) Spore germination.



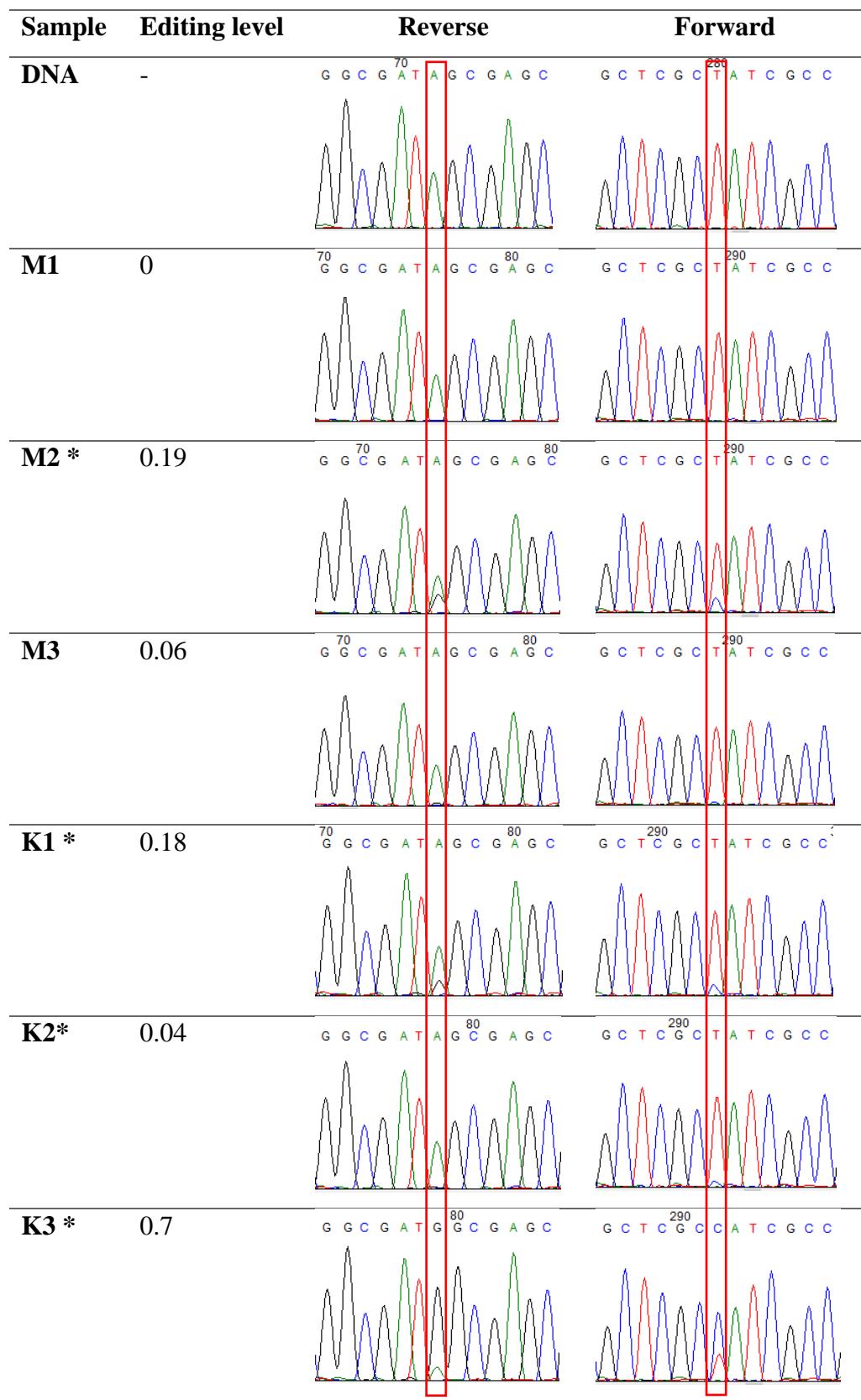
139

140 Figure S15. Statistics on RNA editing sites identified from Muraguchi et al. (2015). (a)
141 Histogram showing editing the frequency of 1050 RNA editing events. (b) Box plots showing
142 RNA editing levels of RNA editing events in different stages/tissues. (c) The number of each
143 type of RNA editing events per million mapped reads in different developmental stages.
144 Sequencing data was summarised in Table S10.

