

Table S1. Geographic information of the 12 *E. breviaristatus* populations.

Pop ID	Pop Size	Collection Site	Latitude	Longitude	Altitude (m)
Pop1	15	Zhubalong, Markam Country, Qamdo Prefecture	29°44'11.950"	98°43'23.122"	3530
Pop2	15	Wangda, Zogang Country, Qamdo Prefecture	29°42'27.821"	97°47'29.187"	3840
Pop3	14	Jida, Baxoi Country, Qamdo Prefecture	29°59'01.579"	96°40'13.665"	3776
Pop4	15	Ranwu, Baxoi Country, Qamdo Prefecture	29°32'26.570"	96°46'40.956"	3820
Pop5	15	Zhaxigang, Maizhokunggar Country, Lhasa Prefecture	29°44'14.377"	90°49'25.706"	4025
Pop6	15	Yala, Sog Country, Nagqu Prefecture	31°49'35.868"	93°33'43.773"	4071
Pop7	15	Bada, Dengqen Country, Qamdo Prefecture	31°41'18.650"	94°53'56.544"	4525
Pop8	15	Bingda, Riwoqe Country, Qamdo Prefecture	31°07'09.215"	96°47'34.984"	3708
Pop9	15	Chaiwei, Karuo District, Qamdo Prefecture	31°28'50.879"	97°14'19.888"	3392
Pop10	15	Qingnidong, Jomda Country, Qamdo Prefecture	31°19'28.580"	97°56'16.266"	3952
Pop11	15	Jiaxing, Gongbo'gyamda Country, Nyingchi Prefecture	29°52'47.348"	92°42'05.058"	3969
Pop12	15	Tiantuo, Zogang Country, Qamdo Prefecture	29°51'06.854"	97°41'04.325"	3909

Table S2. Details of the species used to detect the transferability of molecular markers in this study.

Species	Genome	Accessions PI	Origins
<i>E. dahuricus</i>	StHY	PI639853	Xizang, China
<i>E. dahuricus</i> var. <i>violeus</i>	StHY	HY-3	Sichuan, China
<i>E. atratus</i>	StHY	HY-1	Sichuan, China
<i>E. cylindricus</i>	StHY	HY-4	Sichuan, China
<i>E. excelsus</i>	StHY	G05449	Inner Mongolia, China
<i>E. purpuraristatus</i>	StHY	KD-1	Sichuan, China
<i>E. himalayanus</i>	StHY	H4134	Pakistan
<i>E. drobovii</i>	StHY	H10299	Iran
<i>E. nutans</i>	StHY	Y2196	Xizang, China
<i>E. breviaristatus</i>	StHY	PI504447	China
<i>E. submuticus</i>	StHY	PI531684	China
<i>E. tangutorum</i>	StHY	HY-1	Sichuan, China
<i>R. kamoji</i>	StHY	R273	Sichuan, China
<i>E. tsukushiensis</i>	StHY	PI499623	Japan
<i>E. humidus</i>	StHY	J3279S	Japan
<i>E. schrenkianus</i>	StHY	PI659920	Kyrgyzstan
<i>R. aristiglumis</i>	StHY	PI598486	Xinjiang, China
<i>E. tschimganicus</i>	StStY	W614438	Kazakhstan
<i>E. glaucissimus</i>	StStY	PI611142	Kazakhstan
<i>E. transhyrcanus</i>	StStH	PI383579	Ukraine
<i>E. repens</i>	StStH	PI565006	Russian Federation
<i>E. patagonicus</i>	StHH	PI297898	Argentina
<i>E. scabriglumis</i>	StHH	PI331168	Argentina

Table S3. Detailed information of EST-SSRs based on the number of nucleotide repeat unit.

