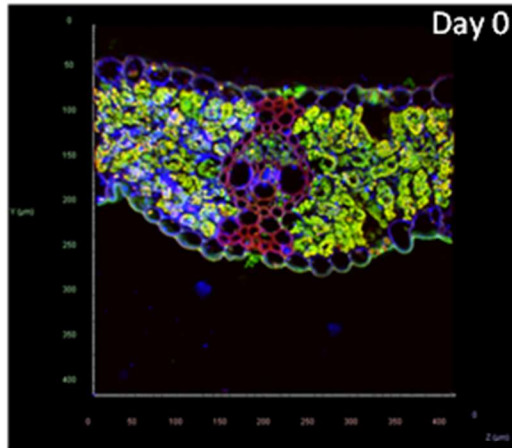
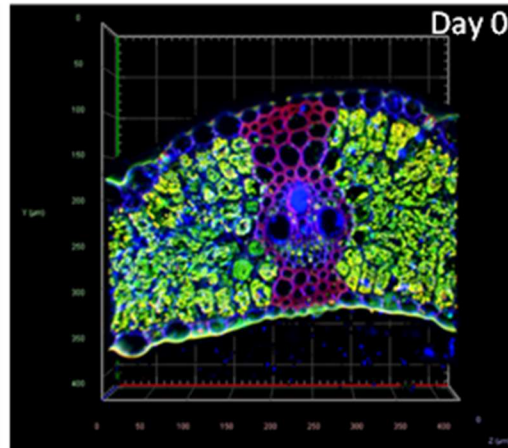


Supplementary Material

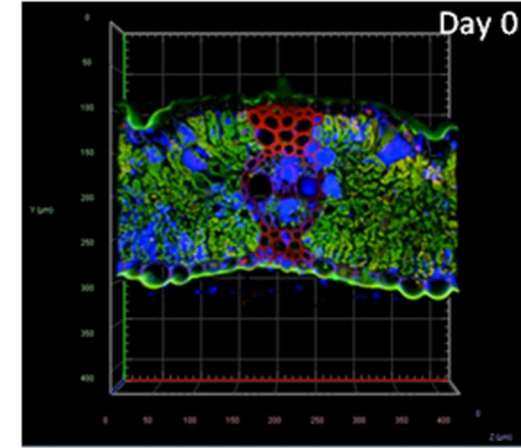
SST 877



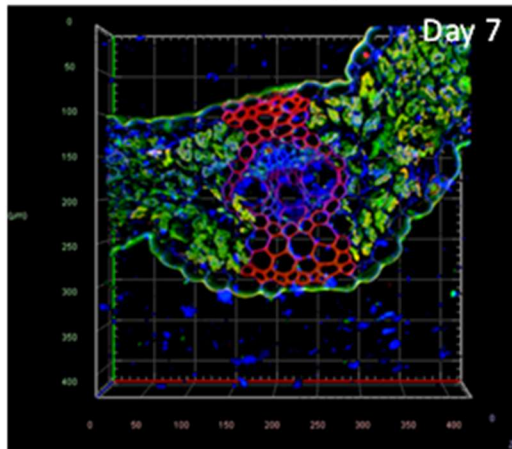
877 SA 11



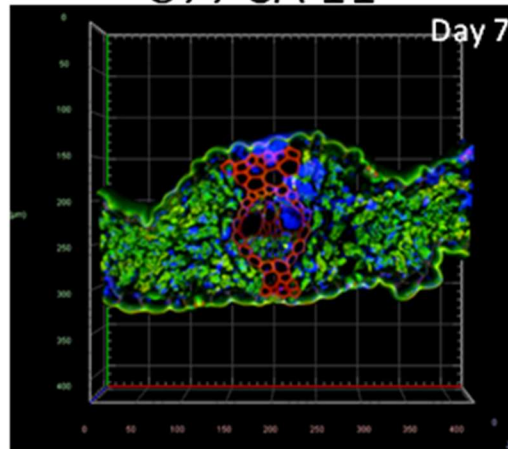
877 SA 12



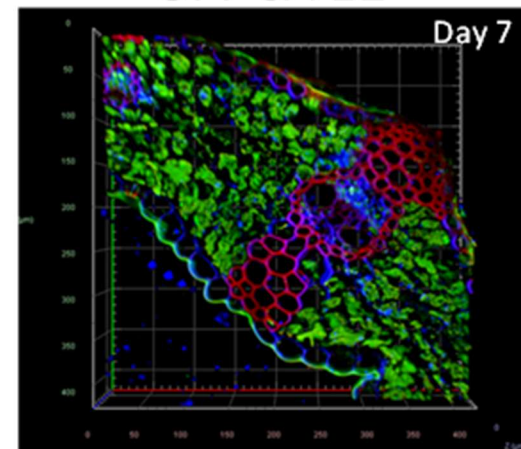
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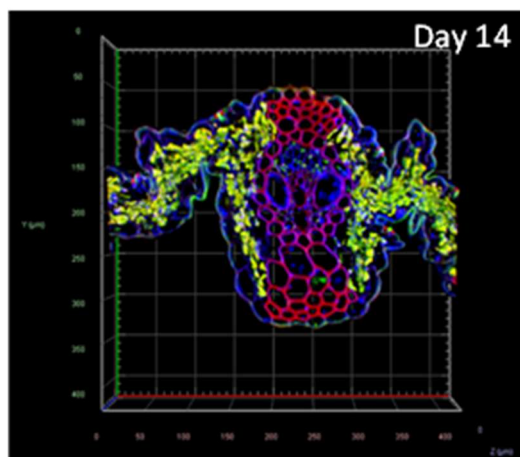
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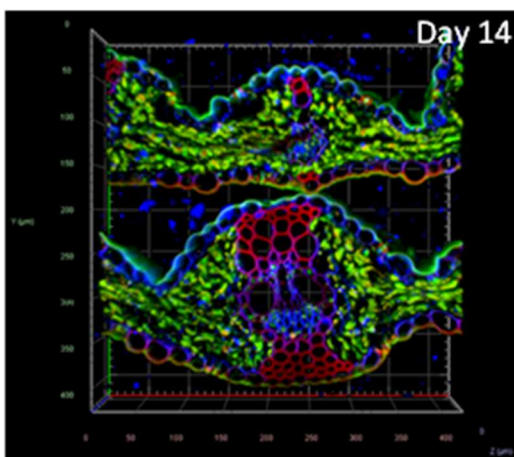
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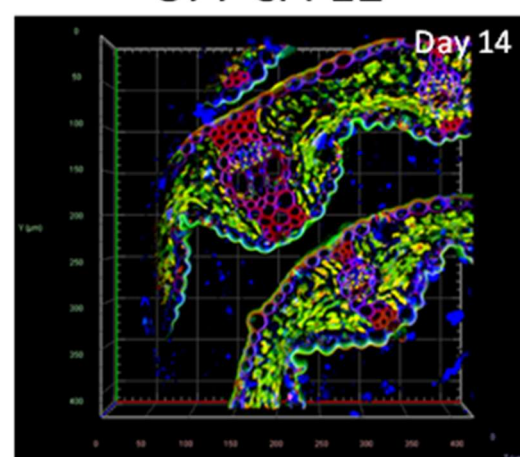
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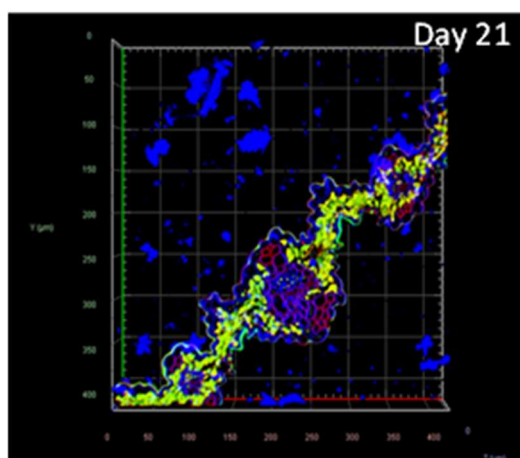
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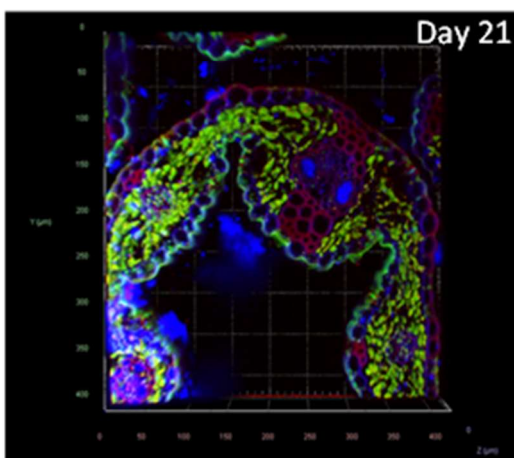
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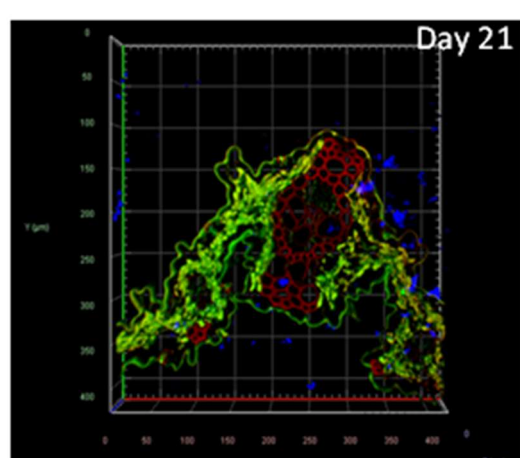
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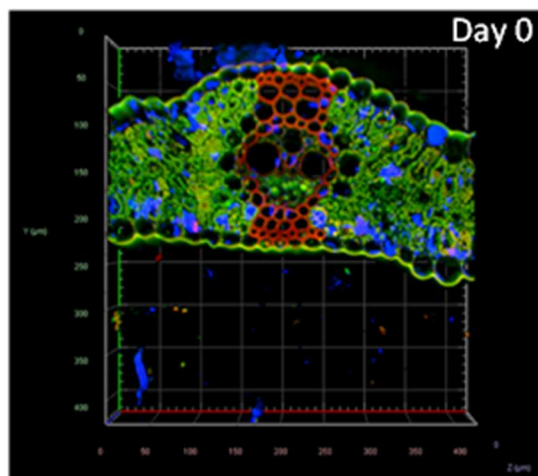
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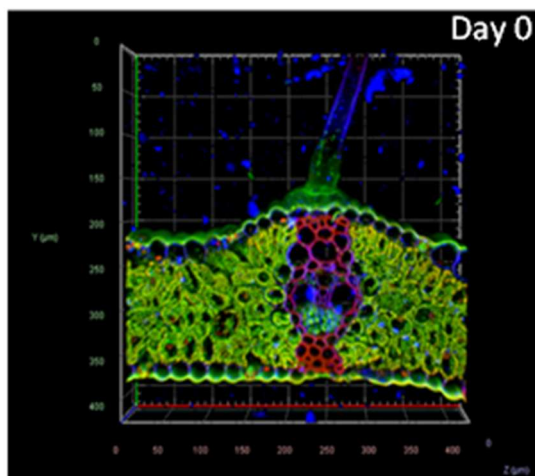
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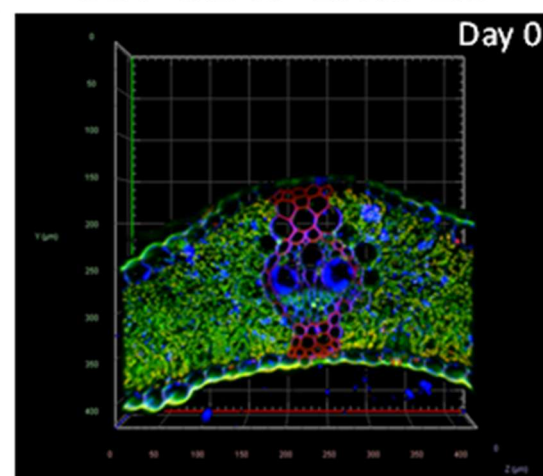
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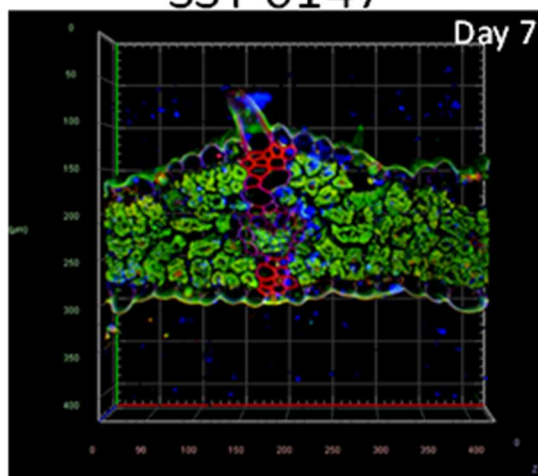
SST 0147 EMS 27



