Supplemental Information

FOXN3 regulates hepatic glucose utilization

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Figure S1. Architecture and population genetics of the rs8004664 SNP in the *FOXN3* **gene, Related to Figure 1.** Linkage disequilibrium (r² values) plots for the 100 kb flanking the rs8004664 are shown for four populations that contributed to the 1000 Genomes project (rendered on the ENSEMBL browser). In none of these populations is this allele in obvious, strong linkage disequilibrium with distant surrounding SNPs, pointing to this intronic region as the causal site.



tcactgaacattttttgaaaacagtccaggatggatgacgatgtcatttctctctttgcacactttccaaatcggtttactgttttcaag atactcatatttggtgtatgacacaatcaactcagtgtttaca tacaactgtggagcataaacatgtaacataagtaaactggtctgctgtcatgtcatttgagggtctgccattgcaccagacagcttgca ttggtgtattctcattctgcgtaccaagattatcattacagtaacactaattaggtgaataaatgtttttataattgatcctggatct acttgtagcaatgattcaagaaatgtgctaaggagccaaataattgaactctggctttagataatgtttttgtgaggtgaggaggaggg tgtcagtcaagaaaaagttttagtgtcagtcattagtgttgttacaatatatacagtaattacattg gatttatatttatacataagcaccaccagttagtttataagtgttttgtgaataaaagatgaagttg

Figure S2. FOXN3 binds a Forkhead sequence in the 3'-UTR of MYC, Related to Figure 4. (A,B) Immunoblot and densitometric analysis was performed for human MYC for the samples shown in Figure 2B (the TUBB immunoblot is reproduced here for clarity). Where indicated, samples were returned to complete medium for the indicated time ('+'). All times are in hours. Mean \pm s.e.m. values are shown. **P* = 0.05 in a 2-sided Student's *t*-test. (C) Structure of the human *MYC* gene (~5 kb shown). A Forkhead binding site and a MYC binding site (E box) are located distal to the 3'-untranslated region (3'UTR) were identified using the ENCODE database. The target PCR product for the ChIP assay is underlined. (D) The gel shows a PCR products from DNA templates precipitated from chromatin extracted from HepG2 cells with the indicated antibodies (MYC or FOXN3), antisera (Rat and Mouse) or controls (input and buffer). As a positive control, ChIP was performed on an additional MYC target gene *APEX1*. (E) Human *MYC* sequences distal to the 3'-UTR where the Forkhead binding site (blue) and E-box (red) were identified in the ENCODE database. (F) Zebrafish *mycb* sequences distal to the 3'-UTR where the Forkhead binding and then validated in Figure 4.



Figure S3. Glycolytic and gluconeogenic gene transcript abundance in the primary human hepatocytes samples, Related to Figure 5. Steady-state transcript abundance of the indicated glycolytic (A) and gluconeogenic (B) transcripts in cryopreserved human hepatocytes from donors with the indicated rs8004664 genotypes, G|G (n=2), A|G (n=8), and A|A (n=6). Horizontal lines indicate the median value. For *PHOSPHOGLYCERATE KINASE 1*, a 1-tailed Student's *t*-test and an outlier test were performed. For *PHOSPHOGLYCERATE MUTASE 1*, a 2-tailed Student's *t*-test and an outlier test were performed. For *TRIOSEPHOSPHATE ISOMERASE*, a 2-tailed Student's *t*-test and an outlier test were performed. FOR *PHOSPHOFRUCTOKINASE, LIVER*, a 2-tailed Student's *t*-test and an outlier test were performed.

| Lot Number | Age (years) | Sex | Body mass | rs8004664 genotype | Transcript abundance (normalized to <i>GAPDH</i>) | | |
|-------------|----------------|--------|------------------|-----------------------|---|----------------|--------|
| | | | index (kg/m²) | | FOXN3- T003 | FOXN3- T004 | MYC |
| ZBH1665 | 15 | Male | 17.6 | G G | 0.015 | 0.518 | 8.697 |
| ZBH2347-P10 | 1.4 | Female | 19.2 | G G | 0.046 | 0.787 | 4.654 |
| | | | | | | | - |
| ZBH0614 | 54 | Male | 25.8 | G A | 0.246 | 0.250 | 2.485 |
| ZBH0129 | 51 | Male | 36.6 | G A | 0.046 | 0.421 | 3.055 |
| HUM4058 | 67 | Female | 28 | G A | 1.271 | 0.808 | 2.101 |
| ZBH0486 | 14 | Female | 20.7 | G A | 0.046 | 0.617 | 7.987 |
| HUM4035 | 51 | Female | 33 | G A | 1.278 | 0.247 | 2.271 |
| ZBH1835 U10 | 17 | Female | 23.5 | G A | 0.068 | 0.318 | 12.831 |
| ZBH012513 | 51 | Female | 33.5 | G A | 0.267 | 0.901 | 15.504 |
| HUM4060B | 23 | Male | 18 | G A | 0.978 | 0.434 | 94.252 |
| | | | | | | | |
| HUM4024 | 77 | Male | 26 | A A | 0.715 | 0.901 | 1.003 |
| HUM4069C | 30 | Male | 25 | A A | 0.652 | 0.455 | 0.668 |
| ZBH1989-P | 25 | Female | 26.1 | A A | 1.041 | 0.371 | 4.660 |
| HUM4031 | 53 | Female | 27 | A A | 0.842 | 0.742 | 1.377 |
| HUM4048 | 43 | Female | 23 | A A | 1.729 | 23.637 | 0.369 |
| HUM4050 | 42 | Female | 29.1 | A A | 1.358 | 0.362 | 0.622 |

 Table S1. Phenotypic characterization of the 16 human hepatocyte samples studied,

 Related to Figures 1 and 4.

| Gene Forward primer Reverse Primer Reference Zebrafish Reference Reference Reference aldoaa CTGCCAGGAGGACATCATAAAG CCTTATCTCCCCAGGAGACACTA (Karanth et al., 2009) enia CTTCATCGCTGAGACTGTGTGTGTG GGAACGGTGTCATTCATCAGGGATTAC (Karanth et al., 2009) gek TGCCAGGAGGACTAAGAA CTGCCTTCTTCTGAGATGGGATTAC (Karanth et al., 2009) gek TGCCAGGAGGACCTAAGAA CTGCCTCTTCTCTGAGATGGGAATTC (Karanth et al., 2009) foxn3 T002 GTGACGACGAGGAGATGAAAG CCTCCTCGCCTTCTTCTTCTCCCCCCTCTTCT (Karanth et al., 2009) mycb CCCTGGACACCACGAGGAGTGAAG CTCCTCTCCCCCCTTGTTGTTT (Karanth et al., 2009) pkth GCTGCTGACGACACCACAGGAGAGTGATAG CTCCTTCGCCAGGAGATTTCT (CCCCGTGTGAACACACACAGGAAGGAGTAAGAGCCCTTGATTTT pgkth AAACACCTGGAGGAGATGAC CTGCTGACGACACTGACGATTATC CTCCTGGCGACACACAGGAGGAAGGCCTGAAGA (Karanth et al., 2014) getra AAGACCTGGAGGAGATGAC CTCCTTGCCTCCTCTTCT (CTCCTGGAGAGCTTAGAAGAGCCCCAAGGAGAGCCTGAAGA (CACGACACCCAGGAGGATGAC (CACGACACCCAGGAGGATGAC (CACGACACCCAGGAGGATGAC (CACGACACCCAGGAGCACAGAGAGCCTGAGGAGCCTTCAGAG (CACGACACCCGGAGAAGACCCCCCCCTCTT | Primers for quantitative PCR | | | | | | | | |
