**88 common exon meQTLs
Based on top 5000   exon s expressed in Neurons**

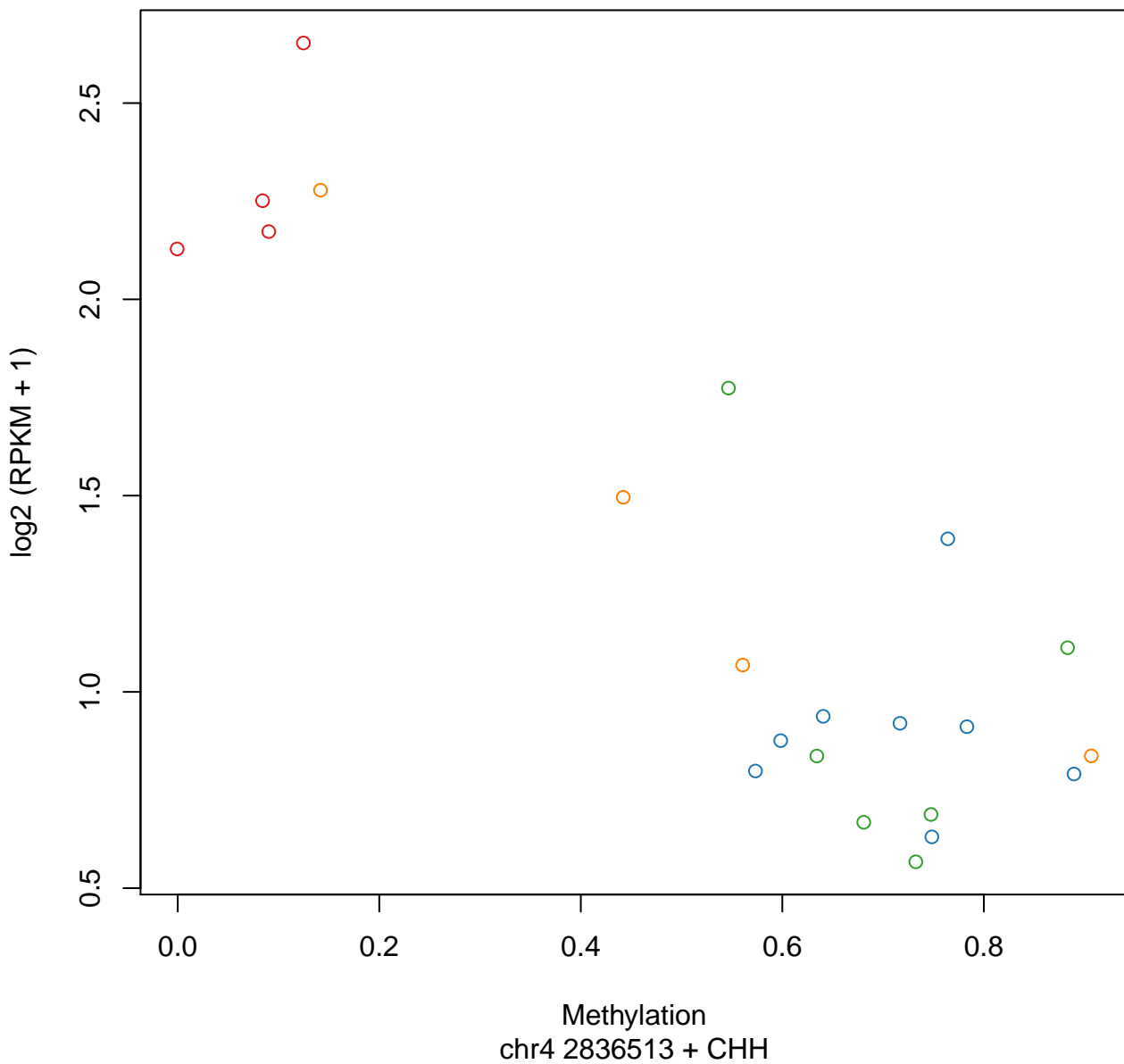Best −log10 FDR p−value with non CpGs

Best −log10 FDR p−value with CpGs
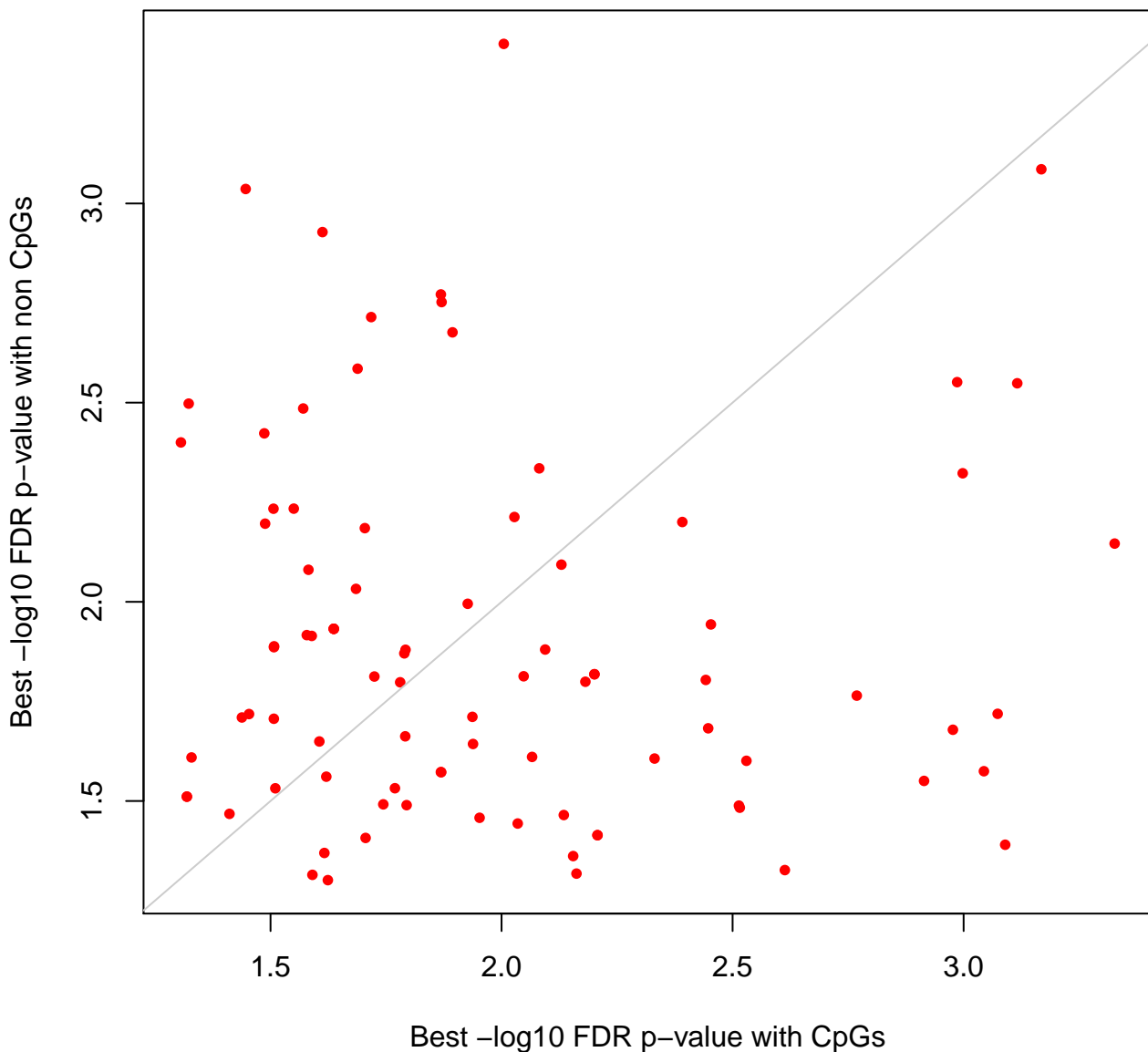
exon ENSE00000926930.1_1 FDR 0.00092
TNC

Methylation
chr9 117848330 + CHH
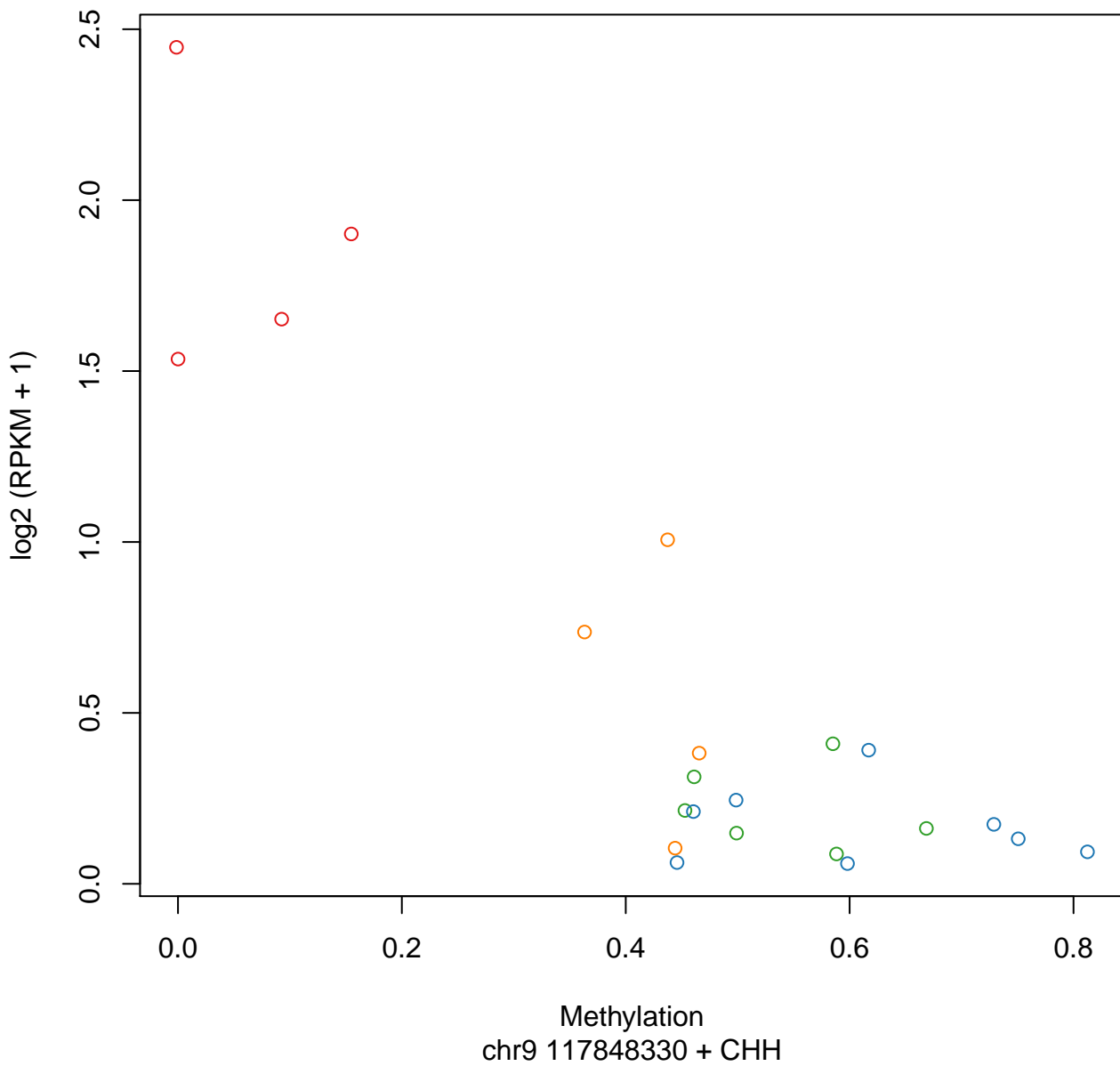
exon ENSE00002039665.1_1 FDR 0.000398
SH3BP2

Methylation
chr4 2836513 + CHH

exon ENSE00001903108.1_1 FDR 0.00118
MASP1

Methylation
chr3 186958992 + CHH
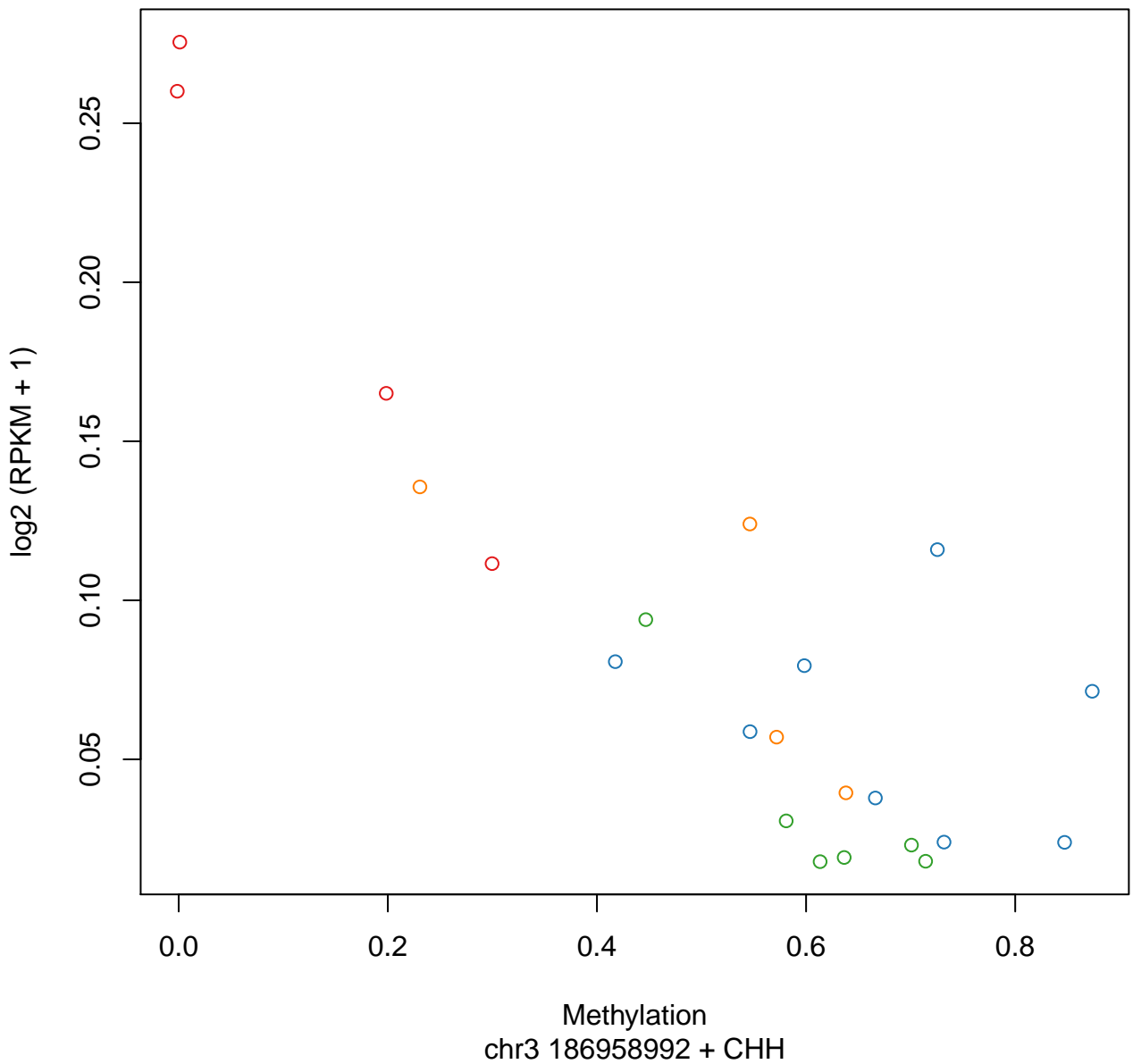
exon ENSE00003474946.1_1 FDR 0.00318
RHBDL3

Methylation
chr17 30643596 + CHH
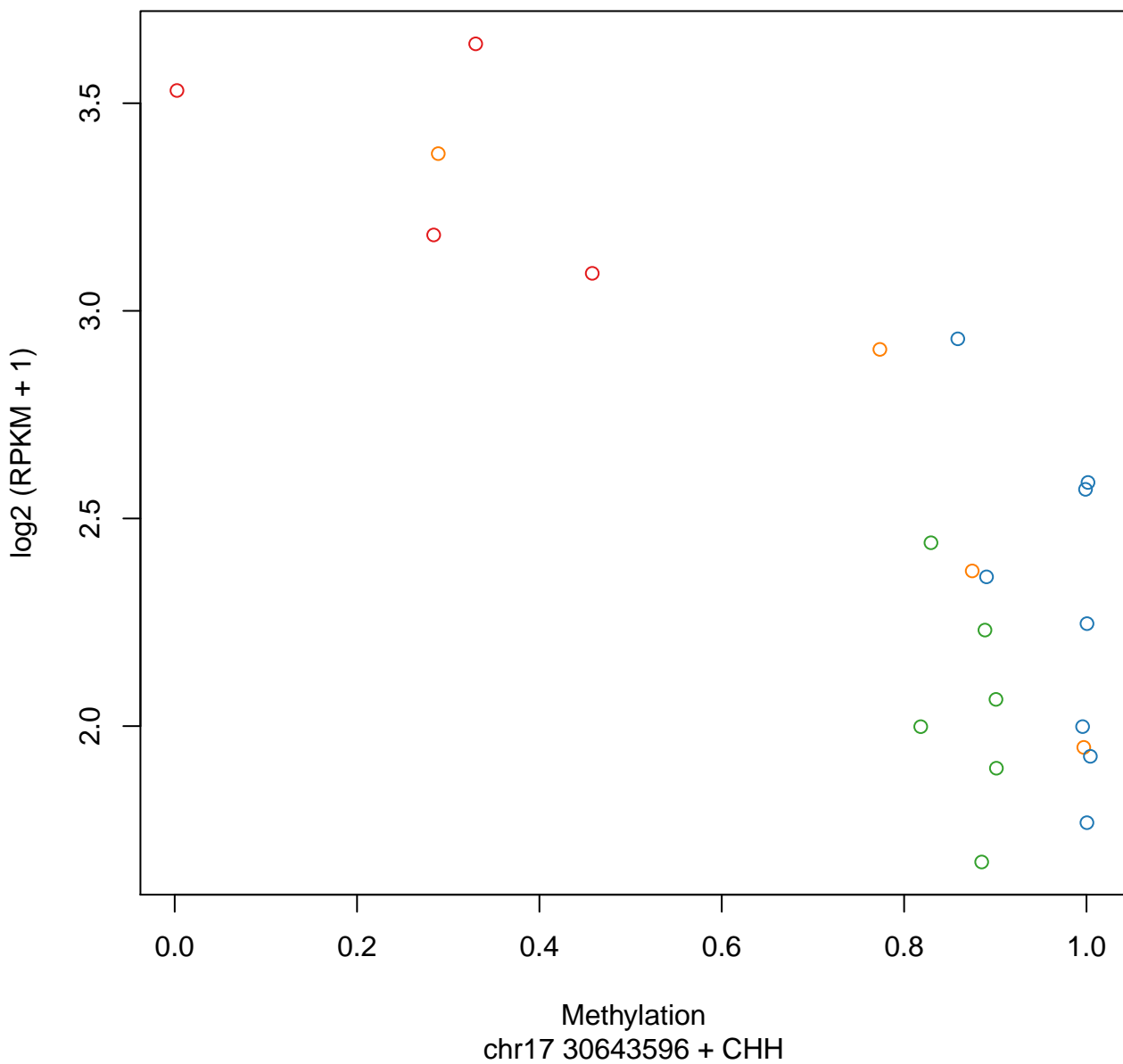
exon ENSE00003512210.1_1 FDR 0.00398
LRP5

