Supplementary Table S3: List of genes, their position and function identified within haploblocks containing the ten most associated SNPs for perinatal mortality.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| BTA | Haploblock position | Gene | Position | Function |
| 14 | 71356288-72195341 | SLC26A7 | [71,722,604-71,871,605](http://jun2011.archive.ensembl.org/Bos_taurus/Location/View?db=core;g=ENSBTAG00000032301;r=14:71722604-71871605;t=ENSBTAT00000045797) | This gene is one member of a family of sulfate/anion transporter genes |
|  |  | **TMEM55A** | [72,033,027-72,105,636](http://jun2011.archive.ensembl.org/Bos_taurus/Location/View?db=core;g=ENSBTAG00000039968;r=14:72033027-72105636;t=ENSBTAT00000028656) | Catalyzes the hydrolysis of the 4-position phosphate of phosphatidylinositol 4,5-bisphosphate. |
|  |  | Tmem64 | [72,195,056-72,229,443](http://jun2011.archive.ensembl.org/Bos_taurus/Location/View?db=core;g=ENSBTAG00000011268;r=14:72195056-72229443;t=ENSBTAT00000045778) |  Transmembrane protein 64 (Tmem64) as a regulator of Ca(2+) oscillation during osteoclastogenesis. |
| 16 | 74717247-75179403 | **DENND1B** | [74,792,846-74,895,655](http://jun2011.archive.ensembl.org/Bos_taurus/Location/View?db=core;g=ENSBTAG00000012433;r=16:74792846-74895655;t=ENSBTAT00000016502) | Members of the connecdenn family, such as DENND1B, function as guanine nucleotide exchange factors (GEFs) for the early endosomal small GTPase RAB35 (MIM 604199) and bind to clathrin and clathrin adaptor protein-2  |
| 10 | 12585173-12899363 | RAB11A | [12,568,783-12,588,033](http://jun2011.archive.ensembl.org/Bos_taurus/Location/View?db=core;g=ENSBTAG00000018959;r=10:12568783-12588033;t=ENSBTAT00000025235)  | The small GTPases Rab are key regulators of intracellular membrane trafficking, from the formation of transport vesicles to their fusion with membranes. In humans Rab11a was involved in the recruitment of TLR4 to phagosomes in a process requiring TLR4 signaling. |
|  |  | MEGF11 | [12,599,062-12,690,387](http://jun2011.archive.ensembl.org/Bos_taurus/Location/View?db=core;g=ENSBTAG00000034140;r=10:12599062-12690387;t=ENSBTAT00000036967) | In humans its thought it may regulate the mosaic spacing of specific neuron subtypes in the retina. Mosaics provide a mechanism to distribute each cell type evenly across the retina, ensuring that all parts of the visual field have access to a full set of processing elements |
| 4 | 24191610-25183065 | AGMO | [24,807,121-25,004,482](http://jun2011.archive.ensembl.org/Bos_taurus/Location/View?db=core;g=ENSBTAG00000034154;r=4:24807121-25004482) | The protein encoded by this gene is a tetrahydrobiopterin- and iron-dependent enzyme that cleaves the ether bond of alkylglycerols. Sequence comparisons distinguish this protein as forming a third, distinct class of tetrahydrobiopterin-dependent enzymes. Variations in this gene have been associated with decreased glucose-stimulated insulin response, type 2 diabetes, and susceptibility to intracranial aneurysms in humans |
|  |  | **MEOX2** | [25,059,437-25,135,467](http://jun2011.archive.ensembl.org/Bos_taurus/Location/View?db=core;g=ENSBTAG00000003238;r=4:25059437-25135467;t=ENSBTAT00000004198) | This gene encodes a member of a subfamily of non-clustered, diverged, antennapedia-like homeobox-containing genes. The encoded protein may play a role in the regulation of vertebrate limb myogenesis. Mutations in the related mouse protein may be associated with craniofacial and/or skeletal abnormalities |
| 2 | 108276539-109093402 | MARCH4 | [108,258,480-108,284,436](http://jun2011.archive.ensembl.org/Bos_taurus/Location/View?db=core;g=ENSBTAG00000016183;r=2:108258480-108284436;t=ENSBTAT00000038261)  | MARCH4 is a member of the MARCH family of membrane-bound E3 ubiquitin ligases (EC 6.3.2.19). MARCH enzymes add ubiquitin (see MIM 191339) to target lysines in substrate proteins, thereby signaling their vesicular transport between membrane compartments. MARCH4 reduces surface accumulation of several membrane glycoproteins by directing them to the endosomal compartment |
