Figure S1

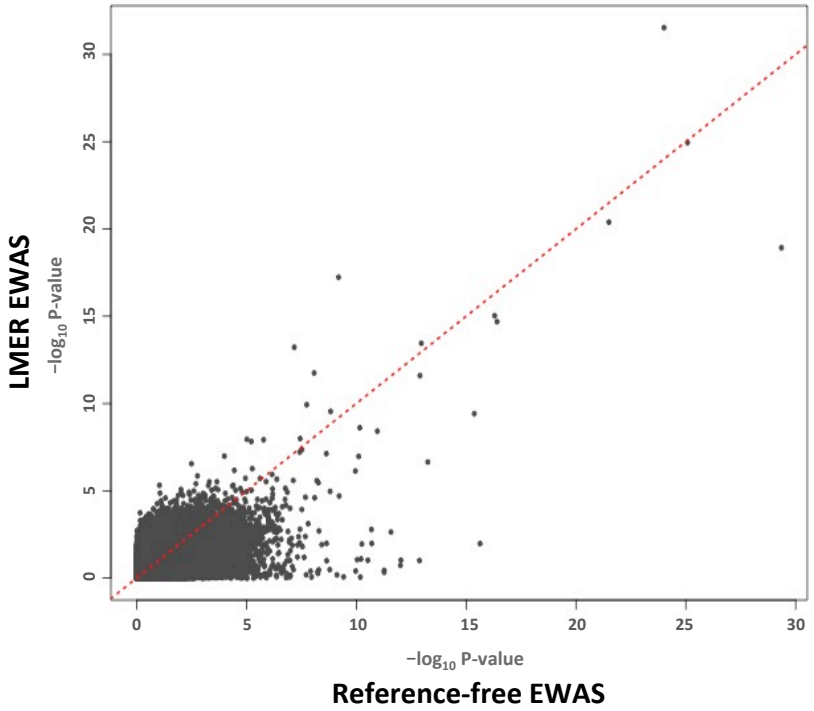
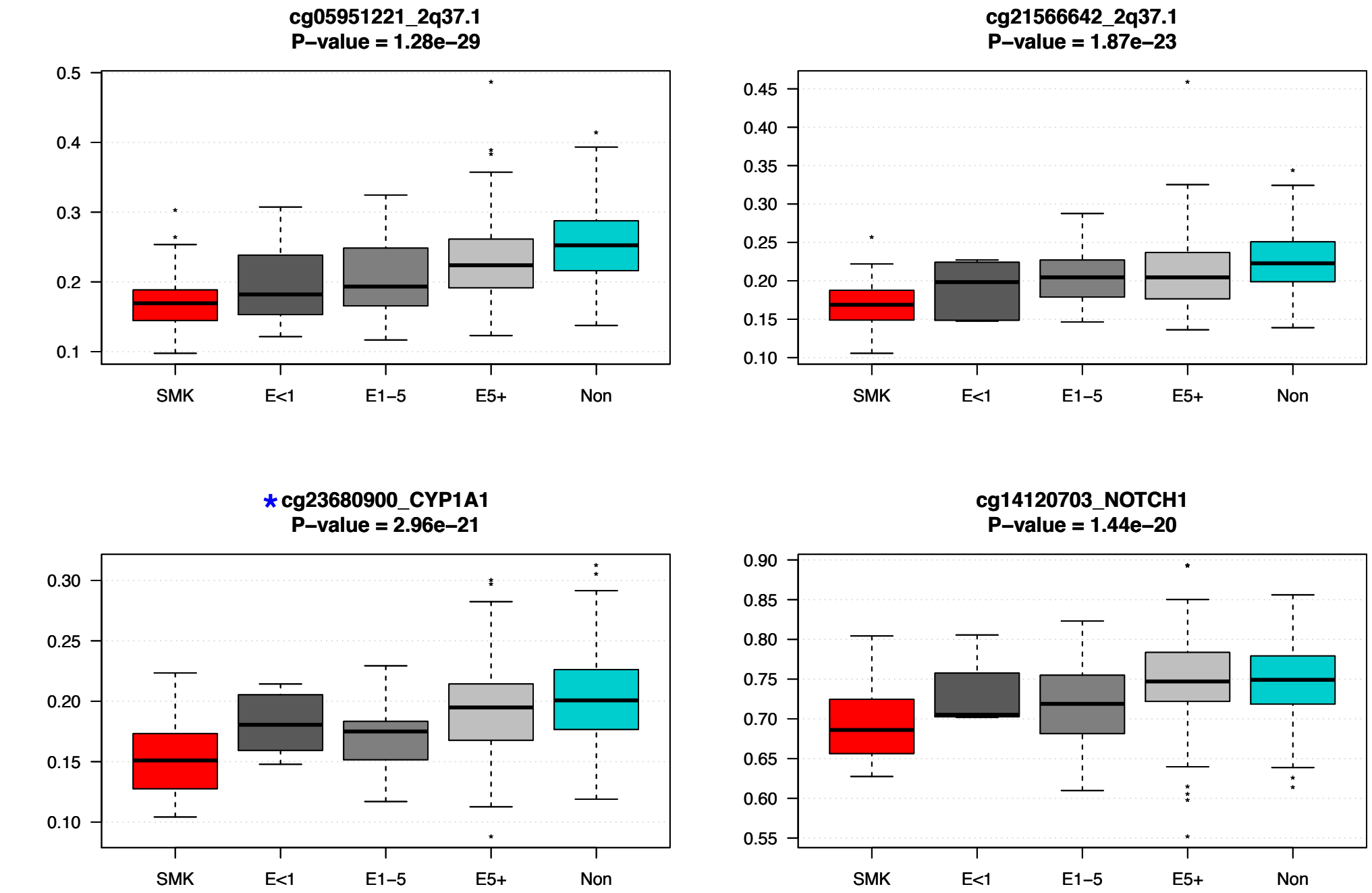
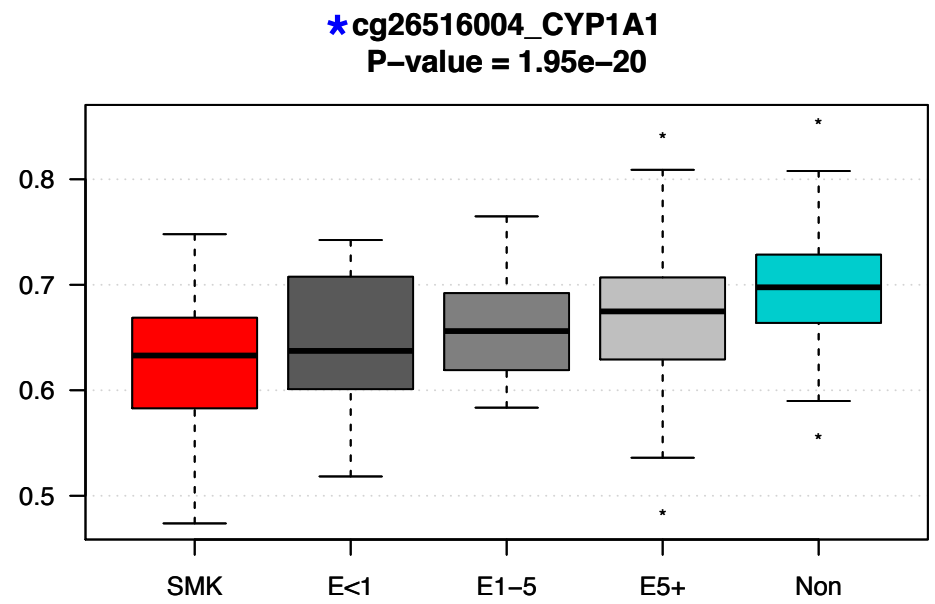
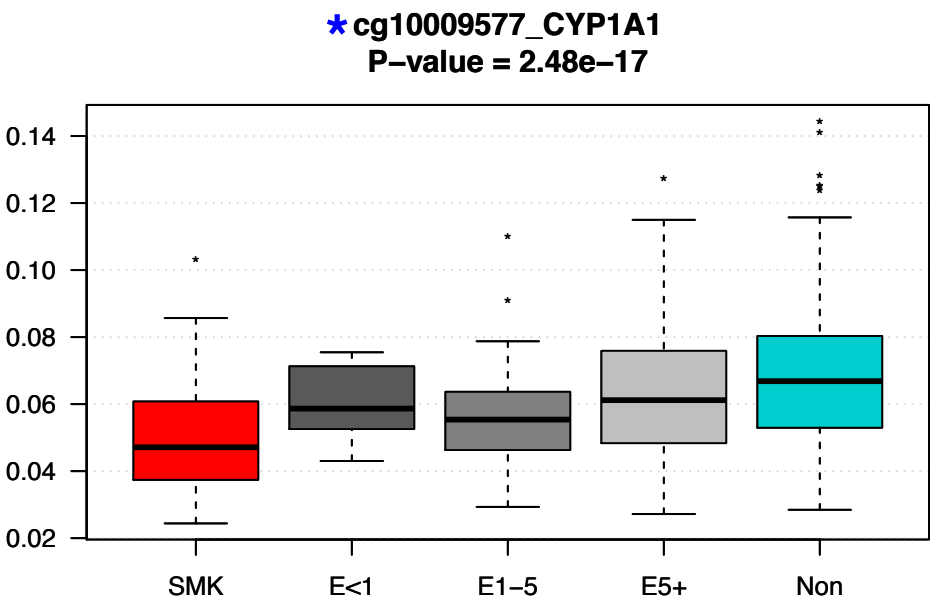
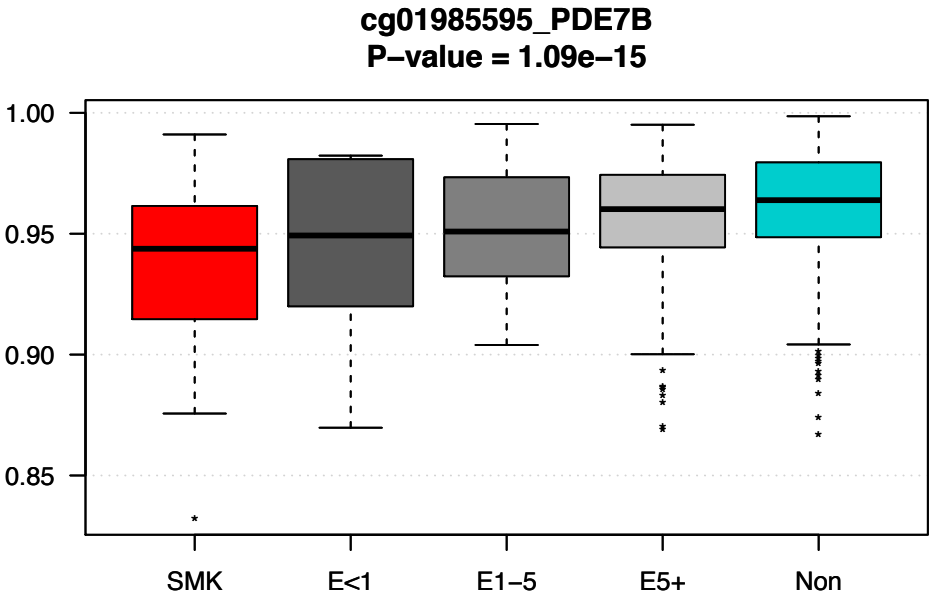

LMER EWAS
−log10 P-value
0
5
10
15
20
25
30
−log10 P-value
Reference-free EWAS

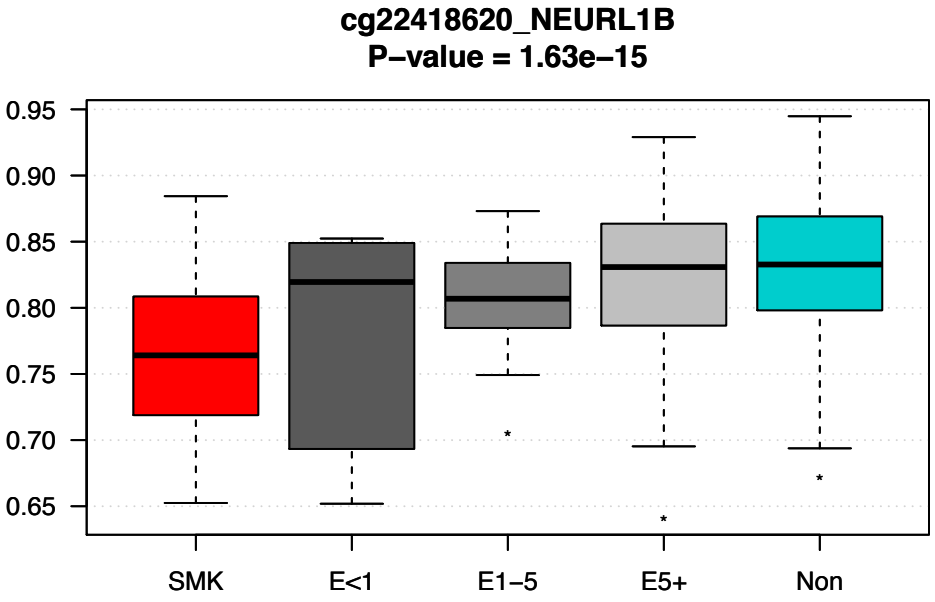
Figure S2

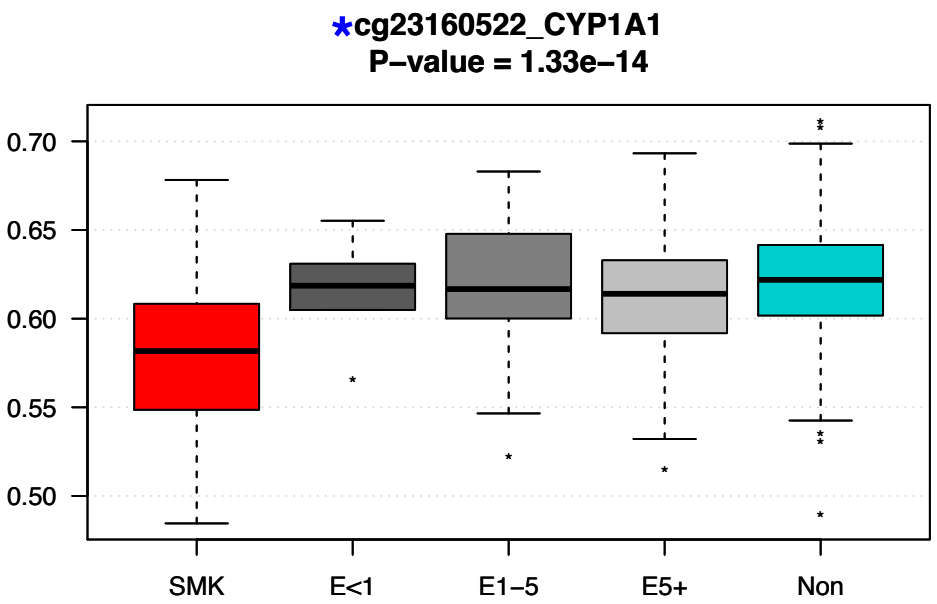

cg05951221_2q37.1
P−value = 1.28e−29
0.5
0.4
0.3
0.2
0.1
SMK
E<1
E1−5
E5+
Non
cg21566642_2q37.1
P−value = 1.87e−23
0.45
0.40
0.35
0.30
0.25
0.20
0.15
0.10
SMK
E<1
E1−5
E5+
Non
* cg23680900_CYP1A1
P−value = 2.96e−21
0.30
0.25
0.20
0.15
0.10
SMK
E<1
E1−5
E5+
Non
cg14120703_NOTCH1
P−value = 1.44e−20
0.90
0.85
0.80
0.75
0.70
0.65
0.60
0.55
SMK
E<1
E1−5
E5+
Non

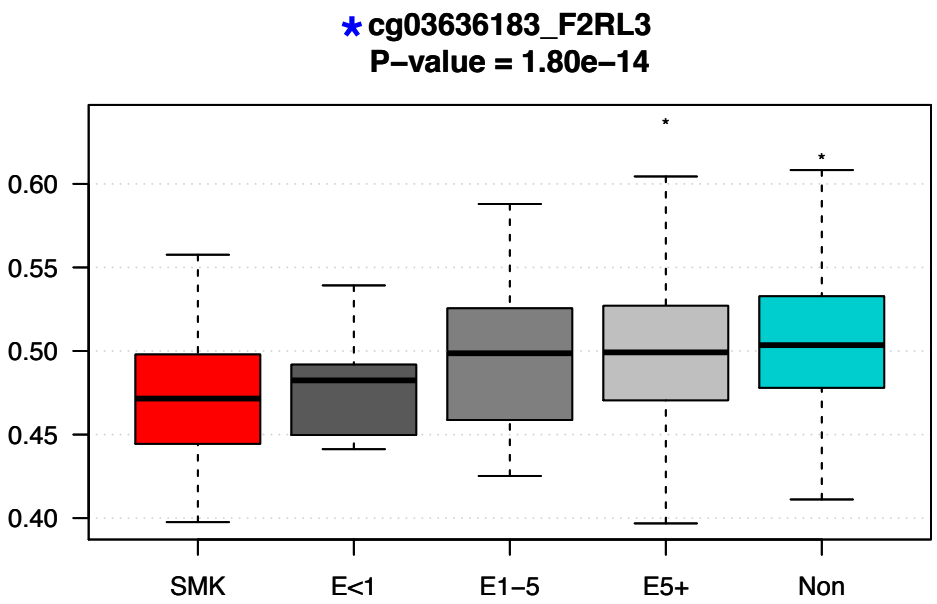

*cg26516004_CYP1A1
P−value = 1.95e−20
0.8
0.7
0.6
0.5
SMK
E<1
E1−5
E5+
Non

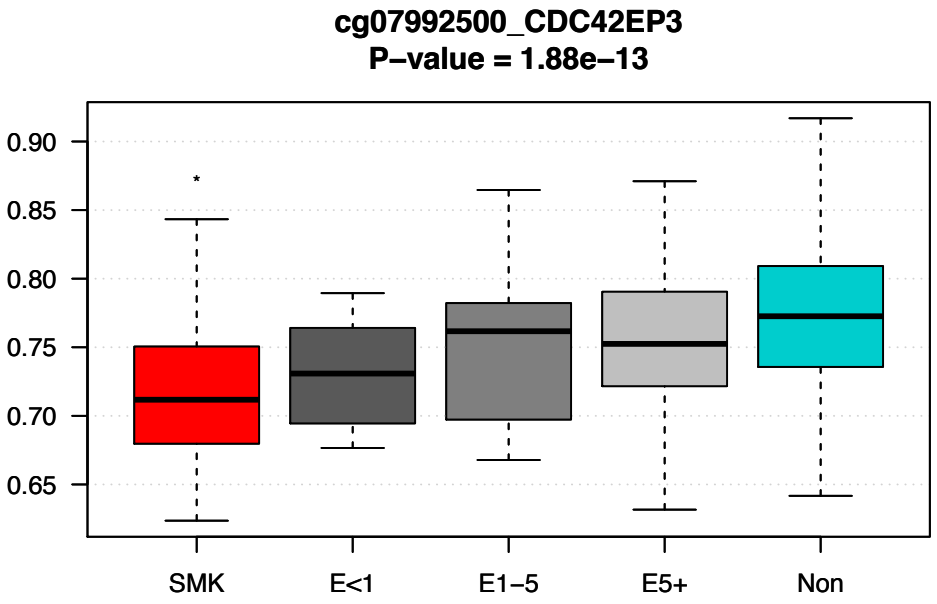

*cg10009577_CYP1A1
P−value = 2.48e−17
0.14
0.12
0.10
0.08
0.06
0.04
0.02
SMK
E<1
E1−5
E5+
Non

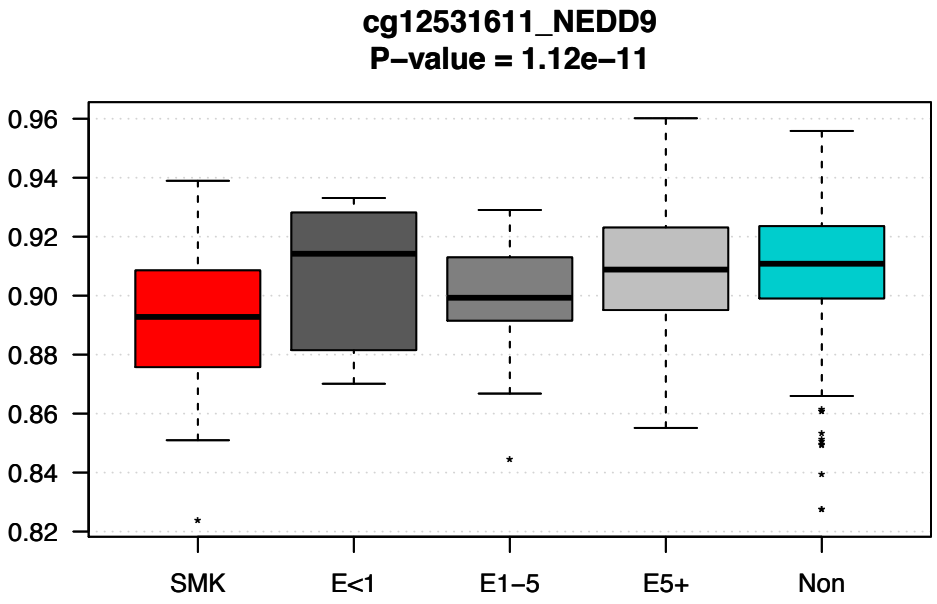

cg01985595_PDE7B
P−value = 1.09e−15
1.00
0.95
0.90
0.85
SMK
E<1
E1−5
E5+
Non


cg22418620_NEURL1B
P−value = 1.63e−15
0.95
0.90
0.85
0.80
0.75
0.70
0.65
SMK
E<1
E1−5
E5+
Non

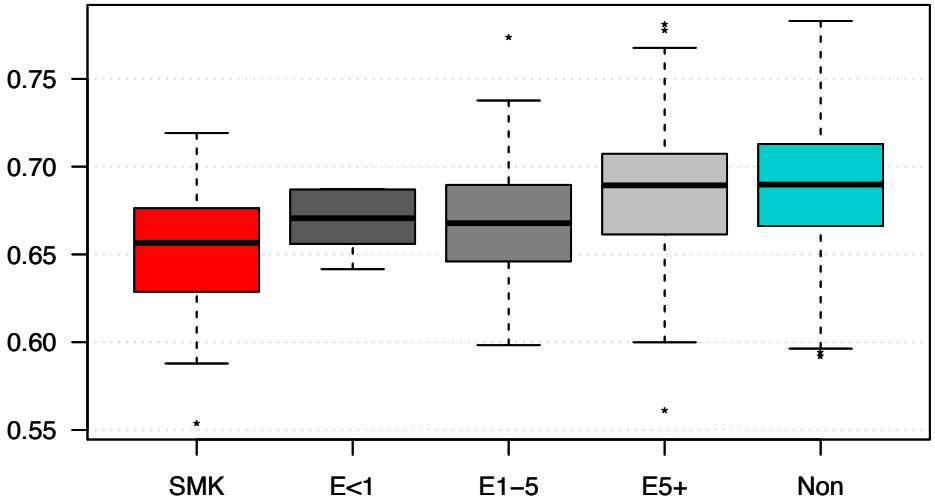

*cg23160522_CYP1A1
P−value = 1.33e−14
0.70
0.65
0.60
0.55
0.50
SMK
E<1
E1−5
E5+
Non


*cg03636183_F2RL3
P−value = 1.80e−14
0.60
0.55
0.50
0.45
0.40
SMK
E<1
E1−5
E5+
Non

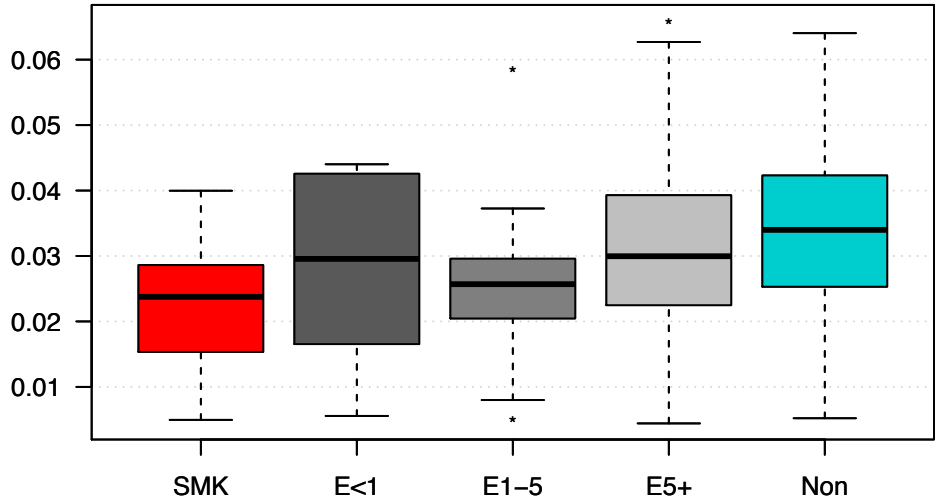

cg07992500_CDC42EP3
P−value = 1.88e−13
0.90
0.85
0.80
0.75
0.70
0.65
SMK
E<1
E1−5
E5+
Non


cg12531611_NEDD9
P−value = 1.12e−11
0.96
0.94
0.92
0.90
0.88
0.86
0.84
0.82
SMK
E<1
E1−5
E5+
Non

