

Table 1 Suppl. List of primer sequences of randomly selected genes used for real time qPCR analysis.

Gene name	Forward	Reverse
<i>DHN2</i>	AGCACGCATGCAGATGTA	CACGGACAAGATCAAGGAGAA
<i>KCR1</i>	CGATCCCTTTGCTTCTGTACTC	CCTACCCGTTCTACTCCATCTA
<i>LOX1.1</i>	CACGTTGGCGCACAAATAA	CACACCGCGGAAATAAGTAAAG
<i>WHAB1.6</i>	TGGATGTAGCCTGTGTGTTG	CACGAAGAGCGACTTCTGATTA
<i>6-FEH</i>	GCAGCATCCTACAATCCTTCT	GGATTTGCCTGCCCAATTATG
<i>Cht2</i>	ACCATGTTGACATCCAGAGC	GCTTGTGTGCCGCAATTC
<i>CYP78A9</i>	CGTGCTTCACGAAAGTGAATAAT	AGACATCACACACGTTAGAAAGA
<i>I-SST</i>	CCTCAACGCCACTGAACTTA	AGCATCAAGGTGGAAAGAGG
<i>RAB15</i>	GCCCTTGGAATCCATCTTAC	CACGACTCACGAACTGTCTTT
<i>HRGPNT3</i>	GAGAGGAAGGAGAGGAAGGAG	CAGCAGCAAGCAGCAAATC
<i>DHN4</i>	ATCCTATCCCGTCGGCTATAA	CTAGTGCTGCTGTTTACCTCTT
<i>MADS7</i>	CCACAGCGTATCCTGATCTAAC	CCAACTTCCTGTATATCCCTCATC
unamed protein	GATACGGAAAGGACCCACATAC	GAATTTCGAGTGGAATGACTTTG
<i>HRGP</i>	GCAGAGCGTCAAGCACTAAA	CAAACCGGCAGCTCATAAGT
<i>TPS6</i>	CGCATCCATCTTCCCTTCTT	GTCTTCGAGAAAGCGTGTAGTC
<i>DREB1B</i>	CCACTTCCTCTTGCTGTTCTT	CCAACTCCTGCTAAGCTTCTAC
<i>LOX2.1</i>	GATAATGAACCTCCTGTCGTCTC	GATCTCCATCATCCTCCCTTTG
<i>CYP90B1</i>	CGCGGTCTCTTGGAATTTA	TTCTCTCTCTCCCTCTCGAAC
<i>RhGT1</i>	GCTGCCGGTTTACTACTTCTAC	GCCAAGCTCCTTTACCTTTCT
<i>CHS1</i>	CACCCAAGTTTGCACTGTATTC	CTCTGGTGCTTGCGATAATTTG
<i>HSP21</i>	GTGCAGGTCCAGTGATGAAT	GGCACACTACGTCTACAAAGAG
<i>CYP86B1</i>	GTGTCGAGCATACGTGATGAA	CTAGGGCTTTGACCTCCTCTA
<i>DREB1H</i>	CGGAGTACCGTCTTCAATTTCT	CCGTATCATTTCTGCCACCT
<i>18S rRNA</i>	GCCTCGTTTCCTGCTCTTAT	CCGCTCCAGAACAACATCT

Table 2 Suppl. Fold change of persistently responsive genes in leaves and crowns of the tolerant Damxung (DX) and the sensitive Gannan (GN) genotypes under cold stress lasting 3 h, 24 h or 5d.

