The SNPstar manual is NOT completely finished! The complete version is available at paper submission!

Manual SNPstar

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1 Use of SNPstar for scientific research

What can SNPstar do for you? SNPstar is a tool to help researchers in different ways. SNPstar serves as some sort of SNP atlas which collects different kinds of information, characteristics and features for each SNP in genic regions based on genomic information from the 1001 genomes project (<u>https://1001genomes.org/</u>) of *Arabidopsis thaliana*. Currently, SNPstar has a focus on nonsynonymous SNPs, thereby serving as a starting point to gather meaningful information about SNPs that potentially affect protein structure and function. This manual provides a step-by-step guideline for gathering this information for SNPs in (a) gene(s) of interest based on the complete or a subset of the naturally occuring accessions present in the 1001 genomes collection.

2 General options

On the landing page you initially select your accession set of interest. Here, we will introduce SNPstar on the basis of the 1001 genomes dataset for *Arabidopsis thaliana*.



- * **Functional impacts of non-synonymous SNPs:** Analysis of amino acid substitutions, changes in physico-chemical properties (polarity, charge), and effects on protein domains.
- * **SNP and haplotype analyses:** Computation of CDS and protein haplotypes, their frequencies, their geographic distributions, and their associations with phenotypic traits or environmental factors.
- * Analysis for chosen set of accessions: All results and tables are available for sets of accessions chosen by the user
- * **GWAS input matrices and computation:** Computation of GWAS with SNP or haplotype subsets chosen by the user

2.1 Gene selection

2.1.1 Select a gene and transcript via AT number

The second step is to select your gene of interest. As an example, we will introduce all the features of SNPstar on the basis of the gene *HMA3* (AT4G30120). You can select any gene of interest either by typing the common gene name (e.g. HMA3) or the AGI identifier in the drop down menu as shown below.

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Select your gene model (transcript) of interest. Here, we select AT4G30120.1, but you can select any of the other known splice variants.

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2.1.2 Select a group of genes

In progress!

2.2 Accession selection

There are several options to select subsets of accessions for your analysis. We will introduce these in the following subchapters 2.2.1 - 2.2.5.

2.2.1. Direct selection all or specified accessions

You can select either the complete set of 1135 accessions or, alternatively, compile a subpopulation by checking the boxes on the left.

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2.2.2 Select a subset of accessions via uploading accession IDs

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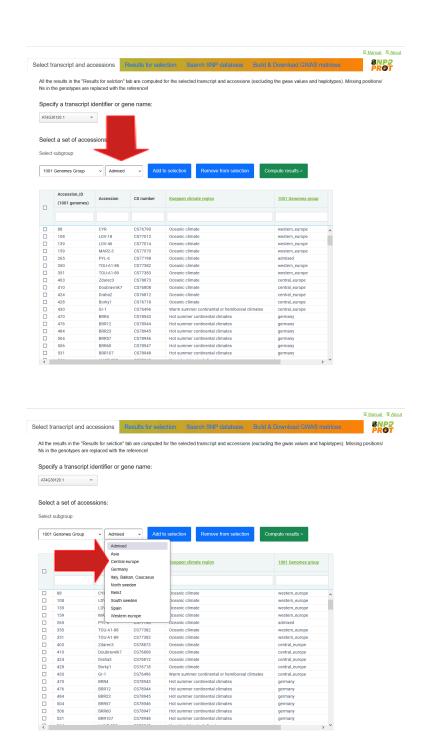
You can always remove the selection via 'Remove from selection' (see chapter 2.2.1).

2.2.3 Selecting accession via 1001 genomes groups

Another straight-forward option to select sub-populations is to select genetic diversity groups from the 1001 genomes project. Use the drop-down menu and select '1001 Genomes Group'.

Koeppen climate region Country	elect	transcript a	and accessions	Results for	selection	Search SNP d	atabase	
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Next, a second drop-down menu appears where you can select the genetic diversity group.



Click 'Add to selection'.

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	430	Gr-1	CS76496	Warm summer continental or hemiboreal climates	central_europe	
	470	BRR4	CS78943	Hot summer continental climates	germany	
	476	BRR12	CS78944	Hot summer continental climates	germany	
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It's possible to add more 1001 Genome groups if you repeat the procedure with other regions of origin. You can remove specific groups via 'Remove from selection' (see chapter 2.2.1).

2.2.4 Select a subset of accessions via Koeppen climate region

If you would like to select a subset of available accession based on the Koeppen climate regions then use the drop-down menu Select subgroup and select Koeppen climate region. The climate regions according to the Koeppen climate classifications.

All the results in the "Results for selection" tab are computed for the selected transcript and accessions (excluding the gwas values an haplotypes). Missing positions/Ns in the genotypes are replaced with the reference! Specify a transcript identifier: Art4G30120.1 Select a set of accessions: Select a set of accessions: Select subgroup: File with accession IDs File with accession IDs File with accession IDs File with accession IDs Compute File with	elect	transcript a	nd accessions	Results for	selection	Search SNP da	tabase
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A second drop-down menu appears. In that menu you can select your climate regions of interest.

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Now you can select your 1001 Genome groups of interest (e.g., Oceanic climate, etc.).

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	350	TOU-A1-88	CS77382	Oceanic climate	western_europe	1
×	351	TOU-A1-89	CS77383	Oceanic climate	western_europe	11
		Zdarec3	CS78873	Oceanic climate	central_europe	
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	410 424 428 430 470 476 484	Draha2 Borky1 Gr-1 BRR4 BRR12 BRR23	CS76812 CS76718 CS76496 CS78943 CS78944 CS78945	Oceanic climate Oceanic climate Warm summer continental or hemiboreal climates Hot summer continental climates Hot summer continental climates	central_europe central_europe central_europe germany germany germany	
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It's possible to select more than one Koeppen climate region. To do this, repeat the procedure with other climate regions. You can remove specific regions if you select the Koeppen climate region of interest and click 'Remove the selection'.

2.2.5 Select a subset of accessions via country

If you would like to select a subset of available accessions based on country of origin, then use the drop-down menu 'Select subgroup' and select 'Country'.

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	108 139 159 265 350 351 403 410 424 428 430 470 476	LDV-18 LDV-46 MAR2-3 PVL-6 TOU-A1-88 TOU-A1-88 TOU-A1-88 Zdarec3 Doubravnik7 Draha2 Borky1 Gr-1 BRR4 BRR12	CS77013 CS77014 CS77070 CS77198 CS77198 CS77382 CS77882 CS76808 CS76808 CS76812 CS76812 CS76718 CS76496 CS76496	Oceanic climate Hot summer continental climates Hot summer continental climates	western_europe western_europe admixed western_europe central_europe central_europe central_europe central_europe central_europe central_europe germany germany
	108 139 159 265 350 403 410 424 428 430 470 476 484	LDV-18 LDV-46 MAR2-3 PVL-6 TOU-A1-88 TOU-A1-89 Zdarec3 Doubravnik7 Draha2 Borky1 Gr-1 BRR4 BRR4 BRR4 BRR23	CS77013 CS77014 CS77070 CS77198 CS77382 CS77383 CS78873 CS78873 CS76808 CS76808 CS76808 CS76808 CS76496 CS76496 CS78943 CS78945	Oceanic climate Hot summer continental climates Hot summer continental climates Hot summer continental climates	western_europe western_europe admixed western_europe western_europe central_europe central_europe central_europe central_europe central_europe central_europe germany germany
	108 139 159 265 350 351 403 410 424 428 430 470 484 504	LDV-18 LDV-46 MAR2-3 PYL-6 TOU-A1-89 Zdarec3 Doubravnik7 Draha2 Borky1 Gr-1 BRR4 BRR12 BRR23 BRR23	CS77013 CS77014 CS77070 CS77198 CS77382 CS77383 CS76808 CS76808 CS76812 CS76812 CS76718 CS76496 CS76943 CS78944 CS78944 CS78945 CS78946	Oceanic climate Hot summer continental climates Hot summer continental climates Hot summer continental climates Hot summer continental climates Hot summer continental climates	western_europe western_europe admixed western_europe central_europe central_europe central_europe central_europe central_europe central_europe germany germany germany germany
	108 139 159 265 350 403 410 424 428 430 470 476 484	LDV-18 LDV-46 MAR2-3 PVL-6 TOU-A1-88 TOU-A1-89 Zdarec3 Doubravnik7 Draha2 Borky1 Gr-1 BRR4 BRR4 BRR4 BRR23	CS77013 CS77014 CS77070 CS77198 CS77382 CS77383 CS78873 CS78873 CS76808 CS76808 CS76808 CS76808 CS76496 CS76496 CS78943 CS78945	Oceanic climate Hot summer continental climates Hot summer continental climates Hot summer continental climates	western_europe western_europe admixed exestern_europe western_europe central_europe central_europe central_europe central_europe central_europe central_europe germany germany

Now you can select your 'Country' of interest (e.g., Sweden, etc.).

001001	transcript and	l accessions	Results for selection	on Search SNP database		
			n" tab are computed for the genotypes are replaced v	e selected transcript and accessions (exclu vith the reference!	ding the gwas values and	
Spec	ify a transcrip	t identifier:				
AT4G3	30120.1	•				
Solor	ct a set of acc	ossions				
Selec		85510115.				
Select	subgroup:					
Count	try	v Sweder	n v Add to sele	ction Remove from selection		
		Geor	gia 🔥		Compute	00
		Germ	any		Computer	103
		Gree	ce 🖉			
	Accession_ID	Acces	p	en climate region	1001 Genomes group	
		Irelan	d	, in the second s		
		Iran				
		Japar				
	9451	Spro 2	khstan n	ic climate	south_sweden	
	9452	Spro 3 Leba	n	ic climate	south_sweden	
	9453	Stenk-	n	ic climate	south_sweden	
	9454	Stenk-	n	ic climate	south_sweden	
	9455	Stenk- Moro	n	ic climate	south_sweden	
	9470	TUT-4		summer continental or hemiboreal climates	south_sweden	
	9471	UII-A-1 Norwa		ic climate	south_sweden	
	9476	VårA 1 Polar		ic climate	germany	
	9481	Yst-1 Portu	-	ic climate	south_sweden	
	9503	11C1 Roma		ic climate	western_europe	
	9506			erranean hot summer climates	admixed	
	9507	IP-Coa Serbi		erranean hot summer climates	spain	
	9508	IF Mo: Switz	shana	erranean hot summer climates	admixed	
	9500	Slova	NIG .	erranean hot summer climates	spain	
			en te	erranean hot summer climates	spain	
	95	Swed	on a second			
	95	Tajiki	stan te	erranean hot summer climates	spain	
	95 9512	IF vid- Turke	stan te y te	erranean hot summer climates	spain	
	95	IF Id- Turke	stan te y te			

Click 'Add to selections'.

Description About

Select transcript and accessions Results for selection Search SNP database

All the results in the "Results for selction" tab are computed for the selected transcript and accessions (excluding the gwas values and haplotypes). Missing positions/Ns in the genotypes are replaced with the reference!

Specify a transcript i	dentifier:				
AT4G30120.1					
Select a set of acces	sions:				
Select subgroup:					
Country	✓ Sweden	✓ Ad	d to selection	Remove from selection	

Compute results

_	Accession_ID	Accession	CS number	Koeppen climate region	1001 Genomes group	
	9451	Spro 2	CS77264	Oceanic climate	south_sweden	
	9452	Spro 3	CS77265	Oceanic climate	south_sweden	
	9453	Stenk-2	CS77274	Oceanic climate	south_sweden	
	9454	Stenk-3	CS77275	Oceanic climate	south_sweden	
	9455	Stenk-4	CS77276	Oceanic climate	south_sweden	
	9470	Tur-4	CS77399	Warm summer continental or hemiboreal climates	south_sweden	
	9471	Ull-A-1	CS78820	Oceanic climate	south_sweden	
	9476	VårA 1	CS78832	Oceanic climate	germany	
	9481	Yst-1	CS78869	Oceanic climate	south_sweden	
	9503	1101	CS76640	Oceanic climate	western_europe	
	9506	IP-Alo-0	CS76662	Mediterranean hot summer climates	admixed	
	9507	IP-Coa-0	CS76775	Mediterranean hot summer climates	spain	
	9508	IP-Mos-1	CS77108	Mediterranean hot summer climates	admixed	
	9509	IP-Reg-0	CS77207	Mediterranean hot summer climates	spain	
	9510	IP-Rei-0	CS77208	Mediterranean hot summer climates	spain	
	9511	IP-Vav-0	CS78835	Mediterranean hot summer climates	spain	
	9512	IP-Vid-1	CS78842	Mediterranean hot summer climates	spain	
	9513	IP-Adc-5	CS76646	Mediterranean hot summer climates	admixed	

Compute results >

Compute results >

🗩 About

Select transcript and accessions Results for selection Search SNP database

All the results in the "Results for selction" tab are computed for the selected transcript and accessions (excluding the gwas values and haplotypes). Missing positions/Ns in the genotypes are replaced with the reference!

Specify a transcript identifier:

AT4G30120.1 👻

Select a set of accessions:

Select subgroup:

Country v Sweden v Add to selection Remove from selection

Koeppen climate region 1001 Genomes group Accession_ID Accession CS number CS77264 Oceanic climate south_sweder 9451 Spro 2 ^ 9452 9453 Spro 3 Stenk-2 CS77265 CS77274 Oceanic climate Oceanic climate south_sweden Stenk-3 9454 CS77275 Oceanic climate south_sweden 9455 9470 Stenk-4 Tur-4 CS77276 CS77399 Oceanic climate Warm summer continental or hemiboreal climates south_sweden south_sweden UII-A-1 9471 CS78820 Oceanic climate south_sweden VårA 1 VårA 1 Yst-1 11C1 IP-Alo-0 IP-Coa-0 9476 9481 CS78832 CS78869 Oceanic climate Oceanic climate germany south_sweden 9503 CS76640 Oceanic climate western_europe 9506 9507 9508 CS76662 CS76775 Mediterranean hot summer climates Mediterranean hot summer climates admixed spain IP-Mos-1 CS77108 Mediterranean hot summer climates admixed 9509 9510 IP-Reg-0 IP-Rei-0 CS77207 CS77208 Mediterranean hot summer climates Mediterranean hot summer climates spain spain 9511 IP-Vav-0 CS78835 Mediterranean hot summer climates spain 9512 9513 IP-Vid-1 IP-Adc-5 CS78842 CS76646 Mediterranean hot summer climates Mediterranean hot summer climates spain admixed · · · .

Compute results >

It's possible to add more 'Countries' when you repeat the procedure with other 'countries'. You can remove specific regions if you select the 'Country' of interest and click 'Remove the selection' (see chapter 2.2.1).

2.3 Compute results

To calculate the result of your selections press 'Compute results'.

elect	transcript and	accessions	Results for	selection Search SNP database	
				ted for the selected transcript and accessions (exclue eplaced with the reference!	ding the gwas values and
Spec	cify a transcrip	t identifier:			
AT4G	30120.1	-			
Solo	ct a set of acc	ossions			
Sele		65510115.			
Select	t subgroup:				
					- A
Com	plete 1135 accessio	ins 🗸 Add	to selection	Remove from selection	
					Compute re:
					Compute re
	Accession_ID	Accession	CS number	Koeppen climate region	1001 Genomes group
				······	
	9451	Spro 2	CS77264	Oceanic climate	south_sweden
~	9452	Spro 3	CS77265	Oceanic climate	south_sweden
~	9453	Stenk-2	CS77274	Oceanic climate	south_sweden
~	9454	Stenk-3	CS77275	Oceanic climate	south_sweden
	9455	Stenk-4	CS77276	Oceanic climate	south_sweden
~	9470	Tur-4	CS77399	Warm summer continental or hemiboreal climates	south_sweden
	9471	Ull-A-1	CS78820	Oceanic climate	south_sweden
_					
	9476	VårA 1	CS78832	Oceanic climate	germany
		VårA 1 Yst-1	CS78832 CS78869	Oceanic climate Oceanic climate	
✓ ✓ ✓	9476				germany south_sweden western_europe
 	9476 9481	Yst-1	CS78869	Oceanic climate	south_sweden western_europe
S S S S S S	9476 9481 9503 9506	Yst-1 11C1 IP-Alo-0	CS78869 CS76640 CS76662	Oceanic climate Oceanic climate Mediterranean hot summer climates	south_sweden western_europe admixed
	9476 9481 9503 9506 9507	Yst-1 11C1 IP-Alo-0 IP-Coa-0	CS78869 CS76640 CS76662 CS76775	Oceanic climate Oceanic climate Mediterranean hot summer climates Mediterranean hot summer climates	south_sweden western_europe admixed spain
	9476 9481 9503 9506 9507 9508	Yst-1 11C1 IP-Alo-0 IP-Coa-0 IP-Mos-1	CS78869 CS76640 CS76662 CS76775 CS77108	Oceanic climate Oceanic climate Mediterranean hot summer climates Mediterranean hot summer climates Mediterranean hot summer climates	south_sweden western_europe admixed spain admixed
	9476 9481 9503 9506 9507 9508 9508 9509	Yst-1 11C1 IP-Alo-0 IP-Coa-0 IP-Mos-1 IP-Reg-0	CS78869 CS76640 CS76662 CS76775 CS77108 CS77207	Oceanic climate Oceanic climate Mediterranean hot summer climates Mediterranean hot summer climates Mediterranean hot summer climates	south_sweden western_europe admixed spain admixed spain
	9476 9481 9503 9506 9507 9508 9509 9509	Yst-1 11C1 IP-Alo-0 IP-Coa-0 IP-Mos-1 IP-Reg-0 IP-Rej-0	CS78869 CS76640 CS76662 CS76775 CS77108 CS77207 CS77208	Oceanic climate Oceanic climate Mediterranean hot summer climates Mediterranean hot summer climates Mediterranean hot summer climates Mediterranean hot summer climates	south_sweden western_europe admixed spain admixed spain spain
	9476 9481 9503 9506 9507 9508 9509 9509 9510 9511	Yst-1 11C1 IP-Alo-0 IP-Coa-0 IP-Mos-1 IP-Reg-0 IP-Rei-0 IP-Vav-0	CS78869 CS76640 CS76662 CS76775 CS77108 CS77207 CS77208 CS78835	Oceanic climate Oceanic climate Mediterranean hot summer climates Mediterranean hot summer climates Mediterranean hot summer climates Mediterranean hot summer climates Mediterranean hot summer climates	south_sweden western_europe admixed spain admixed spain spain spain
	9476 9481 9503 9506 9507 9507 9509 9509 9510 9511 9512	Yst-1 11C1 IP-Alo-0 IP-Coa-0 IP-Mos-1 IP-Reg-0 IP-Rej-0 IP-Vav-0 IP-Vav-0 IP-Vid-1	CS78869 CS76640 CS76662 CS76775 CS77108 CS77207 CS77208 CS78835 CS78842	Oceanic climate Oceanic climate Mediterranean hot summer climates Mediterranean hot summer climates	south_sweden western_europe admixed spain admixed spain spain spain spain
	9476 9481 9503 9506 9507 9508 9509 9509 9510 9511	Yst-1 11C1 IP-Alo-0 IP-Coa-0 IP-Mos-1 IP-Reg-0 IP-Rei-0 IP-Vav-0	CS78869 CS76640 CS76662 CS76775 CS77108 CS77207 CS77208 CS78835	Oceanic climate Oceanic climate Mediterranean hot summer climates Mediterranean hot summer climates Mediterranean hot summer climates Mediterranean hot summer climates Mediterranean hot summer climates	south_sweden western_europe admixed spain admixed spain spain spain

If you hover over any ⁽¹⁾ symbol, additional information (e.g., for tabs or table headers) are shown.

Results: AT4G30120.1		Download	d options	✓ Downlo
ATHMA3: A. THALIAN METAL ATPASE 3; HM atpase 3 Check selected access		I		
Sequence viewer () SNP	s () SNPs <-> Acces	sions 🚯 🛛 Haplotyp	be <-> Accession tal	ble 🚯
Protein haplotype <-> Acces	sion table 🚯			
Please note: Indels are not include starts negative, with the A in the ATC transcripts on the reverse strand the Introns I UTR Protein d	start codon being position 1. The reverse complement is shown.	e SNP labels in the feature	viewer show the genomic	position. For
starts negative, with the A in the ATG transcripts on the reverse strand the Introns I UTR Protein d Position: 0 Zoom: x 1 S	start codon being position 1. The reverse complement is shown.	e SNP labels in the feature NPs ☑ Nonsyn. SNPs	viewer show the genomic	position. For
starts negative, with the A in the ATC transcripts on the reverse strand the Introns UTR Protein d Position: 0 Zoom: x 1 S Sequence 3:UTR	a start codon being position 1. Th reverse complement is shown. Iomains ☑ SNPs ☑ Syn. S	e SNP labels in the feature NPs ☑ Nonsyn. SNPs	viewer show the genomic	position. For
starts negative, with the A in the ATG transcripts on the reverse strand the Introns I UTR Protein d Position: 0 Zoom: x 1 5 Sequence	a start codon being position 1. Th reverse complement is shown. Iomains ☑ SNPs ☑ Syn. S	e SNP labels in the feature NPs ☑ Nonsyn. SNPs	viewer show the genomic	position. For
starts negative, with the A in the ATG transcripts on the reverse strand the Introns Intron Transcripts on the reverse strand the Position: 0 Zoom: x 1 S Sequence 3:UTR CDS Introns	a start codon being position 1. Th reverse complement is shown. Iomains ☑ SNPs ☑ Syn. S	e SNP labels in the feature NPs ☑ Nonsyn. SNPs	viewer show the genomic	position. For
starts negative, with the A in the ATC transcripts on the reverse strand the Introns I UTR Protein d Position: 0 Zoom: x 1 S Sequence S-UTR S-UTR CDS	a start codon being position 1. Th reverse complement is shown. Iomains ☑ SNPs ☑ Syn. S	e SNP labels in the feature NPs ☑ Nonsyn. SNPs	viewer show the genomic	position. For
starts negative, with the A in the ATC transcripts on the reverse strand the Introns I UTR Protein d Position: 0 Zoom: x 1 S Sequence 3-UTR 5-UTR CDS Nonsyn SNPs NoncDS SNPs Syn SNPs	a start codon being position 1. Th reverse complement is shown. Iomains ☑ SNPs ☑ Syn. S	e SNP labels in the feature NPs ☑ Nonsyn. SNPs	viewer show the genomic	position. For
starts negative, with the A in the ATG transcripts on the reverse strand the Introns I UTR Protein d Position: 0 Zoom: x 1 S Sequence 3:UTR CDS Introns Nonsyn, SNPs NonCDS SNPs	a start codon being position 1. Th reverse complement is shown. Iomains ☑ SNPs ☑ Syn. S	e SNP labels in the feature NPs ☑ Nonsyn. SNPs	viewer show the genomic	position. For

2.4 Results for selection

If you compute the results SNPstar shifts directly to the section 'Results for selection'.

