



Supplementary data

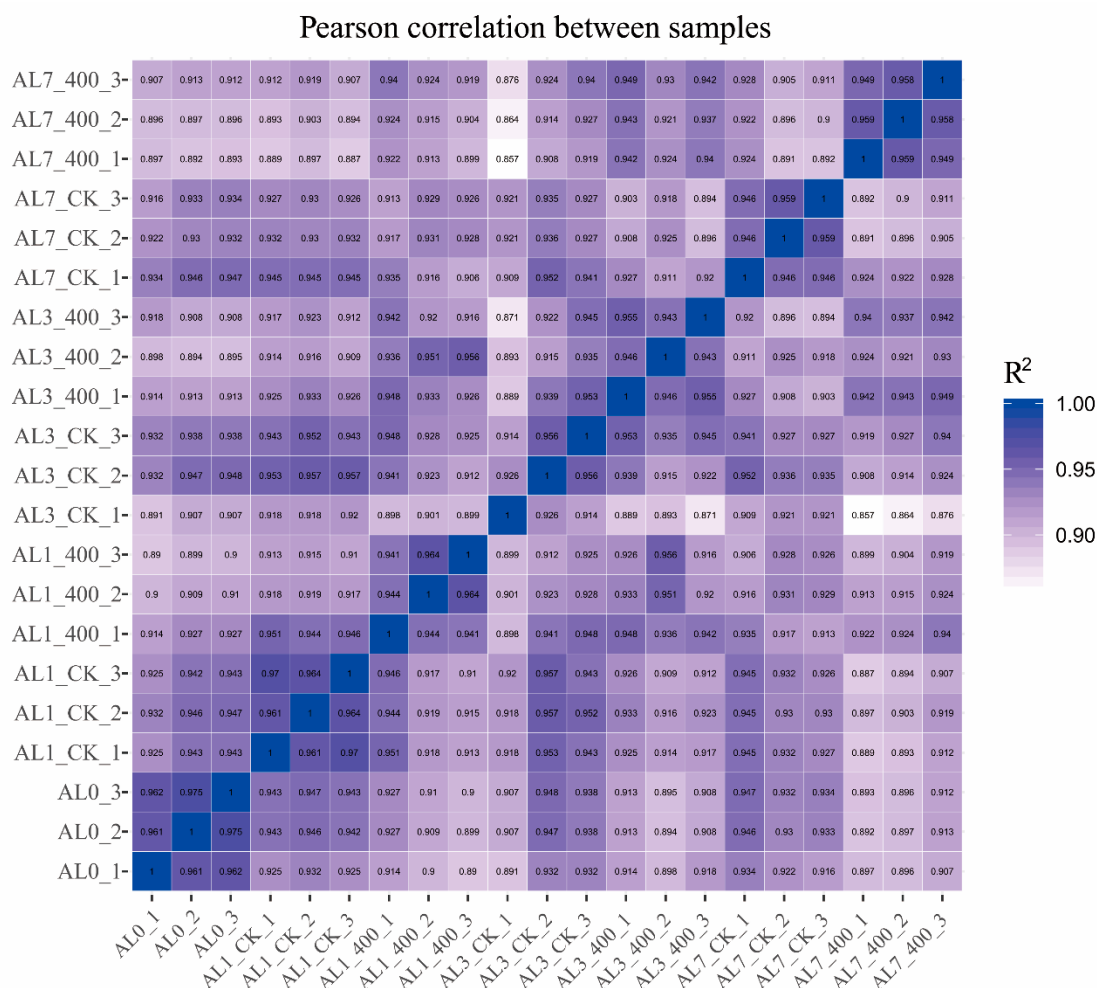
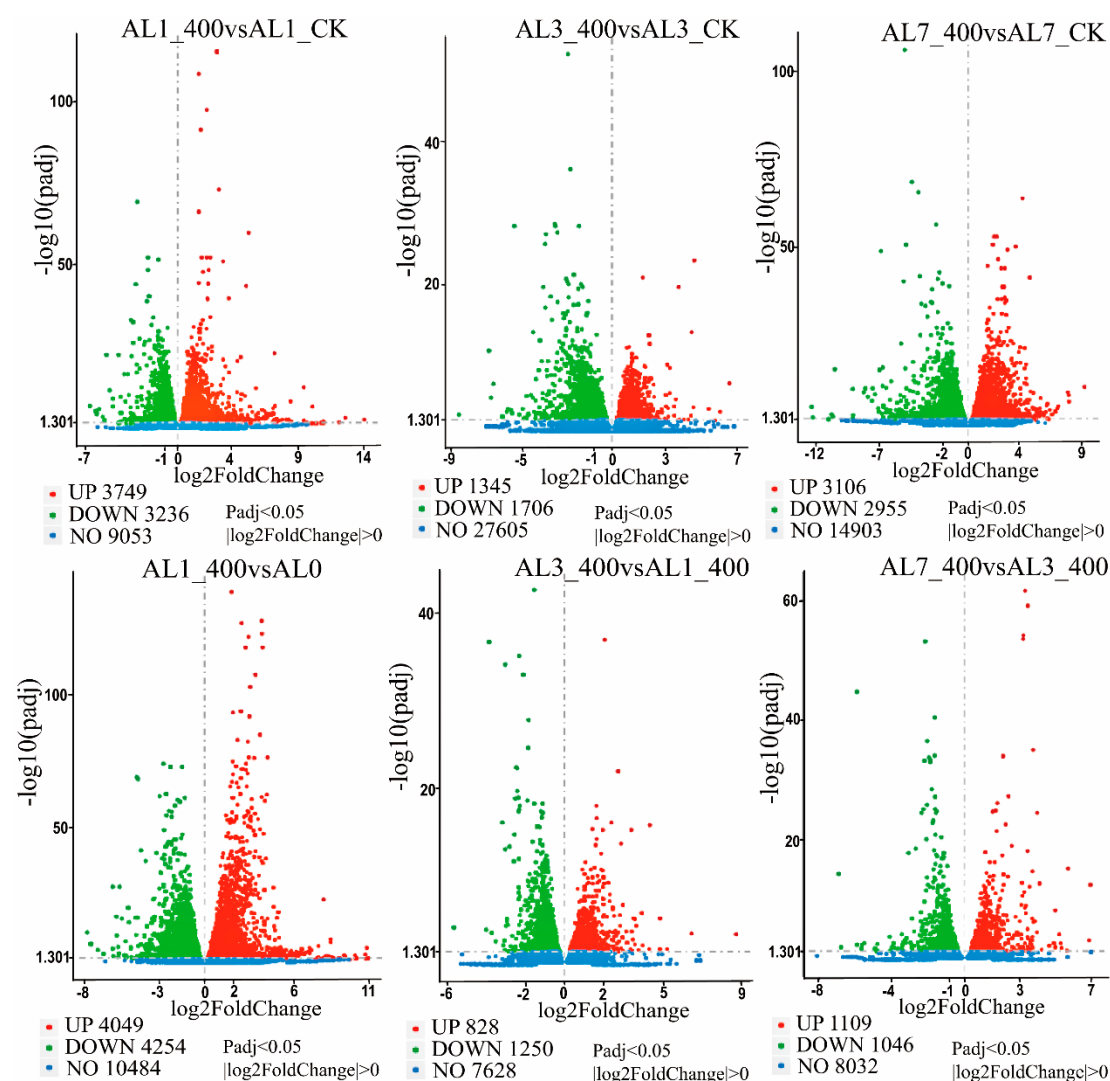


