

## [Supplementary Information]

# The calmodulin fused kinase novel gene family is the major system in plants converting Ca<sup>2+</sup> signals to protein phosphorylation responses

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# Supporting Information

**Table S1.** Samples used in this study.

Species	Code	Common Name	No. of chromosomes/genome	Image	Source	Version	Link	Note
<i>U. Archaeoplasmid</i>								
<i>U. Archaeoplasmid nucleoides</i>								
<i>Cyanophora paradoxa</i>	Cja	NA	NA/78NA	Glaucophyta	Cyanophora genome project	1	<a href="http://cyanophora.rutgers.edu/cyanophora/">http://cyanophora.rutgers.edu/cyanophora/</a>	Genome available
<i>Polyphidiosorus tenuis</i>	PT	NA	NA	Glaucophyta	http://polyphidiosorus.tenuis.genome.jp	1	<a href="http://polyphidiosorus.tenuis.genome.jp">http://polyphidiosorus.tenuis.genome.jp</a>	Genome available
<i>Chlorodesmus ovigerus</i>	CO	Dish moss	NA/185MB-NA	Rhodophyta Florideophyceae	EBI	1	<a href="http://polyphidiosorus.tenuis.genome.jp">http://polyphidiosorus.tenuis.genome.jp</a>	Genome available
<i>Callithamnion heterostromos</i>	CH	NA	NA	Rhodophyta Rhodophyceae/Nemacladophycidae/Callithamniaceae	EBI	1	<a href="http://ebi.udel.edu/ege/selected.html">http://ebi.udel.edu/ege/selected.html</a>	partial genome
<i>Phaeophytis lutea</i>	PL	Zetia or Open Sea Nori	NA	Phaeophytina	http://writs.ra.eafrc.gov.jp	1	<a href="http://ebi.udel.edu/ege/selected.html">http://ebi.udel.edu/ege/selected.html</a>	partial genome
<i>Gracilaria tikvahiae</i>	GT	NA	20/16/25NA	Cyanophytes Cyanophyceae/Cyanidiochlorophytes/Cyanidiales	Yeastlike cyanobacteria Genome Project	1	<a href="http://microbial.chiba-u.ac.jp/yeastlike/">http://microbial.chiba-u.ac.jp/yeastlike/</a>	Genome available
<i>Micromesistia pusilla</i> R.C. 299	MP	NA	17/20/38NA	Chlorophyta Prasinophyceae	EBI	1	<a href="http://microbial.chiba-u.ac.jp/yeastlike/">http://microbial.chiba-u.ac.jp/yeastlike/</a>	Genome available
<i>Desmarestia viridis</i>	DV	NA	NA	Chlorophyta Chlorophyceae	EBI	1	<a href="http://ebi.udel.edu/ege/selected.html">http://ebi.udel.edu/ege/selected.html</a>	Genome available
<i>Ostreococcus tauri</i>	OT	NA	28/12/28NA	Chlorophyta Prasinophyceae	EBI	1	<a href="http://ebi.udel.edu/ege/selected.html">http://ebi.udel.edu/ege/selected.html</a>	Genome available
<i>Harmothoe preissii</i>	HP	NA	NA	Chlorophyta Prasinophyceae	EBI	1	<a href="http://ebi.udel.edu/ege/selected.html">http://ebi.udel.edu/ege/selected.html</a>	Genome available
<i>Thalassiosira weissflogii</i> NCAS	TW	NA	12/20/23NA/797 genes	Chlorophyta Prasinophyceae	EBI	1	<a href="http://ebi.udel.edu/ege/selected.html">http://ebi.udel.edu/ege/selected.html</a>	Genome available
<i>Thalassiosira caroliniana</i>	TC	NA	NA	Chlorophyta Chlorophyceae	EBI	1	<a href="http://ebi.udel.edu/ege/selected.html">http://ebi.udel.edu/ege/selected.html</a>	Genome available
<i>Thalassiosira rotundata</i>	TR	NA	NA	Chlorophyta Chlorophyceae	EBI	1	<a href="http://ebi.udel.edu/ege/selected.html">http://ebi.udel.edu/ege/selected.html</a>	Genome available
<i>Coccomyces hebetulae</i>	CH	NA	NA/85NA	Chlorophyta Chlorophyceae	EBI	1	<a href="http://ebi.udel.edu/ege/selected.html">http://ebi.udel.edu/ege/selected.html</a>	Genome available
<i>Thalassiosira</i>	TH	NA	NA	Chlorophyta Chlorophyceae	EBI	1	<a href="http://ebi.udel.edu/ege/selected.html">http://ebi.udel.edu/ege/selected.html</a>	Genome available
<i>Klebsormidium flaccidum</i>	KF	NA	NA/184MB-NA	Chlorophyta Klembrondiophycaceae	EBI	1	<a href="http://ebi.udel.edu/ege/selected.html">http://ebi.udel.edu/ege/selected.html</a>	Genome available
<i>Volvox nannodes</i>	VN	NA	NA	Breviostomat Anthocerosophyta (hornwort)	EBI	1	<a href="http://www.ncbi.nlm.nih.gov/protein">http://www.ncbi.nlm.nih.gov/protein</a> /308711	Genome not available
<i>Microcoleus thalaciophilus</i>	MT	NA	NA	Breviostomat Marchantiastrigata	EBI	1	<a href="http://www.ncbi.nlm.nih.gov/protein">http://www.ncbi.nlm.nih.gov/protein</a> /8341493	Genome not available
<i>Hypothamnion pellucidum</i>	HP	NA	NA	Breviostomat Marchantiastrigata/Leptosiphon	EBI	1	<a href="http://www.ncbi.nlm.nih.gov/protein">http://www.ncbi.nlm.nih.gov/protein</a> /ADV38623	Genome not available
<i>Phaeophytis lutea</i>	PL	NA	NA	Breviostomat Marchantiastrigata/Leptosiphon	EBI	1	<a href="http://www.ncbi.nlm.nih.gov/protein">http://www.ncbi.nlm.nih.gov/protein</a> /ADV38624	Genome not available
<i>Sargassum polyceratum</i>	SP	NA	NA	Bryozoa Bryozopoda/Bryozoa	EBI	1	<a href="http://www.ncbi.nlm.nih.gov/protein">http://www.ncbi.nlm.nih.gov/protein</a> /V979789	Genome available
<i>Sargassum polyceratum</i>	SP	NA	NA	Bryozoa Bryozopoda/Bryozoa	EBI	1	<a href="http://www.ncbi.nlm.nih.gov/protein">http://www.ncbi.nlm.nih.gov/protein</a> /V979789	Genome available
<i>Volvox carteri</i>	VC	Rever ritter	NA	Ciliophora Ciliophora	EBI	1	<a href="http://www.ncbi.nlm.nih.gov/protein">http://www.ncbi.nlm.nih.gov/protein</a> /V979789	Genome available
<i>Volvox carteri</i>	VC	Rever ritter	NA	Ciliophora Ciliophora	EBI	1	<a href="http://www.ncbi.nlm.nih.gov/protein">http://www.ncbi.nlm.nih.gov/protein</a> /V979789	Genome available
<i>Volvox carteri</i>	VC	Rever ritter	NA	Ciliophora Ciliophora	EBI	1	<a href="http://www.ncbi.nlm.nih.gov/protein">http://www.ncbi.nlm.nih.gov/protein</a> /V979789	Genome available
<i>Gracilaria tikvahiae</i>	GT	NA	NA	Cyanophyta Cyanophyceae	MSB-MPR	1	<a href="http://mpg.mbl.edu/MSB-MPR/">http://mpg.mbl.edu/MSB-MPR/</a>	partial genome data
<i>Emblema trichopoda</i>	ET	Amborella	NA/287MBNA	aglaophytes Angiospermae/Amborellales	AMBELLA genome database	3	<a href="http://ambella-project.lucknow.edu/Public_Ambella/ambella/EVM_27.html">http://ambella-project.lucknow.edu/Public_Ambella/ambella/EVM_27.html</a>	AMBELLA genome database
<i>Thalassiosira</i>	TH	Diat. Palm	NA/272MBNA	aglaophytes Angiospermae/monocots/Araceales	AGAPANGEMONOCOTS/Araceales	1	<a href="http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/">http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/</a>	Genome available
<i>Sertularia mitcheli</i>	SM	Partial mito	NA/272MBNA	aglaophytes Angiospermae/monocots/Pinkalales	AGAPANGEMONOCOTS/Pinkalales	1	<a href="http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/">http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/</a>	Genome available
<i>Desmarestia viridis</i>	DV	NA	NA	aglaophytes Angiospermae/monocots/Pinkalales	AGAPANGEMONOCOTS/Pinkalales	1	<a href="http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/">http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/</a>	Genome available
<i>Oryza sativa</i> indica	OS	rice indica variety	NA/68MBNA	aglaophytes Angiospermae/monocots/Poales	IGCA	NAX	<a href="http://rice.genomics.org.cn/cgi-bin/rice/locus.html">http://rice.genomics.org.cn/cgi-bin/rice/locus.html</a>	Genome available
<i>Oryza sativa</i> japonica	OJ	rice japonica columnar	NA/68MBNA	aglaophytes Angiospermae/monocots/Poales/Magnoliidae	AGAPANGEMONOCOTS/Poales/Magnoliidae	1	<a href="http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/">http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/</a>	Genome available
<i>Filix sibirica</i>	FS	grapeme	NA/68MBNA	aglaophytes Angiospermae/Rilesiales	CRIB	1	<a href="http://genomes.crib.ac.il/FRUIT/FESTIV/">http://genomes.crib.ac.il/FRUIT/FESTIV/</a>	Genome available
<i>Arabidopsis lyrata</i>	AL	Mouse-ear cress	NA/24UNA	aglaophytes Angiospermae/Brassicaceae	AGAPANGEMONOCOTS/Brassicaceae	1	<a href="http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/">http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/</a>	Genome available
<i>Brassica rapa</i>	BR	Chinese Cabbage	NA/24UNA	aglaophytes Angiospermae/Brassicaceae	AGAPANGEMONOCOTS/Brassicaceae	1	<a href="http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/">http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/</a>	Genome available
<i>Crinaria papaya</i>	CP	papaya	NA/24UNA	aglaophytes Angiospermae/Brassicaceae	AGAPANGEMONOCOTS/Brassicaceae	1	<a href="http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/">http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/</a>	Genome available
<i>Thlaspi arvense</i>	TA	field mustard	NA/24UNA	aglaophytes Angiospermae/Brassicaceae	AGAPANGEMONOCOTS/Brassicaceae	1	<a href="http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/">http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/</a>	Genome available
<i>Glycyrrhiza uralensis</i>	GU	licorice	NA/24UNA	aglaophytes Angiospermae/Brassicaceae	AGAPANGEMONOCOTS/Brassicaceae	1	<a href="http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/">http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/</a>	Genome available
<i>Phloxius rotundifolius</i>	PR	old fegum	NA/24UNA	aglaophytes Angiospermae/Brassicaceae	AGAPANGEMONOCOTS/Brassicaceae	1	<a href="http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/">http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/</a>	Genome available
<i>Merluccius productus</i>	MP	Barracudov	NA/232MBNA	aglaophytes Angiospermae/Brassicaceae	AGAPANGEMONOCOTS/Brassicaceae	1	<a href="http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/">http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/</a>	Genome available
<i>Monodelphisi domesticus</i>	MD	dog	NA/232MBNA	aglaophytes Angiospermae/Brassicaceae/Monodelphidales	AGAPANGEMONOCOTS/Monodelphidales	1	<a href="http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/">http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/</a>	Genome available
<i>Thlaspi arvense</i>	TA	arachne	NA/232MBNA	aglaophytes Angiospermae/Brassicaceae/Mustardales	AGAPANGEMONOCOTS/Mustardales	1	<a href="http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/">http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/</a>	Genome available
<i>Cucumis sativus</i>	CS	Cucumber	NA/232MBNA	aglaophytes Angiospermae/Brassicaceae/Malpighiales	AGAPANGEMONOCOTS/Malpighiales	1	<a href="http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/">http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/</a>	Genome available
<i>Populus tremuloides</i>	PT	aspen	NA/232MBNA	aglaophytes Angiospermae/Brassicaceae/Malpighiales	AGAPANGEMONOCOTS/Malpighiales	4.5	<a href="http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/">http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/</a>	Genome available
<i>Ricinus communis</i>	RC	castorbean	NA/232MBNA	aglaophytes Angiospermae/Brassicaceae/Ricidae/Malpighiales	AGAPANGEMONOCOTS/Ricidae/Malpighiales	9	<a href="http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/">http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/</a>	Genome available
<i>Monodelphisi domestica</i>	MD	mouse	NA/232MBNA	aglaophytes Angiospermae/Asteridae/Lamiales	AGAPANGEMONOCOTS/Asteridae/Lamiales	1.1	<a href="http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/">http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/</a>	Genome available
<i>Prunus mume</i>	PM	pepi	NA/285MBNA	aglaophytes Angiospermae/Rileyales	Prunus mume Genome Project	1	<a href="http://prunus.mume.GP/index.html">http://prunus.mume.GP/index.html</a>	Genome available
<i>Quercus rubra</i>	QR	oak	NA/285MBNA	aglaophytes Angiospermae/Rileyales/Fagales	QR	1	<a href="http://qr.vet.virginia.edu/">http://qr.vet.virginia.edu/</a>	Genome available
<i>Thlaspi arvense</i>	TA	cress tree	NA/285MBNA	aglaophytes Angiospermae/Rileyales/Fagales/Mustardales	AGAPANGEMONOCOTS/Fagales/Mustardales	1	<a href="http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/">http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/</a>	Genome available
<i>Thlaspi arvense</i>	TA	arachne	NA/285MBNA	aglaophytes Angiospermae/Rileyales/Fagales/Mustardales	AGAPANGEMONOCOTS/Fagales/Mustardales	1	<a href="http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/">http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/</a>	Genome available
<i>Lactuca sativa</i>	LS	lettuce	NA/303MBNA	aglaophytes Angiospermae/Rileyales/Malpighiales	AGAPANGEMONOCOTS/Malpighiales	1	<a href="http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/">http://qualitec-wellcome.sanger.ac.uk/research/AGAPANGEMONOCOTS/</a>	Genome available
<i>Solanum tuberosum</i>	ST	potato	NA/303MBNA	aglaophytes Angiospermae/Rileyales/Asteridae/Solanaceae	AGAPANGEMONOCOTS/Solanaceae	2.4	<a href="http://solanomics.net/organism/Solanaceae/tuberose.html">http://solanomics.net/organism/Solanaceae/tuberose.html</a>	Genome available
<b>2) Amoebozoa</b>								
<i>Dictyostelium discoideum</i>	DD	NA	NA	Amoebozoa Ciliata	dictyDB	1	<a href="http://www.dictybase.org">http://www.dictybase.org</a>	Genome available
<i>Dictyostelium discoideum</i>	DD	NA	NA	Amoebozoa Ciliata	dictyDB	1	<a href="http://www.ncbi.nlm.nih.gov/gene/330">http://www.ncbi.nlm.nih.gov/gene/330</a>	Genome available
<i>Dictyostelium discoideum</i>	DD	NA	NA	Amoebozoa Mycetozoa	dictyDB	1	<a href="http://www.ncbi.nlm.nih.gov/gene/330">http://www.ncbi.nlm.nih.gov/gene/330</a>	Genome available
<i>Amoebozoa nucleolides</i>	AN	NA	NA	Amoebozoa	dictyDB	1	<a href="http://www.ncbi.nlm.nih.gov/gene/330">http://www.ncbi.nlm.nih.gov/gene/330</a>	Genome available
<b>3) Stramenopiles</b>								
<i>Leptosphaeria major</i>	LM	NA	NA/41MBNA	Oligoflagellida chlorophytes	RGL	current	<a href="http://genome.jgi-psf.org/pages/dynamic/ko/ko.html#ko/ko/Leptosphaeria_major/">http://genome.jgi-psf.org/pages/dynamic/ko/ko.html#ko/ko/Leptosphaeria_major/</a>	Genome available
<i>Centropyxis obliqua</i>	CO	NA	NA/41MBNA	Oligoflagellida chlorophytes	RGL	1	<a href="http://genome.jgi-psf.org/pages/dynamic/ko/ko.html#ko/ko/Centropyxis_obliqua/">http://genome.jgi-psf.org/pages/dynamic/ko/ko.html#ko/ko/Centropyxis_obliqua/</a>	Genome available
<i>Centropyxis obliqua</i>	CO	NA	NA/41MBNA	Oligoflagellida chlorophytes	RGL	1	<a href="http://genome.jgi-psf.org/pages/dynamic/ko/ko.html#ko/ko/Centropyxis_obliqua/">http://genome.jgi-psf.org/pages/dynamic/ko/ko.html#ko/ko/Centropyxis_obliqua/</a>	Genome available
<i>Centropyxis obliqua</i>	CO	NA	NA/41MBNA	Oligoflagellida chlorophytes	RGL	1	<a href="http://genome.jgi-psf.org/pages/dynamic/ko/ko.html#ko/ko/Centropyxis_obliqua/">http://genome.jgi-psf.org/pages/dynamic/ko/ko.html#ko/ko/Centropyxis_obliqua/</a>	Genome available
<b>4) Excavata</b>								
<i>Leptotrichia major</i>	LM	NA	NA/24LMBNA	Excavata Euglenozoa Kinetoplastida	LSA genote	NA	<a href="http://lsagenote.jgi-psf.org/eukaryotes/LSA_genote.html">http://lsagenote.jgi-psf.org/eukaryotes/LSA_genote.html</a>	Genome available
<i>Cryptosporidium hominis</i>	CH	NA	NA/24LMBNA	Excavata Euglenozoa Kinetoplastida	LSA genote	NA	<a href="http://lsagenote.jgi-psf.org/eukaryotes/LSA_genote.html">http://lsagenote.jgi-psf.org/eukaryotes/LSA_genote.html</a>	Genome available
<i>Cryptosporidium hominis</i>	CH	NA	NA/24LMBNA	Excavata Euglenozoa Kinetoplastida	LSA genote	NA	<a href="http://lsagenote.jgi-psf.org/eukaryotes/LSA_genote.html">http://lsagenote.jgi-psf.org/eukaryotes/LSA_genote.html</a>	Genome available
<i>Phytophthora sojae</i>	PS	NA	NA/95MBNA	Chloromyxida Heterokontobionta or stramenopiles/Oomycota	LSA genote	NA	<a href="http://lsagenote.jgi-psf.org/eukaryotes/LSA_genote.html">http://lsagenote.jgi-psf.org/eukaryotes/LSA_genote.html</a>	Genome available
<i>Haemoproteus</i>	HA	NA	NA	Haemoproteus	LSA genote	NA	<a href="http://lsagenote.jgi-psf.org/eukaryotes/LSA_genote.html">http://lsagenote.jgi-psf.org/eukaryotes/LSA_genote.html</a>	Genome available
<i>Archaea</i>	AR	NA	NA	Archaea	LSA genote	NA	<a href="http://lsagenote.jgi-psf.org/eukaryotes/LSA_genote.html">http://lsagenote.jgi-psf.org/eukaryotes/LSA_genote.html</a>	Genome available
<b>5) Chromalveolata</b>								
<i>Radiotilus</i>	RT	NA	NA/7-9MBNA	Chromalveolata Alveolata Apicomplexa	prokaryoids	1.1	<a href="http://prokaryoids.org/common/downloads/Release_1_Blasts.fasta">http://prokaryoids.org/common/downloads/Release_1_Blasts.fasta</a>	Genome available
<i>Cryptosporidium hominis</i>	CH	NA	NA/24LMBNA	Chromalveolata Alveolata Apicomplexa	prokaryoids	4.8	<a href="http://prokaryoids.org/common/downloads/Release_4_Euk_Blasts.fasta">http://prokaryoids.org/common/downloads/Release_4_Euk_Blasts.fasta</a>	Genome available
<i>Trypanosoma brucei</i>	TB	NA	NA/24LMBNA	Chromalveolata Alveolata Apicomplexa	prokaryoids	4.8	<a href="http://prokaryoids.org/common/downloads/Release_4_Euk_Blasts.fasta">http://prokaryoids.org/common/downloads/Release_4_Euk_Blasts.fasta</a>	Genome available
<i>Trypanosoma brucei</i>	TB	NA	NA/24LMBNA	Chromalveolata Alveolata Apicomplexa	prokaryoids	4.8	<a href="http://prokaryoids.org/common/downloads/Release_4_Euk_Blasts.fasta">http://prokaryoids.org/common/downloads/Release_4_Euk_Blasts.fasta</a>	Genome available
<i>Phytophthora sojae</i>	PS	NA	NA/95MBNA	Chromalveolata Heterokontobionta or stramenopiles/Oomycota	prokaryoids	1	<a href="http://prokaryoids.org/common/downloads/Release_1_Blasts.fasta">http://prokaryoids.org/common/downloads/Release_1_Blasts.fasta</a>	Genome available
<b>6) Transcription data</b>								
<i>Grigori</i>	GR	NA	NA					
<i>Trichoplasmoides</i>	TM	NA	NA					
<i>Oryza sativa</i>	OS	rice	rice/plantbiology/rice_cgi/expression.shtml					
<i>Psidium guajava</i>	PG	NA	NA/24LMBNA	supplementary file in <a href="http://www.ncbi.nlm.nih.gov/genomes/GenBank/psidium_guajava/psidium_guajava.html">http://www.ncbi.nlm.nih.gov/genomes/GenBank/psidium_guajava/psidium_guajava.html</a>				
<i>Grigori</i>	GR	NA	NA	Grigori				
<i>Grigori</i>	GR	NA	NA	Grigori				

**Table S2.** CFKs from *Arabidopsis thaliana* enrolled in pollen development from D

subfamily.

<b>pollen development</b>	<b>myristoylation</b>	<b>palmytoylation</b>	<b>group</b>
At2g17290	y	y	d3
At2g38910	y	y	d3
At3G10660	y	y	d3
At2g35890	y	y	d3
At5G04870	y	y	d3
At4G35310	y	y	d3
At1g18890	y	y	d2
At1g74740	y	y	d2
At2g41860	y	y	d2
At3g57530	y	y	d2
At5g19450	y	y	d2
At5g12480	y	y	d2
At3g51850	y	y	d2
At2g31500	y	y	d2
At5g19360	y	y	d1
At5g12180	y	y	d1
At4g23650	y	y	d1
At3g20410	y	y	d1
At4g04740	y	y	d1
At4g21940	y	y	d1
At4g04710	y	y	d1
At4G04700	y	y	d1

**Figure S1** The details of the phylogenetic tree in Figure 1. The maximum-likelihood local supporting value was produced by FastTree software. Branches are colored to represent the origins from the five eukaryotic supergroups. Green: Archaeplastida, Blue: Opisthokonta, Red: SAR, Black: Amoebozoa, Purple: Excavata.

**Figure S2** The four characteristic insertions in the kinase domain are represented as sequence logo format.

Insertion 1 and 3 each has one amino acid, insertion 2 and 4 each has three amino acids.

**Figure S3** Distribution of X-monophylic members in eukaryotic supergroups.

**Figure S4** X-monophylic members in Eukaryotes other than plants are possibly derived from plant X-monophylic members via horizontal gene transfers.

The plant X-monophylic members are shown in green, and the non-plant X-monophylic members are shown in red. The arrow indicates the possible horizontal gene transfer events.

**Figure S5** The whole maximum-likelihood phylogenetic tree of CFK genes generated with CFKs from all sampled plants.

Abbreviations of species are shown in Table S1.

**Figure S6** Enrichment and expansion of CFKs in the order Brassicales.

(A) The genome density of CFKs amongst green plant representatives. (B) Expansion of CFKs via various forms, and rounds of duplication.

**Figure S7** Expression profile of CFKs in *Arabidopsis thaliana* and a B5 member in *Medicago truncatula*.

Expression profile of AtCFKs includes developmental stages of 8 organs/parts, cold, osmotic stress, salt, drought, genotoxic, oxidative, UV-B, wounding, and heat treatment, pseudomonas, phytophthora, and elicitors treatments. Expression profile of *M. truncatula* CFK includes different organs and developmental stages.

**Figure S8** Functions of CFKs in *Arabidopsis thaliana*.

Domains, motifs, and modifications along with corresponding subcellular localizations are shown. Functions on three aspects (development, abiotic and biotic Stress, Plant-microbe communication) are based on expressional analyses as in Fig. S7 and previous reports (Boudsocq & Sheen, 2013). \* indicates that it was reported by Boudsocq and Sheen (Boudsocq & Sheen, 2013). #\\$ represents reports by Aldous et al. (Aldous, 2014) and Yang et al. (Yang, 2015), respectively.

**Figure S9** Expression profile of four CFKs from *P. patens* under the treatments of salt and drought stresses, respectively.

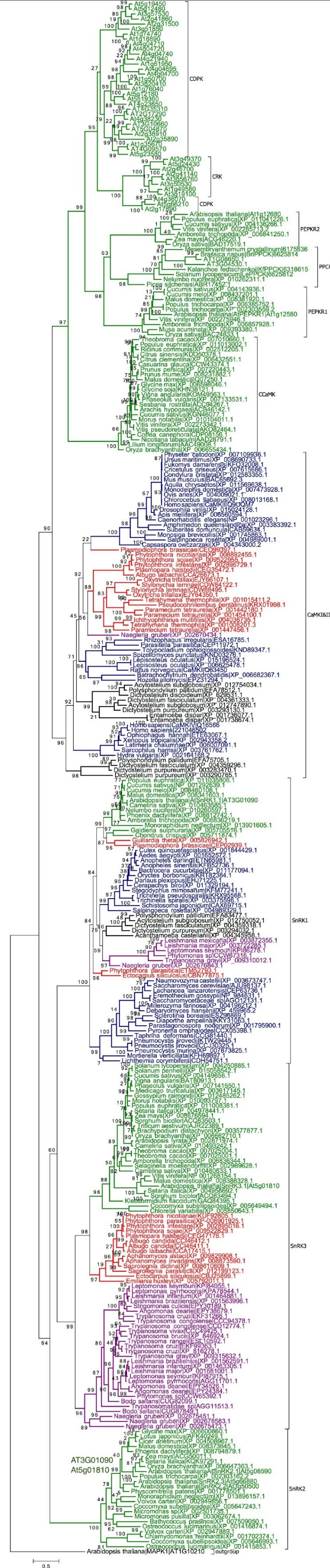
**Figure S10** The expressional profiles of subfamily D CFKs from *Physcomitrella patens* between the sporophyte stage (mean\_spores) and the gametophyte stage (mean\_gametophore).

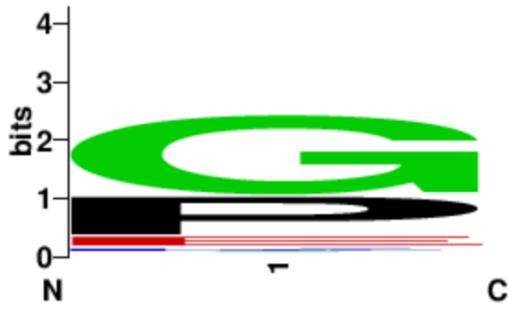
Details of the samples and the experiment could be found by Khraiwesh et al. 2015 (Khraywesh, 2015).

**File S1.** Representative sequences that have innovative gene structure compared to the typical structure composed of a KD and a CaM-LD.

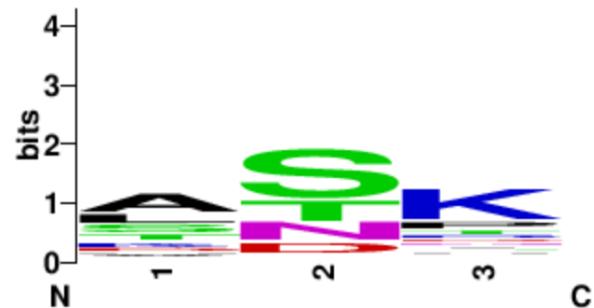
## References

- Aldous S.** 2014. Evolution of the phosphoenolpyruvate carboxylase protein kinase family in C3 and C4 Flaveria spp. *Plant Physiol* **165**: 1076–1091.
- Boudsocq M, Sheen J.** 2013. CDPKs in immune and stress signaling. *Trends Plant Sci* **18**: 30–40.
- Khraiwesh B.** 2015. Genome-wide expression analysis offers new insights into the origin and evolution of *Physcomitrella patens* stress response. *Sci Rep* **5**: 17434.
- Yang X.** 2015. A roadmap for research on crassulacean acid metabolism (CAM) to enhance sustainable food and bioenergy production in a hotter, drier world. *New Phytol* **207**: 491–504.

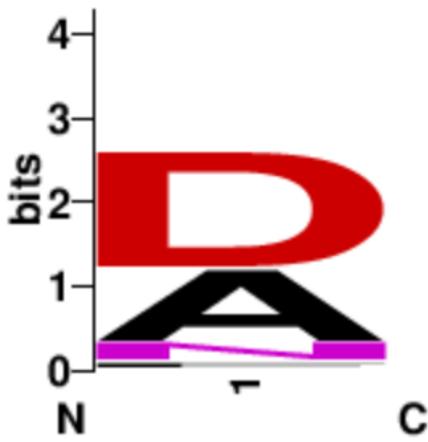




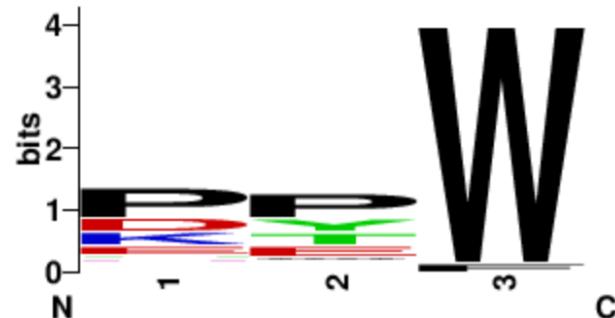
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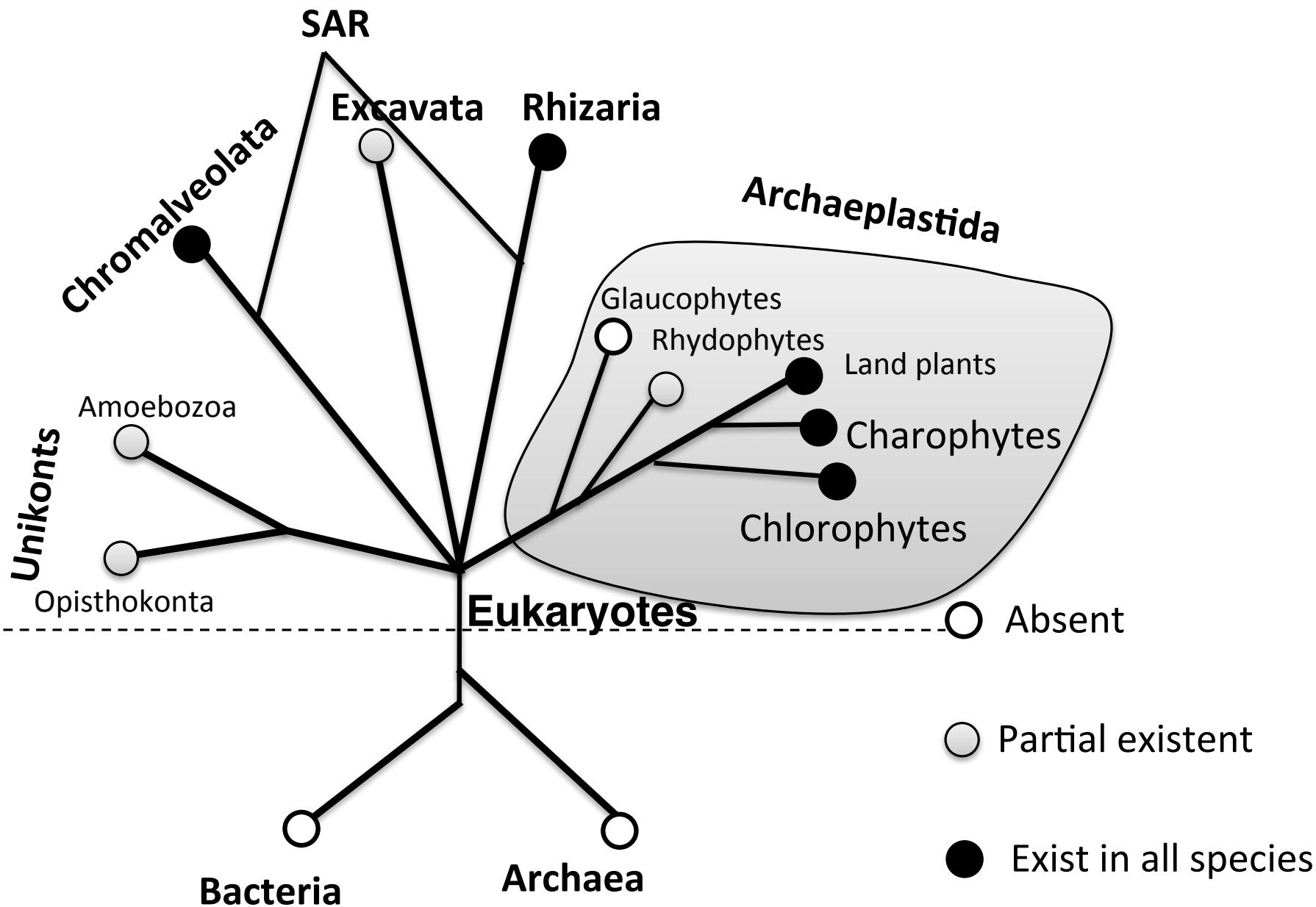
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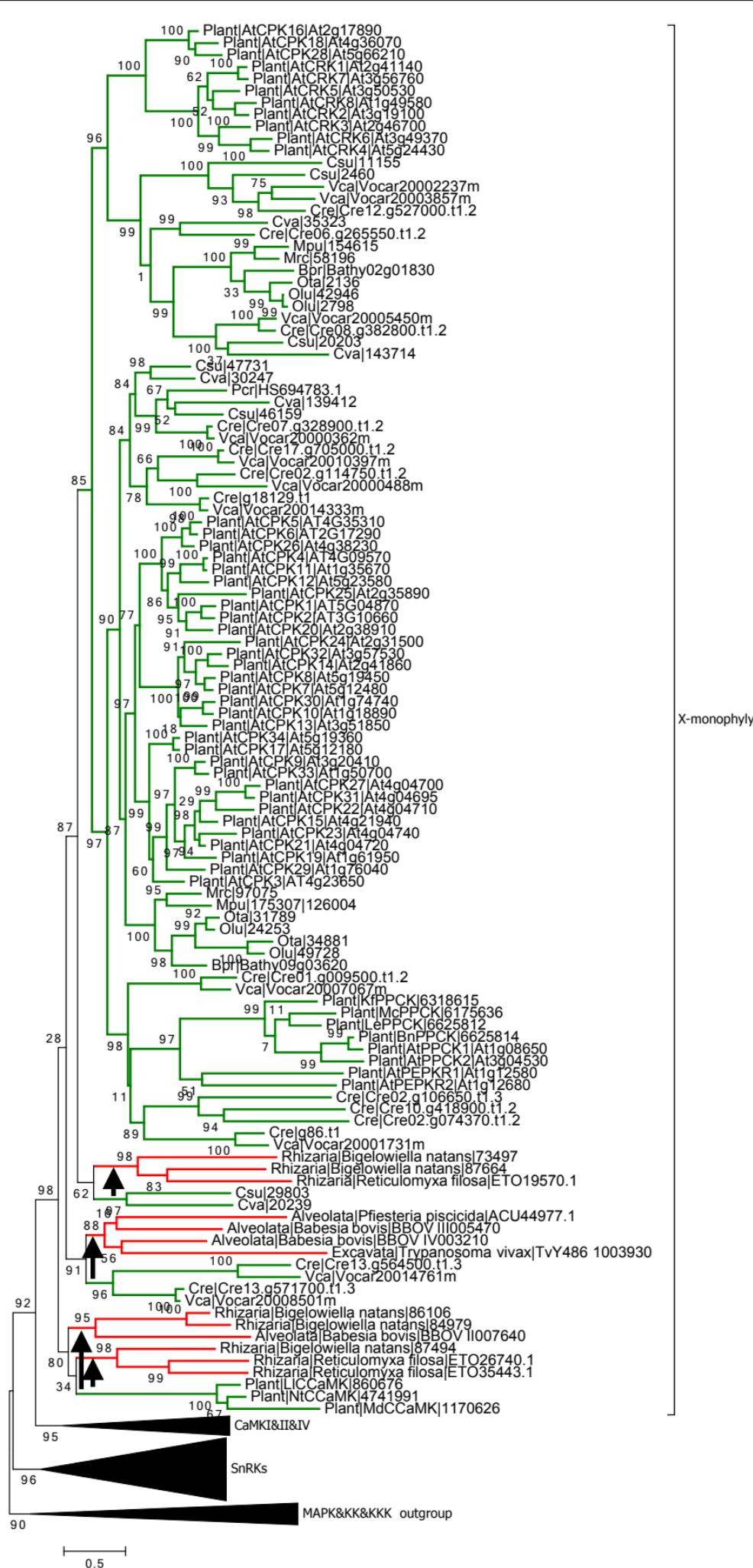


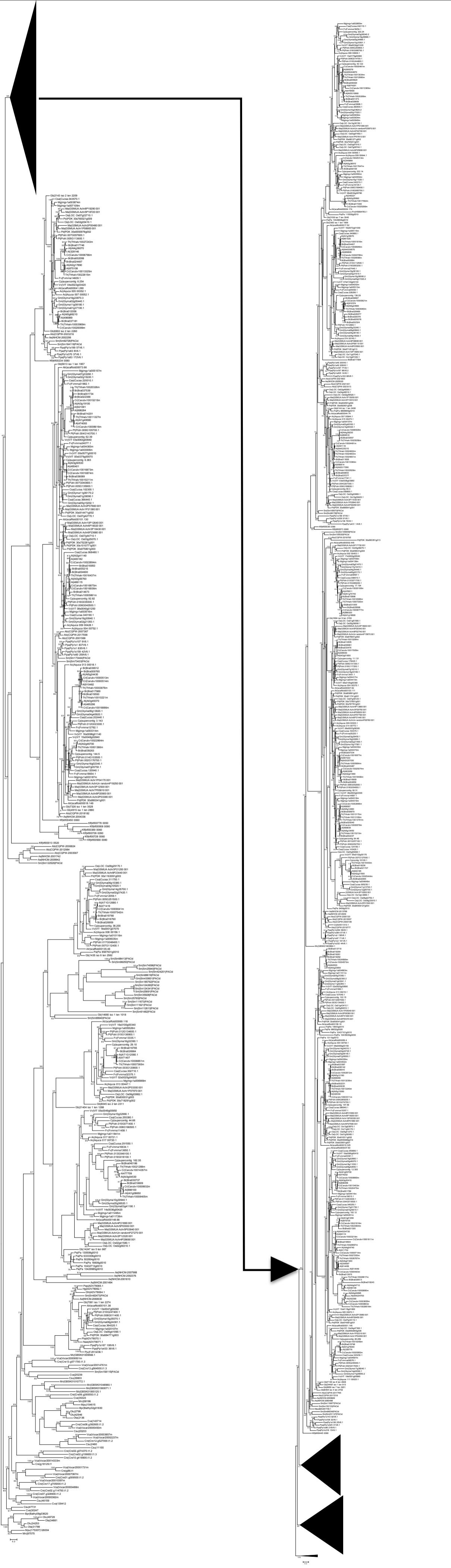
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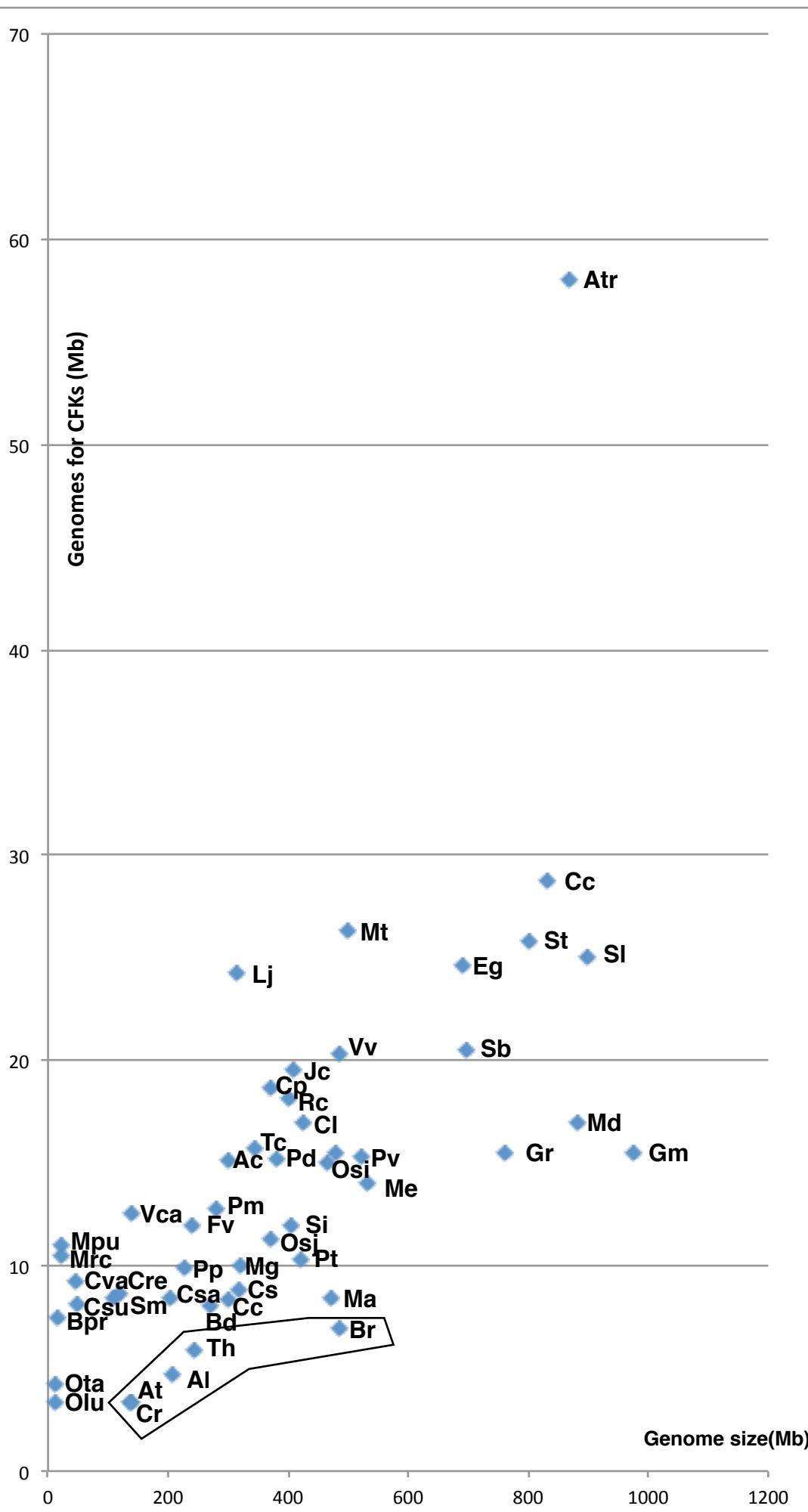
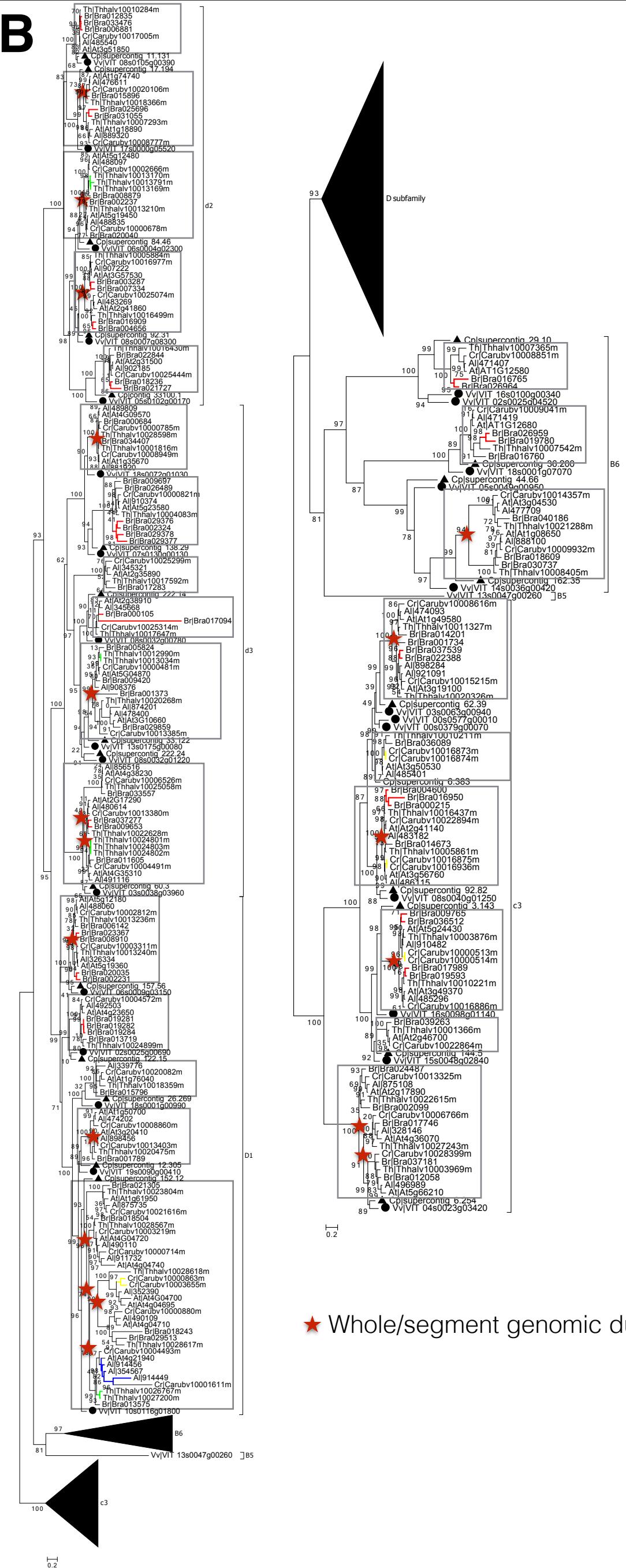


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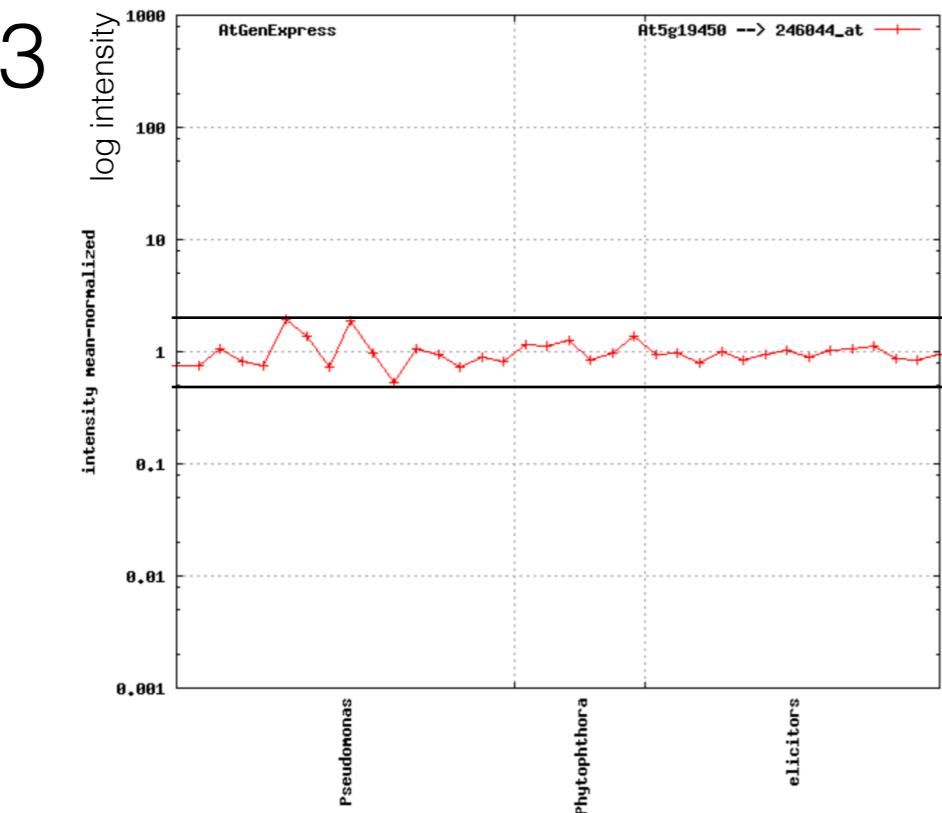
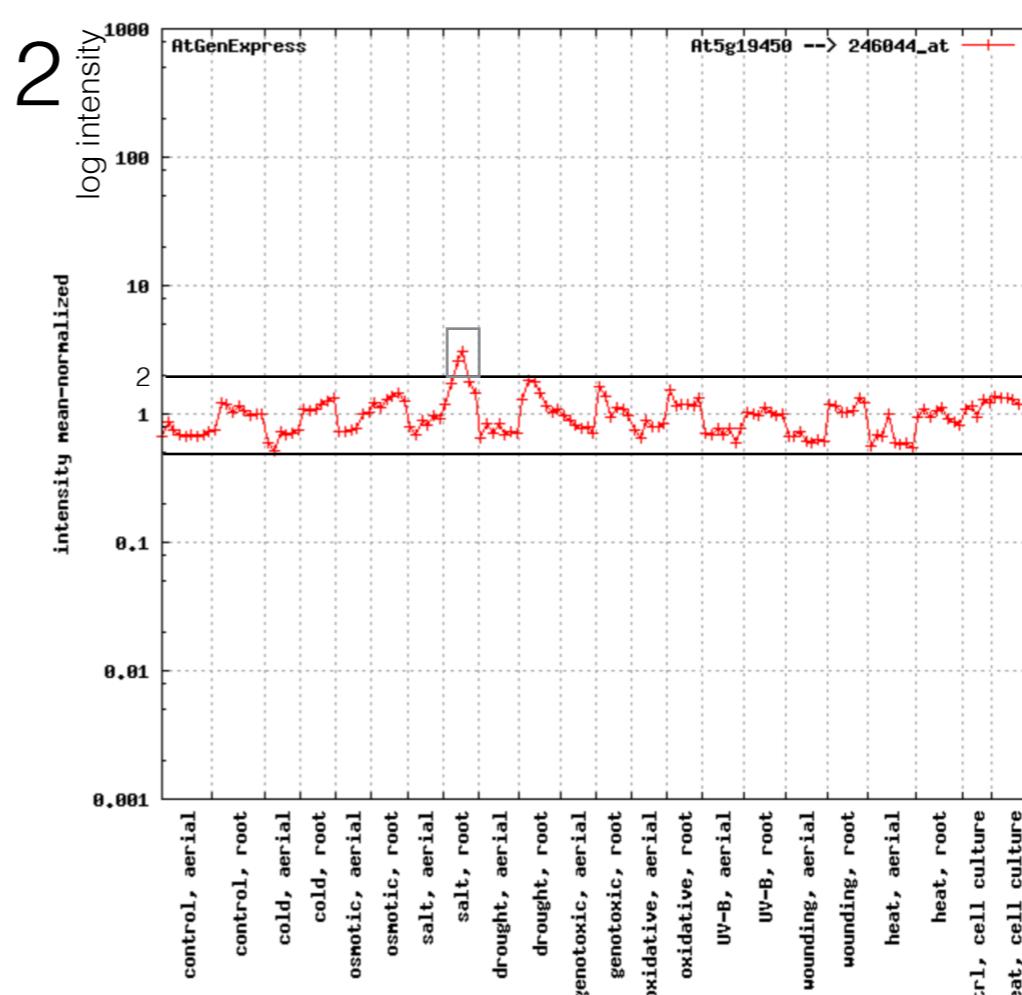
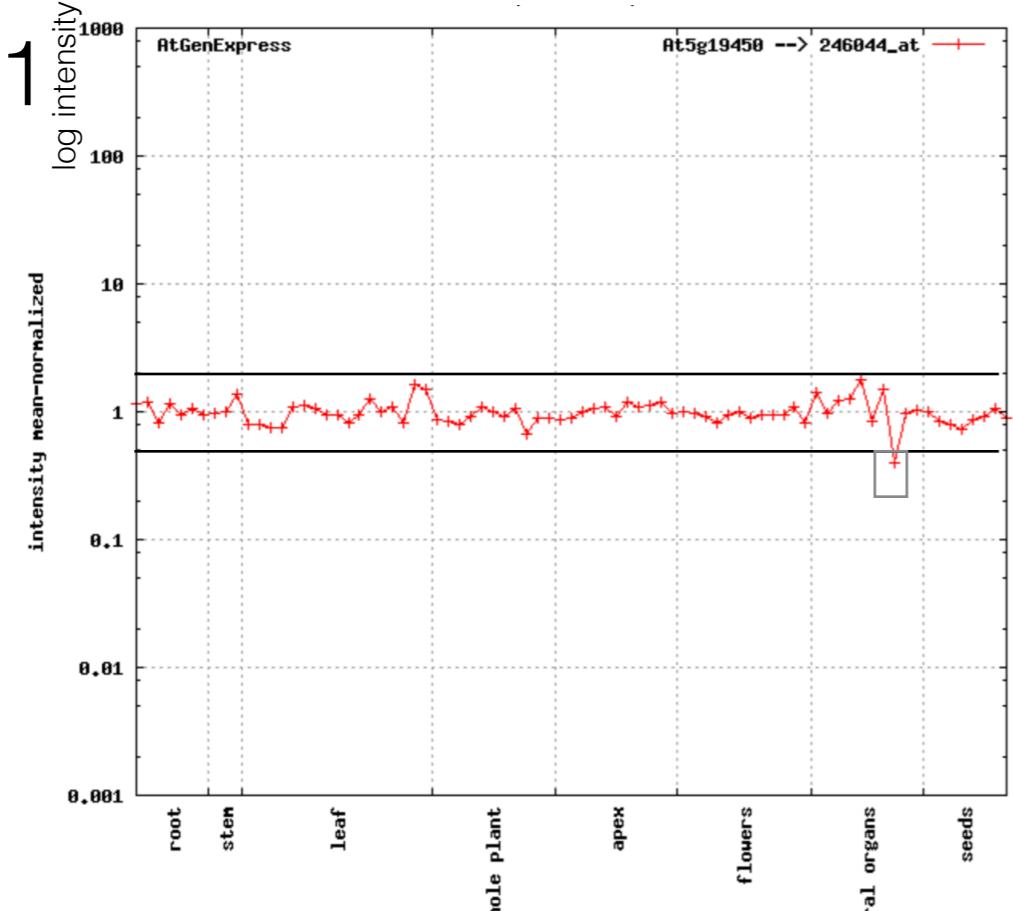




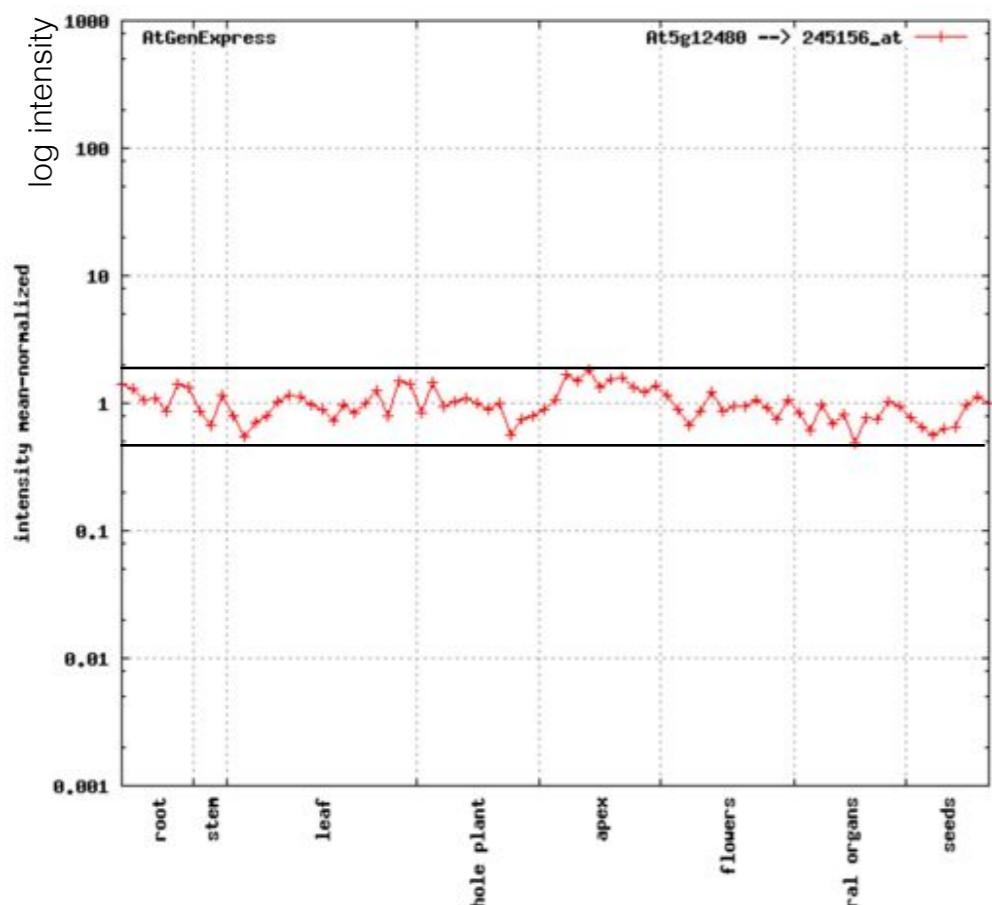


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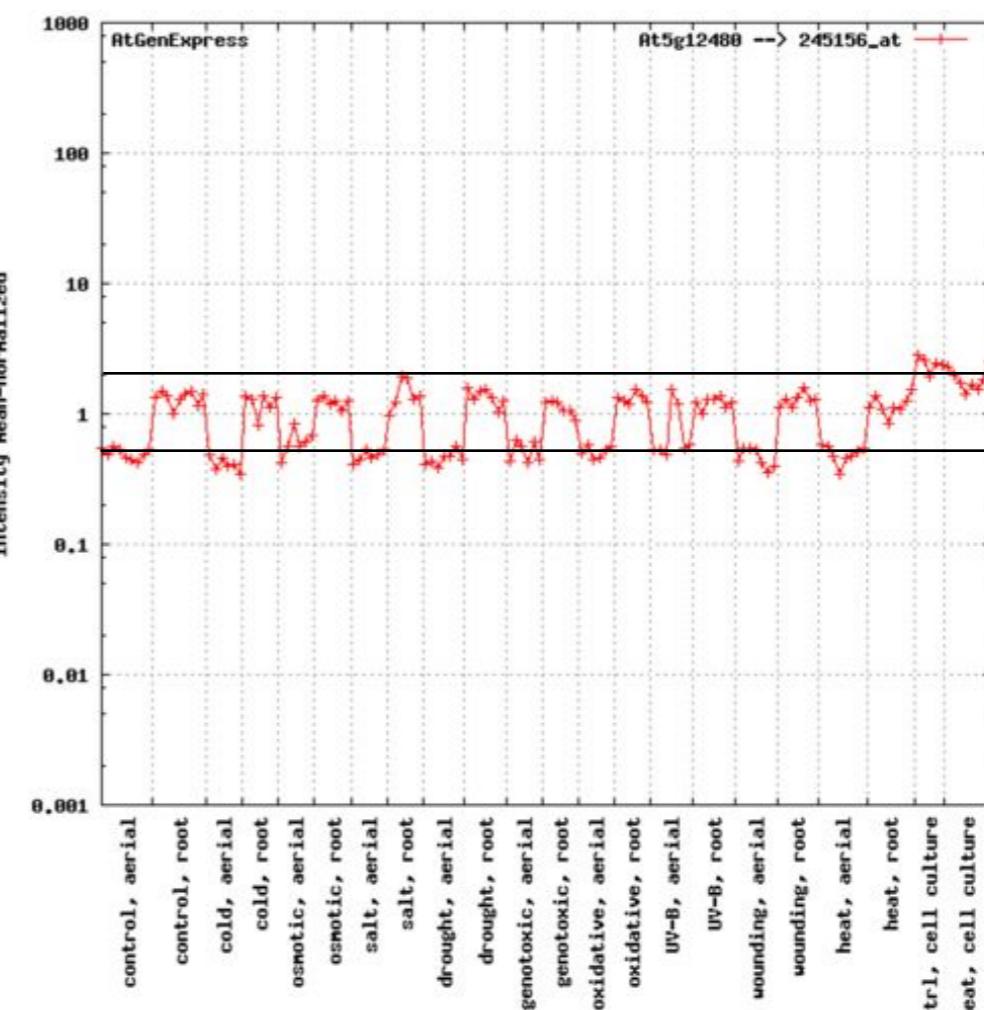
★ Whole/segment genomic duplication



