**Figure S1.** Principal component analysis (PCA) for correlation among *VvHsp70* genes in different tissues. The data were based on transcription data of GSE36128. Different color graphics represent different tissues. rincipal component analysis (PCA) for correlation among *VvHsp70* genes in different tissues. The data were based on transcription data of GSE36128. Different color graphics represent different tissues. Blue, brown, deeppink, green, grey, orchid, palegreen, purple, red, tan color graphics represents the genes expression in seedling, root, stem, leaf, tendril, bud, rachis, flower, berry and seed, respectively. The pca package of R was used for construction of principal component analysis.
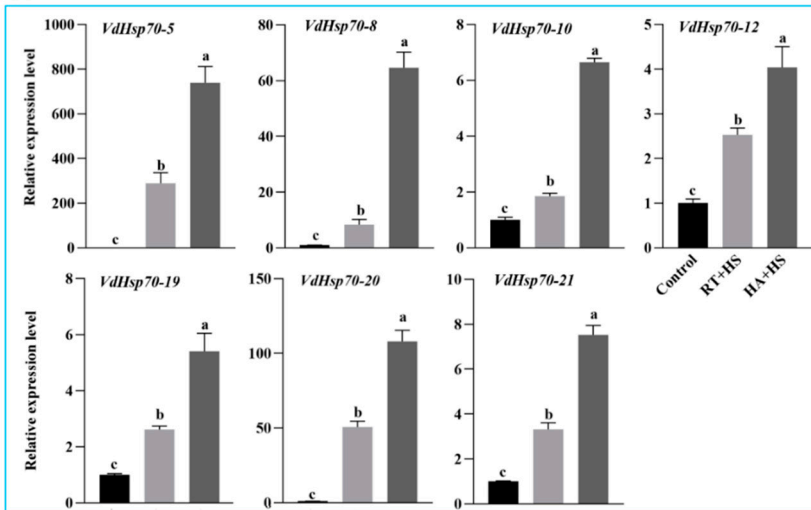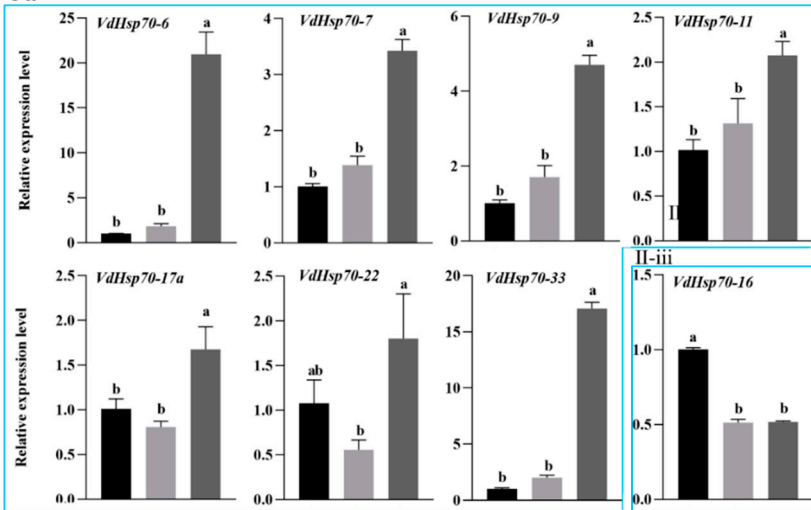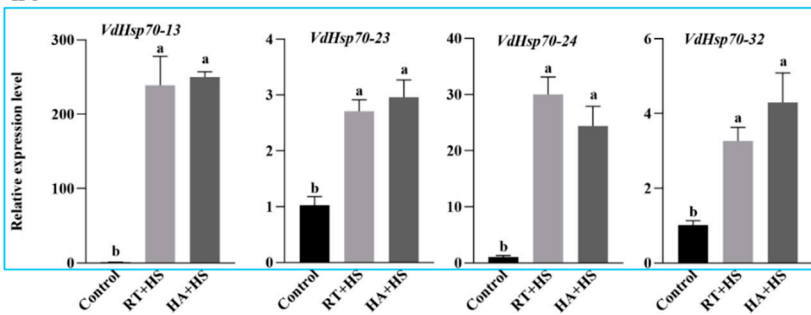
**Figure S2.** Expression of *VdHsp70* in *V. davidii* grapevine leaves in response to high temperatures. Grape leaves treated with 1): 25ºC 2 h and 40 min, 2): 25 ºC 2 h and 47 ºC 40 min, and 3): 38 ºC 2 h and 47 ºC 40 min were marked as Control, RT+HS and HA+HS, respectively. Group I, II and III refer to up-regulated, unchanged and down-regulated in compare treatments of HA+HS with RT+HS. Subgroup i, ii and iii refer to up-regulated, unchanged and down-regulated in compare treatments of RT+HS with Control.
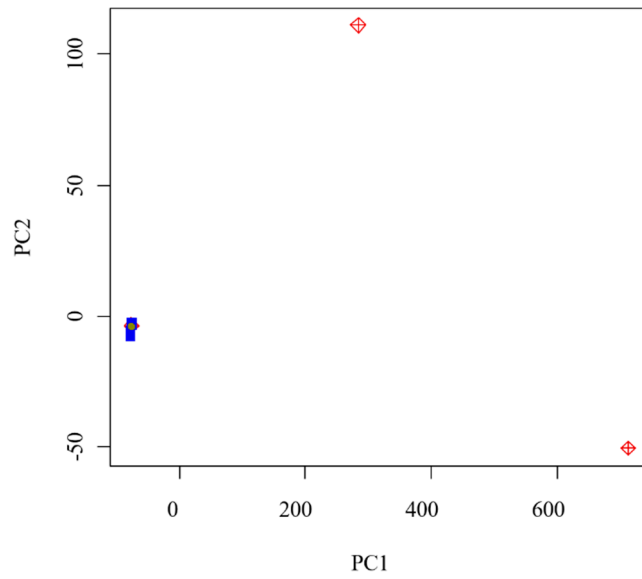
**Figure S3.** Principal component analysis (PCA) for correlation among grape *Hsp70* genes in different abiotic stress. The data were based on our qRT-PCR. Red, yellow and blue graphics represents the genes response heat, osmotic and cold, respectively. Yellow and blue graphics had some overlap. The pca package of R was used for construction of principal component analysis.