

**Supplemental Table S6. Top 25 highly expressed transcription factors in HEMs**

Gene Name (Gene ID)	Average FPKM $\pm$ SEM
<b>Y box binding protein 1 (YBX1)</b>	<b>463.6 <math>\pm</math> 49.3</b>
high mobility group 20B (HMG20B)	210.4 $\pm$ 84.3
activating transcription factor 4 (ATF4)	200.0 $\pm$ 27.6
endothelial differentiation-related factor 1 (EDF1)	176.7 $\pm$ 17.5
<b>SRY (sex determining region Y)-box 10 (SOX10)</b>	<b>171.0 <math>\pm</math> 39.4</b>
<b>microphthalmia-associated transcription factor (MITF)</b>	<b>159.3 <math>\pm</math> 58.4</b>
eukaryotic translation initiation factor 3, subunit K (EIF3K)	154.8 $\pm$ 13.0
prohibitin 2 (PHB2)	141.6 $\pm$ 10.1
upstream transcription factor 2, c-fos interacting (USF2)	140.4 $\pm$ 38.6
transcription factor AP-2 alpha (TFAP2A)	133.0 $\pm$ 41.7
cold shock domain containing E1, RNA-binding (CSDE1)	125.9 $\pm$ 19.2
v-ets avian erythroblastosis virus E26 oncogene homolog 1 (ETS1)	122.7 $\pm$ 14.6
interferon, gamma-inducible protein 16 (IFI16)	117.2 $\pm$ 39.9
plexin C1 (PLXNC1)	114.9 $\pm$ 22.6
nuclear factor, erythroid 2-like 1 (NFE2L1)	106.5 $\pm$ 23.2
H1 histone family, member 0 (H1F0)	103.8 $\pm$ 18.9
snail family zinc finger 2 (SNAI2)	101.2 $\pm$ 24.3
ceramide synthase 2 (CERS2)	98.8 $\pm$ 6.7
sterol regulatory element binding transcription factor 2 (SREBF2)	93.5 $\pm$ 15.5
high mobility group box 1 (HMGB1)	84.2 $\pm$ 32.2
EWS RNA-binding protein 1 (EWSR1)	82.1 $\pm$ 14.5
transcription elongation factor A (SII)-like 8 (TCEAL8)	81.6 $\pm$ 14.5
zinc finger protein 106 (ZFP106)	80.9 $\pm$ 13.2
ets variant 5 (ETV5)	78.0 $\pm$ 11.3
signal transducer and activator of transcription 6 (STAT6)	76.6 $\pm$ 13.8

**Supplemental Table S6. Top 25 highly expressed transcription factor genes in HEMs.** The highest expressed transcription factors in melanocytes were obtained by averaging their FPKM from each library. Transcription factors important for melanocyte function are in bold.