**Table S1a.** Evidence supporting five previously unreported neuropeptide genes in the chicken EST database

<table>
<tr><th>Peptide</th><th>EST</th></tr>
<tr><td>**APEL**</td><td>
Human[1]  30   DGNGLEDGNVRHLVQPRGSRNGPGPWQGGRRKFRRQRPRLSHKGPMPF  77
               DG   EDG +R LV+PRG+R G     GG R+ RR RPR+SH+GPMPF
Chicken  410   DGMDPEDGLIRTLVRPRGARRGNVRRPGGWRRLRRSRPRVSHRGPMPF  554

Chick EST         511  CCGGTCCCCGGCCACGGGTGTCCCATAGGGGCCCCATGCCCTTCTGATGGAGG     563
                       ||| ||||||||||||| ||||||||| |||||||||||||||||||||||||
Chick Genome  1632634  CCG-TCCCCGGCCACGGCTGTCCCATAAGGGCCCCATGCCCTTCTGATGGAGG 1632685
</td></tr>
<tr><td>**CART**</td><td>
Human     47   ASHEKELIEALQEVLKKLKSKRVPIYEKKYGQVPMCDAGEQCAVRKGARIGKLCDCPRGT  106
               AS EKELIEALQEVL+KLKSKRVP YEKK+GQVPMCDAGEQCAVRKGARIGKLCDCPRGT
Chicken  85    ASREKELIEALQEVLEKLKSKRVPHYEKKFGQVPMCDAGEQCAVRKGARIGKLCDCPRGT  264

Human     107  SCNSFLLKCL  116
               SCNSFLLKCL
Chicken  265   SCNSFLLKCL  294
</td></tr>
<tr><td>**INSL5**</td><td>
Human     25   SVRLCGLEYIRTVIYICASSRWRR  48
                V+LCG E+IR VI+ C  SRW+R
Chicken  63    GVKLCGREFIRAVIFTCGGSRWKR  134
</td></tr>
<tr><td>**NPB**</td><td>
Human  21   PGLAWYKPAAGHSSYSVGRAAGLLSGLRRSPYARRSQPYRGAE--PPGGAGASPELQLHP  78
            P   WY+ AA   SY VGRA+GLLSGLR  PY+RRS     AE  PP          LHP
Chicken 439 PAAPWYRQAAAPLSYPVGRASGLLSGLRL-PYSRRSDSEGAAERRPPA---------LHP  588

Human  79   R----LRSLAVCVQDVAPNLQRCERLPDGRGTYQCK  110
                 LR+   CV DV P L+ C  L  G G  QC+
Chicken 589 GSAAPLRTAVPCVTDVDPKLRSCRPLSGGPGALQCR  696
</td></tr>
<tr><td>**NPS**</td><td>
Human     58  LKPILEKMFVKRSFRNGVGTGMKKTSFQRAKS  89
              L+P LE  F KRSFRNGVG+G+KKTSF+RAKS
Chicken  3    LEPHLEMPFNKRSFRNGVGSGIKKTSFRRAKS  98
</td></tr>
</table>

[1]: Human protein sequence from the Gene database, chicken protein sequence from the EST database

**Table S1b.** Evidence supporting five previously unreported neuropeptide genes in the chicken genome

| Peptide | GENOME |
|---|---|
| **APEL** | Human[1]      30       DGNGLEDGNVRHLVQPRGSRNGPGPWQGGRRKFRRQRPRLSHKGPMPF  77<br>                      DG   EDG +R LV+PRG+R G      GG R+ RR RPRLSHKGPMPF<br>Chicken  1632533   DGMDPEDGLIRTLVRPRGARRGNVRRPGGWRRLRRPRPRLSHKGPMPF  1632676 |
| **CART** | Human      79  VPMCDAGEQCAVRKGARIGKLCDCPRGTSCNSFLLKC  115<br>                V  C  GE CAVR GAR GK C CP GT+CN ++L+C<br>Chicken  584  VSQCHLGEPCAVRVGARYGKRCSCPPGTACNLYVLRC  474 |
| **INSL5** | Human  24         ESVRLCGLEYIRTVIYICASSRWRR  48<br>                    +V+LCG +++R +++ C  SRW+R<br>Chicken 17631628  NAVKLCGRDFVRAIVFTCGGSRWKR  17631554 |
| **NPS** | Human      9       LILVLSLSTMHVFWCYPVPSSKVSGKSDYFLILLNSCPTRLDRSKELAFLKPILEKMFVK  68<br>                   L L  SL + + F+     + ++ GKSDY L+LLNSC  ++ RS+E+A L+P LE  F K<br>Chicken  287705   LSLFFSLQSSNPFYL----NCQLYGKSDYCLVLLNSCLAKVGRSEEVALLEPHLEMPFNK  287872 |
|  | Human      69      RSFRNGVGTGMKKTSFQRAKS  89<br>                   RSFRNGVG+G+KKTSF+RAKS<br>Chicken  287873   RSFRNGVGSGIKKTSFRRAKS  287935 |
|  | Human              33aa  GKSDYFLILLNSCPTRLDRSKELAFLKPILEKMFVKRSFRNGVGTGMKKTSFQRAKS  89<br>                         GKSDY L+LLNSC  ++ RS+E+A+L+P LE  F KRSFRNGVG+G+KKTSF+RAKS<br>Predicted Chick  82782bp GKSDYCLVLLNSCLAKVGRSEEVALLEPHLEMPFNKRSFRNGVGSGIKKTSFRRAKS 82936 |
| **NPB** | Human   21       PGLAWYKPAAGHSSYSVGRAAGLLSGLRRSPYARRSQPYRGAE--PP-------------  65<br>                  P   WY+ AA   SY VGRA+GLLSGLR  PY+RRS     AE  PP<br>Chicken  681263  PAAPWYRQAAAPLSYPVGRASGLLSGLRL-PYSRRSDSEGAAERRPPALHPGSAAPLRTA  681439 |
|  | Human      66      -------------------GGAGASPELQLHP-----RLRSLAV-CVQDVAPNLQRCERL  100<br>                                      G   A+P  + HP      + SL V CV DV P L+ C  L<br>Chicken  681440  VSTGMLRSWTVLGPGLPTRGAPWAAPLQRSHPGTWVSVMLSLQVPCVTDVDPELRSCRPL  681619 |
|  | Human  101       PDGRGTYQCKANVFLSLRAADCLAA  125<br>                      G  QC+  V +SL + +C  A<br>Chicken 681620   SGVPGALQCRVAVTVSLVSTECAGA  681694 |
|  | Human               3aa    RSATLAAAALALCLLLAPPGLAWYKPAAGHSSYSVGRAAGLLSGLRRSP<br>                           R+A   A A+A+ LL  P    WY+ AA   SY VGRA+GLLSGLR  P<br>Predicted Chick  1910bp    RAARCLALAVAVALLCRP-AAPWYRQAAAPLSYPVGRASGLLSGLRL-P |
|  | Human               52aa  YARRSQPYRGAE--PPGGAGASPELQLHPR----LRSL<br>                          Y+RRS     AE  PP           LHP     LR+<br>Predicted Chick   2051bp  YSRRSDSEGAAERRPPA---------LHPGSAAPLRTA |
|  | Human               84aa                         AVCVQDVAPNLQRCERLPDGRGTYQC<br>                                                  +  V +SL + +C  A<br>Predicted Chick   2138bp                        VPCVTDVDPELRSCRPLSGVPGALQC |

