Supplementary information to

Homologous cell type markers highlight subdivisions of domestic chick hippocampal formation

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List of supplementary material:

- **Supplementary Figure Legends**
- **Supplementary Figure 1**
- **Supplementary Figure 2**
- **Supplementary Figure 3**
- **Supplementary Figure 4**
- **Supplementary Figure 5**
- **Supplementary Figure 6**
- **Supplementary Figure 7**
- **Supplementary Figure 8**
- **Supplementary Figure 9**
- **Supplementary Table 1**
- **Supplementary Table 2**

Supplemental Figure Legends

Supplementary Figure 1. *In situ* hybridisation of *CPA6* in the P1 chick brains

DIG-labelled RNA antisense (a-f) and sense (a'-f') *CPA6* probes were used for *in situ* hybridisation in coronal sections of P1 chick brains. To evaluate the expression patterns of *CPA6*, sections of nine chicks were analysed and representative images are shown. (a''–f'') Diagrams of coronal sections are shown on the rightmost panels. The levels of the sections (A 8.0 to A 5.4) are in accordance with the chick atlas by Kuenzel and Masson[34]. A, arcopallium; CDL, area corticoidea dorsolateralis; DL, dorsal lateral region; DM, dorsal medial region; HF, hippocampal formation; LSt, lateral striatum; M: mesopallium; N: nidopallium; V, V-shaped complex. Scale bars = 2.5 mm (**c)** and **c')** for **a)**-**c)** and **a')**-**c')**) and 500 µm (**d)**–**f)**, **d')**–**f')**).

Supplementary Figure 2. Comparison of the expression patterns of HF cell type markers in the P1 chick at level A7.2-7.0

In situ hybridisation using DIG-labelled RNA antisense and sense *PROX1* (**a)** and **a')**), *LEF1* (**b)** and **b')**), *ZBTB20* (**c)** and **c')**), and *KIT* (**d)** and **d')**) probes in coronal sections of P1 chick brains. **a'')** Schematic diagrams showing the location of panels **a)**. The levels are in accordance with the chick atlas by Kuenzel and Masson[34]. A, arcopallium; HF, hippocampal formation; LSt, lateral striatum; M: mesopallium; N: nidopallium. Scale bar = 2.5 mm.

Supplementary Figure 3. Comparison of the expression patterns of HF cell type markers in the P1 chick at level A5.6-5.4

In situ hybridisation using DIG-labelled RNA antisense and sense *PROX1* (**a)** and **a')**), *LEF1* (**b)** and **b')**), *ZBTB20* (**c)** and **c')**), and *KIT* (**d)** and **d')**) probes in coronal sections of P1 chick brains. **a'')** Schematic diagrams showing the location of panels **a)**. The levels are in accordance with the chick atlas by Kuenzel and Masson[34]. HF, hippocampal formation; N: nidopallium. Scale bar = 2.5 mm.

Supplementary Figure 4. Comparison of the expression patterns of *GRIK1, GRIK2, GRIK3* in the P1 chick at level A8.8

In situ hybridisation using DIG-labelled RNA antisense and sense *GRIK1* (**a), e)** and **a'), e')**), *GRIK2* (**b), f)** and **b'), f')**), and *GRIK3* (**c), g)** and **c'), g')**) probes in coronal sections of P1 chick brains. **d)** Schematic diagrams showing the location of panels **a)-c)** and **a')-c')**. **d')** Schematic diagrams showing the location of panels **e)-g)** and **e')-g')**. The levels are in accordance with the chick atlas by Kuenzel and Masson[34]. DL, dorsal lateral region; DM, dorsal medial region; E, entopallium; H, hyperpallium; HF, hippocampal formation; LSt, lateral striatum; M: mesopallium; N: nidopallium. Scale bar = 2.5 mm (**a)-c)** and **a')-c')**) and 500 µm (**e)**–**g)**, **e')**–**g')**).

Supplementary Figure 5. Comparison of the expression patterns of *GRIK1, GRIK2, GRIK3* in the P1 chick at level A5.8

In situ hybridisation using DIG-labelled RNA antisense and sense *GRIK1* (**a), e)** and **a'), e')**), *GRIK2* (**b), f)** and **b'), f')**), and *GRIK3* (**c), g)** and **c'), g')**) probes in coronal sections of P1 chick brains. **d)** Schematic diagrams showing the location of panels **a)-c)** and **a')-c')**. **d')** Schematic diagrams showing the location of panels **e)-g)** and **e')-g')**. The levels are in accordance with the chick atlas by Kuenzel and Masson[34]. A, arcopallium; D, diencephalon; DL, dorsal lateral region; DM, dorsal medial region; HF, hippocampal formation; M: mesopallium; N: nidopallium; V, V-shaped complex. Scale bar = 2.5 mm (**a)-c)** and **a')-c')**) and 1 mm (**e)**–**g)**, **e')**–**g')**).

Supplementary Figure 6. *In situ* hybridisation of *GRIK4* in the P1 chick brains

DIG-labelled RNA antisense (**a)**, **b)**)and sense(**a')**, **b')**)*GRIK4* probes were used for *in situ* hybridisation in coronal sections of P1 chick brains. To evaluate the expression patterns of *GRIK4*, sections of five chicks were analysed and representative images are shown. (**a''), b'')**) Diagrams of coronal sections are shown on the rightmost panels. The levels of the sections (A 7.4) are in accordance with the chick atlas by Kuenzel and Masson[34]. A, arcopallium; DL, dorsal lateral region; DM, dorsal medial region; HF, hippocampal formation; LSt, lateral striatum; M: mesopallium; N: nidopallium; V, V-shaped complex. Scale bars = 2.5 mm (**a)** and **a')**) and 1 mm (**b)** and **b')**).

Supplementary Figure 7. Comparison of the expression patterns of *GRIK1, GRIK2, GRIK3* and HF cell type markers using neighboring sections in the P1 chick

In situ hybridisation using DIG-labelled RNA antisense and sense *PROX1* (**a)** and **a')**), *GRIK1* (**b)** and **b')**), *GRIK2* (**c)** and **c')**), *GRIK3* (**d)** and **d'),** and *LEF1* (**e)** and **e')**) probes in coronal sections of P1 chick brains. **a'')** Schematic diagrams showing the panels **a)**.The levels are in accordance with the chick atlas by Kuenzel and Masson[34]. A, arcopallium; FL, field L; HF, hippocampal formation; M: mesopallium; N: nidopallium. Scale bar = 2.5 mm (**a)**–**e)**, **a')**–**e')**).

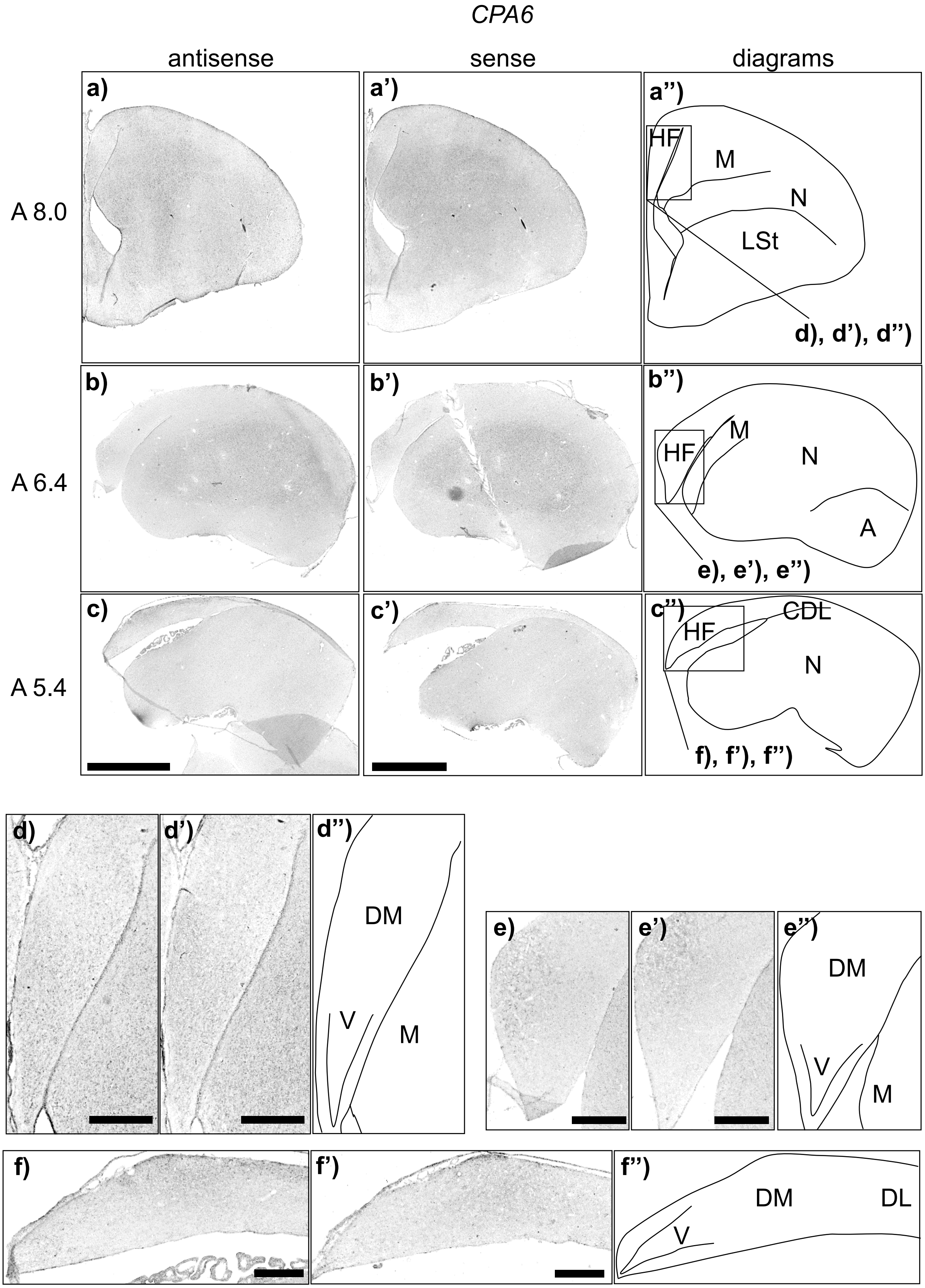
Supplementary Figure 8. Schematic summary

