

Table S3. ITS2 variants which have been verified by PCR products cloned or directly sequenced.

ITS2 variant*	Method	Confirmed (clone number)
<i>Alpinia_hainanensis_1_33.84</i>	Clone	Yes(2)
<i>Alpinia_hainanensis_2_30.06</i>	Clone	Yes(2)
<i>Alpinia_hainanensis_3_28.78</i>	Clone	Yes(5)
<i>Brucea_javanica_1_89.32</i>	PCR	Yes
<i>Brucea_mollis_1_62.64</i>	PCR	Yes
<i>Cerasus_glandulosa_1_14.08</i>	Clone	Yes(9)
<i>Cerasus_glandulosa_6_10.52</i>	Clone	Yes(16)
<i>Cerasus_glandulosa_7_6.26</i>	Clone	Yes(6)
<i>Cerasus_glandulosa_8_3.56</i>	Clone	No
<i>Cerasus_glandulosa_10_2.7</i>	Clone	Yes(1)
<i>Cerasus_glandulosa_12_2.24</i>	Clone	No
<i>Cerasus_japonica_1_20.47</i>	Clone	Yes(15)
<i>Cerasus_japonica_6_8.84</i>	Clone	Yes(7)
<i>Cerasus_japonica_7_8.42</i>	Clone	Yes(6)
<i>Cerasus_japonica_8_4.92</i>	Clone	Yes(3)
<i>Cerasus_japonica_10_2.64</i>	Clone	No
<i>Cerasus_japonica_11_1.78</i>	Clone	No
<i>Citrus_limonum_1_45.53</i>	PCR	Yes
<i>Citrus_maxima_3_8.37</i>	PCR	Yes
<i>Citrus_medica_1_75.75</i>	PCR	Yes
<i>Citrus_reticulata_3_17.46</i>	PCR	Yes
<i>Epimedium_acuminatum_1_77.27</i>	PCR	Yes
<i>Epimedium_pubescens_1_72.55</i>	PCR	Yes
<i>Epimedium_pubescens_2_21.97</i>	PCR	Yes
<i>Epimedium_sagittatum_1_50.86</i>	PCR	Yes
<i>Epimedium_sagittatum_2_44.44</i>	PCR	Yes
<i>Ipomoea_purpurea_1_97.87</i>	PCR	Yes
<i>Ligusticum_jeholense_1_28.63</i>	PCR	Yes
<i>Ligusticum_jeholense_2_22.29</i>	PCR	Yes
<i>Ligusticum_sinense_1_42.72</i>	PCR	Yes
<i>Ligusticum_sinense_2_36.02</i>	PCR	Yes
<i>Ligusticum_sinense_4_4.84</i>	PCR	Yes
<i>Ligusticum_sinense_cv._Chuanxiong_1_40.92</i>	PCR	Yes
<i>Ligusticum_sinense_cv._Chuanxiong_3_11.2</i>	PCR	Yes

Panax_quinquefolius_1_98.44	PCR	Yes
Pinus_strobilus_1_77.01	PCR	Yes
Pinus_wallichiana_1_24.24	PCR	Yes
Pinus_wallichiana_4_9.44	PCR	Yes
Potentilla_chinensis_6_4.72	Specific Primer	Yes
Potentilla_nivea_4_2.27	Specific Primer	Yes
Torreya_fargesii_var._yunnanensis_1_94.4	PCR	Yes
Torreya_grandis_2_28.82	PCR	Yes
Torreya_nucifera_1_92.69	PCR	Yes

*Showing the name of species following the rank of the variant and the relative variant abundance.