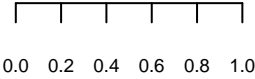
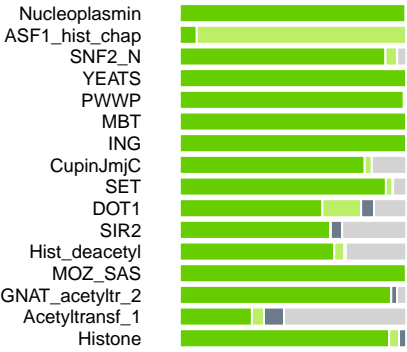
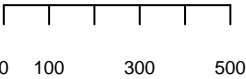
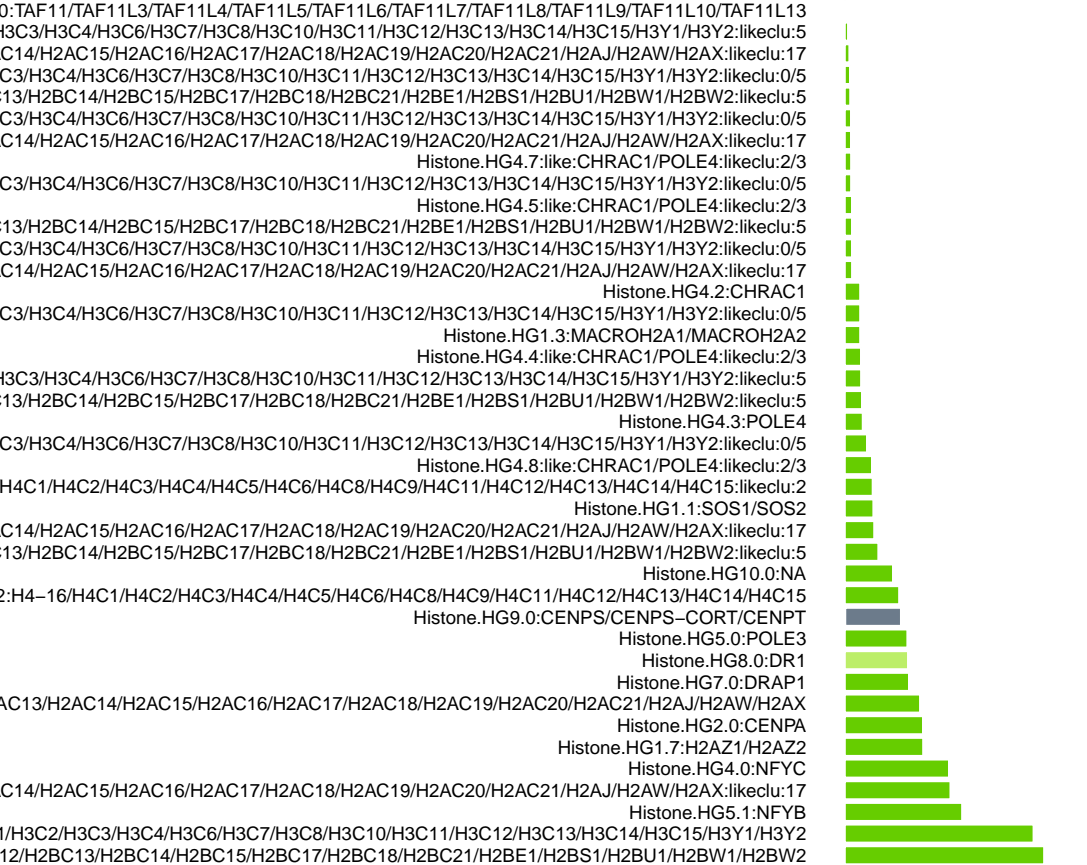


