

SI Materials and Methods

Whole Genome Re-sequencing of Wild Barley Genotypes from the Tabigha

Evolution Slope. Genomic DNA was extracted from the third fully expanded leaves of 13 barley plants using QIAamp Plant DNA Mini Kit (Qiagen, Germantown, MD, USA). DNA concentration and quality was analyzed using Qubit dsDNA HS Assay Kit (Life Technologies, Carlsbad, CA, USA) and agarose gels. DNA libraries were constructed using an Illumina Nextera DNA Library Prep Kit (Illumina, San Diego, CA, USA). DNA paired-end libraries were subjected to 2×150 bp sequencing using a whole genome shotgun sequencing strategy (Illumina HiSeq X Ten sequencing platform, San Diego, CA, USA).

Variant Calling. Clean reads of each sample were aligned against the reference genome of barley, cv. Zangqing320 (1) using BWA v0.7.5a-r405 (2). SAM files were sorted, converted to BAM files, and duplicated reads removed using Picard v1.9 (<http://picard.sourceforge.net>). Uniquely mapped reads were used for the SNVs and *InDels* calling with the Genome Analysis ToolKit (GATK) v3.6 (3). Raw SNVs were filtered according to the criterion that there were at most 3 and 2 gaps in wild barley populations inhabiting Terra Rossa and Basalt soils, respectively. As a result, we obtained 19,615,087 high-quality SNVs randomly distributed on all chromosomes for further population structure analysis and genetic divergence analysis.

Drought Treatment and Sampling of Wild Barley Genotypes from Evolution

Canyon I in Mount Carmel (ECI). Ten wild barley genotypes from ECI (Table S3)

were used to perform transcriptome analysis under drought treatment: five genotypes

from Station 2 (African Slope, AS) and five genotypes from Station 6 (European Slope, ES) (4). Seeds of all genotypes were sown in plastic pots (170 mm × 220 mm) filled with peat in a net house on November 14th 2015. All the pots were well watered before sown and stopped watering after the third leaf stage, except the control. All of the plants continued to grow for another 80 days in winter. During the 80 days growth, the water content of the peat was reduced slowly and treated plants were exposed to a long-term mild drought treatment. After treatment, the fully expanded leaves of both control and treated plants were sampled with three biological replicates, and flash frozen in liquid nitrogen for RNA extraction. Sampling time for all samples occurred four hours into the light phase.

Transcriptome Sequencing Analysis. Total RNA extraction, purification, quality-checking, library construction and paired-end (2×150 bp) sequencing were performed as described previously (5-7). After removing all adaptor sequences, empty reads and low quality reads (Q < 30 and length < 50 bp) from raw reads, clean reads were obtained. Hisat2 v2.0.4 (8) was used to map clean reads to the reference genome of barley, cv. Zangqing320 (1), with parameters of ‘--dta --score-min L,0,-0.8 -5 10 -3 10’. SAM files created by Hisat2 were converted to BAM files using SAM-tools view (9), and then BAM files were analyzed using bam_stat.py of RSeQC v 2.6.4 (10) for quality control analysis, which includes the statistics of unmapped reads, splice reads, and reads mapped in proper pairs. Raw SNVs and *InDels* were called with SAM-tools mpileup and bcftools (9) and then filtered with mapping quality scores ≥ 25 and reads coverage > 2 . HTSeq v 0.6.1 (11) was used to count the mapped reads based on the SAM

files created by Hisat2. The edgeR package (version 3.14.0) (12) was used for differential expression analysis of transcripts based on counts generated by HTSeq. Read counts were normalized using the method of counts per million (CPM), and differentially expressed genes (DEGs) were selected according to the criterion of “FDR < 0.01 and $|\log_2(\text{fold-change})| > 2$ ”. Fold-change referred to the ratio of [CPM (drought treatment)] / [CPM (control)] or [CPM (control)] / [CPM (drought treatment)]. Volcano plots were constructed using $-\log_{10}(\text{FDR})$ versus the $\log_2(\text{fold change})$, and the red points located in the upper-left and upper-right quadrants represented DEGs (Fig. S3). The genes, differentially expressed in at least four samples from the AS (or ES), but not differentially expressed in samples from the other slope were identified as DEGs. Gene annotation was conducted using Blast2GO v4.1.5 (13). In order to determine the genetic divergence of the two populations from ECI, we constructed a data set containing 120,474 SNVs with homozygous loci and without missing data in the ten wild barley genotypes to avoid unreliable inferences caused by missing and multiple variation sites.

Gas exchange measurement

For phenotypic analysis, seeds of ten wild barley genotypes (see Fig. S1) from the Evolution Canyon I were sown in 4 L pots with potting mixture (peat:vermiculite = 1:1). Seedlings were thinned to 5 healthy and uniform plants per pot 10 days after sowing with 3 replicates for both control and drought treatment. Plants were grown in a greenhouse at 22 ± 2 °C (day) and 20 ± 2 °C (night) ~60 % relative humidity (RH), 12 h/12 h light/dark cycle with the average photo-synthetically active radiation (PAR) of $\sim 400 \mu\text{mol m}^{-2} \text{s}^{-1}$. All plants were well-watered to maintain a water holding capacity

(~50% v/v) before drought treatment. Slow release fertilizer was applied before sowing and after tillering. Drought treatment was commenced at Week 5 by controlled watering (50 ml H₂O in each pot every other day) until the water holding capacity decreased to 10% (v/v), which was maintained for 3 weeks. Leaf samples were used for gas exchange measurement (14, 15) at Week 8. Net CO₂ assimilation (*A*) and stomatal conductance (*g_s*) were measured on third fully expanded leaves using an LI-6400 infrared gas analyzer (Li-Cor Inc., Lincoln, NE, USA). The measurements were conducted at both control (three days before drought) and treatment (nine days after drought) with six replicates for each genotype and treatment. Intrinsic leaf water use efficiency was calculated as *A/g_s*. The conditions in measuring chamber were controlled at a flow rate of 500 mol s⁻¹, a saturating PAR of 1500 mol m⁻² s⁻¹, 400 mmol mol⁻¹ CO₂, and a relative humidity of 60%.

