**FIGURE S1. Characterization of ten UCNEs inside FTO gene ( alpha-ketoglutarate dependent dioxygenase).**

**Figure S1a. Screenshot of NCBI genomic viewer of FTO gene on chromosome 16.**

Positions of ten UCNEs inside extra-large introns of FTO gene are shown by red arrows. Their sequences are shown beneath the scheme. Their UCNEbase identifiers are the following: IRXB\_Mateo, IRXB\_Molly, IRXB\_Napoleon, IRXB\_Oberon, IRXB\_Othell, IRXB\_Pablo, IRXB\_Pandora, IRXB\_Penelope, IRXB\_Poseidon, IRXB\_Roxane.



>IRXB\_Mateo id=15047 pos=chr16:53756950-53757285 (FTO-1)

AAGTTACTTTAGTGTAACTGCTGCTGTCACCTTTGCCCTTAGCTAATCAA

ATAGTTTACCTTGAGGGAAGCATTTATCTCCCACTTTCATTATTATTATT

TTTGTAGCTGTAAAGATATATATTTTATGTCTGCAGAAGGCTGTAACAGT

GAAACGAGGTATTGATCTGCTGTATTTAGCAATTTCTTTCCACCTTGCCA

TCAATAGCATGTCAGCATCTGTCTGTACCGTGGTTGACCTCACAAATAGC

TCTTTATGCTCCCATTGGATTCAAATGATATAGTATGCTGAAAACTAAAT

CAATGAATGATTATAAAGTTTTTAGTATTATTTCAT

>IRXB\_Molly id=15052 pos=chr16:53929295-53929573

CGAAAGCACAAAGGACTGTGTTTATGATTCTCTTTGAAGTGTTTTTGCAA

CTGGATAAGGAAAATTTTAGAAACCGTCTGATAGTGTTCAGGGTAAATAC

TTAAACCCCTTTAGAGAATTTCACACACAGATACTGTGCAGCAGAAAAAA

GGGATACTTATGTTTCTTAAAGCTGCTACAGCCTACAGCTTTGTACTTAA

AGACAGAGGTGTTGAATAGAATTCTACTGAGGATACATCCAGTGACAGTA

TCTCCAGGAACATCAGAGCAAACCAGTGG

>IRXB\_Napoleon id=15056 pos=chr16:53957123-53957516

AGTAGTTAATGTACTGTATGTGAAAGATTTAAGACTGGTTGGAAAGCTCT

GCTTCTGTTTTATTAGGCTGCTATTGAAAAGCCAACAGCATAACTTCGAC

TAGGTGCTTTGAGATTTCTTAATGGGCTGTCAGGGGCAAGACACCAGGGC

TGTGCTATACTAGCTCTTTCCTGTACATTAAAACAACAGGGGCCAAACGA

TCACATACAGAAGTATGAATTACTTGATGCTTTCTCTGTTCCATATGGCC

AGCCATGTCTTTGGCAATTAATCATGTACAAAATCAGTCGAGTGCTCTCT

GAAGCATTGAAGTCAACATTTAGTTGTACCTGTGCCAGTAGGGGCAGTGG

GGTTGCAGGCGTAAAATAGCAGGATGAGGGGCTGCTGGCGCCAA

>IRXB\_Oberon id=15058 pos=chr16:53980805-53981054

TTGCTTCATTTCCAGTTTCACCATCAATTACGCCATGTGTTTCATCCAGT

TGGTGCTACCCTCCCAGTGTTAATTATAACCTACAAGACTGTTACAGTTA

ATTTTATGGCAAGCATATTGTCTCTTCAAGGCTCCAGAGCAGCTCATAAA

TTATCTTGAAGGTAAAATGTAACTTGGGGAACTAGTTATGAAAATTCCAT

CCATCTCGCTTAGGAGCTGCAGCTGCTACTGTCAGCTGCCTTGCTGCTGC

>IRXB\_Othell id=15069 pos=chr16:54020764-54020989

AAAGACCAACTCAAATTCTGTCTGCTGTAGCTTTGATCCTTTTCATTTAA

TTCTAAGTACACTTGTTATTATAGTAACTGTTGTTTGTATGTTATTTTAG

CTTTTTACTTAAGTAGCTATTTAGCAATTTAAATGAAAATGTAATTAGGT

TACATCTGTTTTACATGCATGTAATACCACGCAGATGTAAACTTCTATTA

AAGCCATATTTTCTTTTTGGCAAGAA

>IRXB\_Pablo id=15074 pos=chr16:54056490-54056818

