

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

3

4 Yichun Xie,^a Po Lam Chan,^b Hoi Shan Kwan,^b Jinhui Chang^{c,#}

5

6 Supplementary materials

7 **Supplementary Datasets**

- 8
- 9 Dataset1. Gene count matrix by Trimmed Mean of M-values (TMM).
10 (Dataset1_Gene_count_log2TMMmatrix.xlsx)
- 11 Dataset2. Alternative splicing events and percent spliced in (PSI) value in *C. cinerea*
12 development. (Dataset2_Alternative_splicing.exp5.minor05.jad6.psi.xlsx)
- 13 Dataset3. Alternatively spliced genes.
14 (Dataset3_Alternative_splicing.exp5.minor05.jad6.feature.xlsx)
- 15 Dataset4. Wilcoxon test on PSI score differences across eight AS types in nine developmental
16 stages. (Dataset4_AS.type-stage.violin.KWcomparison.xlsx)
- 17 Dataset5. Wilcoxon test on PSI score differences across nine developmental stages of eight
18 AS types. (Dataset5_AS.stage-type.violin.KWcomparison.xlsx)
- 19 Dataset6. RNA editing identified in *C. cinerea* development with matrix of editing level.
20 (Dataset6_RNA_editing.editing_level.xlsx)
- 21 Dataset7. Annotation of RNA editing sites found in *C. cinerea*.
22 (Dataset7_RNA_editing.feature.xlsx)
- 23 Dataset8. Full genome alignment of strain #326 genome (Muraguchi et al., 2015) to (Xie et
24 al., 2021).
25 (Dataset8_full_genome_alignment_of_Muraguchi2015_against_Xie2021.xlsx)
- 26

27 **Supplementary Tables**

28

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

30 Table S2. Primers used in this study.

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

33 Table S4. Functional enrichment summary of DEGs.

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

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

36 Table S6. Wilcoxon test on PSI score of eight AS types.

37 Table S7. Number of RNA editing sites identified during *C. cinerea* development.

38 Table S8. Wilcoxon test on RNA editing levels of nine developmental stages.

39 Table S9. Wilcoxon test on RNA editing levels of twelve editing types.

40 Table S10. Sequencing quality and alignment rate of Muraguchi et al. (2015).

41 Table S11. Summary on impacts of RNA editing.

42

43 **Supplementary Figures**

- 44
- 45 Figure S1. Cross dissection of pileus under high power microscope (400 ×).
- 46 Figure S2. Pie chart showing the summary of gene expression levels.
- 47 Figure S3. Volcano plot showing the distribution of gene expression changes.
- 48 Figure S4. KOG enrichment analysis on gene clusters.
- 49 Figure S5. KEGG enrichment analysis on gene clusters.
- 50 Figure S6. GO enrichment analysis on gene clusters.
- 51 Figure S7. PSI score of AS events identified in nine developmental stages.
- 52 Figure S8. PSI score of eight AS types in nine developmental stages.
- 53 Figure S9. PSI score of nine developmental stages in eight AS types.
- 54 Figure S10. Quantitative relation of gene expression and PSI value of alternatively spliced
55 genes.
- 56 Figure S11. Scatter plots showing the changes on expression levels of alternative spliced
57 genes and their PSI scores.
- 58 Figure S12. Summary on differentially spliced events between stages.
- 59 Figure S13. KOG annotation on developmentally regulated alternative splicing specific to the
60 developmental process.
- 61 Figure S14. Common RNA editing sites among different stages.
- 62 Figure S15. Statistics on RNA editing sites identified from Muraguchi et al. (2015).
- 63 Figure S16. Common RNA editing sites identified from transcriptome data generated by
64 Muraguchi et al. (2015).
- 65 Figure S17. Functional annotation of genes with RNA editing.
- 66 Figure S18. KO annotation of genes with RNA editing.
- 67 Figure S19. Validation of RNA editing on hypothetical protein (CC2G_003350, scaffold_11:
68 1716350U>C).
- 69 Figure S20. Expression levels of nucleoside deaminase annotated in *C. cinerea*.
- 70

71 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

73 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

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

Stage	(Abb.)	Number of genes
Vegetative mycelia	(Myc)	11333
Oidia forming mycelia	(Oidia)	11269
Sclerotia forming mycelia	(Scl)	11075
Mycelia with hyphal knots	(Knot)	11396
Primordia undergoing meiosis	(Pri)	11392
Young fruiting bodies undergoing spore formation	(YFB)	10722
Mature basidiospores	(BS)	10043
Half germinating basidiospores	(BS12h)	10301
Fully germinated basidiospores	(BS24h)	10060
Total		12450

78 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

80 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

82 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	*

84 Table S6. Wilcoxon test on PSI score of eight AS types.

Group1	Group2	p	p.adj	p.format	p.signif
IR	A3SS	1.88E-08	4.10E-07	1.90E-08	****
IR	A3SS	7.90E-63	2.20E-61	< 2e-16	****
IR	AltStart	1.32E-06	3.20E-05	1.30E-06	****
IR	A5SS	3.75E-61	1.00E-59	< 2e-16	****
IR	Cassette	8.43E-14	2.20E-12	8.40E-14	****
IR	Cassette_multi	0.355936	1	0.3559	ns
IR	MXE	9.77E-06	0.00022	9.80E-06	****
IR	AltEnd	5.50E-10	1.40E-08	5.50E-10	****
A3SS	AltStart	0.068109	1	0.0681	ns
A3SS	A5SS	0.187893	1	0.1879	ns
A3SS	Cassette	0.628477	1	0.6285	ns
A3SS	Cassette_multi	0.186512	1	0.1865	ns
A3SS	MXE	0.173202	1	0.1732	ns
A3SS	AltEnd	0.001982	0.042	0.002	**
AltStart	A5SS	0.115084	1	0.1151	ns
AltStart	Cassette	0.03331	0.53	0.0333	*
AltStart	Cassette_multi	0.008635	0.16	0.0086	**
AltStart	MXE	0.609603	1	0.6096	ns
AltStart	AltEnd	0.382457	1	0.3825	ns
A5SS	Cassette	0.233201	1	0.2332	ns
A5SS	Cassette_multi	0.125803	1	0.1258	ns
A5SS	MXE	0.268719	1	0.2687	ns
A5SS	AltEnd	0.00467	0.093	0.0047	**
Cassette	Cassette_multi	0.217052	1	0.2171	ns
Cassette	MXE	0.117014	1	0.117	ns
Cassette	AltEnd	0.001851	0.041	0.0019	**
Cassette_multi	MXE	0.031051	0.53	0.0311	*
Cassette_multi	AltEnd	0.00546	0.1	0.0055	**
MXE	AltEnd	0.258554	1	0.2586	ns

86 Table S7. 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

88 Table S8. 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

90 Table S9. 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	

92 Table S10. Sequencing quality and alignment rate of Muraguchi et al. (2015).

Sample	Before filtering				After filtering				Mapping rate	Mapped reads (duplicates removed)
	Clean	Clean	Q20	Q30	Clean	Clean	Q20	Q30		
	Reads	Bases	(%)	(%)	Reads	Bases	(%)	(%)		
1a	31,205,060	3,120,506,000	96.67	92.62	30,588,537	3,058,853,700	97.85	93.84	90.12	21,198,168
1b	37,134,290	3,713,429,000	96.45	91.78	36,323,040	3,632,304,000	97.75	93.12	87.70	23,921,279
2a	31,223,972	3,122,397,200	96.32	92.34	30,444,327	3,044,432,700	97.83	93.89	90.72	21,599,742
2b	34,762,388	3,476,238,800	96.34	91.84	33,909,128	3,390,912,800	97.80	93.36	89.47	23,169,615
3a	29,580,744	2,958,074,400	96.65	92.54	28,998,689	2,899,868,900	97.82	93.76	93.70	21,949,736
3b	37,690,666	3,769,066,600	96.96	92.53	37,043,009	3,704,300,900	97.98	93.60	91.74	26,818,599
4a	32,147,942	3,214,794,200	95.63	91.43	31,121,759	3,112,175,900	97.58	93.43	88.17	21,399,283
4b	34,817,668	3,481,766,800	96.52	92.01	34,063,717	3,406,371,700	97.84	93.37	91.00	24,173,608
5a	37,244,680	3,724,468,000	95.98	91.73	36,237,503	3,623,750,300	97.61	93.41	89.69	25,750,544
5b	48,903,482	4,890,348,200	96.77	92.34	47,958,309	4,795,830,900	97.93	93.56	89.04	33,203,947
6a	34,887,484	3,488,748,400	96.16	92.03	33,982,615	3,398,261,500	97.73	93.64	90.44	24,292,984
6b	42,412,510	4,241,251,000	96.84	92.38	41,625,122	4,162,512,200	97.96	93.54	90.93	29,228,770
7a	49,589,664	4,958,966,400	87.44	79.59	46,053,761	4,605,376,100	90.91	82.99	92.76	27,418,221
7b	26,740,264	2,674,026,400	97.33	93.77	26,296,838	2,629,683,800	98.36	94.85	90.73	19,797,800
8a	51,622,648	5,162,264,800	88.12	80.35	48,251,483	4,825,148,300	91.31	83.48	80.28	26,627,919
8b	33,568,462	3,356,846,200	97.86	94.48	33,185,693	3,318,569,300	98.56	95.22	85.48	23,935,077

93

94

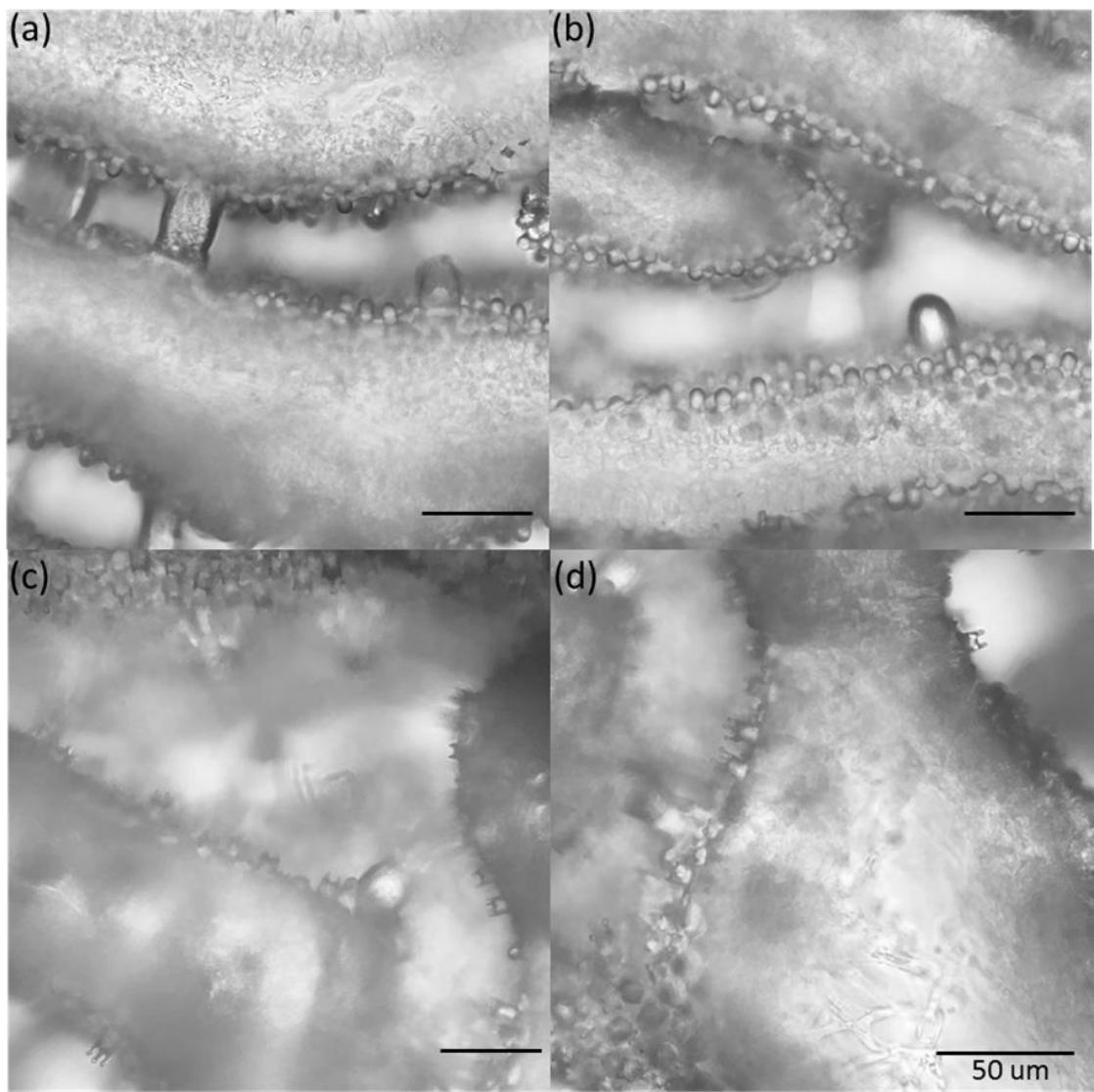
95 Table S10. Sequencing quality and alignment rate of Muraguchi et al. (2015).

