

**Supplementary Table S1.** Annotation of the predicted gene models in the chromosome interval of wild olive corresponding to the DSI locus in 'Leccino'.

ID in Fig.3	Gene ID	Location	Coding strand	Functional annotation
1	LOC111367381	chr18:8,528,227..8,538,408	-	Chaperone-like protein of POR1
2	LOC111367383	chr18:8,570,307..8,585,694	+	Zinc finger CCCH domain-containing protein 44
3	LOC111367384	chr18:8,612,415..8,618,260	-	Uncharacterized protein
4	LOC111366697	chr18:8,620,048..8,623,927	+	FAR1-related sequence 5
5	LOC111367385	chr18:8,649,039..8,655,863	-	SHI related sequence 1 (STYLISH 1)
6	LOC111366698	chr18:8,715,988..8,716,048	+	61-bp pseudogene, probable methyltransferase PMT27
7	LOC111367386	chr18:8,765,216..8,766,001	-	Uncharacterized protein
8	LOC111367387	chr18:8,819,582..8,821,267	+	GATA transcription factor 5
9	LOC111367389	chr18:8,915,356..8,917,792	+	Cytochrome P450 84A1
10	LOC111367390	chr18:8,932,208..8,940,148	-	Uncharacterized protein
11	LOC111366699	chr18:8,978,278..8,981,237	+	Uncharacterized protein
12	LOC111366700	chr18:8,986,696..8,988,082	-	Uncharacterized protein
13	LOC111367391	chr18:8,989,633..8,990,335	-	ncRNA
14	LOC111367392	chr18:8,995,947..9,012,004	-	Transmembrane and coiled-coil domain-containing protein 4
15	LOC111367393	chr18:9,019,094..9,023,583	-	Zinc finger CCCH domain-containing protein 44, partial
16	LOC111366701	chr18:9,031,220..9,033,134	+	60S ribosomal protein L18-2, partial
17	LOC111366702	chr18:9,053,580..9,055,405	-	Uncharacterized protein

**Supplementary Table S2.** List of olive genotypes (cultivars and LexDA offsprings) phenotyped by a stigma test and genotyped by re-sequencing the alleles identified within the incompatibility locus in the map of cv. Leccino. The group of incompatibility, the haplotype combinations and the diagnostic SNP combinations (at 63 and 283 bp position, respectively) are reported for all samples.

<b>Cultivars</b>	<b>Country of diffusion</b>	<b>Group of incompatibility</b>	<b>Haplotype combination</b>	<b>Diagnostic SNPs</b>
Gordal Sevillana	Spain	G1	S-A/s-a	TT/TC
Leccino	Italy	G1	S-A/s-a	TT/TC
Piantone di Falerone	Italy	G1	S-A/s-a	TT/TC
Arbequina	Spain	G1	S-A/s-b	TG/TT
Cornicabra	Spain	G1	S-A/s-b	TG/TT
Dritta di Muscufo	Italy	G1	S-A/s-b	TG/TT
Gentile di Montone	Italy	G1	S-A/s-b	TG/TT
Gentile Grande	Italy	G1	S-A/s-b	TG/TT
Sirole	Italy	G1	S-A/s-b	TG/TT
Frantoio	Italy	G1	S-A/s-c	TG/TT
Moraiolo	Italy	G1	S-A/s-c	TG/TT
Vera Umbra	Italy	G1	S-A/s-c	TG/TT
Moresca	Italy	G1	S-B/s-b	TG/TT
Cornezuelo de Jaen	Spain	G1	S-B/-*	TT/-
Hojiblanca	Spain	G1	S-B/-*	TT/-
Lechin de Sevilla	Spain	G1	S-B/-*	TT/-
Orbetana	Italy	G1	S-B/-*	TT/-
Sevillenca	Spain	G1	S-B/-*	TT/-
Verdial de Badajoz	Spain	G1	S-B/-*	TT/-
Leccio del Corno	Italy	G1	S-A/-*	TT/-
Bottone di Gallo	Italy	G2	s-a/s-a	TT/CC
Machorron	Spain	G2	s-a/s-a	TT/CC
Manzanilla Cacerena	Spain	G2	s-a/s-a	TT/CC
Mollar de Cieza	Spain	G2	s-a/s-a	TT/CC
Picual	Spain	G2	s-a/s-a	TT/CC
Picudo	Spain	G2	s-a/s-a	TT/CC
Arauco	Argentina	G2	s-a/s-b	TG/CT
Borgiona	Italy	G2	s-a/s-b	TG/CT
Carolea	Italy	G2	s-a/s-b	TG/CT
Itrana	Italy	G2	s-a/s-b	TG/CT
Manzanilla de Sevilla	Spain	G2	s-a/s-b	TG/CT
Mastoidis	Greece	G2	s-a/s-b	TG/CT
Nocellara del Belice	Italy	G2	s-a/s-b	TG/CT
Passalunara	Italy	G2	s-a/s-b	TG/CT
Piangente	Italy	G2	s-a/s-b	TG/CT
Picholine Marocaine	Morocco	G2	s-a/s-b	TG/CT
Maurino	Italy	G2	s-a/s-c	TG/CT
Nostrale di Rigali	Italy	G2	s-a/s-c	TG/CT
Semidana	Italy	G2	s-a/s-c	TG/CT
Verdale	France	G2	s-a/s-c	TG/CT

