

Supplementary Table S1. List of putative transcription factor binding sites detected in mouse FTH1 upstream 1.0-kb predicted with a dissimilarity margin level less or equal than 15% in PROMO ALGGEN.

| Factor name | Start position | End position | Dissimilarity | String | RE equally | RE query |
|-------------------------|----------------|--------------|---------------|-----------|------------|----------|
| AP-1 [T00029] | 597 | 605 | 5.354713 | TGACTCCCA | 0.03815 | 0.02927 |
| AP-1 [T00029] | 946 | 954 | 13.075412 | CCAAAGTCA | 0.14496 | 0.17976 |
| AP-1 [T00032] | 597 | 605 | 9.544233 | TGACTCCCA | 0.06104 | 0.03719 |
| AP-1 [T01140] | 508 | 514 | 14.285714 | TGAGACA | 1.28174 | 1.33865 |
| AP-1 [T01140] | 597 | 603 | 14.285714 | TGACTCC | 1.28174 | 1.33865 |
| C/EBP [T01388] | 148 | 154 | 1.299659 | CTGAGCA | 0.48828 | 0.26141 |
| C/EBP [T01388] | 283 | 289 | 2.84092 | TGCCCAC | 0.12207 | 0.04332 |
| C/EBP [T01388] | 328 | 334 | 0 | TTGTGCA | 0.36621 | 0.31784 |
| C/EBP [T01388] | 368 | 374 | 1.541262 | ATGGGCA | 0.48828 | 0.26141 |
| C/EBP [T01388] | 979 | 985 | 1.299659 | CTGTGCA | 0.48828 | 0.26141 |
| C/EBP α [T00104] | 28 | 31 | 0 | AAAT | 3.90625 | 9.71949 |
| C/EBP α [T00104] | 162 | 165 | 0 | ATTT | 3.90625 | 9.71949 |
| C/EBP α [T00104] | 217 | 220 | 0 | AAAT | 3.90625 | 9.71949 |
| C/EBP α [T00104] | 318 | 321 | 0 | AAAT | 3.90625 | 9.71949 |
| C/EBP α [T00104] | 423 | 426 | 0 | AAAT | 3.90625 | 9.71949 |
| C/EBP α [T00104] | 582 | 585 | 0 | AAAT | 3.90625 | 9.71949 |
| C/EBP α [T00104] | 584 | 587 | 0 | ATTT | 3.90625 | 9.71949 |
| C/EBP α [T00104] | 637 | 640 | 0 | ATTT | 3.90625 | 9.71949 |
| C/EBP α [T00104] | 694 | 697 | 0 | AAAT | 3.90625 | 9.71949 |
| C/EBP α [T00104] | 696 | 699 | 0 | ATTT | 3.90625 | 9.71949 |
| C/EBP α [T00104] | 734 | 737 | 0 | ATTT | 3.90625 | 9.71949 |
| C/EBP α [T00104] | 754 | 757 | 0 | ATTT | 3.90625 | 9.71949 |

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|-------------------------|-----|-----|-----------|----------|---------|---------|
| C/EBP α [T00104] | 776 | 779 | 0 | ATTT | 3.90625 | 9.71949 |
| C/EBP α [T00104] | 782 | 785 | 0 | AAAT | 3.90625 | 9.71949 |
| C/EBP α [T00104] | 798 | 801 | 0 | ATTT | 3.90625 | 9.71949 |
| C/EBP α [T00104] | 857 | 860 | 0 | ATTT | 3.90625 | 9.71949 |
| C/EBP α [T00104] | 862 | 865 | 0 | AAAT | 3.90625 | 9.71949 |
| C/EBP α [T00104] | 914 | 917 | 0 | ATTT | 3.90625 | 9.71949 |
| C/EBP α [T00104] | 920 | 923 | 0 | ATTT | 3.90625 | 9.71949 |
| C/EBP α [T00105] | 5 | 10 | 2.897783 | TTGCAA | 0.48828 | 0.52285 |
| C/EBP α [T00105] | 363 | 368 | 2.443272 | TTGCTA | 0.97656 | 1.0805 |
| C/EBP α [T00105] | 370 | 375 | 0.681767 | GGGCAA | 0.48828 | 0.32078 |
| C/EBP α [T00105] | 586 | 591 | 2.514221 | TTGCCT | 0.97656 | 1.0805 |
| C/EBP α [T00107] | 470 | 477 | 14.367318 | TTTGTTT | 0.36621 | 0.46209 |
| C/EBP α [T00107] | 646 | 653 | 5.228028 | TGGCCAAA | 0.06104 | 0.04527 |
| C/EBP α [T00107] | 689 | 696 | 10.446297 | ATTCCAAA | 0.42725 | 0.36963 |
| C/EBP α [T00107] | 697 | 704 | 4.011491 | TTTGGATA | 0.12207 | 0.20872 |
| C/EBP α [T00107] | 943 | 950 | 10.446297 | GTACCAAA | 0.42725 | 0.36963 |
| C/EBP α [T00108] | 5 | 7 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP α [T00108] | 8 | 10 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP α [T00108] | 74 | 76 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP α [T00108] | 78 | 80 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP α [T00108] | 139 | 141 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP α [T00108] | 164 | 166 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP α [T00108] | 259 | 261 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP α [T00108] | 307 | 309 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP α [T00108] | 328 | 330 | 0 | TTG | 15.625 | 18.2634 |

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|-------------------------|-----|-----|---|-----|--------|---------|
| C/EBP α [T00108] | 350 | 352 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP α [T00108] | 363 | 365 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP α [T00108] | 373 | 375 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP α [T00108] | 391 | 393 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP α [T00108] | 398 | 400 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP α [T00108] | 415 | 417 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP α [T00108] | 467 | 469 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP α [T00108] | 471 | 473 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP α [T00108] | 480 | 482 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP α [T00108] | 489 | 491 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP α [T00108] | 494 | 496 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP α [T00108] | 499 | 501 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP α [T00108] | 504 | 506 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP α [T00108] | 507 | 509 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP α [T00108] | 554 | 556 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP α [T00108] | 573 | 575 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP α [T00108] | 586 | 588 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP α [T00108] | 604 | 606 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP α [T00108] | 650 | 652 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP α [T00108] | 659 | 661 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP α [T00108] | 665 | 667 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP α [T00108] | 673 | 675 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP α [T00108] | 693 | 695 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP α [T00108] | 698 | 700 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP α [T00108] | 738 | 740 | 0 | CAA | 15.625 | 18.2634 |

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|-------------------------|-----|-----|----------|-------|---------|---------|
| C/EBP α [T00108] | 750 | 752 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP α [T00108] | 813 | 815 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP α [T00108] | 816 | 818 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP α [T00108] | 859 | 861 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP α [T00108] | 917 | 919 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP α [T00108] | 947 | 949 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP α [T00108] | 962 | 964 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP β [T00017] | 18 | 22 | 4.211117 | CGTGT | 1.95312 | 1.69217 |
| C/EBP β [T00017] | 58 | 62 | 2.100568 | ACAGT | 1.95312 | 2.09573 |
| C/EBP β [T00017] | 97 | 101 | 2.980795 | GGTGT | 0.97656 | 0.6208 |
| C/EBP β [T00017] | 118 | 122 | 2.460644 | ACATA | 2.92969 | 3.89193 |
| C/EBP β [T00017] | 130 | 134 | 2.100568 | ACAGT | 1.95312 | 2.09573 |
| C/EBP β [T00017] | 138 | 142 | 1.050284 | ACAAT | 1.95312 | 2.82176 |
| C/EBP β [T00017] | 193 | 197 | 3.33089 | ACAGC | 2.92969 | 3.62307 |
| C/EBP β [T00017] | 198 | 202 | 2.100568 | ACAGT | 1.95312 | 2.09573 |
| C/EBP β [T00017] | 247 | 251 | 4.561212 | ACAGA | 1.95312 | 1.75703 |
| C/EBP β [T00017] | 327 | 331 | 1.050284 | ATTGT | 1.95312 | 2.82176 |
| C/EBP β [T00017] | 375 | 379 | 4.211117 | ACACA | 1.95312 | 1.69217 |
| C/EBP β [T00017] | 377 | 381 | 2.460644 | ACATA | 2.92969 | 3.89193 |
| C/EBP β [T00017] | 393 | 397 | 4.211117 | ACACA | 1.95312 | 1.69217 |
| C/EBP β [T00017] | 395 | 399 | 0 | ACATT | 0.97656 | 1.76092 |
| C/EBP β [T00017] | 397 | 401 | 1.050284 | ATTGT | 1.95312 | 2.82176 |
| C/EBP β [T00017] | 405 | 409 | 2.460644 | TATGT | 2.92969 | 3.89193 |
| C/EBP β [T00017] | 414 | 418 | 3.510928 | CTTGT | 2.92969 | 3.62307 |
| C/EBP β [T00017] | 466 | 470 | 3.510928 | TTTGT | 2.92969 | 3.62307 |