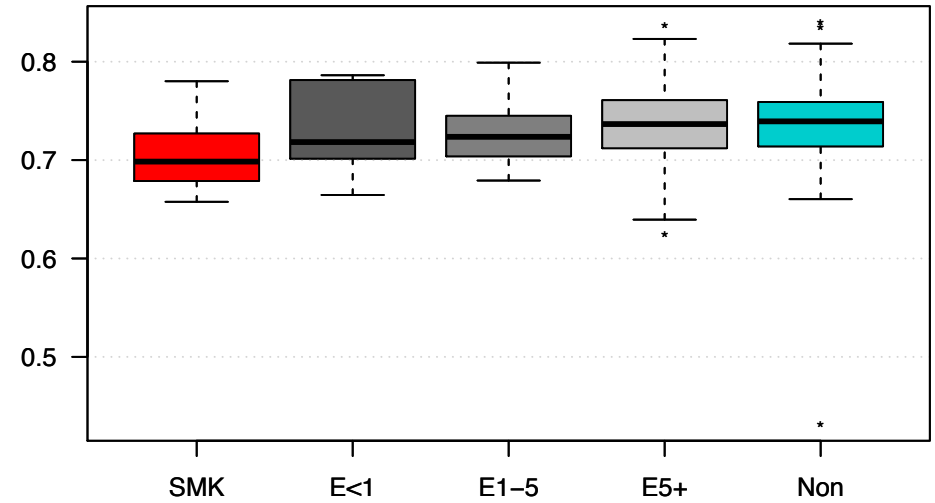
cg03646542_NEURL1B
P−value = 1.87e−10



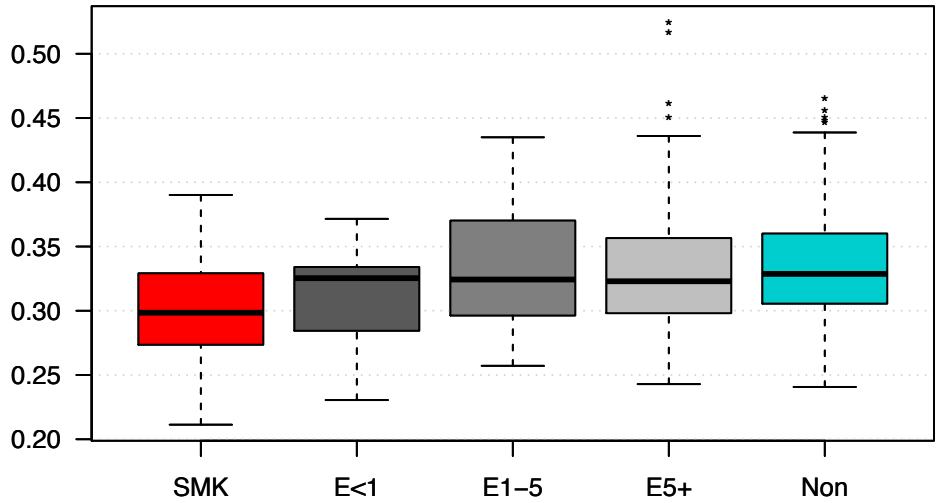
* cg00353139_CYP1A1
P−value = 4.47e−10

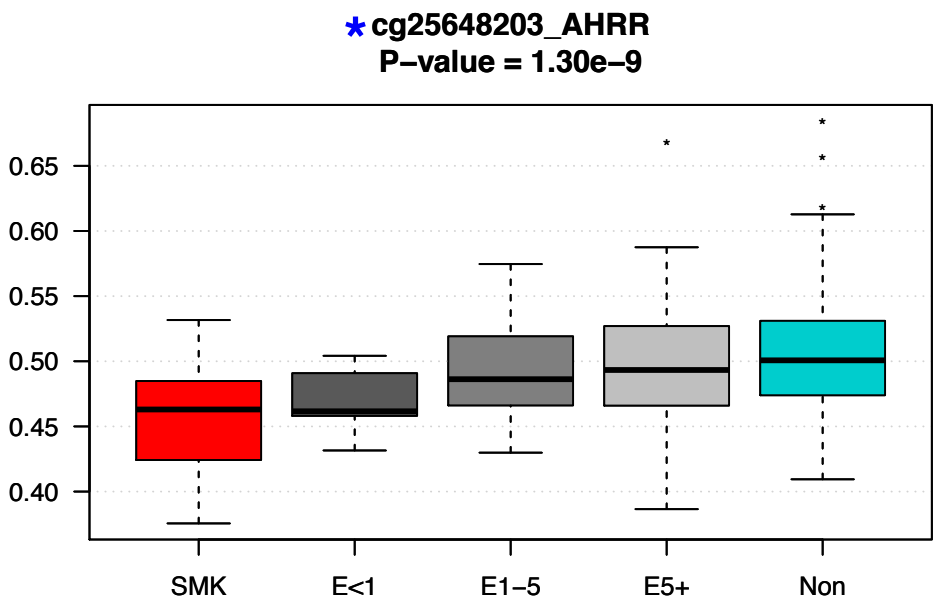


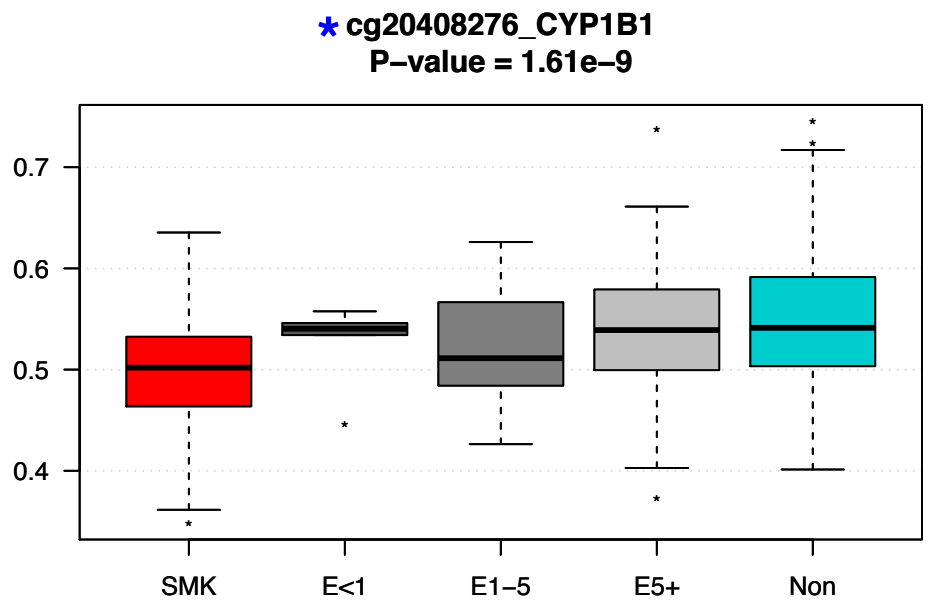
cg21124714_P2RY6
P−value = 5.15e−10

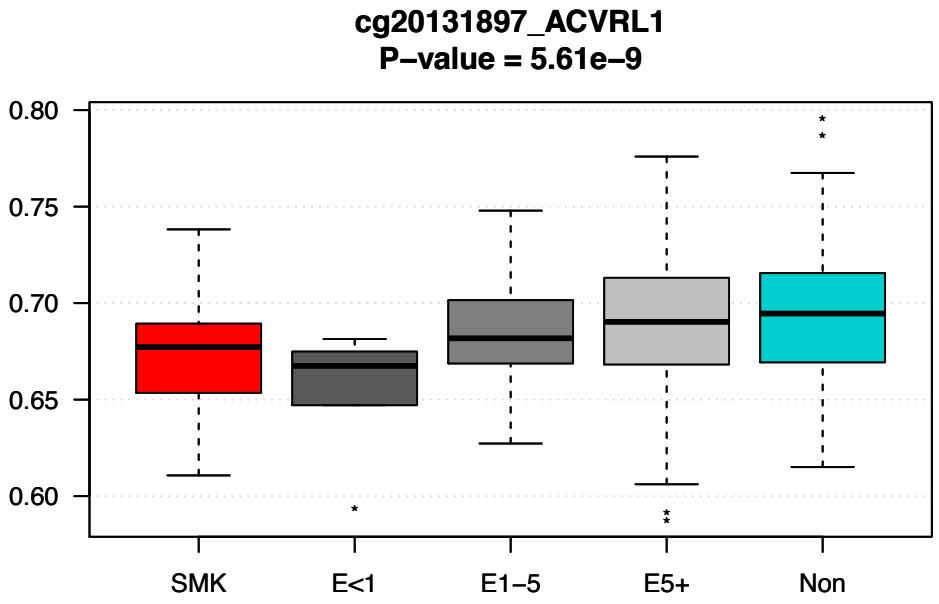


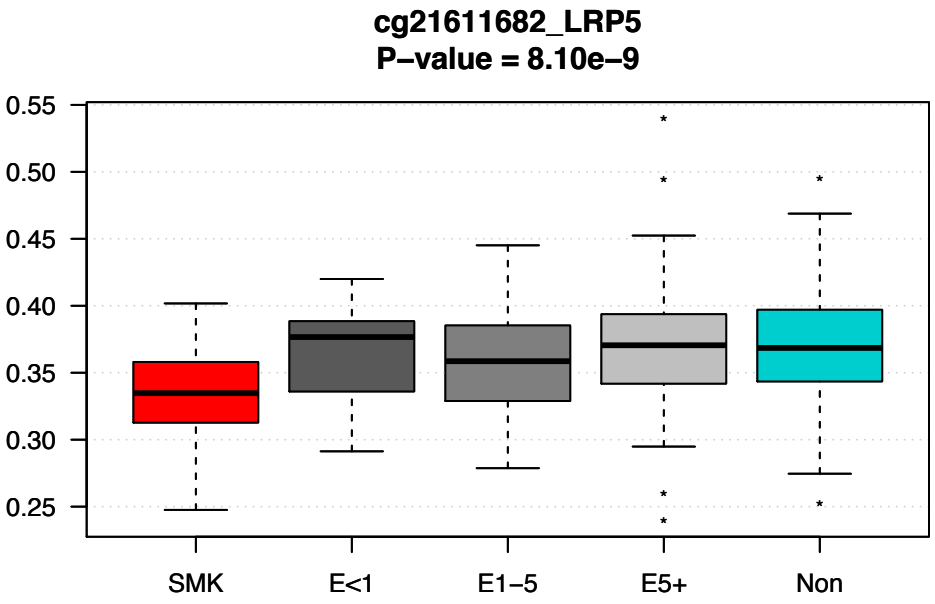
cg01940273_2q37.1
P−value = 8.93e−10

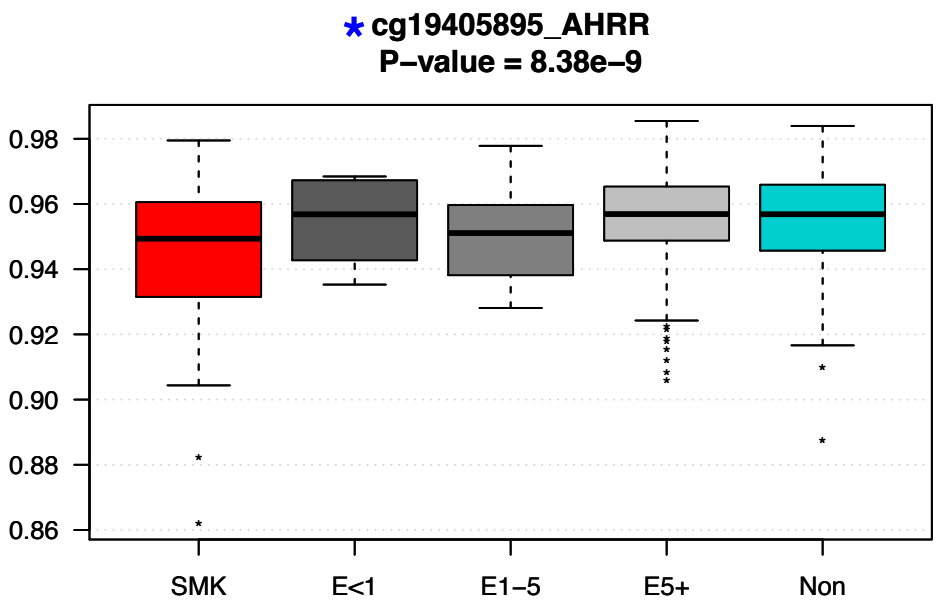


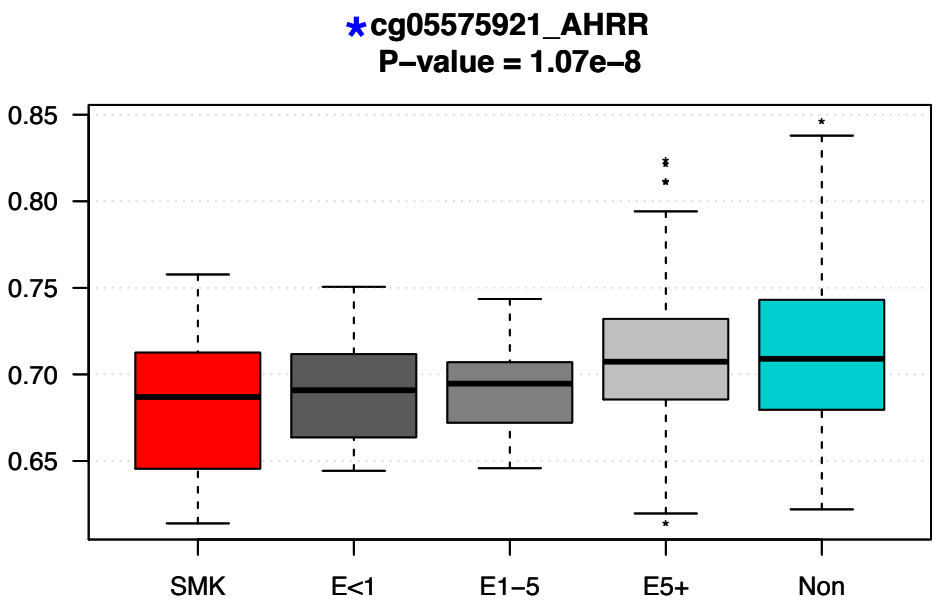

* cg25648203_AHRR
P−value = 1.30e−9
0.65
0.60
0.55
0.50
0.45
0.40
SMK
E<1
E1−5
E5+
Non

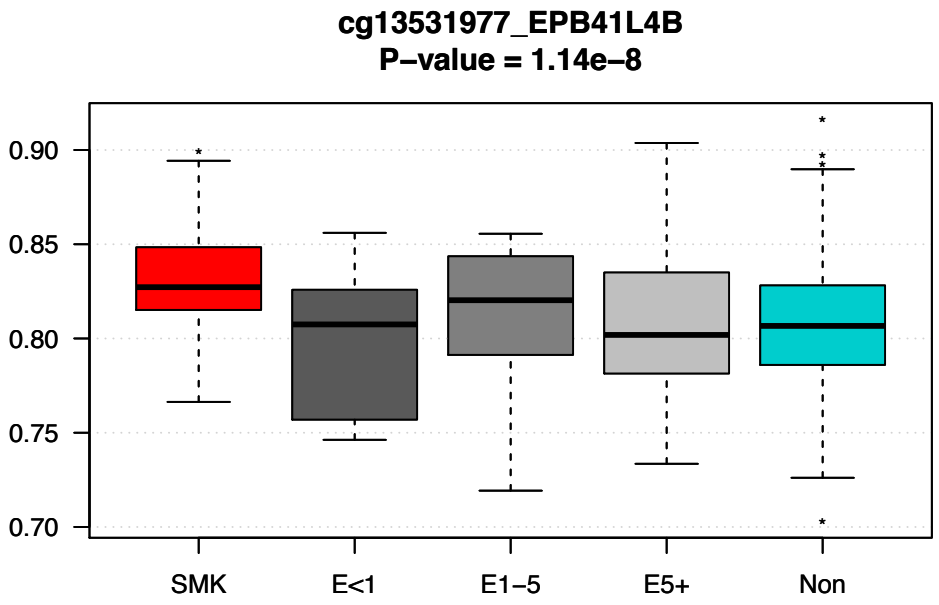

* cg20408276_CYP1B1
P−value = 1.61e−9
0.7
0.6
0.5
0.4
SMK
E<1
E1−5
E5+
Non

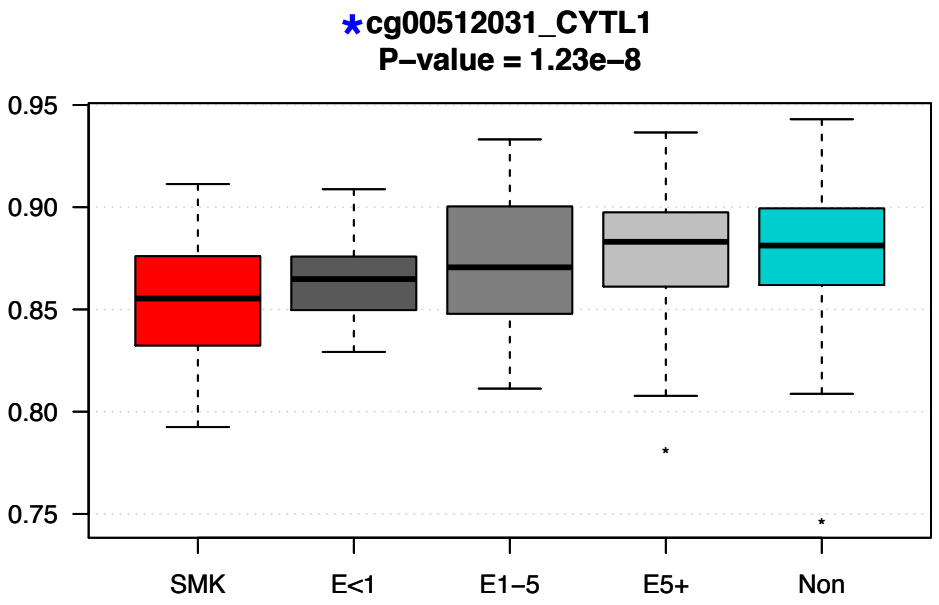

cg20131897_ACVRL1
P−value = 5.61e−9
0.80
0.75
0.70
0.65
0.60
SMK
E<1
E1−5
E5+
Non


cg21611682_LRP5
P−value = 8.10e−9
0.55
0.50
0.45
0.40
0.35
0.30
0.25
SMK
E<1
E1−5
E5+
Non

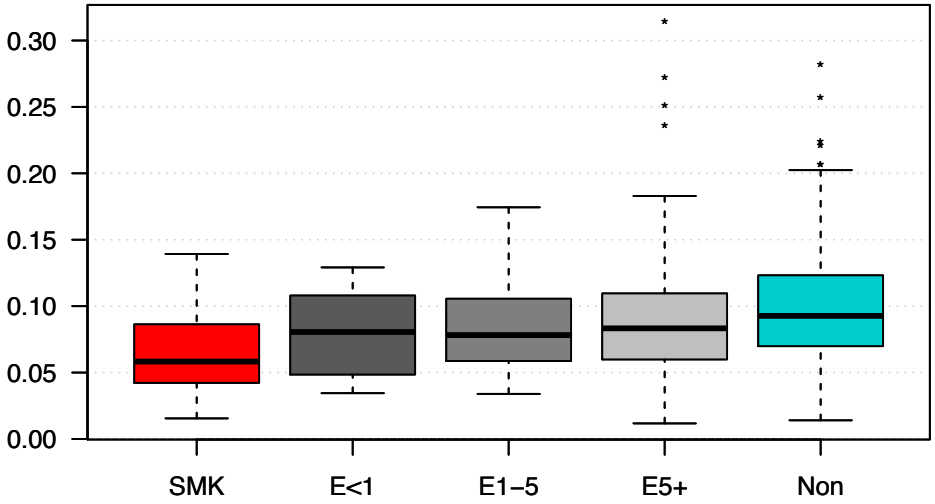

*cg19405895_AHRR
P−value = 8.38e−9
0.98
0.96
0.94
0.92
0.90
0.88
0.86
SMK
E<1
E1−5
E5+
Non


*cg05575921_AHRR
P−value = 1.07e−8
0.85
0.80
0.75
0.70
0.65
SMK
E<1
E1−5
E5+
Non

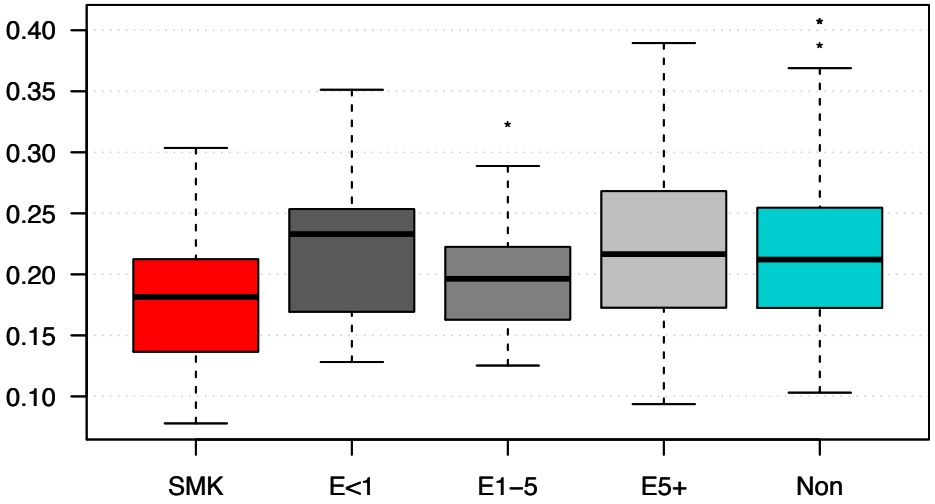

cg13531977_EPB41L4B
P−value = 1.14e−8
0.90
0.85
0.80
0.75
0.70
SMK
E<1
E1−5
E5+
Non


*cg00512031_CYTL1
P−value = 1.23e−8
0.95
0.90
0.85
0.80
0.75
SMK
E<1
E1−5
E5+
Non

