Supplementary Table 1 Sequencing output of thirteen *Caragana* species

Samples	Raw Reads(M)	Clean Reads(M)	Clean Bases(Gb)	Q20(%)	Q30(%)	Number of Unigene
C. tibetica(IM)_1	42.33	42.33	4.23	98.08	90.97	56,105
C. tibetica(IM)_2	42.33	42.33	4.23	97.84	90.33	63,832
C. tibetica(IM)_3	42.33	42.33	4.23	97.81	90.3	69,322
*C. korshinskii*_1	43.82	42.11	6.32	97.59	93.53	64,058
*C. korshinskii*_2	43.82	42.12	6.32	97.7	93.85	66,741
*C. korshinskii*_3	45.57	42.77	6.41	97.62	93.63	67,649
*C. microphylla*_1	43.82	42.26	6.34	97.55	93.44	69,203
*C. microphylla*_2	45.57	43.6	6.54	97.53	93.42	66,787
*C. microphylla*_3	45.57	42.88	6.43	97.61	93.6	61,667
C. tibetica(T)_1	42.34	42.34	4.23	97.5	88.97	60,421
C. tibetica(T)_2	42.34	42.34	4.23	97.38	88.7	63,945
C. tibetica(T)_3	42.34	42.34	4.23	97.53	88.96	63,882
*C. jubata*_1	43.82	42.09	6.31	97.16	92.72	66,130
*C. jubata*_2	39.49	37.55	5.63	97.12	92.73	59,497
*C. opulens*_1	42.33	42.33	4.23	98.41	91.84	47,372
*C. opulens*_2	42.33	42.33	4.23	98.41	91.84	51,818
*C. opulens*_3	42.33	42.33	4.23	98.05	90.81	66,130
*C. roborovskyii*_1	42.33	42.33	4.23	97.78	90.35	89,740
*C. roborovskyii*_2	42.33	42.33	4.23	97.73	89.95	86,689
*C. roborovskyii*_3	42.33	42.33	4.23	97.99	90.92	87,483
*C. polourensis*_1	42.61	42.61	4.26	98	91.03	53,124
*C. polourensis*_2	42.61	42.61	4.26	97.92	90.68	60,410
*C. polourensis*_3	42.61	42.61	4.26	97.89	90.63	58,969
*C. intermedia*_1	42.33	42.33	4.23	97.87	90.57	76,508
*C. intermedia*_2	42.33	42.33	4.23	97.78	90.23	112,247
*C. intermedia*_3	42.33	42.33	4.23	97.83	90.13	85,253
*C. pygmaea*_1	42.33	42.33	4.23	97.85	90.31	66,621
*C. pygmaea*_2	42.33	42.33	4.23	97.96	90.55	71,544
*C. pygmaea*_3	42.33	42.33	4.23	98.37	91.61	65,407
*C. stenophylla*_1	42.33	42.33	4.23	97.79	89.89	52,692
*C. stenophylla*_2	42.33	42.33	4.23	97.36	88.6	46,457
*C. stenophylla*_3	42.34	42.34	4.23	98.33	91.42	59,649
*C. stenophylla*_1	42.34	42.34	4.23	97.67	89.62	47,146
*C. stenophylla*_2	42.34	42.34	4.23	97.41	89.83	52,942
*C. stenophylla*_3	42.34	42.34	4.23	97.54	89.97	52,508
*C. brachypoda*_1	42.33	42.33	4.23	97.72	89.97	87,097
*C. brachypoda*_2	42.33	42.33	4.23	97.25	89.28	57,667
*C. brachypoda*_3	42.33	42.33	4.23	97.84	90.06	56,365