ID number	Description	Gene name	DX			GN		
leaves			3 h	24 h	5 d	3 h	24 h	3d
gi 475588850 gb EMT20996.1	protein argonaute 2	AGO2	8.23	10.55	10.25	7.89	9.6	9.81
gi 590114105 emb CDI59408.1	dehydration-responsive element-binding protein 1H	DREB1H	8.67	8.07	6.82	3.38	-0.81	-1.41
gi 474340936 gb EMS62689.1	tyrosine-sulfated glycopeptide receptor 2	PSYR2	6.66	4.73	5.75	6.89	8.76	10.07
gi 61657606 emb CAI65404.1	dehydrin COR410	COR410	6.65	6.65	6.79	6.77	8.39	6.5
gi 475589368 gb EMT21131.1	cold-regulated protein 2	CR2	6.37	9.43	10.8	6.67	8.63	9.47
gi 326520247 dbj BAK07382.1	phytosulfokine receptor 2	PSKR2	6.33	7.97	7.65	4.73	5.38	7.46
gi 669030397 emb CDM84910.1	zinc finger protein ZAT7	ZAT7	6.11	7.41	6.94	8.24	4.83	6.64
gi 326491521 dbj BAJ94238.1	protein LE25	LE25	5.93	5.97	5.5	4.53	4.08	3.98
gi 475610566 gb EMT27771.1	probable glutathione S-transferase	GSTU6	5.7	5.96	5.44	4.37	4.46	3.75
gi 115485731 ref NP_001068009.1	chalcone synthase 1	CHS1	5.54	8.98	7.05	-4.14	-0.92	-4.14
gi 326514426 dbj BAJ96200.1	lipoxygenase 2.1, chloroplastic	LOX2.1	4.89	3.47	4.51	1.04	-0.54	0.52
gi 474009141 gb EMS52512.1	lipid transfer protein EARLI 1	EARLI1	4.84	4.87	5.65	6.13	5.7	5.38
gi 6017936 gb AAF01693.1 AF181455_1	cold-shock protein CS120	CS120	4.8	7.2	6.8	6.46	7.47	6.99
gi 326534292 dbj BAJ89496.1	heavy metal-associated isoprenylated plant protein 26	HIPP26	4.56	3.84	4.13	3.97	3.58	3.29
gi 475533780 gb EMT08450.1	tyrosine-sulfated glycopeptide receptor 1	PSYR1	4.54	5.18	6	4.85	7.07	8.86
gi 474110039 gb EMS55576.1	late embryogenesis abundant protein	LEA14-B	4.46	5.49	4.54	4.14	5.05	4.23
gi 197726080 gb ACH73191.1	sucrose:sucrose 1-fructosyltransferase	1-SST	4.22	4.56	6.37	2.32	-1.15	0.7
gi 1657845 gb AAB18202.1	dehydrin-/LEA group 2-like protein	LEA2-like	4.06	6.45	6.04	2.36	3.58	2.73
gi 475533782 gb EMT08452.1	probable inactive receptor kinase	At3g02883	4.01	7.21	7.59	4.85	5.17	7.15
gi 6561859 gb AAF17098.1 AF207545_1	cold-regulated protein 1	CR1	4.01	8.01	8.02	4	7.11	6.73
gi 11066101 gb AAG28460.1 AF195612_1	putative lipoxygenase 8, chloroplastic	CM-LOX2	3.98	4.71	3.67	2.26	3.21	3.07

gi 669029199 emb CDM83324.1	late embryogenesis abundant protein	LEA14-A	3.93	7.83	10	4.54	5.88	4.62
gi 4105121 gb AAD02262.1	cold shock protein 66	CS66	3.92	5.06	4.08	6.76	7.76	7.22
gi 475580656 gb EMT18654.1	putative lipoxygenase 8, chloroplastic	CM-LOX2	3.91	4.1	4.22	1.24	1.32	4.64
gi 2970211 gb AAC05921.1	cold-shock protein	COR14	3.9	8.05	8.08	6.14	7.02	6.72
gi 326533280 dbj BAJ93612.1	cytochrome P450 90B1	CYP90B1	3.72	2.57	3.24	1.96	1.85	1.85
gi 10799810 emb CAC12881.1	oleosin-B6	OlnB6	3.63	6.29	5.69	4.04	6.86	6.22
gi 326524582 dbj BAK00674.1	4-coumarate--CoA ligase-like 10	4CLL10	3.62	4.65	5.02	-1.12	2.85	-1.89
gi 475533783 gb EMT08453.1	probable inactive receptor kinase	At3g02880	3.61	5.38	5.56	7.32	8.38	9.74
gi 326489937 dbj BAJ94042.1	predicted glutathione S-transferase T3-like	GSTT3	3.35	4.31	6.79	3.15	5.27	7.11
gi 20067423 emb CAC94005.1	glutathione S-transferase 4	GAST4	3.2	3.48	4.07	7.59	7.24	5.62
gi 326487522 dbj BAJ89745.1	low-temperature-induced 65 kDa protein	LTI65	3.18	3.77	3.63	3.82	3.07	3.18
gi 7188335 gb AAF37732.1 AF052221_1	4-coumarate--CoA ligase 4CL2	4CL2	3.09	3.08	3.83	-0.16	-1.78	-0.42
gi 473888536 gb EMS48364.1	β -glucosidase 31	BGLU31	3.07	5.2	5.32	2.83	2.99	3.01
gi 26017213 dbj BAC41494.1	vegetative cell wall protein gp1	GP1	2.93	6.04	5.88	4.24	5.86	5.65
gi 475623679 gb EMT32324.1	photosystem II reaction center PSB28 protein	PSB28	2.75	2.92	3.72	0.43	-1.2	-0.49
gi 353453150 gb AER00467.1	low temperature-induced protein lt101.1	LT101.1	2.69	4.15	3.57	3.89	5.05	4.03
gi 474396558 gb EMS65749.1	cold-regulated protein 2.2	CR2.2	2.66	3.83	4.25	5.18	4.95	6.48
gi 326500898 dbj BAJ95115.1	Fflavonoid 3'-monooxygenase	CYP75B2	2.66	3.64	4.67	-0.03	-4.7	-3.32
gi 76363564 sp P68178.1 ESI3_THIEL	Llow temperature-induced protein lt101	LT101	2.65	4.03	3.36	4.08	5	4.16
gi 326534182 dbj BAJ89441.1	cold-regulated 413 plasma membrane protein 2	COR413PM2	2.62	4.01	3.31	3.98	5.61	5.34
gi 326500056 dbj BAJ90863.1	36.4 kDa proline-rich protein	TPRP-F1	2.5	4.24	5.5	3.21	5.03	5.42
gi 1657855 gb AAB18207.1	cold-regulated 413 plasma membrane protein 1	COR413PM1	2.42	4.02	3.45	3.93	5.74	5.33
gi 475466922 gb EMT02225.1	chlorophyll a-b binding protein	CAB3C	1.61	3.33	6.13	-0.17	-1.07	-1.64
gi 326511894 dbj BAJ92091.1	cytochrome P450 93A3	CYP93A3	1.42	2.35	3.18	-0.15	-3.07	-2.58
gi 357150179 ref XP_003575369.1	two-component response regulator-like PRR1	PRR1	1.36	0.34	0.67	-3.76	-2.99	-3.37