References

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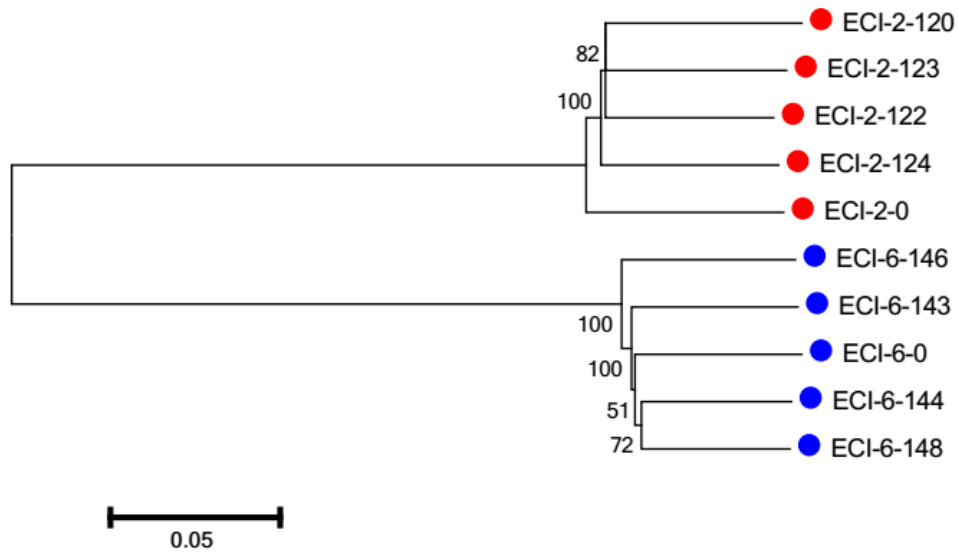
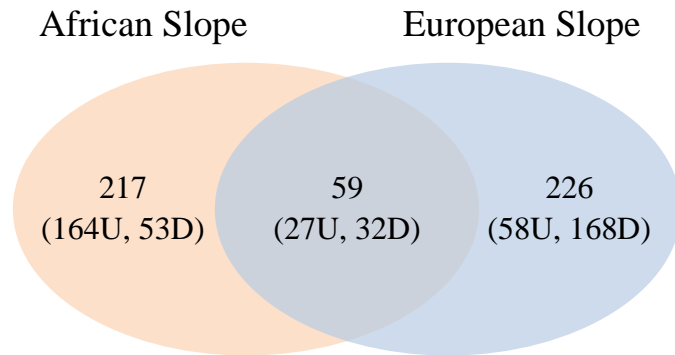


Figure S1. Phylogenetic tree of wild barley genotypes from the two slopes at Evolution Canyon I (ECI) at Mount Carmel, Israel. ECI-2: Station 2 of ECI on the African Slope. ECI-6: Station 6 of ECI on the European Slope. Phylogenetic tree was constructed using the neighbor-joining methods and the percentages of trees from 1,000 bootstrap replications in which the associated taxa clustered together are shown next to the branches.

A



B

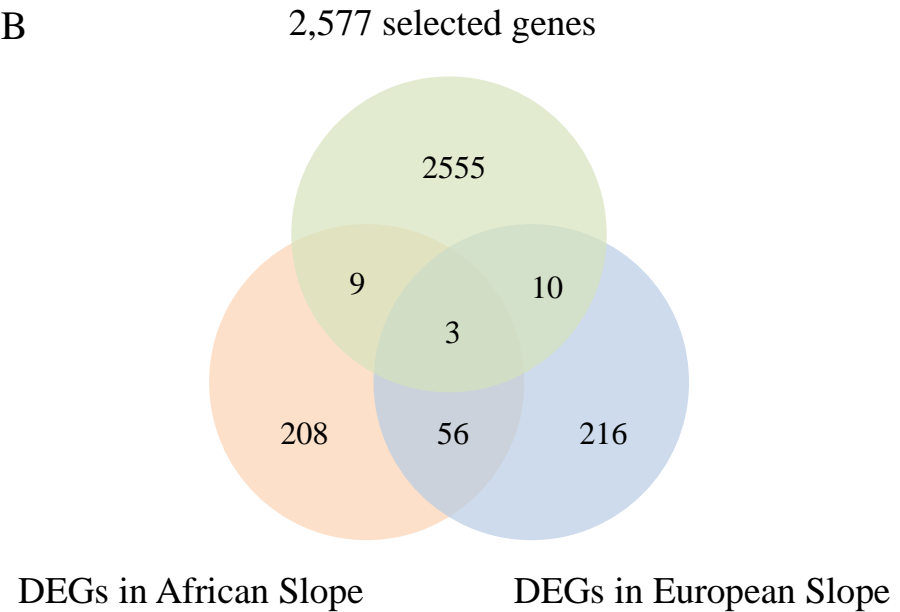


Figure S2. Venn diagrams of common and specific genes in wild barley. (A) Common and specific differentially expressed genes (DEGs) under drought stress in wild barley populations from the African and European Slope of Evolution Canyon I at Mount Carmel (ECI), Israel. U: up-regulated; D: down-regulated. (B) Common and unique genes between the 2,577 selected genes in the selected regions of genotypes from Terra Rossa and Basalt soil types at the Tabigha Evolution Slope and 502 DEGs in the populations of the African and European Slopes of ECI.

