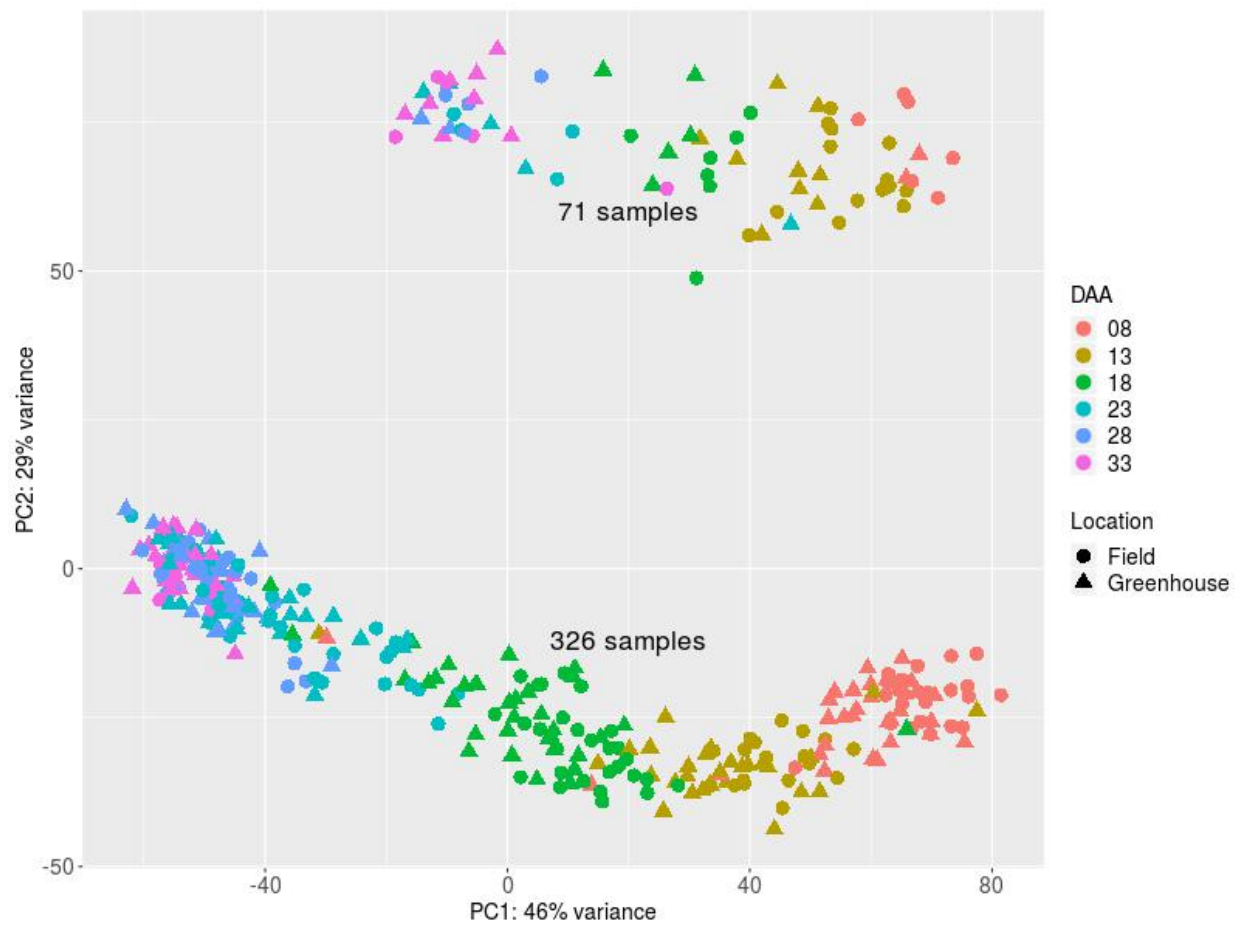1

2 **Figure S1** Transcript length distribution of the 131,457 transcripts included in the RTA

3

Figure S2 PCA plot of 397 samples with more than 0.5 million mapped reads based on the 500 transcripts with highest variance.