|--|---|--|---|-----------------------------------|--------------------------------|--------------------------|--------------------------|--|--|
| Zebrafish effa CTGCCAGGAGGAGTTCATAAAG CCTTATCTCCCGAGGACACATA effa TTGCAGGAGAGATAACGGTGGTGCTG GGAACGGGTGATGAGGGAGATAA (Karanth et al., 2009) enota CTTCATCGCTGACCTTGTAGTC TCAGTGGCTGACCTTGTAGTG (Karanth et al., 2009) gkt TGCCAGGAGAGATGAGAG CTGCCTTCTCTGGCGGATAAA (GTGCGGACGAGGAGAGTGAAAG CCTCGGCGTTGTGTGTGTGT foxn3 T001 GCTACCTGTCTCTGTGTGATC CCTCGGCACCCCACCCTAC CTCTTGTCCTCTCTCTTCT myca TCCTGGACACCTCAACGGTAAC CCTCGGCAGTTAGCACTTAC CCACACACACTACCCACGGAGTAAAG foxn3 T001 GCTGCTGACCCAGAGGATAAG CCTCTCTCCCCTCTTCTT myca foxn3 T002 CCACACACACTACACGAGGA TCGTCGACACCACAAGGAGATAAG CTGCCGAGAGAGCATTACACGCGAGAGACTTACCTTCC myca CCACACACATTCACAGGATAGC CCTACGTGGCATCACCATTAC CCTACGTGGCATCACCATTAC TTCCAGAGAGAGCCTCGAAGA gkt1 AACTGCTGGGCATCACACATTAC CCTGCGGCACACACAAGAGCCTCACGAAG TTCCAGAGCAGCACCCAAGAGCCTCACAAG gkt2 CCACGGCCACAGCAGTAAG GCTGCGCACCACAGCATTACA Lumman ALDOA GTTGTGGGCATCAAGGTAGA GCTGCGCACCAAGCAGAGAGCCTCAGGAGACCTCACGAG fDNX3 T003 | Gene | Forward pri | mer | | Reverse Primer | | Reference | | |
| aldoaa CTGCCAGGAGGAGTTCATAAAG CCTTATCTCCCCGAGGAGAACATC erfia TTGAGAGAAAATCGGTGGTGCTG GGAACGGTGTGATTGAGGGAAATTC (Karanth et al., 2009) enota CTTCATCGCTGACCTTGTAGTC TCCAGGGGAATTC (Karanth et al., 2009) gok TGCCAGGAGGAGAAAGAG CTGCCTTCTGTGATTC ACCTCATCCACAGACAACACTC faw3 T002 GTGACGACGAGGAGATGAAAG CTCCTTGCCTCTCTTCTTCTCCTCCTC Impose faw3 T010 GCTACCTGTCTGTGTGTGTTC CTCCTTGCCTCCTCTTCT Impose faw3 T02C GCTACGACACTCCACCTGACAGGATAC CTCCTTGCCCTCCTCTTCT Impose faw3 TCCTGGACACCTCCACCTGAACA CTCGTCGACGCGATCACCACATATC CTCCTGCGCGACACACACACACACAGGATATC Impose pkh GCTGCTGCAGCACACACACAGGAATATC CCACGTCCACCGACACACACACACACACACACACACACAC | | | | | Zebrafish | | | | |
| effa TTGAGAAGAAAATCGGTGGTGCTG GGAACGGGTAGATTTAGTC (Karanth et al., 2009) eno ta CTTCGTCGCTGACCTTGATCC CCAGGGAGAATGGAGGCTAACA CTGCCTCGATCGAGAGGAGCTAACA (Karanth et al., 2009) glub ti CAACGGAGCAAGGAGGAAGTGAACA CTGCCGTCTTCTGCAGTGGATATGT (Karanth et al., 2009) glub ti CAACGGAGCAGGAGGAGGTGAACA CTGCGGCTTGTTCTGTCTGGCTGATC (CACGGACGACGAGGAGGTGAAG myca TCCTGGACACCTCACCCTAC CTCTTCTCCTCTCTTCTTCT (Karanth et al., 2008) myca CCCTGGACACGTACACGCTAAC CCCTCGCTCTTCTTCTCTCCTCCTCT (Karanth et al., 2008) pkh CCACGACACCACAGGAGGTAAG CCTCTCTCCTCCTCTTCT (Karanth et al., 2008) pkh CACCGGACGACATATCC CTAGCGAAGGTTAAGCCCGAAGCTTACC (Karanth et al., 2013) pgk1 AAACGCTGGAGGAAGTGT CATAGGCTCAAAGCTAAGCTAAG (Karanth et al., 2013) glub 1 AACCCTGGGCGAAGGTAAG CCTCCTCCTCCTCAAAG (Karanth et al., 2013) glub 1 AAACACTGGGCGCAAGACTTAC CTTCCACAGAGACCTCAAAGCTAAG (Karanth et al., 2013) glub 1 AACACTGGGCGCAAGACTTAC CTTCCACAGAGCACCAAGACTCACAGA (CaTCTCCACAGCCAAGACCAGA glub 1 AACACCT | aldoaa | CTGCCAGG | GAGGAGTT | CATAAAG | CCTTATCTCCCGAGGAC | ACATA | | | |
| enota CTTCATCGCTGACCTTGTAGTC TCAGTGCTTCAGATGGGTTTC gck TGCCAGGAGGAGACTAAAGA CTGCCTTTCTGACTGGATAATA gludb1 CAACGGAGAGATGGGAGATGGAAAGG CTGCCTTCTTGTCTGACTGGATAATA gludb1 CAACGGAGAGATGGGAGATGGAAAGG CTGCCTCGCGGTTGATATGT toxn3 T202 GTGACGACGGAGATGGCACC CCCCCGGTTGGTGGTGATATTGT myca GCTACCTGTCTGTCTGATAC CTCTTCTTCTCCCTCTCTCTTT myca TCCTGGACACTCCACCTGAAC CCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC | ef1a | TTGAGAAG | AGAAGAAAATCGGTGGTGCTG GGAACGGTGTGATTGAGGGAAATTC | | | GGAAATTC | (Karanth et al., 2009) | | |
| gek TGCCAGGAGGAGCTAAAGA CTGCCTTCTTCTGACTGGATAAA fund1 CAACGGACGAGAGTGATAGC AACCTGATCCACAGACACATC fan3 1002 GTGACGACGGAGGAGATGAAAG CGTCCGGTTGGTGATATTGT fan3 1201 GCTACCTGTCTCTGTGTGATATC CTCTTGGCCTTGTTGTTTTT myca TCCTGGACACACCACACCTCAC CTCTTGCTCTCTCTTTTTTTTTTTTTTTTTTTTTTTTT | eno1a | CTTCATCG | CTGACCTT | GTAGTC | TCAGTGCTTCAGATGGG | | | | |
| gludb1 CAACGGAGAATGGGAGGTTATC AACCTCATCCACAGACACATC [foxn3_T02] GGTACCACGCAGGAGAGAGAGAC CGTCCGTGGTGGTATTTGT [foxn3_T201 GCTACCTGTCTGTGTGATAATGC CCCTCGTGGTGGTGATTTGT] mycb CCACAGACTTCCACCTAAC CTCTTCTCCTCCTCTCT] pkl GCTGCTGAACACACAGGGAGATGC CCACGCAAGTTATAGCCGAAG] pkl GCTGCTGAACACAAGGGTAAAG CTGACGAAGTGGTGTGTATTT] pgm1b AAACACTGGAGGAGATGTC CACGAGAAGAGCGGTGTAAA [pgk1 AAATGGCTGCACCAGGA TCC CATGGGCGAAGGGCGTAAA] sc2az CCACGTCCAGCAGGTATT GCTCGGCAGAAGGGCGTAAA] pi1a ACTCTGTGGGCATCAGGATTC CTCTGGCGAGAGGGCCTTAA] pi1a ACTCTGTGGGCATCAGGATTC CTCTGGCAGAAGAGCCCTCACAA] pi1a ACTCTGTGGGCATCAGGATGTC HUman ADDA GTTGTGGGCATCAGGATGACGATGTC CTGTGGCGAGAGAGCCCTCACG [Barrilleaux et al., 2013]] NO TCCCTGGTTGGGCATCAAGGTAGA GCGCGCGAACTGGGCTGAGG] ADDA GTTGTGGGCATCAAGGTAGA GCGGTTGCACACAACTGGGCTGAGG] ADDA GTTGTGGGCATCAAGGTAGA GCGGTTGCACACAACTGGG [Barrilleaux et al., 2013] [NO T GCCCTGGTTGGCAGAACC GCGTTGCCACGAACCTAGG [Barrilleaux et al., 2013] [NO T GCCCGGTTGCAGAGACCAGG CTAAGGAGACCTGGGTCACGAACTGGG] ADDA GTTGTGGGCATCAAGGTGGCTACACGAAG [CTAGGCAGAGACCTGGGTAGG]] NO CCTTCTCCAAGTTGCACGGA ACAAGAGCGCGGGGGGAGG] ADDA GCTTGTCGCAGGA CAAGC GCGTTGCACGCAACTTGGG [Barrilleaux et al., 2013] [NO T GCCCGGTTGCAAGCAACC GCGTTGCACGCTACGTGGGGAAGG [CLCINNA1]] NO CACGGCAAACCCAGACCTGGGA ACAAGAGTGGGTCACCTCAGG [Barrilleaux et al., 2013] [NO T GCCCGGTTCCAAGGG ACAACCAGGCTTGGAGAGC [CLCINNA1]] NO CACGGCAAAGCCGGAAACCAGG GGGAAGCCTTGGCACGTCGGGGAAGG] NO CACGGCAAGAGCCGGGGAAAA ACGAGGGCTTGCACGCTGGTCACGCTCGTGAGA [CLCINNA1]] NO CACGGCAAGGCGGAAAGCTC CCCCACAGAGTGGGCCAAGG [CLCINNA1]] NO CACGGCGCGAAGCCTCCACGGGGAAGG] PCK1 ACGGGACAACCTGGGCGTAAA ACGAGGGCTTGAAG [CLCINNA1]] PGM1 CATCGAGGCGGAAGGCC ACCCAGGGCGAAGG [CGAAGTGGTCACTGGTGAAT [PI AAGATGAACGGGGGGGAGAG [CCCCACAGGGGGAGAG]] PCKL AGGGACAAGCTGGACGGCGAAG [GGGAAGGTTGGTAAAGGCAGGGCAAGG [CGGAAGGCGGAGGAG]] PCKL AGGGACAAGCTGGGCGAAG [GGGAAGGTTGGTAAAGGGGGGGACGGGGAGGAG]] PCKL AGGGGACAAGCTGGGCGAAG [GGGAAGGTTGGTAAAGGGGGGGACGGGTAGAGGCGAGGGGGGAGG] PCKL AGGGGCACAGCTGGTCACC CCCCACAGGGGGGAAGG] PCKL AGGGGACAAGGT | gck | TGCCAGGA | GGAGCTA | AGA | CTGCCTTCTTCTGACTG | | | | |
