**SUPPLEMENTARY FILE 1**

**Supplementary Table 1.** Transcription factor binding motif enrichment in genomic regions accessible in E14.5 atrioventricular junctions

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Motif enrichment** |  |  |  |
| **Motif name** | **AVJ (67) vs Ctrl (273)** | **P-value** | **Ventricle (67) vs Ctrl (248)** | **P-value** |
| Smad3 | 50 (74.6%); 104 (38.0%) | 10-7 | 36 (53.7%); 88 (35.2%) | 10-2 |
| Hand2 | 12 (17.9%); 8 (2.9%) | 10-4 | 9 (13.4%); 16 (6.5%) | 10-1 |
| Smad2 | 40 (59.7%); 89 (32.4%) | 10-4 | 23 (34.3%); 69 (27.6%) | 1 |
| Gata6 | 19 (28.4%); 24 (8.8%) | 10-4 | 112 (74.7%); 31 (12.3%) | 10-1 |
| Tcf4 | 11 (16.4%); 9 (3.1%) | 10-3 | 6 (9.0%); 8.9 (3.6%) | 10-1 |
| Smad4 | 36 (53.7%); 83 (30.5%) | 10-3 | 21 (31.3%); 70 (28.1%) | 10 |
| Sox9 | 21 (31.3%); 45 (16.6%) | 10-2 | 14 (20.9%); 24 (9.7%) | 10-1 |
| Tcf3 | 6 (9.0%); 5 (1.8%) | 10-2 | 3 (4.5%); 9 (3.7%) | 10 |
| Tbx20 | 8 (11.9%); 9 (3.2%) | 10-2 | 7 (10.5%); 2.5 (1.0%) | 10-3 |
| Gata4 | 21 (31.3%); 44 (16.3%) | 10-2 | 15 (22.4%); 35 (14.2%) | 10-1 |
| MyoD | 12 (17.9%); 18 (6.7%) | 10-2 | 13 (19.4%); 19 (7.78%) | 10-2 |

Transcription factor binding motif enrichment in 67 genomic regions accessible in E14.5 atrioventricular junctions (AVJ) or E14.5 ventricles. Enrichment was compared to enrichment in a number of random control sequences. Enrichment is depicted as total number of regions with the motif and the percentage of the total number of tested regions. P-values depict statistical significance of enrichment.

**Supplementary Table 2.** Transcription factor binding motif enrichment in active STARR-regions

**A**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Motif enrichment (mouse)** | | |  |
| **Motif name** | **SG4 (216) vs Ctrl (837)** | **P-value** | **Wnt (257) vs Ctrl (987)** | **P-value** |
| Smad3 | 168 (77.8%); 481 (57.4%) | 10-7 | 190 (75.1%); 551 (55.9%) | 10-8 |
| Smad4 | 141 (65.3%); 354 (42.3%) | 10-8 | 152 (60.1%); 369 (37,4%) | 10-10 |
| Smad2 | 128 (59.3%); 358 (42.8%) | 10-4 | 138 (54.6%); 381 (38.6%) | 10-5 |
| Tbox:Smad | 22 (10.2%); 30 (3.5%) | 10-3 | 21 (8.3%); 60 (6.1%) | 1 |
| Gata6 | 94 (43.5%); 328 (39.2%) | 1 | 10 (3.9%); 64 (6.5%) | 1 |
| Gata4 | 71 (32.3%); 244 (29.2%) | 1 | 82 (32.4%); 292 (29.6%) | 1 |
|  |  |  |  |  |
| Tcf4 | 50 (23.1%); 101 (12.1%) | 10-4 | 51 (20.1%); 90 (9.1%) | 10-5 |
| Tcf3 | 24 (11.1%); 61 (7.3%) | 10-1 | 31 (12.2%); 53 (5.4%) | 10-3 |
| Tcf12 | 70 (32.4%); 118 (41.1%) | 10-8 | 112 (44.3%); 131 (13.3%) | 10-24 |
| Tcf21 | 74 (34.3%); 130 (15.5%) | 10-1 | 115 (45.5%); 147 (14.8%) | 10-22 |

**B**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Motif enrichment (human)** | | | |
| **Motif name** | **SG4 (216) vs Ctrl (537)** | **P-value** | **Wnt (257) vs Ctrl (591)** | **P-value** |
| Smad3 | 112 (74.7%); 278 (51.8%) | 10-6 | 104 (69.3%); 1276 (46.8%) | 10-6 |
| Smad4 | 79 (52.7%); 197 (36.7%) | 10-3 | 71 (47.3%); 160 (27.1%) | 10-5 |
| Smad2 | 84 (56.0%); 196 (36.5%) | 10-4 | 74 (49.3%); 168 (28.5%) | 10-5 |
| Tbox:Smad | 15 (10.0%); 12 (2.3%) | 10-4 | 10 (6.7%); 18 (3.0%) | 10-1 |
| Gata6 | 75 (50.0%); 197 (36.7%) | 10-2 | 59 (39.3%); 209 (35.3%) | 1 |
| Gata4 | 80 (53.3%); 218 (40.1%) | 10-2 | 65 (43.3%); 236 (40.0%) | 1 |
|  |  |  |  |  |
| Tcf4 | 39 (26.0%); 79 (14.8%) | 10-2 | 40 (26.7%); 67 (11.4%) | 10-5 |
| Tcf3 | 22 (14.7%); 45 (8.3%) | 10-1 | 27 (18.0%); 35 (6.0%) | 10-4 |
| Tcf12 | 41 (27.3%); 59 (11.0%) | 10-5 | 58 (38.7%); 51 (8.6%) | 10-16 |
| Tcf21 | 48 (32.0%); 72 (13.4%) | 10-6 | 57 (38.0%); 75 (12.8%) | 10-10 |

Transcription factor binding motif enrichment in genomic regions within both mouse (A) and human (B) *TBX3* locus that respond to Smad/Gata (SG4) or Tcf (Wnt) factors as demonstrated by STARR-seq. Enrichment of binding motifs for Smad/Gata- and Tcf-factors is depicted. Enrichment was compared to enrichment in a number of random control sequences. Enrichment is depicted as total number of regions with the motif and the percentage of the total number of tested regions. P-values depict statistical significance of enrichment.