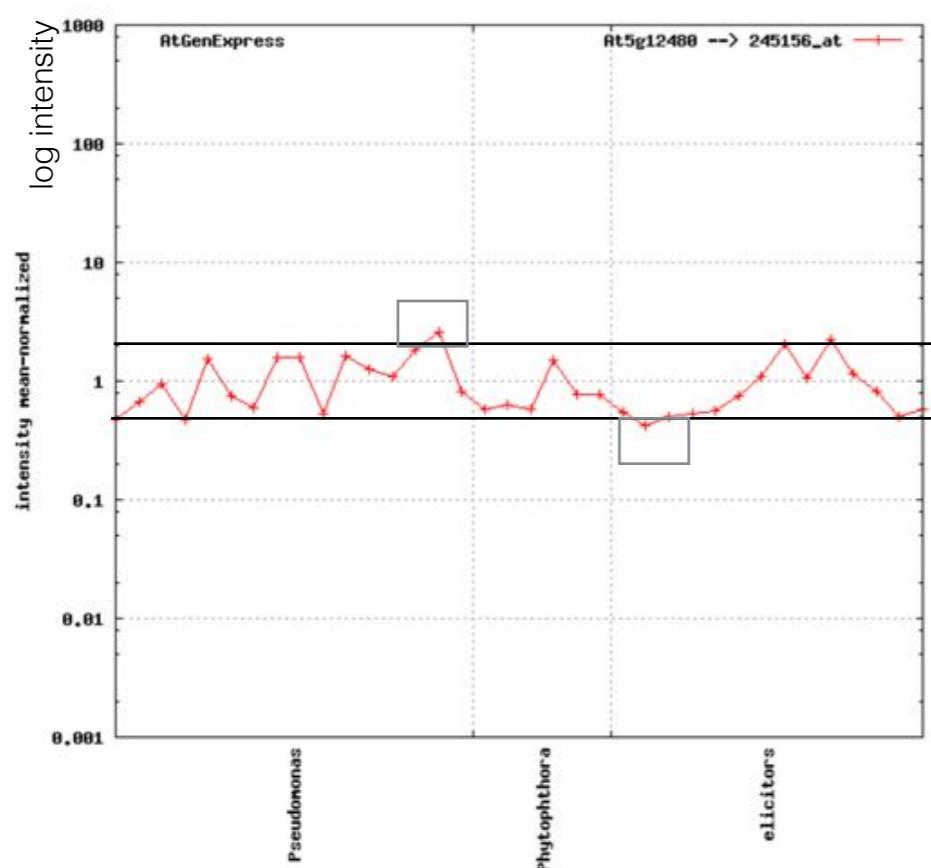
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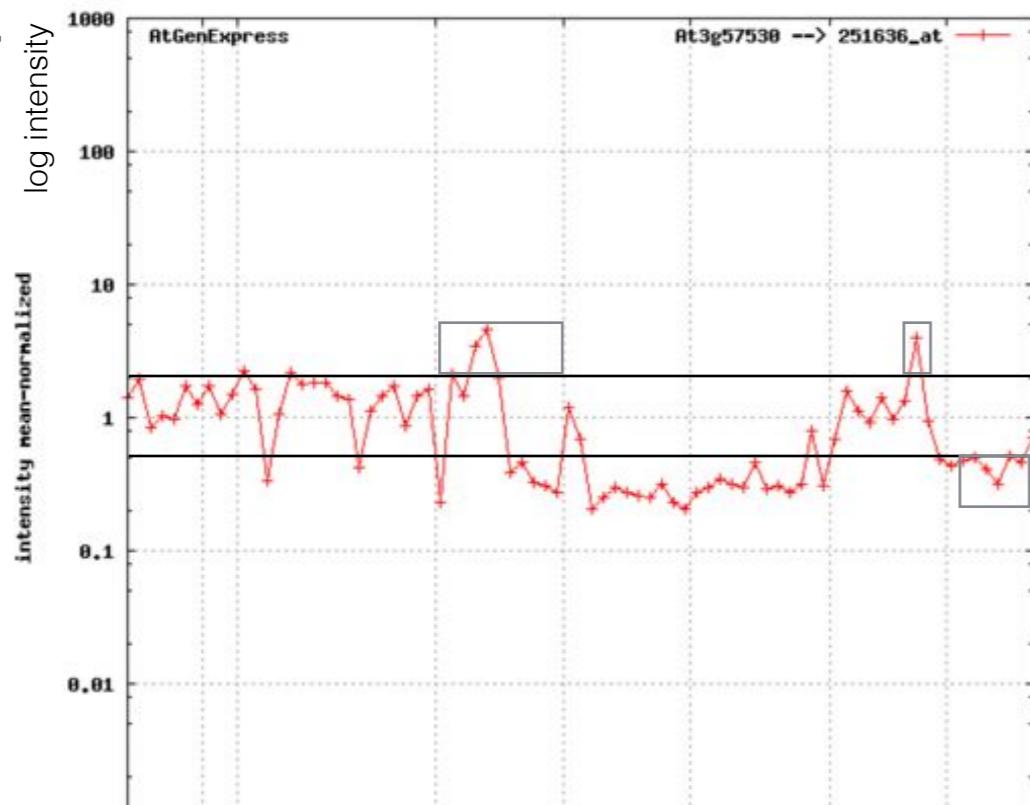
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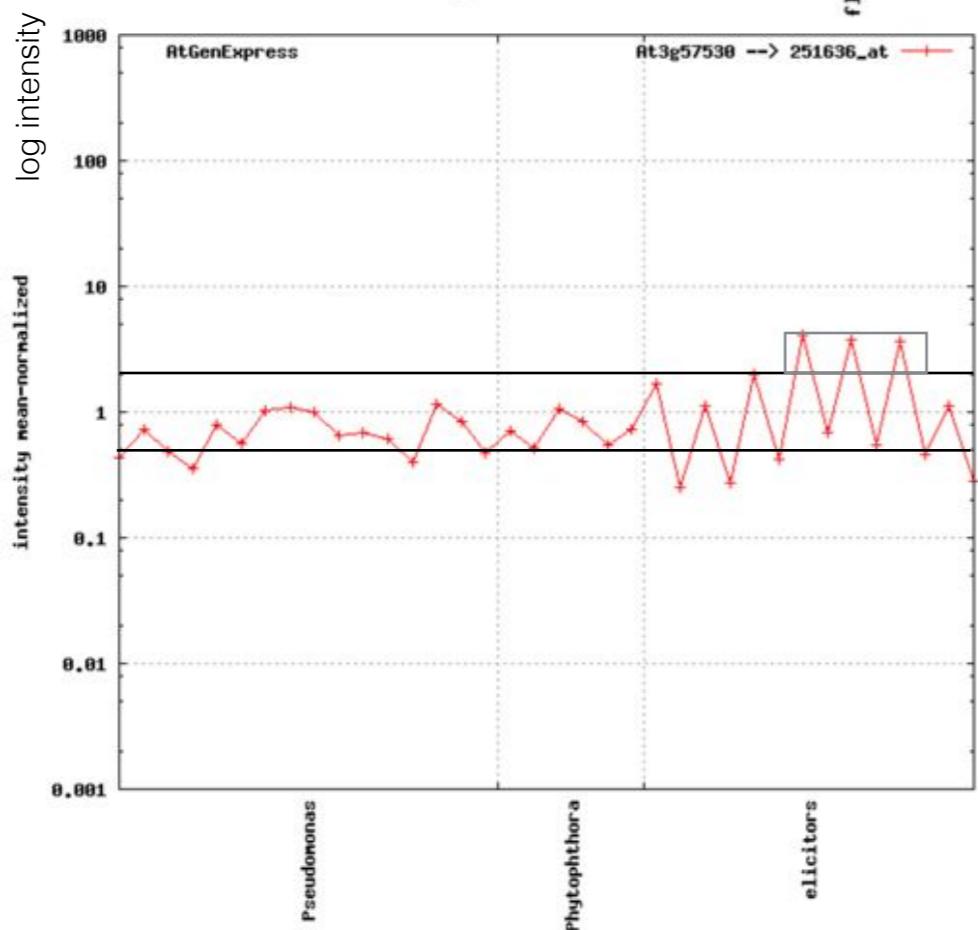
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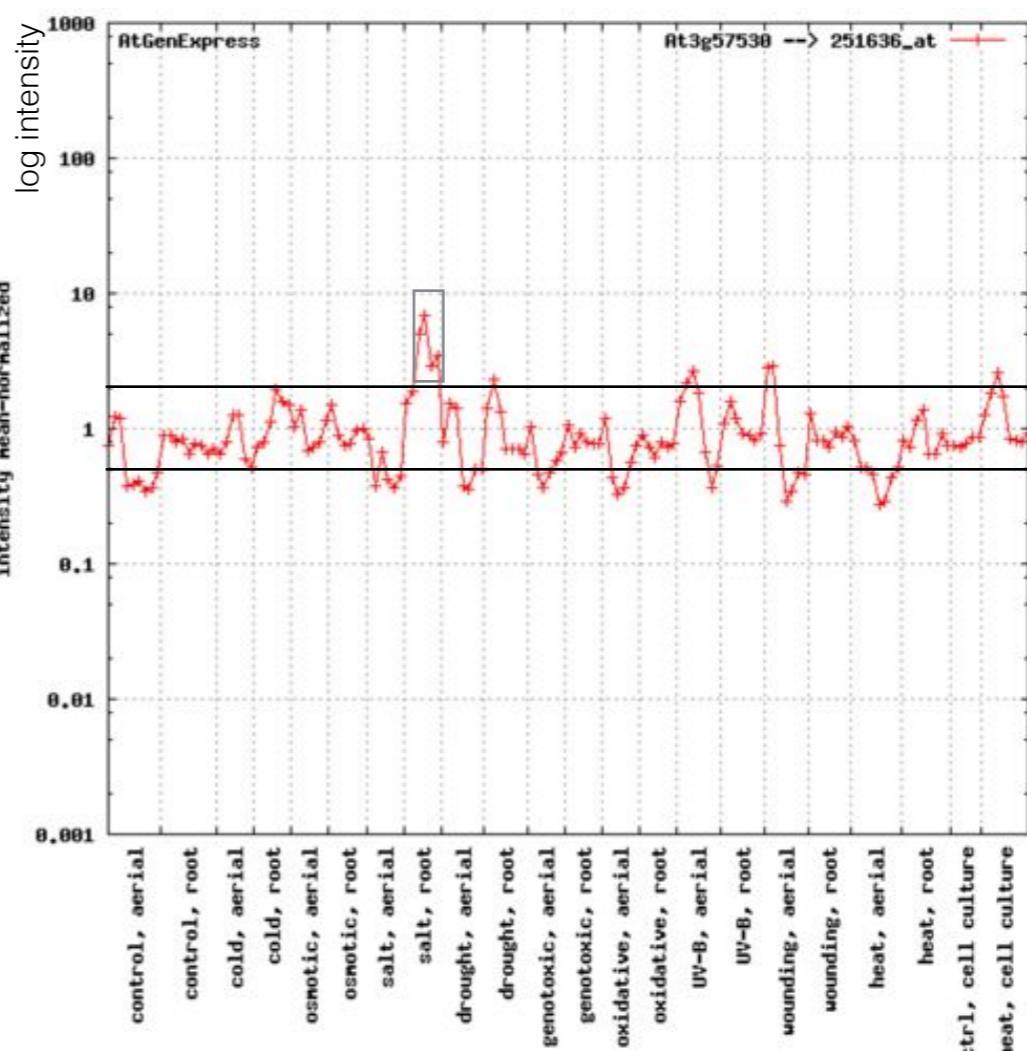
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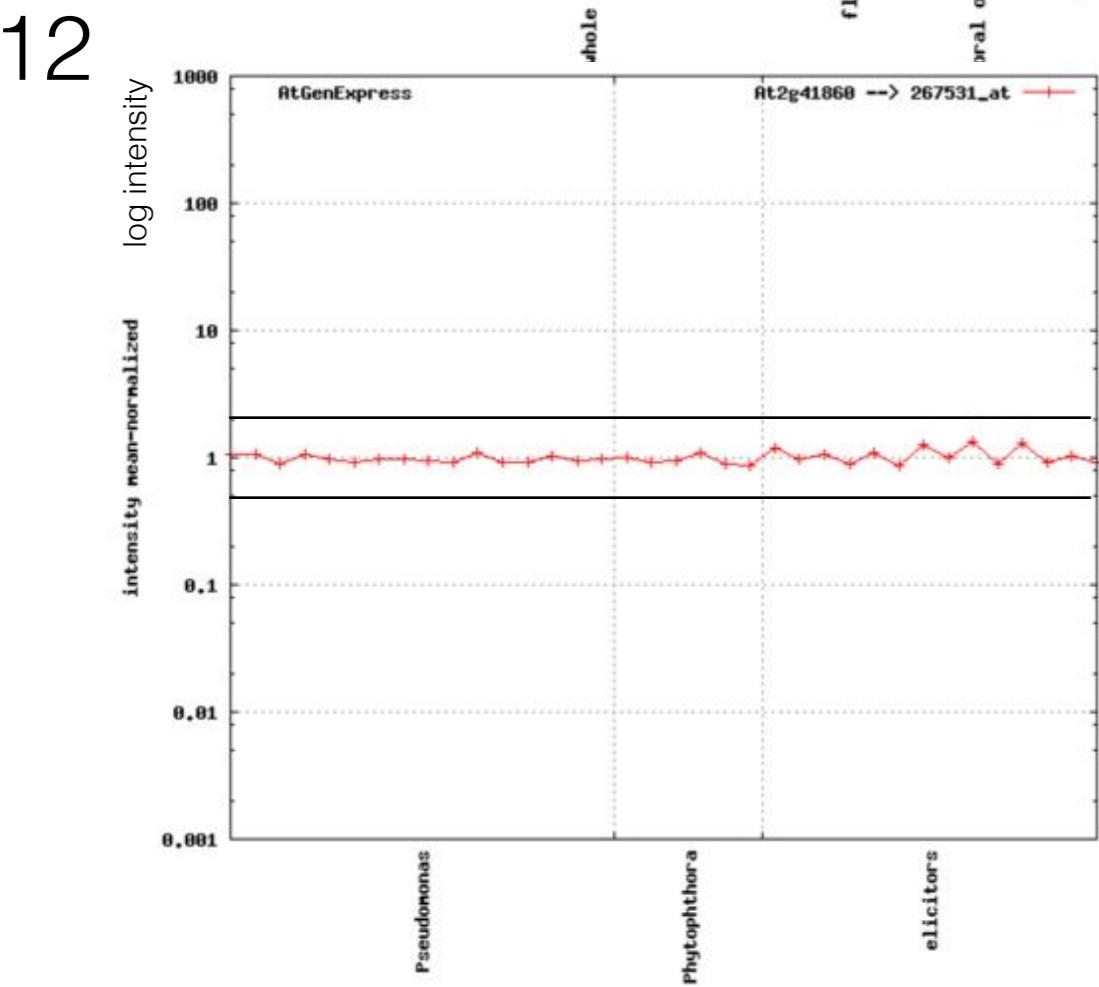
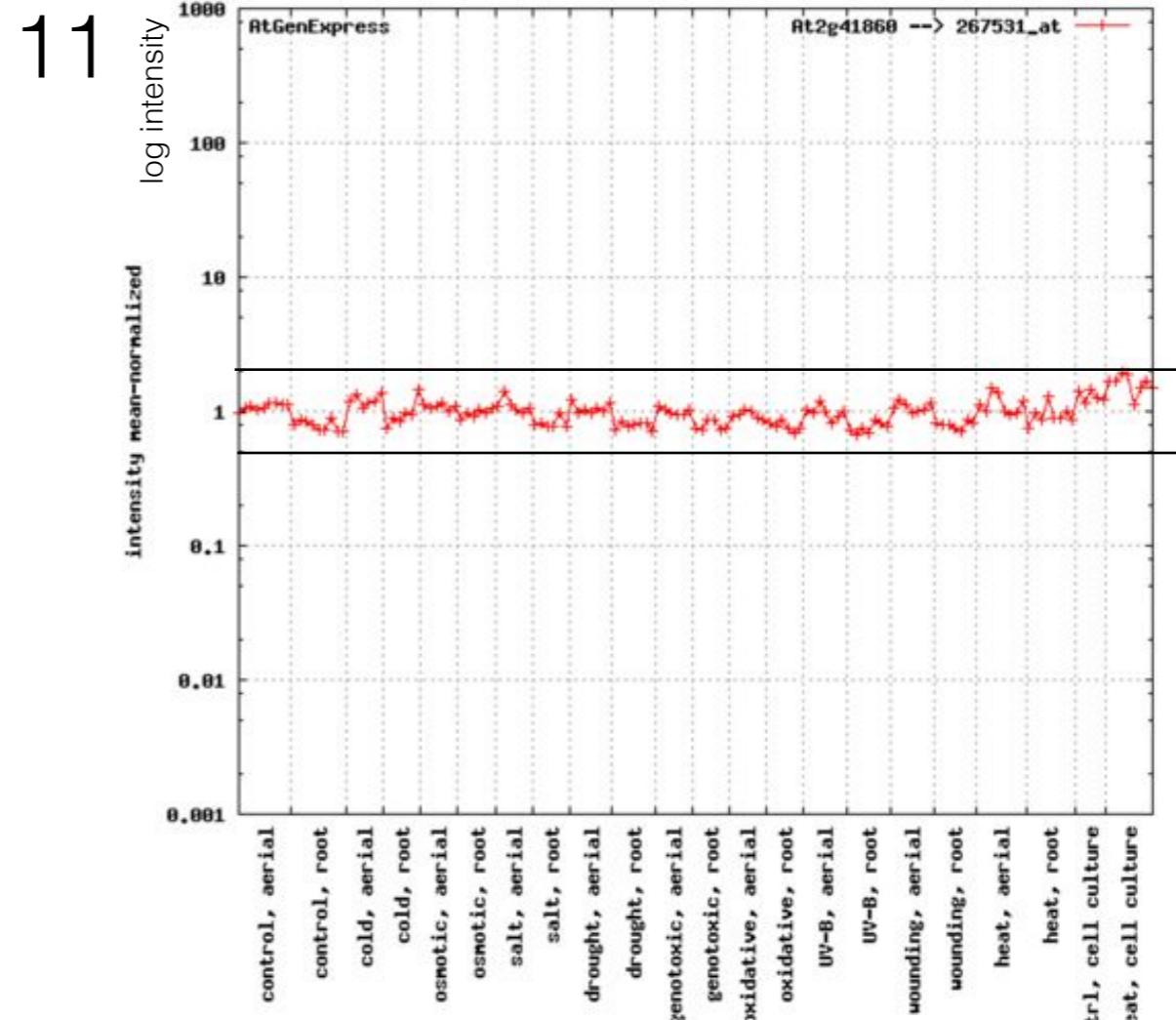
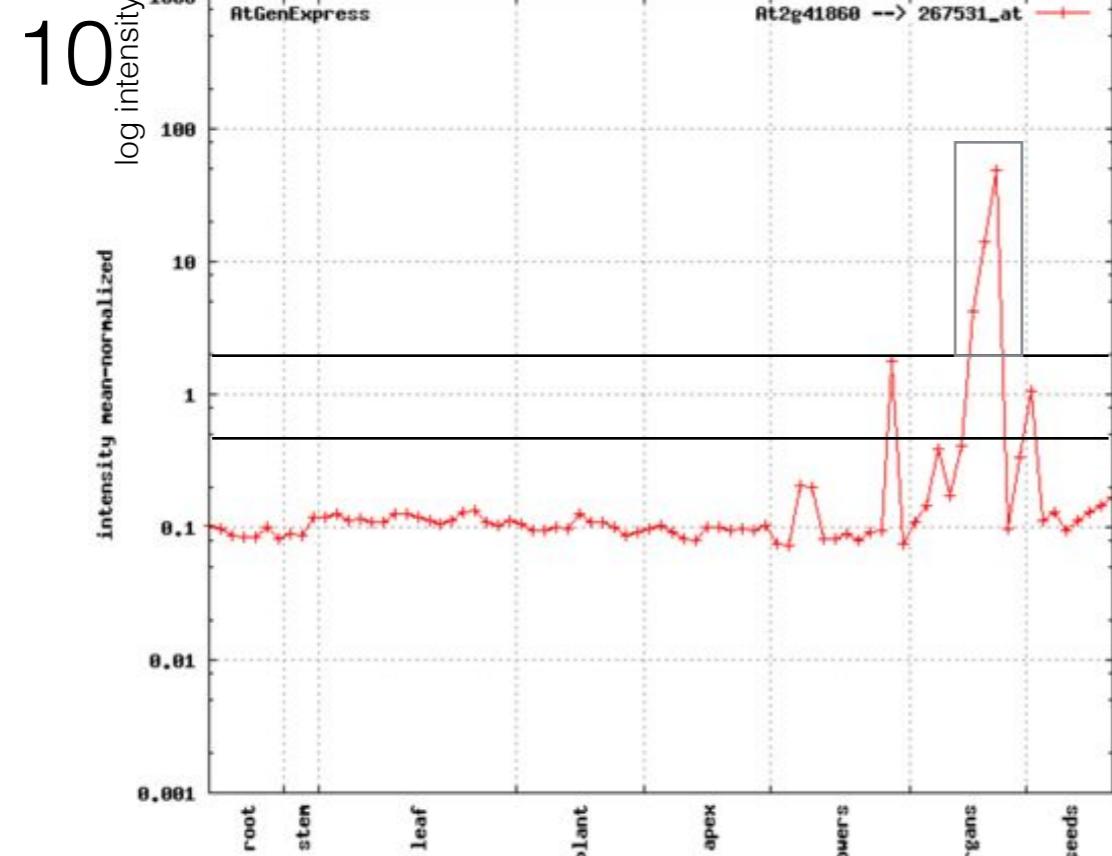


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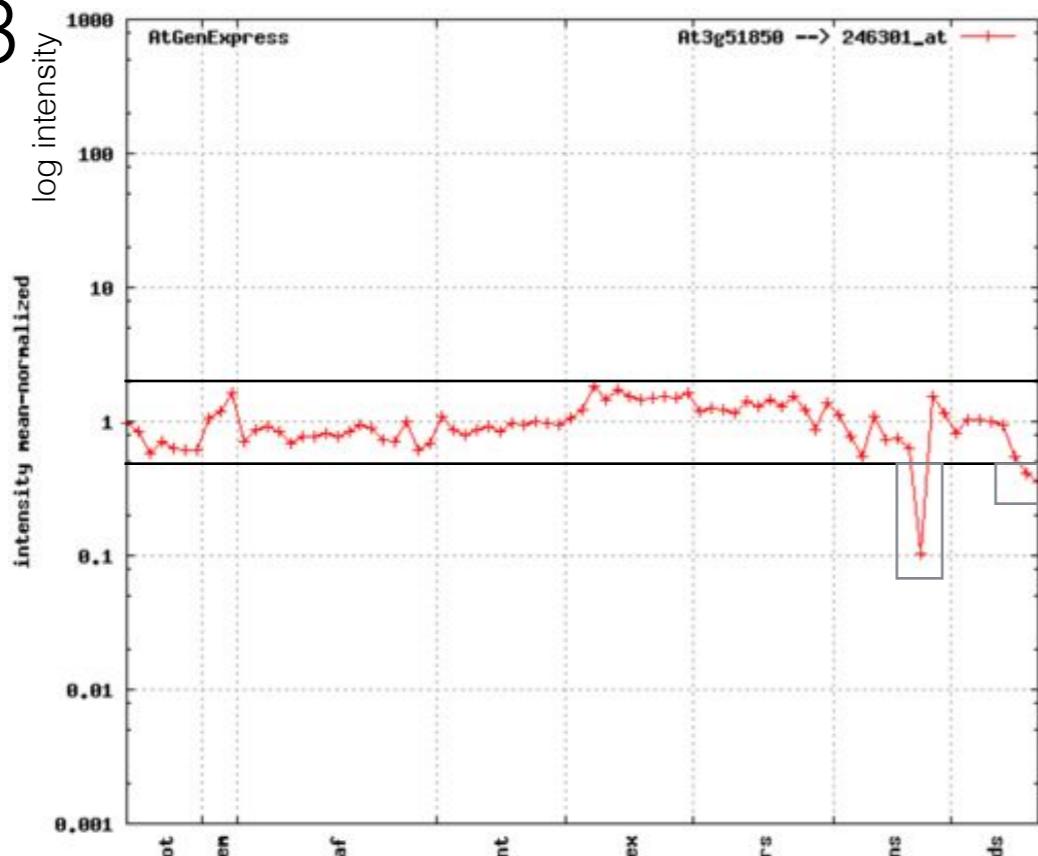


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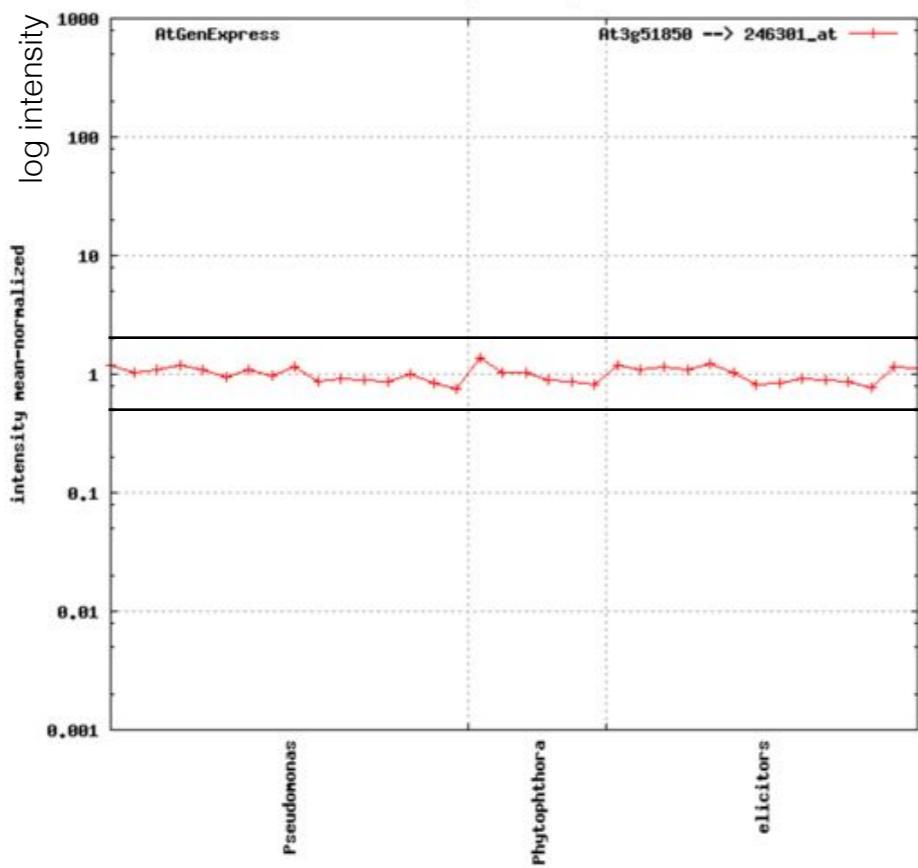