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[1]: Human sequence from the Gene database, chicken sequence from the Genome database,  Predicted Chick sequences predicted from the chicken Genome database using Wise2

**Table S1c.** Evidence supporting five previously unreported neuropeptide genes in the chicken high-throughput genome sequence

| Peptide | HTGS |
|---|---|
| **APEL** | Human[1]     5      LCVQALLLLWL-----SLTAVCGGSLMPLPDGNGLEDGNVRHLVQPRGSRNGPGPWQGGRRKF  62<br>                  +C+Q+    +L     SL  +C    + + +  G  D NV  LVQ R S N P  W G +<br>Chicken  124188   ICIQSYFFFFLLCKKLSLCILCVSVELSVCE*RGSADSNVFCLVQLRRSSNLPTAW-GFKSKF  124003 |
| **CART** | Human      80     PMCDAGEQCAVRKGARIGKLCDCPRGTSCNSFLLKCL  116<br>                  P CDAGEQCAVRKGARIGKLCDCPRGTSCNSFLLKCL<br>Chicken  31027    PQCDAGEQCAVRKGARIGKLCDCPRGTSCNSFLLKCL  31137<br>**OR**<br>Human      54     IEALQEVLKKLKSKRVPIYEKKYGQVPM  81<br>                  IEALQEVL+KLKSKRVP YEKK+GQVPM<br>Chicken  30786    IEALQEVLEKLKSKRVPHYEKKFGQVPM  30869 |
| **INSL5** | Human      26     VRLCGLEYIRTVIYICASSRWRR  48<br>                  V+LCG E+IR VI+ C  SRW+R<br>Chicken  155946   VKLCGREFIRAVIFTCGGSRWKR  156014 |
| **NPS** | Human      9      LILVLSLSTMHVFWCYPVPSSKVSGKSDYFLILLNSCPTRLDRSKELAFLKP-ILEKM  65<br>                  +I +L L+ M  FW      +K+    DYFL    +   +LD  K L FL+P I EK+<br>Chicken  22401    VI*LLDLN*MSSFWMATSKQNKIQSHRDYFL----TATYQLDDCKYLDFLEPNIHEKV  22562 |
| **NPB** | Human  21      PGLAWYKPAAGHSSYSVGRAAGLLSGLRRSPYARRSQPYRGAE--PP-------------  65<br>                P   WY+ AA   SY VGRA+GLLSGLR  PY+RRS     AE  PP<br>Chicken 113131 PAAPWYRQAAAPLSYPVGRASGLLSGLRL-PYSRRSDSEGAAERRPPALHPGSAAPLRTA  113307<br><br>Human  66      -------------------GGAGASPELQLHP-----RLRSLAV-CVQDVAPNLQRCERL  100<br>                                   G   A+P  + HP      + SL V CV DV P L+ C  L<br>Chicken 113308 VSTGMLRSWTVLGPGLPTRGAPWAAPLQRSHPGTWVSVMLSLQVPCVTDVDPELRSCRPL  113487<br><br>Human  101     PDGRGTYQCKANVFLSLRAADCLAA  125<br>                    G  QC+  V +SL + +C  A<br>Chicken 113488 SGVPGALQCRVAVTVSLVSTECAGA  113562 |

[1]: Human sequence from the Gene database, chicken sequence from the High Throughput Genome Sequence database

**Table S2.** Comprehensive distribution of neuropeptide and converatase gene EST across tissues and stages

| Neuropeptide Prohormones | Unigene ID[1] | Blood | Brain | Burse of Fabricius | Cecum | Connective Tissue | Embryonic Tissue | Epiphyseal Growth Plate | Gonad | Head | Heart | Limb | Liver | Muscle | Ovary | Pancreas | Small Intestine | Spleen | Testis | Thymus | Embryo Stage | Hatchling Stage | Juvenile Stage | Adult Stage |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ADML | Gga.12006 | 1[2] | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| ANF | Gga.5157 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| ANFC | Gga.12392 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| C-RF AMIDE | Gga.3202 | 0 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 1 |
| CALCA | Gga.4991 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| CCKN | Gga.2441 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 0 | 1 |
| CMGA | Gga.19002 | 1 | 1 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 1 | 1 | 1 |
| COLI | Gga.6271 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| ECRG4 | Gga.8435 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| EDN1 | Gga.25090 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| EDN2 | Gga.8238 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| EDN3 | Gga.22840 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 1 |
| GALA | Gga.12649 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| GHRL | Gga.16 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 |
| GIP | Gga.7981 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| GLUC | Gga.704 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| GRP | Gga.43422 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| IAPP | Gga.780 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| IGF1 | Gga.850 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| IGF2 | Gga.8511 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| INS | Gga.673 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| MCH | Gga.14659 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| NEU2 | Gga.652 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 1 |
| NEUT | Gga.10167 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 1 |
| NMB | Gga.8071 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| NMU | Gga.18392 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| NPY | Gga.837 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| OREX | Gga.11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| OSTN | Gga.13448 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| PACA | Gga.616 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 1 |
| PDGFA | Gga.3899 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 0 | 0 | 1 | 1 | 0 | 0 | 1 |
| PDGFB | Gga.71 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 1 |
| PDGFD | Gga.43662 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| PENK | Gga.11430 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 1 | 1 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 1 | 1 |
| PNOC | Gga.10041 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| PROK2 | Gga.10528 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |

| | | | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PRRP | Gga.10552 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| PTHR | Gga.2626 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| REL3 | Gga.37019 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| RFRP | Gga.9285 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| SCG1 | Gga.10025 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 0 | 1 | 1 |
| SCG2 | Gga.11999 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 1 |
| SECR | Gga.14227 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| SLIB | Gga.11231 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| SMS | Gga.742 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| TKN1 | Gga.12286 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| UCN3 | Gga.11141 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| UTS2D | Gga.9482 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| VEGFC | Gga.12347 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| VEGFD | Gga.3219 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 1 | 1 | 1 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 1 |
| VIP | Gga.666 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| | **Total** | **4** | **33** | **3** | **2** | **4** | **7** | **8** | **2** | **21** | **13** | **6** | **5** | **10** | **18** | **4** | **16** | **1** | **5** | **1** | **39** | **5** | **11** | **42** |
| **Prohormone Convertases** | | | | | | | | | | | | | | | | | | | | | | | | |
| PCSK1 similar | Gga.31439 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 0 | 1 |
| PCSK2 | Gga.9404 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| PCSK3 | Gga.1751 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| PCSK5 | Gga.12660 | 0 | 1 | 0 | 0 | 1 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| PCSK6 | Gga.21090 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| PCSK7 | Gga.5311 | 0 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | 1 | 1 | 1 | 0 | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 1 |
| | **Total** | **0** | **5** | **2** | **0** | **3** | **0** | **2** | **1** | **2** | **1** | **0** | **3** | **2** | **3** | **0** | **5** | **0** | **1** | **1** | **5** | **0** | **2** | **6** |