a) Representative expression patterns in sections A5.0, A7.0, and A8.0 are shown by coloured areas (magenta, *ZBTB20*; blue, *PROX1*; yellow, *KIT*) in the HF. Crossed arrows indicate anterior-posterior and lateral-medial directions. The levels are in accordance with the chick atlas by Kuenzel and Masson.[34] **b)** Schematic diagram of the expression regions of HF molecular markers in the chick and mouse HFs. The color code indicates pan-HF markers such as *ZBTB20* in magenta, DG markers such as *PROX1* in blue, CA3 markers in green, and CA1 markers such as *KIT* in chicken in yellow. It is unclear whether molecular marker expression in the border region between the chick DM and DL overlaps or is mutually exclusive. CA1, cornu ammonis field 1; CA3, cornu ammonis field 3; DG, dentate gyrus; DL, dorsal lateral region; DM, dorsal medial region; V, V-shaped complex.

Supplementary Figure 9. Probe sequencing and alignment prepared in this study

Subcloned template sequences and alignment results of **a)** *ZBTB20*, **b)** *PROX1*, **c)** *CPA6*, **d)** *KIT*, **e)** *GRIK1*, **f)** *GRIK2*, **g)** *GRIK3*, **h)** *GRIK4*, and **i)** *SOX11* probes were shown.

