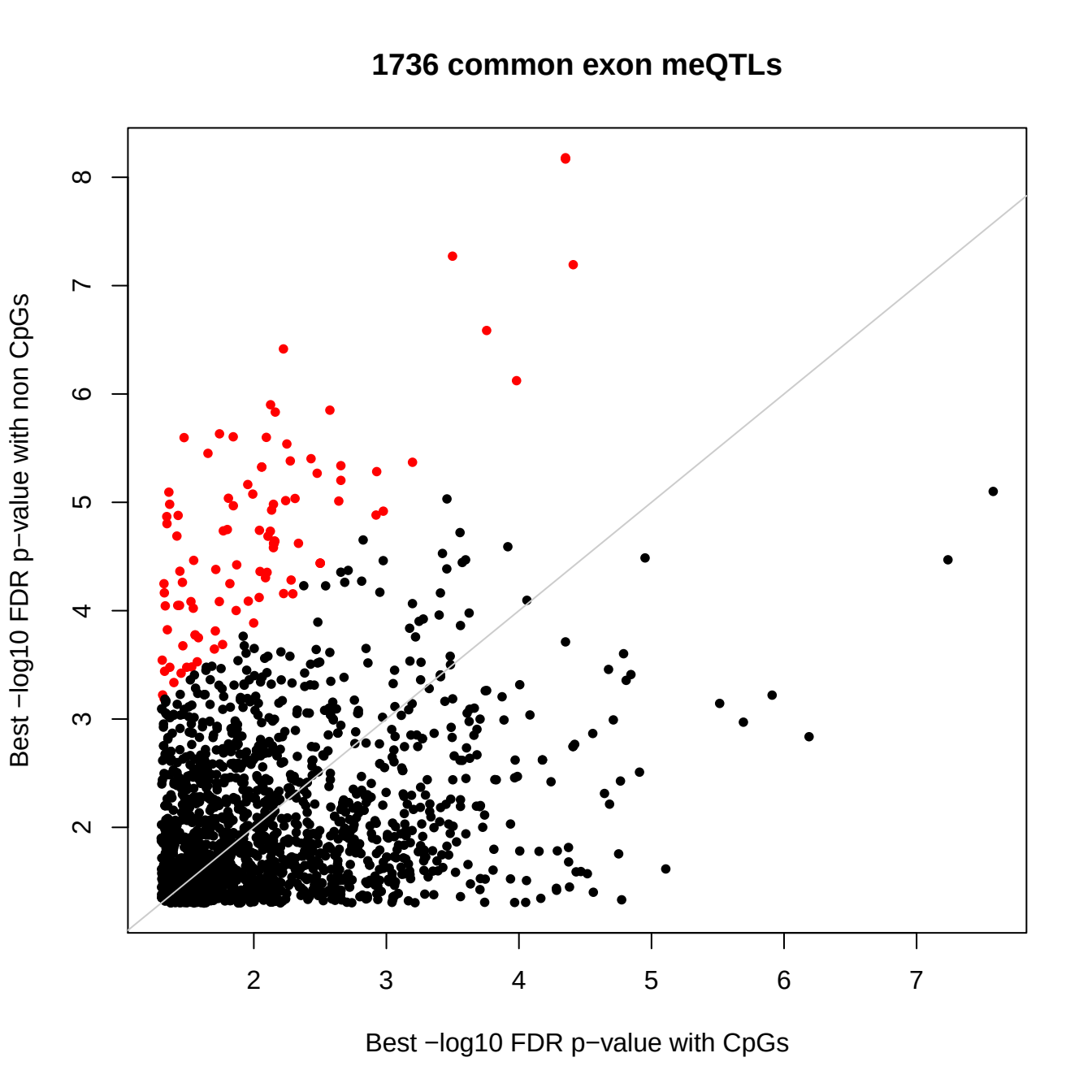
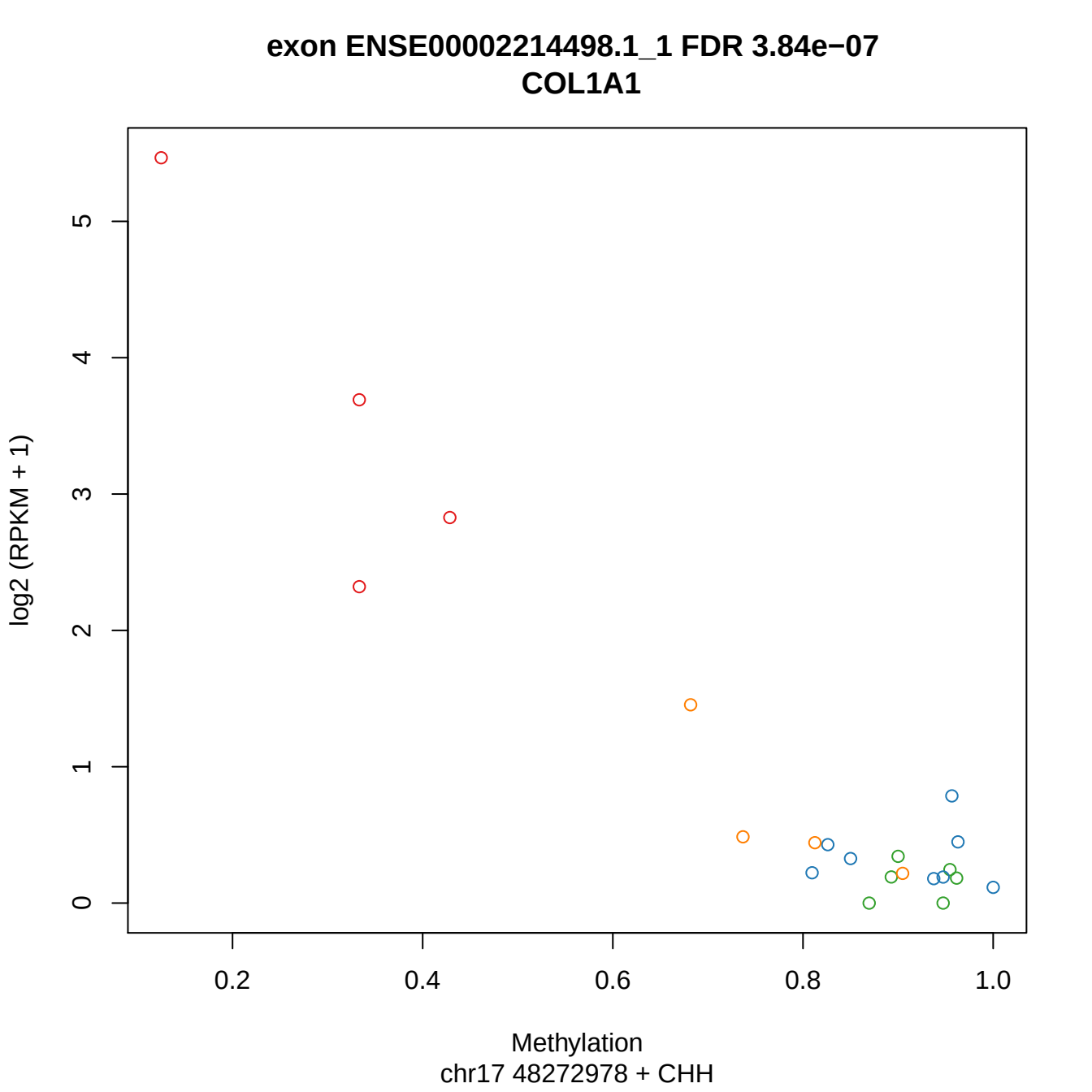
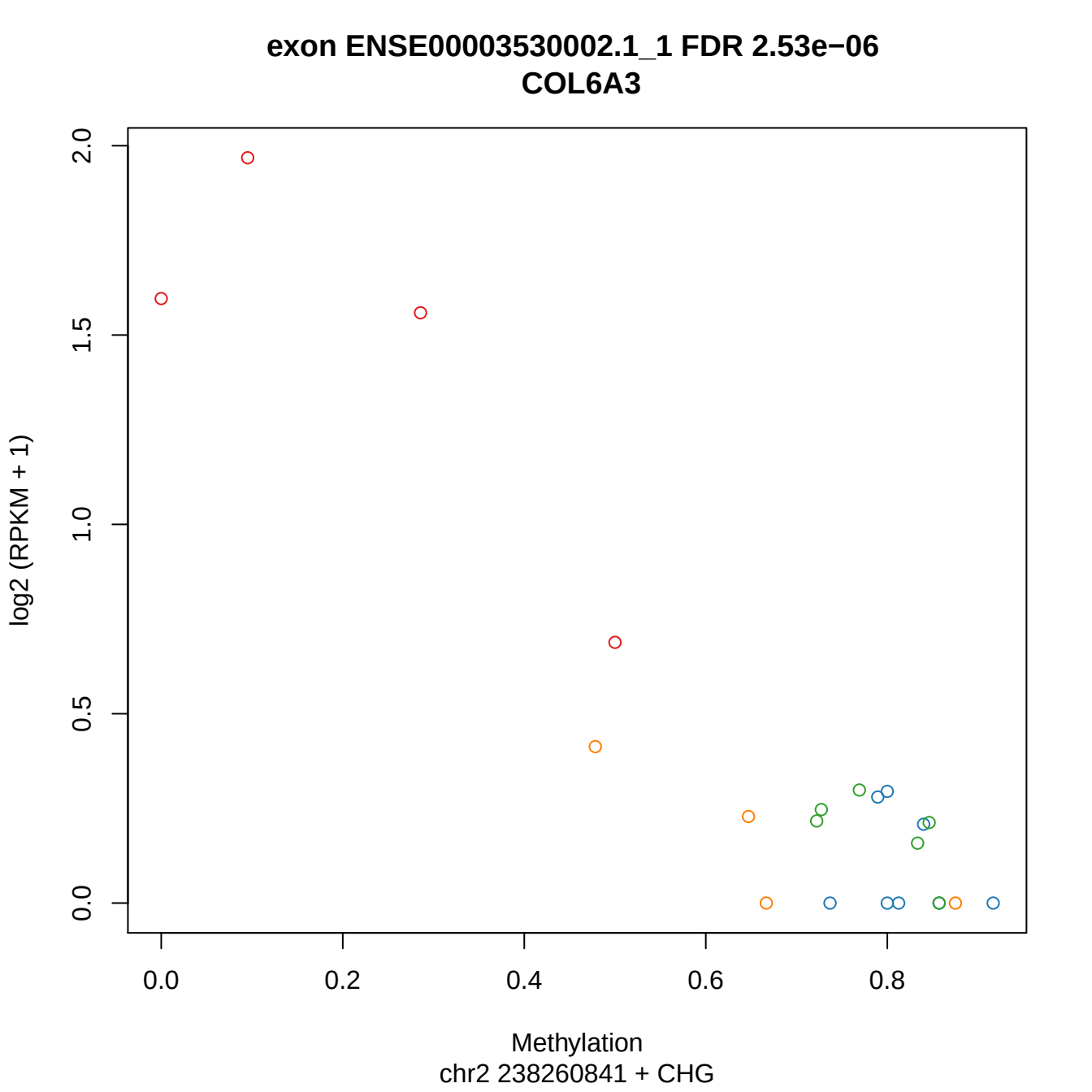
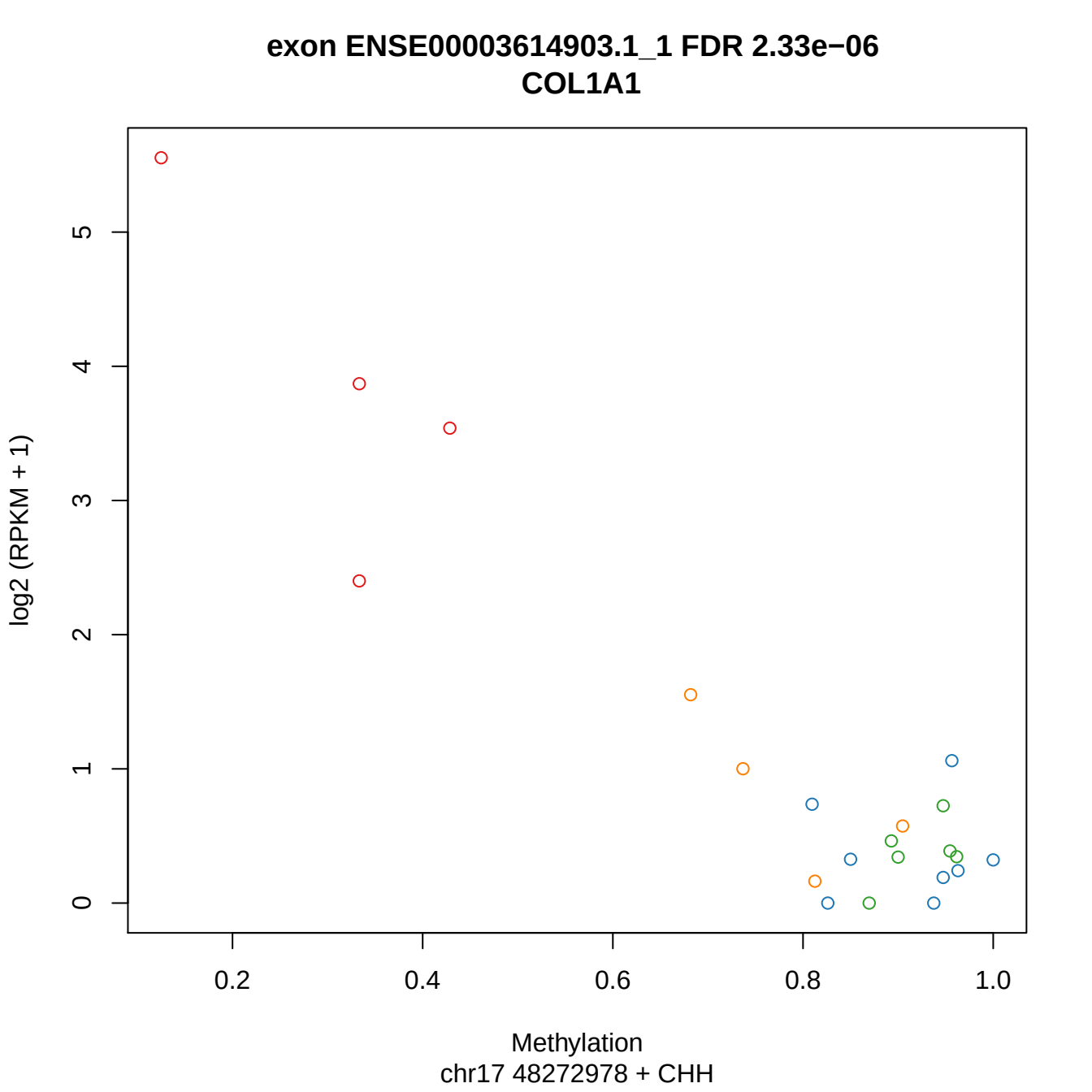
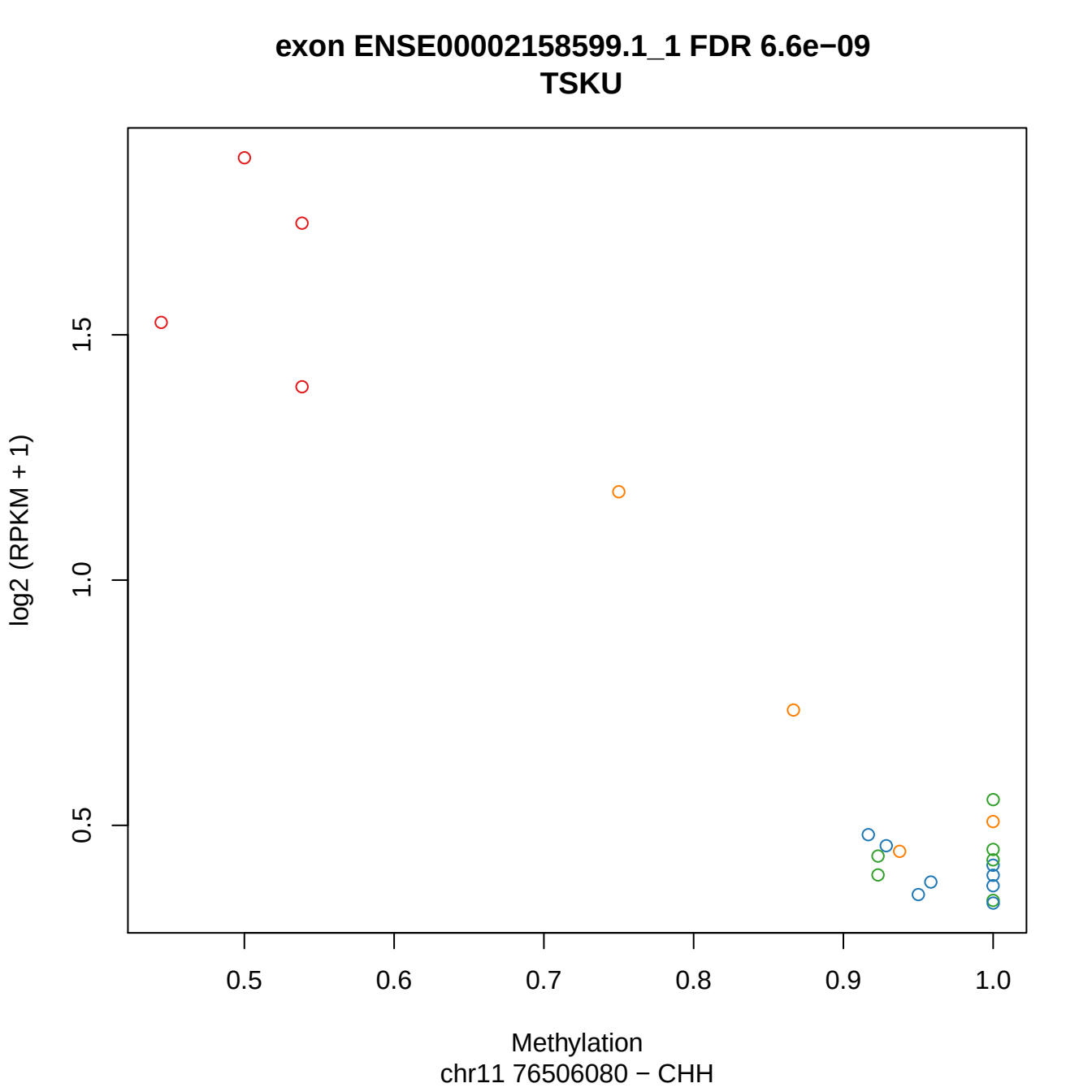
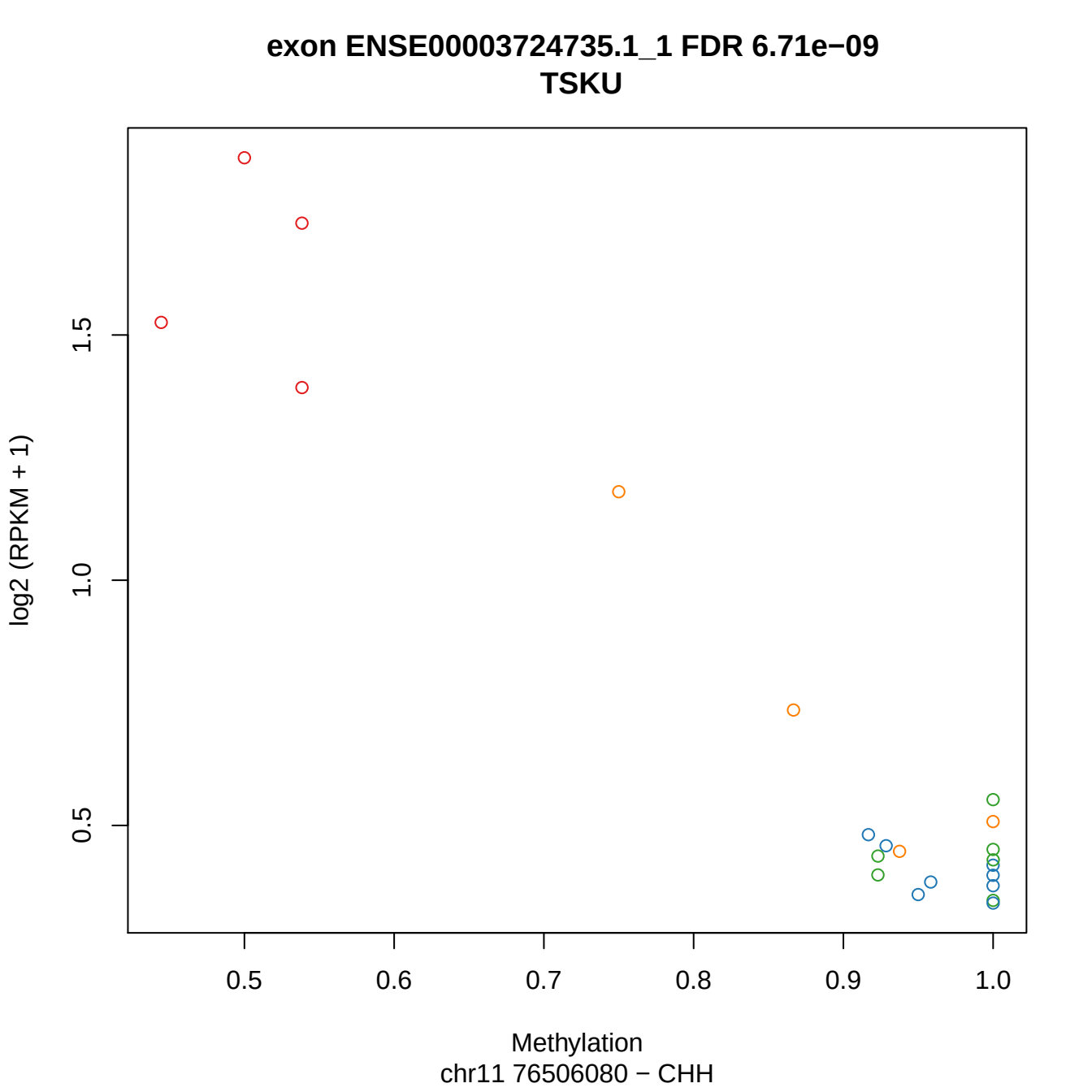

1736 common exon meQTLs
Best −log10 FDR p−value with non CpGs
Best −log10 FDR p−value with CpGs
2
3
4
5
6
7
8

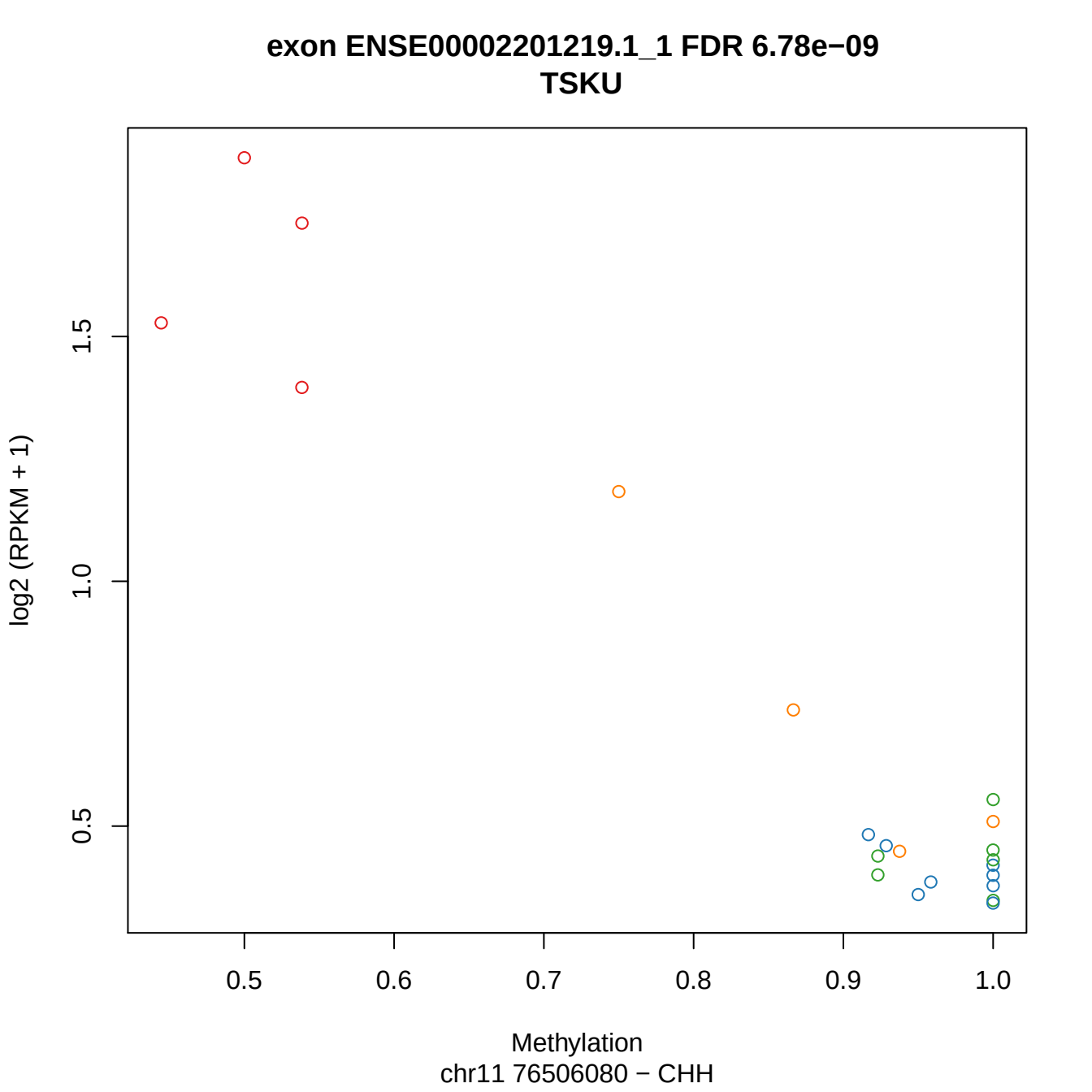

exon ENSE00002214498.1_1 FDR 3.84e−07
COL1A1
log2 (RPKM + 1)
0
1
2
3
4
5
0.2
0.4
0.6
0.8
1.0
Methylation
chr17 48272978 + CHH

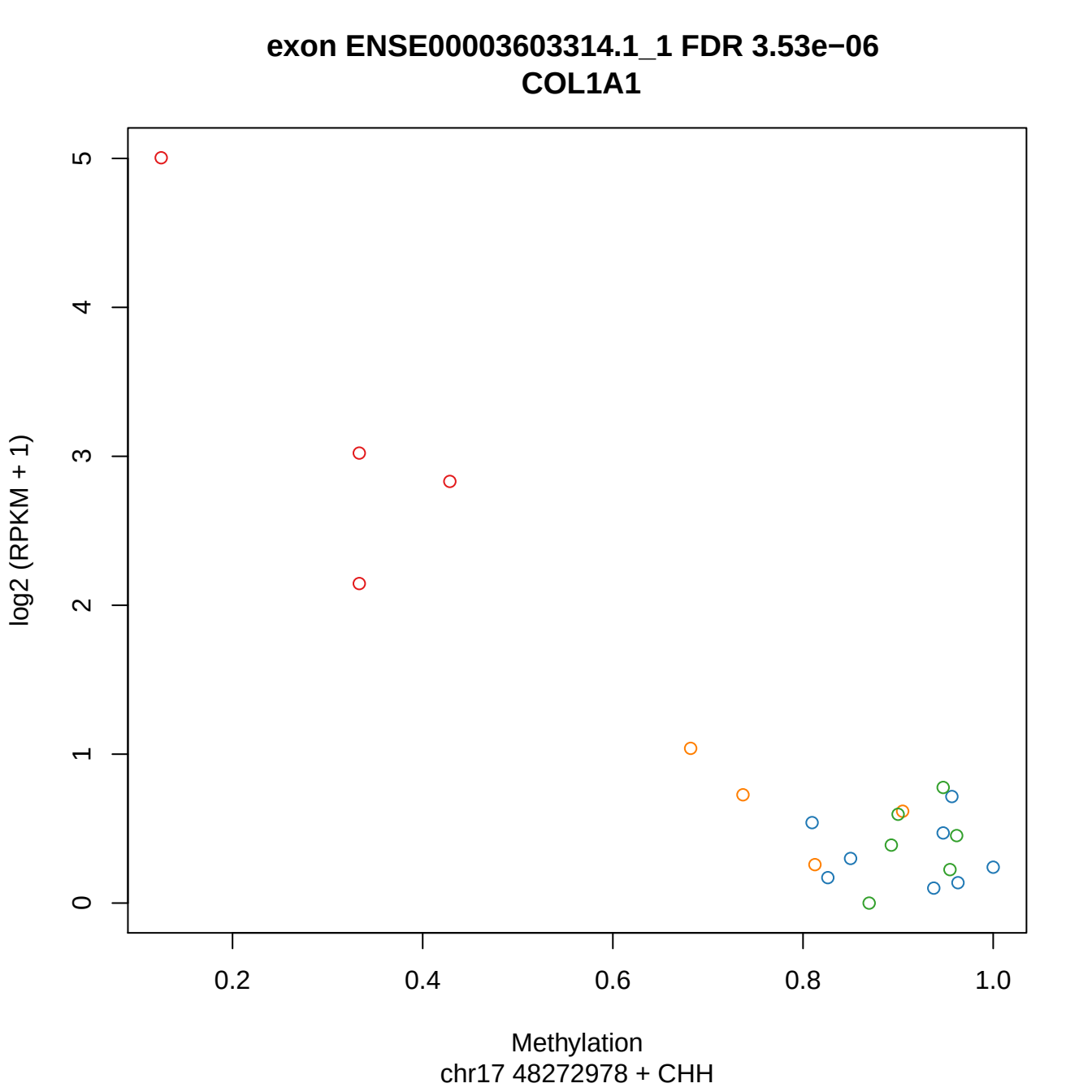

exon ENSE00003530002.1_1 FDR 2.53e−06
COL6A3
log2 (RPKM + 1)
0.0
0.5
1.0
1.5
2.0
0.0
0.2
0.4
0.6
0.8
Methylation
chr2 238260841 + CHG

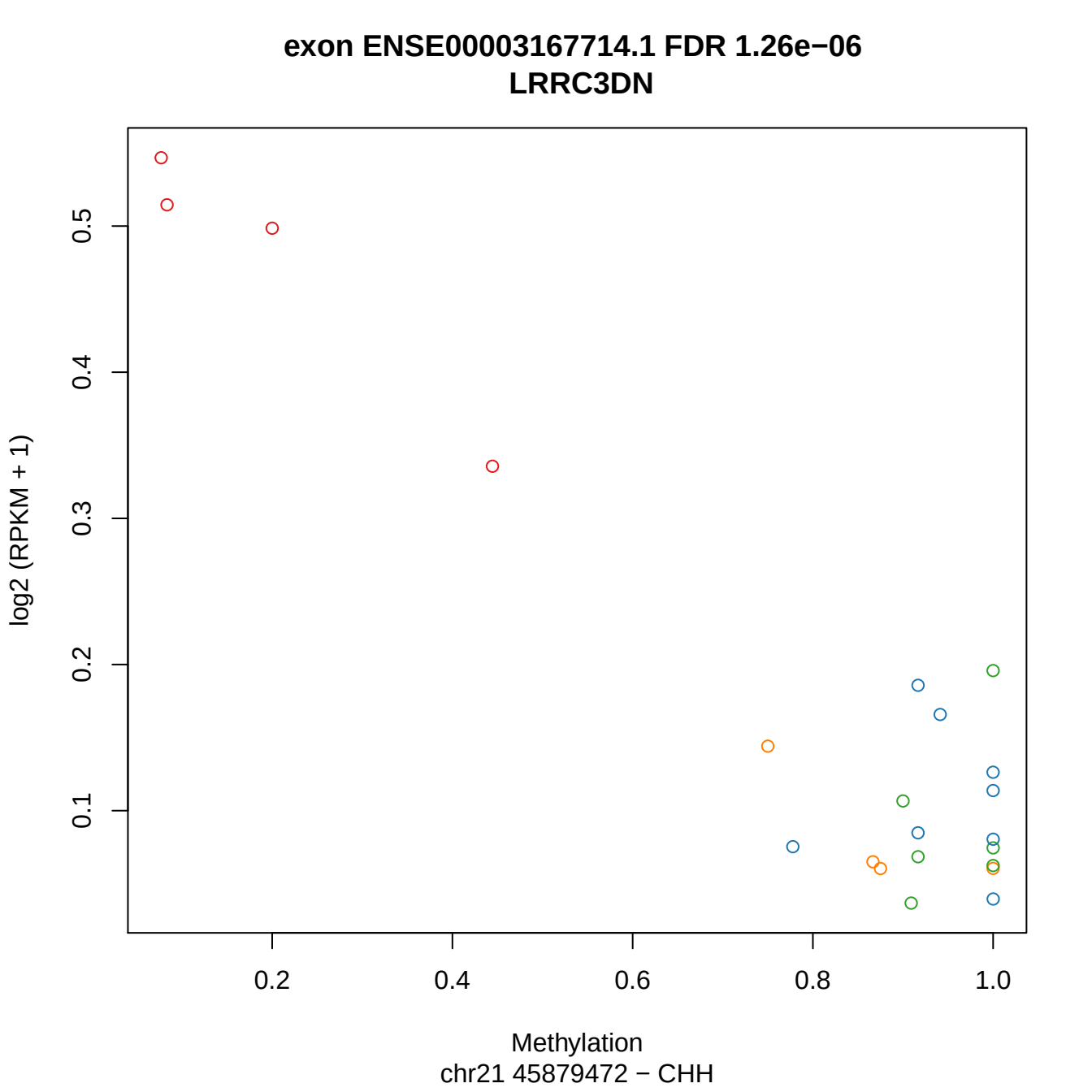

exon ENSE00003614903.1_1 FDR 2.33e−06
COL1A1
log2 (RPKM + 1)
0
1
2
3
4
5
0.2
0.4
0.6
0.8
1.0
Methylation
chr17 48272978 + CHH

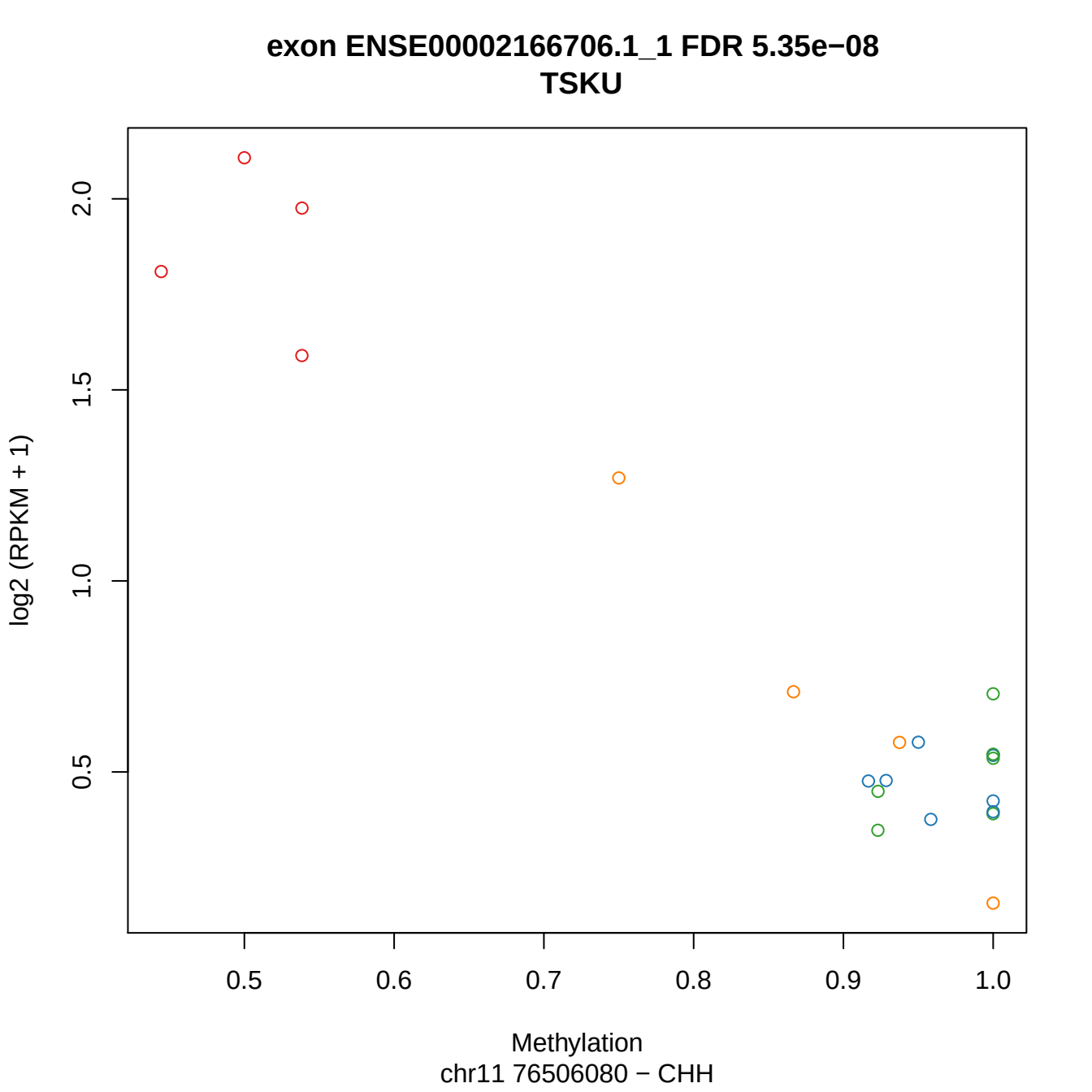

exon ENSE00002158599.1_1 FDR 6.6e−09
TSKU
log2 (RPKM + 1)
0.5
1.0
1.5
0.5
0.6
0.7
0.8
0.9
1.0
Methylation
chr11 76506080 − CHH

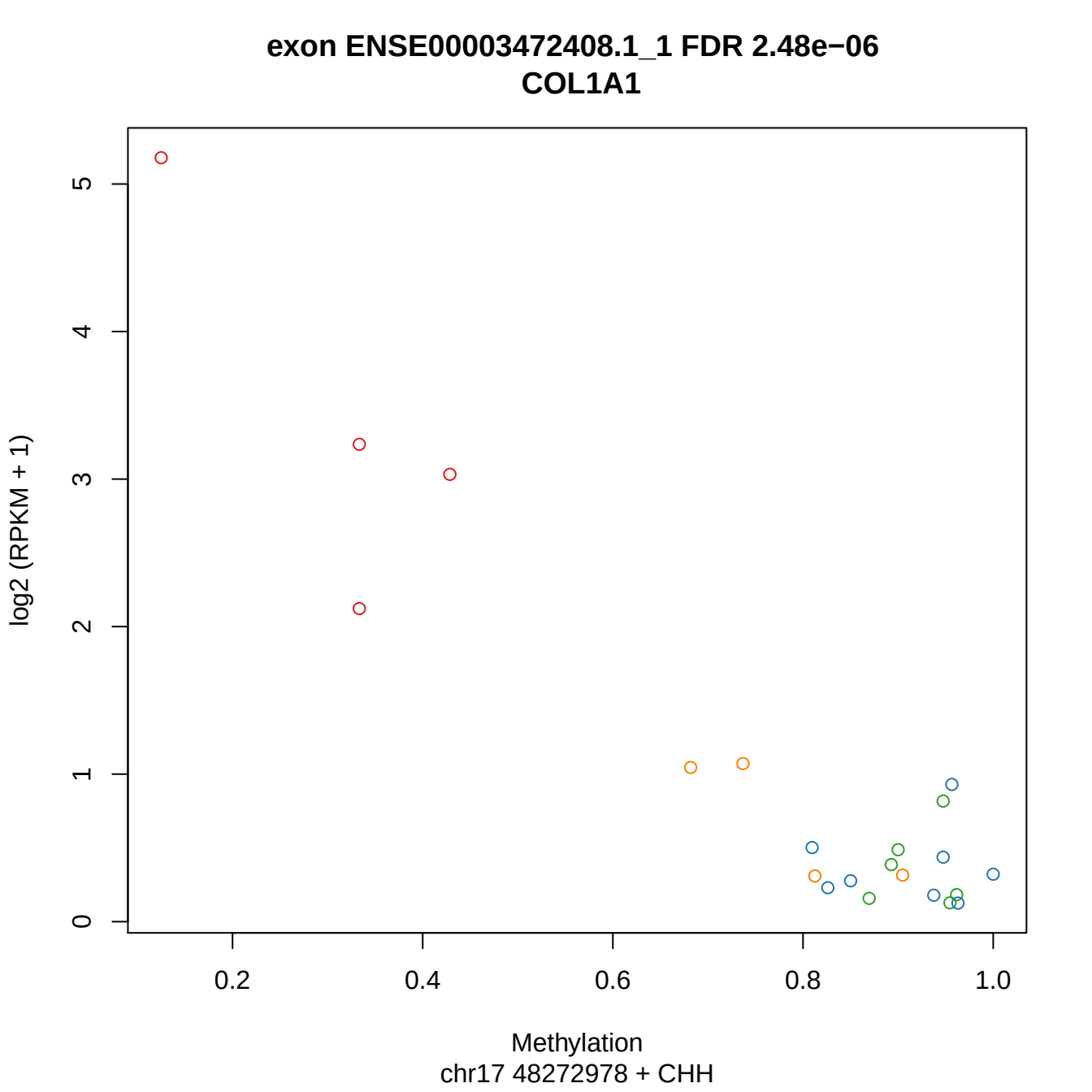

exon ENSE00003724735.1_1 FDR 6.71e−09
TSKU
log2 (RPKM + 1)
0.5
1.0
1.5
0.5
0.6
0.7
0.8
0.9
1.0
Methylation
chr11 76506080 − CHH

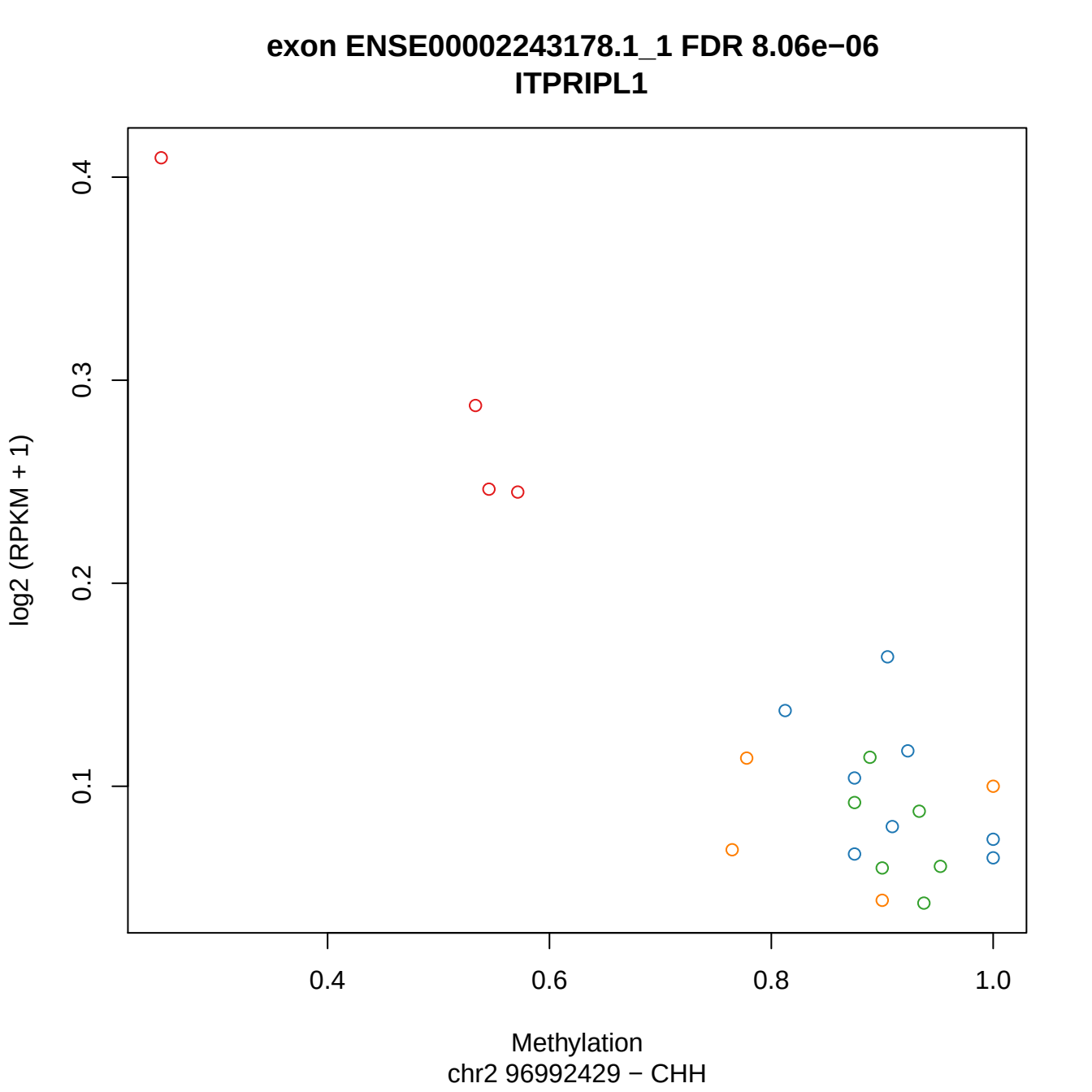

exon ENSE00002201219.1_1 FDR 6.78e−09
TSKU
log2 (RPKM + 1)
0.5
1.0
1.5
0.5
0.6
0.7
0.8
0.9
1.0
Methylation
chr11 76506080 − CHH

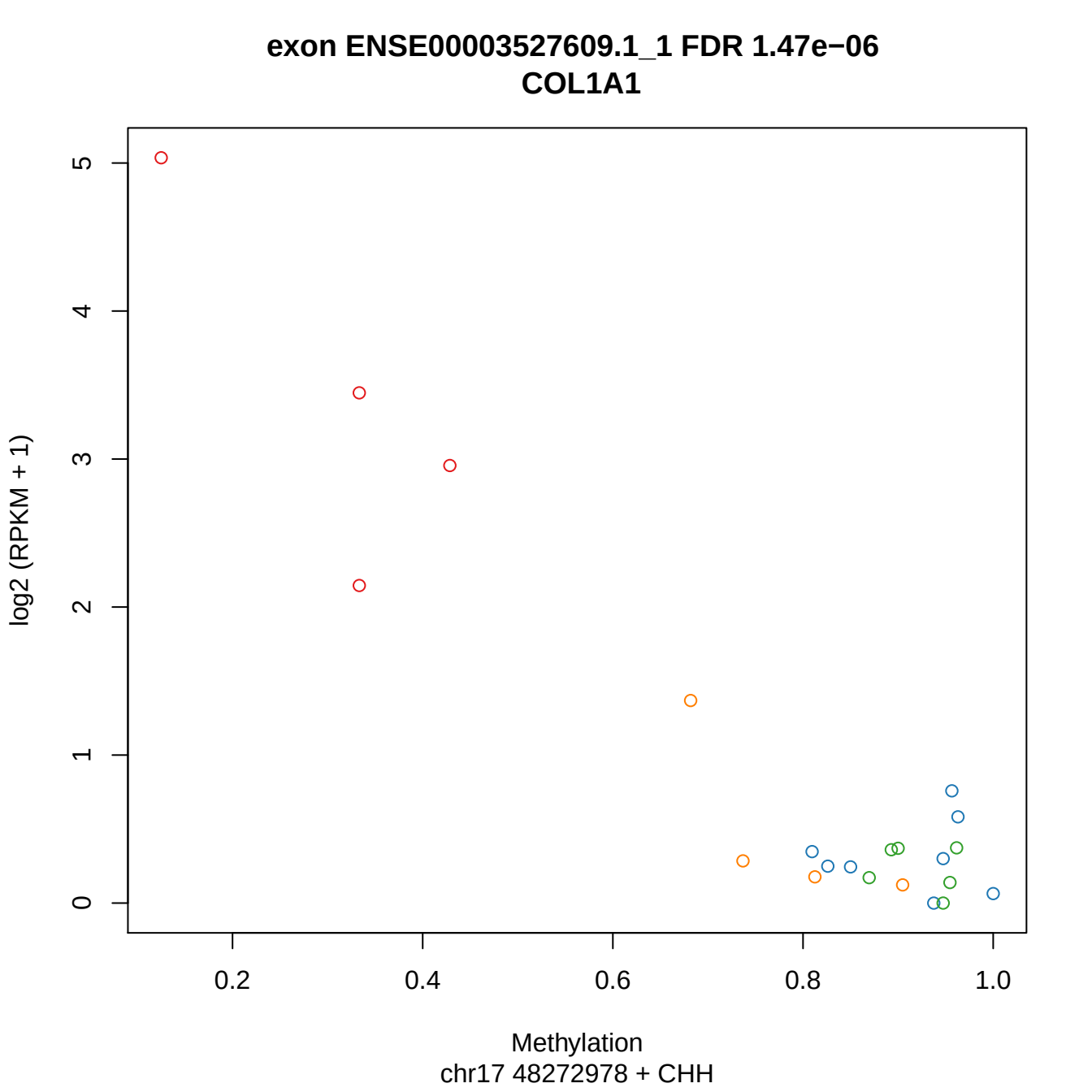

exon ENSE00003603314.1_1 FDR 3.53e−06
COL1A1
log2 (RPKM + 1)
0
1
2
3
4
5
0.2
0.4
0.6
0.8
1.0
Methylation
chr17 48272978 + CHH