elect transcript and accessions	Results for selection	Search SN	IP database	
		_		
Results: AT4G30120.	1		Download options v	Down
ATHMA3: A. THALIAI	NA HEAVY			
METAL ATPASE 3; H	MA3: Heavy meta	I		
atpase 3				
Check selected accessions				
Sequence viewer () SN	Ps () SNPs <-> Acces	sions 🛈 🛛 H	laplotype <-> Accession table ()	
Protein haplotype <-> Acce	ssion table O			
1. 31				
		in the feature view	ver starts with 0 while the genomic position	n in the 5'U
Please note: Indels are not includ	ed in this tab. For now the positior		wer starts with 0, while the genomic position ne feature viewer show the genomic position	
Please note: Indels are not includ	ed in this tab. For now the position FG start codon being position 1. Th			
Please note: Indels are not includ starts negative, with the A in the A' transcripts on the reverse strand th	ed in this tab. For now the position I'G start codon being position 1. Th he reverse complement is shown.	ne SNP labels in th		n. For
Please note: Indels are not includ starts negative, with the A in the A' transcripts on the reverse strand th	ed in this tab. For now the position I'G start codon being position 1. Th he reverse complement is shown.	ne SNP labels in th	e feature viewer show the genomic position	n. For
Please note: Indels are not includ starts negative, with the A in the A' transcripts on the reverse strand th	ed in this tab. For now the position I'G start codon being position 1. Th he reverse complement is shown.	ne SNP labels in th SNPs ☑ Nonsyr	ne feature viewer show the genomic position	n. For
Please note: Indels are not includ starts negative, with the A in the A' transcripts on the reverse strand the Introns VUTR Protein	ed in this tab. For now the position IG start codon being position 1. Th he reverse complement is shown. domains I SNPs I Syn. S	ne SNP labels in th SNPs ☑ Nonsyr	ne feature viewer show the genomic position	n. For
Please note: Indels are not includ starts negative, with the A in the A' transcripts on the reverse strand II Infrons II UTR IP Protein Position: 0 Zoom: x 1 Sequence 3/UTR	ed in this tab. For now the position IG start codon being position 1. Th he reverse complement is shown. domains I SNPs I Syn. S	ne SNP labels in th SNPs ☑ Nonsyr	ne feature viewer show the genomic position	n. For
Please note: Indels are not includ starts negative, with the A in the A' transcripts on the reverse strand th I Introns I UTR I Protein Position: 0 Zoom: x 1 Sequence	ed in this tab. For now the position IG start codon being position 1. Th he reverse complement is shown. domains I SNPs I Syn. S	ne SNP labels in th SNPs ☑ Nonsyr	ne feature viewer show the genomic position	n. For
Please note: Indels are not includ stars negative, with the A in the A' transcripts on the reverse strand the Introns I UTR I Protein Position: 0 Zoom: x 1 Sequence 3'-UTR COS Introns	ed in this tab. For now the position IG start codon being position 1. Th he reverse complement is shown. domains I SNPs I Syn. S	ne SNP labels in th SNPs ☑ Nonsyr	ne feature viewer show the genomic position	n. For
Please note: Indels are not includ starts negative, with the A in the A' transcripts on the reverse strand the lintrons line of the area of the area of the Position: 0 Zoom: x 1 Sequence 3'-UTR D'SUTR CDS Introns Nonsyn, SNPs	ed in this tab. For now the position IG start codon being position 1. Th he reverse complement is shown. domains I SNPs I Syn. S	ne SNP labels in th SNPs ☑ Nonsyr	ne feature viewer show the genomic position	n. For
Please note: Indels are not includ starts negative, with the A in the A' transcripts on the reverse strand the local starts of the reverse strand the local starts of the reverse strand the local starts of the reverse strand the Position: 0 Zoom: x 1 Sequence 3'-UTR S-UTR CDS Infroms Nonsyn SNPs NonCDS SNPs	ed in this tab. For now the position IG start codon being position 1. Th he reverse complement is shown. domains I SNPs I Syn. S	ne SNP labels in th SNPs ☑ Nonsyr	ne feature viewer show the genomic position	n. For
Please note: Indels are not includ stars negative, with the A in the A' transcripts on the reverse strand the line of the area of the area of the area of the Position: 0 Zoom: x 1 Sequence 3-UTR Dostrons Nonsyn SNPs NonCDS SNPs Syn SNPs Prot domains	ed in this tab. For now the position IG start codon being position 1. The reverse complement is shown. domains SNPs SSNPs SSNPs SNP with minor allele frequency SNP with minor allele frequency Henry Henry Henry Henry Henry Henry Henry Henry Henry Henry Henry Henry Henry Henry Henry Henry Henry Hen	ne SNP labels in th SNPs ☑ Nonsyr	ne feature viewer show the genomic position	n. For
Please note: Indels are not includ stars negative, with the A in the A' transcripts on the reverse strand the local strange of the strange of the strange of the strange of the strange of the strange Position: 0 Zoom: x 1 Sequence 3'-UTR 0'-DS Nonsyn SNPs Syn SNPs Prot. domains	ed in this tab. For now the position 1. The reverse complement is shown. domains SNPs SNPs Syn. 5 SNP with minor allele frequency Humpher and the state of the state of the state Humpher and the state of the state of the state Humpher and the state of the state of the state Humpher and the state of the state of the state Humpher and the state of the state of the state of the state Humpher and the state of the	ne SNP labels in th SNPs ☑ Nonsyr	ne feature viewer show the genomic position	n. For
Please note: Indels are not includ stars negative, with the A in the A' transcripts on the reverse strand the local strange of the strange of the strange of the strange of the strange of the strange Position: 0 Zoom: x 1 Sequence 3'-UTR 0'-DS Nonsyn SNPs Syn SNPs Prot. domains	ed in this tab. For now the position IG start codon being position 1. Th ne reverse complement is shown. domains SNPs SNPs SNPs SNP. SNP with minor allele frequency	ne SNP labels in th SNPs ☑ Nonsyr	ne feature viewer show the genomic position	n. For
Please note: Indels are not includ stars negative, with the A in the A' transcripts on the reverse strand the local strange of the strange of the strange of the strange of the strange of the strange Position: 0 Zoom: x 1 Sequence 3'-UTR 0'-DS Nonsyn SNPs Syn SNPs Prot. domains	ed in this tab. For now the position 1. The reverse complement is shown. domains SNPs SNPs Syn. 5 SNP with minor allele frequency Humpher and the state of the state of the state Humpher and the state of the state of the state Humpher and the state of the state of the state Humpher and the state of the state of the state Humpher and the state of the state of the state of the state Humpher and the state of the	ne SNP labels in th SNPs ☑ Nonsyr	ne feature viewer show the genomic position	n. For

Here, you have different options to display your results as described in the following chapters.

2.4.1 Sequence viewer

The first tab of results is the 'Sequence viewer'.

• Top: Graphical overview of SNP positions in relation to nucleotide and amino acid sequence features like UTRs, intron, protein domains. Bottom: Plain genomic, coding and amino acid sequence with SNPs color coded by SNP type. Amino acid substitution (not context dependent but for single SNPs).

All options and possibilities are described in the following.

Select transcript and accessions	Results for selection	Search SNP da	alabase	
Results: AT4G30120.1		Down	load options	▼ Do
ATHMA3: A. THALIAN METAL ATPASE 3; HM		I		
atpase 3				
Sequence viewer 1 SNP	s () SNPs <-> Acces	sions 🚯 🛛 Haplo	otype <-> Accessio	n table 🕕
Protein haplotype <-> Access	sion table 🚯			
Please note: Indels are not included starts negative, with the A in the ATC transcripts on the reverse strand the Introns I UTR Protein d	start codon being position 1. The reverse complement is shown.	e SNP labels in the feat	ture viewer show the ger	nomic position. For
starts negative, with the A in the ATC transcripts on the reverse strand the Introns I UTR Protein d Position: 0 Zoom: x 1 S Sequence 3-UTR	start codon being position 1. The reverse complement is shown.	e SNP labels in the feat NPs ☑ Nonsyn. SN	ture viewer show the ger	nomic position. For
starts negative, with the A in the ATG transcripts on the reverse strand the introns I UTR Protein d Position: 0 Zoom: x 1 S Sequence	start codon being position 1. Th reverse complement is shown. omains 🗹 SNPs 🗹 Syn. S	e SNP labels in the feat NPs ☑ Nonsyn. SN	ture viewer show the ger	nomic position. For
starts negative, with the A in the ATG transcripts on the reverse strand the Introns © UTR © Protein d Position: 0 Zoom: x 1 S Sequence 3'-UTR S-UTR CDS Introns Nonsyn_SNPs	start codon being position 1. Th reverse complement is shown. omains 🗹 SNPs 🗹 Syn. S	e SNP labels in the feat NPs ☑ Nonsyn. SN	ture viewer show the ger	nomic position. For
starts negative, with the A in the ATG transcripts on the reverse strand the Introns © UTR © Protein d Position: 0 Zoom: x 1 S Sequence S-UTR S-UTR CDS Introns	start codon being position 1. Th reverse complement is shown. omains 🗹 SNPs 🗹 Syn. S	e SNP labels in the feat NPs ☑ Nonsyn. SN	ture viewer show the ger	nomic position. For
stats negative, with the A in the ATC transcripts on the reverse strand the Introns © UTR © Protein d Position: 0 Zoom: x 1 S Sequence 3-UTR CDS Nonsyn. SNPS NonCDS SNPS Prot. domains	start codon being position 1. Th reverse complement is shown. omains 🗹 SNPs 🗹 Syn. S	e SNP labels in the feat NPs ☑ Nonsyn. SN	ture viewer show the ger	nomic position. For
starts negative, with the A in the ATG transcripts on the reverse strand the Introns © UTR © Protein d Position: 0 Zoom: x 1 S Sequence 3:-UTR CDS Introns Nonsyn: SNPs NonCDS SNPs Syn: SNPs Prot. domains	start codon being position 1. Th reverse complement is shown. omains 🗹 SNPs 🗹 Syn. S	e SNP labels in the feat NPs ☑ Nonsyn. SN	ture viewer show the ger	nomic position. For
starts negative, with the A in the ATG transcripts on the reverse strand the Introns © UTR © Protein d Position: 0 Zoom: x 1 S Sequence 3'-UTR S'-UTR CDS Introns Nonsyn: SNPs NonCDS SNPs Prot. domains	start codon being position 1. There exerce complement is shown. omains I SNPs I Syn. S INP with minor allele frequency	e SNP labels in the feat NPs ☑ Nonsyn. SN	ture viewer show the ger	nomic position. For

You have different possible selections for 'Sequence viewer'. You can mark none or all of the available genomic features for display.

		_		
Results: AT4G30120.1			ownload options	✓ Do
ATHMA3: A. THALIAN	A HEAVY			
METAL ATPASE 3; HM	1A3: Heavy meta			
atpase 3				
Check selected accessions -				
Sequence viewer () SNP	s () SNPs <-> Acces	sions 🟮 🛛 Ha	plotype <-> Acces	sion table 🚯
	ter teles o			
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nothing selected: shown is the whole sequence in base pairs (bp) and coding sequence (CDS)

Introns: shown is the whole sequence (in bp), CDS and introns of selected gene **UTR (untranslated region):** shown is the whole sequence (in bp), 3'-UTR, 5'-UTR and coding sequence (CDS) of selected gene

Prot. domains (protein domains): shown is the whole sequence (in bp), coding sequence (CDS) and protein domains of selected gene

Noncoding SNPs (Noncoding single nucleotide polymorphisms): shown is the whole sequence (in bp), coding sequence (CDS) and SNPs in non coding regions (NonCDS SNPs)

Syn. SNPs (Synonymous SNPs): shown is the whole sequence (in bp), coding sequence (CDS) and synonymous SNPs in coding regions

Nonsyn. SNPs (Nonsynonymous SNPs): shown is the whole sequence (in bp), coding sequence (CDS) and nonsynonymous SNPs in coding regions

CDS only (coding sequence only): shown is the whole sequence (in bp),

nonsynonymous SNPs, synonymous SNPs and protein domains

Protein sequence only: shown is the whole sequence (in amino acids [AA]),

nonsynonymous SNPs, synonymous SNPs and protein domains

To show multiple features, mark all elements of interest. As an example shown are introns, protein domains and nonsynonymous SNPs.

Select transcript and accession	Results for selection	Search SNP database	Build & Download GWAS matrix	El <u>Manua</u>
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It's possible to zoom in. Click and hold the left mouse button to mark a region of interest.

Select transcript and accessions	Results for selection	Search SNP database	
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The zoom factor is shown as well.

ATHMA3: A. THALIANA HEAVY METAL ATPASE 3; HMA3: Heavy metal atpase 3 Cireck indecide accessions Sequence viewer SNPs SNPs SNPs <-> Accessions Haplotype <-> Accession table Protein haplotype <-> Accession table Protein haplotype <-> Accession table Hease note: Indels are experimentation on the position in the feature viewer starts with 0, while the genomic position in the 50 starts negative, with the start codon being position 1. The SNP labels in the feature viewer show the genomic position. For reverse complement is shown.	Results: AT4G30120.1 Download options Download ATHMA3: A. THALIANA HEAVY METAL ATPASE 3; HMA3: Heavy metal atpase 3 Image: Constraint of the state of the	bout								
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To zoom out (to zoom factor 1) click with the right mouse button on the figure.

SNPs are displayed as vertical lines. Gray color indicates a SNP with a minor allele frequency <1%, while and black vertical lines indicate SNPs with a minor allele frequency >1%.

elect transcript and accessions	Results for selection	Search SNP database	
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If you hover with the mouse cursor over a SNP the sequence position (in bp) and specific base are shown (e.g. 1107T).

ATHMA3: A. THALIANA HEAVY METAL ATPASE 3; HMA3: Heavy metal atpase 3	Describes ATAOOOAOO				
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With the mouse cursor on a specific SNP the position in bp (1107 - 1108), chromosome:whole chromosome position (4:14732522), polymorphism with CDS position in bp (C981T) and minor allele frequency (0.18%) are shown.

elect transcript and accession	ns Results for selection	Search SNP database	
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You can download the 'Sequence viewer' figure (as svg file) by clicking the 'Download view' button.

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Beneath of the above described figure, you can find DNA or amino acid sequence views.

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Prot. (Jomains						
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		500	1000	1000			

There are three different sequence types available.

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genomic sequence: shows the whole sequence region of selected gene **CDS:** shows only coding sequence of selected gene

Amino acid sequence: shows AA sequence of selected protein

Genomic sequence CDS A AGCCTANACC ANATARTIA TITICCCCCC CG ACATCATCE GTANANGAT CTCTCCCG CDS A AGACTCANAG MARTCANS MARTCAGAT TACAGACAN TACTAGA CGATAGAT TACAGACAN TACTAGAC CANANGAT CTCTCCG A AGACTCANAG MARTCANS MARTCAGAT TACAGACAN TACTAGAC CANANGAT TACAGACAN TACAGACAN TACAGACAN TACAGACAN ACTITITICA ACTITITICA ACCOMPACT AND ACCOMPACT AND ACCOMPACT AND ACCOMPACT ACTIONAL CANANGAT TACAGACAN TACAGACAN TACAGACAN ACTITITICA ACTITITICA ACCOMPACT AND ACCOMPACT AND ACCOMPACT AND ACCOMPACT ACTIONAL CANANGAT TACAGACANAG TACAGACANAG TACAGACANAG TACAGACANAG TACAGACANAG TACAGACANAG TACAGACANAGAT ANTAGATACANAGA TACAGACANAGATACANAGA TACAGACANAGATACANAGA TACAGACANAGATACANAGA TACAGACANAGATACANAG								~	sequence	Genomic	ience ty	Sequ
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681 («Витасттт тальятсас тралеваст (Стататат ассавяенае ставаятт сселатст «Влажансте терстлася салавая Э81 Васствала саласветст састетлает оставтама Дасаматест титесствае сателевства тоття) та табаветам атематес Э81 ПТВеттамт ття така са ваталаса лессятата техновант содамает сталемате всталемате в терсти?												
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The different colors indicate (for all three sequence types): black letters: intron sequence purple letters: CDS red letters: 5' and 3' UTR sequence yellow background: Nonsynonymous SNP blue background: Synonymous SNP green background: a SNP in a UTR or intron region

2.4.2 SNPs

The next tab of results is 'SNPs'. This part describes the characteristics of all detected SNPs in detail.

SNPs ①: Information about each polymorphic position in the selected transcript computed for the selected accessions (GWAS, always for all accessions); e.g. base frequencies, protein description, amino acid frequencies, GWAS results etc. All options and possibilities are described in the following.

Select transcript and acce		sults for selection	Search SNF	^o database		
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Introns						
NonCDS SNPs						
Syn. SNPs Prot. domains						
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					L.	Download view

SNP_ID (Genomic position): ^① Chromosome number:genomic position e.g. 4:14730221. SNP identification number. Shown are chromosome:bp position (4:14730221) of each SNP of the selected gene. The empty field below the header can be used for a specific SNP ID search.

Base frequencies: ① You can sort according to the highest base frequency for each SNP and you can input a cutoff for the lowest allowed minor allele frequency. Shown are polymorphisms (base \rightarrow base) and the frequencies (number behind) specific SNPs. The polymorphism with the same bases (e.g. $C \rightarrow C$) is for the reference genotype (Col-0).

Genic position: 1 Position 1, is the A in the ATG start codon. The 5'-UTR has negative indices. For isoforms on the reverse strand we count the same position, but in the reverse complement. SNP base pair position of selected gene gDNA (genomic DNA).

mRNA Position: • Position 1 is the A in the ATG start codon. The 5'-UTR has negative indices. Introns are not included. For isoforms on the reverse strand we count the same position, but in the reverse complement. SNP base pair position of selected gene mRNA.

SNP location: Gene structure location (e.g. 3' UTR (untranslated region), INTRON etc.) of SNP and selected gene.

SNP effects: 1 This includes the effect of the SNP at this position in the reference, ignoring other SNPs in the neighborhood. Canonical motif in splice site means the first dinucleotides in the intron of the splice site (donor GT, acceptor AG). Splice site region describes the region 1 – 3 in the flanking exon and the positions 3 – 8 in the flanking intron of the splice site. Effects are equally defined to SnpEff (A program for annotating and predicting the effects of single nucleotide polymorphisms, SnpEff: SNPs in the genome of *Drosophila melanogaster* strain w1118; iso-2; iso-3., Cigolani P; Platts A, Wang le L, Coon M, Nguyen T, Wang L, Land SJ, Lu W, Ruden DM. Fly (Austin): 2012). Effect of SNP on AA sequence of selected gene (e.g. stop codon (premature stop codon), nonsynonymous (AA substitution), canonical motif in splice site etc.)

Amino acid substitution: ^① Amino acid exchange caused by a nonsynonymous SNP in the codon (example: Q -> H means a glutamine in the reference sequence was substituted by a histidine in the SNP harboring allele).

Chemical properties: Physicochemical properties of AA substitution (e.g. non-polar \rightarrow polar, basic \rightarrow acidic etc.)

	Select transcript	and access	sions Re	sults for selec	tion Search SNP database			
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(Genomic position) 4:14732045		position ()	Position 🕄	INTRON		substitution 🕄	Chemical properties	Inter
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4:14732045	$\begin{tabular}{ c c c c c } \hline Default: No cutoff \\ \hline C &\sim C: 0.70485 \\ \hline C &\sim T: 0.29515 \\ \hline G &\sim G: 0.72863 \\ \hline G &\sim T: 0.27137 \\ \hline T &\sim A: 0.29163 \\ \hline \end{tabular}$	1458		INTRON	nonsynonymous			Inter
4:14732045 4:14731525 4:14731691	$\begin{tabular}{ c c c c c } \hline Default: No cutoff \\ \hline C &> C: 0.70485 \\ \hline C &> T: 0.29515 \\ \hline G &> G: 0.72863 \\ \hline G &> T: 0.27137 \\ \hline T &> A: 0.29163 \\ \hline T &> T: 0.70837 \\ \hline \end{tabular}$	1458 1978 1812	1343	INTRON CDS CDS	nonsynonymous	R->1	basic -> non-polar	Inter
4:14732045 4:14731525	$\begin{tabular}{ c c c c c c c c c c c c c c c c c c c$	1458	1343	INTRON		R->1	basic -> non-polar	Inter
4:14732045 4:14731525 4:14731691 4:14730093	$\label{eq:constraints} \hline \begin{tabular}{ c c c c c } \hline Default: No cutoff \\ \hline C \sim C: 0.70485 \\ \hline C \sim T: 0.29515 \\ \hline G \sim T: 0.27137 \\ \hline T \sim X: 0.29163 \\ \hline T \sim T: 0.70837 \\ \hline A \sim X: 0.60784 \\ \hline A \sim T: 0.33216 \\ \hline \end{tabular}$	1458 1978 1812 2510	1343	INTRON CDS CDS INTRON	nonsynonymous canonical motif in splice site	R->1	basic -> non-polar	Inter
4:14732045 4:14731525 4:14731691	Default: No cutoff C ~ C: 0.70485 C ~ T: 0.29515 G ~ G: 0.72863 G ~ T: 0.27137 T ~ A: 0.29163 T ~ T: 0.70837 A ~ A: 0.66784 A ~ T: 0.33216 C ~ A: 0.33304	1458 1978 1812	1343	INTRON CDS CDS	nonsynonymous	R->1	basic -> non-polar	Inter
4:14732045 4:14731525 4:14731691 4:14730093	$\begin{tabular}{ c c c c } \hline Default: No cutoff \\ \hline C -> C: 0.70485 \\ \hline C -> T: 0.29515 \\ \hline G -> C: 0.72863 \\ \hline G -> T: 0.27137 \\ \hline T -> A: 0.29163 \\ \hline T -> T: 0.70837 \\ \hline A -> A: 0.66784 \\ \hline A -> T: 0.33216 \\ \hline C -> C: 0.86696 \\ \hline \end{tabular}$	1458 1978 1812 2510	1343	INTRON CDS CDS INTRON INTRON	nonsynonymous canonical mobil in splice site canonical mobil in splice site	R->1	basic -> non-polar	Inter
4:14732045 4:14731525 4:14731691 4:14730993 4:14730994	Default: No cutoff C ~ C: 0.70485 C ~ T: 0.29515 G ~ G: 0.72863 G ~ T: 0.27137 T ~ A: 0.29163 T ~ T: 0.70837 A ~ A: 0.66784 A ~ T: 0.33216 C ~ A: 0.33304	1458 1978 1812 2510 2509	1343 1276	INTRON CDS CDS INTRON	nonsynonymous canonical motif in splice site	R->1	basic -> non-polar	
4:14732045 4:14731525 4:14731691 4:14730993 4:14730994	$\begin{tabular}{ c c c c c } \hline Default: No cutoff \\ \hline \hline C \rightarrow C: 0.70485 \\ \hline C \sim T: 0.29515 \\ \hline G $<$ C: 0.72863 \\ \hline G \sim T: 0.27137 \\ \hline T \rightarrow A: 0.27163 \\ \hline T \rightarrow T: 0.70837 \\ \hline A \rightarrow A: 0.66784 \\ \hline A \rightarrow T: 0.33216 \\ \hline C \rightarrow C: 0.36096 \\ \hline G \rightarrow C: 0.5022 \\ \hline \end{tabular}$	1458 1978 1812 2510 2509	1343 1276	INTRON CDS CDS INTRON INTRON	nonsynonymous canonical mobil in splice site canonical mobil in splice site	R->1	basic -> non-polar	Inter
4:14732045 4:14731525 4:14731691 4:14730993 4:14730994 4:14733389	$\label{eq:constraint} \hline \begin{array}{ c c c c c c c c c c c c c c c c c c c$	1458 1978 1812 2510 2509 114	1343 1276 114	INTRON CDS CDS INTRON INTRON CDS	nonsynonymous canonical motif in splice site canonical motif in splice site synonymous	R → 1 Y → N	basic -> non-polar polar -> polar	
4:14732045 4:14731525 4:14731691 4:14730993 4:14730994 4:14733389	$\label{eq:constraints} \begin{bmatrix} Default: No cutoff \\ C \leftrightarrow C: 0.70485 \\ C \to T: 0.29515 \\ G \to G: 0.72683 \\ G \to T: 0.27137 \\ T \leftrightarrow A: 0.29163 \\ T \to T: 0.70837 \\ A \to A: 0.60784 \\ A \to T: 0.33216 \\ C \leftrightarrow A: 0.33204 \\ C \to C: 0.6666 \\ G \to G: 0.5022 \\ G \to T: 0.4978 \\ A \to A: 0.50338 \\ \end{bmatrix}$	1458 1978 1812 2510 2509 114	1343 1276 114	INTRON CDS CDS INTRON INTRON CDS	nonsynonymous canonical motif in splice site canonical motif in splice site synonymous	R → 1 Y → N	basic -> non-polar polar -> polar	
4:14732045 4:14731525 4:14731691 4:14730993 4:14730994 4:14733399 4:14733393	$\label{eq:constraint} \begin{bmatrix} Default No cutoff \\ C \Rightarrow C: 0.70485 \\ c \Rightarrow T: 0.27853 \\ G \Rightarrow C: 0.72863 \\ G \Rightarrow T: 0.27137 \\ T \Rightarrow X: 0.29163 \\ T \Rightarrow X: 0.29163 \\ T \Rightarrow X: 0.06784 \\ A \Rightarrow T: 0.33216 \\ C \Rightarrow C: 0.06076 \\ C \Rightarrow C: 0.3324 \\ C \Rightarrow C: 0.06778 \\ A \Rightarrow C: 0.4978 \\ A \Rightarrow C: 0.4978 \\ A \Rightarrow C: 0.4978 \\ A \Rightarrow C: 0.49692 \\ \end{bmatrix}$	1458 1978 1812 2510 2509 114 110	1343 1276 114	INTRON CDS CDS INTRON INTRON CDS CDS	nonsynonymous canonical motif in splice site canonical motif in splice site synonymous	R → 1 Y → N	basic -> non-polar polar -> polar	
4:14732045 4:14731525 4:14731691 4:14730993 4:14730994 4:14733399 4:14733393	$\label{eq:constant} \begin{split} Default 140 contoff \\ C &\sim C: 0.70485 \\ C &\sim T: 0.29515 \\ G &\sim T: 0.29515 \\ G &\sim T: 0.27137 \\ T &\sim X: 0.27137 \\ T &\sim X: 0.27137 \\ T &\sim X: 0.5724 \\ X &\sim X: 0.33216 \\ C &\sim X: 0.66784 \\ X &\sim X: 0.33216 \\ C &\sim X: 0.5022 \\ G &\sim T: 0.4678 \\ A &\sim C: 0.40962 \\ T &\sim X: 0.4348 \\ G &\sim X: 0.4348 \\ C &\sim X: 0.4348 \end{split}$	1458 1978 1812 2510 2509 114 110	1343 1276 114	INTRON CDS CDS INTRON INTRON CDS CDS	nonsynonymous canonical motif in splice site canonical motif in splice site synonymous	R → 1 Y → N	basic -> non-polar polar -> polar	
4:14732045 4:14731525 4:14731691 4:14730993 4:14733994 4:14733393 4:14733393	$\label{eq:constraint} \begin{array}{c} \mbox{Default No cutoff} \\ \mbox{C} \rightarrow Cr. 0.70485 \\ \mbox{C} \rightarrow Cr. 0.72851 \\ \mbox{G} \rightarrow Cr. 0.29515 \\ \mbox{G} \rightarrow Cr. 0.29515 \\ \mbox{G} \rightarrow Cr. 0.29516 \\ \mbox{T} \rightarrow Cr. 0.29163 \\ \mbox{T} \rightarrow Cr. 0.29163 \\ \mbox{T} \rightarrow Cr. 0.06076 \\ \mbox{G} \rightarrow Cr. 0.0502 \\ \mbox{G} \rightarrow Cr. 0.05062 \\ \mbox{T} \rightarrow Cr. 0.05062 \\ \mbox{T} \rightarrow Cr. 0.3548 \\ \end{array}$	1458 1978 1812 2510 2509 114 110 1247	1343 1276 114 110	INTRON CDS CDS INTRON INTRON CDS CDS CDS CDS	canonscar modif in splice site canonscar modif in splice site canonical modif in splice site synonymous nonsynonymous	R → 1 Y → N	basic -> non-polar polar -> polar	

Interpro ID: Protein domain ID in which the AA substitutions are located. This information is based on the InterPro database (functional analysis of proteins by classifying them into families and predicting domains and important sites).

