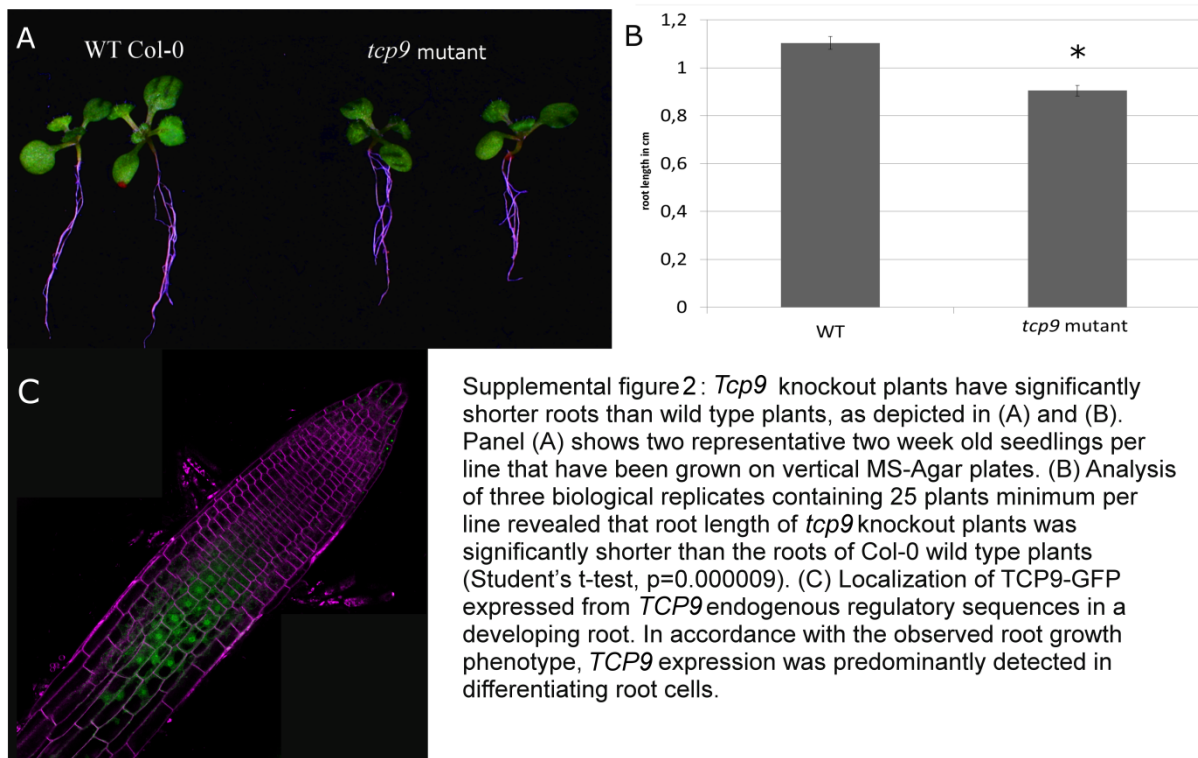
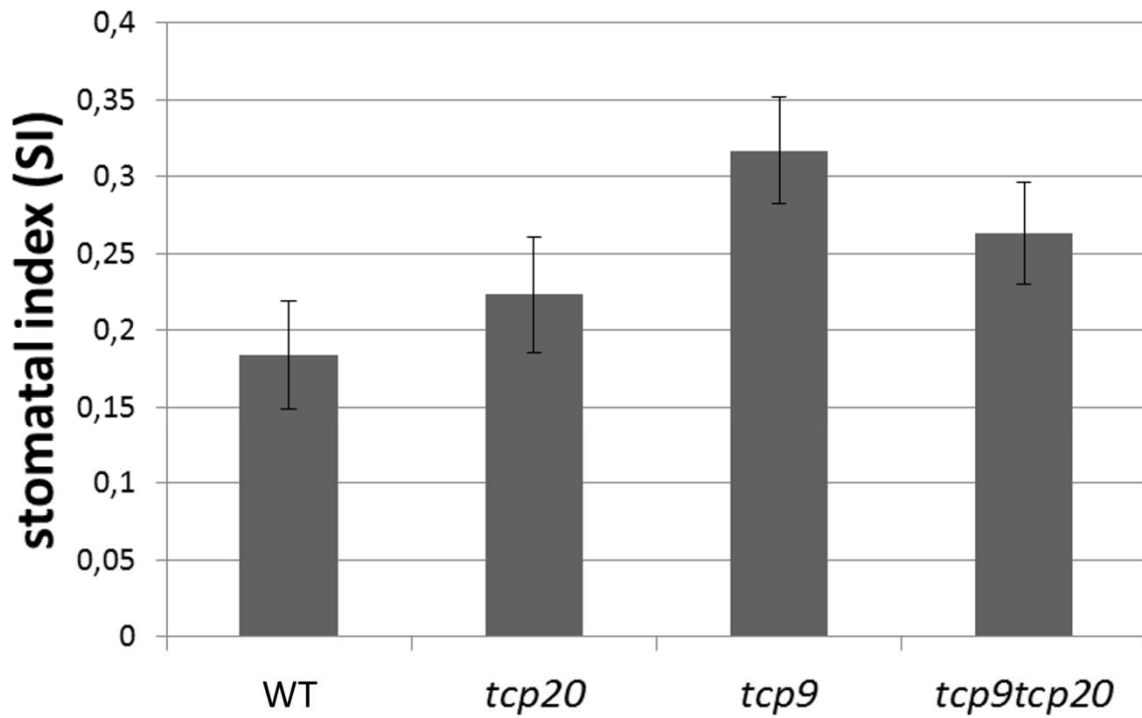


Supplemental figure 1: Expression of *TCP20* in *tcp20* knockout vs. Col-0 wild type plants. Expression was analyzed using Realtime RT-PCR (primers given in Supplemental table 2). *TCP20* expression is hardly detectable in the knockout plants.