Methylation
chr11 68202230 – CHH
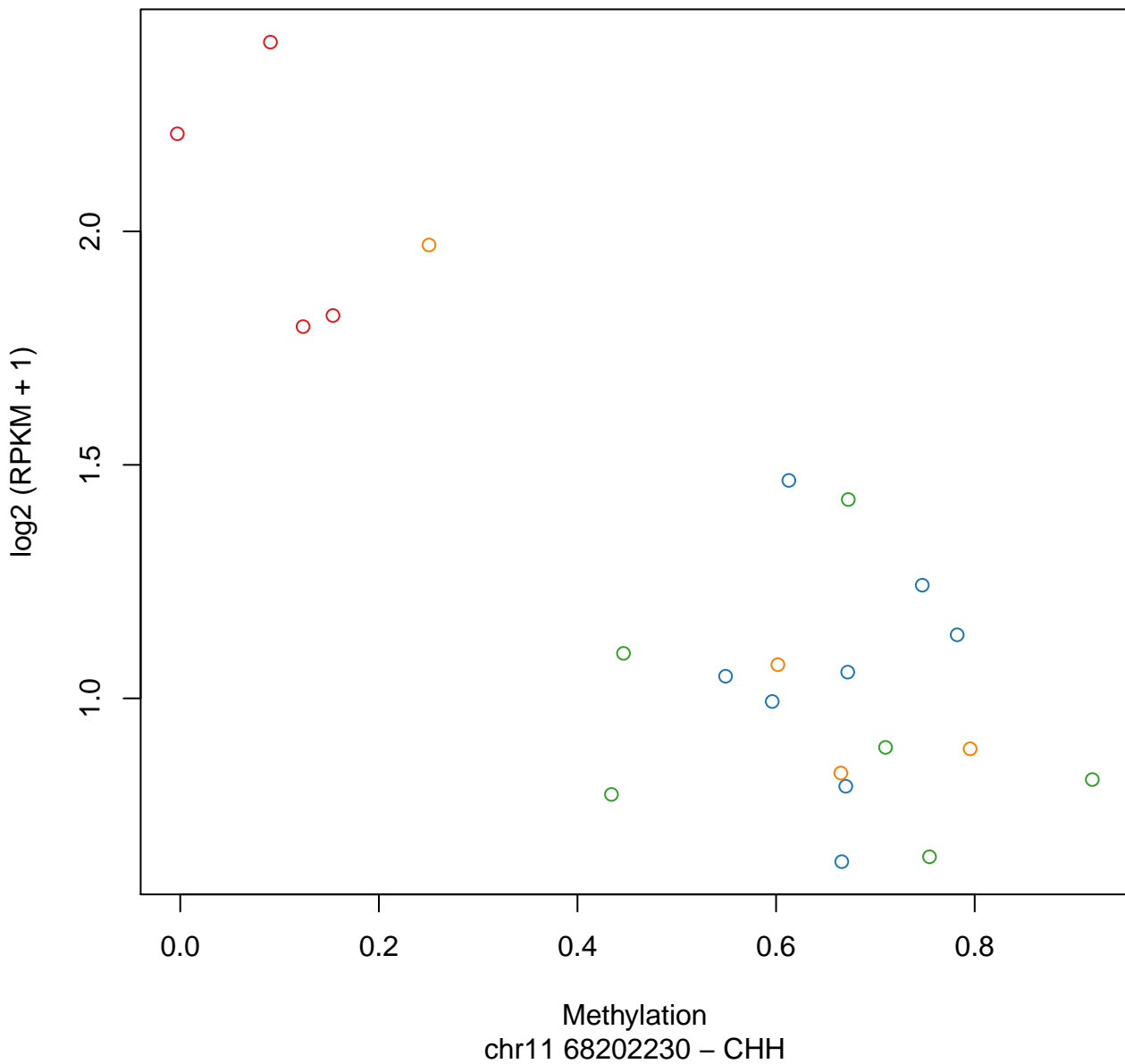
exon ENSE00001498709.2_1 FDR 0.00193
FBLN2

Methylation
chr3 13680314 − CHH
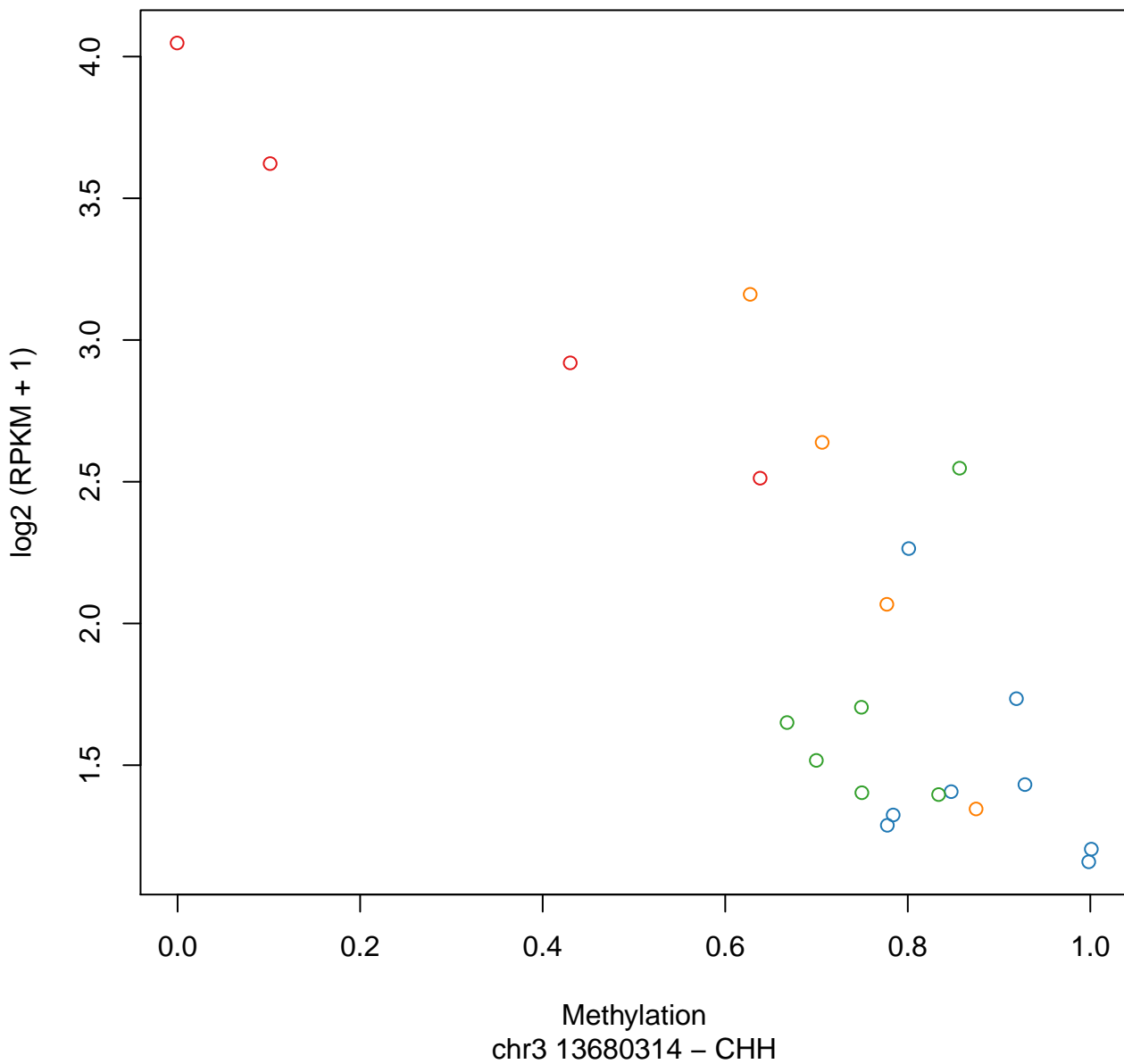
exon ENSE00001635550.1_1 FDR 0.00378
FBLN2

Methylation
chr3 13680314 – CHH
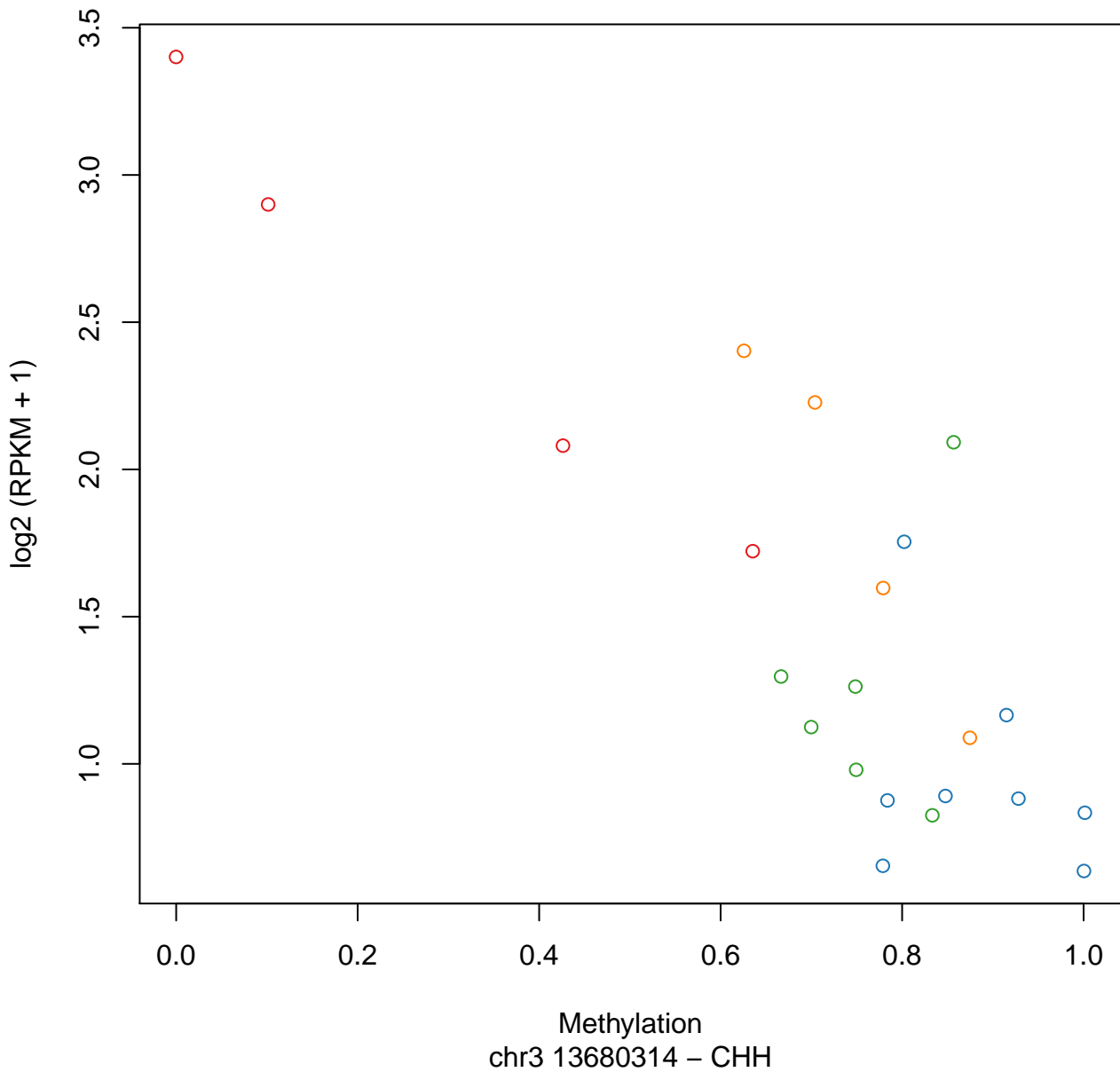
exon ENSE00001736763.1_1 FDR 0.00327
FBLN2

Methylation
chr3 13680314 – CHH
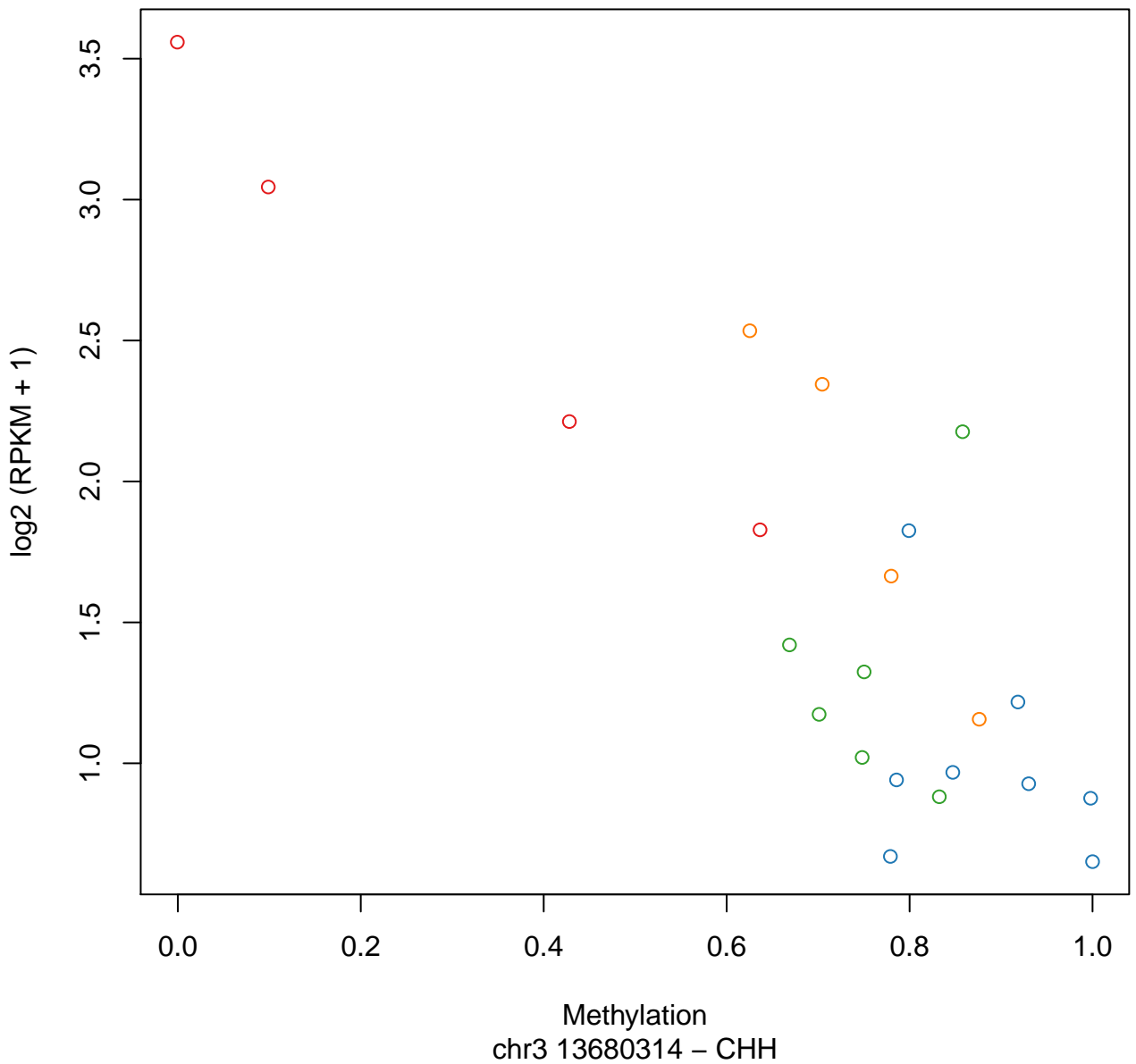
exon ENSE00002509379.1_1 FDR 0.00169
RGMA

Methylation
chr15 93588732 + CHH
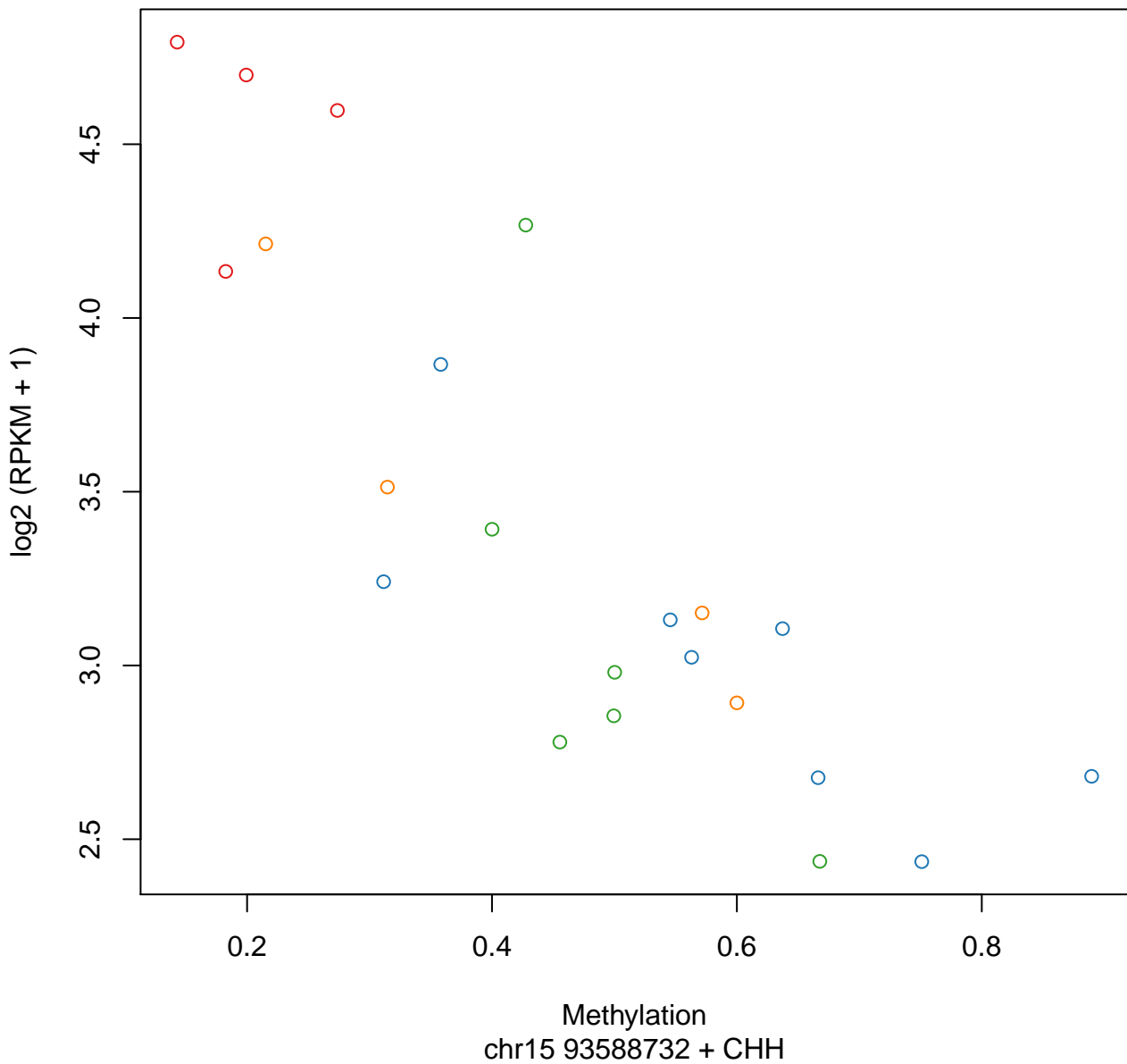
exon ENSE00001863256.1_1 FDR 0.0026
FBLN2