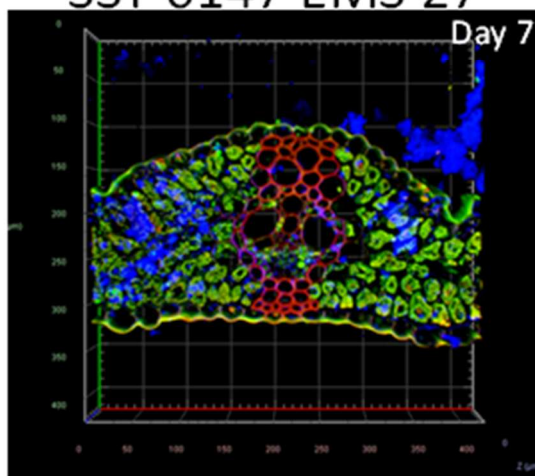
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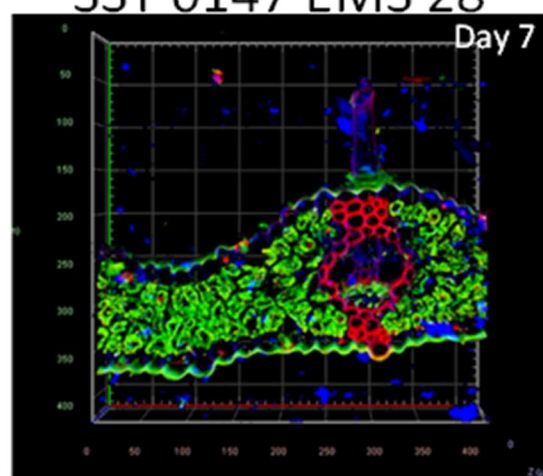
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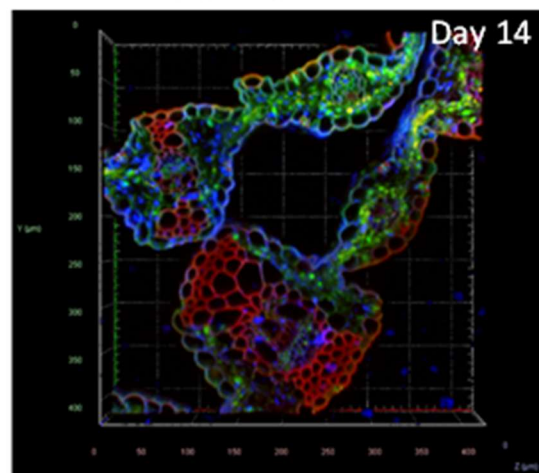
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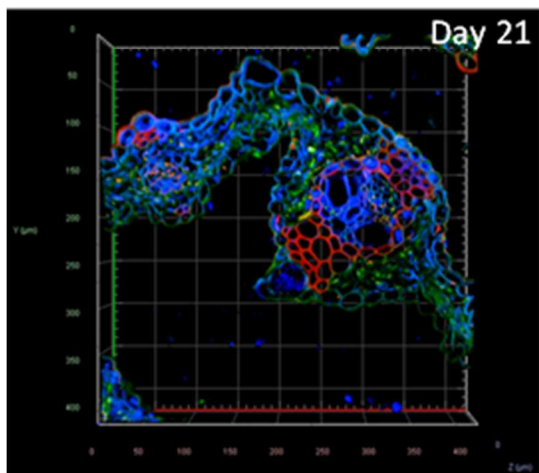
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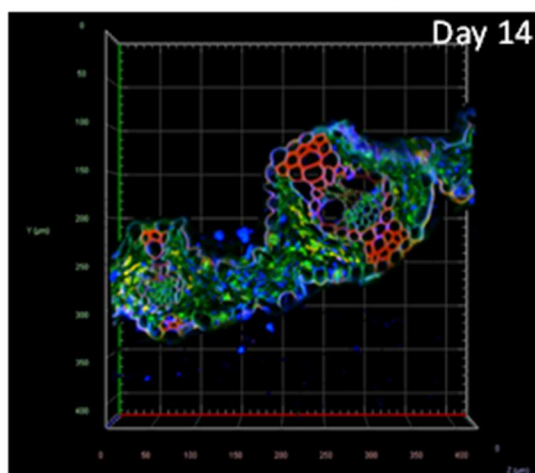
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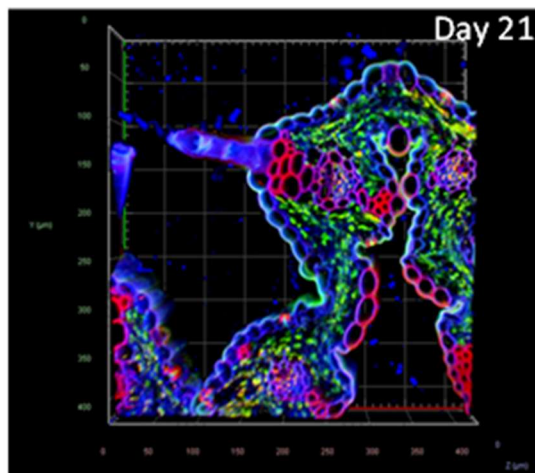
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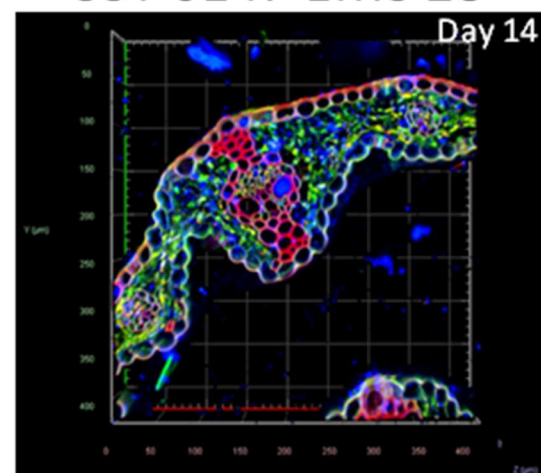
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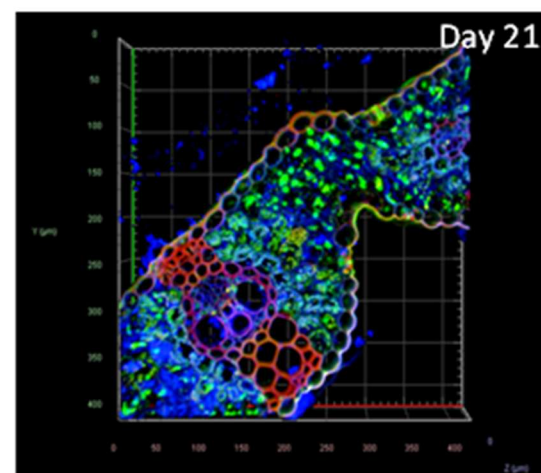
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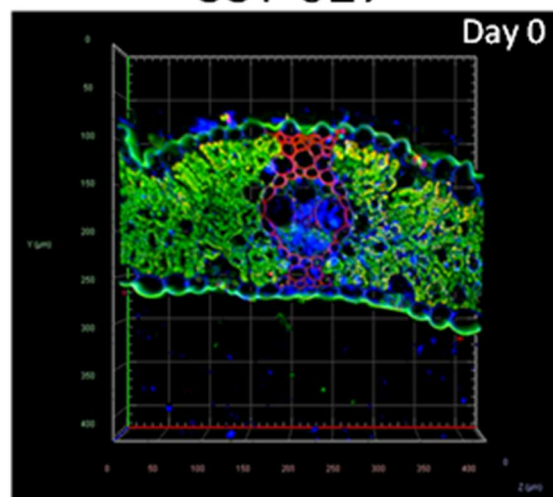
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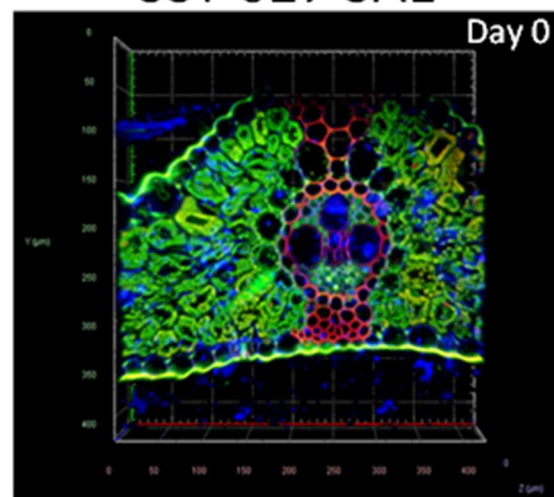
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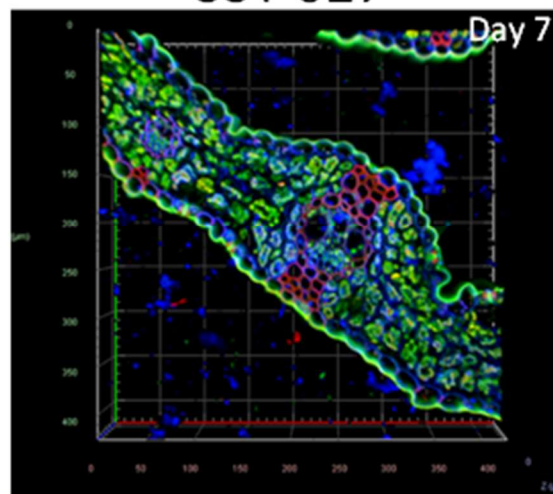
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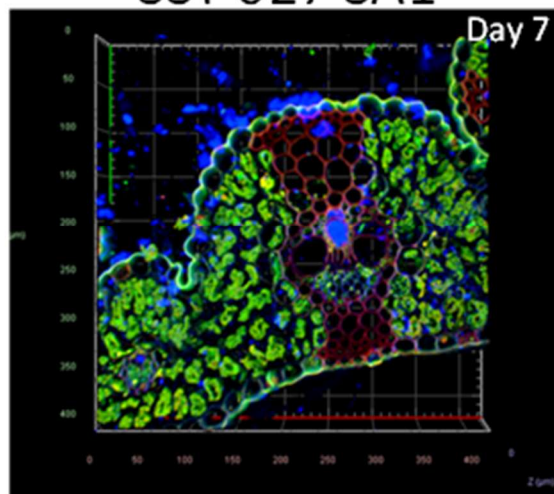
SST 027 SA1



