Strawberry is a large consumed and cultivated fruit, rich in a varied range of functional compounds. Since studies on transcriptomic and metabolic level can provide informations to biofortify food with functional compounds of interest, in this study the antioxidant activity and content of phenolic compounds as well as the expression of genes **phal** (coding for phenylalanine ammonium lyase), **ufgt** (coding for UDP flavonoid glucosyltransferase) and **ans** (coding for anthocyanin synthase) were evaluated in 10 strawberry cultivars. Total RNA from ripe fruits was extracted with a CTAB-based method, cDNA synthesized using MMLV and the gene expression was performed by RT-qPCR. Antioxidant activity was quantified by a DPPH-based method and Total phenolic compounds by spectrophotometry. The cultivar Aroma showed antioxidant activity statistically higher than the others, while Camarosa stood out on the content of phenolic compounds, which was concomitant with the highest expression of **phal**, **ufgt** and **ans** in this cultivar. The expression of **ufgt** was directly related to the expression of **phal**, which was not true to the levels of **ans** transcripts, suggesting that there is trade-off, specific for each cultivar, that determines whether the metabolic pathway branch to be prioritized is the one related to the production of anthocyanins and proanthocyanidins or another **ufgt**-dependent and **ans**-independent such as the one related to the synthesis of flavonoids. Thus, there is a genetic variability in these cultivars that can be exploited by conventional breeding and metabolic engineering in order to improvement of nutritional and functional quality of fruits.