Figure Supplementary 1. Pearson correlation between samples. Taking the square of the Pearson correlation coefficient (R^2) greater than 0.92 (under ideal sampling and experimental conditions), in specific project operations, R^2 is required to be at least greater than 0.8 as the test index for the correlation of gene expression levels between samples, thereby verifying the reliability of the experiment and strictness of sample selection. The closer the correlation coefficient is to 1, the higher the similarity of the expression patterns between samples. The abscissa and ordinate are the log10 (FPKM+1) of the compared samples, and the ordinate is the sample type.



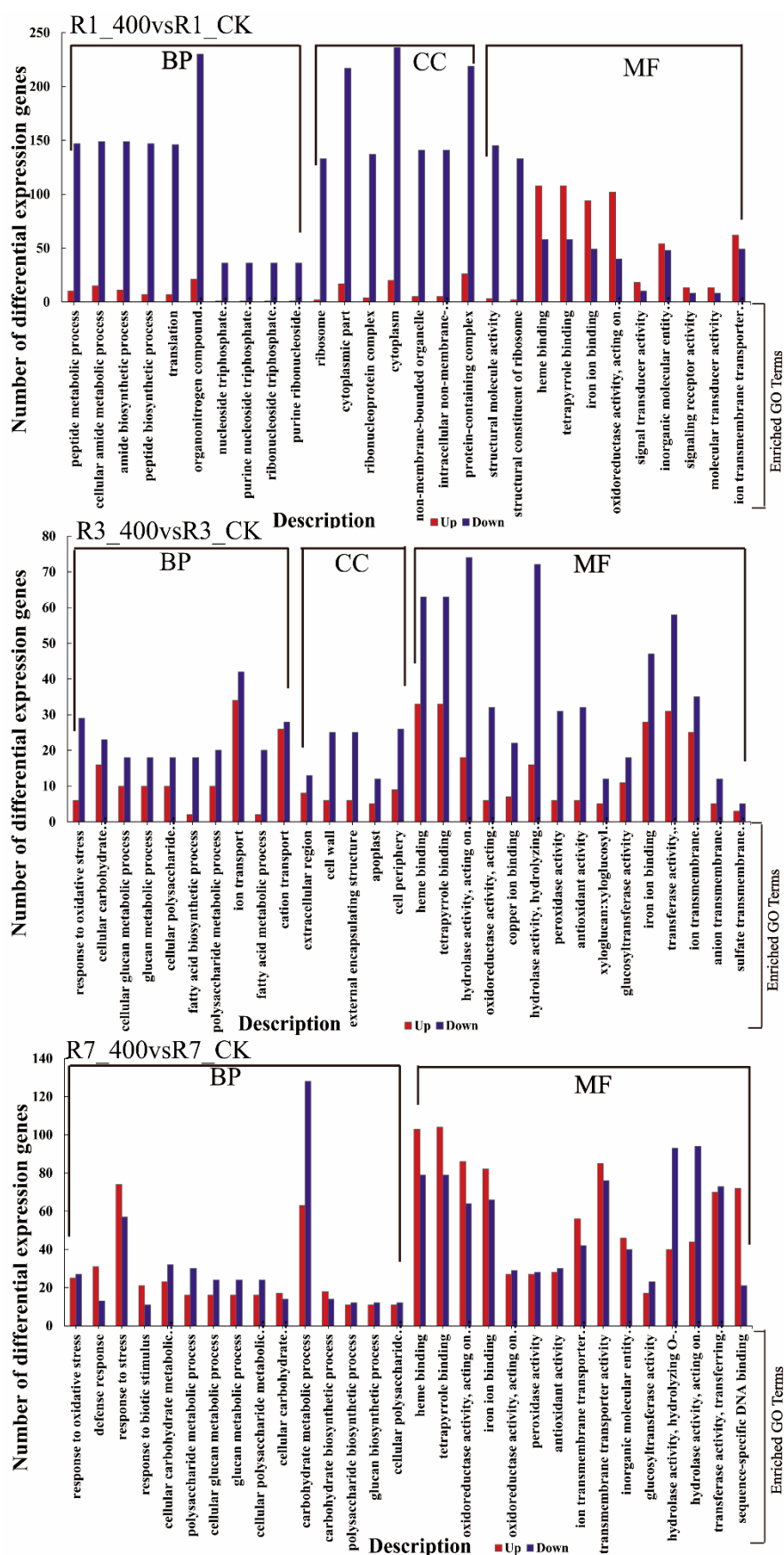


Figure Supplementary 3. GO enrichment of three comparative combinations of aluminum stress in different periods. The DEGs in the first 10 pathways that were significantly enriched in different periods of aluminum stress were