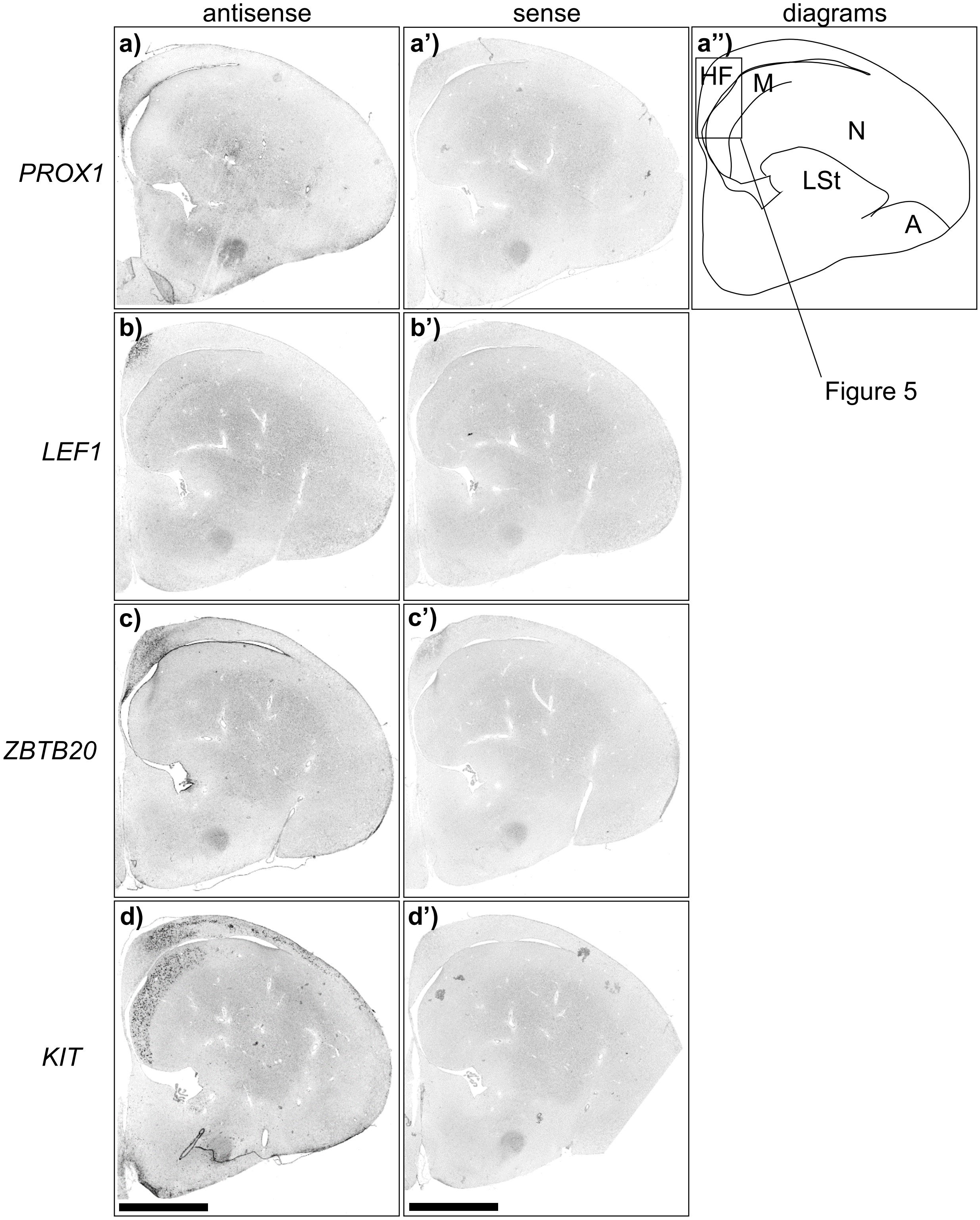
Supplemental Figure 1



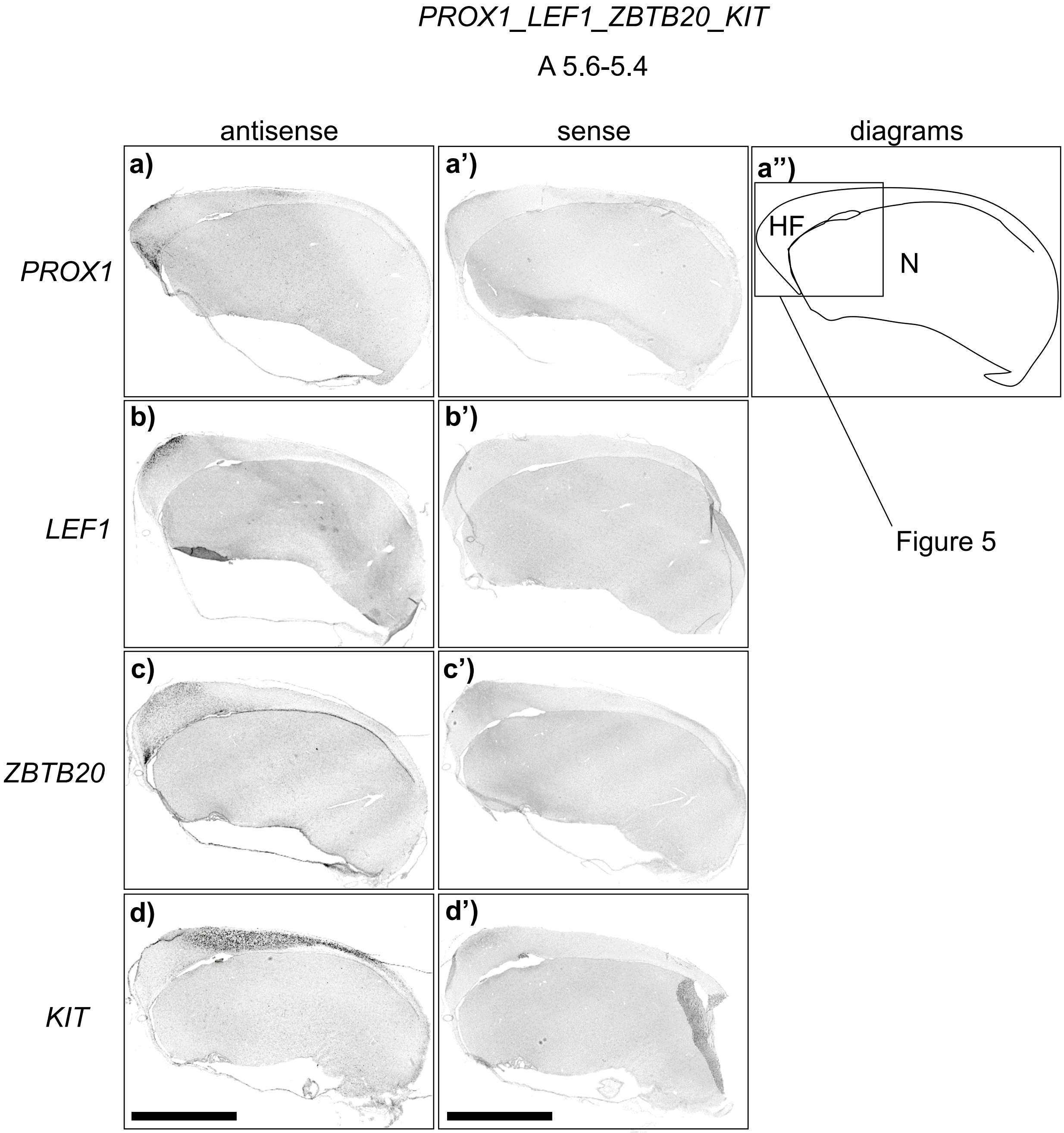
Supplemental Figure 2

PROX1_LEF1_ZBTB20_KIT

A 7.2-7.0



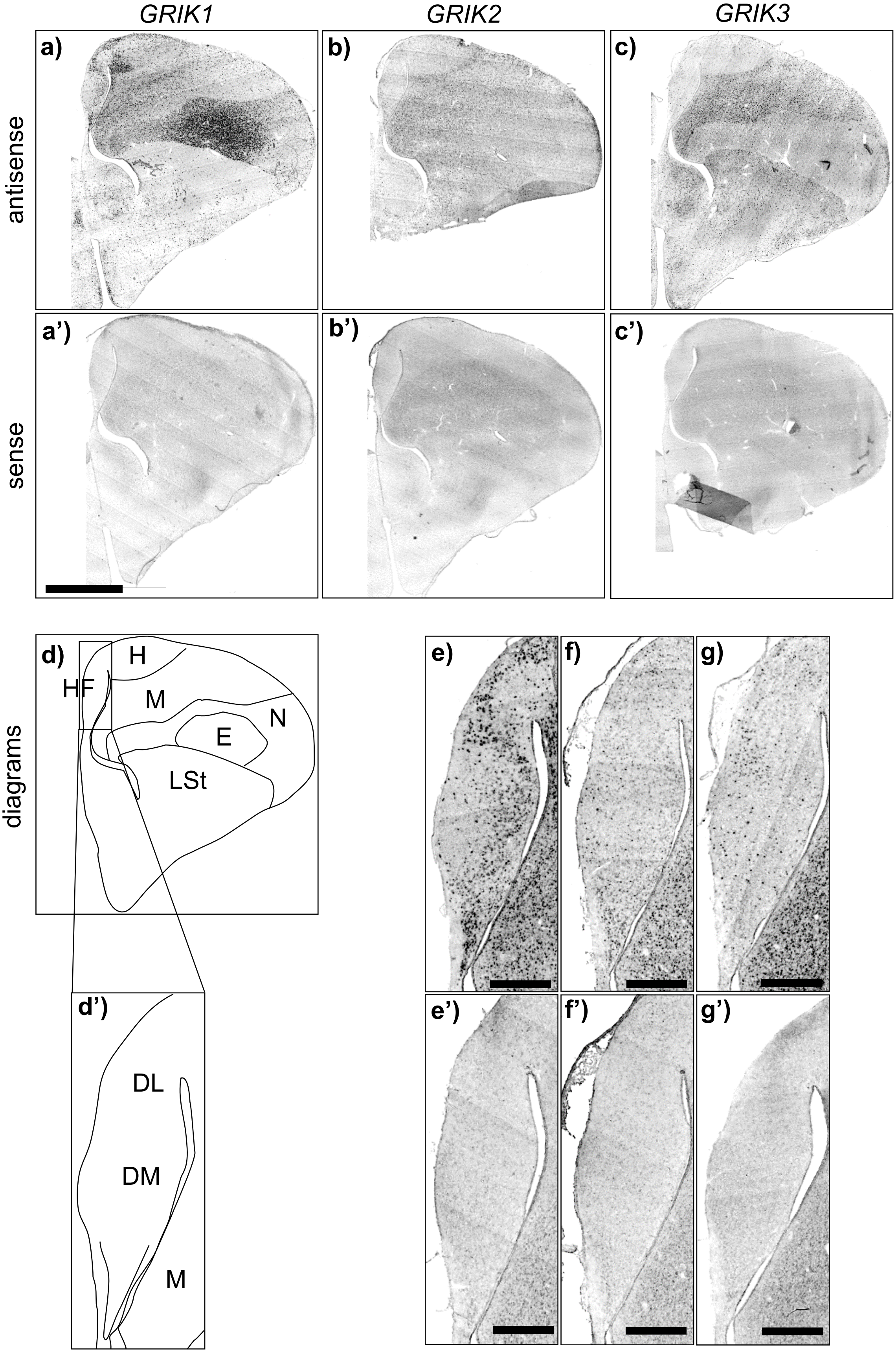
Supplemental Figure 3



Supplemental Figure 4

GRIK1_GRIK2_GRK3