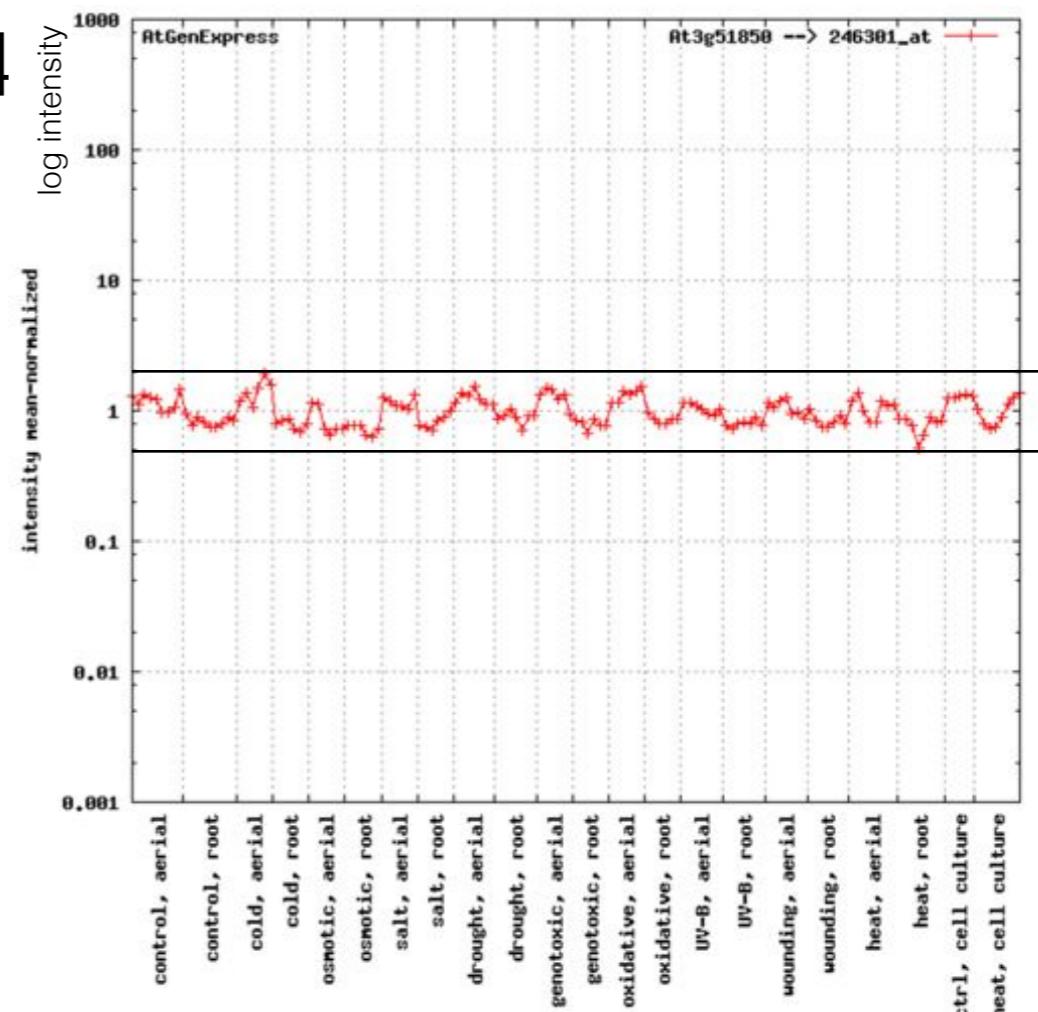
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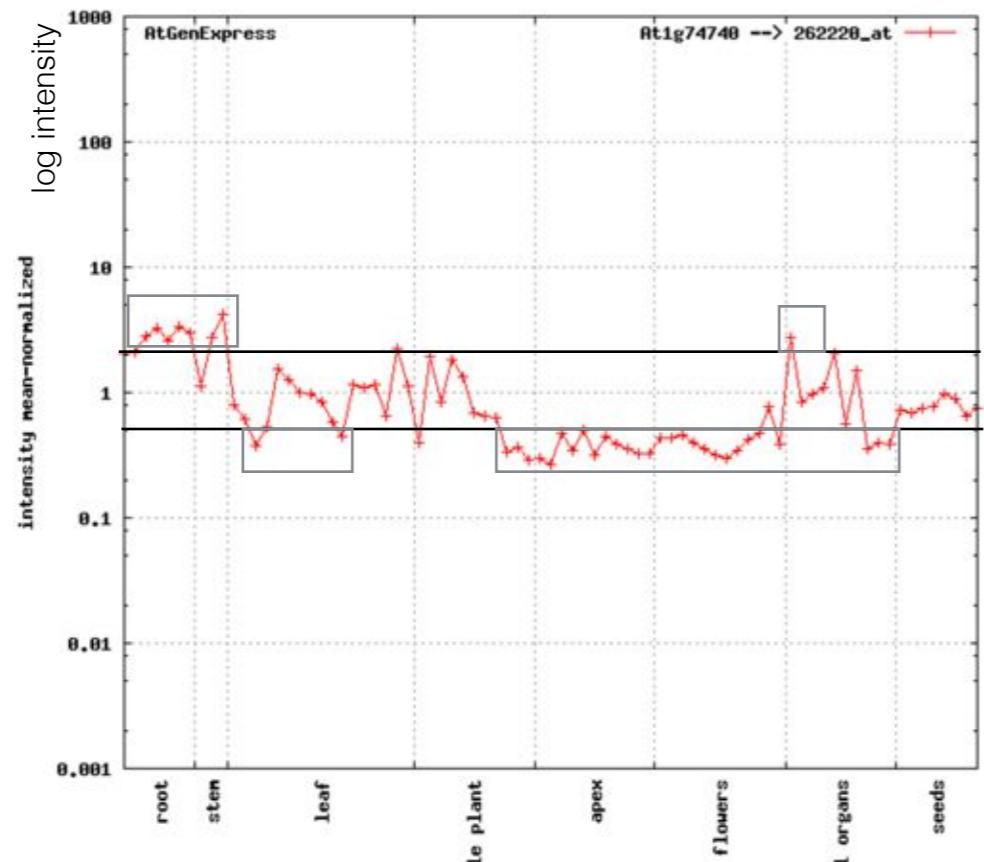
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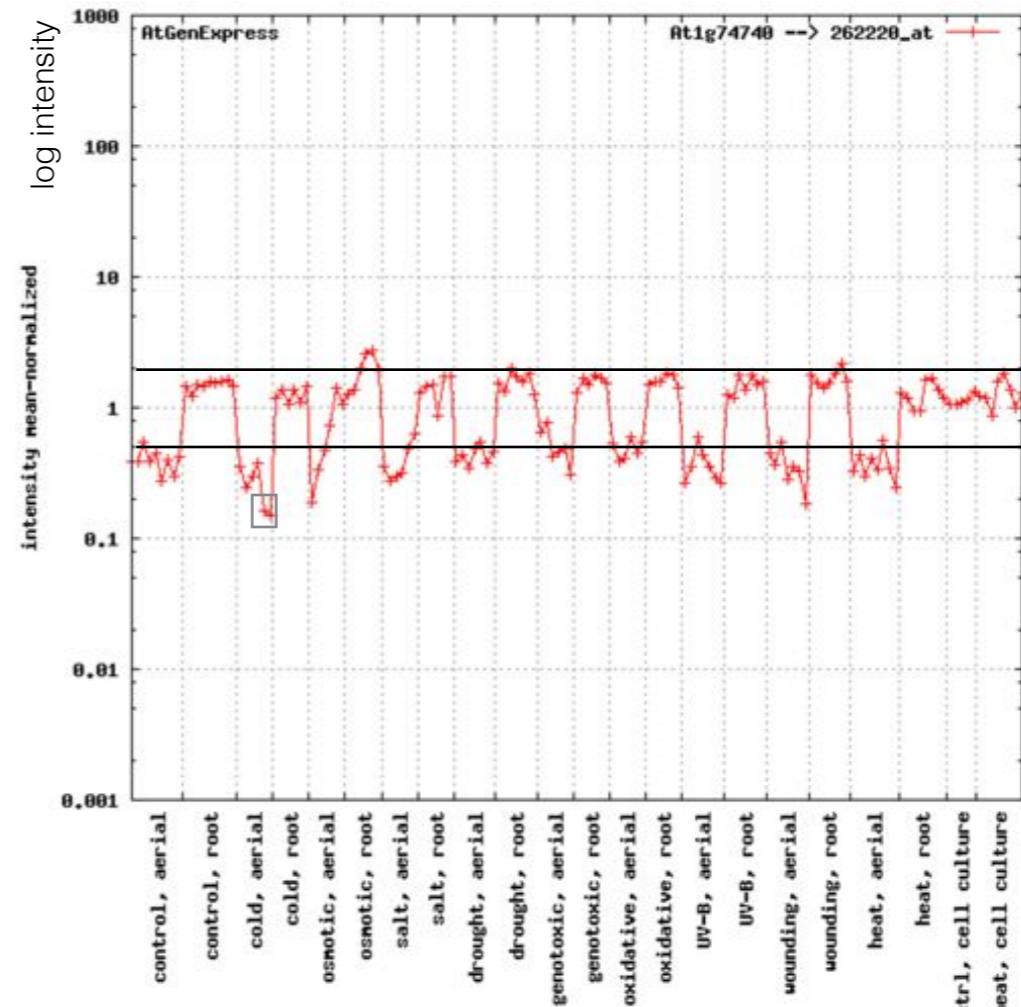
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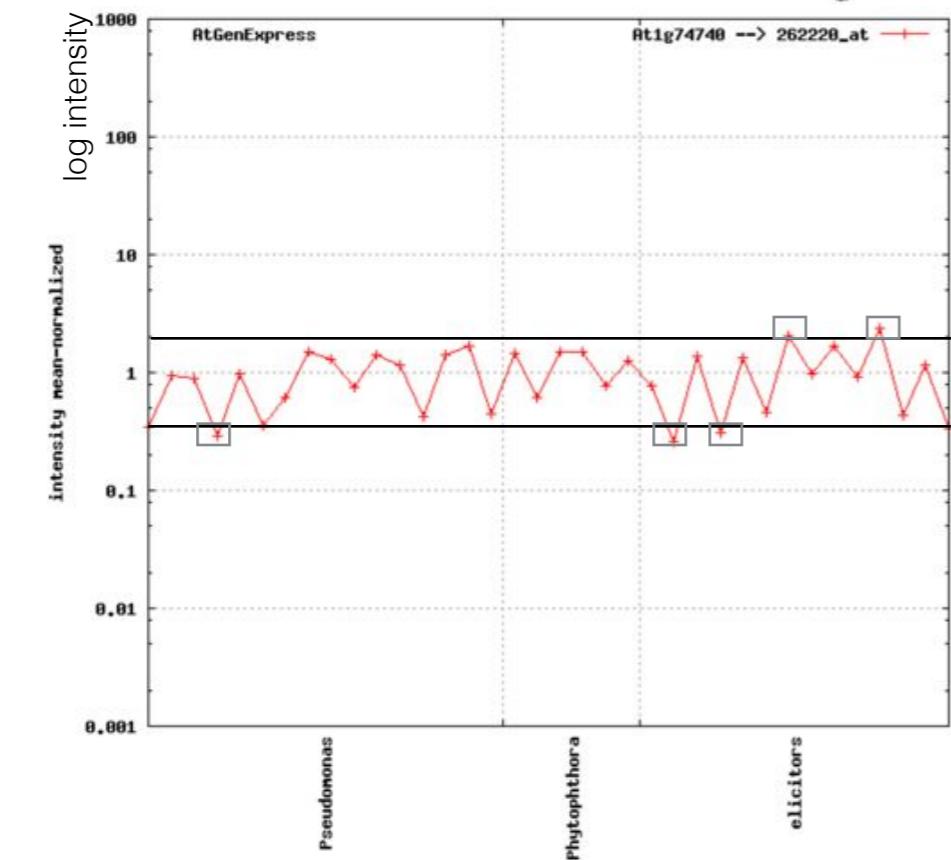
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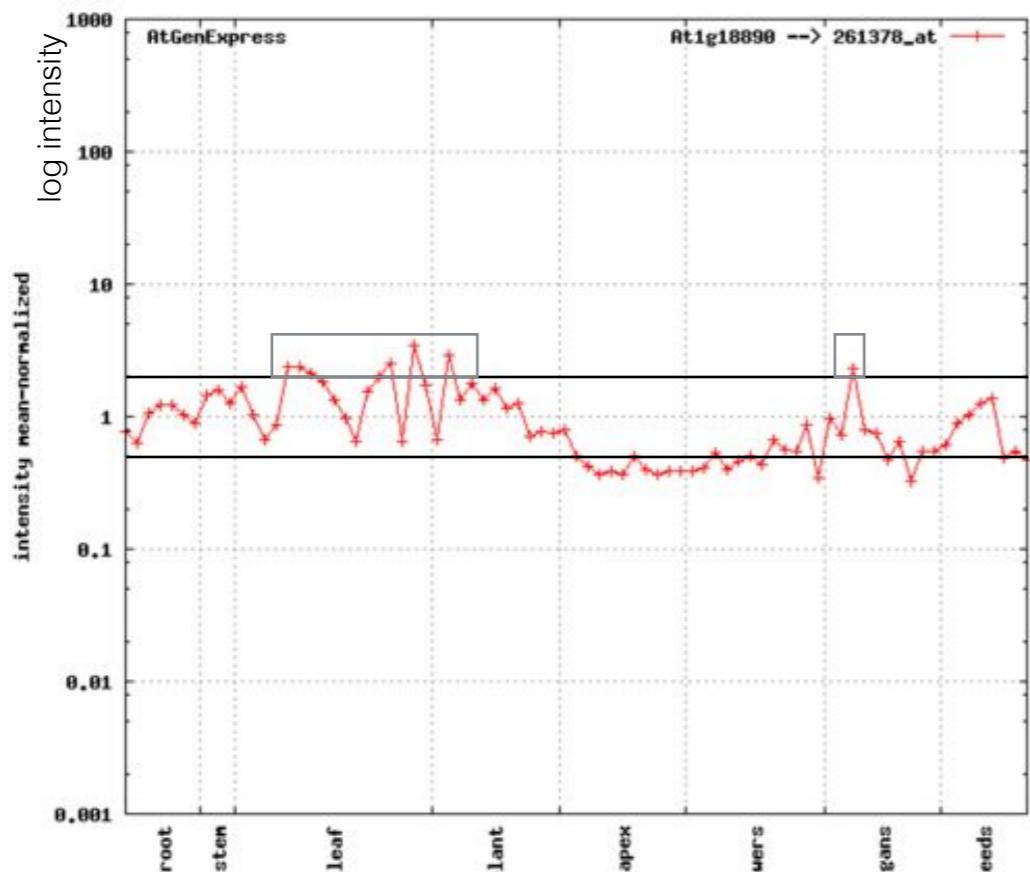
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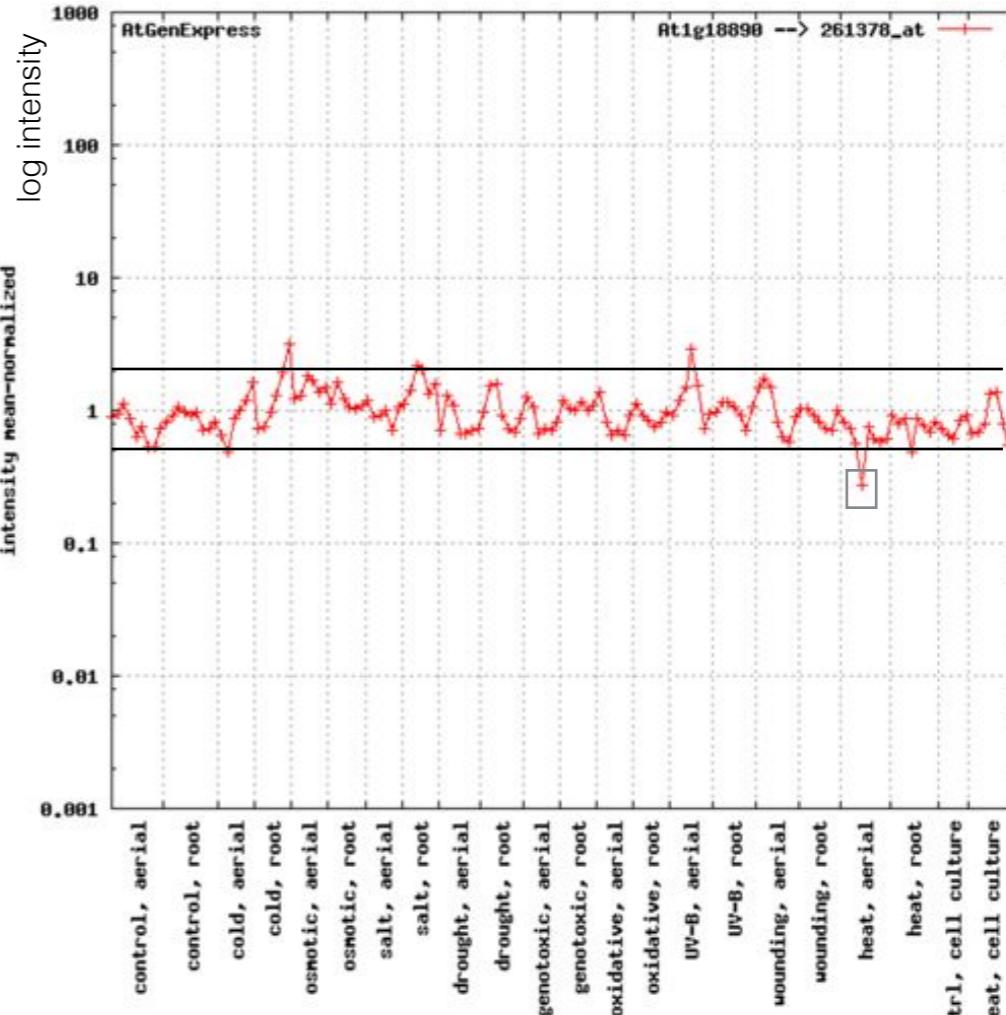
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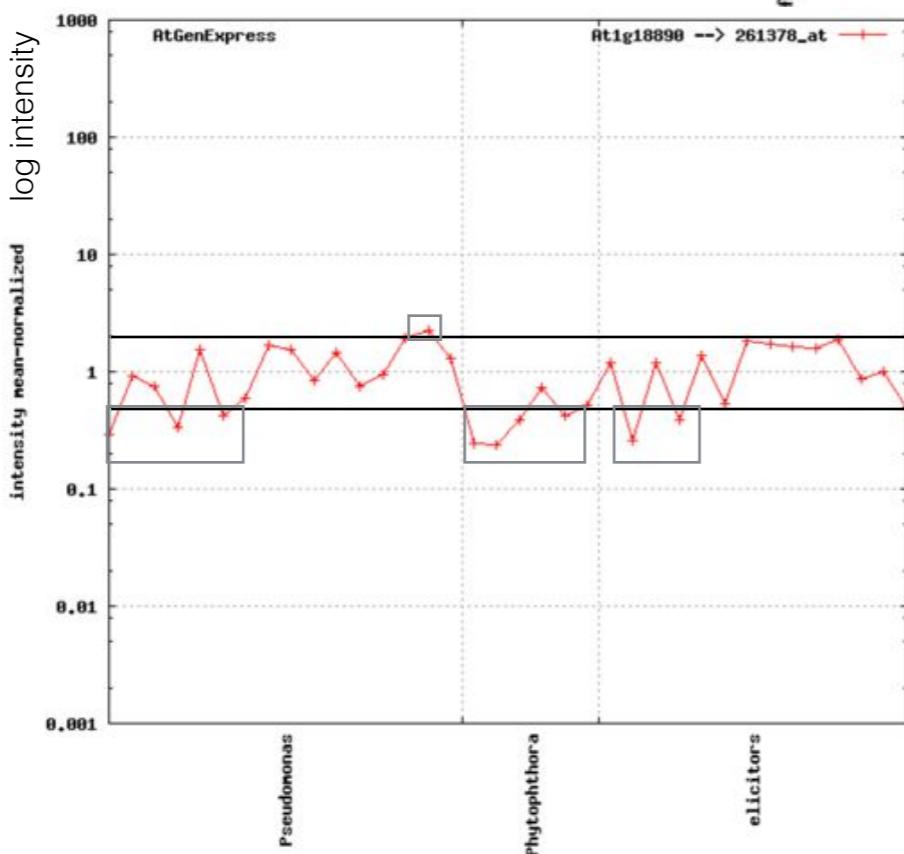
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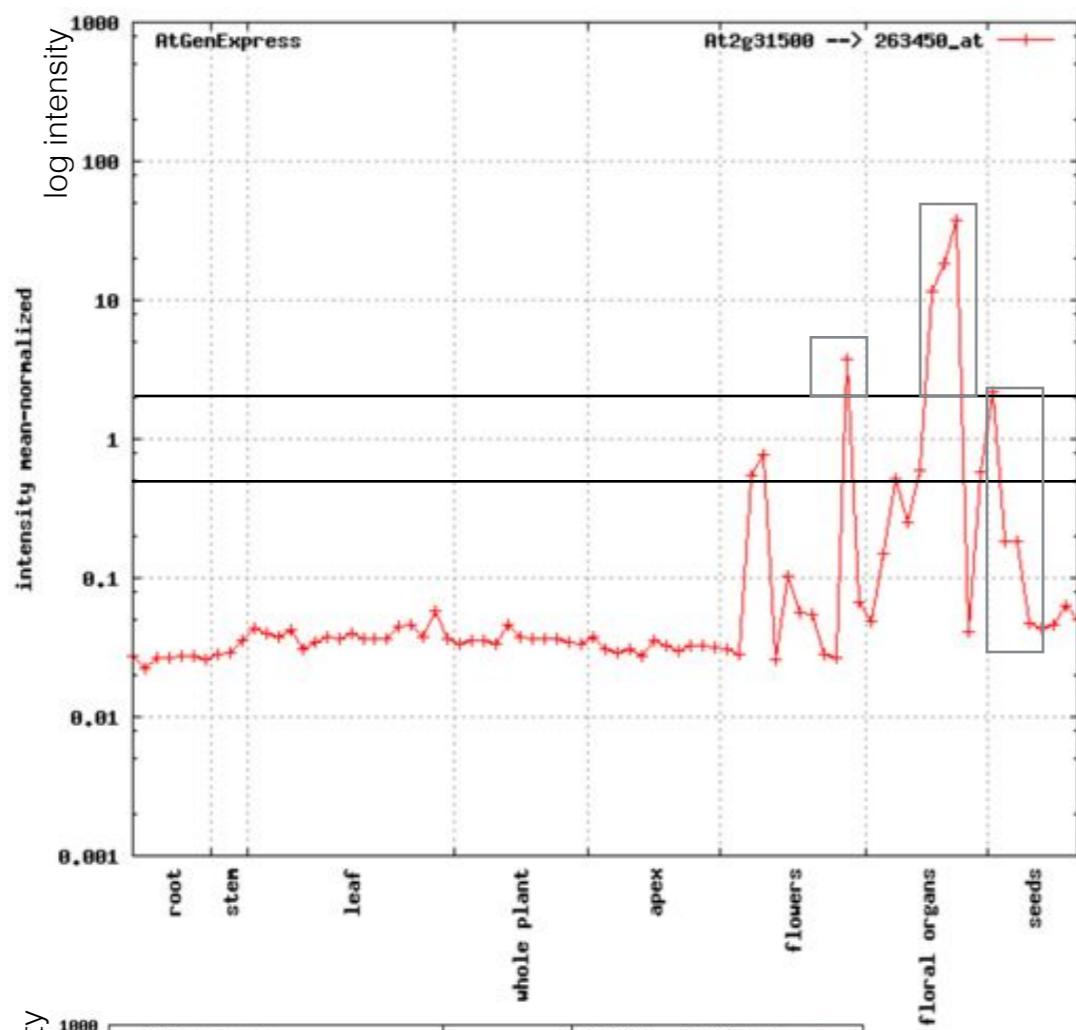
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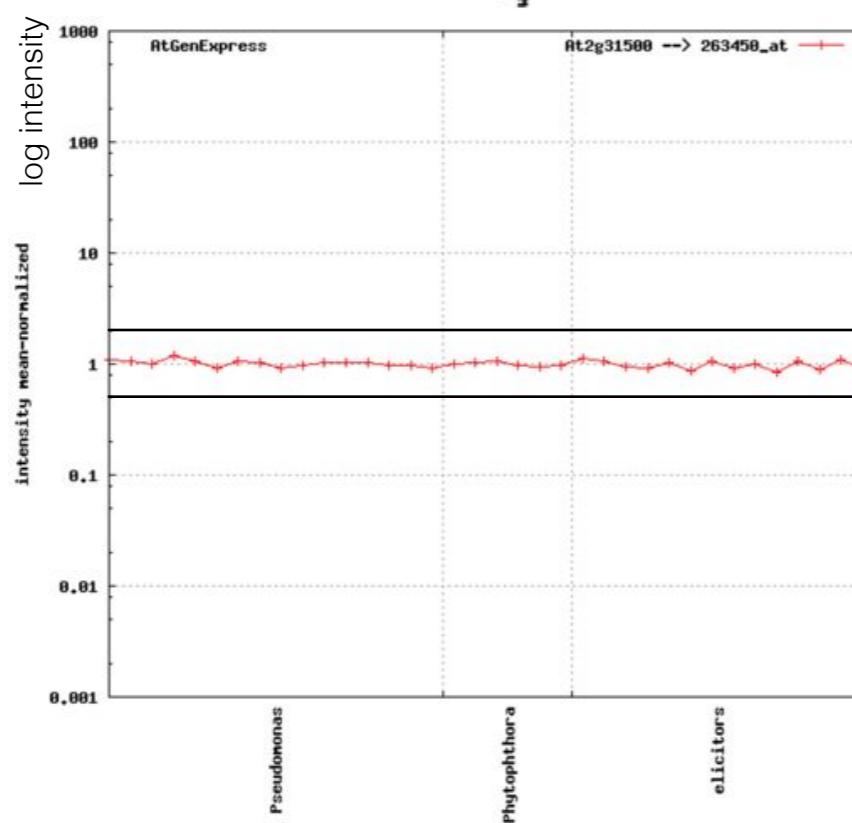
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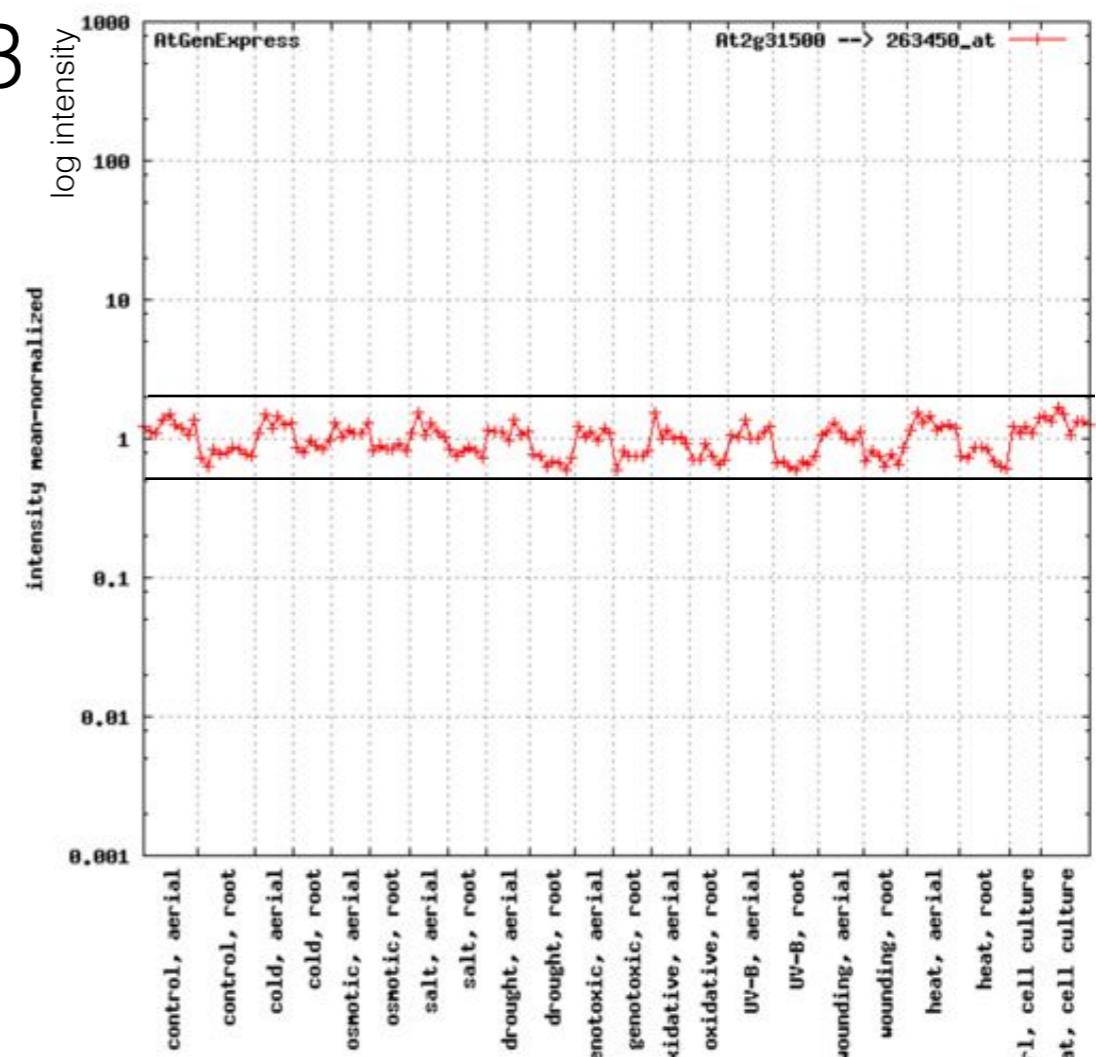
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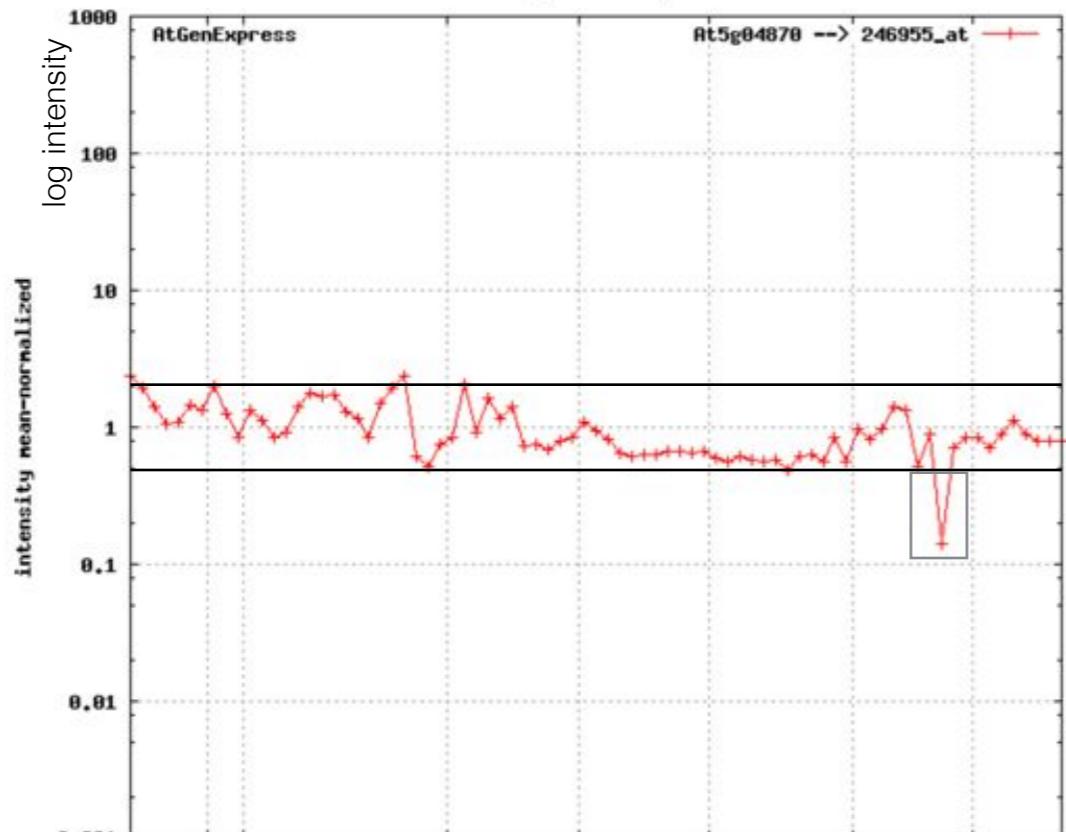
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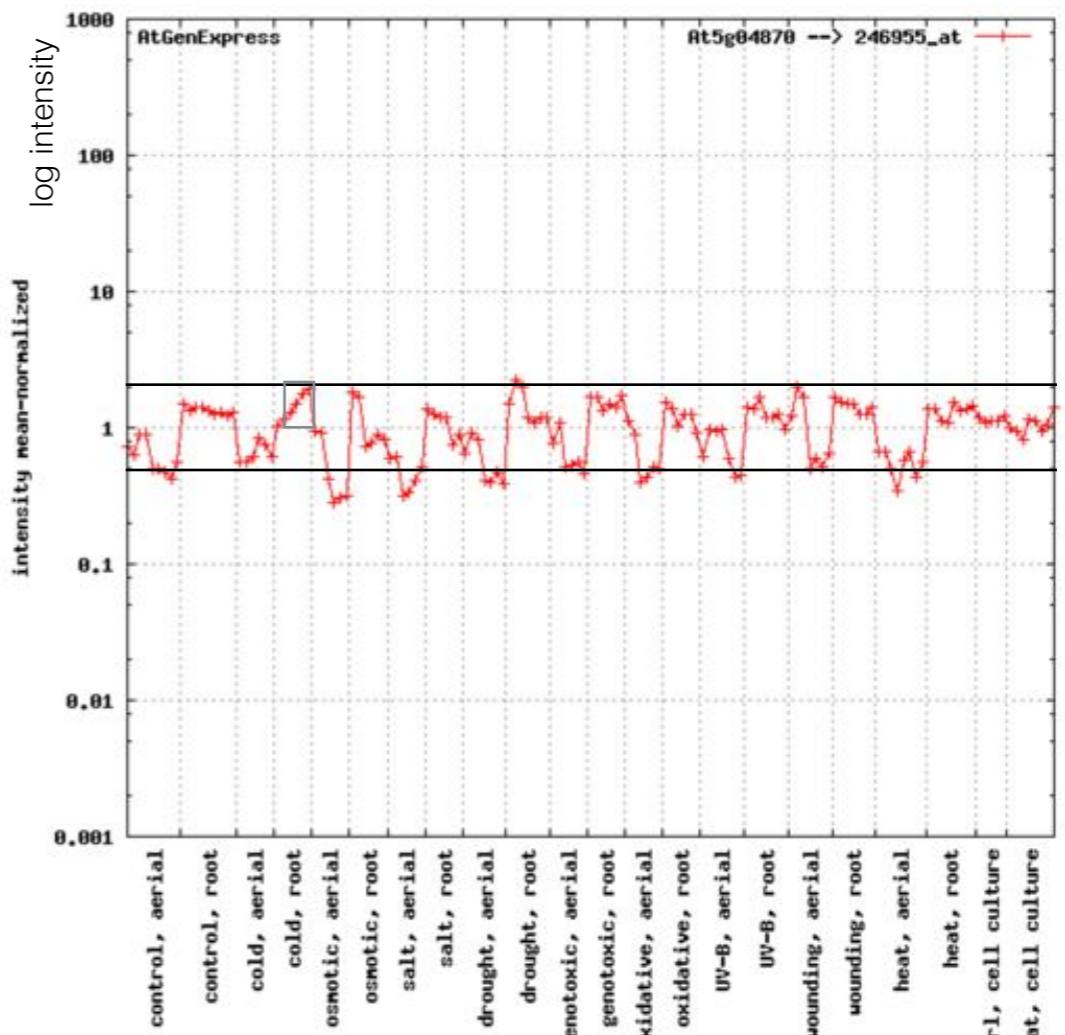
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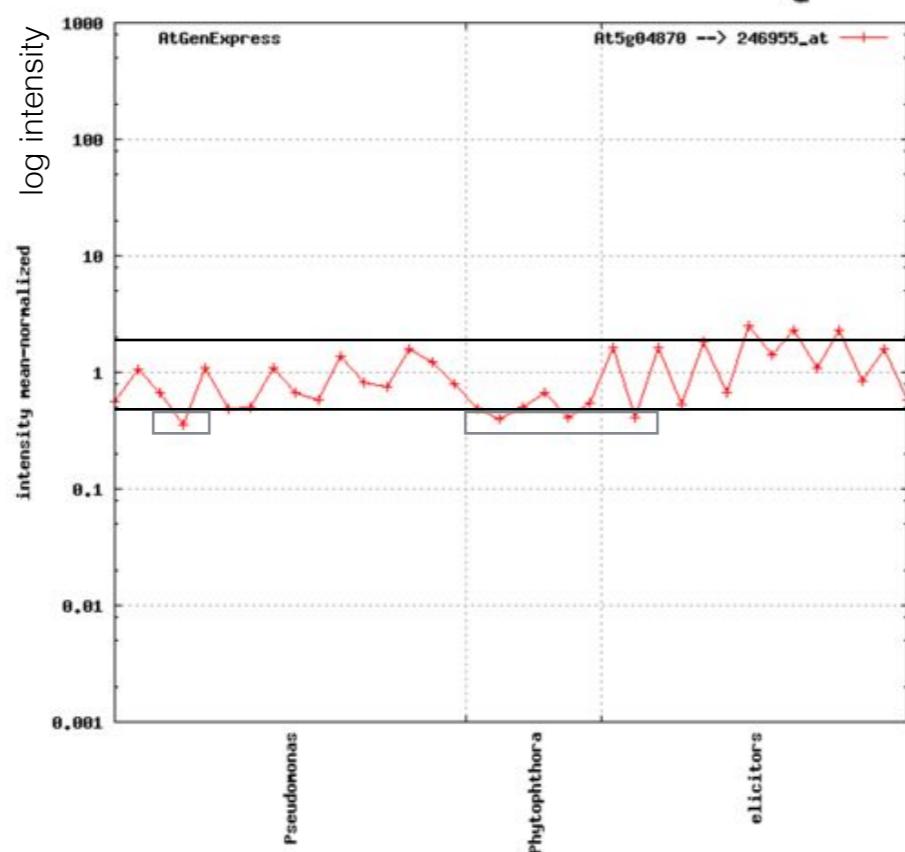
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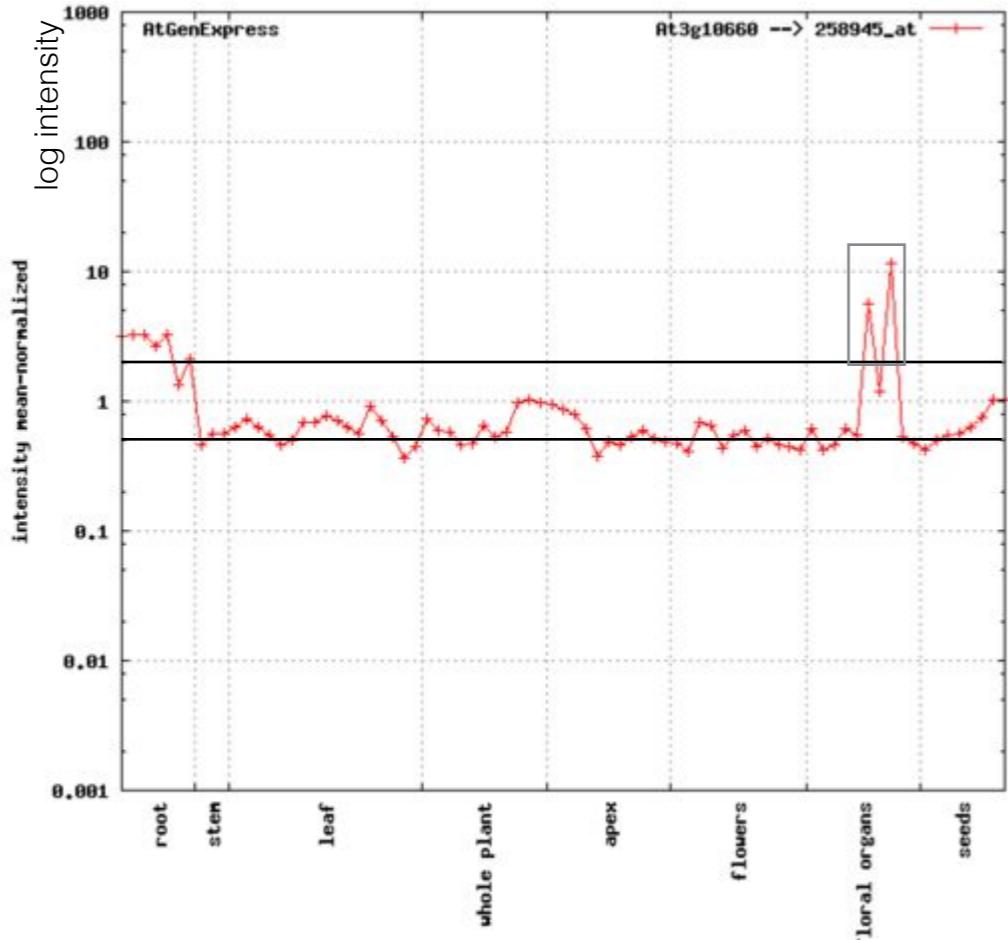
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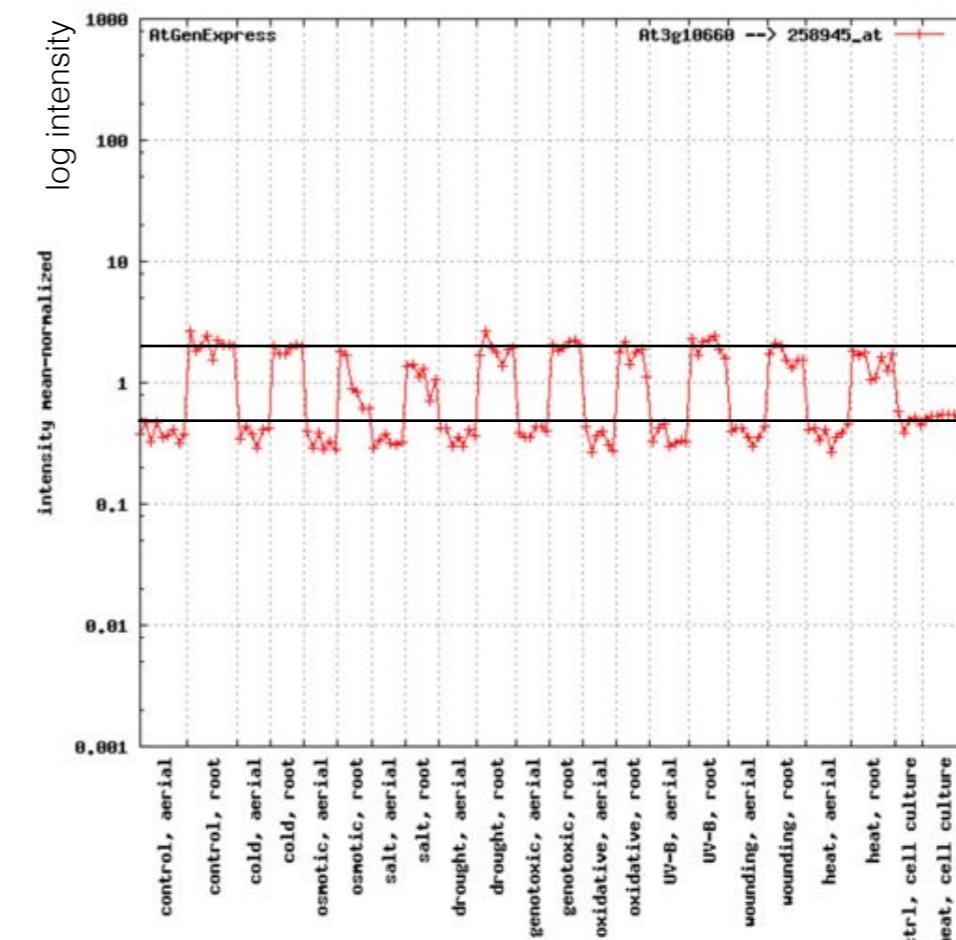
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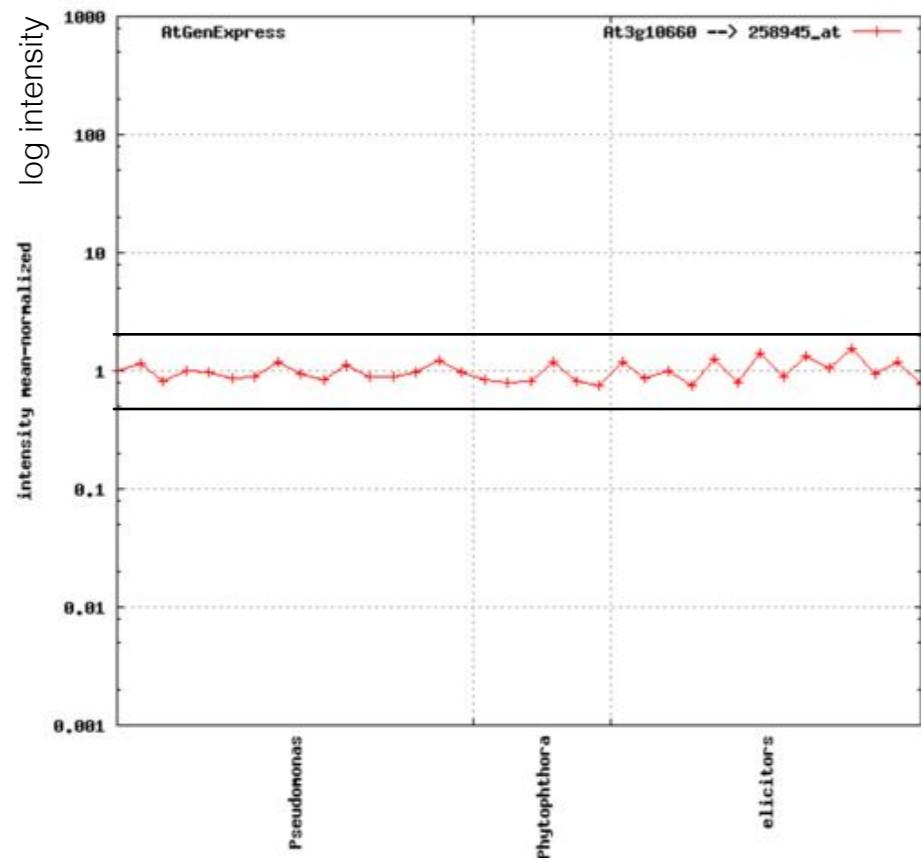
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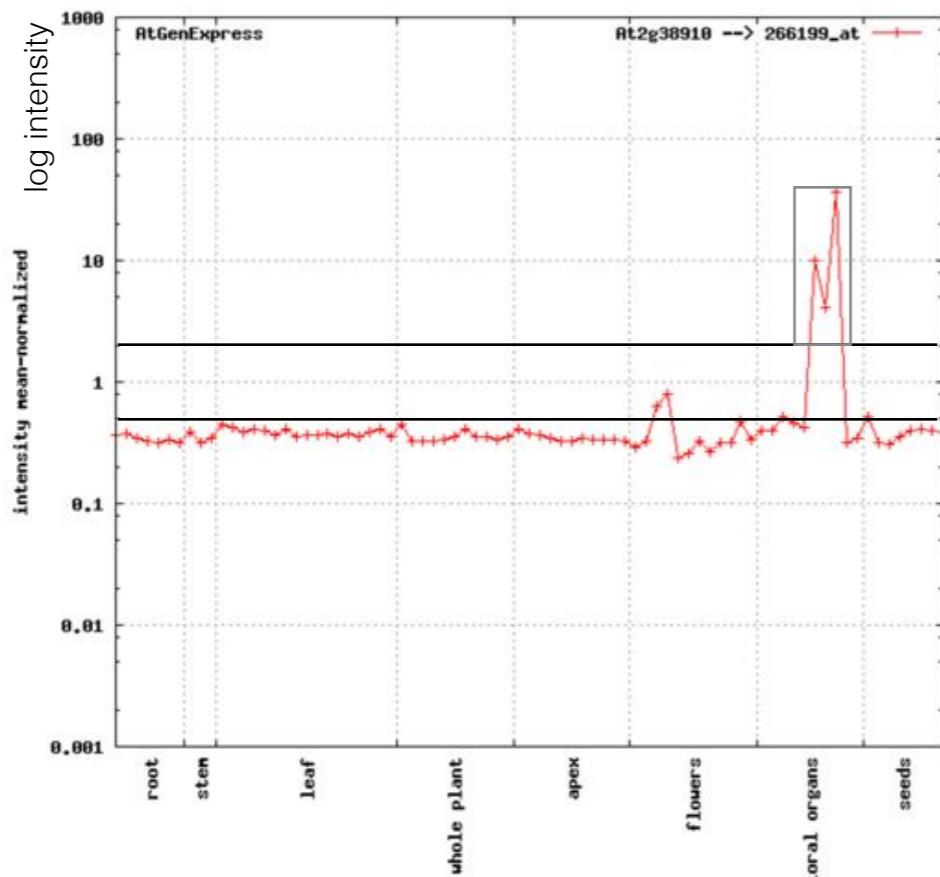
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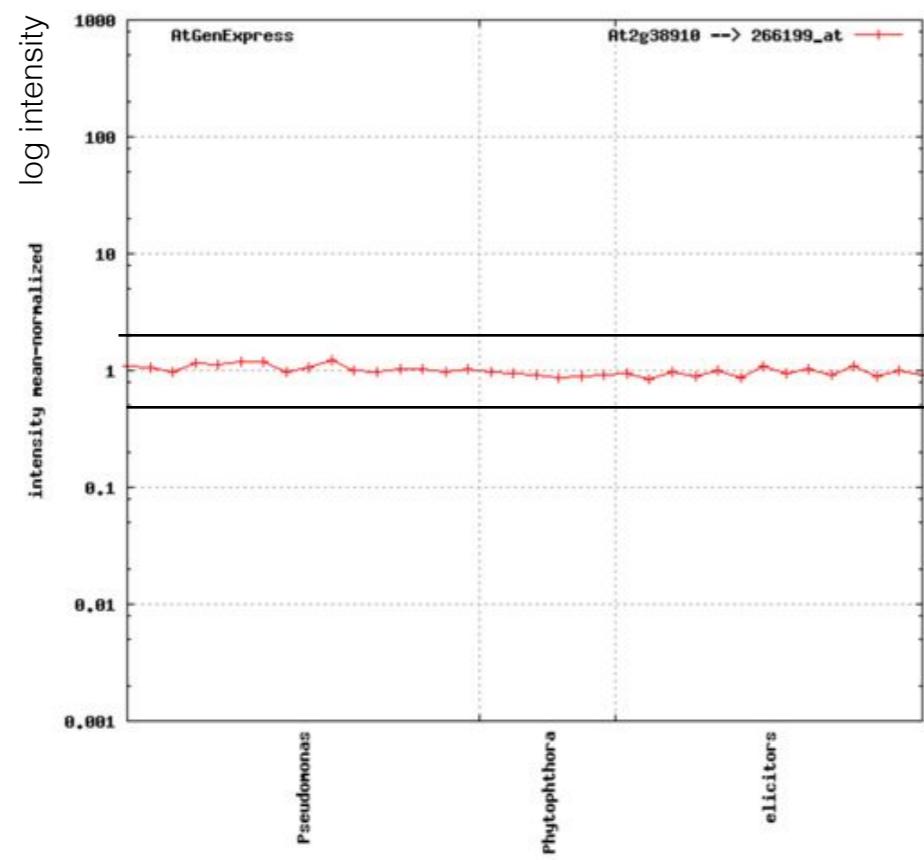
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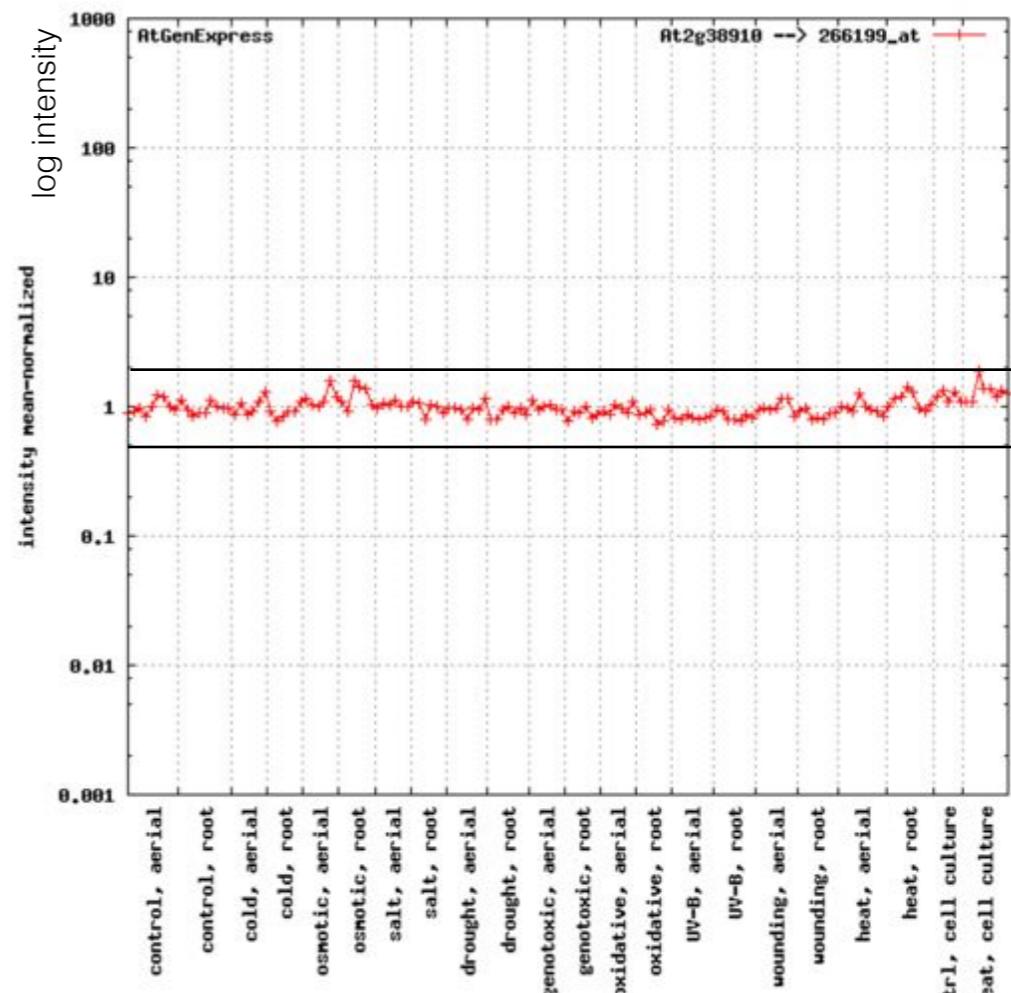
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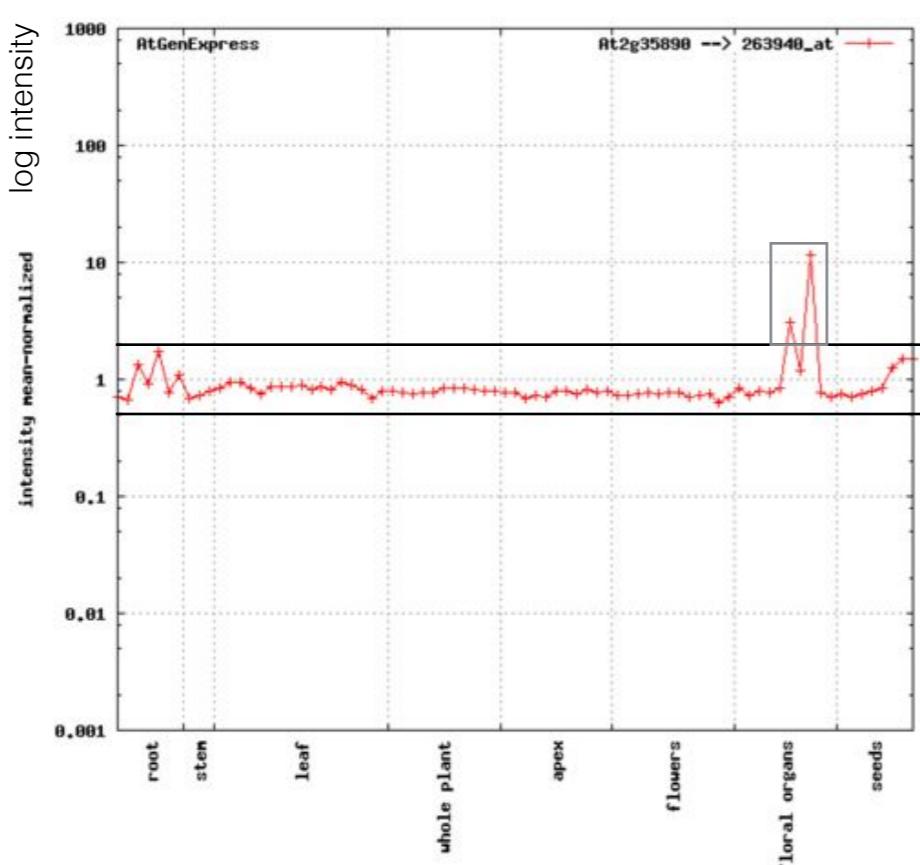
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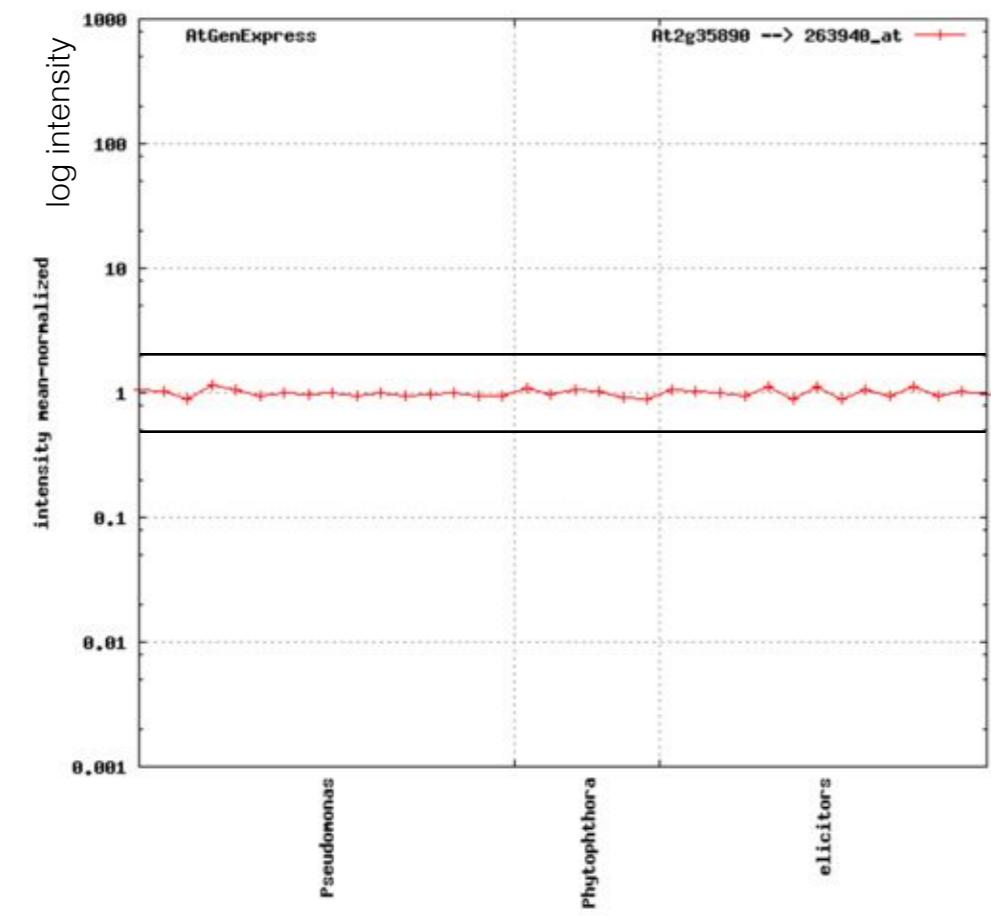
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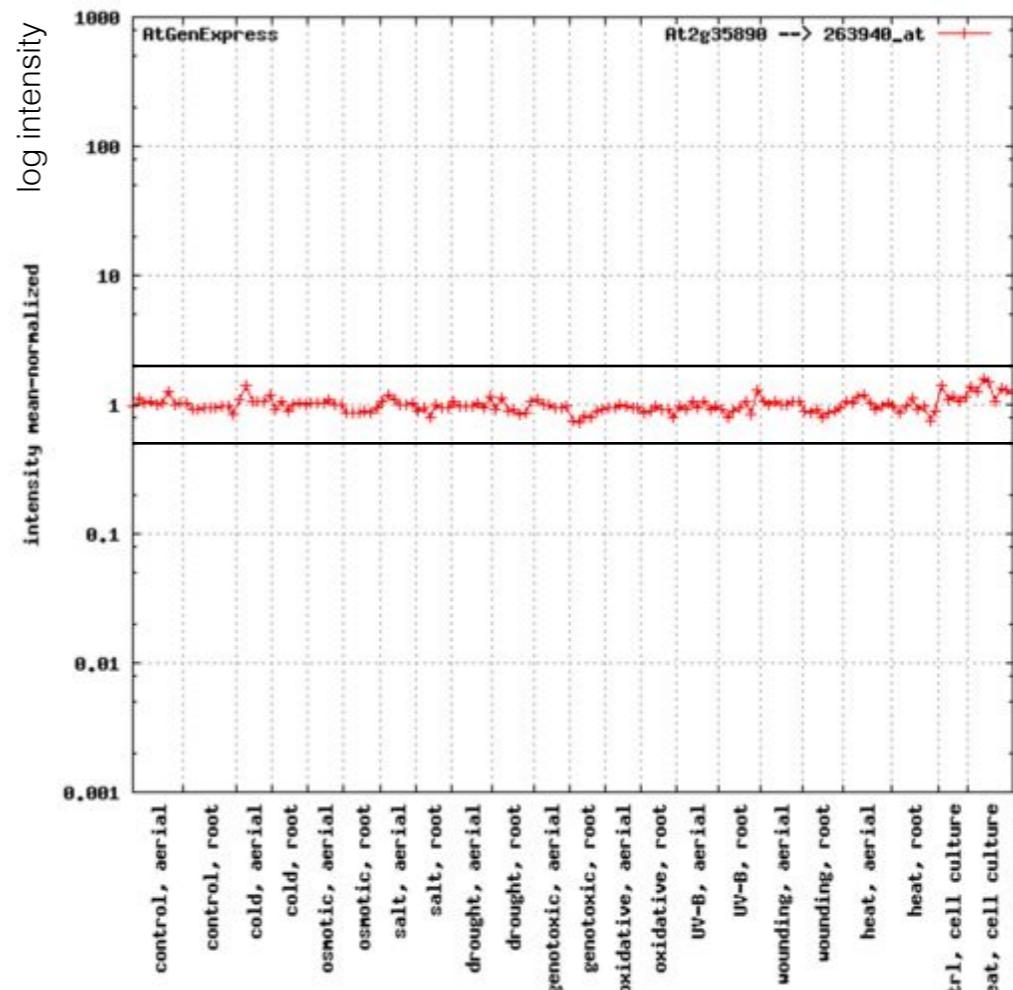
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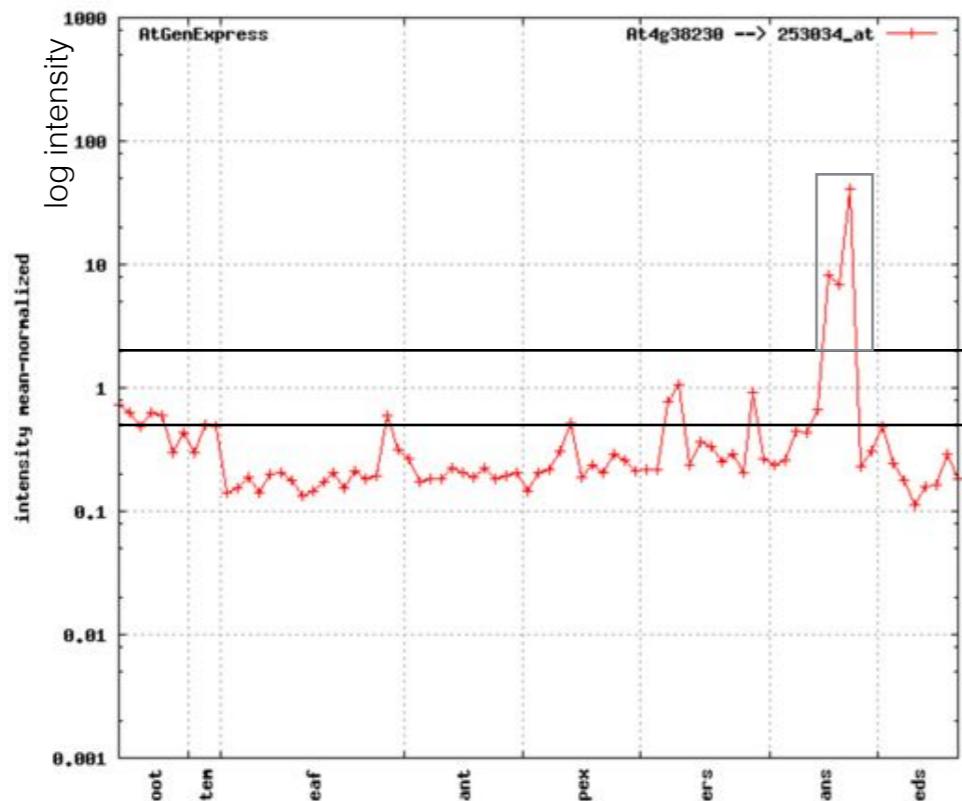