gi 473939672 gb EMS50269.1	ribulose biphosphate carboxylase small chain PW9, chloroplastic	RBCS	0.99	-0.27	-3.57	0.28	-2.3	-2.52
gi 474018958 gb EMS52770.1	two-component response regulator ARR6	ARR6	0.79	-1.22	0.35	-4.42	-3.99	-3.4
gi 475575679 gb EMT17346.1	photosystem II 10 kDa polypeptide	PSBR	-1.81	-4.75	-4.08	0.55	-3.01	-7.25
gi 475515435 gb EMT05854.1	xyloglucan endotransglycosylase /hydrolase protein 8	XTH8	-2.58	-3.33	-6.36	-0.18	0.72	0.7
gi 357452919 ref XP_003596736.1	extensin	HRGPNT3	-5.08	-3.78	-3.89	6.04	-7	-7.64
gi 226069348 dbj BAH36898.1	polyphenol oxidase, chloroplastic	PPO	-8.58	-8.58	-7.85	2.64	3.33	3.31
crown								
gi 147225070 emb CAI96511.1	small heat shock protein, chloroplast	HSP21	1.91	5.14	4.6	-3.65	-0.87	-1.63
gi 474163697 gb EMS57375.1	BI1-like protein	At4g15470	4.66	7.65	8.29	-2.08	1.09	0.8
gi 310656772 gb ADP02203.1	acyl-[acyl-carrier-protein] desaturase 1, chloroplastic	Os01g08808003.38	3.23	4.14	-1.67	-0.69	-4.87	
gi 676378005 ref XP_009032281.1	MADS-box transcription factor 7	MADS7	3.01	0.03	5.89	-4.71	-2.05	-8.37
gi 475531591 gb EMT08103.1	CASP-like protein	Os02g0134500-4.45	-3.19	-6.87	5.45	6.57	7.15	
gi 573922507 ref XP_006648837.1	uncharacterized protein	At4g06744	-5.99	-9.17	-8.14	8.96	9.69	-7.93
gi 551636864 ref XP_005821254.1	extensin	HRGPNT3	-6.25	-5.89	7.29	4.65	2.98	4.05
gi 551606910 ref XP_005784781.1	leucine-rich repeat extensin-like protein 5	LRX5	-7.85	-7.85	-7.85	6.7	5.89	5.24
gi 676385245 ref XP_009035901.1	formin-like protein 6	FH6	-7.94	-4.57	6.68	6.91	8.52	8.66
gi 474049172 gb EMS53591.1	formin-like protein 5	FH5	-8.81	-4.93	-8.81	5.89	5.47	5.46

