**Transcriptome analysis of flower color reveals the correlation between SNP and differential expression genes in *Phalaenopsis***

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Table S1. Functional annotation of unigene

|  |  |  |
| --- | --- | --- |
| Database | No. of unigene | Percentage (%) |
| Nr | 21,143 | 90.7 |
| Swiss-Prot | 15,062 | 64.6 |
| GO | 10,827 | 46.4 |
| KEGG | 9,854 | 42.3 |
| COG | 18,954 | 81.3 |
| Total | 23314 | 100 |

Table S3. Functional annotation of DEGs

|  |  |  |
| --- | --- | --- |
| Database | No. of DEGs | Percentage (%) |
| Nr | 1163 | 98.9 |
| Swiss-prot | 898 | 76.4 |
| GO | 474 | 40.3 |
| KEGG | 431 | 36.7 |
| COG | 882 | 75.1 |
| Total | 1175 | 100 |

Table S7. Statistics of variation types of SNP

|  |  |  |
| --- | --- | --- |
| SNP type | Number of SNP | Percentage (%) |
| G/A | 27947 | 13.45 |
| A/G | 27864 | 13.41 |
| C/T | 27738 | 13.35 |
| T/C | 27670 | 13.32 |
| T/A | 17876 | 8.60 |
| A/T | 17632 | 8.49 |
| G/T | 11887 | 5.72 |
| A/C | 11783 | 5.67 |
| C/A | 11762 | 5.66 |
| T/G | 11537 | 5.55 |
| G/C | 7067 | 3.40 |
| C/G | 6996 | 3.37 |
| total | 207759 | 100.00 |

