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GLOBAL CROP - GOLDEN OPPORTUNITIES

Mining the strong pod shattering resistance gene in Ogu restorer lines

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Pod shatter – rapeseed production obstacle

- **Seed yield lose 6-10%**
- **Harvest time and extremely weather**
- **Volunteer enlarge seed bank in soil**

Swathing or Combining



Seed lose



Volunteer



Quantitative method of pod shattering resistance Index (PSRI)

Random Impact Method



Resistance level of PSRI

High susceptible (HS) : PSRI ≤ 0.20

Susceptible (S) : 0.20 < PSRI ≤ 0.40

Low resistance (LR) : 0.40 < PSRI ≤ 0.60

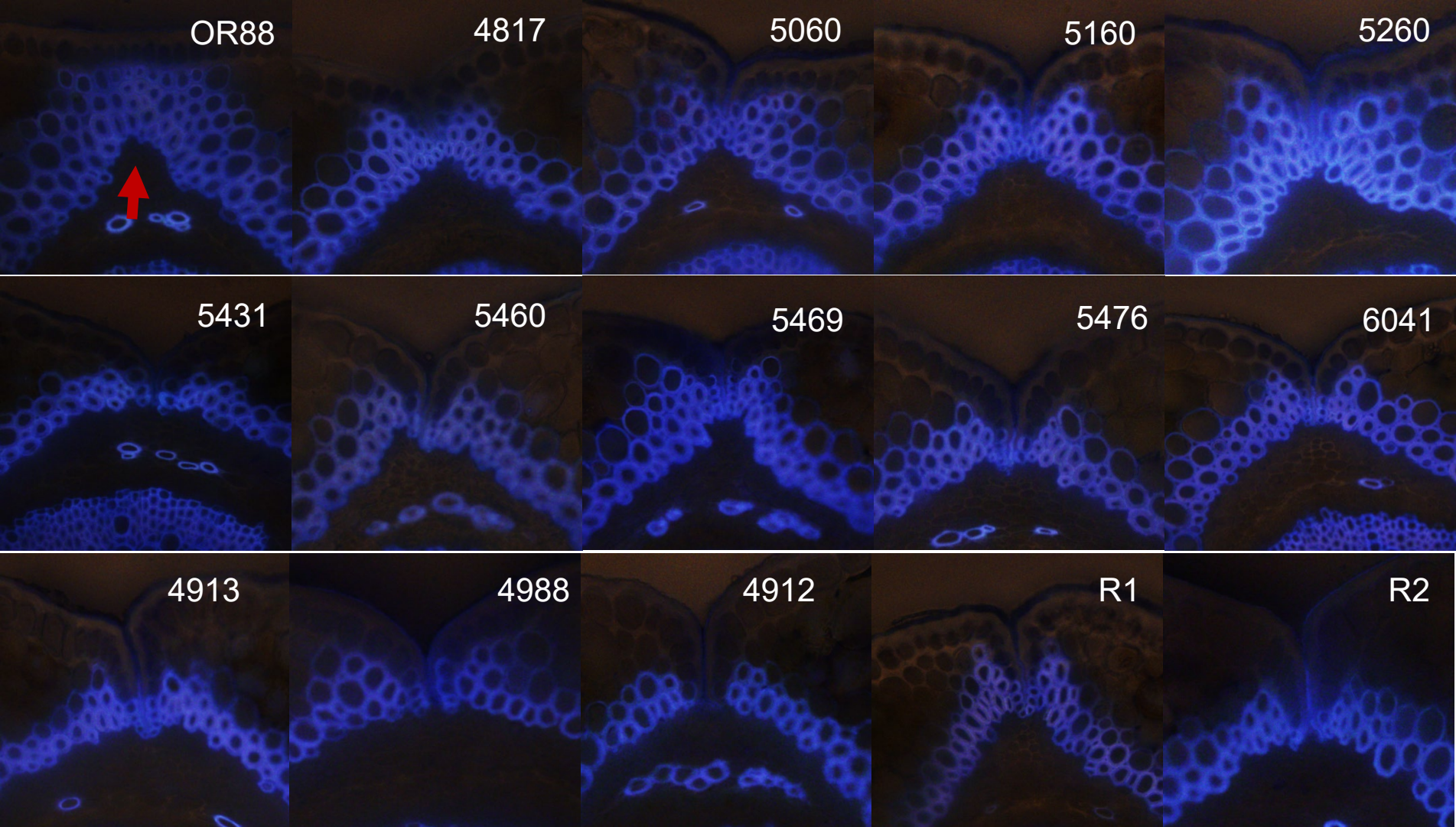
Middle resistance (MR) : 0.60 < PSRI ≤ 0.80