Methylation
chr3 13680314 – CHH
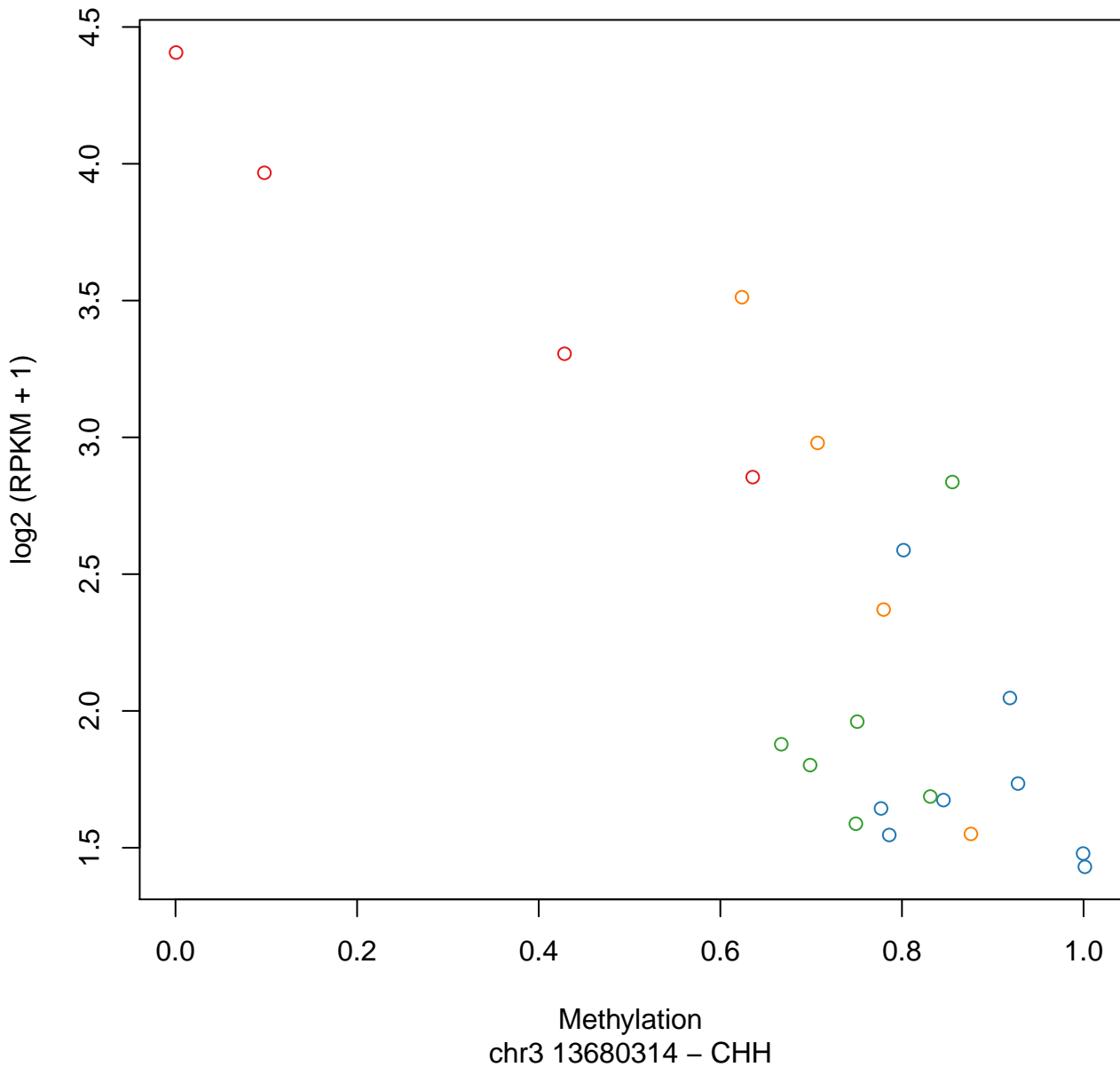
exon ENSE00002451737.1_1 FDR 0.00177
RGMA

log2 (RPKM + 1)

Methylation
chr15 93588732 + CHH
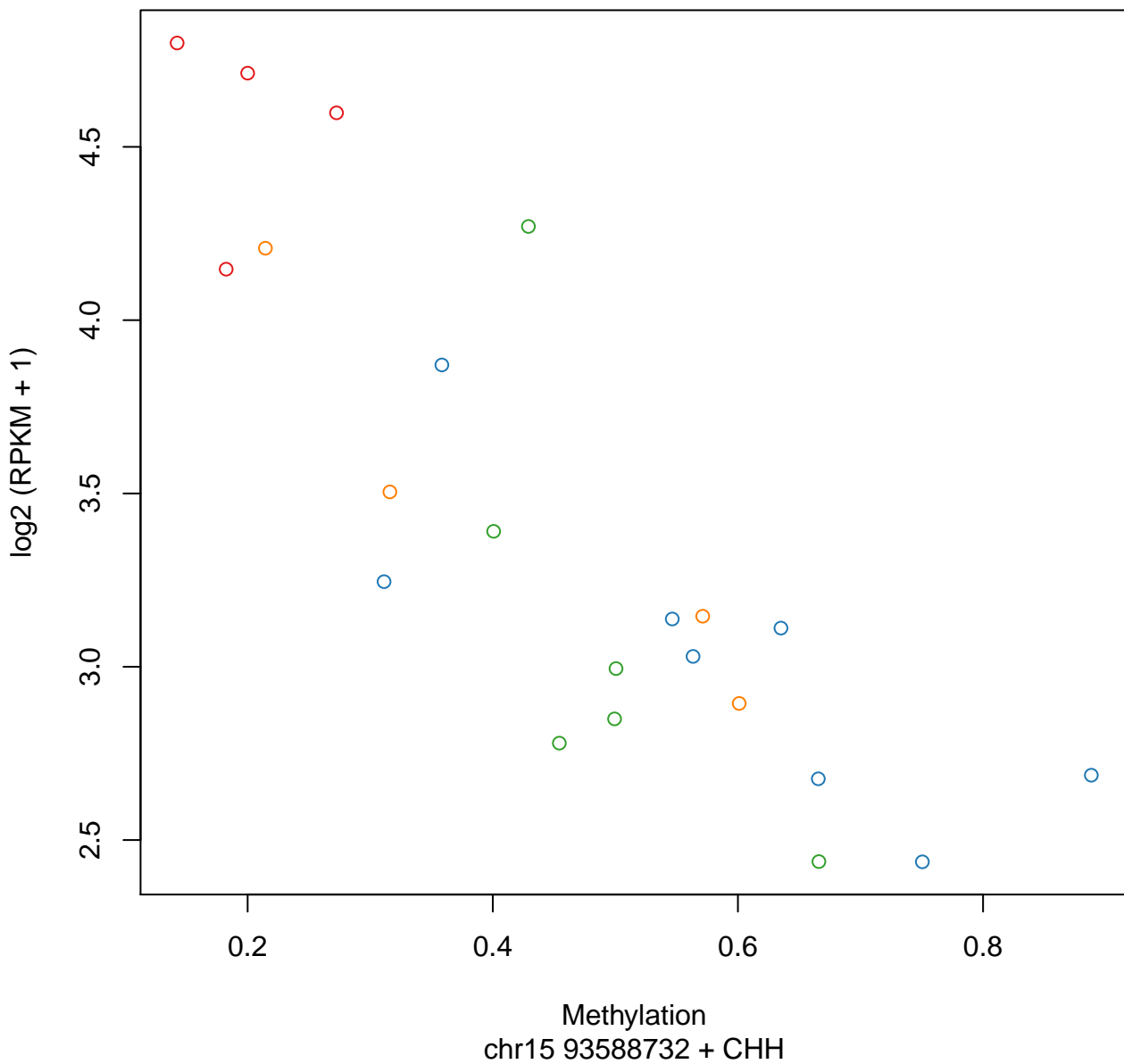
exon ENSE00002476975.1_1 FDR 0.00211
RGMA

log2 (RPKM + 1)

Methylation
chr15 93588732 + CHH
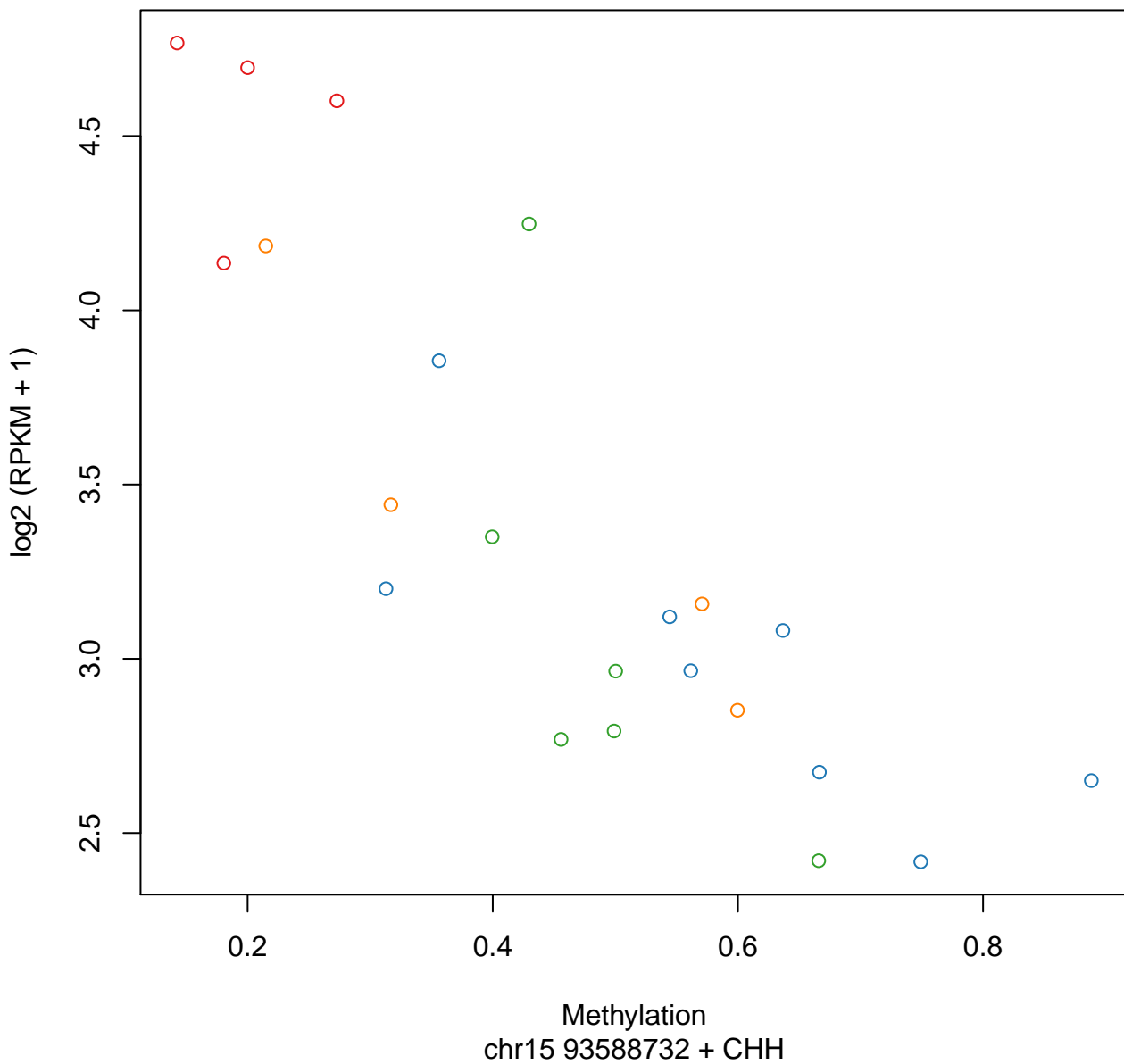
exon ENSE00001863074.1_1 FDR 0.00584
STAB1

log2 (RPKM + 1)

Methylation
chr3 52555238 + CHG
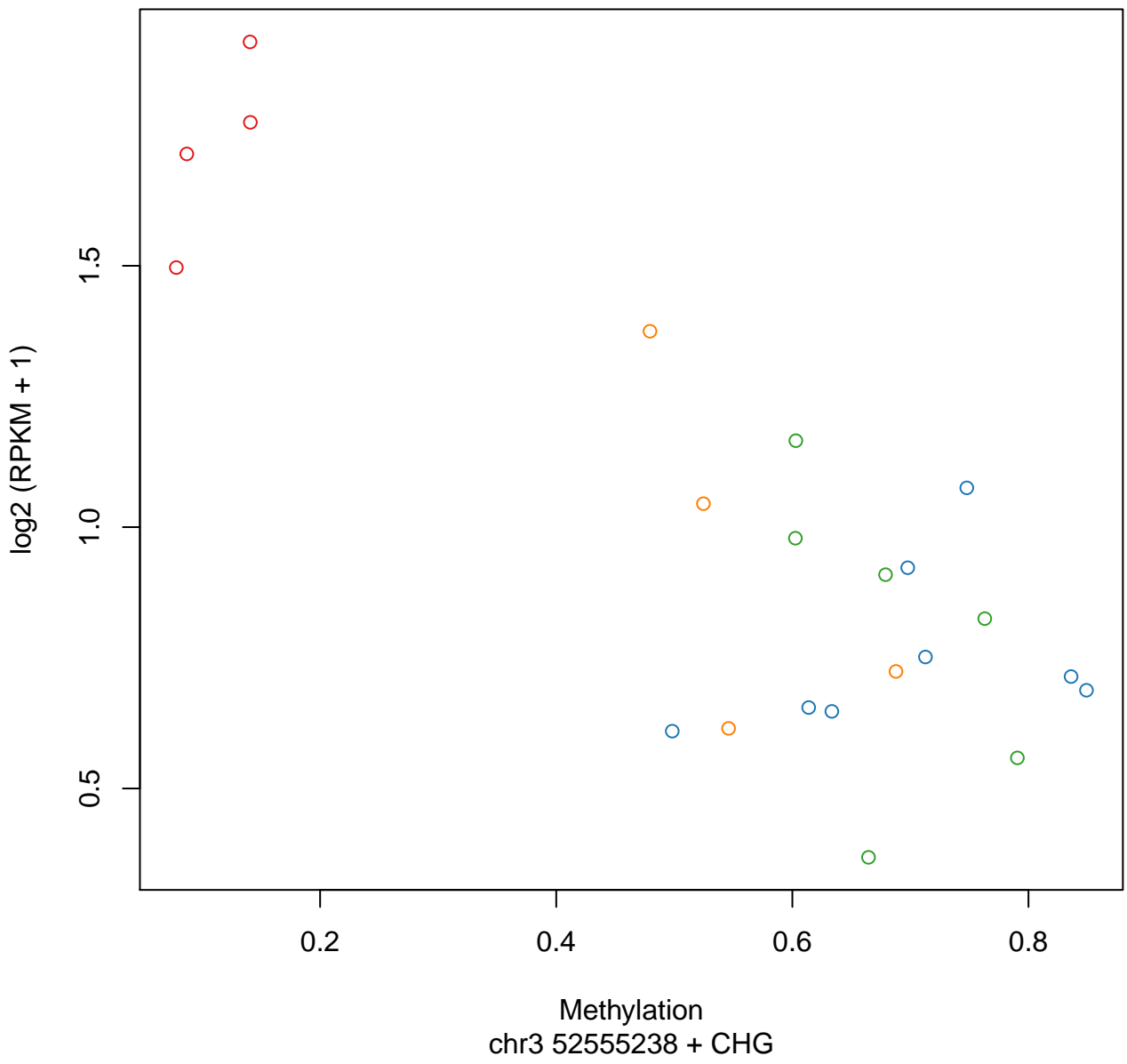
exon ENSE00001937579.1_1 FDR 0.00636
TF

log2 (RPKM + 1)

Methylation
chr3 133467992 − CHH
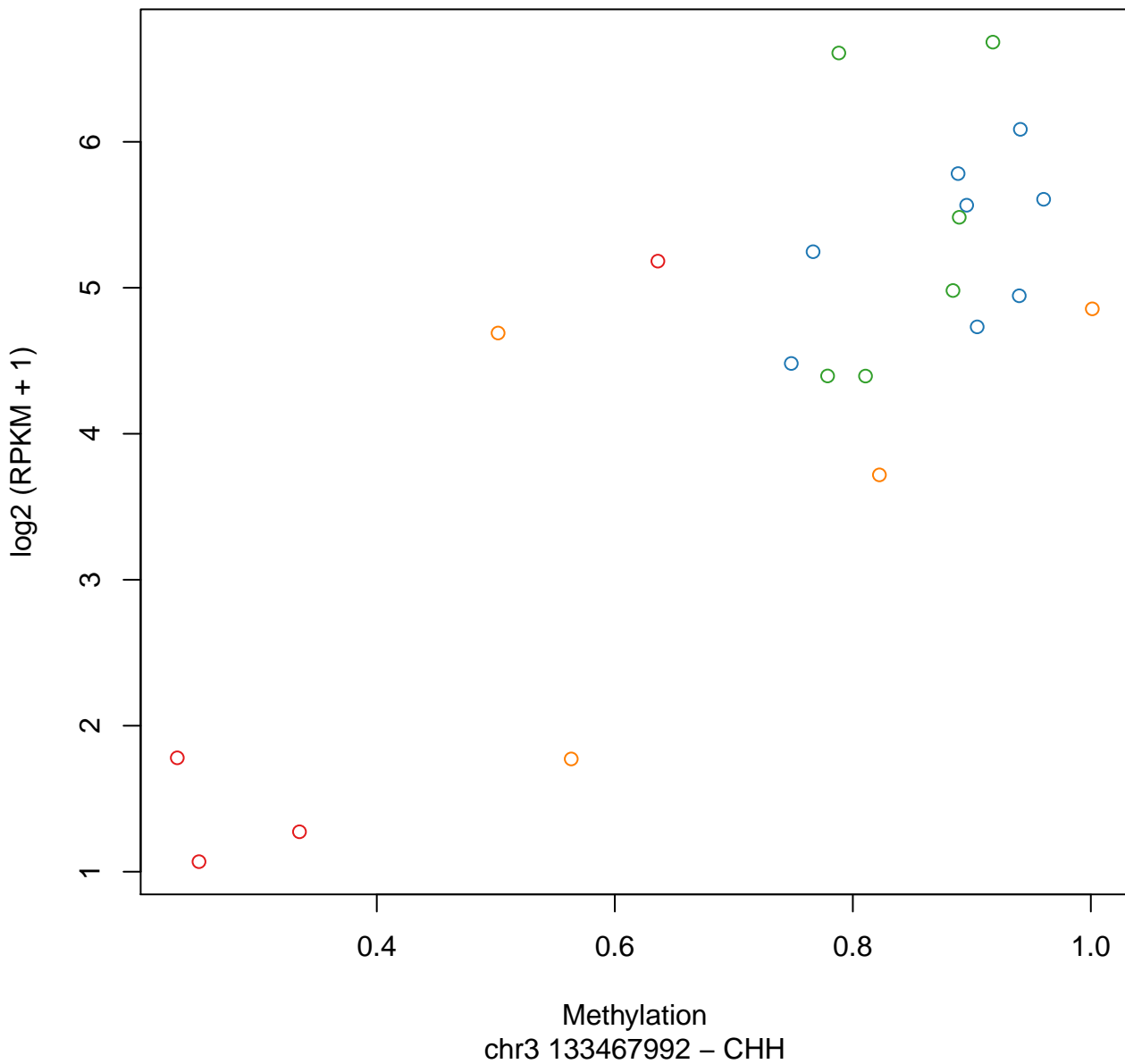
exon ENSE00003596005.1_1 FDR 0.00584
PDGFRA

log2 (RPKM + 1)