[1]: UniGene identifier of microarray gene probe

[2]: 1 denotes presence and 0 denotes absence

**Table S3.** Comprehensive description of the 22 chicken microarray experiments analyzed

| **Exp. ID**[1] | **Title** | **Tissue** | **Gender** | **Age** | **Line** | **Variables** | **Treatment** | **Reference** |
|---|---|---|---|---|---|---|---|---|
| **GSE6543** | Chick myopia | Retina/RPE | Female | One week | Leghorn Chicks | 3 day control retina; 3 day experimental retina; 6 hour retina; 6 hour experimental retina | After either 6 hours or 3 days of goggle wear on the periorbital feathers (to induce myopia), chicks were killed, and the retina/RPE was dissected for expression profiling by array. | McGlinn et al.. (2007) |
| **GSE7176** | Develomental Time Course of the Retinal Pigment Epithelial Transcriptome | Retinal pigment epithelium | NA[2] | 7 day old embryo | NA | Chicken retinal pigment epithelium for embryonic day E7, E10, E14, and E18 | Retinal Pigment Epithelium was isolated from E7, E10, E14 and E18 chick embryos and total RNA extracted for probing the entire genome on Affymetrix microarray chips. | Rizzolo et al. (2007) |
| **GSE11439** | Retinal gene expression in chicks during imposed myopic defocus | Retina | Male | 9 Days | NA | 4 samples of retina of both eyes of +6.9 diopter lens-treated chicks (plus_lens), 4 samples of retina of both eyes untreated control chicks (control) | Chick microarrays were uesed to analyze the changes in retinal mRNA expression after myopic defocus was imposed by positive lens-wear.Four male white leghorn chicks wore +6.9D spectacle lenses over both eyes for 24 hours. Four untreated age-matched male chicks from the same batch served as controls. The retinae from both eyes of each chick were pooled for RNA isolation. | Schippert et al. (2008) |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **GSE15382** | Gene expression profile of embryonic retinas expressing c-hairy1, Delta-1, or Wnt2b | Retina | NA | Embryo | NA | 2 samples of E6.5 retina RCAS c-hairy1 ; 2 samples of E6.5 retina RCAS control; 2 samples of E6.5 retina RCAS Delta; 2 samples of E6.5 retina RCAS Wnt2b | Total RNA was purified from E6.5 retinas transfected either with c-hairy1, Wnt2b, Delta, or mock-expressing RCAS plasmid using Trizol reagent. Expression profiles of embryonic retinas expressing exogenous c-hairy1, Delta-1, or Wnt2b were generated. These genes inhibit neuronal differentiation, and the results provide insight into the mechanism that keeps retinal progenitor cells undifferentiated. | Kubo et al. (2009) |
| **GSE6843** | Male and female embryonic chicken hearts (arnol-affy-chick-445639) | Embryonic chicken heart | Male/Female | Late stage embryo | NA | 5 male hearts; 5 female hearts | In the late stage embryos, the heart is removed and RNA extracted. Gene expression is measured using Affymetrix chicken arrays, and male vs female results are compared. | Itoh et al. (2007) |
| **GSE8693** | Sex-biased gene expression in 18 day embryonic chicken heart, brain, and gonad | Embryonic chicken heart | Male/Female | 18 day embryo | White Leghorn fowl | 3 male hearts; 3 female hearts | Fertilized eggs were purchased and incubated for 18 days. The embryos were then euthanized by decapitation and a piece from the apical part of the heart was collected for expression profiling by array. | Ellegren et al. (2007) |
| **GSE9251** | Systematic identification of genes involved in chicken muscle development | Pectoralis major muscles | Female | Postnatal 1 day, 2 weeks, 4 weeks, 6 weeks and 8 weeks | Broiler/Layer | Broilers at postnatal 1 day, 2 weeks, 4 weeks, 6 weeks and 8 weeks; Layers at postnatal 1 day, 2 weeks, 4 weeks, 6 weeks and 8 weeks. | Pectoralis major muscles were sampled from broilers and layers at indicated developmental stage (postnatal 1 day, 2 weeks, 4 weeks, 6 weeks and 8 weeks). | Zheng et al. (2009) |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **GSE6844** | Male and female embryonic chicken brains (arnol-affy-chick-345142) | Embryonic chicken brain | Male/Female | Late stage embryo | NA | 5 male brains; 5 female brains | In the late stage embryos, the brain is removed and RNA extracted. Gene expression is measured using Affymetrix chicken arrays, and male vs female results are compared. | Itoh et al. (2007) |
| **GSE6868** | Homocysteine induced alterations in gene expression in neural crest cells | Neural tube explants | NA | Stage 9+ embryo | NA | 3 control (media exposed) arrays; 3 homocysteine-treated (100uM final concnetration). | Neural tube explants were obtained from stage 9+ chicken embryos to generate neural crest cell cultures. After 4 hours in culture the cells were exposed to either media or homocysteine for 6 hours. The cultures were then processed for gene expression using the affymetrics chicken chip. | Rosenquist et al. (2007) |
| **GSE8018** | Gene expression in the quail MBH under short and long day conditions. | Mediobasal hypothalamus (MBH) | NA | NA | Quail | Short day condition at ZT2, ZT6, ZT10, ZT14, ZT18, AND ZT22; Long day condition at ZT2, ZT6, ZT10, ZT14, ZT18, AND ZT22. | The mediobasal hypothalamus (MBH) of quail kept under short day condition (6h light:18h dark) or long day condition (20h light:4h dark) were collected for RNA extraction.Samples were collected from 6 birds every 4h during a 24 h cycle and were analyzed in duplicate set of array (two biological replicates). | Nakao et al. (2008) |
