

Supplement Table. Published papers on lncRNAs in major vegetable crops

Title	Species	Year of publication	Publication
BcMF11, a putative pollen-specific non-coding RNA from <i>Brassica campestris</i> ssp. <i>chinensis</i>	<i>Brassica campestris</i> ssp. <i>chinensis</i>	2007	Journal of plant physiology
Transcript Profiling Analysis and ncRNAs' Identification of Male-Sterile Systems of <i>Brassica campestris</i> Reveal New Insights Into the Mechanism Underlying Anther and Pollen Development	<i>Brassica campestris</i>	2022	Frontiers in plant science
BcMF11, a novel non-coding RNA gene from <i>Brassica campestris</i> , is required for pollen development and male fertility	<i>Brassica campestris</i> ssp. <i>chinensis</i> Makino	2013	Plant Cell Reports
Whole-transcriptome sequencing reveals a vernalization-related ceRNA regulatory network in chinese cabbage ( <i>Brassica campestris</i> L. ssp. <i>pekinensis</i> )	<i>Brassica campestris</i> ssp. <i>pekinensis</i>	2021	BMC Genomics
Whole-transcriptome analysis and construction of an anther development-related ceRNA network in Chinese cabbage ( <i>Brassica campestris</i> L. ssp. <i>pekinensis</i> )	<i>Brassica campestris</i> ssp. <i>pekinensis</i>	2022	Scientific Reports
Integrating long noncoding RNAs and mRNAs expression profiles of response to <i>Plasmodiophora brassicae</i> infection in Pakchoi ( <i>Brassica campestris</i> ssp. <i>chinensis</i> Makino)	<i>Brassica campestris</i> ssp. <i>chinensis</i> Makino	2019	PLoS One
Non-coding RNAs: Functional roles in the regulation of stress response in Brassica crops	<i>Brassica crops</i>	2020	Genomics
Genome-wide investigation of regulatory roles of lncRNAs in response to heat and drought stress in <i>Brassica juncea</i> (Indian mustard)	<i>Brassica juncea</i>	2020	Environmental and Experimental Botany
Genome-wide identification of oil biosynthesis-related long non-coding RNAs in allopolyploid <i>Brassica napus</i>	<i>Brassica napus</i>	2018	BMC Genomics
Genome-wide analysis of long non-coding RNAs (lncRNAs) in two contrasting rapeseed ( <i>Brassica napus</i> L.) genotypes subjected to drought stress and re-watering	<i>Brassica napus</i>	2020	BMC Plant Biology
Identification of lncRNAs Responsive to Infection by <i>Plasmodiophora brassicae</i> in Clubroot-Susceptible and -Resistant <i>Brassica napus</i> Lines Carrying Resistance Introgressed from Rutabaga	<i>Brassica napus</i>	2019	Molecular Plant-Microbe Interactions
A global survey of the transcriptome of allopolyploid <i>Brassica napus</i> based on single-molecule long-read isoform sequencing and Illumina-based RNA sequencing data	<i>Brassica napus</i>	2020	Plant Journal
Genome wide identification and functional prediction of long non-coding RNAs responsive to <i>Sclerotinia sclerotiorum</i> infection in <i>Brassica napus</i>	<i>Brassica napus</i>	2016	PLoS One

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Characterization of long non-coding RNAs involved in cadmium toxic response in <i>Brassica napus</i>	<i>Brassica napus</i>	2016	RSC Advances
Genome-wide identification, putative functionality and interactions between lncRNAs and miRNAs in <i>Brassica</i> species	<i>Brassica napus</i> , <i>B. oleracea</i> and <i>B. rapa</i>	2018	Scientific Reports
Pol III-Dependent Cabbage BoNR8 Long ncRNA Affects Seed Germination and Growth in <i>Arabidopsis</i>	<i>Brassica oleracea</i>	2019	Plant and Cell Physiology
