Table 1 Suppl. Primer sequences for quantitative PCR.

Genes	Forward primer (5'–3')	Reverse primer (5'–3')	Tm [°C]
Glyma06G01990	TTCTTCACTGTTCTGGCACT	ATTGTAATCACCAGATAGCCTA	58
Glyma08G22730	GCCTCACTCTACCGTGGAA	CGTTATTGATGACTTTTGCGTTT	58
Glyma019G05140	GACATCGCTATTAGGCTTT	CACAACATTAAGCGCACA	58
Glyma06G20160	GCCCCAAATACCATATTCTGA	GTTACCTATCCAGATTTGCCTA	58
Actin	GTCACTAGCTCTGTGCATT	TCCAGCCTTAACCATTCCT	58

Table 2 Suppl. Statistical results of sample sequencing.

Sample	Clean reads	Clean bases	Error rate [%]	Q20 [%]	Q30 [%]	GC content [%]
LDCK_1	55464946	8260161891	0.0237	98.64	95.39	46.19
LDCK_2	47506852	7072207852	0.024	98.52	95.04	45.78
LDCK_3	61729812	9236976669	0.024	98.54	95.08	46.16
LDHS_1	41197716	6158253436	0.0237	98.65	95.39	45.74
LDHS_2	50654326	7563589311	0.0236	98.68	95.45	46.1
LDHS_3	49094284	7343196191	0.024	98.52	95	45.85
LDLS_1	47556660	7099596230	0.0237	98.65	95.4	46.02
LDLS_2	41804376	6247321958	0.0254	98.02	93.59	45.82
LDLS_3	44316264	6618375671	0.0239	98.57	95.2	45.97
QHCK_1	52253446	7800118474	0.024	98.51	95.07	46.13
QHCK_2	54542890	8140361929	0.024	98.53	95.11	46.23
QHCK_3	49500846	7395354913	0.024	98.5	95.02	46.2
QHHS_1	44885826	6690651344	0.024	98.51	95	46.35
QHHS_2	52149074	7778538385	0.0237	98.66	95.4	45.96
QHHS_3	45950892	6869658562	0.0239	98.56	95.12	45.9
QHLS_1	45193730	6756428651	0.0238	98.6	95.28	46.06
QHLS_2	48631072	7262418158	0.0237	98.62	95.34	46.49
QHLS_3	51267008	7652699387	0.0237	98.62	95.35	46.02
WDCK_1	48800854	7281480892	0.0235	98.7	95.54	45.9
WDCK_2	52705606	7864168523	0.0235	98.69	95.53	45.74
WDCK_3	52436172	7821177957	0.0236	98.67	95.48	47.85
WDHS_1	44732212	6693635889	0.0235	98.72	95.59	46.62
WDHS_2	52275314	7818540530	0.0238	98.59	95.22	47.45
WDHS_3	49004310	7327653472	0.0236	98.66	95.45	46.81
WDLS_1	50612300	7540259029	0.0239	98.54	95.16	45.9
WDLS_2	53680736	7996337386	0.024	98.5	95.05	46.1
WDLS_3	51995384	7752108239	0.0238	98.59	95.3	46.28

Table 3 Suppl. Genes obtained by cross-comparing between genes in *Magenta* module and DEGs of the three strains.

No.	Gene_id	log2fc
1	GLYMA06G01990	-5.095
2	GLYMA08G22730	-3.977
3	GLYMA03G42140	-3.331
4	GLYMA07G34560	-3.108
5	GLYMA19G05140	-2.837
6	GLYMA06G20160	-2.288
7	GLYMA01G25830	-2.254
8	GLYMA11G00550	-2.153
9	GLYMA03G38180	-2.046
10	GLYMA09G04980	-1.964
11	GLYMA14G02350	-1.87
12	GLYMA11G09230	-1.841
13	GLYMA04G34450	-1.786
14	GLYMA08G27000	-1.744
15	GLYMA07G03370	-1.738
16	GLYMA11G14720	-1.722
17	GLYMA01G36145	-1.709
18	GLYMA03G42470	-1.704
19	GLYMA01G38360	-1.598
20	GLYMA03G25510	-1.547
21	GLYMA07G08360	-1.469
22	GLYMA17G11030	-1.417
23	GLYMA20G27261	-1.412
24	GLYMA14G40620	-1.396
25	GLYMA16G33470	-1.354
26	GLYMA11G07380	-1.328
27	GLYMA12G36760	-1.323
28	GLYMA04G43080	-1.29
29	GLYMA12G06540	-1.282
30	GLYMA11G35760	-1.271
31	GLYMA02G03040	-1.227
32	GLYMA02G43410	-1.218
33	GLYMA13G44630	-1.079
34	GLYMA16G29420	-1.03
35	GLYMA03G33990	-1.001