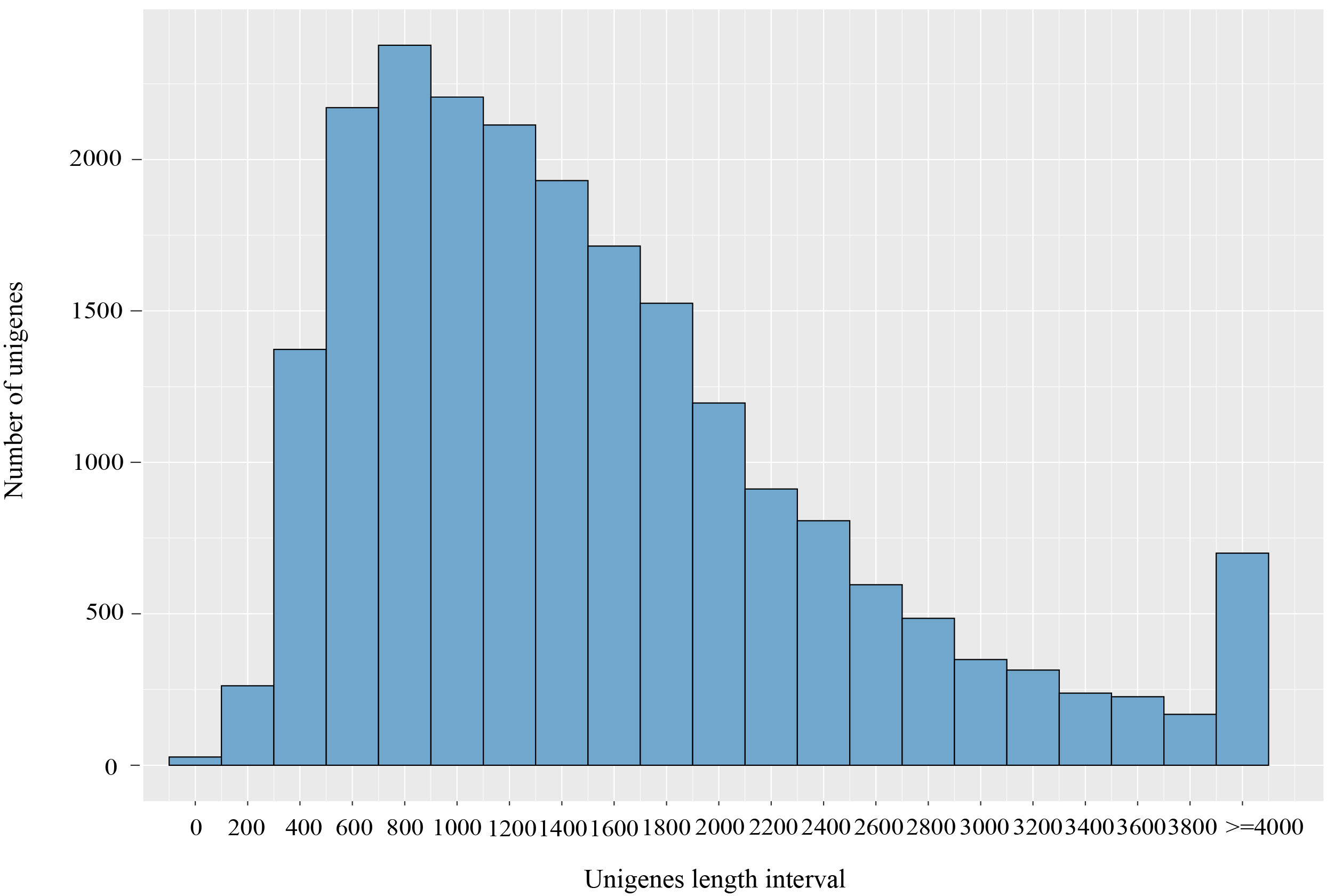


Figure S1 Distribution of unigenes length

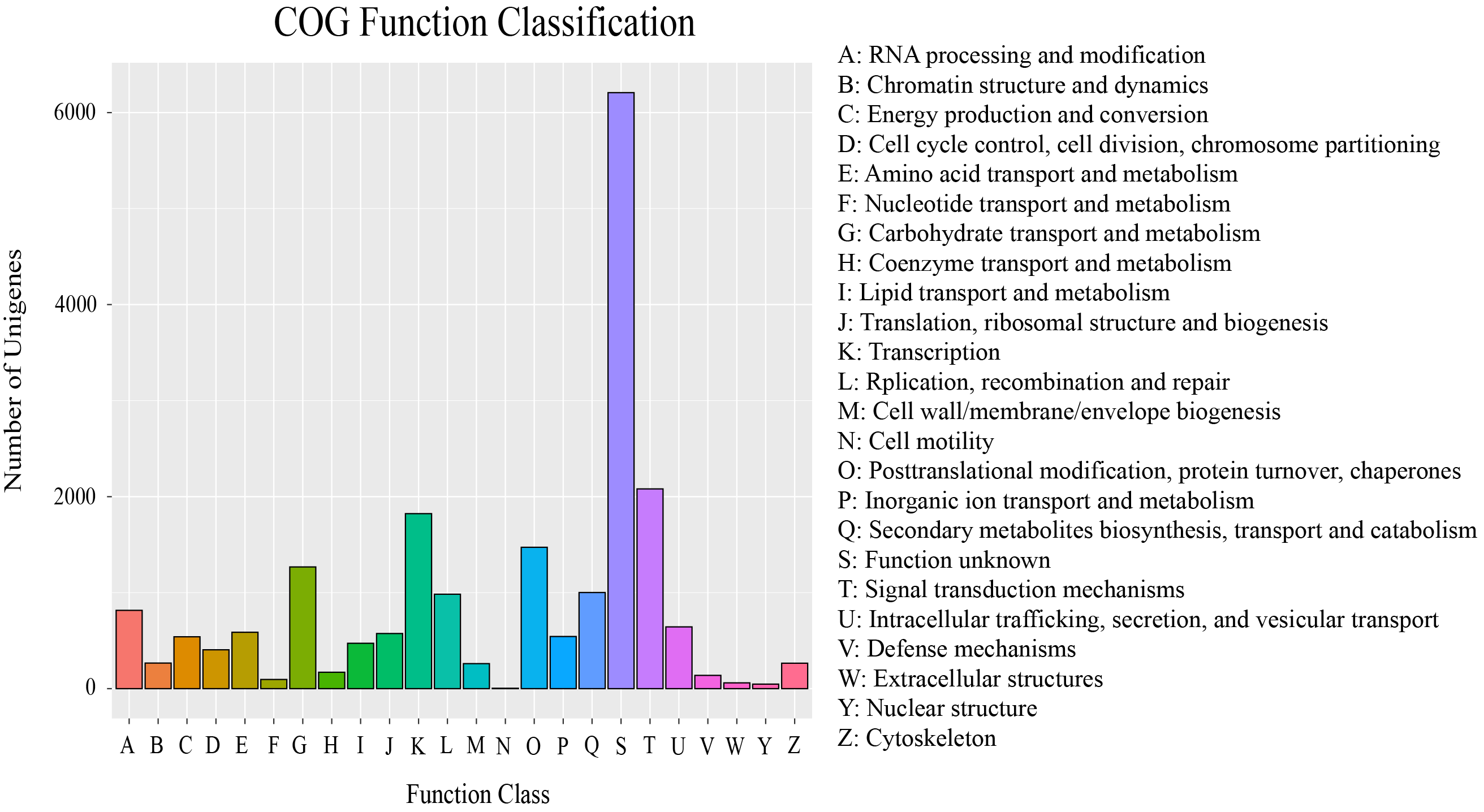


Figure S2 The COG annotation of unigenes