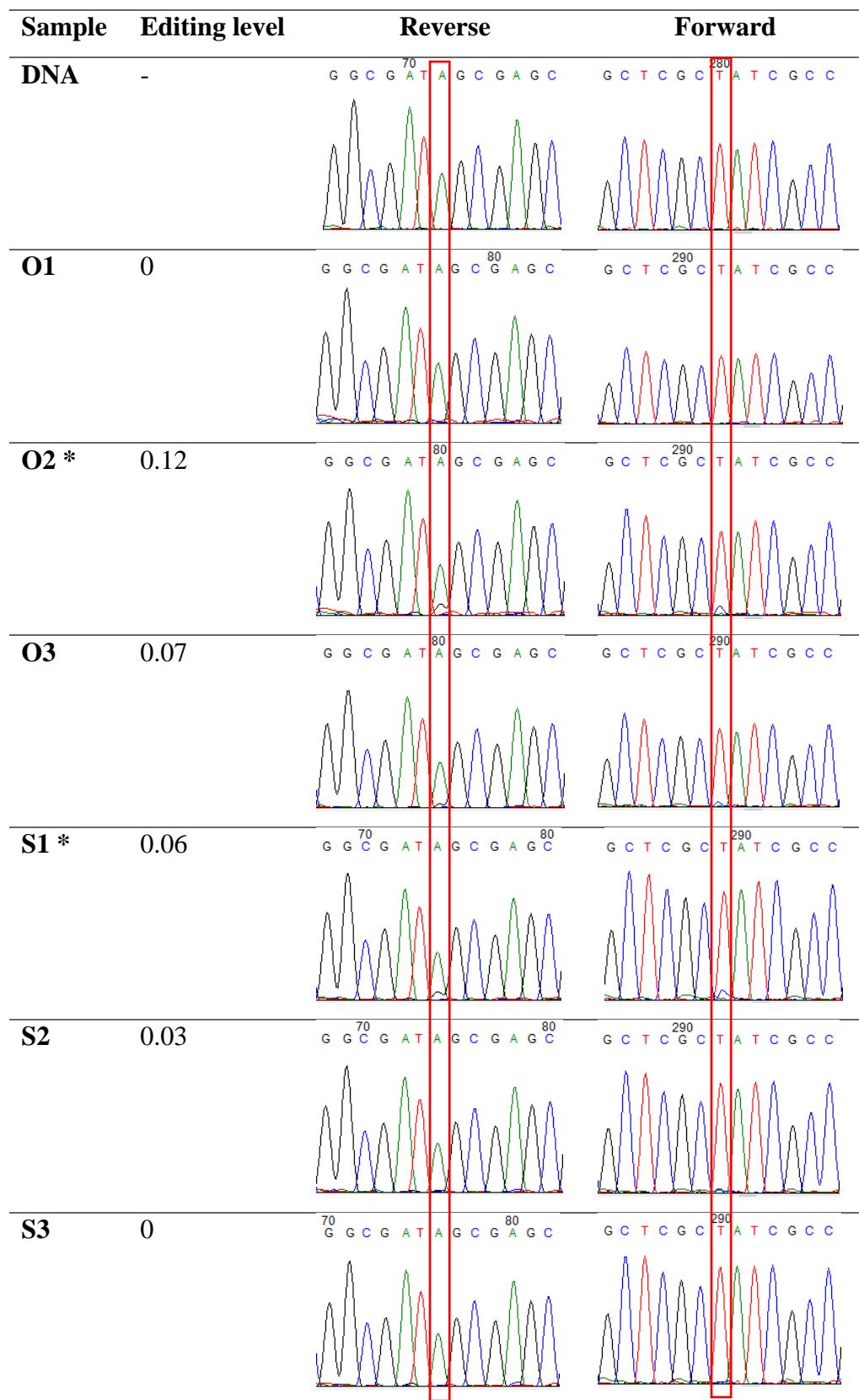
145



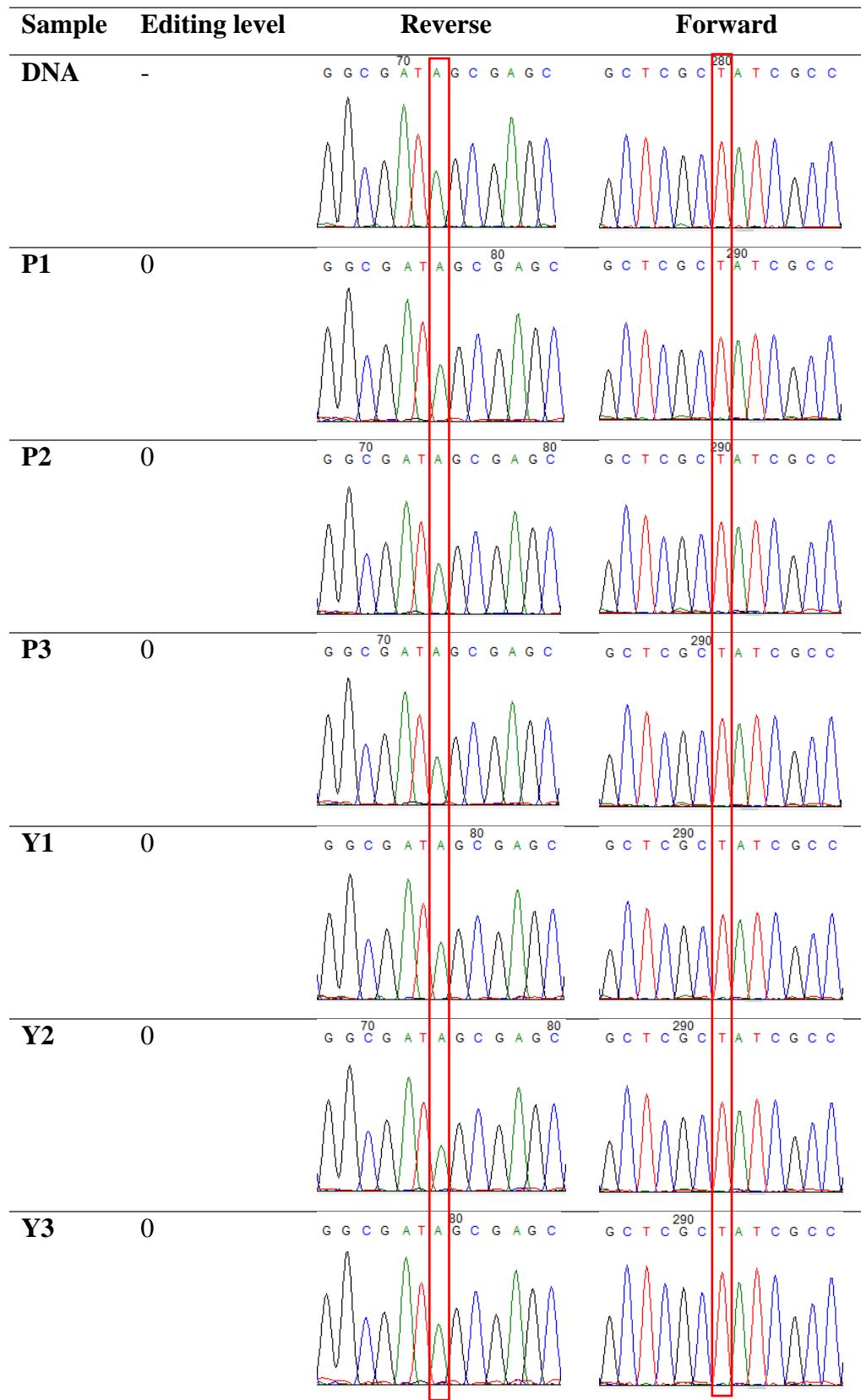
147 Figure S16. Common RNA editing sites identified from transcriptome data generated by
148 Muraguchi et al. (2015). (a) Vegetative mycelium to fruiting body primordia 12 h; (b) Cap of
149 fruiting body from 12 h to 39 h; (c) Stipe of fruiting body from 12 h to 39 h; (d-g) fruiting
150 body, 24 h/30 h/36 h/39 h after the light triggering.



