

Plant growth-promoting bacteria mitigate drought stress in a new forage oat variety (*Avena sativa* AV25T)

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Figure S1. Expression of genes associated with mild stress responses. Antioxidant enzymes—encoding genes **a** superoxide dismutase (*SOD*), **b** catalase (*CAT*), and **c** ascorbate peroxidase (*APX*). **d** Drought-responsive transcription factor Dehydration-Responsive Element-Binding (*DREB*). As well genes involved in the proline metabolic pathway **e** Pyrroline-5-carboxylate synthase (*P5CS1*) and **f**. proline dehydrogenase 1 (*PDH1*). The red line corresponds to oat plants without bacteria inoculation, and the blue line to oat plants inoculated with *Pseudomonas fluorescens* N7 and *Bacillus amyloliquefaciens* XT17.

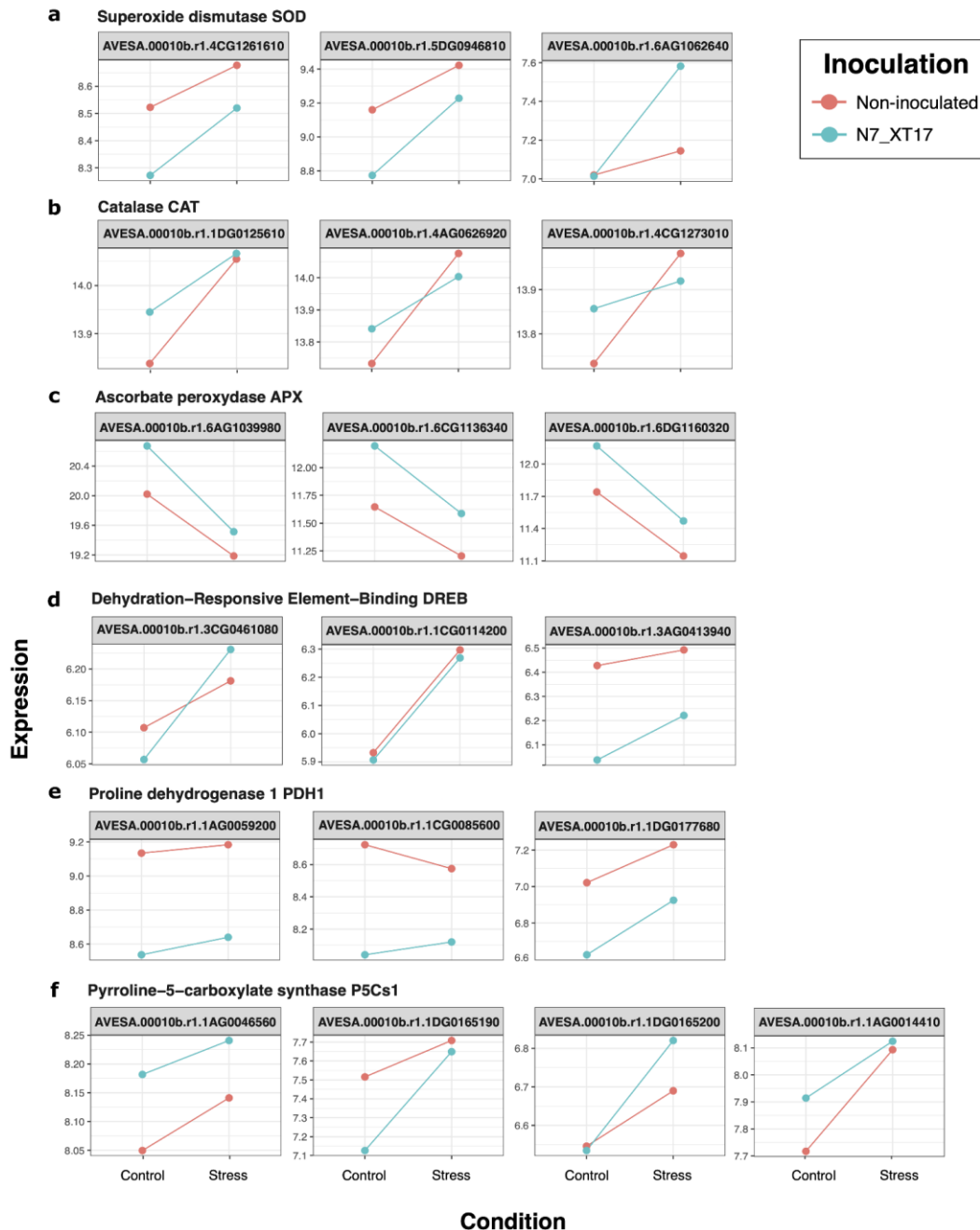


Table S1. Statistics of 12 libraries sequenced by Illumina Hiseq X system and reads mapped to Oat reference genome.

Sample Name	Clean reads	Mapped reads	Mapped ratio	Q20 (%)	Q30 (%)	GC content
Control_R1	66,284,901	41,400,351	62%	98.3	95.9	55.3
Control_R2	24,167,003	17,217,165	71%	98.4	96.2	56.4
Control_R3	126,714,549	87,466,499	69%	98.3	95.9	55.0
Drought_R1	26,648,539	17,016,249	64%	98.3	95.9	56.6
Drought_R2	109,300,141	74,747,752	69%	98.2	95.9	55.2
Drought_R3	58,263,885	38,940,384	67%	98.1	95.5	55.2
N7_XT17_R1	11,874,156	8,449,187	71%	98.5	96.3	60.3
N7_XT17_R2	32,957,216	22,621,348	69%	98.4	96.1	55.7
N7_XT17_R3	50,242,357	35,123,672	70%	98.2	95.9	56.7
Drought_N7XT17_R1	47,891,164	32,871,181	69%	97.9	95.3	55.0
Drought_N7XT17_R2	48,602,487	31,535,030	65%	98.3	95.9	55.6
Drought_N7XT17_R3	73,150,609	49,906,165	68%	98.2	95.7	54.6