Supplementary Figures

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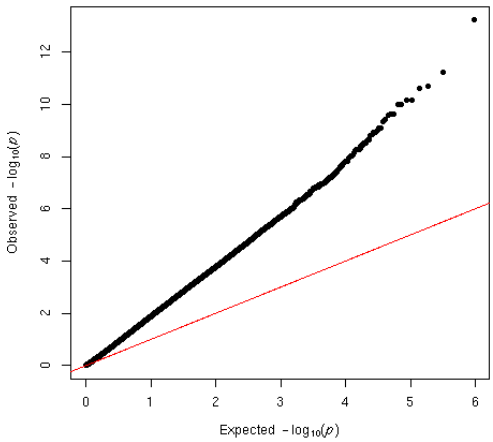
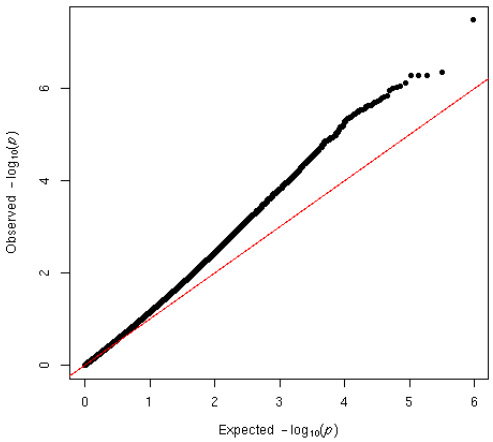
QQ-plots for cell-adjusted continuous BMI model

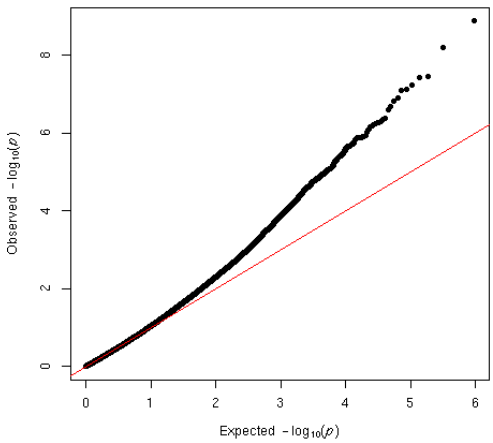
Fixed-effects meta-analysis - Lambda =2.409



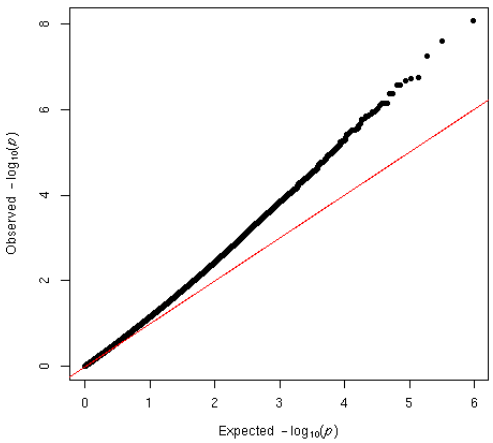
ALSPAC Lambda = 1.179



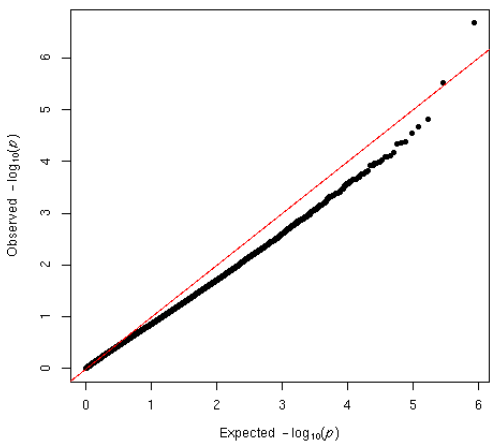
CBC_hispanic Lambda = 0.926



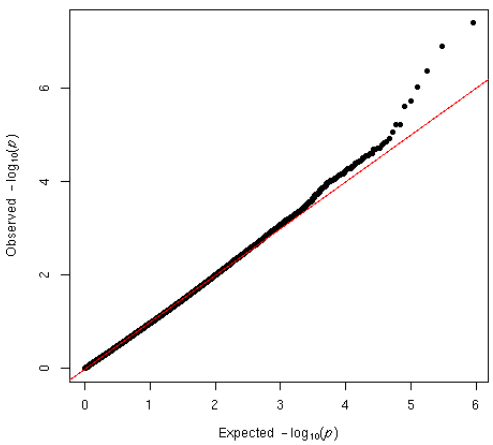
CBC_white Lambda = 1.162



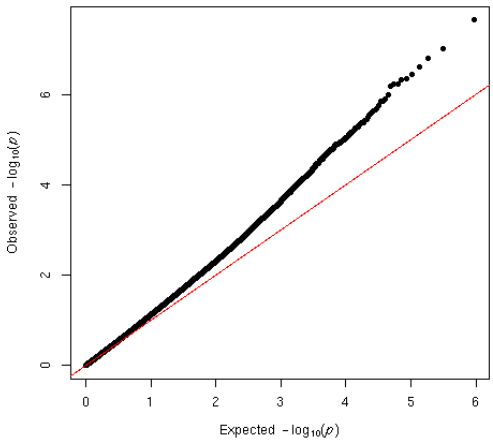
CHAMACOS Lambda = 0.834



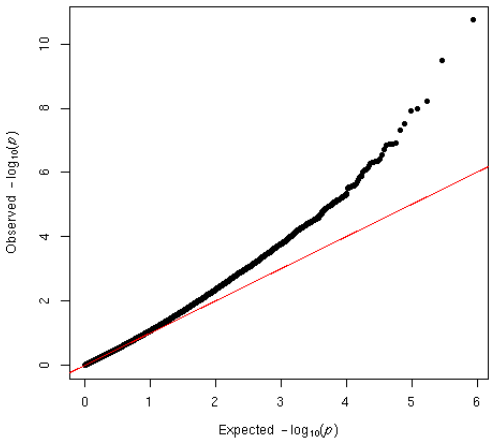
EARLI Lambda = 0.923



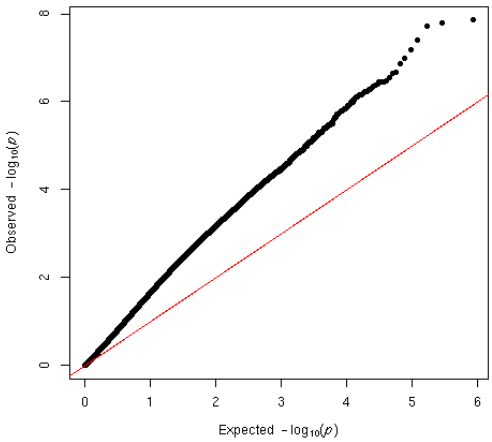
GECKO Lambda = 1.153



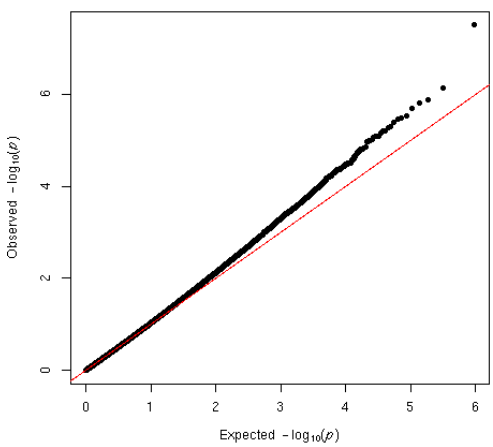
GEN3G Lambda = 1.039



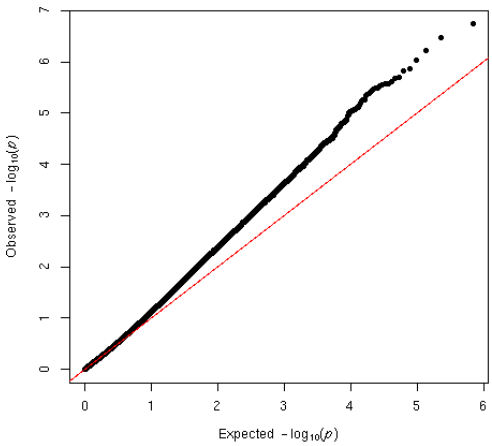
GENR Lambda = 1.996



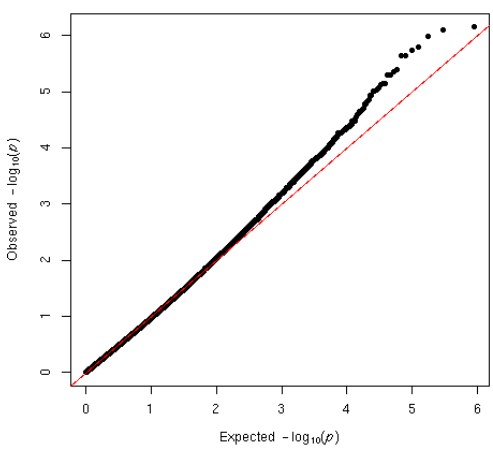
GOYArandom Lambda = 1.01



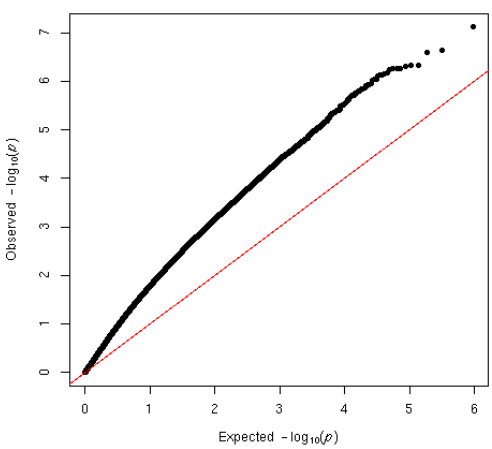
IOW Lambda = 1.05



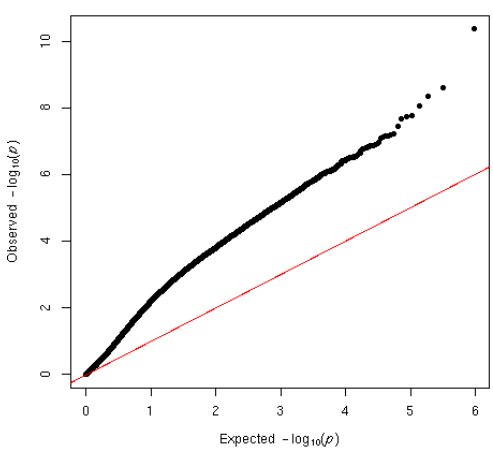
MEDALL Lambda = 0.917



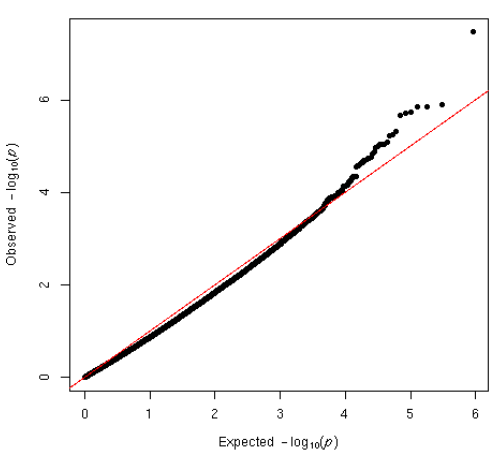
MOBA1 Lambda = 2.739



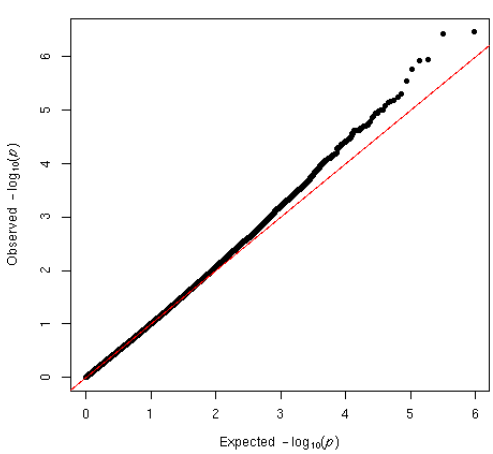
MOBA2 Lambda = 2.763

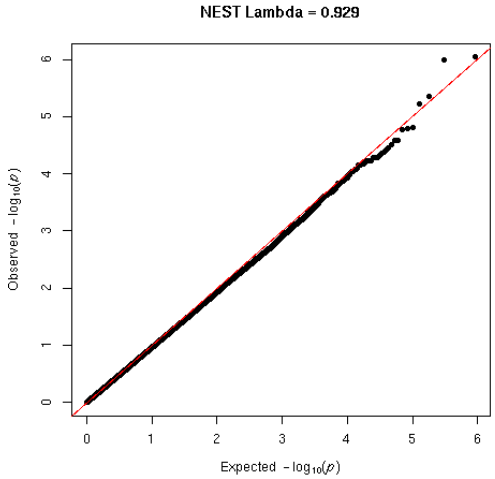


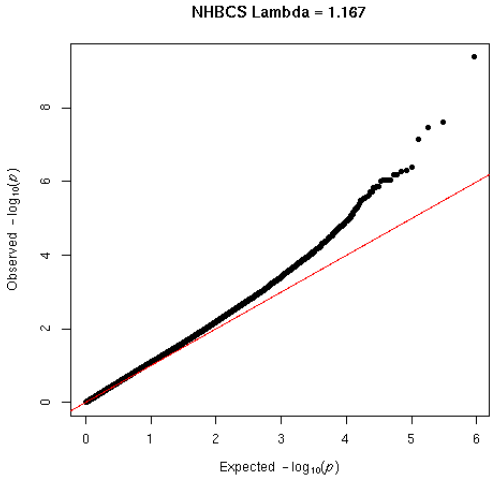
MOBA3 Lambda = 0.759

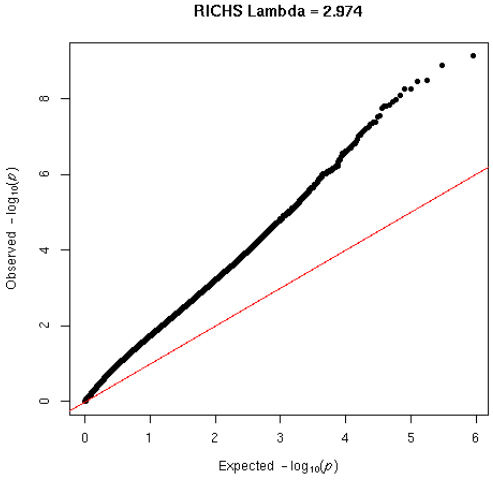


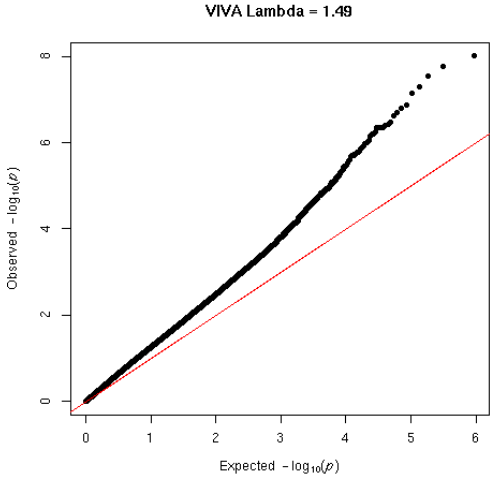
NCL Lambda = 0.985




NEST Lambda = 0.929
Observed $-\log_{10}(p)$
Expected $-\log_{10}(p)$

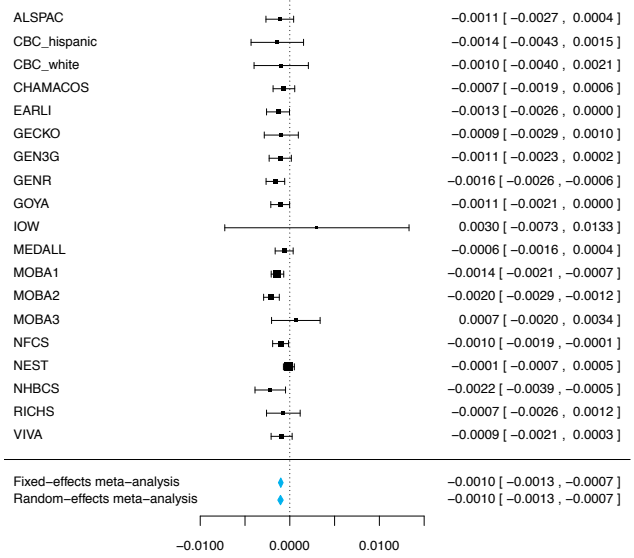

NHBCS Lambda = 1.167
Observed $-\log_{10}(p)$
Expected $-\log_{10}(p)$


RICHS Lambda = 2.974
Observed $-\log_{10}(p)$
Expected $-\log_{10}(p)$

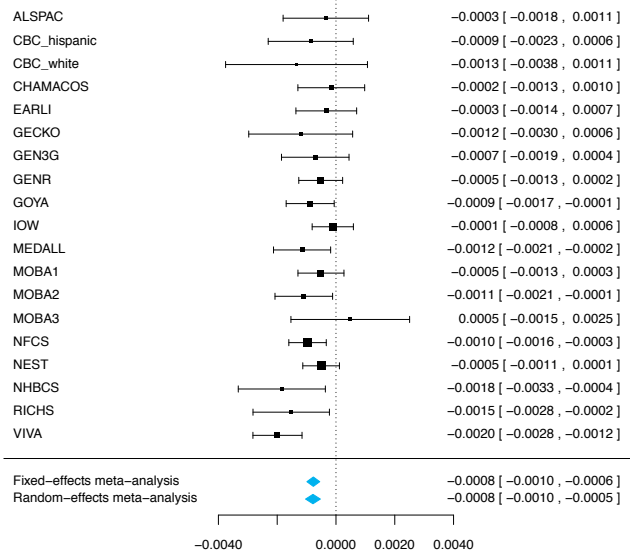

VIVA Lambda = 1.49
Observed $-\log_{10}(p)$
Expected $-\log_{10}(p)$

Forest plots for the cell-adjusted continuous BMI model

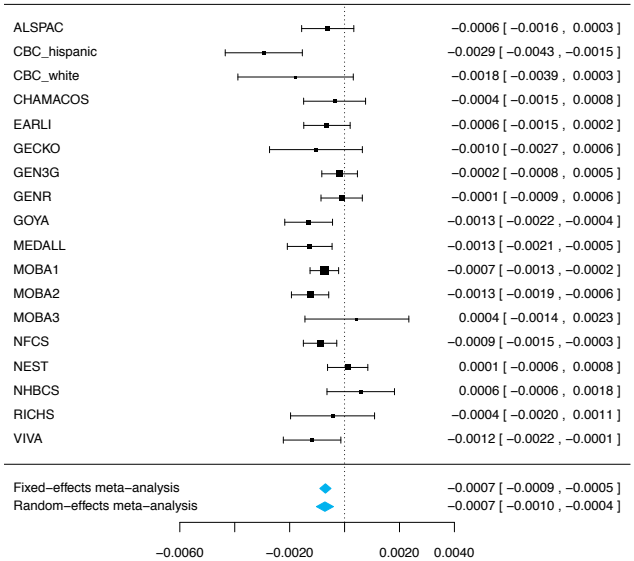
Forest plot for probe: cg12009398 [VIPR2]



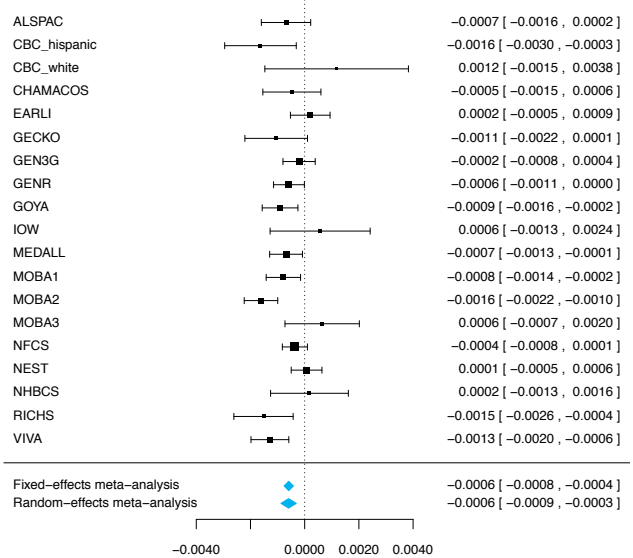
Forest plot for probe: cg09285795 [AK055145]



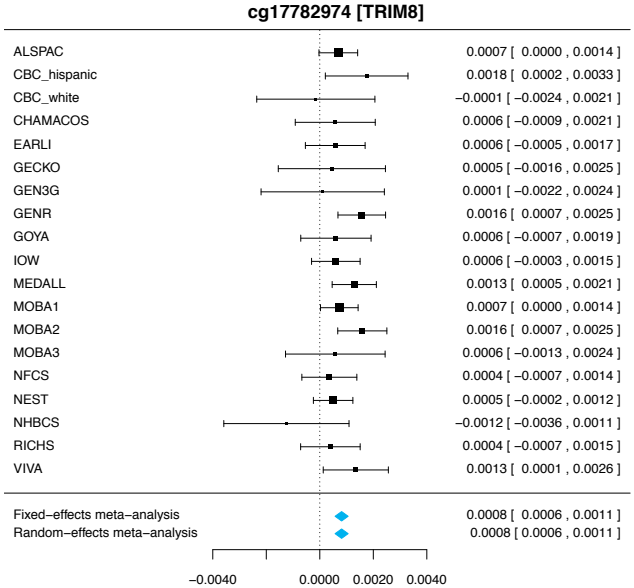
Forest plot for probe: cg23080818 [RBMS1]



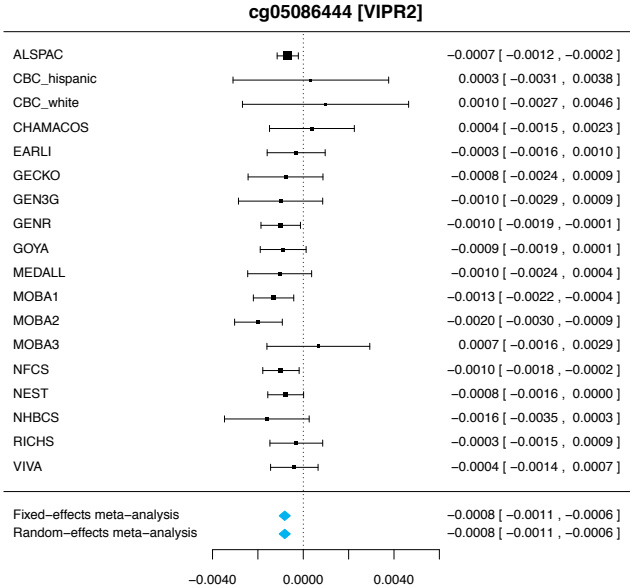
Forest plot for probe: cg25213362 [TMPRSS12]



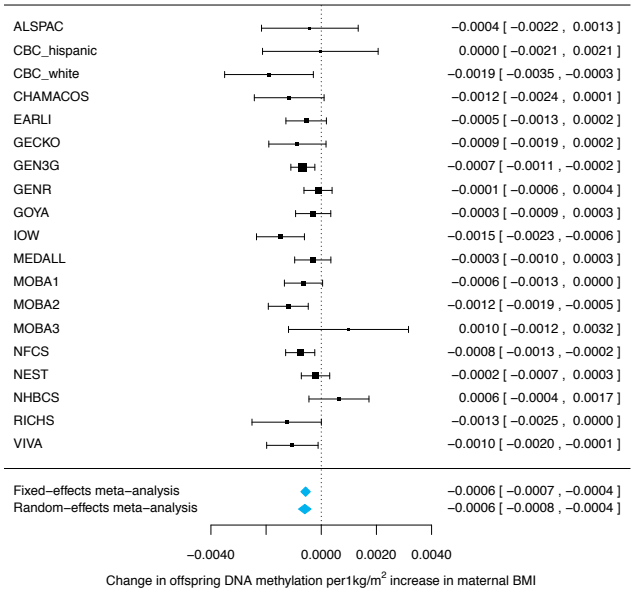
Forest plot for probe: cg17782974 [TRIM8]



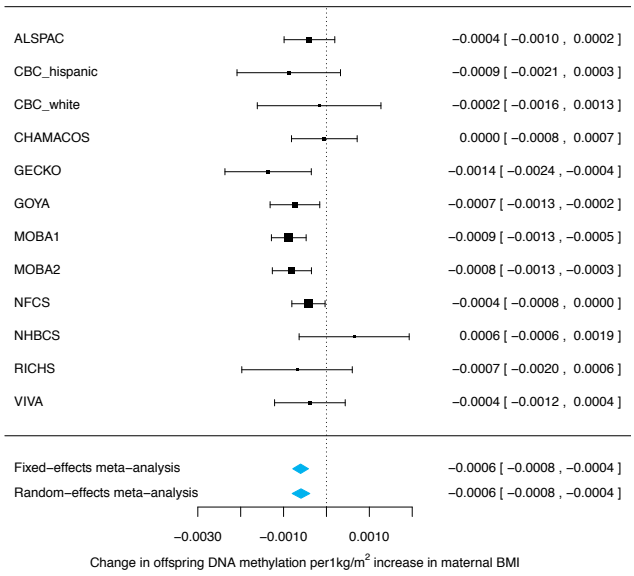
Forest plot for probe: cg05086444 [VIPR2]



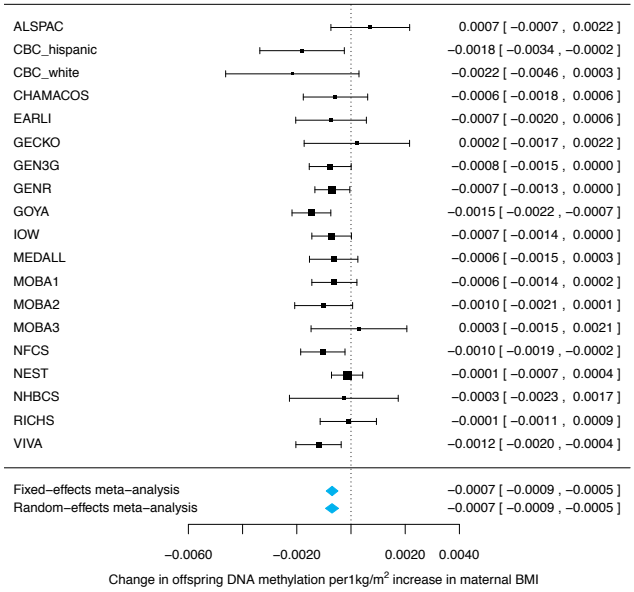
Forest plot for probe: cg03258665 [EPHA2]



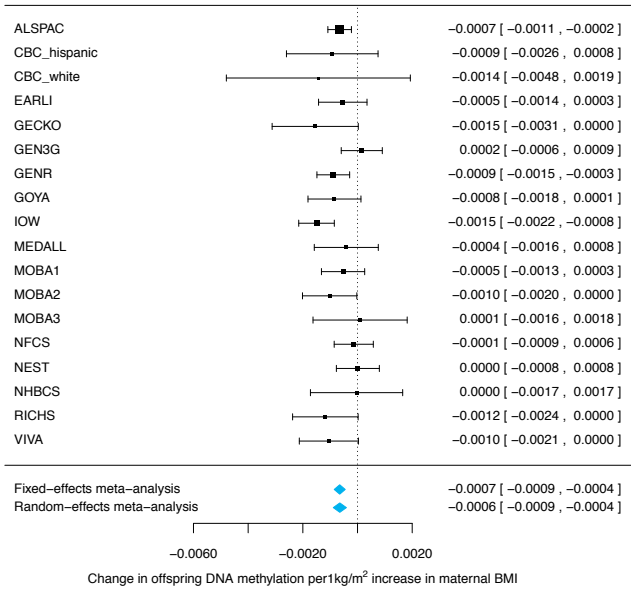
Forest plot for probe: cg20065216 [DUSP16]



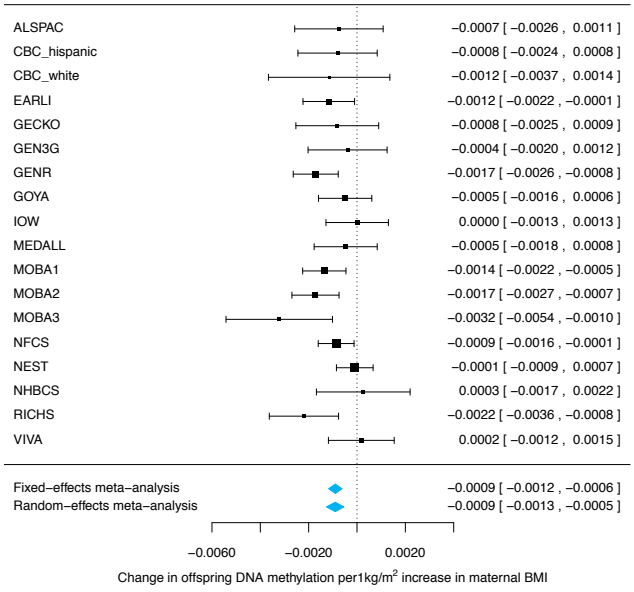
Forest plot for probe: cg26434090 [DSCAML1]



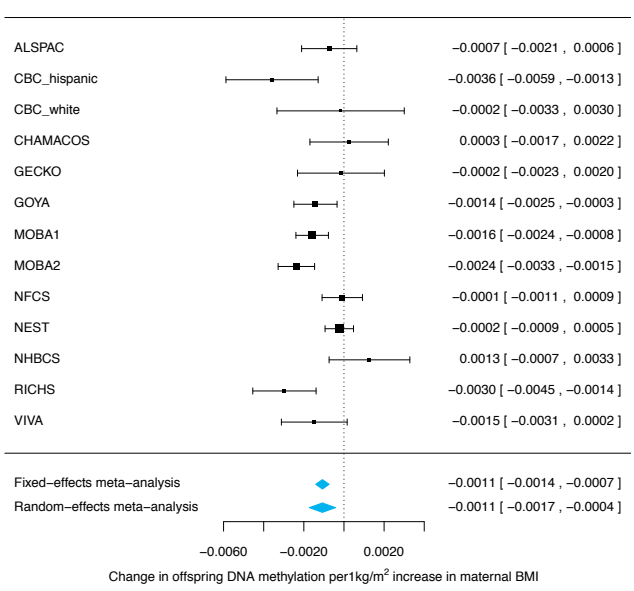
Forest plot for probe: cg18268562 [FOXR1]

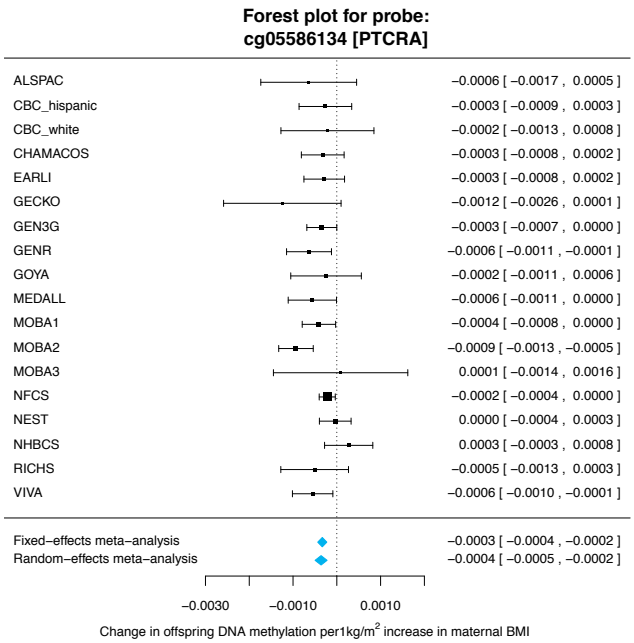


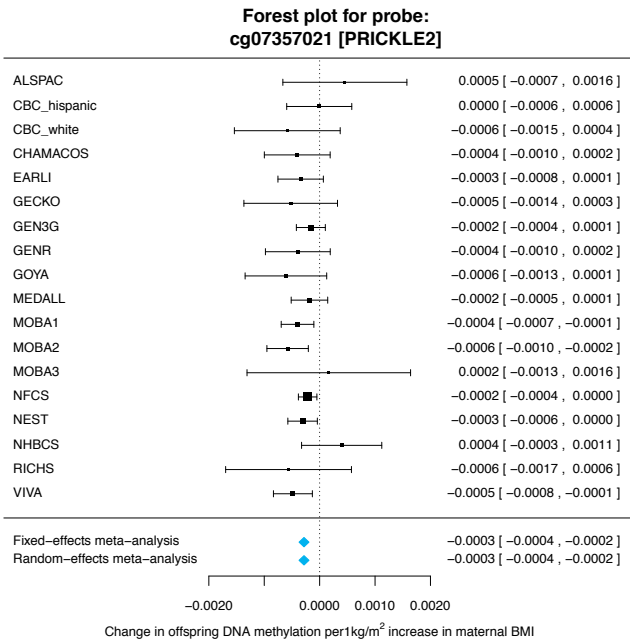
Forest plot for probe: cg00285394 [SQLE]

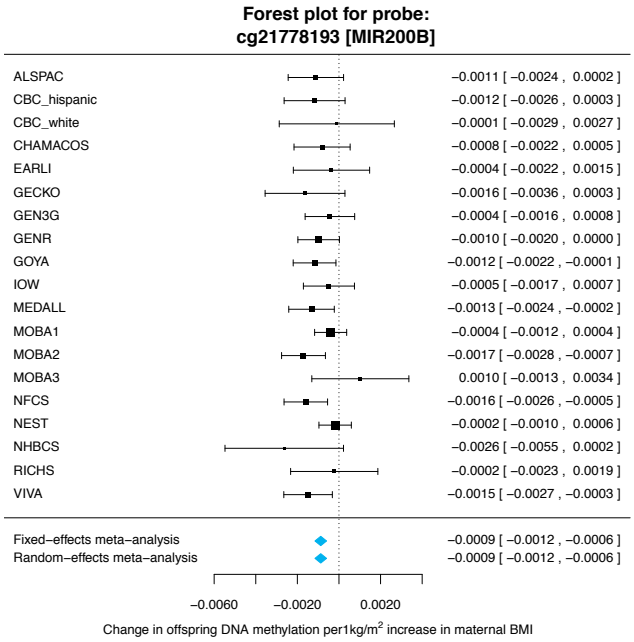


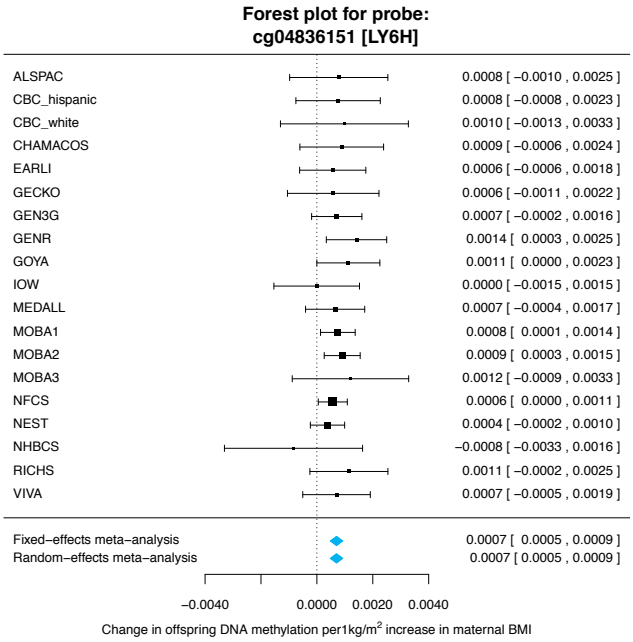
Forest plot for probe: cg27179375 [POM121L1P]

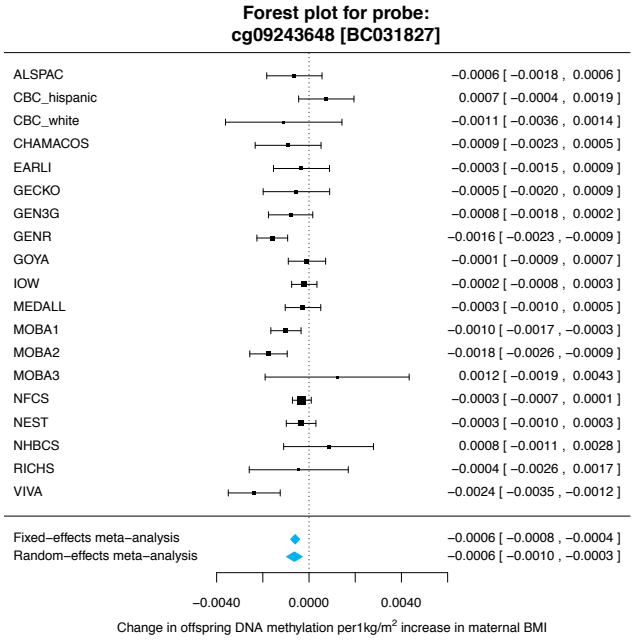


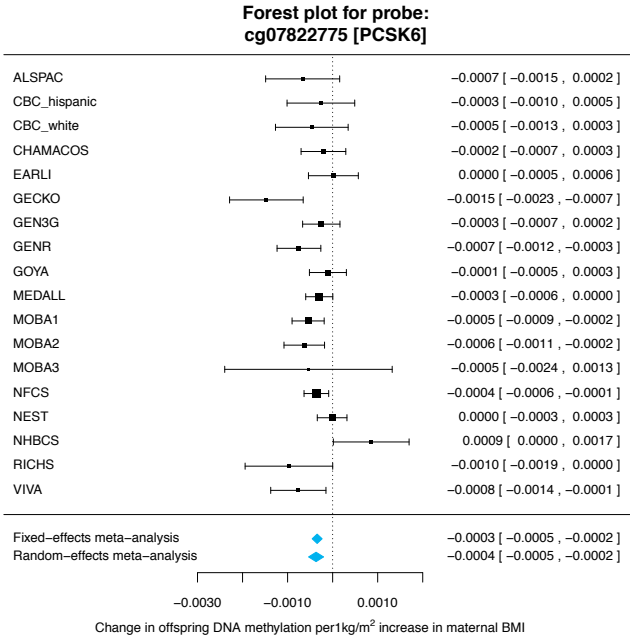

Forest plot for probe:
cg05586134 [PTCRA]
ALSPAC −0.0006 [−0.0017 , 0.0005]
CBC_hispanic −0.0003 [−0.0009 , 0.0003]
CBC_white −0.0002 [−0.0013 , 0.0008]
CHAMACOS −0.0003 [−0.0008 , 0.0002]
EARLI −0.0003 [−0.0008 , 0.0002]
GECKO −0.0012 [−0.0026 , 0.0001]
GEN3G −0.0003 [−0.0007 , 0.0000]
GENR −0.0006 [−0.0011 , −0.0001]
GOYA −0.0002 [−0.0011 , 0.0006]
MEDALL −0.0006 [−0.0011 , 0.0000]
MOBA1 −0.0004 [−0.0008 , 0.0000]
MOBA2 −0.0009 [−0.0013 , −0.0005]
MOBA3 0.0001 [−0.0014 , 0.0016]
NFCS −0.0002 [−0.0004 , 0.0000]
NEST 0.0000 [−0.0004 , 0.0003]
NHBCS 0.0003 [−0.0003 , 0.0008]
RICHS −0.0005 [−0.0013 , 0.0003]
VIVA −0.0006 [−0.0010 , −0.0001]
Fixed−effects meta−analysis −0.0003 [−0.0004 , −0.0002]
Random−effects meta−analysis −0.0004 [−0.0005 , −0.0002]
−0.0030 −0.0010 0.0010
Change in offspring DNA methylation per1kg/m2 increase in maternal BMI


Forest plot for probe:
cg07357021 [PRICKLE2]
ALSPAC 0.0005 [−0.0007 , 0.0016]
CBC_hispanic 0.0000 [−0.0006 , 0.0006]
CBC_white −0.0006 [−0.0015 , 0.0004]
CHAMACOS −0.0004 [−0.0010 , 0.0002]
EARLI −0.0003 [−0.0008 , 0.0001]
GECKO −0.0005 [−0.0014 , 0.0003]
GEN3G −0.0002 [−0.0004 , 0.0001]
GENR −0.0004 [−0.0010 , 0.0002]
GOYA −0.0006 [−0.0013 , 0.0001]
MEDALL −0.0002 [−0.0005 , 0.0001]
MOBA1 −0.0004 [−0.0007 , −0.0001]
MOBA2 −0.0006 [−0.0010 , −0.0002]
MOBA3 0.0002 [−0.0013 , 0.0016]
NFCS −0.0002 [−0.0004 , 0.0000]
NEST −0.0003 [−0.0006 , 0.0000]
NHBCS 0.0004 [−0.0003 , 0.0011]
RICHS −0.0006 [−0.0017 , 0.0006]
VIVA −0.0005 [−0.0008 , −0.0001]
Fixed−effects meta−analysis −0.0003 [−0.0004 , −0.0002]
Random−effects meta−analysis −0.0003 [−0.0004 , −0.0002]
−0.0020 0.0000 0.0010 0.0020
Change in offspring DNA methylation per1kg/m2 increase in maternal BMI

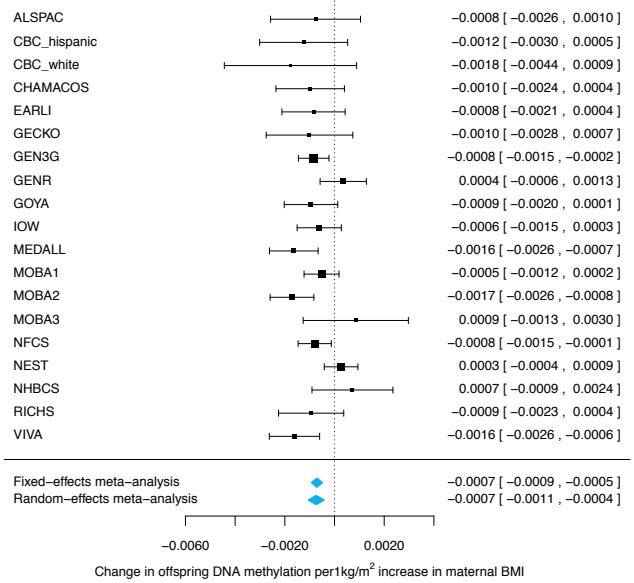

Forest plot for probe:
cg21778193 [MIR200B]
ALSPAC −0.0011 [−0.0024 , 0.0002]
CBC_hispanic −0.0012 [−0.0026 , 0.0003]
CBC_white −0.0001 [−0.0029 , 0.0027]
CHAMACOS −0.0008 [−0.0022 , 0.0005]
EARLI −0.0004 [−0.0022 , 0.0015]
GECKO −0.0016 [−0.0036 , 0.0003]
GEN3G −0.0004 [−0.0016 , 0.0008]
GENR −0.0010 [−0.0020 , 0.0000]
GOYA −0.0012 [−0.0022 , −0.0001]
IOW −0.0005 [−0.0017 , 0.0007]
MEDALL −0.0013 [−0.0024 , −0.0002]
MOBA1 −0.0004 [−0.0012 , 0.0004]
MOBA2 −0.0017 [−0.0028 , −0.0007]
MOBA3 0.0010 [−0.0013 , 0.0034]
NFCS −0.0016 [−0.0026 , −0.0005]
NEST −0.0002 [−0.0010 , 0.0006]
NHBCS −0.0026 [−0.0055 , 0.0002]
RICHS −0.0002 [−0.0023 , 0.0019]
VIVA −0.0015 [−0.0027 , −0.0003]
Fixed−effects meta−analysis −0.0009 [−0.0012 , −0.0006]
Random−effects meta−analysis −0.0009 [−0.0012 , −0.0006]
−0.0060 −0.0020 0.0020
Change in offspring DNA methylation per1kg/m2 increase in maternal BMI