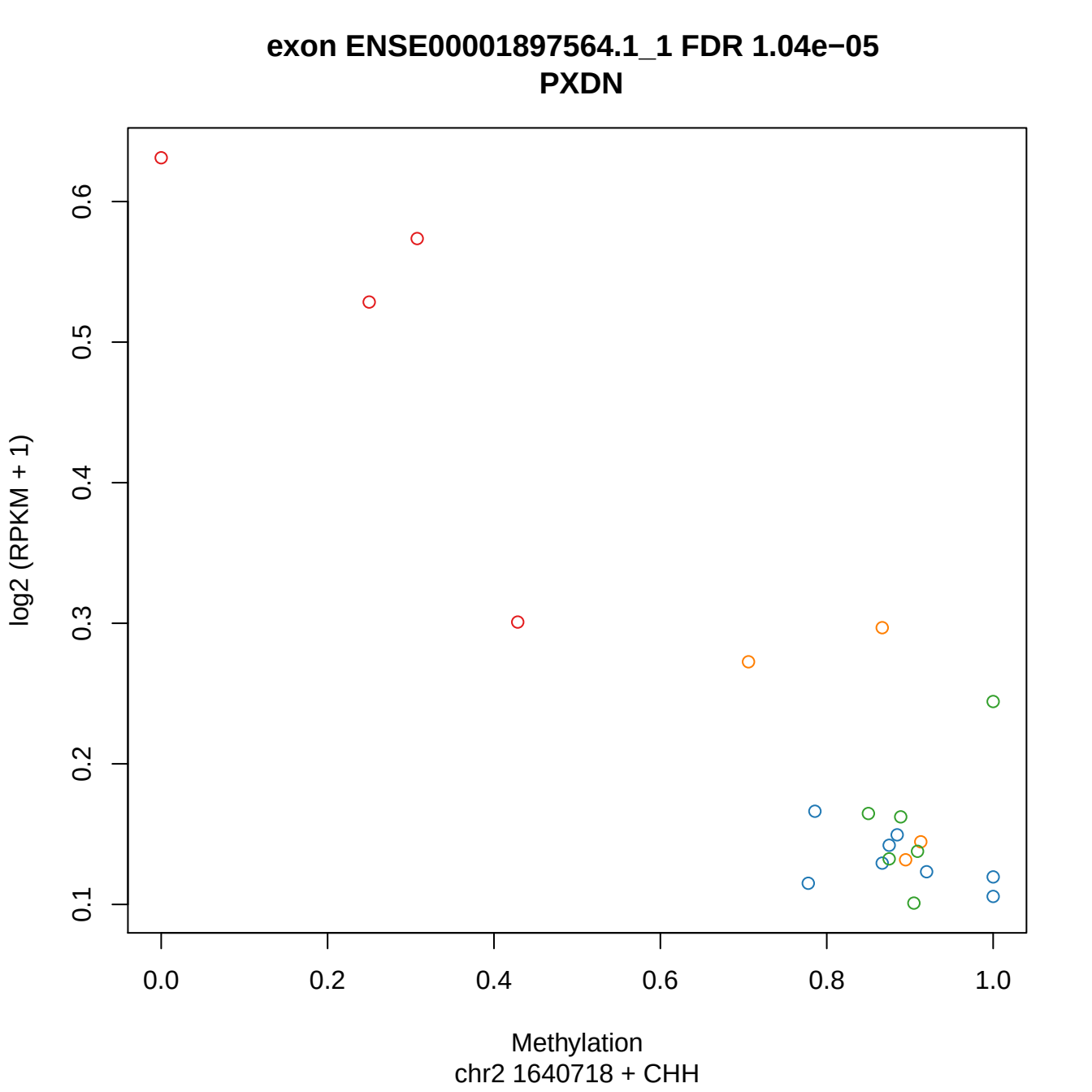

exon ENSE00003167714.1 FDR 1.26e−06
LRRC3DN
log2 (RPKM + 1)
0.1
0.2
0.3
0.4
0.5
0.2
0.4
0.6
0.8
1.0
Methylation
chr21 45879472 − CHH

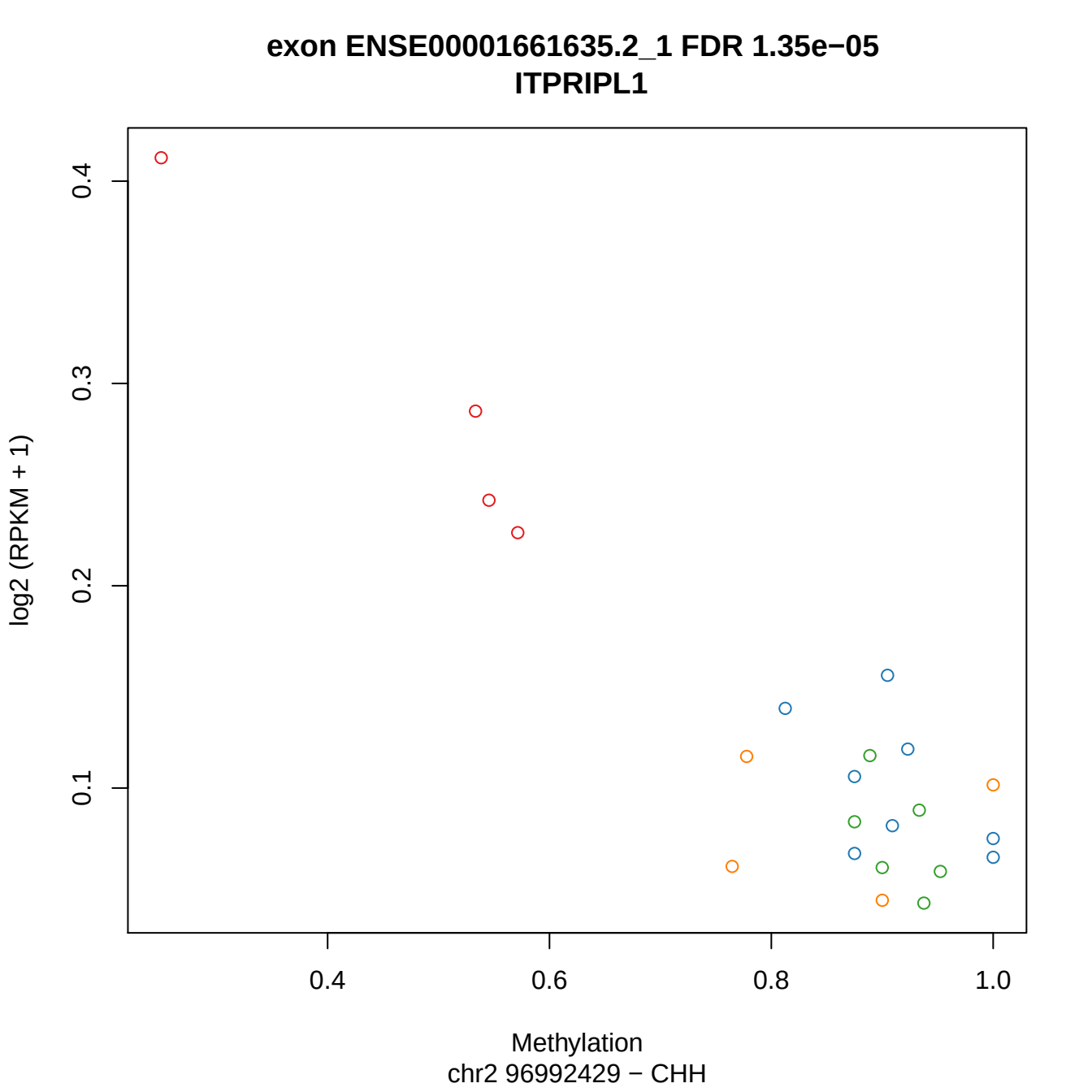

exon ENSE00002166706.1_1 FDR 5.35e−08
TSKU
log2 (RPKM + 1)
0.5
1.0
1.5
2.0
0.5
0.6
0.7
0.8
0.9
1.0
Methylation
chr11 76506080 − CHH

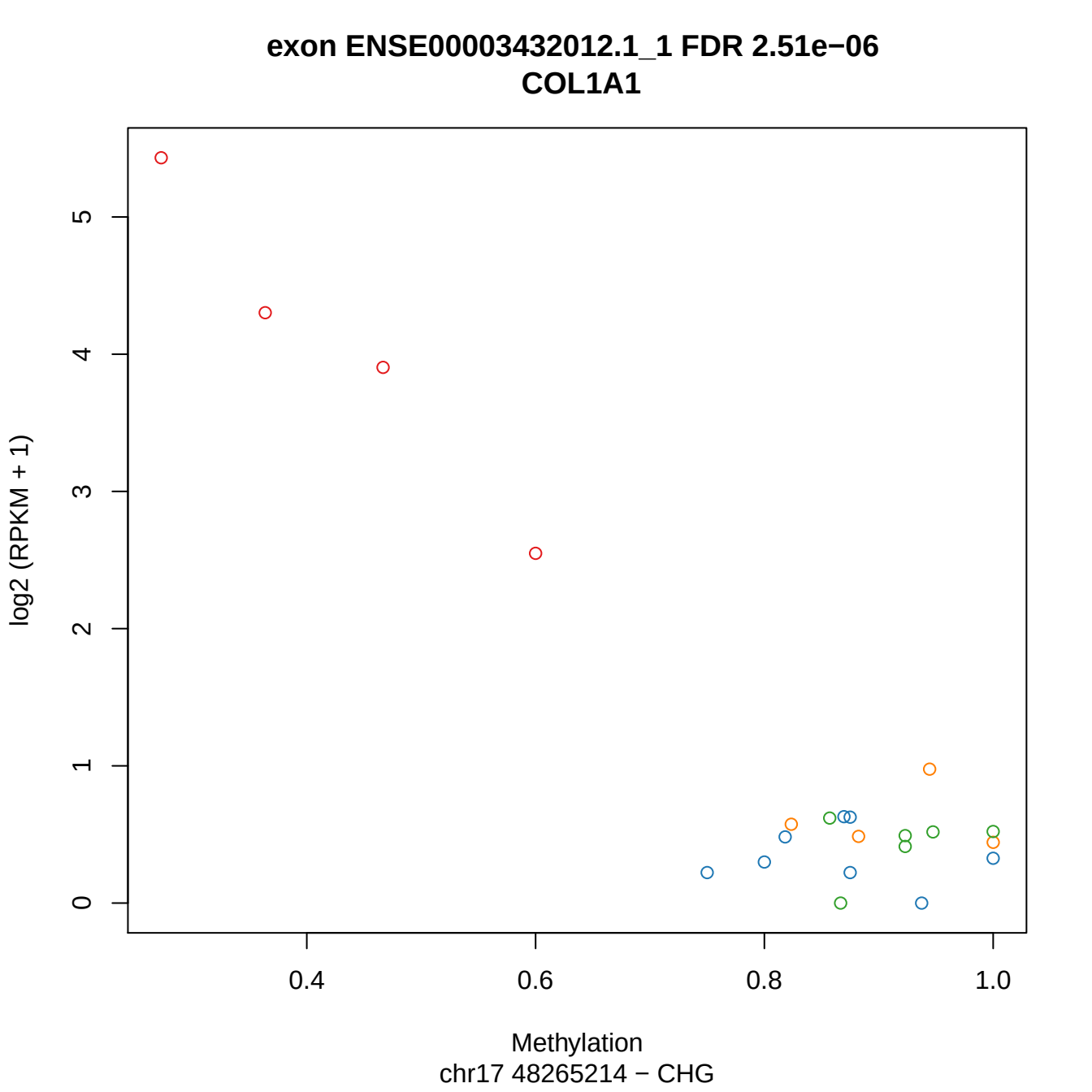

exon ENSE00003472408.1_1 FDR 2.48e−06
COL1A1
log2 (RPKM + 1)
0
1
2
3
4
5
0.2
0.4
0.6
0.8
1.0
Methylation
chr17 48272978 + CHH

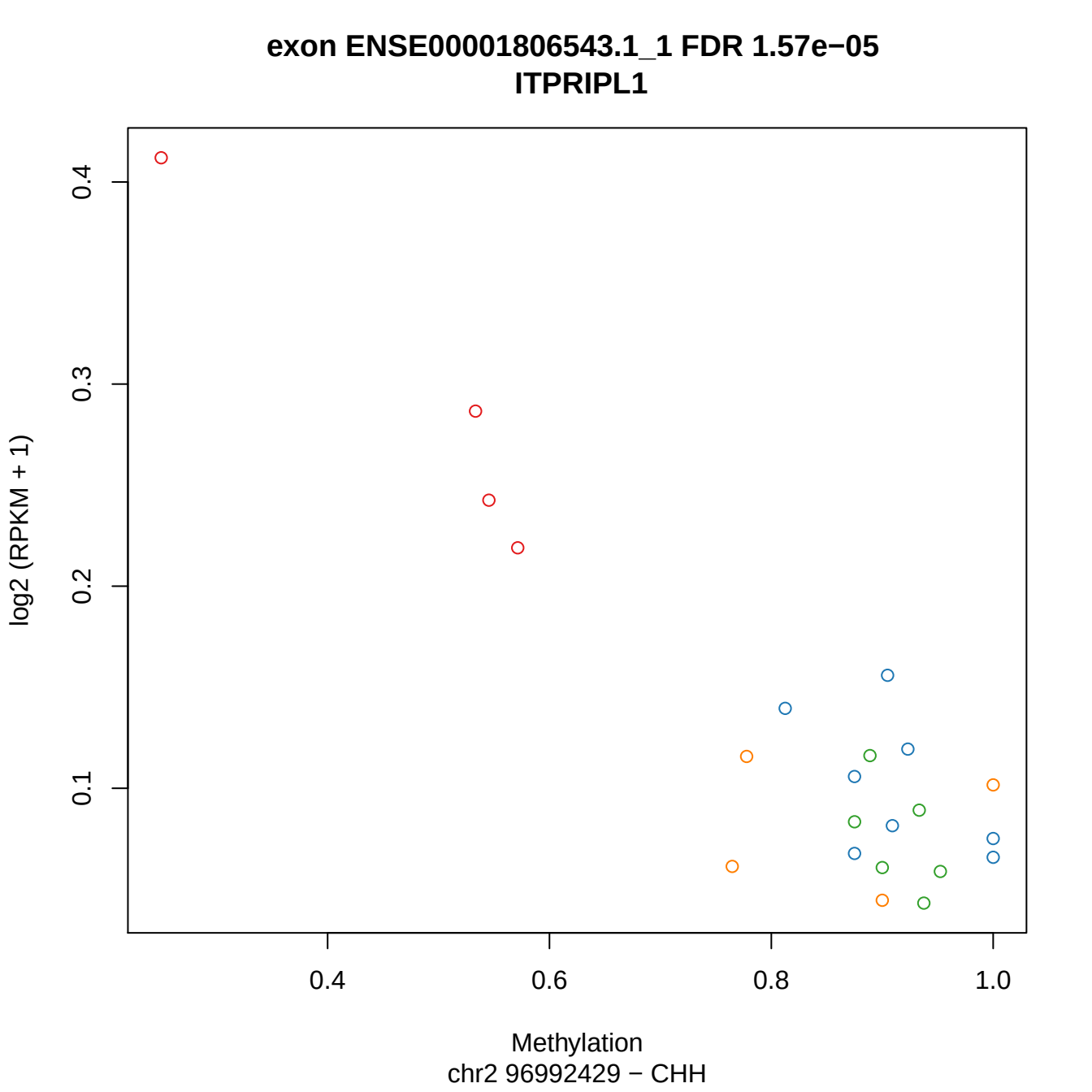

exon ENSE00002243178.1_1 FDR 8.06e−06
ITPRIPL1
log2 (RPKM + 1)
0.1
0.2
0.3
0.4
0.4
0.6
0.8
1.0
Methylation
chr2 96992429 − CHH

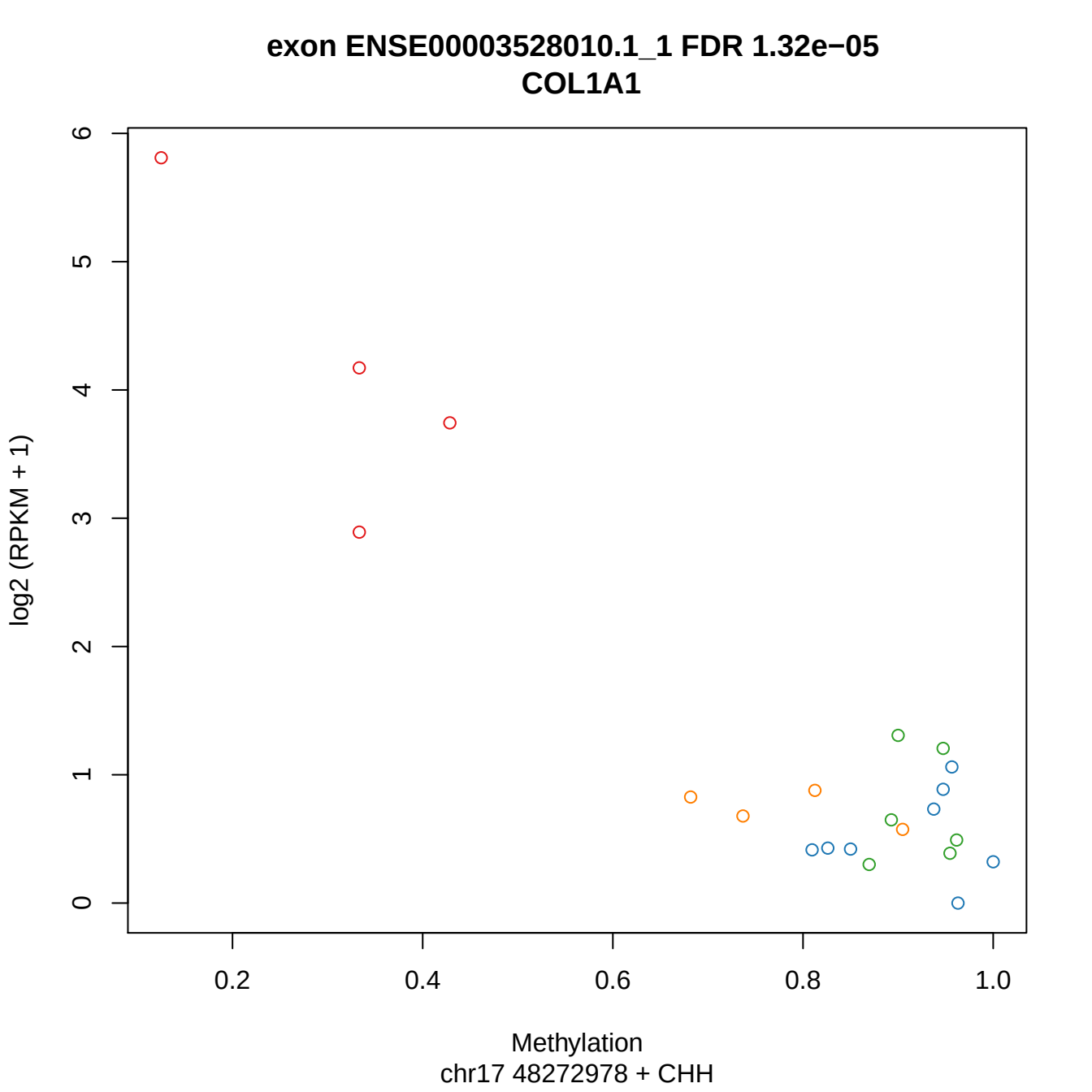

exon ENSE00003527609.1_1 FDR 1.47e−06
COL1A1
log2 (RPKM + 1)
0
1
2
3
4
5
0.2
0.4
0.6
0.8
1.0
Methylation
chr17 48272978 + CHH

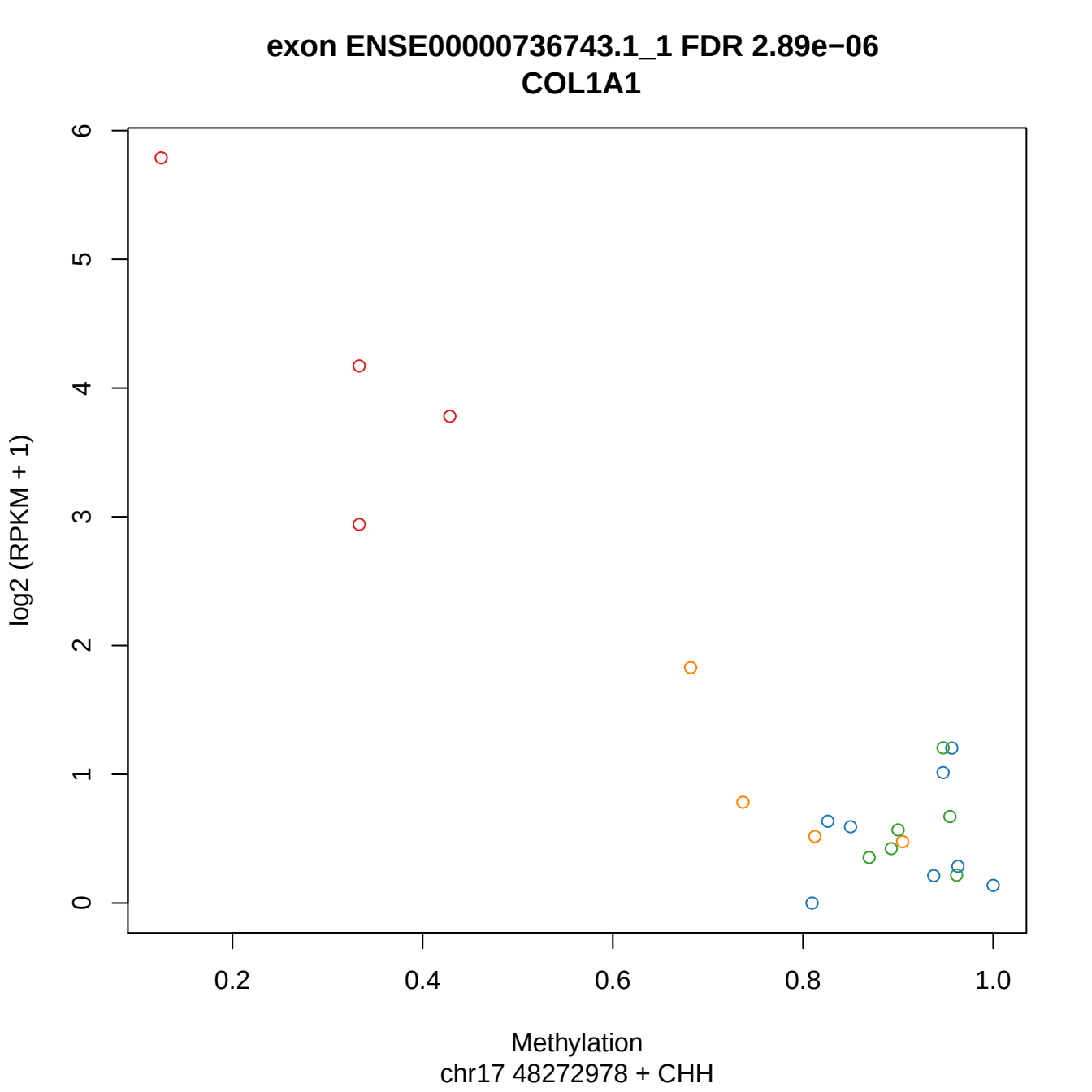

exon ENSE00001897564.1_1 FDR 1.04e−05
PXDN
log2 (RPKM + 1)
0.1
0.2
0.3
0.4
0.5
0.6
0.0
0.2
0.4
0.6
0.8
1.0
Methylation
chr2 1640718 + CHH

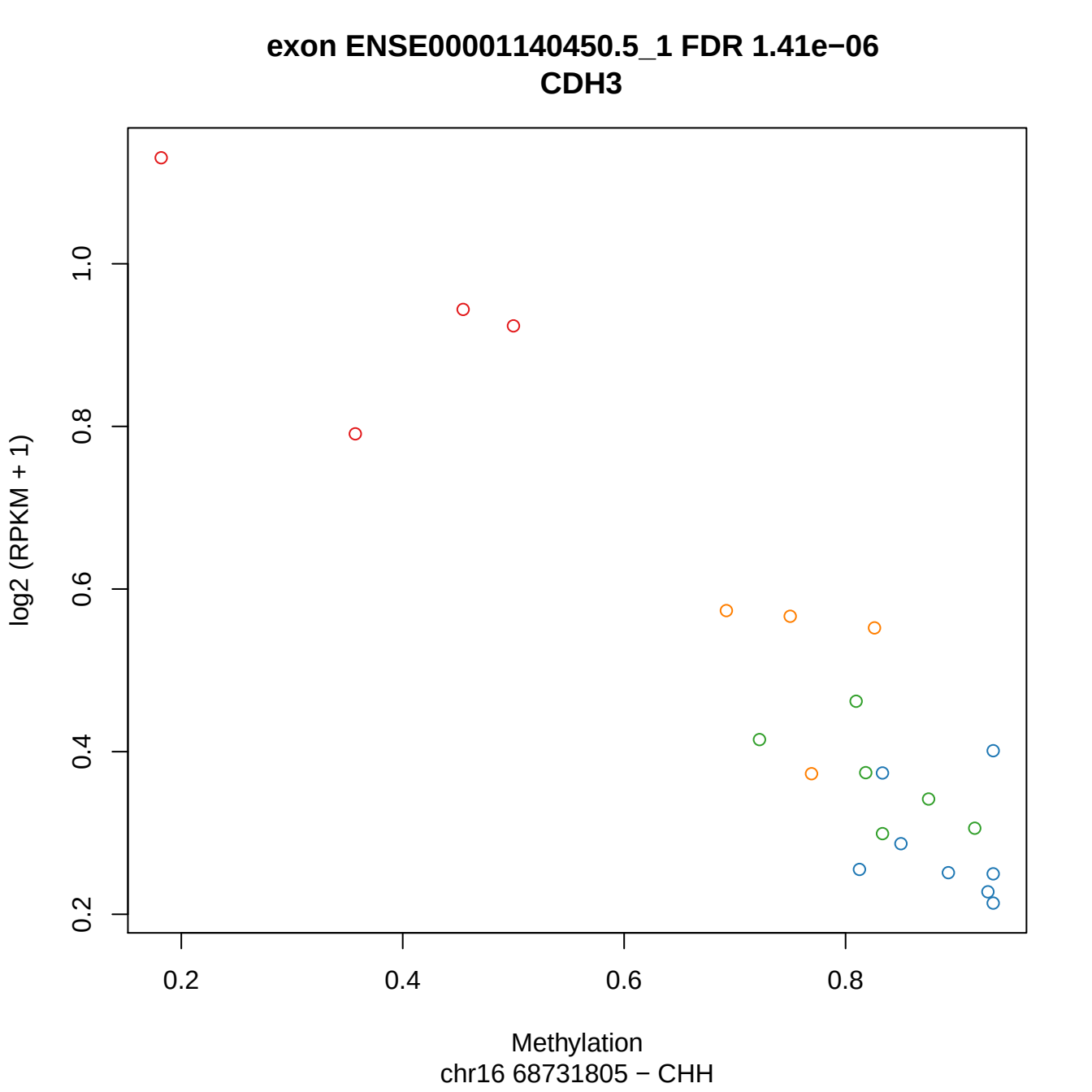

exon ENSE00001661635.2_1 FDR 1.35e−05
ITPRIPL1
log2 (RPKM + 1)
0.1
0.2
0.3
0.4
0.4
0.6
0.8
1.0
Methylation
chr2 96992429 − CHH

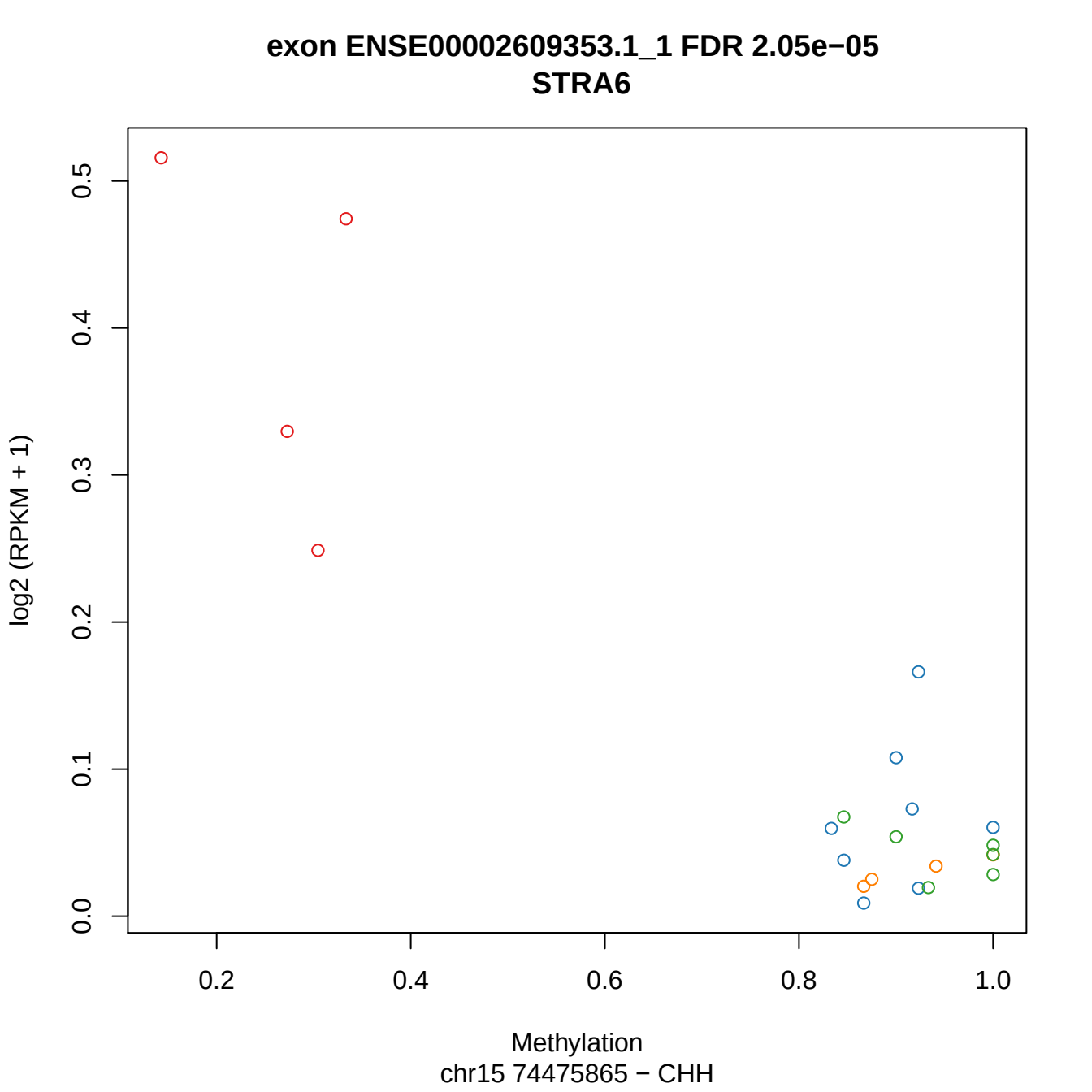

exon ENSE00003432012.1_1 FDR 2.51e−06
COL1A1
log2 (RPKM + 1)
0
1
2
3
4
5
0.4
0.6
0.8
1.0
Methylation
chr17 48265214 − CHG

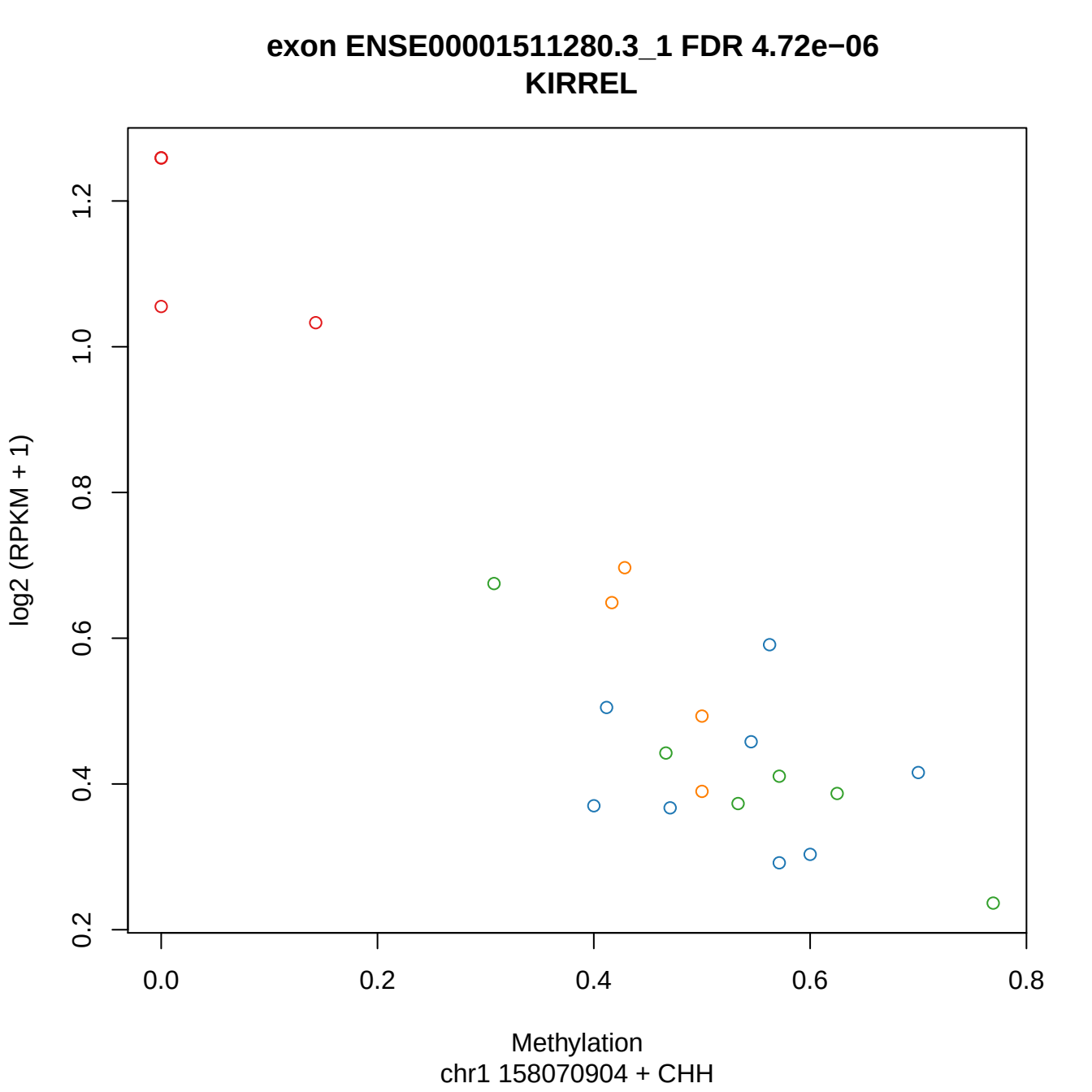

exon ENSE00001806543.1_1 FDR 1.57e−05
ITPRIPL1
log2 (RPKM + 1)
0.1
0.2
0.3
0.4
0.4
0.6
0.8
1.0
Methylation
chr2 96992429 − CHH

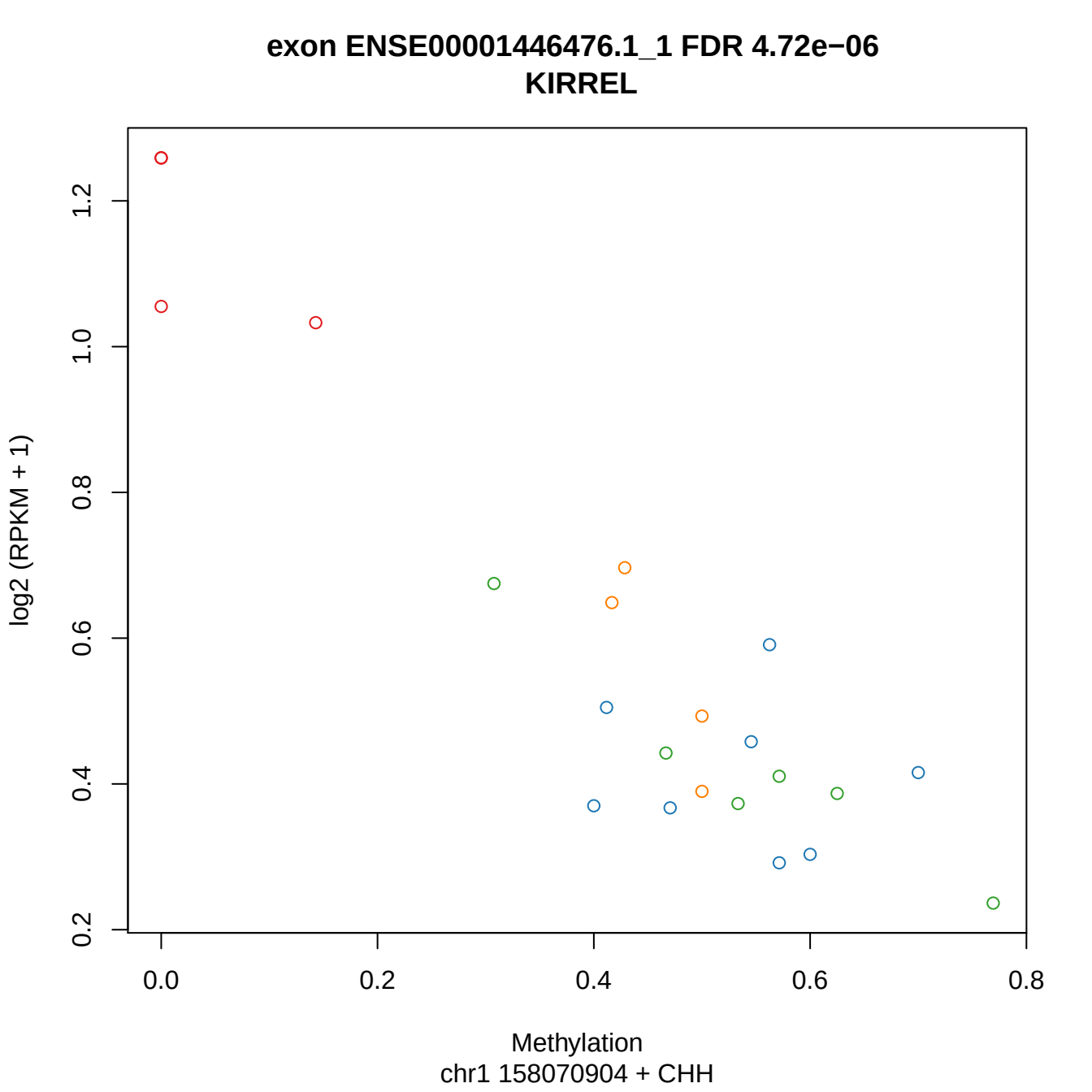

exon ENSE00003528010.1_1 FDR 1.32e−05
COL1A1
log2 (RPKM + 1)
0
1
2
3
4
5
6
0.2
0.4
0.6
0.8
1.0
Methylation
chr17 48272978 + CHH

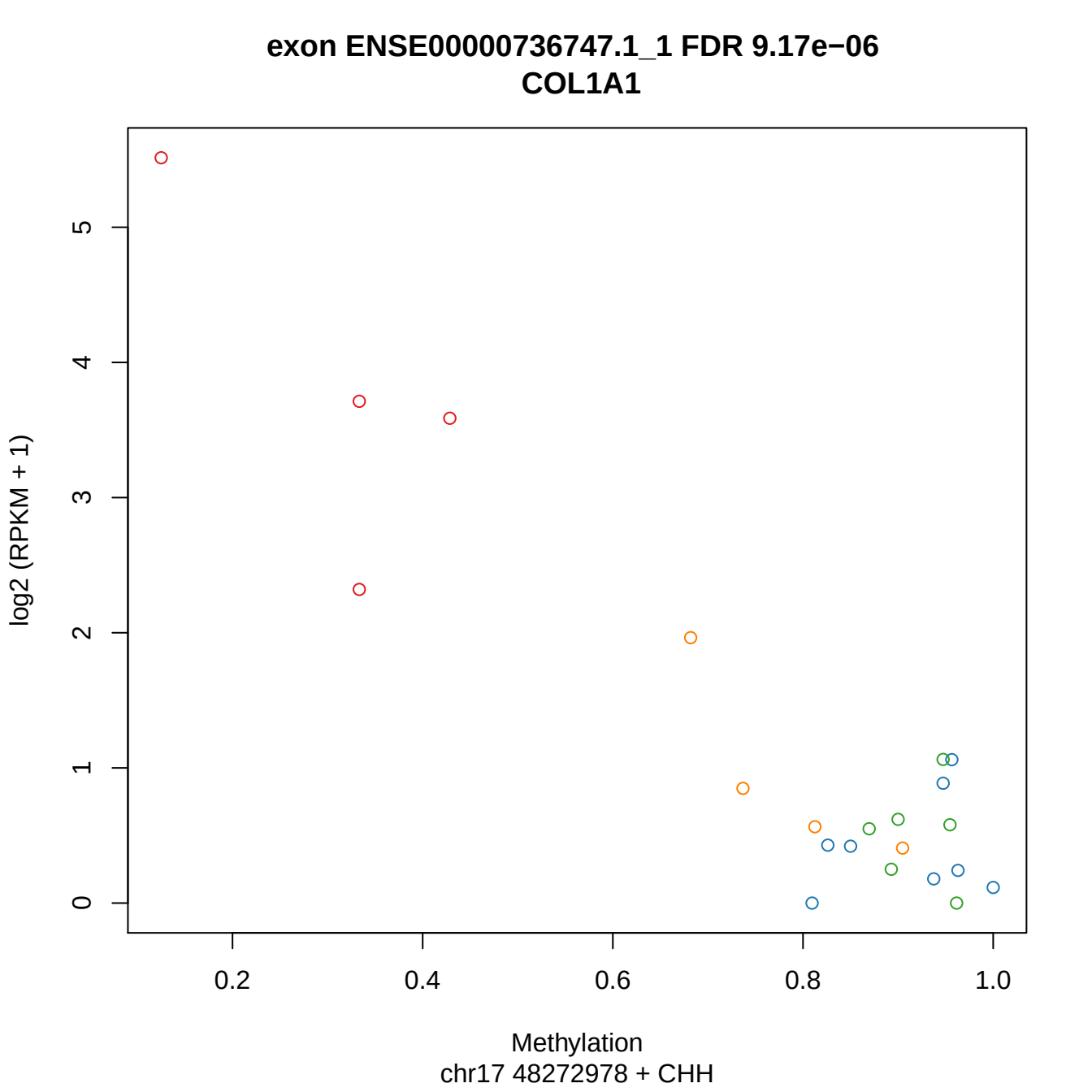

exon ENSE00000736743.1_1 FDR 2.89e−06
COL1A1
log2 (RPKM + 1)
0
1
2
3
4
5
6
0.2
0.4
0.6
0.8
1.0
Methylation
chr17 48272978 + CHH

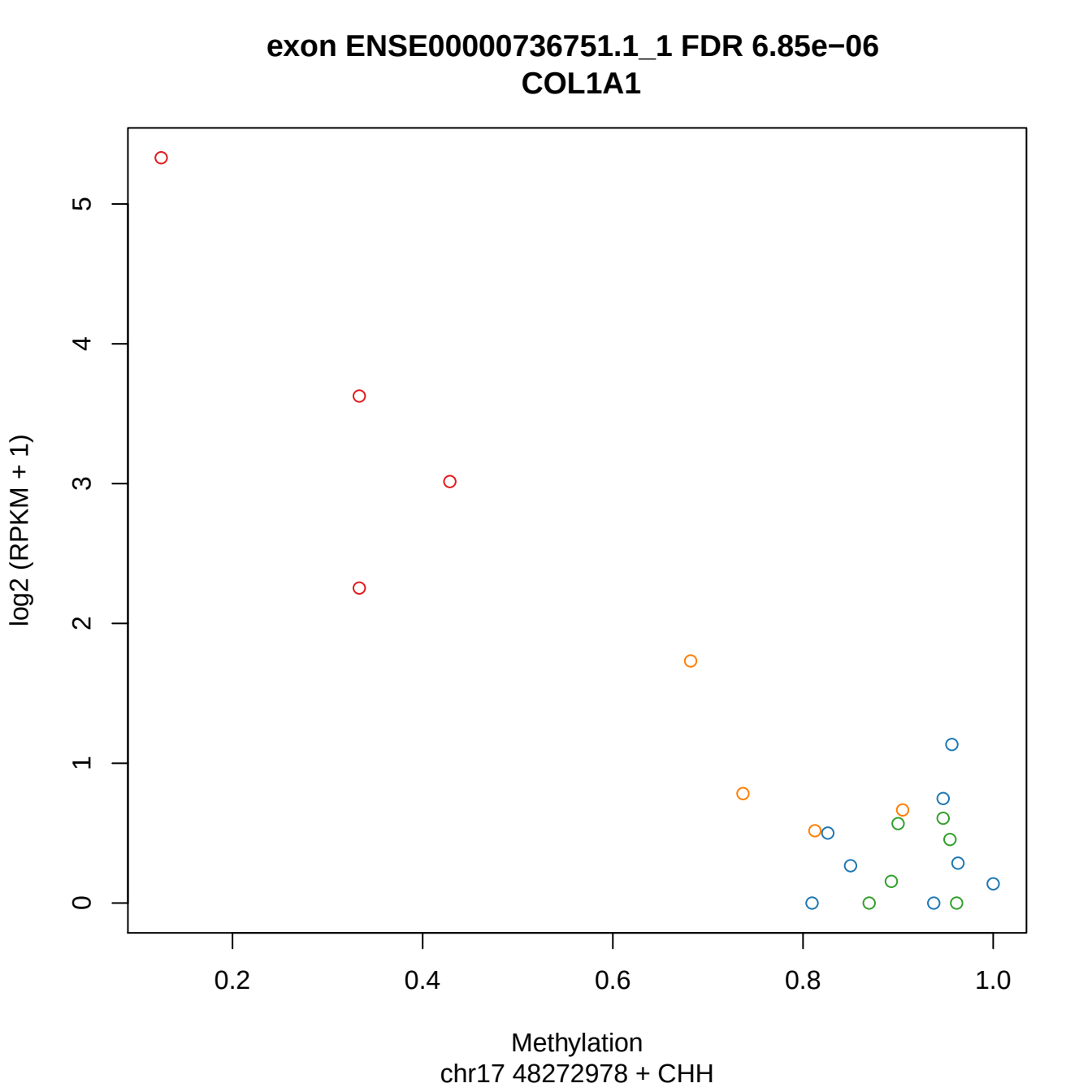

exon ENSE00001140450.5_1 FDR 1.41e−06
CDH3
log2 (RPKM + 1)
0.2
0.4
0.6
0.8
1.0
0.2
0.4
0.6
0.8
Methylation
chr16 68731805 − CHH