152 Figure S17. Validation of RNA editing on hypothetical protein (CC2G_003350, scaffold_11:
 153 1716350U>C).

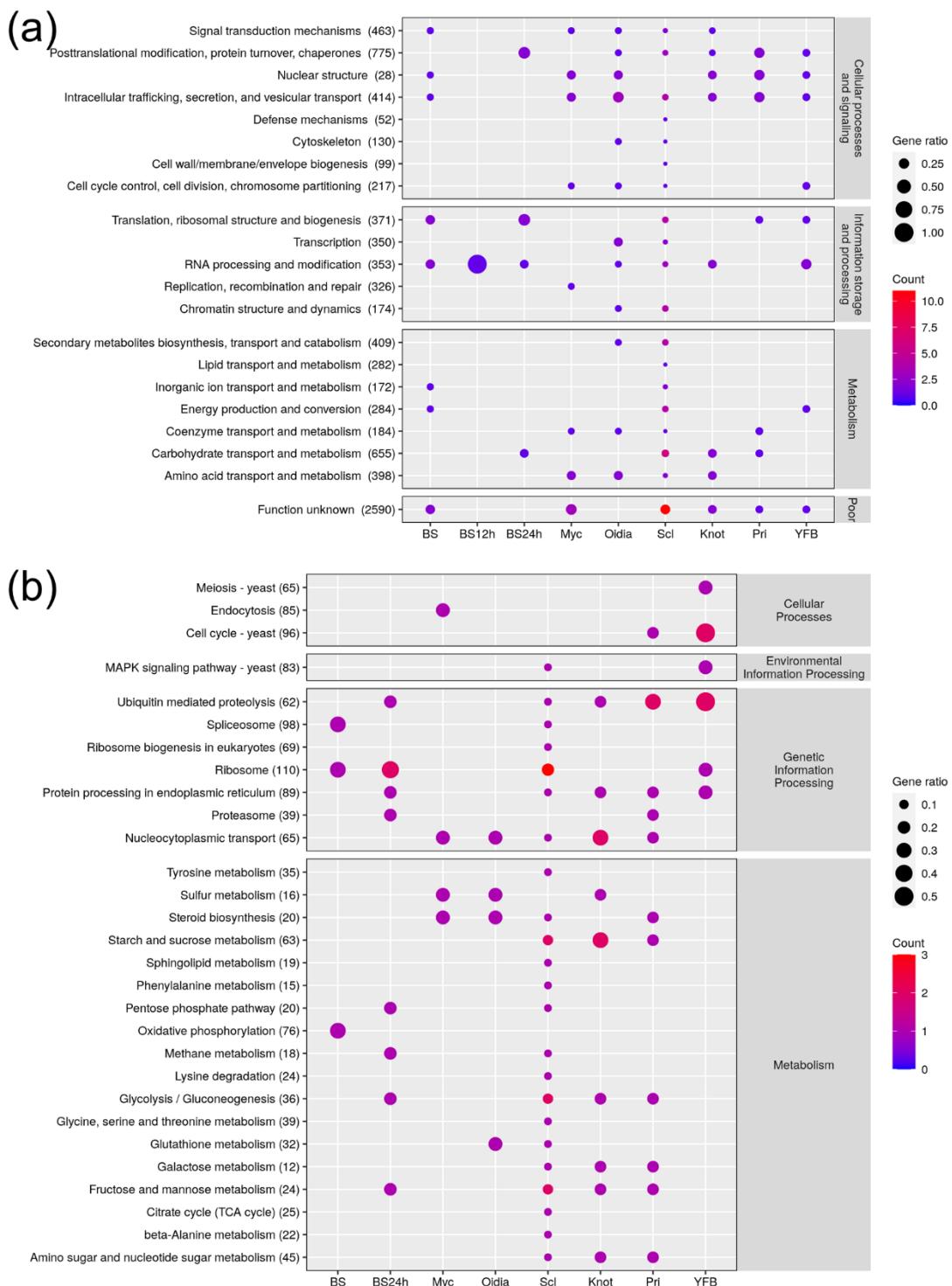


154 Figure S17. Validation of RNA editing on hypothetical protein (CC2G_003350, scaffold_11:
 155 1716350U>C), continued.



