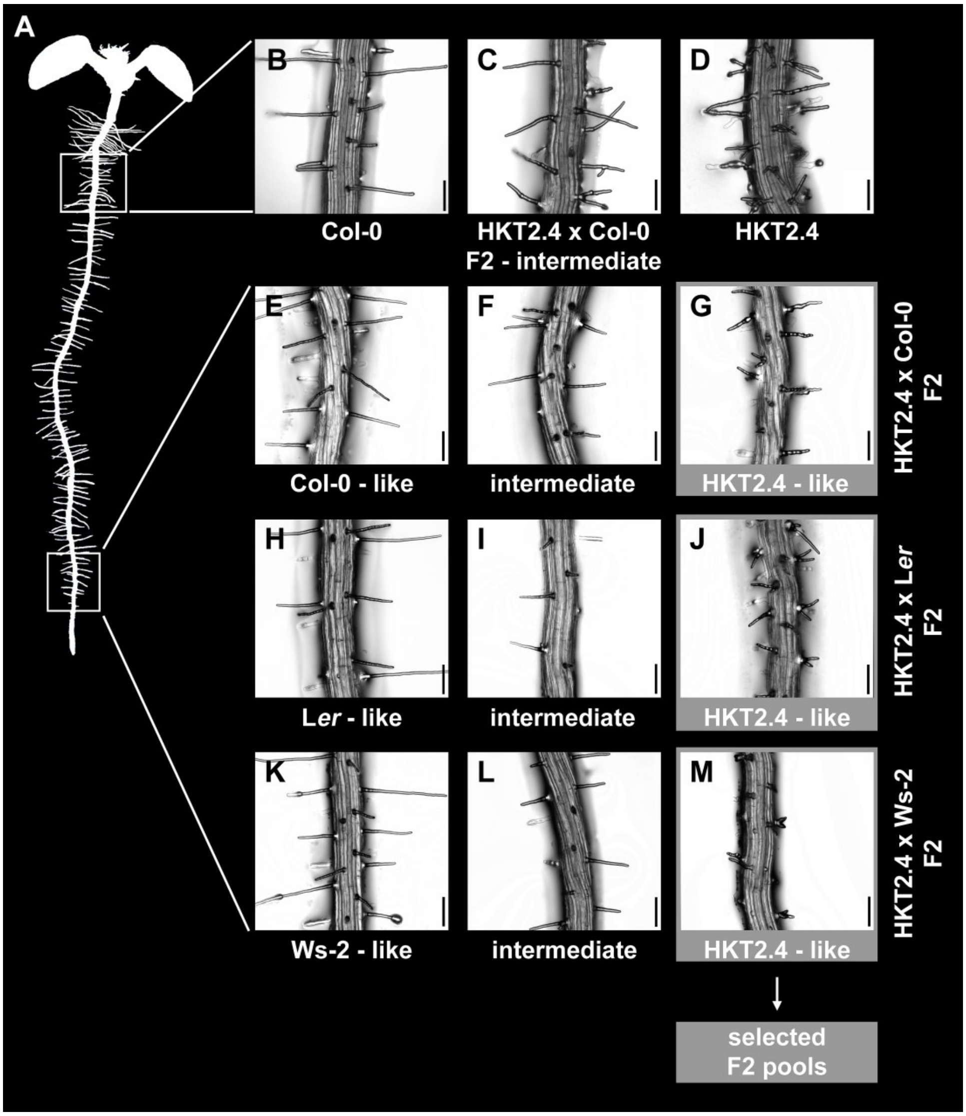
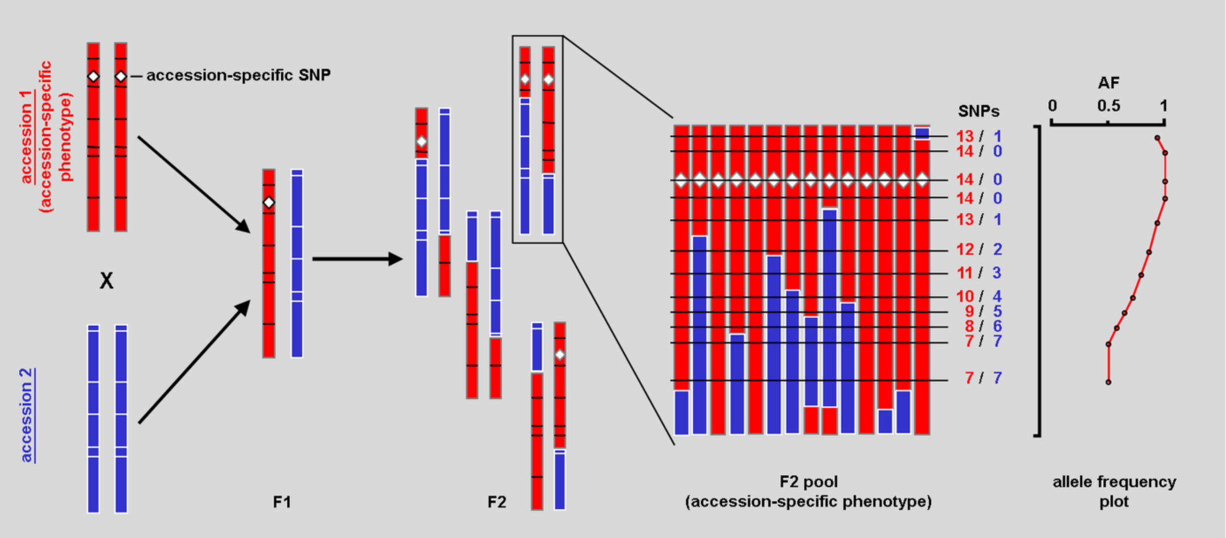
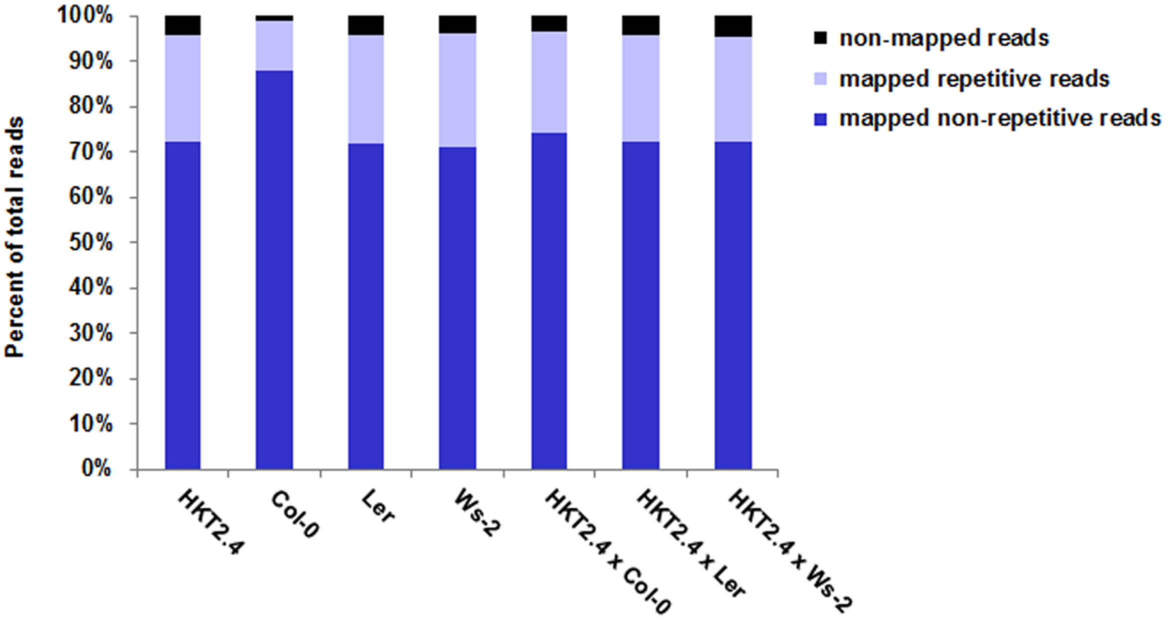


Supplemental Figure S1: Selection of seedlings for F2 pools used for mapping-by-sequencing.
A) The white squares indicate the upper and lower analyzed zones of the root. B) Col-0 has unbranched root hairs in the upper zone C) F2 plants of HKT2.4 crossed to Col-0 with the intermediate phenotype have both, branched and unbranched root hairs in the upper zone. D) HKT2.4 has branched root hairs in the upper zone. E-M) Lower zone of F2 seedlings of HKT2.4 crossed to either Col-0, L*er* or Ws-2. E, H, K) seedlings have unbranched root hairs F, I, L) Seedlings that exhibit the intermediate phenotype in the upper zone (C) show no branching in the lower zone. G, J, M) F2 seedlings with branched root hairs (HKT2.4-like) were pooled for DNA extraction. Scale bar= 250 µm.

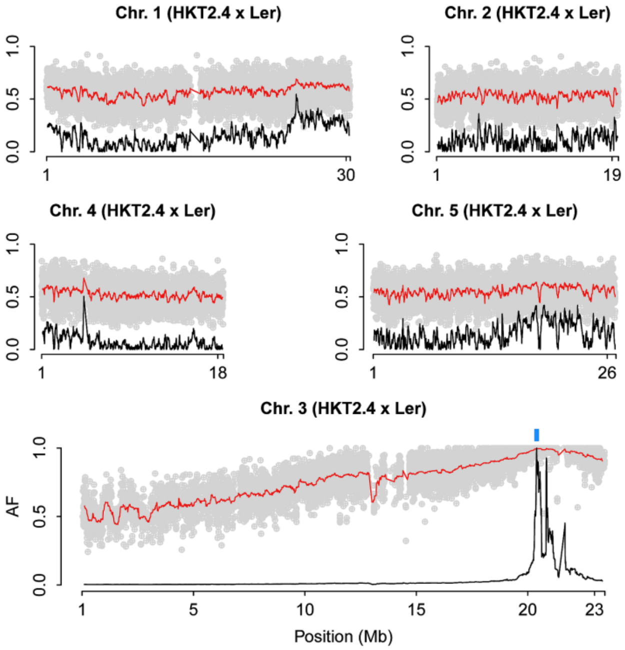


Supplemental Figure S2: Scheme of mapping-by-sequencing using accessions to generate a mapping interval.
Accession 1 has a monogenic SNP causing an accession-specific phenotype compared to accession 2 that uniquely segregates in the F2 generation of the crossing. The scheme illustrates the generation of an F2 mapping population by out-crossing a mutant plant (accession 1) to a non-mutant plant (accession 2), followed by allele frequency (AF) analysis according to the pooled whole-genome sequencing data. The skew of allele frequencies will reveal a mapping interval that is linked to the causal mutation. Black and white lines: accessions-specific markers (SNPs).



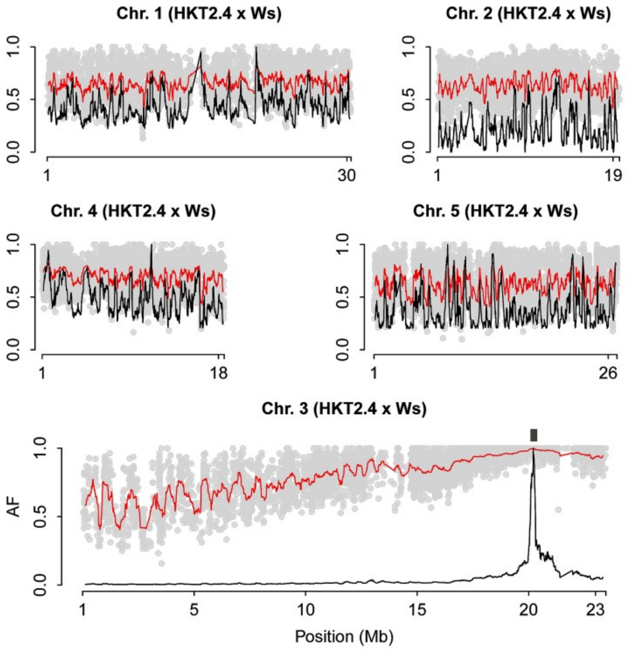
Supplemental Figure S3: Alignment statistics of short reads of parental lines and the mapping populations.

A single read can be mapped to the reference genome when it has up to 10% edit distance and 7% gaps based on its own length. Non-mapped reads are the percent of reads that cannot be mapped to the reference genome. Mapped repetitive reads are the percent of reads that can be mapped to multiple regions of the reference genome. Mapped non-repetitive reads are the percent of reads that can be mapped exactly to one region of the reference genome.