8

Figure S3 Distribution of Pearson correlation coefficients of biological replicates from Greenhouse samples, Field samples and among samples across the two sites
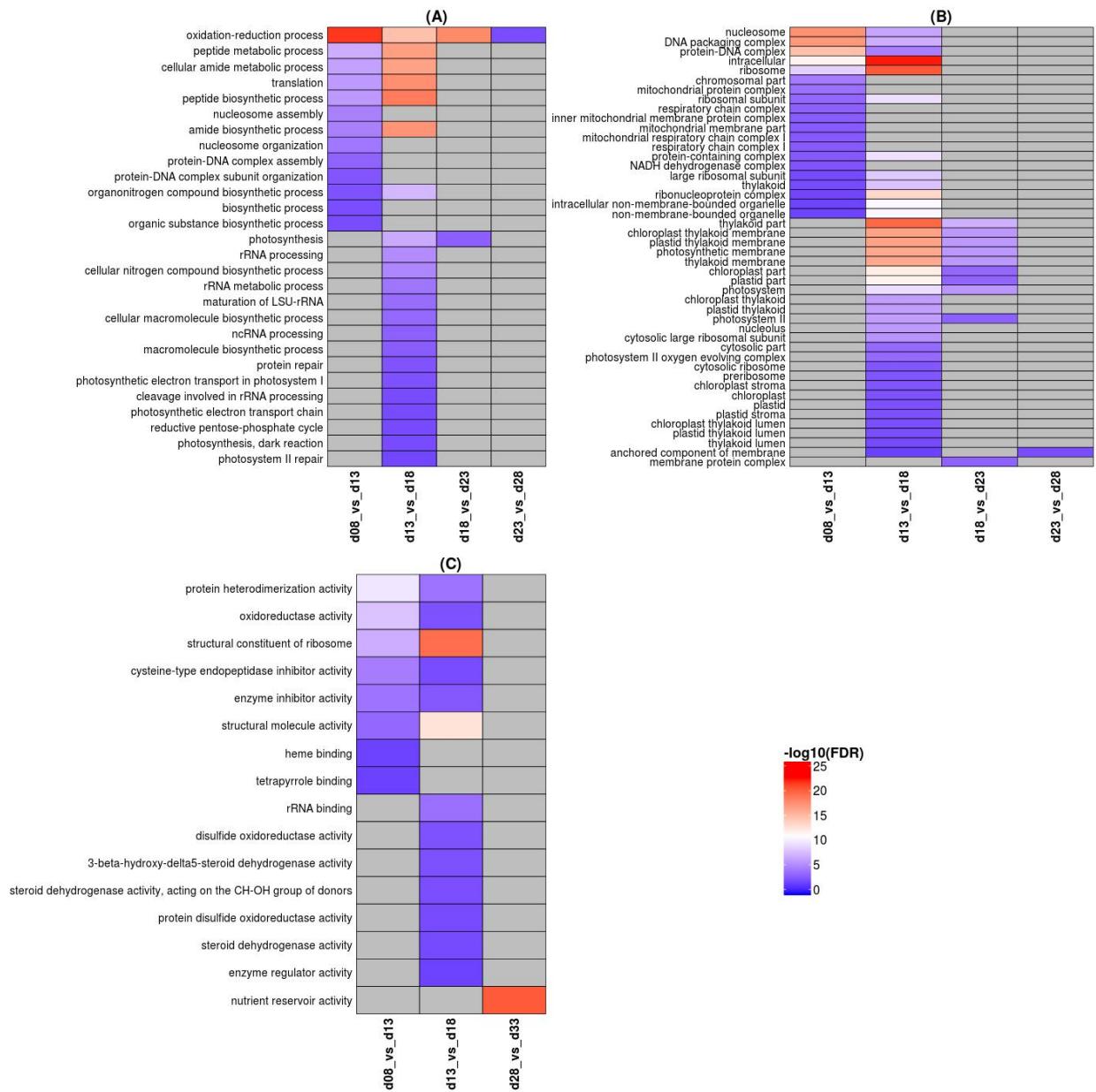
Figure S4 Biological process (A), cellular compartments (B) and molecular function (C) GO terms enriched for differentially expressed transcript sets between adjacent time points. FDR adjusted p-values < 0.01 (in -log10 scale) were colored between blue and red, and cells without GO terms assigned were colored in gray.
