

Altitudes differences impact gene expression and accumulation of main medicinal ingredients of *Zanthoxylum planispinum* var. *Dintanensis* in rocky desertification control areas

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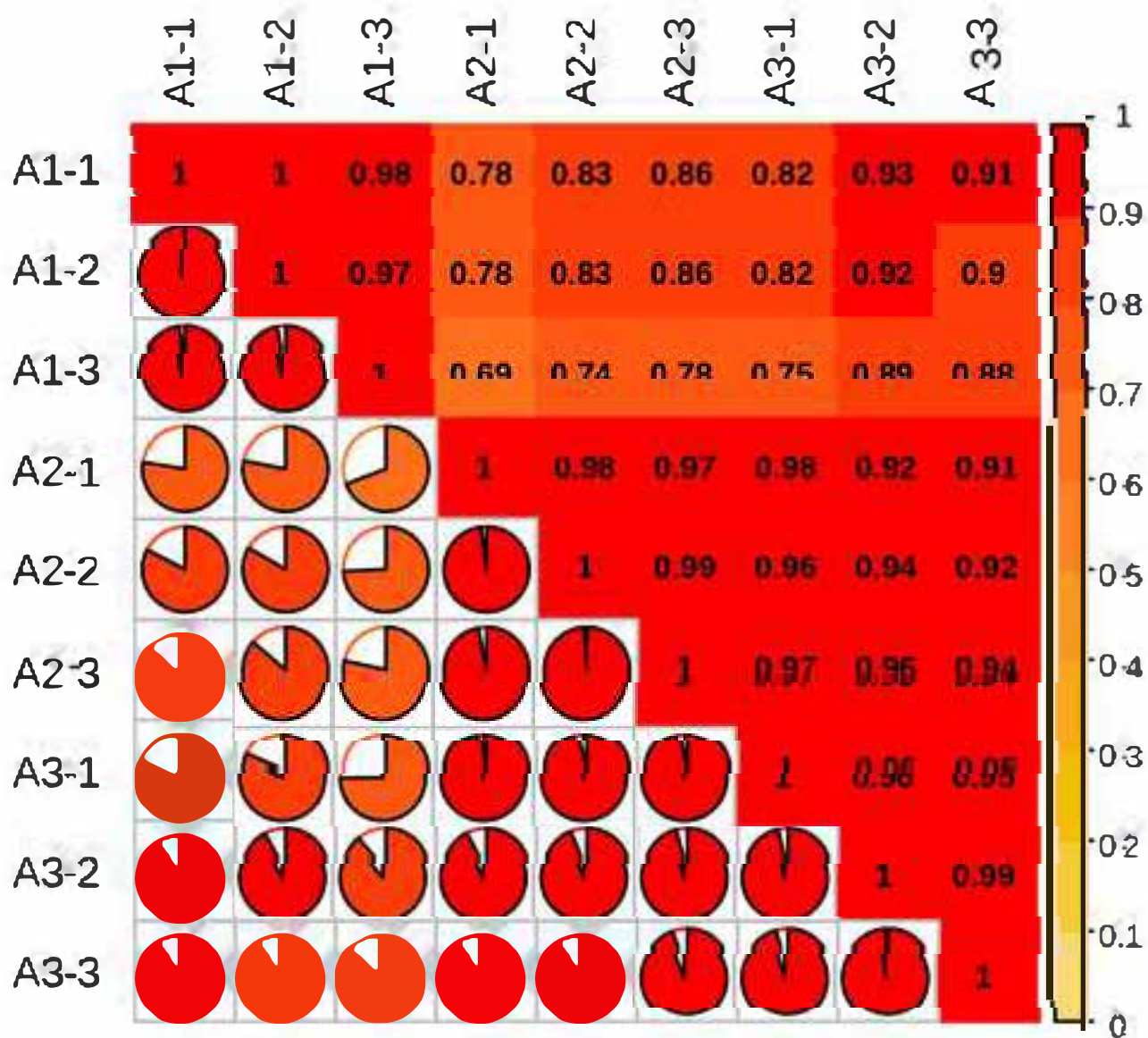


Figure S1. Correlation analysis between samples.

