

Table 1. Summary statistics of faba bean genome assembly versions

Quality category	Metric	V1	V2
Continuity	Contig N50	2.7 Mb	2.7 Mb
	Hybrid scaffold N50	-	100 Mb
	No. of gaps	5,195	335
	LTR Assembly Index (LAI)	10.5	12.9
Chromosome status	Chromosome anchoring rate	93.9 %	97.5 %
	Chromosome anchored size	11.2 Gb	11.7 Gb
	Unanchored size	648 Mb	295 Mb
Structural accuracy	False duplications	0.08 %	0.08 %
	Curation (Hi-C)	Manual	Manual
Base accuracy	Consensus quality value (QV)	60.5	59.7
	<i>K</i> -mer completeness (%)	96.33 %	96.36 %
Functional completeness	BUSCO (n=5366)	97.0 %	97.1 %