

Supplementary Table S1. Two-way ANOVA of the effects of cultivar and drought stress on the phenotypic characteristics of *Poa* forage

Trait	factor	square sum	mean square	F	Partial Eta Squared	<i>P</i>
Plant height	Variety	130.637	65.318	114.053	0.58	0.00
	Drought stress	1207.585	301.896	527.142	0.927	0.00
	Variety × Drought stress	92.987	11.623	20.296	0.496	0.00
Leaf width	Variety	13.829	6.915	461.621	0.848	0.00
	Drought stress	3.334	0.834	55.651	0.574	0.00
	Variety × Drought stress	0.208	0.026	1.733	0.078	0.09
Dry weight	Variety	0.026	0.013	105.048	0.56	0.00
	Drought stress	0.248	0.062	496.988	0.923	0.00
	Variety × Drought stress	0.02	0.002	20.036	0.493	0.00

Supplementary Table S2. Two-way ANOVA of the effects of cultivar and drought stress on the physiological characteristics of *Poa* forage

Trait	factor	square sum	mean square	F	Partial Eta Squared	<i>P</i>
Chl(a+b)	Variety	1.24	0.62	305.58	0.931	0.00
	Drought stress	0.91	0.23	112.66	0.909	0.00
	Variety × Drought stress	0.15	0.02	9.24	0.622	0.00
SS	Variety	6.51	3.26	33.72	0.600	0.00
	Drought stress	51.22	12.81	132.64	0.922	0.00
	Variety × Drought stress	32.66	4.08	42.28	0.883	0.00
Pro	Variety	53210.03	26605.02	2404.81	0.991	0.00
	Drought stress	77396.21	19349.05	1748.95	0.994	0.00
	Variety × Drought stress	46111.06	5763.88	520.99	0.989	0.00
SP	Variety	142.02	71.01	808.53	0.973	0.00
	Drought stress	36.62	9.16	104.25	0.903	0.00
	Variety × Drought stress	100.90	12.61	143.61	0.962	0.00
SOD	Variety	309705.27	154852.63	1162.96	0.981	0.00
	Drought stress	3620.97	905.24	6.80	0.377	0.00
	Variety × Drought stress	64953.03	8119.13	60.98	0.916	0.00
CAT	Variety	15436757.37	7718378.69	14754.43	0.998	0.00
	Drought stress	4747268.84	1186817.21	2268.72	0.995	0.00
	Variety × Drought stress	7206959.91	900869.99	1722.10	0.997	0.00
POD	Variety	5360474.14	2680237.07	1077.20	0.980	0.00
	Drought stress	612301.51	153075.38	61.52	0.845	0.00
	Variety × Drought stress	3335916.90	416989.61	167.59	0.968	0.00
O ₂ ⁻	Variety	12323.88	6161.94	2031.70	0.989	0.00
	Drought stress	4985.82	1246.46	410.98	0.973	0.00
	Variety × Drought stress	1882.06	235.26	77.57	0.932	0.00
H ₂ O ₂	Variety	1.16	0.58	4023.33	0.994	0.00
	Drought stress	0.18	0.05	310.29	0.965	0.00
	Variety × Drought stress	0.25	0.03	214.88	0.974	0.00
OH ⁻	Variety	20398319.47	10199159.73	1300.73	0.983	0.00
	Drought stress	4606085.76	1151521.44	146.86	0.929	0.00
	Variety × Drought stress	2083697.42	260462.18	33.22	0.855	0.00
MDA	Variety	349.02	174.51	418.46	0.949	0.00
	Drought stress	37.04	9.26	22.21	0.664	0.00
	Variety × Drought stress	11.89	1.49	3.57	0.388	0.00
RPP	Variety	81.48	40.74	30.48	0.575	0.00
	Drought stress	4658.88	1164.72	871.49	0.987	0.00
	Variety × Drought stress	79.15	9.89	7.40	0.568	0.00

Supplementary Table S3. Coefficient and contribution rate of various comprehensive indicators

