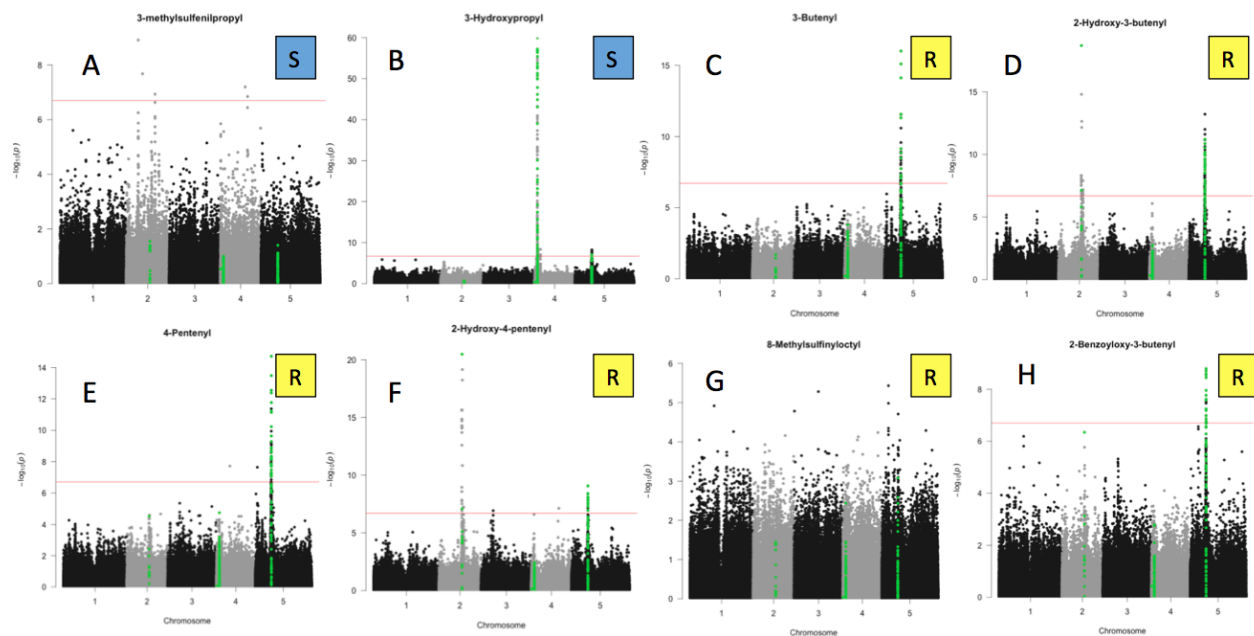
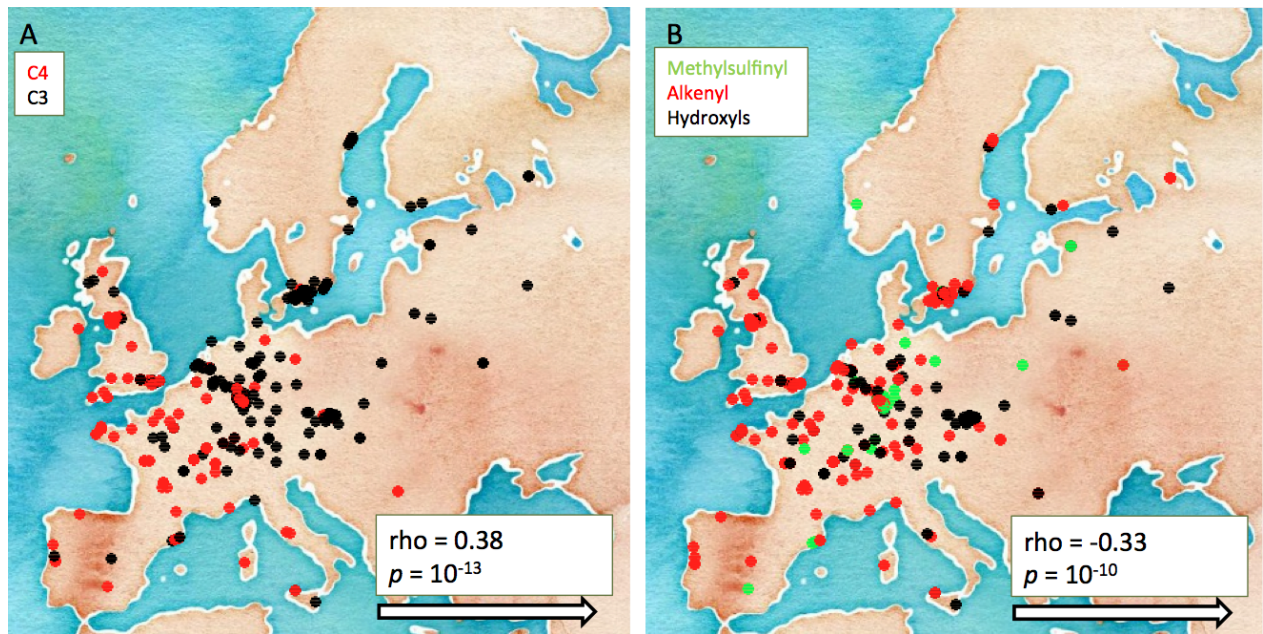


