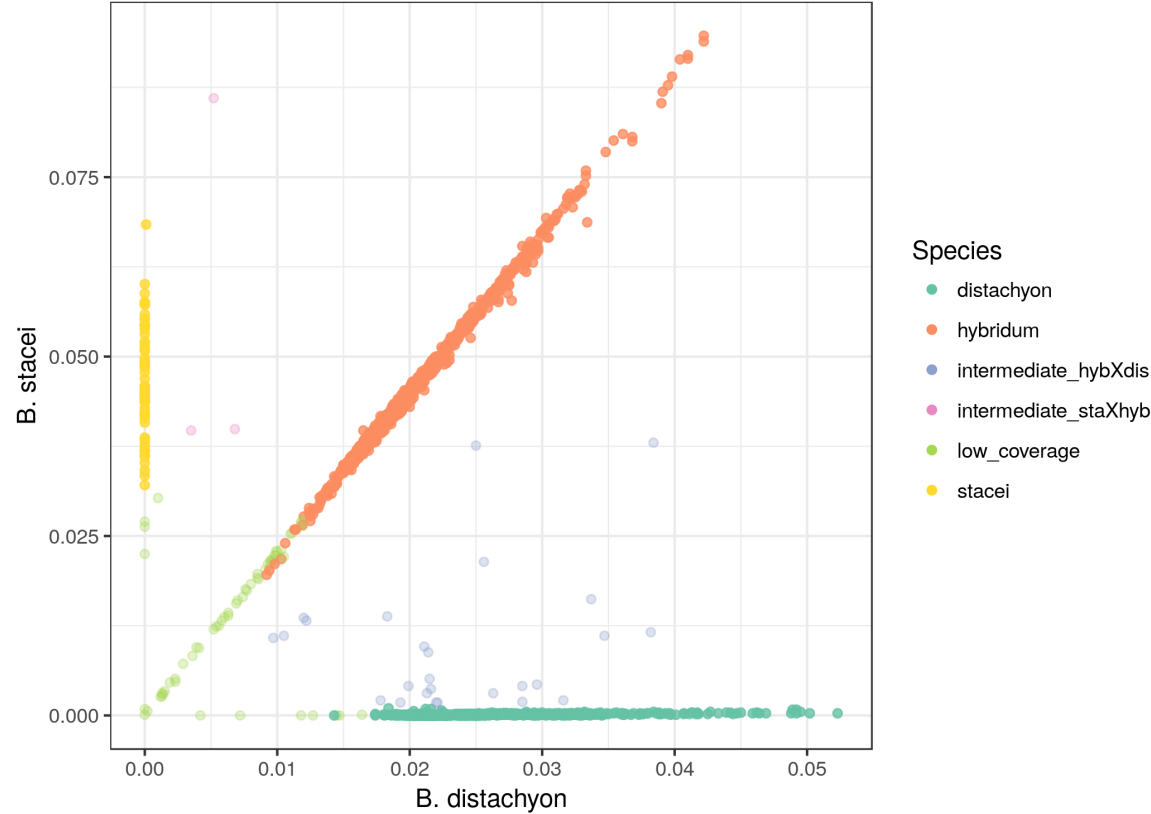
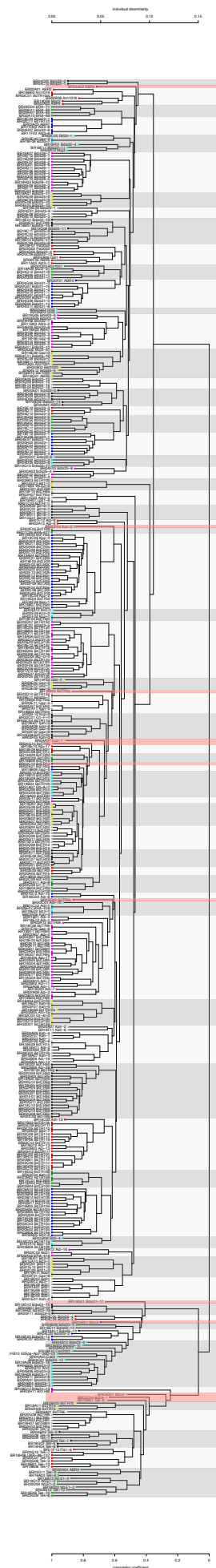


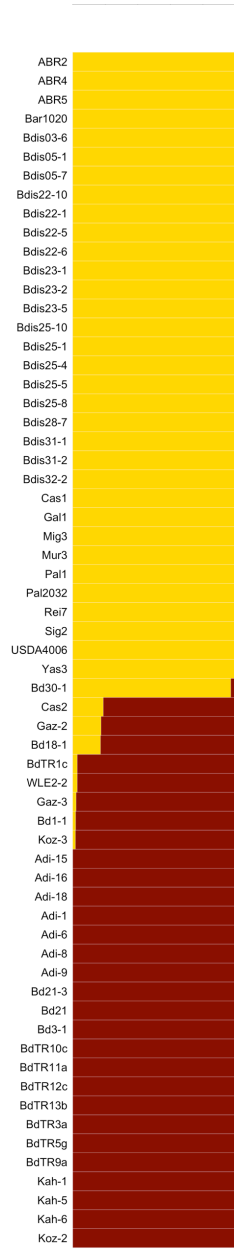
S01. Coverage of *B. stacei* and *B. distachyon* Genomes for Species ID



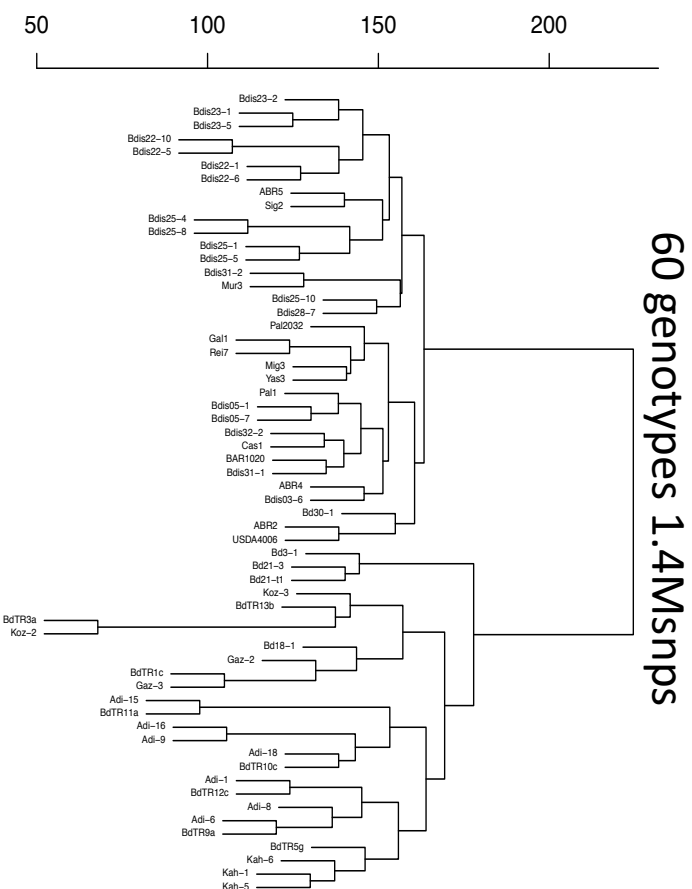
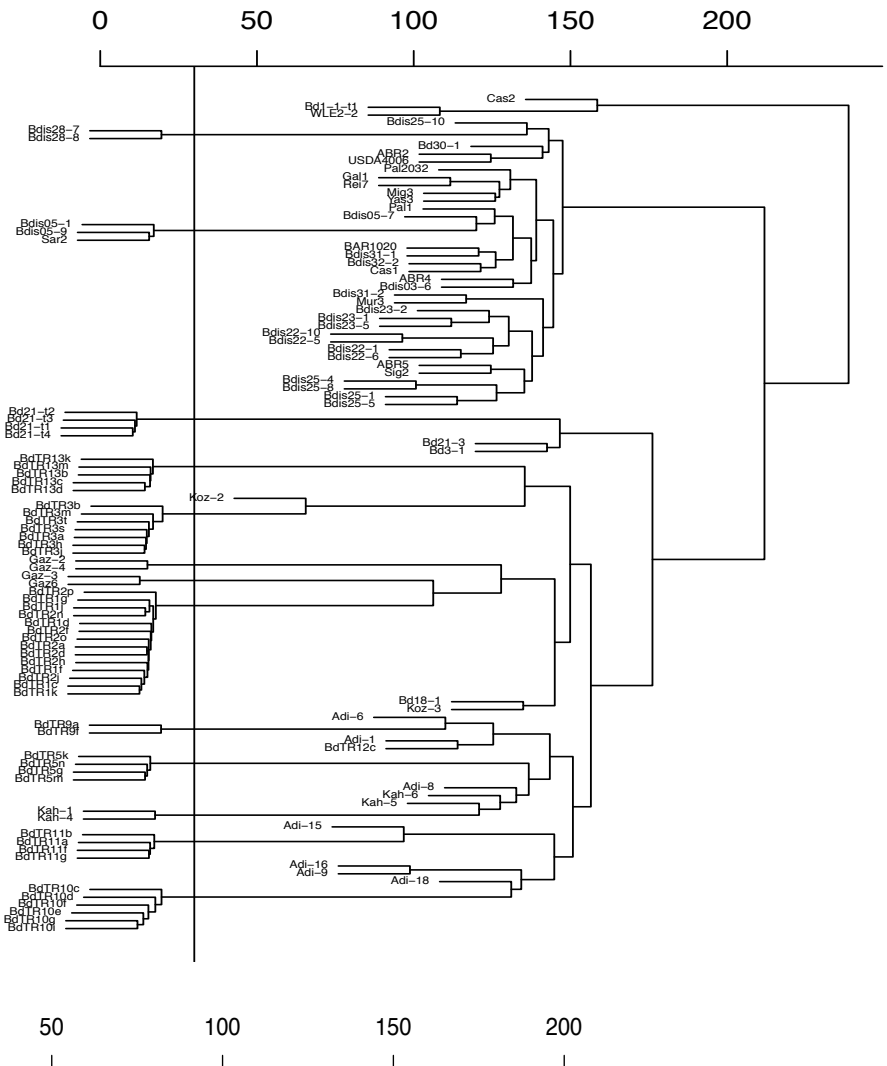
S02. Structure of *B. distachyon* collection as sequenced by GBS



S03. *B. distachyon* reduced set STRUCTURE plots for k=2

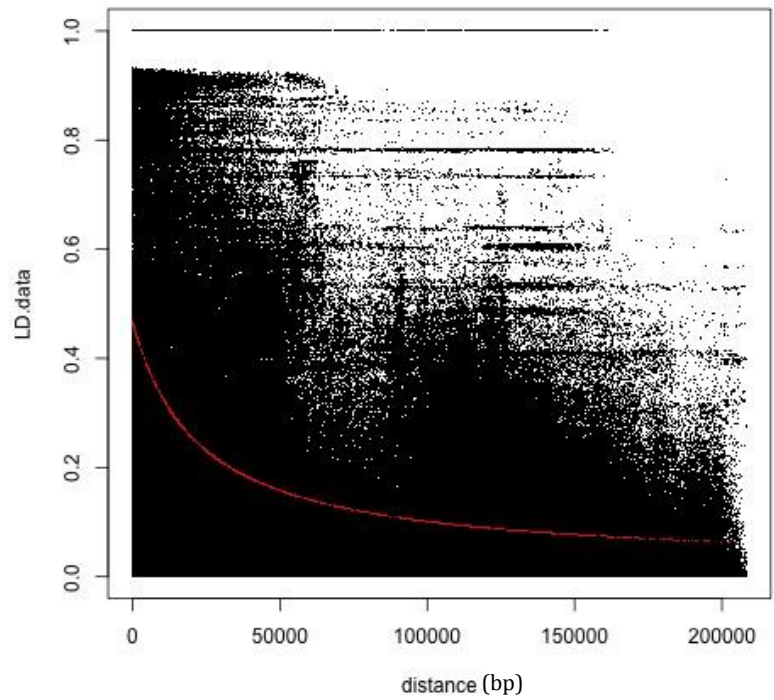
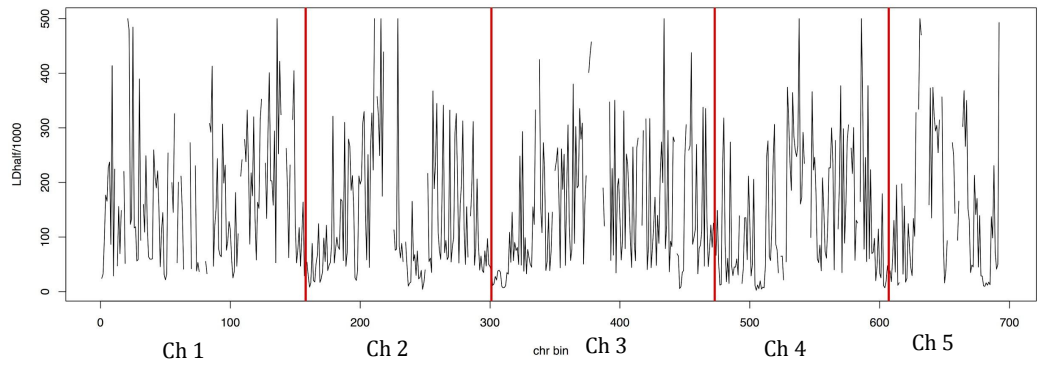


S04. Dendrograms of genomic distance of *B. distachyon* collection at ~2M SNPs. Left - Accessions within a genotype showed very little divergence relative to variation between. Right - A single accession for each genotype was selected and three outlier accessions belonging to subgroup B were removed for linkage disequilibrium and association analysis.



60 genotypes 1.4Msnps

S05. Linkage disequilibrium (LD) across the *B. distachyon* genome
Top – LD as calculated across the five chromosomes (Ch); Bottom – LD at representative section of the genome.