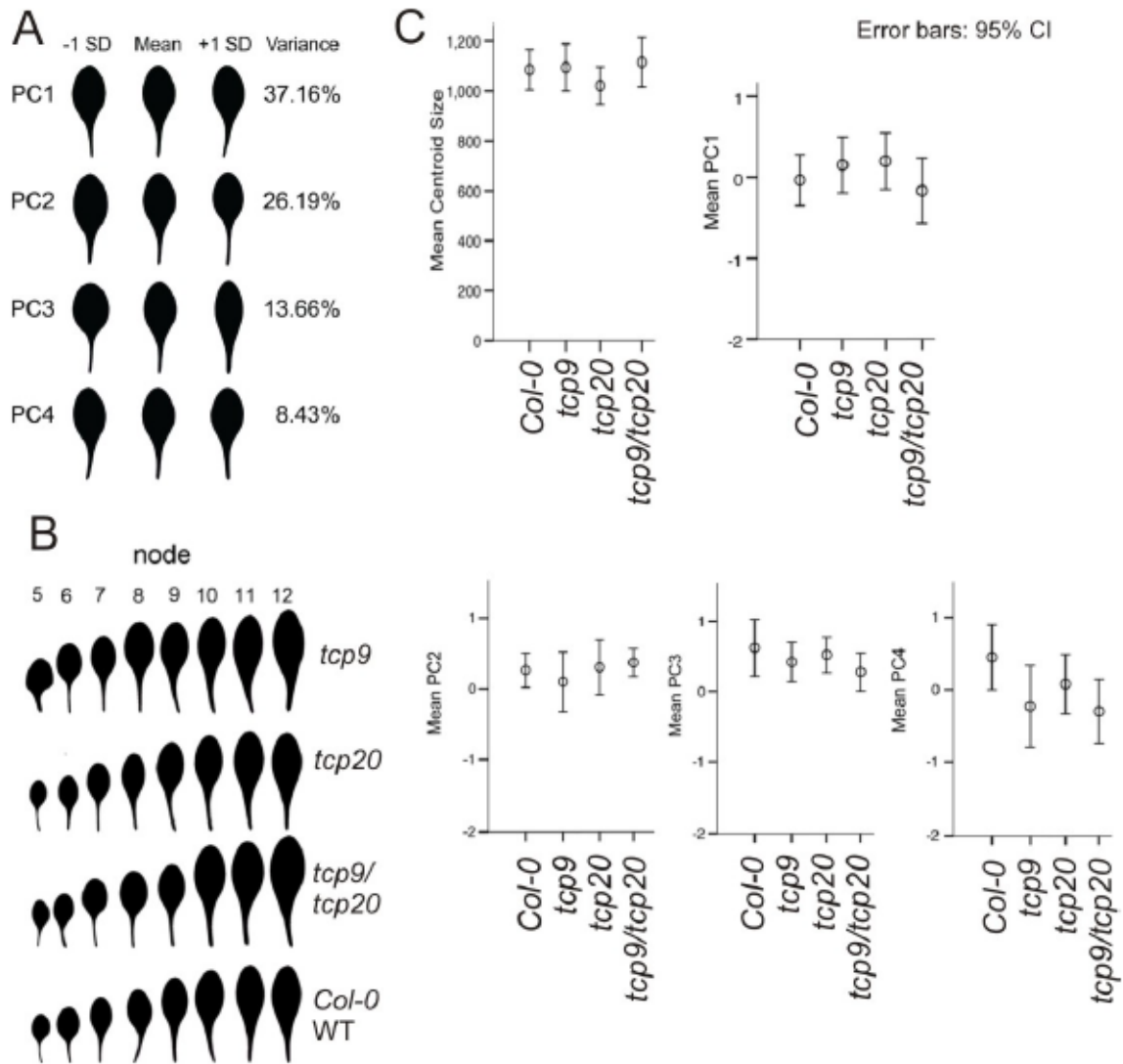
Supplemental figure 3: Stomatal index of class I *tcp* single and double mutants. Calculations were made based on cell drawings as described previously (Andriankaja et al., 2012).

Supplemental data 1: Leaf size and shape analysis by LeafAnalyser.

LeafAnalyser was used to assess differences in leaf shape and size between plant lines (Weight et al., 2008). We had previously defined the natural variation in Arabidopsis leaf shape using a library of 1500 leaves from 10 accessions (Kieffer et al., 2011). For this analysis a full Procrustes fit was applied to all leaves in leaf library. This is a standard method in geometric morphometrics that separates size from variation in shape. A leaf is measured using 48 landmarks along the margin. The landmarks have coordinate values and the average of the x and y coordinate values determines the centroid. Centroid size is then determined by the distance from the centroid to each landmark. Centroid size is used, because it is approximately uncorrelated with every shape variable. This is important because in a geometric sense it is possible that width, length or area correlates with a shape variable (especially in the mean leaf where the position of each landmark is determined by a mean value). A Principal Component analysis was then applied to the dataset of 1500 Procrustes fitted leaf-point models using LeafAnalyser to calculate variation in leaf shape.