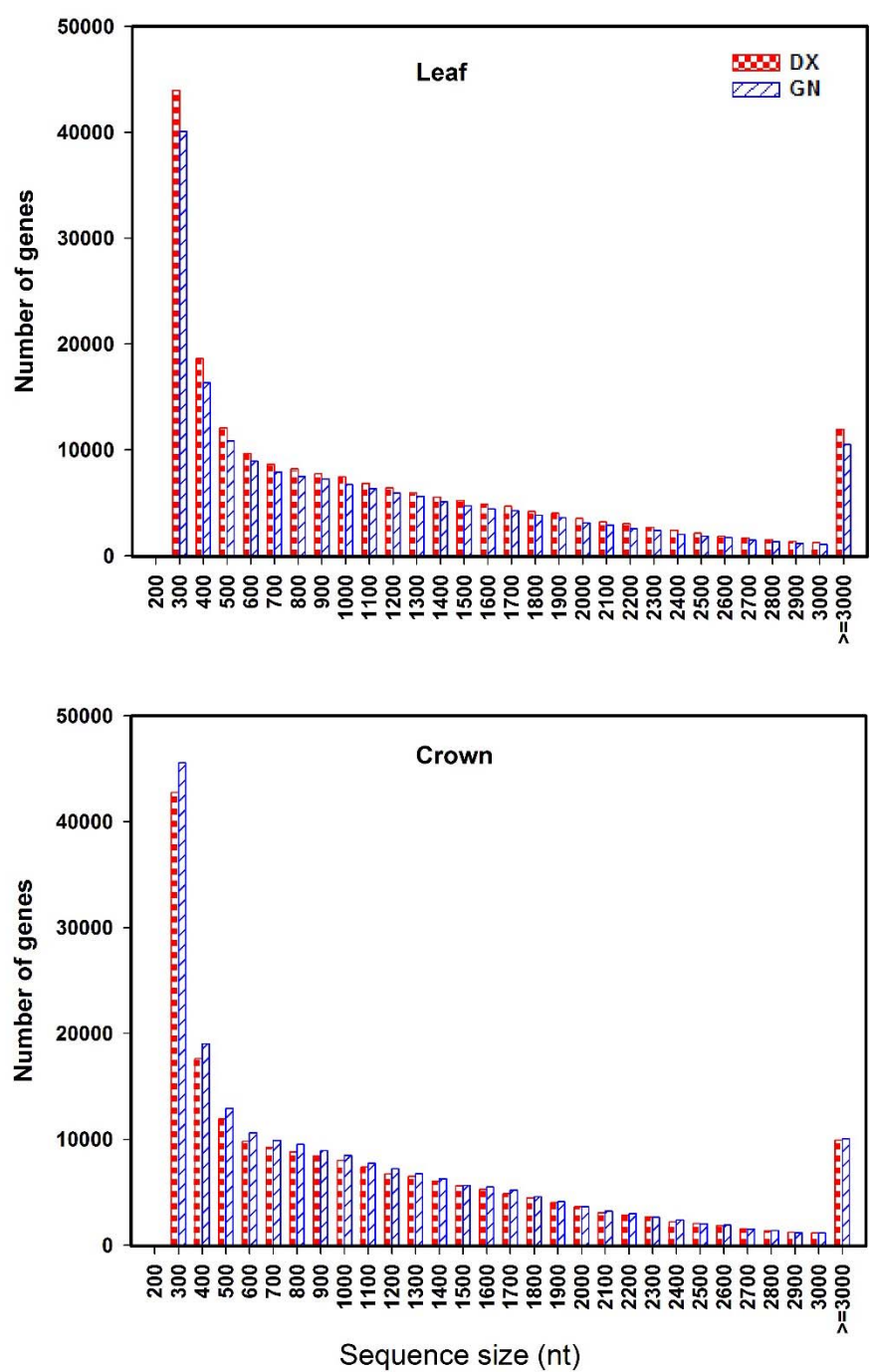


Fig. 1 Suppl. Length distribution of transcripts in both genotypes.

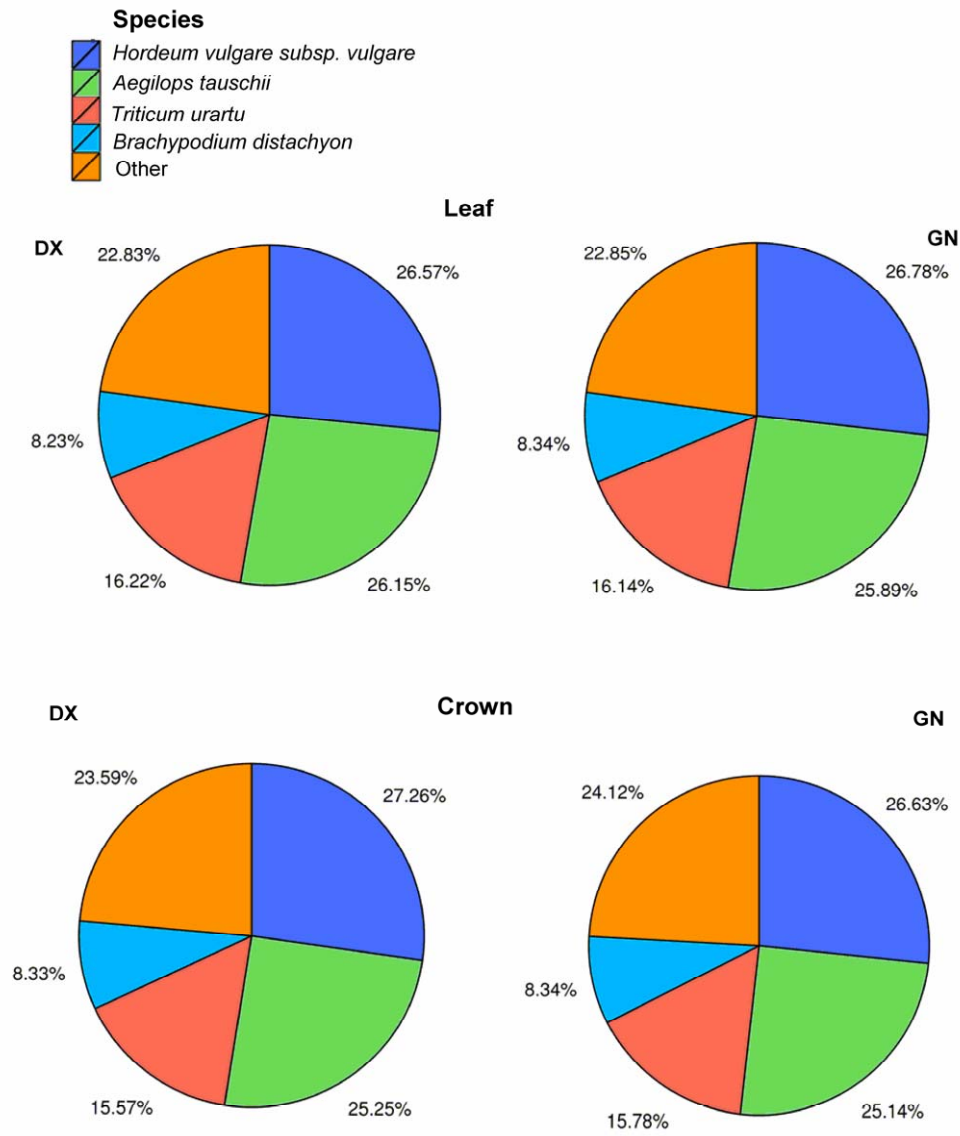


Fig. 2 Suppl. Similarity of *Elymus nutans* sequences with those of other species.