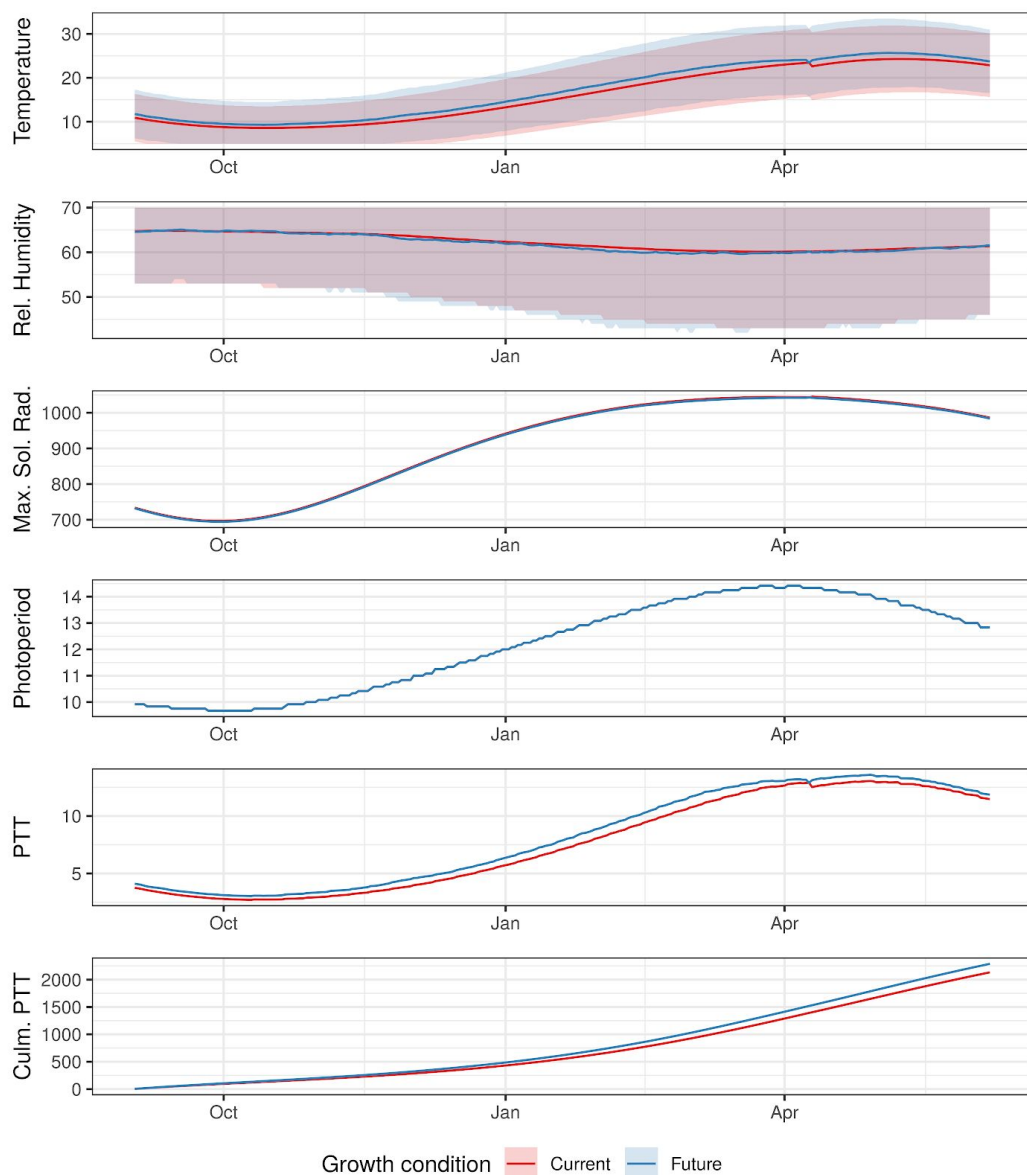
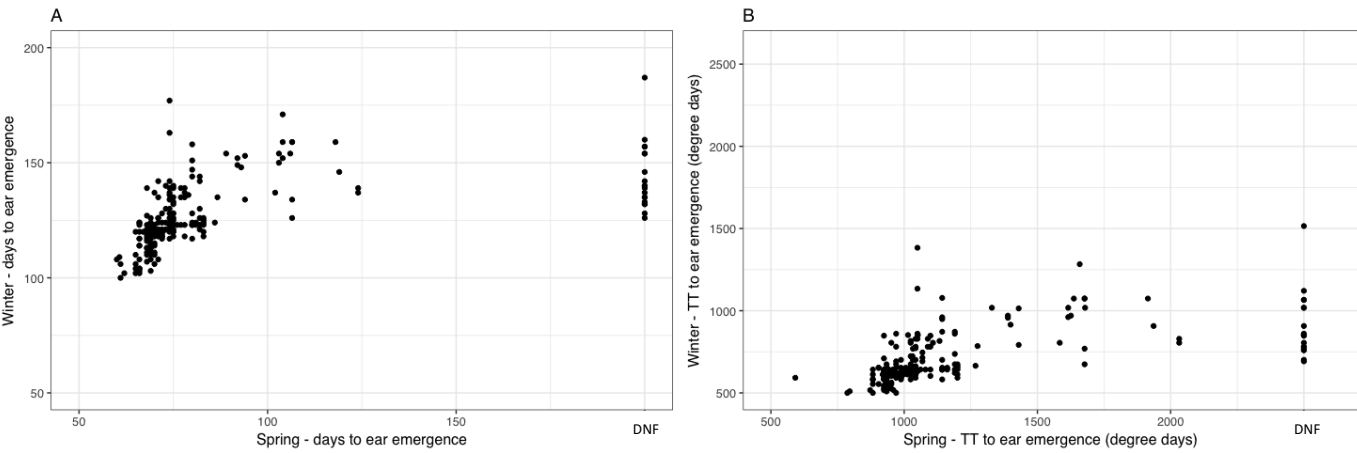


Figure S6: Dynamic growth conditions mimicking current and future climates. From top to bottom, for each simulated climate: mean daily temperature (°C), and diurnal temperature range; mean daily relative humidity (%) and diurnal range; daily maximum solar radiation (Watt/m²); photoperiod (hours daylight); photo-thermal time (degree-days above 2°C with non-zero solar radiation); cumulative photo-thermal time over the growth season. An exploration of relevant climate change models is included as Table S11. Full SolarCalc output files are available at <https://doi.org/10.6084/m9.figshare.7028039.v1>

S08. Flowering time experiment across 266 *B. distachyon* accessions (BVZ0032)



S09 - Phenotypic correlation of traits from the early vigour validation experiment

A. Experimental design

10 replicates of 10 lines:

- Bd21
- Bd21-3
- ABR5
- ABR2
- Bd30-1
- Bdis23-05
- BdTR11a
- BdTR2n

	No. Leaves	No. Tillers	Leaf #3 Width	Leaf #3 Length	Total Leaf Area	Seedling Height	AGBM
Days to Germination	-0.12**	-0.00	-0.07*	-0.09*	-0.14**	-0.07*	-0.12**
No. Leaves		0.05	0.16**	0.06*	0.41**	0.21**	0.42**
No. Tillers			-0.08*	-0.07*	0.13**	-0.04	0.02
Leaf #3 Width				0.53**	0.29**	0.50**	0.46**
Leaf #3 Length					0.35**	0.66**	0.48**
Total Leaf Area						0.56**	0.88**
Seedling Height							0.74**

Table B. Phenotypic correlations (r^2) between surrogate early vigour measurements and destructive harvest. AGBM – above ground biomass dry mass; ** $p < 0.01$, * $p < 0.05$

	Leaf No	Tiller No	Leaf #3 Width	Leaf #3 Length	Total Leaf Area	Height	Biomass
$h^2_{\text{accession}}$	0.43	0.45	0.60	0.64	0.33	0.74	0.51

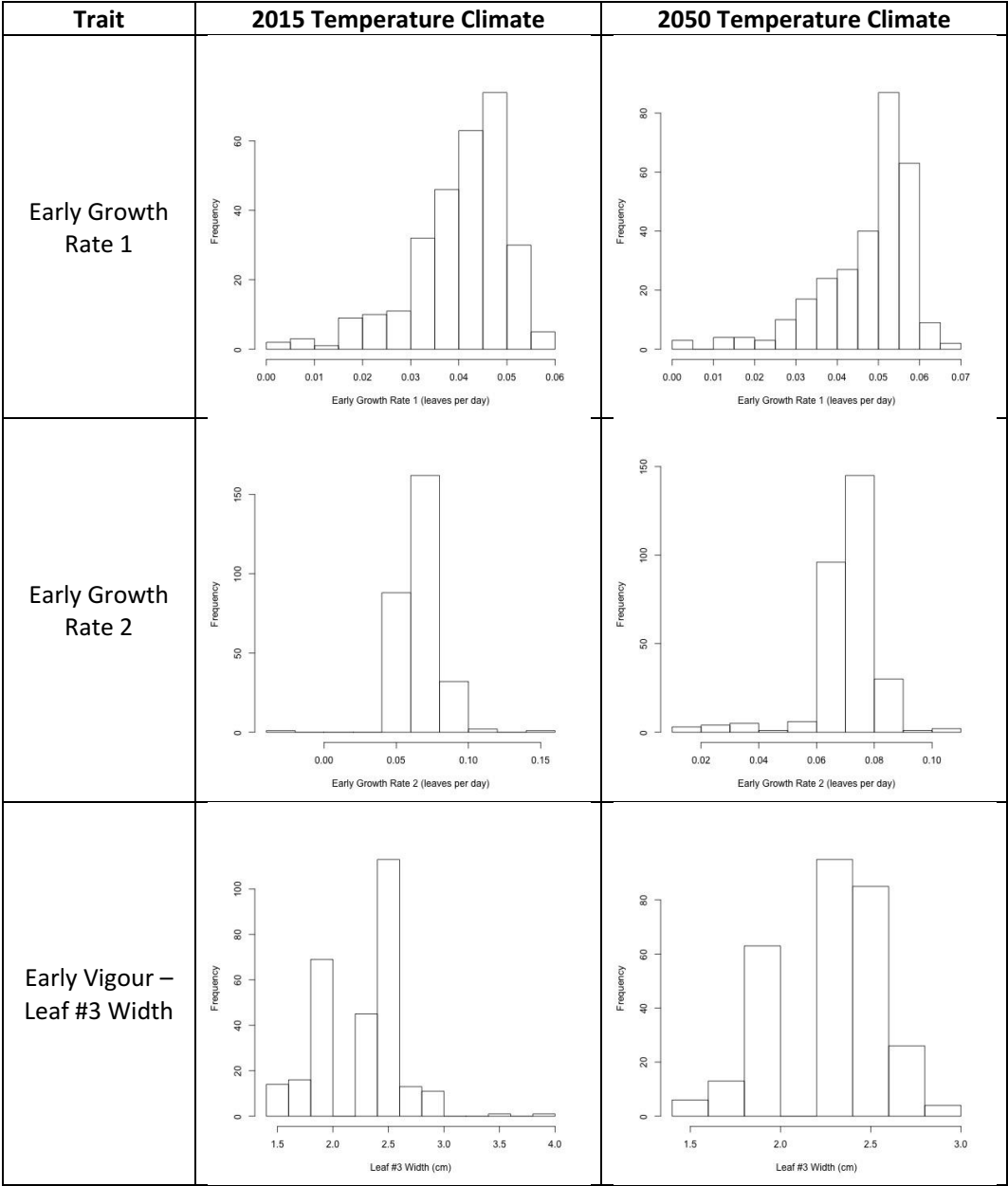
Table C. Heritability of early vigour traits from trait validation study. All results highly significant $p < 0.001$

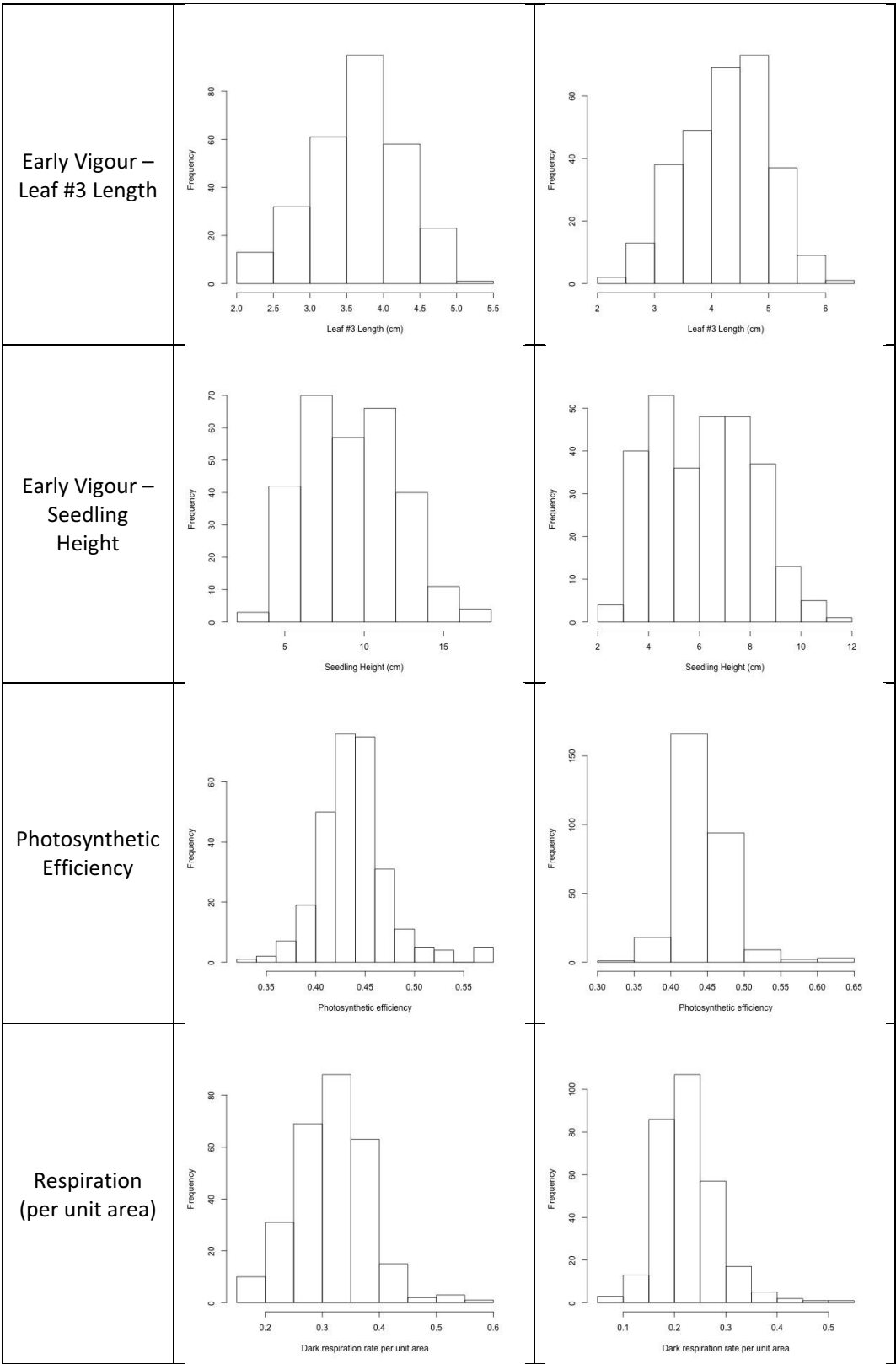
S13. Heritability of traits of interest from 2015 temperature and 2050 temperature climate experiment (BVZ0055)

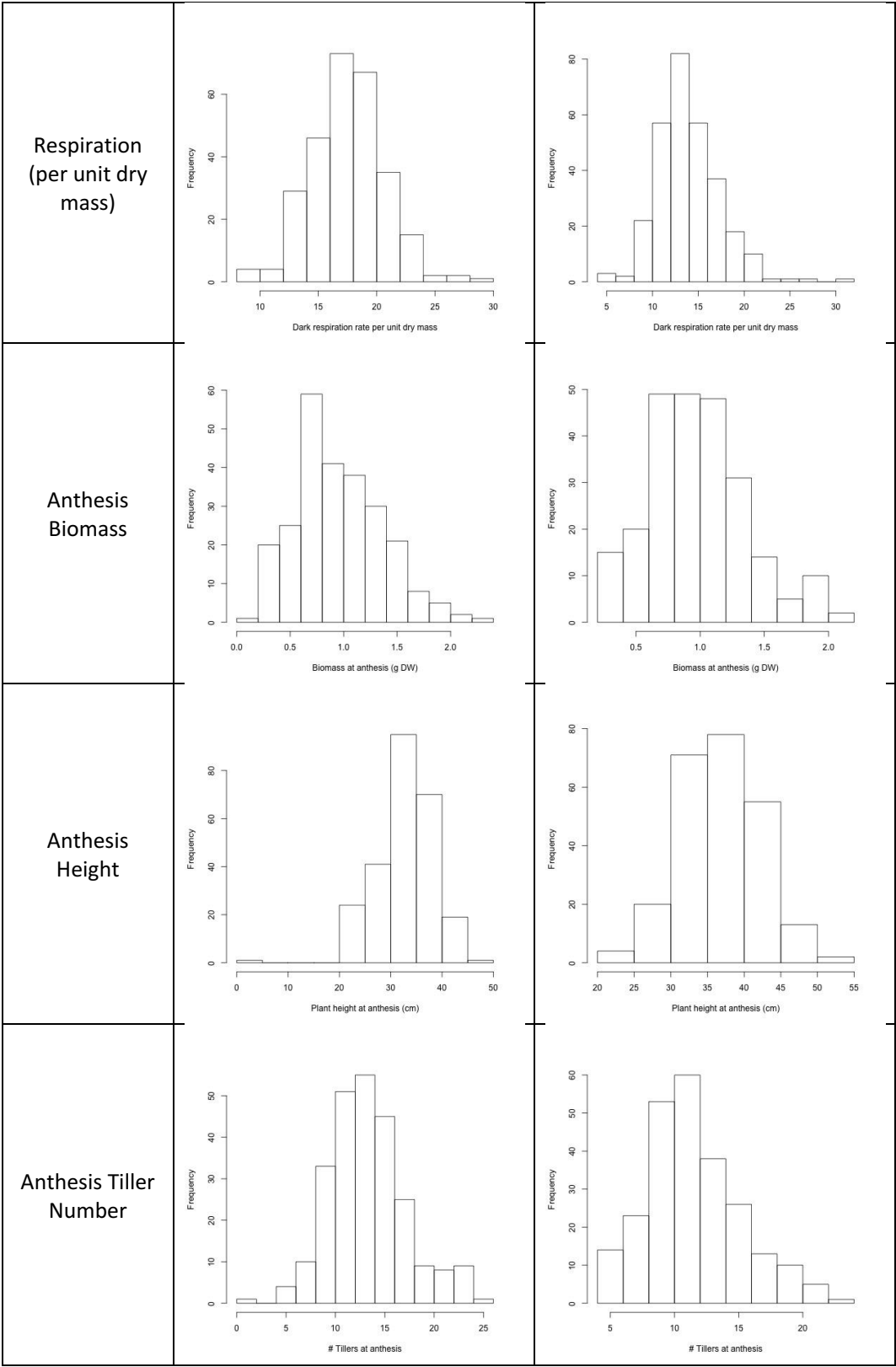
Trait Group	Trait	Heritability - 2015 temperature	Heritability - 2050 temperature
Early Vigour	Early Growth Rate 1	0.44	0.43
	Early Growth Rate 2	0.08	0.13
	Early Vigour – Huan Stage	0.56	0.49
	Early Vigour - # Tillers	0.15	0.30
	Early Vigour – Leaf 3 Width	0.53	0.48
	Early Vigour – Leaf 3 Length	0.70	0.63
	Early Vigour – Seedling Height	0.79	0.84
Energy	Photosynthetic Efficiency	0.24	0.26
	Respiration (per unit area)	0.14	0.15
	Respiration (per unit DM)	*	0.21
	Energy Use Efficiency 1	0.15	0.23
	Energy Use Efficiency 2	0.62	0.56
	Energy Use Efficiency 3	0.42	0.32
	Energy Use Efficiency 4	0.61	0.57
Ear Emergence	Ear Emergence (days)	0.92	0.88
	Ear Emergence (TT)	0.92	0.89
	Ear Emergence (PTU)	0.92	0.89
Growth and Development	Biomass at Ear Emergence	0.62	0.53
	Height at Ear Emergence	0.57	0.57
	Tiller Number at Ear Emergence	0.48	0.37
	Seedling Emergence (TT)	0.21	0.18
	Phyllachron Interval (TT)	0.46	0.42
	Phyllachron Interval (PTU)	0.45	0.44
	Final Growth Efficiency 1 (g/unit TT)	0.40	0.17
	Final Growth Efficiency 2 (g/PTU)	0.39	0.38