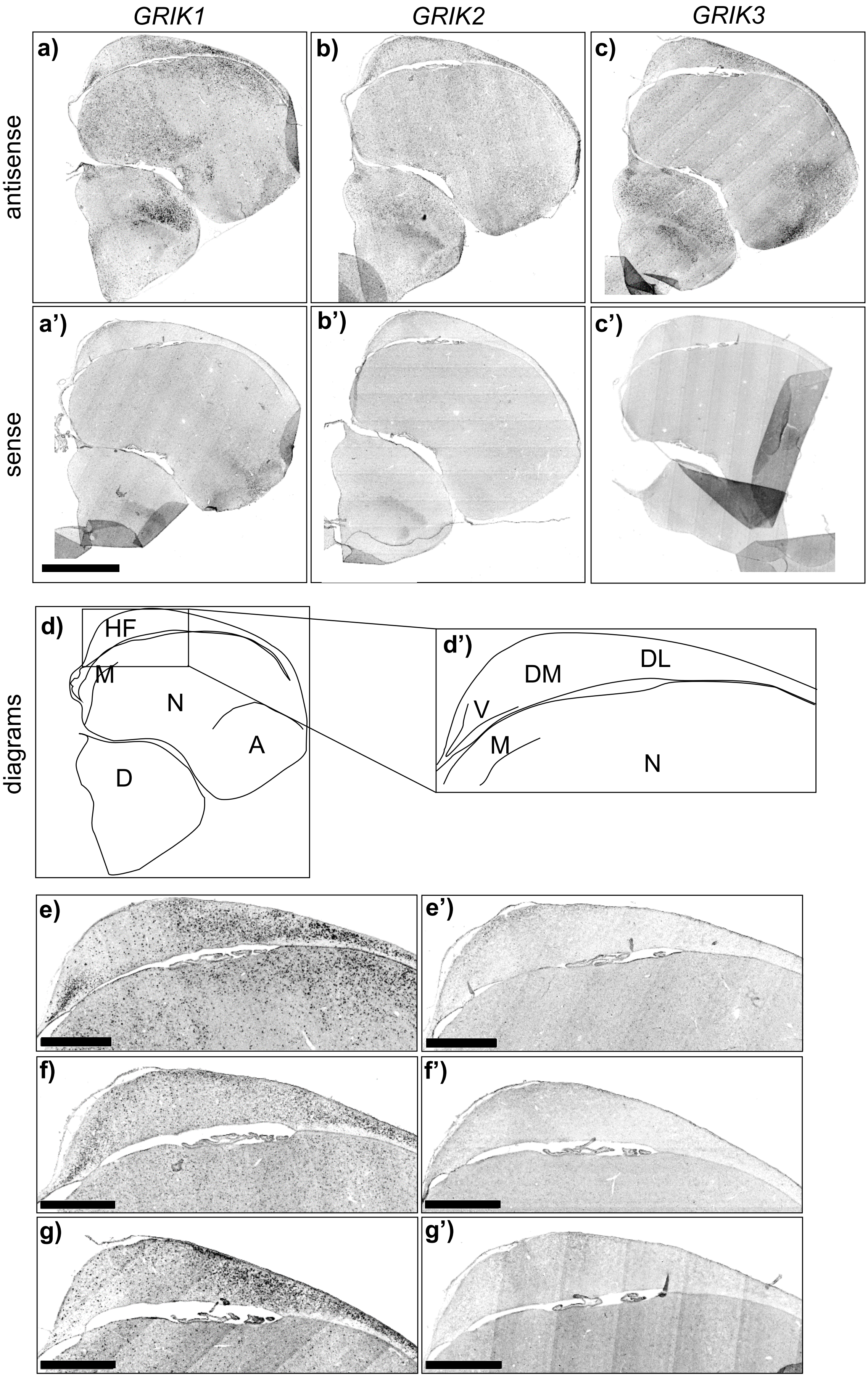
A 8.8



Supplemental Figure 5

GRIK1_GRIK2_GRK3

A 5.8



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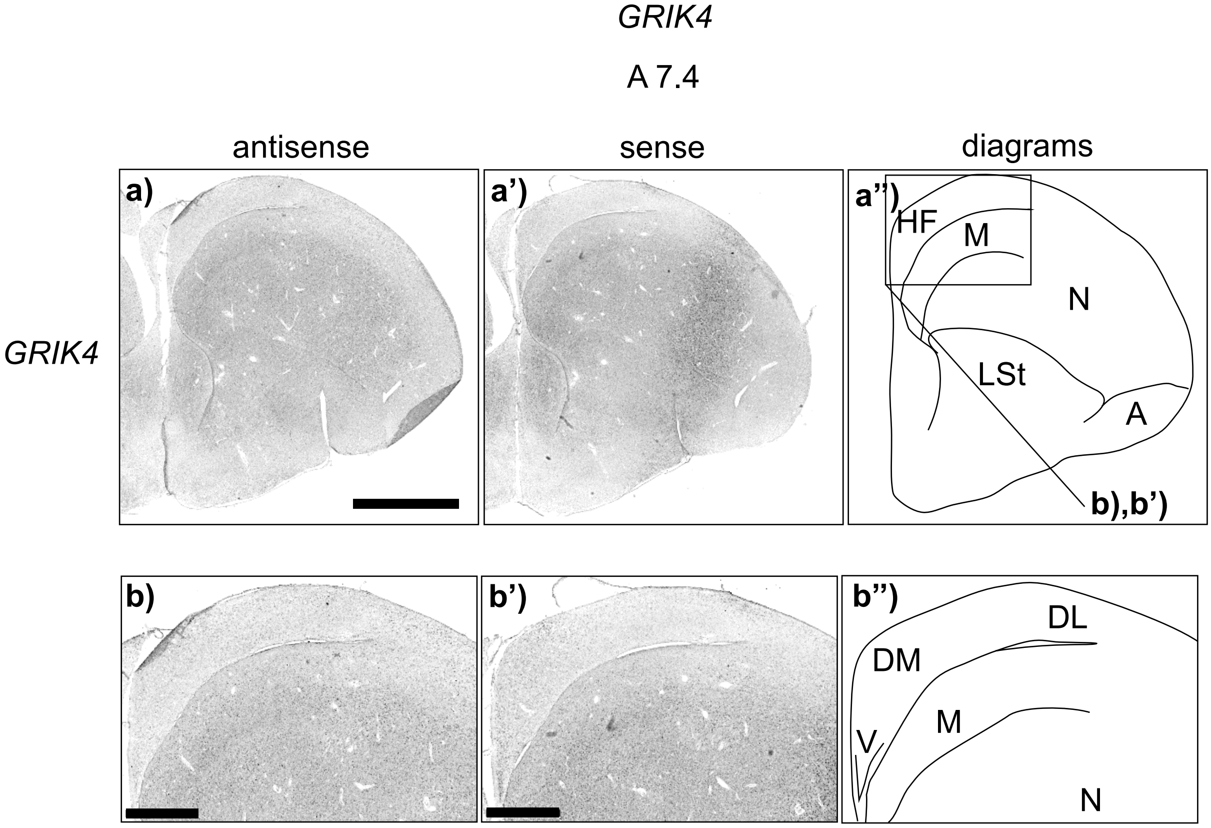
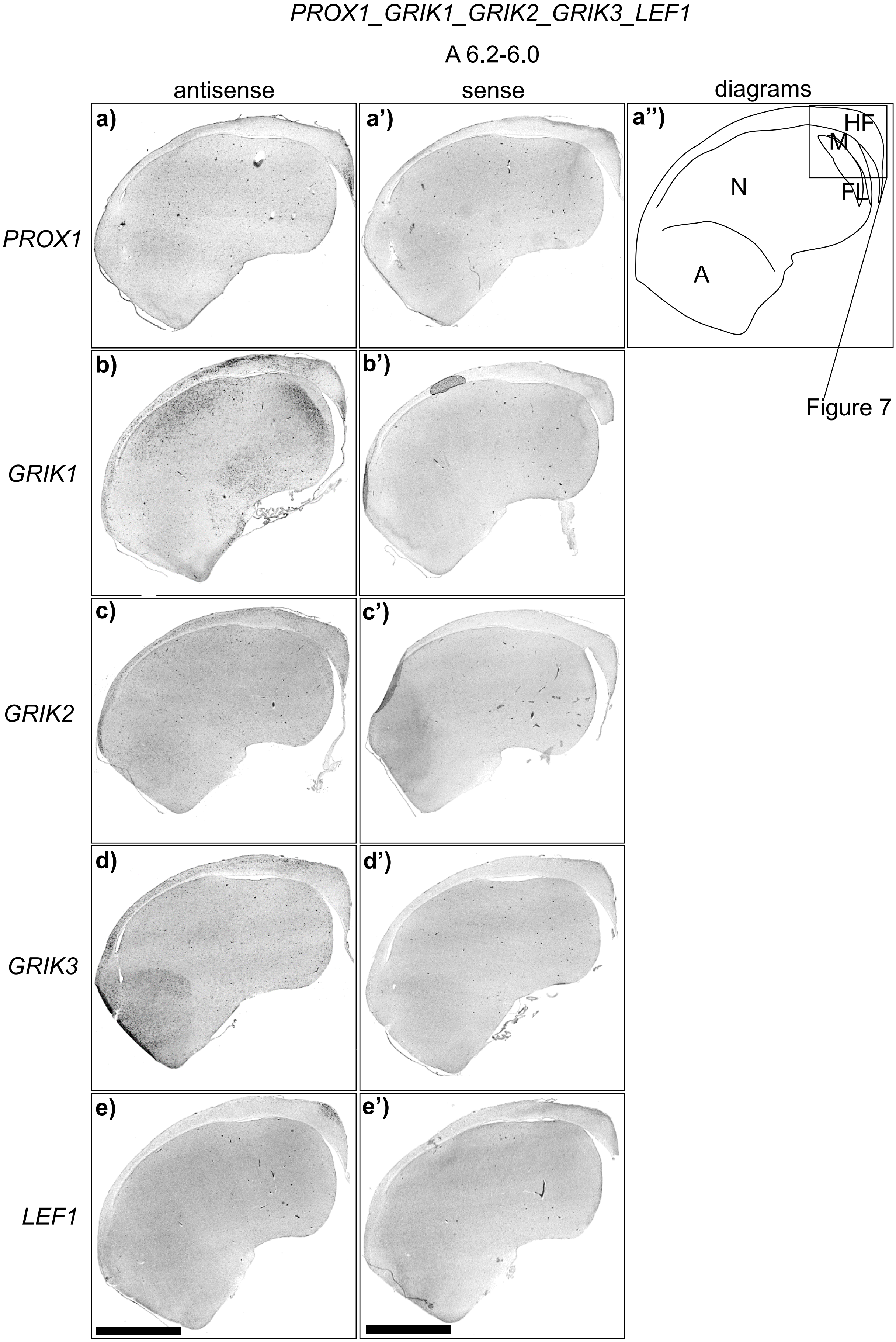
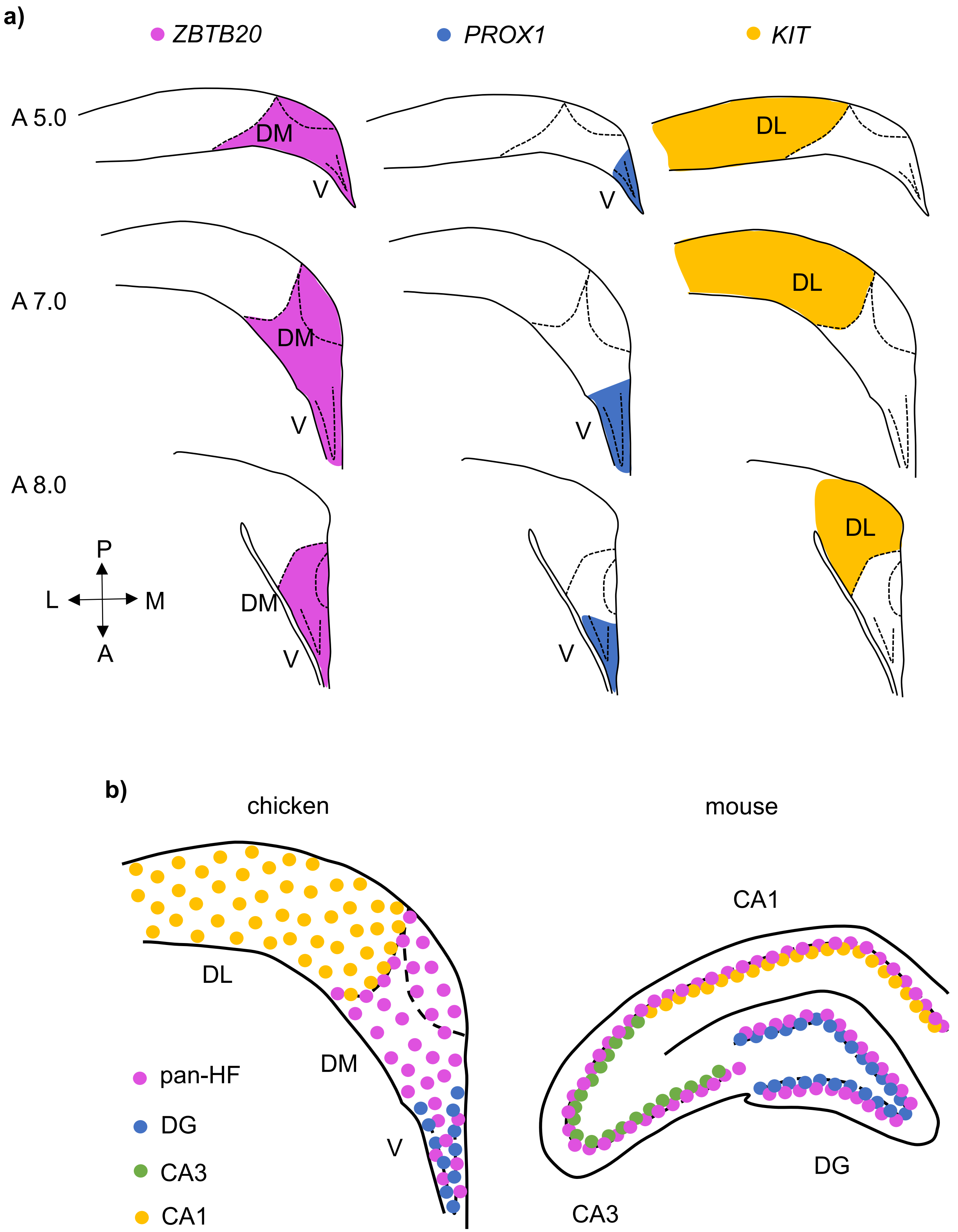