Methylation
chr4 55156578 + CHH
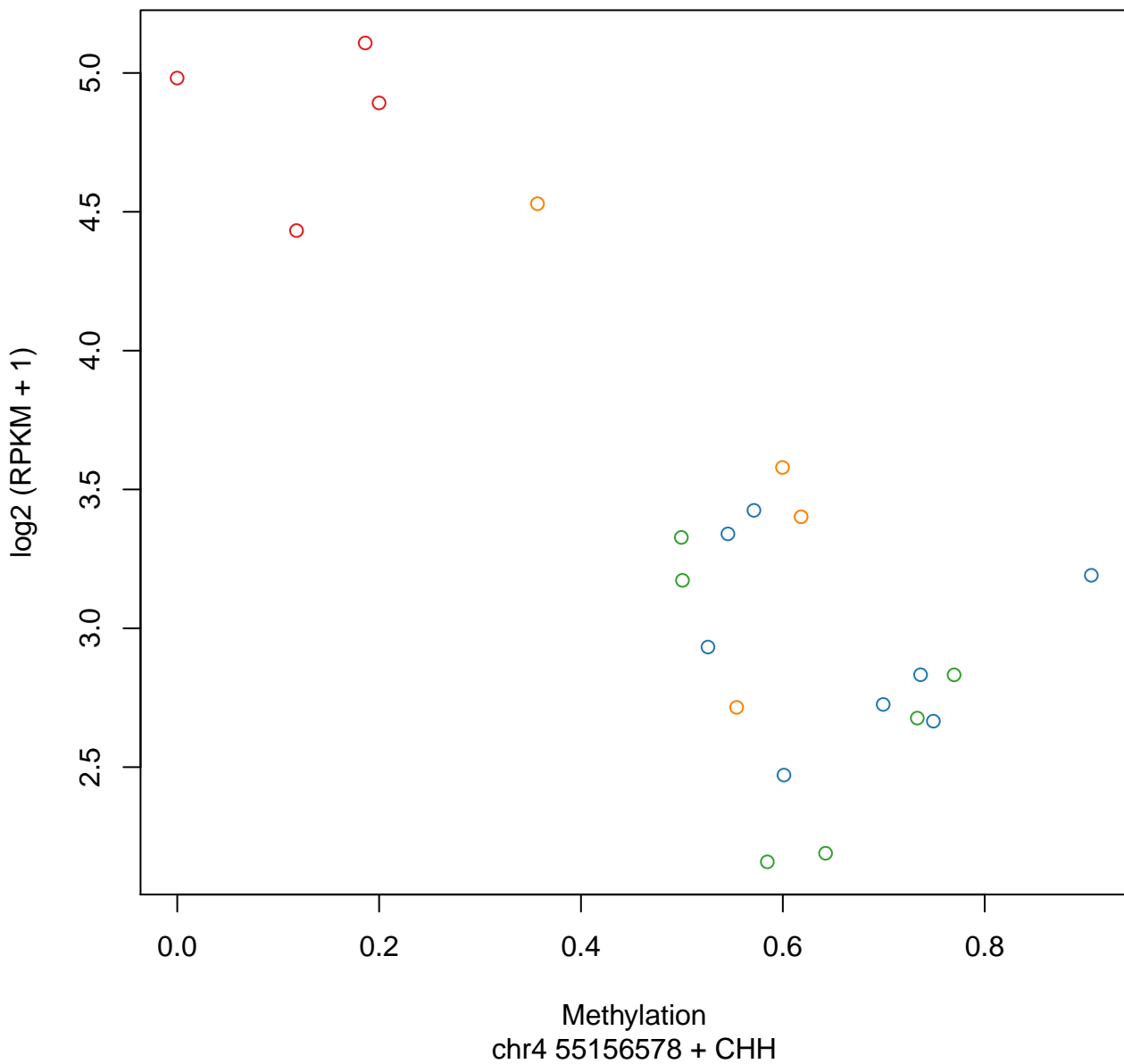
exon ENSE00001891405.1_1 FDR 0.00831
LIMS2

Methylation
chr2 128414319 − CHH
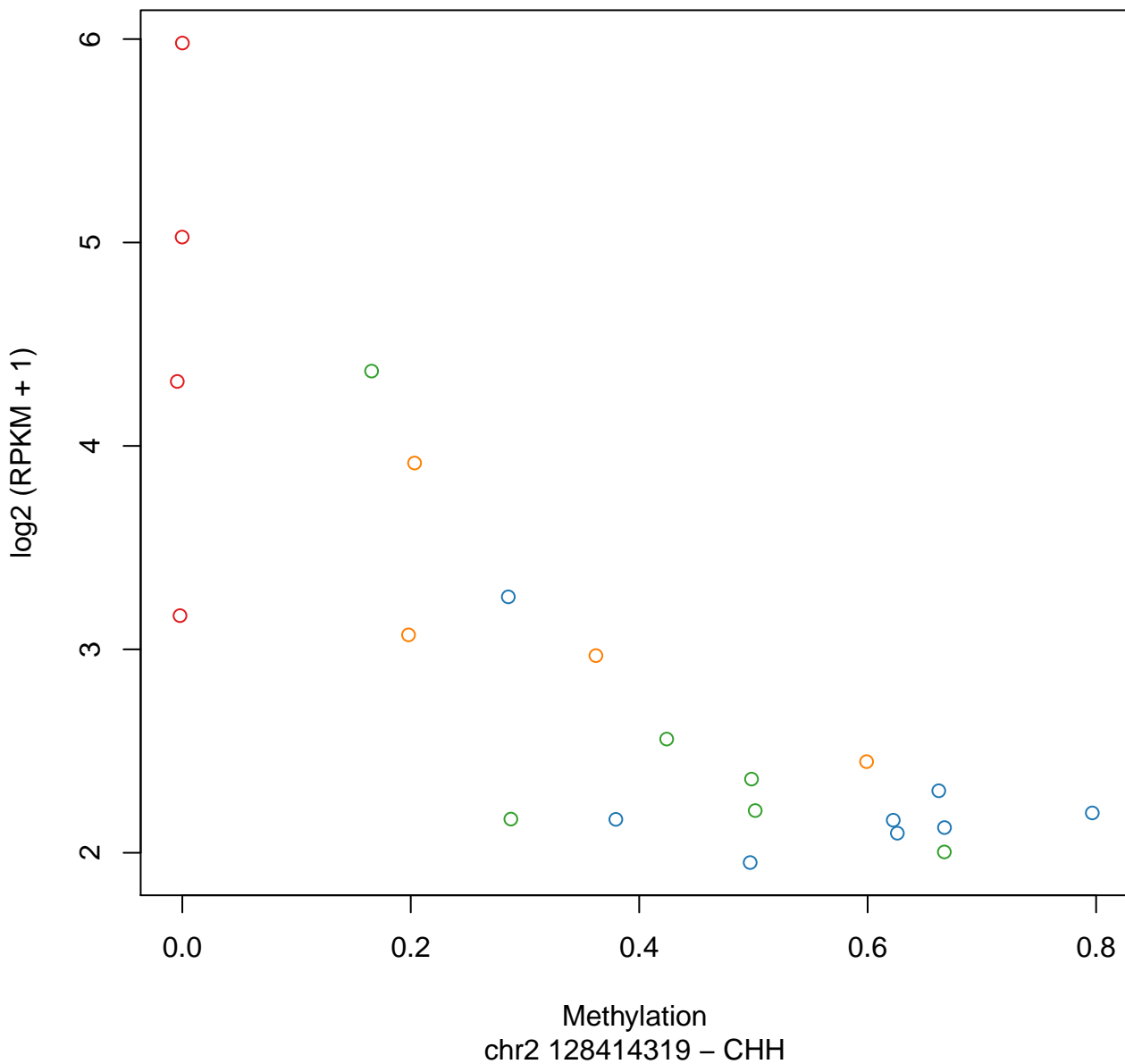
exon ENSE00001925266.1_1 FDR 0.00653
ASIC4

Methylation
chr2 220399277 + CHH
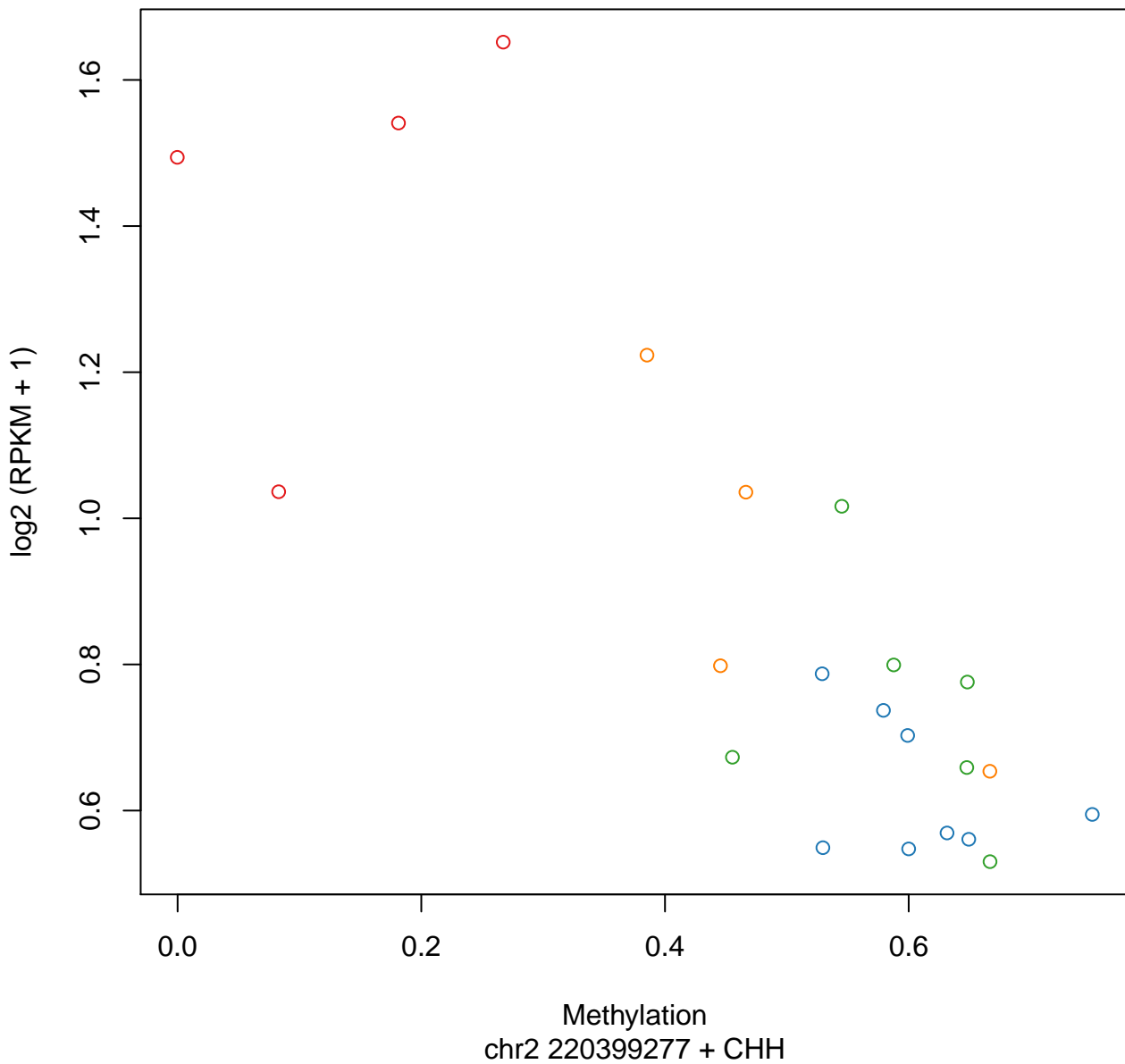
exon ENSE00001914149.1_1 FDR 0.0129
CERCAM

log2 (RPKM + 1)

Methylation
chr9 131184509 + CHH
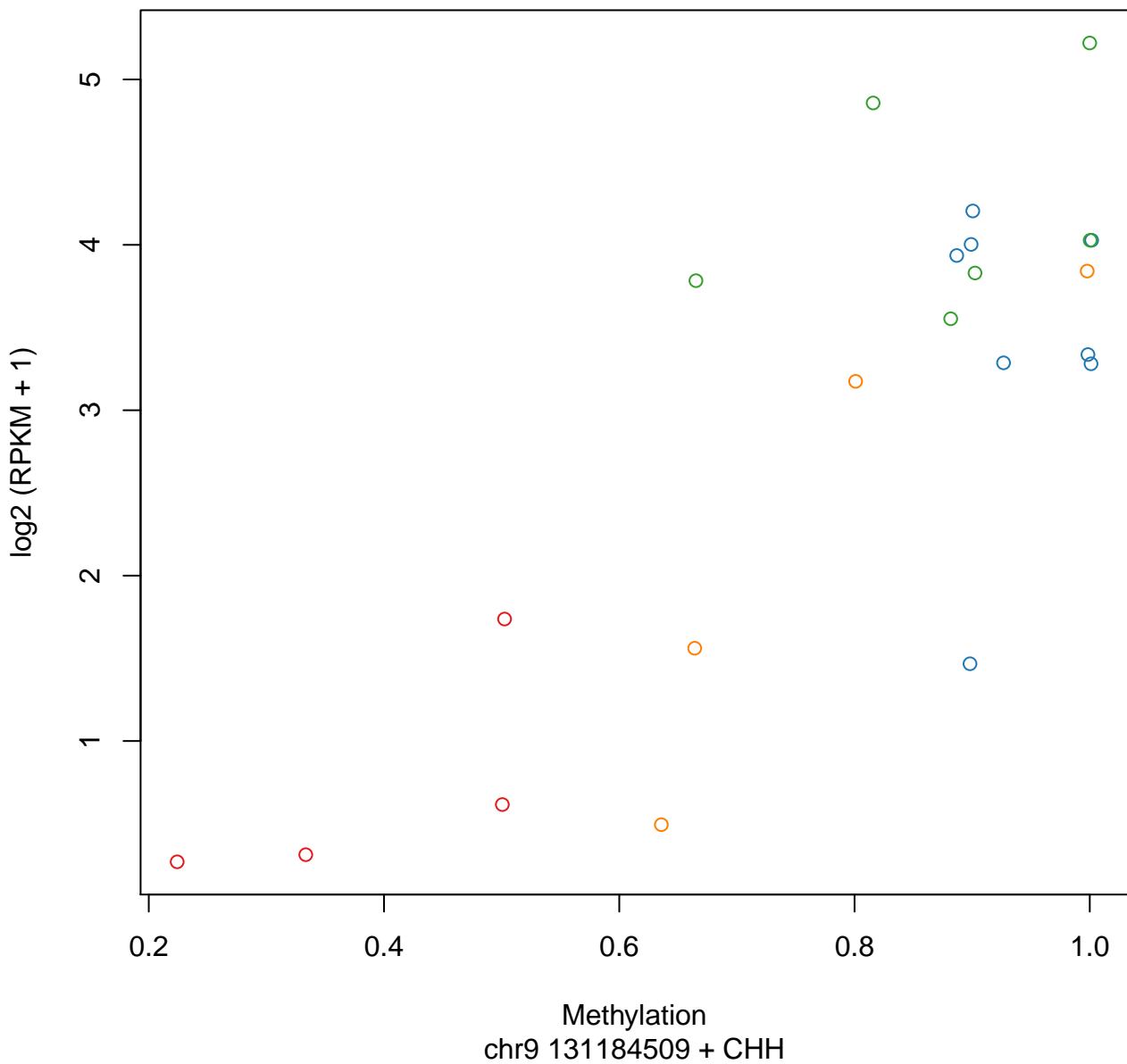
exon ENSE00001761877.1_1 FDR 0.013
CERCAM

log2 (RPKM + 1)

Methylation
chr9 131184509 + CHH
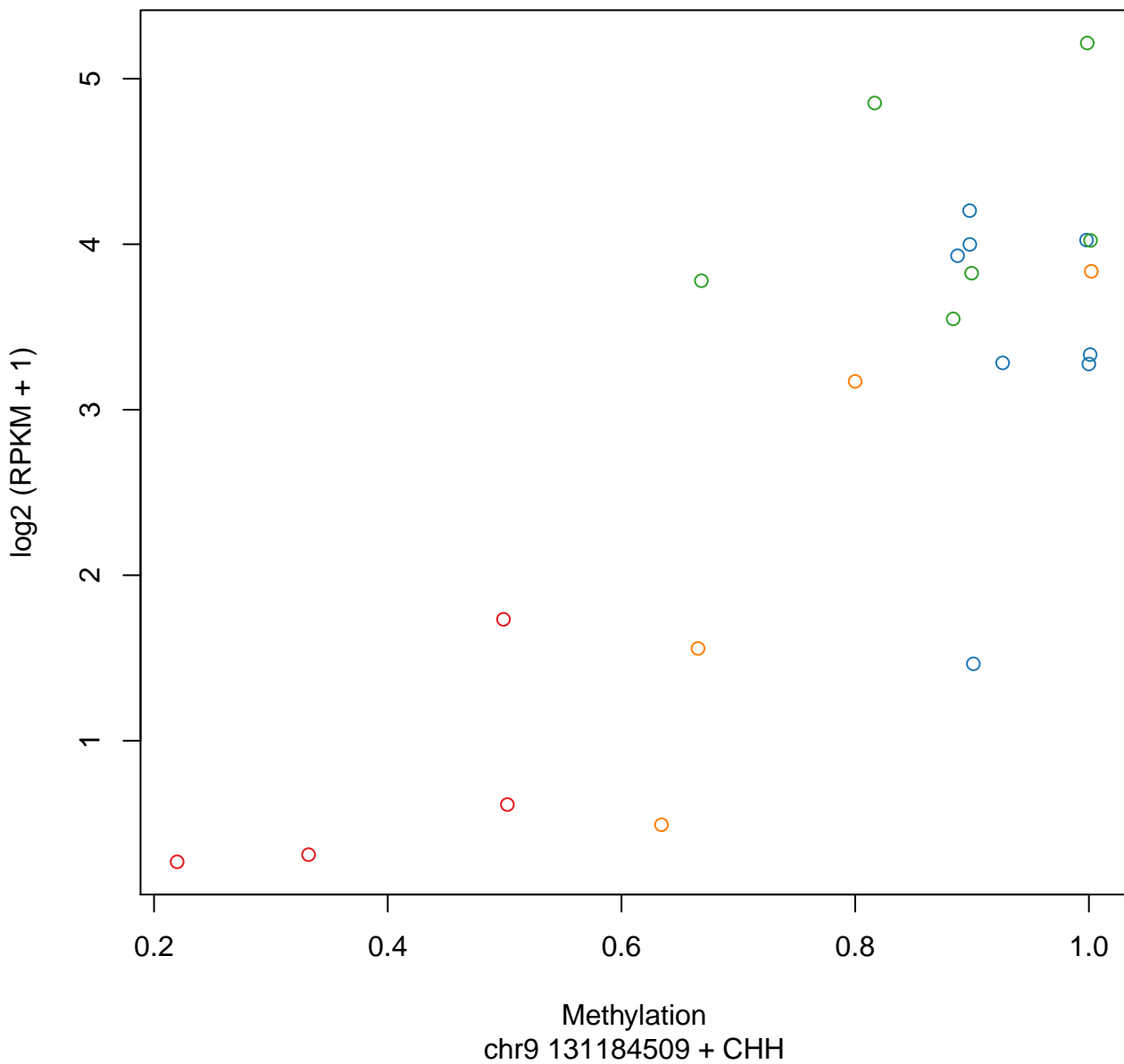
exon ENSE00003742644.1_1 FDR 0.00928
FLJ16779

log2 (RPKM + 1)