The first four principal components (PCs) accounted for 85.44% of the variance in leaf shape and were examined as standard deviations from the mean leaf (Supplemental Fig.4A). Variation along PC1 accounts for 37.16% of the variance in leaf shape. A higher value along PC1 corresponds to a leaf that curves to the left and a lower value with the leaf that curves to the right. Leaves with a higher PC2 value have narrower and elongated petioles with more distally positioned lamina. PC2 accounts for 26.19% of variation in shape. PC3 captures leaf aspect ratio (leaf length:leaf width), and accounts for 13.66% of the variance. Variation along PC4 captures a combination of left right asymmetry and curvature within the leaf and represents 8.43% of variation in shape.

We used LeafAnalyser to generate leaf-point models for the leaves from 8 plants for each of WT, *tcp9*, *tcp20*, and *tcp9 tcp20* lines. We then applied the PCA from the leaf library to these leaf-point models to generate standardized PC scores for each leaf in all four lines. These values were then used reconstruct individual leaves, which were then scaled using the corresponding mean centroid size for each leaf (Supplemental Fig. 4B). We plotted mean PC scores for WT, *tcp9*, *tcp20*, and *tcp9 tcp20* lines (Supplemental Fig. 4C) and used a one-way anova to confirm that there were no significant differences in leaf size and shape between lines.



Supplemental figure 4: Analysis of leaf shape and size. (A) Variation along the first four PCs for the Arabidopsis leaf-point model after a full Procrustes fit and a Principle Component (PC) analysis. The mean leaf of 1500 leaves together with leaves for 1 SD either side of the mean leaf are shown for each PC. Together, the four PCs represent 85.44% of the total variation in leaf shape. (B) Leaf point models for *Col-0* wild type (WT), *tcp9*, *tcp20* and *tcp9 tcp20* mutant plants. Leaves in node positions 5–12 have been calculated from mean PC1, PC2, PC3 and PC4 values for each leaf and then scaled to the appropriate mean size for each leaf. (C) Mean centroid size (in pixels) and PC scores for all leaves from nodes 5–11 for WT, *tcp9*, *tcp20* and *tcp9tcp20*. Error bars represent 95% confidence intervals. No significant differences in shape and size were detected.

Supplemental table 1: Potential direct TCP20 target genes

Values are given as difference between TCP20 JGR and WT experiment (each experiment consists of four arrays, TCP20 JGR, eight hours and zero hours after DEX treatment and the wild type controls)

AGI	experiment 1	experiment 2	Encoded protein (TAIR10)
AT1G01580	-3,476	-5,439	FERRIC REDUCTION OXIDASE 2 (FRO2)
AT1G02205	-3,941	-3,262	ECERIFERUM 1 (CER1)
AT1G03230	-2,190	-2,049	Eukaryotic aspartyl protease family protein
AT1G04040	-2,320	-4,728	HAD superfamily, subfamily IIIB acid phosphatase
AT1G04400	-2,181	-2,243	CRYPTOCHROME 2 (CRY2)
AT1G04430	2,616	2,106	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT1G04800	-2,698	-2,415	glycine-rich protein
AT1G05560	-2,869	-2,804	UDP-glucose transferase (UGT1)
AT1G06100	-2,660	-2,054	Fatty acid desaturase family protein
AT1G06360	-2,302	-2,431	Fatty acid desaturase family protein
AT1G06475	4,179	4,259	unknown protein
AT1G07400	4,067	4,295	HSP20-like chaperones superfamily protein
AT1G08570	-2,211	-2,729	ATYPICAL CYS HIS RICH THIOREDOXIN 4 (ACHT4)
AT1G08900	-3,310	-2,761	Major facilitator superfamily protein
AT1G09200	-2,413	-3,006	Histone superfamily protein
AT1G09240	3,635	3,229	NICOTIANAMINE SYNTHASE 3 (NAS3)
AT1G09380	2,884	2,076	nodulin MtN21 /EamA-like transporter family protein
AT1G09750	-2,530	-2,373	Eukaryotic aspartyl protease family protein
AT1G13300	-2,460	-3,479	HYPERSENSITIVITY TO LOW PI-ELICITED PRIMARY ROOT SHORTENING 1 (HRS1)
AT1G13607	-3,576	-5,245	Encodes a defensin-like (DEFL) family protein
AT1G13608	-4,555	-4,376	Encodes a defensin-like (DEFL) family protein
AT1G13609	-5,319	-8,077	Encodes a defensin-like (DEFL) family protein
AT1G15125	-2,797	-2,690	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT1G17345	2,965	3,382	SAUR-like auxin-responsive protein family
AT1G19510	2,508	2,335	RAD-like 5 (RL5)
AT1G21680	-2,884	-2,466	DPP6 N-terminal domain-like protein
AT1G22710	-3,283	-3,714	SUCROSE-PROTON SYMPORTER 2 (SUC2)
AT1G23020	-2,487	-2,614	FERRIC REDUCTION OXIDASE 3 (FRO3)
AT1G23110	-2,458	-2,095	unknown protein
AT1G23720	-2,648	-5,660	Proline-rich extensin-like family protein
AT1G24145	-2,652	-2,730	unknown protein
AT1G24147	-3,903	-2,876	unknown protein
AT1G25425	2,389	2,647	CLAVATA3/ESR-RELATED 43 (CLE43)
AT1G31580	-6,893	-4,848	Encodes cell wall protein (ECS1)

