

**Table S3.** Microsatellite loci used to examine the genetic uniformity of regenerants and their respective donor plants of *Helianthus verticillatus*.

Core Loci <sup>A</sup>	Renamed Loci <sup>B</sup>	Forward and Reverse Primers 5'-3'	Repeat Motif	Number of Alleles	Allele Size Range (bp)
BL0006	HV006	F: CATGGGTGATCAATGGAGTG R: CGGCACATAACAAGTGCTTC	(gtga) <sub>3</sub>	2	230–265
BL0013	HV012	F: CGAGACGGTTAAGAGCTTGC R: GGTGTACAACCAACTCACACC	(gtta) <sub>3</sub>	4	337–349
BL0022	HV017	F: ACTTACCGTTGCATTTGGTG R: GCTTATCCCTAGAACACGATTACAG	(taa) <sub>4</sub>	2	105–108
BL0015	HV024	F: AATTGGAGCGGATGGTATTG R: AATATCTCTTATTTCAATAGTCCAACG	(atg) <sub>4</sub>	1	360
BL0019	HV026	F: GAGTCCTGGCCTGAACAGAG R: CAAACTGCAATGTACCTTCTTGAC	(gaaa) <sub>3</sub>	1	296
BL0024	HV028	F: CTCCCGCACTTCAAGCTAAC R: CATAACCTTTGCGGTTTCC	(gtaa) <sub>3</sub>	1	119
BL0031	HV031	F: CCGGAAGATAACGACGAGTG R: TCCATCGCTTTCCTAAATC	(gac) <sub>4</sub>	1	424
BL0033	HV033	F: GGGAGTTACACGCCTCCAG R: CACAACCATACGCCATCAAG	(cac) <sub>4</sub>	2	265–268
BL0034	HV034	F: GGTCGTCTACTACGGCTTCG R: TAACCGAACGACCATTCTTC	(tgtt) <sub>4</sub>	3	154–162
BL0037	HV037	F: GGTTAGGGTGAGGGTGGTG R: AAGCCATAGTAAGTTCCTCTTACAAAC	(tgca) <sub>3</sub>	3	152–176
BL0041	HV041	F: ACATTTGGACGTTTGGAAGC R: TCCATCGAGATGTTGACACG	(ctt) <sub>4</sub>	1	190
BL0042	HV042	F: GGTTACAACGGTGGAAGTCG R: TCCGGTTCACCAATTCATTC	(ggc) <sub>4</sub>	2	368–374
BL0046	HV046	F: GAACCAACACAACCAAATCC R: TGTCGCTTCAACGCATAAAC	(aaca) <sub>3</sub>	1	317
BL0048	HV048	F: TTGTGGAGACGGTGAATGAG R: TAACCGAACGACCATTCTTC	(gaa) <sub>4</sub>	1	224

<sup>A</sup>—All core loci taken from Pashley et al. [91]; <sup>B</sup>—Loci renamed by Edwards et al. [5].