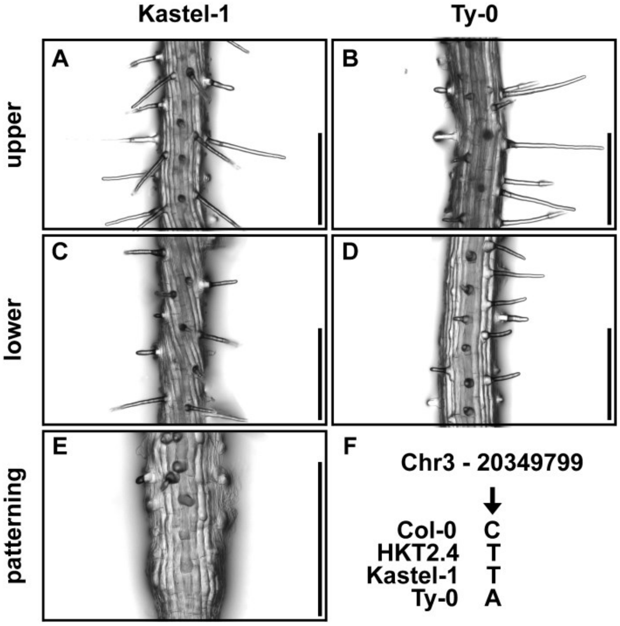


Supplemental Figure S4: Allele frequency plots from the phenotypically selected F2 mapping population of HKT2.4 x L*er.*

The points in gray are individual AFs at the markers, which were created by using SHOREmap according to the resequencing information of parental lines, namely HKT2.4 and L*er*. The red line shows the average AFs at the markers within 200kb sliding windows (10kb step). The black line is the sliding-window based boost-value, a slightly modified version of the r-value as introduced with SHOREmap. Chromosome 3 is shown enlarged. It carries the mapping interval for the phenotype selected for. The peak of boost-values is expected to be linked to the causal mutations. The blue rectangle marks the SHOREmap-derived mapping interval (see Fig. S2 for a scheme).

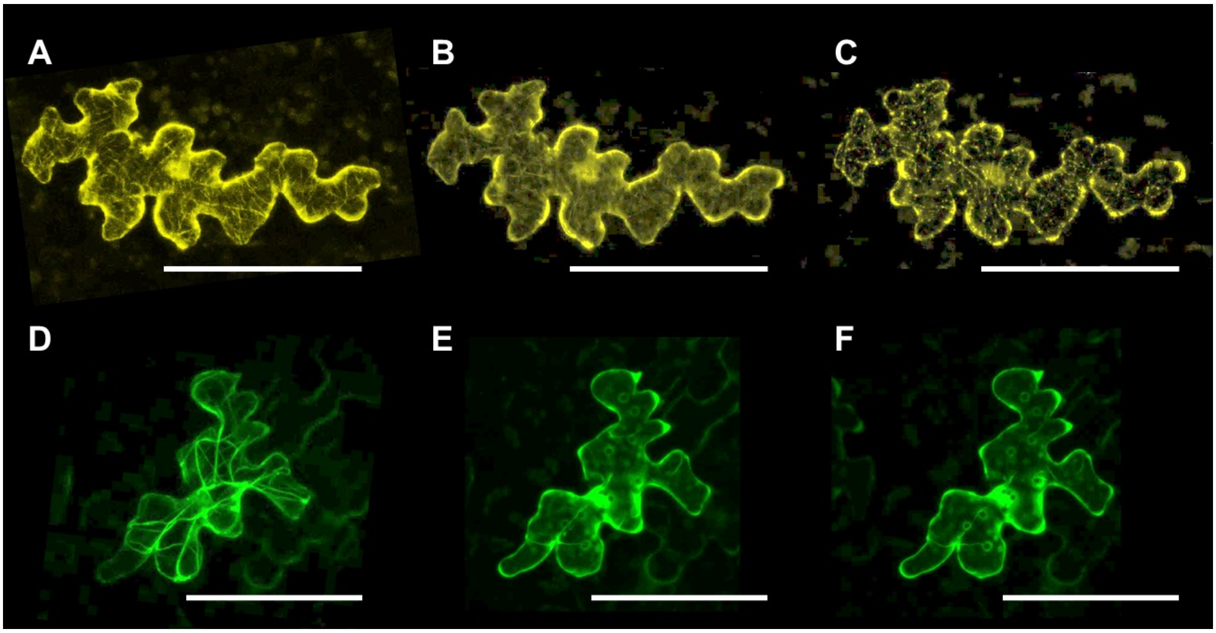


Supplemental Figure S5: Allele frequency plots from the phenotypically selected F2 mapping population of HKT2.4 x Ws-2.
The points in gray are individual AFs at the markers, which were created by using SHOREmap according to the resequencing information of parental lines, namely HKT2.4 and Ws-2. The red line shows the average AFs at the markers within 200kb sliding windows (10kb step). The black line is the sliding-window based boost-value, a slightly modified version of the r-value as introduced with SHOREmap. Chromosome 3 is shown enlarged. It carries the mapping interval for the phenotype selected for. The peak of boost-values is expected to be linked to the causal mutations. The black rectangle marks the SHOREmap-derived mapping interval (see Fig. S2 for a scheme).



Supplemental Figure S6: Root hair phenotypes of accessions with different candidate SNP-alleles in AT3G54925.

A –D) Neither Kastel-1 nor Ty-0 show branched root hairs in the upper or lower regions of the root. E) Kastel-1 shows ectopic root hairs in the patterning zone. F) A scheme showing the position and nucleotide exchange for HKT2.4, Kastel-1 and Ty-0 as compared to Col-0 at the candidate SNP in AT3G54925. Sequence information for Col-0 (Max Planck Institute for Developmental Biology (Tuebingen, Germany)), HKT2.4, Kastel-1 (Cao *et al.*, 2011) and Ty-0 (Salk Institute Genomic Analysis Laboratory (La Jolla, USA)) were extracted from GEBrowser (http://signal.salk.edu/atg1001/3.0/gebrowser.php). See Table SV for additional accessions. Scale bar= 250 µm.



Supplemental Figure S7: Latrunculin B treatment can not abolish YFP-ARK1$^{Col\text{-}0}$ cytoskeletal localization.

Localization of YFP-ARK1$^{Col\text{-}0}$ and Lifeact-eGFP before (A, D) and after (B-C, E-F) latrunculin B treatment (for 1.5h: B, E; and 2h: C, F). Transient expression using the YFP-ARK1$^{Col\text{-}0}$ rescue construct (A-C) and Lifeact-eGFP (D-F) in *A. thaliana* leaf epidermal cells. The localization of Lifeact-eGFP shows the effect of the treatment. Shown are Confocal Laser Scanning Microscopy z-stacks (step size 2µm). Scale bar: 100 µm.

Table S1. List of accessions analyzed for root hair branching phenotype in the lower zone.

name of accessions	HKT2.4-specific root hair branching
Del-10	no
Ey15-2	no
Fei-0	no
HKT2.4	yes
ICE1	no
ICE102	no
ICE104	no
ICE106	no
ICE107	no
ICE112	no
ICE119	no
ICE120	no
ICE127	no
ICE130	no
ICE134	no
ICE138	no
ICE150	no
ICE152	no
ICE153	no
ICE163	no
ICE169	no
ICE173	no
ICE181	no
ICE213	no
ICE216	no
ICE226	no
ICE228	no
ICE29	no
ICE36	no
ICE49	no
ICE50	no
ICE60	no
ICE61	no
ICE63	no
ICE7	no
ICE70	no
ICE71	no
ICE72	no
ICE73	no
ICE75	no
ICE79	no
ICE91	no

ICE92	no
ICE93	no
ICE97	no
Koch-1	no
Lag2.2	no
Leo-1	no
Mer-6	no
Nie1-2	no
Qui-0	no
Rue3-1-31	no
Sha	no
Star-8	no
TueSB30-3	no
Tuescha9	no
TueV13	no
TueWa1-2	no
Vash-1	no
Vie-0	no
WalhaesB4	no
Yeg-1	no

Table S2: Root hair branching percentages. The branching phenotype of 7-day old seedlings was analyzed in the lower region (see Figure 1A). Values are the means of 30 seedlings (20 for HKT2.4 x *ark1-1* (F1)) ± the standard deviation.

Ecotype/mutant	Branching [%]
Col-0	3.9 ± 4.1
L*er*	10.9 ± 4.1
Ws	4.8 ± 1.8
HKT2.4	96.8 ± 4.1
ark1-1	95.0 ± 5.7
HKT2.4 x *ark1-1* (F1)	95.1 ± 2.8

Most of the data sets are non-normally distributed according to the Anderson Darling test. Mann-Whitney U test was applied. No statistical difference was found for Col-0/Ws-2, HKT2.4/*ark1*-1, ark1-*1*/HKT2.4 x *ark1-1* (F1), HKT2.4/HKT2.4 x *ark1-1* (F1) (P>0.05). All other combinations were significantly different (P<0.001).

Table S3: HKT2.4-specific SNPs and their sequence quality and annotation. Anntation by TAIR 10 (ftp://ftp.arabidopsis.org/home/tair/Genes/TAIR10_genome_release/TAIR10_gff3/). See text for details.