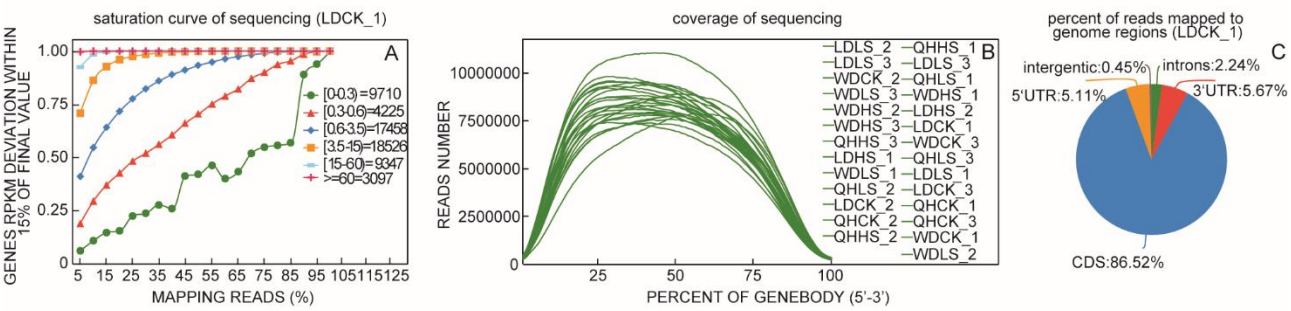

Fig. 1 Suppl. Gene alignment quality analysis. *A* - saturation curves of sequencing. The *x*-axis is the percentage of random mapped reads in the total number of mapped reads (*e.g.*, 60 means 60 % of random mapped reads were used to calculate the expression level of the gene). The *y*-axis is the deviation ratio between the expression level and the final value (within 15 % deviation), and the closer the value approaches to 1, the more saturated the expression level is. The saturation curves of a gene at different expression levels were represented by lines of different colors. RPKM - reads per kilobase of transcript per million mapped reads. *B* - coverage of sequencing. In the *x*-axis, 0 represents the 5' end of a gene, and 100 represents the 3' end of a gene. The *y*-axis shows the read numbers of sequences aligned to the *horizontal* axis corresponding to the regions of a gene. *C* - percent of reads mapped to genome regions. CDS - coding regions, intergenic - gene intergenic regions, introns - gene intron regions, UTR non-coding regions.