Variable	Load matrix		
	PCA1	PCA2	PCA3
Chl(a+b)	0.18	0.15	0.32
SS	0.16	-0.55	0.29
Pro	0.28	-0.35	-0.19
SP	0.23	0.36	0.46
SOD	-0.28	-0.06	0.26
CAT	0.30	0.29	0.42
POD	-0.25	-0.20	0.41
O ₂ ^{·-}	0.37	-0.06	-0.05
H ₂ O ₂	0.37	0.03	-0.12
OH [·]	0.35	-0.02	-0.26
MDA	0.38	0.09	0.01
RPP	-0.19	0.52	-0.28
Eigenvalues	6.19	1.92	1.28
Contribution/%	51.55	16.01	10.66
Cumulative contribution/%	51.55	67.56	78.22

Supplementary Table S4. Summary of RNA-seq data of *Poa* forage

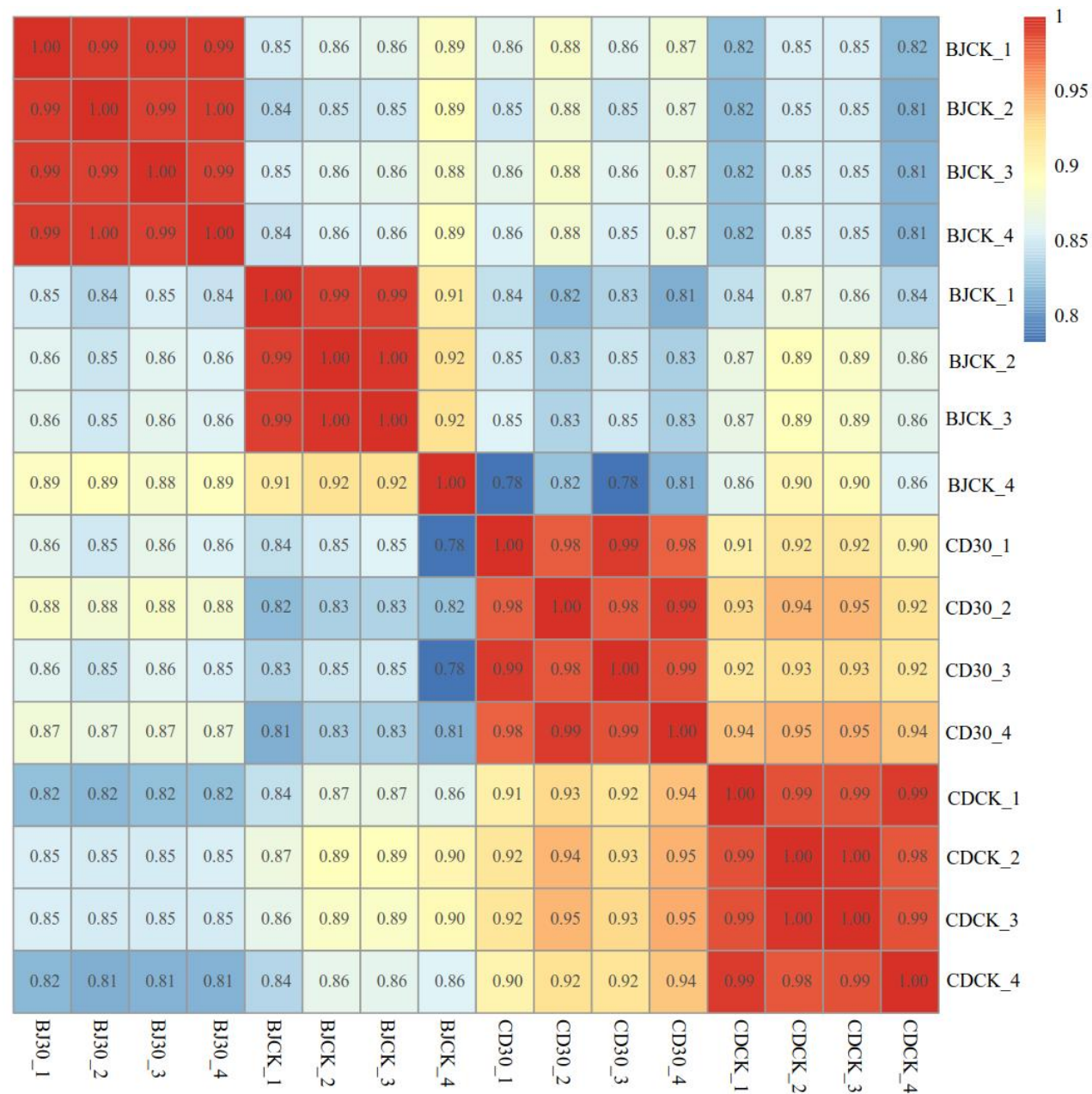
Sample	Raw reads	Raw bases(G)	Clean reads	Clean bases(G)	Error rate(%)	Q20(%)	Q30(%)	GC content(%)
BJ30_1	43385116	6.55	43112766	6.504	0.01	99.33	96.75	51.87
BJ30_2	47365000	7.15	47063218	7.099	0.01	99.33	96.75	51.87
BJ30_3	40755558	6.15	40480468	6.107	0.01	99.32	96.7	51.82
BJ30_4	52358054	7.91	52004326	7.845	0.01	99.33	96.76	51.88
BJ CK_1	44494822	6.72	44180996	6.665	0.01	99.29	96.58	52.71
BJ CK_2	44030452	6.65	43738718	6.598	0.01	99.32	96.7	52.76
BJ CK_3	46763866	7.06	46412176	7.002	0.01	99.28	96.53	52.68
BJ CK_4	41527508	6.27	41213046	6.217	0.01	99.28	96.56	53.00
CD30_1	49275148	7.44	48933372	7.382	0.01	99.31	96.64	51.98
CD30_2	49177988	7.43	48875610	7.373	0.01	99.35	96.81	51.98
CD30_3	43612622	6.59	43344398	6.539	0.01	99.32	96.65	52.00
CD30_4	42775924	6.46	42511522	6.412	0.01	99.32	96.71	52.14
CD CK_1	39506020	5.97	39222838	5.917	0.01	99.3	96.67	52.46
CD CK_2	43735726	6.6	43428920	6.551	0.01	99.29	96.55	52.27
CD CK_3	47444030	7.16	47128404	7.11	0.01	99.31	96.64	52.32
CD CK_4	45901588	6.93	45590892	6.878	0.01	99.29	96.59	52.97