**Suppl. Figure 1. Correlation of 3-ALK GSL content and thrips feeding damage. a.** Correlation between 3-ALK (gluconapin) and thrips feeding damage. **b.** Correlation between 3-ALK and thrips feeding damage; accessions without 3-ALK were omitted from this analysis.



**Suppl. Figure 2. Examples of GWAS on thrips-resistance correlating glucosinolates and thrips feeding damage. a,b** Glucosinolates that significantly correlated with thrips susceptibility. **c-h** Glucosinolates that significantly correlated with thrips resistance.



**Suppl. Figure. 3. Geographic distribution of glucosinolate chemotypes in Europe.** **a.** Geographic distribution pattern of the ratio of C3/C4 glucosinolates. The inset displays the results of a Spearman correlation test on the proportion of C3 GSL over all short chain GSL, with longitude. **b.** Geographic distribution pattern of presence of hydroxy or alkenyl glucosinolates, or their precursor methylsulfinyl glucosinolates. The inset displays the result of a Spearman correlation test on the levels of hydroxyl glucosinolates with longitude.

**Suppl. Table 1. Biotic and abiotic stresses used in for GWAS and correlative study with glucosinolates.**

<b>Trait name</b>	<b>Section of Supplementary Methods in Chapter 5</b>	<b>Trait phenotype</b>	<b>Treatment</b>
Salt_5	SM.2	Biomass	25 mM NaCl
Drought_1	SM.2	Biomass	Drought
Drought_2	SM.9	Biomass	Drought
Osmotic	SM.2	Biomass	PEG8000
Heat	SM.2	Number of siliques	35 °C
Parasitic plant	SM.4	Attachments	<i>Phelipanche ramosa</i>
Nematode	SM.3	Offspring, eggmass	<i>Meloidogyne incognita</i>
Whitefly_1	SM.5	Survival, whiteflies	<i>Aleyrodes proletella</i>
Whitefly_2	SM.5	Reproduction, eggs	<i>A. proletella</i>
Aphid_1	SM.6	Behavior T1, probing	<i>Myzus persicae</i>
Aphid_2	SM.6	Behavior T2, probing	<i>M. persicae</i>
Aphid_3	SM.6	Offspring, aphids	<i>M. persicae</i>
Thrips_1	SM.7	Feeding damage	<i>Frankliniella occidentalis</i>
Thrips_2	SM.7	Behavior T1	<i>F. occidentalis</i>

Thrips_3	SM.7	Behavior T2	<i>F. occidentalis</i>
Caterpillar_1	SM.8	Leaf area consumed	<i>Pieris rapae</i>
Caterpillar_2	SM.9	Biomass	<i>P. rapae</i>
Caterpillar_3	SM.9	Number of damaged leaves and feeding sites	<i>P. rapae</i>
Fungus	SM.10	Number of spreading lesions	<i>Botrytis cinerea</i>
Fungus and caterpillar_1	SM.9	Biomass	<i>B. cinerea</i> and <i>P. rapae</i>
Fungus and caterpillar_2	SM.9	Number of damaged leaves and feeding sites	<i>B. cinerea</i> and <i>P. rapae</i>
Caterpillar and fungus	SM.10	Number of spreading lesions	<i>P. rapae</i> and <i>B. cinerea</i>
Drought and fungus	SM.10	Number of spreading lesions	Drought and <i>B. cinerea</i>
Drought and caterpillar	SM.9	Number of damaged leaves and feeding sites	Drought and <i>P. rapae</i>
Caterpillar and osmotic_1	SM.8	Projected leaf area	<i>P. rapae</i> and PEG8000
Caterpillar and osmotic_2	SM.8	Biomass	<i>P. rapae</i> and PEG8000