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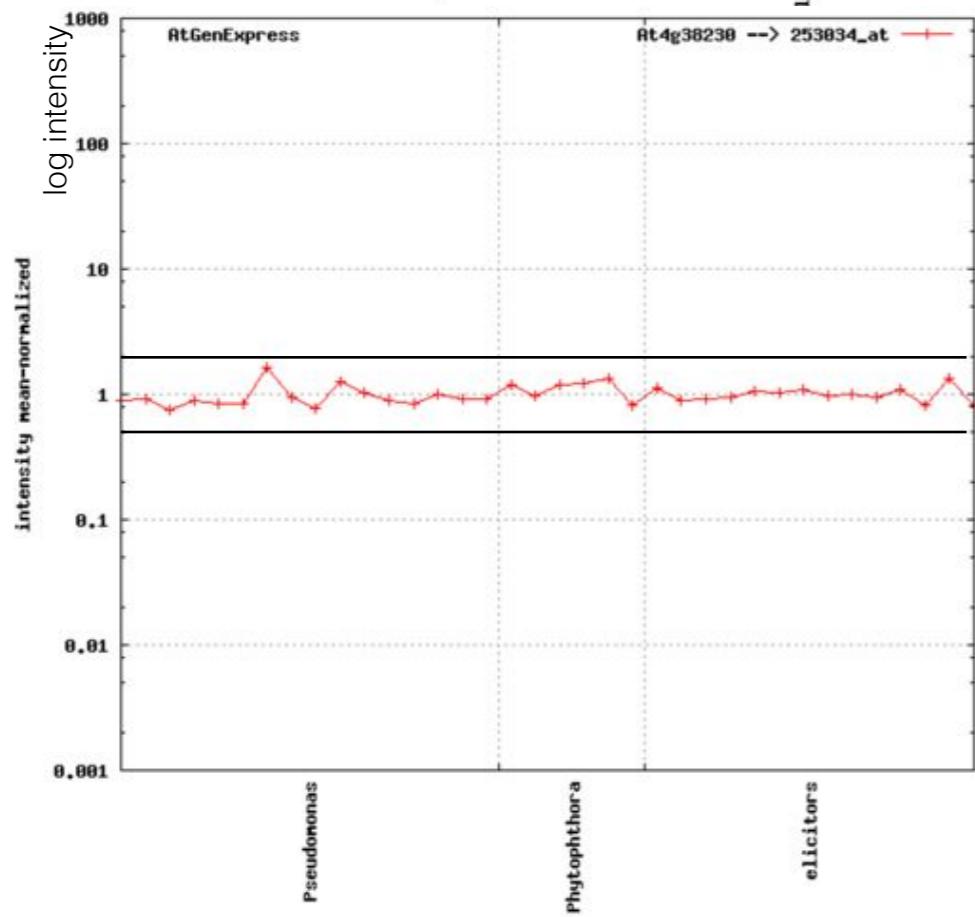
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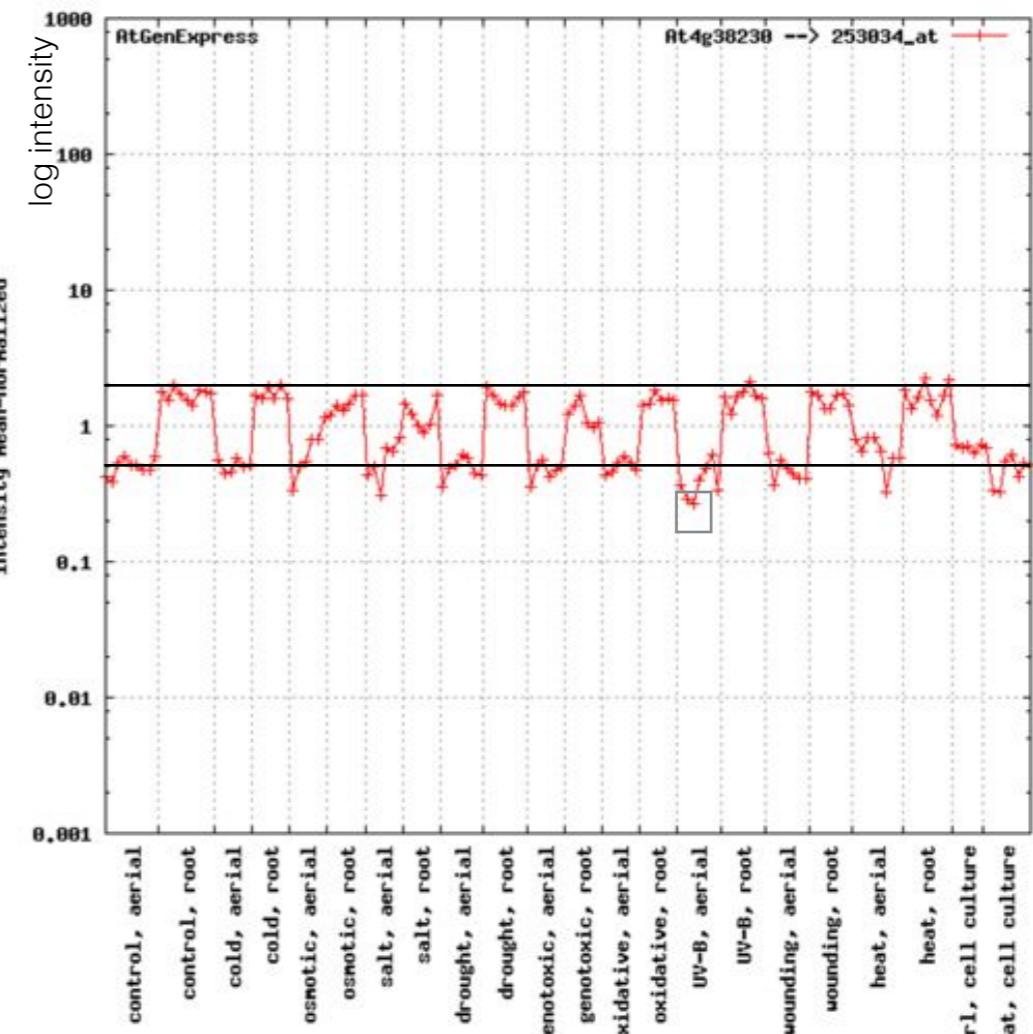
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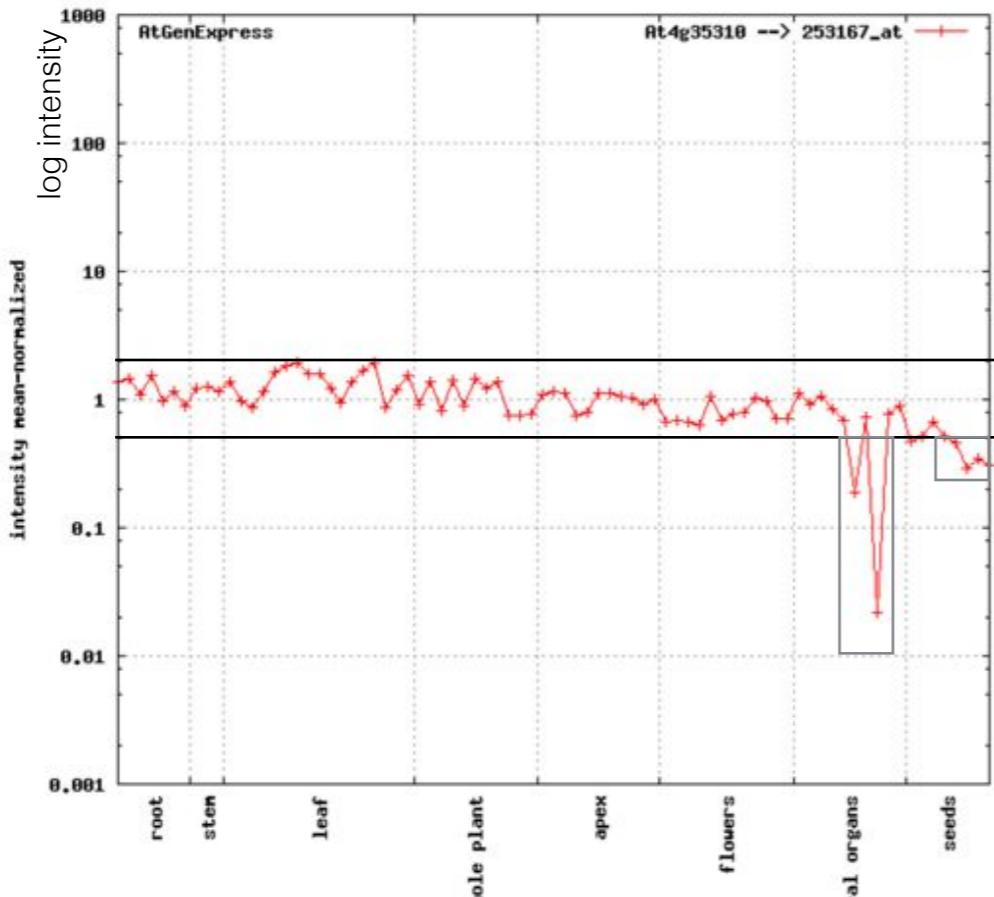
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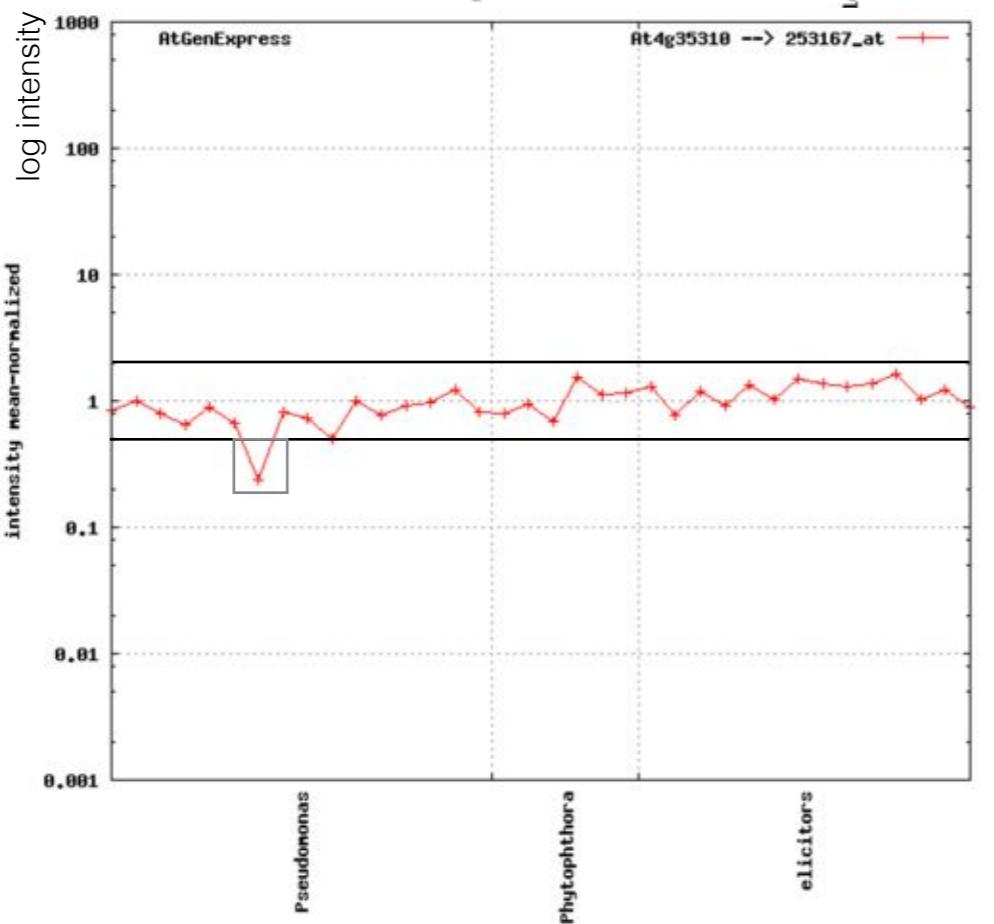
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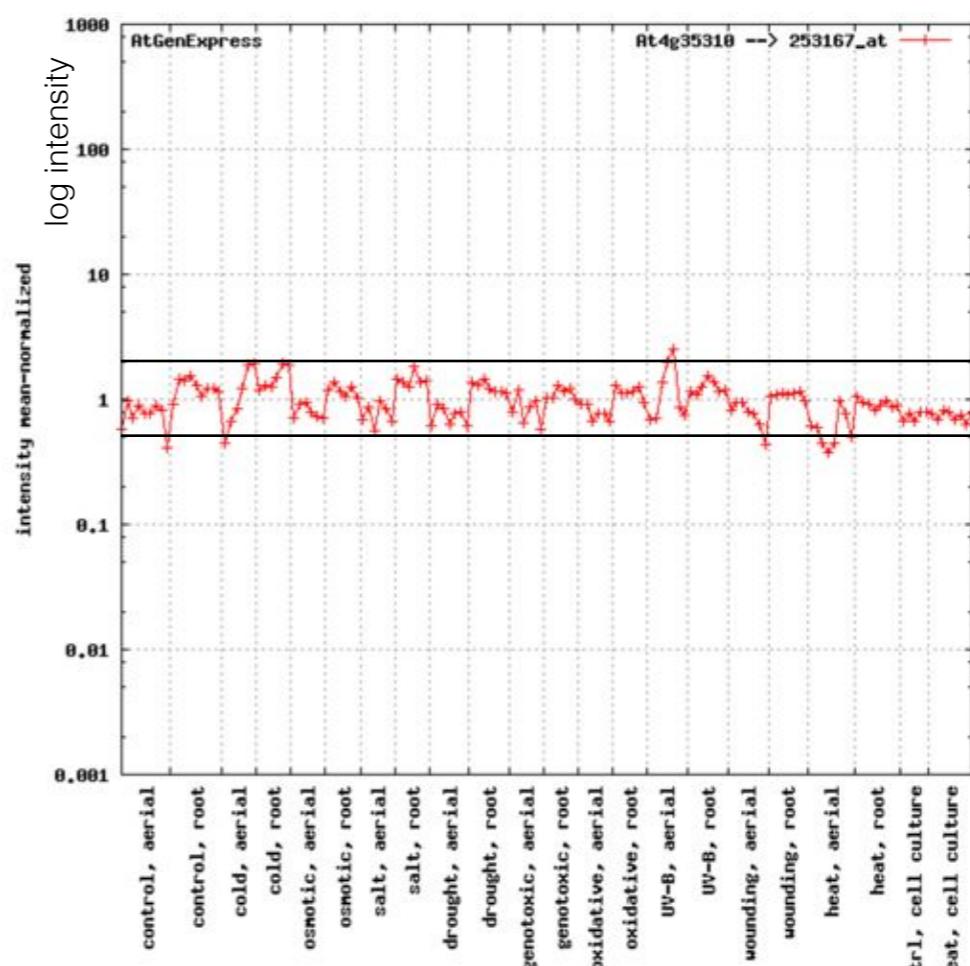
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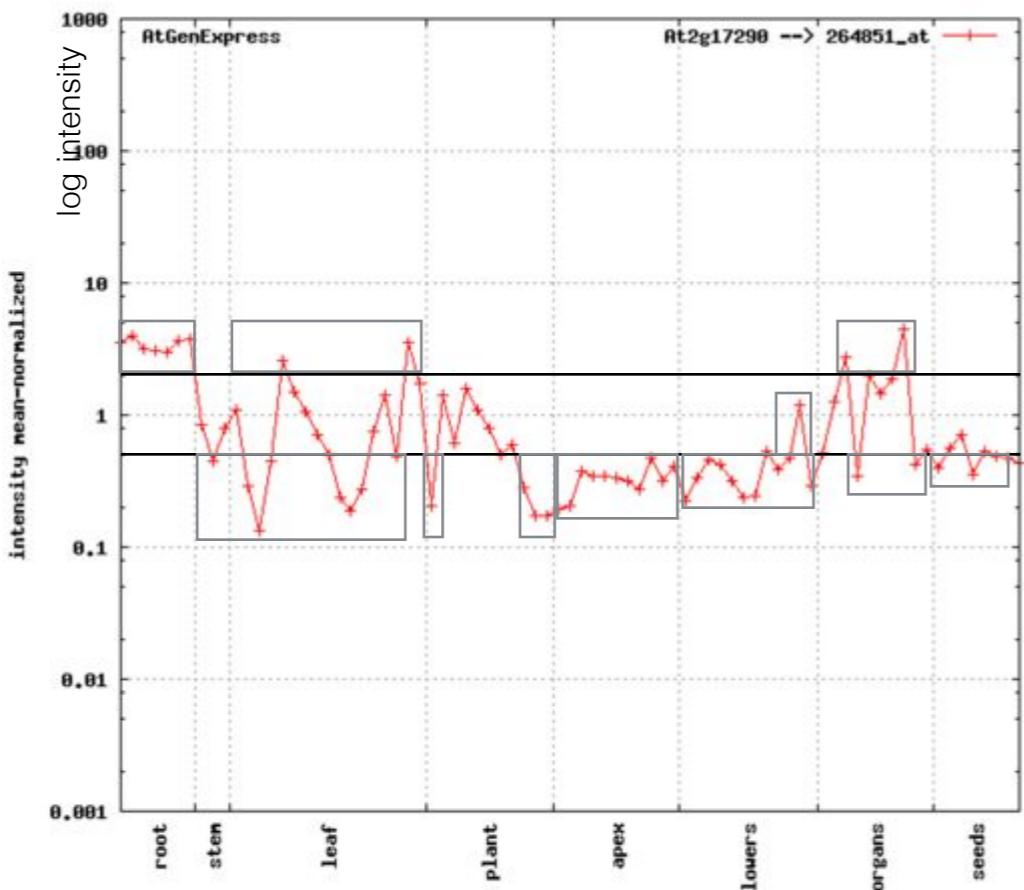
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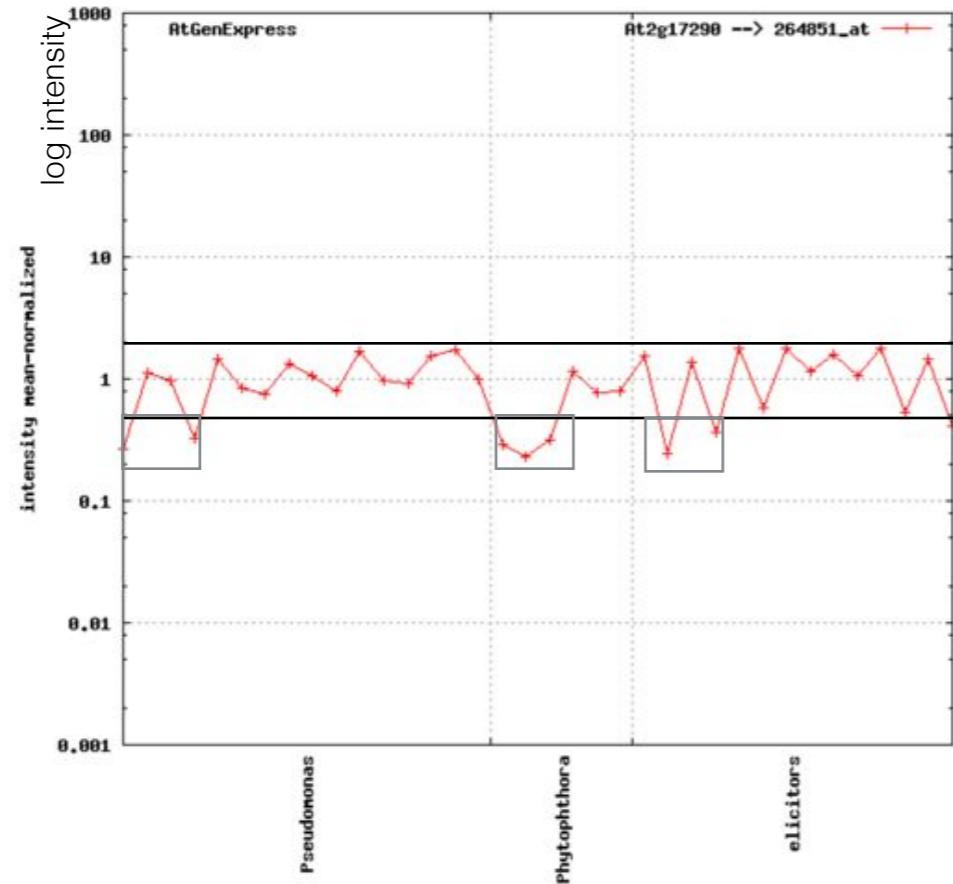
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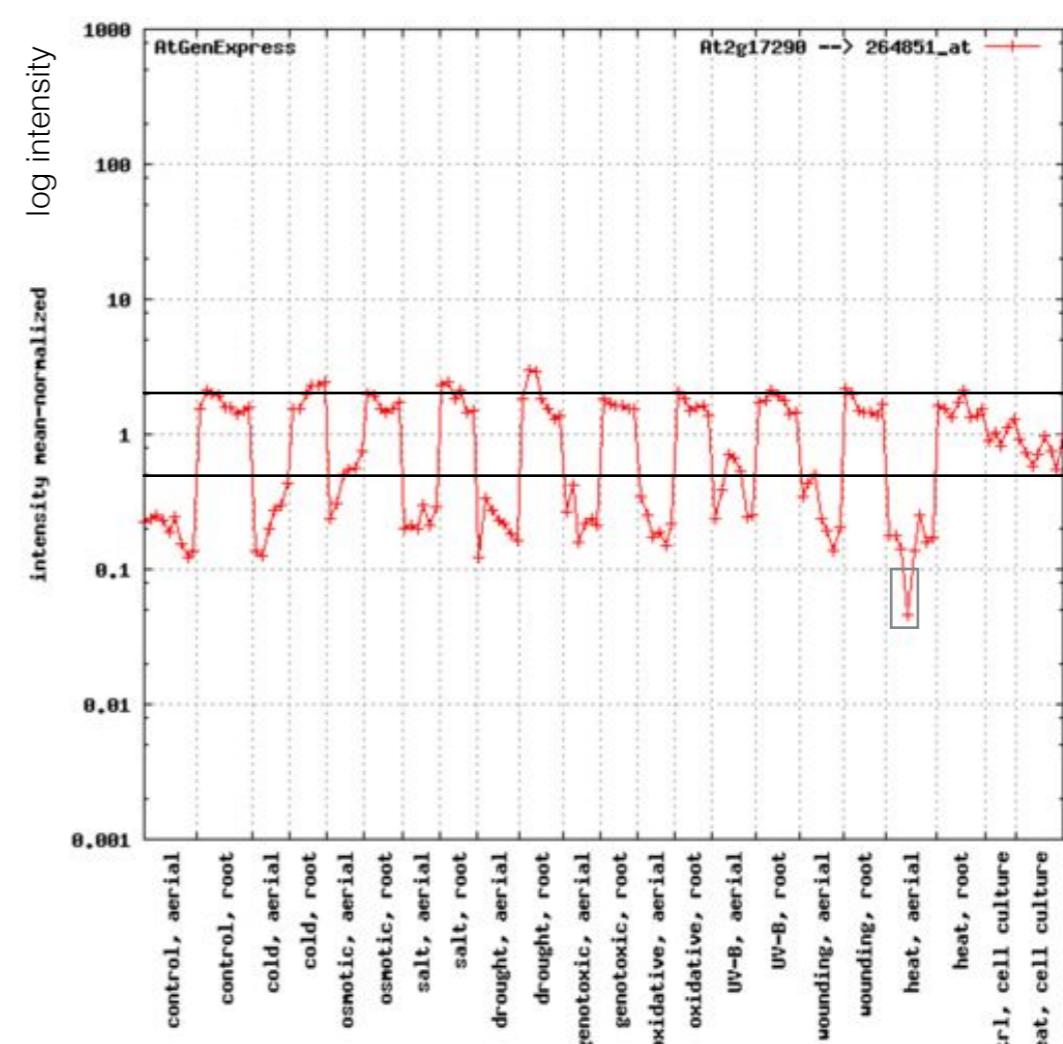
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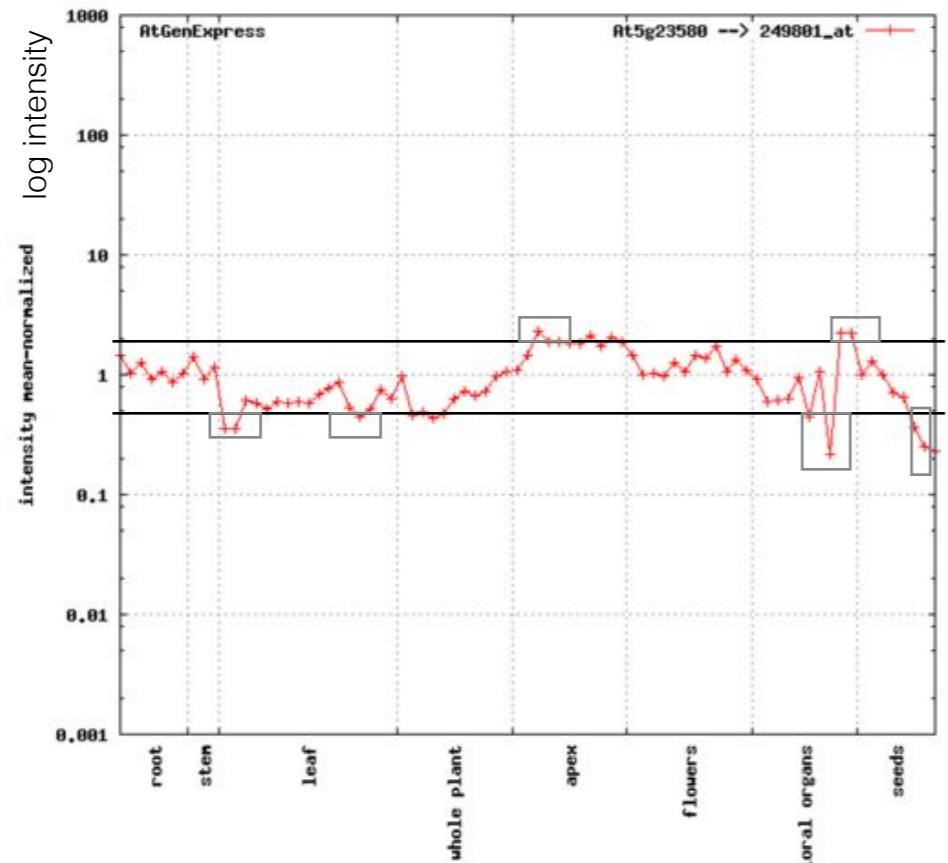
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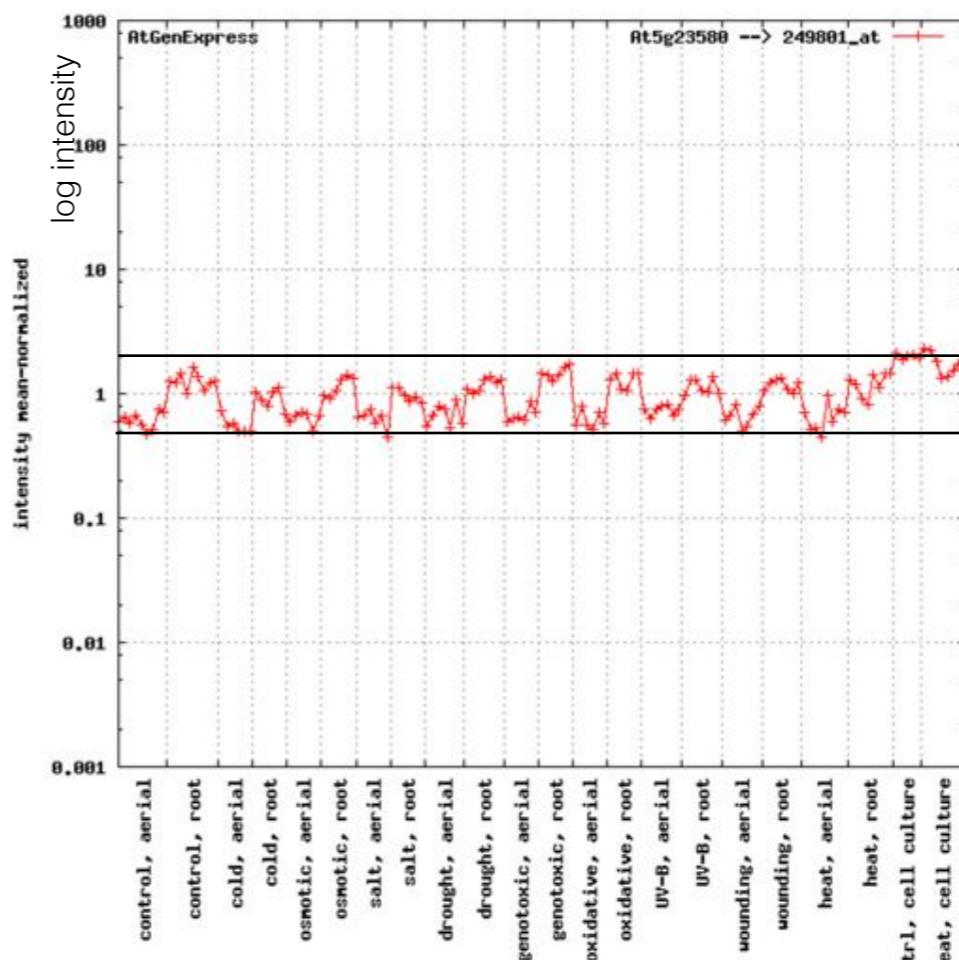
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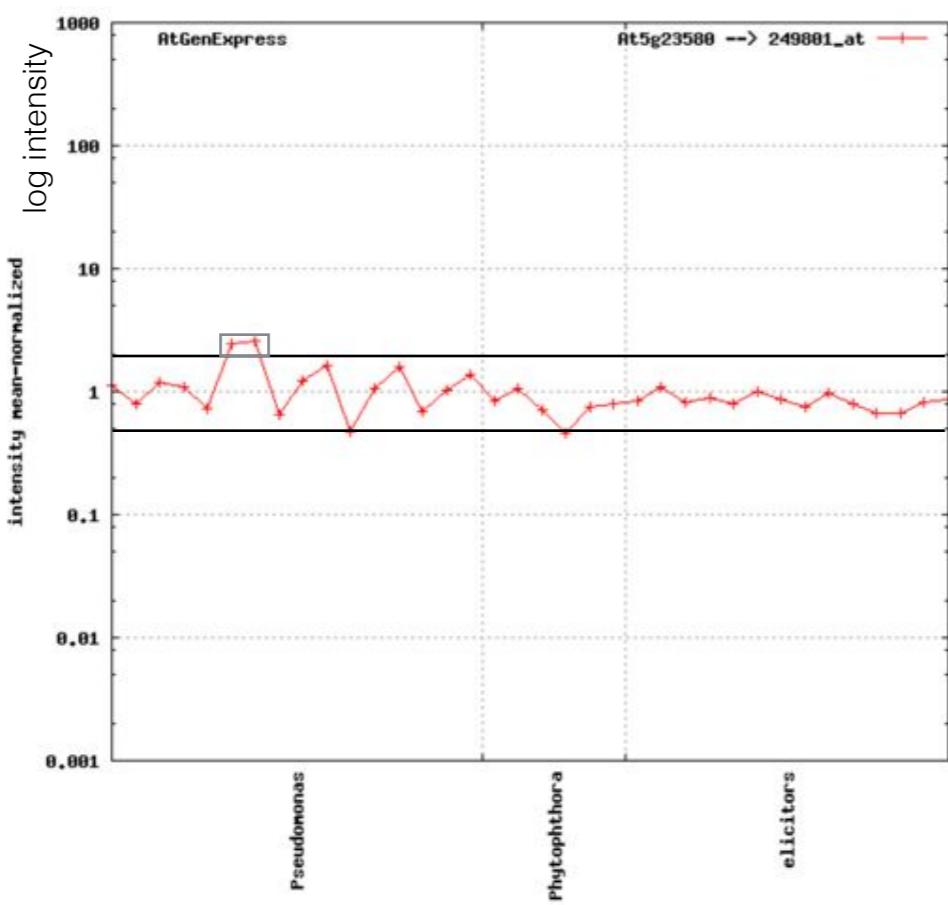
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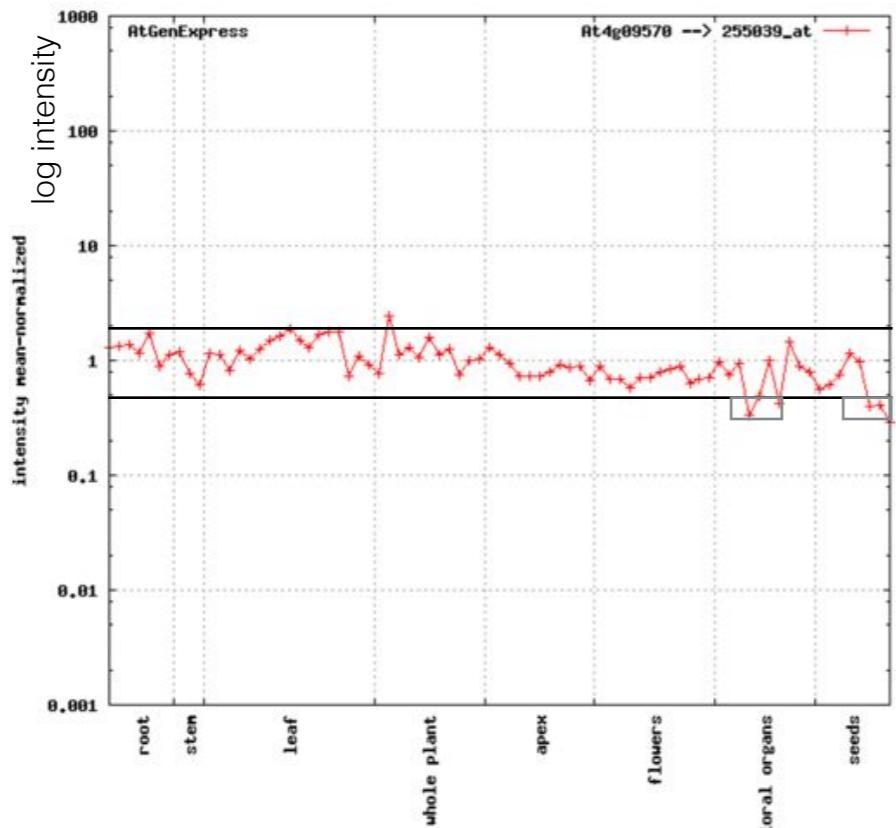
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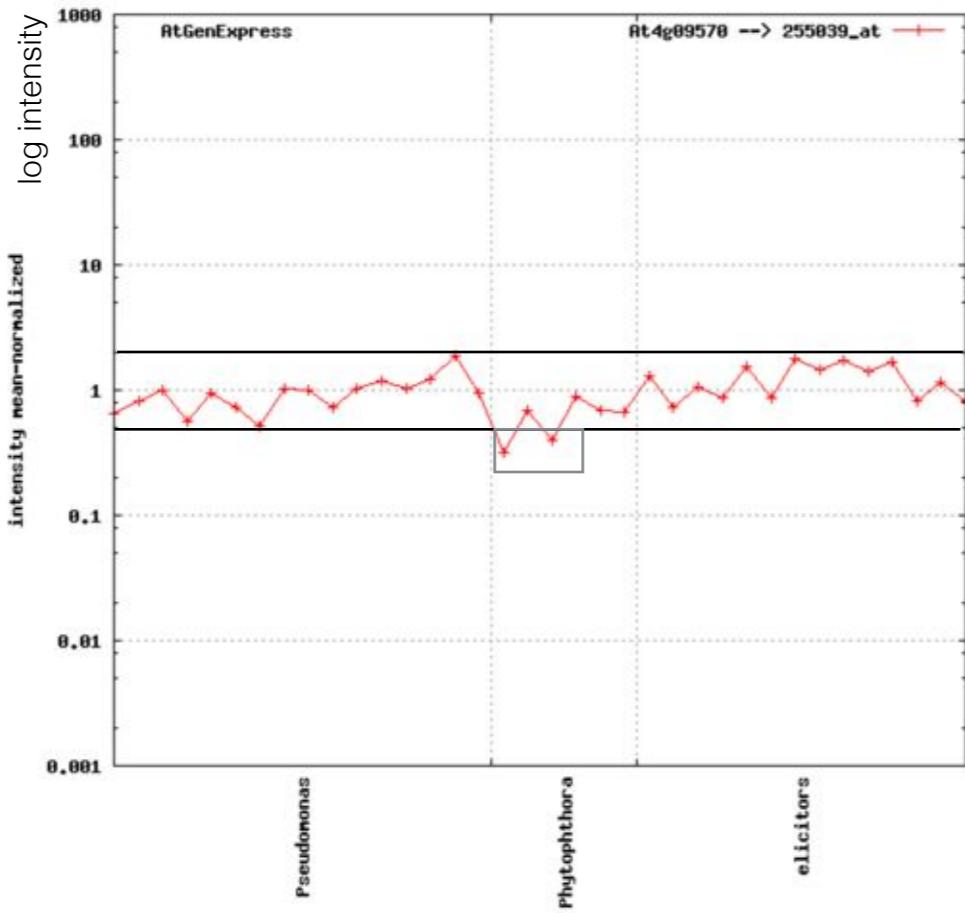
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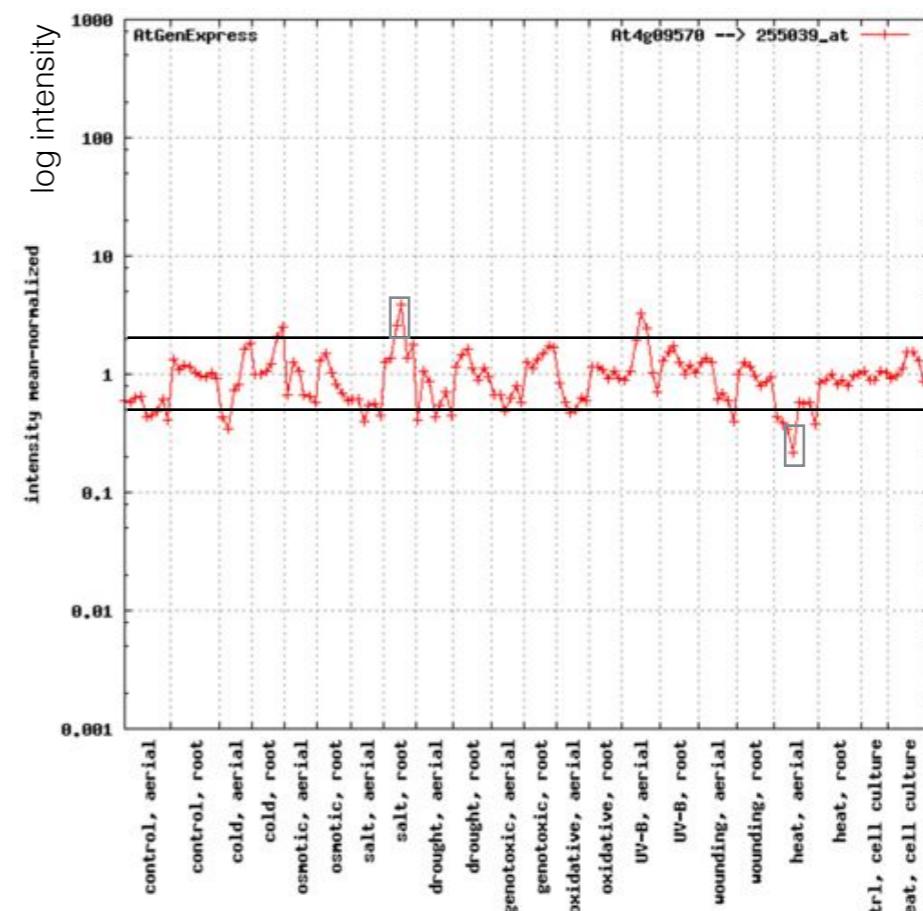
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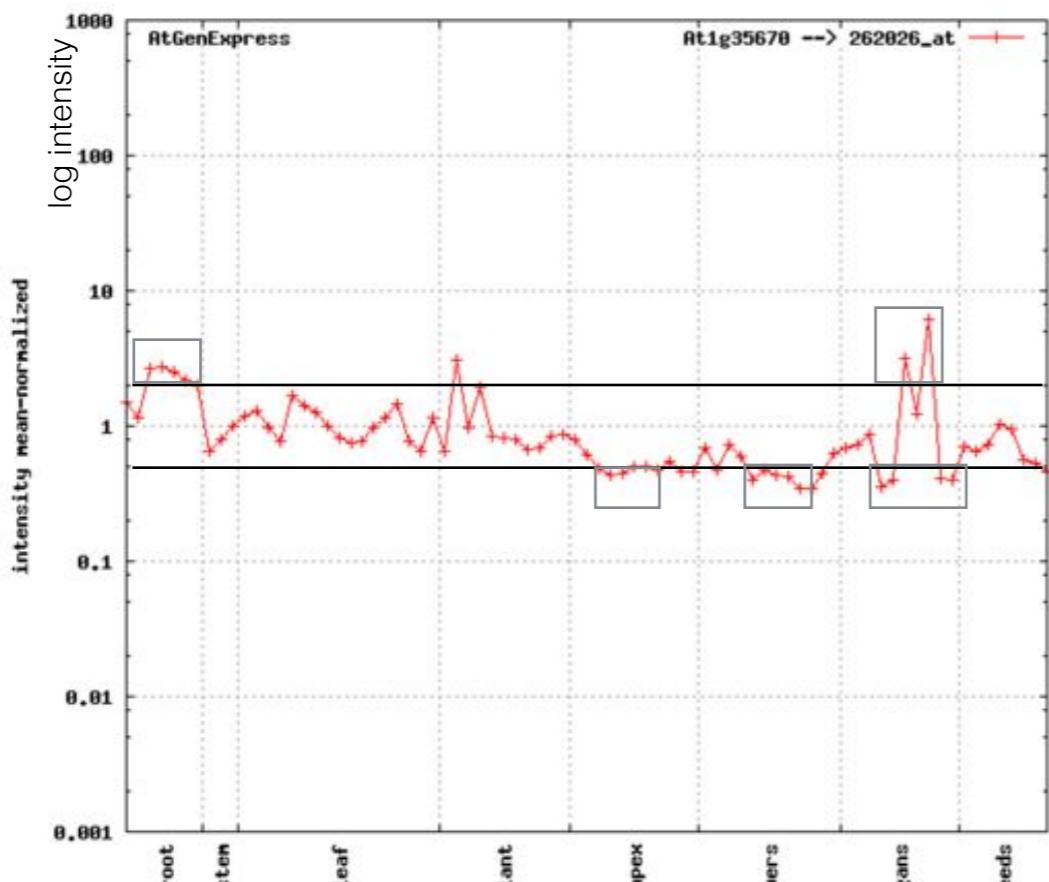
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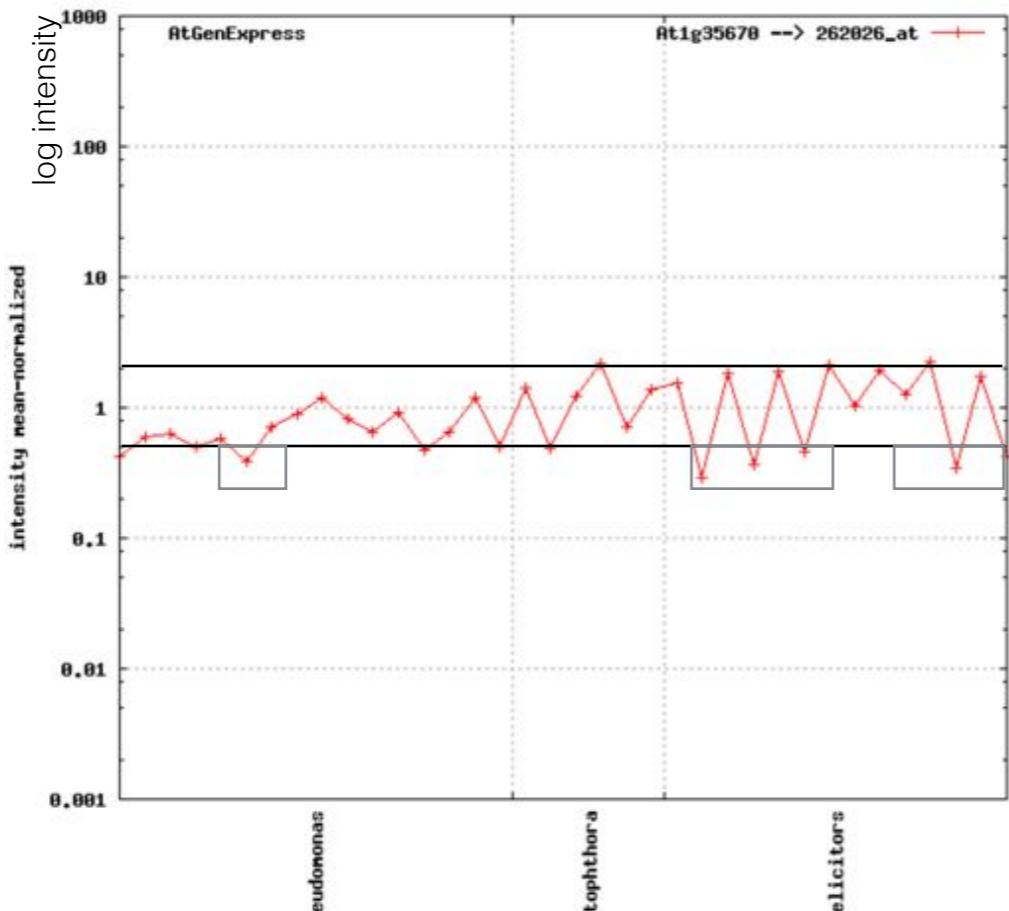
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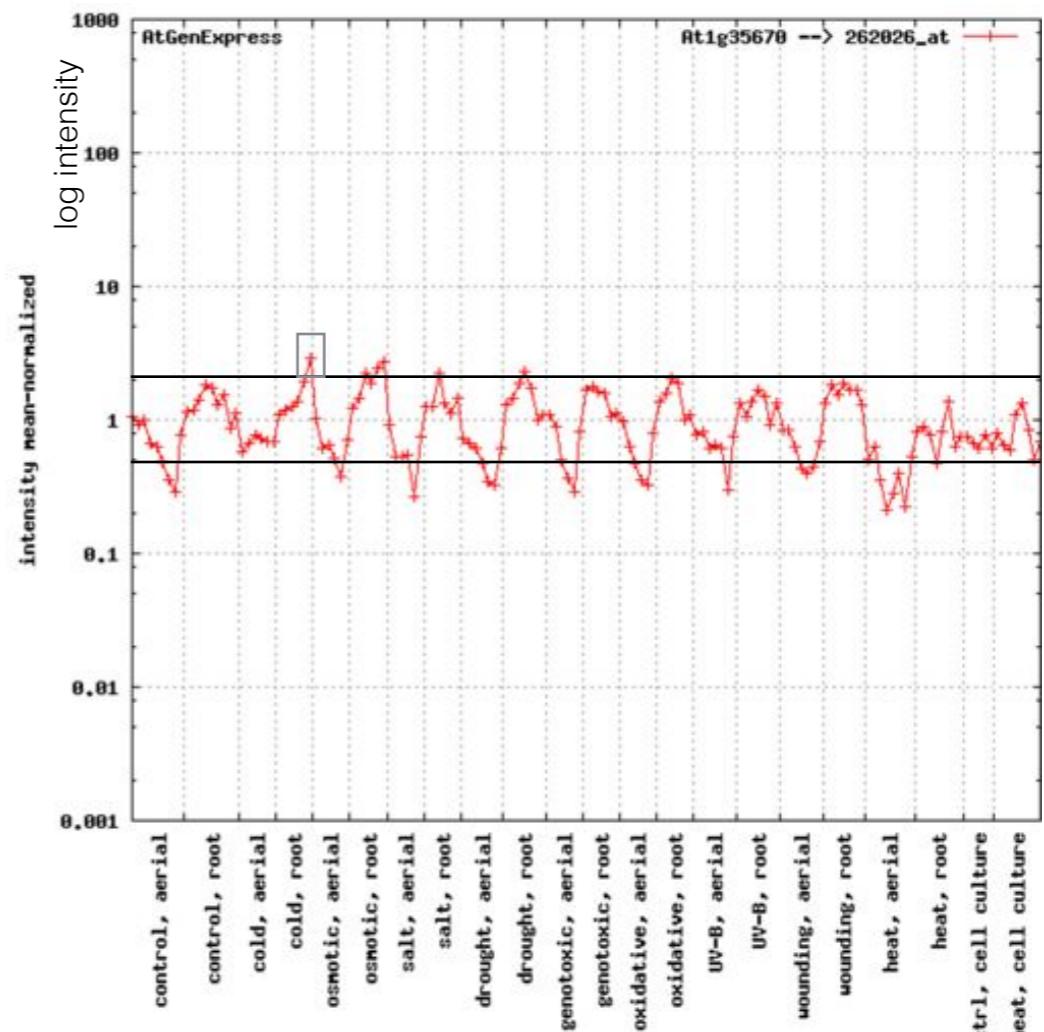
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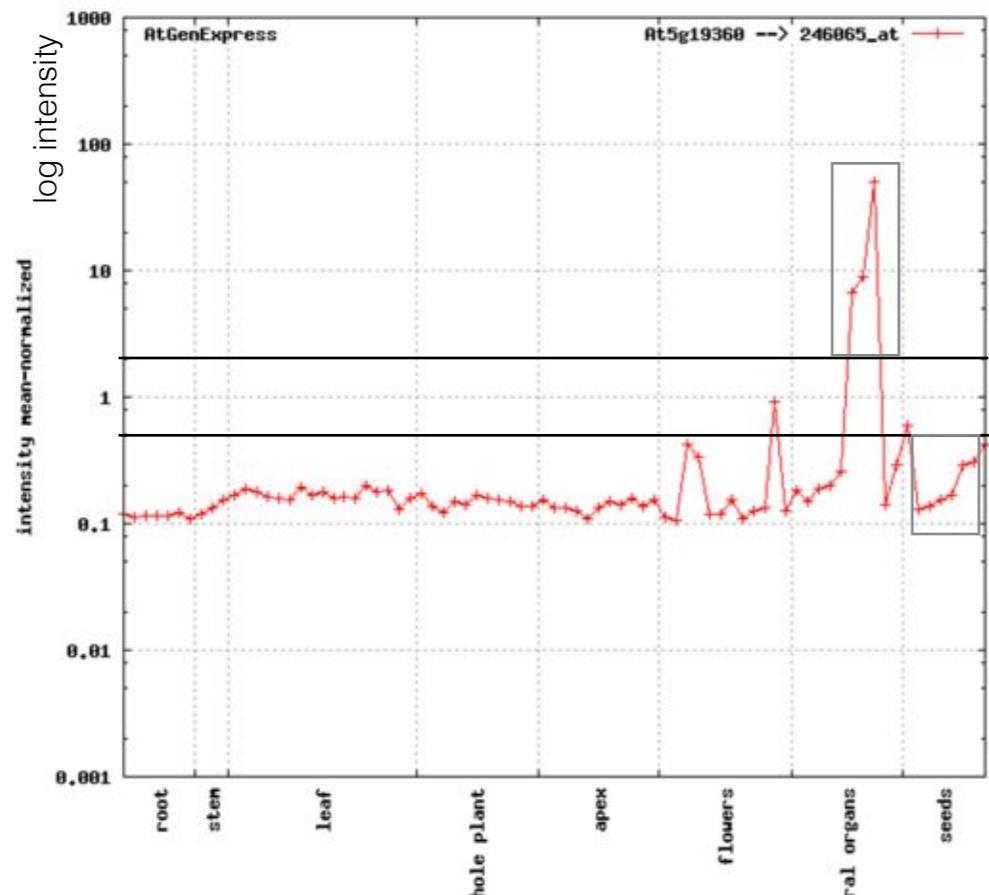
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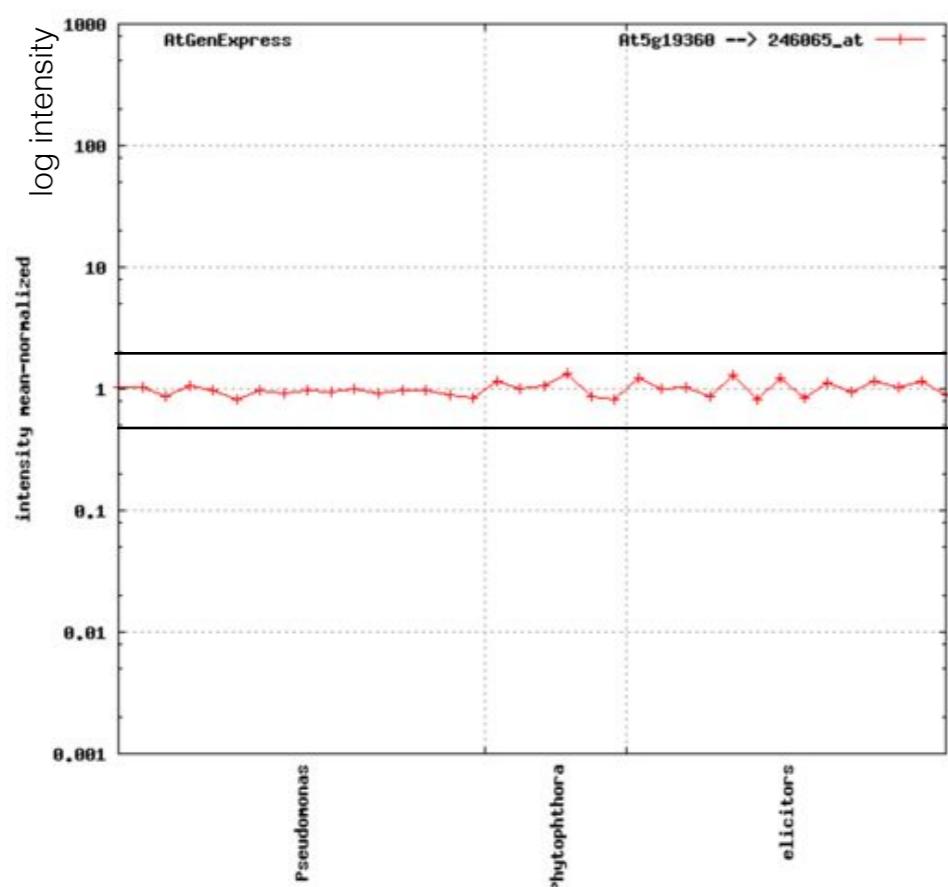
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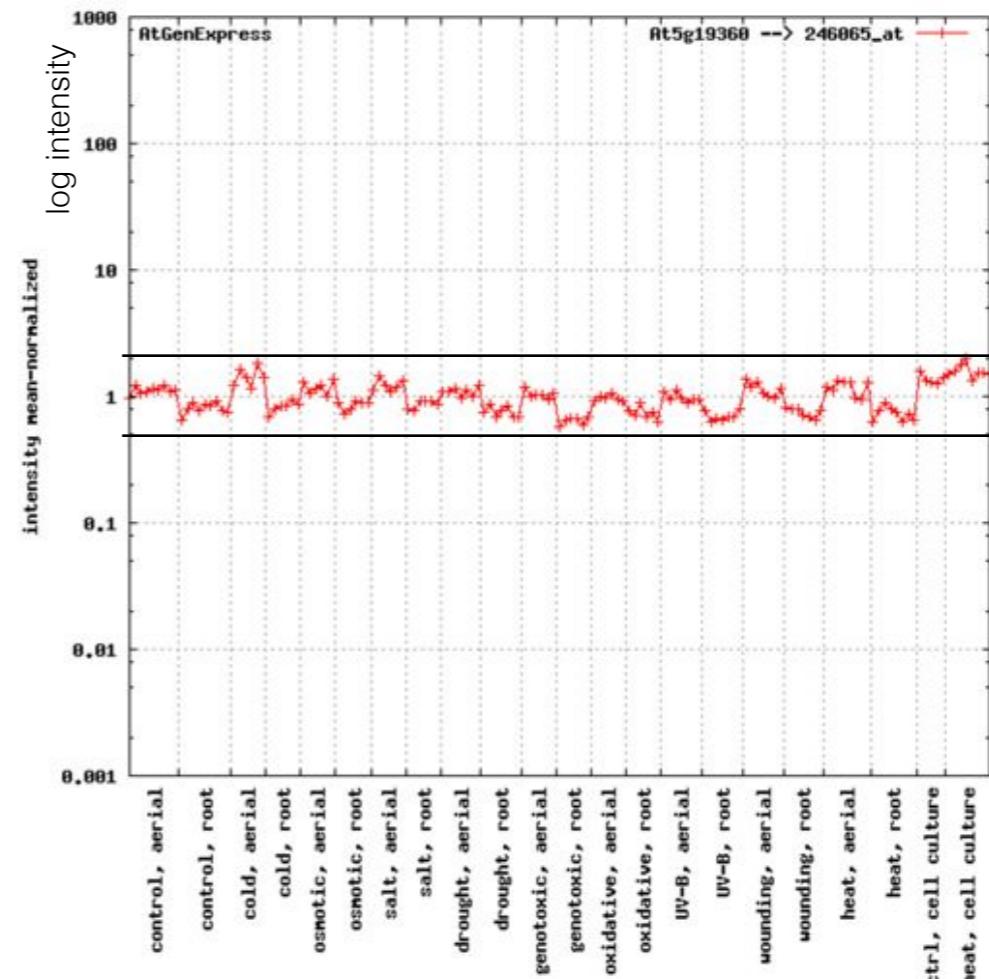
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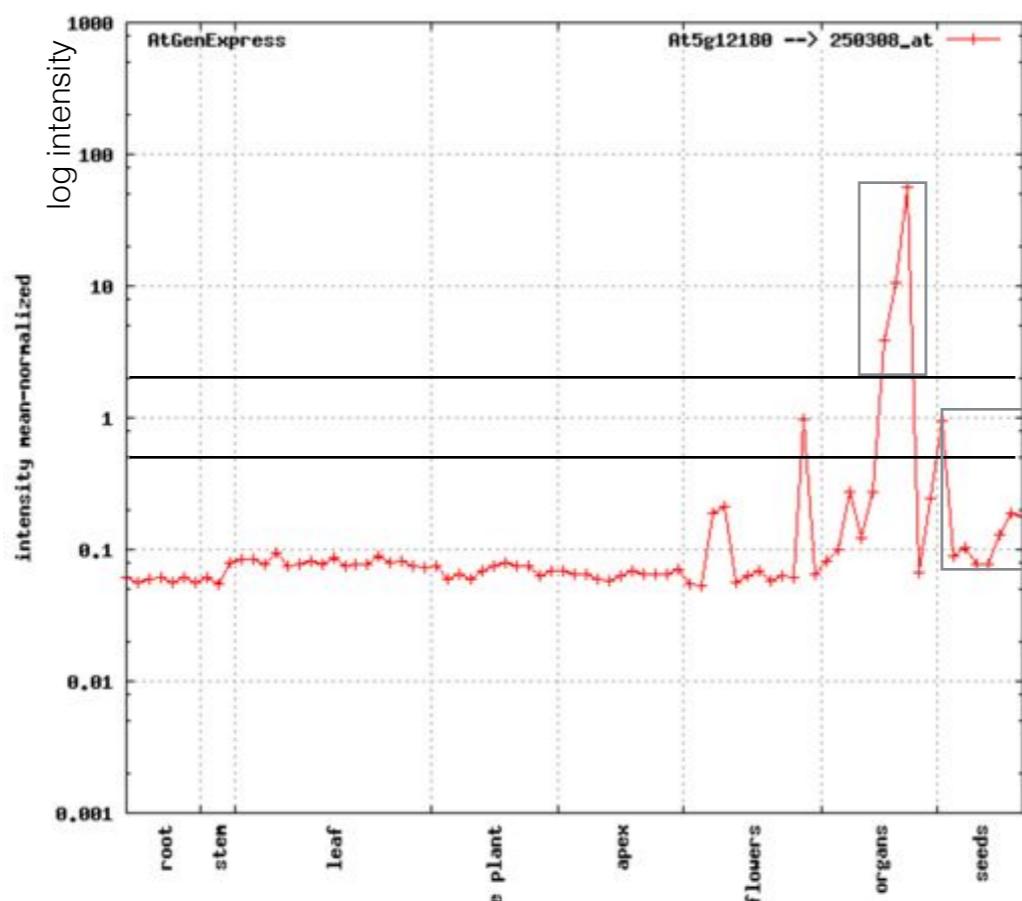
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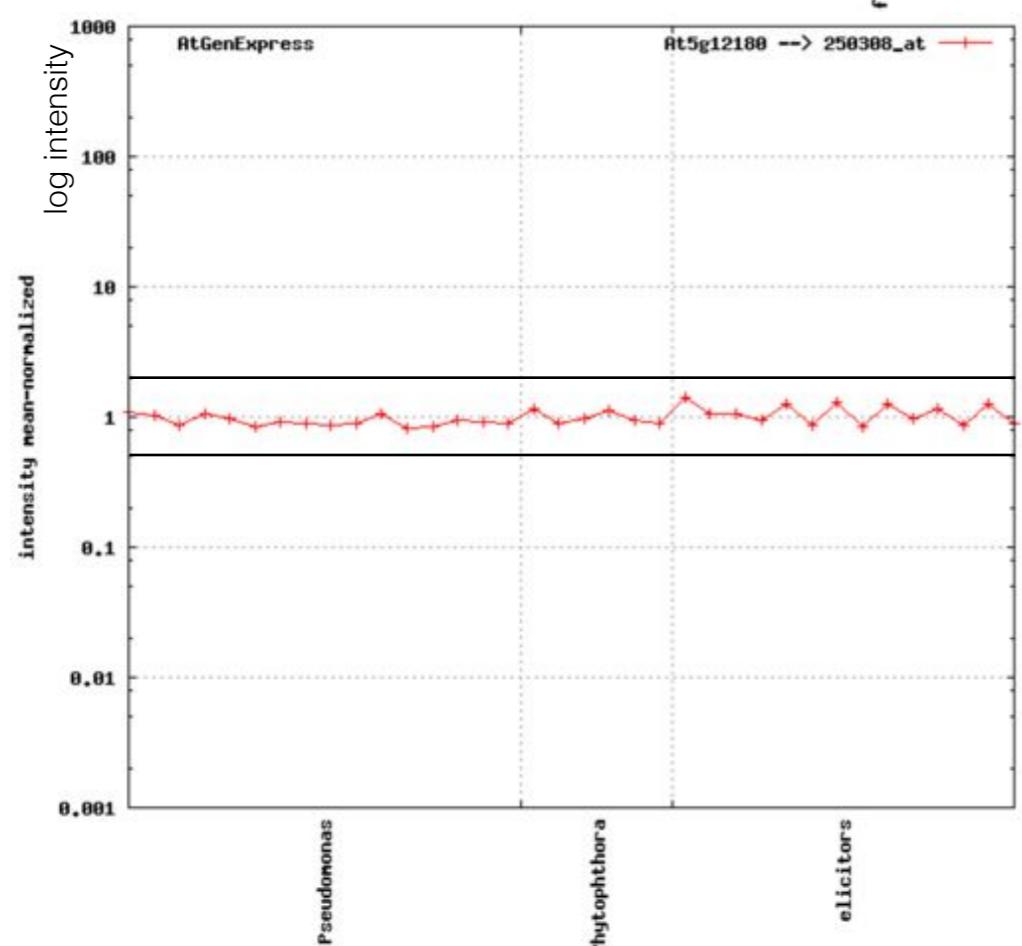