Methylation
chr20 61886474 − CHG
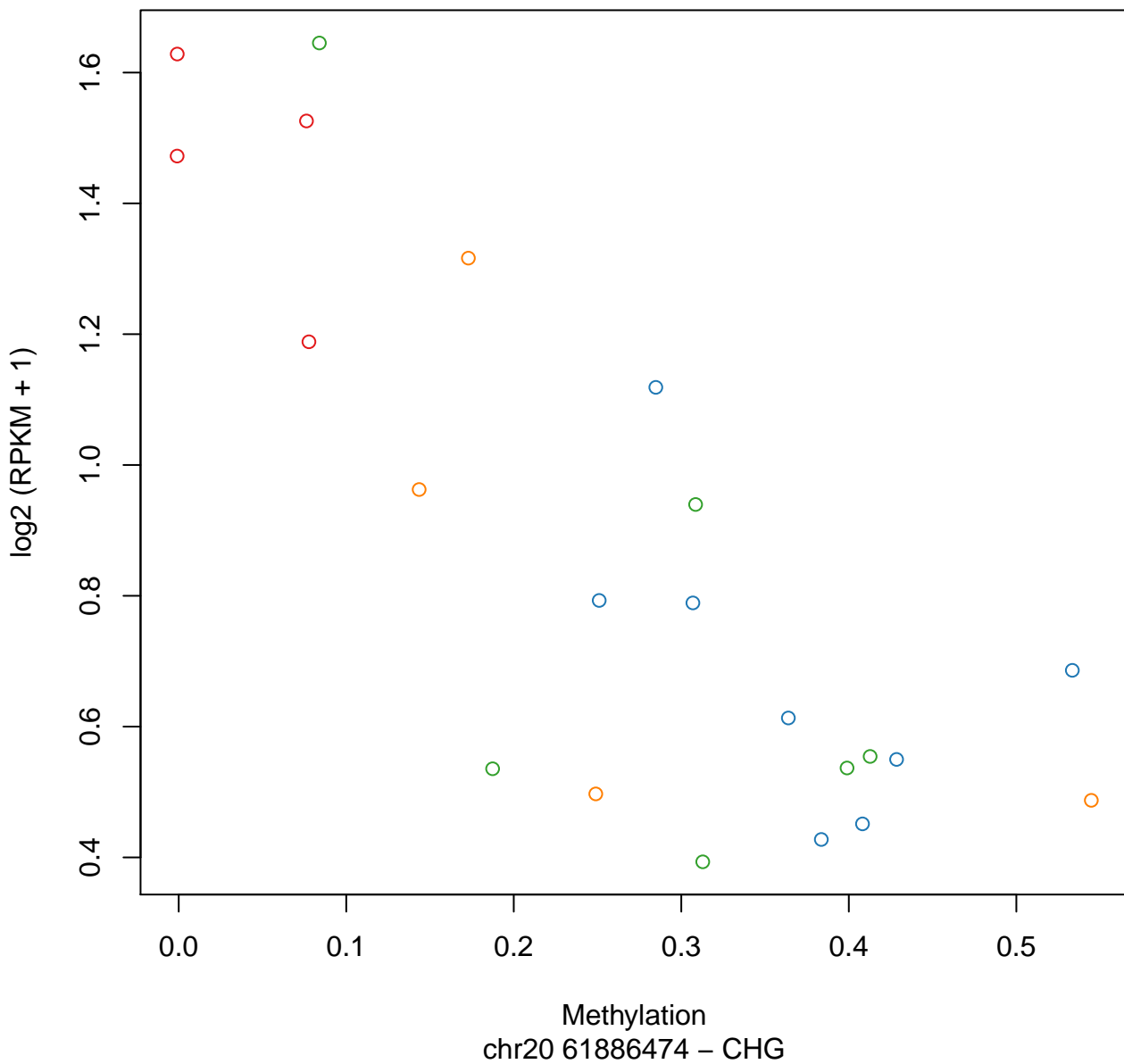
exon ENSE00001868090.1_1 FDR 0.0121
NKAIN4

log2 (RPKM + 1)

Methylation
chr20 61880685 + CHH
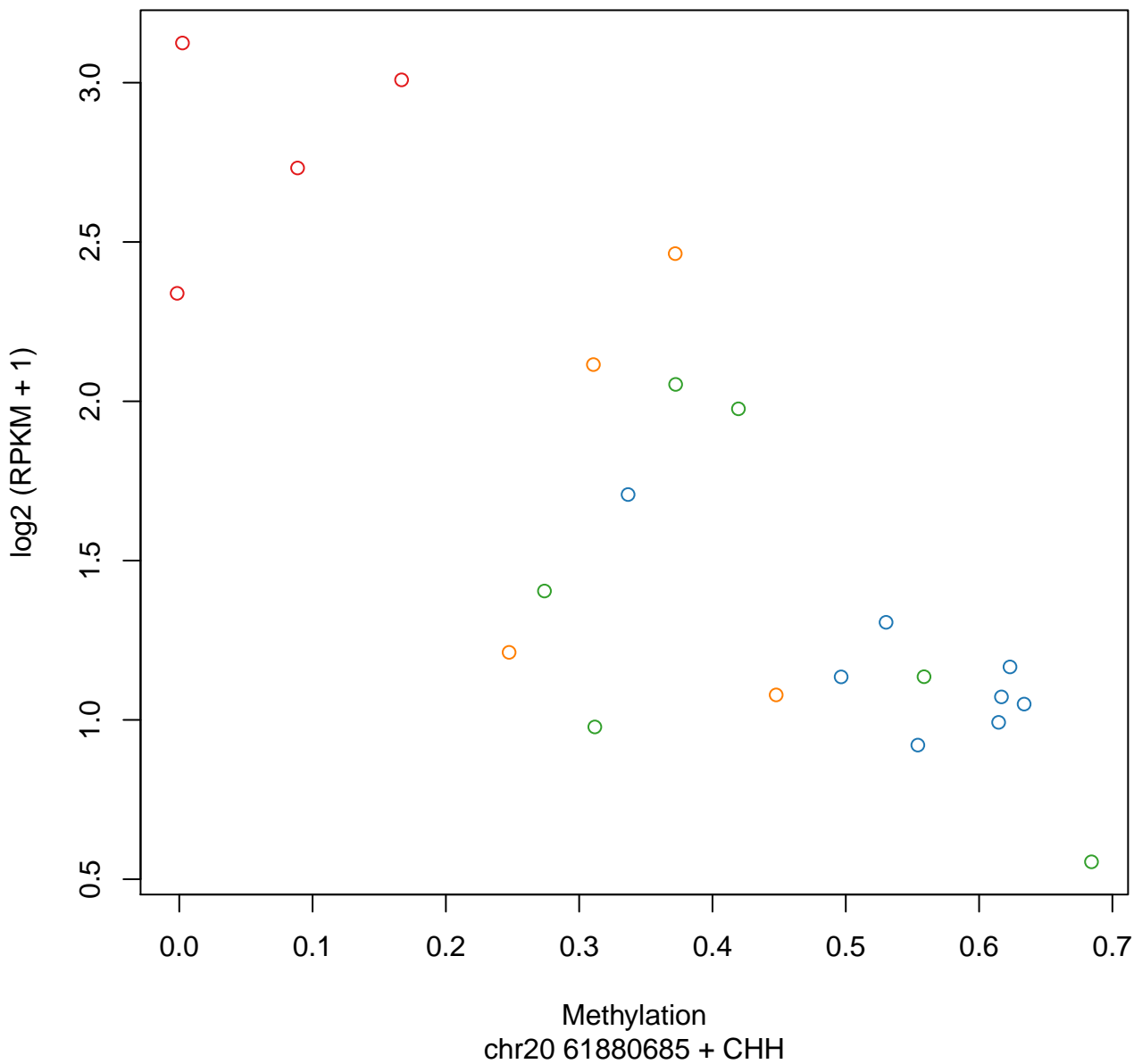
exon ENSE00001864162.1_1 FDR 0.0122
NKAIN4

Methylation
chr20 61880685 + CHH

log2 (RPKM + 1)
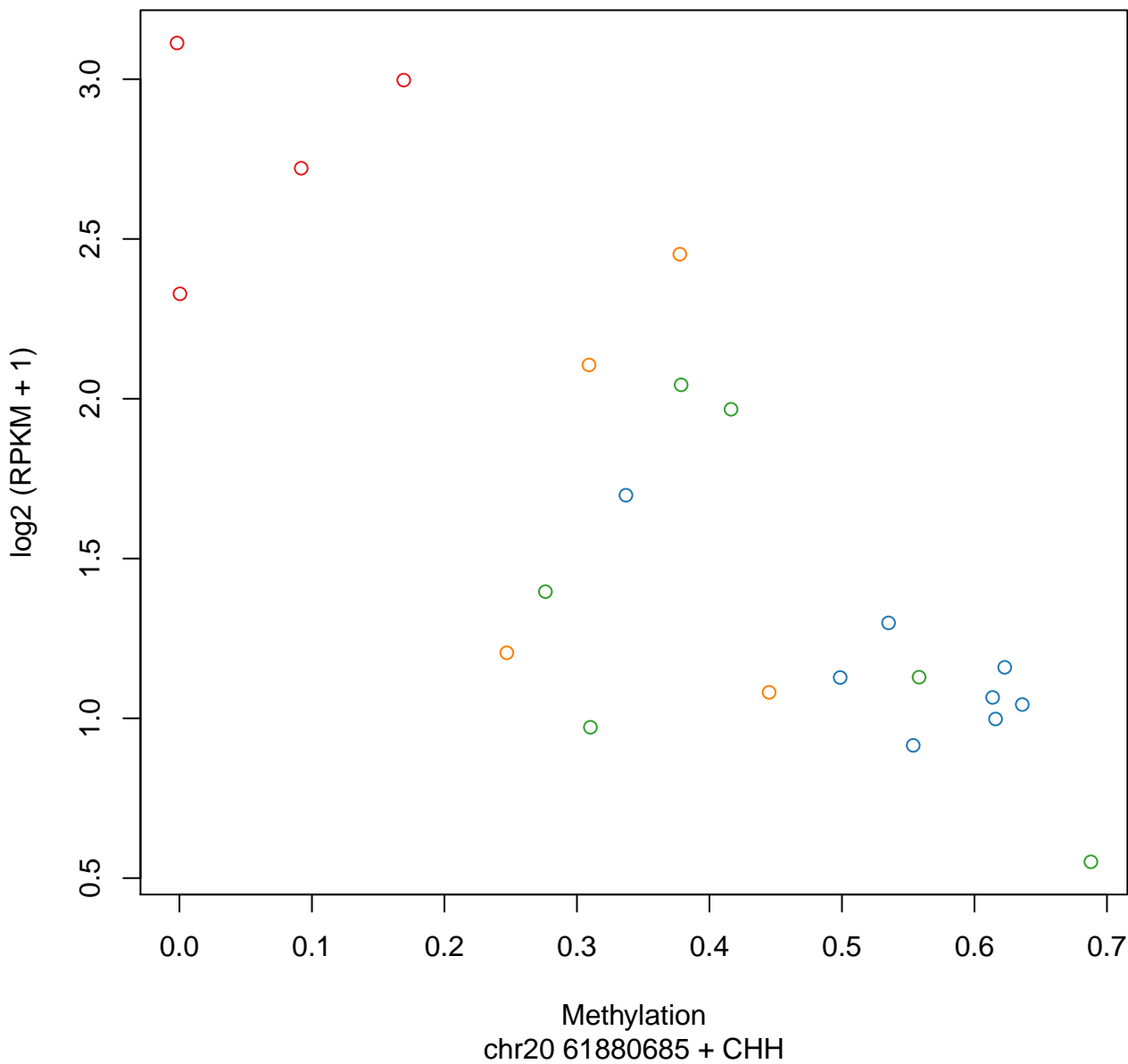
exon ENSE00002459935.1_1 FDR 0.0117
RGMA

log2 (RPKM + 1)

Methylation
chr15 93588732 + CHH
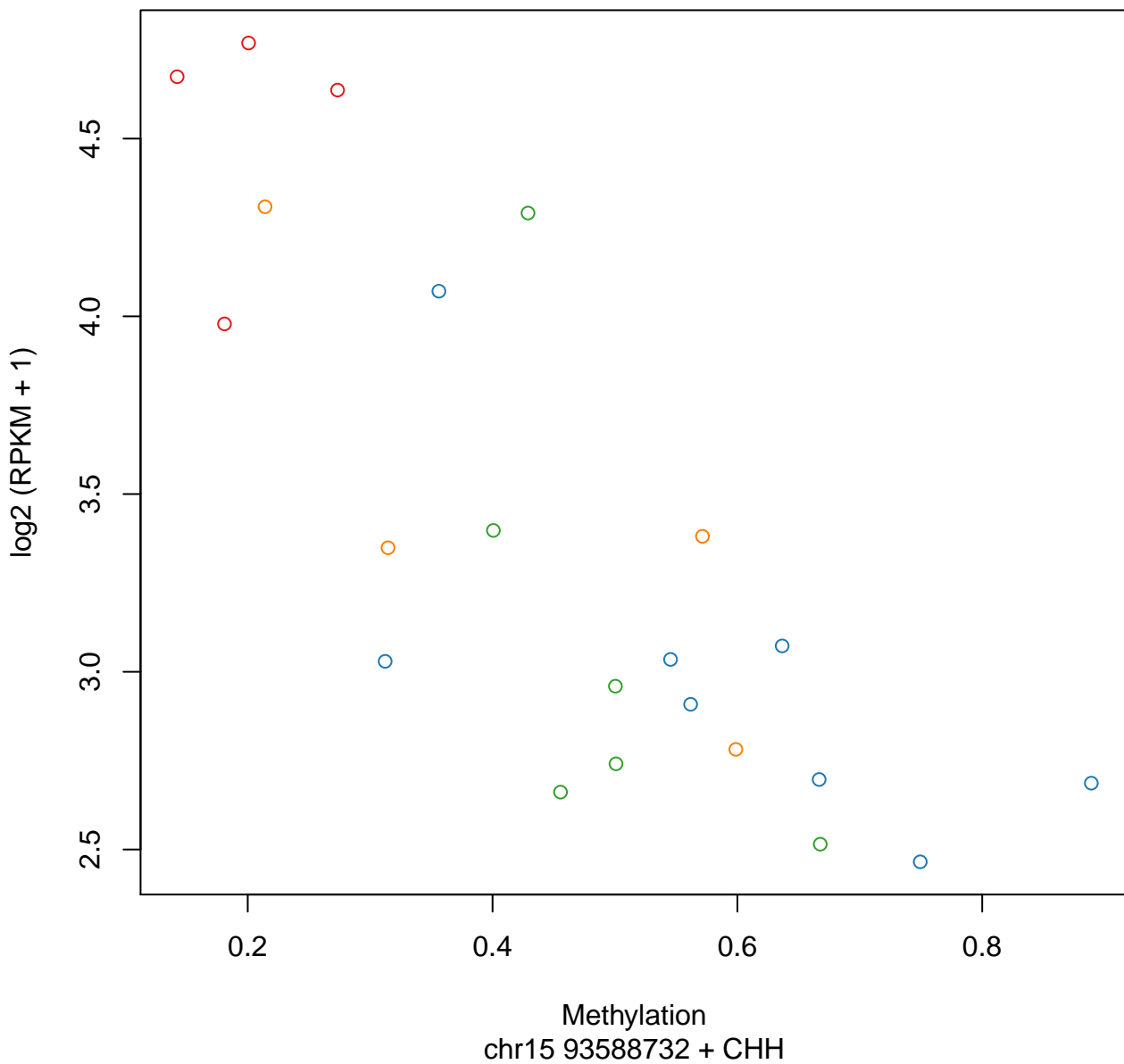
exon ENSE00003630378.1_1 FDR 0.0117
RGMA

log2 (RPKM + 1)

Methylation
chr15 93588732 + CHH
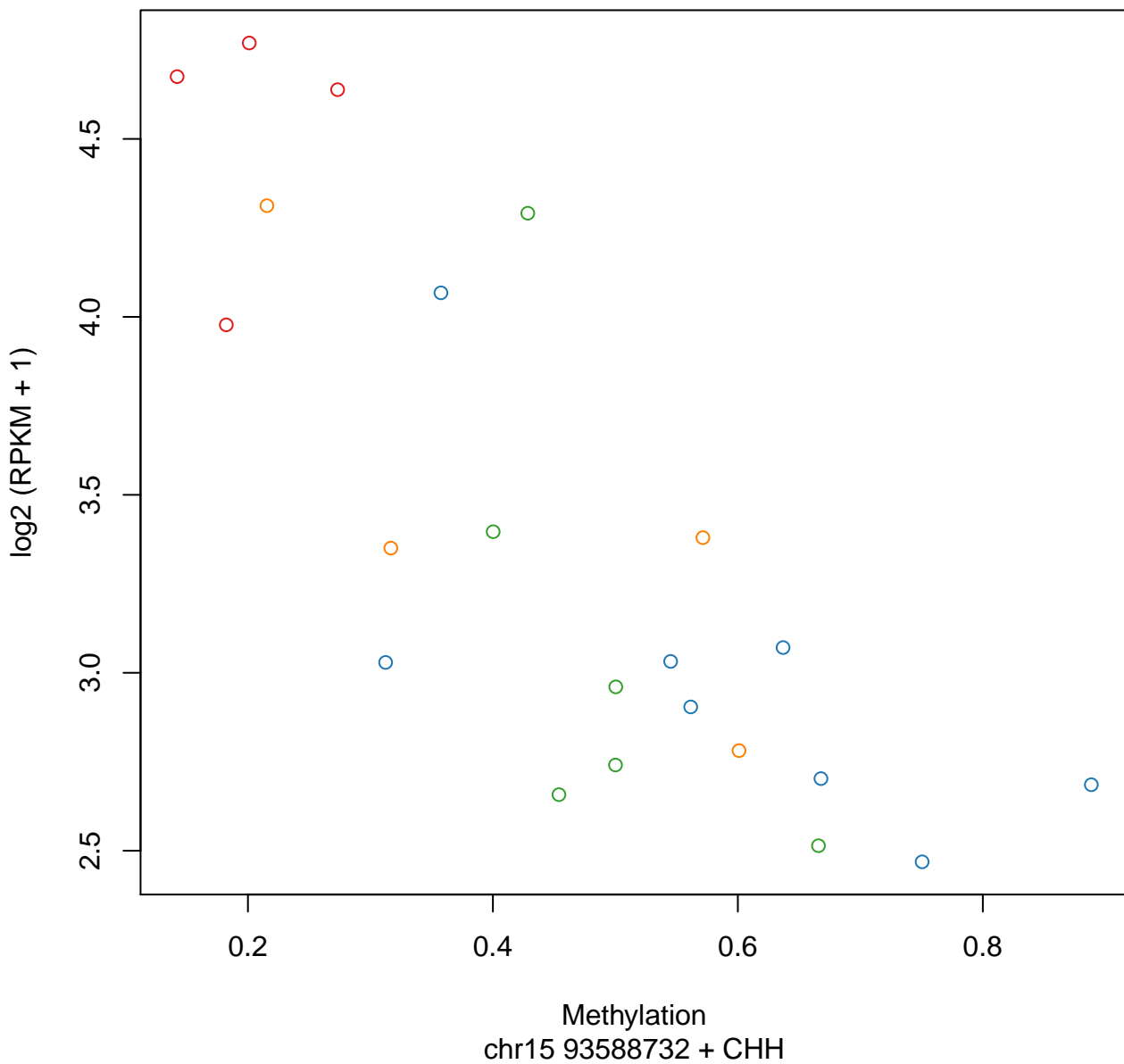
exon ENSE00002296152.1_1 FDR 0.0117
RGMA

log2 (RPKM + 1)

Methylation
chr15 93588732 + CHH
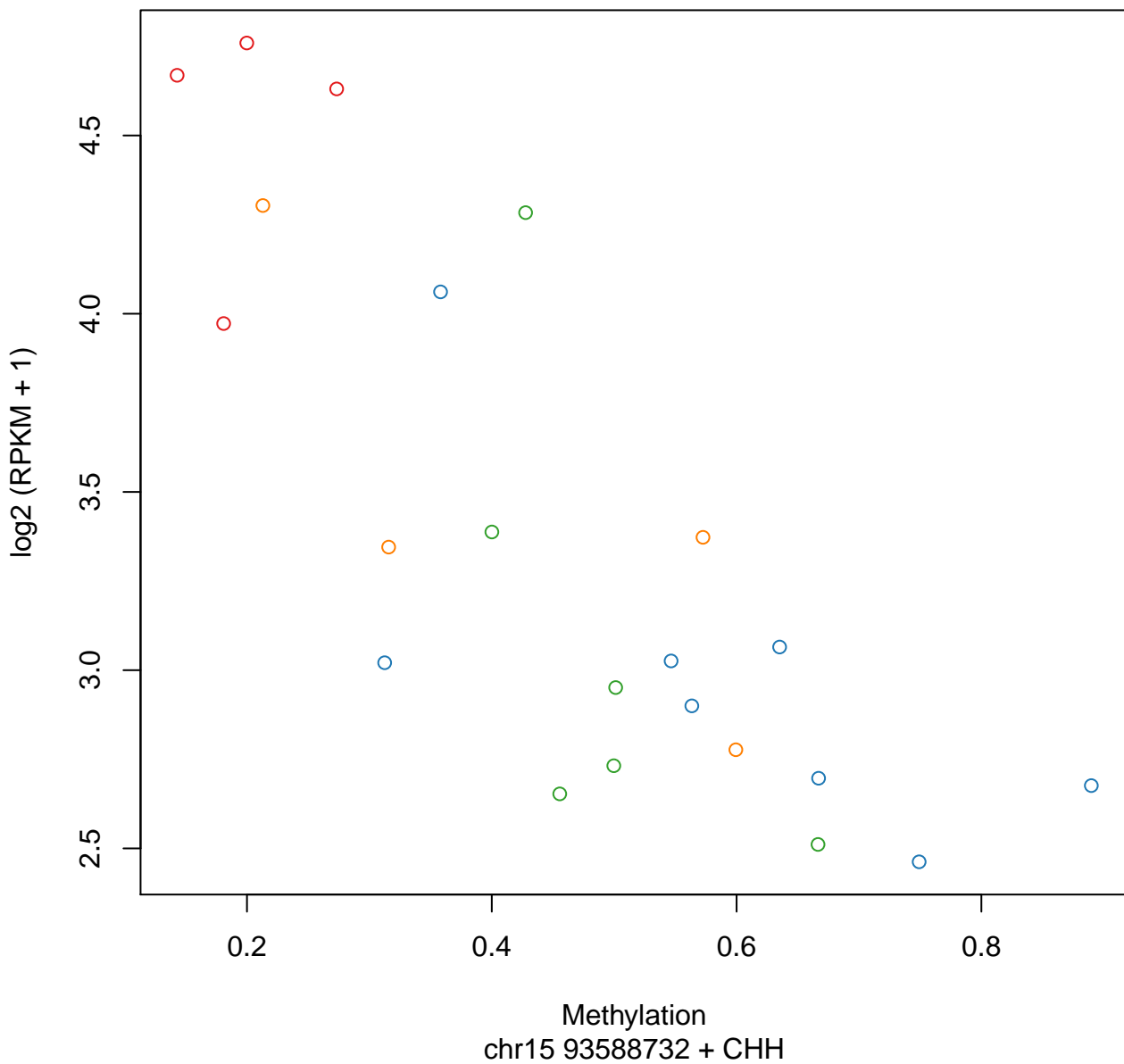
exon ENSE00001042401.1_1 FDR 0.0246
NOTCH1

log2 (RPKM + 1)

