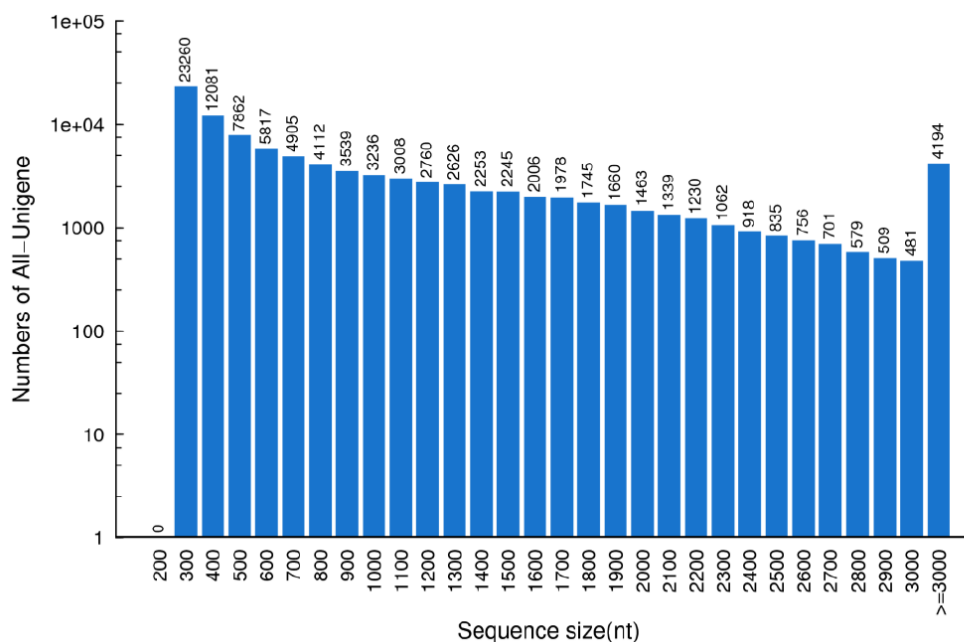


Comparative transcriptome analysis of two *Gerbera hybrida* cultivars revealed cold tolerance mechanismShenchong Li^{1,2,3}, Qinli Shan^{2,3}, Rongpei Yu^{2,3}, Abu Nasar Siddique⁴, Xia Li^{2,3}, Chunmei Yang^{2,3}, Jiwei Ruan^{2,3}, Mingyang Li^{1*}**Supplementary materials****Table S1. Statistics of functional annotation for all unigene.**

Item	Nr	Nt	Swiss-Prot	KEGG	COG	GO	All
All unigene	55660	45646	36939	33611	21709	41360	58127

**FigS1. Length distribution of all unigenes**