Supplementary Table S5. Transcripts and unigenes identified in *de novo* assembled transcriptome of *Poa* forage

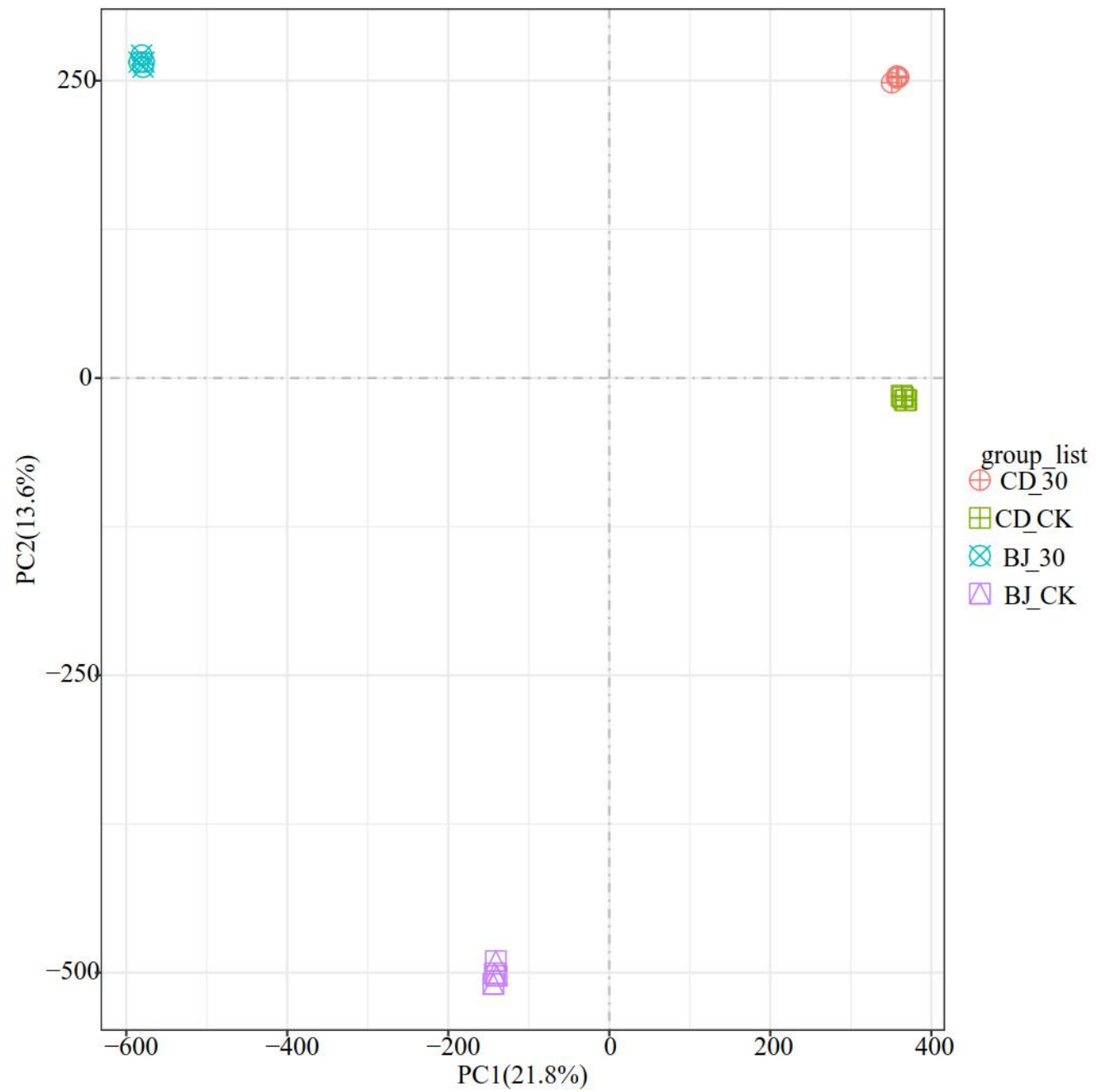
Assembly	Total length	Total seqs	Average length	Median length	N50 length	Max length	Min length
Trinity	807945467	1107505	729.5	483	974	19365	171
Transcript	737779855	881804	836.7	578	1090	19365	177
unigene	736032296	875512	840.7	582	1094	19365	177

