

Supplementary Tables and Figures

Supplementary Table S1. Details of Single nucleotide polymorphism (SNPs), Insertions/ deletions (InDels), and their haplotyping information for nutritional and cooking quality related genes. The deleterious effect mutations are represented with an asterisk

Gene Name	RAP ID	Feature	Total SNPs (Rice Var Map 2.0)	Total SNPs (SNP-SEEK IRRI)	Number of Missense mutations	Functional Impact of Missense Mutations	Number of haplotypes	Haplotype with the highest frequency	Number of accessions under haplotype with the highest frequency	Number of InDels
SSG4	Os01g0179400	Starch size in endosperm	58	65	6	I17V,E69D,I114V,D135G,K406R,I638S	8	3	1931	64
GW5L	Os01g0190500	Grain weight	82	8	3	V58G,A70S,H235R*,V58A	12	1	1349	70
OsROS1 TA2	Os01g0218032	Aleurone thickness	0	31	0		0	9	0	64
RBP-P	Os01g0265800	Endosperm protein localization	24	10	0		5	1	2473	87
PHD1	Os01g0367100	Galactolipid biosynthesis	72	48	6	D63V,F335I*,S321C*,G305V*,D288N*,F273V*	12	1	2707	186
OsAPL2 osagpl2-3 OsAGPL2 GIF2	Os01g0633100	Grain filling	109	37	0		19	5	1247	43
glu4a	Os01g0762500	Glutelin content	29	15	8	Y5H*	8	2	1224	7
OsAAP6 qPC1	Os01g0878700	Grain protein content	55	12	2	R361S,A113T	10	3	1768	39
sd1 GA20	Os01g088	Grain	66	21	9	A82N*,A82N*,E100G,H101D*,H101D*,C	11	2	2051	105

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ox2	3800	protein content				193S*,P240L*,L266F*,Q340R,D349H				
OsIRO2	Os01g0952800	Iron utilization	430	296	20	K240N,V184I,L151M,S149N,T136A,T135A,A55T	7	1	1596	404
OsHAC1;1	Os02g0102300	Arsenic accumulation	59	30	1	Y5H	4	1	2227	162
OsUgp2 Ugp2	Os02g0117700	Starch accumulation	45	22	2	G406R,A62E	11	1	1847	68
OsHMA4	Os02g0196600	Copper accumulation	47	20	8	I55M,F303L,T316M,A553V,S660A,I704M,G818S,V914A*	12	1	1521	64
OsBT1-1 OsBT1	Os02g0202400	Endosperm granule formation	65	18	17	V25A,C46R,R102K,M107I,S115A,H127Q,R130Q,R152C*,R170H,M173I,R183H*,G184D*,T205R*,Y209C,P217L,V224I,Y209F	9	2	2240	70
GW2	Os02g0244100	Grain width and weight	106	36	4	E189D,R262C,R394C,R260C	17	1	1295	84
GluB-1	Os02g0249900	Seed storage protein	0	1	0		0	0	0	0
Du3	Os02g0612300	Grain amylose content	107	35	7	S96F*,Y237F,R189K	21	1	1686	116
OsYSL2	Os02g0649900	Iron nutrition	87	6	3	R588H,R103W,D21V	15	3	1461	4
OsMADS6	Os02g0682200	Endosperm nutrient	107	22	3	M93L,M182I,P203S	7	1	1793	251

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OsFAD2 OsFAD2-1	Os02g0716500	accumulation Grain lipid accumulation	124	47	3	K443Q,A163T,T50A	15	2	1820	177
OsCDPK1 OsCDPK13 OsCDPK11 OsCPK11 OsCDPK12	Os03g0128700	Grain starch structure	67	6	8	I143T*,E259Q*,A265S*,I268V*,Q284P,F288Y*,R355W*,V474I	8	3	2768	54
OsGAPDHB	Os03g0129300	Grain aroma	34	9	0		10	2	2891	36
XS-lpa2-1	Os03g0142800	Seed phytic acid	41	9	6	N6T,A19T,R32L,A350T,N645K*,L1469F*	10	3	1946	28
OsPht1;2 OsPT2	Os03g0150800	Selenite uptake	20	2	5	H398R,N335D,P269S,S258C*,V185I	9	2	2819	6
RINO1	Os03g0192700	Phytic acid	74	10	5	L376P,I43V,Q25G,Q25G,D23E,Q25R,Q25K	12	2	2255	53
OsFRDL1	Os03g0216700	Grain iron distribution	132	69	4	A409T,V227L,P56L,V30A	14	2	2014	197
lpa1	Os03g0237250	Phytic acid content	68	25	4	G420S,A351S,G132S,G127A	9	3	1534	130
OASA2	Os03g0264400	Grain tryptophan content	78	31	6	E585D,G527R*,P446S,R303P,E79K,R68P	17	1	1315	85
OsNAS2	Os03g0307200	Grain zinc content	30	5	4	A87T,N91S,G216E,I252V	6	3	1956	14

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OsLTPL36	Os03g0369100	Grain development	30	0	0		9	4	1576	31
OsCCX2	Os03g0656500	Grain cadmium content	61	9	5	H90N,D292N,F412V*,V448L*,L532V	7	1	3833	12
OsIRT1	Os03g0667500	Grain iron and zinc content	243	128	20	V369I,R307K,R304K,R281K,I227M,V213A,R189W,H180R,V174I,N122S,N121S,G93R,L82F,V71A,A58V*,D49E,I29L,I27F,L21V,P9A	5	1	3828	217
lpaN15-186	Os03g0737701	Phytic acid	50	11	2	M355I,A150T	9	2	1498	6
OsMADS34 PAP2	Os03g0753100	Grain yield	90	20	5	Q89H*,Q106K*,Q71K*,T20A*,R10P*	8	1	1992	140
pho1	Os03g0758100	Starch structure in endosperm	33	15	11	T268N*,V165I,E153K,R550H*,R501C*,P391S*,T268N*,I254F*,S203L*,L60F*,M1del*	9	1	2713	37
CysR10	Os03g0766000	Grain protein bodies	40	16	2	V40A	7	1	2341	64
OASA1D	Os03g0826500	Tryptophan accumulation	85	30	3	R498L,G395E,G22E	9	2	1830	85
sug1	Os04g0164900	Rice endosperm development	0	412	0		0	0	0	607
OsVIT1	Os04g0463400	Iron translocation	72	28	5	A170T*,V136A*,Q105K	10	1	3814	70

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Osvpe1	Os04g0537900	Seed glutelin	33	12	3	E384G*,Q90R,Y86C*	5	1	3293	27
OsYSL9	Os04g0542200	Iron distribution	48	13	4	S511N,T368R,L256F,R90L*	8	3	1503	22
Kala4 OsS1	Os04g0557500	Grain pericarp colour	1140	118	6	E308D,D173N,L140V,D101H,P84L,A29V*	14	3	1506	448
OsPTR6 PTR6 OsNPF7.3	Os04g0597800	Grain yield	111	27	3	I31V,I427V,M561L	13	2	2265	72
OsABCC1 MRP1	Os04g0620000	Arsenic accumulation	245	19	40	S1468T,R1398G*,R1300Q,E1231V*,R990Q,L933F,K892R,Q879L,V814L,R712H*,P642H*,A524S,R518C*,A449V,L285I,N283S,R276Q,T216S,P206L*,L176V,A156S,I150S,I134M,A107V,A92V,R90Q,T61A,G47S,T33S,N23Y*,V21L,S1468N,F708L*,A409T*,R383H*,S266I*,F252T*,A233V*,C228F*,C83F*,T29A*	23	3	810	135
FLO2	Os04g0645100	Grain size	117	59	30	A274T,L399P,I466T,R579K,P599L,G804D,S1203L,N1319D,A1608T,F195L*,H200N*,P204T*,S306P*,N323D*,M348R*,M348I*,L369F*,A378S*,G452S*,P515T*,W589C*,R725K*,A748V*,A789S*,N829Y*,R892Q*,G926C*,R987H*,A1060V*,L1107F*,Y1146F*	9	3	2953	217
OsSULTR3;3	Os04g0652400	Metabolite content	49	30	3	F655I,I600V,A452S	9	3	2039	94
OsMKP1 G8 LARG8 GLA1	Os05g0115800	Grain number and size	88	26	9	V731A,T707M,T618I,D406N,V380L,S378I,V191I,R123H,G40R	16	1	1151	28
Chalk5	Os05g0156900	Chalkiness	212	96	19	R525L,I497V,V412I,K401M,A379T,A364V,G237R*,A215V,A139G,R137S,T125P,V62D,G61V,G59V,D58G,S52N,E49D,V48G,M	11	2	1371	143

Gene Name	RAP ID	Feature	Total SNPs (Rice Var Map 2.0)	Total SNPs (SNP-SEEK IRRI)	Number of Missense mutations	Functional Impact of Missense Mutations	Number of haplotypes	Haplotype with the highest frequency	Number of accessions under haplotype with the highest frequency	Number of InDels
GSE5	Os05g0187500	Grain size	25	4	2	30V D229N,A431G	5	1	2317	30
OsZIP7a OsZIP7	Os05g0198400	Grain zinc and cadmium content	76	31	7	G11S,S18P,E32D,S77N,L210V,G217D,V263M	10	1	2047	119
OsSPL9	Os05g0408200	Grain copper accumulation	79	47	7	A132V,A200T,P309S,I576V,S751T,I789V,S248F*	8	2	2743	114
OsPCS1	Os05g0415200	Arsenic content	39	15	1	H108R	8	2	2561	23
OsMATE2	Os05g0554000	Plant growth and development	83	17	4	T133A,F439Y,A462V,V493A	10	3	2316	71
Wx	Os06g0133000	Grain characteristics	137	45	4	D166G*,Y224S*,P415S,D528Y*,D528N	14	2	1253	205
SPDT	Os06g0143700	Phosphorus accumulation	281	152	6	Q385L*,I251V,L247F,V71G*,A47V,A21V	7	3	2072	308
OsSSI	Os06g0160700	Grain starch content	197	66	12	S596L,K438E*,H420Y*,S319G,D214N*,L86F,A78S,T74A,L60M,R29L,R343S*,C251Y*	10	2	1589	138
ALK SSIIa	Os06g0229800	Grain starch quality	98	65	9	P56A,T117P,A148S,D161E,E208D,D283E,S604G,M737V,L781F*	16	1	842	65
OsLCT1	LOC_Os06g38120	Cadmium in grains	236	0	31	E15D,D26A,E35Q,P43L,P48S,A54S,I60T,L67H,L70Q,A71D,G73D,A77T,A80S,N84K,E87K,V95I,L101F,T147S,R152S,V183A,V21	4	1	4215	218

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OsHMA2 OsHMA2v	Os06g0700700	Grain zinc and cadmium content	104	153	3	1L,L215F,K223N,M241V,Q246H,E258L,M310V,L380F,T480S,V494M,L495F* C19R*,R7W	8	3	1706	261
OsPK2 W59 OsPKpal pha1	Os07g0181000	Grain filling	110	42	6		5	2	2108	94
qCdT7 OsHMA3	Os07g0232900	Grain zinc content	142	19	56	G990A,E975D,C960G,T953I,G930R,D926G,K912R,A908G,A908T,S873G,G787S,E775D,G770A,D768A,A759P,A758S,V752A,E733K,C678R,A638V,S614D,S614D,G595A,G594S*,S575T,D556H,V550I,T526I,S525T,R493Q,G490A,A381V*,S380R*,D338N*,T333M*,F299L,N298I*,Q269R,G268S*,V259I,E257K*,G256D*,G256S*,V250I,E238D,A234V,I233L,V229A,A184S,T134M,G130S*,A95V,E93A,P92S,A91T,R80H*,S614G,P92T,N725H*,L708F*,V697A*,N686K*,G642D*,E607A*,A341T*,V323G*,W293C*,P283L*,D267G*,D262N*,A252V*,R163C*,A99V*,D87N*,V82A*	10	2	2306	50
OsNRAMP5	Os07g0257200	Grain cadmium	163	73	3	A375T,S183F,S182A	18	2	1404	430
GW7 GL7 SLG7	Os07g0603300	Grain quality and yield	60	22	10	I915M,S647A,S620G,N605K,P518S,A462S,R361H,R361C,L259F*	10	3	1667	75
RSUS3 SUS3	Os07g0616800	Grain starch content	45	12	7	A26T,E541K*,L551S,S559N,N634D,E637K,S15G*	12	3	1592	47
OsHMA7	Os07g062	Grain	75	13	4	A32V,C37R,L147V*,R159C	10	1	1361	5

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	3200	iron and zinc content								
OsGZF1	Os07g0668600	Seed storage protein	26	7	9	R255H,A219S,S179P,M174I,L169V,A111P,A102V,R100H,E47K*,A111T	7	1	2276	12
OsNAS3	Os07g0689600		52	7	2	D87E,A327T	11	2	2434	34
OsMOT1;1	Os08g0101500	Grain molybdenum content	52	4	9	A125S,P183H,Q215E,M262I,I448T	16	1	1268	37
SSIIIa	Os08g0191433	Endosperm appearance	186	137	35	A33T,M38K,T43N,A62S,R109H,K116N,E142D,A184T,A195V,A217T,G226E,E231K,A268V,S350L,F401S,D427G,V480L,T486I,A503T,R576K,E641V,S681N,G686E,R702Q,R748H,E790V,G817D,V843E,L957M,Y964C*,K1006N*,R1118K,R1240H,A1528S,T1755I	14	4	1182	136
Badh2	Os08g0424500	Grain aroma	156	59	5	A190V,K244I*,A316E,P458S*,G468V*	21	2	1040	123
qGW8 OsSPL16 GW8	Os08g0531600	Grain quality and shape	69	36	8	P79L,A110V,D172N*,T274N,Q285K,G315S,M364I,A397T	10	2	1842	222
OsVIT2	Os09g0396900	Iron content in rice	38	12	0		8	1	4268	21
osal7	Os09g0440300	Endosperm colour	135	19	2	K242E,R226K	5	1	1531	107
GS9	Os09g0448500	Grain shape and appearance	75	7	8	L15M,P202Q,A223S,P250L,A257P,A258P,A260P,R268C	8	2	1982	36

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OsVPS22	Os09g0529700	e Grain chalkiness	128	9	1	H77R	10	3	1548	35
OsPCR1	Os10g0112100	Grain weight/ zinc accumulation	153	48	9	P185R,H156L,F100L,A58S,A46G,P33S,A15P,S13A,E11G	6	2	3404	132
FLO16	Os10g0478200	Grain development	66	27	0		5	2	2501	72
OsDCL3b	Os10g0485600	Seed quality	59	37	14	H89L*,A115V*,P129S*,N149D,S155A,T181A,F205L,I355M,G712S,R811S,V874L,R1063Q,F1101V,I1320L	11	3	1585	135
OsCAO1 PGL	Os10g0567400	Grain yield and quality	28	8	4	L394F*,T181P,V35L	5	2	4422	39
Rab5a	Os12g0631100	Endosperm storage protein transport	170	63	7	V129I,Q174R,A178V,A178V,P184L,H197Q	7	3	1443	120

Supplementary Table S2. Details of RNASeq datasets used in the present study. All the raw data was retrieved from NCBI SRA database and analyzed using CLC Genomics workbench.

Illumina RNA Sequencing (RNA-Seq) of Oryza sativa, Nipponbare for the Conserved Poaceae Specific Genes project				
SRA Experiment	SRA Study:SRP008821	Samples		
SRX100741	SRR352184	20 Day Leaves		
SRX100743	SRR352187	Emerging Inflorescence		
SRX100745	SRR352189	Early Inflorescence		
SRX100746	SRR352190	Anther		
SRX100747	SRR352192	Pistil		
SRX100749	SRR352194	Seeds 5 days after pollination		
SRX100753	SRR352204	Embryo 25 days after pollination		
SRX100754	SRR352206	Endosperm 25 days after pollination		
SRX100755	SRR352207	Seed 10 days after pollination		
SRX100756	SRR352209	Endosperm 25 days after pollination		
SRX100757	SRR352211	20 day leaves		
The novel quantitative trait locus qTGW3 encodes a GSK3-like kinase and negatively regulates grain size and weight in rice				
BioProject: PRJNA386888		SRA Experiment	SRA Study: SRP107231	Samples
		SRX2823832	SRR5560727	wild type
		SRX2823833	SRR5560728	wild type
		SRX2823834	SRR5560729	wild type
		SRX2823835	SRR5560730	GSK5-/-
		SRX2823836	SRR5560731	GSK5-/-
		SRX2823837	SRR5560732	GSK5-/-
		SRX2823838	SRR5560733	ARF4-/-
		SRX2823839	SRR5560734	ARF4-/-
		SRX2823840	SRR5560735	ARF4-/-
Transcriptome of different rice cultivars research the flavonoid biosynthetic pathway				
BioProject:PRJNA475636		SRA Experiment	SRA Study:SRP150289	Samples
		SRX4195869	SRR7293214	grain

	SRX4195870	SRR7293213	grain
	SRX4195868	SRR7293215	endosperm
	SRX4195872	SRR7293211	pericarp
	SRX4195871	SRR7293212	pericarp
	SRX4195875	SRR7293208	grain
	SRX4195874	SRR7293209	grain
	SRX4195873	SRR7293210	endosperm
	SRX4195877	SRR7293206	grain
	SRX4195876	SRR7293207	grain
Transcriptome analysis of Heugjinju, seed development and heading date using Illumina HiSeq 2000			
Accession: ERP009858	Experiment: ERX779709		
Transcriptome analysis of Heugjinju, seed development and heading date + 7days using Illumina HiSeq 2000			
Accession: ERP009859	Experiment:ERX779710		
Transcriptome analysis of Heugjinju, seed development and heading date + 14days using Illumina HiSeq 2000			
Accession: ERP009860	Experiment:ERX779711		
Transcriptome analysis of Heugseol, seed development and heading date using Illumina HiSeq 2000			
Accession: ERP009861	Experiment:ERX779712		
Transcriptome analysis of Heugseol, seed development and heading date + 7days using Illumina HiSeq 2000			
Accession: ERP009862	Experiment:ERX779713		
Transcriptome analysis of Heugseol, seed development and heading date + 14days using Illumina HiSeq 2000			
Accession: ERP009863	Experiment:ERX779715		
Transcriptome analysis of Heugnam, seed development and heading date using Illumina HiSeq 2000			
Accession: ERP009864	Experiment:ERX779716		
Transcriptome analysis of Heugnam, seed development and heading date + 7days using Illumina HiSeq 2000			
Accession: ERP009866	Experiment:ERX779717		
Transcriptome analysis of Heugnam, seed development and heading date + 14days using Illumina HiSeq 2000			
Accession: ERP009867	Experiment:ERX779718		
Transcriptome analysis of Josaengheug_chal, seed development and heading date using Illumina HiSeq 2000			
Accession: ERP009879	Experiment:ERX780238		
Transcriptome analysis of Josaengheug_chal, seed development and heading date + 7days using Illumina HiSeq 2000			

Accession: ERP009880	Experiment:ERX782739
Transcriptome analysis of Josaengheug_chal, seed development and heading date + 14days using Illumina HiSeq 2000	
Accession: ERP009881	Experiment:ERX784240
Transcriptome analysis of Boseogheug_chal, seed development and heading date using Illumina HiSeq 2000	
Accession: ERP009892	Experiment:ERX808969
Transcriptome analysis of Boseogheug_chal, seed development and heading date + 7days using Illumina HiSeq 2000	
Accession: ERP009893	Experiment:ERX808970
Transcriptome analysis of Boseogheug_chal, seed development and heading date + 14days using Illumina HiSeq 2000	
Accession: ERP009894	Experiment:ERX808971
Accession: Transcriptome analysis of Sinnongheug_chal, seed development and heading date using Illumina HiSeq 2000	
Accession: ERP009895	Experiment:ERX808972
Transcriptome analysis of Sinnongheug_chal, seed development and heading date + 7days using Illumina HiSeq 2000	
Accession: ERP009896	Experiment:ERX808973
Transcriptome analysis of Sinnongheug_chal, seed development and heading date + 14days using Illumina HiSeq 2000	
Accession: ERP009897	Experiment:ERX808974
Transcriptome analysis of Dongjin, seed development and heading date using Illumina HiSeq 2000	
Accession: ERP009898	Experiment:ERX808975
Transcriptome analysis of Dongjin, seed development and heading date + 7days using Illumina HiSeq 2000	
Accession: ERP009899	Experiment:ERX808976
Transcriptome analysis of Dongjin, seed development and heading date + 14days using Illumina HiSeq 2000	
Accession: ERP009900	Experiment:ERX808977
Transcriptome analysis of Dongjin_chal, seed development and heading date using Illumina HiSeq 2000	
Accession: ERP009901	Experiment:ERX808978
Transcriptome analysis of Dongjin_chal, seed development and heading date + 7days using Illumina HiSeq 2000	
Accession: ERP009902	Experiment:ERX808979
Transcriptome analysis of Dongjin_chal, seed development and heading date + 14days using Illumina HiSeq 2000	
Accession: ERP009904	Experiment:ERX808980

Supplementary Table S3: Diversity analysis of 80 nutritional and cooking quality-related genes in terms of average pairwise divergence (π), estimated mutation rate (θ) and Tajima's D values

GeneID	Chromosome	StartChrPosition	SiteCount	AvgSiteCount	SegSites	PiPerBP	ThetaPerBP	TajimaD
Os01g0179400	1	41,27,288	65	63.54892	65	0.30854	0.1167	4.21853
Os01g0190500	1	48,26,604	8	6.96345	8	0.36419	0.1183	3.58516
Os01g0218032	1	64,53,022	31	29.88297	31	0.20937	0.11689	1.86053
Os01g0265800	1	90,64,023	10	9.6397	10	0.33072	0.11689	3.35153
Os01g0367100	1	1,49,93,220	48	45.98122	48	0.19151	0.11698	1.58801
Os01g0633100	1	2,53,54,168	37	36.12483	37	0.25503	0.11672	2.85729
Os01g0762500	1	3,20,76,774	15	14.87794	15	0.23852	0.1165	2.13264
Os01g0878700	1	3,81,33,892	12	11.86881	12	0.3329	0.11654	3.5725
Os01g0883800	1	3,83,83,221	21	19.47555	21	0.25489	0.11742	2.57653
Os01g0952800	1	4,19,71,749	296	281.5608	296	0.20628	0.11707	2.10697
Os02g0102300	2	1,24,668	30	28.90787	30	0.34151	0.1169	4.49553
Os02g0117700	2	9,26,294	22	21.80287	22	0.20007	0.11652	1.58654
Os02g0196600	2	54,04,813	20	19.79248	20	0.20332	0.11654	1.61676
Os02g0202400	2	57,36,616	18	17.55343	18	0.27491	0.11674	2.87973
Os02g0244100	2	81,15,283	36	35.04904	36	0.29831	0.11676	3.73573
Os02g0249900	2	84,65,269	1	0.64408	1	0.40658	0.12268	1.76462
Os02g0612300	2	2,41,00,241	35	34.47124	35	0.15387	0.1166	0.76441
Os02g0649900	2	2,61,71,875	6	5.67171	6	0.21622	0.11716	1.31731
Os02g0682200	2	2,78,76,185	22	21.47139	22	0.24847	0.11672	2.49947
Os02g0716500	2	2,97,25,380	47	46.40889	47	0.25344	0.11657	2.9154
Os03g0128700	3	16,27,188	6	5.88418	6	0.44617	0.11666	4.3887
Os03g0129300	3	16,62,783	9	8.91235	9	0.22767	0.11653	1.69058
Os03g0142800	3	23,68,355	9	8.85542	9	0.19769	0.11661	1.23281
Os03g0150800	3	28,15,656	2	1.99405	2	0.07489	0.11643	-0.35763
Os03g0192700	3	48,25,797	10	9.94124	10	0.09982	0.11647	-0.26146
Os03g0216700	3	61,31,883	69	67.94186	69	0.18969	0.1166	1.61629

GeneID	Chromosome	StartChrPosition	SiteCount	AvgSiteCount	SegSites	PiPerBP	ThetaPerBP	TajimaD
Os03g0237250	3	72,37,375	25	23.87344	25	0.31927	0.11702	3.92384
Os03g0264400	3	87,02,596	31	30.46896	31	0.34251	0.11663	4.54996
Os03g0307200	3	1,09,26,483	5	4.49415	5	0.25522	0.11785	1.70803
Os03g0656500	3	2,56,13,922	9	8.15331	9	0.13527	0.11775	0.26548
Os03g0667500	3	2,62,86,278	128	122.533	128	0.10003	0.11699	-0.38952
Os03g0737701	3	3,02,44,613	11	10.25179	11	0.38413	0.11735	4.28906
Os03g0753100	3	3,10,48,492	20	19.34461	20	0.34321	0.11685	4.21168
Os03g0758100	3	3,13,32,056	15	14.71875	15	0.32238	0.11665	3.59371
Os03g0766000	3	3,17,26,165	16	15.8537	16	0.21357	0.11652	1.72223
Os03g0826500	3	3,47,15,941	30	29.22926	30	0.27022	0.11675	3.07397
Os04g0164900	4	44,08,409	412	396.4897	412	0.27339	0.11691	3.72288
Os04g0463400	4	2,31,34,671	28	27.59705	28	0.12753	0.11659	0.21679
Os04g0537900	4	2,69,04,203	12	11.91487	12	0.11668	0.11649	0.00312
Os04g0542200	4	2,71,54,447	13	12.37409	13	0.3775	0.11707	4.38333
Os04g0557500	4	2,79,15,619	118	101.702	118	0.29913	0.11844	4.1006
Os04g0597800	4	3,01,61,862	27	24.29714	27	0.18638	0.11784	1.34277
Os04g0620000	4	3,15,02,980	19	18.84306	19	0.14903	0.1165	0.59969
Os04g0645100	4	3,28,35,576	59	57.50056	59	0.25349	0.11674	2.9799
Os04g0652400	4	3,32,15,661	30	29.51568	30	0.317	0.11661	4.01606
Os05g0115800	5	8,58,506	26	25.76784	26	0.19447	0.11652	1.52627
Os05g0156900	5	33,35,388	96	88.19535	96	0.4029	0.11755	6.43074
Os05g0187500	5	53,65,256	4	3.31698	4	0.30845	0.11899	2.15946
Os05g0198400	5	60,90,807	31	30.5758	31	0.23536	0.11658	2.39305
Os05g0408200	5	1,99,23,998	47	46.17985	47	0.26167	0.11663	3.08827
Os05g0415200	5	2,03,02,417	15	14.79456	15	0.32518	0.11658	3.64483
Os05g0554000	5	2,75,42,160	17	16.37206	17	0.33183	0.1169	3.86115
Os06g0133000	6	17,65,761	45	43.34151	45	0.2732	0.1169	3.30681
Os06g0143700	6	22,92,676	152	147.4325	152	0.07764	0.11681	-0.90746
Os06g0160700	6	30,79,977	66	63.76309	66	0.37409	0.11686	5.6591
Os06g0229800	6	67,48,443	65	61.69255	65	0.19583	0.1171	1.72753

GeneID	Chromosome	StartChrPosition	SiteCount	AvgSiteCount	SegSites	PiPerBP	ThetaPerBP	TajimaD
Os06g0700700	6	2,94,73,748	153	148.4848	153	0.35977	0.1168	5.63172
Os07g0181000	7	42,66,889	42	39.97037	42	0.15931	0.11707	0.88566
Os07g0232900	7	74,05,972	19	18.39385	19	0.2357	0.11683	2.18823
Os07g0257200	7	88,71,767	73	70.65909	73	0.22392	0.11683	2.37606
Os07g0603300	7	2,46,64,520	22	21.68465	22	0.19962	0.11659	1.57623
Os07g0616800	7	2,54,29,921	12	11.90566	12	0.16957	0.1165	0.87654
Os07g0623200	7	2,57,91,175	13	12.89911	13	0.16963	0.1165	0.89606
Os07g0668600	7	2,82,33,372	7	6.90671	7	0.12424	0.11658	0.10758
Os07g0689600	7	2,93,23,445	7	6.86686	7	0.16426	0.11665	0.66818
Os08g0101500	8	86,771	4	3.9624	4	0.23901	0.11652	1.40525
Os08g0191433	8	53,52,201	137	134.2537	137	0.19903	0.11667	1.90138
Os08g0424500	8	2,03,79,846	59	57.8951	59	0.1761	0.11665	1.29607
Os08g0531600	8	2,65,01,258	36	35.3934	36	0.25308	0.11662	2.80962
Os09g0396900	9	1,38,31,895	12	11.8905	12	0.08845	0.11652	-0.46351
Os09g0440300	9	1,63,30,652	19	18.45389	19	0.2426	0.11679	2.3167
Os09g0448500	9	1,67,66,211	7	6.34739	7	0.20727	0.11773	1.25255
Os09g0529700	9	2,07,45,597	9	8.68011	9	0.36865	0.11689	3.8247
Os10g0112100	10	8,24,973	48	44.50129	48	0.1741	0.11743	1.20475
Os10g0478200	10	1,79,13,836	27	26.54252	27	0.25749	0.11663	2.77459
Os10g0485600	10	1,83,60,613	37	36.3006	37	0.34851	0.11665	4.79117
Os10g0567400	10	2,24,83,116	8	7.95773	8	0.10478	0.11646	-0.17132
Os12g0631100	12	2,70,22,270	63	62.51149	63	0.08756	0.1165	-0.63516

Supplementary Table S4. Details of hub genes and their interactions identified by co-expression network using RNAseq data

Hotspot gene	SUID	Average Shortest Path Length	bait_gene	Betweenness Centrality	Clustering Coefficient	Degree	Neighborhood Connectivity	Number Of Directed Edges	Stress
1	64	1.866667	os10g0567400	0.127522	0.242105	20	9.8	20	3216
2	86	1.983333	os06g0160700	0.137596	0.391813	19	11.84211	19	2066
3	97	1.9	os04g0645100	0.112704	0.327485	19	10.15789	19	2250
4	96	2.016667	os04g0652400	0.070166	0.385621	18	10.66667	18	1554
5	118	1.95	os03g0129300	0.14301	0.125	17	8.882353	17	3646
6	99	2.083333	os04g0597800	0.036403	0.483333	16	12.625	16	1124
7	114	2.15	os03g0216700	0.027757	0.483516	14	12.64286	14	850
8	74	2.283333	os08g0191433	0.061271	0.538462	13	10.30769	13	934
9	81	2.15	os07g0257200	0.011252	0.666667	13	13.92308	13	454
10	125	2.083333	os02g0244100	0.060028	0.564103	13	12.53846	13	1598
11	77	2.416667	os07g0668600	0.024494	0.681818	12	10.66667	12	736
12	79	2.416667	os07g0616800	0.020373	0.681818	12	10.66667	12	668
13	82	2.2	os07g0232900	0.005035	0.742424	12	14.41667	12	232
14	85	2.416667	os06g0229800	0.024494	0.681818	12	10.66667	12	736
15	106	2.316667	os03g0758100	0.022093	0.636364	12	11.91667	12	426
16	127	2.15	os02g0196600	0.017487	0.606061	12	14.25	12	656
17	102	2.25	os04g0537900	0.053353	0.636364	11	11.45455	11	704
18	104	2.216667	os03g0826500	0.031869	0.577778	10	12.8	10	1060
19	134	2.45	os01g0633100	0.008528	0.8	10	11.6	10	242
	94	2.716667	os05g0156900	0.007576	0.722222	9	10.11111	9	258
	103	2.383333	os04g0463400	0.062503	0.277778	9	10.22222	9	1112
	116	2.333333	os03g0150800	0.003624	0.75	9	14.66667	9	122
	138	2.4	os01g0190500	0.061841	0.416667	9	11.11111	9	1818
	84	2.4	os06g0700700	0.016197	0.214286	8	12.625	8	682
	105	2.416667	os03g0766000	0.063427	0.285714	8	9.875	8	1412
	109	2.383333	os03g0667500	0.001049	0.892857	8	14.25	8	62
	129	2.566667	os02g0102300	0.0181	0.678571	8	12.125	8	228

Hotspot gene	SUID	Average Shortest Path Length	bait_gene	Betweenness Centrality	Clustering Coefficient	Degree	Neighborhood Connectivity	Number Of Directed Edges	Stress
	113	2.5	os03g0237250	0.028467	0.47619	7	13	7	1084
	135	2.6	os01g0367100	0.007796	0.333333	7	9.428571	7	176
	139	2.533333	os01g0179400	0.080958	0.142857	7	5	7	1028
	72	3.183333	os08g0531600	0.024035	0.266667	6	4.166667	6	480
	83	2.316667	os07g0181000	0.030286	0.4	6	12.16667	6	812
	117	2.383333	os03g0142800	0.047426	0.133333	6	9.333333	6	842
	120	2.9	os02g0716500	0.046637	0.266667	6	5	6	1022
	131	2.65	os01g0883800	0.019819	0.066667	6	7.833333	6	432
	68	2.566667	os09g0529700	0.022586	0.4	5	8.2	5	558
	75	2.433333	os08g0101500	0.03657	0.3	5	14.2	5	610
	78	2.733333	os07g0623200	0.005018	0.4	5	10.2	5	138
	89	2.516667	os05g0554000	4.75E-04	0.7	5	17.6	5	28
	91	2.5	os05g0408200	0.007101	0.6	5	14.4	5	134
	69	3.283333	os09g0448500	5.18E-04	0.833333	4	6.5	4	6
	92	2.616667	os05g0198400	0.0416	0.166667	4	14.5	4	832
	93	3.283333	os05g0187500	5.18E-04	0.833333	4	6.5	4	6
	111	3.333333	os03g0369100	0	1	4	11.25	4	0
	137	3	os01g0218032	0.028768	0.166667	4	4.5	4	444
	65	2.633333	os10g0485600	0.014287	0	3	14.33333	3	438
	73	2.966667	os08g0424500	0.004986	0.333333	3	6.333333	3	88
	98	3.333333	os04g0620000	0.002252	0.666667	3	5.666667	3	36
	121	3.183333	os02g0682200	0.019997	0.333333	3	5.666667	3	234
	123	3.266667	os02g0612300	9.23E-04	0.666667	3	5.333333	3	12
	124	3.216667	os02g0249900	0	1	3	11.66667	3	0
	126	3.366667	os02g0202400	0	1	3	11	3	0
	80	2.866667	os07g0603300	0	1	2	13.5	2	0
	107	3.8	os03g0753100	0	1	2	4.5	2	0
	108	3.466667	os03g0737701	0.0126	0	2	3	2	258
	110	3.833333	os03g0656500	0.003426	0	2	3	2	32
	119	3.016667	os03g0128700	0.002408	0	2	9.5	2	36

Hotspot gene	SUID	Average Shortest Path Length	bait_gene	Betweenness Centrality	Clustering Coefficient	Degree	Neighborhood Connectivity	Number Of Directed Edges	Stress
	122	1	os02g0649900	1	0	2	1	2	2
	66	3.516667	os10g0478200	0	0	1	7	1	0
	71	1.5	os09g0396900	0	0	1	2	1	0
	101	3.883333	os04g0542200	0	0	1	6	1	0
	115	2.966667	os03g0192700	0	0	1	19	1	0
	130	1.5	os01g0952800	0	0	1	2	1	0
	132	2.883333	os01g0878700	0	0	1	19	1	0
	62	0	loc_os06g38120	0	0	0	0	0	0
	63	0	os12g0631100	0	0	0	0	0	0
	67	0	os10g0112100	0	0	0	0	0	0
	70	0	os09g0440300	0	0	0	0	0	0
	76	0	os07g0689600	0	0	0	0	0	0
	87	0	os06g0143700	0	0	0	0	0	0
	88	0	os06g0133000	0	0	0	0	0	0
	90	0	os05g0415200	0	0	0	0	0	0
	95	0	os05g0115800	0	0	0	0	0	0
	100	0	os04g0557500	0	0	0	0	0	0
	112	0	os03g0264400	0	0	0	0	0	0
	128	0	os02g0117700	0	0	0	0	0	0
	133	0	os01g0762500	0	0	0	0	0	0
	136	0	os01g0265800	0	0	0	0	0	0

Supplementary Table S5. Details of genetic variations previously reported for nutritional and cooking quality related genes

Gene	RAPdb	Chromosome_location	MSU	Mutations/role
Rab5a	Os12g0631100	chr12:27021987-27025197	LOC_Os12g43550	G->A splice donor first intron, Gly->Asp(45),Gln->Stop(176)
Rab5a	Os12g0631100	chr12:27021987-27025197	LOC_Os12g43550	13 bp deletion in the third exon
OsCAO1 PGL	Os10g0567400	chr10:22482881-22486532 (complement)	LOC_Os10g41780	L253F,A106V
OsDCL3b	Os10g0485600	chr10:18360057-18372796	LOC_Os10g34430	Knockdown
FLO16	Os10g0478200	chr10:17913821-17917768	LOC_Os10g33800	4 bp deletion in the fifth exon
OsPCR1	Os10g0112100	chr10:824623-826321 (complement)	LOC_Os10g02300	Knockdown and Knockout
OsVPS22	Os09g0529700	chr9:20744818-20748508 (complement)	LOC_Os09g36020	Knockout
GS9	Os09g0448500	chr9:16765820-16767992	LOC_Os09g27590	Null allele
osaldh7	Os09g0440300	chr9:16330101-16338641 (complement)	LOC_Os09g26880	Insertion mutants
osaldh7	Os09g0440300	chr9:16330101-16338641 (complement)	LOC_Os09g26880	C to T (985) substitution in the tenth exon
OsVIT2	Os09g0396900	chr9:13831851-13833641	LOC_Os09g23300	Knockdown
OsVIT2	Os09g0396900	chr9:13831851-13833641	LOC_Os09g23300	Knockout
qGW8 OsSPL16 G	Os08g0531600	chr8:26500458-26506276	LOC_Os08g41940	Loss of function mutation results in slender grains
W8	Os08g0424500	chr8:20379779-20386042	LOC_Os08g32870	19 alleles
Badh2	Os08g0191433	chr8:5349928-5363361	LOC_Os08g09230	Knockout
SSIIa	Os08g0101500	chr8:86166-87855	LOC_Os08g01120	Sequence variation in promoter
OsMOT1;1	Os07g0689600	chr7:29323078-29324696	LOC_Os07g48980	Activation of NAS Gene
OsNAS3	Os07g0668600	chr7:28233219-28235926 (complement)	LOC_Os07g47240	Downregulation
OsGZF1	Os07g0623200	chr7:25790365-25792702	LOC_Os07g43040	Downregulation
OsHMA7	Os07g0616800	chr7:25429550-25435142	LOC_Os07g42490	SNPs in promoter region
RSUS3 S				
US3				

Gene	RAPdb	Chromosome_location	MSU	Mutations/role
GW7 GL 7 SLG7 OsNRAM P5 OsNRAM P5 qCdT7 O sHMA3 qCdT7 O sHMA3 OsPK2 W59 Os PKpalpha 1 OsHMA2 OsHMA 2v ALK SSIIa ALK SSIIa	Os07g0603300 Os07g0257200 Os07g0257200 Os07g0232900 Os07g0232900	chr7:24664276-24669347 (complement) chr7:8871580-8878943 (complement) chr7:8871580-8878943 (complement) chr7:7405544-7409595 (complement) chr7:7405544-7409595 (complement)	LOC_Os07g41200 LOC_Os07g15370 LOC_Os07g15370 LOC_Os07g12900 LOC_Os07g12900	Gene upregulation Knockout Functionally deficient OsNRAMP5 affects metal accumulation Ser380Arg Loss of function allele Promoter Sequence variations
OsPK2 W59 Os PKpalpha 1 OsHMA2 OsHMA 2v ALK SSIIa ALK SSIIa	Os07g0181000 Os06g0700700 Os06g0229800 Os06g0229800	chr7:4266867-4271499 chr6:29473272-29481042 (complement) chr6:6748306-6753338 chr6:6748306-6753338	LOC_Os07g08340 LOC_Os06g48720 LOC_Os06g12450 LOC_Os06g12450	Ser296Leu Insertion mutations Leu781Phe,Val737Met GC4327, 4328TT,A4196G Polymorphism at -916 bp in the SSSI promoter Indel, an A/G SNP in exon 6, a C/T SNP in exon 8, a C/A SNP
OsSSI SPDT SPDT Wx Wx Wx OsMATE 2	Os06g0160700 Os06g0143700 Os06g0143700 Os06g0133000 Os06g0133000 Os06g0133000 Os05g0554000	chr6:3079058-3086803 (complement) chr6:2292641-2298815 (complement) chr6:2292641-2298815 (complement) chr6:1765524-1770644 chr6:1765524-1770644 chr6:1765524-1770644 chr5:27542040-27545926	LOC_Os06g06560 LOC_Os06g05160 LOC_Os06g05160 LOC_Os06g04200 LOC_Os06g04200 LOC_Os06g04200 LOC_Os05g48040	Val330Ala Knockout GT to TT mutation at the 5' splice site of the first intron G/T intron 1 Splice donor site at intron 1, 224 and 415 positions in exon 6 and 10 Expression

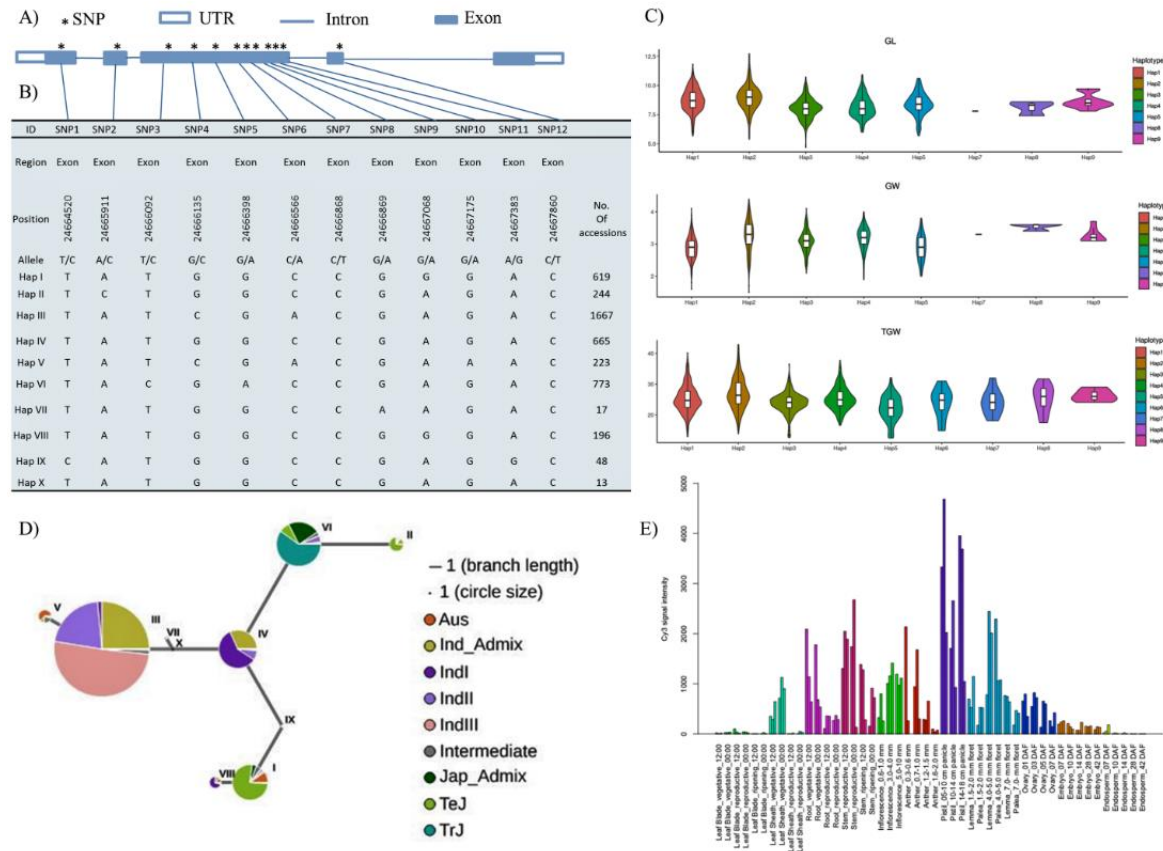
Gene	RAPdb	Chromosome_location	MSU	Mutations/role
OsPCS1	Os05g0415200	chr5:20301984-20305758	LOC_Os05g34290	Alternative splicing
OsSPL9	Os05g0408200	chr5:19923172-19932449	LOC_Os05g33810	Glu561Lys
OsZIP7a OsZIP7	Os05g0198400	chr5:6090719-6094071	LOC_Os05g10940	Loss of function
GSE5	Os05g0187500	chr5:5364877-5367038	LOC_Os05g09520	950-bp deletion in indica and 1212-bp deletion in japonica varieties
Chalk5	Os05g0156900	chr5:3335334-3339834(complement)	LOC_Os05g06480	CATGCA at 721,CACT tetranucleotide at 485 and 2 SNPs in promoter
OsMKP1 GSN1 L ARGE8 G LA1	Os05g0115800	chr5:858395-862791 (complement)	LOC_Os05g02500	Loss of function
OsMKP1 GSN1 L ARGE8 G LA1	Os05g0115800	chr5:858395-862791 (complement)	LOC_Os05g02500	SNP (861,675; G to A) exon 1
OsSULTR 3;3	Os04g0652400	chr4:33215039-33220693 (complement)	LOC_Os04g55800	(1-bp) deletion 12th exon-stop codon and 6-bp deletion first exon
FLO2	Os04g0645100	chr4:32835149-32848270	LOC_Os04g55230	3 SNPs
OsABCC1 MRP1	Os04g0620000	chr4:31502901-31515366 (complement)	LOC_Os04g52900	Knockout
OsPTR6 PTR6 Os NPF7.3	Os04g0597800	chr4:30161413-30165517	LOC_Os04g50950	Overexpression
Kala4 Os S1	Os04g0557500	chr4:27939824-27915598 chr4:27154293-27159796 (complement)	LOC_Os04g47059	6 SNPs, 1 InDel
OsYSL9	Os04g0542200	chr4:26903954-26908730 (complement)	LOC_Os04g45860	knockdown
Osvpe1	Os04g0537900	chr4:23134255-23137105 (complement)	LOC_Os04g45470	Cys269Gly
OsVIT1	Os04g0463400	(complement)	LOC_Os04g38940	expression
sug1	Os04g0164900	chr4:4405753-4418895		80 SNP in the gene

Gene	RAPdb	Chromosome_location	MSU	Mutations/role
OASA1D	Os03g0826500	chr3:34715402-34721077 (complement)		
CysR10	Os03g0766000	chr3:31725962-31732275 (complement)		
		chr3:31332021-31339259		
pho1	Os03g0758100	(complement)	LOC_Os03g55090	Knockout
OsMADS		chr3:31048350-31055281		
34 PAP2	Os03g0753100	(complement)	LOC_Os03g54170	null mutation
OsMADS		chr3:31048350-31055281		
34 PAP2	Os03g0753100	(complement)	LOC_Os03g54170	1014-bp deletion
			Sequence analysis of the N15-186 allele of this orthologue (Os03g52760) revealed a single base pair change (C/G to T/A) in the first exon of the gene, which results in a nonsense mutation. Our results indicate that lpa N15-186 is a mutant allele of the	
lpaN15-186	Os03g0737701	chr3:30244152-30247443 (complement)	rice myo-inositol kinase (OsMIK) gene.	nonsense mutation in first exon
		chr3:26286207-26292159		
OsIRT1	Os03g0667500	(complement)	LOC_Os03g46470	Overexpression
OsCCX2	Os03g0656500	chr3:25613813-25616205	LOC_Os03g45370	Knockout
OsLTPL3				
6	Os03g0369100	chr3:14491725-14492433	LOC_Os03g25350	Knockout
OsNAS2	Os03g0307200	chr3:10926452-10927926	LOC_Os03g19420	Overexpression
OASA2	Os03g0264400	chr3:8702913-8707788 (complement)		site directed S126F/L530D mutations
		chr3:7237067-7241524		insertion in 3rd exon premature transcriptional
lpa1	Os03g0237250	(complement)	LOC_Os03g13400	termination

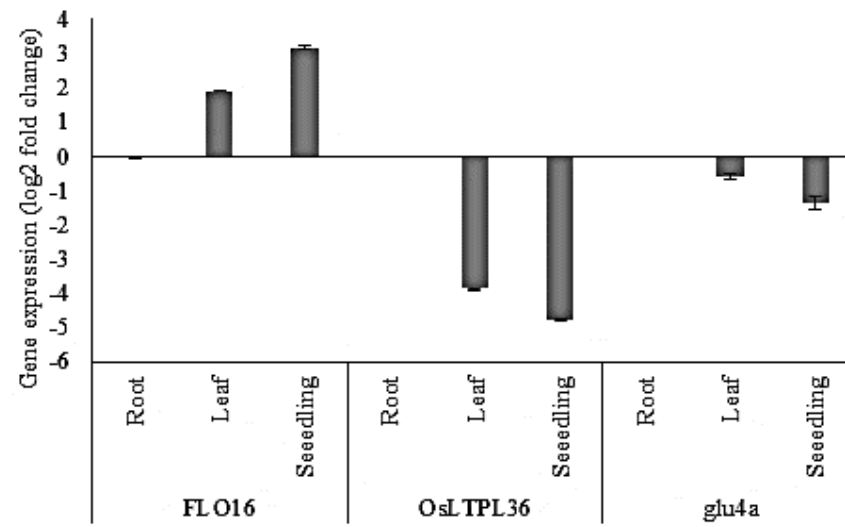
Gene	RAPdb	Chromosome_location	MSU	Mutations/role
OsFRDL1	Os03g0216700	chr3:6131845-6142900 (complement)	LOC_Os03g11734	Knockout
RINO1	Os03g0192700	chr3:4825696-4829742 (complement)		Expression
OsPht1;2		chr3:2815495-2822792		
OsPT2	Os03g0150800	(complement)	LOC_Os03g05640	Leu218Pro
OsPht1;2		chr3:2815495-2822792		
OsPT2	Os03g0150800	(complement)	LOC_Os03g05640	Overexpression 1 SNP (C/G-T/A transition) 6th exon of XS-lpa2-1 and a 5-bp deletion 1st exon of XS-lpa2-2
XS-lpa2-1	Os03g0142800	chr3:2367836-2374429		
OsGAPD				
HB	Os03g0129300	chr3:1662177-1665491		P425S mutation
OsCDPK1	Os03g0128700	chr3:1624884-1629492	LOC_Os03g03660	expression and gene silencing
OsFAD2				
OsFAD2-		chr2:29725325-		
1	Os02g0716500	29730369(complement)	LOC_Os02g48560	gene silencing
OsMADS				
6	Os02g0682200	chr2:27875934-27884005 chr2:26170543-26175198 (complement)	LOC_Os02g45770	Null allele
OsYSL2	Os02g0649900	(complement)	LOC_Os02g43370	Knockdown
Du3	Os02g0612300	chr2:24100127-24103567 (complement)		3 alleles
GluB-1	Os02g0249900	chr2:8465040-8467045	LOC_Os02g15169	Regulator
GW2	Os02g0244100	chr2:8114930-8121836	LOC_Os02g14720	A314 deletion
GW2	Os02g0244100	chr2:8114930-8121836	LOC_Os02g14720	Knockdown
OsBT1-				
1 OsBT1	Os02g0202400	chr2:5736568-5738793	LOC_Os02g10800	1 bp deletion GT->G exon 1
OsHMA4	Os02g0196600	chr2:5404709-5410739	LOC_Os02g10290	V914A
OsUgp2		chr2:926052-930040		
Ugp2	Os02g0117700	(complement)	LOC_Os02g02560	5' deletion promoter and gain-of-function
OsHAC1;				
1	Os02g0102300	chr2:124618-127140 chr1:41972004-41978403 (complement)	LOC_Os02g01220	Knockout
OsIRO2	Os01g0952800	(complement)	LOC_Os01g72370	Transcriptional activator

Gene	RAPdb	Chromosome_location	MSU	Mutations/role
sd1 GA2 Oox2	Os01g0883800	chr1:38382358-38385504	LOC_Os01g66100	Loss of function
OsAAP6 qPC1	Os01g0878700	chr1:38133432-38137790 (complement)	LOC_Os01g65670	(-7 to -12 bp, -32 bp) variations in the cis-regulatory elements of 5' UTR
glu4a OsAPL2 osagpl2- 3 OsAGP L2 GIF2	Os01g0762500	chr1:32076723-32078653		2 mutations L827S and G878E
PHD1	Os01g0633100	chr1:25354534-25361907 chr1:14993203-14998127	LOC_Os01g44220	Single missense mutation (G-to-T) in exon 2,(A-to-T) in exon 7,3-bp Insertion between exon 3 and exon 4
RBP-P OsROS1 TA2	Os01g0367100	chr1:9063927-9066803 (complement)	LOC_Os01g26920	3 mutations A252T, G373E, and G401S
GW5L	Os01g0218032	chr1:6443035-6456074	LOC_Os01g11900	Knockout
SSG4	Os01g0190500	chr1:4826355-4828739	LOC_Os01g09470	Negative regulator
OsLCT1	Os01g0179400	chr1:4127233-4140749	LOC_Os01g08420	1 mutation G to A
	None	chr6:22566775-22571982	LOC_Os06g38120	Knockdown

Supplementary Figure S1: Representative illustration showing genetic variations observed in *GL7* gene defining haplotypic diversity, evolution, and expression profile in different tissues. A) Intron-exon organization of *GL7* gene showing single nucleotide polymorphism sites; B) haplotypic grouping based on the SNPs present in the *GL7* gene; C) Violin plot showing the frequency

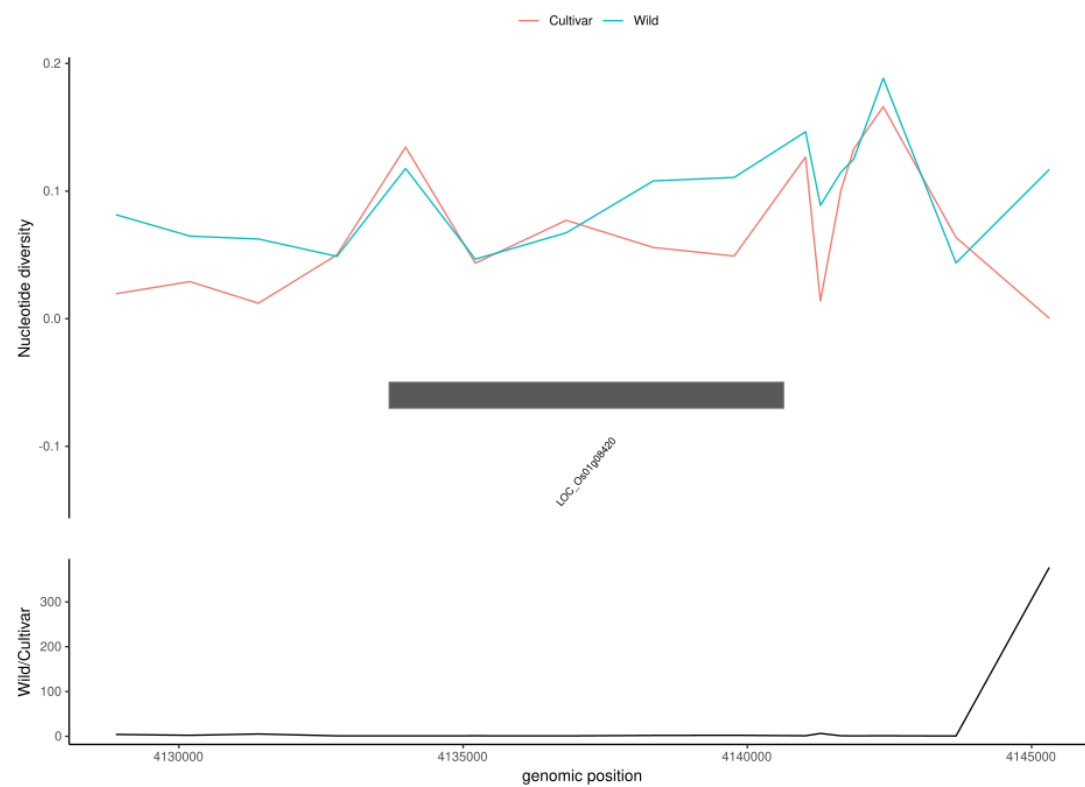


distribution of haplotypes; D) haplotypic network showing relatedness and allelic evolution of *GL7* gene; E) expression profiling of *GL7* gene in different tissues.

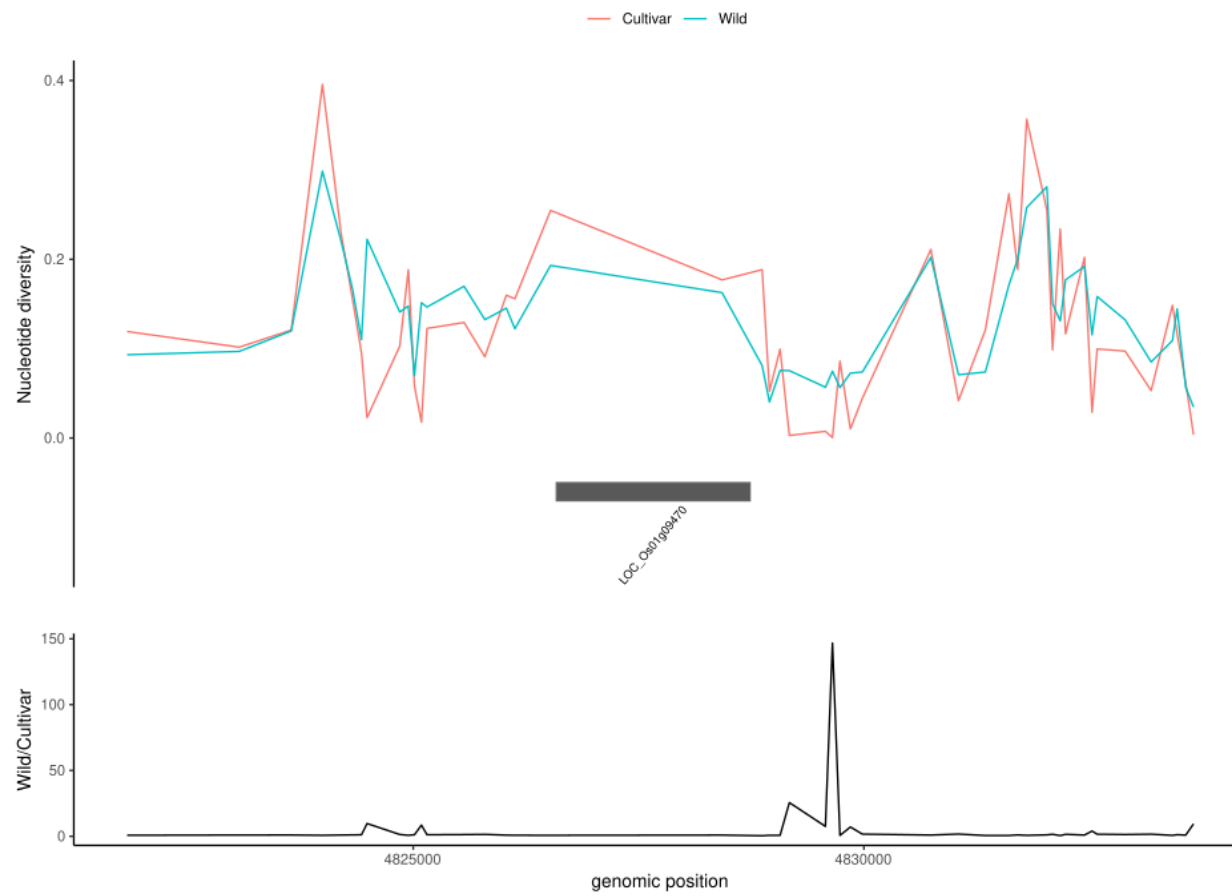


Supplementary Figure S2. The relative expression level of *FLO16*, *OsLTPL36*, and *glu4a* in root, leaf, and seedling, measured with real-time quantitative PCR (RT-qPCR). Bars show mean log(2) fold change \pm SEM of three biological samples.

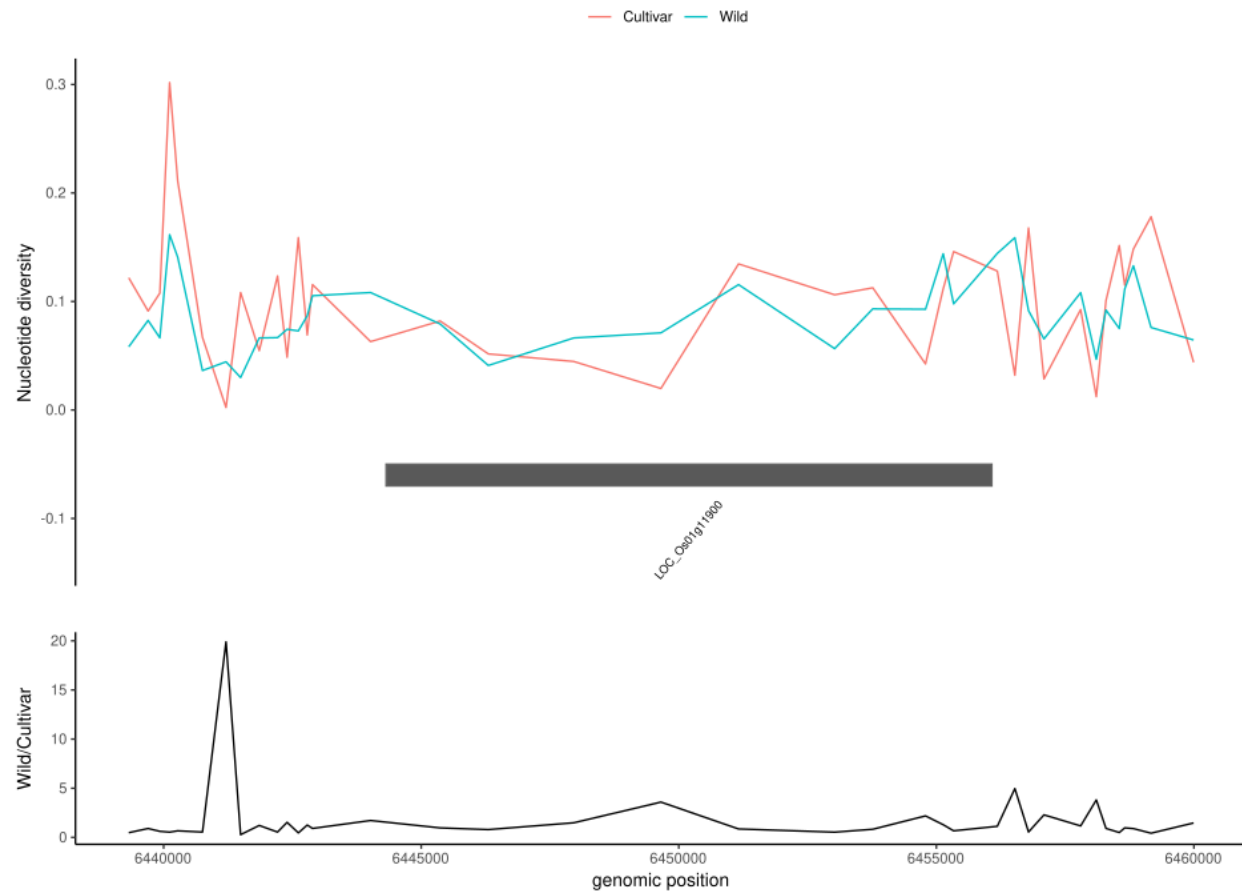
Supplementary Dataset 2. Diversity analysis between cultivated and wild rice accessions for 80 nutritional and cooking quality related genes.