High resistance (HR) : 0.80 < PSRI ≤ 1

Revised from Morgan et al., 2003

$$PSRI = 1 - \sum_{i=1}^{i=5} xi \times (6 - i) / 100$$

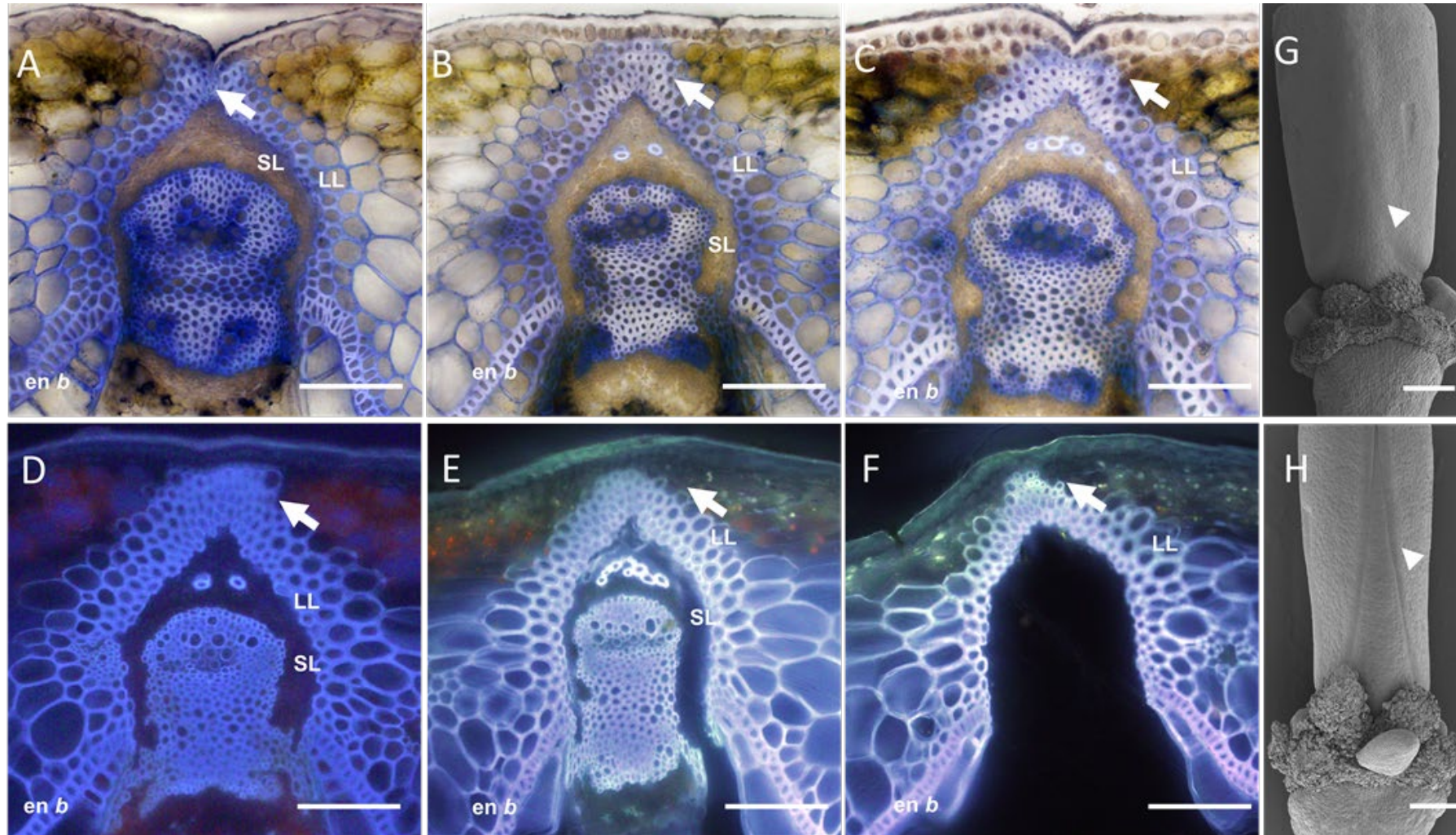
OR88: elite resistant resource (Ogu restorer line)