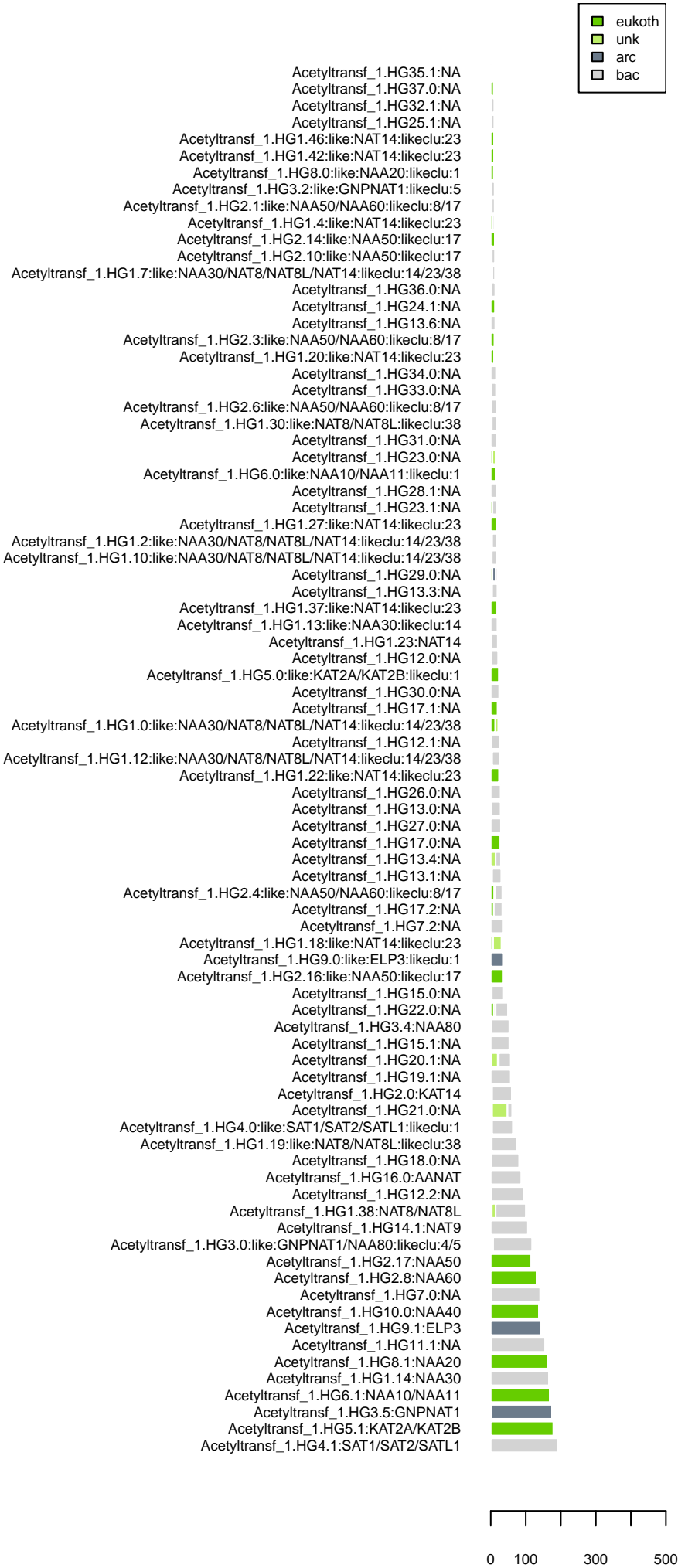
all



Histone



Acetyltransf_1



GNAT_acetyltr_2

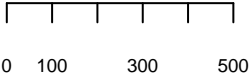


GNAT_acetyltr_2.HG1.0:like:NAT10:likeclu:1
GNAT_acetyltr_2.HG1.1:NAT10

