

S4 Table. Summary of the diversity parameters for each collection site where *V. floribundum* individuals were collected.

Collection site	N _A	N _{PA}	A _R	H _O	H _E	F _{IS}
CS1	43	-	2.31	0.54	0.48	0.03
CS2	45	2	2.28	0.54	0.52	0.12
CS3	49	-	2.25	0.53	0.53	0.12
CS4	40	4	2.04	0.47	0.5	0.07
CS5	40	1	2.02	0.55	0.5	-0.05
CS6	36	1	1.83	0.46	0.42	0.11
CS7	42	3	1.97	0.34	0.46	0.33
CS8	28	2	1.31	0.14	0.21	0.4
CS9	29	1	1.37	0.23	0.27	0.19
CS10	42	2	2.05	0.42	0.46	0.15
CS11	37	-	1.78	0.35	0.38	0.14
CS12	26	1	1.23	0.07	0.21	0.78
CS13	53	5	2.15	0.46	0.5	0.2
CS14	60	6	2.54	0.58	0.6	0.17
CS15	42	1	2.16	0.46	0.42	0.08
CS16	42	1	2.23	0.58	0.49	-0.07
CS17	45	-	2.1	0.5	0.47	-0.01
CS18	65	5	2.49	0.55	0.6	0.1
CS19	39	1	1.99	0.52	0.46	-0.04
CS20	51	-	2.33	0.36	0.53	0.44
CS21	45	1	2.33	0.48	0.5	0.19
CS22	34	2	1.65	0.09	0.36	0.82
CS23	26	1	1.42	0.1	0.24	0.58
CS24	28	3	1.5	0.06	0.28	0.76
CS25	41	1	2.03	0.52	0.48	0.06
CS26	48	5	2.49	0.56	0.52	0.09
CS27	51	4	2.25	0.61	0.54	-0.02

N_A (number of alleles); N_{PA} (number of private alleles); A_R (mean allelic richness calculated using rarefaction); H_O (observed heterozygosity); H_E (expected heterozygosity); and F_{IS} (fixation index) are given for all 100 individuals genotyped at 16 SSR loci across 27 collection sites in three geographic regions.