

Supplementary Figure S2: (a) Genetic Similarity matrix of 15 *Lavandula* individuals based the BLASTN analysis against *S. splendens* exome, and relative observed homozygosity (Obs. Ho) and heterozygosity (Obs. He). (b) Average genetic similarity of Clusters identified through the construction of the UPGMA dendro-gram, and average observed homozygosity (Avg. Obs. Ho)

(a)

Obs. He			Genetic similarity (GS)															
32.3%	Cluster A	1603	100.0%															
39.3%		2601	82.5%	100.0%														
25.4%		2604	79.1%	77.0%	100.0%													
22.2%	Cluster B	1605	81.0%	78.5%	74.7%	100.0%												
21.6%		1841	79.3%	77.3%	72.5%	86.8%	100.0%											
21.4%		1826	80.7%	78.0%	75.6%	87.1%	87.4%	100.0%										
13.9%		SD-014	77.6%	75.0%	71.7%	88.6%	84.5%	83.7%	100.0%									
10.2%	Cluster C	BPI	75.9%	74.0%	69.8%	83.8%	80.5%	84.4%	85.3%	100.0%								
14.8%		ST-913	76.2%	75.4%	71.6%	86.4%	81.8%	87.0%	84.8%	94.1%	100.0%							
16.4%		SD-332	77.0%	75.8%	71.9%	84.3%	80.3%	85.3%	86.4%	94.3%	93.9%	100.0%						
10.8%		1811	76.7%	74.0%	69.5%	86.5%	85.8%	86.0%	87.2%	90.4%	92.4%	90.0%	100.0%					
21.8%	Cluster D	ST-103	77.0%	74.2%	70.8%	82.1%	81.0%	78.7%	83.4%	83.7%	83.1%	83.1%	83.3%	100.0%				
23.0%		3601	74.3%	72.4%	69.7%	79.4%	78.1%	76.2%	80.8%	77.8%	78.5%	78.5%	81.5%	87.2%	100.0%			
13.1%	Cluster E	2603	66.1%	66.9%	68.2%	58.9%	62.3%	60.1%	58.1%	56.8%	57.1%	57.0%	55.5%	58.2%	57.3%	100.0%		
28.9%		2605	68.5%	69.8%	70.2%	64.1%	68.4%	65.1%	62.5%	60.7%	62.4%	62.1%	61.7%	65.8%	66.3%	74.2%	100.0%	
			1603	2601	2604	1605	SD-014	1841	1826	BPI	ST-913	SD-332	1811	ST-103	3601	2603	2605	
			Cluster A			Cluster B				Cluster C				Cluster D		Cluster E		

(b)

Obs. Ho	Sample	Avg. Genetic similarity					
67.7% ± 4.0%	Cluster A	79.5% ± 1.6%					
80.2% ± 2.0%	Cluster B	76.8% ± 0.9%	86.4% ± 0.8%				
86.9% ± 1.5%	Cluster C	74.0% ± 0.8%	84.7% ± 0.5%	92.5% ± 0.8%			
77.6% ± 0.4%	Cluster D	73.1% ± 1.1%	80.0% ± 0.8%	81.2% ± 0.9%	87.2% ± N/A		
79.0% ± 7.9%	Cluster E	68.3% ± 0.7%	62.5% ± 1.2%	59.2% ± 1.0%	61.9% ± 2.4%	74.2% ± N/A	
79.0% ± 2.3%	A+B+C+D					62.7% ± 0.9%	80.7% ± 0.7%
	Cluster A		Cluster B	Cluster C	Cluster D	Cluster E	A+B+C+D