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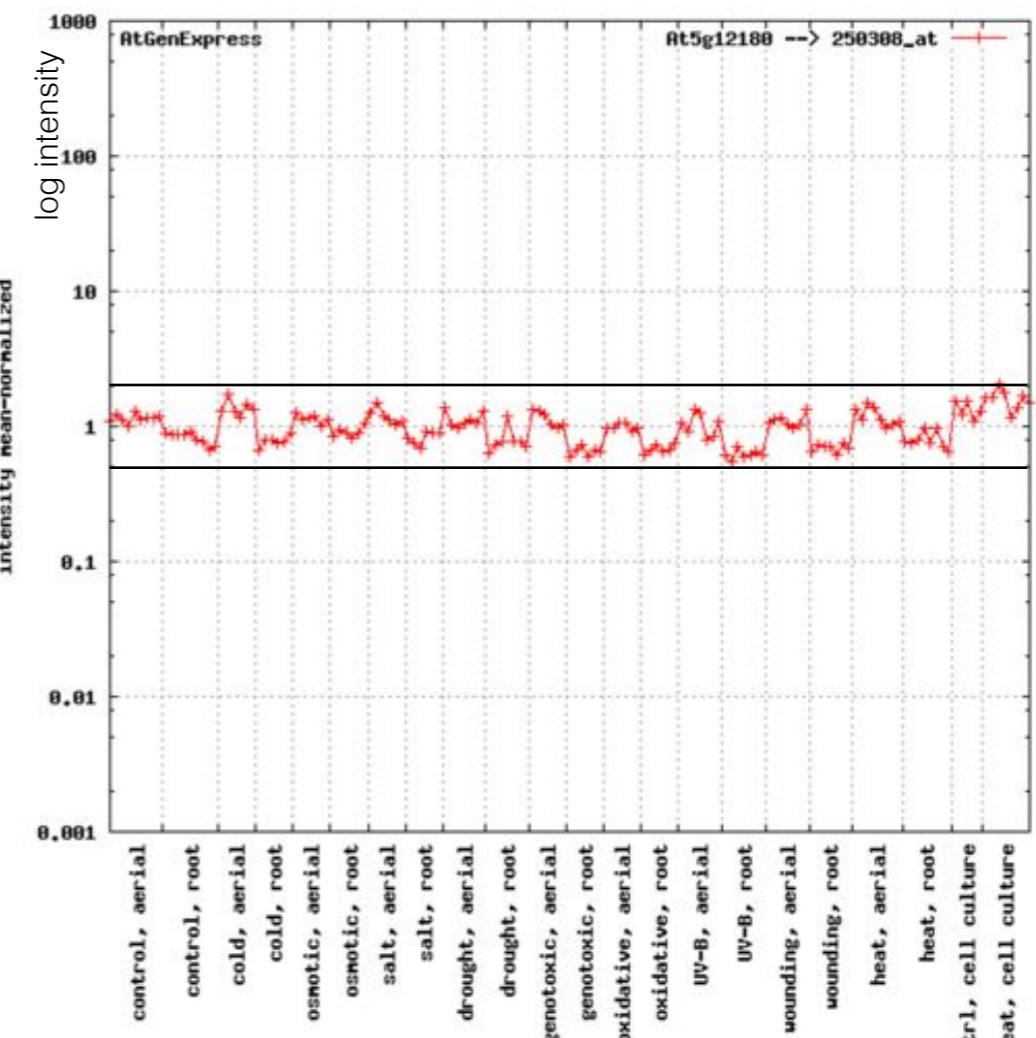
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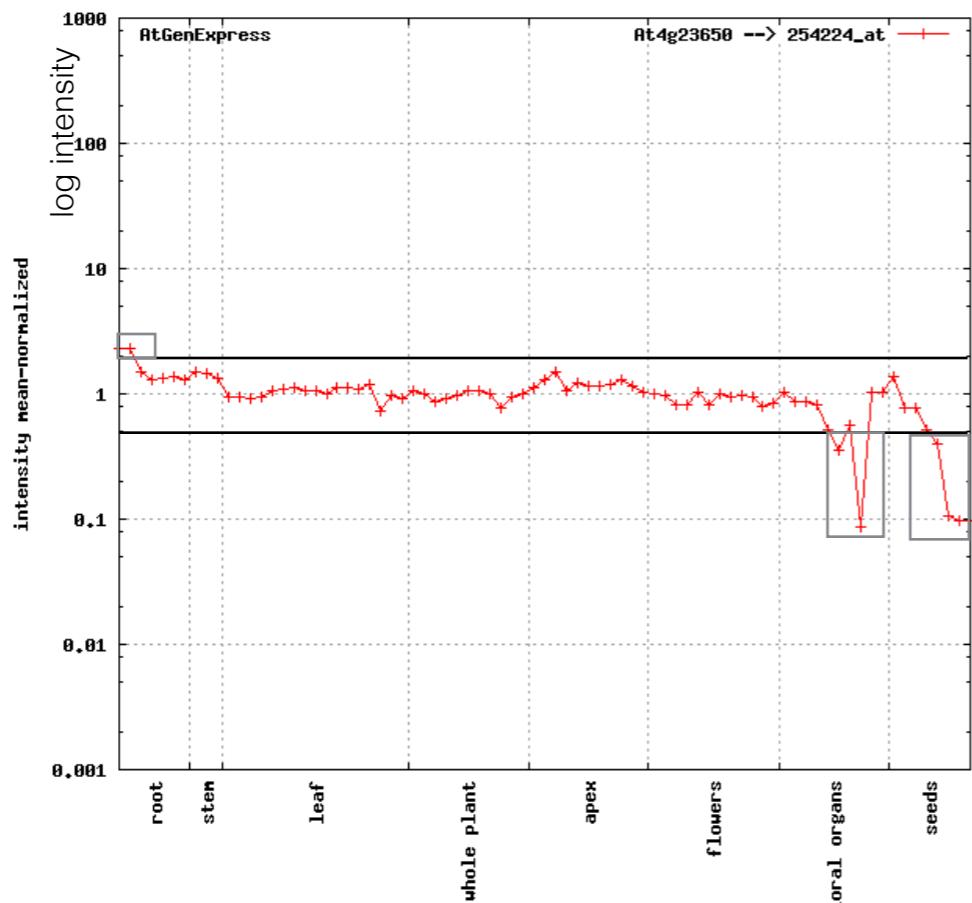
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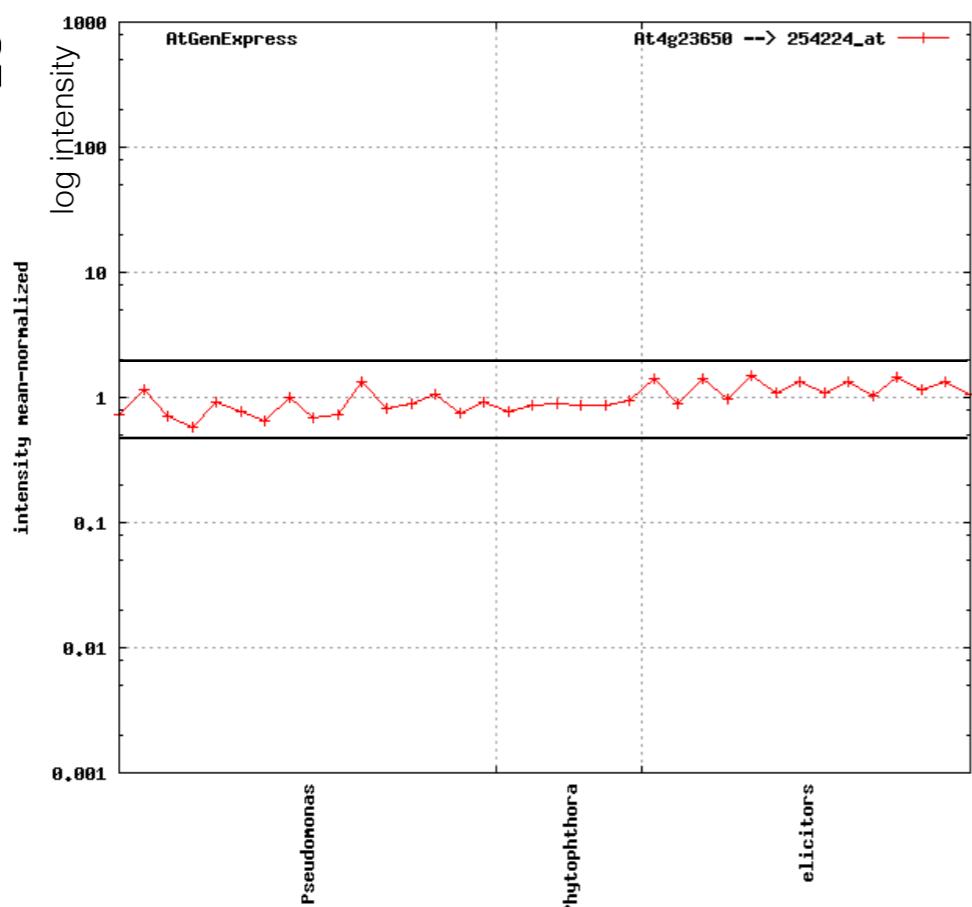
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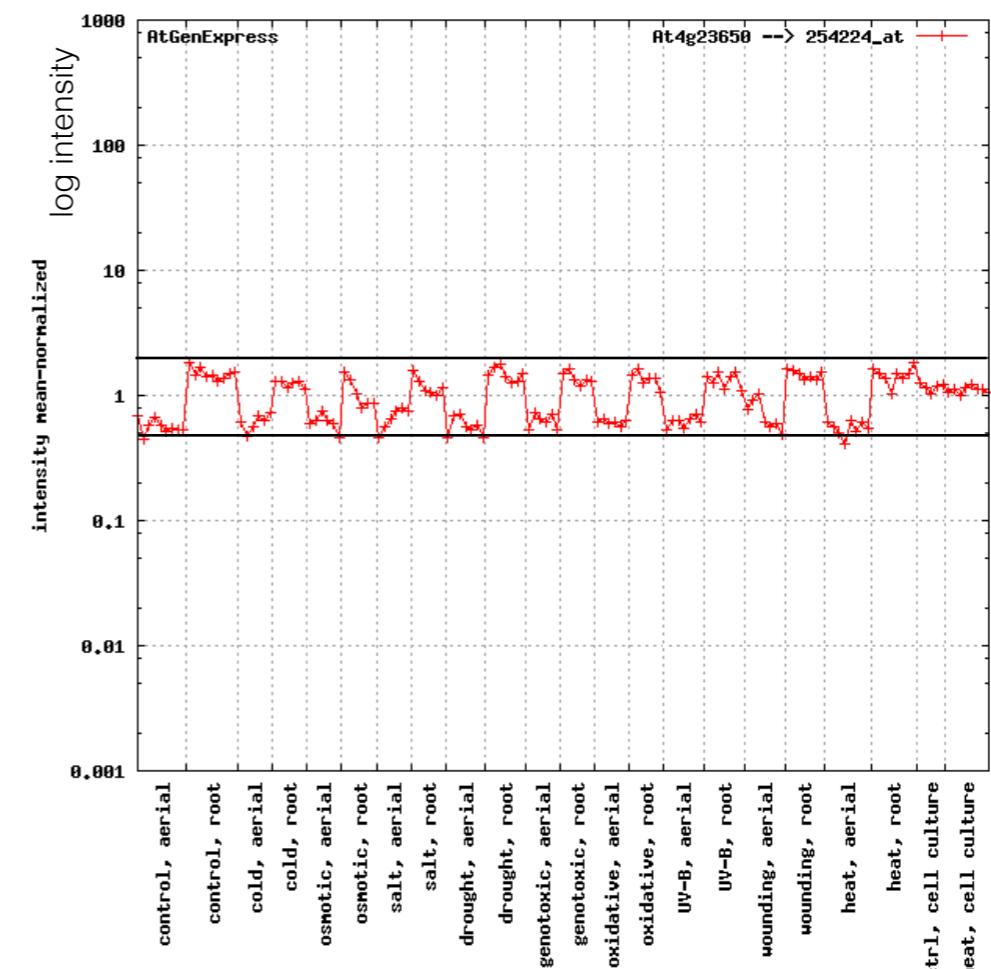
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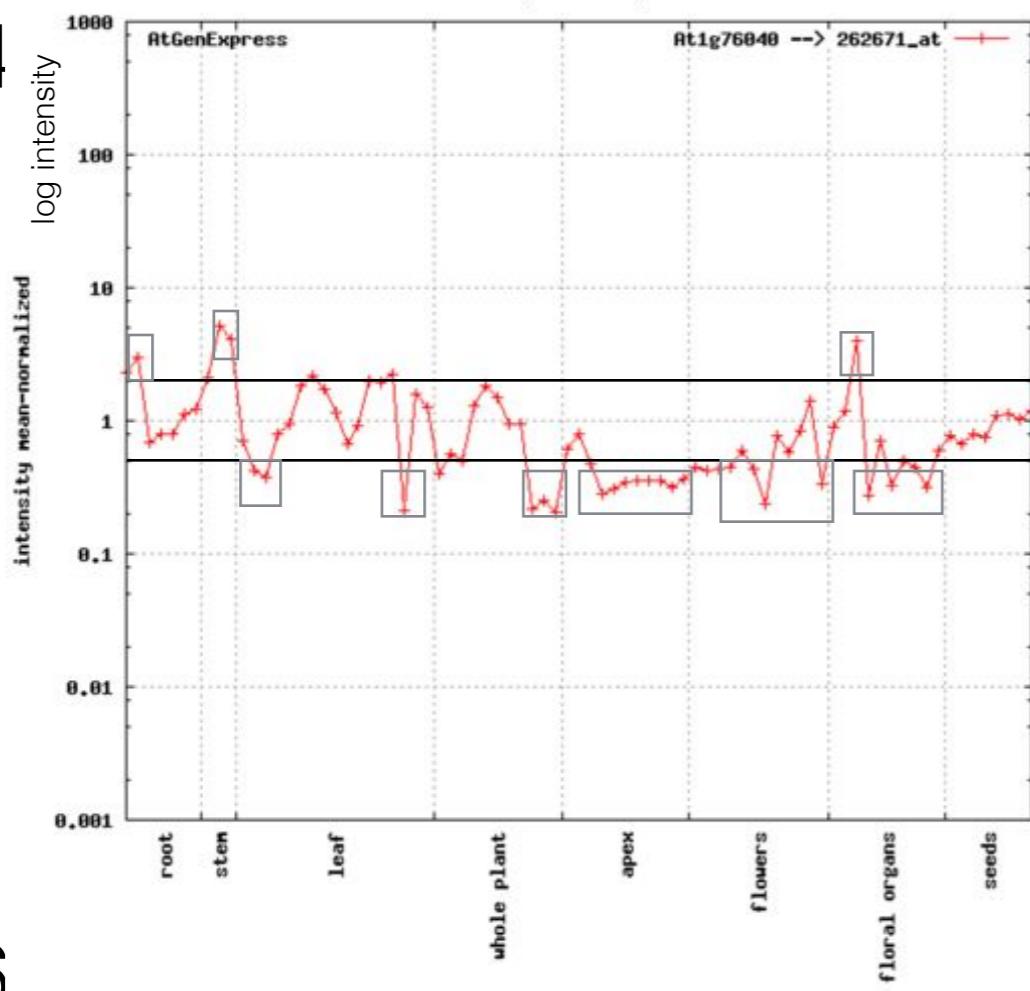
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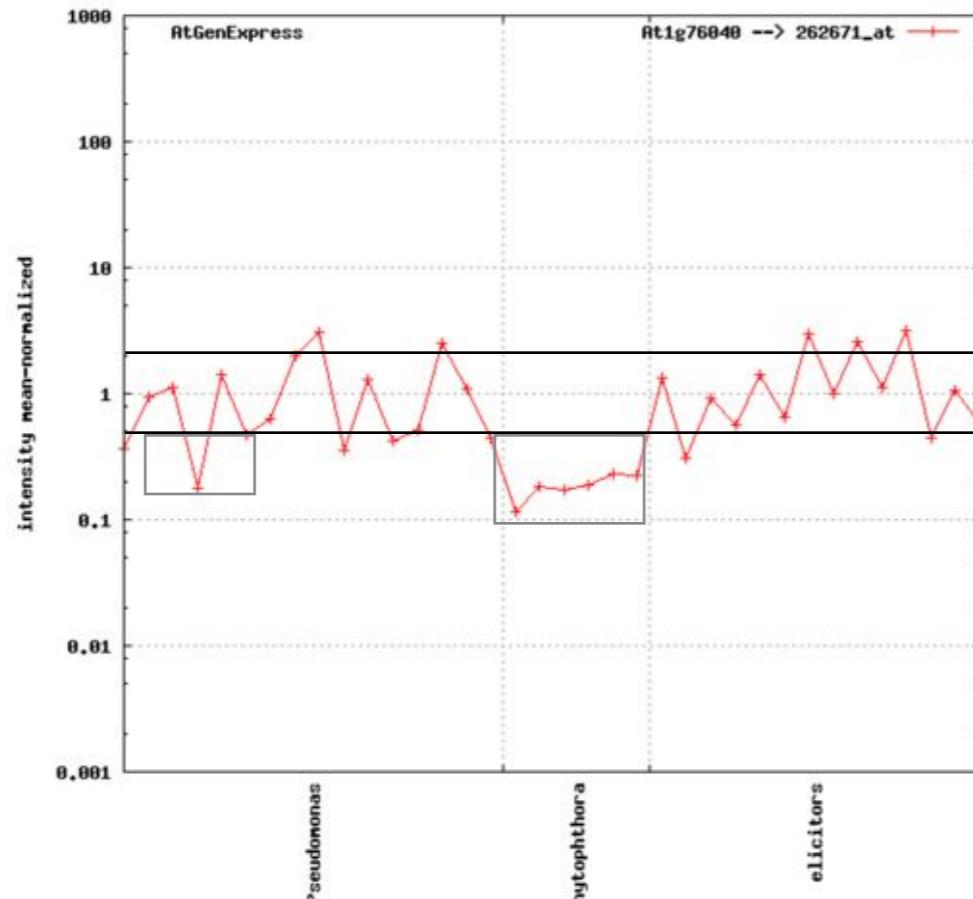
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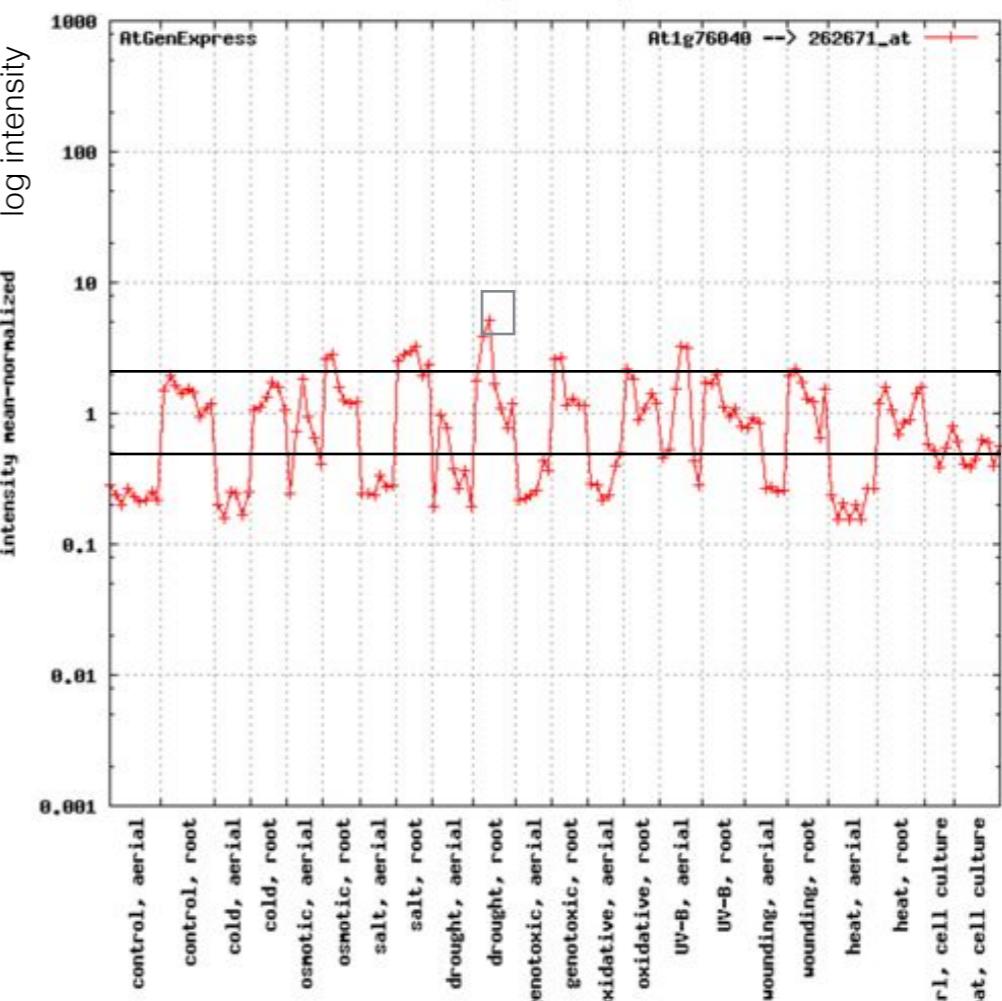
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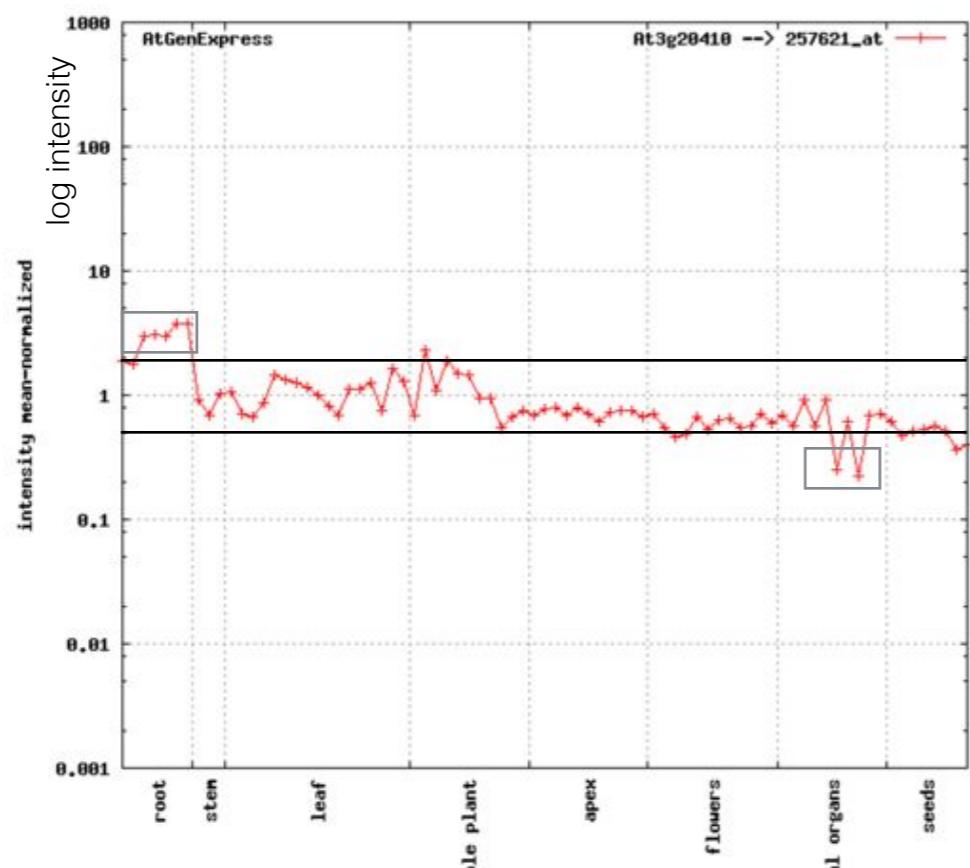
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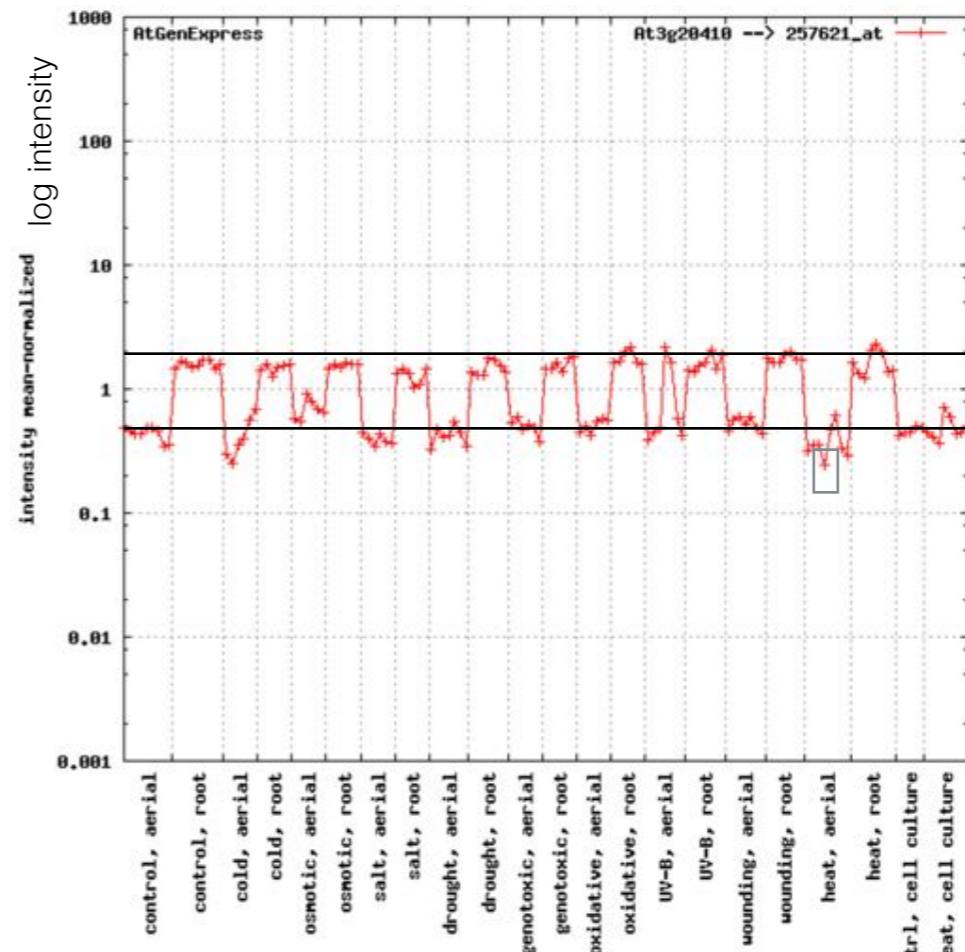
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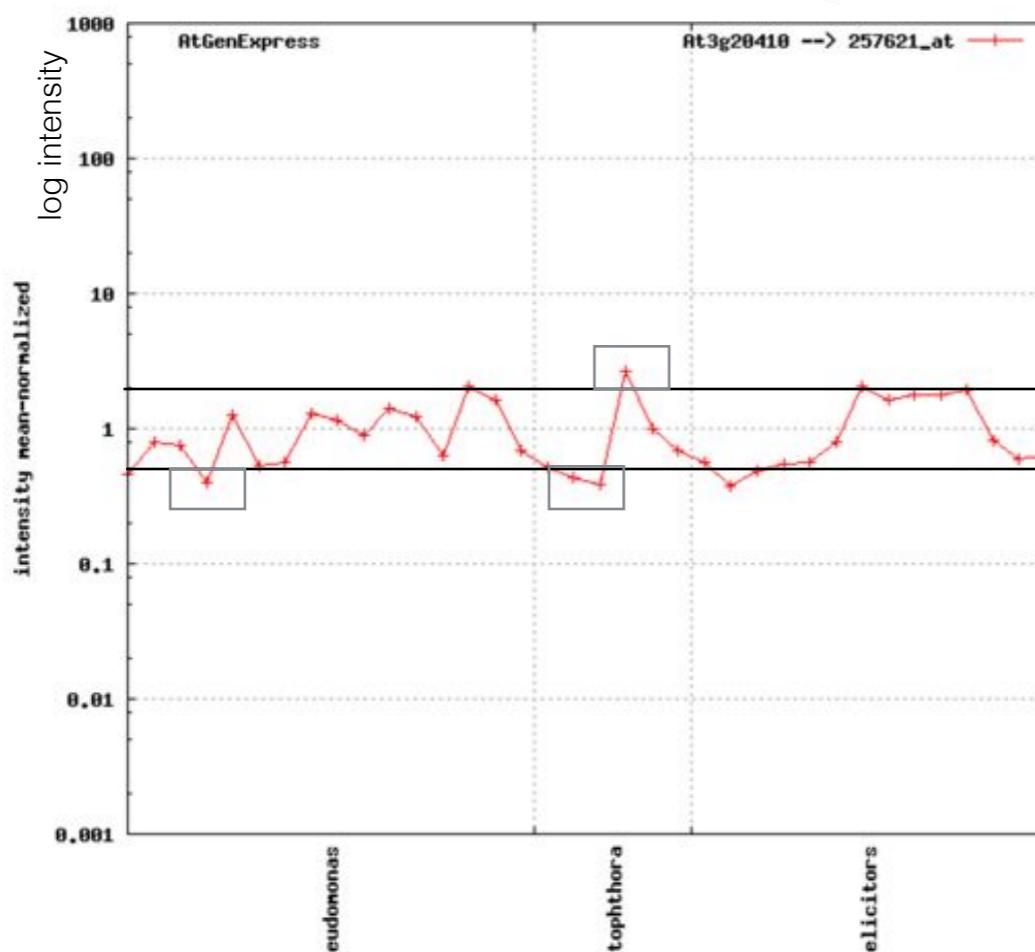
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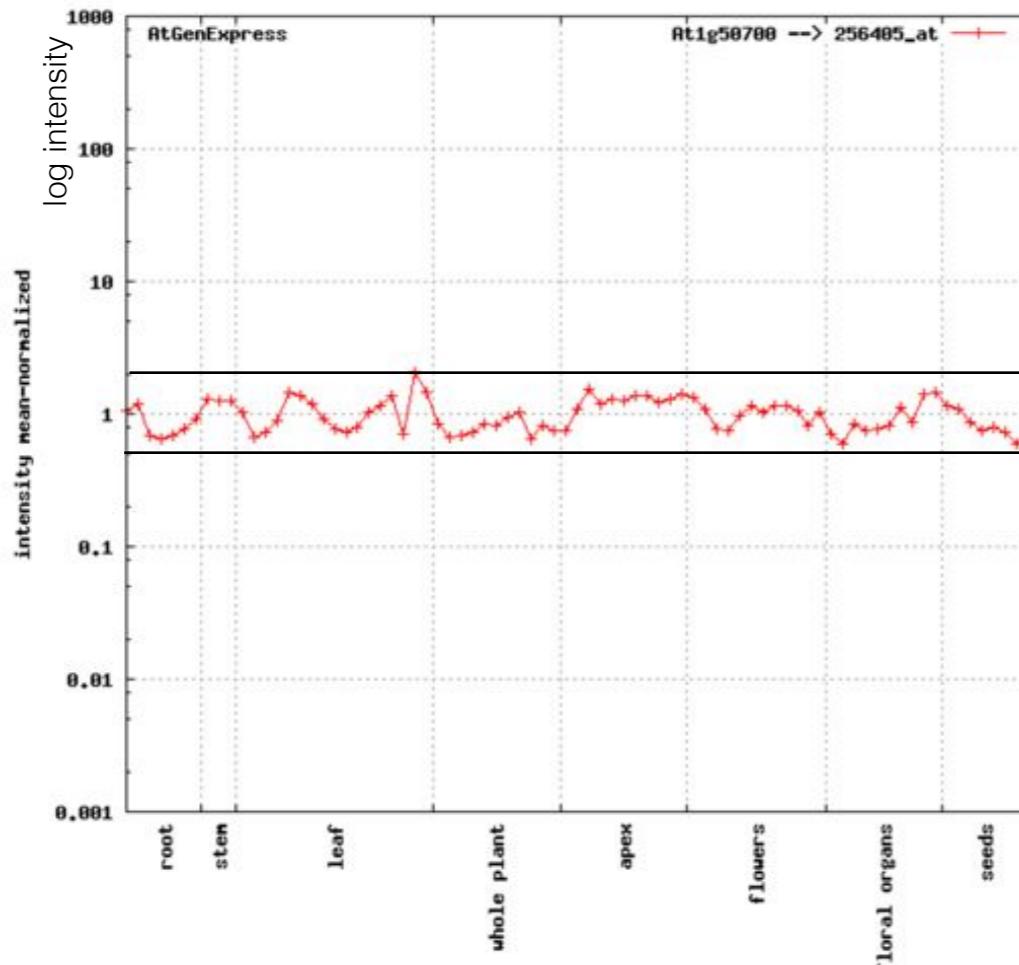
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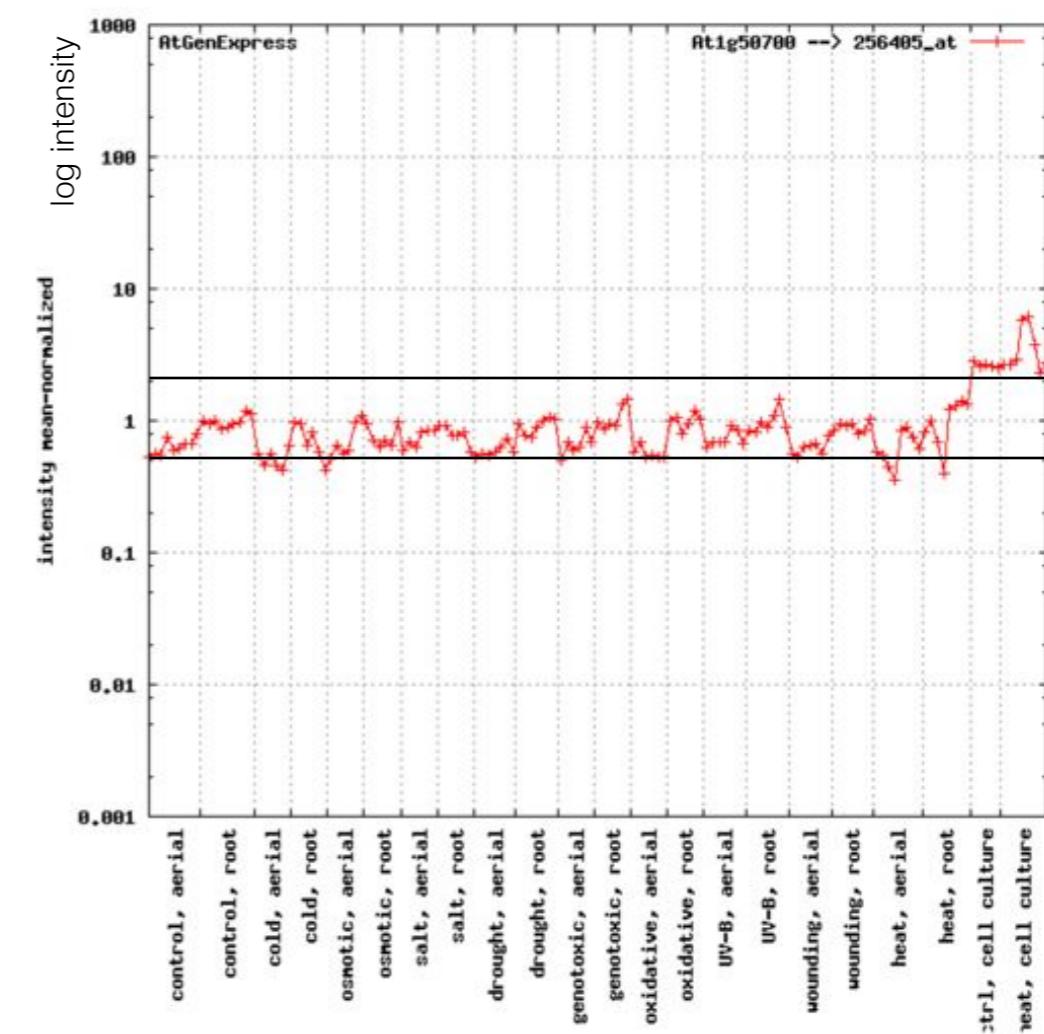
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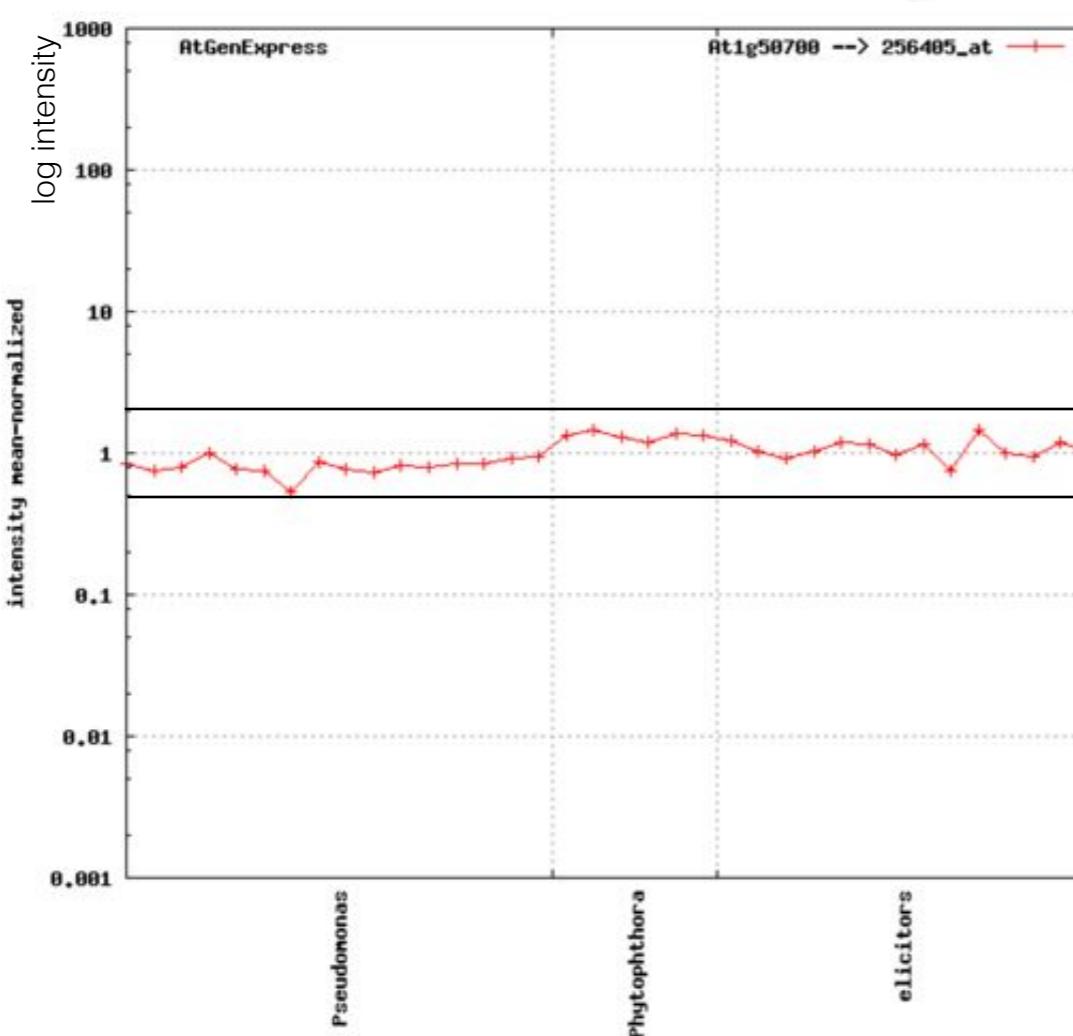
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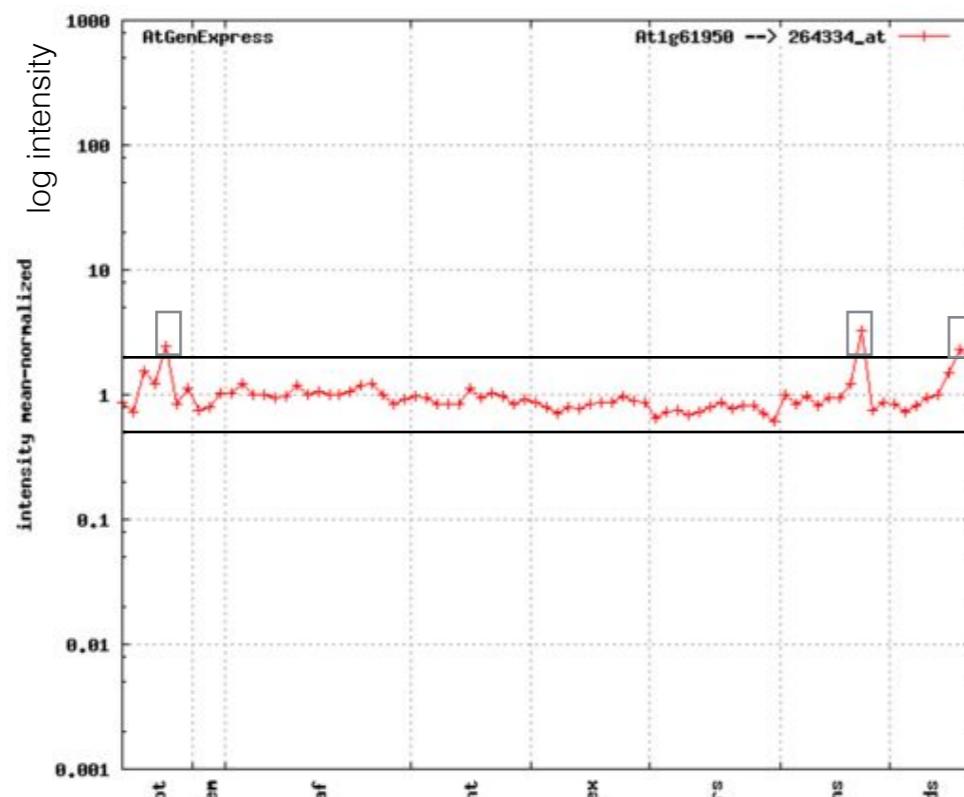
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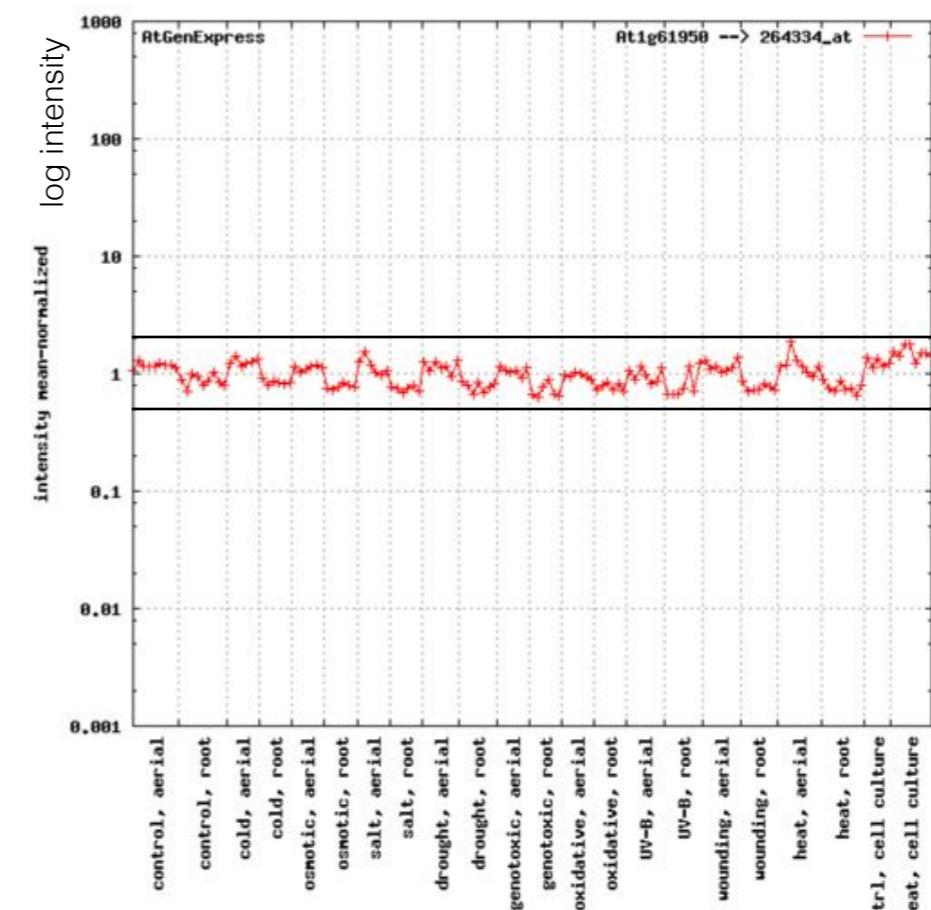
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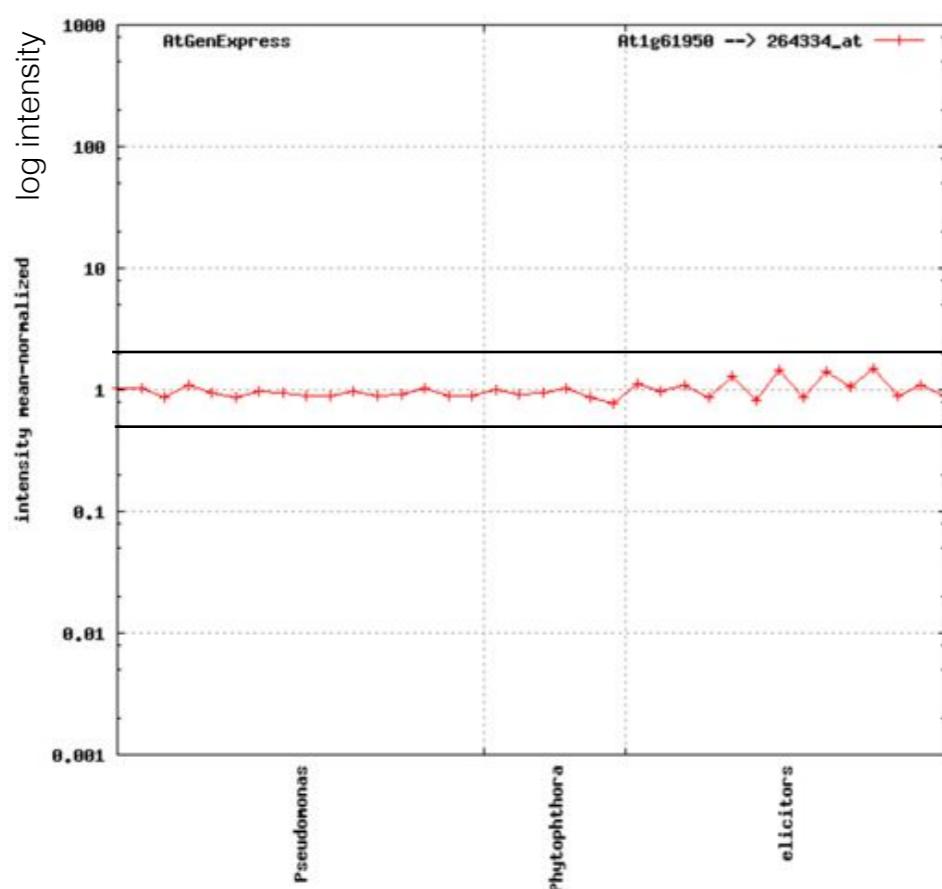
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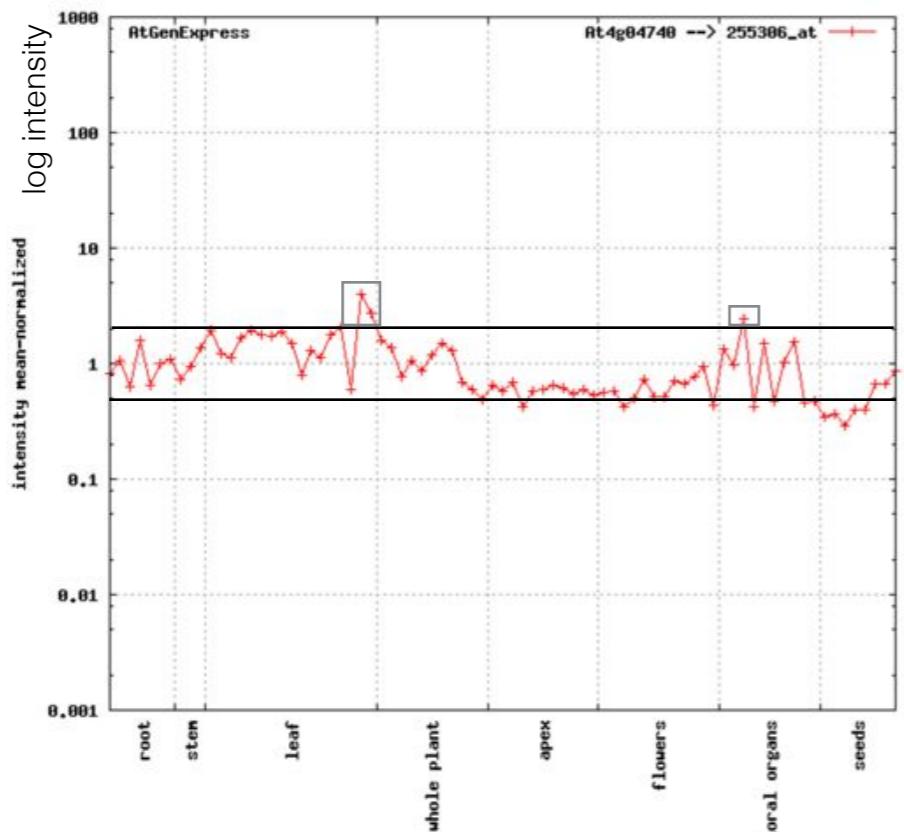
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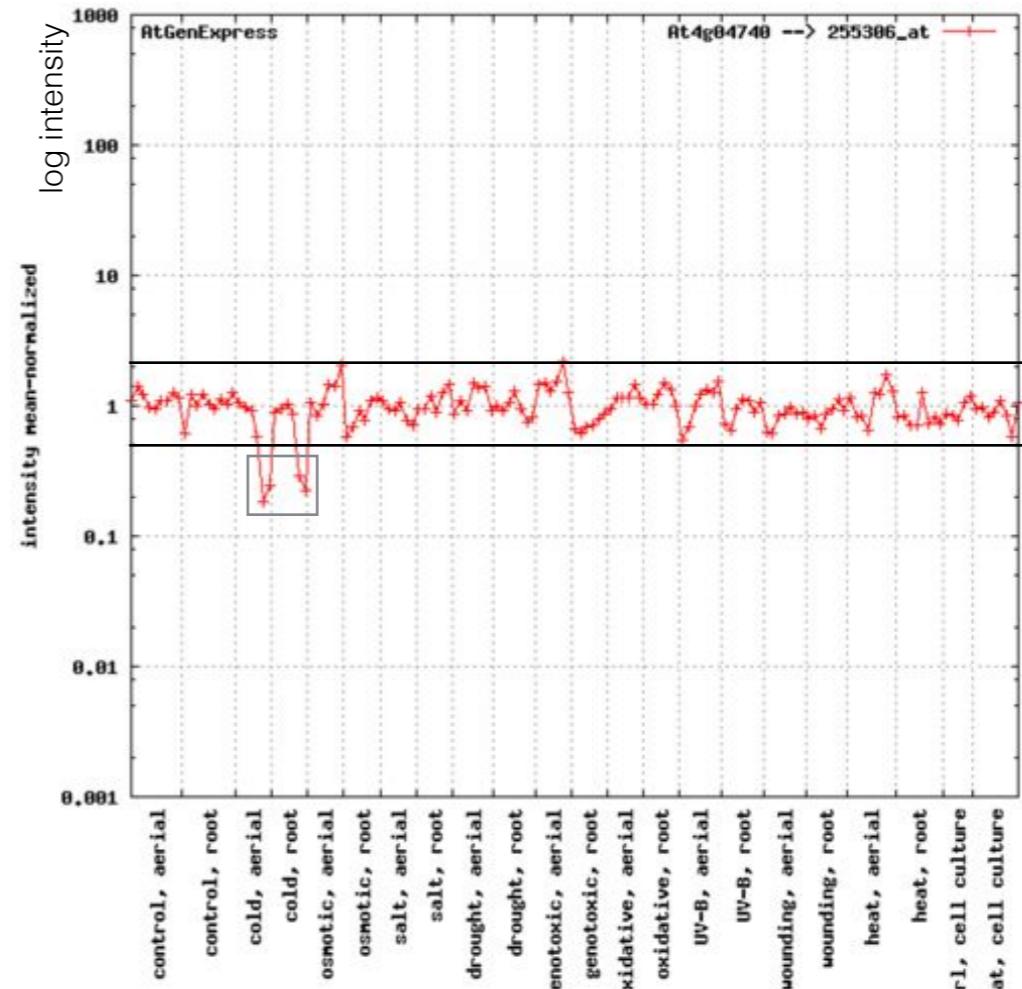
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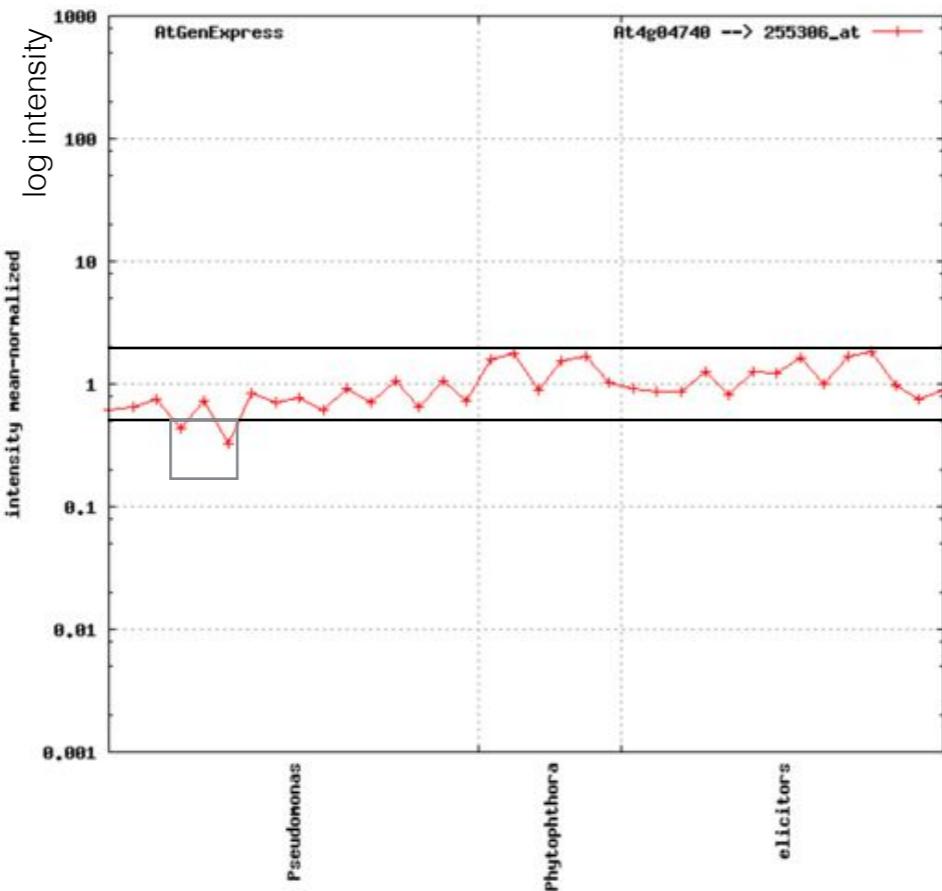
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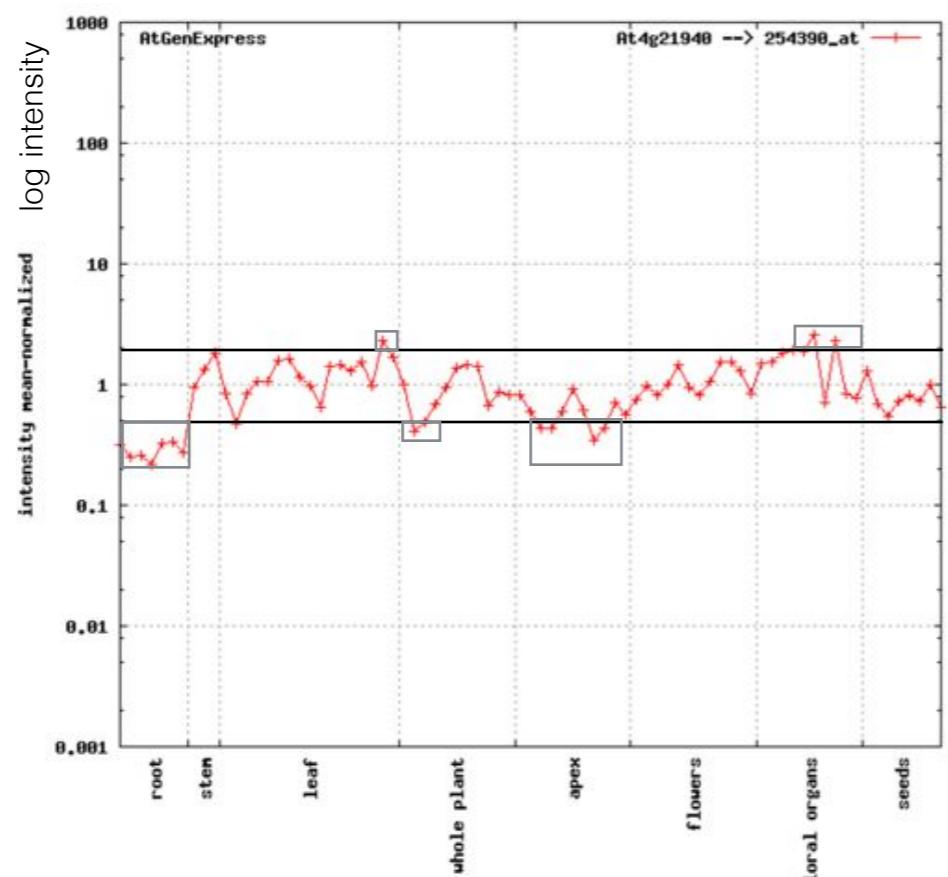
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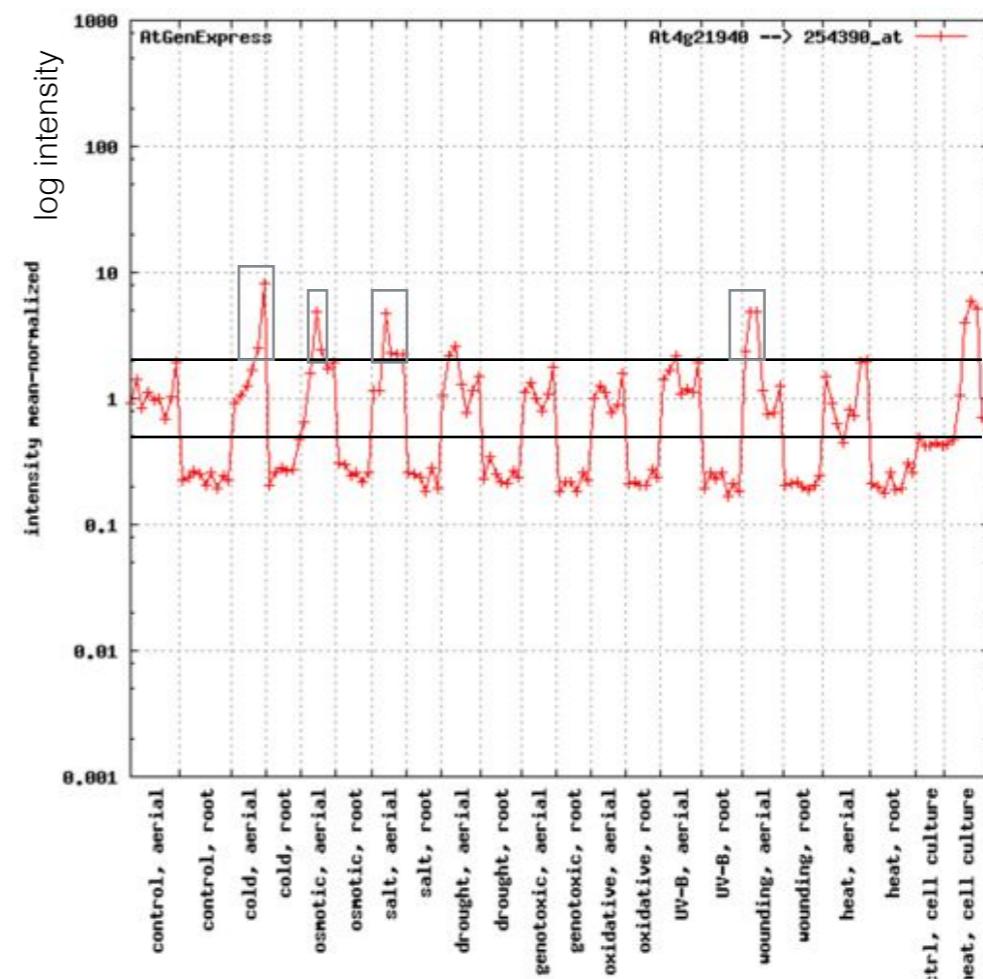
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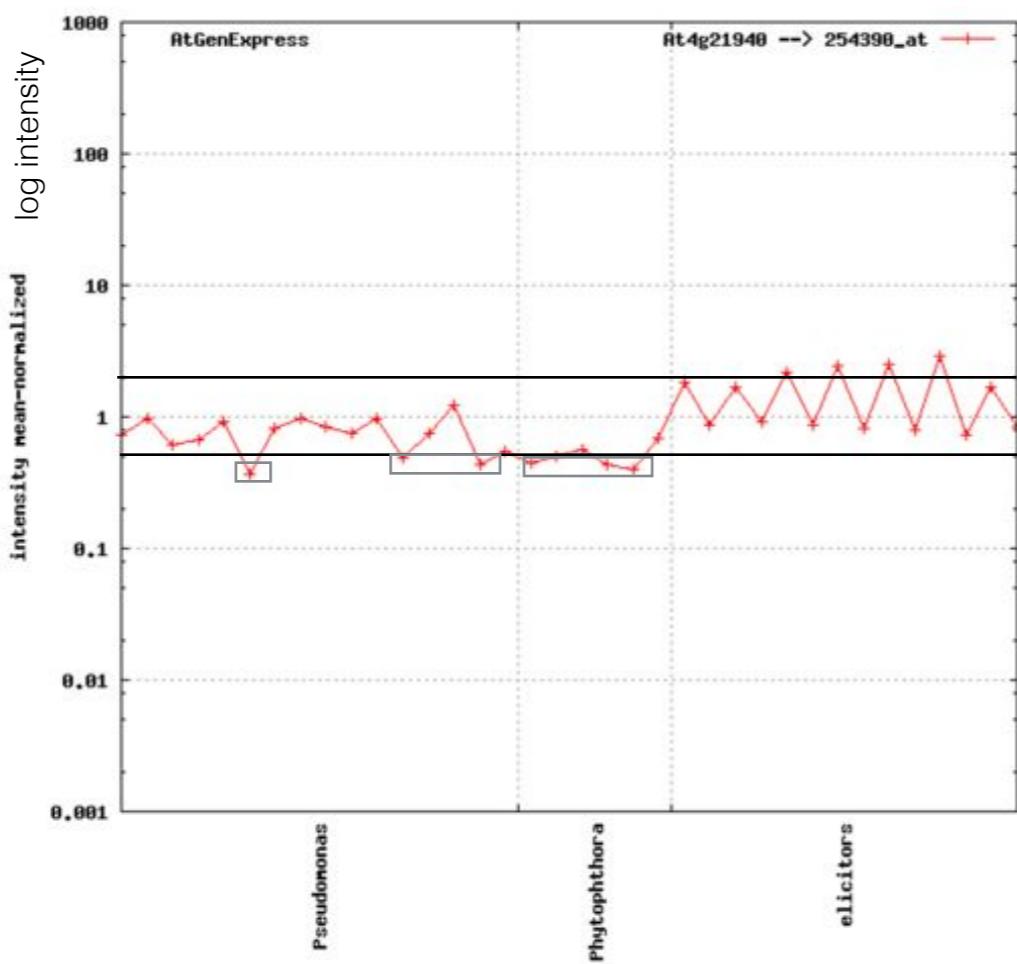