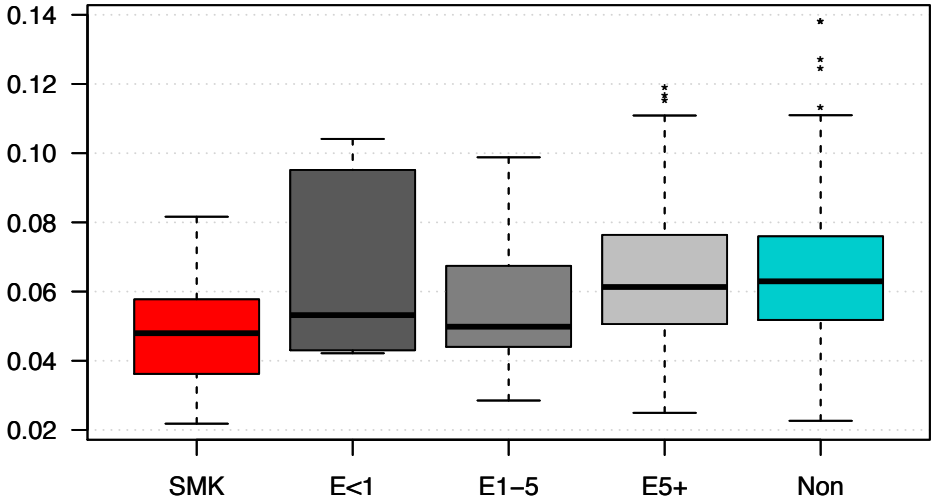
cg25189904_GNG12
P−value = 1.48e−8



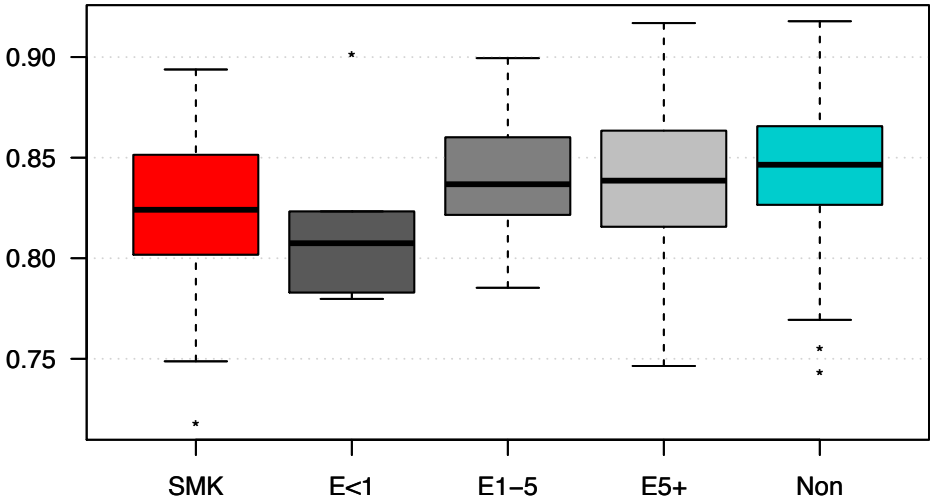
cg00378510_LINGO3
P−value = 1.53e−8



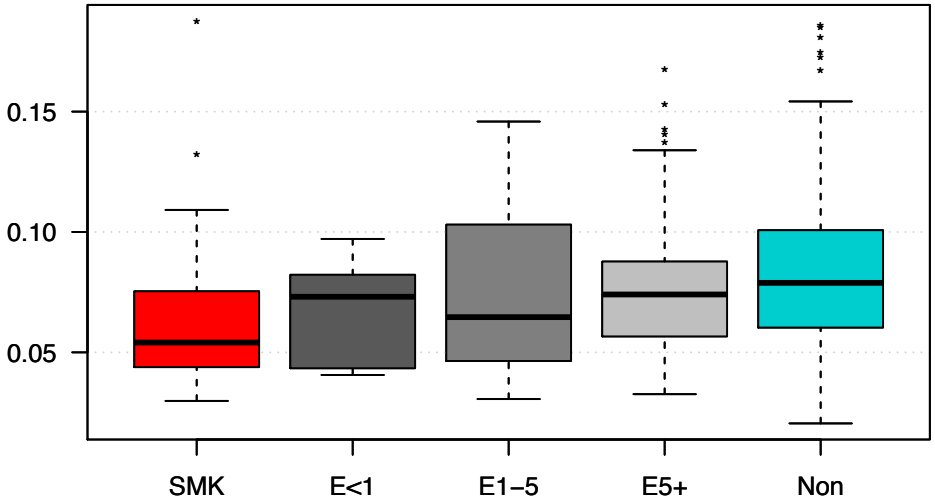
* cg11554391_AHRR
P−value = 2.00e−8



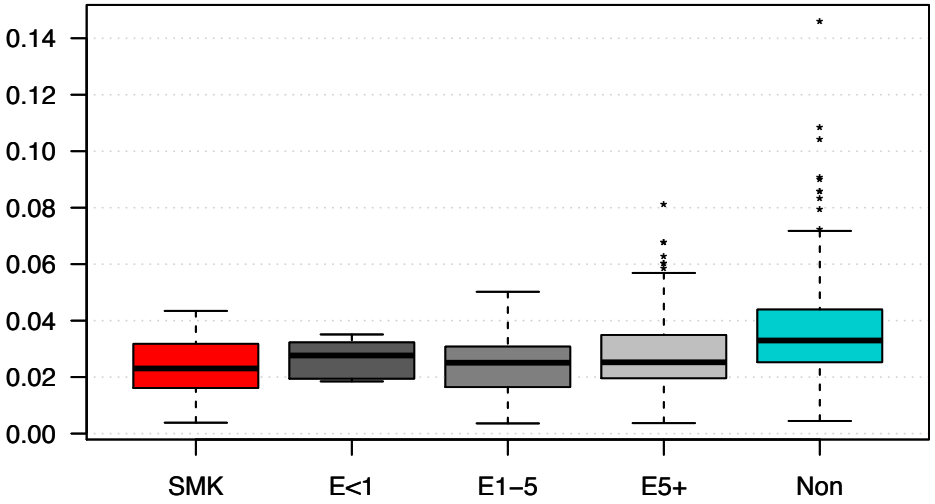
cg01802380_FAM155A
P−value = 5.69e−8



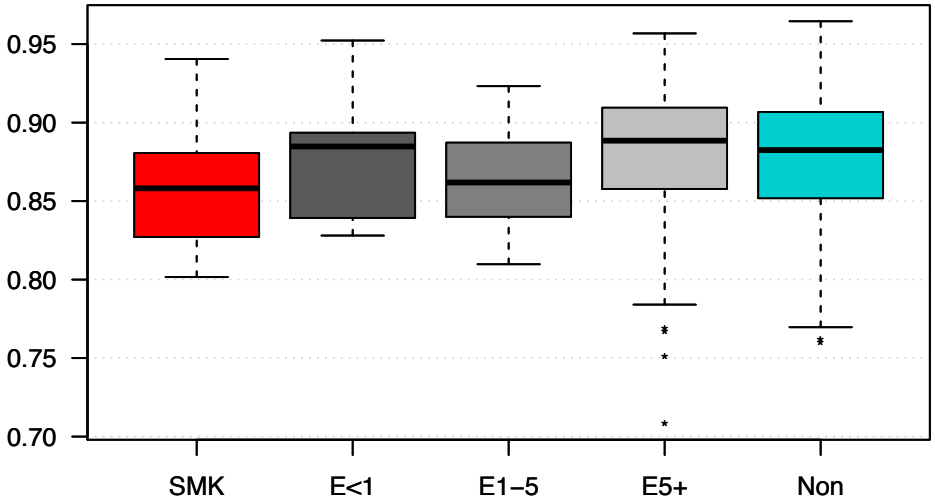
cg14179389_GFI1
P−value = 1.07e−7



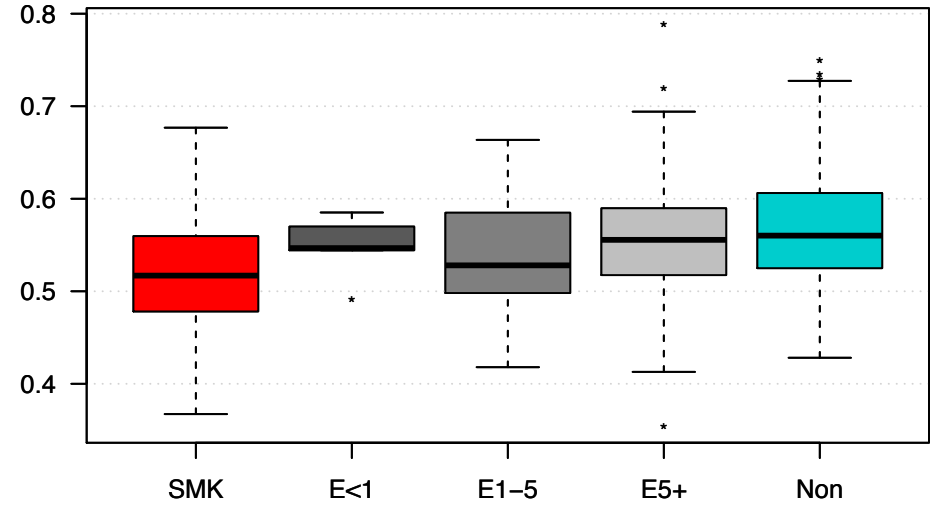
cg06644428_2q37.1
P−value = 1.61e−7

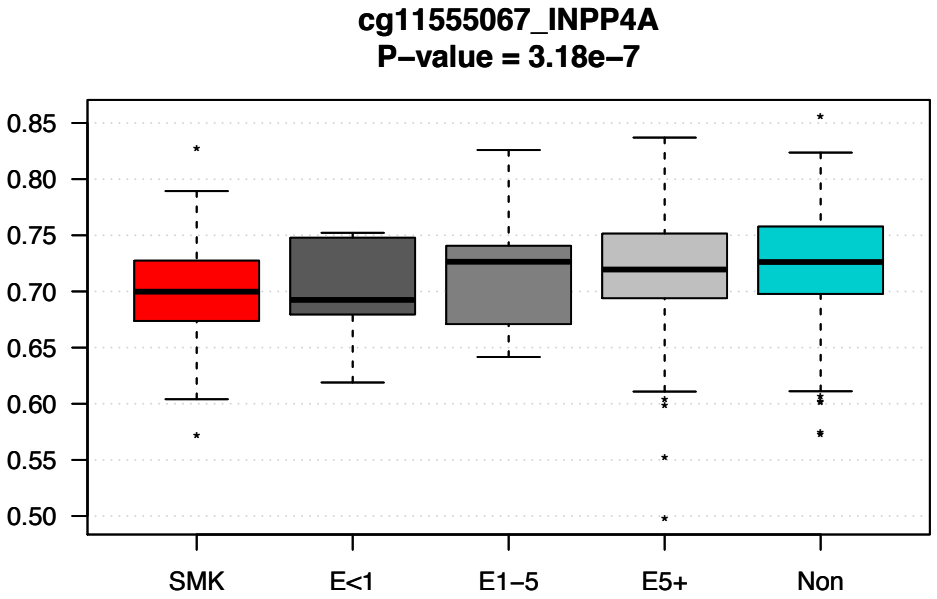


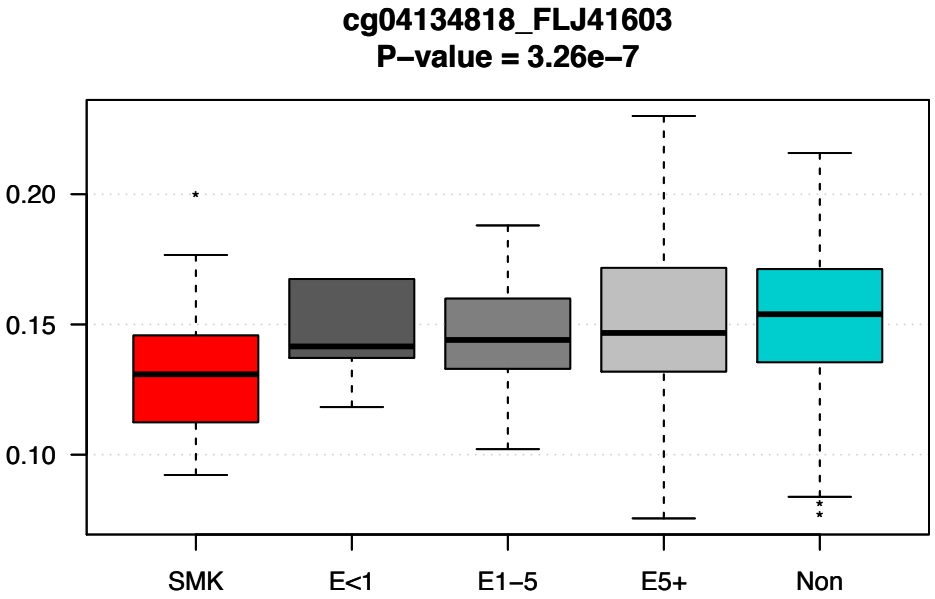
cg12081267_TMEM131
P−value = 1.97e−7

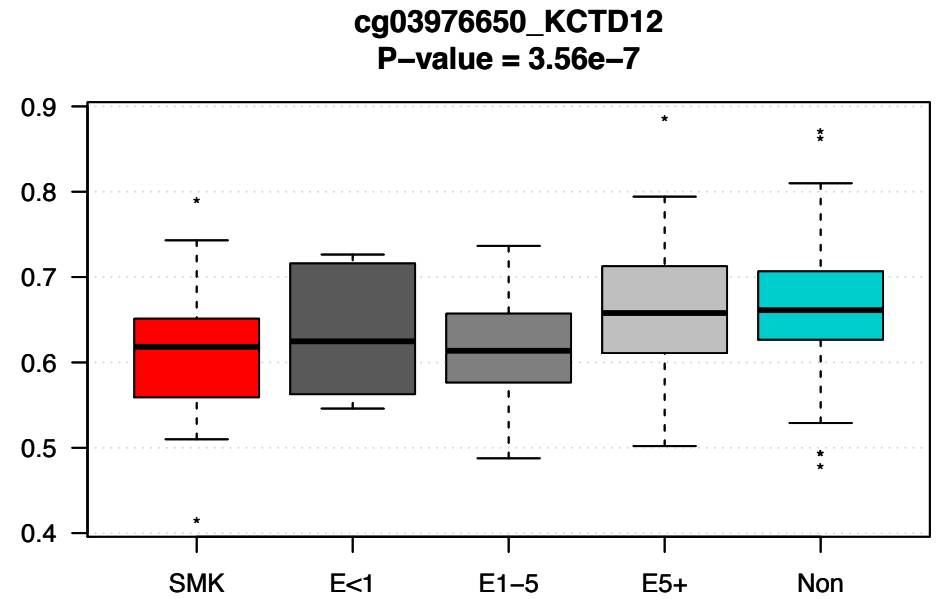


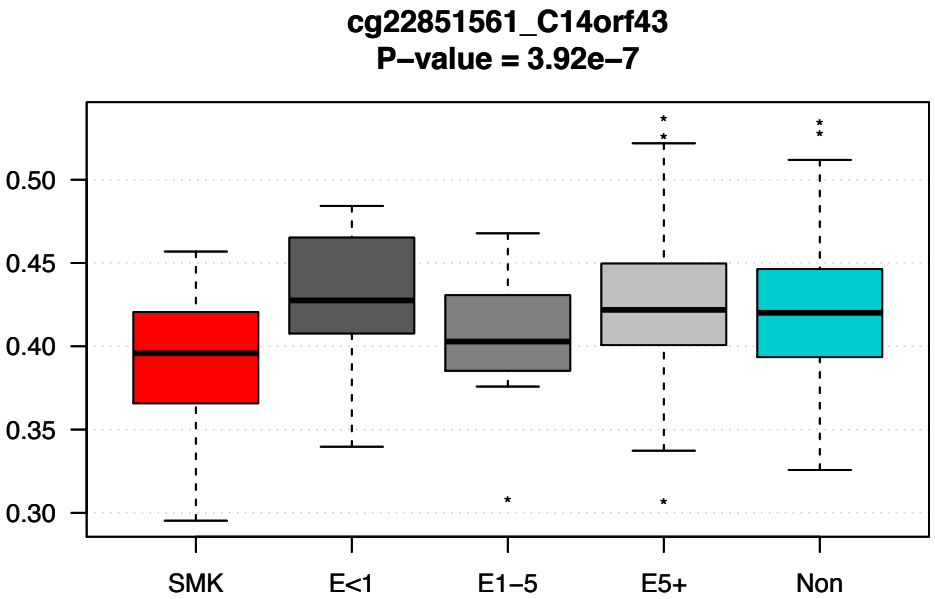
*cg02162897_CYP1B1
P−value = 2.89e−7



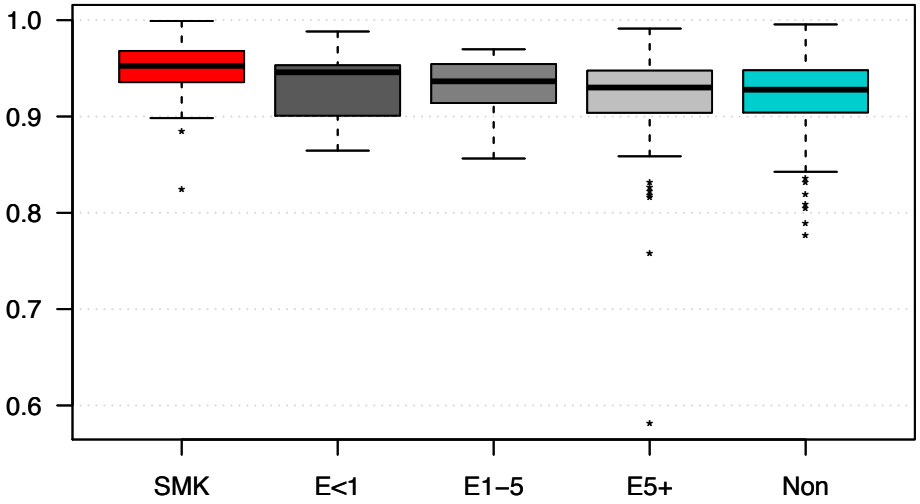

cg11555067_INPP4A
P−value = 3.18e−7
0.85
0.80
0.75
0.70
0.65
0.60
0.55
0.50
SMK
E<1
E1−5
E5+
Non


cg04134818_FLJ41603
P−value = 3.26e−7
0.20
0.15
0.10
SMK
E<1
E1−5
E5+
Non

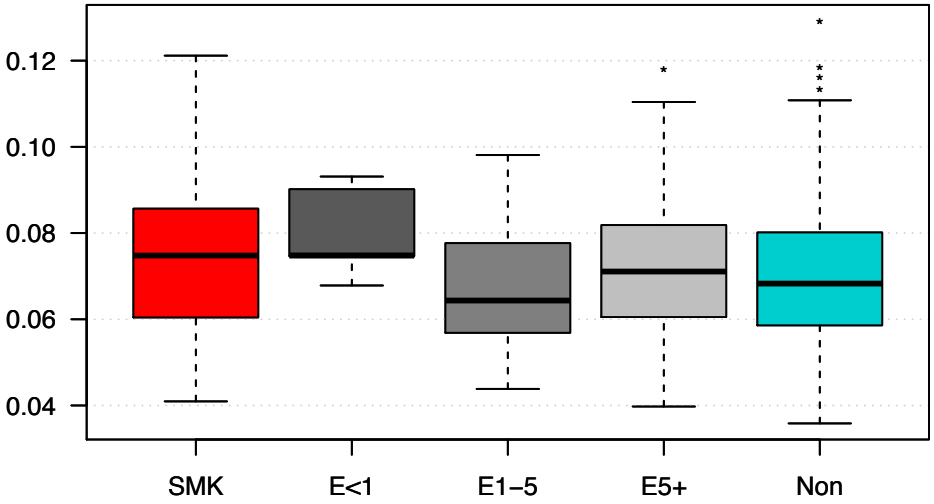

cg03976650_KCTD12
P−value = 3.56e−7
0.9
0.8
0.7
0.6
0.5
0.4
SMK
E<1
E1−5
E5+
Non


cg22851561_C14orf43
P−value = 3.92e−7
0.50
0.45
0.40
0.35
0.30
SMK
E<1
E1−5
E5+
Non

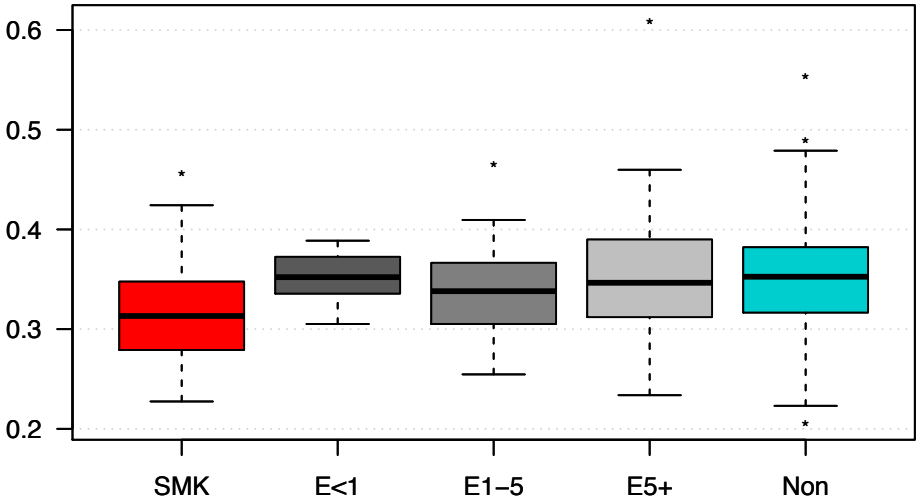
cg10376100_LYST;MIR1537
P−value = 4.03e−7



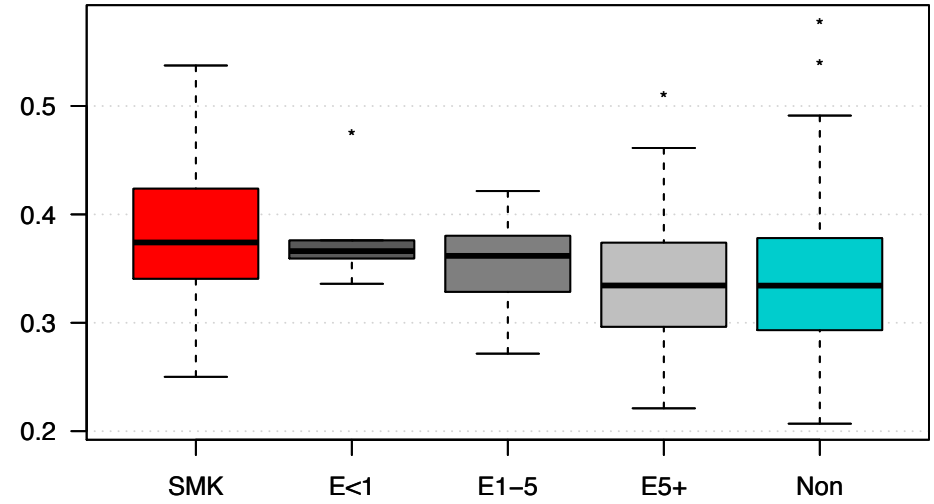
cg04063216_FAM84A
P−value = 4.39e−7

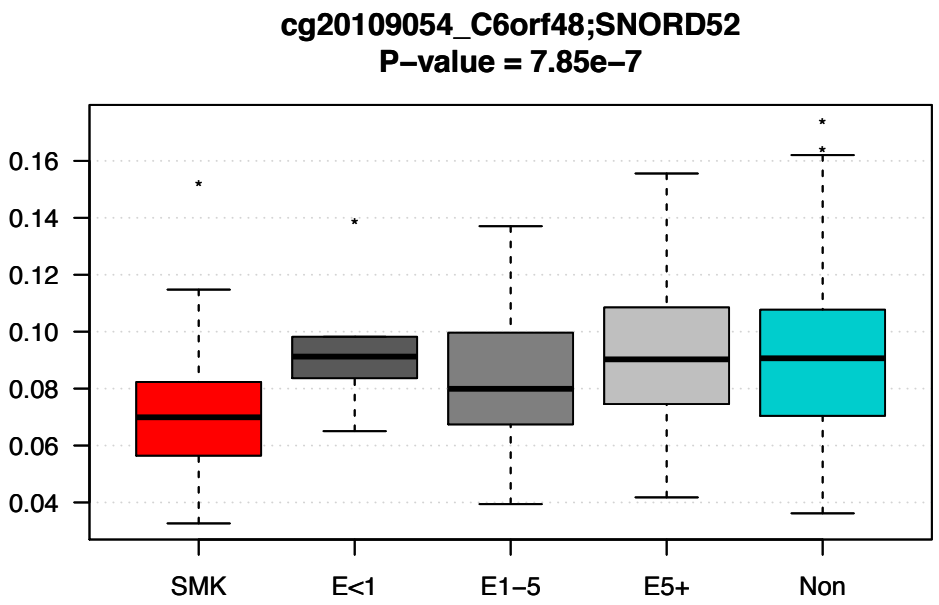


cg16320419_BHLHE40
P−value = 4.88e−7



*cg04135110_AHRR
P−value = 5.34e−7




cg20109054_C6orf48;SNORD52
P−value = 7.85e−7
0.16
0.14
0.12
0.10
0.08
0.06
0.04
SMK
E<1
E1−5
E5+
Non

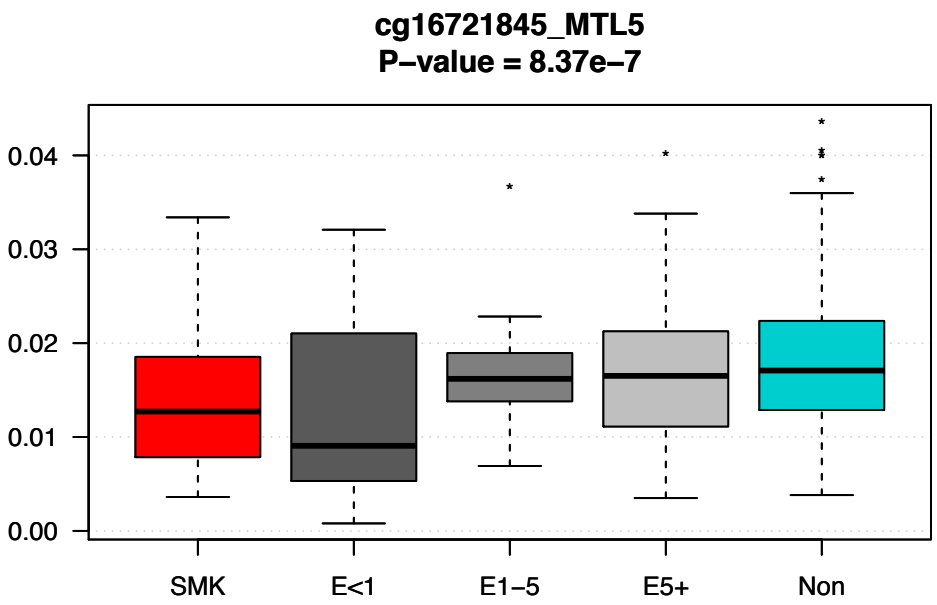
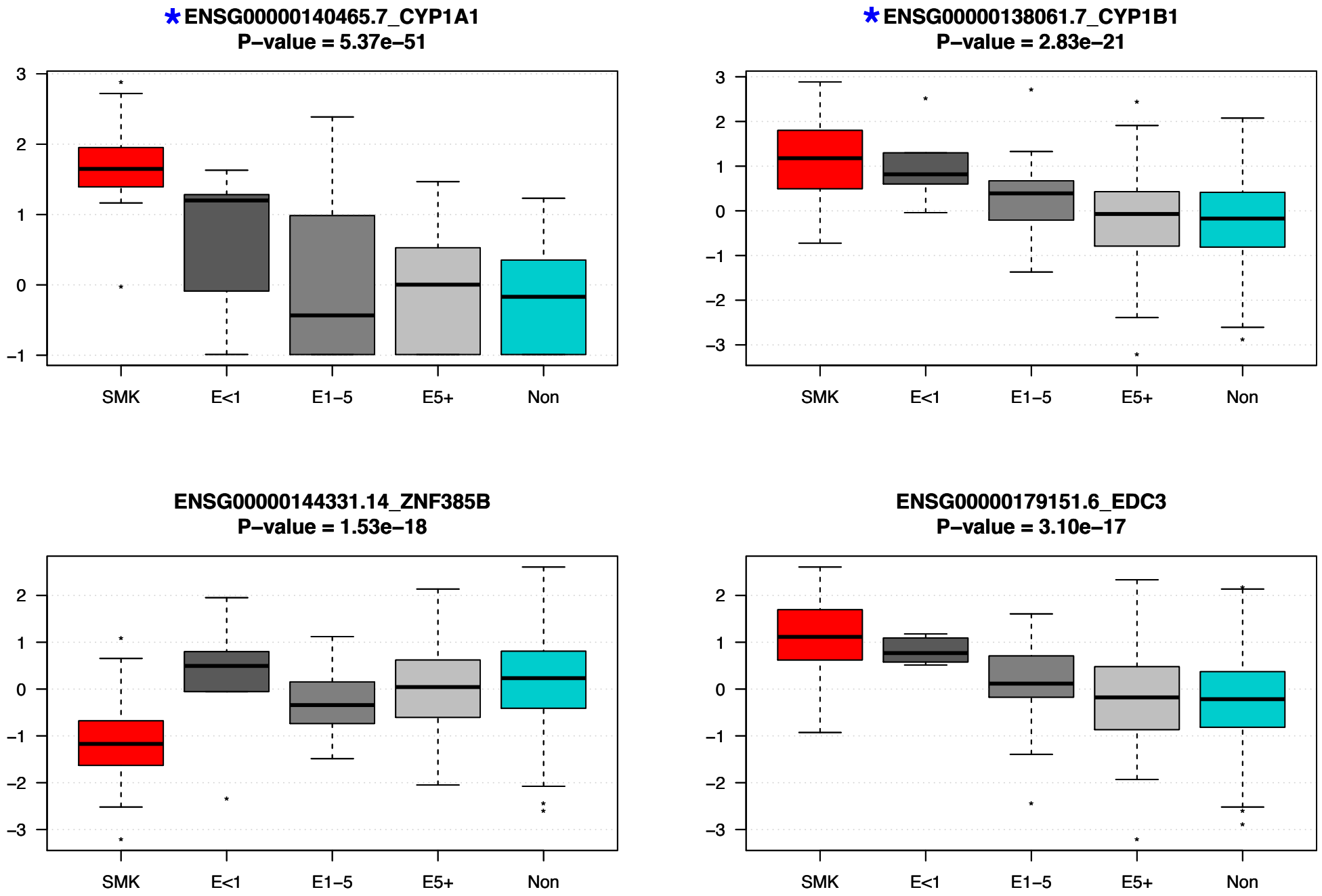
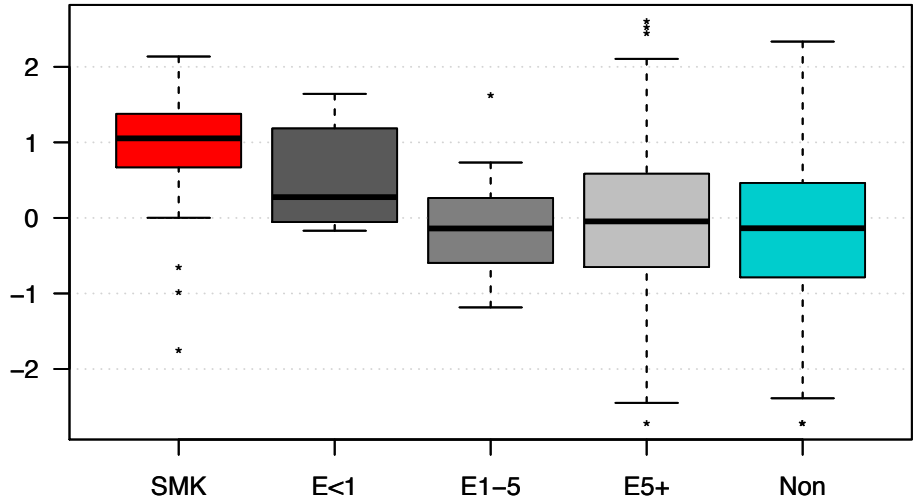

cg16721845_MTL5
P−value = 8.37e−7
0.04
0.03
0.02
0.01
0.00
SMK
E<1
E1−5
E5+
Non

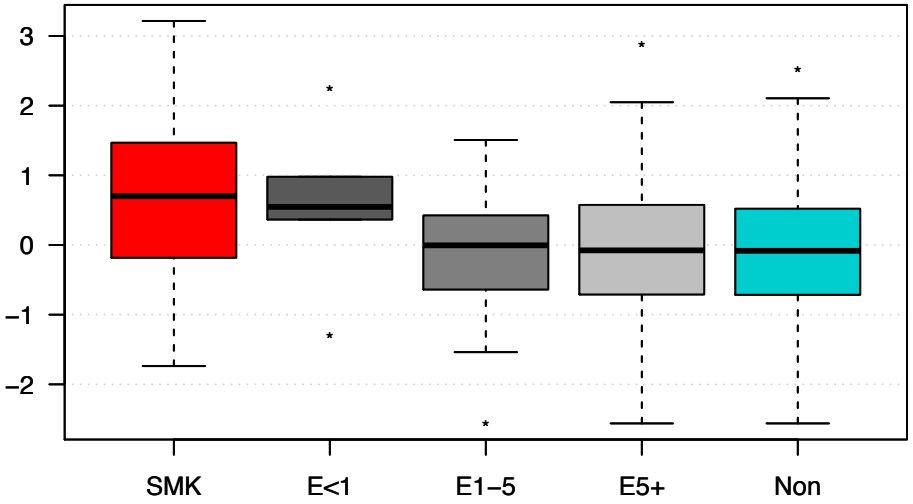
Figure S3


*ENSG00000140465.7_CYP1A1
P−value = 5.37e−51
*ENSG00000138061.7_CYP1B1
P−value = 2.83e−21
ENSG00000144331.14_ZNF385B
P−value = 1.53e−18
ENSG00000179151.6_EDC3
P−value = 3.10e−17
SMK
E<1
E1−5
E5+
Non