Supplementary Table S6. Statistics of the annotated unigenes in *Poa* forage

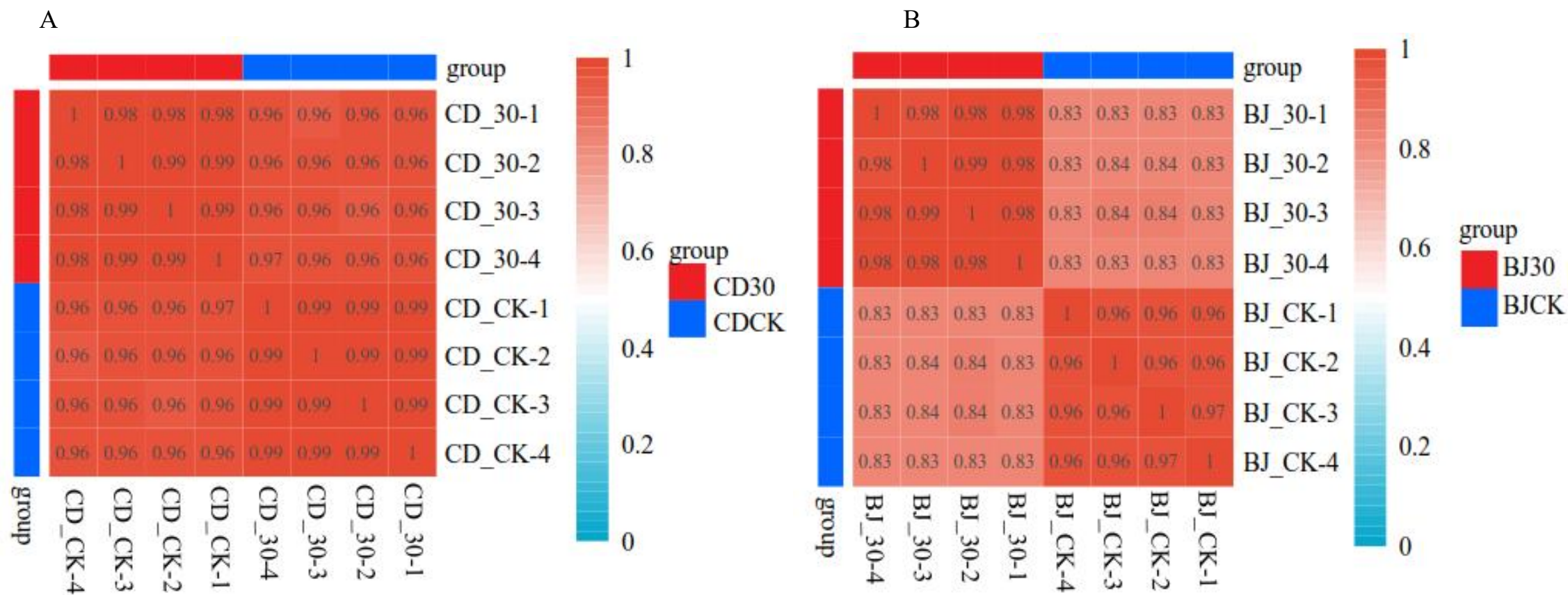
Database	KOG	KEGG	NR	SwissProt	GO	Pfam	Total unigene	Overall annotated
Gene_Number	219965	60839	510256	304568	208185	196788	875512	514446
Annotation_Ratio	25.12%	6.95%	58.28%	34.79%	23.78%	22.48%	100%	58.76%