screened, and all DEGs in less than 10 pathways were displayed. The abscissa represents the different GO term enriched genes, the ordinate represents the number of

DEGs. The red bar represents the up-regulated genes, the blue bar represents the down-regulated genes. BP represents DEGs enriched in biological processes, MF represents DEGs enriched in molecular functions, and CC represents DEGs enriched in cellular component.

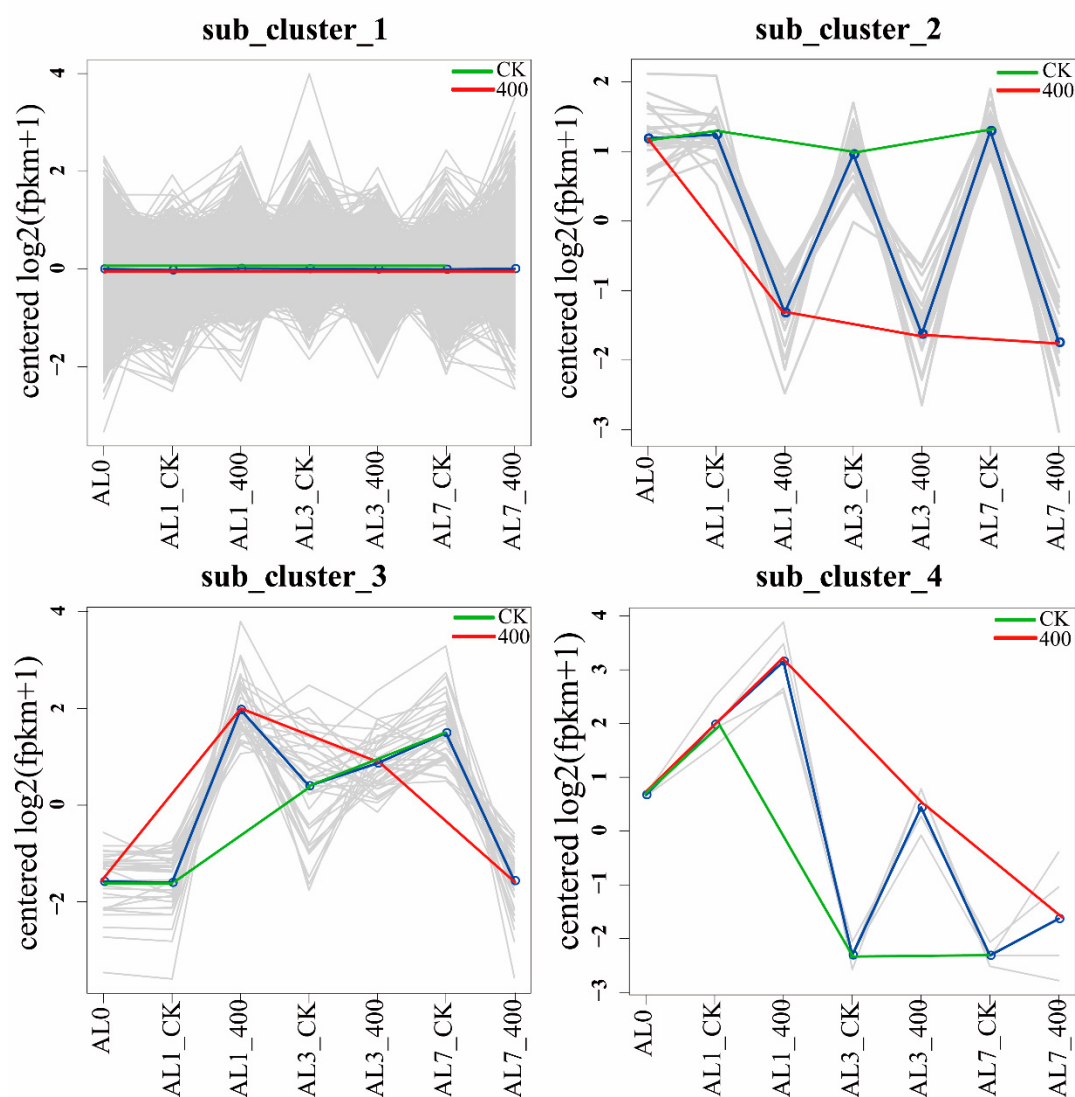


Figure Supplementary 4. Trend clustering of DEGs. The green lines indicate the trend of gene clustering in the control group; the red lines indicate the trend of gene clustering in the treatment group; the blue line shows the average relative expression of all genes in this cluster under different experimental conditions; The gray lines in each subgraph represent a line chart of the relative expression of genes in a cluster under different experimental conditions.