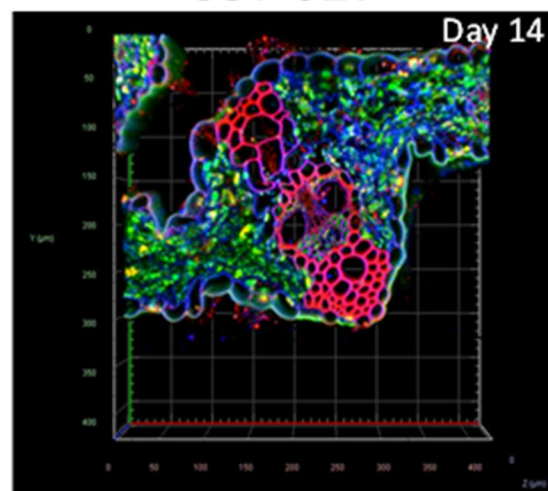
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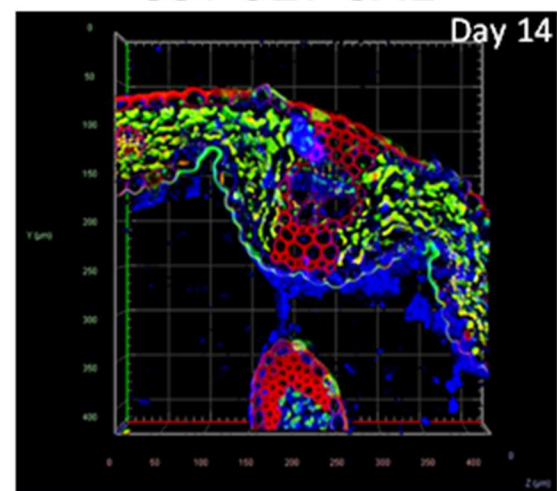
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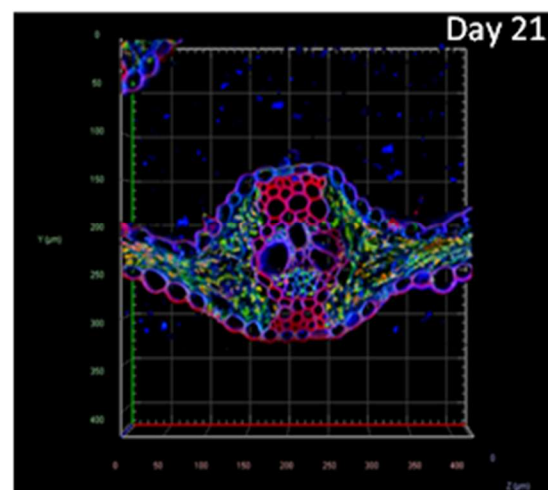
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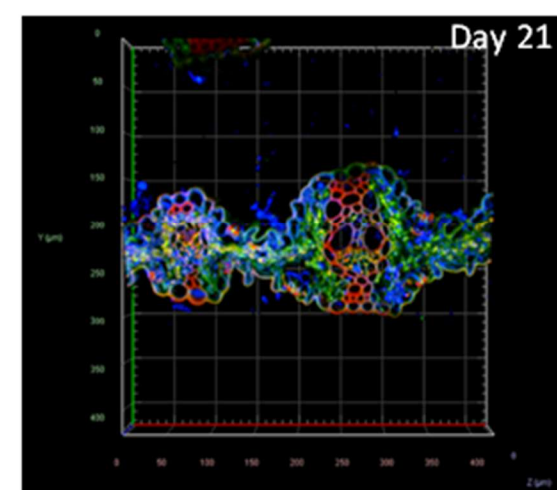
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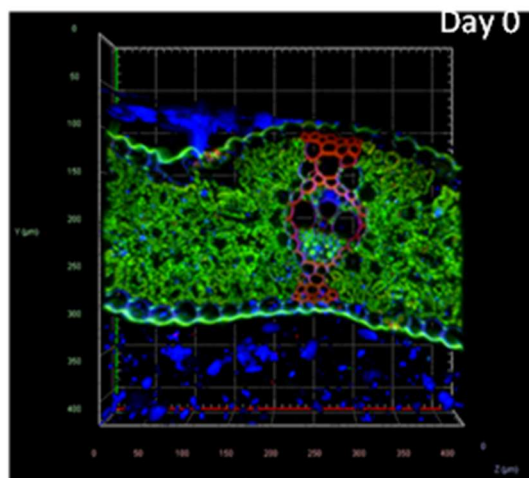
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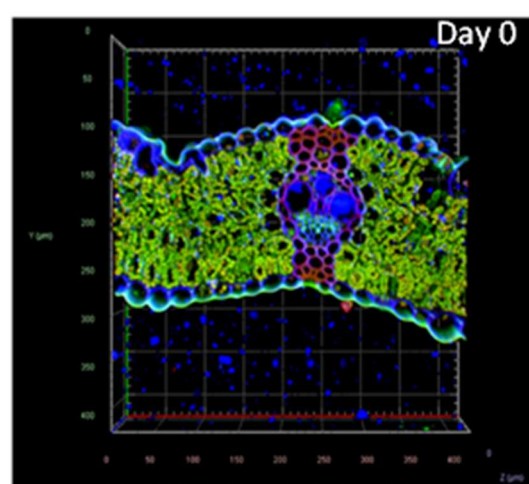
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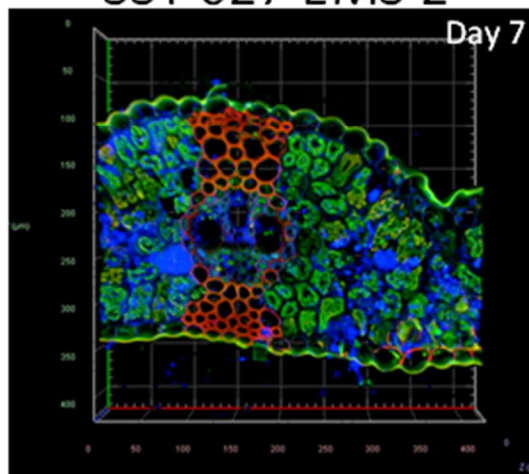
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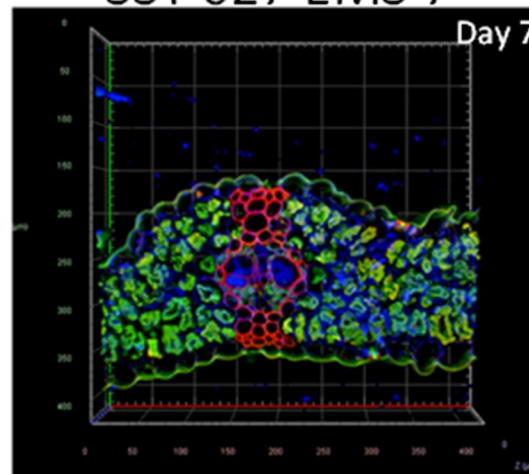
SST 027 EMS 7



