Table 1 Suppl. Gene names, accession numbers of genes in *NCBI*, primer sequences, and amplified fragment lengths (F - forward, R - reverse).

| Gene	Accession number	Primer sequences (5'-3')	Length [bp]
18SrRNA	AJ272181.1	F: CGCGCAAATTACCCAATCCTG	214
		R: GCCCAAGGTCCAACTACGAG	
ChlCu/ZnSOD	U69632.1	F: AAATGCTGGTGGAAGACT	174
		R: ACACTGATACAAACGATCAAC	
tAPX	EF184291.1	F: CACAGCCAGAGCCCTTCGT	176
		R: CAAGAATGCCAACCCTGCGAT	
MDAR	KC884831	F: AGACCTTGCTCATCGCCACTG	175
		R: ATGTAGCCACCTCCAACAACG	
DHAR	AY074784.1	F: AAGTGAACCCGTAAGCCCTC	197
		R:ACACACATATCACCCACACCC	
ChlGR	AB277096.1	F: GCTGCTGTTTTCTCCCAACCAC	205
		R:CATCACCACACATATGCACTCC	
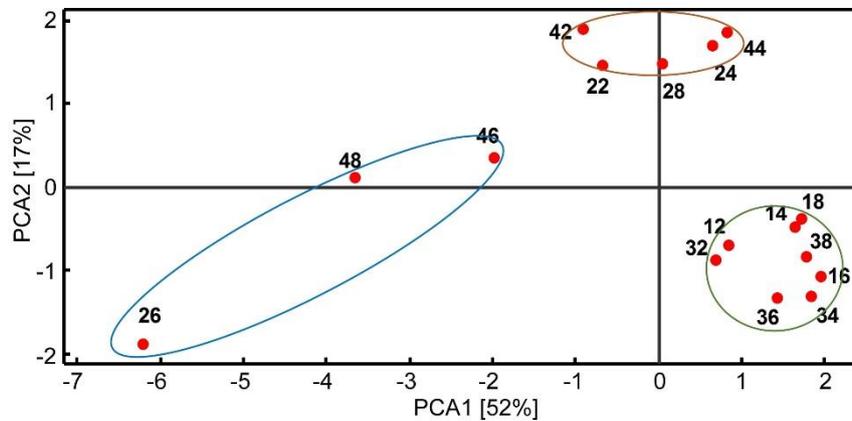
Fig. 1 Suppl. Principal component analysis (PCA) of wheat genotypes at different times of dehydration stress using all attributes under study. The first digit represents cultivar (1- Arta, 2 - Arg, 3- Navid, and 4 - Roshan); the second digit indicates hours of dehydration stress (PCA1 and PCA2 - first and second principal components, respectively).