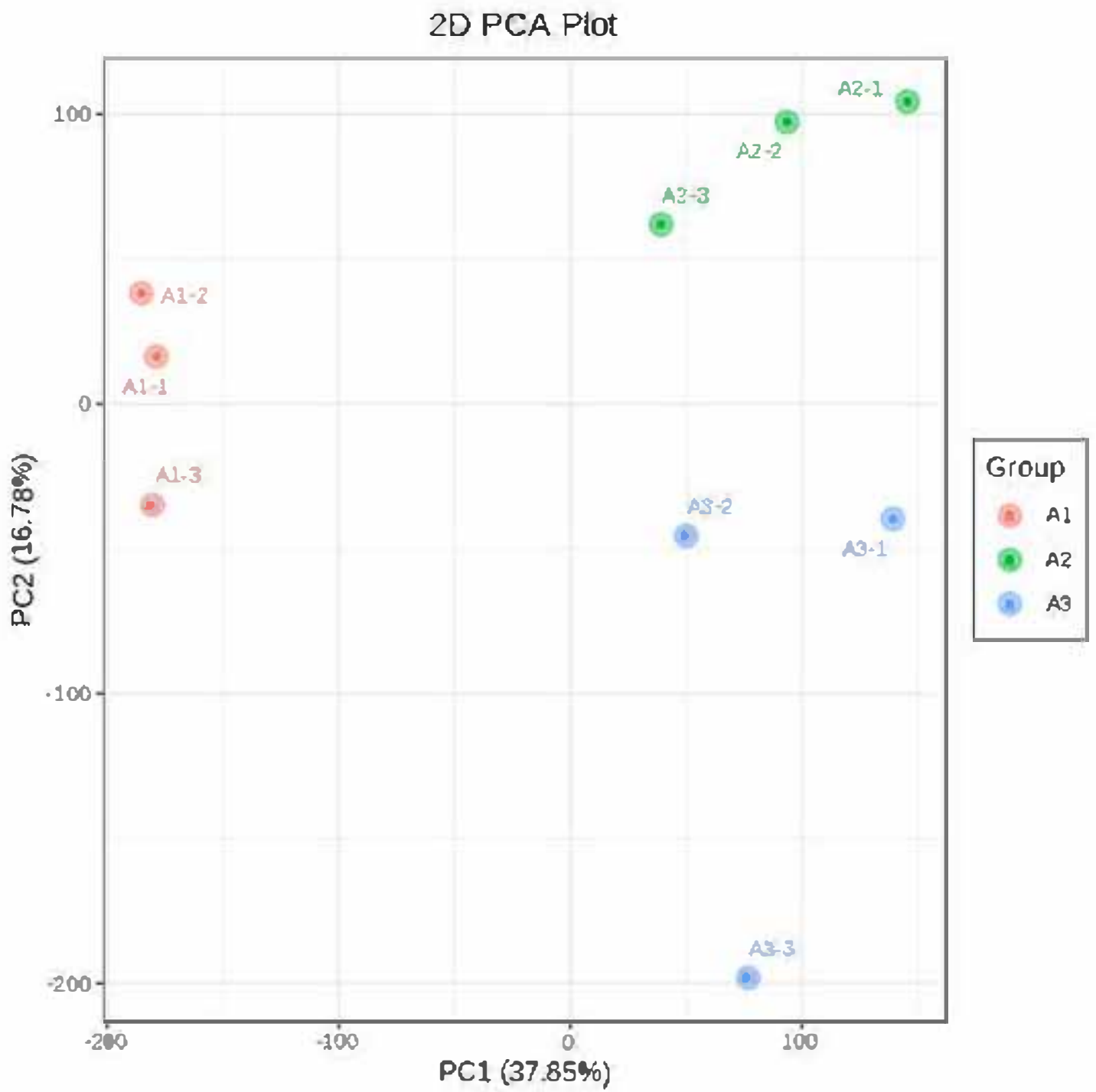
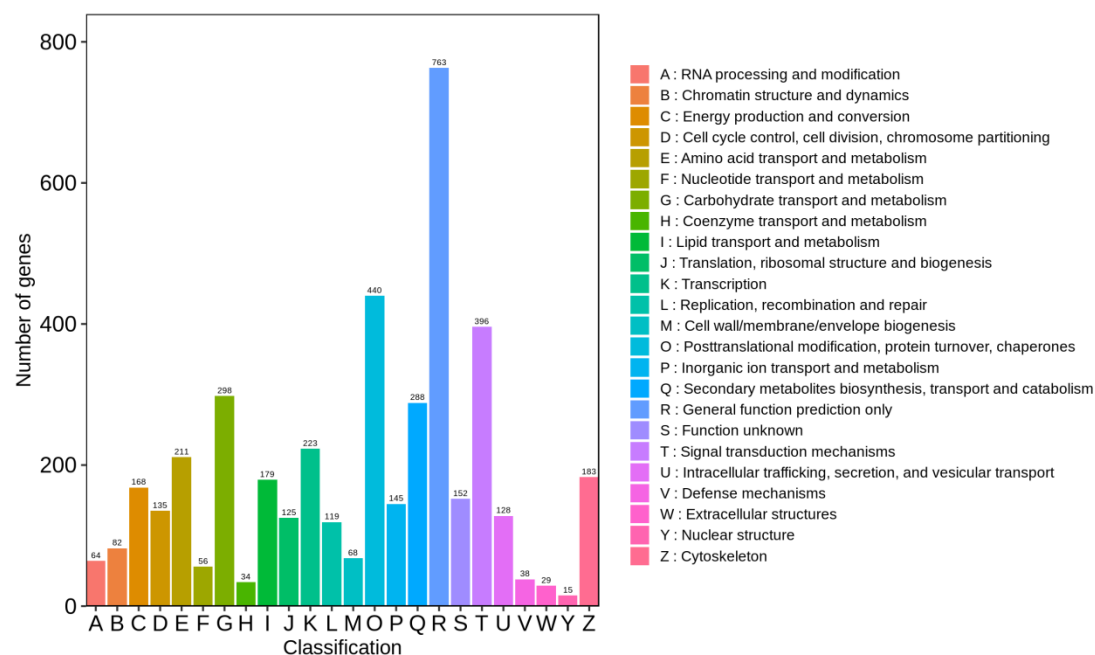