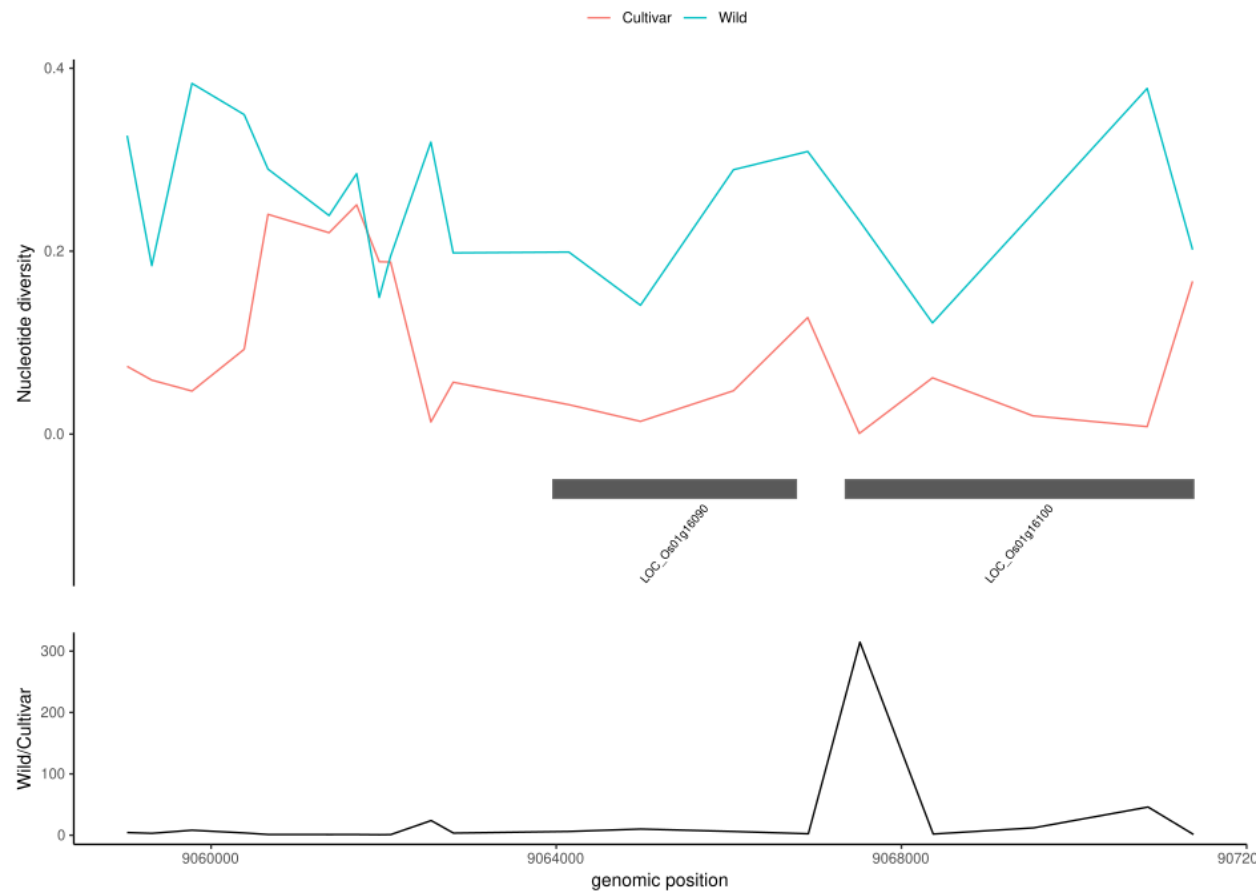
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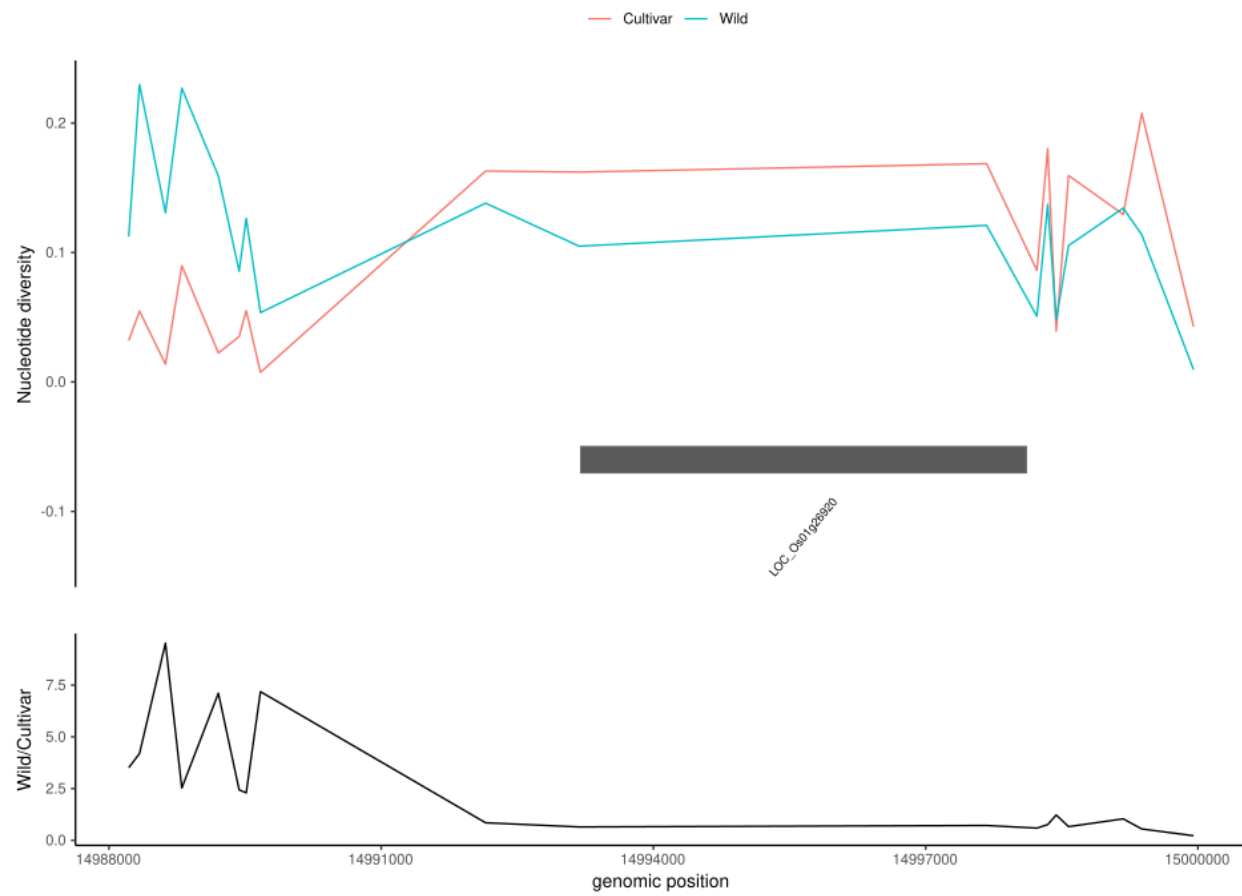
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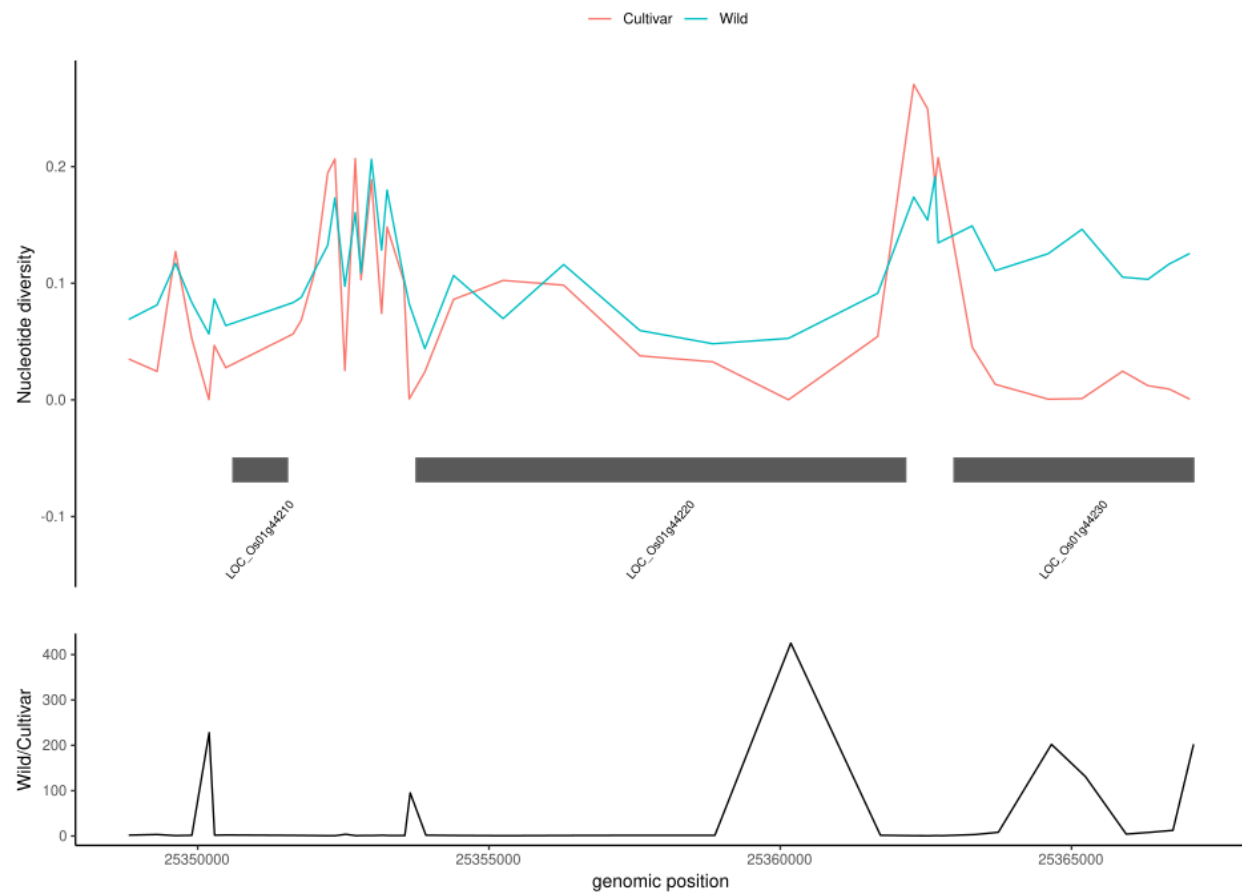
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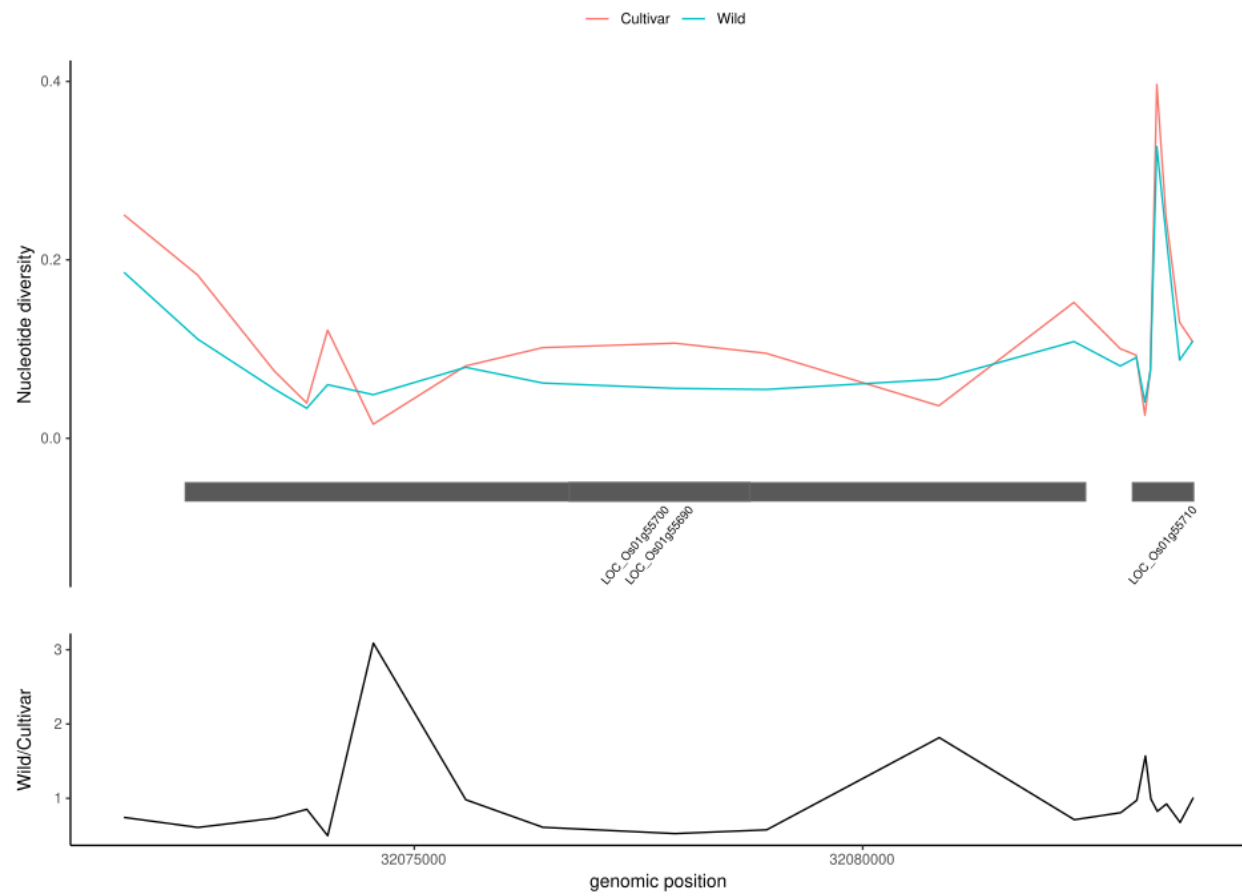
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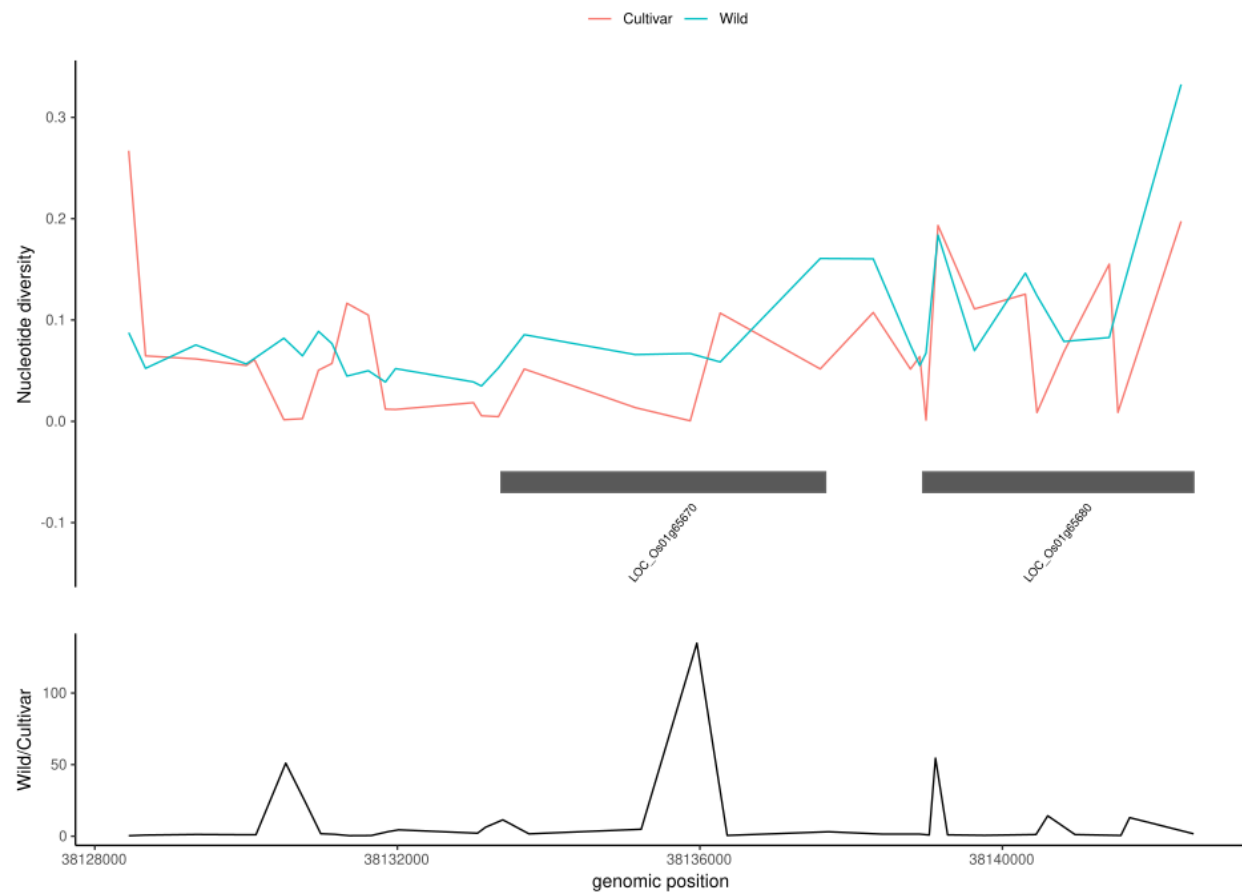
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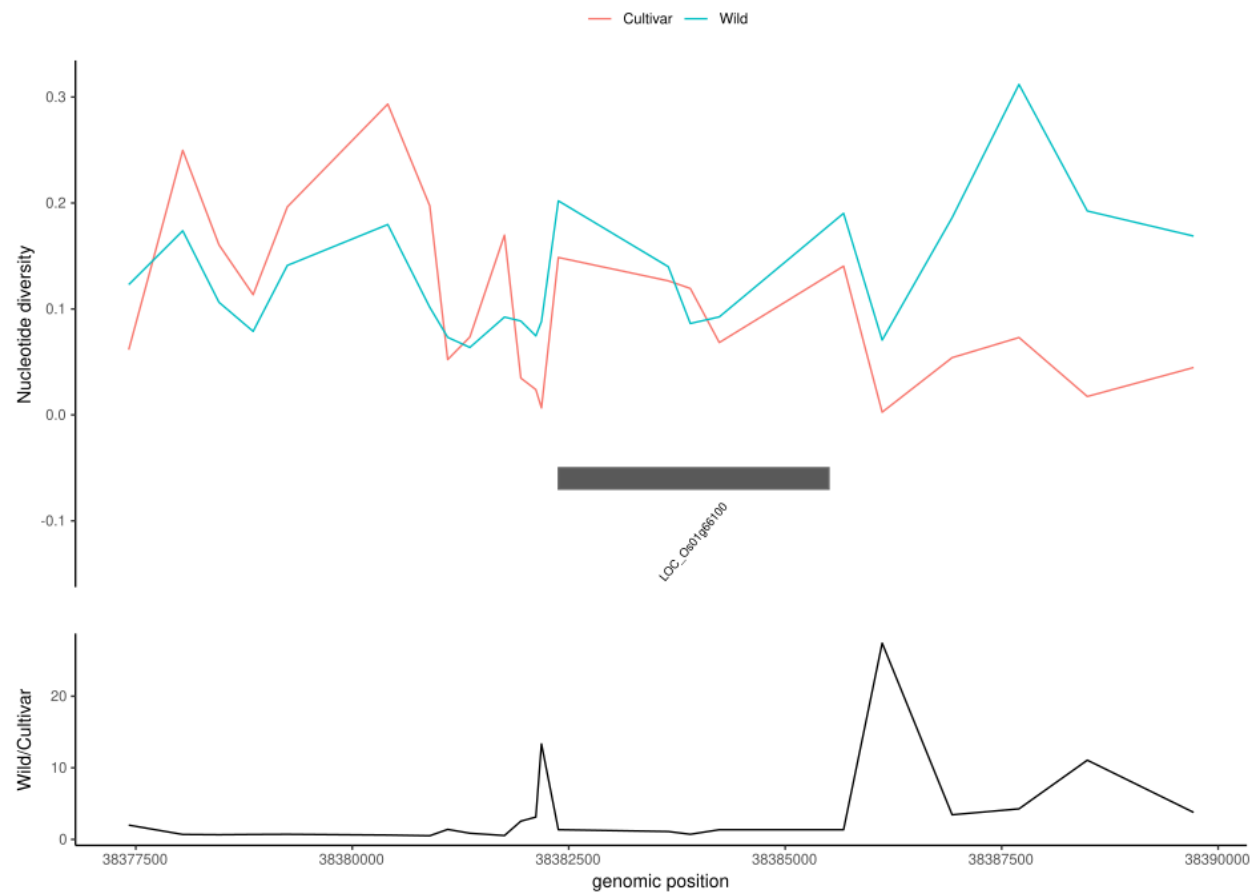
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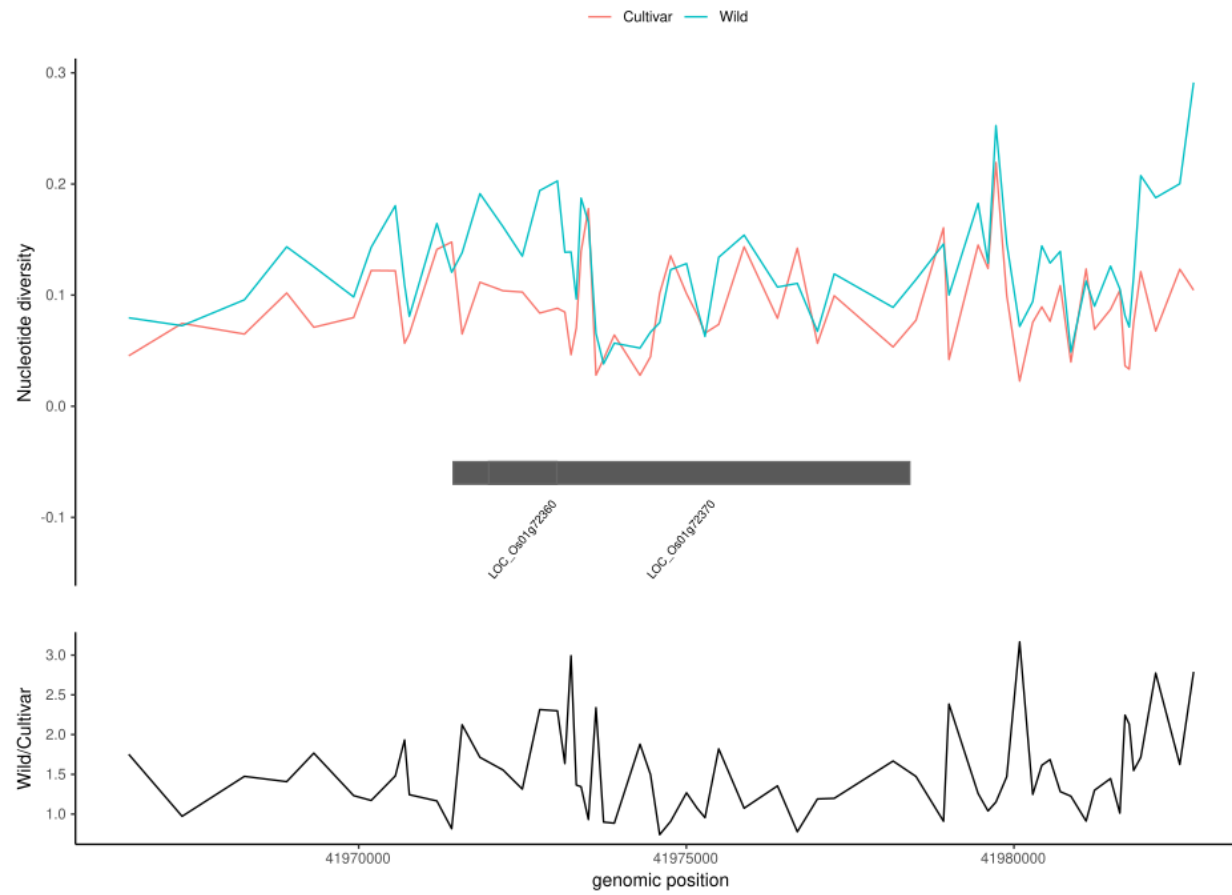
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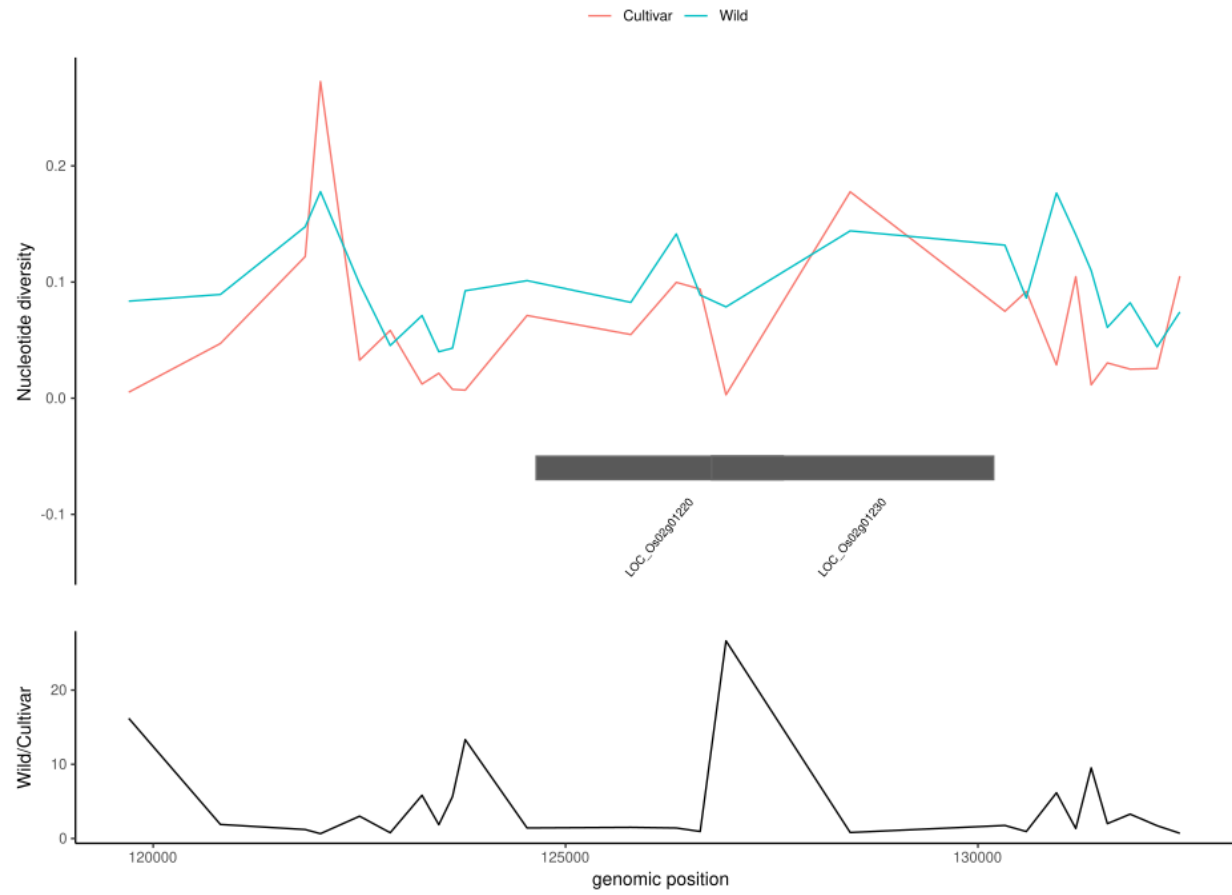
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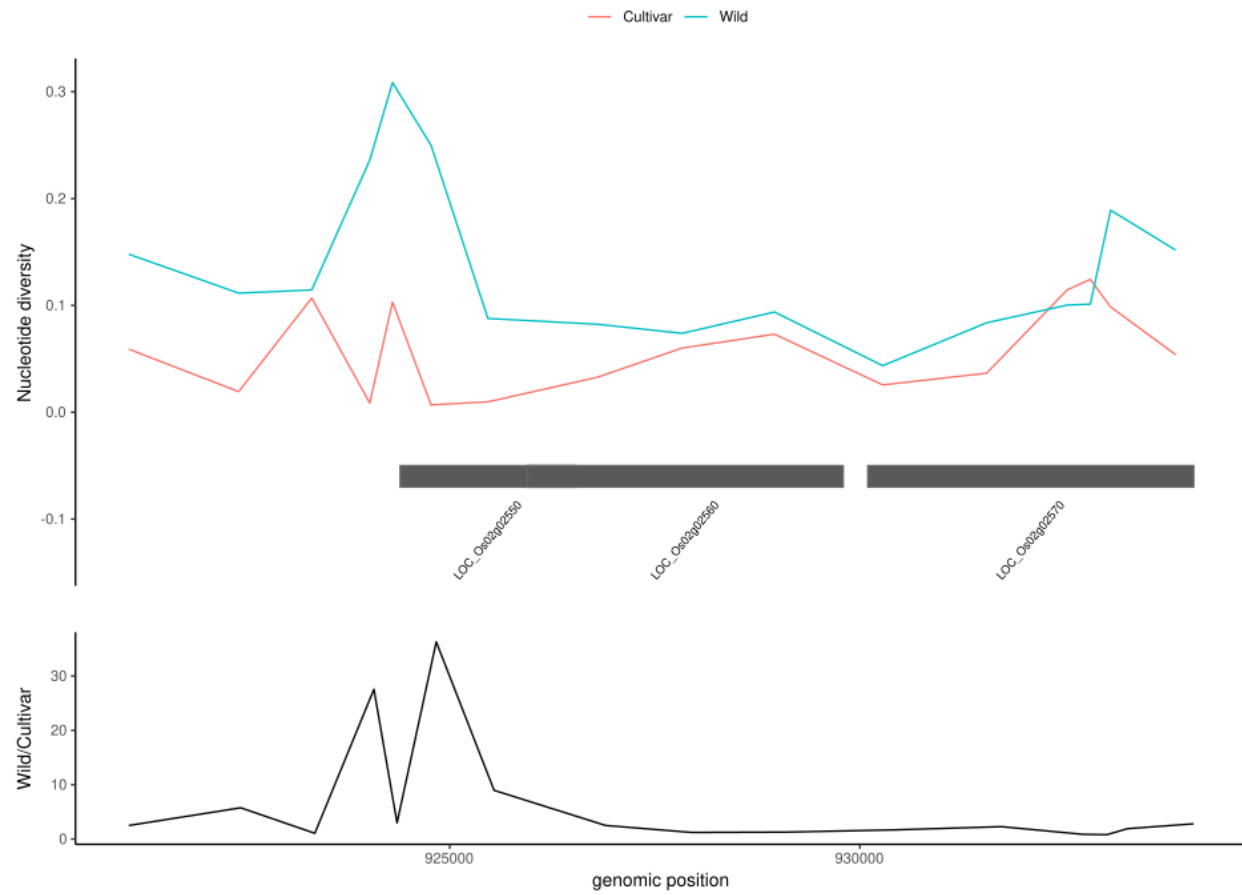
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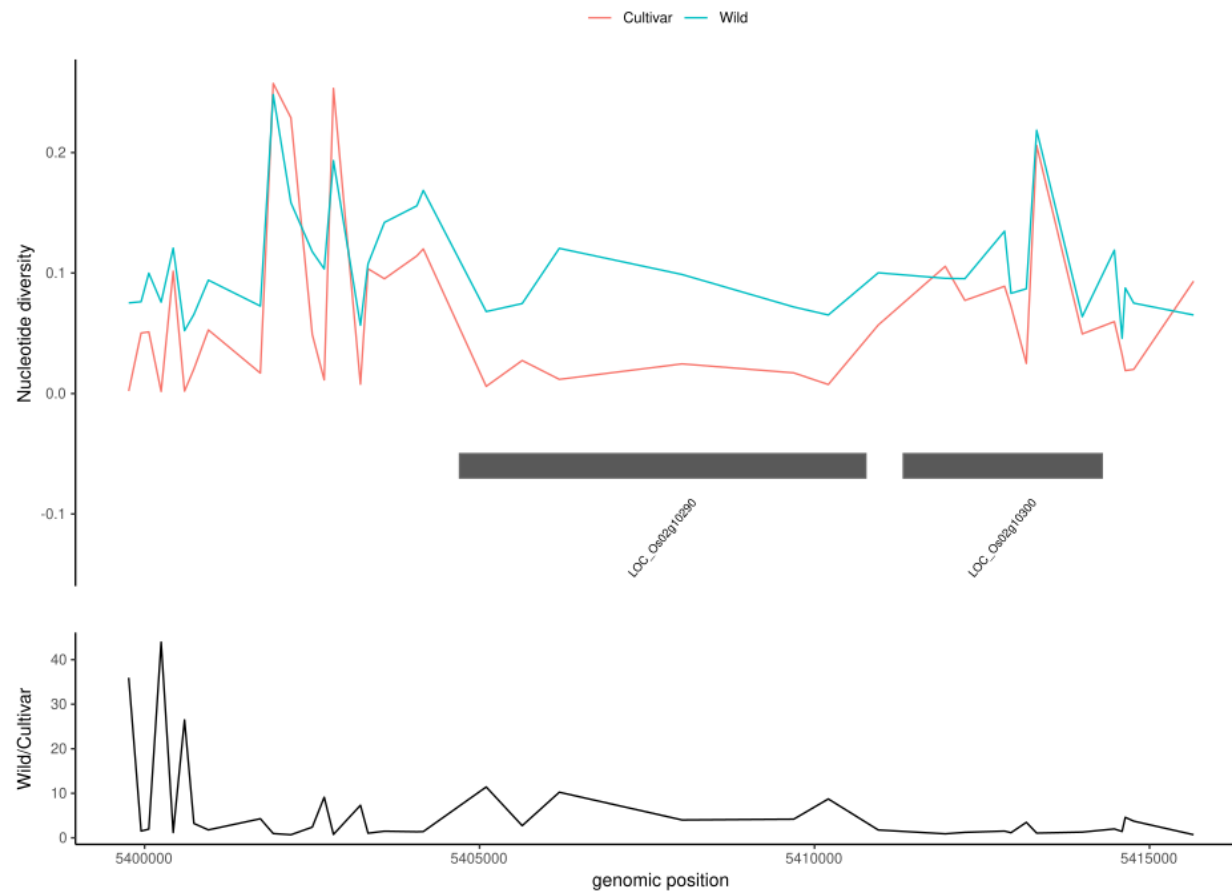
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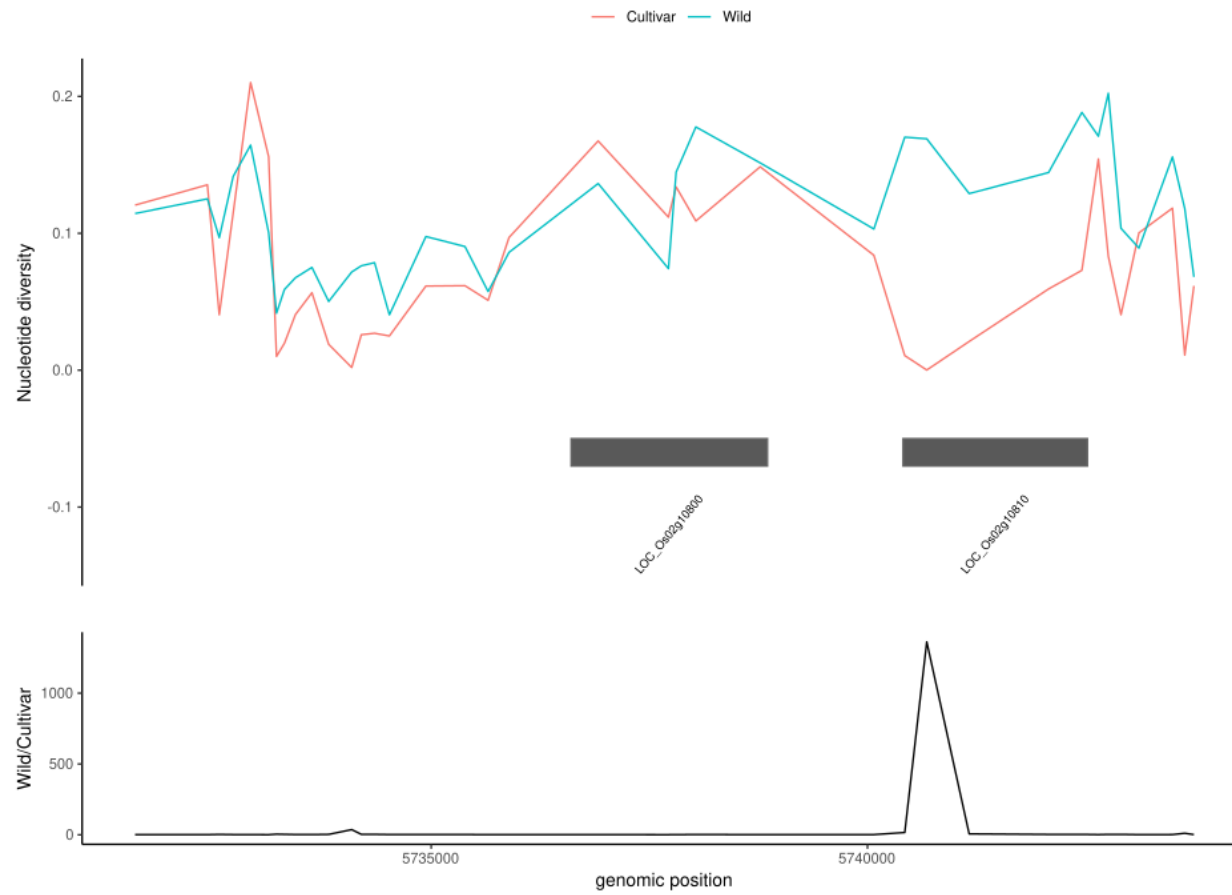
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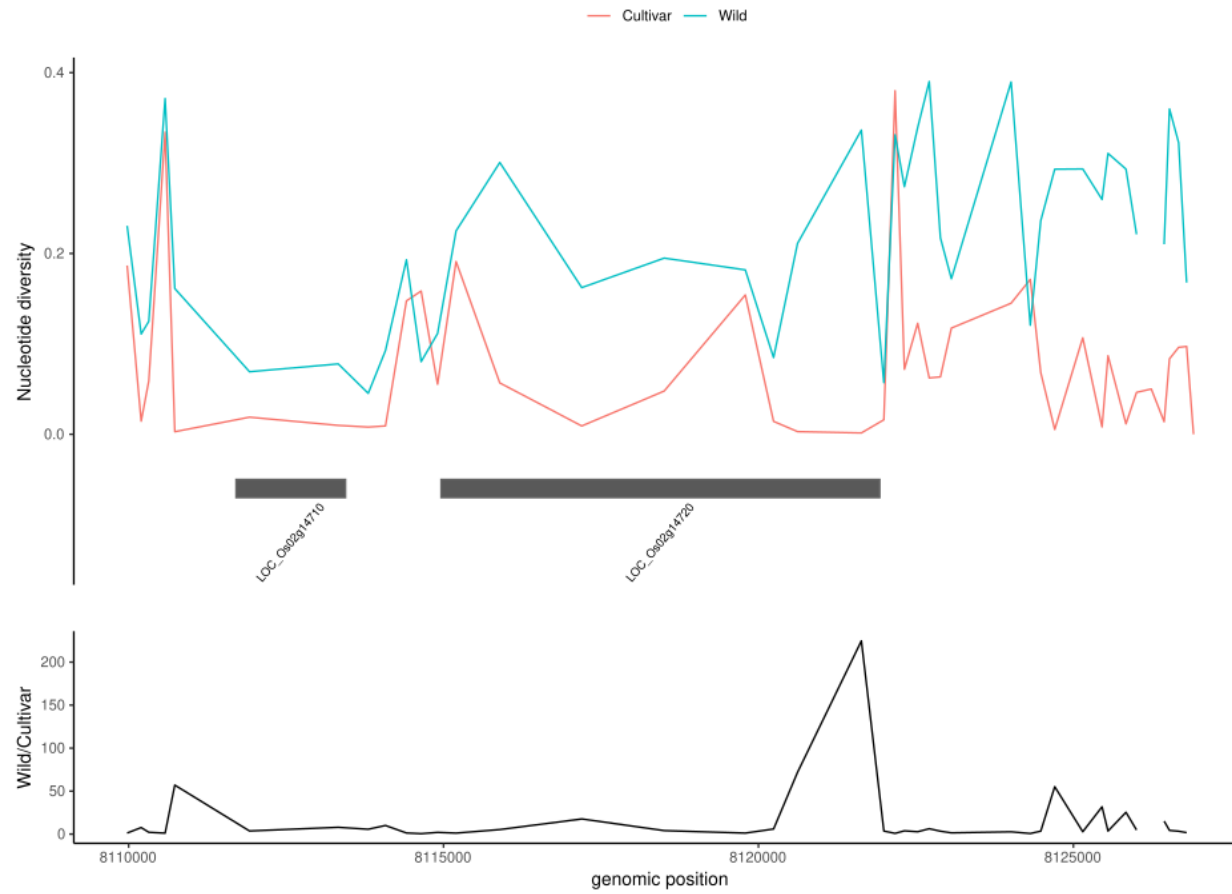
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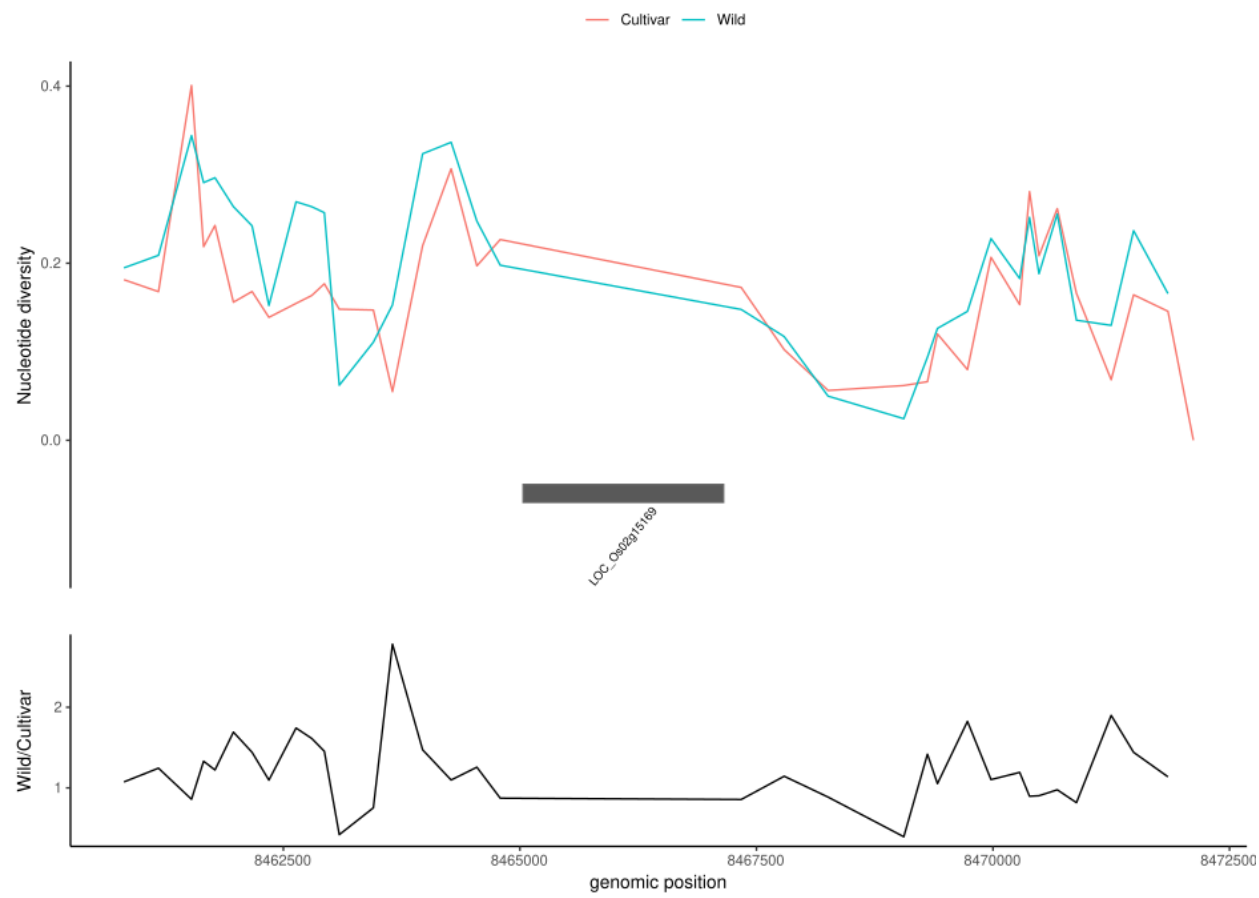
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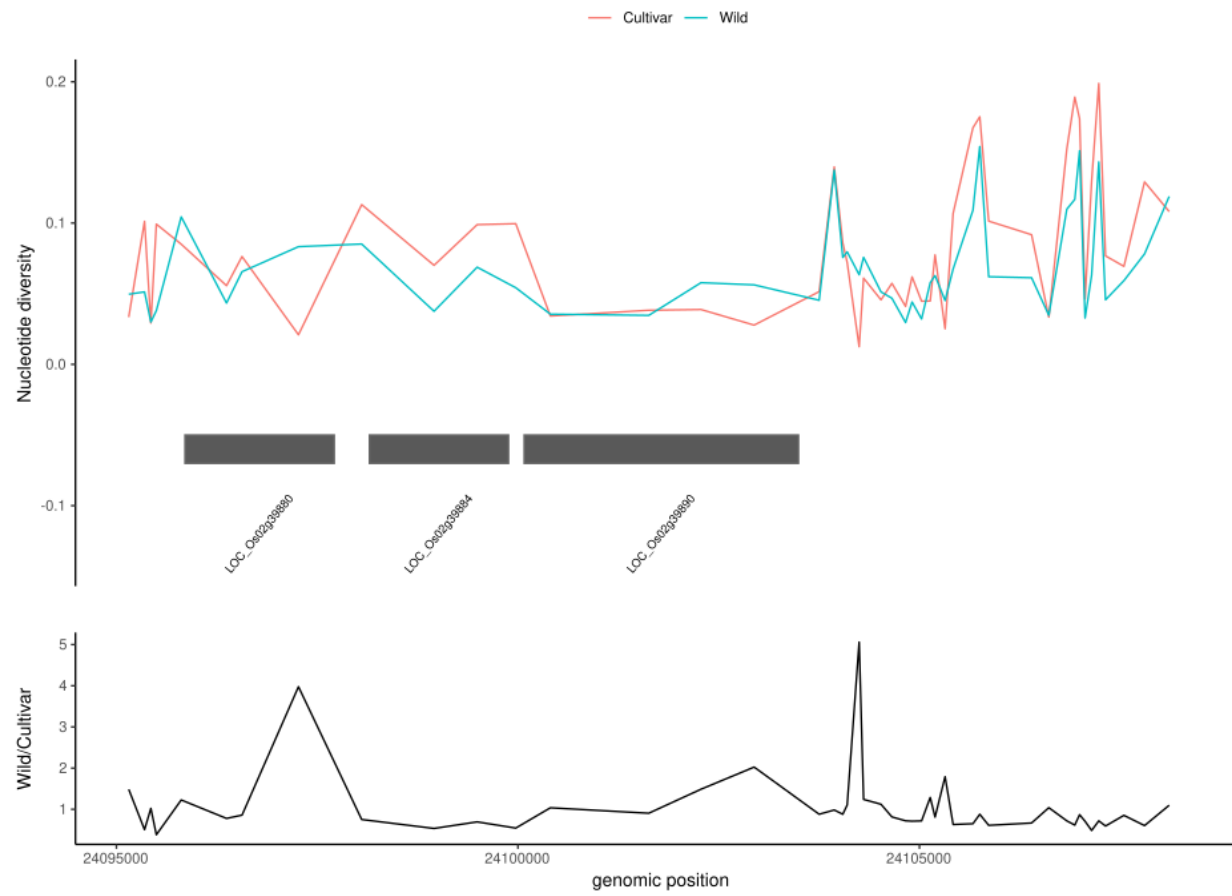
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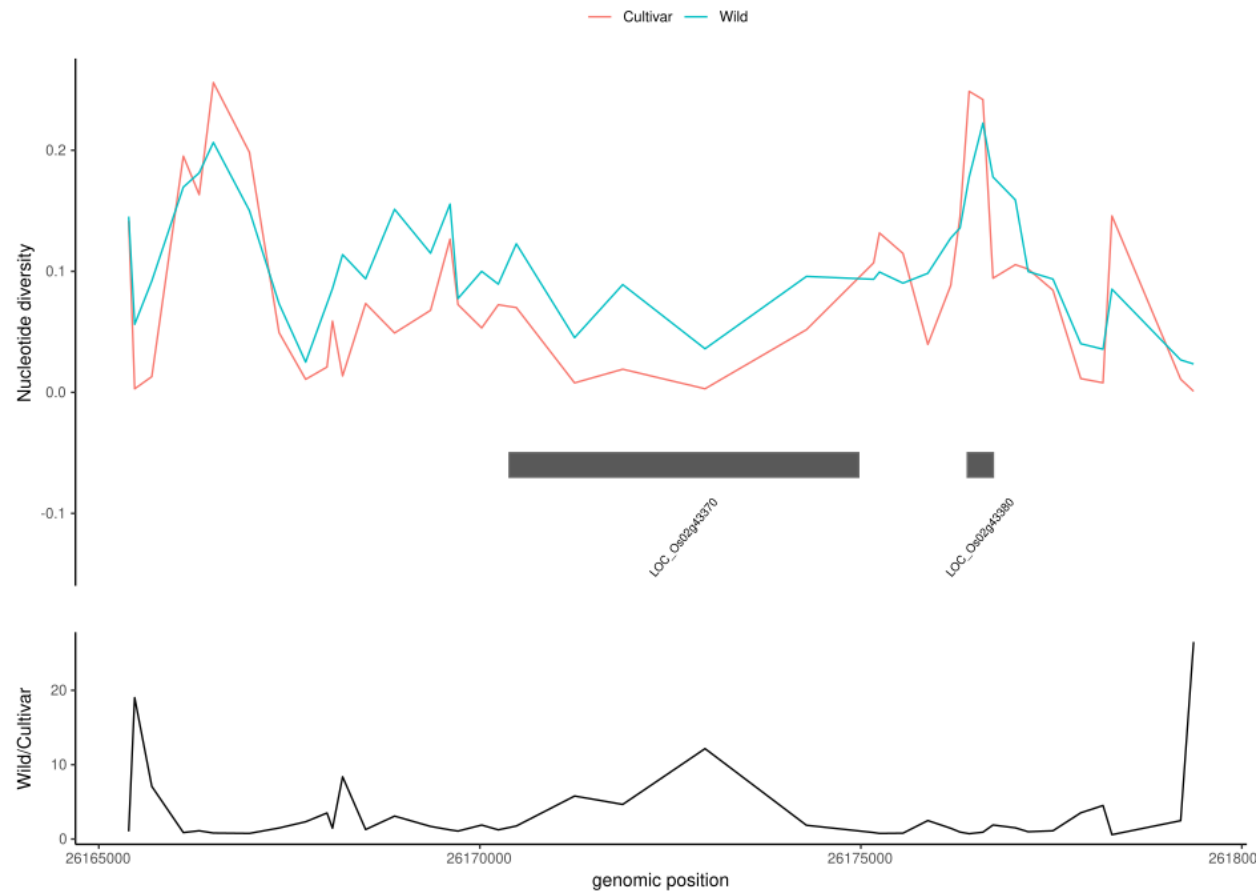
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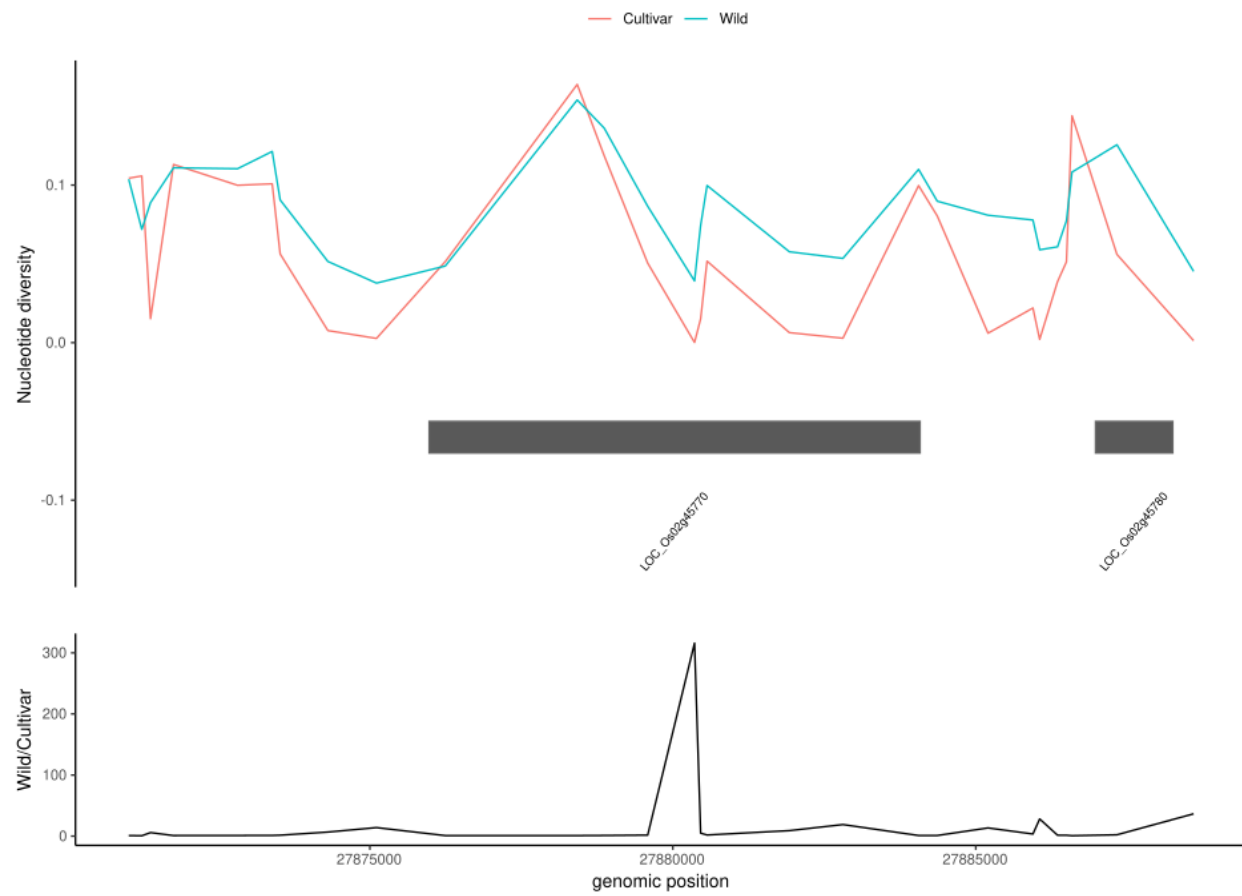


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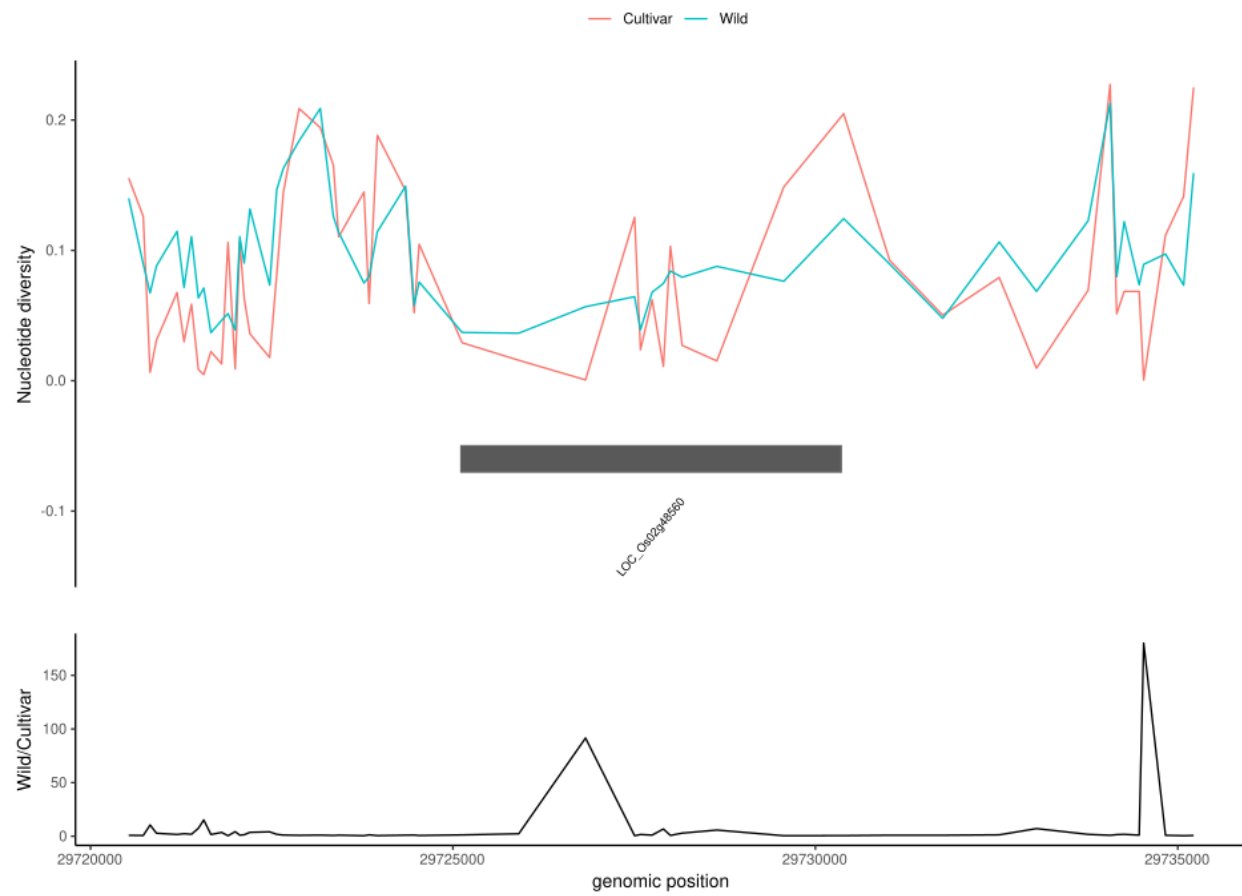


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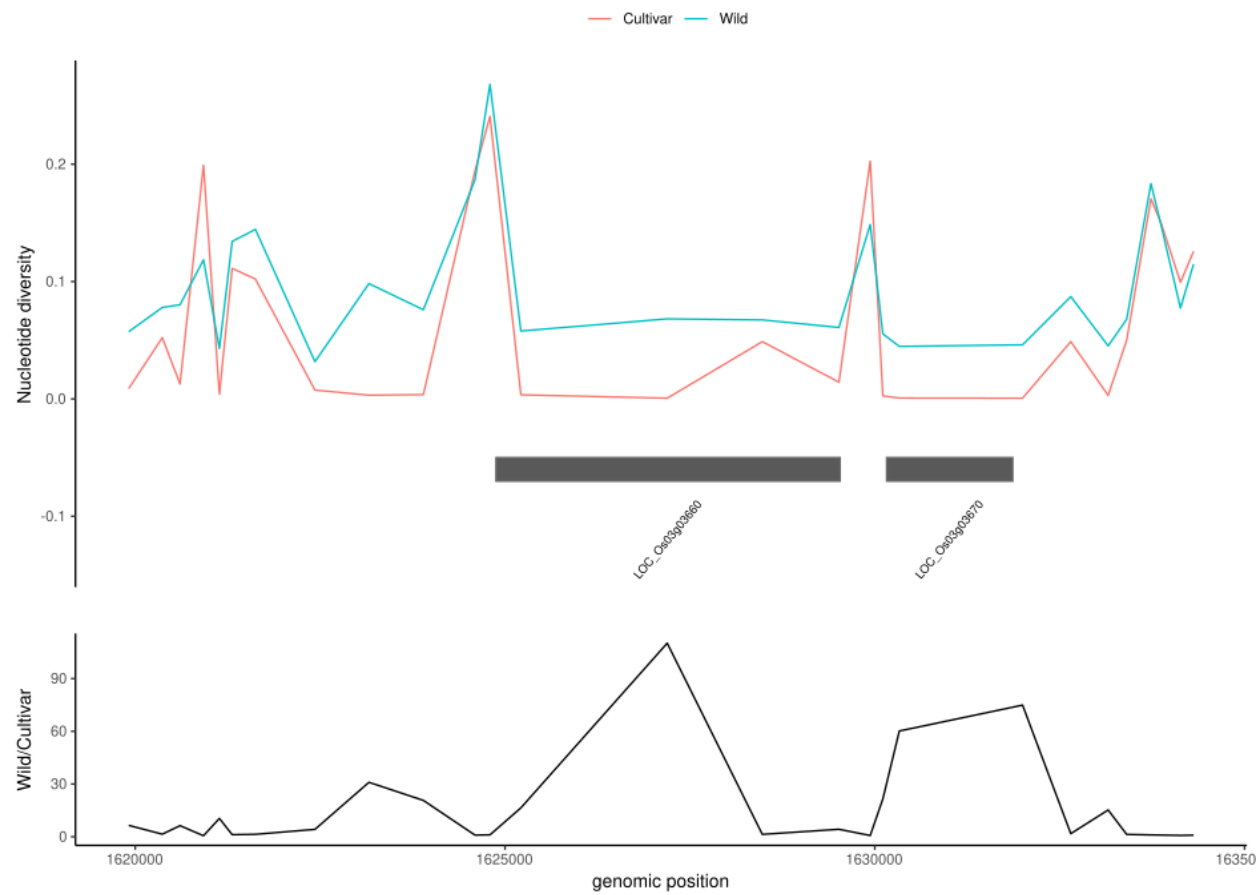