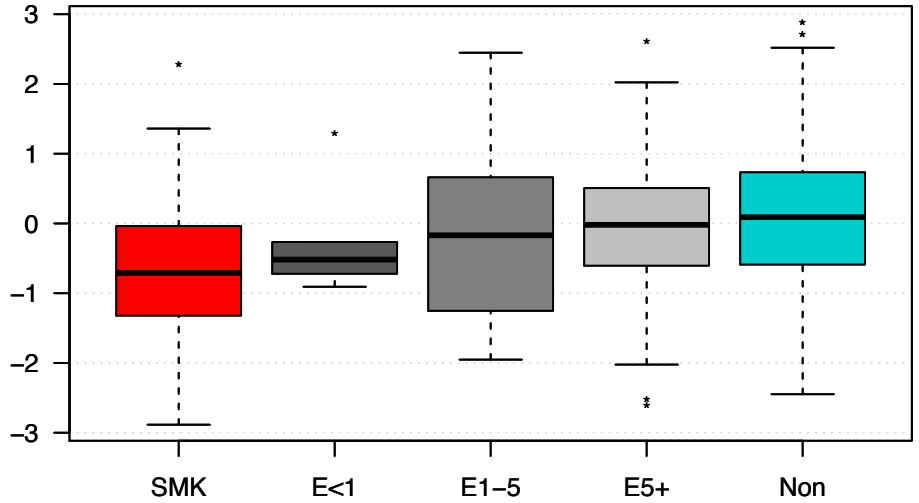
*ENSG00000063438.12_AHRR
P−value = 6.03e−12



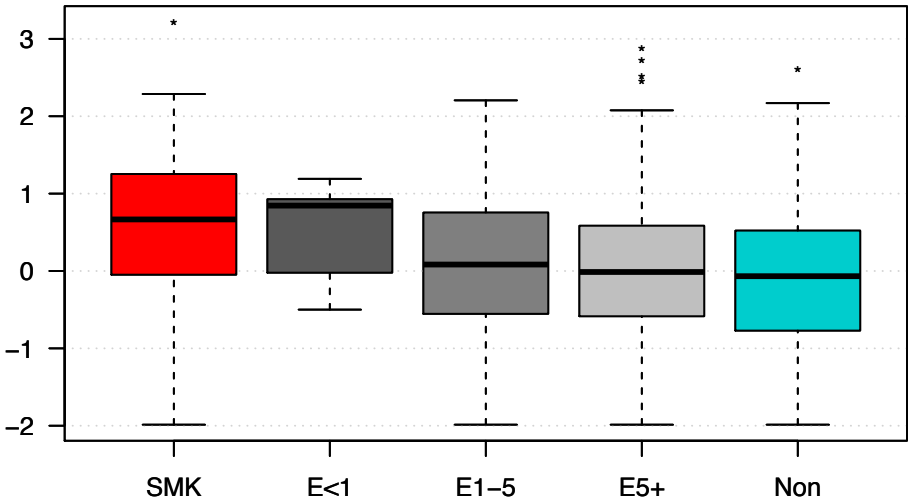
ENSG00000175267.8_VWA3A
P−value = 2.18e−10



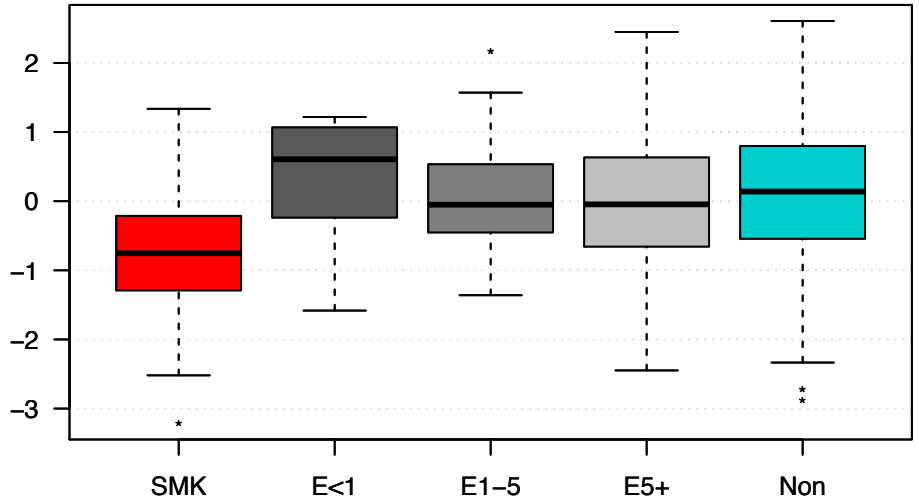
ENSG00000170381.7_SEMA3E
P−value = 8.35e−09



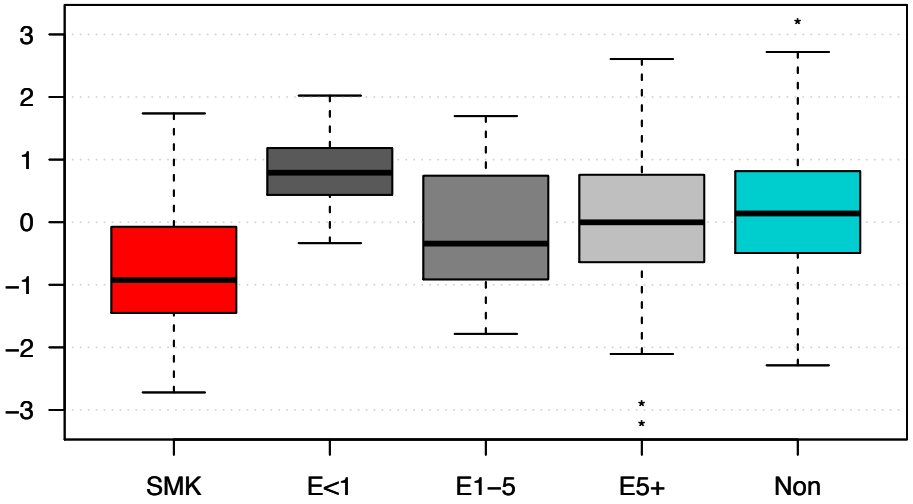
*ENSG00000170891.6_CYTL1
P−value = 2.82e−08



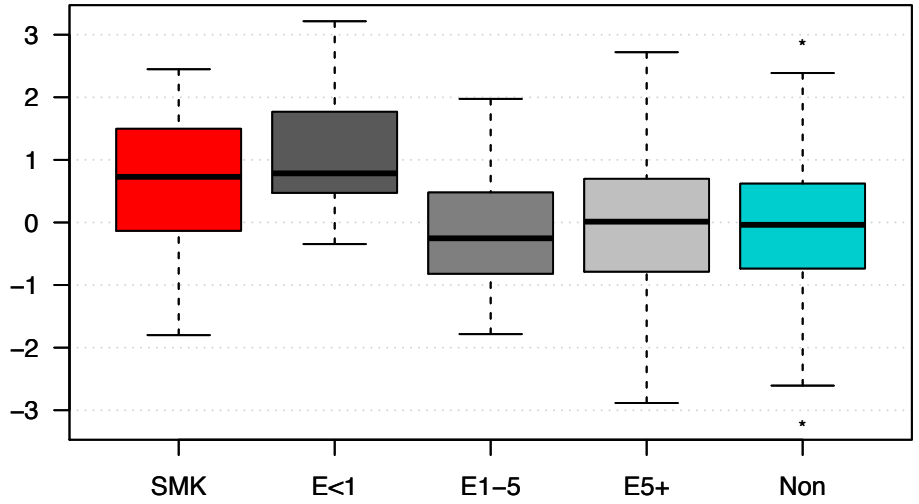
ENSG00000187486.5_KCNJ11
P−value = 3.27e−08



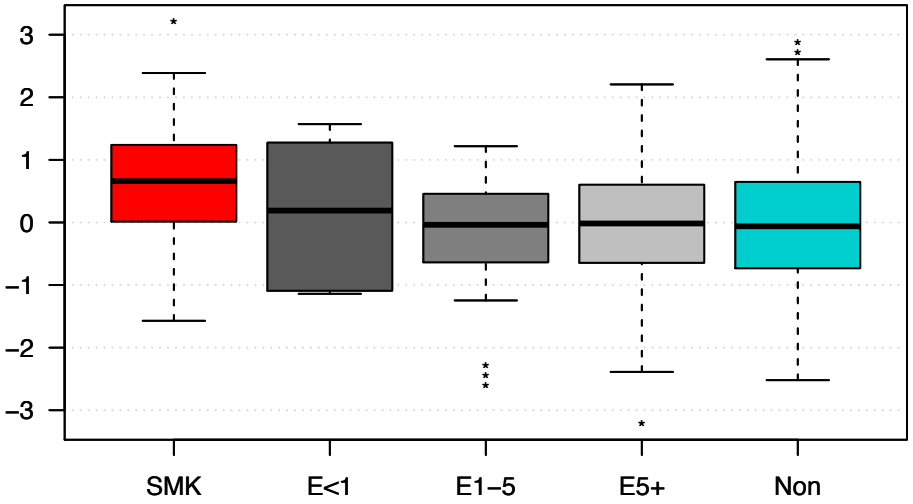
ENSG00000168280.11_KIF5C
P−value = 4.74e−08



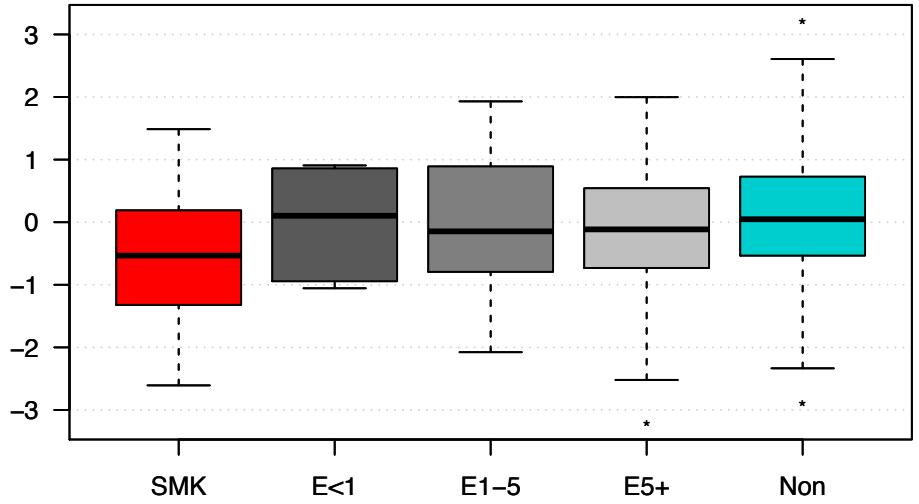
ENSG00000006016.5_CRLF1
P−value = 2.53e−07



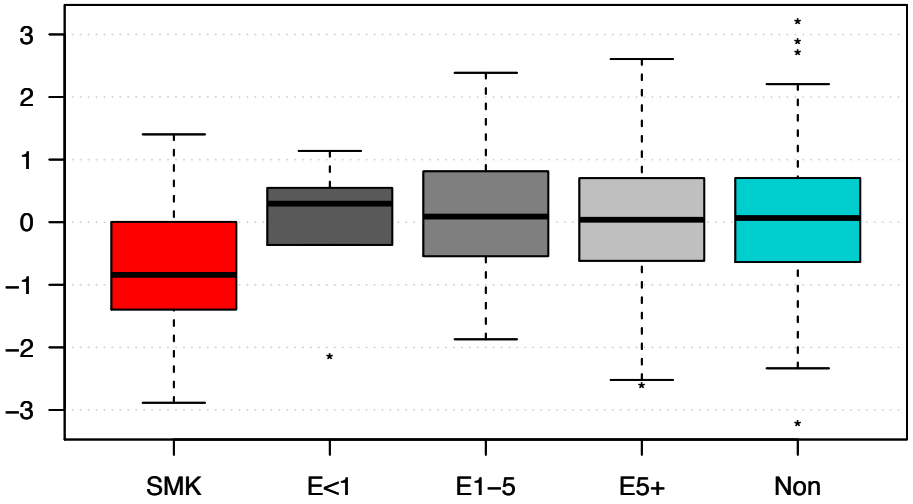
* ENSG00000127533.2_F2RL3
P−value = 2.89e−07



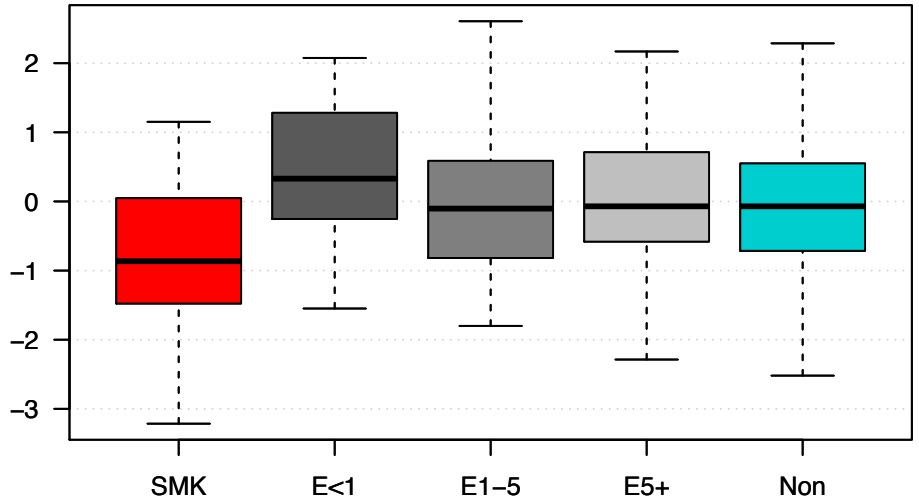
ENSG00000149294.11_NCAM1
P−value = 3.03e−07



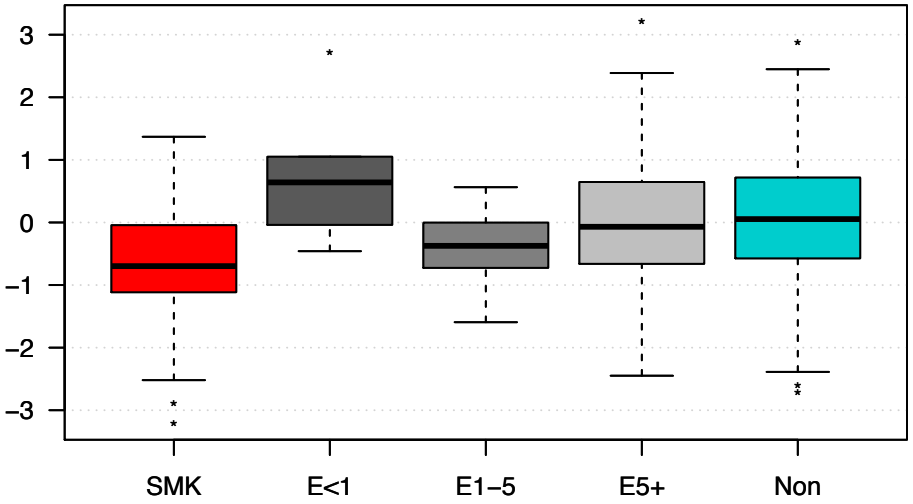
ENSG00000120693.9_SMAD9
P−value = 4.76e−07



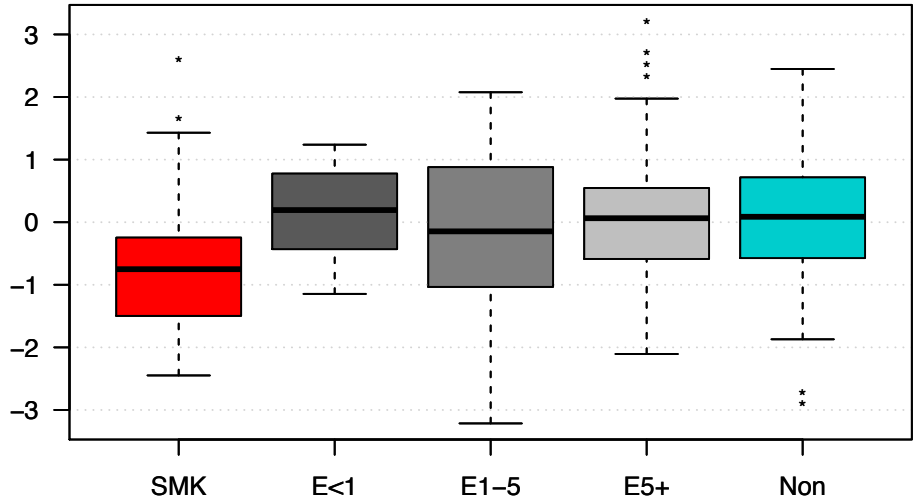
ENSG00000169116.7_PARM1
P−value = 6.76e−07



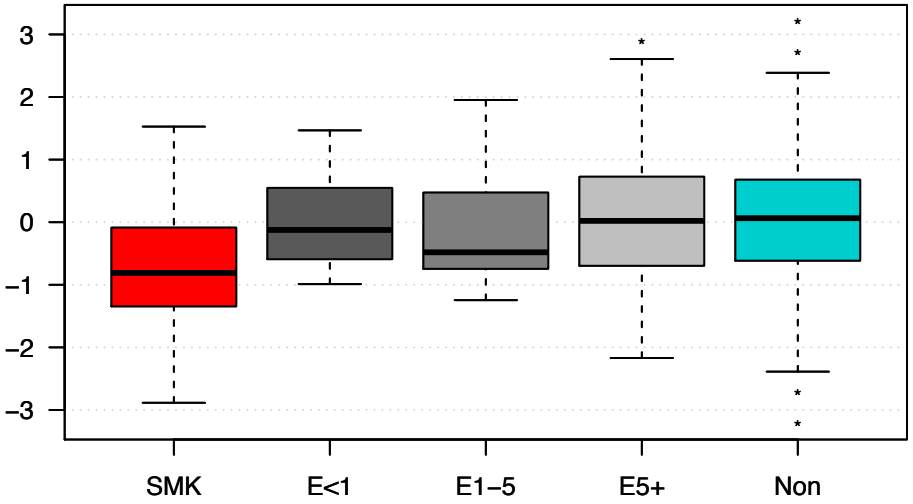
ENSG00000154330.6_PGM5
P−value = 1.72e−06



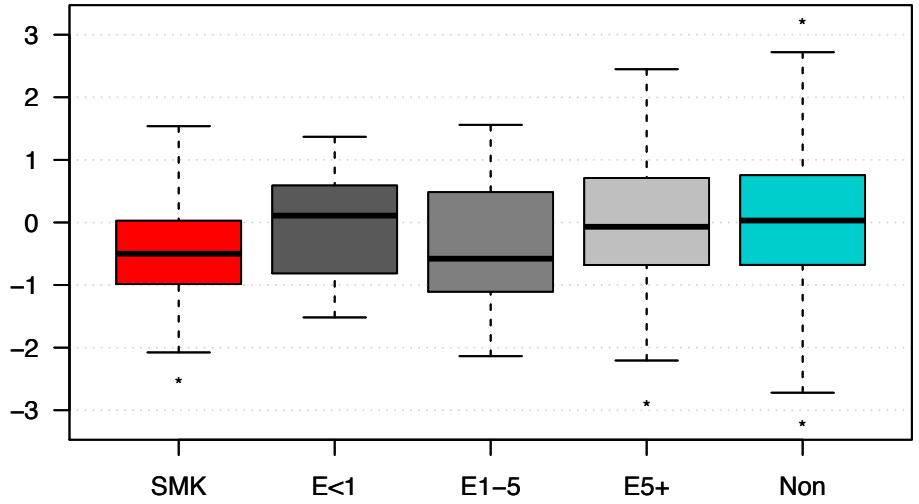
ENSG00000162430.12_SEPN1
P−value = 1.82e−06



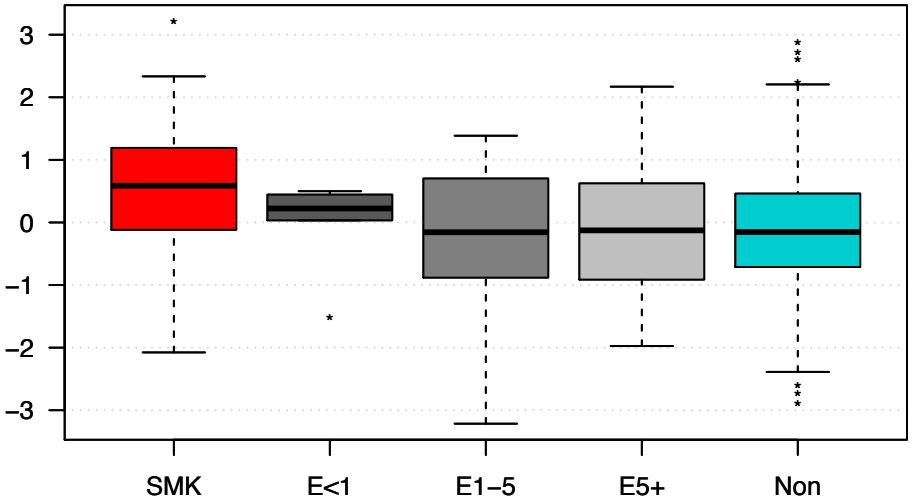
ENSG00000154721.9_JAM2
P−value = 2.23e−06



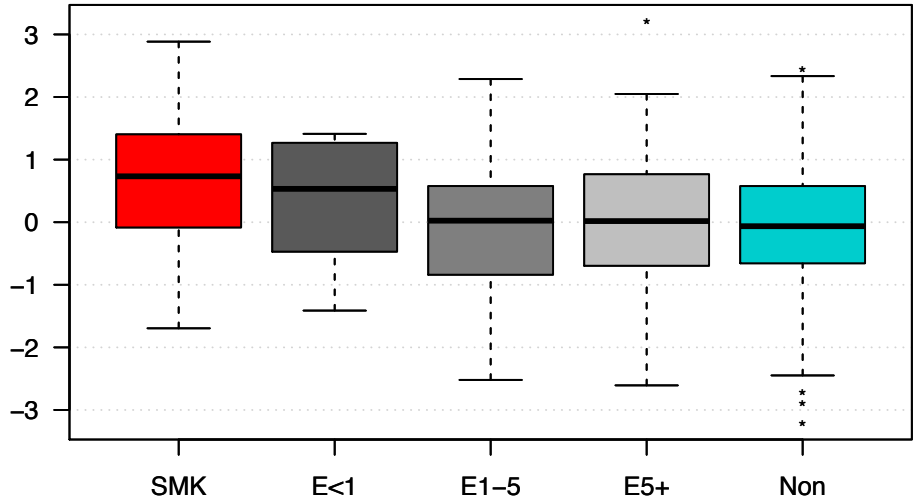
ENSG00000177303.4_CASKIN2
P−value = 2.90e−06