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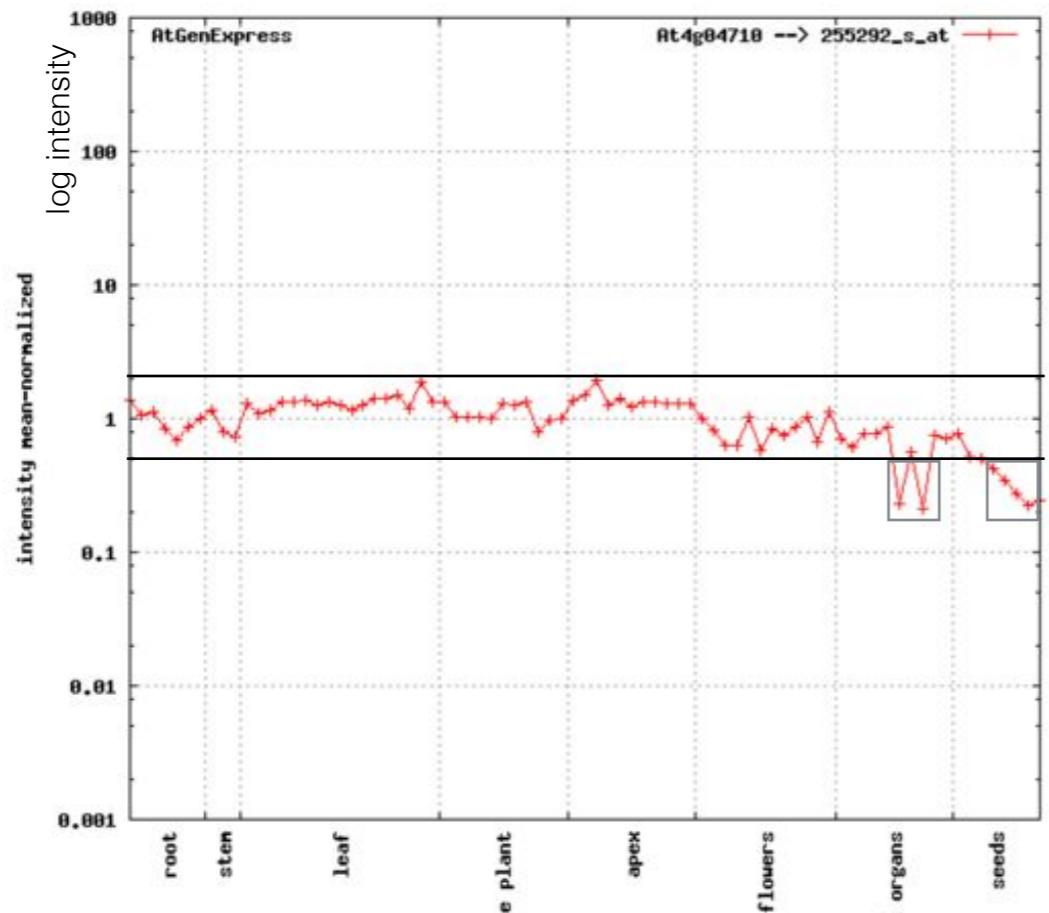
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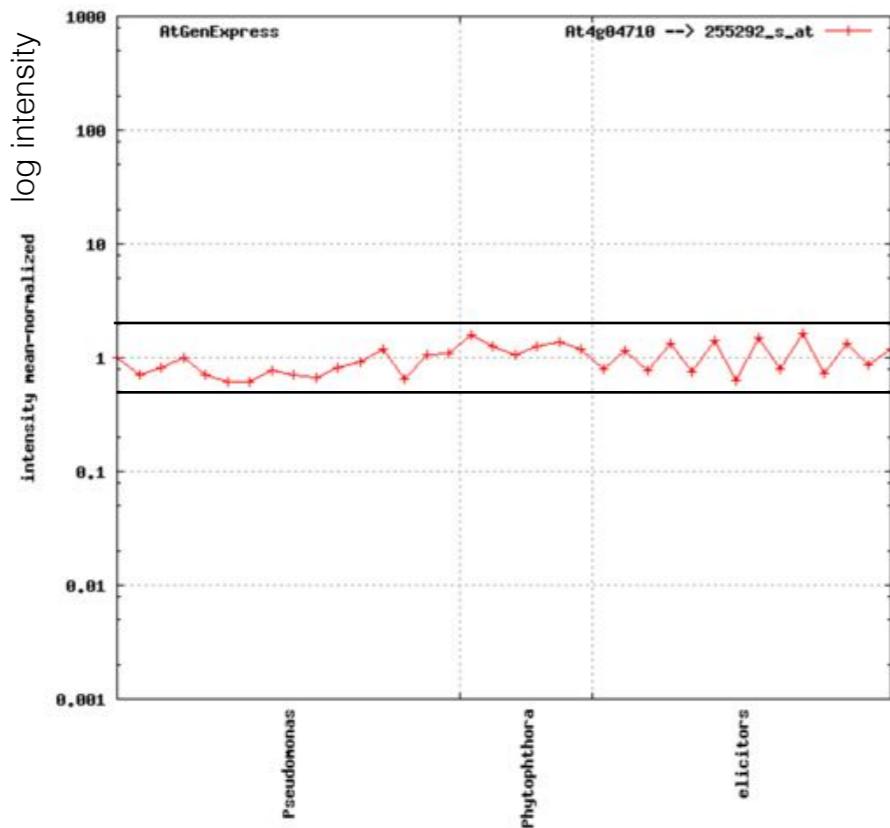
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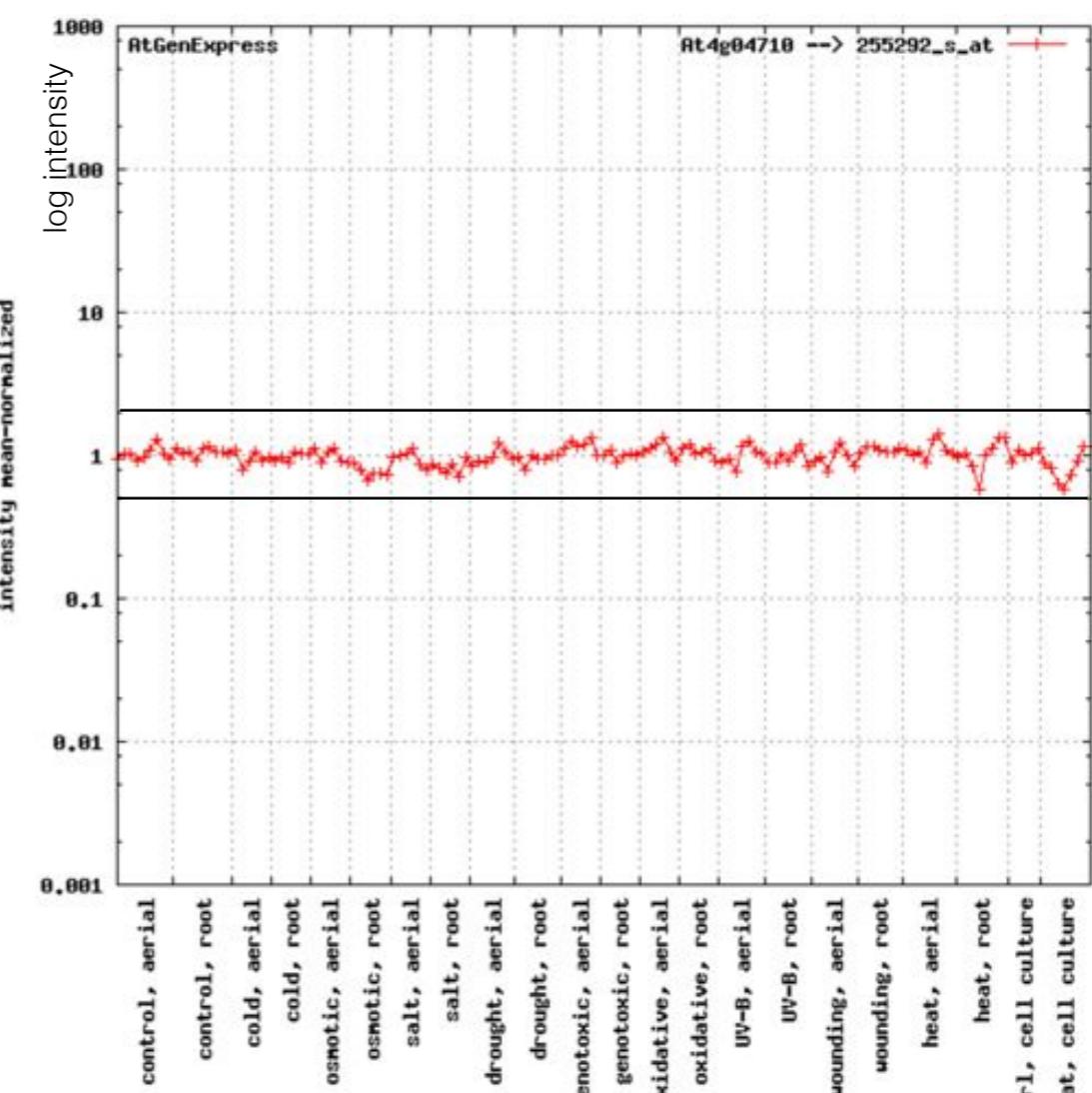
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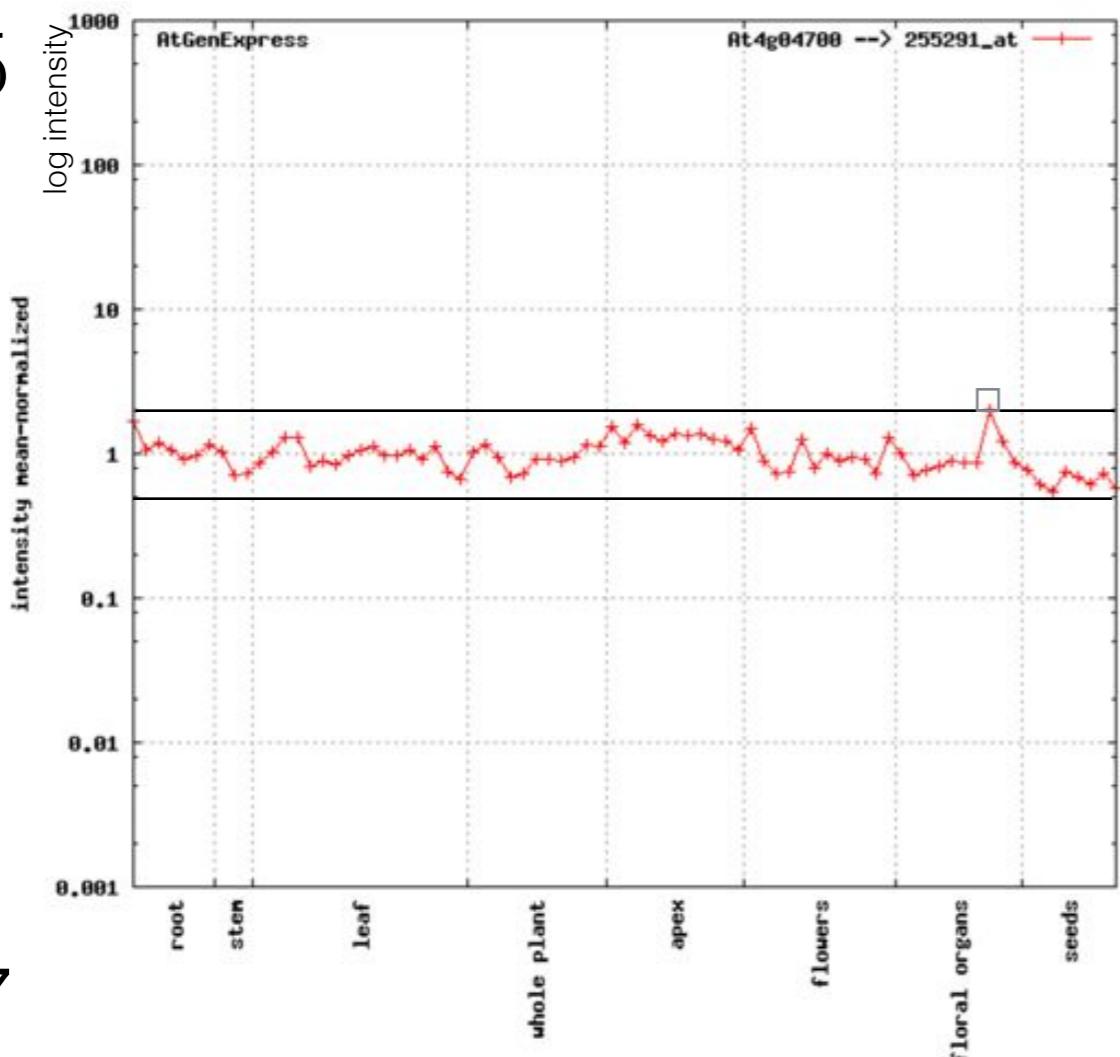
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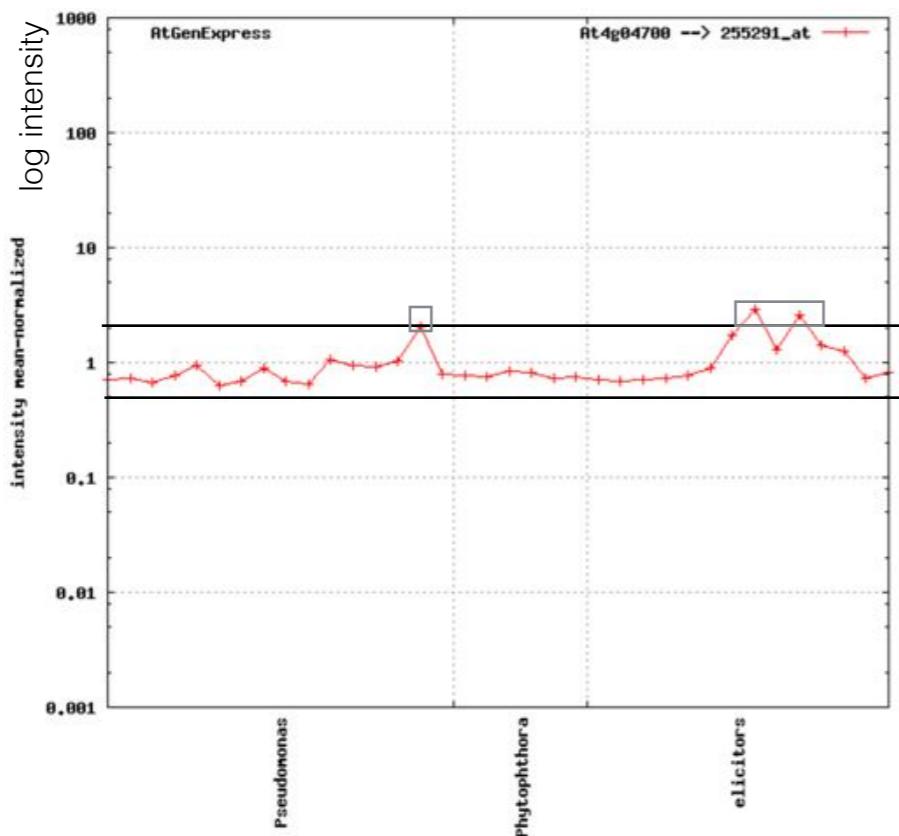
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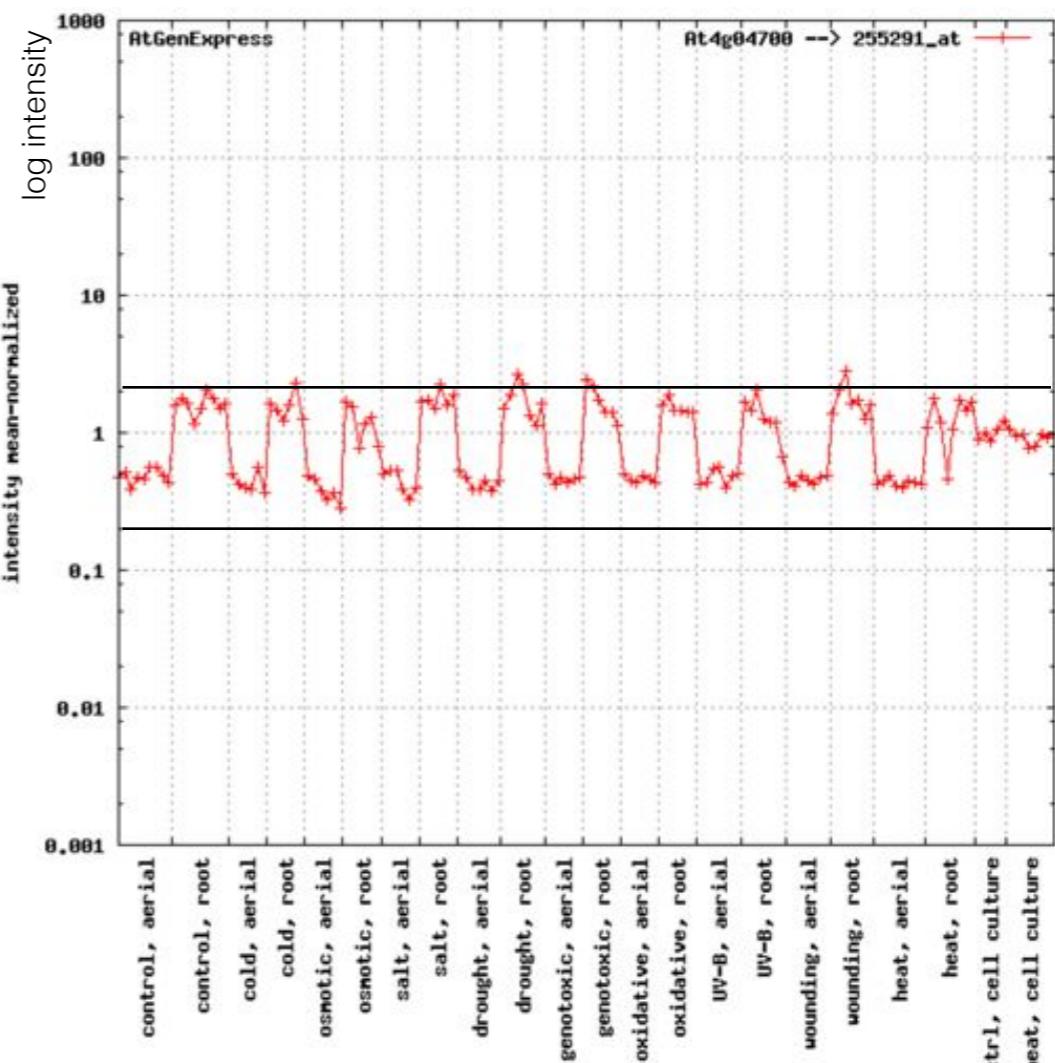
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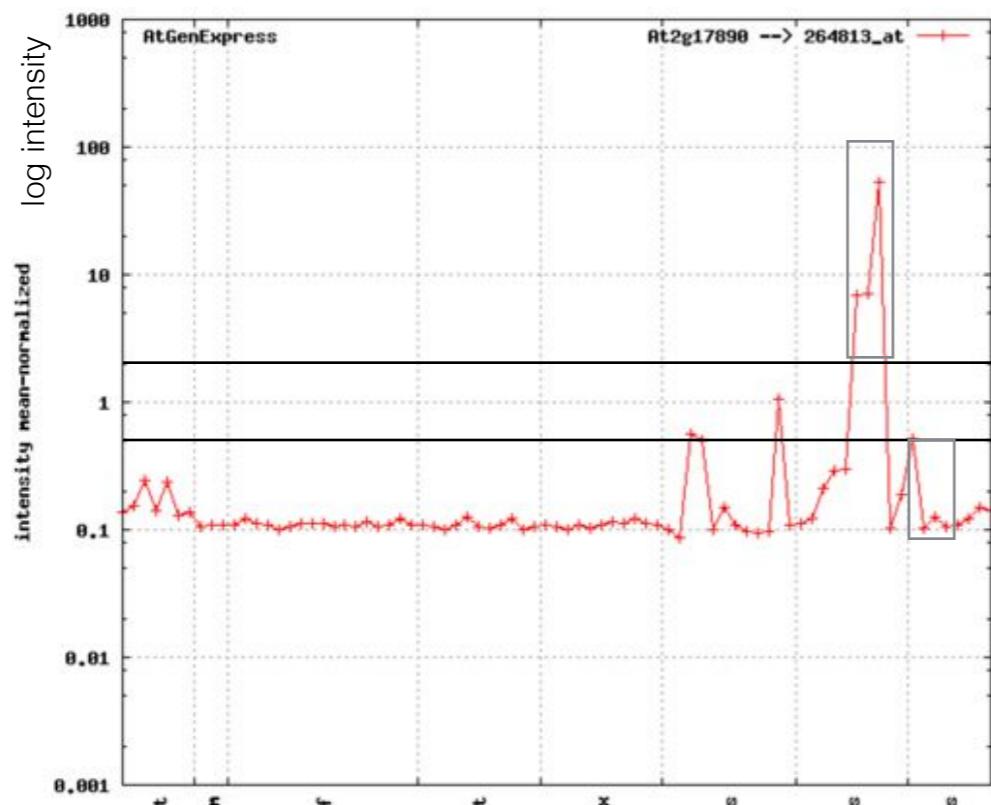
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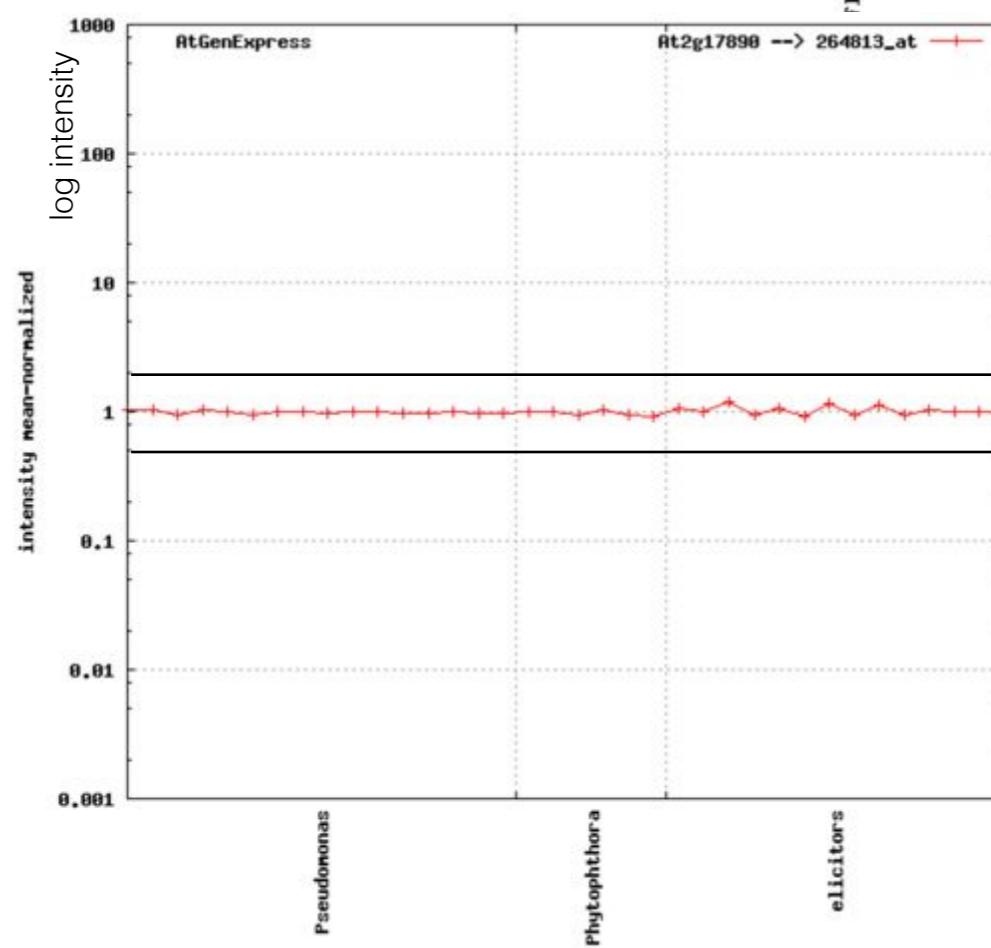
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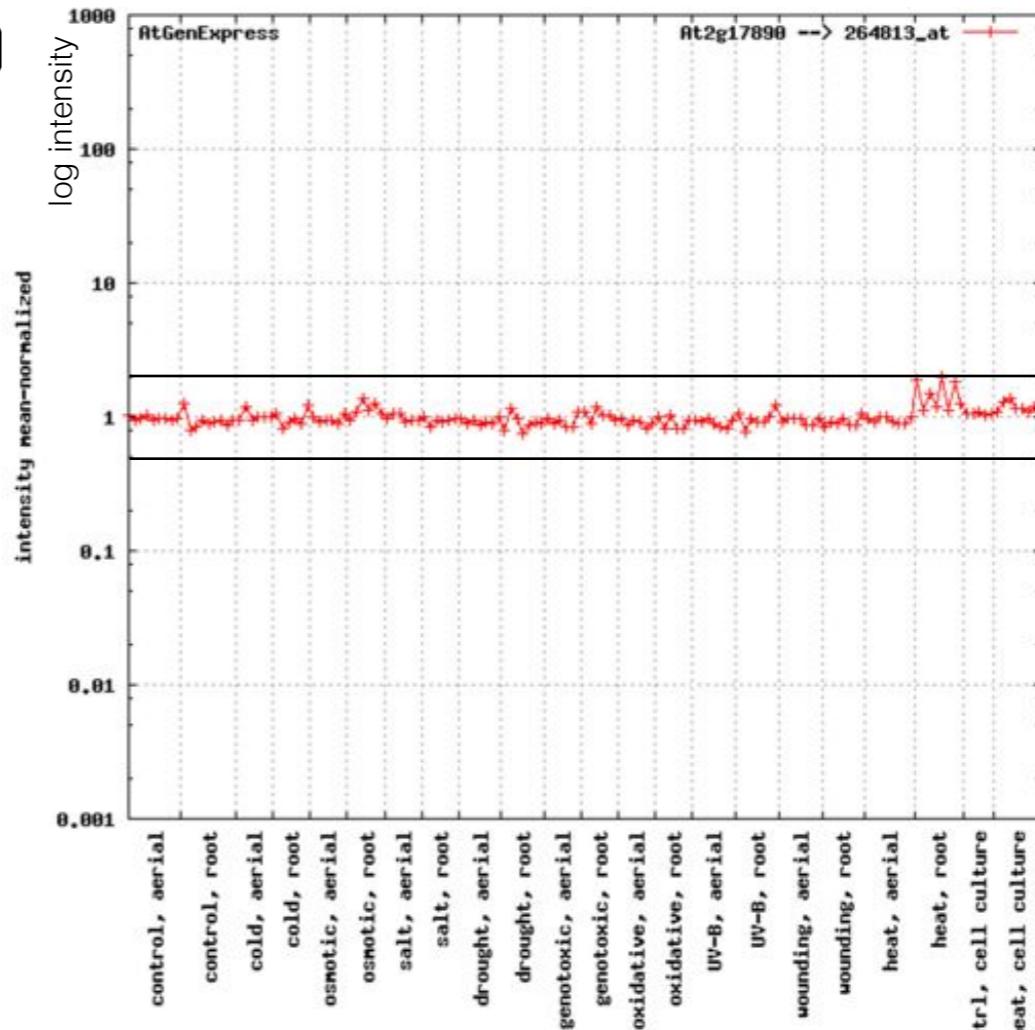
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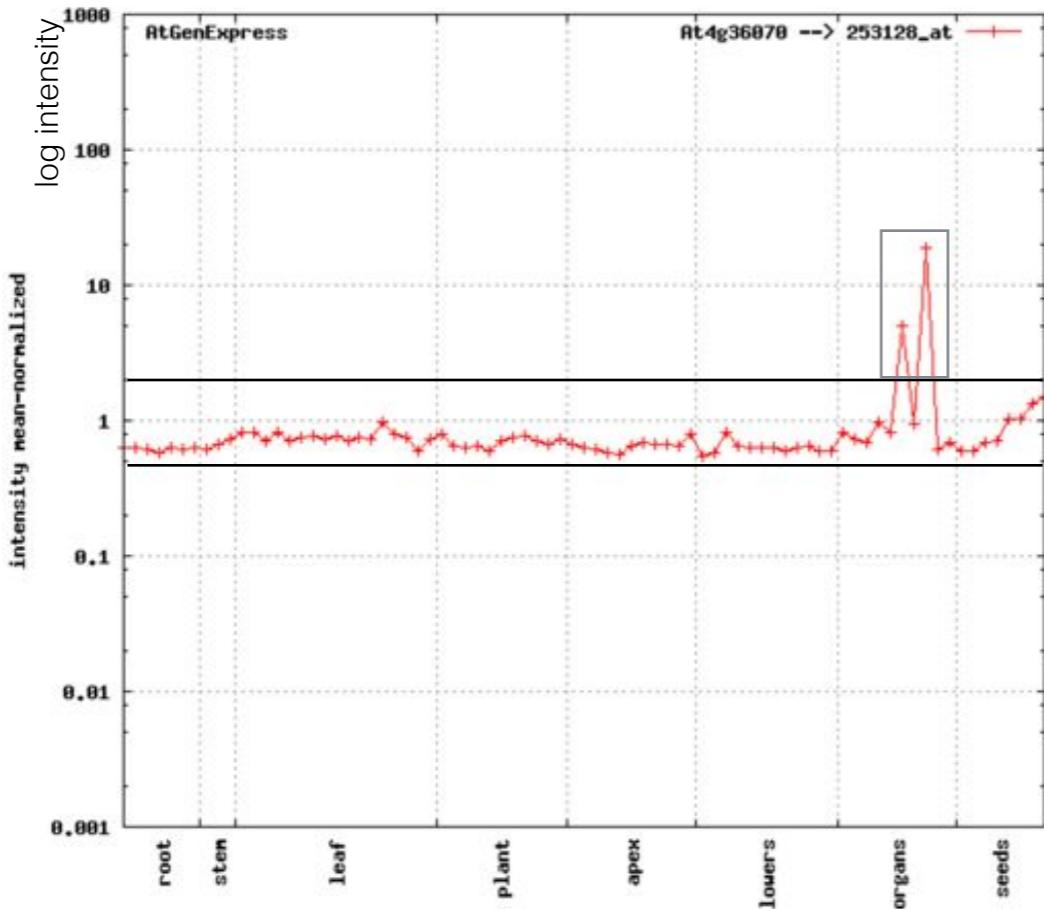
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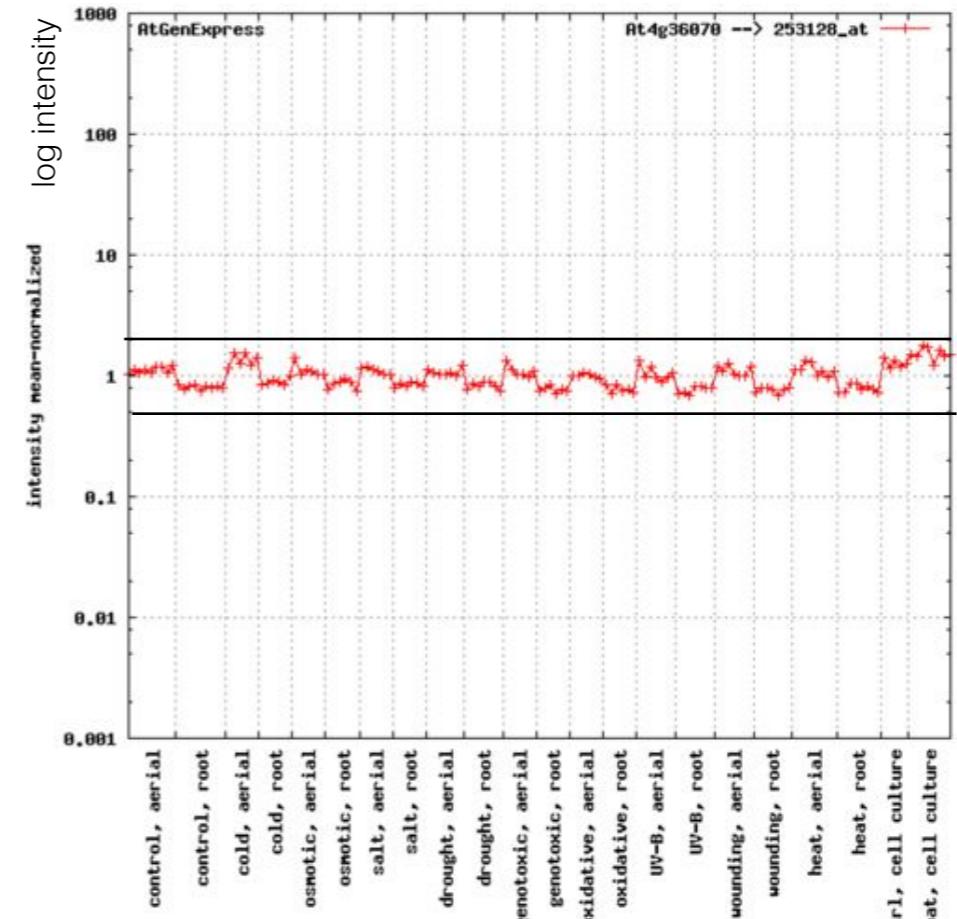
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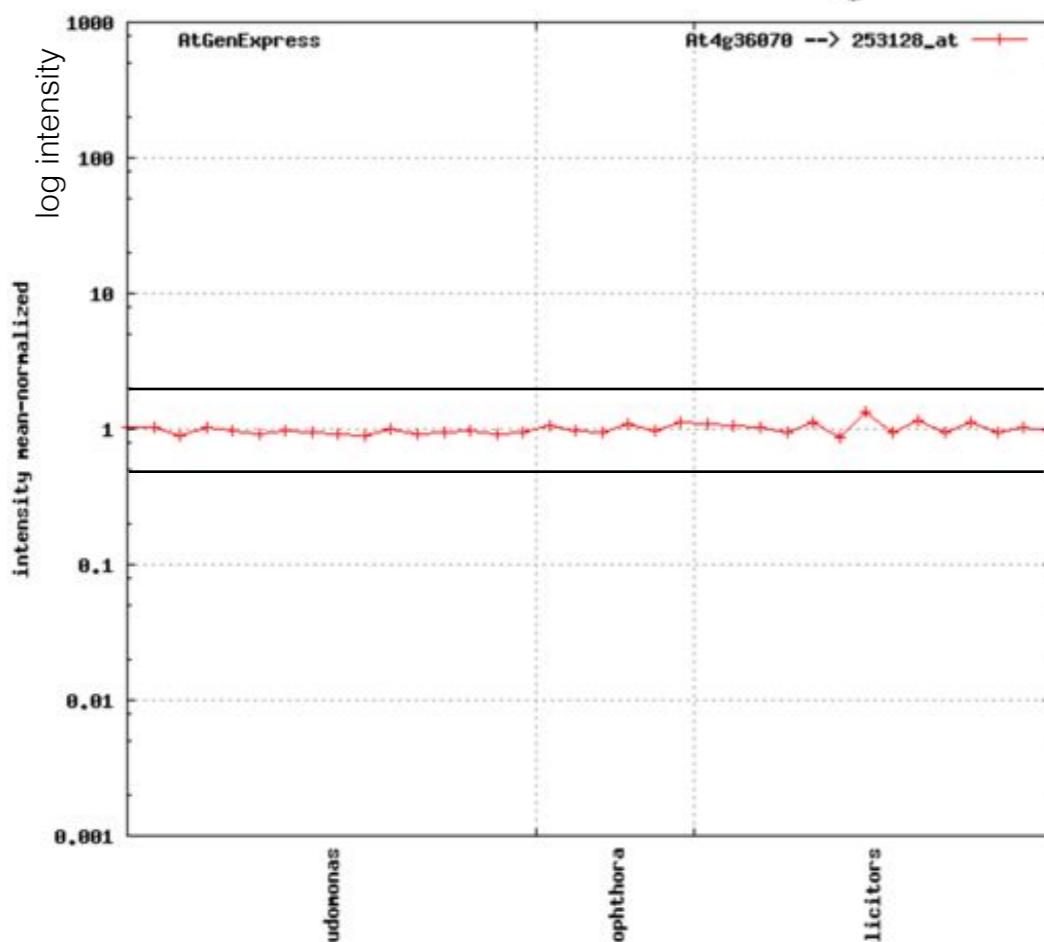
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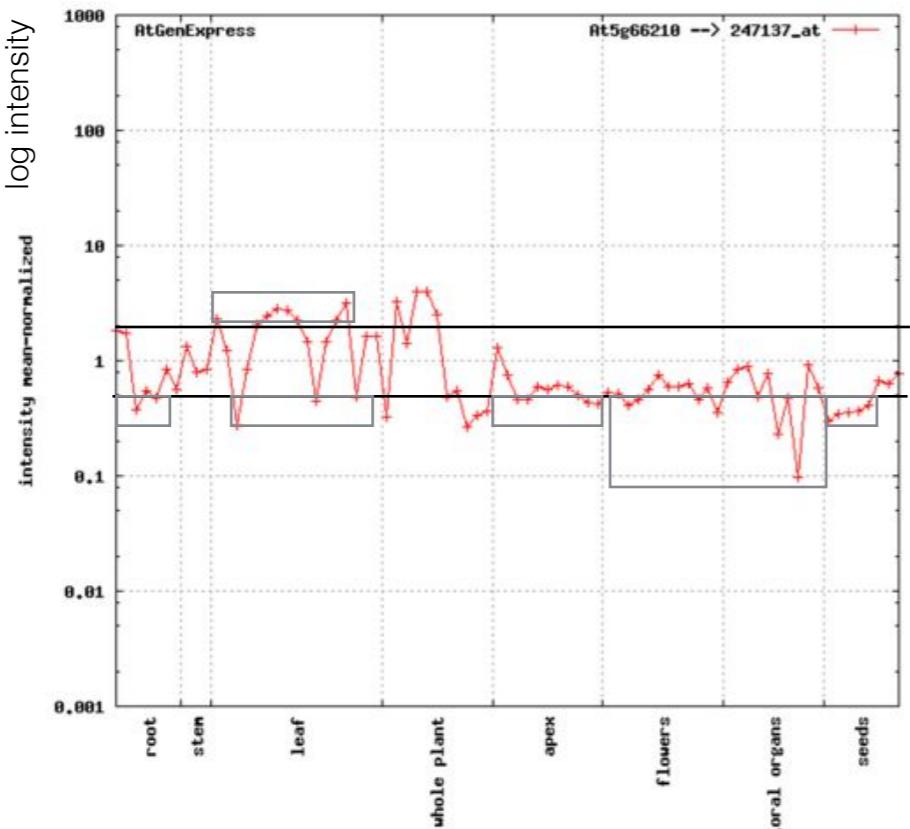
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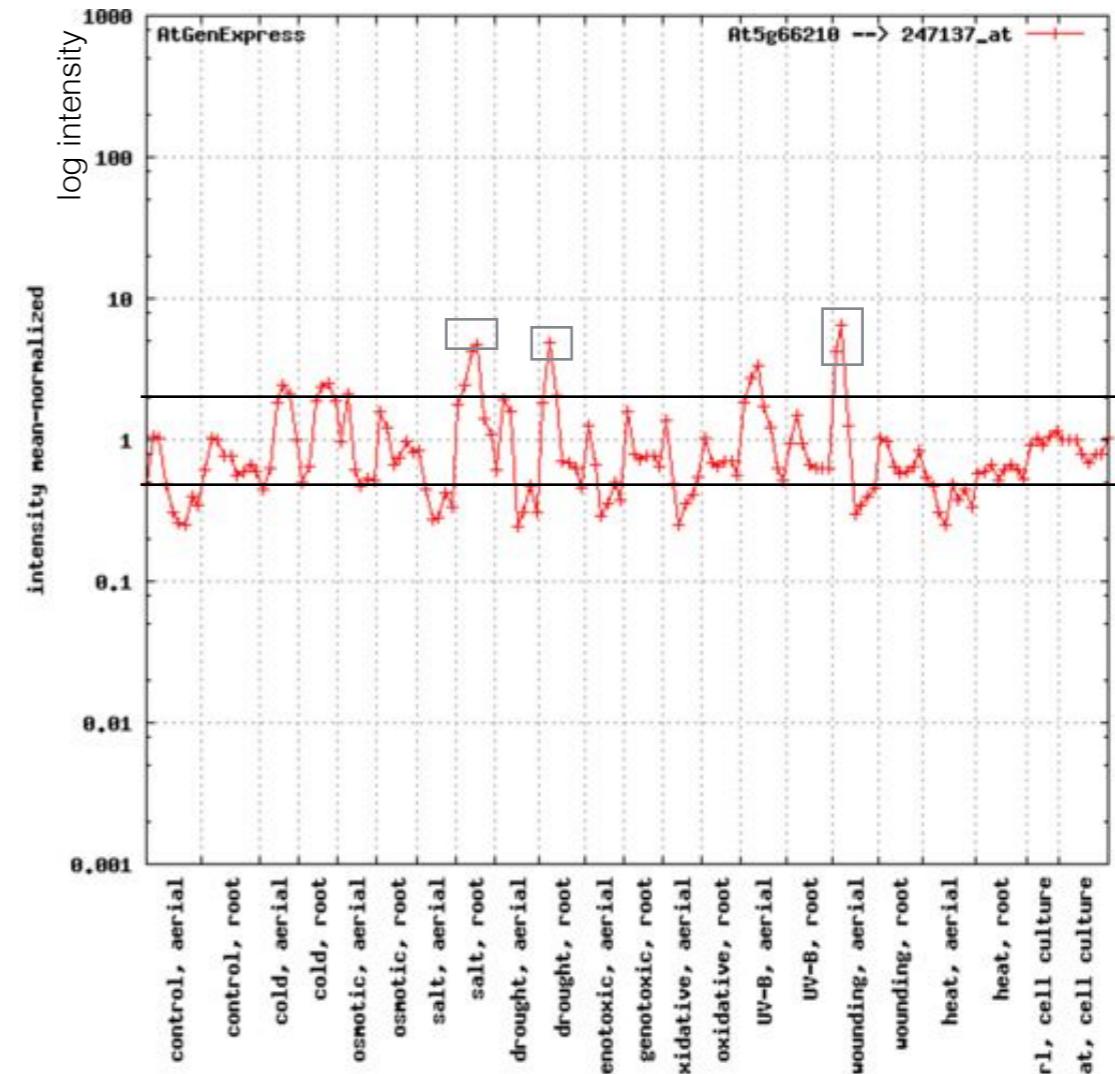
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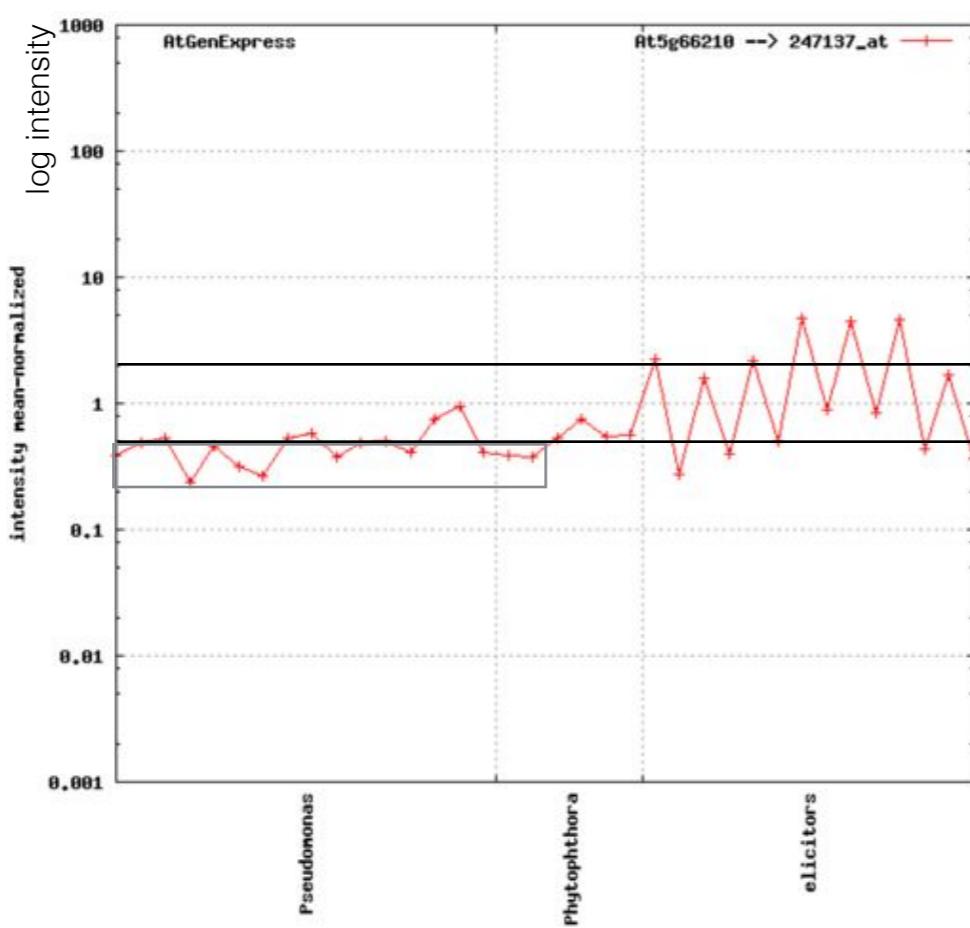
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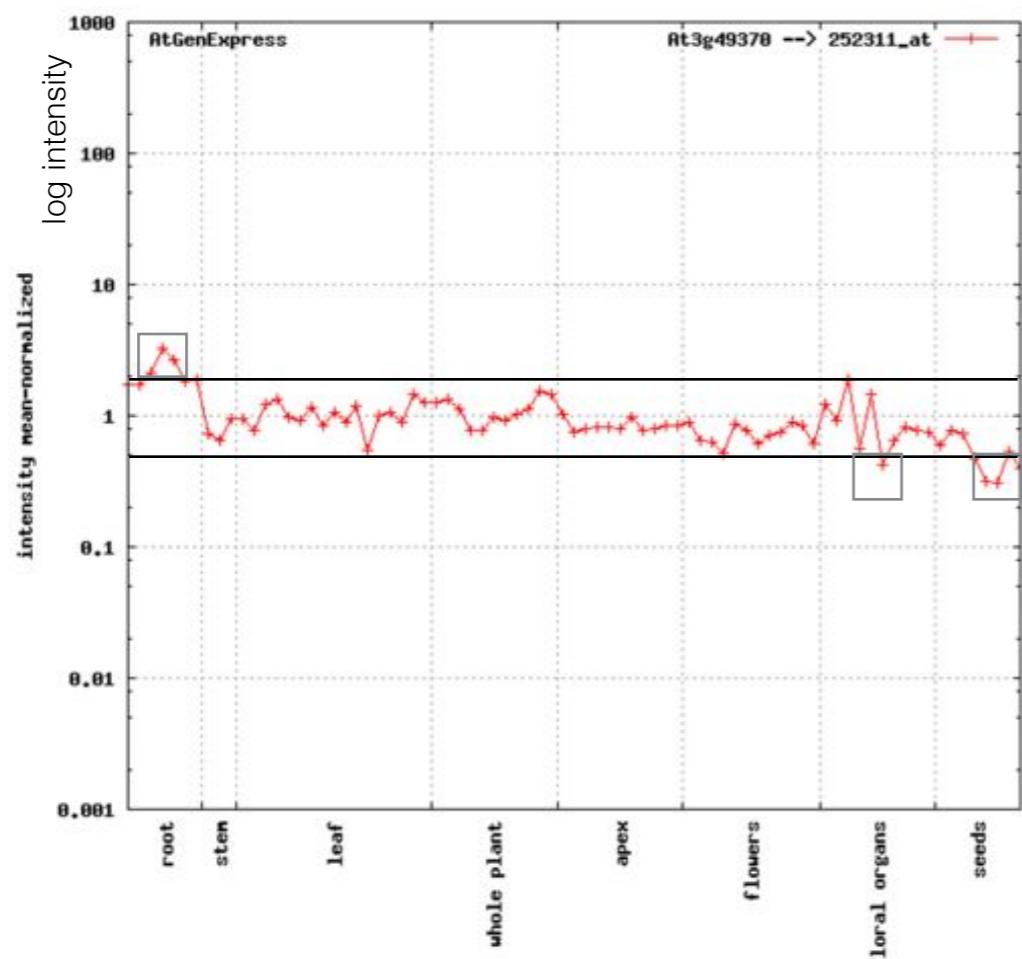
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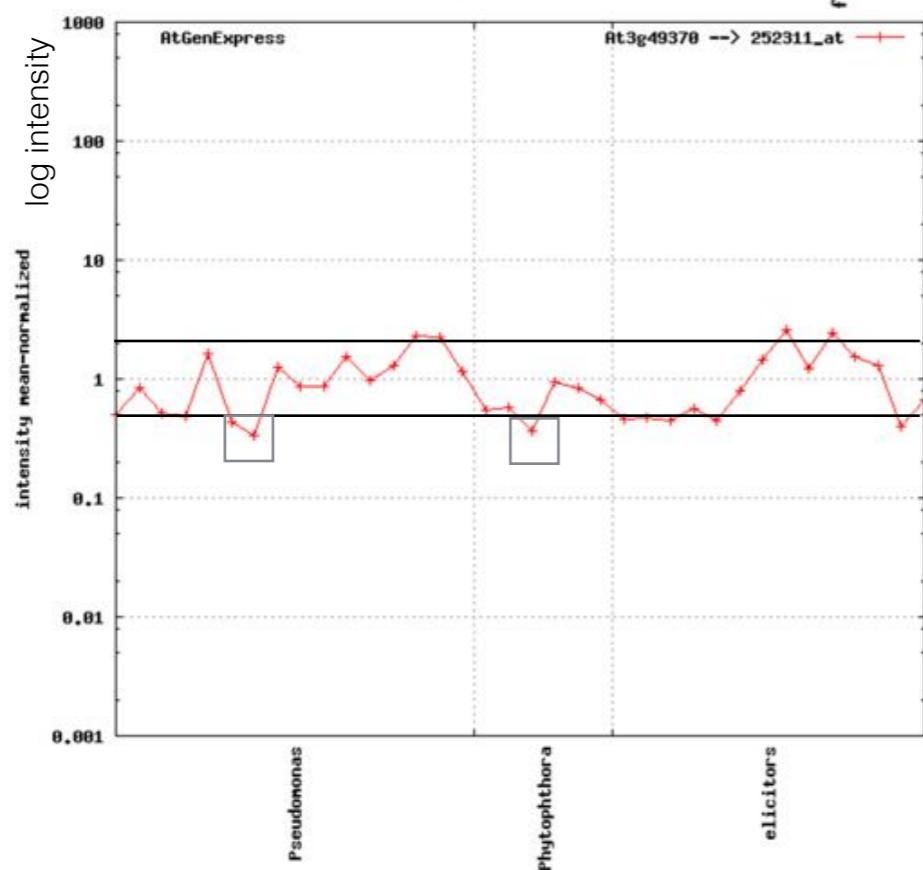
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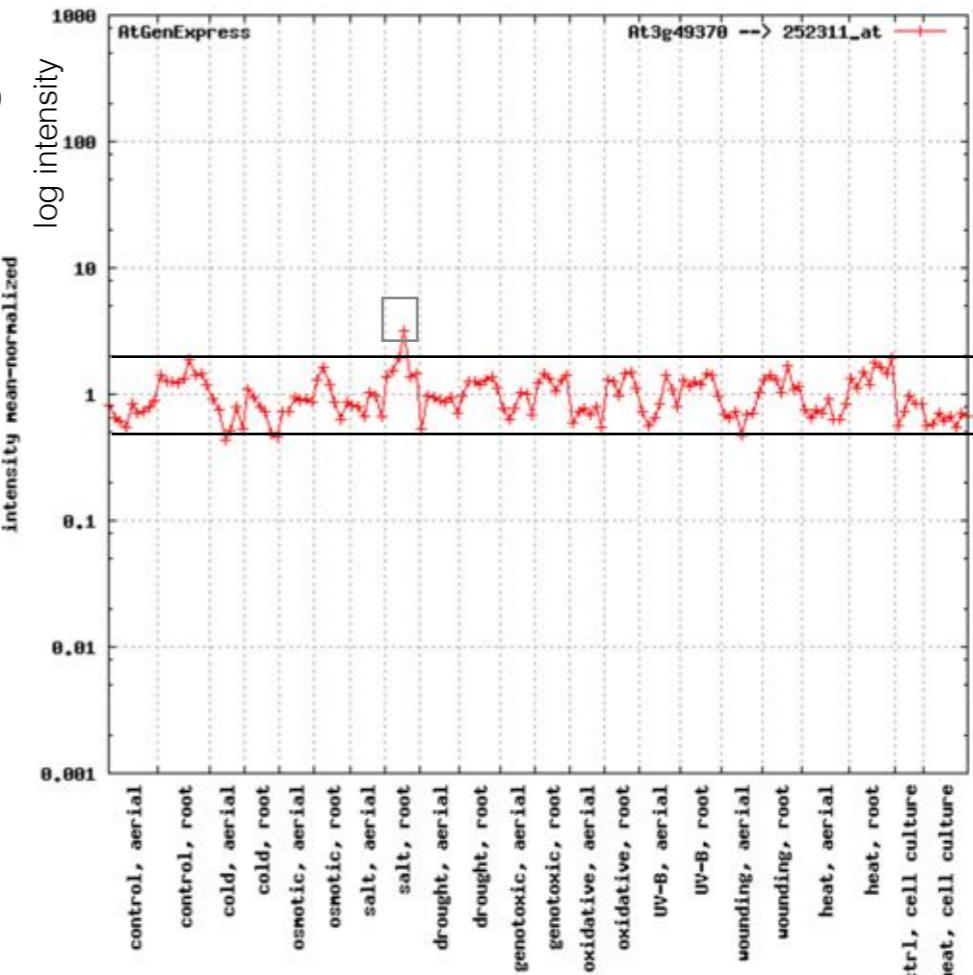
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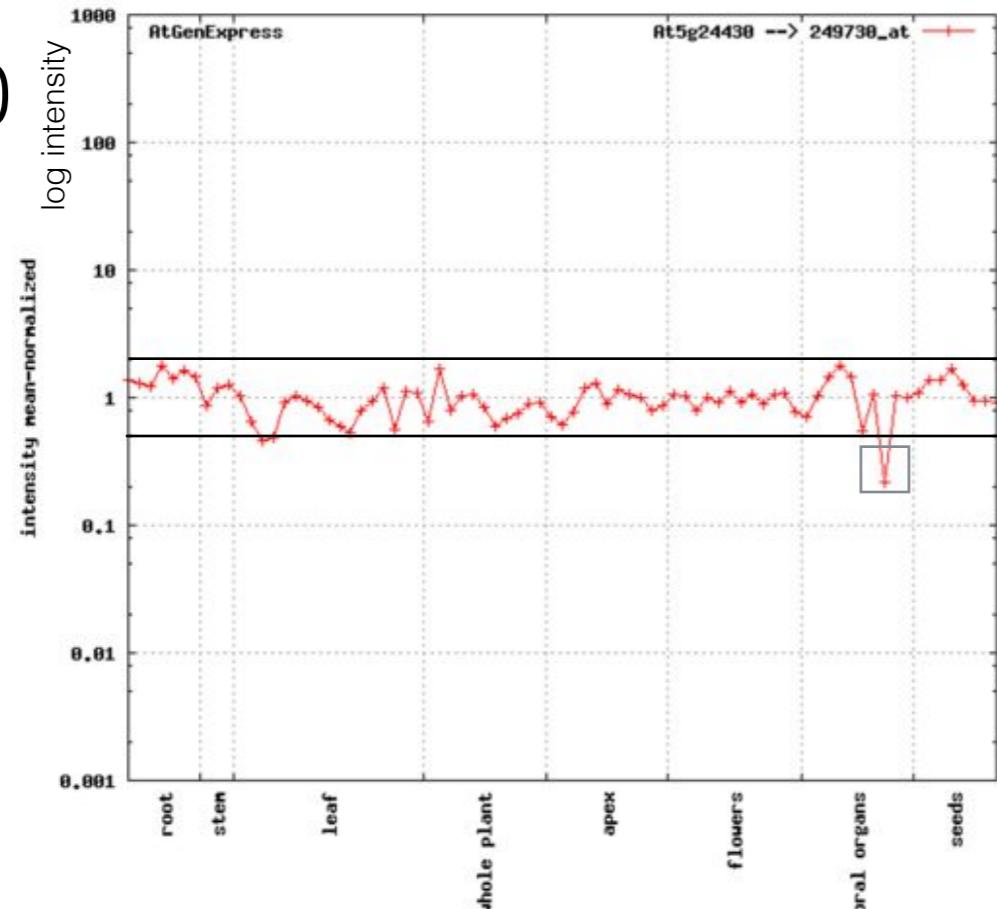
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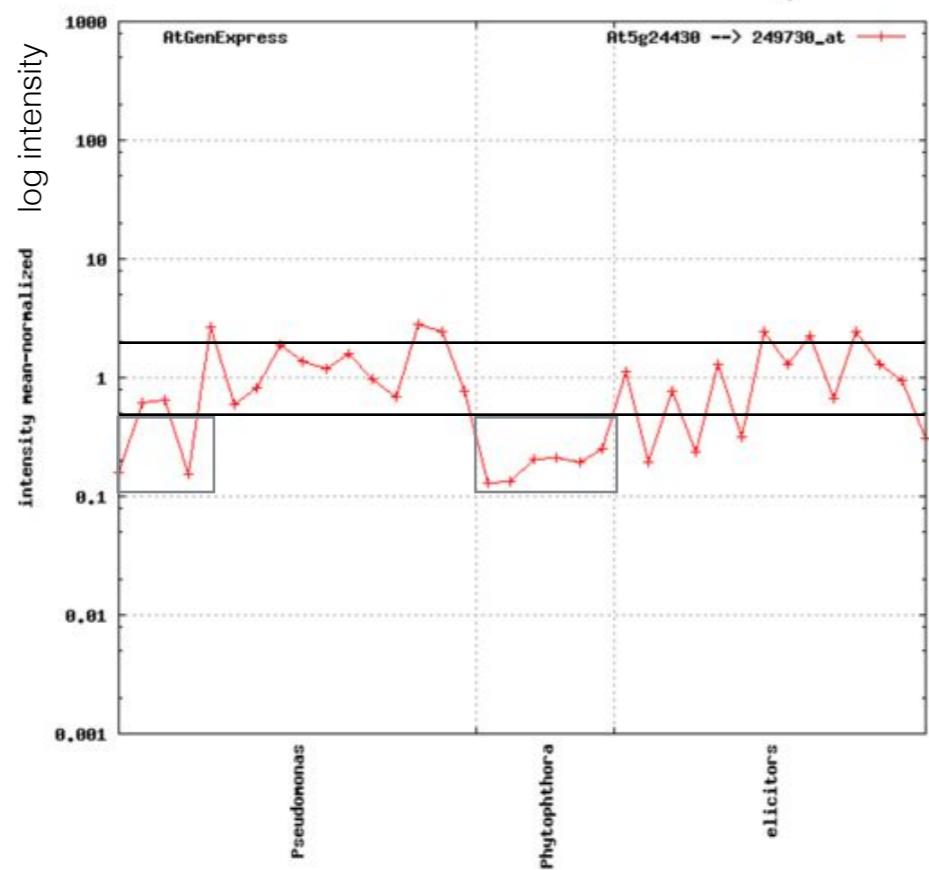
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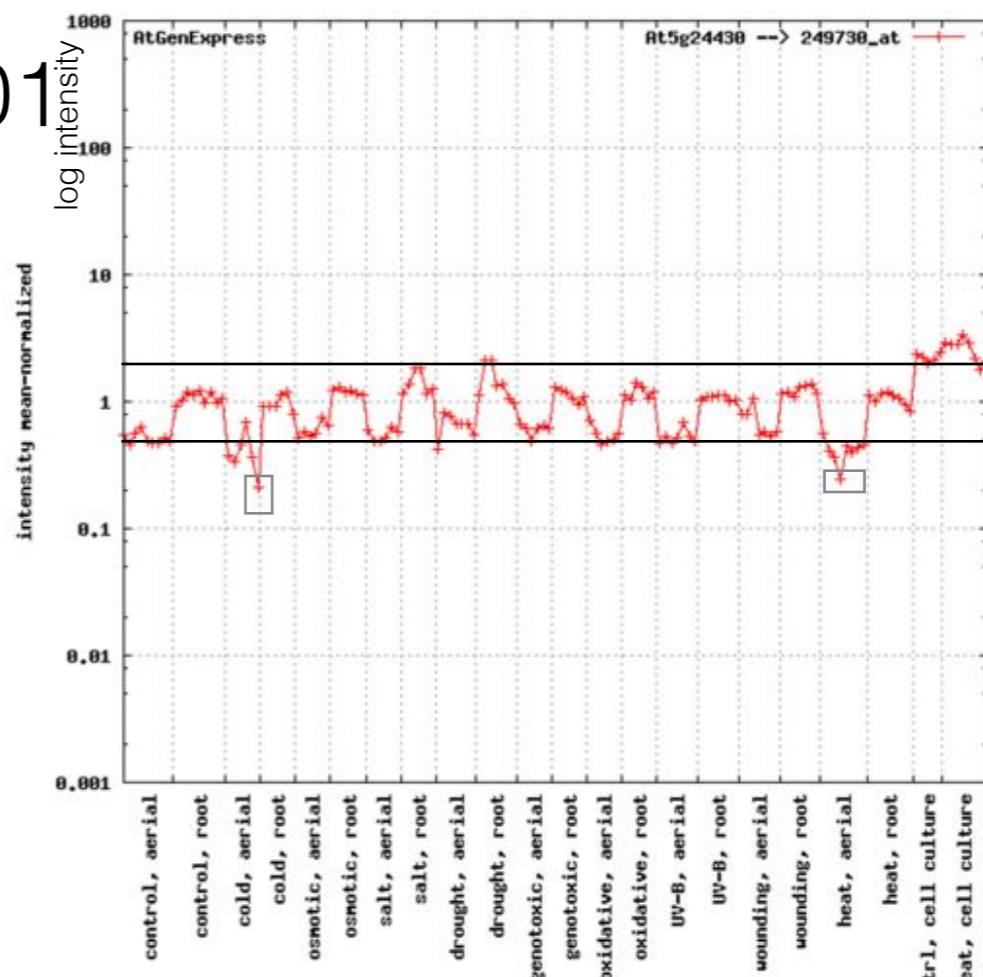
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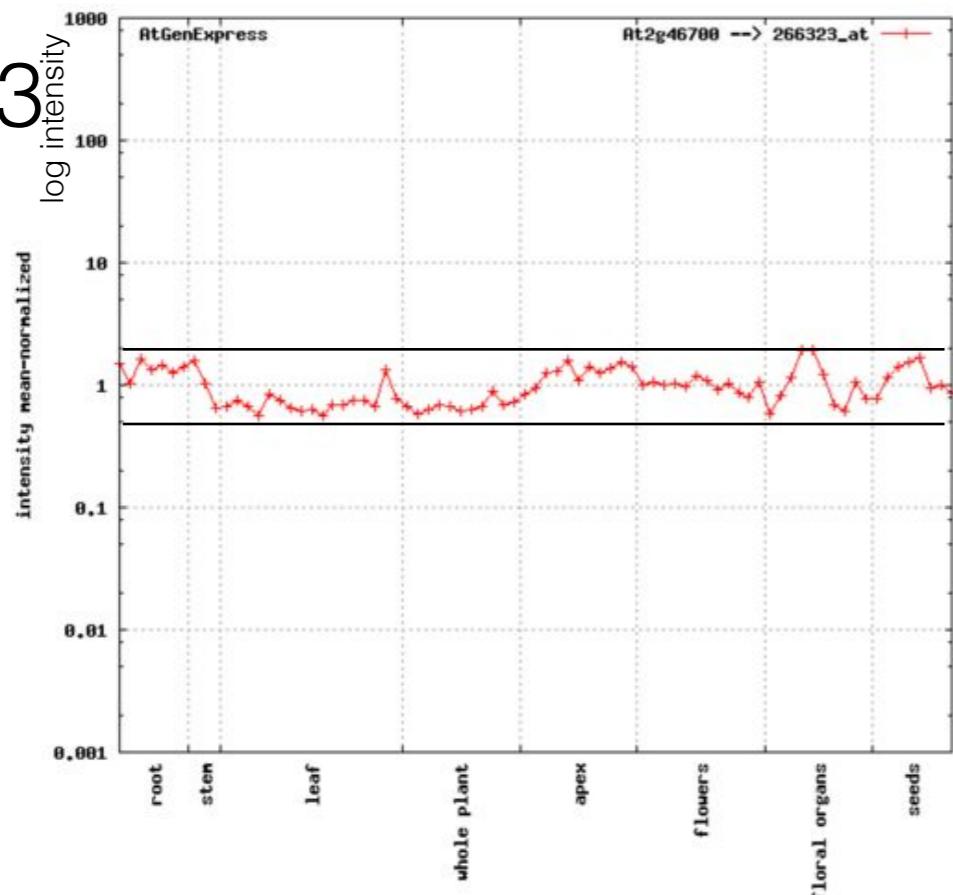
102