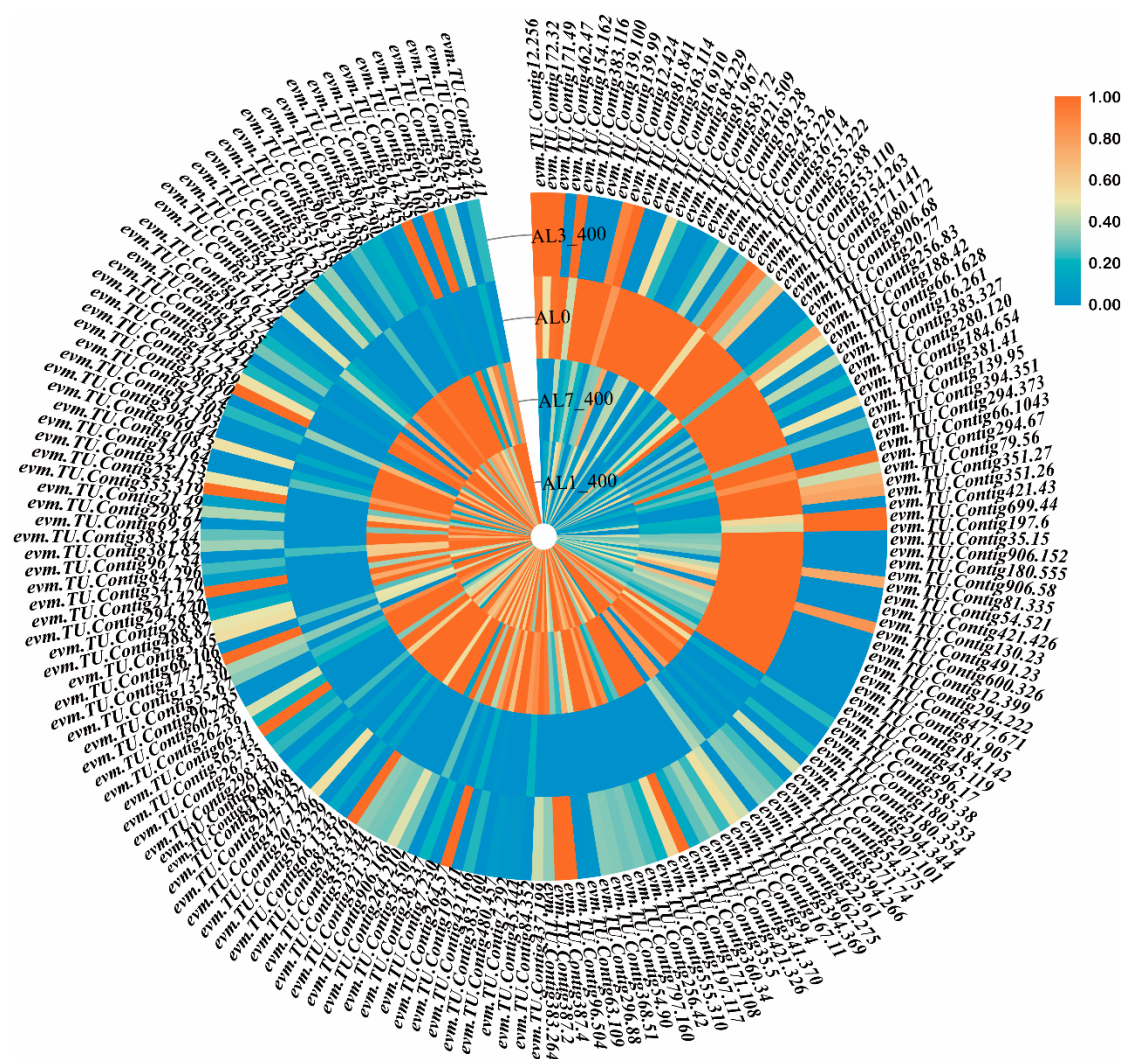


Figure Supplementary 5. Heat map of DEGs expression in response to aluminum stress in various periods. The FDR ($FDR < 0.05$) and the fold change ($|\log_2(\text{FoldChange})| > 1$) were used as the differential gene screening threshold to compare the changes of differential gene expression between different the treatment groups and control group on the 1st day.

Table Supplementary 1. Quality evaluation of sequencing data

Sample name	Raw reads	Clean reads	clean bases	Error rate(%)		GC content(%)	
				Q20(%)	Q30(%)		
AL0_1	61194292	60187436	9.03G	0.02	98.36	94.76	43.64
AL0_2	68003714	66818940	10.02G	0.02	98.17	94.29	43.69
AL0_3	63752868	62619194	9.39G	0.02	98.41	94.88	43.58
AL1_CK_1	68026854	66863458	10.03G	0.02	98.3	94.58	43.52
AL1_CK_2	60377232	59463000	8.92G	0.02	98.26	94.51	43.58
AL1_CK_3	55716572	54928798	8.24G	0.03	98.03	93.92	43.53
AL1_400_1	70108628	68863288	10.33G	0.03	96.8	91.39	43.33
AL1_400_2	56905498	56051598	8.41G	0.02	98.28	94.59	43.45
AL1_400_3	66808072	65804690	9.87G	0.03	96.73	91.26	43.32
AL3_CK_1	60255320	59122780	8.87G	0.02	98.27	94.52	43.66
AL3_CK_2	51855712	50304222	7.55G	0.02	98.25	94.47	43.66
AL3_CK_3	55026252	53363844	8.0G	0.03	96.96	91.71	43.44
AL3_400_1	56693196	55530186	8.33G	0.02	98.31	94.62	43.55
AL3_400_2	61127434	59615668	8.94G	0.03	97.37	92.49	43.41
AL3_400_3	60287314	59056562	8.86G	0.02	98.4	94.87	43.55
AL7_CK_1	64215260	62625458	9.39G	0.02	98.27	94.51	43.49
AL7_CK_2	54868194	52896640	7.93G	0.03	96.98	91.72	43.4
AL7_CK_3	64744542	63356668	9.5G	0.03	98.06	93.98	43.65
AL7_400_1	66694232	65272288	9.79G	0.02	98.45	94.95	44.23
AL7_400_2	46326344	43991788	6.6G	0.02	98.45	95.03	43.73
AL7_400_3	66692556	65368558	9.81G	0.02	98.29	94.52	43.78

