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| --- | --- |
| **Table S2.** Single nucleotide polymorphism (SNP)-based regional annotation. | |
| **SNP location** | **No.** |
| Exonic | 4 (3.28%) |
| Intronic | 53 (43.44%) |
| ncRNA intronic | 5 (4.10%) |
| 5’ UTR | 0 (0.00%) |
| 3’ UTR | 1 (0.82%) |
| Intergenic | 58 (47.54%) |
| Upstream | 0 (0.00%) |
| Downstream | 0 (0.00%) |
| w/o annotation | 1 (0.82%) |
| Total | 122 (100.00%) |