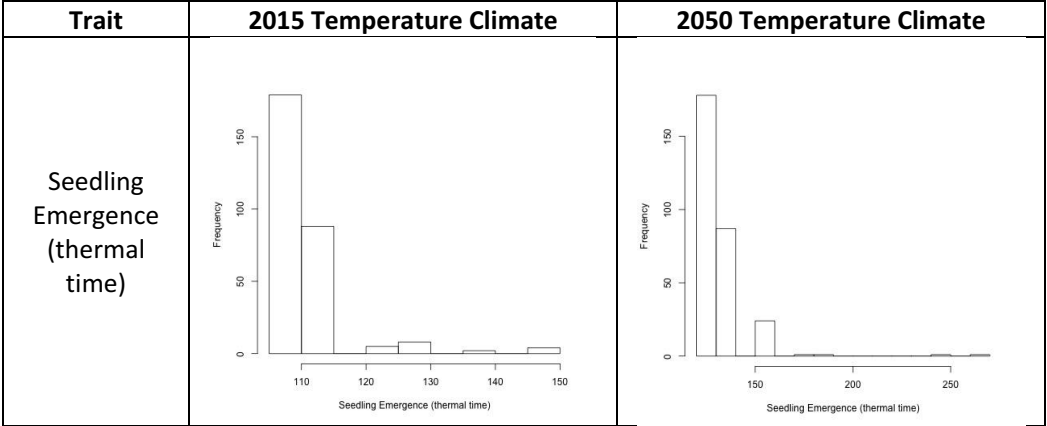
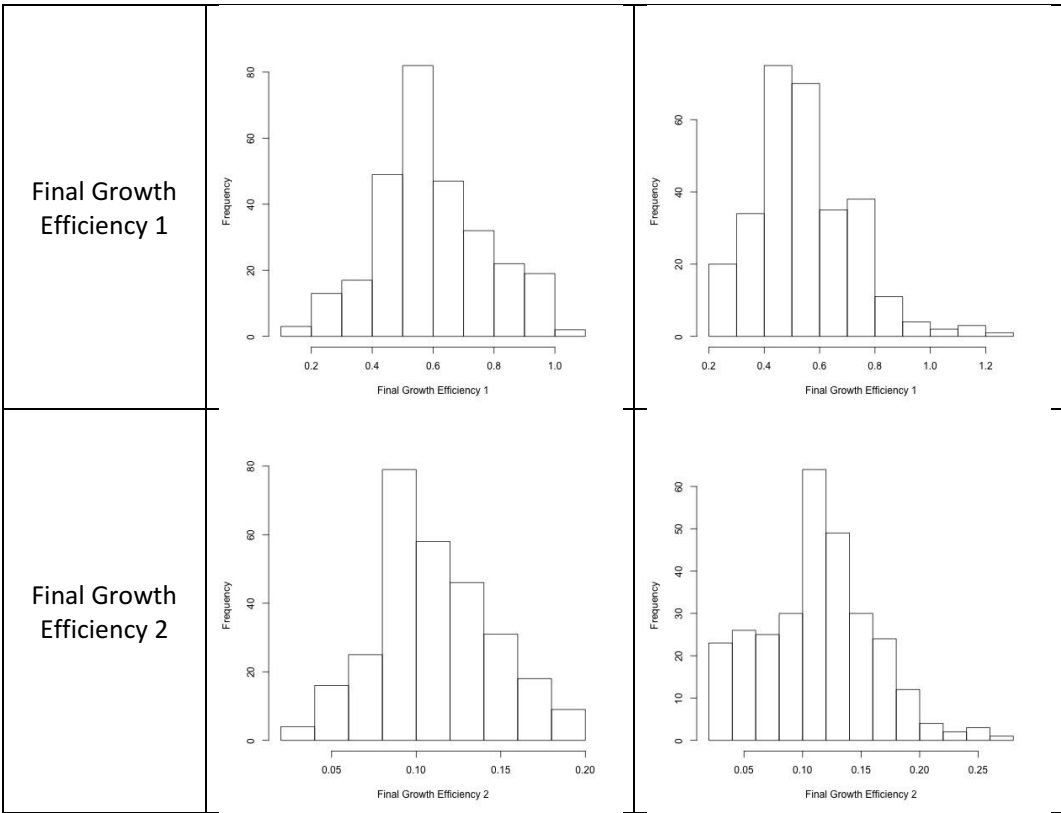
NB: Heritability calculations for BVZ0055 calculated from all data

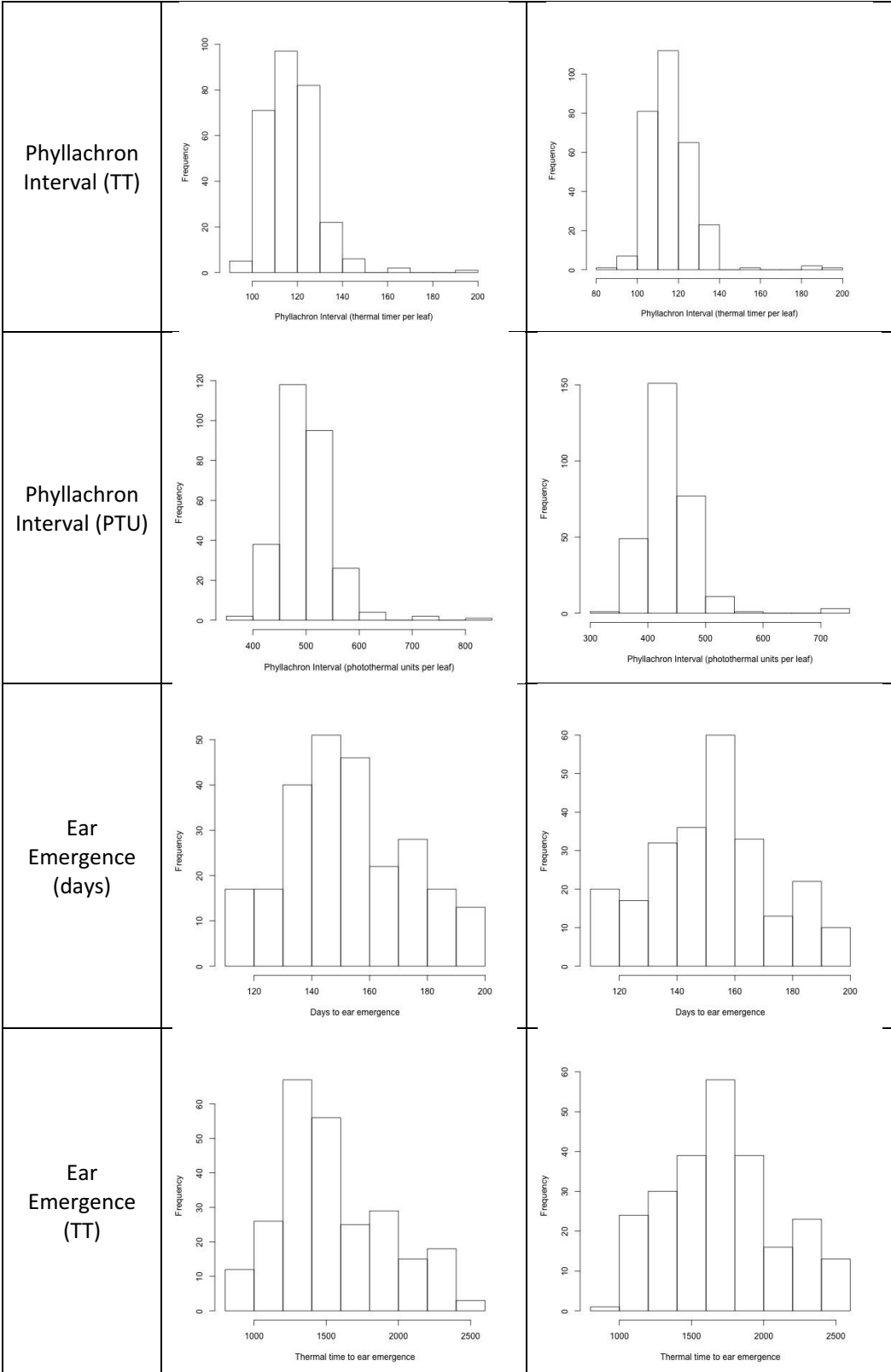
S14. Histograms of all traits in 2015 temperature and 2050 temperature climate experiment

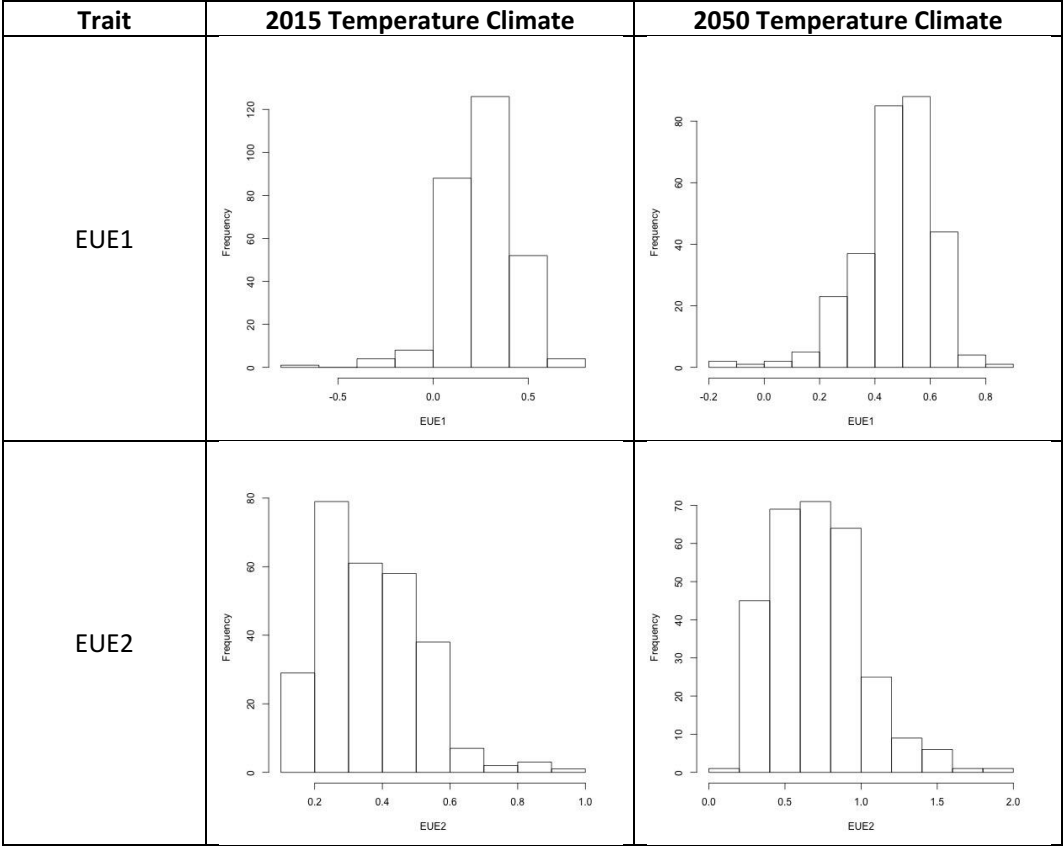
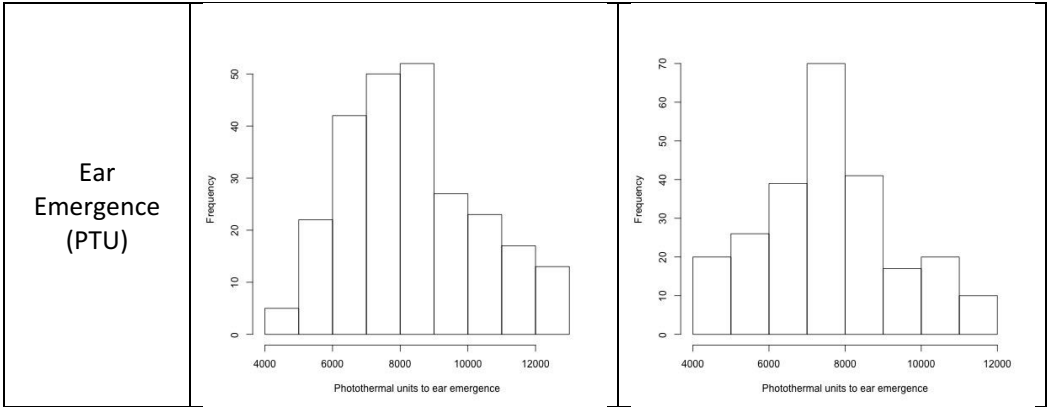


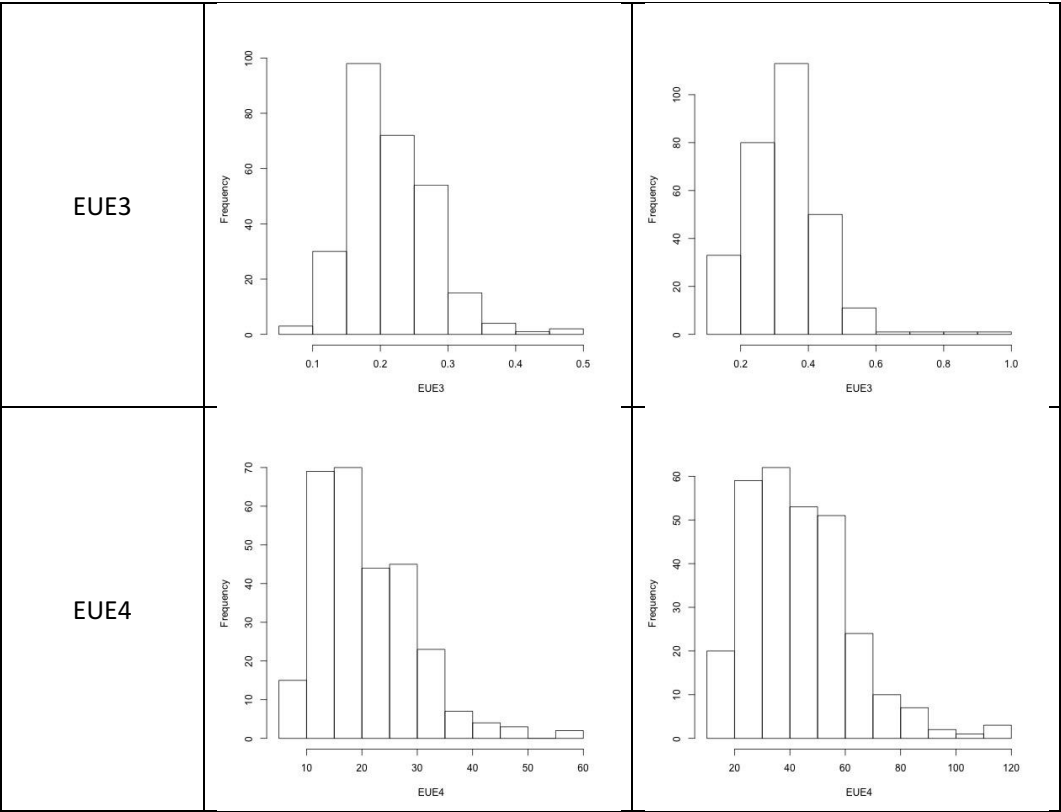












S15. List of QTL identified for traits of interest in 2015 temperature and 2050 temperature climate experiment