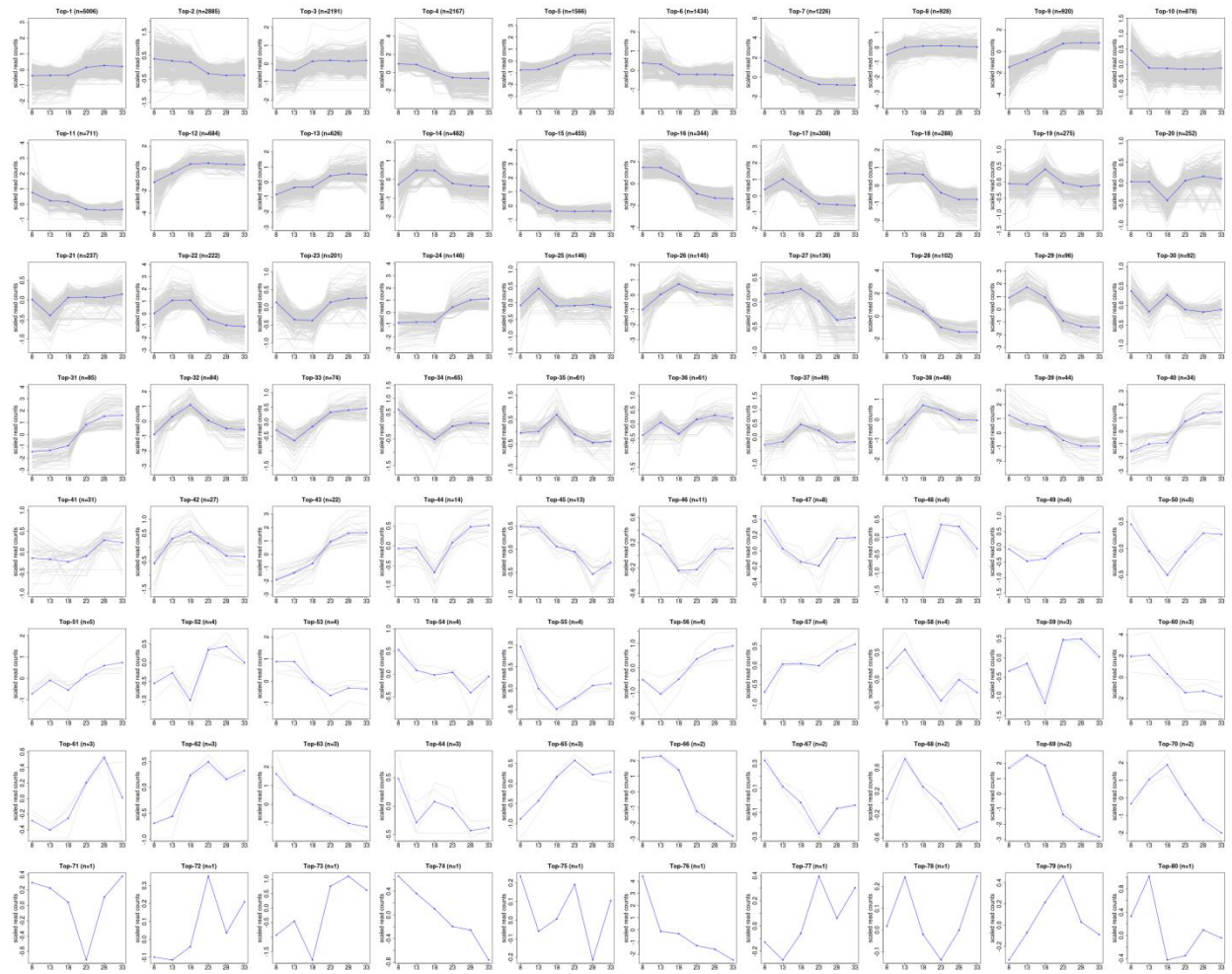
Figure S5 The 80 observed temporal transcript expression patterns identified from 25,971 differentially expressed transcripts between five pairs of adjacent time points
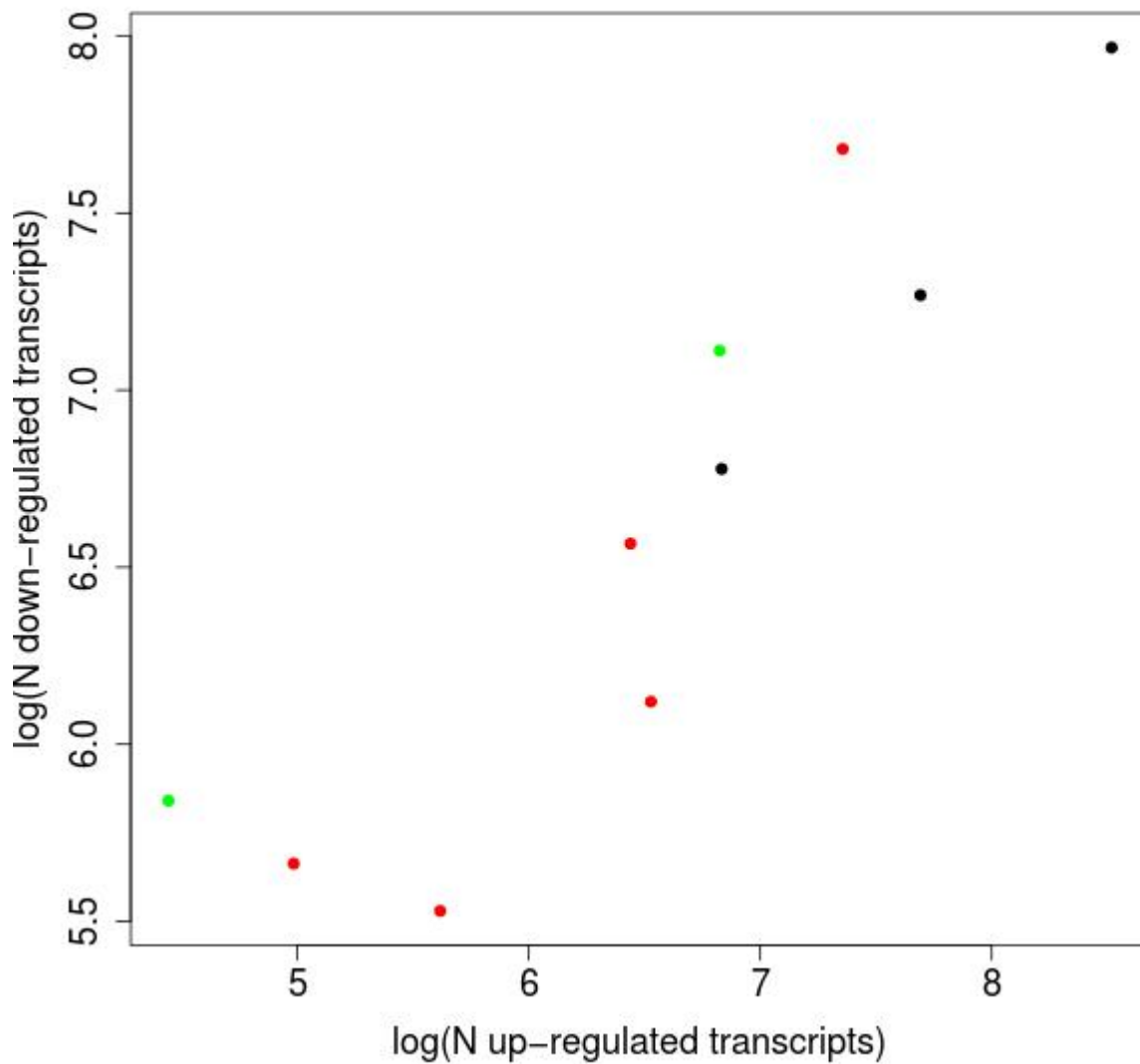
**Figure S6** Correlation of transcript numbers (log scale) between each pair of symmetrical up- and down-regulated expression patterns. Each point represents a pair of symmetrical up- and down-regulated expression patterns. The