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|------------------------|-----|-----|----------|-------|---------|---------|
| C/EBP β [T00017] | 479 | 483 | 3.510928 | TTTGT | 2.92969 | 3.62307 |
| C/EBP β [T00017] | 488 | 492 | 3.510928 | TTTGT | 2.92969 | 3.62307 |
| C/EBP β [T00017] | 493 | 497 | 3.510928 | TTTGT | 2.92969 | 3.62307 |
| C/EBP β [T00017] | 498 | 502 | 3.510928 | TTTGT | 2.92969 | 3.62307 |
| C/EBP β [T00017] | 503 | 507 | 3.510928 | TTTGT | 2.92969 | 3.62307 |
| C/EBP β [T00017] | 512 | 516 | 4.561212 | ACAGG | 1.95312 | 1.75703 |
| C/EBP β [T00017] | 522 | 526 | 4.561212 | TCTGT | 1.95312 | 1.75703 |
| C/EBP β [T00017] | 536 | 540 | 3.33089 | GCTGT | 2.92969 | 3.62307 |
| C/EBP β [T00017] | 553 | 557 | 3.510928 | TTTGT | 2.92969 | 3.62307 |
| C/EBP β [T00017] | 623 | 627 | 2.460644 | CATGT | 2.92969 | 3.89193 |
| C/EBP β [T00017] | 725 | 729 | 2.100568 | ACTGT | 1.95312 | 2.09573 |
| C/EBP β [T00017] | 749 | 753 | 2.280606 | GTTGT | 2.92969 | 3.89193 |
| C/EBP β [T00017] | 807 | 811 | 2.460644 | ACATG | 2.92969 | 3.89193 |
| C/EBP β [T00017] | 812 | 816 | 1.050284 | ACAAT | 1.95312 | 2.82176 |
| C/EBP β [T00017] | 815 | 819 | 1.050284 | ATTGT | 1.95312 | 2.82176 |
| C/EBP β [T00017] | 817 | 821 | 4.211117 | TGTGT | 1.95312 | 1.69217 |
| C/EBP β [T00017] | 894 | 898 | 4.211117 | ACACA | 1.95312 | 1.69217 |
| C/EBP β [T00017] | 896 | 900 | 2.460644 | ACATA | 2.92969 | 3.89193 |
| C/EBP β [T00017] | 899 | 903 | 2.460644 | TATGT | 2.92969 | 3.89193 |
| C/EBP β [T00017] | 936 | 940 | 4.561212 | CCTGT | 1.95312 | 1.75703 |
| C/EBP β [T00017] | 961 | 965 | 1.050284 | ATTGT | 1.95312 | 2.82176 |
| C/EBP β [T00017] | 972 | 976 | 2.460644 | TATGT | 2.92969 | 3.89193 |
| C/EBP β [T00017] | 978 | 982 | 4.561212 | TCTGT | 1.95312 | 1.75703 |
| C/EBP β [T00459] | 5 | 7 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP β [T00459] | 8 | 10 | 0 | CAA | 15.625 | 18.2634 |

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|------------------------|-----|-----|---|-----|--------|---------|
| C/EBP β [T00459] | 74 | 76 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP β [T00459] | 78 | 80 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP β [T00459] | 139 | 141 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP β [T00459] | 164 | 166 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP β [T00459] | 259 | 261 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP β [T00459] | 307 | 309 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP β [T00459] | 328 | 330 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP β [T00459] | 350 | 352 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP β [T00459] | 363 | 365 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP β [T00459] | 373 | 375 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP β [T00459] | 391 | 393 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP β [T00459] | 398 | 400 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP β [T00459] | 415 | 417 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP β [T00459] | 467 | 469 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP β [T00459] | 471 | 473 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP β [T00459] | 480 | 482 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP β [T00459] | 489 | 491 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP β [T00459] | 494 | 496 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP β [T00459] | 499 | 501 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP β [T00459] | 504 | 506 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP β [T00459] | 507 | 509 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP β [T00459] | 554 | 556 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP β [T00459] | 573 | 575 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP β [T00459] | 586 | 588 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP β [T00459] | 604 | 606 | 0 | CAA | 15.625 | 18.2634 |

| | | | | | | |
|------------------------|-----|-----|-----------|----------|---------|---------|
| C/EBP β [T00459] | 650 | 652 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP β [T00459] | 659 | 661 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP β [T00459] | 665 | 667 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP β [T00459] | 673 | 675 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP β [T00459] | 693 | 695 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP β [T00459] | 698 | 700 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP β [T00459] | 738 | 740 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP β [T00459] | 750 | 752 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP β [T00459] | 813 | 815 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP β [T00459] | 816 | 818 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP β [T00459] | 859 | 861 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP β [T00459] | 917 | 919 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP β [T00459] | 947 | 949 | 0 | CAA | 15.625 | 18.2634 |
| C/EBP β [T00459] | 962 | 964 | 0 | TTG | 15.625 | 18.2634 |
| C/EBP β [T00581] | 4 | 10 | 4.018292 | CTTGCAA | 0.36621 | 0.425 |
| C/EBP β [T00581] | 5 | 11 | 2.809597 | TTGCAAT | 0.18311 | 0.2651 |
| C/EBP β [T00581] | 363 | 369 | 3.71163 | TTGCTAT | 0.42725 | 0.49093 |
| C/EBP β [T00581] | 369 | 375 | 1.804066 | TGGGCAA | 0.30518 | 0.25219 |
| C/EBP β [T00581] | 586 | 592 | 6.263409 | TTGCCTG | 0.12207 | 0.07468 |
| CP2 [T00152] | 125 | 132 | 13.249285 | CTGGTACA | 0.36621 | 0.18906 |
| CP2 [T00152] | 343 | 350 | 12.549128 | CTGGCTCT | 0.27466 | 0.16666 |
| CP2 [T00152] | 378 | 385 | 4.144927 | CATACCAG | 0.09155 | 0.05896 |
| CP2 [T00152] | 533 | 540 | 12.549128 | CTGGCTGT | 0.27466 | 0.16666 |
| CP2 [T00152] | 566 | 573 | 11.78931 | CTGGCCTC | 0.12207 | 0.04869 |
| CP2 [T00152] | 610 | 617 | 8.214579 | CTGGGTTT | 0.35095 | 0.15773 |

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|-----------------|-----|-----|-----------|----------|---------|---------|
| CP2 [T00152] | 767 | 774 | 7.531367 | CTGGGAGG | 0.13733 | 0.05611 |
| GATA-1 [T00267] | 698 | 705 | 6.590036 | TTGGATAA | 0.04578 | 0.08525 |
| GATA-1 [T00267] | 827 | 834 | 1.204329 | TTATCGGC | 0.01526 | 0.0115 |
| GATA-1 [T00305] | 698 | 705 | 4.723851 | TTGGATAA | 0.16785 | 0.27481 |
| GATA-1 [T00305] | 827 | 834 | 3.712083 | TTATCGGC | 0.03052 | 0.03103 |
| GATA-1 [T00306] | 114 | 119 | 1.174121 | TATCAC | 0.48828 | 0.65506 |
| GATA-1 [T00306] | 133 | 138 | 1.174121 | GTGATA | 0.48828 | 0.65506 |
| GATA-1 [T00306] | 254 | 259 | 0.298794 | TATCTC | 0.73242 | 1.50427 |
| GATA-1 [T00306] | 426 | 431 | 0.469533 | TATCTT | 0.73242 | 1.50427 |
| GATA-1 [T00306] | 699 | 704 | 2.76306 | TGGATA | 0.48828 | 0.65506 |
| GATA-1 [T00306] | 821 | 826 | 2.76306 | TGGATA | 0.48828 | 0.65506 |
| GATA-1 [T00306] | 828 | 833 | 2.250843 | TATCGG | 1.46484 | 1.47715 |
| GATA-1 [T00306] | 882 | 887 | 2.76306 | TATCGA | 0.48828 | 0.65506 |
| GATA-1 [T00306] | 976 | 981 | 0 | TATCTG | 0.24414 | 0.33435 |
| GATA-2 [T01302] | 110 | 117 | 8.983724 | CGGCTATC | 0.18311 | 0.21354 |
| GATA-2 [T01302] | 135 | 142 | 12.627873 | GATACAAT | 0.36621 | 0.5447 |
| GATA-2 [T01302] | 701 | 708 | 11.858188 | GATAATCT | 0.27466 | 0.49807 |
| GATA-2 [T01302] | 823 | 830 | 13.806911 | GATATTAT | 0.36621 | 0.537 |
| GATA-2 [T01302] | 824 | 831 | 6.518613 | ATATTATC | 0.18311 | 0.35322 |
| GATA-2 [T01302] | 878 | 885 | 12.627873 | TTTATATC | 0.36621 | 0.5447 |
| GATA-3 [T00311] | 251 | 258 | 5.011765 | AAGTATCT | 0.10681 | 0.17988 |
| GATA-3 [T00311] | 423 | 430 | 4.331086 | AAATATCT | 0.07629 | 0.16485 |
| GATA-3 [T00311] | 973 | 980 | 5.011765 | ATGTATCT | 0.10681 | 0.17988 |
| GR [T00333] | 20 | 22 | 0 | TGT | 15.625 | 18.2634 |
| GR [T00333] | 58 | 60 | 0 | ACA | 15.625 | 18.2634 |