| **GSE8693** | Sex-biased gene expression in 18 day embryonic chicken heart, brain, and gonad | Embryonic chicken brain | Male/Female | 18 day embryo | White Leghorn fowl | 3 male brains, 3 female brains | Fertilized eggs were purchased and incubated for 18 days. The embryos were then euthanized by decapitation and the brain was collected for expression profiling by array. | Ellegren et al. (2007) |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **GSE12268** | Sexually dimorphic gene expression in the chick brain at stage 29 | Brain | Male/Female | Stage 29 embryo | NA | 3 replicates of female brain sample at stage 29; 3 replicates of male brain sample at stage 29 | The Affymetrix data from male and female brain samples at stage 29 were generated. The male and female brain samples by genetic sexing were pooled and homogenized. Probe synthesis from total RNA samples, hybridization, detection, and scanning were performed according to standard protocols from Affymetrix. | NA |
| **GSE15413** | Gene expression profiles for liver, breast, and duodenum obtained from newly hatched (day 0) and 7 day-old broiler chickens | Brain | NA | Newly hatched/7 days | Broiler | 3 replicates of chick brain at day 0; 3 replicates of chick brain at day 7 | Tissue samples were collected at hatch and 7 days post-hatch for RNA extraction and hybridization on Affymetrix chicken genome GeneChip microarrays. | NA |
| **GSE15413** | Gene expression profiles for liver, breast, and duodenum obtained from newly hatched (day 0) and 7 day-old broiler chickens | Duodenum | NA | Newly hatched/7 days | Broiler | 3 replicates of chick duodenum at day 0; 3 replicates of chick duodenum at day 7 | Tissue samples were collected at hatch and 7 days post-hatch for RNA extraction and hybridization on Affymetrix chicken genome GeneChip microarrays. | NA |
| **GSE8693** | Sex-biased gene expression in 18 day embryonic chicken heart, brain, and gonad | Embryonic chicken gonad | Male/Female | 18 day embryo | White Leghorn fowl | 3 male gonads, 3 female gonads | Fertilized eggs were purchased and incubated for 18 days. The embryos were then euthanized by decapitation and left gonad was collected for expression profiling by array. | Ellegren et al. (2007) |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **GSE10231** | Gene expression oocyte quality in the hen | F1 oocyte stage | Female | NA | Hen | DPF+ F1 (2 samples); DPF- F1 (2 samples); HG+ F1 (2 samples); HG- F1 (2 samples) | All the samples were bissected from the F1 oocyte stage , and DPF+ and DPF- samples were compared in order to find differentially expressed genes that could explain the difference in fertility occuring between the two divergently selected lines. HG+ and HG- samples were compared in order to find differentially expressed genes that could explain the difference in fertility occuring between a single line. | NA |
| **GSE6868** | Homocysteine induced alterations in gene expression in neural crest cells | Neural tube explants | NA | Stage 9+ embryo | NA | 3 control (media exposed) arrays; 3 homocysteine-treated (100uM final concnetration). | Neural tube explants were obtained from stage 9+ chicken embryos to generate neural crest cell cultures. After 4 hours in culture the cells were exposed to either media or homocysteine for 6 hours. The cultures were then processed for gene expression using the affymetrics chicken chip. | Rosenquist et al. (2007) |
| **GSE8010** | Expression data from chicken adipose tissue at 7-week of age | Adipose Tissue | Female | 7 weeks | Broiler | Adipose tissue of lean lines; adipose tissue of fat lines | Birds were slaughtered at 7 weeks and abdominal fat was isolated. The ten birds used in the present study were chosen by the percentage of abdominal fat (AFP): five had the highest AFP and the other five had the lowest for RNA extraction and hybridization on Affymetrix microarrays. | Wang et al. (2007) |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **GSE8483** | Gene expression in Histone H1 null mutant cells | DT40 cells | NA | NA | Chicken | Gene expression pattern in wild-type; K11; and K11-5 cells | Floxed H1R-eGFP and mer-cre-mer were introduced into 11 out of 12 H1 knock out DT40 cells. Then, the last enedogenous H1 was targeted and successfully established conditional H1 KO cells (K11). Next, they were treated with tamoxifen to loop out floxed H1R-eGFP, and cloning H1 completely null cells (K11-5, and K11-7). Apoptosis is induced in H1 null cells, so it was inhibited with pan-caspase inhibitor, Z-VAD-FMK, and RNA was extracted. Gene expression patterns in wild-type, K11, and K11-5 cells were then analyzed. | Takami et al. (1997) |
| **GSE9884** | Expression Profiling of Circulating Red Blood Cells and Non Red Blood Cells in the Chicken Embryo (E4 and E6) | Blood from embryonic heart | NA | Embryo | NA | E4 Circulating Red blood Cells (2 samples), Non-Red blood cells (2 samples); E6 Circulating Red blood Cells (2 samples), Non-Red blood cells (2 samples) | Blood was extracted from embryonic hearts at E4 and E6 and non-red blood was separated by density gradient centrifugation. | McIntyre et al. (2008) |