			HKT2.4-specific SNPs (sequencing based approach, SHOREmap-derived)					HKT2.4-specific SNPs (accession based approach)	HKT2.4-specific SNPs (both approaches)				
SNP position on Chr3	Col-0 (TAIR10) sequence	HKT2.4 sequence from gebrowser	HKT2.4 sequence	HKT2.4-specific SNPs	coverage	concordance	base quality	identified by sequence analysis of the accession set	identified by both approaches	region of HKT2.4-specific SNP (TAIR10)	gene isoform	reference amino acid (Col-0, TAIR10)	HKT2.4 amino acid (sequencing, this study)
20300113	a	g	g	+	18	1	40	+	+	intergenic	-	-	-
20300318	t	c	c	+	30	1	40	-	-	intergenic	-	-	-
20300334	a	a	-	+	25	0.86	32	-	-	intergenic	-	-	-
20300335	a	a	-	+	25	0.86	40	-	-	intergenic	-	-	-
20300337	t	t	-	+	25	0.86	38	-	-	intergenic	-	-	-
20300338	t	t	-	+	25	0.89	32	-	-	intergenic	-	-	-
20301347	g	t	t	+	20	1	40	-	-	intergenic	-	-	-
20302279	a	g	g	+	32	1	40	-	-	CDS	AT3G54820.1	I	V
20302339	a	g	g	+	24	1	40	-	-	CDS	AT3G54820.1	T	A
20302514	g	a	a	+	36	1.00	40	-	-	intronic/noncoding	AT3G54820.1	-	-
20302632	c	t	t	+	31	1.00	40	-	-	CDS	AT3G54820.1	L	L
20303797	g	a	a	+	23	1	40	+	+	three_prime_UTR	AT3G54820.1	-	-
20304627	t	t	-	+	9	0.69	30	-	-	intergenic	-	-	-
20304728	c	t	t	+	18	1.00	40	-	-	intergenic	-	-	-
20304745	a	t	t	+	18	1.00	40	-	-	intergenic	-	-	-
20304857	a	g	g	+	23	1.00	40	-	-	intergenic	-	-	-
20304970	c	t	t	+	21	1.00	40	+	+	intergenic	-	-	-
20304997	t	t	a	+	20	1.00	40	-	-	intergenic	-	-	-
20305858	g	a	a	+	23	1.00	40	-	-	intergenic	-	-	-
20305859	g	a	a	+	22	0.96	40	+	+	intergenic	-	-	-
20307363	c	a	a	+	23	1.00	40	+	+	intergenic	-	-	-
20307365	a	-	-	+	23	0.96	40	-	-	intergenic	-	-	-
20307534	t	a	a	+	39	1.00	40	+	+	intergenic	-	-	-
20308384	a	c	c	+	36	1.00	40	-	-	intergenic	-	-	-
20308533	c	t	t	+	32	1.00	40	+	+	intergenic	-	-	-
20308580	A	-	-	+	37	0.97	38	-	-	intergenic	-	-	-
20309307	c	t	t	+	46	1.00	40	+	+	intergenic	-	-	-
20309308	c	t	t	+	46	1.00	40	+	+	intergenic	-	-	-
20311131	t	-	-	+	18	0.90	38	-	-	intronic/noncoding	AT3G54826.1	-	-
20312020	t	g	g	+	29	1.00	40	+	+	intronic/noncoding	AT3G54830.1	-	-
20314279	t	-	-	+	28	1.00	40	-	-	intronic/noncoding	AT3G54830.1		
20314331	g	-	-	+	28	1.00	40	+	+	intronic/noncoding	AT3G54830.1	-	-
20315046	c	t	t	+	30	1.00	40	+	+	intergenic	-	-	-
20315877	a	-	-	+	17	0.85	38	-	-	intergenic	-	-	-
20318502	a	a	t	+	3	0.38	34	-	-	five_prime_UTR	AT3G54840.1/2	-	-
20318503	a	a	t	+	3	0.38	34	-	-	five_prime_UTR	AT3G54840.1/2	-	-
20318507	g	g	t	+	2	0.29	27	-	-	five_prime_UTR	AT3G54840.1/2	-	-
20318509	t	t	c	+	2	0.25	10	-	-	five_prime_UTR	AT3G54840.1/2	-	-
20318511	c	c	a	+	2	0.25	10	-	-	five_prime_UTR	AT3G54840.1/2	-	-
20318513	a	a	t	+	2	0.22	9	-	-	five_prime_UTR	AT3G54840.1/2	-	-
20320049	t	c	c	+	24	1.00	40	-	-	intronic/noncoding	AT3G54840.1/2	-	-
20320716	g	a	a	+	26	1.00	40	-	-	intronic/noncoding	AT3G54840.1/2	-	-
20322147	a	g	g	+	29	1.00	40	-	-	CDS	AT3G54850.1	V	V
20324012	t	c	c	+	29	1	40	+	+	three_prime_UTR	AT3G54850.1	-	-
20325602	c	g	g	+	33	1.00	40	+	+	intronic/noncoding	AT3G54860.1/2	-	-
20326208	a	g	g	+	27	1.00	40	+	+	intronic/noncoding	AT3G54860.1/2	-	-
20326975	c	t	t	+	24	1.00	40	+	+	intronic/noncoding	AT3G54860.1/2	-	-
20329247	c	a	a	+	30	1.00	40	+	+	intronic/noncoding	AT3G54860.1/2	-	-
20330599	a	g	g	+	24	1.00	40	+	+	intergenic	-	-	-
20332575	g	a	a	+	32	1	40	+	+	splice_site_change	AT3G54870.1	-	-
20342541	c	c	t	+	3	0.23	10	-	-	intergenic	-	-	-
20342542	c	c	t	+	5	0.33	18	-	-	intergenic	-	-	-
20342543	g	g	t	+	6	0.38	19	-	-	intergenic	-	-	-
20342544	g	g	t	+	6	0.38	38	-	-	intergenic	-	-	-
20342548	g	g	t	+	9	0.47	38	-	-	intergenic	-	-	-
20342549	g	g	c	+	5	0.26	36	-	-	intergenic	-	-	-
20342550	t	t	g	+	5	0.28	38	-	-	intergenic	-	-	-
20342966	c	c	a	+	1	0.33	6	-	-	three_prime_UTR	AT3G54910.1/2/3	-	-
20342971	t	t	a	+	1	0.33	14	-	-	CDS	AT3G54910.1/2/3	D	I
20342972	c	c	t	+	2	0,67	12	-	-	CDS	AT3G54910.1/2/3	D	I
20342974	a	a	c	+	3	1	24	-	-	CDS	AT3G54910.1/2/3	F	S
20342975	a	a	t	+	3	1	28	-	-	CDS	AT3G54910.1/2/3	F	S
20342977	a	a	t	+	4	1	28	-	-	CDS	AT3G54910.1/2/3	V	E
20342979	g	a	a	+	4	1.00	30	+	+	CDS	AT3G54910.1/2/3	L	L
20343252	a	a	c	+	6	0.33	18	-	-	intronic/noncoding	AT3G54910.1/2/3	-	-
20343253	g	g	t	+	7	0.35	19	-	-	intronic/noncoding	AT3G54910.1/2/3	-	-
20343254	a	a	c	+	7	0.35	19	-	-	intronic/noncoding	AT3G54910.1/2/3	-	-
20344588	c	-	-	+	1	0,5	3	-	-	five_prime_UTR	AT3G54910.1/2/3	-	-
20344589	a	-	-	+	1	0,5	3	-	-	five_prime_UTR	AT3G54910.1/2/3	-	-
20344590	g	-	-	+	1	0,5	3	-	-	five_prime_UTR	AT3G54910.1/2/3	-	-
20344593	c	-	t	+	1	0,5	3	-	-	five_prime_UTR	AT3G54910.1/2/3	-	-
20344791	g	g	-	+	1	0,5	11	-	-	intronic_noncoding/five_prime_UTR	AT3G54910.1/3	-	-
20344792	g	g	-	+	1	0,5	11	-	-	intronic_noncoding/five_prime_UTR	AT3G54910.1/3	-	-
20344794	c	c	a	+	1	0,5	7	-	-	intronic_noncoding/five_prime_UTR	AT3G54910.1/3	-	-
20344795	a	-	-	+	1	0,5	3	-	-	intronic_noncoding/five_prime_UTR	AT3G54910.1/3	-	-
20344946	g	-	a	+	4	0.25	10	-	-	intergenic	-	-	-
20344950	a	a	g	+	7	0.37	30	-	-	intergenic	-	-	-
20346526	a	a	t	+	2	0.22	9	-	-	intronic/noncoding	AT3G54920.1	-	-
20346527	a	a	t	+	2	0.22	9	-	-	intronic/noncoding	AT3G54920.1	-	-
20346821	g	a	a	+	29	1.00	40	-	-	intronic/noncoding	AT3G54920.1	-	-
20346868	a	c	c	+	28	1.00	40	-	-	intronic/noncoding	AT3G54920.1	-	-
20349485	g	a	a	+	21	1	40	-	-	three_prime_UTR	AT3G54925.1		
20349605	t	a	a	+	23	1	40	-	-	CDS	AT3G54925.1	L	F
20349784	c	t	t	+	18	1	40	-	-	CDS	AT3G54925.1	V	I
20349799	c	t	t	+	18	1	40	+	+	CDS	AT3G54925.1	V	I
20349948	g	a	a	+	22	1	40	-	-	CDS	AT3G54925.1	T	I
20350721	c	t	t	+	30	0.97	40	-	-	intergenic	-	-	-
20353230	g	a	a	+	15	1.00	40	+	+	intergenic	-	-	-
20353247	c	t	t	+	14	1.00	40	-	-	intergenic	-	-	-
20353330	t	g	g	+	20	1.00	40	+	+	intergenic	-	-	-
20353447	c	c	t	+	24	0.65	40	-	-	intergenic	-	-	-
20353552	g	g	t	+	19	0.50	40	-	-	intergenic	-	-	-
20353799	c	c	t	+	5	0.33	38	-	-	intergenic	-	-	-
20353847	c	c	t	+	11	0.42	40	-	-	intergenic	-	-	-
20353926	g	g	a	+	17	0.85	40	-	-	intergenic	-	-	-
20353947	g	c	c	+	13	1.00	38	-	-	intergenic	-	-	-
20354169	t	c	c	+	19	1.00	40	-	-	intergenic	-	-	-
20354171	t	c	c	+	18	1.00	38	-	-	intergenic	-	-	-
20356315	c	-	-	+	27	0.93	38	-	-	three_prime_UTR	AT3G54940.2	-	-
20356316	c	-	-	+	27	0.93	38	-	-	three_prime_UTR	AT3G54940.2	-	-
20356318	c	a	a	+	28	0.97	40	-	-	three_prime_UTR	AT3G54940.2	-	-
20356837	a	-	-	+	18	0.78	40	-	-	intergenic	-	-	-
20356838	a	-	-	+	18	0.82	38	-	-	intergenic	-	-	-

20356976	t	c	c	+	16	1.00	40	+	+	intergenic	-	-	-
20357265	c	t	t	+	5	1.00	32	-	-	intergenic	-	-	-
20357268	c	t	t	+	5	0.83	38	-	-	intergenic	-	-	-
20357275	a	a	c	+	2	0.40	19	-	-	intergenic	-	-	-
20357277	a	a	t	+	2	0.40	19	-	-	intergenic	-	-	-
20357278	t	t	c	+	2	0.40	20	-	-	intergenic	-	-	-
20357280	g	g	t	+	3	0.50	34	-	-	intergenic	-	-	-
20357281	a	a	c	+	4	0.57	36	-	-	intergenic	-	-	-
20357638	a	a	-	+	24	0.96	38	-	-	intergenic	-	-	-
20357640	t	t	-	+	24	0.96	40	-	-	intergenic	-	-	-
20357641	c	c	-	+	24	0.89	40	-	-	intergenic	-	-	-
20357642	t	t	-	+	24	0.89	32	-	-	intergenic	-	-	-
20357644	a	a	-	+	25	0.93	32	-	-	intergenic	-	-	-
20357711	a	c	c	+	22	1.00	40	-	-	intergenic	-	-	-
20358293	a	a	-	+	21	0.88	40	-	-	intergenic	-	-	-
20358294	t	t	-	+	21	0.91	40	-	-	intergenic	-	-	-
20358296	c	c	-	+	21	0.95	40	-	-	intergenic	-	-	-
20358297	g	g	-	+	21	0.95	38	-	-	intergenic	-	-	-
20358337	a	g	g	+	28	1.00	40	-	-	intergenic	-	-	-
20358739	a	t	t	+	19	0.86	40	+	+	intergenic	-	-	-
20358880	no change	a	no change	-	-	-	-	+	-	intergenic	-	-	-
20361078	**c**	**c**	**a**	**+**	**4**	**0.25**	**12**	**-**	**-**	**five_prime_UTR**	**AT3G54950.1**	**-**	**-**
20361079	**c**	**c**	**g**	**+**	**4**	**0.25**	**12**	**-**	**-**	**five_prime_UTR**	**AT3G54950.1**	**-**	**-**
20361082	**t**	**t**	**g**	**+**	**4**	**0.27**	**34**	**-**	**-**	**five_prime_UTR**	**AT3G54950.1**	**-**	**-**
20361084	**t**	**t**	**a**	**+**	**4**	**0.27**	**34**	**-**	**-**	**five_prime_UTR**	**AT3G54950.1**	**-**	**-**
20361085	**a**	**a**	**g**	**+**	**4**	**0.27**	**34**	**-**	**-**	**five_prime_UTR**	**AT3G54950.1**	**-**	**-**
20361534	t	c	c	+	14	1.00	40	+	+	intergenic	-	-	-
20362272	c	g	g	+	12	1.00	40	-	-	intergenic	-	-	-
20362290	a	c	c	+	12	1.00	40	-	-	intergenic	-	-	-
20362333	t	t	-	+	14	0.93	40	-	-	intergenic	-	-	-
20362428	g	a	a	+	12	1.00	40	+	+	intergenic	-	-	-
20362553	a	a	t	+	9	1.00	40	-	-	intergenic	-	-	-
20365834	**g**	**a**	**a**	**+**	**32**	**1.00**	**40**	**+**	**+**	**intronic/noncoding**	**AT3G54960.1/2**	**-**	**-**
20366883	c	c	-	+	3	0.25	32	-	-	intergenic	-	-	-
20366884	a	a	-	+	3	0.30	34	-	-	intergenic	-	-	-
20367392	a	c	c	+	27	1.00	40	+	+	intergenic	-	-	-
20367755	a	-	-	+	19	1.00	38	-	-	intergenic	-	-	-
20367854	t	t	g	+	4	0.22	17	-	-	intergenic	-	-	-
20367881	c	g	g	+	19	1.00	40	+	+	intergenic	-	-	-
20370185	c	c	t	+	2	0.25	26	-	-	intergenic	-	-	-
20370270	**a**	**t**	**t**	**+**	**20**	**1**	**40**	**+**	**+**	**five_prime_UTR**	**AT3G54980.1**	**-**	**-**
20371399	**c**	**a**	**a**	**+**	**39**	**1.00**	**40**	**+**	**+**	**CDS**	**AT3G54980.1**	**G**	**G**
20371687	**a**	**g**	**g**	**+**	**31**	**1.00**	**40**	**+**	**+**	**CDS**	**AT3G54980.1**	**L**	**L**
20372462	**c**	**a**	**a**	**+**	**34**	**1**	**40**	**-**	**-**	**CDS**	**AT3G54980.1**	**L**	**M**
20373862	**c**	**t**	**t**	**+**	**24**	**1.00**	**40**	**-**	**-**	**CDS**	**AT3G54990.1**	**T**	**T**
20373862	**c**	**t**	**t**	**+**	**24**	**1.00**	**40**	**-**	**-**	**intronic/noncoding**	**AT3G54990.1/2**	**-**	**-**
20375316	**a**	**a**	**c**	**+**	**1**	**0.25**	**4**	**-**	**-**	**intronic/noncoding**	**AT3G54990.1/2**	**-**	**-**
20375317	**t**	**t**	**g**	**+**	**1**	**0.25**	**4**	**-**	**-**	**intronic/noncoding**	**AT3G54990.1/2**	**-**	**-**
20375321	**t**	**t**	**c**	**+**	**1**	**0.50**	**13**	**-**	**-**	**intronic/noncoding**	**AT3G54990.1/2**	**-**	**-**
20375476	**a**	**t**	**t**	**+**	**16**	**1.00**	**40**	**-**	**-**	**intronic/noncoding**	**AT3G54990.1/2**	**-**	**-**
20375522	**a**	**c**	**c**	**+**	**12**	**1.00**	**40**	**-**	**-**	**intronic/noncoding**	**AT3G54990.1/2**	**-**	**-**
20375665	**t**	**t**	**a**	**+**	**4**	**0.24**	**14**	**-**	**-**	**intronic/noncoding**	**AT3G54990.1/2**	**-**	**-**
20376722	t	t	-	+	14	0.82	40	-	-	intergenic	-	-	-
20377689	a	-	g	+	1	0.33	3	-	-	intergenic	-	-	-
20377690	a	-	t	+	1	0.33	3	-	-	intergenic	-	-	-
20377691	c	-	t	+	1	0.50	3	-	-	intergenic	-	-	-
20377692	a	-	g	+	1	0.50	3	-	-	intergenic	-	-	-
20377894	t	-	a	+	4	1.00	28	-	-	intergenic	-	-	-
20379585	t	c	c	+	14	1.00	40	-	-	intergenic	-	-	-
20379888	t	a	a	+	24	1.00	40	+	+	intergenic	-	-	-
20379916	c	t	t	+	27	1.00	40	+	+	intergenic	-	-	-
20379944	t	a	a	+	24	1.00	40	+	+	intergenic	-	-	-
20379965	a	t	t	+	25	1.00	40	-	-	intergenic	-	-	-

legend for the format:

intragenic region border seperates positions from intra- and intergenic SNPs intergenic region "-" is either a gap or a sequencing error/non-unique position, coverage, concordance and base quality was only extracted for HKT2.4-specififc SNPs from the sequencing approach.