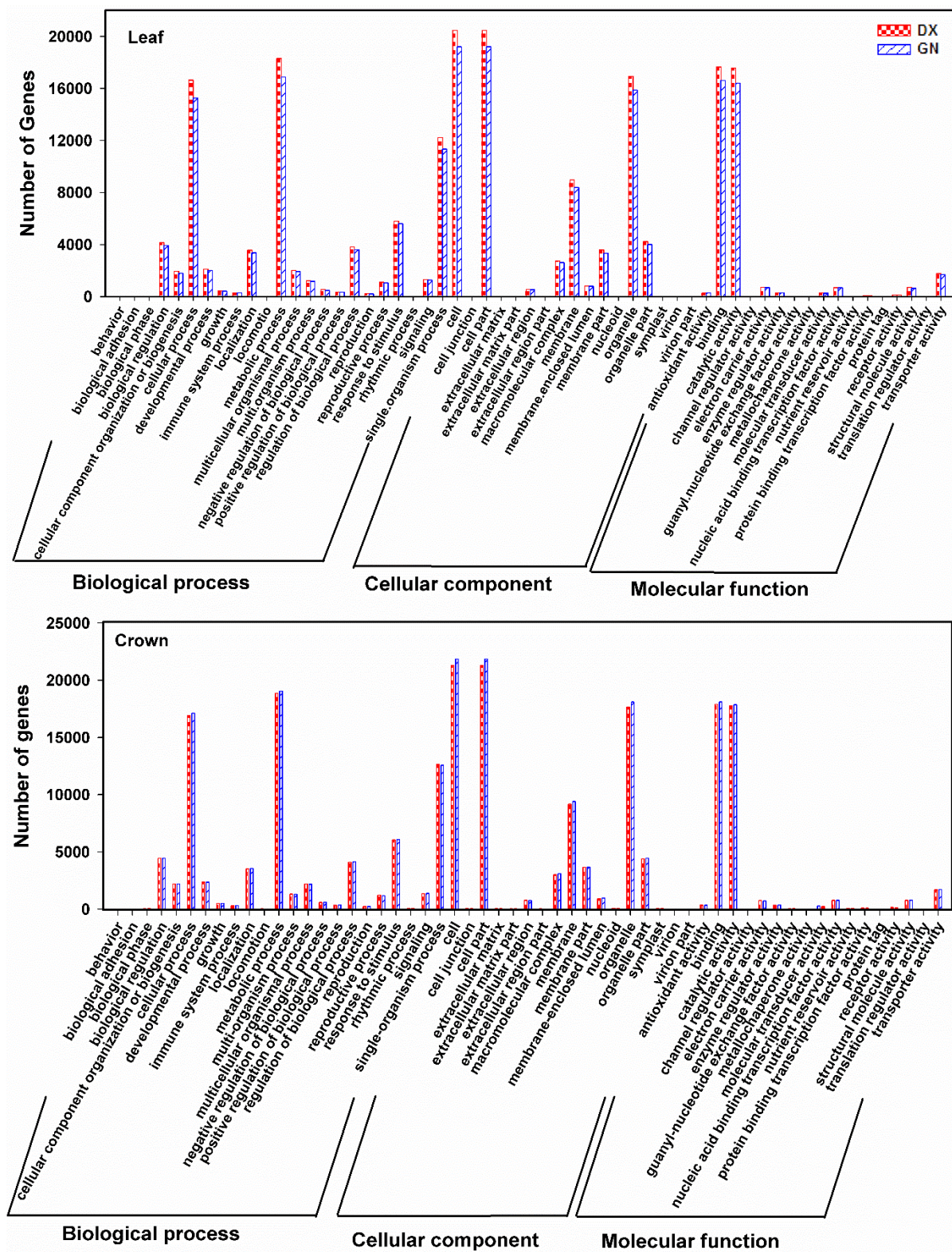


Fig. 3 Suppl. GO functional annotation of genes in both genotypes.

