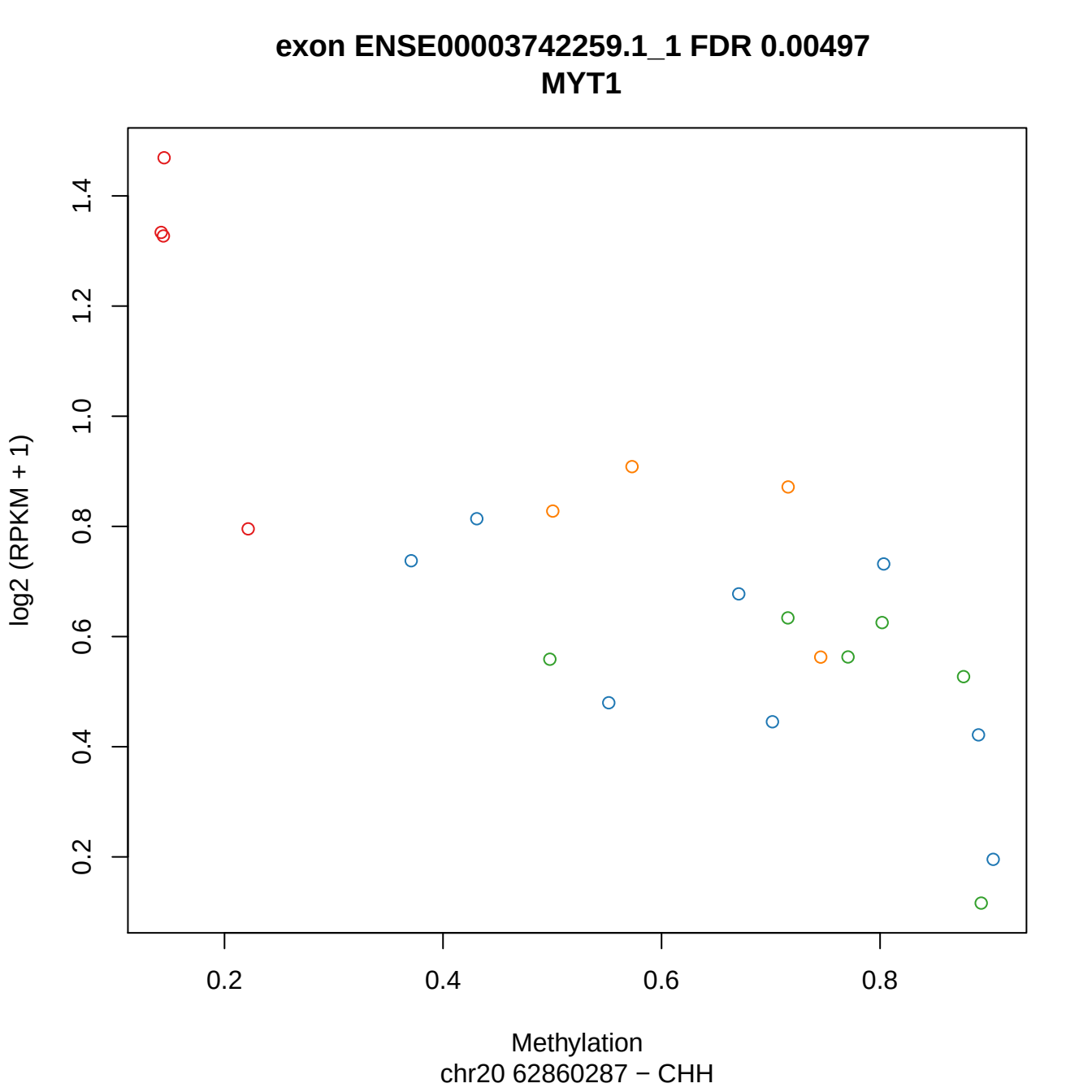
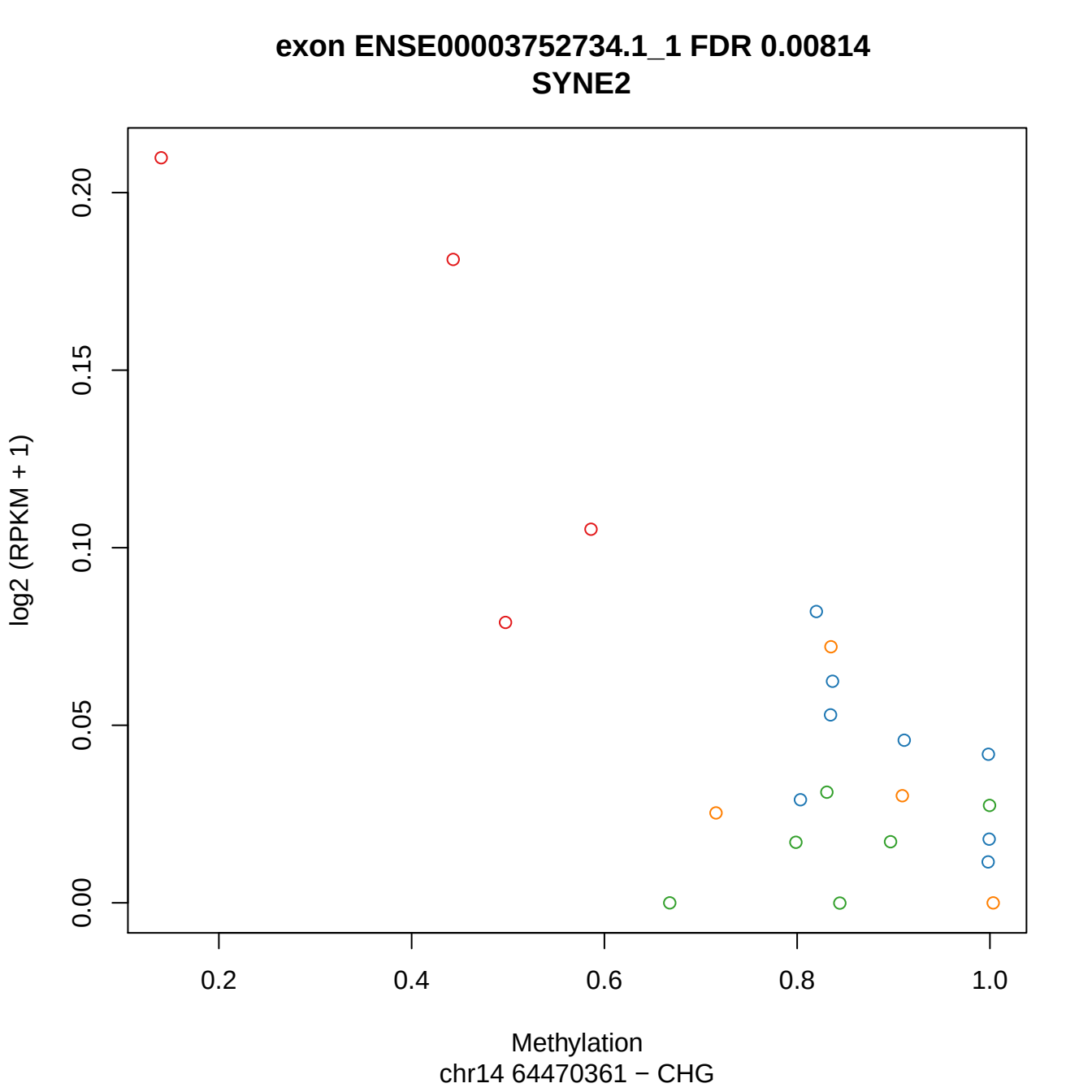
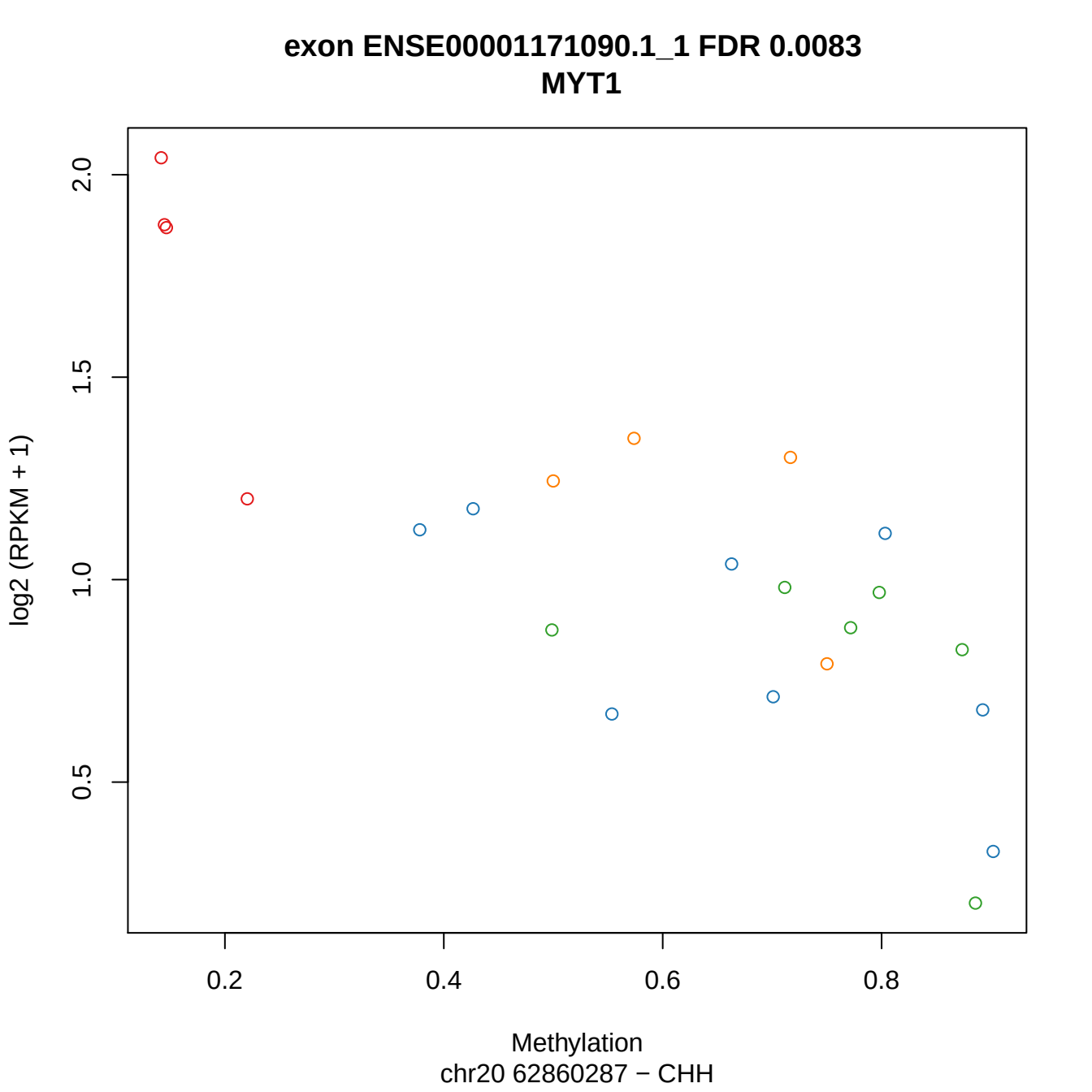
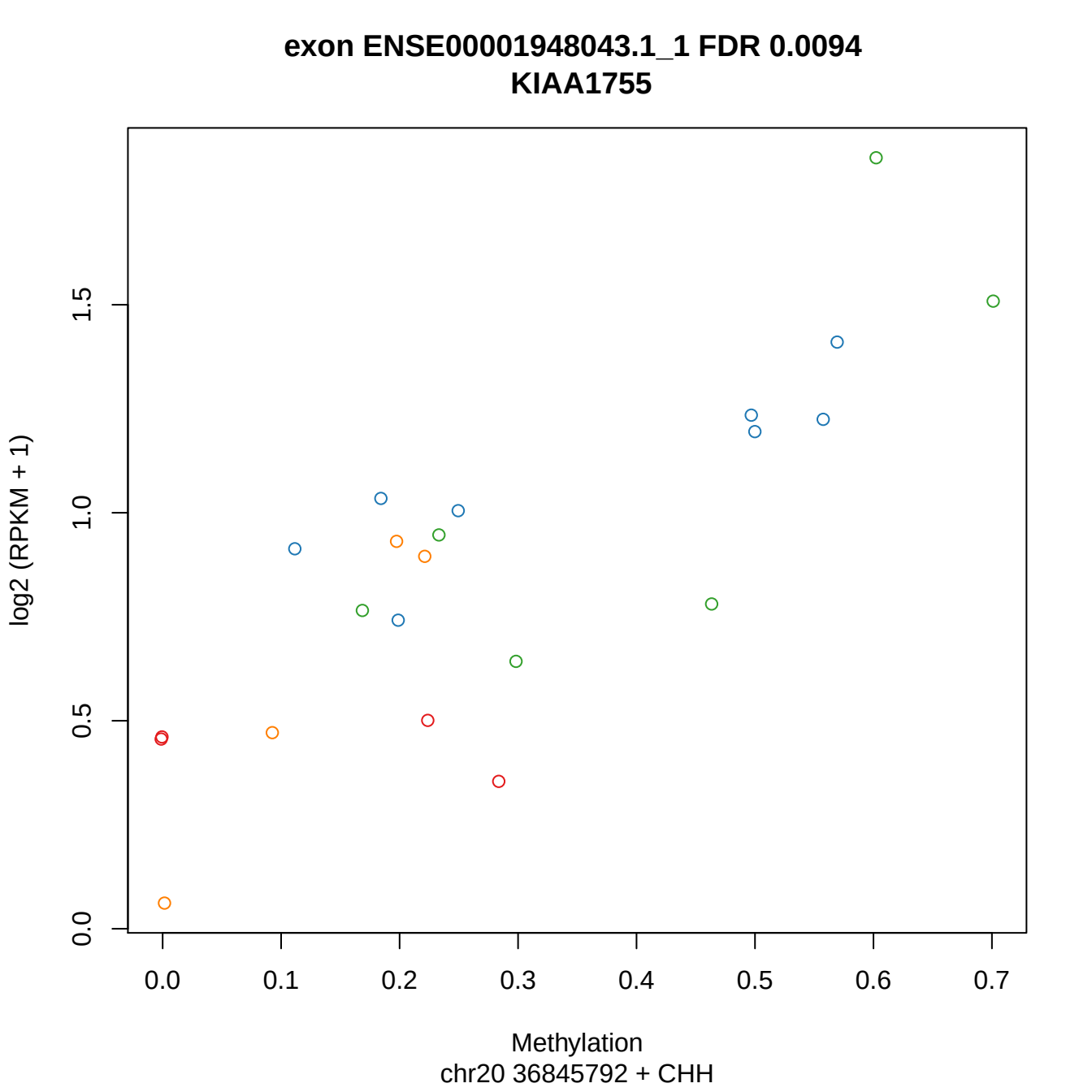
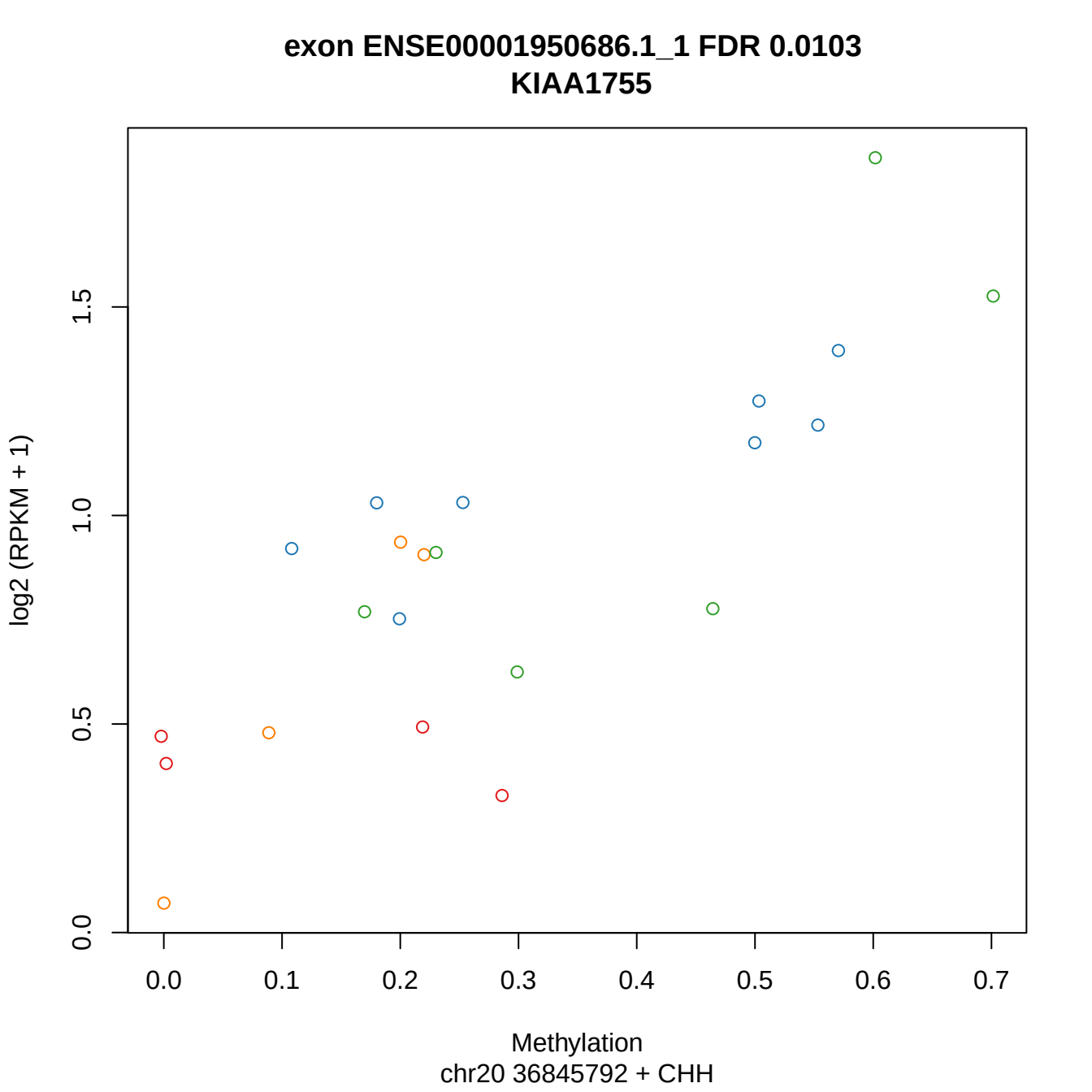
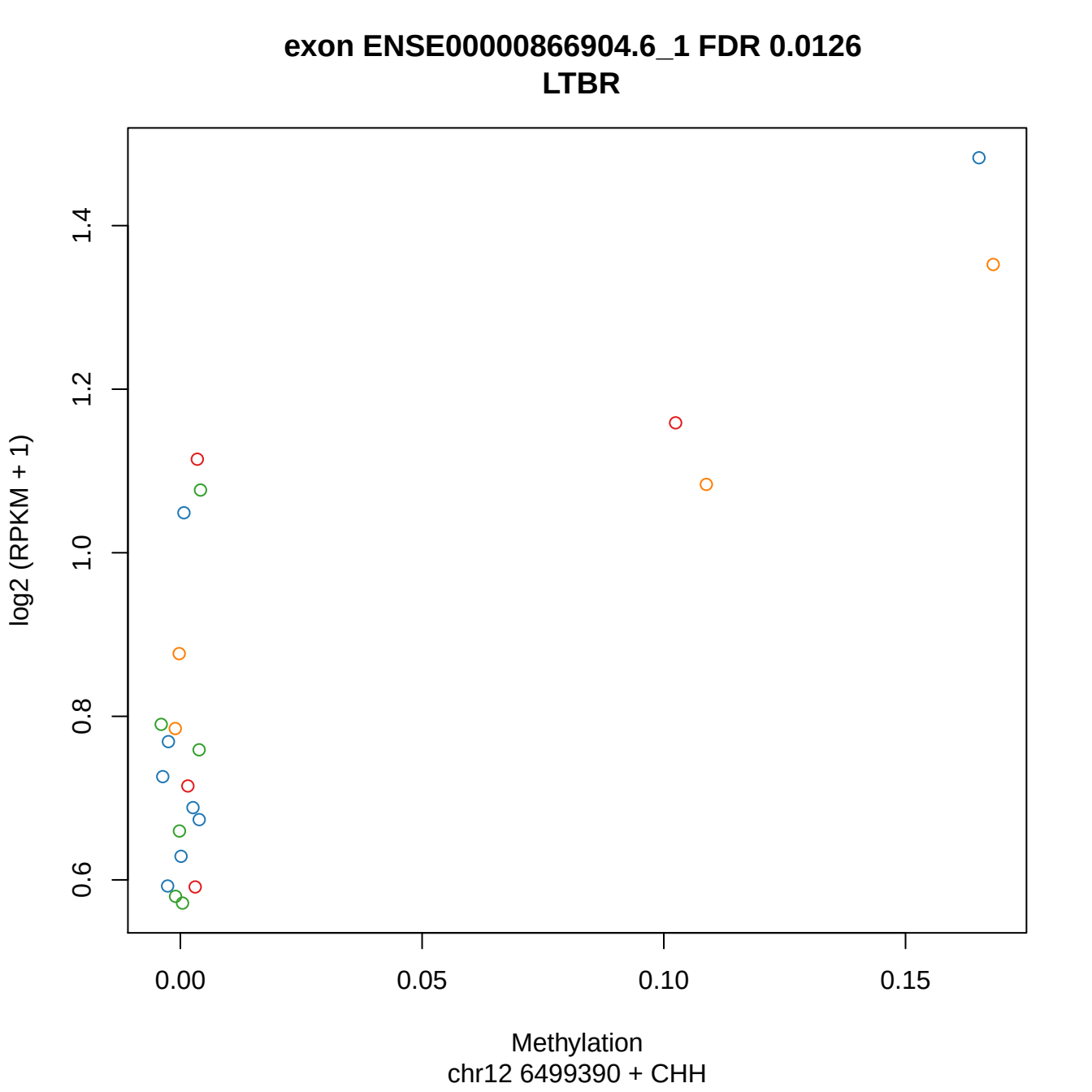