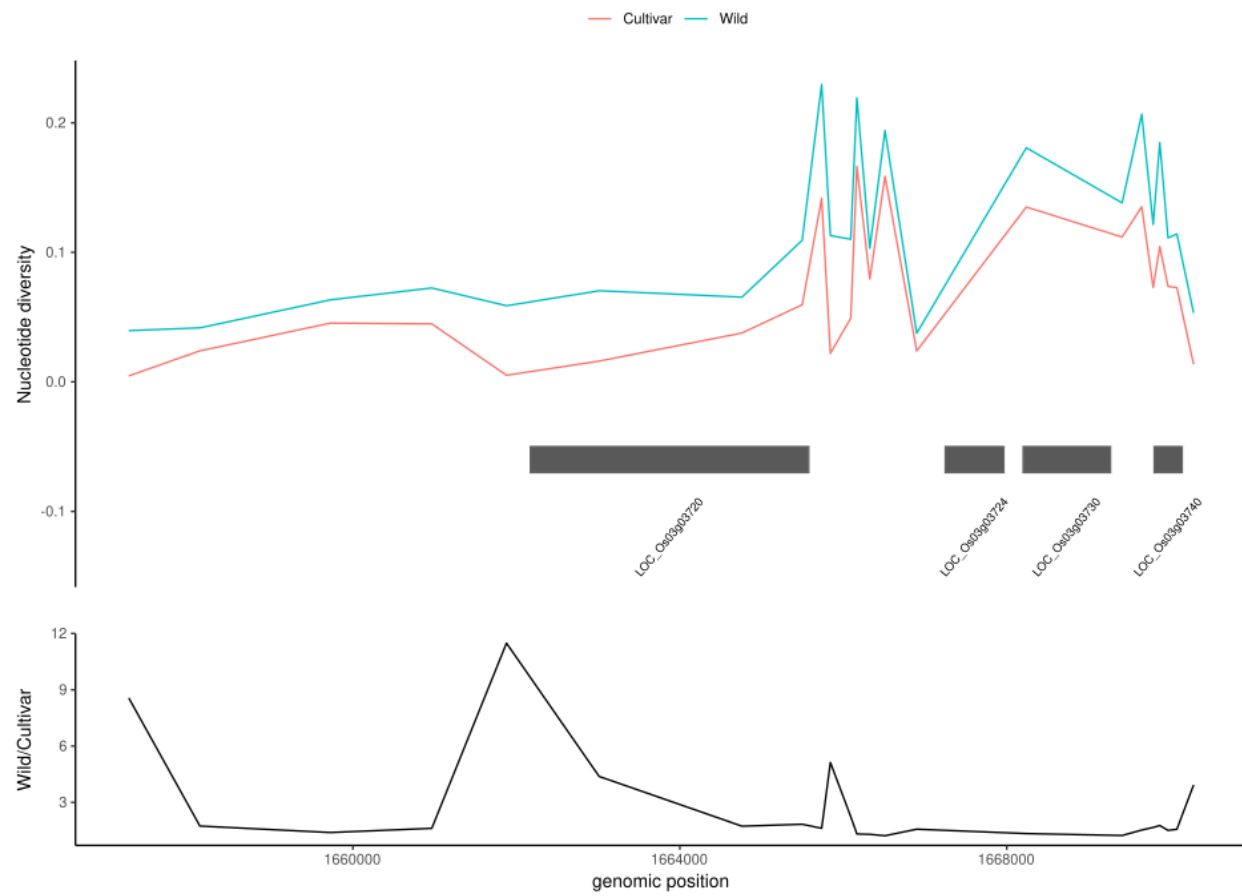
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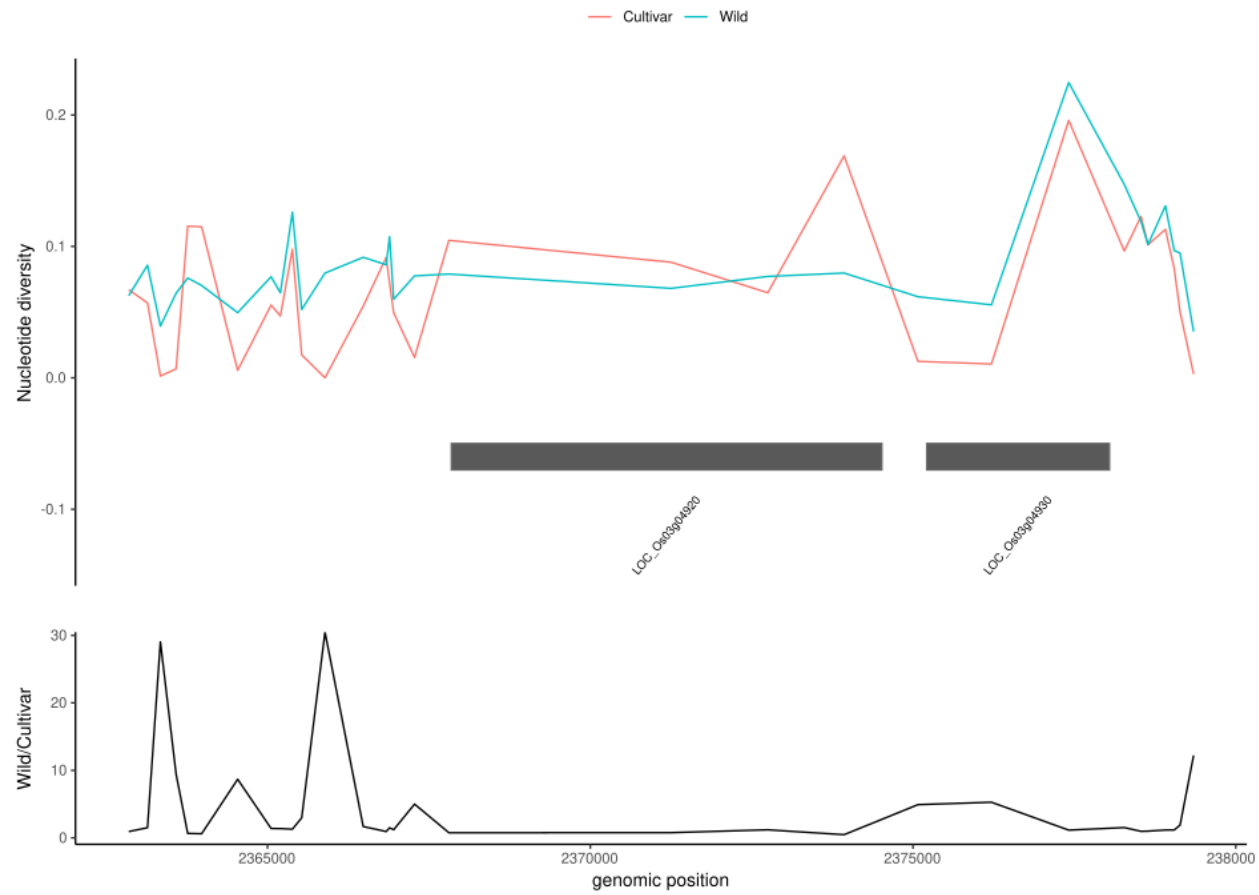
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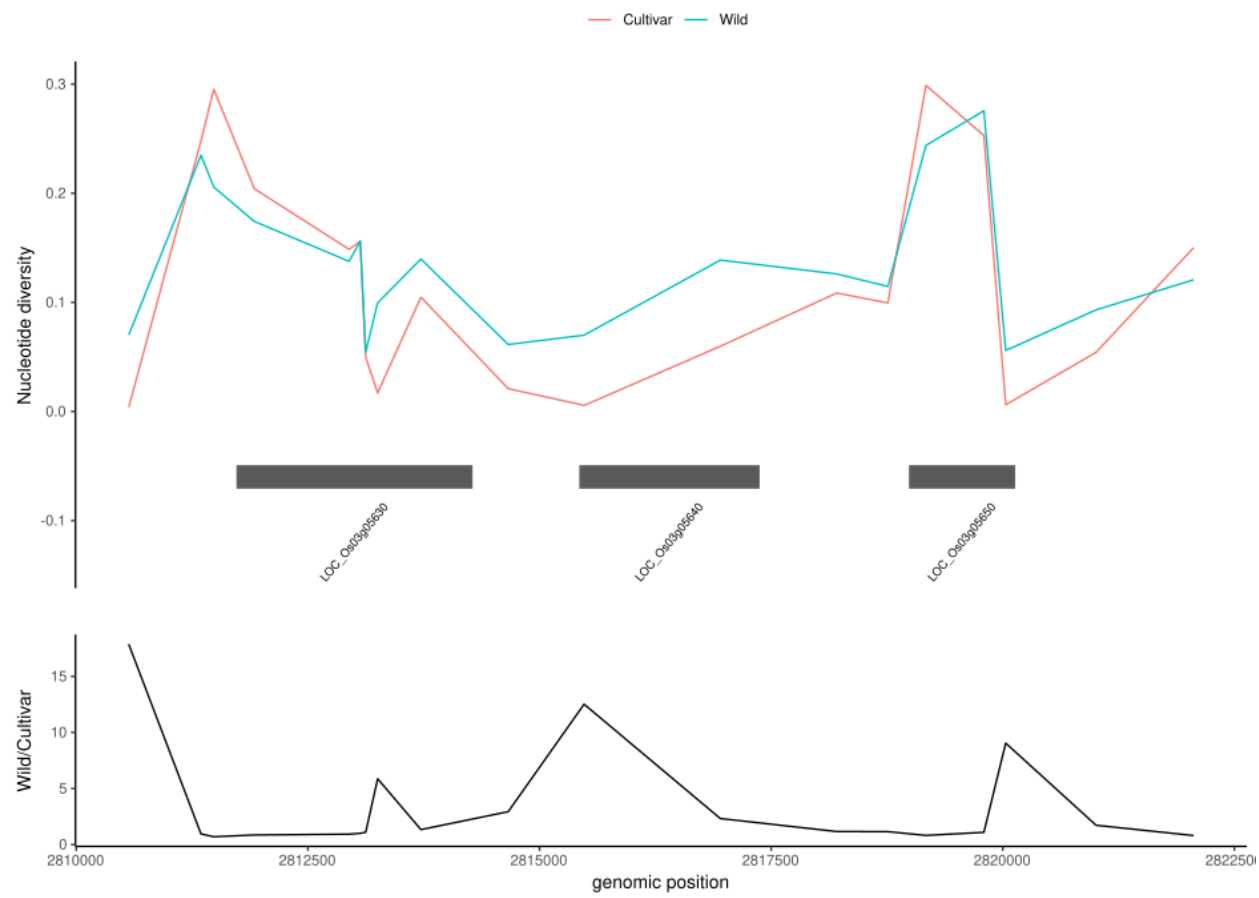
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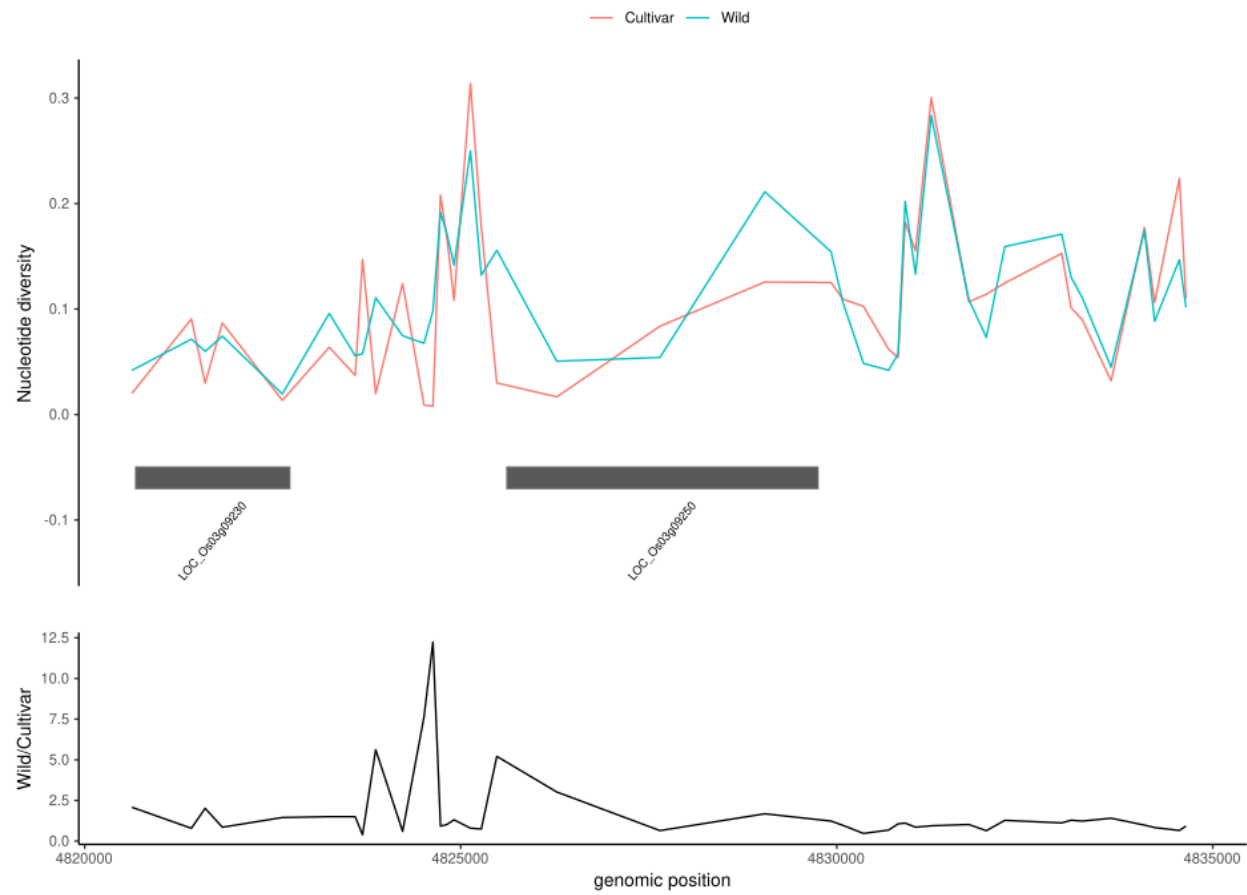
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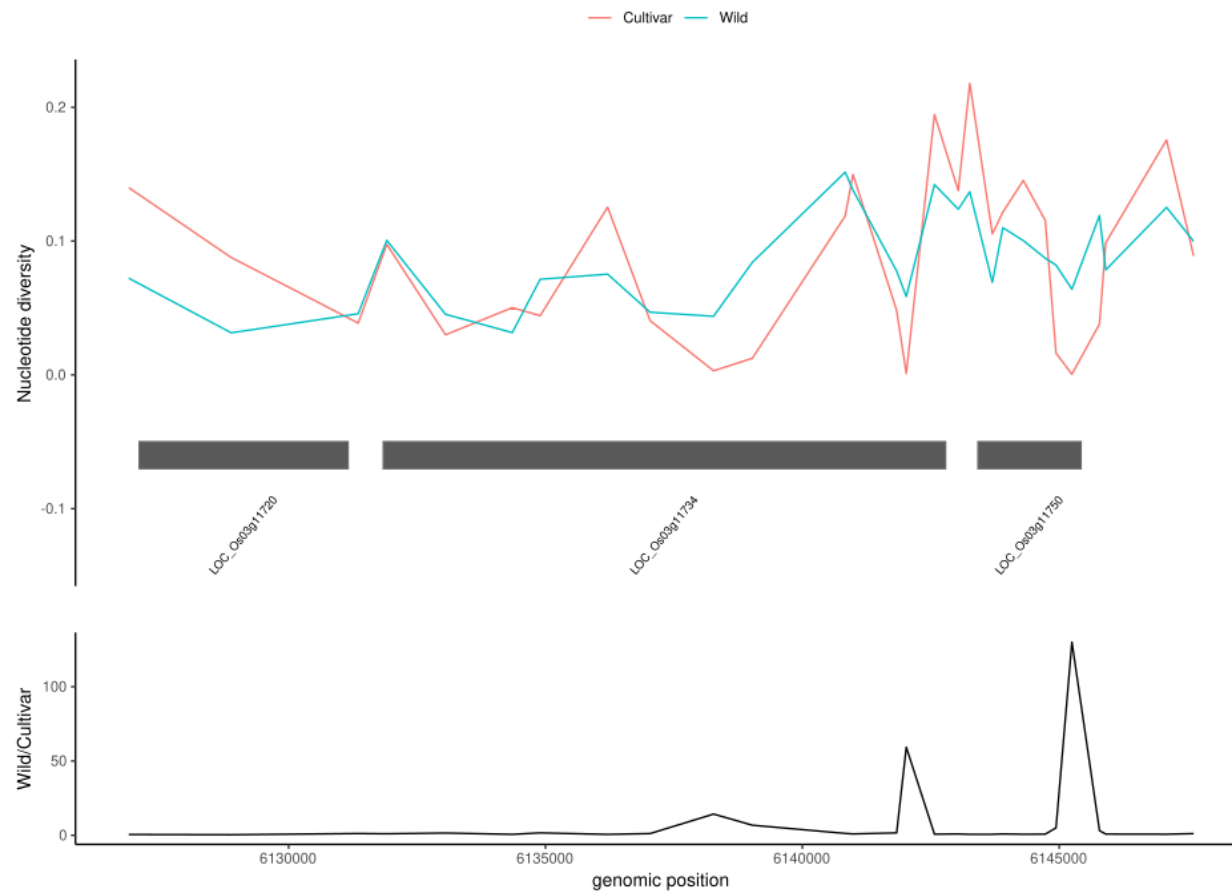
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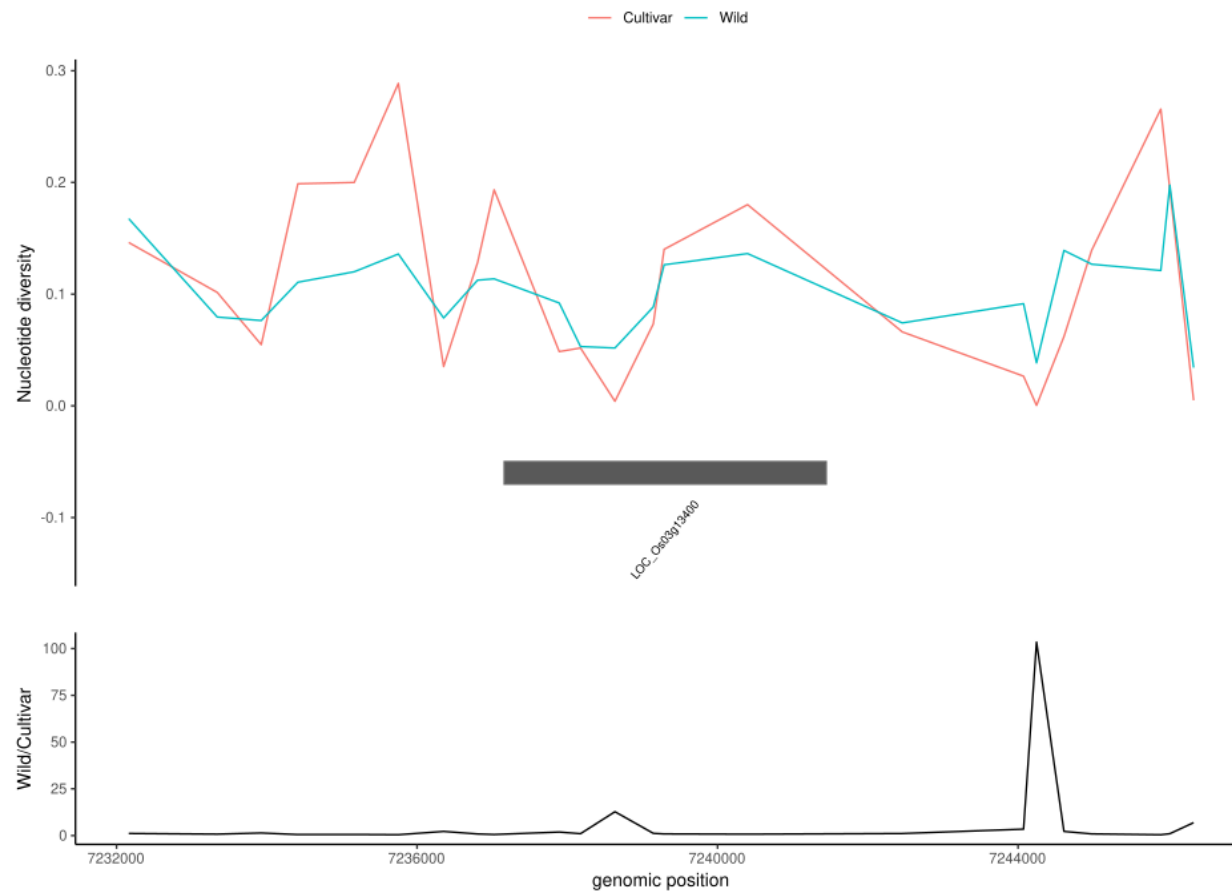
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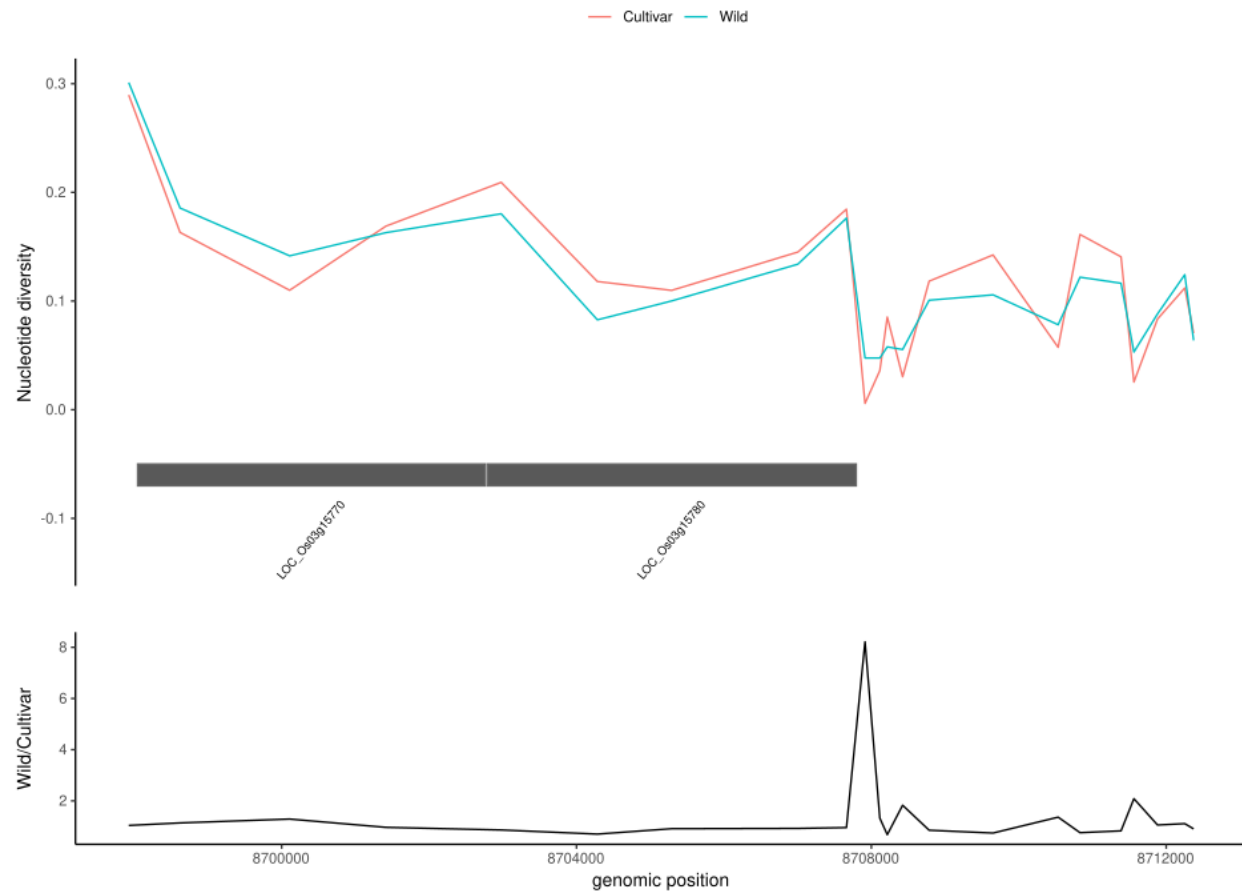
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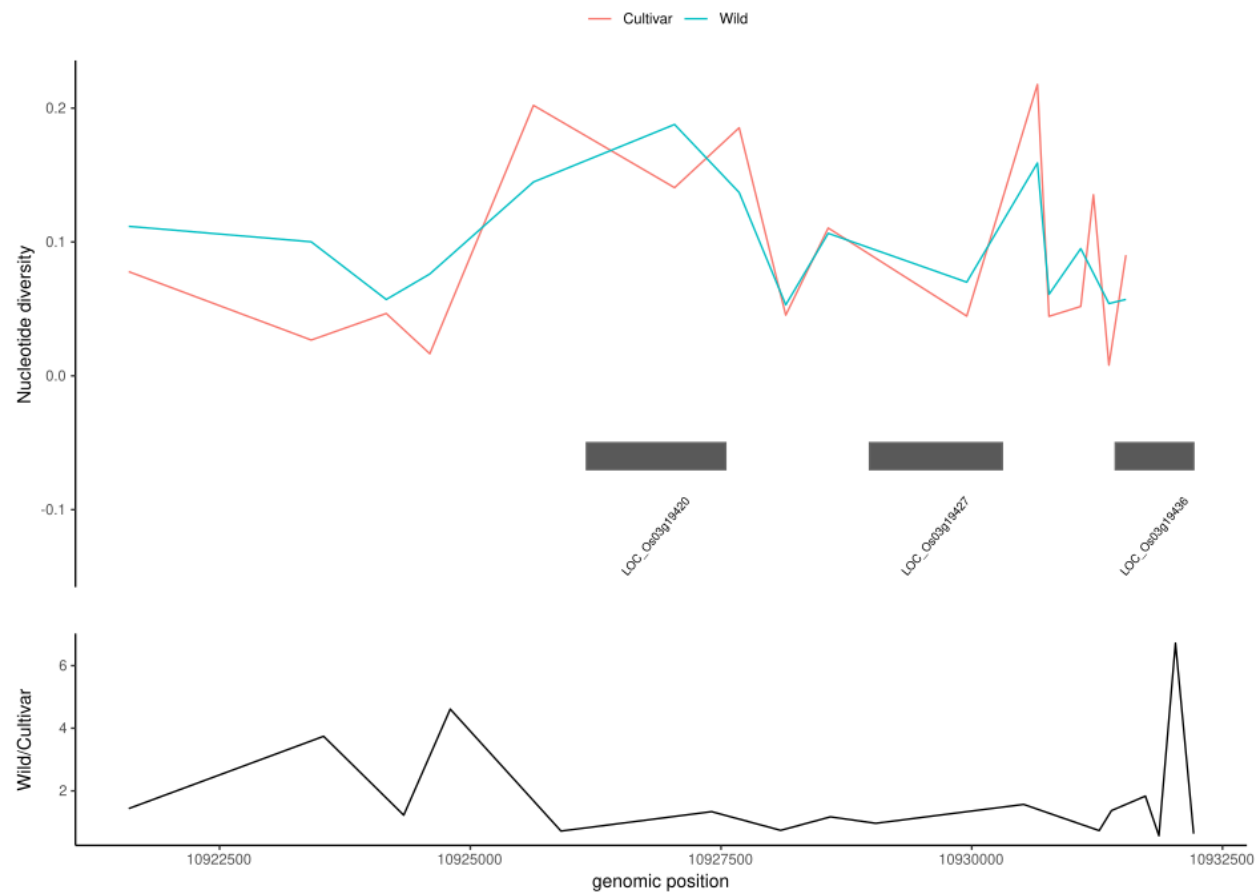
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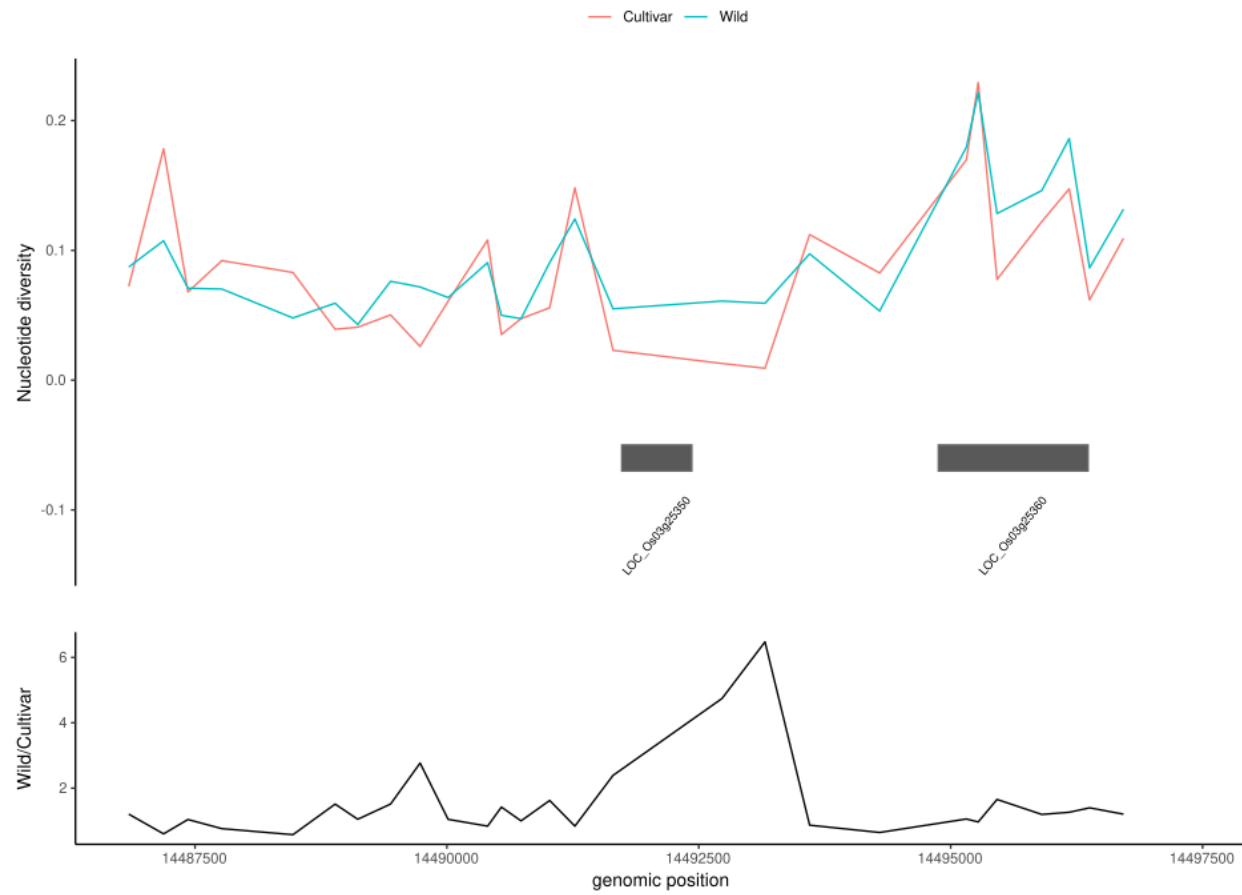
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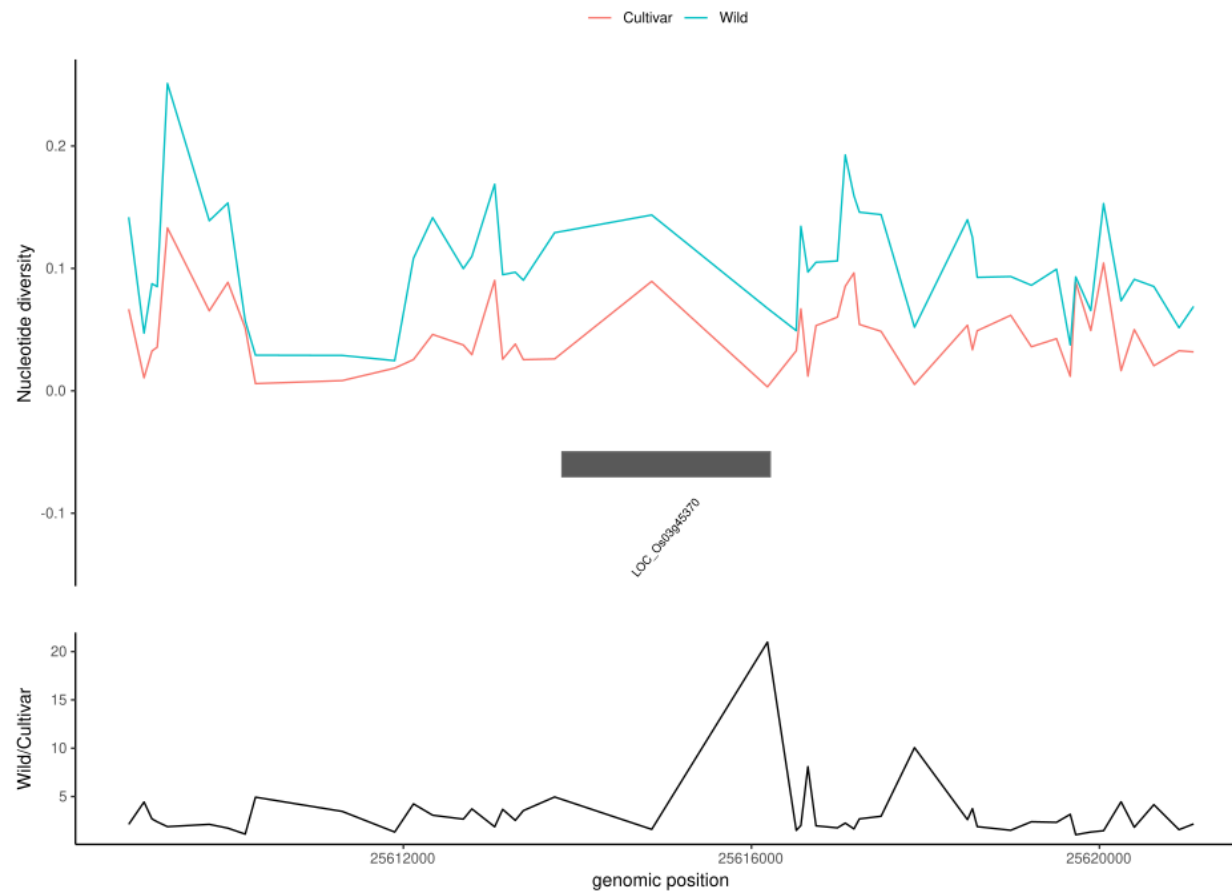
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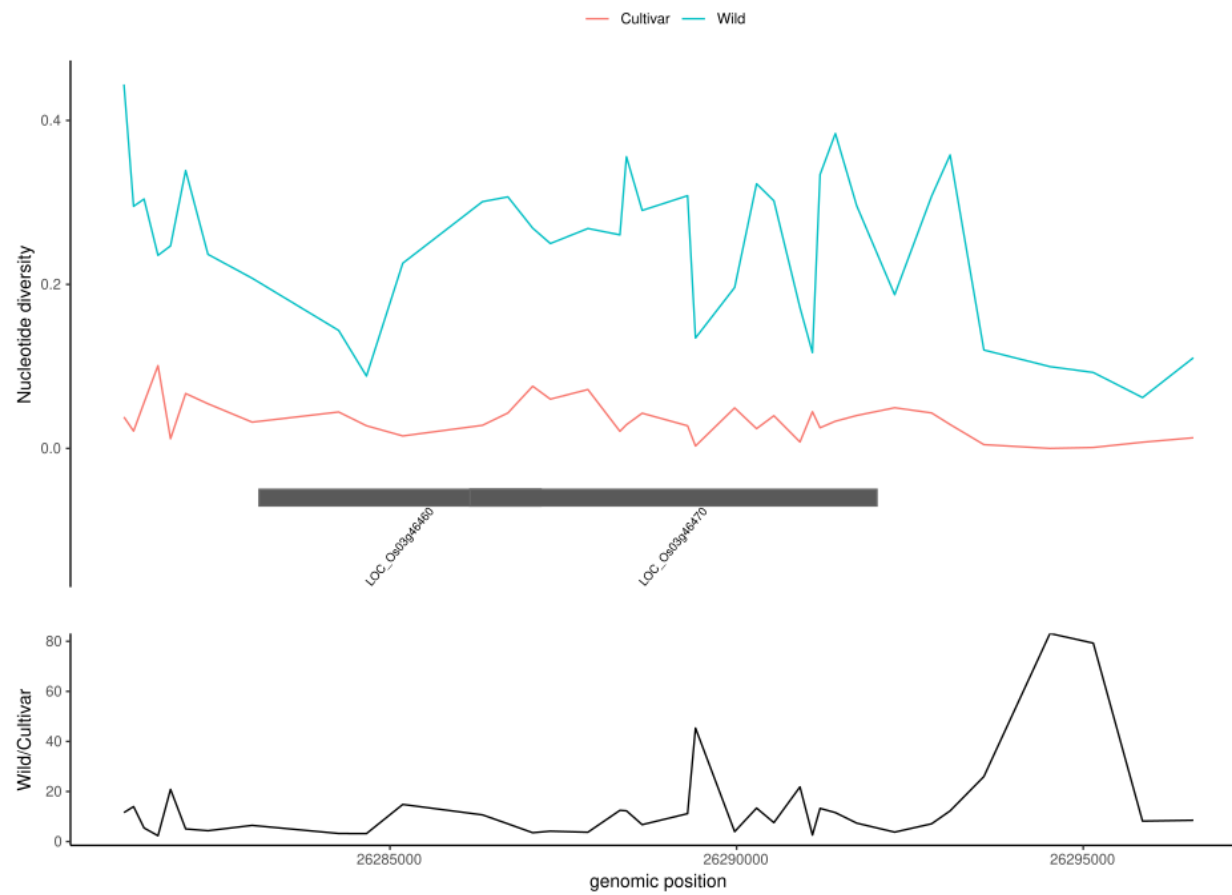
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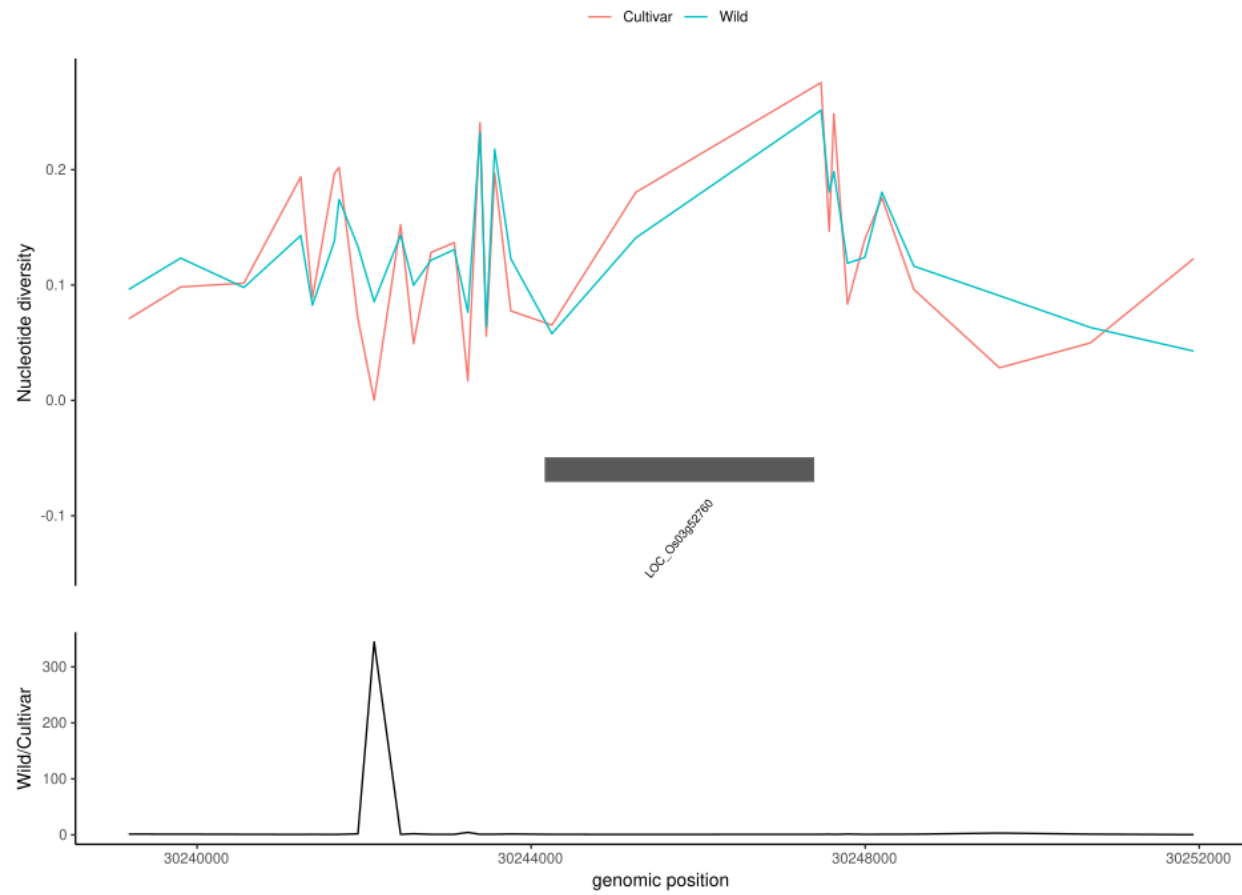
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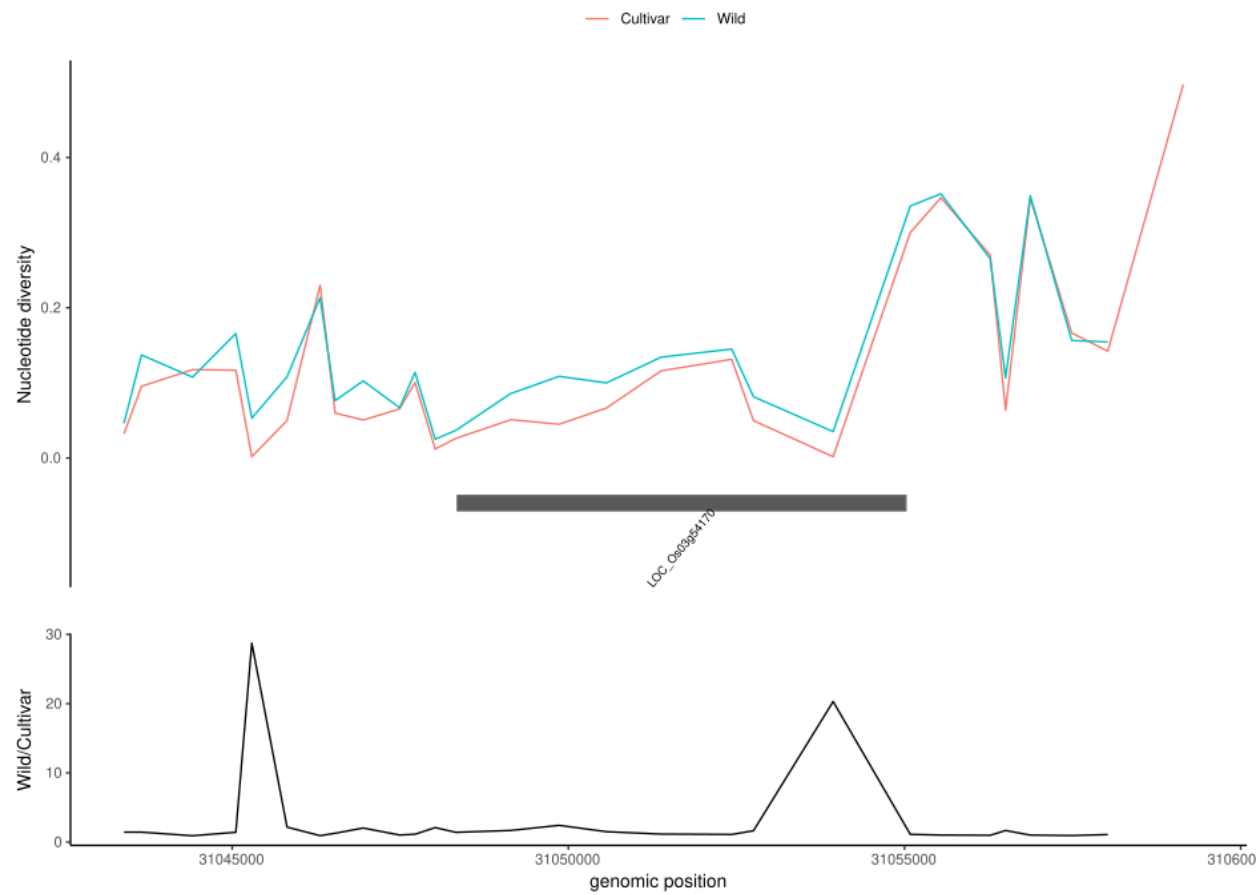
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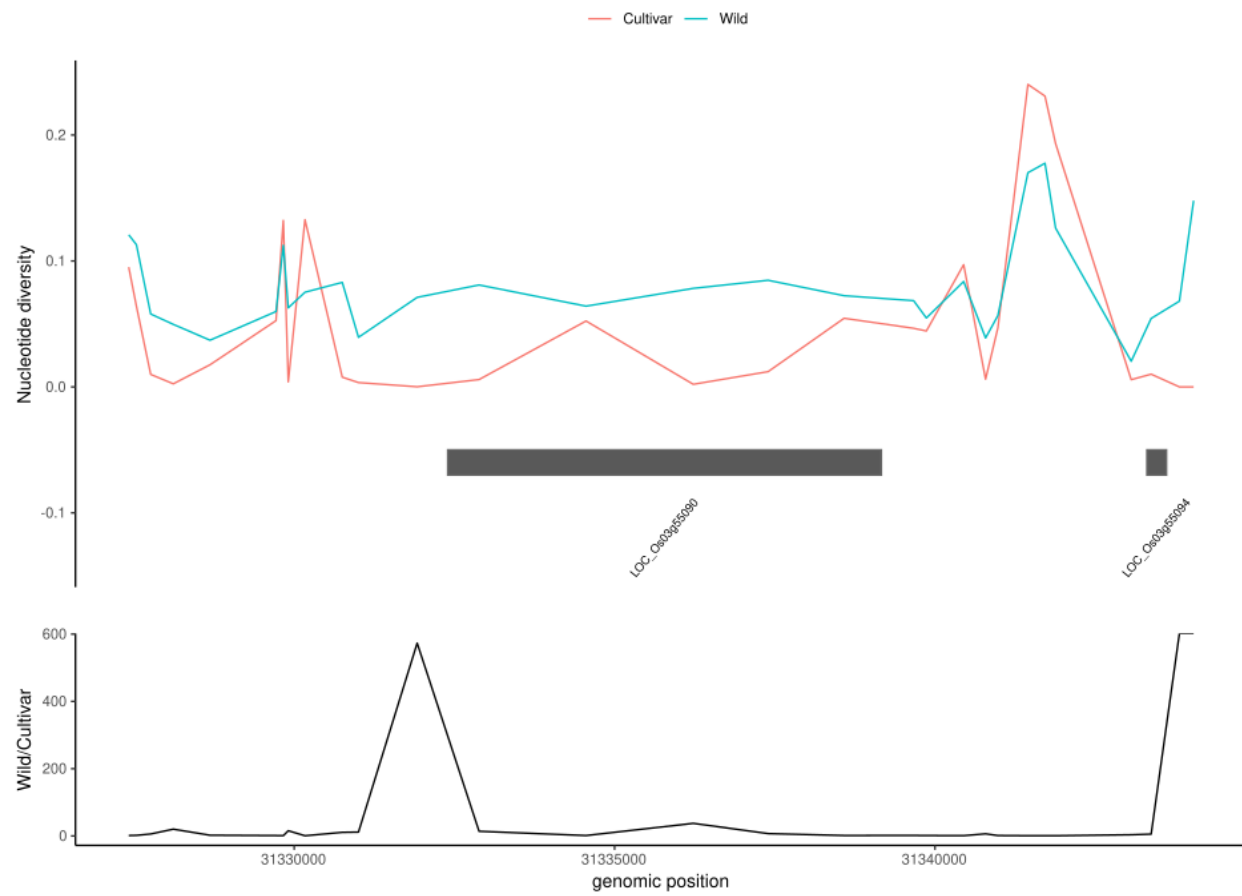
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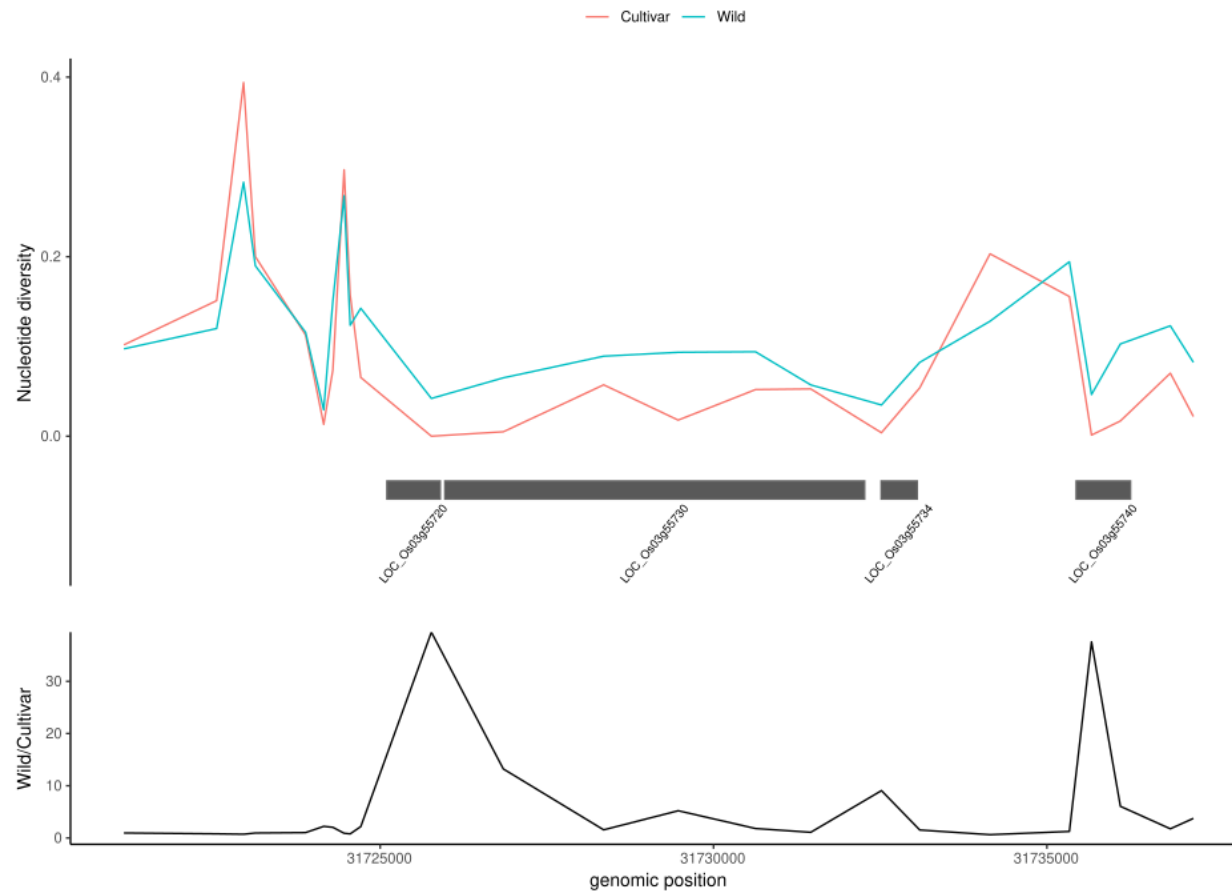
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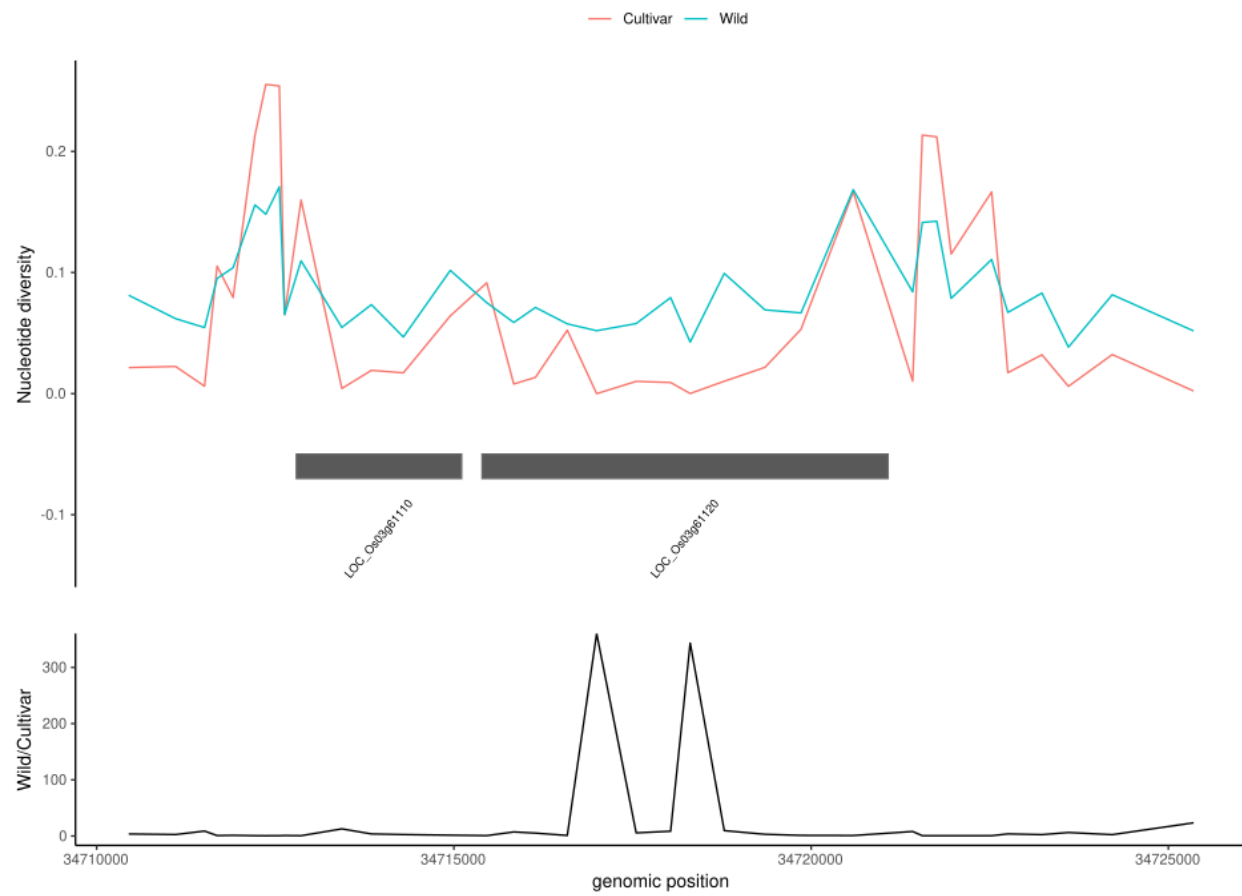
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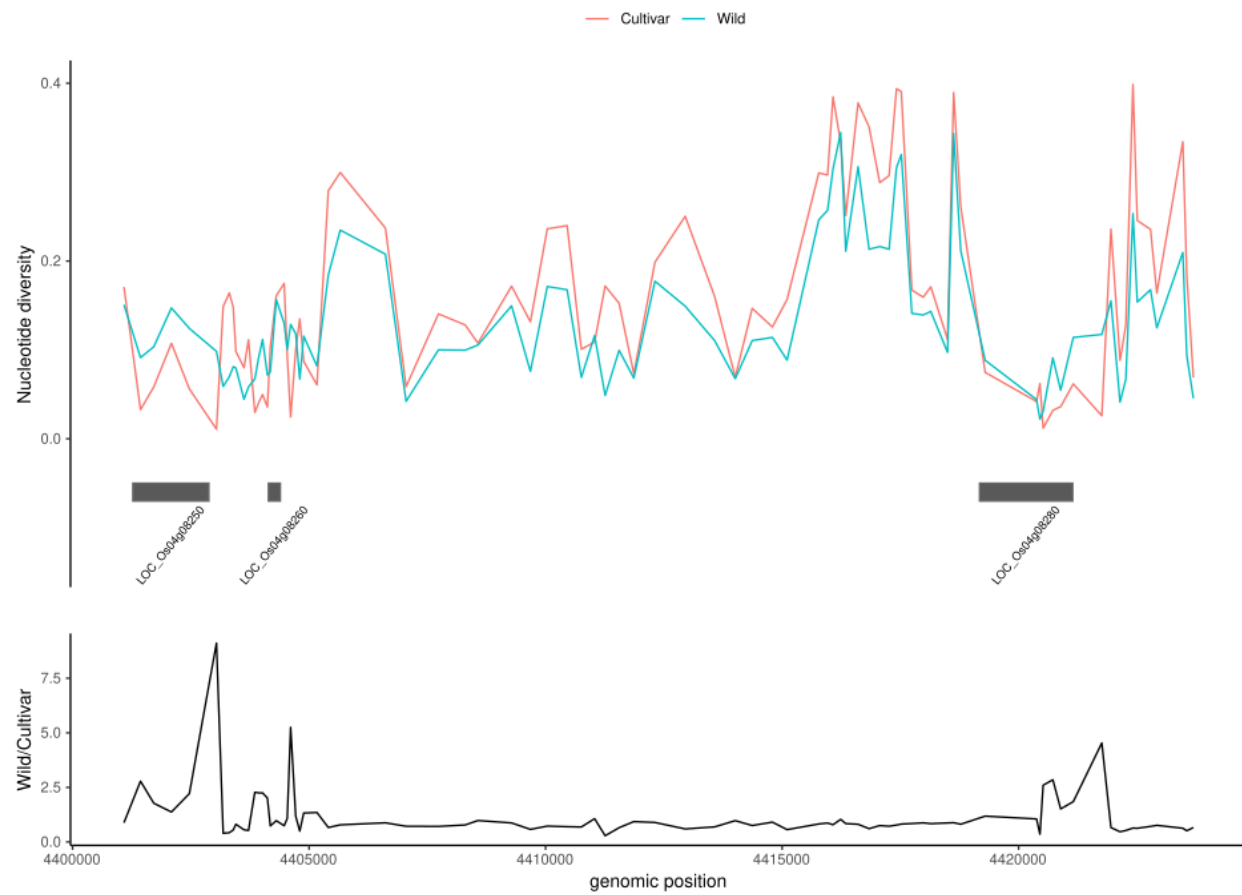


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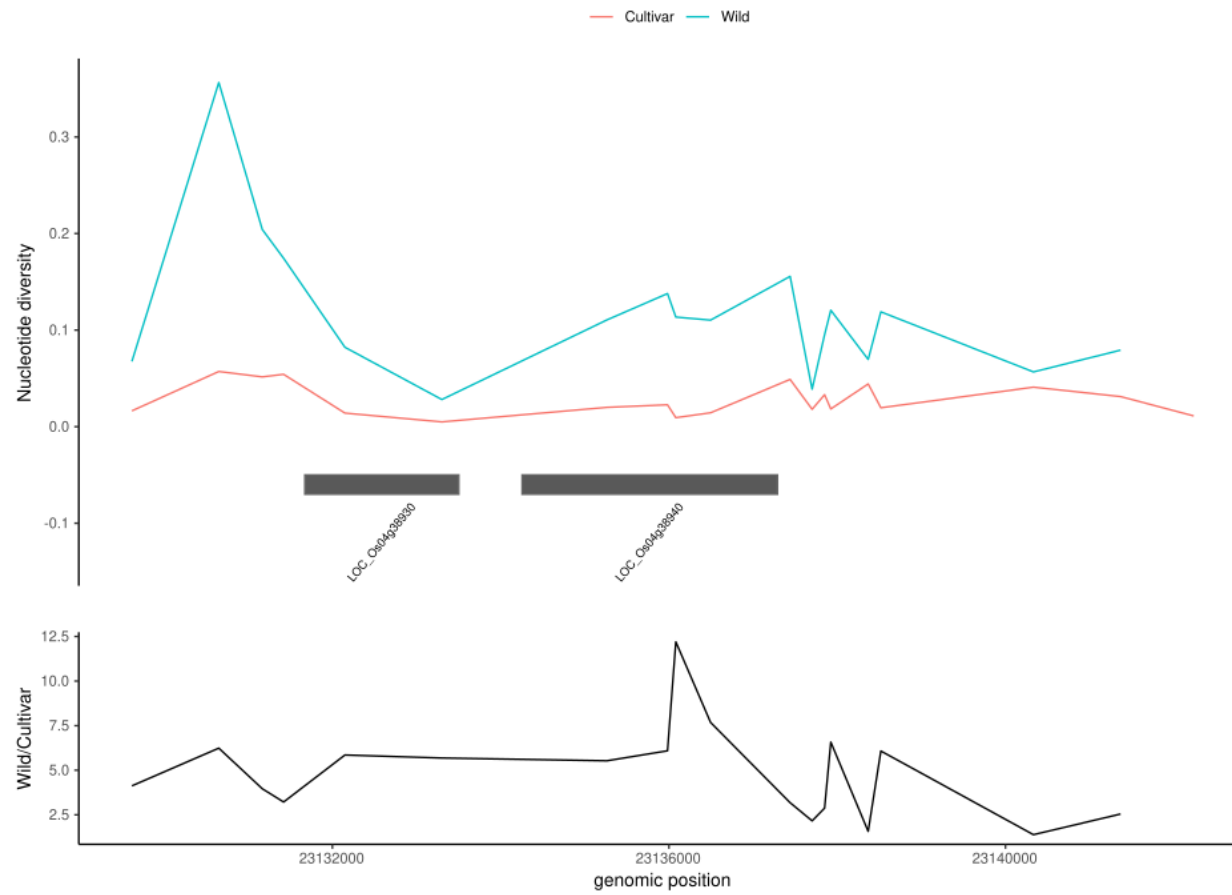


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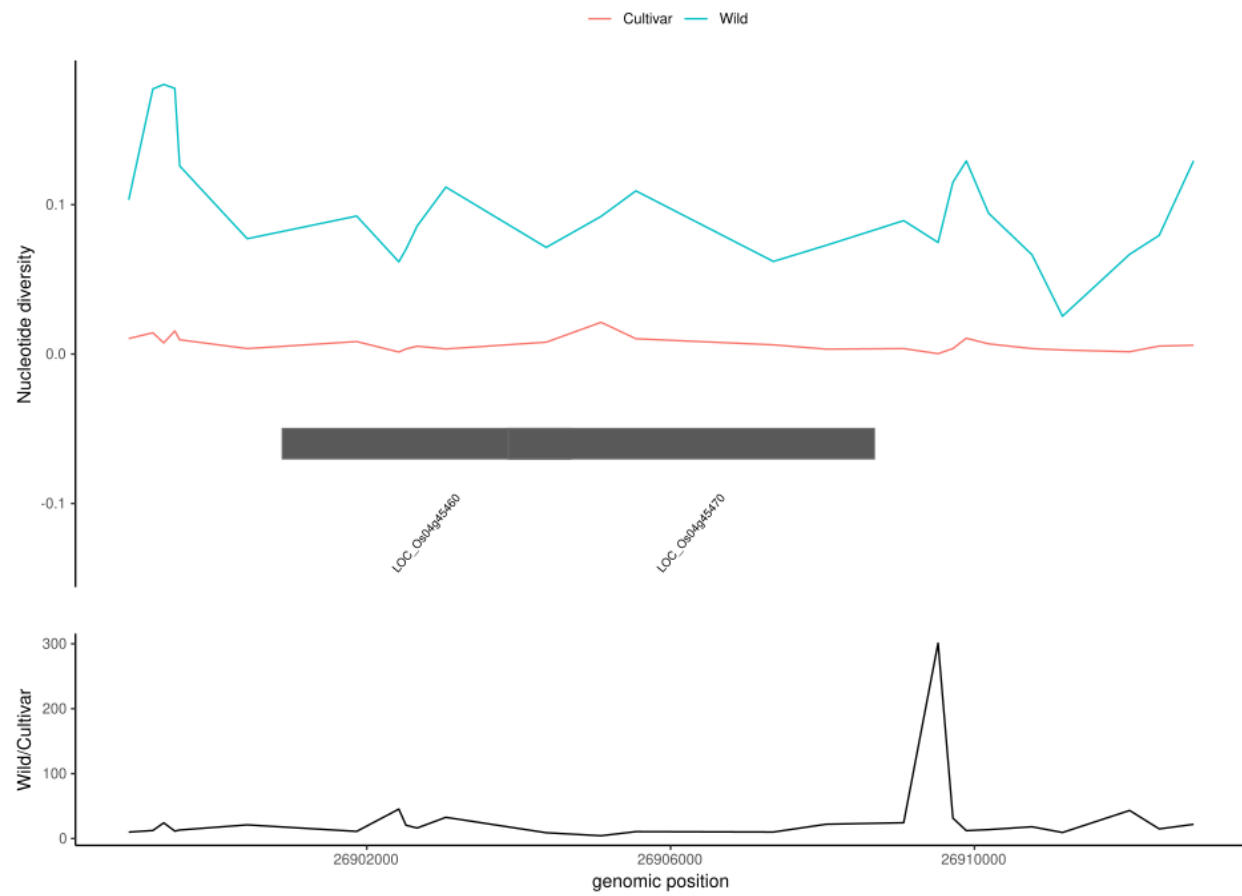