The number of reads in the raw data; clean_reads: the number of reads filtered from the original data; clean_bases: the number of bases filtered from the original data; error_rate: error rate of overall data sequencing; Q20: the percentage of bases with a Phred value greater than 20 to the total base; Q30: the percentage of

bases with a Phred value greater than 30 in the total base; GC content: the percentage of G and C in four bases in clean reads.

Table Supplementary 2. Statistics on the alignment of lean reads and reference genomes

Sample name	total_reads	total_map	unique_map	multi_map	read1_map	read2_map
AL0_1	60187436	56418328(93.74%)	54541126(90.62%)	1877202(3.12%)	27323351(45.4%)	27217775(45.22%)
AL0_2	66818940	62458819(93.47%)	60330247(90.29%)	2128572(3.19%)	30256890(45.28%)	30073357(45.01%)
AL0_3	62619194	58666811(93.69%)	56687286(90.53%)	1979525(3.16%)	28388327(45.33%)	28298959(45.19%)
AL1_CK_1	66863458	63613029(95.14%)	61621016(92.16%)	1992013(2.98%)	30873659(46.17%)	30747357(45.99%)
AL1_CK_2	59463000	55711716(93.69%)	53945557(90.72%)	1766159(2.97%)	27030193(45.46%)	26915364(45.26%)
AL1_CK_3	54928798	51970207(94.61%)	50381570(91.72%)	1588637(2.89%)	25283906(46.03%)	25097664(45.69%)
AL1_400_1	68863288	64624456(93.84%)	62560046(90.85%)	2064410(3.0%)	31438883(45.65%)	31121163(45.19%)
AL1_400_2	56051598	53231186(94.97%)	51505558(91.89%)	1725628(3.08%)	25810115(46.05%)	25695443(45.84%)
AL1_400_3	65804690	61894880(94.06%)	59857820(90.96%)	2037060(3.1%)	30074252(45.7%)	29783568(45.26%)
AL3_CK_1	59122780	56202972(95.06%)	54270913(91.79%)	1932059(3.27%)	27201549(46.01%)	27069364(45.78%)
AL3_CK_2	50304222	47146214(93.72%)	45595077(90.64%)	1551137(3.08%)	22851487(45.43%)	22743590(45.21%)
AL3_CK_3	53363844	49968720(93.64%)	48323788(90.56%)	1644932(3.08%)	24267845(45.48%)	24055943(45.08%)
AL3_400_1	55530186	52779055(95.05%)	51110254(92.04%)	1668801(3.01%)	25601973(46.1%)	25508281(45.94%)
AL3_400_2	59615668	56260050(94.37%)	54480814(91.39%)	1779236(2.98%)	27315745(45.82%)	27165069(45.57%)
AL3_400_3	59056562	55828623(94.53%)	54050775(91.52%)	1777848(3.01%)	27061792(45.82%)	26988983(45.7%)
AL7_CK_1	62625458	58136633(92.83%)	56212441(89.76%)	1924192(3.07%)	28166155(44.98%)	28046286(44.78%)
AL7_CK_2	52896640	49258323(93.12%)	47633351(90.05%)	1624972(3.07%)	23889000(45.16%)	23744351(44.89%)
AL7_CK_3	63356668	59346469(93.67%)	57330146(90.49%)	2016323(3.18%)	28760173(45.39%)	28569973(45.09%)

Total_reads : clean reads number of sequencing data after quality control;
total_map : compare the number and percentage of reads on the genome;
multi_map: the number and percentage of reads mapped to multiple locations of the reference genome; unique_map: the number and percentage of reads compared to the unique location of the reference genome; read1_map: the number and percentage of read1 compared to the reference genome; read2_map: the number and percentage of read2 compared to the reference genome.

Table Supplementary 3. Primer pairs used to verify gene fluorescence quantification