exon ENSE00003742259.1_1 FDR 0.00497
MYT1
log2 (RPKM + 1)
0.2
0.4
0.6
0.8
1.0
1.2
1.4
0.2
0.4
0.6
0.8
Methylation
chr20 62860287 − CHH

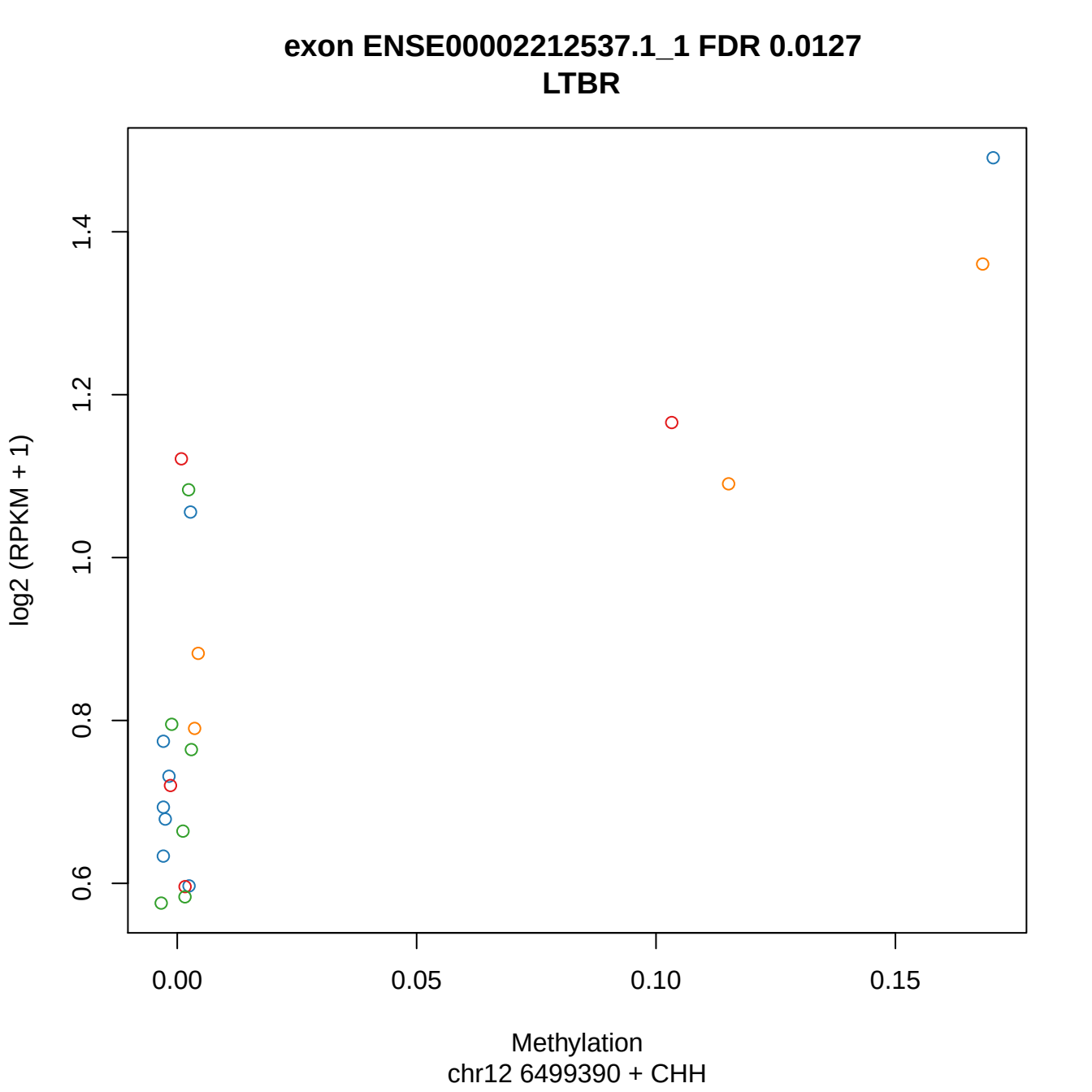

exon ENSE00003752734.1_1 FDR 0.00814
SYNE2
log2 (RPKM + 1)
0.00
0.05
0.10
0.15
0.20
0.2
0.4
0.6
0.8
1.0
Methylation
chr14 64470361 − CHG

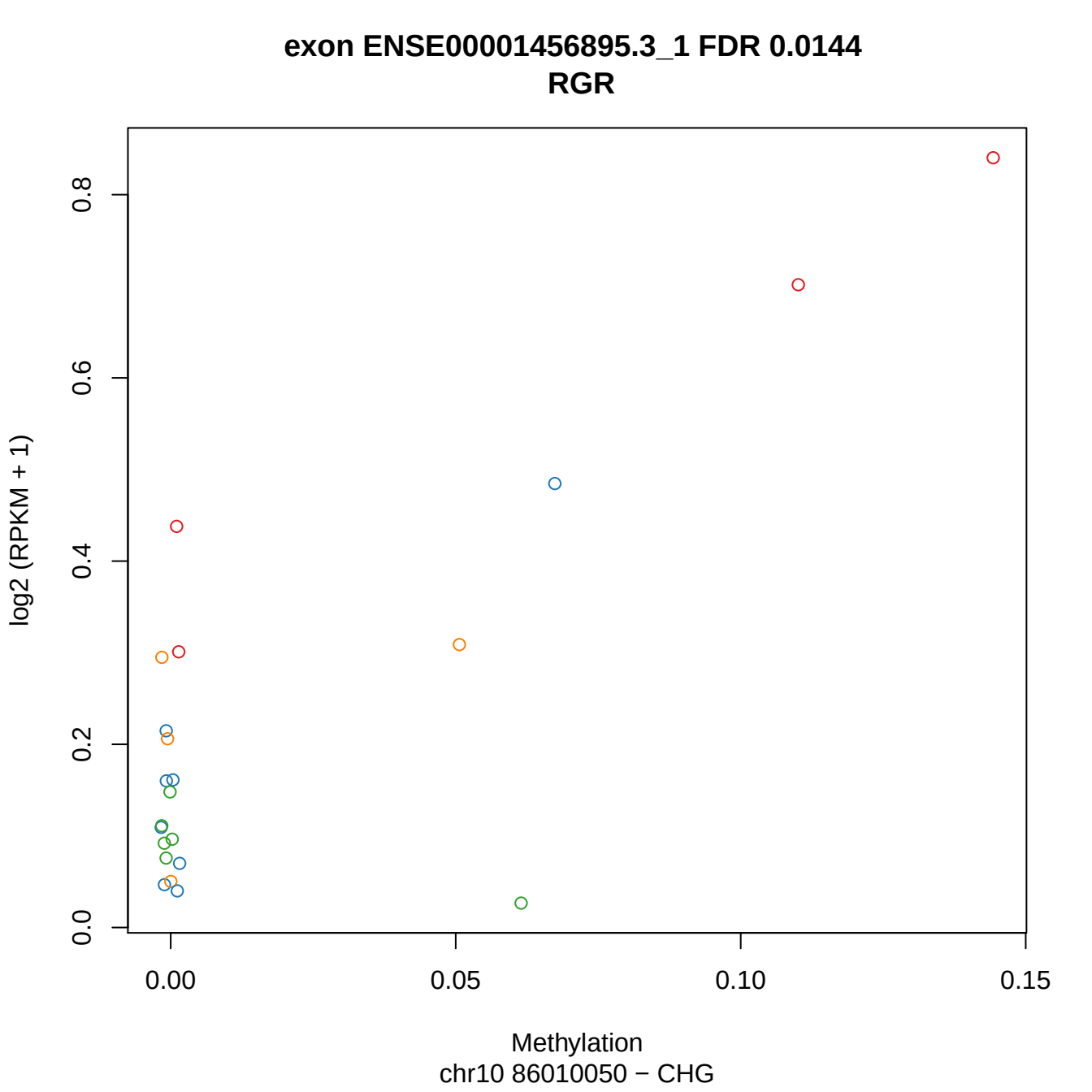

exon ENSE00001171090.1_1 FDR 0.0083
MYT1
log2 (RPKM + 1)
2.0
1.5
1.0
0.5
0.2
0.4
0.6
0.8
Methylation
chr20 62860287 − CHH