Forest plot for probe:
cg04836151 [LY6H]
ALSPAC 0.0008 [−0.0010 , 0.0025]
CBC_hispanic 0.0008 [−0.0008 , 0.0023]
CBC_white 0.0010 [−0.0013 , 0.0033]
CHAMACOS 0.0009 [−0.0006 , 0.0024]
EARLI 0.0006 [−0.0006 , 0.0018]
GECKO 0.0006 [−0.0011 , 0.0022]
GEN3G 0.0007 [−0.0002 , 0.0016]
GENR 0.0014 [0.0003 , 0.0025]
GOYA 0.0011 [0.0000 , 0.0023]
IOW 0.0000 [−0.0015 , 0.0015]
MEDALL 0.0007 [−0.0004 , 0.0017]
MOBA1 0.0008 [0.0001 , 0.0014]
MOBA2 0.0009 [0.0003 , 0.0015]
MOBA3 0.0012 [−0.0009 , 0.0033]
NFCS 0.0006 [0.0000 , 0.0011]
NEST 0.0004 [−0.0002 , 0.0010]
NHBCS −0.0008 [−0.0033 , 0.0016]
RICHS 0.0011 [−0.0002 , 0.0025]
VIVA 0.0007 [−0.0005 , 0.0019]
Fixed−effects meta−analysis 0.0007 [0.0005 , 0.0009]
Random−effects meta−analysis 0.0007 [0.0005 , 0.0009]
−0.0040 0.0000 0.0020 0.0040
Change in offspring DNA methylation per1kg/m2 increase in maternal BMI

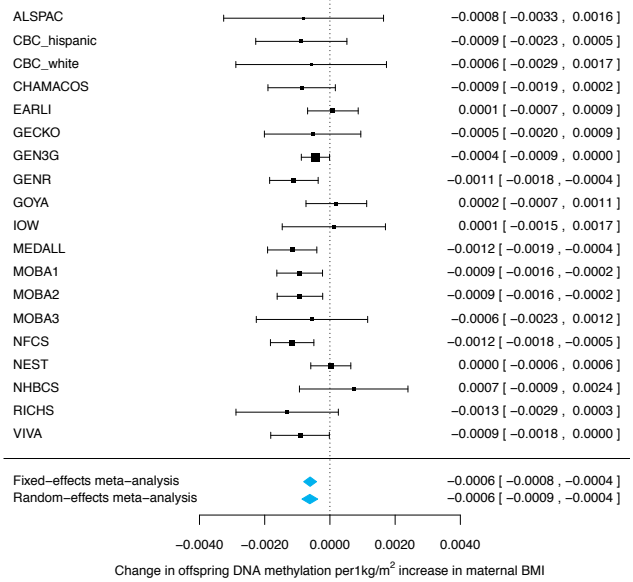

Forest plot for probe:
cg09243648 [BC031827]
ALSPAC −0.0006 [−0.0018 , 0.0006]
CBC_hispanic 0.0007 [−0.0004 , 0.0019]
CBC_white −0.0011 [−0.0036 , 0.0014]
CHAMACOS −0.0009 [−0.0023 , 0.0005]
EARLI −0.0003 [−0.0015 , 0.0009]
GECKO −0.0005 [−0.0020 , 0.0009]
GEN3G −0.0008 [−0.0018 , 0.0002]
GENR −0.0016 [−0.0023 , −0.0009]
GOYA −0.0001 [−0.0009 , 0.0007]
IOW −0.0002 [−0.0008 , 0.0003]
MEDALL −0.0003 [−0.0010 , 0.0005]
MOBA1 −0.0010 [−0.0017 , −0.0003]
MOBA2 −0.0018 [−0.0026 , −0.0009]
MOBA3 0.0012 [−0.0019 , 0.0043]
NFCS −0.0003 [−0.0007 , 0.0001]
NEST −0.0003 [−0.0010 , 0.0003]
NHBCS 0.0008 [−0.0011 , 0.0028]
RICHS −0.0004 [−0.0026 , 0.0017]
VIVA −0.0024 [−0.0035 , −0.0012]
Fixed−effects meta−analysis −0.0006 [−0.0008 , −0.0004]
Random−effects meta−analysis −0.0006 [−0.0010 , −0.0003]
−0.0040 0.0000 0.0040
Change in offspring DNA methylation per1kg/m2 increase in maternal BMI


Forest plot for probe:
cg07822775 [PCSK6]
ALSPAC −0.0007 [−0.0015 , 0.0002]
CBC_hispanic −0.0003 [−0.0010 , 0.0005]
CBC_white −0.0005 [−0.0013 , 0.0003]
CHAMACOS −0.0002 [−0.0007 , 0.0003]
EARLI 0.0000 [−0.0005 , 0.0006]
GECKO −0.0015 [−0.0023 , −0.0007]
GEN3G −0.0003 [−0.0007 , 0.0002]
GENR −0.0007 [−0.0012 , −0.0003]
GOYA −0.0001 [−0.0005 , 0.0003]
MEDALL −0.0003 [−0.0006 , 0.0000]
MOBA1 −0.0005 [−0.0009 , −0.0002]
MOBA2 −0.0006 [−0.0011 , −0.0002]
MOBA3 −0.0005 [−0.0024 , 0.0013]
NFCS −0.0004 [−0.0006 , −0.0001]
NEST 0.0000 [−0.0003 , 0.0003]
NHBCS 0.0009 [0.0000 , 0.0017]
RICHS −0.0010 [−0.0019 , 0.0000]
VIVA −0.0008 [−0.0014 , −0.0001]
Fixed−effects meta−analysis −0.0003 [−0.0005 , −0.0002]
Random−effects meta−analysis −0.0004 [−0.0005 , −0.0002]
−0.0030 −0.0010 0.0010
Change in offspring DNA methylation per1kg/m2 increase in maternal BMI

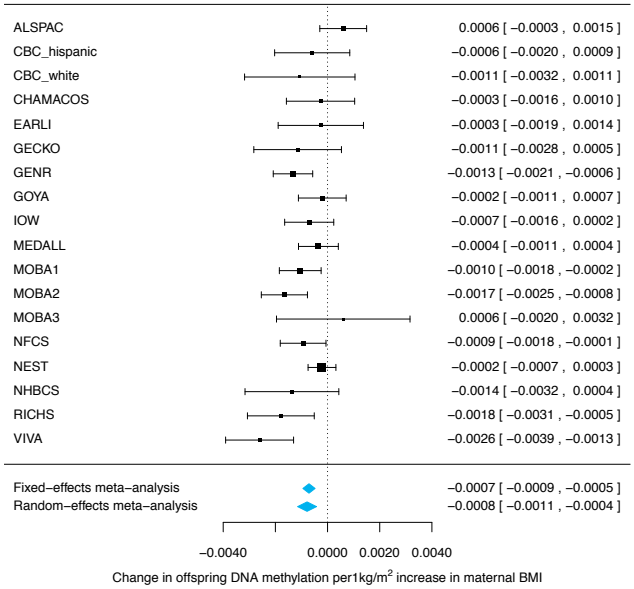
Forest plot for probe: cg14906690 [KAT6B]



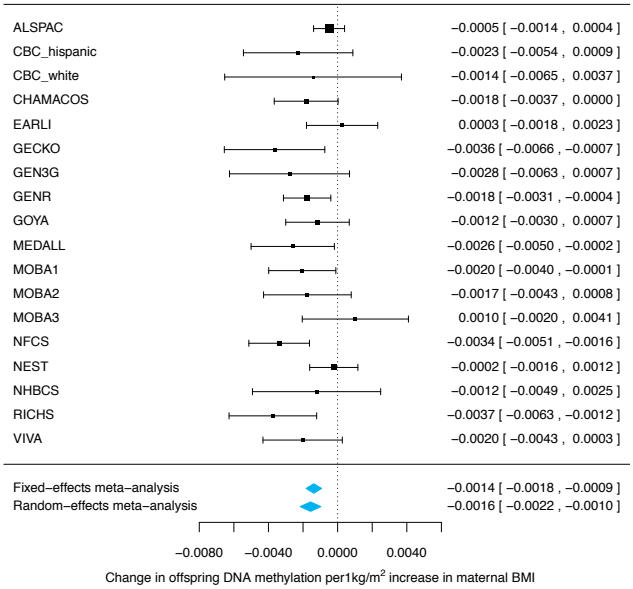
Forest plot for probe: cg05309280 [GORASP2]



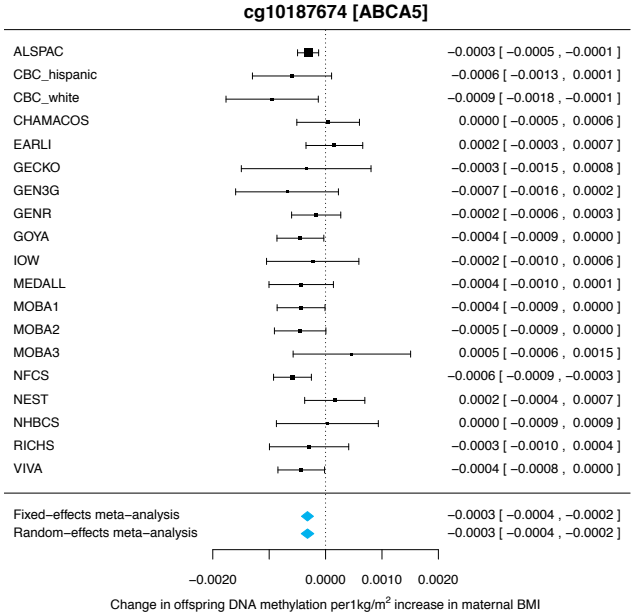
Forest plot for probe: cg10635092 [ZFYVE28]



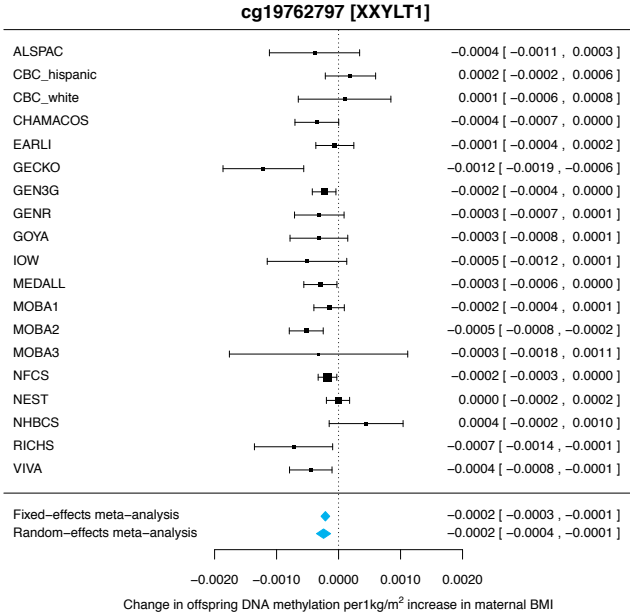
Forest plot for probe: cg13403462 [ACTL10]



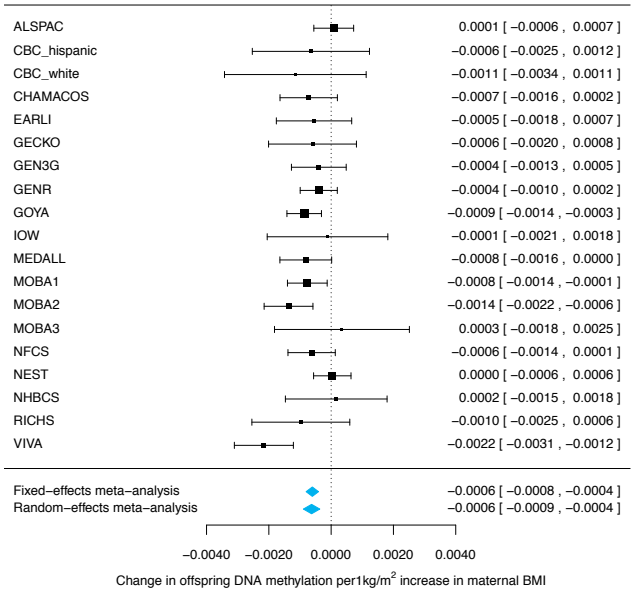
Forest plot for probe: cg10187674 [ABCA5]



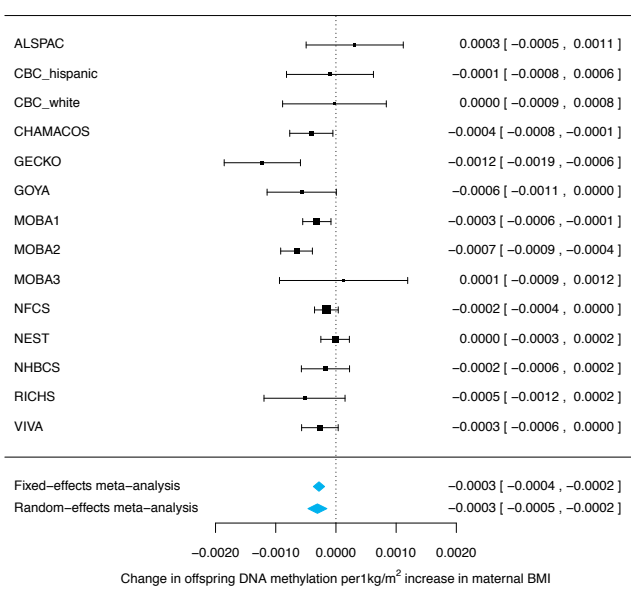
Forest plot for probe: cg19762797 [XXYLT1]



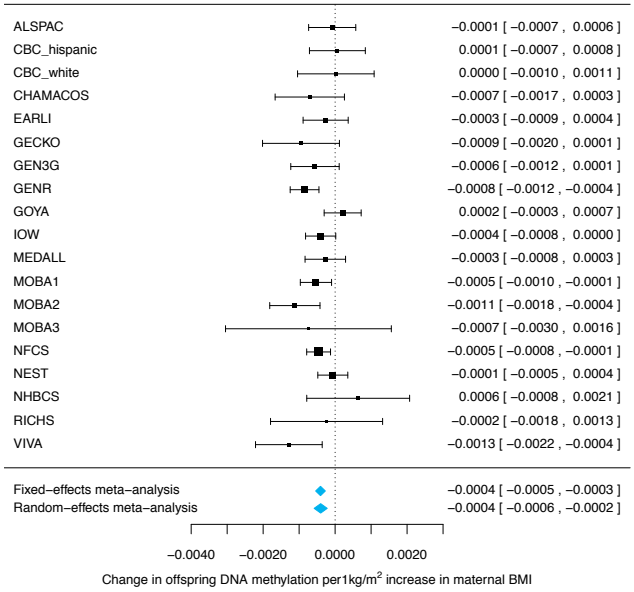
Forest plot for probe: cg09230763 [MAP3K6]



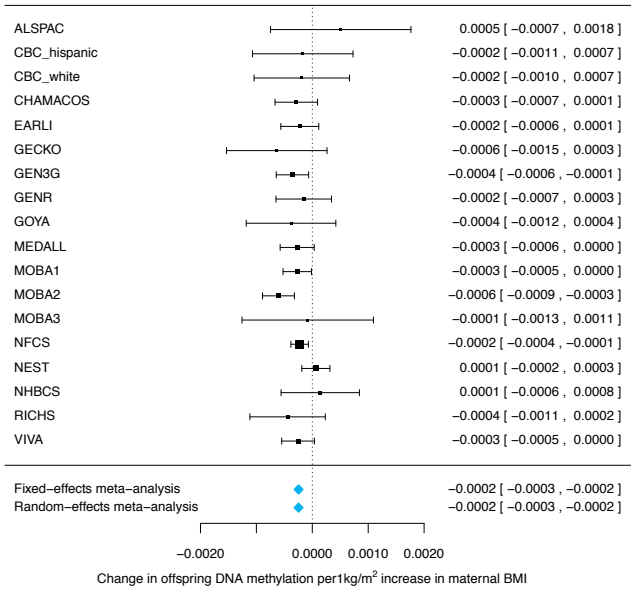
Forest plot for probe: cg18156417 [MAP2K2]



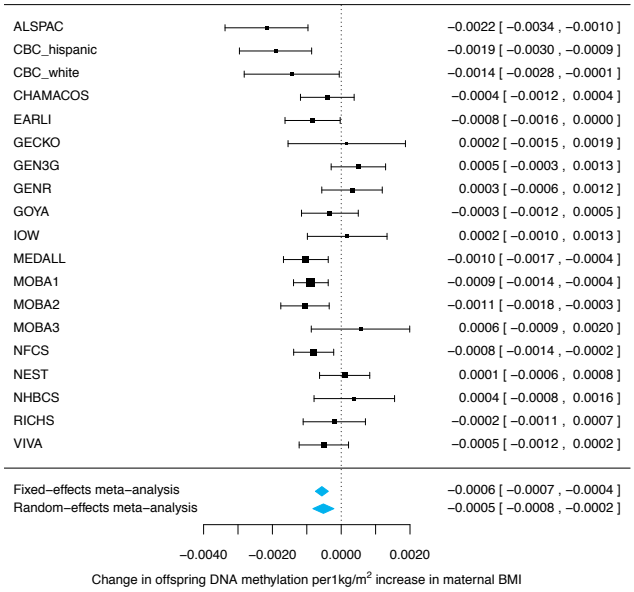
Forest plot for probe: cg26220185 [AK127048]



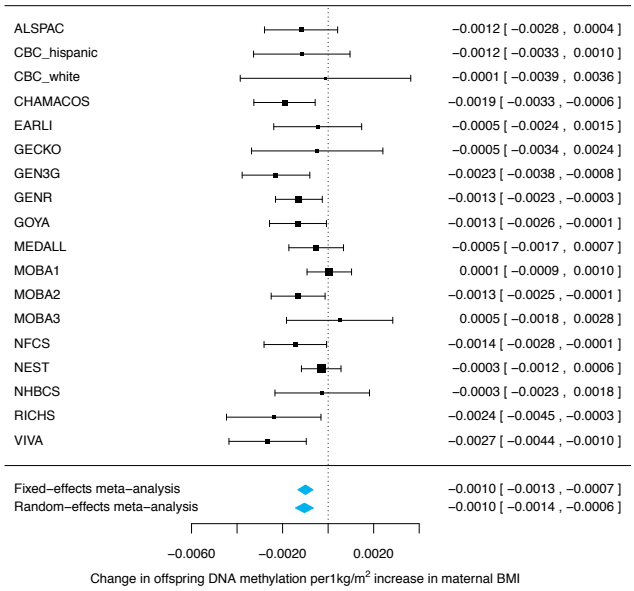
Forest plot for probe: cg13540311 [SEPT9]



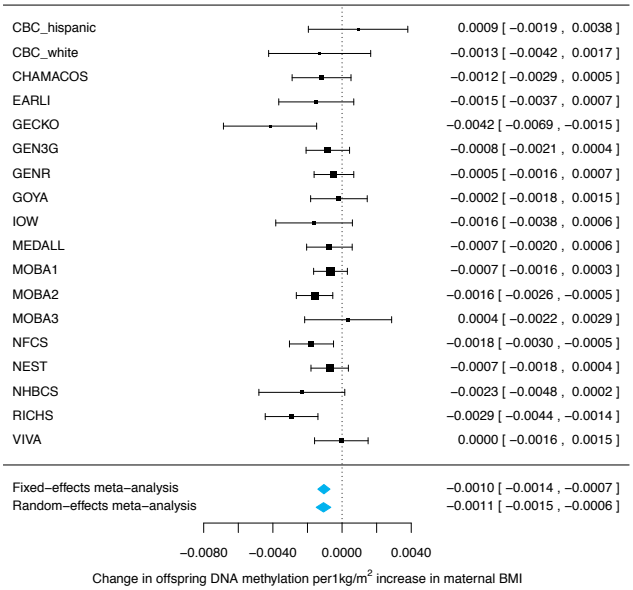
Forest plot for probe: cg16877087 [RBMS1]



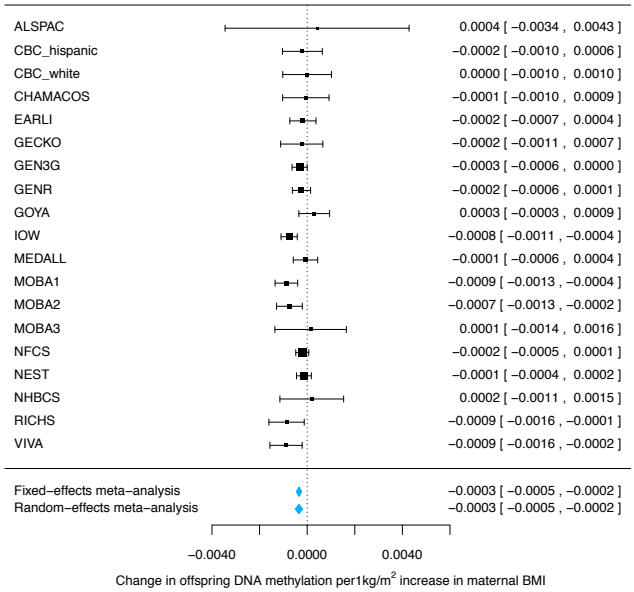
Forest plot for probe: cg20594982 [AGRN]



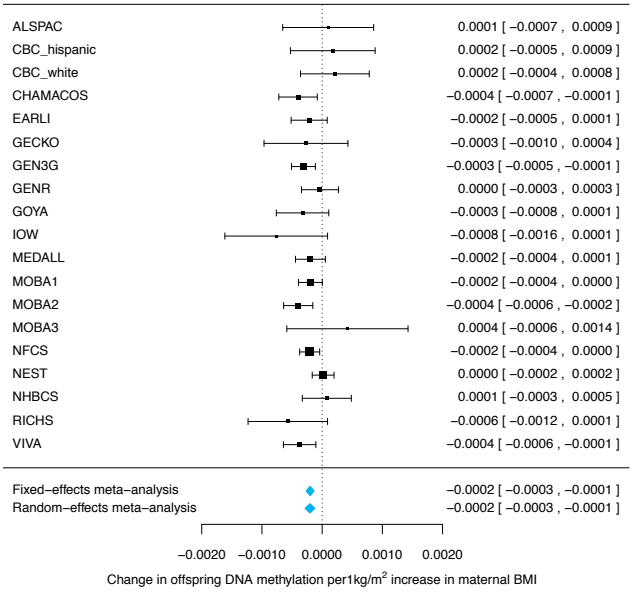
Forest plot for probe: cg14660676 [SQLE]



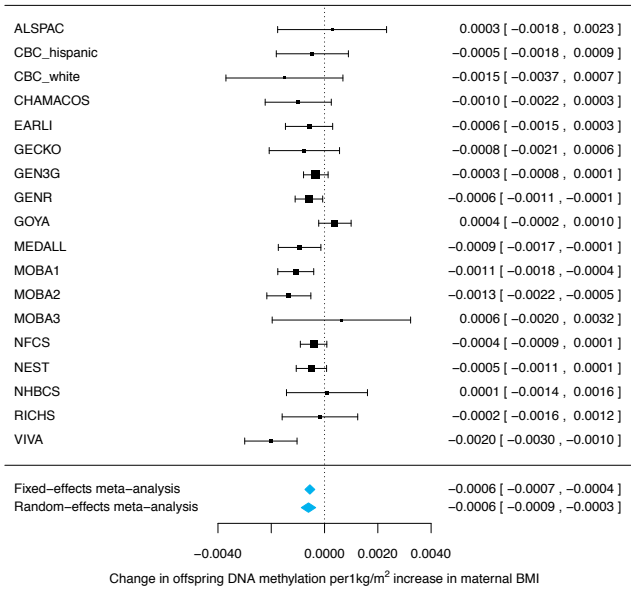
Forest plot for probe: cg09723488 [LHX6]



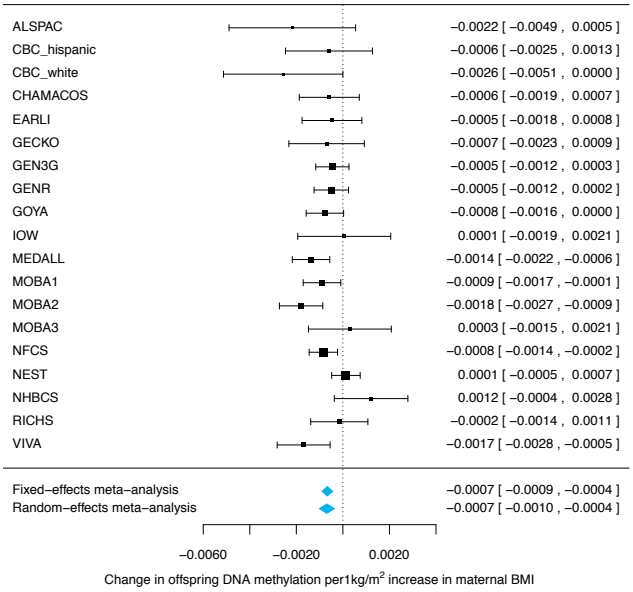
Forest plot for probe: cg13176454 [ST3GAL1]



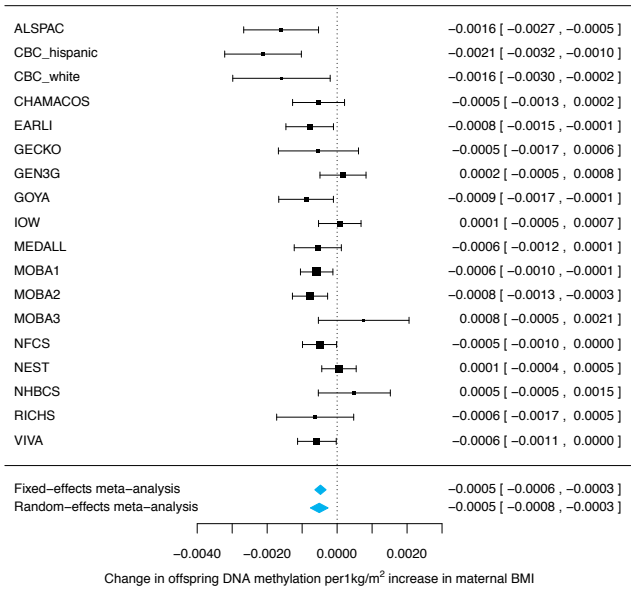
Forest plot for probe: cg14030674 [ANK1]

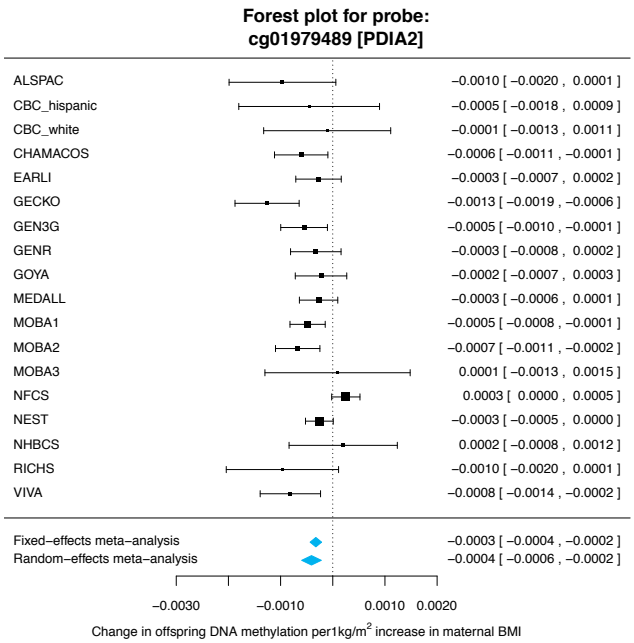


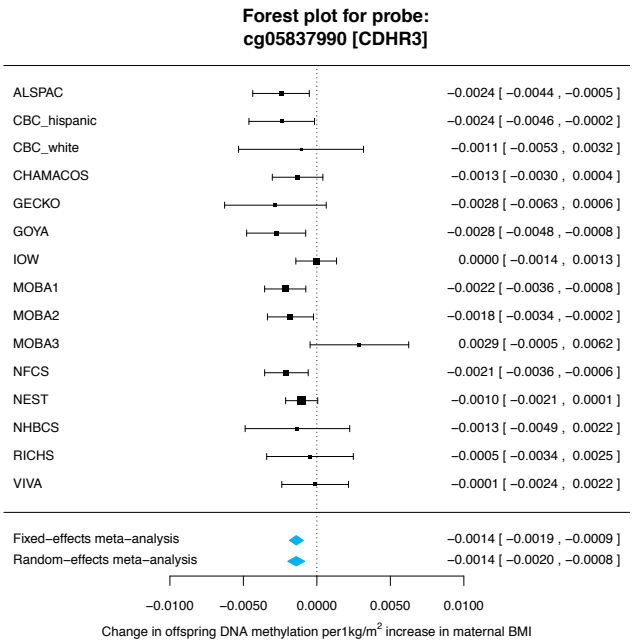
Forest plot for probe: cg27102629 [KAT6B]

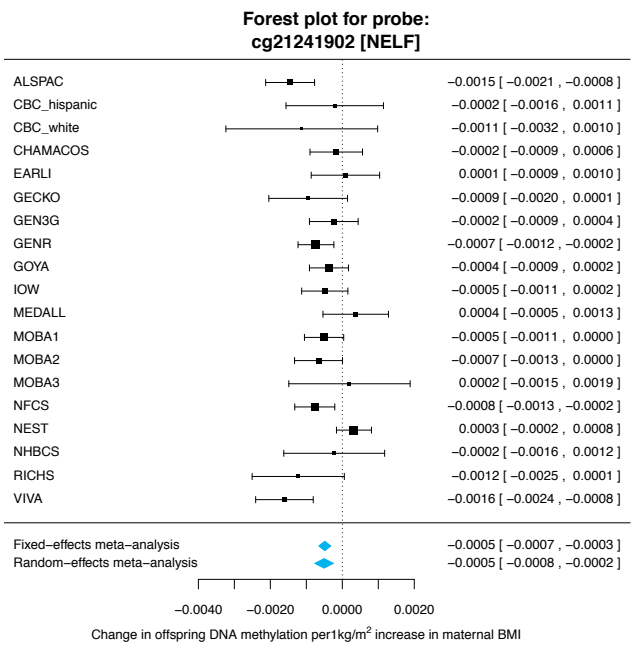


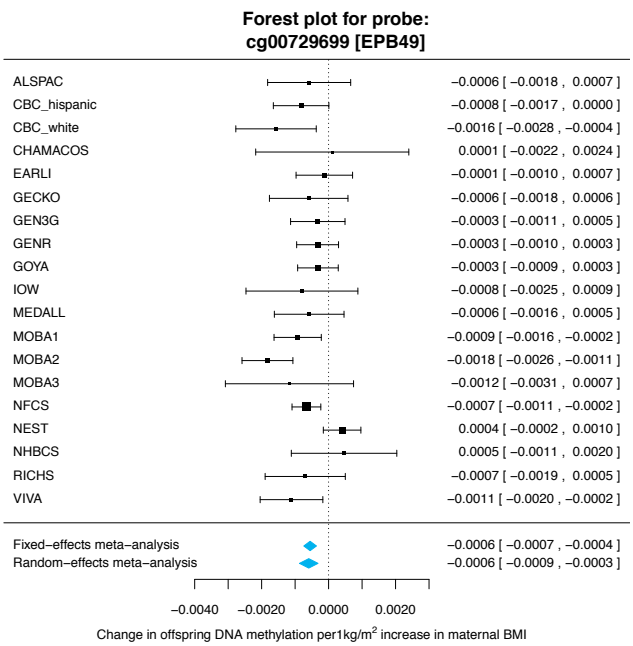
Forest plot for probe: cg06399427 [RBMS1]

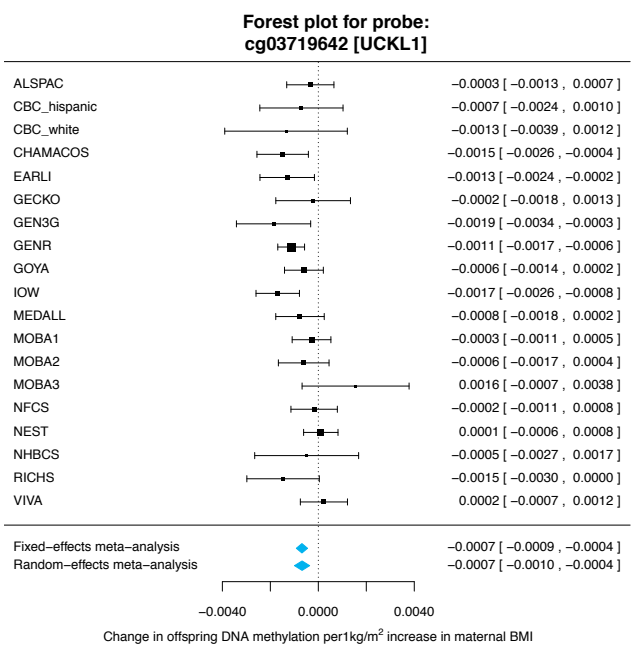


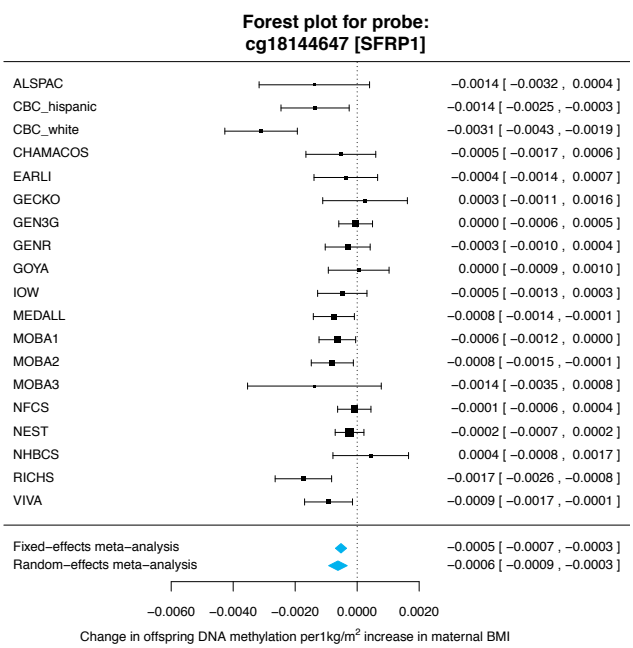

Forest plot for probe:
cg01979489 [PDIA2]
ALSPAC −0.0010 [−0.0020 , 0.0001]
CBC_hispanic −0.0005 [−0.0018 , 0.0009]
CBC_white −0.0001 [−0.0013 , 0.0011]
CHAMACOS −0.0006 [−0.0011 , −0.0001]
EARLI −0.0003 [−0.0007 , 0.0002]
GECKO −0.0013 [−0.0019 , −0.0006]
GEN3G −0.0005 [−0.0010 , −0.0001]
GENR −0.0003 [−0.0008 , 0.0002]
GOYA −0.0002 [−0.0007 , 0.0003]
MEDALL −0.0003 [−0.0006 , 0.0001]
MOBA1 −0.0005 [−0.0008 , −0.0001]
MOBA2 −0.0007 [−0.0011 , −0.0002]
MOBA3 0.0001 [−0.0013 , 0.0015]
NFCS 0.0003 [0.0000 , 0.0005]
NEST −0.0003 [−0.0005 , 0.0000]
NHBCS 0.0002 [−0.0008 , 0.0012]
RICHS −0.0010 [−0.0020 , 0.0001]
VIVA −0.0008 [−0.0014 , −0.0002]
Fixed−effects meta−analysis −0.0003 [−0.0004 , −0.0002]
Random−effects meta−analysis −0.0004 [−0.0006 , −0.0002]
−0.0030 −0.0010 0.0010 0.0020
Change in offspring DNA methylation per1kg/m2 increase in maternal BMI


Forest plot for probe:
cg05837990 [CDHR3]
ALSPAC −0.0024 [−0.0044 , −0.0005]
CBC_hispanic −0.0024 [−0.0046 , −0.0002]
CBC_white −0.0011 [−0.0053 , 0.0032]
CHAMACOS −0.0013 [−0.0030 , 0.0004]
GECKO −0.0028 [−0.0063 , 0.0006]
GOYA −0.0028 [−0.0048 , −0.0008]
IOW 0.0000 [−0.0014 , 0.0013]
MOBA1 −0.0022 [−0.0036 , −0.0008]
MOBA2 −0.0018 [−0.0034 , −0.0002]
MOBA3 0.0029 [−0.0005 , 0.0062]
NFCS −0.0021 [−0.0036 , −0.0006]
NEST −0.0010 [−0.0021 , 0.0001]
NHBCS −0.0013 [−0.0049 , 0.0022]
RICHS −0.0005 [−0.0034 , 0.0025]
VIVA −0.0001 [−0.0024 , 0.0022]
Fixed−effects meta−analysis −0.0014 [−0.0019 , −0.0009]
Random−effects meta−analysis −0.0014 [−0.0020 , −0.0008]
−0.0100 −0.0050 0.0000 0.0050 0.0100
Change in offspring DNA methylation per1kg/m2 increase in maternal BMI

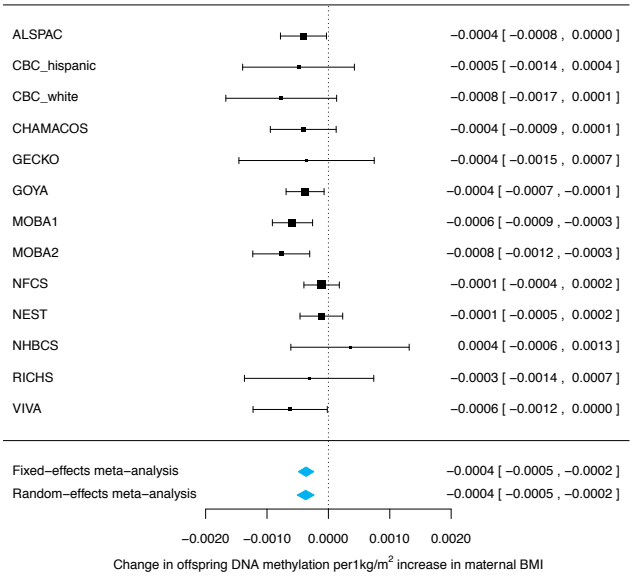

Forest plot for probe:
cg21241902 [NELF]
ALSPAC −0.0015 [−0.0021 , −0.0008]
CBC_hispanic −0.0002 [−0.0016 , 0.0011]
CBC_white −0.0011 [−0.0032 , 0.0010]
CHAMACOS −0.0002 [−0.0009 , 0.0006]
EARLI 0.0001 [−0.0009 , 0.0010]
GECKO −0.0009 [−0.0020 , 0.0001]
GEN3G −0.0002 [−0.0009 , 0.0004]
GENR −0.0007 [−0.0012 , −0.0002]
GOYA −0.0004 [−0.0009 , 0.0002]
IOW −0.0005 [−0.0011 , 0.0002]
MEDALL 0.0004 [−0.0005 , 0.0013]
MOBA1 −0.0005 [−0.0011 , 0.0000]
MOBA2 −0.0007 [−0.0013 , 0.0000]
MOBA3 0.0002 [−0.0015 , 0.0019]
NFCS −0.0008 [−0.0013 , −0.0002]
NEST 0.0003 [−0.0002 , 0.0008]
NHBCS −0.0002 [−0.0016 , 0.0012]
RICHS −0.0012 [−0.0025 , 0.0001]
VIVA −0.0016 [−0.0024 , −0.0008]
Fixed−effects meta−analysis −0.0005 [−0.0007 , −0.0003]
Random−effects meta−analysis −0.0005 [−0.0008 , −0.0002]
−0.0040 −0.0020 0.0000 0.0020
Change in offspring DNA methylation per1kg/m2 increase in maternal BMI


Forest plot for probe:
cg00729699 [EPB49]
ALSPAC −0.0006 [−0.0018 , 0.0007]
CBC_hispanic −0.0008 [−0.0017 , 0.0000]
CBC_white −0.0016 [−0.0028 , −0.0004]
CHAMACOS 0.0001 [−0.0022 , 0.0024]
EARLI −0.0001 [−0.0010 , 0.0007]
GECKO −0.0006 [−0.0018 , 0.0006]
GEN3G −0.0003 [−0.0011 , 0.0005]
GENR −0.0003 [−0.0010 , 0.0003]
GOYA −0.0003 [−0.0009 , 0.0003]
IOW −0.0008 [−0.0025 , 0.0009]
MEDALL −0.0006 [−0.0016 , 0.0005]
MOBA1 −0.0009 [−0.0016 , −0.0002]
MOBA2 −0.0018 [−0.0026 , −0.0011]
MOBA3 −0.0012 [−0.0031 , 0.0007]
NFCS −0.0007 [−0.0011 , −0.0002]
NEST 0.0004 [−0.0002 , 0.0010]
NHBCS 0.0005 [−0.0011 , 0.0020]
RICHS −0.0007 [−0.0019 , 0.0005]
VIVA −0.0011 [−0.0020 , −0.0002]
Fixed−effects meta−analysis −0.0006 [−0.0007 , −0.0004]
Random−effects meta−analysis −0.0006 [−0.0009 , −0.0003]
−0.0040 −0.0020 0.0000 0.0020
Change in offspring DNA methylation per1kg/m2 increase in maternal BMI

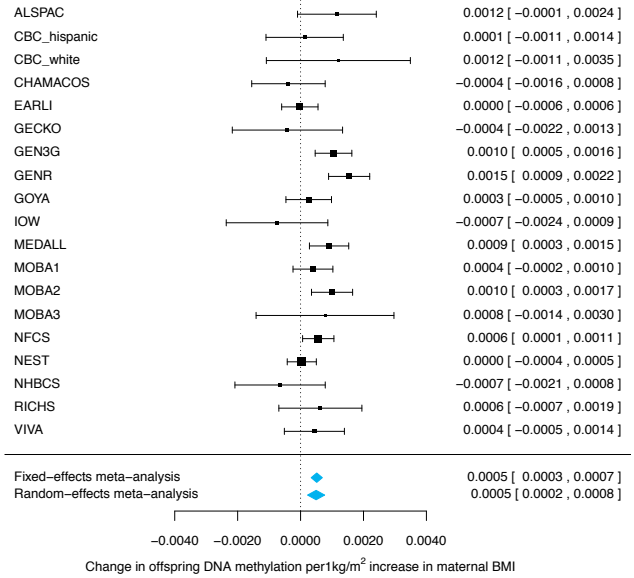

Forest plot for probe:
cg03719642 [UCKL1]
ALSPAC −0.0003 [−0.0013 , 0.0007]
CBC_hispanic −0.0007 [−0.0024 , 0.0010]
CBC_white −0.0013 [−0.0039 , 0.0012]
CHAMACOS −0.0015 [−0.0026 , −0.0004]
EARLI −0.0013 [−0.0024 , −0.0002]
GECKO −0.0002 [−0.0018 , 0.0013]
GEN3G −0.0019 [−0.0034 , −0.0003]
GENR −0.0011 [−0.0017 , −0.0006]
GOYA −0.0006 [−0.0014 , 0.0002]
IOW −0.0017 [−0.0026 , −0.0008]
MEDALL −0.0008 [−0.0018 , 0.0002]
MOBA1 −0.0003 [−0.0011 , 0.0005]
MOBA2 −0.0006 [−0.0017 , 0.0004]
MOBA3 0.0016 [−0.0007 , 0.0038]
NFCS −0.0002 [−0.0011 , 0.0008]
NEST 0.0001 [−0.0006 , 0.0008]
NHBCS −0.0005 [−0.0027 , 0.0017]
RICHS −0.0015 [−0.0030 , 0.0000]
VIVA 0.0002 [−0.0007 , 0.0012]
Fixed−effects meta−analysis −0.0007 [−0.0009 , −0.0004]
Random−effects meta−analysis −0.0007 [−0.0010 , −0.0004]
−0.0040 0.0000 0.0040
Change in offspring DNA methylation per1kg/m2 increase in maternal BMI