Genome-Wide Analysis of Coding and Long Non-Coding RNAs Involved in Cuticular Wax Biosynthesis in Cabbage ( <i>Brassica oleracea</i> L. var. <i>capitata</i> )	<i>Brassica oleracea</i> var. <i>capitata</i>	2019	International journal of molecular sciences
Global Survey of the Full-Length Cabbage Transcriptome ( <i>Brassica oleracea</i> Var. <i>capitata</i> L.) Reveals Key Alternative Splicing Events Involved in Growth and Disease Response	<i>Brassica oleracea</i> var. <i>capitata</i> L.	2021	International journal of molecular sciences
Genome wide identification and functional prediction of long non-coding RNAs in <i>Brassica rapa</i>	<i>Brassica rapa</i>	2016	Genes & Genomics
Transcriptional Association between mRNAs and Their Paired Natural Antisense Transcripts Following <i>Fusarium oxysporum</i> Inoculation in <i>Brassica rapa</i> L	<i>Brassica rapa</i>	2022	Horticulturae
Comparative transcriptome discovery and elucidation of the mechanism of long noncoding RNAs during vernalization in <i>Brassica rapa</i>	<i>Brassica rapa</i>	2018	Plant Growth Regulation
Systematic identification of long non-coding RNAs during pollen development and fertilization in <i>Brassica rapa</i>	<i>Brassica rapa</i>	2018	Plant Journal
Genome-wide analysis of long noncoding RNAs, 24-nt siRNAs, DNA methylation and H3K27me3 marks in <i>Brassica rapa</i>	<i>Brassica rapa</i>	2021	PLoS One
Long noncoding RNAs in <i>Brassica rapa</i> L. following vernalization	<i>Brassica rapa</i>	2019	Scientific Reports
Genome-wide analysis of mRNA and lncRNA expression and mitochondrial genome sequencing provide insights into the mechanisms underlying a novel cytoplasmic male sterility system, BVRC-CMS96, in <i>Brassica rapa</i>	<i>Brassica rapa</i>	2020	Theoretical and Applied Genetics
Single-molecule real-time sequencing facilitates the analysis of transcripts and splice isoforms of anthers in Chinese cabbage ( <i>Brassica rapa</i> L. ssp. <i>pekinensis</i> )	<i>Brassica rapa</i> ssp. <i>pekinensis</i>	2019	BMC Plant Biology
Identification and functional prediction of long non-coding RNAs responsive to heat stress in heading type Chinese cabbage	<i>Brassica rapa</i> ssp. <i>pekinensis</i>	2021	Zemdirbyste-Agriculture
Temperature expression patterns of genes and their coexpression with lncRNAs revealed by RNA-Seq in non-heading Chinese cabbage	<i>Brassica rapa</i> ssp. <i>chinensis</i>	2016	BMC Genomics

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Comparative analysis of long noncoding RNAs in angiosperms and characterization of long noncoding RNAs in response to heat stress in Chinese cabbage	<i>Brassica rapa</i> ssp. <i>pekinensis</i>	2021	Hortic Research
Identification of long noncoding RNAs involved in resistance to downy mildew in Chinese cabbage	<i>Brassica rapa</i> ssp. <i>pekinensis</i>	2021	Hortic Research
Genome-wide analysis of long non-coding RNAs unveils the regulatory roles in the heat tolerance of Chinese cabbage ( <i>Brassica rapa</i> ssp. <i>chinensis</i> )	<i>Brassica rapa</i> ssp. <i>chinensis</i>	2019	Scientific Reports
Integrative analysis of genome-wide lncRNA and mRNA expression in newly synthesized <i>Brassica</i> hexaploids	<i>Brassica rapa</i> , <i>B. carinata</i> , and <i>B. hexaploid</i>	2018	Ecology and evolution
Identification and functional deciphering suggested the regulatory roles of long intergenic ncRNAs (lincRNAs) in increasing grafting pepper resistance to <i>Phytophthora capsici</i>	<i>Capsicum annuum</i>	2021	BMC Genomics