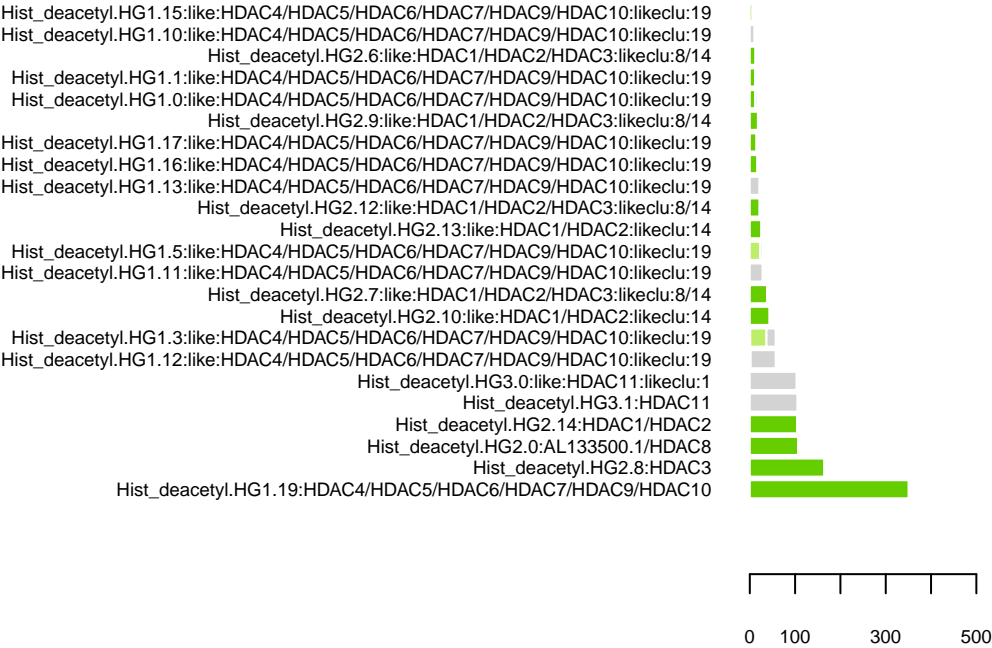


0 100 300 500

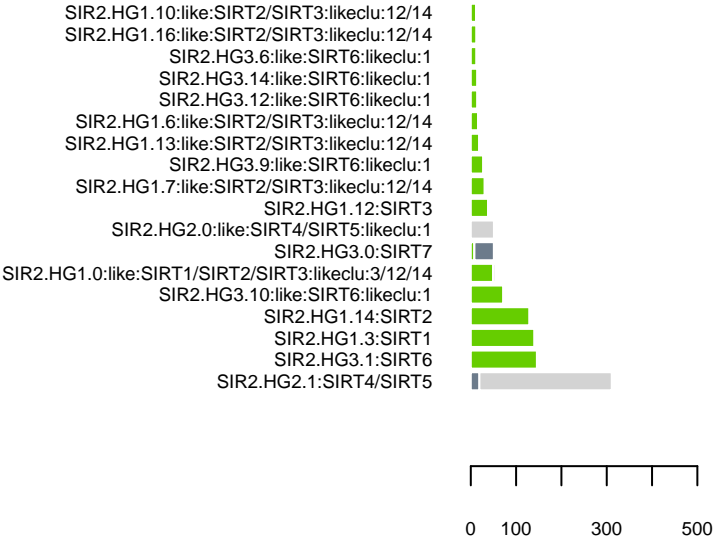
MOZ_SAS



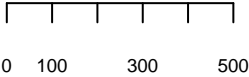
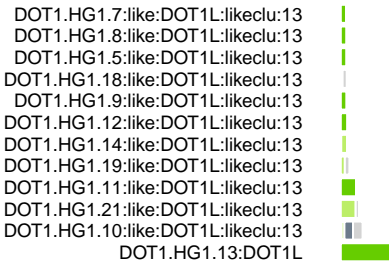
Hist_deacetyl



