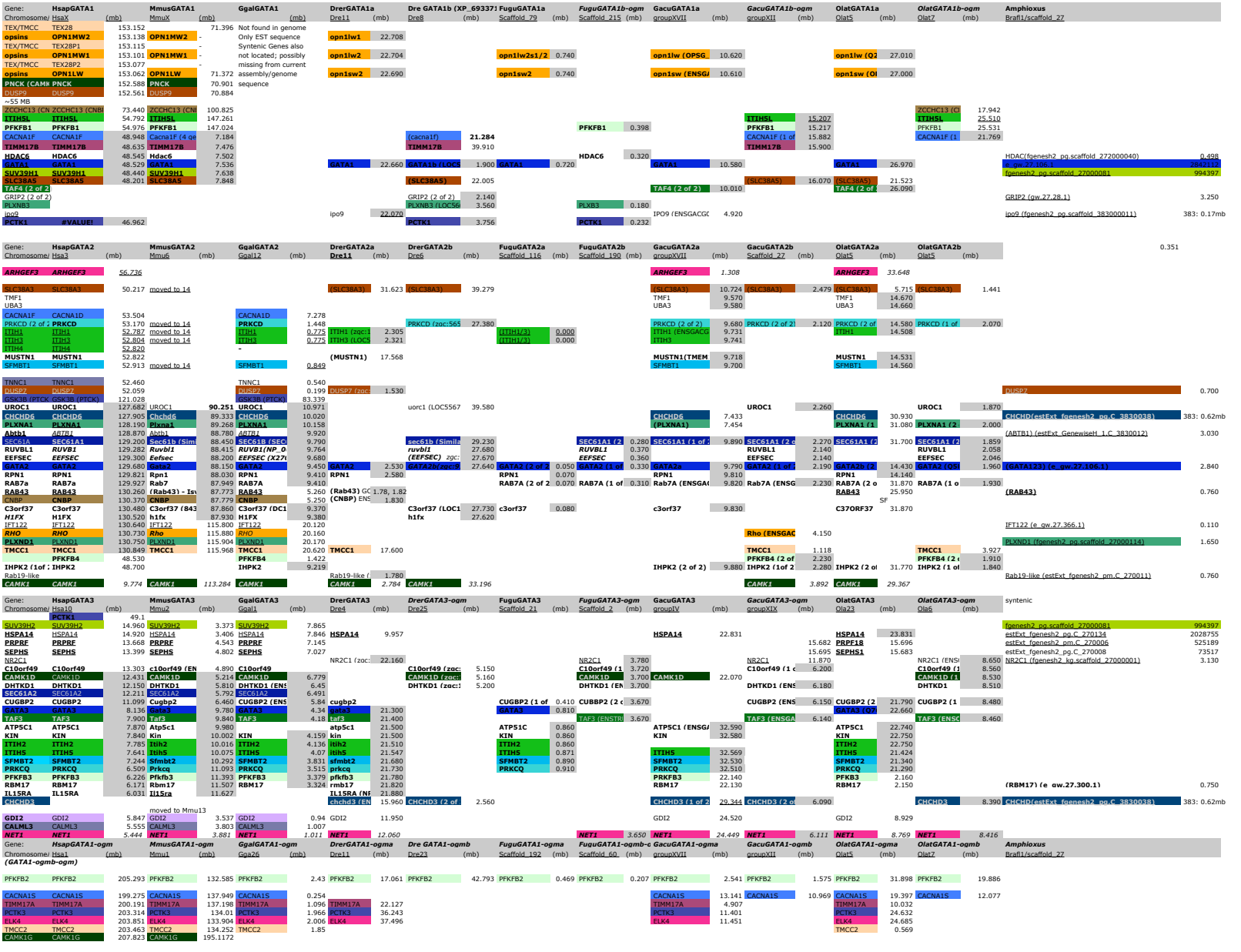
Gene: HsapGATA1
Chromosome/ HsaX (mb)
TEX/TMCC TEX28 153.152
opsins OPN1MW2 153.138
TEX/TMCC TEX28P1 153.115
opsins OPN1MW1 153.101
TEX/TMCC TEX28P2 153.077
opsins OPN1LW 153.062
PNCK (CAMK PNCK 152.588
DUSP9 DUSP9 152.561
~55 MB
ZCCHC13 (CN ZCCHC13 (CNB 73.440
ITIH5L ITIH5L 54.792
PFKFB1 PFKFB1 54.976
CACNA1F CACNA1F 48.948
TIMM17B TIMM17B 48.635
HDAC6 HDAC6 48.545
CATA1 GATA1 48.529
SUV39H1 SUV39H1 48.440
SLC38A5 SLC38A5 48.201
TAF4 (2 of 2
GRIP2 (2 of 2)
PLXNB3
ipo9
PCTK1 #VALUE!