Interpro description: Description of InterPro domain

Domain id: Protein domain ID in which the AA substitutions are located. This information is based on Interproscan.

Domain description: Description of domain.

	🗩 About		
	Select trans	cript and accessions Results for selection Search SNP database	60
	Build & Dow	nload GWAS matrices	
	Results	: AT4G30120.1 Download options	 Download
	METAL atpase	ed accessions	
		Accessions (1) Haplotype	<-> Accession table 19
	Protein	haplotype <-> Accession table ()	
Interpro Id	Interpro description	Domain Id	Domain description
			·
		PTHR11939:SF31,PTHR11939,G3DSA:2.70.150.10	HEAVY METAL CATION TRANSPORT ATPASE (CADMI
		PTHR11939:SF31,PTHR11939,G3DSA:2.70.150.10	HEAVY METAL CATION TRANSPORT ATPASE (CADM
		PTHR11939:SF31,PTHR11939,SSF81660	HEAVY METAL CATION TRANSPORT ATPASE (CADMI
		PF00122,TIGR01494,PTHR11939:SF31,PTHR11939,SSF81653,SSF81665,G3DSA:2.70.150.1	0 E1-E2_ATPase,ATPase_P-type: HAD ATPase, P-type, fr
		PTHR11939:SF31,PTHR11939,SSF81665,SSF81660	HEAVY METAL CATION TRANSPORT ATPASE (CADMI

Strand: Strand direction of sequence (e.g. - and +).

AraGWAS top hits: 1 Top associations imported from the AraGWAS tool as of 10/11/20242024. The score is -log10(p-value) of the hit. The link links to the study on AraGWAS. The table can be sorted according to the lowest score in each cell. e.g. study ID: 29.528 (AraGWAS SNP)

AraGWAS Catalog link of study information of selected SNP and gene. AraGWAS score (-log₁₀ (*p*-value)) of selected SNP and gene. AraGWAS Catalog link of GWAS information of selected SNP and gene.

AraGWAS data based on the AraGWAS Catalog, which is a publicly and manually curated database for standardized GWAS (genome wide association study) results for *Arabidopsis thaliana*. Database is published on the 1001 genome homepage (<u>https://aragwas.1001genomes.org/#/</u>).

GWAS corrected p-values: GWAS analysis was performed with the software GEMMA. Every climate factor was used as a phenotype and for every climate factor, one analysis run was carried out. Only SNPs with a minor allele frequency of 1% or higher were analysed. The obtained p-values were corrected for multiple comparisons using the Benjamini-Yekutiel method. In this column you can see all the correlations between SNPs and the 200 climate factors which have a corrected p-value lower than or equal to the threshold. You can sort the column according to the lowest p-value in each cell.

Number of associated climate factors: (1) Number of associated climate factors with a corrected P-value in the GWAS lower than or equal to the threshold.

	About				
	Select transcript and accessions	Results for selection	Search SNP database		
	Build & Download GWAS matrices				
	Results: AT4G30120.1		Download options	 Download 	
	ATHMA3: A. THALIAN METAL ATPASE 3; HN atpase 3		I		
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	_		AraGWAS top hits	GWAS corrected	Number of
		Stran	d 0	p-values	associated
		Stran	P-value cutoff def.: <0.05	p-values P-value cutoff def.: <0.05	climate factors
		Stran	-	-	
		Stran -	P-value cutoff def.: <0.05	-	climate factors
		Stran - -	P-value cutoff def.: <0.05 study_ID: 287: 29.528 (AraGWAS SNP)	-	climate factors
		Stran - - -	P-value cutoff def: <0.05	-	climate factors () 0
		Stan ·	P-value cutoff def. = 0.05 study_ID: 287: 29.528 (AraGWAS SNP) study_ID: 287: 24.146 (AraGWAS SNP) study_ID: 287: 21.205 (AraGWAS SNP)	-	climate factors 0 0 0
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2.4.3 SNPs \leftrightarrow Accessions

The tab 'SNPs \leftrightarrow Accessions' shows a table for SNP/accession associations.

 $SNPs \leftarrow Accessions$ **1**: Information about each polymorphism in the selected transcript computed for the selected accession. List of accessions in which the polymorphism exists, effect of the polymorphism, amino acid change and SNP quality. All options and possibilities are described in the following.

Results: AT40	220120 1					Down
Results: AT40	530120.1			ownload options	*	Down
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starts negative, with transcripts on the r Introns Introns Sequence S-UTR CDS Introns Nonsyn, SNPS	h the A in the ATG start codo everse strand the reverse co R ☑ Protein domains	n being position 1. The omplement is shown. SNPs VSyn. St	e SNP labels i NPs ☑ Nor	n the feature viewer sh	now the genomic po	osition. For

All empty fields beneath column titles can be used for specific searching (it is important to use the correct format!)

SNP Id: 1 Chr.Pos e.g. 4:14731188. SNP identification number. Shown are chromosome:bp positions (4:14731188) of each SNP of the selected gene. **Polymorphism:** List of polymorphisms (SNPs or InDels). For example: $C \rightarrow G$, always the first base (C) is from Col-0 (reference genotype) \rightarrow the second base (G) from other accessions.

CS numbers and accessions: Download link for a list of genotypes different to Col-0. Shown are accessions with 1001 genome project Id, accession name and CS numbers. **Accession_IDs (1001 genomes):** List of genotypes different to Col-0. Shown are accession IDs from 1001 Genome project.

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Results: AT4	IG30120.1		Download options
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		CS numbers and	
SNP_ID	Polymorphism	accessions	Accession_IDs (1001genomes)
4:14731188	C -> G	Download CS numbers	9824
4:14731200	C -> T	and accessions Download CS numbers	6911
		and accessions	
4:14731132	A -> TA	Download CS numbers and accessions	88, 139, 159, 265, 410, 428, 470, 476, 484, 504, 506, 531, 544, 546, 62 680, 681, 685, 687, 728, 742, 763, 765, 766, 768, 772, 801, 853, 854, 8
			868, 870, 915, 932, 992, 997, 1002, 1006, 1061, 1062, 1063, 1066, 116
			1313, 1317, 1612, 1622, 1651, 1652, 1676, 1684, 1739, 1741, 1756, 17
			1793, 1797, 1819, 1820, 1829, 1834, 1835, 1851, 1852, 1853, 1872, 18
			1925, 1942, 1943, 1954, 2016, 2017, 2053, 2057, 2081, 2091, 2106, 21 2141, 2159, 2166, 2191, 2202, 2212, 2239, 2240, 2276, 2285, 2286, 23
			2412, 4779, 4807, 4826, 4840, 4857, 4900, 4939, 4958, 5023, 5165, 52
			5249, 5253, 5276, 5279, 5349, 5353, 5395, 5577, 5651, 5717, 5720, 57
			5741, 5748, 5776, 5779, 5784, 5798, 5822, 5831, 5832, 5836, 5837, 58
			5741, 5748, 5776, 5779, 5784, 5798, 5822, 5831, 5832, 5836, 5837, 58 5860, 5865, 5867, 5921, 5950, 5984, 6008, 6009, 6010, 6011, 6012, 60
			5741, 5748, 5776, 5779, 5784, 5798, 5822, 5831, 5832, 5836, 5837, 58
			5741, 5748, 5776, 5779, 5784, 5798, 5822, 5831, 5832, 5836, 5837, 56 5860, 5865, 5867, 5921, 5950, 5984, 6008, 6009, 6010, 6011, 6012, 60 6016, 6017, 6019, 6020, 6021, 6022, 6023, 6024, 6025, 6030, 6034, 60

2.4.4 DNA Haplotype ↔ Accessions

The tab 'DNA Haplotype \leftrightarrow Accessions' shows a table for DNA haplotype/accession associations.

DNA Haplotype \leftrightarrow Accessions ①: Accessions with the same polymorphisms in the selected CDS of the selected transcript have the same transcript specific haplotype. All options and possibilities are described in the following.

Select transcript and	accessions	Results for selection	Search SNP database	
Build & Download G	WAS matrices			
Results: AT4	G30120.1		Download options	- Download
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starts negative, w transcripts on the	Is are not included th the A in the ATG reverse strand the	in this tab. For now the position start codon being position 1. Tl reverse complement is shown.	he SNP labels in the feature viewer sh	
Please note: Inde starts negative, w transcripts on the	Is are not included th the A in the ATG reverse strand the FR Z Protein de	in this tab. For now the position start codon being position 1. Tl reverse complement is shown.	he SNP labels in the feature viewer st SNPs ☑ Nonsyn, SNPs □ CDS	low the genomic position. For
Please note: Inde starts negative, w transcripts on the ☑ Introns ☑ U	Is are not included th the A in the ATG reverse strand the FR Z Protein de	in this tab. For now the position start codon being position 1. Ti reverse complement is shown. omains SNPs SNPs, Syn. 9	he SNP labels in the feature viewer st SNPs ☑ Nonsyn, SNPs □ CDS	low the genomic position. For
Please note: Inde starts negative, w transcripts on the Introns I U Position: 0	Is are not included th the A in the ATG reverse strand the FR Z Protein de	in this tab. For now the position start codon being position 1. Ti reverse complement is shown. omains SNPs SNPs, Syn. 9	he SNP labels in the feature viewer st SNPs ☑ Nonsyn, SNPs □ CDS	low the genomic position. For
Please note: Indi starts negative, w transcripts on the Introns I U Position: 0 Sequence 3'-UTR	Is are not included th the A in the ATG reverse strand the FR Z Protein de	in this tab. For now the position start codon being position 1. Ti reverse complement is shown. omains SNPs SNPs, Syn. 9	he SNP labels in the feature viewer st SNPs ☑ Nonsyn, SNPs □ CDS	low the genomic position. For
Please note: Inde starts negative, w transcripts on the Introns I U Position: 0 Sequence 3'-UTR CDS Introns	Is are not included th the A in the ATG reverse strand the FR Z Protein de	in this tab. For now the position start codon being position 1. Ti reverse complement is shown. omains SNPs SNPs, Syn. 9	he SNP labels in the feature viewer st SNPs ☑ Nonsyn, SNPs □ CDS	low the genomic position. For
Please note: Inde starts negative, w transcripts on the Introns I U Sequence 3-UTR CDS Introns Nonsyn, SNPs	Is are not included In the A in the ATG reverse strand the IR I Protein du Zoom: x1 S	in this tab. For now the position start codon being position 1. Ti reverse complement is shown. omains SNPs SNPs, Syn. 9	he SNP labels in the feature viewer st SNPs ☑ Nonsyn, SNPs □ CDS	low the genomic position. For
Please note: Indi starts negative, w transcripts on the Introns I U Position: 0 Sequence 3:-UTR 5:-UTR CDS Introns Nonsyn. SNPs Syn. SNPs	Is are not included th the A in the ATG reverse strand the IR Protein di Zoom: x 1 S	in this tab. For now the position start codon being position 1. Ti reverse complement is shown. omains SNPs SNPs, Syn. 9	he SNP labels in the feature viewer st SNPs ☑ Nonsyn, SNPs □ CDS	low the genomic position. For

All empty fields beneath column titles can be used for specific searching (use the correct format!)

Haplotype color: Color of each DNA haplotype which is shown in the map of all haplotypes (map is beneath the table!)

Haplotype ID: Transcript Id.Haplotype number_dna (e.g. AT4G30120.1_dna). AT4G30120.1 1 dna

Gene ID haplotype number type of sequence

Accessions: Count of accessions of each haplotype.

SNPs: Count of SNPs of each haplotype compared to reference (Col-0). The haplotype group with a SNP number of 0 is the reference haplotype group (accession haplotype group with Col-0).

Sequence: Download link of CDS haplotype sequence of each haplotype (FASTA file).

SNP list: • A list of the SNPs/InDels that differentiate this haplotype from the haplotype of the reference accession (Col-0). List of each SNP per each haplotype. Shown are SNP IDs in chromosome:bp position (4:14732536) of each SNP.

		script and acces wnload GWAS r		Results for selection	n Search SNP database	
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Haplotyp		in haplotype <->	Accessi	on table 🟮		
	ie	#Accessions	#SNPs			
color	Haplotype_ID	#Accessions	*50178	Sequence	SNP list	
	AT4G30120.1.1_dna	#Accessions 88	•SNPS 0	Sequence Download Sequence	SNP list U	
					4:14732536,4:14733425	
	AT4G30120.1.1_dna	88	0	Download Sequence		
	AT4G30120.1.1_dna	88	0	Download Sequence	4:14732536,4:14733425	
	AT4G30120.1.1_dna AT4G30120.1.2_dna AT4G30120.1.3_dna	88 1 1	0 2 5	Download Sequence Download Sequence Download Sequence	4 1473259, A 14733425 A 1473259, A 1473398, A 1473398, A 1473398, A 1473398, A 14733414	
	AT4G30120.1.1_dna AT4G30120.1.2_dna AT4G30120.1.3_dna AT4G30120.1.3_dna AT4G30120.1.4_dna	88 1 1 1 1	0 2 5 5	Download Sequence Download Sequence Download Sequence Download Sequence	4 14722596,4 147334923 4 14722556,4 14733599,4 14733591,4 14735591,4 14735591,4 14735591,4 1473591,4 1475590,4 1475590,4 1475590,4 1475590,4 1475590,4 1475590,4 1475590,4 1475590,4 1475590,4 1475590,4 1475590,4 1475590,4 1475590,4 140000000000000000000000000000000000	
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	AT4630120.1.1_dna AT4630120.1.2_dna AT4630120.1.3_dna AT4630120.1.4_dna AT4630120.1.4_dna AT4630120.1.4_dna	88 1 1 1 1	0 2 5 5 5 5 5	Download Sequence Download Sequence Download Sequence Download Sequence Download Sequence Download Sequence	4.14722596,4.147235425 4.14722556,4.14733589,4.14733591,4.14733593,4.14733514 4.14722556,4.14733599,4.14733593,4.14733596 4.14721450,4.14722556,4.14733597,4.14733596 4.14721450,4.14722556,4.1472317,4.14733598,4.14733391	

CS numbers and accessions: Download link for all accessions of specific haplotype. In the table 1001 genome ID, genotype name and CS number are shown.

Accession_IDs (1001 genomes): ^① The haplotype of one transcript might be the same for several accessions. So for each haplotype there is an accession list with the different accession IDs. The Accession_IDs originate from the 1001 genomes project. Genotype list of all haplotype groups of selected gene. Shown are accession IDs from the 1001 Genomes project.

	Select transcript and accessions Results for selection Search SNP database
	Build & Download GWAS matrices
	Results: AT4G30120.1 Tourniead options Download
	ATHMA3: A. THALIANA HEAVY METAL ATPASE 3; HMA3: Heavy metal atpase 3
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accessions Download CS numbers and accessions	Accession_UDr (1001 personnes)

Beneath of the 'DNA Haplotype \leftrightarrow Accessions' table a 'Map of all haplotypes' is shown.

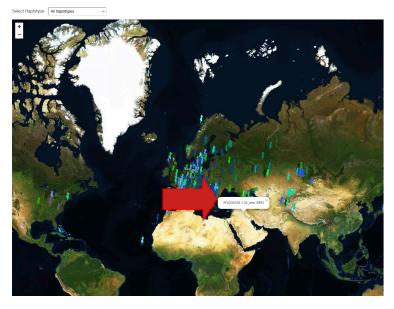
		script and acce wnload GWAS		Results for selectic	n Search SNP database
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				A HEAVY A3: Heavy me	tal
	Check sele	cted accessions	*		
	Haplotype_ID	#Accessions	#SNPs	Senuence	SNP list 0
	Haplotype_ID	#Accessions	#SNPs	Sequence	SNP list
	Haplotype_ID	#Accessions 88	#SNPs 0	Sequence Download Sequence	SMP list O
Haplotype color					590P list 0 414772556,414735425
	AT4G30120.1.1_dna	88	0	Download Sequence	
	AT4G30120.1.1_dna AT4G30120.1.2_dna	88	0	Download Sequence	4.14732536,41.4733425
	AT4G30120.1.1_dna AT4G30120.1.2_dna AT4G30120.1.3_dna	88 1 1	0 2 5	Download Sequence Download Sequence Download Sequence	414772536,4147353425 414772536,414735399,414735991,414735993,414735914
	AT4G30120.1.1_dna AT4G30120.1.2_dna AT4G30120.1.3_dna AT4G30120.1.3_dna AT4G30120.1.4_dna	88 1 1 1 1	0 2 5 5	Download Sequence Download Sequence Download Sequence Download Sequence	4.14772538,4.14735389,4.14735391,4.14733993,4.1473514.4 4.14772536,4.14735389,4.1473591,4.14733993,4.1473514.4 4.14732558,4.14733598,4.14733591,4.14733994,4.1473396
	AT4G30120.1.1_dna AT4G30120.1.2_dna AT4G30120.1.3_dna AT4G30120.1.3_dna AT4G30120.1.3_dna	88 1 1 1 1 1 1	0 2 5 5 5 5	Download Sequence Download Sequence Download Sequence Download Sequence Download Sequence	4.14772536,4.1472539,4.14725391,4.14725393,4.14725394,4.1472594,4.1472564,4.1472564,4.1472566,4.1472566,4.1472566,4.1472566,4.1472566,4.1472566,4.1472566,4.1472566,4.1472566,4.1472566,4.1472566,4.1472566,4.1472566,4.1472566,4.1472666666666666666666666666666666666666

The 'Map of all haplotypes' shows the geographic origin of all selected accessions. Each color is specific for a group of haplotypes. The zoom works via the buttons in the left upper corner or the mouse wheel. With holding the left mouse button and moving the mouse cursor the map can be shifted.

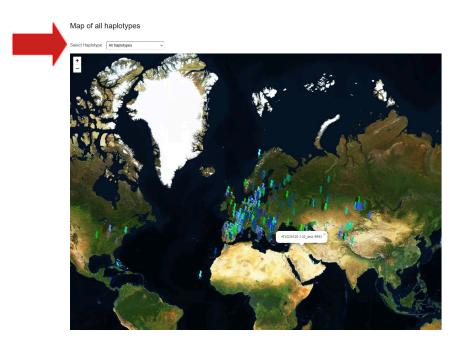


Left mouse click on a mark of the map shows haplotype and accession IDs (1001 genome ID). Both parameters are separated via a double colon (:).





Select haplotype groups (accessions with the same haplotype) via the 'Select Haplotype' option.



Selection of a specific haplotype (haplotype ID).



The geographic origins of all accessions within the haplotype AT4G30120.1.1_dna (haplotype ID) are shown as an example.



2.4.5 Proteotype \leftrightarrow Accession

The tab 'Proteotype \leftrightarrow Accessions' shows a table for protein haplotype/accession associations. The proteotype describes the protein haplotype.

Proteotype \leftarrow Accessions 0: Accessions with polymorphisms in the selected CDS of the selected transcript that result in the same protein sequence have the same haplotype. All options and possibilities are described in the following.

Select t	ranscript and acce	essions	Results for selection	Search SNP	database	
Build &	Download GWAS	matrices				
Res	ults: AT4G30	120.1		Downloa	d options	~ Dow
			A HEAVY A3: Heavy meta	I		
· ·	selected accessions	v				
Se	quence viewer 🕄	SNPs	SNPs <-> Acces	sions 🚯 Hap	olotype <-> Acce	ession table ()
Pr						
P s tr	arts negative, with the A anscripts on the reverse	not included i A in the ATG s strand the r	n this tab. For now the position start codon being position 1. Th everse complement is shown. mains Z SNPs Z Syn. S	e SNP labels in the f	eature viewer show th	e genomic position. For
P s tr S S S S S S S S S S S S S S S S S S	lease note: Indels are i arts negative, with the <i>i</i> anscripts on the reverse Introns VUTR Position: 1622T Zoo iequence -UTR -UTR -UTR DS	not included i A in the ATG set and the restrand the restrand the restrand the restrand the restrict do	n this tab. For now the position start codon being position 1. Th everse complement is shown.	e SNP labels in the fi SNPs ☑ Nonsyn. \$	eature viewer show th	e genomic position. For
P s tr S S S S C U II N	lease note: Indels are i arts negative, with the <i>k</i> anscripts on the reverse introns UTR Position: 1622T Zoo iequence UTR UTR DDS	not included i A in the ATG set and the restrand the restrand the restrand the restrand the restrict do	n this tab. For now the position start codon being position 1. Th everse complement is shown. mains SNPs Syn. S	e SNP labels in the fi SNPs ☑ Nonsyn. \$	eature viewer show th	e genomic position. For
P s tr S S S S C U I I I N S S S S S S S S S S S S S S S S	lease note: Indels are I arts negative, with the A anscripts on the reversion introns II UTR II Position: 1022T Zoo equence UTR UTR DDS DDS Introns Ionsyn, SNPs	not included i A in the ATG set and the restrand the restrand the restrand the restrand the restrict do	n this tab. For now the position start codon being position 1. Th everse complement is shown. mains SNPs Syn. S	e SNP labels in the fi SNPs ☑ Nonsyn. \$	eature viewer show th	e genomic position. For

All empty fields beneath column titles can be used for specific searching (use the correct format!)

Proteotype color: Color of each AA haplotype which is shown in the map of all haplotypes (map is beneath the table!)

Proteotype ID: Transcript Id.Haplotype number_prot (e.g. AT4G30120.1.1_prot). AT4G30120.1.1 prot

Gene ID haplotype number type of sequence

Accessions: Count of accessions of each haplotype.

SNPs: Count of SNPs of each proteotype compared to reference (Col-0). The proteotype group with a SNP number of 0 is the reference proteotype group (accession proteotype group with Col-0).

Sequence: Download link of AA sequence of each proteotype (FASTA file).

SNP list: • A list of the SNPs/InDels that differentiate this proteotype from the proteotype of the reference accession (Col-0). List of SNPs causing AA substitutions per each proteotype. Shown are chromosome:bp positions (4:14732536) of each SNP.

		script and acce wnload GWAS		Results for selecti	n Search SNP database	
	Result	is: AT4G30	120.1		Download options v Download	
	ATHMA3: A. THALIAN/ METAL ATPASE 3; HM atpase 3 Oteck telected accessions					
	Sequ	ence viewer 🚯	SNPs	SNPs> Ac	cessions () Haplotype <-> Accession table ()	
	Prote	in haplotype <-	> Access	ion table 🕄		
Haplotype	Haplotype_ID	#Accessions	#SNPs	Sequence	SNP list	
					SNP list 🖲	
	Haplotype_ID	#Accessions	#SNPs 0	Sequence Download Sequence	SNP list O	
					SNP list 0	
	AT4G30120.1.1_prot	172	0	Download Sequence		
	AT4G30120.1.1_prot AT4G30120.1.2_prot	172 1	0	Download Sequence	4.14732556,4.14733389,4.14733391,4.14733393,4.14733396	
	AT4G30120.1.1_prot AT4G30120.1.2_prot AT4G30120.1.3_prot	172 1 1 1	0 5 7	Download Sequence Download Sequence Download Sequence	414732536,414733399,414733391,414733391,414733396,414733396 414731430,414721955,414723596,414733390,414733396,414733396 414731430,414722556,414723520,414733396,414733399,414733398	
	AT4G30120.1.1_prot AT4G30120.1.2_prot AT4G30120.1.2_prot AT4G30120.1.3_prot AT4G30120.1.4_prot AT4G30120.1.5_prot	172 1 1 1 1 4	0 0 5 7 6 6 6	Download Sequence Download Sequence Download Sequence Download Sequence Download Sequence Download Sequence	4.14732556,4.14733399,4.14733390,4.14733390,4.14733399,4.1473399,4.147339,4.147349	
	AT4G30120.1.1_prot AT4G30120.1.2_prot AT4G30120.1.2_prot AT4G30120.1.3_prot AT4G30120.1.4_prot	172 1 1 1 1 1 1	0 5 7 6	Download Sequence Download Sequence Download Sequence Download Sequence	414732536,414733399,414733391,414733391,414733396,414733396 414731430,414721955,414723596,414733390,414733396,414733396 414731430,414722556,414723520,414733396,414733399,414733398	
	AT4G30120.1.1_prot AT4G30120.1.2_prot AT4G30120.1.2_prot AT4G30120.1.3_prot AT4G30120.1.4_prot AT4G30120.1.5_prot	172 1 1 1 1 4	0 0 5 7 6 6 6	Download Sequence Download Sequence Download Sequence Download Sequence Download Sequence Download Sequence	4.14732556,4.14733399,4.14733390,4.14733390,4.14733399,4.1473399,4.147339,4.147349	

CS numbers and accessions: Download link for all accessions of specific haplotype. In the table 1001 genome Id, genotype name and CS number are shown.

Accession_IDs (1001 genomes): ① The proteotype of one transcript might be the same for several accessions. So far for each proteotype there is an accession list with the different accession IDs. The Accession_IDs originate from the 1001 genomes project. Genotype list of all proteotype groups of selected gene. Shown are accession IDs from the 1001 Genomes project.

•	About		
	Select transcript and accessions Results for	or selection Search SNP database	
	Build & Download GWAS matrices		
	Results: AT4G30120.1	Download options	
	ATHMA3: A. THALIANA HEAV METAL ATPASE 3; HMA3: Hea atpase 3		
	Check selected accessions		
	Sequence viewer SNPs SNP	Accessions I Haplotype> Accession table I	
	Protein haplotype <-> Accession table 0		
CS numbers and accessions	Accession_IDs (1001 genomes)		
Download CS numbers and accessions	403,410,424,630,801,1070,1158,1166,4807,5104,5486,5757,	,5768,5772,5800,5811,5837,5921,5984,5993,6074,6088,6094,6115,6137,6180,6191,6193,6680,6909,6918,6919,	,6922,6945,699
Download CS numbers and accessions	9554		
Download CS numbers and accessions	9512		
Download CS numbers and accessions	9507,9510,9511,9515,9522,9530,9541,9560,9577,9873,9943	3	
Download CS numbers and accessions	9545,9600,9832,9871		
Download CS numbers and accessions	9555,9743,9764		
Download CS numbers and accessions	9710		
<		1 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	> ~

Map of all haplotypes

Map of all proteotypes is shown beneath the table.