SIR2



DOT1



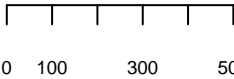
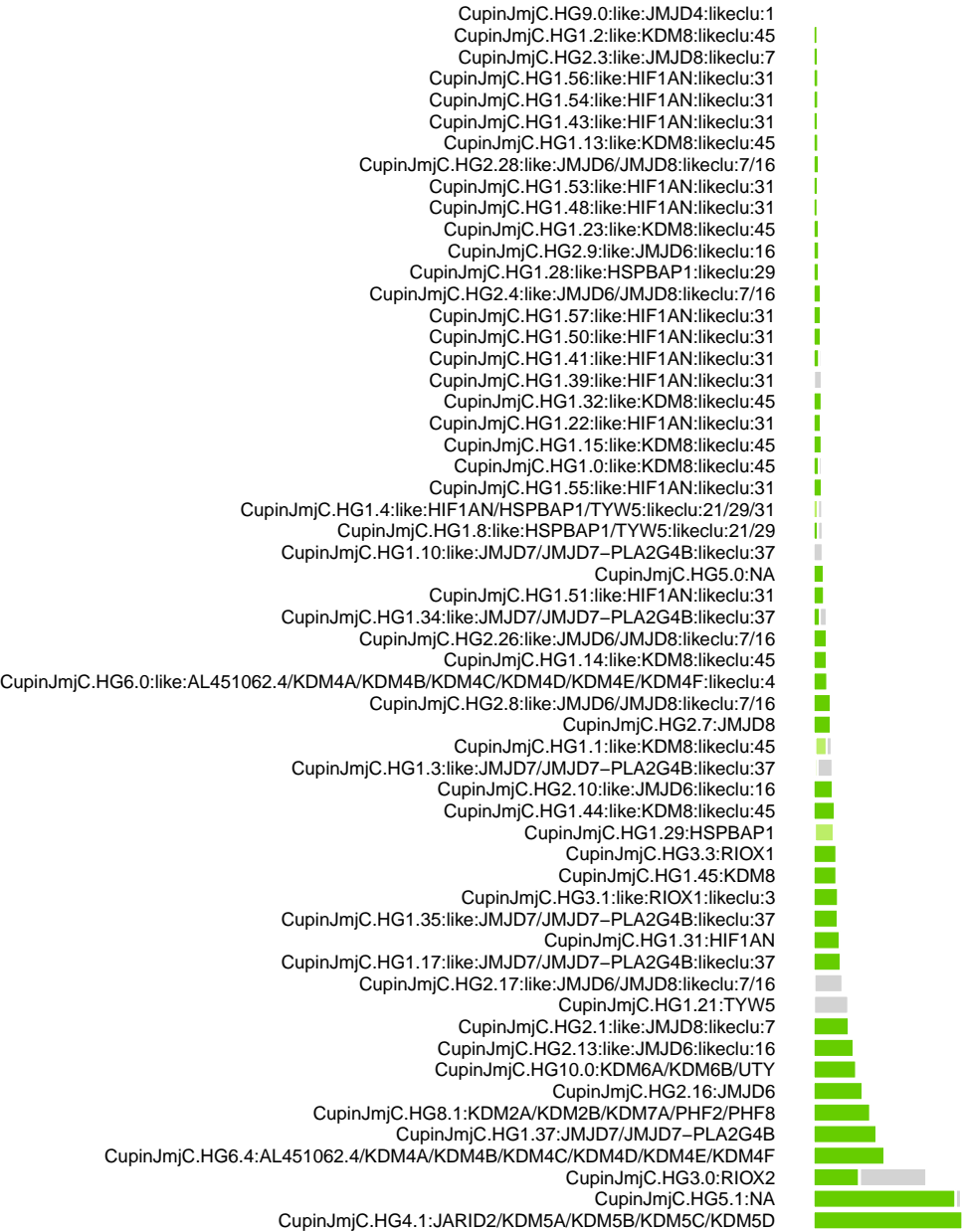
SET.HG1.42:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71
SET.HG3.11:like:KMT2A/KMT2B/KMT2C/KMT2D/SETD1A/SETD1B:likeclu:13/21/22
SET.HG2.39:like:SETD3/SETD4:likeclu:16/17
SET.HG10.0:NA
SET.HG1.70:like:SMYD5:likeclu:71
SET.HG1.27:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71
SET.HG1.0:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71
SET.HG2.14:like:SETD3/SETD4:likeclu:16/17
SET.HG12.0:NA
SET.HG1.8:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71
SET.HG1.53:like:SMYD5:likeclu:71
SET.HG1.36:like:SMYD5:likeclu:71
SET.HG6.2:like:KMT5A:likeclu:6
SET.HG6.0:like:KMT5A:likeclu:6
SET.HG3.14:like:KMT2A/KMT2B/KMT2C/KMT2D:likeclu:21/22
SET.HG2.34:like:SETD3/SETD4:likeclu:16/17
SET.HG1.14:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71
SET.HG1.44:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71
SET.HG1.38:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71
SET.HG1.26:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71
SET.HG5.4:like:EHMT1/EHMT2/SETDB1/SETDB2/SUV39H1/SUV39H2:likeclu:16/7
SET.HG2.35:like:SETD3/SETD4:likeclu:16/17
SET.HG11.0:NA
SET.HG5.2:like:SETMAR:likeclu:3
SET.HG2.26:like:SETD3/SETD4:likeclu:16/17
SET.HG2.12:like:SETD3/SETD4:likeclu:16/17
SET.HG1.66:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71
SET.HG1.58:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71
SET.HG1.18:like:SMYD1/SMYD2/SMYD3:likeclu:19
SET.HG5.5:like:EHMT1/EHMT2/SETDB1/SETDB2/SUV39H1/SUV39H2:likeclu:16/7
SET.HG4.8:like:NSD1/NSD2/NSD3:likeclu:9
SET.HG2.9:like:SETD3/SETD4:likeclu:16/17
SET.HG2.3:like:SETD3/SETD4:likeclu:16/17
SET.HG1.61:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71
SET.HG1.2:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71
SET.HG3.0:like:KMT2A/KMT2B/KMT2C/KMT2D/SETD1A/SETD1B:likeclu:13/21/22
SET.HG2.24:like:SETD3/SETD4:likeclu:16/17
SET.HG6.3:like:KMT5A:likeclu:6
SET.HG3.19:like:KMT2A/KMT2B/KMT2C/KMT2D/SETD1A/SETD1B:likeclu:13/21/22
SET.HG2.41:like:SETD3/SETD4:likeclu:16/17