Repeats	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	> 20	Total
A/T	-	-	-	-	-	3469	1337	747	359	319	240	231	129	66	67	40	760	7764
C/G	-	-	-	-	-	147	123	93	122	83	92	51	51	39	36	57	438	1332
AC/GT	-	559	220	223	97	89	93	83	20	45	38	27	18	15	34	21	45	1627
AG/CT	-	1173	563	369	396	170	171	209	67	71	85	76	59	41	38	23	91	3602
AT/AT	-	242	132	61	43	26	36	15	20	10	15	7	9	7	6	6	26	661
CG/CG	-	289	46	15	1												0	351
AAC/GTT	140	66	40	46	10	4	6		3								0	315
AAG/CTT	614	204	90	58	6	18	13	7	14	3	1						0	1028
AAT/ATT	59	37	9	15	3	11			2						1		0	137
ACC/GGT	490	232	60	14	2	10			1								0	809
ACG/CGT	503	165	50	17	4	3											0	742
ACT/AGT	81	42	12	4	9										5		0	153
AGC/CTG	1349	584	189	99	16	15	2	1					1	2			0	2258
AGG/CCT	1533	660	214	106	9	16	3	5	2								0	2548
ATC/ATG	377	118	68	22	4	11		1		2							0	603
CCG/CGG	3541	1436	628	179	25	8	3	3									0	5823
AAAC/GTTT	7	2															0	9
AAAG/CTTT	28	12	3	1	1												0	45
AAAT/ATTT	11	1															0	12
AACC/GGTT	14	3															0	17
AACG/CGTT	1	1															0	2
AAGC/CTTG	22	2															0	24
AAGG/CCTT	43	18	1														0	62
AATC/ATTG	10	8															0	18
AATG/ATTC	8	9	2														0	19
AATT/AATT	1																0	1
ACAG/CTGT	4																0	4
ACAT/ATGT	17	21	1	9													0	48
ACCC/GGGT	1																0	1
ACCG/CGGT	10																0	10
ACCT/AGGT	4	3															0	7
ACGC/CGTG	57	11															0	68
ACGG/CCGT	14	2	2														0	18
ACGT/ACGT	7																0	7
ACTC/AGTG	1	2															0	3
ACTG/AGTC	6	1															0	7
AGAT/ATCT	5	10	1		2		1	2									0	21
AGCC/CTGG	18	4															0	22
AGCG/CGCT	23	7															0	30
AGCT/AGCT	6																0	6
AGGC/CCTG	41	18															0	59
AGGG/CCCT	51	17															0	68
ATCC/ATGG	28	8	12														0	48
ATCG/ATCG	2																0	2
ATGC/ATGC	10																0	10
CCCG/CGGG	44	6		2													0	52
CCGG/CCGG	11																0	11

AAAAC/GTTTT	6	0	6
AAAAG/CTTTT	3	0	3
AAAAT/ATTTT	2	0	2
AAACC/GGTTT	3 1	0	4
AAAGG/CCTTT	2	0	2
AAATC/ATTTG	5	0	5
AACAC/GTGTT	1	0	1
AACCC/GGGTT	1	0	1
AACTC/AGTTG	1	0	1
AACTG/AGTTC	3	0	3
AAGAG/CTCTT	8 4	0	12
AAGCC/CTTGG	5	0	5
AAGCT/AGCTT	1	0	1
AAGGG/CCCTT	12	0	12
AATAC/ATTGT	2 1	0	3
AATCT/AGATT	2	0	2
ACAGC/CTGTG	1	0	1
ACATC/ATGTG	2	0	2
ACCCC/GGGGT	6	0	6
ACCCG/CGGGT	1	0	1
ACCCT/AGGGT	6	0	6
ACCTC/AGGTG	1	0	1
ACCTG/AGGTC	2	0	2
ACGAG/CGTCT	2	0	2
ACGCC/CGTGG	2	0	2
ACGGG/CCCGT	1	0	1
ACTCC/AGTGG	1	0	1
AGAGC/CTCTG	5	0	5
AGAGG/CCTCT	5 2	0	7
AGATG/ATCTC	2	0	2
AGCCC/CTGGG	1	0	1
AGCGC/CGCTG	1	0	1
AGCGG/CCGCT	1	0	1
AGCTC/AGCTG	3	0	3
AGGCG/CCTCG	1	0	1
AGGGC/CCCTG	8	0	8
AGGGG/CCCCT	2	0	2
ATATC/ATATG	1	0	1
ATCCC/ATGGG	7	0	7
ATGCC/ATGGC	1	0	1
CCCCG/CGGG	4	0	4
G			
AAAATG/ATTT	1	0	1
TC			
AAAGCC/CTTT	3	0	3
GG			
AACGGC/CCGT	2	0	2
TG			
AAGAGG/CCT	2 1	0	3
CTT			