Forest plot for probe:
cg18144647 [SFRP1]
ALSPAC −0.0014 [−0.0032 , 0.0004]
CBC_hispanic −0.0014 [−0.0025 , −0.0003]
CBC_white −0.0031 [−0.0043 , −0.0019]
CHAMACOS −0.0005 [−0.0017 , 0.0006]
EARLI −0.0004 [−0.0014 , 0.0007]
GECKO 0.0003 [−0.0011 , 0.0016]
GEN3G 0.0000 [−0.0006 , 0.0005]
GENR −0.0003 [−0.0010 , 0.0004]
GOYA 0.0000 [−0.0009 , 0.0010]
IOW −0.0005 [−0.0013 , 0.0003]
MEDALL −0.0008 [−0.0014 , −0.0001]
MOBA1 −0.0006 [−0.0012 , 0.0000]
MOBA2 −0.0008 [−0.0015 , −0.0001]
MOBA3 −0.0014 [−0.0035 , 0.0008]
NFCS −0.0001 [−0.0006 , 0.0004]
NEST −0.0002 [−0.0007 , 0.0002]
NHBCS 0.0004 [−0.0008 , 0.0017]
RICHS −0.0017 [−0.0026 , −0.0008]
VIVA −0.0009 [−0.0017 , −0.0001]
Fixed−effects meta−analysis −0.0005 [−0.0007 , −0.0003]
Random−effects meta−analysis −0.0006 [−0.0009 , −0.0003]
−0.0060 −0.0040 −0.0020 0.0000 0.0020
Change in offspring DNA methylation per1kg/m2 increase in maternal BMI

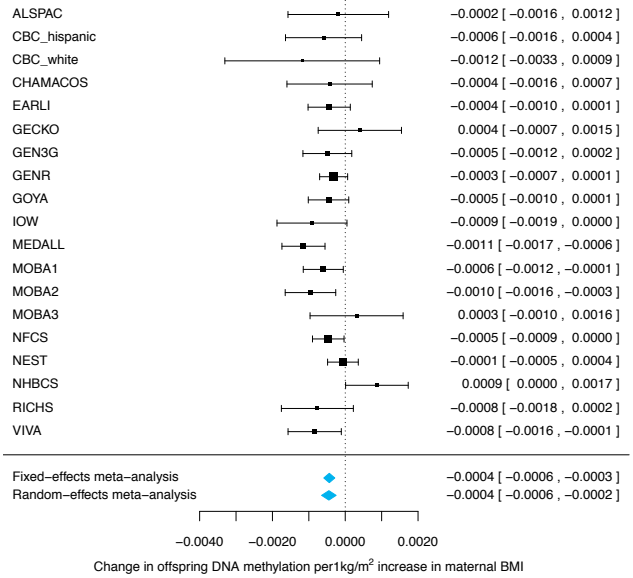
Forest plot for probe: cg21814615 [HCAR1]



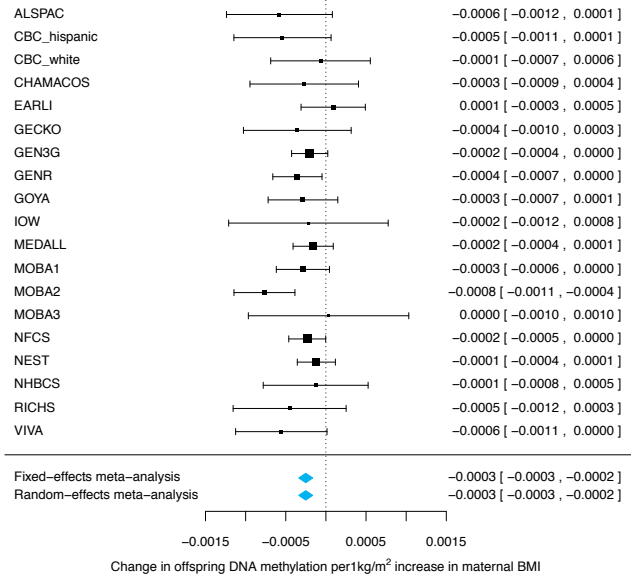
Forest plot for probe: cg14528056 [GBAP1]



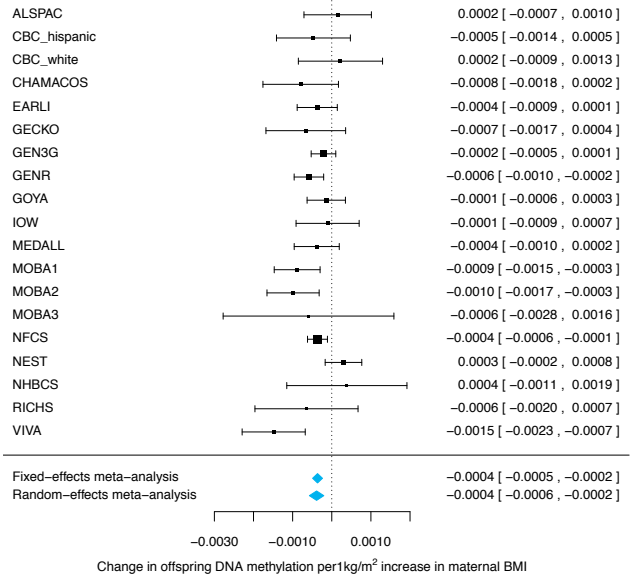
Forest plot for probe: cg22820188 [LMNA]



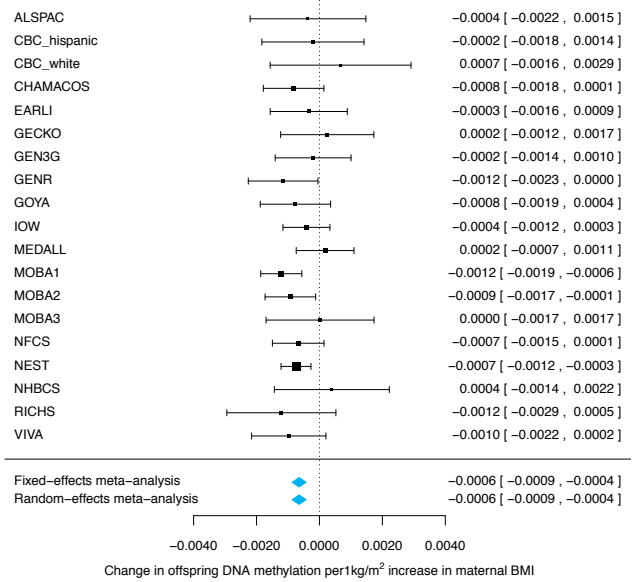
Forest plot for probe: cg08289937 [DDHD1]



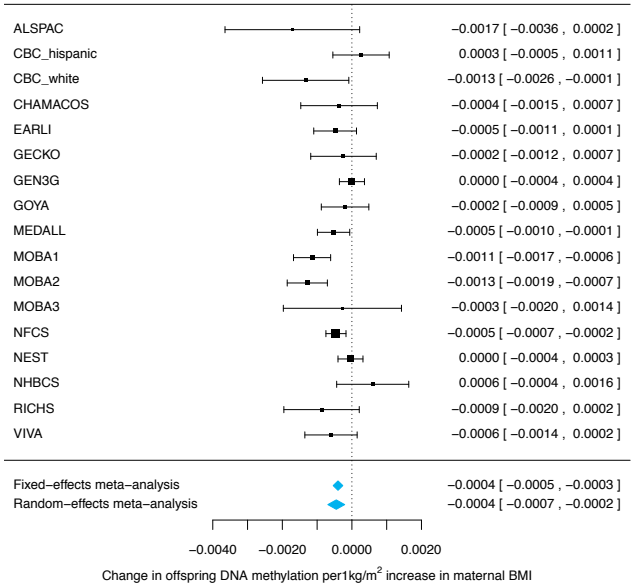
Forest plot for probe: cg21186778 [AK021739]



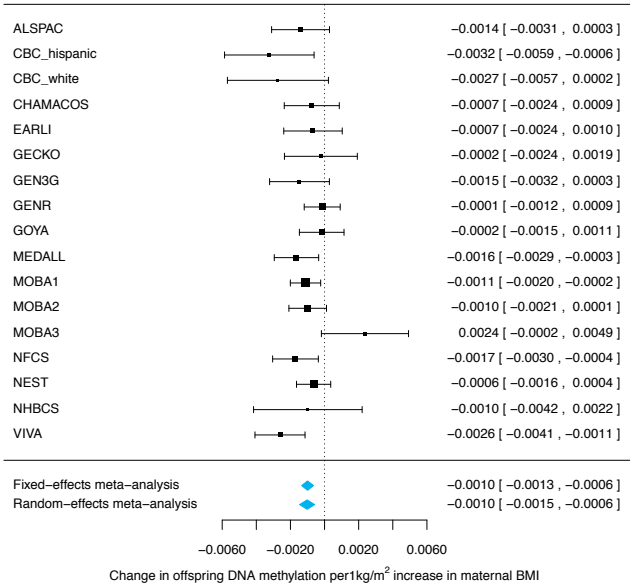
Forest plot for probe: cg17514558 [PCDHB19P]



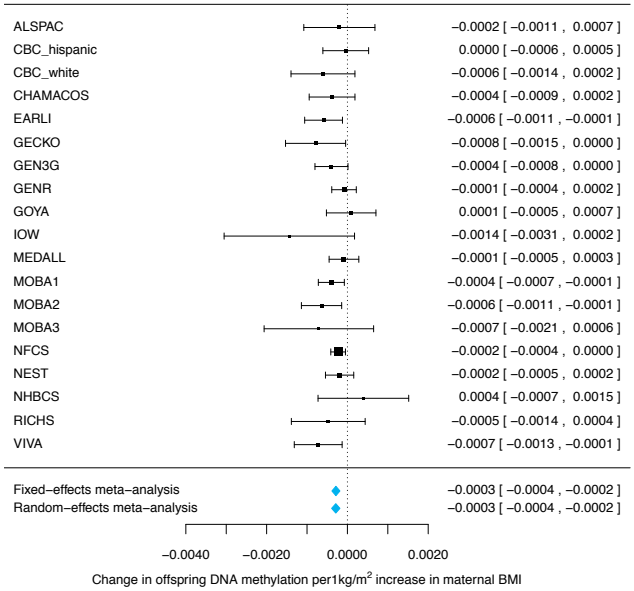
Forest plot for probe: cg15240102 [LOC286083]



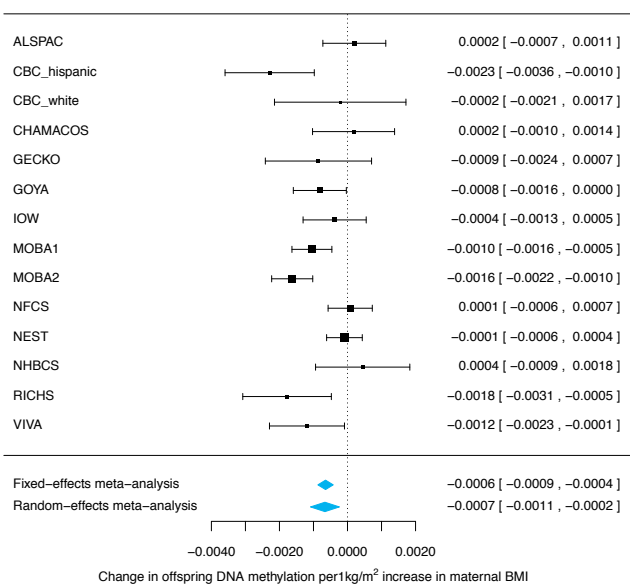
Forest plot for probe: cg21026022 [CABYR]



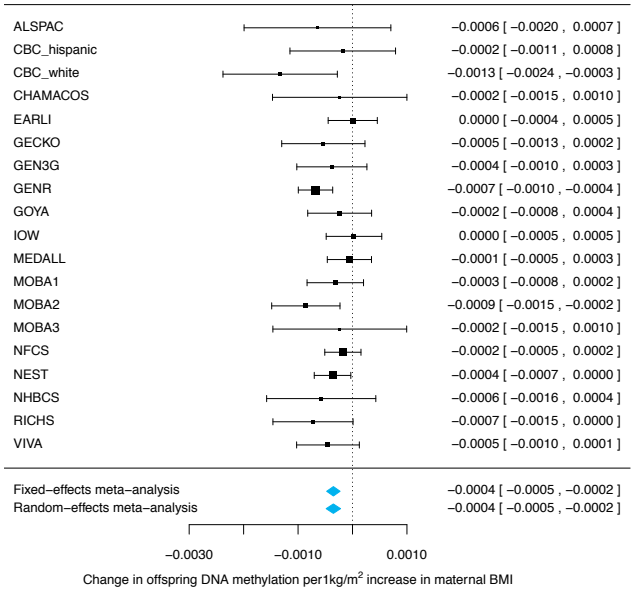
Forest plot for probe: cg18995031 [RASA3]



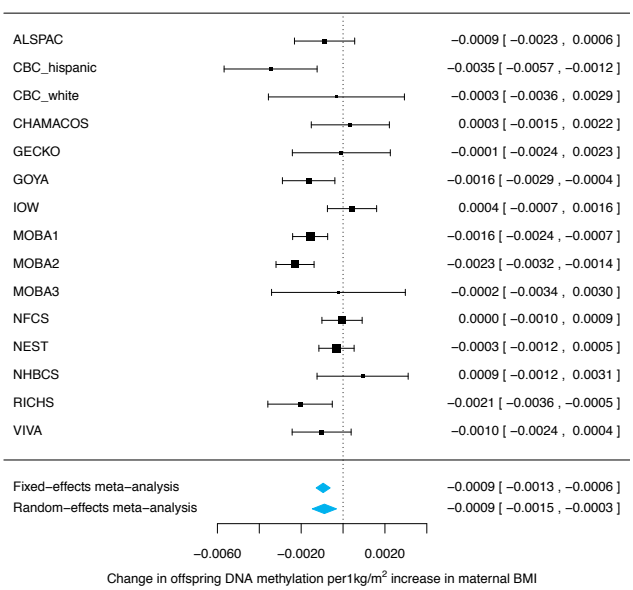
Forest plot for probe: cg04027757 [POM121L1P]



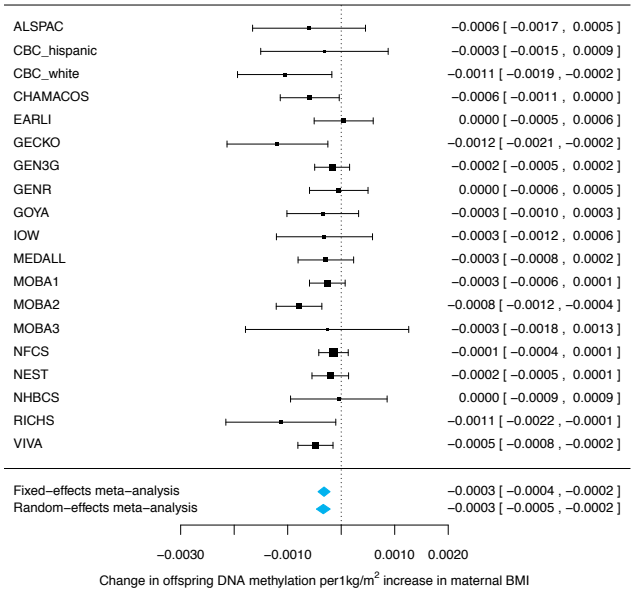
Forest plot for probe: cg01963618 [LOC285768]



Forest plot for probe: cg21445553 [GGTLC1]

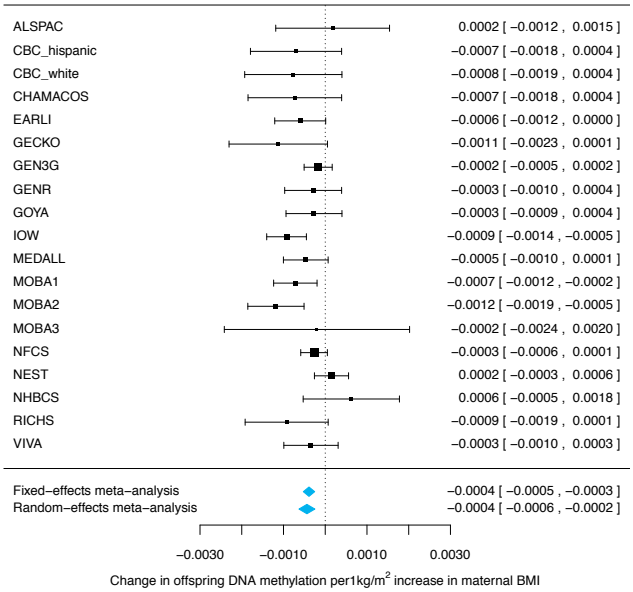


Forest plot for probe: cg05976575 [CMTM2]



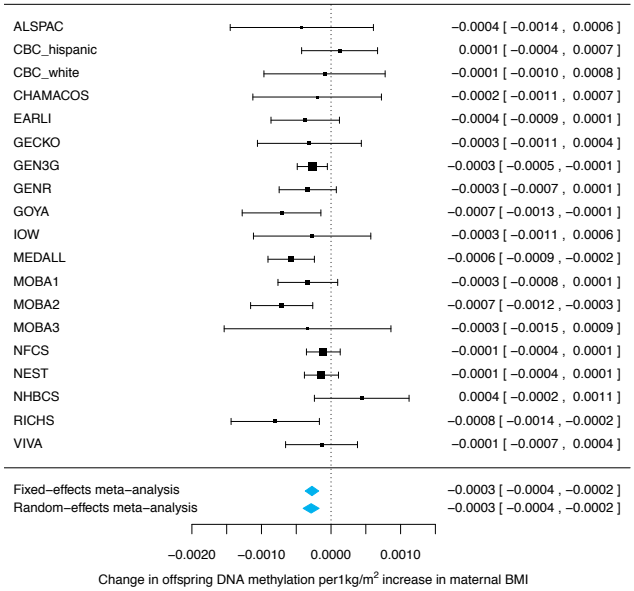
Change in offspring DNA methylation per1kg/m^2 increase in maternal BMI

Forest plot for probe: cg13758186 [CREG2]



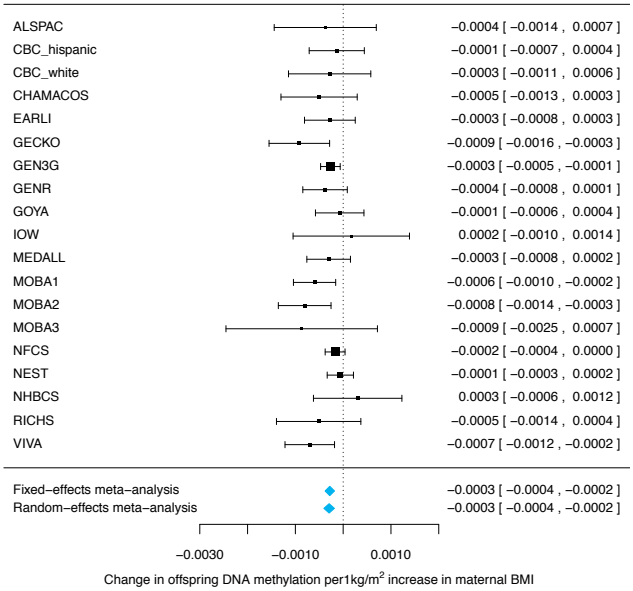
Change in offspring DNA methylation per1kg/m^2 increase in maternal BMI

Forest plot for probe: cg20710902 [DQ594093]



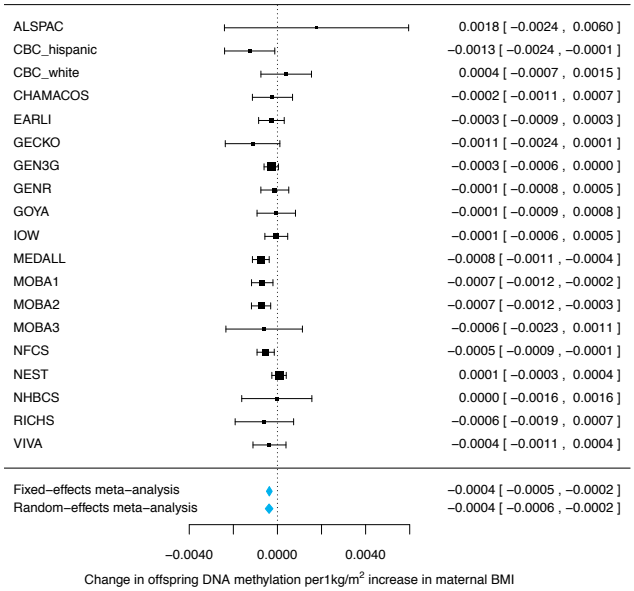
Change in offspring DNA methylation per1kg/m^2 increase in maternal BMI

Forest plot for probe: cg03046925 [TRIM15]



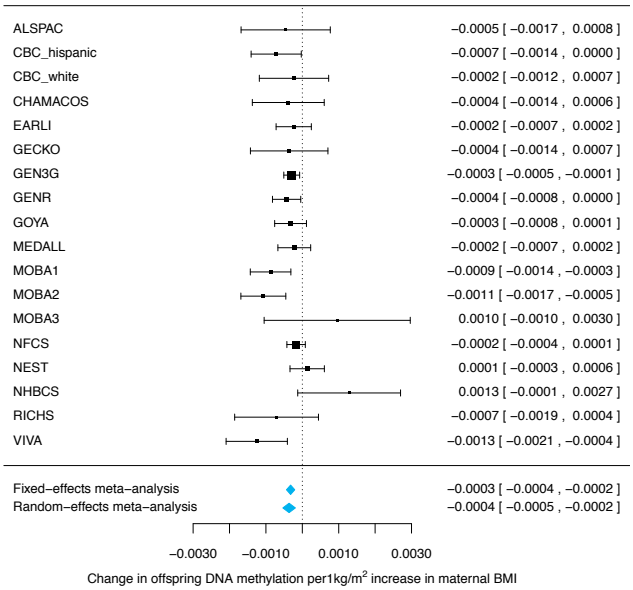
Change in offspring DNA methylation per1kg/m^2 increase in maternal BMI

Forest plot for probe: cg18330571 [MIR4297]

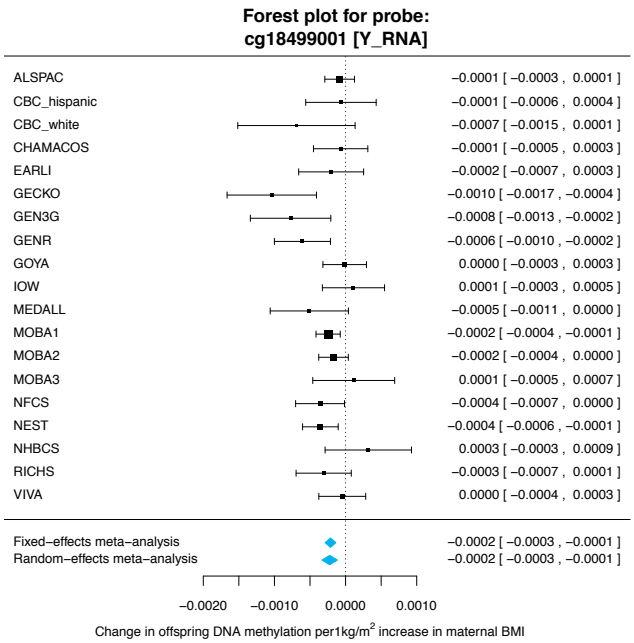


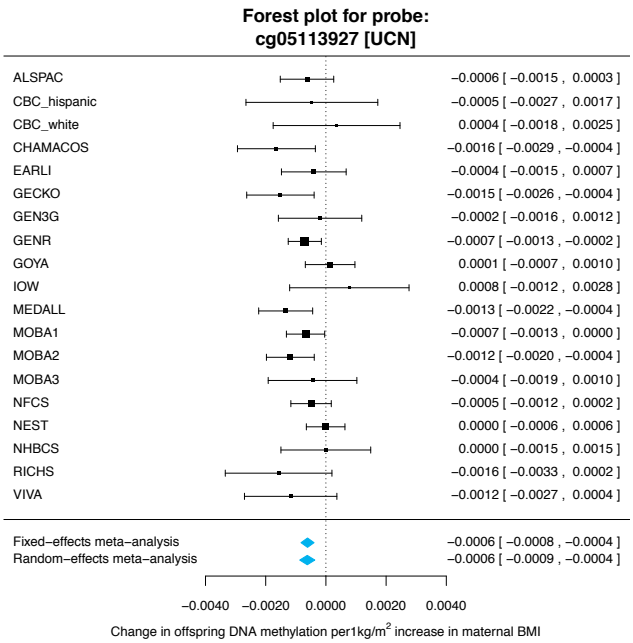
Change in offspring DNA methylation per1kg/m^2 increase in maternal BMI

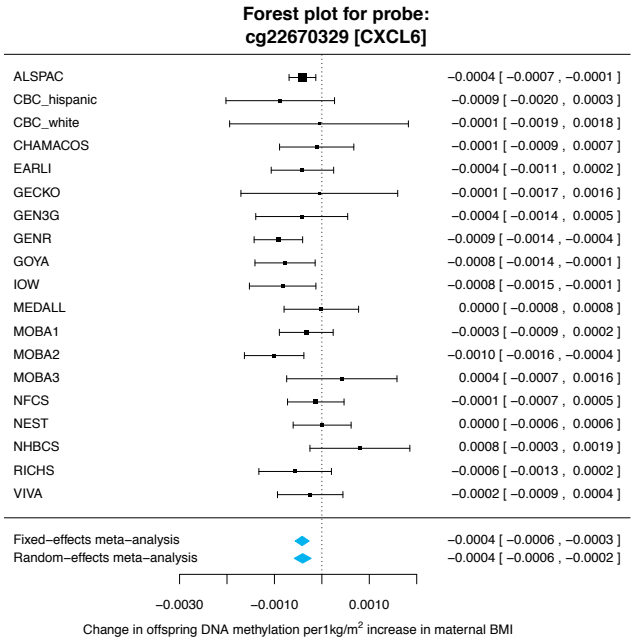
Forest plot for probe: cg11156132 [PRKCD]

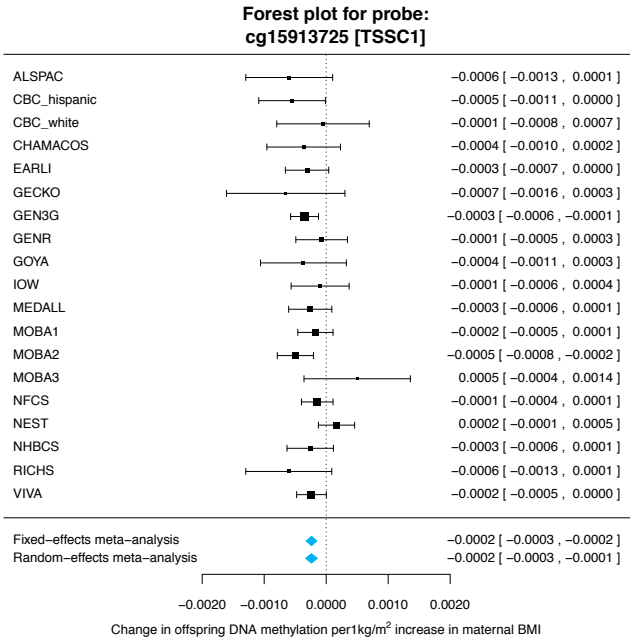


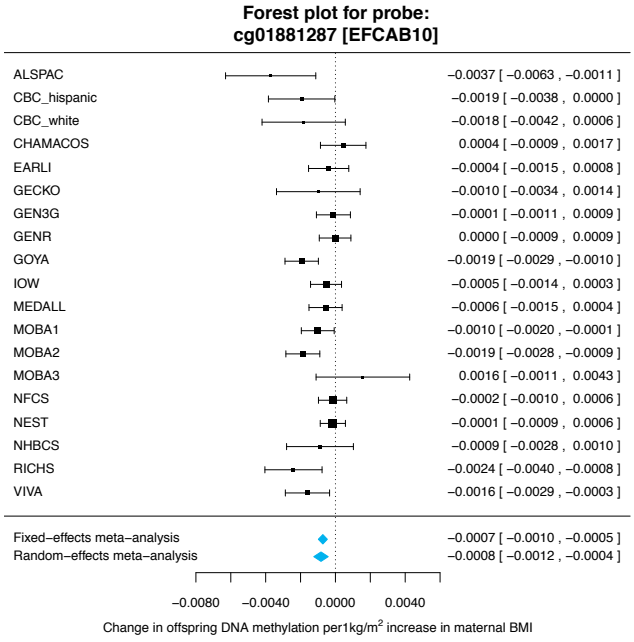
Change in offspring DNA methylation per1kg/m^2 increase in maternal BMI

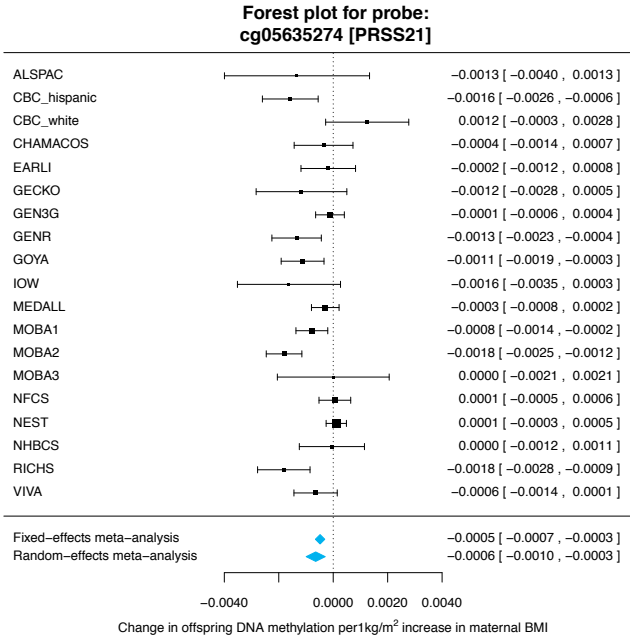

Forest plot for probe:
cg18499001 [Y_RNA]
ALSPAC −0.0001 [−0.0003 , 0.0001]
CBC_hispanic −0.0001 [−0.0006 , 0.0004]
CBC_white −0.0007 [−0.0015 , 0.0001]
CHAMACOS −0.0001 [−0.0005 , 0.0003]
EARLI −0.0002 [−0.0007 , 0.0003]
GECKO −0.0010 [−0.0017 , −0.0004]
GEN3G −0.0008 [−0.0013 , −0.0002]
GENR −0.0006 [−0.0010 , −0.0002]
GOYA 0.0000 [−0.0003 , 0.0003]
IOW 0.0001 [−0.0003 , 0.0005]
MEDALL −0.0005 [−0.0011 , 0.0000]
MOBA1 −0.0002 [−0.0004 , −0.0001]
MOBA2 −0.0002 [−0.0004 , 0.0000]
MOBA3 0.0001 [−0.0005 , 0.0007]
NFCS −0.0004 [−0.0007 , 0.0000]
NEST −0.0004 [−0.0006 , −0.0001]
NHBCS 0.0003 [−0.0003 , 0.0009]
RICHS −0.0003 [−0.0007 , 0.0001]
VIVA 0.0000 [−0.0004 , 0.0003]
Fixed−effects meta−analysis −0.0002 [−0.0003 , −0.0001]
Random−effects meta−analysis −0.0002 [−0.0003 , −0.0001]
−0.0020 −0.0010 0.0000 0.0010
Change in offspring DNA methylation per1kg/m2 increase in maternal BMI


Forest plot for probe:
cg05113927 [UCN]
ALSPAC −0.0006 [−0.0015 , 0.0003]
CBC_hispanic −0.0005 [−0.0027 , 0.0017]
CBC_white 0.0004 [−0.0018 , 0.0025]
CHAMACOS −0.0016 [−0.0029 , −0.0004]
EARLI −0.0004 [−0.0015 , 0.0007]
GECKO −0.0015 [−0.0026 , −0.0004]
GEN3G −0.0002 [−0.0016 , 0.0012]
GENR −0.0007 [−0.0013 , −0.0002]
GOYA 0.0001 [−0.0007 , 0.0010]
IOW 0.0008 [−0.0012 , 0.0028]
MEDALL −0.0013 [−0.0022 , −0.0004]
MOBA1 −0.0007 [−0.0013 , 0.0000]
MOBA2 −0.0012 [−0.0020 , −0.0004]
MOBA3 −0.0004 [−0.0019 , 0.0010]
NFCS −0.0005 [−0.0012 , 0.0002]
NEST 0.0000 [−0.0006 , 0.0006]
NHBCS 0.0000 [−0.0015 , 0.0015]
RICHS −0.0016 [−0.0033 , 0.0002]
VIVA −0.0012 [−0.0027 , 0.0004]
Fixed−effects meta−analysis −0.0006 [−0.0008 , −0.0004]
Random−effects meta−analysis −0.0006 [−0.0009 , −0.0004]
−0.0040 −0.0020 0.0000 0.0020 0.0040
Change in offspring DNA methylation per1kg/m2 increase in maternal BMI

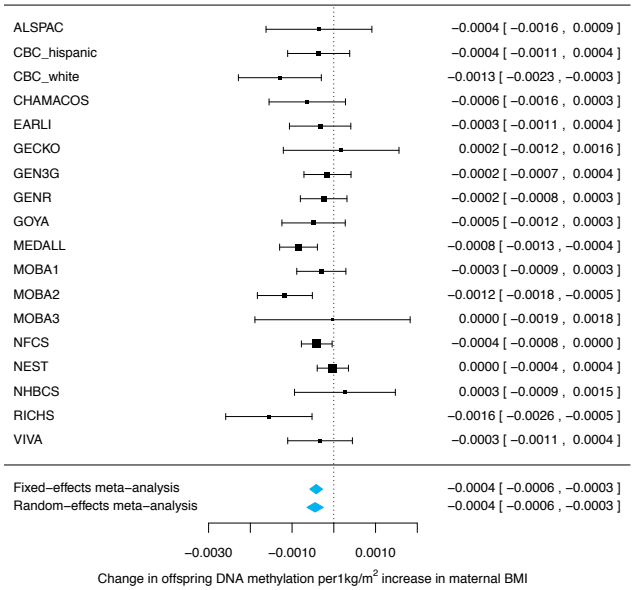

Forest plot for probe:
cg22670329 [CXCL6]
ALSPAC −0.0004 [−0.0007 , −0.0001]
CBC_hispanic −0.0009 [−0.0020 , 0.0003]
CBC_white −0.0001 [−0.0019 , 0.0018]
CHAMACOS −0.0001 [−0.0009 , 0.0007]
EARLI −0.0004 [−0.0011 , 0.0002]
GECKO −0.0001 [−0.0017 , 0.0016]
GEN3G −0.0004 [−0.0014 , 0.0005]
GENR −0.0009 [−0.0014 , −0.0004]
GOYA −0.0008 [−0.0014 , −0.0001]
IOW −0.0008 [−0.0015 , −0.0001]
MEDALL 0.0000 [−0.0008 , 0.0008]
MOBA1 −0.0003 [−0.0009 , 0.0002]
MOBA2 −0.0010 [−0.0016 , −0.0004]
MOBA3 0.0004 [−0.0007 , 0.0016]
NFCS −0.0001 [−0.0007 , 0.0005]
NEST 0.0000 [−0.0006 , 0.0006]
NHBCS 0.0008 [−0.0003 , 0.0019]
RICHS −0.0006 [−0.0013 , 0.0002]
VIVA −0.0002 [−0.0009 , 0.0004]
Fixed−effects meta−analysis −0.0004 [−0.0006 , −0.0003]
Random−effects meta−analysis −0.0004 [−0.0006 , −0.0002]
−0.0030 −0.0010 0.0010
Change in offspring DNA methylation per1kg/m2 increase in maternal BMI


Forest plot for probe:
cg15913725 [TSSC1]
ALSPAC −0.0006 [−0.0013 , 0.0001]
CBC_hispanic −0.0005 [−0.0011 , 0.0000]
CBC_white −0.0001 [−0.0008 , 0.0007]
CHAMACOS −0.0004 [−0.0010 , 0.0002]
EARLI −0.0003 [−0.0007 , 0.0000]
GECKO −0.0007 [−0.0016 , 0.0003]
GEN3G −0.0003 [−0.0006 , −0.0001]
GENR −0.0001 [−0.0005 , 0.0003]
GOYA −0.0004 [−0.0011 , 0.0003]
IOW −0.0001 [−0.0006 , 0.0004]
MEDALL −0.0003 [−0.0006 , 0.0001]
MOBA1 −0.0002 [−0.0005 , 0.0001]
MOBA2 −0.0005 [−0.0008 , −0.0002]
MOBA3 0.0005 [−0.0004 , 0.0014]
NFCS −0.0001 [−0.0004 , 0.0001]
NEST 0.0002 [−0.0001 , 0.0005]
NHBCS −0.0003 [−0.0006 , 0.0001]
RICHS −0.0006 [−0.0013 , 0.0001]
VIVA −0.0002 [−0.0005 , 0.0000]
Fixed−effects meta−analysis −0.0002 [−0.0003 , −0.0002]
Random−effects meta−analysis −0.0002 [−0.0003 , −0.0001]
−0.0020 −0.0010 0.0000 0.0010 0.0020
Change in offspring DNA methylation per1kg/m2 increase in maternal BMI

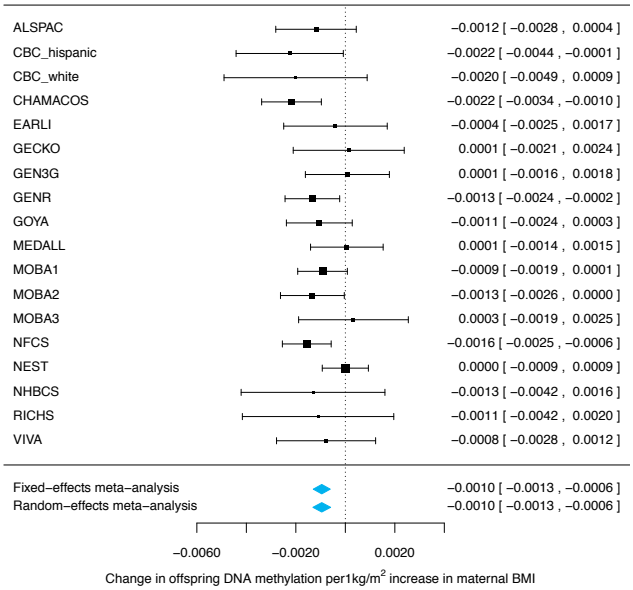

Forest plot for probe:
cg01881287 [EFCAB10]
ALSPAC −0.0037 [−0.0063 , −0.0011]
CBC_hispanic −0.0019 [−0.0038 , 0.0000]
CBC_white −0.0018 [−0.0042 , 0.0006]
CHAMACOS 0.0004 [−0.0009 , 0.0017]
EARLI −0.0004 [−0.0015 , 0.0008]
GECKO −0.0010 [−0.0034 , 0.0014]
GEN3G −0.0001 [−0.0011 , 0.0009]
GENR 0.0000 [−0.0009 , 0.0009]
GOYA −0.0019 [−0.0029 , −0.0010]
IOW −0.0005 [−0.0014 , 0.0003]
MEDALL −0.0006 [−0.0015 , 0.0004]
MOBA1 −0.0010 [−0.0020 , −0.0001]
MOBA2 −0.0019 [−0.0028 , −0.0009]
MOBA3 0.0016 [−0.0011 , 0.0043]
NFCS −0.0002 [−0.0010 , 0.0006]
NEST −0.0001 [−0.0009 , 0.0006]
NHBCS −0.0009 [−0.0028 , 0.0010]
RICHS −0.0024 [−0.0040 , −0.0008]
VIVA −0.0016 [−0.0029 , −0.0003]
Fixed−effects meta−analysis −0.0007 [−0.0010 , −0.0005]
Random−effects meta−analysis −0.0008 [−0.0012 , −0.0004]
−0.0080 −0.0040 0.0000 0.0040
Change in offspring DNA methylation per1kg/m2 increase in maternal BMI


Forest plot for probe:
cg05635274 [PRSS21]
ALSPAC −0.0013 [−0.0040 , 0.0013]
CBC_hispanic −0.0016 [−0.0026 , −0.0006]
CBC_white 0.0012 [−0.0003 , 0.0028]
CHAMACOS −0.0004 [−0.0014 , 0.0007]
EARLI −0.0002 [−0.0012 , 0.0008]
GECKO −0.0012 [−0.0028 , 0.0005]
GEN3G −0.0001 [−0.0006 , 0.0004]
GENR −0.0013 [−0.0023 , −0.0004]
GOYA −0.0011 [−0.0019 , −0.0003]
IOW −0.0016 [−0.0035 , 0.0003]
MEDALL −0.0003 [−0.0008 , 0.0002]
MOBA1 −0.0008 [−0.0014 , −0.0002]
MOBA2 −0.0018 [−0.0025 , −0.0012]
MOBA3 0.0000 [−0.0021 , 0.0021]
NFCS 0.0001 [−0.0005 , 0.0006]
NEST 0.0001 [−0.0003 , 0.0005]
NHBCS 0.0000 [−0.0012 , 0.0011]
RICHS −0.0018 [−0.0028 , −0.0009]
VIVA −0.0006 [−0.0014 , 0.0001]
Fixed−effects meta−analysis −0.0005 [−0.0007 , −0.0003]
Random−effects meta−analysis −0.0006 [−0.0010 , −0.0003]
−0.0040 0.0000 0.0020 0.0040
Change in offspring DNA methylation per1kg/m2 increase in maternal BMI

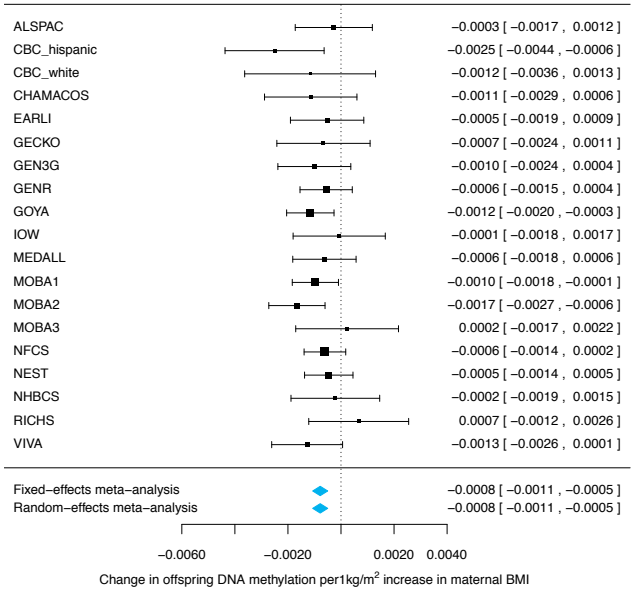
Forest plot for probe: cg03221837 [IRX3]



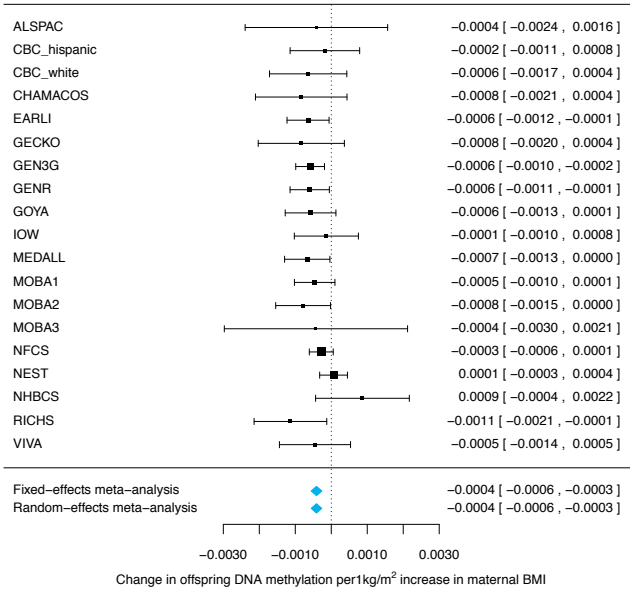
Forest plot for probe: cg13557773 [RASA3]