**Supplementary Table 3.** Murine RE candidates within VR1 and VR2.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **ATAC** |  |  | ***m*STARR** | |  | **ChIP** | | |
|  | **AVJ** | **EMERGE** |  | **SG4** | **Wnt** |  | **Gata4** | **Hand2** | **H3K27ac** |
| mRE1 | + |  |  |  |  |  |  |  |  |
| mRE2 | + | + |  |  |  |  | +/- |  | + |
| mRE3 | + |  |  |  |  |  |  |  | + |
| mRE4 | + |  |  | + | + |  |  |  | +/- |
| mRE5 | + |  |  | + |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |
| mRE6 | + | + |  | + |  |  | +/- | + | + |
| mRE7 | + |  |  |  |  |  |  |  |  |
| mRE8 | + | + |  | + | + |  | + |  |  |
| mRE9 |  | + |  |  |  |  | +/- |  |  |
| mRE10 | + |  |  |  |  |  |  |  |  |
| mRE11 | + | + |  | + |  |  | + | + |  |

Murine RE candidates selected based on accessible chromatin in AV junction cardiomyocytes (ATAC\_AVJ), EMERGE prediction, or mSTARR\_SG4/Wnt activity. Overlap is depicted of candidate regions with ChIP-seq peaks from publicly available datasets for Gata4 (differentiated cardiomyocytes) (Luna-Zurita et al., 2016), Hand2 (E10.5 heart) (Laurent et al., 2017) and H3K27ac (E11.5 heart) (Nord et al., 2013).

**Supplementary Table 4.** Human RE candidates within VR1 and VR2.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | ***m*RE** |  | **hSTARR** | |  |  |  |  |
|  | **RE** | **Liftover** | **EMERGE** | **SG4** | **Wnt** | **SNP** | **trait** | **p-value** |  |
|  | *h*RE3 | *m*RE2 | + |  |  | rs12314403 | PR | 1.7x10-31 |  |
|  | *h*RE4 |  |  |  | + |  |  |  |  |
|  | *h*RE5 | *m*RE3 |  |  | + | rs7310299 | PR | 4.7x10-2 |  |
|  | *h*RE6 | *m*RE4 |  |  |  | rs10744836 | PR;QRS | 5.0x10-27;2.3x10-11 |  |
|  | *h*RE7 | *m*RE5 |  |  |  | rs1896329 | PR;QRS | 7.4x10-28;3.1x10-10 |  |
|  |  |  |  |  |  | rs2114669 | PR | 2.9x10-2 |  |
|  |  |  |  |  |  | rs2384552 | PR;QRS | 2.1x10-23;4.4x10-9 |  |
|  | *h*RE8 |  |  | + |  | rs6489991 | PR | 7.5x10-6 |  |
|  |  |  |  |  |  | rs1991391 | PR | 4.4x10-7 |  |
|  |  |  |  |  |  | rs2384550 | PR | 4.1x10-7 |  |
|  |  |  |  |  |  | rs6489992 | PR | 6.7x10-6 |  |
|  | *h*RE9 |  |  |  | + | rs1896312 | PR;QRS | 1.2x10-34;5.0x10-11 |  |
|  |  |  |  |  |  | rs1863707 | PR | 1.4x10-11 |  |
|  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |
|  | *h*RE10 | *m*RE6 |  |  |  |  |  |  |  |
|  | *h*RE11 | *m*RE7 |  |  |  | rs2062717 | PR | 5.3x10-11 |  |
|  | *h*RE12 |  |  | + |  |  |  |  |  |
|  | *h*RE13 |  |  |  | + | rs7314370 | PR | 1.5x10-3 |  |
|  | *h*RE14 | *m*RE8 | + |  |  | rs11067264 | PR | r2 0.82 w/ rs11067251; rs6488974 |  |
|  | *h*RE15 | *m*RE9 |  |  |  | rs11067258 | PR | 4.4x10-3 |  |
|  |  |  |  |  |  | rs2062712 | PR | 4.2x10-2 |  |
|  | *h*RE16 |  |  |  | + | rs11067251 | PR | 3.2x10-17 |  |
|  |  |  |  |  |  | rs12322585 | PR | 9.2x10-4 |  |
|  |  |  |  |  |  | rs12297161 | PR | 7.0x10-4 |  |
|  |  |  |  |  |  | rs2384479 | PR | 3.3x10-16 |  |
|  |  |  |  |  |  | rs7316851 | PR | 1.4x10-3 |  |
|  |  |  |  |  |  | rs6489974 | PR | 4.5x10-17 |  |
|  |  |  |  |  |  | rs16944593 | PR | 6.9x10-2 |  |
|  |  |  |  |  |  | rs6489975 | PR | 7.2x10-2 |  |
|  | *h*RE17 | *m*RE10 |  |  |  |  |  |  |  |
|  | *h*RE18 | *m*RE11 | + | + | + | rs35789998 |  | r2 0.52 w/ rs11067251 |  |
|  |  |  |  |  |  | rs1354155 |  | r2 0.53 w/ rs11067251 |  |
|  |  |  |  |  |  | rs61931165 |  | r2 0.53 w/ rs11067251 |  |
|  | *h*RE19 |  |  |  | + |  |  |  |  |
|  | *h*RE20 |  |  | + |  |  |  |  |  |
|  | *h*RE21 |  |  | + |  |  |  |  |  |
|  | *h*RE22 |  |  | + |  |  |  |  |  |
|  |  |  |  |  |  |  | |  |  |

Human RE candidates selected based on mouse RE homology (mm9 liftover), EMERGE prediction, or hSTARR\_SG4/Wnt activity. Regions overlapping GWAS SNPs (SNP id, trait association and respective p-value are listed) were selected for further analysis.