AAGCCG/CGG CTT	1	0	1
AAGGAG/CCTT CT	1	0	1
AATGGC/ATTG CC	1	0	1
AATGTG/ACAT TC	2	0	2
ACACAT/ATGT GT	1 2	0	3
ACACGC/CGTG TG	4	0	4
ACAGGC/CCTG TG	1	0	1
ACCAGC/CTGG TG	4	0	4
ACCTCC/AGGT GG	3 2	0	5
ACCTCG/AGGT CG	1	0	1
ACGAGG/CCTC GT	1	0	1
ACGCAG/CGTC TG	3	0	3
ACGGCG/CCGT CG	3	0	3
AGAGGC/CCTC TG	1	0	1
AGATGG/ATCT CC	3	0	3
AGCAGG/CCT GCT	7 2	0	9
AGCGGC/CCG CTG	1	0	1
AGCTCC/AGCT GG	1	0	1
AGGATG/ATCC TC	2	0	2
AGGCGG/CCG CCT	7	0	7
ATCCCC/ATGG GG	2	0	2
ATCGCC/ATGG CG	1	0	1
ATCGGC/ATGC CG	5	0	5
CCCCCG/CGGG GG	1	0	1

Table S4. List of the 58 primer pairs with expected size of PCR products.

Primers	Repeat Motif	Forward Primer (5'-3')	Tm (°C)	Reverse Primer (5'-3')	Tm (°C)	Note
MDEB002	(CT)9	AGTCCTTAGCCCCTAGGACG	60.106	AAAGAGAGGAGGGCTGGGAT	59.955	Polymorphic
MDEB024	(CAT)5	ATGTATGGGGCGGGCATATG	60.034	CAAACCGACGAGAGGTGTCA	59.968	Polymorphic
MDEB025	(CCA)5	GATCCGACGACCTCAGCTTC	60.249	CCATCTGCAGCTGGTCAAGA	60.036	Polymorphic
MDEB027	(CCG)5	CATCGACATCACCTGGGTGT	59.75	TTCTTGTTCCCCACGGCTTC	60.536	Polymorphic
MDEB046	(CTA)6	TACATCAAAGCGCAGGCAGA	60.036	AAGGAGTTGACATGGCTCAGG	60.036	Polymorphic
MDEB050	(CTG)5	CGCCTACACAAGATGGTGGT	60.036	CACTCTGTCGAAATGCAGCG	59.906	Polymorphic
MDEB051	(CTG)5	GCCTGCTGAAGATGCTCAGA	60.108	CCAGCAGTACAACCAGAGCA	59.965	Polymorphic
MDEB054	(GAC)6	ACCGGCATTTCTTACACTGG	60.035	TCCTCACAGCTCTCACCAACA	60.47	Polymorphic
MDEB063	(GCG)5	CACTTCTCCCCTCGCGATG	60.227	AACATGAGCAGGCTCTCGAC	60.108	Polymorphic
MDEB065	(GCG)5	CAAGAGCGACCTGGTGAAGT	59.966	CTCGTTCCCATCATCCGCAAA	60.462	Polymorphic
MDEB067	(GCG)6	AATGGTTCGTTGTCGTCGGA	59.968	GTGGTGGACAAGTAGCTGCT	59.965	Polymorphic
MDEB068	(GCT)5	GTAAGTGTCTTCGGCGGGA	60.038	CCACCGAAGAACGACTACCC	60.109	Polymorphic
MDEB076	(GGC)5	ATCCACGTTTCCCTCTGCTG	60.036	CCAGTCCCCACTACCAGCTA	60.325	Polymorphic
MDEB083	(GTC)5	TGAGGCTGGGACTGAAGAGT	60.179	CTTCTCAGCTGCTGACCTCC	60.108	Polymorphic
MDEB091	(TCA)6	ACCCCCAGCTACTACCATGT	59.956	GAGATGGAGCCTACCGAAGC	59.967	Polymorphic
MDEB094	(TCG)5	CGCCTCTTCCACGTCTTTGA	60.32	GATGGTGCTCCTCGAGATCG	60.04	Polymorphic
MDEB095	(TGT)5	CAGCTGTTCTGGAGGGTGAAG	59.896	TCAGAAGGTGACGACGCTTC	59.969	Polymorphic
MDEB100	(TGT)5	TGGTCGCGAGATCTTATGGG	59.326	TAAACAACAGCACCTGGCCT	59.815	Polymorphic
MDEB003	(GA)9	AATCGACATGAGAGCACCGG	60.179	CGGCCCTTTTATCCCCTGT	60.034	Monomorphic
MDEB004	(AAC)6	TTCAGGCATCCCGCTAACAG	60.108	TCCTACCTCCAAGCCCTCTT	59.582	Monomorphic
MDEB009	(ACG)6	GGCCTCTACGAGTTCCCCTA	60.106	GGCACACCCTACACGTACTC	60.109	Monomorphic
MDEB010	(ACT)5	AGGAACGCATAGGCACACTC	60.108	ATTCACCCCGTGATCGATCG	59.968	Monomorphic
MDEB012	(AGC)5	CGTCGTGGAAGCTGAGGTAG	60.179	CTTGCAAGTTACTTCCGCCG	59.834	Monomorphic
MDEB014	(AGG)6	TTCTTGAACGCCACCTCAGG	60.25	AGAGAGAAGCCAAGAACCGC	60.037	Monomorphic