AGI	experiment 1	experiment 2	Encoded protein (TAIR10)
AT1G32560	3,080	3,110	LATE EMBRYOGENESIS ABUNDANT 4-1 (AtLEA4-1)
AT1G43970	-2,848	-2,110	unknown protein
AT1G45070	3,161	3,259	transposable element gene
AT1G45201	-4,143	-4,474	TRIACYLGLYCEROL LIPASE-LIKE 1 (TLL1)
AT1G45688	2,094	2,143	unknown protein
AT1G47400	-3,376	-4,359	unknown protein
AT1G48300	-2,528	-2,450	unknown protein
AT1G50160	2,798	2,020	BEST Arabidopsis thaliana protein match is: Polynucleotidyl transferase
AT1G52100	-2,508	-3,143	Mannose-binding lectin superfamily protein
AT1G52400	-2,589	-2,409	BETA GLUCOSIDASE 18 (BGLU18)
AT1G53690	3,210	2,724	Protein of unknown function that is homologous to At5g41010
AT1G54010	-2,168	-3,999	GDSL-like Lipase/Acylhydrolase superfamily protein
AT1G54740	2,023	2,308	Protein of unknown function (DUF3049)
AT1G54820	-2,032	-2,497	Protein kinase superfamily protein
AT1G55850	-2,970	-2,983	CELLULOSE SYNTHASE LIKE E1 (CSLE1)
AT1G56300	2,133	2,912	Chaperone DnaJ-domain superfamily protein
AT1G56430	-2,704	-3,283	NICOTIANAMINE SYNTHASE 4 (NAS4)
AT1G56600	-2,423	-2,617	GALACTINOL SYNTHASE 2 (GolS2)
AT1G59860	2,993	3,309	HSP20-like chaperones superfamily protein
AT1G61800	4,647	5,059	GLUCOSE-6-PHOSPHATE/PHOSPHATE TRANSLOCATOR 2 (GPT2)
AT1G62000	-2,272	-2,176	unknown protein
AT1G64370	-4,076	-3,040	unknown protein
AT1G64400	-2,859	-2,548	long-chain acyl-CoA synthetase 3 (LACS3)
AT1G65610	2,359	2,004	KORRIGAN 2 (KOR2)
AT1G66100	-2,673	-2,608	Predicted to encode a PR (pathogenesis-related) protein
AT1G66270	-2,259	-3,980	BETA GLUCOSIDASE 21 (BGLU21)
AT1G66940	-2,072	-2,342	protein kinase-related
AT1G67360	2,399	2,009	Rubber elongation factor protein (REF)
AT1G67865	-2,418	-3,321	unknown protein
AT1G67870	-3,287	-2,580	glycine-rich protein
AT1G67910	-2,392	-2,764	unknown protein
AT1G68190	-2,204	-2,037	B-box zinc finger family protein
AT1G69160	-2,402	-2,258	unknown protein
AT1G69530	-2,018	-2,309	EXPANSIN A1 (EXPA1)
AT1G71030	-2,768	-2,118	MYB-LIKE 2 (MYBL2)
AT1G71450	3,011	3,188	encodes a member of the DREB subfamily A-4 of ERF/AP2 transcription factor family
AT1G73260	2,644	2,094	KUNITZ TRYPSIN INHIBITOR 1 (KTI1)
AT1G73330	-3,107	-4,913	DROUGHT-REPRESSED 4 (DR4)