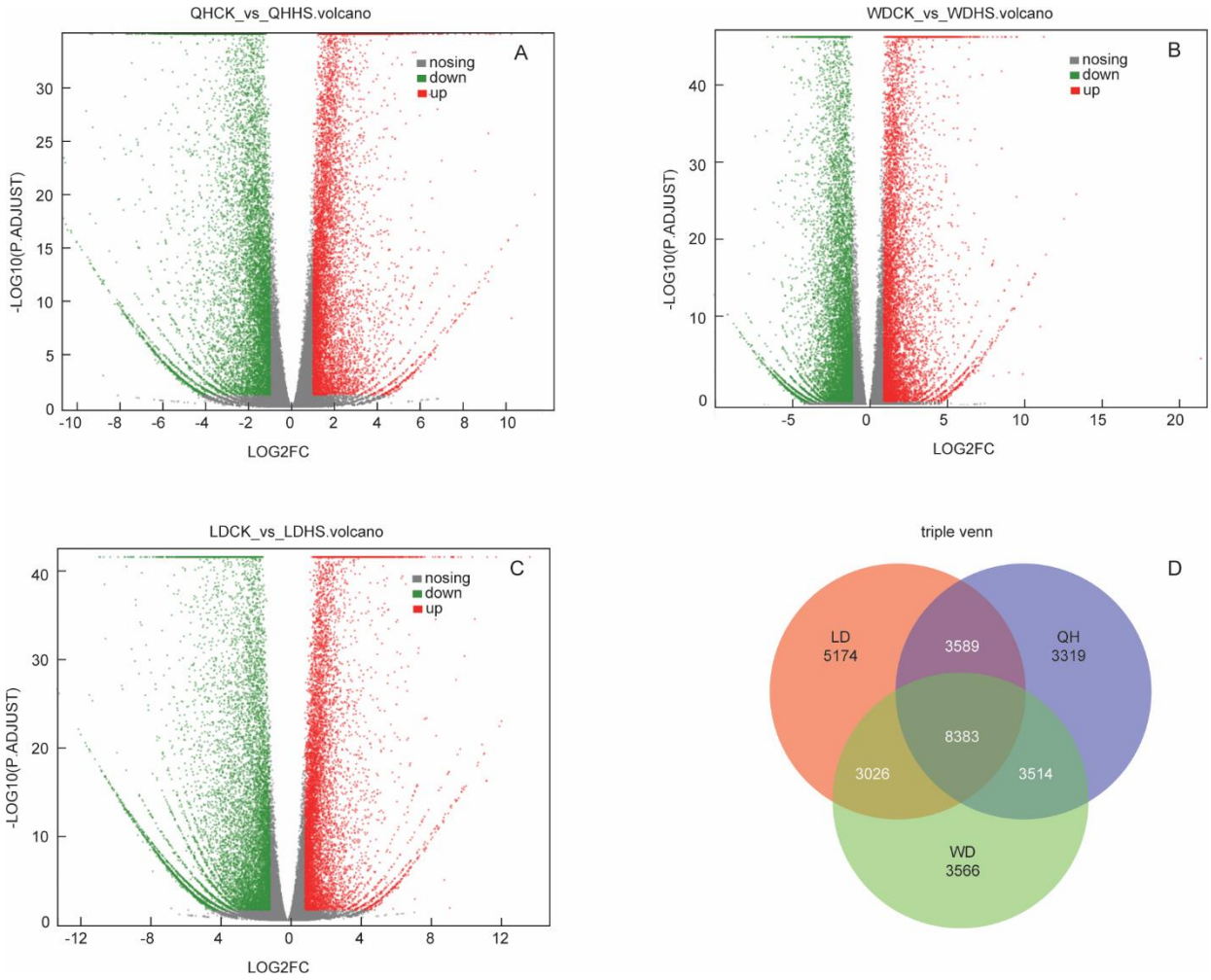

Fig. 2 Suppl. Identification of differentially expressed genes (DEGs). Volcano plots of DEGs between the control group (CK) and the high concentration of salt treatment group (HS) in QH (*A*), WD (*B*), and LD (*C*) strains. The *green* dots represent down-regulated genes, and the *red* dots represent up-regulated genes. *D* - iThe Venn diagram; numbers of unique and common DEGs within each strain.

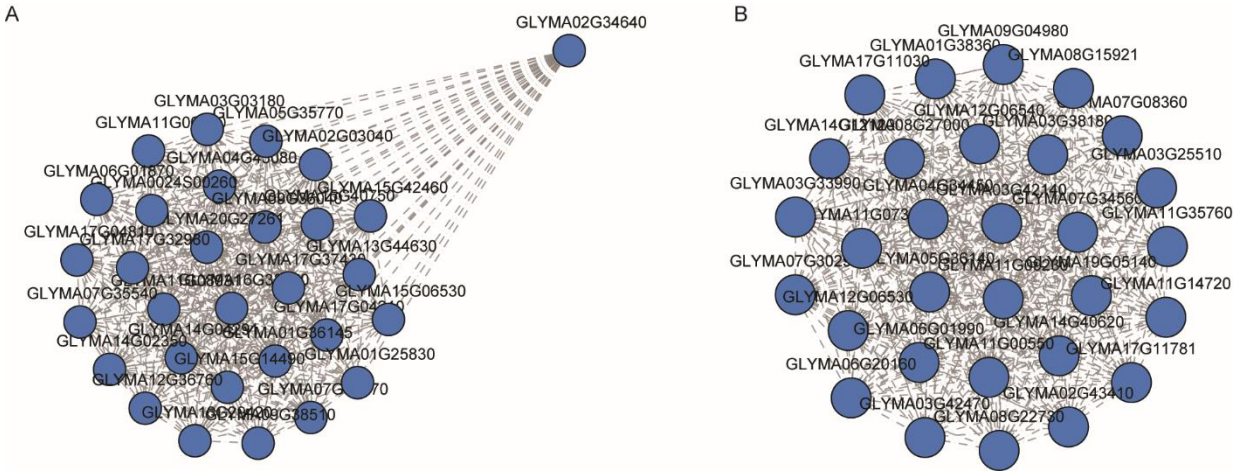

Fig. 3 Suppl. Module visualization. *A* - visualization of genes in the *Magenta* module. *B* - visualization of top 60 genes with strong relationships in the *Magenta* module.