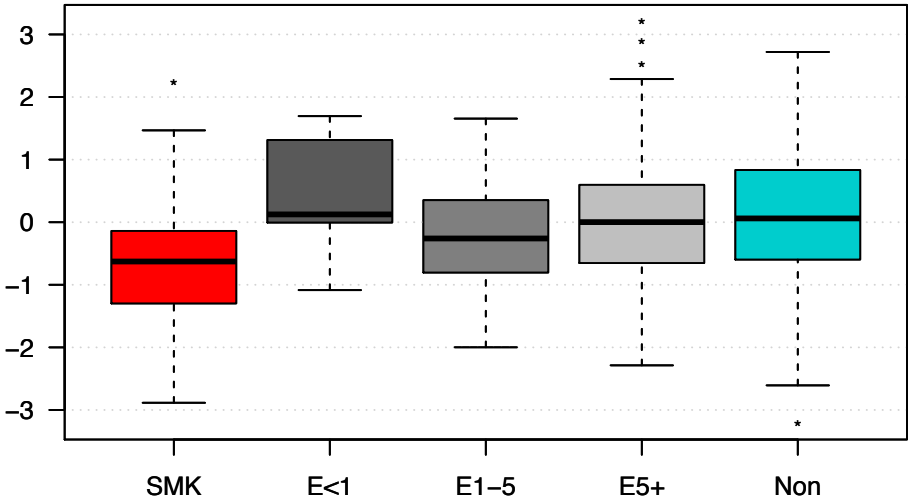
ENSG00000157404.10_KIT
P−value = 3.31e−06



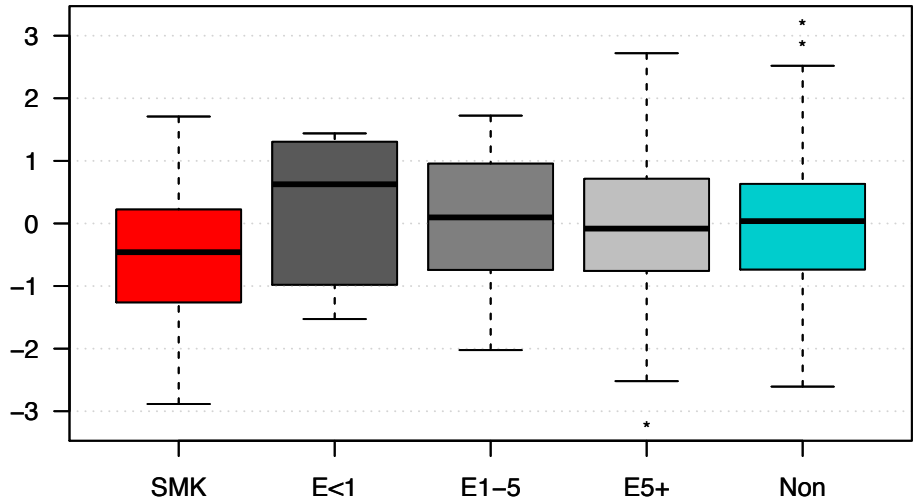
ENSG00000161544.4_CYGB
P−value = 3.42e−06



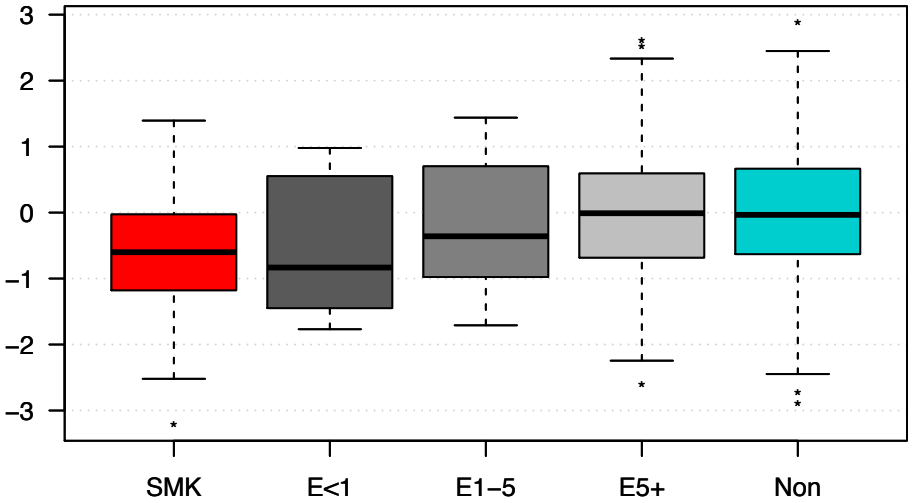
ENSG00000154065.9_ANKRD29
P−value = 3.49e−06

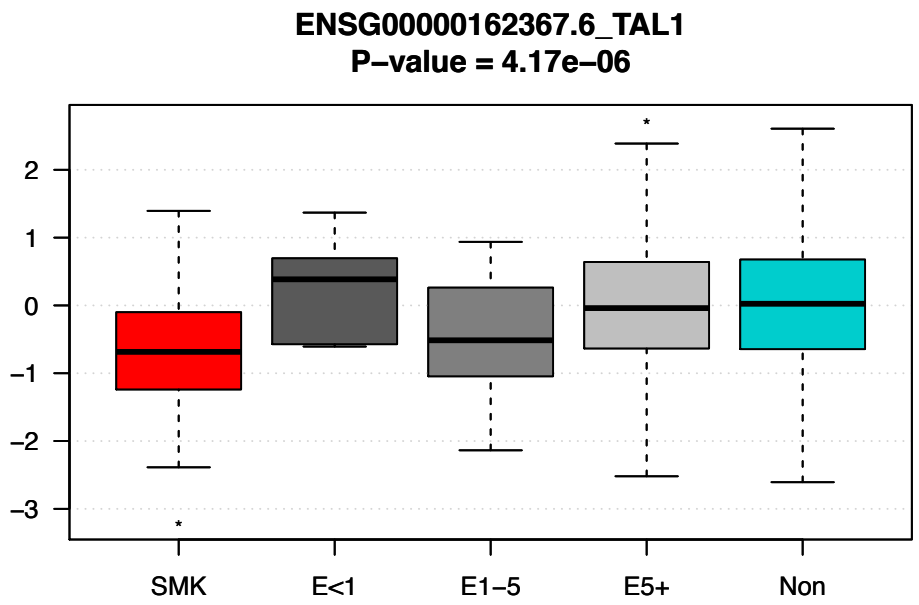


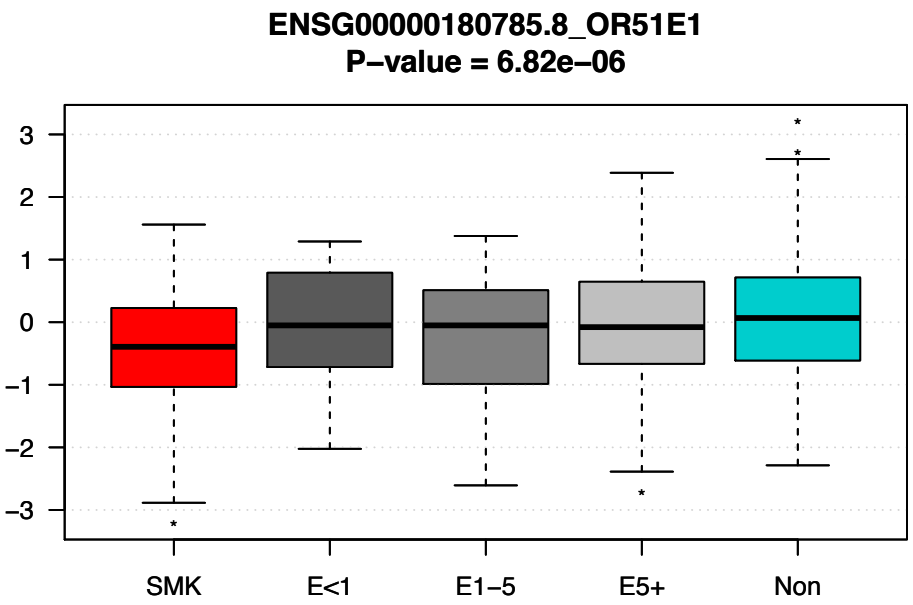
ENSG00000176907.3_C8orf4
P−value = 3.56e−06

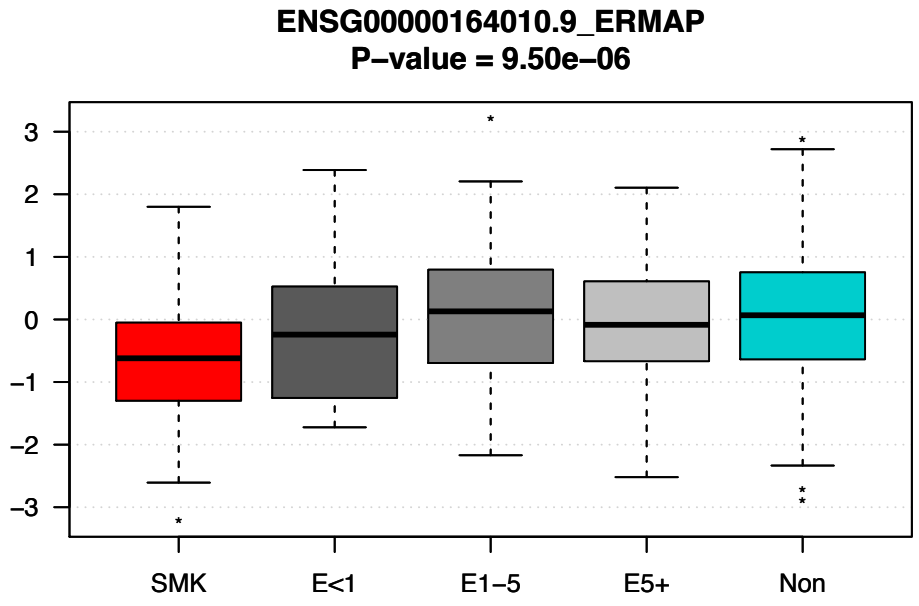


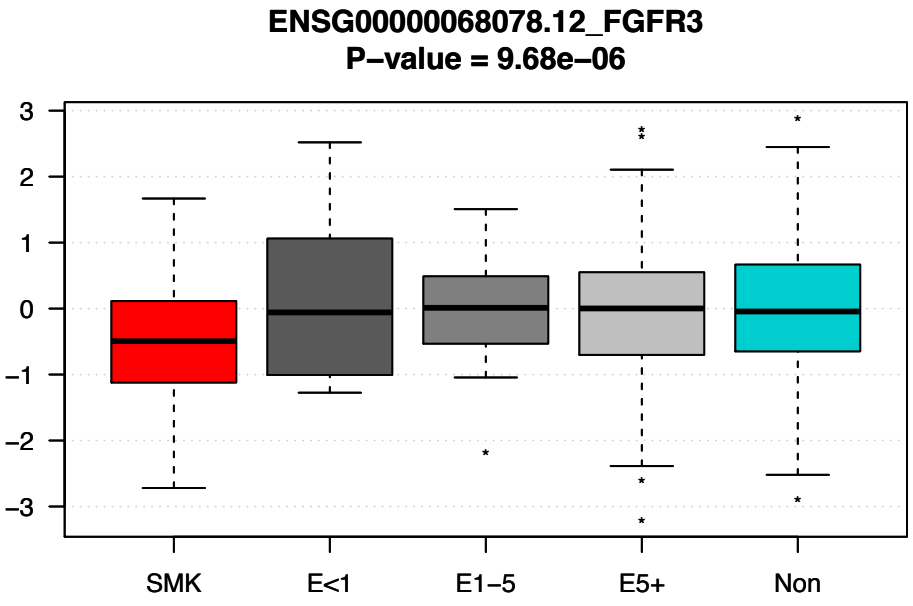
ENSG00000168032.4_ENTPD3
P−value = 3.86e−06



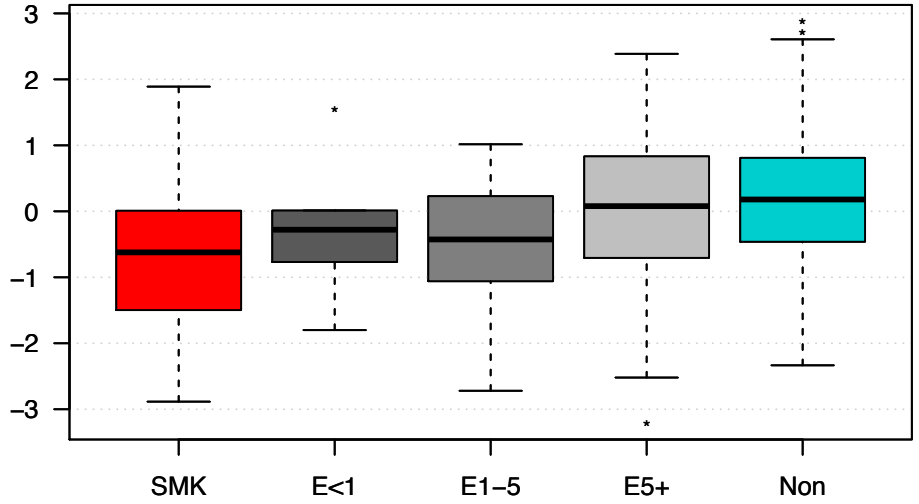

ENSG00000162367.6_TAL1
P−value = 4.17e−06
2
1
0
−1
−2
−3
SMK
E<1
E1−5
E5+
Non


ENSG00000180785.8_OR51E1
P−value = 6.82e−06
3
2
1
0
−1
−2
−3
SMK
E<1
E1−5
E5+
Non

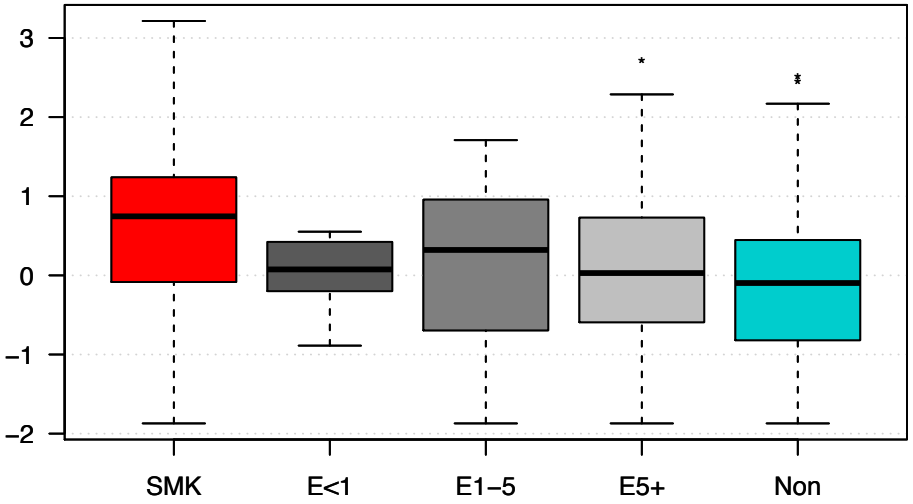

ENSG00000164010.9_ERMAP
P−value = 9.50e−06
3
2
1
0
−1
−2
−3
SMK
E<1
E1−5
E5+
Non


ENSG00000068078.12_FGFR3
P−value = 9.68e−06
3
2
1
0
−1
−2
−3
SMK
E<1
E1−5
E5+
Non

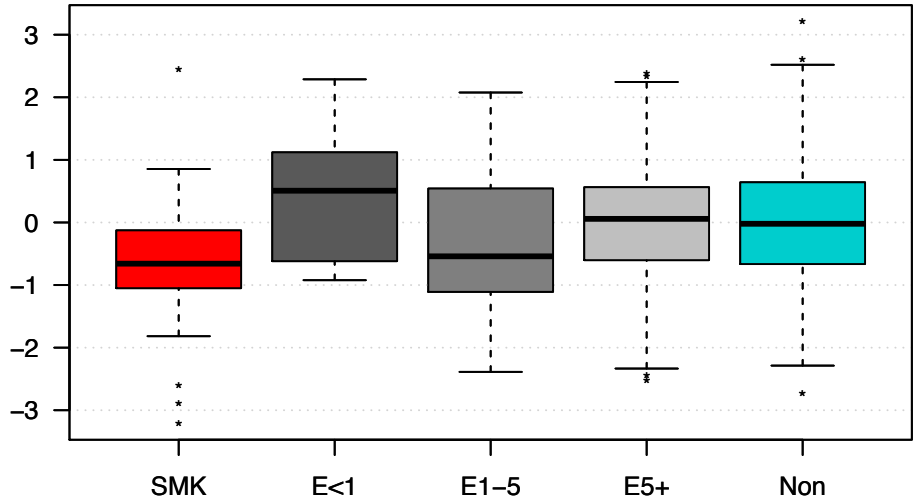
ENSG00000246223.4_C14orf64
P−value = 1.44e−05



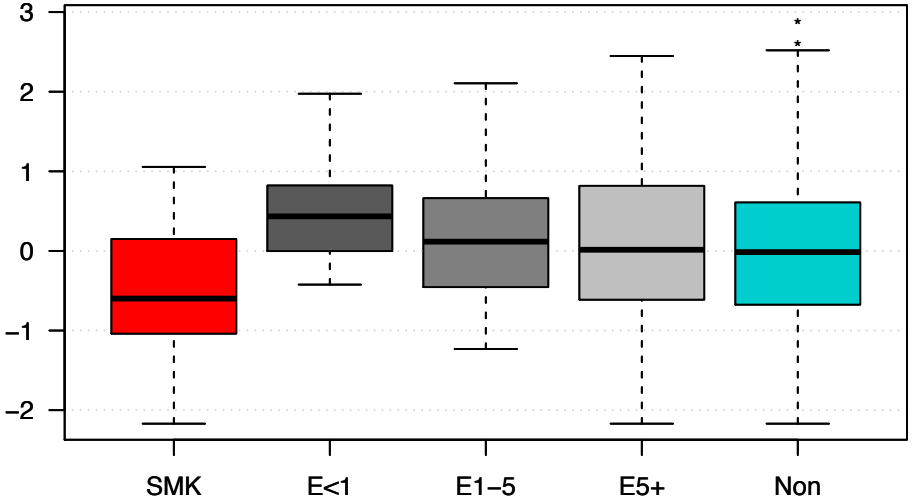
ENSG00000145506.9_NKD2
P−value = 1.46e−05

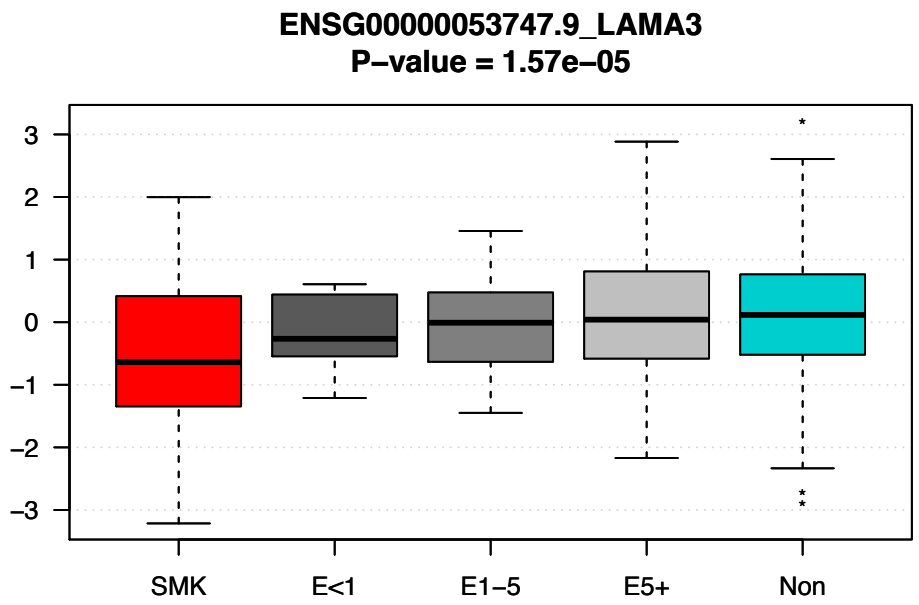


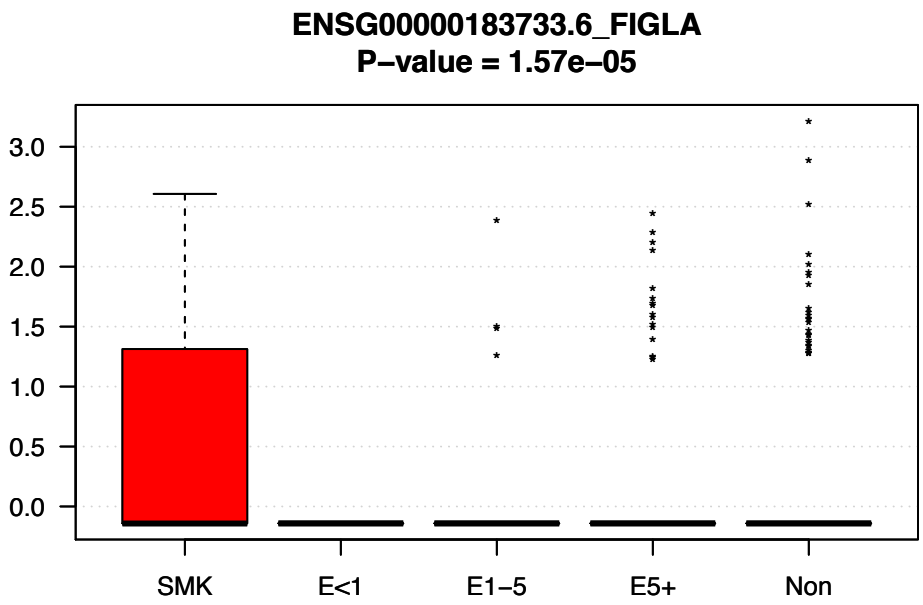
ENSG00000161649.7_CD300LG
P−value = 1.48e−05

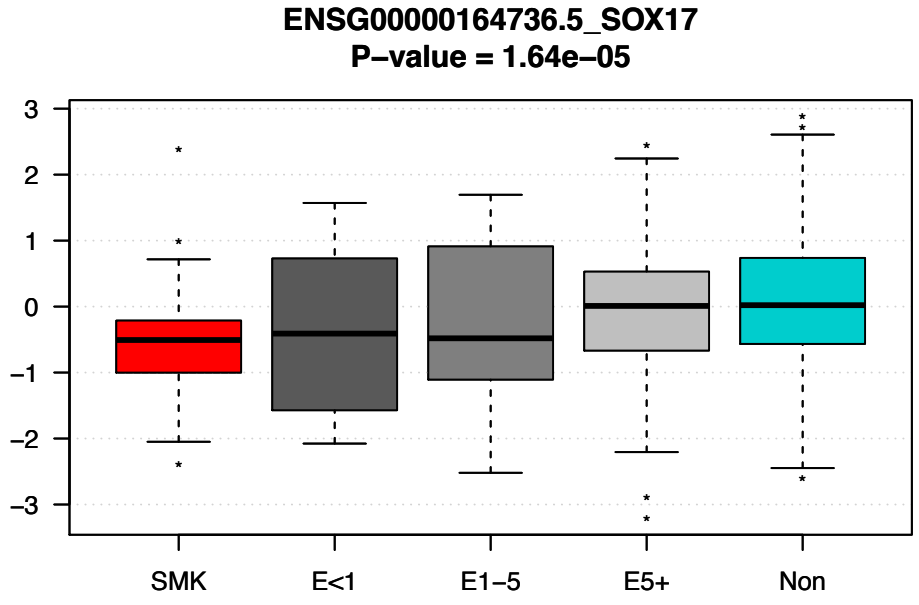


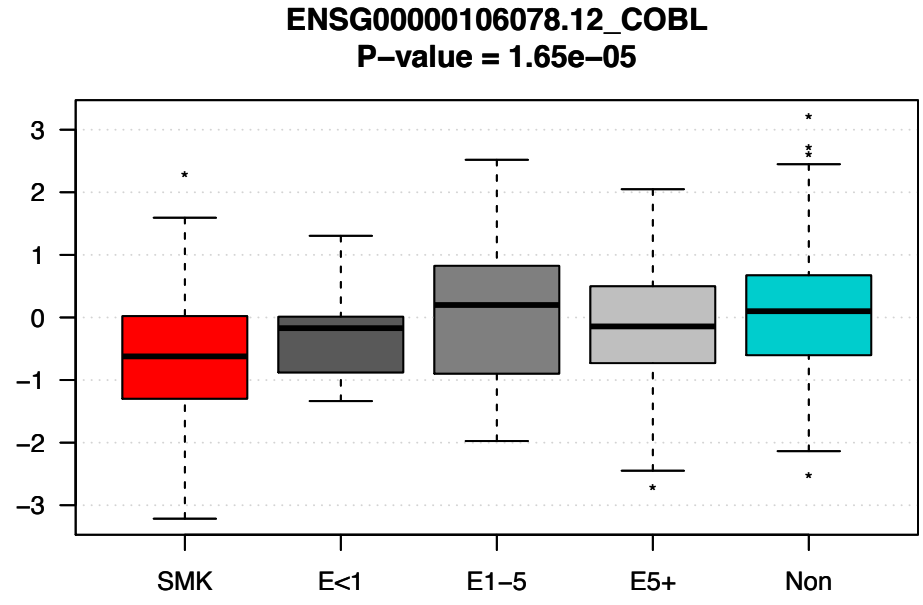
ENSG00000163873.5_GRIK3
P−value = 1.50e−05