SST 027 EMS 2



SST 027 EMS 7



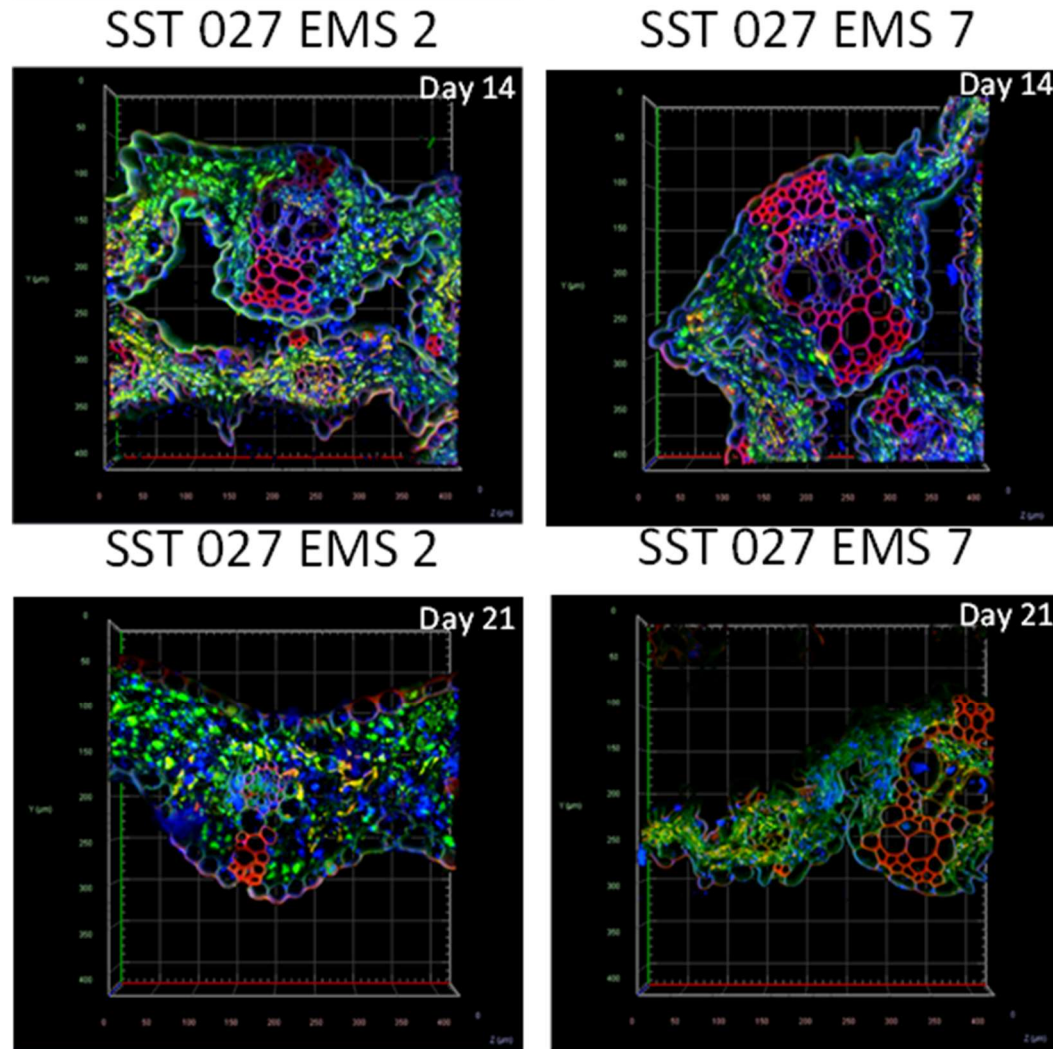
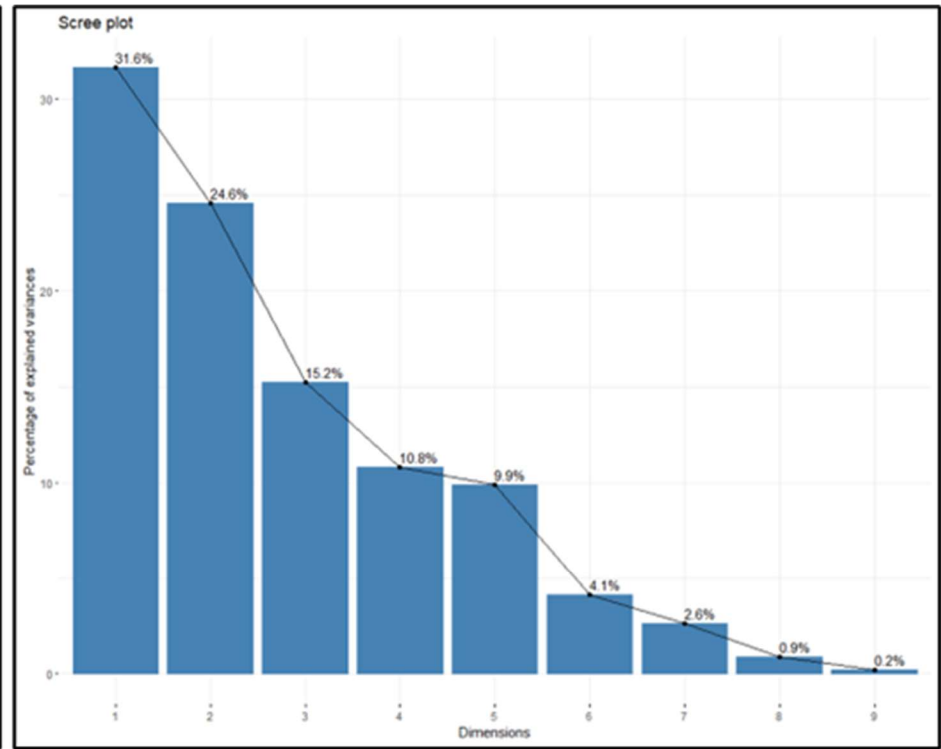
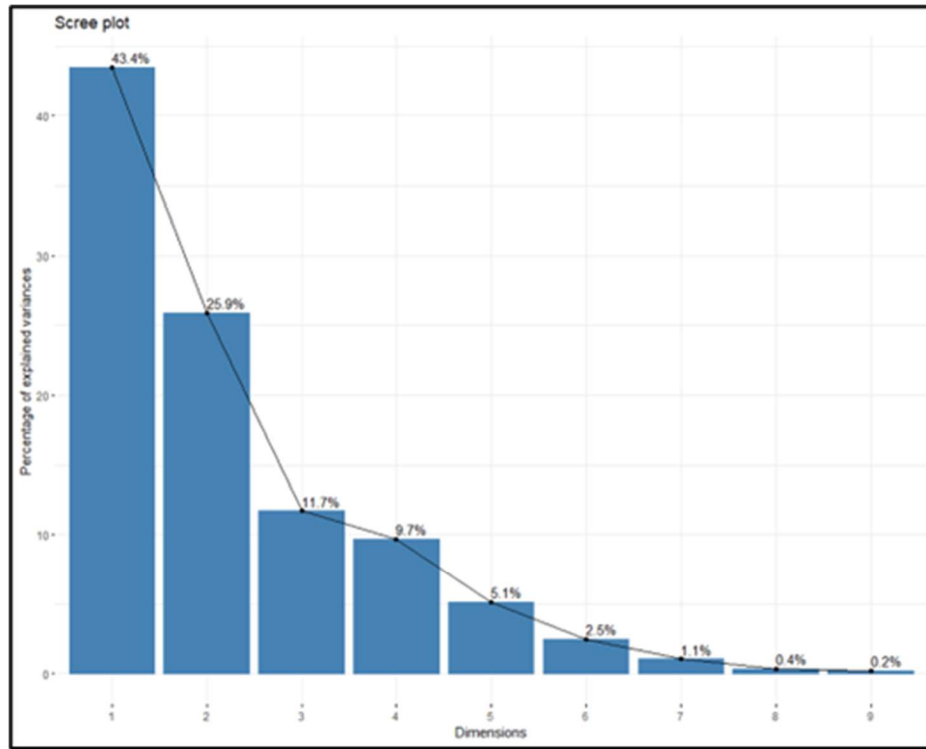


Figure S1. Confocal microscopy images of FFA treated SST wheat leaf cross-sections under water deficit stress. Images were generated at 20x objective magnification utilizing captured light emissions of 591nm, 610nm and 443nm utilizing the fluoresces of chlorophyll (green), propidium iodide (red) and calcofluor white (blue). Images were captured at day 0, 7 14 and 21 of a drought trial.