MmusGATA1
MmuX (mb)
71.396 Not found in genome
- Only EST sequence
- Syntenic Genes also
- not located; possibly
- missing from current
71.372 assembly/genome
70.901 sequence
70.884
100.825
147.261
147.024
7.184 Cacna1f (4 ge
7.476
7.502
7.536
7.638
7.848
GgalGATA1
Dre11 (mb)
opn1lw1 22.708
opn1lw2 22.704
opn1sw2 22.690
GATA1 22.660
DreGATA1a
Dre GATA1b (XP_693377
Dre8 (mb)
(cacna1f) 21.284
TIMM17B 39.910
GATA1b (LOC5 1.900
(SLC38A5) 22.005
GRIP2 (2 of 2) 2.140
PLXNB3 (LOC56 3.560
ipo9 22.070
PCTK1 3.756
FuguGATA1a
Scaffold_79 (mb)
opn1lw2s1/2 0.740
opn1sw2 0.740
GATA1 0.720
FuguGATA1b-ogm
Scaffold_215 (mb)
PFKFB1 0.398
HDAC6 0.320
PLXB3 0.180
TPO9 (ENSGACG 4.920
PCTK1 0.232
GacuGATA1a
groupXVII (mb)
opn1lw (OPSG 10.620
opn1sw (ENSG 10.611
GATA1 10.580
TAF4 (2 of 2) 10.010
GacuGATA1b-ogm
groupXII (mb)
ITIH5L 15.207
PFKFB1 15.217
CACNA1F (1 of 15.882
TIMM17B 15.900
(SLC38A5) 16.070
OlatGATA1a
Olat5 (mb)
opn1lw (Q2 27.010
opn1sw (Ol 27.000
GATA1 26.970
(SLC38A5) 21.523
TAF4 (2 of 2 26.090
OlatGATA1b-ogm
Olat7 (mb)
ZCCHC13 (Cl 17.942
ITIH5L 25.510
PFKFB1 25.531
CACNA1F (1 21.769
Amphioxus
Braf1/scaffold_27
HDAC(fgenesh2_pg.scaffold_272000040) 0.498
c_gw_27.106.1 2842132
fgenesh2_pg.scaffold_27000081 994397
GRIP2 (gw_27.28.1) 3.250
ipo9 (fgenesh2_pg.scaffold_383000011) 383: 0.17mb
Gene: HsapGATA2
Chromosome/ Hsa3 (mb)
ARHGEF3 ARHGEF3 56.736
SLC38A3 SLC38A3 50.217
TMF1 UBA3
CACNA1F CACNA1F 53.504
PRKCD (2 of 2 PRKCD 53.170
ITIH1 ITIH1 52.787
ITIH3 ITIH3 52.804
ITIH4 ITIH4 52.820
MUSTN1 MUSTN1 52.822
SFMBT1 SFMBT1 52.913
TNNC1 TNNC1 52.460
DUSP7 DUSP7 52.059
UROC1 UROC1 121.682
CHCHD6 CHCHD6 127.905
PLXNA1 PLXNA1 128.190
Abtb1 ABTB1 128.870
SEC61A1 SEC61A1 129.200
RUVBL1 RUVBL1 129.282
EEFSEC EEFSEC 129.300
GATA2 GATA2 129.680
RPN1 RPN1 129.821
RAB7a RAB7a 129.927
RAB43 RAB43 130.260
CNBP CNBP 130.370
C3orf37 C3orf37 130.480
H1FX H1FX 130.520
IFT122 IFT122 130.640
RHO RHO 130.730
PLXND1 PLXND1 130.750
TMCC1 TMCC1 130.849
PFKFB4 48.530
IHPK2 (1of 2 48.700
Rab19-like
CAMK1 CAMK1 9.774