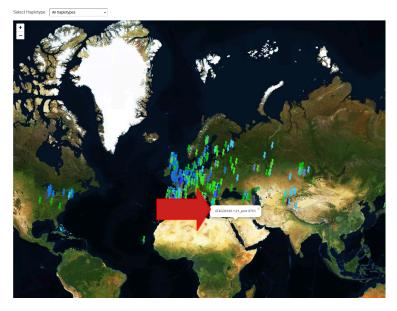
		script and acce wnload GWAS		Results for selection	on Search SNP database
	_				
	Result	ts: AT4G30	120.1		Download options
				A HEAVY A3: Heavy me	tal
	Check sel	cted accessions	*		
Haplotype	Haplotype_ID	#Accessions	#SNPs	Sequence	SNP list
				aequeitoe	
	AT4G30120.1.1_prot	172	0	Download Sequence	
	AT4G30120.1.1_prot AT4G30120.1.2_prot	172	0	Download Sequence	4:14732536,4:14733389,4:14733391,4:14733393,4:14733396
	AT4G30120.1.2_prot AT4G30120.1.3_prot	1	5	Download Sequence	4:14731430,4:14731955,4:14732536,4:14733320,4:14733389,4:14733391,4:1473339
	AT4G30120.1.2_prot AT4G30120.1.3_prot AT4G30120.1.4_prot	1 1 1 1	5 7 6	Download Sequence Download Sequence Download Sequence	4.14731430,4.14731955,4.14732536,4.14733320,4.14733389,4.14733391,4.1473339 4.14731430,4.14732536,4.14733320,4.14733389,4.14733391,4.14733393
	AT4G30120.1.2_prot AT4G30120.1.3_prot AT4G30120.1.4_prot AT4G30120.1.5_prot	1 1 11 4	5 7 6 6	Download Sequence Download Sequence Download Sequence Download Sequence	4:14731430,4:14731955,4:14732536,4:14733320,4:14733389,4:14733391,4:1473339
	AT4G30120.1.2_prot AT4G30120.1.3_prot AT4G30120.1.4_prot	1 1 1 1	5 7 6	Download Sequence Download Sequence Download Sequence	4.14731430,4.14731955,4.14732536,4.14733320,4.14733389,4.14733391,4.1473339 4.14731430,4.14732536,4.14733320,4.14733389,4.14733391,4.1473393
	AT4G30120.1.2_prot AT4G30120.1.3_prot AT4G30120.1.4_prot AT4G30120.1.5_prot	1 1 11 4	5 7 6 6	Download Sequence Download Sequence Download Sequence Download Sequence	4.14731400,414731955,41472256,41472320,41472320,414723304,414723301,41473300 414731400,414722556,414722556,414723300,414723304,14723301,414723393 414731234,414722556,414732226,41473320,414723304,414723394
ζ	AT4G30120.1.2_prot AT4G30120.1.3_prot AT4G30120.1.4_prot AT4G30120.1.4_prot AT4G30120.1.5_prot AT4G30120.1.6_prot	1 1 11 4 3	5 7 6 6 5	Download Sequence Download Sequence Download Sequence Download Sequence Download Sequence	4.14731400,414731955,414722556,414723322,414733396,41473396,41473391,4147339 4.14731430,414722556,414723322,414723397,41472391,41473391 4.14731234,41472556,414723320,414723390,41472391,41472391 4.14731224,414722556,414723220,414723390,41472399

The 'Map of all proteotypes' shows the geographical origin of all selected accessions. Each color is specific for a group of proteotypes. The zoom works via the buttons in the left upper corner or the mouse wheel. With holding the left mouse button and moving the mouse cursor the map can be shifted.



Left mouse click on a mark of the map shows protein haplotype and accession IDs (1001 Genomes ID). Both parameters are separated via a space.

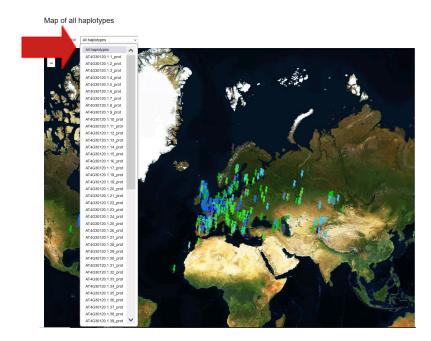
Map of all haplotypes



Select protein haplotype groups (accessions with the same protein haplotype) via 'Select Proteotype' option.



Selection of a specific proteotype (protetype ID).



The origin of all accessions from the protein haplotype AT4G30120.1.1_prot group (proteotype ID) are shown as an example.



2.4.6 Download options

In this chapter we describe download options for the data from the result tables.

2.4.6.1 Download all

To download all available result tables, open the drop-down menu on the upper right corner of the 'Results for selection' tab. Select the option 'All'.

bout					
Select transcript and	accessions	Results for selection	Search SNP data	base	
Results: AT40	G30120.1		Download optio	ins v	Download
ATHMA3: A. METAL ATPA atpase 3	SE 3; HN		Download opt All SNPs SNPs <-> Acc DNA haplotyp DNA haplotyp	essions e <-> Accessions table	
Sequence view Protein haploty			Protein haplo	type <-> Accessions table type fasta	
starts negative, wit transcripts on the	th the A in the ATG reverse strand the	in this tab. For now the position start codon being position 1. Th reverse complement is shown. omains	e SNP labels in the feature	viewer show the genomic p	position. For
Position: 0	Zoom: x 1 S	NP with minor allele frequency	<1% Grey, >1% Black		
Sequence CDS Nonsyn. SNPs					
Prot. domains					
	500	0 1000	1500 2000	2500 30	00

Press the 'Download' button.

🗩 Abou

ect transcript and accession	Results for selection	Search SNP database	
esults: AT4G30120	.1	All v Downloa	ad
THMA3: A. THALIA			
IETAL ATPASE 3; H	IMA3: Heavy meta		
tpase 3			
Check selected accessions			
Sequence viewer () SI	NPs () SNPs <-> Acces	sions () Haplotype <-> Accession table ()	
Protein haplotype <-> Acc	ession table 🚯		
		in the feature viewer starts with 0, while the genomic position in the 5'UTF	R
starts negative, with the A in the a transcripts on the reverse strand	ATG start codon being position 1. Th the reverse complement is shown.	n the feature viewer starts with 0, while the genomic position in the 5'UTF s SNP labels in the feature viewer show the genomic position. For VPS VONSYN. SNPs CDS only Protein sequence only	R
starts negative, with the A in the transcripts on the reverse strand	ATG start codon being position 1. Th the reverse complement is shown. in domains SNPs Syn. S	e SNP labels in the feature viewer show the genomic position. For	R
starts negative, with the A in the. transcripts on the reverse strand Introns UTR Prote Position: 1522C Zoom: x 1	ATG start codon being position 1. Th the reverse complement is shown.	e SNP labels in the feature viewer show the genomic position. For	R
starts negative, with the A in the transcripts on the reverse strand Introns UTR Prote Position: 1522C Zoom: x1 Sequence CDS	ATG start codon being position 1. Th the reverse complement is shown. in domains SNPs Syn. S	e SNP labels in the feature viewer show the genomic position. For	R
starts negative, with the A in the transcripts on the reverse strand Introns UTR Prote Position: 1522C Zoom: x 1 Sequence COS Nonsyn, SNPS	ATG start codon being position 1. Th the reverse complement is shown. in domains SNPs Syn. S	e SNP labels in the feature viewer show the genomic position. For	R
starts negative, with the A in the transcripts on the reverse strand Introns UTR Prote Position: 1522C Zoom: x1 Sequence CDS	ATG start codon being position 1. Th the reverse complement is shown. in domains SNPs Syn. S	e SNP labels in the feature viewer show the genomic position. For	R
starts negative, with the A in the transcripts on the reverse strand Introns UTR Prote Position: 1522C Zoom: x 1 Sequence COS Nonsyn, SNPS	ATG start codon being position 1. Th the reverse complement is shown. in domains SNPs Syn. S	e SNP labels in the feature viewer show the genomic position. For	R
starts negative, with the A in the, transcripts on the reverse strand Introns UTR Prote Position: 1522C Zoom: x1 Sequence CDS Nonsyn, SNPs	ATG start codon being position 1. Th the reverse complement is shown. in domains SNPs Syn. S	e SNP labels in the feature viewer show the genomic position. For	R
starts negative, with the A in the, transcripts on the reverse strand Introns UTR Prote Position: 1522C Zoom: x1 Sequence CDS Nonsyn, SNPs	ATG start codon being position 1 Th the reverse complement is shown. In domains SNPs SNPs SNPs SNP with minor allele frequency -	e SNP labels in the feature viewer show the genomic position. For	R

For all other download options select your file of interest and download it as described above.

For the description of the download options and the corresponding output files, see the following manual sections:

- For 'DNA haplotype \leftrightarrow Accession table' download see chapter 2.4.6.2.
- For 'Protein haplotype fasta' download see chapter 2.4.6.3.

- For 'DNA haplotype fasta' download see chapter 2.4.6.4.
- For 'Protein haplotype \leftrightarrow Accession table' download see chapter 2.4.6.5.
- For 'SNPs' download see chapter 2.4.6.6.
- For 'SNPs \leftrightarrow Accessions' download see chapter 2.4.6.7.
- For 'Accession information' download see chapter 2.4.6.8.

elect transcript and accession	Results for	selection Sea	rch SNP database		
Results: AT4G30120	.1		Download options	~	Download
ATHMA3: A. THALIA METAL ATPASE 3; H atpase 3 Check selected accessions	IMA3: Heav		Download options Au SNPs SNPs <> Accessions DNA haplotype <> Acce DNA haplotype fasta Protein haplotype <> Acce Protein haplotype fasta		
Sequence viewer ③ SI Protein haplotype <-> Acc Please note: Indels are not inclu- starts negative, with the A in the. transcripts on the reverse strand Introns UTR ② Prote Position: 0 Zoom: x1	Added in this tab. For non ATG start codon being the reverse complement in domains SNP	position 1. The SNP lai ent is shown.	Accession information	w the genomic positi	ion. For
Protein haplotype <-> Acc Please note: Indels are not inclustaris negative, with the A in the. transcripts on the reverse strand Introns UTR Prote Position: 0 Zoom: x 1 Sequence	Added in this tab. For non ATG start codon being the reverse complement in domains SNP	w the position in the fee position 1. The SNP la ent is shown. s □ Syn. SNPs ₹	Accession information	w the genomic positi	ion. For
Protein haplotype <-> Acc Please note: Indels are not inclustars negative, with the A in the. transcripts on the reverse strand Infroms UTR Prote Position: 0 Zoom: x 1	Added in this tab. For non ATG start codon being the reverse complement in domains SNP	w the position in the fee position 1. The SNP la ent is shown. s □ Syn. SNPs ₹	Accession information	w the genomic positi	ion. For
Protein haplotype <-> Acc Please note: Indels are not inclu- starts negative, with the A in the. transcripts on the reverse strand Introns UTR Prote Position: 0 Zoom: x 1 Sequence CDS	Added in this tab. For non ATG start codon being the reverse complement in domains SNP	w the position in the fee position 1. The SNP la ent is shown. s □ Syn. SNPs ₹	Accession information	w the genomic positi	ion. For

2.4.6.2 DNA haplotype table

The 'dna_haplotype_table' is dumped as a csv file.

,	AT4G30120.1_dna_haplotype_table AT4G30120.1_haplotype_sequences_completeAA AT4G30120.1_haplotype_sequences_completeC	17/10/2024 16:27 17/10/2024 16:27 17/10/2024 16:27	OpenOffice.org 1.1 S FASTA DNA FASTA DNA	199 KB 41 KB 187 KB
	AT4G30120.1_protein_haplotype_table AT4G30120.1_snp_table AT4G30120.1_snp_accession_table	17/10/2024 16:27 17/10/2024 16:27 17/10/2024 16:27	OpenOffice.org 1.1 S OpenOffice.org 1.1 S OpenOffice.org 1.1 S	50 KB 42 KB 252 KB

DNA haplotype table shows:

haplotype _ID: AT4G30120.1 1 dna

Gene ID haplotype number type of sequence

number_of_accessions: Count of accessions of each haplotype.

list_of_snps: List of each SNP per each haplotype. Shown are chromosome:bp positions (4:14732536) of each SNP.

A	В	c
1 #all	accessions	selected
2 haplotype_ID	number_of_accessions	list_of_snps
AT4G30120.1.1 dna	88	
AT4G30120.1.2 dna	1	4:14732536,4:14733425
5 AT4G30120.1.3 dna	1	4:14732536,4:14733389,4:14733391,4:14733393,4:14733414
5 AT4G30120.1.4 dna	1	4:14732536,4:14733389,4:14733391,4:14733393,4:14733396
7 AT4G30120.1.5 dna	1	4:14731430,4:14732536,4:14733117,4:14733389,4:14733391
AT4G30120.1.6 dna	1	4:14732323,4:14732536,4:14733389,4:14733391
AT4G30120.1.7 dna	4	4:14731430,4:14732536,4:14733389,4:14733391
o AT4G30120.1.8 dna	4	4:14732536,4:14733389,4:14733391
1 AT4G30120.1.9 dna	1	4:14732536,4:14733110,4:14733389,4:14733391
2 AT4G30120.1.10 dna	1	4:14731525,4:14731691,4:14732176,4:14733044,4:14733376

list_accession_IDs: All accessions belonging to the specified haplotype. **haplotype_sequence_complete_CDS:** Coding sequence of haplotypes. **length_haplotype_sequence:** Sequence length of haplotypes in bp.

	D	E	F
1			
2	list_accession_IDs	haplotype_sequence_completeCDS	length_haplotype_sequence
3	630,1070,5104,5486,5757,5768,5800,581	ATGGCGGAAGGTGAAGAGTCAAAGA	1629
4	403	ATGGCGGAAGGTGAAGAGTCAAAGA	1629
5	7106	ATGGCGGAAGGTGAAGAGTCAAAGA	1629
6	9554	ATGGCGGAAGGTGAAGAGTCAAAGA	1629
7	10015	ATGGCGGAAGGTGAAGAGTCAAAGA	1629
8	9964	ATGGCGGAAGGTGAAGAGTCAAAGA	1629

2.4.6.3 Proteotype sequence complete AA

The 'proteotype_sequence_completeAA' is dumped as a FASTA file.

AT4G30120.1_dna_haplotype_table	17/10/2024 16:27	OpenOffice.org 1.1 S	199 KB
AT4G30120.1_haplotype_sequences_completeAA	17/10/2024 16:27	FASTA DNA	41 KB
AT4G30120.1_haplotype_sequences_completeC	17/10/2024 16:27	FASTA DNA	187 KB
AT4G30120.1_protein_haplotype_table	17/10/2024 16:27	OpenOffice.org 1.1 S	50 KB
at4G30120.1_snp_table	17/10/2024 16:27	OpenOffice.org 1.1 S	42 KB
AT4G30120.1_snp_accession_table	17/10/2024 16:27	OpenOffice.org 1.1 S	252 KB

This file contains all AA sequences of each selected haplotype.

- AFI4G30120.1.1. prot MAGGESKMMLGTSYFDVVGICCSSEVSIVGNVLRQVDGVKEFSVIVPSRTVIVH0TFLISPLQIVALNQARLEASVRPVGETSLKSQWPSPFATVSGVLLVLSFRVFYSPLEW VPPILAKAVASVTRFRLDINALTLAVIATLCNQOPTEAATTVFLFSVGMVLESSAAHKASIVMSSLMSLAPRAKAVLADTGLEVDVDEVGINTVSVKAGESIPIDGVVUGSCDVDEK SKRESTVMAAKALARDEVAKAVITLALEQKQSTKTQFRUSKESVTFMVVASACCAVIPULLVGDLSWFHLAUVUSGCGCLISTVATFACTALAR DCLETLAKILVMPEXTGTTTAEPMVSPFLSSFILHKLIVWSSIECKSSHPMAAALIDVARSVSVEPKPDIVENPQNPGEGVVGRIDGQDIYIGMKRIAQRAGCLIDNVPDI 5/4TG30120.1.2 ptdr	TLTGESFPV ISGFLIKTG
MBEGESKKMILGTS/TDYVGICCSSEVSIVGNU/HE/DGWEFSVIV/PSRTVI/WOTTLSFLQWKLIAQARLASVPYGFISLSQWIPSFAVSGU/LLSFFKVTSELEWE VPFLAKAVSVFTSRLDIALTLAUATIALT_MQOFTEASUU/HESAMKSIVMSULALARKAVIATOLLEVDVEVGINT/VSVKGESTIPOGVVGCST SKQRESTVMATTINI.NGTIKKTTALARDCVMAKMTKLIKEAQKSQTKTQRFDKCSRVTFMAV/SACFAVIPULKVQDLSHWFHALUVVJSCCFCGLLSTFVATEALTMA DCLETLAKIKUTRKTGTTIALEMPSFRSLSPSINLHKLIYWSSIECKSSHPMAALIDVARSVSVERKPDIVENFQNFPGEGV/GRIDGQDIYIGIKRIAQRAGCLTDNVPDI GYTYMGAKITGSFNLLDGCRYGVAQALKELKS	CTLTGESFPV FSGFLIKTG
MIEGEESKKMILGTSFDJVGICCSSEVSIVGNURELDGWEFSDVIPSRTVIVHOTTFSPLQWKLIAQARLEASVRPVCFSUSCAPPGFGALSQFFGALSQFFFQFSDGVLUSSFFQFFGALAUSSFFQFGALSQFFGALSQFFGALSQFFGALSQFFQFFGALSQFFQFFGALSQFFQFFGALSQFFQFFGALSQFFGALSQFFQFFGALSQFFQFFGALSQFFGALSQFFQFFGALSQFFQFFGALSQFFGALSQFFGALSQFFQFFGALSQFF	CTLTGESFPV TSGFLIKTG
MIEGEESKKMILGTSFDJVGICCSSEVSIVGNURELOGWEESUUPSRTVIVHOTFFSPLQWKLIAQARLEASVRYGETSLSQHOPSPLJVGOLLUSFFXYFSPLSWE VPFLAKAVSSFTRIDINALTUARITALCMOPTEASUUPESRTVIVHSTFFSPLQWEAKASIWSSIUSALSARRKAIJATOLEUVDEVGINTVOSKAGESTIPOGVVOGEST SKQRESTVAATTILIAGTIKKITTALABOLVVAKATTILUEEQKSQTKTQRFDKCSRVTFAVVSAACFAUPULLVVQDLSHWFHLAUVUVSGCPCGLLSTVATECATKAS DCLETLAKITVARTIRTITALENTSFFSLSFSILIHKLLYWVSSIECKSSHPMAAALDVARSVSVERKPDIVENFQNFPGEGVVGRIDGQDIDIGNRRIAQRAGCLTDNVPDI IGYTWGAKITGSFNLLDCCRVCVAQALKELKS	TLTGESFPV FSGFLIKTG
MAGEGESKKMILGTSYDYVGICCSSEYSIYGKNURPLOGWEFSYDUPSRTVIVHOTTFISPLQWKLIAQARLEASVPYGETSUSQWISPFALYSQULLSFFKYT95PLEW VPPLIAXXASVFTRIDINALTUAIIATLONOPTEANTUFTSYDUVESSAMKSIYMSSUSALSAPKKAIJADISLENDVDEVGINTVSYKAGESTIDOSVVOGCSUS SKQRESTVMAATINI.NGYTKKTTAABOCVAKMTKLVEEQKSQTKTQRFIDKCSRYTPAVX5ACFAVIPVLLKVQDLSHWFH.AUVUVSGCFCGLISTVATEALTKAA DCLETLAKIKTURKTGTTIAEBTVSFFSLSPSIILIHKLLYWVSSIECKSSHPMAAALIDVARSVSVEPKPDIVENFQNFPGESVGRIDGQODTYGIKRIAQRAGLIDNVPDI GYTYMGAKITGSFNLLDCCRYGVAQALKELKS 374fG30120.16 prdt	TLTGESFPV FSGFLIKTG
MAGGESKKMILGTSYDVGICCSSEVSTUGNURED.DGWEESVUPPSRTV/WHOTFISPLQWKLINQARLEASVRPVGETSUS/GWIPSPRAT/SGVLIU,SFRW/RFBLEW VPFILAKANASVTRFRLDINALTLAVIATLCMQDFTEATIVFLFSVADWLESSAMKASIVMSSLMSLAPRKAVIADTGLEVDVDEVGINTV/SVKAGESIPDGW/WDGSCDVPG SKRESTVMAATINLNGYIKVKTTALARDC/WARMTLUEAQKSQTKTQRFIDKCSRVTFAW/VSAACFAVIP/LLKVQDLSHIMFHLU/VL/SGCFCGLILSTFW/RFCATKAA DCLETLAKIKIVAPDKTGTTRLAEPMVSDFSLSPSINLHKLI/WVSSIECKSSHPMAAALIDVARSVSVEPKPDIVENFQNPGGESVGRIDGQDVIGMKRIAQRAGCLIDNVDDI IGYTYMGAKLTGSRILLDGCRVGAQLKELKS_	(TLTGESFPV ISGFLIKTG

2.4.6.4 Haplotype sequences complete CDS

The 'haplotype_sequence_completeCDS' is dumped as a FASTA file.

	AT4G30120.1_dna_haplotype_table	17/10/2024 16:27	OpenOffice.org 1.1 S	199 KB
	🗈 AT4G30120.1_haplotype_sequences_completeAA	17/10/2024 16:27	FASTA DNA	41 KB
	AT4G30120.1_haplotype_sequences_completeC	17/10/2024 16:27	FASTA DNA	187 KB
	AT4G30120.1_protein_haplotype_table	17/10/2024 16:27	OpenOffice.org 1.1 S	50 KB
· · · ·	AT4G30120.1_snp_table	17/10/2024 16:27	OpenOffice.org 1.1 S	42 KB
	AT4G30120.1_snp_accession_table	17/10/2024 16:27	OpenOffice.org 1.1 S	252 KB

This file contains all CDS sequences of each selected haplotype.

>AT4G30120.1.1 dna
ATGGCGGAAGGTGAAGAGTCAAAGAAGTGAATTTACAGACAAGTTACTTCGACGTCGTTGGAATCTGCTGTTCATCGGAGGTTTCTATCGTAGGTAACGTTCTCCGTCAAGTGG
TICACTIAGCACTIGTAGTGTIAGTGATGGTIGTCCCLGTGGGLCTIATCCACACCTGTIGCIACCTTTTGTGCLCTCACTAAGGCAGCCACGTCAGGGLTTCTGATCAA
>AT4G30120.1.2 dna
A TGGC GGAAGGT GAAGAGT CAAAGAAGAT GAATT TACAGACAAGT TACT TCGACGT CGT TGGAAT CTGC TGT TCAT CAGAGGT TTCT AT CGT AGGT AG
TICACTIAGCACTIGTAGTGTIAGTAGTGGTIGTCCCLGTGGTCTIATCCTATCCACACCTGTIGCIACCTTTTGTGCTCTCACTAAGGCAGCCACGTCAGGGTTTCTGATCAA
>AT4G30120.1.3 dna
ATGGCGGAAGGTGAAGGATCAAAGAAGATGAATTTACAGACAAGTTACTTCGACGTCGTTGGAATCTGCTGTTGATCGGAGGTTTCTACCGTAGGTAACGTTCTCCGGTCGACTTG
TTCACTTAGCACTTGTAGTGTTAGTAAGTGGTTGTCCCTGTGGTCTTATCCTATCCACACCTGTTGCTACCTTTTGTGCTCTCACTAAGGCAGCCACGTCAGGGTTTCTGATCAA
>AT4G30120.1.4 dna
ATGGCGGAAGGTGAAGAGTCAAAGAAGATGAATTTACAGACAAGTTACTTCGACGTCGTTGGAATCTGCTGTTCATCGGAGGTTTCTATCGTAGGTAACGTTCTCCATCCA
TTCACTTAGCACTTGTAGTGTTAGTAAGTGGTTGTCCCTGTGGTCTTATCCTATCCACACCTGTTGCTACCTTTTGTGCTCTCACTAAGGCAGCCACGTCAGGGTTTCTGATCAA
>AT4G30120.1.5 dna
ATGGCGGAAGGTGAAGAGGTCAAAGAAGATGAATTTACAGACAAGTTACTTCGACGTCGTTGGAATCTGCTGTTGATCGGAGGTTTCTATCGTAGGTAACGTTCTCCGGTCAACTTG
TTCACTTAGCACTTGTAGTGTTAGTAAGTGGTTGTCCCTGTGGTCTTATCCTATCCACACCTGTTGCTACCTTTTGTGCTCTCACTAAGGCAGCCACGTCAGGGTTTCTGATCAA
>AT4G30120.1.6_dna
ATGGCGGAAGGTGAAGAGTCAAAGAAGATGAATTTACAGACAAGTTACTTCGACGTCGTTGGAATCTGCTGTTCATCGGAGGTTTCTATCGTAGGTAACGTTCTCCGTCAACTTG
TTCACTTAGCACTTGTAGTGTTAGTAGTGGTTGTCCCTGTGGTCTTATCCTATCCACACCTGTTGCTACCTTTTGTGCTCTCACTAAGGCAGCCACGTCAGGGTTTCTGATCAA
>AT4G30120.1.7_dna
ATGGCGGAAGGTGAAGAGTCAAAGAAGATGAATTTACAGACAAGTTACTTCGACGTCGTTGGAATCTGCTGTTGATCGGAGGTTTCTATCGTAGGTAACGTTCTCCGGTCAACTTG
TTCACTTAGCACTTGTAGTGTTAGTAGTGGTTGTCCCTGTGGTCTTATCCTATCCACACCTGTTGCTACCTTTTGTGCTCTCACTAAGGCAGCCACGTCAGGGTTTCTGATCAA

2.4.6.5 Proteotype table

The 'proteotype_table' is dumped as a csv file.