[1]: ID = Identifer

[2]: NA = Not Available

**Table S4.** Neuropeptide and convertase gene differential expression *P-values* across 22 microarray studies grouped by tissue type

| | | Retina | | | | Heart-breast | | | | Brain-head | | | | Liver-duodenum | | | | Oocyte-gonad | | Others | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Neuropeptide Prohormone** | **UniGene Probe ID[1]** | **GSE 6543** | **GSE 7176** | **GSE 11439** | **GSE 15382** | **GSE 6843** | **GSE8693 -HEART** | **GSE 9251** | **GSE15413 -BREAST** | **GSE 6844** | **GSE 6868** | **GSE8693 -BRAIN** | **GSE 12268** | **GSE 6856** | **GSE 8483** | **GSE15413 -LIVER** | **GSE15413- DUODENUM** | **GSE8693 GONAD** | **GSE 10231** | **GSE 8010** | **GSE 8016** | **GSE 8018** | **GSE 8483** | **GSE 9884** |
| **ADML** | **Gga.12006.1.S1_at** | 0.880 | 0.000 | 0.580 | 0.450 | 0.440 | 0.330 | 0.000 | 0.000 | 0.450 | 0.450 | 0.160 | 0.920 | 0.570 | 0.440 | 0.230 | 0.220 | 0.004 | 0.380 | 0.940 | 0.001 | 0.290 | 0.44000 | 0.630 |
| **ANF** | **Gga.5157.1.S1_at** | 0.570 | 0.760 | 0.510 | 0.270 | 0.300 | 0.360 | 0.130 | 0.076 | 0.690 | 0.190 | 0.740 | 0.210 | 0.970 | 0.120 | 0.180 | 0.900 | 0.023 | 0.370 | 0.440 | 0.230 | 0.550 | 0.12000 | 0.620 |
| **ANFC** | **Gga.12392.1.S1_a_at** | 0.580 | 0.730 | 0.460 | 0.760 | 0.160 | 0.520 | 0.002 | 0.019 | 0.580 | 0.290 | 0.460 | 0.200 | 0.180 | 0.150 | 0.690 | 0.850 | 0.016 | 0.570 | 0.560 | 0.003 | 0.008 | 0.15000 | 0.810 |
| **CALCA** | **Gga.4991.2.S1_a_at** | 0.490 | 0.000 | 0.630 | 0.150 | 0.160 | 0.250 | 0.290 | 0.040 | 0.440 | 0.930 | 0.950 | 0.740 | 0.570 | 0.380 | 0.140 | 0.780 | 0.057 | 0.440 | 0.930 | 0.880 | 0.140 | 0.38000 | 0.480 |
| **CCKN** | **GgaAffx.21834.1.S1_s_at** | 0.950 | 0.540 | 0.740 | 0.032 | 0.430 | 0.460 | 0.140 | 0.190 | 0.340 | 0.760 | 0.120 | 0.700 | 0.056 | 0.400 | 0.120 | 0.056 | 0.710 | 0.390 | 0.920 | 0.240 | 0.000 | 0.40000 | 0.700 |
| **CCKN** | **Gga.2441.1.S1_at** | 0.350 | 0.710 | 0.820 | 0.430 | 0.400 | 0.520 | 0.260 | 0.150 | 0.260 | 0.210 | 0.730 | 0.460 | 0.098 | 0.500 | 0.370 | 0.170 | 0.930 | 0.028 | 0.540 | 0.470 | 0.040 | 0.50000 | 0.860 |
| **CMGA** | **GgaAffx.21576.1.S1_s_at** | 0.052 | 0.000 | 0.840 | 0.033 | 0.350 | 0.490 | 0.000 | 0.160 | 0.740 | 0.630 | 0.230 | 0.740 | 0.740 | 0.001 | 0.990 | 0.220 | 0.029 | 0.660 | 0.480 | 0.038 | 0.038 | 0.00050 | 0.310 |
| **CMGA** | **Gga.12437.2.S1_at** | 0.015 | 0.044 | 0.670 | 0.036 | 0.150 | 0.270 | 0.000 | 0.025 | 0.320 | 0.680 | 0.160 | 0.840 | 0.590 | 0.340 | 0.890 | 0.480 | 0.098 | 0.880 | 0.730 | 0.034 | 0.007 | 0.34000 | 0.780 |
| **COLI** | **Gga.6271.1.S1_at** | 0.390 | 0.670 | 0.260 | 0.610 | 0.160 | 0.110 | 0.001 | 0.019 | 0.540 | 0.080 | 0.640 | 0.290 | 0.270 | 0.270 | 0.740 | 0.790 | 0.011 | 0.079 | 0.470 | 0.200 | 0.000 | 0.27000 | 0.830 |
| **CRF** | **Gga.11323.1.S1_at** | 0.340 | 0.700 | 0.590 | 0.570 | 0.180 | 0.740 | 0.310 | 0.013 | 0.520 | 0.180 | 0.810 | 0.017 | 0.290 | 0.470 | 0.400 | 0.830 | 0.003 | 0.062 | 0.490 | 0.640 | 0.180 | 0.47000 | 0.610 |
| **ECRG4** | **Gga.8435.1.S1_at** | 0.610 | 0.240 | 0.350 | 0.090 | 0.460 | 0.330 | 0.000 | 0.001 | 0.930 | 0.880 | 0.550 | 0.010 | 0.250 | 0.290 | 0.011 | 0.520 | 0.010 | 0.025 | 0.160 | 0.000 | 0.510 | 0.29000 | 0.820 |
| **ECRG4** | **Gga.11232.1.A1_at** | 0.230 | 0.660 | 0.230 | 0.300 | 0.210 | 0.490 | 0.002 | 0.024 | 0.630 | 0.150 | 0.800 | 0.110 | 0.250 | 0.390 | 0.450 | 0.750 | 0.009 | 0.059 | 0.620 | 0.800 | 0.610 | 0.39000 | 0.830 |
| **GALA** | **Gga.12649.1.S1_at** | 0.070 | 0.006 | 0.730 | 0.500 | 0.150 | 0.270 | 0.005 | 0.120 | 0.500 | 0.410 | 0.500 | 0.190 | 0.250 | 0.300 | 0.280 | 0.074 | 0.056 | 0.130 | 0.620 | 0.100 | 0.940 | 0.30000 | 0.510 |
| **GAST** | **Gga.782.1.S1_at** | 0.490 | 0.430 | 0.360 | 0.400 | 0.190 | 0.330 | 0.000 | 0.046 | 0.830 | 0.180 | 0.460 | 0.460 | 0.390 | 0.200 | 0.290 | 0.270 | 0.010 | 0.130 | 0.940 | 0.130 | 0.410 | 0.20000 | 0.850 |
| **GHRL** | **Gga.16.1.S1_at** | 0.720 | 0.630 | 0.330 | 0.060 | 0.380 | 0.540 | 0.089 | 0.035 | 0.490 | 0.560 | 0.870 | 0.240 | 0.720 | 0.300 | 0.380 | 0.770 | 0.660 | 0.540 | 0.480 | 0.810 | 0.470 | 0.30000 | 0.710 |
| **GIP** | **Gga.7981.1.S1_at** | 0.220 | 0.610 | 0.330 | 0.022 | 0.160 | 0.360 | 0.000 | 0.025 | 0.620 | 0.440 | 0.940 | 0.490 | 0.180 | 0.620 | 0.260 | 0.370 | 0.023 | 0.140 | 0.490 | 0.470 | 0.690 | 0.62000 | 0.820 |
| **GLUC** | **GgaAffx.21780.2.S1_s_at** | 0.065 | 0.650 | 0.008 | 0.330 | 0.110 | 0.980 | 0.064 | 0.051 | 0.280 | 0.630 | 0.120 | 0.560 | 0.430 | 0.600 | 0.110 | 0.055 | 0.001 | 0.400 | 0.740 | 0.630 | 0.780 | 0.60000 | 0.710 |
| **IAPP** | **Gga.780.1.S1_at** | 0.210 | 0.720 | 0.390 | 0.096 | 0.140 | 0.570 | 0.000 | 0.050 | 0.710 | 0.260 | 0.340 | 0.580 | 0.140 | 0.380 | 0.210 | 0.240 | 0.260 | 0.083 | 0.510 | 0.180 | 0.220 | 0.38000 | 0.740 |
| **IGF1** | **Gga.850.1.S1_at** | 0.009 | 0.560 | 0.820 | 0.170 | 0.150 | 0.220 | 0.000 | 0.000 | 0.730 | 0.310 | 0.870 | 0.120 | 0.220 | 0.380 | 0.000 | 0.860 | 0.004 | 0.110 | 0.590 | 0.048 | 0.570 | 0.38000 | 0.720 |
| **IGF2** | **Gga.8511.1.S1_at** | 0.100 | 0.760 | 0.420 | 0.100 | 0.130 | 0.660 | 0.000 | 0.025 | 0.810 | 0.150 | 0.740 | 0.085 | 0.190 | 0.140 | 0.200 | 0.750 | 0.120 | 0.230 | 0.690 | 0.004 | 0.750 | 0.14000 | 0.780 |
| **INS** | **Gga.673.1.S1_at** | 0.110 | 0.760 | 0.370 | 0.600 | 0.180 | 0.210 | 0.650 | 0.310 | 0.290 | 0.140 | 0.580 | 0.690 | 0.280 | 0.420 | 0.052 | 0.000 | 0.950 | 0.820 | 0.630 | 0.004 | 0.660 | 0.42000 | 0.750 |
| **MCH** | **Gga.14659.1.S1_at** | 0.032 | 0.710 | 0.890 | 0.710 | 0.140 | 0.580 | 0.006 | 0.030 | 0.340 | 0.120 | 0.880 | 0.003 | 0.160 | 0.220 | 0.940 | 0.760 | 0.024 | 0.058 | 0.550 | 0.540 | 0.300 | 0.22000 | 0.710 |
| **NEU2** | **Gga.652.1.S1_at** | 0.310 | 0.840 | 0.210 | 0.680 | 0.590 | 0.990 | 0.150 | 0.250 | 0.280 | 0.045 | 0.970 | 0.240 | 0.270 | 0.290 | 0.380 | 0.470 | 0.006 | 0.220 | 0.430 | 0.100 | 0.620 | 0.29000 | 0.710 |

| | | | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **NEUT** | **Gga.10167.1.S1_at** | 0.002 | 0.810 | 0.005 | 0.220 | 0.200 | 0.920 | 0.024 | 0.010 | 0.850 | 0.810 | 0.830 | 0.240 | 0.160 | 0.380 | 0.150 | 0.190 | 0.110 | 0.230 | 0.850 | 0.290 | 0.930 | 0.38000 | 0.620 |
| **NMB** | **Gga.8071.1.S1_a_at** | 0.180 | 0.042 | 0.900 | 0.690 | 0.480 | 0.410 | 0.019 | 0.310 | 0.780 | 0.180 | 0.380 | 0.330 | 0.140 | 0.480 | 0.930 | 0.110 | 0.010 | 0.200 | 0.750 | 0.064 | 0.430 | 0.48000 | 0.560 |
| **NMU** | **Gga.18392.1.S1_at** | 0.710 | 0.006 | 0.330 | 0.660 | 0.140 | 0.510 | 0.001 | 0.027 | 0.500 | 0.062 | 0.510 | 0.300 | 0.950 | 0.120 | 0.390 | 0.002 | 0.170 | 0.210 | 0.630 | 0.001 | 0.350 | 0.12000 | 0.690 |
| **NPY** | **Gga.837.1.S1_a_at** | 0.950 | 0.650 | 0.700 | 0.005 | 0.430 | 0.930 | 0.180 | 0.150 | 0.500 | 0.680 | 0.970 | 0.690 | 0.140 | 0.360 | 0.470 | 0.150 | 0.017 | 0.009 | 0.520 | 0.000 | 0.190 | 0.36000 | 0.570 |
| **OREX** | **Gga.11.1.S1_at** | 0.460 | 0.520 | 0.100 | 0.480 | 0.280 | 0.280 | 0.340 | 0.048 | 0.960 | 0.120 | 0.830 | 0.026 | 0.490 | 0.220 | 0.540 | 0.460 | 0.045 | 0.410 | 0.490 | 0.460 | 0.950 | 0.22000 | 0.810 |
| **OSTN** | **Gga.13448.1.S1_at** | 0.150 | 0.570 | 0.240 | 0.530 | 0.390 | 0.690 | 0.002 | 0.034 | 0.390 | 1.000 | 0.560 | 0.290 | 0.180 | 0.390 | 0.880 | 0.820 | 0.068 | 0.540 | 0.096 | 0.630 | 0.540 | 0.39000 | 0.840 |
| **PACA** | **Gga.11409.1.S1_at** | 0.660 | 0.680 | 0.150 | 0.220 | 0.240 | 0.450 | 0.001 | 0.640 | 0.120 | 0.190 | 0.280 | 0.350 | 0.280 | 0.160 | 0.680 | 0.550 | 0.170 | 0.065 | 0.520 | 0.083 | 0.380 | 0.16000 | 0.055 |
| **PACA** | **Gga.616.1.S1_s_at** | 0.025 | 0.670 | 0.011 | 0.025 | 0.680 | 0.140 | 0.010 | 0.022 | 0.900 | 0.980 | 0.260 | 0.240 | 0.220 | 0.210 | 0.880 | 0.490 | 0.400 | 0.085 | 0.540 | 0.077 | 0.170 | 0.21000 | 0.930 |
| **PAHO** | **Gga.308.1.S1_at** | 0.500 | 0.600 | 0.350 | 0.480 | 0.580 | 0.270 | 0.230 | 0.020 | 0.920 | 0.430 | 1.000 | 0.790 | 0.350 | 0.050 | 0.098 | 0.018 | 0.004 | 0.420 | 0.550 | 0.280 | 0.550 | 0.05000 | 0.840 |
| **PDGFA** | **Gga.3899.3.S1_a_at** | 0.017 | 0.000 | 0.073 | 0.730 | 0.850 | 0.056 | 0.760 | 0.000 | 0.920 | 0.690 | 0.230 | 0.750 | 0.900 | 0.870 | 0.290 | 0.780 | 0.001 | 0.410 | 0.880 | 0.035 | 0.450 | 0.87000 | 0.200 |
| **PDGFB** | **Gga.71.1.S1_at** | 0.030 | 0.970 | 0.210 | 0.660 | 0.096 | 0.670 | 0.010 | 0.000 | 0.890 | 0.190 | 0.210 | 0.067 | 0.130 | 0.120 | 0.061 | 0.150 | 0.011 | 0.390 | 0.066 | 0.110 | 0.960 | 0.12000 | 0.150 |
| **PDGFD** | **Gga.9675.1.S1_at** | 0.021 | 0.120 | 0.140 | 0.280 | 0.220 | 0.044 | 0.000 | 0.000 | 0.760 | 0.390 | 0.810 | 0.390 | 0.300 | 0.400 | 0.067 | 0.054 | 0.004 | 0.730 | 0.430 | 0.190 | 0.660 | 0.40000 | 0.860 |
| **PENK** | **Gga.11430.1.S1_at** | 0.006 | 0.700 | 0.023 | 0.046 | 0.270 | 0.150 | 0.000 | 0.001 | 0.390 | 0.700 | 0.510 | 0.350 | 0.170 | 0.390 | 0.680 | 0.000 | 0.043 | 0.400 | 0.390 | 0.028 | 0.480 | 0.39000 | 0.054 |
| **PNOC** | **Gga.10041.1.S1_a_at** | 0.350 | 0.700 | 0.660 | 0.520 | 0.013 | 0.610 | 0.000 | 0.000 | 0.920 | 0.930 | 0.460 | 0.810 | 0.082 | 0.560 | 0.630 | 0.790 | 0.380 | 0.150 | 0.380 | 0.008 | 0.060 | 0.56000 | 0.850 |
| **PNOC** | **Gga.10041.2.A1_at** | 0.068 | 0.700 | 0.220 | 0.520 | 1.000 | 0.520 | 0.660 | 0.003 | 0.870 | 0.680 | 0.290 | 0.096 | 0.500 | 0.490 | 0.880 | 0.770 | 0.960 | 0.024 | 0.530 | 0.000 | 0.680 | 0.49000 | 0.850 |
| **PNOC** | **GgaAffx.20191.1.S1_s_at** | 0.200 | 0.690 | 0.340 | 0.140 | 0.720 | 0.320 | 0.046 | 0.850 | 0.790 | 0.180 | 0.760 | 0.350 | 0.820 | 0.260 | 0.160 | 0.730 | 0.017 | 0.055 | 0.490 | 0.039 | 0.940 | 0.26000 | 0.720 |
| **PROK2** | **Gga.10528.1.S1_a_at** | 0.180 | 0.490 | 0.056 | 0.520 | 0.440 | 0.270 | 0.026 | 0.043 | 0.100 | 0.093 | 0.360 | 0.100 | 0.770 | 0.530 | 0.004 | 0.880 | 0.053 | 0.280 | 0.520 | 0.140 | 0.067 | 0.53000 | 0.810 |