Sample	Before filtering				After filtering				Mapping rate	Mapped reads (duplicates removed)
	Clean	Clean	Q20	Q30	Clean	Clean	Q20	Q30		
	Reads	Bases	(%)	(%)	Reads	Bases	(%)	(%)		
9a	37,849,696	3,784,969,600	87.31	79.41	35,094,893	3,509,489,300	90.89	82.91	84.43	19,872,417
9b	33,878,678	3,387,867,800	97.11	93.44	33,236,197	3,323,619,700	98.27	94.65	89.75	24,372,755
10a	45,779,870	4,577,987,000	87.72	79.87	42,630,128	4,263,012,800	91.07	83.15	87.11	23,375,496
10b	34,043,780	3,404,378,000	97.72	94.25	33,615,981	3,361,598,100	98.48	95.06	77.84	19,996,237
11a	36,752,246	3,675,224,600	88.24	80.52	34,355,776	3,435,577,600	91.42	83.64	88.88	19,619,235
11b	28,338,818	2,833,881,800	97.58	94.18	27,918,615	2,791,861,500	98.50	95.13	79.94	18,056,930
12a	44,203,804	4,420,380,400	88.94	81.39	41,603,239	4,160,323,900	91.84	84.24	84.81	20,552,917
12b	19,762,202	1,976,220,200	97.45	94.06	19,473,089	1,947,308,900	98.37	95.03	94.05	13,094,674
13a	37,052,022	3,705,202,200	87.42	79.68	34,265,670	3,426,567,000	91.18	83.34	84.65	18,874,582
13b	22,922,628	2,292,262,800	97.46	93.80	22,588,180	2,258,818,000	98.35	94.74	95.48	16,649,720
DNA	160,188,596	24,028,289,400	81.69	72.20	139,722,400	20,958,360,000	87.29	77.67	88.55	87,789,310

97 Table S11. Summary on impacts of RNA editing.

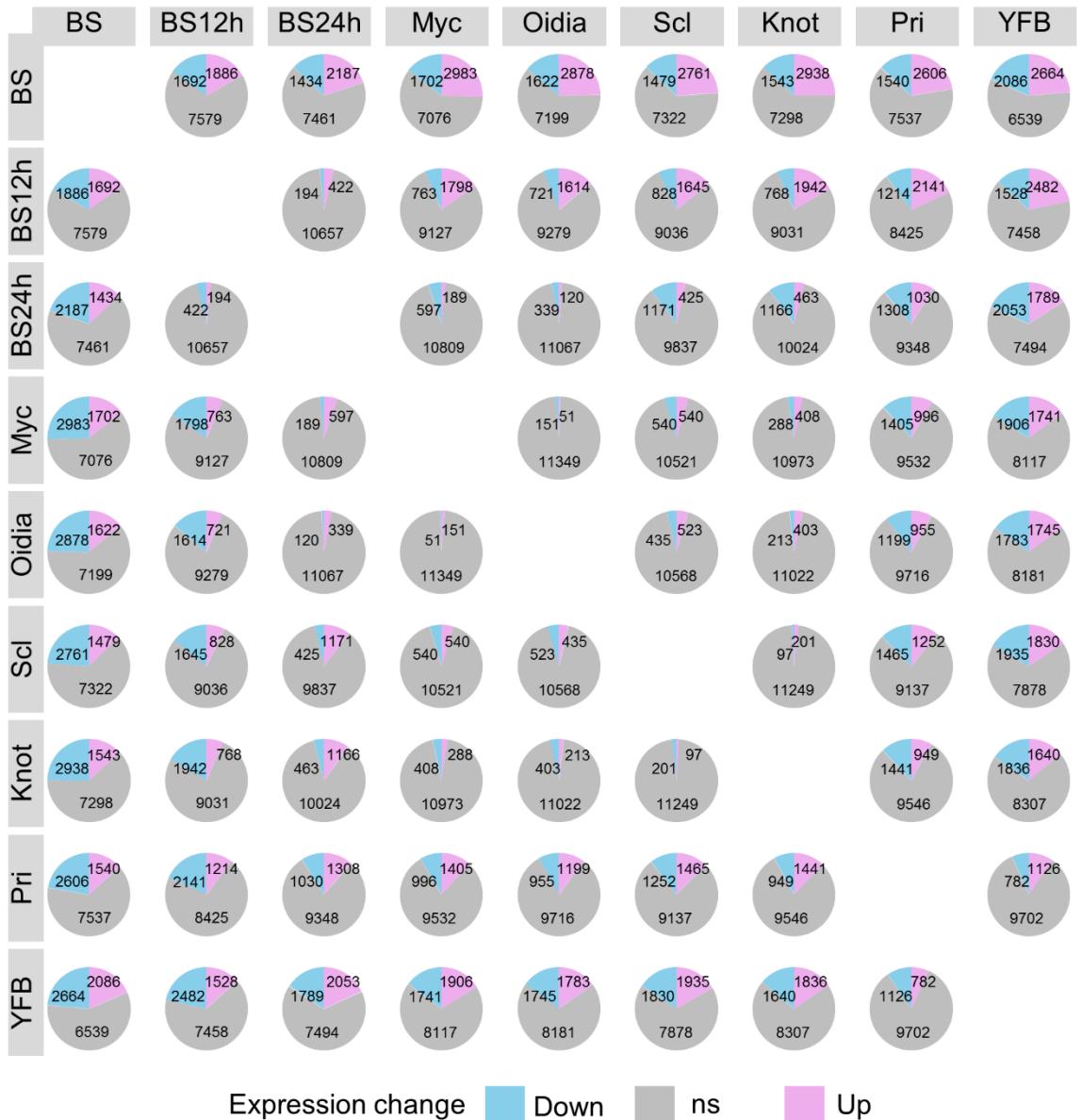
Impact	Number of sites
Upstream gene variant	85
5'-UTR premature start codon gain variant	1
5'-prime UTR variant	6
Synonymous variant	29
Missense variant	26
Stop lost&splice region variant	1
Stop gained	2
3'-UTR variant	63
Downstream gene variant	4