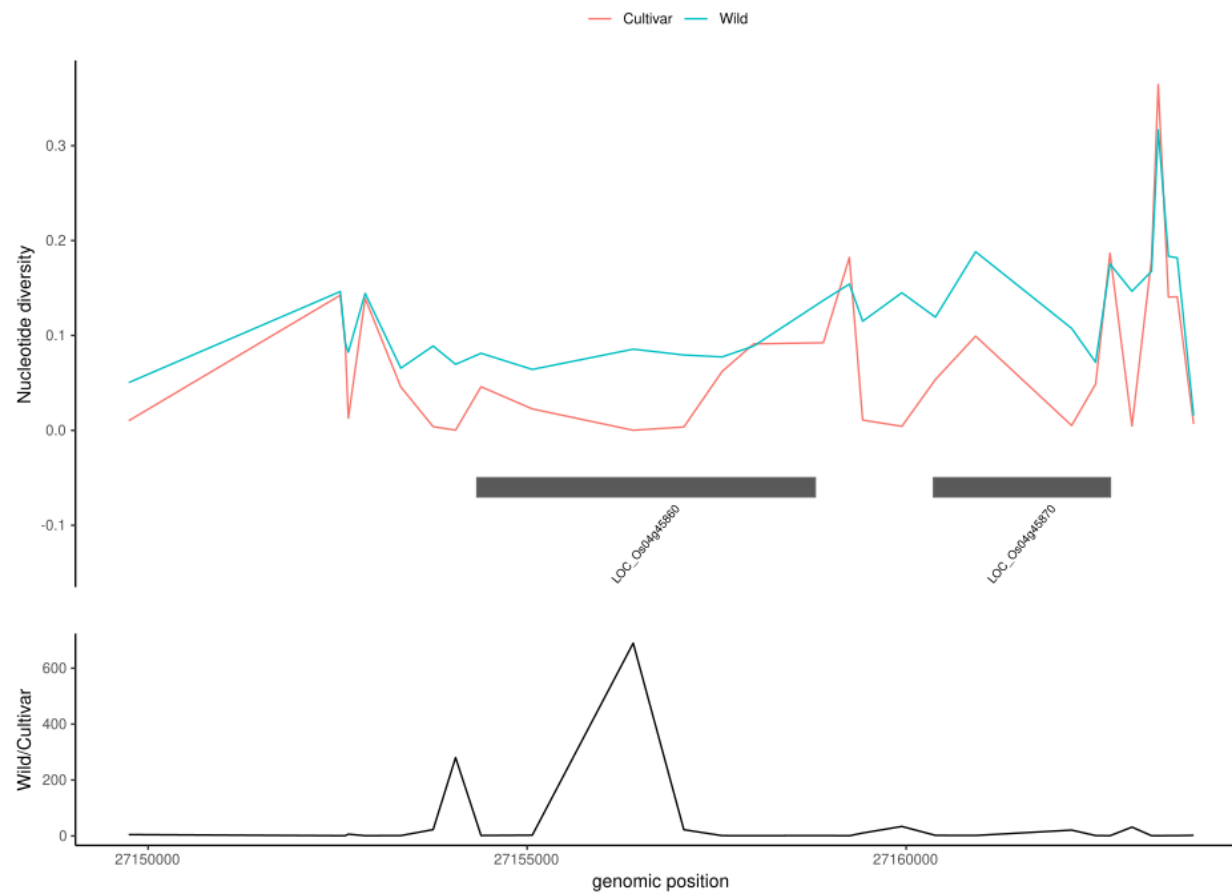
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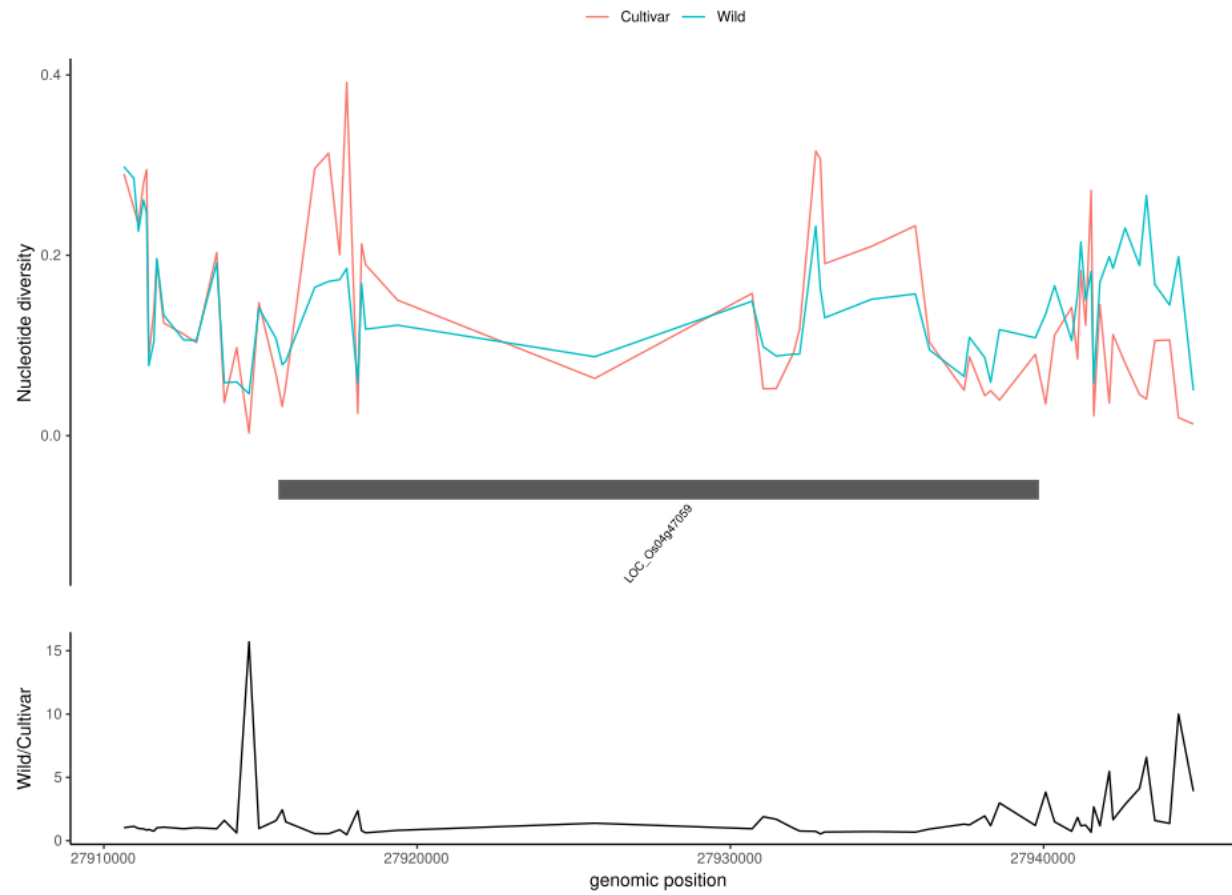
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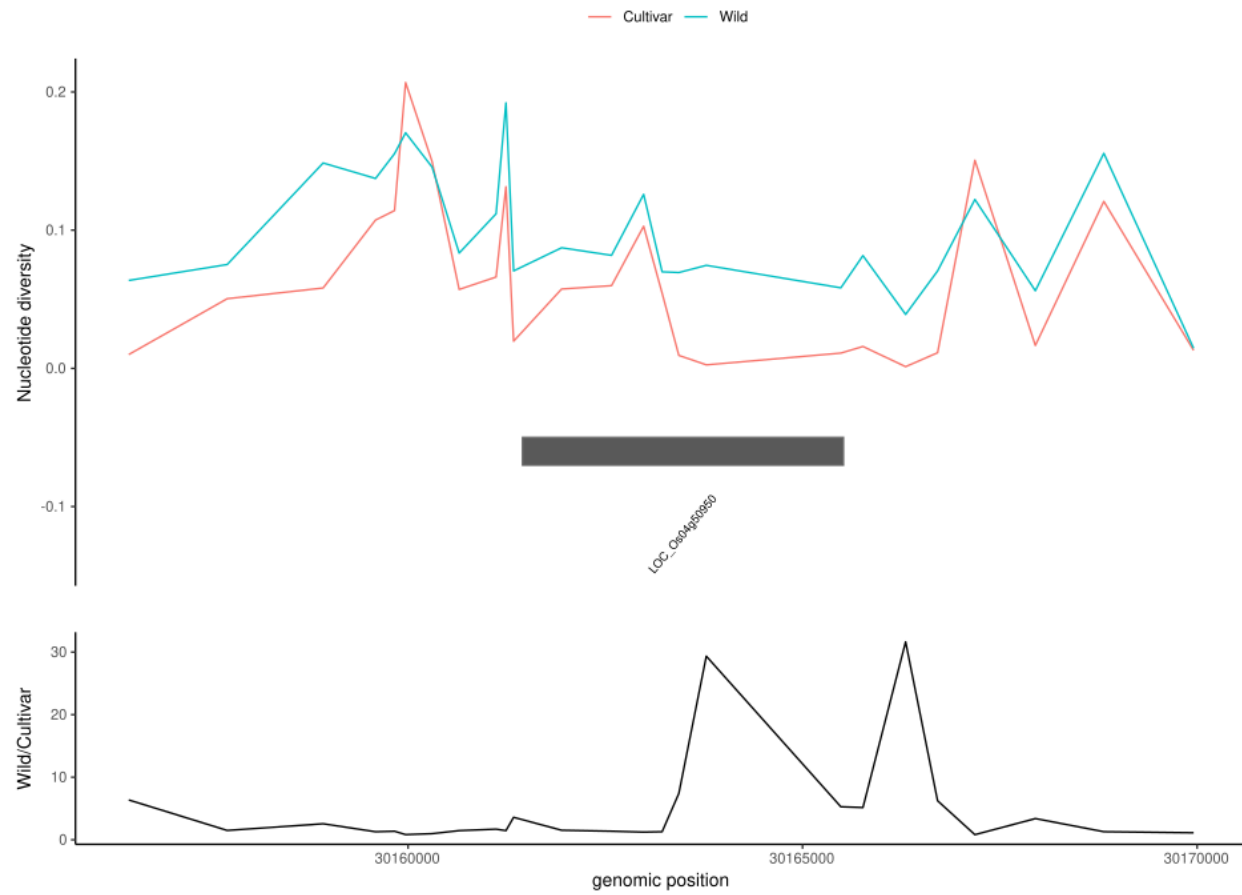
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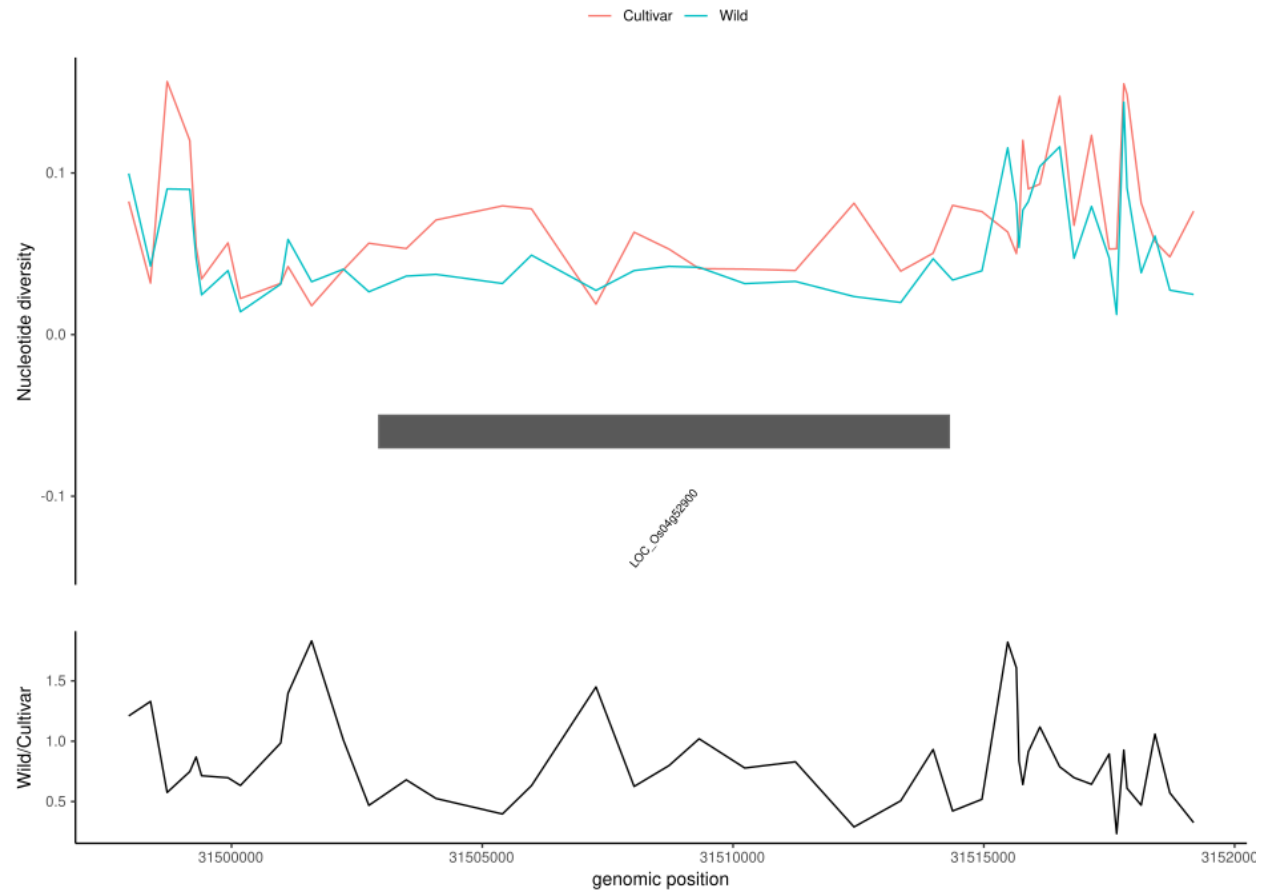
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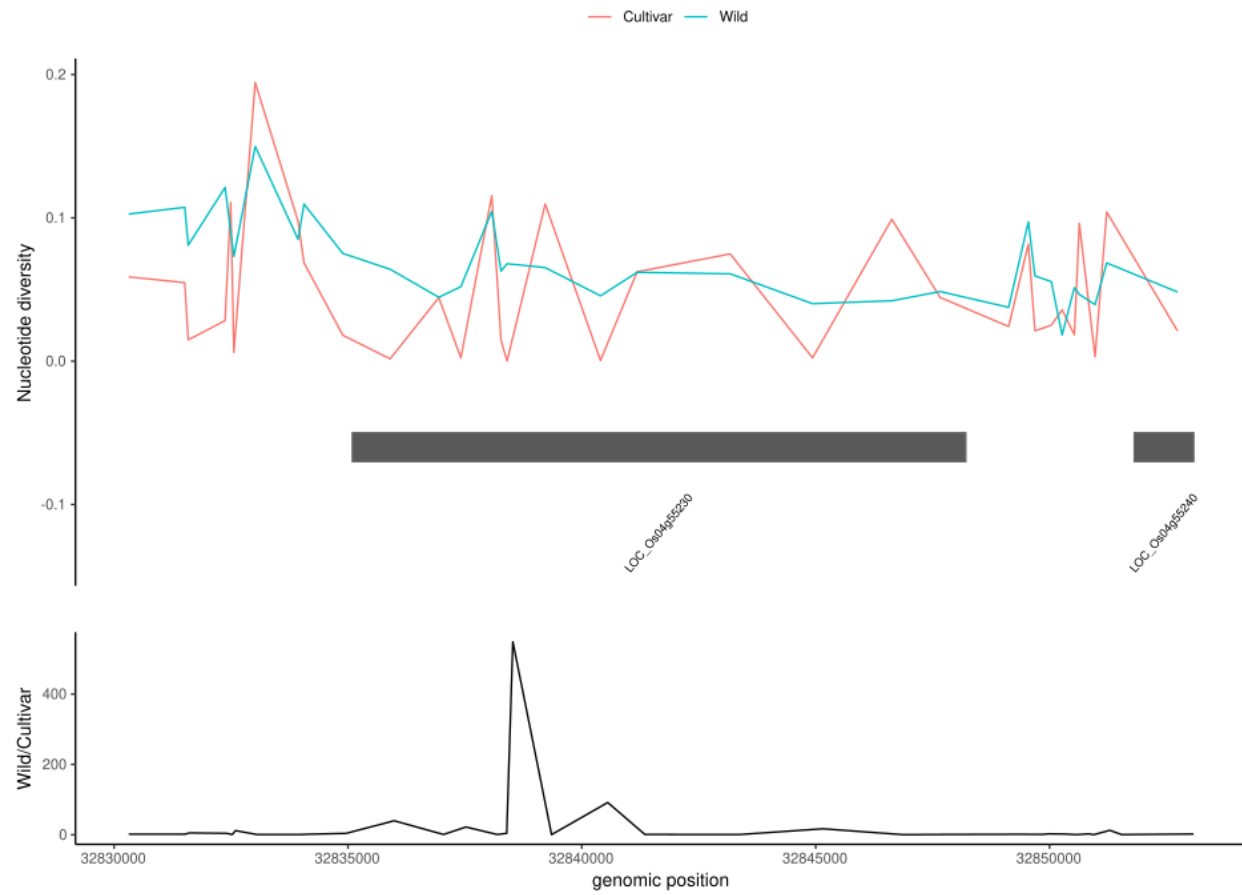
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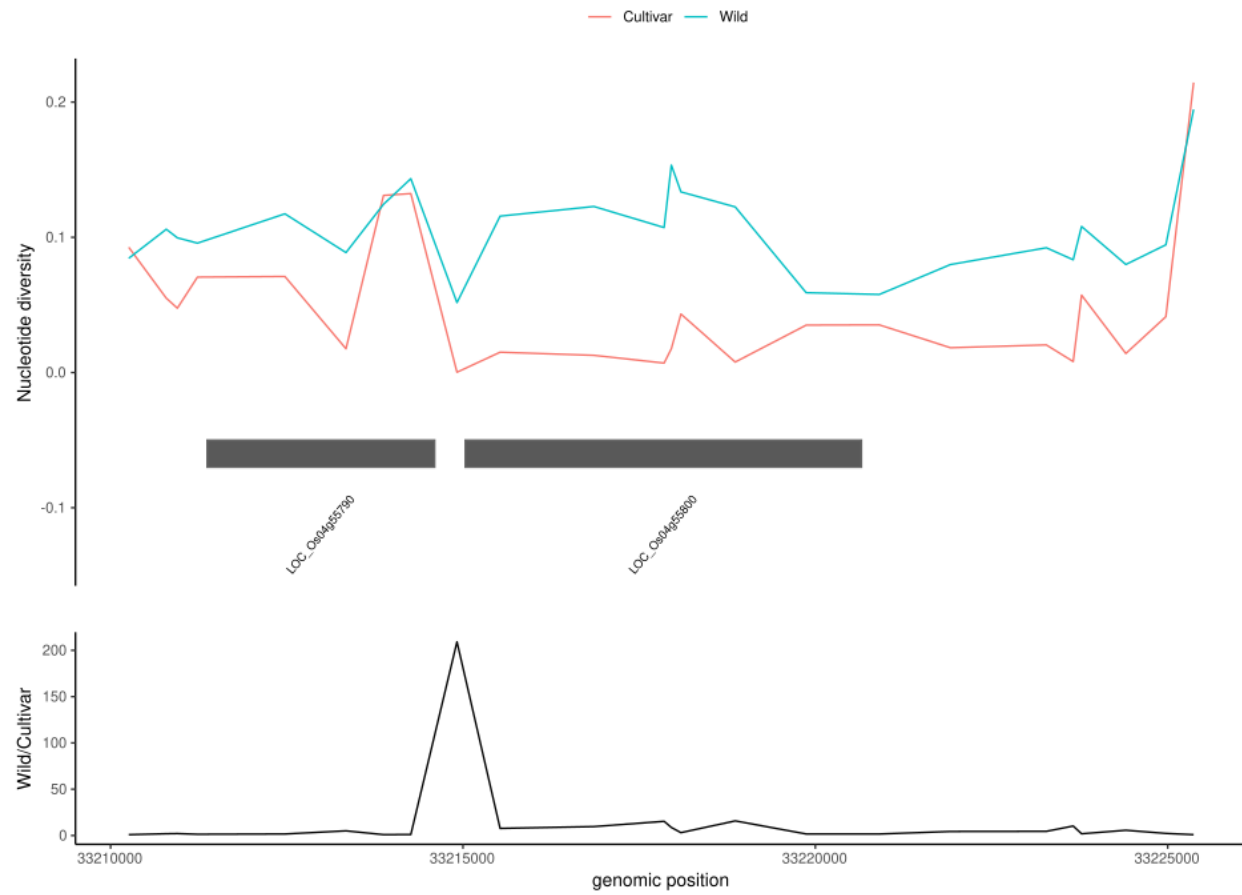
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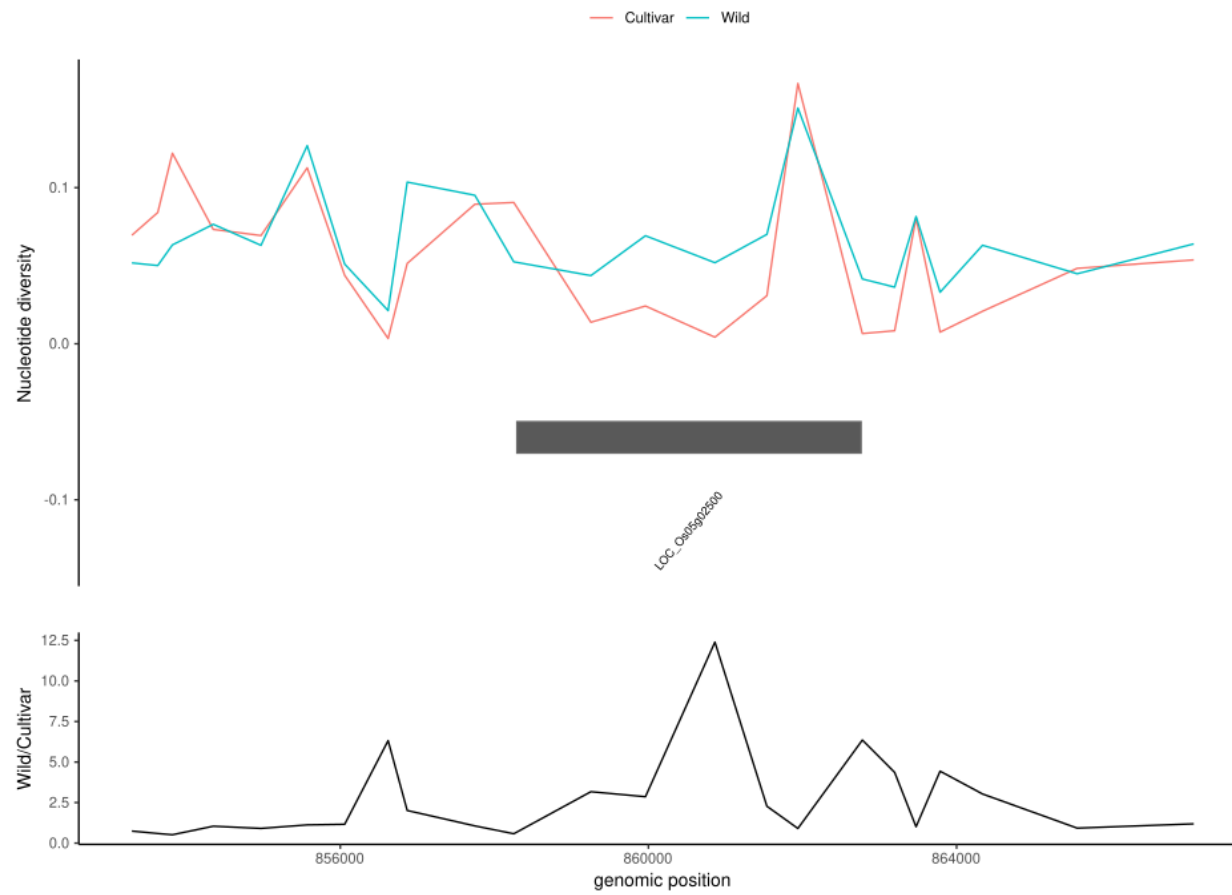
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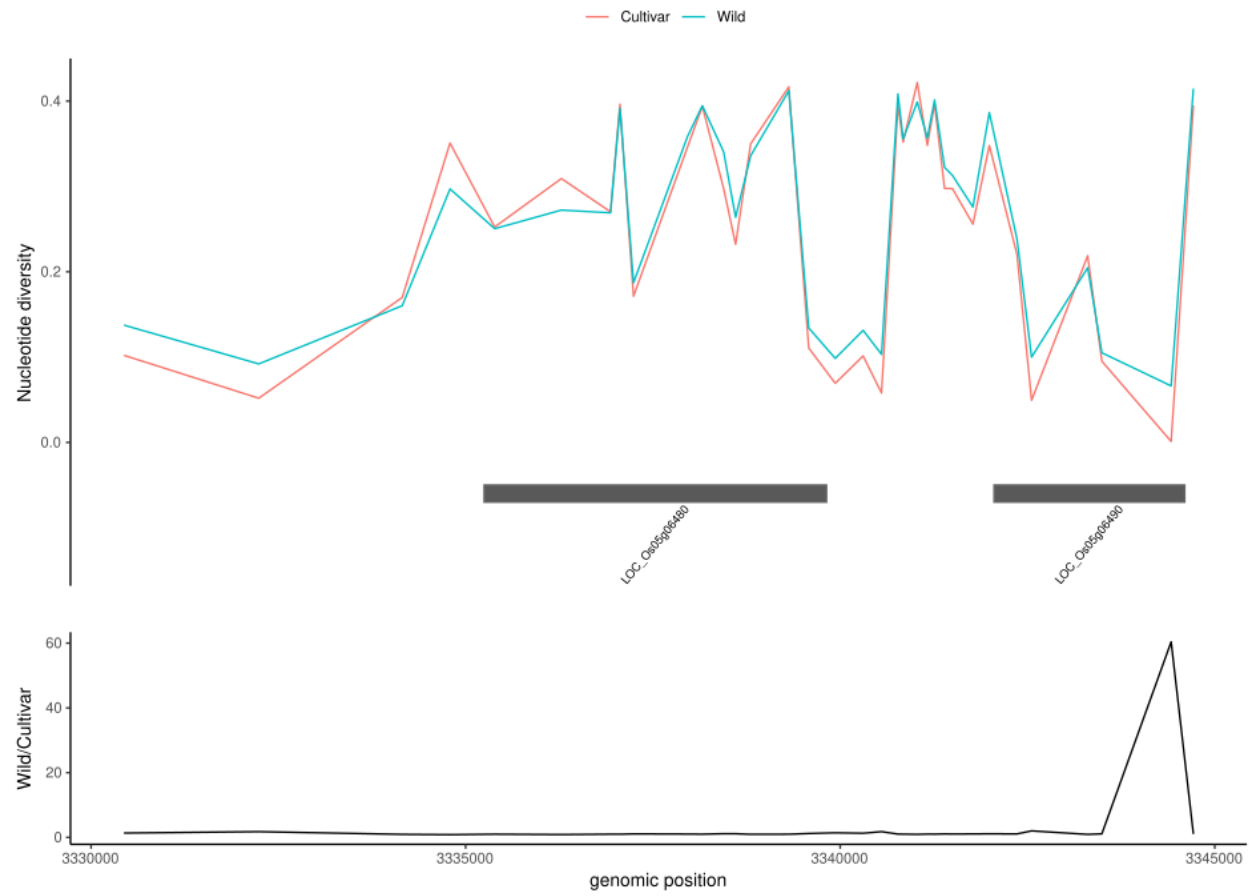
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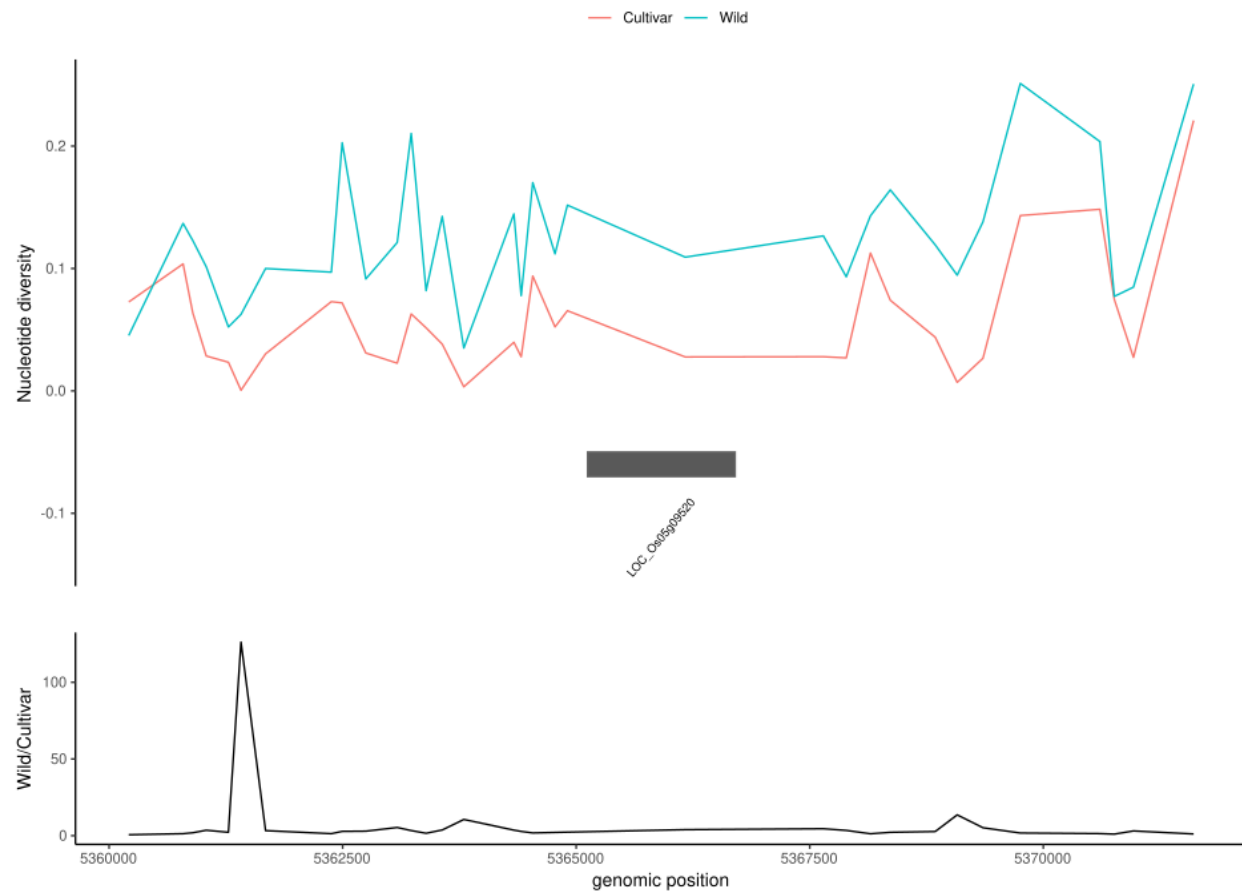
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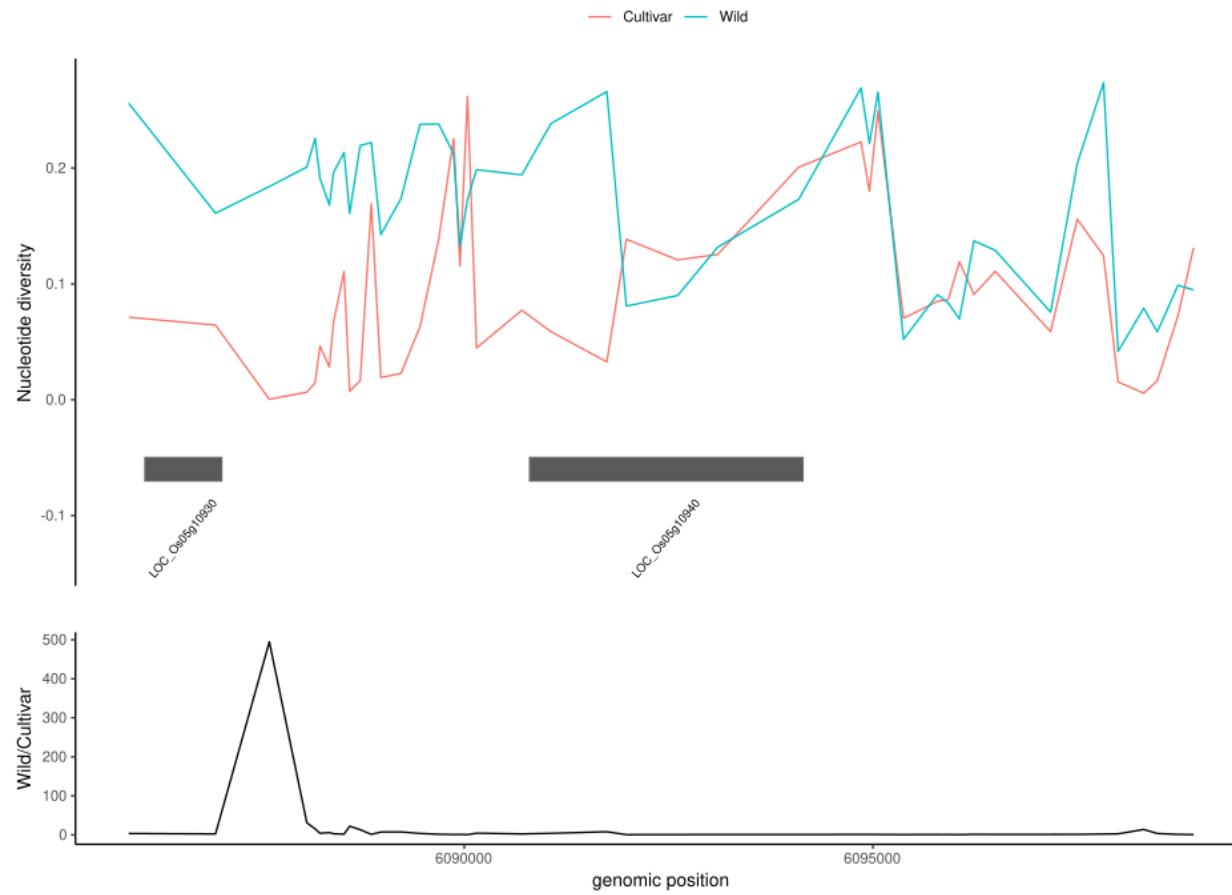
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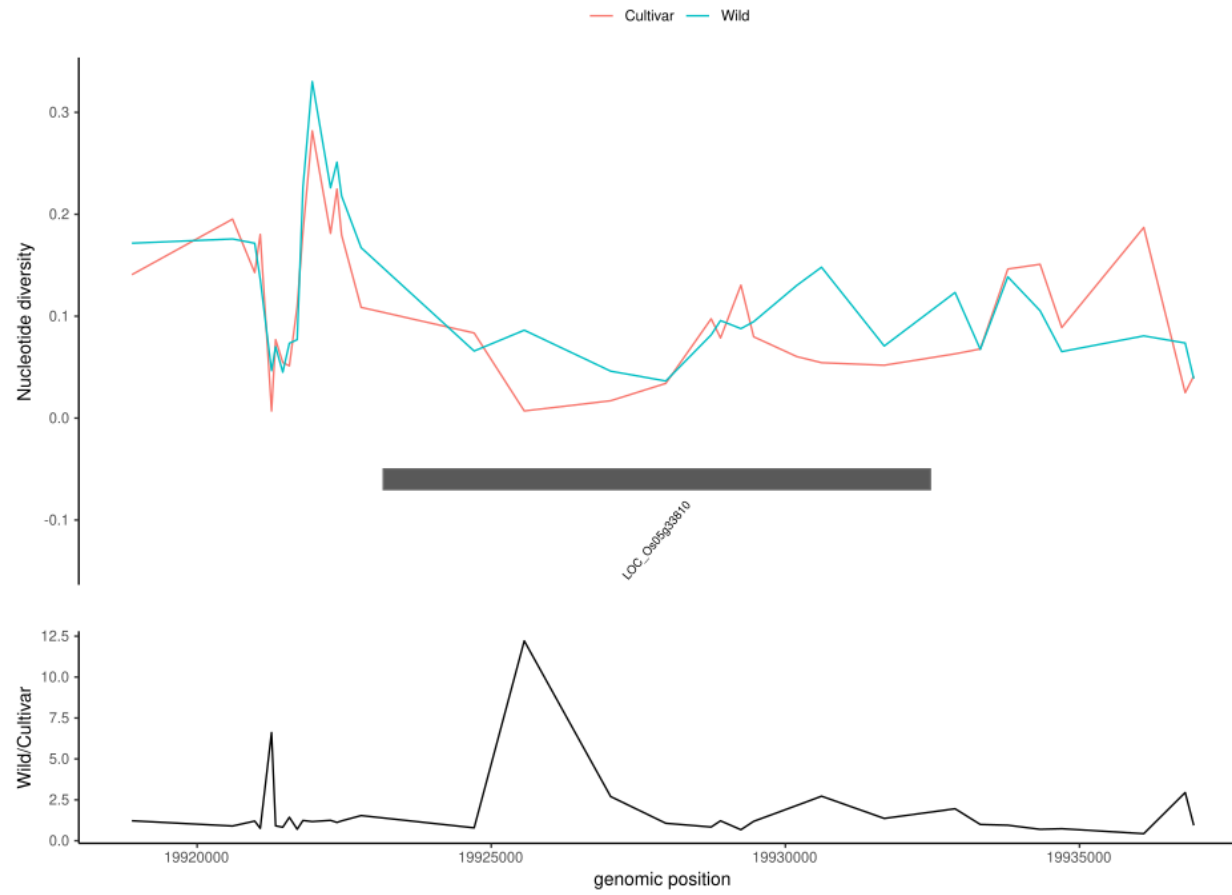
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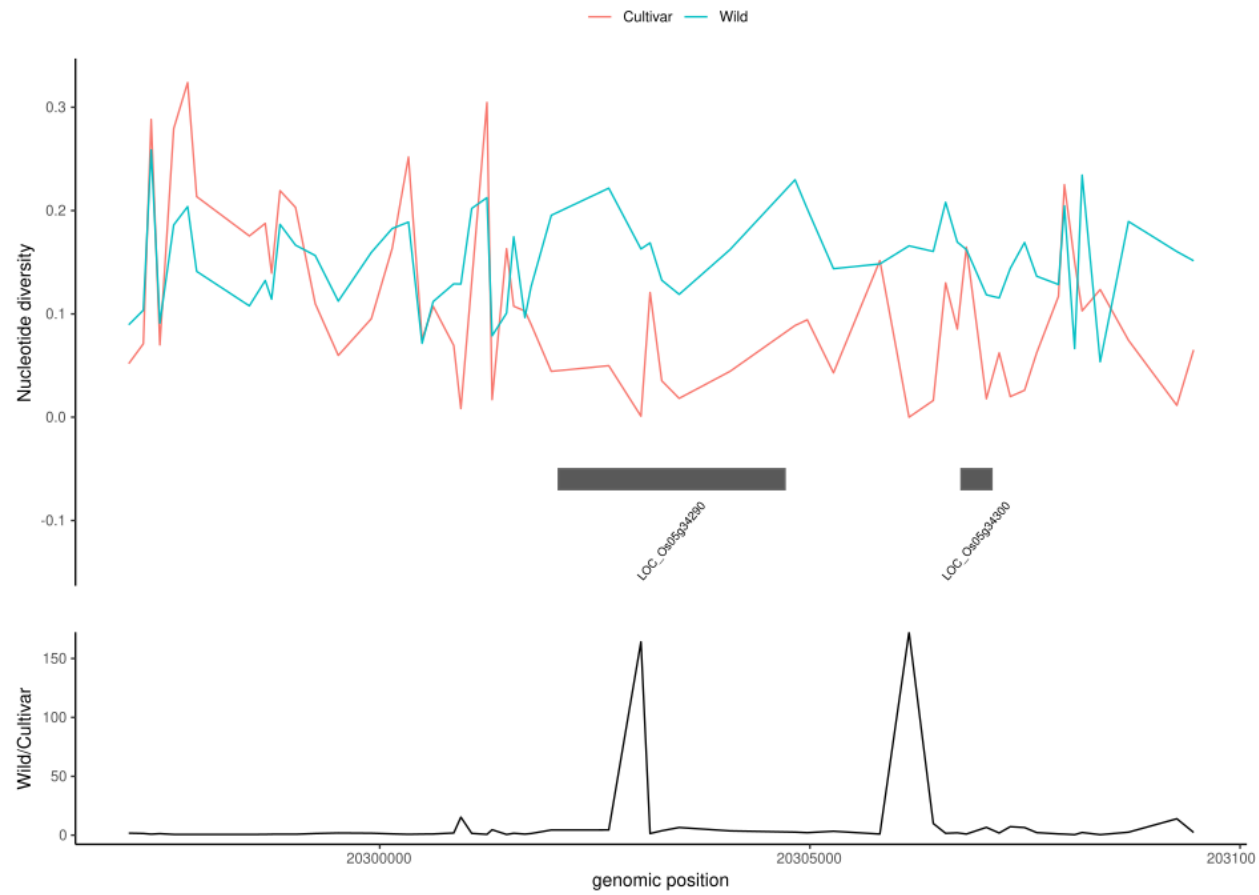
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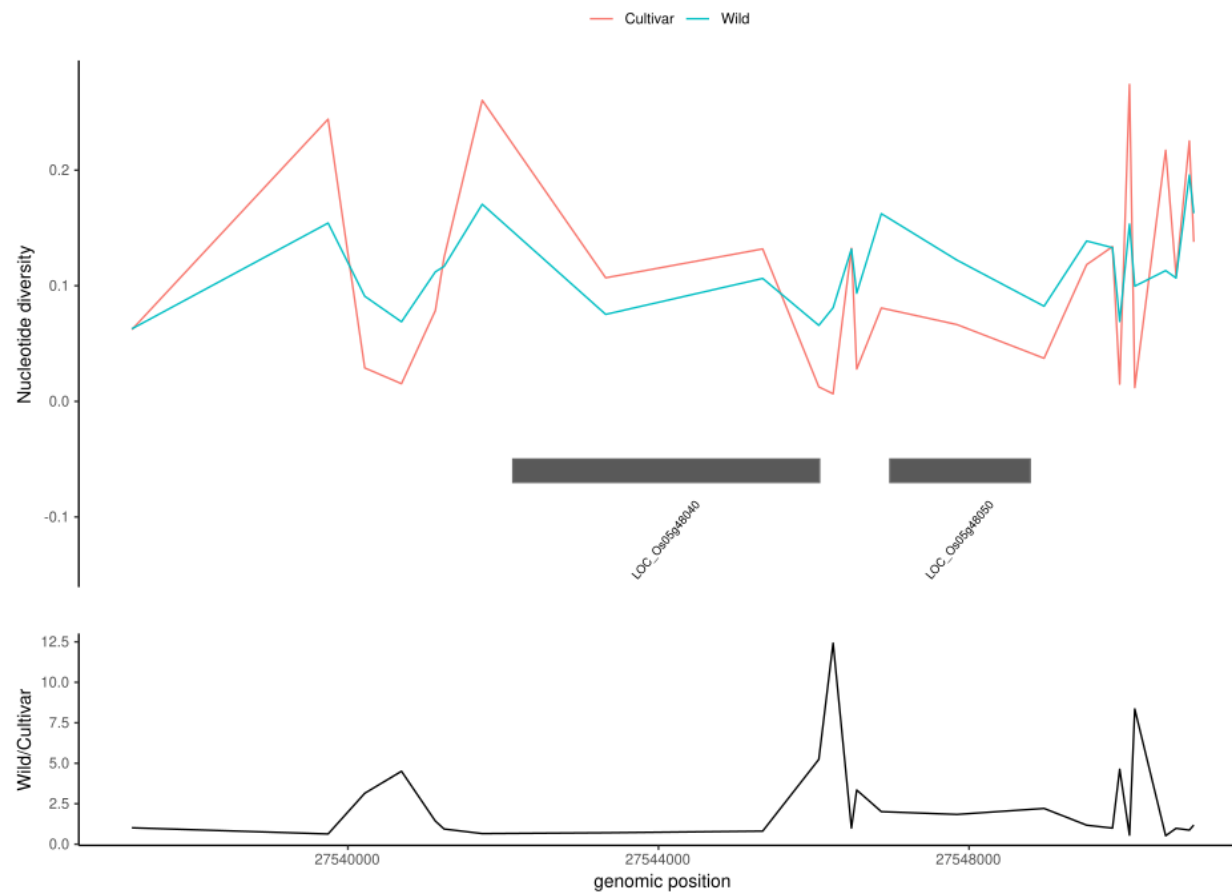
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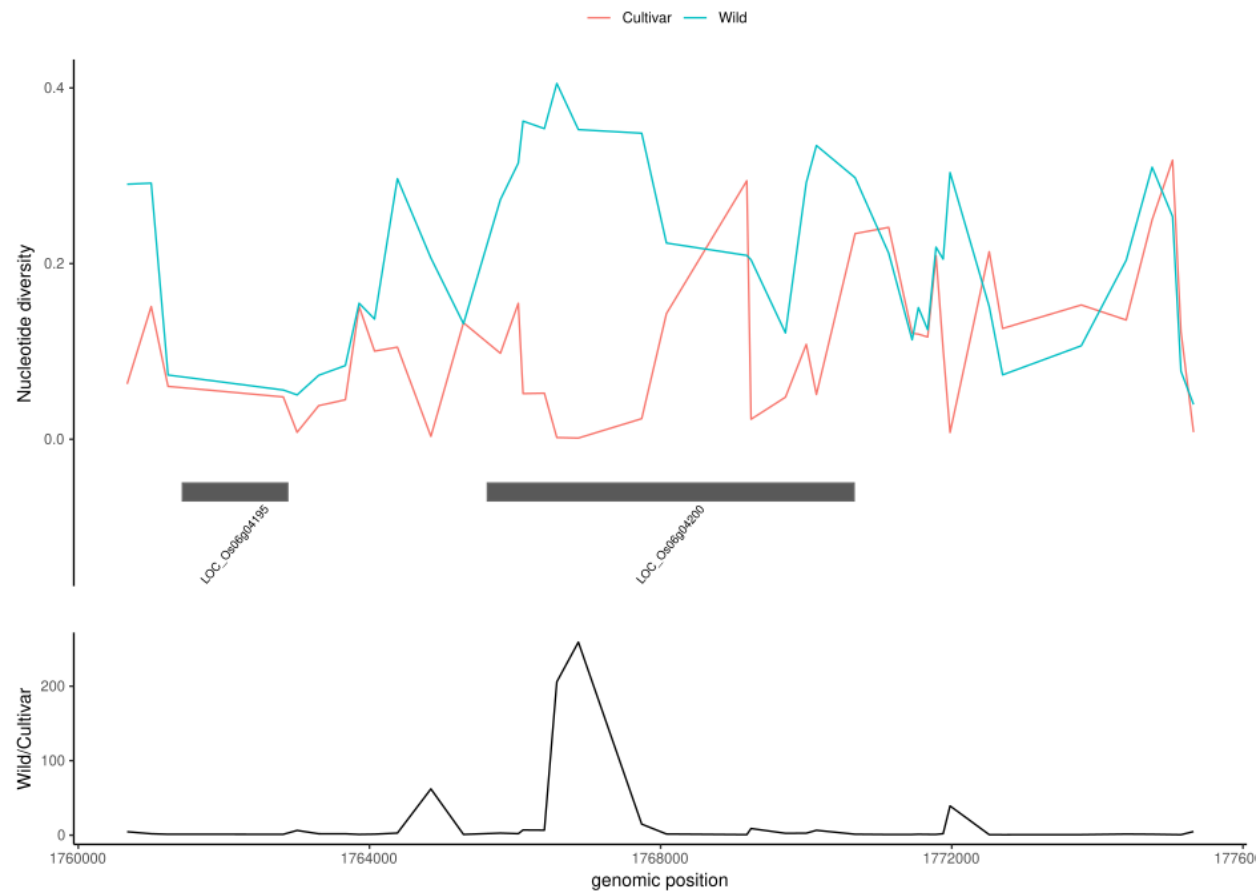
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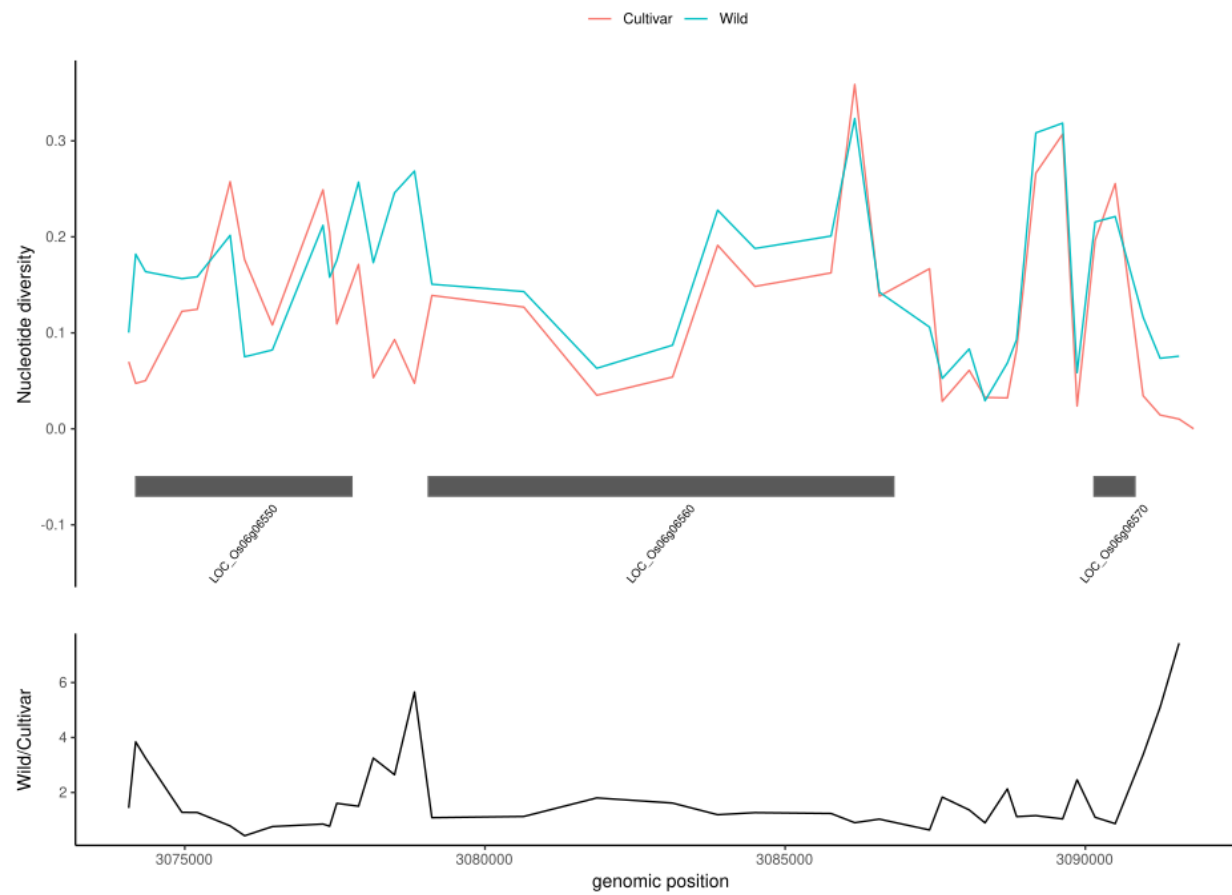
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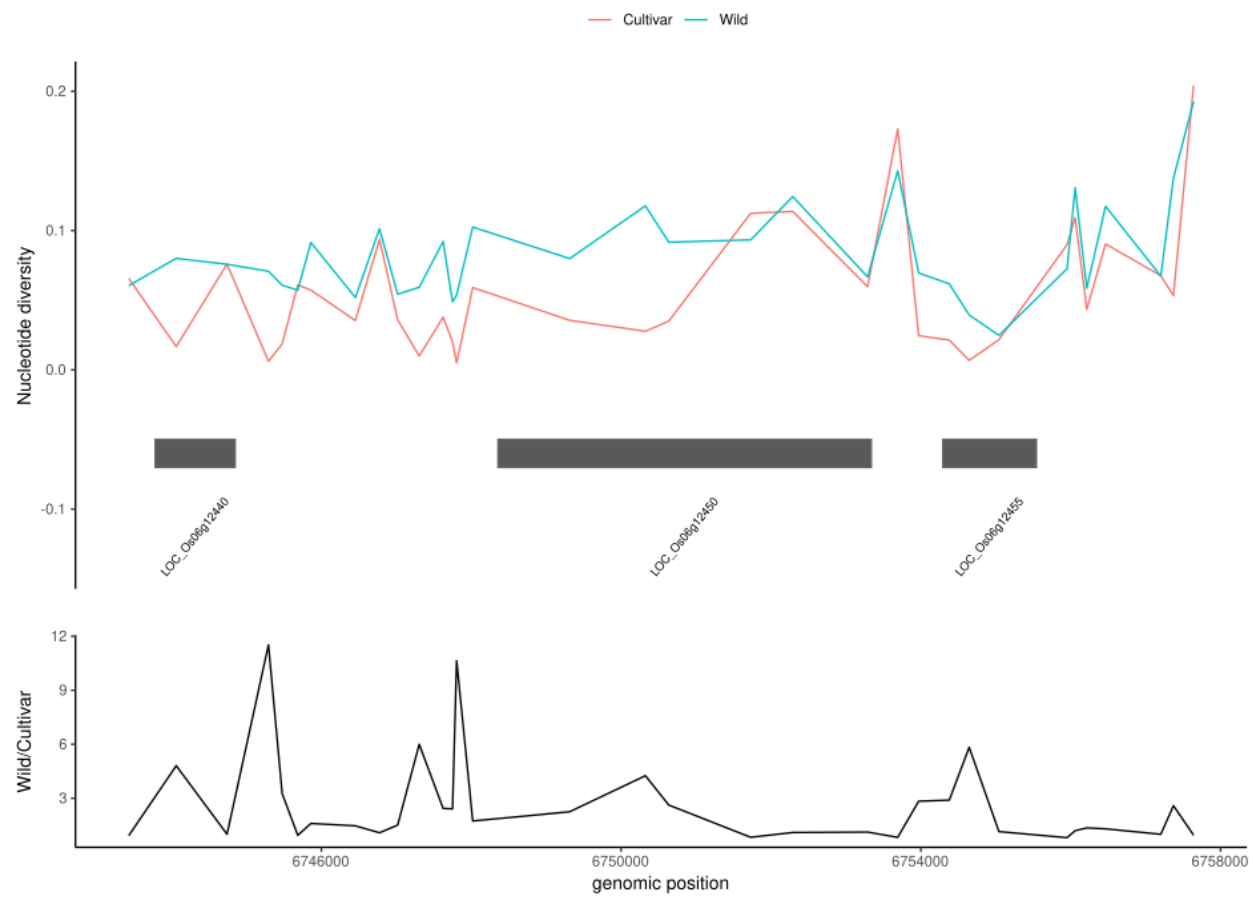
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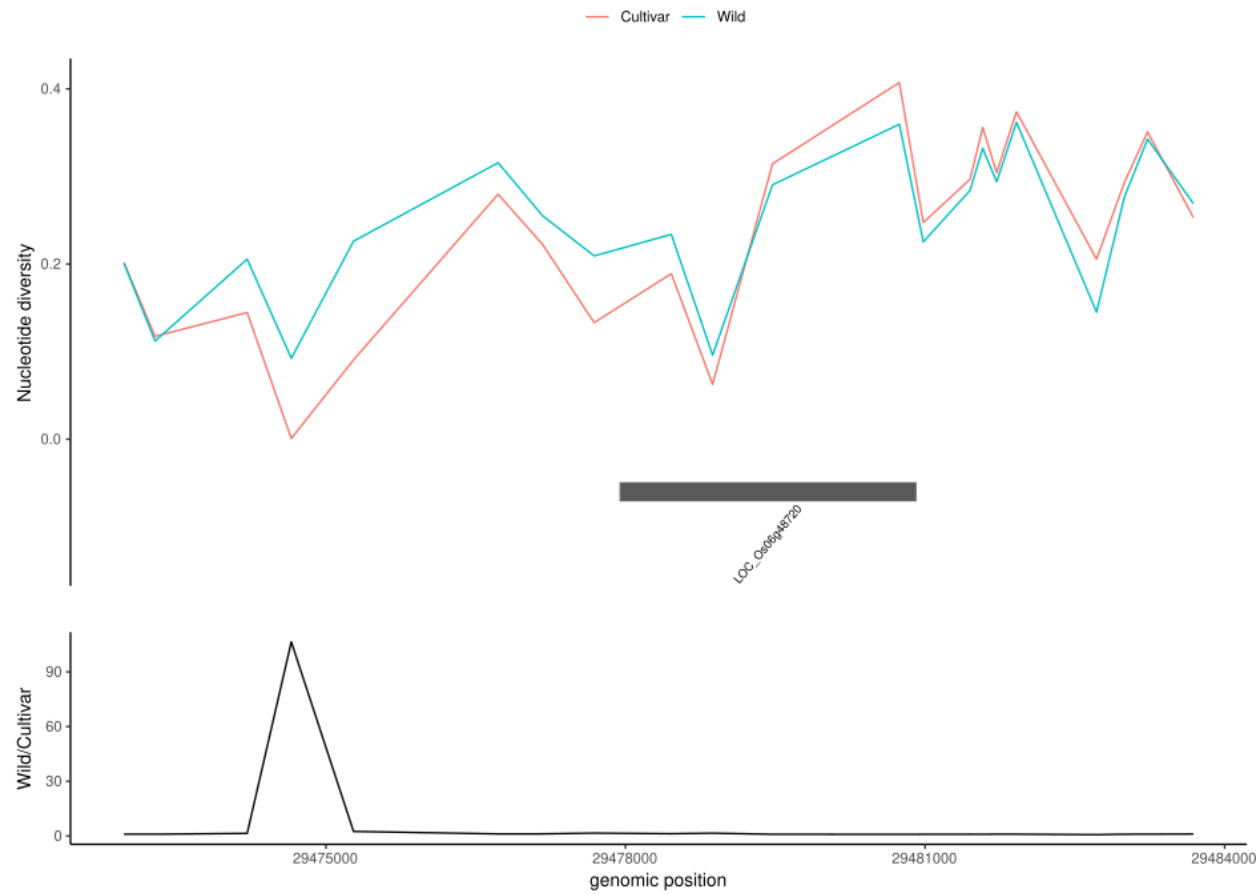
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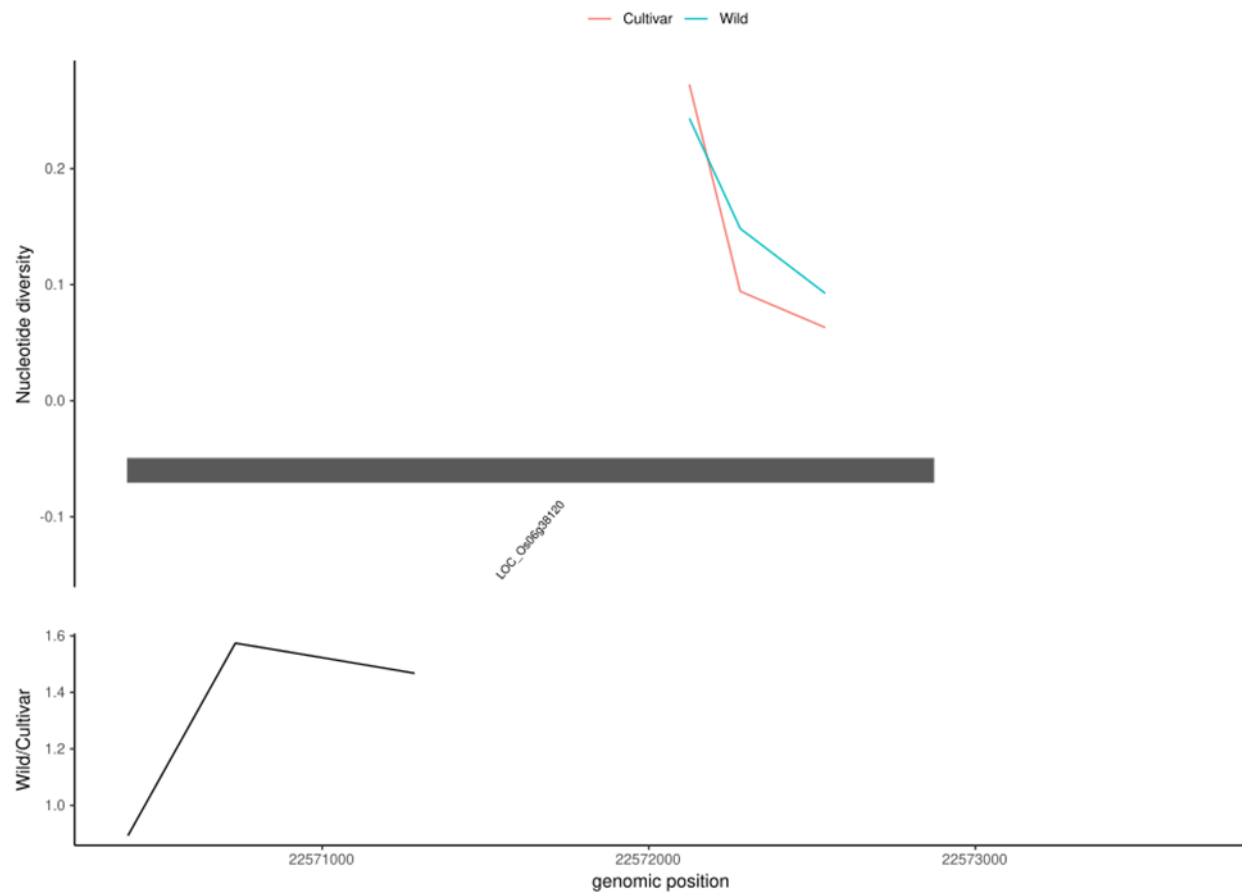
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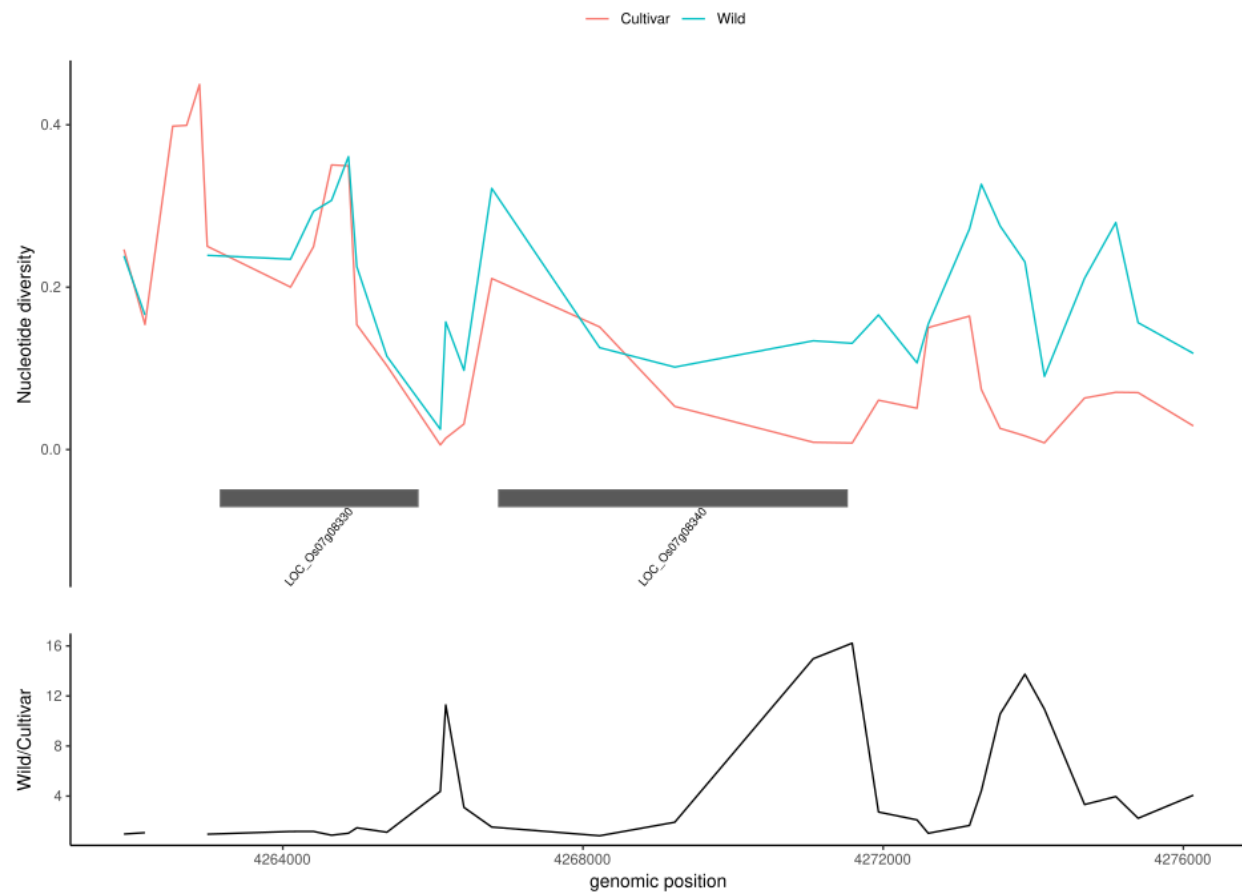
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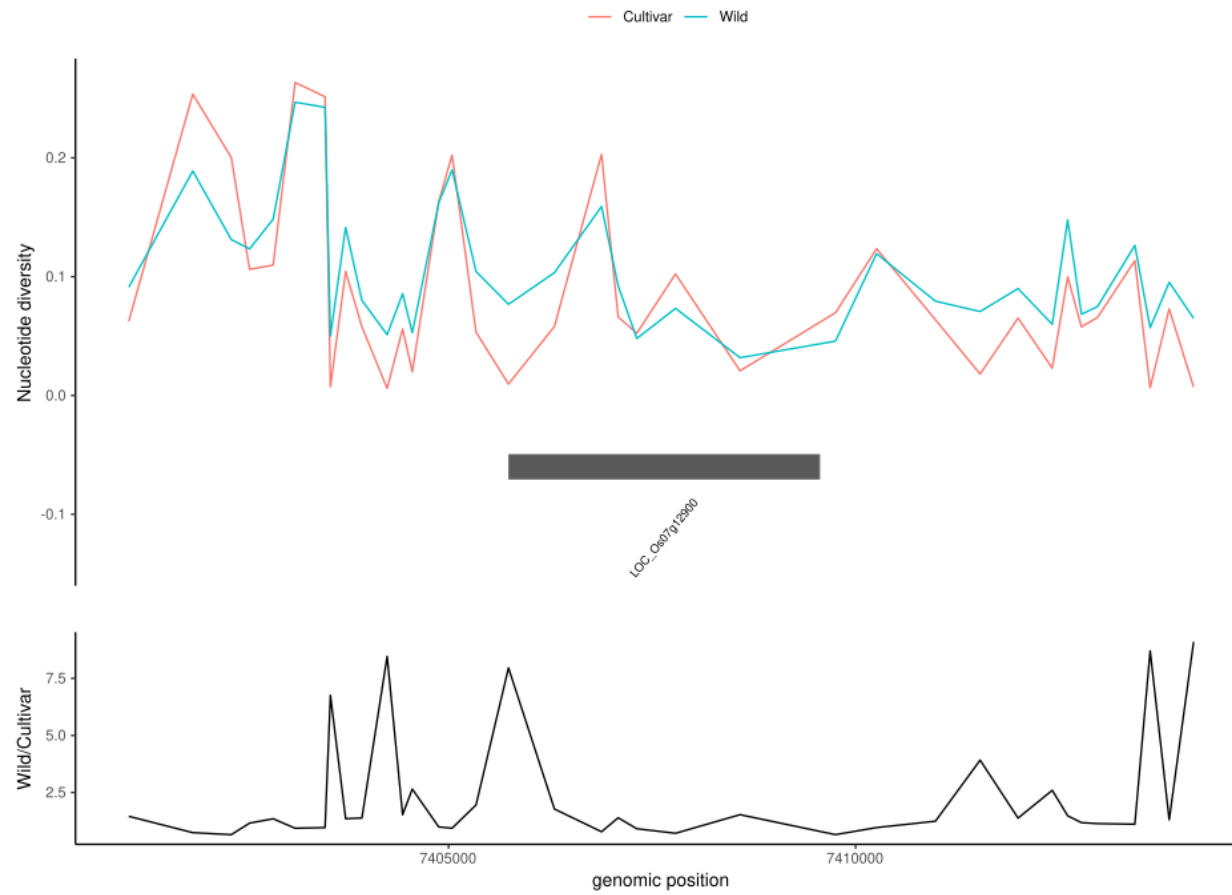
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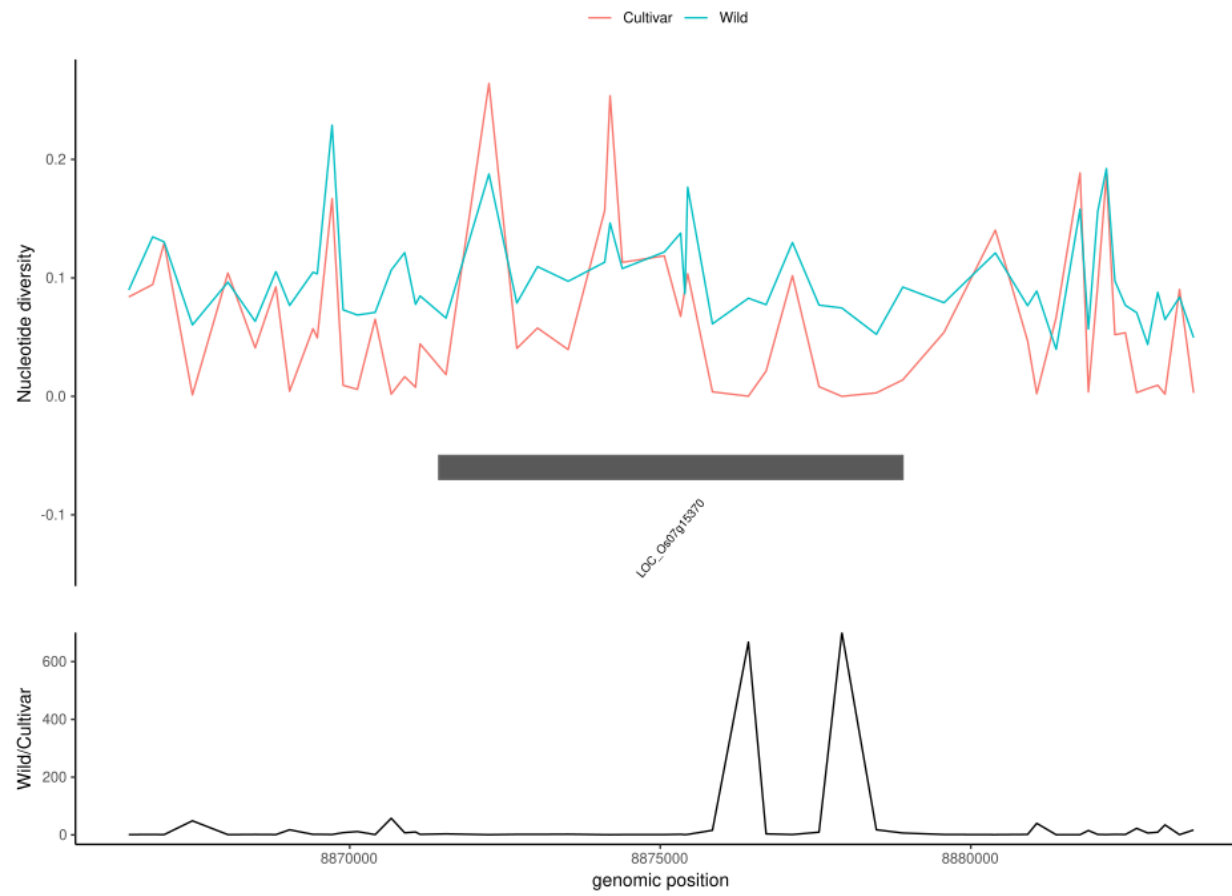
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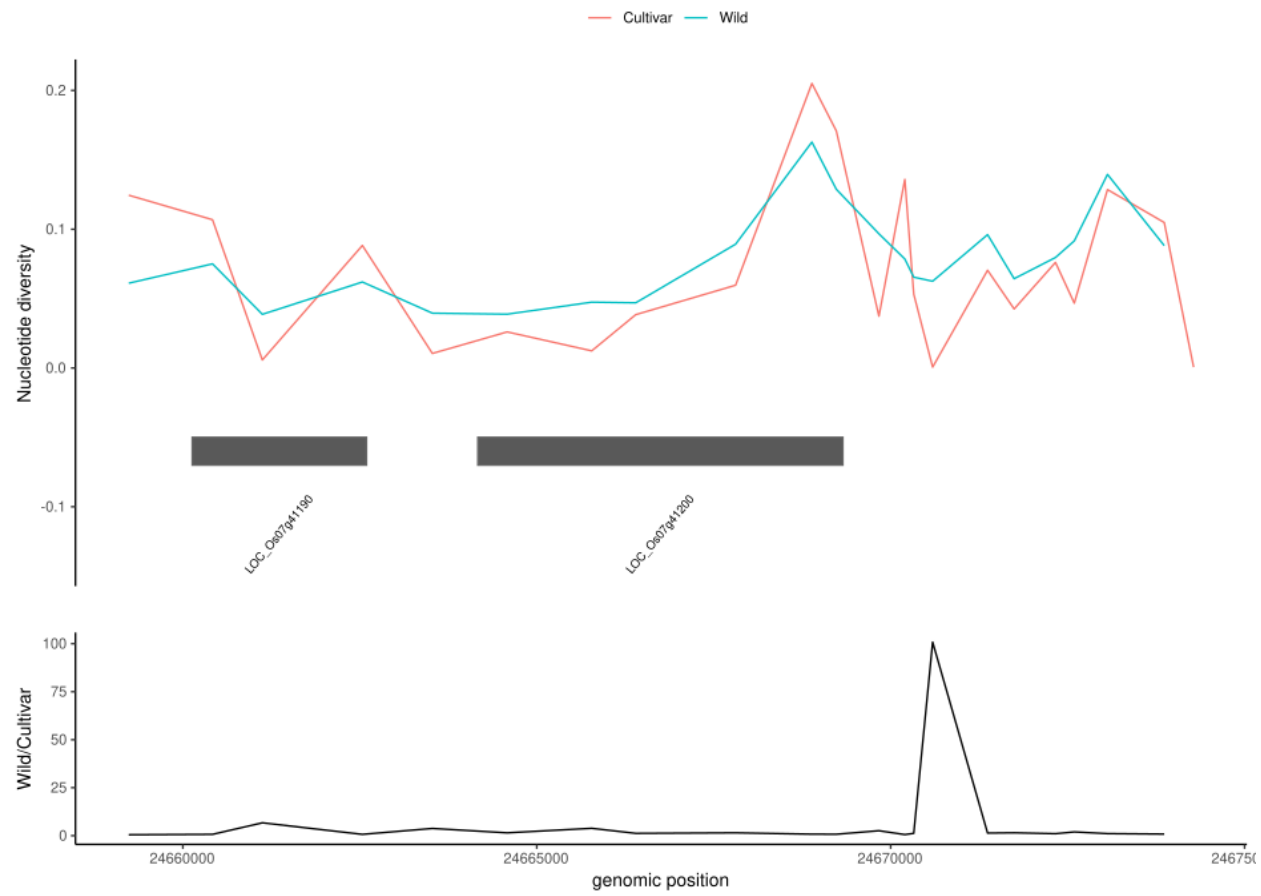
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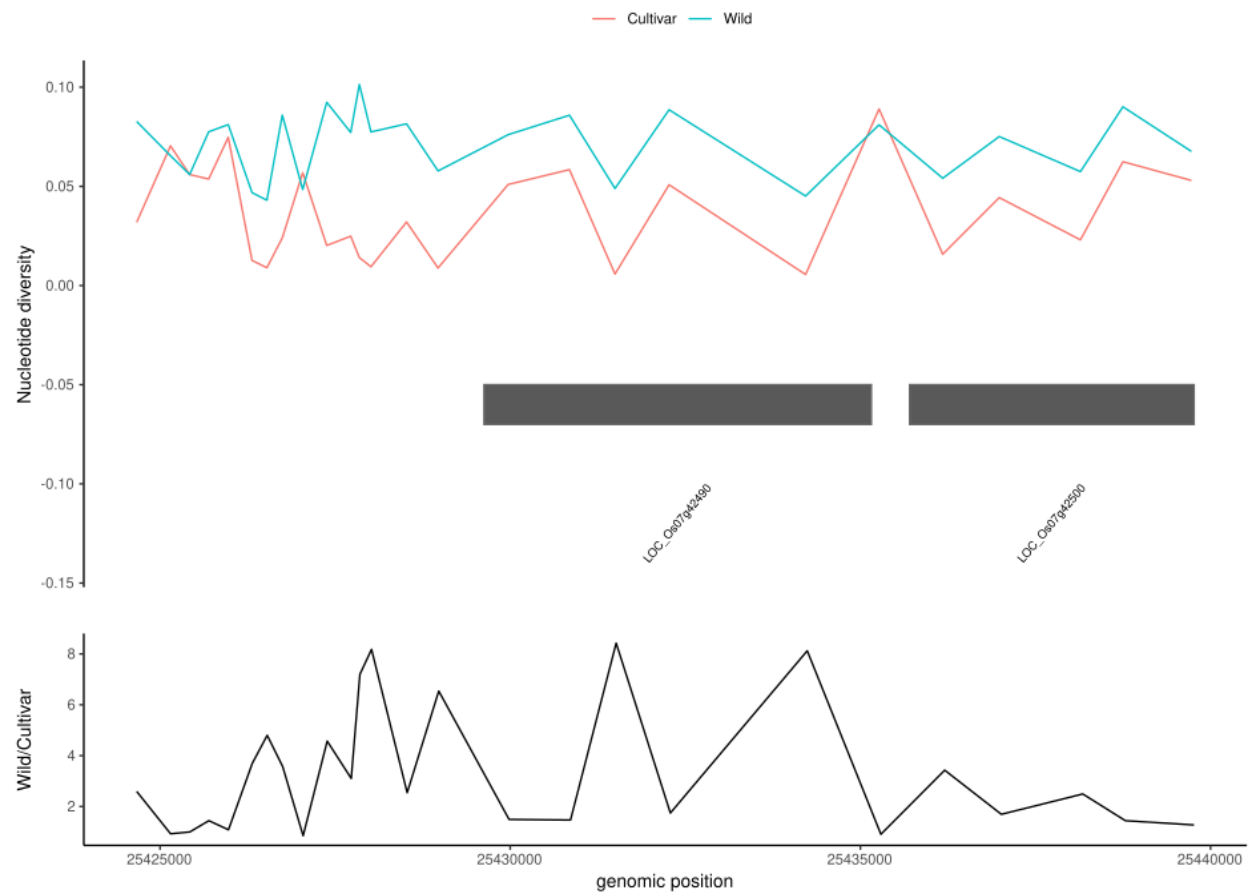
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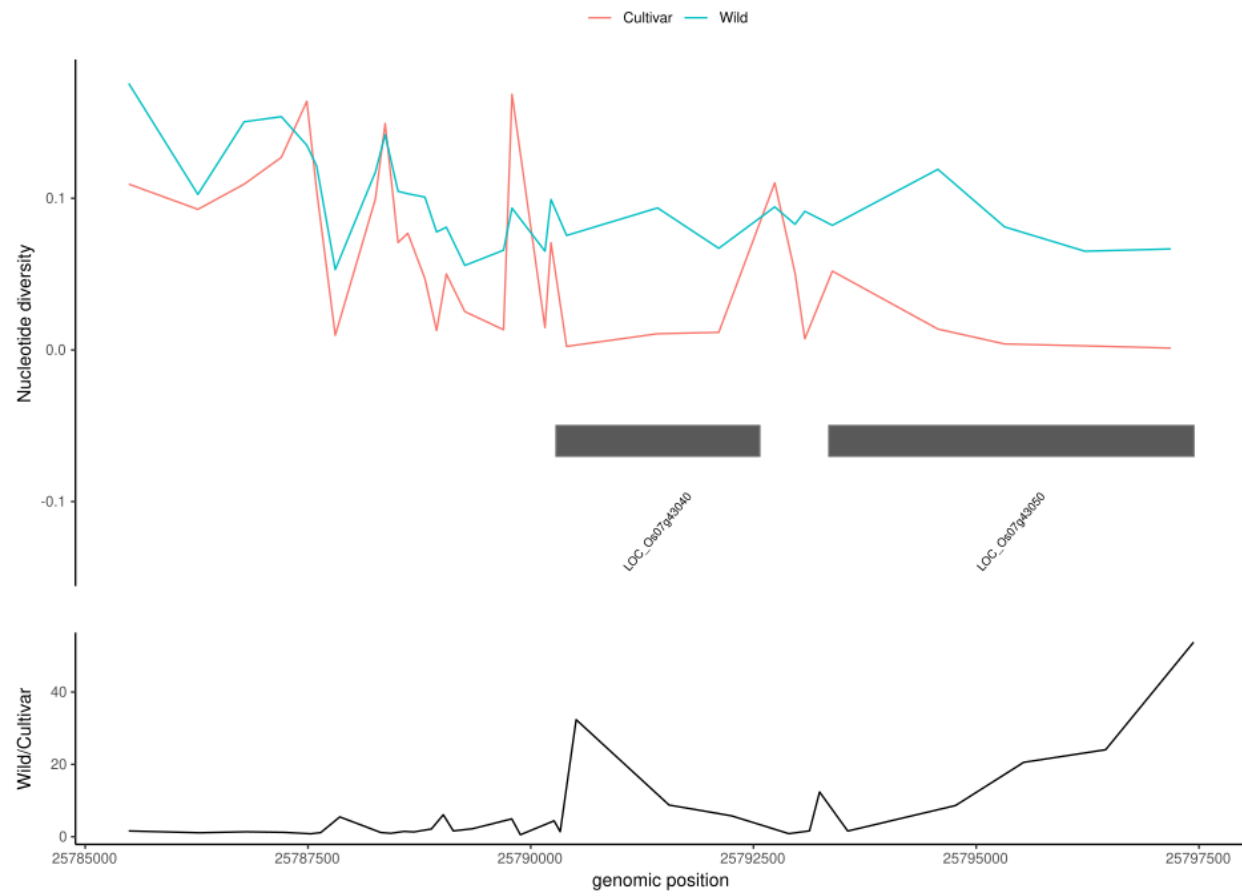
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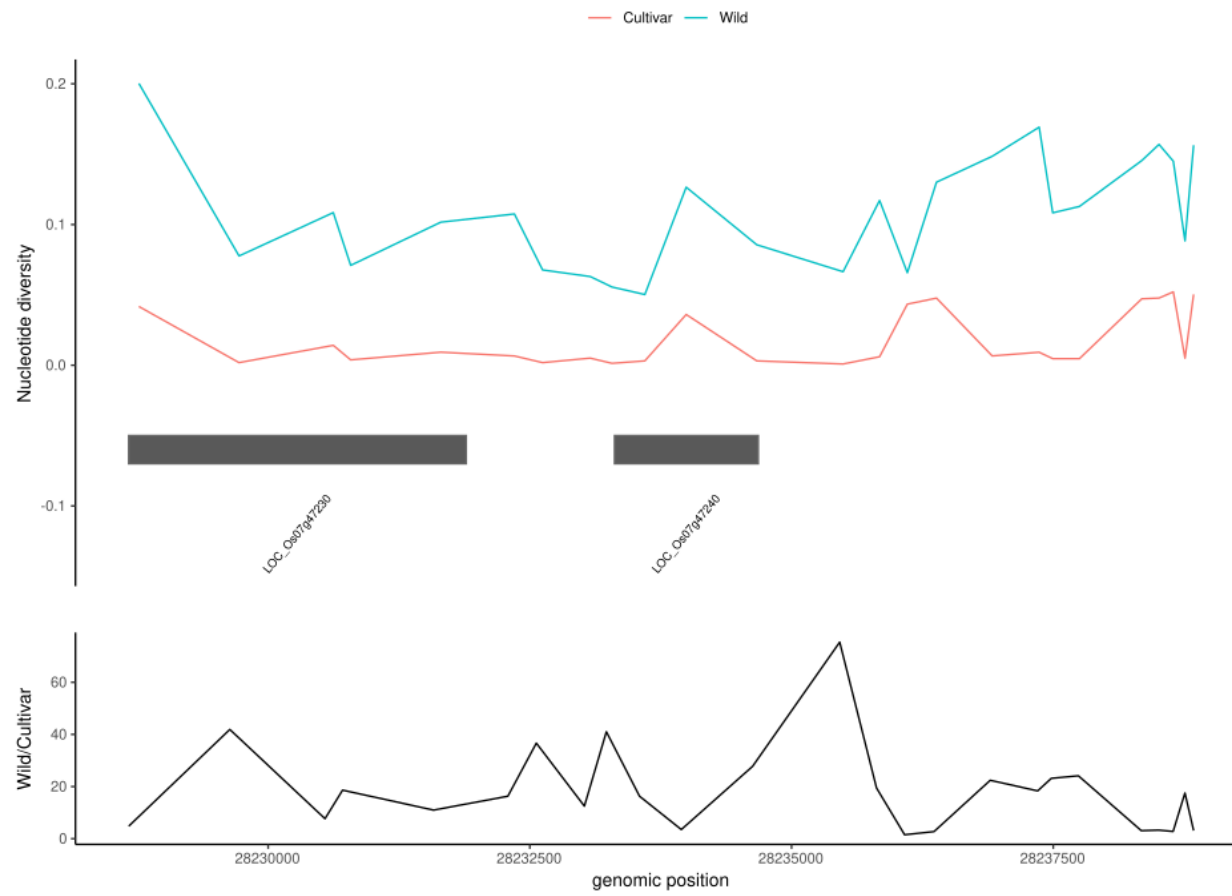
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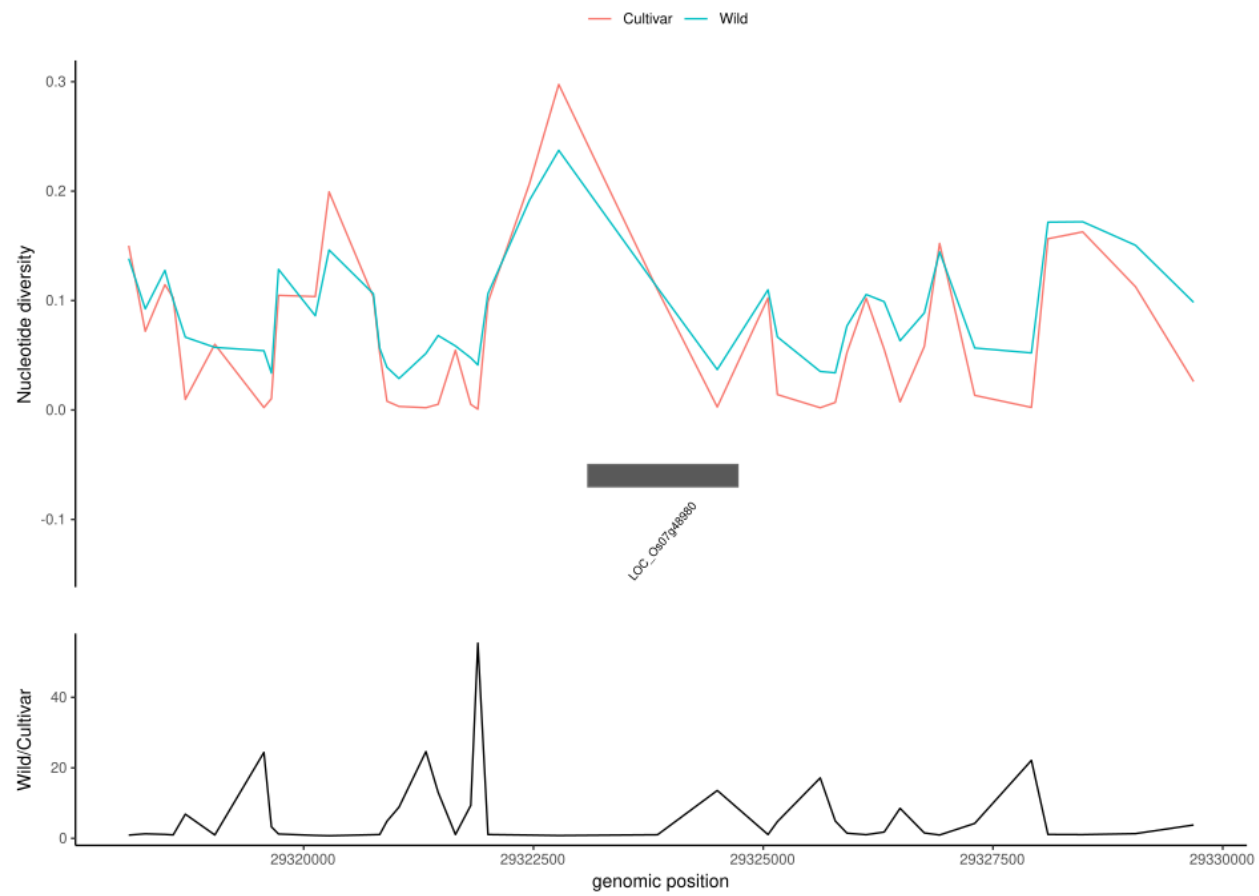
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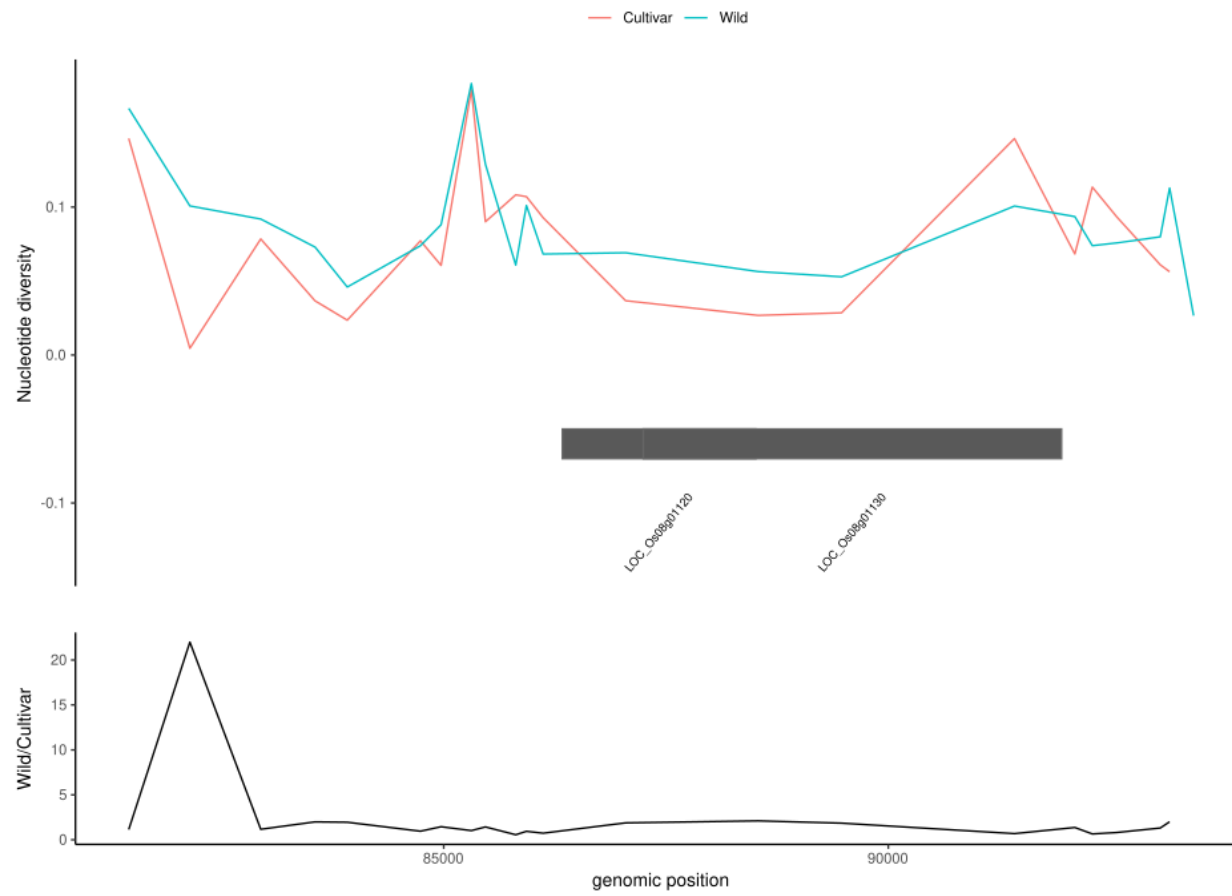
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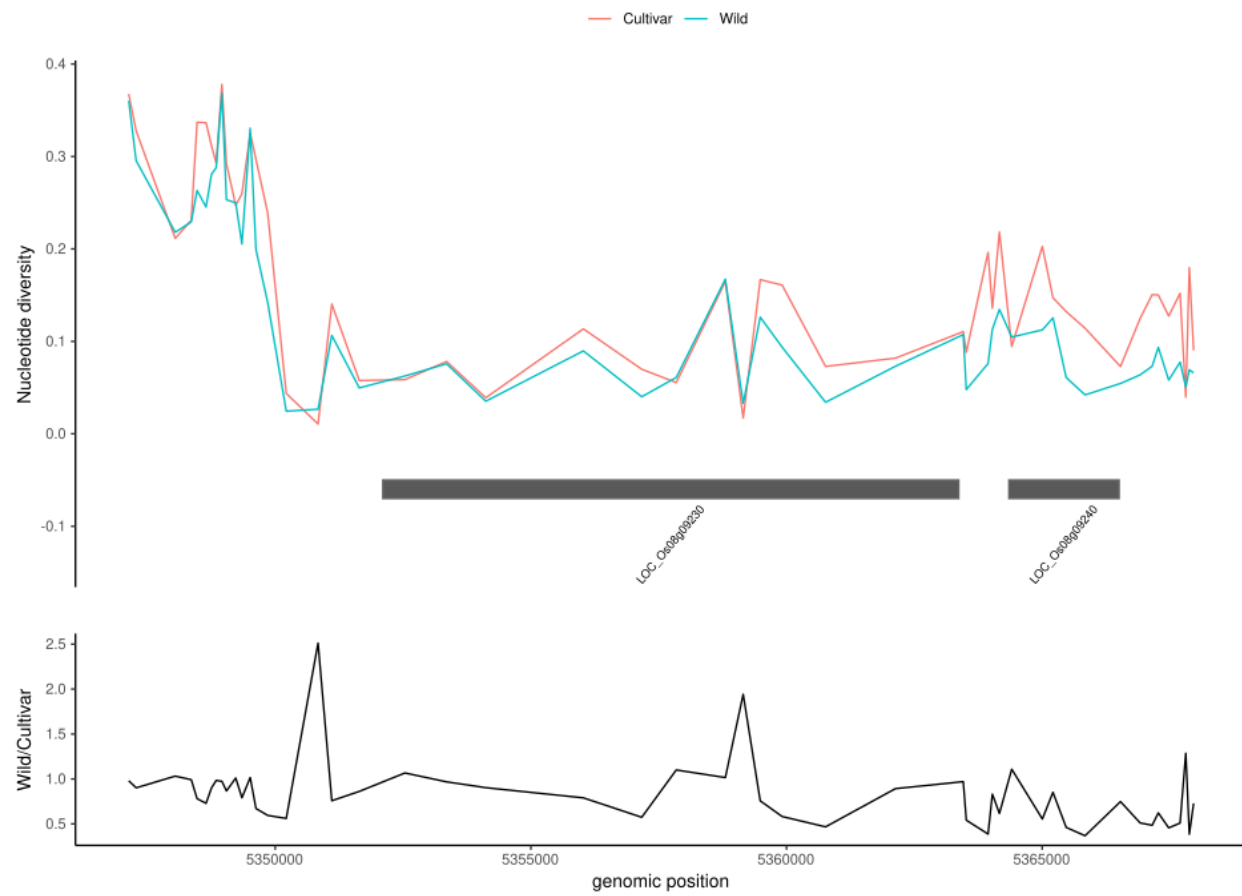
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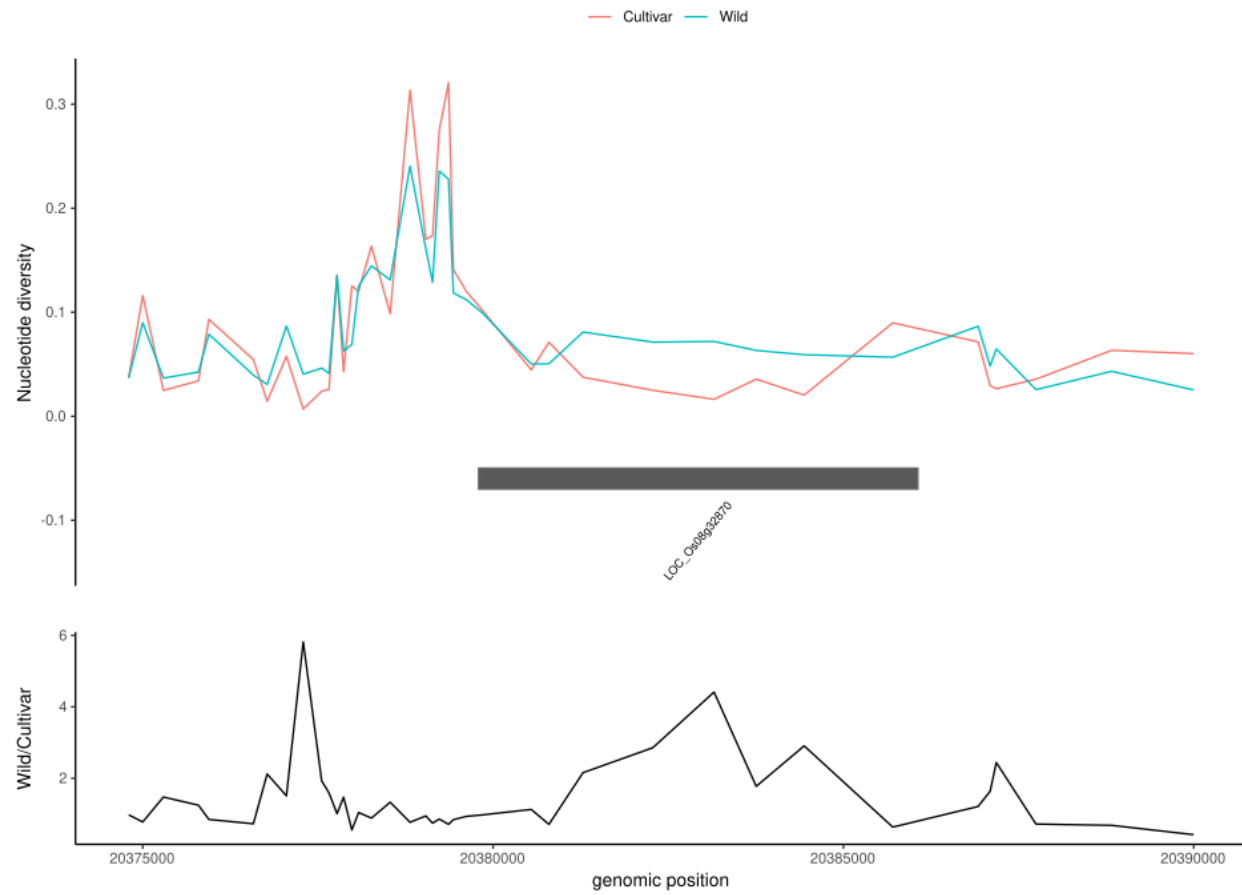
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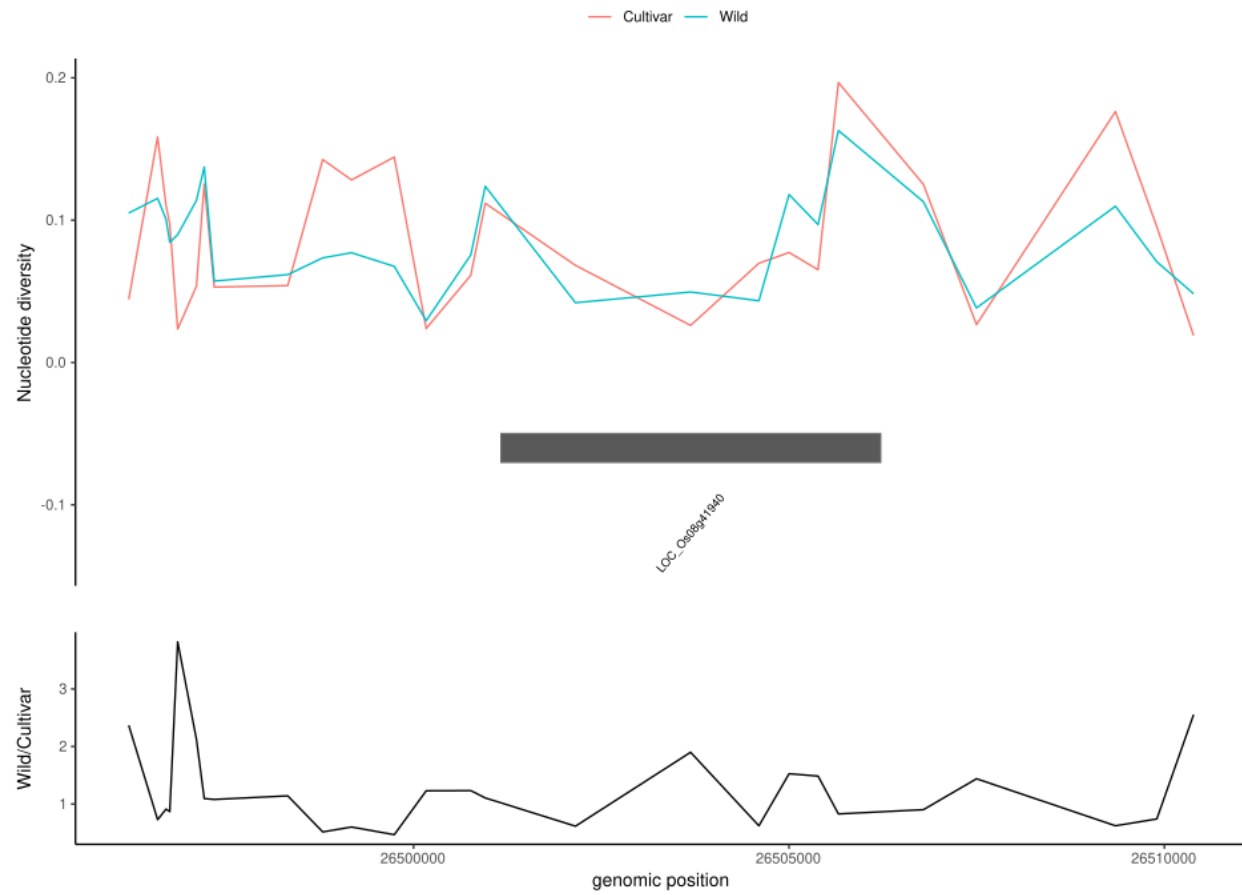
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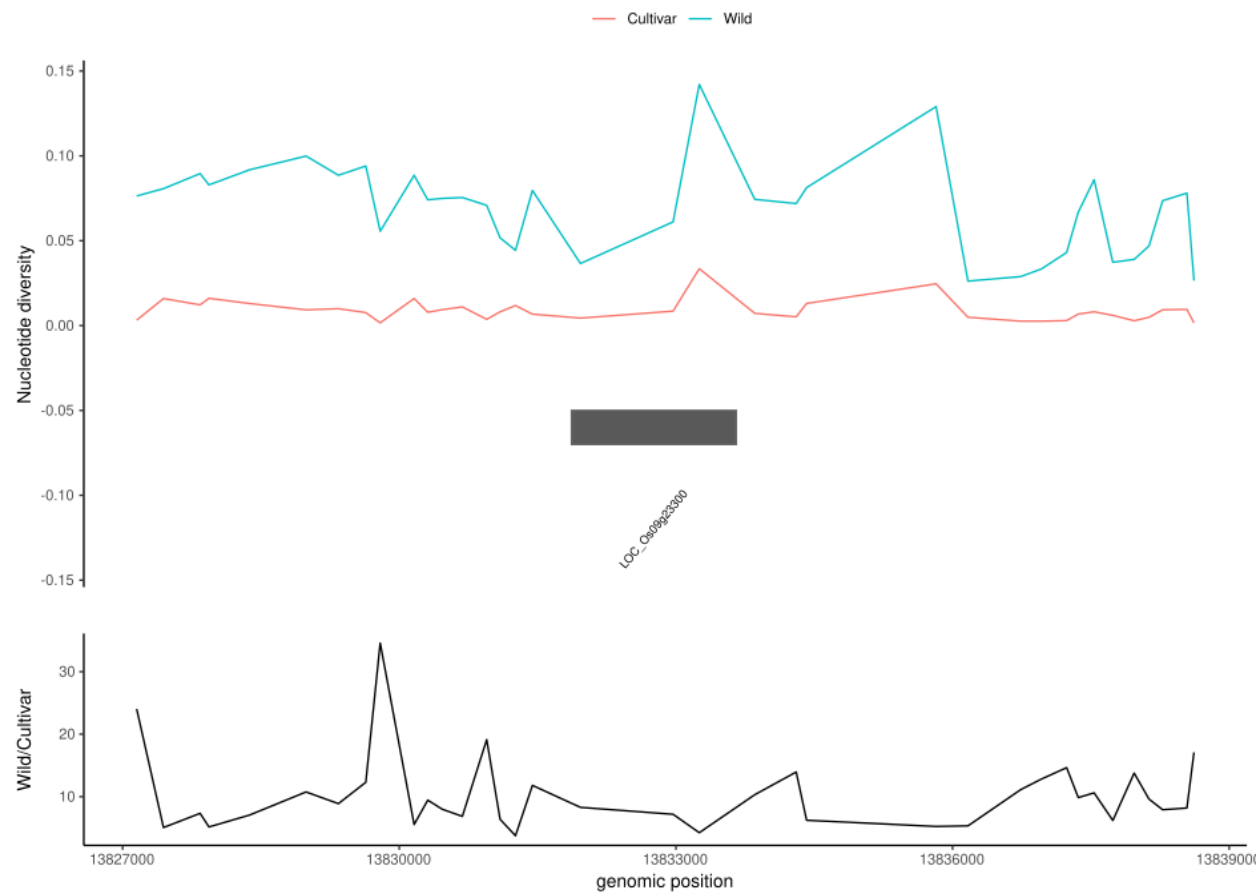
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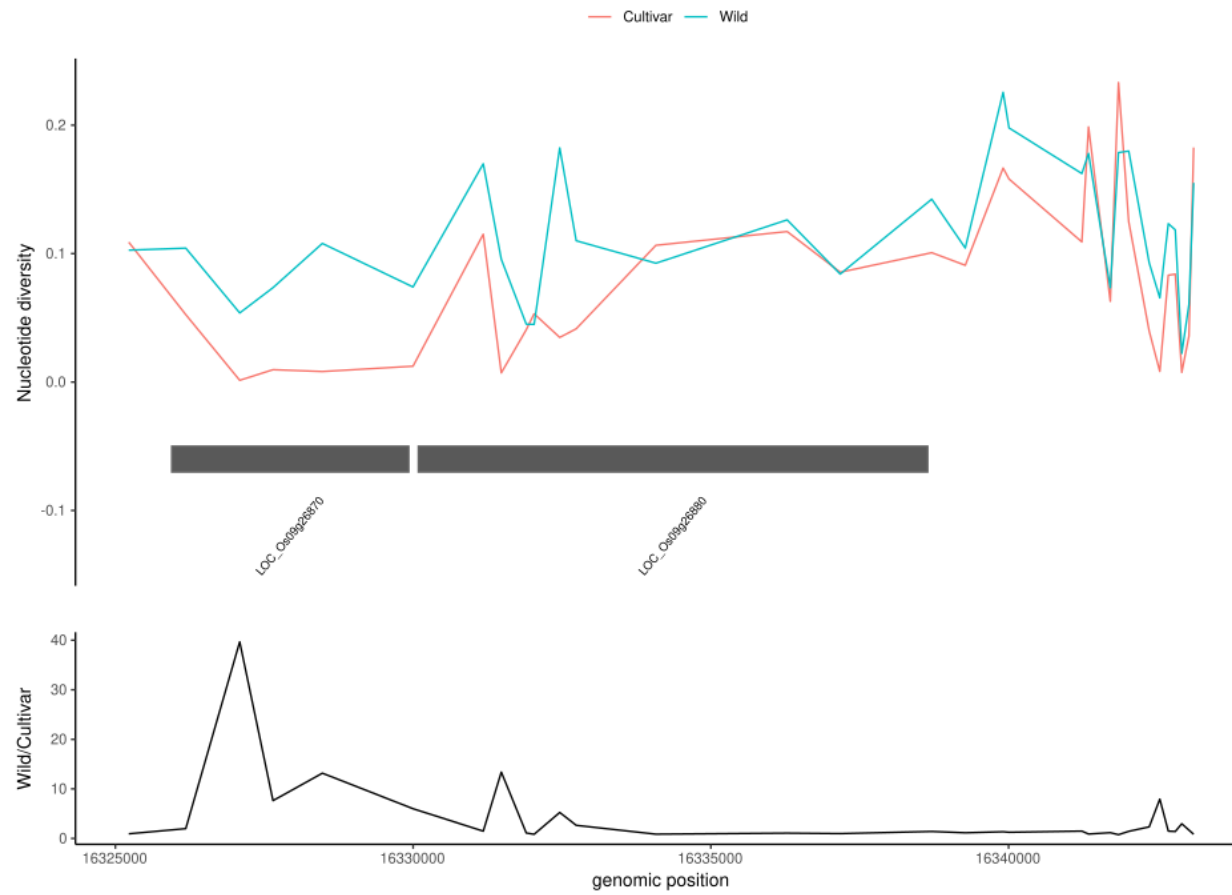
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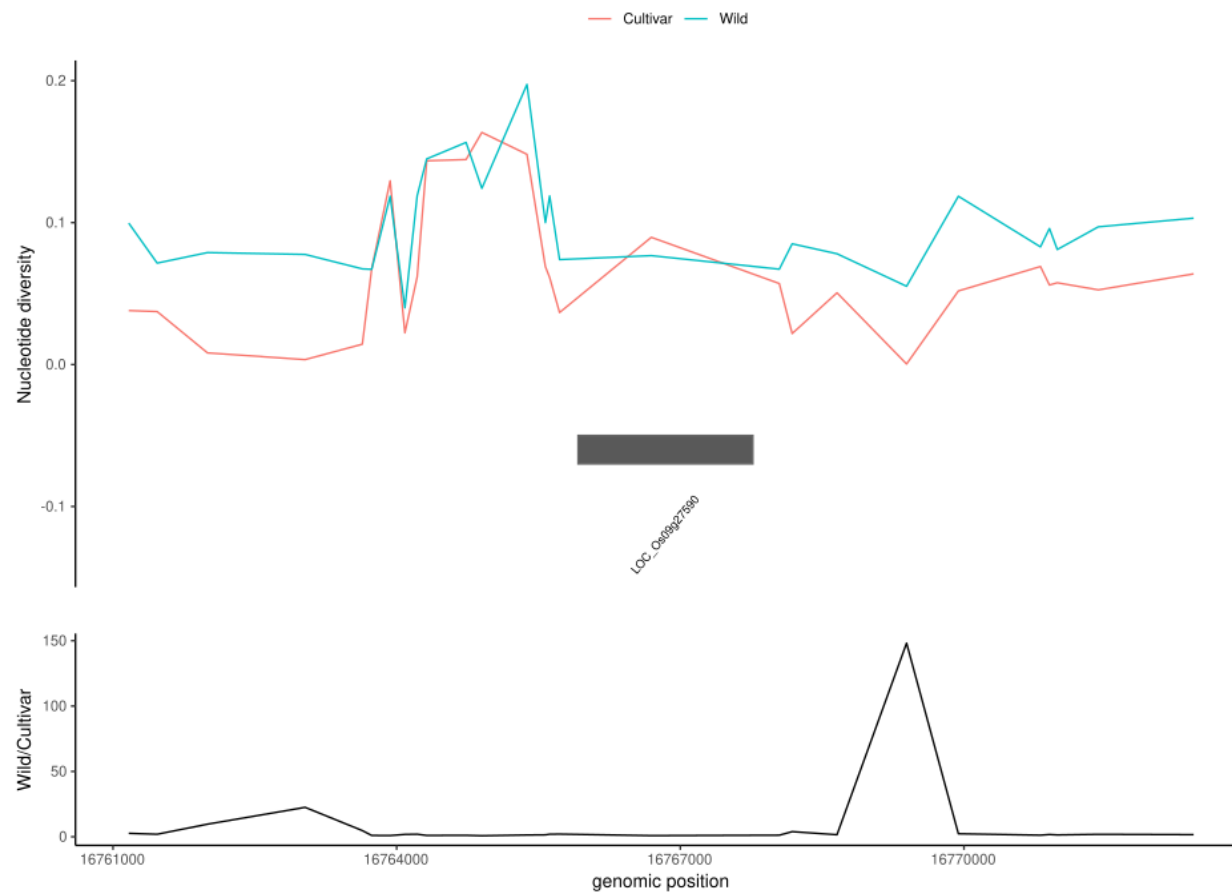
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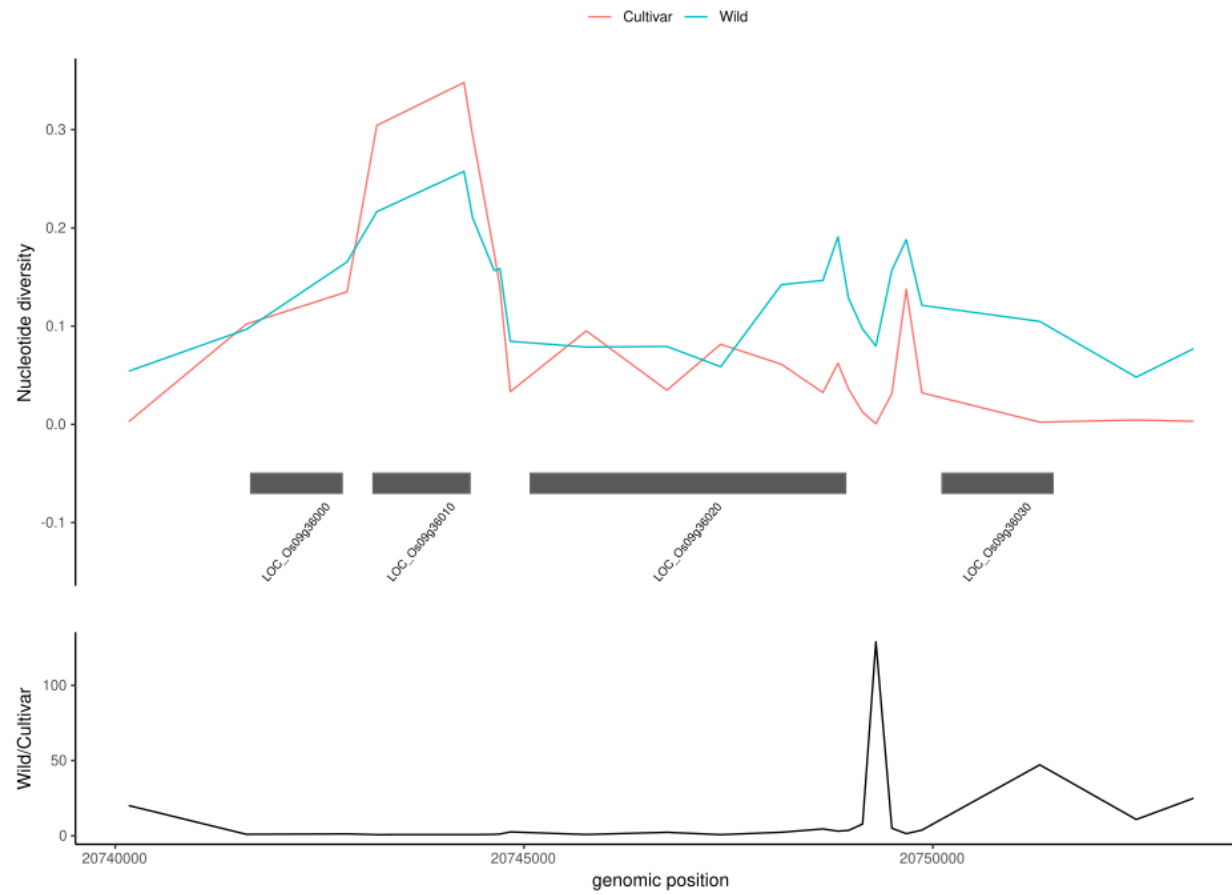
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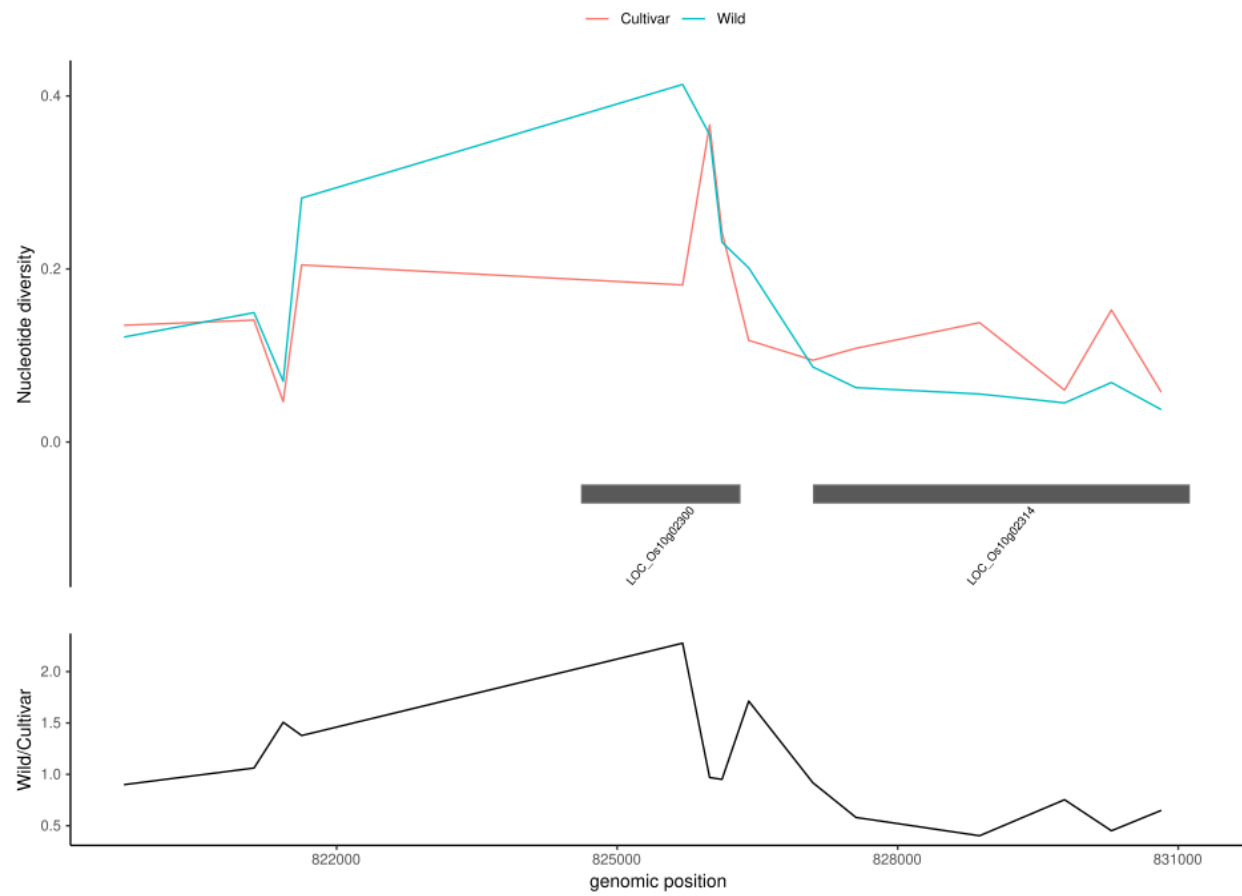
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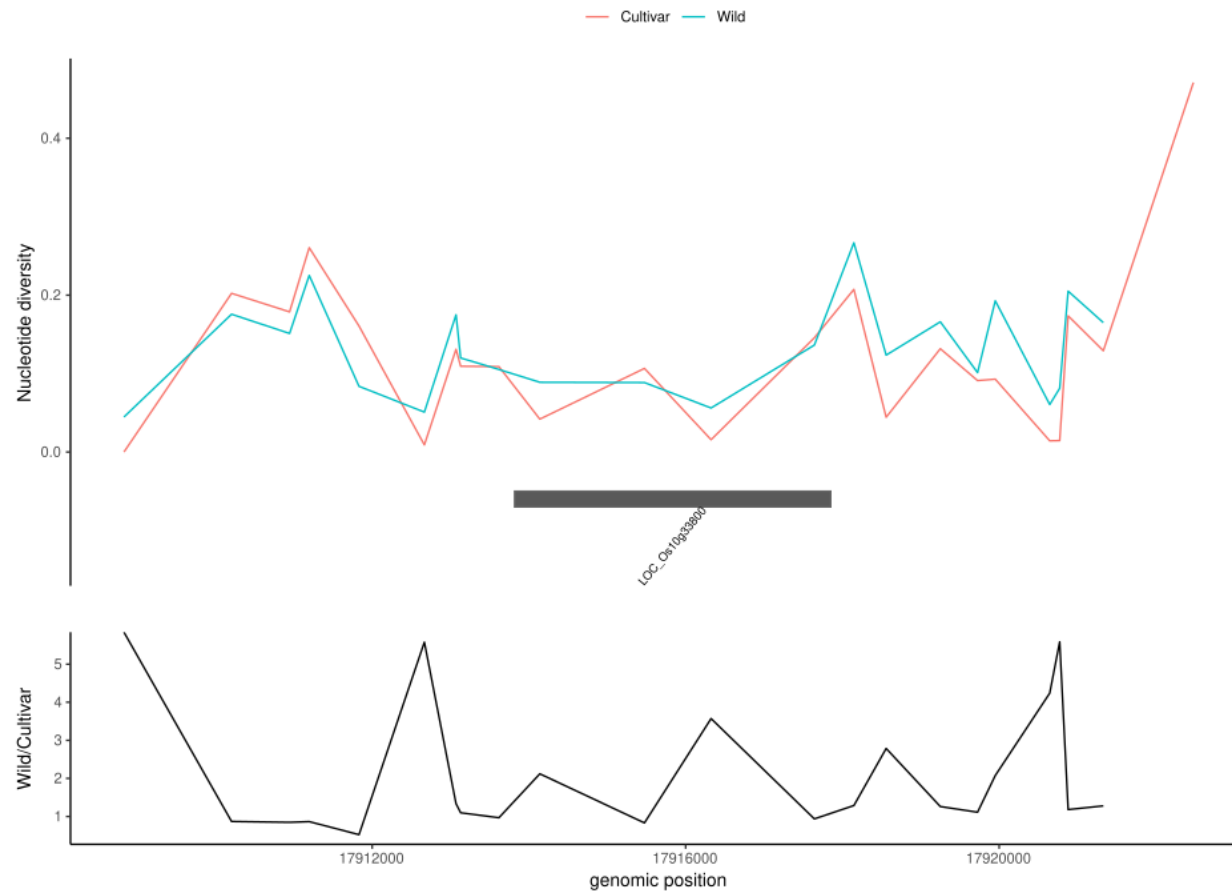
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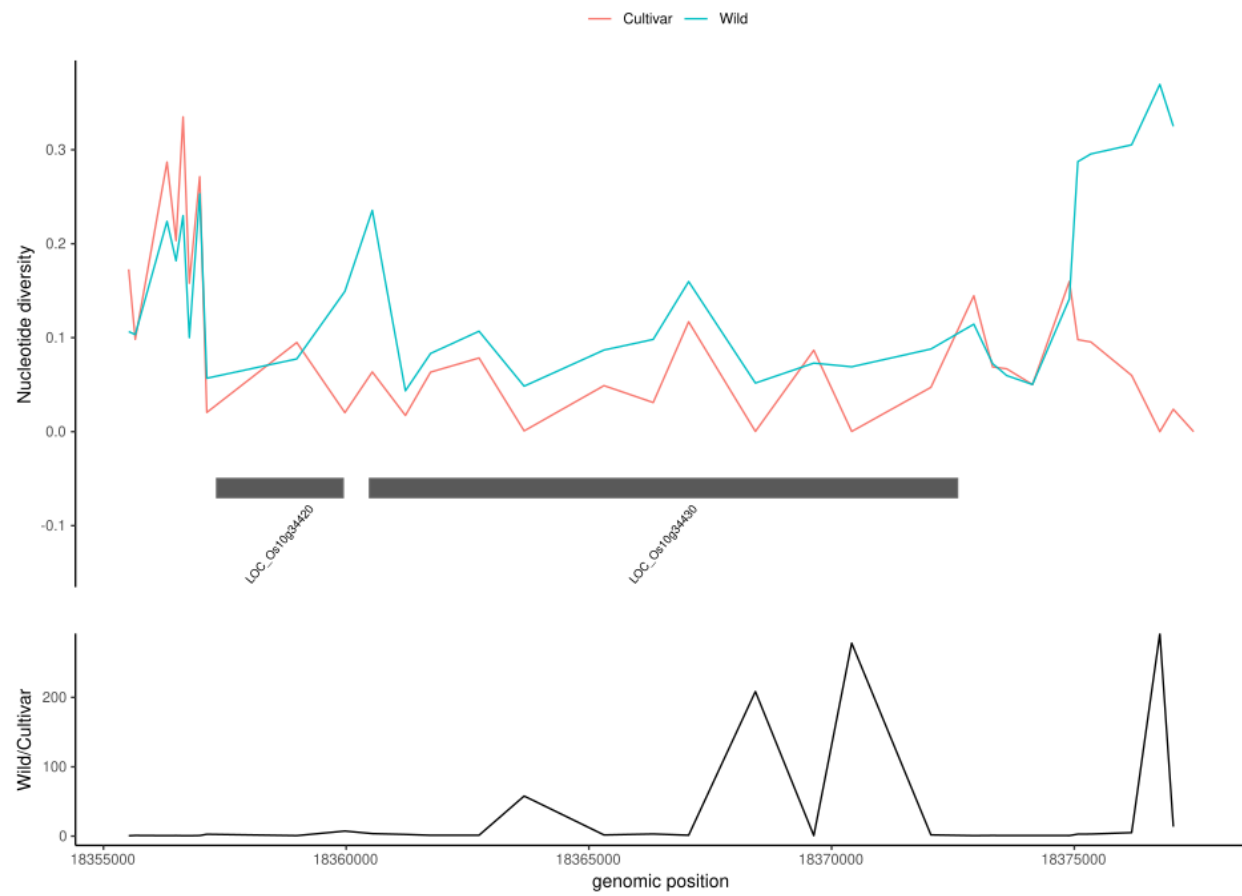
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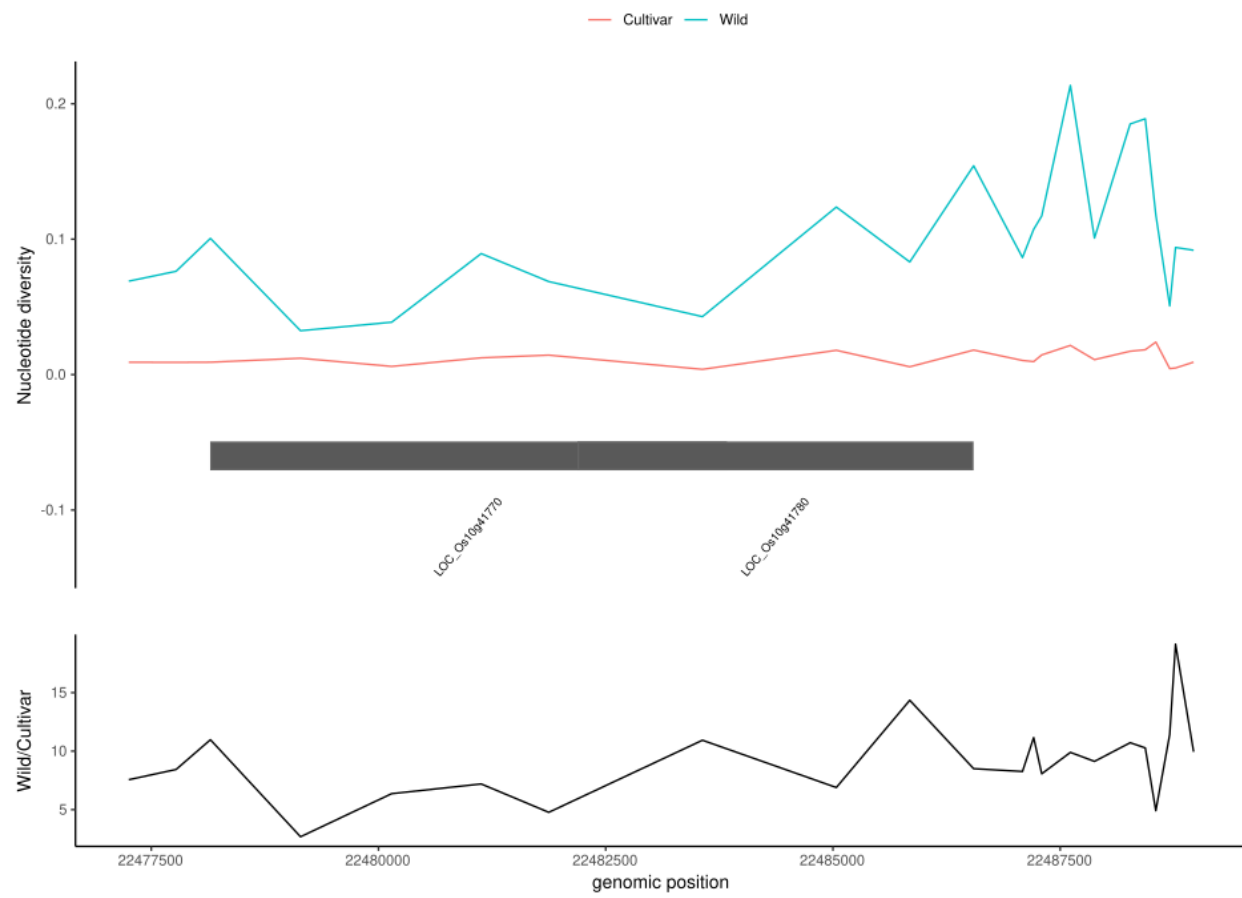
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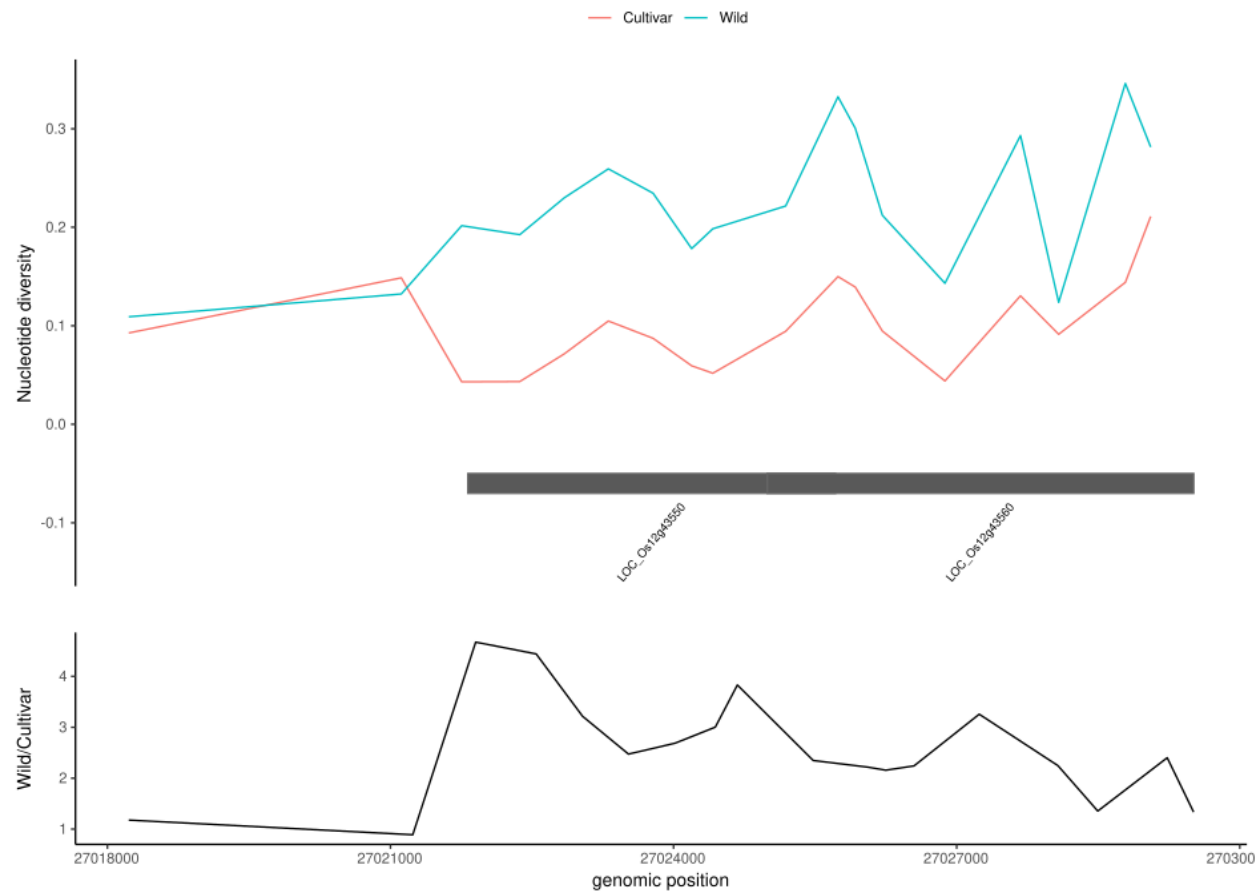
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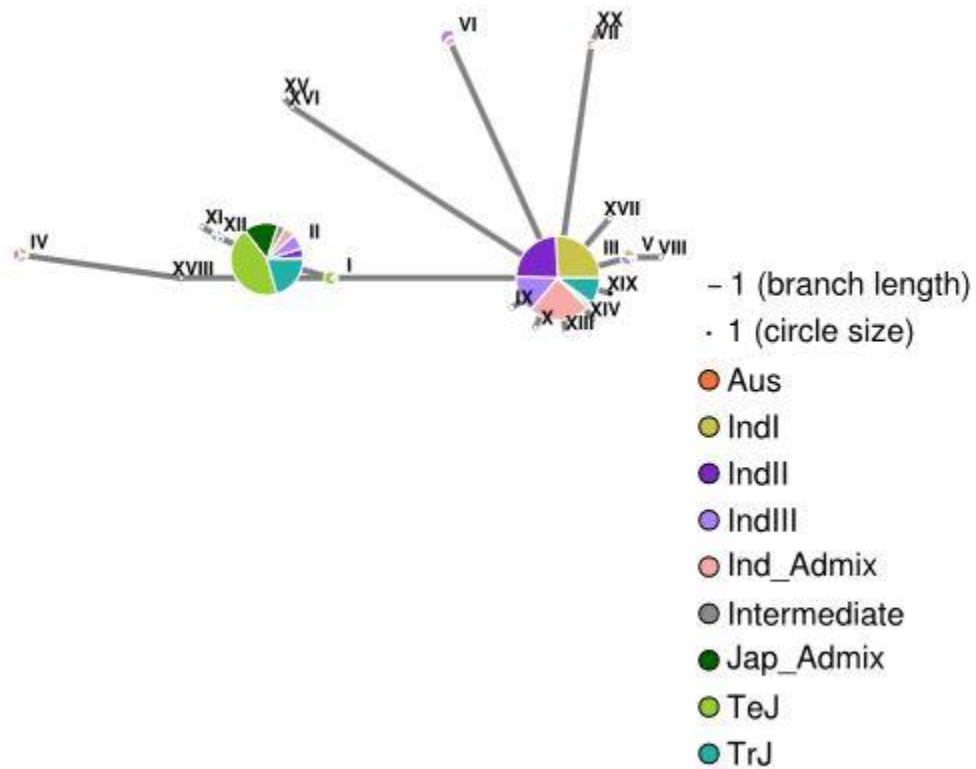
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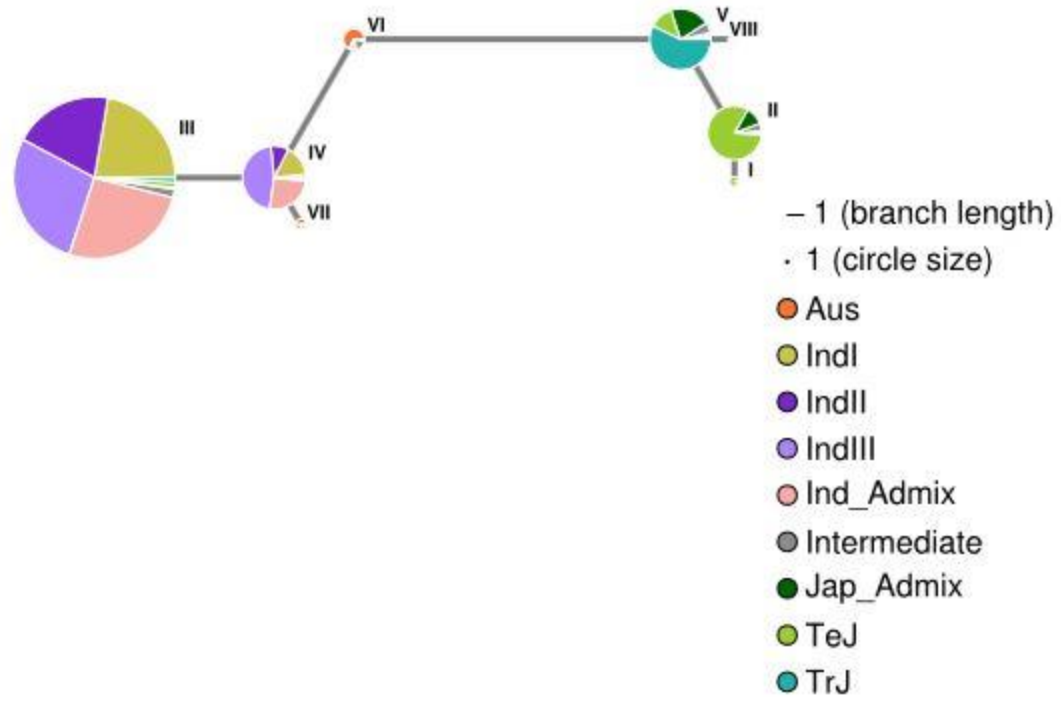