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|-------------|-----|-----|---|-----|--------|---------|
| GR [T00333] | 99 | 101 | 0 | TGT | 15.625 | 18.2634 |
| GR [T00333] | 118 | 120 | 0 | ACA | 15.625 | 18.2634 |
| GR [T00333] | 130 | 132 | 0 | ACA | 15.625 | 18.2634 |
| GR [T00333] | 138 | 140 | 0 | ACA | 15.625 | 18.2634 |
| GR [T00333] | 193 | 195 | 0 | ACA | 15.625 | 18.2634 |
| GR [T00333] | 198 | 200 | 0 | ACA | 15.625 | 18.2634 |
| GR [T00333] | 247 | 249 | 0 | ACA | 15.625 | 18.2634 |
| GR [T00333] | 329 | 331 | 0 | TGT | 15.625 | 18.2634 |
| GR [T00333] | 375 | 377 | 0 | ACA | 15.625 | 18.2634 |
| GR [T00333] | 377 | 379 | 0 | ACA | 15.625 | 18.2634 |
| GR [T00333] | 393 | 395 | 0 | ACA | 15.625 | 18.2634 |
| GR [T00333] | 395 | 397 | 0 | ACA | 15.625 | 18.2634 |
| GR [T00333] | 399 | 401 | 0 | TGT | 15.625 | 18.2634 |
| GR [T00333] | 407 | 409 | 0 | TGT | 15.625 | 18.2634 |
| GR [T00333] | 416 | 418 | 0 | TGT | 15.625 | 18.2634 |
| GR [T00333] | 468 | 470 | 0 | TGT | 15.625 | 18.2634 |
| GR [T00333] | 481 | 483 | 0 | TGT | 15.625 | 18.2634 |
| GR [T00333] | 490 | 492 | 0 | TGT | 15.625 | 18.2634 |
| GR [T00333] | 495 | 497 | 0 | TGT | 15.625 | 18.2634 |
| GR [T00333] | 500 | 502 | 0 | TGT | 15.625 | 18.2634 |
| GR [T00333] | 505 | 507 | 0 | TGT | 15.625 | 18.2634 |
| GR [T00333] | 512 | 514 | 0 | ACA | 15.625 | 18.2634 |
| GR [T00333] | 524 | 526 | 0 | TGT | 15.625 | 18.2634 |
| GR [T00333] | 538 | 540 | 0 | TGT | 15.625 | 18.2634 |
| GR [T00333] | 555 | 557 | 0 | TGT | 15.625 | 18.2634 |

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|--------------------|-----|-----|----------|----------|---------|---------|
| GR [T00333] | 625 | 627 | 0 | TGT | 15.625 | 18.2634 |
| GR [T00333] | 727 | 729 | 0 | TGT | 15.625 | 18.2634 |
| GR [T00333] | 751 | 753 | 0 | TGT | 15.625 | 18.2634 |
| GR [T00333] | 807 | 809 | 0 | ACA | 15.625 | 18.2634 |
| GR [T00333] | 812 | 814 | 0 | ACA | 15.625 | 18.2634 |
| GR [T00333] | 817 | 819 | 0 | TGT | 15.625 | 18.2634 |
| GR [T00333] | 819 | 821 | 0 | TGT | 15.625 | 18.2634 |
| GR [T00333] | 894 | 896 | 0 | ACA | 15.625 | 18.2634 |
| GR [T00333] | 896 | 898 | 0 | ACA | 15.625 | 18.2634 |
| GR [T00333] | 901 | 903 | 0 | TGT | 15.625 | 18.2634 |
| GR [T00333] | 938 | 940 | 0 | TGT | 15.625 | 18.2634 |
| GR [T00333] | 963 | 965 | 0 | TGT | 15.625 | 18.2634 |
| GR [T00333] | 974 | 976 | 0 | TGT | 15.625 | 18.2634 |
| GR [T00333] | 980 | 982 | 0 | TGT | 15.625 | 18.2634 |
| GR [T00333] | 996 | 998 | 0 | ACA | 15.625 | 18.2634 |
| GR [T00335] | 234 | 239 | 0 | AGAACT | 0.24414 | 0.33435 |
| GR [T00335] | 517 | 522 | 6.726303 | GGTTCT | 0.48828 | 0.4118 |
| GR [T00335] | 544 | 549 | 0 | AGAACT | 0.24414 | 0.33435 |
| MyoD [T00526] | 194 | 201 | 12.73119 | CAGCACAG | 0.2594 | 0.20736 |
| MyoD [T00526] | 383 | 390 | 2.345634 | CAGCAGCC | 0.12207 | 0.05525 |
| MyoD [T00526] | 605 | 612 | 11.00374 | AAGTGCTG | 0.16785 | 0.11647 |
| Nrf2:MafK [T05666] | 58 | 64 | 5.316619 | ACAGTAG | 0.48828 | 0.46583 |
| Nrf2:MafK [T05666] | 178 | 184 | 1.541262 | TCAGGAT | 0.48828 | 0.44145 |
| Nrf2:MafK [T05666] | 193 | 199 | 5.316619 | ACAGCAC | 0.48828 | 0.46583 |
| Nrf2:MafK [T05666] | 247 | 253 | 5.316619 | ACAGAAG | 0.48828 | 0.46583 |

| | | | | | | |
|--------------------|-----|-----|-----------|--------------|---------|---------|
| Nrf2:MafK [T05666] | 340 | 346 | 8.033921 | TTTCTGG | 0.73242 | 0.65091 |
| Nrf2:MafK [T05666] | 382 | 388 | 9.33358 | CCAGCAG | 0.97656 | 0.53743 |
| Nrf2:MafK [T05666] | 578 | 584 | 0 | TCAGAAA | 0.36621 | 0.5362 |
| Nrf2:MafK [T05666] | 607 | 613 | 9.33358 | GTGCTGG | 0.97656 | 0.53743 |
| Nrf2:MafK [T05666] | 934 | 940 | 5.558222 | TTCCTGT | 0.48828 | 0.46583 |
| Nrf2:MafK [T05666] | 940 | 946 | 1.299659 | TCAGTAC | 0.48828 | 0.44145 |
| p53 [T00671] | 281 | 287 | 5.253995 | AATGCCC | 0.12207 | 0.05784 |
| p53 [T00671] | 287 | 293 | 3.057625 | CACGCCC | 0.12207 | 0.03427 |
| p53 [T00671] | 370 | 376 | 5.084756 | GGGCAAC | 0.24414 | 0.06544 |
| p53 [T00671] | 385 | 391 | 7.965283 | GCAGCCC | 0.48828 | 0.10994 |
| p53 [T00671] | 527 | 533 | 8.842914 | ATAGCCC | 0.36621 | 0.11232 |
| Sp1 [T00755] | 286 | 294 | 6.497596 | CCACGCCCT | 0.03815 | 0.00765 |
| Sp1 [T01228] | 285 | 295 | 13.898109 | CCCACGCCCTA | 0.06652 | 0.01606 |
| SRF [T00763] | 692 | 701 | 12.836461 | CCAAATTTGG | 0.06008 | 0.07257 |
| SRF [T00766] | 690 | 701 | 13.481114 | TTCCAAATTTGG | 0.03552 | 0.04218 |
| SRF [T00766] | 692 | 703 | 13.341643 | CCAAATTTGGAT | 0.03552 | 0.04218 |
| YY1 [T00278] | 108 | 118 | 14.35951 | TGCGGCTATCA | 0.08011 | 0.02862 |
| YY1 [T00865] | 10 | 15 | 0.700325 | ATGGAC | 0.73242 | 0.87617 |
| YY1 [T00865] | 141 | 146 | 0 | ATGGAG | 0.24414 | 0.20504 |
| YY1 [T00865] | 207 | 212 | 2.965889 | TCCCAT | 0.73242 | 0.59472 |
| YY1 [T00865] | 261 | 266 | 0.350162 | ATGGAA | 0.73242 | 0.87617 |
| YY1 [T00865] | 368 | 373 | 3.316052 | ATGGGC | 0.73242 | 0.77254 |
| YY1 [T00865] | 430 | 435 | 0.350162 | TTCCAT | 0.73242 | 0.87617 |
| YY1 [T00865] | 838 | 843 | 3.14097 | ACCCAT | 0.73242 | 0.59472 |
| YY1 [T00915] | 10 | 15 | 1.17887 | ATGGAC | 1.2207 | 0.98802 |