| foxm3_T002 GTGACGACGAGGAGATGAAAG CGTCCGGTTGGTGTTT foxm3_T201 GCTACCGTGTCGTGTCGTATC CTCTTGCCCTTGCTTTT myca TCCTGGACACCACGCTAAC CTCTTCTTCCTCCTCC mycb CCACAACACTTCCACTGGATAC CCTCGCGAGATTTTCTCCTCCTC pkh GCTGCTGAACACAAGAGGATAC CCACGGCAGAGTTTAGCCGAAG pkh ACACGCTGAGACCAAGGA TCGTCGAAACTGGCTGATATTT pgam1b AAACACCTGGAGGAATGTC CATCAGCGTTCAATGCCTAAA gk1 AAATGCCTGCACACGACATT GCTTCCACAGAGAGCCTTAAA slc2a2 CCACGTCCACGCACATCTAC TTTCGAGAGCATCAAGA tpi1a ACTCTGTGGGCATCAAGGTAGA GCTCCGTCGTGGTTGGAGA ACCTGTGGGCATCAAGGTAGA GCTCCGCCCAACTTGGA (Barrilleaux et al., 2013) ENO1 TGCCCGGTAGCAGAAAC GCGTCGGCCCCACATTAGA (Cicinnati et al., 2013) F0XN3 T003 CAGGCATATCAAGCACTCAC AAGTGCAGGAGAGC (Cicinnati et al., 2008) GCK1 M1 CCGGCGACAACCGCGGTGCT CCCCACACAGGCCTGCAAA ACGGACTGCACCAACTTCACA GAPDH TGCACCGCGGAGAAAAA ACGCAGCTGCAGAACTGCCCCCCAGA (Cicinnati et al., 2008) GCK1 M1 CCGGCGACACACTGCTTAAGC CCCCCACAGACTGCAGCAGCTCCCCAGA (Cicinnati et al., 2014) (Cicinnati et a | gludb1 | CAACGGAG | GAATGGGA | GGTTATC | AACCTCATCCACAGACA | | | | |
| form3_t201 GCTACCTGTCTGTGTGTGATTC CTCCTTGGCCTTTGTTGTTGTTT myca TCCTGGACACTCACCCTAAC CTCGTTGCTGTCTGTTGTTGTTGTTT mycb CCACAACACTTCGACCTGAAC CTCACGAACTGTGTCCTGTTGTTT pkth GCTGGTGAACACAAAGGTAAAG CTGACCGAACTGTGACAGGA pgk1 AAACACCTGGAGGGAATGTC CATAGGCTTGAACATGGTCAA ggk1 AAAAGCCTGCAGCAGCATTATC CTCTGGCAGAAGGCTTAAA ggk2 CCACGTCCACCAGCAGTATC CTCTGGCAGAAGCTCACTAAA tpifa ACTCTGTGCCACCAGGAGCATTAC GCTCGTCTGCTTGTACA pgk1 AAATGCCTGGCAACGTAAG GCTCGTCTGTGTGAG tpifa ACTCTGTGCCACACAGGTAGA GCTCGTCTGTGTGACG ACTCTGTGGCACACACGCAAGAGA GCTCGTCTTGTGTACTG ACAGAACACCCAGAAGCAAG ADDA GTTGTGGGCATCAAGGTAGA GCTCGTCTTGCTGCGCCACACCGG (Barrilleaux et al., 2013) ENO1 TGCCCTGGTTAGCAAGAAAC GCCGTCGCCCCACACACTAGG ACAGACACCTGAGGACACTCAGG FOXN3_T004 CCTTCTCCAAGTCCTCCAGGA ACAGAGTGCACGCCGCCAGGAG ACAGAGCTTGACGC FOXN3_T004 CCTTCTCCAAGTGGTC GCCCAAGCTGCAGGCGCAGAAA ACGAGCGTGAGGACATTGCA (Zhang et al., 2014) HMBS TGCACACCACACCACGTGGT CCCCCCACAGATGGCCTCCCGGTGGCCCCGGGAG ACCTG | foxn3_T002 | GTGACGAC | GAGGAGA | TGAAAG | CGTCCGGTTGGTGATAT | | | | |
| myca TCCTGGACACTCCACCTAAC CTCTTCTTCCTCCTCCTCT mycb CCACAACACTTCCACTGGATAC CCTGACCAATTCTTCCTCCTCCTC pk1 GCTGCTGAACACCAGGA TCGTGGAACTCGGTTCA pgm1b AAACCCTCGAGAGACA CATAGGCTTCAATTCTTCCTCCTCAT pgm1b AAACCCTGGAGGAATGTC CATAGGCTTCAATAA slc2a2 CCACGTCCACGCAGCTATT CCTCGGCACACAGGACTCACCTAGA y1a ACTCTGTGGGCATCACGAGA GCTCCGTCGTTGATGAA ACTCTGTGGGCATCACGAGAAC GCTCCGTCGTTGTGTGGTGAG Wmman ACTCTGTGGGCAACCAAGGAAC GCCTCGCCTCTCTGTGTAGA ACCAACCCAAGACCAAGA GCTCCGCCCTCACGAGAGAGC GATTGTGGGCAACCAAGAAC ADDOA GTTGTGGGCAATCAAGGAAACC GCGTCGCCCCCACAGAGGAGAGC GATGTGAGAGAGC FDN1 TGCCCTGGTTAGCAAGAAAC GCGTTCGCACCAAAACTCTGAGAGA GCTCGTCTGCAAGGA FDN3 TGCACCACCAACACGACACAAC ACATGTCAGGACTCTCAGAG FOXN3 1003 CAGGCATATCAAGGACATCAC GCK1 M1 GCGCGGAAGAAAA GCGCATGACCTCTCCAAGG ACAGAGTTTCCTCAAGG (Clainnati et al., 2008) GCK1 M1 GCGCGGAGAGAAAA ACGAGGCTTCCATGGC (Clainnati et al., 2008) GCK1 M1 GCGACTGAACCTCGCTGCT CCCCCACAGAAGCTGGCCCCCGGAGA AACTGCTGCTGAGCT | foxn3_T201 | GCTACCTG | TCTCTGTC | TGATTC | CTCCTTCGCCTTTGTTTC | | | | |
| mycb CCACAACACTTCCACTGGATAC CCACGTCATTTCTCTCCTC pck1 GCTGCTGAACACAAGGTAAAG CTGACCGAAGTTAGCCCAAGGA TGTCACCGAAGTAGCA pgk1 CACAGACTTTGAGCACAAGGA TCGTCGAACAGGACTATT TGCTCGACAGGACCTTAA pgk1 AAATGCCTGGACGCAACTATC CATAGGCTCATCACTGGCTTCA pgk1 AAATGCGCGACACACCATATC CTTCGACGAGAGGCCTTAAA pffa slc2a2 CCACGTCCAGCGCACCATCTCC TTTCGAGGCGTCGATGAGG tpira ACTCTGTGCGCATCAAGGTAGA GCTCCCTCTTGTACTG ALDOA GTTGTGGGCATCAAGGTAGA GCTCCCCTCTTGTACTGA ADPX1 ACGAACAACCCAGGAACCAAG CTAAGCCAGGACACCAAG (Barrilleaux et al., 2013) ENOT TGCCCTGGTTAGCAAGGAAAC GCGTCCACCAAGGTACAAAGCACACAGA ACGAGATCGACCAACGG F0XN3 T004 CCTCTCCAAGGTTAGACAGCACATCAG AACAAGATGGCTCACTTGGAG (Clcinnati et al., 2008) F0XN3 T004 CCTCTCCCAACGTGGT GCCACGGGCGAAAAA ACGAGCTTCACATCTGGTG (Clcinnati et al., 2014) MMBS TGCACCACCCACGGGAAAAA ACGAGGCTTCACATCTGCAGG (Clcinnati et al., 2014) MMBS TGCACCACCCTGGTTTAAGC GCCATTGGCACTCCCTCCTTCTGAA ACAAGGCTTTGCAACTTGTGCC | туса | TCCTGGAC | ACTCCACC | TAAC | CTCTTCTTCCTCCTCCTC | | | | |
| pck1 GCTGCTGAACACAAAGGTAAAG CTGACCGAAGGTTATAGCCGAAG ptkib CACAGACTTTGAGCACAGGA TCGTCGAAACTGGTCGATATTT D pgm1b AAACCCTGGAGGGAATGTC CATAGGCTTCACTGGCTTCA D pgk1 AAATGGCTGCATCACCATTATC CTCTGGCAGAAGAGCCTTAAA St2a2 CCCACCGTCCAGCGACGCTATTC CTTTCACACAGTTAAA St2a2 CCACCGTCCAGCGCATCATCAC TTTCAGAGCGTCGGTGGAG Imman ALDOA GTTGTGGCATCAAGGTAGA GCTCCCCACAGGCCCGGAG Imman ALDOA GTTGTGGCATCAAGGTAGA GCTCCCCACCAGACCCAGG IBarrilleaux et al., 2013) FDX13 ACGAACCACACACACAGGAAC GCGTTCGCACCAAACTTAGA FOXN3_T003 CAGGCATATCAAAGCCACTACA AATGTCAGGACCTTGCAGAG FOXN3_T004 CCTTCTCCACGTTCGCAGGA ACAAGATGGCTCACCTGCTGGT GCAAGCTGGACCTTGCATGAG FOXN3_T004 CCTTCTCACAGTCCTCACGAGA GCAAGCTGGACCTTCATGGACTTTCACCTTCTCTCT GGPC GGACACCCTAACGTGGTAGC GCATGGACGTCACCCACACTGGTGGT CCAAGCGGGAAGA ACGAGGCTTCACTGGTGGT CCCCACAGAGGCGCTCACACG (Zinang et al., 2014) HMBS TGCACACCCCACACTGGTGGT CCCCCACAGATGGACGCTTCACAGG (Zinang et al., 2014) FKL AGGGCAGCAGCTGGT CCCCCACAG | mycb | CCACAACA | CTTCCACT | GGATAC | CCACGTCAATTTCTTCC ⁻ | | | | |