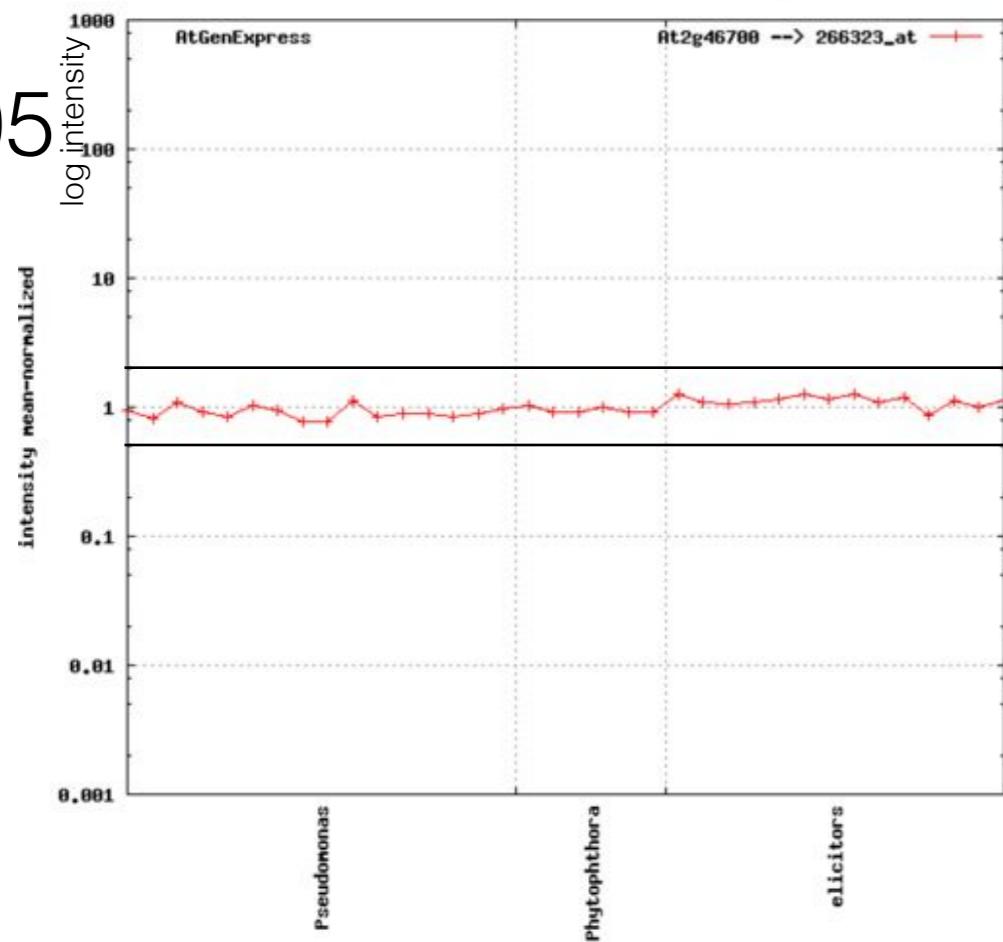
101



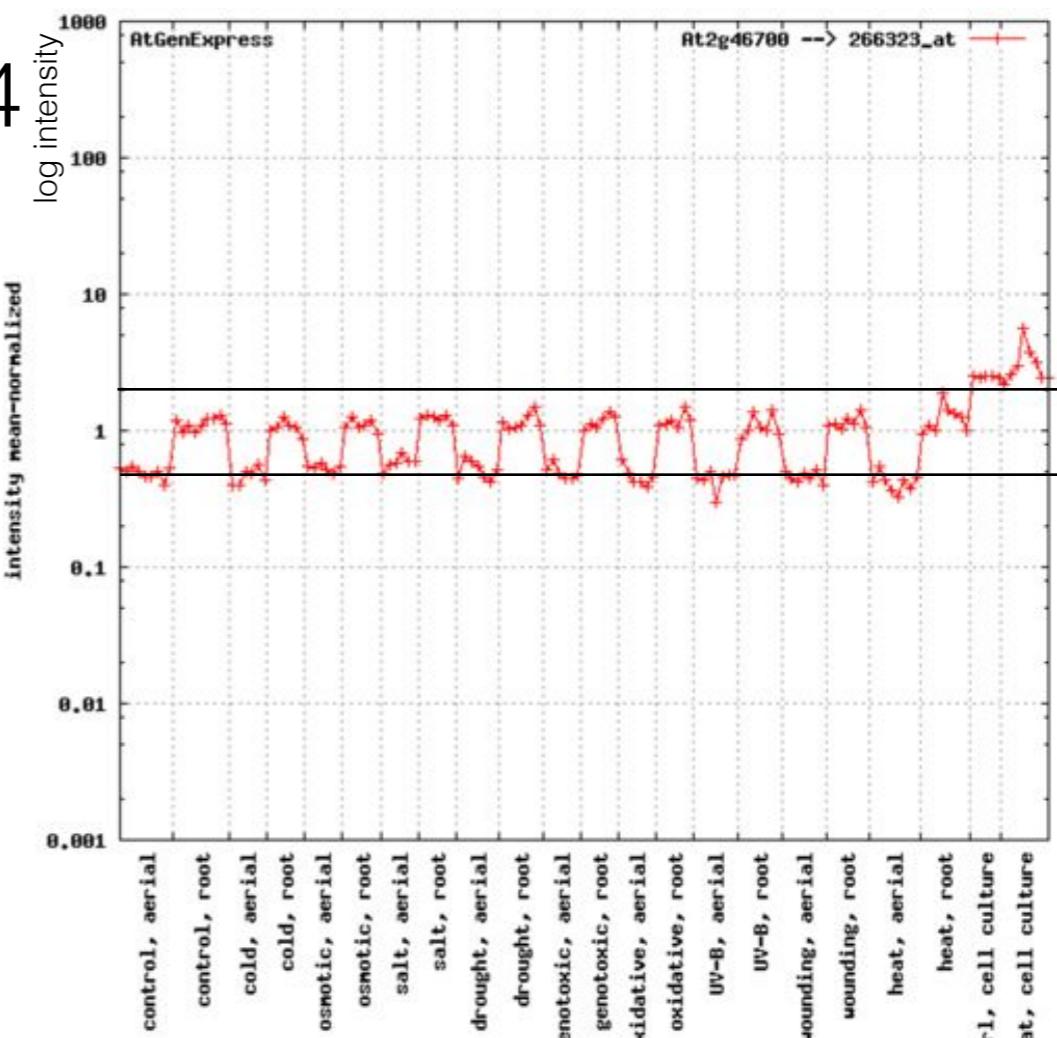
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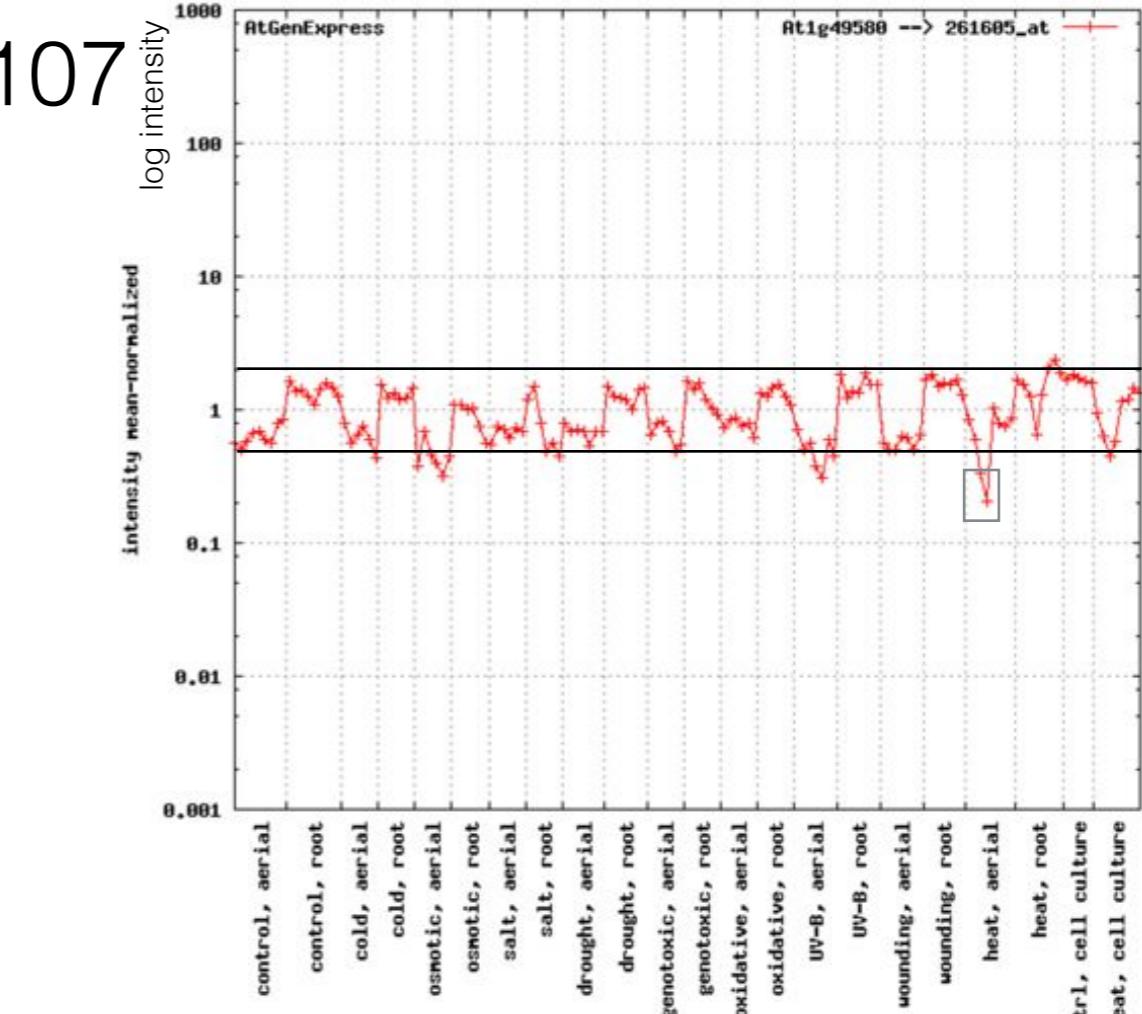
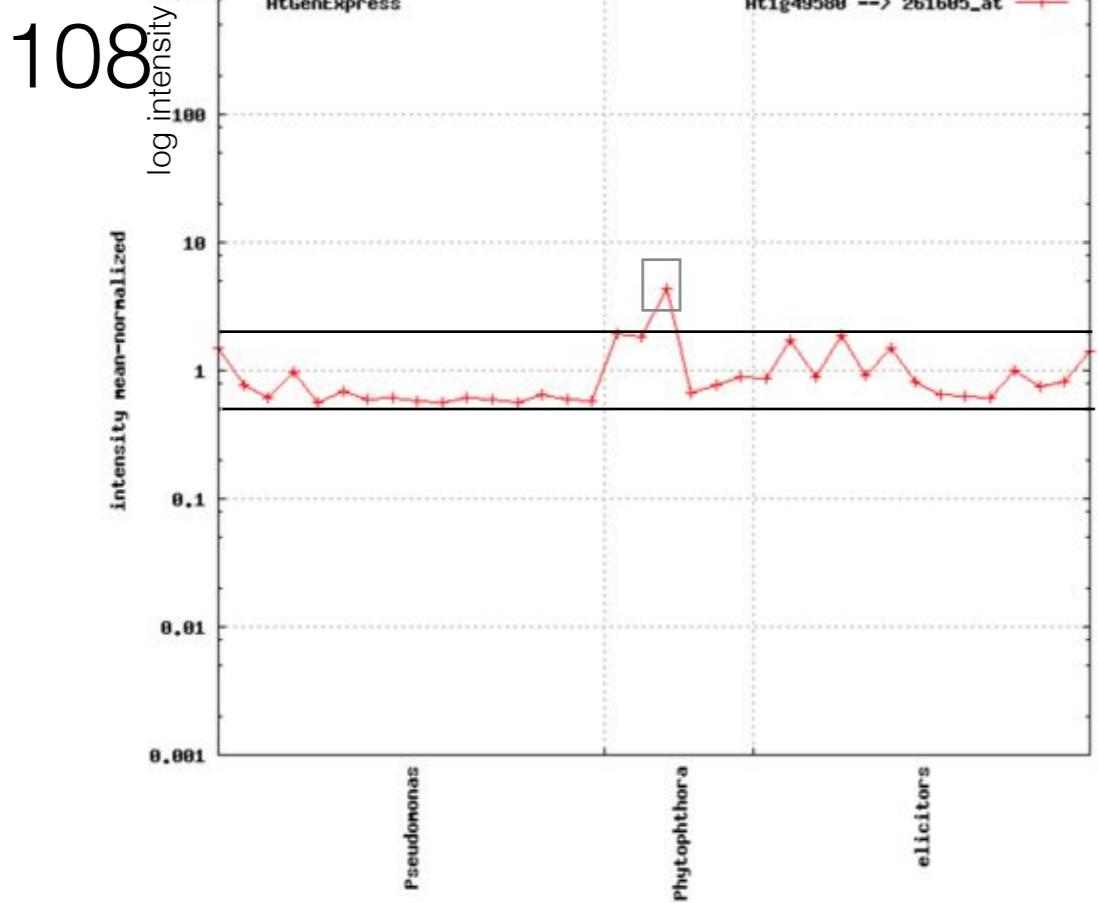
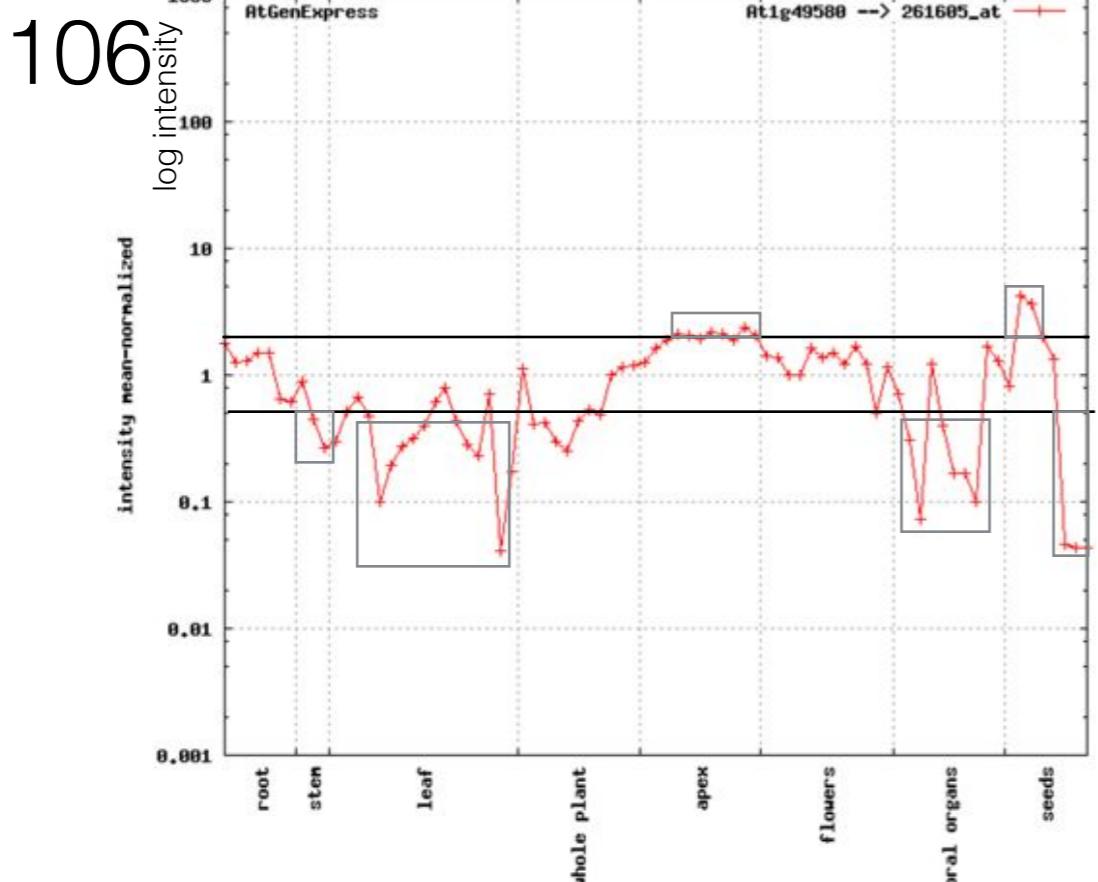


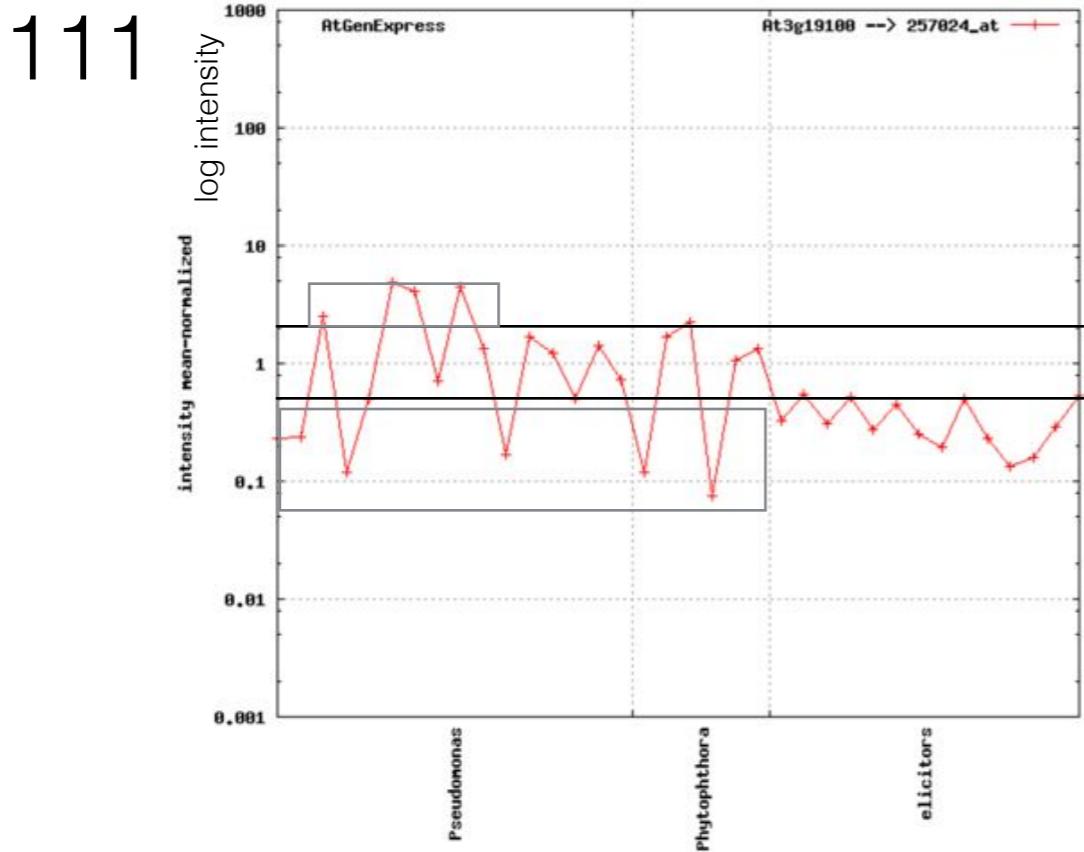
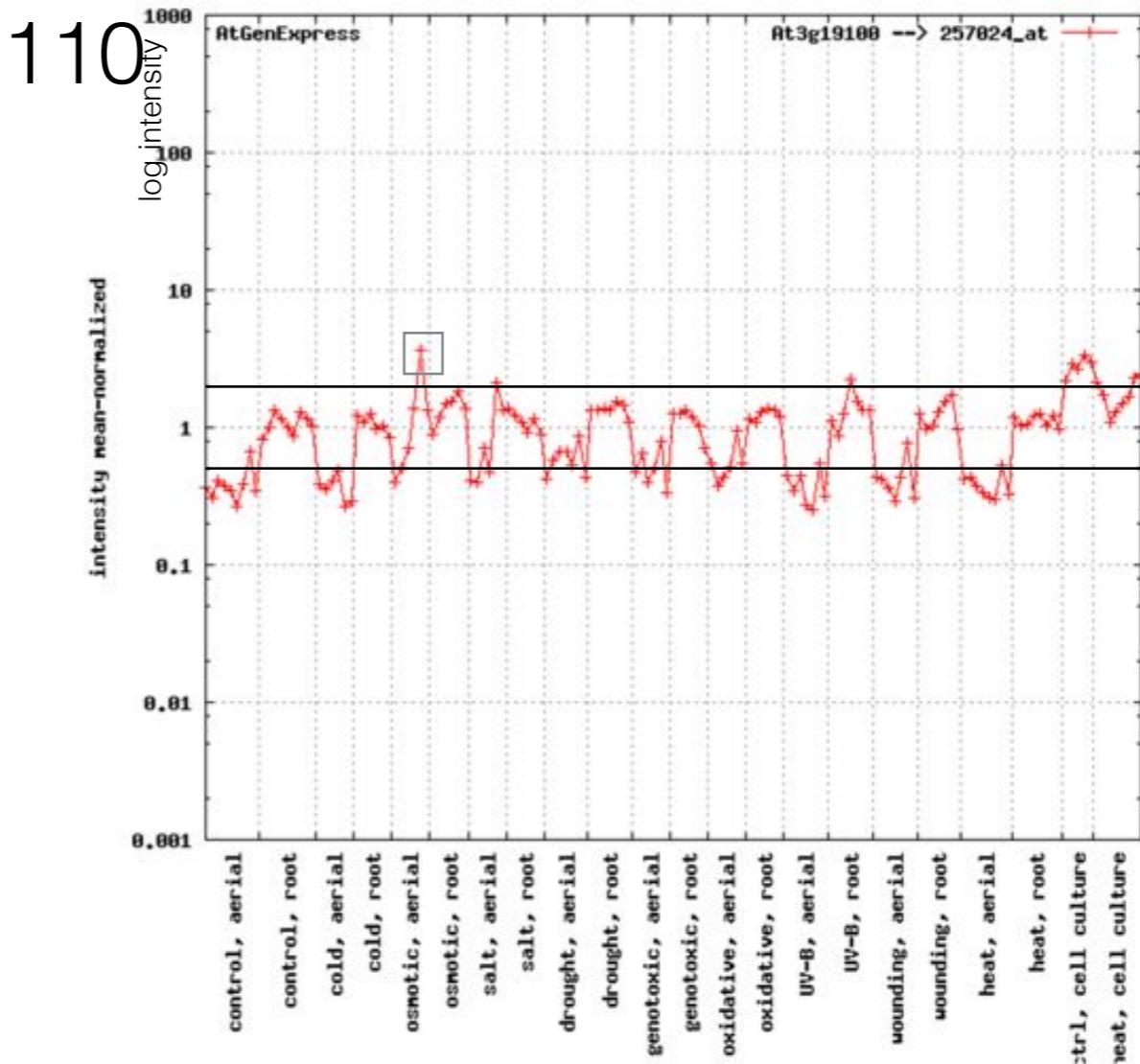
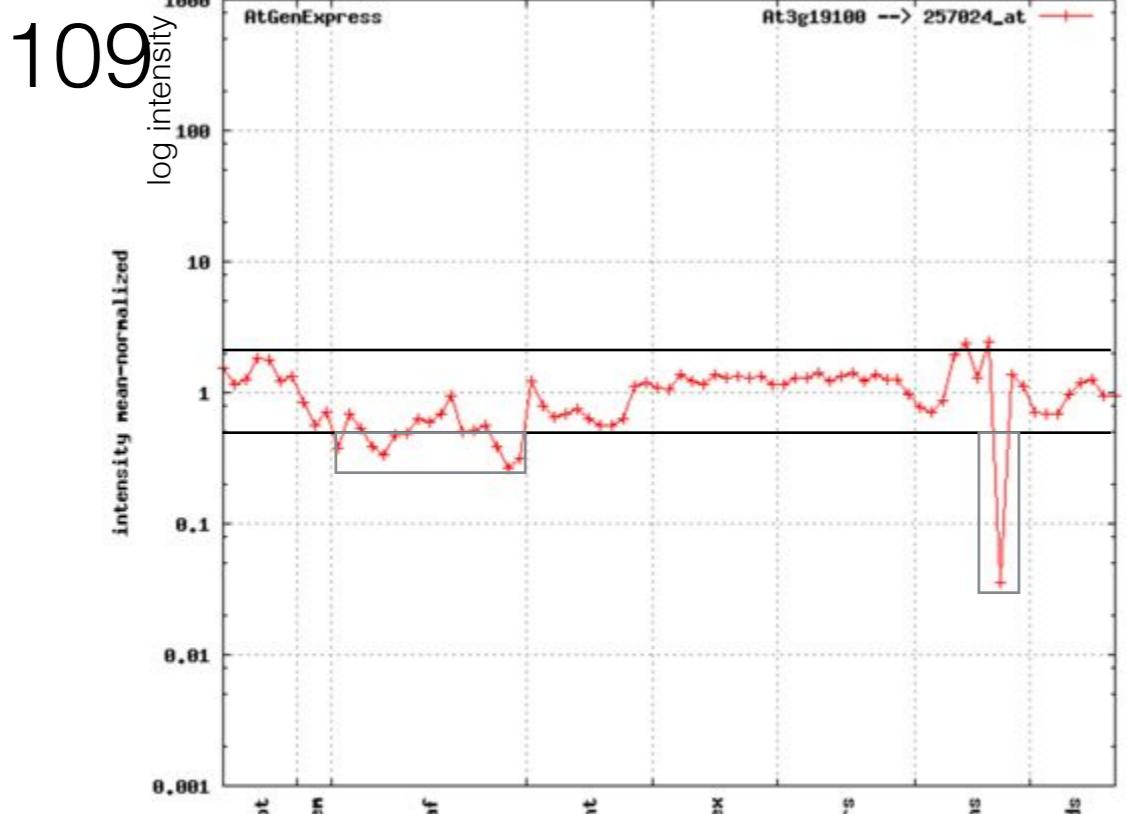
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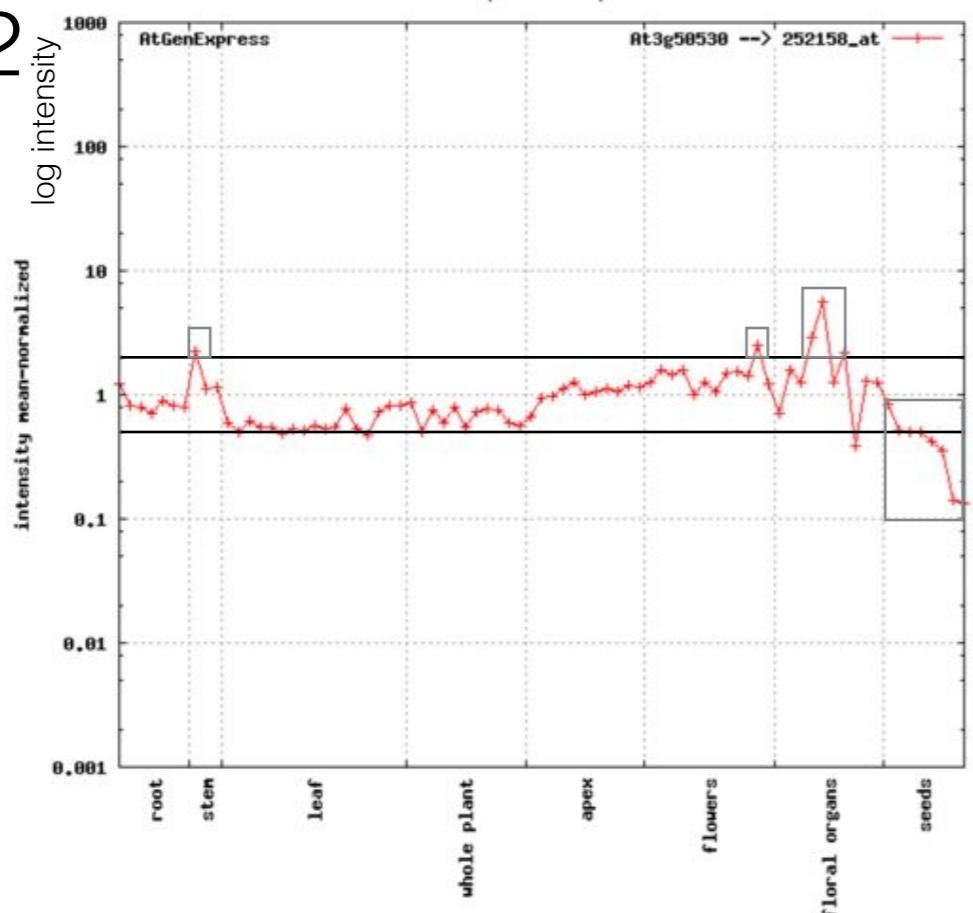
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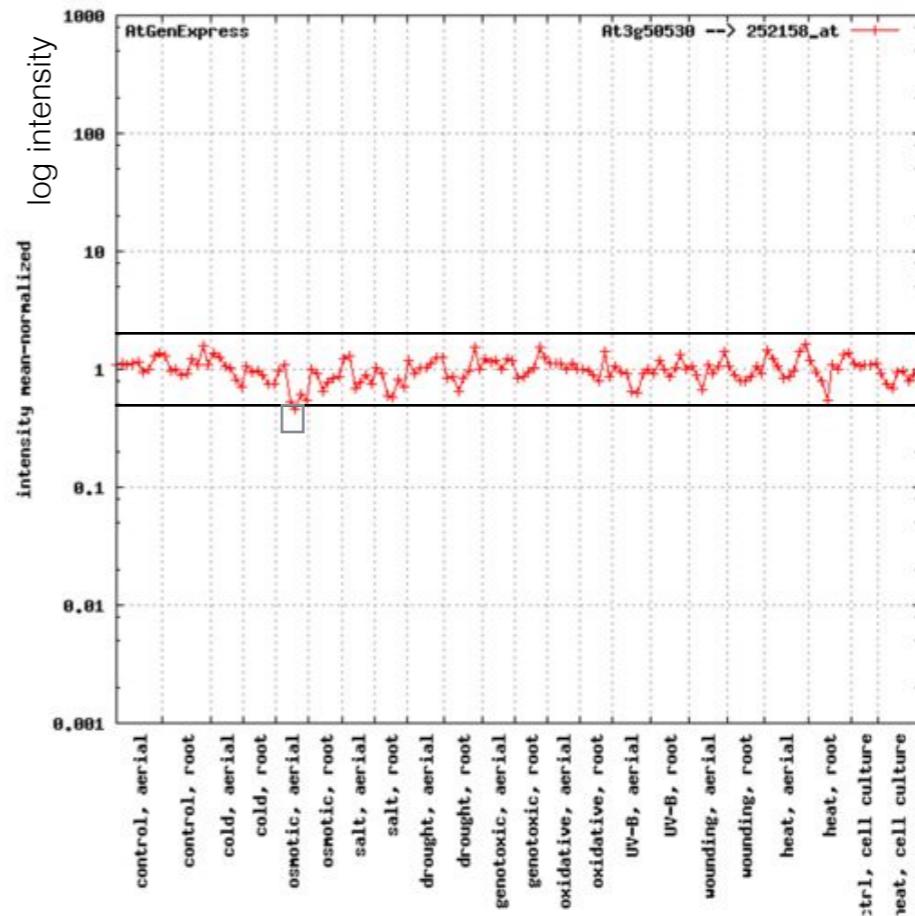




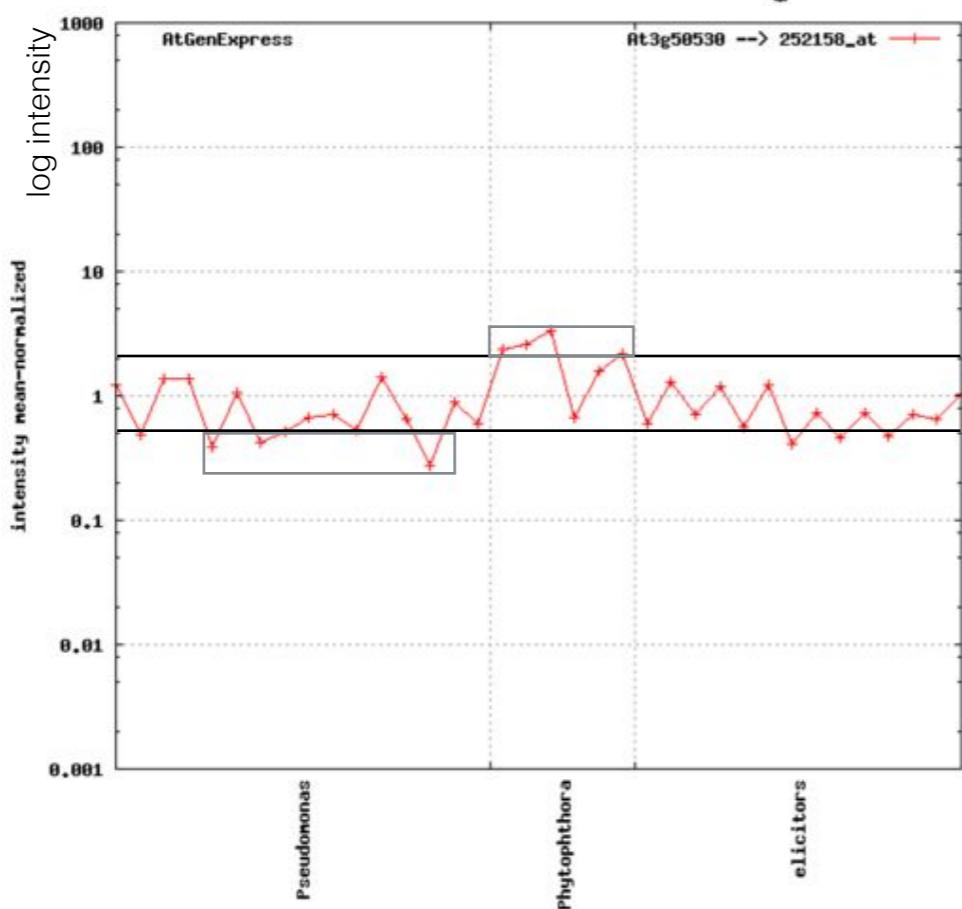
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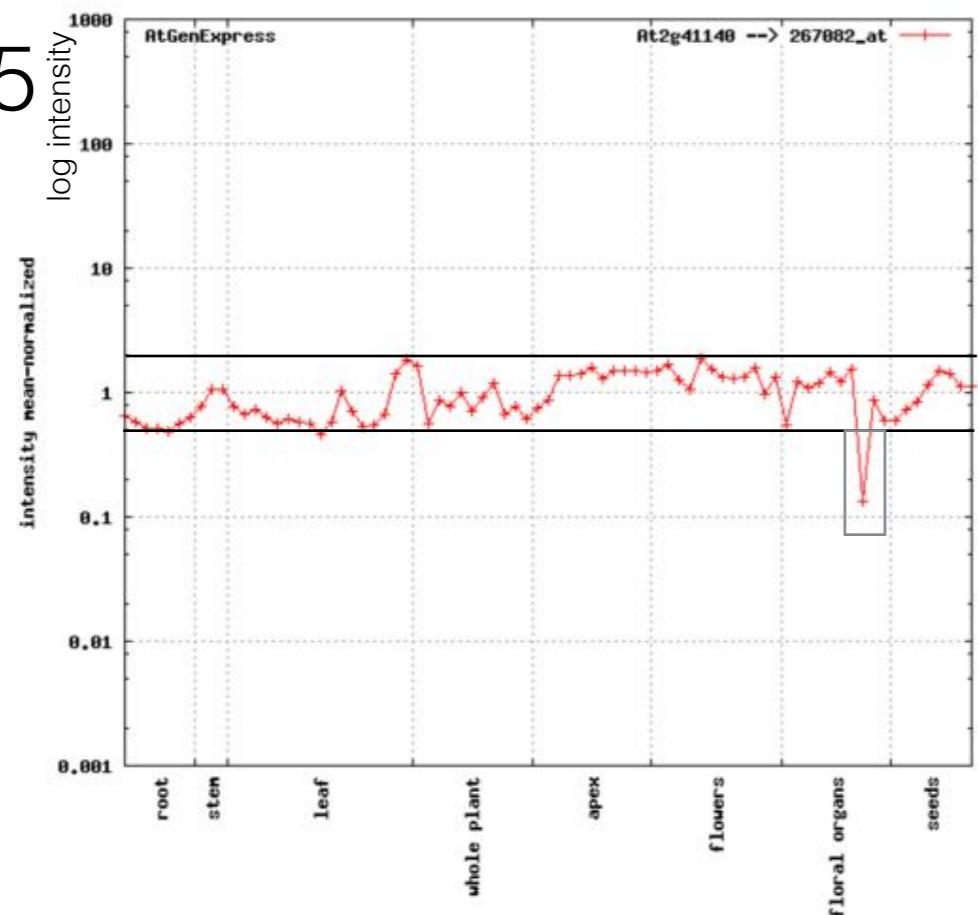
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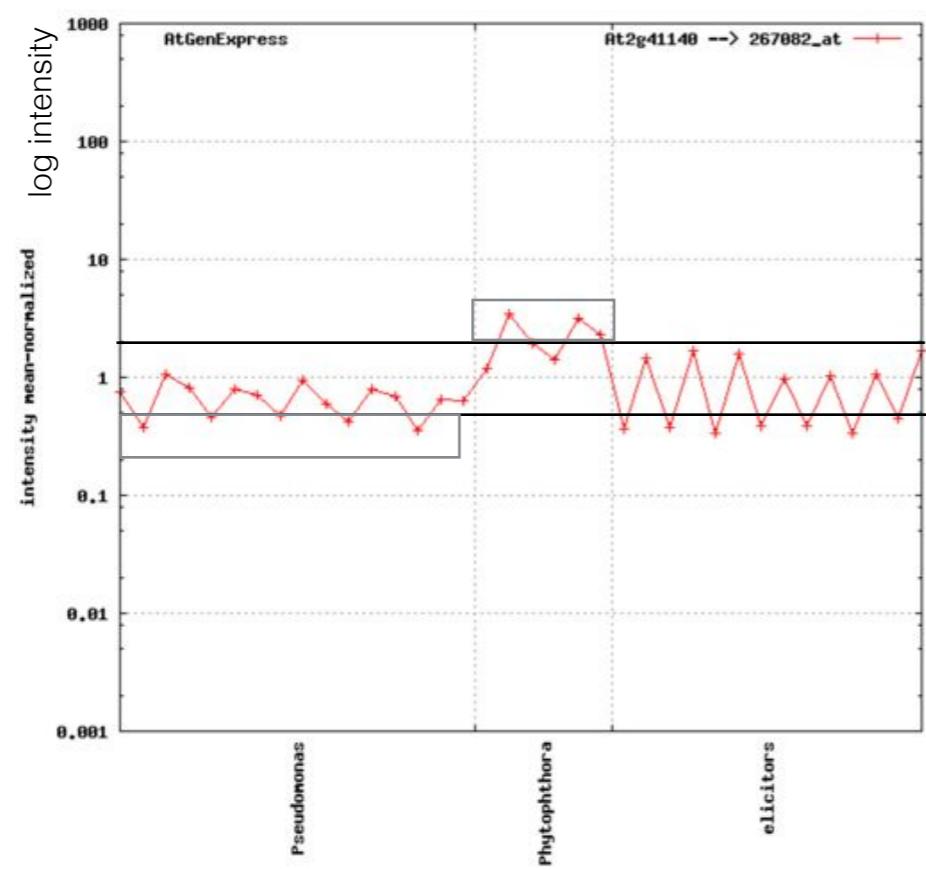
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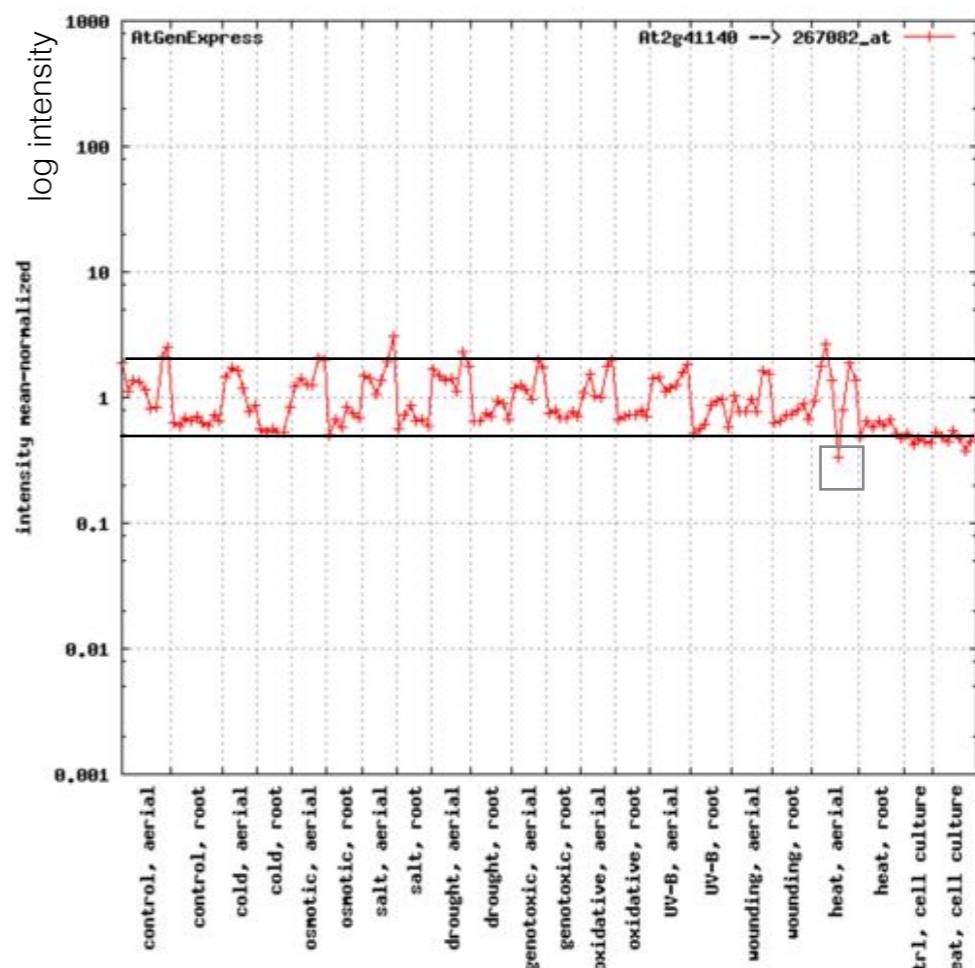
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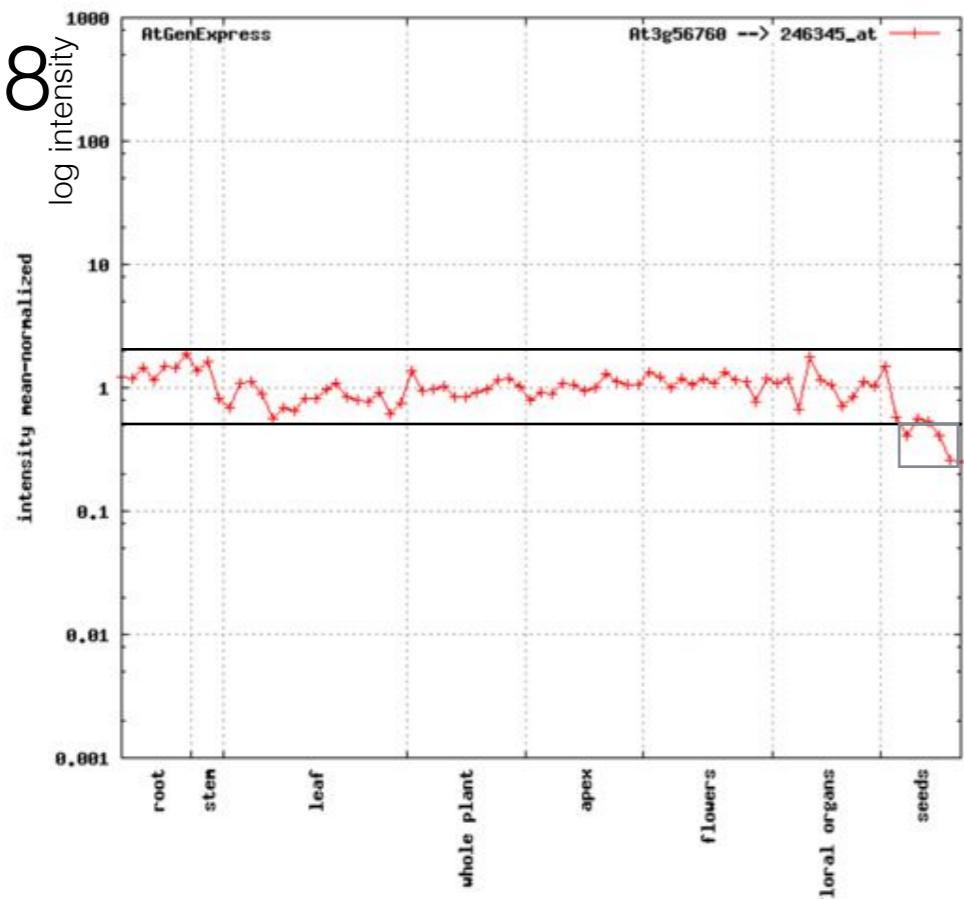
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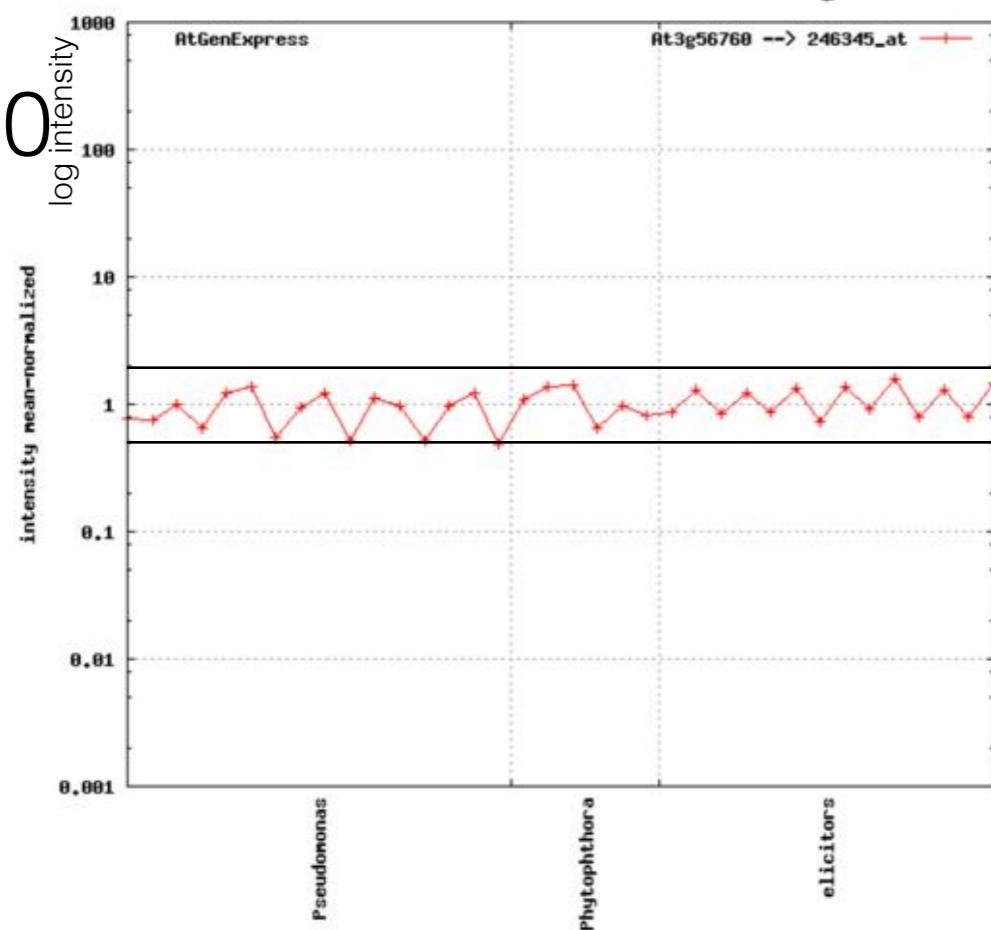
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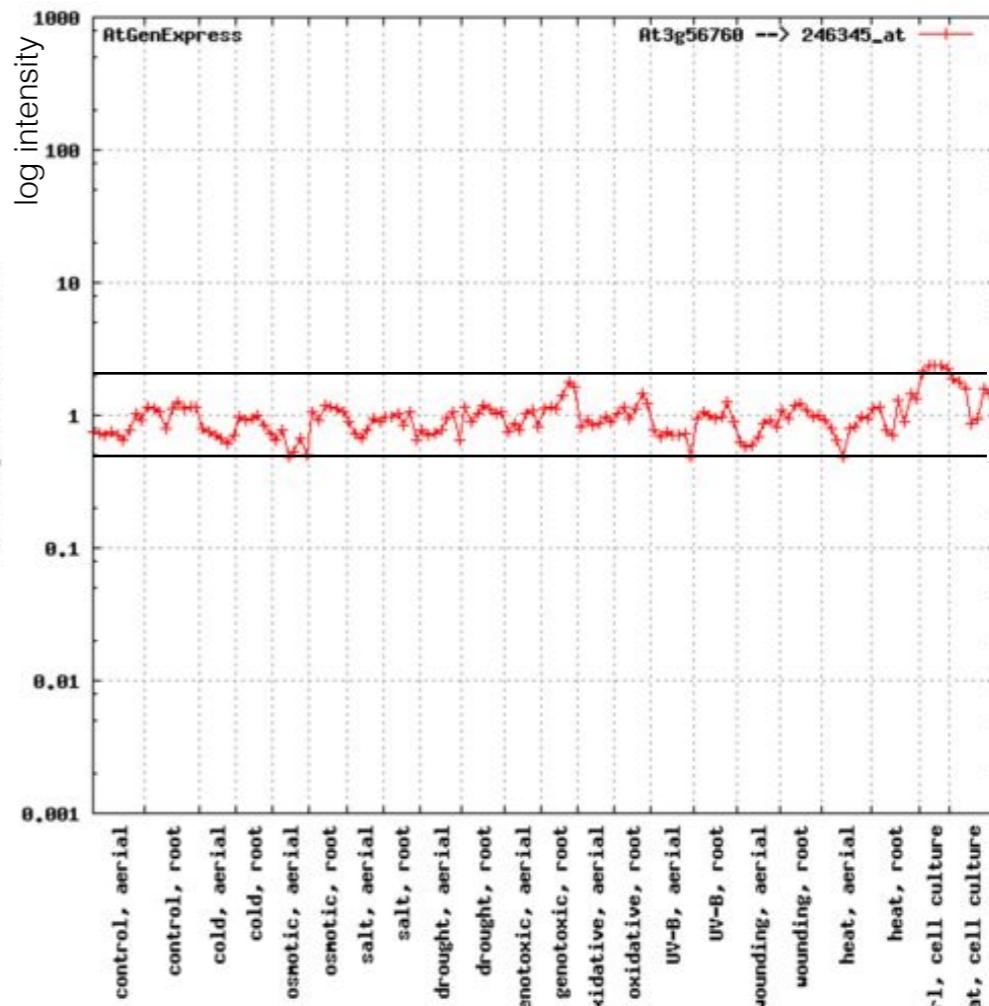
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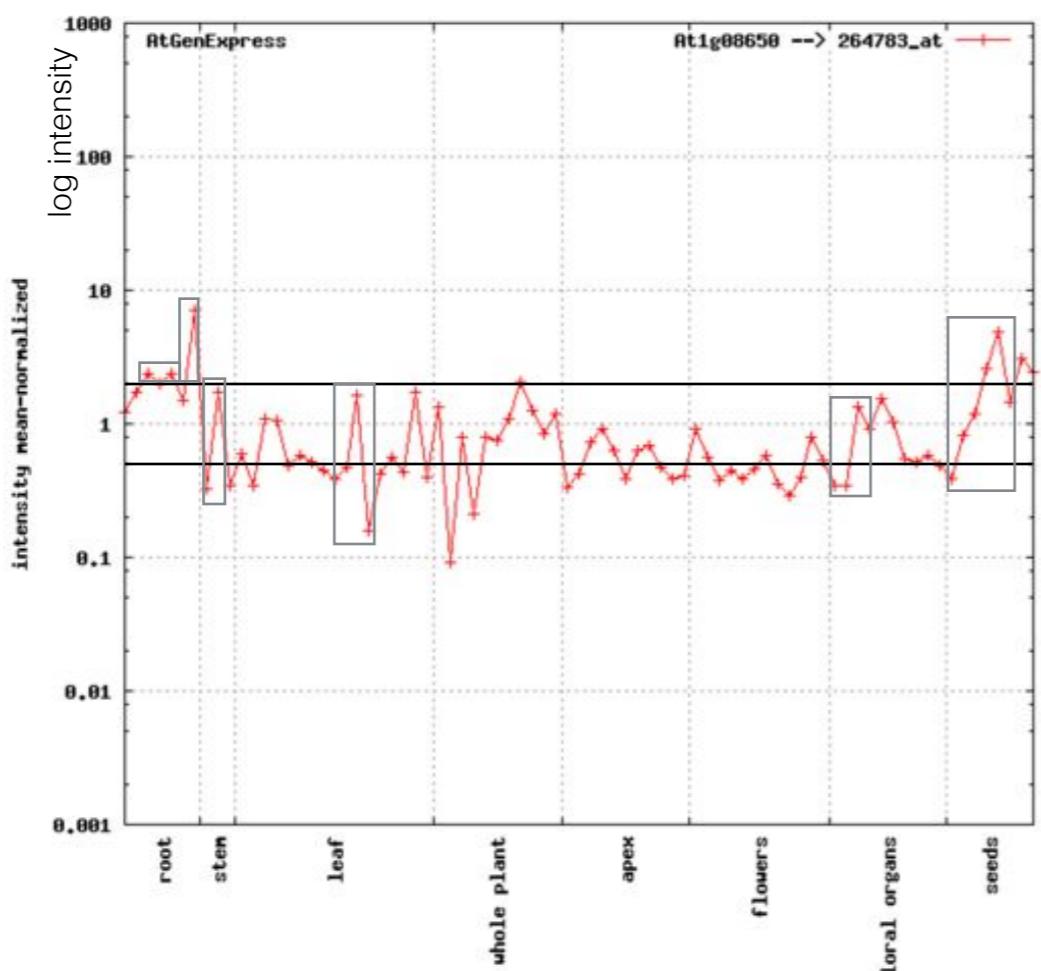
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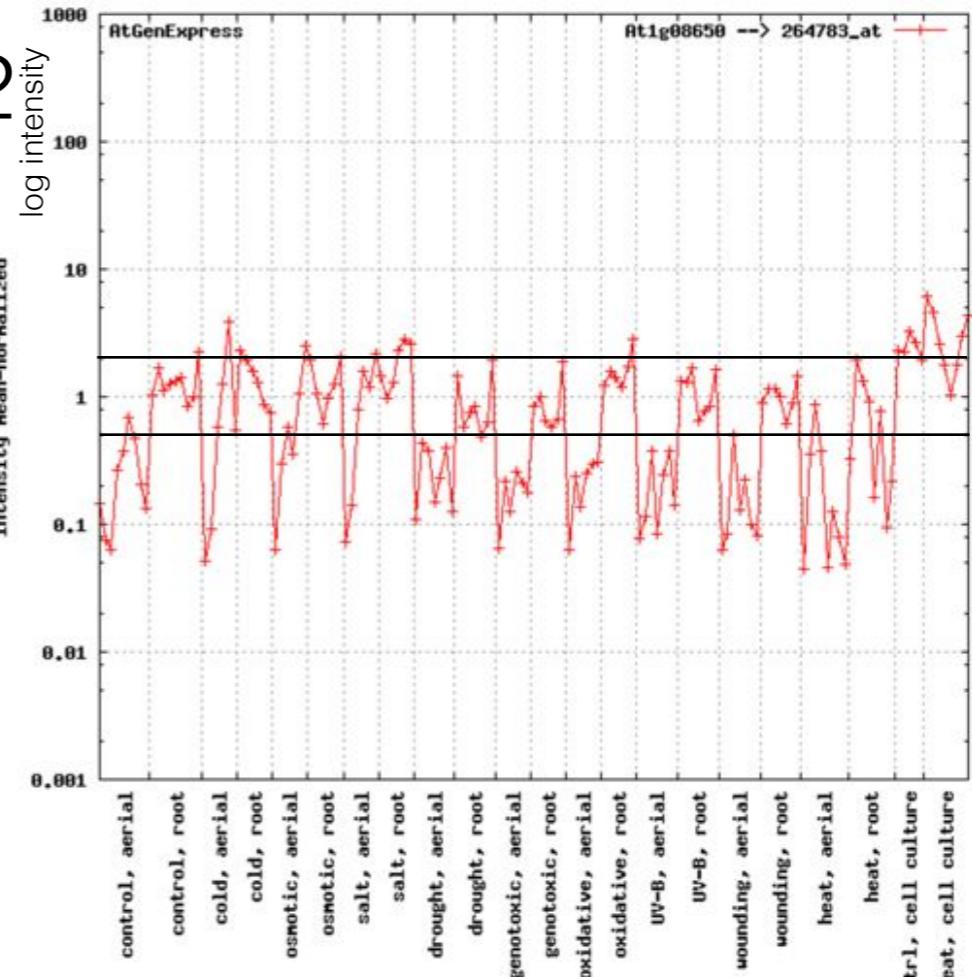
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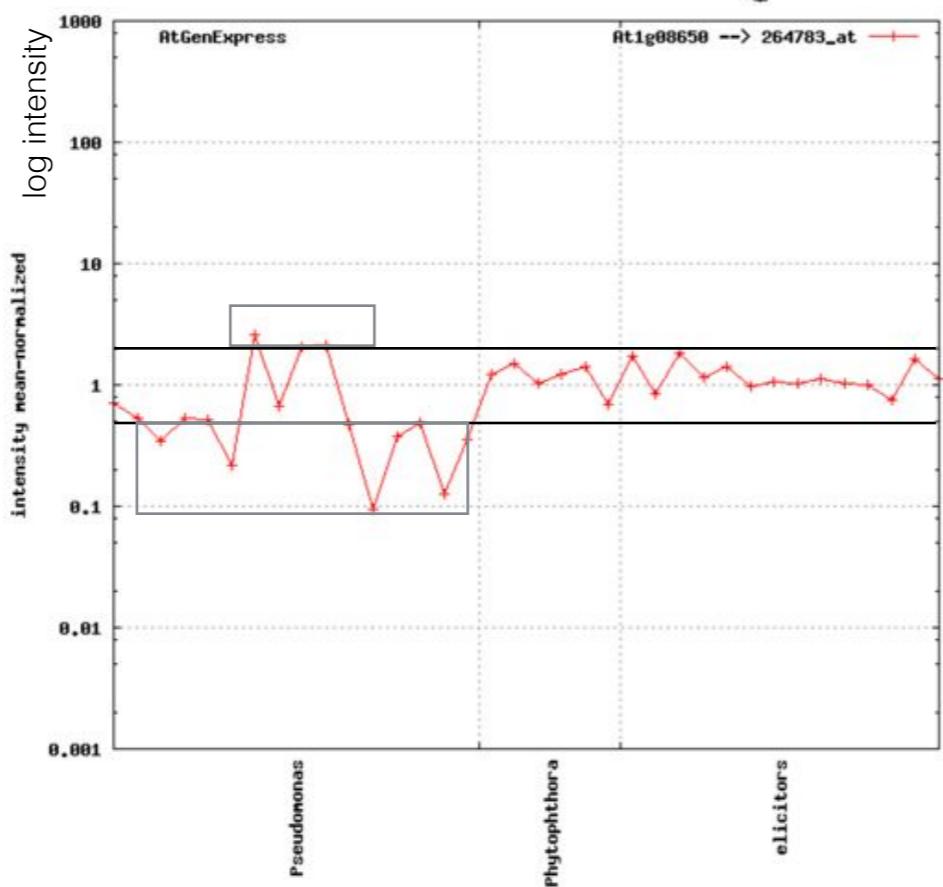
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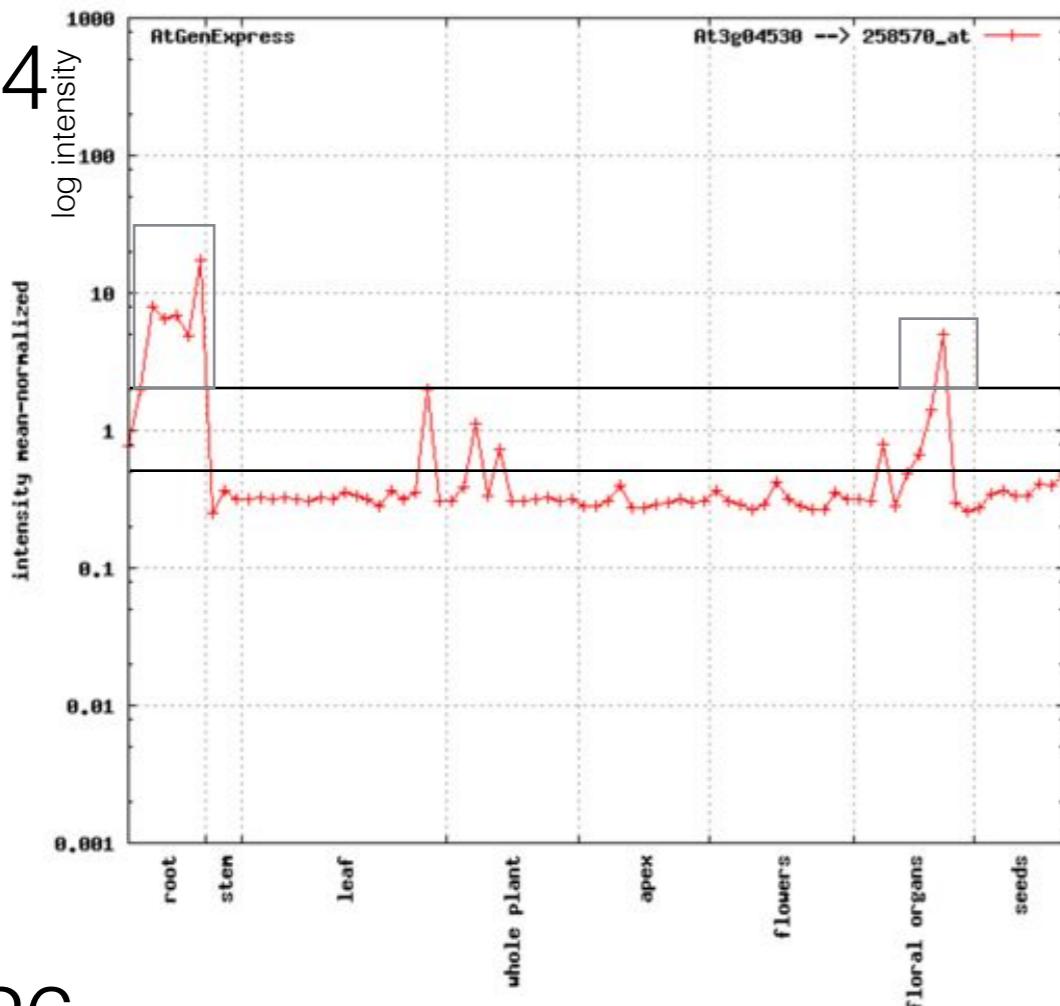
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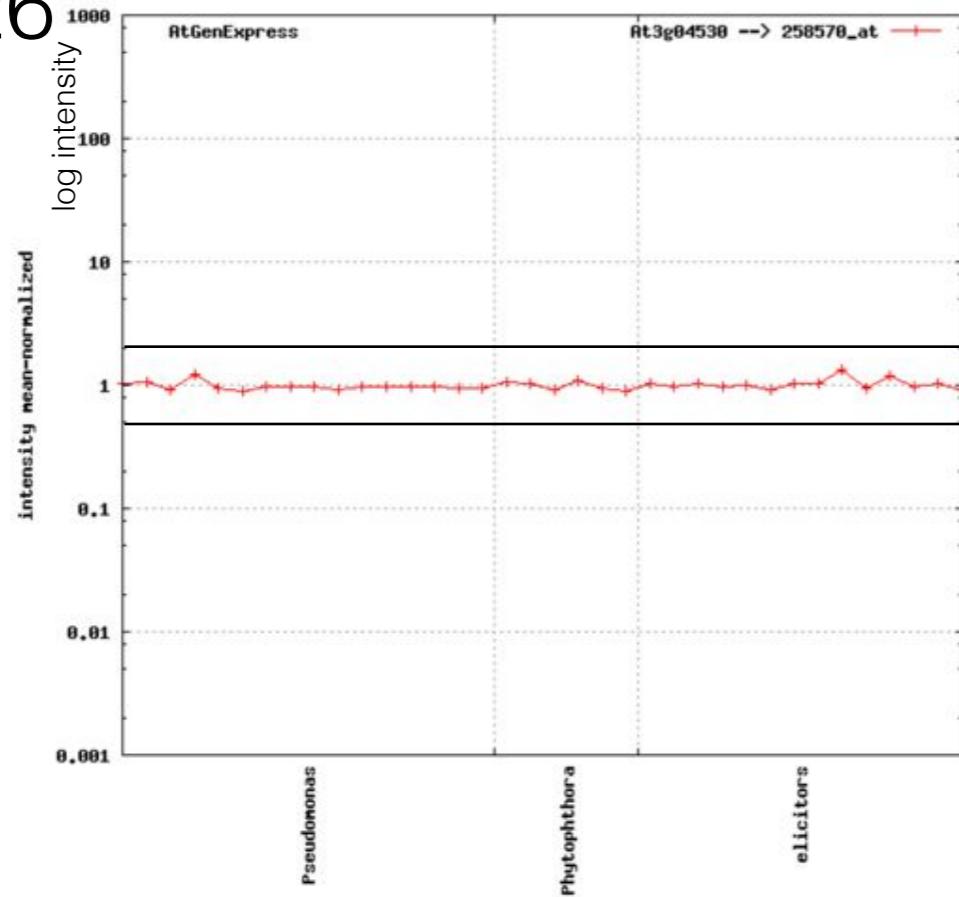
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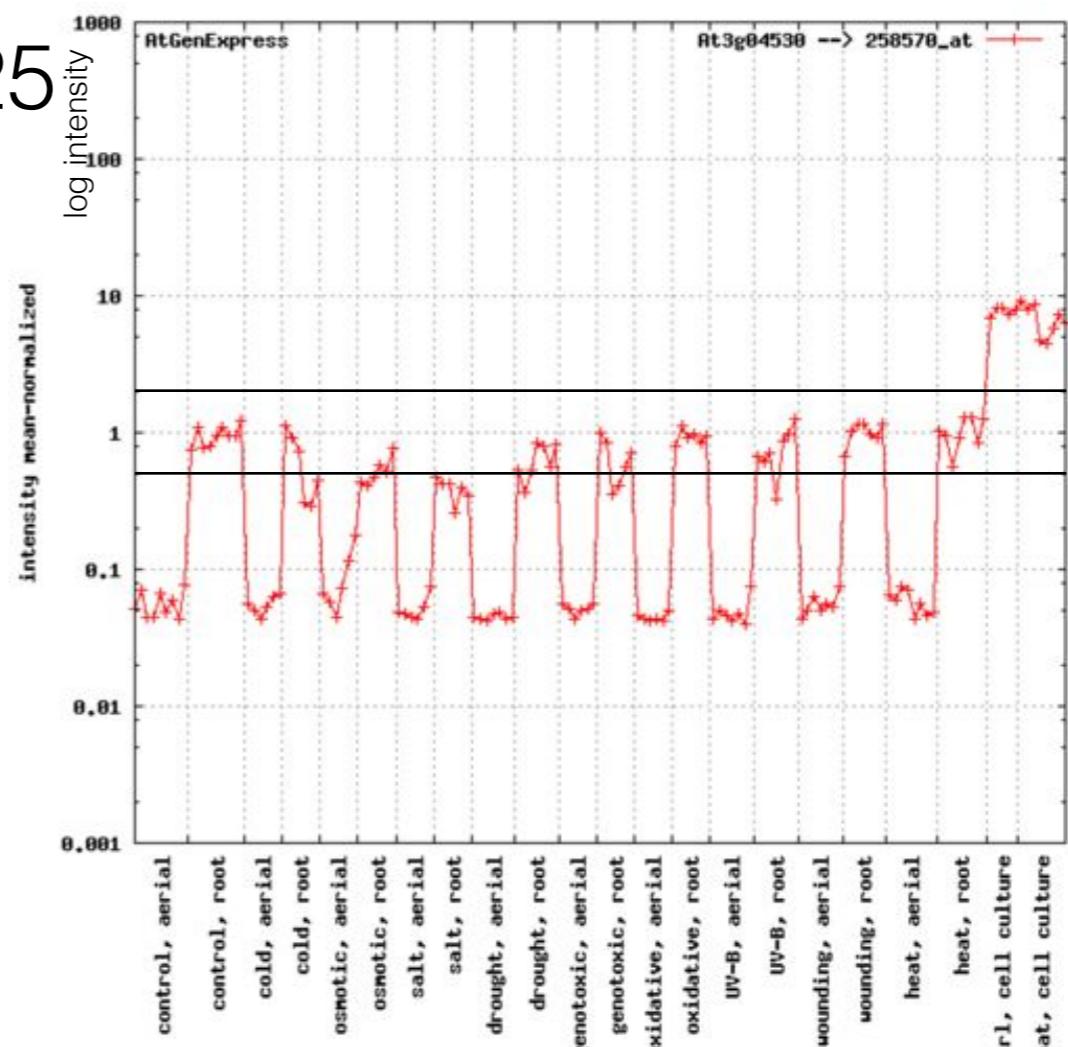
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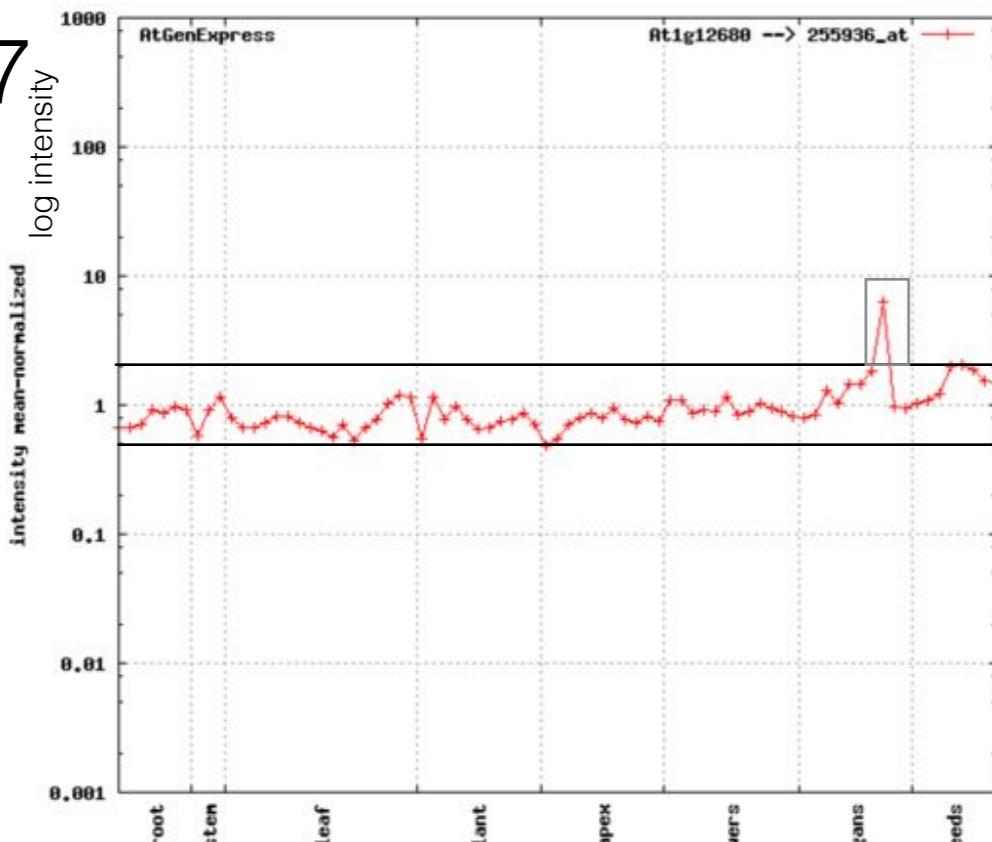
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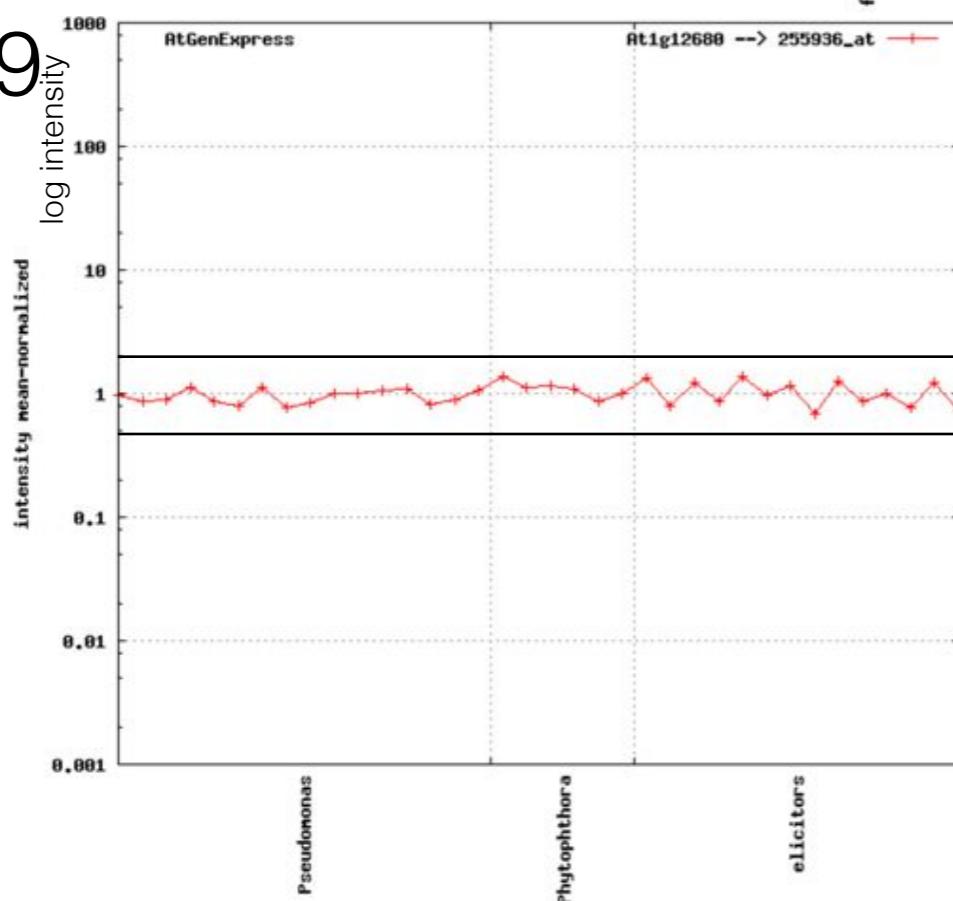
125