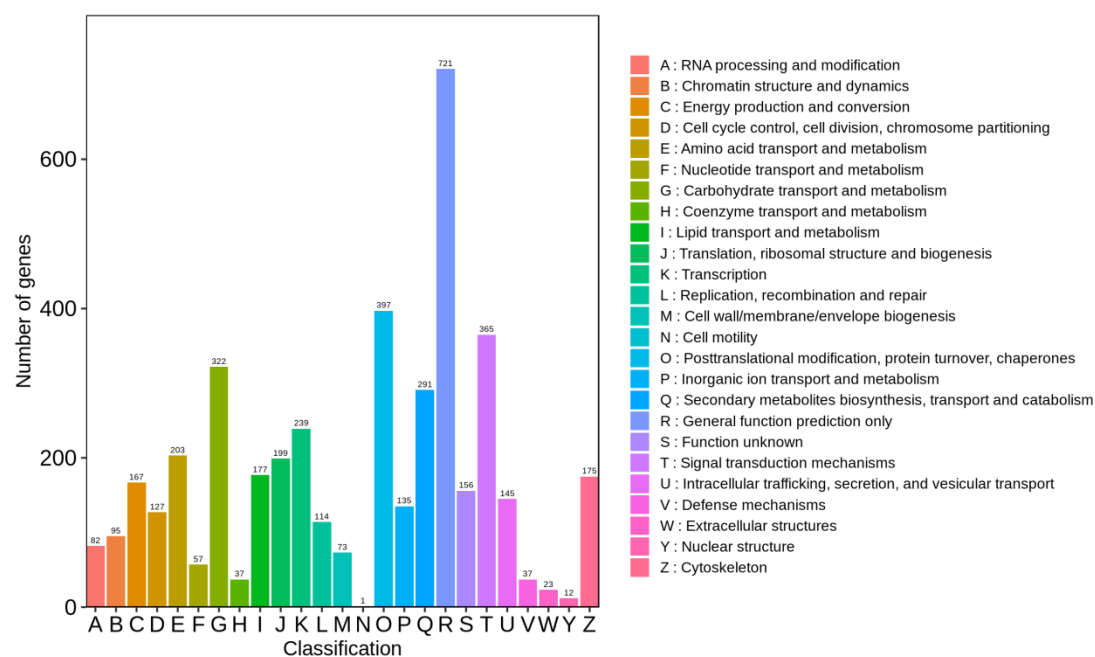