QTL	Locus ID	LOD score for conditions and traits where QTL is significant								
		2015 Temperature			2050 Temperature			Temperature G x E		
		Days	TT	PTU	Days	TT	PTU	Days	TT	PTU
EarEmerg_QTL2.1	s2_31474143							4.81	4.56	
EarEmerg_QTL3.1	s3_00392324					4.46				
EarEmerg_QTL4.1	s4_02984287							4.44		
EarEmerg_QTL4.2	s4_08616700		4.44							
EarEmerg_QTL4.3	s4_13237914							4.92		
EarEmerg_QTL5.1	s5_07006866							5.22		
EarEmerg_QTL5.2	s5_09698141							5.22		
EarEmerg_QTL5.3	s5_20347474				5.06	5.01	5.01			

[illegible]

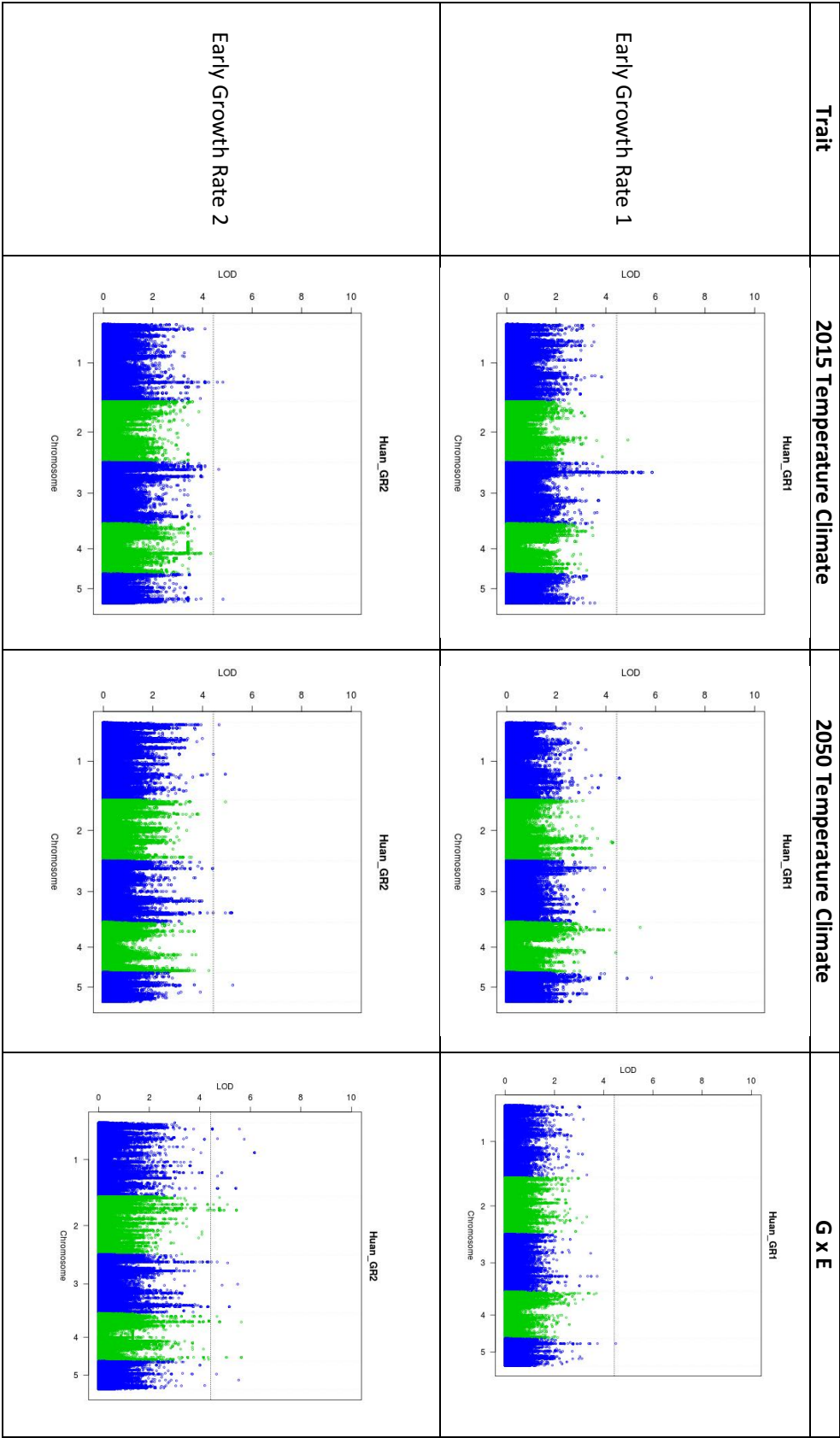
Energy QTLs

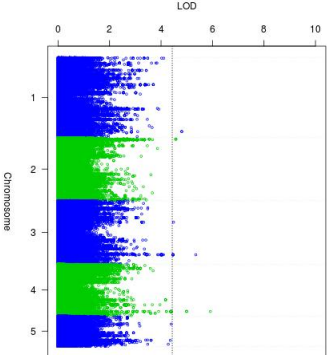
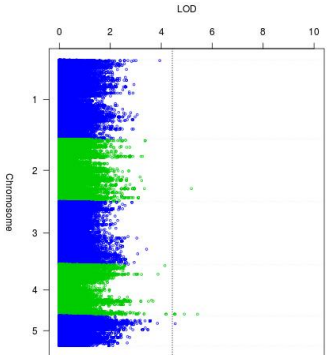
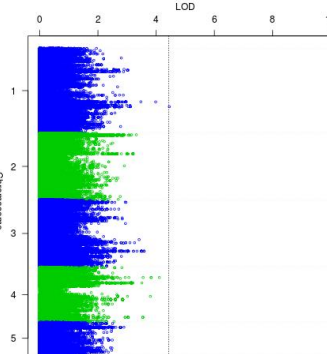
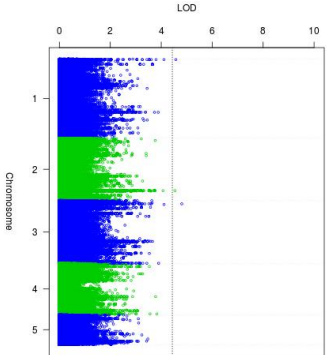
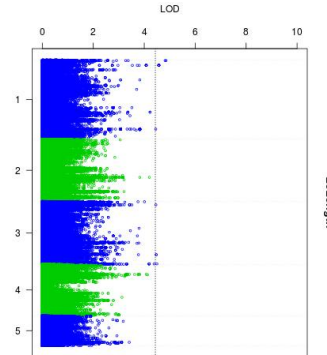
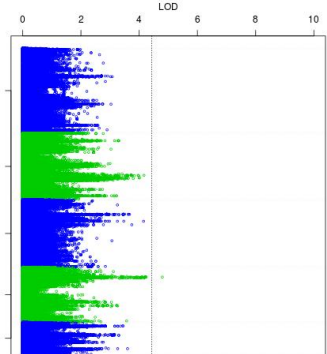
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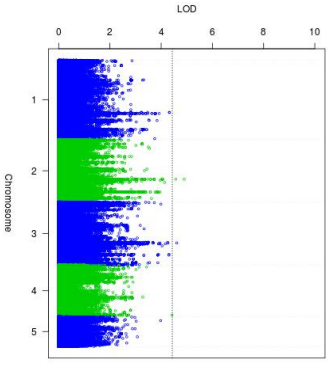
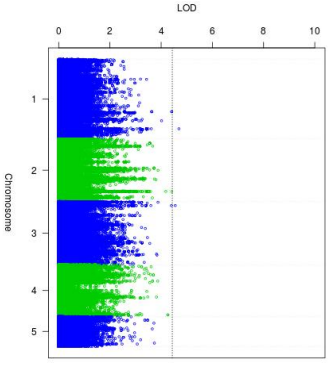
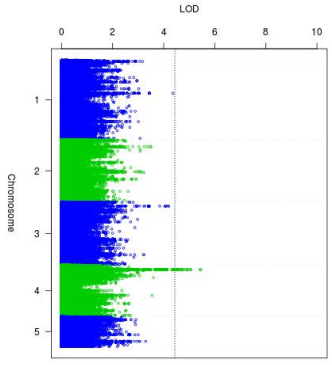
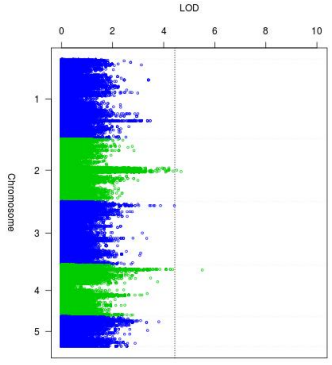
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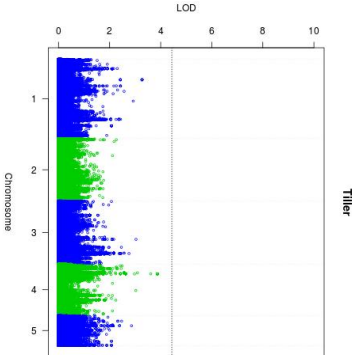
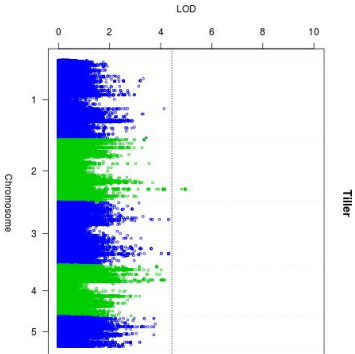
QTL	Locus ID	LOD score for conditions and traits where QTL is significant																							
		2015 Temperature								2050 Temperature								G x E							
		Rd_ area	Rd_ DM	Avg QY	EUE 1	EUE 2	EUE3	EUE 4	Rd_ area	Rd_ DM	Avg QY	EUE 1	EUE 2	EUE 3	EUE 4	EUE 1	EUE2	EUE3	EUE4						
Energy_ QTL3.11	s3_22178931	4.83																							
Energy_ QTL3.12	s3_21991169					4.63		4.31																	
Energy_ QTL3.13	s3_26318303																								
Energy_ QTL3.14	s3_29452743																								
Energy_ QTL3.15	s3_36443490									4.99															
Energy_ QTL3.16	s3_38770516																								
Energy_ QTL3.17	s3_43426288									5.49		5.62													
Energy_ QTL4.1	s4_04046773									4.46															
Energy_ QTL4.2	s4_09202179																				4.54				
Energy_ QTL4.3	s4_09599265			4.60																					
Energy_ QTL4.4	s4_12956633										5.37 1														
Energy_ QTL4.5	s4_13096699													4.80											
Energy_ QTL4.6	s4_13189084																						4.54		
Energy_ QTL4.7	s4_13379767																					5.26			
Energy_ QTL5.1	s5_01570510																4.90				4.45				
Energy_ QTL5.2	s5_04535375									5.17	4.37														
Energy_ QTL5.3	s5_22500232									5.04															

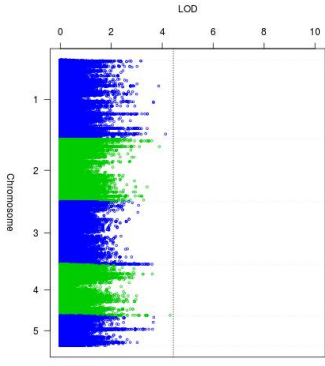
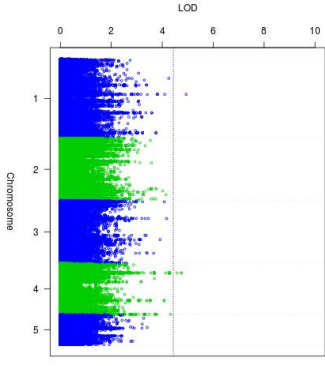
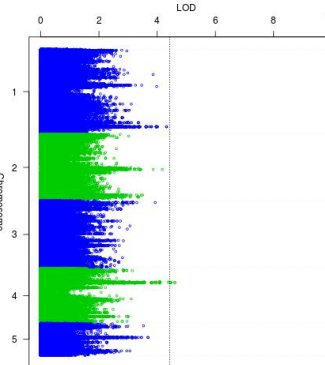
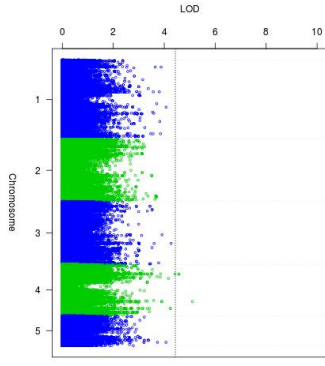
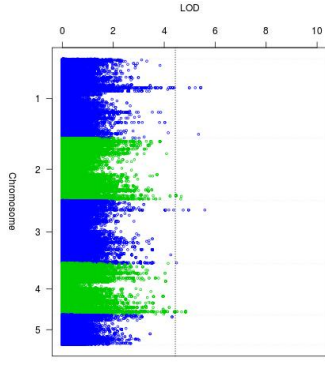
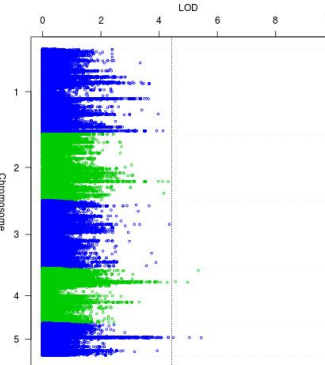
S16: Manhattan Plots for all traits in 2015 temperature and 2050 temperature climate experiment



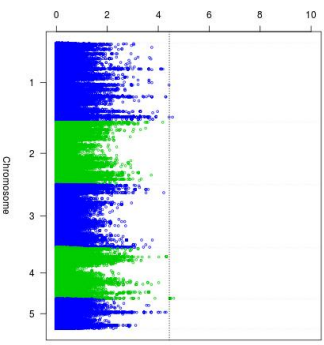
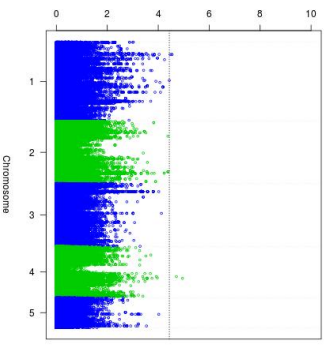
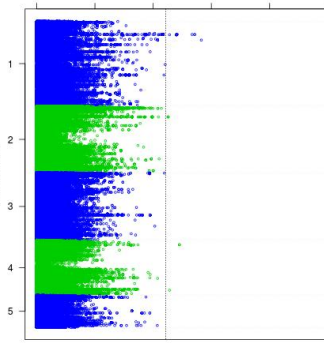
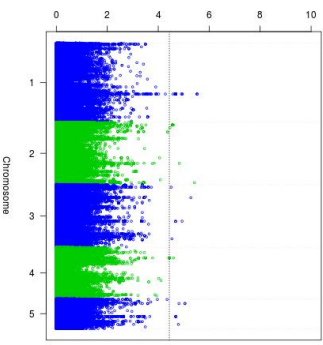
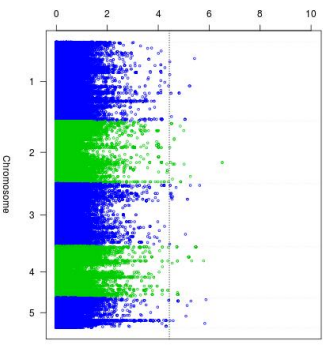
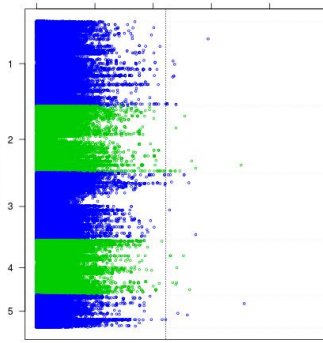
Trait	2015 Temperature Climate	2050 Temperature Climate	G x E
Early Vigour – Leaf 3 Width			
Early Vigour – Leaf 3 Length			

