1011.188

```
ACAAGATCGTGTATCCTTTGCCTGCT······AAATGGAATGACCTTAATCTGGGGTTCTAGCCACTTTTCT  Hsap NM_000379 i03            11 1 2 OK
ACAAGATTGTGTATCCTTTGCCTGGT······CAATGAAACAACCTTAATCTGTGGTTCTAGTCATTTTTCT  Rnor NM_017154 i03            11 1 2 OK
AGAAAATCCTGTATCCTTTGCAGTCT······AAATGAAATGACCTTAATCTATCATTTTAGCCACCATACT  Ggal chr3_4307816_4308333      11 1 2 OK
```

1011.190

```
TTTTGGAAACGTATCCTTTGTTTCAC······GAGAAATGTGATTCTTGACTGGAAAAATAGATGTGTCGTG  Hsap NM_000968 i03            11 1 1 OK
CTTTGGAAACGTATCCTTTGTTGGTG······AAAAGAAAAATTCTTGACAAAAGAAATCAGATGTGTCGTG  Rnor NM_022510 i03            11 1 1 OK
CTTTGGAAATGTATCCTTTGATATCT······GAAAGGTTGTTCTTAACTGTAGATACTTAGATGTGTCGTG  Ggal chr10_1716825_1717468     11 1 1 OK
```

1011.193

```
AGTTTGTGGAGTATCCTTGAGGTTTC······CCTTGGCTAGGGTCCTAAACTCAGGGACAGCTACAACAAG  Hsap NM_004573 i17            11 2 1 OK
AGTTTGTGGAGTATCCTTGAGGCTTT······GCCTTGGCTAGCTCCTATACCCAACAACAGCTATAATAAA  Rnor NM_053478 i17            11 2 2 OK
AGTTTGTGGAGTATCCTTTTGGCAGT······CCAGTTTGGGTTCCAATAGAGCAATTATAGATACAACAAG  Ggal chr5_2788180_2788814      10 0 0 OK
```

1011.195

```
TGCCTTCAGTGTATCCTTTGGGCGCT······GAATTGATTTTTCTTGAGCAGATTGATTAGATGGAGCTGC  Hsap NM_006141 i06            11 1 2 OK
TGCCTCCAGTGTATCCTTGGGACGCT······GAATTGGTTTTCCTTAAGCAAATGGATCAGATGGAGCTGC  Rnor NM_031026 i06            11 1 1 OK
TGCTTACAGTGTATCCTTTCCTGCTC······CTATGTATTTTTCCTTAAATAAATGATCAGATGGAGCTGC  Ggal chr11_11675855_11676572   11 1 1 OK
```