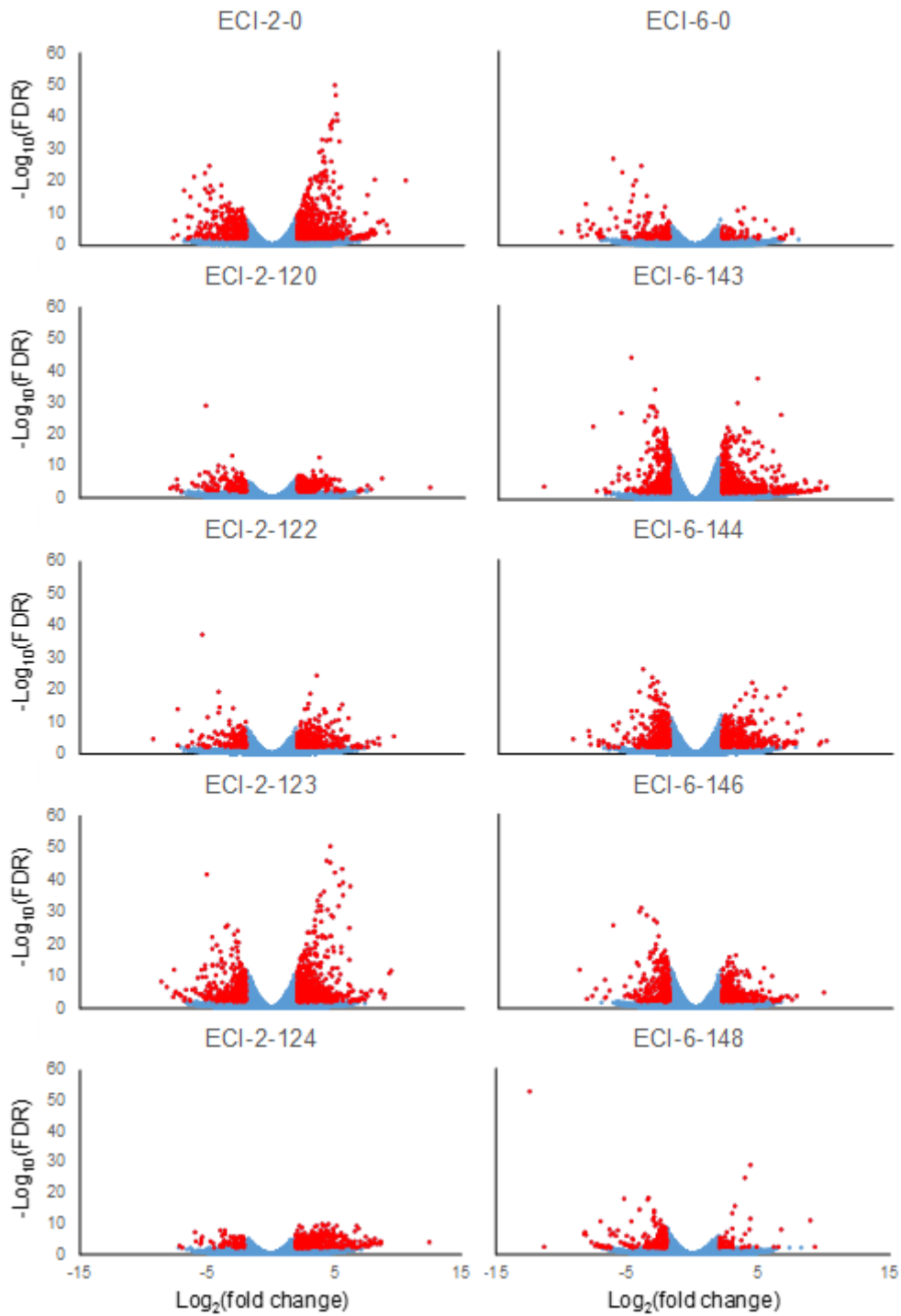


Figure S3. Volcano plot of differentially expressed genes in genotypes from Evolution Canyon I at Mount Carmel.