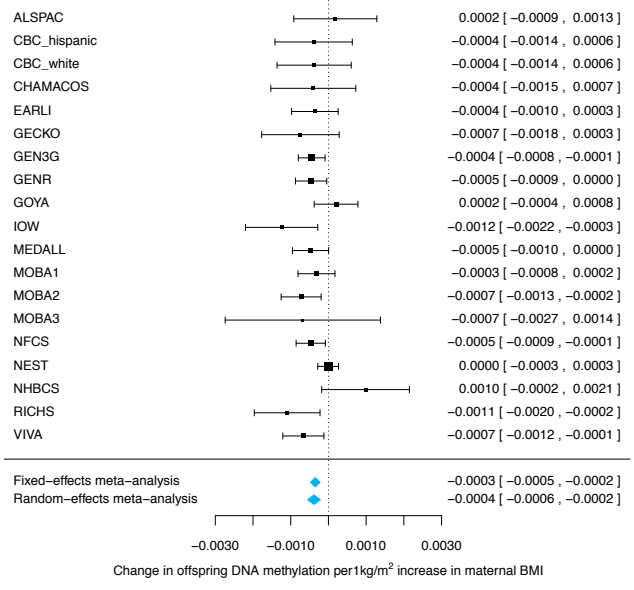
Forest plot for probe: cg14434213 [RNF5P1]



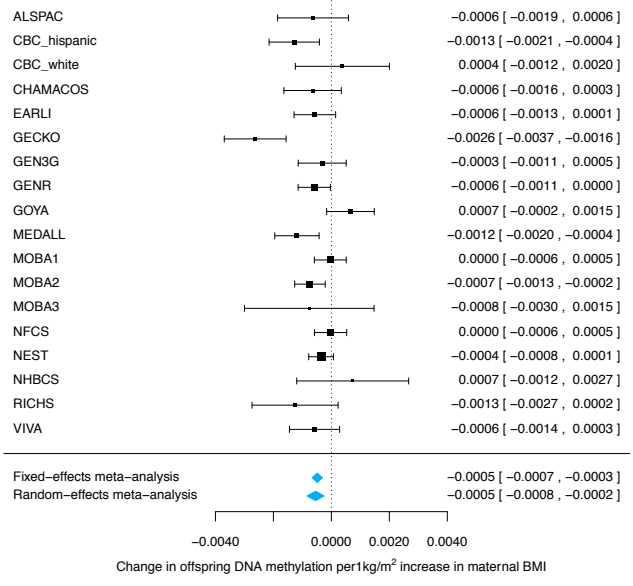
Forest plot for probe: cg05659486 [AK056584]



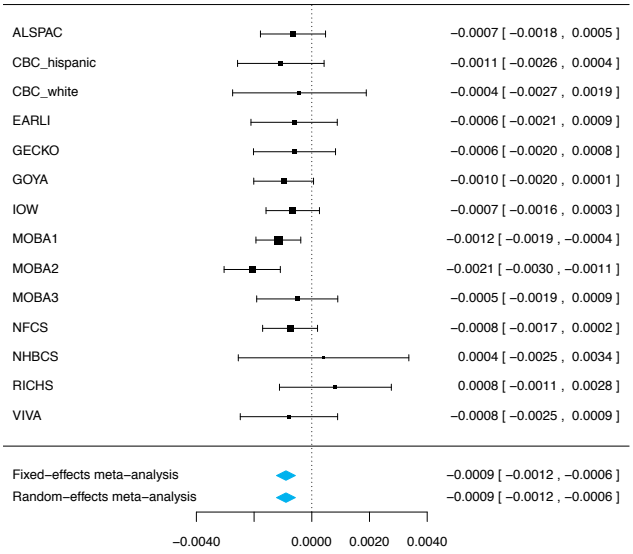
Forest plot for probe: cg22545168 [LAIR1]



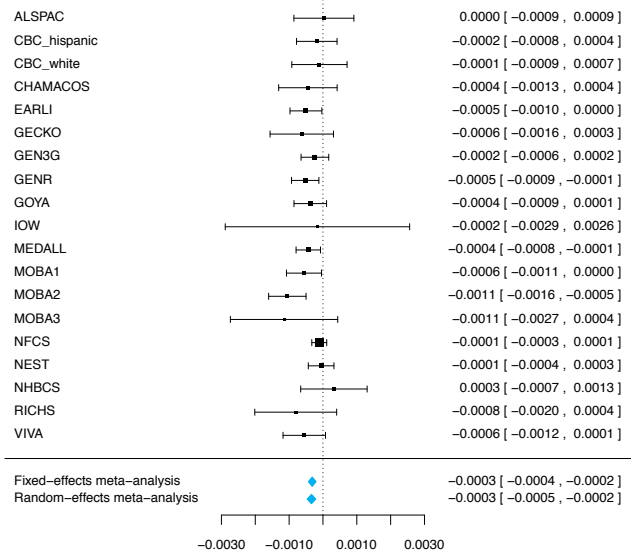
Forest plot for probe: cg15029475 [C5orf38]



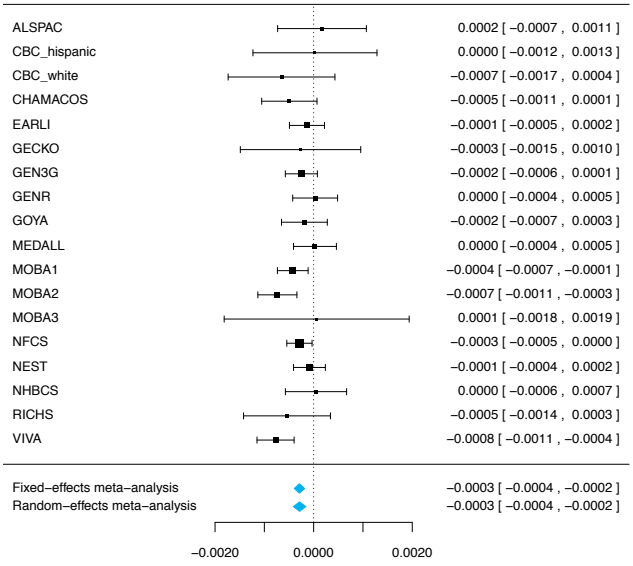
Forest plot for probe: cg23749005 [PTPRN2]



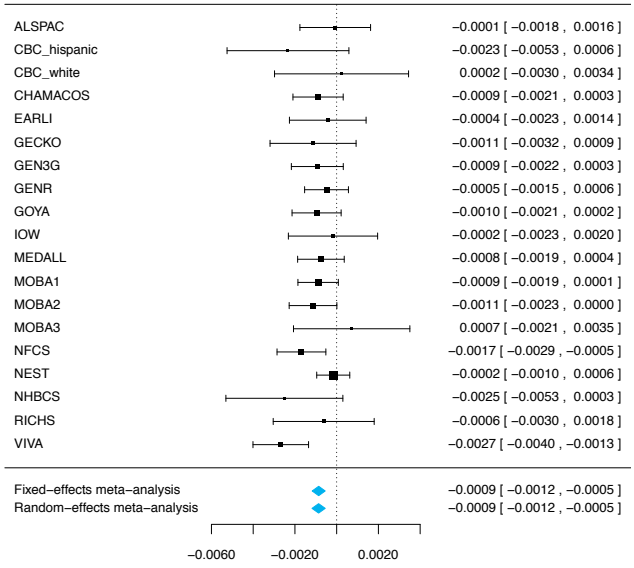
Forest plot for probe: cg23111106 [AK126213]



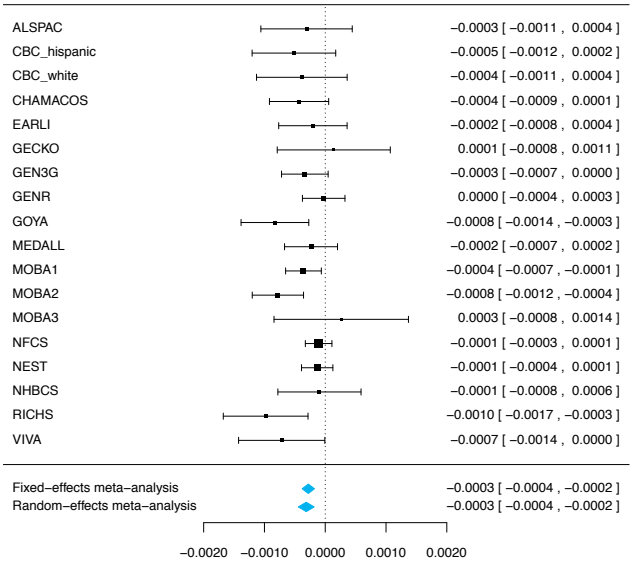
Forest plot for probe: cg21937867 [PRCD]



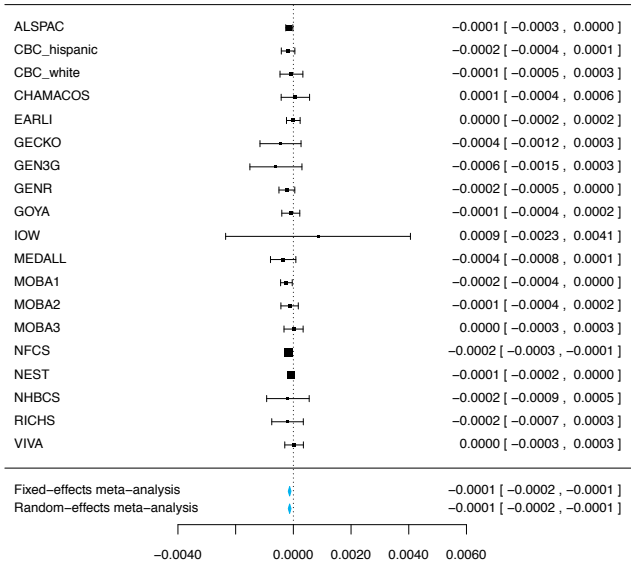
Forest plot for probe: cg04972348 [MIR200B]

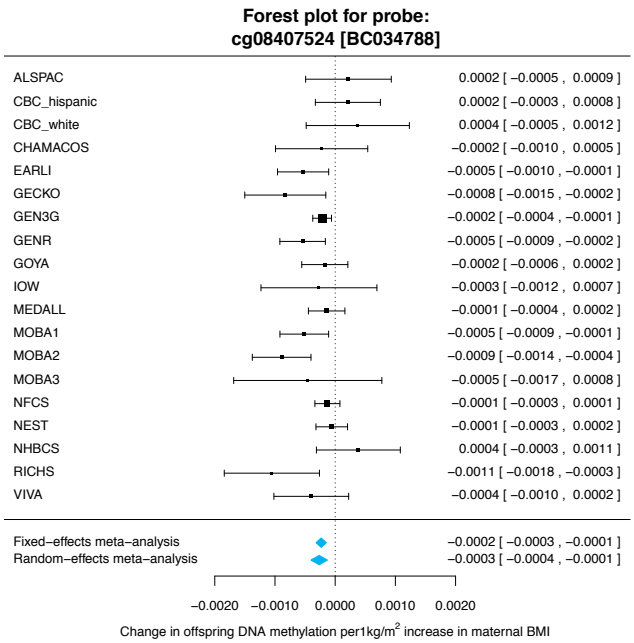


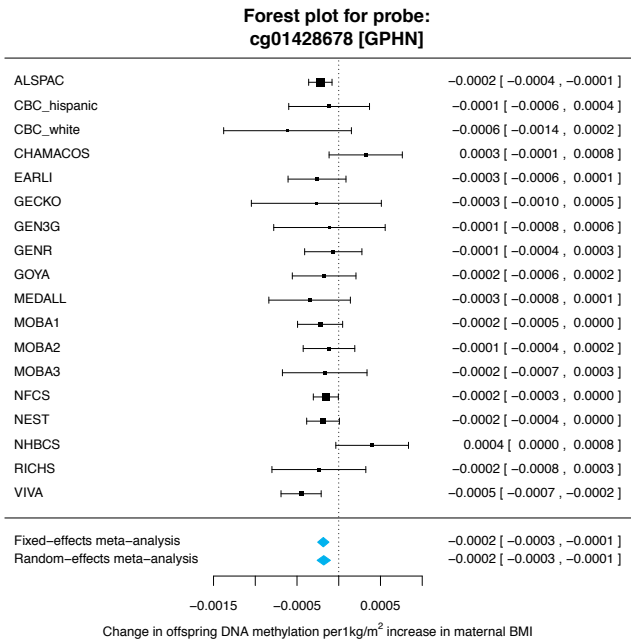
Forest plot for probe: cg05881436 [SNAPC1]

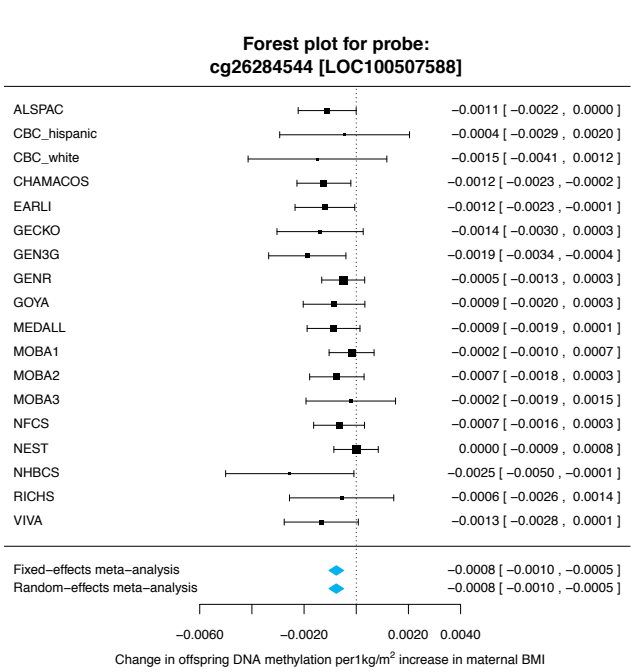


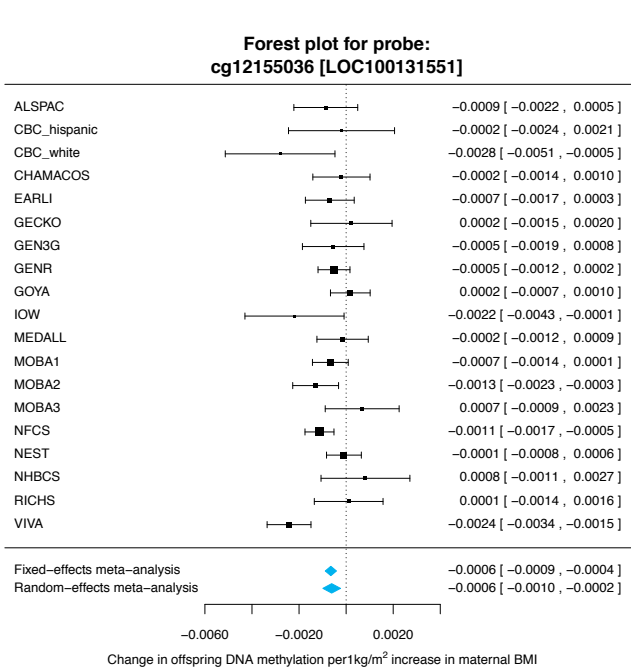
Forest plot for probe: cg23166970 [MCCC1]

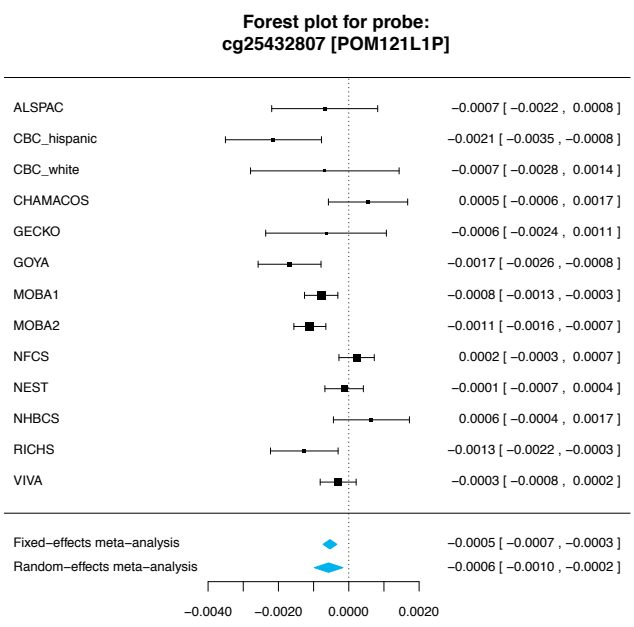


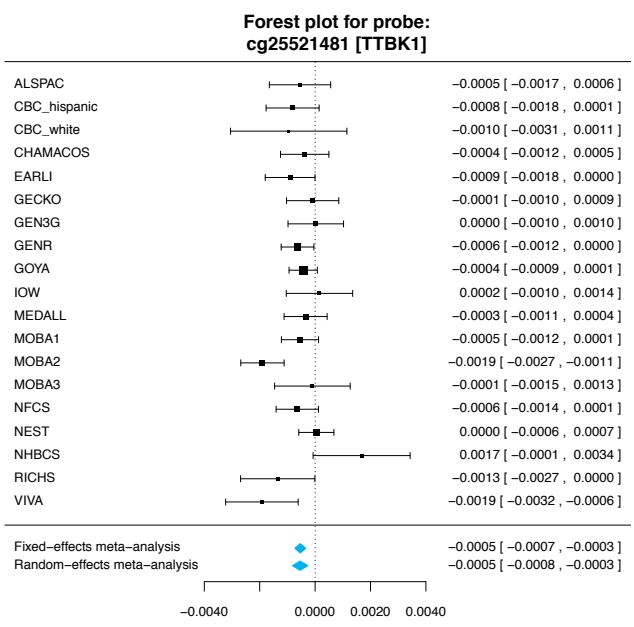

Forest plot for probe:
cg08407524 [BC034788]
ALSPAC 0.0002 [−0.0005 , 0.0009]
CBC_hispanic 0.0002 [−0.0003 , 0.0008]
CBC_white 0.0004 [−0.0005 , 0.0012]
CHAMACOS −0.0002 [−0.0010 , 0.0005]
EARLI −0.0005 [−0.0010 , −0.0001]
GECKO −0.0008 [−0.0015 , −0.0002]
GEN3G −0.0002 [−0.0004 , −0.0001]
GENR −0.0005 [−0.0009 , −0.0002]
GOYA −0.0002 [−0.0006 , 0.0002]
IOW −0.0003 [−0.0012 , 0.0007]
MEDALL −0.0001 [−0.0004 , 0.0002]
MOBA1 −0.0005 [−0.0009 , −0.0001]
MOBA2 −0.0009 [−0.0014 , −0.0004]
MOBA3 −0.0005 [−0.0017 , 0.0008]
NFCS −0.0001 [−0.0003 , 0.0001]
NEST −0.0001 [−0.0003 , 0.0002]
NHBCS 0.0004 [−0.0003 , 0.0011]
RICHS −0.0011 [−0.0018 , −0.0003]
VIVA −0.0004 [−0.0010 , 0.0002]
Fixed−effects meta−analysis −0.0002 [−0.0003 , −0.0001]
Random−effects meta−analysis −0.0003 [−0.0004 , −0.0001]
−0.0020 −0.0010 0.0000 0.0010 0.0020
Change in offspring DNA methylation per1kg/m2 increase in maternal BMI


Forest plot for probe:
cg01428678 [GPHN]
ALSPAC −0.0002 [−0.0004 , −0.0001]
CBC_hispanic −0.0001 [−0.0006 , 0.0004]
CBC_white −0.0006 [−0.0014 , 0.0002]
CHAMACOS 0.0003 [−0.0001 , 0.0008]
EARLI −0.0003 [−0.0006 , 0.0001]
GECKO −0.0003 [−0.0010 , 0.0005]
GEN3G −0.0001 [−0.0008 , 0.0006]
GENR −0.0001 [−0.0004 , 0.0003]
GOYA −0.0002 [−0.0006 , 0.0002]
MEDALL −0.0003 [−0.0008 , 0.0001]
MOBA1 −0.0002 [−0.0005 , 0.0000]
MOBA2 −0.0001 [−0.0004 , 0.0002]
MOBA3 −0.0002 [−0.0007 , 0.0003]
NFCS −0.0002 [−0.0003 , 0.0000]
NEST −0.0002 [−0.0004 , 0.0000]
NHBCS 0.0004 [0.0000 , 0.0008]
RICHS −0.0002 [−0.0008 , 0.0003]
VIVA −0.0005 [−0.0007 , −0.0002]
Fixed−effects meta−analysis −0.0002 [−0.0003 , −0.0001]
Random−effects meta−analysis −0.0002 [−0.0003 , −0.0001]
−0.0015 −0.0005 0.0005
Change in offspring DNA methylation per1kg/m2 increase in maternal BMI

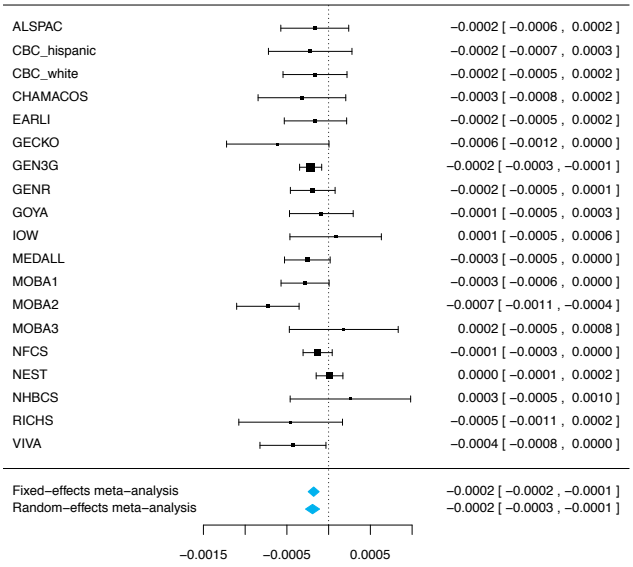

Forest plot for probe:
cg26284544 [LOC100507588]
ALSPAC −0.0011 [−0.0022 , 0.0000]
CBC_hispanic −0.0004 [−0.0029 , 0.0020]
CBC_white −0.0015 [−0.0041 , 0.0012]
CHAMACOS −0.0012 [−0.0023 , −0.0002]
EARLI −0.0012 [−0.0023 , −0.0001]
GECKO −0.0014 [−0.0030 , 0.0003]
GEN3G −0.0019 [−0.0034 , −0.0004]
GENR −0.0005 [−0.0013 , 0.0003]
GOYA −0.0009 [−0.0020 , 0.0003]
MEDALL −0.0009 [−0.0019 , 0.0001]
MOBA1 −0.0002 [−0.0010 , 0.0007]
MOBA2 −0.0007 [−0.0018 , 0.0003]
MOBA3 −0.0002 [−0.0019 , 0.0015]
NFCS −0.0007 [−0.0016 , 0.0003]
NEST 0.0000 [−0.0009 , 0.0008]
NHBCS −0.0025 [−0.0050 , −0.0001]
RICHS −0.0006 [−0.0026 , 0.0014]
VIVA −0.0013 [−0.0028 , 0.0001]
Fixed−effects meta−analysis −0.0008 [−0.0010 , −0.0005]
Random−effects meta−analysis −0.0008 [−0.0010 , −0.0005]
−0.0060 −0.0020 0.0020 0.0040
Change in offspring DNA methylation per1kg/m2 increase in maternal BMI


Forest plot for probe:
cg12155036 [LOC100131551]
ALSPAC −0.0009 [−0.0022 , 0.0005]
CBC_hispanic −0.0002 [−0.0024 , 0.0021]
CBC_white −0.0028 [−0.0051 , −0.0005]
CHAMACOS −0.0002 [−0.0014 , 0.0010]
EARLI −0.0007 [−0.0017 , 0.0003]
GECKO 0.0002 [−0.0015 , 0.0020]
GEN3G −0.0005 [−0.0019 , 0.0008]
GENR −0.0005 [−0.0012 , 0.0002]
GOYA 0.0002 [−0.0007 , 0.0010]
IOW −0.0022 [−0.0043 , −0.0001]
MEDALL −0.0002 [−0.0012 , 0.0009]
MOBA1 −0.0007 [−0.0014 , 0.0001]
MOBA2 −0.0013 [−0.0023 , −0.0003]
MOBA3 0.0007 [−0.0009 , 0.0023]
NFCS −0.0011 [−0.0017 , −0.0005]
NEST −0.0001 [−0.0008 , 0.0006]
NHBCS 0.0008 [−0.0011 , 0.0027]
RICHS 0.0001 [−0.0014 , 0.0016]
VIVA −0.0024 [−0.0034 , −0.0015]
Fixed−effects meta−analysis −0.0006 [−0.0009 , −0.0004]
Random−effects meta−analysis −0.0006 [−0.0010 , −0.0002]
−0.0060 −0.0020 0.0020
Change in offspring DNA methylation per1kg/m2 increase in maternal BMI

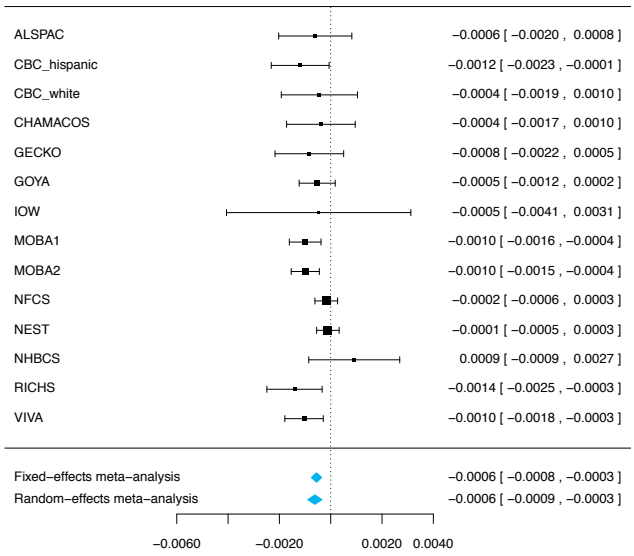

Forest plot for probe:
cg25432807 [POM121L1P]
ALSPAC −0.0007 [−0.0022 , 0.0008]
CBC_hispanic −0.0021 [−0.0035 , −0.0008]
CBC_white −0.0007 [−0.0028 , 0.0014]
CHAMACOS 0.0005 [−0.0006 , 0.0017]
GECKO −0.0006 [−0.0024 , 0.0011]
GOYA −0.0017 [−0.0026 , −0.0008]
MOBA1 −0.0008 [−0.0013 , −0.0003]
MOBA2 −0.0011 [−0.0016 , −0.0007]
NFCS 0.0002 [−0.0003 , 0.0007]
NEST −0.0001 [−0.0007 , 0.0004]
NHBCS 0.0006 [−0.0004 , 0.0017]
RICHS −0.0013 [−0.0022 , −0.0003]
VIVA −0.0003 [−0.0008 , 0.0002]
Fixed−effects meta−analysis −0.0005 [−0.0007 , −0.0003]
Random−effects meta−analysis −0.0006 [−0.0010 , −0.0002]
−0.0040 −0.0020 0.0000 0.0020
Change in offspring DNA methylation per1kg/m2 increase in maternal BMI


Forest plot for probe:
cg25521481 [TTBK1]
ALSPAC −0.0005 [−0.0017 , 0.0006]
CBC_hispanic −0.0008 [−0.0018 , 0.0001]
CBC_white −0.0010 [−0.0031 , 0.0011]
CHAMACOS −0.0004 [−0.0012 , 0.0005]
EARLI −0.0009 [−0.0018 , 0.0000]
GECKO −0.0001 [−0.0010 , 0.0009]
GEN3G 0.0000 [−0.0010 , 0.0010]
GENR −0.0006 [−0.0012 , 0.0000]
GOYA −0.0004 [−0.0009 , 0.0001]
IOW 0.0002 [−0.0010 , 0.0014]
MEDALL −0.0003 [−0.0011 , 0.0004]
MOBA1 −0.0005 [−0.0012 , 0.0001]
MOBA2 −0.0019 [−0.0027 , −0.0011]
MOBA3 −0.0001 [−0.0015 , 0.0013]
NFCS −0.0006 [−0.0014 , 0.0001]
NEST 0.0000 [−0.0006 , 0.0007]
NHBCS 0.0017 [−0.0001 , 0.0034]
RICHS −0.0013 [−0.0027 , 0.0000]
VIVA −0.0019 [−0.0032 , −0.0006]
Fixed−effects meta−analysis −0.0005 [−0.0007 , −0.0003]
Random−effects meta−analysis −0.0005 [−0.0008 , −0.0003]
−0.0040 0.0000 0.0020 0.0040
Change in offspring DNA methylation per1kg/m2 increase in maternal BMI

Forest plot for probe: cg25185429 [EGOT]

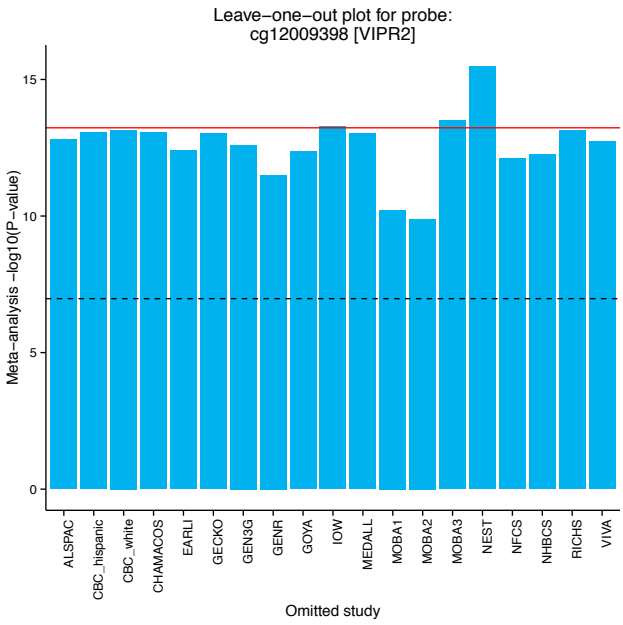


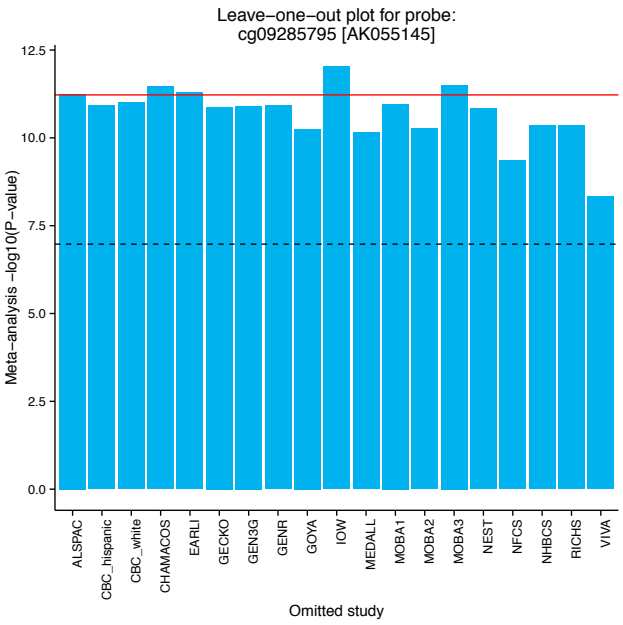
Forest plot for probe: cg01517690 [ZSWIM2]

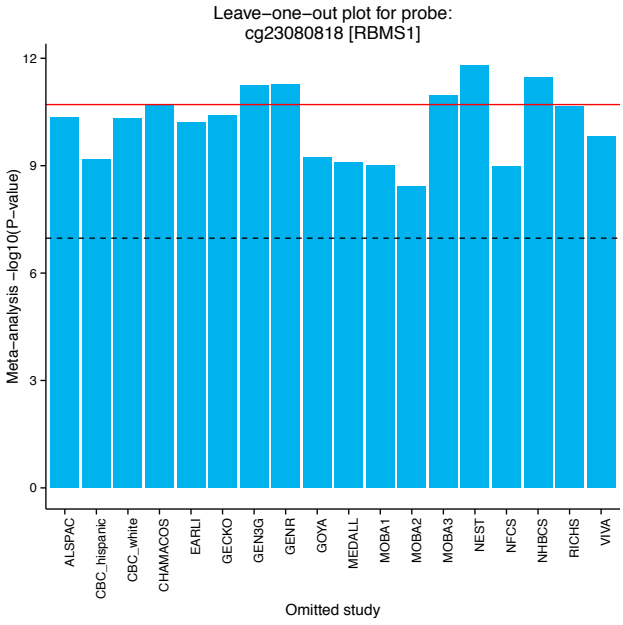


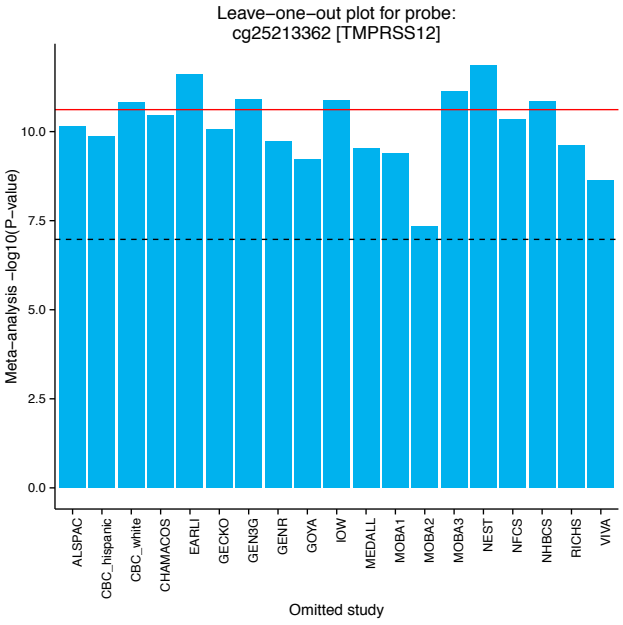
Leave-one-out plots for the cell-adjusted continuous BMI model

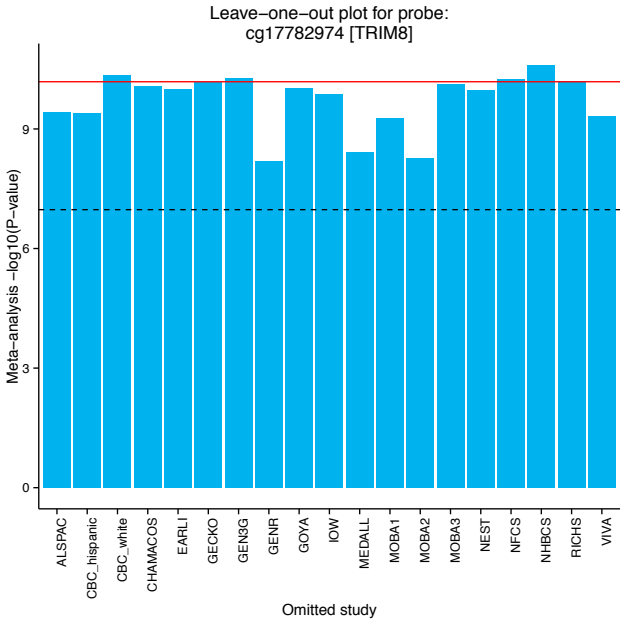
Plots show –log10 P-values for meta-analyses with each cohort (x-axis) omitted. The red, full horizontal line indicates the –log10 P-value for the meta-analysis with all cohorts included. The black, dashed horizontal line indicates the Bonferroni cut off for genome-wide significance ($1.06 * 10^{-7}$).

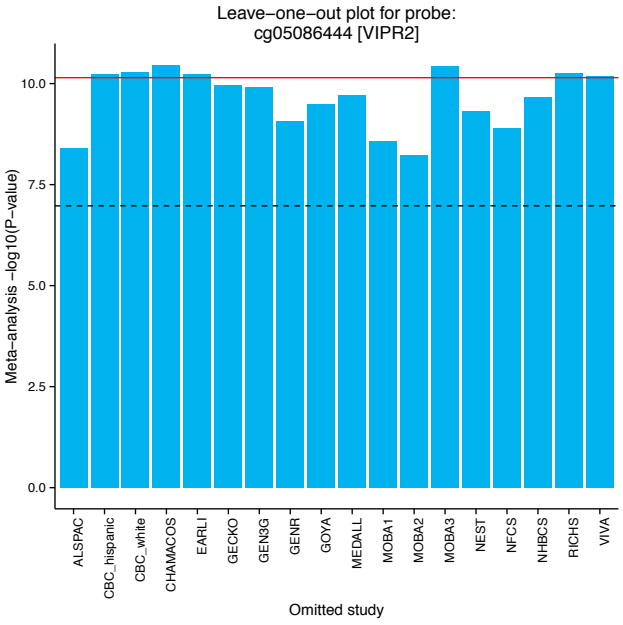

Leave−one−out plot for probe:
cg12009398 [VIPR2]
Meta−analysis −log10(P−value)
0
5
10
15
ALSPAC
CBC_hispanic
CBC_white
CHAMACOS
EARLI
GECKO
GEN3G
GENR
GOYA
IOW
MEDALL
MOBA1
MOBA2
MOBA3
NEST
NFCS
NHBCS
RICHS
VIVA
Omitted study

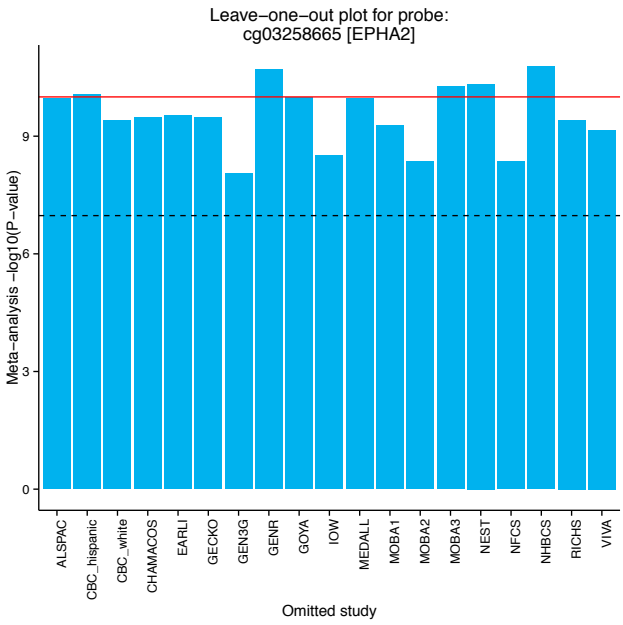

Leave−one−out plot for probe:
cg09285795 [AK055145]
Meta−analysis −log10(P−value)
0.0
2.5
5.0
7.5
10.0
12.5
ALSPAC
CBC_hispanic
CBC_white
CHAMACOS
EARLI
GECKO
GEN3G
GENR
GOYA
IOW
MEDALL
MOBA1
MOBA2
MOBA3
NEST
NFCS
NHBCS
RICHS
VIVA
Omitted study

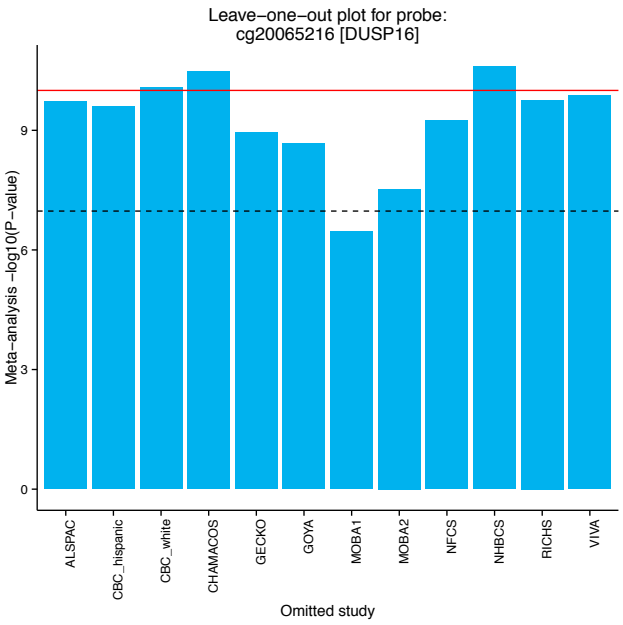

Leave−one−out plot for probe:
cg23080818 [RBMS1]
Meta−analysis −log10(P−value)
0
3
6
9
12
ALSPAC
CBC_hispanic
CBC_white
CHAMACOS
EARLI
GECKO
GEN3G
GENR
GOYA
MEDALL
MOBA1
MOBA2
MOBA3
NEST
NFCS
NHBCS
RICHS
VIVA
Omitted study

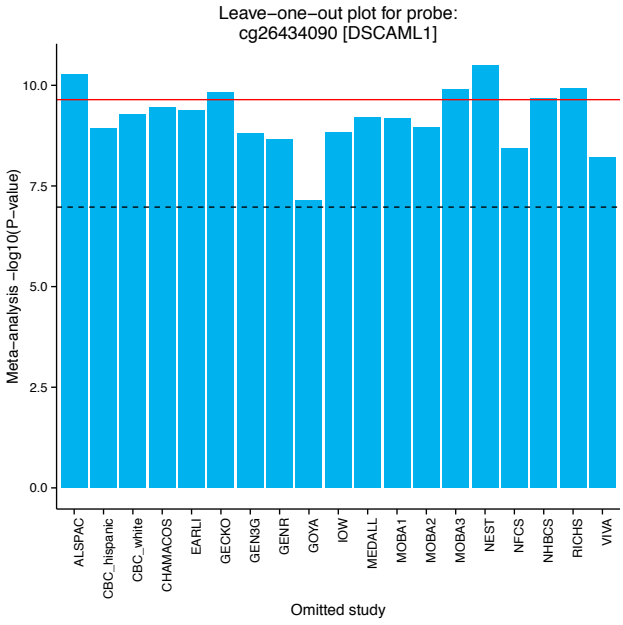

Leave−one−out plot for probe:
cg25213362 [TMPRSS12]
Meta−analysis −log10(P−value)
0.0
2.5
5.0
7.5
10.0
ALSPAC
CBC_hispanic
CBC_white
CHAMACOS
EARLI
GECKO
GEN3G
GENR
GOYA
IOW
MEDALL
MOBA1
MOBA2
MOBA3
NEST
NFCS
NHBCS
RICHS
VIVA
Omitted study

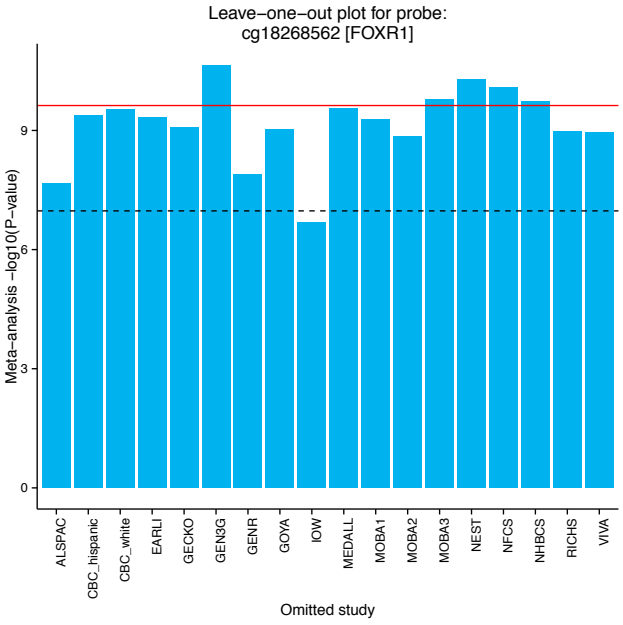

Leave−one−out plot for probe:
cg17782974 [TRIM8]
Meta−analysis −log10(P−value)
0
3
6
9
ALSPAC
CBC_hispanic
CBC_white
CHAMACOS
EARLI
GECKO
GEN3G
GENR
GOYA
IOW
MEDALL
MOBA1
MOBA2
MOBA3
NEST
NFCS
NHBCS
RICHS
VIVA
Omitted study