**Suppl. Table 2. Cvi x Ler RIL QTL mapping Candidate gene list of genes in a 100 KB region of the significant QTL for resistance to thrips on chromosome 2.**

Locus Identifier	Gene Description	All Gene Symbols
<a href="#">AT2G26370</a>	MD-2-related lipid recognition domain-containing protein	
<a href="#">AT2G26450</a>	Plant invertase/pectin methylesterase inhibitor superfamily	
<a href="#">AT2G26490</a>	Transducin/WD40 repeat-like superfamily protein	
<a href="#">AT2G26380</a>	Leucine-rich repeat (LRR) family protein; INVOLVED IN: signal transduction, defense response	
<a href="#">AT2G26360</a>	Mitochondrial substrate carrier family protein; FUNCTIONS IN: binding; INVOLVED IN: transport, mitochondrial transport, transmembrane transport	
<a href="#">AT2G26520</a>	unknown protein	
<a href="#">AT2G26270</a>	unknown protein	
<a href="#">AT2G26440</a>	Plant invertase/pectin methylesterase inhibitor superfamily; FUNCTIONS IN: enzyme inhibitor activity, pectinesterase activity; INVOLVED IN: cell wall modification	
<a href="#">AT2G26455</a>	pseudogene, similar to Ubiquitin conjugating enzyme 7 interacting protein	
<a href="#">AT2G26600</a>	Glycosyl hydrolase superfamily protein	
<a href="#">AT2G26355</a>	Potential natural antisense gene, locus overlaps with AT2G26360	
<a href="#">AT2G26390</a>	inhibitor (SERPIN) family protein	
<a href="#">AT2G26470</a>	unknown protein;	
<a href="#">AT2G26340</a>	unknown protein.	
<a href="#">AT2G26530</a>	unknown function	(AR781) (HEMD)
<a href="#">AT2G26540</a>	Encodes a uroporphyrinogen-III synthase involved in tetrapyrrole biosynthesis.	UROPORPHYRINOGEN III SYNTHASE (UROS)
<a href="#">AT2G26420</a>	Encodes a phosphatidylinositol-4-phosphate 5-kinase. Exclusively expressed in roots.	1-PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE 3 (PIP5K3) ACIREDUCTONE DIOXYGENASE 3 (ARD3)
<a href="#">AT2G26400</a>	Encodes a protein predicted to belong to the acireductone dioxygenase (ARD/ARD?)family.	ACIREDUCTONE DIOXYGENASE 3 (ATARD3)  ACIREDUCTONE DIOXYGENASE (ARD)
<a href="#">AT2G26320</a>	GAMOUS-like 33 (AGL33); FUNCTIONS IN: DNA binding, sequence-specific DNA binding transcription factor activity;	AGAMOUS-LIKE 33 (AGL33)
<a href="#">AT2G26430</a>	Encodes an ania-6a type arginine-rich cyclin which confers tolerance to LiCl and NaCl when expressed in yeast.	ARGININE-RICH CYCLIN 1 (ATRCY1)  ARGININE-RICH CYCLIN 1 (RCY1)
<a href="#">AT2G26280</a>	smr (Small MutS Related) domain-containing protein mRNA, complete cds	CTC-INTERACTING DOMAIN 7 (CID7)