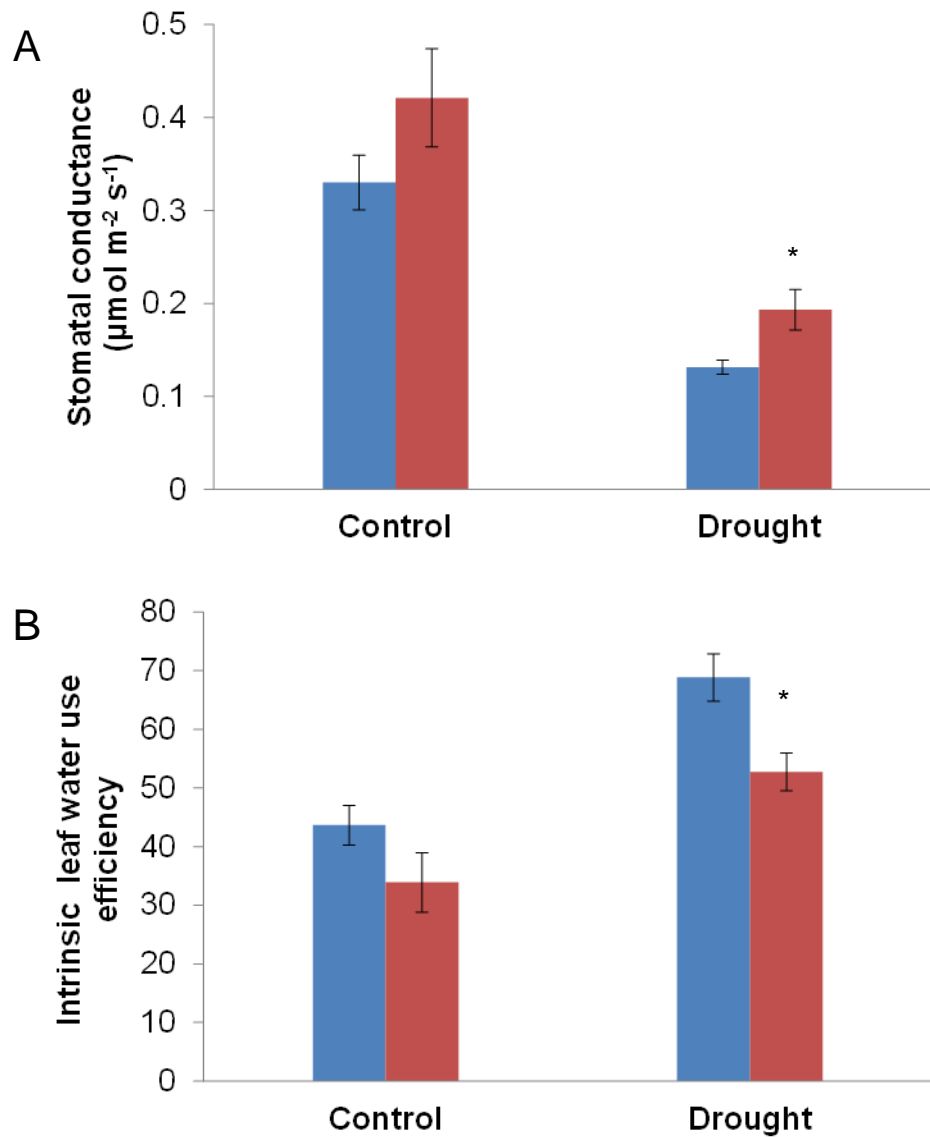


Figure S4. Photosynthetic performance of ten different barley genotypes from Evolution Canyon I (ECI) at Mount Carmel with contrasting drought tolerance. Stomatal conductance (g_s , A) and intrinsic leaf water use efficient (B) were measured in the control and under drought treatment. Data are averages of five genotypes from both African Slope (blue bars) and European Slope (red bars). * $P < 0.05$.

Table S1. Output statistics of whole-genome re-sequencing of wild barley genotypes from the Tabigha Evolution Slope.

| Sample | Raw Reads | Raw Data (Gb) | Clean Reads | Clean Data (%) | Mapped Ratio (%) | SNVs/ <i>InDels</i> | Data Accession |
|----------------|-------------|---------------|-------------|----------------|------------------|---------------------|----------------|
| Terra Rossa110 | 835,596,946 | 125.34 | 806,351,052 | 87.83 | 86.79 | 24,783,387 | SRR6281634 |
| Terra Rossa169 | 781,935,470 | 117.29 | 758,477,406 | 88.29 | 88.4 | 26,237,698 | SRR6281638 |
| Terra Rossa104 | 749,858,260 | 112.48 | 712,365,346 | 86.49 | 89.21 | 25,031,804 | SRR6281632 |
| Terra Rossa109 | 767,760,476 | 115.16 | 745,495,422 | 88.29 | 85.99 | 26,637,793 | SRR6281633 |
| Terra Rossa122 | 767,090,304 | 115.06 | 740,242,144 | 88.24 | 85.96 | 24,710,134 | SRR6281635 |
| Terra Rossa161 | 834,786,770 | 125.22 | 805,569,234 | 89.32 | 88.24 | 26,270,537 | SRR6281636 |
| Terra Rossa166 | 752,785,468 | 112.92 | 703,854,412 | 87.67 | 89.2 | 26,937,684 | SRR6281637 |
| Basalt63 | 724,028,218 | 108.6 | 684,206,666 | 88.5 | 89.42 | 16,053,119 | SRR6281626 |
| Basalt59 | 714,752,782 | 107.21 | 675,441,378 | 90.72 | 91.01 | 18,847,951 | SRR6281627 |
| Basalt99 | 710,181,162 | 106.53 | 671,121,198 | 90.32 | 89.95 | 17,492,176 | SRR6281631 |
| Basalt60 | 727,748,214 | 109.16 | 687,722,062 | 90.1 | 88.3 | 27,020,003 | SRR6281628 |
| Basalt76 | 684,304,838 | 102.65 | 646,668,070 | 90.47 | 88.99 | 25,684,369 | SRR6281629 |
| Basalt77 | 692,651,544 | 103.9 | 654,555,708 | 90.77 | 89.13 | 26,666,170 | SRR6281630 |