MmusGATA2
Mmu6 (mb)
moved to 14
moved to 14
moved to 14
moved to 14
MUSTN1 52.822
moved to 14
90.251 UROC1 10.971
89.333 Chchd6 10.020
89.268 Plxna1 10.158
88.780 ABTB1 9.920
88.450 Sec61b (Sim
88.415 Ruvbl1 9.764
88.200 Eefsec 9.680
88.150 Gata2 9.450
88.030 Rpn1 9.410
87.949 Rab7a 9.410
87.773 Rab43 - Isv 5.260
87.779 CNBP 5.250
87.860 C3orf37 (DC1 9.370
87.930 H1FX 9.380
115.800 IFT122 20.120
115.880 Rho 20.160
115.904 PLXND1 20.170
115.968 TMCC1 20.620
PFKFB4 1.422
IHPK2 9.219
CAMK1 113.284
GgalGATA2
Gga12 (mb)
CACNA1D 7.278
PRKCD 1.448
ITIH1 0.772
ITIH3 0.775
- 0.849
SFMBT1 0.849
TNNC1 0.540
DUSP7 0.199
UROC1 83.339
CHCHD6 10.020
PLXNA1 10.158
ABTB1 9.920
SEC61A1 (SEC 9.764
RUVBL1 9.764
GATA2 9.450
RAB43 5.260
CNBP 5.250
C3orf37 (DC1 9.370
H1FX 9.380
IFT122 20.120
Rho 20.160
PLXND1 20.170
TMCC1 20.620
PFKFB4 1.422
IHPK2 9.219
CAMK1 113.284
DreGATA2a
Dre11 (mb)
(SLC38A3) 31.623
ITIH1 (zgc: 2.305
ITIH3 (LOC5 2.321
(MUSTN1) 17.568
DUSP7 (zgc: 1.530
GATA2 2.530
(Rab43) GC 1.78, 1.82
(CNBP) ENS 1.830
TMCC1 17.600
Rab19-like (1.780
CAMK1 2.784
DreGATA2b
Dre6 (mb)
(SLC38A3) 39.279
sec61b (Simila 29.230
ruvbl1 27.680
(EEFSEC) zgc: 27.670
GATA2b(zgc:8 27.640
uorc1 (LOC5567 39.580
C3orf37 (LOC1 27.730
h1fx 27.620
CAMK1 33.196
FuguGATA2a
Scaffold_116 (mb)
(ITIH1/3) 0.000
(ITIH1/3) 0.000
GATA2 (2 of 2 0.050
RPN1 0.070
RAB7A (2 of 2 0.070
c3orf37 0.080
FuguGATA2b
Scaffold_190 (mb)
SEC61A1 (2 0.280
RUVBL1 0.370
EEFSEC 0.360
GATA2 (3 of 0.330
RAB7A (1 of 0.310
GacuGATA2a
groupXVII (mb)
ARHGEF3 1.308
(SLC38A3) 10.724
(PLXNA1) 7.454
PRKCD (2 of 2) 9.680
ITIH1 (ENSGACG 9.731
ITIH3 9.741
MUSTN1(TMEM 9.718
SFMBT1 9.700
CHCHD6 7.433
GATA2a 9.790
Rab7A (ENSG 9.820
c3orf37 9.830
IHPK2 (2 of 2) 9.880
GacuGATA2b
Scaffold_27 (mb)
(SLC38A3) 2.479
UROC1 2.260
PRKCD (2 of 2) 2.120
GATA2 (1 of 2 2.190
Rab7A (ENSG 2.230
Rho (ENSGAC 4.150
TMCC1 1.118
PKFB4 (2 of 2.230
IHPK2 (1of 2 2.280
CAMK1 3.892
OlatGATA2a
Olat5 (mb)
ARHGEF3 33.648
(SLC38A3) 5.715
TIMM17B 14.670
UBA3 14.660
PRKCD (2 of 14.580