**Supplementary Table 5.** TALEN/CRISPR target sequences for deletion of VR1 and VR2 from the murine genome.

|  |  |
| --- | --- |
| **Target site** | **Target sequence** |
| TALEN\_VR1\_1 | TTCTCAGGGGCCTTTCAAagaagaaagcttcgcAGCCCAGCTTCATCCAGAA | |
| TAL1 RVD sequence | NG-HD-NG-HD-NI-NH-NH-NH-NH-HD-HD-NG-NG-NG-HD-NI-NI | |
| TAL2 RVD sequence | NG-HD-NG-NH-NH-NI-NG-NH-NI-NI-NH-HD-NG-NH-NH-NH-HD-NG | |
|  |  | |
| TALEN\_VR1\_2 | TGTGGGAGAACCCTGCCccctctgcagaagcaGCTGGAGCCTTCTGCATGGA | |
| TALEN\_VR1\_2\_RVD sequence TAL1 | NH-NG-NH-NH-NH-NI-NH-NI-NI-HD-HD-HD-NG-NH-HD-HD | |
| TALEN\_VR1\_2\_RVD sequence TAL2 | HD-HD-NI-NG-NH-HD-NI-NH-NI-NI-NH-NH-HD-NG-HD-HD-NI-NH-HD | |
|  |  |
|  |  |
| **Target site** | **Target sequence** |
| CRISPR\_VR2\_1 | GGCTTTGAAGAAGAGTATCA |
| sgRNA oligonucleotide sequence 1 | TAGGCTTTGAAGAAGAGTATCA |
| sgRNA oligonucleotide sequence 2 | AAACTGATACTCTTCTTCAAAG |
|  |  |
| CRISPR\_VR2\_2 | GGGTTTCTCCTGGAGGGTCG |
| sgRNA oligonucleotide sequence 1 | TAGGGTTTCTCCTGGAGGGTCG |
| sgRNA oligonucleotide sequence 2 | AAACCGACCCTCCAGGAGAAAC |

**Supplementary Table 6.** qPCR primer sequences.

|  |  |
| --- | --- |
| **Primer** | **Primer sequence (5'--3')** |
| Tbx3\_F | GTCTCAGGCCTAGAATCCAC |
| Tbx3\_R | GCCATGTATGTGTAGGGGTA |
| Tbx2\_F | CGCAGGCGGGCTAGGTC |
| Tbx2\_R | AAGAGGCCTCCGAAAGTGGG |
| Tbx5\_F | CCCGGAGACAGCTTTTATCG |
| Tbx5\_F | TGGTTGGAGGTGACTTTGTG |
| Med13l\_F | CACGGAGTTTAGGATGGAAGTGG |
| Med13l\_R | AAGGCTGGAACTGCGGCACTTT |
| Rbm19\_F | TACGGAACCTGTCCTACACCAG |
| Rbm19\_R | AGGTGACGAAGGCAAAGCCCTT |
| Isl1\_F | GCAACCCAACGACAAAACTAA |
| Isl1\_R | CCATCATGTCTCTCCGGACT |
| Eef2\_F | TGGAGCCTATCTATCTGGTGG |
| Eef2\_R | GTCTCAGCTACCACTTGGCT |
| Scn5a\_F | GGGACTCATTGCCTACATGA |
| Scn5a\_R | GCACTGGGAGGTTATCACTG |
| Cacna1g\_F | GAAGGTGTCAATAGCCCTGA |
| Cacna1g\_R | GACACCAGACTTCCTCACAG |
| Hcn4\_F | GCGTGCTCACTAAGGGCAAC |
| Hcn4\_R | GGCAATAAGTATCCGCTCTGAC |
| Gja5\_F | GCCTGAAGAAGCCAACTCCAGG |
| Gja5\_R | GCTTGTGGACCTCCTCCAGG |
| Gja1\_F | AGTACCCAACAGCAGCAGAC |
| Gja1\_R | AAAATGAAGAGCACCGACAG |
| Ryr2\_F | CAAATCCTTCTGCTGCCAAG |
| Ryr2\_R | CGAGGATGAGATCCAGTTCC |

**Supplementary Table 7.** Overview of BACs used for the generation of STARR-seq libraries

|  |  |  |
| --- | --- | --- |
| **Murine BACs** |  |  |
| **BAC name** | **Size [bp]** | **Genomic coordinates [mm9]** |
| RP23-27G24 | 237655 | chr5:120519399-120745441 |
| RP23-183L13 | 212708 | chr5:120318246-120519341 |
| RP23-376N10 | 152322 | chr5:120182858-120323567 |
| RP23-366H17 | 171534 | chr5:120038644-120198565 |
| RP23-459M16 | 181931 | chr5:119874765-120045083 |
| RP24-250N7 | 151066 | chr5:119741090-119878692 |
| RP23-308O19 | 206616 | chr5:119565148-119760151 |
| RP24-371D5 | 208802 | chr5:119387623-119582961 |
| RP23-296H19 | 209394 | chr5:119203312-119401093 |
| RP23-34B9 | 207424 | chr5:119035452-119231263 |
| RP23-335A14 | 227475 | chr5:118828656-119044518 |
|  |  |  |
| **Human BACs** |  |  |
| **BAC name** | **Size [bp]** | **Genomic coordinates [hg19]** |
| RP11-597C16 | 168854 | chr12:116697763-116866617 |
| RP11-379F8 | 167988 | chr12:116533799-116701787 |
| RP11-1130I19 | 141901 | chr12:116391900-116533801 |
| RP11-412G23 | 169878 | chr12:116224958-116394836 |
| RP11-36E12 | 149382 | chr12:116075502-116224884 |
| RP11-346N22 | 162603 | chr12:115966759-116129362 |
| RP11-809J20 | 180445 | chr12:115786239-115966684 |
| RP11-42O13 | 155240 | chr12:115640724-115795964 |
| RP11-992D2 | 185118 | chr12:115458557-115643675 |
| RP11-693B4 | 203971 | chr12:115272432-115476403 |
| RP11-879D18 | 173123 | chr12:115102051-115275174 |
| RP11-125E3 | 165503 | chr12:114956460-115121963 |
| RP11-91M21 | 171499 | chr12:114821528-114993027 |
| RP11-333I15 | 170736 | chr12:114694877-114865613 |
| RP11-100F15 | 185941 | chr12:114546237-114732178 |
| RP11-269C10 | 200600 | chr12:114351967-114552567 |
| RP11-37N9 | 177697 | chr12:114166377-114344074 |

**Supplementary Table 8.** Primer sequences for the amplification of active STARR-seq regions for validation by luciferase reporter assay.