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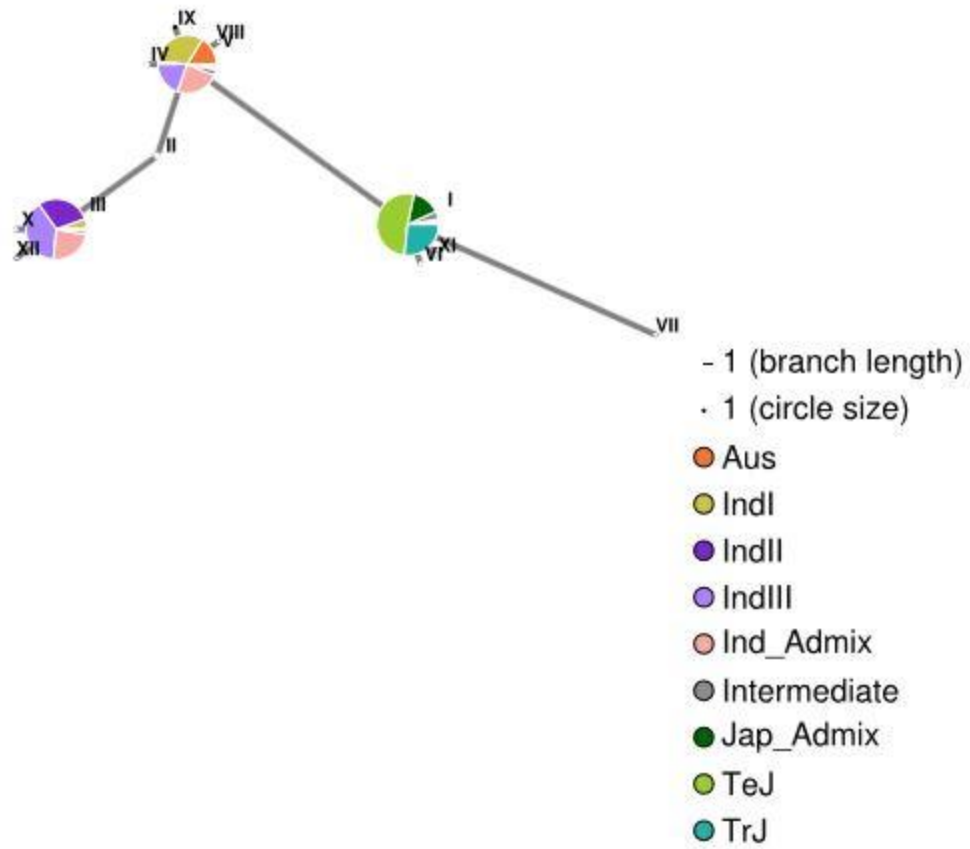
Supplementary Dataset 1. Haplotypic network of 80 nutritional and cooking quality related genes depicting number of haplotypes and their interactions with different rice types