TGTTCATTACTGCTCAAGTGACGGCTTGTCAATAGCAGTGCTTTTTAGTT

TGTTCTAGTCAGCACTTGCTGTGCATTTTGTTGGACCACTGGGAAATAAA

TACAACAAGATTATACATTTGGAATACCACAAGAGTTCACAAAAAAAACC

ACAAATGATAAATTATACACTTGGTAGAAAGTGACATGCTATCTTGTGCT

ATTAACAACCAAAGATAATTGCAACGAATTGTAATTGCAGTTTGCAACTT

ACAGTACAGTGTGTCCAACATCAATCTTAATAGTGAACAAAGCAATTTAT

ATTAAAACTTAATTCACTTGGTAACTTTC

>IRXB\_Pandora id=15083 pos=chr16:54093096-54093465

ATTTACCTTGCAGCCGAGTGAAAAATGATCAGAATATTAGACTCATCTAG

CCCACATTAAGGAGCCATTGCATTTCCCGACAATTGTATGCTATCTCAAT

ATGAAAACAGAGCAATTTCAACTCATATCAGGTTATGATCGGCAATTACA

GTTGCATAATTCACCTAGTCATCTCTTTGCAGGGCCTTTATTTTCCCTCT

TGGTGACATTCCTGAGAAAGTGCCTGATAAAAATGTCATATATCATCCCA

GCTTTAGAACTCGTGAGGGGGTAATCTGCTATGCCTTGCTGAGCCCATAT

TCATCACTGGATTTTTGACTTGGAGGGGTCATGGCACTCATAATTTCCTG

TTTGATATTGTCCTCACCAG

>IRXB\_Penelope id=15084 pos=chr16:54093563-54093797

ATGCTGGAGTTGGCCGTTTCGAAGATAATTAGATTTGATGTCAACATTTC

TTTATCACCTGCATCCTTTTGTGCATCTGTGTGTCAAGTTGTTCTTTCCG

GATTTATTAGCACCCTCAGAGCTACTCTCTATCTGTCAGCTTGTGTGCTG

TTTGTGTTGACAGTTGTAAAGTTAATTACTAGTACTAATGAGCATCGGGC

TTTTGGTGGACATGGCGTTTTGGACATTTAAAACT

>IRXB\_Poseidon id=15090 pos=chr16:54101268-54101623

CTAAATTAAGCTAGCTATTGCTGGAGAGTGGATAAGCGGCCATTATGAAT

TATCCTTAATTATAGCGATTTCCTAAACTAATAAACCTGCTAAATCTTTA

TTGCAAAGGTTAGTTTACGCAGTGCATATAAAATCCGCATGTGCTCCGCA

TCAGCCACCAGCTGTCTGACAGTGTGTTGCTATTGCAGTGAGTGTTCACA

TAAATTTTATGTTGGTTATATTAACAGTCCGTCCATATCACTACCCACAG

ATGCCAGTAGACATAAAAATTGCTCTCTAGTGAGCCTAAATATCCCTAGA

AGCTAGTTGTGTCTAATGTTCCATGTAGTATTTGAACGTGAAAGCACCAG

ATTGGA

>IRXB\_Roxane id=15096 pos=chr16:54144134-54144343

AGCTTATCAGTGCAAACAGTTTAATATTTATGCTAAGAGGATTGTCAAAA

GCAGCTTCTGTTGCTTTAATTCTTGTTTTAAATAAATAATGAGAACATTT

AAACACATTACTCTTCTTGGGGCCCCGGGGTCAGCTAATCTTATTATTTA

TGAAGTGATGTGCTACATAATAGTACTTAGTGCATGTTAACAGACGCTAT

TATCAGGGCC

**Figure S1b. Pairwise BLAST alignments of HUMAN vs CHIKEN UCNE-Mateo inside FTO gene.**

**(IRXB\_Mateo id=15047 pos=chr16:53756950-537572 (h37.p13))**

Human UCNE element highlighted in green. Flanking regions are not highlighted

Human 2906 ttttttaaaagagtTATGTCTGAACCACCTA---TGTGTCCCGATTCATTTTGCCATTTC 2962

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Chick 4511822 TTTTATAAAAGAACGACATCTATACCTCCTAGAATTTGCTCAGTTTCATTTTGCCCCTTT 4511763

Human 2963 ATCTActgctcttcctcctgtttttatttaagACTATGAAGTTACTTTAGTGTaactgct 3022