ITIH1 14.508
MUSTN1 14.531
SFMBT1 14.560
CHCHD6 30.930
PLXNA1 (1 31.080
SEC61A1 (2 31.700
GATA2b (2 14.430
RAB43 25.950
SF
C370RF37 31.870
IHPK2 (2 of 31.770
OlatGATA2b
Olat5 (mb)
(SLC38A3) 1.441
UROC1 1.870
PLXNA1 (2 2.000
RUVBL1 2.058
SEC61A1 (2 1.859
EEFSEC 2.046
GATA2 (QS 1.960
RAB7A (1 o 1.930
(RAB43)
TMCC1 3.927
PKFB4 (2 1.910
IHPK2 (1 of 1.840
CAMK1 3.667
Amphioxus
0.351
CHCHD(estExt_fgenesh2_pg.C_3830038) 383: 0.62mb
(ABTB1) (estExt_GenewiseH_1.C_3830012) 3.030
(GATA123) (e_gw.27.106.1) 2.840
0.760
IFT122 (e_gw.27.366.1) 0.110
PLXND1 (fgenesh2_pg.scaffold_27000114) 1.650
Rab19-like (estExt_fgenesh2_pm.C_270011) 0.760
Gene: HsapGATA3
Chromosome/ Hsa10 (mb)
PCTK1 49.1
SUV39H2 14.960
HSPA14 14.920
PRPRF 13.668
SEPHS 13.399
NR2C1
C10orf49 13.303
CAMK1D 12.431
DHTKD1 12.150
SEC61A2 12.211
CUGBP2 11.099
GATA3 8.136
TAF3 7.900
ATP5C1 7.870
KIN 7.840
ITIH2 7.785
ITIH5 7.641
SFMBT2 7.244
PRKCQ 6.509
PFKFB3 6.226
RBM17 6.171
IL15RA 6.031
CHCHD3
GDI2 5.847
CALML3 5.555
NET1 5.444
MmusGATA3
Mmu2 (mb)
SUV39H2 3.373
HSPA14 3.406
PRPRF 4.543
SEPHS 4.802
c10orf49 (EN 4.890
CAMK1D 5.214
DHTKD1 5.810
SEC61A2 5.792
Cugbp2 6.460
Gata3 9.780
Taf3 9.840
Atp5c1 9.980
Kin 10.002
Itih2 10.016
Itih5 10.075
Sfmbt2 10.292
Prkcq 11.093
Pfkfb3 11.393
Rbm17 11.507
Il15ra 11.627
moved to Mmu13
GDI2 3.537
CALML3 3.803
NET1 3.881
GgalGATA3
Gga1 (mb)
SUV39H2 7.865
HSPA14 7.846
PRPRF 7.145
SEPHS 7.027
CAMK1D 6.779
DHTKD1 (ENS 5.845
SEC61A2 6.491
CUGBP2 (ENS 5.84
GATA3 4.34
TAF3 4.18
KIN 4.159
ITIH2 4.136
ITIH5 4.07
SFMBT2 3.831
PRKCQ 3.515
PFKFB3 3.479
RBM17 3.324
GDI2 0.94
CALML3 1.007
NET1 1.011
DreGATA3
Dre4 (mb)
HSPA14 9.957
NR2C1 (zgc: 22.160
cugbp2 21.300
gata3 21.300
taf3 21.400
atp5c1 21.500
kin 21.500
itih2 21.510
itih5 21.547
sfmbt2 21.680
prkcq 21.730
pfkfb3 21.780
rmb17 21.820
IL15RA (NS 21.880
chchd3 (EN 15.960
GDI2 11.950
NET1 12.060
DreGATA3-ogm
Dre25 (mb)
C10orf49 (zgc: 5.150
CAMK1D (zgc 5.160
DHTKD1 (zgc: 5.200
CHCHD3 (2 of 2.560
FuguGATA3
Scaffold_21 (mb)
CUGBP2 (1 of 0.410
GATA3 0.810