Response of anthocyanin biosynthesis to light by strand-specific transcriptome and miRNA analysis in <i>Capsicum annuum</i>	<i>Capsicum annuum</i>	2022	BMC Plant Biology
Analysis of the Coding and Non-Coding RNA Transcriptomes in Response to Bell Pepper Chilling	<i>Capsicum annuum</i>	2018	International journal of molecular sciences
Noncoding and coding transcriptome analysis reveals the regulation roles of long noncoding RNAs in fruit development of hot pepper ( <i>Capsicum annuum</i> L.)	<i>Capsicum annuum</i>	2017	Plant Growth Regulation
Systematic identification and characterization of long non-coding RNAs involved in cytoplasmic male sterility in pepper ( <i>Capsicum annuum</i> L.)	<i>Capsicum annuum</i>	2020	Plant Growth Regulation
Network analysis of noncoding RNAs in pepper provides insights into fruit ripening control	<i>Capsicum annuum</i>	2019	Scientific Reports
Integrated Analysis of mRNA and Non-coding RNA Transcriptome in Pepper ( <i>Capsicum chinense</i> ) Hybrid at Seedling and Flowering Stages	<i>Capsicum chinense</i>	2021	Frontiers in Genetics
Transcriptomic profile analysis of non-coding RNAs involved in <i>Capsicum chinense</i> Jacq. fruit ripening	<i>Capsicum chinense</i>	2020	Scientia Horticulturae
Global Profiling of lncRNAs Expression Responsive to Allopolyploidization in <i>Cucumis</i>	<i>Cucumis hytivus</i>	2020	Genes
Waterlogging-Stress-Responsive lncRNAs, Their Regulatory Relationships with miRNAs and Target Genes in Cucumber ( <i>Cucumis sativus</i> L.)	<i>Cucumis sativus</i>	2021	International journal of molecular sciences
Plant lncRNAs are enriched in and move systemically through the phloem in response to phosphate deficiency	<i>Cucumis sativus</i>	2019	Journal of Integrative Plant Biology

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Systematic identification and analysis of heat-stress-responsive lncRNAs, circRNAs and miRNAs with associated co-expression and ceRNA networks in cucumber ( <i>Cucumis sativus</i> L.)	<i>Cucumis sativus</i>	2020	Physiologia plantarum
Characterization of lncRNAs and mRNAs Involved in Powdery Mildew Resistance in Cucumber	<i>Cucumis sativus</i>	2021	Phytopathology
Genome-wide identification, characterization and evolutionary analysis of long intergenic noncoding RNAs in cucumber	<i>Cucumis sativus</i>	2015	PLoS One
Insights into long non-coding RNA regulation of anthocyanin carrot root pigmentation	<i>Daucus carota</i>	2021	Scientific Reports International
Early Response of Radish to Heat Stress by Strand-Specific Transcriptome and miRNA Analysis	<i>Raphanus sativus</i>	2019	journal of molecular sciences
Genome-wide identification of long non-coding RNA targets of the tomato MADS box transcription factor RIN and function analysis	<i>Solanum lycopersicum</i>	2019	Annals of botany
Overexpression of lncRNA08489 enhances tomato immunity against <i>Phytophthora infestans</i> by decoying miR482e-3p	<i>Solanum lycopersicum</i>	2022	Biochemical and Biophysical Research Communications
Identification and Characterization of Long Non-Coding RNA in Tomato Roots under Salt Stress	<i>Solanum lycopersicum</i>	2021	bioRxiv
Re-analysis of long non-coding RNAs and prediction of circRNAs reveal their novel roles in susceptible tomato following TYLCV infection	<i>Solanum lycopersicum</i>	2018	BMC Plant Biology
Genome-wide profiling of long non-coding RNAs from tomato and a comparison with mRNAs associated with the regulation of fruit ripening	<i>Solanum lycopersicum</i>	2018	BMC Plant Biology