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Chick 4511762 GTCTGCTGCTCATCCCACCACTTTTATTTAAGACTGTAAAGTTACTTCAGTGTAACTGCT 4511703

Human 3023 gctgtcaccttTGCCCTTAGCTAATCAAATAGTTTACCTTGAGGGAAGCATTTATCTCCc 3082

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Chick 4511702 GTTGTCACCTTTGCCCTCAGCTAATCAAATAGTTTACCTTGAGGGAAACATTTATCTCCC 4511643

Human 3083 actttcattattattatttttgtagctgtaaagatatatattttatgtcTGCAGAAGGCT 3142

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Chick 4511642 ACTTTCATTATTATTATTTTCGTAGCTGTAAAGATATATATTTTATGTCTGCAGAAGGCT 4511583

Human 3143 GTAACAGTGAAACGAGGTATTGATCTGCTGTATTTAGCAATTTCTTTCCACCTTGCCATC 3202

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Chick 4511582 GTAACGGTGAAACGAGGTATTGATCTGCTGTATTTGGCAATTTCTTTCCACCTTGCCATC 4511523

Human 3203 AATAGCATGTCAGCATCTGTCTGTACCGTGGTTGACCTCACAAATAGCTCTTTATGCTCC 3262

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Chick 4511522 GATATCATGTCAGCCTCTGTCTGTACTGTGGTTGACCTCACAAATAGCTCTTTATGTTCC 4511463

Human 3263 CATTGGATTCAAATGATATAGTATGCTGAAAACTAAATCAATGAATGATTATAAAGTTTT 3322

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Chick 4511462 CATTGGATTCAAATGATATACTATTCTCAAAACTAAATCAATGAATGATTATAAAGTTTT 4511403

Human 3323 TAGTATTATTTCATGACCTGGAGGCAACTGGTACT 3357

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Chick 4511402 TAGTATTATTTCATAAGCCCCAGGCAACTGGTACT 4511368

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| **Figure S1c. Pairwise BLAST alignments of HUMAN vs CHIKEN FTO mRNAs.** >NM\_001363894.1 human FTO mRNA; CDS=223..1803>NM\_001185147.1 Gallus gallus FTO mRNA; CDS 81..1604Start codons ATG are highlighted in yellow**Alignment statistics for match #1** |
| Score | Expect | Identities | Gaps | Strand |
| 427 bits(473) | 4e-122 | 487/654**(74%)** | 10/654(1%) | Plus/Plus |

Human 807 CAGAGCAGCATACAACGTAACTTTGCTGAATTTCATGGATCCTCAGAAAATGCCATACCT 866

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Chick 683 CAGAACATCTTATAACTTGACTTTATTAAATTATATGGATCCACTACAAATGCCATACTT 742

Human 867 GAAAGAGGAACCTTATTTTGGCATGGGGAAAATGGCAGTGAGCTGGCATCATGATGAAAA 926

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Chick 743 GAAACAAGAGCCTTATTTTGAAATGGGGAACATGGCAGTGAGTTGGCATCATGATGAGAA 802

Human 927 TCTGGTGGACAGGTCAGCGGTGGCAGTGTACAGTTATAGCTGTGAAGGCCCTGAAGAGGA 986

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Chick 803 TCTGGTTGAGAGGTCAACAGTTGCTGTGTACAGCTACAGCTGTGAAGGTTCATCAGCTGA 862