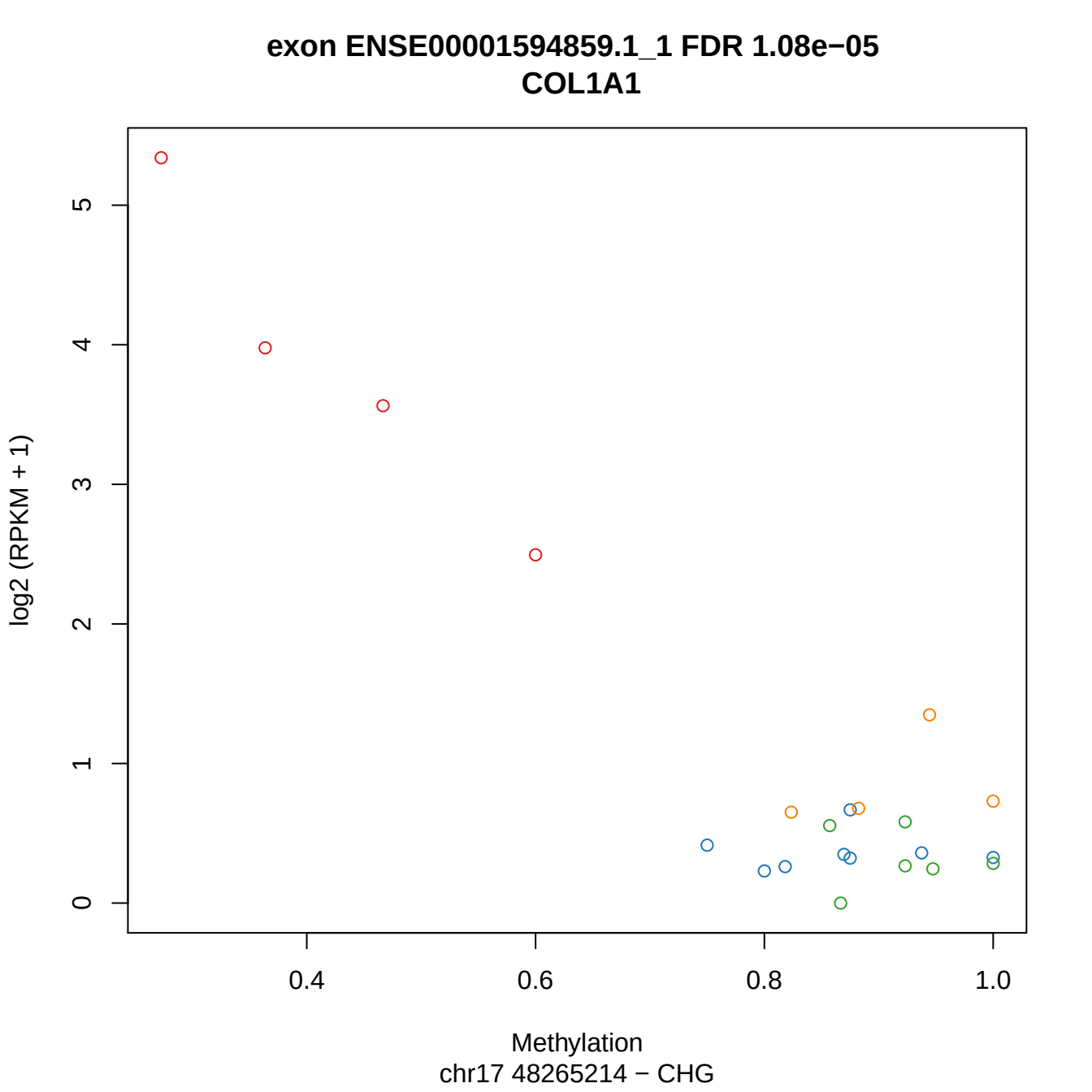

exon ENSE00002609353.1_1 FDR 2.05e−05
STRA6
log2 (RPKM + 1)
0.0
0.1
0.2
0.3
0.4
0.5
0.2
0.4
0.6
0.8
1.0
Methylation
chr15 74475865 − CHH

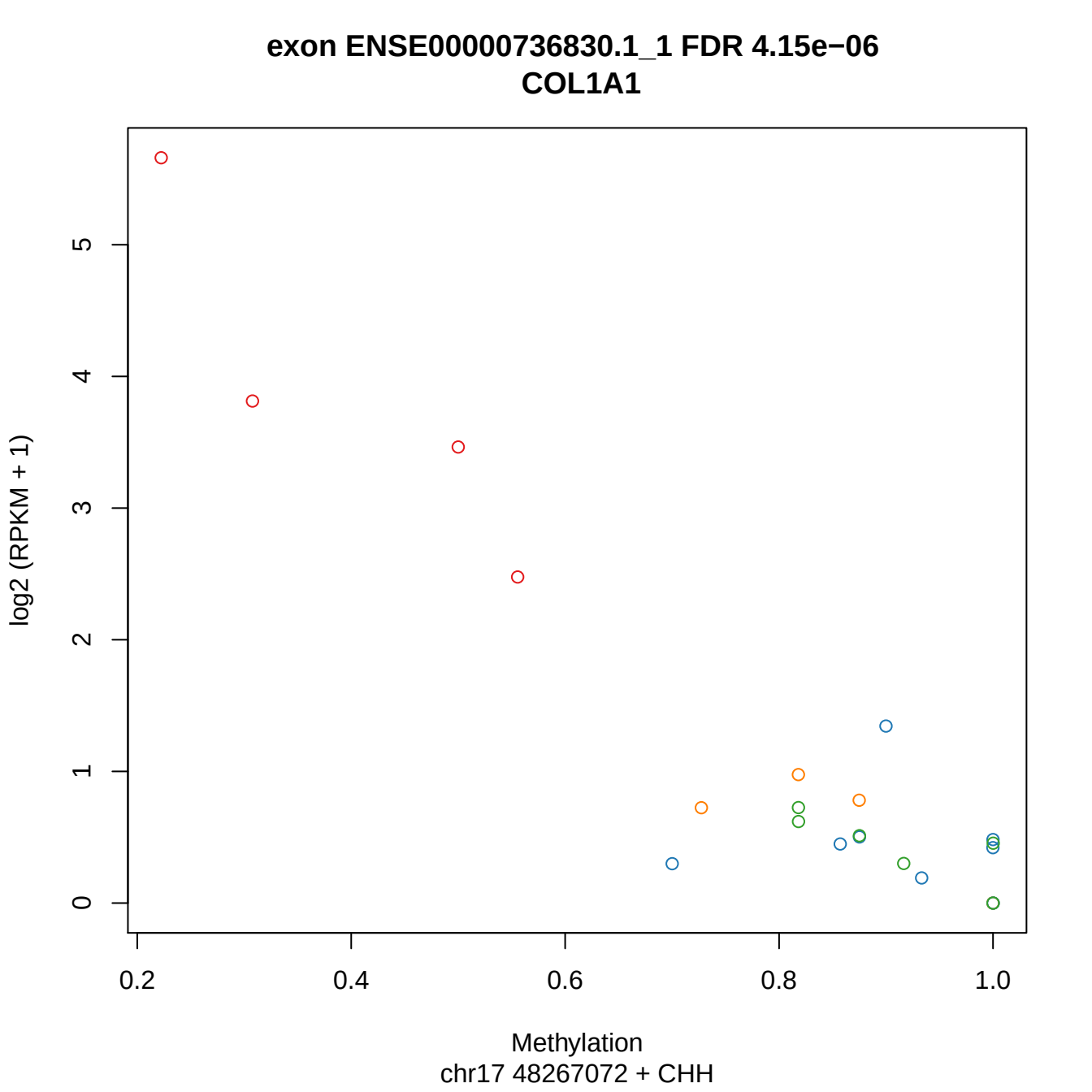

exon ENSE00001511280.3_1 FDR 4.72e−06
KIRREL
log2 (RPKM + 1)
0.2
0.4
0.6
0.8
1.0
1.2
0.0
0.2
0.4
0.6
0.8
Methylation
chr1 158070904 + CHH

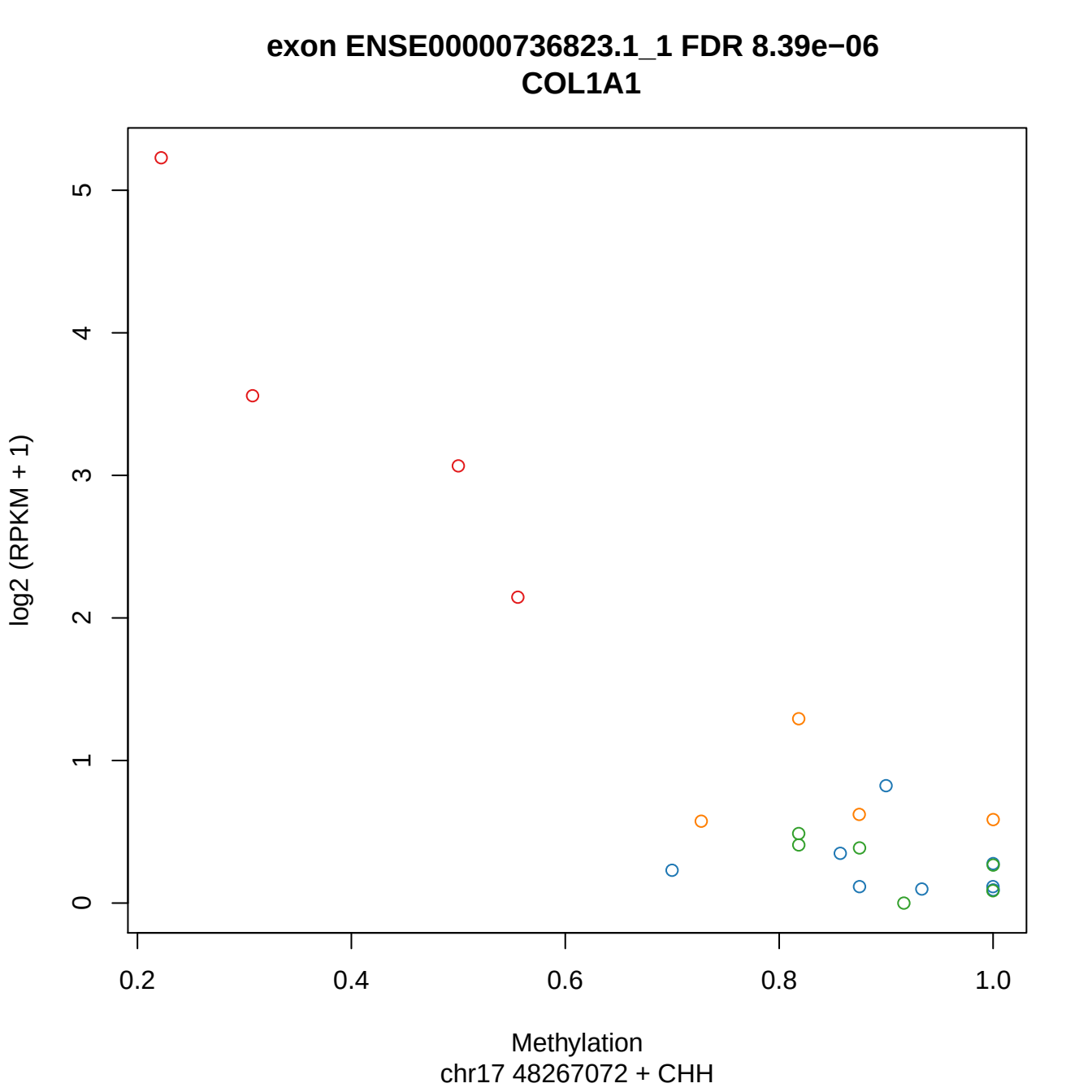

exon ENSE00001446476.1_1 FDR 4.72e−06
KIRREL
log2 (RPKM + 1)
0.2
0.4
0.6
0.8
1.0
1.2
0.0
0.2
0.4
0.6
0.8
Methylation
chr1 158070904 + CHH

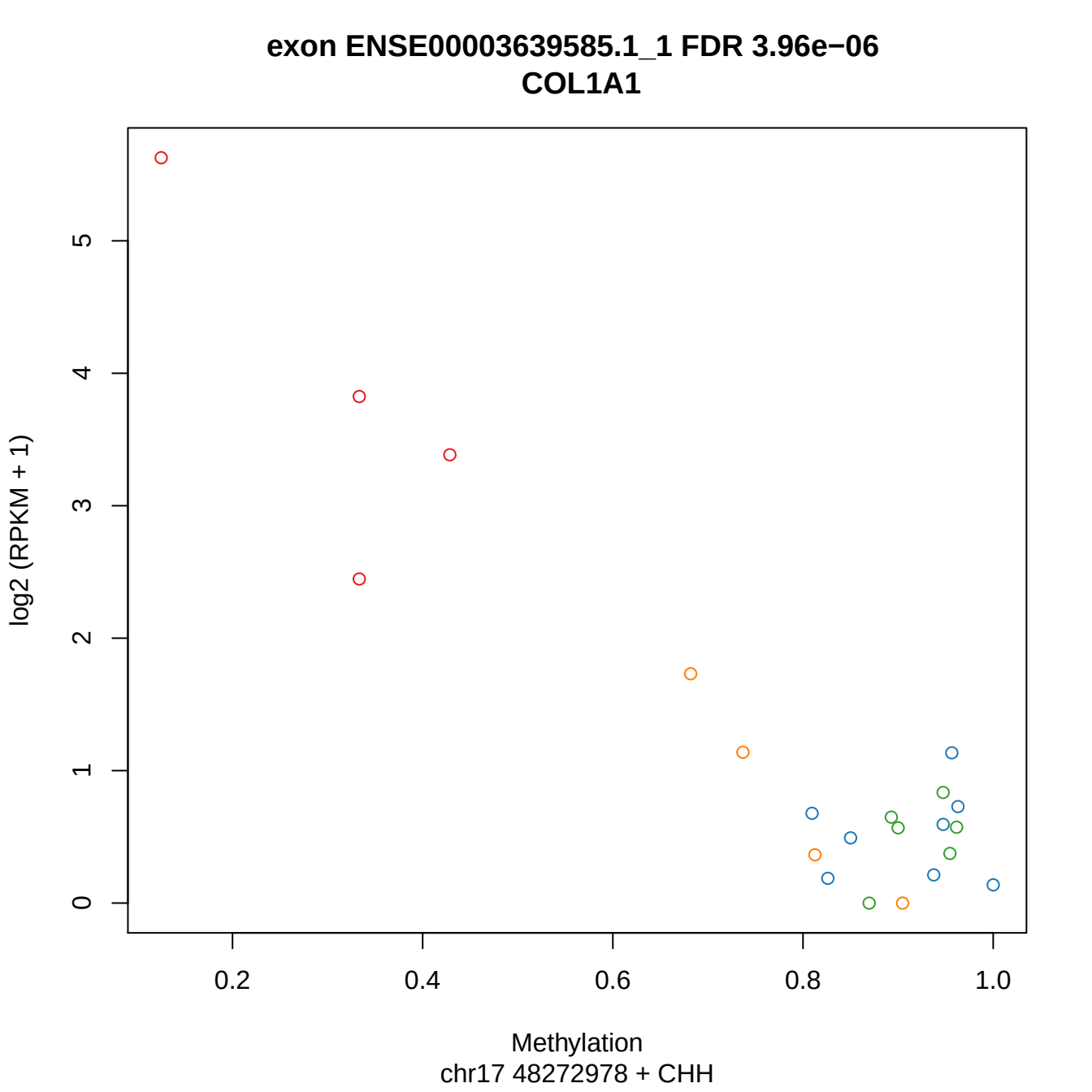

exon ENSE00000736747.1_1 FDR 9.17e−06
COL1A1
log2 (RPKM + 1)
0
1
2
3
4
5
0.2
0.4
0.6
0.8
1.0
Methylation
chr17 48272978 + CHH

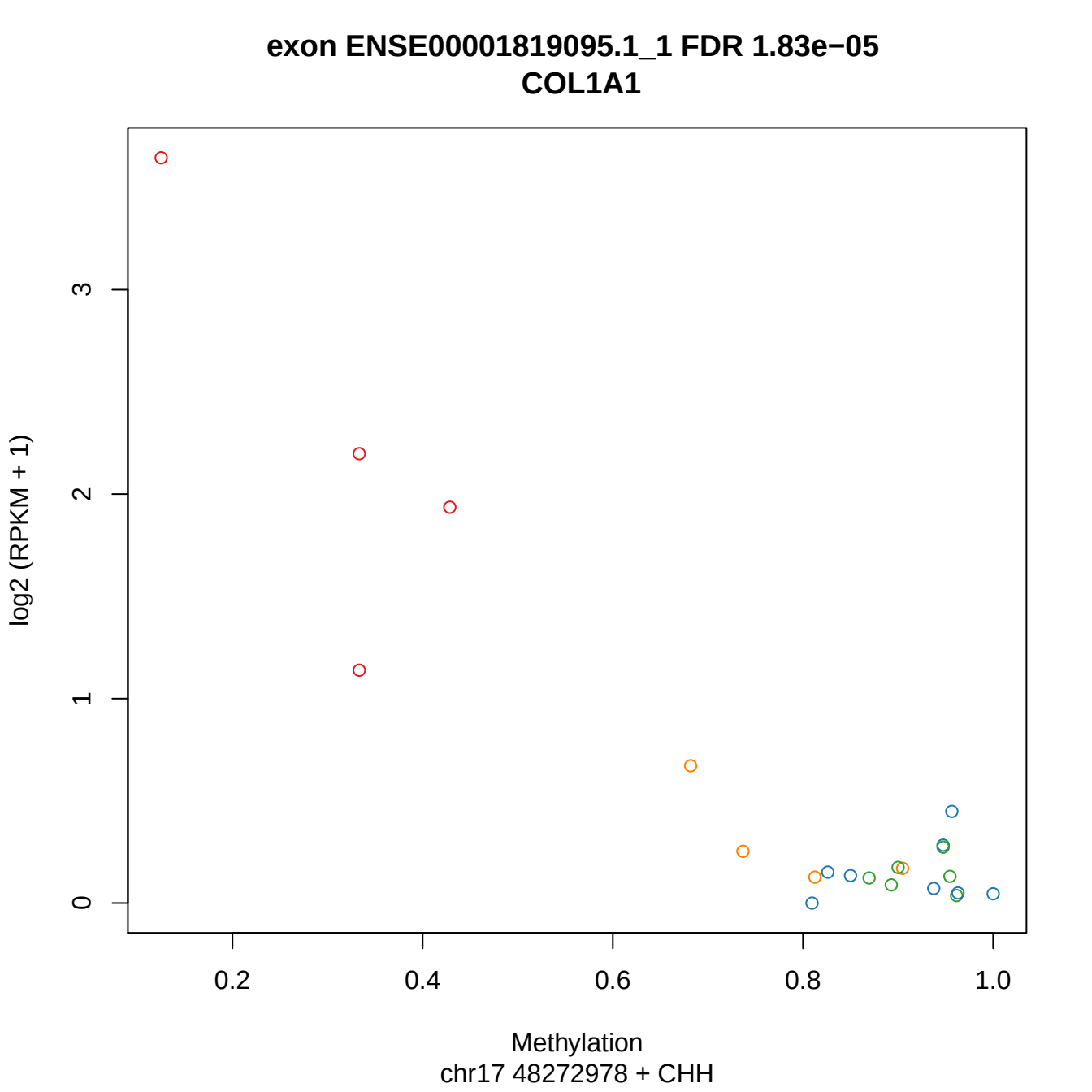

exon ENSE00000736751.1_1 FDR 6.85e−06
COL1A1
log2 (RPKM + 1)
0
1
2
3
4
5
0.2
0.4
0.6
0.8
1.0
Methylation
chr17 48272978 + CHH

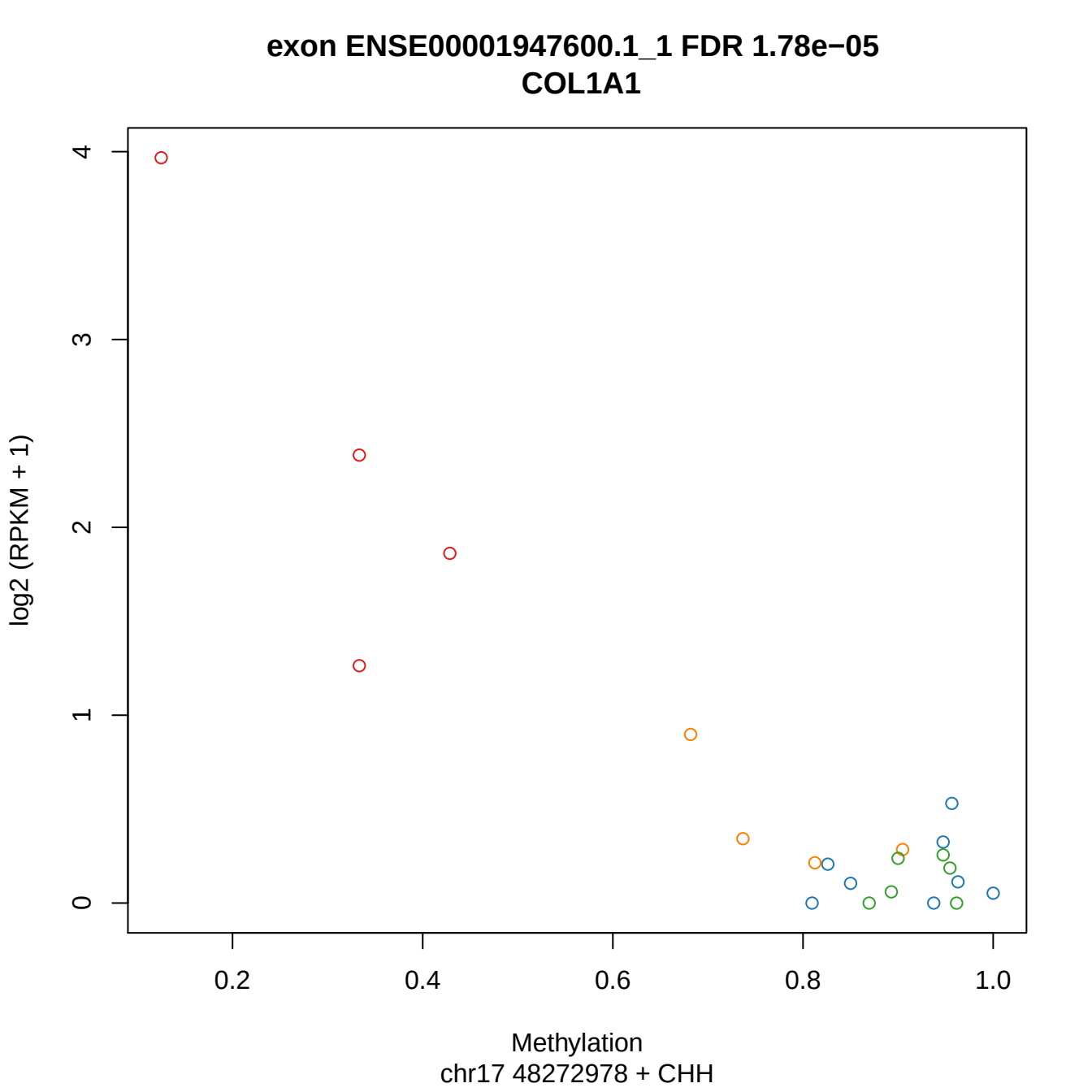

exon ENSE00001594859.1_1 FDR 1.08e−05
COL1A1
log2 (RPKM + 1)
0
1
2
3
4
5
0.4
0.6
0.8
1.0
Methylation
chr17 48265214 − CHG

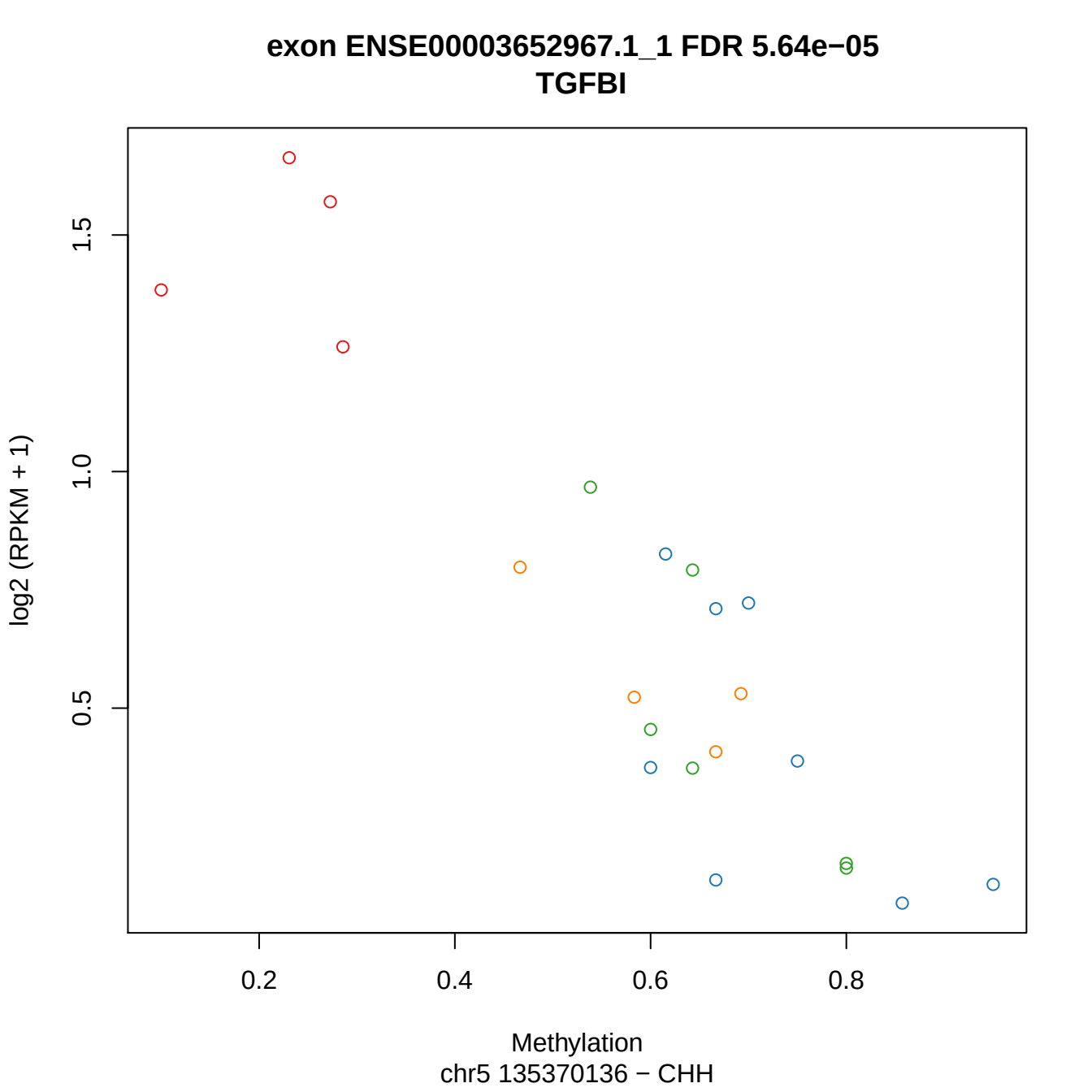

exon ENSE00000736830.1_1 FDR 4.15e−06
COL1A1
log2 (RPKM + 1)
0
1
2
3
4
5
0.2
0.4
0.6
0.8
1.0
Methylation
chr17 48267072 + CHH

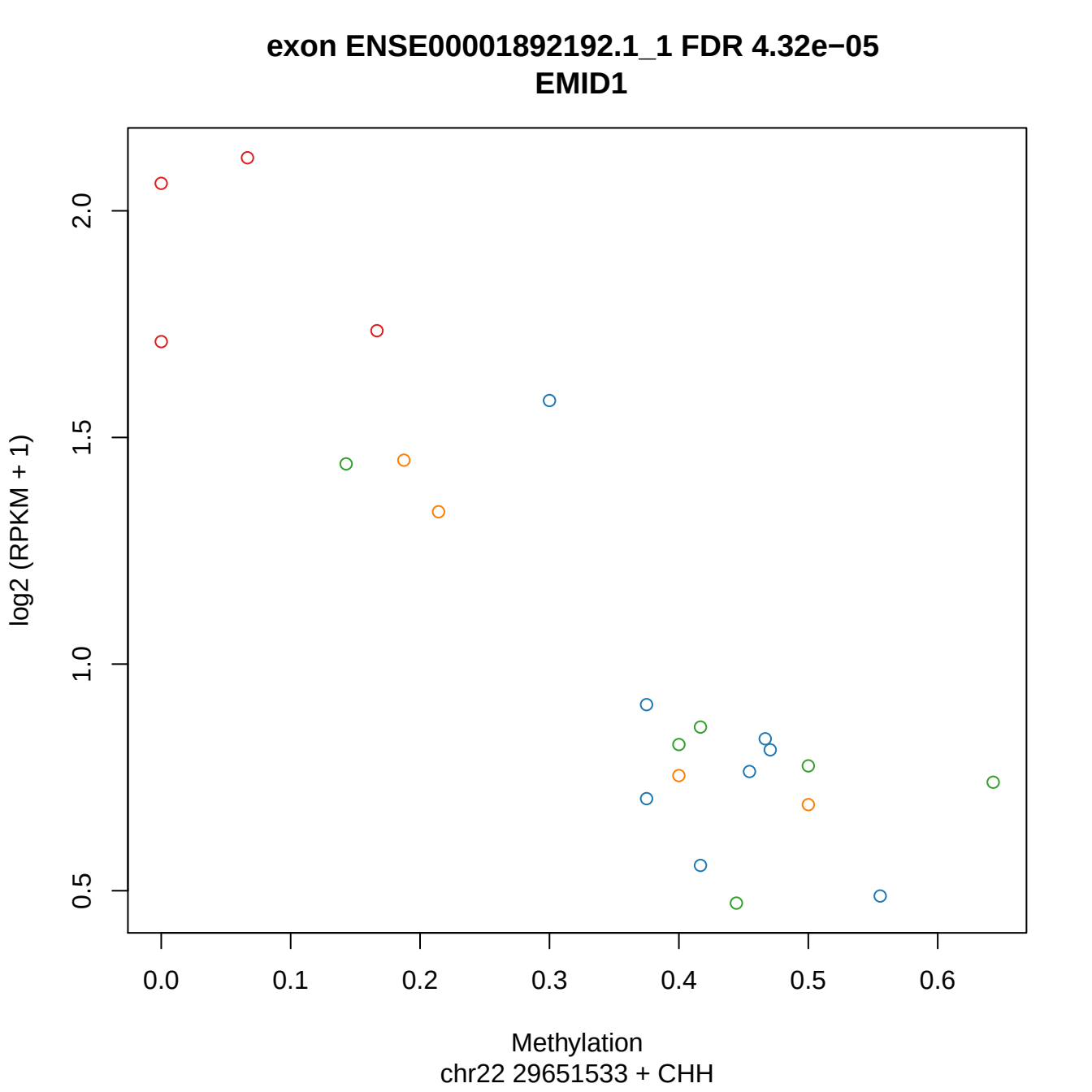

exon ENSE00000736823.1_1 FDR 8.39e−06
COL1A1
log2 (RPKM + 1)
0
1
2
3
4
5
0.2
0.4
0.6
0.8
1.0
Methylation
chr17 48267072 + CHH

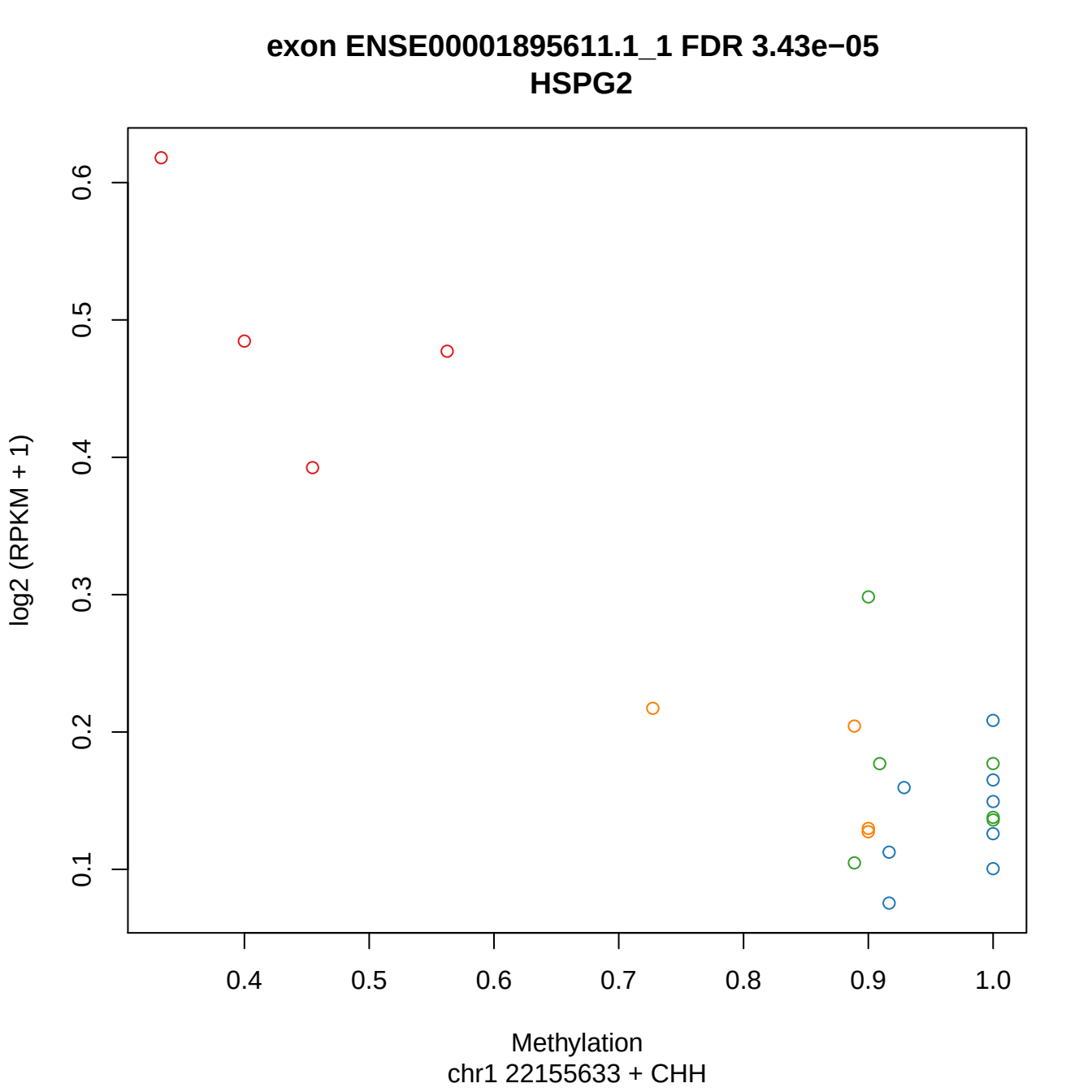

exon ENSE00003639585.1_1 FDR 3.96e−06
COL1A1
log2 (RPKM + 1)
0
1
2
3
4
5
0.2
0.4
0.6
0.8
1.0
Methylation
chr17 48272978 + CHH

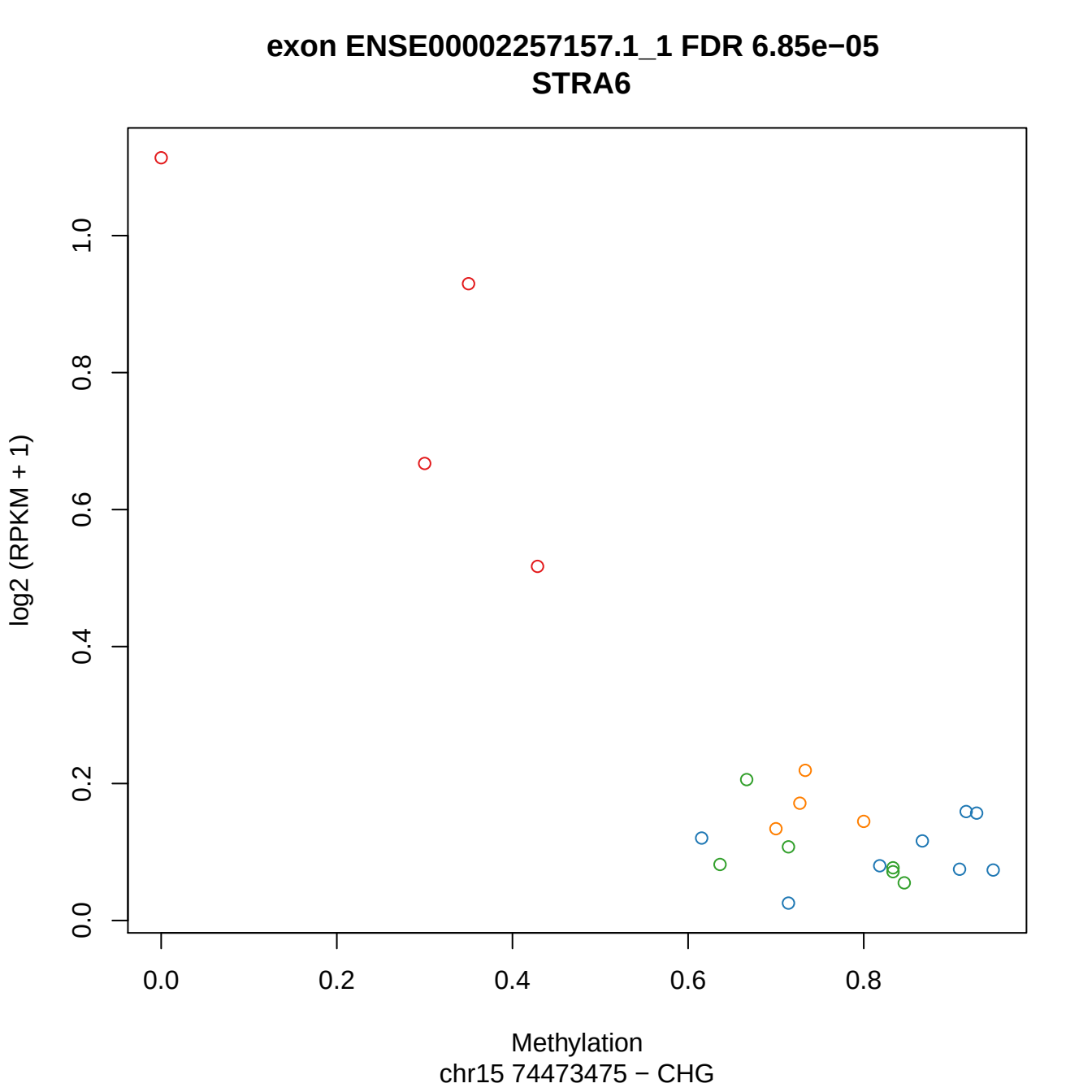

exon ENSE00001819095.1_1 FDR 1.83e−05
COL1A1
log2 (RPKM + 1)
0
1
2
3
0.2
0.4
0.6
0.8
1.0
Methylation
chr17 48272978 + CHH

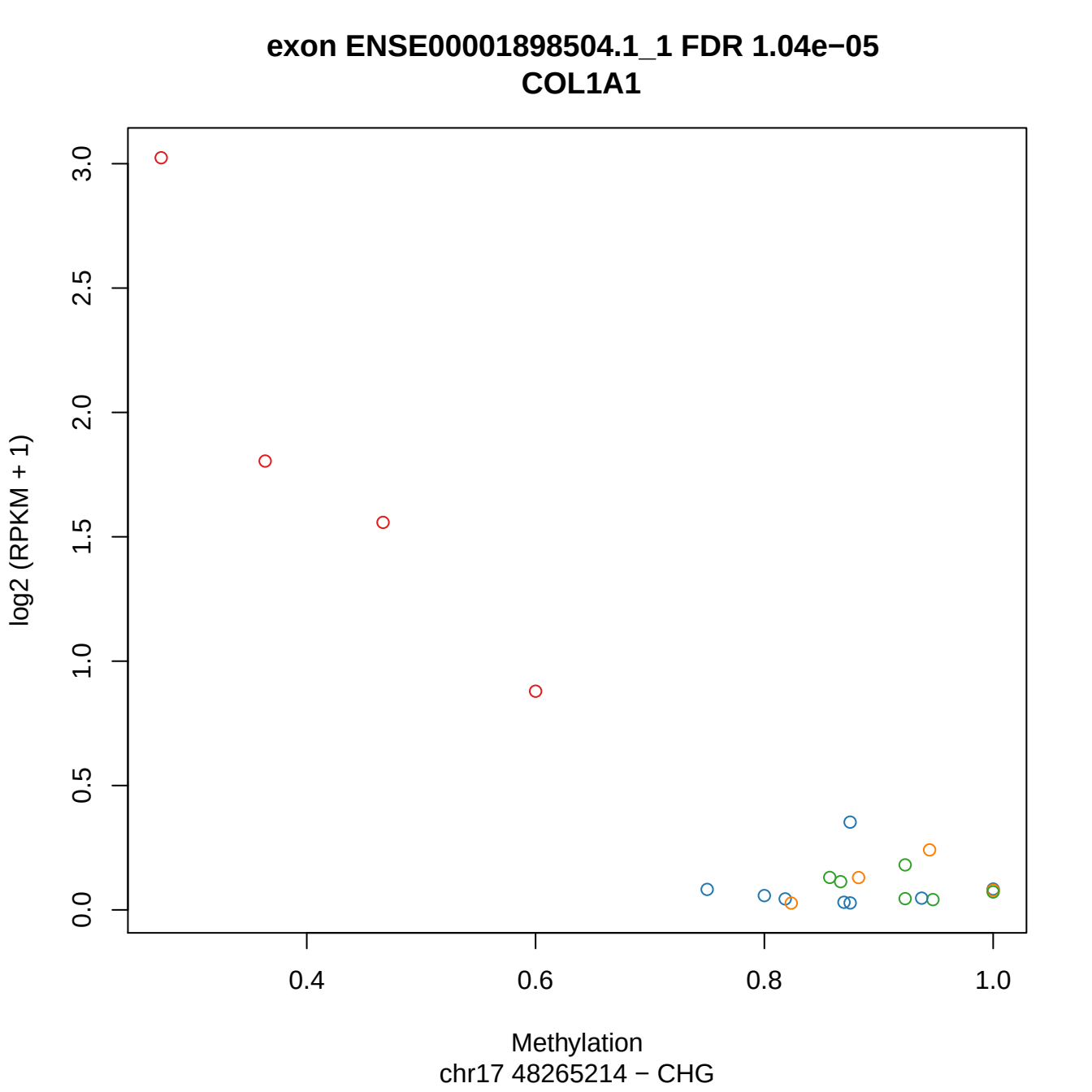

exon ENSE00001947600.1_1 FDR 1.78e−05
COL1A1
log2 (RPKM + 1)
0
1
2
3
4
0.2
0.4
0.6
0.8
1.0
Methylation
chr17 48272978 + CHH

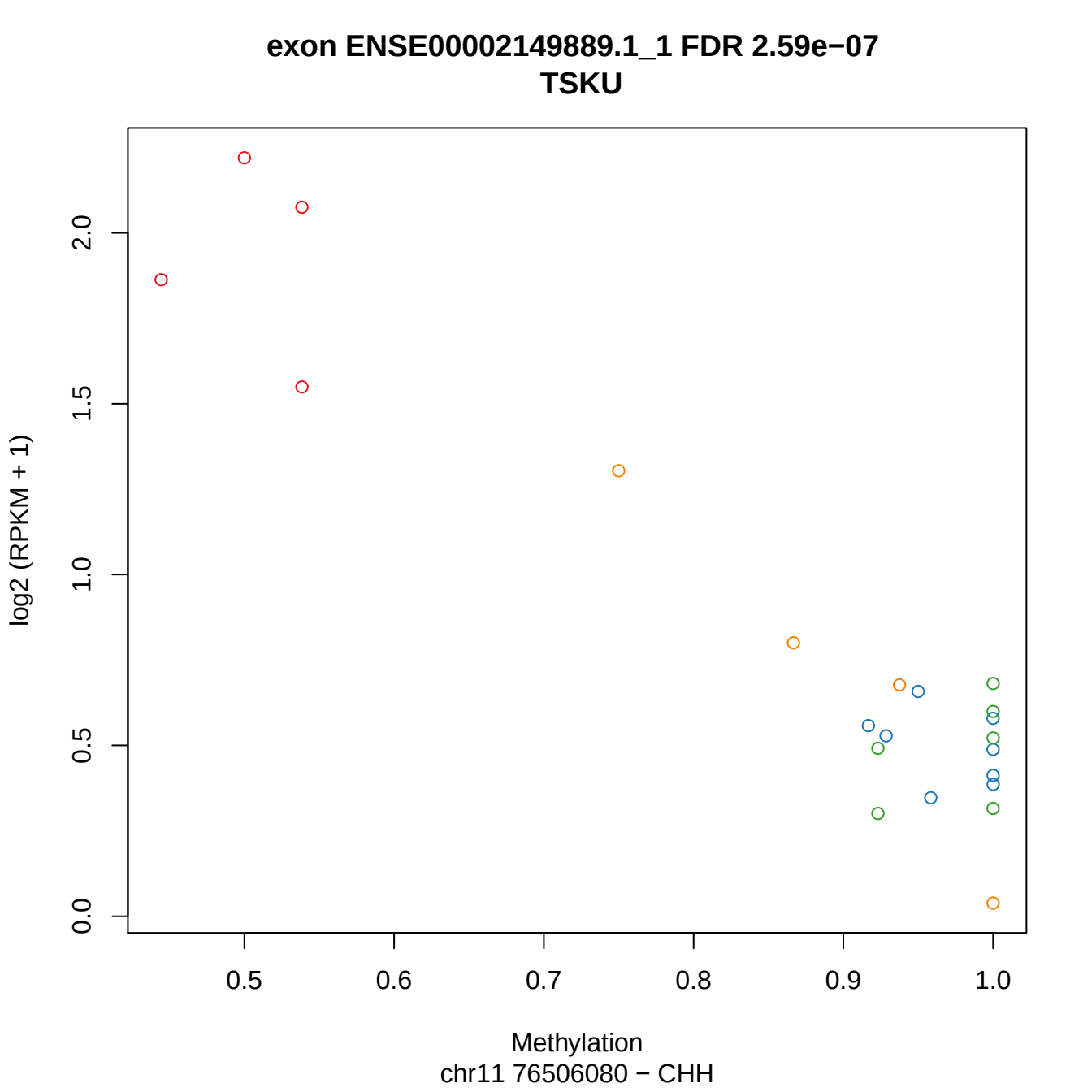

exon ENSE00003652967.1_1 FDR 5.64e−05
TGFBI
log2 (RPKM + 1)
0.5
1.0
1.5
0.2
0.4
0.6
0.8
Methylation
chr5 135370136 − CHH

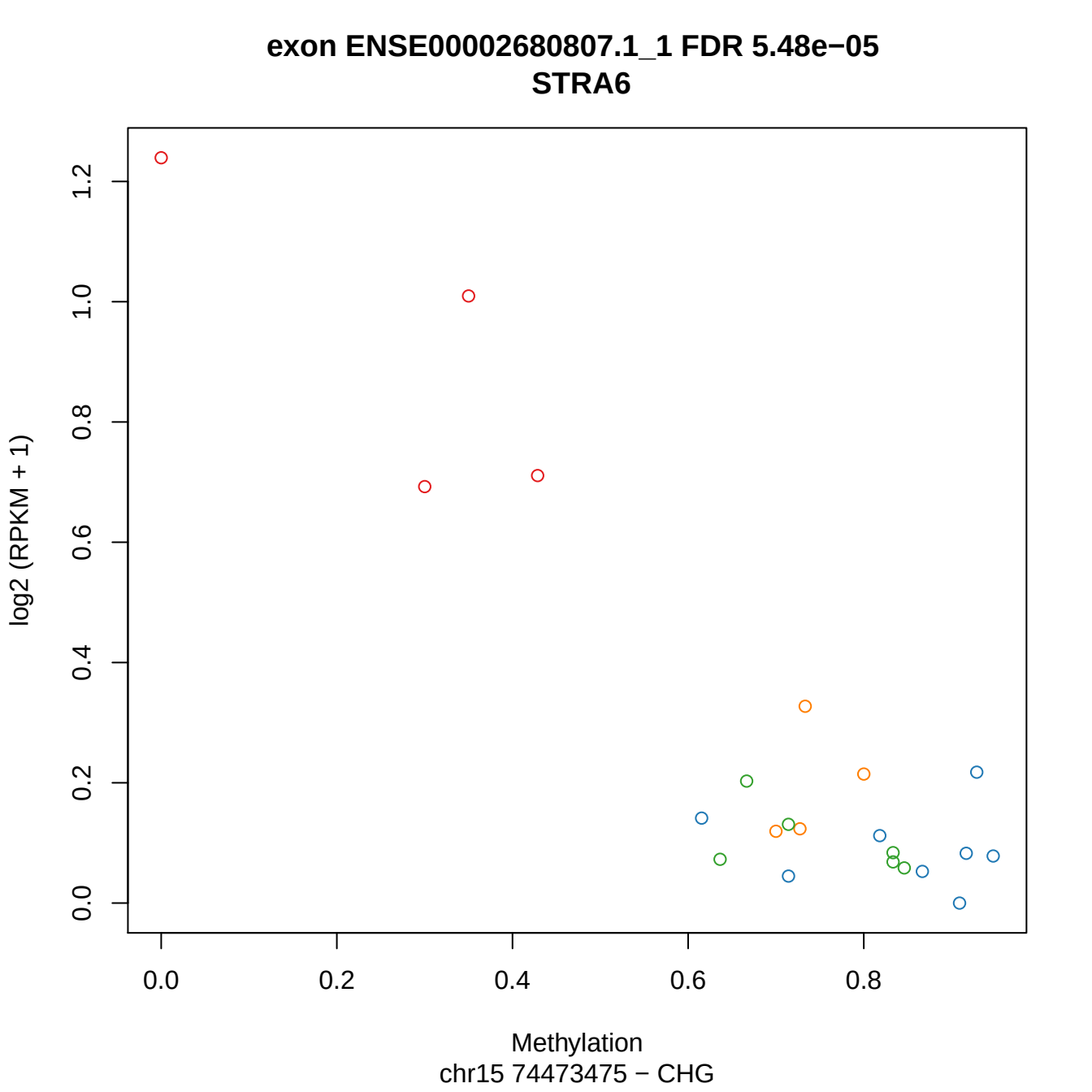

exon ENSE00001892192.1_1 FDR 4.32e−05
EMID1
log2 (RPKM + 1)
0.5
1.0
1.5
2.0
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Methylation
chr22 29651533 + CHH