number of transcripts in the up-regulated pattern on the x-axis and the number of transcript in the down-regulated pattern on the y-axis. Black points have one differential expression event, red points two, and green points three such events.
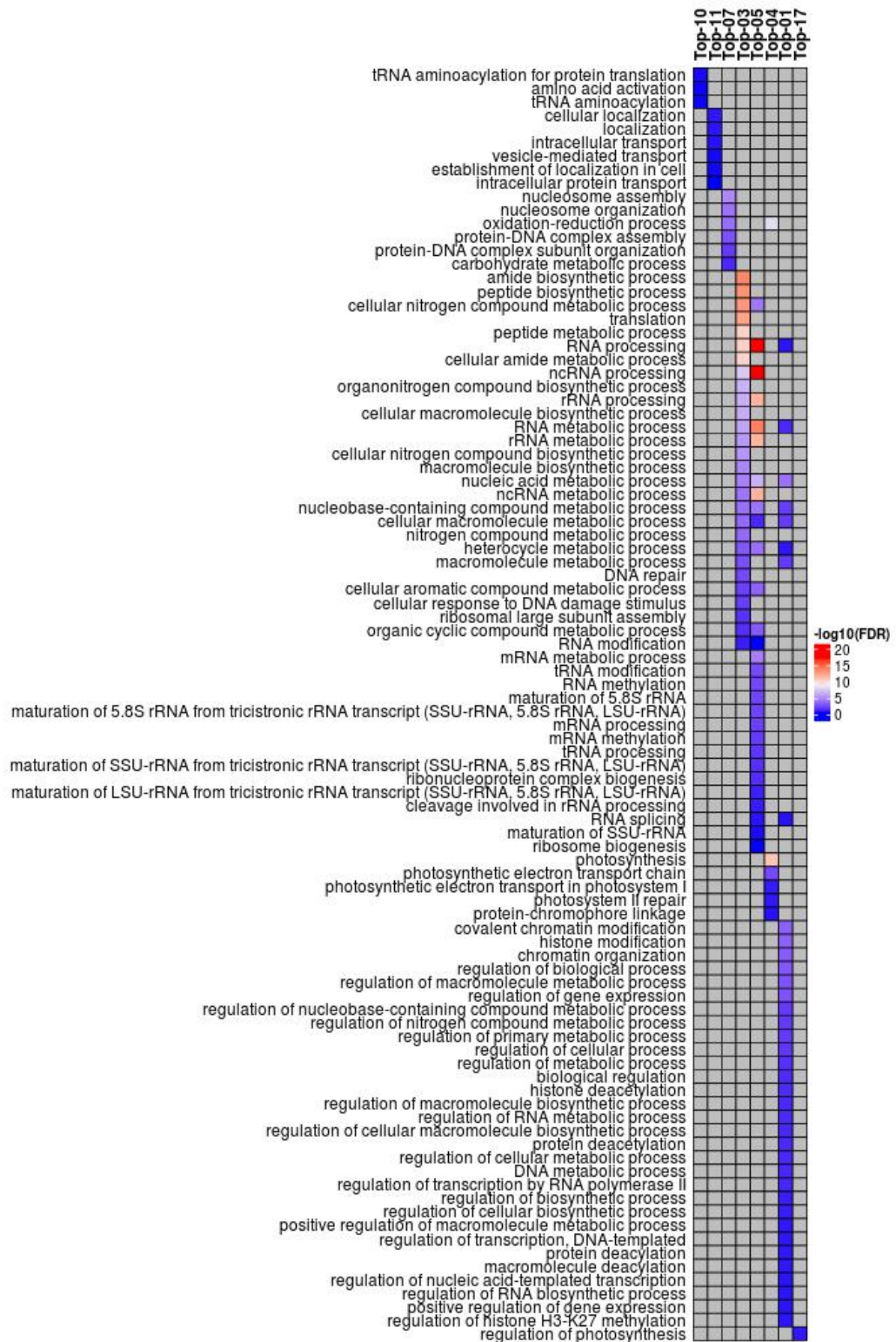
28
Figure S7 GO categories enriched for 8 temporal transcript co-expression sets. FDR adjusted
p-values < 0.01 (in -log10 scale) were colored between blue and red, and cells without GO
terms assigned were colored in gray.