Human 987 AAGTGAGGATGACTCTCATCTCGAAGGCAGGGATCCTGATATTTGGCATGTTGGTTTTAA 1046

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Chick 863 AGAAGCTACTGATTGGAACCTGAAGGGAAGAGACCCAGCTGTTTGGCATGTAGGCTTGAA 922

Human 1047 GATCTCATGGGACATAGAGACACCTGGTTTGGCGATACCCCTTCACCAAGGAGACTGCTA 1106

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Chick 923 GGTAGCGTGGGACATAGAGACACCTGGATTAGCAATACCACTTCACCAAGGCGACCTCTA 982

Human 1107 TTTCATGCTTGATGATCTCAATGCCACCCACCAACACTGTGTTTTGGCCGGTTCACAACC 1166

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Chick 983 CTTGATGCTTGATGATCTCAATATGACACACCAGCACTGTGTTCTGGCTGGCTTTTCACC 1042

Human 1167 TCGGTTTAGTTCCACCCACCGAGTGGCAGAGTGCTCAACAGGAACCTTGGATTATATTTT 1226

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Chick 1043 TCGGTTCAGCTCCACCCACAGAGTGGCAGATTGTTCAAGAGGAACATTGGAATACATATT 1102

Human 1227 ACAACGCTGTCAGTTGGCTCTGCAGAATGT-----CTGTGACGATGTGGACAATGATGAT 1281

 | ||| | |||| || |||||| | ||| | | | ||| | |

Chick 1103 TGGGCAATGTGAACTGGCACTCCAGAATTTGCAAACTGATTCTAATTCAACA-----GCT 1157

Human 1282 GTCTCTTTGAAATCCTTTGAGCCTGCAGTTTTGAAACAAGGAGAAGAAATTCATAATGAG 1341

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Chick 1158 TTATCTCTGAAATCACTGGAAACTGCAGTTATAAAGCAAATGGAAGAAATACATAATGAG 1217

Human 1342 GTCGAGTTTGAGTGGCTGAGGCAGTTTTGGTTTCAAGGCAATCGATACAGAAAGTGCACT 1401

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Chick 1218 GTTGAATTTGAGTGGCTTAGGCAGTTTTGGTTTCAAGGCGAGCGGTATTTGAAATGCACT 1277

Human 1402 GACTGGTGGTGTCAACCCATGGCTCAACTGGAAGCACTGTGGAAGAAGATGGAG 1455

 ||||||||| | | || |||||| ||||||||| | | |||| || ||||||

Chick 1278 GACTGGTGGCTTAAGCCTATGGCTAAACTGGAAGAATTTTGGAGAAAAATGGAG 1331

Range 2: 75 to 543[Graphics](https://www.ncbi.nlm.nih.gov/projects/sviewer/?RID=1NFYV7KV114&id=lcl|Query_61207&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments|Refseq%20Alignments|Gnomon%20Alignments|Unnamed,shown:false%5d&v=52:566&appname=ncbiblast&link_loc=fromHSP)Next MatchPrevious Match[First Match](https://blast.ncbi.nlm.nih.gov/Blast.cgi#hspQuery_61207_1)

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| **Alignment statistics for match #2** |
| Score | Expect | Identities | Gaps | Strand |
| 150 bits(166) | 4e-39 | 326/480(68%) | 16/480(3%) | Plus/Plus |

Human 217 GGCAGCATGAAGCGCACCCCGACTGCCGAGGAACGAGAGCGCGAAGCTAAGAAACTGAGG 276

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Chick 75 GGCAGCATGAAGAGGA----GA--GCAGGGGAGCGGGAGAAGGAACTGAAGAAAAAAAAG 128

Human 277 CTTCTTGAAGAGCTTGAAGACACTTGGCTCCCTTATCTGACCCCCAAAGATGATGAATTC 336

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Chick 129 CTTCTTGAAGAGCTTGGAGAGGGCAAACTTCCATACCTGACACCAGCTGATGCTGATTT- 187