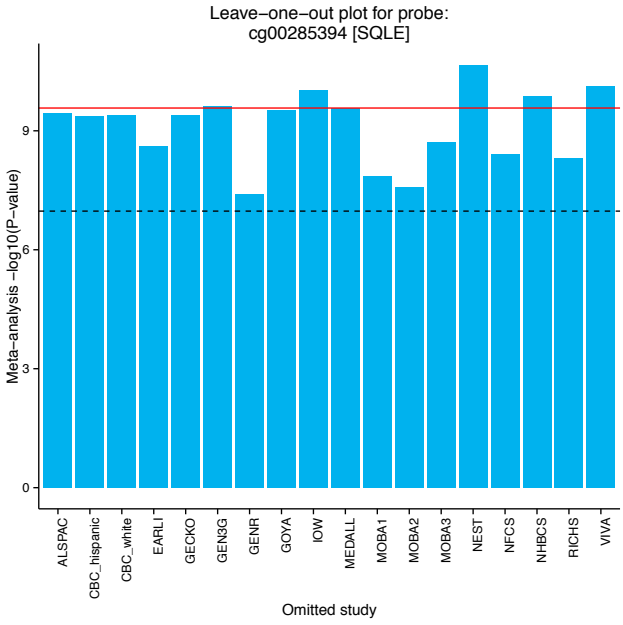

Leave−one−out plot for probe:
cg05086444 [VIPR2]
Meta−analysis −log10(P−value)
0.0
2.5
5.0
7.5
10.0
ALSPAC
CBC_hispanic
CBC_white
CHAMACOS
EARLI
GECKO
GEN3G
GENR
GOYA
MEDALL
MOBA1
MOBA2
MOBA3
NEST
NFCS
NHBCS
RICHS
VIVA
Omitted study

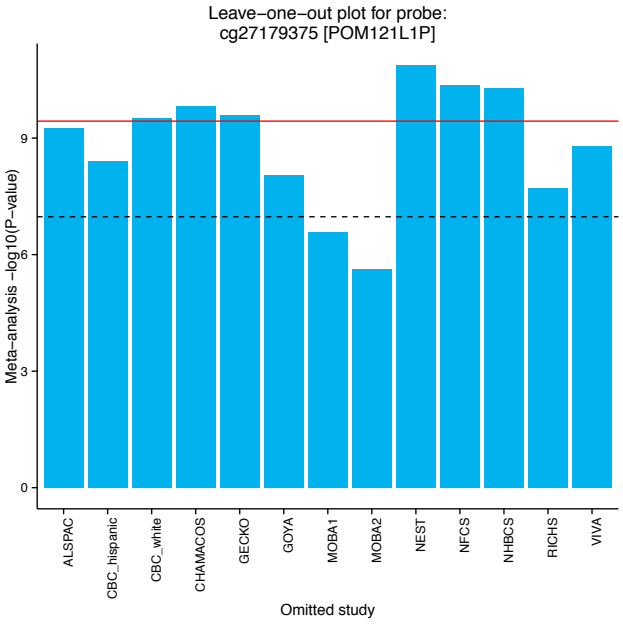

Leave−one−out plot for probe:
cg03258665 [EPHA2]
Meta−analysis −log10(P−value)
0
3
6
9
ALSPAC
CBC_hispanic
CBC_white
CHAMACOS
EARLI
GECKO
GEN3G
GENR
GOYA
IOW
MEDALL
MOBA1
MOBA2
MOBA3
NEST
NFCS
NHBCS
RICHS
VIVA
Omitted study

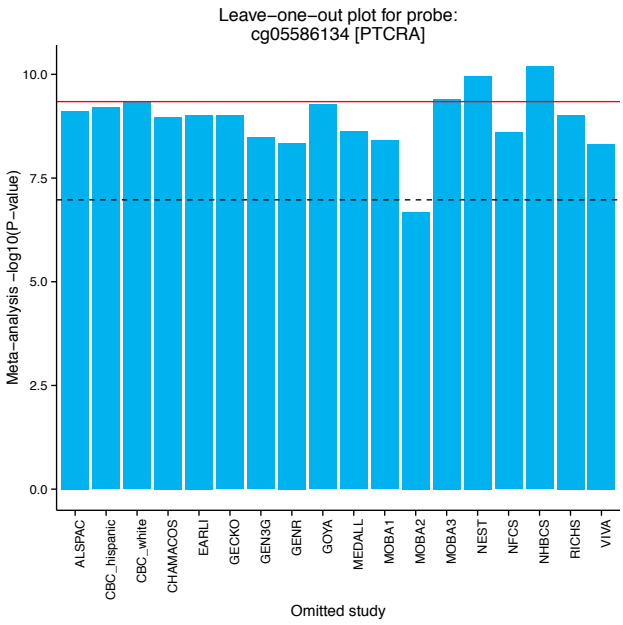

Leave−one−out plot for probe:
cg20065216 [DUSP16]
Meta−analysis −log10(P−value)
0
3
6
9
ALSPAC
CBC_hispanic
CBC_white
CHAMACOS
GECKO
GOYA
MOBA1
MOBA2
NFCS
NHBCS
RICHS
VIVA
Omitted study

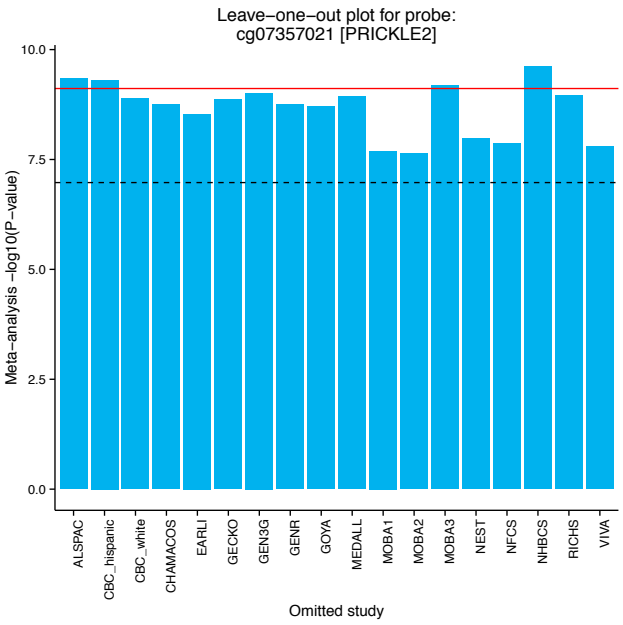

Leave−one−out plot for probe:
cg26434090 [DSCAML1]
Meta−analysis −log10(P−value)
0.0
2.5
5.0
7.5
10.0
ALSPAC
CBC_hispanic
CBC_white
CHAMACOS
EARLI
GECKO
GEN3G
GENR
GOYA
IOW
MEDALL
MOBA1
MOBA2
MOBA3
NEST
NFCS
NHBCS
RICHS
VIVA
Omitted study

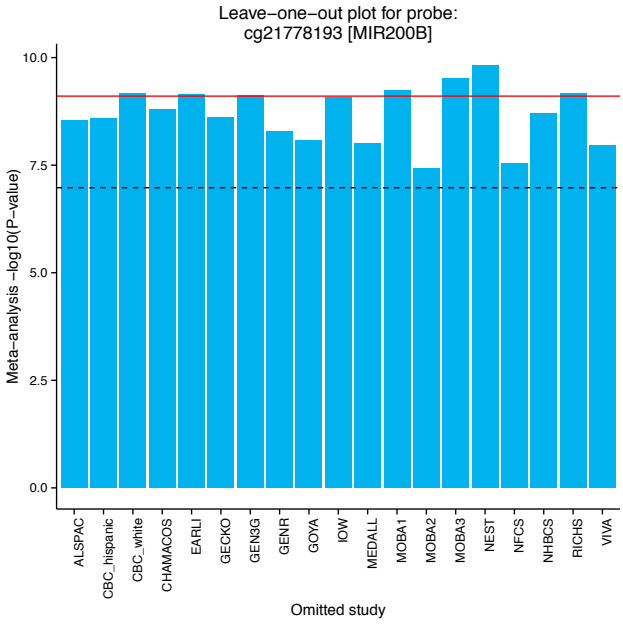

Leave−one−out plot for probe:
cg18268562 [FOXR1]
Meta−analysis −log10(P−value)
0
3
6
9
ALSPAC
CBC_hispanic
CBC_white
EARLI
GECKO
GEN3G
GENR
GOYA
IOW
MEDALL
MOBA1
MOBA2
MOBA3
NEST
NFCS
NHBCS
RICHS
VIVA
Omitted study

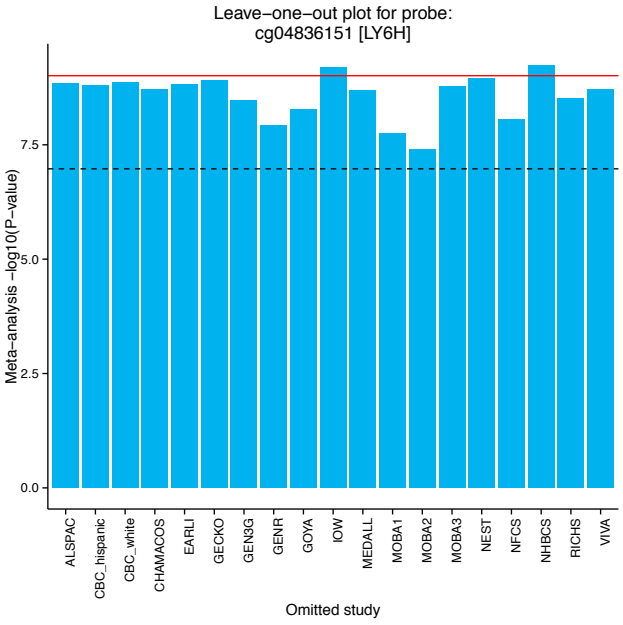

Leave−one−out plot for probe:
cg00285394 [SQLE]
Meta−analysis −log10(P−value)
0
3
6
9
ALSPAC
CBC_hispanic
CBC_white
EARLI
GECKO
GEN3G
GENR
GOYA
IOW
MEDALL
MOBA1
MOBA2
MOBA3
NEST
NFCS
NHBCS
RICHS
VIVA
Omitted study

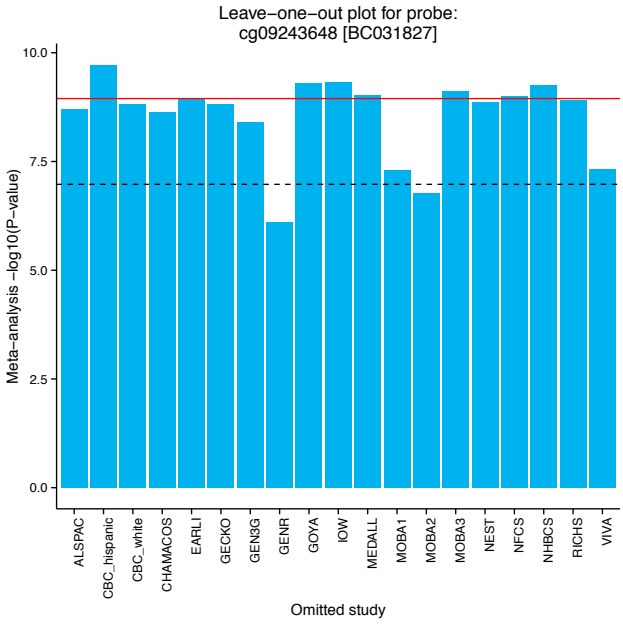

Leave−one−out plot for probe:
cg27179375 [POM121L1P]
Meta−analysis −log10(P−value)
0
3
6
9
ALSPAC
CBC_hispanic
CBC_white
CHAMACOS
GECKO
GOYA
MOBA1
MOBA2
NEST
NFCS
NHBCS
RICHS
VIVA
Omitted study

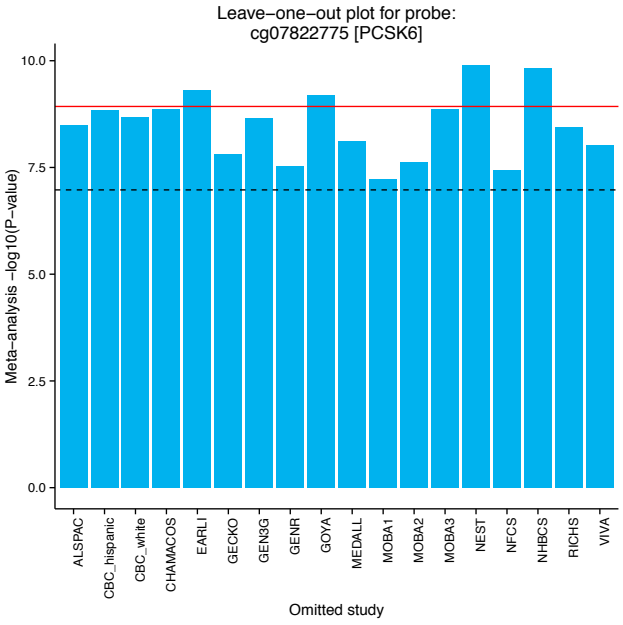

Leave−one−out plot for probe:
cg05586134 [PTCRA]
Meta−analysis −log10(P−value)
10.0
7.5
5.0
2.5
0.0
ALSPAC
CBC_hispanic
CBC_white
CHAMACOS
EARLI
GECKO
GEN3G
GENR
GOYA
MEDALL
MOBA1
MOBA2
MOBA3
NEST
NFCS
NHBCS
RICHS
VIVA
Omitted study


Leave−one−out plot for probe:
cg07357021 [PRICKLE2]
Meta−analysis −log10(P−value)
10.0
7.5
5.0
2.5
0.0
ALSPAC
CBC_hispanic
CBC_white
CHAMACOS
EARLI
GECKO
GEN3G
GENR
GOYA
MEDALL
MOBA1
MOBA2
MOBA3
NEST
NFCS
NHBCS
RICHS
VIVA
Omitted study


Leave−one−out plot for probe:
cg21778193 [MIR200B]
Meta−analysis −log10(P−value)
10.0
7.5
5.0
2.5
0.0
ALSPAC
CBC_hispanic
CBC_white
CHAMACOS
EARLI
GECKO
GEN3G
GENR
GOYA
IOW
MEDALL
MOBA1
MOBA2
MOBA3
NEST
NFCS
NHBCS
RICHS
VIVA
Omitted study


Leave−one−out plot for probe:
cg04836151 [LY6H]
Meta−analysis −log10(P−value)
7.5
5.0
2.5
0.0
ALSPAC
CBC_hispanic
CBC_white
CHAMACOS
EARLI
GECKO
GEN3G
GENR
GOYA
IOW
MEDALL
MOBA1
MOBA2
MOBA3
NEST
NFCS
NHBCS
RICHS
VIVA
Omitted study