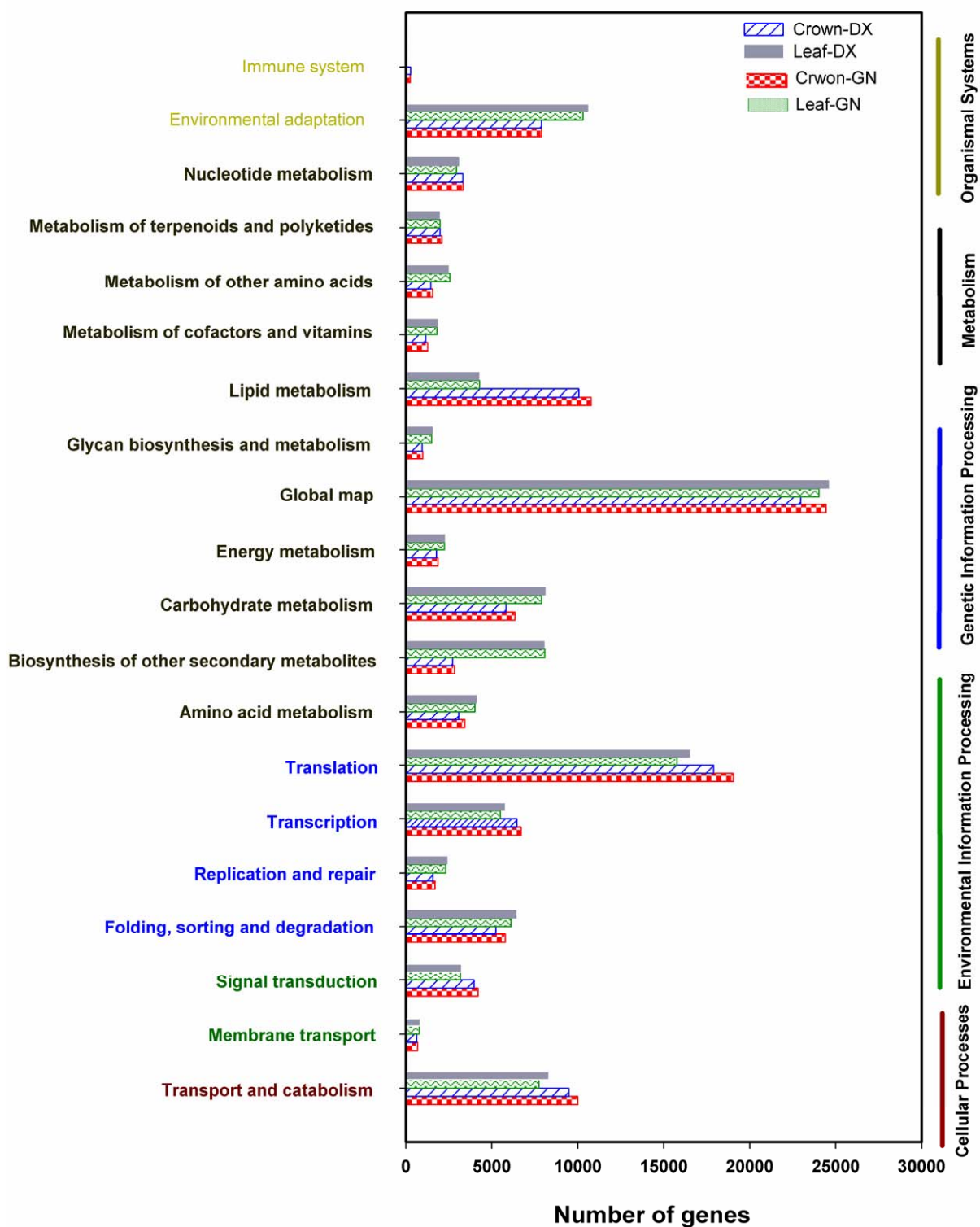


Fig. 4 Suppl. *KEGG* function classification of genes in both genotypes.

