a.
CHEQ−seq Intron MM001
MITF ChIP−seq
SOX10 ChIP−seq
H3K27ac ChIP−seq
SGCD_15−I
KIT_114−D
MLANA_5−I
SOX10_−56−D
CDH1_49−I
TYR_−9−D
TYR_−1−D
SGCD_26−I
ABCC3_11−I
SERPINE1_−27−D
IRF4_4−I
SERPINE1_−5−D
COL5A1_−39−D
COL5A1_−139−D
SERPINE1_−110−I
SOX10_−35−D
ALPK2_44−I
MITF_P
TYR_P
RRAGD_P
SOX10_−34−D
FLNC_−2−D
FOSL2_−117−I
BLK_−13−D
COL5A1_−17−D
COL5A1_−89−D
COL5A1_−50−D
AXL_4−I
SOX10_15−3U
COL5A1_21−I
ALPK2_49−E
GPR39_207−I
HEG1_16−I
EDN1_P
COL5A1_−4−D
CDH1_24−I
COL1A2_−93−D
SOX10_−3−D
BLK_−19−D
GPR39_23−I
MAP3K14_−2−D
BLK_22−I
BLK_21−I
EDN1_283−D
GPR39_P
SMURF2_−47−D
BDNF_P
FGF2_−44−D
GPM6B_P
Log2 FC
4
2
0
−2
−4
Mean score
0.5
0.4
0.3
0.2
0.1
Mean score
0.15
0.10
0.05
Mean score
2.0
1.5
1.0
0.5

b.
MITF ChIP-seq
SOX10 ChIP-seq
0.08
0.06
0.04
0.02
MES
MEL
-250bp
+250bp
-250bp
+250bp
MES specific H3K27ac ChIP-seq regions
MEL specific H3K27ac ChIP-seq regions
0.25
0.20
0.15
0.10
0.05
0.00
-250bp
+250bp
-250bp
+250bp