Table S1. List of primers used for real-time PCR.

Gene name		Primer sequence
BrMYB28.1	F	5´-TTCCTGACAAATACTCTCGCC-3´
	R	5´-CCGAGATCAGAAGTAGCGTTG-3´
BrMYB28.2	F	5´-GGTTTCAACACGGTTTTCGAG-3´
	R	5´-AAGCCTTGATGTAGAACTTGATTTC-3´
BrMYB28.3	F	5´-CCTGGGAACTTGCATTCTCTAG-3´
	R	5´-GAAAGAGGACGAGACATGGAAG-3´
BrMYB29.1	F	5´-GAACCTTGATCCCCTCTACAAC-3´
	R	5´-ATTGCTCCAGAAACTCCGAG-3´
BrMYB34.1	F	5´-GGATCATGTTGGTCTTATGGAGG-3´
	R	5´-CTCCAAGTCCAGATCGTCATTC-3´
BrMYB34.2	F	5´-ACCAAGAATTCGACCTCCAC-3´
	R	5´-AGAACAGTTGTCGGAGAAACC-3´
BrMYB34.3	F	5´-GAACATTCAACGTCCACACTG-3´
	R	5´-GAAAGAACCGGGAGAAGTCG-3´
BrMYB34.4	F	5´-TGCATTATGGAAGAGTTGAGGG-3´
	R	5´-AGAACCAAGAAACTCCATCCC-3´
BrMYB51.1	F	5´-ATTTGCAGGATATTCTGGAG-3´
	R	5´-GAACCTAGCCGACTTCTCCATCTT-3´
BrMYB51.2	F	5´-TCTTTCACACCAACCTCAGATC-3´
	R	5´-ATCATTAACGGATGCCTCAGAG-3´
BrMYB51.3	F	5´-ACAGGGTGGCTAATAGGTTTG-3´
	R	5´-ACTTATCTGAAATAGAGTCAACGGTG-3´
BrMYB122.1	F	5´-CTCTCCACACCAAACTCTTCG-3´
	R	5´-TGAGCGGAGGTATCGTTAGAG-3´
BrMYB122.2	F	5´-ACAAATCACTTAATGGTAAATCA-3´
	R	5´-AGAACCGAGCTGATAATGATCC-3´
BrActin	F	5´-GAACCGGGTGCTCCTCAGGA-3´
	R	5´-ATGGTACCGGAATGGTCAAGGC-3´

Table S2. Correlation analysis of relative expression level of *BrMYB* TFs related to GSL biosynthesis and GSL content in 19 accessions of *B. rapa* ssp. *pekinensis* .