98



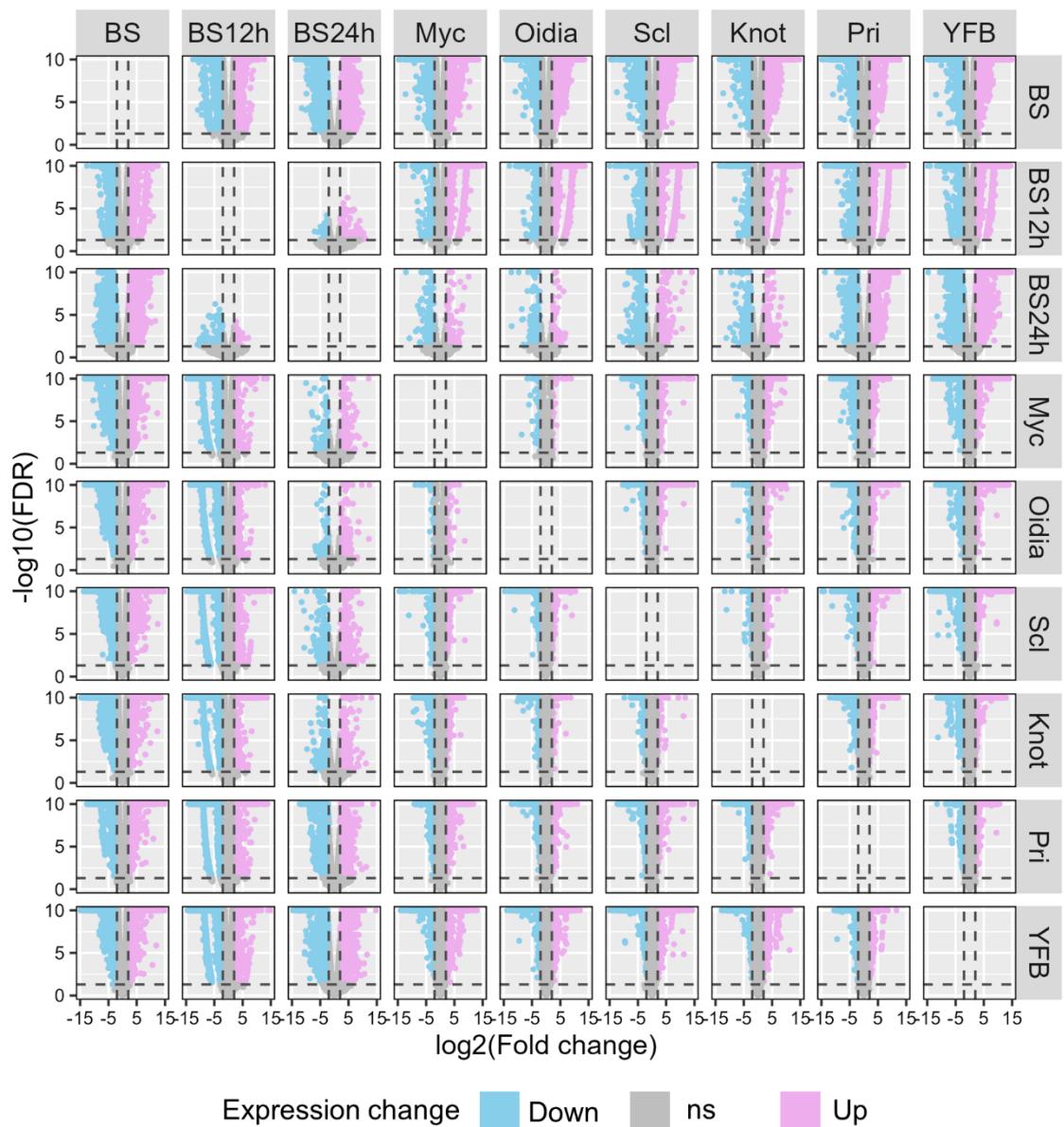
99

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



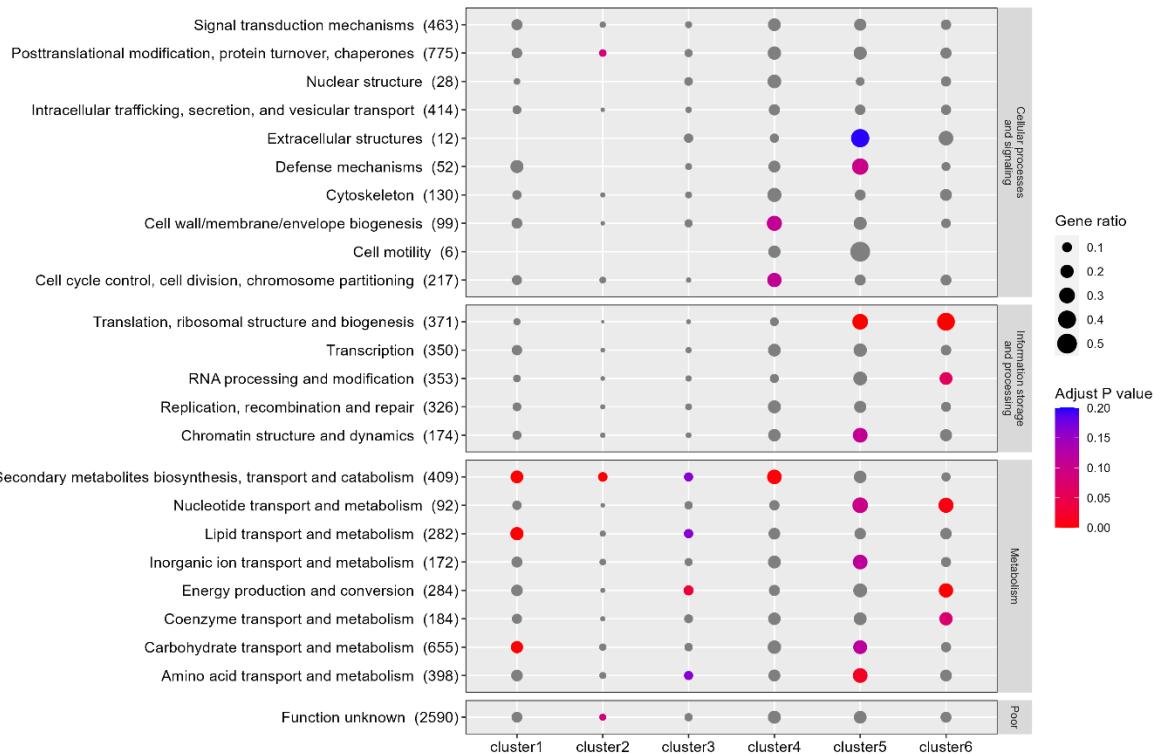
103

104 Figure S2. Pie chart showing the summary of gene expression levels. Sample of each column
 105 were compared against sample of each row, for example, compare to BS, 1886 genes were
 106 up-regulated and 1692 genes were down-regulated in BS12h.



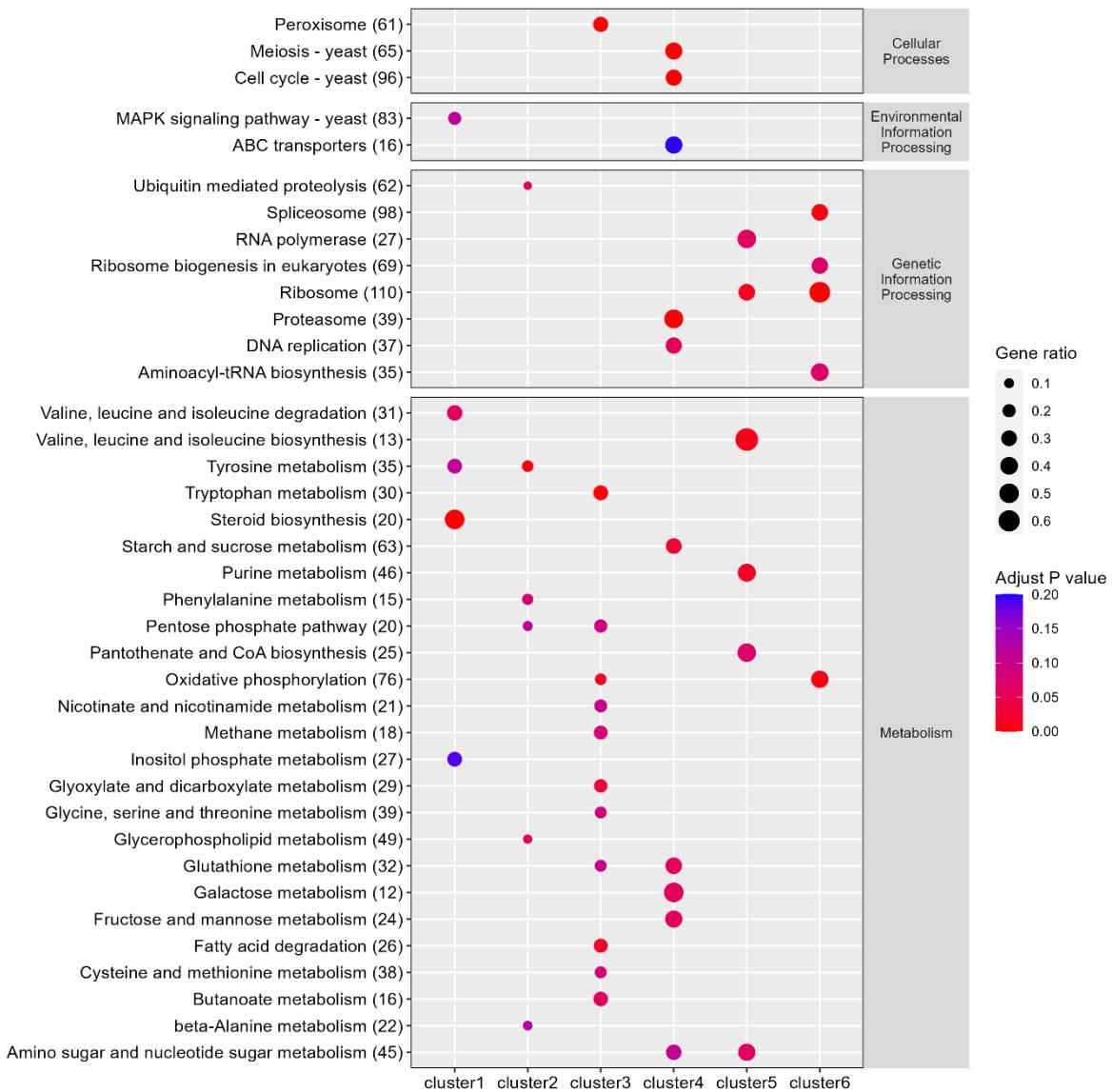
107

108 Figure S3. Volcano plot showing the distribution of gene expression changes. Sample of each
 109 column were compared against sample of each row, for example, compare to BS, 1886 genes
 110 were up regulated and 1692 genes were down regulated in BS12h.



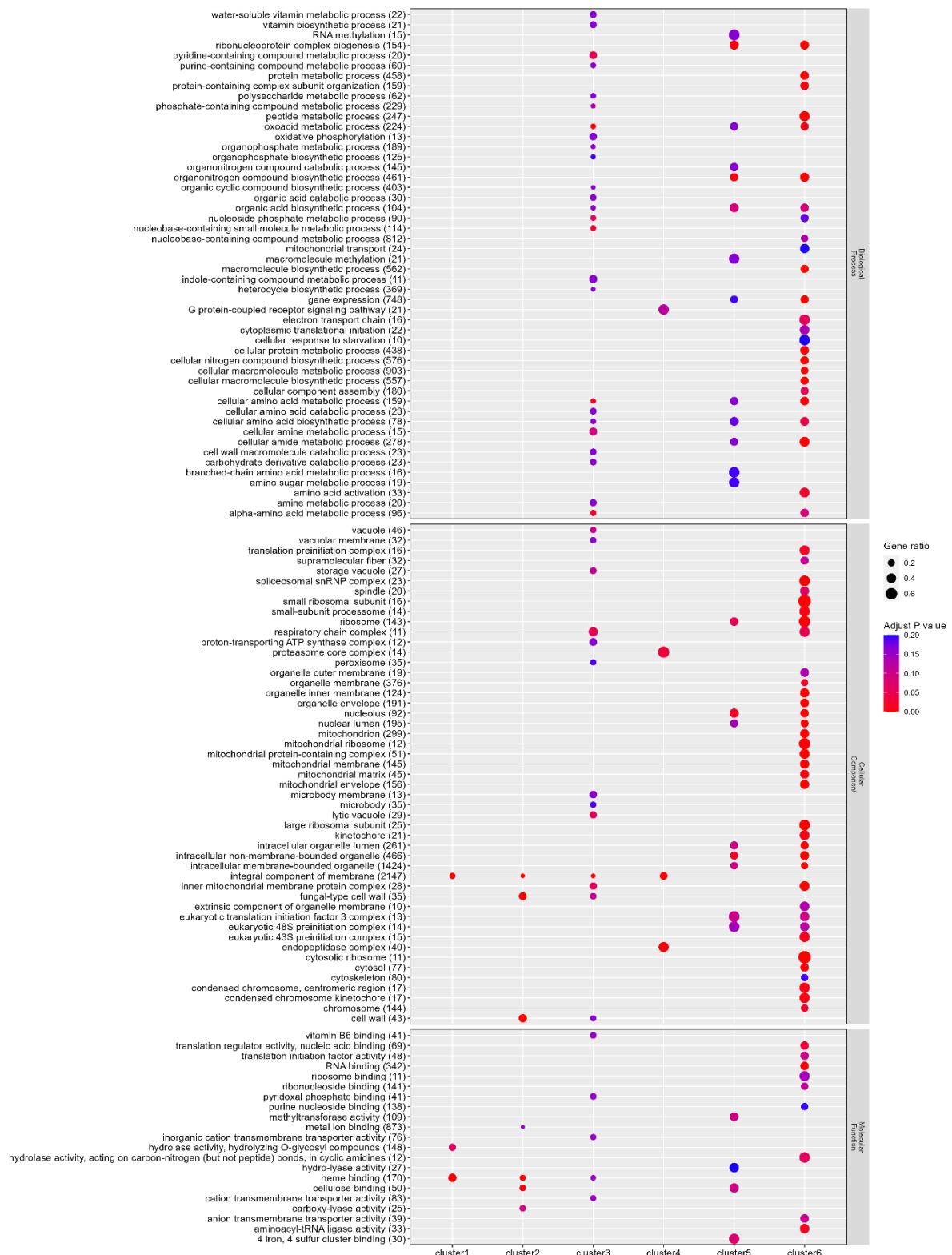
111

112 Figure S4. KOG enrichment analysis on gene clusters. Numbers of genes annotated to
 113 specific KOG term are listed beside the term. Gene ratio is calculated by annotated genes of
 114 specific KOG term in each cluster over annotated genes of specific KOG term in the genome
 115 background. Enriched groups with Benjamini and Hochberg method (BH) adjusted p value \leq
 116 0.20 are coloured red to blue, others are in grey.