Figure 2. PCA Results.

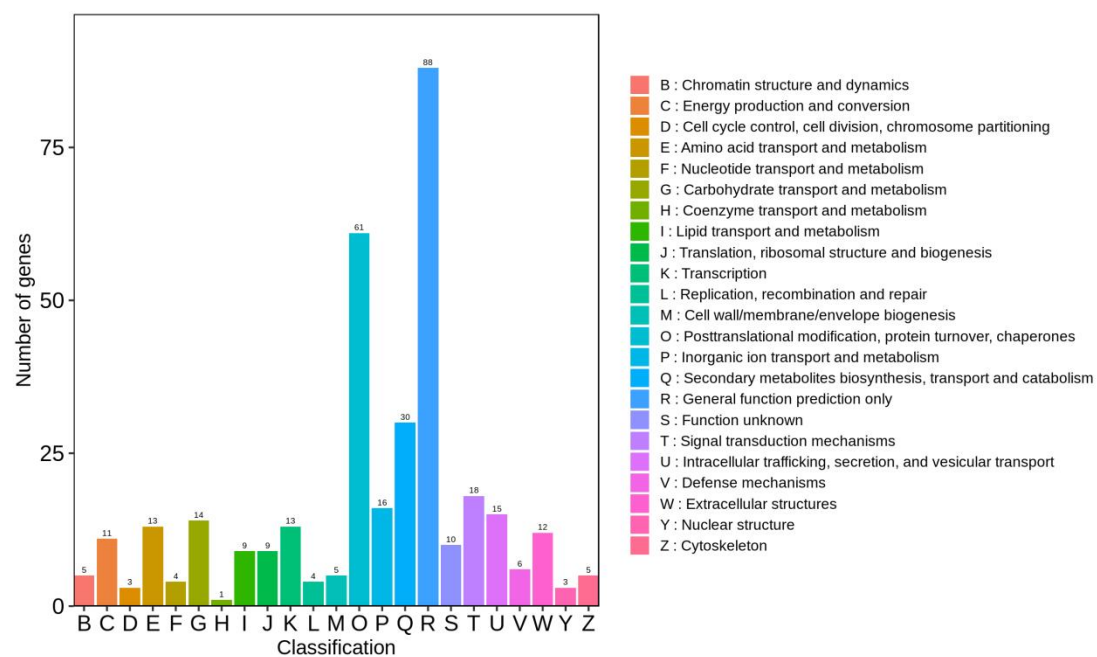


A



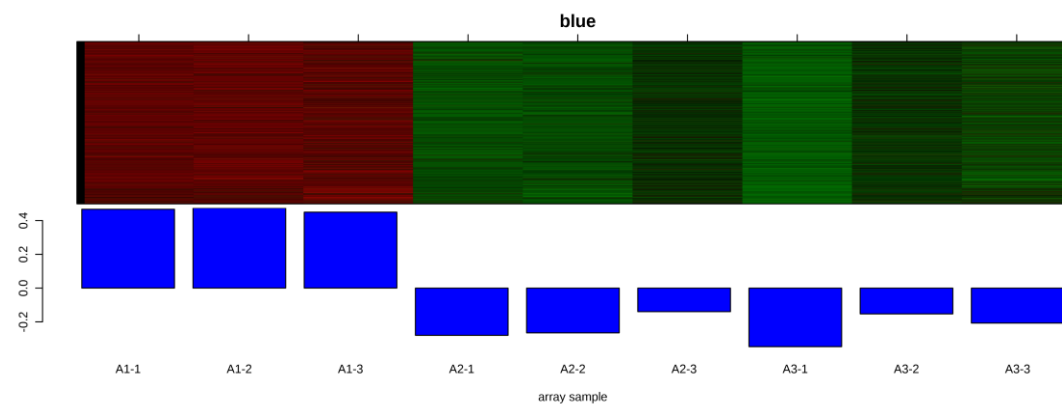
B

Figure S3. KOG function classification. A: A1-vs-A2 group, B: A1-vs-A3 group.

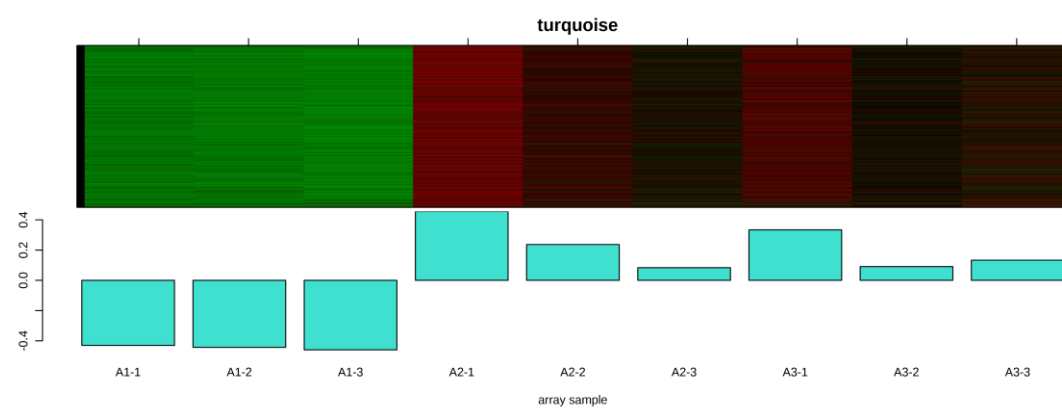


C

Figure S3 (continued). KOG function classification. C: A2-vs-A3 group.



A



B

Figure S4. Gene expression patterns of module. A: blue module, B: turquoise module.

Table S1 Summary of mapping reads

Sample	Total Reads	Reads mapped	Unique mapped	Multi mapped	Read1 mapped	Read2 mapped	+' mapped	-' mapped
A1-1	48925570	42133081(86.12%)	37789721(77.24%)	4343360(8.88%)	18925666(38.68%)	18864055(38.56%)	18898298(38.63%)	18891423(38.61%)
A1-2	42941472	36689365(85.44%)	32836391(76.47%)	3852974(8.97%)	16437056(38.28%)	16399335(38.19%)	16404495(38.20%)	16431896(38.27%)