💩 AT4G30120.1_dna_haplotype_table	17/10/2024 16:27	OpenOffice.org 1.1 S	199 KB
AT4G30120.1_haplotype_sequences_completeAA	17/10/2024 16:27	FASTA DNA	41 KB
AT4G30120.1_haplotype_sequences_completeC	17/10/2024 16:27	FASTA DNA	187 KB
aT4G30120.1_protein_haplotype_table	17/10/2024 16:27	OpenOffice.org 1.1 S	50 KB
🖊 🔤 AT4G30120.1_snp_table	17/10/2024 16:27	OpenOffice.org 1.1 S	42 KB
AT4G30120.1_snp_accession_table	17/10/2024 16:27	OpenOffice.org 1.1 S	252 KB
	 AT4G30120.1_haplotype_sequences_completeAA AT4G30120.1_haplotype_sequences_completeC AT4G30120.1_protein_haplotype_table 	Image: Art4G30120.1_haplotype_sequences_completeAA 17/10/2024 16:27 Image: Art4G30120.1_haplotype_sequences_completeC 17/10/2024 16:27 Image: Art4G30120.1_protein_haplotype_table 17/10/2024 16:27 Image: Art4G30120.1_snp_table 17/10/2024 16:27	AT4G30120.1_haplotype_sequences_completeAA 17/10/2024 16:27 FASTA DNA AT4G30120.1_haplotype_sequences_completeC 17/10/2024 16:27 FASTA DNA AT4G30120.1_protein_haplotype_table 17/10/2024 16:27 CopenOffice.org 1.1 S AT4G30120.1_protein_haplotype_table 17/10/2024 16:27 OpenOffice.org 1.1 S

The proteotype table shows:

proteotype _ID: AT4G30120.1 1 prot

Gene ID proteotype number type of sequence

number_of_accessions: count of accessions of each haplotype list_of_snps: list of each SNP per each proteotype per gene. Shown are chromosome:bp positions (4:14732536) of each SNP

	A	В	с
1	#all	accessions	selected
2	haplotype_ID	number_of_accessions	list_of_snps
3	AT4G30120.1.1 prot	172	
4	AT4G30120.1.2_prot	1	4:14732536,4:14733389,4:14733391,4:14733393,4:14733396
5	AT4G30120.1.3_prot	1	4:14731430,4:14731955,4:14732536,4:14733320,4:14733389,4:14733391,4:14733393
6	AT4G30120.1.4 prot	11	4:14731430,4:14732536,4:14733320,4:14733389,4:14733391,4:14733393
7	AT4G30120.1.5_prot	4	4:14731234,4:14732536,4:14733320,4:14733389,4:14733391,4:14733393
8	AT4G30120.1.6 prot	3	4:14732536,4:14733320,4:14733389,4:14733391,4:14733393

list_accession_IDs: all accession belonging to the specified haplotype **proteotype_sequence_complete_AA:** AA sequence of proteotype **length_proteotype_sequence:** AA sequence length of proteotype

	D	E	F	
1				
2	list_accession_IDs	haplotype_sequence_completeAA	length_haplotype_	sequence
3	403,410,424,630,801,1070,1158,1166,4807,5104,5486,5757,576	MAEGEESKKMNLQTSYFDVVGICCSSEVSIVGNVLRQVDGVKB		543
4	9554	MAEGEESKKMNLQTSYFDVVGICCSSEVSIVGNVLHPLDGVKE		543
5	9512	MAEGEESKKMNLQTSYFDVVGICCSSEVSIVGNVLRPLDGVKD		543
6	9507,9510,9511,9515,9522,9530,9541,9560,9577,9873,9943	MAEGEESKKMNLQTSYFDVVGICCSSEVSIVGNVLRPLDGVKE		543
7	9545,9600,9832,9871	MAEGEESKKMNLQTSYFDVVGICCSSEVSIVGNVLRPLDGVKE		543
8	9555,9743,9764	MAEGEESKKMNLOTSYFDVVGICCSSEVSIVGNVLRPLDGVKE		543

2.4.6.6 SNP table

The 'SNP_table' is dumped as a csv file.

AT4G30120.1_dna_haplotype_table	17/10/2024 16:27	OpenOffice.org 1.1 S	199 KB
AT4G30120.1_haplotype_sequences_completeAA	17/10/2024 16:27	FASTA DNA	41 KB
AT4G30120.1_haplotype_sequences_completeC	17/10/2024 16:27	FASTA DNA	187 KB
aT4G30120.1_protein_haplotype_table	17/10/2024 16:27	OpenOffice.org 1.1 S	50 KB
📄 🗟 AT4G30120.1_snp_table	17/10/2024 16:27	OpenOffice.org 1.1 S	42 KB
AT4G30120.1_snp_accession_table	17/10/2024 16:27	OpenOffice.org 1.1 S	252 KB

The SNP table shows:

SNP ID: SNP identification number. Shown are chromosome:bp position (4:14730221) of each SNP of selected gene.

Variant_0: Base pair variant on a specific position with the highest frequency of selected gene.

Frequency_0: Base frequency of variant 0 from selected gene.

Variant_1: Base pair variant on a specific position with the second highest frequency of selected gene.

Frequency_1: Base frequency of variant 1 from selected gene.

Variant_2: Base pair variant on a specific position with the third highest frequency of selected gene.

Frequency_2: Base frequency of variant 2 from selected gene.

SNP relative position mRNA: SNP base pair position of selected gene mRNA.

SNP relative position genome: SNP base pair position of selected gene gDNA (genomic DNA).

	A	B	C	D	E	F	G	н	1
1	#all accessions selected								
2	SNP Id	Variant_0	Frequency_0	Variant_1	Frequency_1	Variant_2	Frequency_2	SNP relative position mma	SNP relative position genome
3	4:14730221	C -> C	0.99824	C -> A	0.00176	Snoval	noval	2463	3 328
4	4:14730223	T -> T	0.9859	T -> C	0.014	L noval	noval	2461	L 328
5	4:14730234	C -> C	0.99912	C -> A	0.0008	3 noval	noval	2450	3269
6	4:14730241	G -> T	0.70749	G -> G	0.2925	Lnoval	noval	2443	3 326
7	4:14730247	A -> A	0.99031	A -> T	0.00969	noval	noval	2437	7 3256
8	4:14730252	T -> G	0.67489	T -> T	0.3251	Lnoval	noval	2432	2 325:
9	4:14730270	C -> C	0.99912	C -> T	0.0008	3 noval	noval	2414	1 3233
10	4:14730277	C -> C	0.99912	C -> A	0.0008	3 noval	noval	2407	7 322
11	4:14730312	G -> G	0.99824	G -> A	0.00176	Snoval	noval	2372	2 319:
12	4:14730332	A -> A	0.99912	A -> G	0.0008	3 noval	noval	2352	2 317:
13	4:14730350	C -> C	0.9815	C -> T	0.018	5 noval	noval	2334	1 3153
14	4:14730354	A -> A	0.95419	A -> G	0.0458	Lnoval	noval	2330	3149
15	4:14730358	T -> T	0.99648	T -> A	0.00352	2 noval	noval	2326	3 3145
16	4:14730360	A -> A	0.99648	A -> T	0.00353	2 noval	noval	2324	3143

SNP location: Gene structure location (e.g. 3' UTR, INTRON etc.) of SNP and selected gene.

SNP effects: Effect of SNP on AA sequence of selected gene (e.g. stop codon (premature stop codon), nonsynonymous (AA substitution), canonical motif in splice site etc.) **Substitution_0:** AA substitution on a specific position with the highest frequency of

selected gene.

Substitution_frequency_0: AA substitution of substitution 0 from selected gene.

Substitution_1: AA substitution on a specific position with the second highest frequency of selected gene.

Substitution_frequency_1: AA substitution of substitution 1 from selected gene.

Substitution_properties: Physico-chemical properties of AA substitution (e.g. non-polar \rightarrow polar, basic \rightarrow acidic etc.)

Domain Id: Protein domain ID in which the AA substitutions are located.

	J	ĸ	L	M	N	0	P	Q
1								
2	SNP location	SNP effects	Substitution_0	Substitution_frequency_0	Substitution_1	Substitution_frequency_1	Substitution properties	Domain Id
51	INTRON	noval	noval	noval	noval	noval	noval	noval
52	INTRON	noval	noval	noval	noval	noval	noval	noval
53	INTRON	noval	noval	noval	noval	noval	noval	noval
54	3UTR	noval	noval	noval	noval	noval	noval	noval
55	3UTR	noval	noval	noval	noval	noval	noval	noval
56	3UTR	noval	noval	noval	noval	noval	noval	noval
57	3UTR	noval	noval	noval	noval	noval	noval	noval
58	3UTR	noval	noval	noval	noval	noval	noval	noval
59	3UTR	noval	noval	noval	noval	noval	noval	noval
60	CDS	stop codon	stop codon	frame shift	synonymous	noval	noval	noval
61	CDS	nonsynonymous	N -> K	0.00088	noval	noval	polar -> basic	PTHR11939:SF31
62	CDS	synonymous	noval	noval	noval	noval	noval	noval
63	CDS	nonsynonymous	M -> T	0.00088	noval	noval	non-polar -> polar	PTHR11939:SF31
64	CDS	synonymous	noval	noval	noval	noval	noval	noval
65	CDS	nonsynonymous	G -> D	0.00088	noval	noval	non-polar -> acidic	PTHR11939:SF31
66	CDS	nonsynonymous	T -> N	0.00617	noval	noval	polar -> polar	PTHR11939:SF31
67	CDS	synonymous	noval	noval	noval	noval	noval	noval
68	CDS	nonsynonymous	1-> T	0.00088	noval	noval	non-polar -> polar	PTHR11939:SF31
69	CDS	splice site region	noval	noval	noval	noval	noval	noval
70	INTRON	canonical motif in splice site	noval	noval	noval	noval	noval	noval
71	INTRON	splice site region	noval	noval	noval	noval	noval	noval

Domain description: Description of domain.

	R
1	
2	Domain description
51	noval
52	noval
53	noval
54	noval
55	noval
56	noval
57	noval
58	noval
59	noval
60	noval
61	HEAVY METAL CATION TRANSPORT ATPASE (CADMIUM/ZINC TRANSPORTING ATPASE), CATION-TRANSPORTING ATPASE, HMA_2, HMA, heavy metal-associated domain
62	noval
63	HEAVY METAL CATION TRANSPORT ATPASE (CADMIUM/ZINC TRANSPORTING ATPASE), CATION-TRANSPORTING ATPASE HMA_2, HMA, heavy metal-associated domain
64	noval
65	HEAVY METAL CATION TRANSPORT ATPASE (CADMIUM/ZINC TRANSPORTING ATPASE),CATION-TRANSPORTING ATPASE,HMA_2,HMA, heavy metal-associated domain
66	HEAVY METAL CATION TRANSPORT ATPASE (CADMIUM/ZINC TRANSPORTING ATPASE), CATION-TRANSPORTING ATPASE, HMA_2, HMA, heavy metal-associated domain
67	noval
68	HEAVY METAL CATION TRANSPORT ATPASE (CADMIUM/ZINC TRANSPORTING ATPASE),CATION-TRANSPORTING ATPASE,HMA_2,HMA, heavy metal-associated domain
69	noval
70	noval
71	noval

Strand: Strand direction (e.g. - and +) of sequence.

AraGWAS_score: AraGWAS score (-log₁₀ (p-value)) of selected SNP and gene. **AraGWAS_links:** AraGWAS Catalog links of GWAS and study information of selected SNP and gene.

	s	т	U
	Strand	AraGWAS_score	AraGWAS_links
1	-	noval	noval
2	-	noval	noval
3		noval	noval
4	-	noval	noval
5	-	24.1462113508663	SNP_link: https://aragwas.1001genomes.org/#/study/287/associations/4_14731525, study_link: https://aragwas.1001genomes.org/#/study/287, score: 24.1
5		noval	noval
7	-	noval	noval
В		noval	noval
9	-	noval	noval
0	-	noval	noval
1		noval	noval
2	-	noval	noval
3		noval	noval
4	-	noval	noval
5	-	21.204987069462	SNP_link: https://aragwas.1001genomes.org/#/study/287/associations/4_14731691, study_link: https://aragwas.1001genomes.org/#/study/287, score: 21.2

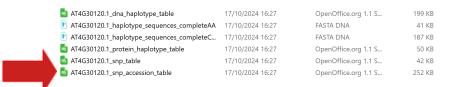
GWAS corrected: GWAS analysis was performed with the software GEMMA. Every climate factor was used as a phenotype and for every climate factor, one analysis run was carried out. Only SNPs with a minor allele frequency of 1% or higher were analysed. The obtained p-values were corrected for multiple comparisons using the Benjamini-Yekutiel method. In this column you can see all the correlations between SNPs and the 200 climate factors which have a corrected p-value lower than or equal to the threshold. You can sort the column according to the lowest p-value in each cell.

Number of associated climate factors: Number of associated climate factors, with a corrected P-value in the GWAS lower than or equal to the threshold.

	V	W
1		
2	GWAS corrected	Number of associated climate factors
81	noval	0
82	noval	0
83	noval	0
84	noval	0
85	noval	0
86	noval	0
87	noval	0
88	noval	0
89	noval	0
90	noval	0
91	noval	0
92	noval	0
93	noval	0
94	noval	0
95	noval	0
96	noval	0

2.4.6.7 SNP accession table

The 'SNP_accession_table' is dumped as a csv file.



The SNP accession table shows:

SNP ID: List of SNP IDs of selected gene. Shown are chromosome:bp position (4:14731188) of each SNP

Polymorphism: List of polymorphisms (SNPs or InDels). For example: $C \rightarrow G$, always the first base (C) is from Col-0 (reference genotype) and his group \rightarrow the second base (G) from other accessions.

Genotypes: List of genotypes different to Col-0. Shown are accession IDs from 1001 Genome project.

CS number: List of genotypes different to Col-0. Shown are the CS accession IDs. **Accession:** List of genotypes different to Col-0. Shown are accession names.

	A	В	с	D	E
1	#all accessions selected				
2	SNP id	Polymorphism	Genotypes	CS number	Accession
3	4:14731188	C -> G	9824	CS76702	Bes-5
4	4:14731200	C -> T	6911	CS76789	Cvi-0
5	4:14731132	A -> TA	88,139,159,265,410,428,	CS76790,CS77014,CS77	CYR.LDV-46,MAR2-3,PY
6	4:14731216	T -> C	6911	CS76789	Cvi-0
7	4:14731221	A -> T	9508,9518,9524,9528,95	CS77108,CS76660,CS78	IP-Mos-1,IP-Alm-0,IP-Ber
8	4:14731228	G -> A	9828	CS76721	Bra-0
9	4:14731234	C -> A	9533,9542,9545,9574,96	CS76763,CS76872,CS70	IP-Cem-0,IP-Fun-0,IP-He
10	4:14731260	T -> A	9543	CS76886	IP-Gra-0
11	4:14731261	T -> C	9879	CS77169	Per-0
12	4:14731275	T -> C	1158,1166,7169,8337,90	CS76656,CS77651,CS70	Aledal-6-49, Aledal-14-73,
13	4:14731393	G -> A	6090,7305,8343,9544,95	CS77288,CS78915,CS70	T1000,Pt-0,Na-1,IP-Gua-
14	4:14731395	GA -> A	9777	CS76880	Gn-1
15	4:14731396	G -> A	6897,9534,9841,9910	CS76430,CS76774,CS70	Ag-0,IP-Cmo-3,Ees-0,BR
16	4:14731430	T -> G	628,763,765,766,768,772	CS78951,CS76522,CS70	LI-OF-061,Kar-1,Sus-1,D
17	4:14731450	G -> A	9759,10013	CS76439,CS76388	Anz-0,Lerik1-3
18	4:14731471	AGAACTTTCC -> C	9099	CS76953	Istisu-9
19	4:14731480	A -> G	9991	CS76391	Vash-1

2.4.6.8 Accession information

The 'accession_information' is dumped as a csv file.

The accession information shows:

accession_id: Accession identification number based on the 1001 Genomes project. **accession**: Name of accession.

cs_number: CS accession lds.

country: Country of origin.

group: Population structure computed in 1001 genomes paper.

	А	В	С	D	E
1	accession_id	accession	cs_number	country	group
2	88	CYR	CS76790	FRA	western_europe
3	108	LDV-18	CS77013	FRA	western_europe
4	139	LDV-46	CS77014	FRA	western_europe
5	159	MAR2-3	CS77070	FRA	western_europe
6	265	PYL-6	CS77198	FRA	admixed
7	350	TOU-A1-88	CS77382	FRA	western_europe
8	351	TOU-A1-89	CS77383	FRA	western_europe
9	403	Zdarec3	CS78873	CZE	central_europe
10	410	Doubravnik7	CS76808	CZE	central_europe
11	424	Draha2	CS76812	CZE	central_europe
12	428	Borky1	CS76718	CZE	central_europe
13	430	Gr-1	CS76496	AUT	central_europe
14	470	BRR4	CS78943	USA	germany
15	476	BRR12	CS78944	USA	germany
16	484	BRR23	CS78945	USA	germany
17	504	BRR57	CS78946	USA	germany
18	506	BRR60	CS78947	USA	germany
19	531	BRR107	CS78948	USA	germany
20	544	LI-WP-039	CS78949	USA	germany
21	546	LI-WP-041	CS78950	USA	germany
22	628	LI-OF-061	CS78951	USA	western_europe
23	630	LI-OF-065	CS77036	USA	western_europe
24	680	LI-RR-096	CS78952	USA	germany
25	681	LI-RR-097	CS78953	USA	germany

2.5 Search SNP database

This database can be used to retrieve SNP information and accessions for SNPs. To get that information you need to identify SNP IDs of interest.

ut				
elect transcript and	accessions	Results for selection	Search SNP database	
uild & Download G	NAS matrices			
Results: AT40	G30120.2		Accession information	v Downlo
ATHMA3: A. METAL ATPA atpase 3		A HEAVY A3: Heavy meta	I	
Check selected accession	s 🔻			
	s are not included	ion table () in this tab. For now the position		while the genomic position in the 5'U
Protein haploty Please note: Inde starts negative, wit transcripts on the r	s are not included h the A in the ATG everse strand the R Z Protein do	ion table () in this tab. For now the position start codon being position 1. T reverse complement is shown	in the feature viewer starts with 0, e SNP labels in the feature viewer INPs Z Nonsyn, SNPs C	while the genomic position in the 5'U
Protein haploty Please note: Inde starts negative, with transcripts on the r Introns I UT Position: 0 Sequence 3: UTR 5: UTR CDS Introns, SNPS	s are not included h the A in the ATG everse strand the R Z Protein do	ion table 3 in this tab. For now the position start codon being position 1. T reverse complement is shown mains 2 SNPs 2 Syn. :	in the feature viewer starts with 0, e SNP labels in the feature viewer INPs Z Nonsyn, SNPs C	while the genomic position in the 5'U show the genomic position. For
Protein haploty Please note: Inde stats negative, will transcripts on the r Introns I UT Position: 0 Sequence 3-UTR CDS Introns	s are not included h the A in the ATG everse strand the R Z Protein do	ion table 3 in this tab. For now the position start codon being position 1. T reverse complement is shown mains 2 SNPs 2 Syn. :	in the feature viewer starts with 0, e SNP labels in the feature viewer INPs Z Nonsyn, SNPs C	while the genomic position in the 5'U show the genomic position. For

2.5.1 Get SNP information



Copy SNP ID or IDs of interest into the empty field.

Sele	ct transcript and access	ions	Results for selection	Search SNP data
Build	& Download GWAS ma	atrices		
	Get SNP information	Get a	ccessions for SNPs	
	1:5787 1:5808			
7	-			
			11.	
	Download SNP informa			
	Download Style Informa	ation U		
	Download SNF Informa			
oout				
			Results for selection	Search SNP data
	ct transcript and access	ions	Results for selection	Search SNP data
Selec	ct transcript and access	ions	Results for selection	Search SNP data
Selec Build	ct transcript and access	ions atrices	Results for selection	Search SNP data
Selec Build	ct transcript and access & Download GWAS ma Get SNP information	ions atrices		Search SNP data
Selec Build	ct transcript and access & Download GWAS ma	ions atrices		Search SNP data
Selec Build	t transcript and access & Download GWAS ma Get SNP information 4:14730221 4:14730223 4:14730234	ions atrices		Search SNP data
Selec Build	et transcript and access & Download GWAS ma Get SNP information 4:14730221 4:14730223 4:14730234 4:14730241	ions atrices		Search SNP data
Selec Build	t transcript and access & Download GWAS ma Get SNP information 4:14730221 4:14730223 4:14730234	ions atrices		Search SNP data
Selec Build	et transcript and access & Download GWAS ma Get SNP information 4:14730221 4:14730223 4:14730234 4:14730241	ions atrices		Search SNP data
Selec Build	et transcript and access & Download GWAS ma Get SNP information 4:14730221 4:14730223 4:14730234 4:14730241	ions atrices		Search SNP data
Selec Build	et transcript and access & Download GWAS ma Get SNP information 4:14730221 4:14730223 4:14730234 4:14730241	ions atrices		Search SNP data

Click 'Download SNP information'.

Download SNP information ⁽¹⁾: For each SNP ID in the list all the transcripts covering the SNP are listed. Additional information like SNP effect, SNP region and base frequency are added.

Build & Download GWAS m		ults for selection	Search SNP databa
Get SNP information	Get access	sions for SNPs	
4:14730221 4:14730223 4:14730234 4:14730241 4:14730247			
		11.	

Transcript ID: Shown are *A. thaliana* gene lds and splicing variant (e.g. AT4G30120.1) in which the selected SNPs are located

SNP ID: SNP identification number. Shown are chromosome:bp positions (4:14730221) of each SNP of selected gene.

Variant_0: Base pair variant on a specific position with the highest frequency of selected gene.

Frequency_0: Base frequency of variant 0 from selected gene.

Variant_1: Base pair variant on a specific position with the second highest frequency of selected gene.

Frequency_1: Base frequency of variant 1 from selected gene.

SNP relative position mRNA: SNP base pair position of selected gene mRNA.

SNP relative position genome: SNP base pair position of selected gene gDNA (genomic DNA).

SNP location: Gene structure location (e.g. 3' UTR (untranslated region), INTRON etc.) of SNP and selected gene.

SNP effects: Effect of SNP on AA sequence of selected gene (e.g. stop codon (premature stop codon), nonsynonymous (AA substitution), canonical motif in splice site etc.)

	A	В	c	D	E	F	G	н	1	1
1	Transcript id	SNP Id	Variant_0	Frequency_0	Variant_1	Frequency_1	SNP relative position mrna	SNP relative position genome	SNP location	SNP effects
2	AT4G30120.2	4:14730221	C -> C	0.99824	C -> A	0.00176	2296	2967	3UTR	noval
3	AT4G30120.2	4:14730223	T -> T	0.9859	T -> C	0.0141	2294	2965	3UTR	noval
-4	AT4G30120.2	4:14730234	C -> C	0.99912	C -> A	0.00088	2283	2954	3UTR	noval
5	AT4G30120.2	4:14730241	G -> T	0.70749	G -> G	0.29251	2276	2947	3UTR	noval
6	AT4G30120.2	4:14730247	A -> A	0.99031	A -> T	0.00969	2270	2941	3UTR	noval
7	AT4G30120.1	4:14730221	C -> C	0.99824	C -> A	0.00176	2589	3408	3UTR	noval
8	AT4G30120.1	4:14730223	T -> T	0.9859	T -> C	0.0141	2587	3406	3UTR	noval
9	AT4G30120.1	4:14730234	C -> C	0.99912	C -> A	0.00088	2576	3395	3UTR	noval
10	AT4G30120.1	4:14730241	G -> T	0.70749	G -> G	0.29251	2569	3388	3UTR	noval
11	AT4G30120.1	4:14730247	A -> A	0.99031	A -> T	0.00969	2563	3382	3UTR	noval

Substitution_properties: Physico-chemical properties of AA substitution (e.g. non-polar \rightarrow polar, basic \rightarrow acidic etc.)

Domain ID: Protein domain ID in which the AA substitutions are located.

Domain description: Description of domain.

Strand: Strand direction (e.g. - and +) of sequence.

GWAS corrected: GWAS analysis was performed with the software GEMMA. Every climate factor was used as a phenotype and for every climate factor, one analysis run was carried out. Only SNPs with a minor allele frequency of 1% or higher were analysed. The obtained p-values were corrected for multiple comparisons using the Benjamini-Yekutiel method. In this column you can see all the correlations between SNPs and the 200 climate factors which have a corrected p-value lower than or equal to the threshold. You can sort the column according to the lowest p-value in each cell.

Number of associated climate factors: Number of associated climate factors, with a corrected P-value in the GWAS lower than or equal to the threshold.