Table S4: Candidate SNP in AT3G54870 extracted for 855 *A. thaliana* accessions. The nucleotide at the candidate SNP position 20,332,575 on chromosome 3 (AT3G54870) was extracted for all available accessions from the 1001 genome project`s GEBowser (http://signal.salk.edu/atg1001/3.0/gebrowser.php). The Col-0 reference nucleotide is shown in the first line, all other same nucleotides are grouped and separated by lines, accessions within these groups are sorted alphabetically. CeBiT: IGS of the Center for Biotechnology of the University of Bielefeld (Bielefeld, Germany), GMI: Gregor Mendel Institute of Molecular Plant Biology (Vienna, Austria), JGI: DOE Joint Genome Institute (Walnut Creek, USA), MPI: Max Planck Institute for Developmental Biology (Tuebingen, Germany), MON: Monsanto Company (St. Louis, USA), SALK: Salk Institute Genomic Analysis Laboratory (La Jolla, USA), WTC: Wellcome Trust Center for Human Genetics (Oxford, UK). Published sources are: Cao et al., 2011; Gan et al., 2011; Long et al., 2013; Schmitz et al., 2013.

accession label from GEBrowser	nucleotide (chr3:20332575)
Col-0.MPI	G
HKT2.4.MPI	A
11C1.9503.MON-MPI	G
Aa_0.SALK	G
Abd_0.SALK	G
Adam-1.9609.MON-MPI	G
Aedal-1.GMI	G
Aedal-3.GMI	G
Ag_0.SALK	G
Agu-1.MPI	G
Aiell-1.9646.MON-MPI	G
Aitba-1.9606.MON-MPI	G
Ak_1.SALK	G
Alc-0.JGI	G
Ale-Stenar-44-4.GMI	G
Ale-Stenar-56-14.GMI	G
Ale-Stenar-64-24.GMI	G
Algutsrum.GMI	G
Alst_1.SALK	G
Alt-1.9774.MON-MPI	G
Altai_5.SALK	G
Amel_1.SALK	G
An_1.SALK	G
Ang_0.SALK	G
Anholt_1.SALK	G
Ann_1.SALK	G
Anz_0.SALK	G
App1-12.GMI	G
App1-14.GMI	G
App1-16.GMI	G
Appt_1.SALK	G
ARGE-1-15.9911.MON-MPI	G
ARR-17.9927.MON-MPI	G
Ba_1.SALK	G
Baa_1.SALK	G

Baa1-2.GMI	G
Baa4-1.GMI	G
Baa5-1.GMI	G
Bach2-1.9796.MON-MPI	G
Bach-7.9778.MON-MPI	G
Bai-10.9779.MON-MPI	G
Bak-2.MPI	G
Bak-7.MPI	G
Balan-1.9613.MON-MPI	G
Basta-1.9619.MON-MPI	G
Basta-2.9620.MON-MPI	G
Bay-0.JGI	G
Bch_1.SALK	G
Bd_0.SALK	G
Bela-1.9730.MON-MPI	G
Bela-2.9733.MON-MPI	G
Benk_1.SALK	G
Ber.SALK	G
Berg-1.9775.MON-MPI	G
BEZ-9.9928.MON-MPI	G
Bg_2.SALK	G
Bl-4.9813.MON-MPI	G
Bijisk-4.9622.MON-MPI	G
Bik_1.SALK	G
Bil-5.GMI	G
Bil-7.GMI	G
Bivio-1.9649.MON-MPI	G
Bl_1.SALK	G
Bla_1.SALK	G
Bla-1.7015.MON-MPI	G
Blh-1.JGI	G
Boo2-1.8266.MON-MPI	G
Boot_1.SALK	G
Bor_1.SALK	G
Bor_4.SALK	G
Borky1.428.MON-MPI	G
Br_0.SALK	G
BRE-14.9919.MON-MPI	G
BRI-2.9910.MON-MPI	G
Broesarp-34-145.GMI	G
Broet1-6.GMI	G
Bs_1.SALK	G
Bsch_0.SALK	G
Bu_0.SALK	G
Buckhorn_Pass.SALK	G
Bur-0.MPI	G
Bur-0.WTC	G
C24.MPI	G
Ca_0.SALK	G
Cal_0.SALK	G

Can-0.WTC	G
Castelfed-1-197.9681.MON-MPI	G
Castelfed-4-211.9695.MON-MPI	G
Castelfed-4-214.9696.MON-MPI	G
CATS-6.9937.MON-MPI	G
Cdm-0.MPI	G
Cerv_1.SALK	G
CHA-41.932.MON-MPI	G
Chaba-2.9624.MON-MPI	G
Chat_1.SALK	G
Chi_0.SALK	G
CIBC_17.SALK	G
CIBC_5.SALK	G
Cimin-1.9661.MON-MPI	G
Cnt_1.SALK	G
Cnt-1.5726.MON-MPI	G
Co.SALK	G
Co_1.SALK	G
Com_1.SALK	G
CON-7.9913.MON-MPI	G
Corig-1.9650.MON-MPI	G
CSHL-5.6744.MON-MPI	G
Ct-1.WTC	G
Cvi_0.SALK	G
Cvi-0.SALK	G
CYR.88.MON-MPI	G
Da1_12.SALK	G
Db_1.SALK	G
Del-10.MPI	G
Dem_4.SALK	G
Di_G.SALK	G
DIR-9.9920.MON-MPI	G
Dja_1.SALK	G
Do_0.SALK	G
Doer-10.GMI	G
Dog-4.MPI	G
Dolen-1.9697.MON-MPI	G
Dolna-1.9712.MON-MPI	G
Don-0.MPI	G
Dospa-1.9706.MON-MPI	G
Doubravnik7.410.MON-MPI	G
Dr_0.SALK	G
Dra_0.SALK	G
Dra2-1.GMI	G
Dra3-1.GMI	G
Draha2.424.MON-MPI	G
DraII_1.SALK	G
DraII-6.5874.MON-MPI	G
DraIII_1.SALK	G
DraIV.5893.MON-MPI	G

DraIV.5907.MON-MPI	G
DraIV.5950.MON-MPI	G
DraIV.5984.MON-MPI	G
DraIV.5993.MON-MPI	G
Duk.SALK	G
Durh_1.SALK	G
Eden-1.GMI	G
Eden-2.GMI	G
Eden-7.GMI	G
Eden-9.GMI	G
Edi-0.WTC	G
Eds-1.GMI	G
Eds-9.GMI	G
Ei_2.SALK	G
El_0.SALK	G
Ema_1.SALK	G
En_1.SALK	G
En_2.SALK	G
En_D.SALK	G
ENC-2-1.9907.MON-MPI	G
Epidauros-1.9725.MON-MPI	G
Er_0.SALK	G
Erg2-6.9784.MON-MPI	G
Es_0.SALK	G
ESP-1-11.9908.MON-MPI	G
Est.SALK	G
Est-1.MPI	G
Et_0.SALK	G
Etna_2.SALK	G
Ey15-2.MPI	G
Faeb-2.GMI	G
Faeb-4.GMI	G
Fael-1.GMI	G
Faneronemi-3.9726.MON-MPI	G
Fei-0.MPI	G
Fell1-10.9814.MON-MPI	G
Fell2-4.9780.MON-MPI	G
Fell3-7.9776.MON-MPI	G
Fi_0.SALK	G
Filet-1.9651.MON-MPI	G
Fjae1-1.GMI	G
Fjae1-2.GMI	G
Fjae1-5.GMI	G
Fjae2-4.GMI	G
Fly2-1.GMI	G
Fly2-2.GMI	G
Fondi-1.9652.MON-MPI	G
Fr_2.SALK	G
Fri_2.GMI	G
Furni-1.9743.MON-MPI	G

Ga_0.SALK	G
Ge_0.SALK	G
Geg-14.9125.MON-MPI	G
Gel_1.SALK	G
GEN-8.9909.MON-MPI	G
Gie_0.SALK	G
Giffo-1.9653.MON-MPI	G
Gifu_2.SALK	G
Gn-1.9777.MON-MPI	G
Gn2-3.9790.MON-MPI	G
Goced-1.9698.MON-MPI	G
Gol-2.9314.MON-MPI	G
Got_22.SALK	G
Got_7.SALK	G
Gr_1.SALK	G
Gr-5.7158.MON-MPI	G
Gradi-1.9645.MON-MPI	G
Gre_0.SALK	G
Grivo-1.9714.MON-MPI	G
Gro-3.GMI	G
Groen-12.GMI	G
Groen-14.GMI	G
Groen-5.GMI	G
Gu_0.SALK	G
Gy_0.SALK	G
Ha_0.SALK	G
Had-1.GMI	G
Had-2.GMI	G
Haes-1.9791.MON-MPI	G
Hag-2.GMI	G
Ha-HBT1-2.9785.MON-MPI	G
Ha-HBT2-10.9797.MON-MPI	G
Ha-HBT3-11.9815.MON-MPI	G
Hal-1.GMI	G
Ham-1.GMI	G
Ha-P-13.9786.MON-MPI	G
Ha-P2-1.9798.MON-MPI	G
Hart-2.9799.MON-MPI	G
Ha-S-B.9800.MON-MPI	G
Ha-SP-2.9801.MON-MPI	G
Hau_0.SALK	G
HE-1.9769.MON-MPI	G
Hel-3.GMI	G
Hey_1.SALK	G
Hh_0.SALK	G
Hi-0.WTC	G
Hn_0.SALK	G
Hod.SALK	G
Hof-1.9772.MON-MPI	G
Hola_1_2.GMI	G

Hola-1-1.GMI	G
Hola-2-2.GMI	G
Hov1-10.GMI	G
Hov1-7.GMI	G
Hov3-2.GMI	G
Hov3-5.GMI	G
Hov4-1.GMI	G
Hovdala-2.GMI	G
HR_10.SALK	G
HR_5.SALK	G
Hs_0.SALK	G
HSm.SALK	G
Iasi-1.9744.MON-MPI	G
ICE1.MPI	G
ICE102.MPI	G
ICE104.MPI	G
ICE106.MPI	G
ICE107.MPI	G
ICE111.MPI	G
ICE112.MPI	G
ICE119.MPI	G
ICE120.MPI	G
ICE127.MPI	G
ICE130.MPI	G
ICE134.MPI	G
ICE138.MPI	G
ICE150.MPI	G
ICE152.MPI	G
ICE153.MPI	G
ICE163.MPI	G
ICE169.MPI	G
ICE173.MPI	G
ICE181.MPI	G
ICE21.MPI	G
ICE212.MPI	G
ICE213.MPI	G
ICE216.MPI	G
ICE226.MPI	G
ICE228.MPI	G
ICE29.MPI	G
ICE33.MPI	G
ICE36.MPI	G
ICE49.MPI	G
ICE50.MPI	G
ICE60.MPI	G
ICE61.MPI	G
ICE63.MPI	G
ICE7.MPI	G
ICE70.MPI	G
ICE71.MPI	G

ICE72.MPI	G
ICE73.MPI	G
ICE75.MPI	G
ICE79.MPI	G
ICE91.MPI	G
ICE92.MPI	G
ICE93.MPI	G
ICE97.MPI	G
ICE98.MPI	G
In_0.SALK	G
IP-Adm-0.9514.MON-MPI	G
IP-Ala-0.9515.MON-MPI	G
IP-All-0.9517.MON-MPI	G
IP-Alm-0.9518.MON-MPI	G
IP-Alo-0.9506.MON-MPI	G
IP-Ang-0.9519.MON-MPI	G
IP-Ara-4.9520.MON-MPI	G
IP-Bar-1.9521.MON-MPI	G
IP-Bea-0.9522.MON-MPI	G
IP-Ben-0.9523.MON-MPI	G
IP-Ber-0.9524.MON-MPI	G
IP-Bis-0.9525.MON-MPI	G
IP-Cab-3.9526.MON-MPI	G
IP-Cad-0.9527.MON-MPI	G
IP-Cal-0.9528.MON-MPI	G
IP-Cap-1.9529.MON-MPI	G
IP-Car-1.9530.MON-MPI	G
IP-Cdc-3.9531.MON-MPI	G
IP-Cdo-0.9532.MON-MPI	G
IP-Cem-0.9533.MON-MPI	G
IP-Cmo-3.9534.MON-MPI	G
IP-Coa-0.9507.MON-MPI	G
IP-Coc-1.9535.MON-MPI	G
IP-Cor-0.9536.MON-MPI	G
IP-Cum-1.9537.MON-MPI	G
IP-Cur-4.9538.MON-MPI	G
IP-Deh-1.9539.MON-MPI	G
IP-Elb-0.9540.MON-MPI	G
IP-Fue-2.9541.MON-MPI	G
IP-Fun-0.9542.MON-MPI	G
IP-Gra-0.9543.MON-MPI	G
IP-Gua-1.9544.MON-MPI	G
IP-Her-12.9545.MON-MPI	G
IP-Hom-4.9546.MON-MPI	G
IP-Hor-0.9547.MON-MPI	G
IP-Hum-2.9549.MON-MPI	G
IP-Iso-4.9550.MON-MPI	G
IP-Jim-1.9551.MON-MPI	G
IP-Lab-7.9552.MON-MPI	G
IP-Ldd-0.9553.MON-MPI	G