Genes	Forward Primer (5' - 3')	Reverse Primer (5' - 3')
<i>evm.TU.Contig491.4</i>	CTTGGCTCCGTTGTTGCTTG	AAGTTGCCCCCTCTTTGGGTC
<i>evm.TU.Contig368.51</i>	AGGCAGCATTGAACCCTGAT	AGCCCTCATCCTGCCAATTC
<i>evm.TU.Contig81.157</i>	TGCGAAAAGCGACAAATCCC	CCACTGCTGGAGAACCAAGT
<i>evm.TU.Contig583.176</i>	TTTGTGGCCTTGAGTTCCCC	ACGTTCTGTTACGGTGTCGTC
<i>evm.TU.Contig207.236</i>	CATCGGGTGGTCGTGTTTTTC	CATGCTTCTTAGGCTTCCGC
<i>evm.TU.Contig63.553</i>	TCCCGTTGCAGGAATGATGG	CACTGGGGACAGGGCAATAA
<i>evm.TU.Contig154.214</i>	ACCGCCTTGAAATCCCTTCC	AAGCGGTACAATTCTGGGCT
<i>evm.TU.Contig154.133</i>	ACTTCAGCTTCCAGCATCCC	CAATGCCGTATGCACAGTCG
<i>evm.TU.Contig66.895</i>	CCTGATTCTGTCCGAGCCAT	TGTTGGCACCCTTTTCGTCT
<i>evm.TU.Contig519.36</i>	ACAGAAAAGGATGGTGGCAGA	TGCCAAAGGACAGTGATCCG
<i>evm.TU.Contig21.81</i>	AAATGGACCGACCCGCATAG	AACGCTCTTGTAATTGCGCC
<i>evm.TU.Contig488.39</i>	CCGACATCCTTGGGGACAAT	AGGGAGTCAAGACGATAGGCA
<i>evm.TU.Contig171.52</i>	GGTGCCTTTGCTTTGCATGA	TGGTGATGATGGTGCTTTCCA
<i>evm.TU.Contig96.340</i>	TTGAAGCAACTACCCCGACC	TTGCGTCTCAGCCTTCAGTT
<i>evm.TU.Contig948.4</i>	AGTGGACGAGGTATCGAGGT	GCCCGATCATAAGCCAATGC
<i>evm.TU.Contig151.18</i>	CAGAGTGGTCGGATTGCCTC	GCACGTAGCACACGTTACAG
<i>evm.TU.Contig84.515</i>	CCCCGATCTTCCTTTTGCT	TGGTCTCATTGGGCATGAAGT

Table Supplementary 4. High expression of transporters-encoding and protein kinases
encoding genes

Gene_id		log ₂ FoldChange			Gene Name
		AL1_400vsAL1_CK	AL3_400vsAL3_CK	AL7_400vsAL7_CK	
		up	25	29	
		down	21	18	
Transporter	<i>evm.TU.Contig14.261</i>	-0.121622481	-1.44918	-1.24121	ABCB13
	<i>evm.TU.Contig383.77</i>	1.758411228	0.682502	2.997459	ABCB15
	<i>evm.TU.Contig66.296</i>	-0.280714207	0.976585	2.446902	ABCB19
	<i>evm.TU.Contig98.26</i>	1.34272343	0.644218	3.402411	ABCB9
	<i>evm.TU.Contig1.102</i>	0.587820918	1.885543	2.940956	ABCC2
	<i>evm.TU.Contig341.248</i>	-0.332416975	-1.36422	-0.82942	ABCC5
	<i>evm.TU.Contig967.193</i>	0.841170134	0.870238	1.34585	ABCC8
	<i>evm.TU.Contig184.120</i>	-0.134403036	0.333368	-1.39083	ABCC9
	<i>evm.TU.Contig583.11</i>	-0.31016166	-1.13194	-0.45071	ABCF1
	<i>evm.TU.Contig16.373</i>	-1.028430204	-3.20704	-2.57766	ABCG10
	<i>evm.TU.Contig694.215</i>	-1.685158875	4.033051	3.007732	ABCG11
	<i>evm.TU.Contig486.7</i>	1.15134808	0.861225	1.343725	ABCG14
	<i>evm.TU.Contig66.774</i>	2.480825243	-0.36736	0.037733	ABCG17
	<i>evm.TU.Contig184.885</i>	-0.71639939	-0.95938	-1.56852	ABCG21
	<i>evm.TU.Contig468.8</i>	-0.077036887	-1.17795	-0.40441	ABCG23
	<i>evm.TU.Contig81.396</i>	0.025017427	-0.51158	-1.36486	ABCG24
	<i>evm.TU.Contig63.68</i>	1.015241478	0.853779	0.594683	ABCG30
	<i>evm.TU.Contig180.280</i>	-0.933270576	0.59209	1.051397	ABCG32
	<i>evm.TU.Contig63.72</i>	-0.130994072	-0.39352	-1.15944	ABCG40
	<i>evm.TU.Contig860.17</i>	-1.990284054	-3.56959	-3.42524	ABCG40
	<i>evm.TU.Contig81.1119</i>	-1.345854341	0.307669	1.156213	ABCG6

	<i>evm.TU.Contig860.19</i>	-0.449622089	1.358583	1.705097	ABCI20
	<i>evm.TU.Contig477.252</i>	1.327312091	-0.40422	-0.59885	ALMT10
	<i>evm.TU.Contig154.52</i>	2.823423011	1.096949	2.266489	ALMT10
	<i>evm.TU.Contig969.22</i>	-0.937404989	1.595426	1.68336	ALMT12
	<i>evm.TU.Contig63.261</i>	4.355505406	0.880934	5.371157	ALMT2
	<i>evm.TU.Contig12.396</i>	1.103505998	1.5693	3.211727	SLC47A1
	<i>evm.TU.Contig84.309</i>	0.463048282	-4.66038	-5.51479	POT2
	<i>evm.TU.Contig421.490</i>	1.531208376	-0.54127	-0.42175	POT5
	<i>evm.TU.Contig69.71</i>	-0.601655184	1.548719	1.581654	POT5
	<i>evm.TU.Contig694.68</i>	-0.307176684	-1.77064	-1.39112	At1g71900
	<i>evm.TU.Contig437.189</i>	-0.779874862	-1.24489	-0.87962	At5g11960
	<i>evm.TU.Contig166.25</i>	1.581465915	5.447464	-0.03108	ZIP10
	<i>evm.TU.Contig16.637</i>	0.411911777	-1.22009	-1.18417	ABCB8
	<i>evm.TU.Contig765.15</i>	-0.634892748	-1.09606	-1.33446	At1g54730
	<i>evm.TU.Contig5.75</i>	2.163089269	0.195573	0.055891	ZIP1
	<i>evm.TU.Contig139.260</i>	0.551929662	0.9105	1.330903	ZIP2
	<i>evm.TU.Contig5.266</i>	0.206621403	1.332927	0.261797	ZIP4
	<i>evm.TU.Contig672.2</i>	-0.317357347	1.958847	1.678213	ZIP5
	<i>evm.TU.Contig481.169</i>	0.811530726	1.179202	2.72664	ZIP5
protein	<i>evm.TU.Contig141.53</i>	4.12081016	-0.52841	-0.66694	SOBIR1
kinase	<i>evm.TU.Contig141.52</i>	3.203429024	0.312604	0.094061	SOBIR1
	<i>evm.TU.Contig81.601</i>	0.272979453	0.885326	1.633123	MAKR4
	<i>evm.TU.Contig60.245</i>	0.163565932	0.666918	1.227542	PKS1
	<i>evm.TU.Contig130.60</i>	/	3.901552	5.317494	PKS3
	<i>evm.TU.Contig201.48</i>	0.38196684	1.543087	1.988568	At3g51990
	<i>evm.TU.Contig766.72</i>	-0.632039789	1.934396	1.290876	CCR1

