**Table S3. Ranking of the candidate reference genes by *BestKeeper\****

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Gene | GM[*Ct*] | AM | Min | Max | SD | CV | [r] | p-value | Ranking |
|  | [*Ct*] | [*Ct*] | [*Ct*] | [±*Ct*] | [%Ct] |  |  | [r] | SD |
| *18S* | 10.06 | 10.09 | 9.26 | 11.14 | 0.60 | 5.90 | 0.355 | 0.389 | *HSP60* | *EF1A* |
| *28S* | 13.10 | 13.16 | 10.72 | 14.51 | 1.07 | 8.12 | 0.900 | 0.002 | *HSP90* | *HSP70* |
| *Actin* | 31.25 | 31.26 | 29.75 | 32.69 | 0.57 | 1.81 | 0.379 | 0.355 | *28S* | *RPL32* |
| *ATPase* | 19.57 | 19.59 | 18.33 | 21.08 | 0.81 | 4.13 | 0.860 | 0.006 | *HSP70* | *HSP60* |
| *EF1A* | 19.33 | 19.34 | 18.48 | 20.63 | 0.50 | 2.58 | 0.748 | 0.033 | *NADH* | *Actin* |
| *HSP60* | 24.62 | 24.63 | 23.26 | 25.50 | 0.56 | 2.27 | 0.924 | 0.001 | *ATPase* | *18S* |
| *HSP70* | 20.81 | 2082 | 19.84 | 21.89 | 0.52 | 2.50 | 0.882 | 0.004 | *RPL32* | *Tubulin* |
| *HSP90* | 22.52 | 22.55 | 20.85 | 23.84 | 0.91 | 4.06 | 0.917 | 0.001 | *EF1A* | *ATPase* |
| *NADH* | 21.87 | 21.89 | 20.10 | 23.23 | 0.89 | 4.09 | 0.870 | 0.005 | *Actin* | *NADH* |
| *RPL32* | 22.10 | 22.11 | 21.02 | 23.67 | 0.56 | 2.51 | 0.858 | 0.006 | *18S* | *HSP90* |
| *Tubulin* | 26.71 | 26.72 | 25.71 | 28.44 | 0.78 | 2.93 | 0.276 | 0.508 | *Tubulin* | *28S* |

"\*": Two criteria are considered: Pearson’s correlation coefficient and *BestKeeper* computed SD values. The stability of a gene is directly proportional to the [r] value, while it is inversely proportional to the SD value. GM: the geometric mean of Ct; AM: the arithmetic mean of Ct; Min and Max: the extreme values of Ct, respectively; SD: the standard deviation of Ct; CV: the coefficient of variance expressed as a percentage on Ct level; r: Pearson’s correlation coefficient.