**PSRI > 0.8;
stable high
resistance**

**Lignified layer
binding (LLB)**

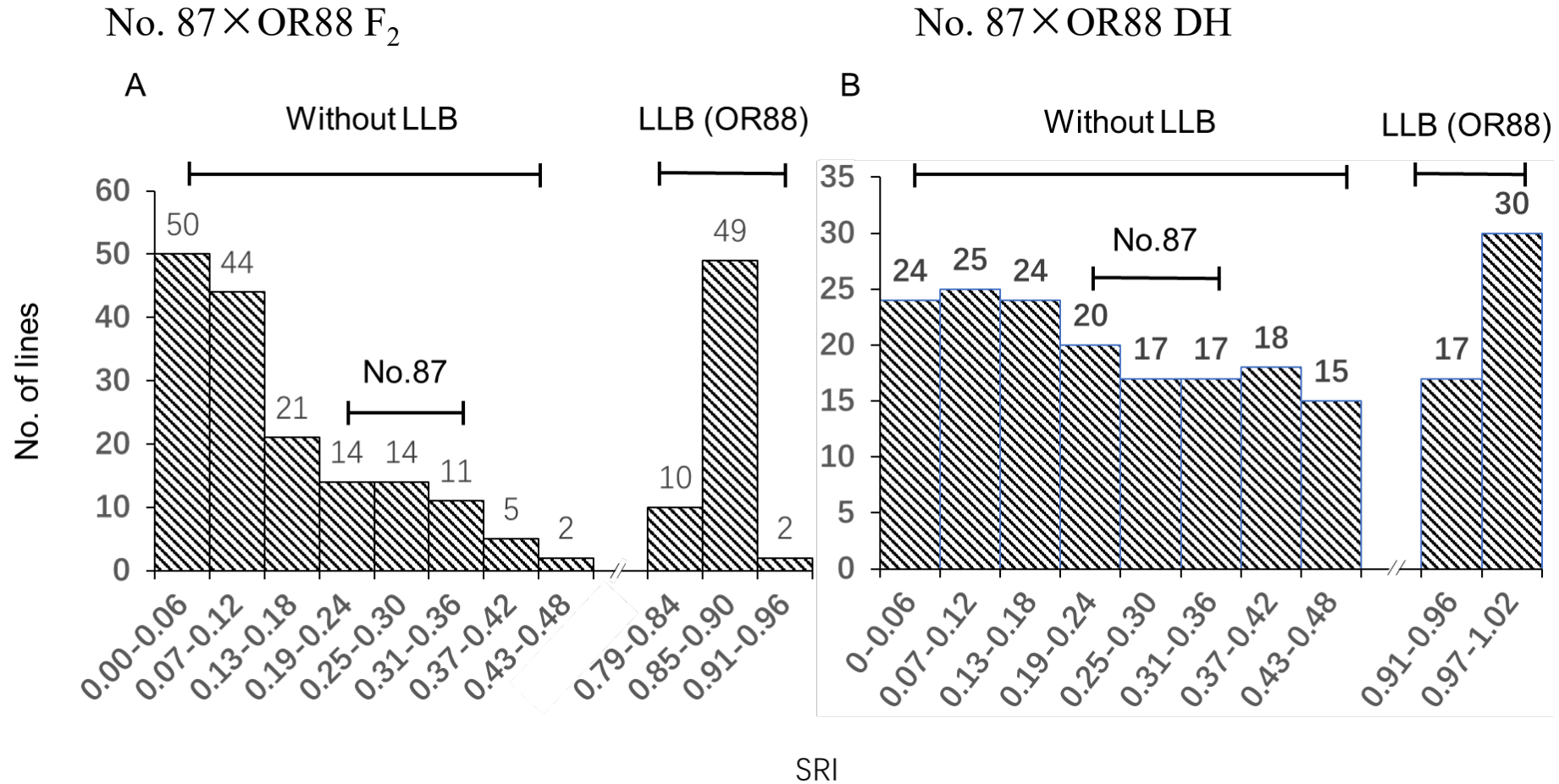
Lignified layer binding (LLB)