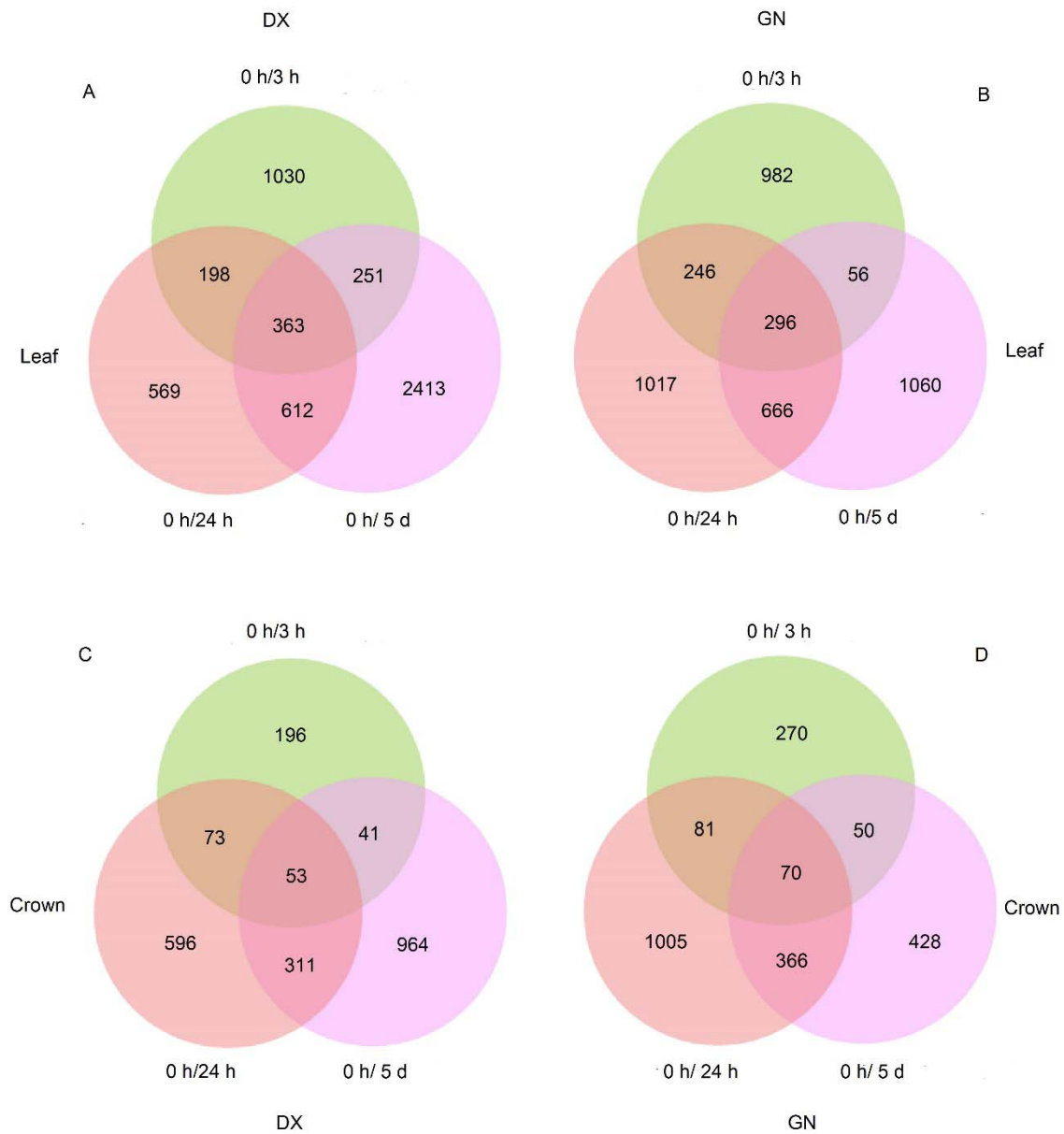


Fig. 5 Suppl. Venn diagram showing the number of DEGs in leaves (*A, B*) and crowns (*C, D*) of DX and GN genotypes under cold stress compared with control plants.

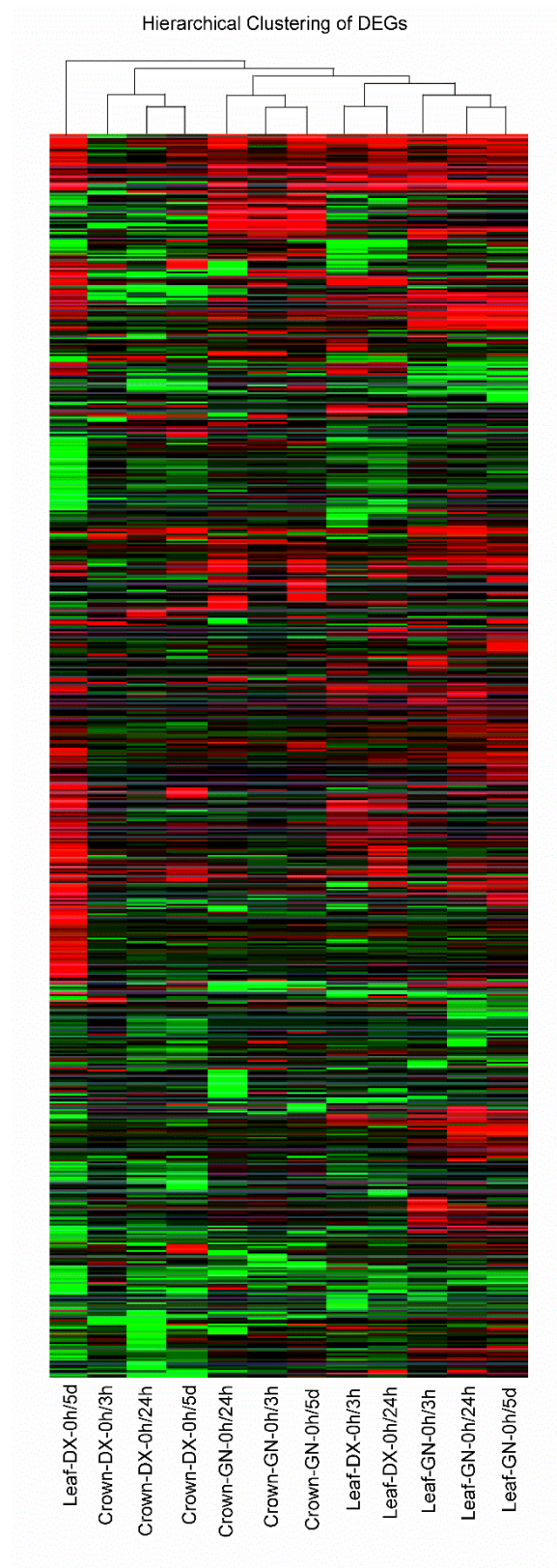


Fig. 6 Suppl. Hierarchical clustering analysis of 5600 DEGs in leaves and crowns of both genotypes (*red* - induced genes; *green* - repressed genes)