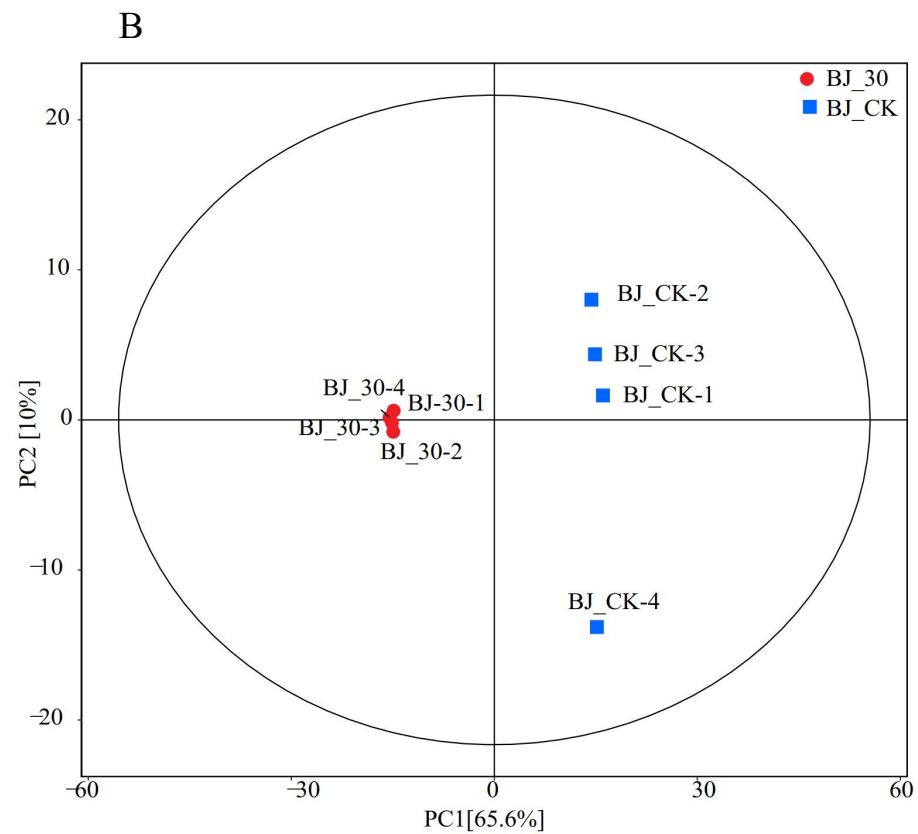
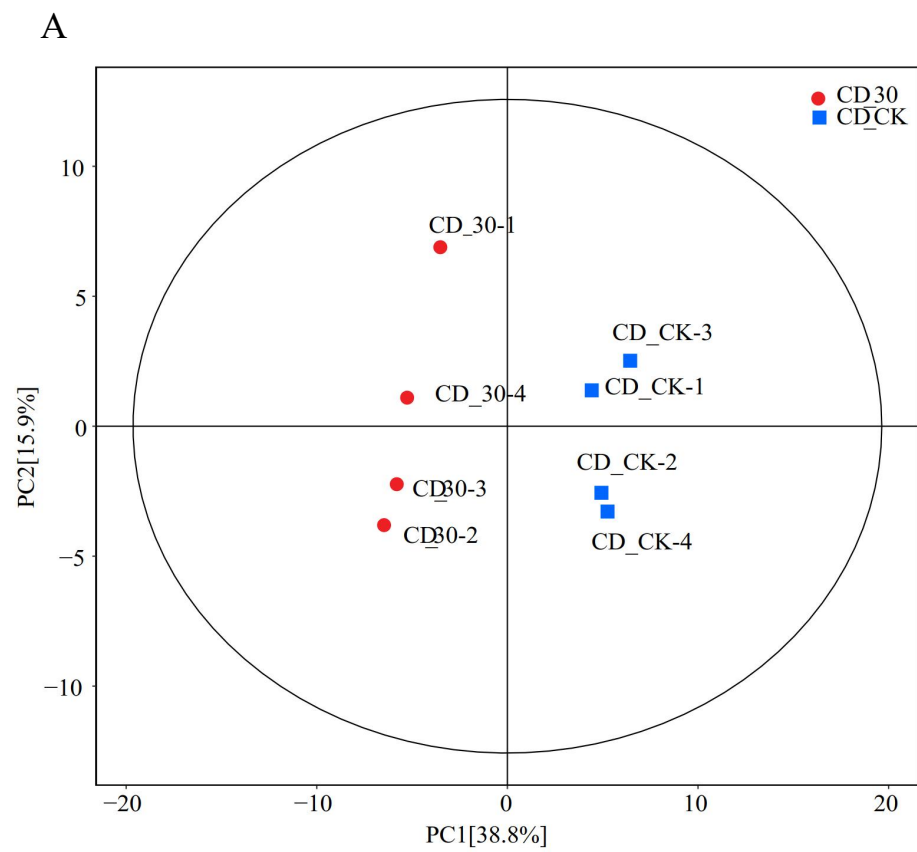
Supplementary Fig. S1. Heatmap of Pearson correlation matrix of transcriptomics