Leave−one−out plot for probe:
cg09243648 [BC031827]
Meta−analysis −log10(P−value)
10.0
7.5
5.0
2.5
0.0
ALSPAC
CBC_hispanic
CBC_white
CHAMACOS
EARLI
GECKO
GEN3G
GENR
GOYA
IOW
MEDALL
MOBA1
MOBA2
MOBA3
NEST
NFCS
NHBCS
RICHS
VIVA
Omitted study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GECKO
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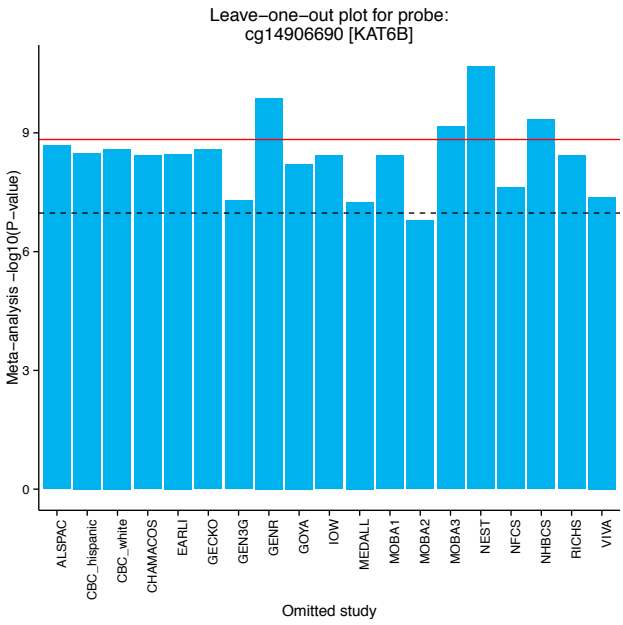
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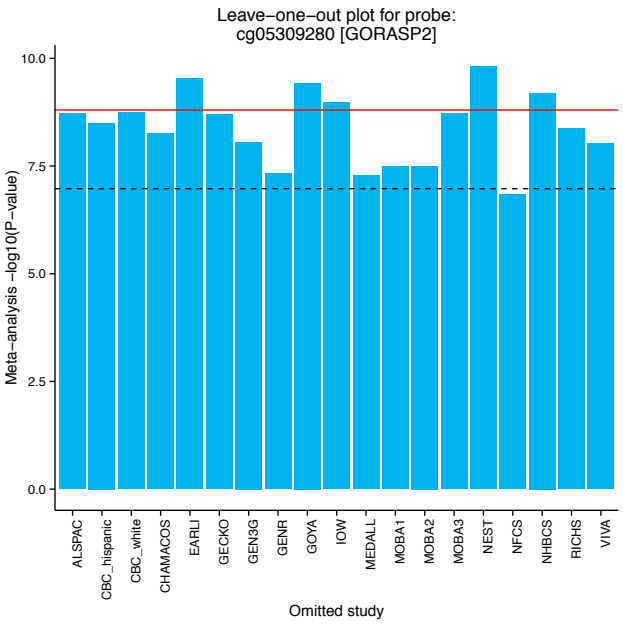
Omitted study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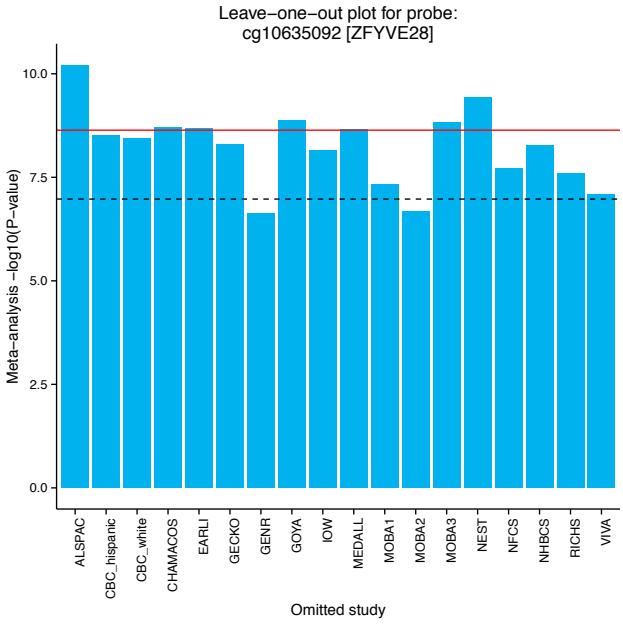
Omitted study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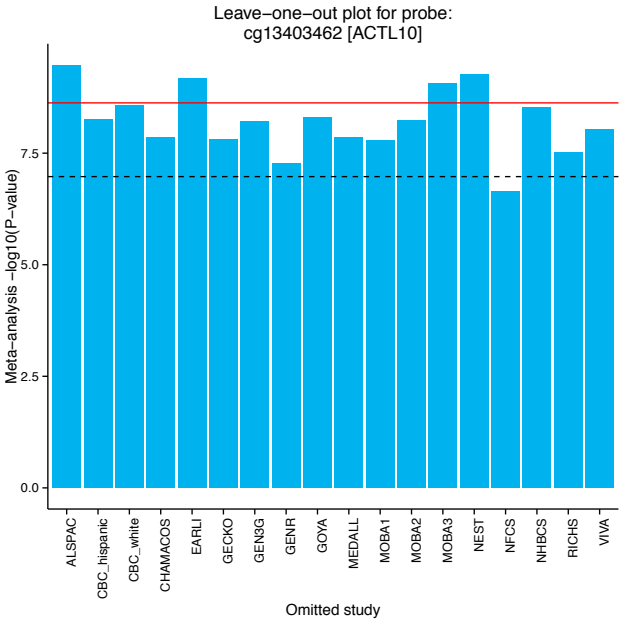
Omitted study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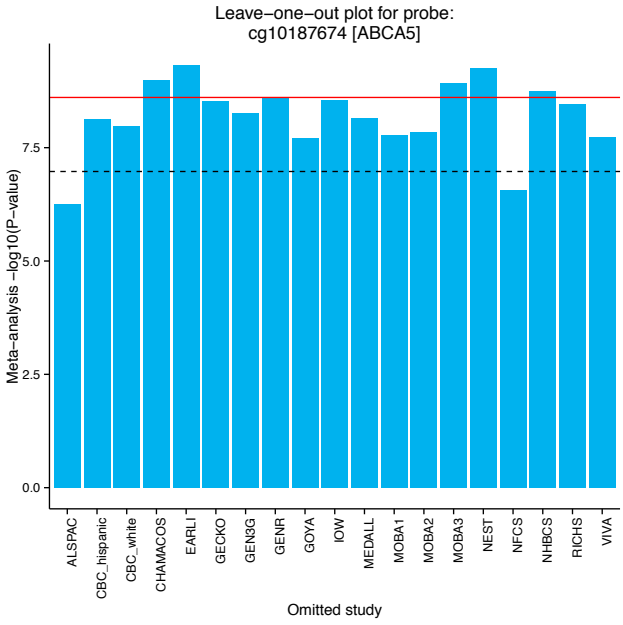
Omitted study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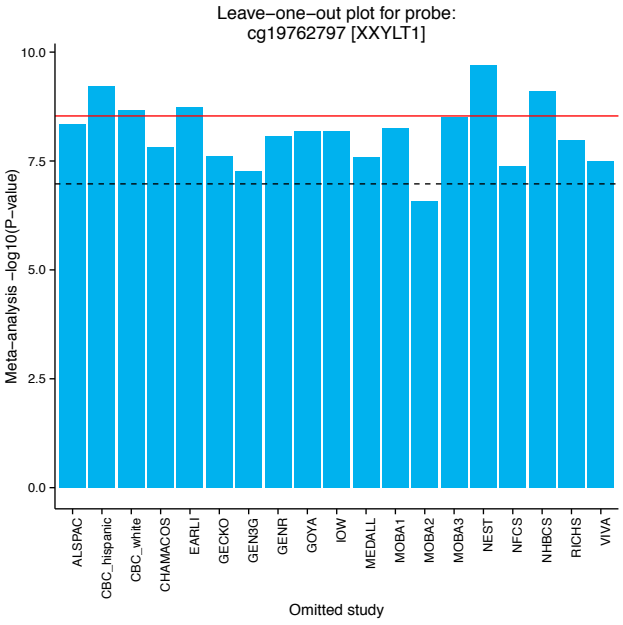
Omitted study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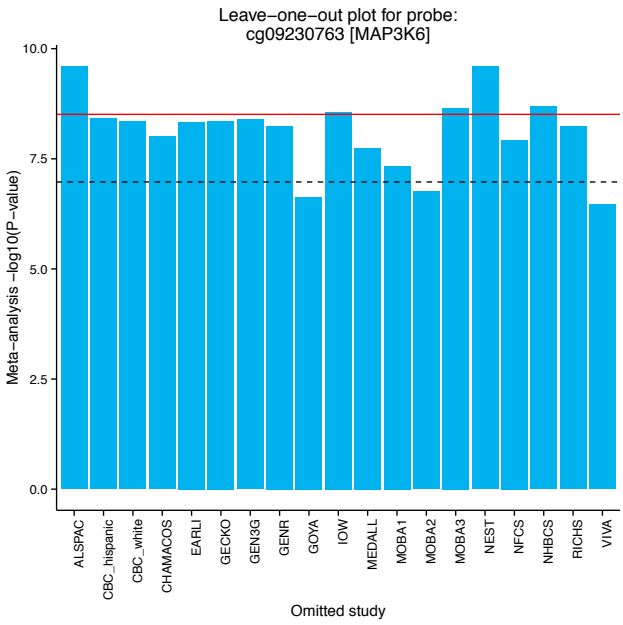
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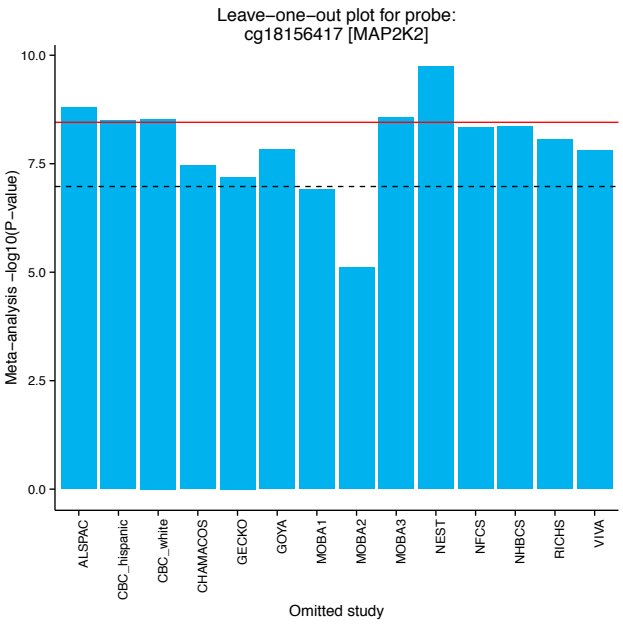
Omitted study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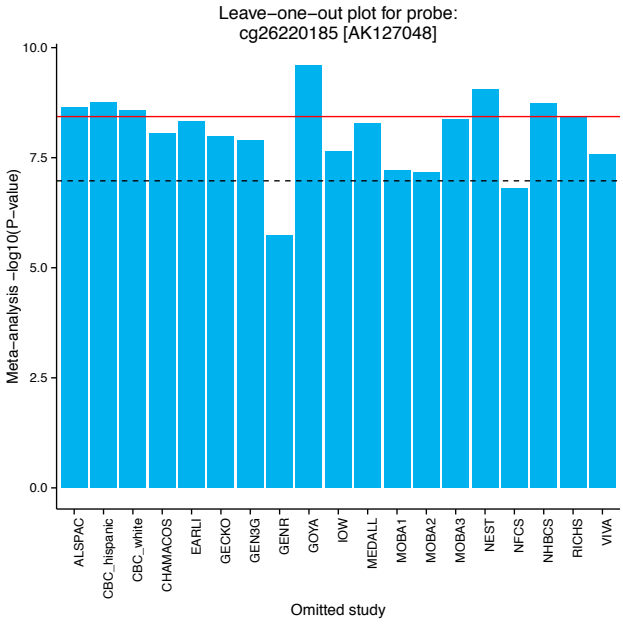
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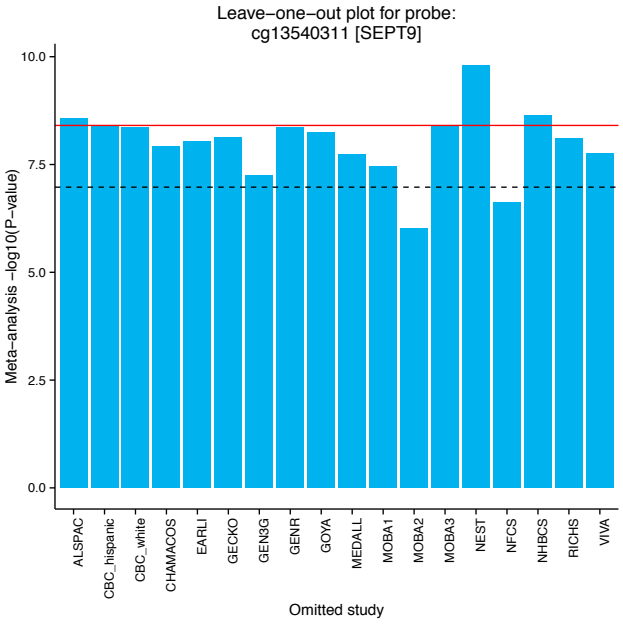
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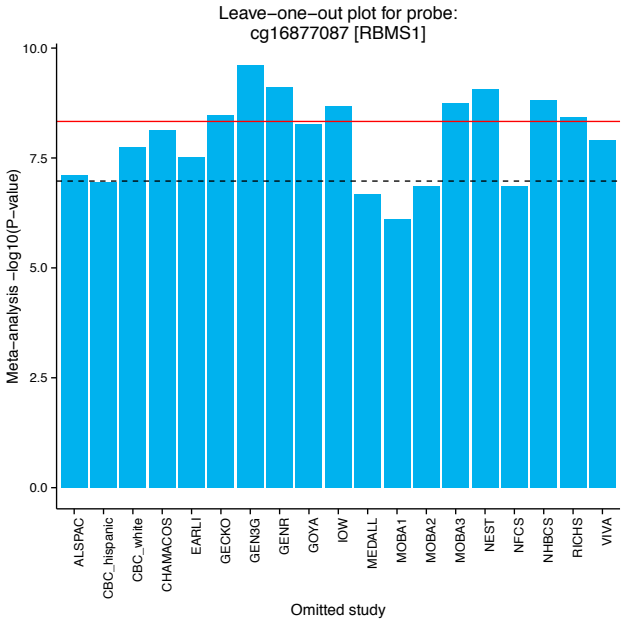
Omitted study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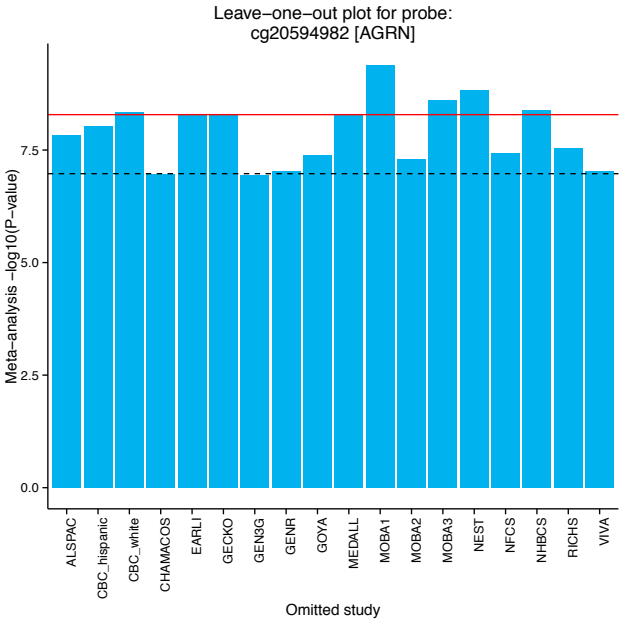
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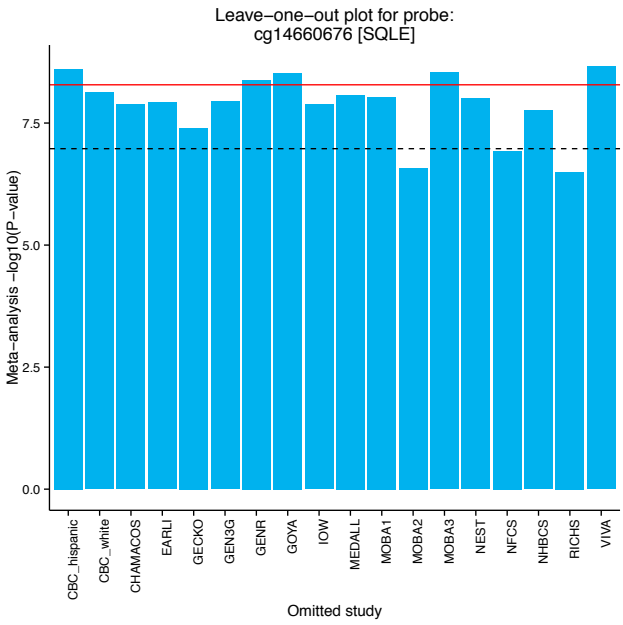
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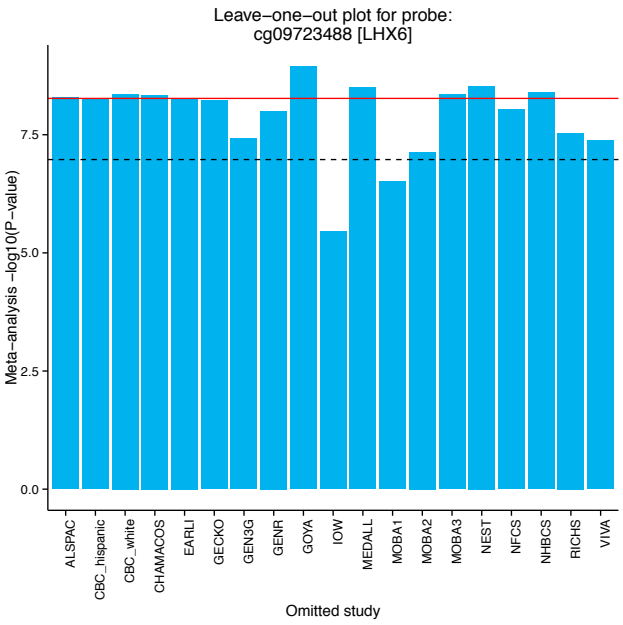
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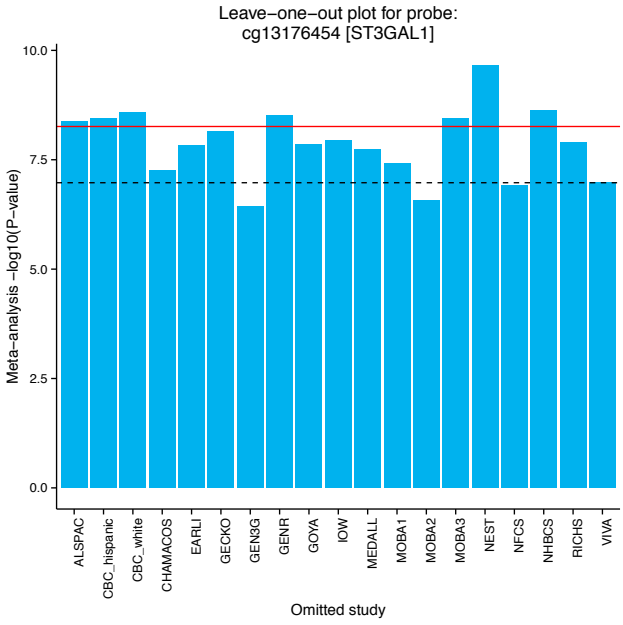
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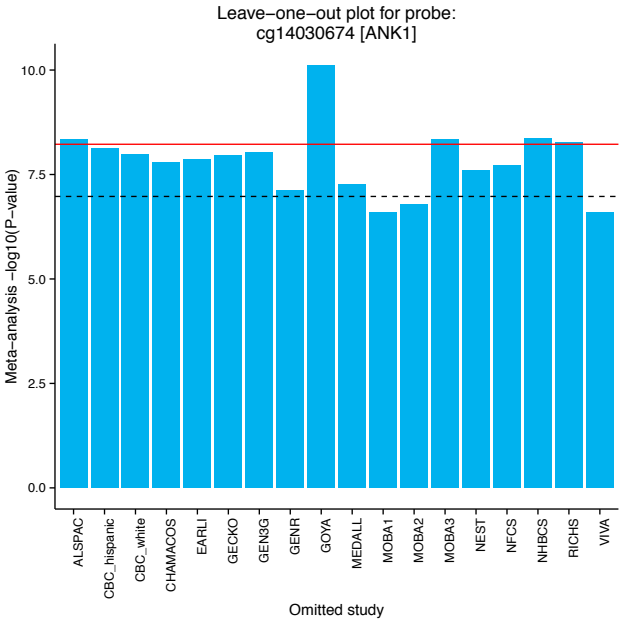
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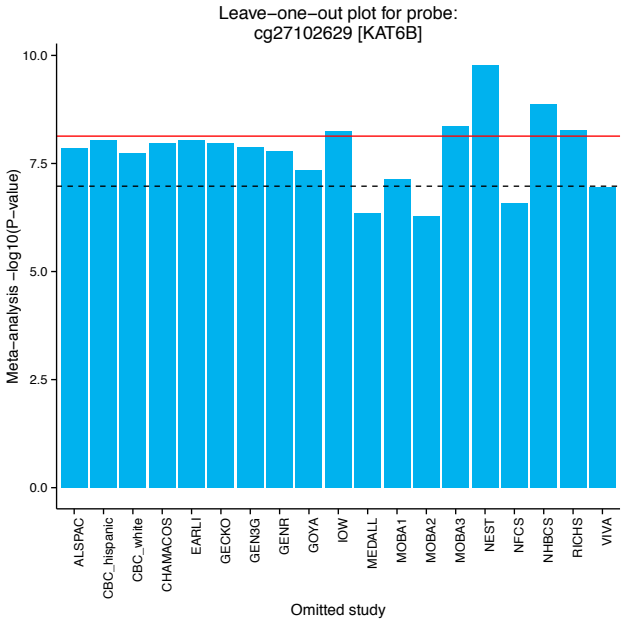
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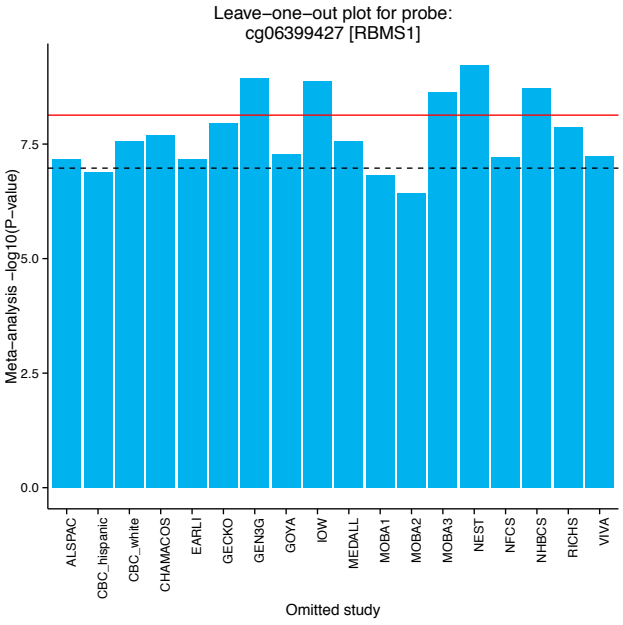
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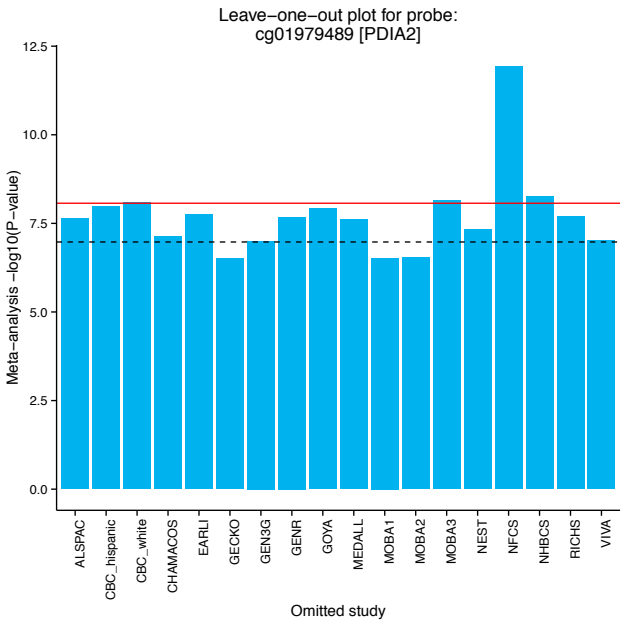
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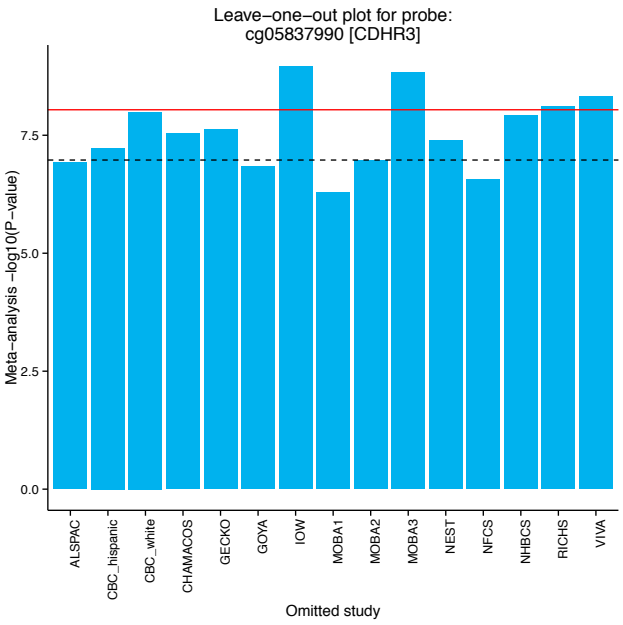
Omitted study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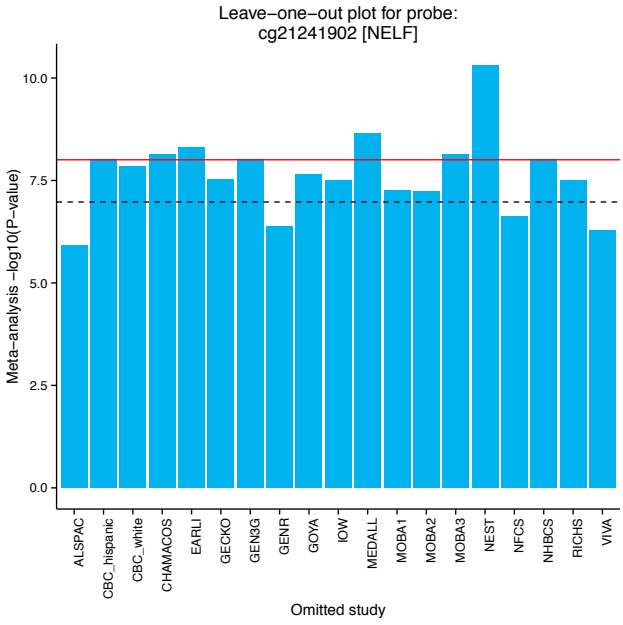
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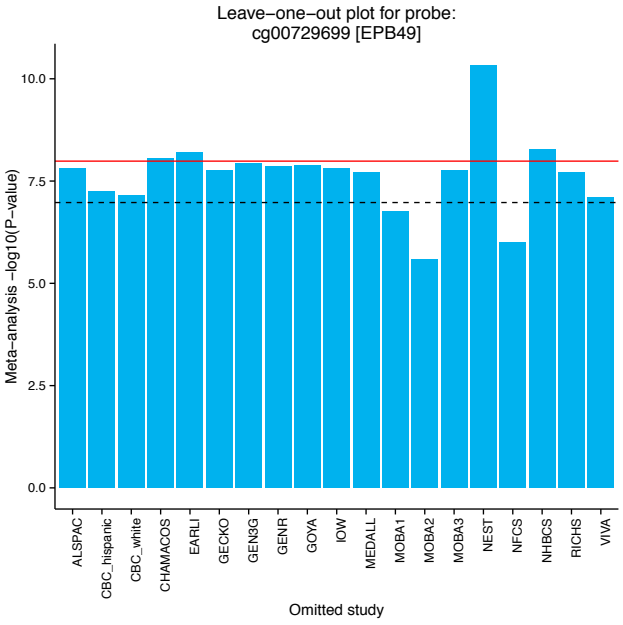
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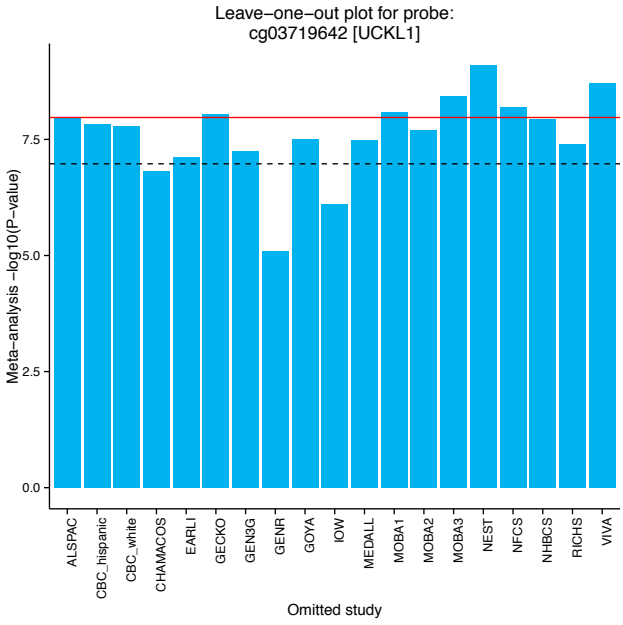
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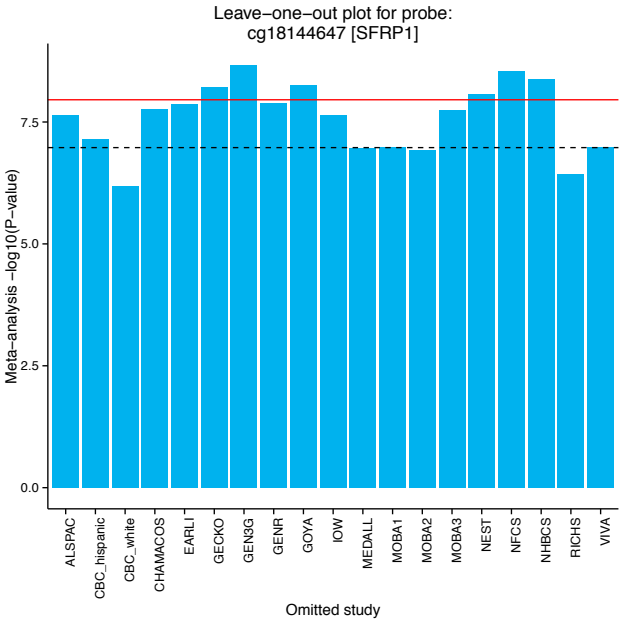
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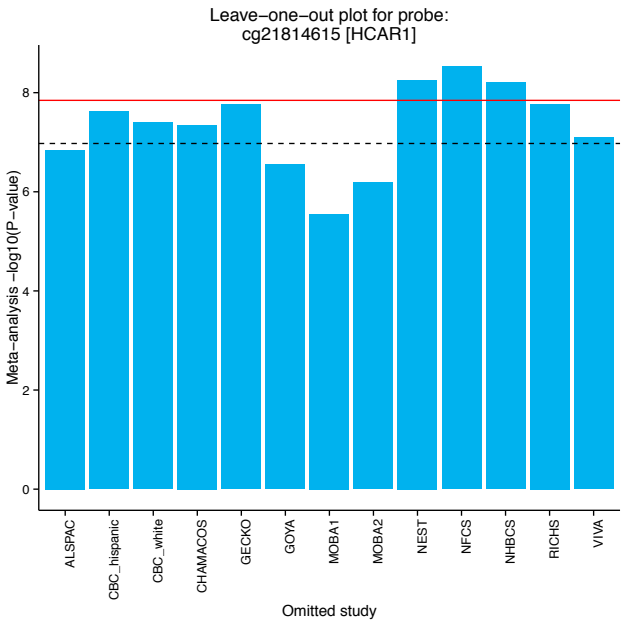
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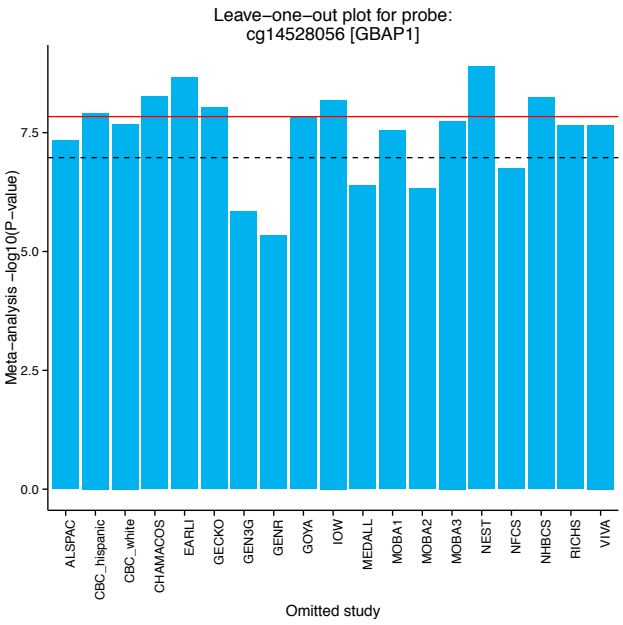
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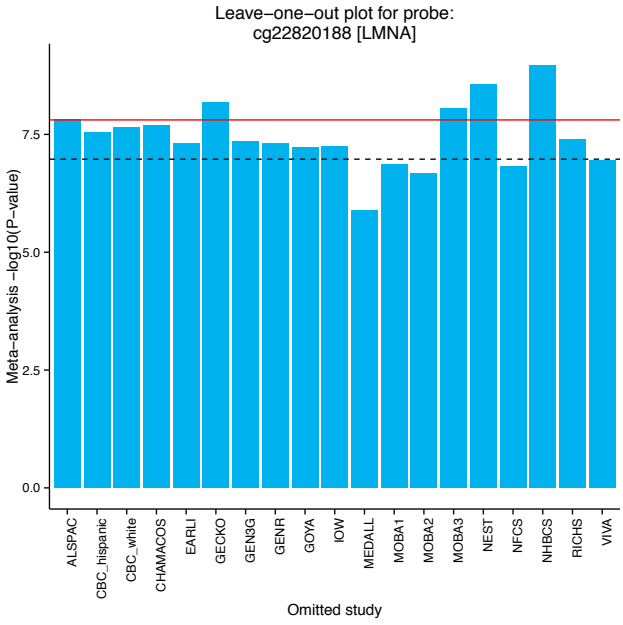
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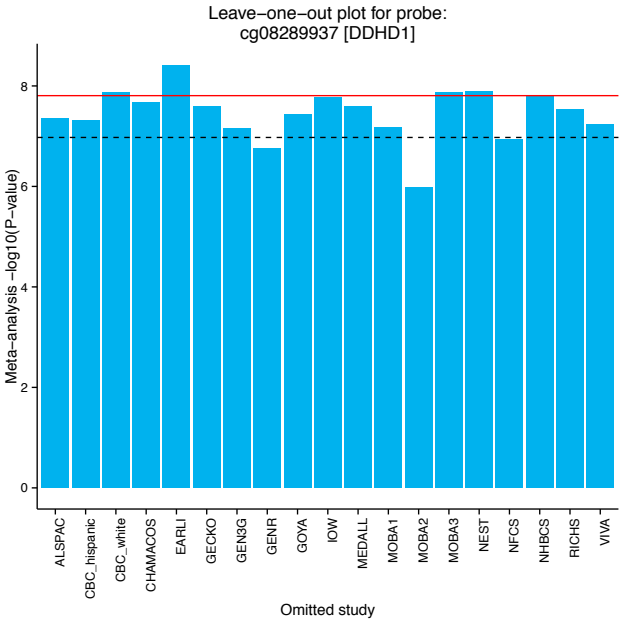
Omitted study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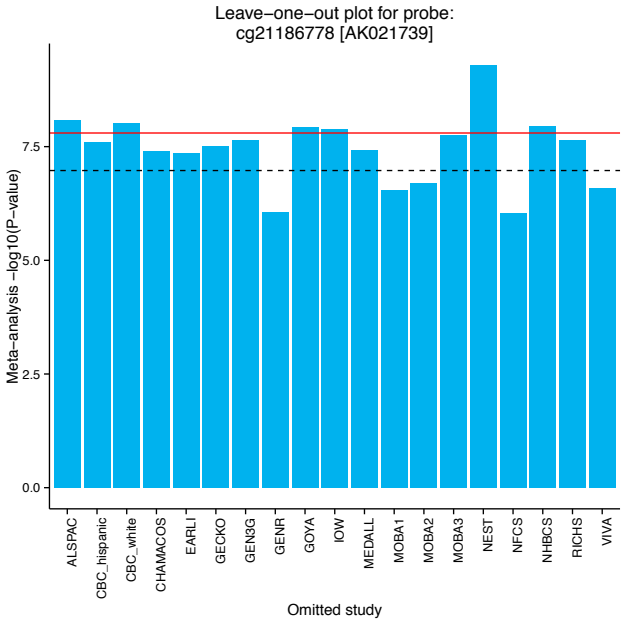
Omitted study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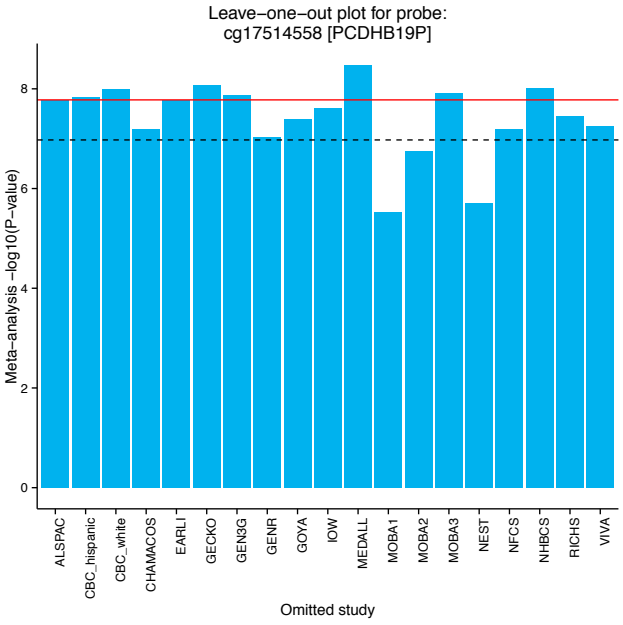
Omitted study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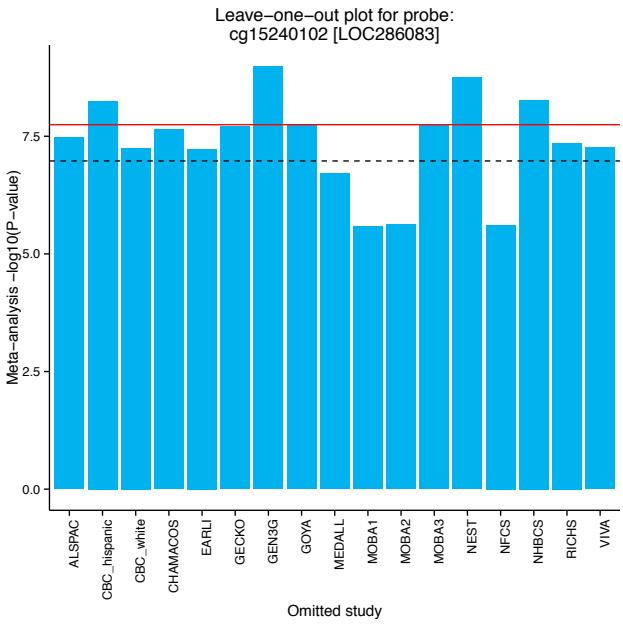
Omitted study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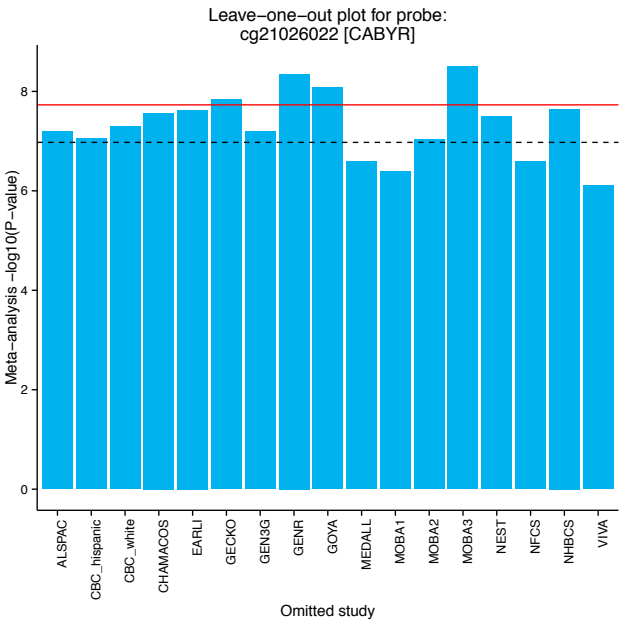
Omitted study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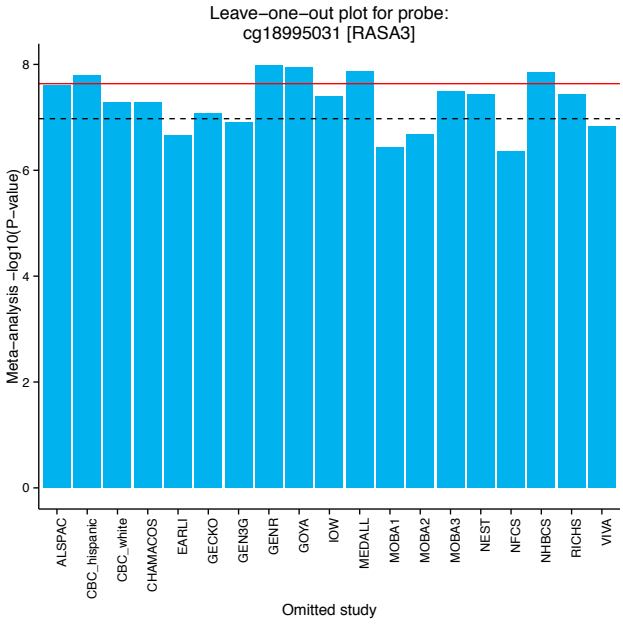