Gene	PRO	GRA	SNG	GAL	GNL	GNA	GCC	GBN	Aliphatic GSLs	GBS	4-MOGBS	NGBS	Indolic GSLs	GNT	Total GSLs
BrMYB28.1	-0.183	-0.185	-0.163	-0.092	-0.229	-0.108	-0.080	-0.149	-0.149	-0.146	0.106	-0.283	-0.150	-0.111	-0.178
BrMYB28.2	-0.186	-0.208	0.221	-0.377	-0.234	-0.131	-0.103	-0.087	-0.164	0.139	0.251	-0.331	0.038	-0.053	-0.147
BrMYB28.3	0.214	-0.208	0.433	-0.027	-0.111	0.352	0.294	**0.530***	0.428	-0.133	-0.093	-0.346	-0.243	**0.466***	0.392
BrMYB29.1	0.154	-0.074	**0.495***	-0.239	-0.035	-0.128	-0.085	-0.062	-0.112	0.184	0.101	-0.262	0.032	0.192	-0.088
BrMYB34.1	-0.007	0.097	0.022	-0.273	-0.008	-0.091	-0.291	0.059	-0.078	0.079	0.009	-0.095	0.008	-0.036	-0.077
BrMYB34.2	-0.144	-0.168	-0.004	-0.291	-0.110	-0.197	-0.371	-0.231	-0.259	-0.344	-0.277	-0.395	-0.445	-0.352	-0.349
BrMYB34.3	-0.335	-0.267	-0.005	-0.364	-0.339	-0.235	-0.415	-0.254	-0.318	-0.141	-0.301	-0.429	-0.360	-0.372	-0.387
BrMYB34.4	-0.176	-0.076	-0.021	-0.104	-0.135	-0.170	-0.227	-0.217	-0.217	-0.468	-0.222	-0.208	-0.416	-0.251	-0.297
BrMYB51.1	-0.112	0.347	-0.146	0.390	-0.098	-0.134	-0.123	-0.147	-0.124	**0.590****	0.370	**0.488***	**0.648****	-0.001	-0.005
BrMYB51.2	0.403	0.058	-0.101	-0.155	**0.619****	0.028	-0.177	0.103	0.070	-0.180	-0.296	0.000	-0.208	0.018	0.029
BrMYB51.3	-0.214	-0.216	-0.160	-0.126	-0.253	-0.059	-0.006	-0.114	-0.106	-0.056	0.188	-0.269	-0.065	-0.094	-0.120
BrMYB122.1	-0.248	-0.181	0.304	-0.238	-0.159	-0.191	-0.236	-0.263	-0.260	0.113	-0.020	-0.346	-0.085	-0.149	-0.266
BrMYB122.2	-0.270	-0.104	**0.551***	-0.248	-0.318	0.048	0.052	-0.014	-0.011	0.288	0.079	-0.099	0.144	0.120	0.034

* and ** indicated a significant correlated at the level of P< 0.05, P<0.01, respectively and without any * means not significant.

Table S3. Correlation analysis of relative expression level of *BrMYB* TFs related to GSL biosynthesis and GSL content in five accessions of *B. rapa* ssp. *chinensis*.

Gene	PRO	GRA	SNG	GAL	GNL	GNA	GCC	GBN	Aliphatic GSLs	GBS	4-MOGBS	NGBS	Indolic GSLs	GNT	Total GSLs
BrMYB28.1	-0.414	0.552	0.079	-0.480	-0.514	-0.298	-0.311	-0.751	-0.731	-0.531	0.826	-0.353	-0.271	-0.542	-0.688
BrMYB28.2	-0.111	0.433	0.429	-0.690	-0.129	-0.345	-0.377	-0.923	-0.788	-0.870	0.470	-0.705	-0.833	-0.940	-0.856
BrMYB28.3	**0.928***	-0.805	-0.434	0.648	0.815	-0.789	0.373	0.405	-0.353	0.277	-0.056	-0.680	-0.137	-0.231	-0.346
BrMYB29.1	-0.128	0.402	-0.384	-0.187	-0.249	-0.572	-0.366	-0.431	-0.800	-0.305	**0.977****	-0.319	-0.026	-0.320	-0.701
BrMYB34.1	-0.405	0.722	-0.415	-0.352	-0.423	-0.184	-0.641	-0.331	-0.466	-0.277	**0.905***	0.205	0.222	0.069	-0.356
BrMYB34.2	-0.478	0.767	-0.237	-0.426	-0.337	0.361	-0.732	-0.057	0.156	-0.171	0.335	0.713	0.337	0.474	0.211
BrMYB34.3	-0.314	0.679	-0.445	-0.338	-0.344	-0.301	-0.646	-0.355	-0.570	-0.315	**0.949***	0.085	0.151	-0.020	-0.463
BrMYB34.4	-0.622	**0.968****	-0.004	-0.723	-0.509	0.260	-0.828	-0.490	-0.167	-0.520	0.557	0.430	0.015	0.069	-0.136
BrMYB51.1	-0.370	-0.193	-0.192	0.514	-0.399	0.586	0.471	0.655	0.807	0.823	-0.320	0.824	**0.910***	**0.902***	**0.893***
BrMYB51.2	-0.172	0.435	-0.363	-0.213	-0.289	-0.535	-0.377	-0.448	-0.782	-0.314	**0.978****	-0.288	-0.017	-0.309	-0.684
BrMYB51.3	**0.973****	-0.545	-0.593	0.465	**0.978****	-0.711	-0.071	0.478	-0.273	0.143	-0.047	-0.425	-0.112	-0.037	-0.272
BrMYB122.1	-0.498	0.789	-0.152	-0.485	-0.341	0.414	-0.744	-0.099	0.185	-0.222	0.275	0.711	0.275	0.439	0.223
BrMYB122.2	-0.305	0.273	**0.888***	-0.674	-0.281	0.172	-0.026	-0.834	-0.262	-0.714	-0.118	-0.483	-0.824	-0.815	-0.392

