

```
human  MSSYFVNSTFPVTLASGQESFLGQLPLYSSGYADPLRHYPAPYGPFGQDKGFATSSYYP 60
mouse  MSSYFVNSTFPVTLASGQESFLGQLPLYSSGYADPLRHYPAPYGPFGQDKGFAASSYYP 60
*****
human  PAGGGYGRAAPCDYGPAPAFYREKESACALSGADEQPPFHPEPRKSDCAQDKSVFGETEE 120
mouse  PAGGGYGRAAPCDYGPAPAFYREKDAACALSGADEPPPFHPEPRKSDCAQDKSVFGETEE 120
*****:*****
human  QKCSTPVYPWMQRMNSCNSSSFGPSGRRGRQTYTRYQTLELEKEFHYNRYLTRRRRIEIA 180
mouse  QKCSTPVYPWMQRMNSCNSSSFGPSGRRGRQTYTRYQTLELEKEFHYNRYLTRRRRIEIA 180
*****
human  HALCLTERQIKIWFQNRMRKWKESKLLSASQLSAEEEEKQAE 224
mouse  HALCLTERQIKIWFQNRMRKWKESKLLSASQLSAEEEEKPAE 224
***** **
```

**Figure S1.** Sequence alignment of the mouse and human Hoxb6 proteins. The homeodomain (HD) is highlighted in blue, the hexapeptide (HX) in green and the linker region (LR) in orange.\* indicates positions which have a conserved residue and : indicates conservation between groups of strongly similar properties.

```

human AGGUGUCUGGAAAGGGAGGGAGGACGCGAGGGGAAAGGCCUGUGGGG-AGCCGAGGGCGUC 59
mouse AGGUGUCUGCAAAGGGAGGGGGACGCGAAGGGAGAGGUCUGUGGGGAACCUAGGGCACC 60
*****

human AGAGAGACCCGGGAAGGAAGGCUCU-CGGGUGGGGGAGCCAGGAGACCGUCUCUCCGGCG 118
mouse CGAAAGCCCC-----AGAAGGCUCUGCGGUCGGGGAGUCUGGGGACUUGCUGUCCAGAG 115
** ** **

human CA-GACAGCGGGGCCAGCGCUCUCCUGGACGCCCCCGCCGACAGCUCUCCGGCGGGU 177
mouse CACGACGGGCAGGGCCAGUGCUUGCUGGAUGCCCCUUCUGCAGAGCUCUCCUGGGC 175
** ** **

human GCUUCGAGGCCUCACUACUCGAGCCACCAGCAUCCC--GCGCGCCUUCUUCUCC--GA 234
mouse GCUUGCGGAU-----GCCACCAGCACCCAGCGCCUCCUCCUCCCGA 224
** * **

human GGAACUCGCCUCAGCCUGAUCAGGCUCCUGGUGAGAACUGAGGAGCGGACUCACUUGAU 294
mouse AGAACCACCUUGGCCUCAUCAGGCUUCUGGUGAGAACUGAGAAUCGGACUCACUUGAU 284
**** * **

human GUUUCUGGAAGCAGAGCAAAUUGCUCUUGUCCUGUCGCGUCUCAUUUUGUCCAUUGUC 354
mouse GUCUCCUGGAAGCAGAGCAGAAUUGCUCUUGUCCUGUCGAGUCUCAUUUUGUCCAUUGUC 344
** *****

human CCCGUGCACGGUCAAUGGUAGAUUCGUGUCCUCCAGCGGGGCCUUGAAGACUCCU 414
mouse CCCGUGCACGGUCAAUGGUAGAUUCGUGUCCUCCAGCAGGGACCGAAAGACUCCU 404
*****

human GAUCCAGACCGUCGUCUCCACCCUCCCAAAGCCACUGGAAGGAGCACAUAUC 474
mouse GACCCAGACUUGUC---UCUCCUACCCUCCCAAAGCCACUGGAAGGAGCACAUAUC 461
** *****

human ACCUAGAAGUAAGAAGAGGAGCCUCAGAAGAAAACAAGUUCUAUUUUUAUUUUUCUA 534
mouse ACCUAGAAGGAAGAAGAGGAGCCUCAGAAGAAAACAAGUUCUAUUUUUAUUUUUCUA 521
*****

human UGUGUUGUGUUUGUAGUCUUGUCUAGCUCUGGACGUGAAAACUUCGAUGAUGAUG 594
mouse UGUGUUGUGUUUGUAGUCUUGUCUAGCUCUGGACGUGAAAACUUCGGUAAUAUAUA 581
*****

human AUGAUGAUGAUGAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUA 654
mouse AU---AUUAU-----UAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUA 632
** ** **

human AAACUCGACGUCUGGUCACCUCAAAAAAAAAA 686
mouse AAACUCG-CAAAAAAAAAAAAAAAAAAAAAA 663
***** *

```

**Figure S2.** Sequence alignment of the mouse and human 3'UTRs. \* indicates positions with conserved nucleotides.