SET.HG2.18:like:SETD3/SETD4:likeclu:16/17
SET.HG3.2:like:KMT2A/KMT2B/KMT2C/KMT2D/SETD1A/SETD1B:likeclu:13/21/22
SET.HG2.5:like:SETD3/SETD4:likeclu:16/17
SET.HG1.50:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71
SET.HG1.30:like:SMYD5:likeclu:71
SET.HG2.42:like:SETD3/SETD4:likeclu:16/17
SET.HG2.4:like:SETD6:likeclu:8
SET.HG1.22:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71
SET.HG1.9:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71
SET.HG1.75:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71
SET.HG3.8:like:KMT2A/KMT2B/KMT2C/KMT2D/SETD1A/SETD1B:likeclu:13/21/22
SET.HG2.31:like:SETD3/SETD4:likeclu:16/17
SET.HG3.17:like:KMT2A/KMT2B/KMT2C/KMT2D:likeclu:21/22
SET.HG4.7:like:ASH1L/NSD1/NSD2/NSD3/SETD2:likeclu:9/10/11
SET.HG3.16:like:KMT2A/KMT2B/KMT2C/KMT2D:likeclu:21/22
SET.HG1.45:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71
SET.HG4.6:like:ASH1L/NSD1/NSD2/NSD3/SETD2:likeclu:9/10/11
SET.HG2.10:like:SETD3/SETD4:likeclu:16/17
SET.HG4.1:like:ASH1L/KMT2E/NSD1/NSD2/NSD3/SETD2/SETD5:likeclu:5/9/10/11
SET.HG2.7:like:SETD6:likeclu:8
SET.HG8.0:like:EZH1/EZH2:likeclu:1
SET.HG1.69:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71
SET.HG1.15:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71
SET.HG2.16:SETD3
SET.HG3.21:KMT2C/KMT2D
SET.HG6.11:like:KMT5A:likeclu:6
SET.HG4.10:ASH1L
SET.HG2.8:SETD6
SET.HG4.3:like:KMT2E/SETD5:likeclu:5
SET.HG10.1:NA
SET.HG1.46:like:SMYD5:likeclu:71
SET.HG7.0:SETD7
SET.HG1.71:SMYD5
SET.HG6.6:KMT5A
SET.HG3.22:KMT2A/KMT2B
SET.HG9.0:KMT5B/KMT5C
SET.HG3.15:like:KMT2A/KMT2B/KMT2C/KMT2D:likeclu:21/22
SET.HG1.28:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71
SET.HG4.5:KMT2E/SETD5
SET.HG1.16:like:SMYD5:likeclu:71
SET.HG2.17:SETD4
SET.HG5.3:SETMAR
SET.HG3.20:like:KMT2A/KMT2B/KMT2C/KMT2D/SETD1A/SETD1B:likeclu:13/21/22
SET.HG5.6:EHMT1/EHMT2
SET.HG2.19:like:SETD3/SETD4:likeclu:16/17
SET.HG1.4:SMYD4
SET.HG5.1:SUV39H1/SUV39H2
SET.HG1.5:like:SMYD1/SMYD2/SMYD3/SMYD4/SMYD5:likeclu:4/19/71
SET.HG8.1:EZH1/EZH2
SET.HG4.9:NSD1/NSD2/NSD3
SET.HG3.13:SETD1A/SETD1B
SET.HG1.19:SMYD1/SMYD2/SMYD3
SET.HG4.11:SETD2
SET.HG5.7:SETDB1/SETDB2