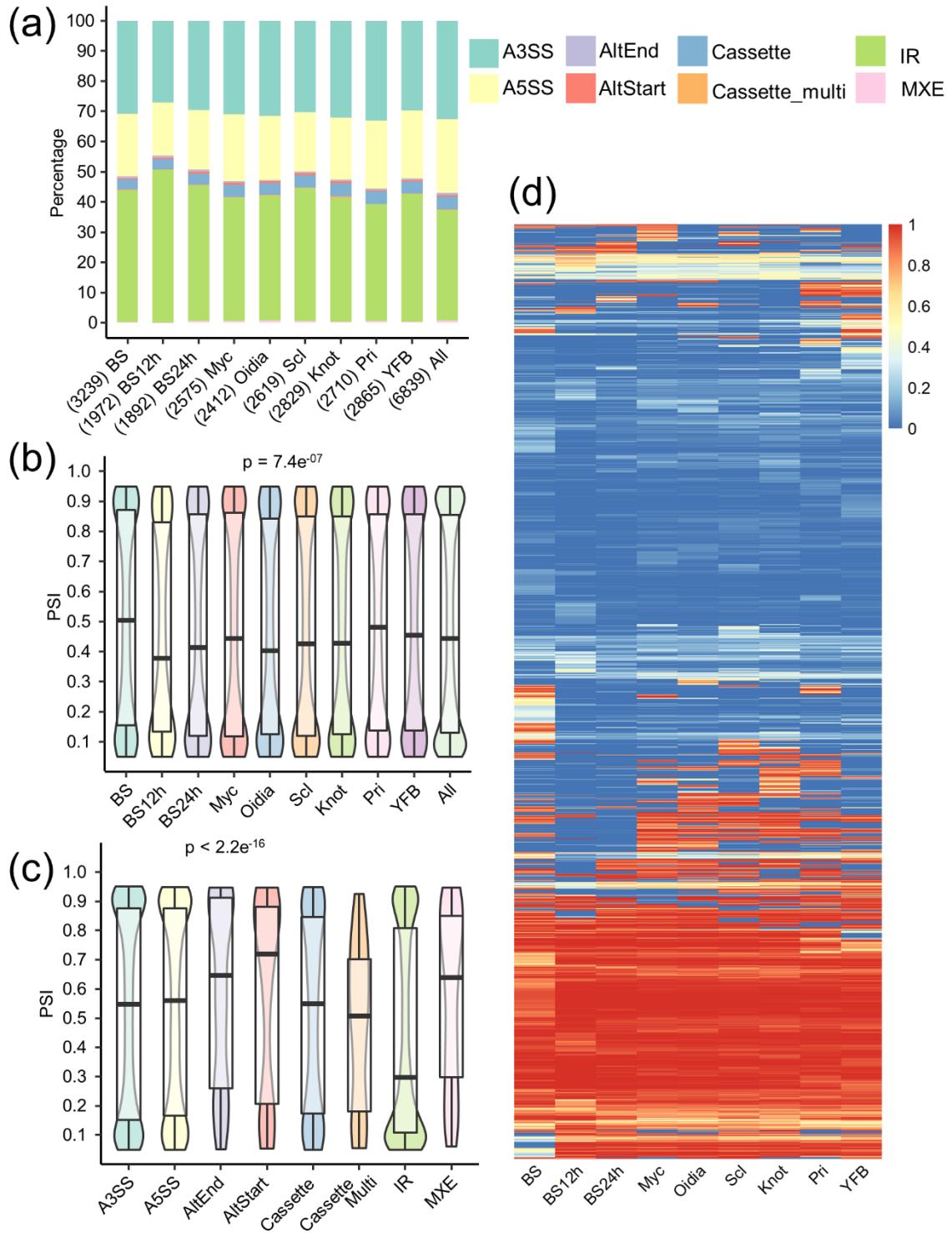
117

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



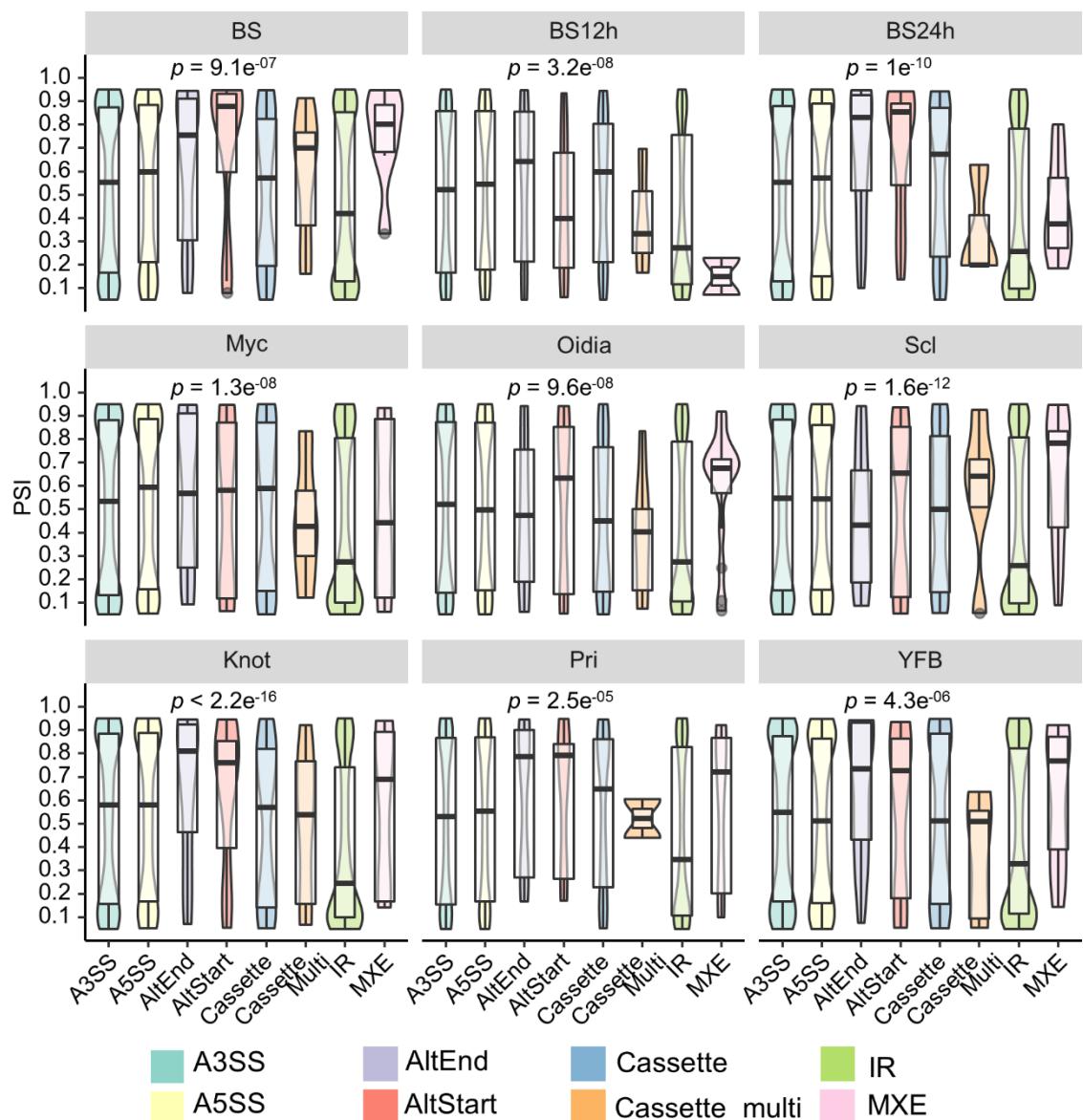
123

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



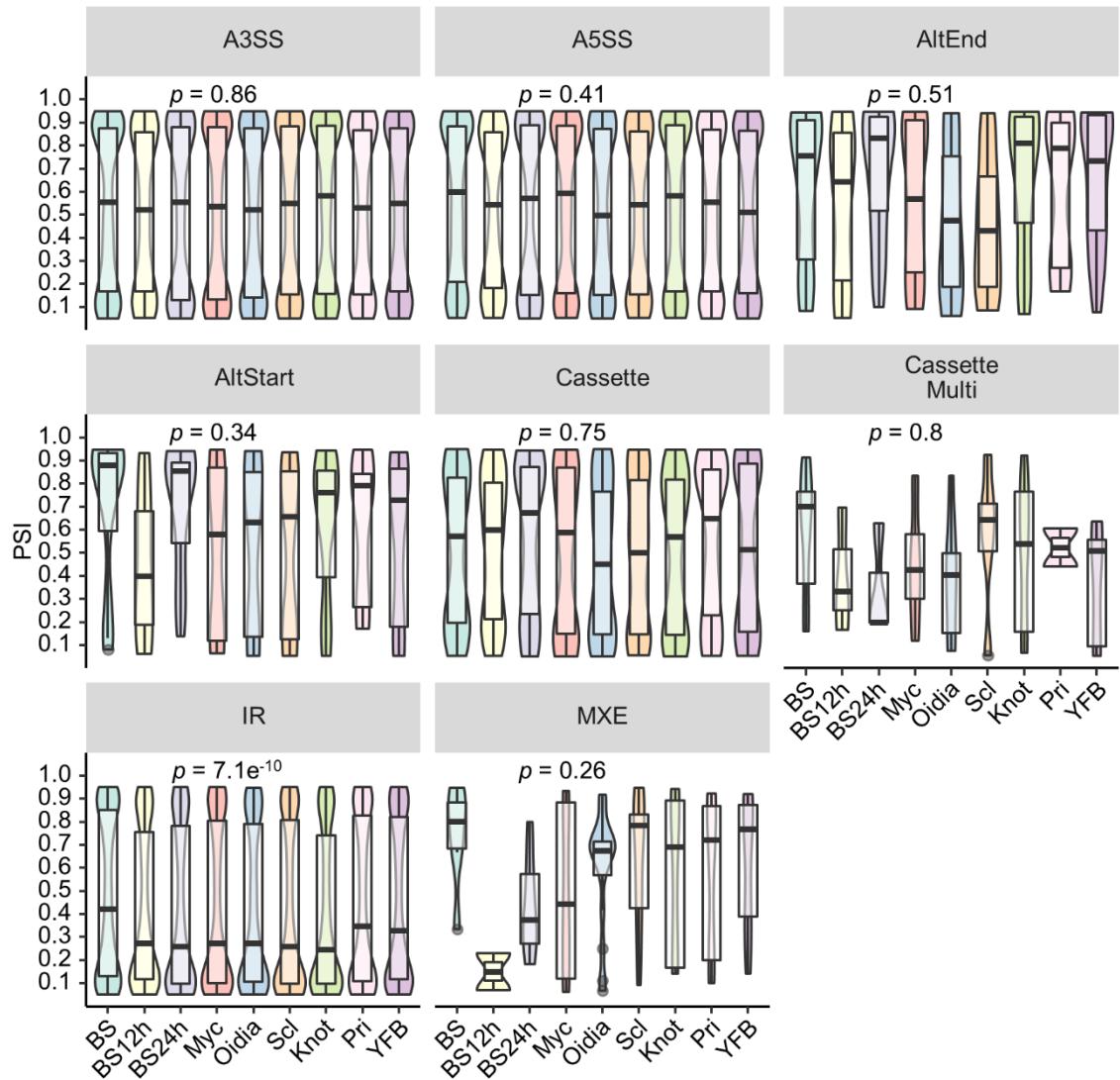
129

130 Figure S7. PSI score of AS events identified in nine developmental stages. (a) Distribution of
 131 eight AS types in nine stages; (b) PSI score of different stages, statistical results were detailed
 132 in table S5; (c) Violin plot summarising the PSI score of each AS types, statistical results
 133 were detailed in Table S6; (d) Heatmap showing the PSI score.