|  |  |
| --- | --- |
| **Primer name** | **Primer sequence (5'--3')** |
| mSTARR\_validation\_1\_F | ACAACAATCTTAGTGCCAGCAA |
| mSTARR\_validation\_1\_R | GCGTCAATCATGGCTTCTCAAC |
| mSTARR\_validation\_2\_F | GCTCACCACAGCCTGTTCA |
| mSTARR\_validation\_2\_R | ATCCTAGCTCAGACTGTCTTCA |
| mSTARR\_validation\_3\_F | CCCTGAGTGTTAGGAGAGTTGT |
| mSTARR\_validation\_3\_R | AATTCACCATGGAGTCAGGTTT |
| mSTARR\_validation\_4\_F | GGGAGATCAGAGGACAACCTAC |
| mSTARR\_validation\_4\_R | TTCCGTGACCCAAAGTTCTCTC |
| mSTARR\_validation\_5\_F | CTTTCACTTCCCTGGTCCACTT |
| mSTARR\_validation\_5\_R | TCAGGGCTGGAAGGAGAAGATA |
| mSTARR\_validation\_6\_F | TGGTTCCTGTAGGAGAGGAGAG |
| mSTARR\_validation\_6\_R | TTTGTTTGGCCAGAGAACAACC |
| mSTARR\_validation\_7\_F | TATGTGGGTGCTGGGAATTCAA |
| mSTARR\_validation\_7\_R | AAGGATCCAGTCTCTGGTCTCA |
| mSTARR\_validation\_8\_F | ATCCAGTCCACTGTCTCAGCAA |
| mSTARR\_validation\_8\_R | ACTCTGCCCTTGACAATTCTGT |
| mSTARR\_validation\_9\_F | GGGTTACAGGTGTGTGTCACTA |
| mSTARR\_validation\_9\_R | TGACTACGGAGTTAGTTCAAGG |
|  |  |
| hSTARR\_validation\_1\_F | CACAACAGAAAGGAAGCTCACA |
| hSTARR\_validation\_1\_R | GCAGAGGCATAATGAACAGGTA |
| hSTARR\_validation\_2\_F | GCATCTGTGTTCATCAAGGATAT |
| hSTARR\_validation\_2\_R | CATGACCTTGCTCTTGACTGCT |
| hSTARR\_validation\_3\_F | GCAGCAACCCATCCCAAAAC |
| hSTARR\_validation\_3\_R | GGACCAGCCGTTTCTCTGTTA |
| hSTARR\_validation\_4\_F | GGGGTAGCAGAGTGATGGAA |
| hSTARR\_validation\_4\_R | CCCGCCCTGAATTTGACTTTTC |
| hSTARR\_validation\_5\_F | TGACAACTTCACCTCTCTGCTT |
| hSTARR\_validation\_5\_R | GCCCTCTACCAACTCGCATT |
| hSTARR\_validation\_6\_F | ACCACTCCATCCCTGCTAAC |
| hSTARR\_validation\_6\_R | GCATGGACAAAGGACAGGGAA |
| hSTARR\_validation\_7\_F | AACAGGCAGACCCTCATCAA |
| hSTARR\_validation\_7\_R | GCTCACAAGGTGGATCCCAA |
| hSTARR\_validation\_8\_F | TTCTCTCGGAGAAGCCAGGTT |
| hSTARR\_validation\_8\_R | TTGAGCCAATGCTCCAACTCA |
| hSTARR\_validation\_9\_F | TGTAAGCATGTGCCTAGTTAGTA |
| hSTARR\_validation\_9\_R | AGACTGGGATTGAGGACATGC |
| hSTARR\_validation\_10\_F | GACAAGGCCGATGGATGCTT |
| hSTARR\_validation\_10\_R | GCATCTGACAACCTCAGAACC |

**Supplementary Table 8,** continued

|  |  |
| --- | --- |
| **Primer name** | **Primer sequence (5’—3’)** |
| mSTARR\_validation\_neg1\_F | AATCCTTCCAGCTTCCTTCCTG |
| mSTARR\_validation\_neg1\_R | TATTGGAAAGAACGCCTGTGGA |
| mSTARR\_validation\_neg2\_F | GAGCCCAGATGTTAAACCCTCA |
| mSTARR\_validation\_neg2\_R | GGGTTCAGAAGGTAGATTGGCA |
| mSTARR\_validation\_neg3\_F | GGATGTCAGTGAGGTGGGATTT |
| mSTARR\_validation\_neg3\_R | TTAGAGGGTGGAGACAGGGTAG |
| mSTARR\_validation\_neg4\_F | GAGCTTTCTCCCAACCCACATA |
| mSTARR\_validation\_neg4\_R | AATGTGGACAGGATGAGGTCAC |
| mSTARR\_validation\_neg5\_F | GCTGTCTTCAGACACTCCAGAA |
| mSTARR\_validation\_neg5\_R | ACTGCTGAGTCACACCTACAAG |
| hSTARR\_validation\_neg1\_F | CACCCTCTTGGATGGATTGTGA |
| hSTARR\_validation\_neg1\_R | ACCTTACCCAAGATGTGCCAAT |
| hSTARR\_validation\_neg2\_F | CAGGTGGAAAGGGCTCAGTAAT |
| hSTARR\_validation\_neg2\_R | GGAGTTTGGCTCCATCAGGTAA |
| hSTARR\_validation\_neg3\_F | ATAAGGAAGGGCACAAGACTGG |
| hSTARR\_validation\_neg3\_R | ATGGACAAATGGAAGGCTGGAT |
| hSTARR\_validation\_neg4\_F | TCTTGCTAAATCACTCGGCTGT |
| hSTARR\_validation\_neg4\_R | TGCCTGTTACCTGTCATTCTCC |
| hSTARR\_validation\_neg5\_F | CTGGGCTGACTCTGAGACATTT |
| hSTARR\_validation\_neg5\_R | AGGGTAGCATGCCAATTCTTCA |