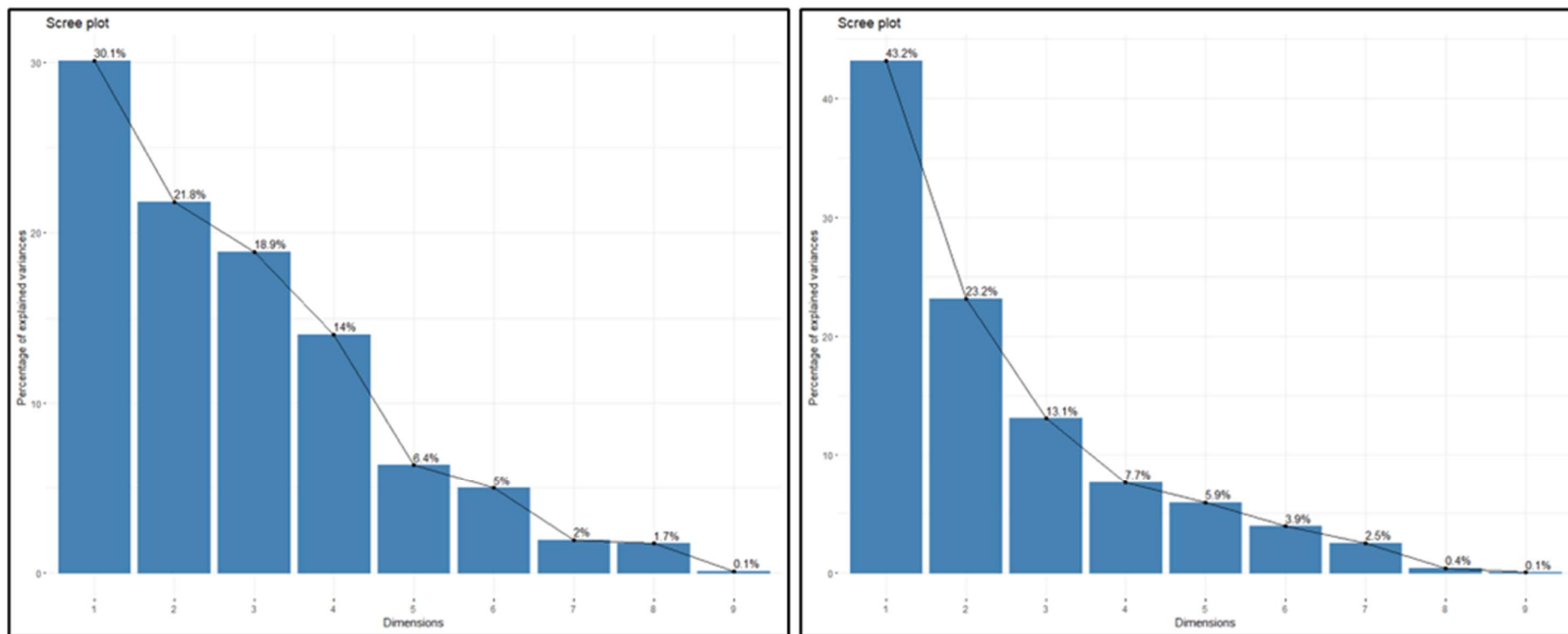
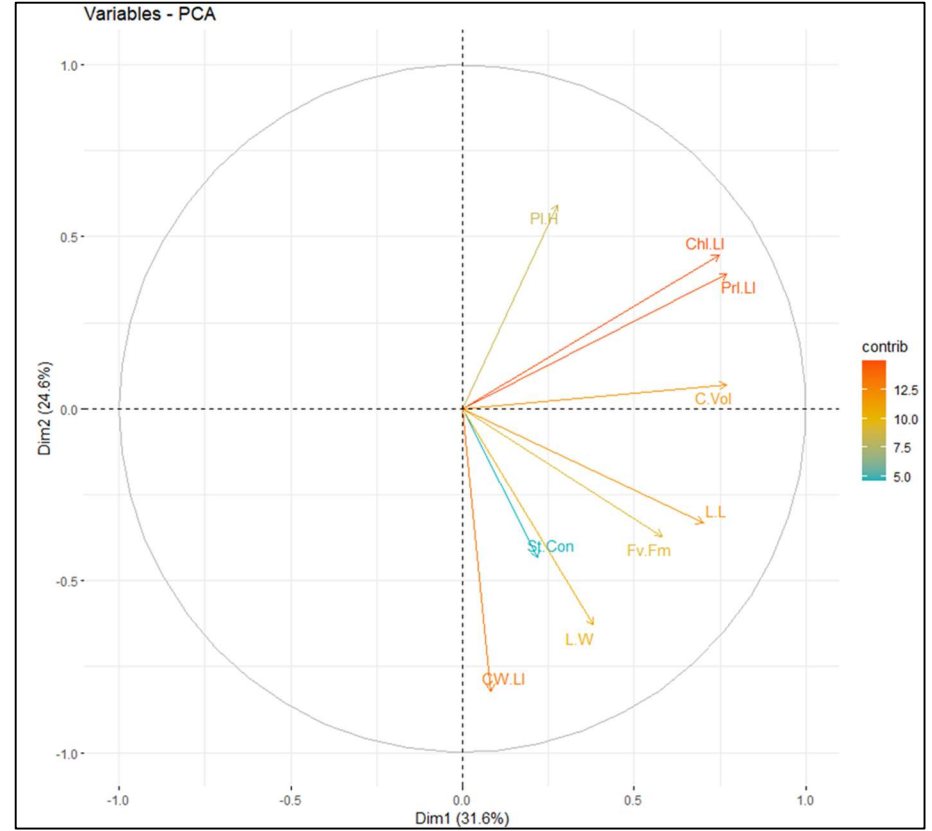
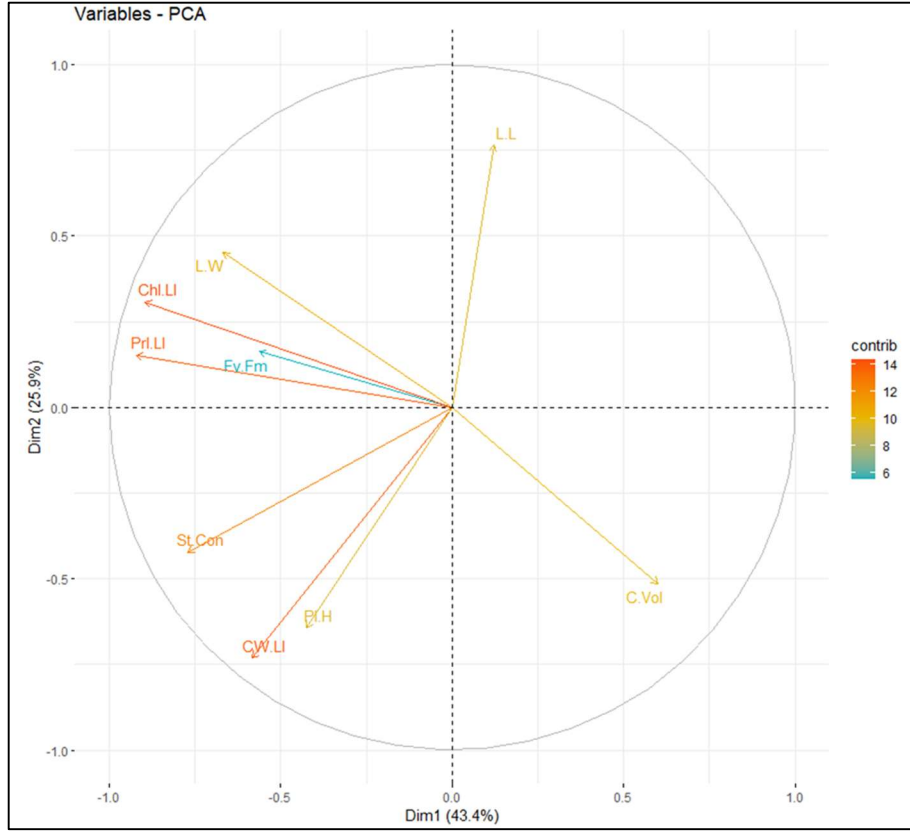


Figure S2. Scree plots generated for BIG and SST lines during PCA analysis.