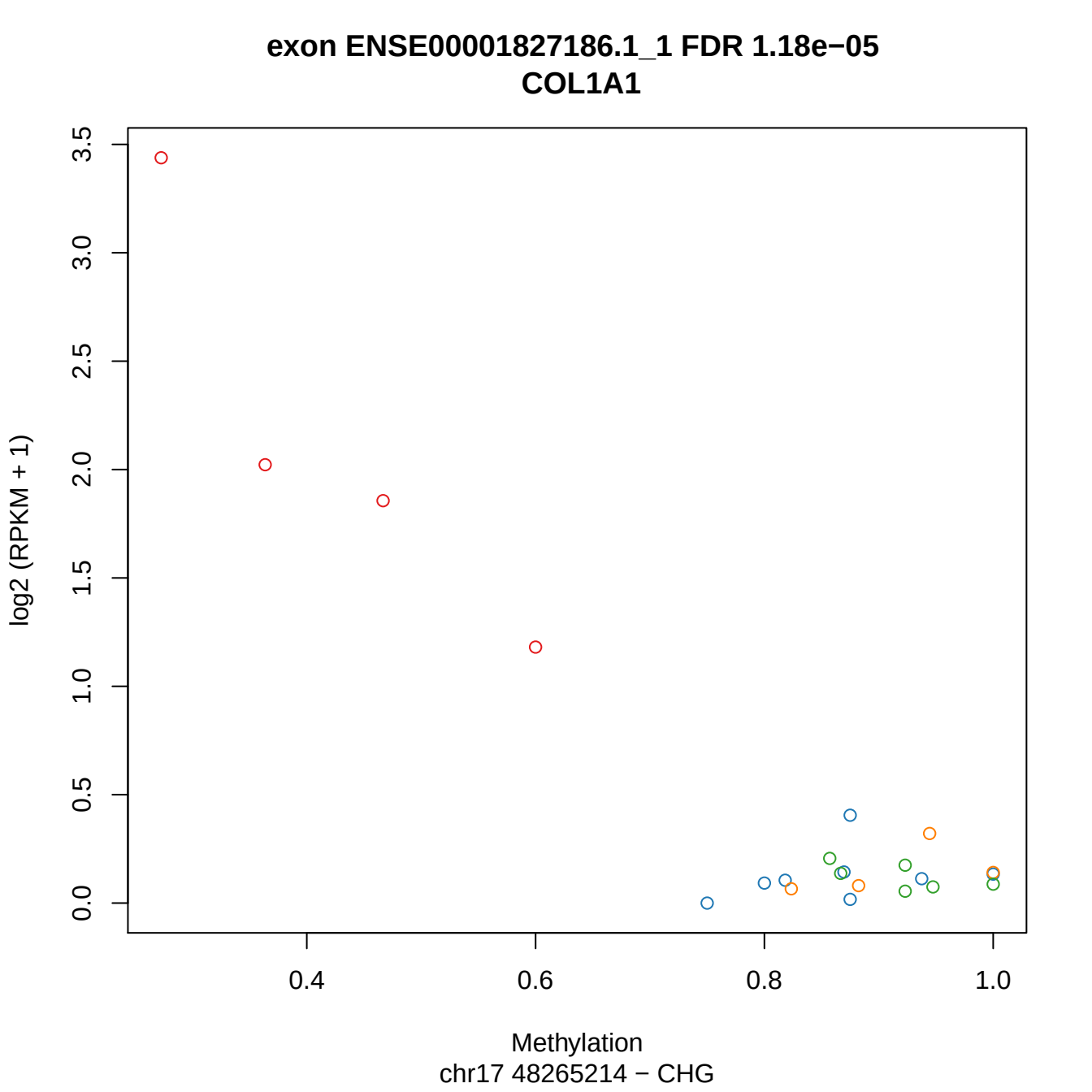

exon ENSE00001895611.1_1 FDR 3.43e−05
HSPG2
log2 (RPKM + 1)
0.1
0.2
0.3
0.4
0.5
0.6
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Methylation
chr1 22155633 + CHH

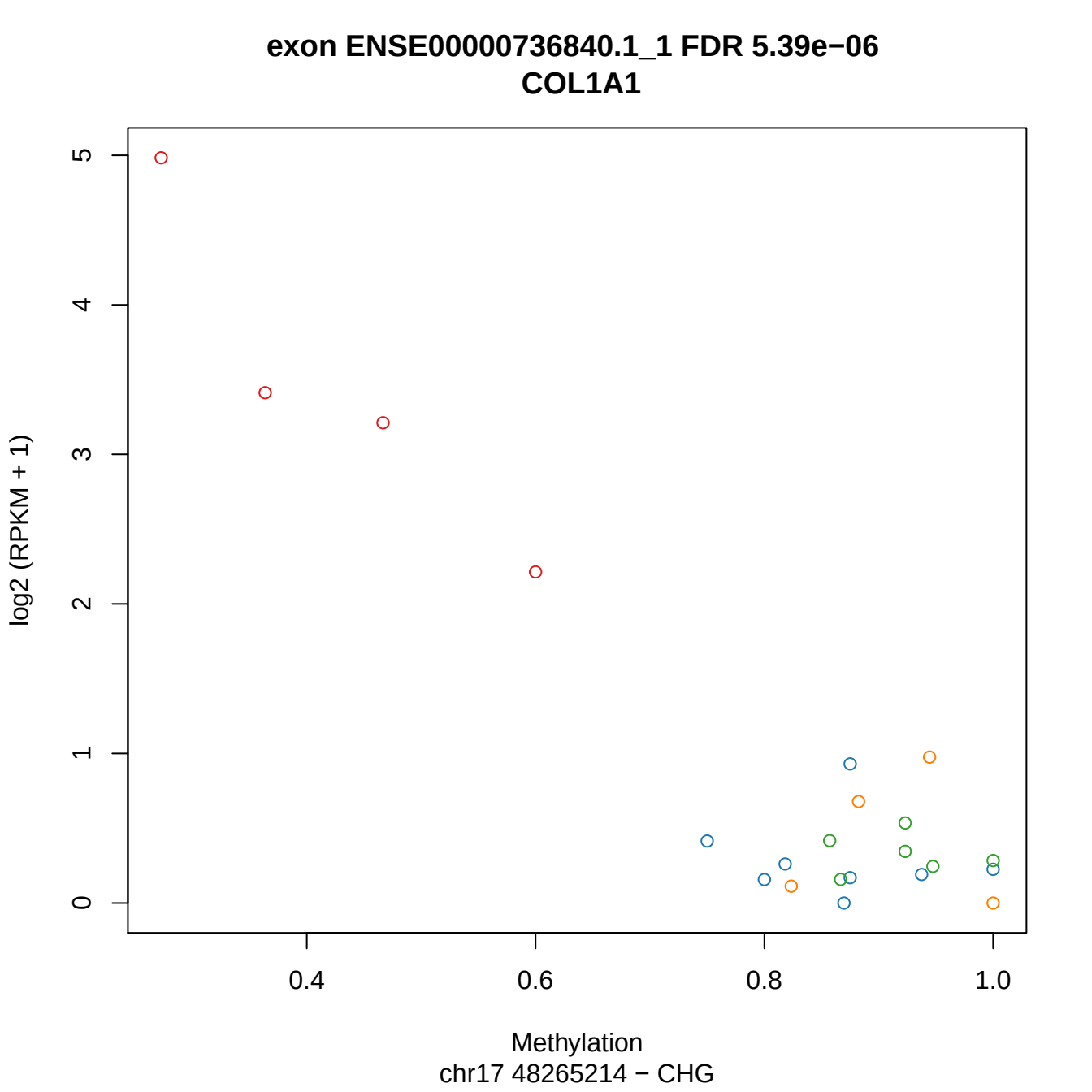

exon ENSE00002257157.1_1 FDR 6.85e−05
STRA6
log2 (RPKM + 1)
0.0
0.2
0.4
0.6
0.8
1.0
0.0
0.2
0.4
0.6
0.8
Methylation
chr15 74473475 − CHG

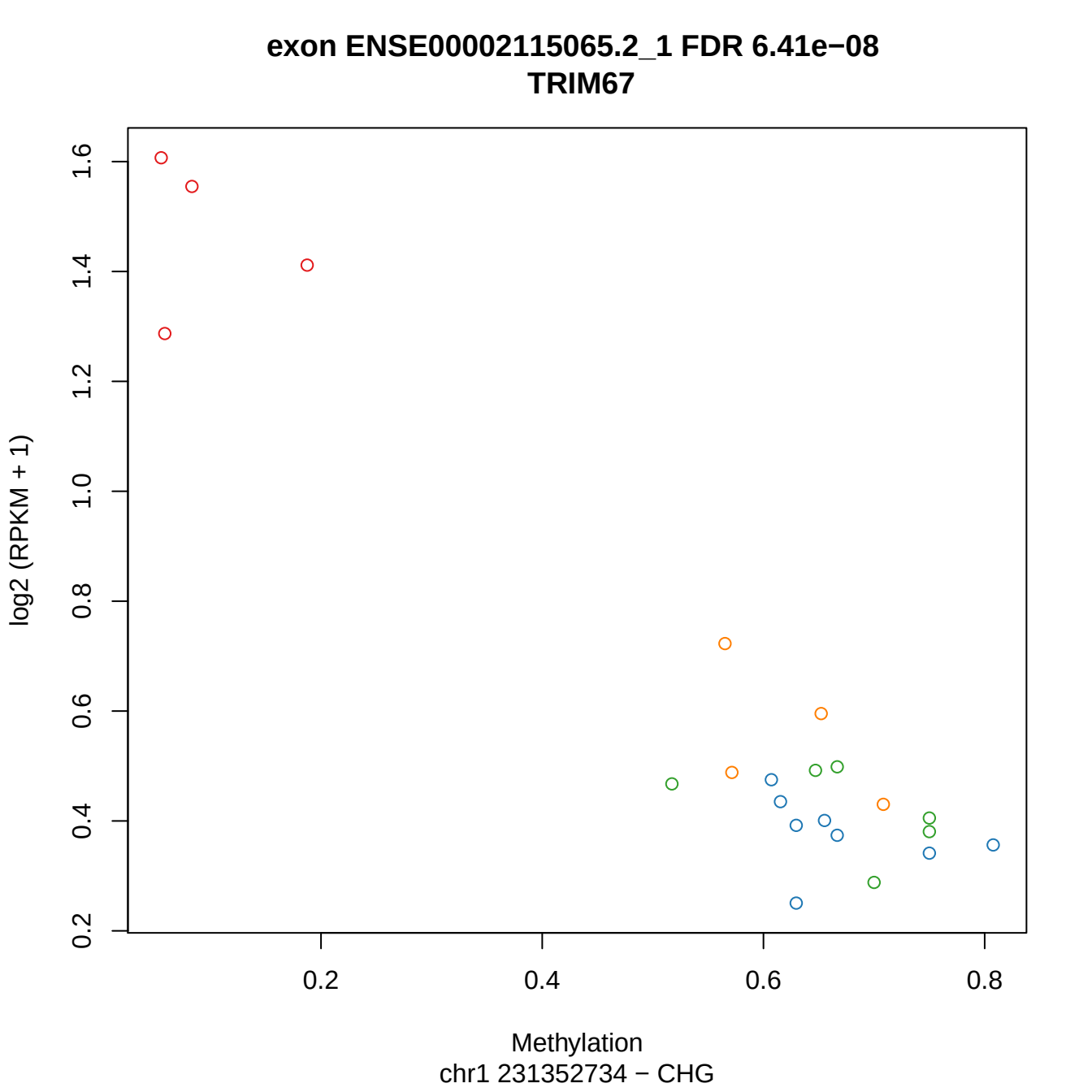

exon ENSE00001898504.1_1 FDR 1.04e−05
COL1A1
log2 (RPKM + 1)
0.0
0.5
1.0
1.5
2.0
2.5
3.0
0.4
0.6
0.8
1.0
Methylation
chr17 48265214 − CHG

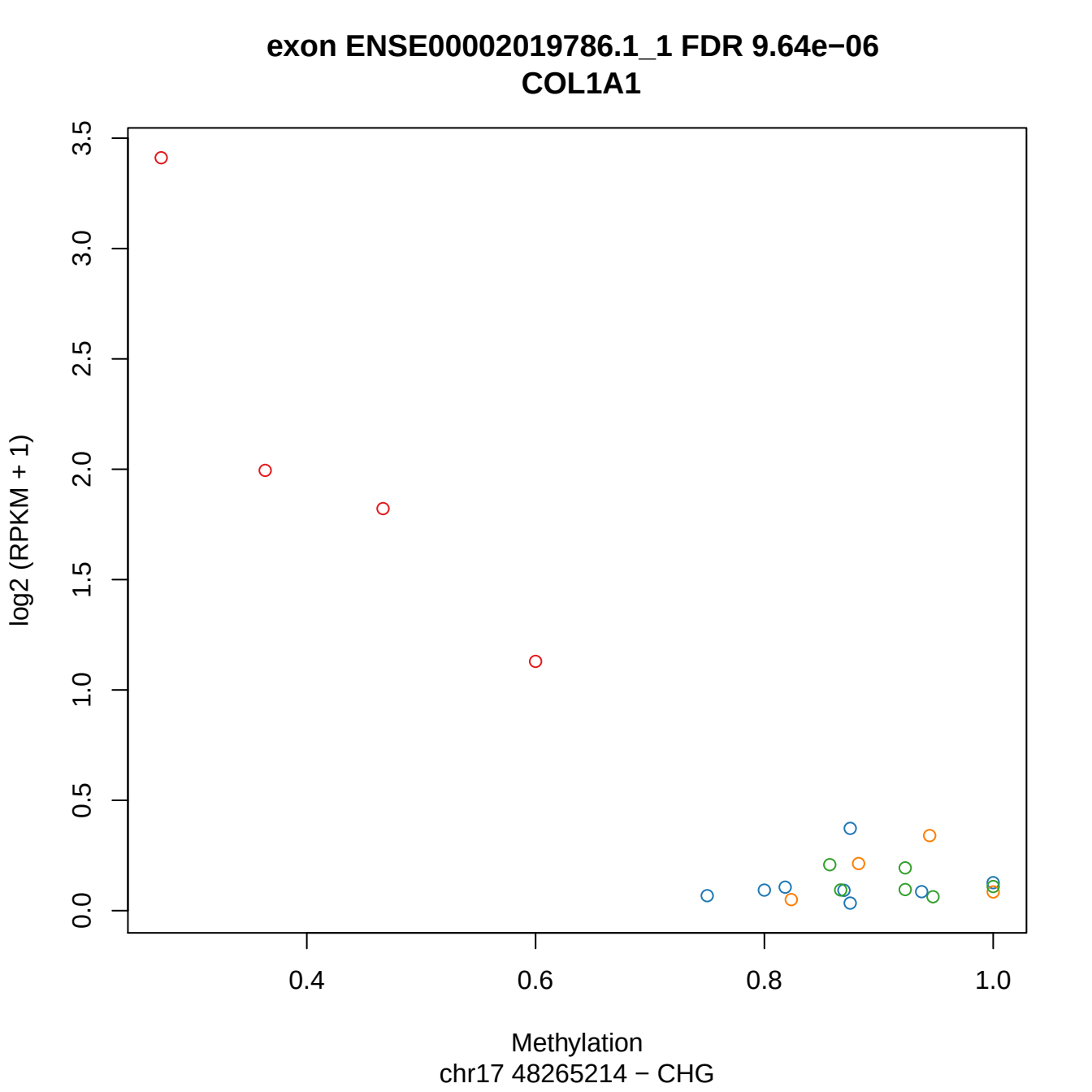

exon ENSE00002149889.1_1 FDR 2.59e−07
TSKU
log2 (RPKM + 1)
0.0
0.5
1.0
1.5
2.0
0.5
0.6
0.7
0.8
0.9
1.0
Methylation
chr11 76506080 − CHH

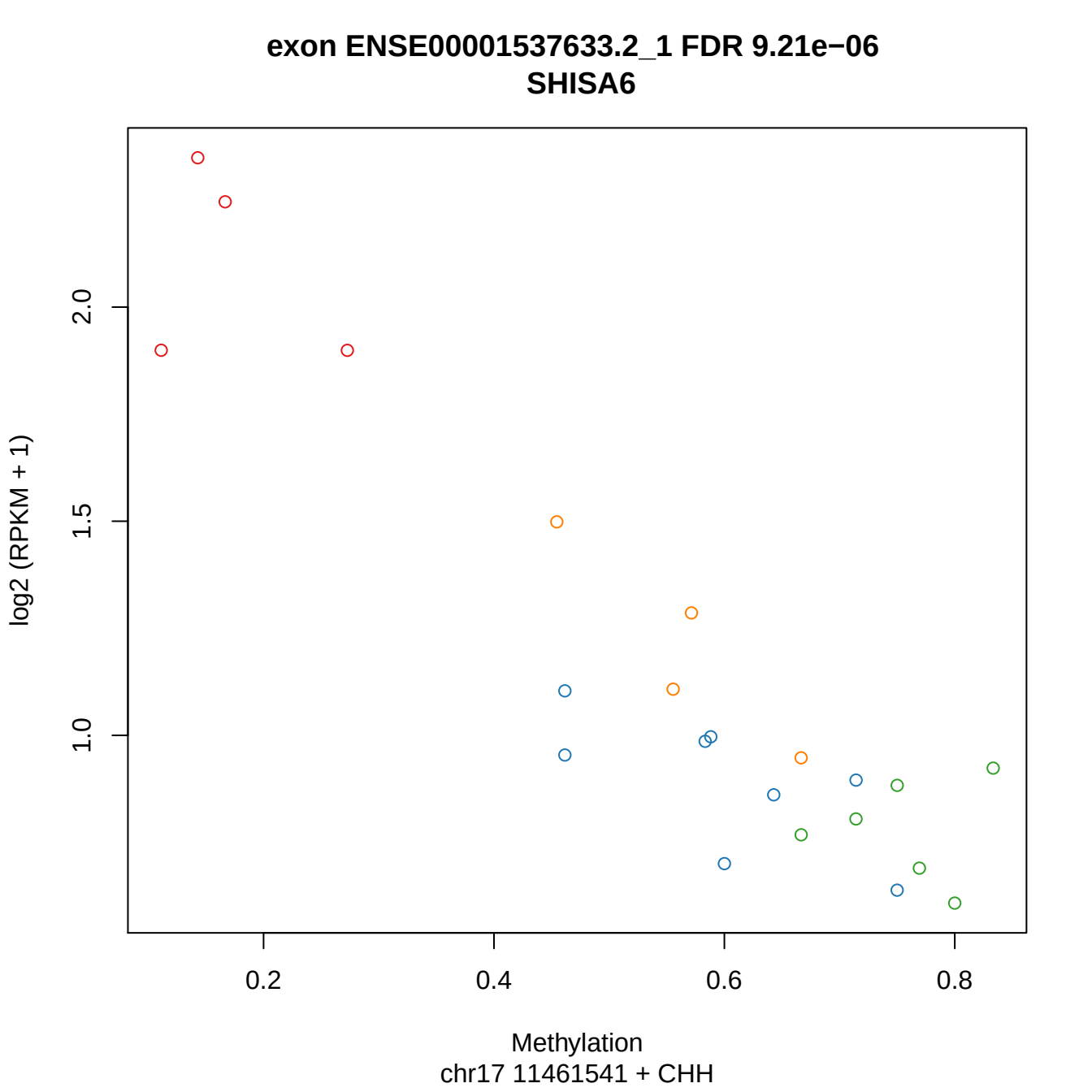

exon ENSE00002680807.1_1 FDR 5.48e−05
STRA6
log2 (RPKM + 1)
0.0
0.2
0.4
0.6
0.8
1.0
1.2
0.0
0.2
0.4
0.6
0.8
Methylation
chr15 74473475 − CHG

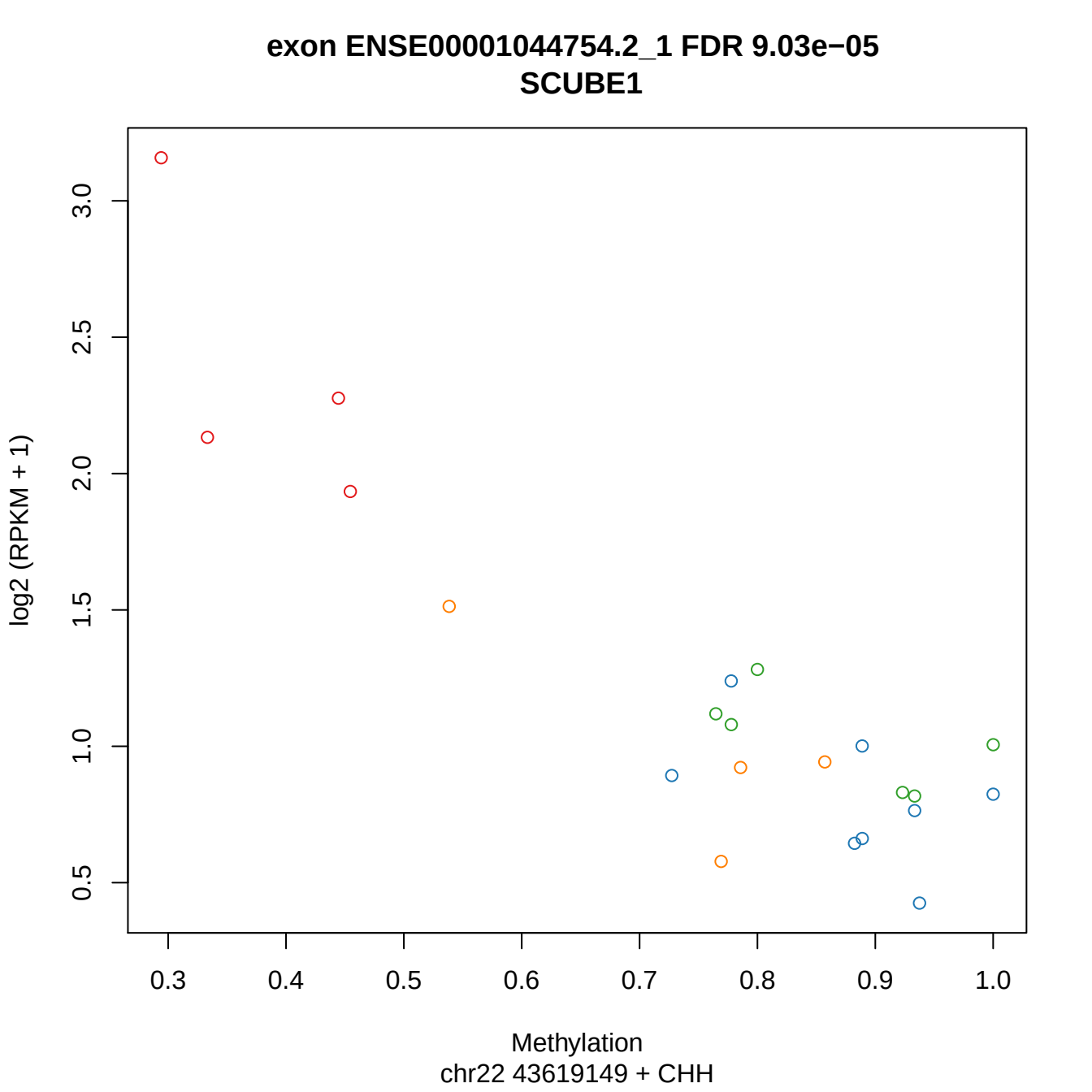

exon ENSE00001827186.1_1 FDR 1.18e−05
COL1A1
log2 (RPKM + 1)
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
0.4
0.6
0.8
1.0
Methylation
chr17 48265214 − CHG

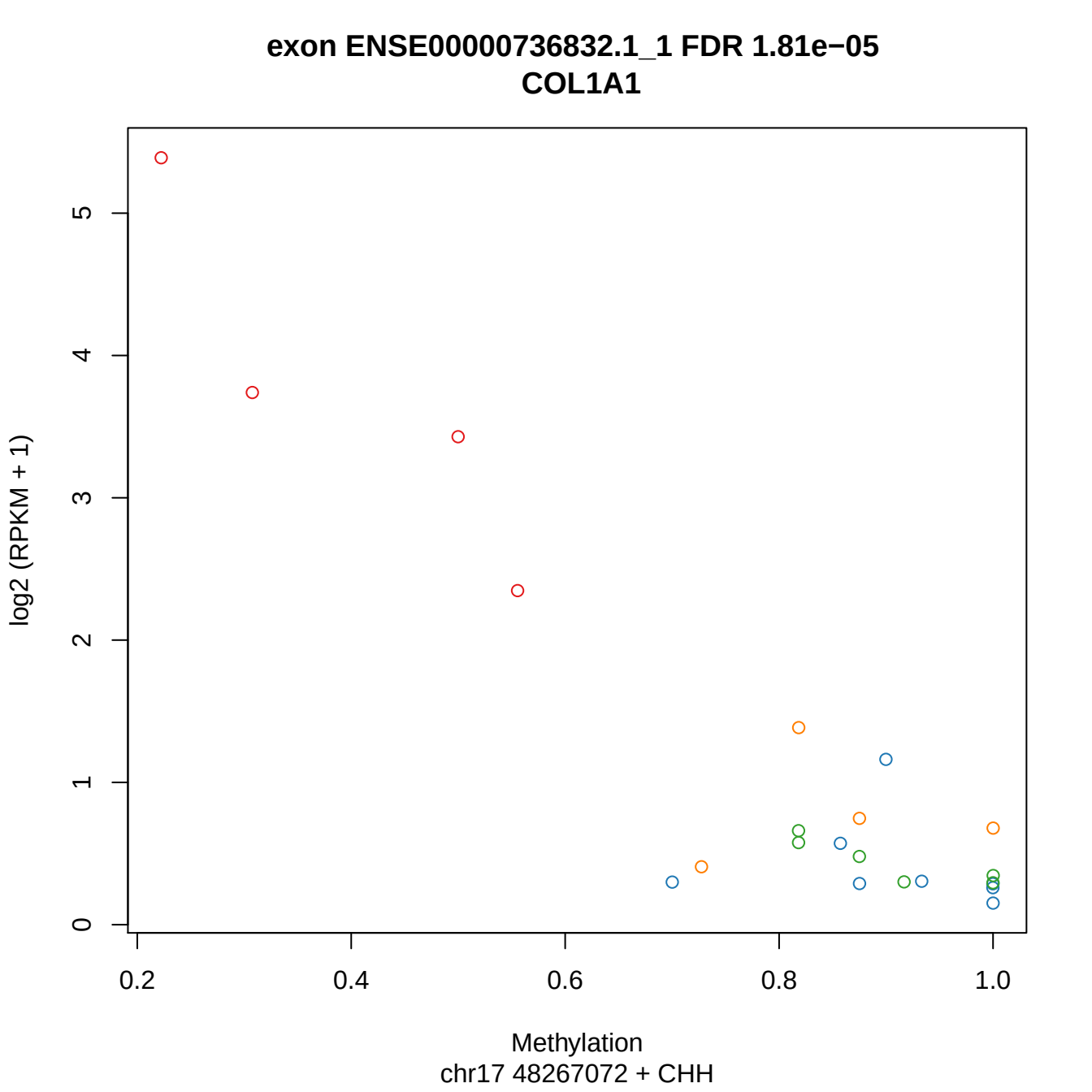

exon ENSE00000736840.1_1 FDR 5.39e−06
COL1A1
log2 (RPKM + 1)
0
1
2
3
4
5
0.4
0.6
0.8
1.0
Methylation
chr17 48265214 − CHG

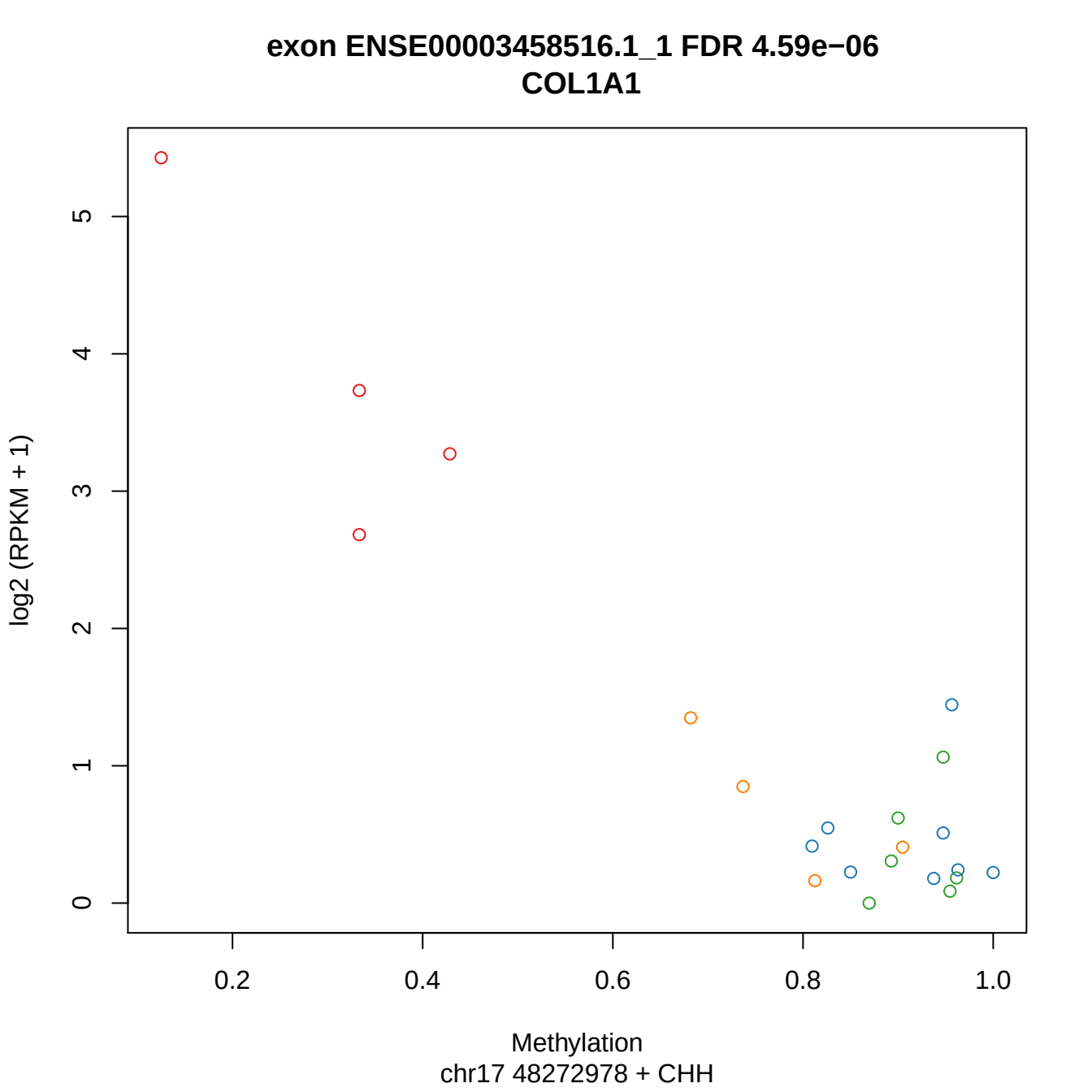

exon ENSE00002115065.2_1 FDR 6.41e−08
TRIM67
log2 (RPKM + 1)
0.2
0.4
0.6
0.8
1.0
1.2
1.4
1.6
0.2
0.4
0.6
0.8
Methylation
chr1 231352734 − CHG

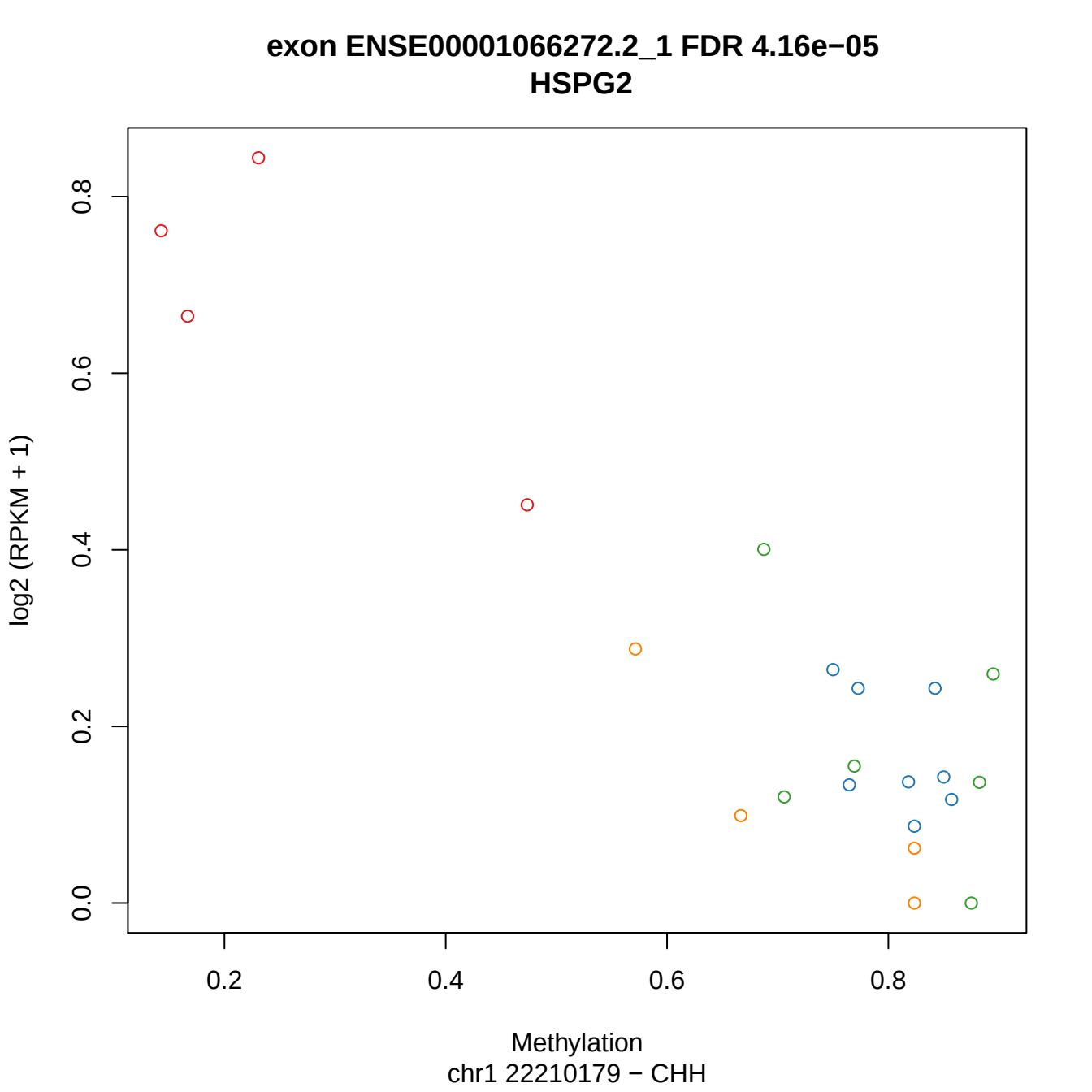

exon ENSE00002019786.1_1 FDR 9.64e−06
COL1A1
log2 (RPKM + 1)
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
0.4
0.6
0.8
1.0
Methylation
chr17 48265214 − CHG

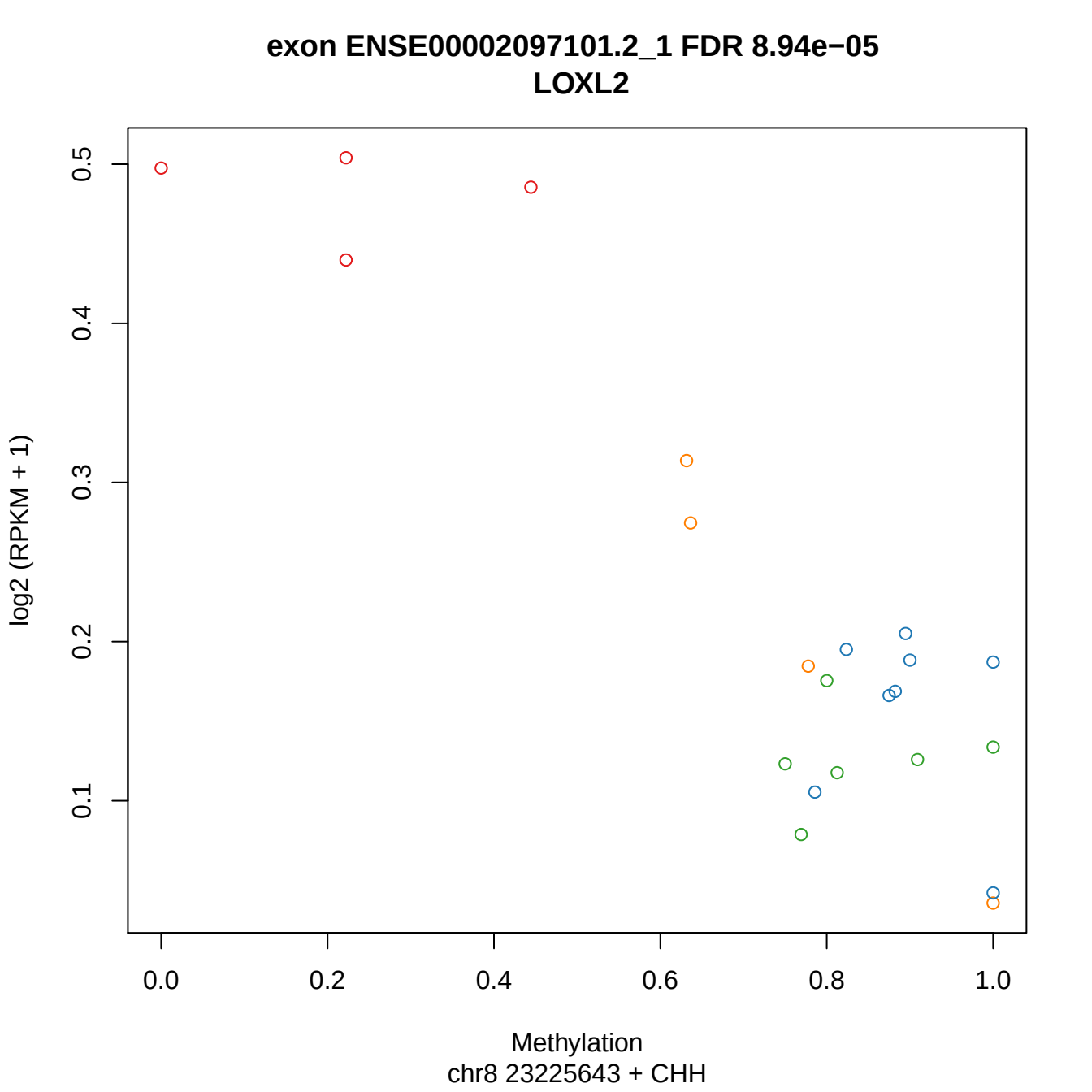

exon ENSE00001537633.2_1 FDR 9.21e−06
SHISA6
log2 (RPKM + 1)
1.0
1.5
2.0
0.2
0.4
0.6
0.8
Methylation
chr17 11461541 + CHH

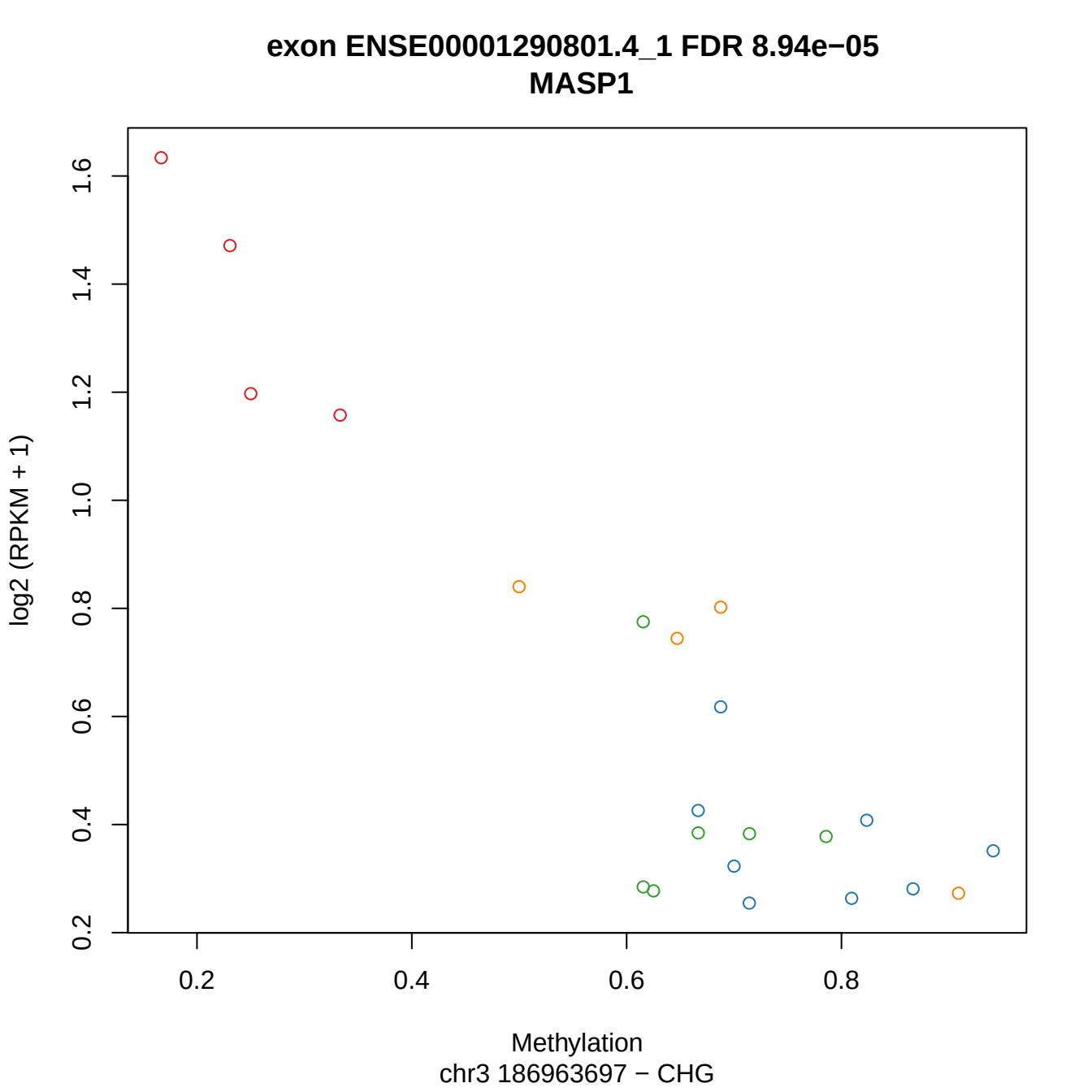

exon ENSE00001044754.2_1 FDR 9.03e−05
SCUBE1
log2 (RPKM + 1)
0.5
1.0
1.5
2.0
2.5
3.0
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Methylation
chr22 43619149 + CHH

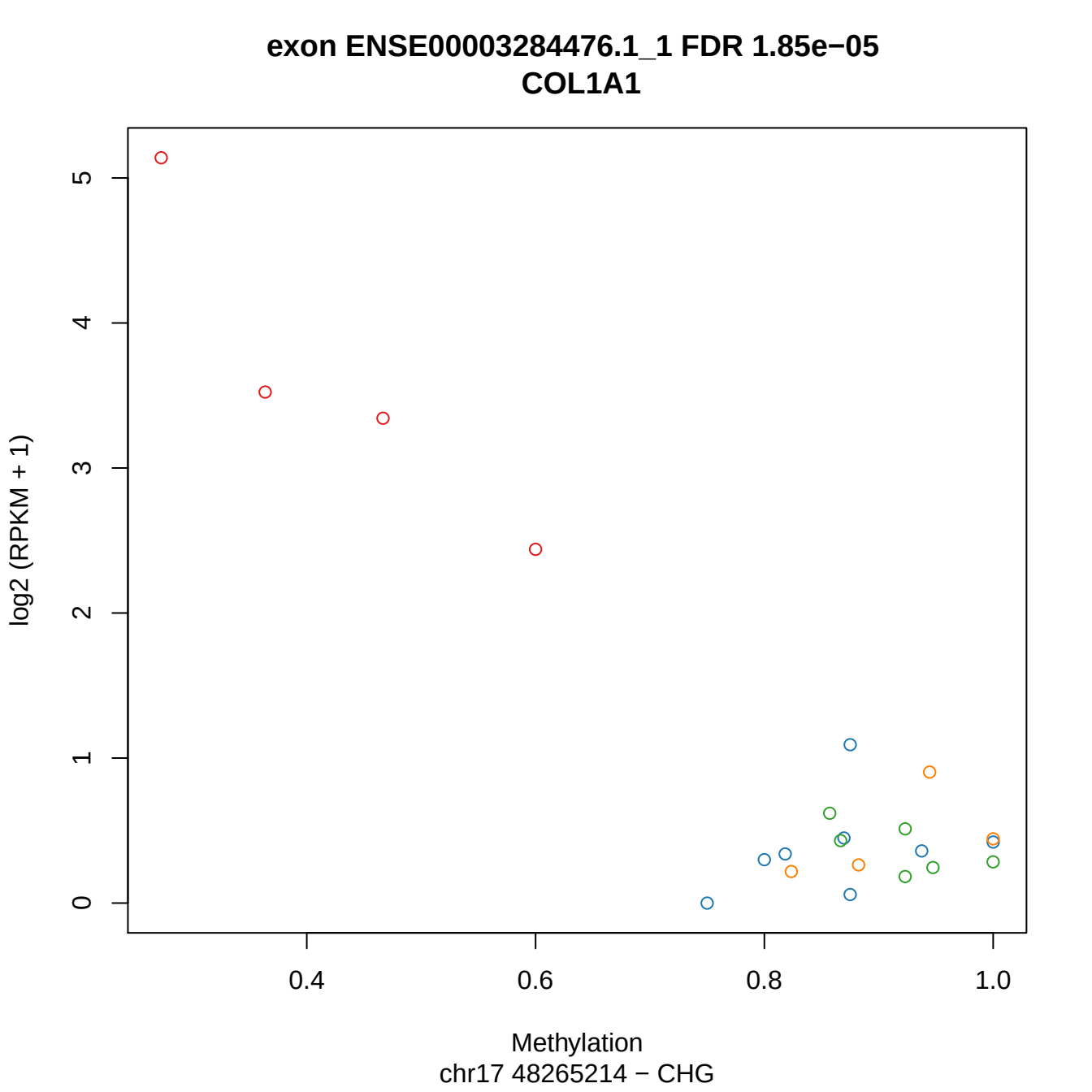

exon ENSE00000736832.1_1 FDR 1.81e−05
COL1A1
log2 (RPKM + 1)
0
1
2
3
4
5
0.2
0.4
0.6
0.8
1.0
Methylation
chr17 48267072 + CHH