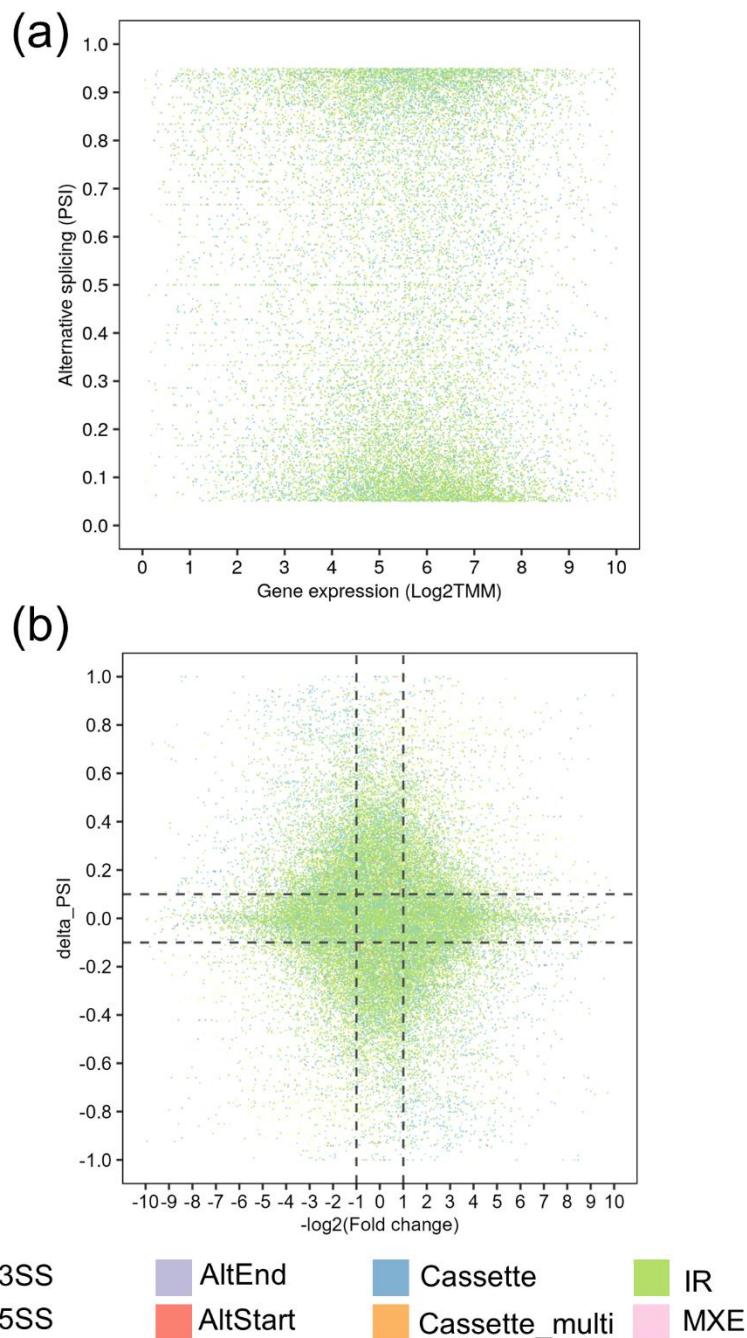
134

135 Figure S8. PSI score of eight AS types in nine developmental stages. Statistical results were
 136 detailed in Dataset4.



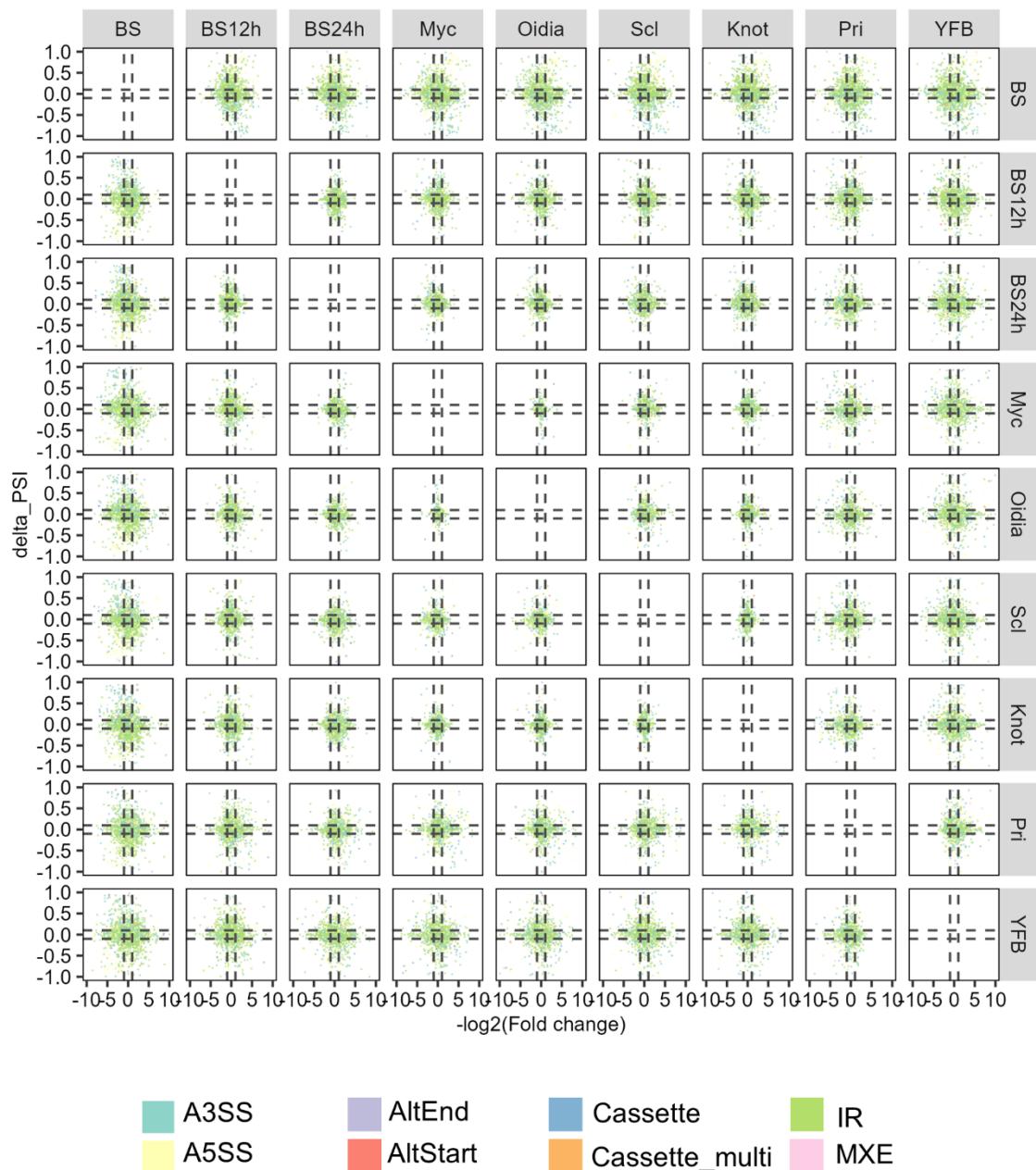
137

138 Figure S9. PSI score of nine developmental stages in eight AS types. Statistical results were
139 detailed in Dataset5.