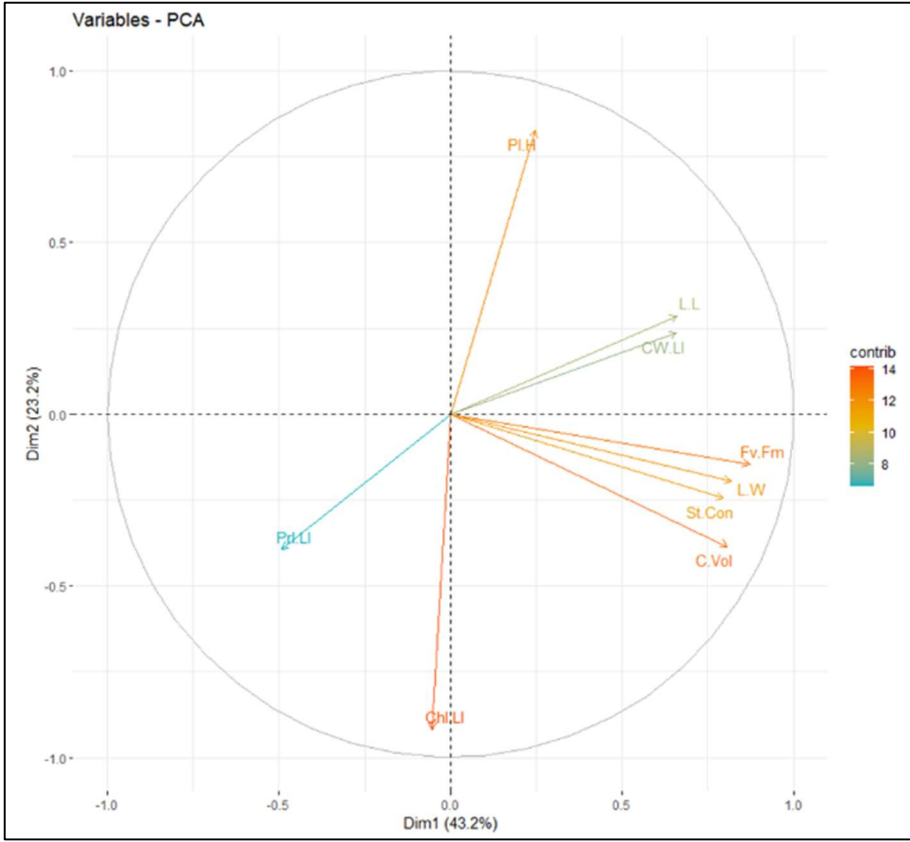
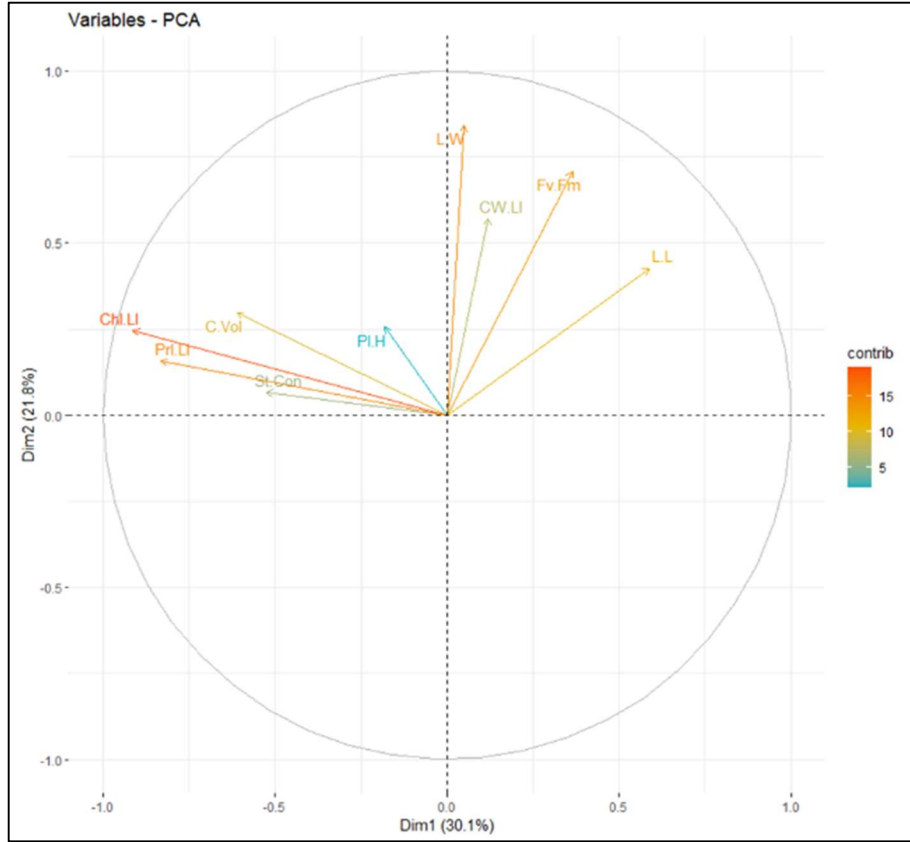
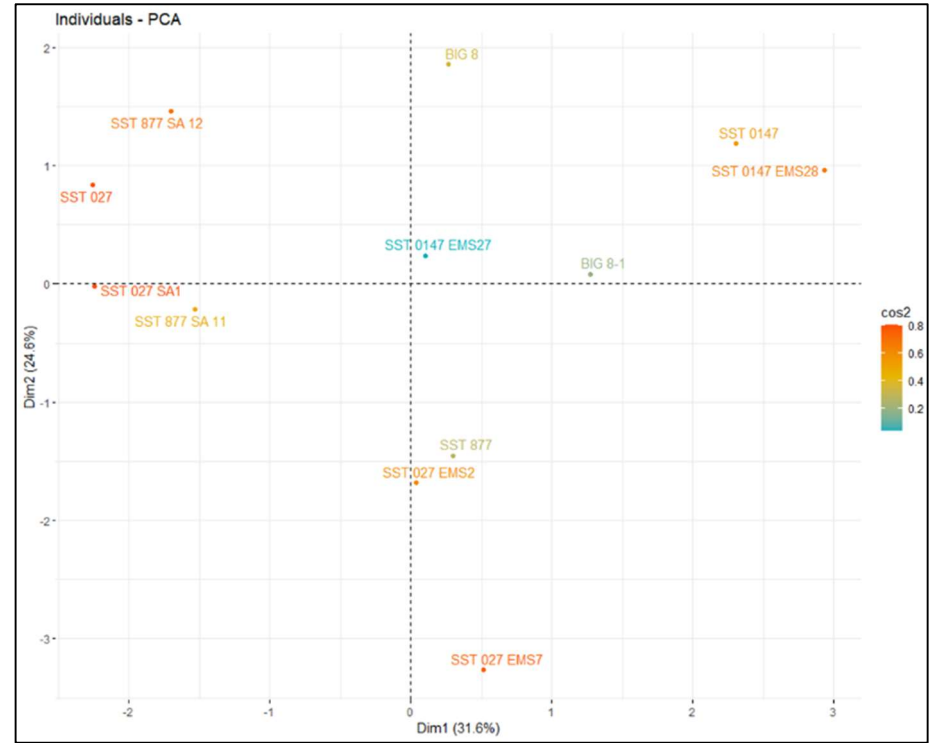
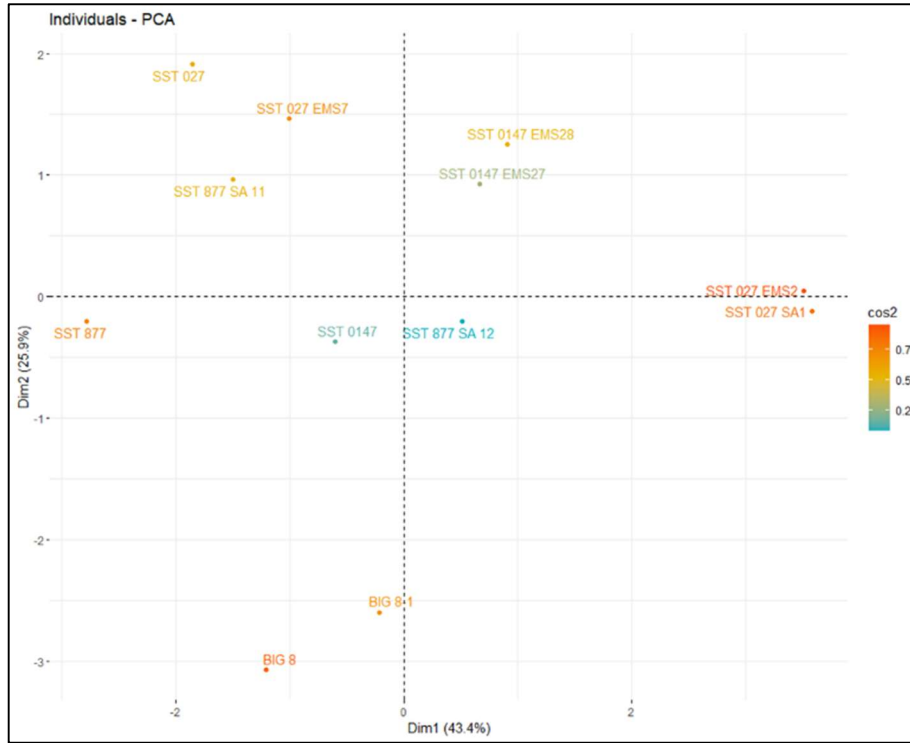


Figure S3. PCA plots of variables for BIG and SST lines generated during PCA analysis.