Methylation
chr9 139418619 + CHH
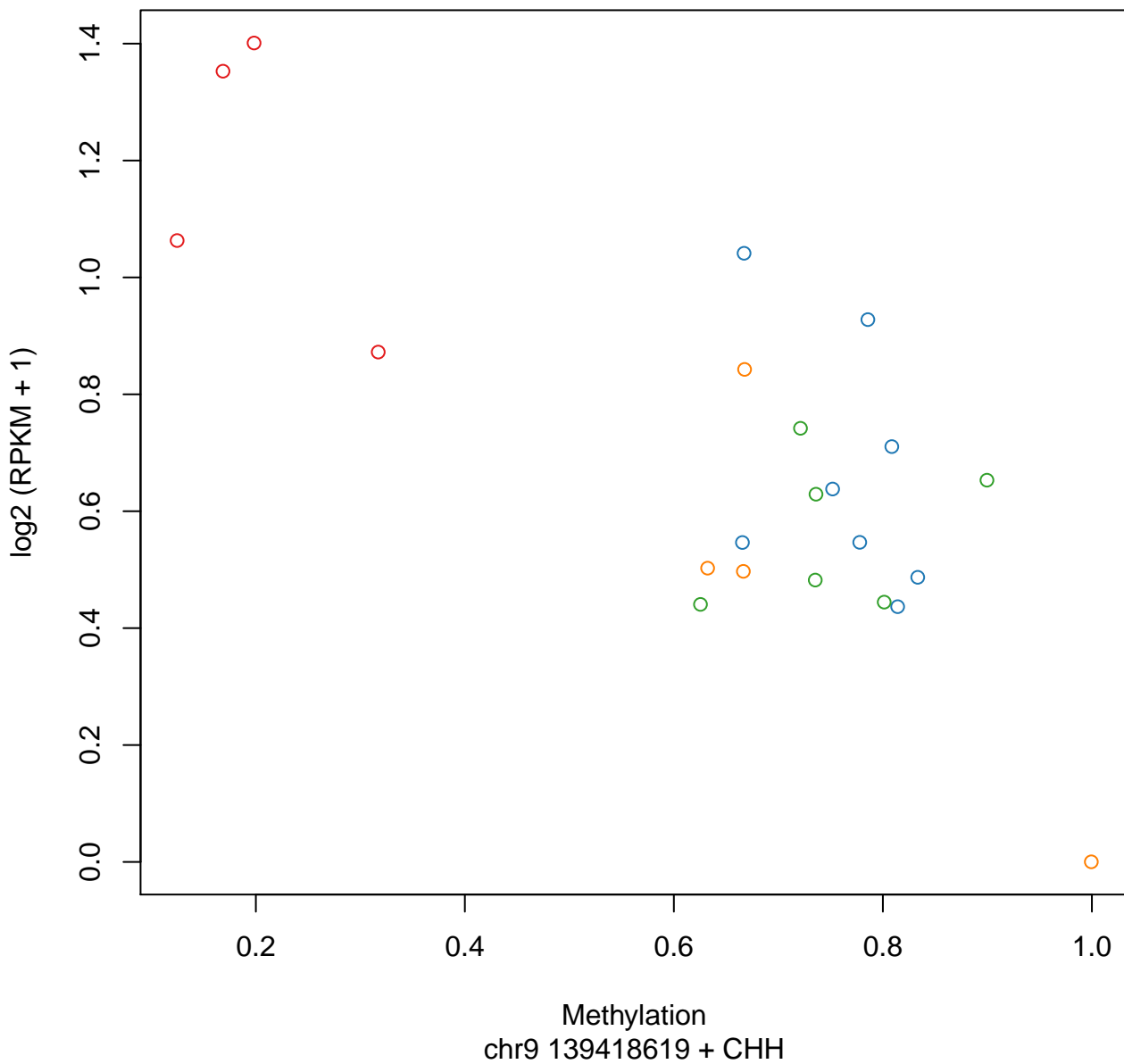
exon ENSE00001424547.1_1 FDR 0.0195
CERCAM

Methylation
chr9 131184509 + CHH
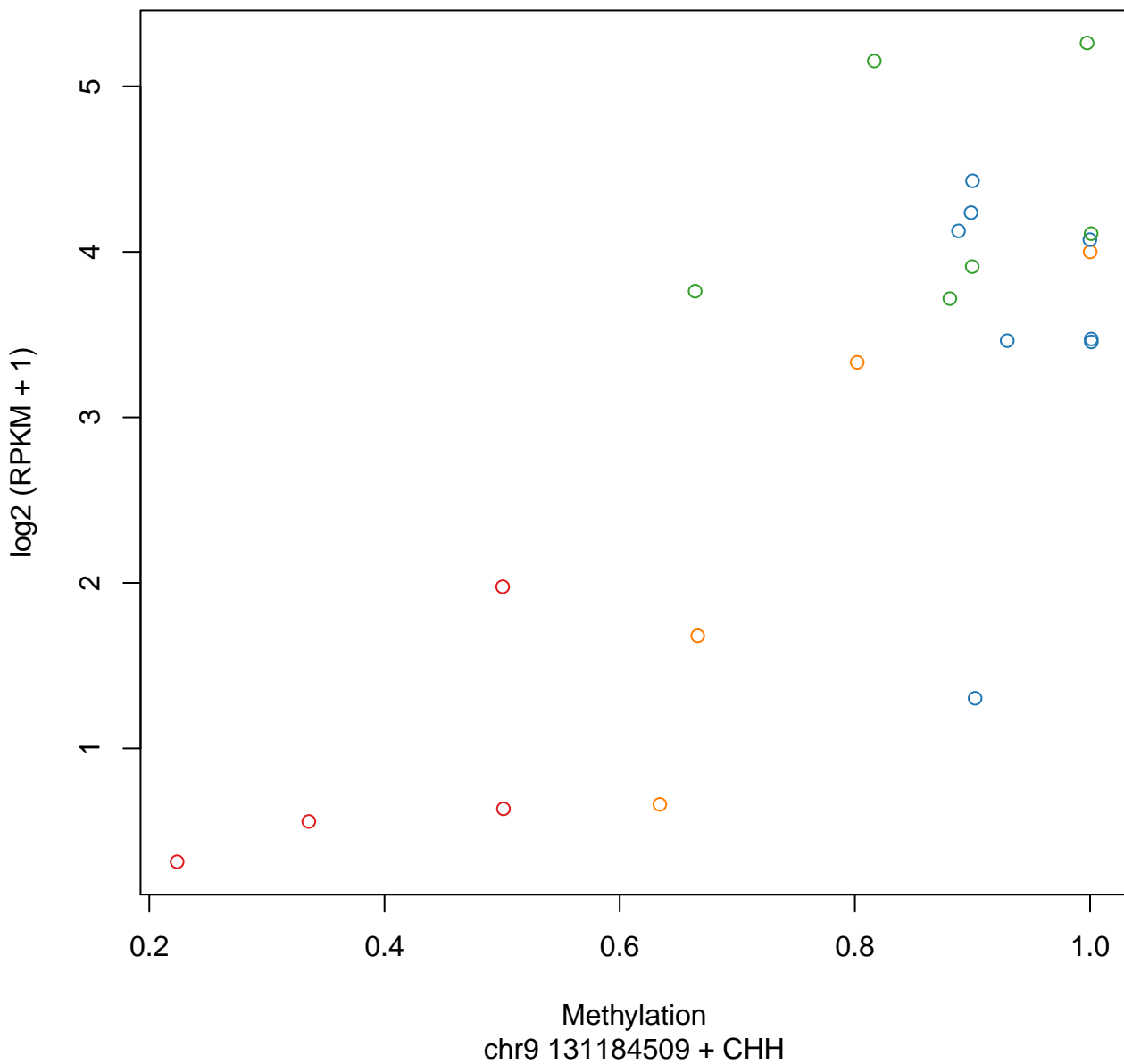
exon ENSE00000967113.5_1 FDR 0.0191
LIMD1

Methylation
chr3 45637580 – CHH

log2 (RPKM + 1)
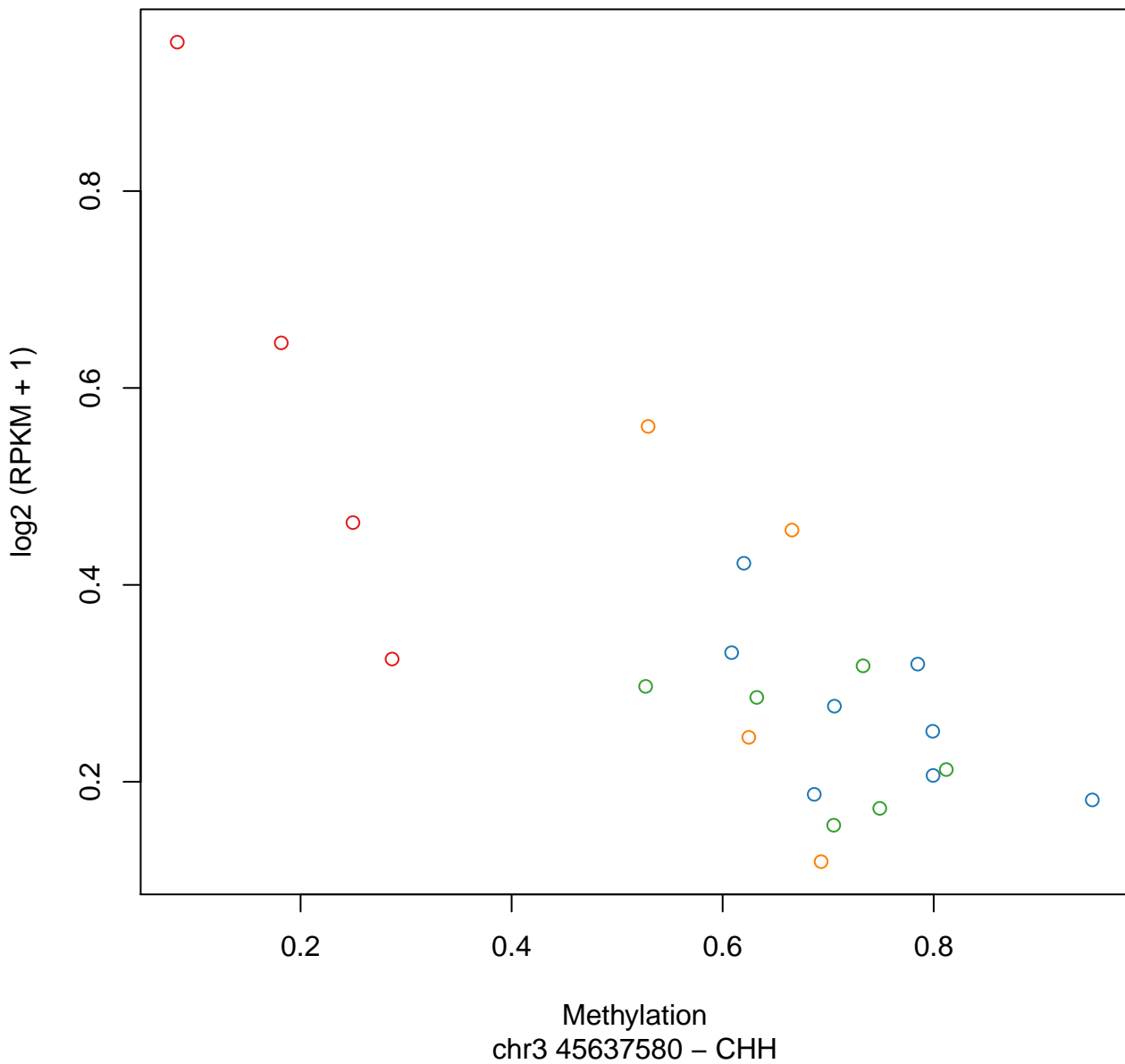
exon ENSE00001945946.1_1 FDR 0.00462
TNC

log2 (RPKM + 1)

Methylation
chr9 117836009 + CHH
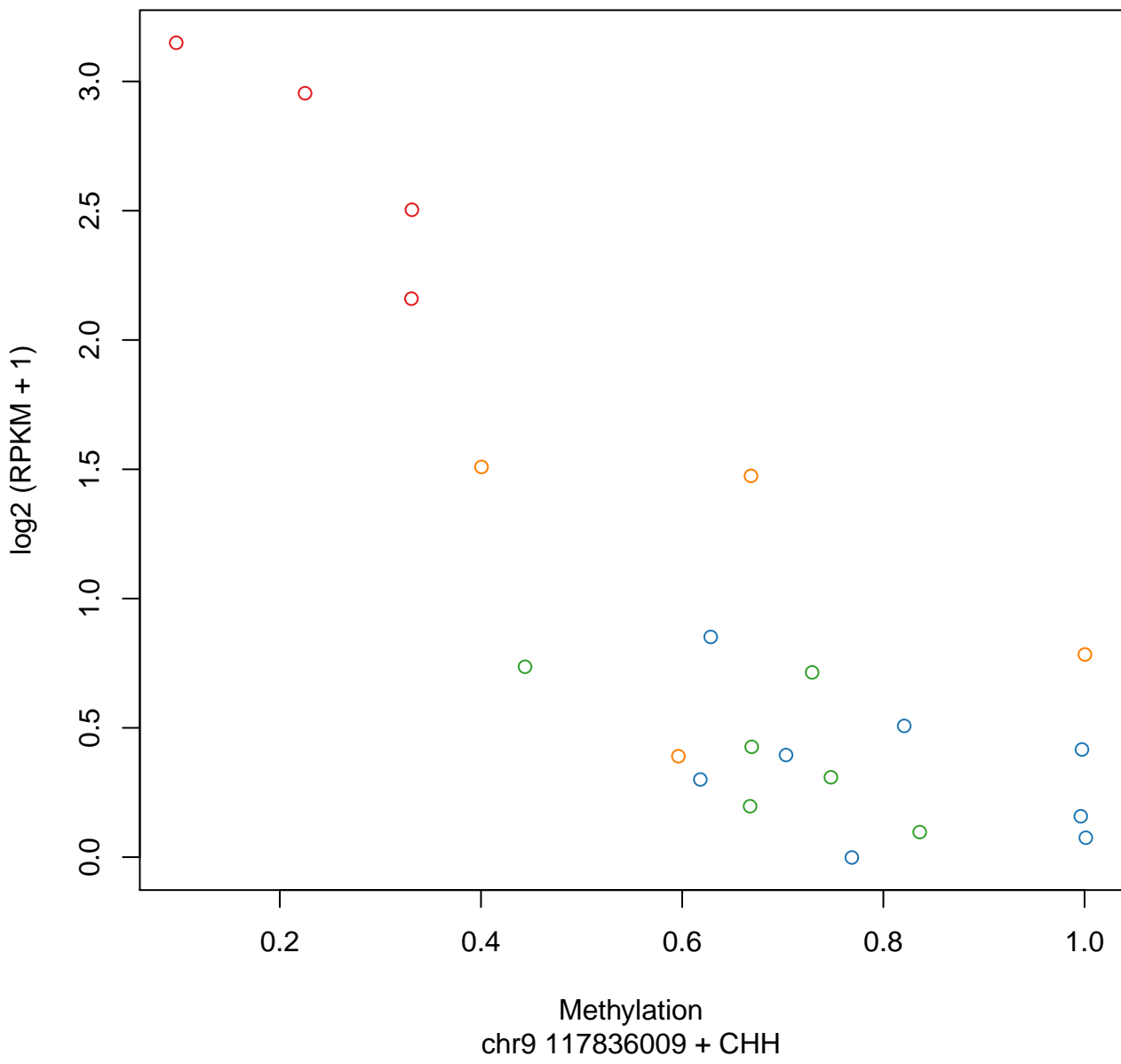
exon ENSE00001720421.1_1 FDR 0.0197
LIMD1

Methylation
chr3 45637580 − CHH
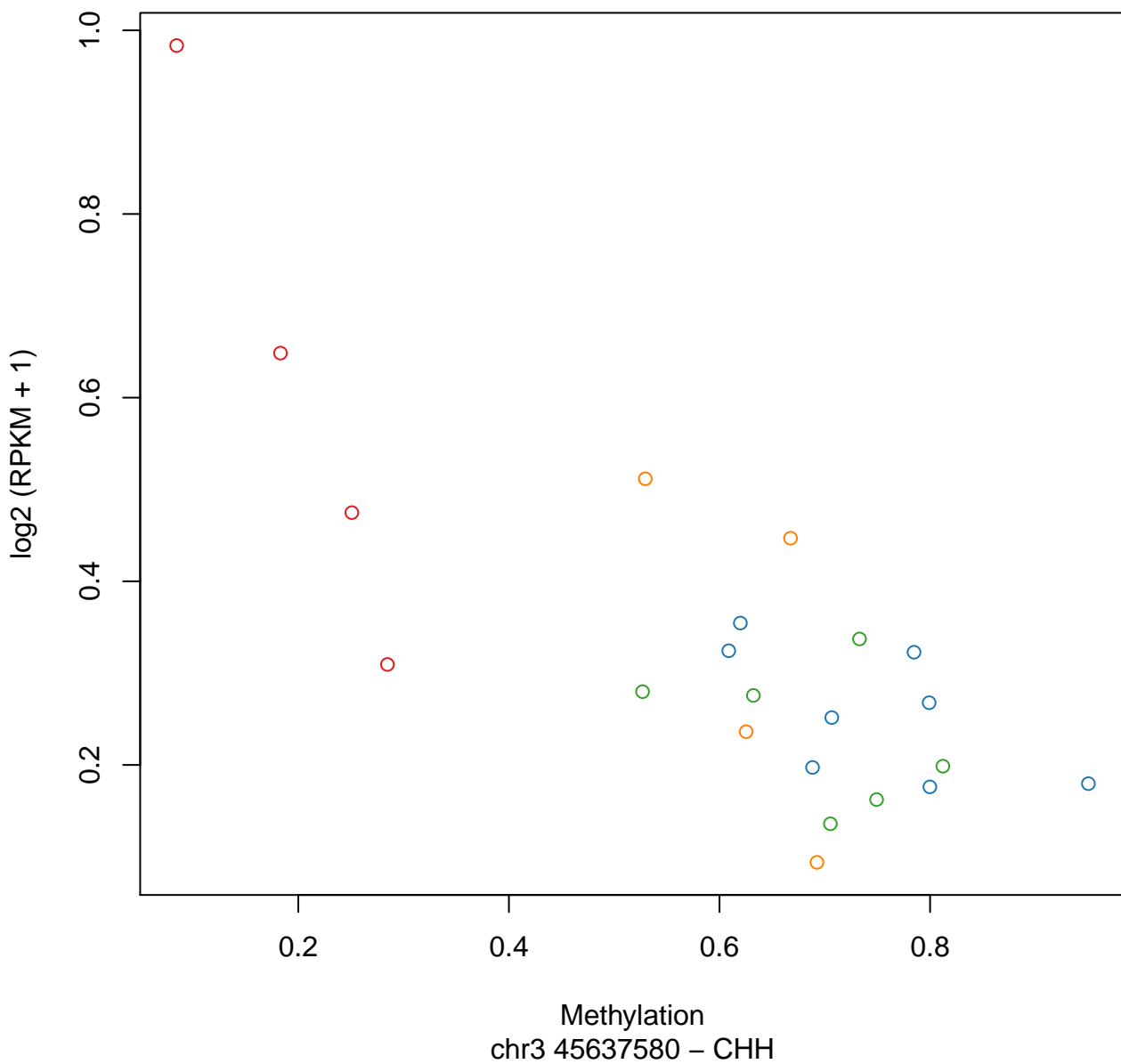
exon ENSE00001422164.1_1 FDR 0.0308
PLAU