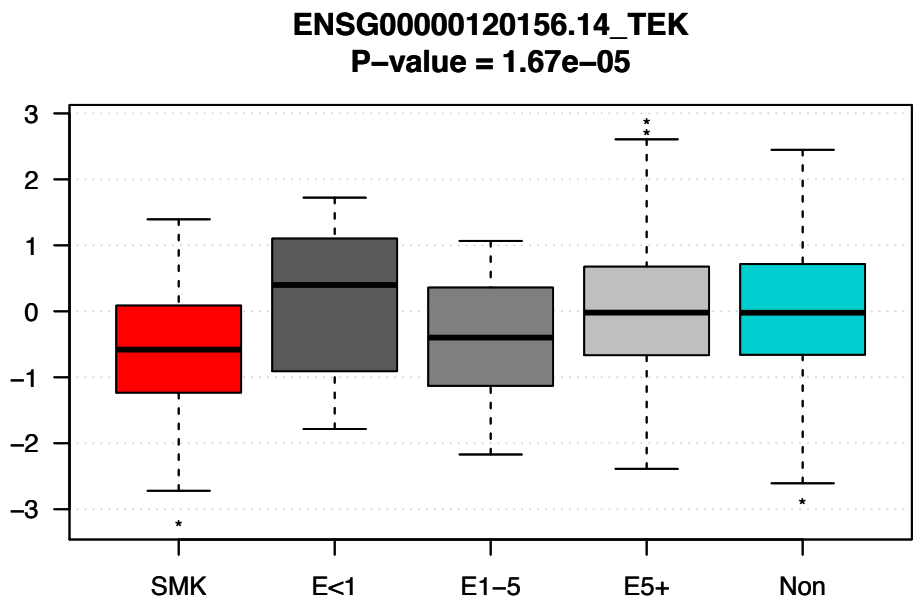


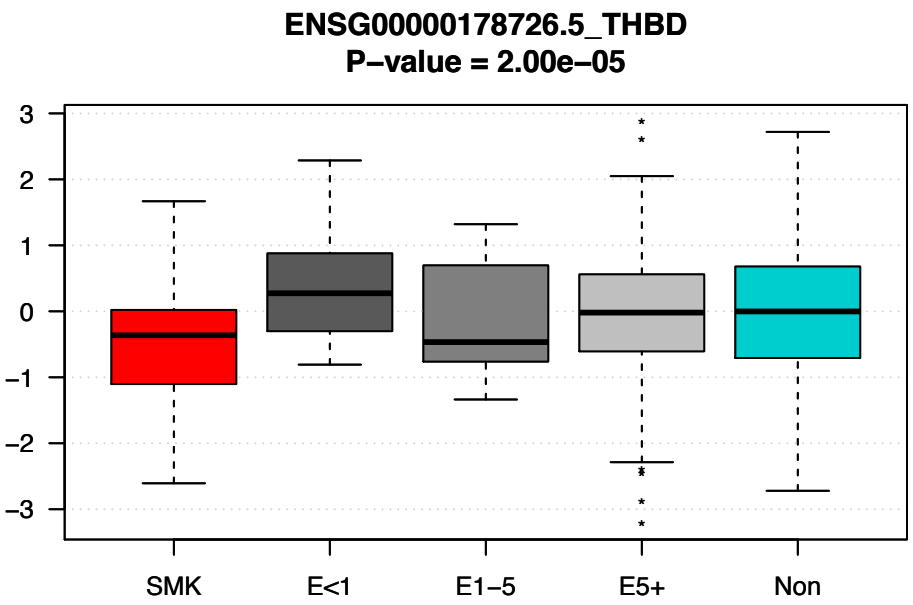

ENSG00000053747.9_LAMA3
P−value = 1.57e−05
3
2
1
0
−1
−2
−3
SMK
E<1
E1−5
E5+
Non

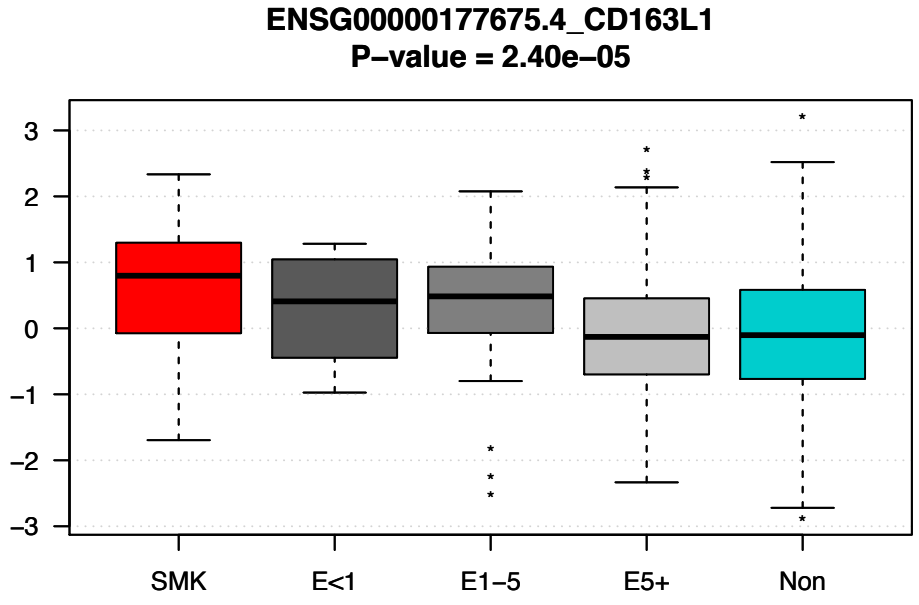

ENSG00000183733.6_FIGLA
P−value = 1.57e−05
3.0
2.5
2.0
1.5
1.0
0.5
0.0
SMK
E<1
E1−5
E5+
Non

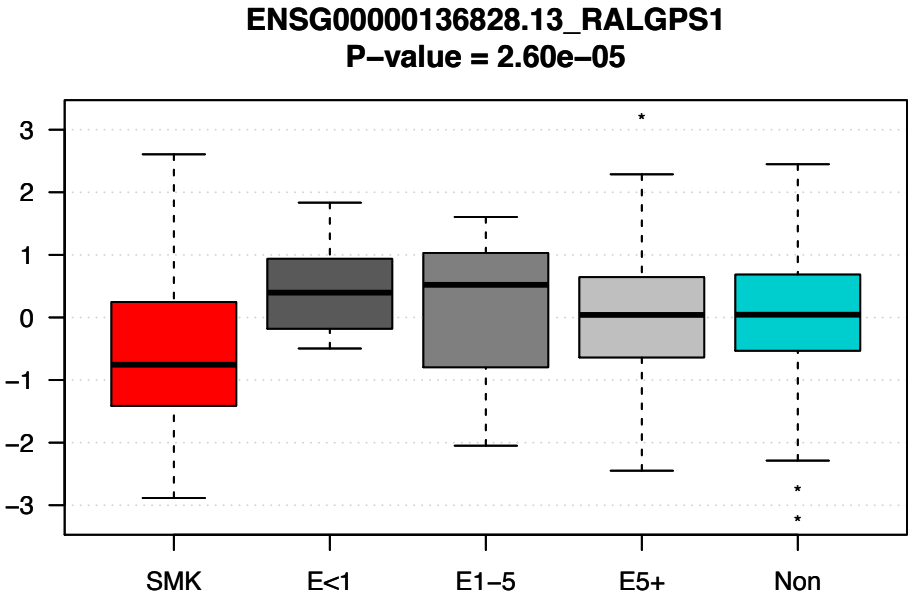

ENSG00000164736.5_SOX17
P−value = 1.64e−05
3
2
1
0
−1
−2
−3
SMK
E<1
E1−5
E5+
Non

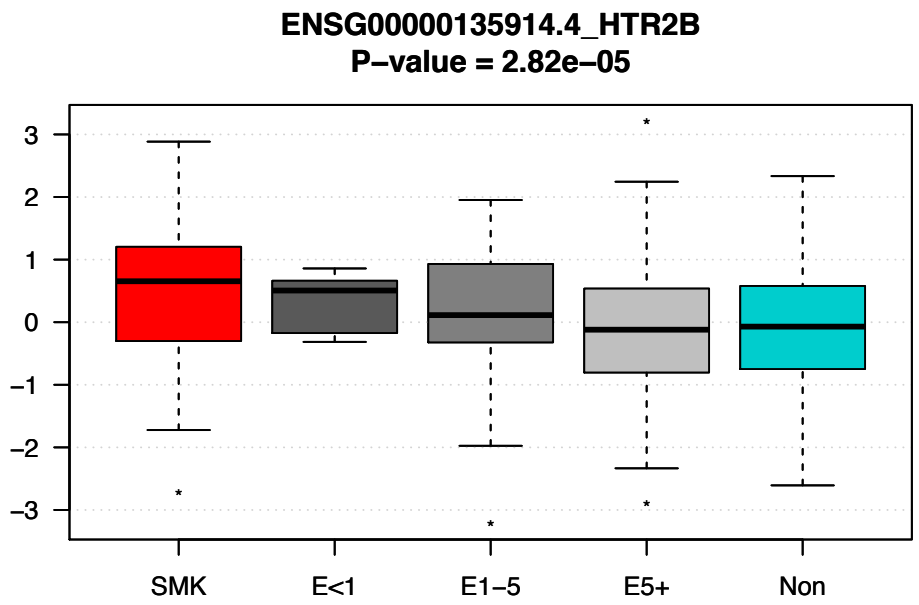

ENSG00000106078.12_COBL
P−value = 1.65e−05
3
2
1
0
−1
−2
−3
SMK
E<1
E1−5
E5+
Non


ENSG00000120156.14_TEK
P−value = 1.67e−05
3
2
1
0
−1
−2
−3
SMK
E<1
E1−5
E5+
Non


ENSG00000178726.5_THBD
P−value = 2.00e−05
3
2
1
0
−1
−2
−3
SMK
E<1
E1−5
E5+
Non


ENSG00000177675.4_CD163L1
P−value = 2.40e−05
3
2
1
0
−1
−2
−3
SMK
E<1
E1−5
E5+
Non


ENSG00000136828.13_RALGPS1
P−value = 2.60e−05
3
2
1
0
−1
−2
−3
SMK
E<1
E1−5
E5+
Non


ENSG00000135914.4_HTR2B
P−value = 2.82e−05
3
2
1
0
−1
−2
−3
SMK
E<1
E1−5
E5+
Non

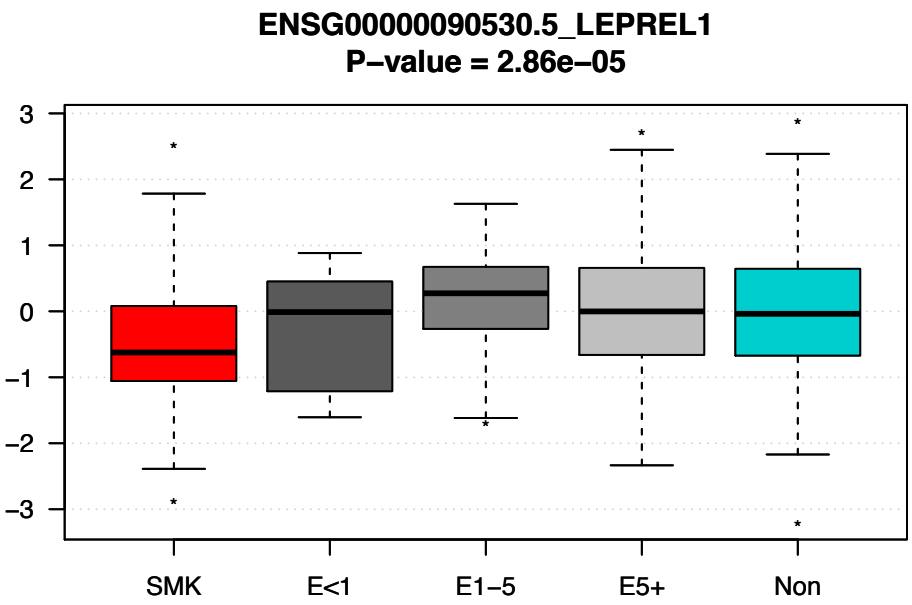
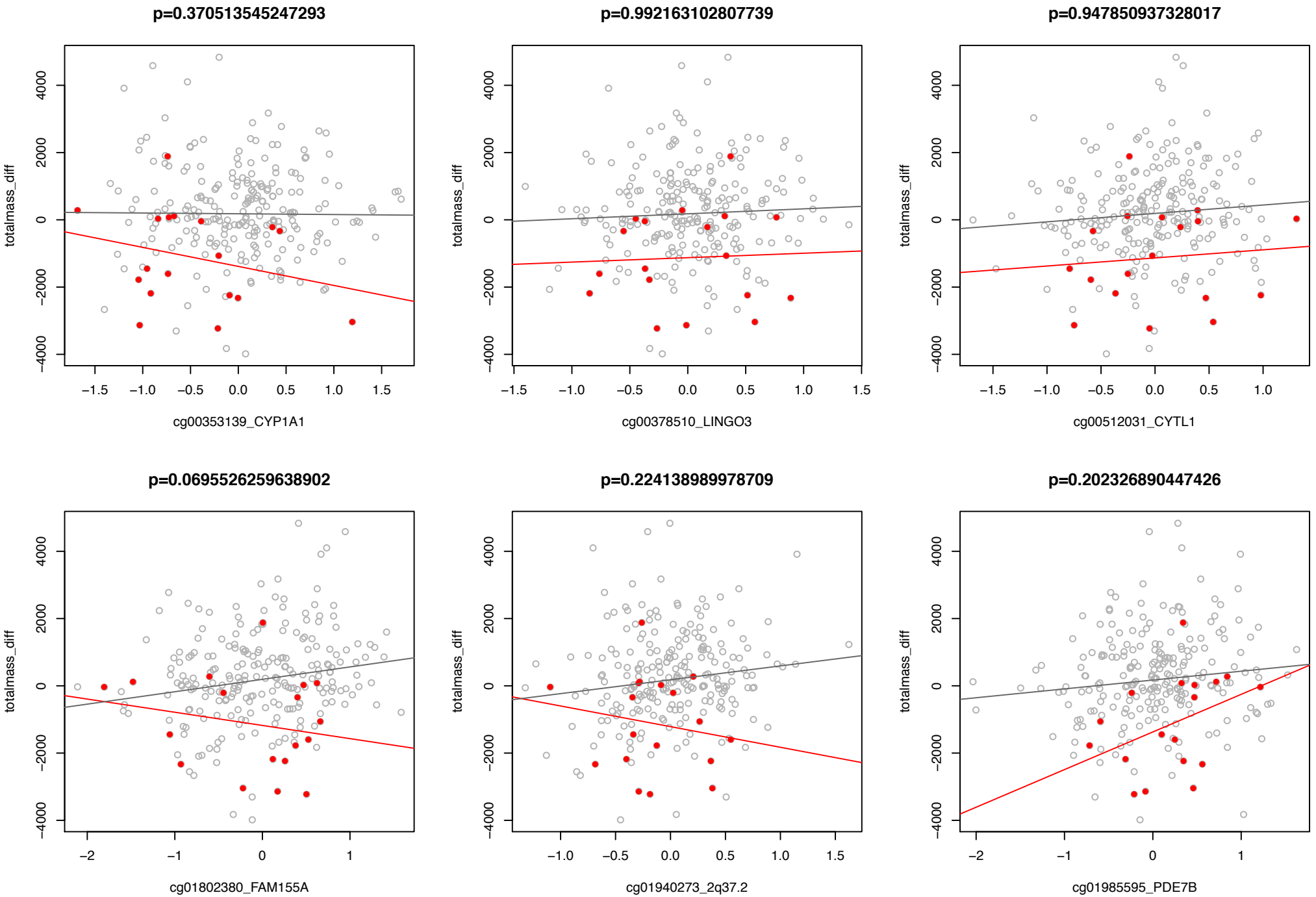
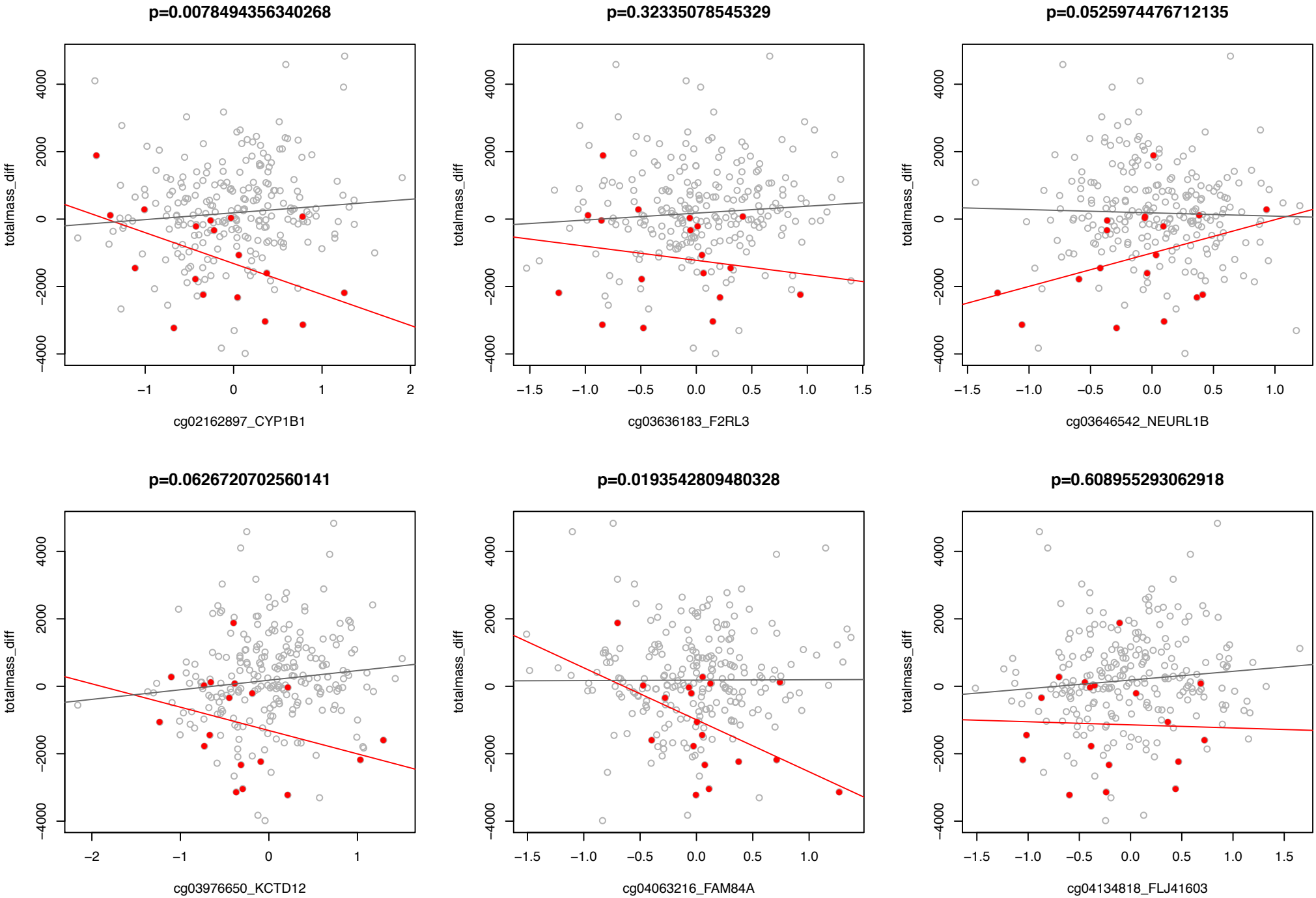
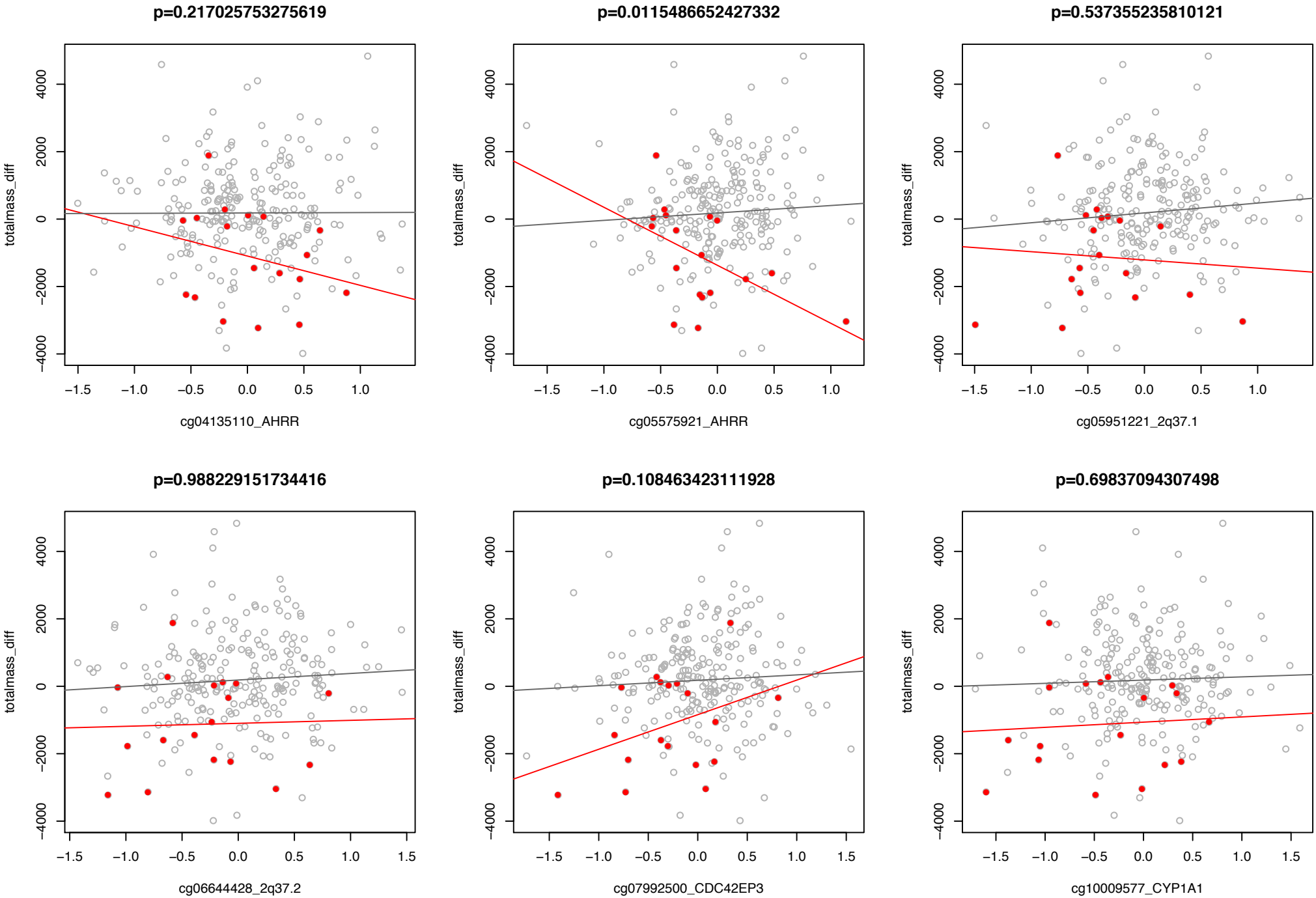
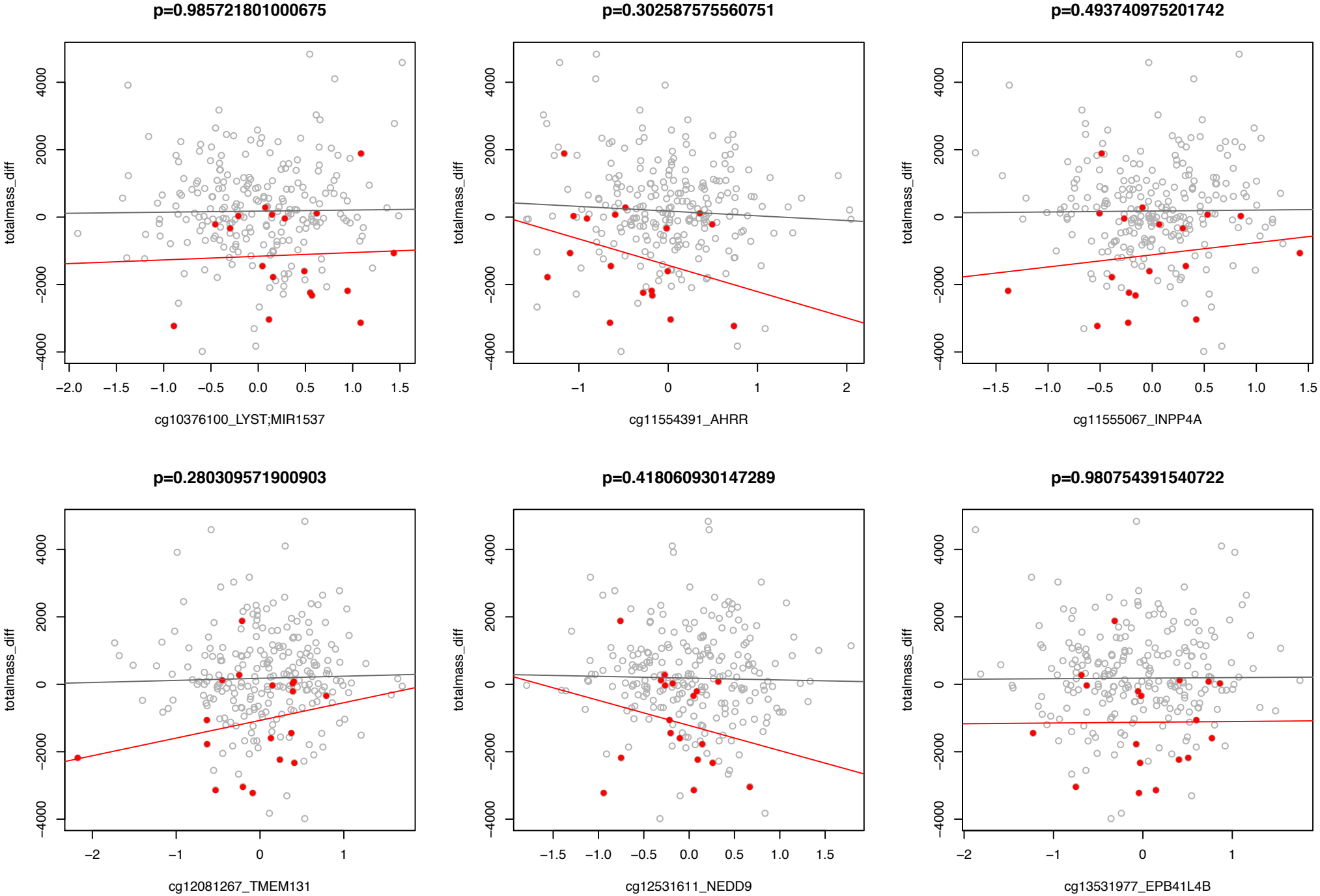

ENSG00000090530.5_LEPREL1
P−value = 2.86e−05
3
2
1
0
−1
−2
−3
SMK
E<1
E1−5
E5+
Non