| | | | | | | |
|--------------|-----|-----|-----------|-----------|---------|---------|
| YY1 [T00915] | 141 | 146 | 0.781798 | ATGGAG | 1.2207 | 0.98802 |
| YY1 [T00915] | 207 | 212 | 2.177379 | TCCCAT | 0.97656 | 1.05597 |
| YY1 [T00915] | 261 | 266 | 1.708301 | ATGGAA | 1.2207 | 1.10967 |
| YY1 [T00915] | 368 | 373 | 1.647949 | ATGGGC | 1.2207 | 1.10967 |
| YY1 [T00915] | 430 | 435 | 1.708301 | TTCCAT | 1.2207 | 1.10967 |
| YY1 [T00915] | 838 | 843 | 2.045022 | ACCCAT | 0.97656 | 1.05597 |
| YY1 [T04970] | 187 | 195 | 5.873209 | GCCTAGACA | 0.18311 | 0.12783 |
| YY1 [T04970] | 506 | 514 | 7.047851 | GTTGAGACA | 0.15259 | 0.11378 |
| YY1 [T04970] | 806 | 814 | 11.458499 | CACATGACA | 0.27466 | 0.19711 |
| YY1 [T04970] | 938 | 946 | 10.571776 | TGTCAGTAC | 0.33569 | 0.24819 |

Supplementary Table S2. List of putative transcription factor binding sites detected in mouse FTH1 upstream 1.0-kb predicted with cut-off matrix similarity > 0.85 in TRANSCFAC.

| factor name | position | strand | core match | matrix match | sequence (always the (+)-strand is shown) |
|-------------|----------|--------|------------|--------------|---|
| AP-1 | 100 | (+) | 0.906 | 0.895 | tgTGATTaatg |
| AP-1 | 101 | (-) | 0.964 | 0.884 | gTGATTaat |
| AP-1 | 544 | (-) | 0.908 | 0.854 | tagaACTCAct |
| AP-1 | 596 | (+) | 0.983 | 0.953 | tCTGACtccca |
| AP-1 | 596 | (+) | 1 | 0.932 | tcTGACTccca |
| AP-1 | 596 | (+) | 1 | 0.951 | tcTGACTccca |
| AP-1 | 596 | (+) | 1 | 0.916 | tcTGACTccca |
| AP-1 | 758 | (-) | 0.903 | 0.894 | tttaATTCAcc |
| AP-1 | 791 | (-) | 0.903 | 0.896 | agttATTCAtt |
| AP-1 | 792 | (+) | 0.955 | 0.878 | gttATTCAt |
| AP-1 | 809 | (+) | 0.975 | 0.907 | cATGACaattg |
| AP-1 | 809 | (+) | 0.967 | 0.872 | caTGACAattg |
| AP-1 | 809 | (+) | 0.936 | 0.871 | caTGACAattg |
| AP-1 | 935 | (-) | 0.983 | 0.933 | ttcctGTCAGt |
| AP-1 | 935 | (-) | 0.967 | 0.92 | ttccTGTCAGt |
| AP-1 | 935 | (-) | 0.936 | 0.868 | ttccTGTCAGt |
| AP-1 | 935 | (-) | 0.935 | 0.855 | ttccTGTCAGt |
| AP-1 | 947 | (-) | 0.975 | 0.919 | ccaaaGTCATa |
| AP-1 | 947 | (-) | 1 | 0.9 | ccaaAGTCAta |
| AP-1 | 947 | (-) | 1 | 0.925 | ccaaAGTCAta |
| AP-1 | 947 | (-) | 1 | 0.89 | ccaaAGTCAta |
| C/EBP | 1 | (-) | 1 | 0.954 | gcaccttGCAATgg |

| | | | | | |
|-------|-----|-----|-------|-------|----------------|
| C/EBP | 3 | (+) | 0.984 | 0.881 | atCTTGCaatggac |
| C/EBP | 98 | (+) | 0.94 | 0.937 | ggTGTGAttaatg |
| C/EBP | 132 | (-) | 0.949 | 0.924 | cagtgaTACAATgg |
| C/EBP | 146 | (+) | 0.885 | 0.852 | agTCTGAgcacta |
| C/EBP | 147 | (-) | 0.876 | 0.874 | gtctgaGCACTag |
| C/EBP | 162 | (+) | 0.961 | 0.921 | caTTTGAGAatat |
| C/EBP | 242 | (-) | 0.889 | 0.893 | aactaaACAGAag |
| C/EBP | 252 | (-) | 0.944 | 0.909 | aagtatTCAATgg |
| C/EBP | 326 | (+) | 0.889 | 0.86 | taATTGTgcataa |
| C/EBP | 326 | (+) | 0.949 | 0.866 | taATTGTgcataaa |
| C/EBP | 327 | (-) | 0.917 | 0.904 | aattgtGCATAaa |
| C/EBP | 328 | (+) | 0.952 | 0.929 | atTGTGCataaac |
| C/EBP | 361 | (+) | 0.984 | 0.875 | tcCTTGctatgggc |
| C/EBP | 366 | (+) | 0.945 | 0.894 | gcTATGGgcaaca |
| C/EBP | 366 | (-) | 0.987 | 0.886 | gctatggGCAACac |
| C/EBP | 404 | (+) | 0.91 | 0.928 | tcTATGTtaacct |
| C/EBP | 413 | (+) | 0.933 | 0.936 | acCTTGTttaaaaa |
| C/EBP | 469 | (+) | 1 | 0.887 | tgTTTGGttttt |
| C/EBP | 478 | (+) | 0.965 | 0.855 | ttTTTGTttttt |
| C/EBP | 487 | (+) | 0.965 | 0.856 | ttTTTGTtttgtt |
| C/EBP | 502 | (+) | 0.965 | 0.946 | gtTTTGTtgagac |
| C/EBP | 502 | (+) | 0.933 | 0.859 | gtTTTGTtgagaca |
| C/EBP | 505 | (+) | 0.931 | 0.904 | ttGTTGAgacaggg |
| C/EBP | 521 | (+) | 0.889 | 0.893 | tcTCTGTatagcc |
| C/EBP | 552 | (+) | 0.965 | 0.938 | acTTTGTtagatca |

| | | | | | |
|----------------|-----|-----|-------|-------|--------------------|
| C/EBP | 584 | (+) | 0.984 | 0.855 | aaTTTGcctgcctc |
| C/EBP | 643 | (+) | 0.904 | 0.869 | taAGTGGccaaac |
| C/EBP | 644 | (-) | 1 | 0.935 | aagtggCCAAAcc |
| C/EBP | 686 | (-) | 0.936 | 0.905 | ccctattCCAAAtt |
| C/EBP | 687 | (-) | 1 | 0.875 | cctattCCAAAtt |
| C/EBP | 696 | (+) | 1 | 0.973 | aaTTTGgataatc |
| C/EBP | 696 | (+) | 0.936 | 0.942 | aaTTTGgataatct |
| C/EBP | 800 | (-) | 0.979 | 0.923 | ttttagCCACAtg |
| C/EBP | 814 | (+) | 0.949 | 0.852 | caATTGTgtggata |
| C/EBP | 816 | (+) | 0.944 | 0.894 | atTGTGTggatat |
| C/EBP | 818 | (+) | 0.979 | 0.962 | tgTGTGGatatta |
| C/EBP | 845 | (-) | 0.941 | 0.855 | tcttcCTTCCctaatttg |
| C/EBP | 887 | (-) | 0.979 | 0.947 | gagttcCCACAc |
| C/EBP | 960 | (+) | 0.949 | 0.915 | ttATTGTaataat |
| C/EBP | 977 | (+) | 0.889 | 0.862 | taTCTGTgcatat |
| C/EBP | 978 | (-) | 0.917 | 0.899 | atctgtGCATAtg |
| C/EBP | 979 | (+) | 0.952 | 0.942 | tcTGTGCatatgc |
| C/EBP α | 1 | (-) | 1 | 0.916 | gcatcttGCAATgg |
| C/EBP α | 132 | (-) | 0.929 | 0.876 | cagtgatACAATgg |
| C/EBP α | 161 | (+) | 0.872 | 0.877 | tcATTTGagaatat |
| C/EBP α | 161 | (-) | 0.858 | 0.879 | tcatttgAGAATat |
| C/EBP α | 213 | (+) | 0.875 | 0.891 | tcTTTAAataaaaa |
| C/EBP α | 213 | (-) | 0.872 | 0.888 | tctttaaATAAAaa |
| C/EBP α | 252 | (-) | 0.932 | 0.864 | aagtatcTCAATgg |
| C/EBP α | 326 | (+) | 0.929 | 0.856 | taATTGTgcataaa |

