

**Table S2.** Number of different alleles ( $N_a$ ), Shannon's information index ( $I$ ), Heterozygosity observed ( $H_o$ ), Heterozygosity expected ( $H_e$ ) and Fixation Index ( $F$ ) of 11 SSR markers used in faba bean collection.

	<b>M9</b>	<b>M22</b>	<b>M25</b>	<b>M27</b>	<b>M36</b>	<b>M41</b>	<b>M43</b>	<b>M46</b>	<b>SSR1</b>	<b>VFG1</b>	<b>VFG41</b>
<b><i>N<sub>a</sub></i></b>	6	3	8	8	9	5	6	3	10	14	22
<b><i>I</i></b>	1.411	0.447	1.368	1.278	1.709	1.347	1.304	0.764	1.808	2.216	2.646
<b><i>H<sub>o</sub></i></b>	0.447	0.250	0.733	0.45	0.897	0.640	0.408	0.600	0.940	0.848	0.237
<b><i>H<sub>e</sub></i></b>	0.674	0.225	0.662	0.603	0.779	0.707	0.66	0.473	0.792	0.866	0.890
<b><i>F</i></b>	0.337	-0.113	-0.107	0.254	-0.151	0.094	0.381	-0.269	-0.187	0.021	0.734