Table S2. Drought adaptive genes in selection sweep regions of the Tabigha Evolution Slope.

| Category | Gene_ID ¹ | Chr | Gene_Start | Sequence Description ² |
|-----------------------|----------------------|------------|--|--|
| ABA signaling pathway | MLOC_7007 | 2H | 666,198,589 | cytochrome P450 704C1-like |
| | MLOC_49654 | 3H | 142,782,985 | abscisic acid receptor PYL2 |
| | ZLOC_8934 | 5H | 74,319,028 | SNF1-type serine-threonine kinase |
| | ZLOC_3966 | 2H | 700,027,349 | ABSCISIC ACID-INSENSITIVE 5 2 |
| | MLOC_10399 | 2H | 700,120,061 | ABSCISIC ACID-INSENSITIVE 5 2 |
| | MLOC_7520 | 3H | 33,302,188 | LRR receptor-like serine threonine- kinase RPK2 |
| | MLOC_12939 | 6H | 290,666,349 | phosphatase 2C 12 |
| | ZLOC_11905 | 6H | 219,505,848 | phosphatase 2C and cyclic nucleotide-binding kinase domain-containing isoform X1 |
| | MLOC_81883 | 6H | 210,951,191 | probable phosphatase 2C 12 |
| | MLOC_15036 | 6H | 246,752,202 | probable phosphatase 2C 14 |
| | ZLOC_21849 | 3H | 201,415,581 | probable phosphatase 2C 38 isoform X1 |
| | MLOC_19687 | 1H | 525,201,985 | probable phosphatase 2C 50 |
| | ZLOC_9683 | 5H | 434,376,296 | probable phosphatase 2C 67 |
| | MLOC_65528 | 3H | 447,897,316 | probable phosphatase 2C 8 |
| | MLOC_67347 | 2H | 665,419,081 | guard cell S-type anion channel SLAC1 |
| | ZLOC_3757 | 2H | 665,504,656 | guard cell S-type anion channel SLAC1 |
| | ZLOC_30254 | 7H | 256,199,517 | S-type anion channel SLAH1-like |
| | ZLOC_21671 | 3H | 150,671,151 | S-type anion channel SLAH2-like |
| | ZLOC_1443 | 1H | 524,774,783 | probable calcium-binding CML11 |
| | MLOC_72577 | 3H | 139,746,142 | V-type proton ATPase subunit E |
| MLOC_34557 | 5H | 72,978,018 | calcium-transporting ATPase plasma membrane-type | |
| Auxin related | ZLOC_14091 | 7H | 243,622,097 | auxin response factor 8-like |
| | MLOC_38622 | 7H | 255,567,804 | auxin-independent growth promoter |
| | ZLOC_30563 | 7H | 376,319,567 | Auxin-induced 5NG4 |

| Category | Gene_ID ¹ | Chr | Gene_Start | Sequence Description ² |
|----------------------------|----------------------|-----|-------------|---|
| Auxin related | ZLOC_29553 | 7H | 68,185,223 | auxin-responsive SAUR36-like |
| Casparian strip regulation | ZLOC_3498 | 2H | 586,705,851 | LRR receptor-like serine threonine- kinase GSO1 |
| | ZLOC_12039 | 6H | 295,114,404 | LRR receptor-like serine threonine- kinase GSO2 |
| Proline related | ZLOC_14223 | 7H | 312,259,072 | hydroxyproline O-galactosyltransferase HPGT1 |
| | MLOC_16417 | 7H | 312,371,346 | hydroxyproline O-galactosyltransferase HPGT1 |
| | MLOC_52074 | 2H | 688,281,282 | kDa proline-rich -like |
| | ZLOC_3871 | 2H | 688,324,355 | kDa proline-rich -like |
| | ZLOC_12177 | 6H | 343,036,273 | proline iminopeptidase |
| | MLOC_40538 | 6H | 273,860,372 | proline-rich 36-like |
| | MLOC_59853 | 7H | 277,519,736 | proline-rich 36-like |
| | ZLOC_30331 | 7H | 289,434,000 | proline-rich 36-like |
| | MLOC_81942 | 3H | 151,509,284 | proline-rich receptor kinase PERK1 |
| | ZLOC_11958 | 6H | 243,448,886 | proline-rich receptor kinase PERK2 |
| Protein phosphorylation | ZLOC_3866 | 2H | 687,790,011 | LRR receptor-like serine threonine- kinase |
| | ZLOC_3867 | 2H | 687,837,207 | LRR receptor-like serine threonine- kinase |
| | ZLOC_18566 | 1H | 525,063,547 | LRR receptor-like serine threonine- kinase FLS2 |
| | MLOC_6082 | 2H | 702,258,838 | LRR receptor-like serine threonine- kinase FLS2 |
| | ZLOC_4949 | 3H | 55,668,676 | LRR receptor-like serine threonine- kinase FLS2 |
| | MLOC_14999 | 2H | 742,055,230 | probable LRR receptor-like serine threonine- kinase At3g47570 |
| | MLOC_57098 | 5H | 389,250,407 | probable LRR receptor-like serine threonine- kinase At4g37250 |
| | ZLOC_11866 | 6H | 196,272,203 | LRR receptor-like serine threonine- kinase MRH1 |
| | ZLOC_11976 | 6H | 251,967,446 | LRR receptor-like serine threonine- kinase |
| | ZLOC_12175 | 6H | 343,007,636 | CBL-interacting kinase 19 |
| | MLOC_57740 | 5H | 461,331,278 | serine threonine- kinase BLUS1 |
| | MLOC_67098 | 2H | 741,342,644 | G-type lectin S-receptor-like serine threonine- kinase B120 |