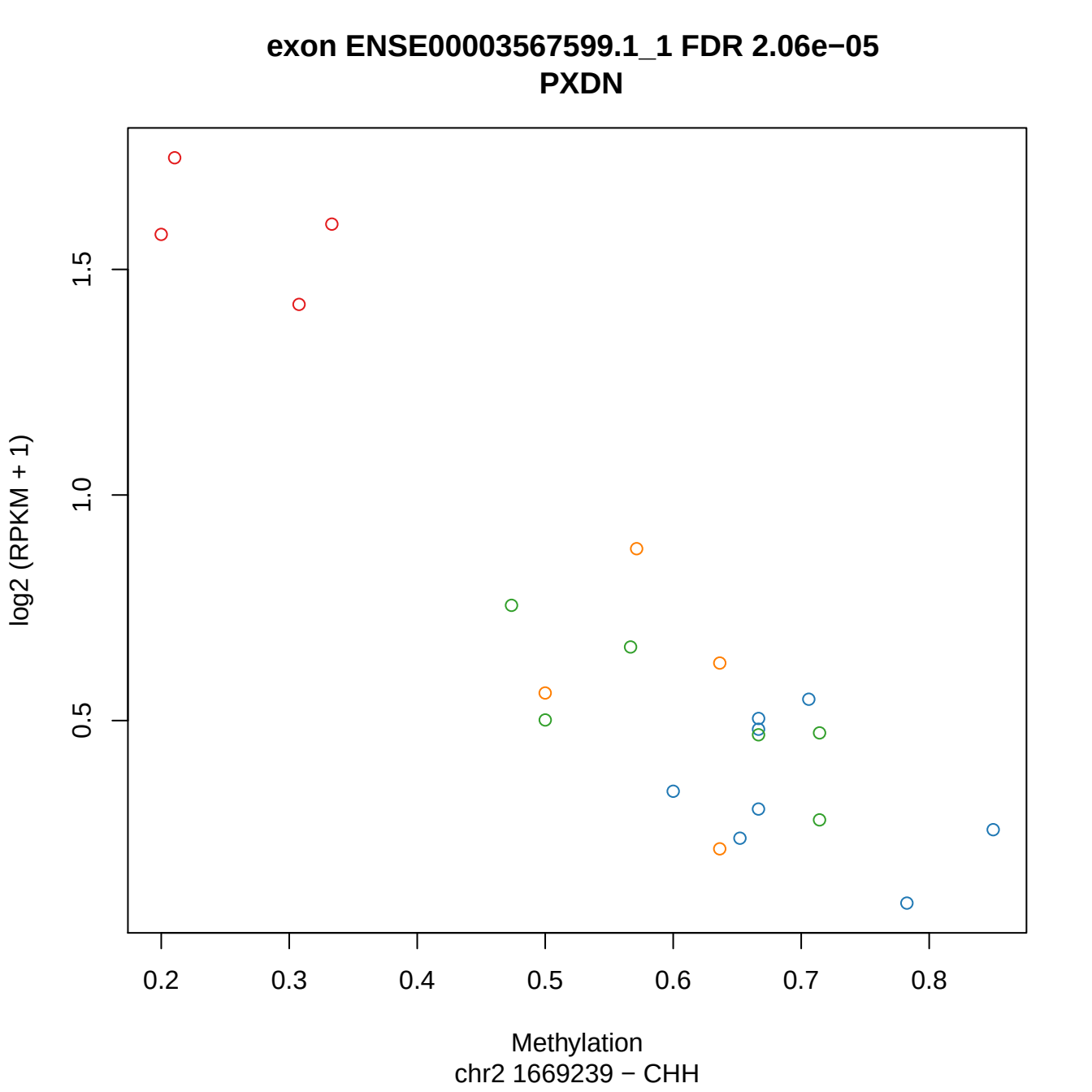

exon ENSE00003458516.1_1 FDR 4.59e−06
COL1A1
log2 (RPKM + 1)
0
1
2
3
4
5
0.2
0.4
0.6
0.8
1.0
Methylation
chr17 48272978 + CHH

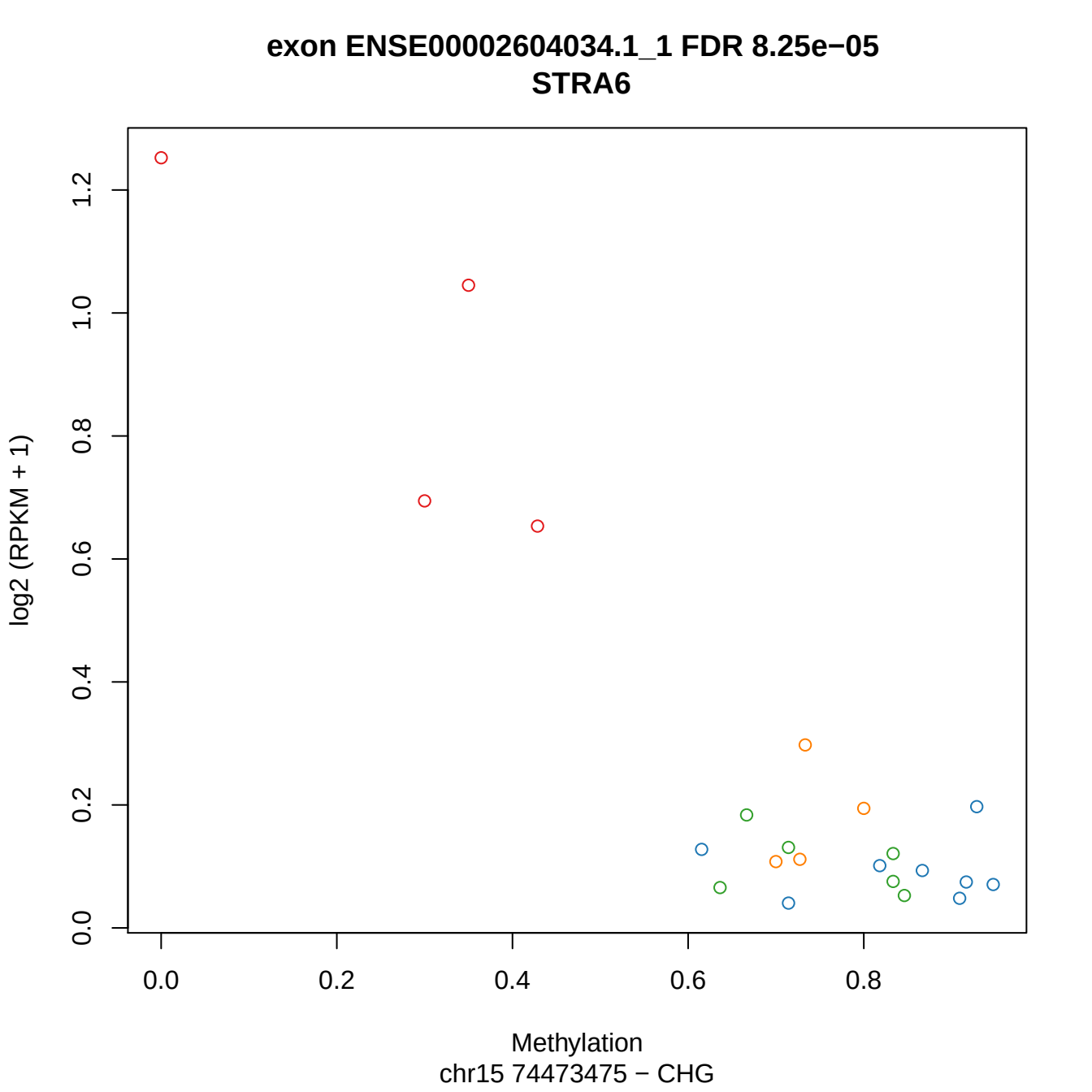

exon ENSE00001066272.2_1 FDR 4.16e−05
HSPG2
log2 (RPKM + 1)
0.0
0.2
0.4
0.6
0.8
0.2
0.4
0.6
0.8
Methylation
chr1 22210179 − CHH

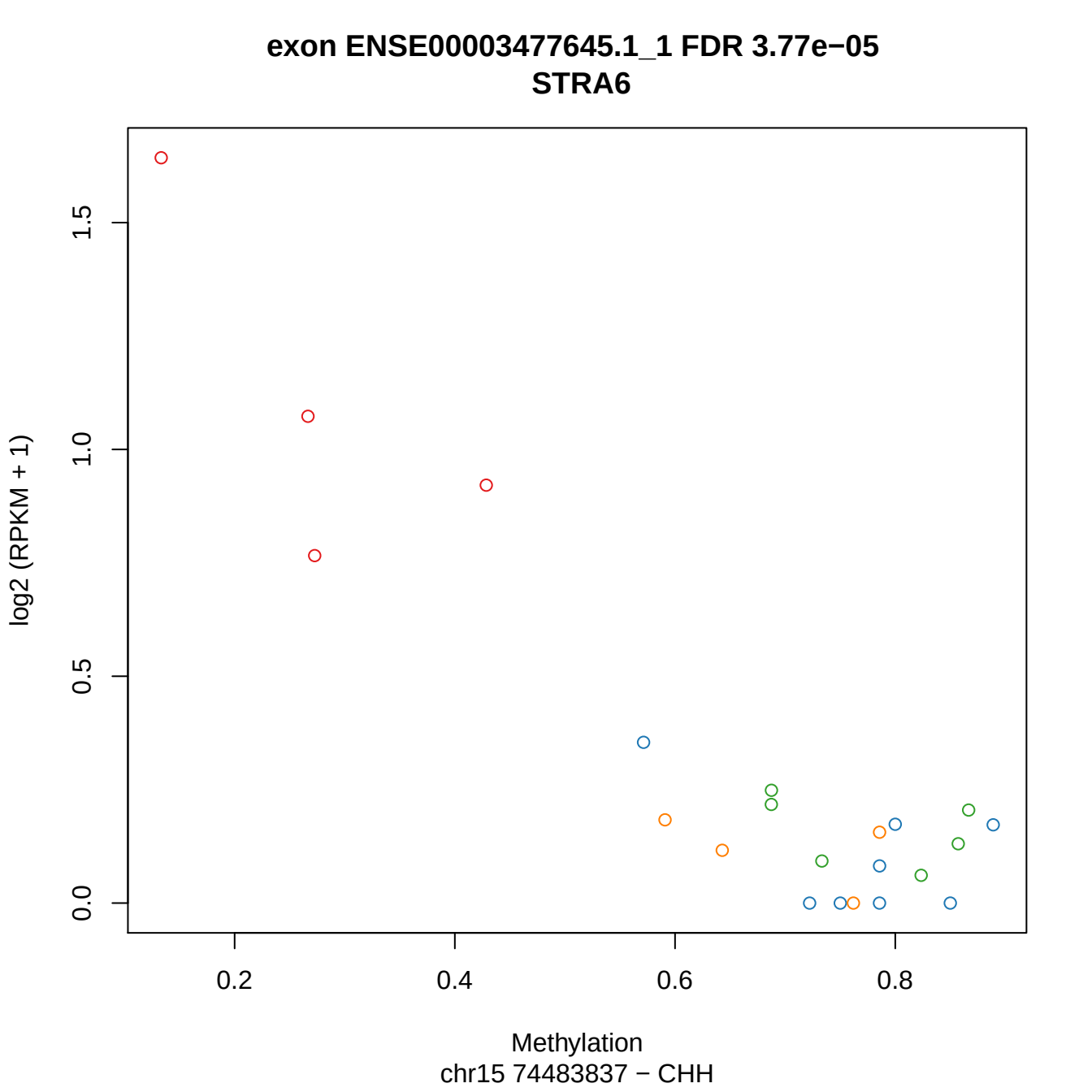

exon ENSE00002097101.2_1 FDR 8.94e−05
LOXL2
log2 (RPKM + 1)
0.1
0.2
0.3
0.4
0.5
0.0
0.2
0.4
0.6
0.8
1.0
Methylation
chr8 23225643 + CHH

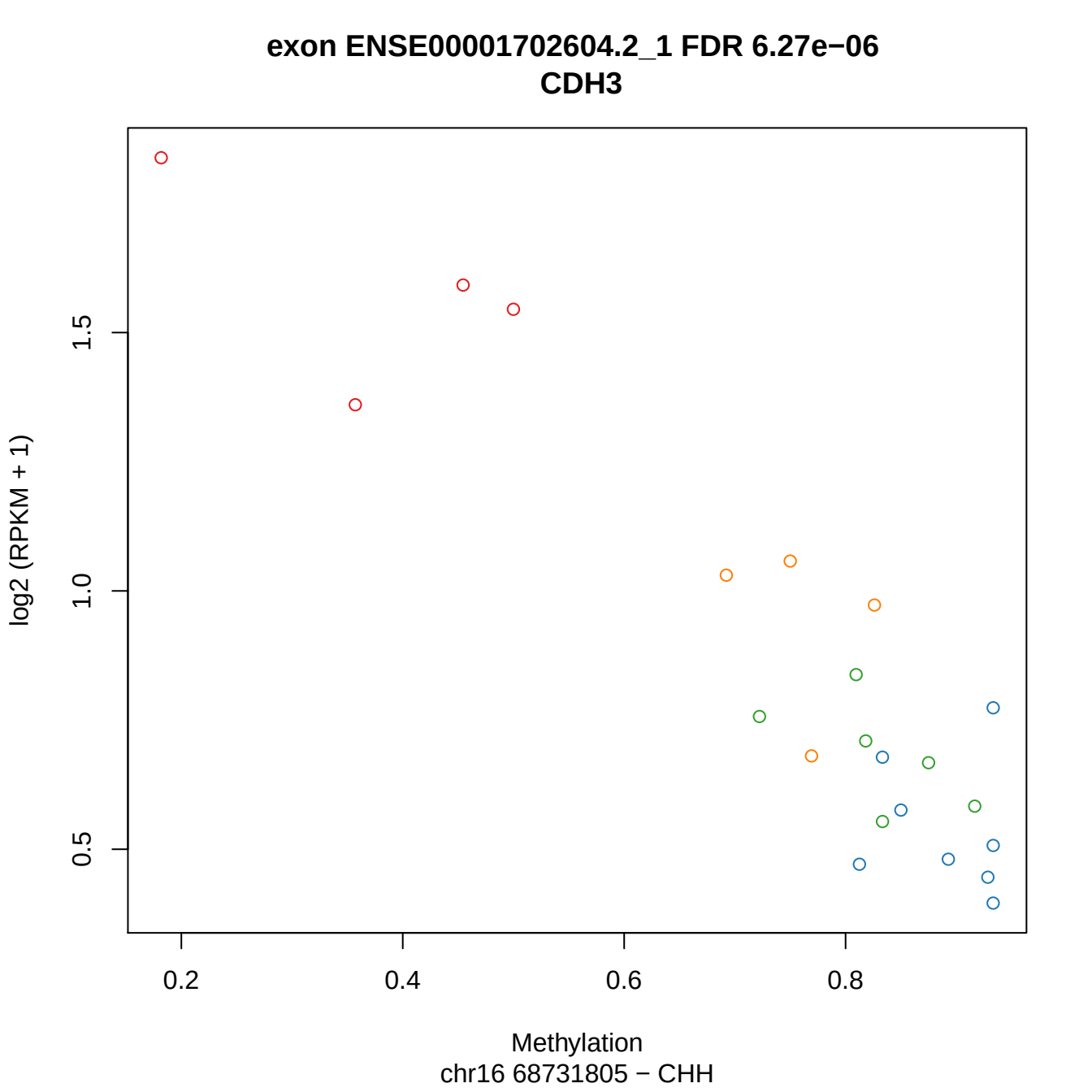

exon ENSE00001290801.4_1 FDR 8.94e−05
MASP1
log2 (RPKM + 1)
0.2
0.4
0.6
0.8
1.0
1.2
1.4
1.6
0.2
0.4
0.6
0.8
Methylation
chr3 186963697 − CHG

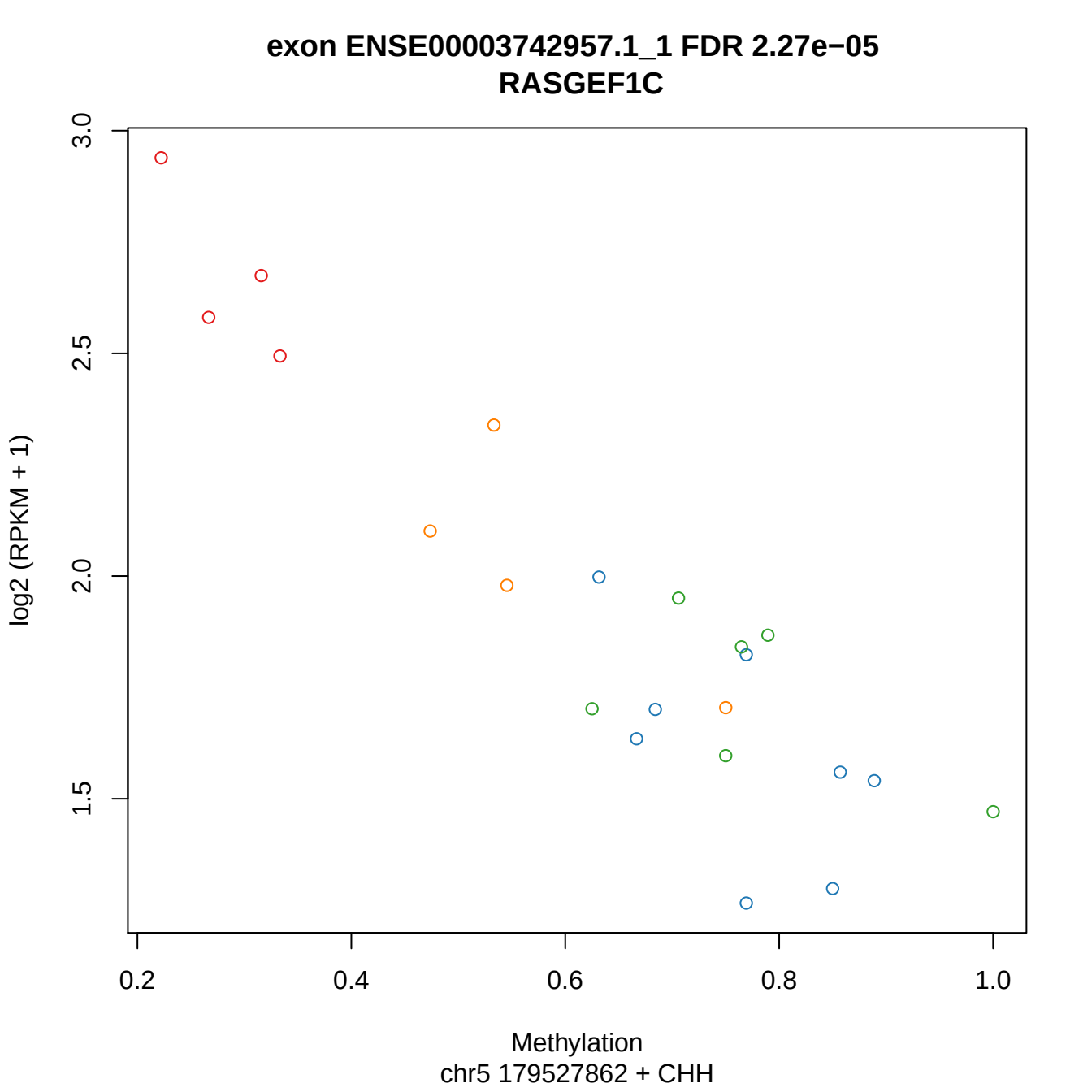

exon ENSE00003284476.1_1 FDR 1.85e−05
COL1A1
log2 (RPKM + 1)
0
1
2
3
4
5
0.4
0.6
0.8
1.0
Methylation
chr17 48265214 − CHG

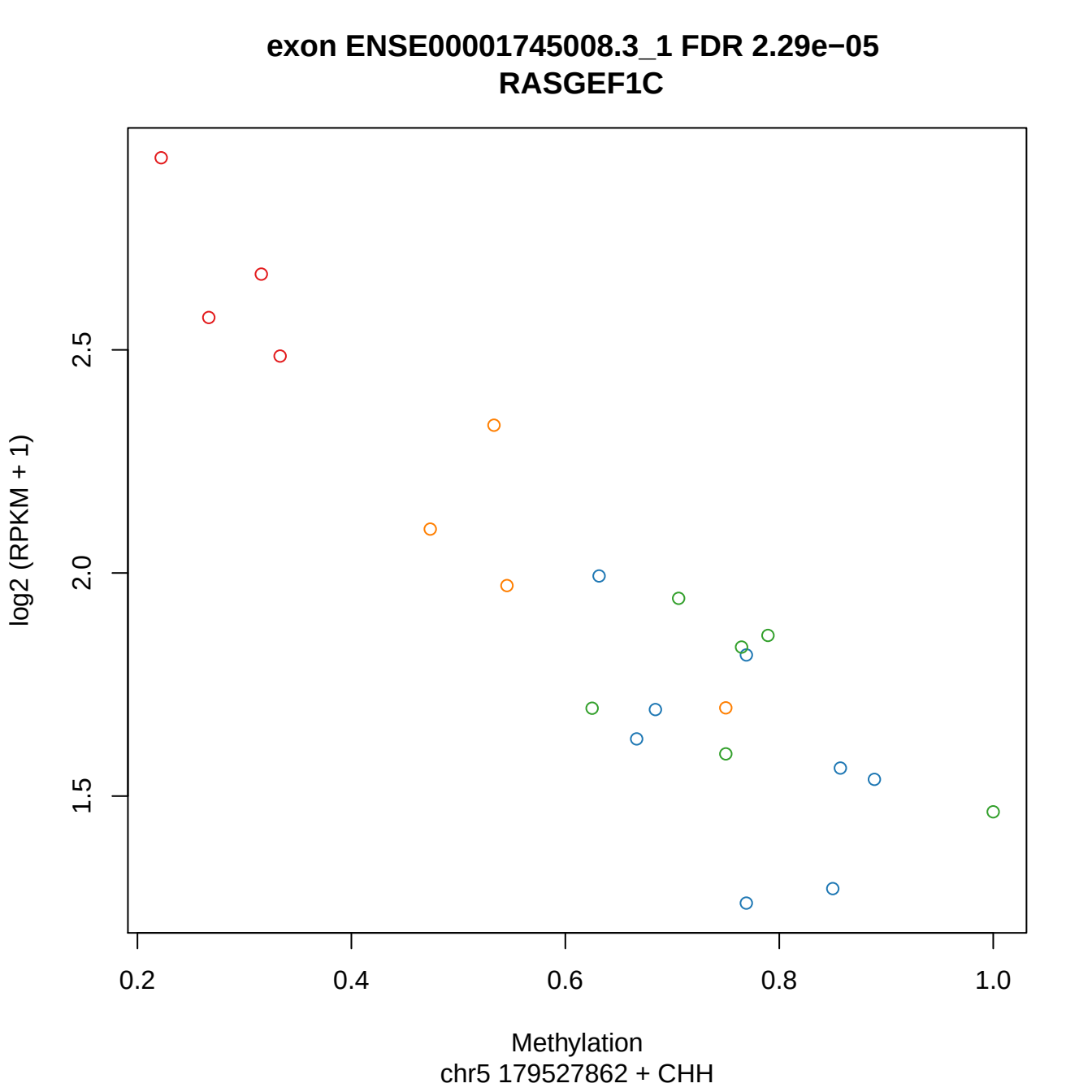

exon ENSE00003567599.1_1 FDR 2.06e−05
PXDN
log2 (RPKM + 1)
0.5
1.0
1.5
0.2
0.3
0.4
0.5
0.6
0.7
0.8
Methylation
chr2 1669239 − CHH

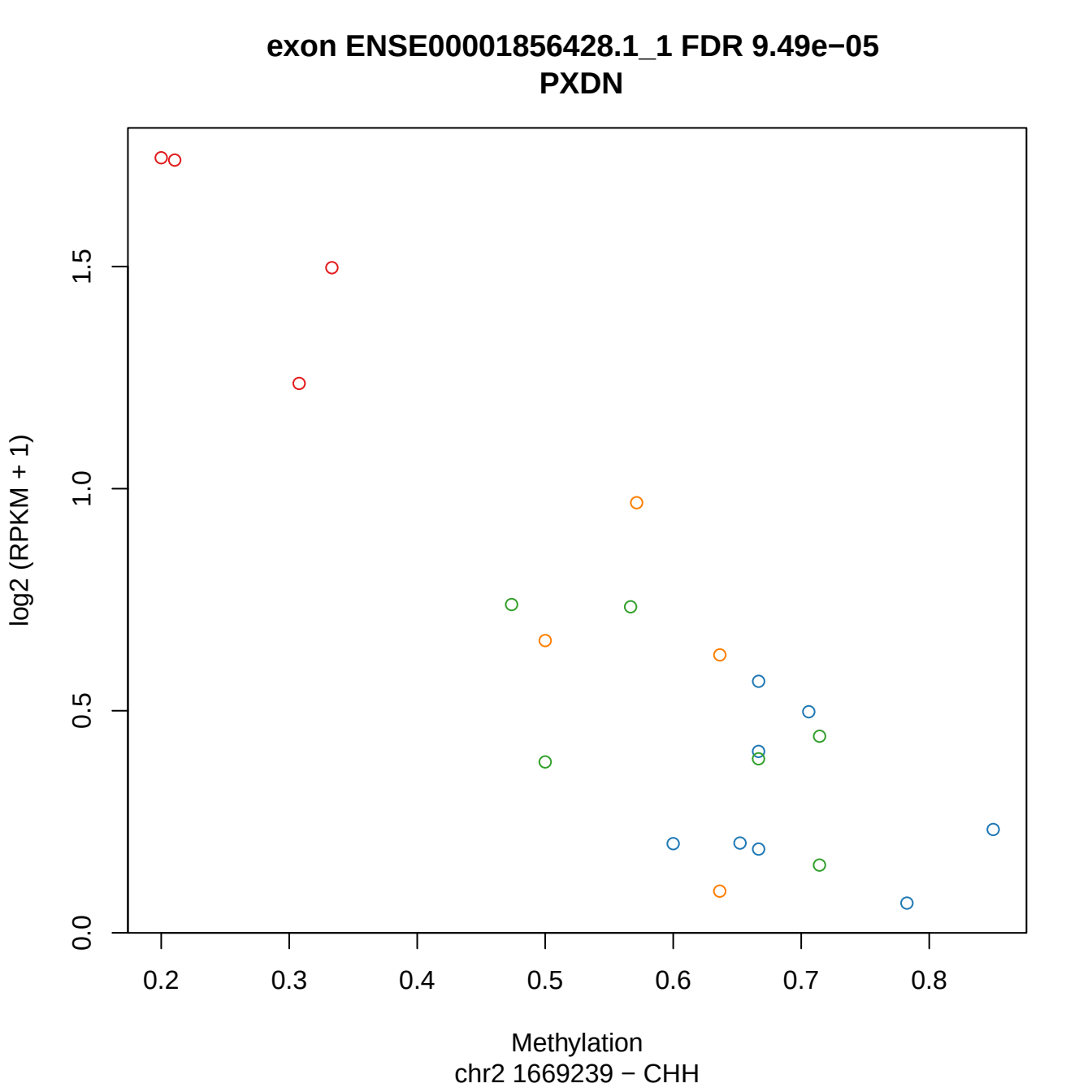

exon ENSE00002604034.1_1 FDR 8.25e−05
STRA6
log2 (RPKM + 1)
0.0
0.2
0.4
0.6
0.8
1.0
1.2
0.0
0.2
0.4
0.6
0.8
Methylation
chr15 74473475 − CHG

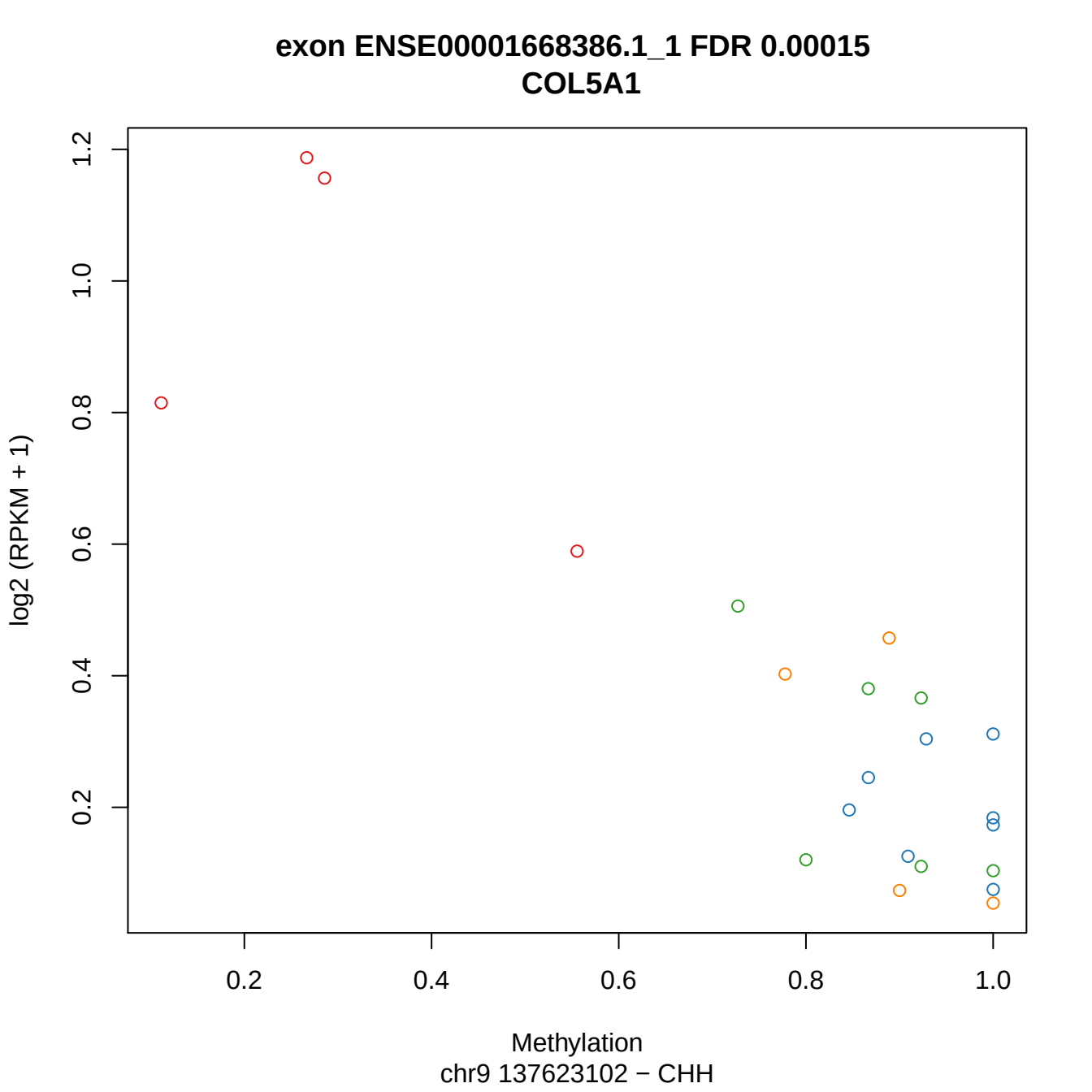

exon ENSE00003477645.1_1 FDR 3.77e−05
STRA6
log2 (RPKM + 1)
0.0
0.5
1.0
1.5
0.2
0.4
0.6
0.8
Methylation
chr15 74483837 − CHH

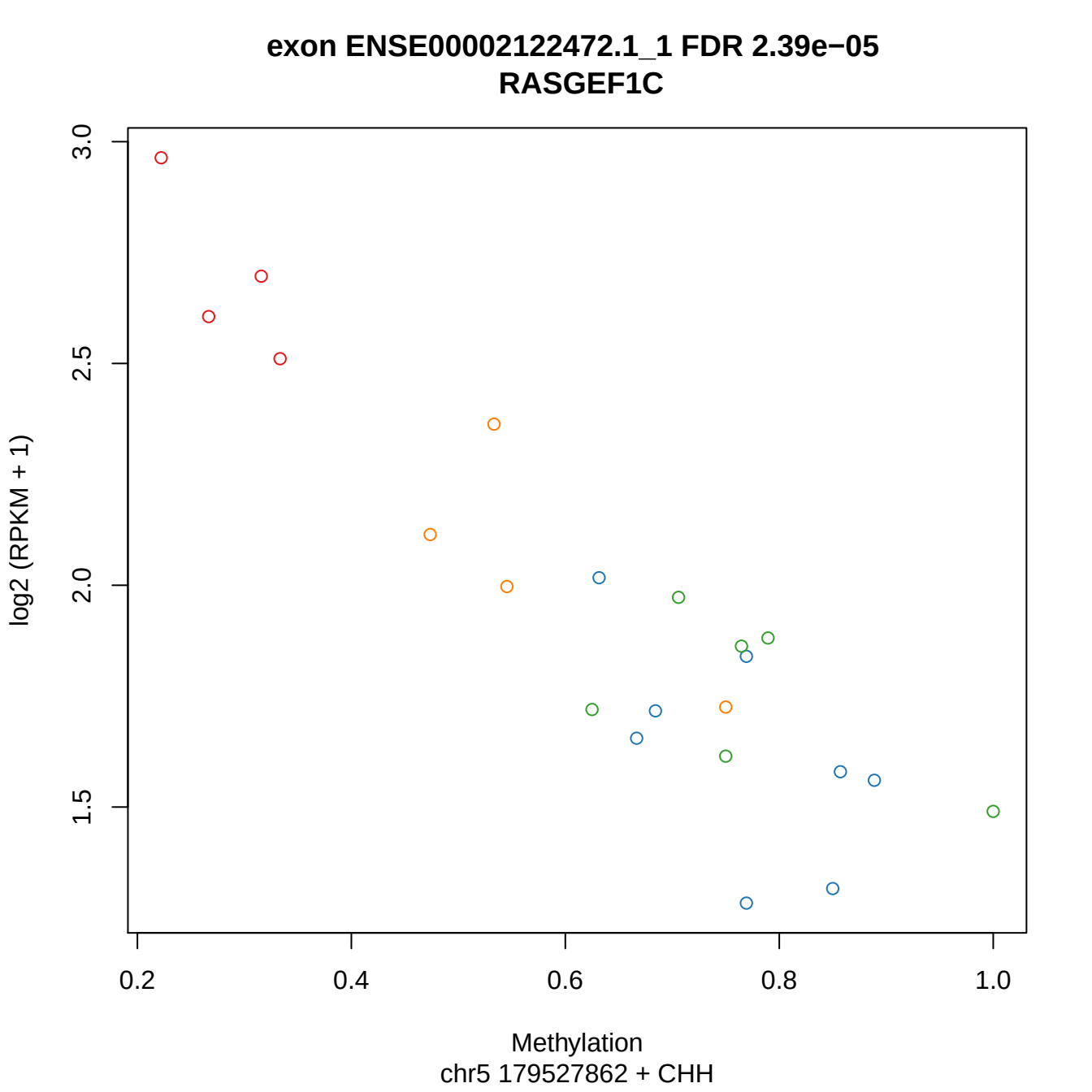

exon ENSE00001702604.2_1 FDR 6.27e−06
CDH3
log2 (RPKM + 1)
0.5
1.0
1.5
0.2
0.4
0.6
0.8
Methylation
chr16 68731805 − CHH

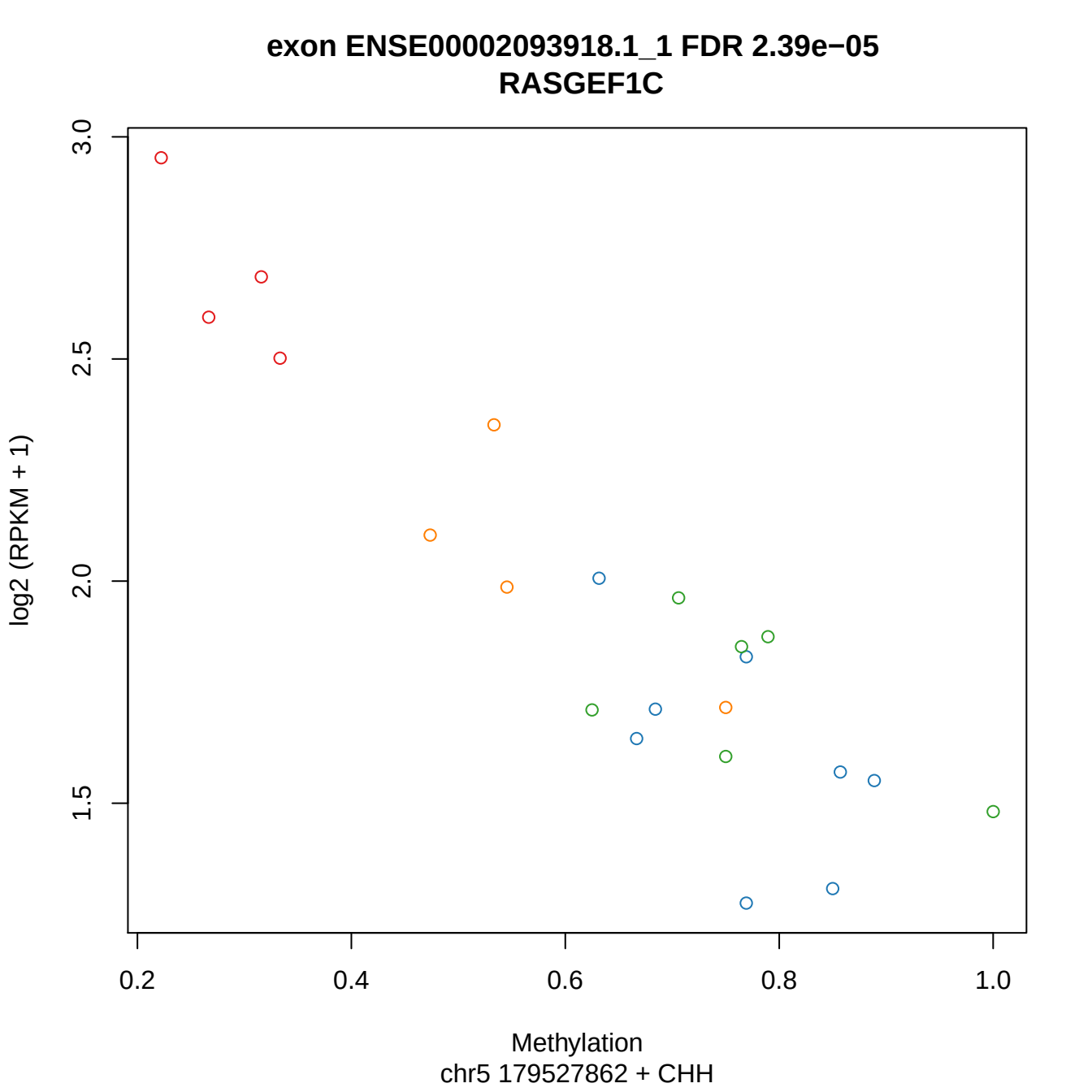

exon ENSE00003742957.1_1 FDR 2.27e−05
RASGEF1C
log2 (RPKM + 1)
3.0
2.5
2.0
1.5
0.2
0.4
0.6
0.8
1.0
Methylation
chr5 179527862 + CHH

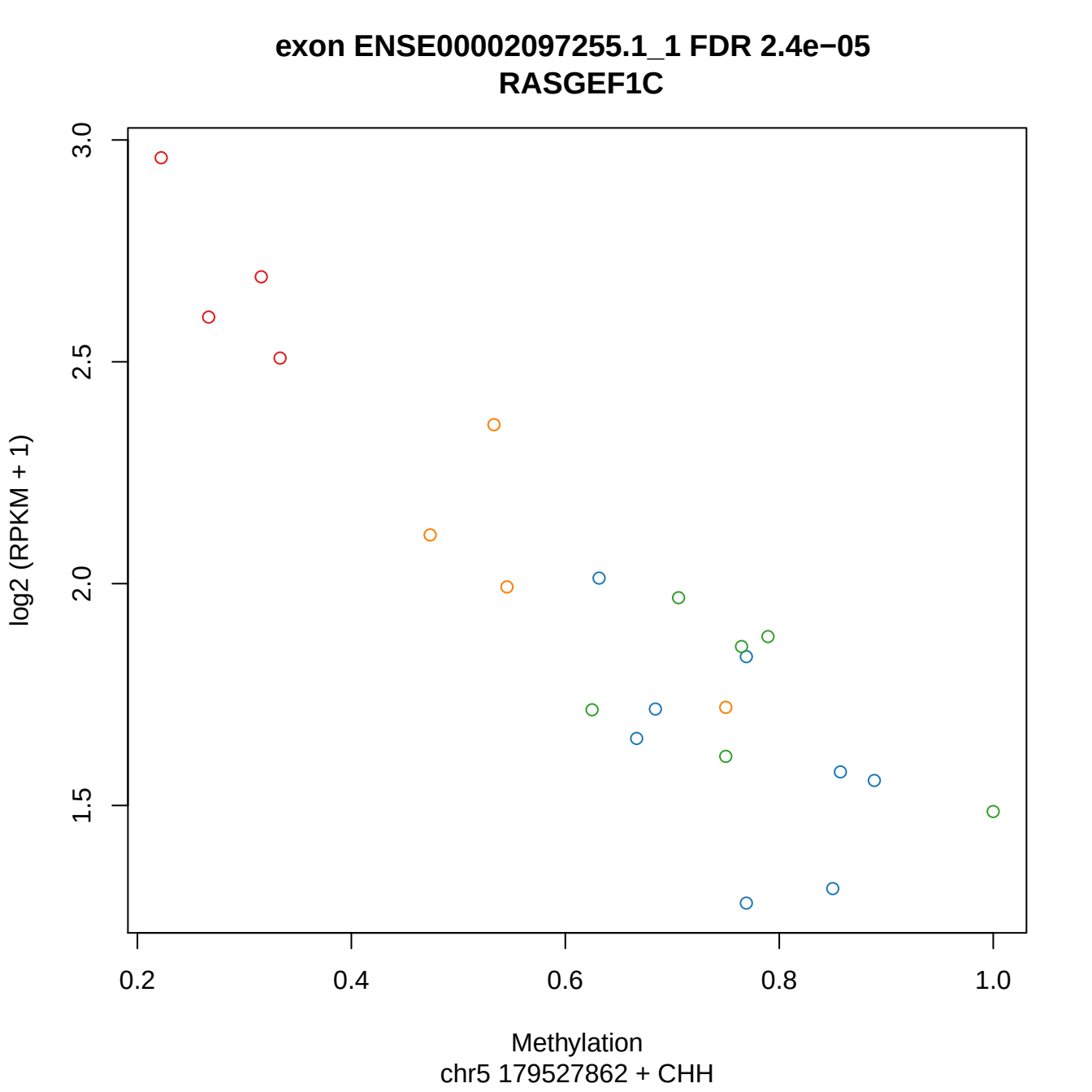

exon ENSE00001745008.3_1 FDR 2.29e−05
RASGEF1C
log2 (RPKM + 1)
2.5
2.0
1.5
0.2
0.4
0.6
0.8
1.0
Methylation
chr5 179527862 + CHH

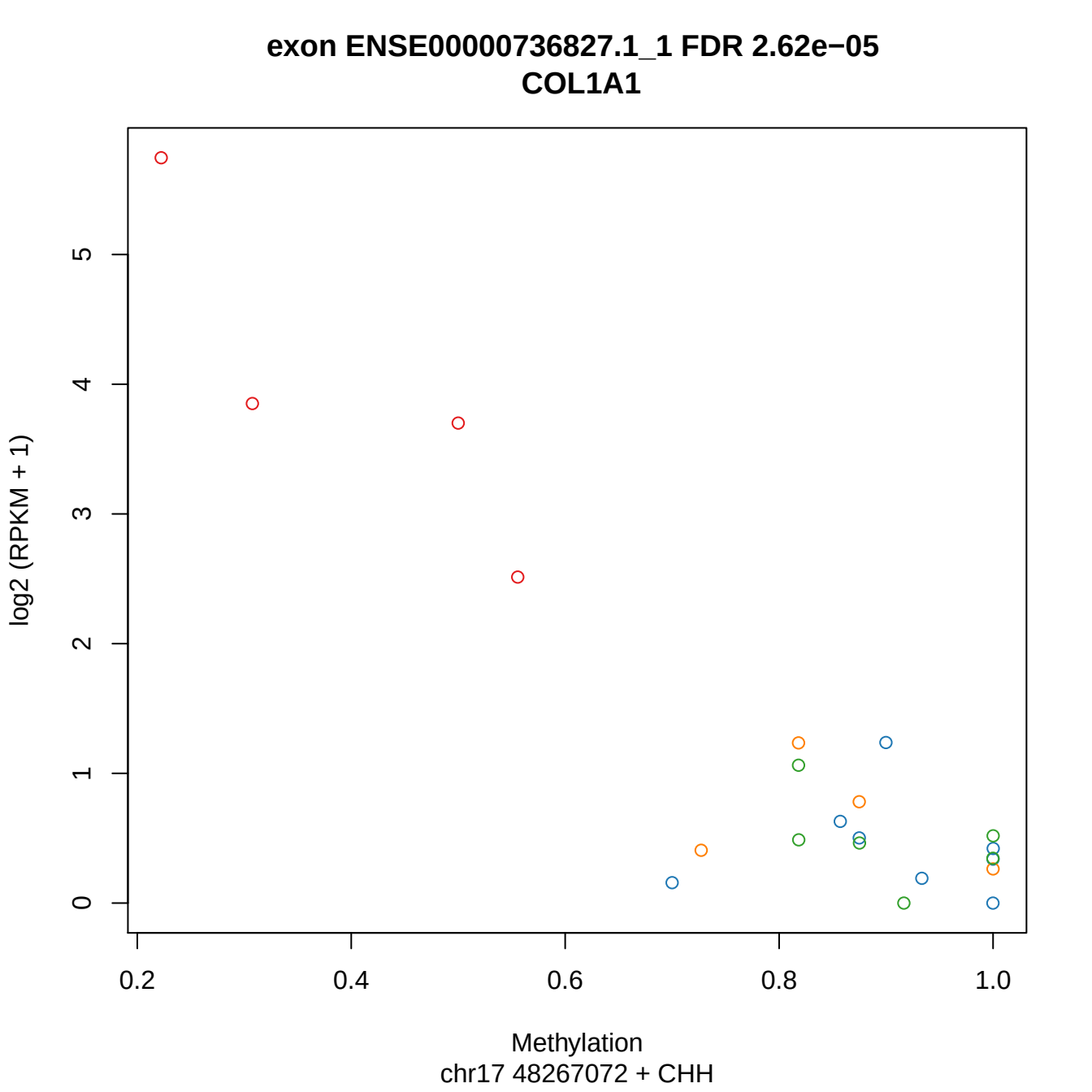

exon ENSE00001856428.1_1 FDR 9.49e−05
PXDN
log2 (RPKM + 1)
0.0
0.5
1.0
1.5
0.2
0.3
0.4
0.5
0.6
0.7
0.8
Methylation
chr2 1669239 − CHH

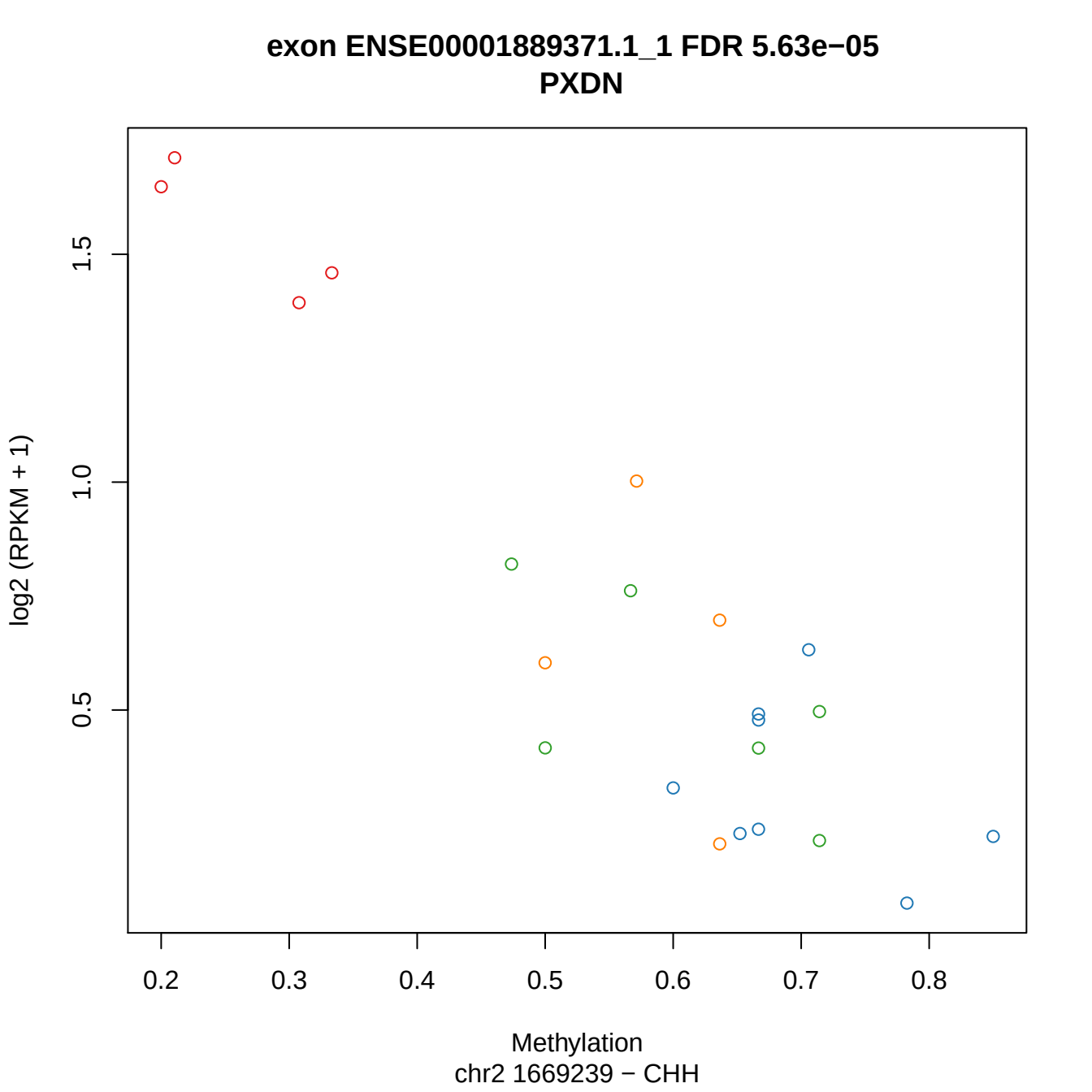

exon ENSE00001668386.1_1 FDR 0.00015
COL5A1
log2 (RPKM + 1)
0.2
0.4
0.6
0.8
1.0
1.2
0.2
0.4
0.6
0.8
1.0
Methylation
chr9 137623102 − CHH