The FDR ($FDR < 0.05$) and the fold change ($|\log_2(\text{FoldChange})| > 1$) were used as indicators to screen the differentially expressed genes between aluminum stress induced group and control group at different time. A negative value of $\log_2\text{FoldChange}$ indicates that the gene expression is down-regulated, while a positive value indicates that the gene expression is up-regulated.

Table Supplementary 5. New DEGs and unnamed DEGs

Gene ID	log ₂ FoldChange			Description
	R1_400vsR1_CK	R3_400vsR3_CK	R7_400vsR7_CK	
	up	25	24	23
	down	52	53	54
<i>evm.TU.Contig12.254</i>	-1.68032	-2.13683	-2.21447	unnamed protein product
<i>evm.TU.Contig139.44</i>	-1.34723	-2.34128	-1.78706	unnamed protein product
<i>evm.TU.Contig14.145</i>	-1.14208	-2.13592	-1.50448	unnamed protein product
<i>evm.TU.Contig14.325</i>	-1.76456	-1.53771	-3.0853	unnamed protein product
<i>evm.TU.Contig14.326</i>	-0.97391	-1.42962	-2.0822	unnamed protein product
<i>evm.TU.Contig143.12</i>	-3.96174	-3.55446	-3.30114	unnamed protein product
<i>evm.TU.Contig151.66</i>	1.95868	1.968553	3.56543	unnamed protein product
<i>evm.TU.Contig154.193</i>	0.885835	2.214445	1.86615	unnamed protein product
<i>evm.TU.Contig154.659</i>	-2.10398	-3.58933	-1.97985	unnamed protein product
<i>evm.TU.Contig184.424</i>	1.205629	2.006807	2.147204	unnamed protein product
<i>evm.TU.Contig184.57</i>	-1.21883	-1.7173	-2.25449	unnamed protein product
<i>evm.TU.Contig184.586</i>	-2.91187	-5.80906	-3.80385	unnamed protein product
<i>evm.TU.Contig21.498</i>	2.137926	1.664477	2.31157	unnamed protein product
<i>evm.TU.Contig256.6</i>	2.115634	1.781262	2.497298	unnamed protein product
<i>evm.TU.Contig271.70</i>	1.664998	1.583371	2.536936	unnamed protein product
<i>evm.TU.Contig271.71</i>	1.371642	1.626755	2.279892	unnamed protein product
<i>evm.TU.Contig280.67</i>	2.241073	1.593307	1.684287	unnamed protein product
<i>evm.TU.Contig296.151</i>	-4.90499	-5.46567	-6.7321	unnamed protein product
<i>evm.TU.Contig368.46</i>	-2.74083	-1.79621	-3.24205	unnamed protein product
<i>evm.TU.Contig368.47</i>	-2.76407	-2.12096	-3.27932	unnamed protein product
<i>evm.TU.Contig447.157</i>	0.96409	-3.35752	-3.48368	unnamed protein product
<i>evm.TU.Contig45.123</i>	-1.34708	-2.3494	-1.53932	unnamed protein product
<i>evm.TU.Contig471.132</i>	-1.23449	-2.04507	-1.51728	unnamed protein product