A1-3	56000682	48206282(86.08%)	43352020(77.41%)	4854262(8.67%)	21742258(38.82%)	21609762(38.59%)	21673949(38.70%)	21678071(38.71%)
A2-1	44705082	38288174(85.65%)	34249642(76.61%)	4038532(9.03%)	17243811(38.57%)	17005831(38.04%)	17110315(38.27%)	17139327(38.34%)
A2-2	39678378	34330905(86.52%)	30739704(77.47%)	3591201(9.05%)	15482776(39.02%)	15256928(38.45%)	15354938(38.70%)	15384766(38.77%)
A2-3	47810308	41439870(86.68%)	37076597(77.55%)	4363273(9.13%)	18566492(38.83%)	18510105(38.72%)	18537285(38.77%)	18539312(38.78%)
A3-1	53666032	46774527(87.16%)	41804174(77.90%)	4970353(9.26%)	20890849(38.93%)	20913325(38.97%)	20907898(38.96%)	20896276(38.94%)
A3-2	40353668	34501400(85.50%)	30831965(76.40%)	3669435(9.09%)	15433142(38.24%)	15398823(38.16%)	15408409(38.18%)	15423556(38.22%)
A3-3	45718786	39316087(86.00%)	35204508(77.00%)	4111579(8.99%)	17596121(38.49%)	17608387(38.51%)	17596121(38.49%)	17608387(38.51%)