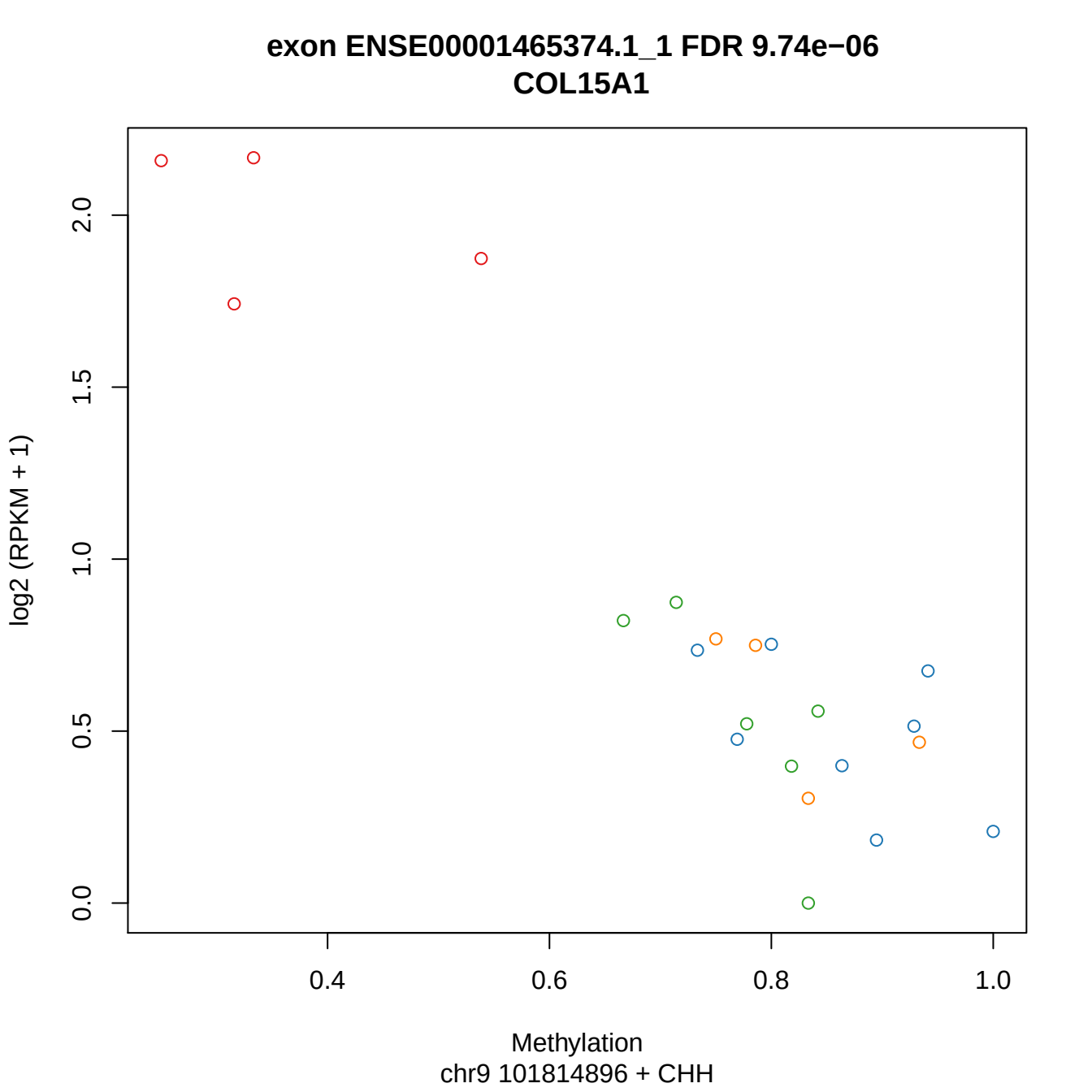

exon ENSE00002122472.1_1 FDR 2.39e−05
RASGEF1C
log2 (RPKM + 1)
3.0
2.5
2.0
1.5
0.2
0.4
0.6
0.8
1.0
Methylation
chr5 179527862 + CHH

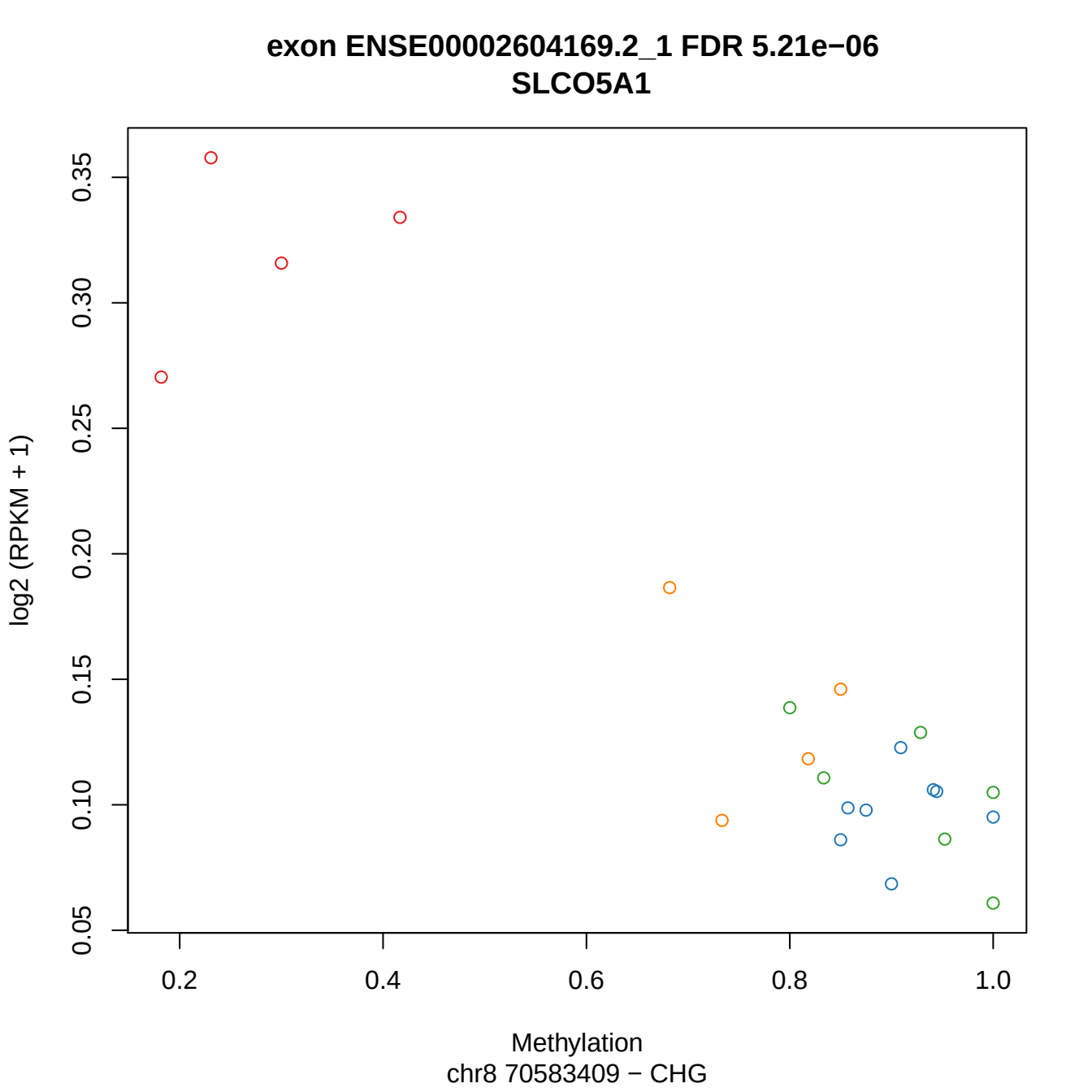

exon ENSE00002093918.1_1 FDR 2.39e−05
RASGEF1C
log2 (RPKM + 1)
3.0
2.5
2.0
1.5
0.2
0.4
0.6
0.8
1.0
Methylation
chr5 179527862 + CHH


exon ENSE00002097255.1_1 FDR 2.4e−05
RASGEF1C
log2 (RPKM + 1)
3.0
2.5
2.0
1.5
0.2
0.4
0.6
0.8
1.0
Methylation
chr5 179527862 + CHH


exon ENSE00000736827.1_1 FDR 2.62e−05
COL1A1
log2 (RPKM + 1)
0
1
2
3
4
5
0.2
0.4
0.6
0.8
1.0
Methylation
chr17 48267072 + CHH


exon ENSE00001889371.1_1 FDR 5.63e−05
PXDN
log2 (RPKM + 1)
0.5
1.0
1.5
0.2
0.3
0.4
0.5
0.6
0.7
0.8
Methylation
chr2 1669239 − CHH


exon ENSE00001465374.1_1 FDR 9.74e−06
COL15A1
log2 (RPKM + 1)
0.0
0.5
1.0
1.5
2.0
0.4
0.6
0.8
1.0
Methylation
chr9 101814896 + CHH


exon ENSE00002604169.2_1 FDR 5.21e−06
SLCO5A1
log2 (RPKM + 1)
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0.10
0.15
0.20
0.25
0.30
0.35
0.2
0.4
0.6
0.8
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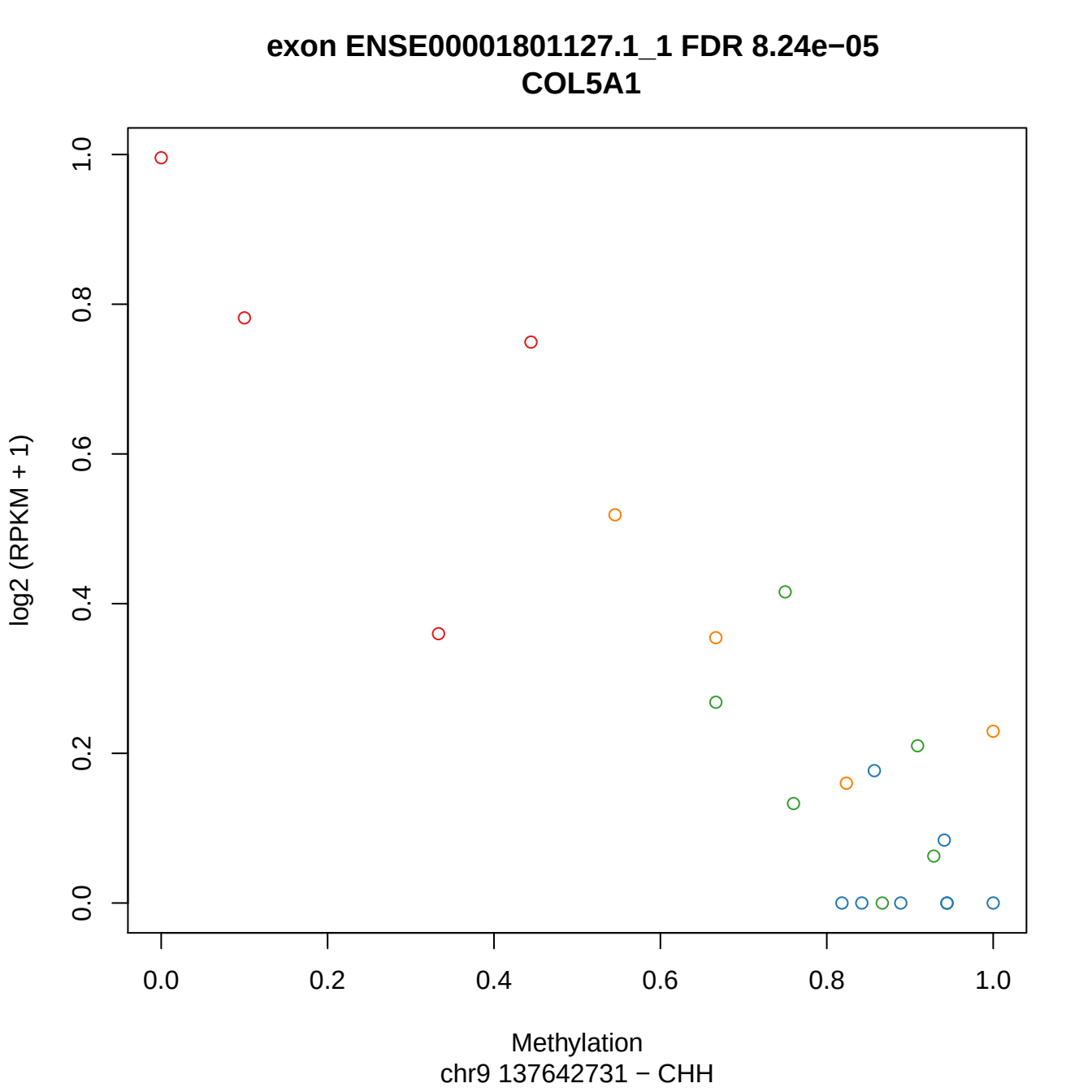
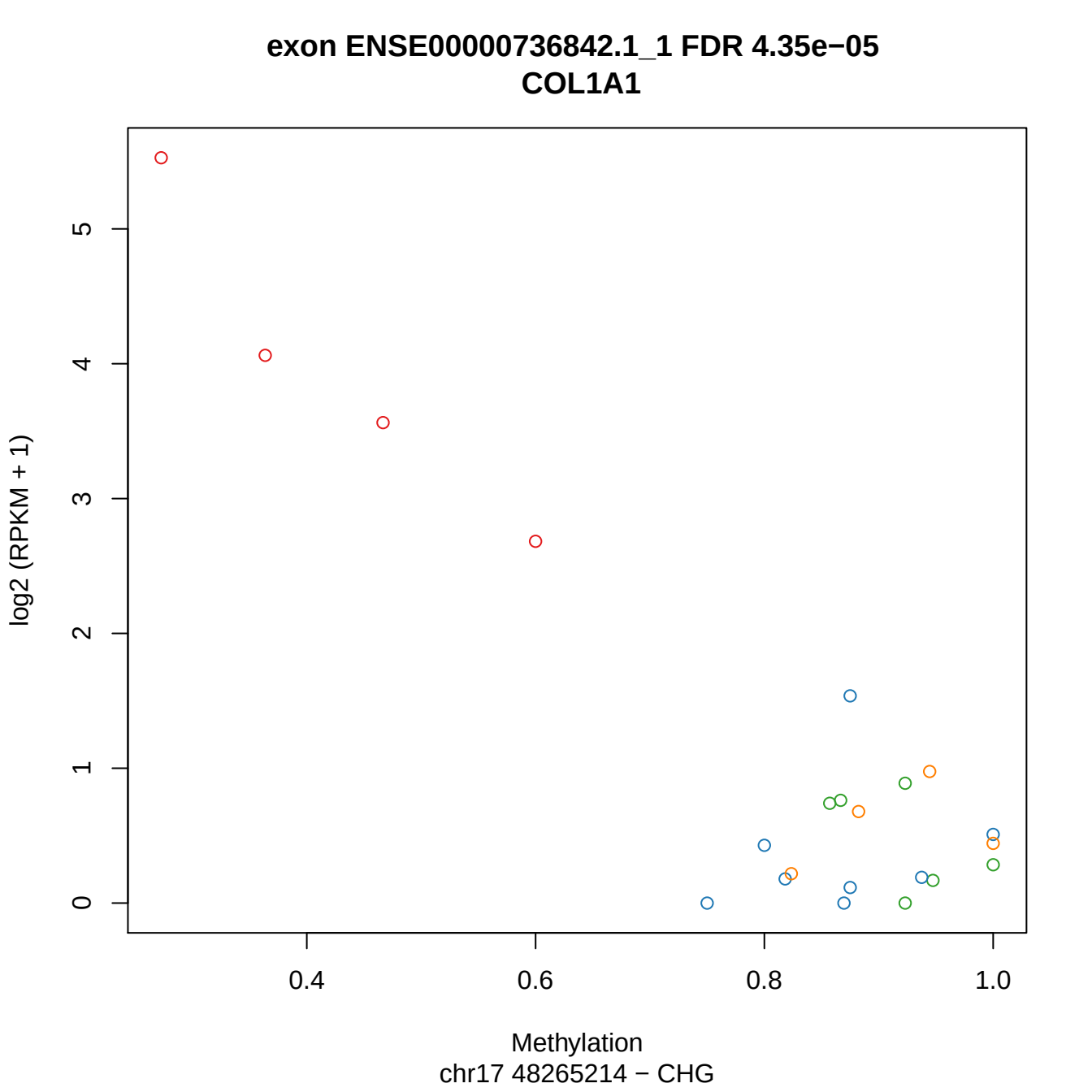
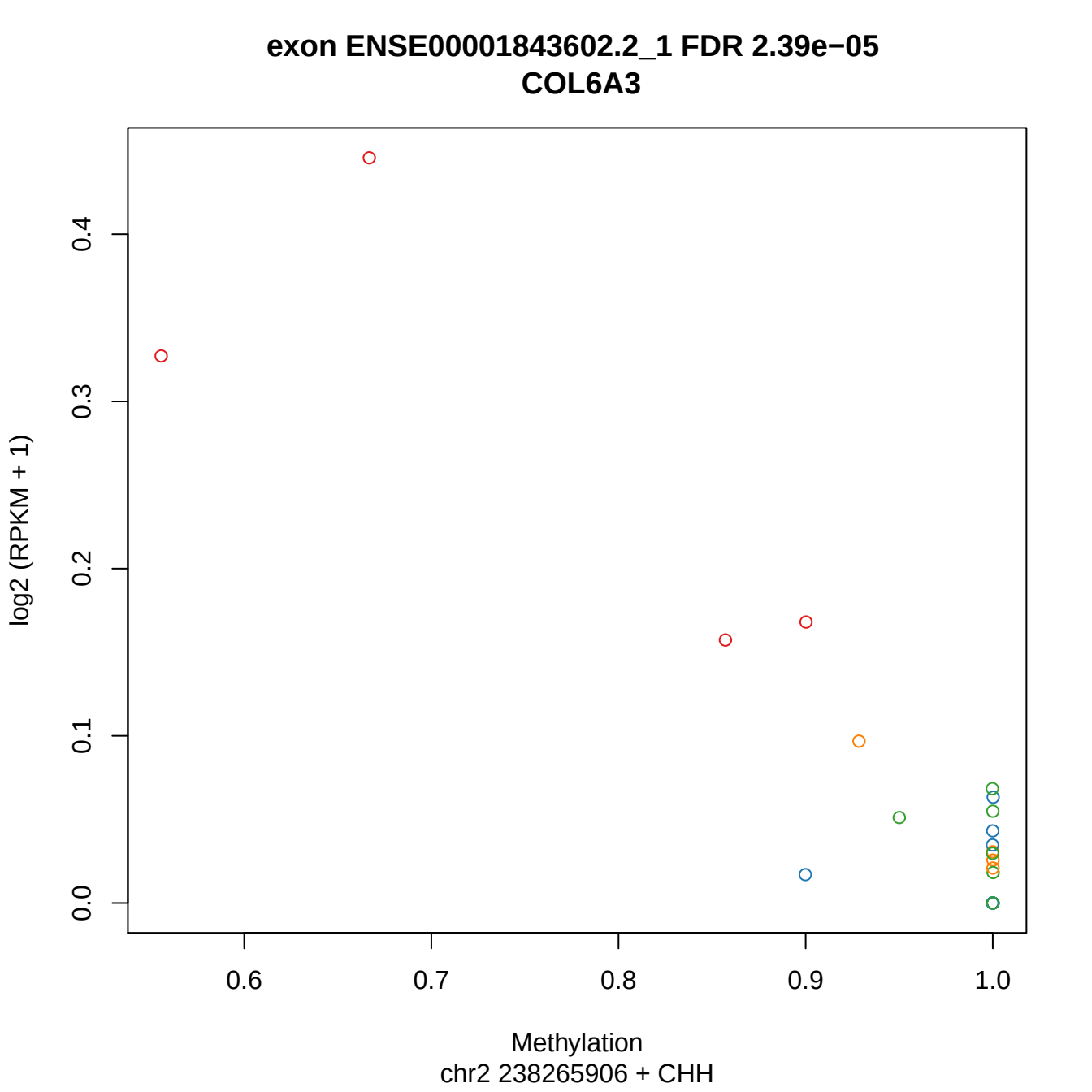
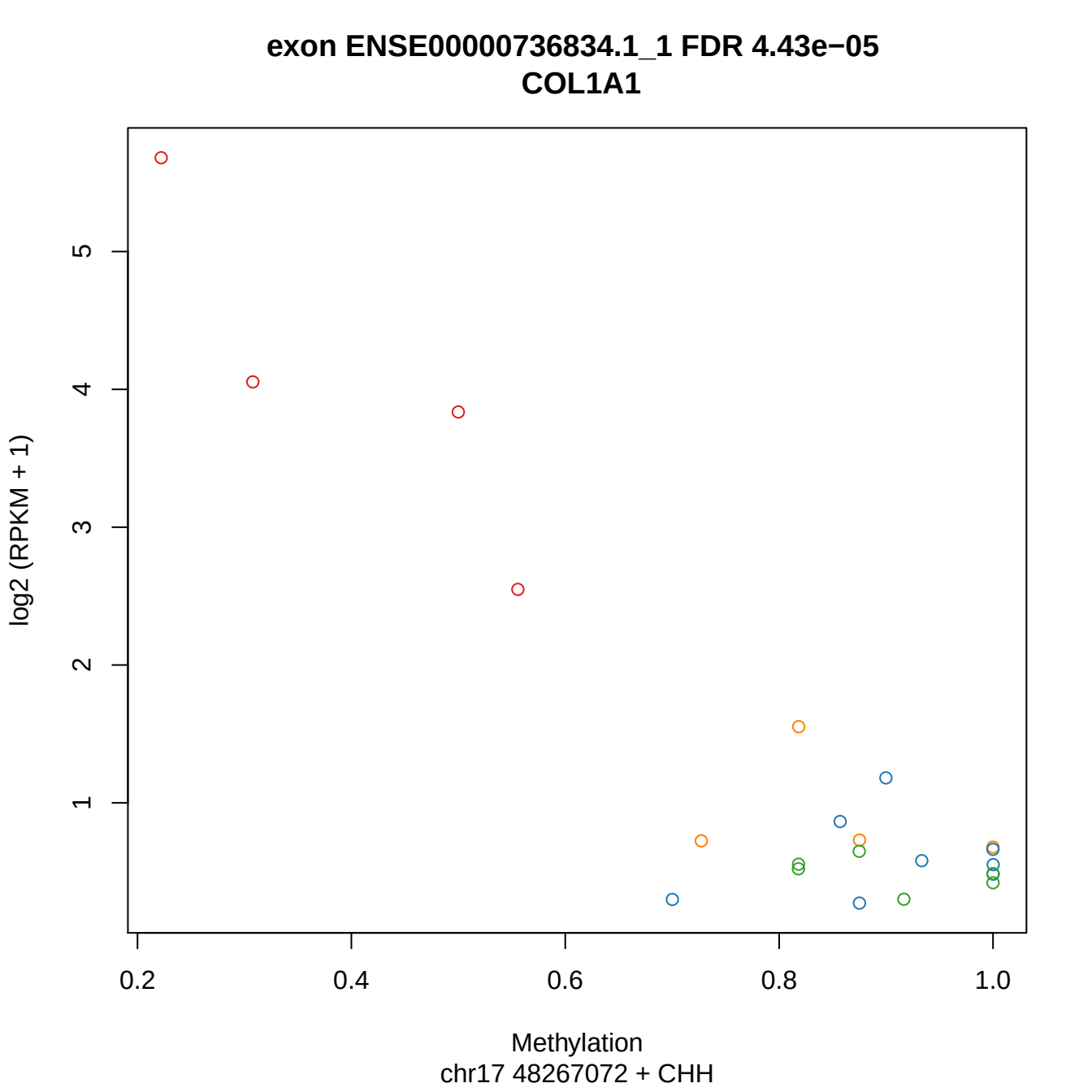
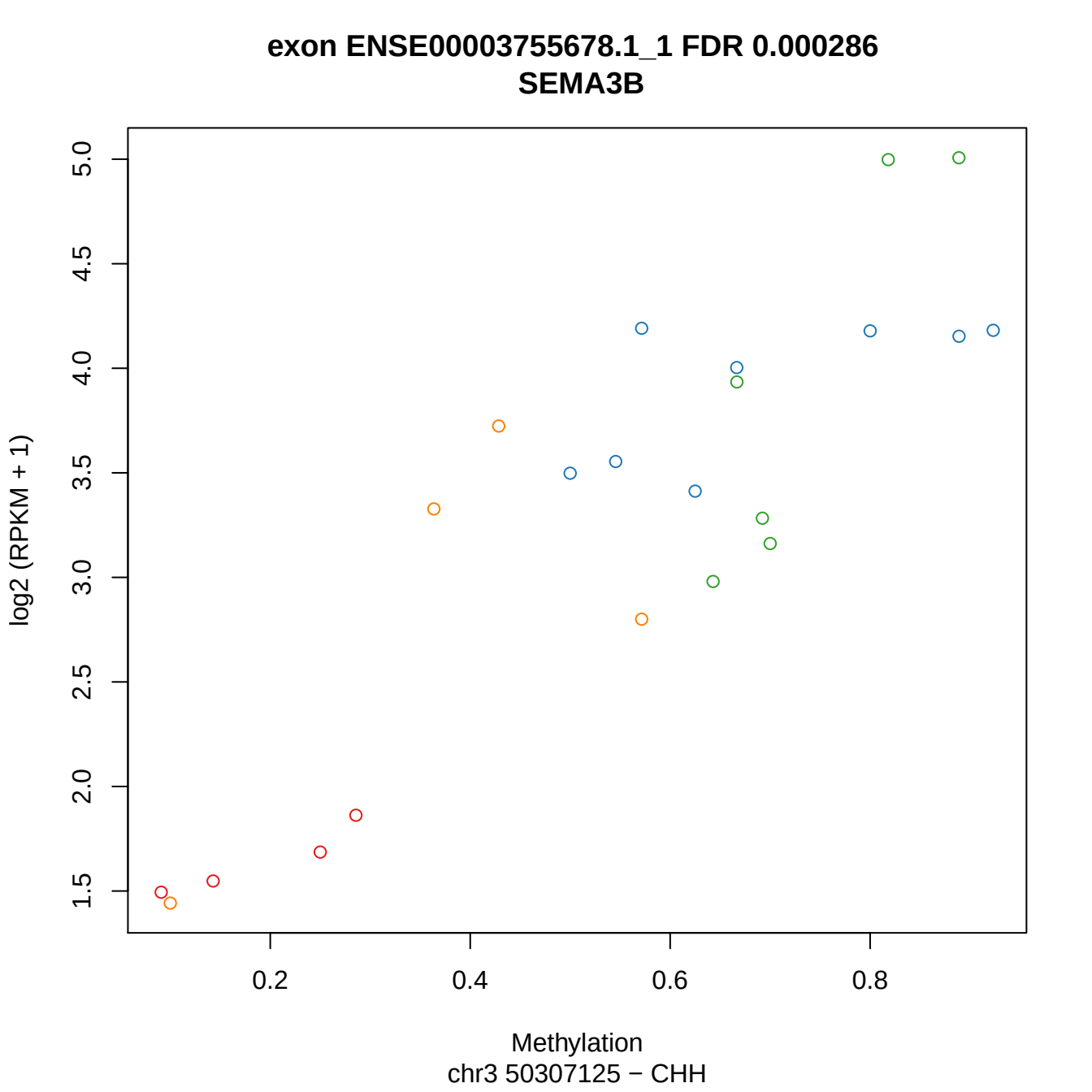
Methylation
chr8 70583409 − CHG

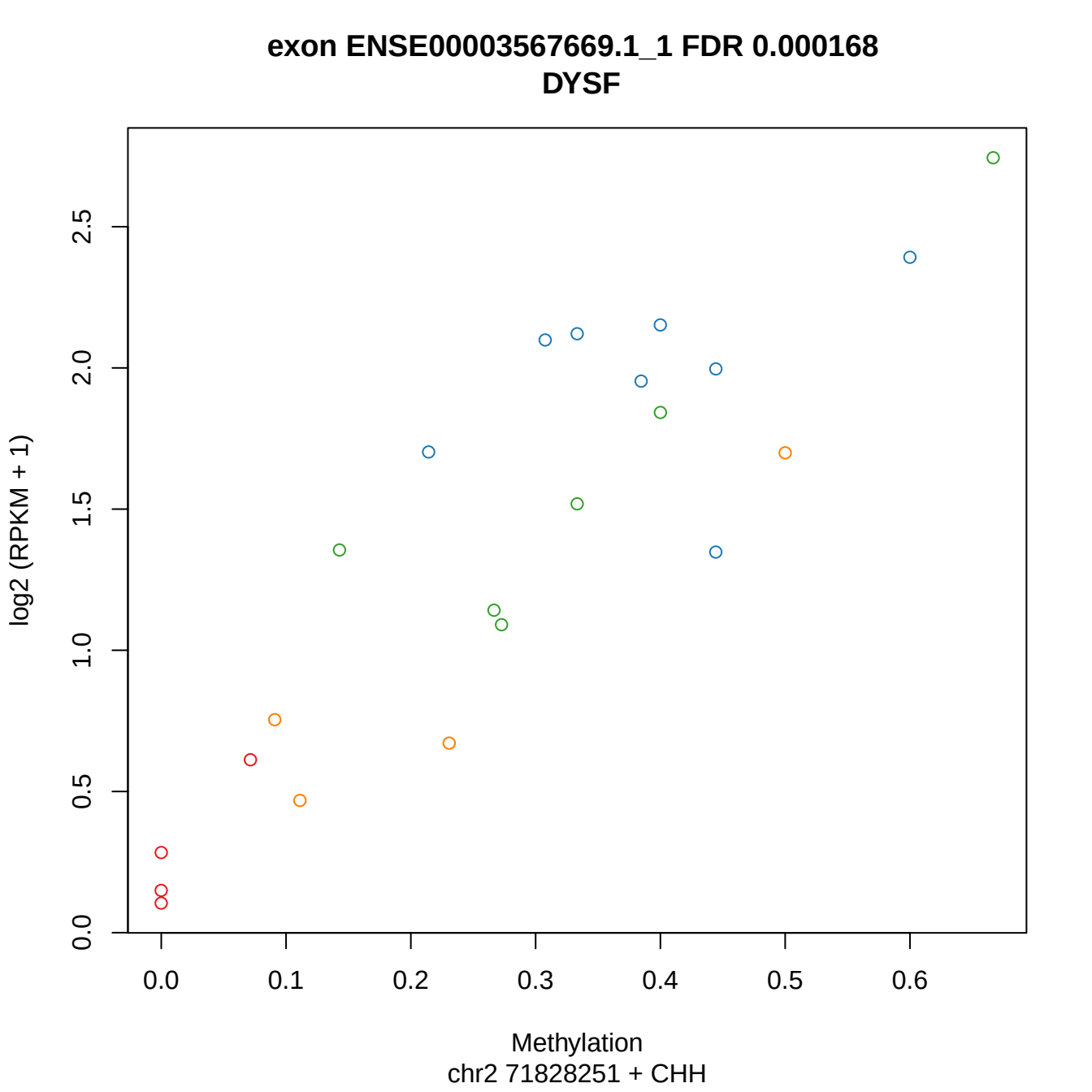

exon ENSE00001801127.1_1 FDR 8.24e−05
COL5A1
log2 (RPKM + 1)
0.0
0.2
0.4
0.6
0.8
1.0
0.0
0.2
0.4
0.6
0.8
1.0
Methylation
chr9 137642731 − CHH

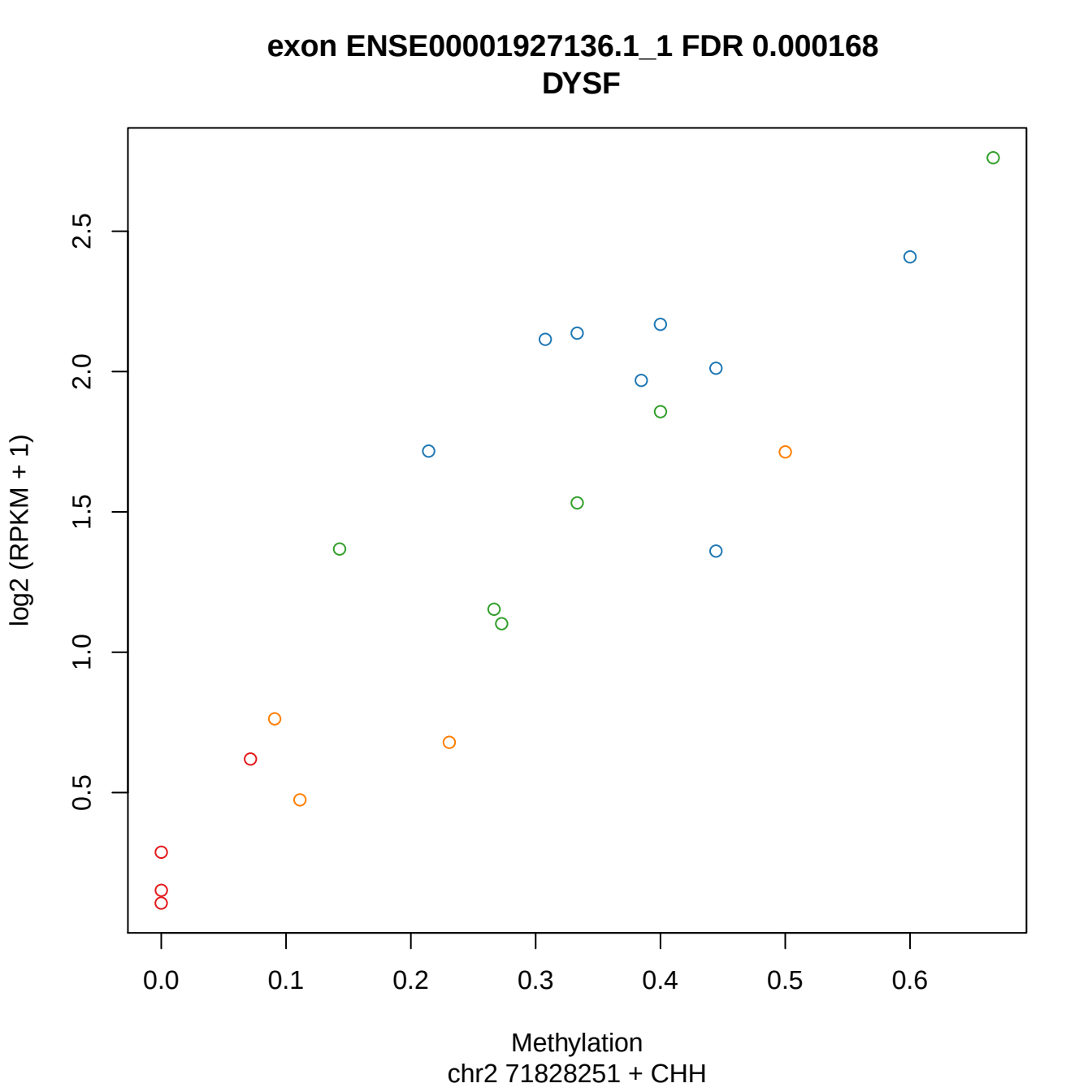

exon ENSE00000736842.1_1 FDR 4.35e−05
COL1A1
log2 (RPKM + 1)
0
1
2
3
4
5
0.4
0.6
0.8
1.0
Methylation
chr17 48265214 − CHG

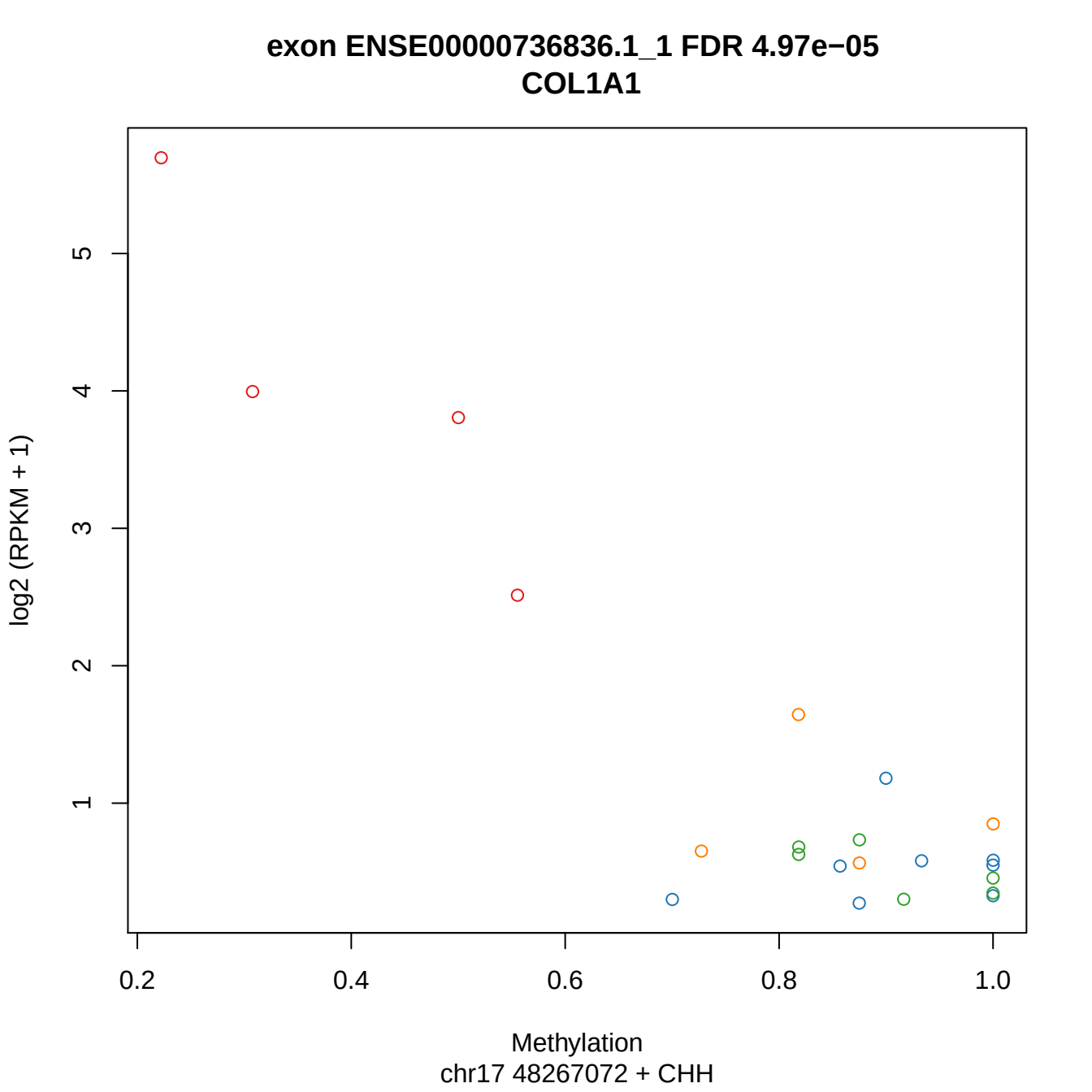

exon ENSE00001843602.2_1 FDR 2.39e−05
COL6A3
log2 (RPKM + 1)
0.0
0.1
0.2
0.3
0.4
0.6
0.7
0.8
0.9
1.0
Methylation
chr2 238265906 + CHH

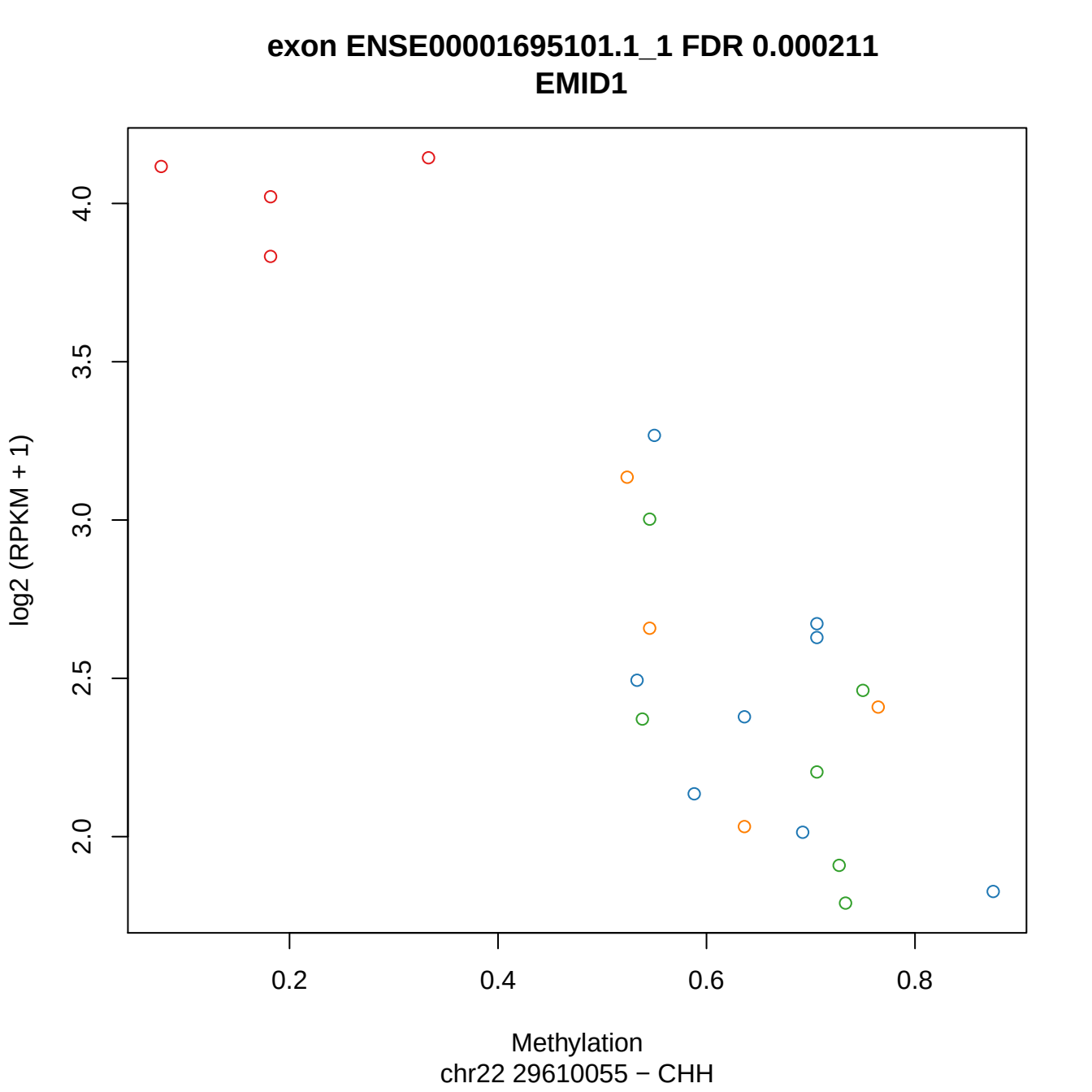

exon ENSE00000736834.1_1 FDR 4.43e−05
COL1A1
log2 (RPKM + 1)
1
2
3
4
5
0.2
0.4
0.6
0.8
1.0
Methylation
chr17 48267072 + CHH

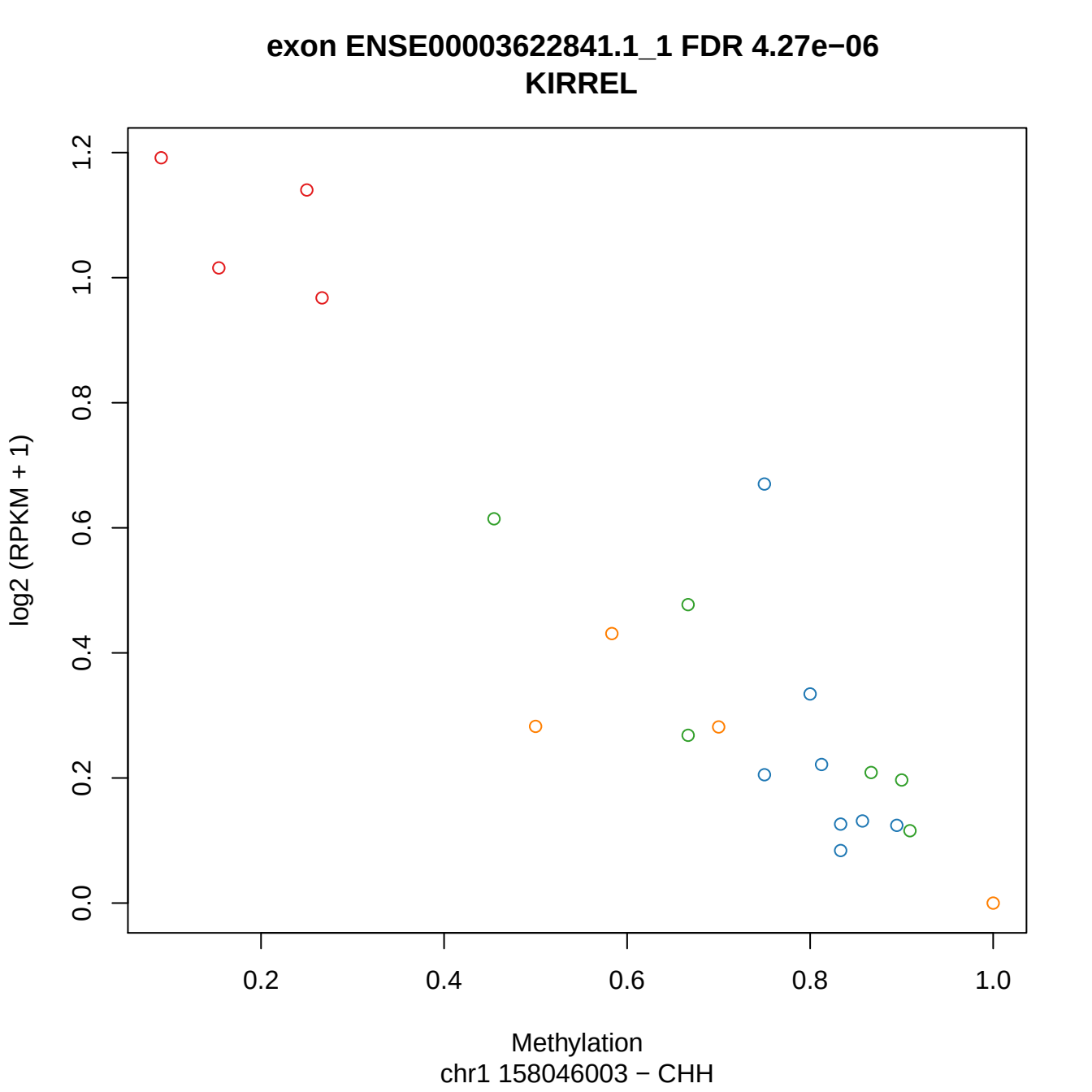

exon ENSE00003755678.1_1 FDR 0.000286
SEMA3B
log2 (RPKM + 1)
1.5
2.0
2.5
3.0
3.5
4.0
4.5
5.0
0.2
0.4
0.6
0.8
Methylation
chr3 50307125 − CHH

