|  |
| --- |
| **S1 Table. Paired primers used for assessing the transcript levels of the NER and BER genes in** ***E. histolytica.*** |
| **Gene** | **Ref Seq\*** | **Use** | **Sequences of paired primers****(5´- 3´)** | **Amplicon size (bp)** | **TM** |
| **NER**  |
| *ehhr23.1*  | XM\_644420.1 | *RT-PCR* | F: GAGTGCTGTTCCTCCTCC R: TCCCATTTCAACTAAATG | 202 | 53.9147.39 |
|  |  | *qRT-PCR* | F: AAGAGTGCTGTTCCTCCTCC R: ACTGGTTGTGTTGAAGGTTGG | 122 | 59.0258.9 |
| *ehddb1* | XM\_648763 | *RT-PCR* | F: GATGAACAAAGGGTTGTTG R: GAAATATCCCTCATTTCC | 210 | 52.1947.49 |
|  |  | *qRT-PCR* | F: GGAATTAGTGGGGTTGTTATTGGG R: AGACAATACAACCCAACAACCC | 158 | 59.658.8 |
| *ehxpb* | XM\_644397.1 | *RT-PCR* | F: TCGTGAAGATGATAGAATTCG R: TAATTTTATCACCATGTGCC | 266 | 53.9852.07 |
|  |  | *qRT-PCR* | F: CGAAGACAAGAGGCTCAACG R: CCCTCTTTAGCAGGGTCTTCC | 253 | 58.9459.79 |
| *ehrpa*  | XM\_645141.1 | *RT-PCR* | F: CTGATTACAAACAAAGTAATGGGR: ATCTACTTCAACAGCATAGC | 281 | 54.2548.13 |
|  |  | *qRT-PCR* | F: AGAAGGGAAGATCGCAGACGR: TGAGATTGCAACAACGAGGG | 265 | 59.5458.48 |
| *ehxpg*  | XM\_646609.2 | *RT-PCR* | F: CCTCTTTATCAGTCTATCCC R:TGGAAGTGTCTGGTGATGGG | 232 | 48.9960.35 |
|  |  | *qRT-PCR* | F: CCATCTTCCTCCTCACTTCCCR:AGAAGGAAGAGGGGAGAGAGG | 100 | 59.5159.71 |
| *ehrcc1* | XM\_647372.1 | *RT-PCR* | F: GATTAAAGGGATAAACTCGCR: TGTTCCGACAATTGGGGAATG | 166 | 51.9063.56 |
|  |  | *qRT-PCR* | F: GCGAGTTGAATATGATCCTGGCR: GCAGCATCAGAATAACTTTGTGC | 282 | 59.5259.14 |
| **BER**  |
| *Ehmuty* | XM\_647968.1 | *RT-PCR* | F: TTACAACAAACACAAGTA R: ATTTATCAACACTAGAAGG  | 214 | 40.0042.39 |
|  |  | *qRT-PCR* | F: TCAAGATATTGCAACAGTAGACGCR:CCAGTTGCAACAAGAGCACC  | 177 | 59.4359.97 |
| *ehnth*  | XM\_649933.2 | *RT-PCR* | F: AAGTTGCATGAAACTCTT R: GGTCCAACACCAGGAAGTG  | 206 | 46.0257.28 |
|  |  | *qRT-PCR* | F: ACACTTCCTGGTGTTGGACC R: TCTGGGGTTGAACCATCTGC | 137 | 59.8259.96 |
| *ehnth-like* | XM\_649024.1 | *RT-PCR* | F: TTAAATGAGTTATTAGATGGR: TGGTCAACAGTAATACCTTC | 206 | 43.3148.47 |
|  |  | *qRT-PCR* | F: ACCTGGTATTGGTCCTAAGTTAGCR: AGGACATTGGTCACATAAAGGG | 259 | 59.8458.03 |
| *Ehapex* | XM\_645440.2 | *RT-PCR* | F: CCTGATATTTTATGTGTTC R: TTTCTCATATTCAACTGT  | 210 | 43.4540.71 |
|  |  | *qRT-PCR* | F: GTTGCAAGTTGGAATGCTGC R: CCAGCATAACCTTTCTTAGCCG  | 170 | 58.8659.39 |
| *ehfen1* | XM\_646178.1 | *RT-PCR* | F: GAAGGTACTTGTGCTGCATTAG R: CATCCAAGTAAAATACAAAGG  | 218 | 55.3550.40 |
|  |  | *qRT-PCR* | F: ACCACCAGAAATGAAGGATGG R: GCAGCACAAGTACCTTCTGC | 231 | 57.9159.48 |
| **Both** **Pathways** |
| *ehpcna* | XM\_646418.1 | *RT-PCR* | F: GCACTTGACAATGATTGTGG R: GTAATTTTGAGGAATTCTGC  | 200 | 55.8950.19 |
|  |  | *qRT-PCR* | F: TCCAGAACTTCAATCTGACGR: AGCACCTTTAGTAGTGAGAG | 142 | 5251 |
| *ehdnaligI*  | XM\_652503.2 | *RT-PCR* | F: GATTATTTAAATGGATTAG R: AGTCTTCAAATGTTCATAC | 259 | 40.1342.52 |
|  | *qRT-PCR* | F: GATTAGCCGATACAGTTGACR: ATCTCCACTGTCTTCATCTC | 113 | 50.551.1 |
| **Positive DNA Damage control** |
| *ehmutS* | XM\_647442.1 | *qRT-PCR* | F: ATTCTATCCGTCCAACAACCR: GAAGTTCAAACCCCTTTTGG | 104 | 55.154.9 |
| **Internal control** |
| *40s rps2* | XM\_643876.2 | *qRT-PCR* | F: ATTCGGAAATAGAAGAGGAGGR: ACTAATCTT CCAAGCTTGGT | 105 | 57.554.3 |

&According to NCBI