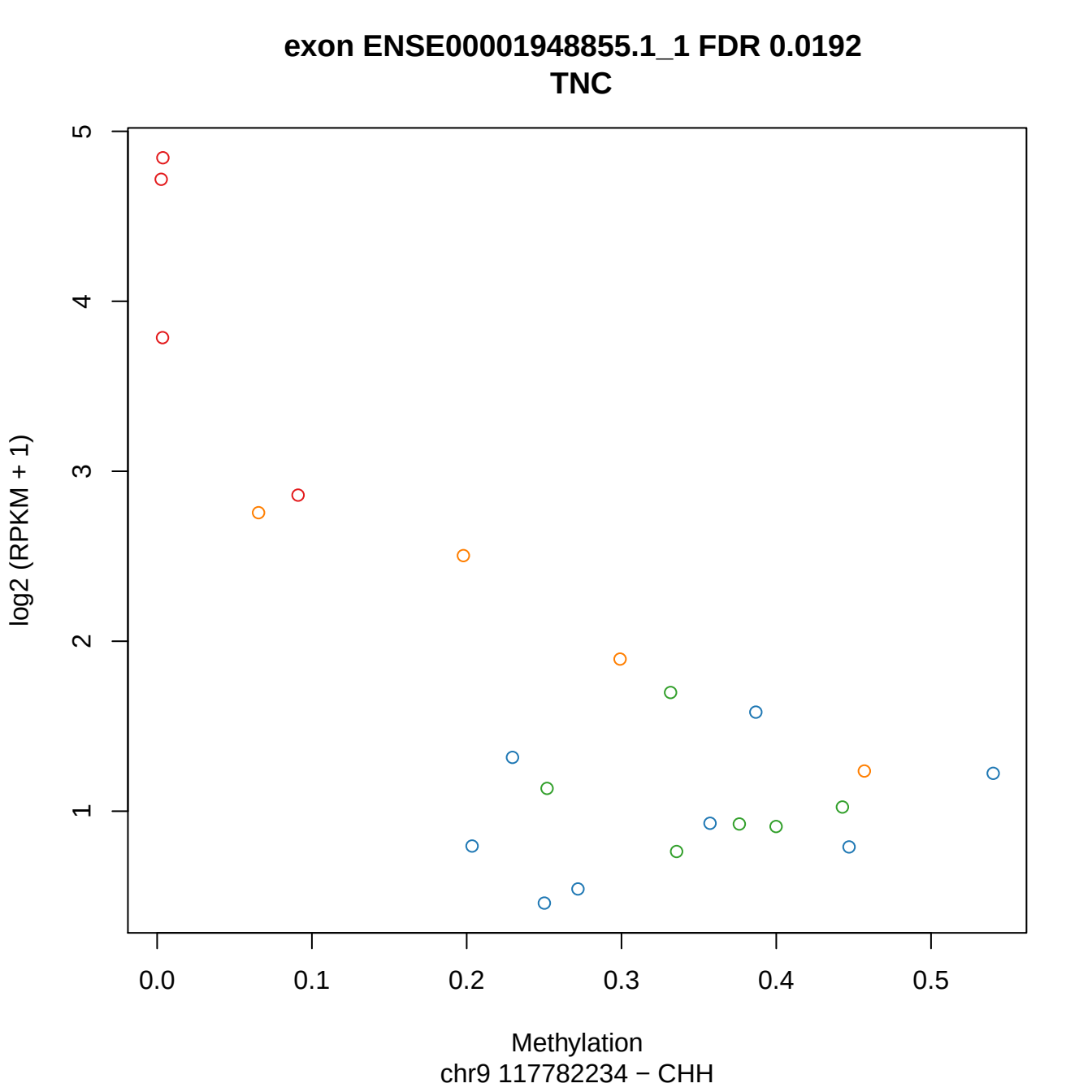

exon ENSE00001948043.1_1 FDR 0.0094
KIAA1755
log2 (RPKM + 1)
0.0
0.5
1.0
1.5
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Methylation
chr20 36845792 + CHH

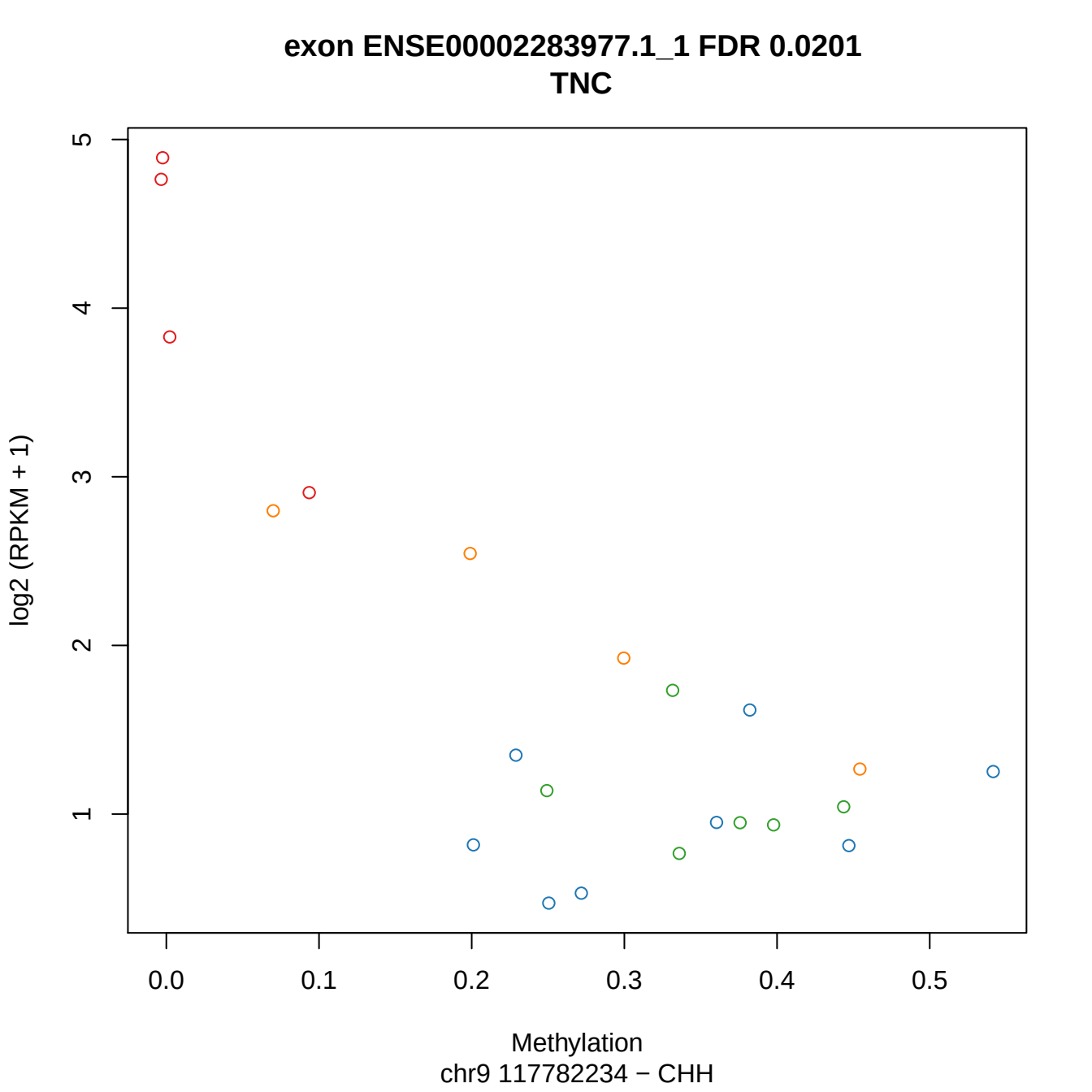

exon ENSE00001950686.1_1 FDR 0.0103
KIAA1755
log2 (RPKM + 1)
0.0
0.5
1.0
1.5
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Methylation
chr20 36845792 + CHH

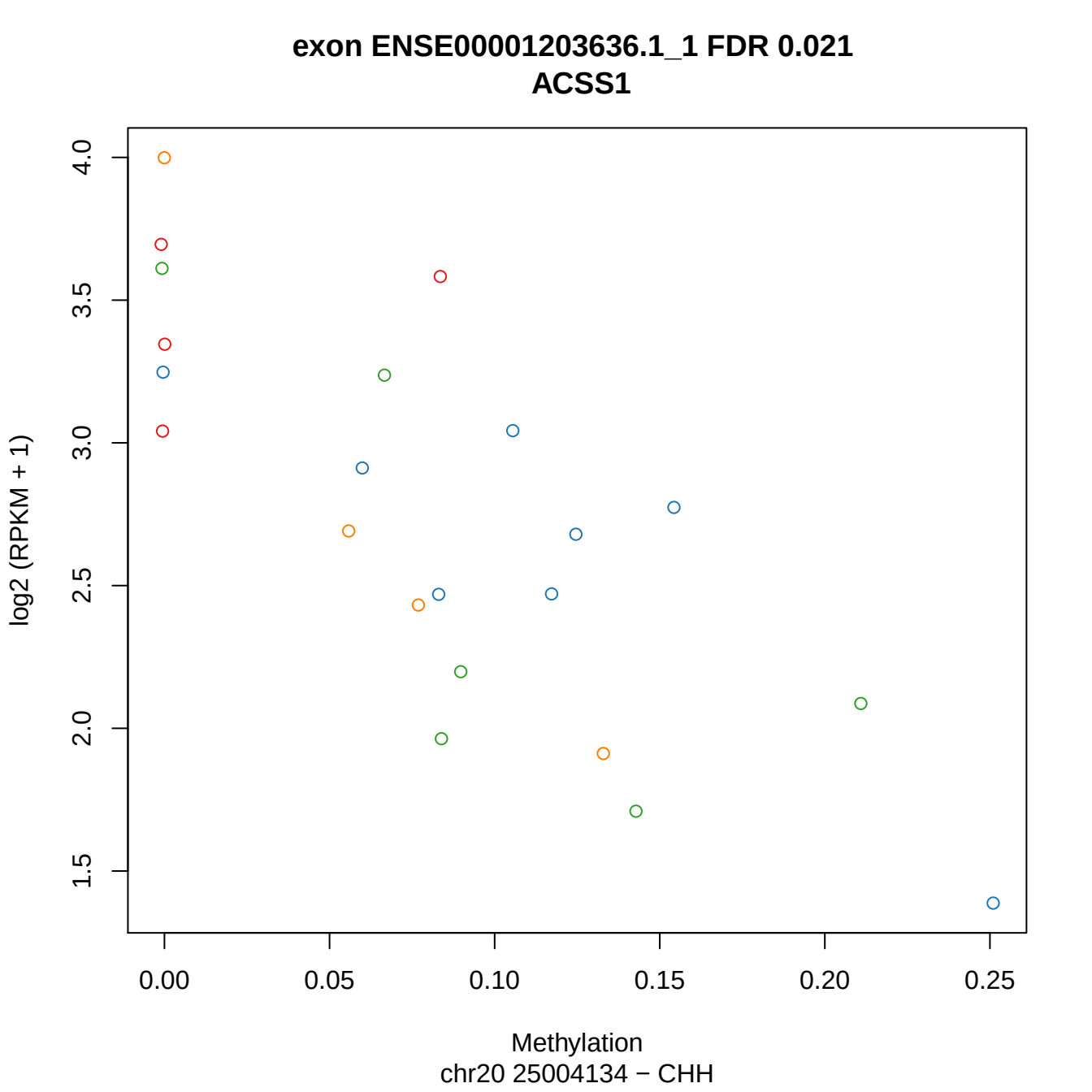

exon ENSE00000866904.6_1 FDR 0.0126
LTBR
log2 (RPKM + 1)
0.6
0.8
1.0
1.2
1.4
0.00
0.05
0.10
0.15
Methylation
chr12 6499390 + CHH