**Supplementary Table 9.** Primer sequences for the amplification of RE candidate fragments.

|  |  |
| --- | --- |
| **Primer name** | **Primer sequence (5'--3')** |
| *h*RE3\_F | AATGGGCTCCTGTCAATATCC |
| *h*RE3\_R | GAAGGACCAAGCCTGGATGT |
| *h*RE5\_F | AAGCTGCAAGTCAAAAGGCATC |
| *h*RE5\_R | CTGGCATTGCTACCTAACATC |
| *h*RE6\_F | TACGGGACAGACCTGACATC |
| *h*RE6\_R | AAATCCCAGAGGCCAAAGGC |
| *h*RE7\_F | GAGTTGGAGGCAACTTTGAAG |
| *h*RE7\_R | AATCACAGAGGGCAGAGGTC |
| *h*RE8\_F | CTCCACTTAGACTCAAATCCTG |
| *h*RE8\_R | GTTGGCTCACATTGTAGAGTG |
| *h*RE9\_F | CTTCTTCCAATGCCCTTTTGC |
| *h*RE9\_R | CAACTGTTTTGTGGCATTGAGC |
| *h*RE11\_F | CCTTCCCAAGACTTCTAATGTG |
| *h*RE11\_R | GGAGAAGGGGAAAGAGAGTG |
| *h*RE13\_F | GCTGAAGATGGAGTGCAATAG |
| *h*RE13\_R | CCAACATCTCAGGCCTTCTC |
| *h*RE15\_F | GTGCCTGACATCAAATACTTGG |
| *h*RE15\_R | TGGACATGGCTGAAGAAACCA |
| *h*RE16\_F | CCACTCAACTGTAATGGCTTC |
| *h*RE16\_R | TATGTTACCCAGGCATAGTGAG |
| *h*RE19\_F | GAGATGGAGAAGACCTGGAC |
| *h*RE19\_R | CGGCTTGGATCTGCATAGAC |
| *h*RE14\_F | CCAGGGTACCCAGCTTATAG |
| *h*RE14\_R | CCTGGCTAGATGTTAAAAGCTA |
| *h*RE18\_F | GGCAGATTGTCCGAGGTTAG |
| *h*RE18\_R | AGAGAGGTTCTCATTCATTAGG |