IP-Lso-0.9554.MON-MPI	G
IP-Mar-1.9555.MON-MPI	G
IP-Men-2.9556.MON-MPI	G
IP-Moa-0.9557.MON-MPI	G
IP-Moc-11.9558.MON-MPI	G
IP-Mon-5.9559.MON-MPI	G
IP-Mos-1.9508.MON-MPI	G
IP-Mot-0.9560.MON-MPI	G
IP-Mun-0.9561.MON-MPI	G
IP-Mur-0.9562.MON-MPI	G
IP-Nav-0.9563.MON-MPI	G
IP-Nog-17.9564.MON-MPI	G
IP-Orb-10.9565.MON-MPI	G
IP-Oso-0.9566.MON-MPI	G
IP-Pal-0.9567.MON-MPI	G
IP-Pan-0.9568.MON-MPI	G
IP-Pds-1.9569.MON-MPI	G
IP-Pob-0.9570.MON-MPI	G
IP-Pro-0.9571.MON-MPI	G
IP-Pue-0.9572.MON-MPI	G
IP-Rds-0.9573.MON-MPI	G
IP-Rei-0.9510.MON-MPI	G
IP-Rel-0.9574.MON-MPI	G
IP-Ren-6.9575.MON-MPI	G
IP-Rev-0.9576.MON-MPI	G
IP-Ria-0.9577.MON-MPI	G
IP-Sac-0.9578.MON-MPI	G
IP-San-10.9579.MON-MPI	G
IP-Scm-0.9580.MON-MPI	G
IP-Sdv-3.9581.MON-MPI	G
IP-Ses-0.9582.MON-MPI	G
IP-Sne-0.9583.MON-MPI	G
IP-Stp-0.9584.MON-MPI	G
IP-Svi-0.9585.MON-MPI	G
IP-Tam-0.9586.MON-MPI	G
IP-Tdc-0.9587.MON-MPI	G
IP-Tol-7.9588.MON-MPI	G
IP-Tor-1.9589.MON-MPI	G
IP-Trs-0.9590.MON-MPI	G
IP-Vad-0.9591.MON-MPI	G
IP-Vae-2.9592.MON-MPI	G
IP-Vav-0.9511.MON-MPI	G
IP-Vaz-0.9593.MON-MPI	G
IP-Vdm-0.9594.MON-MPI	G
IP-Vdt-0.9595.MON-MPI	G
IP-Ver-5.9596.MON-MPI	G
IP-Vid-1.9512.MON-MPI	G
IP-Vig-1.9597.MON-MPI	G
IP-Vim-0.9598.MON-MPI	G
IP-Vin-0.9599.MON-MPI	G

IP-Vis-0.9600.MON-MPI	G
IP-Voz-0.9601.MON-MPI	G
IP-Vpa-1.9602.MON-MPI	G
Is_0.SALK	G
ISS-20.9929.MON-MPI	G
IST-29.9914.MON-MPI	G
Istisu-1.MPI	G
Je_0.SALK	G
Jea.JGI	G
Jl_3.SALK	G
Jm_0.SALK	G
Kaevlinge-1.GMI	G
Kal-2.GMI	G
Kar_1.SALK	G
Karag-1.9617.MON-MPI	G
Karag-2.9608.MON-MPI	G
Kas_1.SALK	G
Kas_2.SALK	G
Kastel-1.MPI	G
Kb_0.SALK	G
KBG1-14.9788.MON-MPI	G
KBG2-13.9770.MON-MPI	G
Kelsterbach_4.SALK	G
Kent.SALK	G
Kia-1.GMI	G
Kil_0.SALK	G
Kin_0.SALK	G
Kl_5.SALK	G
Kn-0.WTC	G
Kni-1.GMI	G
Knjas-1.9749.MON-MPI	G
Knox_18.SALK	G
Ko_2.SALK	G
Koch-1.MPI	G
Kolar-1.9699.MON-MPI	G
Kolar-2.9702.MON-MPI	G
Koln.SALK	G
Kolyv-2.9625.MON-MPI	G
Kolyv-3.9626.MON-MPI	G
Kolyv-5.9627.MON-MPI	G
Kolyv-6.9628.MON-MPI	G
Kondara.SALK	G
Kor-3.GMI	G
Koren-1.9719.MON-MPI	G
K-oze-1.9629.MON-MPI	G
K-oze-3.9630.MON-MPI	G
Kro_0.SALK	G
Kro-0.MPI	G
Krot_0.SALK	G
Kru-3.GMI	G

Kulturen-1.GMI	G
Kus2-2.9781.MON-MPI	G
KYC-33.801.MON-MPI	G
Kyoto.SALK	G
Kz_9.SALK	G
La_0.SALK	G
Lag1-2.9100.MON-MPI	G
Lag1-4.9102.MON-MPI	G
Lag1-6.9104.MON-MPI	G
Lag2.2.MPI	G
Lan_0.SALK	G
Lan-1.GMI	G
LDV-18.108.MON-MPI	G
LDV-46.139.MON-MPI	G
Le_0.SALK	G
Lebja-2.9632.MON-MPI	G
Lebja-4.9633.MON-MPI	G
LEC-25.9930.MON-MPI	G
Leo-1.MPI	G
Ler-0.WTC	G
Ler-1.MPI	G
Ler-1.SALK	G
Lerik1-3.MPI	G
Leska-1.9716.MON-MPI	G
Lesno-1.9611.MON-MPI	G
Lesno-2.9612.MON-MPI	G
Lesno-4.9610.MON-MPI	G
Li_2:1.SALK	G
Li-7.7231.MON-MPI	G
Liarum.GMI	G
Lilloe-1.GMI	G
LI-OF-065.630.MON-MPI	G
Lip_0.SALK	G
Liri-1.9654.MON-MPI	G
Lis-2.GMI	G
Lis-3.GMI	G
Lisse.SALK	G
Litva.SALK	G
LL_0.SALK	G
Lm_2.SALK	G
Lom1-1.GMI	G
love-1.GMI	G
love-5.GMI	G
Lp2_2.SALK	G
Lp2_6.SALK	G
LP3413.41.8472.MON-MPI	G
Lu-1.GMI	G
Lu3-30.9782.MON-MPI	G
Lu4-2.9792.MON-MPI	G
Lund.GMI	G

Malii-1.9746.MON-MPI	G
MAR2-3.159.MON-MPI	G
MAR-4-16.9915.MON-MPI	G
Marce-1.9655.MON-MPI	G
Masl-1.9634.MON-MPI	G
Mc_0.SALK	G
Mdn-1.1829.MON-MPI	G
Melic-1.9657.MON-MPI	G
Melni-2.9704.MON-MPI	G
Mer-6.MPI	G
Mh_0.SALK	G
MIC-31.870.MON-MPI	G
MIL-2.9922.MON-MPI	G
Mir_0.SALK	G
Mitterberg-1-180.9665.MON-MPI	G
Mitterberg-1-182.9666.MON-MPI	G
Mitterberg-1-183.9667.MON-MPI	G
Mitterberg-2-184.9668.MON-MPI	G
Mitterberg-2-185.9669.MON-MPI	G
Mitterberg-3-187.9671.MON-MPI	G
MNF-Che-2.1925.MON-MPI	G
MNF-Jac-12.1954.MON-MPI	G
MNF-Pin-39.2016.MON-MPI	G
MNF-Pot-21.1853.MON-MPI	G
MNF-Pot-75.1872.MON-MPI	G
MNF-Riv-21.1890.MON-MPI	G
Mnz_0.SALK	G
MOL-1.9916.MON-MPI	G
MOU2-25.9931.MON-MPI	G
Ms_0.SALK	G
Mt-0.WTC	G
Muh-2.9803.MON-MPI	G
Mv_0.SALK	G
Mz_0.SALK	G
N13.SALK	G
Naes-2.GMI	G
Nc_1.SALK	G
NC_6.SALK	G
Nd-1.CeBiT	G
Nemrut-1.MPI	G
Neo_6.SALK	G
NFA_10.SALK	G
NFA_8.SALK	G
Nicas-1.9658.MON-MPI	G
Nie1-2.MPI	G
No-0.WTC	G
Nok_3.SALK	G
Nosov-1.9635.MON-MPI	G
Noveg-1.9636.MON-MPI	G
Noveg-2.9637.MON-MPI	G

Noveg-3.9638.MON-MPI	G
NOZ-6.9932.MON-MPI	G
Np_0.SALK	G
Nw_0.SALK	G
Nyl-13.GMI	G
Nyl-2.GMI	G
Nyl-7.GMI	G
Nz_1.SALK	G
Ob_0.SALK	G
Obe1-15.9804.MON-MPI	G
Obh-13.9789.MON-MPI	G
Oede-2.GMI	G
Oemoe1-7.GMI	G
Oemoe2-1.GMI	G
Oer-1.GMI	G
Old_1.SALK	G
Olympia-2.9727.MON-MPI	G
Omn-1.GMI	G
Omn-5.GMI	G
Or_0.SALK	G
Orast-1.9741.MON-MPI	G
Ove_0.SALK	G
Oy-0.JGI	G
Oy-0.WTC	G
Panik-1.9607.MON-MPI	G
Panke-1.9639.MON-MPI	G
Parti-1.9615.MON-MPI	G
Paw-26.2171.MON-MPI	G
Ped-0.MPI	G
Per_1.SALK	G
Petergof.7296.MON-MPI	G
Pfn-10.9805.MON-MPI	G
Pfn-N2.2-6.9771.MON-MPI	G
PHW_2.SALK	G
PHW_34.SALK	G
Pi_0.SALK	G
Pigna-1.9659.MON-MPI	G
Pla_0.SALK	G
PLO-1.9923.MON-MPI	G
PLY-20.9924.MON-MPI	G
Pna_10.SALK	G
Pna_17.SALK	G
PNA3.40.7947.MON-MPI	G
Po-0.WTC	G
Pog_0.SALK	G
Pra-6.MPI	G
Pro_0.SALK	G
Pt_0.SALK	G
PT2.21.8077.MON-MPI	G
Pu2_23.SALK	G

Pu2_7.SALK	G
Pu2_8.SALK	G
Puk-2.GMI	G
PYL-6.265.MON-MPI	G
Qar_8a.SALK	G
Qui-0.MPI	G
QUI-8.9934.MON-MPI	G
Ra_0.SALK	G
RAD-21.9917.MON-MPI	G
Ragl_1.SALK	G
Rak_2.SALK	G
Rakit-1.9640.MON-MPI	G
Rakit-3.9642.MON-MPI	G
Rd_0.SALK	G
Rd-0.8411.MON-MPI	G
Ren_1.SALK	G
Ren_11.SALK	G
Rennes_1.SALK	G
Rev-1.GMI	G
Rev-2.GMI	G
Rhen_1.SALK	G
Ri-0.JGI	G
Rld_1.SALK	G
Rmx_A02.SALK	G
Rmx_A180.SALK	G
RMX3.22.8132.MON-MPI	G
Roed-17-319.GMI	G
Rome_1.SALK	G
Rou_0.SALK	G
RRs_10.SALK	G
RRS_7.SALK	G
Rsch-4.WTC	G
Ru-2.9806.MON-MPI	G
Ru4-16.9768.MON-MPI	G
Rubeznhoe_1.SALK	G
Rue3-1-31.MPI	G
RUM-20.9925.MON-MPI	G
Ru-N2.9793.MON-MPI	G
Sakata.JGI	G
San-2.GMI	G
Sanna-2.GMI	G
Sap_0.SALK	G
Sarno-1.9660.MON-MPI	G
SAUL-24.9918.MON-MPI	G
Schip-1.9721.MON-MPI	G
Schl-7.9807.MON-MPI	G
Se_0.SALK	G
Seattle_0.SALK	G
Sei_0.SALK	G
Set-1.5772.MON-MPI	G

Sever-1.9643.MON-MPI	G
Sf_1.SALK	G
Sf-2.WTC	G
Sg_1.SALK	G
Sha.JGI	G
Sha.MPI	G
Si_0.SALK	G
Sim-1.GMI	G
Slavi-2.9723.MON-MPI	G
SLSP-31.2276.MON-MPI	G
SLSP-35.2278.MON-MPI	G
Smolj-1.9718.MON-MPI	G
Sorbo.SALK	G
Sp_0.SALK	G
Sparta-1.GMI	G
Spr1-2.GMI	G
Spr1-6.GMI	G
Spro-1.GMI	G
Spro-2.GMI	G
Spro-3.GMI	G
Sq_1.SALK	G
Sq_8.SALK	G
Sr:3.GMI	G
Sr:5.GMI	G
St-0.GMI	G
Star-8.MPI	G
Stara-1.9713.MON-MPI	G
Staro-1.9757.MON-MPI	G
Ste-0.7346.MON-MPI	G
Ste-2.GMI	G
Ste-3.GMI	G
Ste-4.GMI	G
Stiav-1.9728.MON-MPI	G
Stilo-1.9662.MON-MPI	G
Stu1-1.GMI	G
Stw_0.SALK	G
Su_0.SALK	G
Sus_1.SALK	G
T1000.GMI	G
T1020.GMI	G
T1070.GMI	G
T1080.GMI	G
T1090.GMI	G
T1110.GMI	G
T1130.GMI	G
T1160.GMI	G
T460.GMI	G
T470.GMI	G
T480.GMI	G
T530.GMI	G

