

Tables S1 The results of the metagenomic workflow

	Sample ID	Raw Reads	Clean Reads	Effective Reads	AvgLen(bp)	GC(%)	Q20(%)	Q30(%)	Effective (%)
Fungi	<i>E. nutans</i>	44563	38200	37456	244	50.4	99.7	99.29	84.05
		78066	67625	66296	249	48	99.6	99.12	84.92
		80147	70714	69250	243	46.12	99.7	99.34	86.4
	<i>E. breviaris</i>	79982	69959	68421	237	49.01	99.76	99.44	85.55
		80220	69799	68180	245	43.26	99.66	99.26	84.99
		79833	71512	70068	239	45.75	99.73	99.39	87.77
	<i>R. pauciflora</i>	79791	70615	69046	242	43.28	99.72	99.36	86.53
		80026	70364	68782	239	46.09	99.74	99.39	85.95
		80139	71201	69720	234	46.49	99.79	99.5	87
	<i>P. crymophila</i>	79967	71976	70603	232	46.09	99.8	99.53	88.29
		80042	70945	68871	240	45.5	99.74	99.41	86.04
		80123	69551	68058	235	49.52	99.79	99.49	84.94
	<i>E. sibircus</i>	80037	69730	68191	240	45.37	99.73	99.38	85.2
		80109	71773	70444	237	46.37	99.78	99.48	87.94
		79824	70226	68709	240	46.43	99.75	99.42	86.08
	<i>E. sinosubmuticus</i>	79942	70774	69250	237	45.3	99.74	99.41	86.63
		80308	71227	69423	246	43.64	99.68	99.3	86.45
		80024	69674	68113	232	46.45	99.78	99.48	85.12
	<i>P. tenuiflora</i>	80076	70336	68913	239	48.8	99.76	99.43	86.06
		80082	68427	66032	242	47.73	99.71	99.32	82.46
		79737	70675	68245	238	46.03	99.76	99.45	85.59
	CK	80227	71579	70022	240	44.64	99.72	99.36	87.28
		79627	68396	66878	260	48.11	99.47	98.84	83.99
		79814	69762	68067	245	46.06	99.66	99.25	85.28
		79944	69684	68192	251	45.16	99.59	99.11	85.3
		79752	70843	69451	257	45.8	99.59	99.11	87.08
		69989	58471	53715	419	56.15	98.14	96.46	76.75
Bacterial	<i>E. nutans</i>	69963	58780	53271	418	56.23	98.21	96.56	76.14
		69937	60022	54778	418	56.12	98.31	96.73	78.32
		70006	58772	55696	418	56.21	98.22	96.6	79.56
	<i>E. breviaris</i>	70045	55848	49960	418	56.17	97.89	96.01	71.33
		69910	58621	54194	419	56.05	98.13	96.45	77.52
		69965	58367	52877	418	56.38	98.19	96.52	75.58
	<i>R. pauciflora</i>	70112	59866	55341	419	56.39	98.31	96.74	78.93
		68796	58675	55084	418	56.57	98.35	96.81	80.07
		69931	59946	56899	418	56.25	98.28	96.69	81.36
	<i>P. crymophila</i>	70053	59862	54369	418	56.19	98.25	96.64	77.61
		70048	56874	50700	418	56.17	98.05	96.29	72.38
		69775	58008	52800	418	56.22	98.08	96.34	75.67
	<i>E. sibircus</i>	69929	60509	55733	418	56.39	98.26	96.65	79.7
		70559	61125	55426	418	56.09	98.32	96.76	78.55

<i>E.</i>	69972	58299	52991	418	56.34	98.18	96.51	75.73
<i>sinosub</i>	70159	59278	53202	418	56.03	98.18	96.53	75.83
<i>muticus</i>	69962	57996	51890	418	55.94	98.16	96.49	74.17
<i>P.</i>	70204	60810	55644	418	56.07	98.35	96.81	79.26
<i>tenuiflor</i>	69910	59597	53805	418	55.87	98.29	96.71	76.96
<i>a</i>	70148	60705	55548	418	56.12	98.34	96.79	79.19
	69978	59810	53600	419	56.46	98.28	96.69	76.6
	69881	58373	53664	420	57.13	98.23	96.57	76.79
CK	70253	59567	54512	420	57.11	98.29	96.67	77.59
	69895	56898	51761	419	56.99	98.03	96.22	74.06
	64757	54639	50369	419	57.25	98.21	96.54	77.78

Tables S2 Soil moisture at artificial and natural grasslands. CK: Natural temperate steppe. The different lowercase letters above the bars denoted significant differences ($P < 0.05$). Values represent means \pm SD

grasslands types	soil moisture (%)
<i>E. nutans</i>	22.12 \pm 1.23a
<i>E. breviaristatus</i>	19.36 \pm 1.86ab
<i>R. pauciflora</i>	15.27 \pm 1.31c
<i>P. crymophila</i>	19.96 \pm 1.19ab
<i>E. sibircus</i>	18.97 \pm 0.62b
<i>E. sinosubmuticus</i>	19.37 \pm 2.09ab
<i>P. tenuiflora</i>	20.64 \pm 1.13ab
CK	24.04 \pm 1.67ab

Figures S1 Effects of artificial grasslands on shannon index of bacteria (Shannon_B) and fungi (Shannon_F) and phylogenetic diversities of bacteria (PD_whole_tree_B) and fungi(PD_whole_tree_F). CK: Natural temperate steppe. E breviaristatus: *Elymus breviaristatus*. E nutans: *Elymus nutans*. E sibircus: *Elymus sibircus*. E sinosubmuticus: *Elymus sinosubmuticus*. P crymophila: *Poa crymophila*. P tenuiflora: *Puccinellia tenuiflora*. R pauciflora: *Roegneria pauciflora*. The different lowercase letters above the bars denoted significant differences ($P < 0.05$).

Values are means \pm SD.