Omitted study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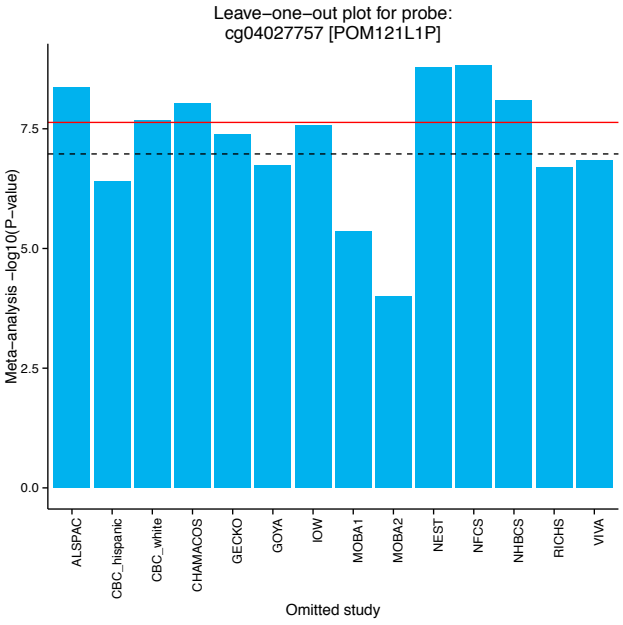
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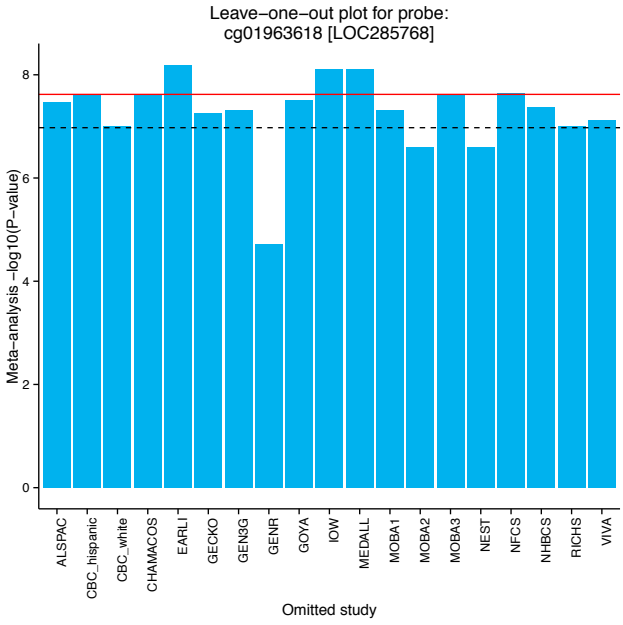
Omitted study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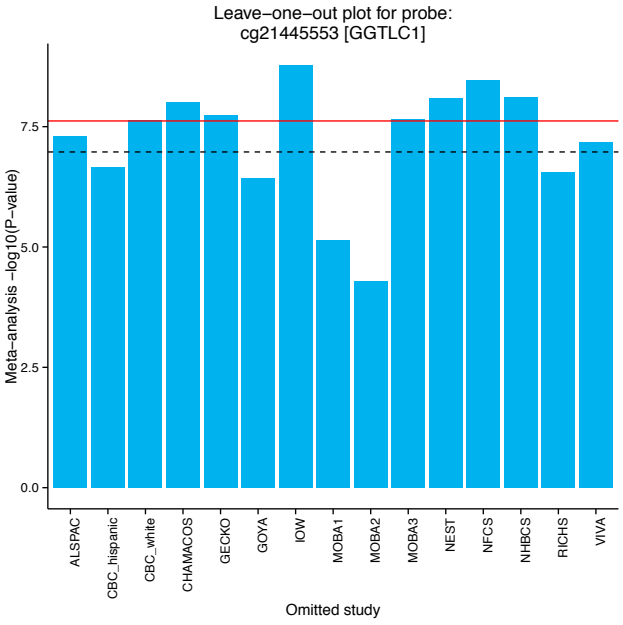
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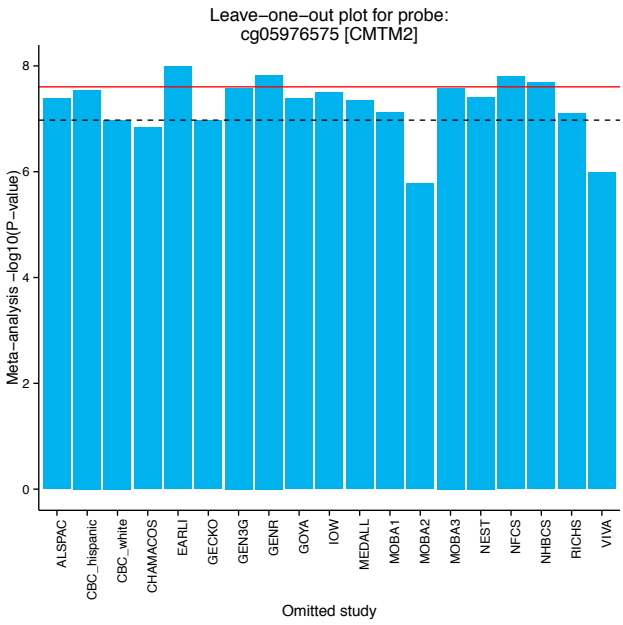
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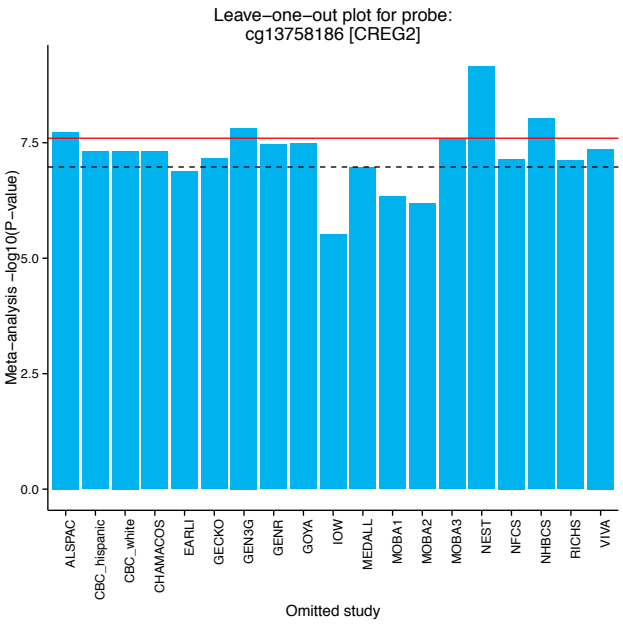
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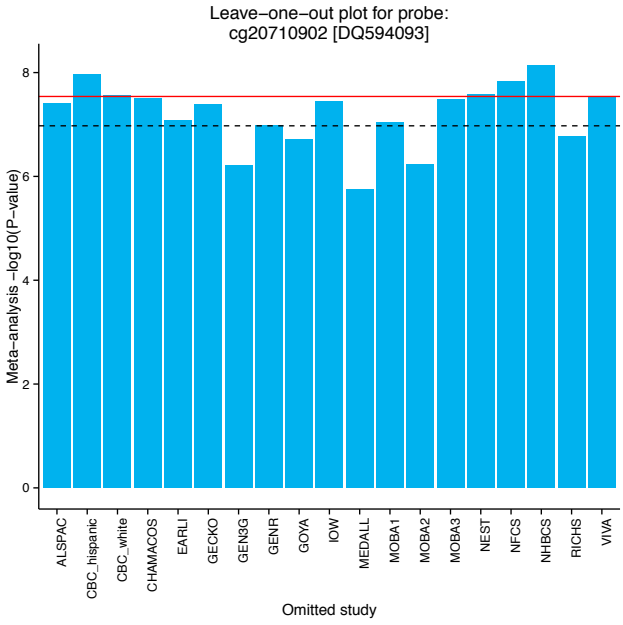
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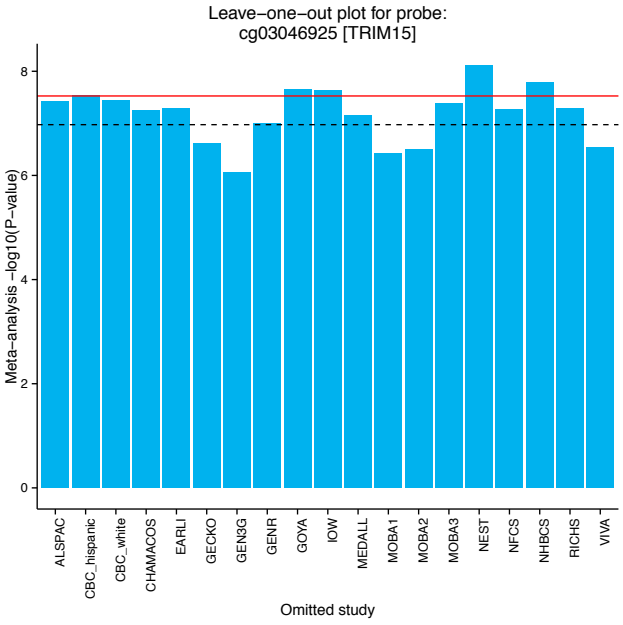
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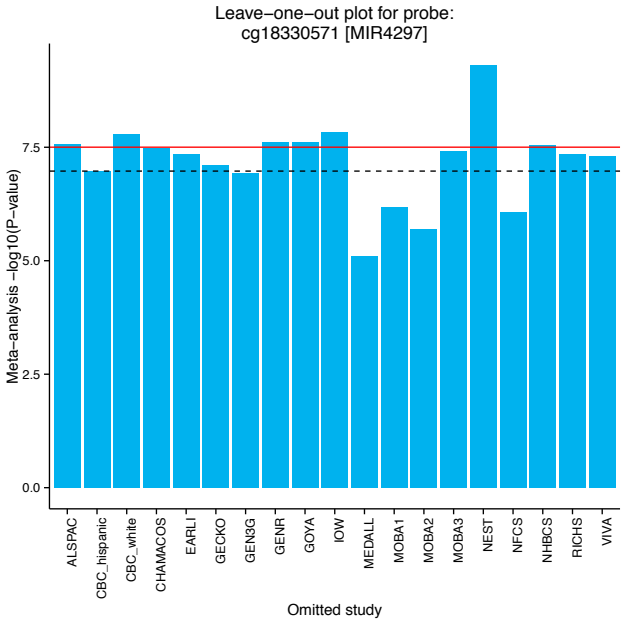
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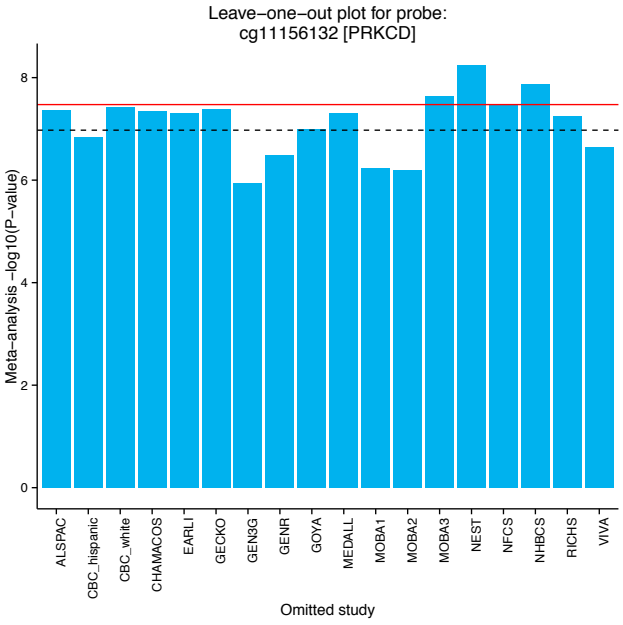
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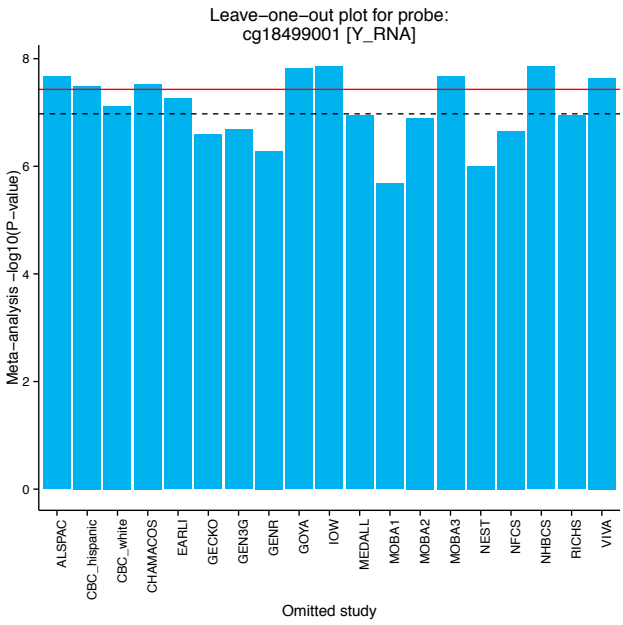
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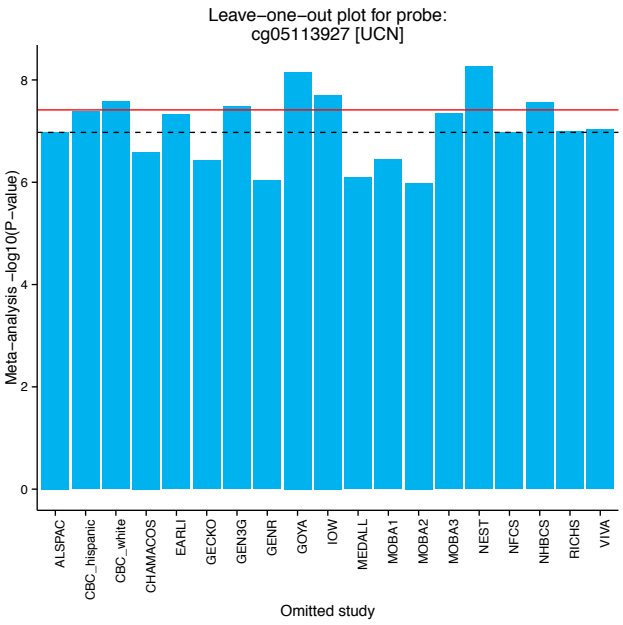
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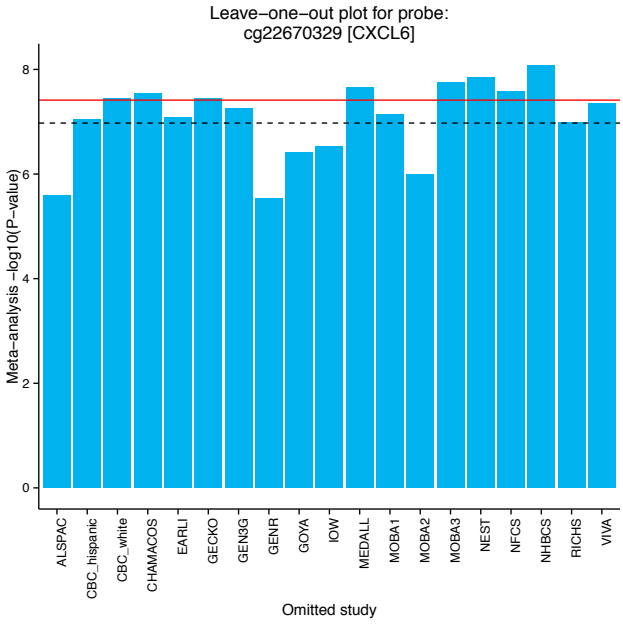
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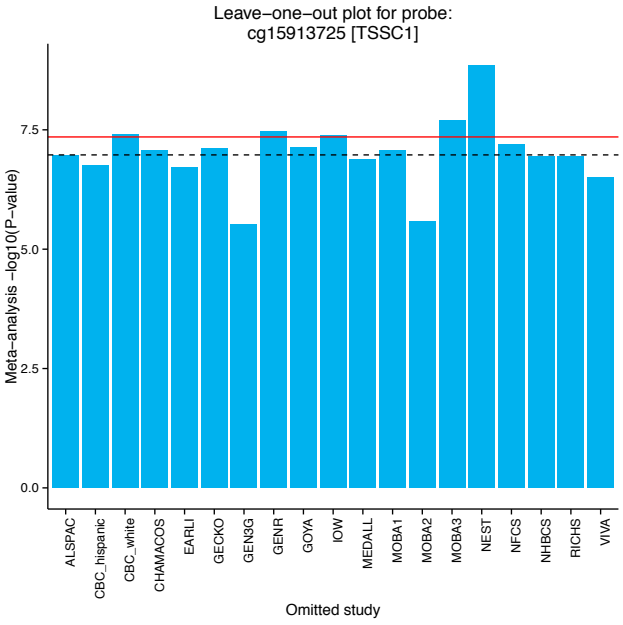
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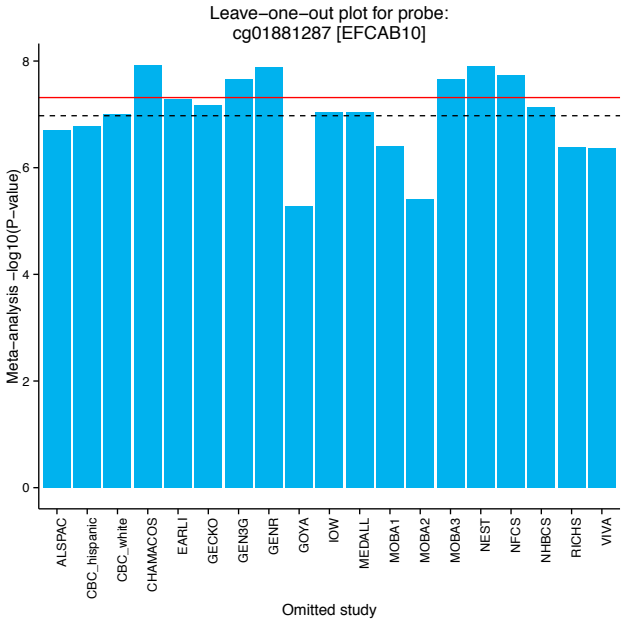
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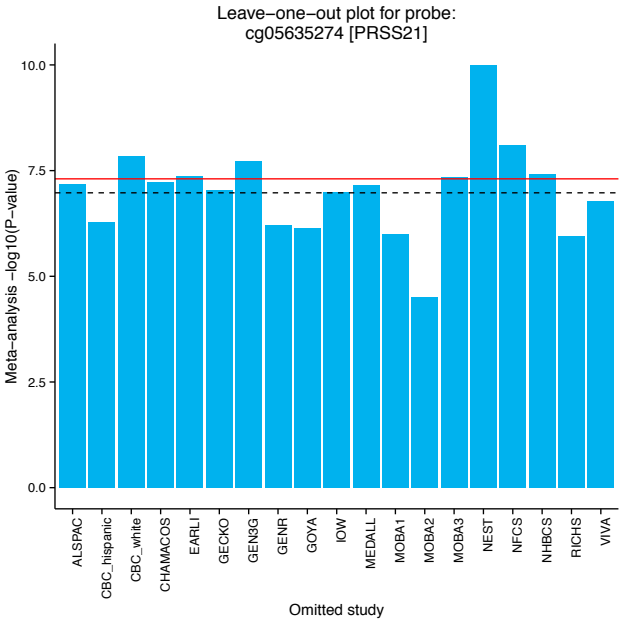
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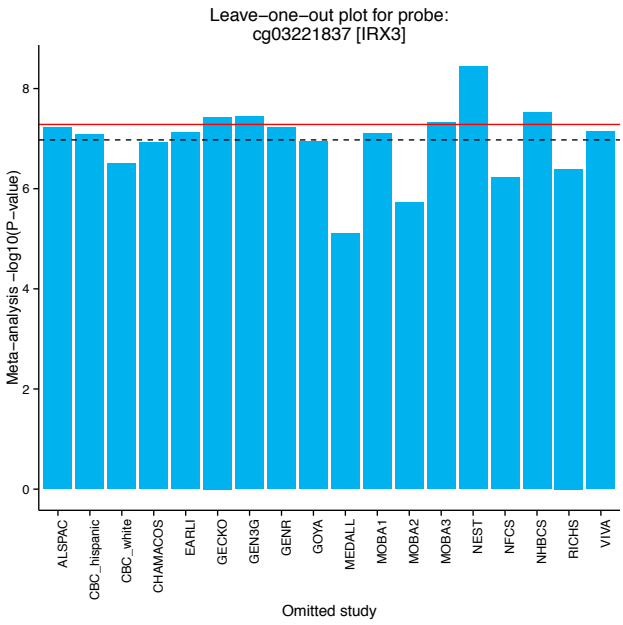
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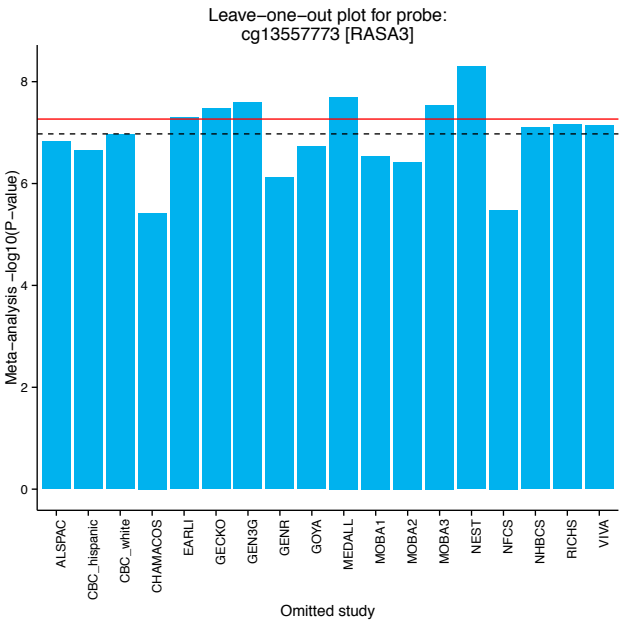
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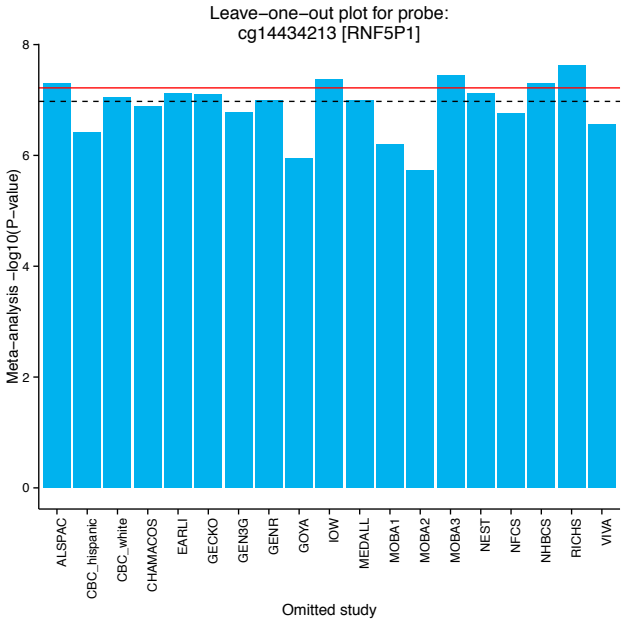
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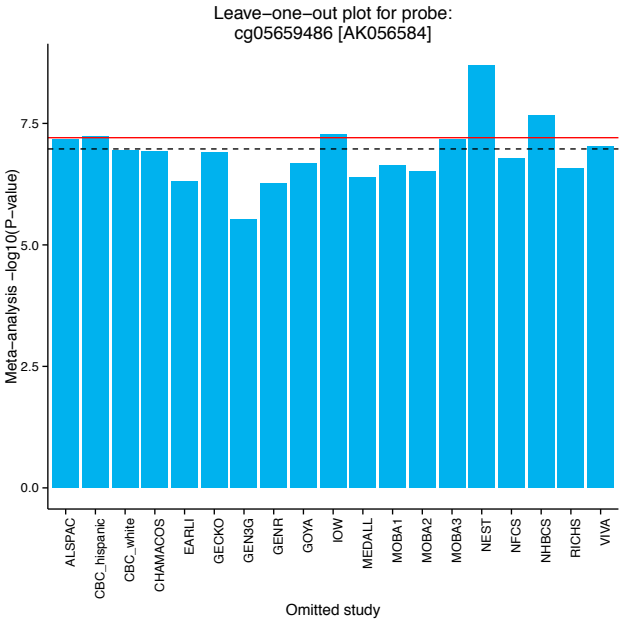
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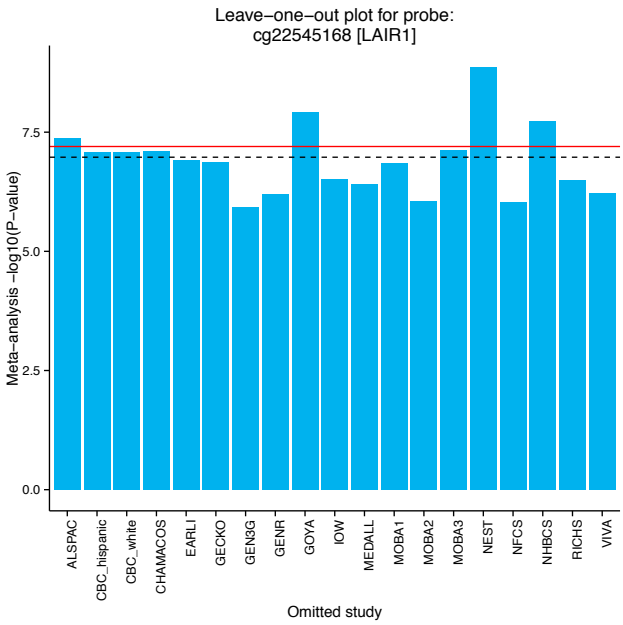
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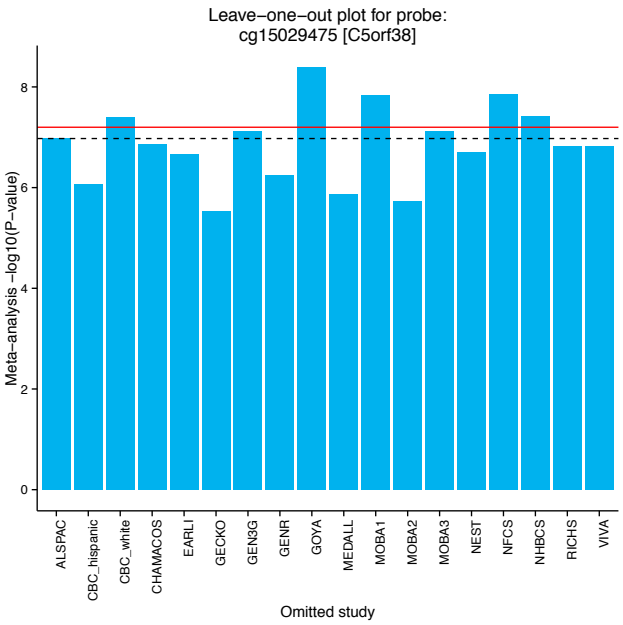
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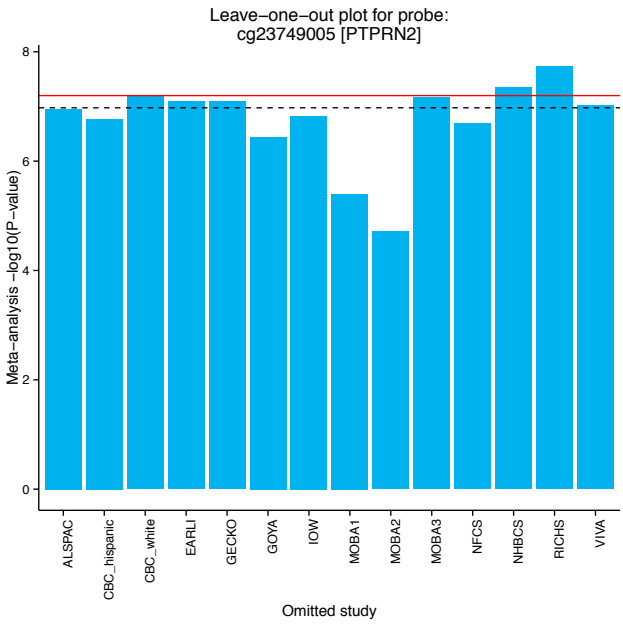
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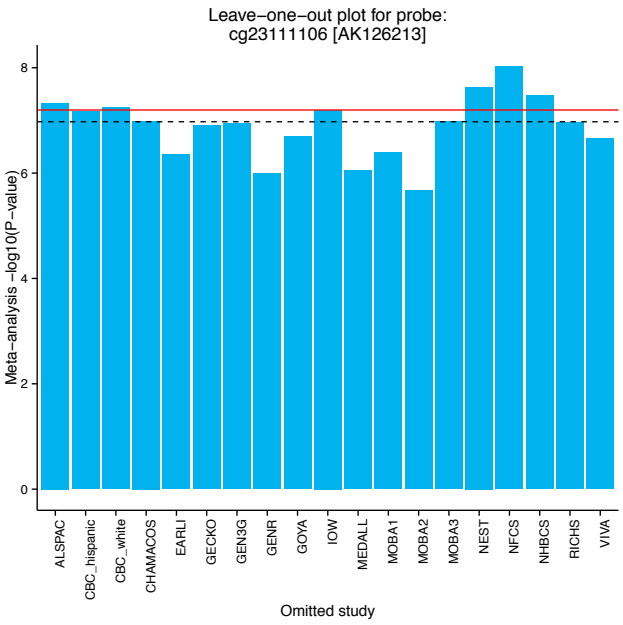
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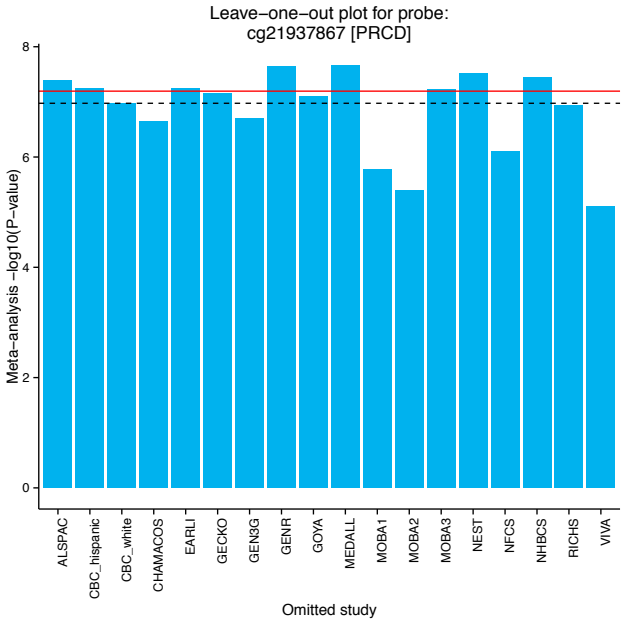
Omitted study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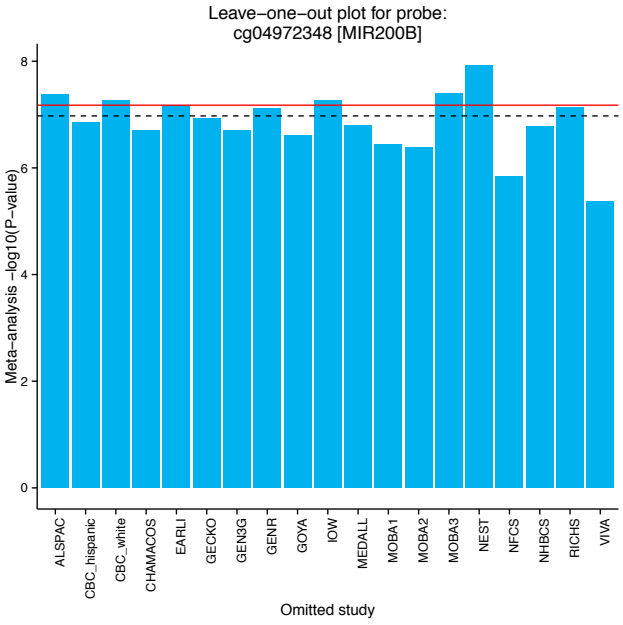
Omitted study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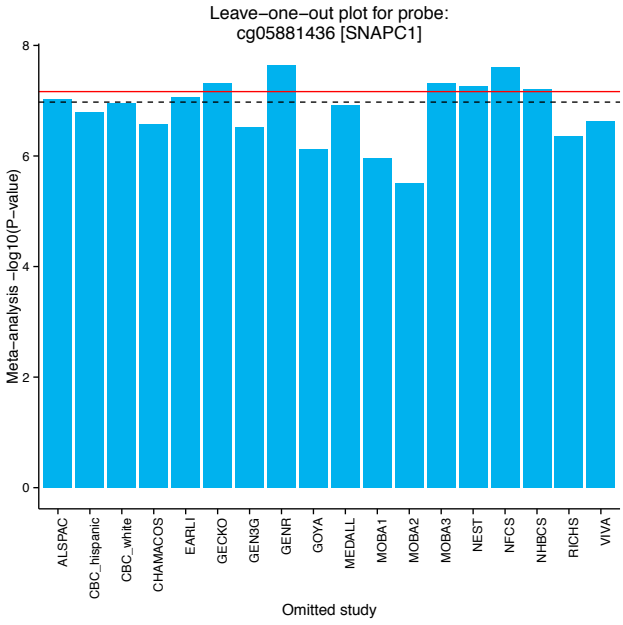
Omitted study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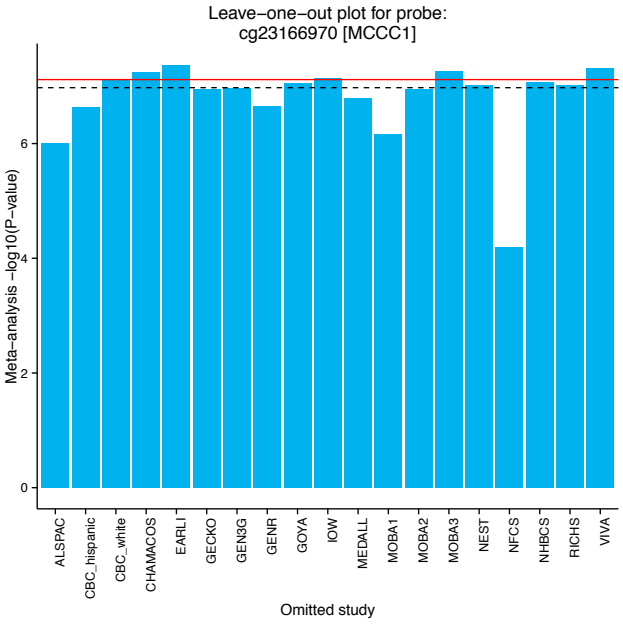
Omitted study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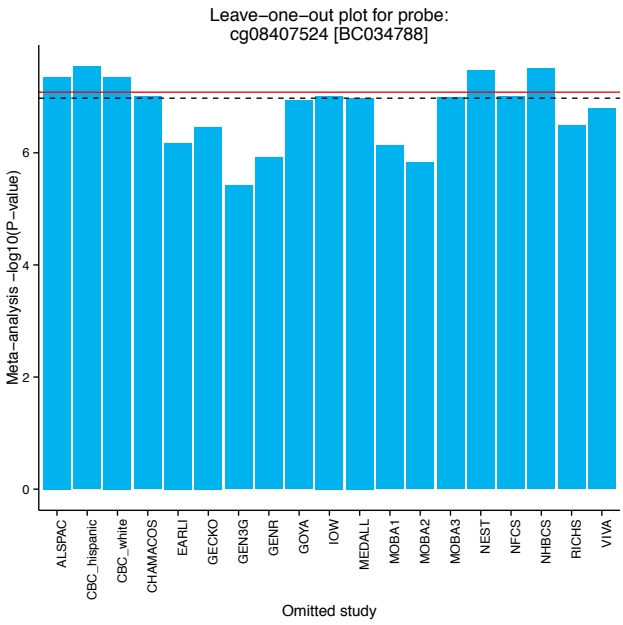
Omitted study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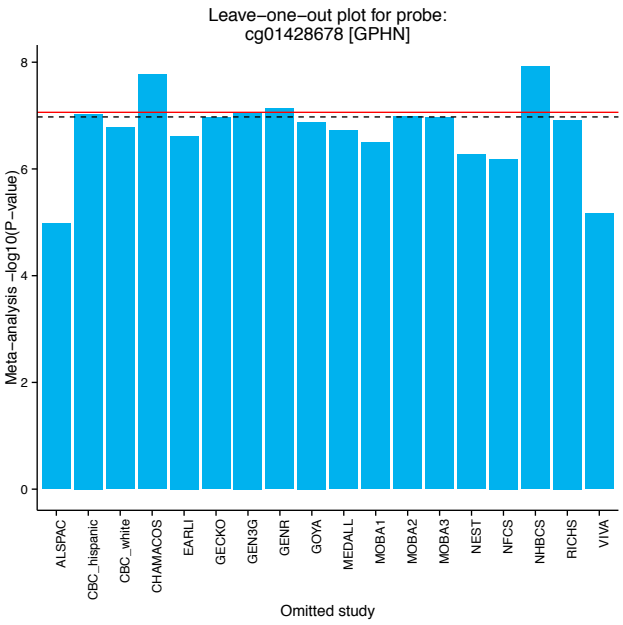
Omitted study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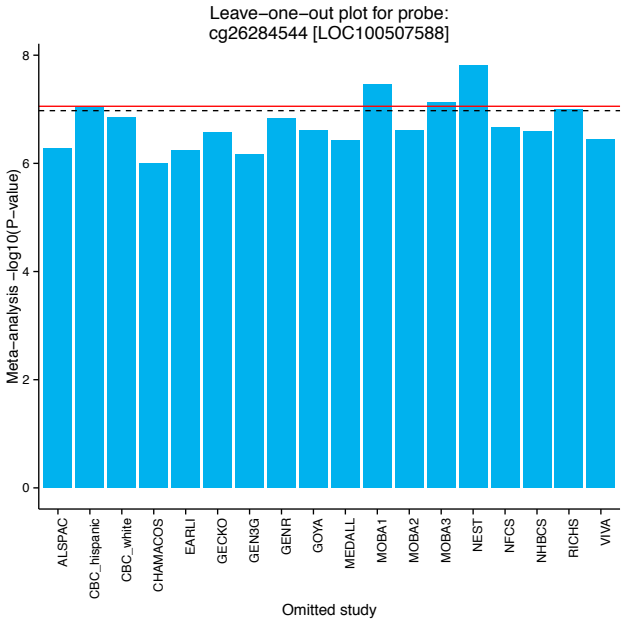
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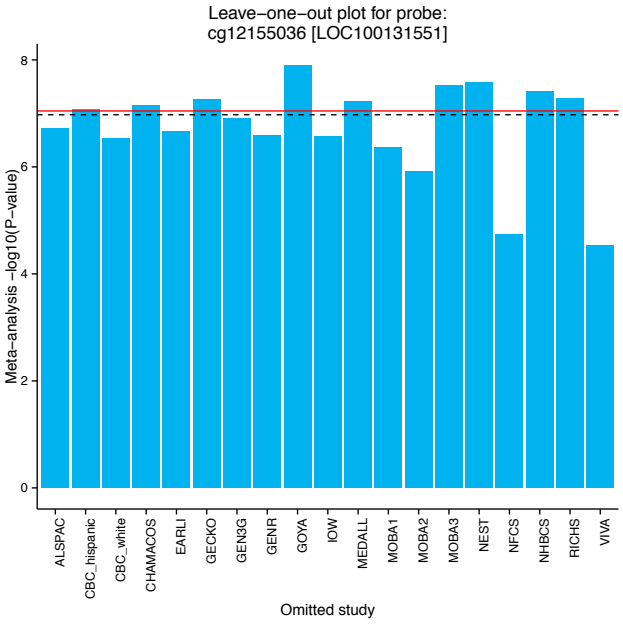
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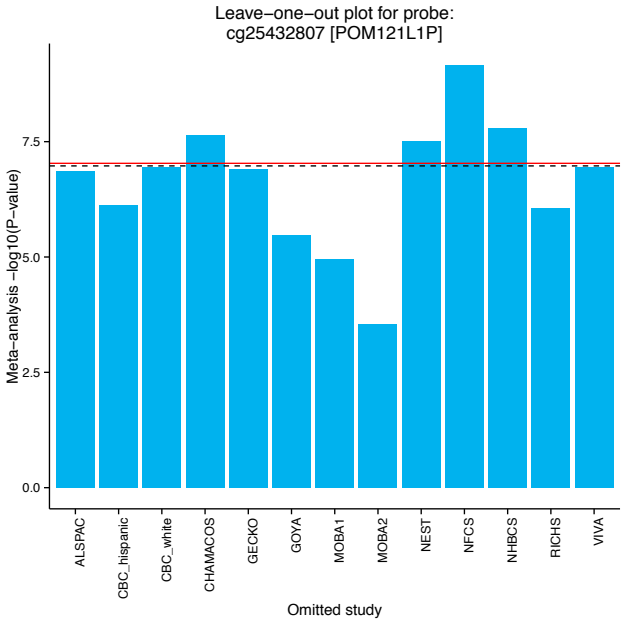
Omitted study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VIVA
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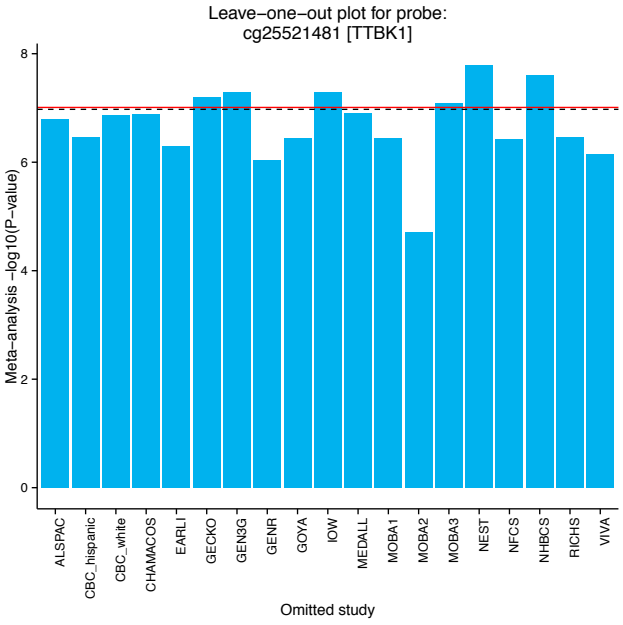
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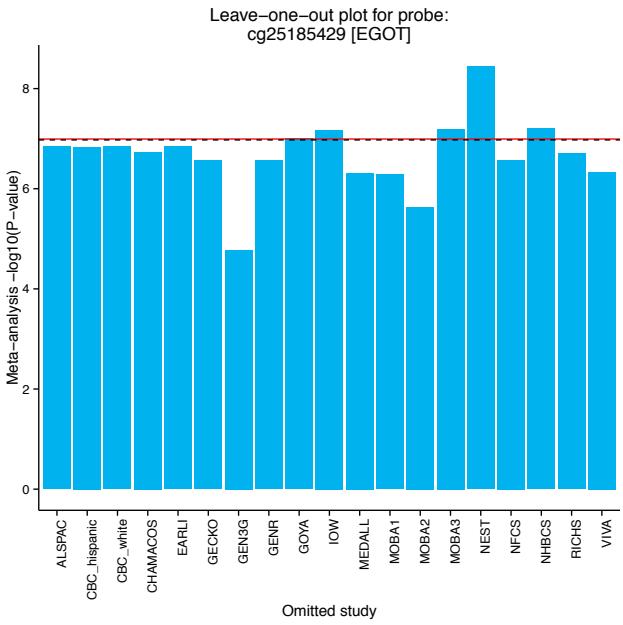
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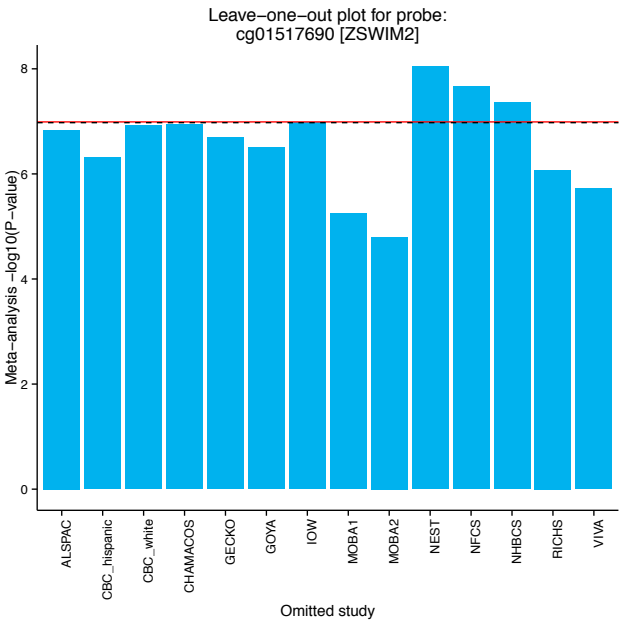
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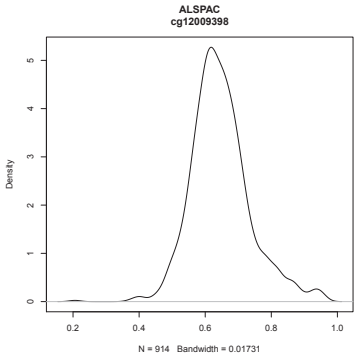
RICHS
VIVA
Omitted study