MDEB017	(ATC)5	TCTTTGACCAGCTGCGAA GT	59.893	CTGGCCGAGAACAAGATC GT	60.109	Monomorphi c
MDEB020	(CAA)5	CAGTTCAGTAGCAGCCA CCA	59.965	TGGGCGTCAAGTTTGGAT GA	59.89	Monomorphi c
MDEB021	(CAC)5	CAGGATCTTCCAGCTCAC CC	59.82	GGAGGAGTTCATGAAGCC GG	60.463	Monomorphi c
MDEB022	(CAG)5	CAATCGACAAGCTCCCC GAG	60.808	GGCCTCCTTGTCTTCACA G	60.322	Monomorphi c
MDEB031	(CCT)5	GACGGTCTGGTCGAACA CTT	59.968	GGAATCCCCTTTGACTCC CG	60.107	Monomorphi c
MDEB032	(CCT)6	CCTCCGGCTTCAAGCTCT TC	60.743	GAACTTGGTCTCCCTGCTC C	60.036	Monomorphi c
MDEB033	(CGA)5	GCAACACGAACCGGAAA TGA	59.411	TGTCTGTACATAGCTGCG GC	60.179	Monomorphi c
MDEB034	(CGA)6	CCTCGCCGCTGGACTACA	61.449	TTCTTCCGTTGCCTCTGAC C	59.965	Monomorphi c
MDEB036	(CGC)5	GCAGTACTACCAGCAGG GAC	59.824	GAGATCTCCGATCCACAG CG	60.04	Monomorphi c
MDEB037	(CGC)5	CCATCACGTGATCTCCGA GG	59.969	CCTCTCGATCCAACCTCGA CG	59.972	Monomorphi c
MDEB041	(CGG)5	TCCACTCTGTCTCGTCGA CT	59.965	GCTGTTGCCACCTCTGATG A	60.322	Monomorphi c
MDEB043	(CGG)6	CGCCGACAAGAACCGAG ATT	60.736	GGACGGGGAAAATGGGG ATT	60.033	Monomorphi c
MDEB047	(CTC)5	GCGACTGGATTAGATGG CGA	59.968	TTCTACGCACCTTCACCGT G	60.319	Monomorphi c
MDEB048	(CTC)5	CGGAAGCTCATCGAGAT GCT	59.968	TGACCCTCCTCAGCAGAT CA	59.958	Monomorphi c
MDEB049	(CTC)6	CGTCATGCCCTTGAATC CT	60.036	AAGACCAGAAGCAGAAG GGC	59.963	Monomorphi c
MDEB053	(GAA)5	TTGAGGTCAGTGGCAAG CAA	60.107	GTTTTCGCGGTCTTGACGA G	59.839	Monomorphi c
MDEB066	(GCG)6	GGACGGCCATGCATAAC AGG	61.447	GAGCAGCTGGTCCATCAT CG	60.879	Monomorphi c