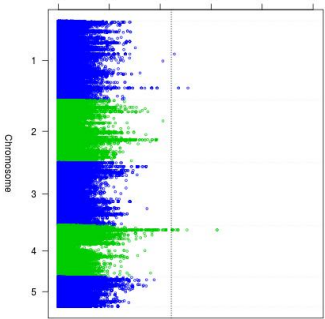
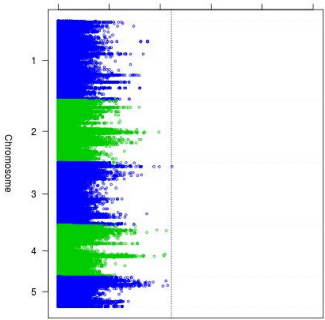
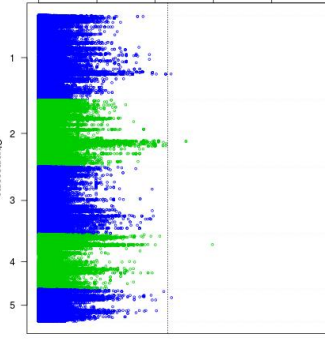
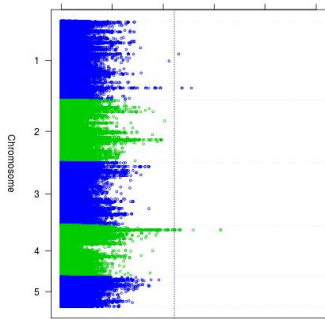
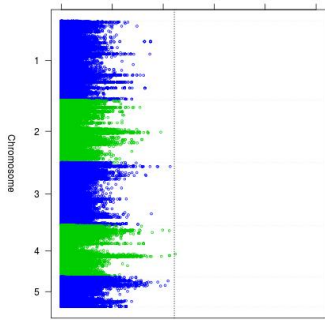
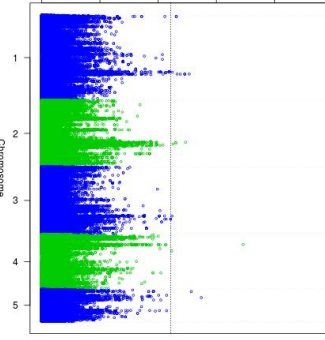
Trait	2015 Temperature Climate	2050 Temperature	G x E
Early Vigour – Seedling Height			NA
Early Vigour - Huan Score			NA

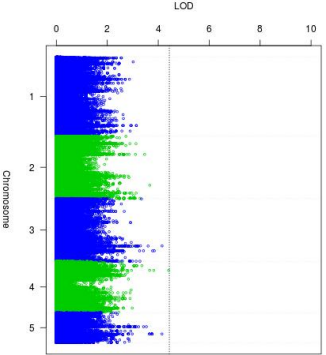
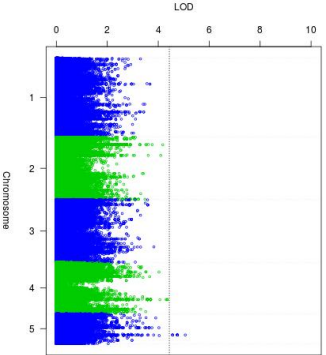
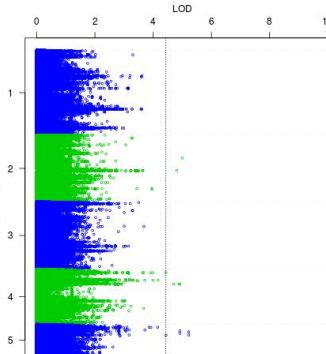
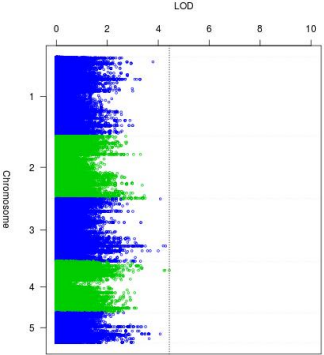
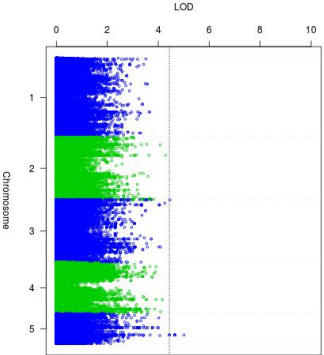
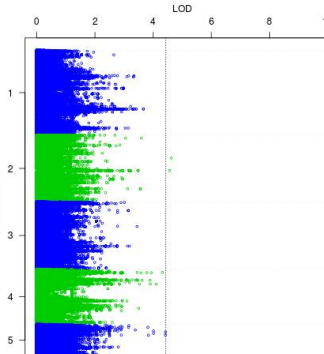
Early Vigour - Number Tillers	 <p>A Manhattan plot showing the association of genetic markers with 'Early Vigour - Number Tillers'. The y-axis is labeled 'Tiller' and ranges from 0 to 10. The x-axis is labeled 'Chromosome' and ranges from 1 to 5. A vertical dashed line is at LOD = 4. The plot shows a dense cluster of blue points on chromosome 1, with a few green points on chromosomes 2, 3, 4, and 5. The highest peak is on chromosome 1, reaching an LOD of approximately 4.5.</p>
	 <p>A Manhattan plot showing the association of genetic markers with 'Early Vigour - Number Tillers'. The y-axis is labeled 'Tiller' and ranges from 0 to 10. The x-axis is labeled 'Chromosome' and ranges from 1 to 5. A vertical dashed line is at LOD = 4. The plot shows a dense cluster of blue points on chromosome 1, with a few green points on chromosomes 2, 3, 4, and 5. The highest peak is on chromosome 1, reaching an LOD of approximately 4.5.</p>
NA	

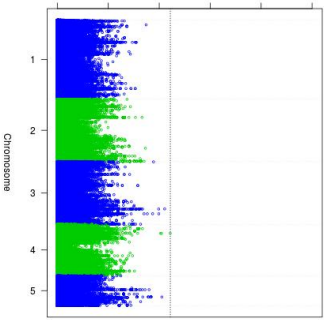
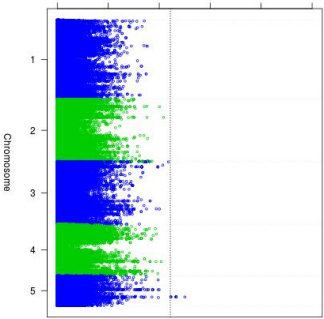
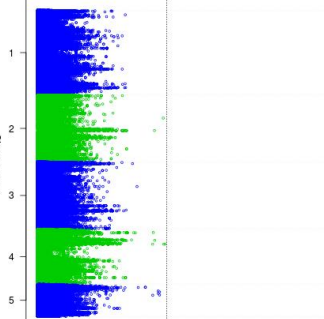
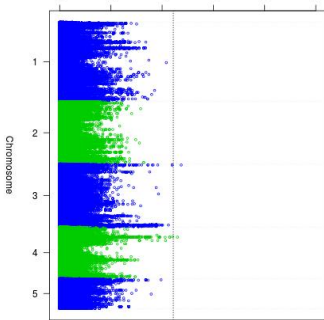
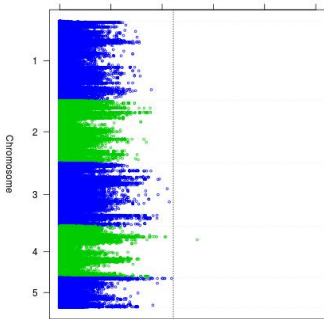
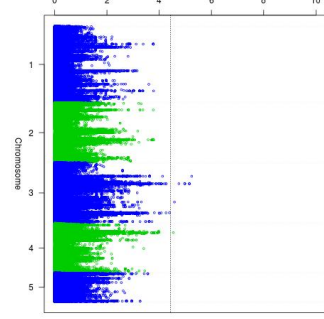
Trait	2015 Temperature Climate	2050 Temperature Climate	G x E
Anthesis Biomass			
Anthesis Height			

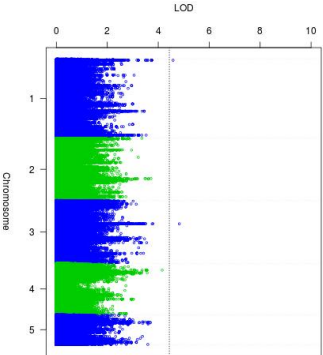
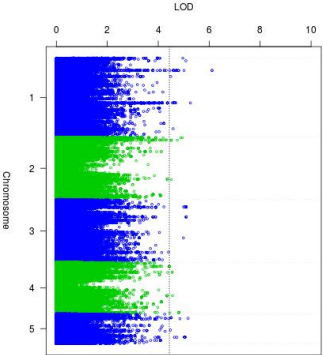
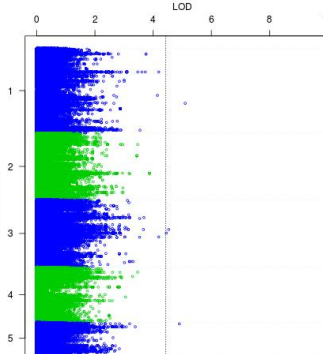
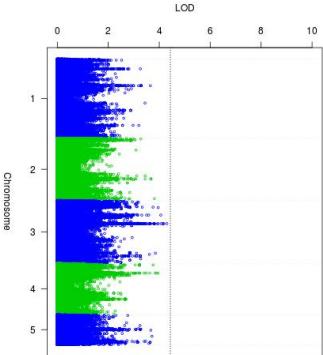
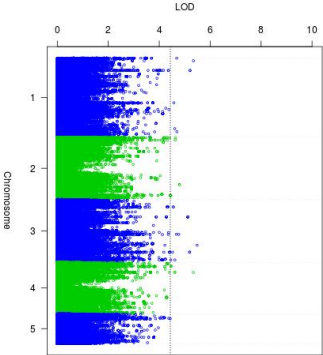
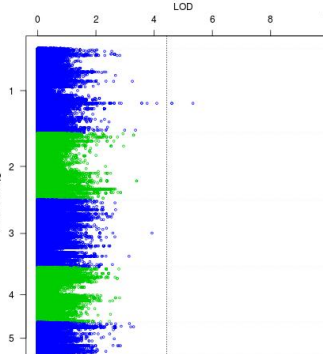
Trait	2015 Temperature Climate			2050 Temperature Climate	G x E
Anthesis Tiller Number					
Final Growth Efficiency 1					

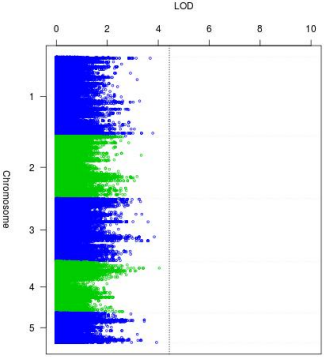
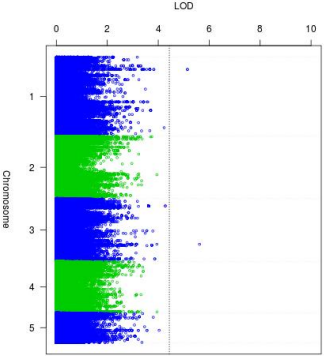
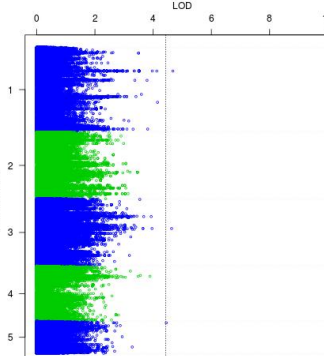
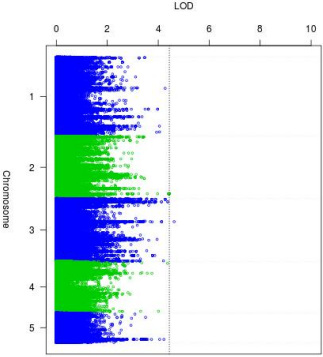
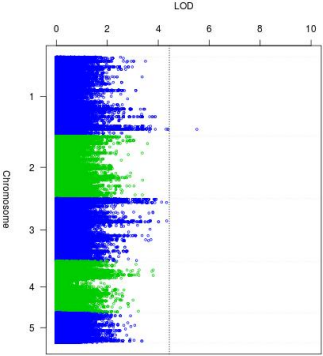
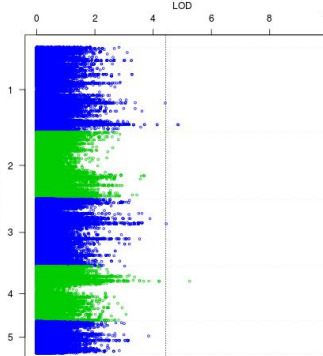
Trait	2015 Temperature Climate	2050 Temperature Climate	G x E
Final Growth Efficiency 2			
Seedling Emergence (TT)			

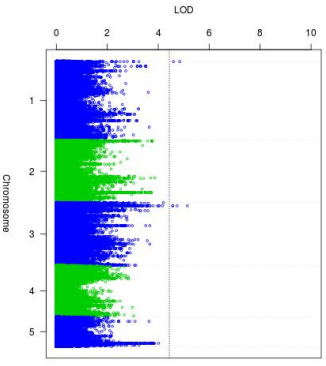
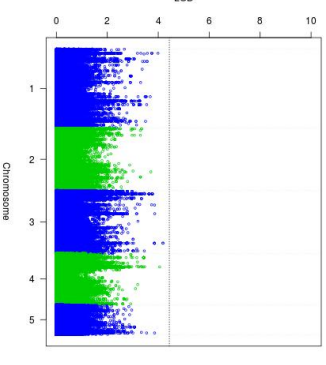
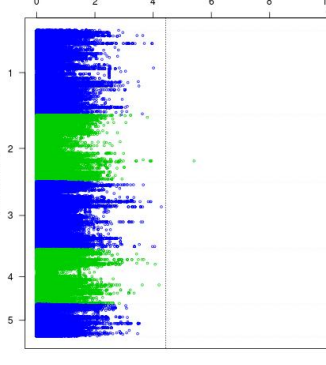
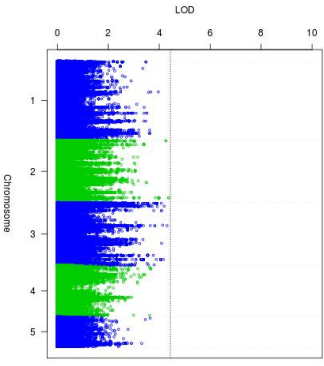
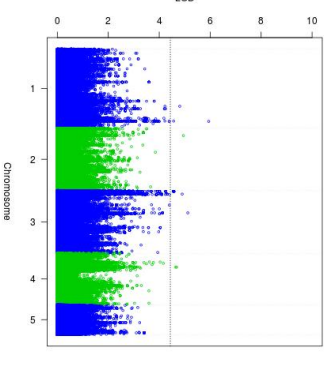
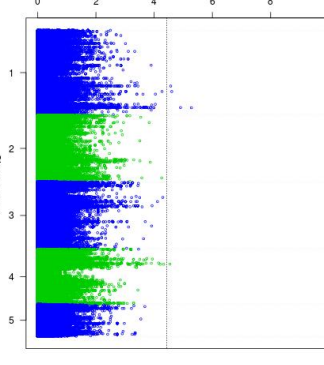
Trait	2015 Temperature Climate	2050 Temperature Climate	G x E
Phyllachron Interval (TT)	<p>Phyllachron Interval (TT)</p> 	<p>Phyll_TT</p> 	<p>Phyll_TT</p> 
Phyllachron Interval (PTU)	<p>Phyll_PTU</p> 	<p>Phyll_PTU</p> 	<p>Phyll_PTU</p> 