Supplemental Figure 7



Supplementary Figure 8



Supplementary Figure 9

a) *ZBTB20*

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transcript variant X29, mRNA
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Range 1: 1574 to 2333

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Identities:759/760(99%),  Gaps:0/760(0%), Strand: Plus/Minus

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b) *PROX1*

```
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>Gallus gallus homeodomain protein (Prox 1) mRNA, complete cds
Sequence ID: U46563.1 Length: 3322
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c) *CPA6*

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d) *KIT*

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transcript variant X1, mRNA
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Range 1: 2260 to 2982

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Sbjct  2380  TCCCCCAAAAGCTGATAAAAAAAGGCCGGTGAAATCTGGATCTTACACCGATCAGGATGT  2439

Query  181   TACCCTTTCCATGTTGGAAGATGACGAACTTGCTCTAGATGTTGAAGATCTATTAAGCTT  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2440  TACCCTTTCCATGTTGGAAGATGACGAACTTGCTCTAGATGTTGAAGATCTATTAAGCTT  2499

Query  241   CTCTTACCAGGTGGCAAAGGGCATGAGCTTCCTGGCCTCTAAAAACTGCATTCATAGGGA  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2500  CTCTTACCAGGTGGCAAAGGGCATGAGCTTCCTGGCCTCTAAAAACTGCATTCATAGGGA  2559

Query  301   TCTGGCAGCAAGAAATATTCTTCTCACTCATGGTCGAATAACAAAAATCTGTGACTTTGG  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2560  TCTGGCAGCAAGAAATATTCTTCTCACTCATGGTCGAATAACAAAAATCTGTGACTTTGG  2619

Query  361   CCTGGCAAGAGATATAAGGAATGACTCAAATTACGTGGTTAAAGGAAATGCTCGTCTCCC  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2620  CCTGGCAAGAGATATAAGGAATGACTCAAATTACGTGGTTAAAGGAAATGCTCGTCTCCC  2679

Query  421   TGTGAAGTGGATGGCACCTGAAAGCATTTTCAACTGCGTTTACACCTTCGAGGGTGATGT  480
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  2680  TGTGAAGTGGATGGCACCTGAAAGCATTTTCAACTGCGTTTACACCTTCGAGAGTGATGT  2739

Query  481   CTGGTCTTATGGAATATTGCTTTGGGAACTCTTCTCCTTAGGAAGCAGCCCTTACCCAGG  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2740  CTGGTCTTATGGAATATTGCTTTGGGAACTCTTCTCCTTAGGAAGCAGCCCTTACCCAGG  2799

Query  541   GATGCCCGTGGACTCCAAGTTCTATAAAATGATCAAGGAGGGATATCGGATGTTCAGCCC  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2800  GATGCCCGTGGACTCCAAGTTCTATAAAATGATCAAGGAGGGATATCGGATGTTCAGCCC  2859

Query  601   CGAGTGCTCACCCCCCGAAATGTACGACATAATGAAGAGTTGCTGGGATGCCGATCCCTT  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2860  CGAGTGCTCACCCCCCGAAATGTACGACATAATGAAGAGTTGCTGGGATGCCGATCCCTT  2919

Query  661   GCAGAGACCCACATTCAAACAGATCGTGCAGCTGATAGAACAGCAGCTTTCCGATAATGC  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2920  GCAGAGACCCACATTCAAACAGATCGTGCAGCTGATAGAACAGCAGCTTTCCGATAATGC  2979

Query  721   CCC  723
             |||
Sbjct  2980  CCC  2982
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e) *GRIK1*

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>PREDICTED: Gallus gallus glutamate ionotropic receptor kainate type subunit 1
(GRIK1), transcript variant X1, mRNA
Sequence ID: XM_015299614.4 Length: 3337
Range 1: 2146 to 2844

Score:1291 bits(699), Expect:0.0,
Identities:699/699(100%),  Gaps:0/699(0%), Strand: Plus/Minus

Query  1     CTGCTCAATATCACTGTTTTTCCTTGATTTATAAATAAATTCACCAATGGCTACGAACAC  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2844  CTGCTCAATATCACTGTTTTTCCTTGATTTATAAATAAATTCACCAATGGCTACGAACAC  2785

Query  61    TGAAAGAACAAGCCCAGCAGCGAGCACTATGAAGATGCCCCCGATATTCTCCACCCCGAG  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2784  TGAAAGAACAAGCCCAGCAGCGAGCACTATGAAGATGCCCCCGATATTCTCCACCCCGAG  2725

Query  121   AGCACTGGCTTCTTTGCTGTCCTCTTCAGGGCAGCCGTTGCCTCGCCACCACTTTTCCTT  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2724  AGCACTGGCTTCTTTGCTGTCCTCTTCAGGGCAGCCGTTGCCTCGCCACCACTTTTCCTT  2665

Query  181   CATCATGTGGAGCTTCCCTTCCTCCTGGAGCTGGAGGATGGCAATGGTGATCTTGTCCCT  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2664  CATCATGTGGAGCTTCCCTTCCTCCTGGAGCTGGAGGATGGCAATGGTGATCTTGTCCCT  2605

Query  241   ATAAGGTGACCCAATAGGGGTTCCCACTCCATAGCCTTTTGAATCGATGAGTCCCCCGAT  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2604  ATAAGGTGACCCAATAGGGGTTCCCACTCCATAGCCTTTTGAATCGATGAGTCCCCCGAT  2545

Query  301   CTGAGTGAGGTTGCAGTTTCTCTGAGTCACATACTCAATGCTGGTGGACTCCATCAGCAG  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2544  CTGAGTGAGGTTGCAGTTTCTCTGAGTCACATACTCAATGCTGGTGGACTCCATCAGCAG  2485

Query  361   CGCATAGTCTGTCGTGAGCACACGCTGGATTCCCTCATCATTGTTCTTCACCAGTGCTGT  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2484  CGCATAGTCTGTCGTGAGCACACGCTGGATTCCCTCATCATTGTTCTTCACCAGTGCTGT  2425

Query  421   CTGCTGCCTGCTGCTCATGAATGCCCACATCTTCTCATATGTTGATATCTTGGATTTCTT  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2424  CTGCTGCCTGCTGCTCATGAATGCCCACATCTTCTCATATGTTGATATCTTGGATTTCTT  2365

Query  481   GAAGAAGGTCATTGTGGATCCATCTCTAACAGCCCCGTACTCTATTTTGGTTTGCTTTGC  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2364  GAAGAAGGTCATTGTGGATCCATCTCTAACAGCCCCGTACTCTATTTTGGTTTGCTTTGC  2305

Query  541   CAAATCGTCGGCTGAATCGATGGGGGATTCCATCCTTTCTACCGTCAGGAAGGCAGCCAG  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2304  CAAATCGTCGGCTGAATCGATGGGGGATTCCATCCTTTCTACCGTCAGGAAGGCAGCCAG  2245

Query  601   GTTGGCAGTATAGGATGAGATTATGATTAAGGTGAAAAACCACCATATTCCTCCAACTAT  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2244  GTTGGCAGTATAGGATGAGATTATGATTAAGGTGAAAAACCACCATATTCCTCCAACTAT  2185

Query  661   TCTGGTGGAAAGAGCTTTGGGCATCAGCTCTGATCCTTG  699
             |||||||||||||||||||||||||||||||||||||||
Sbjct  2184  TCTGGTGGAAAGAGCTTTGGGCATCAGCTCTGATCCTTG  2146
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f) *GRIK2*

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>PREDICTED: Gallus gallus glutamate ionotropic receptor kainate type subunit 2
(GRIK2), transcript variant X11, mRNA
Sequence ID: XM_046939222.1 Length: 2189
Range 1: 1441 to 2156

Score:1317 bits(713), Expect:0.0,
Identities:715/716(99%),  Gaps:0/716(0%), Strand: Plus/Minus

Query  1     ACCCAAGTAAGCCAGCAGAACATACATCCAGATATCAGGGGAGAGAGGATTCAGGAAGGA  60
             |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  2156  ACCCAAGTAAGCCAGCAGAATATACATCCAGATATCAGGGGAGAGAGGATTCAGGAAGGA  2097

Query  61    GAAGACGCCCGGGTTTGTACCATTGGGCTTGCGGTACAAAATACTTATTCCAAGAGTCAT  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2096  GAAGACGCCCGGGTTTGTACCATTGGGCTTGCGGTACAAAATACTTATTCCAAGAGTCAT  2037