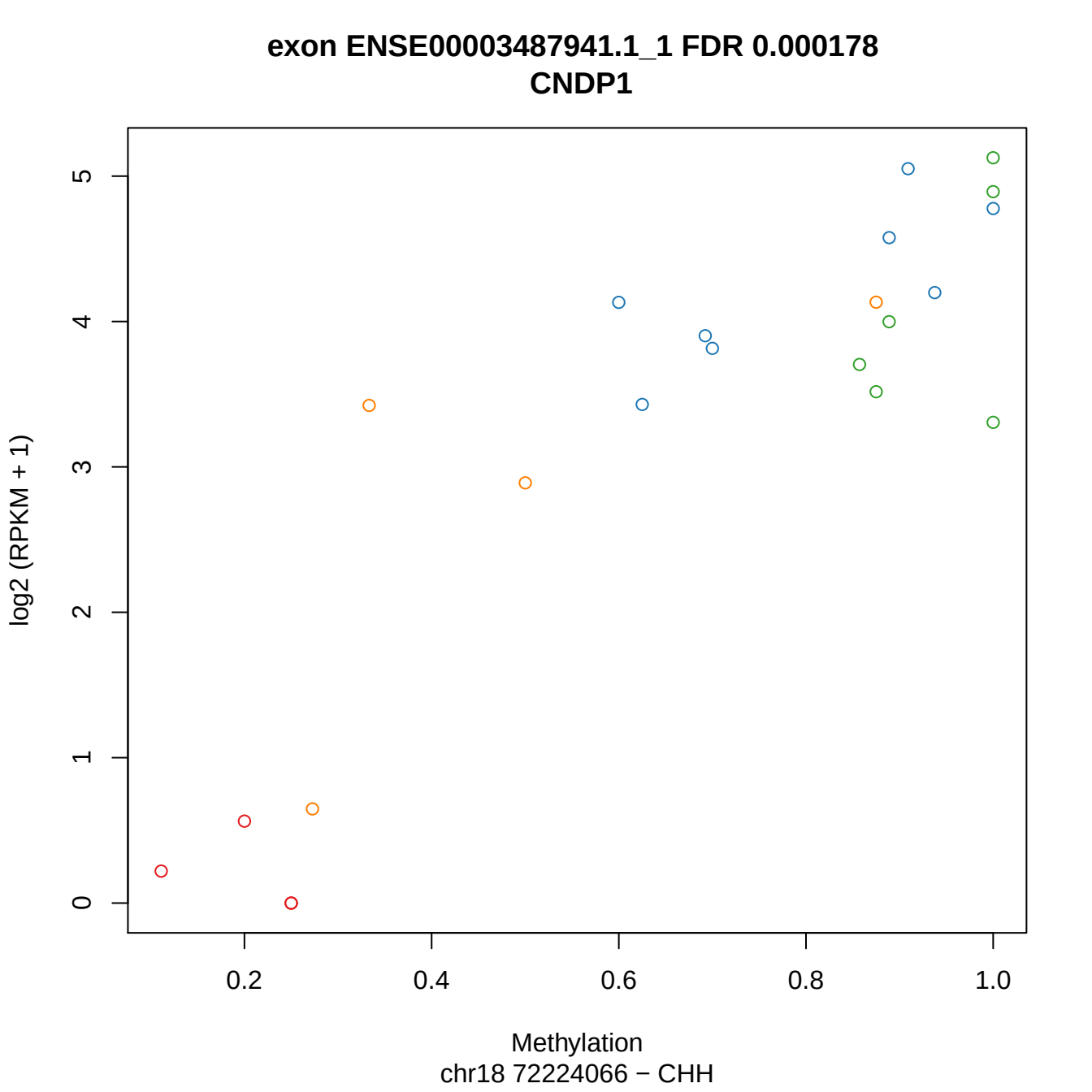

exon ENSE00003567669.1_1 FDR 0.000168
DYSF
log2 (RPKM + 1)
0.0
0.5
1.0
1.5
2.0
2.5
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Methylation
chr2 71828251 + CHH

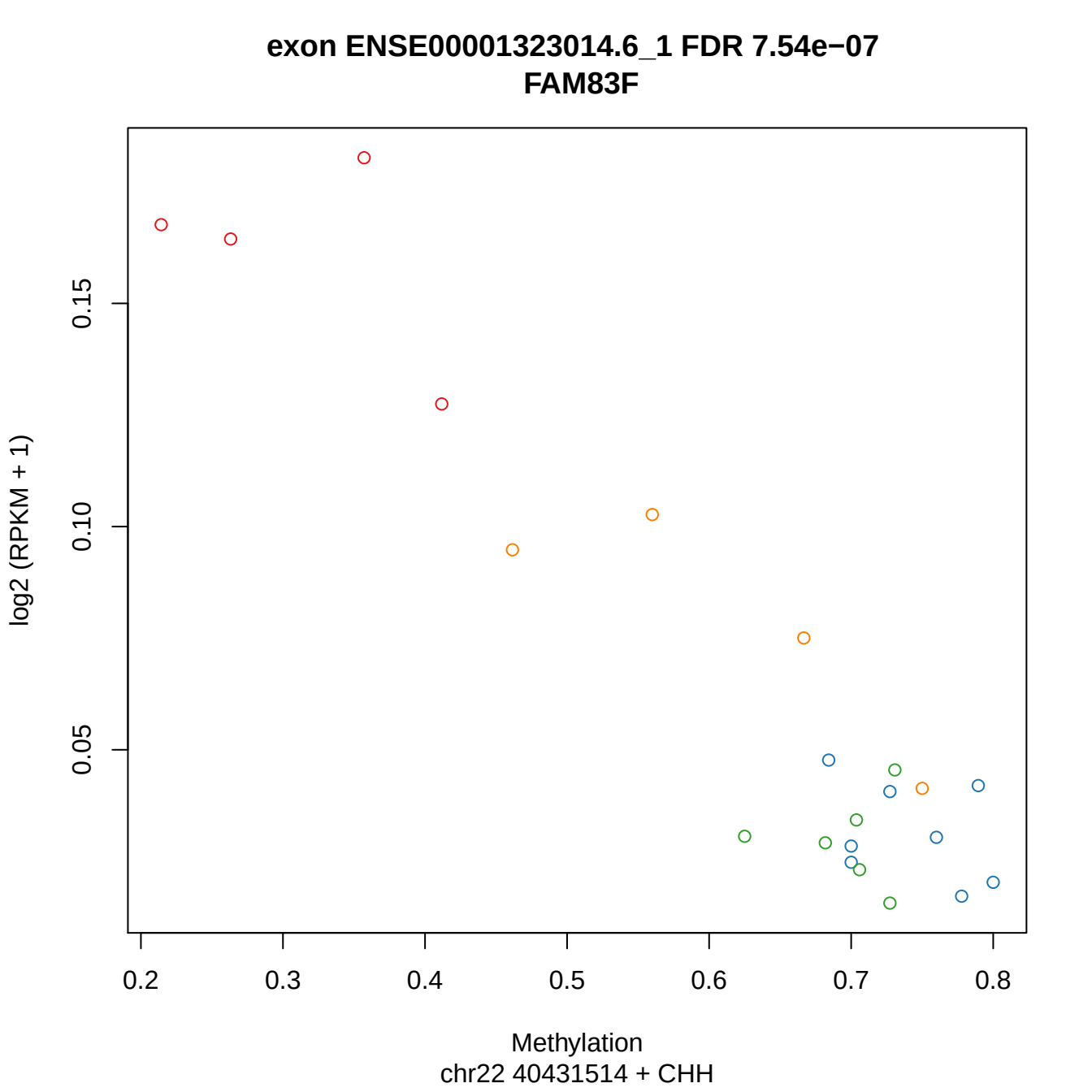

exon ENSE00001927136.1_1 FDR 0.000168
DYSF
log2 (RPKM + 1)
0.5
1.0
1.5
2.0
2.5
0.0
0.1
0.2
0.3
0.4
0.5
0.6
Methylation
chr2 71828251 + CHH

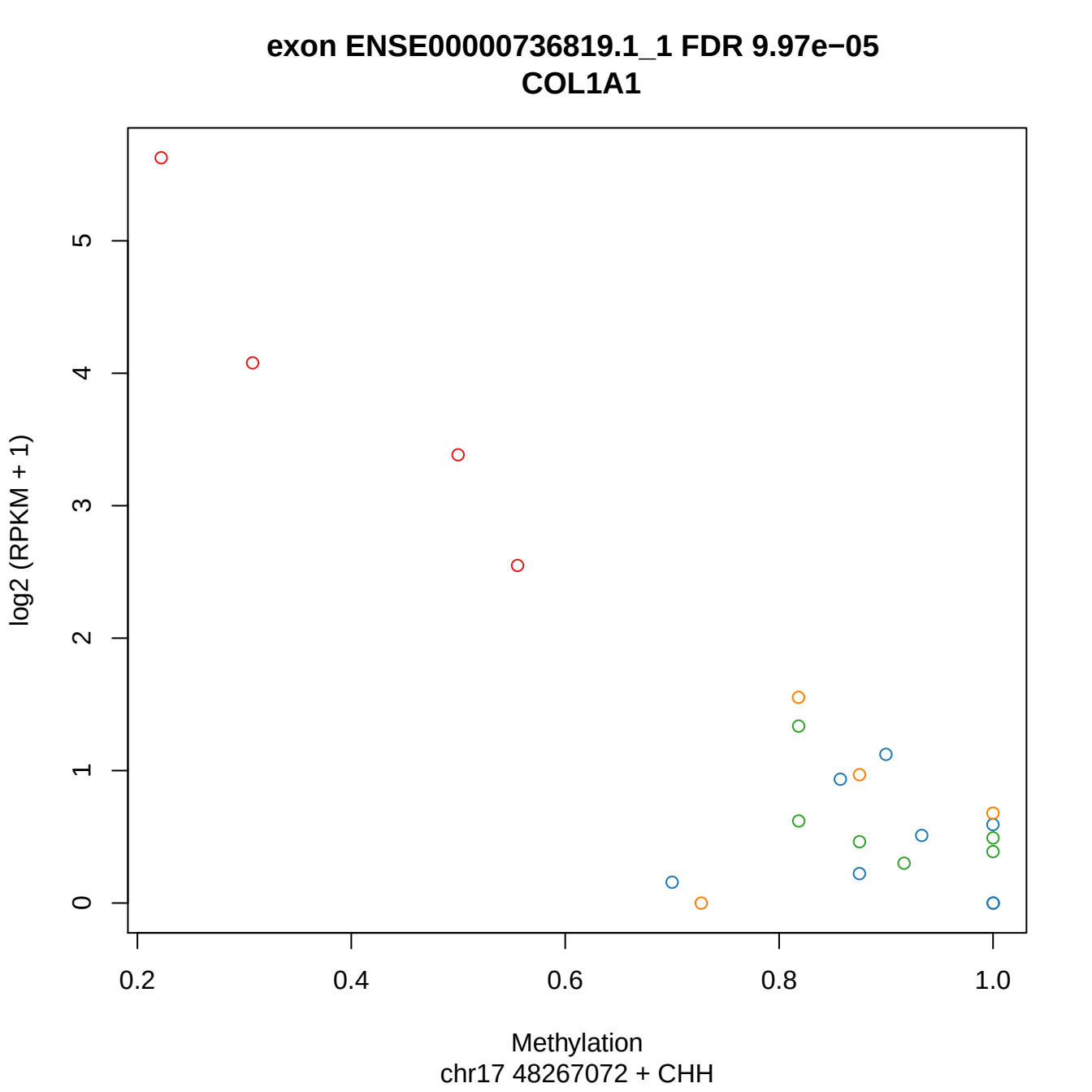

exon ENSE00000736836.1_1 FDR 4.97e−05
COL1A1
log2 (RPKM + 1)
1
2
3
4
5
0.2
0.4
0.6
0.8
1.0
Methylation
chr17 48267072 + CHH

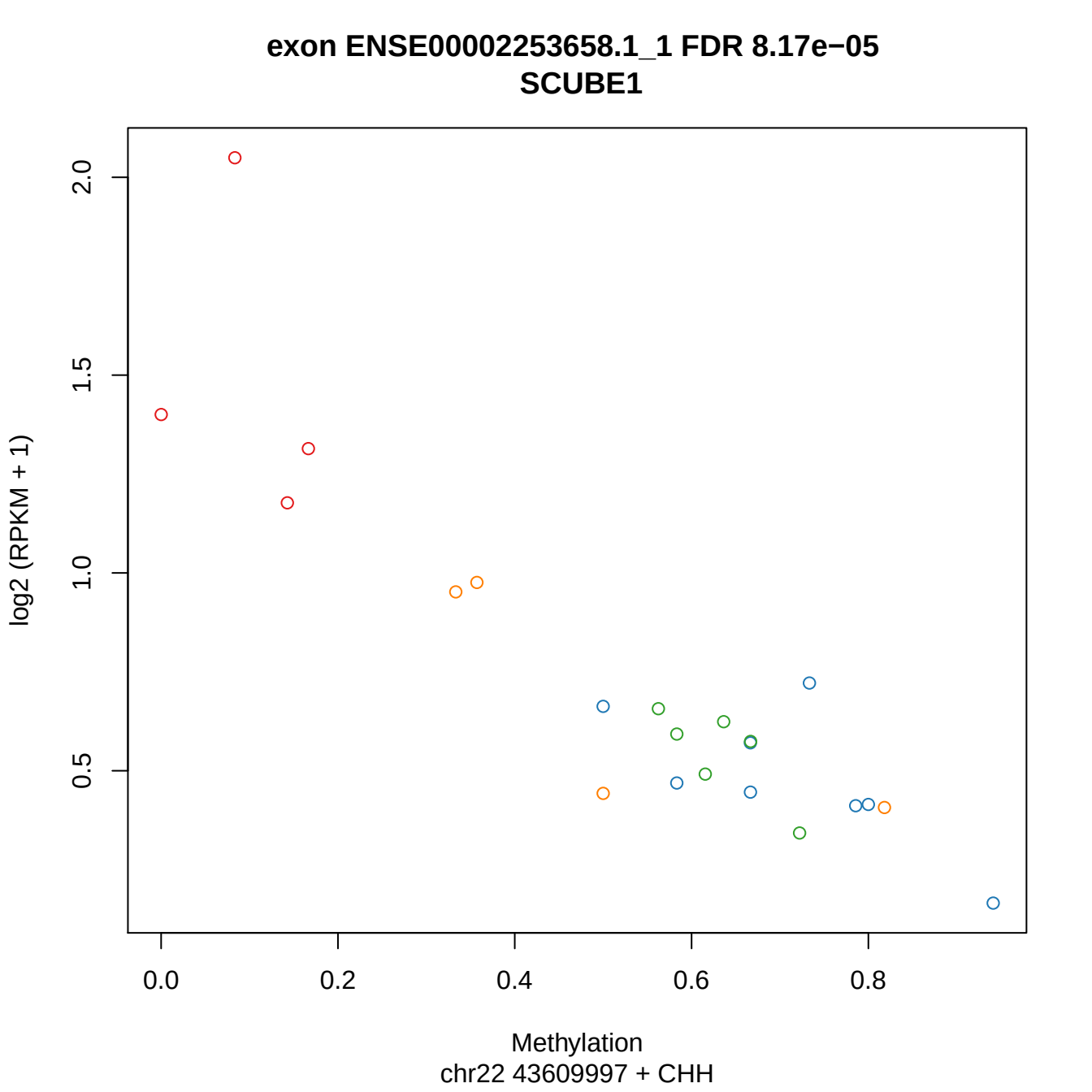

exon ENSE00001695101.1_1 FDR 0.000211
EMID1
log2 (RPKM + 1)
4.0
3.5
3.0
2.5
2.0
0.2
0.4
0.6
0.8
Methylation
chr22 29610055 − CHH

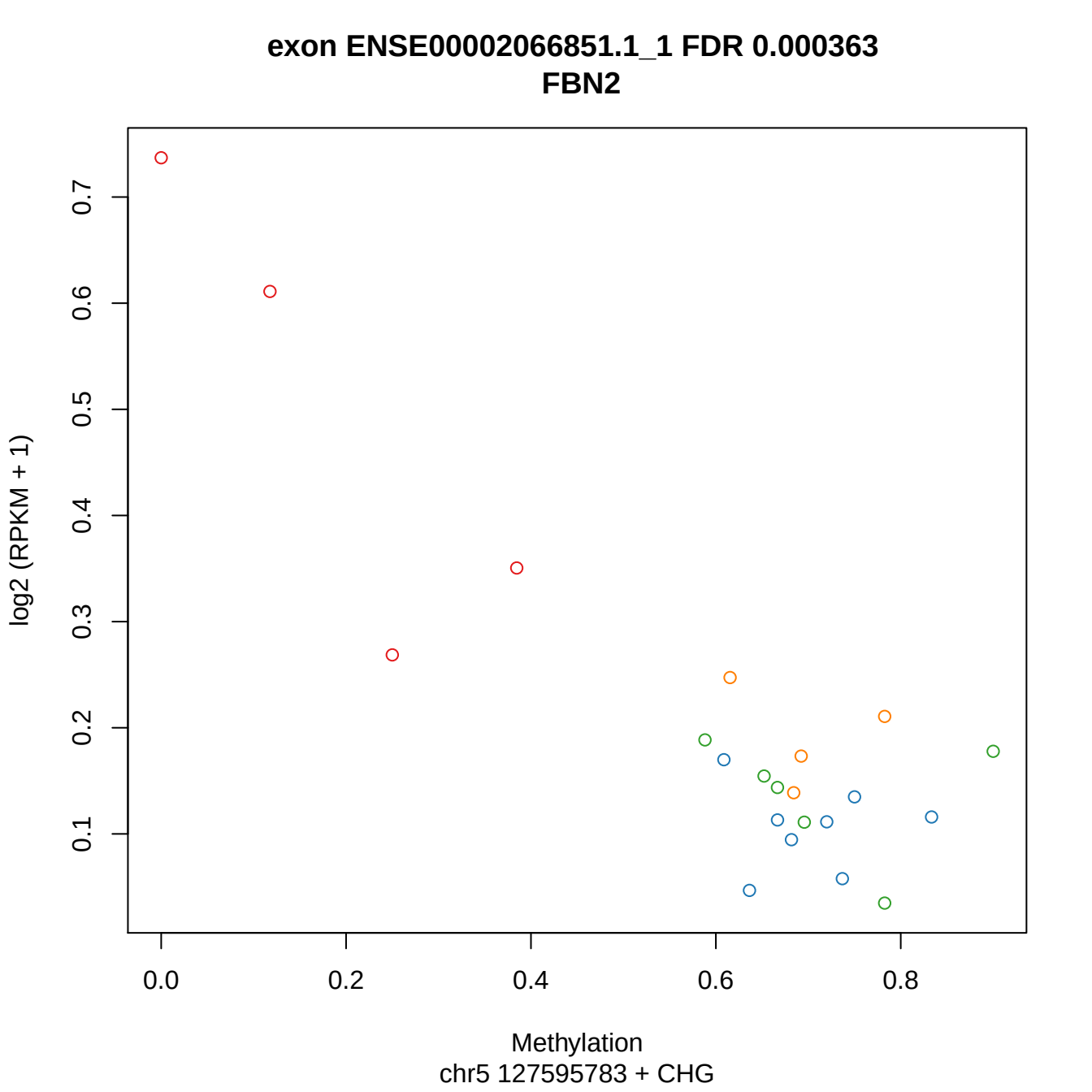

exon ENSE00003622841.1_1 FDR 4.27e−06
KIRREL
log2 (RPKM + 1)
0.0
0.2
0.4
0.6
0.8
1.0
1.2
0.2
0.4
0.6
0.8
1.0
Methylation
chr1 158046003 − CHH

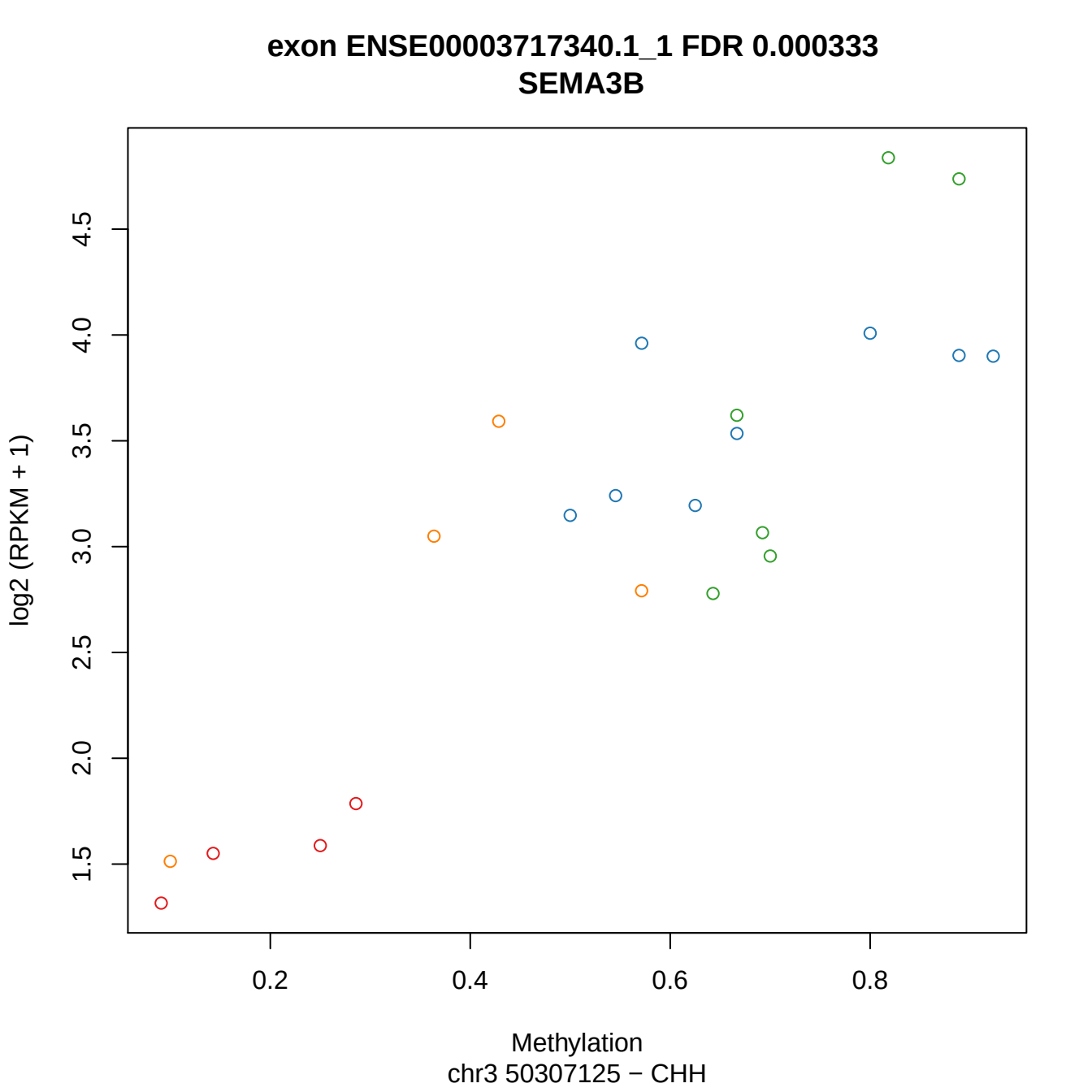

exon ENSE00003487941.1_1 FDR 0.000178
CNDP1
log2 (RPKM + 1)
0
1
2
3
4
5
0.2
0.4
0.6
0.8
1.0
Methylation
chr18 72224066 − CHH

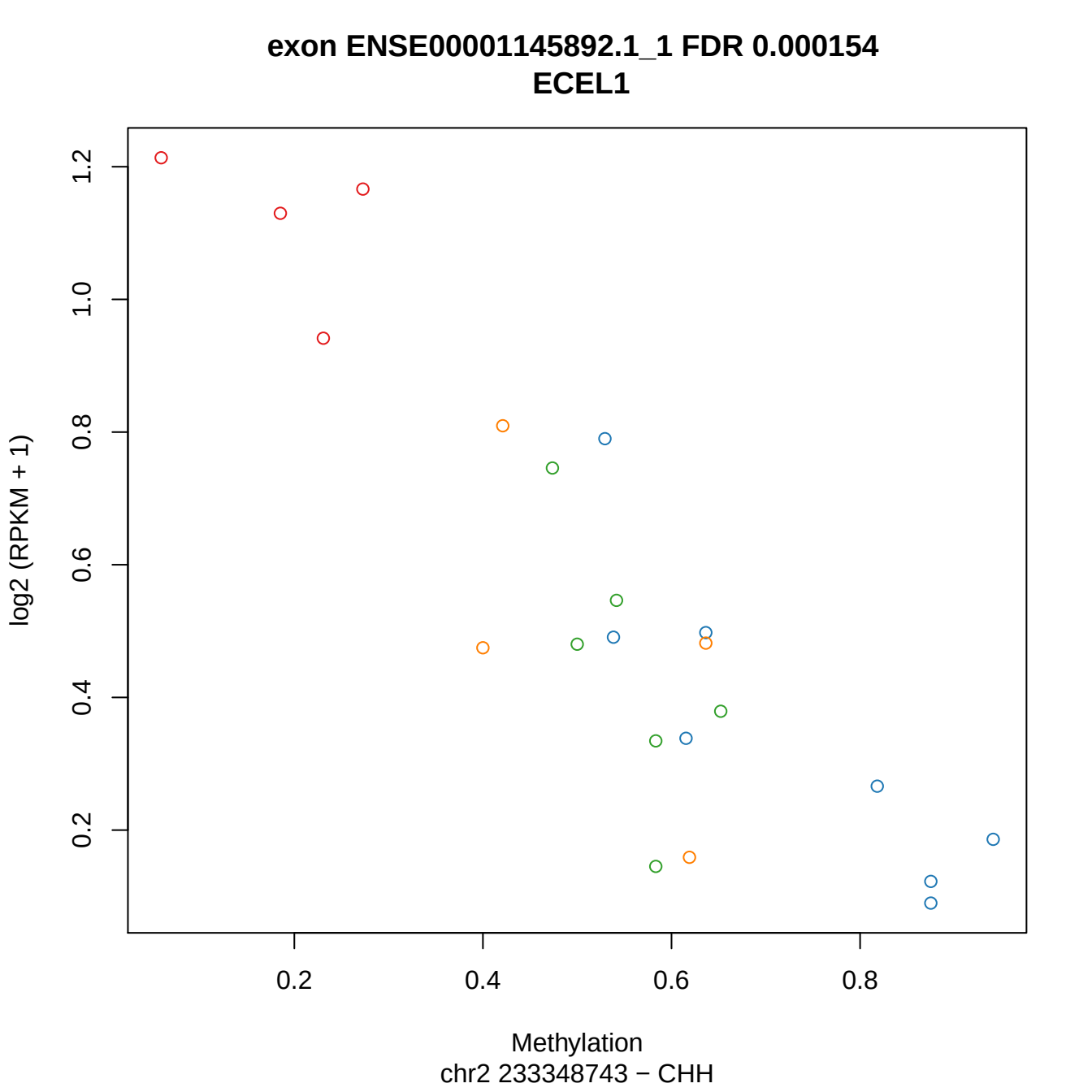

exon ENSE00001323014.6_1 FDR 7.54e−07
FAM83F
log2 (RPKM + 1)
0.05
0.10
0.15
0.2
0.3
0.4
0.5
0.6
0.7
0.8
Methylation
chr22 40431514 + CHH

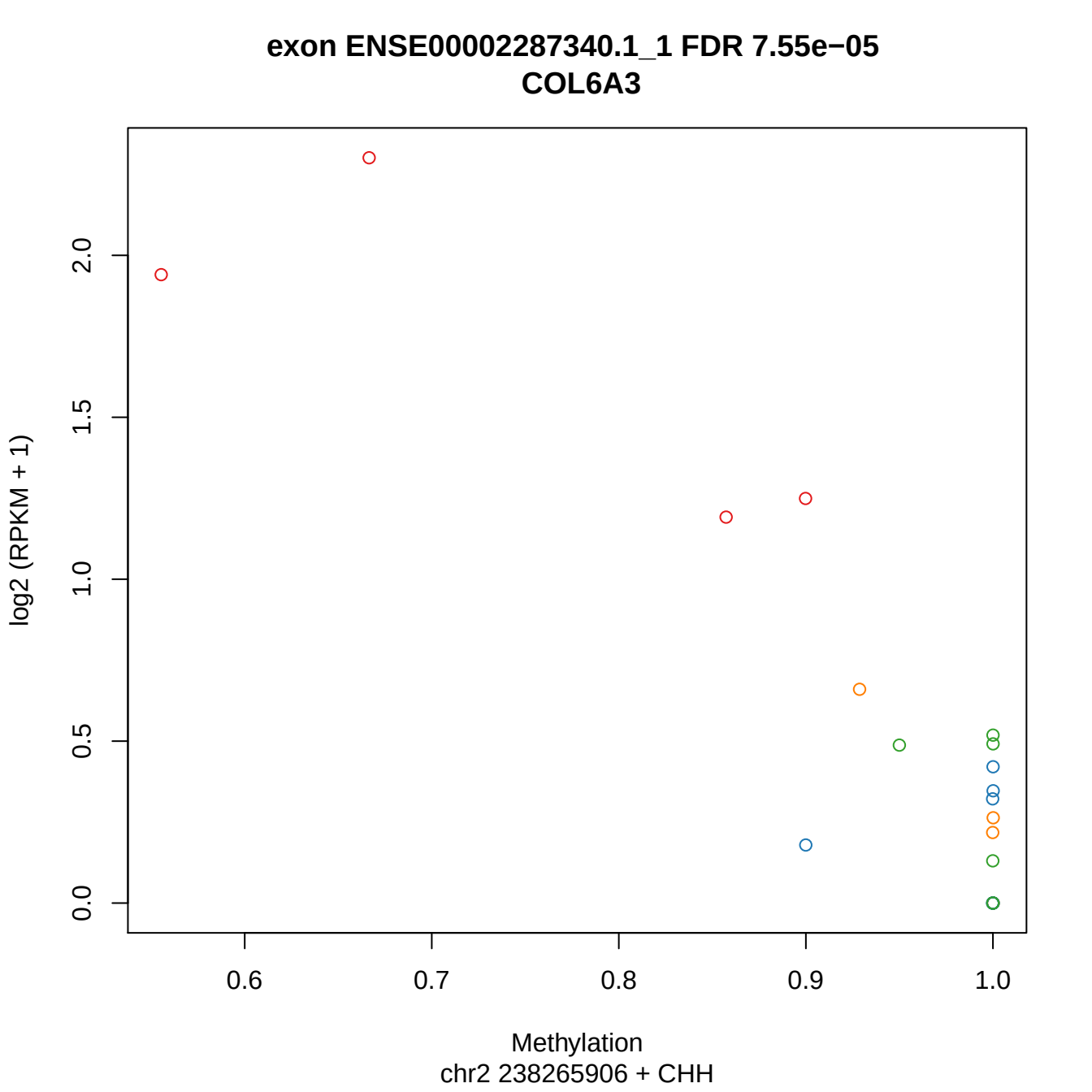

exon ENSE00000736819.1_1 FDR 9.97e−05
COL1A1
log2 (RPKM + 1)
0
1
2
3
4
5
0.2
0.4
0.6
0.8
1.0
Methylation
chr17 48267072 + CHH

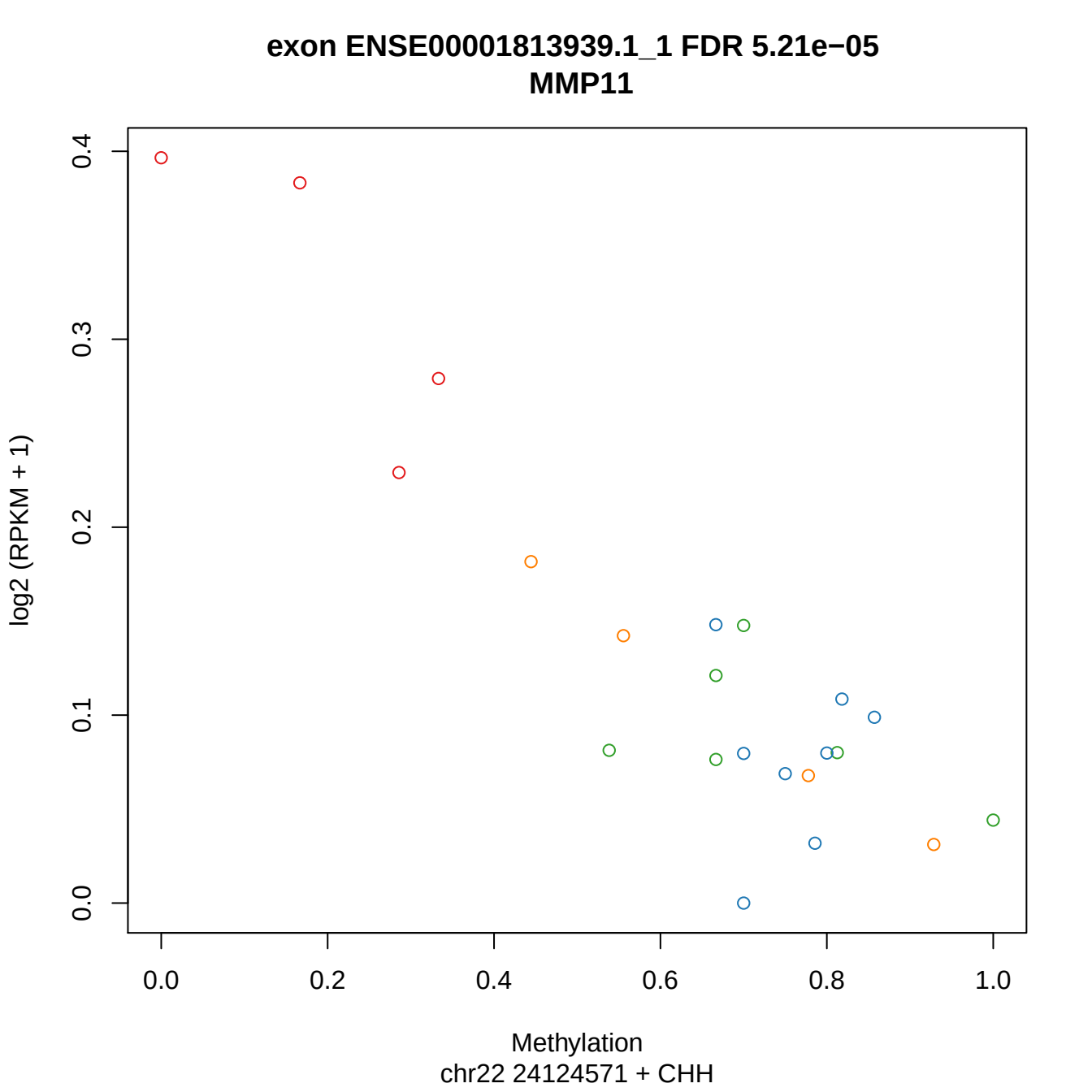

exon ENSE00002253658.1_1 FDR 8.17e−05
SCUBE1
log2 (RPKM + 1)
0.5
1.0
1.5
2.0
0.0
0.2
0.4
0.6
0.8
Methylation
chr22 43609997 + CHH

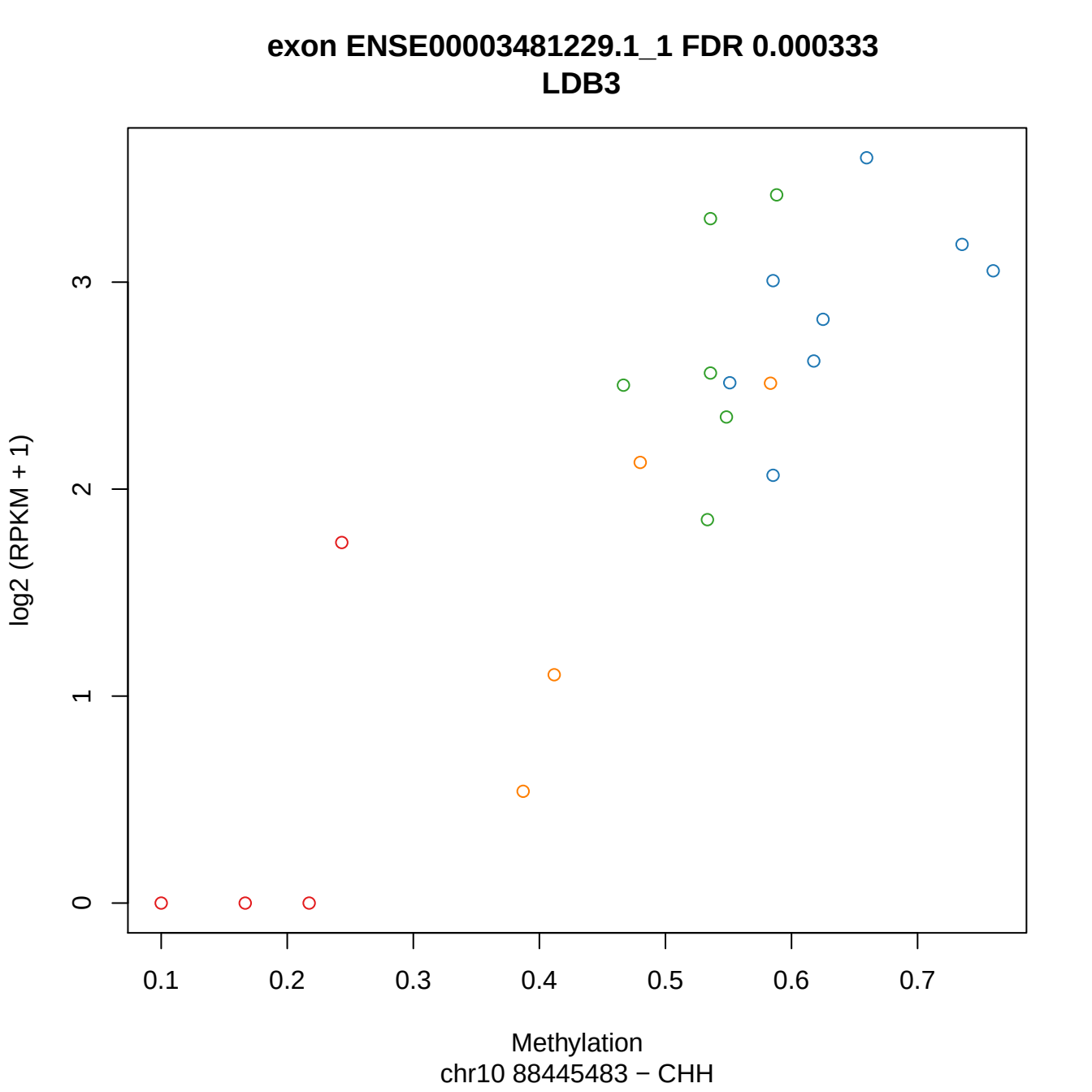

exon ENSE00002066851.1_1 FDR 0.000363
FBN2
log2 (RPKM + 1)
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.0
0.2
0.4
0.6
0.8
Methylation
chr5 127595783 + CHG

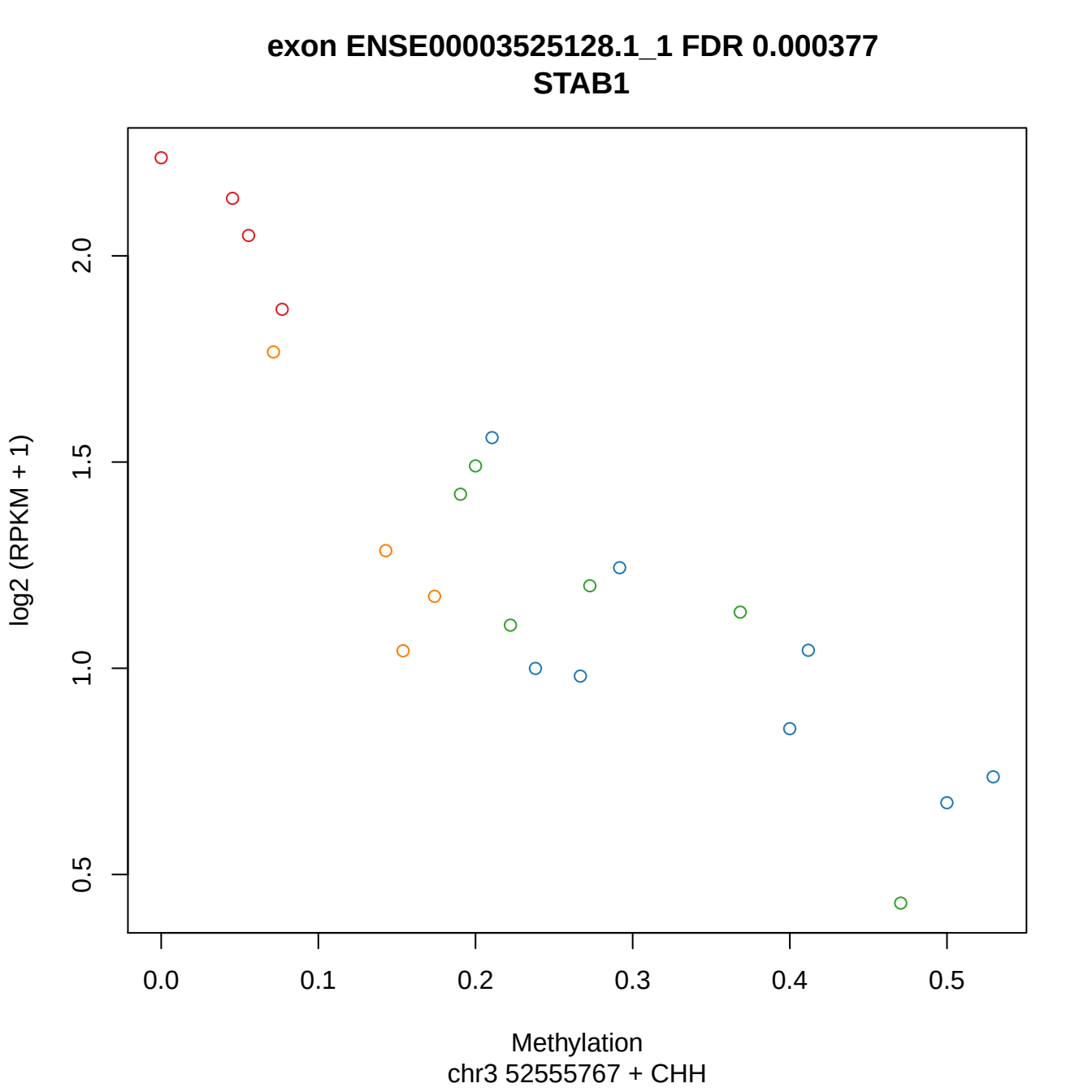

exon ENSE00003717340.1_1 FDR 0.000333
SEMA3B
log2 (RPKM + 1)
1.5
2.0
2.5
3.0
3.5
4.0
4.5
0.2
0.4
0.6
0.8
Methylation
chr3 50307125 − CHH

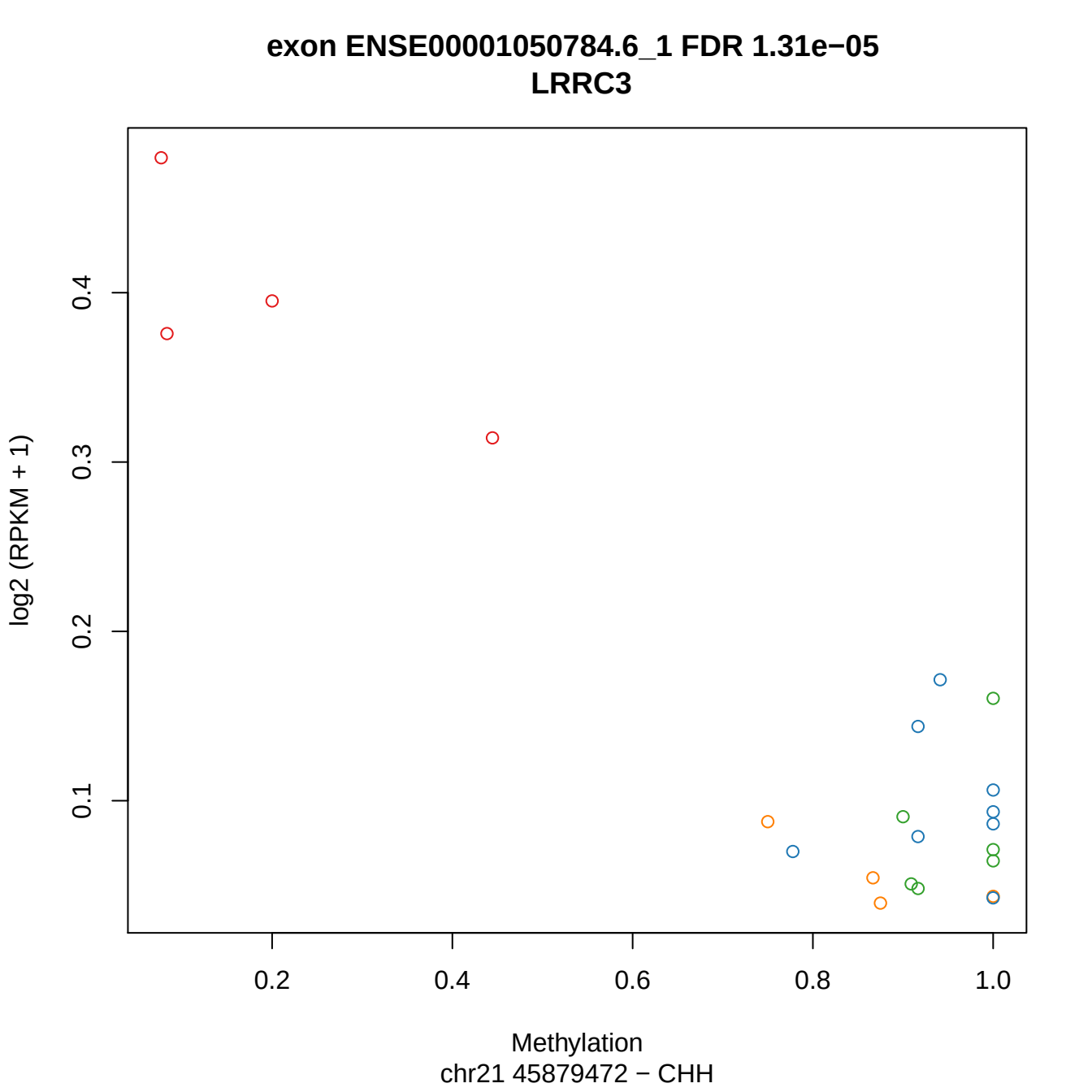

exon ENSE00001145892.1_1 FDR 0.000154
ECEL1
log2 (RPKM + 1)
0.2
0.4
0.6
0.8
1.0
1.2
0.2
0.4
0.6
0.8
Methylation
chr2 233348743 − CHH

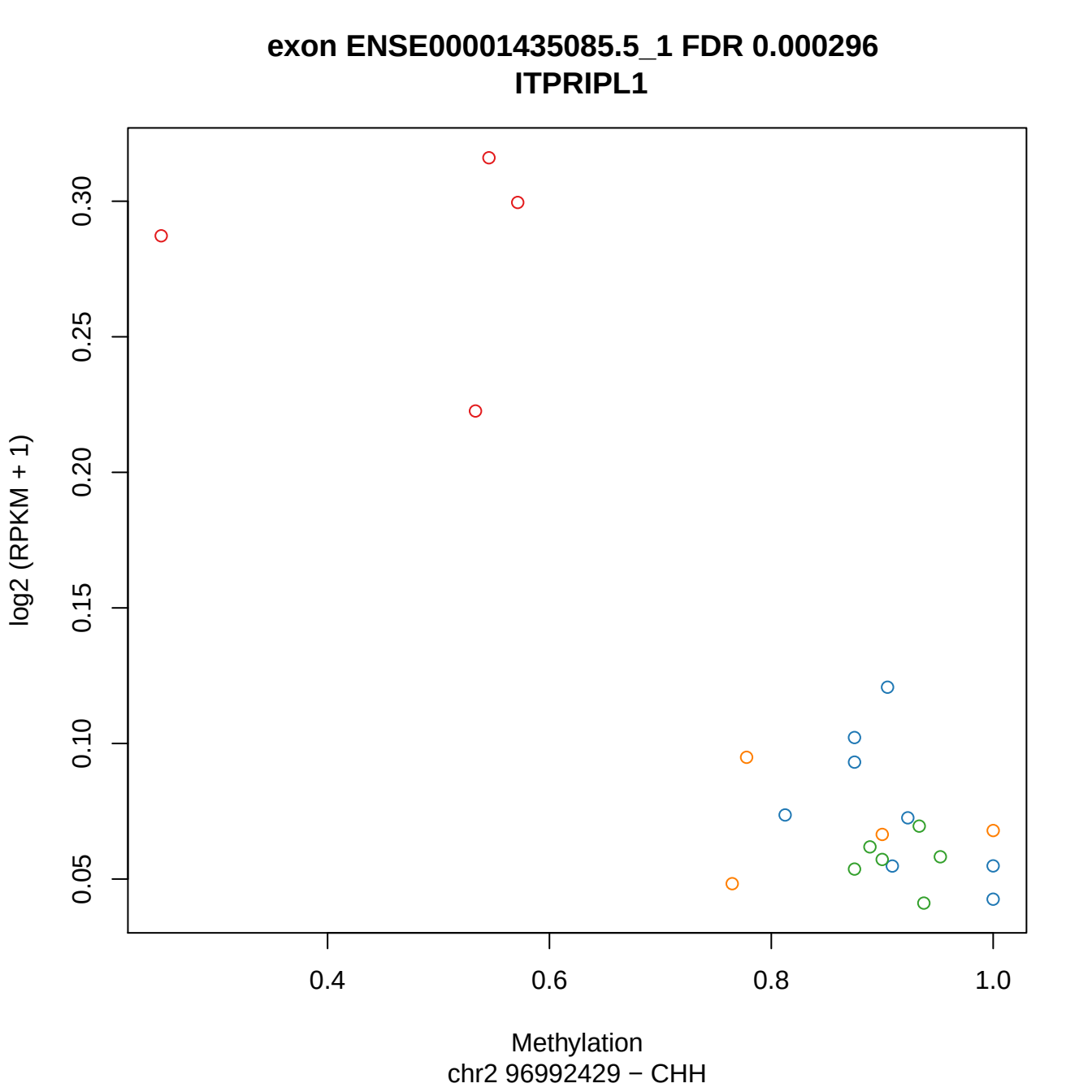

exon ENSE00002287340.1_1 FDR 7.55e−05
COL6A3
log2 (RPKM + 1)
0.0
0.5
1.0
1.5
2.0
0.6
0.7
0.8
0.9
1.0
Methylation
chr2 238265906 + CHH