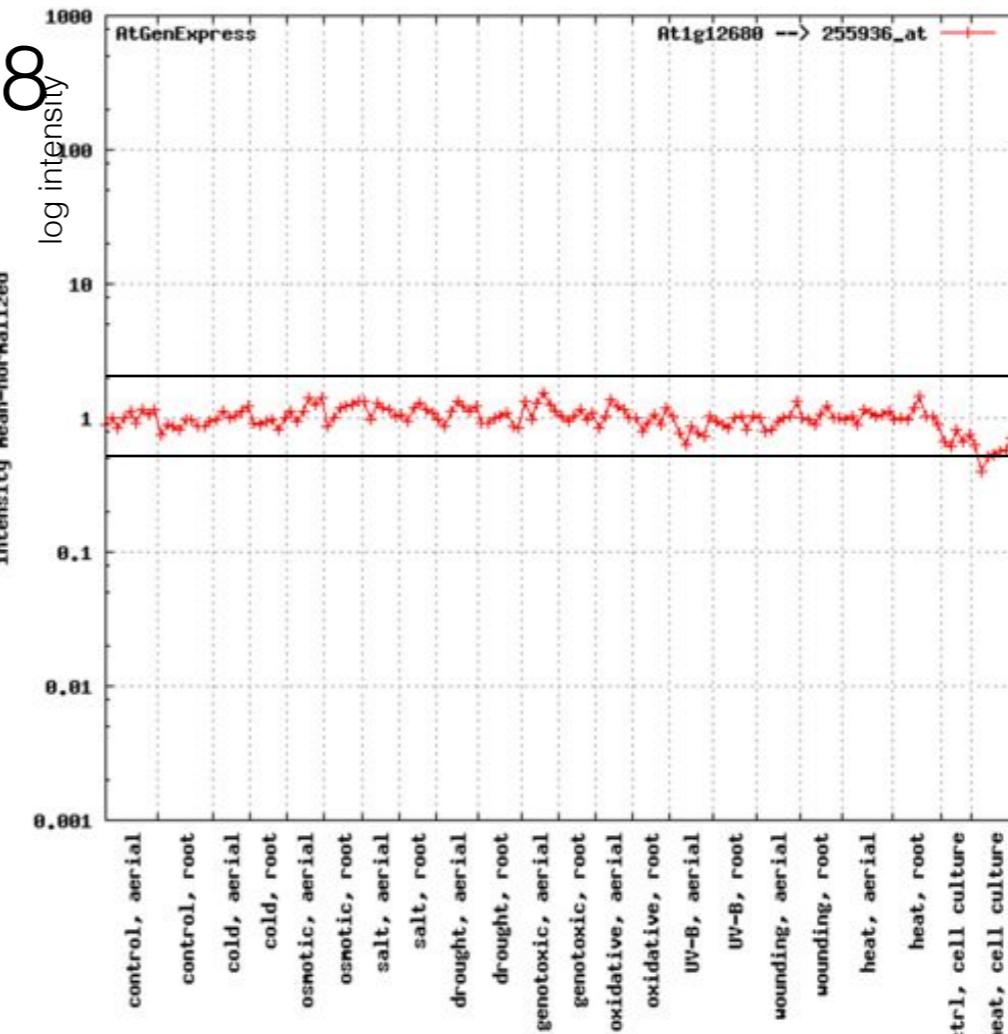
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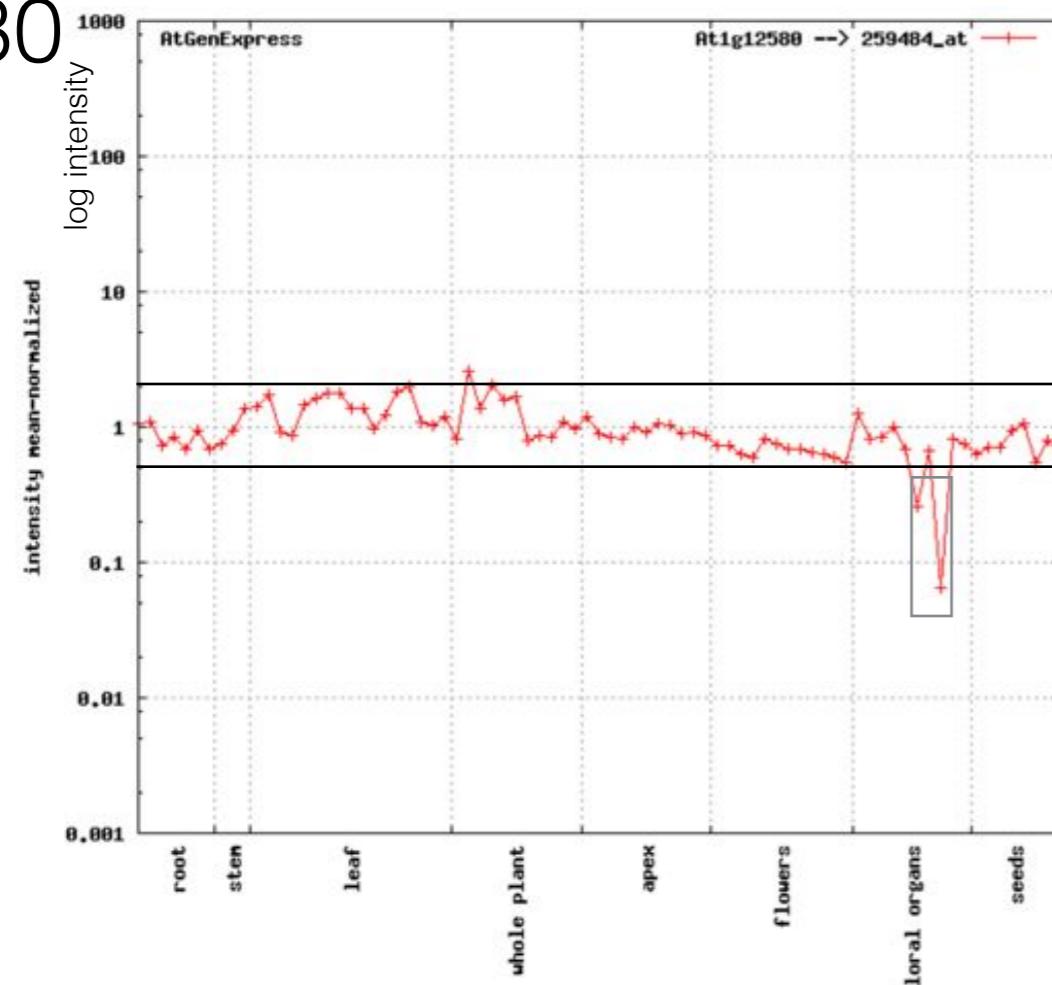
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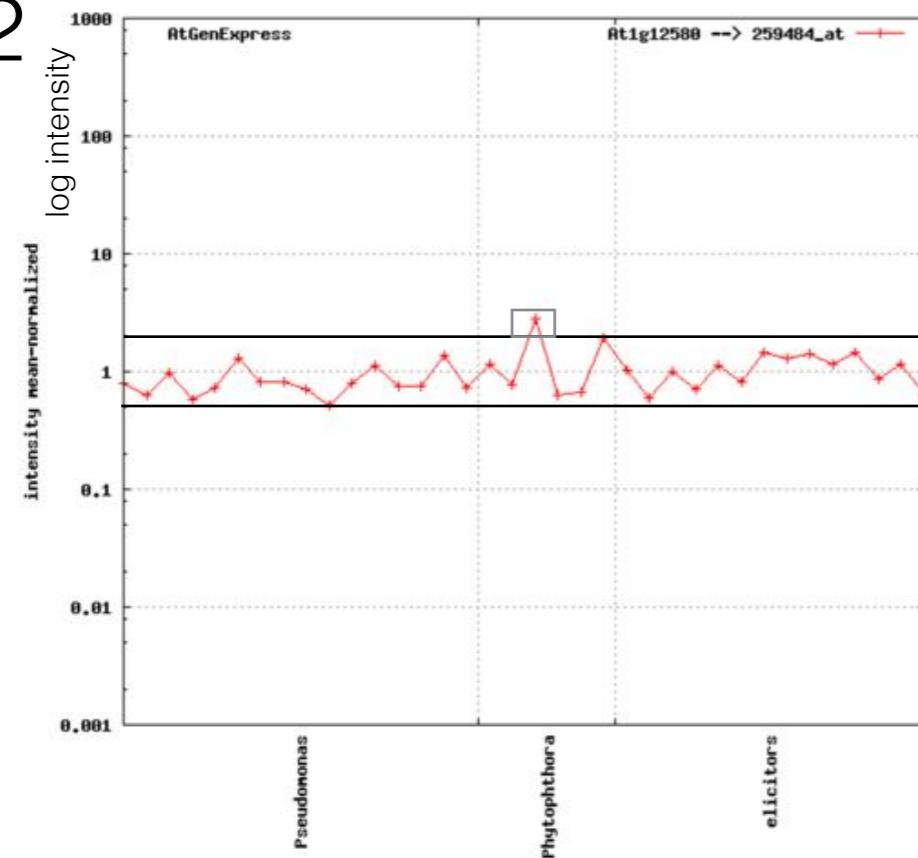
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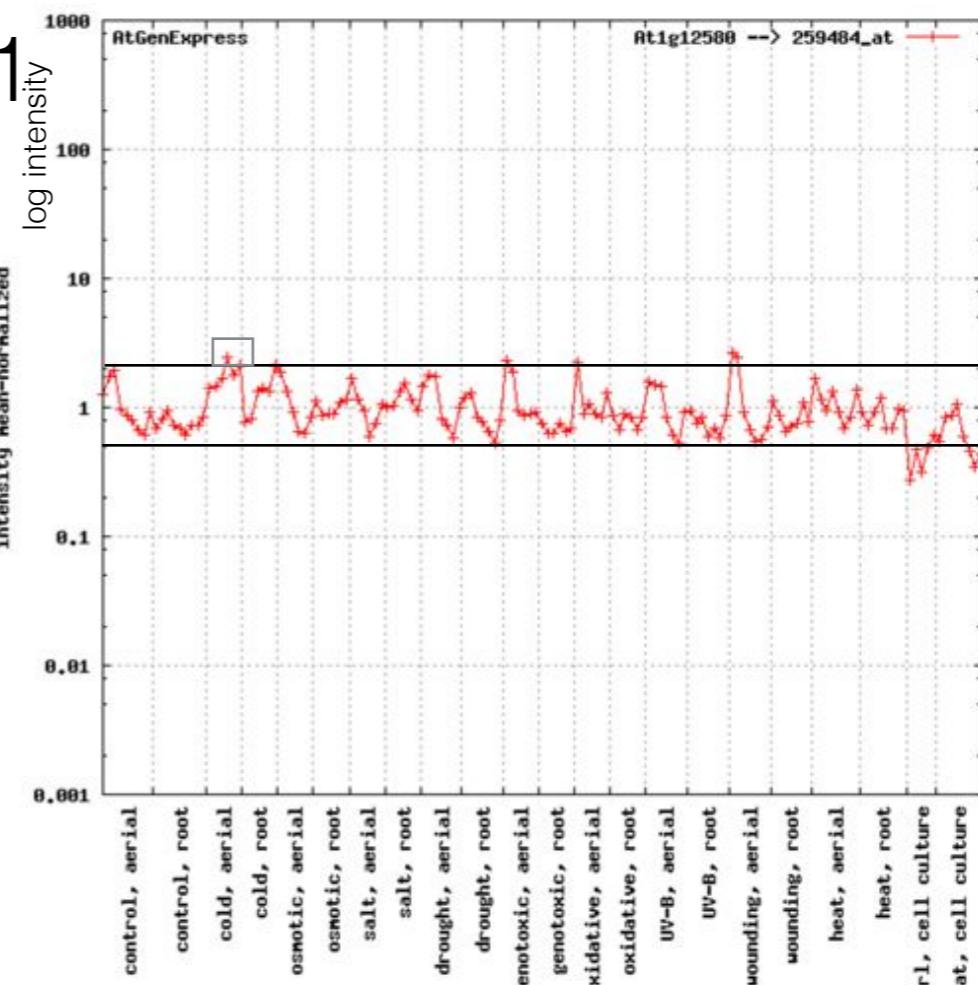
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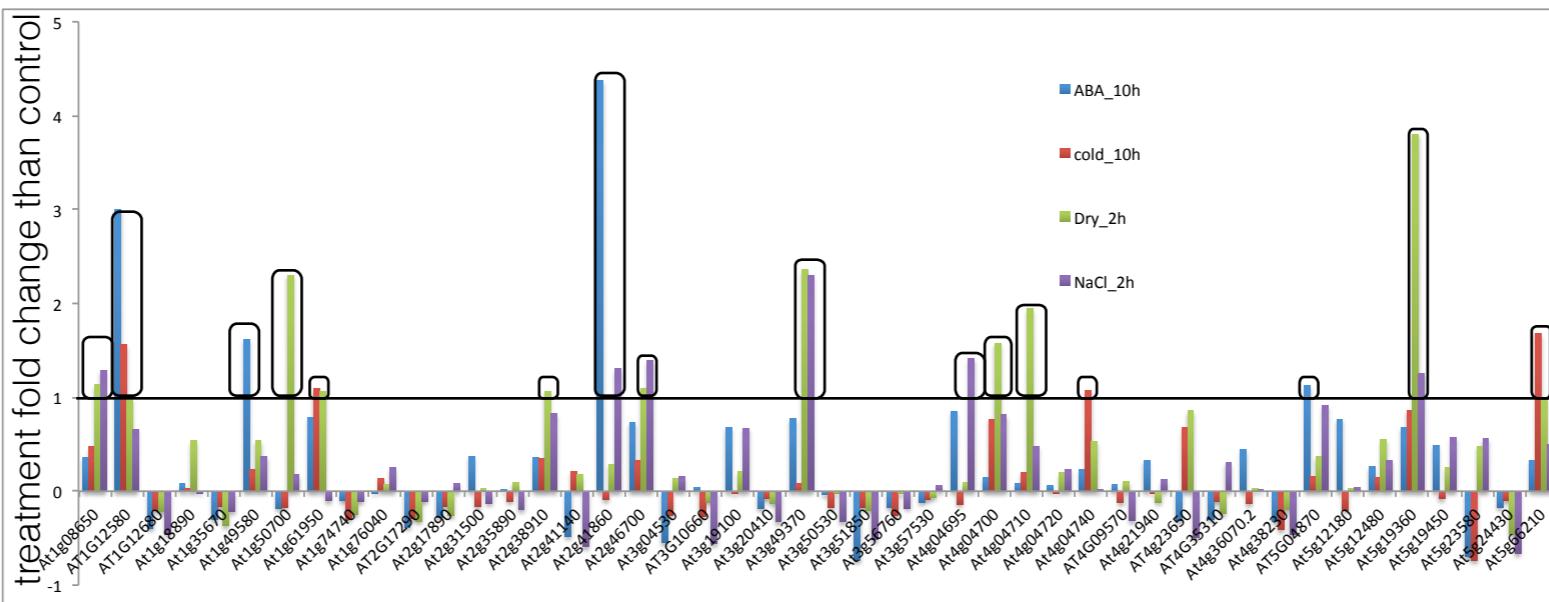
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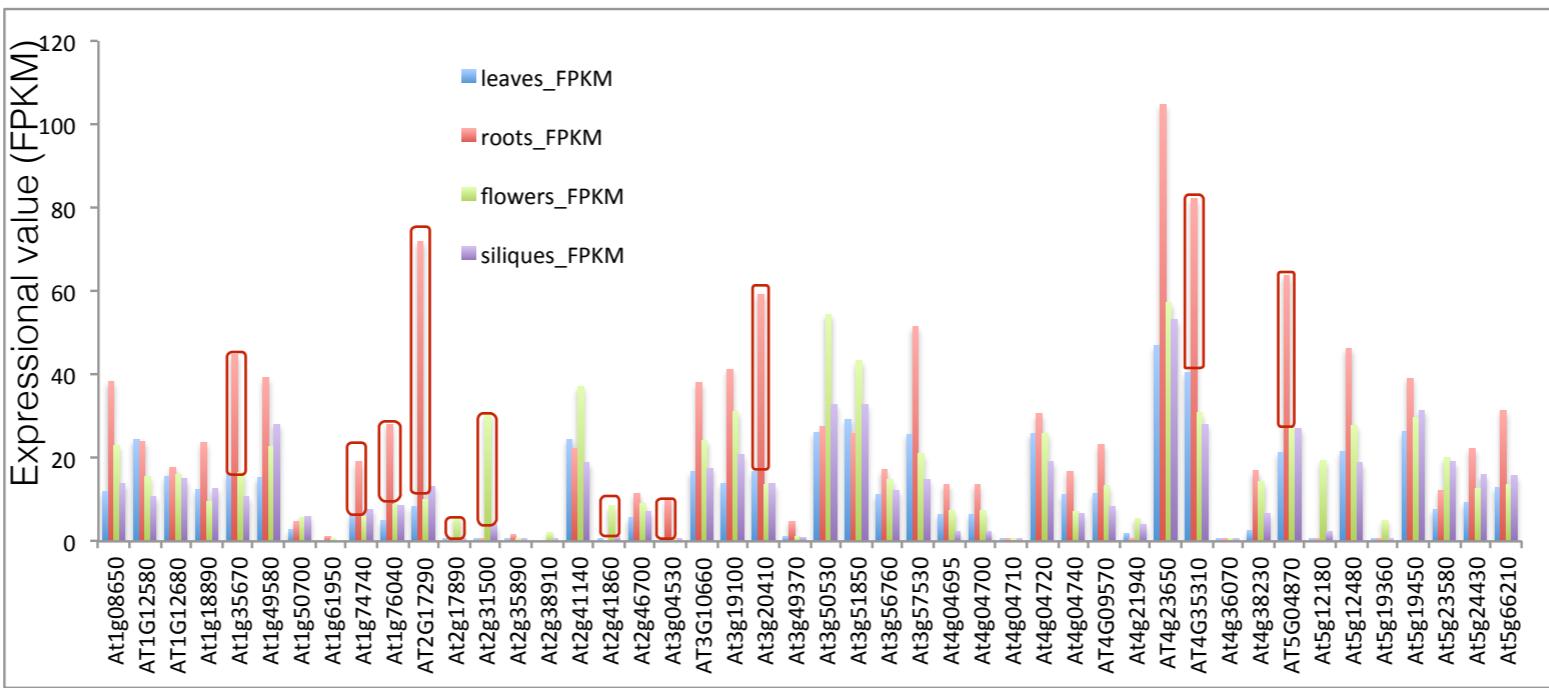
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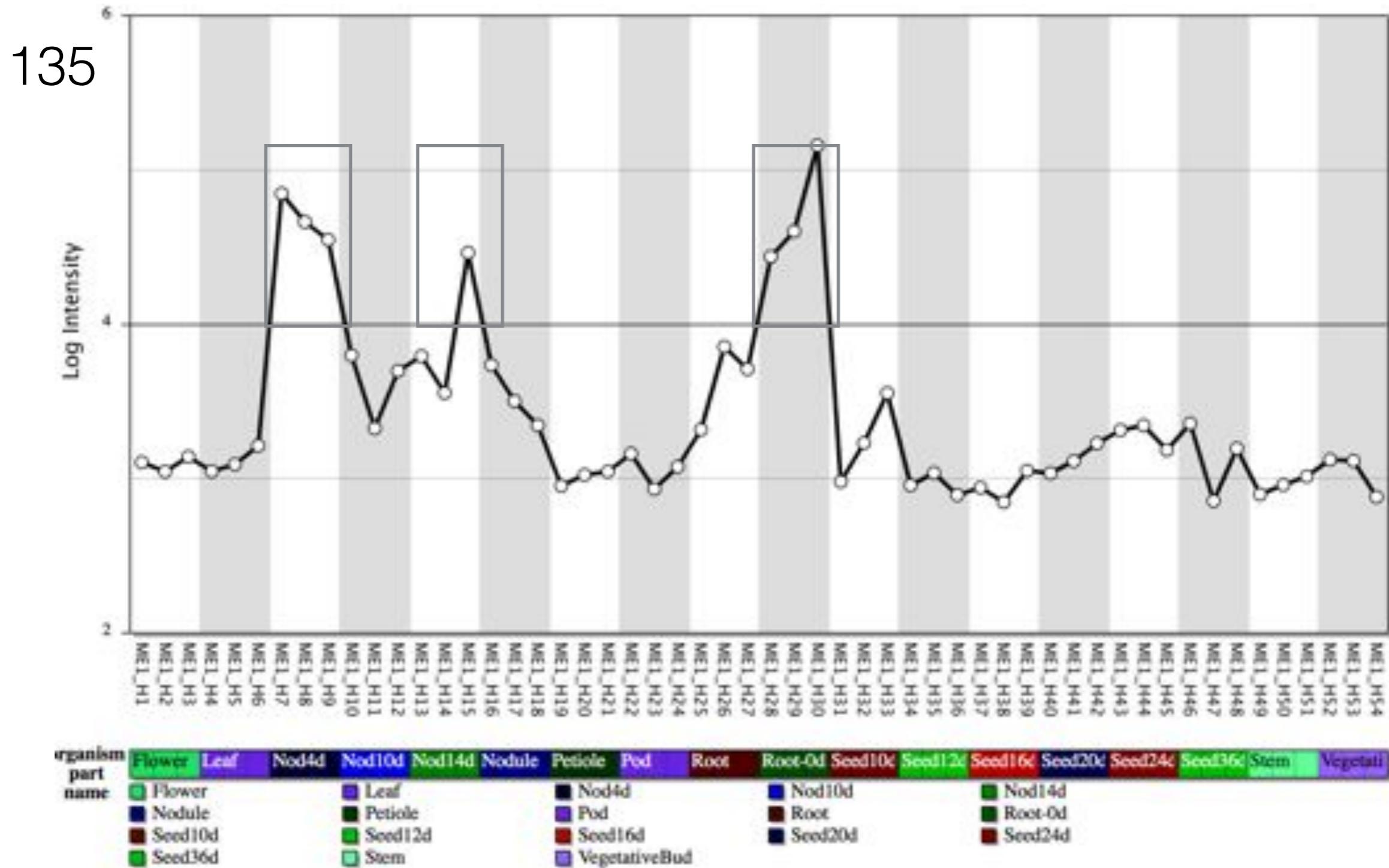


133

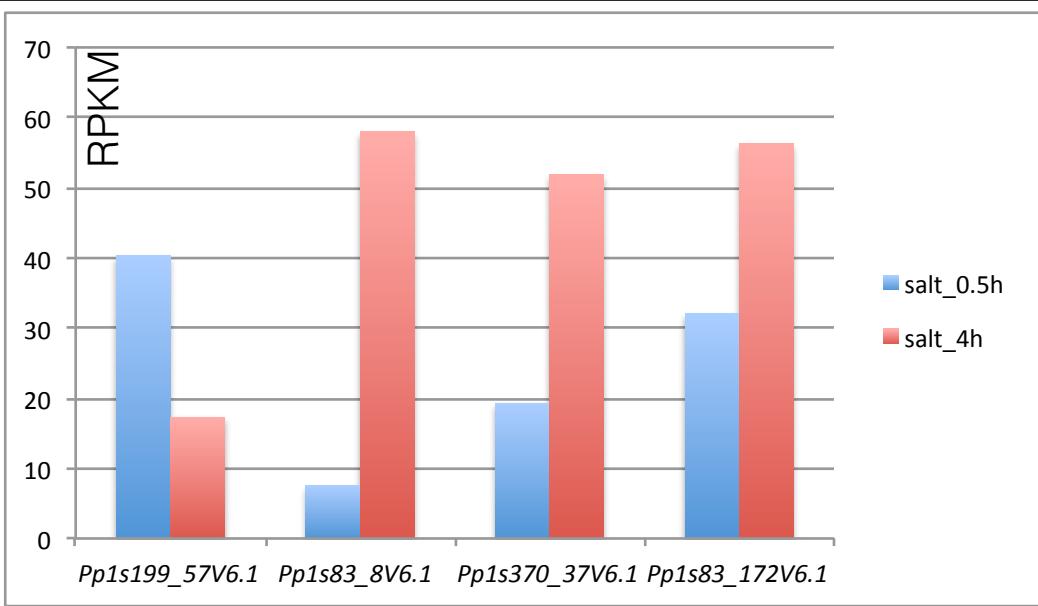
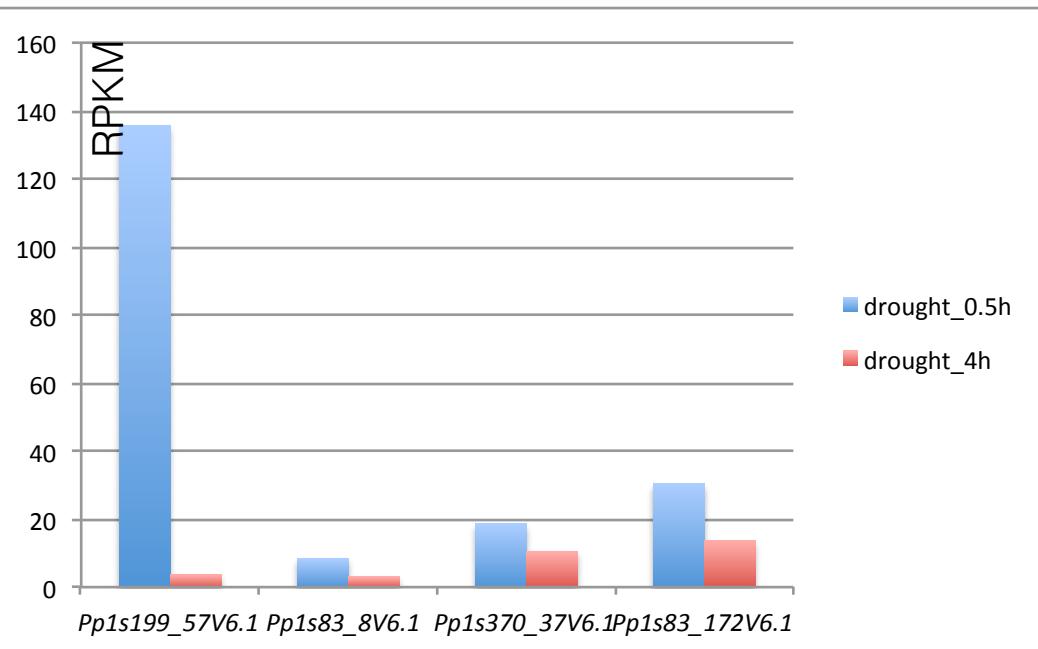


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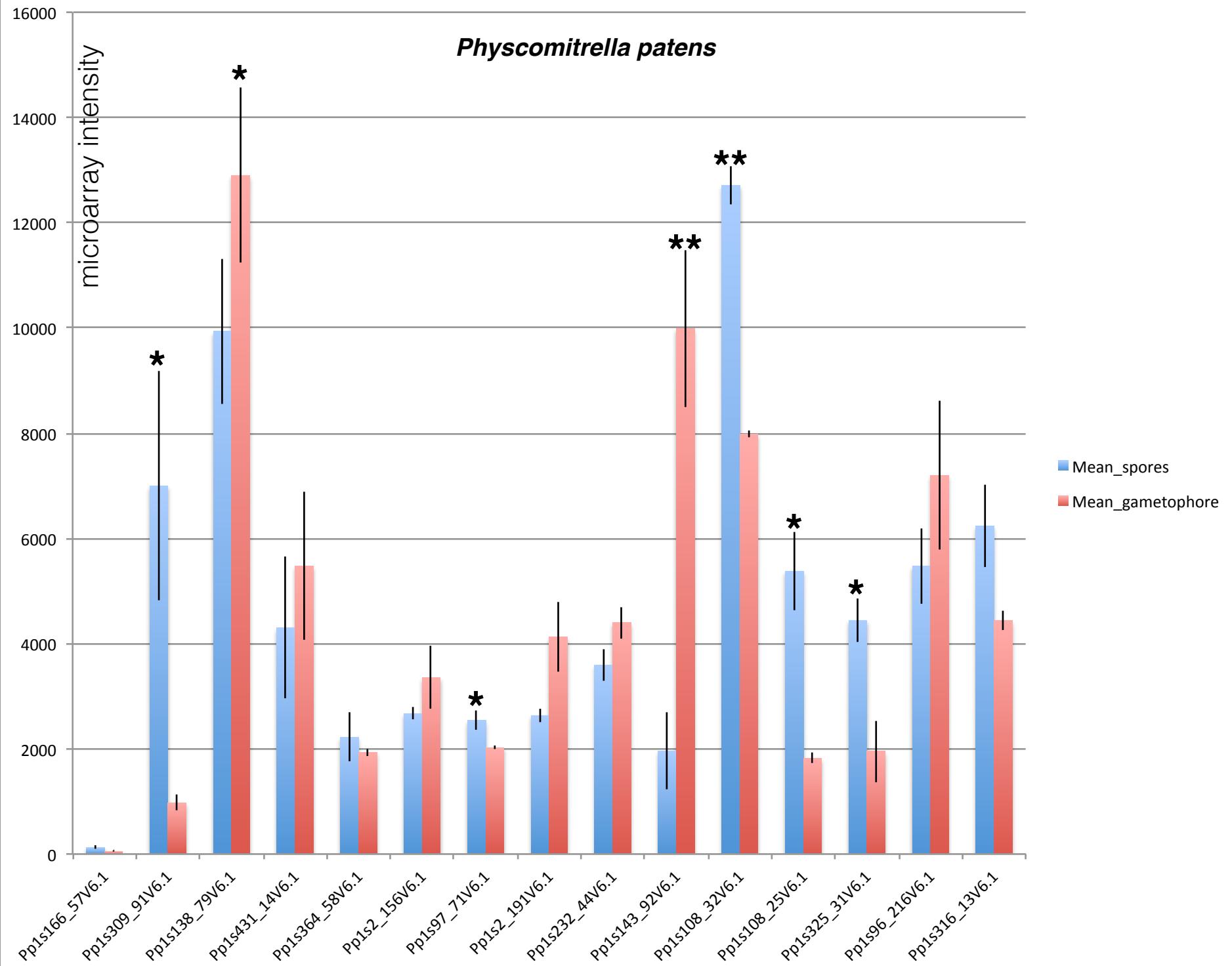




	gene structure	Gene_ID	Subcellular_Localization	development	Abiotic and biotic Stress	Plant-microbe communication
D2	At At5g19450 At At5g12480 At At3G57530 At At2g41860 At At3g51850 At At1g74740 At At1g18890 At At2g31500 At At5G04870 At At3G10660 At At2g38910 At At2g35890 At At4g38230 At At4G35310 At At2G17290 At At5g23580 At At4G09570 At At1g35670 At At5g19360 At At5g12180 At At4g23650 At At1g76040 At At3g20410 At At1g50700 At At1g61950 At At4g04740 At At4G04720 At At4g21940 At At4g04710 At At4G04700 At At4g04695 At At2g17890 At At4g36070 At At5g66210 At At3g49370 At At5g24430 At At2g46700 At At1g49580 At At3g19100 At At3g50530 At At2g41140 At At3g56760 At At1g08650 At At3g04530 At AT1G12680.1 At AT1G12580.1 Mt Medtr8g043970.1	At5g19450 At5g12480 At3g57530 At2g41860 At3g51850 At1g74740 At1g18890 At2g31500 AT5G04870 AT3G10660 At2g38910 At2g35890 At4g38230 AT4G35310 AT2G17290 At5g23580 AT4G09570 At1g35670 At5g19360 At5g12180 AT4g23650 At1g76040 At3g20410 At1g50700 At1g61950 At4g04740 At4g04720 At4g21940 At4g04710 At4g04700 At4g04695 At2g17890 At4g36070 At5g66210 At3g49370 At5g24430 At2g46700 At1g49580 At3g19100 At3g50530 At2g41140 At3g56760 At1g08650 At3g04530 At AT1G12680.1 At AT1G12580.1 Medtr8g043970	PM* PM* Membrane*,nucleus* chlo: 5, cyto: 2, extr: 2, vacu: 2, plas: 1, E.R.: 1 Membrane*,PM* membrane* PM* chlo: 4, mito: 4, cyto: 3, plas: 2 Peroxisomes*,oil bodies* ER and other membranes* chlo: 4, cyto: 3, mito: 2.5, nucl: 2, pero: 2, mito_plas: 2 Peroxisomes,chlo,mito Membrane*, cytosol*, nucleus* Membrane*, cytosol*, nucleus* Cytosol*, nucleus* Cytosol*, nucleus* Cytosol*, nucleus* PM* PM* Soluble*,PM*,tonoplast* cyto,nucl,chlo chlo: 5, cyto_nucl: 4, nucl: 3.5, cyto: 3.5, mito cyto: 8.5, cyto_nucl: 6.5, nucl: 3.5 membrane* PM* PM* cyto: 5.5, cyto_nucl: 4, plas: 3, chlo: 2, nucl: 1.5, mito: 1 cyto: 6, E.R.: 3, nucl: 2, mito: 1, pero: 1 cyto: 12, cysk: 1 chlo: 5, cyto: 4, nucl: 2, mito: 2 PM* cyto: 6, nucl: 4, mito: 3 PM* chlo: 4, nucl: 4, cyto: 4, mito: 1 chlo: 6, nucl: 5, cyto: 1, mito: 1 cyto: 5, E.R.: 5, chlo: 1, nucl: 1, mito: 1 chlo: 5, cyto: 4, nucl: 3, mito: 1 cyto: 7, nucl: 3, chlo: 2, cysk: 2 chlo: 7, nucl: 4, cyto: 1, mito: 1 cyto: 5, nucl: 4, mito: 2, chlo: 1, vacu: 1 cyto: 5, nucl: 4, chlo: 2, mito: 1 cyto: 8, chlo: 2, nucl: 2, cysk: 2 nucl: 10, cyto: 2, chlo: 1 nucl: 10, cyto: 1, extr: 1, vacu: 1 nucl: 6, cyto: 6, chlo: 2	stomata*, mature pollen(Fig.S7_1) all tissues(Fig.S7_4), stomata* pollen, seed maturation (Fig. S7_7) pollen, seed maturation(Fig. S7_10) pollen, seed maturation(Fig.S7_13) whole plant except apex(Fig. S7_16) whole plant(Fig.S7_19) flowers,seed maturation(Fig.S7_22) pollen(Fig.S7_25) pollen(Fig.S7_28) pollen(Fig.S7_31) pollen(Fig.S7_34) pollen(Fig.S7_37) pollen,seed maturation(Fig.S7_40) root,stem,leaf,apex,flowers,seed maturation (Fig. S7_43) whole plant(Fig.S7_46) flower,seed maturation(Fig.S7_49) whole plant(Fig.S7_52) pollen*, seed maturation(Fig.S7_55) pollen, seed maturation*(Fig.S7_58) root,pollen,seed maturation(Fig.S7_61) root,leaf,stem,apex,flower(Fig.S7_64) root,pollen(Fig.S7_67) whole plant(Fig. S7_70) root,pollen,seed maturation(Fig.S7_73) leaf,flower(Fig.S7_76) stomata* root,leaf,apex,flower(Fig.S7_79) flower,seed maturation(Fig.S7_82) pollen(Fig.S7_85) unknown pollen, seed(Fig.S7_88) pollen(Fig.S7_91) root,leaf,apex,pollen,seed maturation(Fig.S7_94) root,flower,seed maturation(Fig.S7_97) pollen(Fig.S7_100) whole plant(Fig. S7_103) stem,leaf,apex,flower,seed maturation(Fig.S7_106) leaf,pollen(Fig.S7_109) stem, flower, seed maturation(Fig.S7_112) pollen(Fig.S7_115) seed maturation(Fig.S7_118) whole plant(Fig.S7_121),C4&CAM photosynthesis#\$ root,pollen(Fig.S7_124),C4&CAM photosynthesis## pollen(Fig.S7_127) pollen (Fig.S7_130) none(Fig.S7_135)	salt(Fig. S7_2) None(Fig.S7_5) ABA*, stomata*, salt(Fig. S7_8) ABA,NaCl (Fig. S7_133),none(Fig.S4_11) Herbivore*,none(Fig.S7_14) ABA*, abiotic stress*,cold(Fig.S7_17) ABA*, drought*, stomata*,heat(Fig.S7_20) None(Fig.S7_133,S7_23) SA&defense&cold&ABA(Fig.S7_26,133)&NaCl&oxidative stress&secondary metabolism* none(Fig.S7_29) Drought(Fig.S7_133),none(Fig.S7_32) none(Fig.S7_35) UV-B(Fig.S7_38) MAMP*,UV-B(Fig.S7_41) MAMP*,ABA*,drought*,salinity*,stomata*, heat(Fig.S7_44) ABA*,none(Fig.S7_47) MAMP*,ABA*,drought*,salinity*,stomata*,salt,heat(Fig.S7_50) MAMP*,ABA*,drought*, salinity*,stomata*,cold(Fig.S7_53) ABA*,cold*,NaCl*&Drought*(Fig.S5),none(Fig.S7_56) ABA*,Drought*, none(Fig.S7_59) Herbivore*,salinity*,stomata*,none(Fig.S7_62) ABA*,Cold*,Drought*(Fig.S7_65) Drought*,NaCl*,heat(Fig.S7_68) none(Fig.S7_71),dry(Fig.S7_133) cold,dry(Fig.S7_133),none(Fig.S7_74) Drought*,salinity*,stomata*,cold(Fig.S7_77,S7_133) Osmotic stress* cold,osmotic stress,salt(Fig.S7_80) dry(Fig.S7_133),none(FigS7_83) none(Fig.S7_86),dry(Fig.S7_133) NaCl(Fig.S5) none(Fig.S7_89) none(Fig.S7_92) salt,drought,wounding(Fig.S4_95),cold(Fig.S7_133) salt(Fig.S7_98,S7_133), dry(Fig.S7_133) cold,heat(Fig.S7_101) none(Fig.S7_104),dry&NaCl(Fig.S7_133) heat(Fig.S7_107),ABA(Fig.S7_133) osmotic stress(Fig.S7_110) osmotic stress(Fig.S7_113) heat(Fig.S7_116) none(Fig.S7_119) none(Fig.S7_122),dry&NaCl(Fig.S7_133) none(Fig.S7_125) none(Fig.S7_128) cold(Fig.S7_131,S7_133),ABA(Fig.S7_133) none(Fig.S7_135)	None(Fig.S7_3) pathogen(Fig. S7_6) pathogen(Fig.S7_9) None(Fig.S7_12) None(Fig.S7_15) pathogen(Fig. S7_18) pathogen(Fig. S7_21) None(Fig.S7_24) pathogen(Fig. S7_27) None(Fig.S7_30) None(Fig.S7_33) none(Fig.S7_36) none(Fig.S7_39) pathogen(Fig. S7_42) pathogen(Fig. S7_45) pathogen(Fig. S7_48) pathogen(Fig. S7_51) pathogen(Fig. S7_54) none(Fig.S7_57) none(Fig.S7_60) none(Fig.S7_63) pathogen(Fig S7_66) pathogen(Fig.S7_69) none(Fig.S7_72) none(Fig.S7_75) pathogen(Fig.S7_78) unknown pathogen(Fig.S7_81) none(Fig.S7_84) pathogen(Fig.S7_87) unknown none(Fig.S7_90) none(Fig.S7_93) pathogen(Fig. S7_96) pathogen(Fig. S7_99) pathogen(Fig. S7_102) none(Fig.S7_105) pathogen(Fig. S7_108) pathogen(Fig. S7_111) pathogen(Fig. S7_114) pathogen(Fig. S7_117) none(Fig.S7_120) pathogen(Fig. S7_123) none(Fig.S7_126) none(Fig.S7_129) pathogen(Fig. S7_132) root symbiosis(*,Fig.S7_135)

**A****B**

*Physcomitrella patens*



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This text file includes the Supplemental File S1, followed by the references to the supplemental figures.

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Supplemental File S1. Representative sequences that have innovative gene structure compared to the typical structure composed of a KD and a CaM-LD.

(1) degenerated kinase domain, distributed in red algae to flowering plants

Pcr|HS694783.1

Vca|Vocar20001731m

Olu|2798

Vitis\_vinifera|VIT\_00s0577g00010

(2) myristoylation at the Nterminal, distributed in Charophytes to flowering plants

Mpu|175307|126004

Cre|Cre13.g564500.t1.3

Kfl|kfl00234\_0080

At|At2G17290

At|At2g41860

At|At5g12180

(3) palmytoylation at the NUterminal, distributed in seawater algae to flowering plants

Mpu|175307|126004

Cre|Cre13.g564500.t1.3

Kfl|kfl00036\_0390

(4) C2 domain at the NUterminal, distributed only in freshwater algae

Cre|Cre17.g705000.t1.2

Vca|Vocar20010397m

(5) PEST motif in the NUterminal, distributed in freshwater algae to flowering plants

Cre|Cre02.g114750.t1.2

Kfl|kfl00013\_0520

Atr|scaffold00018.149

Vv|VIT\_16s0098g01140

(6) Acylation at the NTerminal, distributed in freshwater algae to flowering plants

Cre|Cre02.g114750.t1.2

Kfl|kfl00013\_0520

Atr|scaffold00018.149

Vv|VIT\_16s0098g01140

(7) DnaJ domain in the NTerminal, distributed in flowering plants

Br|Bra009697

Fv|mRNA09567.1

(8) AAA domain in the NTerminal, distributed in flowering plants

Br|Bra001373

Br|Bra029859

(9) Two EF hands in the CTerminal, distributed in red algae to flowering plants

Pcr|HS694783.1

Cva|35323

Cre|Cre06.g265550.t1.2

Cva|20239

Atr|scaffold00073.66

(10) 4 EF hands at the CTerminal, the typical calmodulinUlike domain, distributed in seawater algae to flowering plants

Mpu|175307|126004

Vca|Vocar20000362m

At|At2G17290

At|At2g41860 (11) three EF hands at the CTerminal, distributed in seawater algae to flowering plants

Olu|2798

Csu|20203

Atr|scaffold00101.38

At|At4g23650 (12) one EF hands at the CTerminal, distributed in freshwater

algae to flowering plants

Csu|11155

Csu|2460

Ppa|Pp1s159\_42V6.1

Sm|Sm173444|PACid:15414880

Fv|Fvmrna24077.1

Fv|Fvmrna18654.1

(13) Insertion in the AID, and degeneration of first EF hand, distributed in all streptophytes

Mv|GBSK01009566.1

Pla|ADV78070.1

Atr|scaffold00101.38

Os|LOC\_Os05g41090.1

(14) CTerminal without domain detected

Sm|Sm99940|PACid:15420380

Atr|scaffold00069.118

Vv|VIT\_16s0100g00340

Os|LOC\_Os06g03682.1

(15) no AID nor CaMULD, found in Lycophytes to flowering plants

Sm|Sm99940|PACid:15420380

Atr|scaffold00148.66

At|At3g04530

(16) FBG domain at the C-terminal

Gm|Glyma07g18310.1

Gm|Glyma18g43160.1

Rc|28308.m000065

(17) Transmembrane domain at the C-terminal, found only in flowering plants

Pm|Pm007589

Pm|Pm023987

(18) S4 domain found in the C-terminal, found only in flowering plants

Al|339776

Lu|Lus10005619

### Supplemental References

- Aldous S. 2014. Evolution of the phosphoenolpyruvate carboxylase protein kinase family in C3 and C4 Flaveria spp. *Plant Physiol.* 165: 1076–1091.
- Boudsocq M, Sheen J. 2013. CDPKs in immune and stress signaling. *Trends Plant Sci* 18: 30–40.
- Khraiwesh B. 2015. Genome-wide expression analysis offers new insights into the origin and evolution of *Physcomitrella patens* stress response. *Sci. Rep.* 5: 17434.
- Yang X. 2015. A roadmap for research on crassulacean acid metabolism (CAM) to enhance sustainable food and bioenergy production in a hotter, drier world. *New Phytol.* 207: 491–504.