T540.GMI	G
T550.GMI	G
T570.GMI	G
T710.GMI	G
T720.GMI	G
T740.GMI	G
T780.GMI	G
T790.GMI	G
T800.GMI	G
T840.GMI	G
T850.GMI	G
T860.GMI	G
T880.GMI	G
T900.GMI	G
T930.GMI	G
T960.GMI	G
T980.GMI	G
T990.GMI	G
Ta_0.SALK	G
TAA-04.GMI	G
TAA-14.GMI	G
TAA-18.GMI	G
TAAD-01.GMI	G
TAAD-03.GMI	G
TAAD-04.GMI	G
TAAD-05.GMI	G
TAAD-06.GMI	G
TAAL-03.GMI	G
TAAL-07.GMI	G
Tamm_2.SALK	G
Tamm_27.SALK	G
Tamm-2.GMI	G
TBO-01.GMI	G
TDr-1.GMI	G
TDr-13.GMI	G
TDr-16.GMI	G
TDr-17.GMI	G
TDr-2.GMI	G
TDr-7.GMI	G
TDr-8.GMI	G
TDr-9.GMI	G
Teano-1.9663.MON-MPI	G
TEDEN-02.GMI	G
TEDEN-03.GMI	G
Teiu-2.9736.MON-MPI	G
TFAE-06.GMI	G
TFAE-07.GMI	G
TFAE-08.GMI	G
Tgr-01.GMI	G
Tha_1.SALK	G

Ting_1.SALK	G
Tny-04.GMI	G
Toc-1.9739.MON-MPI	G
Tol_0.SALK	G
TOM-04.GMI	G
TOM-06.GMI	G
TOM-07.GMI	G
Tomegap-2.GMI	G
Tottarp-2.GMI	G
TOU-A1-88.350.MON-MPI	G
TOU-A1-89.351.MON-MPI	G
TRAE-01.GMI	G
TRE-1.9926.MON-MPI	G
Ts_1.SALK	G
Ts_5.SALK	G
Tscha_1.SALK	G
Tsu-0.WTC	G
Tsu-1.MPI	G
Tu_0.SALK	G
Tu-B1-2.9794.MON-MPI	G
Tu-B2-3.9808.MON-MPI	G
TueSB30-3.MPI	G
Tuescha9.MPI	G
TueV13.MPI	G
TueWa1-2.MPI	G
Tu-KB-6.9809.MON-MPI	G
Tu-KS-7.9810.MON-MPI	G
Tul_0.SALK	G
Tu-NK-12.9811.MON-MPI	G
Tu-PK-7.9783.MON-MPI	G
Tur-4.GMI	G
Tu-WH.9816.MON-MPI	G
TV-10.GMI	G
TV-22.GMI	G
TV-30.GMI	G
TV-38.GMI	G
TV-7.GMI	G
Ty_0.SALK	G
Ty-1.5784.MON-MPI	G
UduI.6296.MON-MPI	G
UduI.6390.MON-MPI	G
UduI.6396.MON-MPI	G
Uk_1.SALK	G
UKID107.5811.MON-MPI	G
UKID114.5818.MON-MPI	G
UKID63.5768.MON-MPI	G
UKID74.5779.MON-MPI	G
UKID96.5800.MON-MPI	G
UKNW06-003.5353.MON-MPI	G
UKNW06-403.5577.MON-MPI	G

UKNW06-481.5644.MON-MPI	G
UKSE06-118.5023.MON-MPI	G
UKSE06-252.5104.MON-MPI	G
UKSE06-325.5151.MON-MPI	G
UKSE06-362.5165.MON-MPI	G
UKSE06-432.5210.MON-MPI	G
UKSE06-470.5236.MON-MPI	G
UKSE06-500.5253.MON-MPI	G
UKSE06-533.5276.MON-MPI	G
UKSW06-179.4779.MON-MPI	G
UKSW06-207.4807.MON-MPI	G
UKSW06-226.4826.MON-MPI	G
UKSW06-285.4884.MON-MPI	G
UKSW06-302.4900.MON-MPI	G
UKSW06-333.4931.MON-MPI	G
UKSW06-360.4958.MON-MPI	G
Ulies-1.9737.MON-MPI	G
Ull2-3.GMI	G
Ull2-5.GMI	G
Ull-A-1.GMI	G
Ullapool-8.9312.MON-MPI	G
Uod_1.SALK	G
Uod_7.SALK	G
Uod-2.8428.MON-MPI	G
Utrecht.SALK	G
Vaar-1.GMI	G
Vaar2-1.GMI	G
Vaar2-6.GMI	G
Vaestervik.GMI	G
Van_0.SALK	G
Vash-1.MPI	G
VED-10.9933.MON-MPI	G
Ven_1.SALK	G
Vie-0.MPI	G
Vimmerby.GMI	G
Vind_1.SALK	G
Vinsloev.GMI	G
Wa_1.SALK	G
WalhaesB4.MPI	G
WAR.7477.MON-MPI	G
WAV-8.9938.MON-MPI	G
Wc_1.SALK	G
Wei_0.SALK	G
Westkar_4.SALK	G
Wil_1.SALK	G
Wil-2.WTC	G
Wl_0.SALK	G
Ws_2.SALK	G
Ws-0.WTC	G
Wt_5.SALK	G

Wu-0.WTC	G
Xan-1.MPI	G
Yeg-1.MPI	G
Yeg-2.9128.MON-MPI	G
Yeg-4.9130.MON-MPI	G
Yeg-5.9131.MON-MPI	G
Yeg-7.9133.MON-MPI	G
Yeg-8.9134.MON-MPI	G
Yo_0.SALK	G
Yst-1.GMI	G
Zagub-1.9748.MON-MPI	G
Zal_1.SALK	G
Zdarec3.403.MON-MPI	G
Zdr_1.SALK	G
Zdrl.6424.MON-MPI	G
Zdrl.6434.MON-MPI	G
Zdrl.6445.MON-MPI	G
Zu-0.WTC	G
Zu-1.7418.MON-MPI	G
Zupan-1.9644.MON-MPI	G

Table S5: Candidate SNP in AT3G54925 extracted for 855 *A. thaliana* accessions. The nucleotide at the candidate SNP position 20349799 on chromosome 3 (AT3G54925) was extracted for all available accessions from the 1001 genome project`s GEBowser (http://signal.salk.edu/atg1001/3.0/gebrowser.php). The Col-0 reference nucleotide is shown in the first line, all other same nucleotides are grouped and separated by lines, accessions within these groups are sorted alphabetically. ".": no sequence information. CeBiT: IGS of the Center for Biotechnology of the University of Bielefeld (Bielefeld, Germany), GMI: Gregor Mendel Institute of Molecular Plant Biology (Vienna, Austria), JGI: DOE Joint Genome Institute (Walnut Creek, USA), MPI: Max Planck Institute for Developmental Biology (Tuebingen, Germany), MON: Monsanto Company (St. Louis, USA), SALK: Salk Institute Genomic Analysis Laboratory (La Jolla, USA), WTC: Wellcome Trust Center for Human Genetics (Oxford, UK). Published sources are: Cao et al., 2011; Gan et al., 2011; Long et al., 2013; Schmitz et al., 2013.

accession label from GEBrowser	nucleotide (chr3:20349799)
Col-0.MPI	C
HKT2.4.MPI	T
Kastel-1.MPI	T
Bik_1.SALK	A
IP-Coc-1.9535.MON-MPI	A
IP-Pal-0.9567.MON-MPI	A
IP-Pan-0.9568.MON-MPI	A
IP-Ria-0.9577.MON-MPI	A
IP-Vaz-0.9593.MON-MPI	A
IP-Vdm-0.9594.MON-MPI	A
Old_1.SALK	A
TV-7.GMI	A
Ty_0.SALK	A
Ty-1.5784.MON-MPI	A
Vaar2-6.GMI	.
11C1.9503.MON-MPI	C
Aa_0.SALK	C
Abd_0.SALK	C
Adam-1.9609.MON-MPI	C
Aedal-1.GMI	C
Aedal-3.GMI	C
Ag_0.SALK	C
Agu-1.MPI	C
Aiell-1.9646.MON-MPI	C
Aitba-1.9606.MON-MPI	C
Ak_1.SALK	C
Alc-0.JGI	C
Ale-Stenar-44-4.GMI	C
Ale-Stenar-56-14.GMI	C
Ale-Stenar-64-24.GMI	C
Algutsrum.GMI	C
Alst_1.SALK	C
Alt-1.9774.MON-MPI	C
Altai_5.SALK	C
Amel_1.SALK	C

An_1.SALK	C
Ang_0.SALK	C
Anholt_1.SALK	C
Ann_1.SALK	C
Anz_0.SALK	C
App1-12.GMI	C
App1-14.GMI	C
App1-16.GMI	C
Appt_1.SALK	C
ARGE-1-15.9911.MON-MPI	C
ARR-17.9927.MON-MPI	C
Ba_1.SALK	C
Baa_1.SALK	C
Baa1-2.GMI	C
Baa4-1.GMI	C
Baa5-1.GMI	C
Bach2-1.9796.MON-MPI	C
Bach-7.9778.MON-MPI	C
Bai-10.9779.MON-MPI	C
Bak-2.MPI	C
Bak-7.MPI	C
Balan-1.9613.MON-MPI	C
Basta-1.9619.MON-MPI	C
Basta-2.9620.MON-MPI	C
Bay-0.JGI	C
Bch_1.SALK	C
Bd_0.SALK	C
Bela-1.9730.MON-MPI	C
Bela-2.9733.MON-MPI	C
Benk_1.SALK	C
Ber.SALK	C
Berg-1.9775.MON-MPI	C
BEZ-9.9928.MON-MPI	C
Bg_2.SALK	C
Bl-4.9813.MON-MPI	C
Bijisk-4.9622.MON-MPI	C
Bil-5.GMI	C
Bil-7.GMI	C
Bivio-1.9649.MON-MPI	C
Bl_1.SALK	C
Bla_1.SALK	C
Bla-1.7015.MON-MPI	C
Blh-1.JGI	C
Boo2-1.8266.MON-MPI	C
Boot_1.SALK	C
Bor_1.SALK	C
Bor_4.SALK	C
Borky1.428.MON-MPI	C
Br_0.SALK	C
BRE-14.9919.MON-MPI	C

BRI-2.9910.MON-MPI	C
Broesarp-34-145.GMI	C
Broet1-6.GMI	C
Bs_1.SALK	C
Bsch_0.SALK	C
Bu_0.SALK	C
Buckhorn_Pass.SALK	C
Bur-0.MPI	C
Bur-0.WTC	C
C24.MPI	C
Ca_0.SALK	C
Cal_0.SALK	C
Can-0.WTC	C
Castelfed-1-197.9681.MON-MPI	C
Castelfed-4-211.9695.MON-MPI	C
Castelfed-4-214.9696.MON-MPI	C
CATS-6.9937.MON-MPI	C
Cdm-0.MPI	C
Cerv_1.SALK	C
CHA-41.932.MON-MPI	C
Chaba-2.9624.MON-MPI	C
Chat_1.SALK	C
Chi_0.SALK	C
CIBC_17.SALK	C
CIBC_5.SALK	C
Cimin-1.9661.MON-MPI	C
Cnt_1.SALK	C
Cnt-1.5726.MON-MPI	C
Co.SALK	C
Co_1.SALK	C
Com_1.SALK	C
CON-7.9913.MON-MPI	C
Corig-1.9650.MON-MPI	C
CSHL-5.6744.MON-MPI	C
Ct-1.WTC	C
Cvi_0.SALK	C
Cvi-0.SALK	C
CYR.88.MON-MPI	C
Da1_12.SALK	C
Db_1.SALK	C
Del-10.MPI	C
Dem_4.SALK	C
Di_G.SALK	C
DIR-9.9920.MON-MPI	C
Dja_1.SALK	C
Do_0.SALK	C
Doer-10.GMI	C
Dog-4.MPI	C
Dolen-1.9697.MON-MPI	C
Dolna-1.9712.MON-MPI	C

Don-0.MPI	C
Dospa-1.9706.MON-MPI	C
Doubravnik7.410.MON-MPI	C
Dr_0.SALK	C
Dra_0.SALK	C
Dra2-1.GMI	C
Dra3-1.GMI	C
Draha2.424.MON-MPI	C
DraII_1.SALK	C
DraII-6.5874.MON-MPI	C
DraIII_1.SALK	C
DraIV.5893.MON-MPI	C
DraIV.5907.MON-MPI	C
DraIV.5950.MON-MPI	C
DraIV.5984.MON-MPI	C
DraIV.5993.MON-MPI	C
Duk.SALK	C
Durh_1.SALK	C
Eden-1.GMI	C
Eden-2.GMI	C
Eden-7.GMI	C
Eden-9.GMI	C
Edi-0.WTC	C
Eds-1.GMI	C
Eds-9.GMI	C
Ei_2.SALK	C
El_0.SALK	C
Ema_1.SALK	C
En_1.SALK	C
En_2.SALK	C
En_D.SALK	C
ENC-2-1.9907.MON-MPI	C
Epidauros-1.9725.MON-MPI	C
Er_0.SALK	C
Erg2-6.9784.MON-MPI	C
Es_0.SALK	C
ESP-1-11.9908.MON-MPI	C
Est.SALK	C
Est-1.MPI	C
Et_0.SALK	C
Etna_2.SALK	C
Ey15-2.MPI	C
Faeb-2.GMI	C
Faeb-4.GMI	C
Fael-1.GMI	C
Faneronemi-3.9726.MON-MPI	C
Fei-0.MPI	C
Fell1-10.9814.MON-MPI	C
Fell2-4.9780.MON-MPI	C
Fell3-7.9776.MON-MPI	C