| Category | Gene_ID ¹ | Chr | Gene_Start | Sequence Description ² |
|-------------------------|----------------------|-----|-------------|--|
| Protein phosphorylation | MLOC_21948 | 2H | 743,876,310 | Lectin-domain containing receptor kinase |
| | MLOC_64374 | 3H | 33,599,589 | serine threonine- phosphatase PP1-gamma catalytic subunit |
| | MLOC_44139 | 7H | 67,926,864 | Phosphoinositide phosphatase SAC2 |
| Root morphology | ZLOC_3610 | 2H | 625,736,825 | ROOT PRIMORDIUM DEFECTIVE 1 |
| | MLOC_30847 | 2H | 625,804,675 | ROOT PRIMORDIUM DEFECTIVE 1 |
| | ZLOC_14125 | 7H | 262,421,503 | Root hairless 1 |
| ROS and NO signaling | MLOC_17760 | 7H | 274,187,252 | Cu Zn superoxide dismutase (chloroplast) |
| | MLOC_76615 | 2H | 666,214,528 | Copper chaperone for superoxide dismutase |
| | MLOC_72880 | 2H | 741,549,713 | manganese superoxide dismutase |
| | ZLOC_22743 | 3H | 503,150,926 | Peroxidase 19 |
| | MLOC_3293 | 2H | 701,010,839 | nitrate-induced NOI |
| | ZLOC_22743 | 3H | 503,150,926 | Peroxidase 19 |
| | ZLOC_22744 | 3H | 503,160,467 | peroxidase 19 |
| | ZLOC_26291 | 5H | 433,871,551 | peroxidase 1-like |
| | ZLOC_20810 | 2H | 539,032,335 | Peroxidase 72 |
| | ZLOC_4418 | 2H | 755,300,759 | Peroxidase 9 |
| | MLOC_6127 | 7H | 250,818,888 | probable L-ascorbate peroxidase 4 |
| | MLOC_4571 | 2H | 757,374,943 | probable phospholipid hydroperoxide glutathione peroxidase |
| | MLOC_24804 | 5H | 464,286,186 | glutathione gamma-glutamylcysteinyltransferase 1 |
| | ZLOC_4452 | 2H | 759,052,033 | glutathione S-transferase |
| | ZLOC_4453 | 2H | 759,083,535 | glutathione S-transferase |
| | ZLOC_4454 | 2H | 759,090,571 | glutathione S-transferase |
| | ZLOC_4437 | 2H | 756,549,871 | glutathione S-transferase T3-like |
| | ZLOC_21669 | 3H | 150,394,632 | glutathione S-transferase T3-like |
| | MLOC_3747 | 6H | 249,093,590 | glutathione S-transferase T3-like |

| Category | Gene_ID ¹ | Chr | Gene_Start | Sequence Description ² |
|-----------------------|----------------------|-----|-------------|--|
| ROS and NO signaling | ZLOC_30187 | 7H | 234,643,614 | glutathione S-transferase T3-like |
| | ZLOC_30310 | 7H | 280,735,221 | glutathione S-transferase T3-like |
| | MLOC_25093 | 2H | 675,853,757 | glutathione S-transferase T3-like isoform X1 |
| Stomatal development | MLOC_51546 | 2H | 674,729,589 | mitogen-activated kinase kinase kinase YODA |
| | MLOC_17359 | 2H | 625,729,197 | TOO MANY MOUTHS |
| Transcription factors | MLOC_6171 | 7H | 73,006,176 | MYB-A1 |
| | MLOC_39910 | 7H | 276,679,000 | NAC domain containing 71 |
| Transporters | MLOC_56261 | 2H | 701,170,173 | ABC transporter C family member 2 |
| | MLOC_11780 | 2H | 689,120,698 | potassium transporter 15 |
| | MLOC_60308 | 6H | 337,120,592 | high-affinity nitrate transporter-activating -like |
| | MLOC_55066 | 2H | 691,917,158 | cation transporter HKT4-like |
| | ZLOC_25185 | 5H | 73,840,401 | cation H(+) antiporter 15-like |
| | MLOC_64607 | 7H | 255,782,878 | cation-chloride cotransporter 1 isoform X1 |

¹ refer to Dai F et al. (2017) *Plant Biotechnol J* DOI: 10.1111/pbi.12826. (http://www.ibgs.zju.edu.cn/ZJU_barleygenome.htm), ² detailed in Dataset 1.

Table S3. Mapping RNA-Seq reads of wild barley populations from ECI to the reference genome of barley cv. Zangqing320.