33
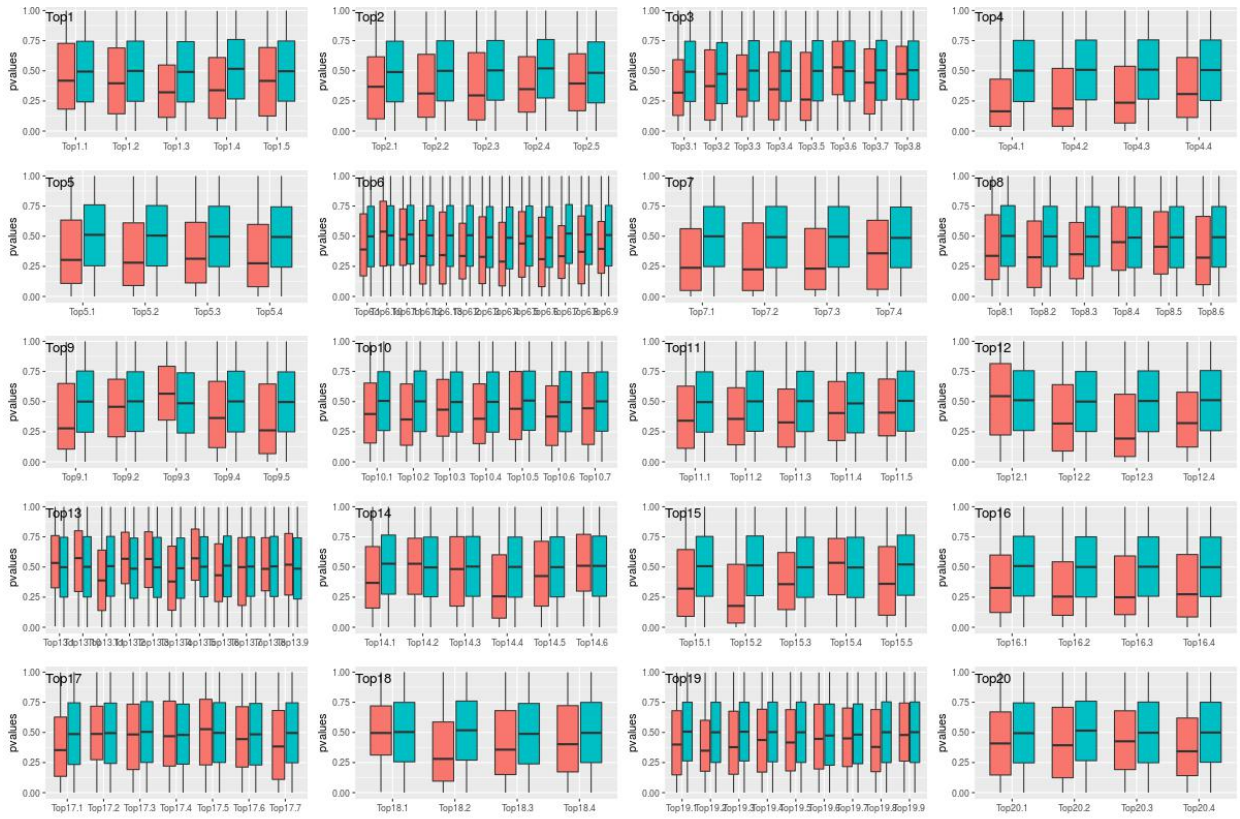
Figure S8 Distribution of P values of simple linear regression between 634 metabolites and PC1 scores of GCoE sets. Red boxes contained p-values from real data, and blue boxes contained p-values from 100 permutations.
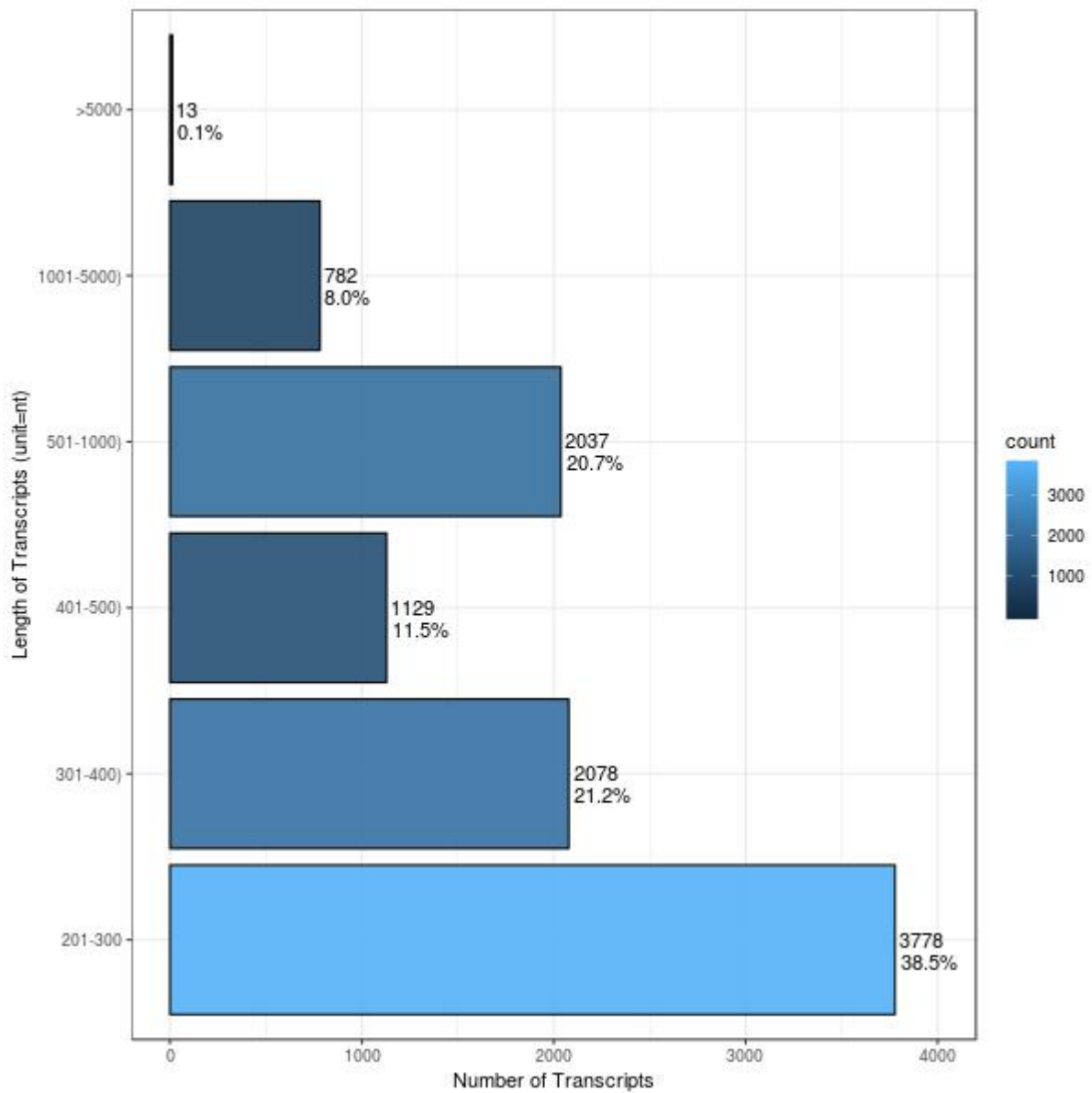
37
Figure S9 Transcript length distribution of the 9,817 transcripts that couldn't be aligned to the
UniRef100
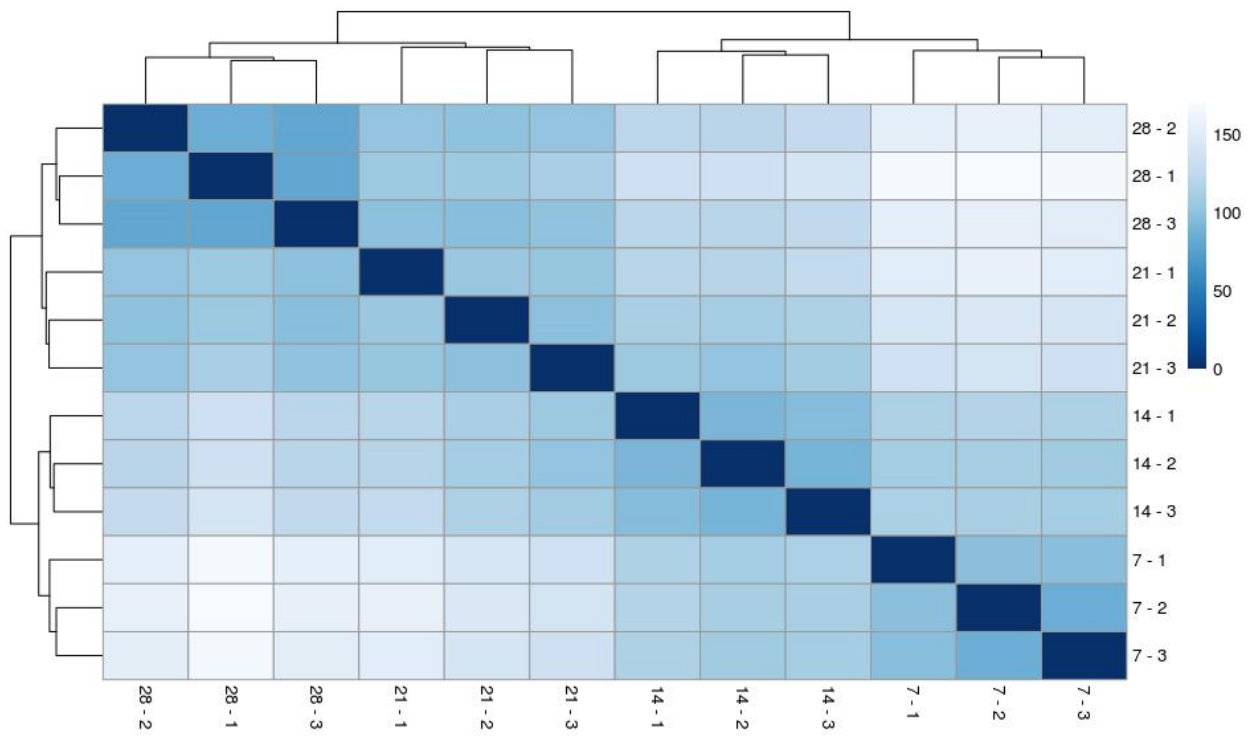
41
42 **Figure S10** clusters of 12 HiSeq samples based on expression profiles. Euclidean distances
43 between samples were colored between dark blue and light blue.
44
45