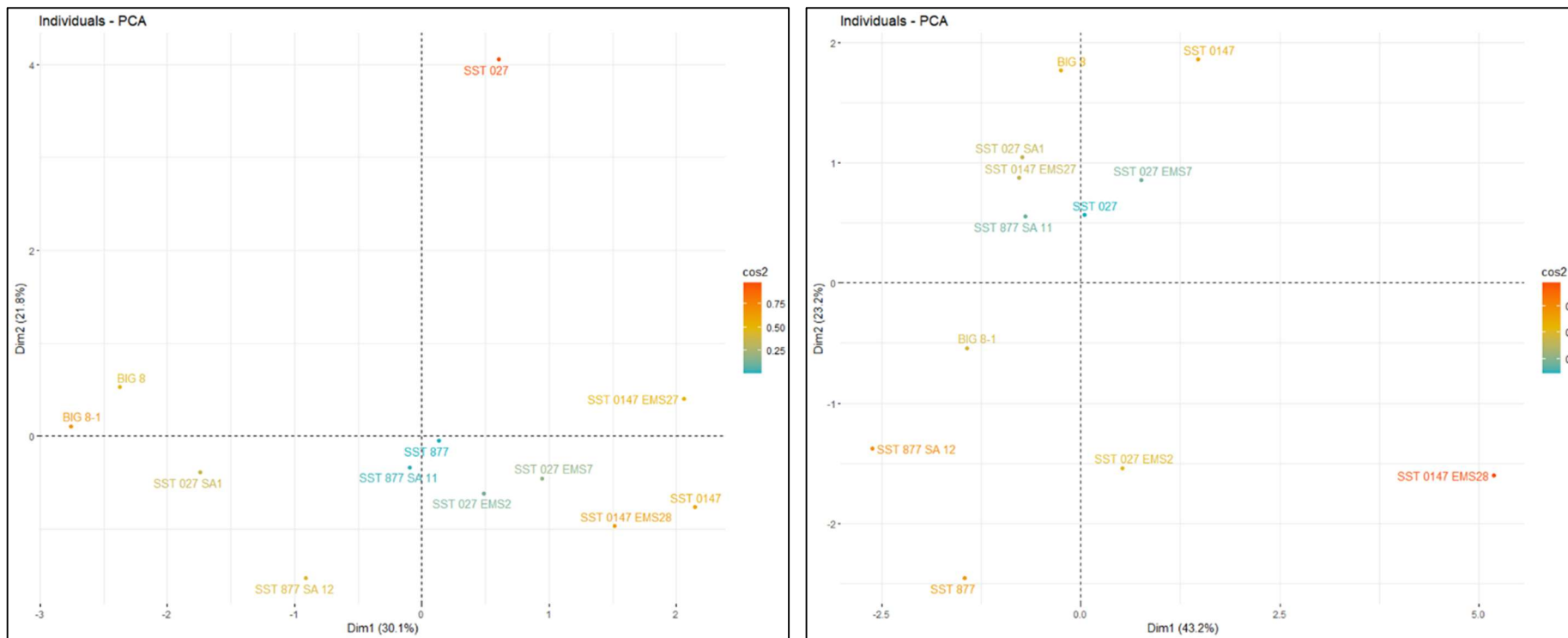
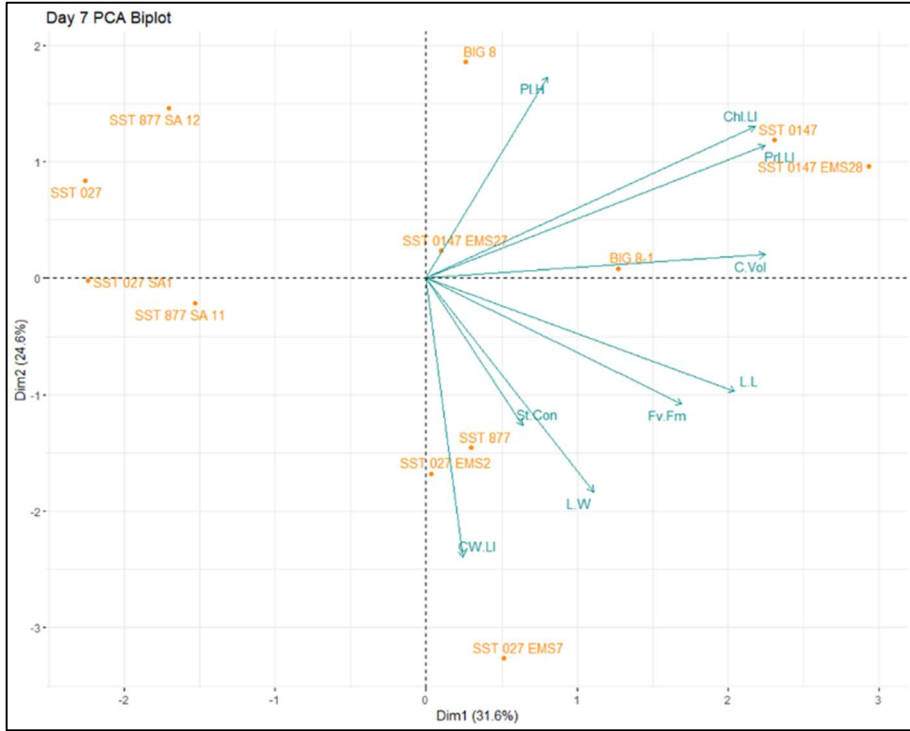
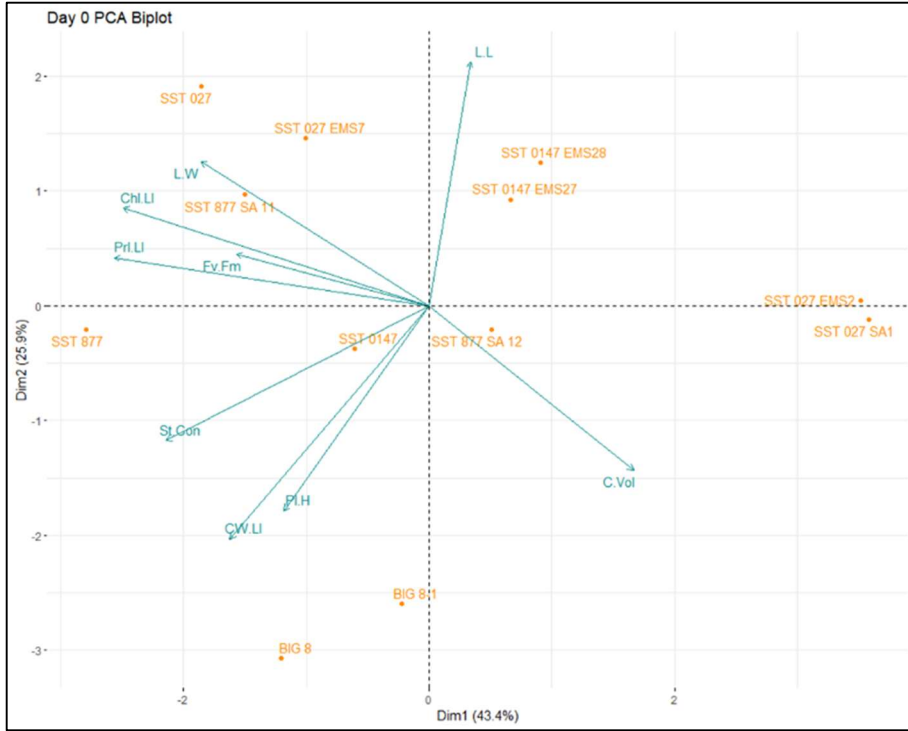


Figure S4. PCA plots of individuals for BIG and SST lines generated during PCA analysis.



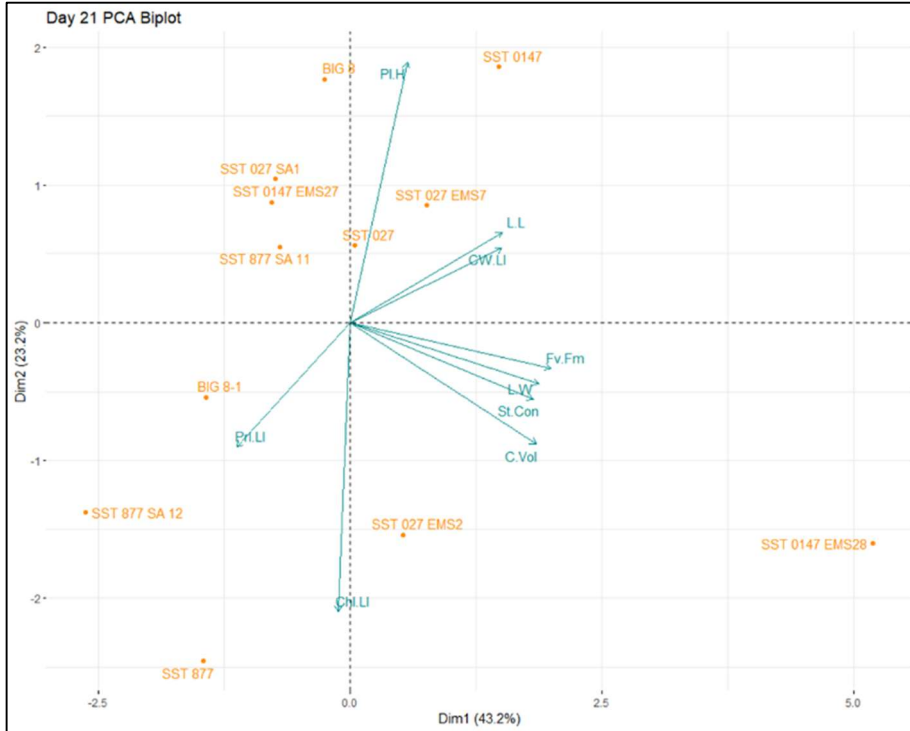
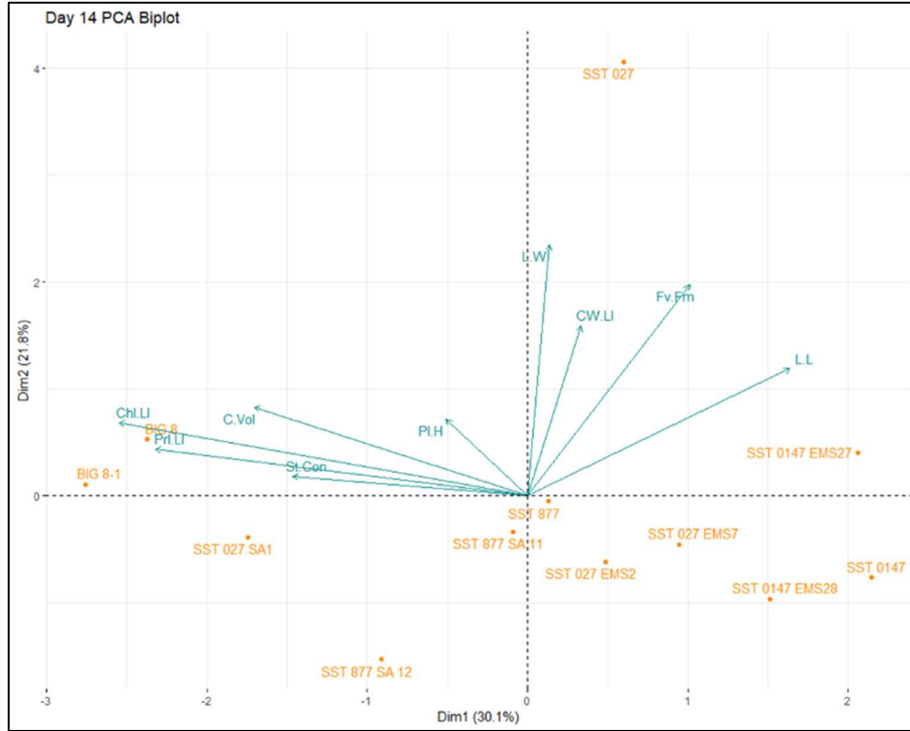


Figure S5. PCA biplots of individuals and variables for BIG and SST wheat lines generated during PCA analysis.