| **PROK2** | **Gga.10528.2.A1_at** | 0.031 | 0.560 | 0.210 | 0.410 | 0.160 | 0.360 | 0.005 | 0.019 | 0.610 | 0.042 | 0.980 | 0.210 | 0.910 | 0.140 | 0.300 | 0.780 | 0.260 | 0.170 | 0.410 | 0.020 | 0.700 | 0.14000 | 0.520 |
| **PRRP** | **Gga.10552.1.S1_at** | 0.160 | 0.750 | 0.310 | 0.320 | 0.160 | 0.410 | 0.002 | 0.044 | 0.480 | 0.170 | 0.440 | 0.340 | 0.520 | 0.400 | 0.750 | 0.740 | 0.310 | 0.130 | 0.460 | 0.054 | 0.690 | 0.40000 | 0.780 |
| **PTHR** | **Gga.2626.1.S1_at** | 0.260 | 0.650 | 0.810 | 0.540 | 0.330 | 0.370 | 0.001 | 0.036 | 0.480 | 0.320 | 0.890 | 0.150 | 0.260 | 0.078 | 0.700 | 0.960 | 0.096 | 0.230 | 0.560 | 0.003 | 0.570 | 0.07800 | 0.840 |
| **PTHY** | **Gga.78.1.A1_at** | 0.370 | 0.530 | 0.510 | 0.510 | 0.160 | 0.550 | 0.005 | 0.023 | 0.690 | 0.160 | 0.940 | 0.130 | 0.170 | 0.260 | 0.490 | 0.970 | 0.019 | 0.084 | 0.280 | 0.160 | 0.410 | 0.26000 | 0.840 |
| **REL3** | **Gga.12454.1.S1_at** | 0.700 | 0.200 | 0.210 | 0.480 | 0.058 | 0.410 | 0.006 | 0.027 | 0.001 | 0.077 | 0.027 | 0.400 | 0.600 | 0.180 | 0.200 | 0.014 | 0.710 | 0.110 | 0.430 | 0.000 | 0.003 | 0.18000 | 0.670 |
| **RFRP** | **Gga.9285.1.S1_at** | 0.085 | 0.110 | 0.860 | 0.690 | 0.280 | 0.380 | 0.023 | 0.200 | 0.420 | 0.230 | 0.330 | 0.440 | 0.170 | 0.440 | 0.850 | 0.740 | 0.010 | 0.320 | 0.550 | 0.002 | 0.900 | 0.44000 | 0.660 |
| **SCG1** | **Gga.10025.1.S1_at** | 0.540 | 0.440 | 0.440 | 0.270 | 0.440 | 0.360 | 0.027 | 0.140 | 0.003 | 0.830 | 0.500 | 0.310 | 0.880 | 0.410 | 0.230 | 0.410 | 0.140 | 0.190 | 0.820 | 0.180 | 0.260 | 0.41000 | 0.760 |
| **SCG2** | **Gga.11999.1.S1_at** | 0.043 | 0.088 | 0.180 | 0.180 | 0.390 | 0.140 | 0.290 | 0.190 | 0.460 | 0.810 | 0.780 | 0.930 | 0.870 | 0.035 | 0.160 | 0.770 | 0.290 | 0.780 | 0.330 | 0.990 | 0.530 | 0.03500 | 0.046 |
| **SCG2** | **Gga.11999.1.A1_s_at** | 0.520 | 0.740 | 0.260 | 0.270 | 0.160 | 0.410 | 0.001 | 0.022 | 0.280 | 0.180 | 0.077 | 0.550 | 0.300 | 0.200 | 0.430 | 0.440 | 0.003 | 0.015 | 0.600 | 0.130 | 0.062 | 0.20000 | 0.810 |
| **SCG2** | **Gga.11999.1.A1_at** | 0.076 | 0.810 | 0.640 | 0.006 | 0.200 | 0.990 | 0.081 | 0.035 | 0.830 | 0.310 | 0.075 | 0.093 | 0.074 | 0.400 | 0.140 | 0.810 | 0.049 | 0.250 | 0.850 | 0.006 | 0.930 | 0.40000 | 0.490 |
| **SECR** | **Gga.14227.1.S1_at** | 0.120 | 0.530 | 0.840 | 0.350 | 0.042 | 0.880 | 0.028 | 0.029 | 0.560 | 0.230 | 0.500 | 0.180 | 0.940 | 0.210 | 0.380 | 0.480 | 0.810 | 0.410 | 0.470 | 0.089 | 0.390 | 0.21000 | 0.740 |
| **SLIB** | **Gga.11231.1.S1_at** | 0.420 | 0.240 | 0.590 | 0.510 | 0.180 | 0.640 | 0.011 | 0.016 | 0.380 | 0.210 | 0.800 | 0.800 | 0.220 | 0.180 | 0.710 | 0.550 | 0.057 | 0.062 | 0.470 | 0.660 | 0.008 | 0.18000 | 0.750 |
| **SMS** | **Gga.742.1.S1_at** | 0.620 | 0.007 | 0.170 | 0.360 | 0.240 | 0.280 | 0.001 | 0.023 | 0.180 | 0.870 | 0.130 | 0.100 | 0.760 | 0.370 | 0.120 | 0.130 | 0.200 | 0.260 | 0.470 | 0.630 | 0.270 | 0.37000 | 0.210 |
| **TKN1** | **Gga.12286.1.S1_at** | 0.190 | 0.630 | 0.390 | 0.056 | 0.370 | 0.770 | 0.002 | 0.120 | 0.300 | 0.100 | 0.940 | 0.820 | 0.820 | 0.250 | 0.880 | 0.620 | 0.001 | 0.180 | 0.470 | 0.005 | 0.790 | 0.25000 | 0.780 |
| **TRH** | **Gga.19489.1.A1_at** | 0.570 | 0.700 | 0.290 | 0.460 | 0.170 | 0.550 | 0.001 | 0.021 | 0.600 | 0.170 | 0.830 | 0.110 | 0.290 | 0.140 | 0.890 | 0.790 | 0.011 | 0.028 | 0.330 | 0.190 | 0.650 | 0.14000 | 0.830 |
| **TRH** | **Gga.19489.1.S1_at** | 0.079 | 0.710 | 0.690 | 0.540 | 0.170 | 0.330 | 0.034 | 0.041 | 0.920 | 0.120 | 0.880 | 0.150 | 0.300 | 0.250 | 0.430 | 0.610 | 0.010 | 0.130 | 0.430 | 0.200 | 0.450 | 0.25000 | 0.790 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **TSHB** | **Gga.551.1.S1_at** | 0.190 | 0.760 | 0.510 | 0.420 | 0.900 | 0.470 | 0.000 | 0.047 | 0.290 | 0.530 | 0.590 | 0.300 | 0.410 | 0.430 | 0.840 | 0.940 | 0.250 | 0.097 | 0.300 | 0.063 | 0.000 | 0.43000 | 0.850 |