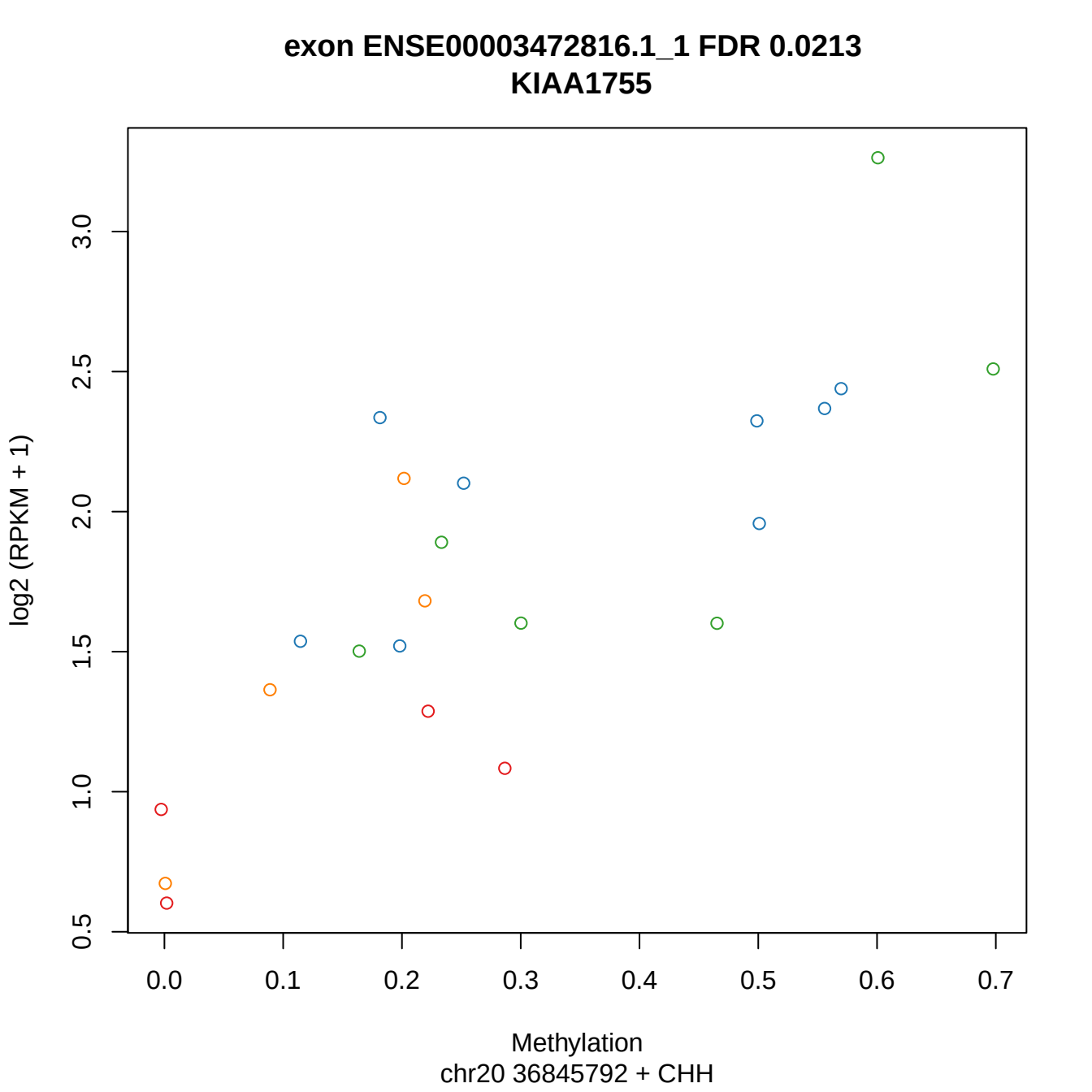

exon ENSE00002212537.1_1 FDR 0.0127
LTBR
log2 (RPKM + 1)
0.6
0.8
1.0
1.2
1.4
0.00
0.05
0.10
0.15
Methylation
chr12 6499390 + CHH

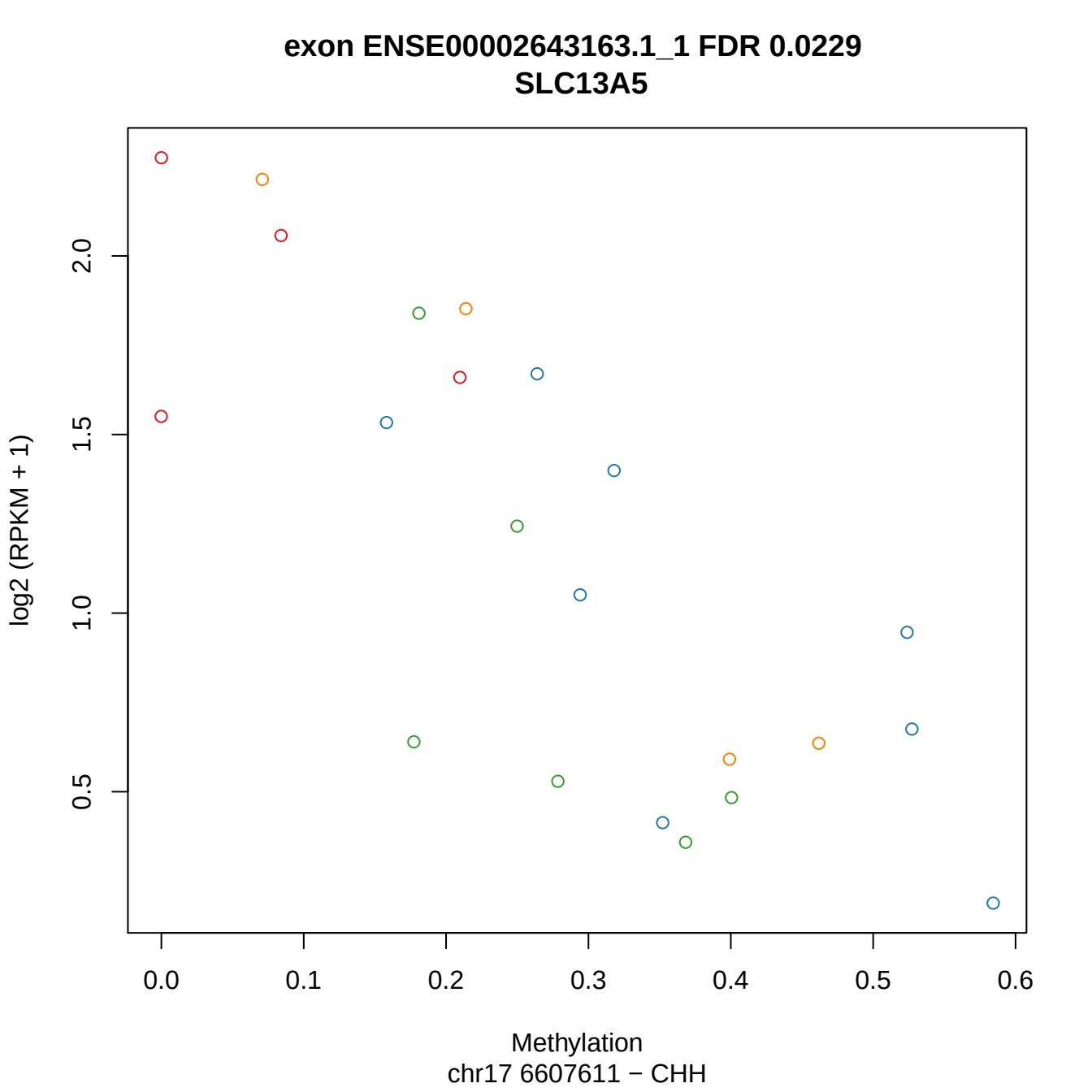

exon ENSE00001456895.3_1 FDR 0.0144
RGR
log2 (RPKM + 1)
0.0
0.2
0.4
0.6
0.8
0.00
0.05
0.10
0.15
Methylation
chr10 86010050 − CHG

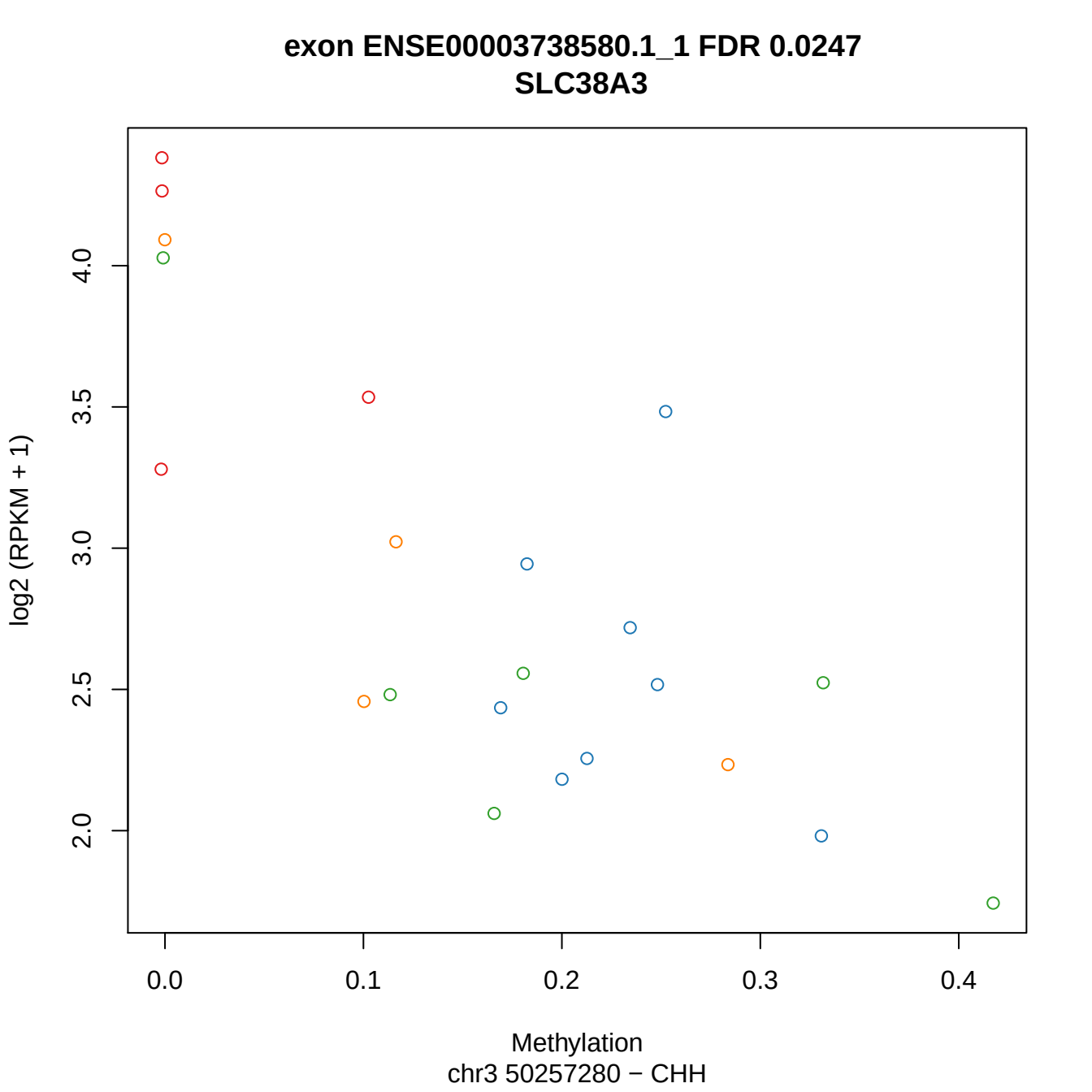

exon ENSE00001948855.1_1 FDR 0.0192
TNC
log2 (RPKM + 1)
1
2
3
4
5
0.0
0.1
0.2
0.3
0.4
0.5
Methylation
chr9 117782234 − CHH

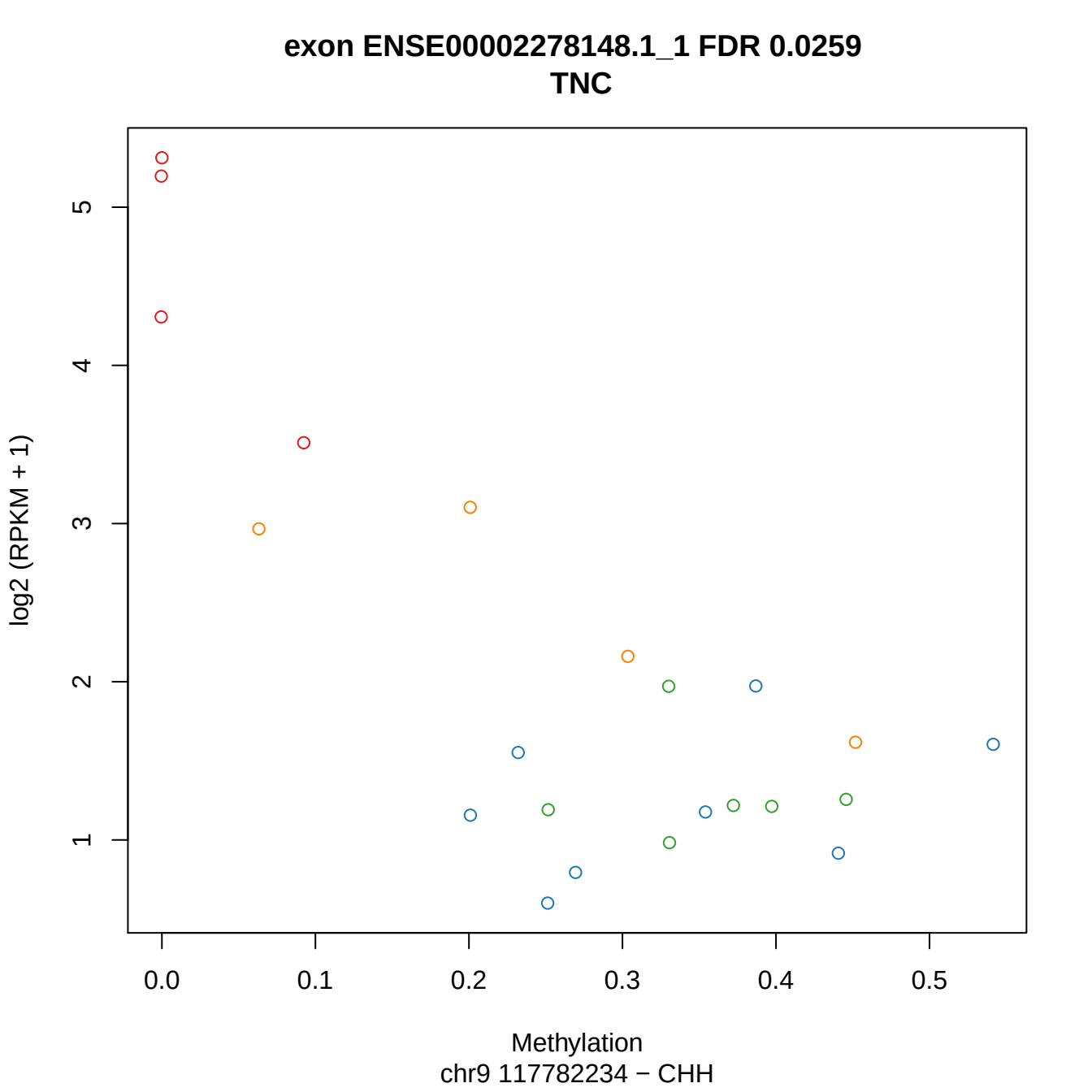

exon ENSE00002283977.1_1 FDR 0.0201
TNC
log2 (RPKM + 1)
1
2
3
4
5
0.0
0.1
0.2
0.3
0.4
0.5
Methylation
chr9 117782234 − CHH