<i>evm.TU.Contig477.396</i>	-2.20047	-3.70606	-2.90498	unnamed protein product
<i>evm.TU.Contig477.721</i>	-1.2679	-2.03637	-2.47889	unnamed protein product
<i>evm.TU.Contig480.386</i>	-3.53075	-1.48989	-5.31566	unnamed protein product
<i>evm.TU.Contig55.215</i>	1.811465	1.525186	2.064504	unnamed protein product
<i>evm.TU.Contig555.77</i>	-2.06753	-1.84046	-2.54481	unnamed protein product
<i>evm.TU.Contig586.8</i>	2.335668	1.465431	3.197961	unnamed protein product
<i>evm.TU.Contig60.474</i>	-0.88135	-2.06653	-1.52982	unnamed protein product
<i>evm.TU.Contig600.222</i>	3.816377	2.304929	2.871286	unnamed protein product
<i>evm.TU.Contig600.57</i>	2.846669	2.078649	2.785662	unnamed protein product
<i>evm.TU.Contig63.371</i>	-1.09605	-1.39256	-2.21673	unnamed protein product
<i>evm.TU.Contig66.311</i>	-1.65001	-1.55028	-2.78768	unnamed protein product
<i>evm.TU.Contig66.781</i>	3.421413	2.077415	1.927894	unnamed protein product
<i>evm.TU.Contig797.219</i>	2.940478	3.055996	3.768322	unnamed protein product
<i>evm.TU.Contig797.67</i>	-1.91577	-2.37416	-2.35697	unnamed protein product
<i>novel.1026</i>	-1.39844	-2.81986	-1.71505	new gene
<i>novel.1040</i>	3.026199	1.250311	1.817744	new gene
<i>novel.109</i>	-1.17115	-3.1877	-1.83652	new gene
<i>novel.116</i>	1.433453	1.243581	2.851857	new gene
<i>novel.122</i>	-3.12123	-3.16949	-3.65924	new gene
<i>novel.125</i>	-2.00935	-1.80948	-3.95399	new gene
<i>novel.1308</i>	-6.09709	-8.55061	-5.96819	new gene
<i>novel.1325</i>	-3.31625	-4.41164	-2.36392	new gene
<i>novel.1326</i>	-2.16862	-2.51953	-3.22303	new gene
<i>novel.1344</i>	-1.08814	-3.7315	-2.47517	new gene
<i>novel.138</i>	-2.31072	-1.97709	-3.20647	new gene
<i>novel.1618</i>	-4.35506	-2.62978	-2.84897	new gene
<i>novel.1777</i>	-1.72736	-0.88269	-2.28467	new gene
<i>novel.1778</i>	-5.38369	-3.85791	-5.0134	new gene
<i>novel.1784</i>	-6.17447	-4.77418	-5.08971	new gene

<i>novel.1834</i>	5.237935	3.577414	5.365558	new gene
<i>novel.1839</i>	4.42903	2.824671	5.120345	new gene
<i>novel.1846</i>	-1.53519	-2.47915	-1.61022	new gene
<i>novel.1871</i>	5.608535	3.67216	-3.68213	new gene
<i>novel.1912</i>	-1.49282	-2.05183	-2.27075	new gene
<i>novel.21</i>	-1.87753	-2.14708	-3.28464	new gene
<i>novel.278</i>	1.612914	1.426325	2.825292	new gene
<i>novel.438</i>	7.140842	3.507089	4.615261	new gene
<i>novel.54</i>	-0.67544	-2.558	-1.16692	new gene
<i>novel.547</i>	-4.45889	-4.23123	-2.71747	new gene
<i>novel.548</i>	-3.11392	-2.85048	-3.11139	new gene
<i>novel.56</i>	-4.06775	-3.4372	-6.07657	new gene
<i>novel.58</i>	-2.39682	-2.12457	-2.99169	new gene
<i>novel.59</i>	-1.33916	-2.92269	-1.92548	new gene
<i>novel.60</i>	-2.89228	-4.39289	-4.30914	new gene
<i>novel.619</i>	-1.11134	-2.20149	-3.84177	new gene
<i>novel.623</i>	-2.06662	-2.57085	-1.71939	new gene
<i>novel.639</i>	2.326975	1.25429	0.79408	new gene
<i>novel.688</i>	-2.3588	-3.48776	-2.41744	new gene
<i>novel.811</i>	2.623409	1.559927	1.512646	new gene
<i>novel.861</i>	-1.82287	-2.25526	-2.4827	new gene
<i>novel.901</i>	2.084617	1.851716	2.822601	new gene
<i>novel.938</i>	-2.11981	-2.07641	-1.17352	new gene
<i>novel.939</i>	-1.4746	-2.11379	-1.13413	new gene
<i>novel.989</i>	-4.29487	-6.88285	-10.5275	new gene
	R1_400vsR0	R3_400vsR1_400	R7_400vsR3_400	
up	25	24	23	
down	52	53	54	
<i>evm.TU.Contig16.712</i>	2.380067495	-1.49085964	1.20212316	unnamed protein product

<i>evm.TU.Contig318.21</i>	-2.189921877	1.4118865	-1.799735417	unnamed protein product
<i>evm.TU.Contig480.393</i>	2.941809	-0.53452	-1.47162	unnamed protein product
<i>evm.TU.Contig60.166</i>	2.027039	0.57279	-0.82097	unnamed protein product
<i>evm.TU.Contig600.222</i>	2.635218	1.532061	1.24221	unnamed protein product
<i>evm.TU.Contig66.901</i>	2.661035	0.498963	-1.03932	unnamed protein product
<i>evm.TU.Contig81.474</i>	3.843881	-0.64851	-1.33899	unnamed protein product
<i>evm.TU.Contig84.318</i>	1.891238	0.93173	-2.69735	unnamed protein product
<i>evm.TU.Contig906.35</i>	4.123436	-0.88732	-2.37734	unnamed protein product
<i>novel.120</i>	-3.28835	2.874898	-3.67847	new gene
<i>novel.1219</i>	-2.00927	1.699088	-2.4735	new gene
<i>novel.1431</i>	5.464379	3.402045	1.979997	new gene
<i>novel.482</i>	-3.46163	1.507224	-2.31423	new gene
<i>novel.619</i>	-1.52041	-0.87076	-2.06521	new gene
<i>novel.950</i>	2.785206	2.367055	1.916898	new gene
<i>novel.976</i>	-1.70888	2.00455	-0.96501	new gene

The FDR ($FDR < 0.05$) and the fold change ($|\log_2(\text{FoldChange})| > 1$) were used as indicators to screen the differentially expressed genes after aluminum stress in contrast to control conditions. A negative value of $\log_2\text{FoldChange}$ indicates that the gene expression is down-regulated, while a positive value indicates that the gene expression is up-regulated.