Query  121   AAACGGCTTGGAAAAGTCGATGACTTTCTCACGAACATAGGTAATTGCCAATGGTGCAAC  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2036  AAACGGCTTGGAAAAGTCGATGACTTTCTCACGAACATAGGTAATTGCCAATGGTGCAAC  1977

Query  181   TGCAAGGTCAGCTTTATGATCAATTAATTCACGAACCATTCCATTCCACTGTCCACTGGC  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1976  TGCAAGGTCAGCTTTATGATCAATTAATTCACGAACCATTCCATTCCACTGTCCACTGGC  1917

Query  241   ATCCTCCTGGGCTCCATATTTTCCATCCTCCACCAGTCTAATCTCATAGGAAAATCCAAG  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1916  ATCCTCCTGGGCTCCATATTTTCCATCCTCCACCAGTCTAATCTCATAGGAAAATCCAAG  1857

Query  301   GATAGTAGACAGCTCCCTGAGGAGGTCAATGCAATAACCTTCAAATCGATCATTTCCATA  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1856  GATAGTAGACAGCTCCCTGAGGAGGTCAATGCAATAACCTTCAAATCGATCATTTCCATA  1797

Query  361   CAAAGGTTTATCTGATTTCTTGAACATTACATATGGCTCTTCCAAGATGGTGGTAACTAT  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1796  CAAAGGTTTATCTGATTTCTTGAACATTACATATGGCTCTTCCAAGATGGTGGTAACTAT  1737

Query  421   TAAAGAACGATTGGACAGGGAATCCGTGATGTTTGCTGGTTTTCCTTTCTGATTCTCTGT  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1736  TAAAGAACGATTGGACAGGGAATCCGTGATGTTTGCTGGTTTTCCTTTCTGATTCTCTGT  1677

Query  481   CATGTTAAGGCCACTCAGTGGATCCCAAGTTCCAACCTTTTCAAGACCTTCTTCCTTGAG  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1676  CATGTTAAGGCCACTCAGTGGATCCCAAGTTCCAACCTTTTCAAGACCTTCTTCCTTGAG  1617

Query  541   GCTTATAACATCTAAATCAAAATCTGTCCTTAAGCCATTGGATTTGTTGAAAGTTATCCT  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1616  GCTTATAACATCTAAATCAAAATCTGTCCTTAAGCCATTGGATTTGTTGAAAGTTATCCT  1557

Query  601   TCCTGTGAGGCCTTCCCAGTGAGCCTCCTTAATGAGACTCATAAAGCGAGTCCCAAAGCG  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1556  TCCTGTGAGGCCTTCCCAGTGAGCCTCCTTAATGAGACTCATAAAGCGAGTCCCAAAGCG  1497

Query  661   CCAAGGTTTGTGGCGATTACACTGTAGTGAACTGACAGTCATCTGTGGGAACTGCT  716
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1496  CCAAGGTTTGTGGCGATTACACTGTAGTGAACTGACAGTCATCTGTGGGAACTGCT  1441
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g) *GRIK3*

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>PREDICTED: Gallus gallus glutamate ionotropic receptor kainate type subunit 3
(GRIK3), transcript variant X1, mRNA
Sequence ID: XM_417766.7 Length: 6097
Range 1: 2109 to 2900

Score:1456 bits(788), Expect:0.0,
Identities:791/792(99%),  Gaps:1/792(0%), Strand: Plus/Plus

Query  1     CTCGCCGCCTTCCTGACAGTGGAGAGGATGGAATCCCCCATTGACTCAGCAGACGACCTG  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2109  CTCGCCGCCTTCCTGACAGTGGAGAGGATGGAATCCCCCATTGACTCAGCAGACGACCTG  2168

Query  61    GCAAAGCAGACCAAAATCGAGTATGGGGCTGTGAAGGATGGGGCAACCATGACCTTCTTC  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2169  GCAAAGCAGACCAAAATCGAGTATGGGGCTGTGAAGGATGGGGCAACCATGACCTTCTTC  2228

Query  121   AAGAAATCCAAAATTTCCACCTTTGAAAAAATGTGGGCTTTCATGAGCAGCAAACCCACG  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2229  AAGAAATCCAAAATTTCCACCTTTGAAAAAATGTGGGCTTTCATGAGCAGCAAACCCACG  2288

Query  181   GCTCTCGTCAAGAACAACGAGGAGGGAATCCAGCGCACCCTGACGGCCGACTACGCCCTG  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2289  GCTCTCGTCAAGAACAACGAGGAGGGAATCCAGCGCACCCTGACGGCCGACTACGCCCTG  2348

Query  241   CTGATGGAGTCCACCACCATCGAGTACATCACCCAGAGGAACTGCAACCTCACCCAGGTC  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2349  CTGATGGAGTCCACCACCATCGAGTACATCACCCAGAGGAACTGCAACCTCACCCAGGTC  2408

Query  301   GGGGGGCTCATCGACTCCAAGGGCTACGGGATTGGGACCCCCATGGGCTCACCGTACCGG  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2409  GGGGGGCTCATCGACTCCAAGGGCTACGGGATTGGGACCCCCATGGGCTCACCGTACCGG  2468

Query  361   GACAAGATCACCATCGCCATCCTGCAGCTGCAGGAGGAGGACAAGCTGCACGTCATGAAG  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2469  GACAAGATCACCATCGCCATCCTGCAGCTGCAGGAGGAGGACAAGCTGCACGTCATGAAG  2528

Query  421   GAGAAGTGGTGGCGGGGGAACGGTTGCCCTGAGGATGAGAACAAGGAGGCCAGTGCCCTG  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2529  GAGAAGTGGTGGCGGGGGAACGGTTGCCCTGAGGATGAGAACAAGGAGGCCAGTGCCCTG  2588

Query  481   GGCATCCAAAACATCGGCGGCATTTTCATCGTGCTGGCAGCAGGCTTGGTGCTGTCGGTC  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2589  GGCATCCAAAACATCGGCGGCATTTTCATCGTGCTGGCAGCAGGCTTGGTGCTGTCGGTC  2648

Query  541   TTTGTGGCCATGGTGGAGTTCATCTACAAGCTGCGGAAGACGGCGGAACGCGAGCAGCGC  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2649  TTTGTGGCCATGGTGGAGTTCATCTACAAGCTGCGGAAGACGGCGGAACGCGAGCAGCGC  2708

Query  601   TCCTTCTGCAGCGCGGTGGCCGATGAGATCCGGCTGTCTCTCACCTGCCAGCGCCGGGTC  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2709  TCCTTCTGCAGCGCGGTGGCCGATGAGATCCGGCTGTCTCTCACCTGCCAGCGCCGGGTC  2768

Query  661   AAGCACAAACCACCACCACCCGTCATGGTGAAGGCGGATGCTGTGATCAACATGCACACC  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2769  AAGCACAAACCACCACCACCCGTCATGGTGAAGGCGGATGCTGTGATCAACATGCACACC  2828

Query  721   TTCAACGACCGGCGGCTGCCAGGGAAGGACAGCATGAGCTGCAACACCGGCCTGACGCCC  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2829  TTCAACGACCGGCGGCTGCCAGGGAAGGACAGCATGAGCTGCAACACCGGCCTGACGCCC  2888

Query  781   GTGTTCC-ATAG  791
             ||||||| ||||
Sbjct  2889  GTGTTCCCATAG  2900
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h) *GRIK4*

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>PREDICTED: Gallus gallus glutamate ionotropic receptor kainate type subunit 4
(GRIK4), mRNA
Sequence ID: XM_015298177.4 Length: 4160
Range 1: 104 to 1286

Score:2135 bits(1156), Expect:0.0,
Identities:1174/1183(99%),  Gaps:0/1183(0%), Strand: Plus/Minus

Query  1     CCTTCAGAAACATGCCAGTGGCCGATCTGCCGGAAGCCGCTGTGTGTGTGCTGCAGGATT  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1286  CCTTCAGAAACATGCCAGTGGCCGATCTGCCGGAAGCCGCTGTGTGTGTGCTGCAGGATT  1227

Query  61    TTCAGGGCATAGTTGGAGCGCTGGCCTTTGCTGTTGAATTCGATGTGGCCGGTGAGACCT  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1226  TTCAGGGCATAGTTGGAGCGCTGGCCTTTGCTGTTGAATTCGATGTGGCCGGTGAGACCT  1167

Query  121   TCCAATTCTACCATGCGCAGGTAGTTCATCAGGCTGGTGCCATGCTGCCAGATCTGGGCA  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1166  TCCAATTCTACCATGCGCAGGTAGTTCATCAGGCTGGTGCCATGCTGCCAGATCTGGGCA  1107

Query  181   GAGCCACAGGACAGCGGCTTCACGCCGATCTCCTGGCTGCGGTTCAGCTCCTGCACGGCG  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1106  GAGCCACAGGACAGCGGCTTCACGCCGATCTCCTGGCTGCGGTTCAGCTCCTGCACGGCG  1047