| Group | Sample | Raw reads | Raw bases | Clean reads | Clean bases | Clean data rate (%) | Mapped reads (%) | Data accession |
|---------------|--------------|-------------|----------------|-------------|----------------|---------------------|------------------|----------------|
| African Slope | ECI-2-0_C1 | 41,720,294 | 6,258,044,100 | 41,555,472 | 6,194,263,132 | 98.98 | 93.35 | SRR3628735 |
| | ECI-2-0_C2 | 40,498,996 | 6,074,849,400 | 40,321,634 | 6,005,988,142 | 98.87 | 89.75 | SRR3628736 |
| | ECI-2-0_C3 | 42,518,958 | 6,377,843,700 | 42,369,218 | 6,326,904,969 | 99.2 | 93.5 | SRR3628737 |
| | ECI-2-0_T1 | 68,547,566 | 10,282,134,900 | 68,312,690 | 10,187,698,658 | 99.08 | 93.02 | SRR3628738 |
| | ECI-2-0_T2 | 63,653,536 | 9,548,030,400 | 63,384,656 | 9,405,777,402 | 98.51 | 92.73 | SRR3628739 |
| | ECI-2-0_T3 | 78,013,364 | 11,702,004,600 | 77,655,744 | 11,537,253,756 | 98.59 | 92.84 | SRR3653597 |
| | ECI-2-120_C1 | 87,629,632 | 13,144,444,800 | 87,279,394 | 13,003,798,025 | 98.93 | 91.47 | SRR3628845 |
| | ECI-2-120_C2 | 67,411,054 | 10,111,658,100 | 67,139,600 | 10,006,719,150 | 98.96 | 95.36 | SRR3628846 |
| | ECI-2-120_C3 | 50,519,956 | 7,577,993,400 | 50,303,826 | 7,502,629,852 | 99.01 | 91.26 | SRR3628847 |
| | ECI-2-120_T1 | 39,652,482 | 5,947,872,300 | 39,494,062 | 5,891,841,794 | 99.06 | 91.91 | SRR3628848 |
| | ECI-2-120_T2 | 43,282,242 | 6,492,336,300 | 43,071,588 | 6,380,591,141 | 98.28 | 93.68 | SRR3628849 |
| | ECI-2-120_T3 | 29,004,742 | 4,350,711,300 | 28,914,094 | 4,319,045,707 | 99.27 | 93.55 | SRR3628850 |
| | ECI-2-122_C1 | 68,412,610 | 10,261,891,500 | 68,126,718 | 10,173,780,754 | 99.14 | 92.12 | SRR3628851 |
| | ECI-2-122_C2 | 27,681,906 | 4,152,285,900 | 27,567,866 | 4,110,297,019 | 98.99 | 90 | SRR3628852 |
| | ECI-2-122_C3 | 31,363,966 | 4,704,594,900 | 31,247,924 | 4,668,121,507 | 99.22 | 94.1 | SRR3628854 |
| | ECI-2-122_T1 | 38,814,674 | 5,822,201,100 | 38,658,764 | 5,752,688,144 | 98.81 | 92.82 | SRR3628855 |
| | ECI-2-122_T2 | 79,997,426 | 11,999,613,900 | 79,760,732 | 11,917,932,650 | 99.32 | 92.82 | SRR3628856 |
| | ECI-2-122_T3 | 66,590,446 | 9,988,566,900 | 66,382,806 | 9,911,907,855 | 99.23 | 93.12 | SRR3628857 |
| | ECI-2-123_C1 | 101,023,592 | 15,153,538,800 | 100,508,132 | 14,970,875,661 | 98.79 | 92.33 | SRR3628858 |
| | ECI-2-123_C2 | 64,095,920 | 9,614,388,000 | 63,771,020 | 9,484,994,596 | 98.65 | 91.94 | SRR3628859 |
| | ECI-2-123_C3 | 47,472,704 | 7,120,905,600 | 47,223,780 | 7,024,382,838 | 98.64 | 92.57 | SRR3628896 |
| | ECI-2-123_T1 | 34,857,756 | 5,228,663,400 | 34,691,102 | 5,153,460,516 | 98.56 | 93.98 | SRR3628905 |
| | ECI-2-123_T2 | 35,376,068 | 5,306,410,200 | 35,246,840 | 5,257,020,238 | 99.07 | 96.67 | SRR3628906 |
| | ECI-2-123_T3 | 77,761,018 | 11,664,152,700 | 77,404,792 | 11,525,688,325 | 98.81 | 94.12 | SRR3628907 |