| | | | | | |
|----------------|-----|-----|-------|-------|----------------|
| C/EBP α | 366 | (-) | 0.979 | 0.893 | gctatggGCAACac |
| C/EBP α | 413 | (+) | 0.903 | 0.916 | acCTTGTttaaaaa |
| C/EBP α | 413 | (-) | 0.875 | 0.889 | accttgtTTAAAAa |
| C/EBP α | 416 | (-) | 0.858 | 0.88 | ttgtttaAAAATat |
| C/EBP α | 505 | (+) | 0.91 | 0.861 | ttGTTGAgacaggg |
| C/EBP α | 575 | (-) | 0.929 | 0.854 | aaactcaGAAATtt |
| C/EBP α | 643 | (-) | 0.92 | 0.859 | taagtggCCAAAcc |
| C/EBP α | 661 | (-) | 0.908 | 0.917 | aacttttGAAACtc |
| C/EBP α | 681 | (+) | 0.929 | 0.858 | atATTCCctattcc |
| C/EBP α | 686 | (-) | 0.92 | 0.855 | ccctattCCAAAtt |
| C/EBP α | 688 | (+) | 0.929 | 0.855 | ctATTCCaaatttg |
| C/EBP α | 696 | (+) | 0.92 | 0.931 | aaTTTGataatct |
| C/EBP α | 696 | (-) | 0.895 | 0.907 | aatttggATAATct |
| C/EBP α | 775 | (+) | 0.858 | 0.875 | gtATTTTtaaatac |
| C/EBP α | 775 | (-) | 0.861 | 0.878 | gtattttTAAATac |
| C/EBP α | 848 | (+) | 0.903 | 0.913 | tcCTTCCctaattt |
| C/EBP α | 848 | (-) | 0.909 | 0.909 | tccttccCTAATtt |
| C/EBP α | 855 | (-) | 0.929 | 0.854 | ctaatttGAAATgc |
| C/EBP α | 887 | (+) | 0.908 | 0.861 | gaGTTCCcacacat |
| C/EBP α | 958 | (-) | 0.966 | 0.893 | ctttattGTAATat |
| C/EBP α | 960 | (+) | 0.929 | 0.863 | ttATTGTaatatat |
| C/EBP β | 1 | (+) | 1 | 0.931 | gcatcttGCAATgg |
| C/EBP β | 1 | (-) | 1 | 0.886 | gcatctTGCAAtgg |
| C/EBP β | 174 | (-) | 0.981 | 0.892 | tgCTTTCaggatta |
| C/EBP β | 661 | (+) | 0.966 | 0.954 | aacttttGAAACtc |

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|---------------|-----|-----|-------|-------|----------------|
| C/EBP β | 661 | (-) | 0.865 | 0.872 | aactttTGAAActc |
| C/EBP β | 848 | (-) | 0.95 | 0.954 | tcCTTCCctaattt |
| C/EBP β | 887 | (-) | 0.935 | 0.911 | gaGTTCCcacacat |
| C/EBP β | 958 | (+) | 0.981 | 0.897 | ctttattGTAATat |
| CP2 | 344 | (-) | 0.974 | 0.853 | CTGGCtcttga |
| GATA1 | 100 | (+) | 0.985 | 0.965 | tgtGATTaAt |
| GATA1 | 110 | (-) | 0.993 | 0.944 | gcggcTATCacata |
| GATA1 | 110 | (-) | 0.96 | 0.913 | gcggCTATCacata |
| GATA1 | 110 | (-) | 0.991 | 0.954 | gcggcTATCacat |
| GATA1 | 112 | (-) | 1 | 0.981 | ggCTATCaca |
| GATA1 | 131 | (+) | 0.993 | 0.935 | acagTGATAcaatg |
| GATA1 | 131 | (+) | 0.945 | 0.898 | acagtGATACaatg |
| GATA1 | 132 | (+) | 0.991 | 0.922 | cagTGATAcaatg |
| GATA1 | 133 | (+) | 0.993 | 0.97 | agtGATACaa |
| GATA1 | 156 | (+) | 0.983 | 0.972 | ctaGATCatt |
| GATA1 | 156 | (-) | 0.985 | 0.96 | ctAGATCatt |
| GATA1 | 180 | (+) | 0.985 | 0.977 | cagGATTAgc |
| GATA1 | 203 | (+) | 0.988 | 0.967 | tgaGATCCca |
| GATA1 | 203 | (-) | 0.985 | 0.964 | tgAGATCcca |
| GATA1 | 208 | (-) | 1 | 0.974 | tcCCATCttt |
| GATA1 | 250 | (-) | 1 | 0.947 | agaagTATCTcaat |
| GATA1 | 250 | (-) | 0.945 | 0.899 | agaaGTATCtcaat |
| GATA1 | 250 | (-) | 1 | 0.936 | agaagTATCTcaa |
| GATA1 | 252 | (-) | 0.993 | 0.975 | aaGTATCtca |
| GATA1 | 299 | (-) | 0.988 | 0.973 | ttTCATCctc |

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|-------|-----|-----|-------|-------|-----------------|
| GATA1 | 350 | (+) | 0.985 | 0.973 | cttGATCTtc |
| GATA1 | 350 | (-) | 0.983 | 0.972 | ctTGATCttc |
| GATA1 | 356 | (-) | 0.988 | 0.962 | ctTCATCctt |
| GATA1 | 422 | (-) | 1 | 0.941 | aaaaaTATCTtcca |
| GATA1 | 422 | (-) | 0.937 | 0.893 | aaaaATATCttcca |
| GATA1 | 422 | (-) | 1 | 0.939 | aaaaaTATCTtcc |
| GATA1 | 424 | (-) | 0.99 | 0.98 | aaATATCttc |
| GATA1 | 557 | (+) | 0.983 | 0.972 | gtaGATCagg |
| GATA1 | 557 | (-) | 0.985 | 0.977 | gtAGATCagg |
| GATA1 | 697 | (+) | 0.986 | 0.939 | atttGGATAatctt |
| GATA1 | 697 | (+) | 1 | 0.945 | atttgGATAAtctt |
| GATA1 | 698 | (+) | 0.965 | 0.932 | tttGGATAatctt |
| GATA1 | 699 | (+) | 0.988 | 0.96 | ttgGATAAtc |
| GATA1 | 699 | (+) | 1 | 0.909 | ttgGATAAtc |
| GATA1 | 699 | (+) | 1 | 0.877 | ttgGATAAtc |
| GATA1 | 702 | (-) | 0.985 | 0.96 | gaTAATCttt |
| GATA1 | 731 | (+) | 0.987 | 0.957 | ataGATTTca |
| GATA1 | 819 | (+) | 0.986 | 0.937 | gtgtGGATAAttatc |
| GATA1 | 819 | (+) | 0.937 | 0.9 | gtgtgGATATtadc |
| GATA1 | 820 | (+) | 0.965 | 0.901 | tgtGGATAAttatc |
| GATA1 | 821 | (+) | 0.99 | 0.974 | gtgGATATta |
| GATA1 | 824 | (-) | 0.991 | 0.946 | gatatTATCGgcta |
| GATA1 | 824 | (-) | 1 | 0.938 | gataTTATCggcta |
| GATA1 | 824 | (-) | 0.965 | 0.952 | gatatTATCGgct |
| GATA1 | 826 | (-) | 0.988 | 0.979 | taTTATCggc |