Anatomy and scanning electron microscope

The relationship between PSRI and LLB structure of pod

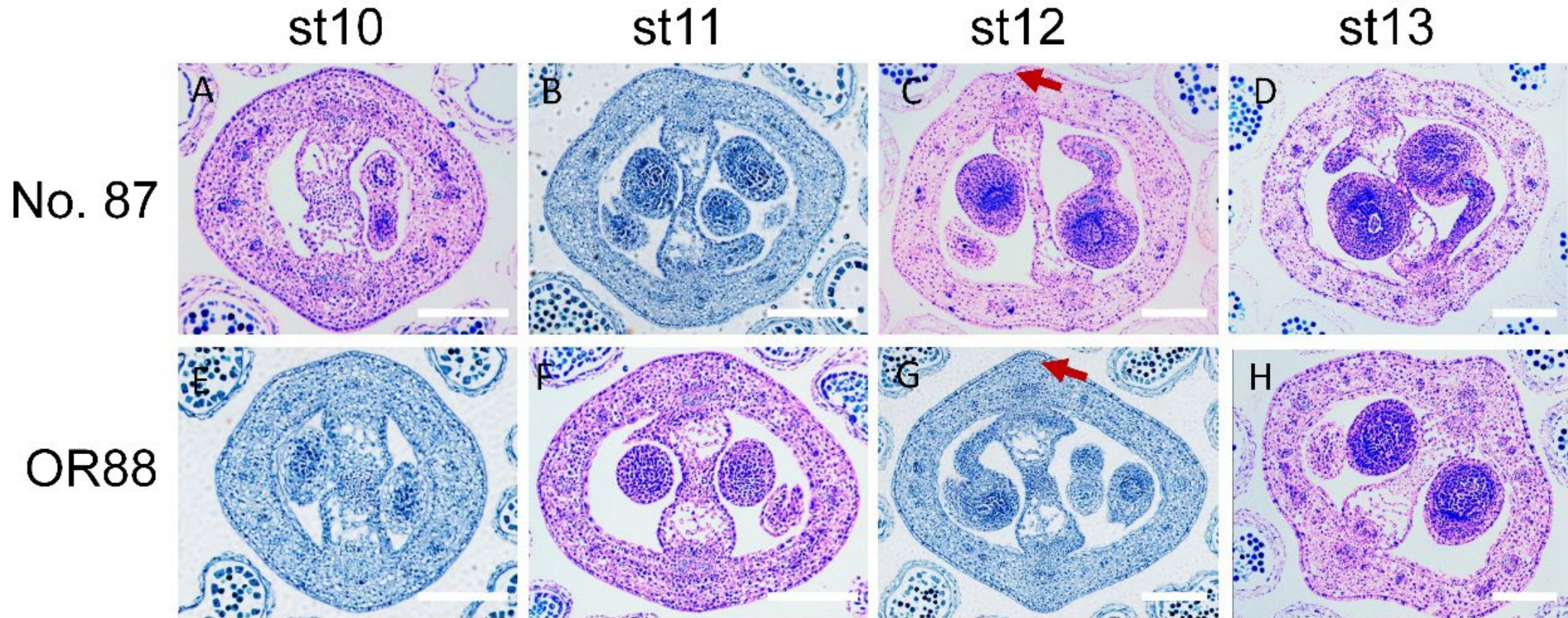
Genetic population



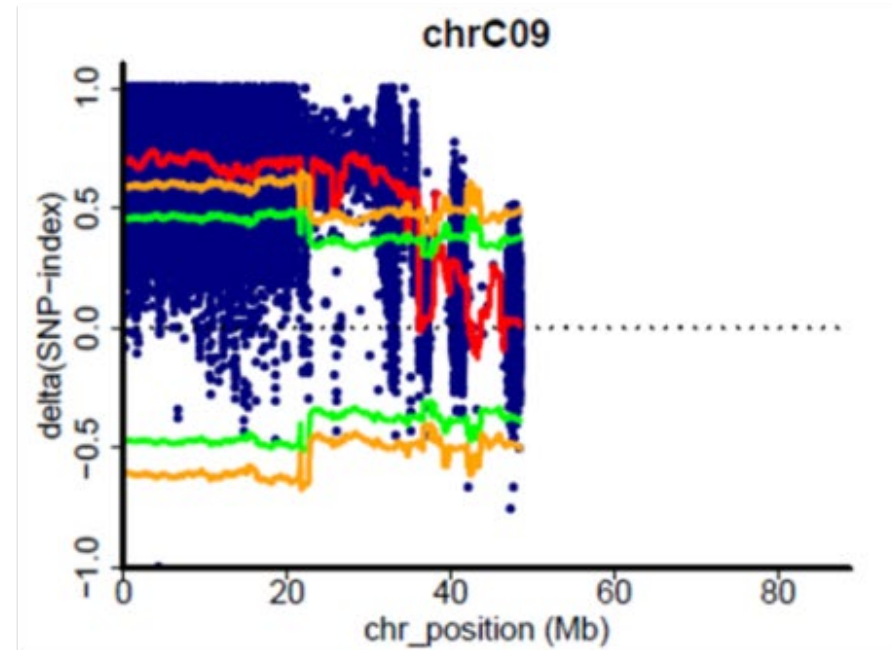
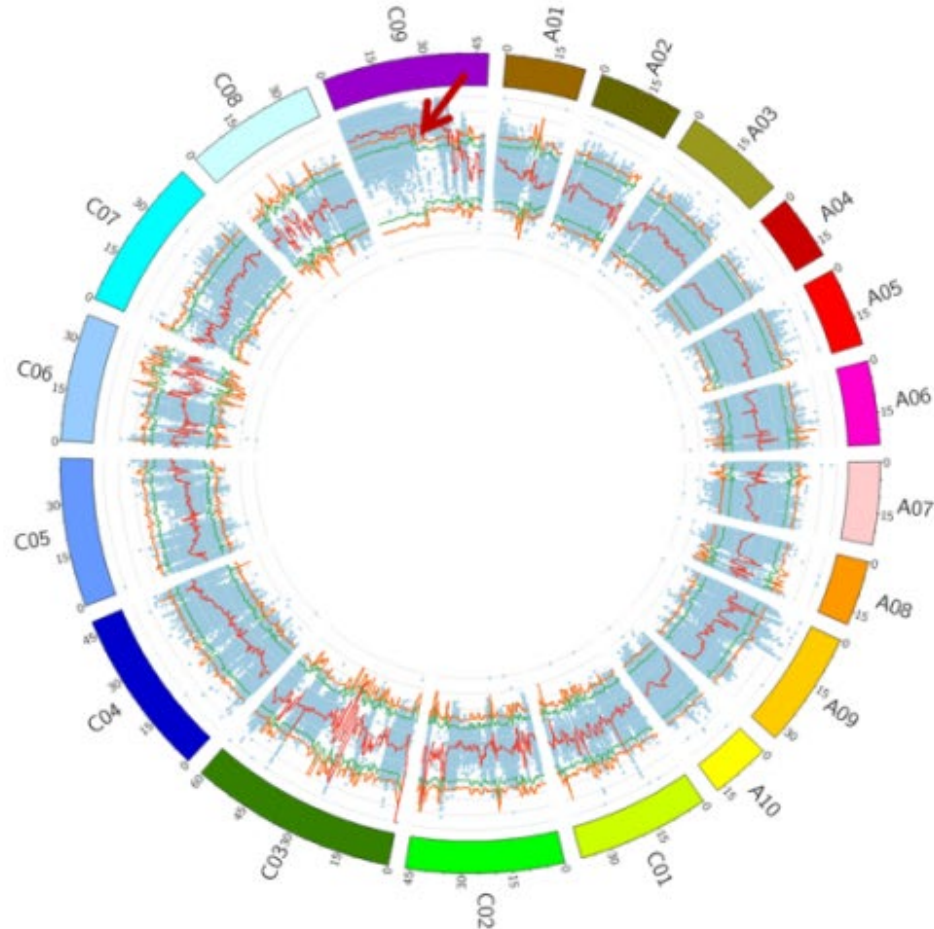
The LLB structure is controlled by one recessive gene.

Material	Total	Phenotype		Observed ratio	Expected ratio	χ^2	<i>P</i>
		Normal	LLB				
OR88	20		20				
87	20	20					
F₁	50	50					
F₂	222	161	61	2.64:1	3: 1	0.73	0.4
BC₁	860	435	425	1.02:1	1: 1	0.12	0.73