<a href="#">AT2G26330</a>	Homologous to receptor protein kinases. Involved in specification of organs originating from the shoot apical meristem. ER has been identified as a quantitative trait locus for transpiration efficiency by influencing epidermal and mesophyll development, stomatal density and porosity of leaves. It has been implicated in resistance to the bacterium <i>Ralstonia solanacearum</i> and to the necrotrophic fungus <i>Plectosphaerella cucumerina</i> . Together with ERL1 and ERL2, ER governs the initial decision of protodermal cells to either divide proliferatively to produce pavement cells or divide asymmetrically to generate stomatal complexes.	QUANTITATIVE RESISTANCE TO PLECTOSPHAERELLA 1 (QRP1)  ERECTA (ER)  (ATFAP2)
<a href="#">AT2G26310</a>	Encodes a plastid stroma localized fatty acid binding protein.	FATTY-ACID-BINDING PROTEIN 2 (FAP2)  G PROTEIN ALPHA SUBUNIT 1 (GPA1)
<a href="#">AT2G26300</a>	Encodes an alpha subunit of a heterotrimeric GTP-binding protein. The active GTP-bound form of GPA1 binds to the GTG1 and GTG2 abscisic acid (ABA) receptors and appears to affect their GTPase and GTP-binding activity, and hence, ABA binding abilities. GPA1 is a positive regulator in ABA-mediated inhibition of stomatal opening.	ARABIDOPSIS THALIANA G PROTEIN ALPHA SUBUNIT 1 (ATGPA1)  G PROTEIN ALPHA SUBUNIT 1 (GP ALPHA 1)
<a href="#">AT2G26550</a>	Encodes a heme oxygenase-like protein lacking the conserved histidine residue at the active site that is usually involved in heme-iron coordination.	HEME OXYGENASE 2 (HO2)
<a href="#">AT2G26410</a>	Q-domain 4 (lqd4); CONTAINS InterPro DOMAIN/s: IQ calmodulin-binding region	IQ-DOMAIN 4 (lqd4)
<a href="#">AT2G26350</a>	Zinc-binding peroxisomal integral membrane protein (PEX10). Inserted directly from the cytosol into peroxisomes and is involved in importing proteins into the peroxisome. Required for embryogenesis.	(ATPEX10)  PEROXIN 10 (PEX10)
<a href="#">AT2G26560</a>	Encodes a lipid acyl hydrolase with wide substrate specificity that accumulates upon infection by fungal and bacterial pathogens. Protein is localized in the cytoplasm in healthy leaves, and in membranes in infected cells. Plays a role in cell death and differentially affects the accumulation of oxylipins. Contributes to resistance to virus.	PHOSPHOLIPASE A 2A (PLP2)  (PLAII ALPHA)  PHOSPHOLIPASE A 2A (PLA2A)  PATATIN-LIKE PROTEIN 2 (PLP2)  PHOSPHOLIPASE A 2A (PLA IIA)
<a href="#">AT2G26510</a>	Encodes a plasma-membrane localized nucleobase transporter capable of transporting adenine, guanine, uracil and hypoxanthine. Likely to be a proton-nucleobase symporter	NAT-3 PIGMENT DEFECTIVE EMBRYO 135 (PDE135)
<a href="#">AT2G26590</a>	regulatory particle non-ATPase 13 (RPN13);	REGULATORY PARTICLE NON-ATPASE 13 (RPN13)
<a href="#">AT2G26290</a>	root-specific kinase 1 (ARSK1)	ROOT-SPECIFIC KINASE 1 (ARSK1)
<a href="#">AT2G26460</a>	Encodes SMU2, a protein involved in RNA splicing.	SUPPRESSORS OF MEC-8 AND UNC-52 2 (SMU2)
<a href="#">AT2G26480</a>	UDP-glucosyl transferase 76D1 (UGT76D1);	UDP-GLUCOSYL TRANSFERASE 76D1 (UGT76D1)

<a href="#">AT2G26570</a>	Encodes a coiled-coil protein WEB1 (weak chloroplast movement under blue light 1). WEB1, together with another coiled-coil protein WEB2/PMI2 (At1g66840), maintains the chloroplast photorelocation movement velocity.	WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1 (WEB1)
<a href="#">AT2G26580</a>	YAB	YAB

**Suppl. Table 3. Lists of all GWAS candidate genes under SNPs (10KB window) that a *P*. value < 10<sup>-5</sup>, for resistance to thrips.**