Methylation
chr10 75675311 − CHH

log2 (RPKM + 1)
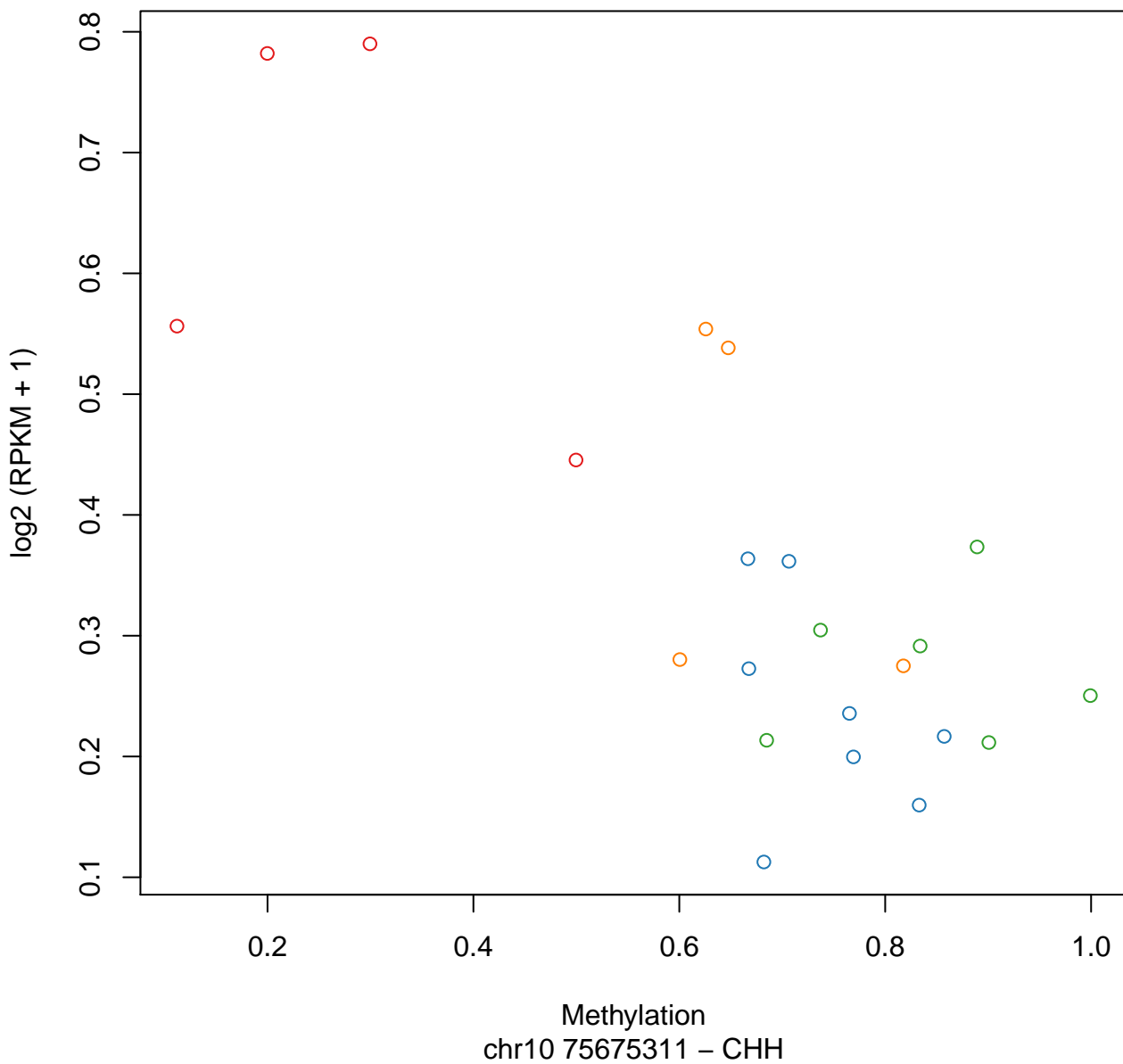
exon ENSE00001892698.1_1 FDR 0.0308
PLAU

Methylation
chr10 75675311 − CHH
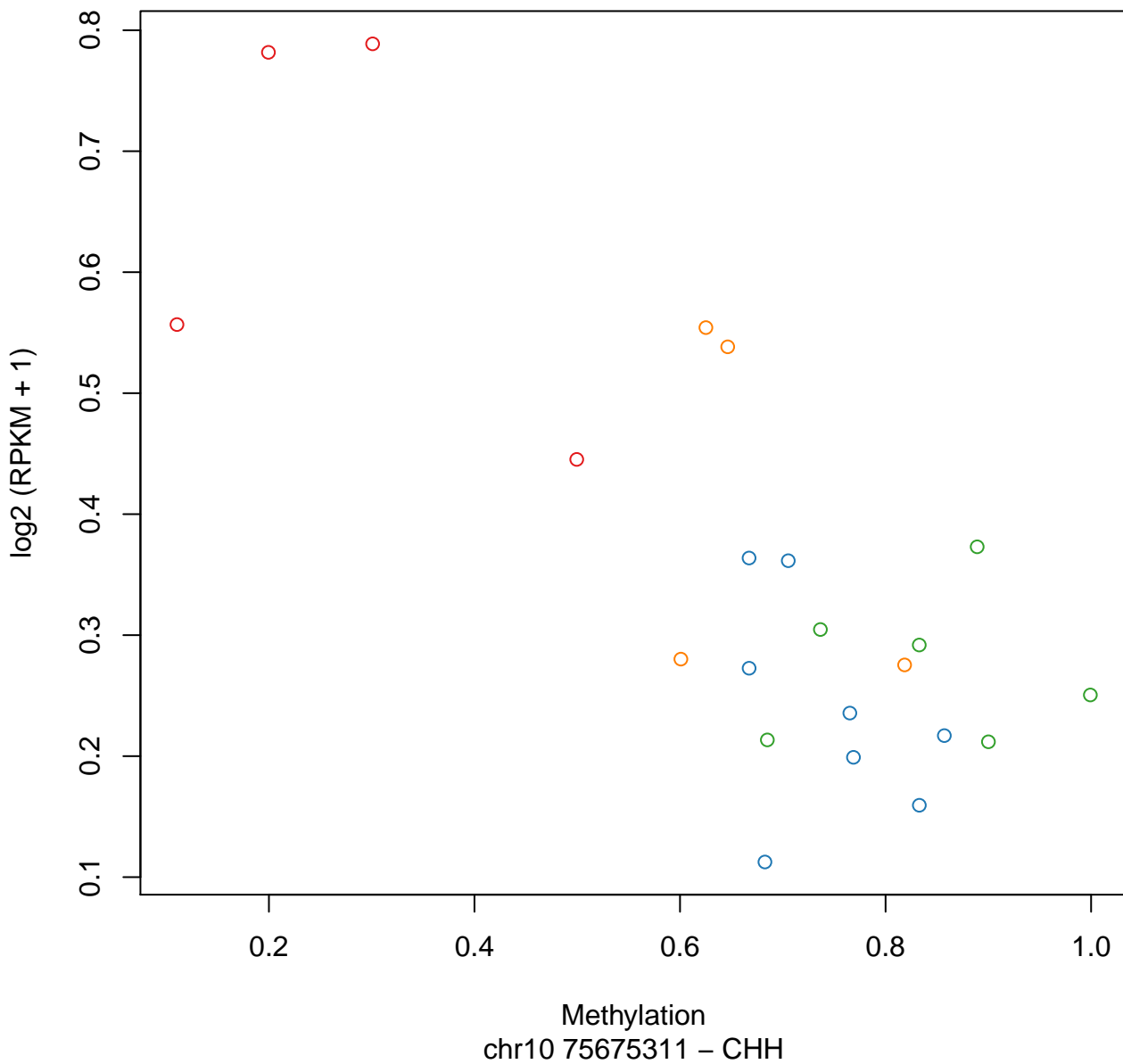
exon ENSE00001844315.1_1 FDR 0.00612
NKAIN4

log2 (RPKM + 1) vs Methylation
chr20 61875836 + CHH
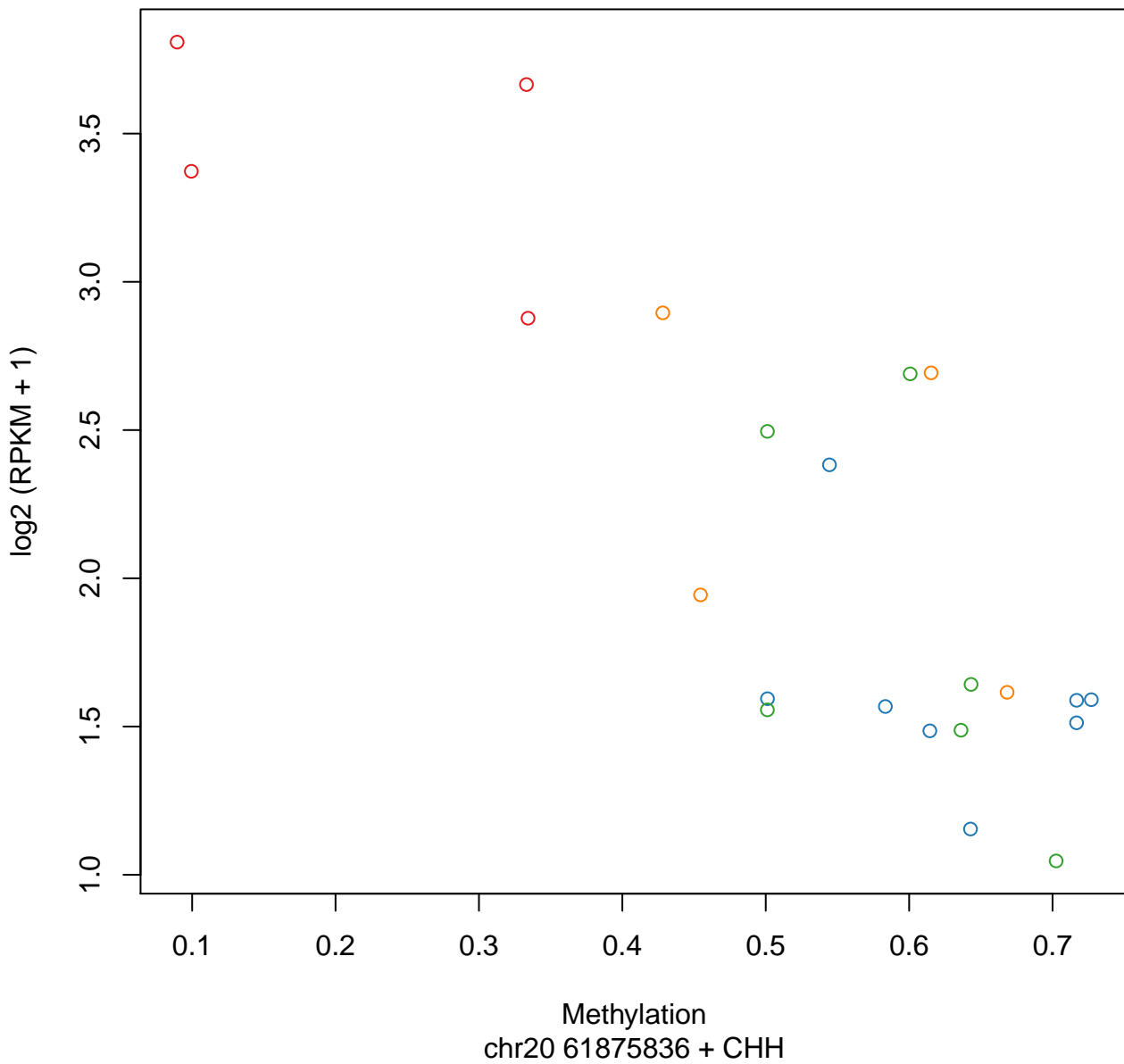
exon ENSE00002519404.2_1 FDR 0.0154
RGMA

log2 (RPKM + 1)

Methylation
chr15 93588732 + CHH
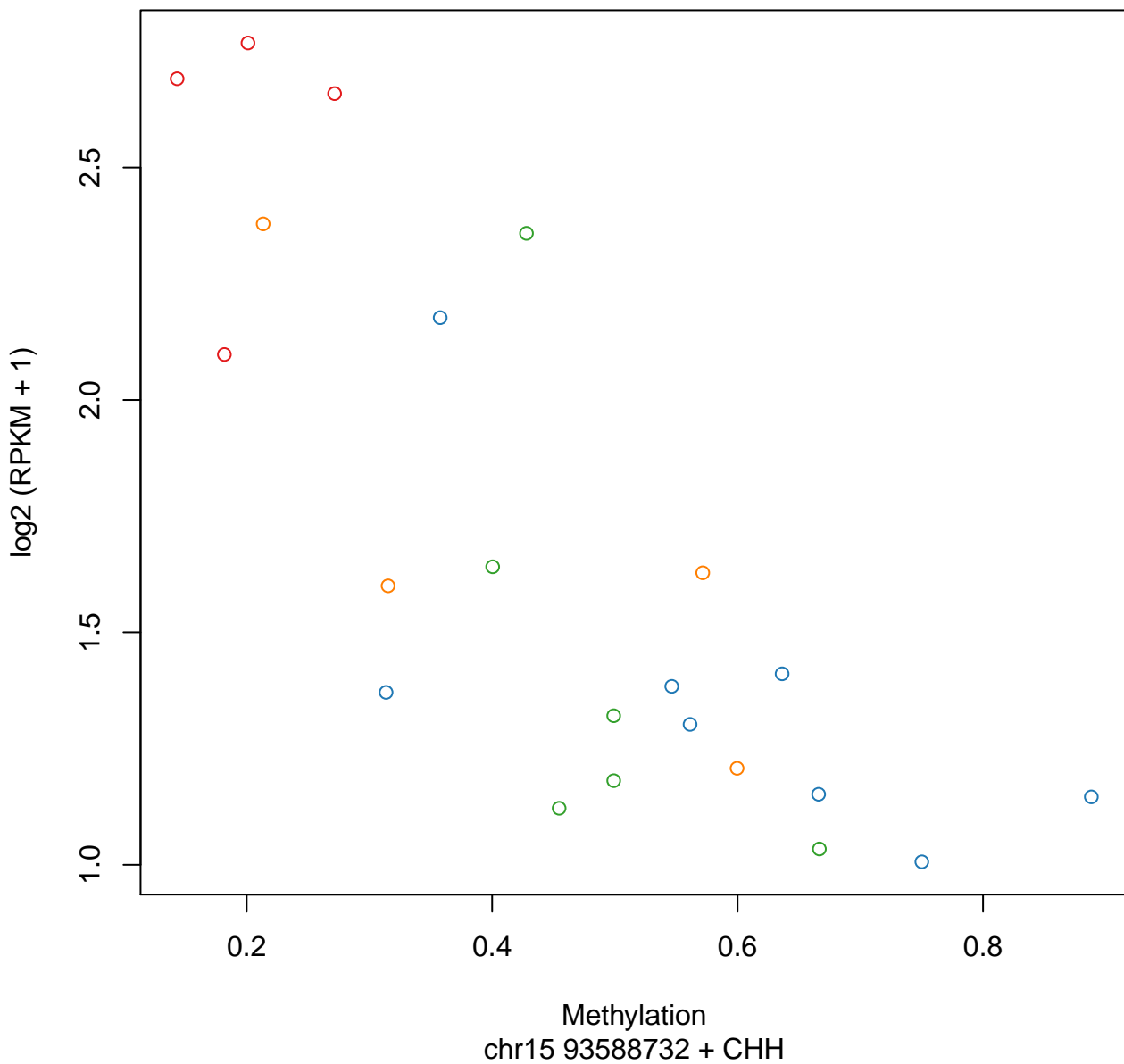
exon ENSE00001927539.1_1 FDR 0.0132
NOTCH1

log2 (RPKM + 1)

Methylation
chr9 139418619 + CHH
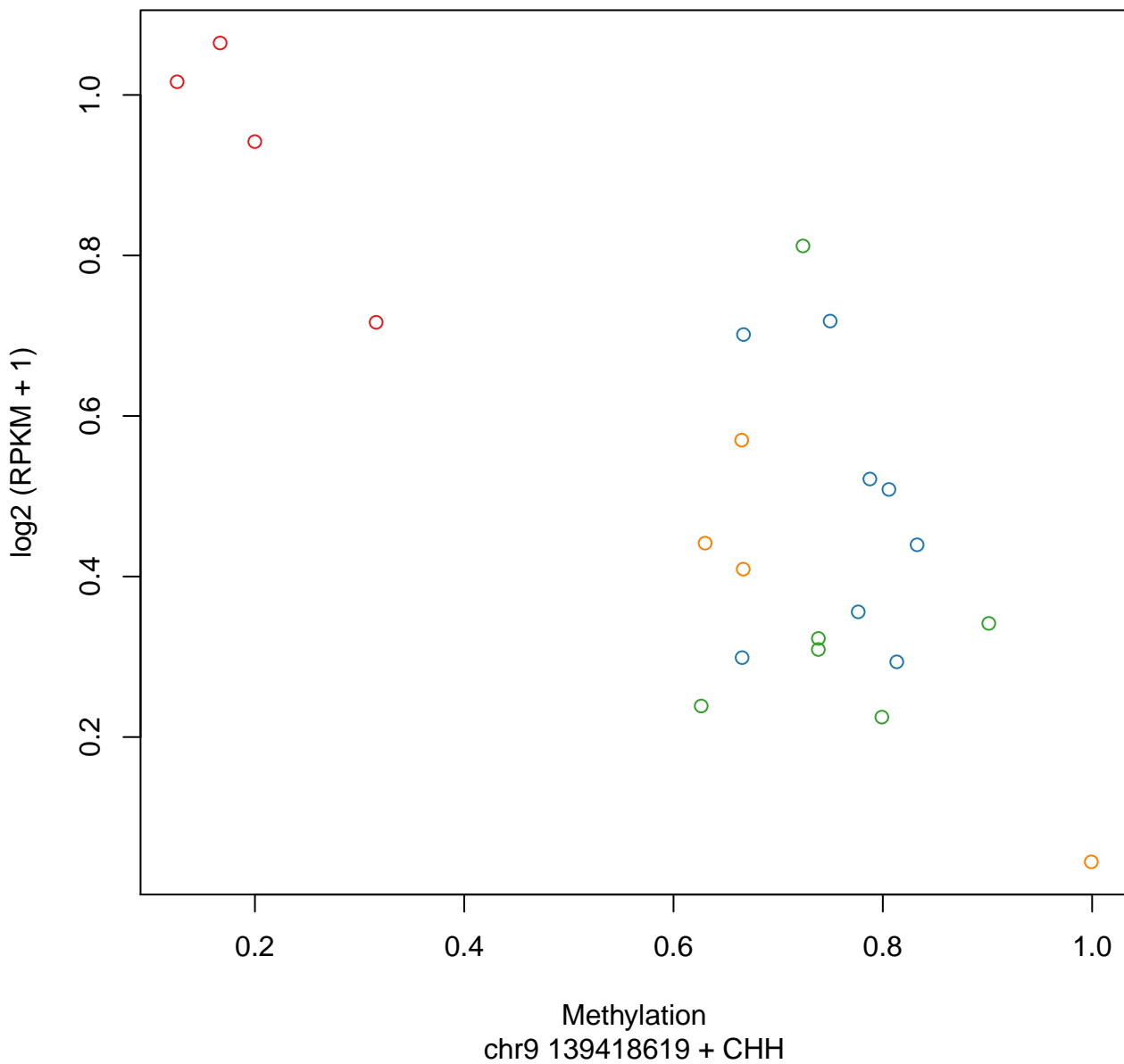
exon ENSE00002526105.1_1 FDR 0.0135
NKAIN4

log2 (RPKM + 1)