TAF3 (ENSTRI 3.670
ATP5C1 0.860
KIN 0.860
ITIH2 0.860
ITIH5 0.871
SFMBT2 0.890
PRKCQ 0.910
NET1 3.650
FuguGATA3-ogm
Scaffold_2 (mb)
NR2C1 3.780
C10orf49 (1 3.720
CAMK1D 3.700
DHTKD1 (EN 3.700
CUGBP2 (2 3.670
GacuGATA3
groupIV (mb)
HSPA14 22.831
ATP5C1 (ENSG 32.590
KIN 32.580
ITIH5 32.569
SFMBT2 32.530
PRKCQ 32.510
PRKFB3 22.140
RBM17 22.130
CHCHD3 (1 of 2 29.344
GDI2 24.520
NET1 24.449
GacuGATA3-ogm
groupXIX (mb)
NR2C1 11.870
C10orf49 (1 c 6.200
DHTKD1 (ENS 6.180
CUGBP2 (ENS 6.150
TAF3 (ENSGA 6.140
CHCHD3 (2 o 6.090
NET1 6.111
OlatGATA3
Ola23 (mb)
HSPA14 23.831
PRPF18 15.696
SEPHS1 15.683
NR2C1 (ENSI 8.650
C10orf49 (1 8.560
CAMK1D (1 8.530
DHTKD1 8.510
CUGBP2 (2 21.790
GATA3 (QY 22.660
TAF3 (ENSG 8.460
ATP5C1 22.740
KIN 22.750
ITIH2 22.750
ITIH5 21.424
SFMBT2 21.340
PRKCQ 21.290
PFKFB3 2.160
RBM17 2.150
CHCHD3 8.390
NET1 8.769
OlatGATA3-ogm
Ola6 (mb)
CUGBP2 (1 8.480
(RBM17) (e_gw.27.300.1) 0.750
CHCHD(estExt_fgenesh2_pg.C_3830038) 383: 0.62mb
NR2C1 (fgenesh2_kg.scaffold_27000001) 3.130
Gene: HsapGATA1-ogm
Chromosome/ Hsa1 (mb)
(GATA1-ogmb-ogm)
PFKFB2 PFKFB2 205.293
CACNA1S CACNA1S 199.275
TIMM17A TIMM17A 200.191
PCTK3 PCTK3 203.314
ELK4 ELK4 203.851
TMCC2 TMCC2 203.463
CAMK1G CAMK1G 207.823
MmusGATA1-ogm
Mmu1 (mb)
PFKFB2 132.585
CACNA1S 137.949
TIMM17A 137.198
PCTK3 134.01
ELK4 133.904
TMCC2 134.252
CAMK1G 195.1172
GgalGATA1-ogm
Gga26 (mb)
PFKFB2 2.43
CACNA1S 0.254
TIMM17A 1.096
PCTK3 1.966
ELK4 2.006
TMCC2 1.85
DreGATA1-ogma
Dre11 (mb)
PFKFB2 17.061
TIMM17A 22.127
PCTK3 36.243
ELK4 37.496
Dre GATA1-ogmb
Dre23 (mb)
PFKFB2 42.793
FuguGATA1-ogma
Scaffold_192 (mb)
PFKFB2 0.469
FuguGATA1-ogmb-c
Scaffold_60 (mb)
PFKFB2 0.207
NET1 3.650
GacuGATA1-ogma
groupXVII (mb)
PFKFB2 2.541
CACNA1S 13.141
TIMM17A 4.907
PCTK3 11.401
ELK4 11.451
GacuGATA1-ogmb
groupXII (mb)
PFKFB2 1.575
CACNA1S 10.969
OlatGATA1-ogma
Olat5 (mb)
PFKFB2 31.898
CACNA1S 19.397
TIMM17A 10.032
PCTK3 24.632
ELK4 24.685
TMCC2 0.569
OlatGATA1-ogmb
Olat7 (mb)
PFKFB2 19.886
CACNA1S 12.077
Amphioxus
Braf1/scaffold_27