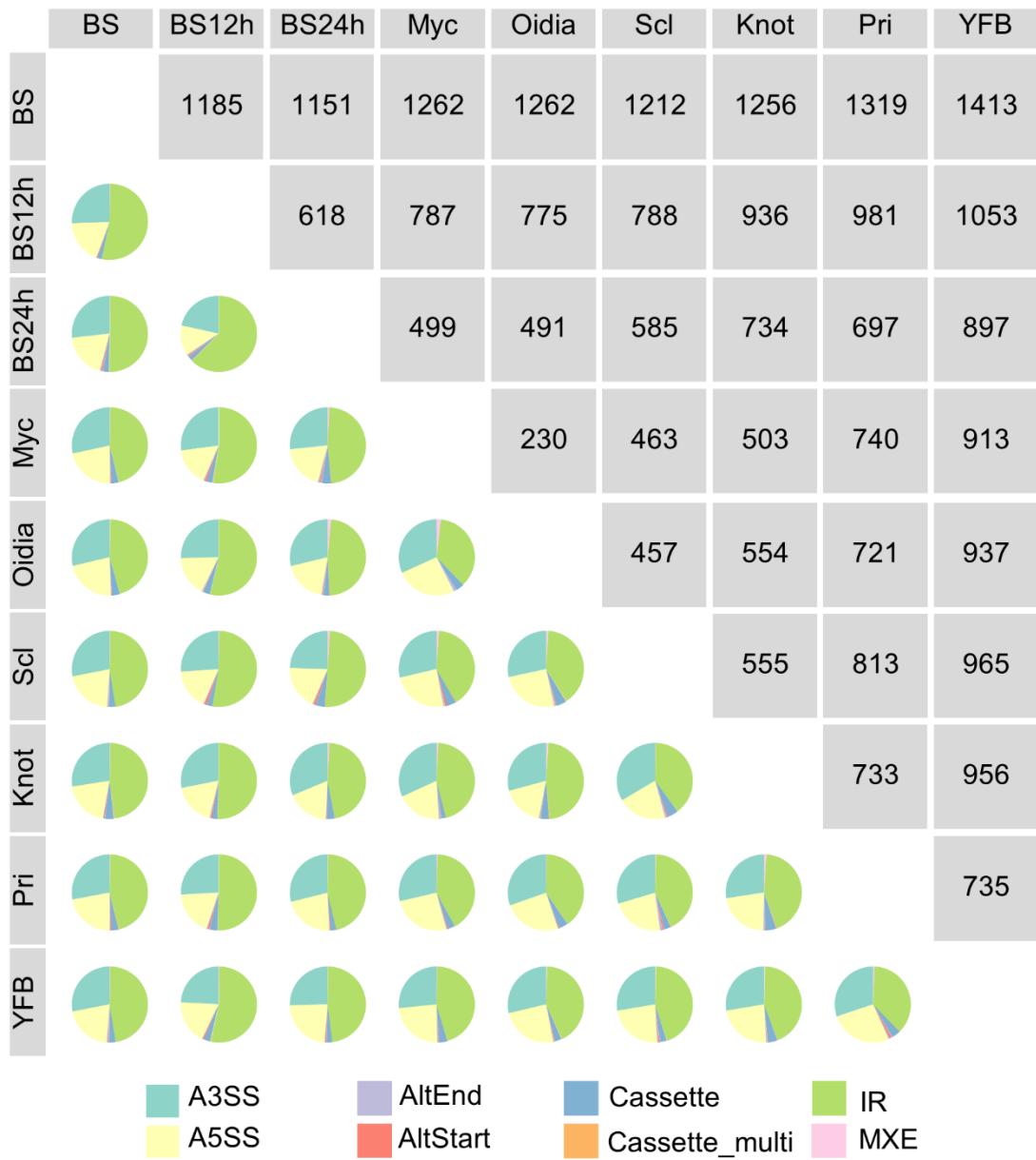
140

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



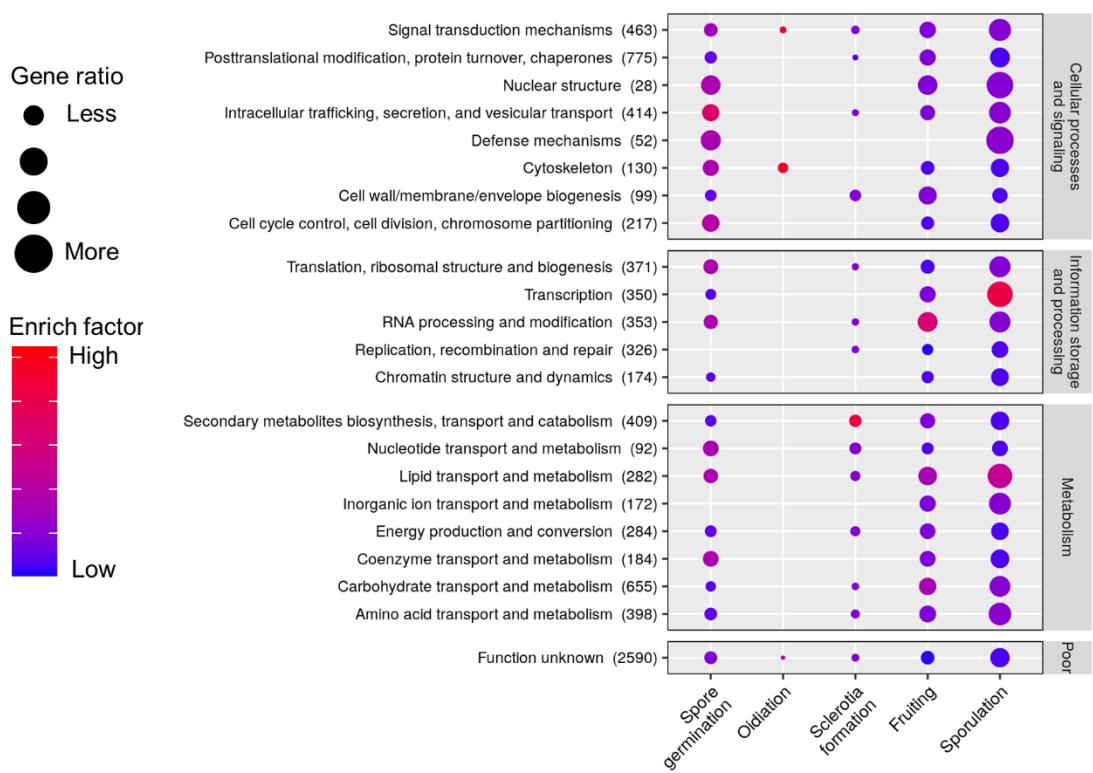
144

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



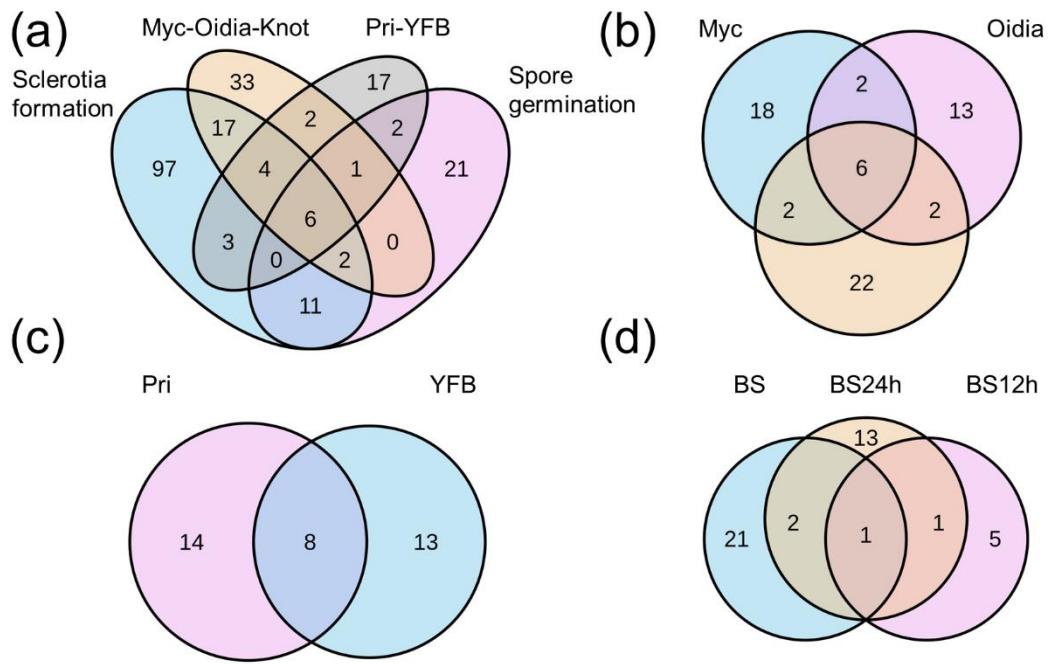
148

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



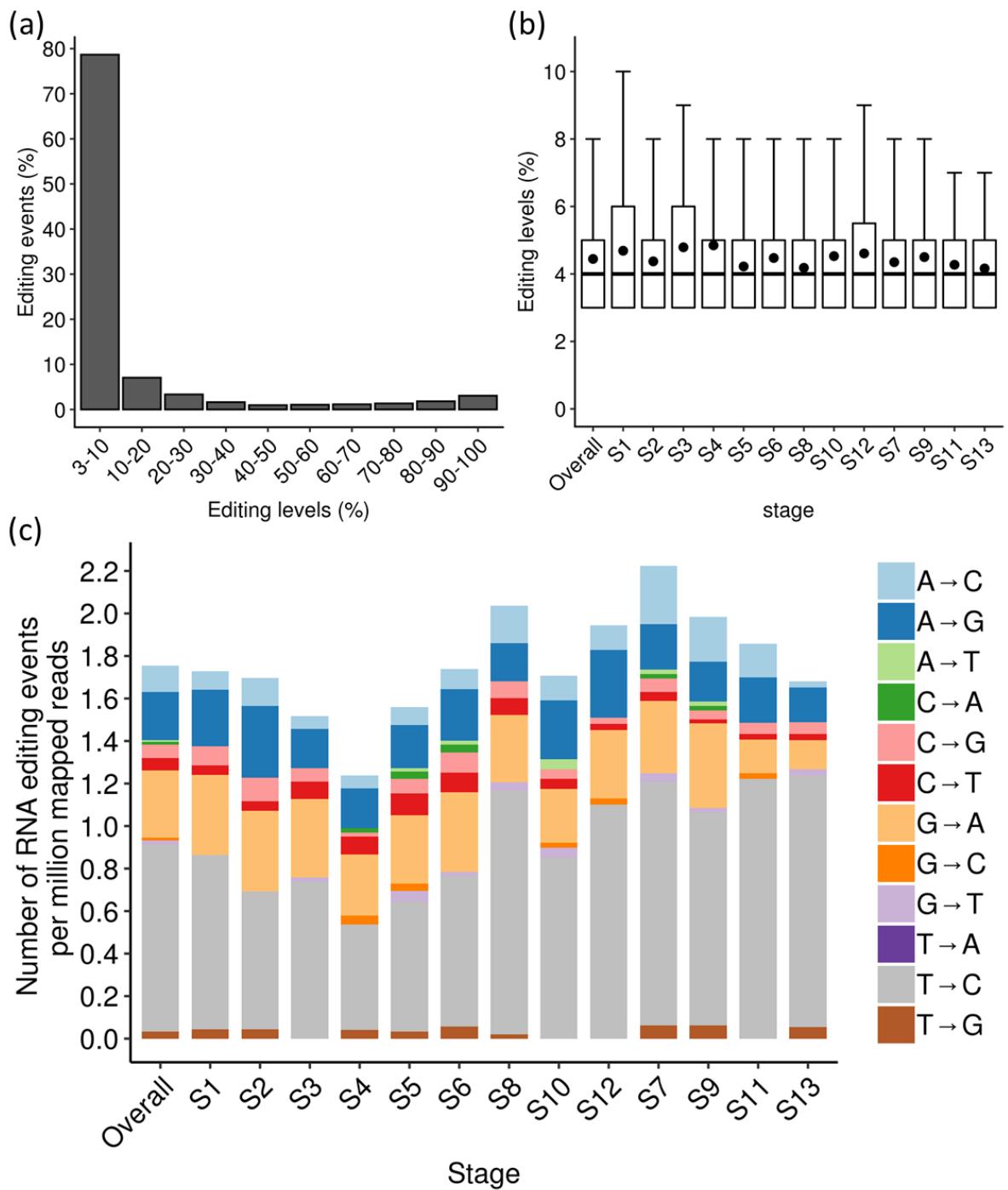
152

153 Figure S13. KOG annotation on developmentally regulated alternative splicing specific to the
154 developmental process.