Human 337 TATCAGCAGTGGCAGCTG---AAATATCCTAAACTAATTCTCCGAGAAGCCAG-CAGTGT 392

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Chick 188 --TCATCATTTGCAGAAGACCAGATATTCCAAGCTAATTTTCAGA-AAGTCGGATACAGT 244

Human 393 ATCTGAGGAGCTCCATAAAGAGGTTCAAGAAGCCTTTCTCACACTGCACAAGCATGGCTG 452

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Chick 245 ACCTGAAGAGCTCCATCAGATGGTACAAGATGGCTTTTTGACCTTGAGGAAACATGGTTG 304

Human 453 CTTATTTCGGGACCTGGTTAGGATCCAAGGCAAAGATCTGCTCACTCCGGTATCTCGCAT 512

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Chick 305 TTTTTTTCAAGATCTTGTAAGGATCAAAGGAAAAGATTTTTTTACCCCAGTGTCTCGTAT 364

Human 513 CCTCATTGGTAATCCAGGCTGCACCTACAAGTACCTGAACACCAGGCTCTTTACGGTCCC 572

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Chick 365 ATTAATTGGAAAGCCAGGATGCACTTACAAGTACTTGAACACAAGATTATTTACAGTTCC 424

Human 573 CTGGCC-AGTGAAAGGGTCTAATATAAAACACACCGAGGCTGAAATAGCCGCTGCTTGTG 631

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Chick 425 TTGGCCTACTG-AGGGTTGTGAAATAAAATATTGCAGTCCTCAAATACATGATGCTTGTA 483

Human 632 AGACCTTCCTCAAGCTCAATGACTACCTGCAGATAGAAACCATCCAGGCTTTGGAAGAAC 691

 | | || |||| || ||||||||| |||| || ||| | || |||| || ||| ||

Chick 484 AAGCATTAATCAAACTTAATGACTACTTGCATATTGAAGCAGTCAAGGCATTACAAGGAC 543

Range 3: 1497 to 1564[Graphics](https://www.ncbi.nlm.nih.gov/projects/sviewer/?RID=KC3CUN4X114&id=lcl|Query_48931&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments|Refseq%20Alignments|Gnomon%20Alignments|Unnamed,shown:false%5d&v=1494:1567&appname=ncbiblast&link_loc=fromHSP)Next MatchPrevious Match[First Match](https://blast.ncbi.nlm.nih.gov/Blast.cgi#hspQuery_48931_1)

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| **Alignment statistics for match #3** |
| Score | Expect | Identities | Gaps | Strand |
| 38.3 bits(41) | 3e-05 | 49/68(72%) | 0/68(0%) | Plus/Plus |

Human 1684 GATCAGAAGCCAGAATGTCGGCCATACTGGGAAAAGGATGATGCTTCGATGCCTCTGCCG 1743

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Chick 1497 GAGCAGAAGCCAGAATGCCATCCCTTCTGGACAAATGAAGAAAGTAACATGCCTCTGCCA 1556

Human 1744 TTTGACCT 1751

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Chick 1557 CTTGATCT 1564

Range 4: 1347 to 1398[Graphics](https://www.ncbi.nlm.nih.gov/projects/sviewer/?RID=KC3CUN4X114&id=lcl|Query_48931&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments|Refseq%20Alignments|Gnomon%20Alignments|Unnamed,shown:false%5d&v=1345:1400&appname=ncbiblast&link_loc=fromHSP)Next MatchPrevious Match[First Match](https://blast.ncbi.nlm.nih.gov/Blast.cgi#hspQuery_48931_1)

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| **Alignment statistics for match #4** |
| Score | Expect | Identities | Gaps | Strand |
| 31.9 bits(34) | 0.001 | 38/52(73%) | 0/52(0%) | Plus/Plus |

Human 1534 GTGCTTCATGAAGTTAAAAGAGAGGGGCTCCCCGTGGAACAAAGGAATGAAA 1585

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Chick 1347 GTCCTCCAAGAAGTTCGAAAAAAGGAGCAAACTGAAGAACAAAGGAATGAAA 1398