|  |  | **SMARCAL1** | [108,615,915-108,666,059](http://jun2011.archive.ensembl.org/Bos_taurus/Location/View?db=core;g=ENSBTAG00000003843;r=2:108615915-108666059;t=ENSBTAT00000005013) | ATP-dependent annealing helicase that catalyzes the rewinding of the stably unwound DNA. Rewinds single-stranded DNA bubbles that are stably bound by replication protein A (RPA). Acts throughout the genome to reanneal stably unwound DNA, performing the opposite reaction of many enzymes, such as helicases and polymerases, that unwind DNA  |
|  |  | RPL37A | [108,679,858-108,682,477](http://jun2011.archive.ensembl.org/Bos_taurus/Location/View?db=core;g=ENSBTAG00000003846;r=2:108679858-108682477;t=ENSBTAT00000005015) | This gene encodes a ribosomal protein that is a component of the 60S subunit of the ribosome. |
|  |  | IGFBP2 | [108,810,787-108,839,273](http://jun2011.archive.ensembl.org/Bos_taurus/Location/View?db=core;g=ENSBTAG00000005596;r=2:108810787-108839273;t=ENSBTAT00000007349) | Inhibits IGF-mediated growth and developmental rates by similarity. IGF-binding proteins prolong the half-life of the IGFs and have been shown to either inhibit or stimulate the growth promoting effects of the IGFs on cell culture. They alter the interaction of IGFs with their cell surface receptors. |
|  |  | **IGFBP5** | [108,851,172-108,854,511](http://jun2011.archive.ensembl.org/Bos_taurus/Location/View?db=core;g=ENSBTAG00000007062;r=2:108851172-108854511;t=ENSBTAT00000009285)  | IGF-binding proteins prolong the half-life of the IGFs and have been shown to either inhibit or stimulate the growth promoting effects of the IGFs on cell culture. They alter the interaction of IGFs with their cell surface receptors. |
| 12 | 6281991-6307016 | NONE | N/A | N/A |
| 15 | 60424410-61035044 | KCNA4 | [60,436,517-60,443,987](http://jun2011.archive.ensembl.org/Bos_taurus/Location/View?db=core;g=ENSBTAG00000020793;r=15:60436517-60443987;t=ENSBTAT00000027710) | Mediates the voltage-dependent potassium ion permeability of excitable membranes. Assuming opened or closed conformations in response to the voltage difference across the membrane, the protein forms a potassium-selective channel through which potassium ions may pass in accordance with their electrochemical gradient. |
|  |  | LOC787432 | [60,620,624-60,626,625](http://jun2011.archive.ensembl.org/Bos_taurus/Location/View?db=core;g=ENSBTAG00000039236;r=15:60620624-60626625;t=ENSBTAT00000052558) | Follicle stimulating hormone that regulates the development, growth, pubertal maturation, and reproductive processes of the body.  |
|  |  | FSHB | [60,683,262-60,687,228](http://jun2011.archive.ensembl.org/Bos_taurus/Location/View?db=core;g=ENSBTAG00000010889;r=15:60683262-60687228) | Stimulates development of follicle and spermatogenesis in the reproductive organs. |
|  |  | **ARL14EP** | [60,753,945-60,767,727](http://jun2011.archive.ensembl.org/Bos_taurus/Location/View?db=core;g=ENSBTAG00000012417;r=15:60753945-60767727) | Through its interaction with ARL14 and MYO1E, **ARL14EP** may connect MHC class II-containing cytoplasmic vesicles to the actin network allowing it to control the movement of these vesicles along the actin cytoskeleton in dendritic cells |
|  |  | **MPPED2** | [60,867,597-61,077,511](http://jun2011.archive.ensembl.org/Bos_taurus/Location/View?db=core;g=ENSBTAG00000020956;r=15:60867597-61077511) | This gene likely encodes a metallophosphoesterase. The encoded protein may play a role a brain development. |
| 6 | 66407840-66809119 | **None** | N/A | N/A |
| 10 | No haploblock | **N/A** | N/A | N/A |