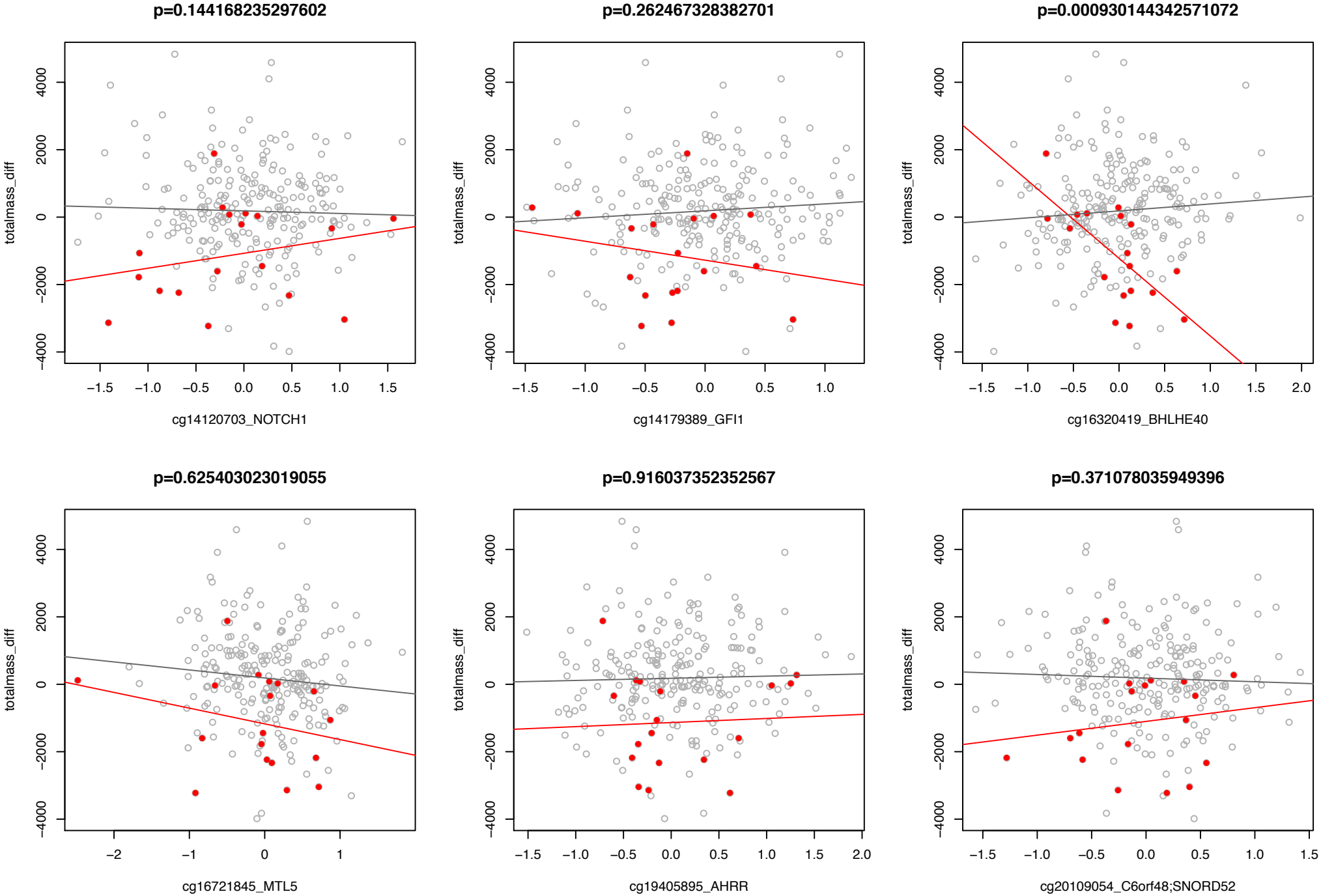
Figure S4

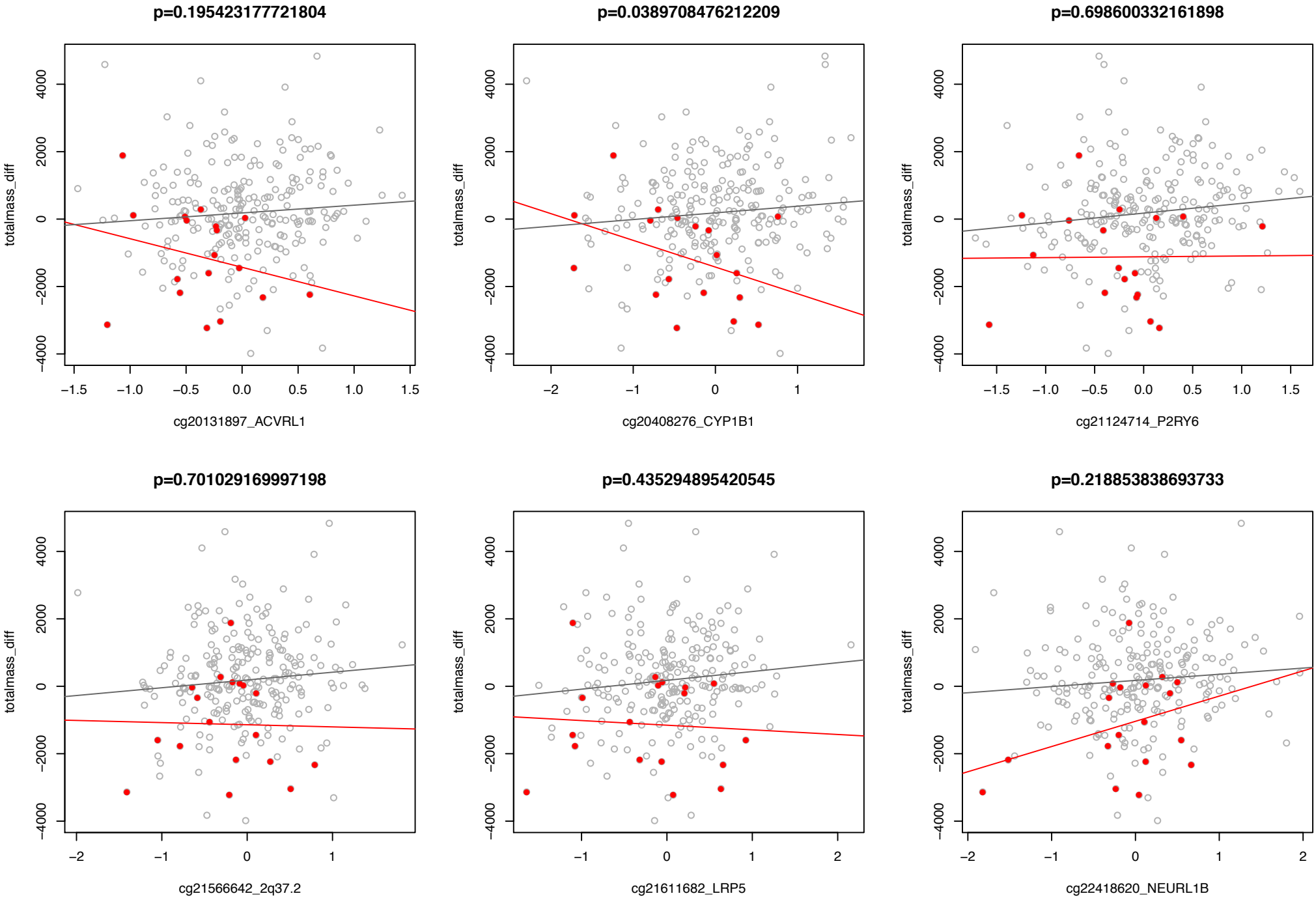

p=0.370513545247293
p=0.992163102807739
p=0.947850937328017
p=0.0695526259638902
p=0.224138989978709
p=0.202326890447426
totalmass_diff
cg00353139_CYP1A1
cg00378510_LINGO3
cg00512031_CYTL1
cg01802380_FAM155A
cg01940273_2q37.2
cg01985595_PDE7B


p=0.0078494356340268
totalmass_diff
cg02162897_CYP1B1
p=0.32335078545329
totalmass_diff
cg03636183_F2RL3
p=0.0525974476712135
totalmass_diff
cg03646542_NEURL1B
p=0.0626720702560141
totalmass_diff
cg03976650_KCTD12
p=0.0193542809480328
totalmass_diff
cg04063216_FAM84A
p=0.608955293062918
totalmass_diff
cg04134818_FLJ41603


p=0.217025753275619
totalmass_diff
cg04135110_AHRR
p=0.0115486652427332
totalmass_diff
cg05575921_AHRR
p=0.537355235810121
totalmass_diff
cg05951221_2q37.1
p=0.988229151734416
totalmass_diff
cg06644428_2q37.2
p=0.108463423111928
totalmass_diff
cg07992500_CDC42EP3
p=0.69837094307498
totalmass_diff
cg10009577_CYP1A1


p=0.985721801000675
totalmass_diff
cg10376100_LYST;MIR1537
p=0.302587575560751
totalmass_diff
cg11554391_AHRR
p=0.493740975201742
totalmass_diff
cg11555067_INPP4A
p=0.280309571900903
totalmass_diff
cg12081267_TMEM131
p=0.418060930147289
totalmass_diff
cg12531611_NEDD9
p=0.980754391540722
totalmass_diff
cg13531977_EPB41L4B


p=0.144168235297602
totalmass_diff
cg14120703_NOTCH1
p=0.262467328382701
totalmass_diff
cg14179389_GFI1
p=0.000930144342571072
totalmass_diff
cg16320419_BHLHE40
p=0.625403023019055
totalmass_diff
cg16721845_MTL5
p=0.916037352352567
totalmass_diff
cg19405895_AHRR
p=0.371078035949396
totalmass_diff
cg20109054_C6orf48;SNORD52


p=0.195423177721804
totalmass_diff
cg20131897_ACVRL1
p=0.0389708476212209
totalmass_diff
cg20408276_CYP1B1
p=0.698600332161898
totalmass_diff
cg21124714_P2RY6
p=0.701029169997198
totalmass_diff
cg21566642_2q37.2
p=0.435294895420545
totalmass_diff
cg21611682_LRP5
p=0.218853838693733
totalmass_diff
cg22418620_NEURL1B

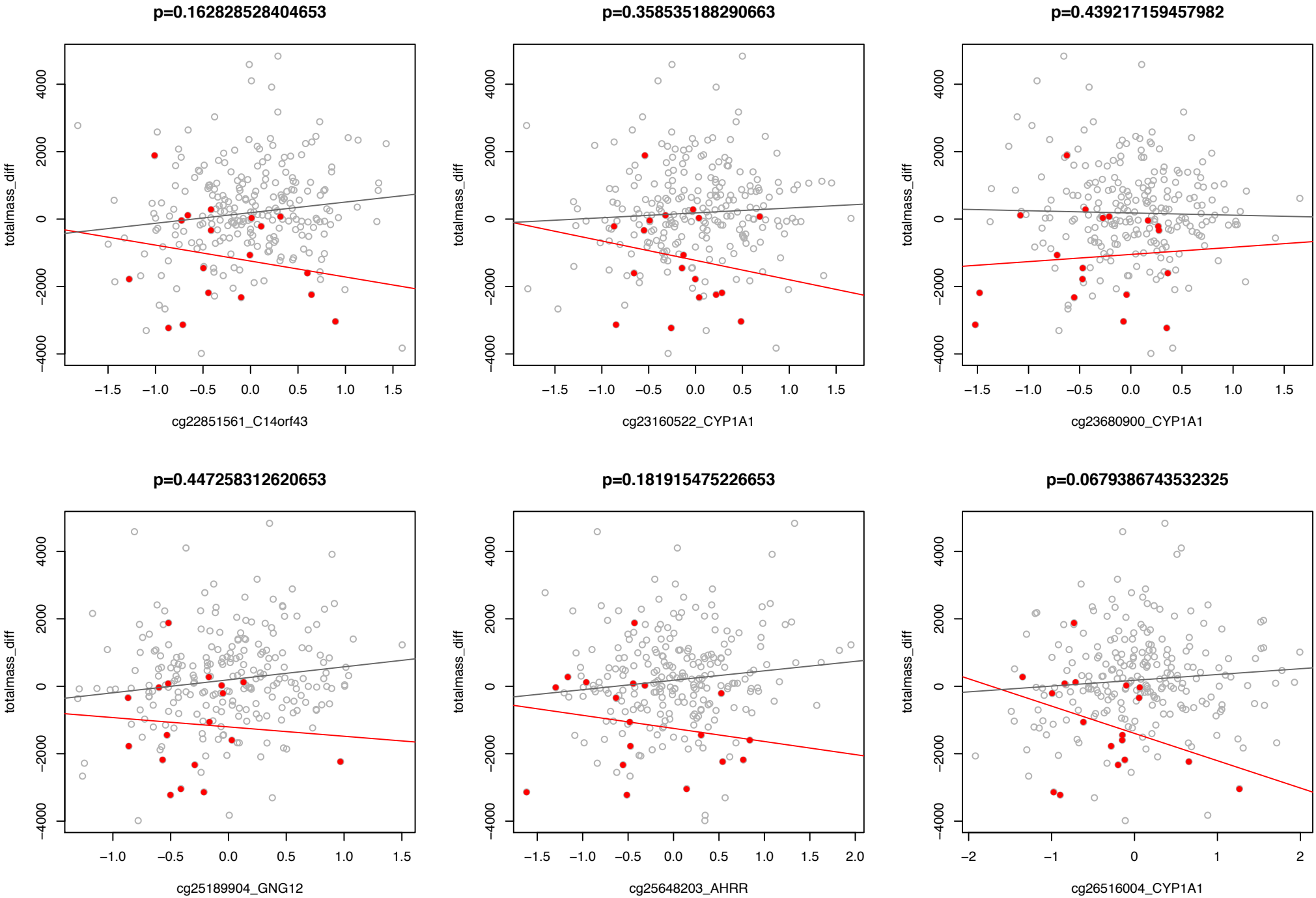
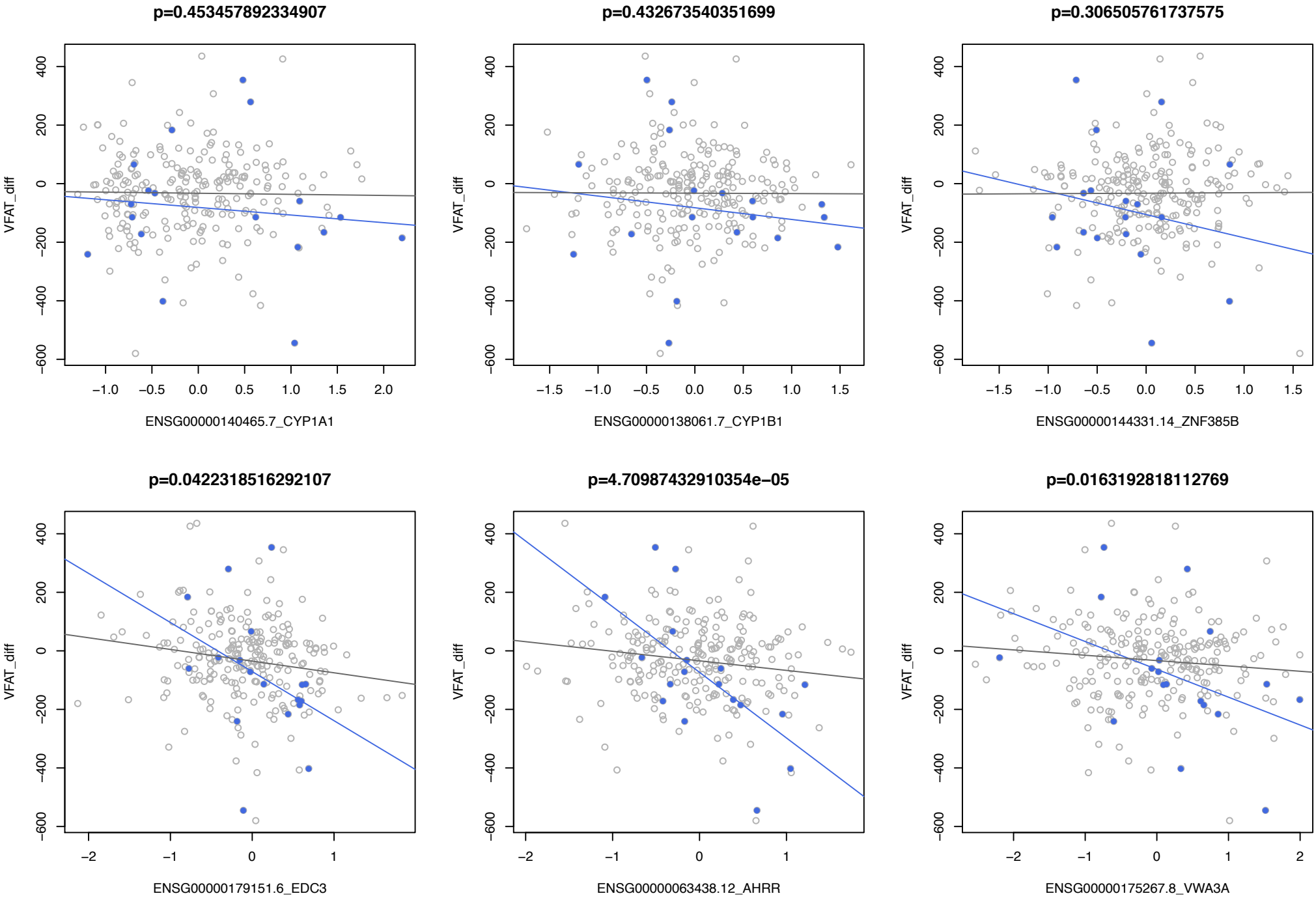
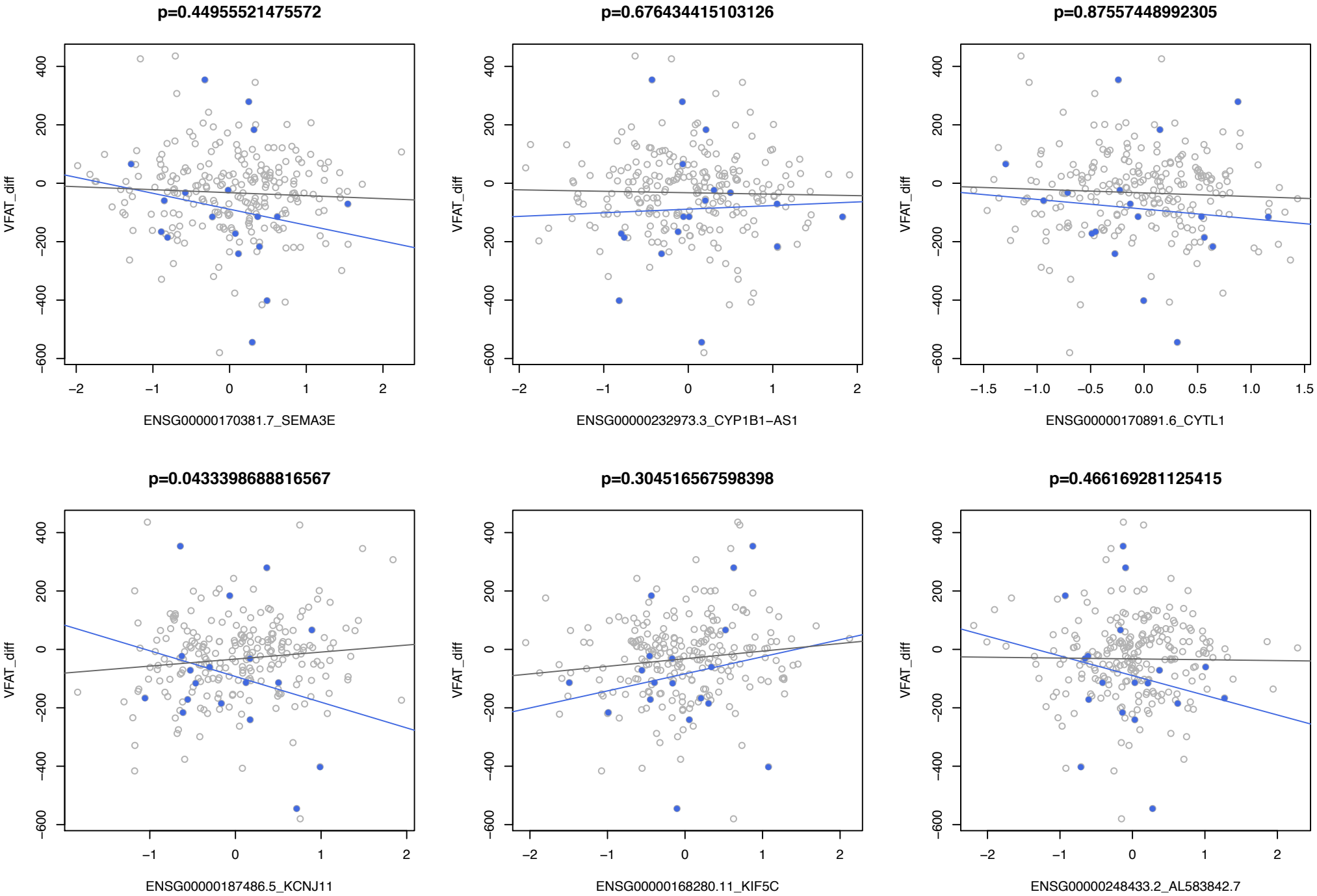
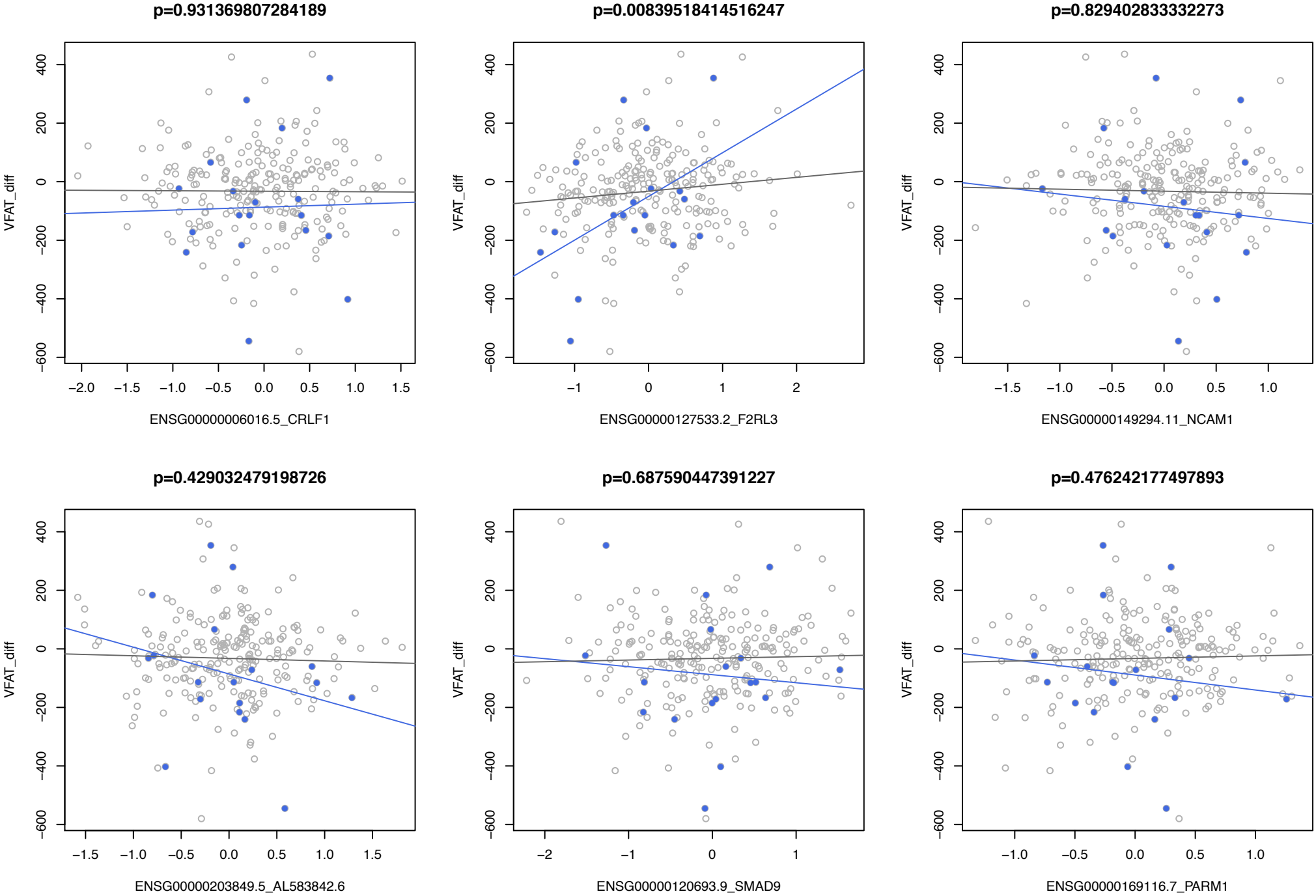
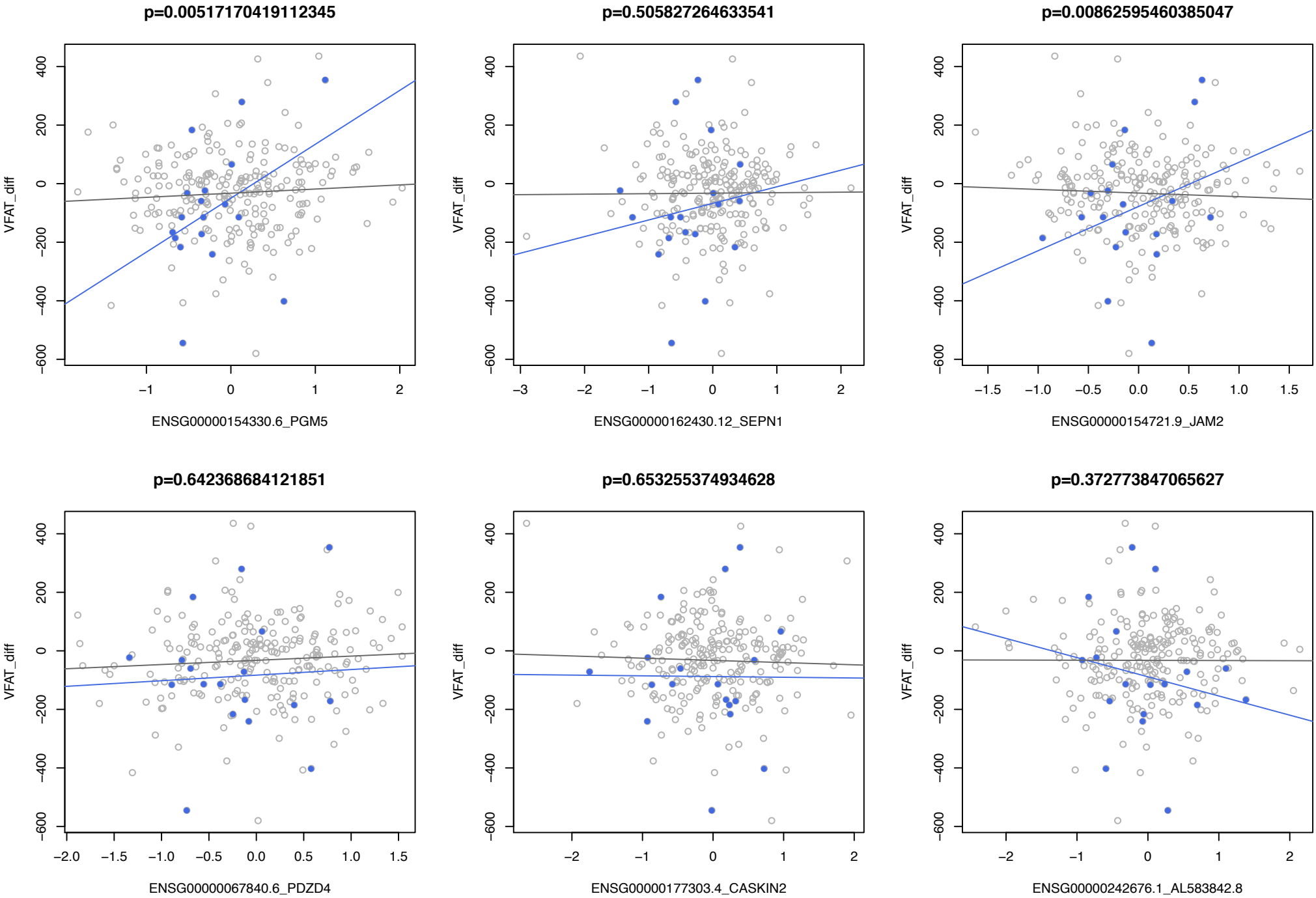

p=0.162828528404653
totalmass_diff
cg22851561_C14orf43
p=0.358535188290663
totalmass_diff
cg23160522_CYP1A1
p=0.439217159457982
totalmass_diff
cg23680900_CYP1A1
p=0.447258312620653
totalmass_diff
cg25189904_GNG12
p=0.181915475226653
totalmass_diff
cg25648203_AHRR
p=0.0679386743532325
totalmass_diff
cg26516004_CYP1A1