MDEB069	(GCT)5	TCCACCATGCTCAGCGAA TT	60.035	TCTCGGTAAACGGTCCTT GC	60.038	Monomorphi c
MDEB070	(GCT)6	CTCCGCATCTTTTTCAGC GG	59.902	CGGCCGGGTAAATTCAA CC	59.828	Monomorphi c
MDEB071	(GGA)5	GGAGAGGTGGAGTCGTC GTC	61.647	TTCCTGTCCTTCACCAACC C	59.523	Monomorphi c
MDEB072	(GGA)5	CCGCCGCCATGATGAAG TAT	60.604	ACCGACTCCTCCTCGTACT C	60.108	Monomorphi c
MDEB078	(GGC)6	GCGAAAGGGAGGGAATG TCA	60.035	CTCCCCAACTTCCCCTCCT A	59.956	Monomorphi c
MDEB082	(GTA)5	GAGCAGTCCAGGCCATT GAT	60.107	TCACCACCTCCTCCTCCA AG	60.545	Monomorphi c
MDEB084	(GTC)6	GGACGCAGAGAAGGAGT ACG	59.901	TGTCCGTATGGCAGCGAT AC	59.968	Monomorphi c
MDEB085	(GTG)5	ACAGATGACACGCGGTA CAG	60.109	TCGCCAAACCTGTCTGAT CC	60.036	Monomorphi c

MDEB087	(GTT)5	ATCACACAAGCCAGAGG AGC	60.036	GCTCCAGTACAACAAACC GC	59.763	Monomorphi c
MDEB088	(TAC)5	GCCTCCTCCGCCTCTAGT AT	60.251	TCATGGCTGGACCCCATC TA	60.03	Monomorphi c
MDEB089	(TAG)5	AAGCAGCGGGTATGCAA AAC	59.756	CAAGTCGCACCAAGAAC AGC	60.041	Monomorphi c
MDEB090	(TAT)5	AGGTGGTTGCTATTGGCT CC	60.034	GCTGTAGATATTTTGGCG CCC	60.288	Monomorphi c
MDEB092	(TCC)5	GCAAAACGAGTGTGACT GGC	60.317	AGAATTCCGGCGCTTCTT CA	60.036	Monomorphi c
MDEB093	(TCC)6	GGTGAAGCTCTAGACCC CCA	60.618	CAAGCTCAAGGACCACG ACT	59.966	Monomorphi c
MDEB098	(TGC)6	CACATTGTCACGCTGCCA AA	59.969	CGAATGCCTTTGGACCGT TG	60.11	Monomorphi c
MDEB099	(TGG)5	CTCACTCGCTATGCAGCT CG	60.934	GAGCTCCAGCACCTCCAT AG	59.608	Monomorphi c
MDEB101	(TTA)5	GCGACATGGGCAAGAAC AAG	60.11	GTCCCGCAAACAAGTCAC AC	59.971	Monomorphi c