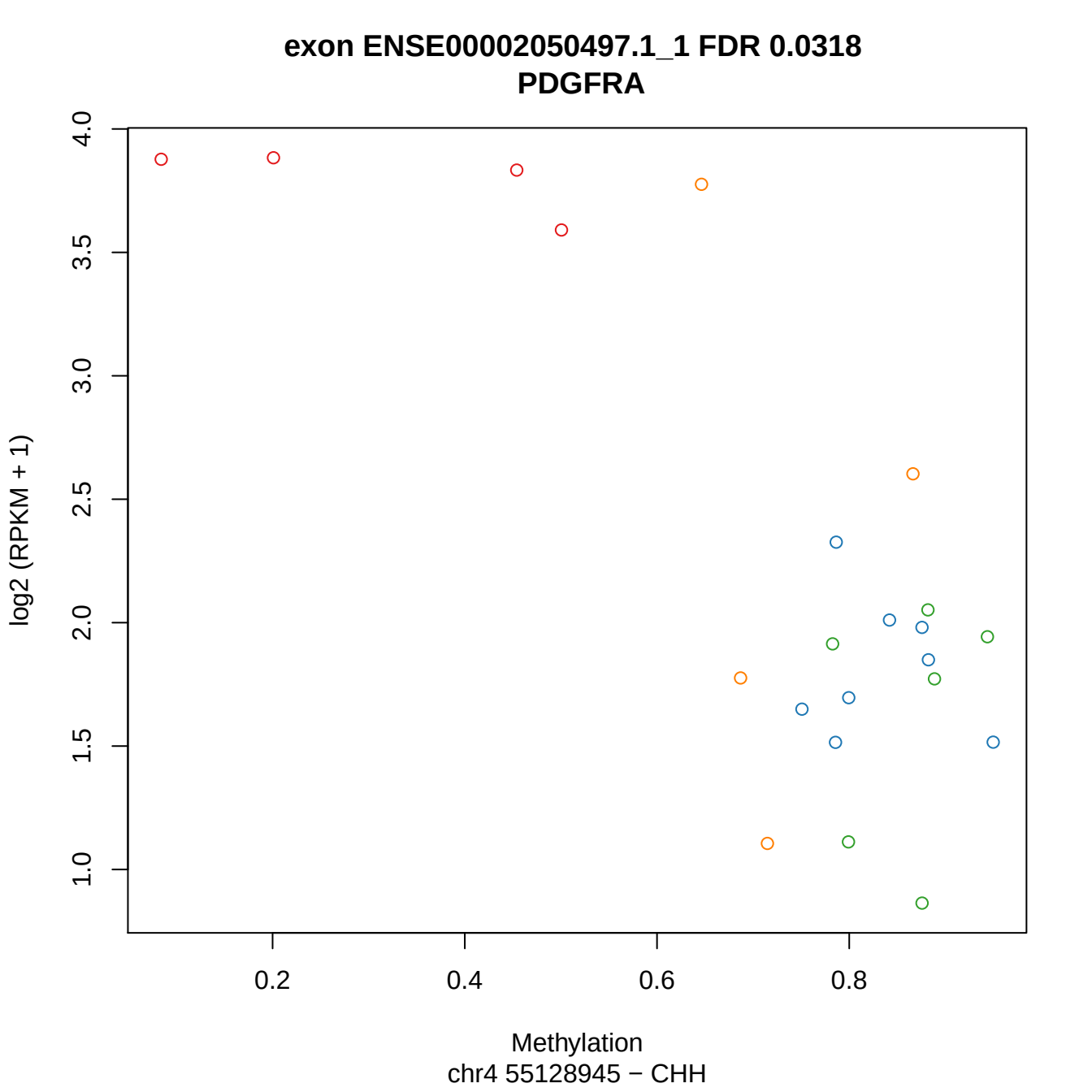

exon ENSE00001203636.1_1 FDR 0.021
ACSS1
log2 (RPKM + 1)
4.0
3.5
3.0
2.5
2.0
1.5
0.00
0.05
0.10
0.15
0.20
0.25
Methylation
chr20 25004134 − CHH

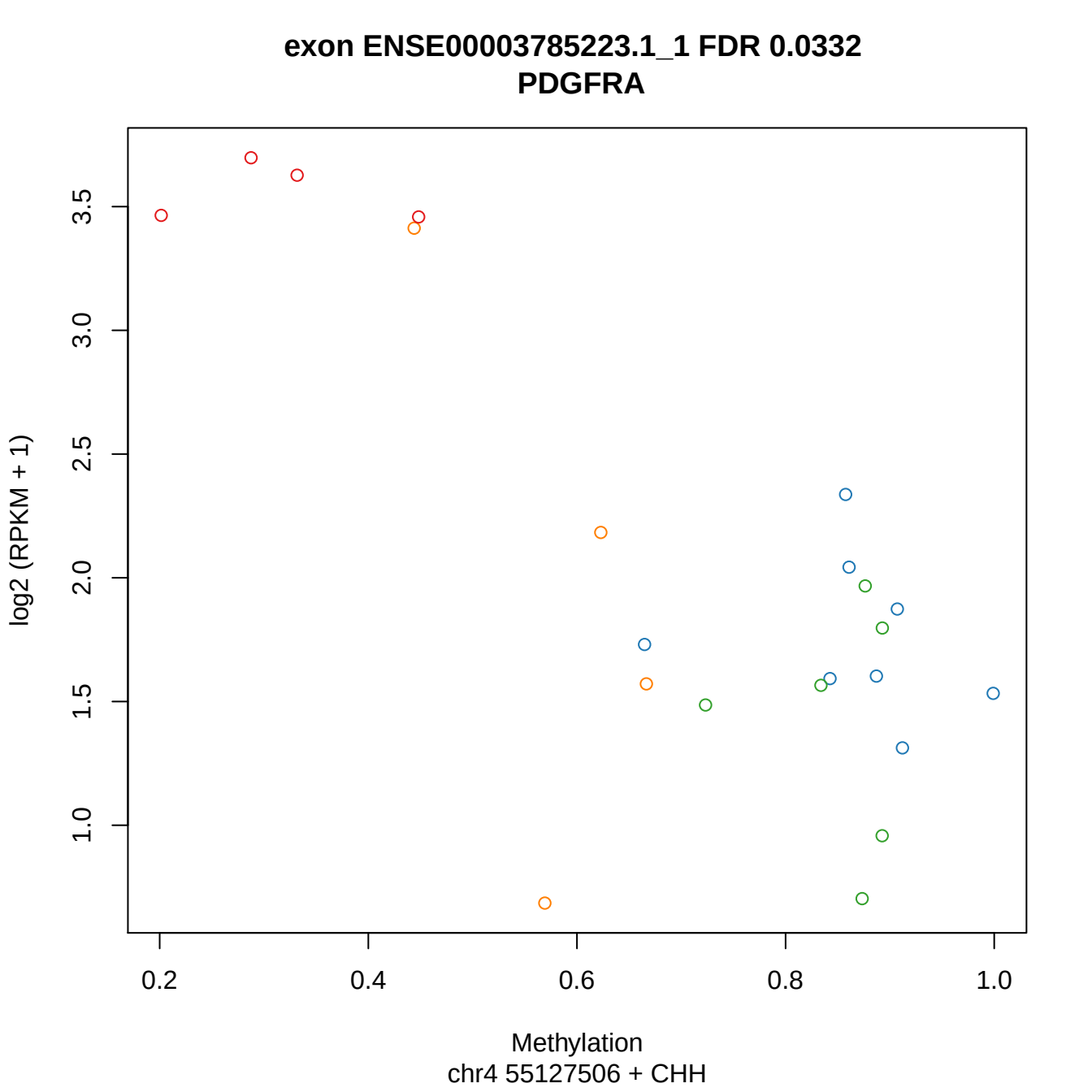

exon ENSE00003472816.1_1 FDR 0.0213
KIAA1755
log2 (RPKM + 1)
0.5
1.0
1.5
2.0
2.5
3.0
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Methylation
chr20 36845792 + CHH

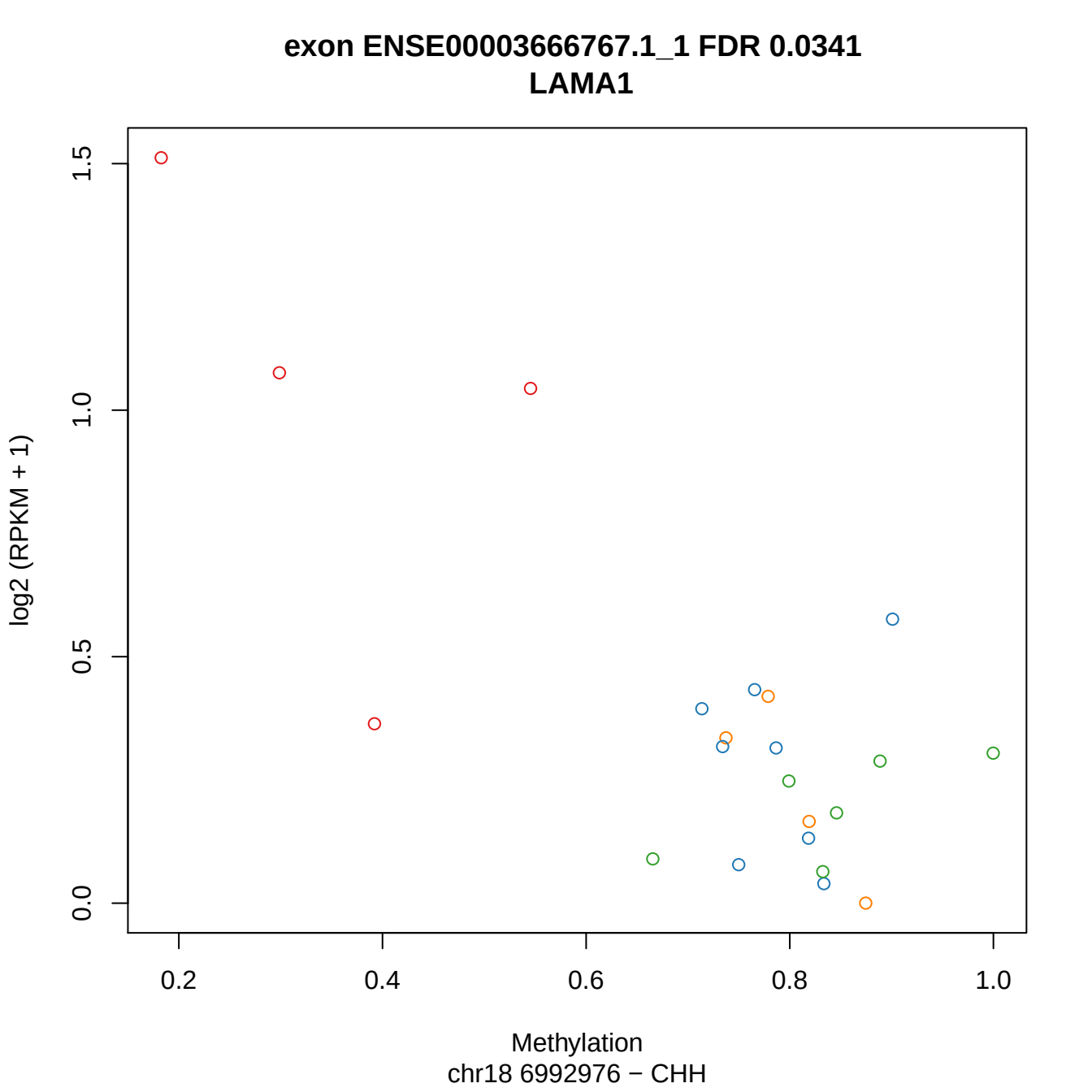

exon ENSE00002643163.1_1 FDR 0.0229
SLC13A5
log2 (RPKM + 1)
0.5
1.0
1.5
2.0
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Methylation
chr17 6607611 − CHH