Locus Identifier	All Gene Symbols	Gene Description
AT3G51050		FG-GAP repeat-containing protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: cell-matrix adhesion; LOCATED IN: integrin complex, integral to membrane, plasma membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; Has 99 Blast hits to 94 proteins in 41 species: Archae - 0; Bacteria - 0; Metazoa - 7; Fungi - 0; Plants - 47; Viruses - 0; Other Eukaryotes - 45 (source: NCBI BLink).
AT2G03970		transposable element gene; pseudogene, similar to SAE1-S9-protein, blastp match of 33% identity and 1.2e-17 P-value to GP 4760708 dbj BAA77394.1  AB012866 SAE1-S9-protein {Brassica rapa}
AT1G30515		unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 16 plant structures; EXPRESSED DURING: 6 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G21740.1); Has 20 Blast hits to 20 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 20; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).
AT4G19633		pseudogene of heat shock factor related protein Pseudogene of AT1G66520; PDE194 (PIGMENT DEFECTIVE 194); formyltetrahydrofolate deformylase/ hydroxymethyl-, formyl- and related transferase
AT3G31005		transposable element gene; gypsy-like retrotransposon family (Athila), has a 7.3e-111 P-value blast match to GB:CAA57397 Athila ORF 1 (Arabidopsis thaliana)
AT3G31340		transposable element gene; similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G60930.1)
AT3G31310		GCK domain-containing protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: GCK (InterPro:IPR012891); BEST Arabidopsis thaliana protein match is: GCK domain-containing protein (TAIR:AT5G57570.1); Has 362 Blast hits to 345 proteins in 84 species: Archae - 0; Bacteria - 11; Metazoa - 131; Fungi - 19; Plants - 81; Viruses - 15; Other Eukaryotes - 105 (source: NCBI BLink).
AT5G57640		
AT2G03972		pseudogene of heat shock protein AAA-type ATPase family protein; FUNCTIONS IN: nucleoside-triphosphatase activity, DNA binding, DNA-directed DNA polymerase activity, nucleotide binding, ATP binding; INVOLVED IN: DNA replication; LOCATED IN: DNA polymerase III complex; CONTAINS InterPro DOMAIN/s: ATPase, AAA+ type, core (InterPro:IPR003593), ATPase, AAA-type, core (InterPro:IPR003959), DNA polymerase III, clamp loader complex, gamma/delta/delta subunit, C-terminal (InterPro:IPR008921), DNA polymerase III, subunit gamma/ tau (InterPro:IPR012763); BEST Arabidopsis thaliana protein match is: AAA-type ATPase family protein (TAIR:AT4G18820.1); Has 13188 Blast hits to 13168 proteins in 2852 species: Archae - 365; Bacteria - 7695; Metazoa -
AT5G45720		