The lignified layered structure appears in the 12th stage of pistil development

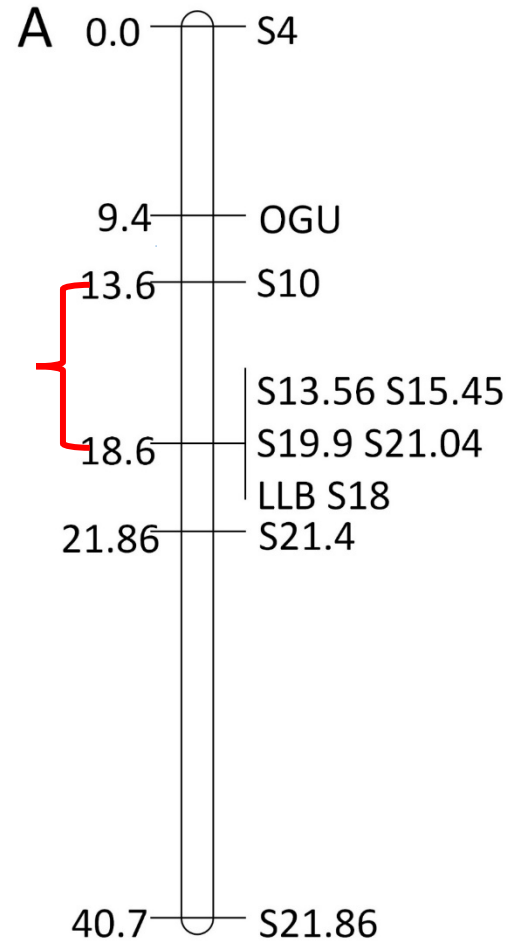


BSA method mapping the resistant gene in C09

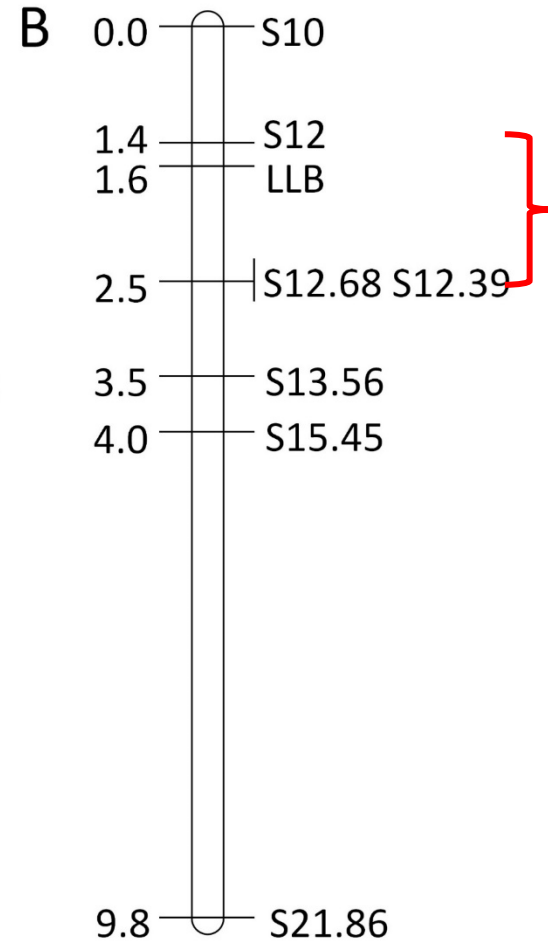


This locus just coincide with the radish introgress region in Ogu CMS restorer.

