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| Sample order (from left to right) | | | | | | | | | | | | | |
| 23-70 | LfSaltT0  (1) | LfSaltT3  (2) | LfSaltT27  (3) | LfPegT0  (4) | LfPegT3  (5) | LfPegT27  (6) | RtSaltT0  (7) | RtSaltT3  (8) | RtSaltT27  (9) | RtPegT0  (10) | RtPegT3  (11) | RtPegT27  (12) |
| 20-40 | LfSaltT0  (13) | LfSaltT3  (14) | LfSaltT27  (15) | LfPegT0  (16) | LfPegT3  (17) | LfPegT27  (18) | RtSaltT0  (19) | RtSaltT3  (20) | RtSaltT27  (21) | RtPegT0  (22) | RtPegT3  (23) | RtPegT27  (24) |

**Figure. S1** Assignment of 15 top-level clusters (marked by red lines) based on the expression profiles of 641 salt- and drought-responsive genes in 20-40 and 23-70 wild barley accessions **(A).** A heatmap of 15 clusters according to the 641 salt and drought responsive genes in 20-40 and 23-70 wild barley genotypes (X axis genotype-tissue-treatment-time) **(B).**