155

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



159

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

165

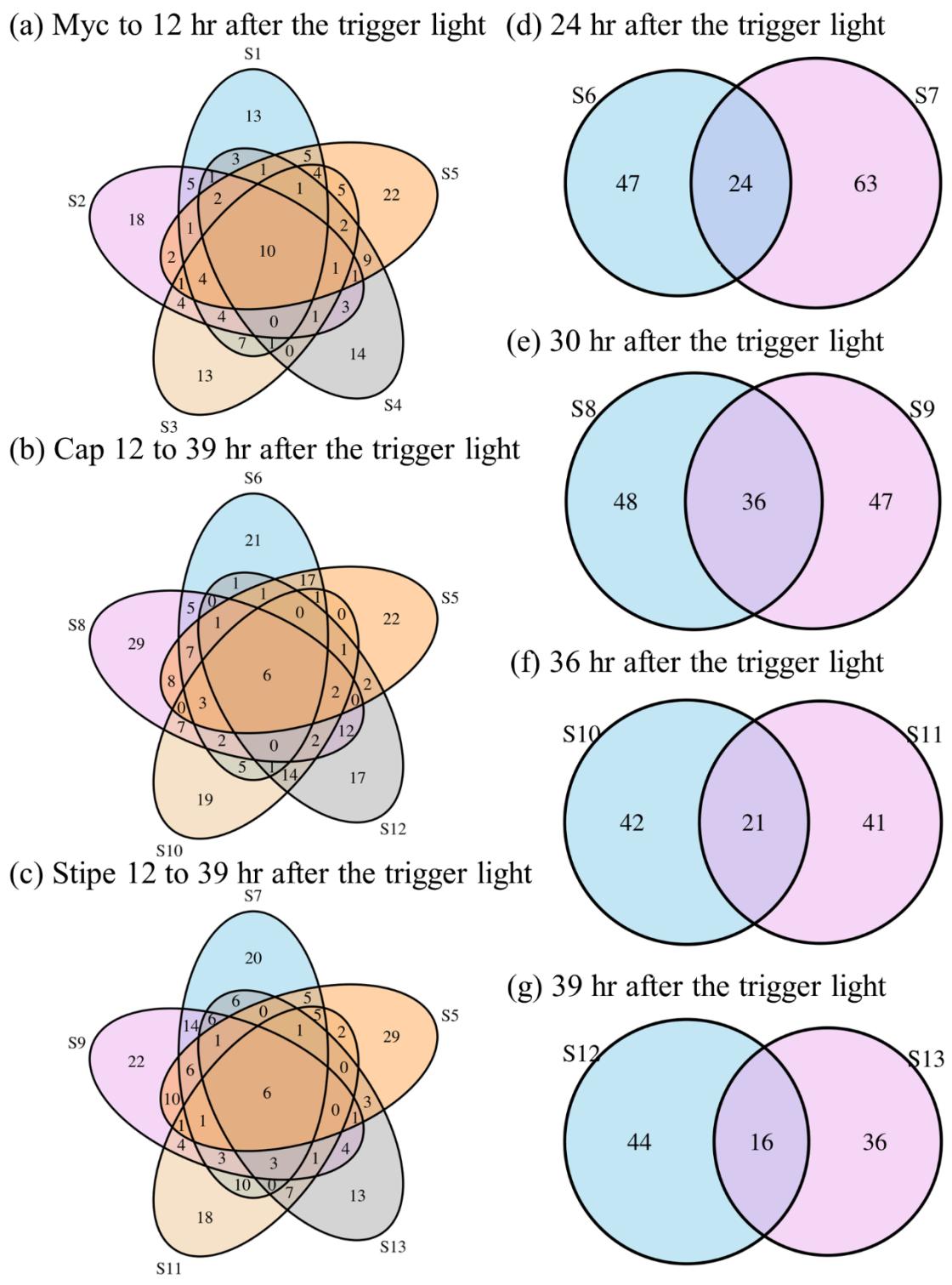
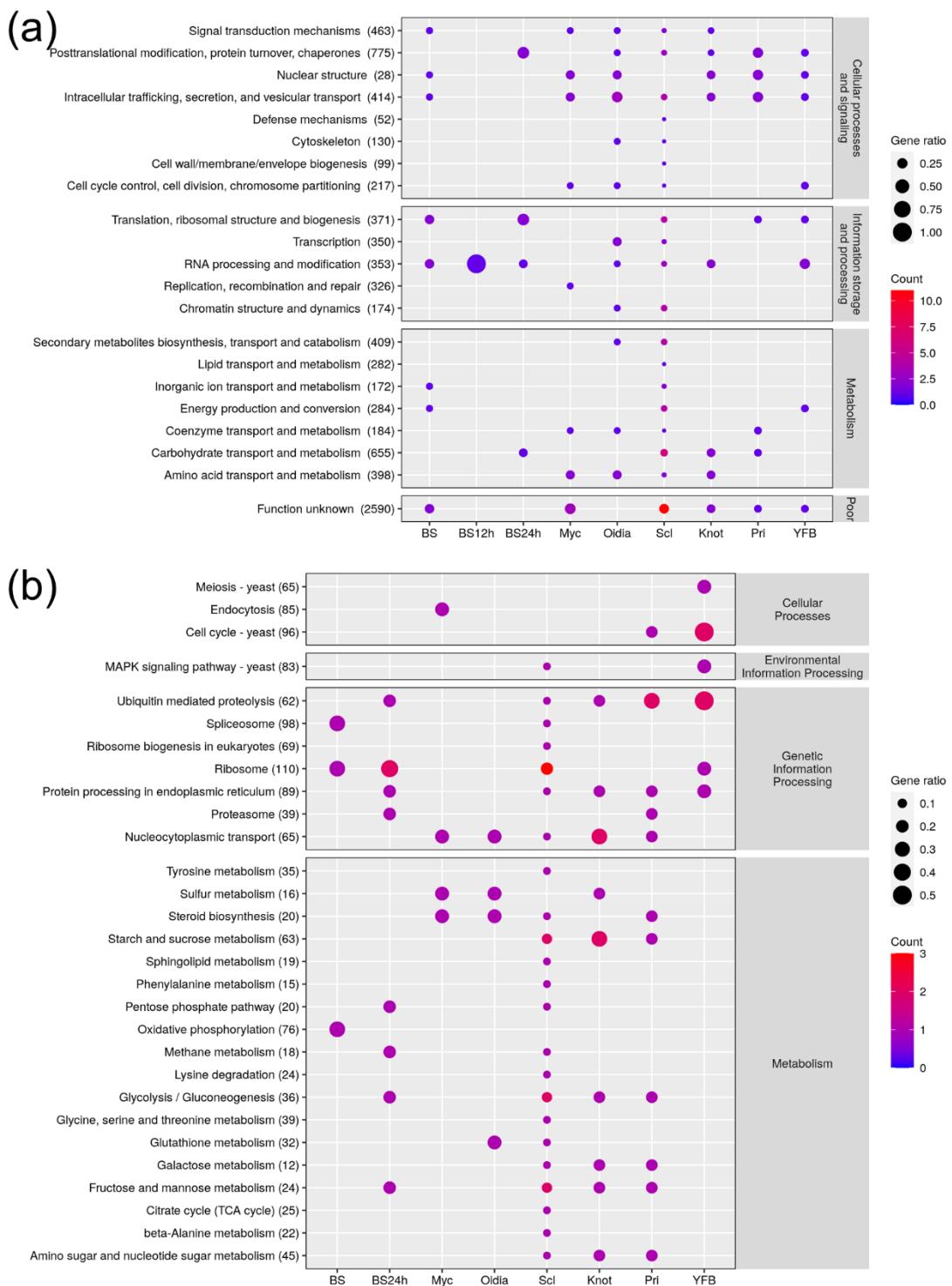


Figure S16. Common RNA editing sites identified from transcriptome data generated by Muraguchi et al. (2015). (a) Vegetative mycelium to fruiting body primordia 12 h; (b) Cap of fruiting body from 12 h to 39 h; (c) Stipe of fruiting body from 12 h to 39 h; (d-g) fruiting body, 24 h/30 h/36 h/39 h after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



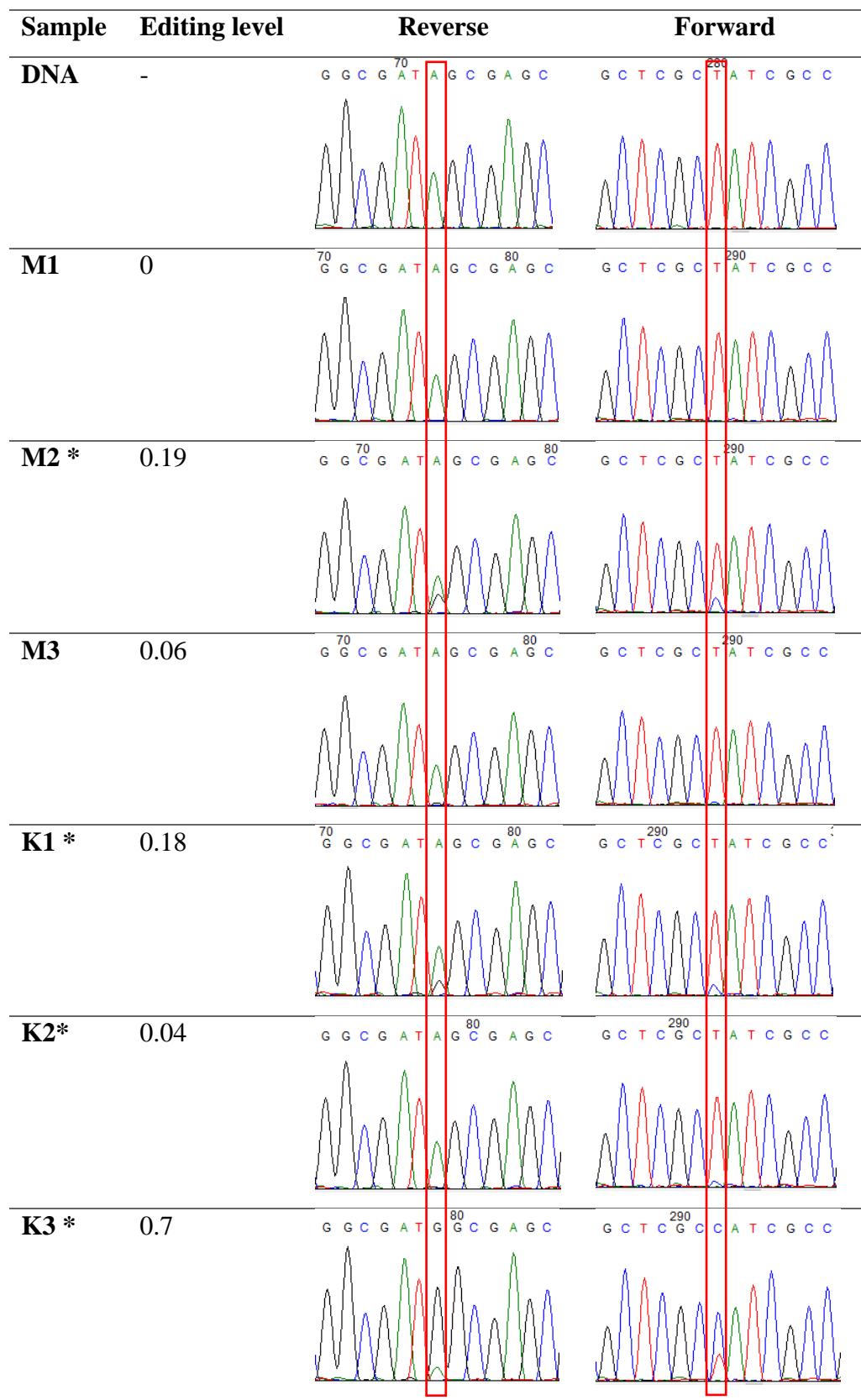
171

172 Figure S17. Functional annotation of genes with RNA editing. Gene ratio is calculated by
 173 annotated genes of specific functional term in each stage over annotated genes of each stage
 174 in the genome background. (a) KOG term annotation; (b) KEGG pathway annotation.