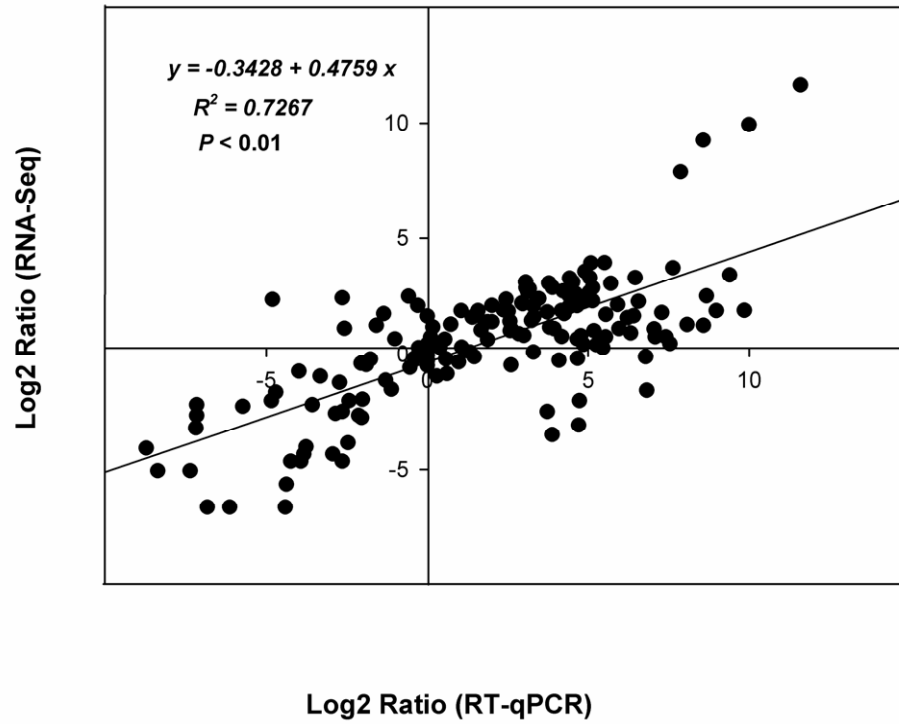


Fig. 7 Suppl. The correlation analysis between RNA-seq data and qRT-PCR results.

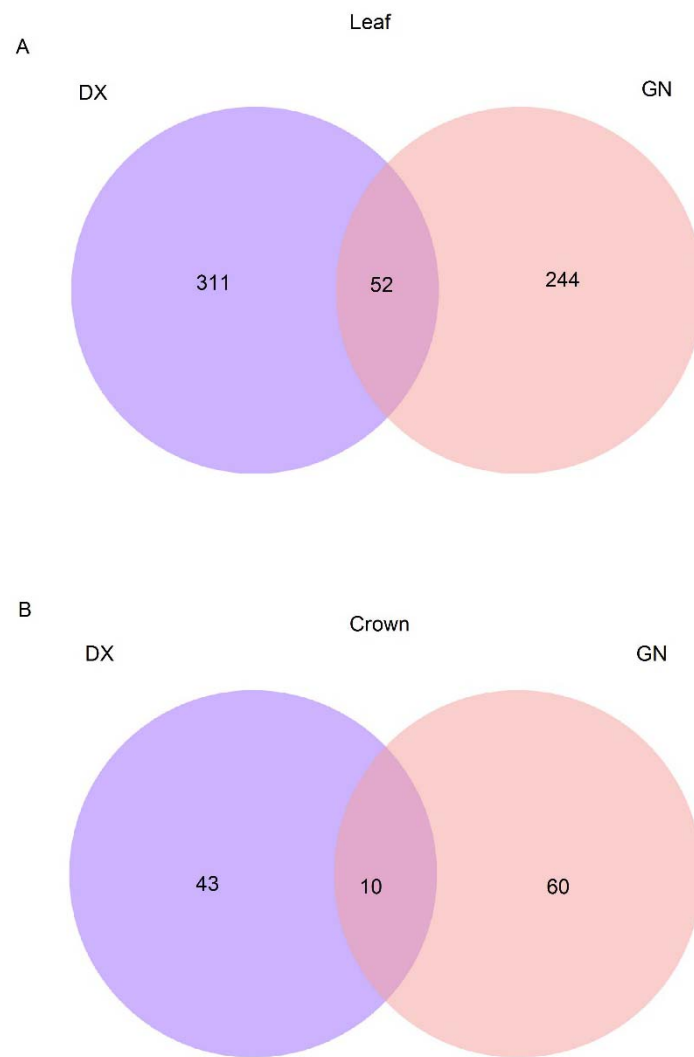


Fig. 8 Suppl. Persistently expressed DEGs in leaves (A) and crowns (B) of both genotypes during the entire cold stress.