SET

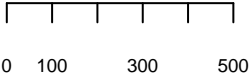
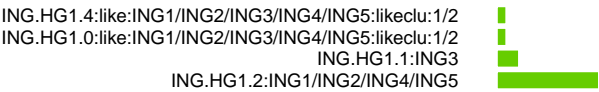


0 100 300 500

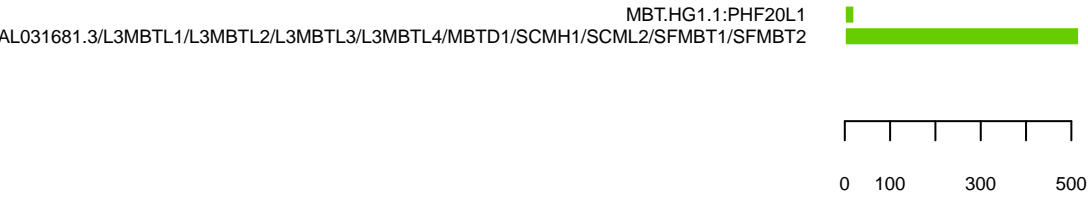
CupinJmjC



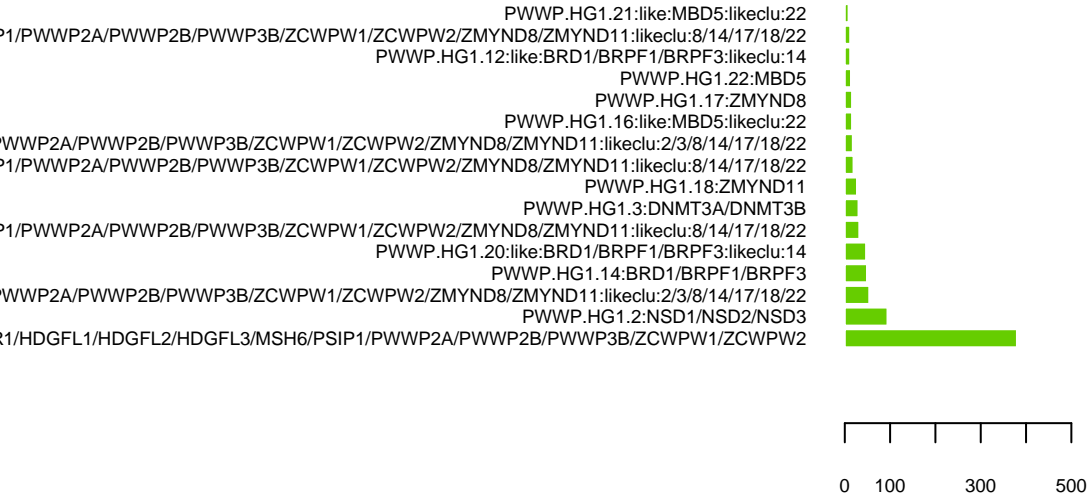
ING



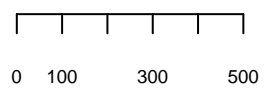
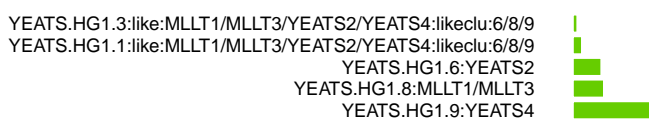
MBT