Trait	2015 Temperature Climate	2050 Temperature Climate	G x E
Ear Emergence (days)			
Ear Emergence (TT)			

Trait	2015 Temperature Climate	2050 Temperature Climate	G x E
Ear Emergence (PTU)	 <p>EarEmerg_PTU</p>	 <p>EarEmerg_PTU</p>	 <p>EarEmerg_PTU</p>
Photosynthetic Efficiency	 <p>Avg_OY</p>	 <p>Avg_OY</p>	 <p>Avg_OY</p>

Trait	2015 Temperature Climate	2050 Temperature Climate	G x E
Respiration (per unit area)			
Respiration (per unit DM)			

Trait	2015 Temperature Climate	2050 Temperature Climate	G x E
EUE1			
EUE2			

Trait	2015 Temperature Climate	2050 Temperature Climate	G x E
EUE3			
EUE4			

S17. List of candidate genes for strong ear emergence QTL

QTL	Candidate Gene	Gene Location (bp)	Distance from QTL (bp)	Description	Rice Protein Homologs	Arabidopsis Homologs
EarEmerg_QTL5.3	Bradi5g16900	20307500 - 20312116	35 358	Glycosyl hydrolase (GH), subfamily GH32	LOC_Os04g45290.1 - glycosyl hydrolases, putative, expressed (61%)	AT1G62660.1 - Glycosyl hydrolases family 32 protein(62.7%)
	Bradi5g16910	20326042 - 20328526	18 948	YABBY transcription factor	LOC_Os04g45330.1 - YABBY14 protein, putative, expressed (76%)	AT2G45190.1 - Plant-specific transcription factor YABBY family protein (45.3%)
	Bradi5g16917	20332204 - 20335948	11 526	No apical meristem (NAM) protein	LOC_Os02g42970.1 - NAC domain containing protein, putative, expressed (67%)	AT1G12260.1 - NAC 007 (66.8%)
	Bradi5g16930	20342797 - 20343495	3 979	RIM domain containing protein similar to putative RNA recognition motif containing protein	LOC_Os06g13839.1 - RNA recognition motif containing protein, putative, expressed (59%)	AT1G71800.1 - cleavage stimulating factor 64 (17.7%)
	Bradi5g16935	20345479 - 20345819	1 655	Expressed gene	None available	None available
	Bradi5g16940	20349458 - 20350336	1 984	AUXIN-REGULATED PROTEIN-RELATED	LOC_Os02g42990.1 - OsSAUR11 - Auxin-responsive SAUR gene family member, expressed (30%)	AT3G60690.1 - SAUR-like auxin-responsive protein family (24.9%)
	Bradi5g16950	20354677 - 20357924	7 203	CYSTEINE-RICH REPEAT SECRETORY PROTEIN	LOC_Os04g45460.1 - cysteine-rich repeat secretory protein precursor, putative, expressed (66%)	AT3G60720.1 - plasmodesmata-located protein 8 (45.7%)
	Bradi5g16960	20357202 - 20362127	9 728	HEMOGLOBINASE FAMILY MEMBER	LOC_Os04g45470.1 - vacuolar-processing enzyme precursor,	AT1G62710.1 - beta vacuolar processing enzyme (59.6%)

				putative, expressed (72%)	
Bradi5g16970	20364622 - 20368114	17 148	HSP70-HSP90 ORGANIZING PROTEIN 1- RELATED	LOC_Os02g43020.1 - heat shock protein S7I, putative, expressed (89%)	AT1G62740.1 - stress-inducible protein, putative (81.5%)
Bradi5g16980	20367655 - 20372866	20 181	GTPase activity	LOC_Os04g45490.1 - elongation factor, putative, expressed (87%)	AT1G62750.1 - Translation elongation factor EFg/EF2 protein (85.4%)
Bradi5g16990	20375286 - 20376509	27 812	ferrous iron transmembrane transporter activity	LOC_Os04g45520.1 - integral membrane protein, putative, expressed (53%)	AT3G643630.1 - Vacuolar iron transporter (VIT) family protein (48.8%)
Bradi5g17000	20378484 - 20384475	31 010	nuclear hormone receptor binding	LOC_Os04g45570.1 - expressed protein (79%)	AT3G49590.2 - Autophagy-related protein 13 (35.4%)
Bradi5g17010	20389545 - 20389880	42 071	Auxin responsive protein	LOC_Os10g36703.1 - CPuORF40 - conserved peptide uORF- containing transcript, expressed (32%)	none
Bradi5g17020	20390119 - 20395891	42 645	plus-end-directed microtubule motor activity	LOC_Os04g45580.1 - kinesin motor domain containing protein, expressed (88%)	AT2G21300.2 - ATP binding microtubule motor family protein (62.8%)

S18. List of candidate genes for strong early vigour QTL

QTL	Candidate Gene	Gene Location (bp)	Distance from QTL (bp)	Description	Rice Protein Homologs	Arabidopsis Protein Homolog
EarlyVigour_QTL1.1 (s1_00506881)	Bradi1g00567	453524 - 460935	45946	WD40 REPEAT PROTEIN // SUBFAMILY NOT NAMED	LOC_Os03g64300.1 - THION30 - Plant thionin family protein precursor, expressed (87.9%)	AT2G32700.6 - LEUNIG_homolog (68.1%)
	Bradi1g00580	461063 - 467208	39673	protein kinase family protein, putative, expressed, subfamily Raf	LOC_Os07g25680.1 - protein kinase domain containing protein, expressed (71.2%)	AT1G79570.1 - Protein kinase superfamily protein with octicosapeptide/Phox/Bem1p domain (57.5%)
	Bradi1g00587	469432 - 472049	34832	DIMETHYLANILINE MONOOXYGENASE // SUBFAMILY NOT NAMED	LOC_Os07g25540.1 - flavin monooxygenase, putative, expressed (66.6%)	AT1G04610.1 - YUCCA 3 (59.3%)
	Bradi1g00600	479483 - 480393	26488	AWPM-19-LIKE FAMILY PROTEIN	LOC_Os07g24000.1 - AWPM-19-like membrane family protein, putative, expressed (73.7%)	AT1G04560.1 - AWPM-19-like family protein (60.3%)
	Bradi1g00607	482858 - 497592	9289	MYOSIN	LOC_Os03g64290.1 - myosin, putative, expressed (90.6%)	AT1G04160.1 - myosin XI B (78.1%)
	Bradi1g00620	498552 - 500965	5916	ISG15 ligase activity, ubiquitin-protein ligase activity	LOC_Os10g31000.1 - ubiquitin-conjugating enzyme, putative, expressed (86.6%)	AT1G63800.1 - ubiquitin-conjugating enzyme 5 (74.7%)
	Bradi1g00625	500986 - 501500	5381	No description	None	None
	Bradi1g00630	501413 - 501868	5013	No description	None	None

	Bradi1g00642	505289 - 506860	21	No description	None	None
	Bradi1g00654	514295 - 517374	7414	Eama-like transporter family	LOC_Os08g31130.1 - integral membrane protein DUF6 containing protein, expressed (79.1%)	AT1G44800.1 - nodulin MtN21 /Eama-like transporter family protein (52.9%)
	Bradi1g00666	519685 - 521001	12804	ethylene-responsive transcription factor 1 (ERF1)	LOC_Os03g64260.1 - AP2 domain containing protein, expressed (25.4%)	AT3G23240.1 - ethylene response factor 1 (29.9%)
	Bradi1g00672	521910 - 523129	15029	No description	None	None
	Bradi1g00678	523410 - 527774	16529	THYROID RECEPTOR INTERACTING PROTEIN RELATED	LOC_Os03g64250.2 - expressed protein (32.2%)	AT2G20410.1 - RNA-binding ASCH domain protein (30.3%)
	Bradi1g00690	531773 - 534582	24892	myosin phosphatase activity	LOC_Os03g16110.1 - Ser/Thr protein phosphatase family protein, putative, expressed (77.6%)	AT2G39840.1 - tyne one serine/threonine protein phosphatase 4 (76.4%)
	Bradi1g00700	539495 - 542936	32614	inorganic phosphate transmembrane transporter activity, manganese ion transmembrane transporter activity	LOC_Os04g10690.1 - inorganic phosphate transporter, putative, expressed (78.6%)	AT3G54700.1 - phosphate transporter 1;7 (75.6%)
	Bradi1g00710	544048 - 547886	37167	Leucine-zipper of ternary complex factor MIP1	LOC_Os03g64230.1 - expressed protein (55.6%)	AT5G60720.1 - Protein of unknown function, DUF547 (40.2%)
	Bradi1g00720	549976 - 553622	43095	OTU DOMAIN CONTAINING PROTEIN	LOC_Os03g64219.1 - OTU-like cysteine protease family	AT5G04250.2 - Cysteine proteinases superfamily

EarlyVigour_QTL3.1 (s3_03204480)					protein, putative, expressed (54.1%)	protein (42.9%)
	Bradi1g00730	553623 - 558060	46742	ATPase activity, coupled	LOC_Os03g64210.1 - T-complex protein, putative, expressed (86.2%)	AT2G28000.1 - chaperonin-60alpha (84.5%)
	Bradi1g00740	555382 - 558935	48501	Enoyl-CoA hydratase 2 / ECH2	LOC_Os05g09370.3 - kinase, pfkB family, putative, expressed (70.6%)	AT5G60335.1 - Thioesterase superfamily protein (62.9%)
	Bradi3g04580	3154480 - 3156693	47787	sugar transmembrane transporter activity	LOC_Os02g06540.1 - transporter family protein, putative, expressed (84.7%)	AT1G11260.1 - sugar transporter 1 (70.1%)
	Bradi3g04585	3158304 - 3160486	43994	Wound-induced protein	LOC_Os06g46970.1 - wound induced protein, putative, expressed (78.3%)	AT4G10265.1 - Wound-responsive family protein (47.8%)
	Bradi3g04590	3161033 - 3162956	41524	F-Box	LOC_Os01g32640.1 - OsFBX9 - F-box domain containing protein, expressed (32.0%)	AT3G20620.1 - F-box family protein-related (20.6%)
	Bradi3g04598	3165923 - 3169372	35108	No description	LOC_Os01g41950.1 - expressed protein (46.8%)	None
Bradi3g04604	3170333 - 3170731	33749	No description	None	None	
Bradi3g04611	3173051 - 3175042	29438	No description	None	None	
Bradi3g04617	3183006 - 3184040	20440	No description	None	None	
Bradi3g04620	3184172 -	17484	F-Box	LOC_Os01g32640.1 - OsFBX9 -	AT3G17530.1 - F-box and	

		3186996			F-box domain containing protein, expressed (41.4%)	associated interaction domains-containing protein (31.4%)
	Bradi3g04630	3187661 - 3192603	11877	CAMK includes calcium/calmodulin dependent protein kinases	LOC_Os02g06570.1 - CAMK_KIN1/SNF1/Nim1_like.1 3 - CAMK includes calcium/calmodulin dependent protein kinases, expressed (78.9%)	AT5G07070.1 - CBL-interacting protein kinase 2 (68.8%)
	Bradi3g04640	3192668 - 3196846	7634	Rho GTPase binding	LOC_Os02g06580.1 - formin, putative, expressed (72.5%)	AT5G54650.2 - formin homologY5 (35.8%)
	Bradi3g04650	3198706 - 3204772	0	ATPase activity, coupled	LOC_Os02g06584.2 - zinc finger C-x8-C-x5-C-x3-H type family protein, expressed (78.1%)	AT3G21810.1 - Zinc finger C-x8-C-x5-C-x3-H type family protein (30.6%)
	Bradi3g04655	3206978 - 3212873	2498	No description	None	None
	Bradi3g04660	3207821 - 3210064	3341	Leucine-rich repeat protein // Ras suppressor protein	LOC_Os02g06600.1 - receptor-like protein kinase 2 precursor, putative, expressed (52.1%)	AT1G35710.1 - Protein kinase family protein with leucine-rich repeat domain (51.6%)
	Bradi3g04671	3211145 - 3215539	6665	PROPROTEIN CONVERTASE SUBTILISIN/KEXIN	LOC_Os09g30250.1 - OsSub58 - Putative Subtilisin homologue, expressed (54.4%)	AT2G04160.1 - Subtilisin-like serine endopeptidase family protein (56.2%)
	Bradi3g04681	3216712 - 3220903	12232	Leucine Rich Repeat	LOC_Os02g06600.1 - receptor-like protein kinase 2 precursor, putative, expressed (48.8%)	AT1G71400.1 - receptor like protein 12 (43.3%)
	Bradi3g04690	3222059 - 3227339	17579	serine-type endopeptidase activity	LOC_Os02g10520.1 - OsSub12 - Putative Subtilisin homologue,	AT2G04160.1 - Subtilisin-like serine endopeptidase family

EarlyVigour_QT13.3 (s3_09601708)					expressed (51.3%)	protein (51.2%)
	Bradi3g04701	3232085 - 3232706	27605	No description	None	None
	Bradi3g04705	3234102 - 3234683	29622	No description	LOC_Os02g15160.1 - OsFBX40 - F-box domain containing protein, expressed (58.1%)	None
	Bradi3g04710	3238168 - 3240567	33688	Leucine Rich Repeat	LOC_Os02g06600.1 - receptor-like protein kinase 2 precursor, putative, expressed (55.5%)	AT4G04220.1 - receptor like protein 46 (40.3%)
	Bradi3g04717	3240879 - 3243367	36399	Peroxidase / Lactoperoxidase	LOC_Os02g06630.1 - peroxidase precursor, putative, expressed (75.6%)	AT4G11290.1 - Peroxidase superfamily protein (57.3%)
	Bradi3g04730	3244701 - 3247978	40221	ubiquitin-protein ligase activity	LOC_Os05g42424.1 - ubiquitin family protein, putative, expressed (100%)	AT5G20620.1 - ubiquitin 4 (99.7%)
	Bradi3g04737	3249676 - 3258707	45196	FBD	LOC_Os12g31340.1 - OsFBD15 - F-box and FBD domain containing protein, expressed (48%)	AT3G28410.1 - F-box/RN1-like superfamily protein (39.4%)
	Bradi3g11120	9554183 - 9559683	42025	CONSERVED OLIGOMERIC GOLGI COMPLEX SUBUNIT 4	LOC_Os02g25840.1 - conserved oligomeric Golgi complex component 4, related, putative, expressed (65.7%)	AT4G01400.2 (67.4%)
	Bradi3g11130	9559943 - 9567535	34173	diaminopimelate decarboxylase activity	LOC_Os02g24354.1 - pyridoxal-dependent decarboxylase protein, putative, expressed (80.2%)	AT5G11880.1 - Pyridoxal-dependent decarboxylase family protein (77%)

	Bradi3g11140	9570245 - 9575774	25934	phosphatidylcholine transmembrane transporter activity	LOC_Os10g03400.2 - phosphatidylinositol transfer, putative, expressed (84.2%)	AT4G39170.1 - Sec14p-like phosphatidylinositol transfer family protein (65.7%)
	Bradi3g11145	9583051 - 9584271	17437	No description	LOC_Os02g25820.1 - B3 DNA binding domain containing protein, expressed (25.8%)	AT4G01500.1 - AP2/B3-like transcriptional factor family protein (19.3%)
	Bradi3g11150	9588169 - 9590496	11212	S-ADENOSYL-L-METHIONINE-DEPENDENT METHYLTRANSFERASE DOMAIN-CONTAINING PROTEIN	LOC_Os03g03470.2 - expressed protein (37.5%)	AT5G63100.1 - S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (50.8%)
	Bradi3g11156	9591855 - 9592133	9575	No description	LOC_Os02g24240.1 - expressed protein (46.7%)	None
	Bradi3g11163	9592708 - 9593625	8083	No description	None	None
	Bradi3g11170	9596208 - 9597278	4430	No description	LOC_Os01g15610.1 - expressed protein (38%)	None
	Bradi3g11175	9605941 - 9606524	4233	Expressed protein	none	none
	Bradi3g11180	9608962 - 9615936	7254	CYCLIN-T1-3	LOC_Os02g24190.1 - cyclin-T1-2, putative, expressed (76.3%)	AT4G19600.1 - Cyclin family protein (33.5%)
	Bradi3g11191	9628090 - 9633334	26382	SENTRIN/SUMO-SPECIFIC PROTEASE	LOC_Os06g13890.1 - expressed protein (49.9%)	none
	Bradi3g11197	9637041 - 9644509	35333	PHOSPHATIDYLINOSITOL/PHOSPHATIDYLCHOLINE TRANSFER PROTEIN SFHG-RELATED	LOC_Os02g04020.1 - expressed protein (73.3%)	AT2G21520.1 - Sec14p-like phosphatidylinositol transfer family protein (71.7%)