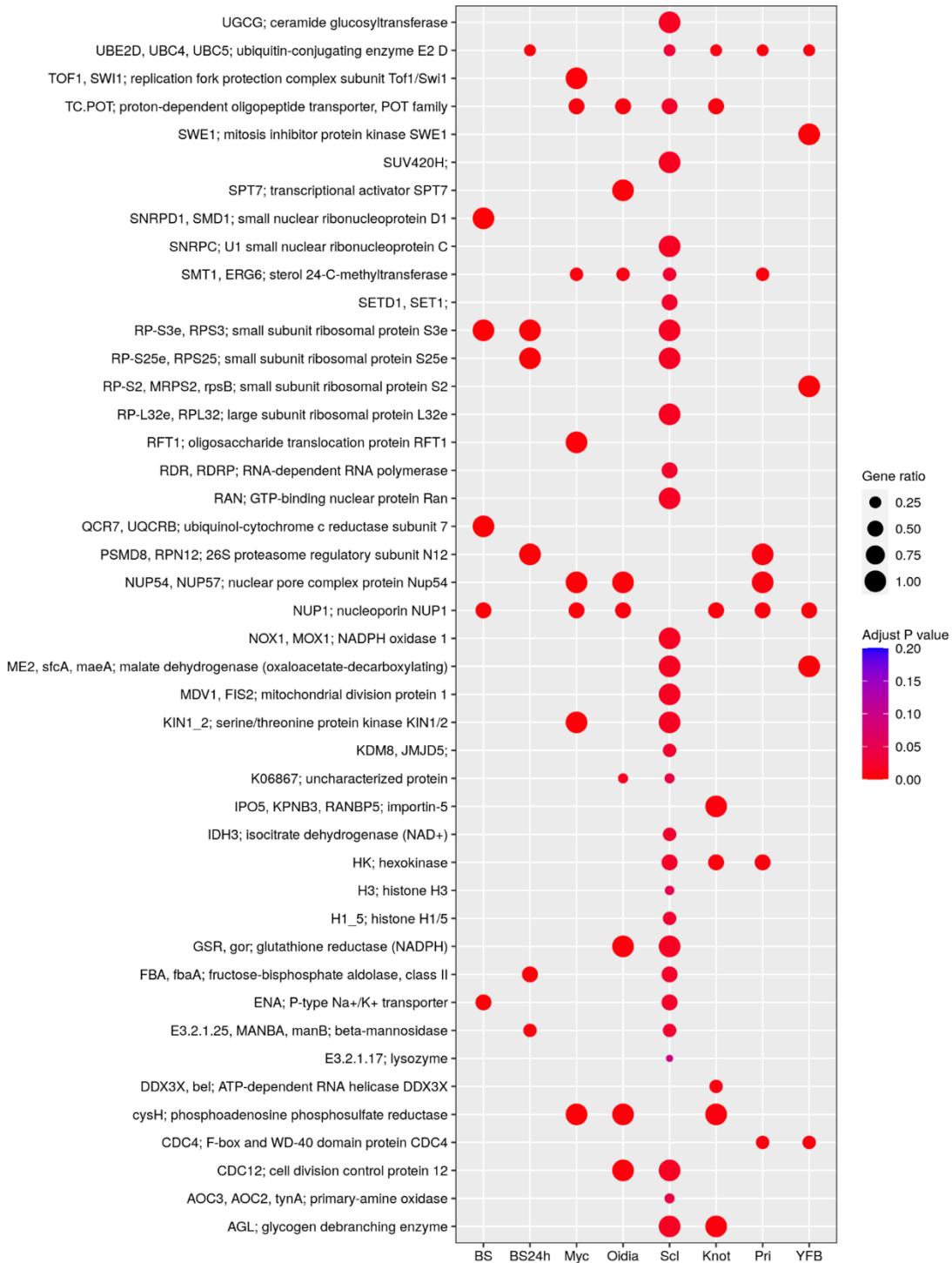
156 Figure S17. Validation of RNA editing on hypothetical protein (CC2G_003350, scaffold_11:
157 1716350U>C), continued.