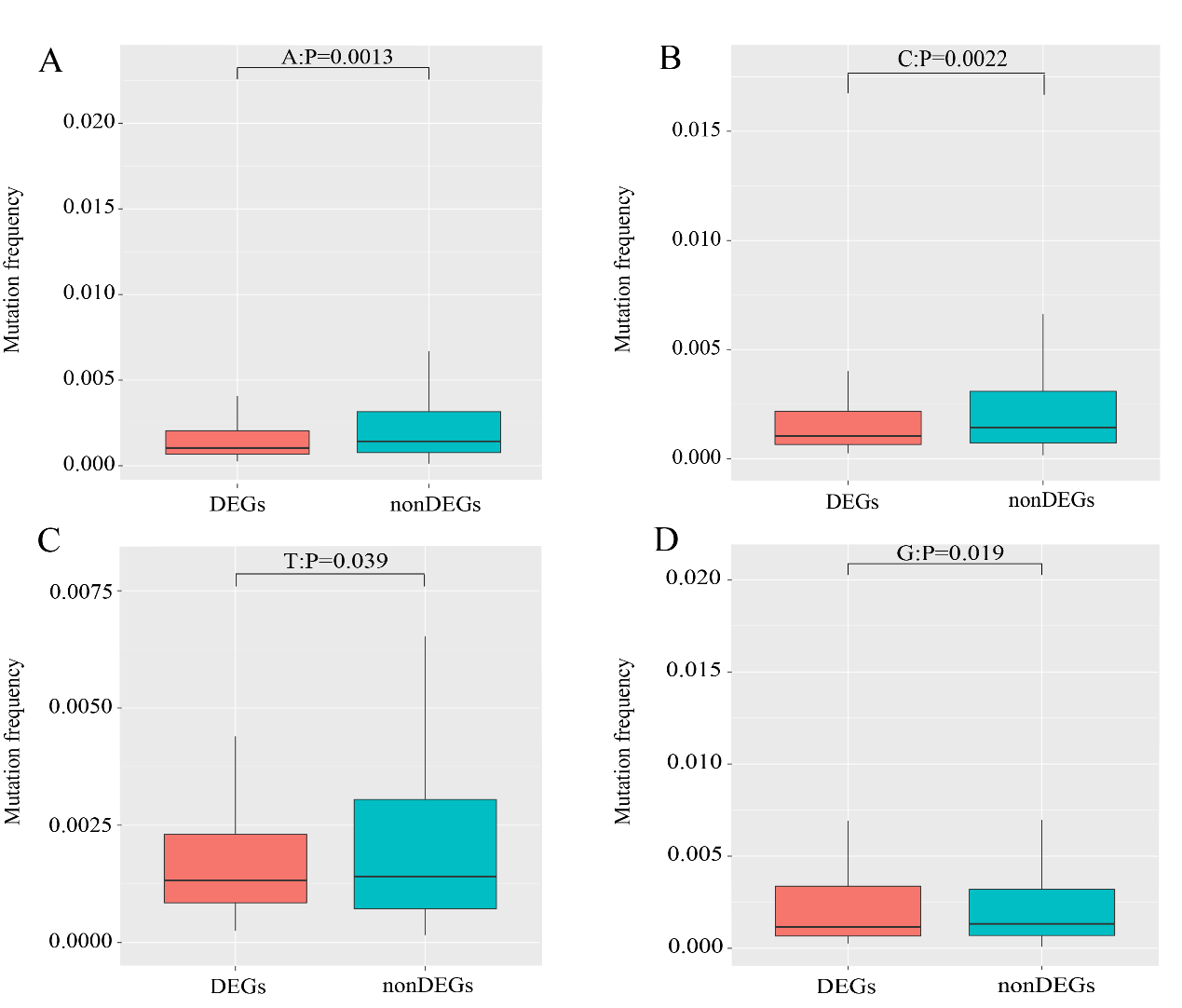


Figure S3 Comparison SNP mutation frequency between DEGs and non-DEGs in A, C, T and G four categories (A: A base; B: C base; C: T base; D: G base)