lncRNA regulates tomato fruit cracking by coordinating gene expression via a hormone-redox-cell wall network	<i>Solanum lycopersicum</i>	2020	BMC Plant Biology
<i>Bacillus subtilis</i> SL18r Induces Tomato Resistance Against <i>Botrytis cinerea</i> , Involving Activation of Long Non-coding RNA, MSTRG18363, to Decoy miR1918	<i>Solanum lycopersicum</i>	2020	Frontiers in plant science
Analysis of long-non-coding RNAs associated with ethylene in tomato	<i>Solanum lycopersicum</i>	2018	Gene
Integrative analysis of long non-coding RNA acting as ceRNAs involved in chilling injury in tomato fruit	<i>Solanum lycopersicum</i>	2018	Gene
Identification and genetic analysis of alternative splicing of long non-coding RNAs in tomato initial flowering stage	<i>Solanum lycopersicum</i>	2020	Genomics

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Long non-coding RNA transcriptome landscape of anthers at different developmental stages in response to drought stress in tomato	<i>Solanum lycopersicum</i>	2022	Genomics
Tomato lncRNA23468 functions as a competing endogenous RNA to modulate NBS-LRR genes by decoying miR482b in the tomato-Phytophthora infestans interaction	<i>Solanum lycopersicum</i>	2019	Hortic Research
Identification of Long Non-Coding RNAs Associated with Tomato Fruit Expansion and Ripening by Strand-Specific Paired-End RNA Sequencing	<i>Solanum lycopersicum</i>	2021	Horticulturae
Functional Analysis of Long Non-Coding RNAs Reveal Their Novel Roles in Biocontrol of Bacteria-Induced Tomato Resistance to Meloidogyne incognita	<i>Solanum lycopersicum</i>	2020	International journal of molecular sciences
RNA sequencing and functional analysis implicate the regulatory role of long non-coding RNAs in tomato fruit ripening	<i>Solanum lycopersicum</i>	2015	Journal of Experimental Botany
Comprehensive Transcriptome Analyses Reveal that Potato Spindle Tuber Viroid Triggers Genome-Wide Changes in Alternative Splicing, Inducible trans-Acting Activity of Phased Secondary Small Interfering RNAs, and Immune Responses	<i>Solanum lycopersicum</i>	2017	Journal of Virology
Expression and diversification analysis reveals transposable elements play important roles in the origin of Lycopersicon-specific lncRNAs in tomato	<i>Solanum lycopersicum</i>	2016	New Phytologist
Genome-Wide Identification of lncRNAs and Analysis of ceRNA Networks During Tomato Resistance to Phytophthora infestans	<i>Solanum lycopersicum</i>	2020	Phytopathology
lncRNA39026 Enhances Tomato Resistance to Phytophthora infestans by Decoying miR168a and Inducing PR Gene Expression	<i>Solanum lycopersicum</i>	2020	Phytopathology
Comparative transcriptome analysis between resistant and susceptible tomato allows the identification of lncRNA16397 conferring resistance to Phytophthora infestans by co-expressing glutaredoxin	<i>Solanum lycopersicum</i>	2017	Plant Journal
CRISPR/Cas9-mediated mutagenesis of lncRNA1459 alters tomato fruit ripening	<i>Solanum lycopersicum</i>	2018	Plant Journal
Transcriptomics analyses reveal the molecular roadmap and long non-coding RNA landscape of sperm cell lineage development	<i>Solanum lycopersicum</i>	2018	Plant Journal
lncRNA33732-respiratory burst oxidase module associated with WRKY1 in tomato-Phytophthora infestans interactions	<i>Solanum lycopersicum</i>	2019	Plant Journal
Sl-lncRNA15492 interacts with Sl-miR482a and affects Solanum lycopersicum immunity against Phytophthora infestans	<i>Solanum lycopersicum</i>	2020	Plant Journal