Query  241   CTCACCACGGCGTACACGGCATCAAACAGCAGGGCAGAAGAGAGTGCTGGCCCAGTAAAA  300
             ||||||||||||||||| ||||| |||||||||||||| |||||||||||||||||||||
Sbjct  1046  CTCACCACGGCGTACACAGCATCGAACAGCAGGGCAGAGGAGAGTGCTGGCCCAGTAAAA  987

Query  301   GGAGCATGATCACAGTTCTCCTGCCAGGACTGGTTGAGGCTCTGGACAAACTCTTGGAAA  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  986   GGAGCATGATCACAGTTCTCCTGCCAGGACTGGTTGAGGCTCTGGACAAACTCTTGGAAA  927

Query  361   AAGGCGTGAGACTGGTTGAAAATGGAAAATCCCAGGATGTTGACTCGGTCATCCAATTGG  420
             |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  926   AAGGCGTGAGACTGGTTGAAAATGGAAAATCCCAGGATGTTGACTCGGTCGTCCAATTGG  867

Query  421   CTGTCCAGGCGCTGGAGTGAAAACTCCAGATTAGTGAAGATATATGTGTAATAGGCAGAT  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  866   CTGTCCAGGCGCTGGAGTGAAAACTCCAGATTAGTGAAGATATATGTGTAATAGGCAGAT  807

Query  481   GCCATTCCCAGCTCGGCTGCCTTCTGCAGGATGGTGTGGGACATGGAGGCGTTGGCATGG  540
             |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  806   GCCATTCCCAGCTCGGCTGCCTTCTGCAGGATGGTGTGGGACATGGAGGCATTGGCATGG  747

Query  541   ACAATGATGGTGGCCGTTTTGTCGTCTCTGATCTCTTTGAGGAGAGGCGTAGGGTCCCGG  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  746   ACAATGATGGTGGCCGTTTTGTCGTCTCTGATCTCTTTGAGGAGAGGCGTAGGGTCCCGG  687

Query  601   CTGTCATCCAGCATCCGGACTGAGAGCGTGTCCTTGGAAATGAGGAACTGCCGAAGCAAC  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  686   CTGTCATCCAGCATCCGGACTGAGAGCGTGTCCTTGGAAATGAGGAACTGCCGAAGCAAC  627

Query  661   TTCTCTAGGTTTAAAAGGCATTCAGCTTTGGCACAGATGAGGCAGGCAGTGGTGCAGTTA  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  626   TTCTCTAGGTTTAAAAGGCATTCAGCTTTGGCACAGATGAGGCAGGCAGTGGTGCAGTTA  567

Query  721   AAGAAGTTGAGGATTCTTGCCACGGCCACACTGATGTCAGTGTTGCTGGGGTGGAGGTTG  780
             |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  566   AAGAAGTTGAGGATTCCTGCCACGGCCACACTGATGTCAGTGTTGCTGGGGTGGAGGTTG  507
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GRIK4 (continued)

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Query  781   AGGGTGGTGAAGCGCTGGAGCTGCAGCTTCAGGAACTCTTCTGGTGCCACTCTGAAGTGA  840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  506   AGGGTGGTGAAGCGCTGGAGCTGCAGCTTCAGGAACTCTTCTGGTGCCACTCTGAAGTGA  447

Query  841   GGAACCTCTTTCTCCCCGCAGATATTGCTGATAATTGAGCTGGAGGCCGGGCTGGAGGAA  900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  446   GGAACCTCTTTCTCCCCGCAGATATTGCTGATAATTGAGCTGGAGGCCGGGCTGGAGGAA  387

Query  901   GGCCCCAGGACGCCCACCACCCCTTTGGGAAGGATCTGGCACATGGTTTCCGCCGTCTCA  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  386   GGCCCCAGGACGCCCACCACCCCTTTGGGAAGGATCTGGCACATGGTTTCCGCCGTCTCA  327

Query  961   TACTCGCTGTCCCGCAGCAGCTCGAAGATGTCCACCTCCACCTTGGCCTTCCCCAGGCGC  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  326   TACTCGCTGTCCCGCAGCAGCTCGAAGATGTCCACCTCCACCTTGGCCTTCCCCAGGCGC  267

Query  1021  TCGGGCGCACGGTTGATGCGGTTCTTGGCCAGGGTGATGGAGAGCCTCTCCCCCCGGCTG  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  266   TCGGGCGCACGGTTGATGCGGTTCTTGGCCAGGGTGATGGAGAGCCTCTCCCCCCGGCTG  207

Query  1081  CACTCCATGGGGTCATCCAGGATGGCGGCAATGCGCAGGGCGTGTGGGCTGGCGGCCGTC  1140
             |||||||||||||||||||||||||| |||||||| ||||||||||||||||| ||||||
Sbjct  206   CACTCCATGGGGTCATCCAGGATGGCAGCAATGCGTAGGGCGTGTGGGCTGGCAGCCGTC  147

Query  1141  CTCATCAGCCACAGCAGAAGGAGCACCAGAGGCGCCCATACAC  1183
             |||||||||||||||||||||||||||||||||||||||||||
Sbjct  146   CTCATCAGCCACAGCAGAAGGAGCACCAGAGGCGCCCATACAC  104
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i) ***SOX11***

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>Gallus gallus SRY-box 11 (SOX11), mRNA
Sequence ID: NM_001396047.1 Length: 1566
Range 1: 523 to 1255

Score:1354 bits(733), Expect:0.0,
Identities:733/733(100%),  Gaps:0/733(0%), Strand: Plus/Plus

Query  1      CGGTGGAAAATGCTGAAGGACAGCGAGAAGATCCCCTTCATCCGGGAGGCGGAGAGGCTG  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  523    CGGTGGAAAATGCTGAAGGACAGCGAGAAGATCCCCTTCATCCGGGAGGCGGAGAGGCTG  582

Query  61     CGGCTCAAGCACATGGCCGATTACCCCGACTACAAGTACCGGCCCAGGAAAAAGCCCAAA  120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  583    CGGCTCAAGCACATGGCCGATTACCCCGACTACAAGTACCGGCCCAGGAAAAAGCCCAAA  642

Query  121    ATGGACCCCTCGGCCAAGCCCAACGCCGGCCAGAGCCCCGAGAAGAACGCTCCCGGCGGC  180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  643    ATGGACCCCTCGGCCAAGCCCAACGCCGGCCAGAGCCCCGAGAAGAACGCTCCCGGCGGC  702

Query  181    GGCAGCAAGAGCGCCAAGAGCTCGGGCAAGAAGTGCAGCAAGCTGAAGgccgccgccgcc  240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  703    GGCAGCAAGAGCGCCAAGAGCTCGGGCAAGAAGTGCAGCAAGCTGAAGGCCGCCGCCGCC  762

Query  241    tcgcccccaagcccggcgccaaagccgccccTCACGGGGACTACGCGGGGGACGAGTAC  300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  763    TCGCCCCCAAGCCCGGCGCCAAAGCCGCCCCTCACGGGGACTACGCGGGGGACGAGTAC  822

Query  301    GTCTTCGGCGCGCTGAAAGTCAGCAGCAAGGCGGTCAAGTGCGTTTTCGTggacgaggag  360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  823    GTCTTCGGCGCGCTGAAAGTCAGCAGCAAGGCGGTCAAGTGCGTTTTCGTGGACGAGGAG  882

Query  361    gaggaggacgaggaggacgaggacgagctgcagctgcggatcaagcaggaggcggacgac  420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  883    GAGGAGGACGAGGAGGACGAGGACGAGCTGCAGCTGCGGATCAAGCAGGAGGCGGACGAC  942

Query  421    gaggaggaggacgaggagCCGGGCCCGCAGCAGCTGCGGCGGTACAACGTGGCCAAAGTG  480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  943    GAGGAGGAGGACGAGGAGCCGGGCCCGCAGCAGCTGCGGCGGTACAACGTGGCCAAAGTG  1002

Query  481    CCGGCCAGCCCCACCTTGAGCTCCTCGGCGGAGTCCACCGAGGGGGCGAGCCTCTACGAG  540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1003   CCGGCCAGCCCCACCTTGAGCTCCTCGGCGGAGTCCACCGAGGGGGCGAGCCTCTACGAG  1062

Query  541    GAGGTGCGGGGCGCGGCGGGCGGCGGCAGACTCTACTACAGCTTCAAGAACATCACCAAG  600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1063   GAGGTGCGGGGCGCGGCGGGCGGCGGCAGACTCTACTACAGCTTCAAGAACATCACCAAG  1122

Query  601    CAGGgcccgccgccgccgcagccgcccgccggcctctcccccgcctcgtcccgcTCCATC  660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1123   CAGGGCCCGCCGCCGCCGCAGCCGCCCGCCGGCCTCTCCCCCGCCTCGTCCCGCTCCATC  1182

Query  661    TCCACCTCGTCGGCCGGCAGCGAGGAGGCGGACGACCTCCTGTTCGACCTCAGCCTCAAC  720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1183   TCCACCTCGTCGGCCGGCAGCGAGGAGGCGGACGACCTCCTGTTCGACCTCAGCCTCAAC  1242

Query  721    TTCTCGCAGCATG  733
              |||||||||||||
Sbjct  1243   TTCTCGCAGCATG  1255
```