46
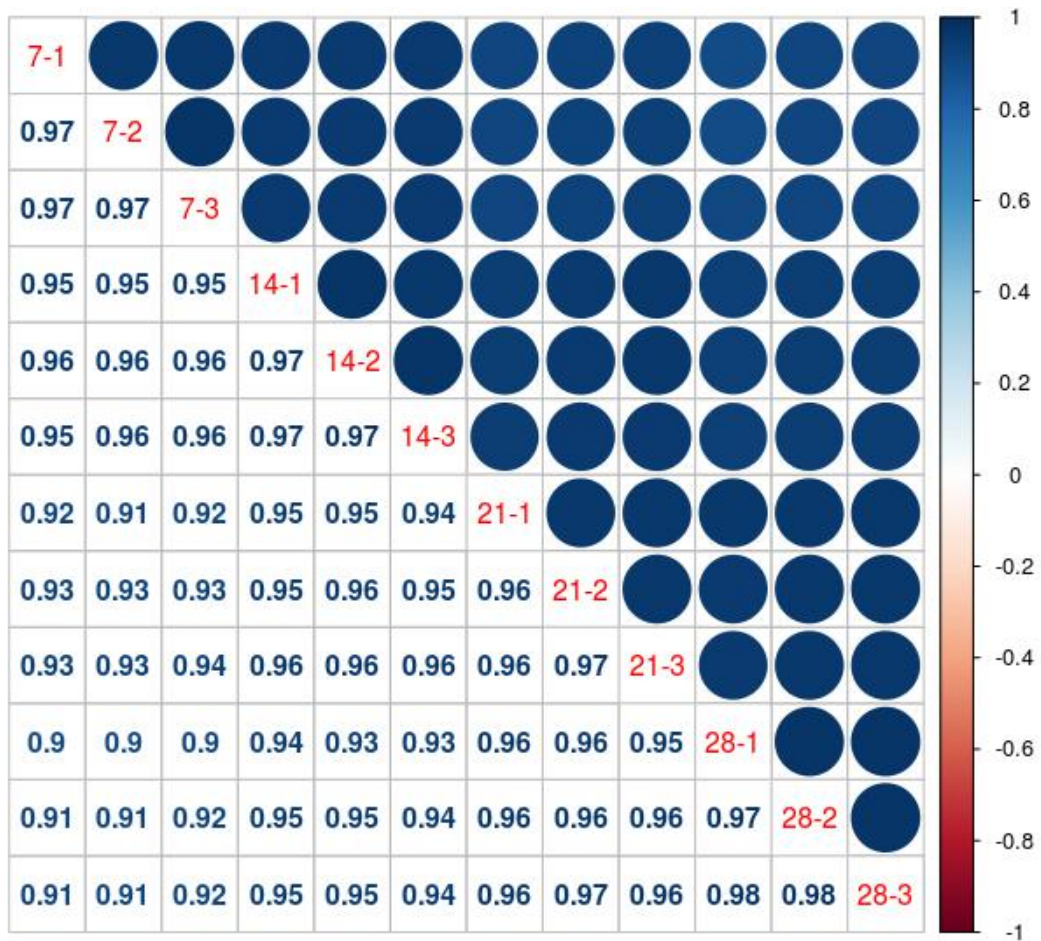
Figure S11 Pearson correlation coefficients of biological replicates from 12 HiSeq samples of
cv.Ogle-C whose developing seeds were collected at 7, 14, 21, and 28 DAA