Fi_0.SALK	C
Filet-1.9651.MON-MPI	C
Fjae1-1.GMI	C
Fjae1-2.GMI	C
Fjae1-5.GMI	C
Fjae2-4.GMI	C
Fly2-1.GMI	C
Fly2-2.GMI	C
Fondi-1.9652.MON-MPI	C
Fr_2.SALK	C
Fri_2.GMI	C
Furni-1.9743.MON-MPI	C
Ga_0.SALK	C
Ge_0.SALK	C
Geg-14.9125.MON-MPI	C
Gel_1.SALK	C
GEN-8.9909.MON-MPI	C
Gie_0.SALK	C
Giffo-1.9653.MON-MPI	C
Gifu_2.SALK	C
Gn-1.9777.MON-MPI	C
Gn2-3.9790.MON-MPI	C
Goced-1.9698.MON-MPI	C
Gol-2.9314.MON-MPI	C
Got_22.SALK	C
Got_7.SALK	C
Gr_1.SALK	C
Gr-5.7158.MON-MPI	C
Gradi-1.9645.MON-MPI	C
Gre_0.SALK	C
Grivo-1.9714.MON-MPI	C
Gro-3.GMI	C
Groen-12.GMI	C
Groen-14.GMI	C
Groen-5.GMI	C
Gu_0.SALK	C
Gy_0.SALK	C
Ha_0.SALK	C
Had-1.GMI	C
Had-2.GMI	C
Haes-1.9791.MON-MPI	C
Hag-2.GMI	C
Ha-HBT1-2.9785.MON-MPI	C
Ha-HBT2-10.9797.MON-MPI	C
Ha-HBT3-11.9815.MON-MPI	C
Hal-1.GMI	C
Ham-1.GMI	C
Ha-P-13.9786.MON-MPI	C
Ha-P2-1.9798.MON-MPI	C
Hart-2.9799.MON-MPI	C

Ha-S-B.9800.MON-MPI	C
Ha-SP-2.9801.MON-MPI	C
Hau_0.SALK	C
HE-1.9769.MON-MPI	C
Hel-3.GMI	C
Hey_1.SALK	C
Hh_0.SALK	C
Hi-0.WTC	C
Hn_0.SALK	C
Hod.SALK	C
Hof-1.9772.MON-MPI	C
Hola_1_2.GMI	C
Hola-1-1.GMI	C
Hola-2-2.GMI	C
Hov1-10.GMI	C
Hov1-7.GMI	C
Hov3-2.GMI	C
Hov3-5.GMI	C
Hov4-1.GMI	C
Hovdala-2.GMI	C
HR_10.SALK	C
HR_5.SALK	C
Hs_0.SALK	C
HSm.SALK	C
Iasi-1.9744.MON-MPI	C
ICE1.MPI	C
ICE102.MPI	C
ICE104.MPI	C
ICE106.MPI	C
ICE107.MPI	C
ICE111.MPI	C
ICE112.MPI	C
ICE119.MPI	C
ICE120.MPI	C
ICE127.MPI	C
ICE130.MPI	C
ICE134.MPI	C
ICE138.MPI	C
ICE150.MPI	C
ICE152.MPI	C
ICE153.MPI	C
ICE163.MPI	C
ICE169.MPI	C
ICE173.MPI	C
ICE181.MPI	C
ICE21.MPI	C
ICE212.MPI	C
ICE213.MPI	C
ICE216.MPI	C
ICE226.MPI	C

ICE228.MPI	C
ICE29.MPI	C
ICE33.MPI	C
ICE36.MPI	C
ICE49.MPI	C
ICE50.MPI	C
ICE60.MPI	C
ICE61.MPI	C
ICE63.MPI	C
ICE7.MPI	C
ICE70.MPI	C
ICE71.MPI	C
ICE72.MPI	C
ICE73.MPI	C
ICE75.MPI	C
ICE79.MPI	C
ICE91.MPI	C
ICE92.MPI	C
ICE93.MPI	C
ICE97.MPI	C
ICE98.MPI	C
In_0.SALK	C
IP-Adm-0.9514.MON-MPI	C
IP-Ala-0.9515.MON-MPI	C
IP-All-0.9517.MON-MPI	C
IP-Alm-0.9518.MON-MPI	C
IP-Alo-0.9506.MON-MPI	C
IP-Ang-0.9519.MON-MPI	C
IP-Ara-4.9520.MON-MPI	C
IP-Bar-1.9521.MON-MPI	C
IP-Bea-0.9522.MON-MPI	C
IP-Ben-0.9523.MON-MPI	C
IP-Ber-0.9524.MON-MPI	C
IP-Bis-0.9525.MON-MPI	C
IP-Cab-3.9526.MON-MPI	C
IP-Cad-0.9527.MON-MPI	C
IP-Cal-0.9528.MON-MPI	C
IP-Cap-1.9529.MON-MPI	C
IP-Car-1.9530.MON-MPI	C
IP-Cdc-3.9531.MON-MPI	C
IP-Cdo-0.9532.MON-MPI	C
IP-Cem-0.9533.MON-MPI	C
IP-Cmo-3.9534.MON-MPI	C
IP-Coa-0.9507.MON-MPI	C
IP-Cor-0.9536.MON-MPI	C
IP-Cum-1.9537.MON-MPI	C
IP-Cur-4.9538.MON-MPI	C
IP-Deh-1.9539.MON-MPI	C
IP-Elb-0.9540.MON-MPI	C
IP-Fue-2.9541.MON-MPI	C

IP-Fun-0.9542.MON-MPI	C
IP-Gra-0.9543.MON-MPI	C
IP-Gua-1.9544.MON-MPI	C
IP-Her-12.9545.MON-MPI	C
IP-Hom-4.9546.MON-MPI	C
IP-Hor-0.9547.MON-MPI	C
IP-Hum-2.9549.MON-MPI	C
IP-Iso-4.9550.MON-MPI	C
IP-Jim-1.9551.MON-MPI	C
IP-Lab-7.9552.MON-MPI	C
IP-Ldd-0.9553.MON-MPI	C
IP-Lso-0.9554.MON-MPI	C
IP-Mar-1.9555.MON-MPI	C
IP-Men-2.9556.MON-MPI	C
IP-Moa-0.9557.MON-MPI	C
IP-Moc-11.9558.MON-MPI	C
IP-Mon-5.9559.MON-MPI	C
IP-Mos-1.9508.MON-MPI	C
IP-Mot-0.9560.MON-MPI	C
IP-Mun-0.9561.MON-MPI	C
IP-Mur-0.9562.MON-MPI	C
IP-Nav-0.9563.MON-MPI	C
IP-Nog-17.9564.MON-MPI	C
IP-Orb-10.9565.MON-MPI	C
IP-Oso-0.9566.MON-MPI	C
IP-Pds-1.9569.MON-MPI	C
IP-Pob-0.9570.MON-MPI	C
IP-Pro-0.9571.MON-MPI	C
IP-Pue-0.9572.MON-MPI	C
IP-Rds-0.9573.MON-MPI	C
IP-Rei-0.9510.MON-MPI	C
IP-Rel-0.9574.MON-MPI	C
IP-Ren-6.9575.MON-MPI	C
IP-Rev-0.9576.MON-MPI	C
IP-Sac-0.9578.MON-MPI	C
IP-San-10.9579.MON-MPI	C
IP-Scm-0.9580.MON-MPI	C
IP-Sdv-3.9581.MON-MPI	C
IP-Ses-0.9582.MON-MPI	C
IP-Sne-0.9583.MON-MPI	C
IP-Stp-0.9584.MON-MPI	C
IP-Svi-0.9585.MON-MPI	C
IP-Tam-0.9586.MON-MPI	C
IP-Tdc-0.9587.MON-MPI	C
IP-Tol-7.9588.MON-MPI	C
IP-Tor-1.9589.MON-MPI	C
IP-Trs-0.9590.MON-MPI	C
IP-Vad-0.9591.MON-MPI	C
IP-Vae-2.9592.MON-MPI	C
IP-Vav-0.9511.MON-MPI	C

IP-Vdt-0.9595.MON-MPI	C
IP-Ver-5.9596.MON-MPI	C
IP-Vid-1.9512.MON-MPI	C
IP-Vig-1.9597.MON-MPI	C
IP-Vim-0.9598.MON-MPI	C
IP-Vin-0.9599.MON-MPI	C
IP-Vis-0.9600.MON-MPI	C
IP-Voz-0.9601.MON-MPI	C
IP-Vpa-1.9602.MON-MPI	C
Is_0.SALK	C
ISS-20.9929.MON-MPI	C
IST-29.9914.MON-MPI	C
Istisu-1.MPI	C
Je_0.SALK	C
Jea.JGI	C
Jl_3.SALK	C
Jm_0.SALK	C
Kaevlinge-1.GMI	C
Kal-2.GMI	C
Kar_1.SALK	C
Karag-1.9617.MON-MPI	C
Karag-2.9608.MON-MPI	C
Kas_1.SALK	C
Kas_2.SALK	C
Kb_0.SALK	C
KBG1-14.9788.MON-MPI	C
KBG2-13.9770.MON-MPI	C
Kelsterbach_4.SALK	C
Kent.SALK	C
Kia-1.GMI	C
Kil_0.SALK	C
Kin_0.SALK	C
Kl_5.SALK	C
Kn-0.WTC	C
Kni-1.GMI	C
Knjas-1.9749.MON-MPI	C
Knox_18.SALK	C
Ko_2.SALK	C
Koch-1.MPI	C
Kolar-1.9699.MON-MPI	C
Kolar-2.9702.MON-MPI	C
Koln.SALK	C
Kolyv-2.9625.MON-MPI	C
Kolyv-3.9626.MON-MPI	C
Kolyv-5.9627.MON-MPI	C
Kolyv-6.9628.MON-MPI	C
Kondara.SALK	C
Kor-3.GMI	C
Koren-1.9719.MON-MPI	C
K-oze-1.9629.MON-MPI	C

K-oze-3.9630.MON-MPI	C
Kro_0.SALK	C
Kro-0.MPI	C
Krot_0.SALK	C
Kru-3.GMI	C
Kulturen-1.GMI	C
Kus2-2.9781.MON-MPI	C
KYC-33.801.MON-MPI	C
Kyoto.SALK	C
Kz_9.SALK	C
La_0.SALK	C
Lag1-2.9100.MON-MPI	C
Lag1-4.9102.MON-MPI	C
Lag1-6.9104.MON-MPI	C
Lag2.2.MPI	C
Lan_0.SALK	C
Lan-1.GMI	C
LDV-18.108.MON-MPI	C
LDV-46.139.MON-MPI	C
Le_0.SALK	C
Lebja-2.9632.MON-MPI	C
Lebja-4.9633.MON-MPI	C
LEC-25.9930.MON-MPI	C
Leo-1.MPI	C
Ler-0.WTC	C
Ler-1.MPI	C
Ler-1.SALK	C
Lerik1-3.MPI	C
Leska-1.9716.MON-MPI	C
Lesno-1.9611.MON-MPI	C
Lesno-2.9612.MON-MPI	C
Lesno-4.9610.MON-MPI	C
Li_2:1.SALK	C
Li-7.7231.MON-MPI	C
Liarum.GMI	C
Lilloe-1.GMI	C
LI-OF-065.630.MON-MPI	C
Lip_0.SALK	C
Liri-1.9654.MON-MPI	C
Lis-2.GMI	C
Lis-3.GMI	C
Lisse.SALK	C
Litva.SALK	C
LL_0.SALK	C
Lm_2.SALK	C
Lom1-1.GMI	C
love-1.GMI	C
love-5.GMI	C
Lp2_2.SALK	C
Lp2_6.SALK	C

LP3413.41.8472.MON-MPI	C
Lu-1.GMI	C
Lu3-30.9782.MON-MPI	C
Lu4-2.9792.MON-MPI	C
Lund.GMI	C
Malii-1.9746.MON-MPI	C
MAR2-3.159.MON-MPI	C
MAR-4-16.9915.MON-MPI	C
Marce-1.9655.MON-MPI	C
Masl-1.9634.MON-MPI	C
Mc_0.SALK	C
Mdn-1.1829.MON-MPI	C
Melic-1.9657.MON-MPI	C
Melni-2.9704.MON-MPI	C
Mer-6.MPI	C
Mh_0.SALK	C
MIC-31.870.MON-MPI	C
MIL-2.9922.MON-MPI	C
Mir_0.SALK	C
Mitterberg-1-180.9665.MON-MPI	C
Mitterberg-1-182.9666.MON-MPI	C
Mitterberg-1-183.9667.MON-MPI	C
Mitterberg-2-184.9668.MON-MPI	C
Mitterberg-2-185.9669.MON-MPI	C
Mitterberg-3-187.9671.MON-MPI	C
MNF-Che-2.1925.MON-MPI	C
MNF-Jac-12.1954.MON-MPI	C
MNF-Pin-39.2016.MON-MPI	C
MNF-Pot-21.1853.MON-MPI	C
MNF-Pot-75.1872.MON-MPI	C
MNF-Riv-21.1890.MON-MPI	C
Mnz_0.SALK	C
MOL-1.9916.MON-MPI	C
MOU2-25.9931.MON-MPI	C
Ms_0.SALK	C
Mt-0.WTC	C
Muh-2.9803.MON-MPI	C
Mv_0.SALK	C
Mz_0.SALK	C
N13.SALK	C
Naes-2.GMI	C
Nc_1.SALK	C
NC_6.SALK	C
Nd-1.CeBiT	C
Nemrut-1.MPI	C
Neo_6.SALK	C
NFA_10.SALK	C
NFA_8.SALK	C
Nicas-1.9658.MON-MPI	C
Nie1-2.MPI	C