Arbosana	Spain	G2	s-b/s-b	GG/TT
Capolga	Italy	G2	s-b/s-b	GG/TT
Fecciaro	Italy	G2	s-b/s-b	GG/TT
Gnacolo	Italy	G2	s-b/s-b	GG/TT
Grappuda	Italy	G2	s-b/s-b	GG/TT
Koroneiki	Greece	G2	s-b/s-b	GG/TT
Morrut	France	G2	s-b/s-b	GG/TT
Raio	Italy	G2	s-b/s-b	GG/TT
Sant'Emiliano	Italy	G2	s-b/s-b	GG/TT
Tombareddu	Italy	G2	s-b/s-b	GG/TT
Dolce Agogia	Italy	G2	s-b/s-c	GG/TT
Bosana	Italy	G2	s-c/s-c	GG/TT
Canino	Italy	G2	s-c/s-c	GG/TT
Coratina	Italy	G2	s-c/s-c	GG/TT
Gentile di Chieti	Italy	G2	s-c/s-c	GG/TT
Mignola	Italy	G2	s-c/s-c	GG/TT
Pendolino	Italy	G2	s-c/s-c	GG/TT

<b>LexDA progeny</b>	<b>Group of incompatibility</b>	<b>Haplotype combination</b>	<b>Diagnostic SNPs</b>
202	G1	S-A/s-b	TG/TT
205	G1	S-A/s-b	TG/TT
210	G1	S-A/s-b	TG/TT
211	G1	S-A/s-b	TG/TT
213	G1	S-A/s-b	TG/TT
214	G1	S-A/s-b	TG/TT
238	G1	S-A/s-b	TG/TT
245	G1	S-A/s-b	TG/TT
247	G1	S-A/s-b	TG/TT
249	G1	S-A/s-b	TG/TT
252	G1	S-A/s-b	TG/TT
268	G1	S-A/s-b	TG/TT
272	G1	S-A/s-b	TG/TT
276	G1	S-A/s-b	TG/TT
284	G1	S-A/s-b	TG/TT
285	G1	S-A/s-b	TG/TT
300	G1	S-A/s-b	TG/TT
312	G1	S-A/s-b	TG/TT
SP10	G1	S-A/s-b	TG/TT
SP15	G1	S-A/s-b	TG/TT
SP26	G1	S-A/s-b	TG/TT
SP33	G1	S-A/s-b	TG/TT
SP73	G1	S-A/s-b	TG/TT
SP75	G1	S-A/s-b	TG/TT
SP89	G1	S-A/s-b	TG/TT
SP90	G1	S-A/s-b	TG/TT
201	G1	S-A/s-c	TG/TT
206	G1	S-A/s-c	TG/TT
230	G1	S-A/s-c	TG/TT
237	G1	S-A/s-c	TG/TT