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Transcriptomic and functional analyses uncover the regulatory role of lncRNA000170 in tomato multicellular trichome formation	<i>Solanum lycopersicum</i>	2020	Plant Journal
Relationships between genome methylation, levels of non-coding RNAs, mRNAs and metabolites in ripening tomato fruit	<i>Solanum lycopersicum</i>	2020	Plant Journal
LncRNA expression profile and ceRNA analysis in tomato during flowering	<i>Solanum lycopersicum</i>	2019	PLoS One
Tomato yellow leaf curl virus intergenic siRNAs target a host long noncoding RNA to modulate disease symptoms	<i>Solanum lycopersicum</i>	2019	PLoS Pathog
Transcription of lncRNA ACoS-AS1 is essential to trans-splicing between SIPsy1 and ACoS-AS1 that causes yellow fruit in tomato	<i>Solanum lycopersicum</i>	2020	RNA Biology
Genome-wide analysis of tomato long non-coding RNAs and identification as endogenous target mimic for microRNA in response to TYLCV infection	<i>Solanum lycopersicum</i>	2015	Scientific Reports
Genome-wide analysis uncovers tomato leaf lncRNAs transcriptionally active upon <i>Pseudomonas syringae</i> pv. tomato challenge	<i>Solanum lycopersicum</i>	2021	Scientific Reports
Identification and Functional Prediction of Drought-Responsive Long Non-Coding RNA in Tomato	<i>Solanum lycopersicum</i>	2019	Agronomy
Function identification of miR394 in tomato resistance to <i>Phytophthora infestans</i>	<i>Solanum lycopersicum</i>	2021	Plant Cell Reports
Noncoding RNAs: functional regulatory factors in tomato fruit ripening	<i>Solanum lycopersicum</i>	2020	Theoretical and Applied Genetics
In Silico identification and annotation of non-coding RNAs by RNA-seq and de novo assembly of the transcriptome of tomato fruits	<i>Solanum lycopersicum</i>	2017	PLoS One
Genome-wide identification of potato long intergenic noncoding RNAs responsive to <i>Pectobacterium carotovorum</i> subspecies <i>brasiliense</i> infection	<i>Solanum tuberosum</i>	2016	BMC Genomics
Anthocyanin regulatory networks in <i>Solanum tuberosum</i> L. leaves elucidated via integrated metabolomics, transcriptomics, and StAN1 overexpression	<i>Solanum tuberosum</i>	2022	BMC Plant Biology
Genome-Wide Identification and Characterization of Potato Long Non-coding RNAs Associated With <i>Phytophthora infestans</i> Resistance	<i>Solanum tuberosum</i>	2021	Frontiers in plant science
Genome-Wide Analysis of Long Non-Coding RNAs in Potato and Their Potential Role in Tuber Sprouting Process	<i>Solanum tuberosum</i>	2017	International journal of molecular sciences
Transcriptomic Reprogramming, Alternative Splicing and RNA Methylation in Potato ( <i>Solanum tuberosum</i> L.) Plants in Response to Potato Virus Y Infection	<i>Solanum tuberosum</i>	2022	Plants

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A Comparative Transcriptome Analysis of Purple and Yellow Fleshed Potato Tubers Reveals Long Non-coding RNAs and their Targets Functioned in Anthocyanin Biosynthesis	<i>Solanum tuberosum</i>	2021	Research Square
Construction of Drought Stress Regulation Networks in Potato Based on SMRT and RNA Sequencing Data	<i>Solanum tuberosum</i>	2021	Research Square
Comparative transcriptome analysis of male and female flowers in <i>Spinacia oleracea</i> L	<i>Spinacia oleracea</i>	2020	BMC Genomics
Global identification of long non-coding RNAs involved in the induction of spinach flowering	<i>Spinacia oleracea</i>	2021	BMC Genomics