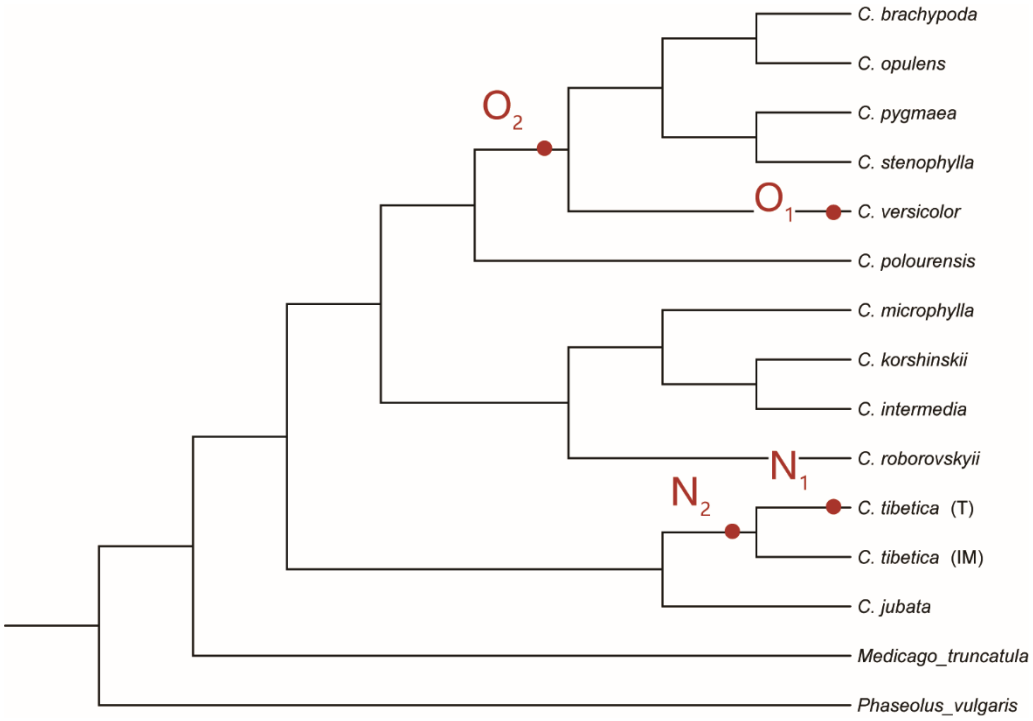
Supplementary Table 2 Members of transcription factor families containing convergent amino acid substitution sites

Group	Gene	TF family	Pfam domain
	isoform_161744	GRAS	GRAS domain family
	isoform_201072	GRAS	GRAS domain family
	isoform_233287	mTERF	mTERF
High altitude Group	isoform_31103	MYB	Myb-like DNA-binding domain
[*C. tibetica* (T)/*C. versicolor*]	isoform_27383	WRKY	WRKY DNA -binding domain
	isoform_244935	NAC	No apical meristem (NAM) protein
	isoform_209364	bHLH	Helix-loop-helix DNA-binding domain
	isoform_236069	C3H	tRNA (Uracil-5-)-methyltransferase
	isoform_117053	AP2-EREBP	AP2 domain
	isoform_33599	AP2-EREBP	AP2 domain
Low altitude Group_1 [*C.tibetica*(IM)/*C.brachypoda*]	isoform_104797	C3H	Zinc finger C-x8-C-x5-C-x3-H type (and similar)
	isoform_203037	C3H	Zinc finger C-x8-C-x5-C-x3-H type (and similar)
	isoform_1522	MYB	NA
	isoform_6819	C2H2	(DUF1356)
	isoform_171850	OFP	Transcriptional repressor, ovate
Low altitude Group_2 [*C. intermedia*/*C. pygmaea*]	isoform_4171	EIL	(DUF2431)
	isoform_259820	C2H2	Zinc finger, C2H2 type
	isoform_155575	mTERF	mTERF

Supplementary Table 3 *Caragana* voucher specimen numbers

Species	Voucher specimen numbers
C. tibetica (IM)	2018-0032
C. korshinskii	2018-2033
C. microphylla	2018-1010
C. tibetica (T)	2018-3066
C. jubata	2018-1003
C. opulens	2018-0721
C. roborovskyii	2018-6022
C. polourensis	2018-8026
C. intermedia	2018-1026
C. pygmaea	2018-0625
C. stenophylla	2018-7045
C. versicolor	2018-3025
C. brachypoda	2018-0053

Supplementary Figure 1



Supplementary Figure 2