	Bradi3g11200	9645536 - 9650291	43828	No description	None	None
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S19. List of candidate genes for strong energy QTL

QTL	Candidate Gene	Gene Location (bp)	Distance from QTL	Description	Rice Protein Homologs	Arabidopsis Protein Homolog
Energy_QTL1.4 (s1_02600962)	Bradi1g03853	2583581 - 2584374	16588	Expressed protein	NA	NA
	Bradi1g03856	2585071 - 2586838	14124	Differentially upregulated in nitrogen Roots vs. Shoots comparison	NA	NA
	Bradi1g03860	2586981 - 2591146	9816	aminopeptidase activity	LOC_Os03g60460.1 - aminopeptidase, putative, expressed (94.9%)	AT5G13520.1 - peptidase M1 family protein (78.1%)
	Bradi1g03867	2595174 - 2592606	8356	Coexpressed along with genes transcribed in shoot tissue during night	LOC_Os12g27790.1 - OsFBX443 - F-box domain containing protein, expressed (14.7%)	NA
	Bradi1g03880	2600038 - 2603789	0	Coexpressed along with genes transcribed in shoot tissue during night	LOC_Os03g60430.2 - AP2 domain containing protein, expressed (62.6%)	AT2G28550.3 - related to AP2.7 (42.2%)
	Bradi1g03890	2608441 - 2611283	7479	BRICK1, putative	NA	AT2G22640.1 - BRICK1, putative (76.5%)
	Bradi1g03900	2613615 - 2617812	12653	DNA-dependent ATPase activity	LOC_Os03g60390.1 - PHD finger protein, putative, expressed (78.1%)	AT5G05610.2 - aifin-like 1 (66.8%)
	Bradi1g03910	2622358 - 2625266	24304	aldo-keto reductase activity, carbonyl reductase (NADPH) activity, steroid dehydrogenase activity, acting on the CH-OH group	LOC_Os03g60380.1 - cinnamoyl CoA reductase, putative, expressed (83.3%)	AT5G58490.1 - NAD(P)-binding Rossmann-fold superfamily protein (63.4%)

				of donors, NAD or NADP as acceptor		
Energy_QTL1.5 (s1_11783844)	Bradi1g14810	11754643 - 11756133	27711	zinc ion binding	LOC_Os03g41110 - C2H2 zinc finger protein, expressed (61%)	AT1G24625 - zinc finger protein 7 (27%)
	Bradi1g14815	11756698 - 11759061	24783	No annotation	none	none
	Bradi1g14820	11759343 - 11761732	22112	CYCCLIN, subfamily CYCA3	LOC_Os03g41100 - cyclin, putative, expressed (62%)	AT1G47230 - CYCCLIN A3;4 (60%)
	Bradi1g14830	11764332 - 11771956	11888	Protein of unknown function (DUF760)	LOC_Os03g41080.1 - seed maturation protein PM23, putative, expressed (93.9%)	AT2G14910.1 - (1 of 8) PF05542 - Protein of unknown function (DUF760) (60.3%)
	Bradi1g14835	11777417 - 11777940	5904	Expressed, Coexpressed along with genes transcribed in shoot tissue during night	LOC_Os08g31460.1 - GTPase of unknown function domain containing protein, putative, expressed (83%)	none
	Bradi1g14840	11782056 - 11785989	0	ferrous iron transmembrane transporter activity	LOC_Os12g39180.1 - natural resistance-associated macrophage protein, putative, expressed (80.4%)	AT1G47240.1 - NRAMP metal ion transporter 2 (72.8%)
	Bradi1g14845	11786471 - 11787344	2627	EXTENSIN, PROLINE-RICH PROTEIN, Coexpressed with genes downregulated during drought stress	LOC_Os03g55290.1 - GASR3 - Gibberellin-regulated GASA/GAST/Snakin family protein precursor, expressed (44.4%)	AT1G10588.1 - Gibberellin-regulated family protein (41.7%)

	Bradi1g14850	11800558 - 11803295	19451	Protein of unknown function (DUF620), Coexpressed along with genes transcribed in shoot tissue during day	LOC_Os03g40930.1 - expressed protein (79.9%)	AT3G19540.1 - Protein of unknown function (DUF620) (69.5%)
	Bradi1g14855	11810840 - 11813999	26996	Expressed protein	none	none
	Bradi1g14860	11819372 - 11823066	35528	SF335 - SUBTILISIN-LIKE PROTEASE, Coexpressed with genes in flower specific coexpression subnetwork	LOC_Os03g55350.1 - OsSub31 - Putative Subtilisin homologue, expressed (72.3%)	AT5G67360.1 - Subtilase family protein (66.1%)
Energy_QT11.10 (s1_53853254)	Bradi1g55216	53796314 - 53807134	46120	GENERAL TRANSCRIPTION FACTOR 3C POLYPEPTIDE 4	LOC_Os01g50690.1 - WD domain, G-beta repeat domain containing protein, expressed (78.4%)	AT3G49400.1 - Transducin/WD40 repeat-like superfamily protein (53.4%)
	Bradi1g55230	53824245 - 53829688	23566	MEMBRANE RELATED PROTEIN-LIKE	LOC_Os07g08760.1 - START domain containing protein, putative, expressed (88.4%)	AT4G14500.1 - Polyketide cyclase/dehydrase and lipid transport superfamily protein (61.6%)
	Bradi1g55240	53840201 - 53849470	3784	protein kinase family protein, putative, expressed, subfamily RLCK-IXb	LOC_Os03g31000.1 - protein kinase, putative, expressed (71.4%)	AT2G45910.1 - U-box domain-containing protein kinase family protein (41.9%)
	Bradi1g55245	53853949 - 53856846	695	SERINE/THREONINE-PROTEIN KINASE	LOC_Os07g38530.2 - STE_PAK_Ste20_Slob_Wnk.4 - STE kinases (62.7%)	AT3G04910.1 - with no lysine (K) kinase 1 (54.4%)
	Bradi1g55250	53857279 - 53869489	4025	ATP-dependent DNA helicase activity	LOC_Os07g08729.1 - ATP-dependent DNA helicase 2	AT1G16970.1 - KU70 homolog (71.8%)

					subunit 1, putative, expressed (93.8%)	
	Bradi1g55260	53870177 - 53871436	16923	histone H1/5	LOC_Os07g08710.2 - AT hook-containing DNA-binding protein, putative, expressed (21.4%)	AT2G30620.2 - winged-helix DNA-binding transcription factor family protein (11.7%)
	Bradi1g55272	53875377 - 53876293	22123	No description	none	none
	Bradi1g55280	53898647 - 53900383	45393	small subunit ribosomal protein S15e	LOC_Os07g08660.1 - 40S ribosomal protein S15, putative, expressed (89.7%)	AT5G09510.1 - Ribosomal protein S19 family protein (90.3%)
Energy_QTL3.3 (s3_00938760)	Bradi3g01377	888056 - 890380	48380	MYB-LIKE DNA-BINDING PROTEIN	LOC_Os02g02370.1 - myb-like DNA-binding domain containing protein, putative, expressed (72.9%)	AT5G52260.1 - myb domain protein 19 (40.9%)
	Bradi3g01390	893855 - 897506	41254	F-Box	LOC_Os07g36870.1 - OsFBX252 - F-box domain containing protein, expressed (48.1%)	none
	Bradi3g01398	898193 - 900018	38742	F-box-like	LOC_Os07g36870.1 - OsFBX252 - F-box domain containing protein, expressed (48.5%)	none
	Bradi3g01406	902533 - 905344	33416	F-box-like	LOC_Os07g36870.1 - OsFBX252 - F-box domain containing protein, expressed (47.3%)	none
	Bradi3g01412	905987 - 907025	31735	F-box-like	LOC_Os07g36870.1 - OsFBX252 - F-box domain containing protein, expressed (54.9%)	AT3G16210.1 - F-box family protein (10%)

	Bradi3g01419	908671 - 911574	27186	F-box-like	LOC_Os07g36870.1 - OsFBX252 - F-box domain containing protein, expressed (32.1%)	none
	Bradi3g01427	914646 - 915980	22780	Expressed protein	LOC_Os09g17530.1 - OsFBX321 - F-box domain containing protein, expressed (7%)	none
	Bradi3g01440	917087 - 918352	20408	nucleoside-triphosphatase activity	LOC_Os02g02380.1 - suppressor of phythochrome A, putative, expressed (47%)	AT5G23730.1 - Transducin/WD40 repeat-like superfamily protein (41.3%)
	Bradi3g01450	921226 - 926408	12352	NUCLEIC ACID-BINDING, OB-FOLD-LIKE PROTEIN	LOC_Os02g02390.1 - S1 RNA binding domain containing protein, expressed (71.1%)	AT1G12800.1 - Nucleic acid-binding, OB-fold-like protein (49.7%)
	Bradi3g01460	925843 - 933040	5720	protein kinase family protein	LOC_Os03g28980.1 - WD40-like Beta Propeller Repeat family protein, expressed (45.9%)	AT1G21680.1 - DPP6 N-terminal domain-like protein (31.4%)
	Bradi3g01470	939007 - 941921	247	aminoacylase activity, catalase activity	LOC_Os02g02400.2 - catalase isozyme A, putative, expressed (86%)	AT1G20630.1 - catalase 1 (79%)
	Bradi3g01477	942486 - 946497	3726	HEAT SHOCK PROTEIN 70KDA	LOC_Os02g02410.1 - DnaK family protein, putative, expressed (87.4%)	AT5G28540.1 - heat shock protein 70 (Hsp 70) family protein (84.5%)
	Bradi3g01483	948294 - 952294	9534	general transcription factor IIIA (GTF3A)	LOC_Os02g02424.1 - ZOS2-02 - C2H2 zinc finger protein, expressed (88.4%)	AT1G72050.2 - transcription factor IIIA (59.3%)
	Bradi3g01489	952729 - 954585	13969	PPR repeat (PPR)	LOC_Os10g26070.1 - pentatricopeptide, putative, expressed (53.6%)	AT5G59200.1 - Tetratricopeptide repeat (TPR)-like superfamily protein (52.5%)
	Bradi3g01497	955118 - 957532	16358	OPT oligopeptide transporter protein (OPT)	LOC_Os02g02450.1 - transposon protein, putative, unclassified, expressed (81.3%)	AT3G17650.1 - YELLOW STRIPE like 5 (57%)

	Bradi3g01510	959098 - 961116	20338	Protein of unknown function, DUF594 (DUF594)	LOC_Os07g16930.1 - expressed protein (53.5%)	AT5G45480.1 - Protein of unknown function (DUF594) (41.2%)
	Bradi3g01515	961177 - 963366	22417	No description	none	none
	Bradi3g01520	965015 - 967462	26255	OPT oligopeptide transporter protein (OPT)	LOC_Os02g02460.1 - transposon protein, putative, unclassified, expressed (82.8%)	AT3G17650.1 - YELLOW STRIPE like 5 (68.9%)
	Bradi3g01527	968355 - 972729	29595	OXIDOREDUCTASE FEY3-RELATED	LOC_Os02g02470.1 - oxidoreductase, short chain dehydrogenase/reductase family domain containing protein (76.9%)	AT4G27760.1 - NAD(P)-binding Rossmann-fold superfamily protein (69.5%)
	Bradi3g01540	971365 - 974693	32605	bHLH transcription factor	LOC_Os02g02480.1 - basic helix-loop-helix DND-binding domain containing protein, expressed (75.6%)	AT1G51070.2 - basic helix-loop-helix (bHLH) DNA-binding superfamily protein (49.2%)
	Bradi3g01550	974981 - 978786	36221	PROTEIN LOW PSII ACCUMULATION 3, CHLOROPLASTIC	LOC_Os02g02520.1 - expressed protein (75.7%)	AT1G73060.1 - Low PSII Accumulation 3 (65.9%)
	Bradi3g01560	979803 - 980696	41043	DNA-directed RNA polymerase activity	LOC_Os02g02510.1 - DNA-directed RNA polymerase II subunit RPB4, putative, expressed (92.9%)	AT5G09920.1 - RNA polymerase II, Rpb4, core protein (86.5%)
	Bradi3g01570	980681 - 984906	41921	galacturonate binding	LOC_Os02g02500.1 - remorin family protein, putative, expressed (84.6%)	AT2G02170.2 - Remorin family protein (53.5%)
	Bradi3g01577	985013 - 989900	46253	Protein kinase domain (Pkinase) // Leucine rich repeat (LRR_8)	LOC_Os02g02490.1 - phyto sulfokine receptor precursor, putative, expressed (66.5%)	AT2G02220.1 - phyto sulfokine receptor 1 (53.9%)

Energy_QTL3.6 (s3_07106643)	Bradi3g08946	7058804 - 7059487	47156	No annotation	none	none
	Bradi3g08960	7075456 - 7079656	26987	1-phosphatidylinositol-4-phosphate 5-kinase activity	LOC_Os02g13890.1 - FYVE zinc finger domain containing protein, expressed (82.3%)	AT1G29800.2 - RING/FYVE/PHD-type zinc finger family protein (61.5%)
	Bradi3g08961	7080630 - 7081434	25209	No annotation	none	none
	Bradi3g08963	7080630 - 7081425	25218	No annotation	none	none
	Bradi3g08967	7083882 - 7087443	19200	BES1/BZR1 HOMOLOG PROTEIN 4	LOC_Os06g35900.1 - BES1/BZR1 homolog protein, putative, expressed (61.1%)	AT1G78700.1 - BES1/BZR1 homolog 4 (55.3%)
	Bradi3g08974	7091746 - 7092224	14419	No annotation	none	none
	Bradi3g08981	7094905 - 7095887	10756	No annotation	none	none
	Bradi3g08990	7097643 - 7106185	458	NHL repeat (NHL)	LOC_Os02g13950.1 - NHL repeat-containing protein, putative, expressed (88.4%)	AT3G14860.2 - NHL domain-containing protein (62.1%)
	Bradi3g09000	7110846 - 7113041	4203	U-box, subfamily	LOC_Os02g13960.1 - spotted leaf 11, putative, expressed (75%)	AT1G29340.1 - plant U-box 17 (48.8%)
	Bradi3g09005	7116111 - 7118594	9468	Protein kinase domain (Pkinase) // D-mannose binding lectin (B_lectin)	LOC_Os02g13965.1 - lectin protein kinase family protein, putative, expressed (83.9%)	AT4G32300.1 - S-domain-2 5 (46.9%)
	Bradi3g09010	7120985 - 7127846	14342	NAD(P)-BINDING ROSSMANN-FOLD SUPERFAMILY PROTEIN	LOC_Os02g13970.1 - Complex I intermediate-associated protein 30 domain containing	AT4G18810.1 - NAD(P)-binding Rossmann-fold superfamily protein (72.7%)

					protein, putative, expressed (87.9%)	
	Bradi3g09013	7128096 - 7129751	21453	No annotation	LOC_Os02g13980.1 - expressed protein (45.6%)	AT4G15140.1 (32.2%)
	Bradi3g09015	7131557 - 7134272	24914	No annotation	none	none
	Bradi3g09017	7138006 - 7142112	31363	No description	LOC_Os03g58930.1 - expressed protein (74.6%)	AT1G20890.1 (63.5%)
	Bradi3g09020	7141024 - 7141755	34381	No annotation	none	none
	Bradi3g09030	7142735 - 7145347	36092	large subunit ribosomal protein L11e	LOC_Os02g14059.1 - ribosomal protein L5, putative, expressed (97.2%)	AT5G45775.2 - Ribosomal L5P family protein (97.2%)
	Bradi3g09032	7149154 - 7149795	42511	No annotation	none	none
	Bradi3g09034	7149796 - 7150700	43153	No annotation	none	none
	Bradi3g09037	7151497 - 7153629	44854	actin related protein 2/3 complex, subunit 3 (ARPC3)	LOC_Os02g14000.1 - actin-related protein 2/3 complex subunit 3, putative, expressed (96%)	AT1G60430.2 - actin-related protein C3 (83.3%)
Energy_QTL3.8 (s3_16587273)	Bradi3g18077	16562829 - 16581852	5421	RING/FYVE/PHD ZINC FINGER DOMAIN-CONTAINING PROTEIN	LOC_Os08g12680.1 - zinc finger domain, LSD1 subclass family protein, expressed (84.1%)	AT1G79350.1 - RING/FYVE/PHD zinc finger superfamily protein (80.9%)
	Bradi3g18090	16582021 - 16585513	1760	protein serine/threonine phosphatase activity	LOC_Os04g52000.1 - protein phosphatase 2C, putative, expressed (84.9%)	AT4G28400.1 - Protein phosphatase 2C family protein (67.6%)