**Supplementary Table 10.** Mouse functional genomic datasets included in merge as possible predictors.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Dataset** | **Type** | **Genome** | **Tissue** | **Overall** | **Stage** | **Source** | **Deposit** | **# of Peaks** |
| Conservation | PhastCons | mm9 | all | all | all | Siepel lab | UCSC | 972010 |
| DHSs | Dnase1 hypersensitivity | mm9 | whole\_brain | brain | E18.5 | ENCODE | GSE37074 | 143557 |
| H3K27ac | ChIP‐seq | mm9 | whole\_brain | brain | E14.5 | ENCODE | GSE49847 | 34012 |
| H3K4me1 | ChIP‐seq | mm9 | whole\_brain | brain | E14.5 | ENCODE | GSE49847 | 152915 |
| H3K4me3 | ChIP‐seq | mm9 | whole\_brain | brain | E14.5 | ENCODE | GSE49847 | 36227 |
| Pol2 | ChIP‐seq | mm9 | whole\_brain | brain | E14.5 | ENCODE | GSE49847 | 17146 |
| Smarca4 | ChIP‐seq | mm9 | forebraim | brain | E11.5 | Pennacchio lab | GSE37151 | 7349 |
| ATAC | ATAC‐seq | mm9 | Ventricle | heart | E12.5 | Christoffels lab | in house | 84667 |
| ATAC | ATAC‐seq | mm9 | right arium | heart | E12.5 | Christoffels lab | in house | 129996 |
| ATAC | ATAC‐seq | mm9 | left atrium | heart | E12.5 | Christoffels lab | in house | 125461 |
| ATAC | ATAC‐seq | mm9 | HL‐1 cells | heart | no stimulation 20k | Christoffels lab | in house | 110206 |
| ATAC | ATAC‐seq | mm9 | HL‐1 cells | heart | no stimulation 50k | Christoffels lab | in house | 150324 |
| ATAC | ATAC‐seq | mm9 | HL‐1 cells | heart | Bmp2 stim 20k | Christoffels lab | in house | 150279 |
| ATAC | ATAC‐seq | mm9 | HL‐1 cells | heart | Bmp2 stim 50k | Christoffels lab | in house | 130868 |
| ATAC | ATAC‐seq | mm9 | atria | heart | Embryonic | Moskowitz | unpublished | 18213 |
| ATAC | ATAC‐seq | mm9 | pSHF | heart | Embryonic | Moskowitz | unpublished | 21318 |
| ATAC | ATAC‐seq | mm9 | ventricles | heart | Embryonic | Moskowitz | unpublished | 33418 |
| Coup‐TFII | ChIP‐seq | mm9 | atria | heart | E14.5 | Tsai lab | GSE46497 | 4359 |
| DHSs | Dnase1 hypersensitivity | mm9 | heart | heart | adult | ENCODE | GSE37074 | 150000 |
| Gata4 | ChIP‐seq | mm9 | heart | heart | adult | Christoffels lab | GSE35151 | 150493 |
| Gata4 | ChIP‐seq | mm9 | heart | heart | E12.5 | Pu lab | GSE52123 | 150033 |
| Gata4 | ChIP‐seq | mm9 | heart | heart | adult | Pu lab | GSE52123 | 150054 |
| Gata4 | ChIP‐exo | mm9 | myocyte cell line | heart | differentiated | Bruneau lab | GSE77548 | 25710 |
| Gata4 | ChIP‐exo | mm9 | myocyte cell line | heart | cardiac\_precursor | Bruneau lab | GSE77548 | 52999 |
| H3ac | ChIP‐seq | mm9 | left ventric~~ | heart | adult | Baker lab | GSE63590 | 150201 |
| H3K27ac | ChIP‐seq | mm9 | avc | heart | E10.5 | Christoffels lab | GSE55611 | 87572 |
| H3K27ac | ChIP‐seq | mm9 | right atrium | heart | E10.5 | Christoffels lab | GSE55611 | 67092 |
| H3K27ac | ChIP‐seq | mm9 | heart | heart | adult | ENCODE | GSE49847 | 53034 |
| H3K27ac | ChIP‐seq | mm9 | heart | heart | E14.5 | ENCODE | GSE49847 | 84442 |
| H3K27ac | ChIP‐seq | mm9 | heart | heart | adult | Pennacchio lab | GSE52386 | 150515 |
| H3K27ac | ChIP‐seq | mm9 | heart | heart | E11.5 | Pennacchio lab | GSE52386 | 32289 |
| H3K27ac | ChIP‐seq | mm9 | heart | heart | E14.5 | Pennacchio lab | GSE52386 | 31815 |
| H3K27ac | ChIP‐seq | mm9 | heart | heart | E17.5 | Pennacchio lab | GSE52386 | 23210 |
| H3K27ac | ChIP‐seq | mm9 | heart | heart | P0 | Pennacchio lab | GSE52386 | 39133 |
| H3K27ac | ChIP‐seq | mm9 | heart | heart | P7 | Pennacchio lab | GSE52386 | 36447 |
| H3K27ac | ChIP‐seq | mm9 | heart | heart | P21 | Pennacchio lab | GSE52386 | 7376 |
| H3K27me3 | ChIP‐seq | mm9 | heart | heart | adult | ENCODE | GSE49847 | 21876 |
| H3K4me1 | ChIP‐seq | mm9 | heart | heart | adult | ENCODE | GSE49847 | 150914 |
| H3K4me3 | ChIP‐seq | mm9 | heart | heart | adult | ENCODE | GSE49847 | 53034 |
| Hand2 (rep1) | ChIP‐seq | mm9 | heart | heart | adult | Zeller lab | confidential? | 150002 |
| Hand2 (rep2) | ChIP‐seq | mm9 | heart | heart | adult | Zeller lab | confidential? | 20446 |
| Hif1a rep1 | ChIP‐seq | mm9 | heart | heart | E12.5 | Keck institute | GSE61247 | 17289 |
| Hopx | ChIP‐seq | mm9 | heart | heart | E9.5 | Won lab | GSE67251 | 3774 |
| Hopx with EGS | ChIP‐seq | mm9 | heart | heart | E9.5 | Won lab | GSE67251 | 178 |
| Isl1 | ChIP‐seq | mm9 | sinus node | heart | p3 | Evans lab | GSE68974 | 2322 |
| Mef2a | ChIP‐exo | mm9 | C2C12 cell line | heart | myoblast | McDermott lab | GSE61204 | 2796 |
| Nkx2‐5 | ChIP‐seq | mm9 | heart | heart | adult | Christoffels lab | GSE35151 | 150227 |
| Nkx2‐5 | ChIP‐seq | mm9 | heart | heart | E12.5 | Chen lab | GSE70332 | 3967 |
| Nkx2‐5 | ChIP‐exo | mm9 | myocyte cell line | heart | differentiated | Bruneau lab | GSE77548 | 62218 |
| Nkx2‐5 | ChIP‐exo | mm9 | myocyte cell line | heart | cardiac\_precursor | Bruneau lab | GSE77548 | 9463 |
| p300 (rep1) | ChIP‐seq | mm9 | heart | heart | adult | ENCODE | GSE49847 | 137325 |
| p300 (rep2) | ChIP‐seq | mm9 | heart | heart | adult | ENCODE | GSE49847 | 116158 |
| Pol2 | ChIP‐seq | mm9 | heart | heart | adult | ENCODE | GSE49847 | 58637 |
| RBFox2 | ChIP‐seq | mm9 | heart | heart | 9w | Palade lab | GSE57926 | 151144 |
| Shox2 | ChIP‐seq | mm9 | heart | heart | E12.5 | Chen lab | GSE70332 | x |
| Smarca4 | ChIP‐seq | mm9 | heart | heart | E11.5 | Pennacchio lab | GSE37151 | 13775 |
| SOX9 | ChIP‐seq | mm9 | AVC~~ | heart | E12.5 | Fox lab | GSE73225 | x |
| ß‐catenin biotin | ChIP‐seq | mm9 | mESC | heart | blastocyst | McMahon lab | GSE43565 | 20408 |
| ß‐catenin flag | ChIP‐seq | mm9 | mESC | heart | blastocyst | McMahon lab | GSE43565 | 20294 |
| Suz12 | ChIP‐seq | mm9 | heart | heart | 9w | Palade lab | GSE57926 | 22476 |
| Tbx20 | ChIP‐seq | mm9 | heart | heart | adult | Evans lab | GSE30943 | 4011 |
| TBX3 | ChIP‐seq | mm9 | heart | heart | adult | Christoffels lab | GSE44821 | 150859 |
| Tbx5 | ChIP‐seq | mm9 | HL‐1 cells | heart | cell line | Pu lab | GSE21529 | 48221 |
| Tbx5 | ChIP‐exo | mm9 | myocyte cell line~ | heart | differentiated | Bruneau lab | GSE77548 | 45540 |
| Tbx5 | ChIP‐exo | mm9 | myocyte cell line~ | heart | cardiac\_precursor | Bruneau lab | GSE77548 | 8587 |
| Tcf3 | ChIP‐seq | mm9 | mESC | heart | blastocyst | Whitehead Inst. | GSE11724 | 7336 |
| Smarca4 | ChIP‐seq | mm9 | limb | limb | E11.5 | Pennacchio lab | GSE37151 | 5251 |
| SOX9 | ChIP‐seq | mm9 | Limb | limb | E12.5 | Fox lab | GSE73225 | 151213 |
| ATAC | ATAC‐seq | mm9 | liver | liver | E12.5 | Christoffels lab | in house | 70760 |
| Hey2 | ChIP‐seq | mm9 | mESC | stem cell | blastocyst | Gessler | TBA | 99750 |
| H3K27ac | ChIP‐seq | mm9 | forebrain | brain | adult | Pennacchio lab | GSE52386 | 33178 |
| H3K27ac | ChIP‐seq | mm9 | forebrain | brain | E11.5 | Pennacchio lab | GSE52386 | 15823 |
| H3K27ac | ChIP‐seq | mm9 | forebrain | brain | E14.5 | Pennacchio lab | GSE52386 | 27288 |
| H3K27ac | ChIP‐seq | mm9 | forebrain | brain | E17.5 | Pennacchio lab | GSE52386 | 20450 |
| H3K27ac | ChIP‐seq | mm9 | forebrain | brain | P0 | Pennacchio lab | GSE52386 | 30308 |
| H3K27ac | ChIP‐seq | mm9 | forebrain | brain | P7 | Pennacchio lab | GSE52386 | 36771 |
| H3K27ac | ChIP‐seq | mm9 | forebrain | brain | P21 | Pennacchio lab | GSE52386 | 15246 |
| H3K27ac | ChIP‐seq | mm9 | forelimb | limb | E11.5 | Menke lab | GSE64055 | 40303 |
| H3K27ac | ChIP‐seq | mm9 | hindlimb | limb | E11.5 | Menke lab | GSE64055 | 35166 |
| Pol2 | ChIP‐seq | mm9 | limb | limb | E14.5 | ENCODE | GSE49847 | 14426 |
| H3K4me1 | ChIP‐seq | mm9 | limb | limb | E14.5 | ENCODE | GSE49847 | 150360 |
| H3K4me3 | ChIP‐seq | mm9 | limb | limb | E14.5 | ENCODE | GSE49847 | 19259 |
| H3K27ac | ChIP‐seq | mm9 | limb | limb | E14.5 | ENCODE | GSE49848 | 30543 |
| DHSs | Dnase1 hypersensitivity | mm9 | forelimb | limb | E11.5 | ENCODE | GSE37074 | 151669 |
| DHSs | Dnase1 hypersensitivity | mm9 | hindlimb | limb | E11.5 | ENCODE | GSE37074 | 150814 |
| H3K27ac | ChIP‐seq | mm9 | forebrain | brain | E12.5 | Rockowitz | GSE66961 | 26863 |
| H3K4me1 | ChIP‐seq | mm9 | forebrain | brain | E12.5 | Rockowitz | GSE66961 | 40773 |
| H3K4me3 | ChIP‐seq | mm9 | forebrain | brain | E12.5 | Rockowitz | GSE66961 | 15407 |