Supplemental Table 1. Subject summary used in this study

	probes											
chick#s	***ZBTB20***	***PROX1***	***CPA6***	***KIT***	***NR4A2***	***LEF1***	***GRIK1***	***GRIK2***	***GRIK3***	***GRIK4***	***SOX11***	RNA extraction
#1	○	○	○	○	-	○	○	○	○	-	-	-
#2	○	-	○	○	-	○	○	○	○	-	-	-
#3	○	○	○	○	-	○	○	○	○	-	○	-
#4	○	○	○	○	-	○	○	○	○	-	○	-
#5	○	○	○	○	-	○	○	○	○	-	○	-
#6	○	○	○	○	○	○	-	-	-	-	-	-
#7	○	○	-	○	○	○	-	-	-	-	-	-
#8	○	-	○	○	-	○	○	○	○	-	-	-
#9	○	-	○	○	-	-	-	-	-	-	○	-
#10	-	○	○	-	-	○	○	○	○	○	○	-
#11	-	○	-	-	-	○	-	-	-	-	○	-
#12	-	○	-	-	-	○	○	○	-	-	-	-
#13	-	-	○	-	-	○	-	-	-	-	-	-
#14	-	-	-	-	-	-	○	○	○	○	-	-
#15	-	-	-	-	-	○	○	○	○	-	○	-
#16	-	-	-	-	-	○	-	-	-	○	○	-
#17	-	-	-	-	-	-	-	-	-	○	-	-
#18	-	-	-	-	-	-	-	-	-	○	-	-
#19	-	-	-	-	-	-	-	-	-	-	○	-
#20	-	-	-	-	-	○	-	-	-	-	○	-
#21	-	-	-	-	-	-	-	-	-	-	-	○

Supplemental Table 2. Overview of gene probes used in this study

Accession number	**Gene symbol**	**Molecular characteristics**	**Probe position**	**Probe size(base)**	**Probe preparation**
XM_046905147.1	*ZBTB20*	transcription factor	CDS	760	this study
NM_001005616.1	*PROX1*	transcription factor	CDS	771	this study
NM_001006344.2	*CPA6*	enzyme	CDS	771	this study
XM_046915417.1	*KIT*	receptor tyrosine kinase	CDS	723	this study
XM_040675955	*NR4A2*	transcription factor	3'-UTR	594	Fujita, et al.(2019)
XM_015276135.2	*LEF1*	transcription factor	CDS	565	Fujita, et al. (2022)
XM_015299614.4	*GRIK1*	ionotropic gutamate receptor subunit	CDS	699	this study
XM_046939222.1	*GRIK2*	ionotropic glutamate receptor subunit	CDS	716	this study
XM_417766.7	*GRIK3*	ionotropic glutamate receptor subunit	CDS	792	this study
XM_015298177.4	*GRIK4*	ionotropic glutamate receptor subunit	CDS	1183	this study
NM_001396047.1	*SOX11*	transcription factor	CDS	733	this study

3’-UTR, three prime untranslated region; CDS, coding sequence