Table S2. Comparison of major *L. edodes* genetic linkage maps.

Reference	**Mapping population size**	**Map size (cM)**	**No. of linkage groups**	**No. of markers**	**Average marker spacing (cM)***	**No. of sequence-based markers**
[8]	32	622.4	14	69	11.3	2
[11]	95	1956.7	11	206	10.0	0
[12]	95	1398.4	11	166	9.0	10
[9]	92	908.8	11	289	3.3	23
[10]	92	908.8	11	301	3.1	35
This study	**20**	**637.1**	**13**	**200**	**3.4**	**200**

* Calculated by dividing the size of map by the number of markers minus the number of linkage groups.