Narrowdown the interval of resistant gene



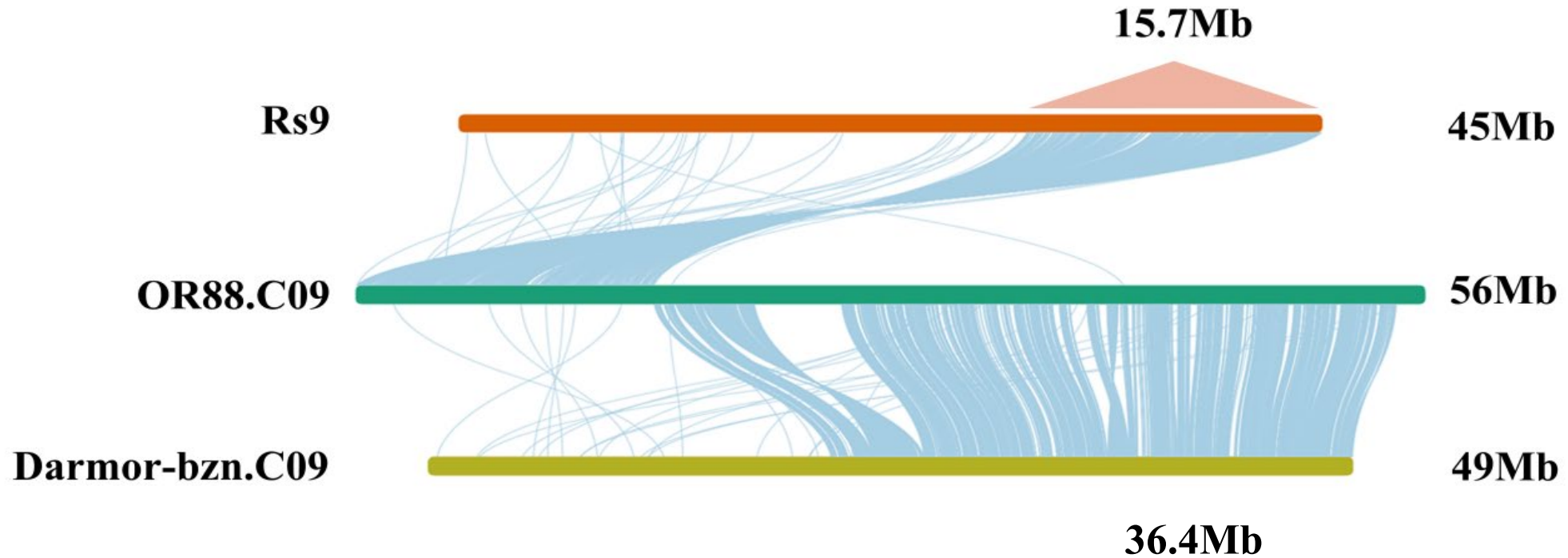
No. 87-OR88 BC₁



OR5-OR88 F₂

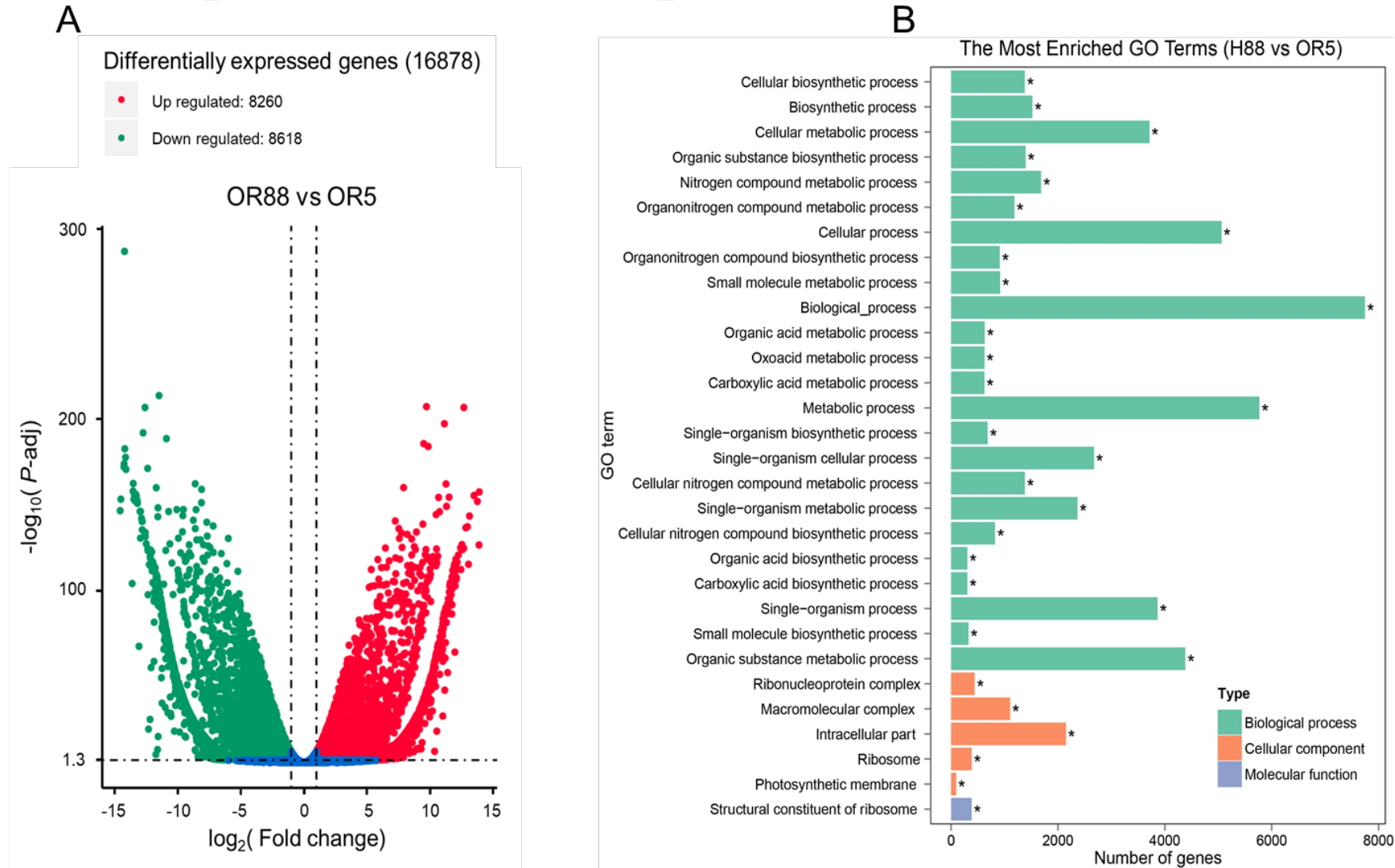
**165 Kb interval
between S12 and
S12.68 markers.**