AGI	experiment 1	experiment 2	Encoded protein (TAIR10)
AT1G73920	-2,575	-2,168	alpha/beta-Hydrolases superfamily protein
AT1G74310	2,106	2,406	HEAT SHOCK PROTEIN 101 (HSP101)
AT1G74430	2,064	2,401	MYB DOMAIN PROTEIN 95 (MYB95)
AT1G74670	-4,022	-4,465	GA-STIMULATED ARABIDOPSIS 6 (GASA6)
AT1G75380	-2,682	-2,404	BIFUNCTIONAL NUCLEASE IN BASAL DEFENSE RESPONSE 1 (BBD1)
AT1G75390	2,139	2,124	basic leucine-zipper 44 (bZIP44)
AT1G76210	2,193	3,250	Arabidopsis protein of unknown function (DUF241)
AT1G76680	-2,781	-2,148	12-OXOPHYTODIENOATE REDUCTASE 1 (OPR1)
AT1G77760	-2,677	-2,563	NITRATE REDUCTASE 1 (NIA1)
AT1G78830	-2,031	-2,198	Curculin-like (mannose-binding) lectin family protein
AT1G80130	2,184	2,163	Tetratricopeptide repeat (TPR)-like superfamily protein
AT1G80180	-2,541	-2,295	unknown protein
AT1G80920	-3,160	-2,604	TRANSLOCON AT THE OUTER ENVELOPE MEMBRANE OF CHLOROPLASTS 12 (Toc12)
AT2G02990	2,822	2,920	RIBONUCLEASE 1 (RNS1)
AT2G06850	2,078	2,601	XYLOGLUCAN ENDOTRANSGLUCOSYLASE/HYDROLASE 4 (XTH4)
AT2G14635	-2,421	-3,338	unknown protein
AT2G16660	2,449	2,376	Major facilitator superfamily protein
AT2G17840	2,374	2,373	EARLY-RESPONSIVE TO DEHYDRATION 7 (ERD7)
AT2G19620	2,381	2,023	N-MYC DOWNREGULATED-LIKE 3 (NDL3)
AT2G20560	3,086	3,650	DNAJ heat shock family protein
AT2G21790	-2,224	-2,008	RIBONUCLEOTIDE REDUCTASE 1 (RNR1)
AT2G22122	-2,109	-2,614	unknown protein
AT2G22860	4,767	5,606	PHYTOSULFOKINE 2 PRECURSOR (PSK2)
AT2G23120	2,628	2,024	Late embryogenesis abundant protein, group 6
AT2G23130	2,402	2,151	ARABINOGALACTAN PROTEIN 17 (AGP17)
AT2G25770	4,179	3,168	Polyketide cyclase/dehydrase and lipid transport superfamily protein
AT2G26150	4,193	4,033	HEAT SHOCK TRANSCRIPTION FACTOR A2 (HSFA2)
AT2G27505	2,398	2,529	FBD-like domain family protein
AT2G27690	2,792	2,195	CYTOCHROME P450, FAMILY 94, SUBFAMILY C, POLYPEPTIDE 1 (CYP94C1)
AT2G29090	2,976	2,680	CYTOCHROME P450, FAMILY 707, SUBFAMILY A, POLYPEPTIDE 2 (CYP707A2)
AT2G29500	5,453	4,549	HSP20-like chaperones superfamily protein

AGI	experiment 1	experiment 2	Encoded protein (TAIR10)
AT2G32870	-2,631	-2,785	TRAF-like family protein
AT2G32880	-5,212	-6,125	TRAF-like family protein
AT2G33330	2,191	2,067	PLASMODESMATA-LOCATED PROTEIN 3 (PDLP3)
AT2G33570	2,517	2,292	Domain of unknown function (DUF23)
AT2G33830	-2,831	-2,707	Dormancy/auxin associated family protein
AT2G33850	-3,547	-4,105	unknown protein
AT2G34300	2,687	2,067	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT2G34430	-2,477	-2,242	LIGHT-HARVESTING CHLOROPHYLL-PROTEIN COMPLEX II SUBUNIT B1 (LHB1B1)
AT2G34600	3,124	2,653	jasmonate-zim-domain protein 7 (JAZ7)
AT2G34930	2,398	2,592	disease resistance family protein / LRR family protein
AT2G38240	3,454	3,021	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AT2G38465	2,757	2,221	unknown protein
AT2G39310	-2,796	-2,286	jacalin-related lectin 22 (JAL22)
AT2G39470	-2,233	-2,855	PsbP-like protein 2 (PPL2)
AT2G39800	-3,032	-2,257	1-PYRROLINE-5-CARBOXYLATE SYNTHASE 1 (P5CS1)
AT2G40020	-3,373	-2,184	Nucleolar histone methyltransferase-related protein
AT2G41240	-5,034	-5,894	BASIC HELIX-LOOP-HELIX PROTEIN 100 (BHLH100)
AT2G42740	-2,030	-2,429	RIBOSOMAL PROTEIN LARGE SUBUNIT 16A (RPL16A)
AT2G42750	-2,228	-2,167	DNAJ heat shock N-terminal domain-containing protein
AT2G42840	-3,336	-3,059	PROTODERMAL FACTOR 1 (PDF1)
AT2G44940	2,330	2,324	encodes a member of the DREB subfamily A-4 of ERF/AP2 transcription factor family
AT2G45170	-2,213	-3,356	AUTOPHAGY 8E (ATG8E)
AT2G45660	-2,823	-2,450	AGAMOUS-LIKE 20 (AGL20)
AT2G45680	2,310	1,910	TCP9
AT2G46220	-2,583	-2,233	Uncharacterized conserved protein (DUF2358)
AT2G46550	-2,110	-2,290	unknown protein
AT2G47270	3,159	2,341	UPBEAT1 (UPB1)
AT3G03280	2,071	2,679	unknown protein
AT3G04210	-2,743	-2,358	Disease resistance protein (TIR-NBS class)
AT3G05730	-3,758	-3,112	Encodes a defensin-like (DEFL) family protein
AT3G08770	-2,295	-2,161	LIPID TRANSFER PROTEIN 6 (LTP6)
AT3G08970	2,249	2,616	THERMOSENSITIVE MALE STERILE 1 (TMS1)
AT3G09260	-2,834	-2,825	Encodes beta-glucosidase (BGLU23)

