**Supplementary File 1**. Cypher query to traverse syntenic blocks encompassing the *FT* locus and collect included QTL. The QTL "q1" serves as an anchor for the FT locus in *L. culinaris*.

MATCH (q1:QTL)<--(:Gene)-->(sb1:Synteny)-[s1:LOCATED\_ON]->(c1:Chromosome)-[:SUBSET\_OF]->(g1:Genome) MATCH (c1)<-[s2:LOCATED\_ON]-(sb2:Synteny)-->(c2:Chromosome)-[:SUBSET\_OF]->(g2:Genome) WHERE q1.qtl\_id = "qDTF.6-2\_1" AND g1.genome\_id in ["mtrun", "psat", "lcul", "vfab"] AND g2.genome\_id in ["mtrun", "psat", "lcul", "vfab"] AND ((s2.start >= s1.start AND s2.end <= s1.end) OR (s2.start <= s1.start AND s2.end >= s1.end) OR (s1.start <= s2.start <= s1.end AND s2.end >= s1.end) OR (s2.start <= s1.start <= s2.end AND s1.end >= s2.end)) WITH COLLECT(DISTINCT sb2) as found\_blocks UNWIND found\_blocks as sb2 MATCH (c1:Chromosome)<-[s1:LOCATED\_ON]-(sb2)-[s2:LOCATED\_ON]->(c2:Chromosome) WHERE id(c1) > id(c2) WITH sb2 as common\_blocks MATCH (c:Chromosome)<-[s:LOCATED\_ON]-(q2:QTL)<--(:Gene)-->(common\_blocks), (t:Trait)<--(q2) WHERE t.trait\_id =~ ".\*flower.\*" RETURN DISTINCT q2.qtl\_id as qtl\_id, c.chromosome\_id as chr, s.start as start, s.end as end