| pfklb CACAGACTTIGAGCACAGGA TCGTCGAAACTGGTCGTCATTIT pgm1b AAACACCTGGAGGGAATGTC CATAGGCTTCACTGGCTTCA MACACACTGGAGGGAATGTC pgk1 AAATGGCTGCATCACCATTATC CTCTGGCAGAGAGCTCACTAAA St2a2 cCACGTCCAGCAGCACTATC GCTTCCACAGGAGCTGATGAA St2a2 cCACGTCCAGCAGCACTATCAC TTTCAGAGGCTTGGTGAGG y1a ACTCTGTGCGCATCAACGTACAC TTTCAGAGGCTTGATGAGGAGA ACTCGTGGCATCAAGGTAGA GCCTCCCTCTTGTGACGAG (Barrilleaux et al., 2013) END1 TGCCCTGGTTAGCAAGGAAAC GCGTTCGACACAACACAGA FOXN3 T004 CCTTCTCCAAGGTCCTCCAGGA ACAAGATGGCTCACCTCTGGTC GACCACCACCACCTGCTTAGC GGCATGGAACGTTGGCATGAG (Cicinnati et al., 2008) GCK1 M1 GCGGAGAAGCCTTGGATAT ATCGTCTCACAGGACGCCTCACA (Zhang et al., 2014) HMBS TGCAACGCACGCAAAAA ACAGAGCTTTCACTTGTCTCTCT GGPC GGCTCAACCTCGTCTTAAGTG (Cicinnati et al., 2008) Cicinnati et al | pck1 | GCTGCTGA | ACACAAAG | GTAAAG | CTGACCGAAGTTATAGC | | | | |
| pgam1b AAACACCTGGAGGGGAATGTC CATAGGCTTCACTGCATCAC pgk1 AAATGGCTGCATCACCATTATC CTCTGGCAGAGAGCCTAAA sic2a2 CCACGTCCAGCAGCATATT GCTTCCACCAGAGCTCACTAAA tpi1a ACTCTGTGCGCATCATCTAC TTTCAGAGGCGTCAGCTAAA tpi1a ACTCTGTGCGCATCATCTAC TTTCAGAGGCGTCTGGTTGAG Human ALDOA GTTGTGGGCATCAAGGTAGA GCTCCGTCCTTCACG APEX1 ACGAACACCCAGAACCAAG CTAAGCCAGAGACCCTTAGA APEX1 ACGAACACCCAGAACCAAG GCTCGGCCTCACGG FON3<003 | pfklb | CACAGACT | TTGAGCAC | AGGA | TCGTCGAAACTGGTCTG | | | | |
| pgk1 AAATGGCTGCATCACCATTATC CTCTGGCAGAAGAGCCTAAA slc2a2 CCACGTCCAGCAGCATT GCTTCCACAGAGACTCATCAA tpi1a ACTCTGTGCGCATCATCTAC TTTCGAGAGCTGGTGAGA ALDOA GTTGTGGGCATCAAGGTAGA GCTCCGTCCTTCTTGTACTG APEX1 ACGAACAACCCCAGAGACCCACAG CTAAGCCAGAGACCCTCACG FOXN3_T003 CAGGCATTACAAAGCACATCAG AATGTCAGGACAACCACAGG FOXN3_T004 CCTTCTCCAAGTCCTCCAGGA ACAAGATGGCTCACTCACAGTC GAPDH TGCACCACCACATGCTTAGCA GGCATGGGCTCATGCAGAGA GCK1 M1 GCGGAGAAGCCTTGGATATT ATCTCGCTGCACGACTGCCC GBPC GGCCCAACCTCGTCTTAAGTG CCCCCACAGAGTGCCC GBPC GGCACAACGCTGGATCATCGAA ACGAGGCTTGACATGTGCC GCACCAGCACGGCGGAAGAAA ACGAGGCTTGACATGTGACC (Cicinnati et al., 2008) PCK1 ACGGACTAACGCTGCTC CCCCCCACAGATTGACAGTT (Zhang et al., 2014) HMBS TGCAACGGCGGAAGCTCC CCCCCCACAGATGATGAGCCT (Cicinnati et al., 2008) PCK1 ACGGACTGAACGTGGCT CCCCCCCACAGATGATGAGCCC (Cicinnati et al., 2014) PFKL ACGGACTGAACGTGGCT CCCCCCACAGATGATCAGAT PRAM1 CATCTGGAGGCTGCTCTCAA PGK1 CTGGAG | pgam1b | AAACACCT | GGAGGGAA | ATGTC | CATAGGCTTCACTGGCT | | | | |
| sic2a2 CCACGTCCAGCAGCTATT GCTTCCACAGAGACTCACTAAA ipifa ACTCTGTGCGCATCATCTAC TTTCAGAGCGTCGGTGAGA Human Human ALDOA GTTGTGGGCATCAAGGTAGA GCTCCGTCTTCTTGTACTG APEX1 ACGACAACCCAGAACCAAG CTAAGCCAGAGACCCTCACG (Barrilleaux et al., 2013) EN01 TGCCCTGGTTAGCAAGAAAC GCGTTCGCACCAAACTTAGA Barrilleaux et al., 2013) EN01 TGCCCTGGTTAGCAAGAAAC GCGTTCGCACCAAACTTAGA Barrilleaux et al., 2013) EN01 TGCACCACCACAAGCATCAG AATGTCAGGACCACTCAGGA Barrilleaux et al., 2013) EN01 TGCACCACCACAGCATCAG AATGTCAGGACACCTACAG (Barrilleaux et al., 2013) ENX3_T003 CAGGCATACAACGCAGAAAC GCGTTCGCAACCTCTCAGGC (Cicinnati et al., 2008) GCK1 M1 GCGAGAAGCCTTGGTTAAGTG CTCCCTGCAGCCCACTCTCCTTCT (Cicinnati et al., 2014) HMBS TGCAACGGCGGAAGAAA ACGAGGCCTTCCAACTCTCCTCAGGCCCCAGCCTTAATC (Cicinnati et al., 2014) PCK1 ACGAGCATGAACGCTGGTCTCTCTGAA AACGCCAGGCCTTCAATGAGGCCTGTAAGG PGK1 CAGGCAAGCTGAAGCTC PGAM1 CATCTGGAAGGCTGGAAGCT CCCCACAATGTGTGTGTGTAAGG TPI AAGATGAACGGCGGGAAG GCGAAAGTTGGTGTGTGTGGTGAA TP | pgk1 | AAATGGCT | GCATCACC | ATTATC | CTCTGGCAGAAGAGCCT | CTCTGGCAGAAGAGCCTTAAA | | | |
| tpi1a ACTCTGTGCGCATCATCTAC TTTCAGAGCGTCTGGTTGAG Human Human Human Human Human ACDACA GCTCCGTCTTCTTGTACTG APEX1 ACGACACCCAGGACCAAG GCTCCGTCTCTCACG (Barrilleaux et al., 2013) EXPEX1 ACGACACCCAGGACCAAG GCGTCCGCACCAAACTTAGA FOXN3_T003 CAGGCATATCAAAGCACATCAG AAAGATGGCAACAACCTCAGG (Barrilleaux et al., 2013) FOXN3_T004 CCTTCTCCAAGTTCCTCCAGGA AACGACACCAACACTCAG AAGATGGCACACAACGTCTAGGG FOXN3_T004 CCTTCTCCCAAGTTCCTCCAGGA AACAAGATGGCTCACTCTCAGTG GCACACCAACACTGCTTAGG GCACATGCAACTGCTGTGGTCATCTGTGGGCATGAGGA GCACACCAACACTGCTTAGG GCGCTCACCCTCCTTCT GGAPDH TGCACACCACACACTGCTTGGTGGTCATCTGTGGTCATCTCTCGAG (Clicinnati et al., 2008) GCK1 M1 GCGGAGAAGAAAA ACGAGGCTTCCAGTCTCCAGGCCTTCCAGGCCTTCCAGGC (Clicinnati et al., 2014) HMBS TGCAACGCCGAAGAAAA ACGAGGCTTCCAGGCCTTCCAGGCCTTAAG (Zhang et al., 2014) PKL AAGGGATTGAACGCTGGCCGTC CCCCCACACAGAGGAGGCTTCCAGGCTTTCATAGGC FOX PGAM1 CATCTGGAGGGTCTCTCTGAA AACTGCACGACGCAGGCTTAACTC PGAM1 CAGGCACAGCTGGACGTTAAC TTGGGACAGCGCGCAGGAG CCCCCACGAGTGGGTCGTCATAGG PGACTGGACAGGTTAGGAGGCGGAAG CCCCCGCAGGAGGCGAGGTGGTGAGGTAA TTGGGACAGGCGGAAG <td>slc2a2</td> <td>CCACGTCC</td> <td>AGCAGCTA</td> <td>ATT</td> <td>GCTTCCACAGAGACTCA</td> <td></td> | slc2a2 | CCACGTCC | AGCAGCTA | ATT | GCTTCCACAGAGACTCA | | | | |
| ALDOA GTTGTGGGCATCAAGGTAGA GCTCCCGTCCTTCTTGACTG APEX1 ACGAACAACCCAAGGAACAAG CTAAGCCAGAGACCTACG (Barrilleaux et al., 2013) EN01 TGCCCTGGTTAGCAAGAAAC GCGTTCGCACCAAACTTAGA FOXN3_T003 CAGGCATATCAAAGCAACTCAG AAAGATGGCACCACAAGAAG FOXN3_T004 CCTTCTCCAAGTTCCTCCAGGA AACGAAGGCTCTGGGTCATGAGA FOXN3_T004 CCTTCTCCAAGTCCTCCAGGA ACAAGATGGCTCACTCTAGAG GAPDH TGCACCACCAACTGCTTGACG GGCATGGACTGTGGTCATGAGA (Cicinnati et al., 2008) GCK1 M1 GCGGAGAAAAA ACGAGGCTTCATGCTTCTCCACCA (Zhang et al., 2014) HMBS TGCAACGGCGGAAAAAA ACGAGGCTTCATGTGTGCC (Cicinnati et al., 2008) PCK1 ACGGATTCAACCCTACGTGGT CCCCCACAGAATGGAGGCACTT (Zhang et al., 2014) PFKL AAGGACTGACGTGCT CCCCCACAGATGGAGCATT (Zhang et al., 2014) PFKL AAGGACTGACGTGCT CCCCCACAGATGGACGCTTAATG PGAM1 CATCTGGAAGCTGGCAGGTTAAA TTGGGACAGCCTTAATG PGK1 CTGGACGAGGGGGAAG GCGATGGAAGTTGAGCT CCCGCATGATATAGGCAGCTTAG PFKL AGGTGATGAACGGGCGGAAG GGGGACCACTTTGTGCGGTAT PGAM1 CATCTGGAAGGCGGGAAG GCGCATGGACGTAG FOTMAGGGAAGCCGGGTAG FOTMAGGGAAGCTGGGTAGT CCGC | tpi1a | ACTCTGTG | CGCATCAT | CTAC | TTTCAGAGCGTCTGGTT | GAG | | | |