AGI	experiment 1	experiment 2	Encoded protein (TAIR10)
AT3G09870	2,005	3,006	SAUR-like auxin-responsive protein family
AT3G12110	2,221	2,252	ACTIN-11 (ACT11)
AT3G12580	2,093	2,608	heat shock protein 70 (HSP70)
AT3G14200	2,375	2,555	Chaperone DnaJ-domain superfamily protein
AT3G14210	-2,573	-3,053	EPITHIOSPECIFIER MODIFIER 1 (ESM1)
AT3G14720	2,322	2,418	MAP KINASE 19 (MPK19)
AT3G14990	-2,029	-2,509	DJ-1 HOMOLOG A (DJ1A)
AT3G15356	-2,780	-2,439	Legume lectin family protein
AT3G15650	5,583	4,968	alpha/beta-Hydrolases superfamily protein
AT3G16400	-3,153	-3,010	NITRILE SPECIFIER PROTEIN 1 (NSP1)
AT3G16450	-3,039	-3,573	Mannose-binding lectin superfamily protein
AT3G16470	-2,755	-2,711	Mannose-binding lectin superfamily protein
AT3G16530	-2,425	-2,429	Lectin like protein
AT3G16700	-2,263	-2,059	Fumarylacetoacetate (FAA) hydrolase family
AT3G18290	-2,723	-2,767	BRUTUS (BTS)
AT3G19615	-2,652	-2,480	unknown protein
AT3G20060	-2,321	-2,772	UBIQUITIN-CONJUGATING ENZYME19 (UBC19)
AT3G20370	-2,339	-3,590	TRAF-like family protein
AT3G21352	2,283	2,543	unknown protein
AT3G25180	3,434	2,136	CYTOCHROME P450, FAMILY 82, SUBFAMILY G, POLYPEPTIDE 1 (CYP82G1)
AT3G25770	-2,213	-2,656	ALLENE OXIDE CYCLASE 2 (AOC2)
AT3G27060	-3,624	-3,043	TSO MEANING 'UGLY' IN CHINESE 2 (TSO2)
AT3G27360	-2,738	-3,015	Histone superfamily protein
AT3G27690	-2,944	-2,978	PHOTOSYSTEM II LIGHT HARVESTING COMPLEX GENE 2.3 (LHCB2.3)
AT3G28210	5,832	2,952	STRESS-ASSOCIATED PROTEIN 12 (SAP12)
AT3G29810	2,379	2,165	COBRA-like protein 2 precursor (COBL2)
AT3G45140	-2,881	-2,832	LIPOXYGENASE 2 (LOX2)
AT3G46230	3,340	2,898	HEAT SHOCK PROTEIN 17.4 (HSP17.4)
AT3G50770	2,476	2,032	calmodulin-like 41 (CML41)
AT3G51860	3,073	3,595	cation exchanger 3 (CAX3)
AT3G51970	2,687	2,355	acyl-CoA sterol acyl transferase 1 (ASAT1)
AT3G52720	-2,765	-2,976	CARBONIC ANHYDRASE 1 (CAH1)
AT3G53230	2,306	2,173	ATPase, AAA-type, CDC48 protein
AT3G54590	-2,099	-5,096	HYDROXYPROLINE-RICH GLYCOPROTEIN (ATHRGP1)
AT3G56360	-3,539	-2,465	unknown protein
AT3G56380	5,358	3,381	RESPONSE REGULATOR 17 (ARR17)
AT3G56970	-5,848	-6,661	BASIC HELIX-LOOP-HELIX PROTEIN 038 (BHLH038)
AT3G56980	-4,135	-4,178	BASIC HELIX-LOOP-HELIX PROTEIN 039 (BHLH039)
AT3G58790	2,972	2,599	GALACTURONOSYLTRANSFERASE 15 (GAUT15)

AGI	experiment 1	experiment 2	Encoded protein (TAIR10)
AT3G61210	-3,851	-2,646	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT3G62200	2,058	2,023	Putative endonuclease or glycosyl hydrolase
AT3G62410	-2,413	-2,503	CP12 DOMAIN-CONTAINING PROTEIN 2 (CP12-2)
AT3G62550	-2,767	-2,978	Adenine nucleotide alpha hydrolases-like superfamily protein
AT3G62760	2,182	2,597	Encodes glutathione transferase belonging to the phi class of GSTs (ATGSTF13)
AT3G63160	-3,284	-2,918	unknown protein
AT4G00695	3,178	2,064	unknown protein
AT4G00780	-4,841	-4,524	TRAF-like family protein
AT4G01250	2,380	2,279	AtWRKY22
AT4G01360	2,340	2,047	unknown protein
AT4G01640	2,974	3,018	F-box associated ubiquitination effector family protein
AT4G02160	2,967	3,533	unknown protein
AT4G02380	-2,841	-2,646	SENESCENCE-ASSOCIATED GENE 21 (SAG21)
AT4G02520	-2,281	-2,396	GLUTATHIONE S-TRANSFERASE PHI 2 (GSTF2)
AT4G03400	2,491	3,378	DWARF IN LIGHT 2 (DFL2)
AT4G05070	-2,311	-2,282	Wound-responsive family protein
AT4G07960	2,655	2,236	CELLULOSE-SYNTHASE-LIKE C12 (CSLC12)
AT4G09030	2,447	2,180	ARABINO GALACTAN PROTEIN 10 (AGP10)
AT4G11250	2,366	3,419	AGAMOUS-like 52 (AGL52)
AT4G11320	-3,898	-4,087	Papain family cysteine protease
AT4G12400	2,363	3,292	HOP3 (Hop3)
AT4G13570	2,081	3,041	HISTONE H2A 4 (HTA4)
AT4G14400	-4,239	-4,128	ACCELERATED CELL DEATH 6 (ACD6)
AT4G17245	-2,372	-2,369	RING/U-box superfamily protein
AT4G17670	2,805	2,869	Protein of unknown function (DUF581)
AT4G17770	2,708	2,591	TREHALOSE PHOSPHATASE/SYNTHASE 5 (TPS5)
AT4G19660	-2,279	-2,138	NPR1-LIKE PROTEIN 4 (NPR4)
AT4G19690	-4,525	-7,865	IRON-REGULATED TRANSPORTER 1 (IRT1)
AT4G19840	-3,184	-3,188	PHLOEM PROTEIN 2-A1 (PP2-A1)
AT4G21320	2,111	2,110	HEAT-STRESS-ASSOCIATED 32 (HSA32)
AT4G21445	-2,329	-2,117	unknown protein
AT4G21680	3,226	2,496	NITRATE TRANSPORTER 1.8 (NRT1.8)
AT4G23700	-2,609	-3,438	CATION/H+ EXCHANGER 17 (CHX17)
AT4G24800	-2,385	-2,019	EIN2 C-TERMINUS INTERACTING PROTEIN 1 (ECIP1)
AT4G25100	2,622	4,110	FE SUPEROXIDE DISMUTASE 1 (FSD1)
AT4G26530	-3,965	-3,695	Aldolase superfamily protein
AT4G27440	-2,607	-2,201	PROTOCHLOROPHYLLIDE OXIDOREDUCTASE B (PORB)