	К	L	M	N	0	P	Q	R
1	Substitution properties	Domain Id	Domain description	Strand	AraGWAS_score	AraGWAS_links	GWAS corrected	Number of associated climate factors
2	noval	noval	noval	-	noval	noval	noval	C
3	noval	noval	noval		noval	noval	noval	C
4	noval	noval	noval	-	noval	noval	noval	C
5	noval	noval	noval		noval	noval	noval	C
6	noval	noval	noval	-	noval	noval	noval	C
7	noval	noval	noval		noval	noval	noval	C
8	noval	noval	noval	-	noval	noval	noval	C
9	noval	noval	noval		noval	noval	noval	C
10	noval	noval	noval	-	noval	noval	noval	C
11	noval	noval	noval		noval	noval	noval	0

2.5.2 Get accessions for SNPs

About		
Select transcript and acces	ssions Results for selection	Search SNP database
Build & Download GWAS	matrices	
Get SNP information	Get accessions for SNPs	
1:5787 1:5808		
	//.	
Download Accession	ns 🚯	

Copy and paste SNP ID or IDs of interest into the empty field.

Selec	et transcript and access	sions	Results f	for selection	Search SNP databas
Build	& Download GWAS m	atrices			
	Get SNP information	Get a	accessions	for SNPs	
	4:14730221 4:14730223 4:14730234 4:14730241				
	4:14730247 				
			//.		

Retrieve accessions for SNPs of interest by clicking 'Download Accessions'.

Download SNP information ①: For each SNP ID in the list all the transcripts covering the SNP are listed. For each combination of transcript, SNP ID and variant all the genotypes with this specific variation are listed.

🗩 Ak	pout					
	Select transcript and access	ions	Results	for selection	Search SNP database	
	Build & Download GWAS ma	atrices				
	Get SNP information	Geta	accession	s for SNPs		
	4:14730221 4:14730223 4:14730234 4:14730241 4:14730247	0	//.			

Transcript ID: Shown are *A. thaliana* gene IDs and splice variants (e.g. AT4G30120.2) in which the selected SNPs are located

SNP_ID: SNP identification number. Shown are chromosome:bp positions (4:14730221) of each SNP of selected gene.

T: Accessions with the base T on this position.

G: Accessions with the base G on this position.

A: Accessions with the base A on this position.

C: Accessions with the base C on this position.

	A	B	C	D	F	F
1	transcript id	snp id c	т	G	A	c
2	AT4G30120.2	4:14730221	9608,9728,	88,108,139,159,265,350,351,403	3,410,424,428,430,470,476,484,5	04,506,531,544,546,628,630,680
3	AT4G30120.2	4:14730223		6074,8231,8235,8243,9646,964	88,108,139,159,265,350,351,403	3,410,424,428,430,470,476,484,5
4	AT4G30120.2	4:14730234	8230,	88,108,139,159,265,350,351,403	3,410,424,428,430,470,476,484,5	04,506,531,544,546,628,630,680
5	AT4G30120.2	4:14730241			265,350,351,403,424,428,430,4	88,108,139,159,410,630,765,768
6	AT4G30120.2	4:14730247	88,108,139,159,265,350,351,403	410,424,428,430,470,476,484	9102,9104,9106,9111,9113,9114	4,9115,9128,9130,9133,9134,
7	AT4G30120.1	4:14730221	9608,9728,	88,108,139,159,265,350,351,403	3,410,424,428,430,470,476,484,5	04,506,531,544,546,628,630,680
8	AT4G30120.1	4:14730223		6074,8231,8235,8243,9646,964	88,108,139,159,265,350,351,403	3,410,424,428,430,470,476,484,5
9	AT4G30120.1	4:14730234	8230,	88,108,139,159,265,350,351,403	3,410,424,428,430,470,476,484,5	04,506,531,544,546,628,630,680
10	AT4G30120.1	4:14730241			265,350,351,403,424,428,430,4	88,108,139,159,410,630,765,768
11	AT4G30120.1	4:14730247	88,108,139,159,265,350,351,403	,410,424,428,430,470,476,484 >	9102,9104,9106,9111,9113,9114	4,9115,9128,9130,9133,9134,

2.6 Build & Download GWAS matrices

SNPstar enables the generation of GWAS matrices of interest. The computed matrix contains accessions and SNPs, DNA haplotypes or protein haplotypes.

Select transcript and accessi	ons Results for selection	Search SNP database	
Build & Download GWAS ma	atrices		
Results: AT4G3012	20.2	Accession information	~ Dow
ATHMA3: A. THAL METAL ATPASE 3; atpase 3	IANA HEAVY HMA3: Heavy meta	1	
Check selected accessions	•		
0		ning O Harlahma ay Ara	i tabla 🗛
		sions () Haplotype <-> Acc	ession table 🕖
Protein haplotype <-> A	ccession table 🚯		
starts negative, with the A in t		in the feature viewer starts with 0, while the SNP labels in the feature viewer show	
starts negative, with the A in the transcripts on the reverse stranscripts on the reve	he ATG start codon being position 1. Th and the reverse complement is shown. otein domains Z SNPs Z Syn. S	ne SNP labels in the feature viewer show	the genomic position. For
starts negative, with the A in the transcripts on the reverse stranscripts on the reverse strain in the transcripts on the reverse strain in the transcripts on the transcripts on the transcripts of the t	he ATG start codon being position 1. Th and the reverse complement is shown. otein domains Z SNPs Z Syn. S	ne SNP labels in the feature viewer show	the genomic position. For
starts negative, with the A in the transcripts on the reverse stranscripts on the reverse stranscripts on the reverse stranscripts on the transcripts on the transcripts on the transcripts of the transcri	he ATG start codon being position 1. Th and the reverse complement is shown. otein domains Z SNPs Z Syn. S	ne SNP labels in the feature viewer show	the genomic position. For
starts negative, with the A in the transcripts on the reverse stranscripts on the reverse stranscripts on the reverse stranscripts on the reverse stranscripts on the Provide Stranscripts on the Provide Stranscripts of the Prov	he ATG start codon being position 1. Ti and the reverse complement is shown. Dotein domains 2 SNPs 2 Syn. S 1 SNP with minor allele frequency	ne SNP labels in the feature viewer show	the genomic position. For

Select three different types of polymorphisms from the drop-down menu 'Select GWAS Matrix Type'.

•	About
	Select transcript and accessions Results for selection Search SNP database
	Build & Download GWAS matrices
	Select GWAS Matrix Type: SNP GWAS Matrix ~
	Per default all transcripts are selected. Upload Transcript CSV File to select subset (IDs in each line): Browse No file selected.
	Select SNP Subset: All SNPs v
	Select accessions:
	File with accession IDs v Browse No file selected.
	Email for notification: Enter your email Compute GWAS Matrix

'Select GWAS Matrix Type' options are 'SNP GWAS Matrix', 'Haplotype GWAS Matrix' and 'Proteotype GWAS Matrix'. If the 'SNP GWAS Matrix' is applied, a matrix for all available SNPs of selected genes is generated. For 'Haplotype GWAS Matrix' only DNA haplotypes (based on bases) and for 'Proteotype GWAS Matrix' only protein haplotypes (or proteotypes based on AAs).

bout	Paralle for a la fina - O cardo OND da la cardo
Select transcript and accessions Build & Download GWAS matrices	Results for selection Search SNP database
Select GWAS Matrix Type: SNP GWAS I Per defait SNP GWAS Haplotype	
Select SNP Subset: All SN Proteotype	e GWAS Matrix
Select accessions:	
File with accession IDs v Browse	No file selected.
Email for notification: Enter your email	Compute GWAS Matrix

You can upload a transcript table (csv file). If the default settings are used, a matrix for all transcripts (genes) is computed. If a download transcript file is used, a matrix for transcripts (genes) of interest is computed. The uploaded file needs to contain gene and transcript numbers (e.g. AT4G30120.1).

	A	В
1	AT4G30110.1	
2	AT4G30110.2	
3	AT4G30120.1	
4	AT4G30120.2	
5		

Click 'Browse' and select your transcript file of interest for upload.

	Results for selection Search SNP database	
Build & Download GWAS matric	es	
Select GWAS Matrix Type: SNP GV	AS Matrix ~	
Por dofault all transcripts are soloctor		No file sele
r er ueraun an nariscripts are selecter	. Upload Transcript CSV File to select subs	No file sele
Select SNP Subset: All SNPs	Upload Transcript CSV File to select subs	No lile sele
		No life sele

To remove the selected transcript (Gene) file, click 'Unselect File/Default all transcripts'.

۶	About
	Select transcript and accessions Results for selection Search SNP database
	Build & Download GWAS matrices
	Select GWAS Matrix Type: SNP GWAS Matrix
	Per default all transcripts are selected. Upload Transcript CSV File to select subset (IDs in each line): Browse, SNPstar_transcript csv
	Unselect File/Default all transcripts
	Select SNP Subset: All SNPs V
	Select accessions:
	File with accession IDs V Browse No file selected.
	Email for notification: Enter your email Compute GWAS Matrix

Next, select a SNP subset.

Select transcript and acc	essions Results for selection Search SNP database
Build & Download GWAS	S matrices
Select GWAS Matrix Type:	SNP GWAS Matrix
Per default all transcripts are	e selected. Upload Transcript CSV File to select subset (IDs in each line): Browse SNPstar_transcript c
Per default all transcripts are	
	npts
Unselect File/Default all transc	npts

'Select SNP Subsets' options are 'All SNPs', 'Coding region only' and 'Nonsynonymous SNPs only'. If 'All SNPs' are selected all SNPs are used. For 'Coding region only' SNPs in coding regions and for 'Nonsynonymous SNPs only' SNPs causing AA substitutions are considered.

Select transcript and accessions	Results for selection	Search SNP data	abase	
Build & Download GWAS matrices				
Select GWAS Matrix Type: SNP GWAS I	Matrix v			
Per default all transcripts are selected. Up	load Transcript CSV File to	select subset (IDs in ea	ach line): Browse SNPstar_tra	nscript.csv
Per default all transcripts are selected. Up Unselect File/Default all transcripts	oload Transcript CSV File to	select subset (IDs in ea	ach line): Browse SNPstar_tra	nscript.csv
	oload Transcript CSV File to	select subset (IDs in ea	ach line): Browse) SNPstar_tra	nscript.cs
Unselect File/Default all transcripts		select subset (IDs in ea	ach line): Browse) SNPstar_tra	nscript.csv
Unselect File/Default all transcripts Select SNP Subset: All SNPs	, ,	select subset (IDs in ea	ach line): Browse) SNPstar_tra	nscript.cs [,]

If you would like to select accessions of interest you can upload an accession file. For the structure of that file see chapter 2.2.2. If the default settings are used a matrix for all accessions is computed. The upload works like for the transcript table (refer to 2.6). To remove the selected accession file use the 'Unselect File/Default all accession' button.

Select transcript and a	accessions	Results for selection	Search SNP database	e
Build & Download GW	AS matrices			
Select GWAS Matrix Typ	e: SNP GWAS	Matrix ~		
Per default all transcripts	are selected. U	pload Transcript CSV File to	select subset (IDs in each lin	e): Browse SNPstar_transcript.csv
Per default all transcripts Unselect File/Default all tra		pload Transcript CSV File to	select subset (IDs in each lin	e): Browse SNPstar_transcript.csv
Unselect File/Default all tra		pload Transcript CSV File to	select subset (IDs in each lin	e): Browse) SNPstar_transcript.csv
Unselect File/Default all tra	nscripts		select subset (IDs in each lin	e): Browse SNPstar_transcript.csv

Provide an email address for notification and press 'Compute GWAS Matrix'.

Select transcript and accession	s Results for selection	Search SNP database	
Build & Download GWAS matrice	ces		
Select GWAS Matrix Type: SNP G	WAS Matrix V		
Per default all transcripts are selecte	d. Upload Transcript CSV File to	select subset (IDs in each line):	Browse SNPstar_transcript.
Unselect File/Default all transcripts			
Select SNP Subset: All SNPs	~		
Select accessions:			
File with accession IDs v Bro	wse SNPstar_accessions.csv	Unselect File/Default all accessions	
Email for notification: Enter your ema			

If the calculation is in progress, an information window is displayed.

			🖩 Manual 🛤
Select transcript and accessions Results for select	ofion Search SNP database	Build & Download GWAS matrices	SNP: PRØ
Select GWAS Matrix Type: SNP GWAS Matrix V			
Per default all transcripts are selected. Upload Transcript CS ⁴	V File to select subset (IDs in each line):	Browse SNPstar_transcript.csv	
Select SNP Subset: All SNPs v			
Select accessions: File with accession IDs V Browse SNPstar_accessi	ons.csv		
Email for notification. re babben@landwuni-halle.de Com	pute GWAS Matrix		
After processing, download GWAS matrix at localhost:5000)/query_result/gwas_matrix_snp_dba1dl	ec6478155759ea8a0f078c35f0 p (Currentl)	Processing)

To retrieve the GWAS matrix click on the green window (only when processing is finished).

Control transmipt and resources - Results for extendion - Support SNP database - Build & Download	I GWAS matrices
Select GWAS Matrix Type: SNP GWAS Matrix ~	
Per default all transcripts are selected. Upload Transcript CSV File to select subset (IDs in each line): Browse SNPstar_t	transcript.csv
Select SNP Subset: All SNPs ~	
Select accessions: File with accession IDs Image: SNPstar_accessions.csv	
Email for notification rebabblen@lands.uni-halle.de Compute GWAS Matrix	
File ready. /query_result/gwas_matrix_srp_dba1dfec6478155759ea8a0I078c35f0.zip	

2.6.1 Layout of SNP GWAS Matrix

In the first horizontal row all selected accessions (IDs from the 1001 Genomes project) are shown.

		В	с	D	E	F	G	н	1	J	K	L	м	N	0	Р	Q
		6145	6148	2053	6149	6150	6151	2057	6153	6154	6163	6166	8214	19950	6169	19951	617
2	AT4G3011 .1	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	(
3	AT4G30110.2	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	(
4	AT4G30120.1	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0	(
5	AT4G30120.2	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0	(

In the first vertical column all selected transcripts are shown.

		В	С	D	E	F	G	н	- 1	J	K	L	М	N	0	P	Q
1		6145	6148	2053	6149	6150	6151	2057	6153	6154	6163	6166	8214	19950	6169	19951	6172
2	AT4G30110.1	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0
3	AT4G30110.2	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0
4	AT4G30120.1	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0	0
5	AT4G30120.2	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0	0

The matrix consists of numbers. The number zero (0) describes the status of Col-0. One (1) describes an allele different from Col-0. This matrix can be used for GWAS and/or kinship calculations.

	A	В	С	D	E	F	G	н	1	J	K	L	м	Ν	0	Р	Q
1											0100			10050		10001	
2	AT4G30110.1	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0
3	AT4G30110.2	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0
4	AT4G30120.1	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0	0
5	AT4G30120.2	0	1	0	0	1	0	0	0	0	1	0	1	0	0	0	0

2.6.2 Layout of Haplotype GWAS Matrix

In the first horizontal row all selected accessions (IDs from the 1001 Genomes project) are shown.

	× 1																
		В	с	D	Е	F	G	н	1	J	К	L	М	N	0	Р	Q
		6145	6148	2053	6149	6150	6151	2057	6153	6154	6163	6166	8214	19950	6169	19951	6172
2	AT4G30110.1	68	68	33	73	33	70	33	33	33	33	33	26	70	10	70	9
3	AT4G30110.2	68	68	33	73	33	70	33	33	33	33	33	26	70	10	70	9
4	AT4G30120.1	38	38	36	38	36	47	36	36	36	36	36	84	84	87	84	80
5	AT4G30120.2	47	47	45	47	45	27	45	45	45	45	45	25	25	32	25	20

In the first vertical column all selected transcripts are shown.

		в	C	D	F	F	G	н	1	1	к	1	м	N	0	р	0
1		6145	6148	2053	-	6150	-		6153	6154	6163	6166		19950	-		
2	AT4G30110.1	68	68	33	73	33	70	33	33	33	33	33	26	70	10	70	9
3	AT4G30110.2	68	68	33	73	33	70	33	33	33	33	33	26	70	10	70	9
4	AT4G30120.1	38	38	36	38	36	47	36	36	36	36	36	84	84	87	84	80
5	AT4G30120.2	47	47	45	47	45	27	45	45	45	45	45	25	25	32	25	20

The matrix consists of numbers which describe a specific haplotype of specific accession and transcript. This matrix can be used for GWAS calculation.

А	В	С	D	E	F	G	н	1	J	К	L	М	N	0	Р	Q
	0145	0110	2050	0110	0150	0151	2057	0150	0154	0100	0100	0211	10050	0100	10051	0172
AT4G30110.1	68	68	33	73	33	70	33	33	33	33	33	26	70	10	70	9
AT4G30110.2	68	68	33	73	33	70	33	33	33	33	33	26	70	10	70	9
AT4G30120.1	38	38	36	38	36	47	36	36	36	36	36	84	84	87	84	80
AT4G30120.2	47	47	45	47	45	27	45	45	45	45	45	25	25	32	25	20
	A AT4G30110.1 AT4G30110.2 AT4G30120.1 AT4G30120.2	AT4G30110.1 68 AT4G30110.2 68 AT4G30120.1 38	AT4G30110.1 68 68 AT4G30110.2 68 68 AT4G30120.1 38 38	AT4G30110.1 68 68 33 AT4G30110.2 68 68 33 AT4G30120.1 38 38 36	AT4G30110.1 68 68 33 73 AT4G30110.2 68 68 33 73 AT4G30120.1 38 38 36 38	AT4G30110.1 68 68 33 73 33 AT4G30110.2 68 68 33 73 33 AT4G30120.1 38 38 36 38 36	AT4G30110.1 68 68 33 73 33 70 AT4G30110.2 68 68 33 73 33 70 AT4G30120.1 38 38 36 38 36 47	AT4G30110.1 68 68 33 73 33 70 33 AT4G30110.2 68 68 33 73 33 70 33 AT4G30120.1 38 38 36 38 36 47 36	AT4G30110.1 68 68 33 73 33 70 33 33 AT4G30110.2 68 68 33 73 33 70 33 33 AT4G30120.1 38 38 36 38 36 47 36 36	AT4G30110.1 68 68 33 73 33 70 33 33 33 AT4G30110.2 68 68 33 73 33 70 33 33 33 AT4G30120.1 38 38 36 38 36 47 36 36 36	AT4G30110.1 68 68 33 73 33 70 33 33 33 33 AT4G30110.2 68 68 33 73 33 70 33 33 33 33 AT4G30120.1 38 38 36 38 36 47 36 36 36 36	AT4G30110.1 68 68 33 73 33 70 33 33 33 33 33 AT4G30110.2 68 68 33 73 33 70 33 33 33 33 33 AT4G30120.1 38 38 36 38 36 47 36 36 36 36 36	0145 0140 0050 0140 0250 0150 0151 0151 0160 0161 <th< th=""><th>04.15 04.16 04.05 04.14 04.05 04.05 04.05 <th< th=""><th>0145 0146 0050 0150 0151 0157 0150 0151 0160 0160 0161 0160 <th< th=""><th>04.15 04.16 <th< th=""></th<></th></th<></th></th<></th></th<>	04.15 04.16 04.05 04.14 04.05 04.05 04.05 <th< th=""><th>0145 0146 0050 0150 0151 0157 0150 0151 0160 0160 0161 0160 <th< th=""><th>04.15 04.16 <th< th=""></th<></th></th<></th></th<>	0145 0146 0050 0150 0151 0157 0150 0151 0160 0160 0161 0160 <th< th=""><th>04.15 04.16 <th< th=""></th<></th></th<>	04.15 04.16 <th< th=""></th<>

2.6.3 Layout of Proteotype GWAS Matrix

¥.

In the first horizontal row all selected accessions (IDs from the 1001 Genomes project) are shown.

		_															
		В	С	D	E	F	G	н	- 1	J	K	L	М	N	0	Р	Q
		6145	6148	2053	6149	6150	6151	2057	6153	6154	6163	6166	8214	19950	6169	19951	6172
2	AT4G3011.1	36	36	30	41	30	36	30	30	30	30	30	30	36	68	36	70
3	AT4G30110.2	36	36	30	41	30	36	30	30	30	30	30	30	36	68	36	70
4	AT4G30120.1	57	57	54	57	54	67	54	54	54	54	54	21	21	19	21	19
5	AT4G30120.2	19	19	16	19	16	29	16	16	16	16	16	1	1	23	1	23

In the first vertical column all selected transcripts are shown.

_		_															
		В	C	D	E	F	G	н	- 1	J	K	L	М	Ν	0	Р	Q
1		6145	6148	2053	6149	6150	6151	2057	6153	6154	6163	6166	8214	19950	6169	19951	6172
2	AT4G30110.1	36	36	30	41	30	36	30	30	30	30	30	30	36	68	36	70
3	AT4G30110.2	36	36	30	41	30	36	30	30	30	30	30	30	36	68	36	70
4	AT4G30120.1	57	57	54	57	54	67	54	54	54	54	54	21	21	19	21	19
5	AT4G30120.2	19	19	16	19	16	29	16	16	16	16	16	1	1	23	1	23

The matrix consists of numbers which describe a specific protein haplotype/proteotype of a specific accession and transcript. This matrix can be used for GWAS calculation.

	A	В	C	D	E	F	G	н	1	J	K	L	М	N	0	Р	Q
1		0145	0110	2050	0110	0150	0151	2057	0150	0151	0100	0100	0211	10050	0100	10051	0172
2	AT4G30110.1	36	36	30	41	30	36	30	30	30	30	30	30	36	68	36	70
3	AT4G30110.2	36	36	30	41	30	36	30	30	30	30	30	30	36	68	36	70
4	AT4G30120.1	57	57	54	57	54	67	54	54	54	54	54	21	21	19	21	19
5	AT4G30120.2	19	19	16	19	16	29	16	16	16	16	16	1	1	23	1	23

3 Use cases

SNPstar covers a number of different use cases. In this chapter, we will explain the most prominent use cases, which can be roughly grouped into single target gene, multiple target genes and GWAS.

3.1 Single target gene

In this first use case, we will consider a single target gene and all SNPs in this gene. We will again use *A. THALIANA HEAVY METAL ATPASE 3* (*HMA3*; *AT4G30120*) as an example.

First, select gene and gene model (AT4G30120.1; see chapter 2.1.1). Then we select all available accessions (see chapter 2.2.1) and click 'Compute results' (see chapter 2.3) to get to the 'Sequence viewer' tab as displayed below.

Results: AT4G	30120.1			Download options	✓ Down
ATHMA3: A. TH METAL ATPAS atpase 3			tal		
Check selected accessions	•				
Sequence viewer	6 SNP:	s 🚯 SNPs <-> Acc	cessions 🕄	Haplotype <-> Access	sion table 🚯
Protein haplotype	<-> Access	sion table 🚯			
✓ Introns ✓ UTR	Protein de		n. SNPs 🗹 Non	syn. SNPs CDS only	Protein sequence only
🗹 Introns 🗹 UTR	Protein de		n. SNPs 🗹 Non		Protein sequence only
Position: 0	Protein de	omains 🗹 SNPs 🗹 Syr	n. SNPs 🗹 Non		Protein sequence only
Introns UTR Position: 0 Sequence 3'-UTR	Protein de	omains 🗹 SNPs 🗹 Syr	n. SNPs 🗹 Non		Protein sequence only
Introns UTR Position: 0 Sequence S-UTR CDS Introns Nonsyn. SNPs	Protein de	omains 🗹 SNPs 🗹 Syr	n. SNPs 🗹 Non		Protein sequence only
Introns UTR Position: 0 Sequence S-UTR CDS Introns Nonsyn. SNPs NonCDS SNPs	Protein de	omains 🗹 SNPs 🗹 Syr	n. SNPs 🗹 Non		Protein sequence only
Introns UTR Position: 0 Sequence S-UTR CDS Introns Nonsyn. SNPs	Protein de	omains 🗹 SNPs 🗹 Syr	n. SNPs 🗹 Non		Protein sequence only
Introns UTR Position: 0 Sequence 3-UTR 5-UTR CDS Introns Nonsyn. SNPs Syn. SNPs Syn. SNPs	Protein de	omains 🗹 SNPs 🗹 Syr	n. SNPs 🗹 Non		Protein sequence only

3.1.1 Identification of SNPs in a single gene of interest

3.1.1.1 General selection and SNP identification

The Sequence viewer tab (see chapter 2.4.1) shows an overview of all SNPs represented in all accessions. Additional information are gene structure (e.g. CDS, Intron, etc.), detected protein domain locations and effect of SNPs (nonsynonymous, synonymous and non-CDS). Beneath the overview figure the sequence is shown.

For a closer look of detected SNPs use the 'SNPs' tab (see chapter 2.4.2). Different selection options can be used depending on your research interest. If you are interested in a specific SNP location use the column 'SNP location' for selection. As an example we use CDS for selection.