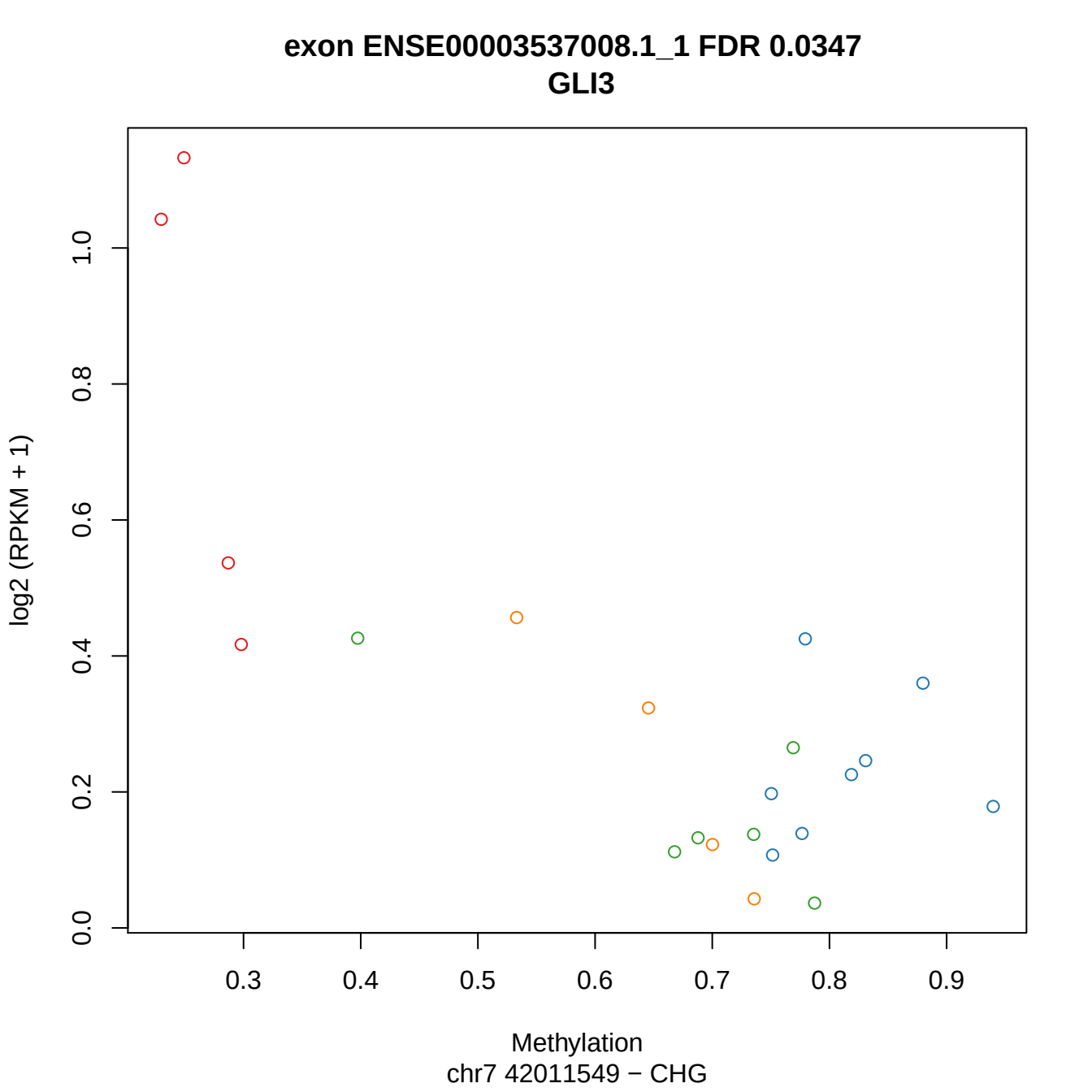

exon ENSE00003738580.1_1 FDR 0.0247
SLC38A3
log2 (RPKM + 1)
2.0
2.5
3.0
3.5
4.0
0.0
0.1
0.2
0.3
0.4
Methylation
chr3 50257280 − CHH

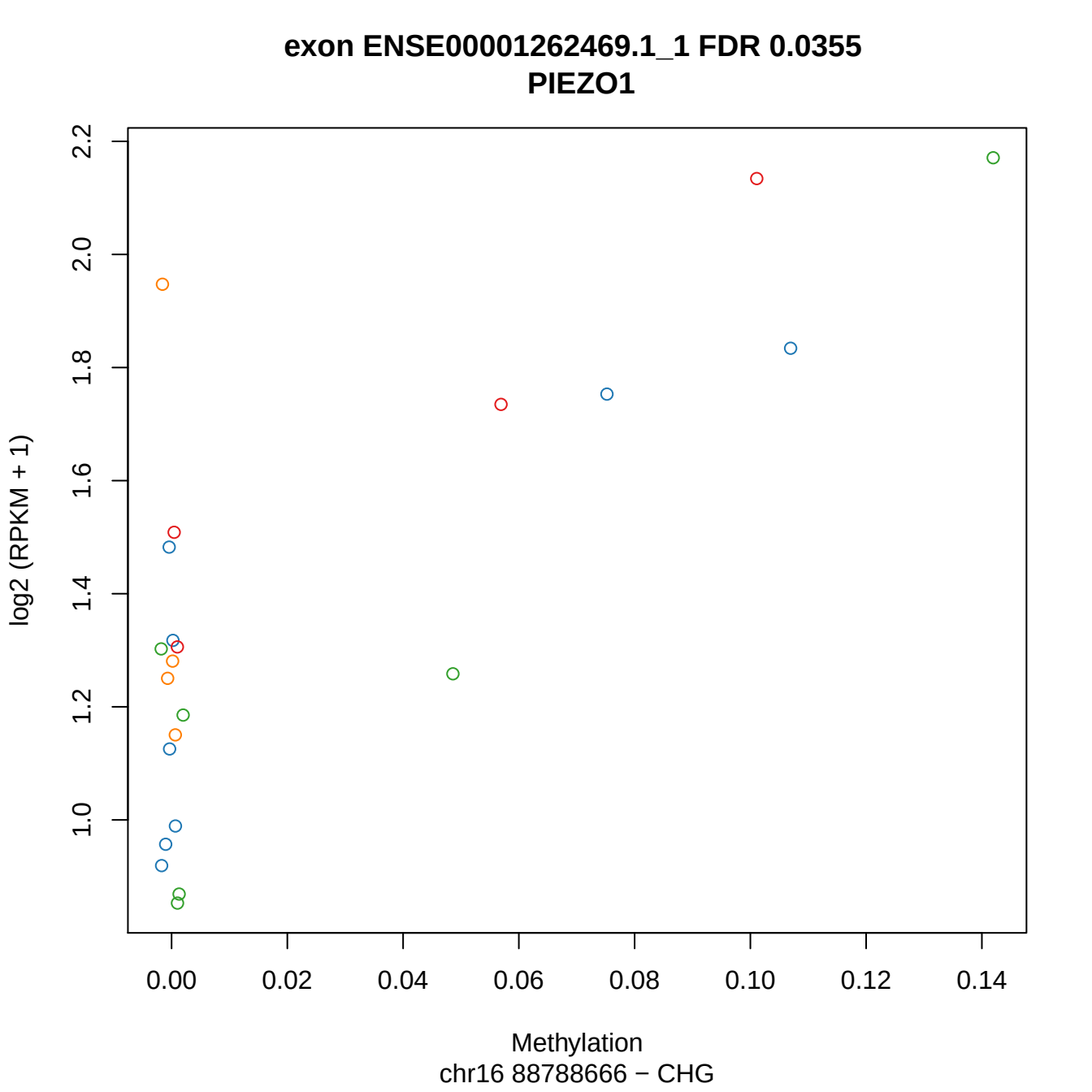

exon ENSE00002278148.1_1 FDR 0.0259
TNC
log2 (RPKM + 1)
1
2
3
4
5
0.0
0.1
0.2
0.3
0.4
0.5
Methylation
chr9 117782234 − CHH

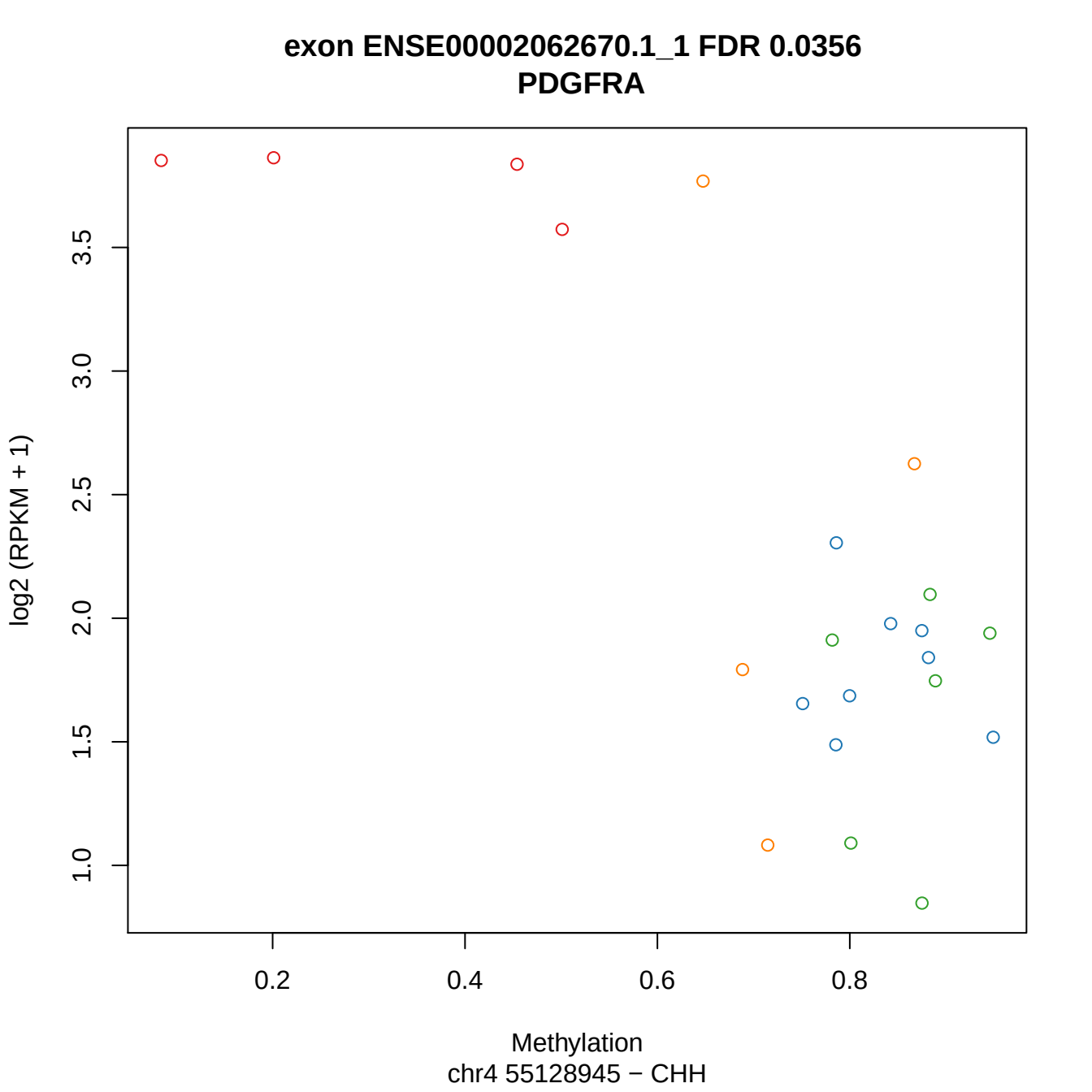

exon ENSE00002050497.1_1 FDR 0.0318
PDGFRA
log2 (RPKM + 1)
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.2
0.4
0.6
0.8
Methylation
chr4 55128945 − CHH

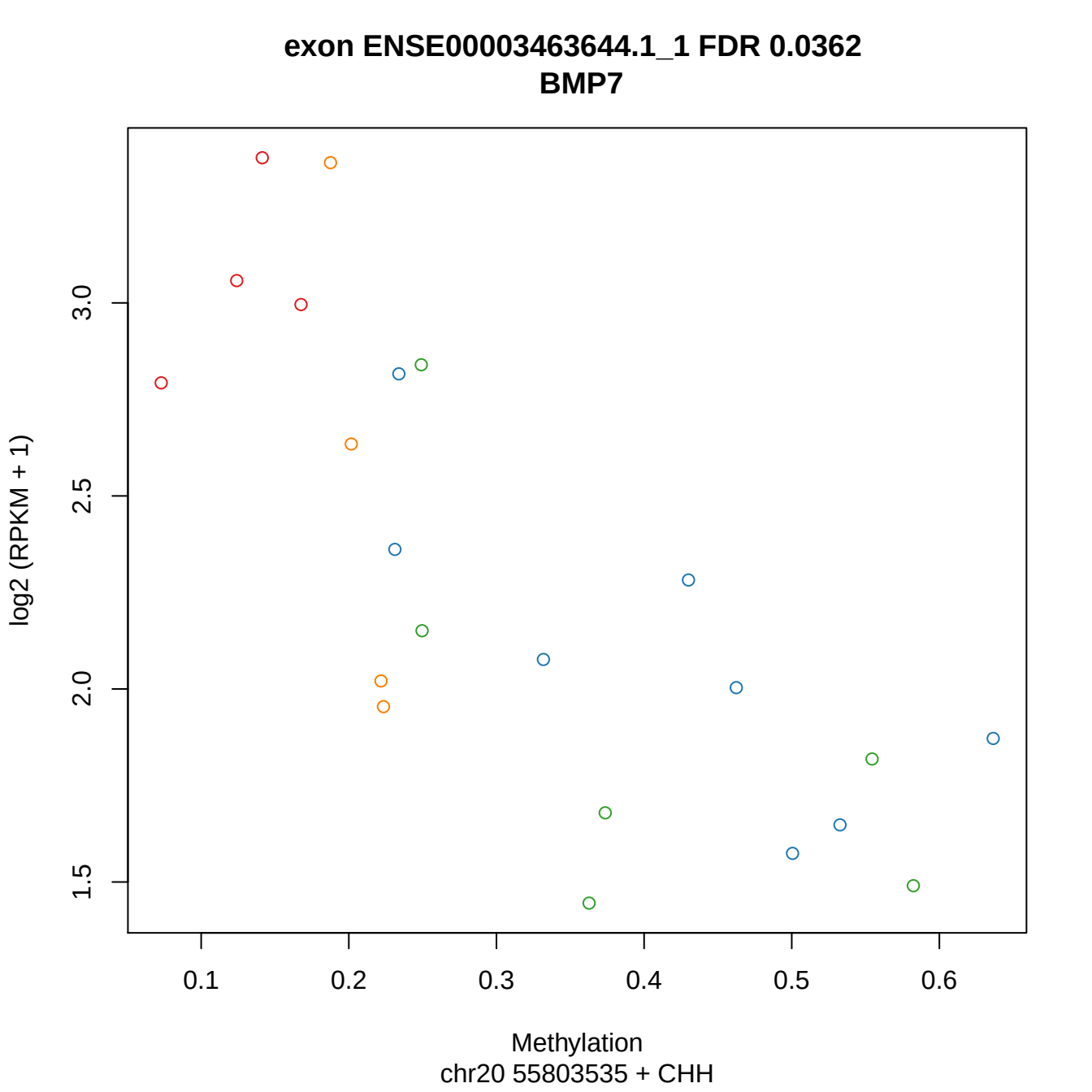

exon ENSE00003785223.1_1 FDR 0.0332
PDGFRA
log2 (RPKM + 1)
1.0
1.5
2.0
2.5
3.0
3.5
0.2
0.4
0.6
0.8
1.0
Methylation
chr4 55127506 + CHH

