

Supplementary Information

Table S1. Off targets prediction of Cs_target1 in the genomes of *Crocus sativus* and its three adulterants

Species	Number of mismatches					
	0	1	2	3	4	5
<i>Crocus sativus</i>	201	13	8	0	4	61
<i>Carthamus tinctorius</i>	0	0	0	0	0	17
<i>Nelumbo nucifera</i>	0	0	0	0	14	63
<i>Zea mays</i>	0	0	0	0	5	26

Table S2. Mismatch sites of Cs_target1 in the genome of *Crocus sativus*

Chromosome	Position	Sequence (5'→3')	Direction of strand	Number of mismatches
chr1	365527282	TTTGTGCCTACTCTtCGTGCCTTG	-	1
chr1	562319670	TTTGTGCCTACTCTCCGTGCCTgG	-	1
chr1	945245496	TTTGTGCCTACTCTtCGTGCCTTG	-	1
chr1	945453723	TTTGTGCCTACTCTcGTGCCTTG	-	1
chr2	16933964	TTTGTGCCTACTCTCCGTGCCTTc	+	1
chr2	9025836	TTTGTGCCTACTCTCCGTGCCTcTG	-	1
chr3	729719	TTTGTGCCTACTCTCCGcGTGCCTTG	-	1
chr3	746190	TTTGTGCCTACTCTCCGcGTGCCTTG	+	1
chr6	208473188	TTTGTGCCTACgCTCCGTGCCTTG	+	1
chr6	209771094	TTTGTGCCTACgCTCCGTGCCTTG	+	1
chr8	127085844	TTTGTGCCTACTCTCCGTGTCaTTG	-	1
chr8	65165634	TTTGTGCCTACTCTtCGTGCCTTG	+	1
chr8	65184893	TTTGTGCCTACTCTcGTGCCTTG	+	1
chr1	560187580	TTTGTGCCTACTCTtCGTGCCTgG	-	2
chr2	50064681	TTTGTGCCcACTCTCCGTGCCTTt	+	2
chr2	79230269	TTTGTGCCcACTCTCCGTGCCTTt	-	2
chr3	518276986	TTTGTGCCTACTCTCCGTGCCTgc	-	2
chr5	448736026	TTTGTGCCTACTCTagGTGCCTTG	+	2
chr5	449535986	TTTGTGCCTACTCTggGTGCCTTG	+	2
chr5	449948285	TTTGTGCCTACTCTagGTGCCTTG	-	2
tig00095233_pilon	187	TTTGTGCCTACTCTCCGTGCCTgc	-	2

The red and lowercase bases are the mismatch sites; tig00095233_pilon is a scaffold that doesn't

assemble into chromosomes.

Table S3. Targets located in the ITS2 region of five plants from different classes

Species	Target name	Target sequence	Copy number
<i>Ricinus communis</i>	Rc_target1	TTTCGATACATCGAGAGGGGGGCGG	222
	Rc_target2	GCCTCGTGCATGCGGTTGGCCTAAA	224
	Rc_target3	TCGGTGGTTGTAAGACTCTCTGAAA	241
<i>Setaria italica</i>	Si_target1	CGCCAAAAGACACTCCCAACCCAAA	19
	Si_target2	TTTGGCTCCCCGTGCTGCAAGGCGC	20
	Si_target3	TTTGGGCTGCCGGCATAACTTGTCG	20
<i>Ginkgo biloba</i>	Gb_target1	TGTCCCCGTGGCGCGGTTGACTAAA	1
	Gb_target2	GAGCGTCTCCACGAACAACCTCAAA	1
<i>Alsophila spinulosa</i>	As_target1	GCGATGGTGCCACGGTCGGCTGAAA	9
	As_target2	ACGTGCCTAGCCCGCTCGATCGAAA	11
<i>Selaginella tamariscina</i>	St_target1	TTTGGCCGTCCGTGGTGTCTCTCC	23

Table S4. List of plants used to verify Genome Analysis and Genome Editing (GAGE)

Class	Family	Species	Locality	Resource type
Angiosperms	Iridaceae	<i>Crocus sativus</i>	Dingzhou, Hebei	Cultivated
Angiosperms	Compositae	<i>Carthamus tinctorius</i>	Urumqi, Xinjiang	Cultivated
Angiosperms	Nelumbonaceae	<i>Nelumbo nucifera</i>	Beijing	Cultivated
Angiosperms	Euphorbiaceae	<i>Ricinus communis</i>	Qingyuan, Guangdong	Wild
Angiosperms	Poaceae	<i>Setaria italica</i>	Suqian, Jiangsu	Cultivated
Angiosperms	Poaceae	<i>Zea mays</i>	Nanning, Guangxi	Cultivated
Gymnosperms	Ginkgoaceae	<i>Ginkgo biloba</i>	Beijing	Cultivated
Ferns	Cyatheaceae	<i>Alsophila spinulosa</i>	Meishan, Sichuan	Cultivated
Lycophytes	Selaginellaceae	<i>Selaginella tamariscina</i>	Nanning, Guangxi	Cultivated

5'-GAGAGGAGAGAGGGGTGGGTGTGAATAAGGGGAAGAGGGGGAGAGGAGGG-3'

Fig. S1. The nucleotide sequence for 50 bp ssDNA reporter¹

Supplementary References

1. Bonini, A. et al. A label-free impedance biosensing assay based on CRISPR/Cas12a collateral activity for bacterial DNA detection. *J. Pharmaceut. Biomed.* **204**, 114268 (2021).