| Human ALDOA GTTGTGGGCATCAAGGTAGA GCTCCGTCTTTTGTACTG APEX1 ACGAACACCCCAAGC CTAAGCCAGAGACCCTACG (Barrilleaux et al., 2013) EN01 TGCCCTGGTTAGCAAGAAAC GCGTTCGCACGAGACCCTACG (Barrilleaux et al., 2013) EN01 TGCCCTGGTTAGCAAGAAAC GCGTTCGCACGACCTTAGG (Barrilleaux et al., 2013) EN01 TGCCCTGGTTAGCAAGACACTCAG AATGTCAGGACTCTGGAGAAG (Cicinnati et al., 2013) F0XN3_T004 CCTTCTCCAAGTTCCTCCAGGA ACAGAGTGGCTCACCTTCTCTCT (GAPDH) TGCACACCACCACATCTCTTAGC GGCATGGACTTGGTCTCCCTTCTCTCT GAPDH TGCACACCACCTCGTCTTTAGC GCCATGGACTTCCCTCTCTCT (Cicinnati et al., 2008) (Cicinnati et al., 2014) GCK1 M1 GCGGAGAAGACCTTGGTTAT ATCTCCTCGTCTCCCCT (Cicinnati et al., 2014) PMBS TGCCAACGCAGGAAAA ACGAGGCTTCAACTCTTCATGTTGAGAGCCC (Cicinnati et al., 2014) PKL ACGGATTCACCCTACGTGGT CCCCCACAGAATGGAGGGCCC (Cicinnati et al., 2014) PFKL AAGGCATGAACGCTGCT CCCCCACAGAATGGAGGGCCTTAAT PRW PGAM1 CATCTGGAGAGCAGCTC CCCCCCATAGATGGGTTAACT PKLR GGCTTTGAACAGCTGGA | | | | | · | | · | | |
| ALDOA GTTGTGGGGCATCAAGGTAGA GCTCCGTCTTGTGTACTG APEX1 ACGAACAACCCAGAAGCAAG CTAAGCCAGAGACCTACG (Barrilleaux et al., 2013) EN01 TGCCCTGGTTAGCAAGAAAC GCGTTCGCACCAAACTTAGA (Barrilleaux et al., 2013) F0XN3_T003 CAGGCATATCAAAGCACATCAG AATGTCAGGAGCAACCTCTGGAGA (Cicinnati et al., 2008) GAPDH CCTTCTCCCAGGTCTGGGAATATT ATCTGCTCACCTTCACTCCTCAGG (Cicinnati et al., 2008) GCK1 M1 GCGGAGAAGCCTTGGATATT ATCTGCTCACCTTCCCTCAA (Zhang et al., 2014) HMBS TGCAACGCGGGAAGAAAA ACGAGGCTTCACATCTCCAA (Zhang et al., 2014) HMBS TGCAACGGCGGAAGAAAA ACGAGGCTTCACAGTCCAAA (Cicinnati et al., 2008) PCK1 ACGGATTCAACCTGTGTTTAAGTG CCCCCACAGAATGGAGGCATTT (Zhang et al., 2014) HMBS TGCAACGCGCGGAAGAAA ACGAGGCTTCAAGGCTGCT (Cicinnati et al., 2008) PCK1 ACGGATGAACGCTGCT CCCCCACAGATGGAGGCTTAAT (Zhang et al., 2014) PFKL AAGGCATGAACGGCGGAAG GCCTTAGCCTCGTAGAT PAGAM1 CATCTGCAAGGGCGGAAG CCCCCCCAGAGCTGATAATAGGCAGGCAGTAG TPI AAGATGAACGGGGCGGAAG GCCAAGTCGATATAGGCTGGTTATAG PAGATGAACGGGGCGGAAG GCCCTAGTGTGGTATGGGTTATG Prime | | | | | Human | | | | |
| APEX1 ACGAACAACCCAGAACCAAG CTAAGCCAGAGACCCTCACG (Barrilleaux et al., 2013) EN01 TGCCCTGGTTAGCAAGAAAC GCGTTCGCAACAACTTAGA FOXN3_T003 CAGGCATATCAAAGCACATCAG AATGTCAGGATCTTGGAAAG FOXN3_T004 CCTTCTCCAAGTTCCTCCAGGA AACAAGATGGCTCACTCTCAGTC (Cicinnati et al., 2008) GAPDH TGCACCACCAACTGCTTAGC GGCATGGACTGTGGTCATCACAGG (Cicinnati et al., 2008) GCK1 M1 GCGGGGAAGACCCTTGGATATT ATCTGCTCTCACAGTGCTCACCA (Zhang et al., 2014) HMBS TGCAACGGCGGAAGAAAA ACGAGGCTTCAACTCACAGTGGT (Cicinnati et al., 2008) PCK1 ACGGAGTTCACCCTACGTGGT CCCCCACAGAAGCTGGAGGCATTT (Zhang et al., 2014) PFKL AAGGCATGAACGCGGGT CCCCTCAAGCTGGAGGATTT (Zhang et al., 2014) PFKL AAGGACGAGGCGGAAGAAA ACGAGGCTTCAACTGAGGCGTGACGTGGT (Cicinnati et al., 2008) PCK1 ACGGAGTAGACGCGGGTGCT CCCCCACAGAGAGGAGGCGCTTCACAGT (Zhang et al., 2014) PFKL AAGGCATGAAGCTGGACGTTAA TTGGGACAGCCTTGATA (Zhang et al., 2014) PFKL AAGGCATGAAGCTGGGACGTTAA TTGGGACAGCCTTGATA (Zhang et al., 2014) PFKL AAGGCATGAAGCTGGACGTTAA ACCCCCTGATACCTTGACAGACGAGCTTATAG (Zhang et al., 20 | ALDOA | GTTGTGGG | CATCAAGO | STAGA | GCTCCGTCCTTCTTGTA | CTG | | | |
| EN01 TGCCCTGGTTAGCAAGAAAC GCGTTCGCACAACTTAGA F0XN3_T003 CAGGCATATCAAAGCACATCAG AACAAGATGGCTCTGAGAAG F0XN3_T004 CCTTCTCCAAGTTCCTCCAGGA ACAAGATGGCTCACCTCAGTC GAPDH TGCACCACCAACTGGTTAGC GGCATGGACTGTGGTATGAG (Cicinnati et al., 2008) GCK1 M1 GCGGAGAAGCCTTGGATATT ATCTGCTCACCTCCAGTCTCACCT (Zhang et al., 2014) HMBS TGCAACGGCGGAAGAAA ACGAGGCTTTCAATGTGCC (Cicinnati et al., 2008) PCK1 ACGGATCAACCTCGTGCT CCCCACAGATGAGGGCATTT (Zhang et al., 2014) PFKL AAGGGATGAACGCTGGT CCCCACAGAATGGAGGCATTT (Zhang et al., 2014) PFKL AAGGGATGAACGCTGGT CCCCACAGAATGGAGGCTTAAT (Zhang et al., 2014) PFKL AAGGCATGAAGCTGGACGTTAA TTGGGACAGCGTGAAG (Zhang et al., 2014) PFKL AAGGCATGAAGCTGGACCTC CCCCCACAGAGTGTGTATAC (Zhang et al., 2014) PFKL CGGATTGAAGTGGACAGCTTGTAA TTGGGACAGCCTGATATC (Zhang et al., 2014) PFKL CAGGACAGCTGGAAG GCCCACAGGCTGATATC (Zhang et al., 2014) PGK1 CTGGACAGCTGGACGCT CCCCCACACAGGCTGATATC (Zhang et al., 2014) PGK1 CTGGACAGGCTGGAAG GC | APEX1 | ACGAACAACCCAGAACCAAG | | | CTAAGCCAGAGACCCTC | CTAAGCCAGAGACCCTCACG | | | |
| FOXN3_T003 CAGGCATATCAAAGCACATCAG AATGTCAGGATCTTGGAGAAG FOXN3_T004 CCTTCTCCAAGTTCCTCCAGGA ACAAGATGGCTCACTCACTCAGTC GAPDH TGCACCACCAACTGCTTAGC GGCATGGACTGTGGTCATGAG (Cicinnati et al., 2008) GCK1 M1 GCGGAGAAGCCTTGGATATT ATCTGCTCACGTCACCTACCA (Zhang et al., 2014) HMBS TGCAACGGCGGAAGAAA ACGAGGCTTCAATGTTGCC (Cicinnati et al., 2008) PCK1 ACGGATTCAACCTCGGTC CCCCACAGAATGGAGGGCATTT (Zhang et al., 2014) PKL AAGGCATGAACGCTGGT CCCCACAGAATGGAGGCATTT (Zhang et al., 2014) PKL AAGGCATGAACGCTGGT CCCCACAGAGAGGGCTTAATGGAGGCATTT (Zhang et al., 2014) PKL AAGGCATGAACGCTGGT CCCCCACAGAGAGGGCTTAATGGAGGCATTT (Zhang et al., 2014) PKL AAGGCATGAACGCTGGT CCCCCACAGAGAGCCTTAATG (PKL) PKL AAGGCATGAAGCTGGACGTTAAA TTGGGACAGCCTTAATC (PALR) PKLR GGCATGAAGCTGGACGTTAAA TTGGGACAGCCTTAATC (PKL) PKLR GGCACAGCTGGAAGCTC CCCCCACAGAGCGAGAG (CCCCACAGCAGCGTAGGTGGTCACTGCGGTAGG Primers GGCACAGCTTGAAGTGGTGCAGTGGTCACTGCGGGTAAG TPI AAGATGAACGGGCGCGAAG GCGCAAGTGGTGGTGGTGTGTGGGGTATGG | ENO1 | TGCCCTGG | TTAGCAAG | GAAAC | GCGTTCGCACCAAACTTAGA | | | | |
| FOXN3_T004 CCTTCTCCAAGTTCCTCCAGGA ACAAGATGGCTCACTCTCAGTC GAPDH TGCACCACCAACTGCTTAGC GGCATGGACTGGTCATGAGA (Cicinnati et al., 2008) GCK1 M1 GCGGGAGAGCCTTGGATATT ATCTGCTCACCTTCTCCTTCT G6PC GGCTCAACCTCGTCTTTAAGTG CTCCCTGGTCACGTCTCACA (Zhang et al., 2014) HMBS TGCAACGCGGGAAGAAAA ACGAGGCTTCAATGTTGCC (Cicinnati et al., 2008) PCK1 ACGGATTCACCCTACGTGGT CCCCCACAGAATGGAGGCCATTT (Zhang et al., 2014) PKL AAGGCATGAACGCTGCT CCCCACAGAATGGAGGCCAGATT (Zhang et al., 2014) PKL AAGGCATGAACGTGGACGTCA CCCCACAGAATGGAGGCCAGAGT PGK1 CTGGACAAGCTGGACGTCT CCCCCACAGACGCCTAAGG PGK1 CTGGACAAGCTGGAAAGCTC CCCCCGCATGATGTTGGTGTA PKLR GGCATTGAAAGTGGAAAGCTC CCCCGCATGATGTTGGTGTA PFI AAGATGAACGGGCGGAAG GCGAAGTCGATATAGGCAGTAG Primers for genotyping SNP rs8004664 Forward primer Reverse Primer GGTCTTTGCACAGGCTCT ACATTATGCTAGTTGTGAAAAAGCGGCTACTGTGGGTCACTGCTGTGACAGGTCACTGCTGTAGACGGGCTCTTGTACAAGAAAGCAGGCTACTGTGGGGCACAGTTTGTACAAGAAAGCAGGCTACTGTGGGGCACAGTTTGTACAAGAAAAGCAGGGCTACTGTGGGGCACAGTTTGTACAAGAAAGCTGGGCTCATGCCTGCC | FOXN3 T003 | CAGGCATA | TCAAAGCA | CATCAG | AATGTCAGGATCTTGGA | | | | |