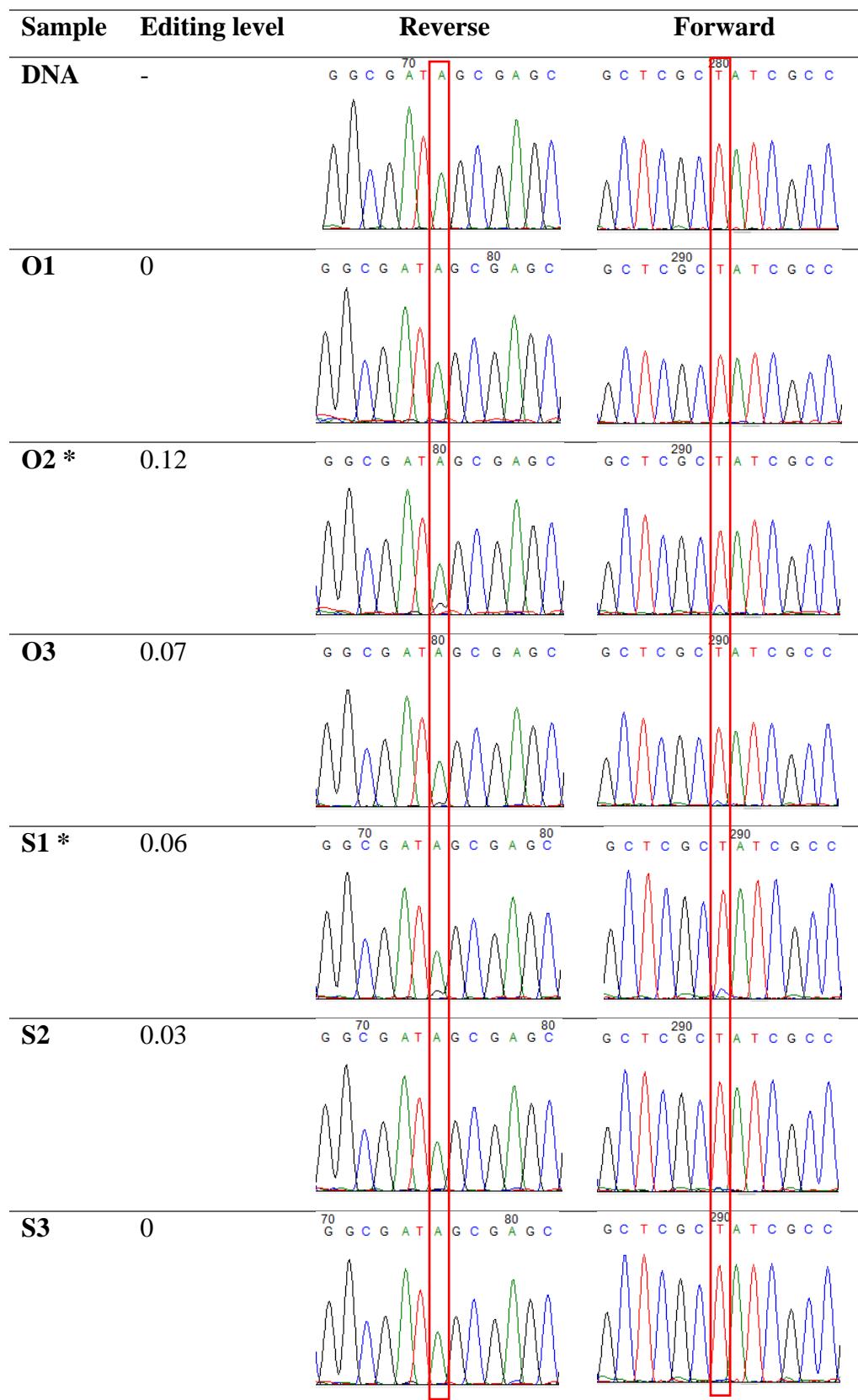


175

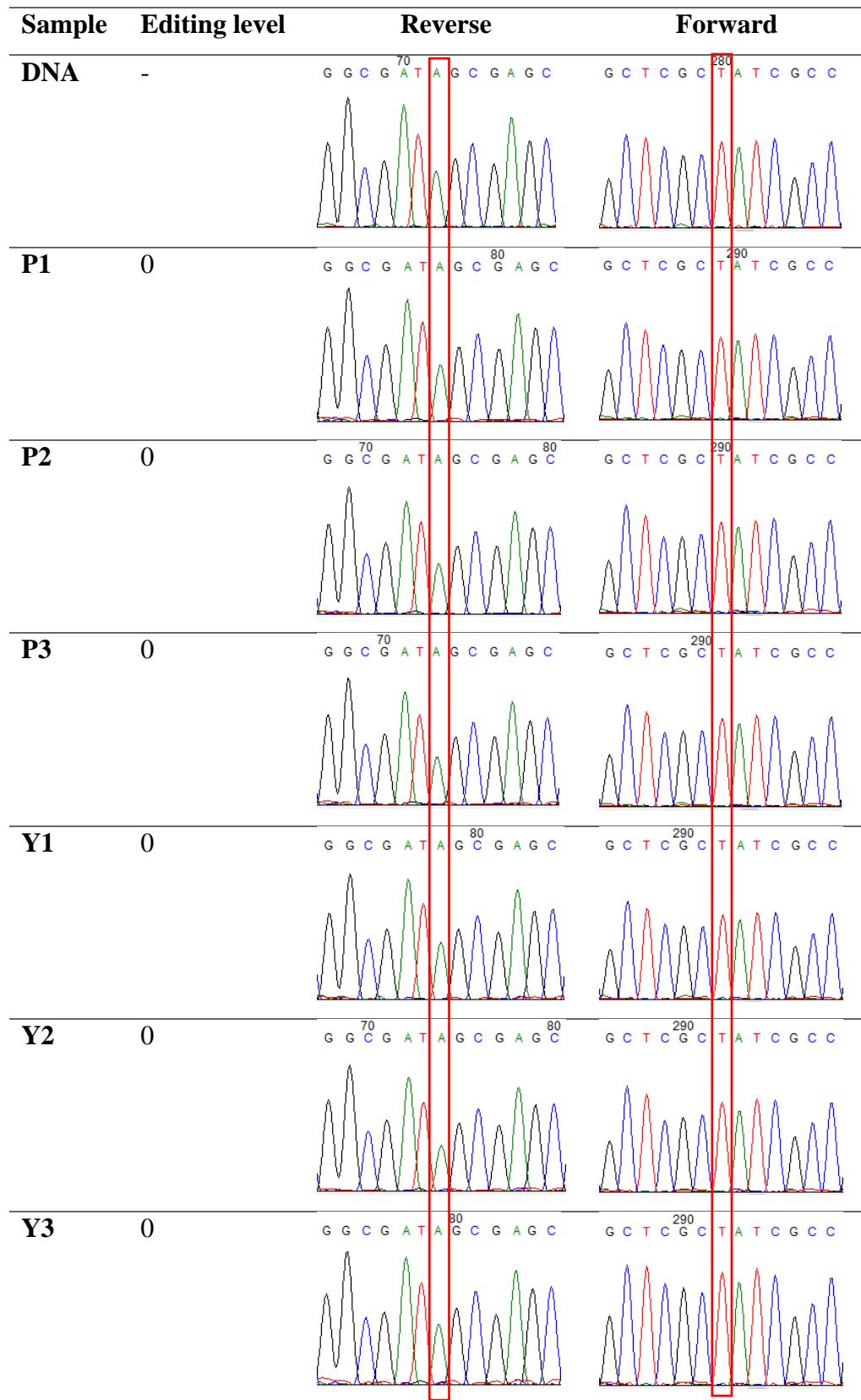
176 Figure S18. KO annotation of genes with RNA editing. Gene ratio is calculated by annotated
 177 genes of specific KO term in each stage over annotated genes of specific KO term in the
 178 genome background. Enriched groups with Benjamini and Hochberg method (BH) adjusted p
 179 value ≤ 0.20 are coloured red to blue.



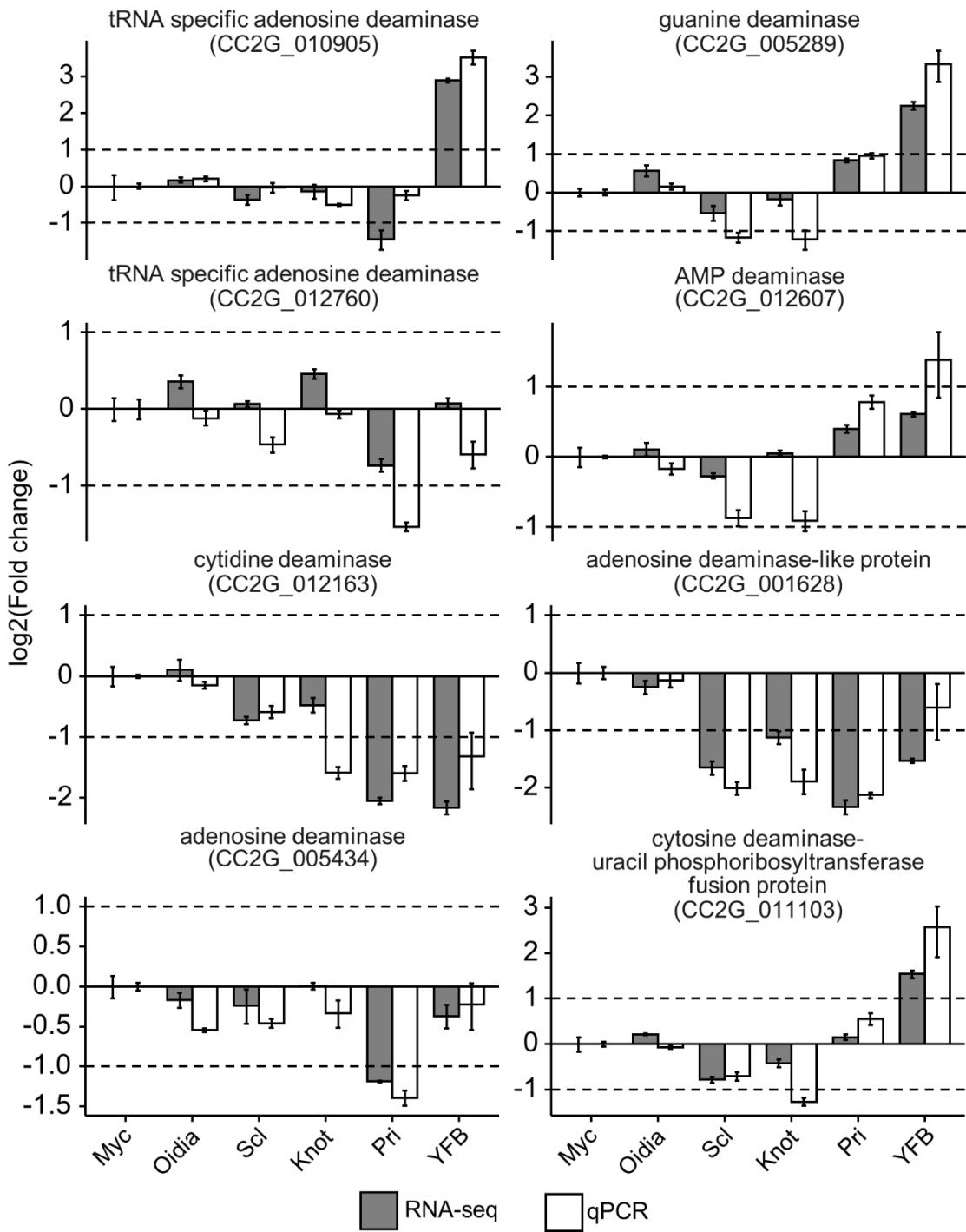
180 Figure S19. Validation of RNA editing on hypothetical protein (CC2G_003350, scaffold_11:
 181 1716350U>C).



182 Figure S19. Validation of RNA editing on hypothetical protein (CC2G_003350, scaffold_11:
 183 1716350U>C), continued.



184 Figure S19. Validation of RNA editing on hypothetical protein (CC2G_003350, scaffold_11:
185 1716350U>C), continued.



186

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