,	About							
	Select transcript	t and access	sions Re	esults for selec	tion Search SNP database			
	Build & Downloa	ad GWAS m	atrices					
	Results: A	T4G301	20.1		All	- Downl	oad	
	ATHMA3: METAL AT atpase 3				etal			
	Check selected acc	cessions	*					
	Sequence Protein hap	viewer () plotype <->	SNPs () Accession		ccessions 0 Haplotype <-> Access	ion table 0		
SNP_ID (Genomic position)	Base frequencies 🚯	Genomic position ()	MRNA Position	SNP location	SNP effects	Amino acid substitution	Chemical properties	Interp
	Default: No cutoff							
4:14732045	C → C: 0.70485 C → T: 0.29515	1458		INTRON				
4:14731525	G → G: 0.72863 G → T: 0.27137	1978	1343	CDS	nonsynonymous	R → I	basic -> non-polar	
4:14731691	T → A: 0.29163 T → T: 0.70837	1812	1276	CDS	nonsynonymous	Y → N	polar -> polar	
4:14730993	A → A: 0.66784 A → T: 0.33216	2510		INTRON	canonical motif in splice site			
4:14730994	C → A: 0.33304 C → C: 0.66696	2509		INTRON	canonical motif in splice site			
4:14733389	G -> G: 0.5022 G -> T: 0.4978	114	114	CDS	synonymous			
4:14733393	A → A: 0.50308 A → C: 0.49692	110	110	CDS	nonsynonymous	Q -> P	polar -> non-polar	
4:14732256	T → C: 0.56652 T → T: 0.43348	1247		INTRON				
4:14732536	G -> A: 0.56388 G -> G: 0.43612	967	600	CDS	synonymous			
4:14732323	T → A: 0.13392 T → T: 0.86608	1180	813	CDS	splice site region, nonsynonymous	N → K	polar -> basic	

Type 'CDS' into the empty field below the column header. The selection works automatically (no need to press enter). Shown are all SNPs which are located in the CDS of the selected target gene.

,	About								
	Select transcript	and access	sions Re	sults for selec	tion Search SNP database				
	Build & Downloa	ad GWAS m	atrices						
	Results: A	T4G301	20.1		Al	- Downl	oad		
	ATHMA3: METAL AT atpase 3				netal		_		
	Check selected ac	ressions	*						
	Sequence	viewer	SNPs 🚯		Accessions () Haplotype <-> Accession	n table 🚯			
	Protein haj	olotype <->	Accession	ta					
			-						
SNP_ID (Genomic position)	Base frequencies 🕄	Genomic position ()	MRNA Position 🕄	SNP location	SNP effects	Amino acid substitution 🕄	Chemical properties	Interp	
	Default: No cutoff			cds			onemen properties	interp	
4:14731525	G → G: 0.72863	1978	1343	CDS	nonsynonymous	R ≫ I	basic -> non-polar		^
4:14731691	G → T: 0.27137 T → A: 0.29163	1812	1276	CDS	nonsynonymous	Y → N	polar -> polar		
	T -> T: 0.70837								
4:14733389	G -> G: 0.5022	114	114	CDS	synonymous				
	G -> T: 0.4978								
4:14733393	A → A: 0.50308	110	110	CDS	nonsynonymous	$Q \Rightarrow P$	polar -> non-polar		
4:14733393	$A \Rightarrow A: 0.50308$ $A \Rightarrow C: 0.49692$ $G \Rightarrow A: 0.56388$	110 967	110	CDS CDS	nonsynonymous synonymous	Q → P	polar -> non-polar		
4:14732536	$A \Rightarrow C: 0.49692$ $G \Rightarrow A: 0.56388$ $G \Rightarrow G: 0.43612$	967	600	CDS	synonymous				
	A -> C: 0.49692 G -> A: 0.56388 G -> G: 0.43612 T -> A: 0.13392					Q → P N → K	polar -> non-polar polar -> basic		
4:14732536 4:14732323	$\begin{array}{l} A \to C; \ 0.49692 \\ G \to A; \ 0.56388 \\ G \to G; \ 0.43612 \\ T \to A; \ 0.13392 \\ T \to T; \ 0.86608 \end{array}$	967 1180	600 813	CDS CDS	synonymous splice site region, nonsynonymous	N -> K	polar -> basic		
4:14732536	A -> C: 0.49692 G -> A: 0.56388 G -> G: 0.43612 T -> A: 0.13392	967	600	CDS	synonymous				
4:14732536 4:14732323	$\begin{array}{c} A \Rightarrow C: \ 0.49692 \\ \hline G \Rightarrow A: \ 0.56388 \\ \hline G \Rightarrow G: \ 0.43612 \\ \hline T \Rightarrow A: \ 0.13392 \\ \hline T \Rightarrow T: \ 0.86608 \\ \hline G \Rightarrow A: \ 0.01674 \end{array}$	967 1180	600 813	CDS CDS	synonymous splice site region, nonsynonymous	N -> K	polar -> basic		
4:14732536 4:14732323 4:14733117 4:14731132	$\begin{array}{l} A \Rightarrow C: 0.49692 \\ \hline G \Rightarrow A: 0.56388 \\ \hline G \Rightarrow G: 0.43612 \\ \hline T \Rightarrow A: 0.13392 \\ \hline T \Rightarrow T: 0.86608 \\ \hline G \Rightarrow A: 0.01674 \\ \hline G \Rightarrow G: 0.08326 \\ \hline A \Rightarrow A: 0.20705 \\ \hline A \Rightarrow TA: 0.79295 \\ \end{array}$	967 1180 386 2371	600 813 238 1628	CDS CDS CDS CDS CDS	synanymous splice site region, nonsynonymous nonsynonymous stop codon, stop codon, frame shift, synonymous	N → K V → I	polar → basic non-polar → non-polar		
4:14732536 4:14732323 4:14733117	$\begin{array}{l} A \to \mathbb{C}: \ 0.49692 \\ G \to A: \ 0.50388 \\ G \to \mathbb{C}: \ 0.43612 \\ T \to A: \ 0.13392 \\ T \to T: \ 0.86008 \\ G \to A: \ 0.01674 \\ G \to \mathbb{C}: \ 0.08326 \\ A \to A: \ 0.20705 \\ A \to TA: \ 0.70255 \\ C \to \mathbb{C}: \ 0.99912 \end{array}$	967 1180 386	600 813 238	CDS CDS CDS	synonymous splice site region, nonsynonymous nonsynonymous	N -> K	polar -> basic		
4:14732536 4:14732323 4:14733117 4:14731132	$\begin{array}{l} A \Rightarrow C: 0.49692 \\ \hline G \Rightarrow A: 0.56388 \\ \hline G \Rightarrow G: 0.43612 \\ \hline T \Rightarrow A: 0.13392 \\ \hline T \Rightarrow T: 0.86608 \\ \hline G \Rightarrow A: 0.01674 \\ \hline G \Rightarrow G: 0.08326 \\ \hline A \Rightarrow A: 0.20705 \\ \hline A \Rightarrow TA: 0.79295 \\ \end{array}$	967 1180 386 2371	600 813 238 1628	CDS CDS CDS CDS CDS	synanymous splice site region, nonsynonymous nonsynonymous stop codon, stop codon, frame shift, synonymous	N → K V → I	polar → basic non-polar → non-polar		

If you are interested in further filtering the SNPs in the CDS for, for example, those causing missense mutations, type 'nonsynonymous' into the empty field below the column header 'SNP effects'. Shown are all SNPs which are located in the CDS with an AA substitution effect.

	About							
	Select transcript	and access	sions Re	esults for selec	tion Search SNP database			
	Build & Downloa	ad GWAS m	atrices					
	Results: A	T4G301	20.1		All		Download	
	ATHMA3: METAL AT atpase 3	A. THAL			netal			
	Check selected acc	essions	*					
	Sequence Protein ha	viewer () blotype <->	SNPs () Accession	SNPs <-> /	Accessic plotype <->	Accession table ()		
SNP_ID (Genomic position)	Base frequencies 0	Genomic position ()	MRNA Position	SNP location	SNP c.	Amino acid substitution (3)	Chemical properties	Interpro Id
	Default: No cutoff			cds	nonsynonymous			
4:14731525	G → G: 0.72863 G → T: 0.27137	1978	1343	CDS	nonsynonymous	R -> I	basic -> non-polar	
4:14731691	T -> A: 0.29163 T -> T: 0.70837	1812	1276	CDS	nonsynonymous	Y -> N	polar -> polar	
4:14733393	A → A: 0.50308 A → C: 0.49692	110	110	CDS	nonsynonymous	Q → P	polar -> non-polar	
4:14732323	T → A: 0.13392 T → T: 0.86608	1180	813	CDS	splice site region, nonsynonymous	N → K	polar -> basic	
4:14733117	G → A: 0.01674 G → G: 0.98326	386	238	CDS	nonsynonymous	V -> 1	non-polar -> non-polar	
4:14731188	C → C: 0.99912 C → G: 0.00088	2315	1572	CDS	nonsynonymous	N → K	polar -> basic	
4:14731216	T → C: 0.00088 T → T: 0.99912	2287	1544	CDS	nonsynonymous	M -> T	non-polar -> polar	
4:14731228	G → A: 0.00088 G → G: 0.99912	2275	1532	CDS	nonsynonymous	$G \twoheadrightarrow D$	non-polar -> acidic	
4:14731234	C → A: 0.00617 C → C: 0.99383	2269	1526	CDS	nonsynonymous	T⇒N	polar -> polar	
4:14731261	T -> C: 0.00088 T -> T: 0.99912	2242	1499	CDS	nonsynonymous	1.+T	non-polar -> polar	

The first column 'SNP ID' shows all SNPs which are selected with the implemented filter steps by now. The SNP IDs are important to identify accessions which contain SNPs of interest (see chapter 3.1.1.2).

	Select transcript	and acces	sions Re	sults for selecti	on Search SNP database			
	Build & Downloa	ad GWAS m	natrices					
	Results: A	T4G301	20.1		All	~	Download	
	ATHMA3: METAL AT atpase 3				etal			
	Check selected act	cessions	*					
	Sequence		SNPs 6	SNPs <-> Ac		Accession table 6		
	Sequence	vieweľ	SINP'S 😈	SINPS <-> AC	cessions • Haplotype <-> /	Accession table		
	Protein har	olotype <->	Accession t	able 🙃				
	Trotoirrid	soupo		0.010				
SNP_ID 🚯	Base frequencies 🛈	Genomic	MRNA	SNP location	SNP effects	Amino acid		
(Genomic position)								
(Genomic position)		position	Position 🕄			substitution 🕄	Chemical properties	Interp
(Genomic position)	Default: No cutoff	position O	Position	cds	nonsynonymous	substitution U	Chemical properties	Interp
4:14731525	Default: No cutoff G -> G: 0.72863	1978	1343	cds CDS	nonsynonymous nonsynonymous	R > 1	Chemical properties	Interp
								Interp
	G -> G: 0.72863							Interp
4:14731525 4:14731691	G → G: 0.72863 G → T: 0.27137 T → A: 0.29163 T → T: 0.70837	1978	1343 1276	CDS CDS	nonsynonymous	R > 1 Y → N	basic -> non-polar polar -> polar	Interp
4:14731525	$G \Rightarrow G: 0.72863$ $G \Rightarrow T: 0.27137$ $T \Rightarrow A: 0.29163$ $T \Rightarrow T: 0.70837$ $A \Rightarrow A: 0.50308$	1978	1343	CDS	nonsynonymous	R⇒I	basic -> non-polar	Interp
4:14731525 4:14731691 4:14733393	$G \rightarrow G: 0.72863$ $G \rightarrow T: 0.27137$ $T \rightarrow A: 0.29163$ $T \rightarrow T: 0.70837$ $A \rightarrow A: 0.50308$ $A \rightarrow C: 0.49692$	1978 1812 110	1343 1276 110	CDS CDS CDS	nonsynonymous nonsynonymous nonsynonymous	R → I Y → N Q → P	basic -> non-polar polar -> polar polar -> non-polar	Interp
4:14731525 4:14731691	$\begin{split} G & \Rightarrow G: 0.72863 \\ G & \Rightarrow T: 0.27137 \\ T & \Rightarrow A: 0.29163 \\ T & \Rightarrow T: 0.70837 \\ A & \Rightarrow A: 0.50308 \\ A & \Rightarrow C: 0.49692 \\ T & \Rightarrow A: 0.13392 \end{split}$	1978	1343 1276	CDS CDS	nonsynonymous	R > 1 Y → N	basic -> non-polar polar -> polar	Interp
4:14731525 4:14731691 4:1473393 4:14732323	$\begin{split} G & \Rightarrow G: 0.72863 \\ G & \Rightarrow T: 0.27137 \\ T & \Rightarrow A: 0.29163 \\ T & \Rightarrow T: 0.70837 \\ A & \Rightarrow A: 0.50308 \\ A & \Rightarrow C: 0.49692 \\ T & \Rightarrow A: 0.13392 \\ T & \Rightarrow T: 0.86608 \end{split}$	1978 1812 110 1180	1343 1276 110 813	CDS CDS CDS CDS CDS	nonsynonymous nonsynonymous nonsynonymous splice site region, nonsynonymous	R → I Y → N Q → P N → K	basic -> non-polar polar -> polar polar -> non-polar polar -> basic	Interp
4:14731525 4:14731691 4:14733393	$\begin{split} G &\to G: 0.72863 \\ G &\to T: 0.27137 \\ T &\to A: 0.29163 \\ T &\to T: 0.70837 \\ A &\to A: 0.50308 \\ A &\to C: 0.49692 \\ T &\to A: 0.13392 \\ T &\to T: 0.86608 \\ G &\to A: 0.01674 \end{split}$	1978 1812 110	1343 1276 110	CDS CDS CDS	nonsynonymous nonsynonymous nonsynonymous	R → I Y → N Q → P	basic -> non-polar polar -> polar polar -> non-polar	Interp
4:14731525 4:14731691 4:14733393 4:14732323 4:14733117	$\begin{split} G & \sim G: 0.72863 \\ G & \sim T: 0.27137 \\ T & \sim X: 0.29163 \\ T & \sim T: 0.70837 \\ A & \sim X: 0.30308 \\ A & \sim C: 0.49692 \\ T & \sim X: 0.13392 \\ T & \sim T: 0.86608 \\ G & \sim X: 0.01674 \\ G & \sim G: 0.98326 \end{split}$	1978 1812 110 1180 386	1343 1276 110 813 238	CDS CDS CDS CDS CDS CDS	nonsynonymous nonsynonymous nonsynonymous splice site region, nonsynonymous nonsynonymous	R → I Y → N Q → P N → K V → I	basic -> non-polar polar -> polar polar -> non-polar polar -> basic non-polar -> non-polar	Interp
4:14731525 4:14731691 4:1473393 4:14732323	$\begin{split} I & = 0 \\ G & > G: 0.72863 \\ G & > I: 0.27137 \\ T & > A: 0.29163 \\ T & > I: 0.70837 \\ A & > A: 0.50308 \\ A & > C: 0.49692 \\ T & > A: 0.13392 \\ T & > I: 0.86608 \\ G & > A: 0.01674 \\ G & > G: 0.98266 \\ C & > C: 0.99912 \end{split}$	1978 1812 110 1180	1343 1276 110 813	CDS CDS CDS CDS CDS	nonsynonymous nonsynonymous nonsynonymous splice site region, nonsynonymous	R → I Y → N Q → P N → K	basic -> non-polar polar -> polar polar -> non-polar polar -> basic	Interp
4:14731525 4:14731691 4:14733393 4:14732323 4:14733117	$\begin{split} G & \sim G: 0.72863 \\ G & \sim T: 0.27137 \\ T & \sim X: 0.29163 \\ T & \sim T: 0.70837 \\ A & \sim X: 0.30308 \\ A & \sim C: 0.49692 \\ T & \sim X: 0.13392 \\ T & \sim T: 0.86608 \\ G & \sim X: 0.01674 \\ G & \sim G: 0.98326 \end{split}$	1978 1812 110 1180 386	1343 1276 110 813 238	CDS CDS CDS CDS CDS CDS	nonsynonymous nonsynonymous nonsynonymous splice site region, nonsynonymous nonsynonymous	R → I Y → N Q → P N → K V → I	basic -> non-polar polar -> polar polar -> non-polar polar -> basic non-polar -> non-polar	Interp
4:14731525 4:14731691 4:147333993 4:14732323 4:14733117 4:14731188	$\begin{split} 0 &> G : 0.72863 \\ G &> G : 0.72863 \\ G &> T : 0.27137 \\ T &> A : 0.29163 \\ T &> T : 0.70837 \\ A &> A : 0.50308 \\ A &> C : 0.49692 \\ T &> A : 0.13392 \\ T &> T : 0.86608 \\ G &> A : 0.11674 \\ G &> G : 0.98326 \\ C &> C : 0.9912 \\ C &> G : 0.0088 \end{split}$	1978 1812 110 1180 386 2315	1343 1276 110 813 238 1572	CDS CDS CDS CDS CDS CDS CDS CDS CDS	nonsynonymous nonsynonymous splice alte region, nonsynonymous nonsynonymous nonsynonymous	R→I Y→N Q→P N→K V→I N→K	basic -> non-polar polar -> polar polar -> non-polar polar -> basic non-polar -> non-polar polar -> basic	Interp
4:14731525 4:14731691 4:147333993 4:14732323 4:14733117 4:14731188	$\begin{array}{c} \mathbf{C} \Rightarrow \mathbb{G}: 0.72863 \\ \mathbf{G} \Rightarrow \mathbb{G}: 0.72863 \\ \mathbf{G} \Rightarrow \mathbb{T}: 0.27137 \\ \mathbf{T} \Rightarrow \mathbb{A}: 0.29163 \\ \mathbf{T} \Rightarrow \mathbb{T}: 0.70837 \\ \mathbf{A} \Rightarrow \mathbb{A}: 0.80308 \\ \mathbf{A} \Rightarrow \mathbb{C}: 0.49692 \\ \mathbf{T} \Rightarrow \mathbb{K}: 0.13392 \\ \mathbf{T} \Rightarrow \mathbb{T}: 0.86608 \\ \mathbf{G} \Rightarrow \mathbb{A}: 0.01674 \\ \mathbf{G} \Rightarrow \mathbb{G}: 0.98326 \\ \mathbf{C} \Rightarrow \mathbb{C}: 0.98912 \\ \mathbf{C} \Rightarrow \mathbb{C}: 0.00088 \\ \mathbf{T} \Rightarrow \mathbb{C}: 0.00088 \end{array}$	1978 1812 110 1180 386 2315	1343 1276 110 813 238 1572	CDS CDS CDS CDS CDS CDS CDS CDS CDS	nonsynonymous nonsynonymous splice alte region, nonsynonymous nonsynonymous nonsynonymous	R→I Y→N Q→P N→K V→I N→K	basic -> non-polar polar -> polar polar -> non-polar polar -> basic non-polar -> non-polar polar -> basic	Interp
4:14731525 4:14731691 4:14733393 4:14732323 4:14732317 4:14731188 4:14731216	$\begin{array}{c} 0 & \rightarrow c \cdot 0.72863 \\ G \rightarrow T \cdot 0.27137 \\ T \rightarrow K \cdot 0.29163 \\ T \rightarrow T \cdot 0.70847 \\ A \rightarrow K \cdot 0.50308 \\ A \rightarrow C \cdot 0.49692 \\ T \rightarrow T \cdot 0.70847 \\ T \rightarrow X \cdot 0.1392 \\ T \rightarrow T \cdot 0.86608 \\ G \rightarrow K \cdot 0.01574 \\ G \rightarrow C \cdot 0.01574 \\ C \rightarrow C \cdot 0.00981 \\ T \rightarrow C \cdot 0.00088 \\ T \rightarrow C \cdot 0.00088 \\ T \rightarrow T \cdot 0.99912 \end{array}$	1978 1812 110 1180 2315 2287	1343 1276 110 813 238 1572 1544	CDS CDS CDS CDS CDS CDS CDS CDS CDS CDS	nonsynonymous nonsynonymous splice site region, nonsynonymous nonsynonymous nonsynonymous nonsynonymous nonsynonymous	R>I Y→N Q>P N→K V>I N→K N→K	basic -> non-polar polar -> polar polar -> non-polar polar -> basic non-polar -> non-polar polar -> basic non-polar -> polar	Interp
4:14731525 4:14731691 4:14733393 4:14732323 4:14732317 4:14731188 4:14731216	$\begin{array}{c} 0 & \sim 0 \cdot 0 \cdot 72863 \\ 0 & \sim 1 \cdot 0 \cdot 72863 \\ 0 & \sim 1 \cdot 0 \cdot 7137 \\ \mathbf{T} & \sim \mathbf{K} \cdot 0 \cdot 29163 \\ \mathbf{T} & \sim \mathbf{K} \cdot 0 \cdot 0 \cdot 0 \\ \mathbf{T} & \sim \mathbf{K} \cdot 0 \cdot 0 \cdot 0 \\ \mathbf{T} & \sim \mathbf{K} \cdot 0 \cdot 13392 \\ \mathbf{T} & \sim \mathbf{K} \cdot 0 \cdot 13392 \\ \mathbf{T} & \sim \mathbf{K} \cdot 0 \cdot 13392 \\ \mathbf{T} & \sim \mathbf{K} \cdot 0 \cdot 0 \cdot 0 \\ \mathbf{G} & \sim \mathbf{K} \cdot 0 \cdot 0 \cdot 0 \\ \mathbf{G} & \sim \mathbf{K} \cdot 0 \cdot 0 \\ \mathbf{G} & \sim \mathbf{K} \cdot 0 \cdot 0 \\ \mathbf{G} & \sim \mathbf{K} \cdot 0 \cdot 0 \\ \mathbf{G} & \sim \mathbf{K} \cdot 0 \cdot 0 \\ \mathbf{G} & \sim \mathbf{K} \cdot 0 \\ \mathbf{G} & = \mathbf{K} \cdot $	1978 1812 110 1180 2315 2287	1343 1276 110 813 238 1572 1544	CDS CDS CDS CDS CDS CDS CDS CDS CDS CDS	nonsynonymous nonsynonymous splice site region, nonsynonymous nonsynonymous nonsynonymous nonsynonymous nonsynonymous	R>I Y→N Q>P N→K V>I N→K N→K	basic -> non-polar polar -> polar polar -> non-polar polar -> basic non-polar -> non-polar polar -> basic non-polar -> polar	Interp
4:14731525 4:14731691 4:14732393 4:14732323 4:14733117 4:14731188 4:14731216 4:14731228	$G \Rightarrow G: 0.72863$ $G \Rightarrow T: 0.27137$ $T \Rightarrow X: 0.27137$ $T \Rightarrow X: 0.27037$ $T \Rightarrow X: 0.30308$ $T \Rightarrow X: 0.30308$ $T \Rightarrow X: 0.30308$ $G \Rightarrow G: 0.06952$ $G \Rightarrow X: 0.00874$ $G \Rightarrow G: 0.00088$ $T \Rightarrow X: 0.0$	1978 1812 110 1180 2315 2287 22275	1343 1276 110 813 238 1572 1544 1532	CDS CDS CDS CDS CDS CDS CDS CDS CDS CDS	nonghongmous nonghongmous songhongmous splice site region, nonghongmous nonghongmous nonghongmous nonghongmous	R>1 Y→N Q>P N>K V>I N>K M>T G>D	basic > non-polar polar > polar polar > non-polar polar > non-polar polar > basic non-polar > non-polar polar > polar non-polar > polar non-polar > polar	Interp

Additional interesting information are the nature of AA substitutions and whether the mutated residue may have different physico-chemical properties to specifically focus on such SNPs with a potential consequence on protein structure and/or function.

	About								
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SNP_ID	Protein hap Base frequencies	Genomic position	MRNA Position	SNP location	SNP effects	Amino acid		1	
(denomic position)	Default: No cutoff	position	r canton Q	cds	nonsynonymous	Substitution C	Chemical properties	In erpro Id	
4:14731525	G → G: 0.72863 G → T: 0.27137	1978	1343	CDS	nonsynonymous	R -> 1	basic -> non-polar		
4:14731691	T → A: 0.29163 T → T: 0.70837	1812	1276	CDS	nonsynonymous	Y -> N	polar -> polar		
4:14733393	A → A: 0.50308 A → C: 0.49692	110	110	CDS	nonsynonymous	Q → P	polar -> non-polar		
4:14732323	T → A: 0.13392 T → T: 0.86608	1180	813	CDS	splice site region, nonsynonymous	N → K	polar -> basic		
4:14733117	G → A: 0.01674 G → G: 0.98326	386	238	CDS	nonsynonymous	V > I	non-polar -> non-polar		
4:14731188	C → C: 0.99912 C → G: 0.00088	2315	1572	CDS	nonsynonymous	N -> K	polar -> basic		
4:14731216	T → C: 0.00088 T → T: 0.99912	2287	1544	CDS	nonsynonymous	M -> T	non-polar -> polar		
4:14731228	G → A: 0.00088 G → G: 0.99912	2275	1532	CDS	nonsynonymous	G → D	non-polar -> acidic		
4:14731234	C → A: 0.00617 C → C: 0.99383	2269	1526	CDS	nonsynonymous	T → N	polar -> polar		
4:14731261	T -> C: 0.00088	22.42	1499	CDS	nonsynonymous	1 -> T	non-polar -> polar		

If you are interested in nonsynonymous SNPs which are located in a protein domain or in combination with already shown information (e.g. physico-chemical property, etc.), scroll to the right to the 'Interpro ID', 'Interpro description', 'Domain ID' and 'Domain description' columns to retrieve this type of information.