* and ** indicated a significant correlated at the level of $P< 0.05$, $P<0.01$, respectively and without any * means not significant.

Table S4. Correlation analysis of relative expression level of *BrMYB* TFs related to GSL biosynthesis and GSLs content in six accessions of *B. rapa* ssp. *rapa*.

Gene	PRO	GRA	SNG	GAL	GNL	GNA	GCC	GBN	Aliphatic GSLs	GBS	4-MOGBS	NGBS	Indolic GSLs	GNT	Total GSLs
BrMYB28.1	0.428	-0.141	-0.064	-0.102	-0.137	0.612	0.310	-0.184	0.664	-0.513	0.165	-0.763	-0.701	-0.367	0.633
BrMYB28.2	0.514	-0.103	-0.726	-0.670	0.600	-0.337	0.765	-0.236	-0.153	0.108	0.114	-0.523	-0.066	-0.924	-0.168
BrMYB28.3	-0.243	-0.444	-0.782	-0.520	**0.876***	-0.893	0.564	0.289	-0.630	0.506	-0.066	0.316	0.555	-0.310	-0.614
BrMYB29.1	0.657	0.481	0.462	0.505	-0.285	0.466	-0.476	0.218	0.431	0.424	-0.518	0.568	0.465	0.251	0.456
BrMYB34.1	0.133	-0.287	-0.909	-0.412	0.627	-0.404	**0.990****	-0.239	-0.155	-0.231	0.452	-0.540	-0.296	-0.866	-0.180
BrMYB34.2	-0.010	-0.467	-0.706	-0.425	0.431	-0.123	**0.844***	-0.183	0.082	-0.455	0.449	-0.740	-0.572	-0.655	0.050
BrMYB34.3	-0.119	-0.731	0.015	-0.338	0.434	-0.027	-0.238	**0.954****	0.188	0.697	-0.821	0.618	0.657	0.570	0.224
BrMYB34.4	-0.122	0.024	0.244	**0.837***	-0.320	0.457	-0.165	0.232	0.498	-0.275	0.064	0.375	-0.096	0.453	0.502
BrMYB51.1	-0.730	0.435	0.235	0.228	-0.453	-0.369	-0.217	-0.656	-0.685	-0.496	0.688	-0.187	-0.350	0.110	-0.701
BrMYB51.2	-0.403	-0.035	0.325	0.549	-0.119	-0.032	-0.481	0.486	-0.032	0.298	-0.287	**0.873***	0.519	0.752	0.000
BrMYB51.3	0.216	-0.208	-0.812	-0.439	0.508	-0.283	**0.935****	-0.345	-0.087	-0.315	0.475	-0.694	-0.422	-0.904	-0.117
BrMYB122.1	-0.133	-0.561	0.300	-0.413	-0.109	0.429	-0.281	0.354	0.420	-0.063	-0.350	-0.304	-0.252	0.382	0.416
BrMYB122.2	-0.302	-0.128	0.310	0.757	-0.331	0.450	-0.258	0.331	0.479	-0.275	0.013	0.384	-0.105	0.615	0.485

* and ** indicated a significant correlated at the level of $P < 0.05$, $P < 0.01$, respectively and without any * means not significant.