**Supplementary Table 10,** continued.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Dataset** | **Type** | **Genome** | **Tissue** | **Overall** | **Stage** | **Source** | **Deposit** | **# of peaks** |
| H3K27me3 | ChIP‐seq | mm9 | forebrain | brain | E12.5 | Rockowitz | GSE66961 | 25473 |
| Pol2 | ChIP‐seq | mm9 | forebrain | brain | E12.5 | Rockowitz | GSE66961 | 1704 |
| H3K4me1 | ChIP‐seq | mm9 | midbrain | brain | E11.5 | Endo | GSE49652 | 19384 |
| H3K27ac | ChIP‐seq | mm9 | midbrain | brain | E11.5 | Endo | GSE49652 | 22752 |
| p300 | ChIP‐seq | mm9 | midbrain | brain | E11.5 | Pennacchio lab | GSE22549 | 2786 |
| p300 | ChIP‐seq | mm9 | heart | heart | E11.5 | Pennacchio lab | GSE22549 | 3597 |
| p300 | ChIP‐seq | mm9 | forebrain | brain | E11.5 | Pennacchio lab | GSE13845 | 2454 |
| p300 | ChIP‐seq | mm9 | midbrain | brain | E11.5 | Pennacchio lab | GSE13845 | 562 |
| p300 | ChIP‐seq | mm9 | limb | limb | E11.5 | Pennacchio lab | GSE13845 | 2106 |
| DHSs | Dnase1 hypersensitivity | mm9 | cerebellum | brain | P7 | Crawford | GSE60731 | 100000 |
| DHSs | Dnase1 hypersensitivity | mm9 | cerebellum | brain | P14 | Crawford | GSE60731 | 100000 |
| DHSs | Dnase1 hypersensitivity | mm9 | cerebellum | brain | Adult | Crawford | GSE60731 | 100000 |