(Os08g0424500)

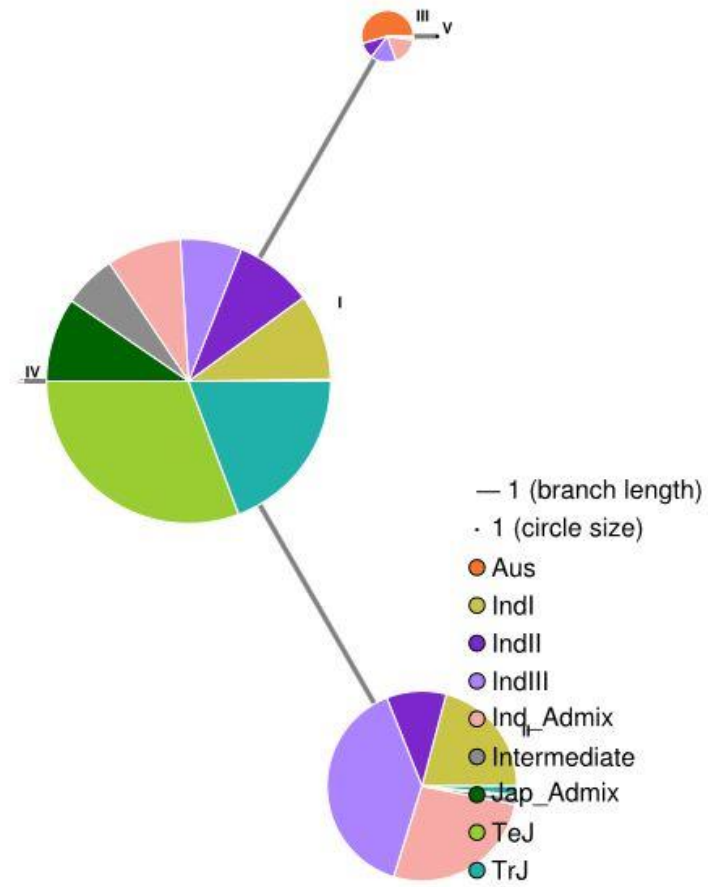




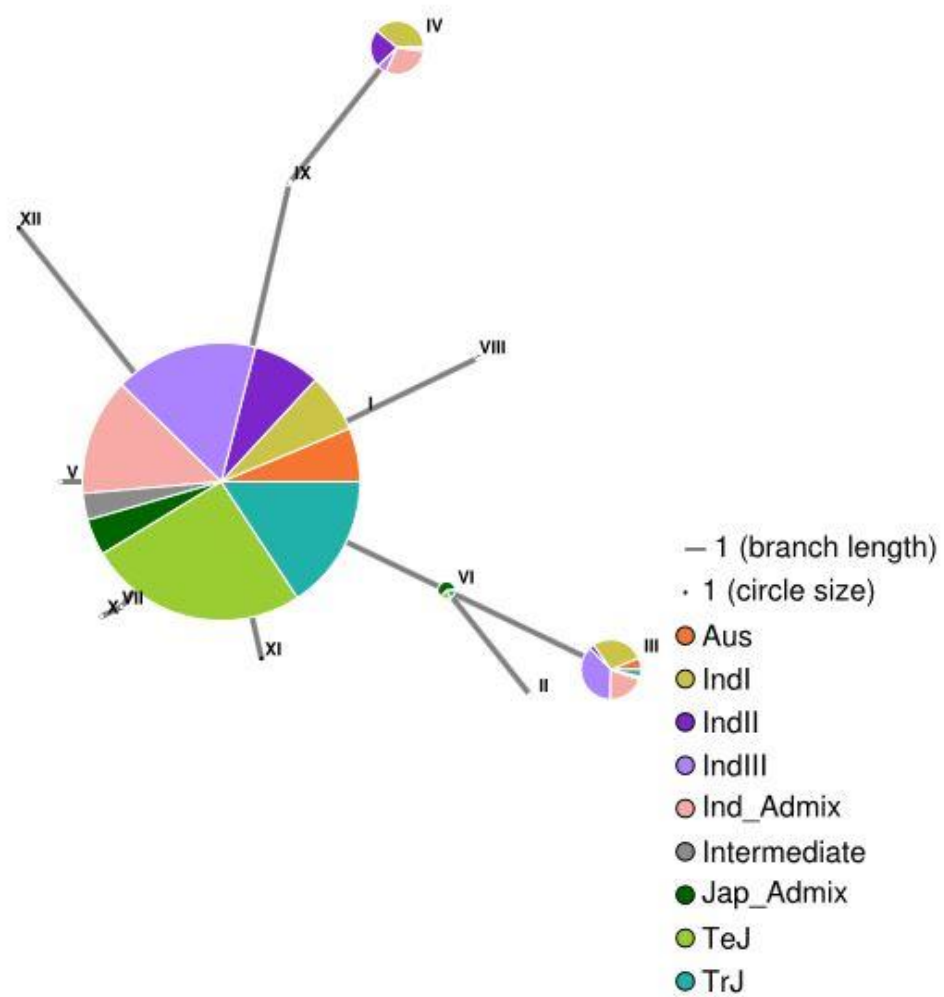
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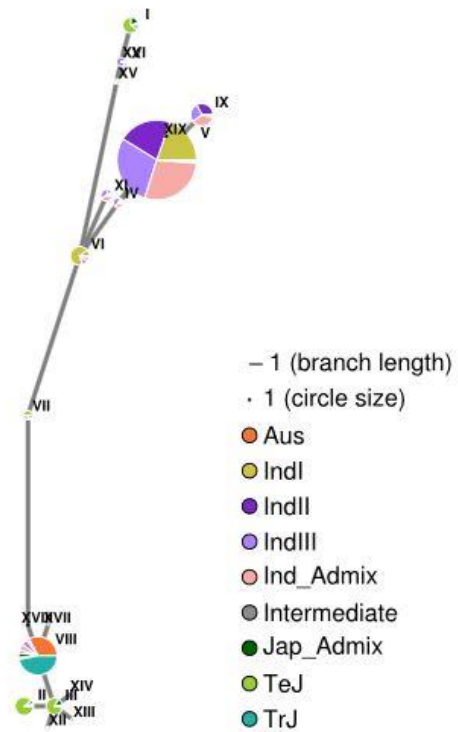
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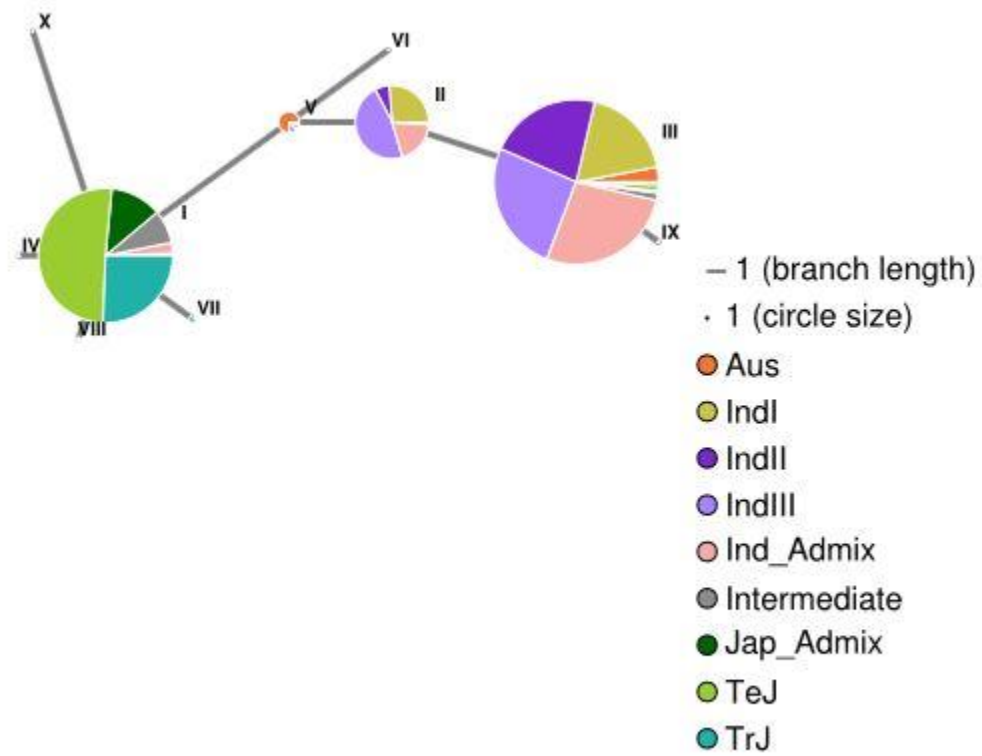
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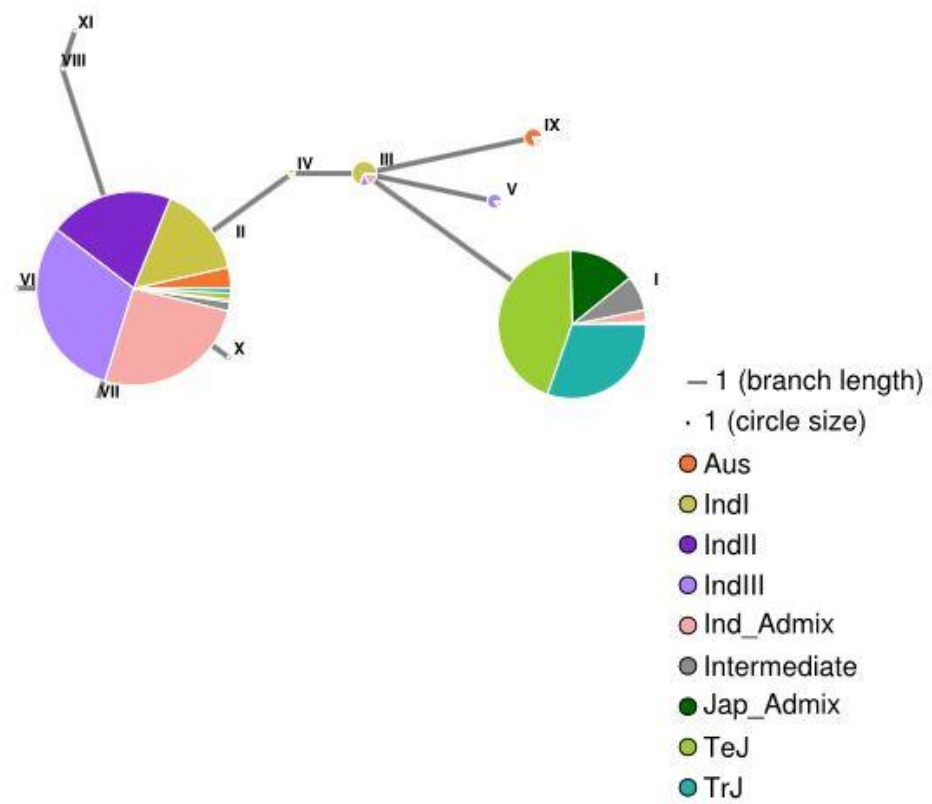
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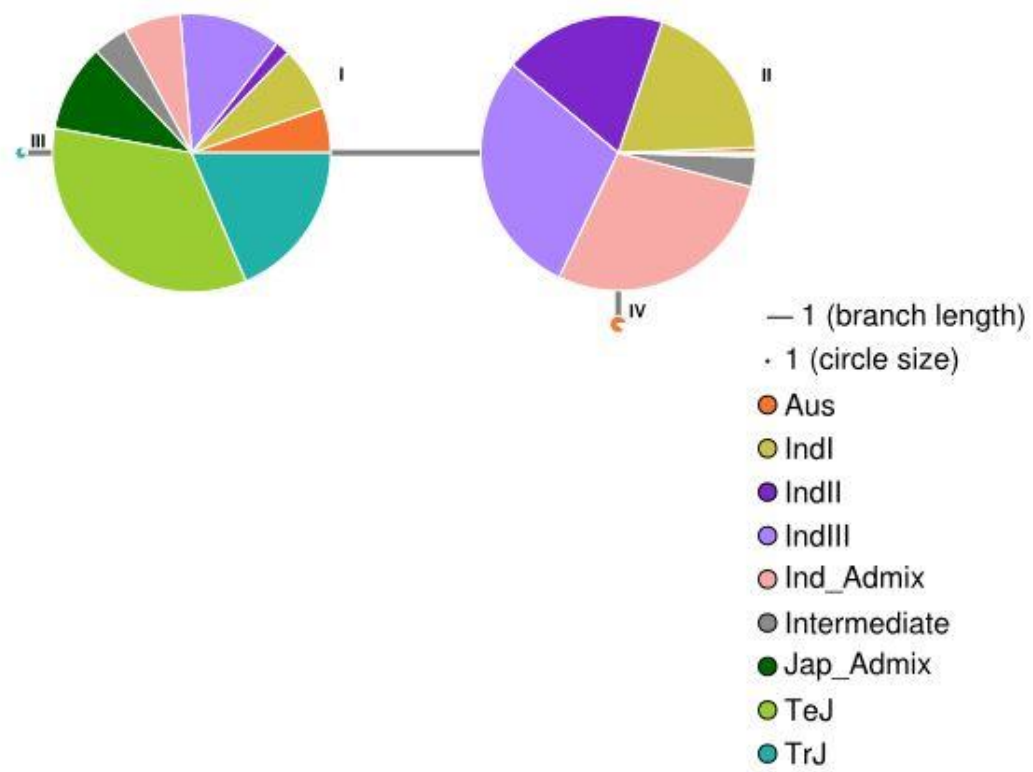
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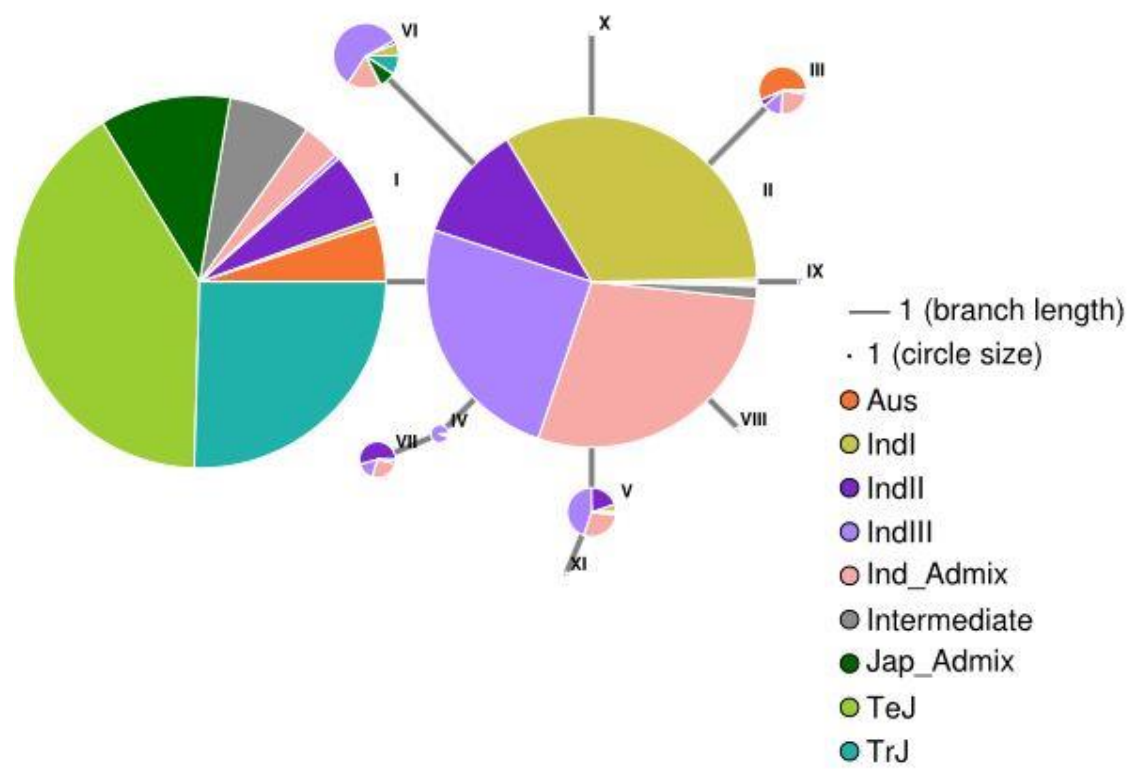
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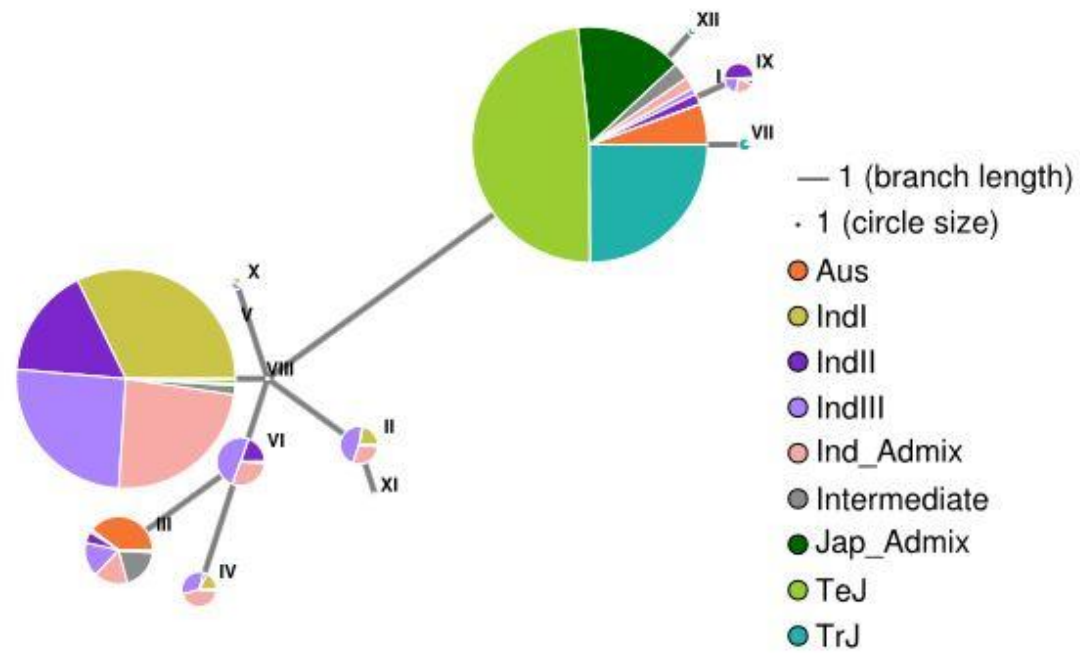
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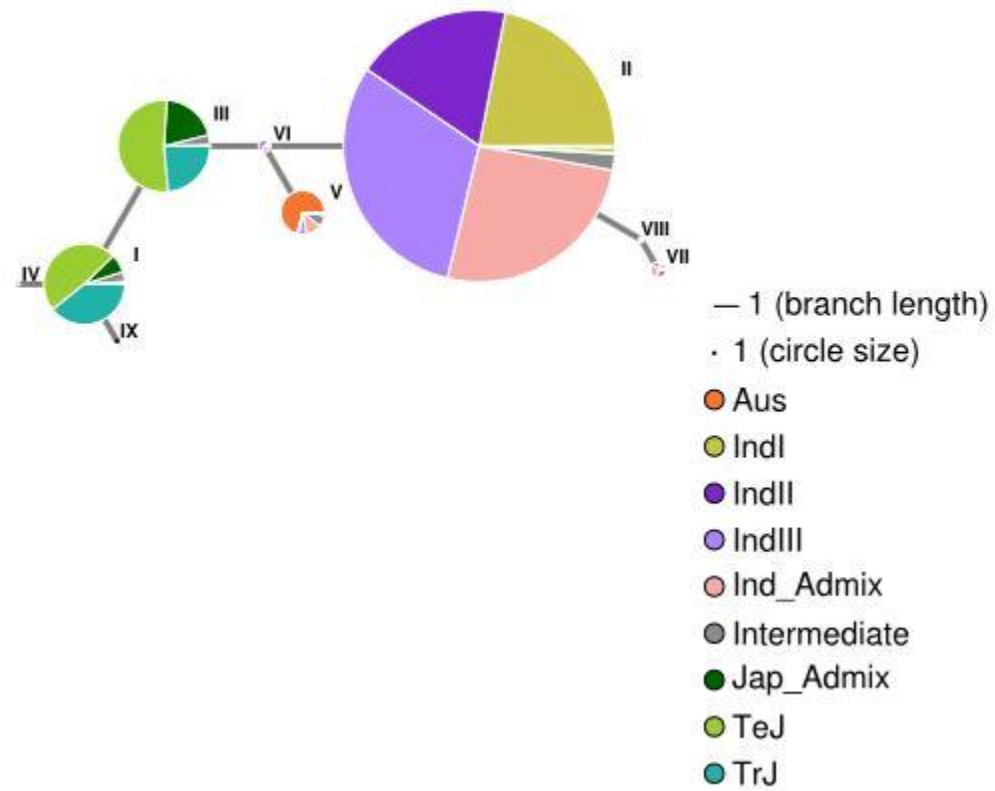
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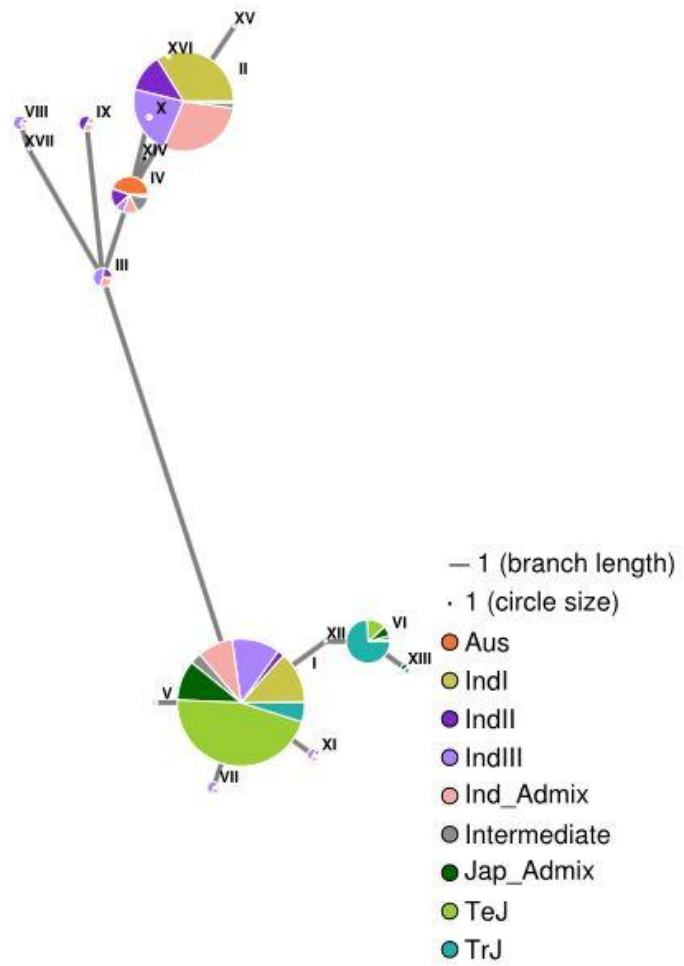
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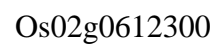
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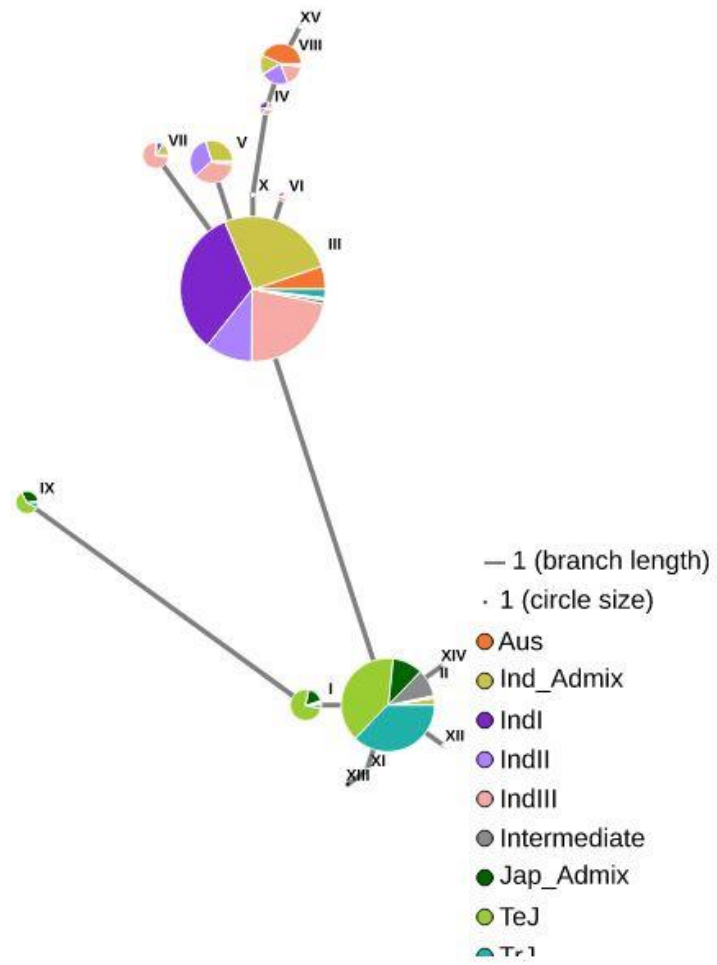


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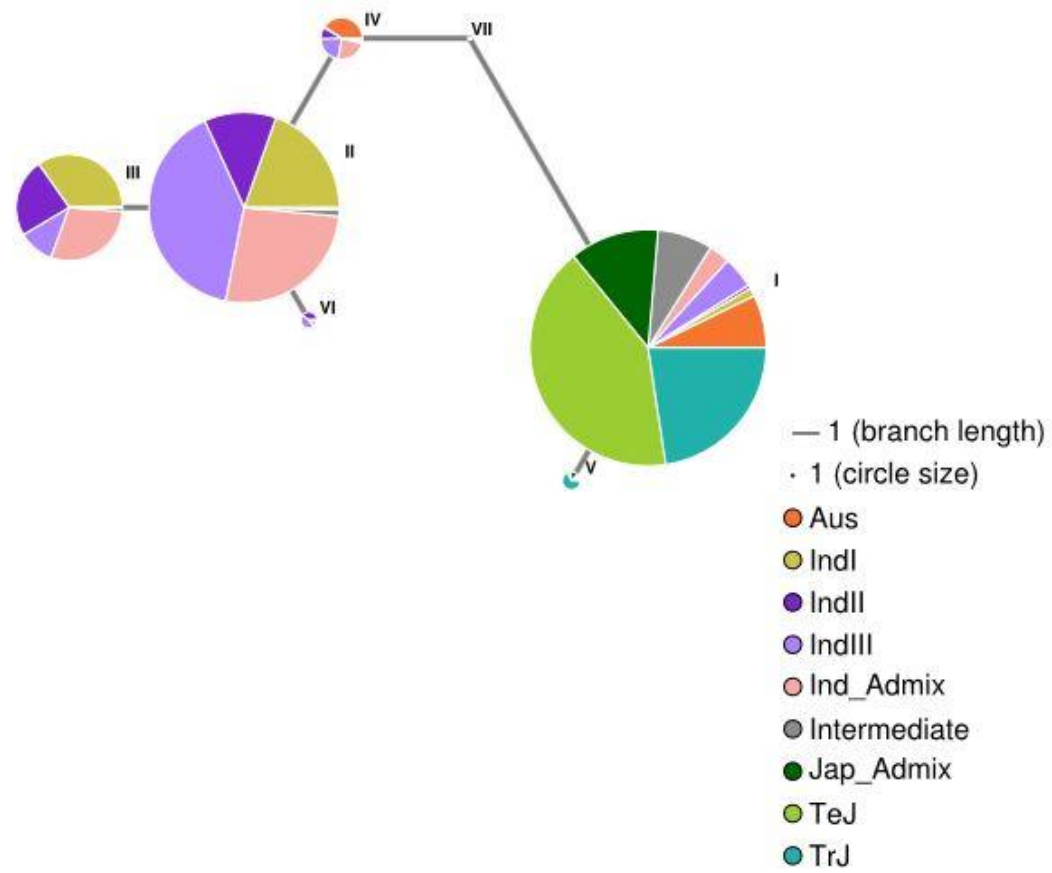


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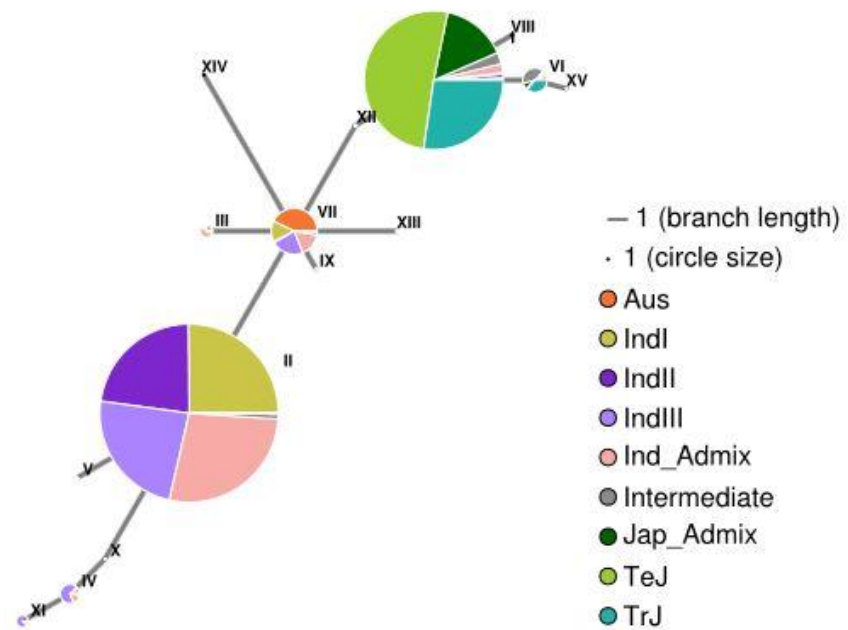