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|-------|-----|-----|-------|-------|----------------|
| GATA1 | 826 | (-) | 1 | 0.957 | taTTATCggc |
| GATA1 | 826 | (-) | 1 | 0.924 | taTTATCggc |
| GATA1 | 878 | (-) | 0.991 | 0.924 | gtttaTATCGagtt |
| GATA1 | 878 | (-) | 0.937 | 0.896 | gtttATATCgagtt |
| GATA1 | 878 | (-) | 0.965 | 0.912 | gtttaTATCGagt |
| GATA1 | 880 | (-) | 0.99 | 0.974 | ttATATCgag |
| GATA1 | 917 | (+) | 0.987 | 0.961 | tttGATTTtt |
| GATA1 | 928 | (-) | 0.988 | 0.977 | tcTCATCttc |
| GATA1 | 972 | (-) | 1 | 0.938 | atatgTATCTgtgc |
| GATA1 | 972 | (-) | 0.945 | 0.897 | atatGTATCtgtgc |
| GATA1 | 972 | (-) | 1 | 0.946 | atatgTATCTgtg |
| GATA1 | 974 | (-) | 0.993 | 0.97 | atGTATCtgt |
| GATA1 | 988 | (-) | 0.993 | 0.972 | atGCATCcca |
| GATA2 | 100 | (+) | 0.971 | 0.961 | tgtGATTAat |
| GATA2 | 112 | (-) | 1 | 0.996 | ggCTATCaca |
| GATA2 | 133 | (+) | 0.995 | 0.98 | agtGATACaa |
| GATA2 | 133 | (+) | 0.931 | 0.909 | agtGATACaa |
| GATA2 | 156 | (+) | 0.971 | 0.952 | ctaGATCatt |
| GATA2 | 156 | (-) | 0.972 | 0.958 | ctAGATCatt |
| GATA2 | 180 | (+) | 0.971 | 0.964 | cagGATTAgc |
| GATA2 | 203 | (+) | 0.974 | 0.969 | tgaGATCCca |
| GATA2 | 203 | (-) | 0.972 | 0.968 | tgAGATCcca |
| GATA2 | 208 | (-) | 0.987 | 0.974 | tcCCATCttt |
| GATA2 | 252 | (-) | 0.995 | 0.988 | aaGTATCtca |
| GATA2 | 299 | (-) | 0.979 | 0.967 | ttTCATCctc |

| | | | | | |
|-------|-----|-----|-------|-------|------------|
| GATA2 | 350 | (+) | 0.972 | 0.953 | cttGATCTtc |
| GATA2 | 350 | (-) | 0.971 | 0.961 | ctTGATCttc |
| GATA2 | 356 | (-) | 0.979 | 0.966 | ctTCATCctt |
| GATA2 | 424 | (-) | 0.994 | 0.986 | aaATATCttc |
| GATA2 | 557 | (+) | 0.971 | 0.955 | gtaGATCagg |
| GATA2 | 557 | (-) | 0.972 | 0.963 | gtAGATCagg |
| GATA2 | 699 | (+) | 0.992 | 0.972 | ttgGATAAtc |
| GATA2 | 699 | (+) | 1 | 0.922 | ttgGATAAtc |
| GATA2 | 702 | (-) | 0.971 | 0.96 | gaTAATCttt |
| GATA2 | 731 | (+) | 0.972 | 0.951 | ataGATTTca |
| GATA2 | 821 | (+) | 0.994 | 0.973 | gtgGATATta |
| GATA2 | 821 | (+) | 0.954 | 0.881 | gtgGATATta |
| GATA2 | 826 | (-) | 0.992 | 0.985 | taTTATCggc |
| GATA2 | 826 | (-) | 1 | 0.948 | taTTATCggc |
| GATA2 | 826 | (-) | 1 | 0.943 | taTTATCggc |
| GATA2 | 880 | (-) | 0.994 | 0.968 | ttATATCgag |
| GATA2 | 880 | (-) | 0.954 | 0.893 | ttATATCgag |
| GATA2 | 917 | (+) | 0.972 | 0.952 | tttGATTTtt |
| GATA2 | 928 | (-) | 0.979 | 0.971 | tcTCATCttc |
| GATA2 | 928 | (-) | 0.871 | 0.881 | tcTCATCttc |
| GATA2 | 974 | (-) | 0.995 | 0.982 | atGTATCtgt |
| GATA2 | 988 | (-) | 0.982 | 0.972 | atGCATCcca |
| GATA3 | 100 | (+) | 0.925 | 0.86 | tgtGATTAat |
| GATA3 | 101 | (+) | 0.962 | 0.932 | gtGATTAat |
| GATA3 | 112 | (-) | 1 | 0.969 | ggCTATCac |

| | | | | | |
|-------|-----|-----|-------|-------|------------|
| GATA3 | 133 | (+) | 0.878 | 0.86 | agtGATACaa |
| GATA3 | 133 | (+) | 0.896 | 0.86 | agtGATACaa |
| GATA3 | 134 | (+) | 0.974 | 0.951 | gtGATACaa |
| GATA3 | 156 | (-) | 0.936 | 0.929 | ctAGATCat |
| GATA3 | 156 | (+) | 0.928 | 0.871 | ctaGATCAtt |
| GATA3 | 156 | (+) | 0.977 | 0.862 | ctaGATCAtt |
| GATA3 | 156 | (-) | 1 | 0.857 | ctAGATCatt |
| GATA3 | 157 | (+) | 0.944 | 0.917 | taGATCAtt |
| GATA3 | 181 | (+) | 0.962 | 0.933 | agGATTAgc |
| GATA3 | 203 | (-) | 0.936 | 0.913 | tgAGATCcc |
| GATA3 | 203 | (+) | 0.915 | 0.869 | tgaGATCCca |
| GATA3 | 203 | (-) | 1 | 0.868 | tgAGATCcca |
| GATA3 | 204 | (+) | 0.933 | 0.915 | gaGATCCca |
| GATA3 | 208 | (-) | 0.969 | 0.952 | tcCCATCtt |
| GATA3 | 208 | (-) | 0.87 | 0.88 | tcCCATCttt |
| GATA3 | 252 | (-) | 0.974 | 0.949 | aaGTATCtc |
| GATA3 | 299 | (-) | 0.954 | 0.928 | ttTCATCct |
| GATA3 | 299 | (-) | 0.917 | 0.867 | ttTCATCctc |
| GATA3 | 350 | (-) | 0.944 | 0.94 | ctTGATCtt |
| GATA3 | 350 | (-) | 0.928 | 0.878 | ctTGATCttc |
| GATA3 | 350 | (-) | 0.977 | 0.854 | ctTGATCttc |
| GATA3 | 351 | (+) | 0.936 | 0.906 | ttGATCTtc |
| GATA3 | 356 | (-) | 0.954 | 0.945 | ctTCATCct |
| GATA3 | 424 | (-) | 0.977 | 0.95 | aaATATCtt |
| GATA3 | 424 | (-) | 0.981 | 0.872 | aaATATCttc |

| | | | | | |
|-------|-----|-----|-------|-------|---------------------|
| GATA3 | 557 | (-) | 0.936 | 0.905 | gtAGATCag |
| GATA3 | 557 | (+) | 0.928 | 0.872 | gtaGATCagg |
| GATA3 | 558 | (+) | 0.944 | 0.943 | taGATCagg |
| GATA3 | 699 | (+) | 1 | 0.892 | ttgGATAAtc |
| GATA3 | 700 | (+) | 0.985 | 0.951 | tgGATAAtc |
| GATA3 | 702 | (-) | 0.962 | 0.935 | gaTAATCtt |
| GATA3 | 702 | (-) | 0.925 | 0.877 | gaTAATCttt |
| GATA3 | 702 | (-) | 0.945 | 0.875 | gaTAATCttt |
| GATA3 | 731 | (+) | 0.968 | 0.943 | ataGATTTca |
| GATA3 | 732 | (+) | 0.953 | 0.931 | taGATTTca |
| GATA3 | 821 | (+) | 0.981 | 0.885 | gtgGATATta |
| GATA3 | 822 | (+) | 0.977 | 0.95 | tgGATATta |
| GATA3 | 826 | (-) | 0.985 | 0.961 | taTTATCgg |
| GATA3 | 826 | (-) | 1 | 0.943 | taTTATCggc |
| GATA3 | 826 | (-) | 0.958 | 0.874 | taTTATCggc |
| GATA3 | 880 | (-) | 0.977 | 0.95 | ttATATCga |
| GATA3 | 880 | (-) | 0.981 | 0.876 | ttATATCgag |
| GATA3 | 918 | (+) | 0.953 | 0.922 | ttGATTTtt |
| GATA3 | 928 | (-) | 0.954 | 0.938 | tcTCATCtt |
| GATA3 | 928 | (-) | 0.917 | 0.905 | tcTCATCttc |
| GATA3 | 928 | (-) | 0.932 | 0.899 | tcTCATCttc |
| GATA3 | 974 | (-) | 0.974 | 0.945 | atGTATCtg |
| GATA3 | 988 | (-) | 0.943 | 0.913 | atGCATCcc |
| GR | 10 | (+) | 0.986 | 0.94 | aatggactgcgTGTGCTag |
| GR | 12 | (+) | 0.96 | 0.852 | tggactgcgtGTGCTa |