49
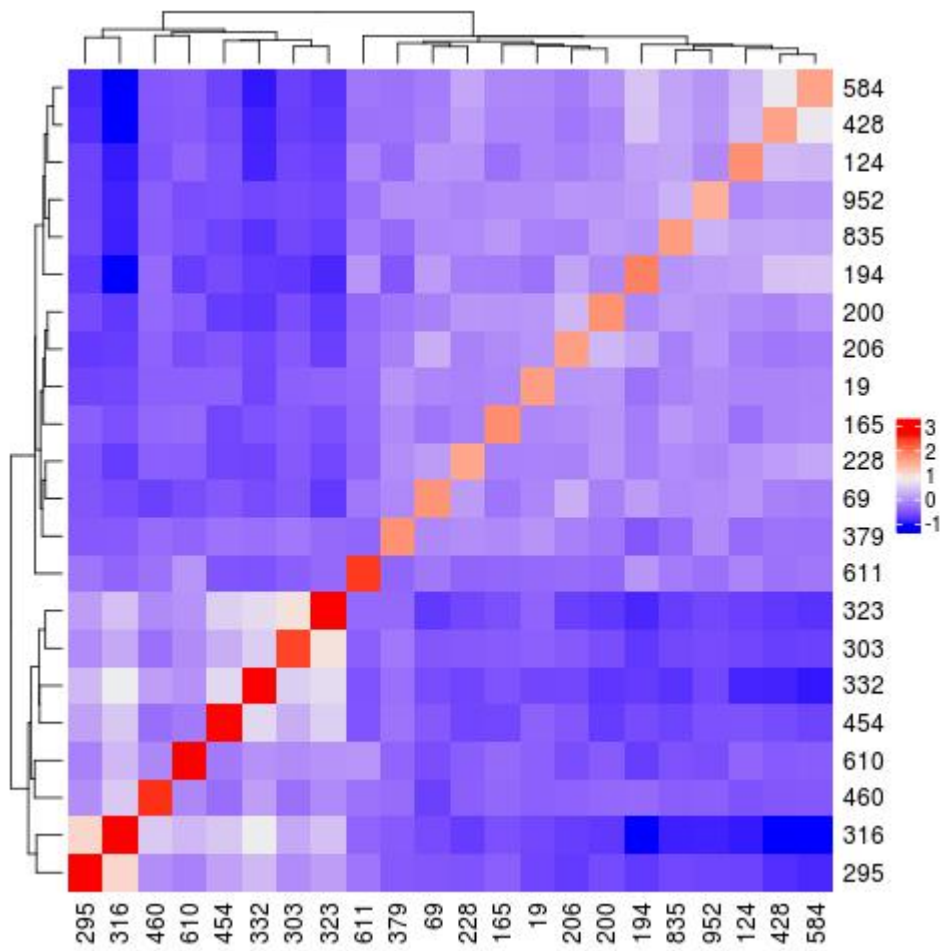
50
51 **Figure S12** Heatmap of genomic relationship among 22 oat lines used in this study