	Bradi3g18100	16586176 - 16587906	633	Expressed protein	LOC_Os03g21600.1 - expressed protein (47.4%)	none
	Bradi3g18120	16588308 - 16594496	1035	No description	LOC_Os01g20110.1 - expressed protein (72.4%)	AT1G36320.1 (52.2%)
	Bradi3g18130	16594488 - 16597664	7215	WAK receptor-like protein kinase, expressed, subfamily WAKL-OS	LOC_Os11g35120.1 - OsWAK116 - OsWAK receptor- like cytoplasmic kinase OsWAK-RLCK, expressed (72.5%)	AT1G21230.1 - wall associated kinase 5 (57.4%)
	Bradi3g18135	16597670 - 16598858	10397	Expressed protein	none	none
	Bradi3g18140	16598165 - 16606217	10892	beta-amyrin synthase activity, alpha-amyrin synthase activity, lanosterol synthase activity	LOC_Os02g04710.1 - cycloartenol synthase, putative, expressed (73.3%)	AT2G07050.1 - cycloartenol synthase 1 (71.6%)
	Bradi3g18150	16621900 - 16630426	34627	protein kinase family protein, putative, expressed, subfamily Raf	LOC_Os08g12750.1 - serine/threonine-protein kinase HT1, putative, expressed (89%)	AT2G24360.1 - Protein kinase superfamily protein (80.1%)
	Bradi3g18160	16630479 - 16634862	42206	FAD binding	LOC_Os08g02230.1 - FAD- binding and arabino-lactone oxidase domains containing protein, putative, expressed (73.9%)	AT2G46750.1 - D-arabinono- 1,4-lactone oxidase family protein (64.2%)
	Bradi3g18170	16636799 - 16638547	49526	FAD binding	LOC_Os04g29210.1 - FAD- binding and arabino-lactone oxidase domains containing protein, putative, expressed (71.0%)	AT2G46760.1 - D-arabinono- 1,4-lactone oxidase family protein (63.5%)

S20. Protocol for measuring phenotypic parameters using a PAM

```
TS=40ms
; Quenching protocol with Actinic1 & Actinic2 8mins + dark 3 mins
; Protocol: Quenching-without-FR1-Lucam.p modified by Keng
;version September, 2015
;high-resolution CCD
;
include default.inc ;Includes standard options, do not remove it !
include light.inc ;Includes standard options, do not remove it !
Shutter=3
Sensitivity=50
Act1=100
Act2=100
Super=100

;-----
;-----
;*** Fo Measurement
*****
*****
;-----
;-----
F0duration = 5s
F0period = 1s
<0,F0period..F0duration>=>mfmsub
;
;Fo definition
<0s>=>checkPoint,"startFo"
<F0duration - F0period>=>checkPoint,"endFo"
;
;-----
;-----
;*** Saturating Pulse & Fm Measurement
*****
*****
;-----
;-----
PulseDuration=800ms;####
a1=F0duration + 2*mfmsub_length;####
;
<a1>=>SatPulse(PulseDuration)
<a1>=>act1(PulseDuration)
<a1>=>act2(PulseDuration)
;
<a1>=>mpulse
;
;Fm definition
<a1 + mfmsub_length>=>checkPoint,"startFm"
<a1 + PulseDuration - mfmsub_length>=>checkPoint,"endFm"
;
;Visual frame definition ## Image
shown in pre-processing window
<a1 + PulseDuration/2 + TS>=>checkPoint,"timeVisual"
;
;-----
;-----
;***** Dark Relaxation Measurement
*****
```

```

;-----
;-----
DarkRelaxation1=17s;####
b1= a1 + PulseDuration + 2*mfmsub_length;####
b2=2s;####
<b1, b1 + 200ms .. b1 + b2>=>mfmsub
<b1 + b2 + 200ms, b1 + 2*b2 .. b1+DarkRelaxation1>=>mfmsub
;
;-----
;-----
;***** Kautsky Effect Measurement
*****
;-----
;-----
;
;***** Actinic light Exposure *****
ALPeriod=450s;####
c1= a1 + PulseDuration + DarkRelaxation1 + mfmsub_length;####
<c1>=>act1(ALPeriod)
<c1>=>act2(ALPeriod)
;
;*****Fast Kautsky kinetics*****
c2=3s;####
;
<c1 + TS, c1 + TS + mfmsub_length.. c1+c2>=>mfmsub;
;
;*****Slow Kautsky kinetics*****
c3=4s;####
period of slow measurement
;
<c1 + c2 + c3/10, c1 + c2+ c3/5, c1 + c2 + c3/2>=>mfmsub
;
<c1 + c2 + c3, c1 + c2 + c3 +12s .. c1 + ALPeriod>=>mfmsub;
;
;Fp definition
<c1>=>checkPoint,"startFp"
<c1 + c2 + c3>=>checkPoint,"endFp"
;
;-----
;-----
;***** Saturating Pulses - Fm' Quenching Analysis
*****
;-----
;-----
;
;***** Saturating Pulses - Fm_L1 *****
f1=c1+<18s>;####
f11=f1#<mfmsub_length,2*mfmsub_length ..PulseDuration - mfmsub_length>;####
f11=>mfmsub
f1 + mfmsub_length=>checkPoint,"startFt_L1"
f1 + PulseDuration - mfmsub_length=>checkPoint,"endFt_L1"
;
f2=f1 + PulseDuration;####
f2=>SatPulse(PulseDuration);
f2=>mpulse
f2+PulseDuration/2=>checkPoint,"startFm_L1"
f2 + PulseDuration - mfmsub_length=>checkPoint,"endFm_L1"
;

```

```

;***** Saturating Pulses - Fm_L2 *****
f3=c1+<38s>;####
f31=f3#<mfmsub_length,2*mfmsub_length ..PulseDuration - mfmsub_length>;####
f31=>mfmsub
f3 + mfmsub_length=>checkPoint,"startFt_L2"
f3 + PulseDuration - mfmsub_length=>checkPoint,"endFt_L2"
;
f4=f3 + PulseDuration;####
f4=>SatPulse(PulseDuration);
f4=>mpulse
f4 + PulseDuration/2=>checkPoint,"startFm_L2"
f4 + PulseDuration - mfmsub_length=>checkPoint,"endFm_L2"
;
;***** Saturating Pulses - Fm_L3 *****
f5=c1+<58s>;####
f51=f5#<mfmsub_length,2*mfmsub_length ..PulseDuration - mfmsub_length>;####
f51=>mfmsub
f5 + mfmsub_length=>checkPoint,"startFt_L3"
f5 + PulseDuration - mfmsub_length=>checkPoint,"endFt_L3"
;
f6=f5 + PulseDuration;####
f6=>SatPulse(PulseDuration);
f6=>mpulse
f6 + PulseDuration/2=>checkPoint,"startFm_L3"
f6 + PulseDuration - mfmsub_length=>checkPoint,"endFm_L3"
;
;***** Saturating Pulses - Fm_L4 *****
f7=c1+<78s>;####
f71=f7#<mfmsub_length,2*mfmsub_length ..PulseDuration - mfmsub_length>;####
f71=>mfmsub
f7 + mfmsub_length=>checkPoint,"startFt_L4"
f7 + PulseDuration - mfmsub_length=>checkPoint,"endFt_L4"
;
f8=f7 + PulseDuration;####
f8=>SatPulse(PulseDuration);
f8=>mpulse
f8 + PulseDuration/2=>checkPoint,"startFm_L4"
f8 + PulseDuration - mfmsub_length=>checkPoint,"endFm_L4"
;
;***** Saturating Pulses - Fm_L5 *****
f9=c1+<98s>;####
f91=f9#<mfmsub_length,2*mfmsub_length ..PulseDuration - mfmsub_length>;####
f91=>mfmsub
f9 + mfmsub_length=>checkPoint,"startFt_L5"
f9 + PulseDuration - mfmsub_length=>checkPoint,"endFt_L5"
;
f10=f9 + PulseDuration;####
f10=>SatPulse(PulseDuration);
f10=>mpulse
f10 + PulseDuration/2=>checkPoint,"startFm_L5"
f10 + PulseDuration - mfmsub_length=>checkPoint,"endFm_L5"
;
;***** Saturating Pulses - Fm_L6 *****
f11=c1+<118s>;####
f111=f11#<mfmsub_length,2*mfmsub_length ..PulseDuration - mfmsub_length>;####
f111=>mfmsub
f11 + mfmsub_length=>checkPoint,"startFt_L6"
f11 + PulseDuration - mfmsub_length=>checkPoint,"endFt_L6"

```



```

;
f12=f11 + PulseDuration;####
f12=>SatPulse(PulseDuration);
f12=>mpulse
f12 + PulseDuration/2=>checkPoint,"startFm_L6"
f12 + PulseDuration - mfmsub_length=>checkPoint,"endFm_L6"
;
;***** Saturating Pulses - Fm_L7 *****
f13=c1+<148s>;####
f131=f13#<mfmsub_length,2*mfmsub_length ..PulseDuration - mfmsub_length>;####
f131=>mfmsub
f13 + mfmsub_length=>checkPoint,"startFt_L7"
f13 + PulseDuration - mfmsub_length=>checkPoint,"endFt_L7"
;
f14=f13 + PulseDuration;####
f14=>SatPulse(PulseDuration);
f14=>mpulse
f14 + PulseDuration/2=>checkPoint,"startFm_L7"
f14 + PulseDuration - mfmsub_length=>checkPoint,"endFm_L7"
;
;***** Saturating Pulses - Fm_L8 *****
f15=c1+<178s>;####
f151=f15#<mfmsub_length,2*mfmsub_length ..PulseDuration - mfmsub_length>;####
f151=>mfmsub
f15 + mfmsub_length=>checkPoint,"startFt_L8"
f15 + PulseDuration - mfmsub_length=>checkPoint,"endFt_L8"
;
f16=f15 + PulseDuration;####
f16=>SatPulse(PulseDuration);
f16=>mpulse
f16 + PulseDuration/2=>checkPoint,"startFm_L8"
f16 + PulseDuration - mfmsub_length=>checkPoint,"endFm_L8"
;
;***** Saturating Pulses - Fm_L9 *****
f17=c1+<238s>;####
f171=f17#<mfmsub_length,2*mfmsub_length ..PulseDuration - mfmsub_length>;####
f171=>mfmsub
f17 + mfmsub_length=>checkPoint,"startFt_L9"
f17 + PulseDuration - mfmsub_length=>checkPoint,"endFt_L9"
;
f18=f17 + PulseDuration;####
f18=>SatPulse(PulseDuration);
f18=>mpulse
f18 + PulseDuration/2=>checkPoint,"startFm_L9"
f18 + PulseDuration - mfmsub_length=>checkPoint,"endFm_L9"
;
;***** Saturating Pulses - Fm_L10 *****
f19=c1+<298s>;####
f191=f19#<mfmsub_length,2*mfmsub_length ..PulseDuration - mfmsub_length>;####
f191=>mfmsub
f19 + mfmsub_length=>checkPoint,"startFt_L10"
f19 + PulseDuration - mfmsub_length=>checkPoint,"endFt_L10"
;
f20=f19 + PulseDuration;####
f20=>SatPulse(PulseDuration);
f20=>mpulse
f20 + PulseDuration/2=>checkPoint,"startFm_L10"
f20 + PulseDuration - mfmsub_length=>checkPoint,"endFm_L10"

```

```

;
;***** Saturating Pulses - Fm_L11 *****
f21=c1+<358s>;####
f211=f21#<mfmsub_length,2*mfmsub_length ..PulseDuration - mfmsub_length>;####
f211=>mfmsub
f21 + mfmsub_length=>checkPoint,"startFt_L11"
f21 + PulseDuration - mfmsub_length=>checkPoint,"endFt_L11"
;
f22=f21 + PulseDuration;####
f22=>SatPulse(PulseDuration);
f22=>mpulse
f22 + PulseDuration/2=>checkPoint,"startFm_L11"
f22 + PulseDuration - mfmsub_length=>checkPoint,"endFm_L11"
;
;***** Saturating Pulses - Fm_L12 *****
f23=c1+<448s>;####
f231=f23#<mfmsub_length,2*mfmsub_length ..PulseDuration - mfmsub_length>;####
f231=>mfmsub
f23 + mfmsub_length=>checkPoint,"startFt_Lss"
f23 + PulseDuration - mfmsub_length=>checkPoint,"endFt_Lss"
;
f24=f23 + PulseDuration;####
f24=>SatPulse(PulseDuration);
f24=>mpulse
f24 + PulseDuration/2=>checkPoint,"startFm_Lss"
f24 + PulseDuration - mfmsub_length=>checkPoint,"endFm_Lss"
;
;-----
-----
;*** Dark relaxation after actinic light period
*****
;-----
-----
DarkRelaxation2=180s;####
h=c1 + ALPeriod +mfmsub_length;####
;
;***** Relaxation measurement*****
;
<h, h+DarkRelaxation2/10..h+DarkRelaxation2>=>mfmsub
;
;***** Saturating Pulses - Fm_D1 *****
g1=h + <28s>;####
g11=g1#<mfmsub_length,2*mfmsub_length ..PulseDuration - mfmsub_length>;####
g11=>mfmsub
g1 + mfmsub_length=>checkPoint,"startFt_D1"
g1 + PulseDuration - mfmsub_length=>checkPoint,"endFt_D1"
;
g2=g1 + PulseDuration;####
g2=>SatPulse(PulseDuration)
g2=>act1(PulseDuration)
g2=>act2(PulseDuration)
g2=>mpulse
g2 + PulseDuration/2=>checkPoint,"startFm_D1"
g2 + PulseDuration - mfmsub_length=>checkPoint,"endFm_D1"
;
;***** Saturating Pulses - Fm_D2 *****
g3=h + <58s>;####
g31=g3#<mfmsub_length,2*mfmsub_length ..PulseDuration - mfmsub_length>;####

```

```

g31=>mfmsub
g3 + mfmsub_length=>checkPoint,"startFt_D2"
g3 + PulseDuration - mfmsub_length=>checkPoint, "endFt_D2"
;
g4=g3 + PulseDuration;####
g4=>SatPulse(PulseDuration)
g4=>act1(PulseDuration)
g4=>act2(PulseDuration)
g4=>mpulse
g4 + PulseDuration/2=>checkPoint,"startFm_D2"
g4 + PulseDuration - mfmsub_length=>checkPoint,"endFm_D2"
;
;***** Saturating Pulses - Fm_D3 *****
g5=h+<118s>;####
g51=g5#<mfmsub_length,2*mfmsub_length ..PulseDuration - mfmsub_length>;####
g51=>mfmsub
g5 + mfmsub_length=>checkPoint,"startFt_D3"
g5 + PulseDuration - mfmsub_length=>checkPoint,"endFt_D3"
;
g6=g5 + PulseDuration;####
g6=>SatPulse(PulseDuration)
g6=>act1(PulseDuration)
g6=>act2(PulseDuration)
g6=>mpulse
g6 + PulseDuration/2=>checkPoint,"startFm_D3"
g6 + PulseDuration - mfmsub_length=>checkPoint,"endFm_D3"
;
;***** Saturating Pulses - Fm_D4 *****
g7=h+<178s>;####
g71=g5#<mfmsub_length,2*mfmsub_length ..PulseDuration - mfmsub_length>;####
g71=>mfmsub
g7 + mfmsub_length=>checkPoint,"startFt_D4"
g7 + PulseDuration - mfmsub_length=>checkPoint,"endFt_D4"
;
g8=g7 + PulseDuration;####
g8=>SatPulse(PulseDuration)
g8=>act1(PulseDuration)
g8=>act2(PulseDuration)
g8=>mpulse
g8 + PulseDuration/2=>checkPoint,"startFm_D4"
g8 + PulseDuration - mfmsub_length=>checkPoint,"endFm_D4"
;
;END *****

```