AGI	experiment 1	experiment 2	Encoded protein (TAIR10)
AT4G27860	-2,175	-2,037	vacuolar iron transporter (VIT) family protein
AT4G28780	-2,796	-2,384	GDSL-like Lipase/Acylhydrolase superfamily protein
AT4G32800	2,263	3,260	encodes a member of the DREB subfamily A-4 of ERF/AP2 transcription factor family
AT4G34560	-2,461	-2,093	unknown protein
AT4G34710	-3,033	-2,609	ARGININE DECARBOXYLASE 2 (ADC2)
AT4G34950	3,700	3,690	Major facilitator superfamily protein
AT4G35320	3,314	2,770	unknown protein
AT4G37925	-2,952	-3,085	SUBUNIT NDH-M OF NAD(P)H:PLASTOQUINONE DEHYDROGENASE COMPLEX (NDH-M)
AT4G37980	-2,772	-2,236	elicitor-activated gene 3-1 (ELI3-1)
AT4G39250	2,067	3,291	RAD-like 1 (RL1)
AT5G01380	3,746	3,197	Homeodomain-like superfamily protein
AT5G02490	3,813	3,643	Heat shock protein 70 (Hsp 70) family protein
AT5G02780	-2,459	-4,130	GLUTATHIONE TRANSFERASE LAMBDA 1 (GSTL1)
AT5G04150	-2,703	-3,125	BASIC-HELIX-LOOP-HELIX PROTEIN 100 (bHLH100)
AT5G04840	2,480	2,606	bZIP protein
AT5G05250	-3,960	-3,052	unknown protein
AT5G05365	4,254	4,687	Heavy metal transport/detoxification superfamily protein
AT5G05600	2,590	2,641	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AT5G06720	3,200	3,284	peroxidase 2 (PA2)
AT5G09220	-2,782	-3,262	AMINO ACID PERMEASE 2 (AAP2)
AT5G11360	2,075	2,196	Interleukin-1 receptor-associated kinase 4 protein
AT5G11790	2,607	2,538	N-MYC DOWNREGULATED-LIKE 2 (NDL2)
AT5G12020	4,664	3,606	17.6 KDA CLASS II HEAT SHOCK PROTEIN (HSP17.6II)
AT5G12030	2,180	2,548	HEAT SHOCK PROTEIN 17.6A (HSP17.6A)
AT5G13740	-2,386	-2,862	ZINC INDUCED FACILITATOR 1 (ZIF1)
AT5G16360	4,387	2,921	NC domain-containing protein-related
AT5G19530	-2,357	-2,204	NC domain-containing protein-related
AT5G20190	2,736	2,387	Tetratricopeptide repeat (TPR)-like superfamily protein
AT5G20630	-3,933	-3,442	GERMIN 3 (GER3)
AT5G21940	-2,517	-2,669	unknown protein
AT5G22545	2,252	2,572	unknown protein
AT5G22880	-2,411	-2,700	HISTONE H2B (H2B)