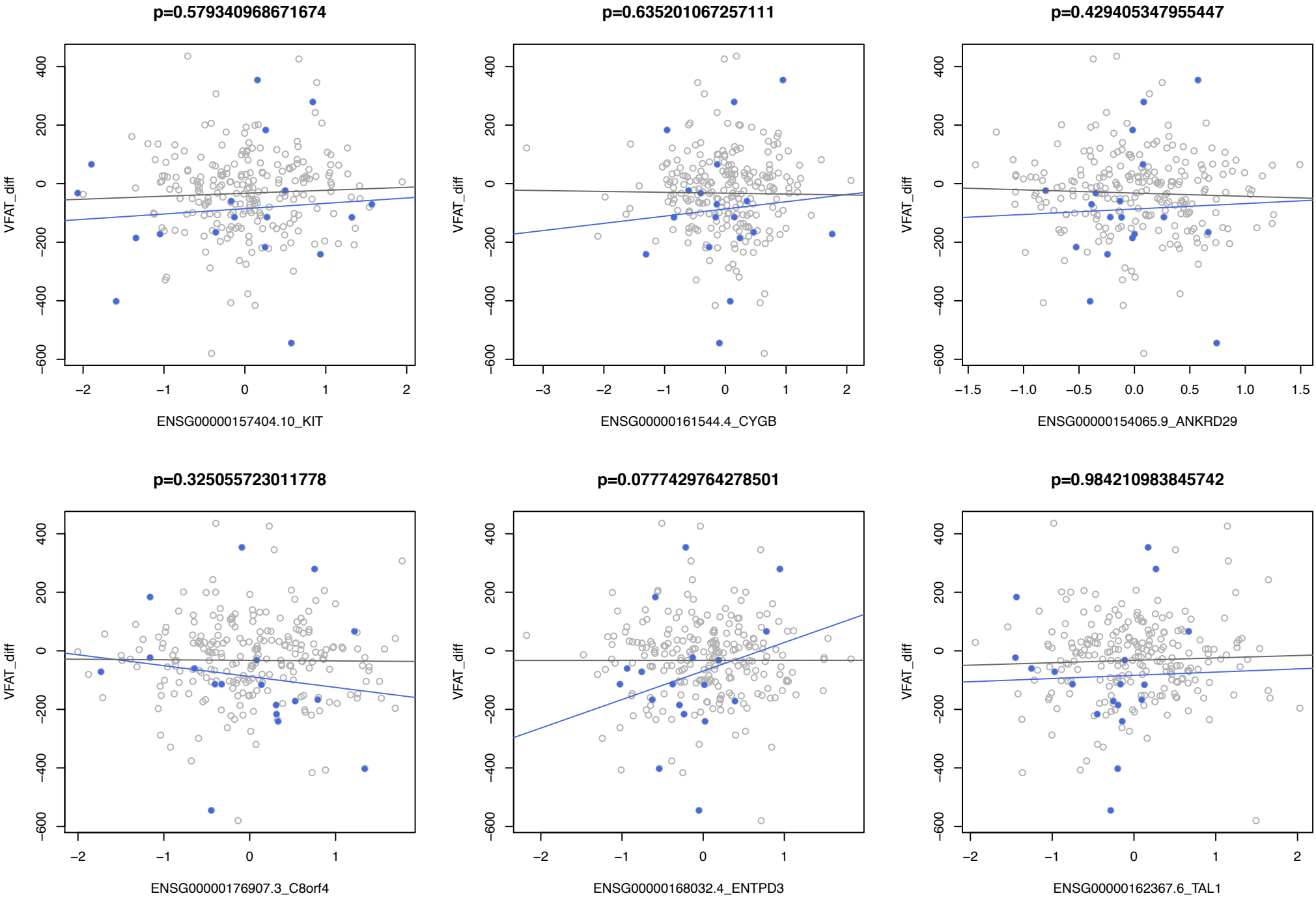
Figure S5

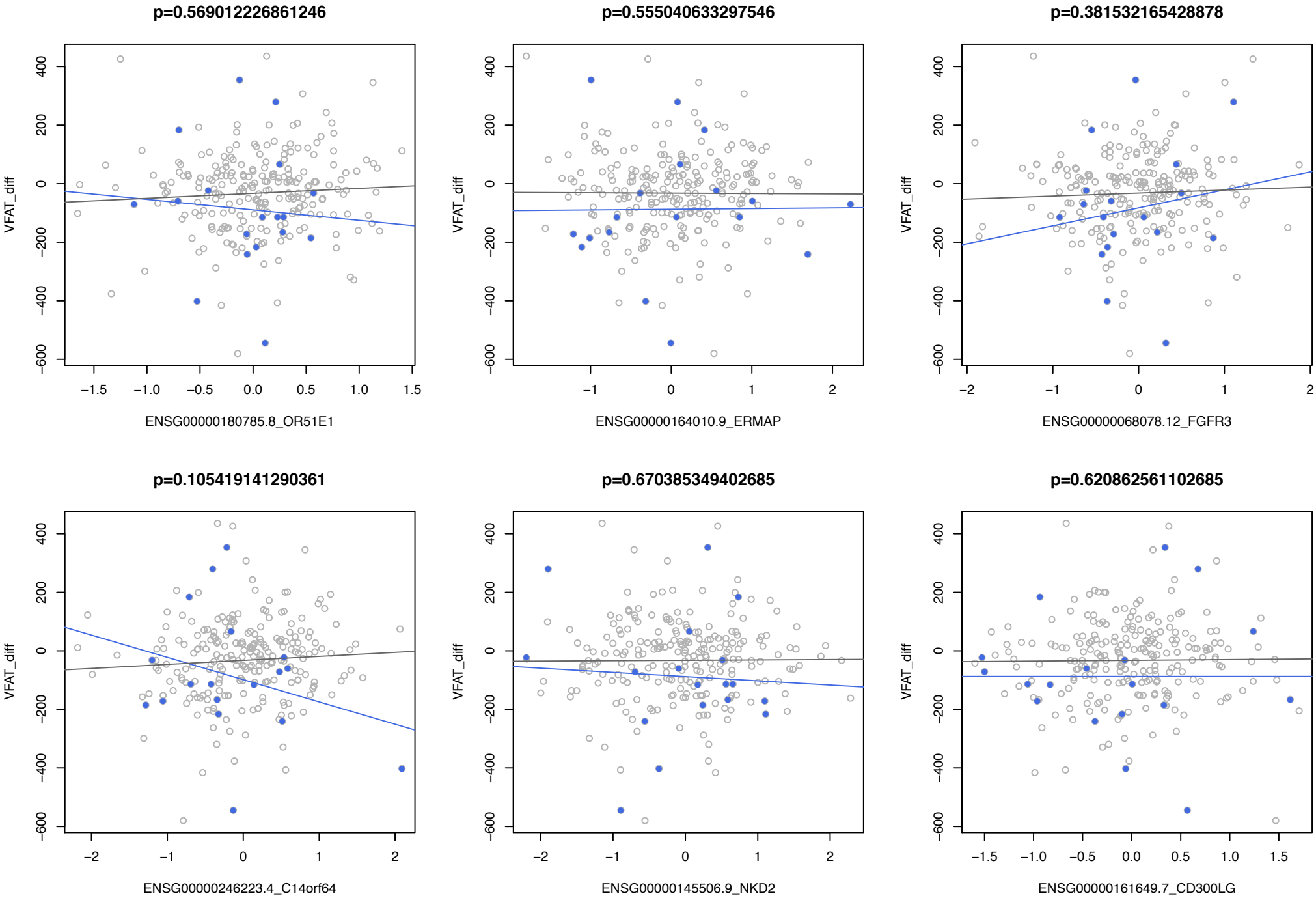

p=0.453457892334907
p=0.432673540351699
p=0.306505761737575
p=0.0422318516292107
p=4.70987432910354e−05
p=0.0163192818112769
VFAT_diff
ENSG00000140465.7_CYP1A1
ENSG00000138061.7_CYP1B1
ENSG00000144331.14_ZNF385B
ENSG00000179151.6_EDC3
ENSG00000063438.12_AHRR
ENSG00000175267.8_VWA3A

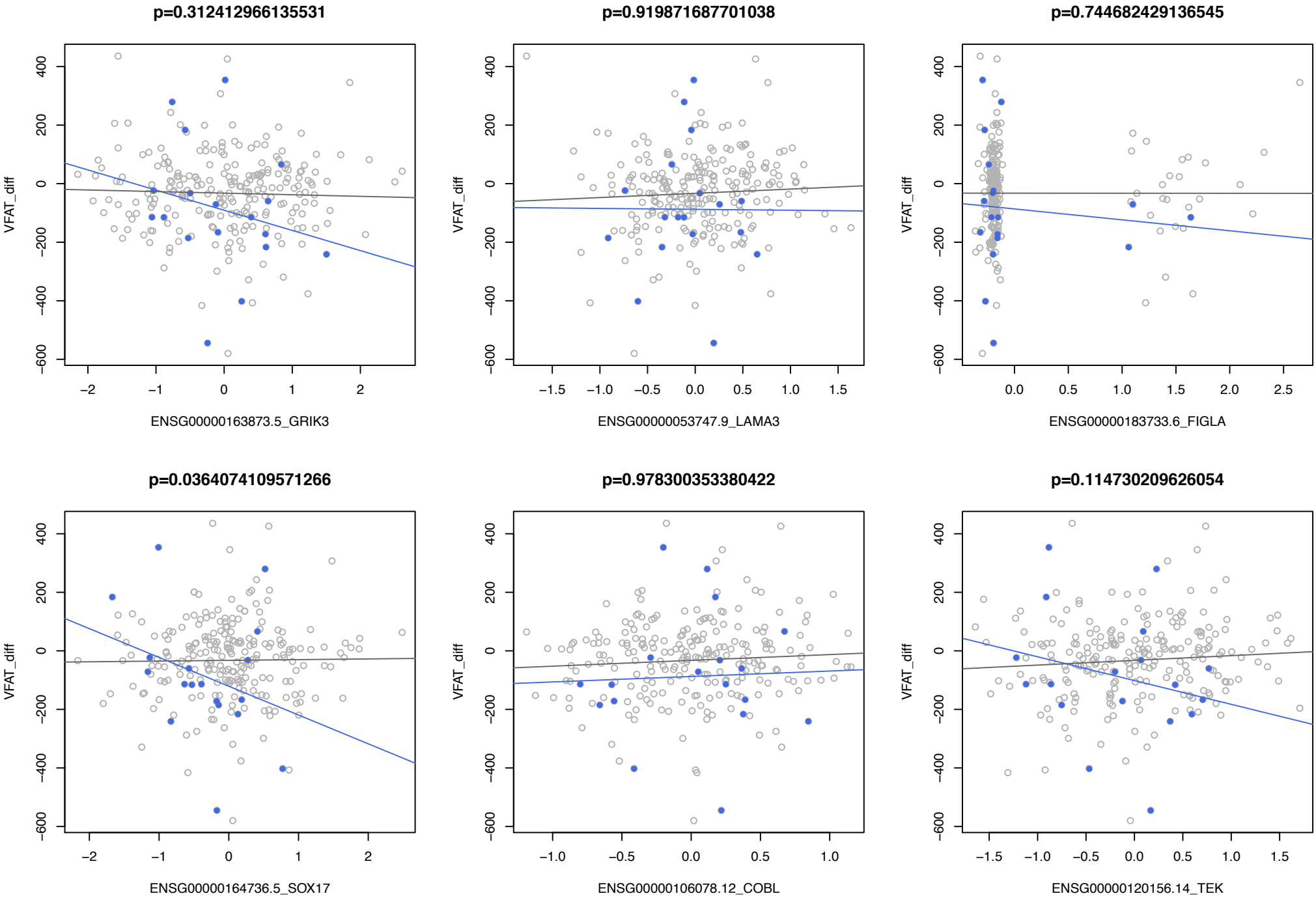

p=0.44955521475572
VFAT_diff
ENSG00000170381.7_SEMA3E
p=0.676434415103126
VFAT_diff
ENSG00000232973.3_CYP1B1−AS1
p=0.87557448992305
VFAT_diff
ENSG00000170891.6_CYTL1
p=0.0433398688816567
VFAT_diff
ENSG00000187486.5_KCNJ11
p=0.304516567598398
VFAT_diff
ENSG00000168280.11_KIF5C
p=0.466169281125415
VFAT_diff
ENSG00000248433.2_AL583842.7

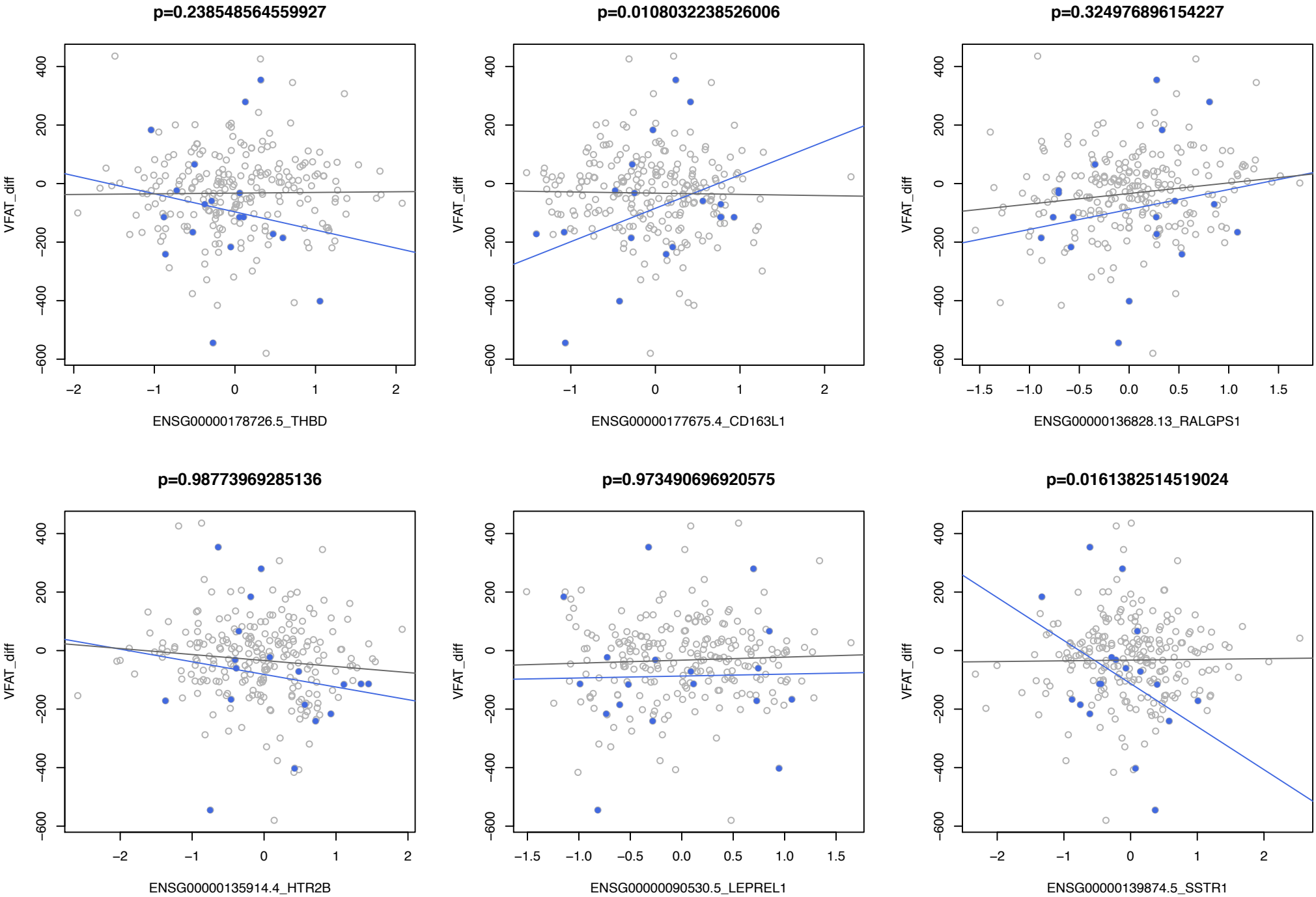

p=0.931369807284189
VFAT_diff
ENSG00000006016.5_CRLF1
p=0.00839518414516247
VFAT_diff
ENSG00000127533.2_F2RL3
p=0.829402833332273
VFAT_diff
ENSG00000149294.11_NCAM1
p=0.429032479198726
VFAT_diff
ENSG00000203849.5_AL583842.6
p=0.687590447391227
VFAT_diff
ENSG00000120693.9_SMAD9
p=0.476242177497893
VFAT_diff
ENSG00000169116.7_PARM1


p=0.00517170419112345
VFAT_diff
ENSG00000154330.6_PGM5
p=0.505827264633541
VFAT_diff
ENSG00000162430.12_SEPN1
p=0.00862595460385047
VFAT_diff
ENSG00000154721.9_JAM2
p=0.642368684121851
VFAT_diff
ENSG00000067840.6_PDZD4
p=0.653255374934628
VFAT_diff
ENSG00000177303.4_CASKIN2
p=0.372773847065627
VFAT_diff
ENSG00000242676.1_AL583842.8

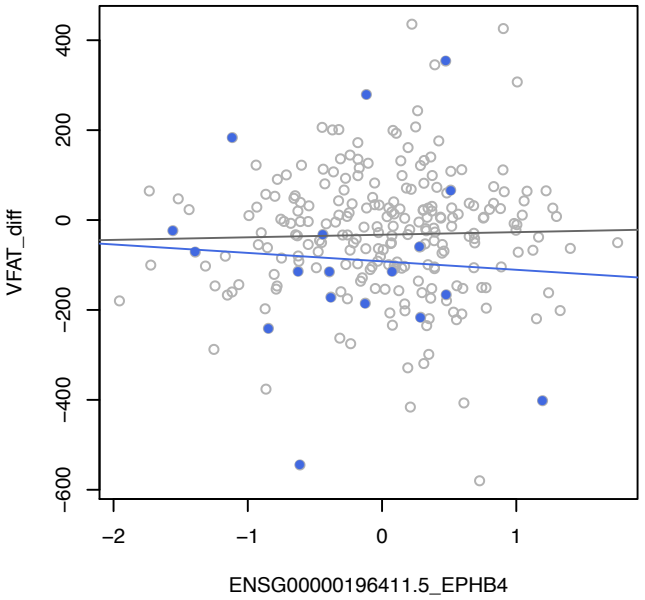

p=0.579340968671674
VFAT_diff
ENSG00000157404.10_KIT
p=0.635201067257111
VFAT_diff
ENSG00000161544.4_CYGB
p=0.429405347955447
VFAT_diff
ENSG00000154065.9_ANKRD29
p=0.325055723011778
VFAT_diff
ENSG00000176907.3_C8orf4
p=0.0777429764278501
VFAT_diff
ENSG00000168032.4_ENTPD3
p=0.984210983845742
VFAT_diff
ENSG00000162367.6_TAL1


p=0.569012226861246
VFAT_diff
ENSG00000180785.8_OR51E1
p=0.555040633297546
VFAT_diff
ENSG00000164010.9_ERMAP
p=0.381532165428878
VFAT_diff
ENSG00000068078.12_FGFR3
p=0.105419141290361
VFAT_diff
ENSG00000246223.4_C14orf64
p=0.670385349402685
VFAT_diff
ENSG00000145506.9_NKD2
p=0.620862561102685
VFAT_diff
ENSG00000161649.7_CD300LG

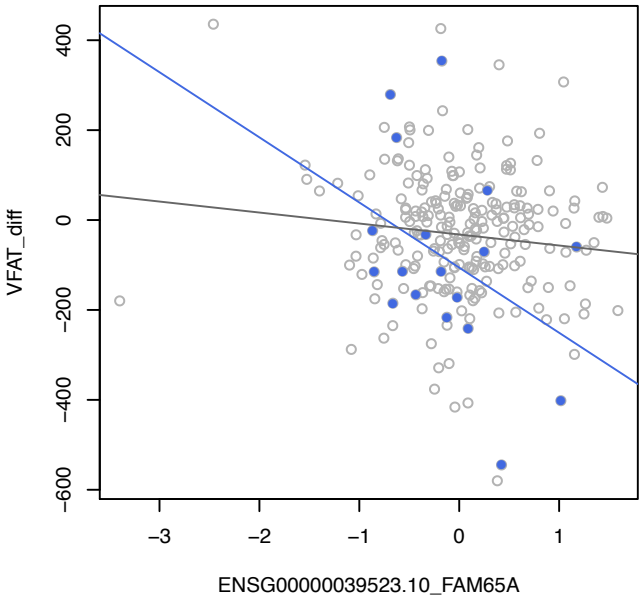

p=0.312412966135531
VFAT_diff
ENSG00000163873.5_GRIK3
p=0.919871687701038
VFAT_diff
ENSG00000053747.9_LAMA3
p=0.744682429136545
VFAT_diff
ENSG00000183733.6_FIGLA
p=0.0364074109571266
VFAT_diff
ENSG00000164736.5_SOX17
p=0.978300353380422
VFAT_diff
ENSG00000106078.12_COBL
p=0.114730209626054
VFAT_diff
ENSG00000120156.14_TEK


p=0.238548564559927
p=0.0108032238526006
p=0.324976896154227
p=0.98773969285136
p=0.973490696920575
p=0.0161382514519024
VFAT_diff
ENSG00000178726.5_THBD
ENSG00000177675.4_CD163L1
ENSG00000136828.13_RALGPS1
ENSG00000135914.4_HTR2B
ENSG00000090530.5_LEPREL1
ENSG00000139874.5_SSTR1

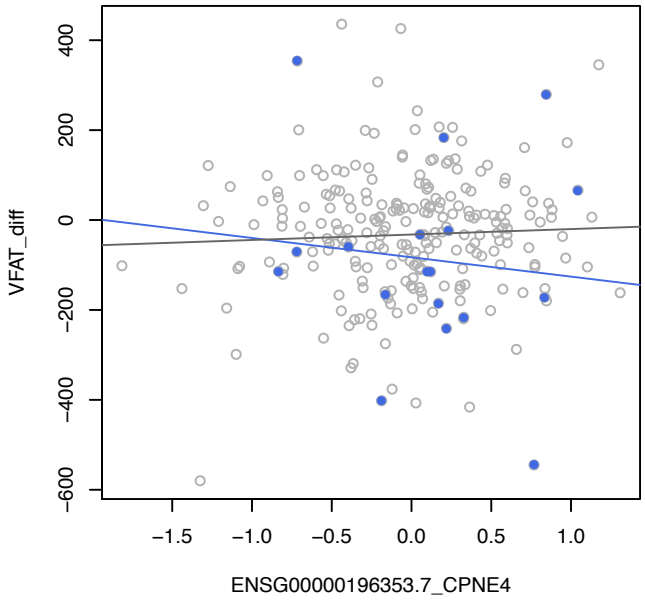
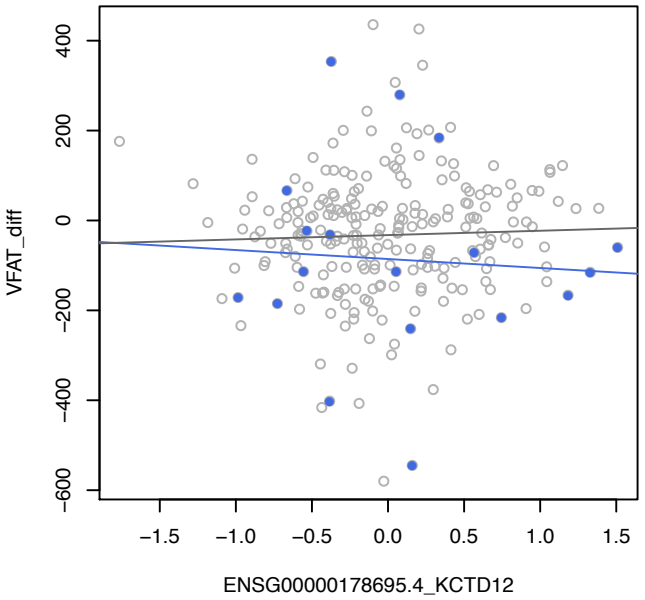
p=0.489970074196403



p=0.0402538228743152



p=0.309989413070512



p=0.860227824879606