| GAPDH TGCACCACCAACTGCTTAGC GGCATGGACTGTGGTCATGAG (Cicinnati et al., 2008) GCK1 M1 GCGGAGAGACCTTGGATATT ATCTGCTCTACCTTCCTTCT GGCCCAACCTCGTCTTAAGTG CTCCCTGGTCCACTCCTCTC G6PC GGCTCAACCTCGTCTTAAGTG CTCCCTGGTCCAGTCTCACA (Zhang et al., 2014) HMBS TGCAACGGCGGAAGAAA ACGAGGCTTCAATGTTGCC (Cicinnati et al., 2008) PCK1 ACGGATTCACCCTACGTGGT CCCCCACAGAAGGGCGCTGAGAT (Zhang et al., 2014) PFKL AAGGCATGAACGCTGCT CCCCCACAGAGAGGCATAGG (Zhang et al., 2014) PFKL AAGGCATGAACGCTGCT CCCCCACAGAGAGCATTGATAGG PGAM1 CATCTGGAGGGGGTCTCTGAA AACTGCACGCCTGTAGAT PGAM1 CATCTGGAGAGGCTGTAAA TTGGGACAGCAGCCTTAAAT TGGGACAAGCTGGGCGGAAG PGKLR GGCATTGAAAGTGGAAAGCTC CCCCGCATGATGTTGGTGTA PKLR GGCATTGAAAGTGGAAAGCTC CCCCGCATGATGTTGGGTAT Primers for genotyping SNP rs8004664 Primers for genotyping SNP rs8004664 Forward primer Reverse Primer GGGCACAGCTGTTATG Primers GGTCTTTGCACAGGCTCAT ACATTATGCTAGTTGTGGGTTATG GGTCTTTGCACAGGCTCT ACATTATGCTAGAAAAAAGCAGGCTGGGTCACTGTGGTGCACTGCTGCAGA AttB1 GGGGGACCACTTTGTACAAAAAAGCAGGCTGGGTCTACTGTGGGTCACTGCCCCCTT Hum | FOXN3 T004 | CCTTCTCC | AAGTTCCT | CCAGGA | ACAAGATGGCTCACTCT | | | | |
| GCK1 M1 GCGGAGAAGCCTTGGATATT ATCTGCTCACCTTCTCTCT G6PC GGCTCAACCTCGTCTTTAAGTG CTCCCTGGTCCAGTCTCACA (Zhang et al., 2014) HMBS TGCAACGCCGGAAGAAAA ACGAGGCTTCAATGTTGCC (Cicinnati et al., 2008) PCK1 ACGGATTCACCCTACGTGGGT CCCCACAGAATGGGGGGGGCGATT (Zhang et al., 2014) PFKL AAGGCATGAACGCTGGT CCCCACAGAATGGGGGGGATT (Zhang et al., 2014) PFKL AAGGCATGAACGCTGGT CCCCACAGAATGGGGGGCATT (Zhang et al., 2014) PFKL AAGGCATGAACGCTGGTCT CCCCACAGAATGGGGGGCATT (Zhang et al., 2014) PFKL AAGGCATGAACGCTGGTCT CCCCACAGAAGGCTGGAGGT (Zhang et al., 2014) PFKL AAGGCATGAACGCTGGACGTT CCCCACAGAGCTGGAGGTTAAGG PGK1 CTGGACAAGCTGGACGTTAAA TTGGGACAGCAGCTGGTGATAGG PKLR GGCATTGAAAGTGGAAAGCTC CCCCGCATGATGTGGTGATATC PKINERS Primers for genotyping SNP rs8004664 Forward primer Reverse Primer GGGTCTTGCACAGGCTCT ACATTATGCTAGTTGTGGGTTATG GGTCTTTGCACAGGCTCT ACATTATGCTAGTTGTAGAAAAAGCAGGCTACTGTGGTCACTGCTGCACTGCTGAA attB1 GGGGGACCACTTTGTACAAAAAAGCAGGGCTACTGTGGTCACTGCACTGCCTGTAA gGTCTTTGCACAGGCCGGAGA attB1 GGGGGACCACTTTGTACAAAAAAGCAGGGTGGGTCAGTGAG | GAPDH | TGCACCAC | CAACTGCT | TAGC | GGCATGGACTGTGGTCA | (Cicinnati et al., 2008) | | | |
| G6PC GGCTCAACCTCGTCTTTAAGTG CTCCCTGGTCCAGTCTCACA (Zhang et al., 2014) HMBS TGCAACGGCGGAAGAAA ACGAGGCTTCAATGTTGCC (Cicinnati et al., 2008) PCK1 ACGGATTCACCCTCGTGGT CCCCACAGAATGGAGGCATTT (Zhang et al., 2014) PFKL AAGGCATGAACGCTGGCT CCCCACAGAATGGAGGCATTT (Zhang et al., 2014) PFKL AAGGCATGAACGCTGCTCTCTGAA AACTGCATGGCCTGAGAT P PGK1 CTGGACGGCTCTCTCTGAA AACTGCATGGCCTTAATGG P PGK1 CTGGACAGCTGGACGTTAAA TTGGGACAGCCGTGATAGG P PKLR GGCATTGAAAGTGGAAAGCTC CCCCGCATGATGTGGGTAA T PVINERS Forward primer Reverse Primer GGTCTTTGCACAGGCTCT ACATTATGCTAGTTGTGGGTTATG Primers for Transgenesis GGGGACCACTTTGTACAAAAAGCAGGGCTACTGTGGTCACTGCTGAA attB1 GGGGACCACTTTGTACAAAAAAGCAGGGATGGGTCCAGTCACTGCCCCCTT Human FOXN3 attB1 GGGGACCACTTTGTACAAAAAAGCAGGATGGGTCCAGTCAGT | GCK1 M1 | GCGGAGAA | AGCCTTGG | ATATT | ATCTGCTCTACCTTCTC | | | | |
| HMBS TGCAACGGCGGAAGAAAA ACGAGGCTTTCAATGTTGCC (Cicinnati et al., 2008) PCK1 ACGGATTCACCCTACGTGGT CCCCACAGAATGGAGGCATTT (Zhang et al., 2014) PFKL AAGGCATGAACGCTGCT CCCCCACAGATGGAGGCATT (Zhang et al., 2014) PGAM1 CATCTGGAGGTCTCTCTGAA AACTGCATGGCCTCTGTAAGG PGAN1 PGKLR GGCATTGAAAGTGGACGTTAAA TTGGGACAGCAGCCTTAATC PKLR PKLR GGCATTGAAAGTGGAAAGCTC CCCCGCATGATGTTGGTGTA PTPI AAGATGAACGGGCGGAAG GCGAAGTCGATATAGGCAGTAG PTPI Primers for genotyping SNP rs8004664 Forward primer Reverse Primer GGTCTTTGCACAGGCTCT ACATTATGCTAGTTGTTGGGTTATG Primers for Transgenesis Gateway multisite cloning - middle Entry clone (pME) attB1 GGGGACCACTTTGTACAAAAAAGCAGGCTACTGTGGTCACTGCTGAA zebrafish foxn3 attB1 GGGGACCACTTTGTACAAAAAAGCAGGACTGGGTCATTTTGCCCCTTT Human FOXN3 attB1 GGGGACCACTTTGTACAAAAAAGCAGGAGGGGTATTTTTTGGGTTCCCTTTGC Chromatin Immunoprecipitation-DNA primers GGGGACCACTTTGTACAAAAAAGCTGGGTATTTTTTGTGGTTCCTTTGC Forkhead binding sites near MYC 3'UTR CAGCCAGAGTTGACAGTTAG TTGTGAAGGCAGCAGCAGCAGTTACTTAT | G6PC | GGCTCAAC | CTCGTCTT | TAAGTG | CTCCCTGGTCCAGTCTCACA | | (Zhang et al., 2014) | | |
| PCK1 ACGGATTCACCCTACGTGGT CCCCACAGAATGGAGGCATTT (Zhang et al., 2014) PFKL AAGGCATGAACGCTGCT CCCTCATAGCCCTCGTAGAT PGAM1 CATCTGGAGGGTCTCTCTGAA AACTGGACGGCTGAAGG PGK1 CTGGACAAGCTGGACGTTAAA TTGGGACAGCCGCAGGCGTAAAG PGK1 CTGGACAAGCTGGACGTTAAA TTGGGACAGCCGCAGGCGTGAA PGK1 CTGGACAAGCTGGACGTTAAA TTGGGACAGCCGCAGGCGGAGG PGK1 CTGGACAAGCTGGACGTTAAA TTGGGACAGCCGCGGAGG PGCCCCGCATGATGTGGGTGTA PKLR GGCATTGAAAGTGGAAAGCTC CCCCGCATGATGTGGGGGAGGAG PGCCGCATGATGGGGCGGAAG PGCCGCGCAAGTTGGGGCGGAAG PGCCGCGCAGTGGGCGCAGTAG PTIP AAGATGAACGGGCGGGAAG GCGAAGTCGATATAGGCAGTAG PGCCGCGCAGGGGCACGGGGAGG PGCCGCGCAGCGGGACGGGGCGACGGGGGGGGGGGGGGG | HMBS | TGCAACGG | GGGAAGA | AAA | ACGAGGCTTTCAATGTTGCC | | (Cicinnati et al., 2008) | | |
| PFKL AAGGCATGAACGCTGCT CCCTCATAGCCCTCGTAGAT PGAM1 CATCTGGAGGGTCTCTCTGAA AACTGCATGGCGCTTGATAGG PGAM1 PGK1 CTGGACAAGCTGGACGTTAAA TTGGGACAGCAGCCCTTAATC PKLR GGCATTGAAAGTGGAAAGCTC CCCGCATGATGTTGGTGTA PKLR GGCATTGAAAGTGGAAAGCTC CCCGCATGATGTTGGTGTA PKLR GGCATTGAAAGTGGAAAGCTC CCCGCATGATGTTGGTGTA PTIMERS PTIMERS PTIMERS Primers for genotyping SNP rs8004664 Forward primer Reverse Primer GGCTTTGCACAGGCTCT ACATTATGCTAGTTGTTGGGTTATG Primers for Transgenesis GGTCTTTGCACAGGCTCT ACATTATGCTAGTTGTAGAAAAAAGCAGGCTACTGTGGTCACTGCTGAA attB1 GGGGACCACTTTGTACAAAAAAGCAGGCTGGGTCACTGCTGCAAA attB2 GGGGACCACTTTGTACAAAAAAGCAGGATGGGTCACTGCTCCCAGT Human FOXN3 attB1 GGGGACCACTTTGTACAAGAAAAGCTGGGTATTTTGGTTTCCTTTTGCCCCTT HUMAN FOXN3 attB1 GGGGACCACTTTGTACAAGAAAAGCTGGGTATTTTTGGCTTTCCTTTTGC Chromatin Immunoprecipitation-DNA primers Forward primer Reverse Primer Forward primer Forkhead binding sites near MYC 3'UTR CAGCCAGAGTTGACAGTTAG TTGTGAAGGCAGCAGAAGG TTGTGAAGGCAGCAGAAGG Forkhead binding sites near mycb 3'UTR AGGCTCTGTTAACTGGTATCAC TGACAGCAGACCAGTTTACTTAT TGAC | PCK1 | ACGGATTC | ACCCTACG | TGGT | CCCCACAGAATGGAGGCATTT | | (Zhang et al., 2014) | | |