| | | | | | |
|-------|-----|-----|-------|-------|---------------------|
| GR | 126 | (-) | 0.984 | 0.87 | ctgGTACAgtgatacaatg |
| GR | 194 | (-) | 0.986 | 0.961 | acaGCACAgtgagatccca |
| GR | 319 | (+) | 0.986 | 0.88 | aaatatataatTGTGCata |
| GR | 471 | (+) | 0.875 | 0.854 | tttggtttttTGTTTttt |
| GR | 480 | (+) | 0.875 | 0.854 | tttggtttttTGTTTtgt |
| GR | 490 | (+) | 0.875 | 0.852 | ttgttttggtTGTTTtgt |
| GR | 528 | (+) | 0.989 | 0.939 | atagccctggcTGTCCtag |
| GR | 615 | (+) | 0.986 | 0.856 | gtttaaaggcaTGTGCcac |
| GR | 970 | (+) | 0.986 | 0.904 | atatatgtatcTGTGCata |
| MyoD | 602 | (+) | 0.873 | 0.851 | tccCAAGTgctg |
| MyoD | 621 | (+) | 0.905 | 0.861 | aggCATGTgcca |
| MyoD | 622 | (+) | 0.851 | 0.889 | ggCATGTgcc |
| MyoD | 762 | (-) | 1 | 0.856 | attcACCTGgga |
| MyoD | 763 | (+) | 1 | 0.921 | ttCACCTggg |
| MyoD | 804 | (-) | 0.905 | 0.861 | agccACATGaca |
| MyoD | 805 | (-) | 0.851 | 0.882 | gccACATGac |
| NRF-2 | 261 | (+) | 1 | 0.868 | aatGGAAGag |
| NRF-2 | 932 | (-) | 1 | 0.901 | atCTTCctgt |
| p53 | 587 | (+) | 0.965 | 0.882 | ttgCCTGCct |
| p53 | 621 | (+) | 1 | 0.87 | aggCATGTgc |
| p53 | 621 | (-) | 1 | 0.922 | agGCATGtgc |
| p53 | 652 | (+) | 0.965 | 0.897 | aaaCCTGCca |
| p53 | 865 | (+) | 1 | 0.91 | atgCATGCct |
| p53 | 865 | (-) | 1 | 0.878 | atGCATGcct |
| Sp1 | 286 | (-) | 0.949 | 0.9 | cccACGCCct |

| | | | | | |
|-----|-----|-----|-------|-------|--------------------|
| Sp1 | 563 | (+) | 0.962 | 0.873 | caGGCTGgcc |
| Sp1 | 588 | (-) | 0.972 | 0.908 | tgcCTGCCtc |
| Sp1 | 653 | (-) | 0.972 | 0.897 | aacCTGCCaa |
| Sp1 | 866 | (-) | 0.921 | 0.852 | tgcATGCCtt |
| Sp1 | 902 | (+) | 0.915 | 0.872 | tgtgGGTGGgagt |
| Sp1 | 903 | (+) | 0.872 | 0.854 | gtGGGTGgga |
| SRF | 691 | (+) | 0.99 | 0.922 | ttCCAAAttggat |
| SRF | 691 | (-) | 0.99 | 0.92 | ttccaaaTTTGat |
| SRF | 692 | (+) | 0.867 | 0.851 | tccaaaTTTGataa |
| YY1 | 3 | (-) | 1 | 0.9 | atcttgcaATGGAActgc |
| YY1 | 134 | (-) | 1 | 0.922 | gtgatacaATGGAgtct |
| YY1 | 156 | (+) | 0.922 | 0.891 | ctagATCATttgagaat |
| YY1 | 165 | (-) | 0.906 | 0.907 | ttgagaatATGCTtca |
| YY1 | 205 | (+) | 0.996 | 0.984 | agatCCCATctttaa |
| YY1 | 254 | (-) | 1 | 0.899 | gtatctcaATGGAagag |
| YY1 | 361 | (-) | 0.996 | 0.869 | tccttgctATGGGcaac |
| YY1 | 428 | (+) | 1 | 0.95 | atctTCCATataaaccc |
| YY1 | 618 | (+) | 0.904 | 0.866 | taaaGGCATgtgccacc |
| YY1 | 792 | (+) | 0.922 | 0.898 | gttaTTCATtttagcca |
| YY1 | 802 | (-) | 0.92 | 0.891 | ttagccacATGACaatt |
| YY1 | 836 | (+) | 0.996 | 0.91 | taaaCCCATcttctctt |
| YY1 | 857 | (-) | 0.906 | 0.875 | aatttgaaATGCAtgcc |
| YY1 | 892 | (+) | 0.902 | 0.86 | cccaCACATatgtgggt |
| YY1 | 893 | (-) | 0.902 | 0.864 | ccacacatATGTGggtg |
| YY1 | 925 | (+) | 0.918 | 0.887 | ttctCTCATcttctgt |

| | | | | | |
|-----|-----|-----|-------|-------|-------------------|
| YY1 | 966 | (-) | 0.906 | 0.887 | taatatatATGTAtctg |
| YY1 | 979 | (+) | 0.906 | 0.864 | tctgTGCATatgcatcc |
| YY1 | 980 | (-) | 0.906 | 0.879 | ctgtgcatATGCAtccc |

Supplementary Table S3. List of putative transcription factor binding sites detected in mouse FTH1 upstream 1.0-kb predicted with cut-off Score > 0.85 in TF BIND.

| ID | Score | Loc. | Str. | Consensus | Sequence |
|----------|----------|------|------|----------------|----------------|
| AP1_C | 0.871429 | 101 | (-) | NTGASTCAG | GTGATTAAT |
| AP1_C | 0.85277 | 597 | (-) | NTGASTCAG | CTGACTCCC |
| AP1_C | 0.856268 | 792 | (-) | NTGASTCAG | GTTATTCAT |
| AP1_Q6 | 0.872508 | 596 | (+) | NNTGACTCANN | TCTGACTCCCA |
| CEBP_01 | 0.883306 | 404 | (+) | NNTKTGGWNANNN | TCTATGTTAACCT |
| CEBP_01 | 0.935494 | 469 | (+) | NNTKTGGWNANNN | TGTTTGTTTTTTT |
| CEBP_01 | 0.871637 | 487 | (+) | NNTKTGGWNANNN | TTTTTGTTTTGTT |
| CEBP_01 | 0.914749 | 687 | (-) | NNTKTGGWNANNN | CCTATTCCAAATT |
| CEBP_01 | 0.947488 | 696 | (+) | NNTKTGGWNANNN | AATTTGGATAATC |
| CEBP_01 | 0.929011 | 818 | (+) | NNTKTGGWNANNN | TGTGTGGATATTA |
| CEBP_01 | 0.926742 | 887 | (-) | NNTKTGGWNANNN | GAGTTCCCACACA |
| CEBP_01 | 0.9141 | 979 | (+) | NNTKTGGWNANNN | TCTGTGCATATGC |
| CEBP_Q2 | 0.859404 | 1 | (-) | NNNTTGCNNAANNN | GCATCTTGCAATGG |
| CEBP_Q2 | 0.860876 | 413 | (+) | NNNTTGCNNAANNN | ACCTTGTTTAAAAA |
| CEBP_Q2 | 0.853147 | 696 | (+) | NNNTTGCNNAANNN | AATTTGGATAATCT |
| CEBPA_01 | 0.876809 | 696 | (+) | NNATTRCNNAANNN | AATTTGGATAATCT |
| CEBPB_01 | 0.867509 | 733 | (-) | RNRTKNNGMAAKNN | AGATTTCAACTTA |
| CEBPB_01 | 0.857355 | 1 | (+) | RNRTKNNGMAAKNN | GCATCTTGCAATGG |
| CEBPB_01 | 0.855869 | 505 | (+) | RNRTKNNGMAAKNN | TTGTTGAGACAGGG |