**Supplementary Table 11.** Human functional genomic datasets included in merge as possible predictors.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Dataset** | **Type** | **Genome** | **Tissue** | **Stage** | **Source** | **Deposit** | **# of Peaks** |
| Conservation | PhastCons | hg19 | all | all | Siepel lab | UCSC | 10121233 (174584)\* |
| CTCF | ChIP‐seq | hg19 | HCM cells | cell line | ENCODE | GSE30263 | 41966 |
| DHSs | Dnase1 hypersensitivity | hg19 | cerebellum | adult | ENCODE | GSE32970 | 104575 |
| DHSs | Dnase1 hypersensitivity | hg19 | cerebrum | adult | ENCODE | GSE32970 | 135930 |
| DHSs | Dnase1 hypersensitivity | hg19 | frontal\_cortex | adult | ENCODE | GSE32970 | 110989 |
| DHSs | Dnase1 hypersensitivity | hg19 | HCM cells | cell line | ENCODE | GSE26328 | 317895 |
| DHSs | Dnase1 hypersensitivity | hg19 | heart | adult | ENCODE | GSE32970 | 124949 |
| H3K27ac | ChIP‐seq | hg19 | brain | fetal 12w post‐gest. | Guo lab | GSE63634 | 77355 |
| H3K27ac | ChIP‐seq | hg19 | cerebellum | adult | Creyghton lab | GSE40465 | 174090 |
| H3K27ac | ChIP‐seq | hg19 | fibroblast cell line | induced myocytes D6 | Cao lab | GSE78096 | 33954 |
| H3K27ac | ChIP‐seq | hg19 | fibroblast cell line | induced myocytes D11 | Cao lab | GSE78096 | 36649 |
| H3K27ac | ChIP‐seq | hg19 | heart | fetal 12w post‐gest. | Guo lab | GSE63634 | 49185 |
| H3K27ac | ChIP‐seq | hg19 | iPSC | induced myocytes | Sakabe lab | GSE77267 | 19528 |
| H3K27ac | ChIP‐seq | hg19 | left ventricle | adult | Ren lab | GSE16256 | 59070 |
| H3K27ac | ChIP‐seq | hg19 | limbs | gest. E33 | Cotney lab | GSE42413 | 72841 |
| H3K27ac | ChIP‐seq | hg19 | limbs | gest. E41 | Cotney lab | GSE42413 | 42284 |
| H3K27ac | ChIP‐seq | hg19 | limbs | gest. E44 | Cotney lab | GSE42413 | 69409 |
| H3K27ac | ChIP‐seq | hg19 | limbs | gest. E47 | Cotney lab | GSE42413 | 54981 |
| H3K27ac | ChIP‐seq | hg19 | liver | fetal 12w post‐gest. | Guo lab | GSE63634 | 27741 |
| H3K27ac | ChIP‐seq | hg19 | right ventricle | adult | Ren lab | GSE16256 | 126802 |
| H3K27me3 | ChIP‐seq | hg19 | brain | fetal 12w post‐gest. | Guo lab | GSE63634 | 50180 |
| H3K27me3 | ChIP‐seq | hg19 | fibroblast cell line | induced myocytes D6 | Cao lab | GSE78096 | 275 |
| H3K27me3 | ChIP‐seq | hg19 | fibroblast cell line | induced myocytes D11 | Cao lab | GSE78096 | 173 |
| H3K27me3 | ChIP‐seq | hg19 | heart | fetal 12w post‐gest. | Guo lab | GSE63634 | 34795 |
| H3K27me3 | ChIP‐seq | hg19 | hESC | induced myocytes 14d | Murry lab | SRR577565 | 86945 |
| H3K27me3 | ChIP‐seq | hg19 | iPSC | induced myocytes | Sakabe lab | GSE77267 | 8952 |
| H3K27me3 | ChIP‐seq | hg19 | liver | fetal 12w post‐gest. | Guo lab | GSE63634 | 41712 |
| H3K36me3 | ChIP‐seq | hg19 | hESC | induced myocytes 14d | Murry lab | SRR577574 | 118126 |
| H3K4me1 | ChIP‐seq | hg19 | brain | fetal 12w post‐gest. | Guo lab | GSE63634 | 58426 |
| H3K4me1 | ChIP‐seq | hg19 | heart | fetal (d105) | BROAD institute | GSE17312 | 113536 |
| H3K4me1 | ChIP‐seq | hg19 | heart | fetal 12w post‐gest. | Guo lab | GSE63634 | 59026 |
| H3K4me1 | ChIP‐seq | hg19 | iPSC | induced myocytes | Sakabe lab | GSE77267 | 13902 |
| H3K4me1 | ChIP‐seq | hg19 | liver | fetal 12w post‐gest. | Guo lab | GSE63634 | 43426 |
| H3K4me3 | ChIP‐seq | hg19 | brain | fetal 12w post‐gest. | Guo lab | GSE63634 | 16745 |
| H3K4me3 | ChIP‐seq | hg19 | fibroblast cell line | induced myocytes D6 | Cao lab | GSE78096 | 18720 |
| H3K4me3 | ChIP‐seq | hg19 | fibroblast cell line | induced myocytes D11 | Cao lab | GSE78096 | 19871 |
| H3K4me3 | ChIP‐seq | hg19 | HCM cells | cell line | ENCODE | GSE35583 | 49247 |
| H3K4me3 | ChIP‐seq | hg19 | heart | fetal (d105) | BROAD institute | GSE17312 | 1238 |
| H3K4me3 | ChIP‐seq | hg19 | heart | fetal 12w post‐gest. | Guo lab | GSE63634 | 86937 |
| H3K4me3 | ChIP‐seq | hg19 | hESC | induced myocytes 14d | Murry lab | SRR577568 | 26960 |
| H3K4me3 | ChIP‐seq | hg19 | iPSC | induced myocytes | Sakabe lab | GSE77267 | 10760 |
| H3K4me3 | ChIP‐seq | hg19 | liver | fetal 12w post‐gest. | Guo lab | GSE63634 | 11799 |
| H3K9ac | ChIP‐seq | hg19 | heart | fetal (d105) | BROAD institute | GSE17312 | 49876 |
| p300 | ChIP‐seq | hg19 | cortex | fetal (gest. week 20) | Pennacchio lab | GSE42881 | 642876 |
| p300 | ChIP‐seq | hg19 | heart | adult | Pennacchio lab | GSE32587 | 139824 |
| p300 | ChIP‐seq | hg19 | heart | fetal (gest. week 16) | Pennacchio lab | GSE32587 | 108384 |
| Pol2 | ChIP‐seq | hg19 | heart | fetal (gest. week 16) | Pennacchio lab | GSE32587 | 223086 |
| Pol2 | ChIP‐seq | hg19 | iPSC | induced myocytes | Sakabe lab | GSE77267 | 11332 |
| ATAC | ATAC‐seq | hg19 | SANLPCs | induced SAN myocytes | Protze lab | unpublished | 45389 |
| ATAC | ATAC‐seq | hg19 | hESC | 0d H1 differentiated myocytes | Snyder lab | GSE85330 | 54378 |
| ATAC | ATAC‐seq | hg19 | hESC | 2d H1 differentiated myocytes | Snyder lab | GSE85330 | 21979 |
| ATAC | ATAC‐seq | hg19 | hESC | 4d H1 differentiated myocytes | Snyder lab | GSE85330 | 28991 |
| ATAC | ATAC‐seq | hg19 | hESC | 30d H1 differentiated myocytes | Snyder lab | GSE85330 | 11931 |
| ATAC | ATAC‐seq | hg19 | hESC | 0d H9 differentiated myocytes | Snyder lab | GSE85330 | 28417 |
| ATAC | ATAC‐seq | hg19 | hESC | 2d H9 differentiated myocytes | Snyder lab | GSE85330 | 10980 |
| ATAC | ATAC‐seq | hg19 | hESC | 4d H9 differentiated myocytes | Snyder lab | GSE85330 | 26580 |
| ATAC | ATAC‐seq | hg19 | hESC | 30d H9 differentiated myocytes | Snyder lab | GSE85330 | 24661 |
| ATAC | ATAC‐seq | hg19 | iPSC | 0d C15 induced myocytes | Snyder lab | GSE85330 | 37100 |
| ATAC | ATAC‐seq | hg19 | iPSC | 2d C15 induced myocytes | Snyder lab | GSE85330 | 35192 |
| ATAC | ATAC‐seq | hg19 | iPSC | 4d C15 induced myocytes | Snyder lab | GSE85330 | 13920 |
| ATAC | ATAC‐seq | hg19 | iPSC | 30d C15 induced myocytes | Snyder lab | GSE85330 | 16191 |
| ATAC | ATAC‐seq | hg19 | iPSC | 0d C20 induced myocytes | Snyder lab | GSE85330 | 27217 |
| ATAC | ATAC‐seq | hg19 | iPSC | 2d C20 induced myocytes | Snyder lab | GSE85330 | 22065 |
| ATAC | ATAC‐seq | hg19 | iPSC | 4d C20 induced myocytes | Snyder lab | GSE85330 | 51994 |
| ATAC | ATAC‐seq | hg19 | iPSC | 30d C20 induced myocytes | Snyder lab | GSE85330 | 19602 |
| ATAC | ATAC‐seq | hg19 | hESC | cardiac mesoderm H7 | Weissman lab | GSE85066 | 180380 |
| ATAC | ATAC‐seq | hg19 | left ventricle | induced LV myocytes | Protze lab | unpublished | 38335 |
| ATAC | ATAC‐seq | hg19 | left atrium | adult | Martin lab | unpublished | 55045 |
| DHSs | Dnase1 hypersensitivity | hg19 | limbs | fetal | ENCODE | GSE90405 | 95652 |
| Med1 | ChIP‐seq | hg19 | iPSC | induced myocytes 32d | Srivastava lab | GSE85631 | 15400 |

\*number of ultra‐conserved phastCons (score≥600)