PWWP



YEATS



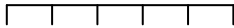
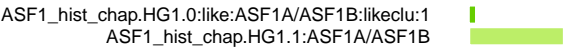
SNF2_N



SNF2_N.HG7.0:like:RAD54B/RAD54L:likeclu:8
 SNF2_N.HG2.5:like:SMARCA1:likeclu:7
 SNF2_N.HG10.0:like:SHPRH:likeclu:1
 SNF2_N.HG4.1:like:CHD1/CHD2:likeclu:6
 SNF2_N.HG2.12:like:SMARCA1/SMARCA5:likeclu:10
 SNF2_N.HG1.20:like:HLTF/TTF2:likeclu:18/26
 SNF2_N.HG1.1:like:HLTF/TTF2:likeclu:18/26
 SNF2_N.HG5.5:like:ATRAX:likeclu:7
 SNF2_N.HG15.0:NA
 SNF2_N.HG6.1:like:SMARCA2/SMARCA4:likeclu:0
 SNF2_N.HG4.2:like:CHD1/CHD2:likeclu:6
 SNF2_N.HG3.4:like:ERCC6L:likeclu:5
 SNF2_N.HG1.23:like:HLTF:likeclu:26
 SNF2_N.HG1.12:like:HLTF/TTF2:likeclu:18/26
 SNF2_N.HG5.1:like:ATRAX/RAD54L2:likeclu:2/7
 SNF2_N.HG1.25:like:HLTF:likeclu:26
 SNF2_N.HG5.4:like:ATRAX/RAD54L2:likeclu:2/7
 SNF2_N.HG5.3:like:ATRAX/RAD54L2:likeclu:2/7
 SNF2_N.HG7.7:like:RAD54B/RAD54L:likeclu:8
 SNF2_N.HG1.7:like:HLTF/TTF2:likeclu:18/26
 SNF2_N.HG4.4:like:CHD1/CHD2:likeclu:6
 SNF2_N.HG2.15:like:SMARCA1/SMARCA5:likeclu:10
 SNF2_N.HG1.27:like:TTF2:likeclu:18
 SNF2_N.HG1.29:like:TTF2:likeclu:18
 SNF2_N.HG5.2:RAD54L2
 SNF2_N.HG5.7:ATRAX
 SNF2_N.HG5.0:like:ATRAX/RAD54L2:likeclu:2/7
 SNF2_N.HG2.0:CHD1L
 SNF2_N.HG1.4:like:HLTF/TTF2:likeclu:18/26
 SNF2_N.HG1.16:like:HLTF/TTF2:likeclu:18/26
 SNF2_N.HG1.26:HLTF
 SNF2_N.HG1.18:TTF2
 SNF2_N.HG3.1:ERCC6L2
 SNF2_N.HG14.0:NA
 SNF2_N.HG3.5:ERCC6L
 SNF2_N.HG4.0:AC006064.6/CHD3/CHD4/CHD5
 SNF2_N.HG2.7:SMARCA1
 SNF2_N.HG2.3:HELLS
 SNF2_N.HG13.0:INO80
 SNF2_N.HG4.6:CHD1/CHD2
 SNF2_N.HG3.3:ERCC6
 SNF2_N.HG12.0:AC106886.6/EP400/SRCAP
 SNF2_N.HG1.17:like:HLTF/TTF2:likeclu:18/26
 SNF2_N.HG11.1:BTAF1
 SNF2_N.HG10.1:SHPRH
 SNF2_N.HG2.10:SMARCA1/SMARCA5
 SNF2_N.HG7.8:RAD54B/RAD54L
 SNF2_N.HG9.2:SMARCA1/ZRANB3
 SNF2_N.HG6.0:SMARCA2/SMARCA4
 SNF2_N.HG8.1:CHD6/CHD7/CHD8/CHD9



ASF1_hist_chap



0 100 300 500

Nucleoplasmin