| | | | | | |
|----------|----------|-----|-----|----------------------|---------------------|
| CEBPB_01 | 0.854631 | 661 | (+) | RNRTKNNGMAAKNN | AACTTTTGAAACTC |
| CP2_01 | 0.914666 | 363 | (-) | GCNMNAMCMAG | CTTGCTATGGG |
| CP2_01 | 0.886364 | 834 | (+) | GCNMNAMCMAG | GCTAAACCCAT |
| CP2_01 | 0.867496 | 344 | (-) | GCNMNAMCMAG | CTGGCTCTGA |
| CP2_01 | 0.858919 | 648 | (+) | GCNMNAMCMAG | GGCCAAACCTG |
| CP2_01 | 0.856775 | 72 | (+) | GCNMNAMCMAG | AGCCAACCAAG |
| GATA1_01 | 0.90079 | 112 | (-) | SNNGATNNNN | GGCTATCACA |
| GATA1_01 | 0.8692 | 252 | (-) | SNNGATNNNN | AAGTATCTCA |
| GATA1_01 | 0.875617 | 424 | (-) | SNNGATNNNN | AAATATCTTC |
| GATA1_01 | 0.857354 | 826 | (-) | SNNGATNNNN | TATTATCGGC |
| GATA1_03 | 0.863792 | 926 | (-) | RNSNNGATAANNGN | TCTCTCATCTTCT |
| GATA1_04 | 0.887255 | 110 | (-) | NNCWGATARNNNN | GCGGCTATCACAT |
| GATA2_01 | 0.943166 | 112 | (-) | NNNGATRNNN | GGCTATCACA |
| GATA2_01 | 0.913848 | 252 | (-) | NNNGATRNNN | AAGTATCTCA |
| GATA2_01 | 0.908886 | 424 | (-) | NNNGATRNNN | AAATATCTTC |
| GATA2_01 | 0.869193 | 826 | (-) | NNNGATRNNN | TATTATCGGC |
| GATA2_01 | 0.85972 | 988 | (-) | NNNGATRNNN | ATGCATCCCA |
| GATA3_01 | 0.87284 | 112 | (-) | NNGATARNG | GGCTATCAC |
| GATA3_01 | 0.894107 | 208 | (-) | NNGATARNG | TCCCATCTT |
| GATA3_01 | 0.863093 | 826 | (-) | NNGATARNG | TATTATCGG |
| GATA3_01 | 0.865751 | 928 | (-) | NNGATARNG | TCTCATCTT |
| GR_Q6 | 0.879464 | 194 | (-) | NNNNNNC NNTNTGTNCTNN | ACAGCACAGTGAGATCCCA |

| | | | | | |
|---------|----------|-----|-----|-----------------|-----------------|
| MYOD_01 | 0.897047 | 621 | (+) | SRACAGGTGKYG | AGGCATGTGCCA |
| MYOD_01 | 0.850197 | 804 | (-) | SRACAGGTGKYG | AGCCACATGACA |
| MYOD_Q6 | 0.874152 | 622 | (+) | NNCANCTGNY | GGCATGTGCC |
| NRF2_01 | 0.925388 | 932 | (-) | ACCGGAAGNS | ATCTTCCTGT |
| NRF2_01 | 0.853924 | 261 | (+) | ACCGGAAGNS | AATGGAAGAG |
| P53_02 | 0.890387 | 564 | (-) | NGRCWTGYCY | AGGCTGGCCT |
| P53_02 | 0.885991 | 564 | (+) | NGRCWTGYCY | AGGCTGGCCT |
| P53_02 | 0.867233 | 583 | (+) | NGRCWTGYCY | AAATTTGCCT |
| P53_02 | 0.899766 | 621 | (-) | NGRCWTGYCY | AGGCATGTGC |
| P53_02 | 0.856975 | 621 | (+) | NGRCWTGYCY | AGGCATGTGC |
| P53_02 | 0.872802 | 652 | (+) | NGRCWTGYCY | AAACCTGCCA |
| P53_02 | 0.862837 | 652 | (-) | NGRCWTGYCY | AAACCTGCCA |
| P53_02 | 0.91823 | 865 | (+) | NGRCWTGYCY | ATGCATGCCT |
| P53_02 | 0.866061 | 865 | (-) | NGRCWTGYCY | ATGCATGCCT |
| SP1_01 | 0.855323 | 280 | (-) | GRGGCRGGGW | AGAATGCCCA |
| SP1_01 | 0.908834 | 588 | (-) | GRGGCRGGGW | TGCCTGCCTC |
| SP1_01 | 0.85051 | 653 | (-) | GRGGCRGGGW | AACCTGCCAA |
| SP1_01 | 0.855606 | 866 | (-) | GRGGCRGGGW | TGCATGCCTT |
| SP1_01 | 0.864666 | 903 | (+) | GRGGCRGGGW | GTGGGTGGGA |
| SRF_C | 0.870696 | 689 | (-) | NCCWTATATGGNCWN | TATTCCAAATTTGGA |
| SRF_C | 0.87052 | 692 | (+) | NCCWTATATGGNCWN | TCCAAATTTGGATAA |
| SRF_Q6 | 0.909975 | 691 | (+) | GNCCAWATAWGGMN | TTCCAAATTTGGAT |

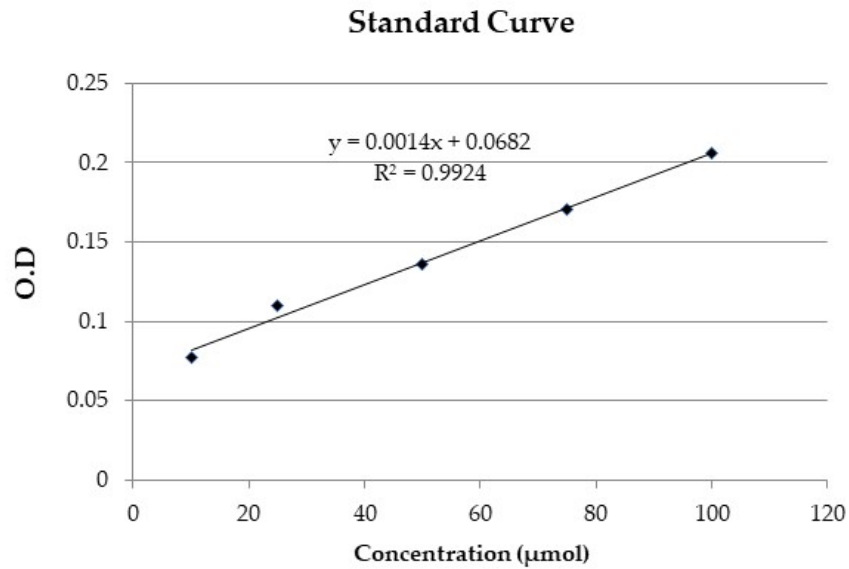
| | | | | | |
|--------|----------|-----|-----|-------------------|-------------------|
| SRF_Q6 | 0.902156 | 691 | (-) | GNCCAWATAWGGMN | TTCCAAATTTGGAT |
| YY1_01 | 0.861402 | 134 | (-) | NNNNNCCATNTWNNNWN | GTGATACAATGGAGTCT |
| YY1_01 | 0.854849 | 205 | (+) | NNNNNCCATNTWNNNWN | AGATCCCATCTTTAAAT |

Supplementary Table S4. Analysis of the correlation between the iron content in the mouse liver and the analyzed genes in microarray

| Gene | RHO | <i>p</i> -value | Regulation | Functions | Reference |
|--------|----------|-----------------|------------|--|-----------|
| Scd1 | -0.57471 | 0.002321 | Down | <ul style="list-style-type: none"> Fatty Acyl-CoA Biosynthesis Regulation of cholesterol biosynthesis by SREBP | [1,2] |
| Acs15 | -0.659 | 0.002321 | n.s. | <ul style="list-style-type: none"> Fatty Acyl-CoA Biosynthesis Regulation of lipid droplet | [3,4] |
| Leptin | 0.608648 | 0.000754 | n.s. | <ul style="list-style-type: none"> AMPK Signaling Adipocytokine signaling pathway | [5] |
| ASXL1 | -0.54461 | 0.003154 | Up | <ul style="list-style-type: none"> Transcriptional regulator of adipogenesis, acting to repress PPARγ adipocyte differentiation | [6] |
| GATA2 | -0.54351 | 0.003225 | n.s. | <ul style="list-style-type: none"> Regulation of differentiation of brown adipocytes Inhibitor of PPARγ | [7] |

All data was given in a study by McLachlan, S., et al. [8]. Abbreviation: Scd1; Stearoyl-CoA desaturase-1, Acs15; Acyl-CoA Synthetase Long Chain Family Member 5, ASXL1; Additional Sex Comb-Like Protein 1, Gata2; GATA Binding Protein

Supplementary Figure S1. The standard curve for measurement of total glutathione (tGSH) contents



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