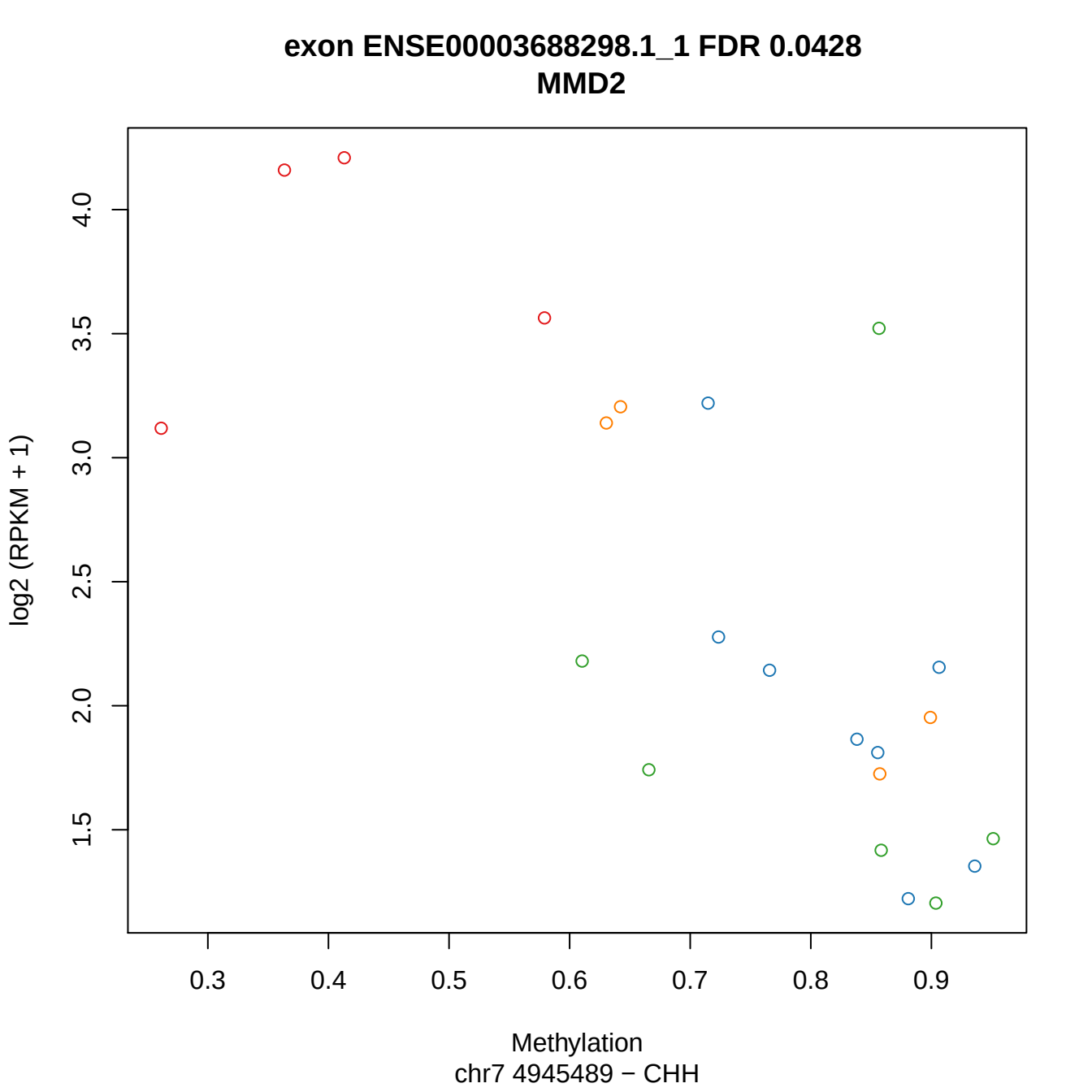

exon ENSE00003666767.1_1 FDR 0.0341
LAMA1
log2 (RPKM + 1)
0.0
0.5
1.0
1.5
0.2
0.4
0.6
0.8
1.0
Methylation
chr18 6992976 − CHH

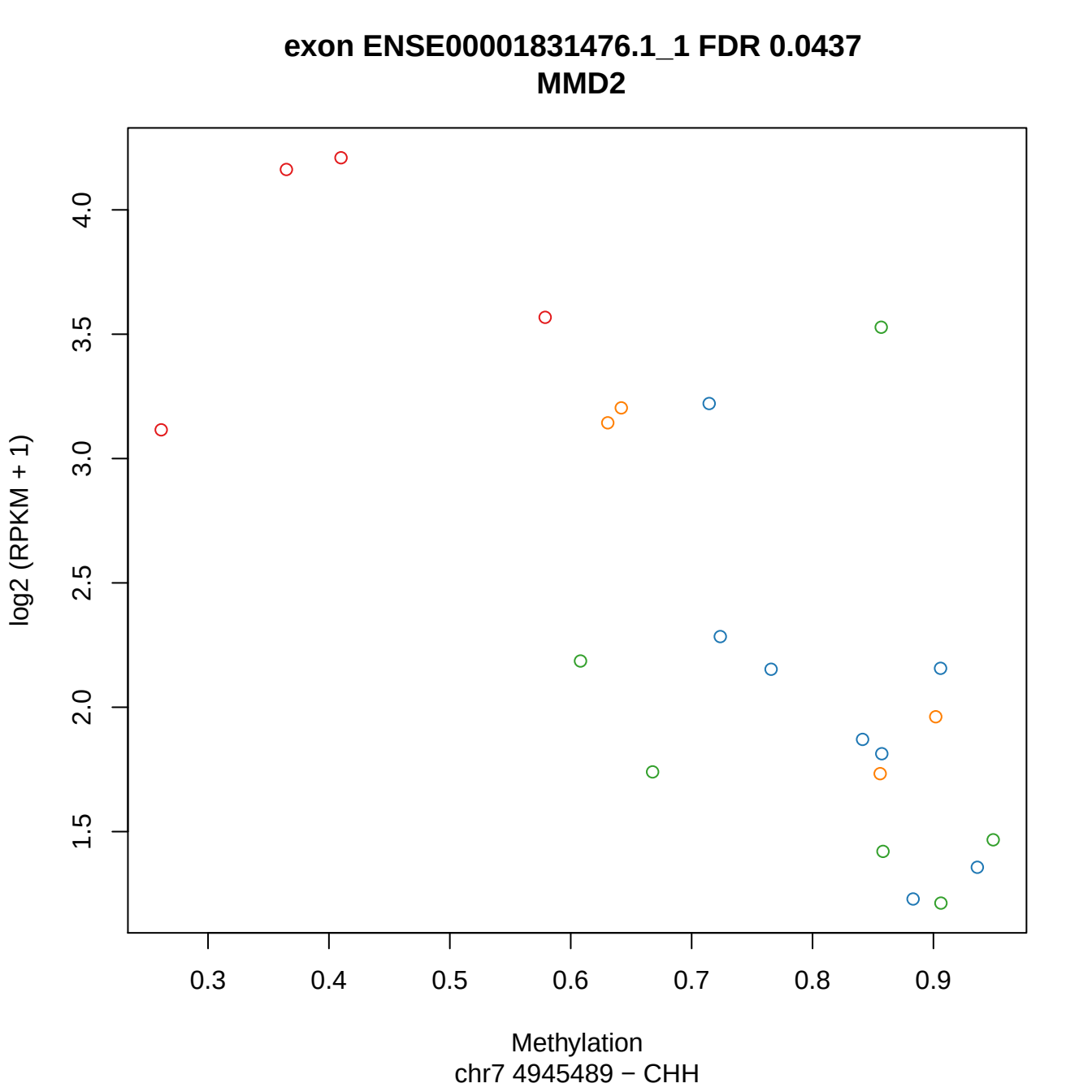

exon ENSE00003537008.1_1 FDR 0.0347
GLI3
log2 (RPKM + 1)
0.0
0.2
0.4
0.6
0.8
1.0
0.3
0.4
0.5
0.6
0.7
0.8
0.9
Methylation
chr7 42011549 − CHG

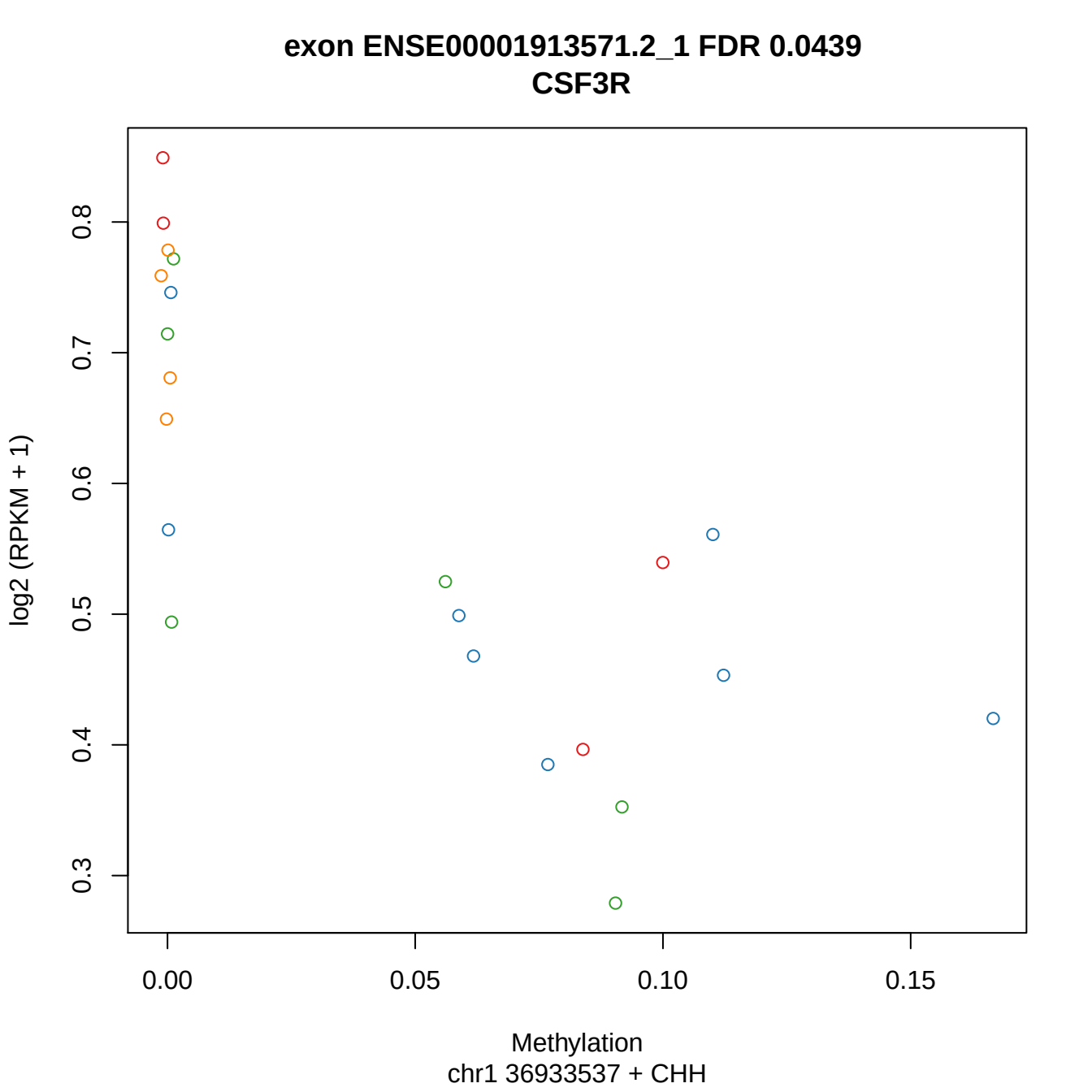

exon ENSE00001262469.1_1 FDR 0.0355
PIEZO1
log2 (RPKM + 1)
2.2
2.0
1.8
1.6
1.4
1.2
1.0
0.00
0.02
0.04
0.06
0.08
0.10
0.12
0.14
Methylation
chr16 88788666 − CHG

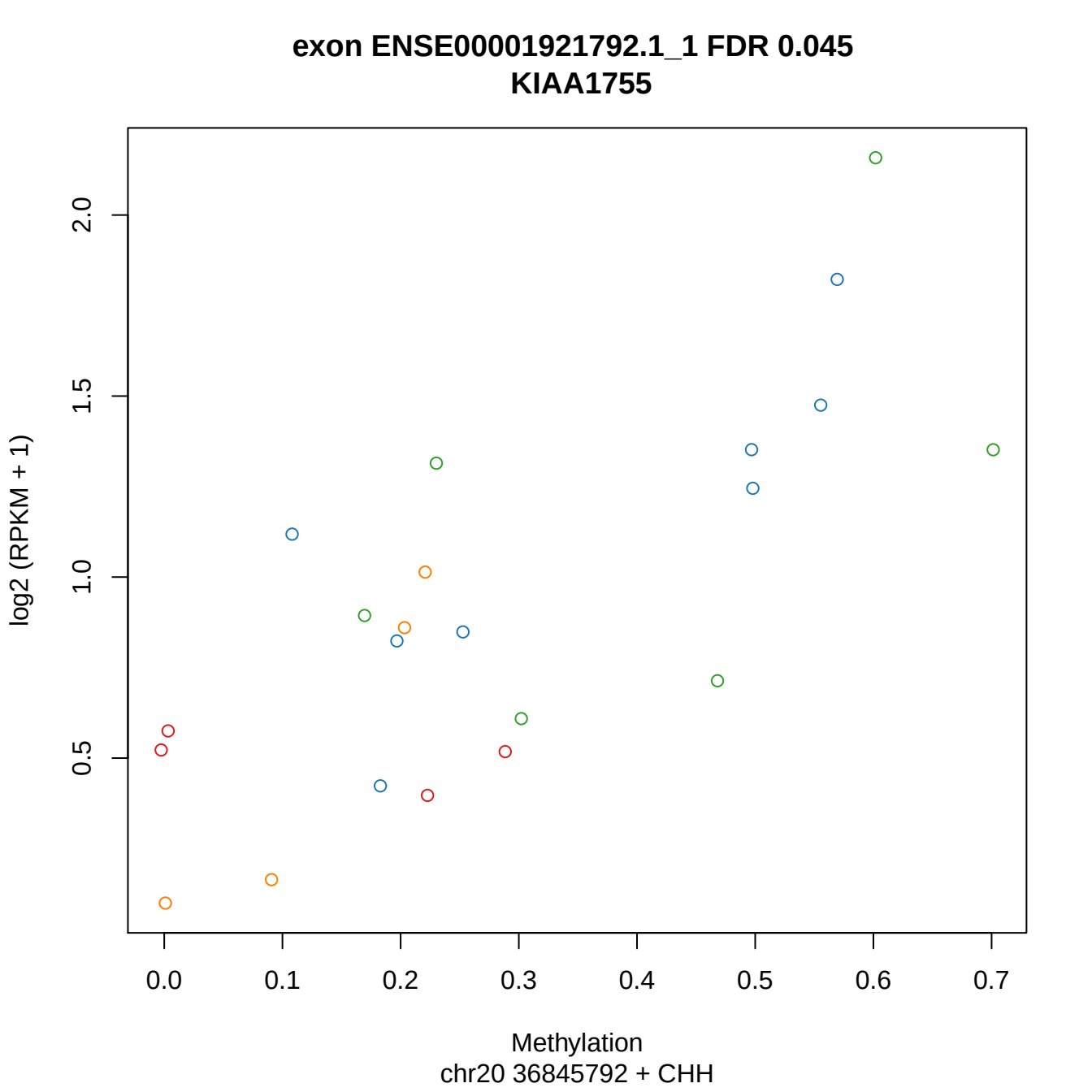

exon ENSE00002062670.1_1 FDR 0.0356
PDGFRA
log2 (RPKM + 1)
1.0
1.5
2.0
2.5
3.0
3.5
0.2
0.4
0.6
0.8
Methylation
chr4 55128945 − CHH