Methylation
chr20 61875836 + CHH
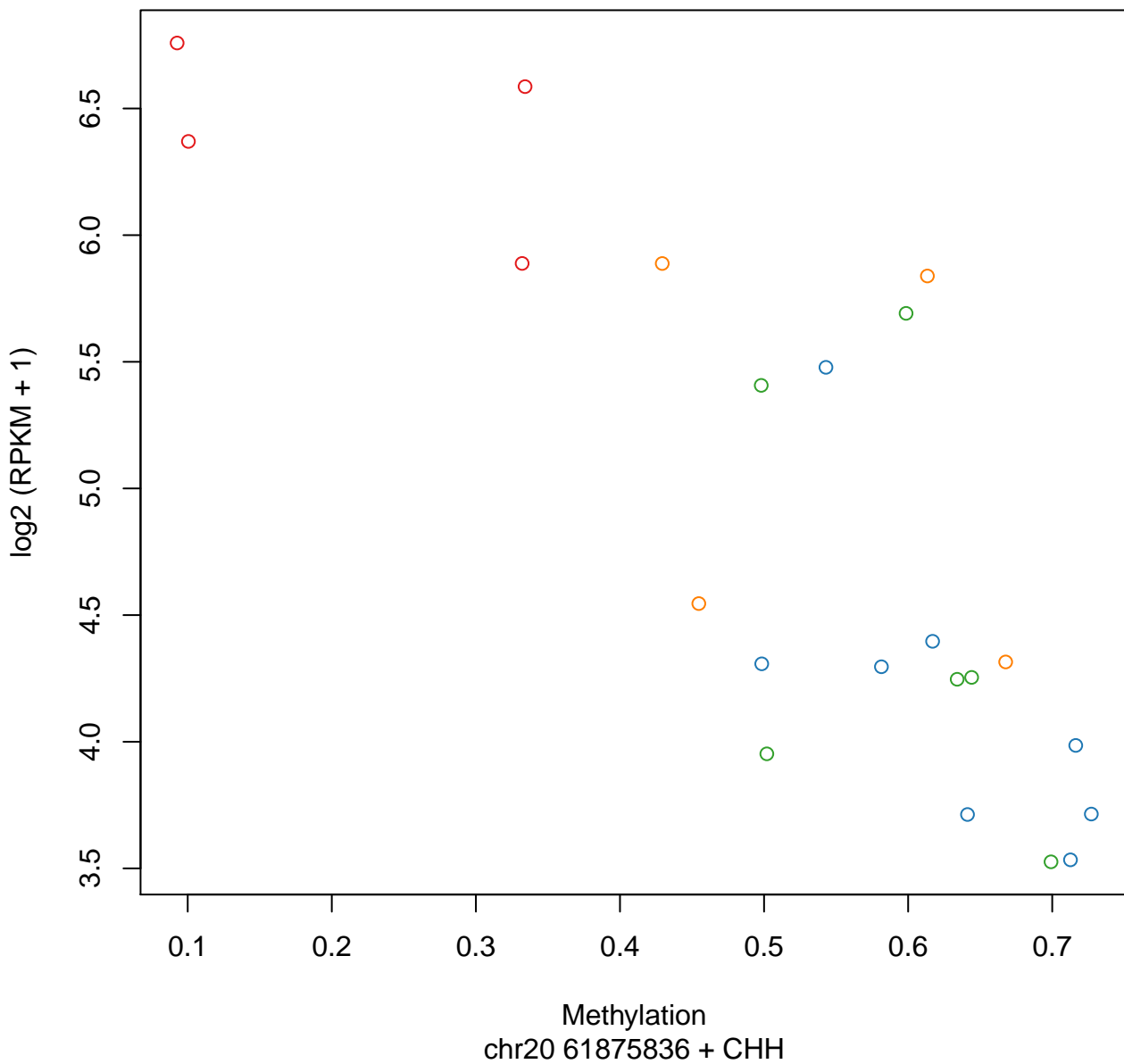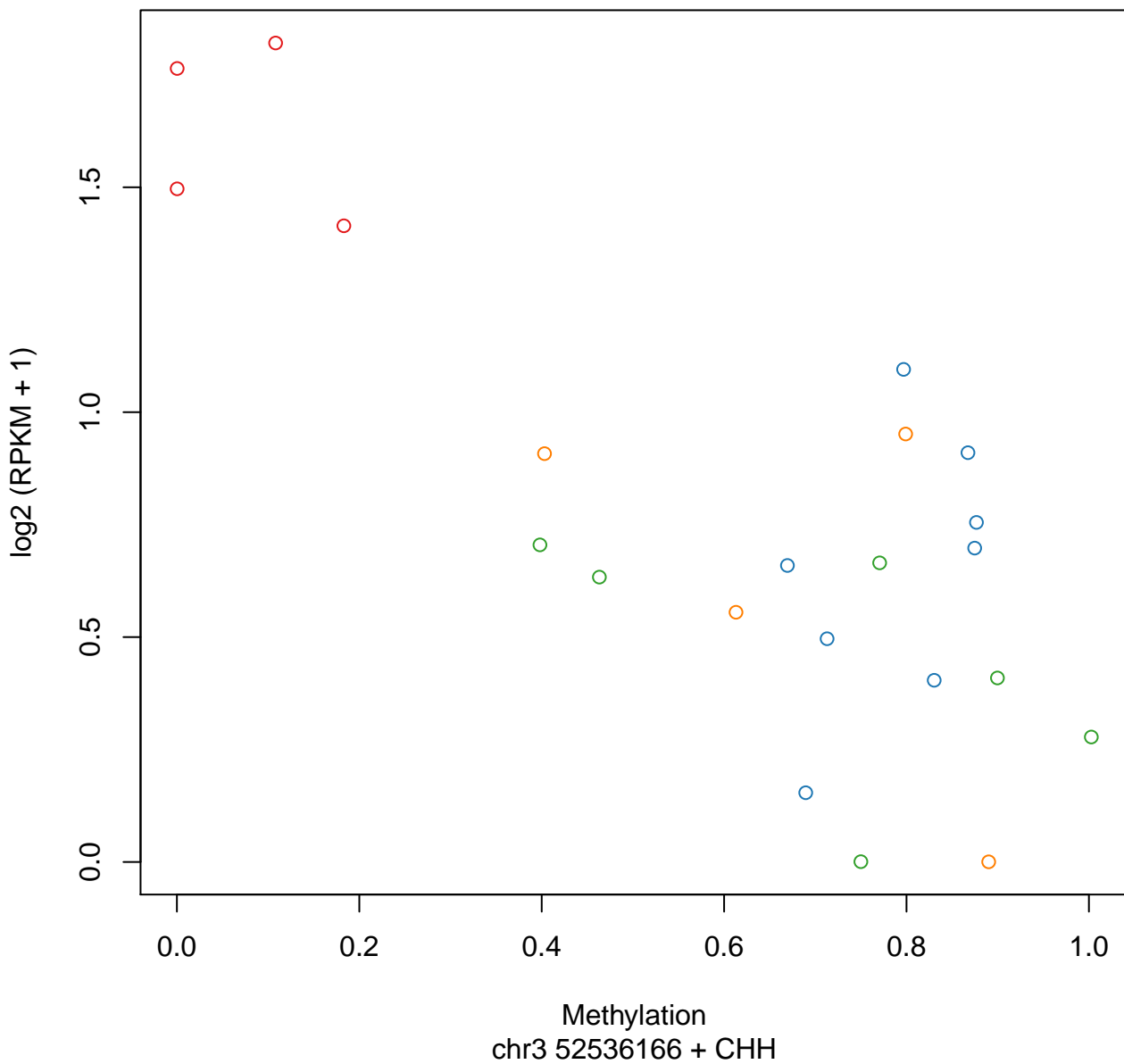
exon ENSE00003612624.1_1 FDR 0.0101
NKAIN4
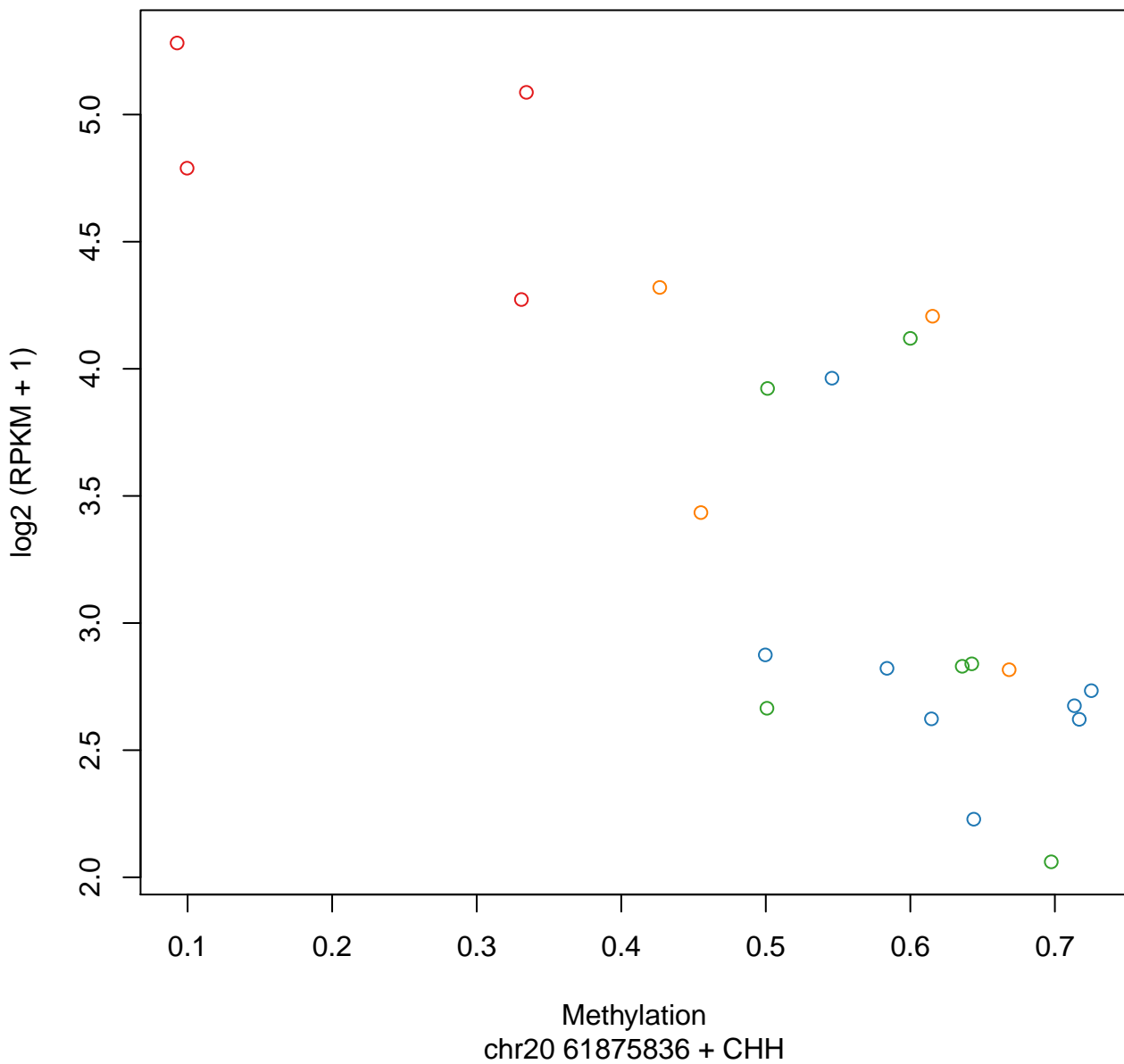
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STAB1

exon ENSE00000985020.1_1 FDR 0.0224
NOTCH1
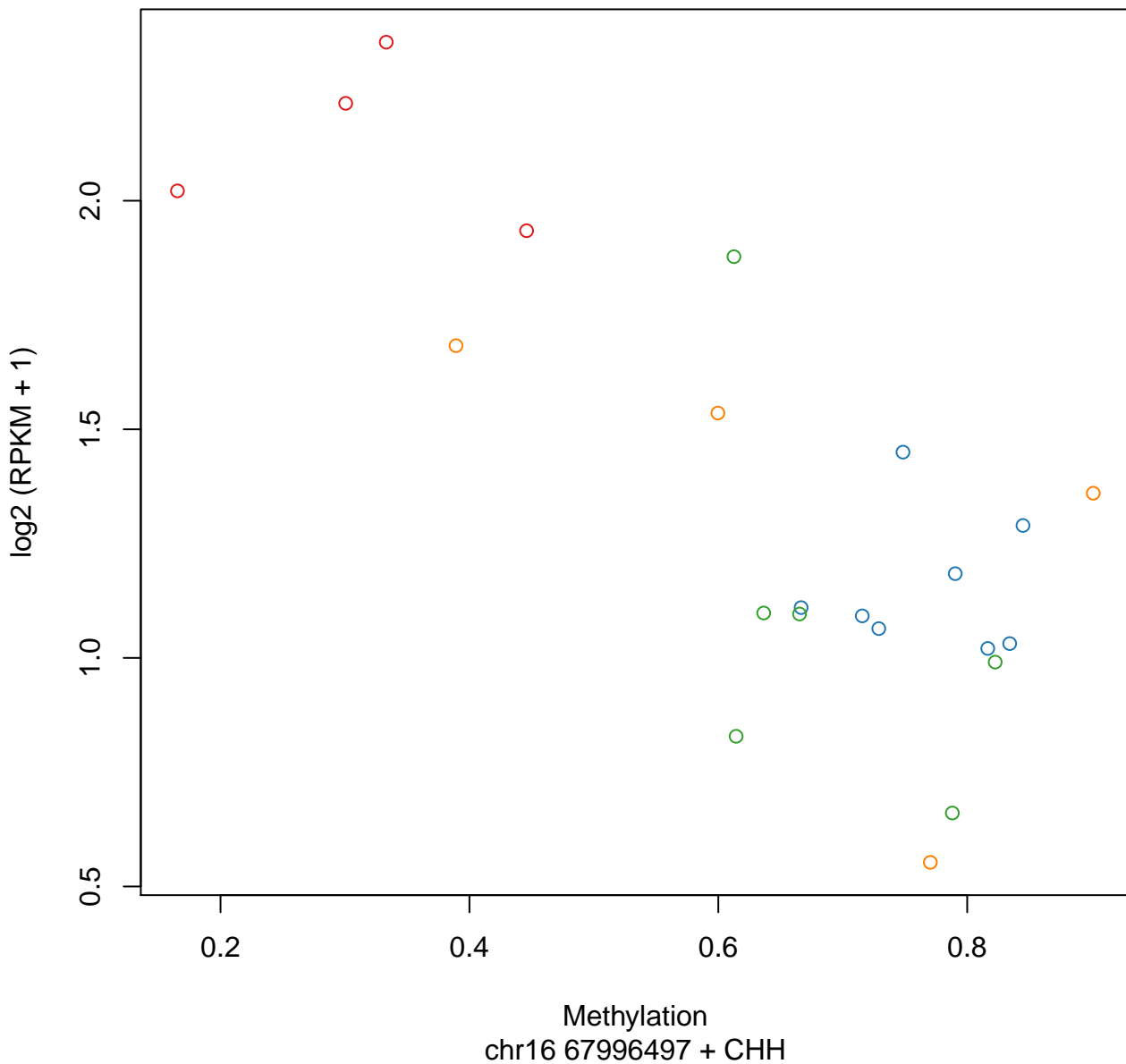
log2 (RPKM + 1) vs Methylation
chr9 139418619 + CHH
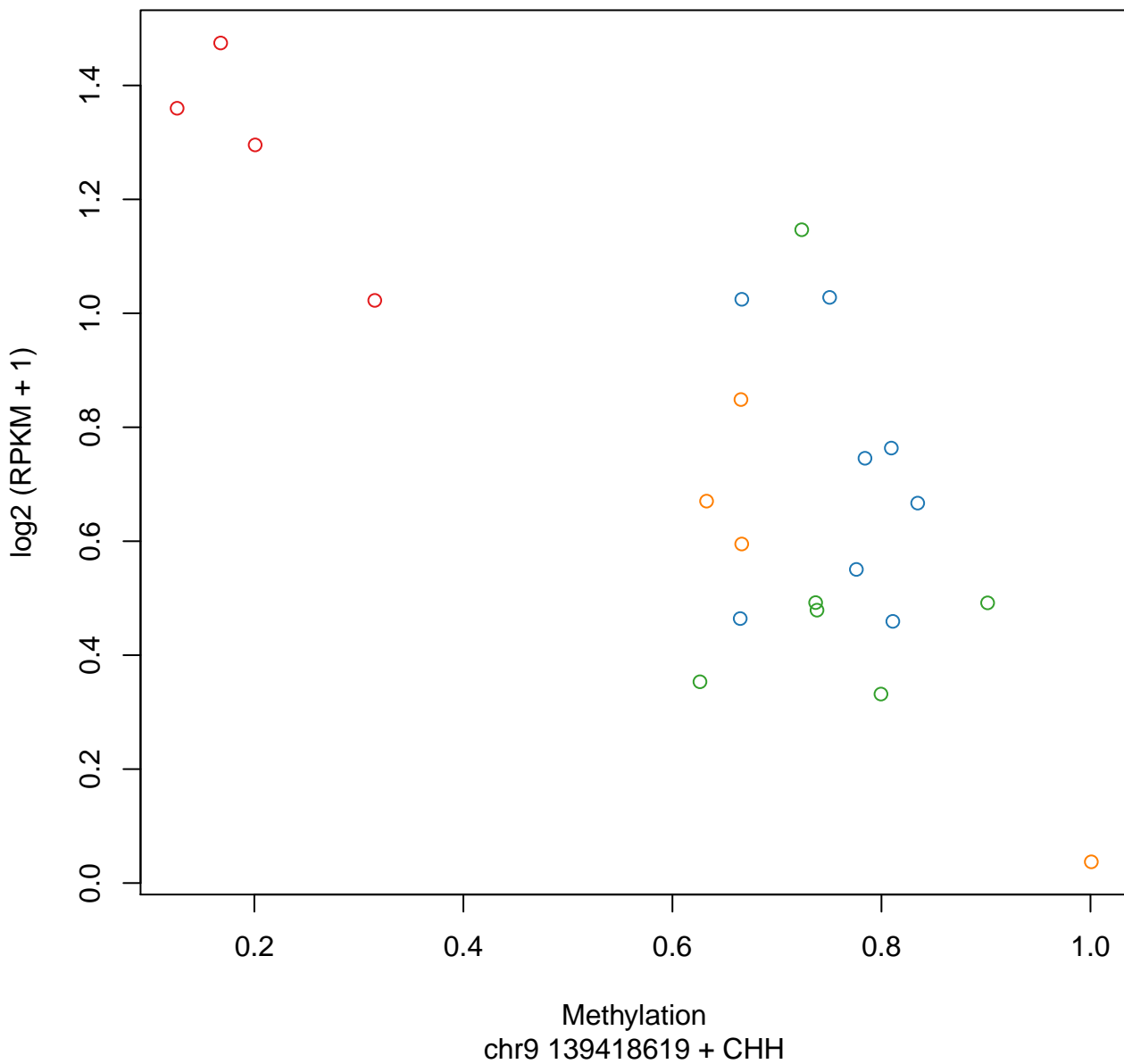
exon ENSE00003670475.1_1 FDR 0.0294
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exon ENSE00002863413.1_1 FDR 0.0159
DOCK6