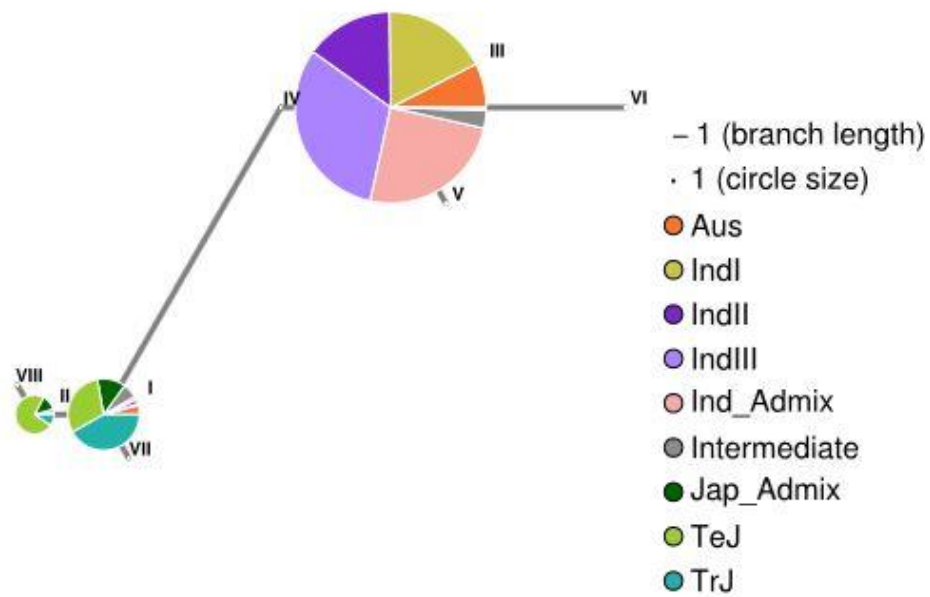
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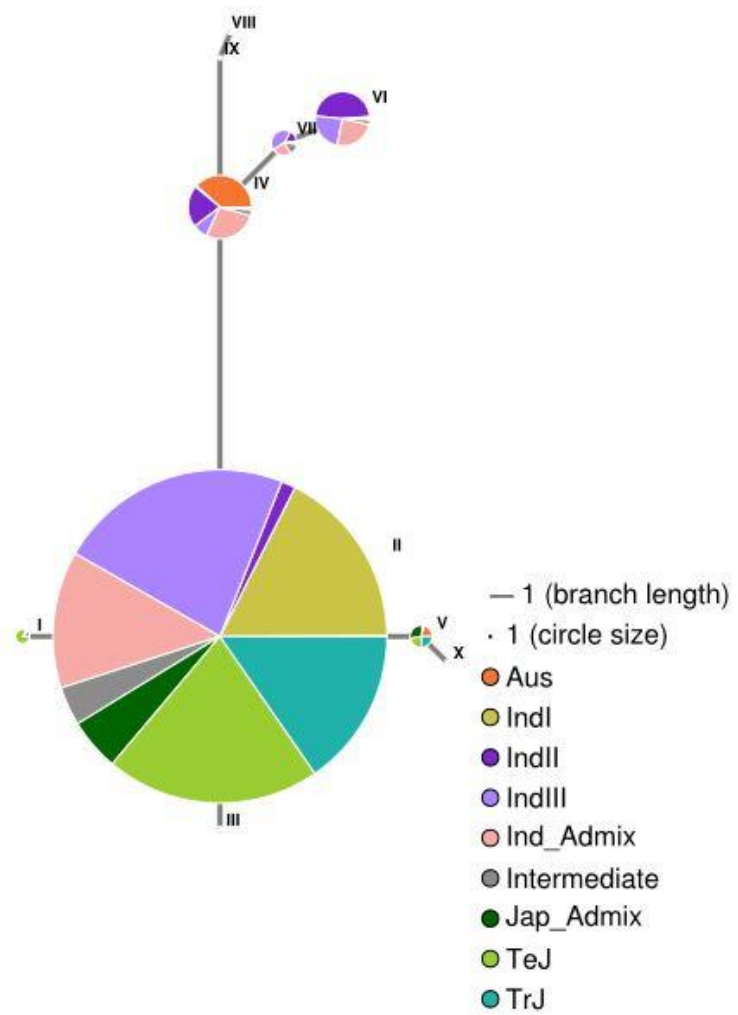
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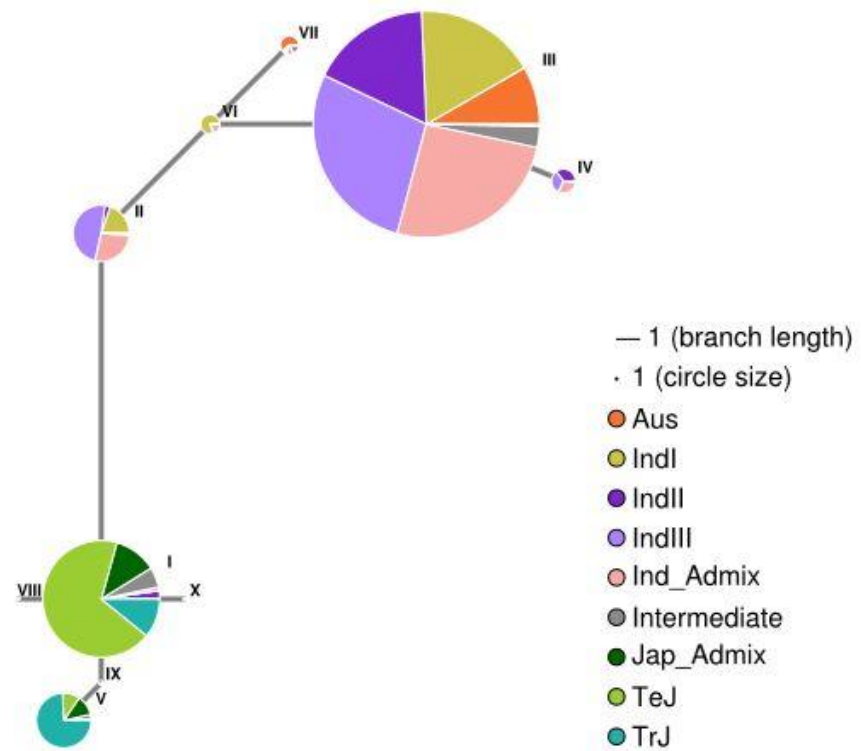
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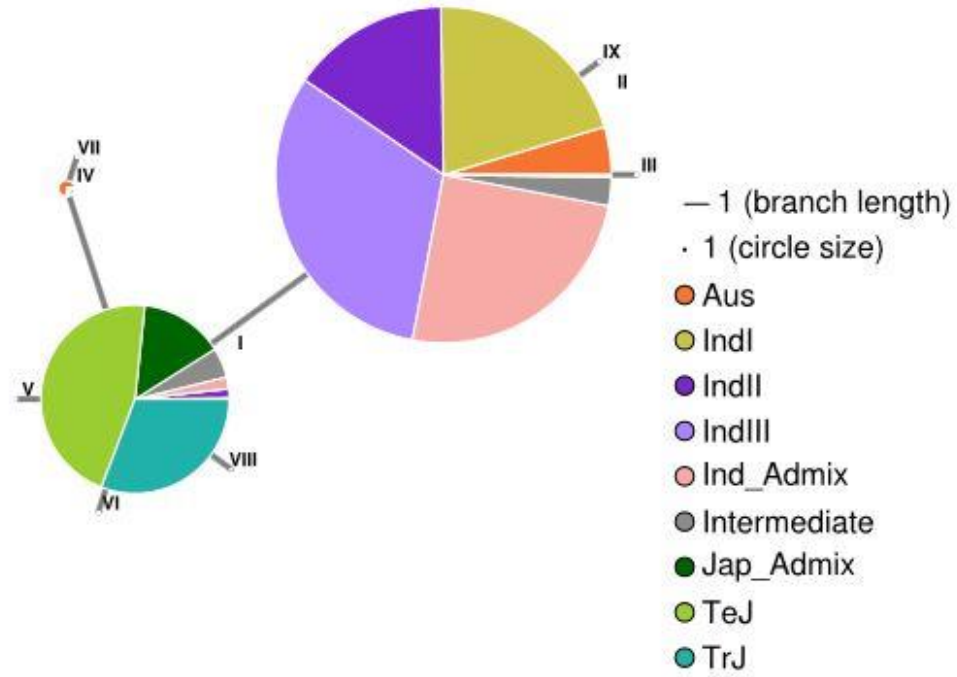
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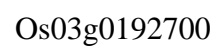
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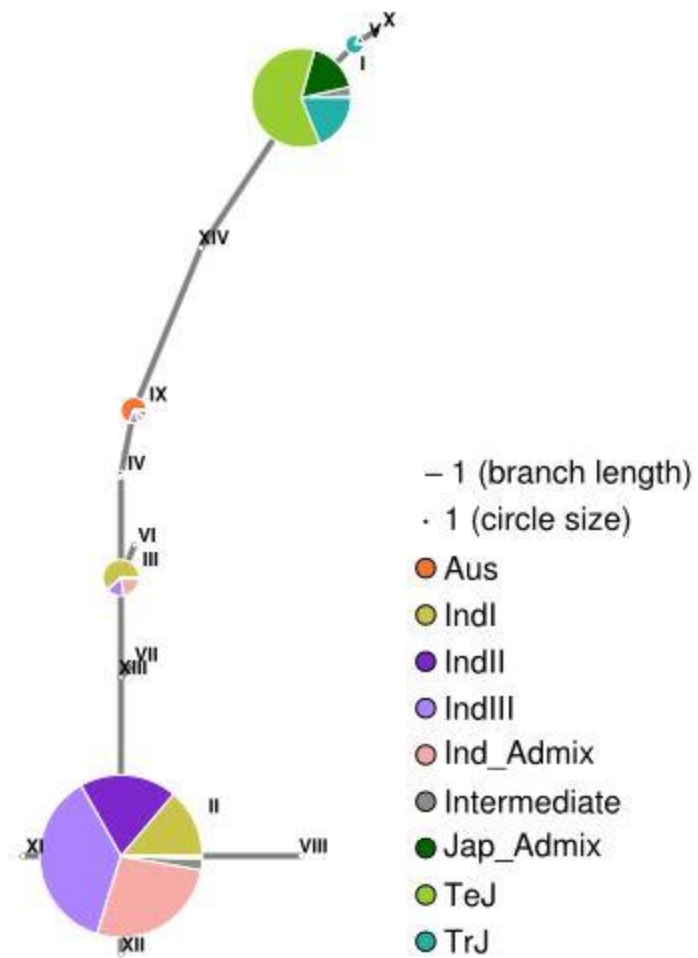
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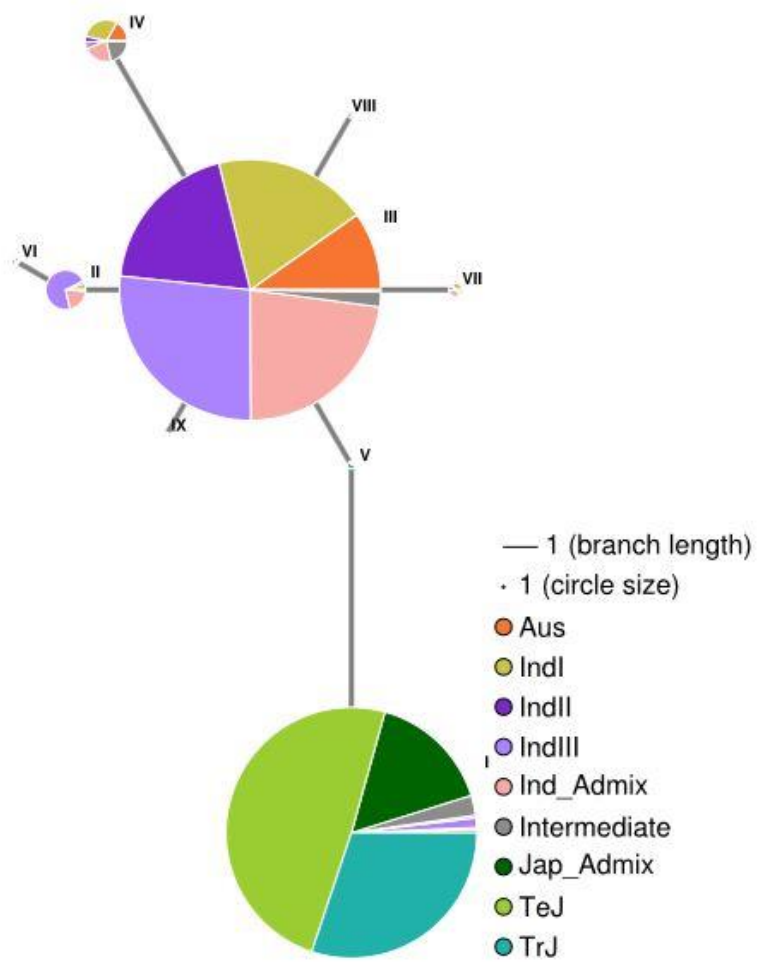
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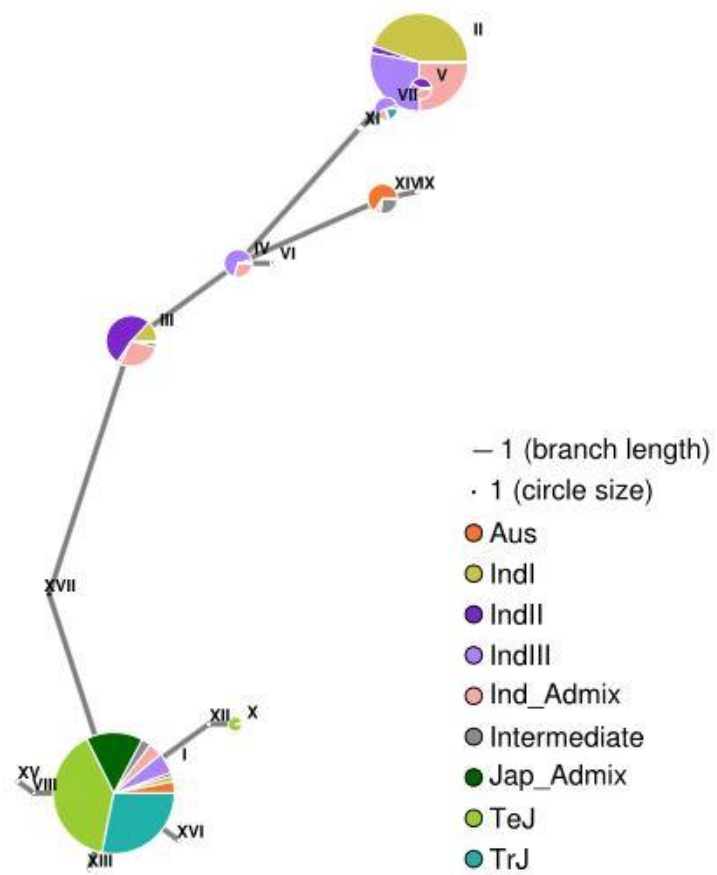
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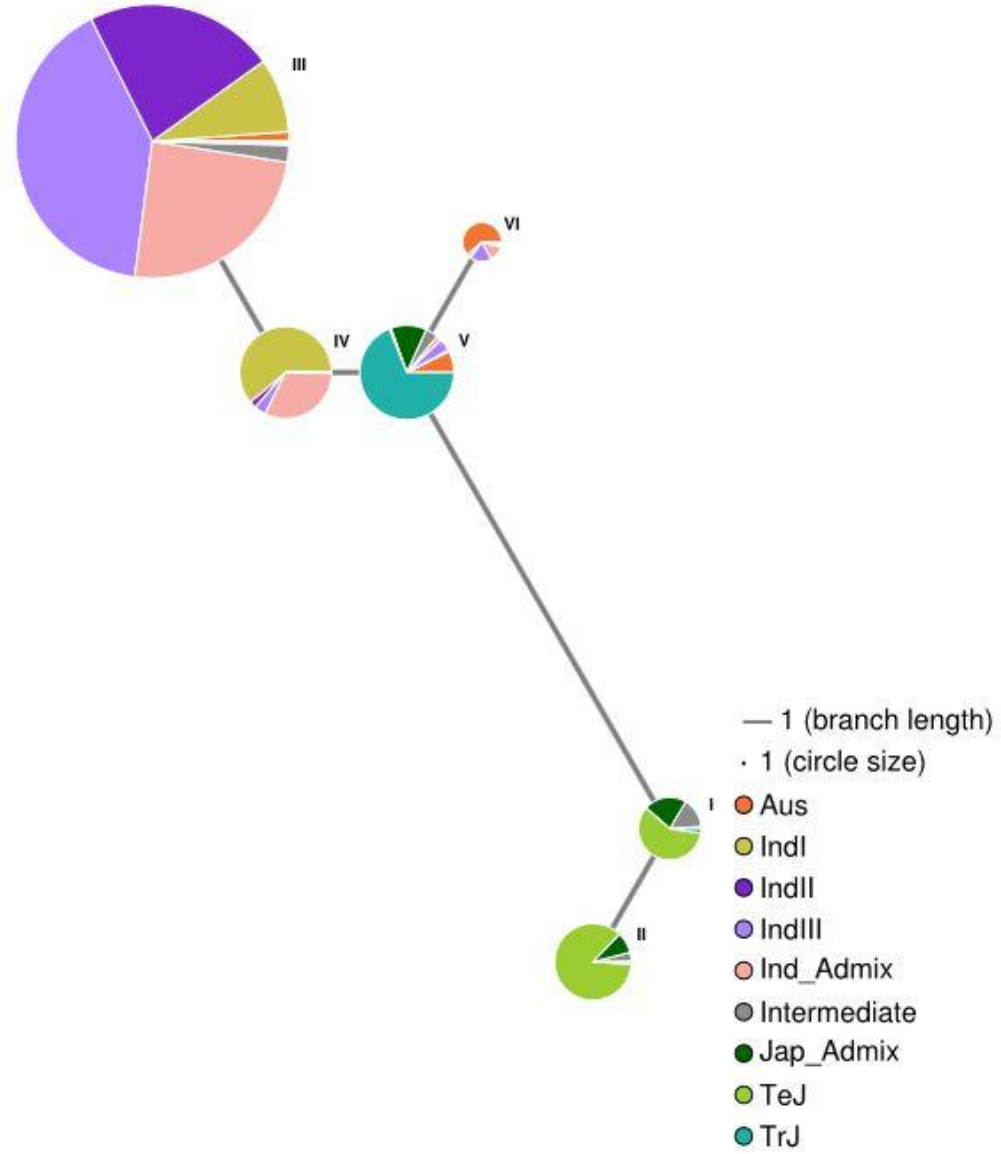
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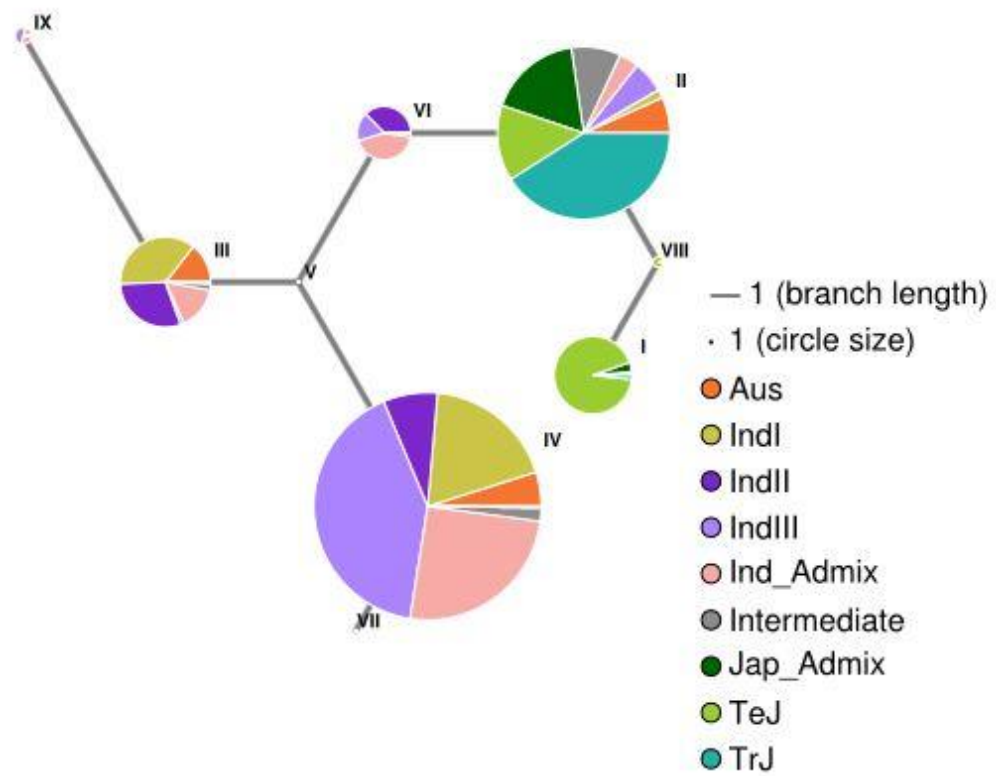
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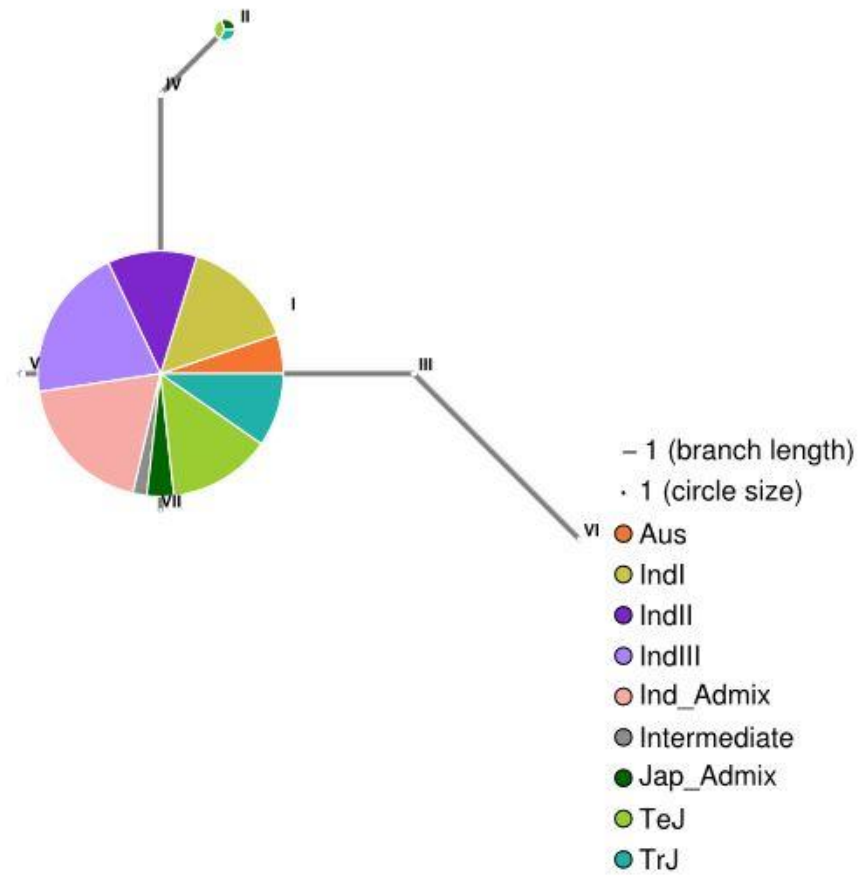
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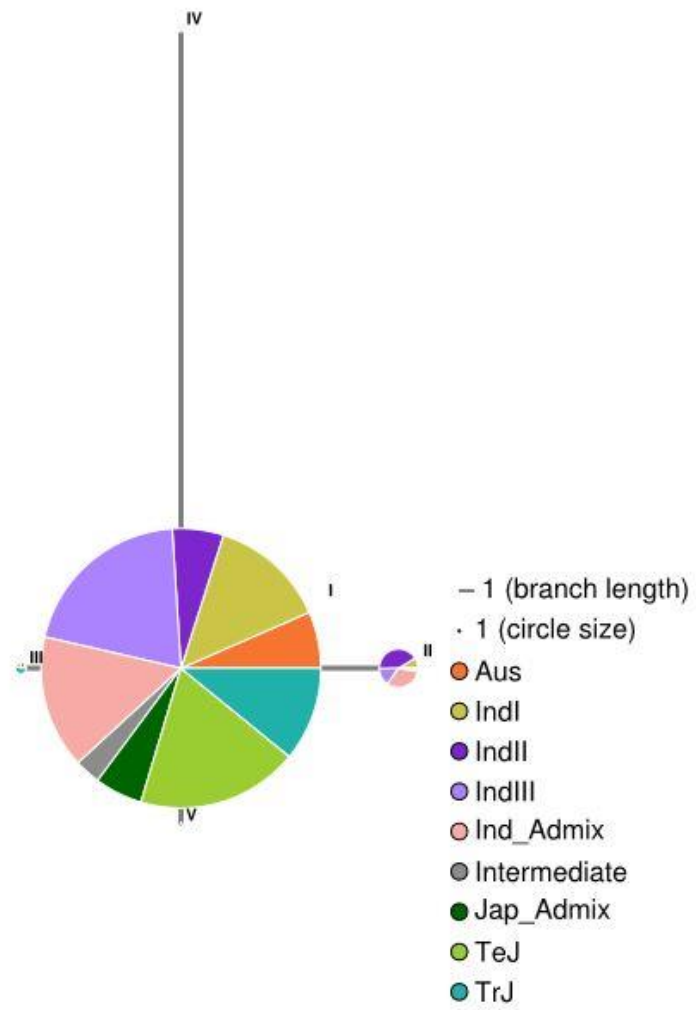
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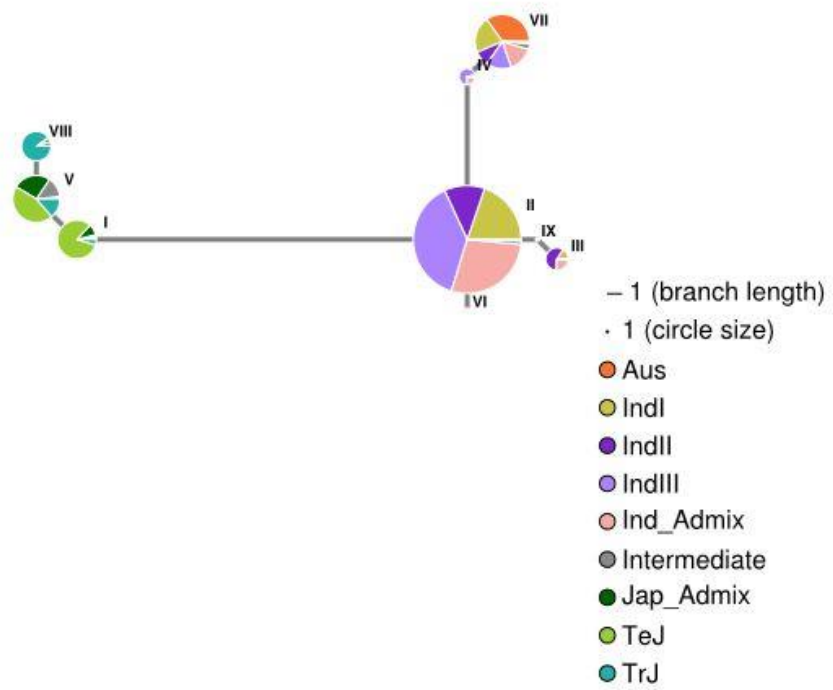
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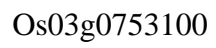
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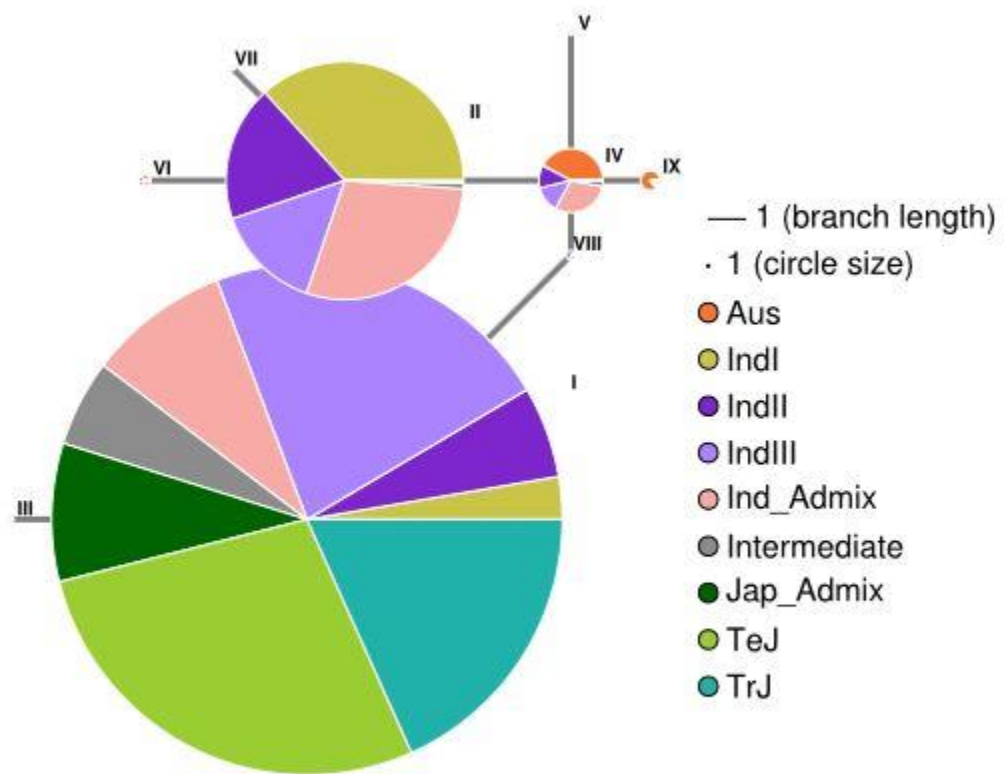
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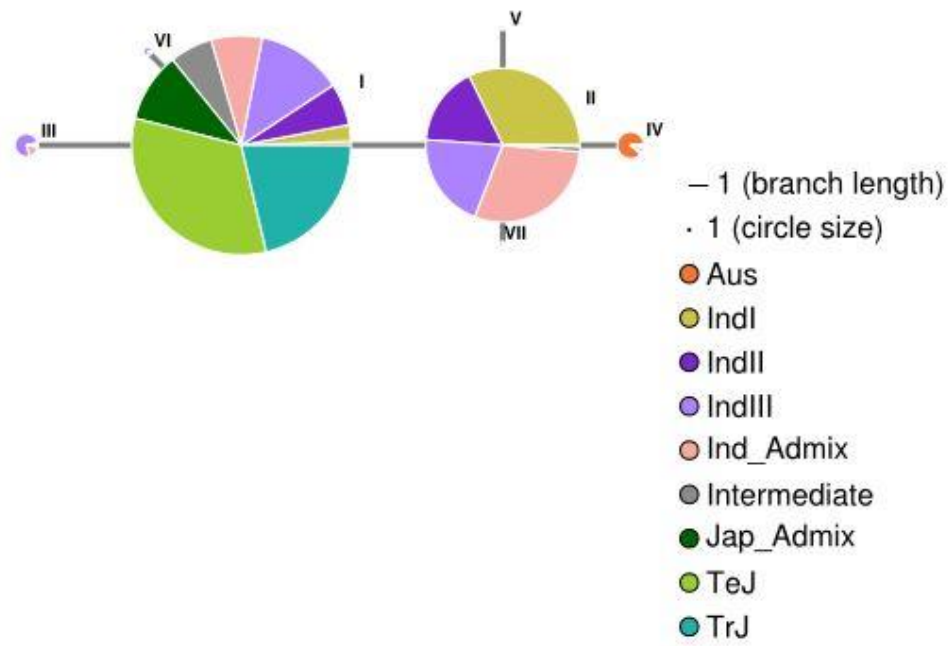
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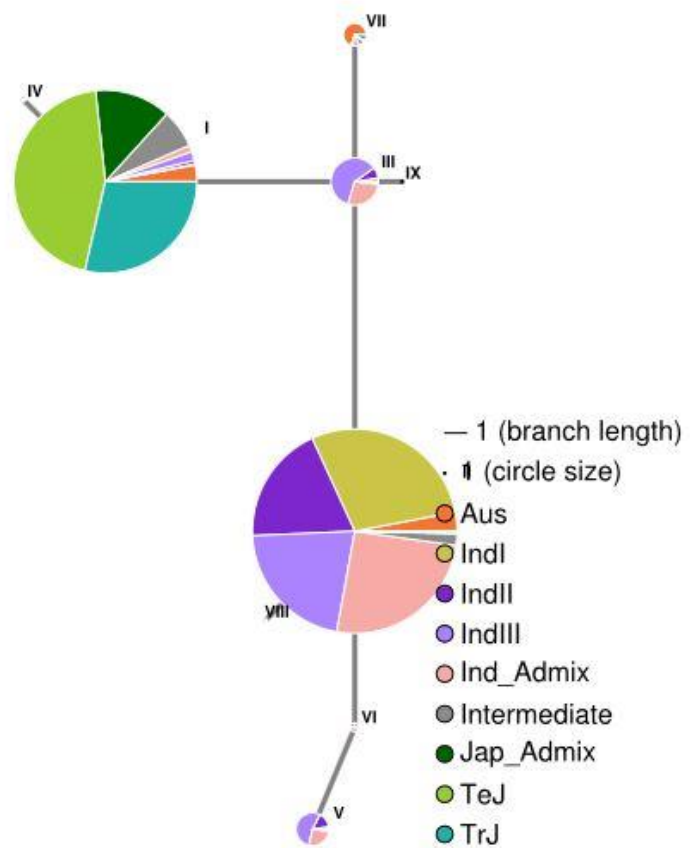
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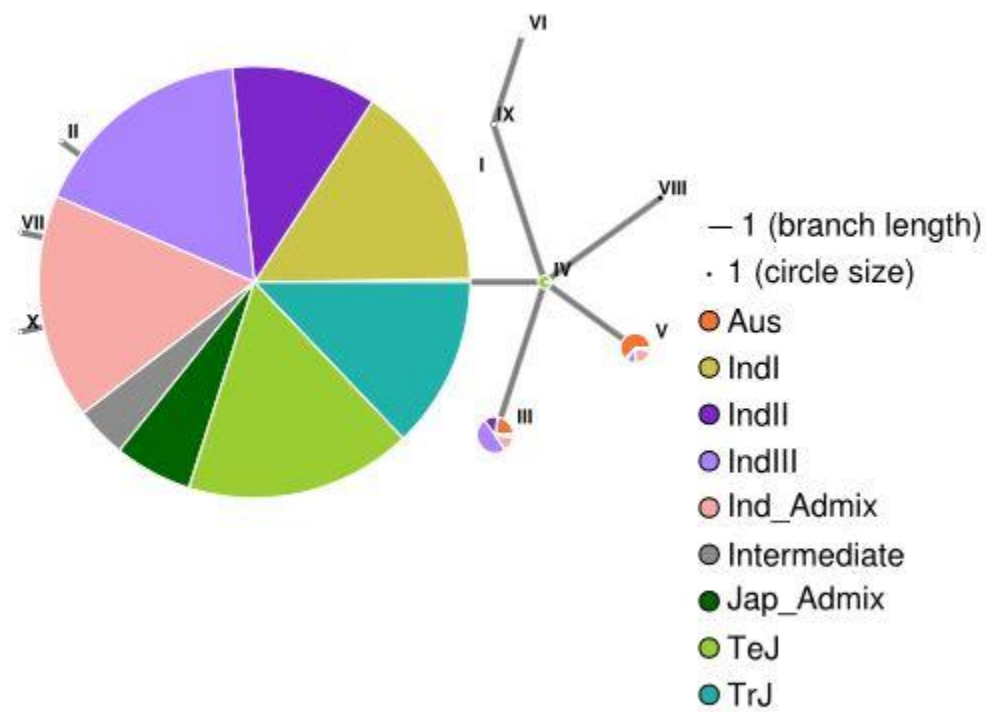
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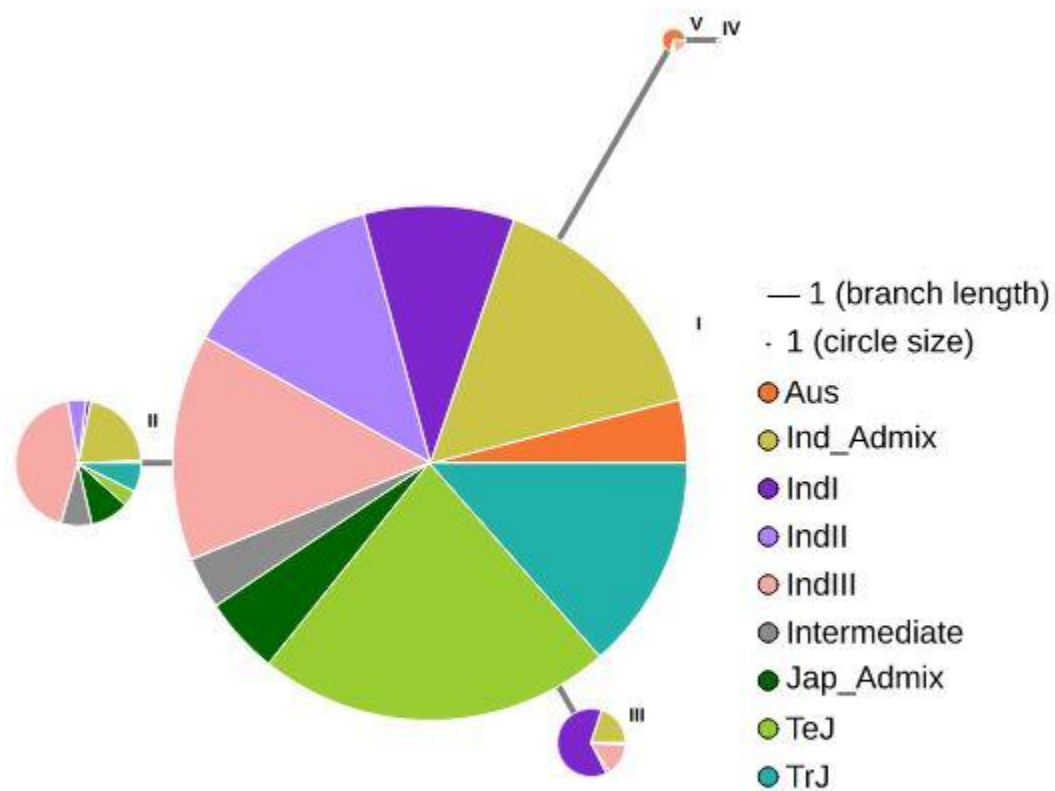
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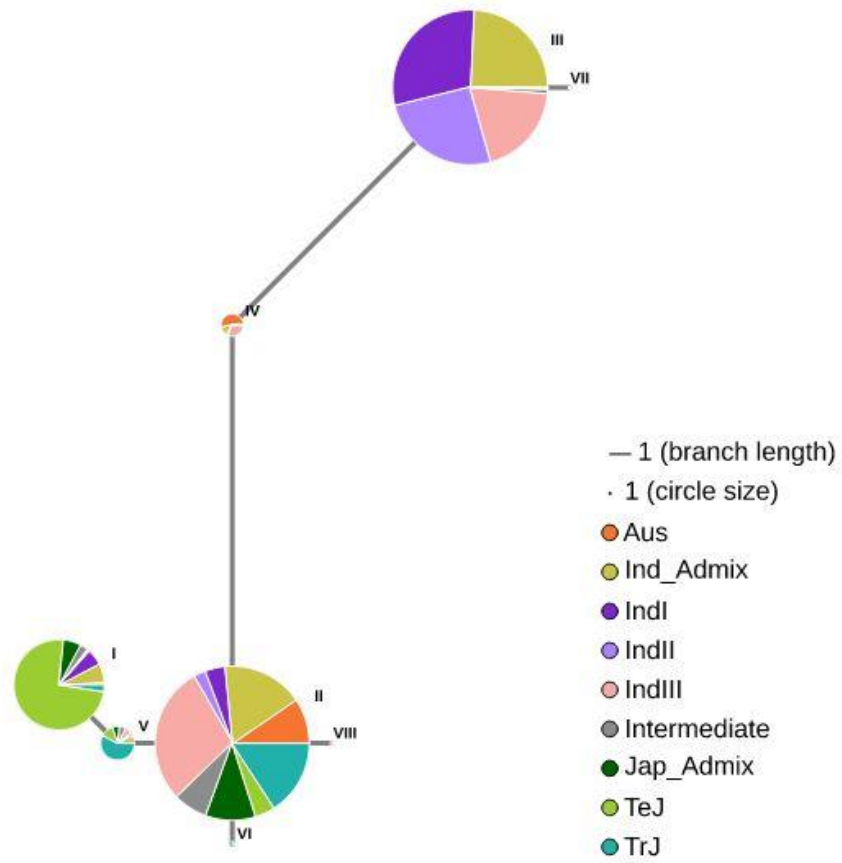
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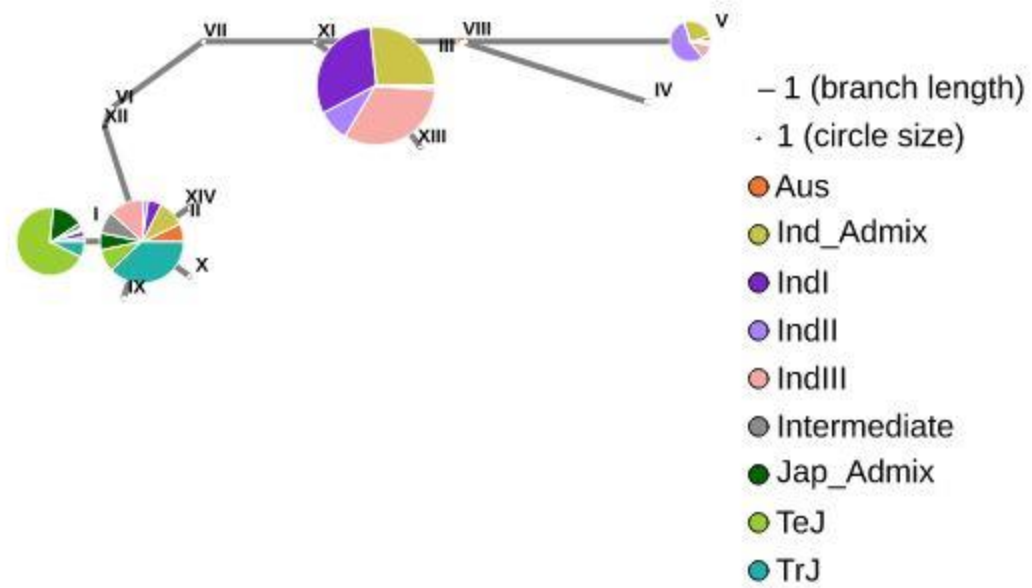
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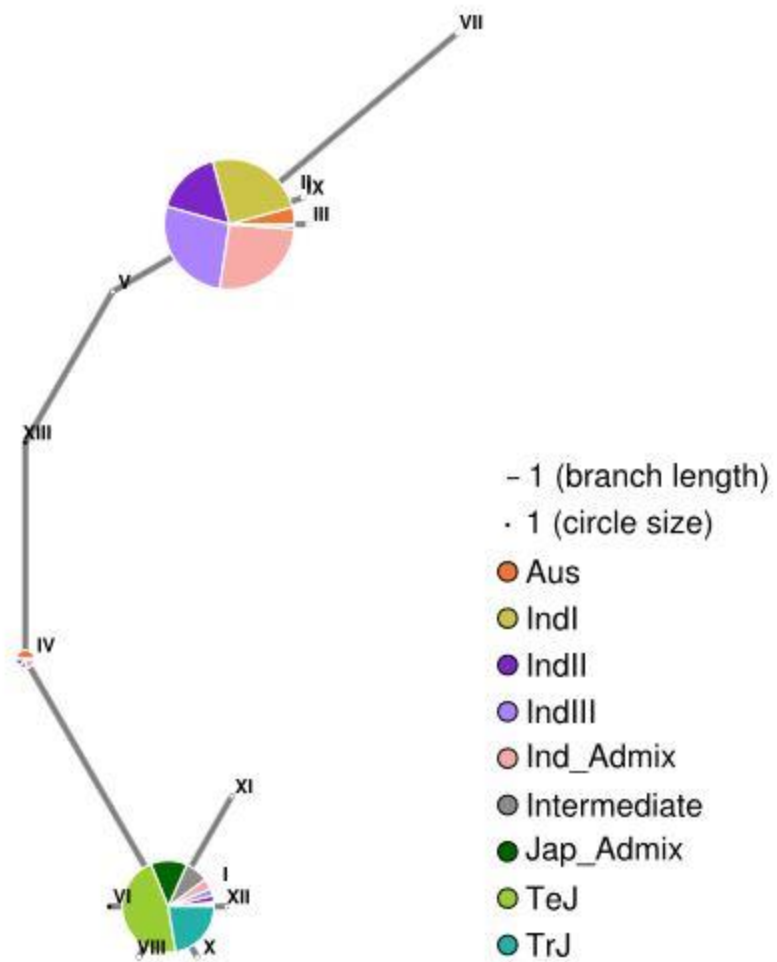
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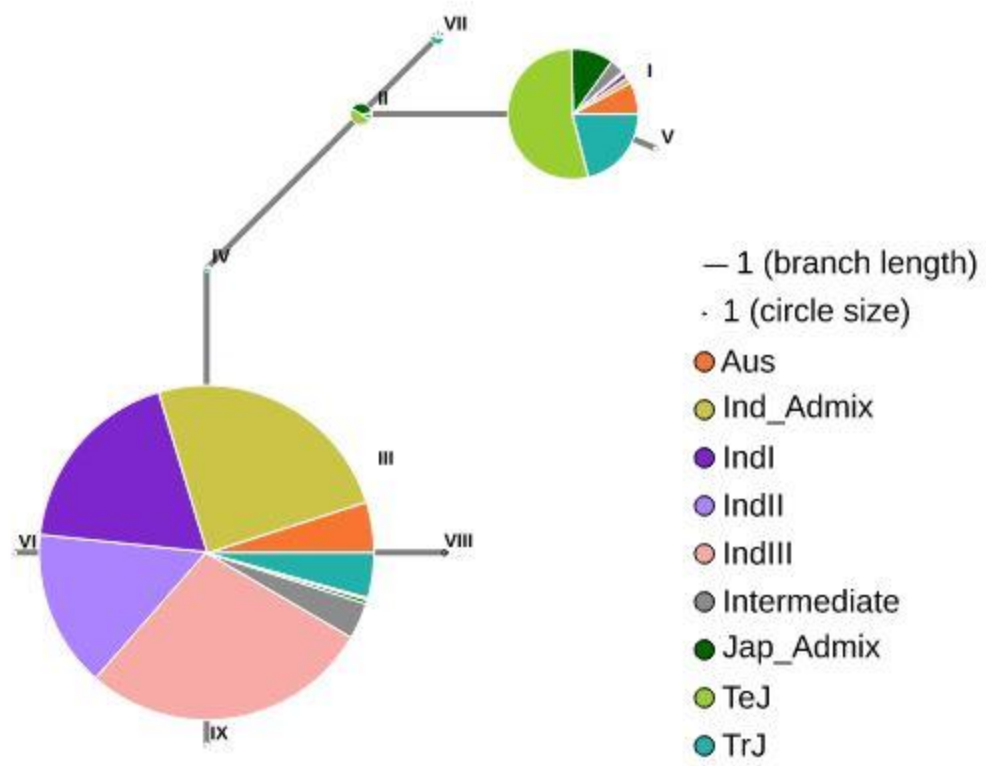
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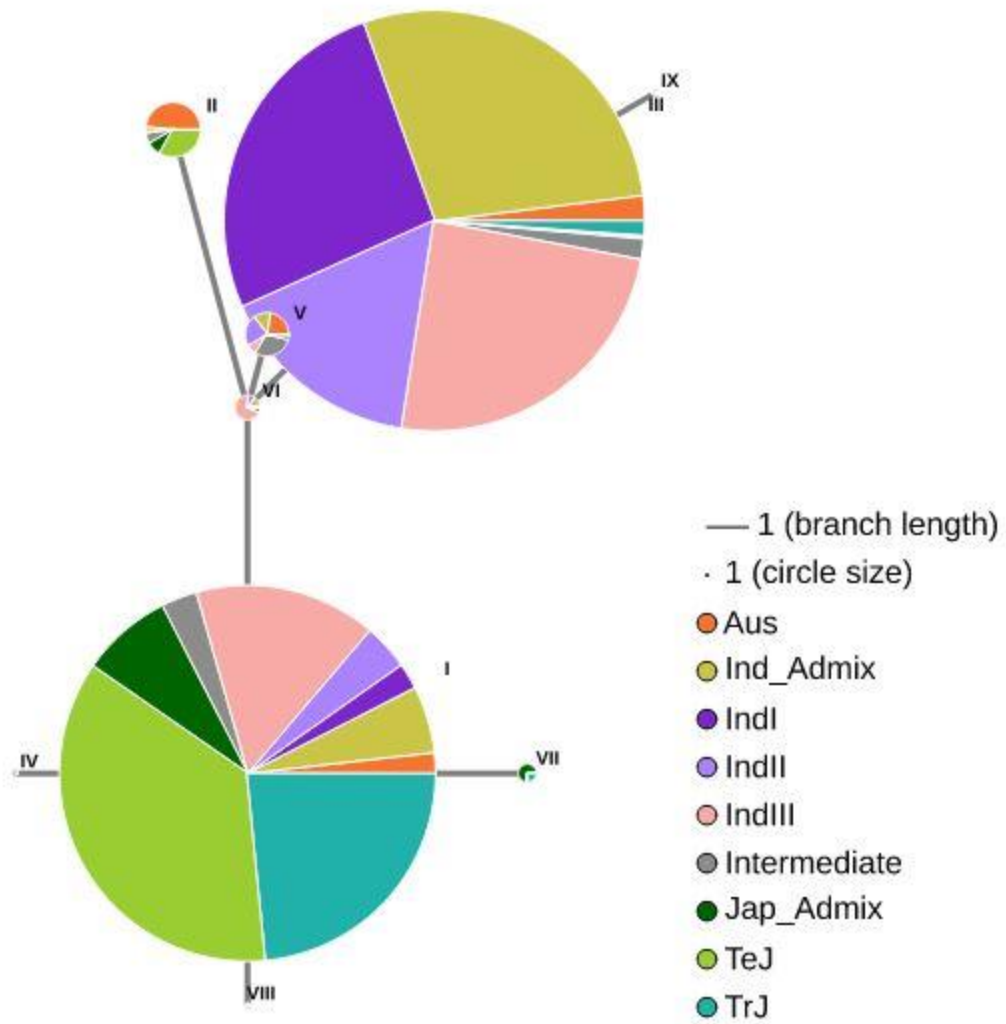
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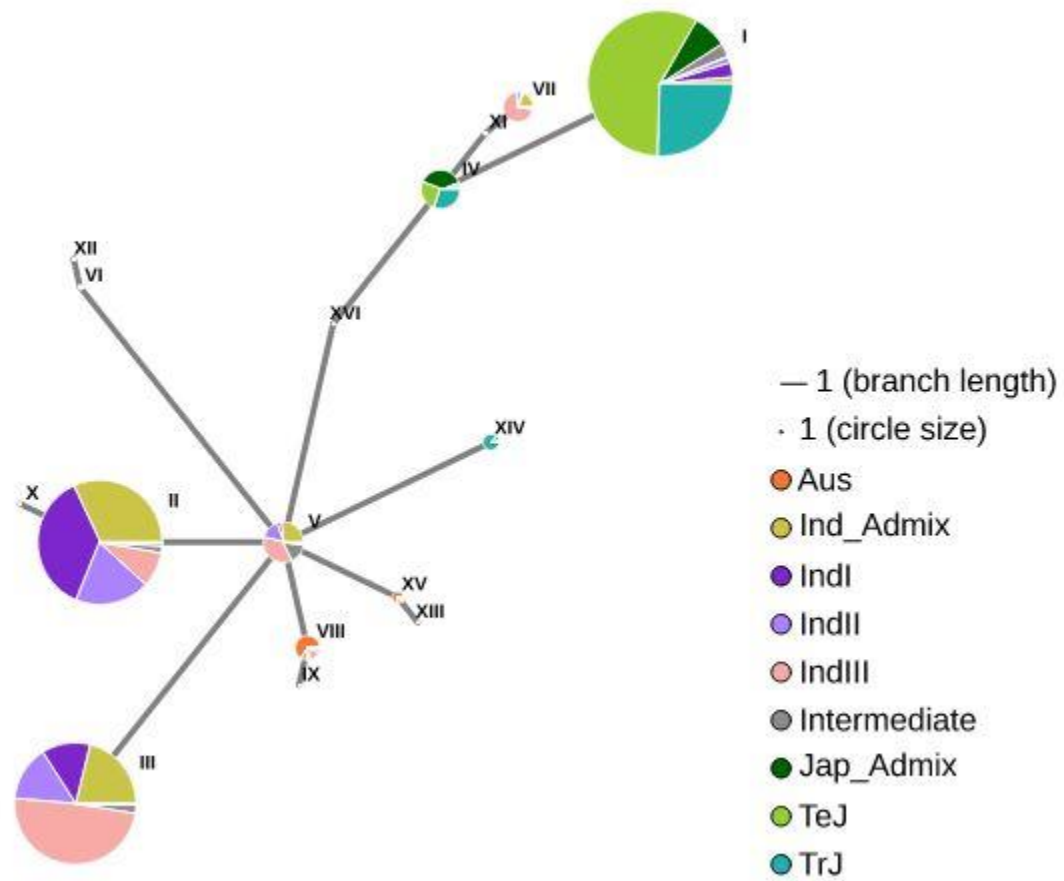
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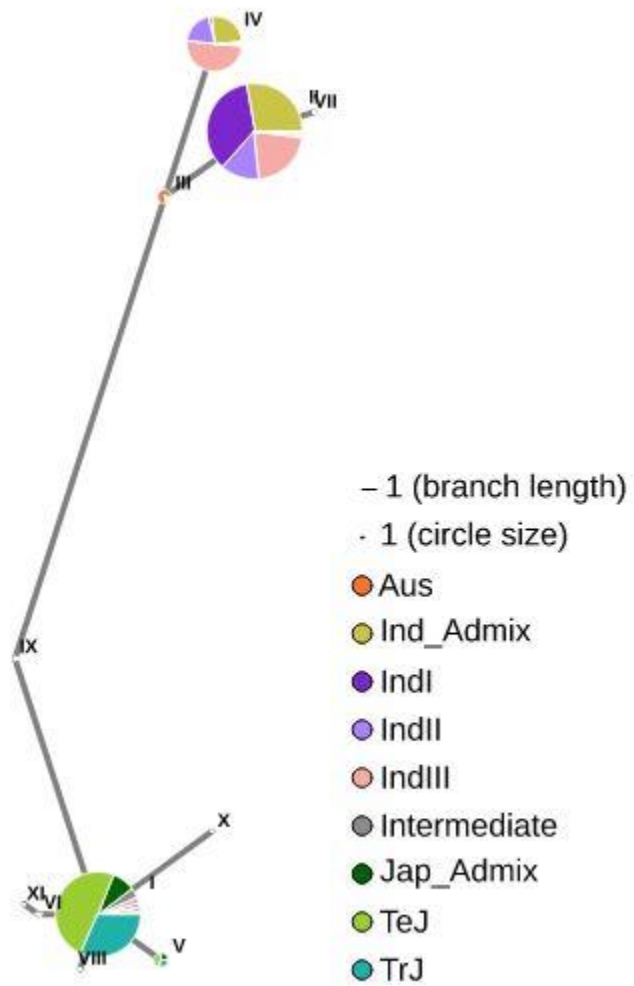
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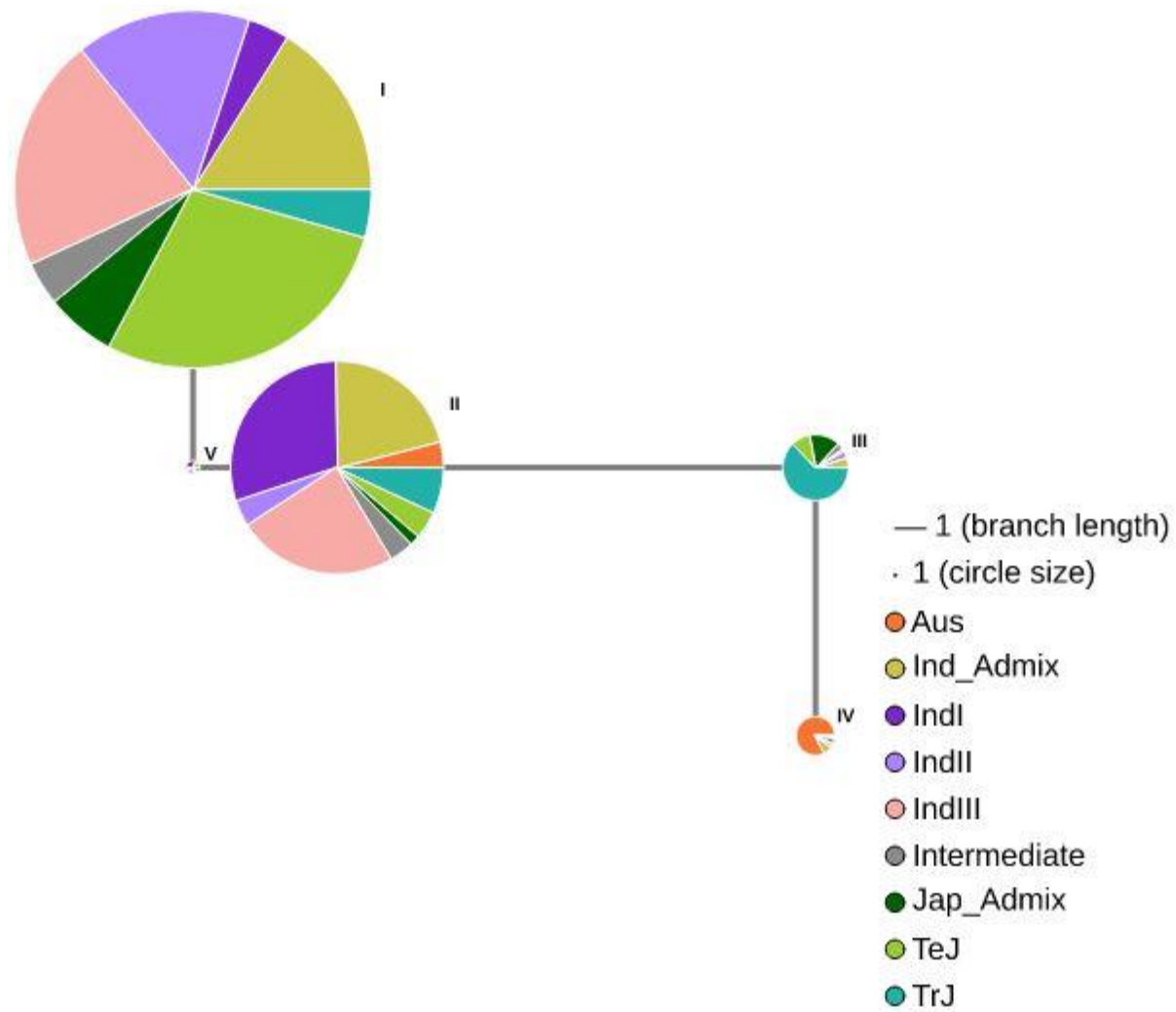
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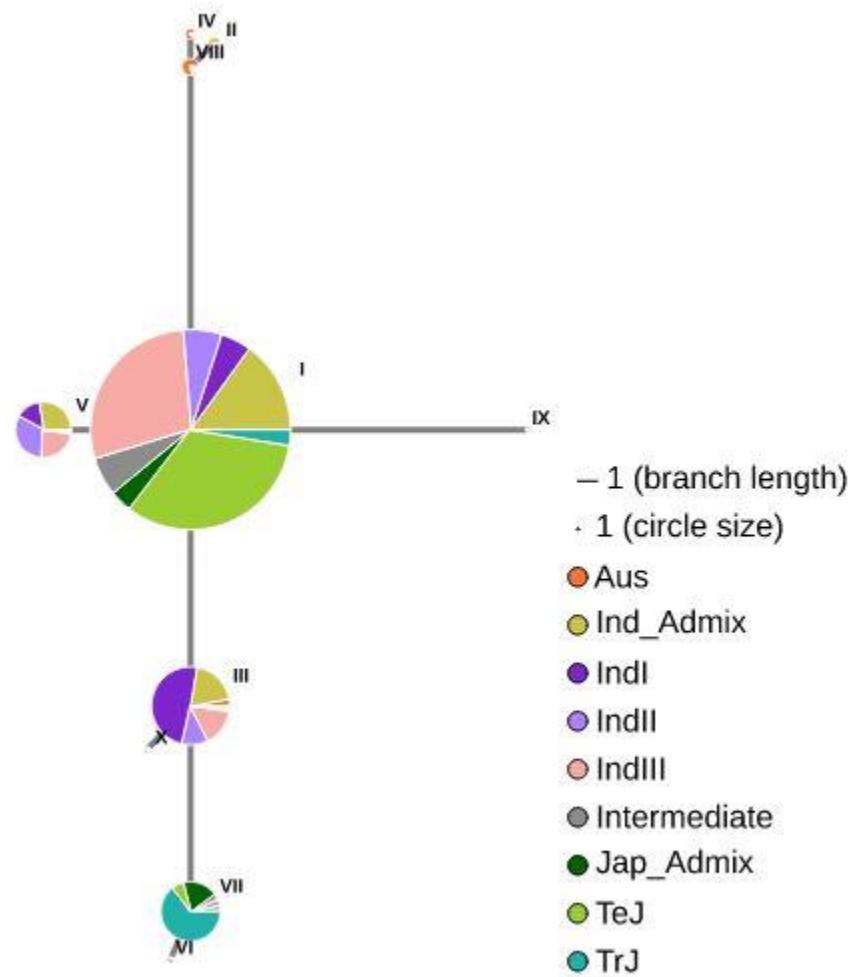
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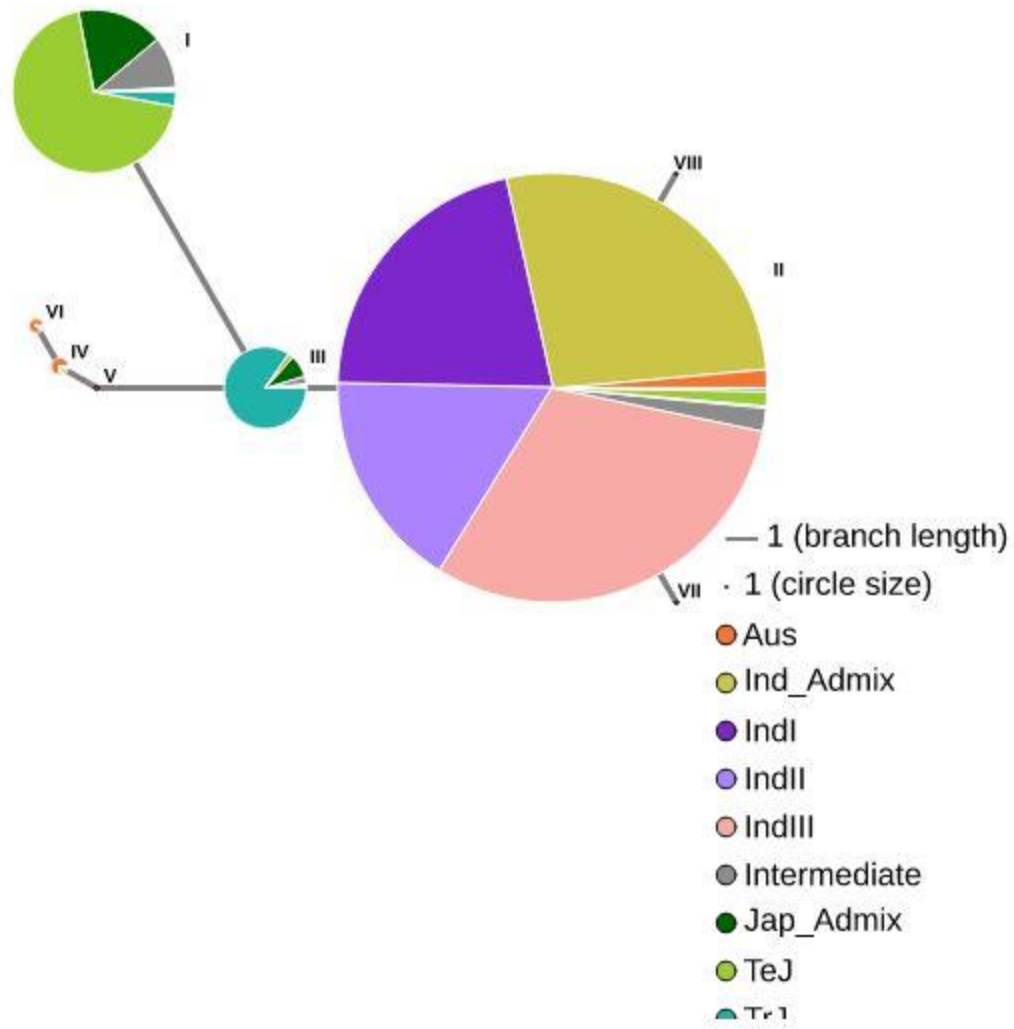
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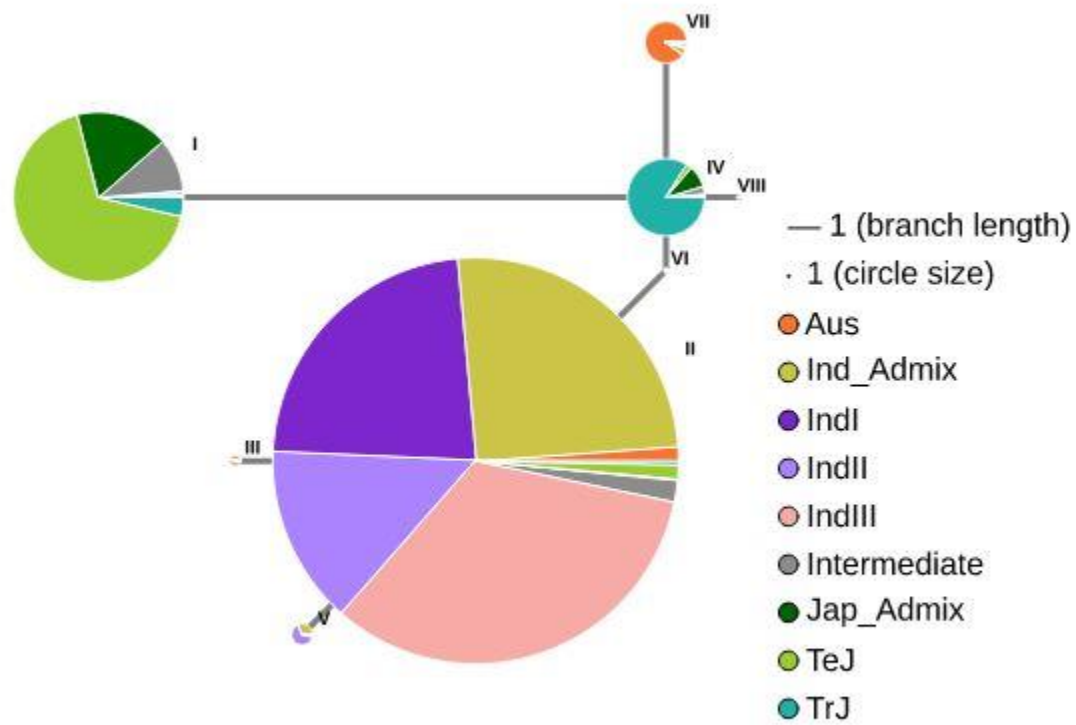
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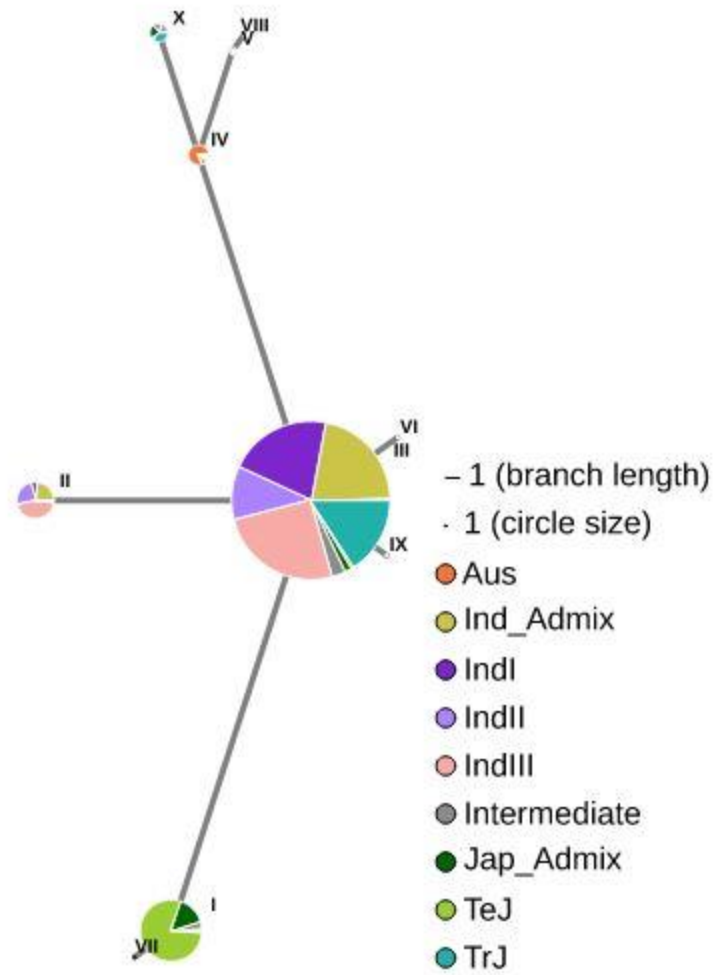
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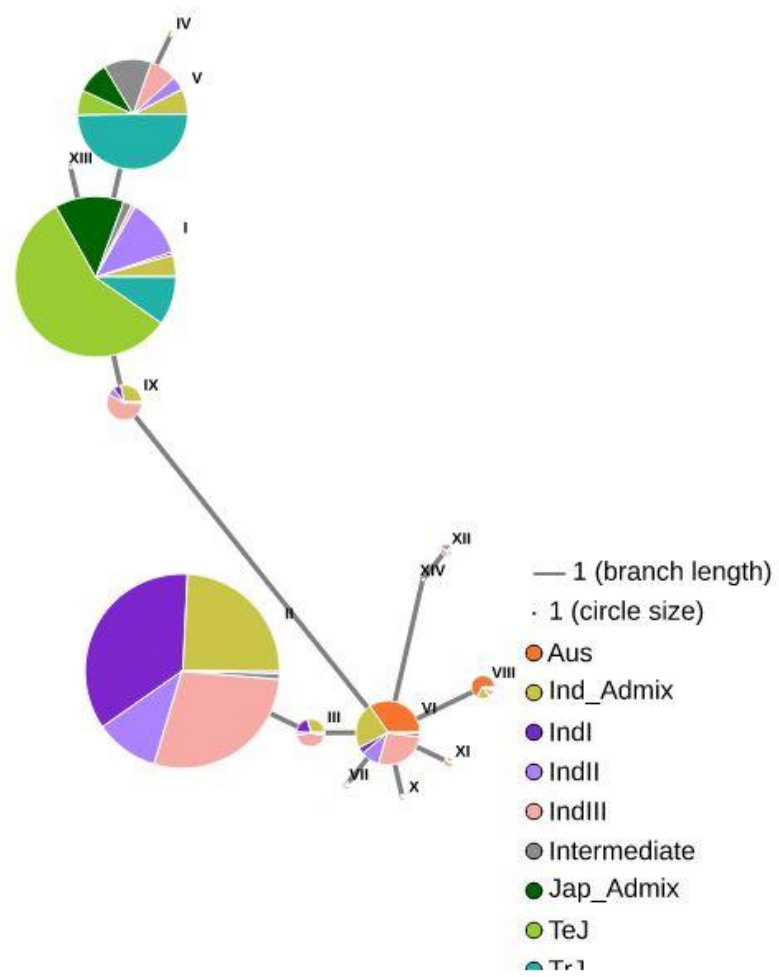
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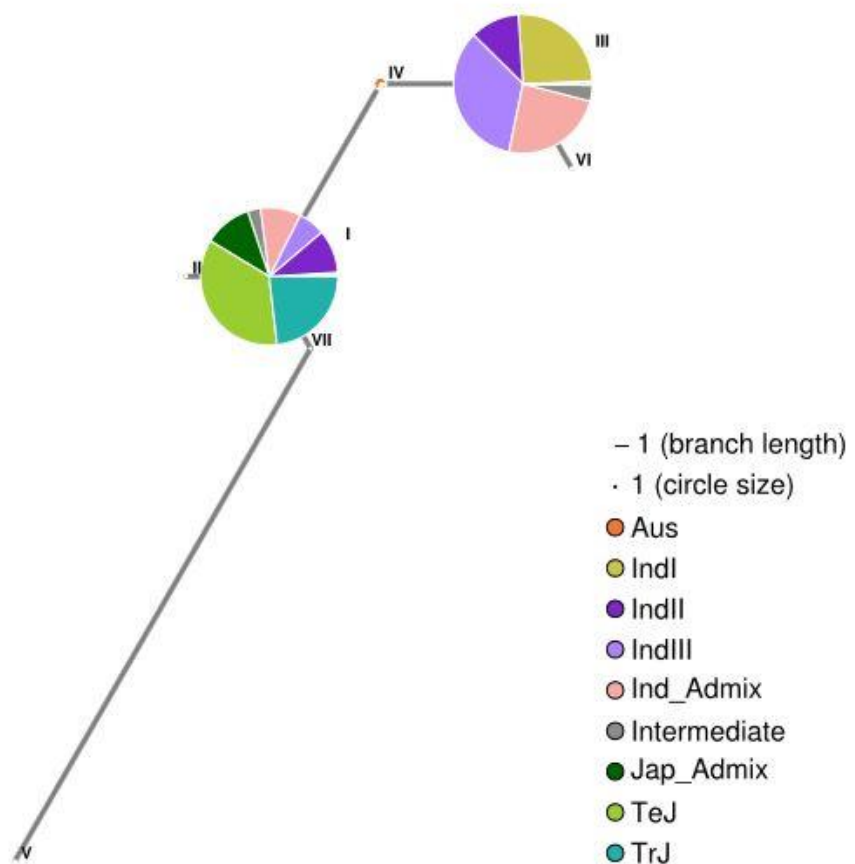