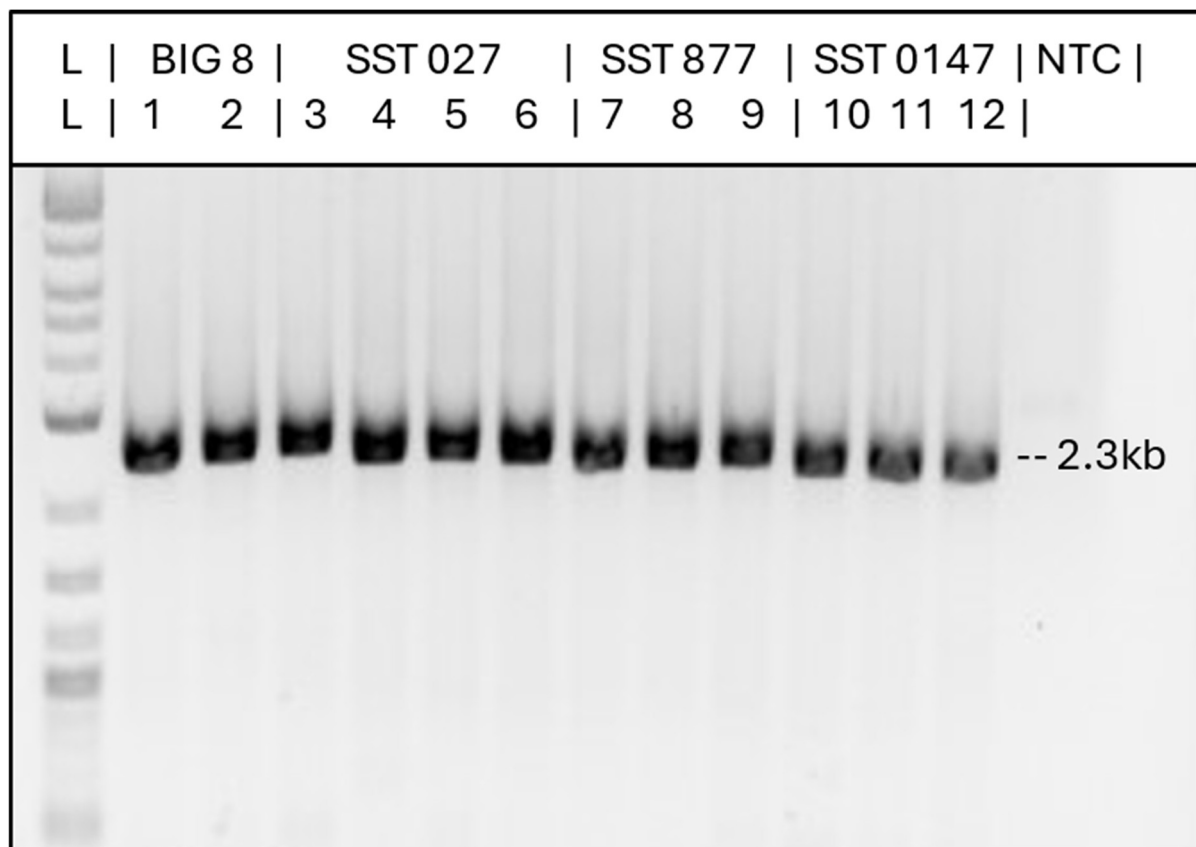


Figure S7. Serpin-Z2B gene fragments, 2300 base pairs, separated by gel electrophoresis on 1% agarose gel and visualized using GelRed staining dye. PCR products were separated against a 1kb Plus DNA ladder (NEB) in lane L. Lanes 1-12 contain PCR products from all 12 wheat lines (BIG 8, BIG 8-1, SST 027, SST 027 SA1, SST 027 EMS2, SST 027 EMS7, SST 877, SST 877 SA11, SST 877 SA12, SST 0147, SST 0147 EMS27 and SST 0147 EMS28). Lane NTC (No template control) is a negative control.

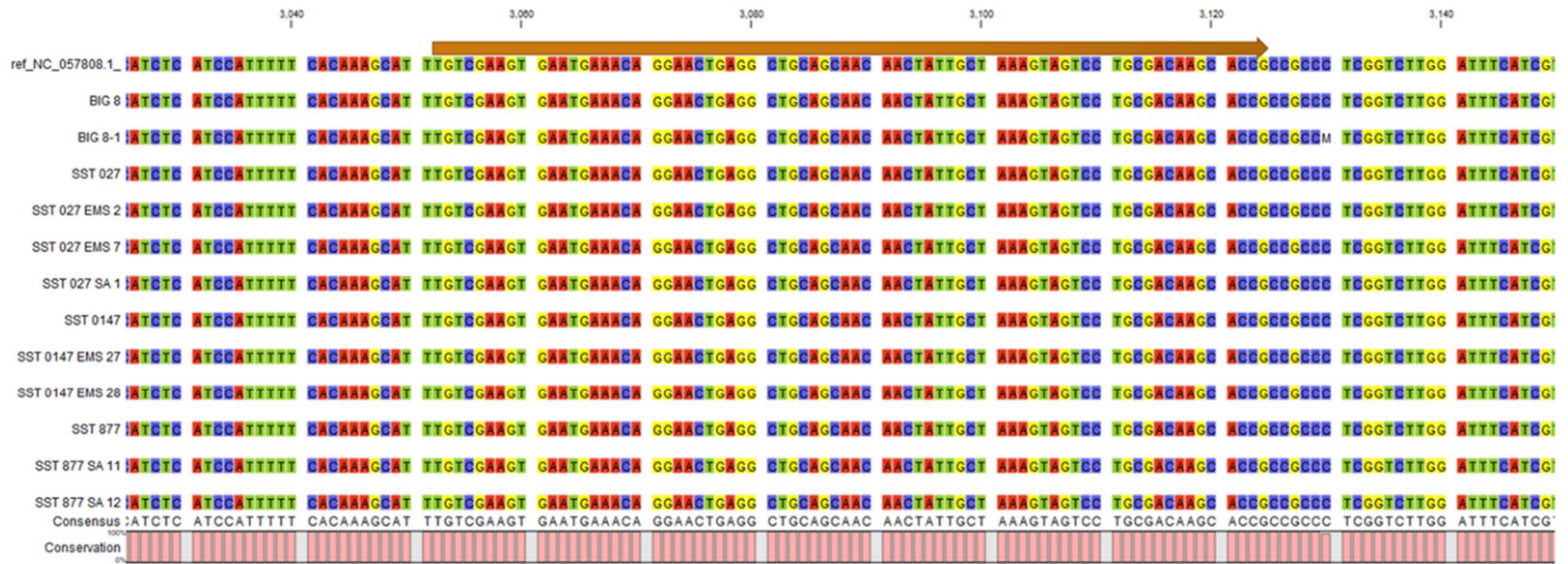


Figure S8. Nucleotide sequence alignment centred around the RCL coding region, highlighted by the arrow from 3052-3124bp, between 3040-3140bp against the Serpin-Z2B reference gene NC_057808.1 and the Serpin-Z2B gene sequences isolated from the 12 BIG and SST wheat lines.

Table S1. Wheat lines assessed within this study.

Wheat line	Line type
BIG 8	Parental
BIG 8-1	EMS derived mutant
SST 027	Parental
SST 027 SA 1	SA derived mutant
SST 027 EMS 2	EMS derived mutant
SST 027 EMS 7	EMS derived mutant
SST 0147	Parental
SST 0147 EMS 27	EMS derived mutant
SST 0147 EMS 28	EMS derived mutant
SST 877	Parental
SST 877 SA 11	SA derived mutant
SST 877 SA 12	SA derived mutant

Table S2. Table reporting the significant differences, according to multiple comparison analysis, between parental wheat lines and their mutations, at which time points they differ, and whether the mutant line performed better (+) or worse (-) than the parental line.

Genotype	Water deficit duration (days)	Significant difference (p-value < 0.05)
SST 027 vs SST 027 SA1	0	-
SST 027 vs SST 027 EMS 2	0	-
SST 027 vs SST 027 EMS 7	7	+
SST 877 vs SST 877 SA 12	14	+
SST 0147 vs SST 0147 EMS 27	0	+
SST 0147 vs SST 0147 EMS 28	0	+
SST 0147 vs SST 0147 EMS 28	7	+