246	G1	S-A/s-c	TG/TT
257	G1	S-A/s-c	TG/TT
259	G1	S-A/s-c	TG/TT
267	G1	S-A/s-c	TG/TT
270	G1	S-A/s-c	TG/TT
273	G1	S-A/s-c	TG/TT
279	G1	S-A/s-c	TG/TT
286	G1	S-A/s-c	TG/TT
289	G1	S-A/s-c	TG/TT
291	G1	S-A/s-c	TG/TT
297	G1	S-A/s-c	TG/TT
298	G1	S-A/s-c	TG/TT
303	G1	S-A/s-c	TG/TT
306	G1	S-A/s-c	TG/TT
307	G1	S-A/s-c	TG/TT
308	G1	S-A/s-c	TG/TT
SP16	G1	S-A/s-c	TG/TT
SP17	G1	S-A/s-c	TG/TT
SP21	G1	S-A/s-c	TG/TT
SP63	G1	S-A/s-c	TG/TT
SP70	G1	S-A/s-c	TG/TT
SP74	G1	S-A/s-c	TG/TT
SP81	G1	S-A/s-c	TG/TT
SP83	G1	S-A/s-c	TG/TT
SP85	G1	S-A/s-c	TG/TT
SP93	G1	S-A/s-c	TG/TT
212	G2	s-a/s-b	TG/TC
218	G2	s-a/s-b	TG/TC
222	G2	s-a/s-b	TG/TC
228	G2	s-a/s-b	TG/TC
232	G2	s-a/s-b	TG/TC
234	G2	s-a/s-b	TG/TC
236	G2	s-a/s-b	TG/TC
242	G2	s-a/s-b	TG/TC
251	G2	s-a/s-b	TG/TC
253	G2	s-a/s-b	TG/TC
258	G2	s-a/s-b	TG/TC
262	G2	s-a/s-b	TG/TC
263	G2	s-a/s-b	TG/TC
266	G2	s-a/s-b	TG/TC
277	G2	s-a/s-b	TG/TC
290	G2	s-a/s-b	TG/TC
296	G2	s-a/s-b	TG/TC
301	G2	s-a/s-b	TG/TC
SP28	G2	s-a/s-b	TG/TC
SP29	G2	s-a/s-b	TG/TC
SP30	G2	s-a/s-b	TG/TC
SP39	G2	s-a/s-b	TG/TC
SP53	G2	s-a/s-b	TG/TC

SP55	G2	s-a/s-b	TG/TC
SP56	G2	s-a/s-b	TG/TC
SP57	G2	s-a/s-b	TG/TC
SP78	G2	s-a/s-b	TG/TC
SP92	G2	s-a/s-b	TG/TC
204	G2	s-a/s-c	TG/TC
207	G2	s-a/s-c	TG/TC
217	G2	s-a/s-c	TG/TC
226	G2	s-a/s-c	TG/TC
229	G2	s-a/s-c	TG/TC
239	G2	s-a/s-c	TG/TC
244	G2	s-a/s-c	TG/TC
255	G2	s-a/s-c	TG/TC
260	G2	s-a/s-c	TG/TC
261	G2	s-a/s-c	TG/TC
264	G2	s-a/s-c	TG/TC
282	G2	s-a/s-c	TG/TC
287	G2	s-a/s-c	TG/TC
294	G2	s-a/s-c	TG/TC
299	G2	s-a/s-c	TG/TC
302	G2	s-a/s-c	TG/TC
311	G2	s-a/s-c	TG/TC
313	G2	s-a/s-c	TG/TC
315	G2	s-a/s-c	TG/TC
SP35	G2	s-a/s-c	TG/TC
SP41	G2	s-a/s-c	TG/TC
SP51	G2	s-a/s-c	TG/TC

---

\*The second allele has not been reported because of the uncertain homozygous status of these genotypes. Null alleles could be considered.