

Supplementary Material

Quality evaluation of dandelion by HPLC five-wavelength fusion fingerprint in combination with antioxidant activity

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Table S1. Origin of 18 batches of samples

Sample	Place of origin
S1	Gansu
S2	Gansu
S3	Gansu
S4	Shaanxi
S5	Shaanxi
S6	Shaanxi
S7	Henan
S8	Shanxi
S9	Inner Mongolia
S10	Chongqing
S11	Henan
S12	Gansu
S13	Guangxi
S14	Sichuan
S15	Anhui
S16	Anhui
S17	Shandong
S18	Jilin

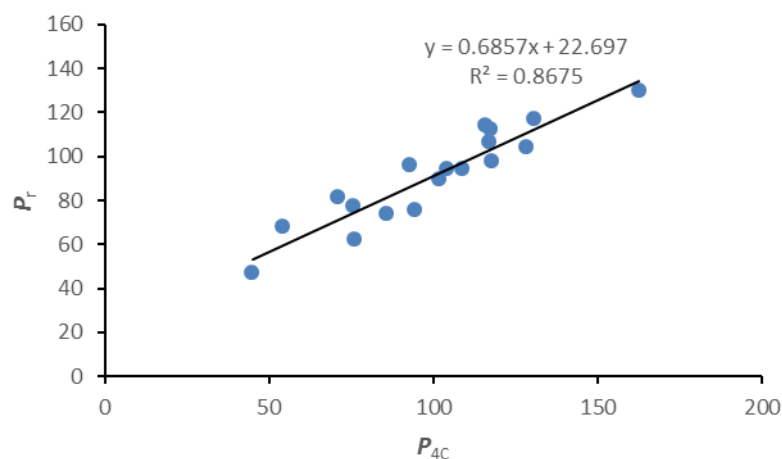


Fig.S1 The linear correlation between the average percentage of four analytes (P_{4C}) and the macro quantitative similarity factors (P_r)

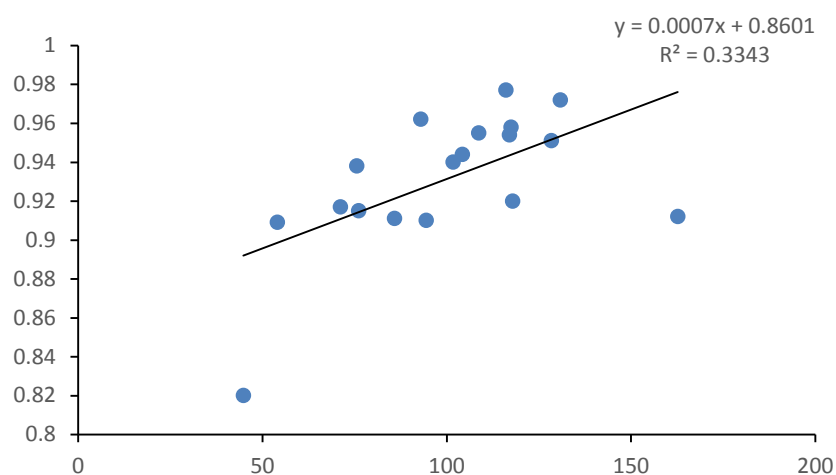


Fig.S2 The linear correlation between the average percentage of four analytes (P_{4C}) and the macro qualitative similarity factors (S_r)

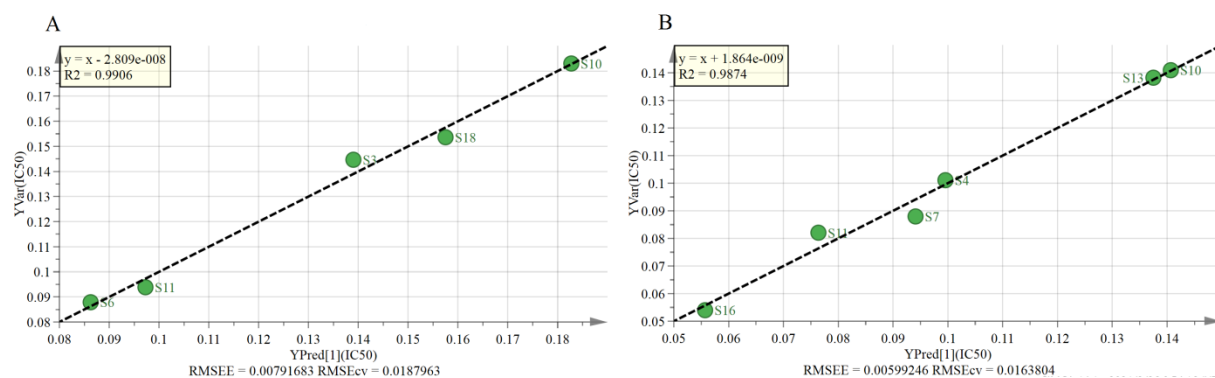


Fig.S3 plot of Y observed versus Y predicted for the prediction model for DPPH test (A) and prediction model for ABTS test (B)

Table S2 Overview of the experimental and predicted values for total antioxidant activity of DPPH and ABTS test obtained by OPLS model

Sample	DPPH			Sample	ABTS		
	Y _{Var} (IC50)	Y _{Pred} (IC50)	RE% ^c		Y _{Var} (IC50)	Y _{Pred} (IC50)	RE% ^c
S1 ^a	0.153	0.137	-10.86	S1 ^a	0.110	0.111	0.54
S2 ^a	0.151	0.138	-8.51	S2 ^a	0.082	0.086	5.40
S4 ^a	0.107	0.122	13.76	S3 ^a	0.124	0.121	-2.17
S5 ^a	0.095	0.103	7.79	S5 ^a	0.106	0.106	-0.40
S7 ^a	0.119	0.129	9.06	S6 ^a	0.060	0.060	0.80
S8 ^a	0.191	0.192	0.58	S8 ^a	0.124	0.129	3.69
S9 ^a	0.081	0.072	-10.89	S9 ^a	0.086	0.083	-3.23
S12 ^a	0.151	0.143	-5.26	S12 ^a	0.096	0.095	-0.67
S13 ^a	0.205	0.212	3.11	S14 ^a	0.201	0.200	-0.66
S14 ^a	0.296	0.282	-4.99	S15 ^a	0.130	0.132	1.66
S15 ^a	0.185	0.209	12.47	S17 ^a	0.095	0.092	-3.20
S16 ^a	0.109	0.108	-0.83	S18 ^a	0.109	0.108	-1.23
S17 ^a	0.156	0.154	-0.93	S4 ^b	0.101	0.100	-1.34
S3 ^b	0.145	0.139	-3.96	S7 ^b	0.088	0.094	6.81
S6 ^b	0.088	0.086	-1.70	S10 ^b	0.141	0.141	-0.16
S10 ^b	0.183	0.183	-0.10	S11 ^b	0.082	0.076	-6.82
S11 ^b	0.094	0.097	3.68	S13 ^b	0.138	0.138	-0.31
S18 ^b	0.154	0.158	2.57	S16 ^b	0.054	0.056	2.97

^aUsed for the validation model.

^bUsed for the prediction model.

^cRE: relative error.