Table S2. GO GESA in A1 vs A2

NAME	GO ID	SIZE	ES	NES
LOCOMOTION	GO:0040011	147	0.5552808	1.4334292
NUTRIENT RESERVOIR ACTIVITY	GO:0045735	23	0.35643333	1.401939
IMMUNE SYSTEM PROCESS	GO:0002376	785	0.29166946	1.3217136
GENERAL TRANSCRIPTION INITIATION FACTOR ACTIVITY	GO:0140223	15	0.6065685	1.2432882
BIOLOGICAL PROCESS INVOLVED IN INTERSPECIES INTERACTION BETWEEN ORGANISMS	GO:0044419	2758	0.21960965	1.2134597
PROTEIN TAG	GO:0031386	20	0.35082665	0.96741635
CARBON UTILIZATION	GO:0015976	25	0.22502321	0.81640565
TOXIN ACTIVITY	GO:0090729	52	-0.666831	-1.8551861
MOLECULAR FUNCTION REGULATOR	GO:0098772	1264	-0.35258442	-1.7536683
ANTIOXIDANT ACTIVITY	GO:0016209	222	-0.42529437	-1.6953052
MOLECULAR CARRIER ACTIVITY	GO:0140104	90	-0.40299073	-1.6599253
GROWTH	GO:0040007	1474	-0.37189227	-1.636863
BIOLOGICAL PROCESS INVOLVED IN INTRASPECIES INTERACTION BETWEEN ORGANISMS	GO:0051703	25	-0.56267035	-1.6064404
REPRODUCTION	GO:0000003	3870	-0.2878866	-1.5312333
MOLECULAR TRANSDUCER ACTIVITY	GO:0060089	543	-0.29972214	-1.5247681
REPRODUCTIVE PROCESS	GO:0022414	3844	-0.28691363	-1.522695
TRANSPORTER ACTIVITY	GO:0005215	2308	-0.2952147	-1.4781028
LOCALIZATION	GO:0051179	4628	-0.2727091	-1.4439822
SMALL MOLECULE SENSOR ACTIVITY	GO:0140299	33	-0.5095702	-1.4184793
STRUCTURAL MOLECULE ACTIVITY	GO:0005198	828	-0.49291703	-1.3917829
RHYTHMIC PROCESS	GO:0048511	408	-0.2557086	-1.3703744
NEGATIVE REGULATION OF BIOLOGICAL PROCESS	GO:0048519	2601	-0.24857748	-1.3699057
BIOLOGICAL ADHESION	GO:0022610	49	-0.6256175	-1.3534654
PIGMENTATION	GO:0043473	60	-0.4199764	-1.3436227
PROTEIN FOLDING CHAPERONE	GO:0044183	46	-0.34417495	-1.3112055
MULTI-ORGANISM PROCESS	GO:0051704	955	-0.26102254	-1.307387
SIGNALING	GO:0023052	3514	-0.22745493	-1.2937692
POSITIVE REGULATION OF BIOLOGICAL PROCESS	GO:0048518	2670	-0.21377203	-1.2578028
TRANSCRIPTION REGULATOR ACTIVITY	GO:0140110	3172	-0.22840562	-1.2341813
NITROGEN UTILIZATION	GO:0019740	29	-0.33935145	-0.983415
DETOXIFICATION	GO:0098754	82	-0.21145007	-0.86656374
MOLECULAR ADAPTOR ACTIVITY	GO:0060090	156	-0.16926783	-0.8034387
TRANSLATION REGULATOR ACTIVITY	GO:0045182	322	-0.14082304	-0.71667486

Note: SIZE represents the number of genes in the enriched gene set, ES represents enrichment ccore, NES represents normalized enrichment score.