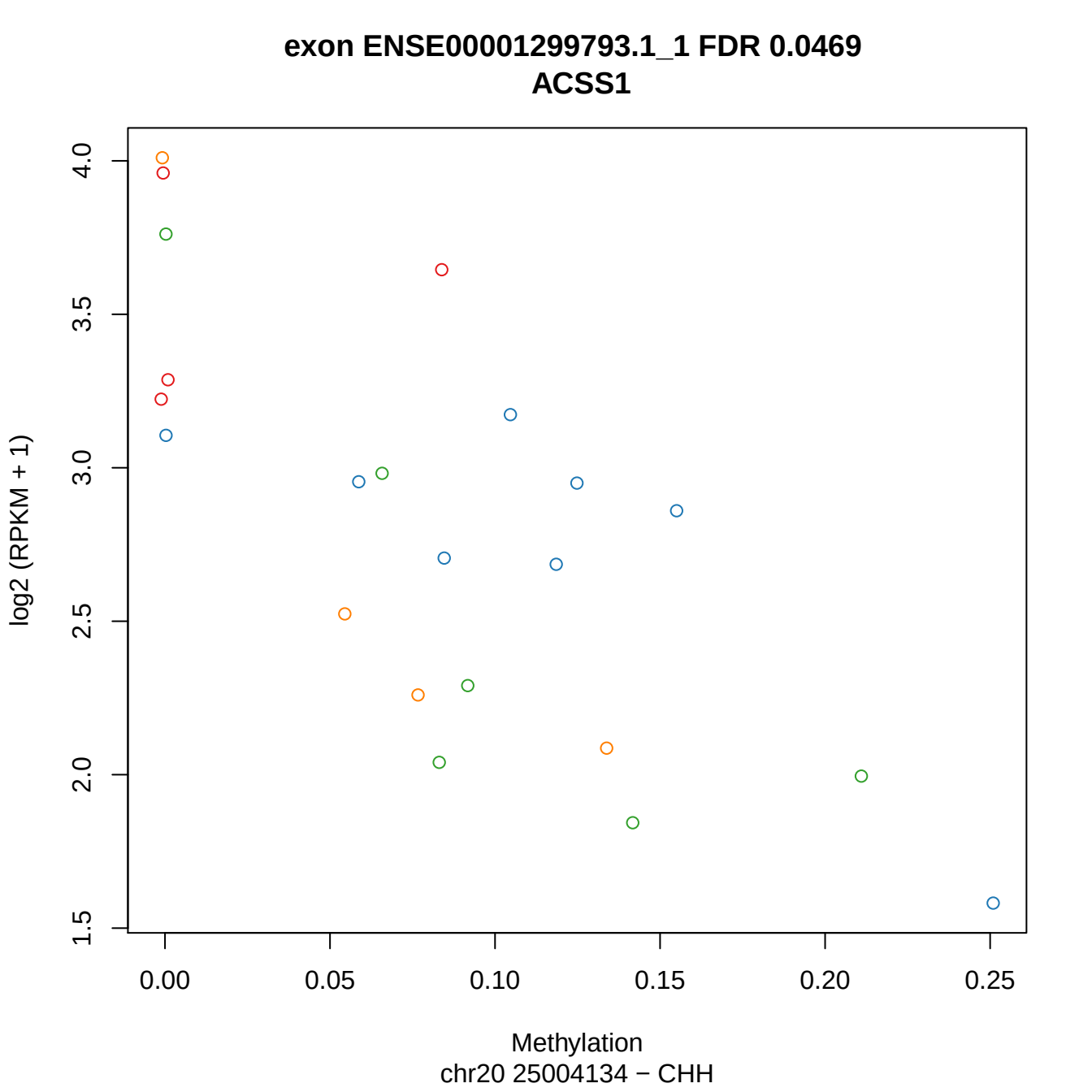

exon ENSE00003463644.1_1 FDR 0.0362
BMP7
log2 (RPKM + 1)
3.0
2.5
2.0
1.5
0.1
0.2
0.3
0.4
0.5
0.6
Methylation
chr20 55803535 + CHH

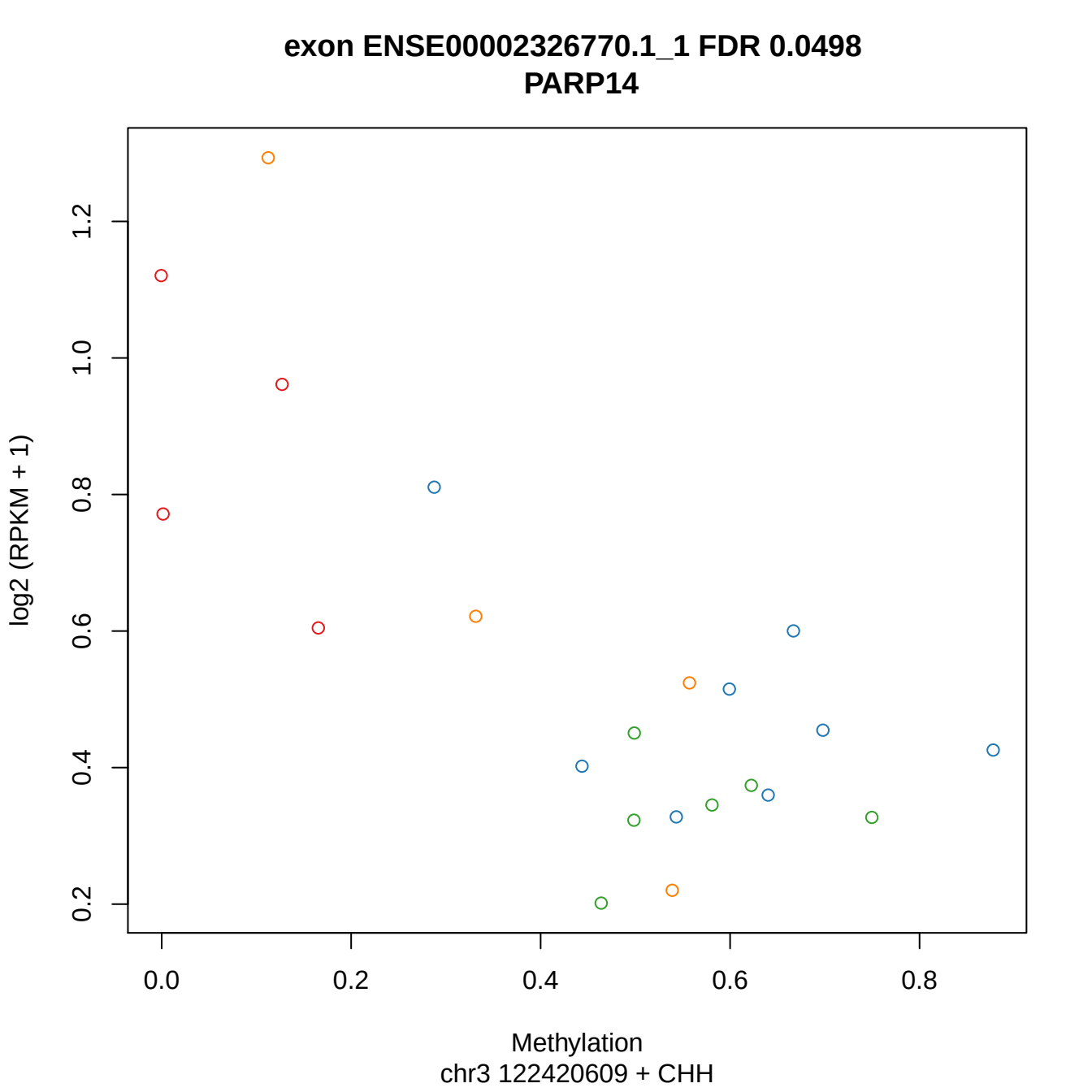

exon ENSE00003688298.1_1 FDR 0.0428
MMD2
log2 (RPKM + 1)
4.0
3.5
3.0
2.5
2.0
1.5
0.3
0.4
0.5
0.6
0.7
0.8
0.9
Methylation
chr7 4945489 − CHH

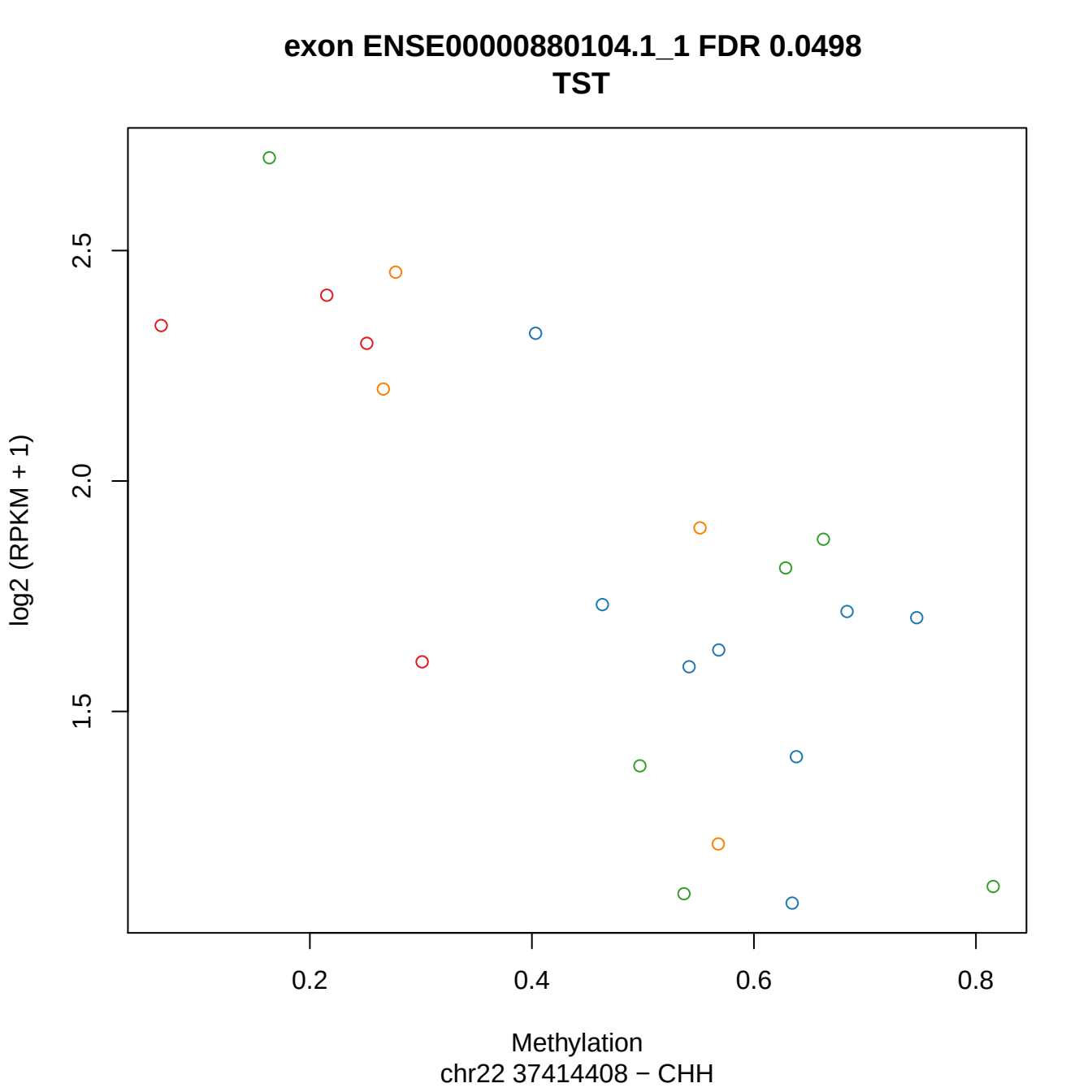

exon ENSE00001831476.1_1 FDR 0.0437
MMD2
log2 (RPKM + 1)
4.0
3.5
3.0
2.5
2.0
1.5
0.3
0.4
0.5
0.6
0.7
0.8
0.9
Methylation
chr7 4945489 − CHH


exon ENSE00001913571.2_1 FDR 0.0439
CSF3R
log2 (RPKM + 1)
0.3
0.4
0.5
0.6
0.7
0.8
0.00
0.05
0.10
0.15
Methylation
chr1 36933537 + CHH


exon ENSE00001921792.1_1 FDR 0.045
KIAA1755
log2 (RPKM + 1)
0.5
1.0
1.5
2.0
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Methylation
chr20 36845792 + CHH


exon ENSE00001299793.1_1 FDR 0.0469
ACSS1
log2 (RPKM + 1)
4.0
3.5
3.0
2.5
2.0
1.5
0.00
0.05
0.10
0.15
0.20
0.25
Methylation
chr20 25004134 − CHH


exon ENSE00002326770.1_1 FDR 0.0498
PARP14
log2 (RPKM + 1)
0.2
0.4
0.6
0.8
1.0
1.2
0.0
0.2
0.4
0.6
0.8
Methylation
chr3 122420609 + CHH


exon ENSE00000880104.1_1 FDR 0.0498
TST
log2 (RPKM + 1)
2.5
2.0
1.5
0.2
0.4
0.6
0.8
Methylation
chr22 37414408 − CHH