No-0.WTC	C
Nok_3.SALK	C
Nosov-1.9635.MON-MPI	C
Noveg-1.9636.MON-MPI	C
Noveg-2.9637.MON-MPI	C
Noveg-3.9638.MON-MPI	C
NOZ-6.9932.MON-MPI	C
Np_0.SALK	C
Nw_0.SALK	C
Nyl-13.GMI	C
Nyl-2.GMI	C
Nyl-7.GMI	C
Nz_1.SALK	C
Ob_0.SALK	C
Obe1-15.9804.MON-MPI	C
Obh-13.9789.MON-MPI	C
Oede-2.GMI	C
Oemoe1-7.GMI	C
Oemoe2-1.GMI	C
Oer-1.GMI	C
Olympia-2.9727.MON-MPI	C
Omn-1.GMI	C
Omn-5.GMI	C
Or_0.SALK	C
Orast-1.9741.MON-MPI	C
Ove_0.SALK	C
Oy-0.JGI	C
Oy-0.WTC	C
Panik-1.9607.MON-MPI	C
Panke-1.9639.MON-MPI	C
Parti-1.9615.MON-MPI	C
Paw-26.2171.MON-MPI	C
Ped-0.MPI	C
Per_1.SALK	C
Petergof.7296.MON-MPI	C
Pfn-10.9805.MON-MPI	C
Pfn-N2.2-6.9771.MON-MPI	C
PHW_2.SALK	C
PHW_34.SALK	C
Pi_0.SALK	C
Pigna-1.9659.MON-MPI	C
Pla_0.SALK	C
PLO-1.9923.MON-MPI	C
PLY-20.9924.MON-MPI	C
Pna_10.SALK	C
Pna_17.SALK	C
PNA3.40.7947.MON-MPI	C
Po-0.WTC	C
Pog_0.SALK	C
Pra-6.MPI	C

Pro_0.SALK	C
Pt_0.SALK	C
PT2.21.8077.MON-MPI	C
Pu2_23.SALK	C
Pu2_7.SALK	C
Pu2_8.SALK	C
Puk-2.GMI	C
PYL-6.265.MON-MPI	C
Qar_8a.SALK	C
Qui-0.MPI	C
QUI-8.9934.MON-MPI	C
Ra_0.SALK	C
RAD-21.9917.MON-MPI	C
Ragl_1.SALK	C
Rak_2.SALK	C
Rakit-1.9640.MON-MPI	C
Rakit-3.9642.MON-MPI	C
Rd_0.SALK	C
Rd-0.8411.MON-MPI	C
Ren_1.SALK	C
Ren_11.SALK	C
Rennes_1.SALK	C
Rev-1.GMI	C
Rev-2.GMI	C
Rhen_1.SALK	C
Ri-0.JGI	C
Rld_1.SALK	C
Rmx_A02.SALK	C
Rmx_A180.SALK	C
RMX3.22.8132.MON-MPI	C
Roed-17-319.GMI	C
Rome_1.SALK	C
Rou_0.SALK	C
RRs_10.SALK	C
RRS_7.SALK	C
Rsch-4.WTC	C
Ru-2.9806.MON-MPI	C
Ru4-16.9768.MON-MPI	C
Rubeznhoe_1.SALK	C
Rue3-1-31.MPI	C
RUM-20.9925.MON-MPI	C
Ru-N2.9793.MON-MPI	C
Sakata.JGI	C
San-2.GMI	C
Sanna-2.GMI	C
Sap_0.SALK	C
Sarno-1.9660.MON-MPI	C
SAUL-24.9918.MON-MPI	C
Schip-1.9721.MON-MPI	C
Schl-7.9807.MON-MPI	C

Se_0.SALK	C
Seattle_0.SALK	C
Sei_0.SALK	C
Set-1.5772.MON-MPI	C
Sever-1.9643.MON-MPI	C
Sf_1.SALK	C
Sf-2.WTC	C
Sg_1.SALK	C
Sha.JGI	C
Sha.MPI	C
Si_0.SALK	C
Sim-1.GMI	C
Slavi-2.9723.MON-MPI	C
SLSP-31.2276.MON-MPI	C
SLSP-35.2278.MON-MPI	C
Smolj-1.9718.MON-MPI	C
Sorbo.SALK	C
Sp_0.SALK	C
Sparta-1.GMI	C
Spr1-2.GMI	C
Spr1-6.GMI	C
Spro-1.GMI	C
Spro-2.GMI	C
Spro-3.GMI	C
Sq_1.SALK	C
Sq_8.SALK	C
Sr:3.GMI	C
Sr:5.GMI	C
St-0.GMI	C
Star-8.MPI	C
Stara-1.9713.MON-MPI	C
Staro-1.9757.MON-MPI	C
Ste-0.7346.MON-MPI	C
Ste-2.GMI	C
Ste-3.GMI	C
Ste-4.GMI	C
Stiav-1.9728.MON-MPI	C
Stilo-1.9662.MON-MPI	C
Stu1-1.GMI	C
Stw_0.SALK	C
Su_0.SALK	C
Sus_1.SALK	C
T1000.GMI	C
T1020.GMI	C
T1070.GMI	C
T1080.GMI	C
T1090.GMI	C
T1110.GMI	C
T1130.GMI	C
T1160.GMI	C

T460.GMI	C
T470.GMI	C
T480.GMI	C
T530.GMI	C
T540.GMI	C
T550.GMI	C
T570.GMI	C
T710.GMI	C
T720.GMI	C
T740.GMI	C
T780.GMI	C
T790.GMI	C
T800.GMI	C
T840.GMI	C
T850.GMI	C
T860.GMI	C
T880.GMI	C
T900.GMI	C
T930.GMI	C
T960.GMI	C
T980.GMI	C
T990.GMI	C
Ta_0.SALK	C
TAA-04.GMI	C
TAA-14.GMI	C
TAA-18.GMI	C
TAAD-01.GMI	C
TAAD-03.GMI	C
TAAD-04.GMI	C
TAAD-05.GMI	C
TAAD-06.GMI	C
TAAL-03.GMI	C
TAAL-07.GMI	C
Tamm_2.SALK	C
Tamm_27.SALK	C
Tamm-2.GMI	C
TBO-01.GMI	C
TDr-1.GMI	C
TDr-13.GMI	C
TDr-16.GMI	C
TDr-17.GMI	C
TDr-2.GMI	C
TDr-7.GMI	C
TDr-8.GMI	C
TDr-9.GMI	C
Teano-1.9663.MON-MPI	C
TEDEN-02.GMI	C
TEDEN-03.GMI	C
Teiu-2.9736.MON-MPI	C
TFAE-06.GMI	C

TFAE-07.GMI	C
TFAE-08.GMI	C
Tgr-01.GMI	C
Tha_1.SALK	C
Ting_1.SALK	C
Tny-04.GMI	C
Toc-1.9739.MON-MPI	C
Tol_0.SALK	C
TOM-04.GMI	C
TOM-06.GMI	C
TOM-07.GMI	C
Tomegap-2.GMI	C
Tottarp-2.GMI	C
TOU-A1-88.350.MON-MPI	C
TOU-A1-89.351.MON-MPI	C
TRAE-01.GMI	C
TRE-1.9926.MON-MPI	C
Ts_1.SALK	C
Ts_5.SALK	C
Tscha_1.SALK	C
Tsu-0.WTC	C
Tsu-1.MPI	C
Tu_0.SALK	C
Tu-B1-2.9794.MON-MPI	C
Tu-B2-3.9808.MON-MPI	C
TueSB30-3.MPI	C
Tuescha9.MPI	C
TueV13.MPI	C
TueWa1-2.MPI	C
Tu-KB-6.9809.MON-MPI	C
Tu-KS-7.9810.MON-MPI	C
Tul_0.SALK	C
Tu-NK-12.9811.MON-MPI	C
Tu-PK-7.9783.MON-MPI	C
Tur-4.GMI	C
Tu-WH.9816.MON-MPI	C
TV-10.GMI	C
TV-22.GMI	C
TV-30.GMI	C
TV-38.GMI	C
Udul.6296.MON-MPI	C
Udul.6390.MON-MPI	C
Udul.6396.MON-MPI	C
Uk_1.SALK	C
UKID107.5811.MON-MPI	C
UKID114.5818.MON-MPI	C
UKID63.5768.MON-MPI	C
UKID74.5779.MON-MPI	C
UKID96.5800.MON-MPI	C
UKNW06-003.5353.MON-MPI	C

UKNW06-403.5577.MON-MPI	C
UKNW06-481.5644.MON-MPI	C
UKSE06-118.5023.MON-MPI	C
UKSE06-252.5104.MON-MPI	C
UKSE06-325.5151.MON-MPI	C
UKSE06-362.5165.MON-MPI	C
UKSE06-432.5210.MON-MPI	C
UKSE06-470.5236.MON-MPI	C
UKSE06-500.5253.MON-MPI	C
UKSE06-533.5276.MON-MPI	C
UKSW06-179.4779.MON-MPI	C
UKSW06-207.4807.MON-MPI	C
UKSW06-226.4826.MON-MPI	C
UKSW06-285.4884.MON-MPI	C
UKSW06-302.4900.MON-MPI	C
UKSW06-333.4931.MON-MPI	C
UKSW06-360.4958.MON-MPI	C
Ulies-1.9737.MON-MPI	C
Ull2-3.GMI	C
Ull2-5.GMI	C
Ull-A-1.GMI	C
Ullapool-8.9312.MON-MPI	C
Uod_1.SALK	C
Uod_7.SALK	C
Uod-2.8428.MON-MPI	C
Utrecht.SALK	C
Vaar-1.GMI	C
Vaar2-1.GMI	C
Vaestervik.GMI	C
Van_0.SALK	C
Vash-1.MPI	C
VED-10.9933.MON-MPI	C
Ven_1.SALK	C
Vie-0.MPI	C
Vimmerby.GMI	C
Vind_1.SALK	C
Vinsloev.GMI	C
Wa_1.SALK	C
WalhaesB4.MPI	C
WAR.7477.MON-MPI	C
WAV-8.9938.MON-MPI	C
Wc_1.SALK	C
Wei_0.SALK	C
Westkar_4.SALK	C
Wil_1.SALK	C
Wil-2.WTC	C
Wl_0.SALK	C
Ws_2.SALK	C
Ws-0.WTC	C
Wt_5.SALK	C

Wu-0.WTC	C
Xan-1.MPI	C
Yeg-1.MPI	C
Yeg-2.9128.MON-MPI	C
Yeg-4.9130.MON-MPI	C
Yeg-5.9131.MON-MPI	C
Yeg-7.9133.MON-MPI	C
Yeg-8.9134.MON-MPI	C
Yo_0.SALK	C
Yst-1.GMI	C
Zagub-1.9748.MON-MPI	C
Zal_1.SALK	C
Zdarec3.403.MON-MPI	C
Zdr_1.SALK	C
Zdrl.6424.MON-MPI	C
Zdrl.6434.MON-MPI	C
Zdrl.6445.MON-MPI	C
Zu-0.WTC	C
Zu-1.7418.MON-MPI	C
Zupan-1.9644.MON-MPI	C

Table S6: Root hair branching in rescued T1 seedlings. The genomic region of *ARK1* from Col-0 was used for rescue experiments of the HKT2.4 root hair branching phenotype. Pro*35S*:*YFP-ARK1* (pENSG) seedlings were grown on MS with BASTA. Pro*35S*:*ARK1* (pFAST) lines were preselected based on the fluorescent seed-marker. The transformation efficiency for HKT2.4 was very low. Root hairs in the upper region of T1 seedlings (see Figure S1) were analyzed.

Pro*35S*:*YFP-ARK1(Col-0)* (HKT2.4)				**Pro*35S*:*ARK1(Col-0)* (HKT2.4)**			
No. of analyzed root hairs	No. of branched root hairs	Branched root hairs [%]	Selection of seedlings	No. of analyzed root hairs	No. of branched root hairs	Branched root hairs [%]	Selection of seedlings
16	2	12.5	BASTA	34	8	23.5	fluorescence of seed
13	1	7.7	BASTA	38	8	21.1	fluorescence of seed
8	1	12.5	BASTA	28	8	28.6	fluorescence of seed
11	1	9.1	BASTA	19	3	15.8	fluorescence of seed
				24	10	41.7	fluorescence of seed
				14	1	7.1	fluorescence of seed
				20	5	25.0	fluorescence of seed
				24	6	25.0	fluorescence of seed

Table S7: List of primers.

Primer name	Sequence 5’ to 3’
Pf-MRH2	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCATGAGTTCGTCAAATTCCTCCTC
Pr-MRH2	GGGGACCACTTTGTACAAGAAAGCTGGGTCTTAATATATCTTTACACATAAGTTGTACAG
Pf-splcing MRH2	GCCATTCCTAGAGTTAGAAAGAG
Pr-splcing MRH2	CAGATGGCCCAATTGTTATTATAAGTG