		381; Fungi - 497; Plants - 312; Viruses - 26; Other Eukaryotes - 3912 (source: NCBI BLink).
AT1G41930		transposable element gene; CACTA-like transposase family (Tnp1/En/Spm), has a 3.8e-118 P-value blast match to ref NP_189784.1  TNP1-related protein (Arabidopsis thaliana) (CACTA-element)
AT3G31317		transposable element gene; non-LTR retrotransposon family (LINE), has a 6.9e-32 P-value blast match to GB:NP_038603 L1 repeat, Tf subfamily, member 23 (LINE-element) (Mus musculus)
AT4G14165		F-box family protein-related; BEST Arabidopsis thaliana protein match is: F-box family protein with a domain of unknown function (DUF295) (TAIR:AT4G22170.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).
AT1G30550		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein; FUNCTIONS IN: methyltransferase activity; INVOLVED IN: RNA capping, RNA methylation; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; CONTAINS InterPro DOMAIN/s: RNA cap guanine-N2 methyltransferase (InterPro:IPR019012); BEST Arabidopsis thaliana protein match is: S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (TAIR:AT1G45231.2); Has 1500 Blast hits to 1060 proteins in 507 species: Archae - 106; Bacteria - 580; Metazoa - 259; Fungi - 264; Plants - 97; Viruses - 3; Other Eukaryotes - 191 (source: NCBI BLink).
AT4G04410		transposable element gene; copia-like retrotransposon family, has a 1.7e-176 P-value blast match to dbj BAA78426.1  polyprotein (AtRE2-1) (Arabidopsis thaliana) (Ty1_Copia-element)
AT5G28190		unknown protein; Has 45 Blast hits to 34 proteins in 11 species: Archae - 0; Bacteria - 2; Metazoa - 1; Fungi - 0; Plants - 7; Viruses - 2; Other Eukaryotes - 33 (source: NCBI BLink).
AT1G21920		Histone H3 K4-specific methyltransferase SET7/9 family protein; CONTAINS InterPro DOMAIN/s: MORN motif (InterPro:IPR003409); BEST Arabidopsis thaliana protein match is: Histone H3 K4-specific methyltransferase SET7/9 family protein (TAIR:AT1G77660.1); Has 24355 Blast hits to 6247 proteins in 541 species: Archae - 0; Bacteria - 3533; Metazoa - 3700; Fungi - 215; Plants - 2241; Viruses - 0; Other Eukaryotes - 14666 (source: NCBI BLink).
AT5G15230	GAST1 PROTEIN HOMOLOG 4 (GASA4)	Encodes gibberellin-regulated protein GASA4. Promotes GA responses and exhibits redox activity.
AT3G43860	GLYCOSYL HYDROLASE 9A4 (GH9A4)	glycosyl hydrolase 9A4 (GH9A4); FUNCTIONS IN: hydrolase activity, hydrolyzing O-glycosyl compounds, catalytic activity; INVOLVED IN: carbohydrate metabolic process; LOCATED IN: endomembrane system; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Six-hairpin glycosidase (InterPro:IPR012341), Six-hairpin glycosidase-like (InterPro:IPR008928), Glycoside hydrolase, family 9 (InterPro:IPR001701); BEST Arabidopsis thaliana protein match is: glycosyl hydrolase 9B13 (TAIR:AT4G02290.1); Has 1796 Blast hits to 1785 proteins in 262 species: Archae - 2; Bacteria - 633; Metazoa - 188; Fungi - 19; Plants - 915; Viruses - 0; Other Eukaryotes - 39 (source: NCBI BLink).
AT3G51040	RTE1-HOMOLOG (RTH)	Encodes a protein of 231 amino acids with 51% identity to RTE1 over 209 amino acids.
AT3G21560	UDP-GLUCOSYL TRANSFERASE 84A2 (UGT84A2)	Encodes a protein with sinapic acid:UDP-glucose glucosyltransferase activity. Mutants defective in this gene are hyper-fluorescent (which accumulate in their trichomes a compound that is likely to be 3',5'-dimethoxynaringenin chalcone or sinapoyltriatic acid lactone, potential products of the concerted action of 4-coumarate CoA ligase and chalcone synthase on sinapic acid).
AT5G41990	WITH NO LYSINE (K) KINASE 8 (WNK8), EMF1-INTERACTING PROTEIN 1 (EIP1),	Encodes a member of the WNK family (9 members in all) of protein kinases, the structural design of which is clearly distinct from those of other known protein kinases, such as receptor-like kinases and mitogen-activated protein kinases. Interacts specifically with and phosphorylates AtVHA-C, subunit C of the vacuolar

(ATWKNK8)

H<sup>+</sup>-ATPase.

**Suppl. Table 4. Correlation of Glucosinolate content with thrips feeding damage on 125 overlapping accessions in Brachi et al (Brachi, Meyer et al. 2015)**

Glucosinolate	rho	adjusted <i>P.</i> value	Significant
2-ALK	0.085589	0.452256	ns
3-ALK	-0.29819	0.004036	**
3-OH	-0.04188	0.676418	ns
4-ALK	-0.3665	0.000595	***
2-OH-3 ALK	-0.30935	0.003306	**
4-OH	-0.14551	0.208021	ns
2-OH-4-ALK	-0.26634	0.011719	*
3-MT	0.094844	0.412618	ns
4-MT	0.134446	0.21975	ns
3-MS	0.133199	0.21975	ns
5-MS	0.052262	0.658351	ns
4-MS	0.131158	0.21975	ns
6-MT	-0.02691	0.766704	ns
5-MS	-0.14581	0.208021	ns
7-MT	-0.16768	0.164539	ns
6-MS	-0.31137	0.003306	**