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| **Table S1.** Primers designed for characterization of complete coding sequences of *RmATG3*, *RmATG4* and *RmATG6* genes and gene expression assessment by qPCR. | | |
| **Characterization of complete coding sequences** | | |
| **Primer name** | **Primer sequence (5’ to 3’)** | |
| RmATG3 | **Foward** | GCA TGT ATG GGT GTG TTT CG |
| RmATG3 | **Reverse** | AAA ATG AGC ACG GTT CCA TC |
| RmATG4 | **Foward** | CTT CTT TCA AGA ATG GCT G |
| RmATG4 | **Reverse** | GGA GGC TGT TGC ATC TCT TC |
| RmATG6 | **Foward** | GTC CGA TCC GTC GTC ACT AT |
| RmATG6 | **Reverse** | GAA GTT GTA CAC GCG GTT GTT |
| **Gene expression *by qPCR*** | | |
| **Primer name** | **Primer sequence (5’ to 3’)** | |
| RmATG3E | **Foward** | CGA ACC TGG CTC TTT AGA CG |
| RmATG3E | **Reverse** | GTC CTG GCT GAT GTC CTC AT |
| RmATG4E | **Foward** | AGC TTG CAG TTG ACC TGG AT |
| RmATG4E | **Reverse** | CTC GAA CAA TGG CTG TTT CA |
| RmATG6E | **Foward** | GGC AAC CAC TCG TAC CTG AT |
| RmATG6E | **Reverse** | TGT TGC TGT CCT CGA TCT TG |
| \*RmELF1A | **Foward** | CGT CTA CAA GAT TGG TGG CAT T |
| \*RmELF1A | **Reverse** | CTC AGT GGT CAG GTT GGC AG |
| \*RmACTB | **Foward** | CCC ATC TAC GAA GGT TAC GCC |
| \*RmACTB | **Reverse** | CGC ACG ATT TCA CGC TCA G |
| \**Elongation factor 1-α* (*ELFIA*) and *β-actin* (*ACTB*) genes were used as endogenous control (Nijhof et al. 2009). | | |