	🗩 About			
	Select tran	script and accessions	Results for selection	Search SNP database
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Interpro Id	Interpro description			
Interpro Id	Interpro description	Domain id PTHR11939:SF31,PTHR1192	39,G3DSA-2.70.150.10	Damain description HEAVY METAL CATION TRANSPORT ATPASE (CAD
Interpro Id	Interpro description			
Interpro Id	Interpro description	PTHR11039:SF31,PTHR119: PTHR11939:SF31,PTHR119:	39,G3DSA:2.70.150.10	HEAVY METAL CATION TRANSPORT ATIVASE (CAD HEAVY METAL CATION TRANSPORT ATIVASE (CAD
interpro id	Interpro description	PTHR11939:SF31,PTHR1193	39,G3DSA:2.70.150.10	HEAVY METAL CATION TRANSPORT ATPASE (CAD
Interpro Id	Interpro description	PTHR11939:SF31,PTHR1192 PTHR11939:SF31,PTHR1192 PTHR11939:SF31,PTHR1192	39,G3DSA:2.70.150.10	HEAVY METAL CATION TRANSPORT ATPAGE (CAD HEAVY METAL CATION TRANSPORT ATPAGE (CAD HEAVY METAL CATION TRANSPORT ATPAGE (CAD
Interpro Id	Interpro description	PTHR11939:SF31,PTHR1192 PTHR11939:SF31,PTHR1192 PTHR11939:SF31,PTHR1192	39,G3DSA:2.70.150.10 39,SSF81660	HEAVY METAL CATION TRANSPORT ATPAGE (CAD HEAVY METAL CATION TRANSPORT ATPAGE (CAD HEAVY METAL CATION TRANSPORT ATPAGE (CAD
Interpro Id	Interpro description	PTHR11939:SF31,PTHR1192 PTHR11939:SF31,PTHR1192 PTHR11939:SF31,PTHR1192	39,G3DSA:2.70.150.10 39,SSF81660 1039:SF31,PTHR11939,SSF81653,	HEAVY METAL CATION TRANSPORT ATPAGE (CAD HEAVY METAL CATION TRANSPORT ATPAGE (CAD HEAVY METAL CATION TRANSPORT ATPAGE (CAD
Interpro Id	Interpro description	PTHR11939.5F31,PTHR119; PTHR11939.5F31,PTHR119; PTHR1939.5F31,PTHR119; PF00122,TIGR01404,PTHR119; PF00122,TIGR01404,PTHR119;	99,G3DSA-2,70.150.10 99,S5F81660 1039:SF31,PTHR11039,S5F81653, 99,S5F81665,S5F81660	HEAVY METAL CATION TRANSPORT ATPAGE (CAD HEAVY METAL CATION TRANSPORT ATPAGE (CAD HEAVY METAL CATION TRANSPORT ATPAGE (CAD HEAVY METAL CATION TRANSPORT ATPAGE (CAD E1422,ATPasc,ATPasc, Physe HAD ATPasc, Physe HEAVY METAL CATION TRANSPORT ATPAGE (CAD
Interpro Id	Interpro description	PTHR11939.SF31,PTHR1192 PTHR11939.SF31,PTHR1192 PTHR11939.SF31,PTHR1192 PTHR11939.SF31,PTHR1193 PF00122,TIGR01494,PTHR1	99,G3DSA-2,70.150.10 99,S5F81660 1039:SF31,PTHR11039,S5F81653, 99,S5F81665,S5F81660	HEAVY METAL CATION TRANSPORT ATMAGE (CAD HEAVY METAL CATION TRANSPORT ATMAGE (CAD HEAVY METAL CATION TRANSPORT ATMAGE (CAD HEAVY METAL CATION TRANSPORT ATMAGE (CAD SIFE1643.0305A.2.70.150.10 E1-62_ATMAGATASA_Physe_Physe.
Interpro Id	Interpro description	PTHR11939.5F31,PTHR119; PTHR11939.5F31,PTHR119; PTHR1939.5F31,PTHR119; PF00122,TIGR01404,PTHR119; PF00122,TIGR01404,PTHR119;	99,G3DSA-2, 70, 150, 10 99,SSF81660 1939:SF31,PTHR11939,SSF81653, 99,SSF81665,SSF81660 19,PS50846,SSF55008	HEAVY METAL CATION TRANSPORT ATPAGE (CAD HEAVY METAL CATION TRANSPORT ATPAGE (CAD HEAVY METAL CATION TRANSPORT ATPAGE (CAD HEAVY METAL CATION TRANSPORT ATPAGE (CAD E1422,ATPasc,ATPasc, Physe HAD ATPasc, Physe HEAVY METAL CATION TRANSPORT ATPAGE (CAD
Interpro Id	Interpro description	PTHRI 1939: SF31, PTHRI 193 PTHRI 1939: SF31, PTHRI 193	99,0308A.2.70.150.10 19,05F81660 1939:SF31,PTHR11939,05F81653, 39,05F81665,05F81660 19,P550846,35F55008	HEAVY METAL CATION TRANSPORT ATPAGE (CAD HEAVY METAL CATION TRANSPORT ATPAGE (CAD
Interpro Id	Interpro description	PTHR11939.5F31,PTHR1192 PTHR11939.5F31,PTHR1192 PTHR11939.5F31,PTHR1192 PF00122,TIGR01494,PTHR1 PF00122,TIGR01494,PTHR1 PTHR11939.5F31,PTHR1192	99,0308A.2.70.150.10 19,05F81660 1939:SF31,PTHR11939,05F81653, 39,05F81665,05F81660 19,P550846,35F55008	HEAVY METAL CATION TRANSPORT ATMAE (CAD HEAVY METAL CATION TRANSPORT ATMAE (CAD HEAVY METAL CATION TRANSPORT ATMAE (CAD HEAVY METAL CATION TRANSPORT ATMAE (CAD E1+22_ATMAE_TABAE_THAS_P + PAPE HEAVY METAL CATION TRANSPORT ATMAE (CAD HEAVY METAL CATION TRANSPORT ATMAE (CAD
Interpro Id	Interpro description	PTHRI 1939: SF31, PTHRI 193 PTHRI 1939: SF31, PTHRI 193	99,0305A-270.150.10 199,05781660 199,0578165,05781660 199,05781665,05781660 199,0550846,05755008 199,0550846,05755008	HEAVY METAL CATION TRANSPORT ATPAGE (CAD HEAVY METAL CATION TRANSPORT ATPAGE (CAD
Interpro Id	Interpro description	PTHRI 1939 SF3L/PTHRI 19 PTHRI 1939 SF3L/PTHRI 19	99,0305A-270.150.10 199,55781660 99,55781653,5771660 99,55781655,55781660 99,755046,55575008 19,755046,55755008	HEAVY METAL CATION TRANSPORT ATPAGE (CAD HEAVY METAL CATION TRANSPORT ATPAGE (CAD

To download information for the SNPs of interest, generate a table with a format as previously described (see 2.5.1) to identify and download accessions carrying your SNP(s) of interest (see 2.5.2).

Another way to identify SNP IDs for SNPs of interest is to download the complete SNP table (see 2.4.6.6). Open the downloaded file in your data processing software of choice (e.g. Excel, etc.) and filter the columns of interest (SNP location, SNP effects, etc.). The resulting lists can also be used for accession identification (chapter 3.1.1.2).

Here we would like to explain filtering for SNP location and SNP effects. Filter CDS in your calculator program of choice (e.g. Excel) in the column SNP location.

3.1.1.2 Identification of accessions with SNPs of interest

If you have identified a single SNP of interest, you might want to do experiments with accessions carrying different alleles at this locus, or simply clone different alleles from original genetic material. You can click on the 'SNP ID' (e.g. 4:14731525) to move directly to the tab 'SNPs \leftrightarrow Accessions' (see chapter 2.4.3).

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For the selected SNP of interest all accessions carrying the allele different from the Col-0 reference are now shown in the column 'Accession_IDs (1001 genomes)'. All shown accessions are different to the reference (Col-0). Now you can search for accessions which are in your lab if you write down the accession ID of interest in the empty field below the column header Accession_IDs (1001 genome).

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			and accessions	685, 687, 728, 742, 853, 854, 867, 868, 870, 915, 932, 1254, 1257, 1612, 1622, 1651, 1652, 1676, 1684, 1739, 1741, 1756, 1757, 1793, 1797, 181	
				1820, 1834, 1835, 1851, 1852, 1853, 1872, 1942, 1943, 2017, 2031, 205	
				2057, 2081, 2091, 2106, 2108, 2141, 2159, 2166, 2171, 2191, 2212, 223	9,
				2240, 2276, 2285, 2286, 2370, 2412, 4779, 4826, 4840, 4857, 4884, 493	
				4958, 5023, 5151, 5165, 5210, 5236, 5249, 5253, 5279, 5349, 5353, 539	
				5577, 5644, 5651, 5717, 5718, 5720, 5726, 5741, 5776, 5779, 5798, 582 5832, 5836, 6016, 6017, 6024, 6025, 6034, 6038, 6040, 6076, 6087, 609	
				6095, 6096, 6099, 6100, 6104, 6105, 6108, 6113, 6118, 6119, 6126, 613	
				6133, 6134, 6138, 6141, 6145, 6148, 6149, 6150, 6153, 6154, 6163, 616	6,
				6217, 6284, 6413, 6739, 6740, 6744, 6749, 6750, 6805, 6806, 6814, 689	7,
				6898, 6907, 6923, 6924, 6926, 6927, 6940, 6943, 6944, 6959, 6966, 698	
				6986, 6989, 6992, 7003, 7008, 7014, 7026, 7028, 7033, 7058, 7061, 706 7071, 7094, 7102, 7107, 7109, 7111, 7119, 7143, 7160, 7162, 7164, 719	
				7202, 7208, 7217, 7248, 7250, 7255, 7276, 7298, 7306, 7307, 7314, 731	
				7320, 7332, 7342, 7344, 7358, 7359, 7377, 7378, 7387, 7411, 7415, 741	
				7471, 7475, 7477, 7515, 7521, 7523, 7529, 7530, 7566, 7568, 7757, 776	7,
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				8422, 8464, 8483, 8699, 8723, 9027, 9057, 9298, 9314, 9380, 9395, 940 9405, 9407, 9427, 9471, 9532, 9534, 9550, 9559, 9565, 9581, 9584, 958	

You can download the accession table by clicking on the link in the column 'CS numbers and accessions' (see in chapter 2.4.3).

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Another way is to move to to the 'SNPs \leftrightarrow Accessions' tab (see chapter 2.4.3) ...

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4:14731691 4:14733393 4:14732323	$\begin{array}{c} C \to G: \ 0.72863 \\ G \to G: \ 0.72863 \\ G \to T: \ 0.27137 \\ T \to A: \ 0.29163 \\ T \to T: \ 0.70837 \\ A \to A: \ 0.50308 \\ A \to C: \ 0.40692 \\ T \to A: \ 0.13992 \\ T \to T: \ 0.86608 \\ G \to A: \ 0.1074 \\ G \to G: \ 0.98326 \\ C \to C: \ 0.9912 \end{array}$	1812 110 1180	1276 110 813	CDS CDS CDS CDS CDS	nonsynonymous nonsynonymous nonsynonymous splice site region, nonsynonymous	R⇒1 Y→N Q→P N→K	basic -> non-polar polar -> polar polar -> non-polar polar -> basic		
1:14731691 1:14733393 1:14732323 1:14733117 1:14731188	$\begin{array}{c} C \to G: \ 0.72863 \\ G \to G: \ 0.72863 \\ G \to T: \ 0.27137 \\ T \to A: \ 0.29163 \\ T \to T: \ 0.70837 \\ A \to A: \ 0.50308 \\ A \to C: \ 0.40692 \\ T \to A: \ 0.13392 \\ T \to T: \ 0.86608 \\ G \to A: \ 0.01674 \\ G \to G: \ 0.09826 \\ C \to C: \ 0.09912 \\ C \to G: \ 0.00088 \\ T \to C: \ 0.00088 \end{array}$	1812 110 1180 386	1276 110 813 238	CDS CDS CDS CDS CDS CDS CDS	nonsynonymous nonsynonymous spilce site region, nonsynonymous nonsynonymous	R→I Y→N Q→P N→K V→I	basic -> non-polar polar -> polar polar -> non-polar polar -> basic non-polar -> non-polar		
114731691 114733393 114732323 114733117 114733117 114731188 114731216	$\begin{array}{c} \mathbf{C} & \sim \mathbf{C} \cdot \mathbf{C} \cdot 22863 \\ \mathbf{G} & \sim \mathbf{C} \cdot \mathbf{C} \cdot 227137 \\ \mathbf{T} & \sim \mathbf{k} \cdot \mathbf{C} \cdot 227137 \\ \mathbf{T} & \sim \mathbf{k} \cdot \mathbf{C} \cdot 227137 \\ \mathbf{T} & \sim \mathbf{k} \cdot \mathbf{C} \cdot \mathbf{C370837} \\ \mathbf{T} & \sim \mathbf{k} \cdot \mathbf{C} \cdot \mathbf{C370837} \\ \mathbf{T} & \sim \mathbf{k} \cdot \mathbf{C} \cdot \mathbf{C370837} \\ \mathbf{T} & \sim \mathbf{k} \cdot \mathbf{C} \cdot \mathbf{C3707} \\ \mathbf{T} & \sim \mathbf{k} \cdot \mathbf{C} \cdot \mathbf{C} \cdot \mathbf{C} \cdot \mathbf{C3707} \\ \mathbf{C} & \sim \mathbf{C} \cdot \mathbf{C} \cdot \mathbf{C} \cdot \mathbf{C3707} \\ \mathbf{C} & \sim \mathbf{C} \cdot \mathbf{C} \cdot \mathbf{C} \cdot \mathbf{C} \cdot \mathbf{C} \cdot \mathbf{C} \\ \mathbf{C} & \sim \mathbf{C} \cdot \mathbf{C} \cdot \mathbf{C} \cdot \mathbf{C} \cdot \mathbf{C} \cdot \mathbf{C} \\ \mathbf{C} & \sim \mathbf{C} \cdot \mathbf{C} \cdot \mathbf{C} \cdot \mathbf{C} \cdot \mathbf{C} \cdot \mathbf{C} \\ \mathbf{T} & \sim \mathbf{T} \cdot \mathbf{C} \\ \mathbf{C} & \sim \mathbf{C} \cdot $	1812 110 1180 386 2315	1276 110 813 238 1572	CDS CDS CDS CDS CDS CDS CDS CDS CDS	nonsynonymous nonsynonymous nonsynonymous splice site region, nonsynonymous nonsynonymous nonsynonymous	R→I Y→N Q→P N→K V→I N→K	basic -> non-polar polar -> polar polar -> non-polar polar -> non-polar non-polar -> non-polar polar -> basic		
1:14731691 1:14733393 1:14732323 1:14733117	$\begin{array}{c} \mathbb{L} & \mathbb{C} \to \mathbb{G}: \ 0.72863 \\ \mathbb{G} \to \mathbb{G}: \ 0.72863 \\ \mathbb{G} \to \mathbb{T}: \ 0.27137 \\ \mathbb{T} \to \mathbb{K}: \ 0.29163 \\ \mathbb{T} \to \mathbb{T}: \ 0.70837 \\ \mathbb{A} \to \mathbb{K}: \ 0.30837 \\ \mathbb{A} \to \mathbb{K}: \ 0.3097 \\ \mathbb{T} \to \mathbb{K}: \ 0.3608 \\ \mathbb{G} \to \mathbb{K}: \ 0.10174 \\ \mathbb{G} \to \mathbb{G}: \ 0.08126 \\ \mathbb{G} \to \mathbb{K}: \ 0.00088 \\ \mathbb{T} \to \mathbb{T}: \ 0.009812 \\ \mathbb{T} \to \mathbb{T}: \ 0.09912 \end{array}$	1812 110 1180 386 2315 2287	1276 110 813 238 1572 1544	CDS CDS CDS CDS CDS CDS CDS CDS CDS CDS	nonsynonymous nonsynonymous spitce site region, nonsynonymous nonsynonymous nonsynonymous nonsynonymous	R>I Y→N Q>P N>K V>I N>K N>K	basic -> non-polar polar -> polar polar -> non-polar polar -> basic non-polar -> non-polar polar -> basic non-polar -> polar		

... and type a single SNP ID of interest (e.g. 4:14731525) into the empty field below the column header 'SNP_ID'.

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If you are interested in more than a single SNP, generate an input list with SNP IDs in your data processing software of choice (e.g. Excel) or, alternatively, use a filtered SNP table (see chapter 3.1.1.1). Next, move to the 'Search SNP database' tab followed by 'Get accessions for SNPs' tab.

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T + T 0.04668 C C Description V + 1 nonpader > nonpder 3317 0 + 0.01674 36 28 CDS nonpmorpmous V + 1 nonpader > nonpder 318 0 + 0.009012 217 CDS nonpmorpmous N + K peder > basic 312.6 0 + 0.00088 2287 1544 CDS nonpmorpmous M + T nonpuder > basic 312.8 0 + 0.00088 2287 1544 CDS nonpmorpmous M + T nonpuder > basic Image: compader > ba	Control Control <t< td=""><td>T + T 0.8668 C C Description N + R Description 3317 0 + 0.01974 386 28 CDS nonsynonymous N + R polar + non-polar 318 0 + 0.009012 217 CDS nonsynonymous N + R polar + basic 118 0 + 0.00088 2287 1544 CDS nonsynonymous M + T non-polar + basic 1216 T + 0.00088 2287 1542 CDS nonsynonymous M + T non-polar + basic 1312.8 0 + 0.00088 2287 1552 CDS nonsynonymous G - D non-polar + basic 1312.8 0 + 0.00088 2287 152 CDS nonsynonymous G - D non-polar + basic 1312.8 0 + 0.00081 2249 128 CDS nonsynonymous T + T non-polar + polar 1312.8 T + T 0.0017 2242 1499 CDS nonsynonymous I + T non-polar + polar</td><td>33393</td><td></td><td>110</td><td>110</td><td>CDS</td><td>nonsynonymous</td><td>Q -> P</td><td>polar -> non-polar</td><td></td><td></td></t<>	T + T 0.8668 C C Description N + R Description 3317 0 + 0.01974 386 28 CDS nonsynonymous N + R polar + non-polar 318 0 + 0.009012 217 CDS nonsynonymous N + R polar + basic 118 0 + 0.00088 2287 1544 CDS nonsynonymous M + T non-polar + basic 1216 T + 0.00088 2287 1542 CDS nonsynonymous M + T non-polar + basic 1312.8 0 + 0.00088 2287 1552 CDS nonsynonymous G - D non-polar + basic 1312.8 0 + 0.00088 2287 152 CDS nonsynonymous G - D non-polar + basic 1312.8 0 + 0.00081 2249 128 CDS nonsynonymous T + T non-polar + polar 1312.8 T + T 0.0017 2242 1499 CDS nonsynonymous I + T non-polar + polar	33393		110	110	CDS	nonsynonymous	Q -> P	polar -> non-polar		
V3117 0 & 0.0154 36 23 CDS nonsprogramus V - I nonsproder - nonspolar 01188 0 - 0.00385 2115 172 CDS nonsprogramus N - K gular - basic 0 - 0.00385 227 1544 CDS nonsprogramus M - T N - Dot M - Dot M - Dot M - Dot M - Dot N - Dot M - Dot M - Dot N - Dot M - Dot </td <td>V3317 0 ~ A 0.0154 86 28 DDS nonsynorymous V ~ I nonsynder ~ honsplar 0.1188 0.~ C.03932 2315 1572 DDS nonsynorymous N ~ K palar ~ basic 0.~ C.03932 2315 1572 DDS nonsynorymous N ~ K palar ~ basic 0.~ C.03088 237 1544 DDS nonsynorymous M ~ T nonsynorymous M + T nonsynorymous M + T nonsynorymous M - T N - M DE DE</td> <td>V3117 0 ~ < & 01164 386 28 DDS nonsynopmous V + I nonsynder = nonspelar 01188 0 ~ < C 08902</td> 2115 1572 DDS nonsynopmous N + X pular ~ basic 0 ~ < C 00008	V3317 0 ~ A 0.0154 86 28 DDS nonsynorymous V ~ I nonsynder ~ honsplar 0.1188 0.~ C.03932 2315 1572 DDS nonsynorymous N ~ K palar ~ basic 0.~ C.03932 2315 1572 DDS nonsynorymous N ~ K palar ~ basic 0.~ C.03088 237 1544 DDS nonsynorymous M ~ T nonsynorymous M + T nonsynorymous M + T nonsynorymous M - T N - M DE	V3117 0 ~ < & 01164 386 28 DDS nonsynopmous V + I nonsynder = nonspelar 01188 0 ~ < C 08902	32323		1180	813	CDS	splice site region, nonsynonymous	$N \twoheadrightarrow K$	polar -> basic		l
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Paste the SNP IDs of interest into the empty field and click 'Download Accessions' to retrieve accession information (see chapter 2.5.2).

3.1.1.3 Identification of accessions with haplotypes of interest

Since SNPs rarely occur in isolation due to phenomena like linkage disequilibrium, you might be interested in identifying haplotypes containing an identical sequence of SNPs for your gene of interest; for example for subsequent cloning projects. We will therefore demonstrate the identification of haplotypes and accessions sharing the same haplotype for a gene of interest.

First, identify SNPs of interest as previously shown (see 3.1.1.2). If you have a list of SNP IDs you can search for a single SNP ID in the tab 'Haplotype \leftrightarrow Accession table'. Type your SNP ID of interest (e.g. 4:14731525) into the column 'SNP list' (see chapter 2.4.4).

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Shown are all haplotypes and the accessions with your SNP of interest.

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If you would like to identify a haplotype which contains only your SNP of interest, write 1 in the search field of column '#SNPs'. Now all haplotypes and accessions which contain only your SNP of interest are shown.

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For our example we identify the haplotype AT4G30120.1.42 with the SNP of interest (4:14731525). Now we can identify accessions which have the haplotype of interest. All accessions are listed in the column 'Accession_IDs'.

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You can also download a list of the selected accessions.

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3.1.1.4 Identification of accessions with protein haplotypes of interest

If you are interested in SNPs which show only AA substitutions then use protein haplotypes. In our example we use the same SNP ID as before (4:14731525) and then move to the tab 'Protein haplotype \leftrightarrow Accession table' (see chapter 2.4.5). Filter for SNP ID 4:14731525.

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	AT4G30120.1. AT4G30120.1. AT4G30120.1. AT4G30120.1. AT4G30120.1.	46_prot 53_prot 54_prot 56_prot 57_prot 58_prot	8 4 255 2 19	3 3 2 3 3 3	Download Sequence Download Sequence Download Sequence Download Sequence Download Sequence Download Sequence	4.14731525,4.14731691,4.147 4.14731525,4.14731691,4.147 4.14731525,4.14731691,4.147 4.14731525,4.14731691 4.14731525,4.14731543,4.147 4.14731525,4.14731564,4.147	31691 31691	accessions Download CS numbers and accessions	915,4840,692 6897,9534,98 108,139,159,2 6100,9897 88,5822,5836

To identify accessions carrying the SNP alleles of interest, follow the same procedure as for haplotype identification described above (see 3.1.1.3).

3.1.2 Identification of known associated SNPs in a gene of interest

In its SNP table SNPstar also lists published associations of SNPs retrieved from the AraGWAS (<u>https://aragwas.1001genomes.org/#/</u>) database and, in addition, associations of SNPs with environmental/climatic factors (eGWAS). You can exploit this information to find out whether SNP(s) in your gene of interest are associated with such phenotypes or environmental/climatic data. Select your gene of interest and all accessions (see 2.1).

Move to tab 'SNPs' and check the columns 'AraGWAS top hits', 'GWAS corrected p-values' and 'Number of associated climate factors' (see 2.4.2) to retrieve this information.

3.2 GWAS

3.2.1 GWAS with all transcripts and a subset of accession.

The initial situation here is the availability of phenotypic data for a subset of accessions or the plan to collect phenotypic data for a subset of accessions that are available in your lab. The widest approach to perform a genome wide association study would include all available SNPs. In this case, you can upload a csv file with the subset of accessions, choose "SNP GWAS Matrix" as matrix type and "All SNPs" as SNP subset and compute the GWAS matrix (see chapter 2.6). This will result in a large dataset. For a more reduced dataset, you could choose a subset of SNPs like "coding SNPs" or "nonsynonymous SNPs" which would focus the subsequent analysis on functional SNPs.

As the conventional GWAS exhibits difficulties in detecting rare alleles and is furthermore limited by the mostly biallelic information of the SNPs, the use of "Haplotype GWAS Matrix" or "Proteotype GWAS Matrix" as matrix type is an effective approach to overcome the limitations of biallelic SNPs and increases the allelic resolution of the candidate genomic region (Qian et al. 2017). The proteotype dataset contains fewer variants per transcript compared to the haplotype dataset as only nonsynonymous SNPs that cause an amino acid exchange are considered (see chapter 2.6).

The computed GWAS matrices can be used directly or with some modification as input for different GWAS tools, e.g. TASSEL etc.

3.2.2 GWAS with a subset of transcripts and a subset of accessions

For this use case, the initial situation is again the availability of phenotypic data for a subset of accessions or the plan to collect phenotypic data for a subset of accessions that are available in you lab. Furthermore, you have already focused your interest on a group of transcripts, may it be the large group of transcription factors, auxin signaling genes or a gene family like ARFs (AUXIN RESPONSE FACTORs). After uploading the csv files of your subset of accession and your transcripts of interest, you could compute the "SNP GWAS Matrix" type with "All SNPs" or a "Haplotype GWAS Matrix", if your analysis should contain all SNPs. If you want to focus more on SNPs that cause an amino acid exchange, you can select the "SNP GWAS Matrix" with "nonsynonymous SNPs" or the "Proteotype GWAS Matrix" (see chapter 2.6). The computed GWAS matrices can be used directly or with some modification as input for different GWAS tools, e.g. TASSEL etc.

3.2.3 GWAS with all or a subset of transcripts and all accessions

This would correspond to the rare occasion that phenotypic data is available for all 1135 accessions. If the GWAS matrix should also contain all transcripts you do not need to upload any file, only choose the SNP matrix type and SNP type and compute the GWAS matrix (see also 3.5.1). If you want to focus on a specific subset of transcripts, you upload only the transcript csv file and then compute the GWAS matrix (see also 3.5.2).