Density plots: ALSPAC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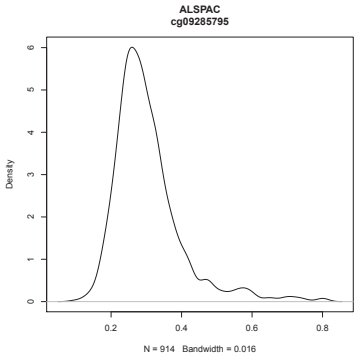
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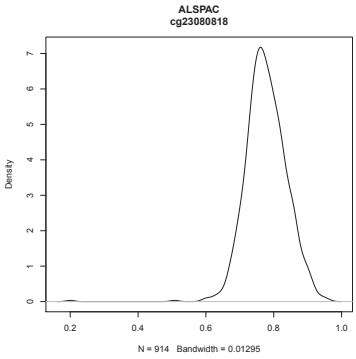
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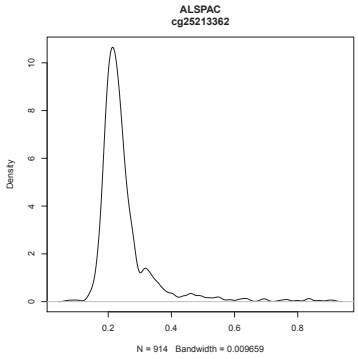
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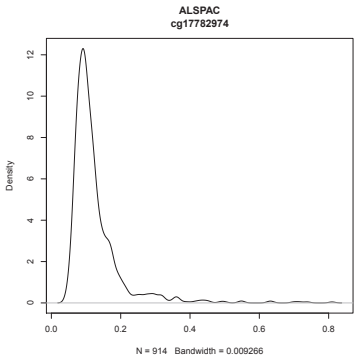
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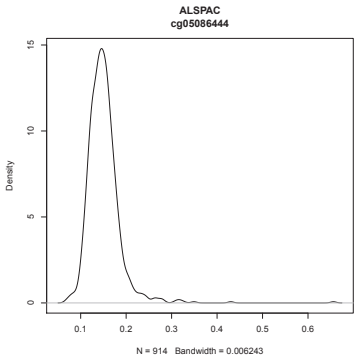
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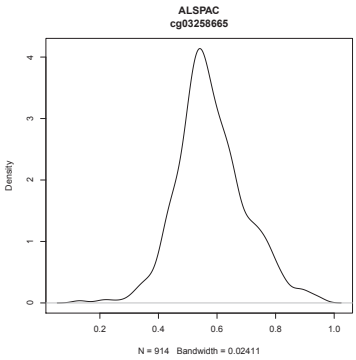
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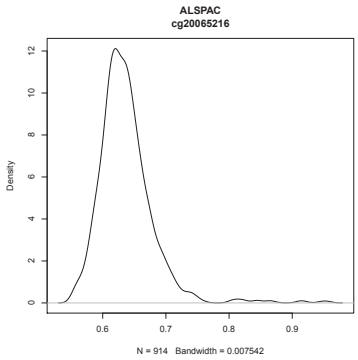
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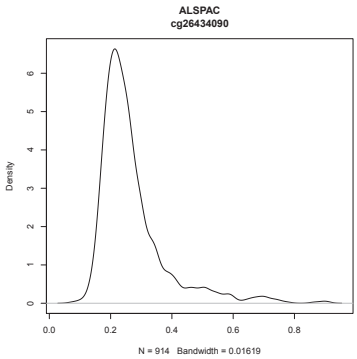
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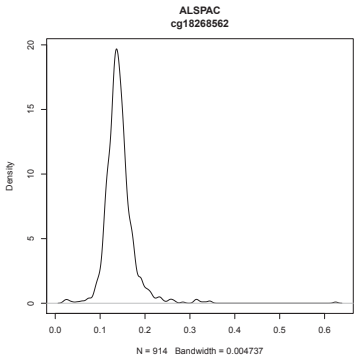
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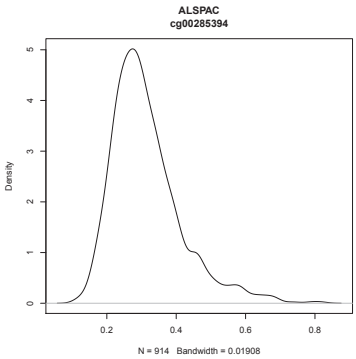
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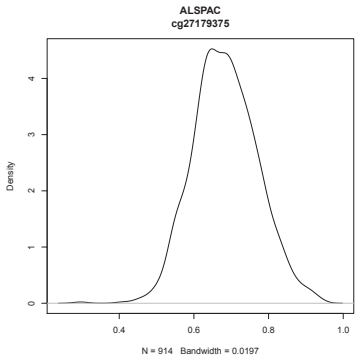
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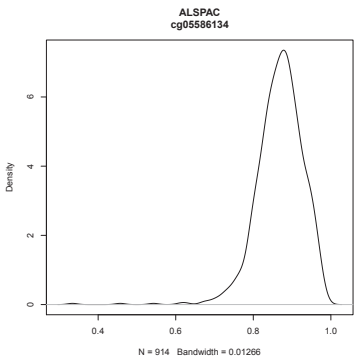
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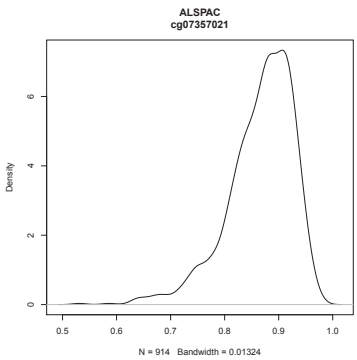
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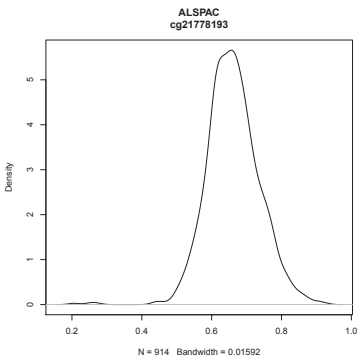
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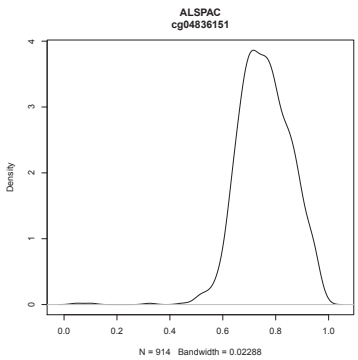
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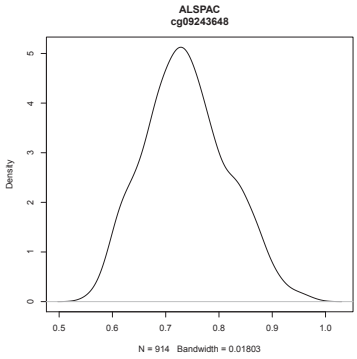
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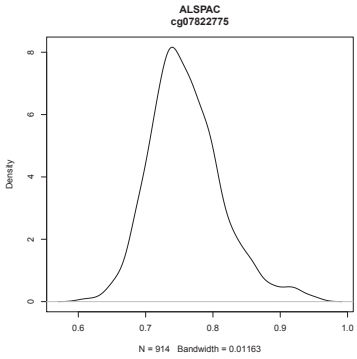
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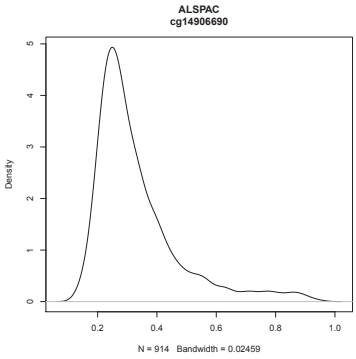
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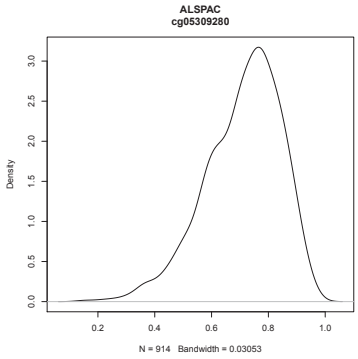
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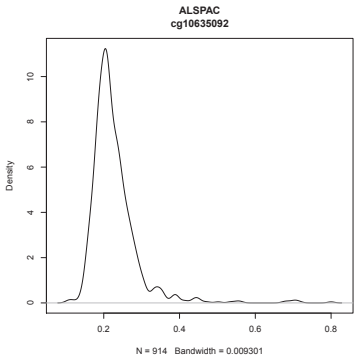
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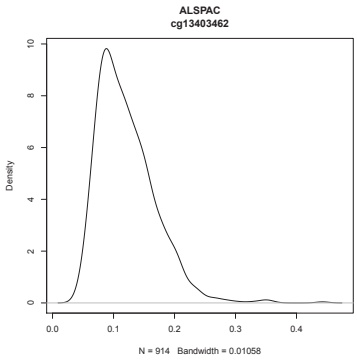
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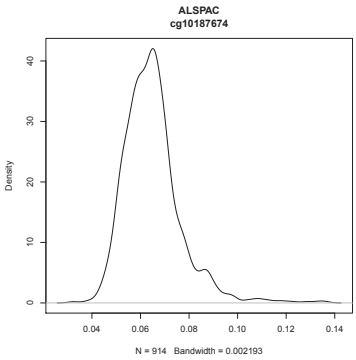
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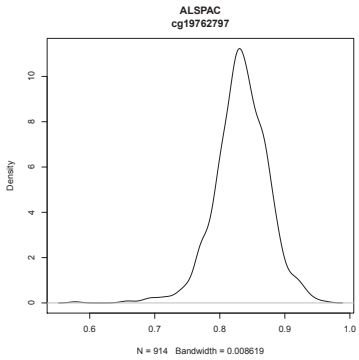
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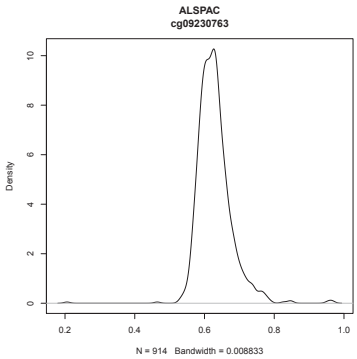
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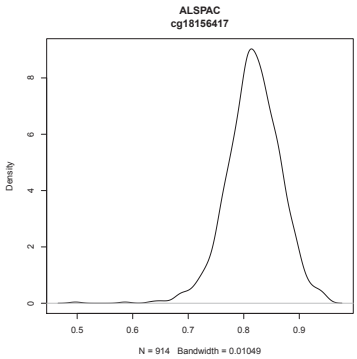
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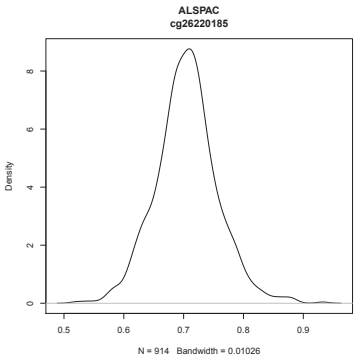
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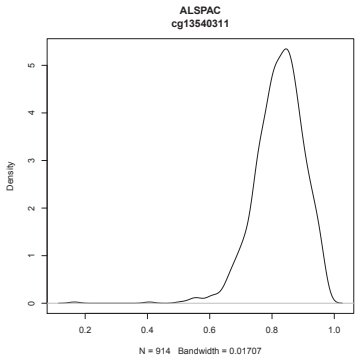
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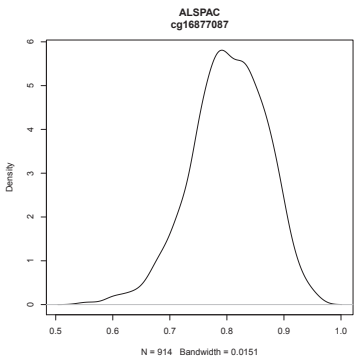
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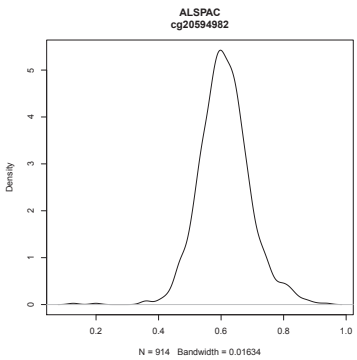
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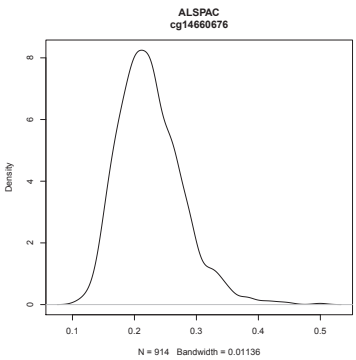
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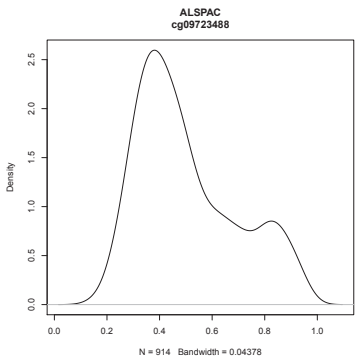
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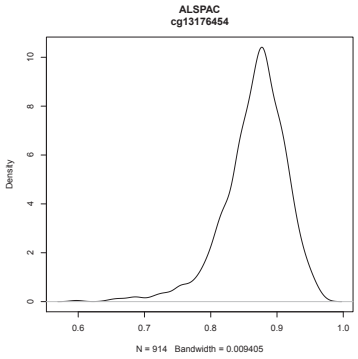
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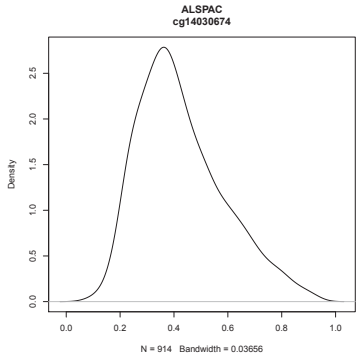
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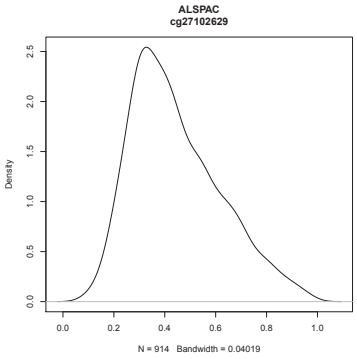
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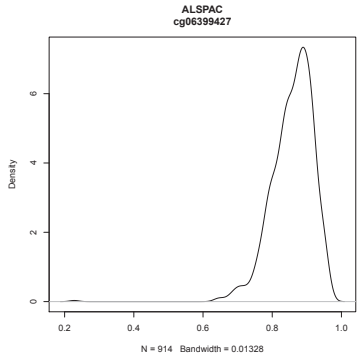
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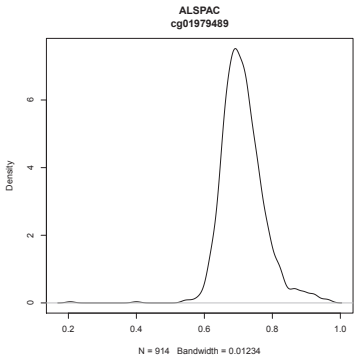
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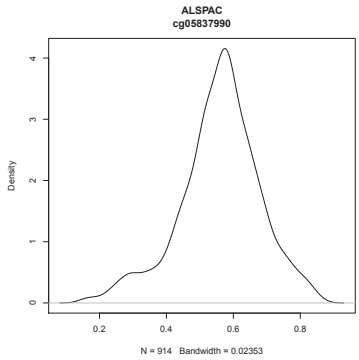
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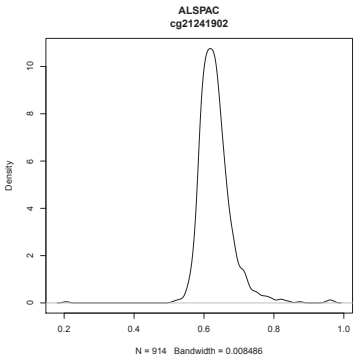
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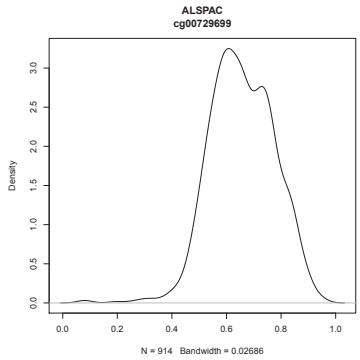
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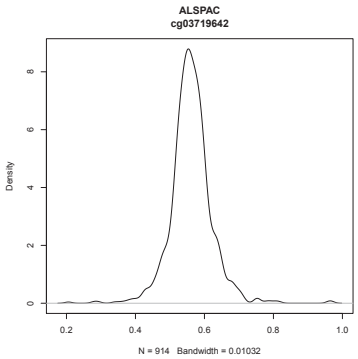
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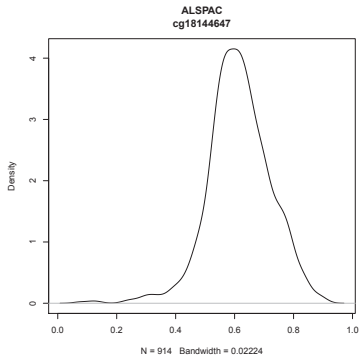
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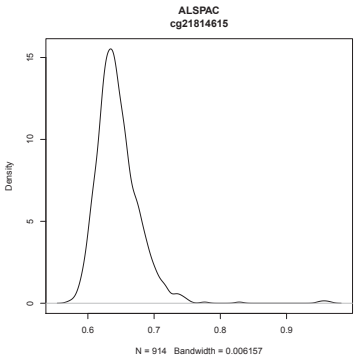
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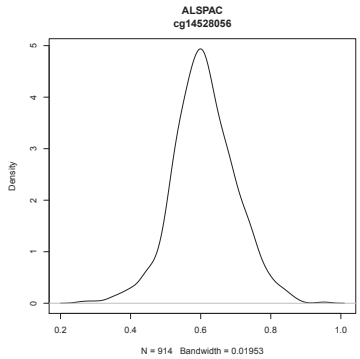
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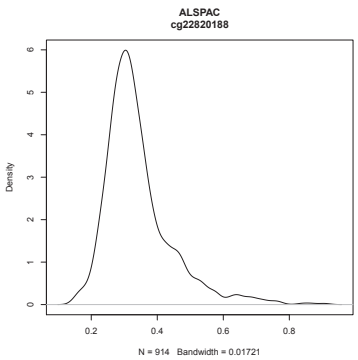
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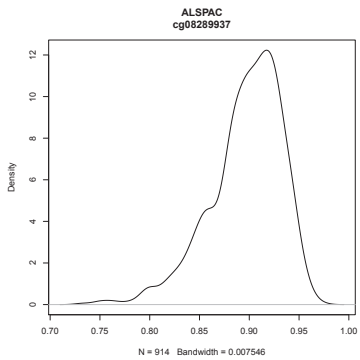
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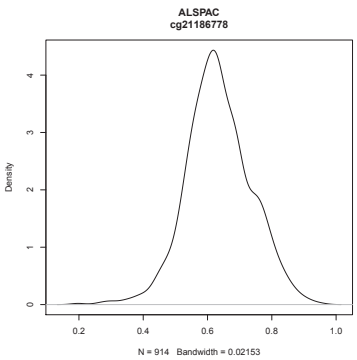
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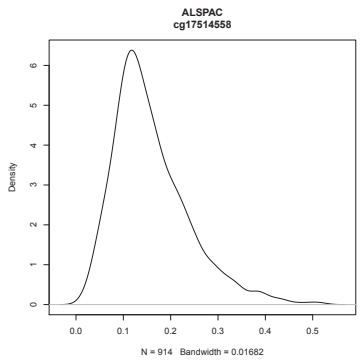
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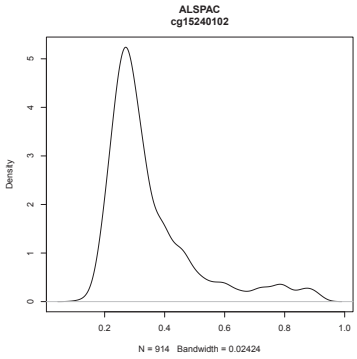
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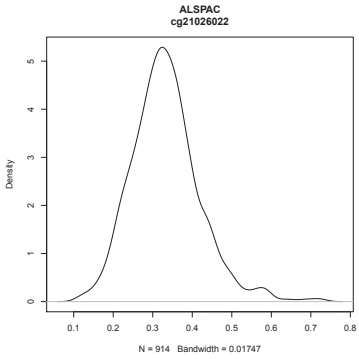
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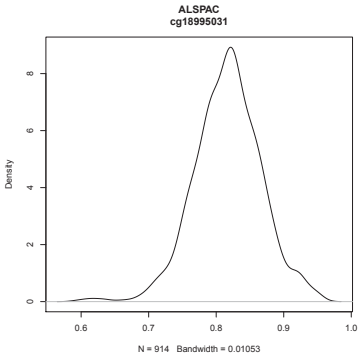
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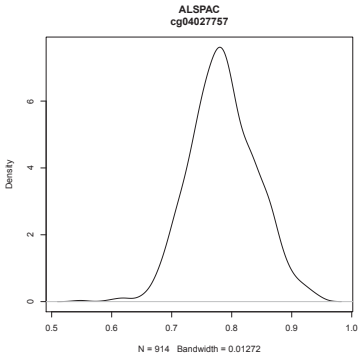
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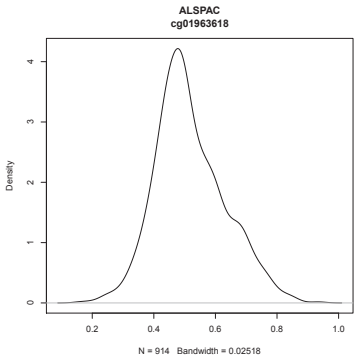
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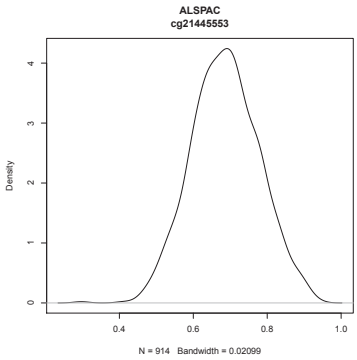
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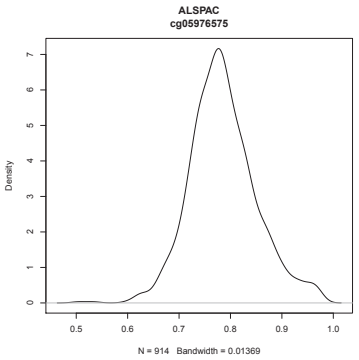
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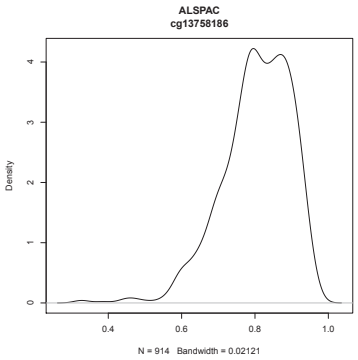
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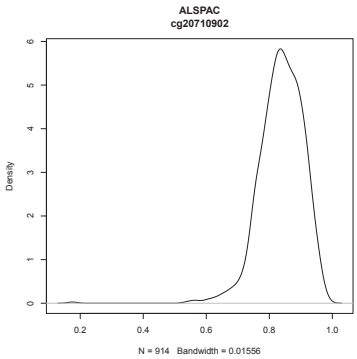
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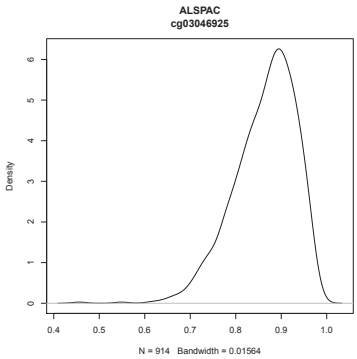
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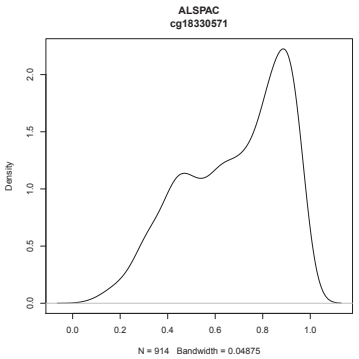
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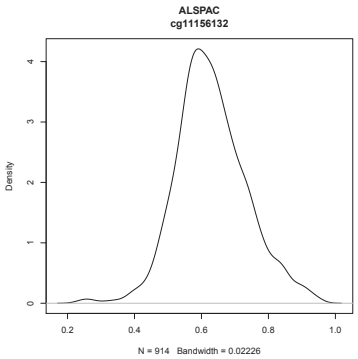
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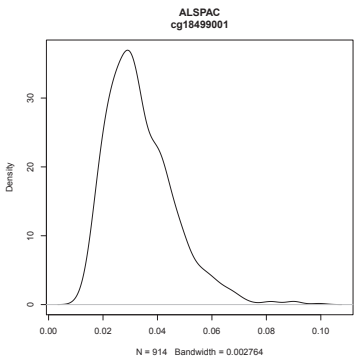
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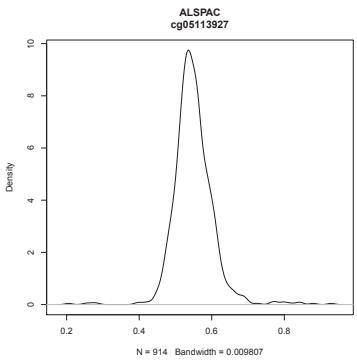
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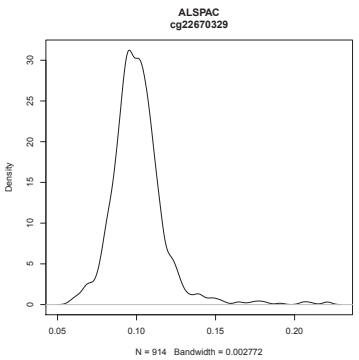
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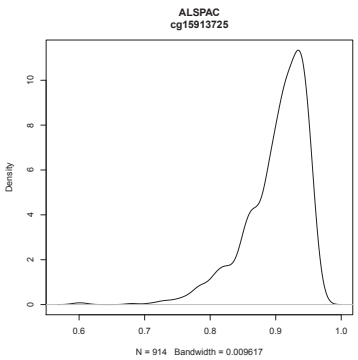
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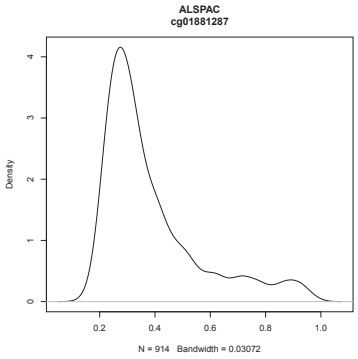
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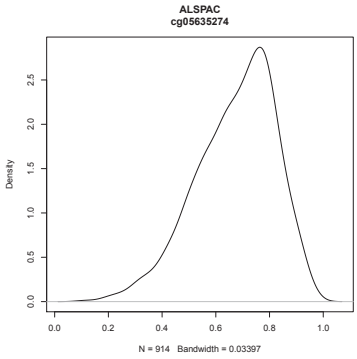
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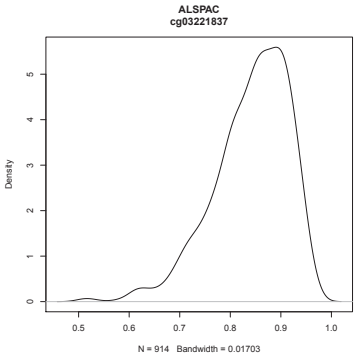
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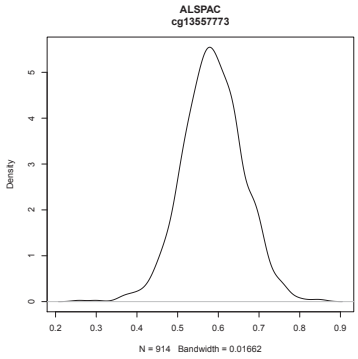
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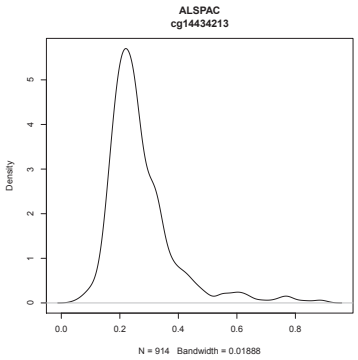
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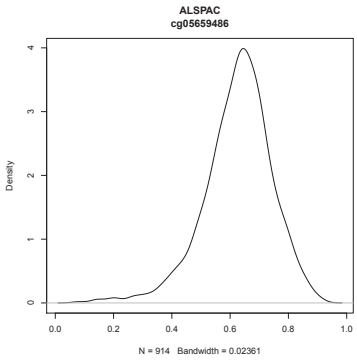
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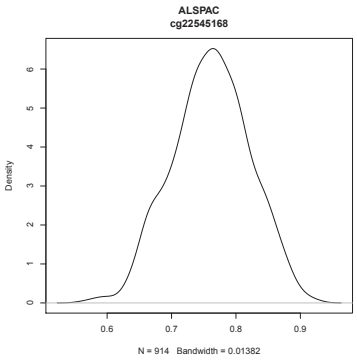
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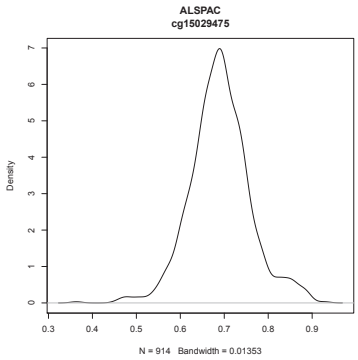
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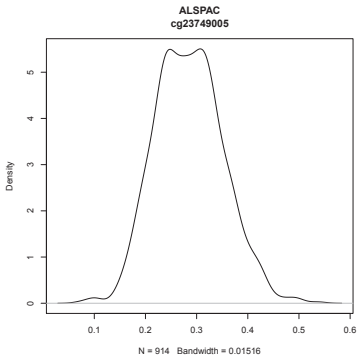
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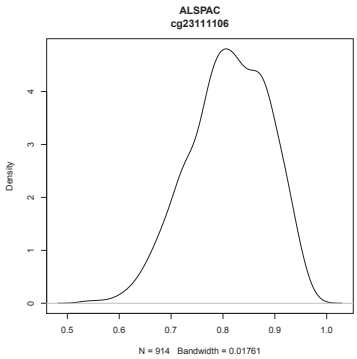
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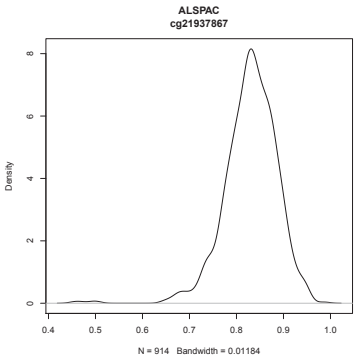
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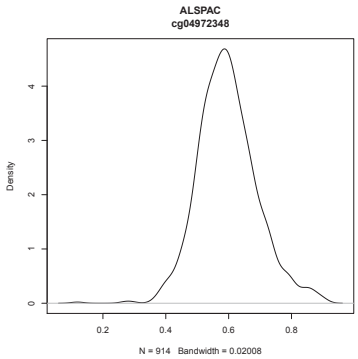
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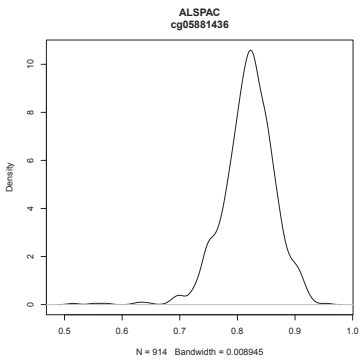
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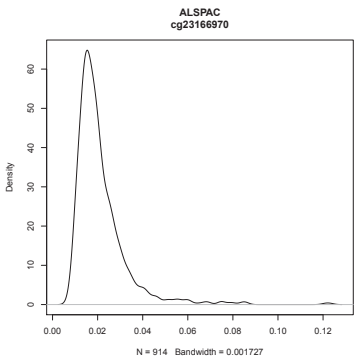
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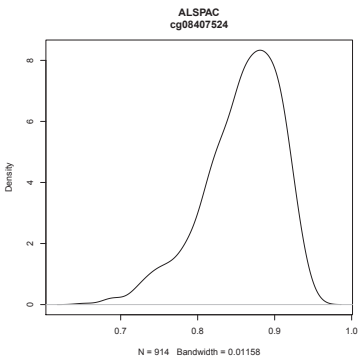
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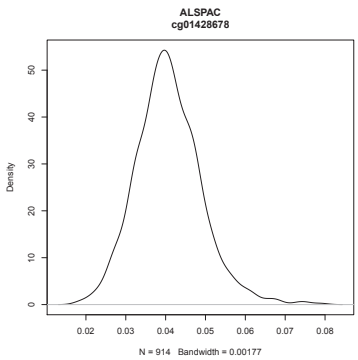
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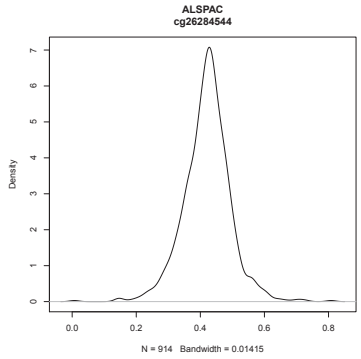
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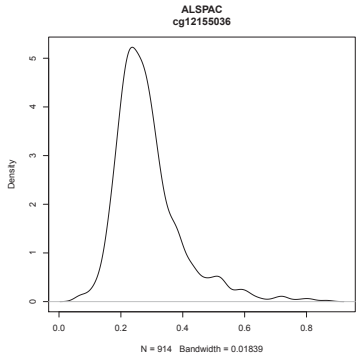
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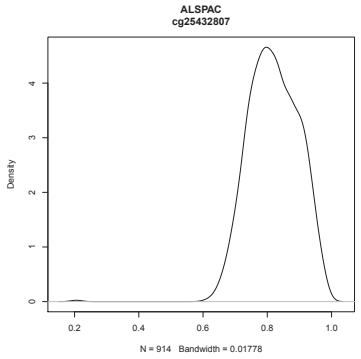
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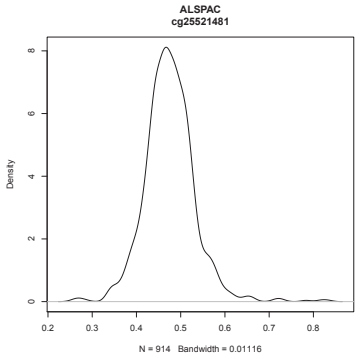
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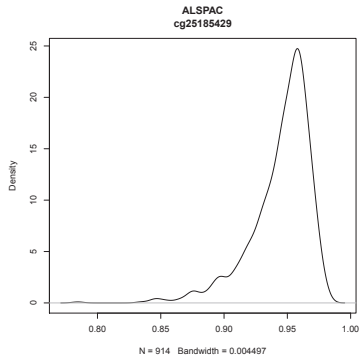
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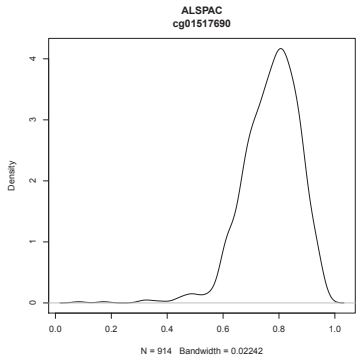
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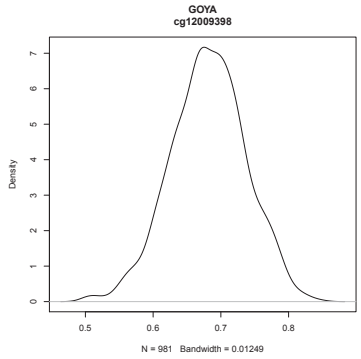
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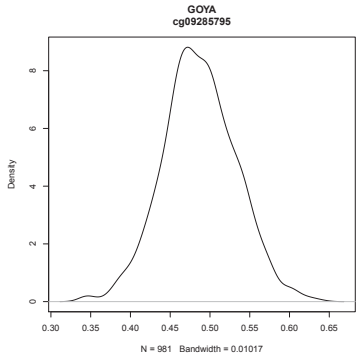
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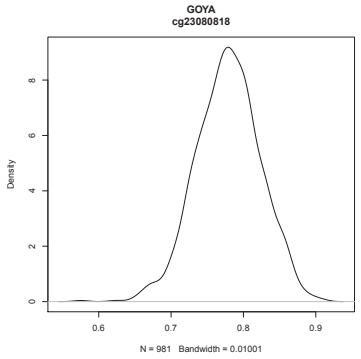
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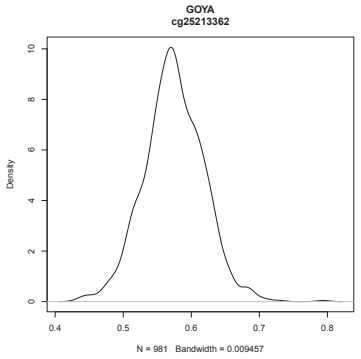
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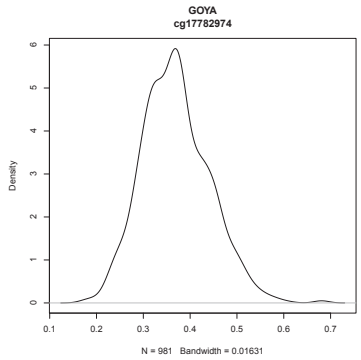
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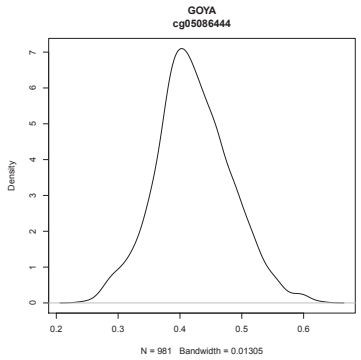
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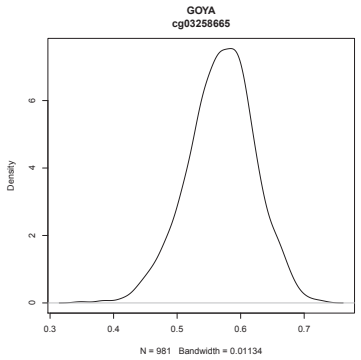
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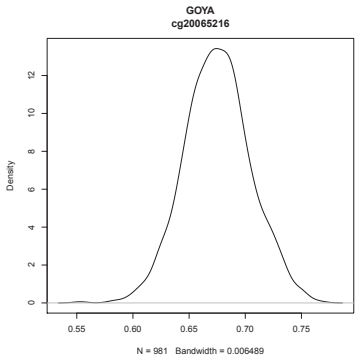
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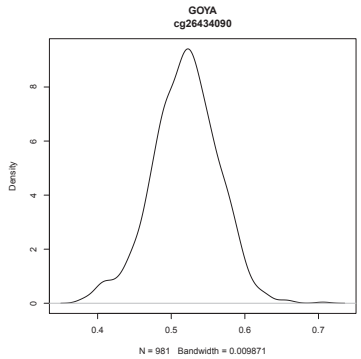
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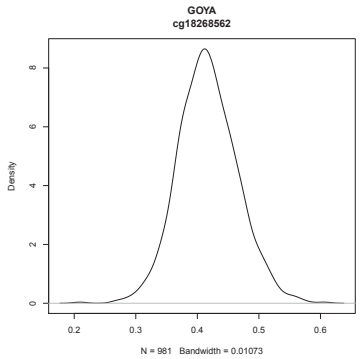
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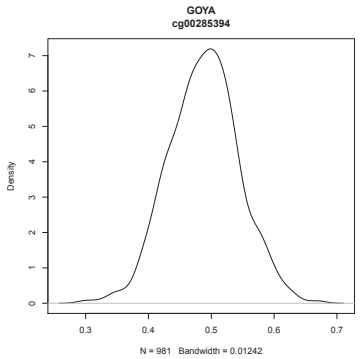
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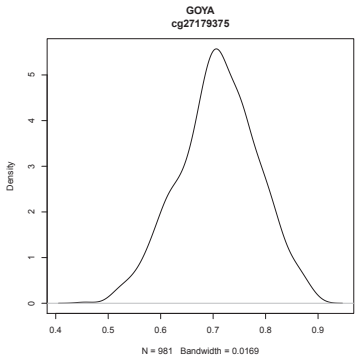
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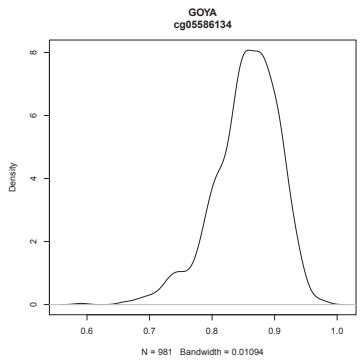
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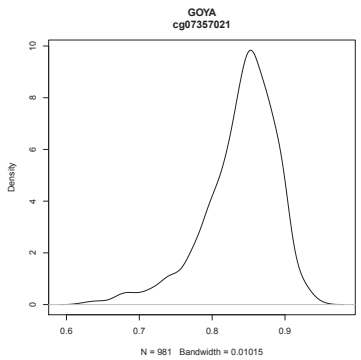
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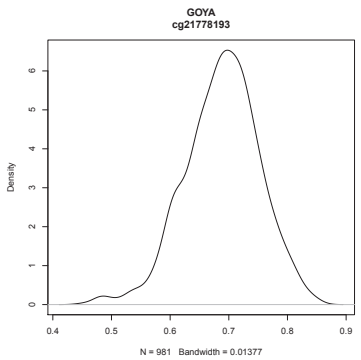
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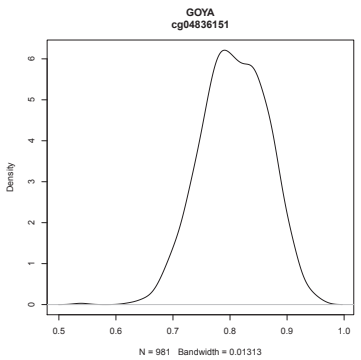
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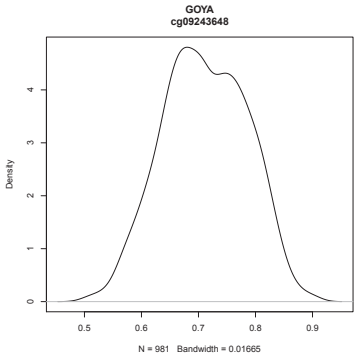
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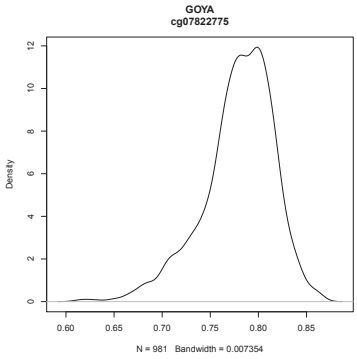
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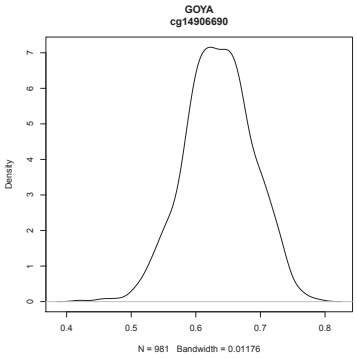
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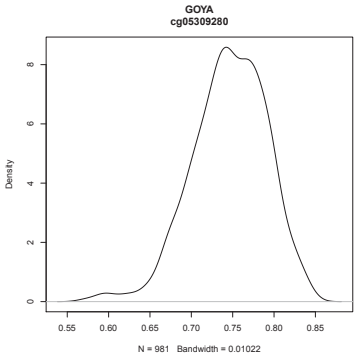
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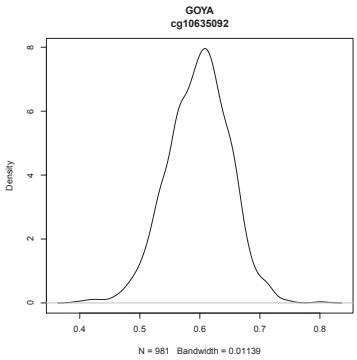
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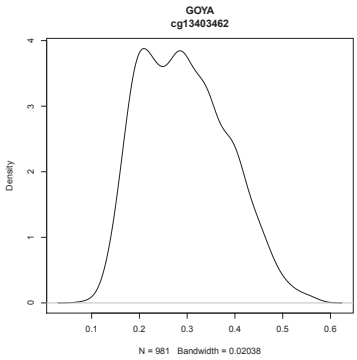
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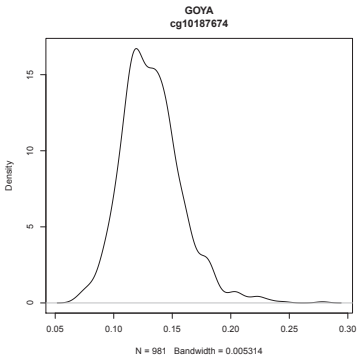
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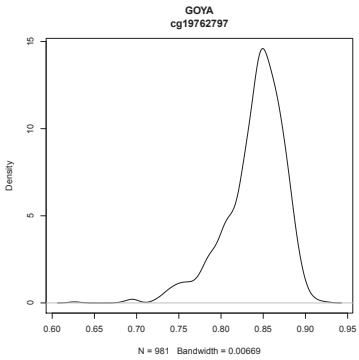
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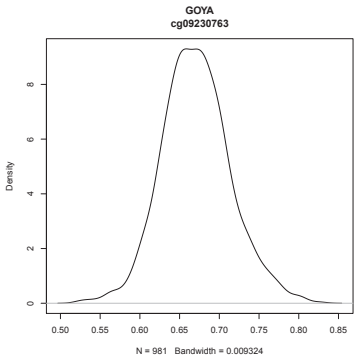
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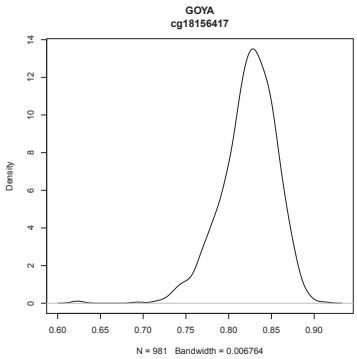
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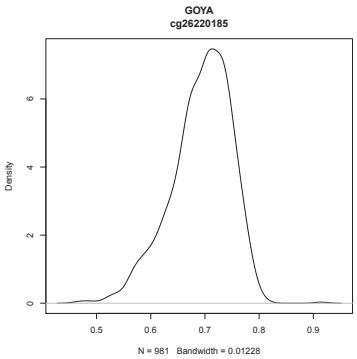
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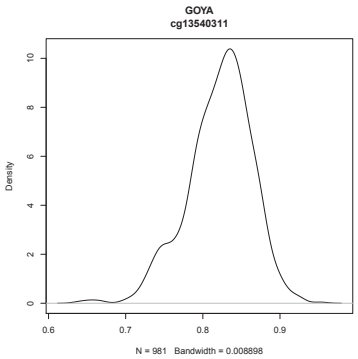
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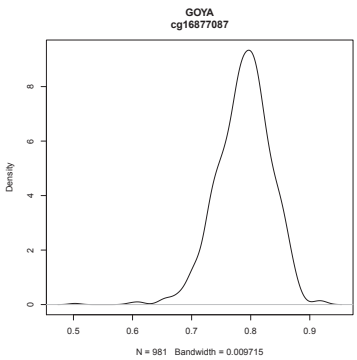
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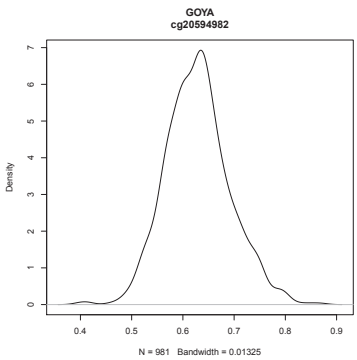
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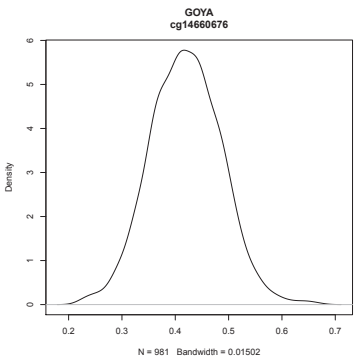
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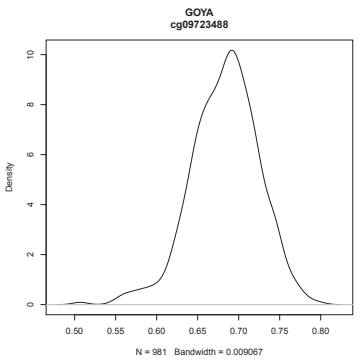
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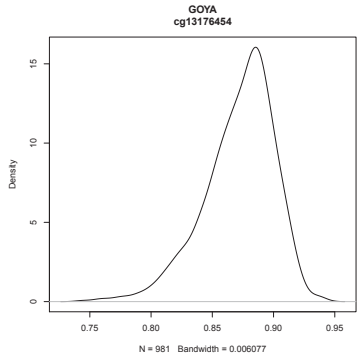
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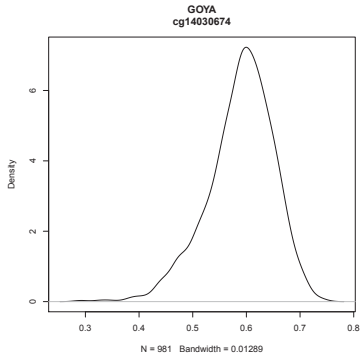
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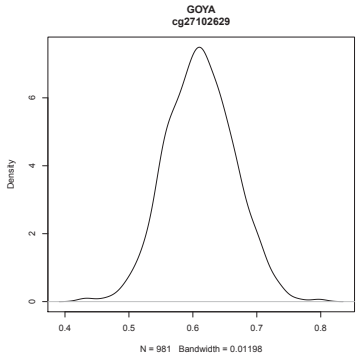
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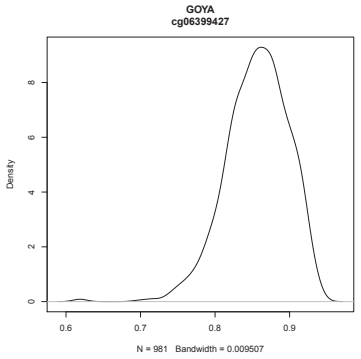
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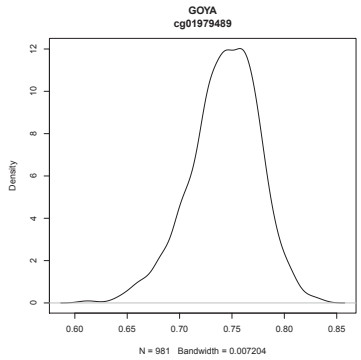
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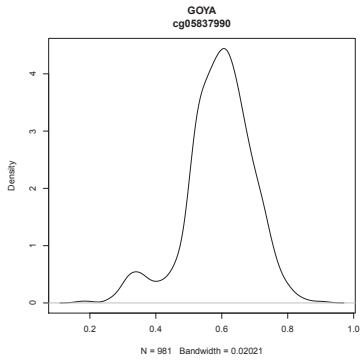
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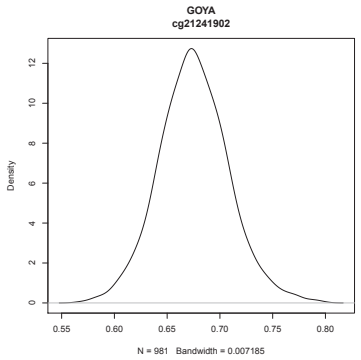
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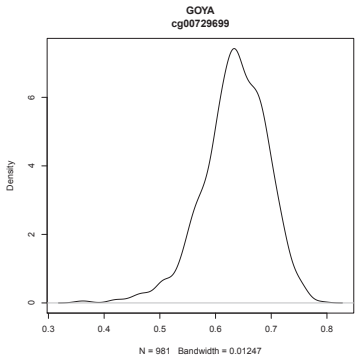
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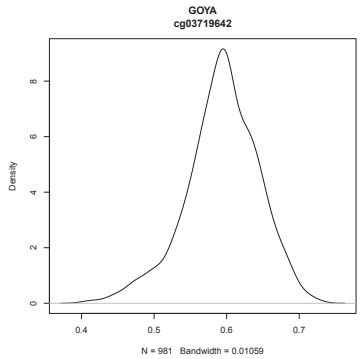
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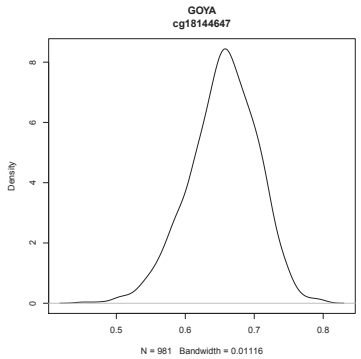
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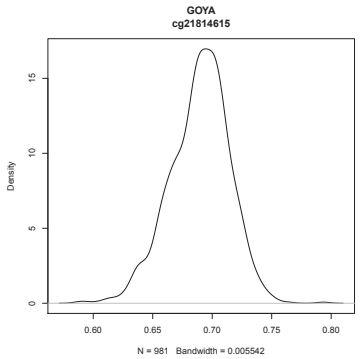
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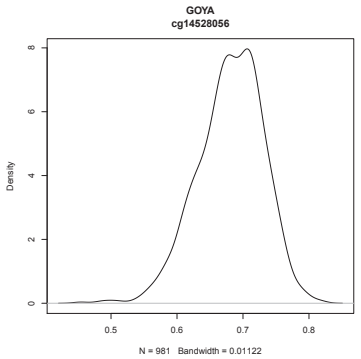
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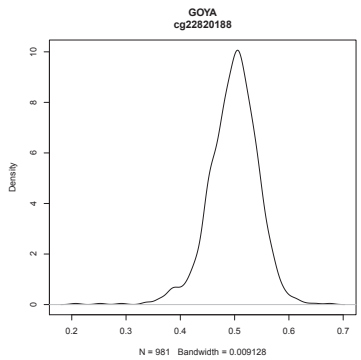
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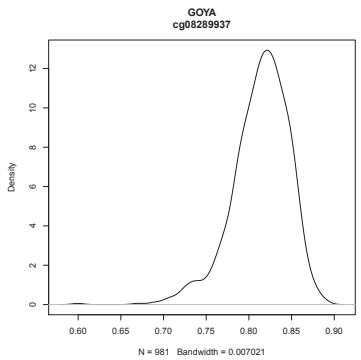
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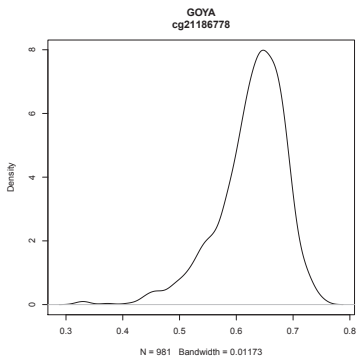
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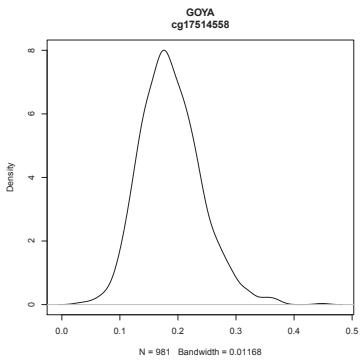
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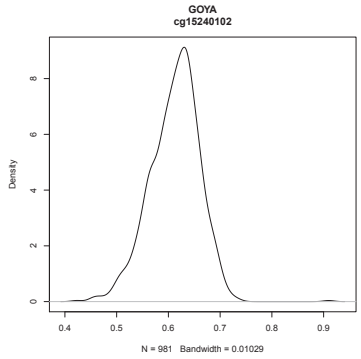
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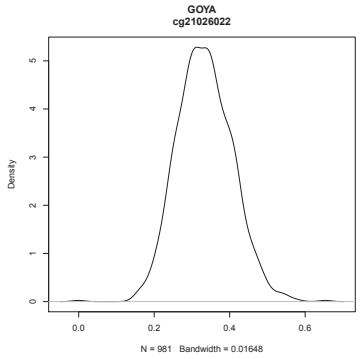
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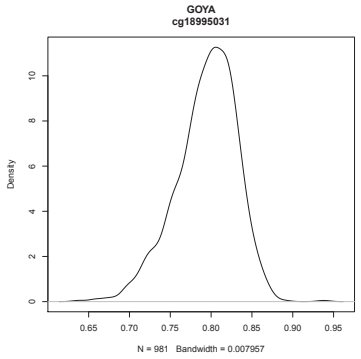
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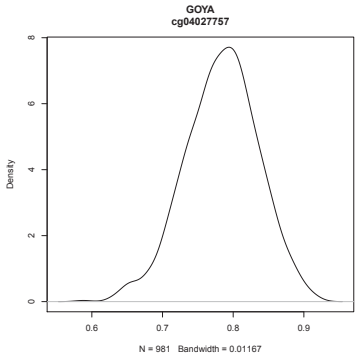
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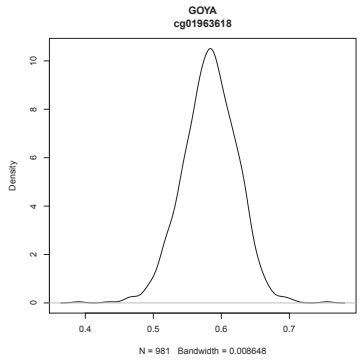
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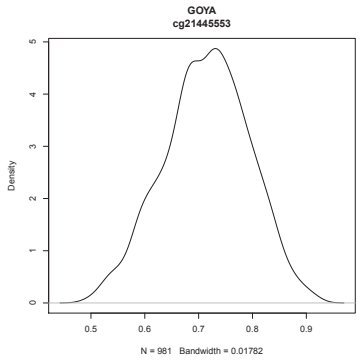
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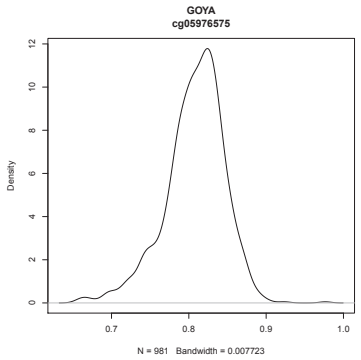
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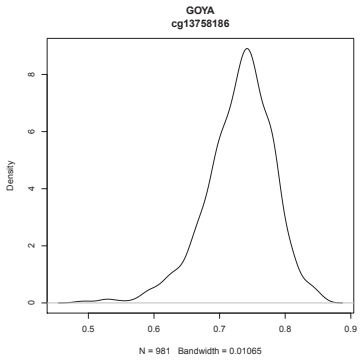
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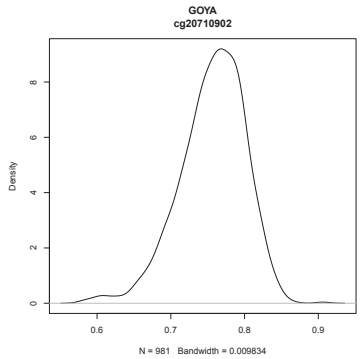
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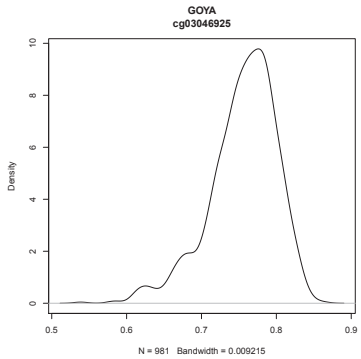
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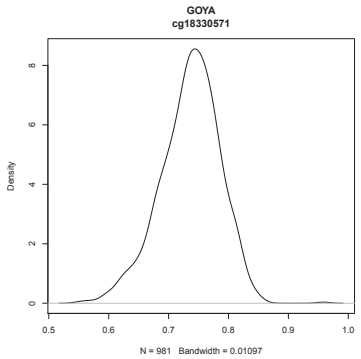
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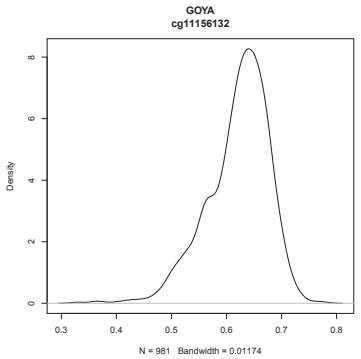
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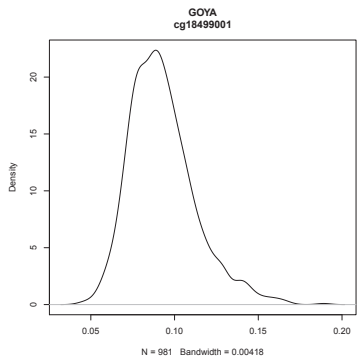
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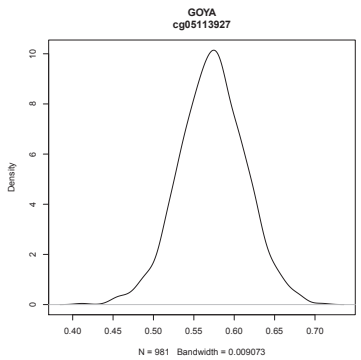
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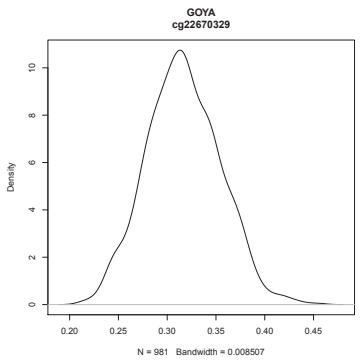
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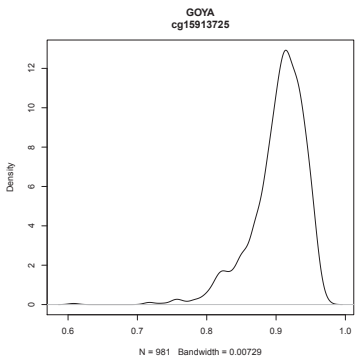
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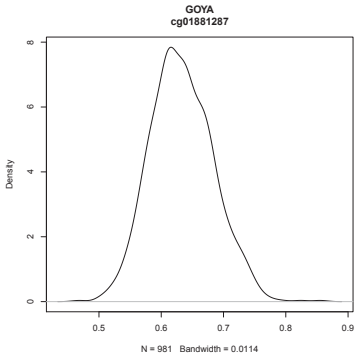
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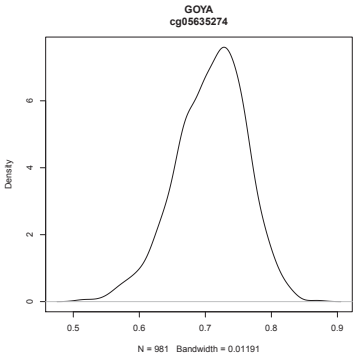
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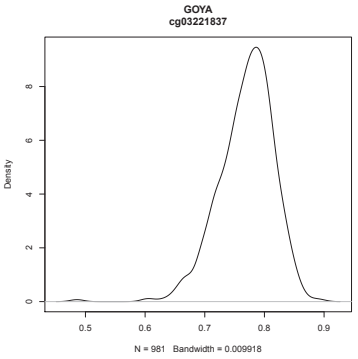
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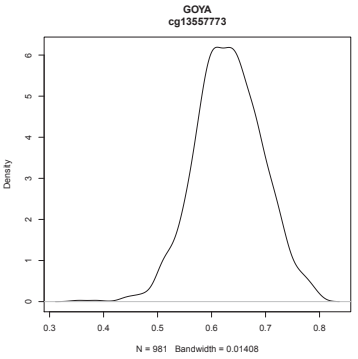
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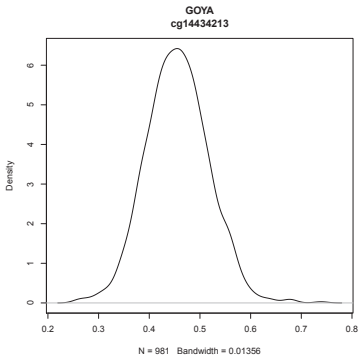
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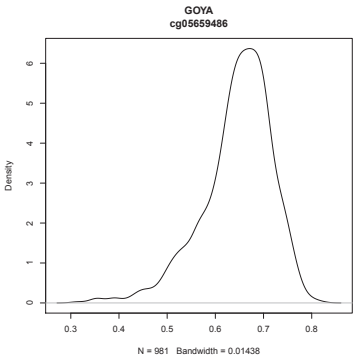
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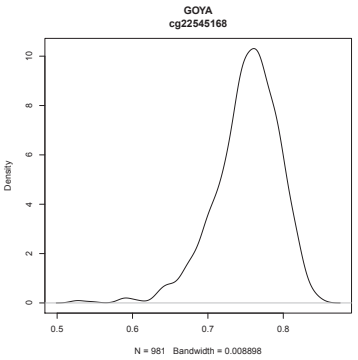
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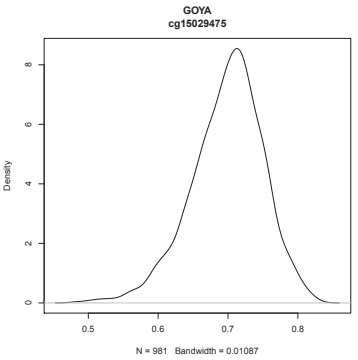
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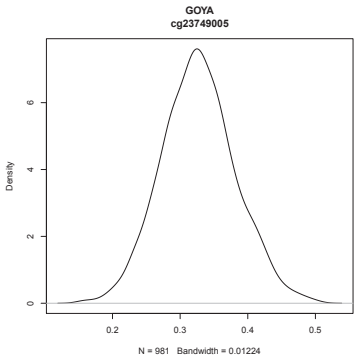
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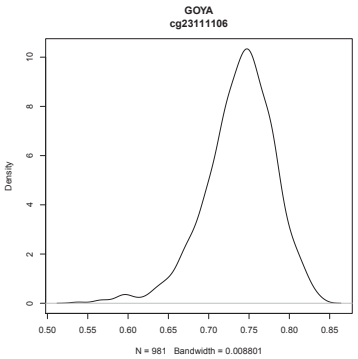
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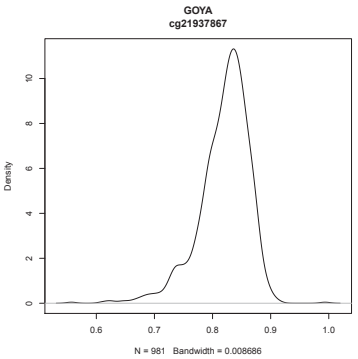
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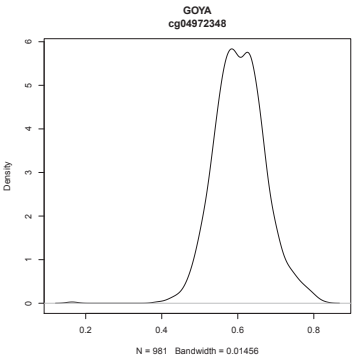
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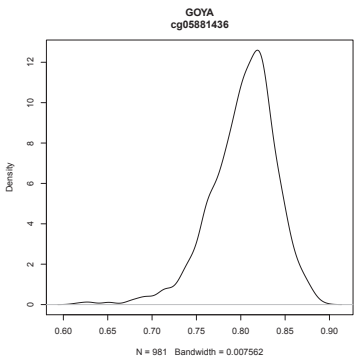
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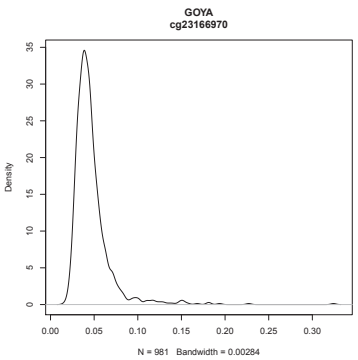
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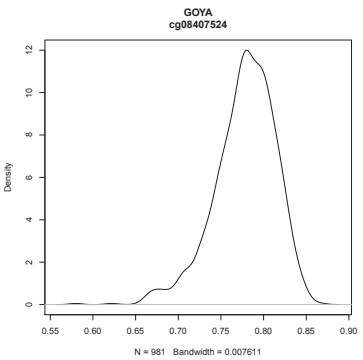
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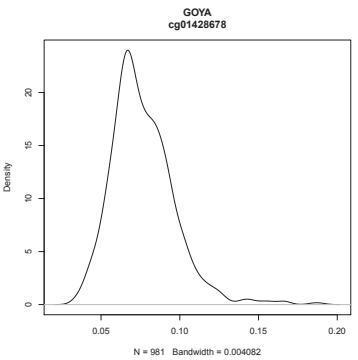
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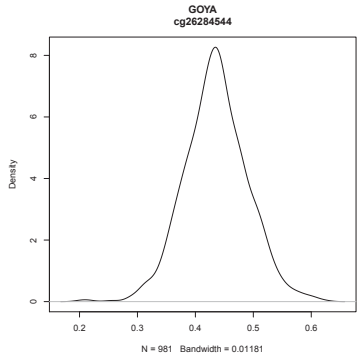
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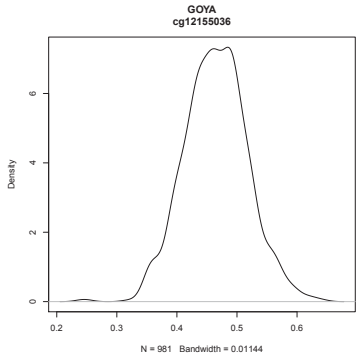
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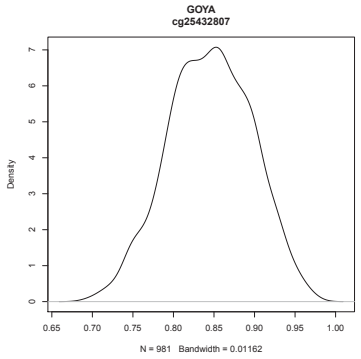
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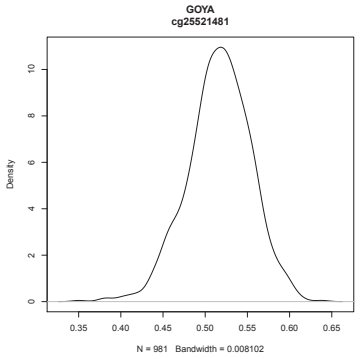
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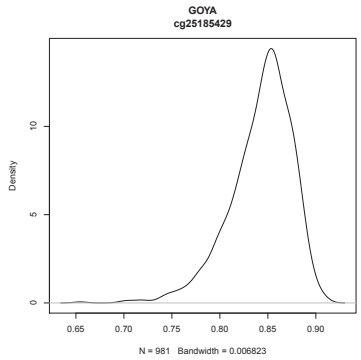
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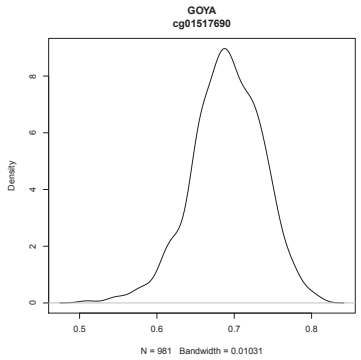
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