158



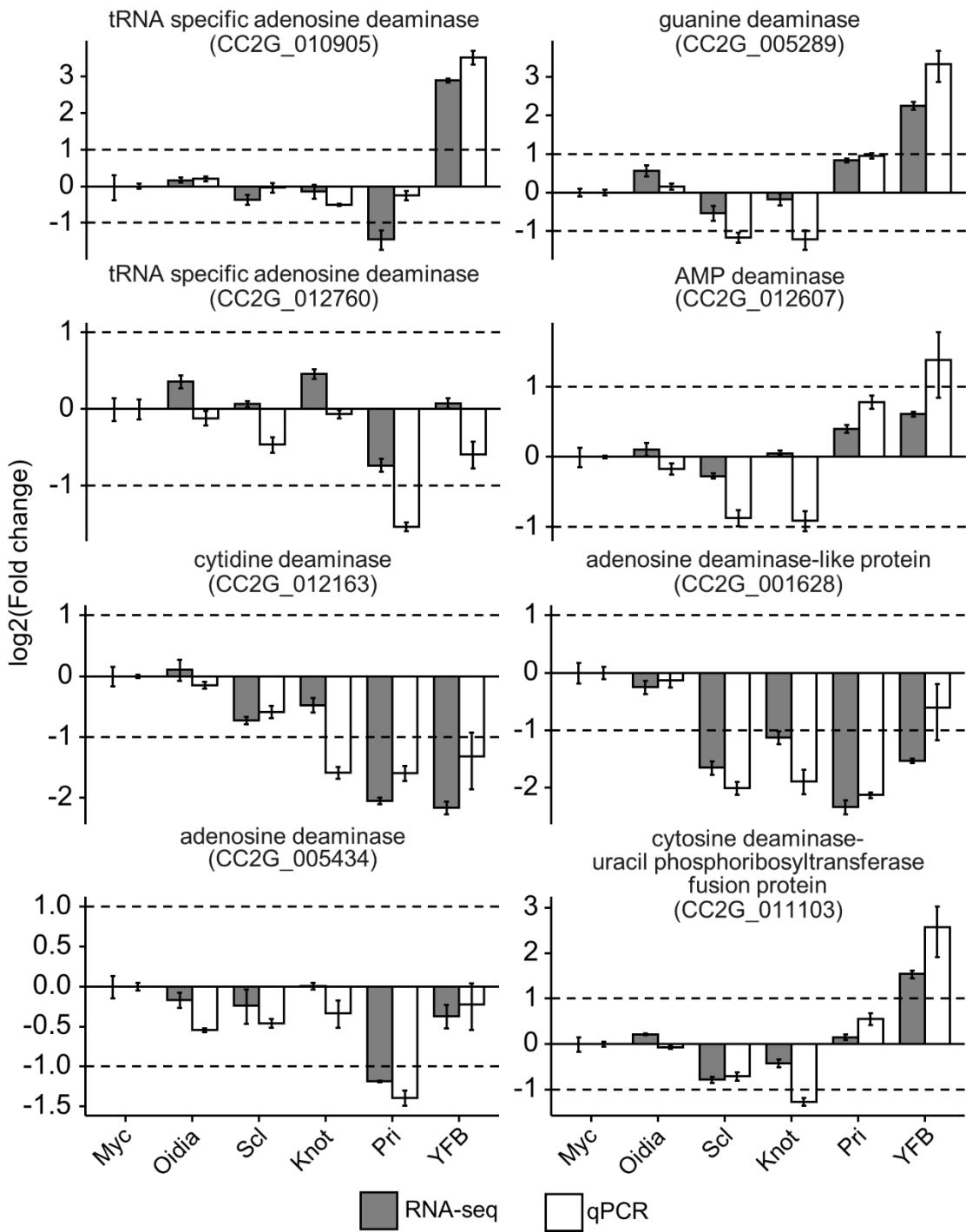
159

160 Figure S18. Functional annotation of genes with RNA editing. Gene ratio is calculated by
 161 annotated genes of specific functional term in each stage over annotated genes of each stage
 162 in the genome background. (a) KOG term annotation; (b) KEGG pathway annotation.



163

164 Figure S19. KO annotation of genes with RNA editing. Gene ratio is calculated by annotated
 165 genes of specific KO term in each stage over annotated genes of specific KO term in the
 166 genome background. Enriched groups with Benjamini and Hochberg method (BH) adjusted p
 167 value ≤ 0.20 are coloured red to blue.



168

169 Figure S20. Expression levels of nucleoside deaminase annotated in *C. cinerea*. Expression
170 fold changes are compared to vegetative mycelia (Myc).