| Group | Sample | Raw reads | Raw bases | Clean reads | Clean bases | Clean data rate (%) | Mapped reads (%) | Data accession |
|----------------|--------------|-------------|----------------|-------------|----------------|---------------------|------------------|----------------|
| | ECI-2-124_C1 | 41,550,694 | 6,232,604,100 | 41,403,510 | 6,181,740,298 | 99.18 | 93.14 | SRR3628908 |
| | ECI-2-124_C2 | 75,318,864 | 11,297,829,600 | 75,083,486 | 11,223,747,472 | 99.34 | 92.32 | SRR3628909 |
| | ECI-2-124_C3 | 43,180,988 | 6,477,148,200 | 43,004,894 | 6,419,091,425 | 99.1 | 91.02 | SRR3628910 |
| | ECI-2-124_T1 | 50,130,816 | 7,519,622,400 | 49,962,228 | 7,447,497,008 | 99.04 | 93.58 | SRR3628911 |
| | ECI-2-124_T2 | 28,204,994 | 4,230,749,100 | 28,121,970 | 4,195,210,882 | 99.16 | 93.03 | SRR3628912 |
| | ECI-2-124_T3 | 135,408,502 | 20,311,275,300 | 133,084,724 | 18,573,637,964 | 91.44 | 94.43 | SRR3628913 |
| European Slope | ECI-6-143_C1 | 93,136,944 | 13,970,541,600 | 92,687,696 | 13,797,482,461 | 98.76 | 92.2 | SRR3628920 |
| | ECI-6-143_C2 | 62,536,610 | 9,380,491,500 | 62,306,292 | 9,307,110,858 | 99.22 | 91.49 | SRR3628921 |
| | ECI-6-143_C3 | 30,911,654 | 4,636,748,100 | 30,792,250 | 4,594,312,034 | 99.08 | 94.63 | SRR3628922 |
| | ECI-6-143_T1 | 33,279,290 | 4,991,893,500 | 33,057,286 | 4,834,236,180 | 96.84 | 93.25 | SRR3628923 |
| | ECI-6-143_T2 | 77,729,986 | 11,659,497,900 | 76,878,888 | 11,094,058,272 | 95.15 | 92.75 | SRR3628924 |
| | ECI-6-143_T3 | 117,474,104 | 17,621,115,600 | 115,984,208 | 16,694,498,019 | 94.74 | 92.51 | SRR3628925 |
| | ECI-6-144_C1 | 60,990,986 | 9,148,647,900 | 60,741,680 | 9,064,390,023 | 99.08 | 92.8 | SRR3628926 |
| | ECI-6-144_C2 | 86,683,526 | 13,002,528,900 | 86,329,912 | 12,897,784,543 | 99.19 | 92.94 | SRR3628927 |
| | ECI-6-144_C3 | 71,825,978 | 10,773,896,700 | 71,575,562 | 10,702,818,550 | 99.34 | 92.83 | SRR3628928 |
| | ECI-6-144_T1 | 34,327,750 | 5,149,162,500 | 34,115,114 | 5,016,731,930 | 97.43 | 93.64 | SRR3628929 |
| | ECI-6-144_T2 | 39,923,670 | 5,988,550,500 | 39,185,794 | 5,487,993,485 | 91.64 | 94.59 | SRR3628930 |
| | ECI-6-144_T3 | 41,191,458 | 6,178,718,700 | 40,661,958 | 5,792,716,603 | 93.75 | 94.16 | SRR3628931 |
| | ECI-6-146_C1 | 35,902,156 | 5,385,323,400 | 35,787,792 | 5,340,202,079 | 99.16 | 92.66 | SRR3628932 |
| | ECI-6-146_C2 | 40,727,694 | 6,109,154,100 | 40,585,756 | 6,063,456,001 | 99.25 | 92.72 | SRR3628933 |
| | ECI-6-146_C3 | 100,811,740 | 15,121,761,000 | 100,423,000 | 14,990,114,758 | 99.13 | 94.71 | SRR3628934 |
| | ECI-6-146_T1 | 40,528,006 | 6,079,200,900 | 40,136,642 | 5,801,146,692 | 95.43 | 92.66 | SRR3628935 |
| | ECI-6-146_T2 | 40,158,520 | 6,023,778,000 | 39,741,560 | 5,735,959,598 | 95.22 | 93.41 | SRR3628936 |
| | ECI-6-146_T3 | 34,961,620 | 5,244,243,000 | 34,807,028 | 5,106,271,819 | 97.37 | 95.1 | SRR3628937 |
| | ECI-6-148_C1 | 80,739,166 | 12,110,874,900 | 80,407,104 | 11,979,744,760 | 98.92 | 92.37 | SRR3628938 |

| Group | Sample | Raw reads | Raw bases | Clean reads | Clean bases | Clean data rate (%) | Mapped reads (%) | Data accession |
|-------|--------------|------------|----------------|-------------|----------------|---------------------|------------------|----------------|
| | ECI-6-148_C2 | 57,424,994 | 8,613,749,100 | 57,182,706 | 8,521,457,624 | 98.93 | 92.95 | SRR3628939 |
| | ECI-6-148_C3 | 54,517,448 | 8,177,617,200 | 54,280,034 | 8,083,831,276 | 98.85 | 94.34 | SRR3628940 |
| | ECI-6-148_T1 | 42,620,250 | 6,393,037,500 | 42,157,010 | 5,955,828,859 | 93.16 | 93.59 | SRR3628941 |
| | ECI-6-148_T2 | 42,991,310 | 6,448,696,500 | 42,551,048 | 6,073,832,150 | 94.19 | 94.43 | SRR3628942 |
| | ECI-6-148_T3 | 42,431,480 | 6,364,722,000 | 42,044,288 | 5,984,128,572 | 94.02 | 95.64 | SRR3628943 |
| | ECI-6-0_C1 | 68,712,206 | 10,306,830,900 | 68,401,404 | 10,184,212,229 | 98.81 | 92.73 | SRR3628914 |
| | ECI-6-0_C2 | 65,847,806 | 9,877,170,900 | 65,664,450 | 9,816,514,491 | 99.39 | 93.04 | SRR3628915 |
| | ECI-6-0_C3 | 46,500,006 | 6,975,000,900 | 46,325,336 | 6,917,813,112 | 99.18 | 94.42 | SRR3628916 |
| | ECI-6-0_T1 | 59,354,406 | 8,903,160,900 | 58,490,430 | 8,085,067,632 | 90.81 | 94.71 | SRR3628917 |
| | ECI-6-0_T2 | 83,657,786 | 12,548,667,900 | 82,952,090 | 11,963,688,981 | 95.34 | 94.99 | SRR3628918 |
| | ECI-6-0_T3 | 78,776,948 | 11,816,542,200 | 78,161,008 | 11,396,313,905 | 96.44 | 92.93 | SRR3628919 |

ECI: Evolution Canyon I, Mount Carmel, Israel. ECI-2: Station 2 of ECI on the African Slope, ECI-6: Station 6 of ECI on the European Slope, C: Control, T: Treatment.