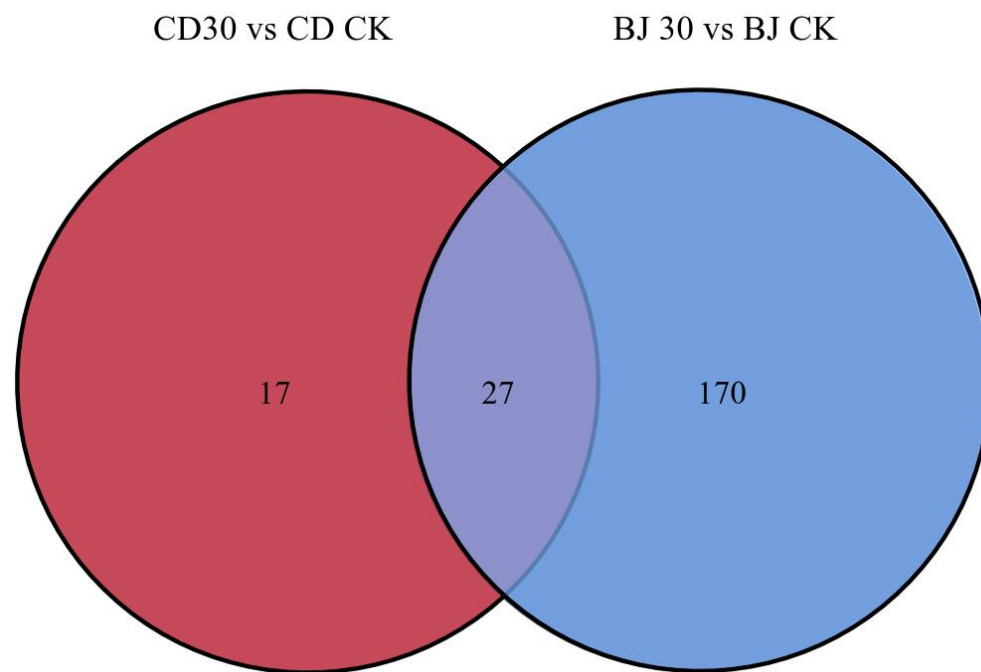
Supplementary Fig. S2. Principal component analysis (PCA) of the transcriptomes of *Poa* forage species



Supplementary Fig. S3. metabolomics replicates of different drought stress groups



Supplementary Fig. S4. Score scatter plot for PCA model total



Supplementary Fig. S5. The number of genes involved in the photosynthetic pathway of *Poa* forage after drought stress