| **UCN3** | **Gga.11141.1.S1_at** | 0.380 | 0.480 | 0.420 | 0.270 | 0.590 | 0.370 | 0.012 | 0.022 | 0.410 | 0.068 | 0.950 | 0.030 | 0.190 | 0.490 | 0.260 | 0.410 | 0.009 | 0.039 | 0.440 | 0.400 | 0.069 | 0.49000 | 0.740 |
| **UTS2** | **Gga.14388.1.S1_at** | 0.490 | 0.510 | 0.250 | 0.420 | 0.140 | 0.430 | 0.022 | 0.140 | 0.410 | 0.700 | 0.890 | 0.120 | 0.290 | 0.390 | 0.350 | 0.650 | 0.300 | 0.006 | 0.460 | 0.032 | 0.590 | 0.39000 | 0.720 |
| **UTS2D** | **Gga.9482.1.S1_at** | 0.000 | 0.430 | 0.001 | 0.490 | 0.160 | 0.440 | 0.140 | 0.018 | 0.960 | 0.120 | 0.530 | 0.520 | 0.230 | 0.160 | 0.950 | 0.510 | 0.290 | 0.190 | 0.710 | 0.190 | 0.740 | 0.16000 | 0.850 |
| **VEGFC** | **Gga.12347.1.S1_at** | 0.900 | 0.000 | 0.067 | 0.240 | 0.250 | 0.300 | 0.000 | 0.140 | 0.520 | 0.600 | 0.960 | 0.510 | 0.190 | 0.240 | 0.610 | 0.064 | 0.059 | 0.250 | 0.240 | 0.019 | 0.870 | 0.24000 | 0.440 |
| **VEGFD** | **Gga.3219.1.S1_at** | 0.570 | 0.000 | 0.060 | 0.480 | 0.250 | 0.560 | 0.000 | 0.600 | 0.940 | 0.890 | 0.670 | 0.540 | 0.730 | 0.340 | 0.110 | 0.008 | 0.150 | 0.760 | 0.130 | 0.750 | 0.150 | 0.34000 | 0.430 |
| **VIP** | **Gga.666.1.S1_a_at** | 0.000 | 0.630 | 0.051 | 0.590 | 0.190 | 0.190 | 0.680 | 0.530 | 0.002 | 0.270 | 0.500 | 0.630 | 0.780 | 0.450 | 0.910 | 0.150 | 0.062 | 0.170 | 0.400 | 0.180 | 0.580 | 0.45000 | 0.140 |
| | Total *P-value* < 0.005 | 3 | 6 | 1 | 0 | 0 | 0 | 27 | 9 | 3 | 0 | 0 | 1 | 0 | 1 | 2 | 3 | 9 | 0 | 0 | 11 | 4 | 1 | 0 |
| **Prohormone Convertase Enzymes** | | | | | | | | | | | | | | | | | | | | | | | | |
| **PCSK2** | **Gga.2786.1.S1_at** | 0.170 | 0.700 | 0.900 | 0.430 | 0.057 | 0.280 | 0.001 | 0.053 | 0.830 | 0.420 | 0.320 | 0.320 | 0.250 | 0.500 | 0.510 | 0.069 | 0.370 | 0.010 | 0.710 | 0.038 | 0.840 | 0.50000 | 0.710 |
| **PCSK2** | **Gga.9404.1.S1_at** | 0.400 | 0.690 | 0.350 | 0.037 | 0.063 | 0.580 | 0.005 | 0.180 | 0.910 | 0.590 | 0.820 | 0.820 | 0.510 | 0.150 | 0.035 | 0.006 | 0.560 | 0.056 | 0.930 | 0.110 | 0.350 | 0.15000 | 0.140 |
| **PCSK3** | **Gga.1751.1.S1_at** | 0.600 | 0.096 | 0.310 | 0.970 | 0.290 | 0.220 | 0.430 | 0.230 | 0.290 | 1.000 | 0.420 | 0.420 | 0.510 | 0.680 | 0.990 | 0.630 | 0.004 | 0.500 | 0.490 | 0.510 | 0.800 | 0.68000 | 0.870 |
| **PCSK5** | **Gga.247.1.S1_at** | 0.001 | 0.760 | 0.086 | 0.410 | 0.170 | 0.490 | 0.570 | 0.036 | 0.180 | 0.250 | 0.490 | 0.490 | 0.670 | 0.150 | 0.300 | 0.110 | 0.200 | 0.400 | 0.680 | 0.016 | 0.090 | 0.15000 | 0.850 |
| **PCSK5** | **Gga.12660.2.S1_a_at** | 0.038 | 0.650 | 0.450 | 0.160 | 0.350 | 0.370 | 0.440 | 0.067 | 0.170 | 0.630 | 0.260 | 0.260 | 0.840 | 0.420 | 0.160 | 0.043 | 0.009 | 0.600 | 0.130 | 0.004 | 0.570 | 0.42000 | 0.790 |
| **PCSK6** | **Gga.20041.1.S1_at** | 0.880 | 0.820 | 0.120 | 0.027 | 0.740 | 0.099 | 0.000 | 0.007 | 0.430 | 0.057 | 0.640 | 0.640 | 0.930 | 0.410 | 0.003 | 0.064 | 0.003 | 0.500 | 0.650 | 0.015 | 0.790 | 0.41000 | 0.065 |
| **PCSK6** | **GgaAffx.20832.1.S1_s_at** | 0.060 | 0.810 | 0.400 | 0.180 | 0.430 | 0.300 | 0.660 | 0.830 | 0.210 | 0.360 | 0.500 | 0.500 | 0.680 | 0.660 | 0.014 | 0.810 | 0.001 | 0.520 | 0.025 | 0.081 | 0.540 | 0.66000 | 0.870 |
| **PCSK6** | **Gga.246.1.S1_at** | 0.560 | 0.350 | 0.150 | 0.520 | 0.190 | 0.350 | 0.290 | 0.046 | 0.420 | 0.340 | 0.410 | 0.410 | 0.260 | 0.240 | 0.750 | 0.460 | 0.011 | 0.084 | 0.560 | 0.110 | 0.450 | 0.24000 | 0.600 |
| **PCSK7** | **GgaAffx.12272.1.S1_s_at** | 0.440 | 0.600 | 0.029 | 0.830 | 0.250 | 0.640 | 0.270 | 0.900 | 0.120 | 0.690 | 0.370 | 0.370 | 0.680 | 0.018 | 0.360 | 0.670 | 0.032 | 0.170 | 0.410 | 0.260 | 0.760 | 0.01800 | 0.700 |
| **PCSK7** | **Gga.17539.1.S1_s_at** | 0.530 | 0.570 | 0.220 | 0.440 | 0.880 | 0.840 | 0.024 | 0.170 | 0.290 | 0.110 | 0.830 | 0.830 | 0.220 | 0.013 | 0.360 | 0.270 | 0.001 | 0.340 | 0.170 | 0.880 | 0.830 | 0.01300 | 0.680 |
| | Total *P-value* < 0.005 | 1 | 0 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 4 | 0 | 0 | 1 | 0 | 0 | 0 |

[1]: UniGene identifier of microarray gene probe