Table S3 GO GESA in A1 vs A3

NAME	GO_ID	SIZE	ES	NES
LOCOMOTION	GO:0040011	147	0.5281227	1.3209519
GENERAL TRANSCRIPTION INITIATION FACTOR ACTIVITY	GO:0140223	15	0.63850564	1.2288884
IMMUNE SYSTEM PROCESS	GO:0002376	785	0.24435487	1.0626987
CARBON UTILIZATION	GO:0015976	25	0.2764965	0.96511114
TRANSLATION REGULATOR ACTIVITY	GO:0045182	322	0.13990986	0.7801411
PIGMENTATION	GO:0043473	60	0.20107378	0.68635267
SMALL MOLECULE SENSOR ACTIVITY	GO:0140299	33	0.1702684	0.5045698
MOLECULAR FUNCTION REGULATOR	GO:0098772	1264	-0.36162502	-1.9046954
TOXIN ACTIVITY	GO:0090729	52	-0.61213195	-1.4508703
STRUCTURAL MOLECULE ACTIVITY	GO:0005198	828	-0.5682868	-1.441199
ANTIOXIDANT ACTIVITY	GO:0016209	222	-0.4403264	-1.4134021
TRANSPORTER ACTIVITY	GO:0005215	2308	-0.2848857	-1.41239
BIOLOGICAL ADHESION	GO:0022610	49	-0.55884176	-1.4080366
LOCALIZATION	GO:0051179	4628	-0.25530943	-1.3951498
NUTRIENT RESERVOIR ACTIVITY	GO:0045735	23	-0.36377132	-1.3544226
GROWTH	GO:0040007	1474	-0.29581913	-1.3346087
MULTI-ORGANISM PROCESS	GO:0051704	955	-0.27717793	-1.3322734
DETOXIFICATION	GO:0098754	82	-0.42341945	-1.2837774
PROTEIN FOLDING CHAPERONE	GO:0044183	46	-0.40605736	-1.2816278
REPRODUCTIVE PROCESS	GO:0022414	3844	-0.25903106	-1.2299156
REPRODUCTION	GO:0000003	3870	-0.2588915	-1.2269136
TRANSCRIPTION REGULATOR ACTIVITY	GO:0140110	3172	-0.22647743	-1.1751968
PROTEIN TAG	GO:0031386	20	-0.4812725	-1.1419796
SIGNALING	GO:0023052	3514	-0.21156059	-1.0940124
MOLECULAR CARRIER ACTIVITY	GO:0140104	90	-0.3268193	-1.0895159
MOLECULAR TRANSDUCER ACTIVITY	GO:0060089	543	-0.24356613	-1.0857776
BIOLOGICAL PROCESS INVOLVED IN INTRASPECIES INTERACTION BETWEEN ORGANISMS	GO:0051703	25	-0.43294144	-1.0790561
BIOLOGICAL PROCESS INVOLVED IN INTERSPECIES INTERACTION BETWEEN ORGANISMS	GO:0044419	2758	-0.20670593	-1.0765493
NEGATIVE REGULATION OF BIOLOGICAL PROCESS	GO:0048519	2601	-0.21006049	-1.0076892
POSITIVE REGULATION OF BIOLOGICAL PROCESS	GO:0048518	2670	-0.19441652	-0.9680842
MOLECULAR ADAPTOR ACTIVITY	GO:0060090	156	-0.17850596	-0.9121554
RHYTHMIC PROCESS	GO:0048511	408	-0.20957606	-0.9100356
NITROGEN UTILIZATION	GO:0019740	29	-0.29902765	-0.8272227