The collinearity relationship among Darmor, OR88 and radish C09/Rs9 genome



- De nova genome of OR88 by 3 generation genome sequencing and assembling
- There are 2398 predicted genes in the 15.7 MB region.

Comparative transcriptome between OR88 and OR5



➤ **Totally 267 differentially expressed genes ($|\log_{2}FC| > 1$) in the radish introgression segment between OR88 and OR5 Ogu lines.**

- The 26 genes are within the 165 Kb segment between the interval of S12 and S12.68.
- **BnaCnng71510D (*BnTCP8.C09*)** is the candidate gene for the pod shattering resistance.

Rapeseed ID	Radish ID	Annotation	log ₂ FC	Seq-diff
<i>BnaC09g15360D</i>	<i>RSAskr1.0R9g89362</i>	protein FAM135B	-2.58	TRUE
<i>BnaC09g15440D</i>	<i>RSAskr1.0R9g89350</i>	glutamyl-tRNA reductase 1, chloroplastic	-3.42	TRUE
<i>BnaC09g15460D</i>	<i>RSAskr1.0R9g89348</i>	cytosolic sulfotransferase 18-like	-	FALSE
<i>BnaC09g15510D</i>	<i>RSAskr1.0R9g89347</i>	cytosolic sulfotransferase 18-like	-	FALSE
<i>BnaC09g15520D</i>	-	60S ribosomal protein L6-2-like;	-	FALSE
<i>BnaC09g15540D</i>	<i>RSAskr1.0R9g89346</i>	protein SABRE	-2.15	TRUE
<i>BnaC09g15550D</i>	<i>RSAskr1.0R9g89345</i>	mucin-17	-6.15	TRUE
<i>BnaC09g15570D</i>	<i>RSAskr1.0R9g89343</i>	uncharacterized protein LOC108826222	-5.24	FALSE
<i>BnaCnng71510D</i>	<i>RSAskr1.0R9g89341</i>	transcription factor TCP8	-8.22	TRUE
<i>BnaC09g15590D</i>	<i>RSAskr1.0R9g89342</i>	uncharacterized protein At4g06598-like	-2.61	TRUE
<i>BnaC09g15600D</i>	<i>RSAskr1.0R9g89339</i>	ATP phosphoribosyltransferase 1, chloroplastic-like	-2.83	TRUE
<i>BnaC09g15610D</i>	<i>RSAskr1.0R9g89336</i>	DExH-box ATP-dependent RNA helicase DExH7, chloroplastic	-2.62	TRUE
<i>BnaC09g15650D</i>	<i>RSAskr1.0R9g89334</i>	uncharacterized protein LOC108828383	-	TRUE
<i>BnaCnng43840D</i>	<i>RSAskr1.0R9g89318</i>	cytochrome P450 86B1-like; K15405 midchain alkane hydroxylase (A)	4.96	FALSE
<i>BnaCnng60030D</i>	<i>RSAskr1.0R9g89321</i>	alkane hydroxylase MAH1-like	-	TRUE
<i>BnaC09g15730D</i>	-	--	-	TRUE
<i>BnaC09g15740D</i>	<i>RSAskr1.0R9g89317</i>	prolycopene isomerase, chloroplastic	-2.55	TRUE

Summary

- **OR88 is a elite breeding line with high resistance for pod shattering.**
- **Specific lignined structure is contributed to resistant phenotype.**
- **One partly recessive gene on C09 original from radish genome take part in the key role.**
- **By genetic mapping and transcriptome analysis, *BnTCP8.C09* is the candidate gene for lignified layer binding.**

Thanks!