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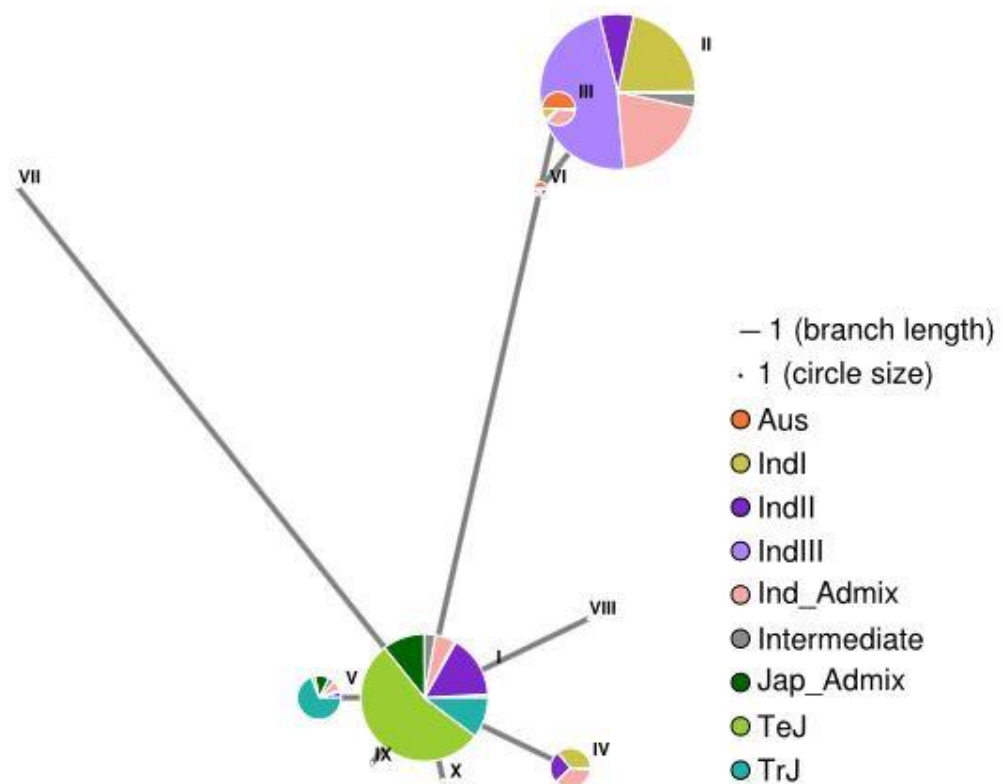
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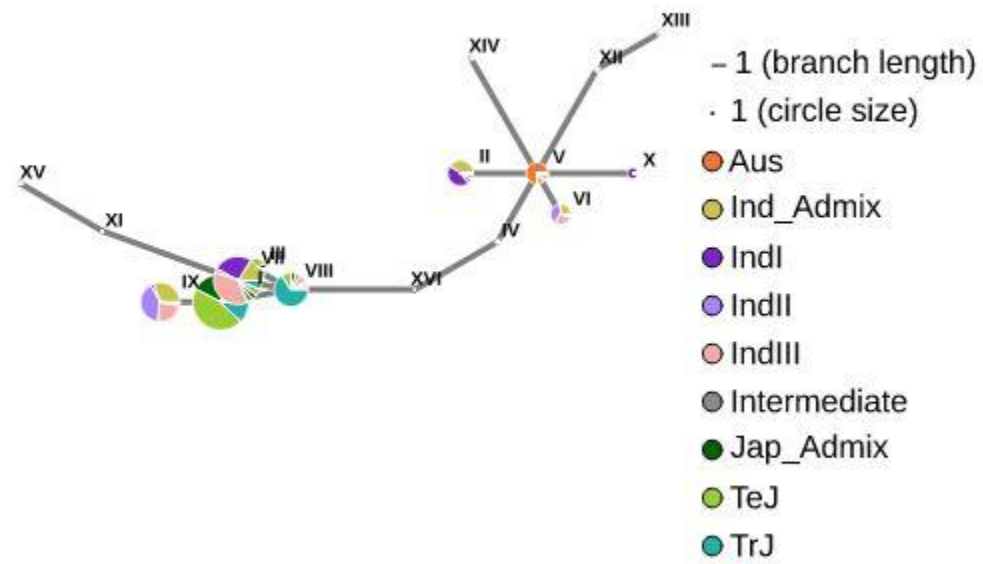
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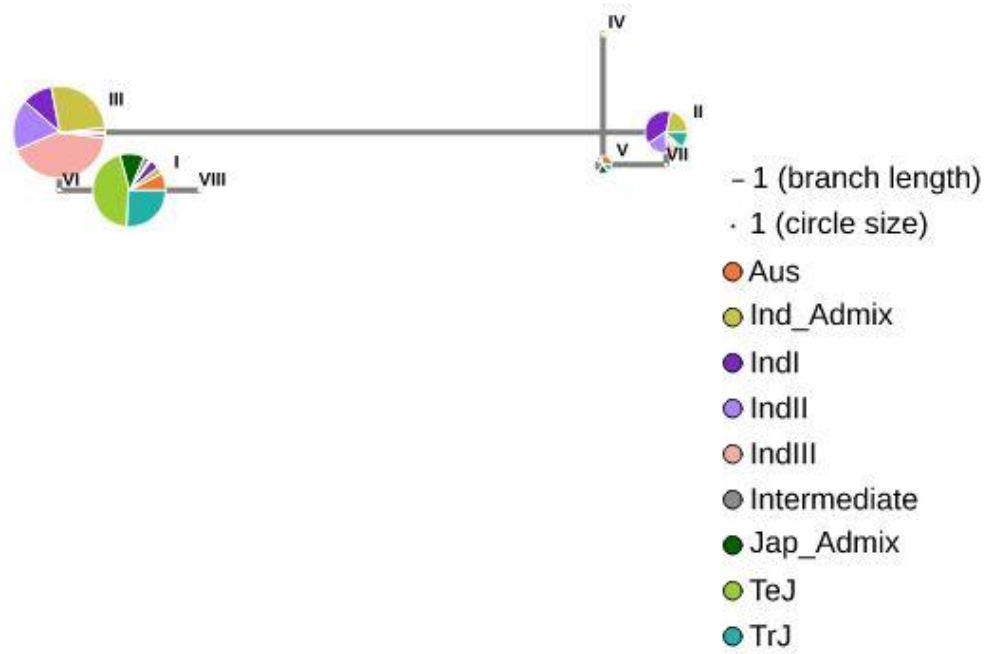
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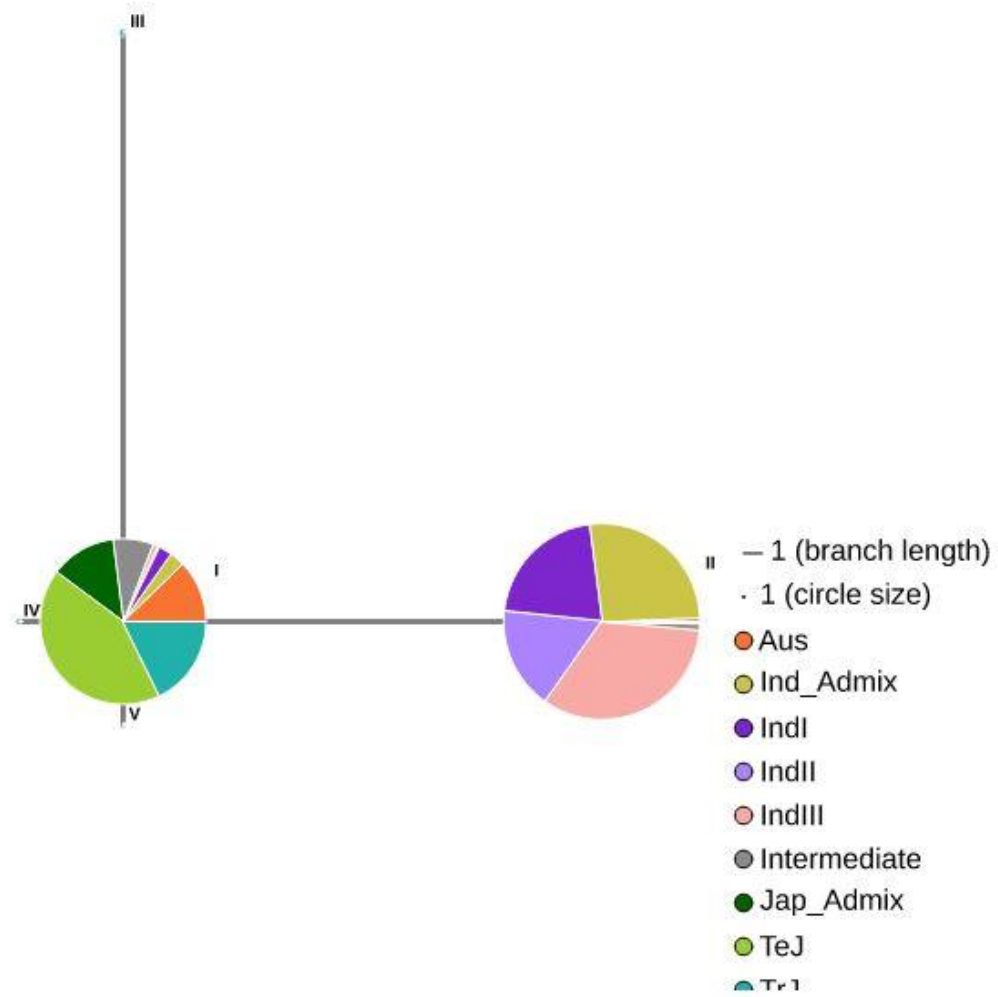
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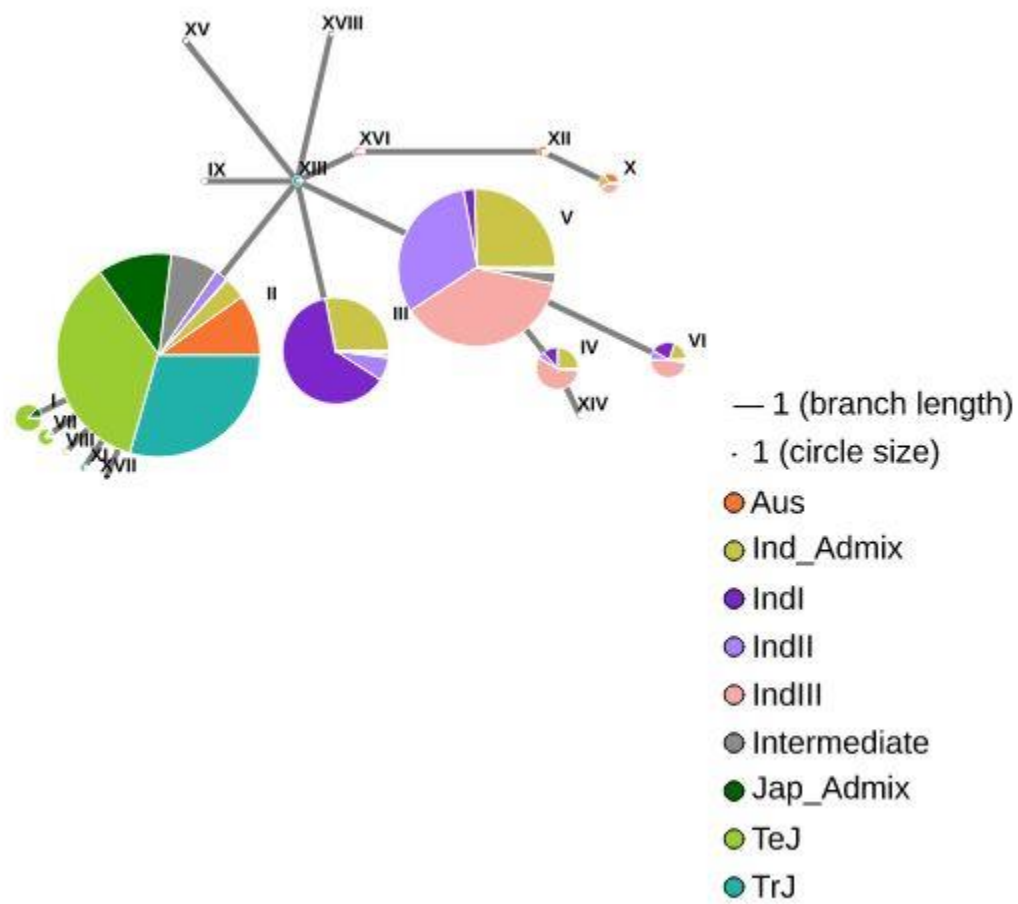
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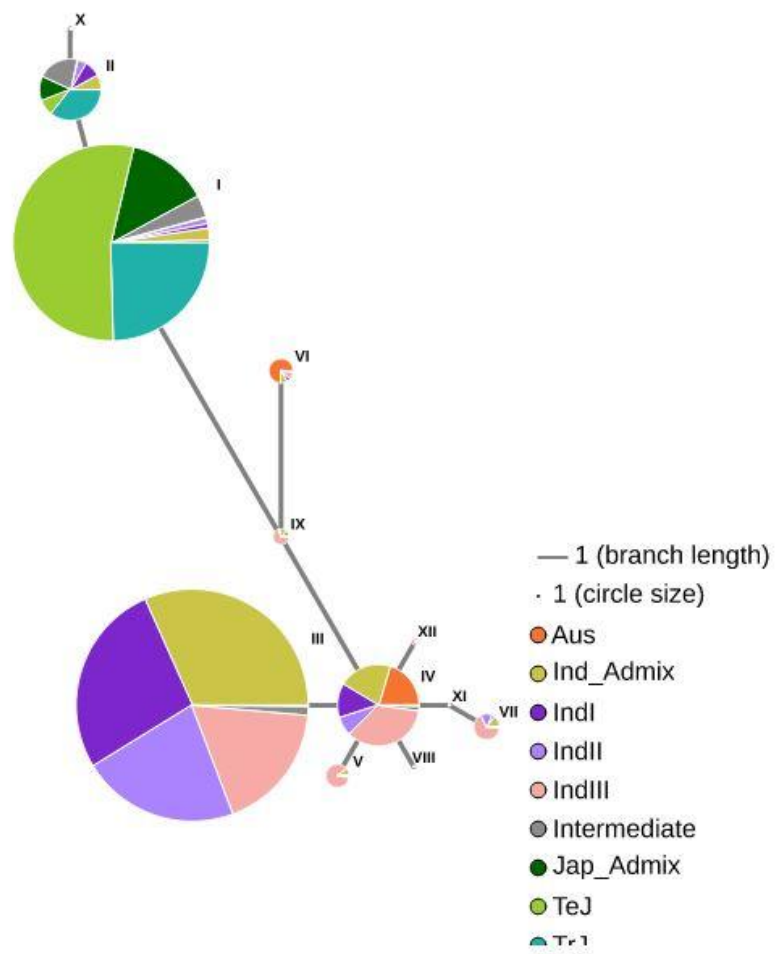
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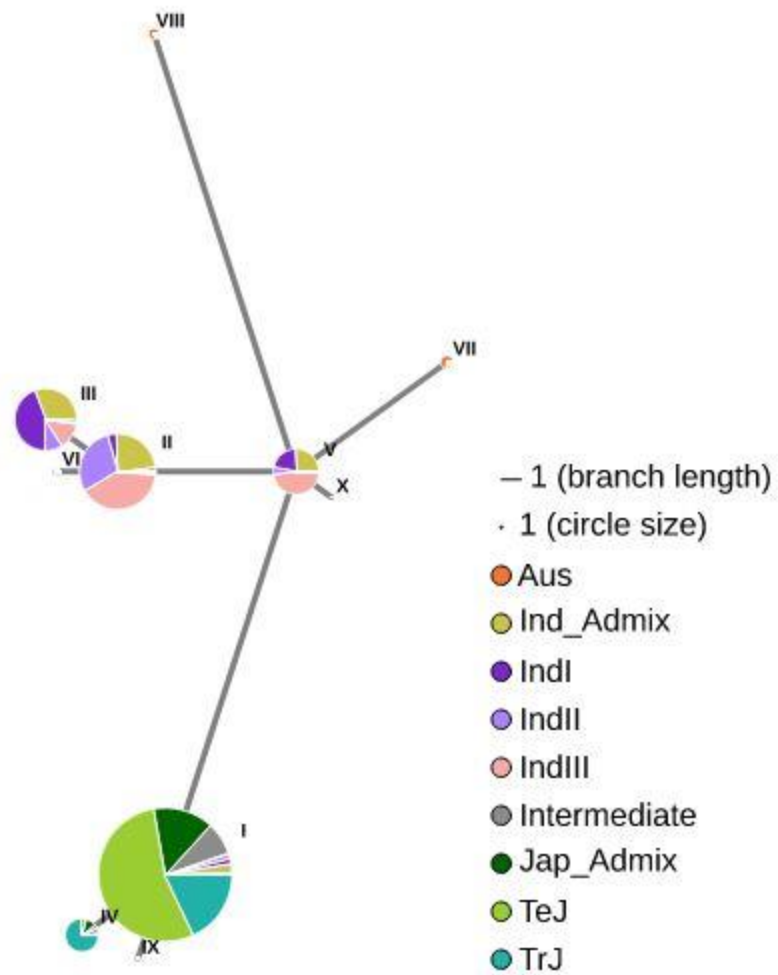
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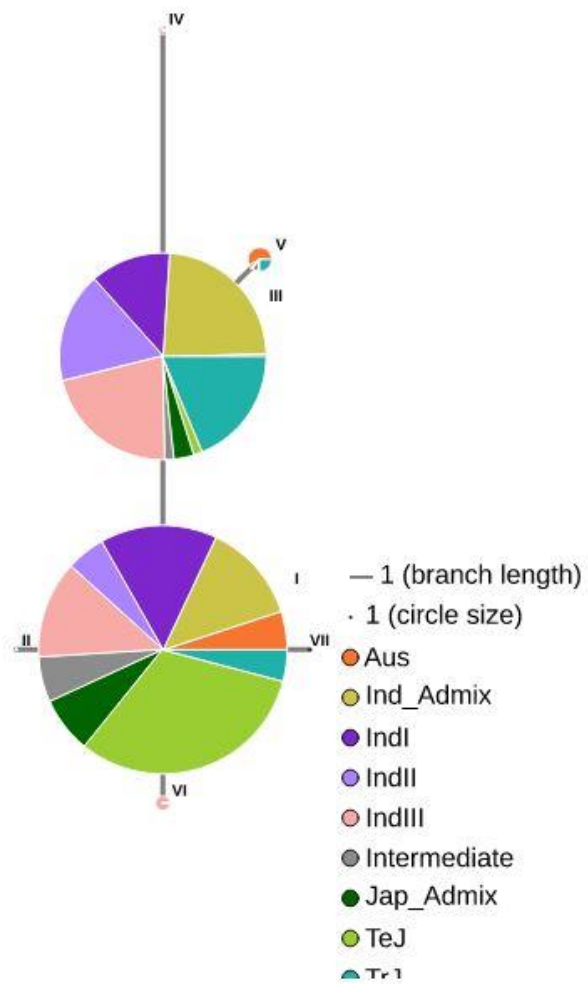
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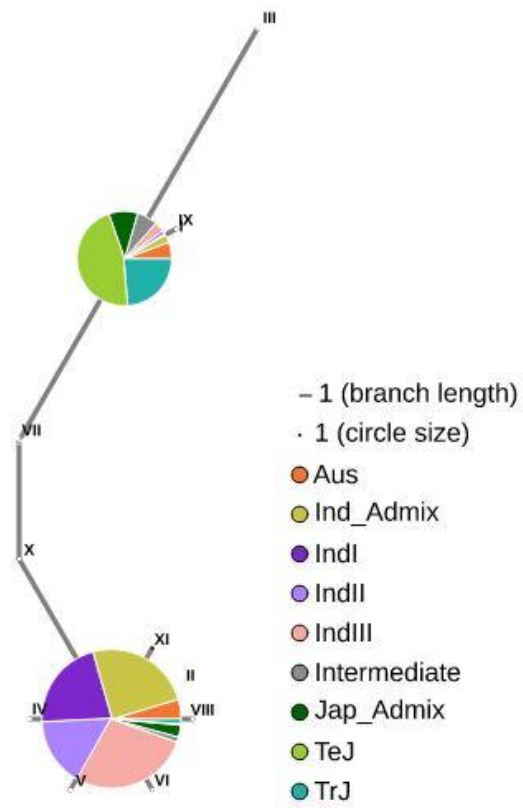
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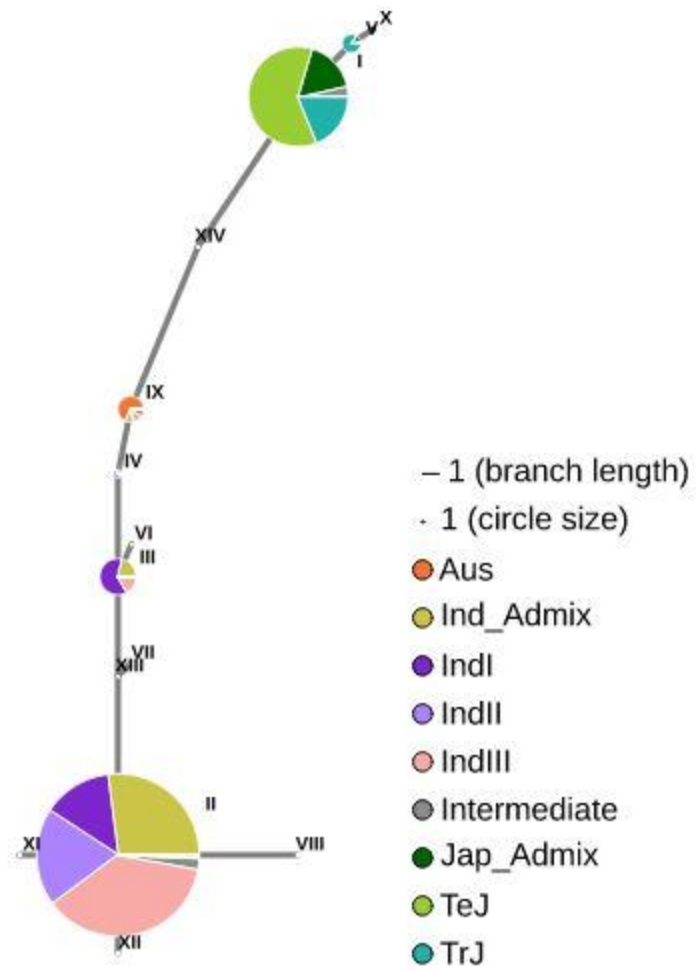
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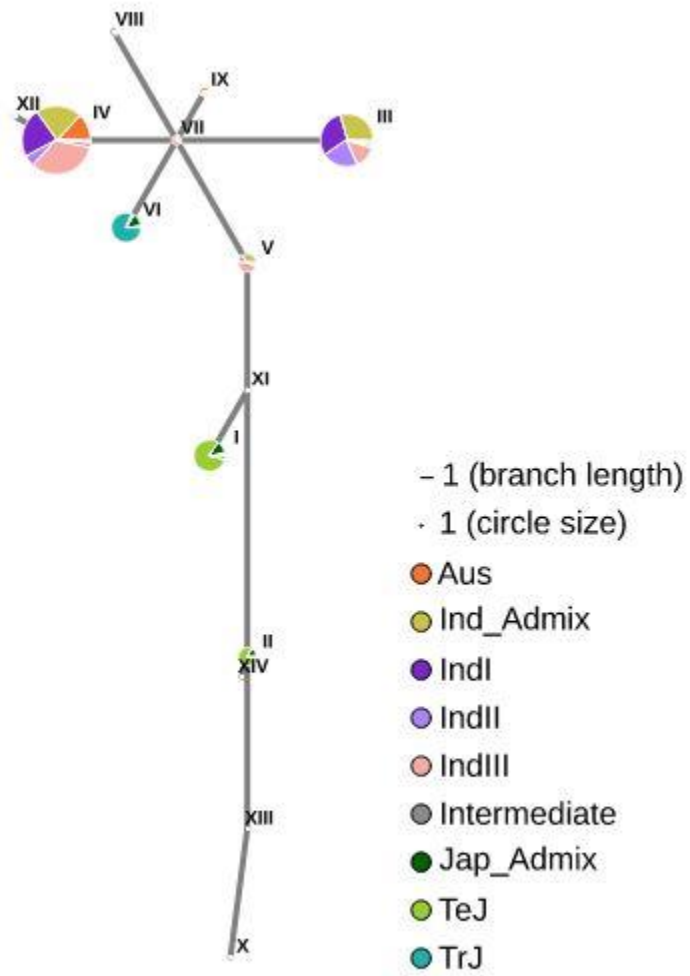
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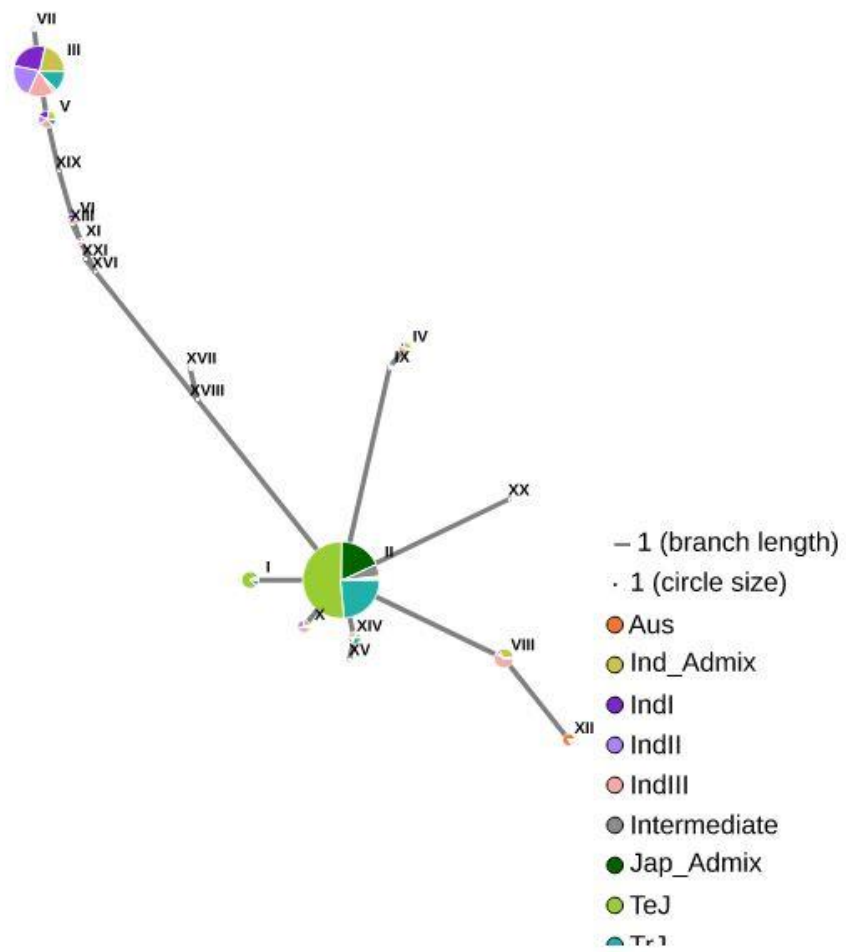
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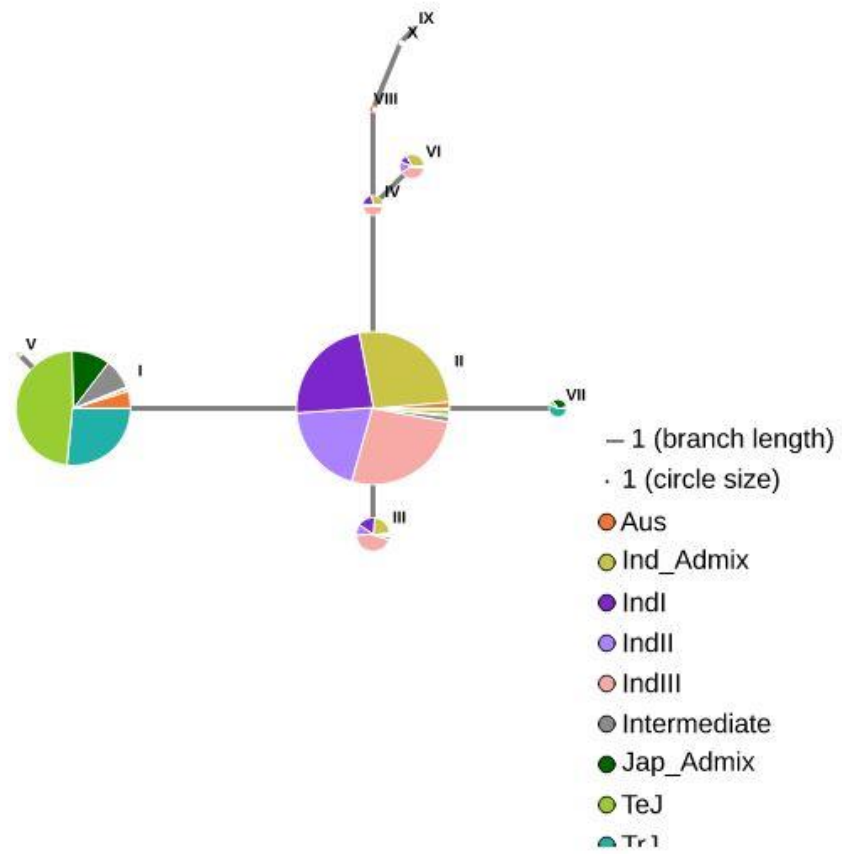
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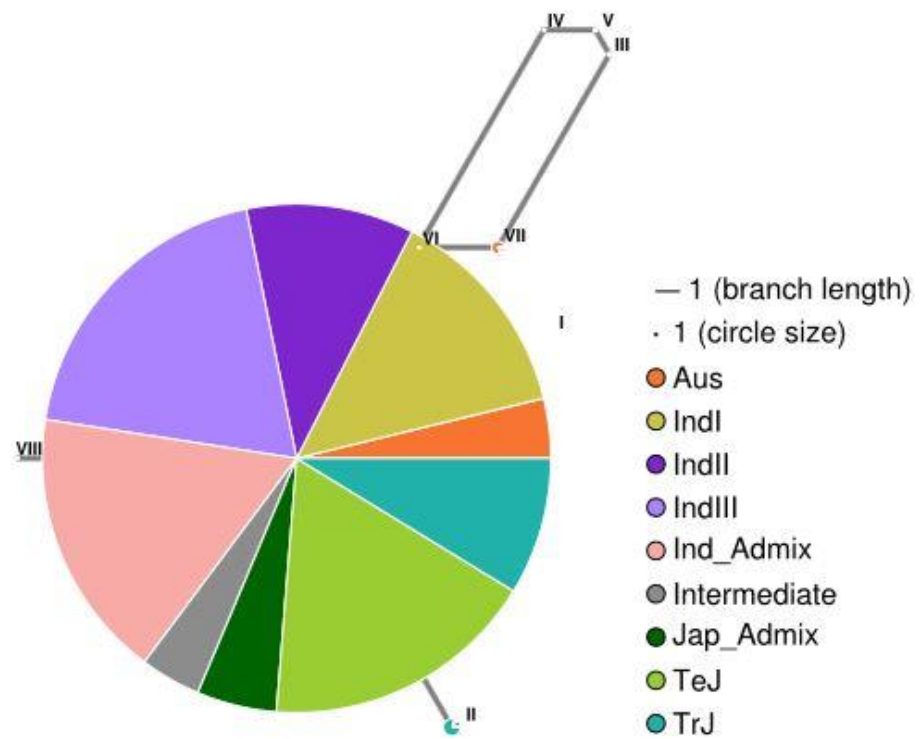
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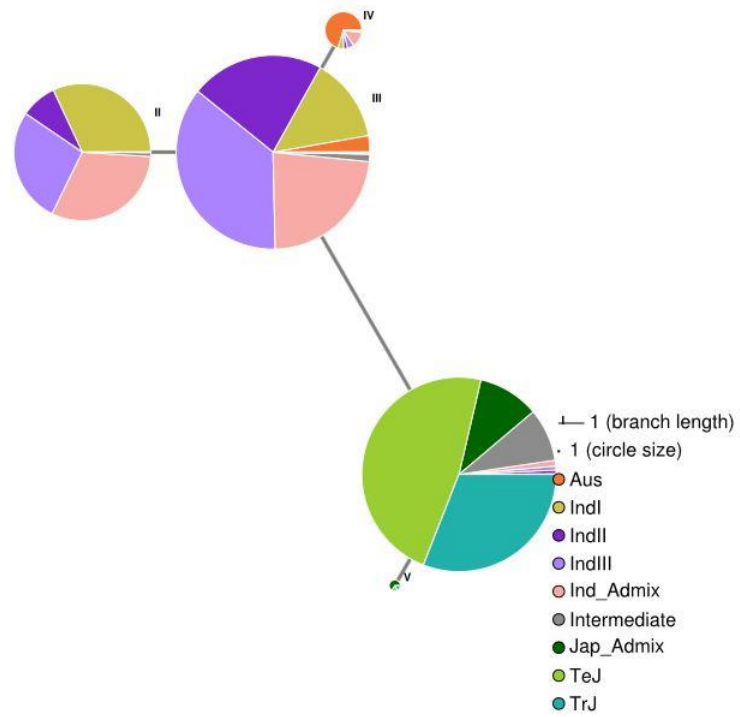
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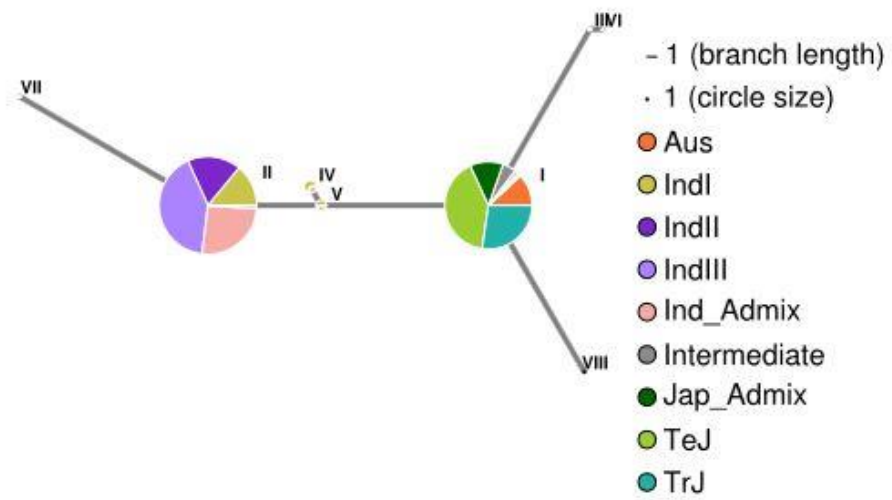
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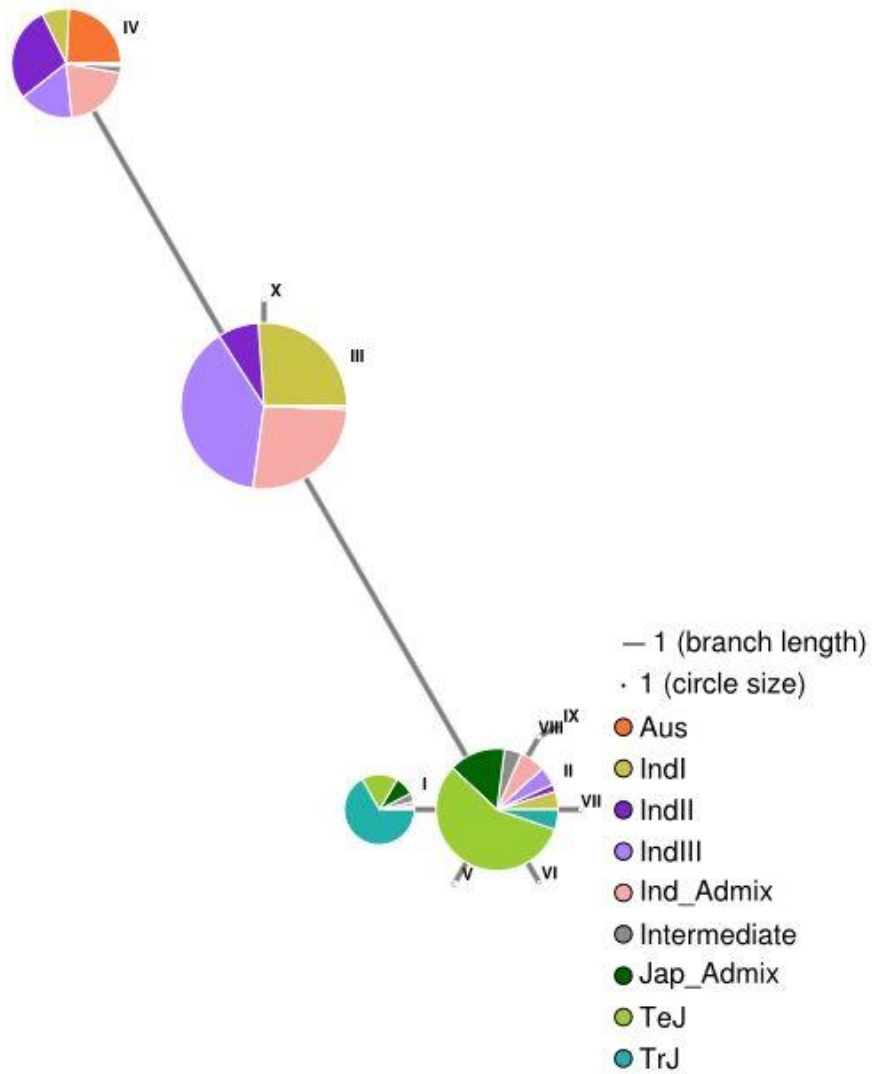
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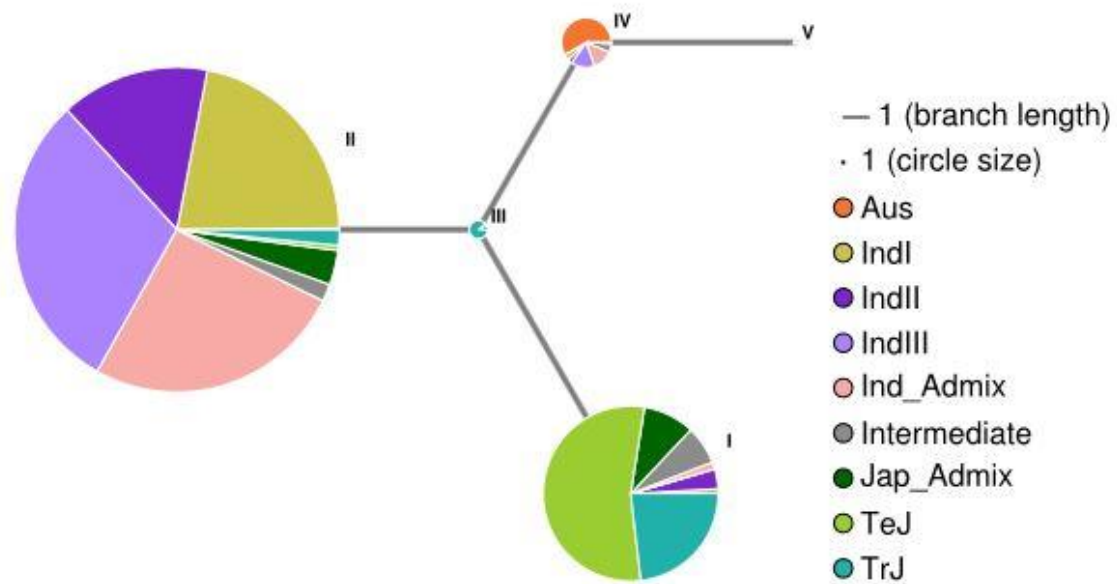
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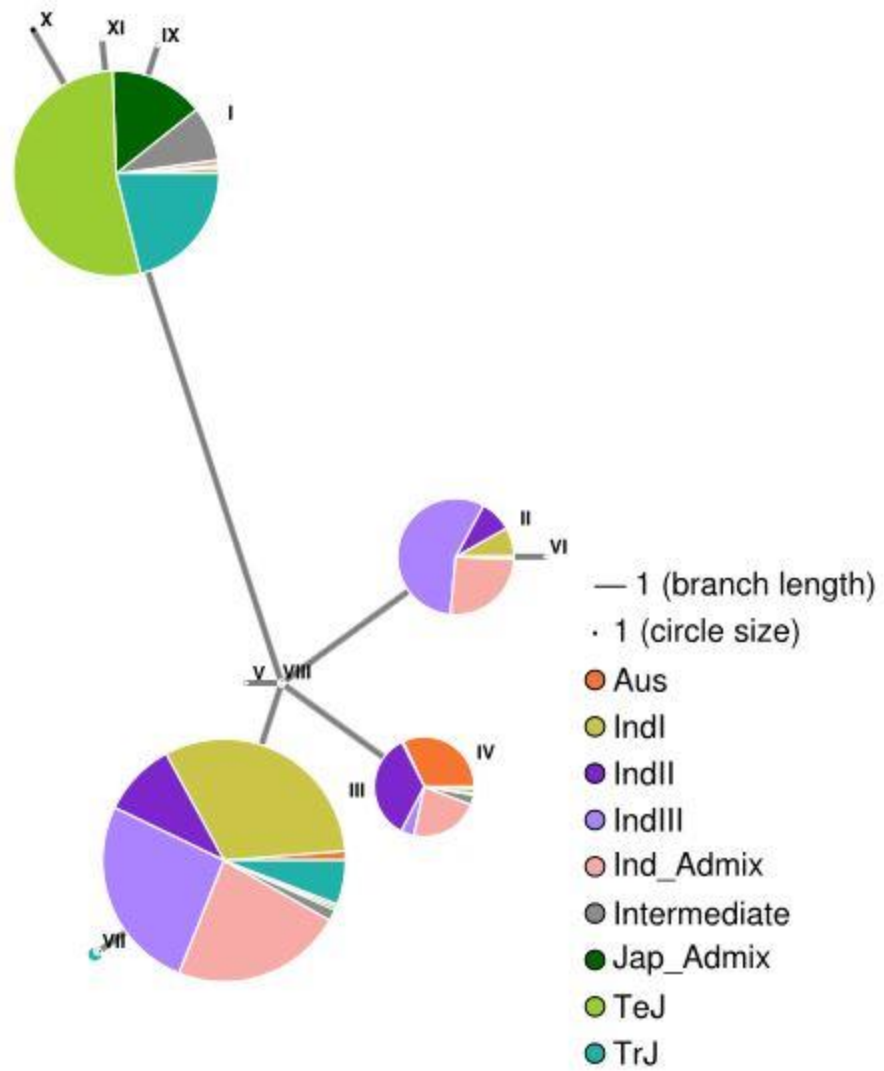
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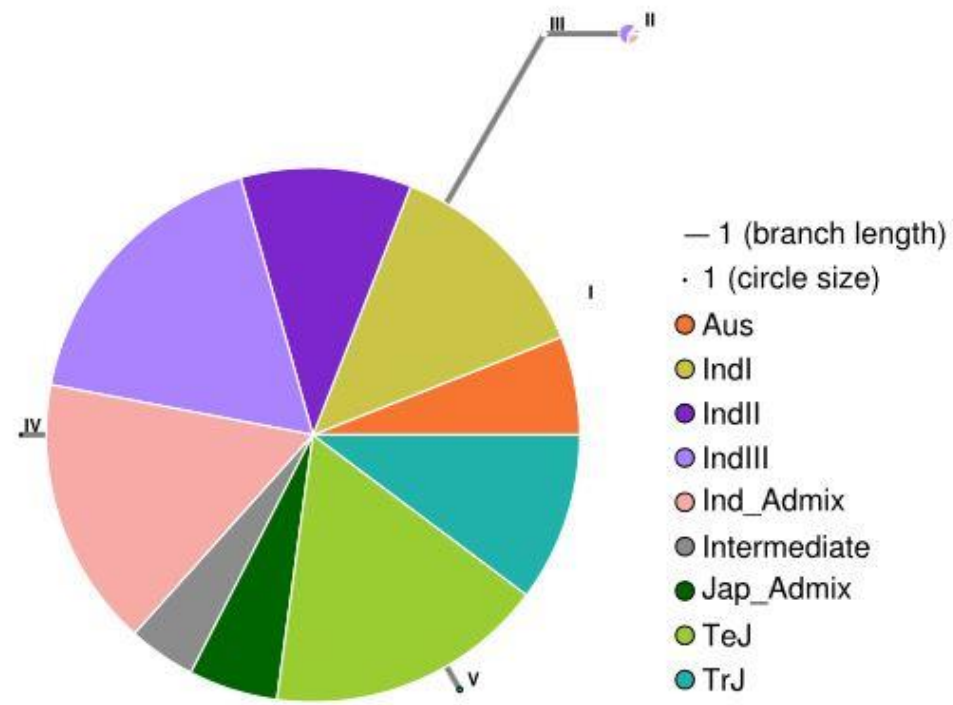
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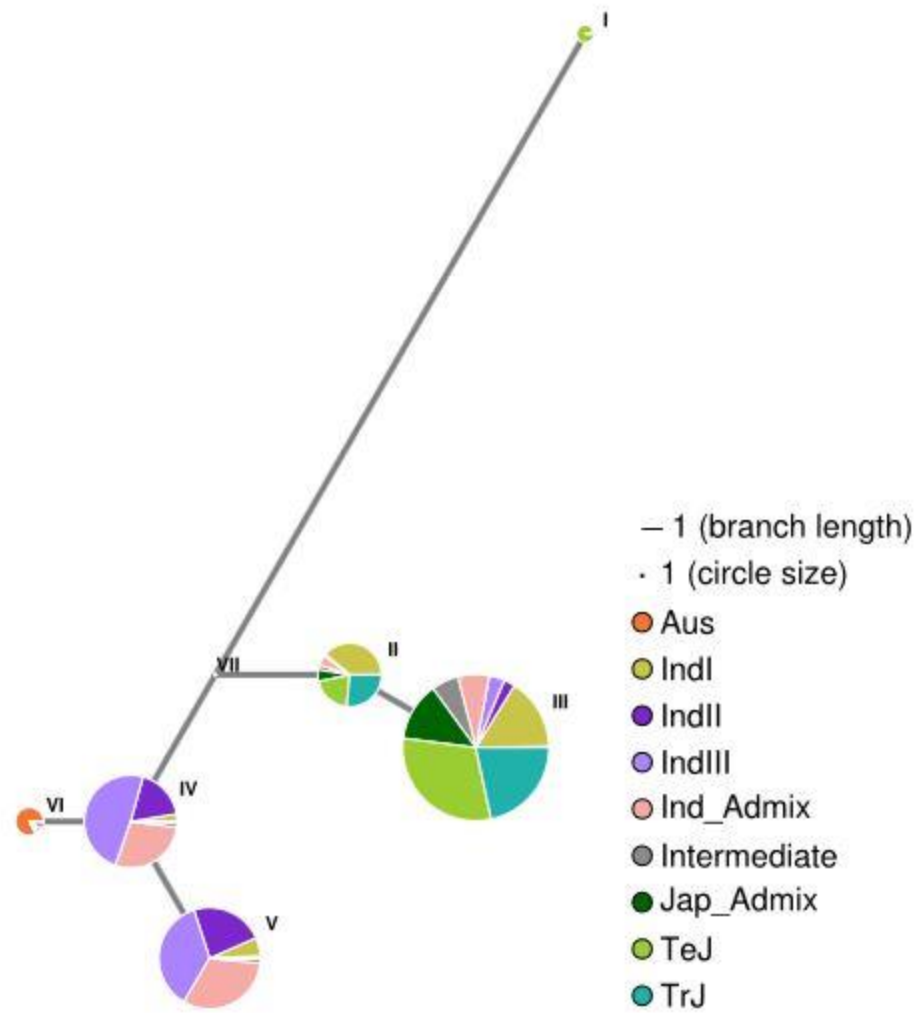
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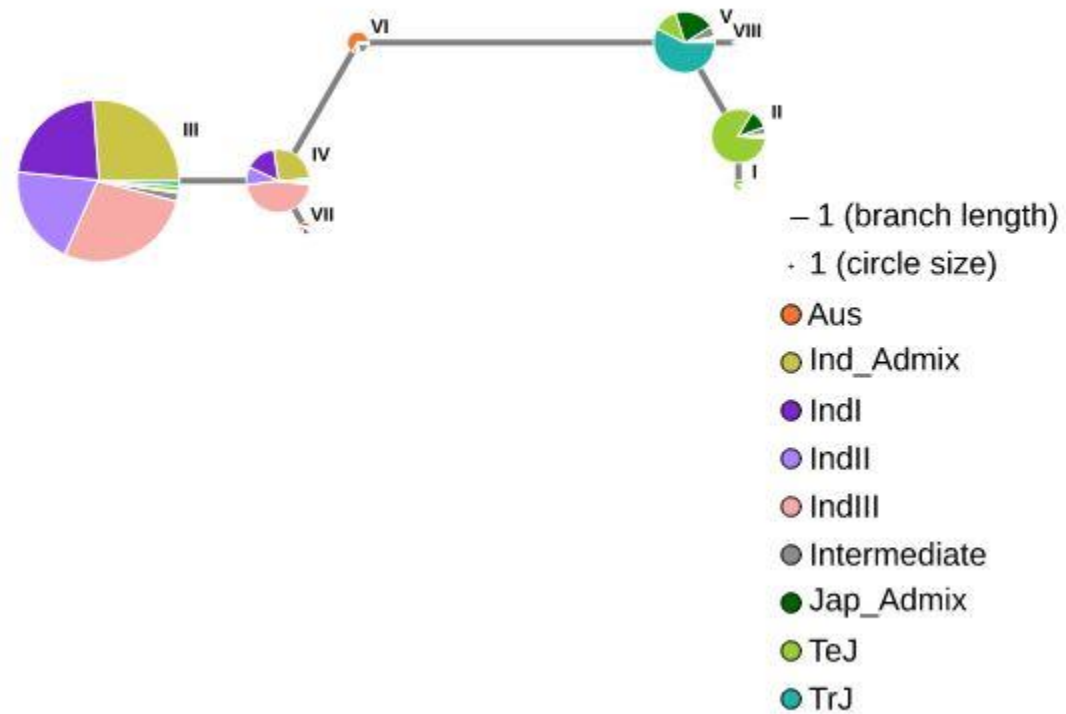
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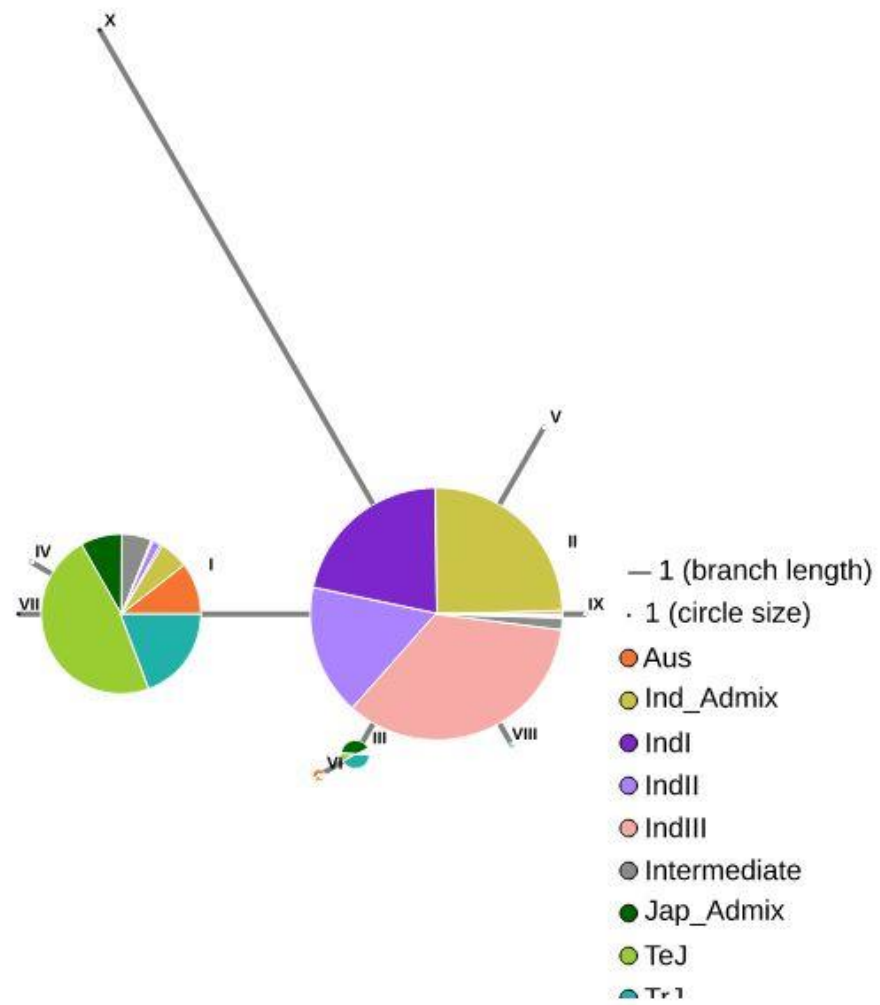
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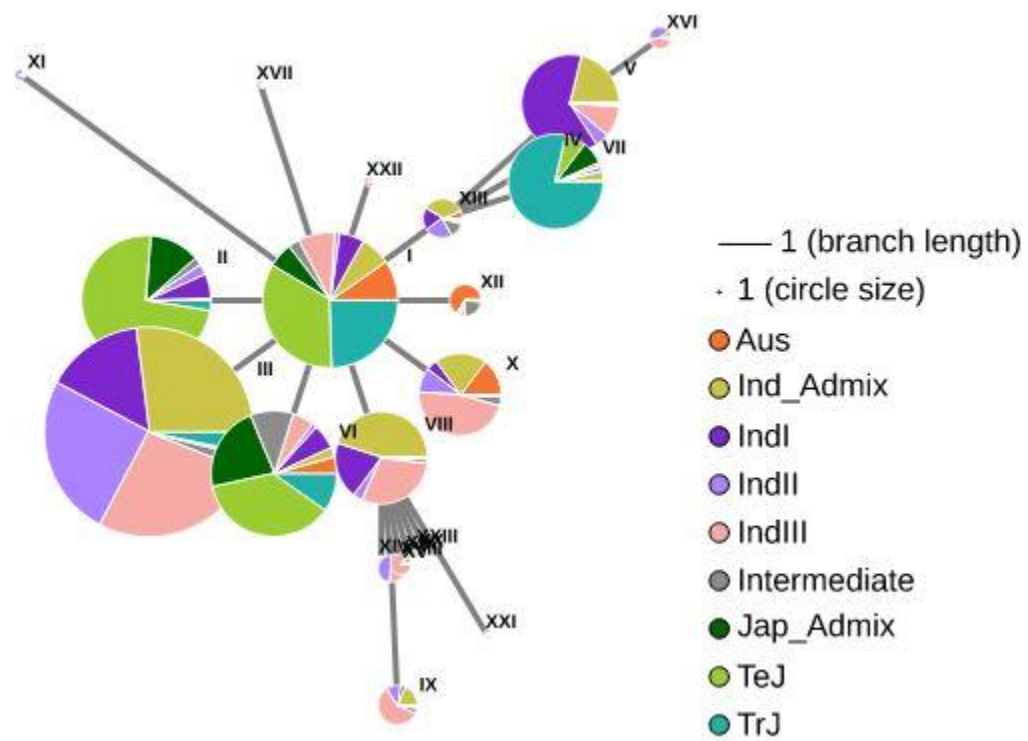
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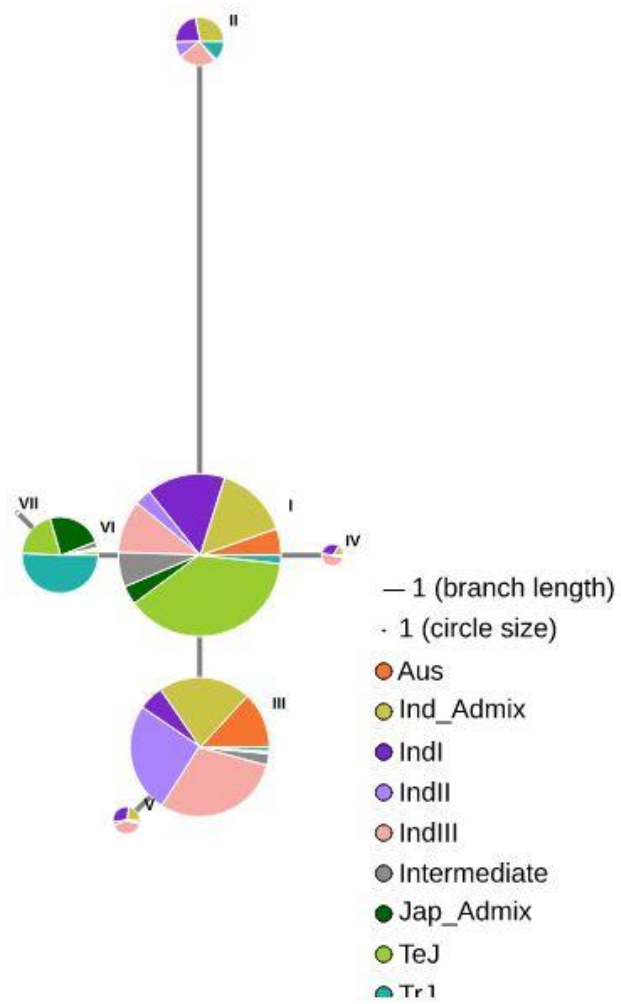
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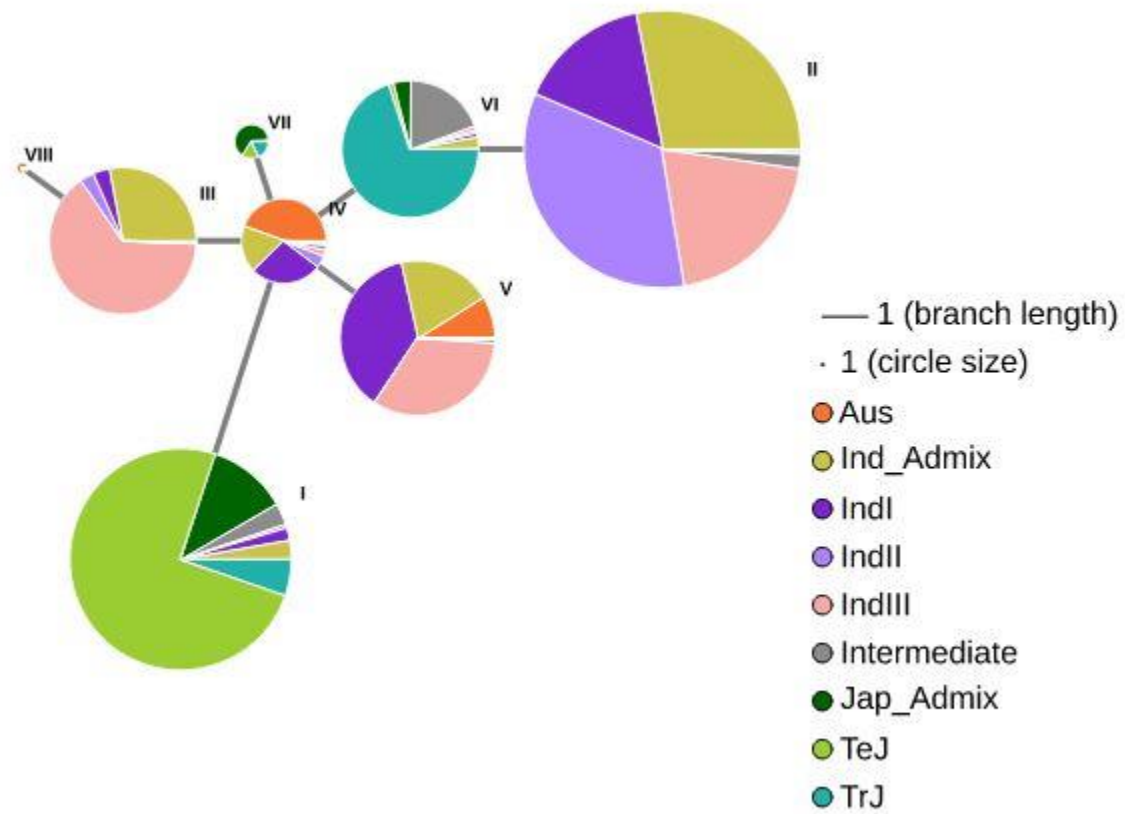
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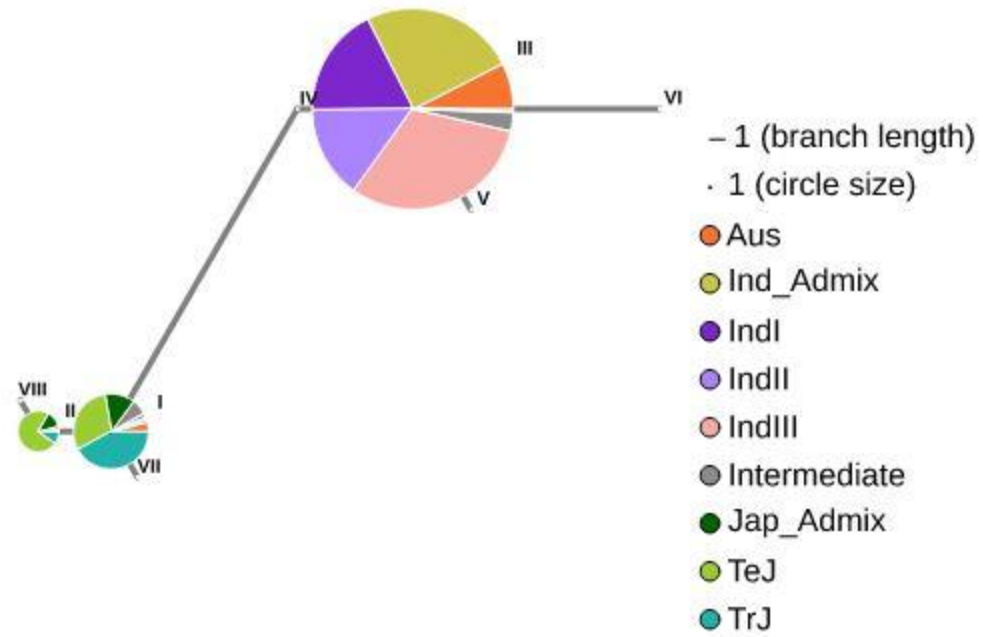
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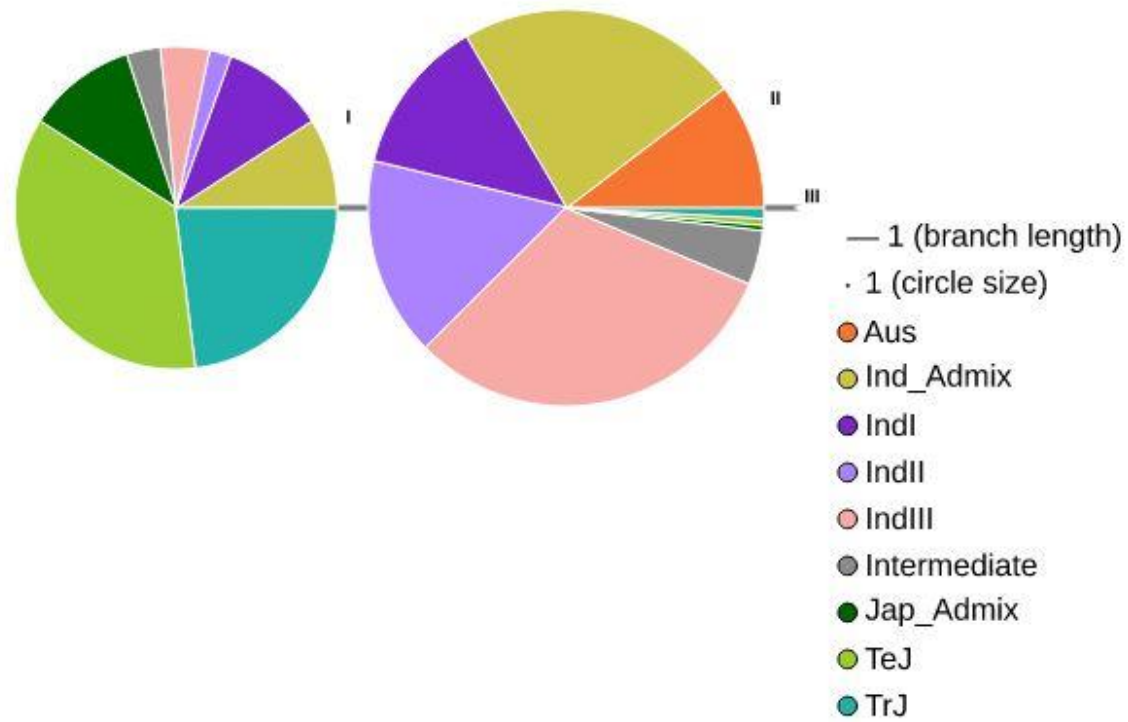
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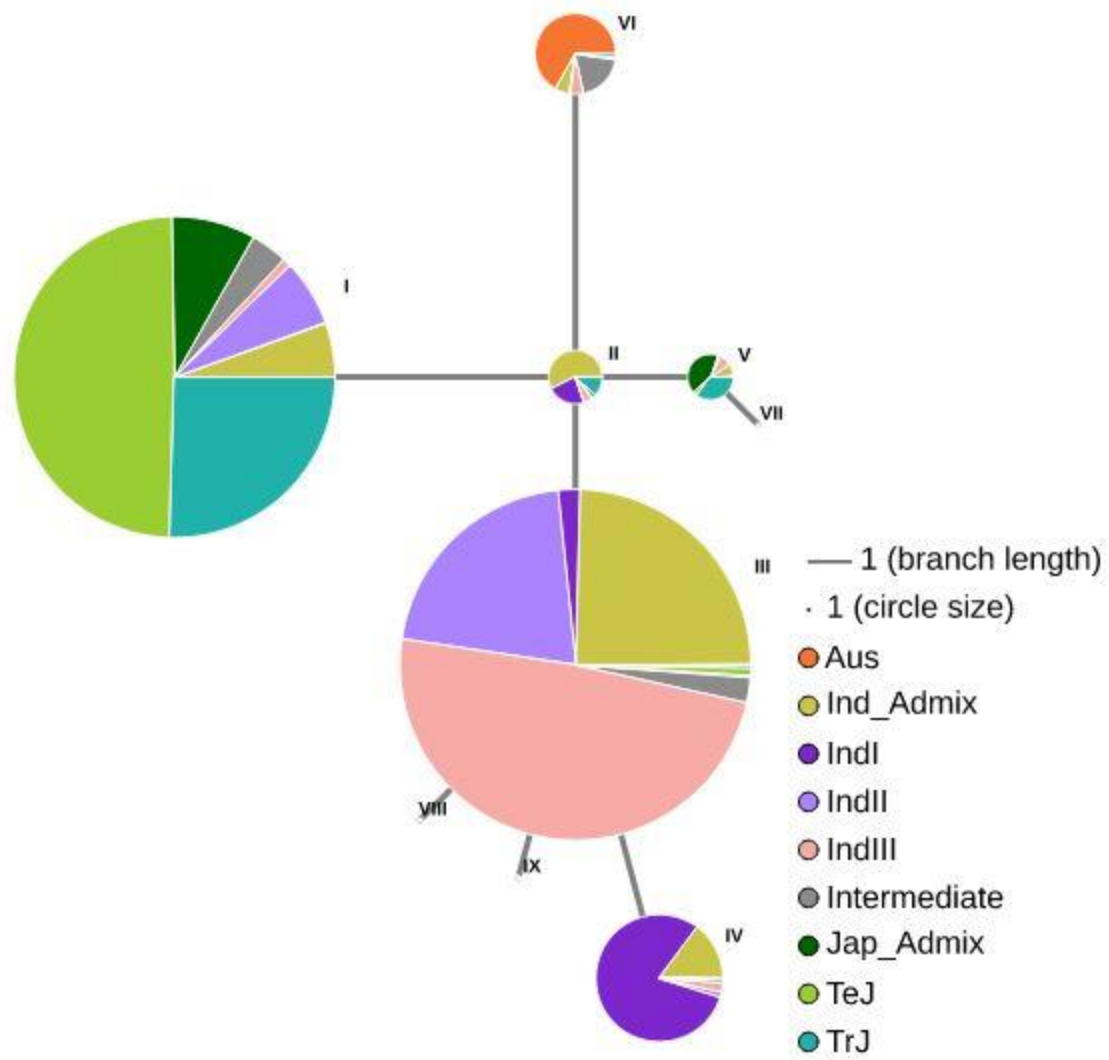
Os01g0762500



LOC_Os06g38120



LOC_Os02g15169



LOC_Os01g11900

Supplementary Dataset 3. Expression in different rice tissues among three cultivars for 80 nutritional and cooking quality related genes. The genes highlighted have specific expression in rice endosperm