Table S4. GO GESA in A2 vs A2

NAME	GO_ID	SIZE	ES	NES
SMALL MOLECULE SENSOR ACTIVITY	GO:0140299	33	0.6856099	1.5951768
BIOLOGICAL ADHESION	GO:0022610	49	0.59116346	1.5294495
GROWTH	GO:0040007	1474	0.33081198	1.3127905
PIGMENTATION	GO:0043473	60	0.40773982	1.2532766
MOLECULAR CARRIER ACTIVITY	GO:0140104	90	0.38360447	1.215418
MOLECULAR TRANSDUCER ACTIVITY	GO:0060089	543	0.27539077	1.1940435
REPRODUCTION	GO:0000003	3870	0.27081585	1.1673399
REPRODUCTIVE PROCESS	GO:0022414	3844	0.2701529	1.1672101
NEGATIVE REGULATION OF BIOLOGICAL PROCESS	GO:0048519	2601	0.2646961	1.1671758
CARBON UTILIZATION	GO:0015976	25	0.30086786	1.1569184
RHYTHMIC PROCESS	GO:0048511	408	0.26791164	1.156115
POSITIVE REGULATION OF BIOLOGICAL PROCESS	GO:0048518	2670	0.24145253	1.1181551
LOCALIZATION	GO:0051179	4628	0.2111572	1.0818332
TRANSCRIPTION REGULATOR ACTIVITY	GO:0140110	3172	0.2165514	1.0594546
MOLECULAR FUNCTION REGULATOR	GO:0098772	1264	0.2176505	1.042795
GENERAL TRANSCRIPTION INITIATION FACTOR ACTIVITY	GO:0140223	15	0.30996624	1.0406257
SIGNALING	GO:0023052	3514	0.19870324	0.99570453
MOLECULAR ADAPTOR ACTIVITY	GO:0060090	156	0.19295609	0.95759916
MULTI-ORGANISM PROCESS	GO:0051704	955	0.18432692	0.86549115
TRANSPORTER ACTIVITY	GO:0005215	2308	0.17868923	0.8318097
TOXIN ACTIVITY	GO:0090729	52	0.27156582	0.7915285
BIOLOGICAL PROCESS INVOLVED IN INTRASPECIES INTERACTION BETWEEN ORGANISMS	GO:0051703	25	0.23764025	0.7525019
LOCOMOTION	GO:0040011	147	0.21613456	0.71382546
DETOXIFICATION	GO:0098754	82	-0.54018205	-1.4867309
PROTEIN TAG	GO:0031386	20	-0.7759457	-1.4578713
ANTIOXIDANT ACTIVITY	GO:0016209	222	-0.374144	-1.4362376
BIOLOGICAL PROCESS INVOLVED IN INTERSPECIES INTERACTION BETWEEN ORGANISMS	GO:0044419	2758	-0.25648308	-1.289833
NUTRIENT RESERVOIR ACTIVITY	GO:0045735	23	-0.40581352	-1.2604636
STRUCTURAL MOLECULE ACTIVITY	GO:0005198	828	-0.42209563	-1.2585585
PROTEIN FOLDING CHAPERONE	GO:0044183	46	-0.36608875	-1.2307667
IMMUNE SYSTEM PROCESS	GO:0002376	785	-0.2239122	-1.0185963
NITROGEN UTILIZATION	GO:0019740	29	-0.35718152	-0.9718953
TRANSLATION REGULATOR ACTIVITY	GO:0045182	322	-0.15182014	-0.77393824

Table S6 Correlations between altitude and main medicinal components, and morphological characterization

Index	Total acylamide	Total flavonoids	Total alkaloidsa	Volatile oil	Yield	Hundred grains mass	Normal mass	Carpopodium mass	Mass of coat-closing fruits
altitude	0.904**	0.935**	0.903**	0.903**	0.892**	0.904**	0.847**	-0.869**	-0.844**