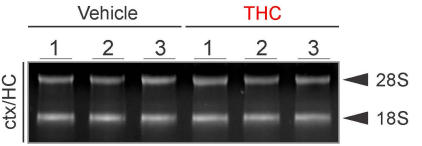
**A**

| GenBank number | Protein | Primer pair | Localization |
|---|---|---|---|
| NM_025285 | SCG10 | 5'-GCAATGGCCTACAAGGAAAA-3' | exon1/2 |
| | | 5'-GGTGGCTTCAAGATCAGCTC-3' | exon3 |
| NM_007726 | $CB_1R$ | 5'-TCTTAGACGGCCTTGCAGAT-3' | exon2 |
| | | 5'-AGGGACTACCCCTGAAGGAA-3' | exon2 |
| NM_008084 | GAPDH | 5'-AACTTTGGCATTGTGGAAGG-3' | exon4 |
| | | 5'-ACACATTGGGGGTAGGAACA-3' | exon5 |
| NM_013684 | TBP | 5'-ACCCTTCACCAATGACTCCTATG-3' | exon3 |
| | | 5'-ATGACTGCAGCAAATCGCTTGG-3' | exon5 |

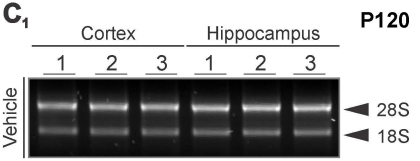
**B**

| SMARTpool | target sequence |
|---|---|
| siRNA (1) | ACAUAAUGCUACUGAACGU |
| siRNA (2) | AGUCAGGGUAGAAGCGAAA |
| siRNA (3) | UAUAAUGGAUCAUGCGAUA |
| siRNA (4) | CCUCAUGGAUUACGCGCUA |

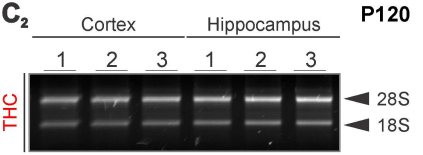
**C** **E18.5**




**$C_1$** **P120**




**$C_2$** **P120**




(1.5 columns)

Table SII **Primer sequences, siRNA targets and RNA quality controls.** (**A**) Quantitative real-time PCR reactions were performed with primer pairs amplifying short fragments for each gene. Primer pairs were designed to efficiently anneal to their target sequence on mouse cDNAs. (**B**) A pool of ON-TARGETplus SMART siRNAs were used (Thermo Scientific), with target sequences of the individual siRNA components shown. (**C-$C_2$**) The integrity of RNA used for gene expression profiling was tested by running total RNA (0.5 µg) from microdissected embryonic (E18.5; **C**) or adult (P120; **$C_1$,$C_2$**) mouse cortices and hippocampi on 1.0% agarose gels pre-loaded with GelRed (Biotium) (Keimpema *et al*, 2010). Sharply segregated 28S and 18S rRNA bands indicated intact total RNA. Three samples (1-3) per group were run in parallel.