| PGAM1 CATCTGGAGGGTCTCTCTGAA AACTGCATGGGCTTGATAGG PGK1 CTGGACAAGCTGGACGTTAAA TTGGGACAGCAGCAGCCTTAATC PKLR GGCATTGAAAGTGGAAAGCTC CCCGCATGATGTTGGTGTA TPI AAGATGAACGGGCGGAAG GCGAAGTCGATATAGGCAGTAG Primers for genotyping SNP rs8004664 Forward primer GGTCTTTGCACAGGCTCT ACATTATGCTAGTTGTGGGTTATG Primers for Transgenesis Gateway multisite cloning - middle Entry clone (pME) AttB1 GGGGACCACTTTGTACAAAAAGCAGGCTACTGTGGTCACTGCTGAA attB1 GGGGACCACTTTGTACAAAAAAGCAGGATCGGGTCCAGTCATGCCCCCTT Human FOXN3 attB1 GGGGACCACTTTGTACAAAAAAGCAGGATGGGTCCAGTCATGCCTCCCAGT Human FOXN3 attB1 GGGGACCACTTTGTACAAAAAAGCAGGATGGGTCCAGTCATGCCTCCCAGT Forward primer | PFKL | AAGGCATG | AACGCTGC | Т | CCCTCATAGCCCTCGTA | | | | |
| PGK1 CTGGACAAGCTGGACGTTAAA TTGGGACAGCAGCAGCCCTTAATC PKLR GGCATTGAAAGTGGAAAGCTC CCCGCATGATGTTGGTGTA TPI AAGATGAACGGGCGGAAG GCGAAGTCGATATAGGCAGTAG Primers for genotyping SNP rs8004664 Reverse Primer GGTCTTTGCACAGGCTCT ACATTATGCTAGTTGTTGGGTTATG Primers for Transgenesis Reverse Primer Gateway multisite cloning - middle Entry clone (pME) QGGGGACCACTTTGTACAAAAAAGCAGGCTACTGTGGTCACTGCTGAA zebrafish foxn3 attB1 GGGGGACCACTTTGTACAAAAAAGCAGGCTACTGTGGTCACTGCTGCAA Human FOXN3 attB1 GGGGACCACTTTGTACAAAAAAGCAGGATGGGTCCAGTCATGCCTCCCAGT Chromatin Immunoprecipitation-DNA primers Forward primer Reverse Primer Forkhead binding sites near MYC 3'UTR CAGCCAGAGTTGACAGTTAG TTGTGAAGGCAGCAGAGG Forkhead binding sites near mycb 3'UTR CAGCCCAGAGTTGACAGTTAG TTGTGAAGGCAGCAGAAGCAGAAG | PGAM1 | CATCTGGA | GGGTCTCT | CTGAA | AACTGCATGGGCTTGATAGG | | | | |
| PKLR GGCATTGAAAGTGGAAAGCTC CCCGCATGATGTTGGTGTA TPI AAGATGAACGGGCGGAAG GCGAAGTCGATATAGGCAGTAG Primers for genotyping SNP rs8004664 Reverse Primer GGTCTTTGCACAGGCTCT ACATTATGCTAGTTGTTGGGTTATG Primers for Transgenesis Reverse Primer Gateway multisite cloning - middle Entry clone (pME) Primers zebrafish foxn3 attB1 GGGGGACCACTTTGTACAAGAAAGCTGGGTCACTGTGGTCACTGCTGAA Human FOXN3 attB1 GGGGACCACTTTGTACAAAAAAGCAGGATGGGTCCAGTCATGCCTCCCAGT Human FOXN3 attB1 GGGGACCACTTTGTACAAAAAAGCAGGATGGGTCCAGTCATGCCTCCCAGT Forward primer Reverse Primer Forward primer Reverse Primer Forkhead binding sites near MYC 3'UTR CAGCCAGAGTTAGCAGTTAG TTGTGAAGGCAGCAGCAGAGG Forkhead binding sites near mycb 3'UTR AGGTCCTGTTAACTTGGTATCAC TGACAGCAGACCAGTTTACTTAT | PGK1 | CTGGACAA | GCTGGACO | GTTAAA | TTGGGACAGCAGCCTTAATC | | | | |
| TPI AAGATGAACGGGCGGAAG GCGAAGTCGATATAGGCAGTAG Primers for genotyping SNP rs8004664 Reverse Primer GGTCTTTGCACAGGCTCT ACATTATGCTAGTTGTTGGGTTATG Primers for Transgenesis ACATTATGCTAGTTGTTGGGTTATG Gateway multisite cloning - middle Entry clone (pME) Primers zebrafish foxn3 attB1 GGGGACAAGTTTGTACAAAAAAGCAGGCTACTGTGGTCACTGCTGAA AttB2 GGGGACCACTTTGTACAAAAAAGCAGGCTCCAGTCATGCCTCCCAGT Human FOXN3 attB1 GGGGACCACTTTGTACAAAAAAGCAGGATGGGTCCAGTCATGCCTCCCAGT Chromatin Immunoprecipitation-DNA primers Forward primer Reverse Primer Forkhead binding sites near MYC 3'UTR CAGCCAGAGTTGACAGTTAG TTGTGAAGGCAGCAGCAGAAG Forkhead binding sites near mycb 3'UTR CAGCCAGAGTTGACAGTTAG TTGTGAAGGCAGCAGCAGAAG | PKLR | GGCATTGA | AAGTGGAA | AGCTC | CCCGCATGATGTTGGTGTA | | | | |
| Primers for genotyping SNP rs8004664 Forward primer Reverse Primer GGTCTTTGCACAGGCTCT ACATTATGCTAGTTGTTGGGTTATG Primers for Transgenesis Gateway multisite cloning - middle Entry clone (pME) Zebrafish foxn3 attB1 GGGGACAAGTTTGTACAAAAAAGCAGGCTACTGTGGTCACTGCTGAA attB2 GGGGACCACTTTGTACAAAAAAGCAGGCTACTGTGGTCACTGCCCCTT Human FOXN3 attB1 GGGGACCACTTTGTACAAAAAAGCAGGATGGGTCCAGTCATGCCTCCCAGT dtB2 GGGGACCACTTTGTACAAAAAAGCAGGATGGGTCCAGTCATGCCTCCCAGT attB2 GGGGACCACTTTGTACAAAAAAGCAGGATGGGTCCAGTCATGCCTCCCAGT dtB2 GGGGACCACTTTGTACAAGAAAGCTGGGTATTTTTTGTGGTTTCCTTTGC Chromatin Immunoprecipitation-DNA primers Forward primer Reverse Primer Forkhead binding sites near MYC 3'UTR CAGCCAGAGTTGACAGTTAG TTGTGAAGGCAGCAGCAGAGA Forkhead binding sites near mycb 3'UTR AGGTCCTGTTAACTTGGTATCAC TGACAGCAGACCAGTTTACTTAT | TPI | AAGATGAA | CGGGCGG | AAG | GCGAAGTCGATATAGGC | CAGTAG | | | |
| Forward primer Reverse Primer GGTCTTTGCACAGGCTCT ACATTATGCTAGTTGTTGGGTTATG Primers for Transgenesis Primers Gateway multisite cloning - middle Entry clone (pME) Primers zebrafish foxn3 attB1 GGGGACAAGTTTGTACAAAAAAGCAGGCTACTGTGGTCACTGCTGAA attB2 GGGGACCACTTTGTACAAAAAAGCAGGGTCCTTTTTGCTCTTTCTGCCCCTT Human FOXN3 attB1 GGGGACCACTTTGTACAAAAAAGCAGGATGGGTCCAGTCATGCCTCCCAGT dtB2 GGGGACCACTTTGTACAAAAAAGCAGGATGGGTCCAGTCATGCCTCCCAGT Chromatin Immunoprecipitation-DNA primers Forward primer Forkhead binding sites near MYC 3'UTR CAGCCAGAGTTGACAGTTAG TTGTGAAGGCAGCAGGAGAG Forkhead binding sites near mycb 3'UTR AGGTCCTGTTAACTTGGTATCAC TGACAGCAGACCAGTTTACTTAT | Primers for | genotypir | na SNP r | \$8004664 | | | | | |
| Individual primer Reverse Primer GGTCTTTGCACAGGCTCT ACATTATGCTAGTTGTTGGGTTATG Primers for Transgenesis Primers Gateway multisite cloning - middle Entry clone (pME) Primers zebrafish foxn3 attB1 GGGGACAAGTTTGTACAAAAAAGCAGGCTACTGTGGTCACTGCTGAA attB2 GGGGACCACTTTGTACAAGAAAGCTGGGTCCTTTTTGCTCTTTCTGCCCCTT Human FOXN3 attB1 GGGGACCACTTTGTACAAAAAAGCAGGATGGGTCCAGTCATGCCTCCCAGT attB2 GGGGACCACTTTGTACAAGAAAGCTGGGTATTGTTGTGGTTTCCTTTGC Chromatin Immunoprecipitation-DNA primers Forward primer Forkhead binding sites near MYC 3'UTR CAGCCAGAGTTGACAGTTAG TTGTGAAGGCAGCAGGAGAG Forkhead binding sites near mycb 3'UTR AGGTCCTGTTAACTTGGTATCAC TGACAGCAGACCAGTTTACTTAT | Forward primer | genetypi | | 2000-00- | rso Primor | | | | |