AGI	experiment 1	experiment 2	Encoded protein (TAIR10)
AT5G23820	-4,168	-6,441	MD-2-related lipid recognition domain-containing protein
AT5G24080	2,063	2,201	Protein kinase superfamily protein
AT5G24490	-2,292	-2,440	30S ribosomal protein, putative
AT5G25140	2,849	3,022	putative cytochrome P450
AT5G25460	-2,177	-2,407	Protein of unknown function, DUF642
AT5G25980	-2,679	-4,507	BETA GLUCOSIDASE 37 (BGLU37)
AT5G26000	-2,474	-2,339	BETA GLUCOSIDASE 38 (BGLU38)
AT5G26850	-2,116	-2,006	Uncharacterized protein
AT5G28800	3,041	2,084	unknown protein
AT5G37260	-4,315	-3,049	REVEILLE 2 (RVE2)
AT5G37540	2,137	2,168	Eukaryotic aspartyl protease family protein
AT5G39050	-2,070	-2,251	PHENOLIC GLUCOSIDE MALONYLTRANSFERASE 1 (PMAT1)
AT5G43380	2,749	2,394	TYPE ONE SERINE/THREONINE PROTEIN PHOSPHATASE 6 (TOPP6)
AT5G43570	4,058	3,399	Predicted to encode a PR (pathogenesis-related) peptide that belongs to the PR-6 proteinase inhibitor family
AT5G46890	-2,778	-5,002	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AT5G48485	-2,914	-2,167	DEFECTIVE IN INDUCED RESISTANCE 1 (DIR1)
AT5G48490	-4,847	-4,317	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AT5G48570	4,195	4,229	Encodes one of the 36 carboxylate clamp (CC)-tetratricopeptide repeat (TPR) proteins
AT5G51000	2,510	3,058	F-box and associated interaction domains-containing protein
AT5G51440	3,385	3,887	HSP20-like chaperones superfamily protein
AT5G52640	2,999	3,716	HEAT SHOCK PROTEIN 90.1 (HSP90.1)
AT5G53420	2,021	2,190	CCT motif family protein
AT5G53450	-3,014	-2,987	OBP3-responsive gene 1 (ORG1)
AT5G54030	2,367	2,446	Cysteine/Histidine-rich C1 domain family protein
AT5G55970	-2,416	-2,838	RING/U-box superfamily protein
AT5G57220	-3,308	-2,858	CYTOCHROME P450, FAMILY 81, SUBFAMILY F, POLYPEPTIDE 2 (CYP81F2)
AT5G58750	2,331	2,674	NAD(P)-binding Rossmann-fold superfamily protein
AT5G59400	3,020	2,410	unknown protein
AT5G59690	-2,453	-3,059	Histone superfamily protein
AT5G59870	-2,457	-2,681	NAD(P)-binding Rossmann-fold superfamily protein

AGI	experiment 1	experiment 2	Encoded protein (TAIR10)
AT5G60680	-2,450	-2,378	unknown protein
AT5G61270	2,686	2,741	PHYTOCHROME-INTERACTING FACTOR7 (PIF7)
AT5G63810	-2,092	-2,253	BETA-GALACTOSIDASE 10 (BGAL10)
AT5G64190	2,547	3,032	unknown protein
AT5G65470	2,525	2,784	O-fucosyltransferase family protein

Supplemental table 2: Primers used in this study

In the first half the primers that have been used for ChIP-PCR analyses detecting binding of TCP20 on the LOX2 and the TCP9 promoters are depicted. Given are the names of the fragments and promoters, product length and the sequences for forward and reverse primers. In the second part primers analyzed for the effect of TCP20 on target gene transcripts are given, along with the AGIs the common gene names of these targets and the forward and reverse primers used for the analysis.

Promoter fragment	Product length (bp)	Forward primer (5'→3')	Reverse primer (5'→3')
pLOX2neg-5283	157	CTCATATATCAAAGGAATTTACAATAT	GAATATTTAACCCAATTTTGAATTCA
pLOX2neg-4464	142	GCAGGTAATGTGGGAGATTAAAA	CTCATCTTATAAATATATAGAGAGGT
pLOX2neg-3663	117	GCATTTTCGTTTTCCATTTACTTAA	CTTTCTTCATACTTAAACTCATAAC
TGGGC	142	CATGAGATGTTTTAACCGTTCTAAGT	ATTAACAATTGTTGGCTATATACTCC
GCCCG	131	CCCACTTTTCTCAAGAAGATCATT	CTCAACATACCATTTTATCACGT
TCP4 BS1	96	TGTTACACATTACTTGATGTTTTTC	TTCTGCGCTTTGTTGTCTAAATAG
TCP4 BS2	93	CCACCTAAAAGTACAGGATATGATTTCT	ATGGCCGGTTCCTCCAAAAGTAC
pTCP9	63	TTGGGCCTAGCCCTCAACAAT	GTCCAGCTCAGGCCACATT
TCP4 BS3	99	GATGAAAAGAGCTGCATTCT	CATCACATGCAATATCGGGTAAGGTCA
AGI	Common gene name	Forward primer (5'→3')	Reverse primer (5'→3')
At2g28390	<i>SAND-family protein</i>	AACTCTATGCAGCATTTGATCCACT	TGATTGCATATCTTTATCGCCATC
At3g15030	<i>TCP4</i>	TTCGGAAGGATTACAGAGACTAGTGG	AGGAGTAGGAGGAGCGAACAGAAAC
At3g27010	<i>TCP20</i>	TTAGGCTTGCTCAAGAAGGGAATG	GCATATGGTGAAGAACCCTACCTTG
At3g45140	<i>LOX2</i>	GATGCCCCAGTTCTCATAACAGGG	CGGGTCTAGTTTGTCTATTAACGGC
At2g45680	<i>TCP9</i>	TGCCGTCGTTTTCAATGTCTTTAGC	TTCTCCCTTCTCTTCAACCTTCG
At4g34270	<i>TIP41-like protein</i>	GTGAAAAGTGTGGAGAGAAGCAA	TCAACTGGATACCTTTTCGCA
At1g72010	<i>TCP22</i>	GTAGTAACTGCACCAATGGGGTCA	CCAAACCATCGCTCTACTGCC
At1g58100	<i>TCP8</i>	CAAATGGAGAGTAGTAGCAACAATA	GTAAGTATCCATCGGAAAAGTAAA