Table S1 A comparison of BUSCOs plant gene completeness between the RTA in this study and the first version of *de novo* oat seed transcriptome assembly (*dn*OST, Gutierrez-Gonzalez et al. 2013)

BUSCO Statistics	the RTA	*dn*OST
Complete BUSCOs	1212 (84.2%)	412 (28.7%)
Complete and single-copy BUSCOs	1188 (82.5%)	116 (8.1%)
Complete and duplicated BUSCOs	24 (1.7%)	296 (20.6%)
Fragmented BUSCOs	148 (10.3%)	201 (14.0%)
Missing BUSCOs	80 (5.5%)	827 (57.3%)
Total BUSCO groups searched	1440	1440

57 **Table S2** Chi-Square test for sub-cluster size distribution of the 22 temporal co-expression sets.

58 At significant level of 0.05, the critical p-value after Bonferroni correction is 0.05/22=0.00227.

59

Temporal co-expression set*	P-value
Top-8	0.994548451
Top-10	0.999286221
Top-12	0.497109215
Top-15	0.003939038
Top-13	0.108831006
Top-11	0.344207141
Top-9	0.380203442
Top-7	0.608797221
Top-3	0.895528366
Top-6	0.419936316
Top-5	0.273601551
Top-4	0.594794097
Top-31	0.021221027
Top-16	0.133281338
Top-1	0.637929437
Top-2	0.83840654
Top-24	0.744979403
Top-18	0.210760149
Top-19	0.980442768
Top-20	0.35296887
Top-14	0.962213032
Top-17	0.549011073

60 *The temporal co-expression sets were ordered the same as in Figure 4.

Genename	Source	Transcript name	reference	query_len[a]	ref_len[b]	aln_length[c]	pct_ident[d]
Avenanthramides biosynthetic genes							
CCoA3H	Arabidopsis	TRINITY_DN6473_c0_g1_i1	NM_180006.2	1942	1885	1362	67.621
CCoA3H	Brachypodium	TRINITY_DN6473_c0_g1_i1	KQK05634	1942	2031	1954	86.131
CCoAOMT	Oat	TRINITY_DN3508_c0_g1_i7	AB076979.1	1238	622	604	99.834
HHT1	Oat	TRINITY_DN5172_c0_g1_i4	AB076980.1	1598	1755	1343	79.449
HHT2	Oat	TRINITY_DN5172_c0_g1_i4	AB076981.1	1598	1770	1343	78.555
HHT3	Oat	TRINITY_DN5172_c0_g1_i4	AB076982.1	1598	1659	1343	79.598
HHT4	Oat	TRINITY_DN5172_c0_g1_i4	AB076983.1	1598	1100	1088	97.151
Fatty Acids biosynthetic genes							
ACCase	Brachypodium	TRINITY_DN146_c0_g1_i8	BRADI_5g03860	7812	8783	7598	88.694
DGAT1/TAG1	Brachypodium	TRINITY_DN151_c0_g1_i4	BRADI_1g37750	2878	3009	925	72.757
FAB1/KAS2	Brachypodium	TRINITY_DN207_c0_g1_i1	BRADI_1g60300	2876	2498	1851	87.088
FAB2	Brachypodium	TRINITY_DN2740_c0_g1_i5	BRADI_2g58930	5078	1792	1610	86.957
FAD2	Brachypodium	TRINITY_DN268_c0_g1_i4	BRADI_3g53370	1883	2351	1665	85.526
FAD3	Brachypodium	TRINITY_DN10818_c0_g1_i3	BRADI_1g65580	1198	2817	1195	82.343
FAE1/KCS18	Brachypodium	TRINITY_DN1011_c0_g1_i5	BRADI_2g16050	1990	2481	1447	81.064
FATB	Brachypodium	TRINITY_DN2629_c0_g1_i1	BRADI_1g51170	2394	4407	1368	88.085
GPAT9	Brachypodium	TRINITY_DN5048_c0_g1_i7	BRADI_1g25790	1490	1540	1460	86.37
LPCAT1	Brachypodium	TRINITY_DN3352_c0_g1_i1	BRADI_3g51577	1846	1671	1634	88.433
PAH1	Brachypodium	TRINITY_DN1042_c0_g1_i6	BRADI_2g23040	4252	4162	2485	82.817
PDAT1	Brachypodium	TRINITY_DN2921_c0_g1_i1	BRADI_4g31540	2494	2601	2531	86.448
WRI1	Brachypodium	TRINITY_DN331_c0_g1_i1	BRADI_4g43877	3900	2035	1223	80.376

63 [a]query_len= query sequence length;

64 [b]ref_len = reference sequence length;

65 [c]aln_length= alignment length;

66 [d]pct_ident= percent identity