| Primers for Transgenesis Gateway multisite cloning - middle Entry clone (pME) Primers 2ebrafish foxn3 attB1 GGGGACAAGTTTGTACAAAAAAGCAGGCTACTGTGGTCACTGCTGAA attB2 GGGGACCACTTTGTACAAGAAAGCTGGGTCTTTTTGCTCTTTCTGCCCCTT Human FOXN3 attB1 GGGGACCACTTTGTACAAGAAAGCAGGATGGGTCCAGTCATGCCTCCCAGT attB2 GGGGACCACTTTGTACAAGAAAGCTGGGTCCAGTCATGCCTCCCAGT Chromatin Immunoprecipitation-DNA primers Forward primer Reverse Primer Forkhead binding sites near MYC 3'UTR CAGCCAGAGTTGACAGTTAG TTGTGAAAGGCAGCAGCAGAAG Forkhead binding sites near mycb 3'UTR AGGTCCTGTTAACTTGGTATCAC TGACAGCAGACCAGTTTACTTAT | GGTCTTTGCAC | AGGCTCT | | | TATECTACTICITECCT | ATG | | | |
| Gateway multisite cloning - middle Entry clone (pME) Primers zebrafish foxn3 attB1 GGGGACAAGTTTGTACAAAAAAGCAGGCTACTGTGGTCACTGCTGAA Human FOXN3 attB1 GGGGACCACTTTGTACAAGAAAGCAGGGTCTTTTGCTCTTTCTGCCCCTT Human FOXN3 attB1 GGGGACCACTTTGTACAAGAAAGCAGGATGGGTCCAGTCATGCCTCCCAGT Thuman FOXN3 attB1 GGGGACCACTTTGTACAAGAAAGCAGGATGGGTCCAGTCATGCCTCCCAGT Thuman FOXN3 attB2 GGGGACCACTTTGTACAAGAAAGCAGGATGGGTCCAGTCATGCCTCCCAGT Thuman FOXN3 attB2 GGGGACCACTTTGTACAAGAAAGCAGGATGGGTCCAGTCATGCCTCCCAGT Forward primer Forward primer Forward primer Forkhead binding sites near MYC 3'UTR CAGCCAGAGTTGACAGTTAG TTGTGAAGGCAGCAGCAGAAG Forkhead binding sites near mycb 3'UTR AGGTCCTGTTAACTTGGTATCAC TGACAGCAGACCAGTTTACTTAT | Primers for | Transgen | esis | 7.07.1 | | | | | |
| middle Éntry clone (pME) Frincers zebrafish foxn3 attB1 GGGGACAAGTTTGTACAAAAAAGCAGGCTACTGTGGTCACTGCTGAA attB2 GGGGACCACTTTGTACAAGAAAGCTGGGTCTTTTGCTCTTTCTGCCCCTT Human FOXN3 attB1 GGGGACCACGTTGTACAAAAAAGCAGGATGGGTCCAGTCATGCCTCCCAGT attB2 GGGGACCACTTTGTACAAAAAAGCAGGATGGGTCCAGTCATGCCTCCCAGT attB2 GGGGACCACTTTGTACAAGAAAGCTGGGTATTTTTTGTGGTTTCCTTTGC Chromatin Immunoprecipitation-DNA primers Forward primer Reverse Primer Forkhead binding sites near MYC 3'UTR CAGCCAGAGTTGACAGTTAG TTGTGAAGGCAGCAGAAG Forkhead binding sites near mycb 3'UTR AGGTCCTGTTAACTTGGTATCAC TGACAGCAGACCAGTTTACTTAT | Gateway multisit | e cloning - | | | Primors | | | | |
| zebrafish foxn3 attB1 GGGGACAAGTTTGTACAAAAAGCAGGCTACTGTGGTCACTGCTGAA attB2 GGGGACCACTTTGTACAAGAAAGCTGGGTCTTTTGCTCTTTCGCCCCTT Human FOXN3 attB1 GGGGACCACTTTGTACAAGAAAGCAGGATGGGTCCAGTCATGCCTCCCAGT attB2 GGGGACCACTTTGTACAAGAAAGCAGGATGGGTCCAGTCATGCCTCCCAGT attB2 GGGGACCACTTTGTACAAGAAAGCTGGGTATTTTTTGTGGTTTCCTTTGC Chromatin Immunoprecipitation-DNA primers Forward primer Reverse Primer Forkhead binding sites near MYC 3'UTR CAGCCAGAGTTGACAGTTAG TTGTGAAGGCAGCAGAAG Forkhead binding sites near mycb 3'UTR AGGTCCTGTTAACTTGGTATCAC TGACAGCAGACCAGTTTACTTAT | middle Entry clone (pME) | | | | | | | | |
| attB2 GGGGACCACTTTGTACAAGAAAGCTGGGTCTTTTTGCTCTTTCTGCCCCTT Human FOXN3 attB1 GGGGACCAAGTTTGTACAAAAAAGCAGGATGGGTCCAGTCATGCCTCCCAGT attB2 GGGGACCACTTTGTACAAGAAAGCTGGGTATGGGTCCAGTCATGCCTCCCAGT Chromatin Immunoprecipitation-DNA primers Forward primer Forkhead binding sites near MYC 3'UTR CAGCCAGAGTTGACAGTTAG TTGTGAAGGCAGCAGAAG Forkhead binding sites near mycb 3'UTR AGGTCCTGTTAACTTGGTATCAC TGACAGCAGACCAGTTTACTTAT | zebrafish foxn3 | | <i>att</i> B1 | GGGGACAAGTTTGTACAAAAAGCAGGCTACTG | | | GGTCACTGCTGAA | | |
| Human FOXN3 attB1 GGGGACAAGTTTGTACAAAAAGCAGGATGGGTCCAGTCATGCCTCCCAGT attB2 GGGGACCACTTTGTACAAGAAAGCTGGGTATTTTTTGTGGTTTCCTTTGC Chromatin Immunoprecipitation-DNA primers Forward primer Reverse Primer Forkhead binding sites near MYC 3'UTR CAGCCAGAGTTGACAGTTAG TTGTGAAGGCAGCAGAAG Forkhead binding sites near mycb 3'UTR AGGTCCTGTTAACTTGGTATCAC TGACAGCAGAACAGTTTACTTAT | Human <i>FOXN3</i> | | attB2 | GGGGACCACTTTGTACAAGAAAGCTGGGTCTTT | | | IGCTCTTTCTGCCCCTT | | |
| attB2 GGGGACCACTTTGTACAAGAAAGCTGGGTATTTTTTGTGGTTTCCTTTTGC Chromatin Immunoprecipitation-DNA primers Reverse Primer Forward primer Reverse Primer Forkhead binding sites near MYC 3'UTR CAGCCAGAGTTGACAGTTAG TTGTGAAGGCAGCAGAAG Forkhead binding sites near mycb 3'UTR AGGTCCTGTTAACTTGGTATCAC TGACAGCAGACCAGTTACTTAT | | | <i>att</i> B1 | GGGGACAAGTTTGTACAAAAAGCAGGATGGGT | | | CAGTCATGCCTCCCAGT | | |
| Chromatin Immunoprecipitation-DNA primers Forward primer Reverse Primer Forkhead binding sites near MYC 3'UTR CAGCCAGAGTTGACAGTTAG TTGTGAAGGCAGCAGAAG Forkhead binding sites near mycb 3'UTR AGGTCCTGTTAACTTGGTATCAC TGACAGCAGACCAGTTACTTAT | | attB2 GGGGACCACTTTGTACAAGAAAGCTGGGTATTTTTGTGGTTTCCTTTTGC | | | | | | | |
| Forward primer Reverse Primer Forkhead binding sites near MYC 3'UTR CAGCCAGAGTTGACAGTTAG TTGTGAAGGCAGCAGAAG Forkhead binding sites near mycb 3'UTR AGGTCCTGTTAACTTGGTATCAC TGACAGCAGACCAGTTACTTAT | Chromatin Immunoprecipitation-DNA primers | | | | | | | | |
| Forkhead binding sites near MYC 3'UTR CAGCCAGAGTTGACAGTTAG TTGTGAAGGCAGCAGAAG Forkhead binding sites near mycb 3'UTR AGGTCCTGTTAACTTGGTATCAC TGACAGCAGACCAGTTACTTAT | | | • | Forward pri | imer | Reverse Primer | | | |
| Forkhead binding sites near <i>mycb</i> 3'UTR AGGTCCTGTTAACTTGGTATCAC TGACAGCAGACCAGTTTACTTAT | Forkhead binding | sites near M | C 3'UTR | CAGCCAGAGTTGACAGTTAG | | TTGTGAAG | GTGAAGGCAGCAGAAG | | |
| | Forkhead binding sites near mych 3'U | | | AGGTCCTGTTAACTTGGTATCAC | | TGACAGCA | TGACAGCAGACCAGTTTACTTAT | | |

Table S2. Primer sequences, Related to Figures 1, 2, and 4.

Supplementary References

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