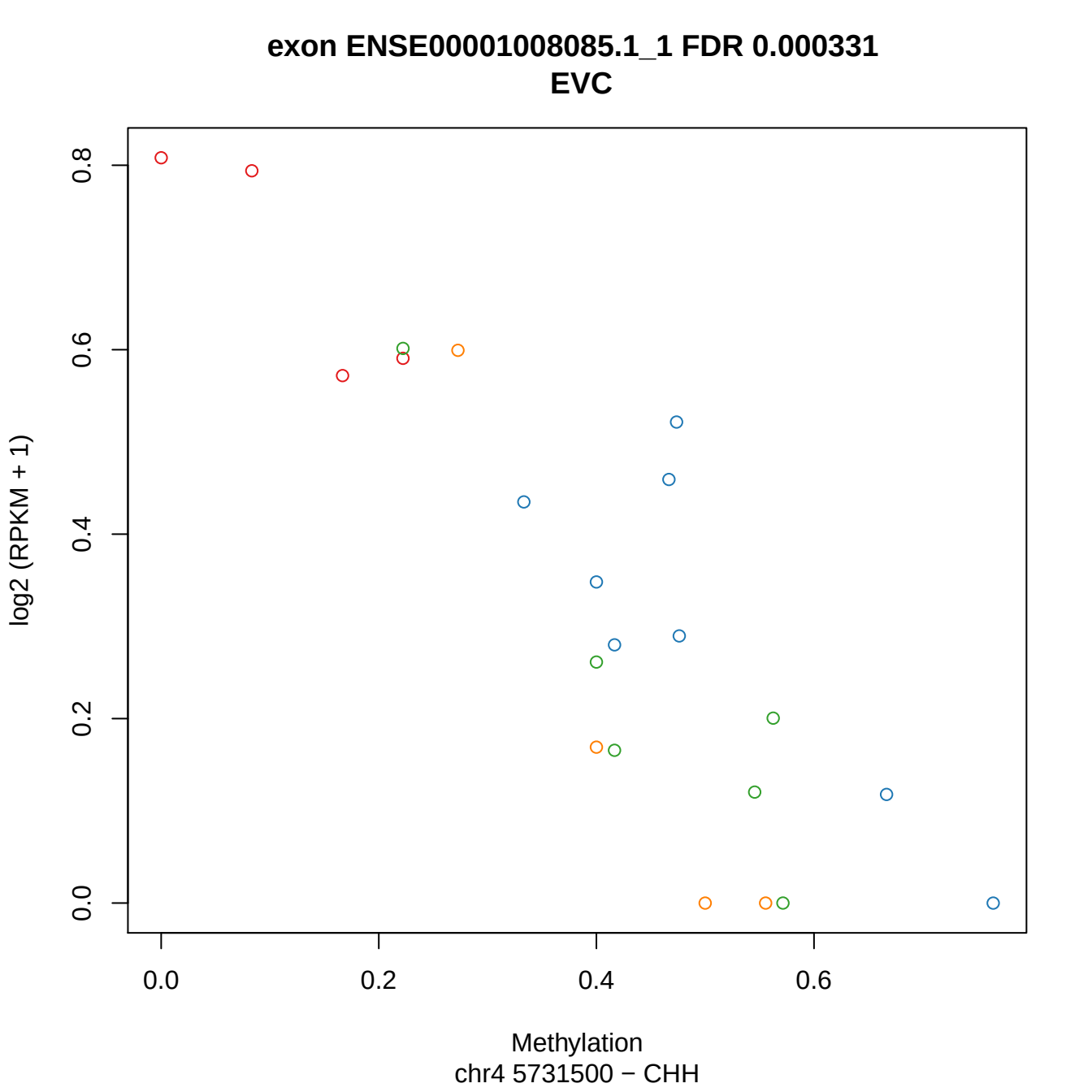

exon ENSE00001813939.1_1 FDR 5.21e−05
MMP11
log2 (RPKM + 1)
0.0
0.1
0.2
0.3
0.4
0.0
0.2
0.4
0.6
0.8
1.0
Methylation
chr22 24124571 + CHH

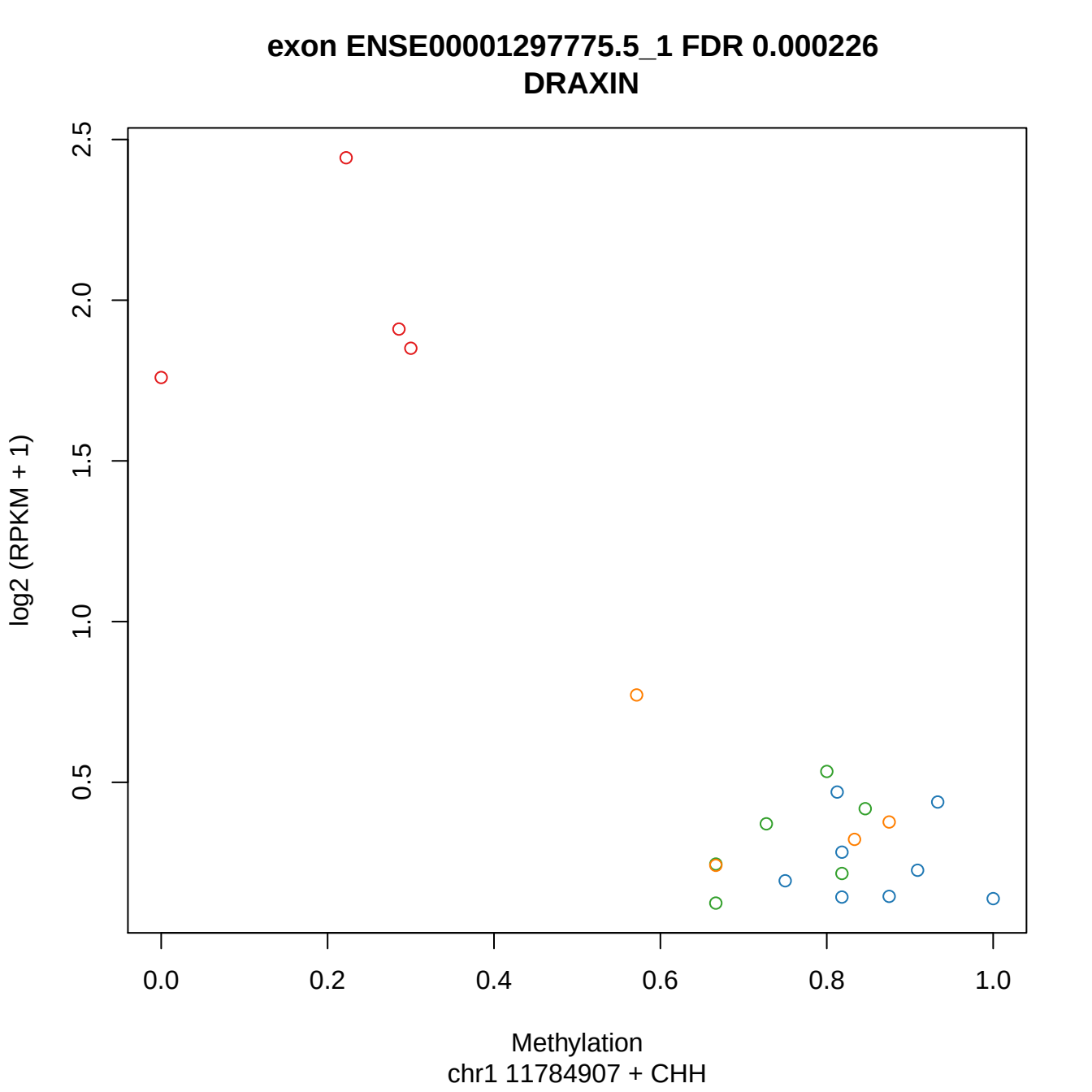

exon ENSE00003481229.1_1 FDR 0.000333
LDB3
log2 (RPKM + 1)
0
1
2
3
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Methylation
chr10 88445483 − CHH

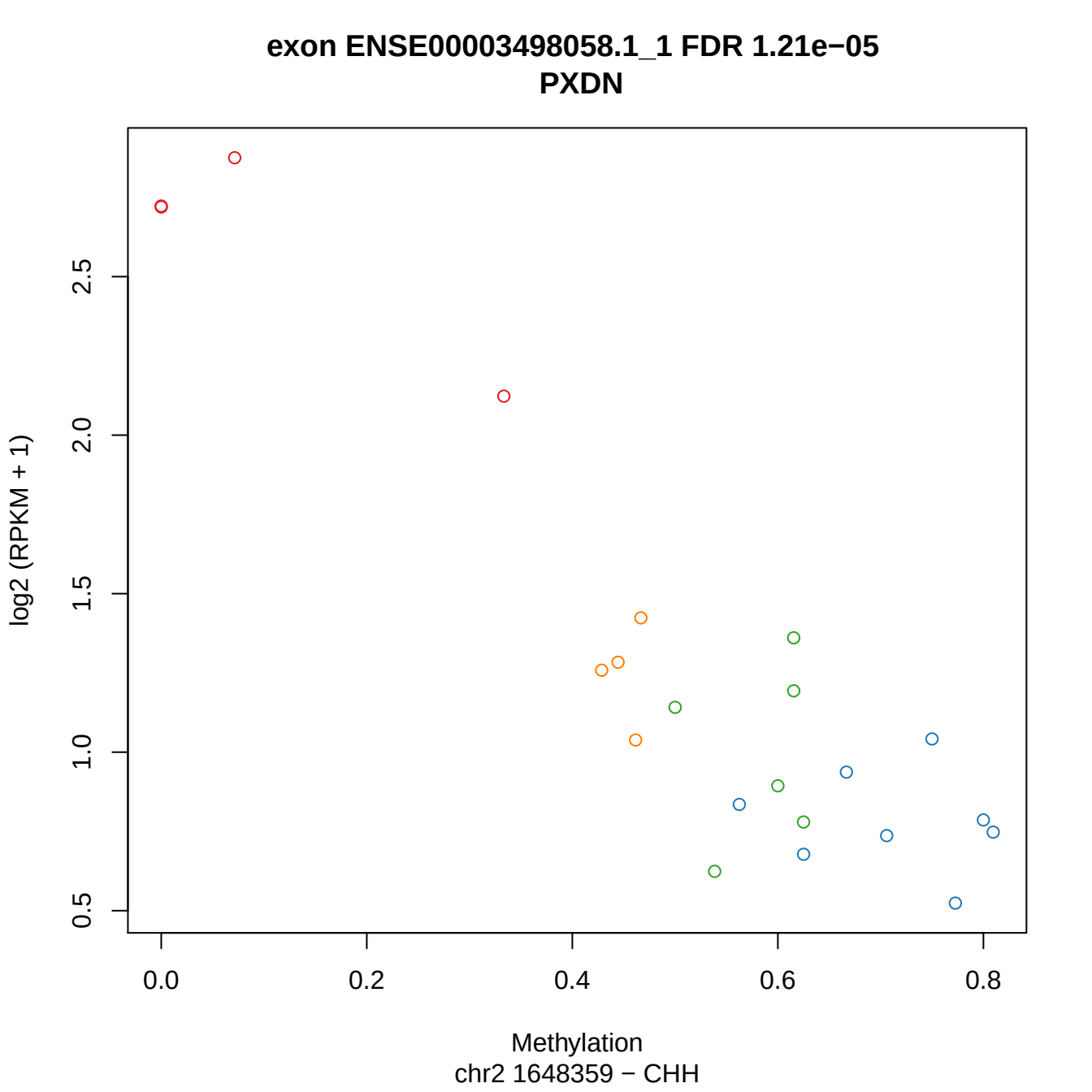

exon ENSE00003525128.1_1 FDR 0.000377
STAB1
log2 (RPKM + 1)
0.5
1.0
1.5
2.0
0.0
0.1
0.2
0.3
0.4
0.5
Methylation
chr3 52555767 + CHH

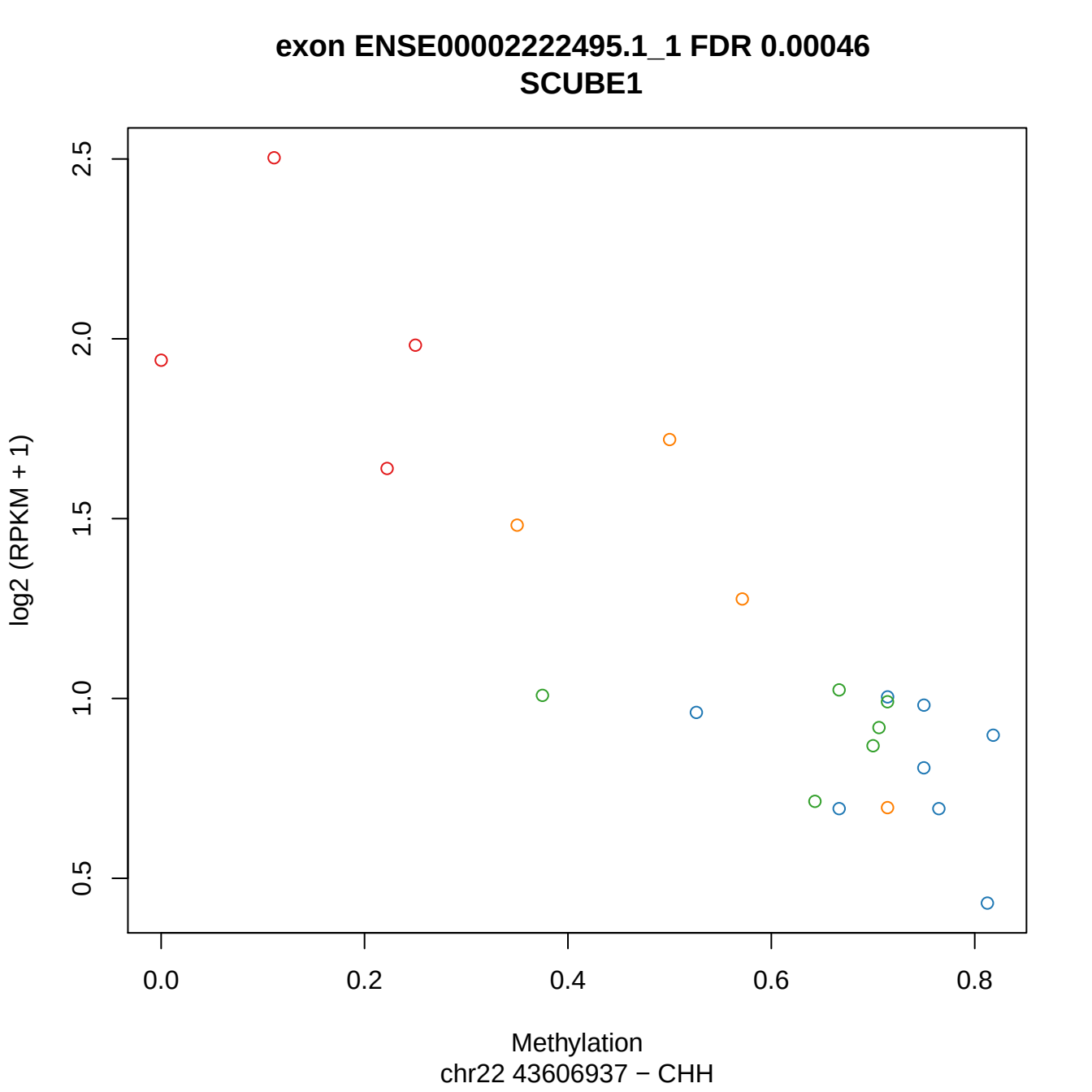

exon ENSE00001050784.6_1 FDR 1.31e−05
LRRC3
log2 (RPKM + 1)
0.1
0.2
0.3
0.4
0.2
0.4
0.6
0.8
1.0
Methylation
chr21 45879472 − CHH

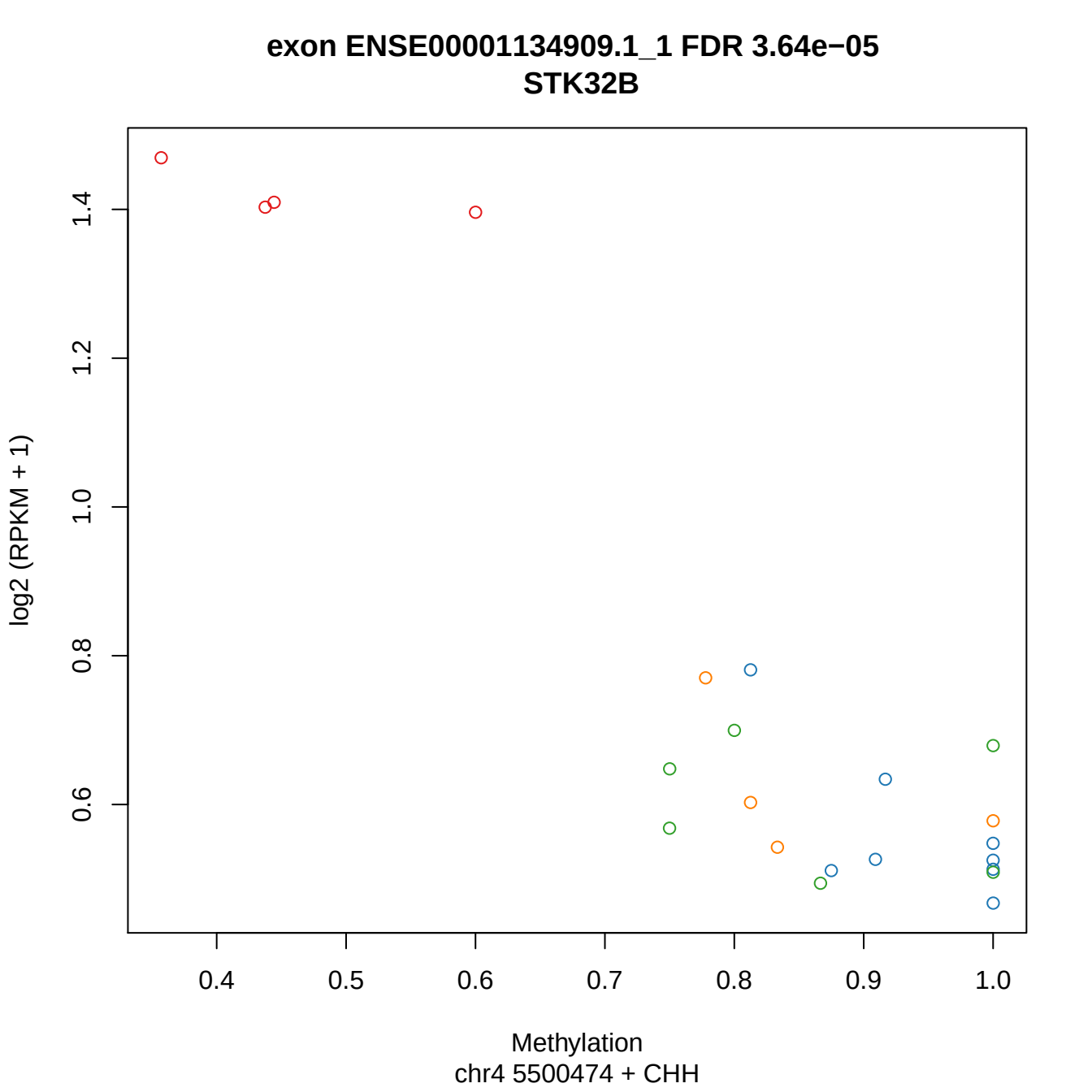

exon ENSE00001435085.5_1 FDR 0.000296
ITPRIPL1
log2 (RPKM + 1)
0.05
0.10
0.15
0.20
0.25
0.30
0.4
0.6
0.8
1.0
Methylation
chr2 96992429 − CHH

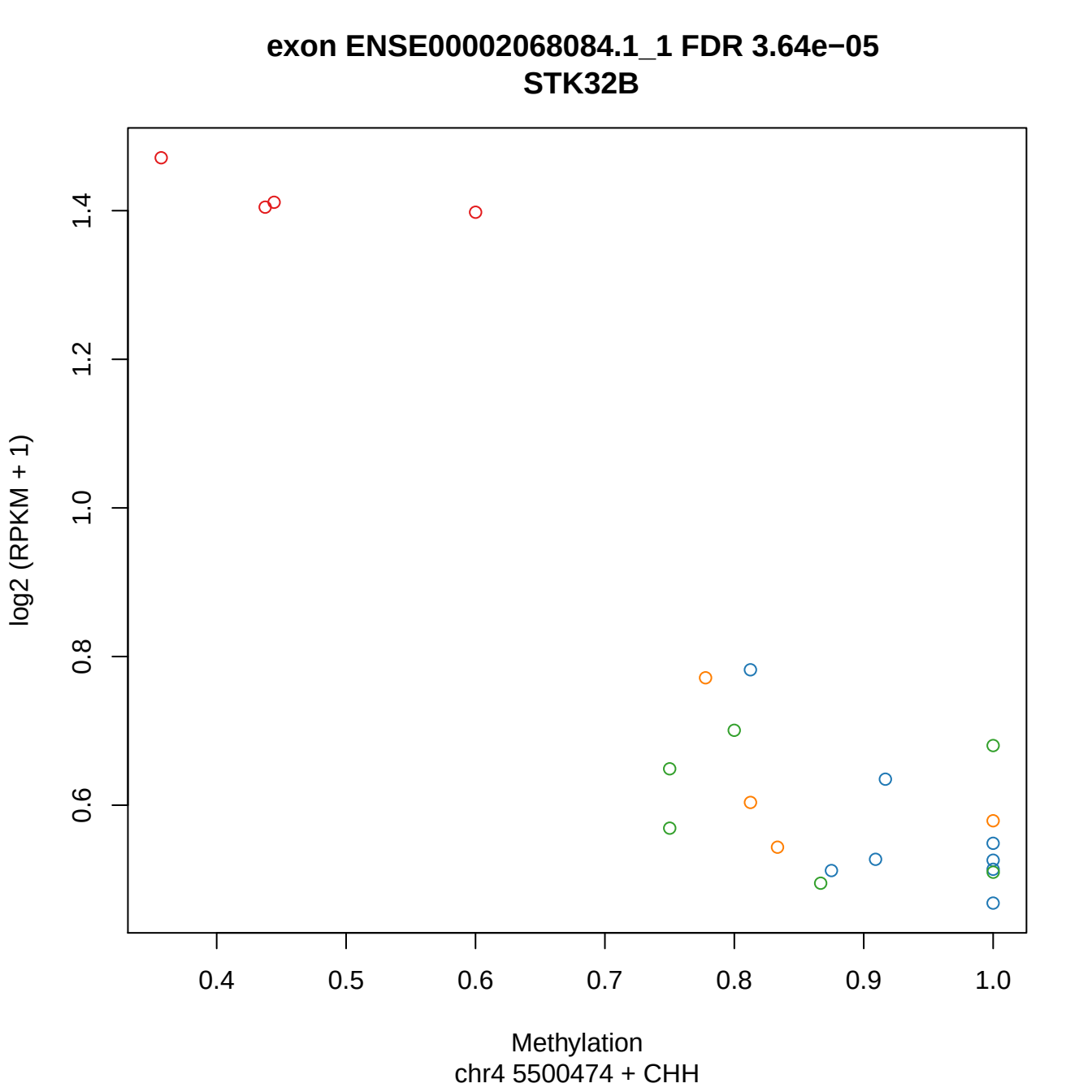

exon ENSE00001008085.1_1 FDR 0.000331
EVC
log2 (RPKM + 1)
0.0
0.2
0.4
0.6
0.8
0.0
0.2
0.4
0.6
Methylation
chr4 5731500 − CHH

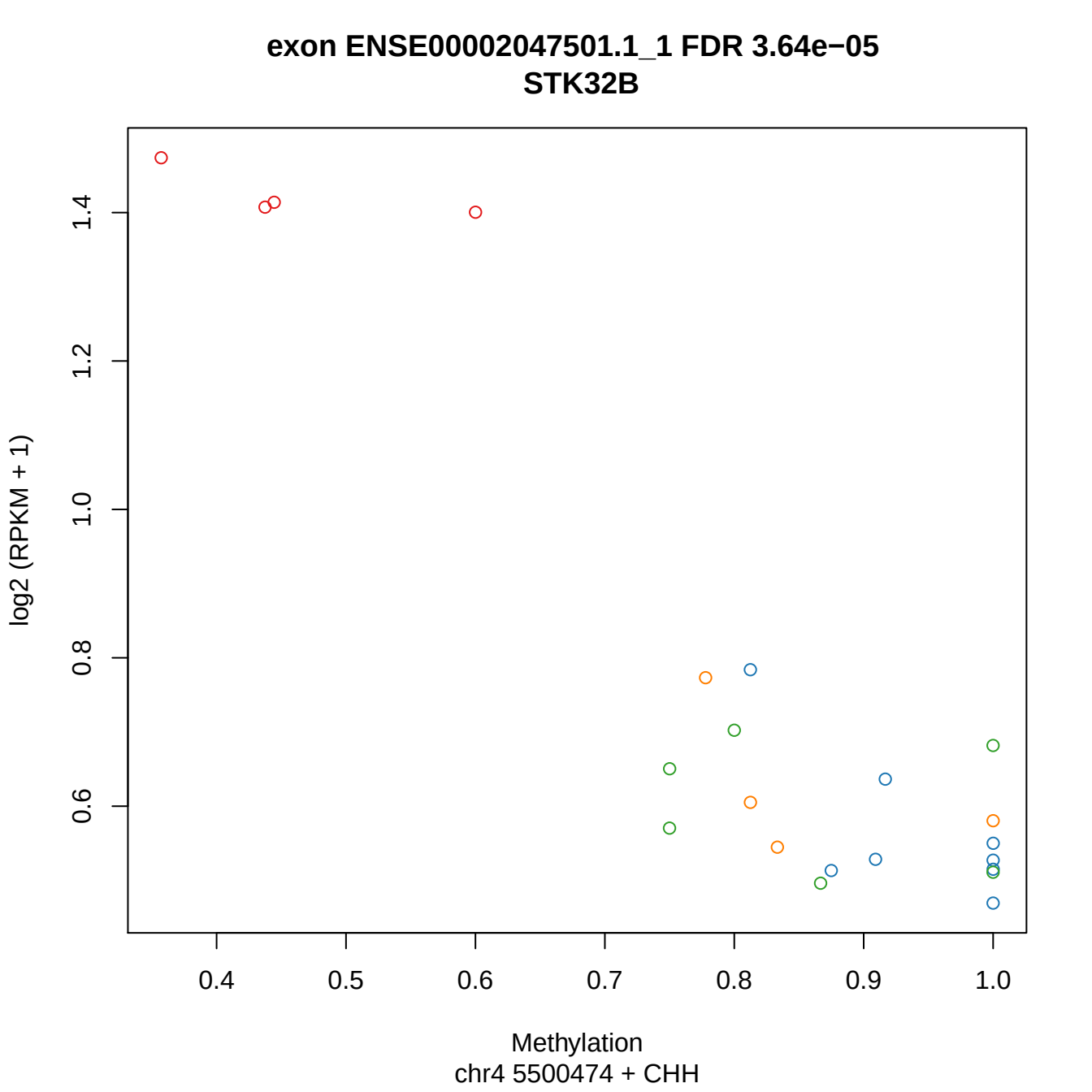

exon ENSE00001297775.5_1 FDR 0.000226
DRAXIN
log2 (RPKM + 1)
2.5
2.0
1.5
1.0
0.5
0.0
0.2
0.4
0.6
0.8
1.0
Methylation
chr1 11784907 + CHH

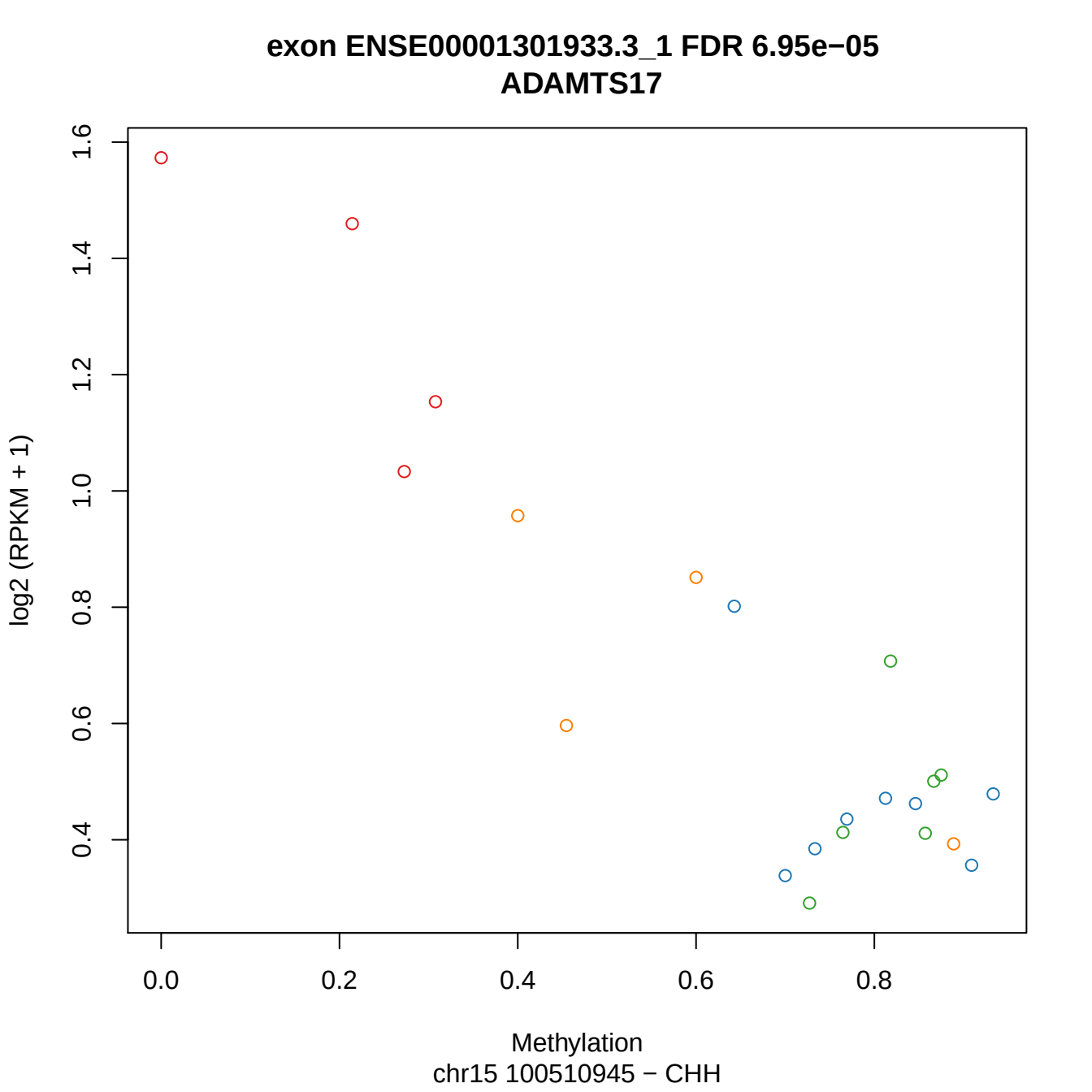

exon ENSE00003498058.1_1 FDR 1.21e−05
PXDN
log2 (RPKM + 1)
0.5
1.0
1.5
2.0
2.5
0.0
0.2
0.4
0.6
0.8
Methylation
chr2 1648359 − CHH

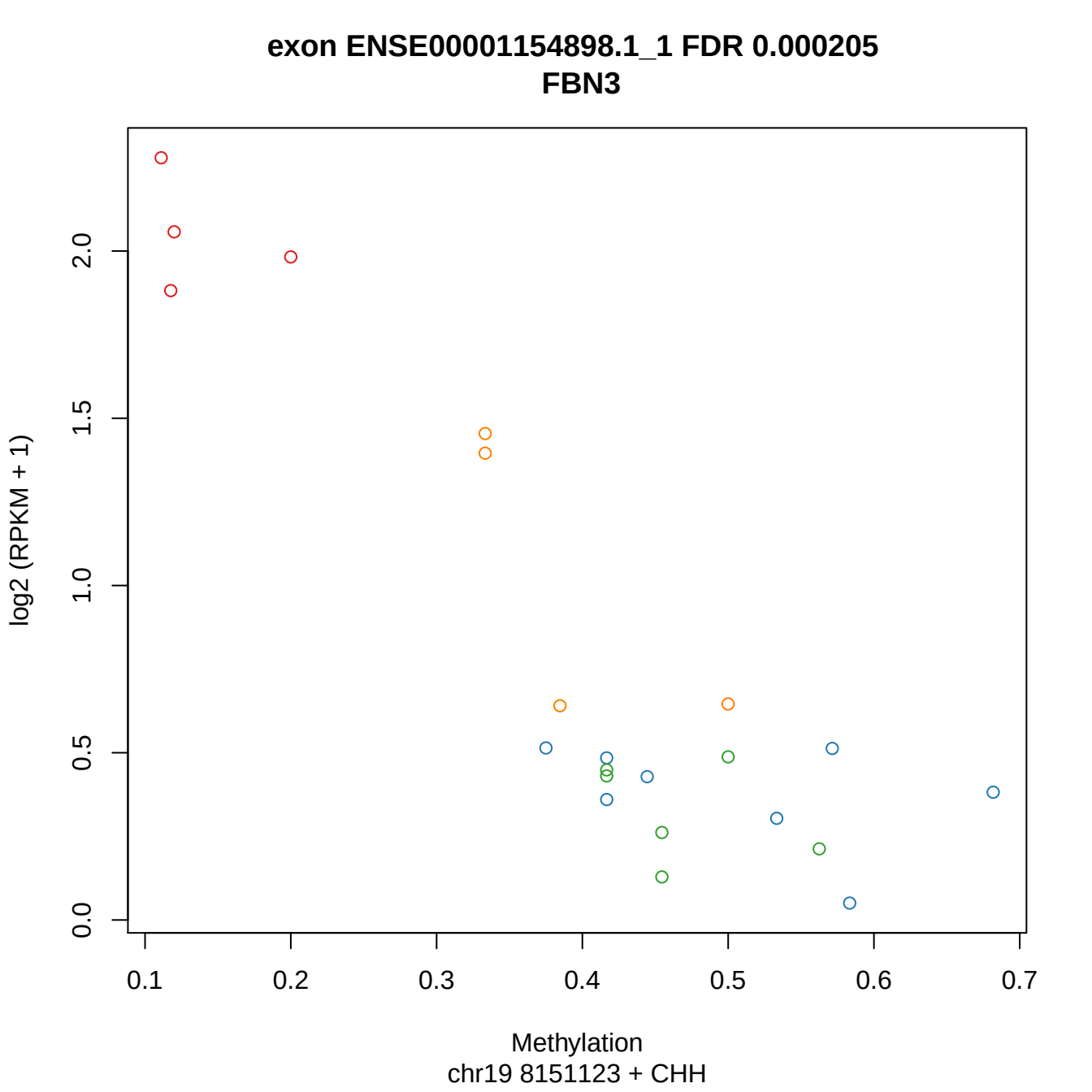

exon ENSE00002222495.1_1 FDR 0.00046
SCUBE1
log2 (RPKM + 1)
2.5
2.0
1.5
1.0
0.5
0.0
0.2
0.4
0.6
0.8
Methylation
chr22 43606937 − CHH

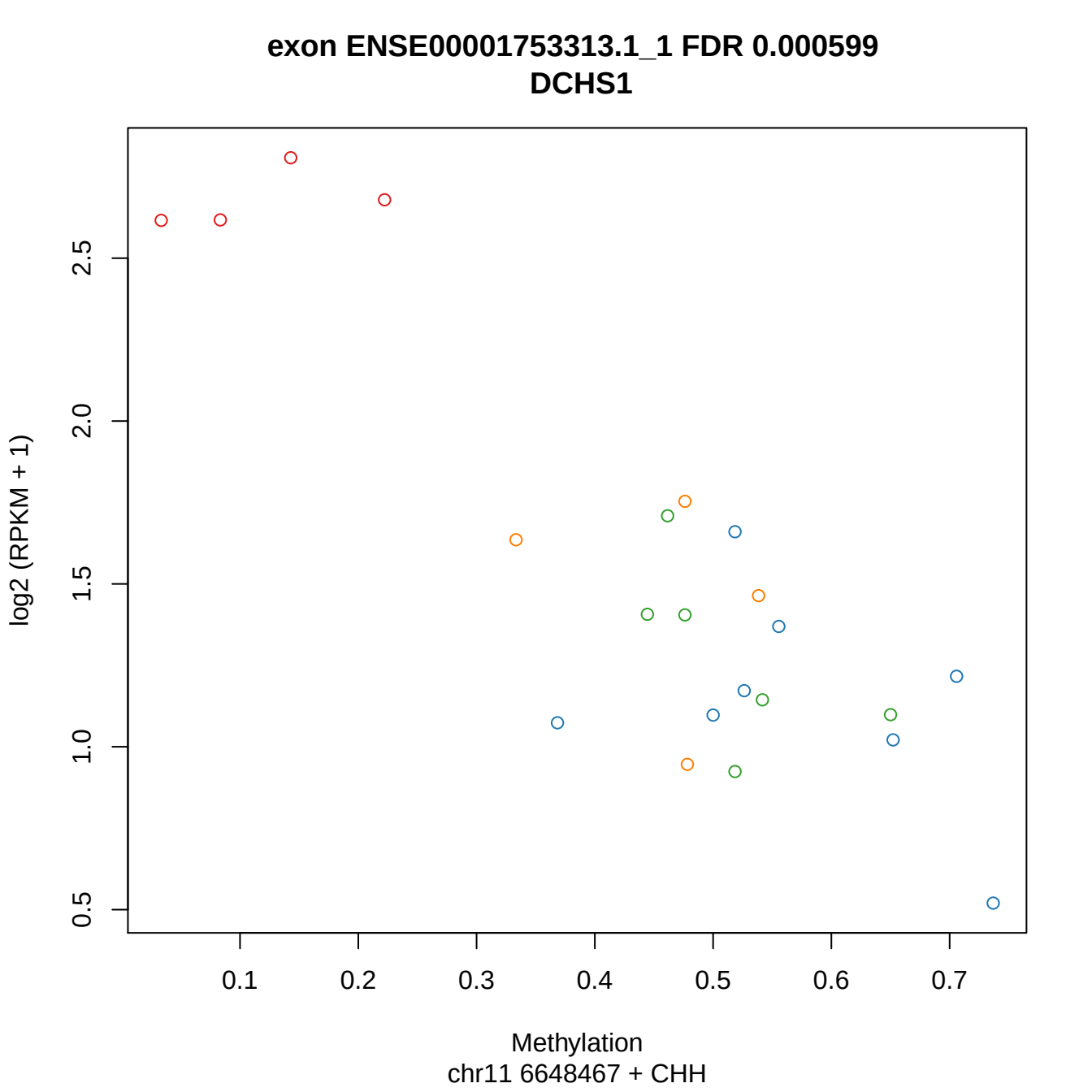

exon ENSE00001134909.1_1 FDR 3.64e−05
STK32B
log2 (RPKM + 1)
0.6
0.8
1.0
1.2
1.4
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Methylation
chr4 5500474 + CHH

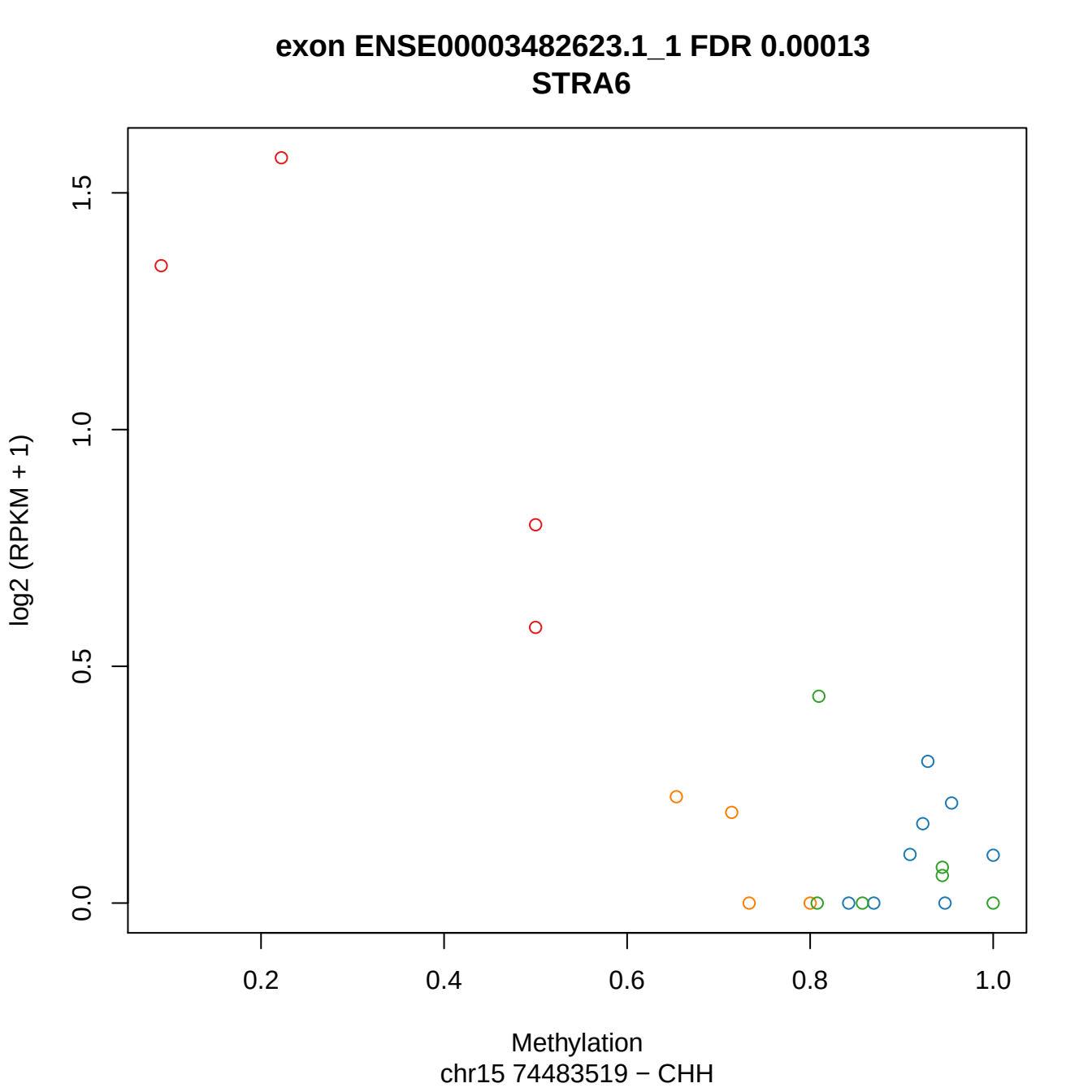

exon ENSE00002068084.1_1 FDR 3.64e−05
STK32B
log2 (RPKM + 1)
0.6
0.8
1.0
1.2
1.4
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Methylation
chr4 5500474 + CHH

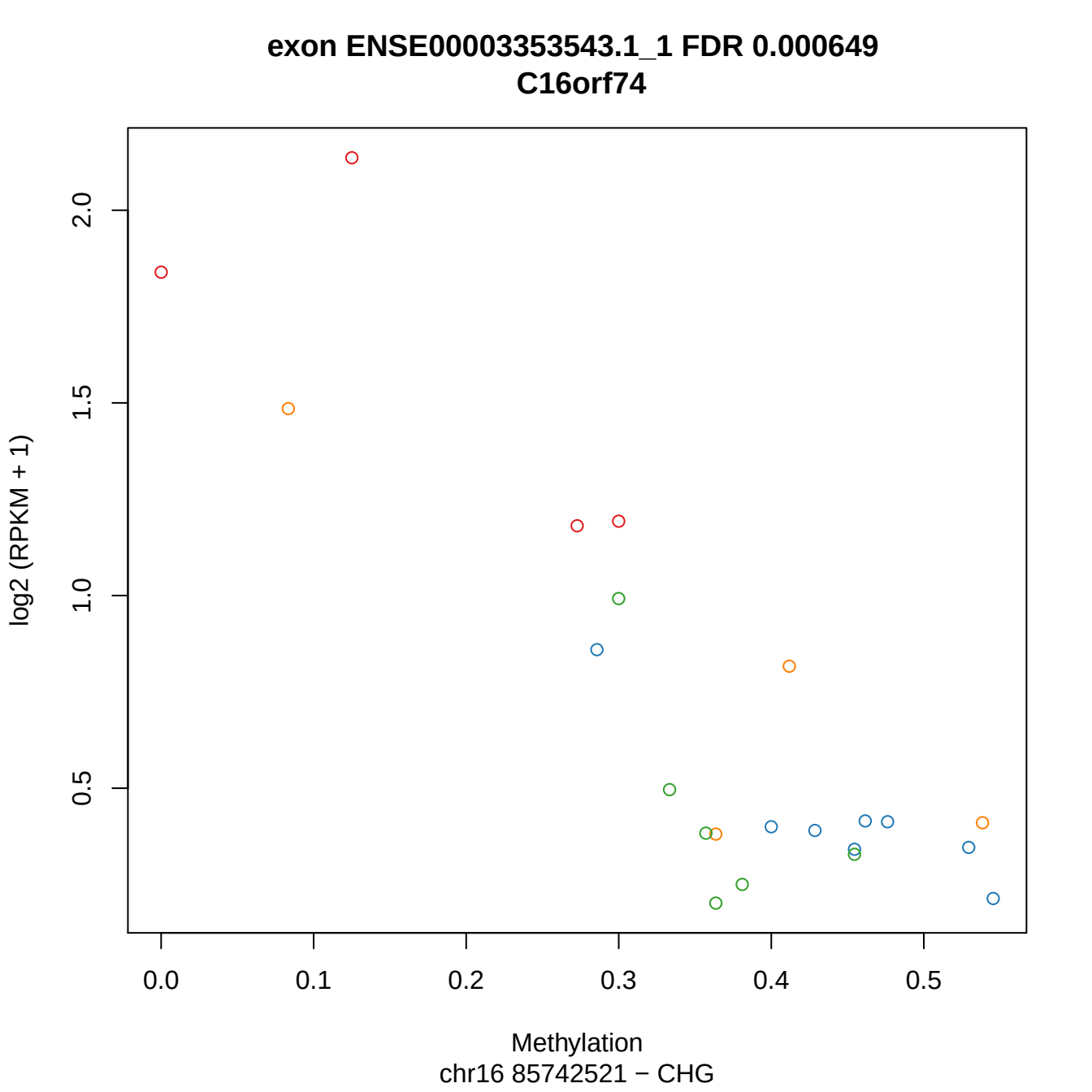

exon ENSE00002047501.1_1 FDR 3.64e−05
STK32B
log2 (RPKM + 1)
0.6
0.8
1.0
1.2
1.4
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Methylation
chr4 5500474 + CHH

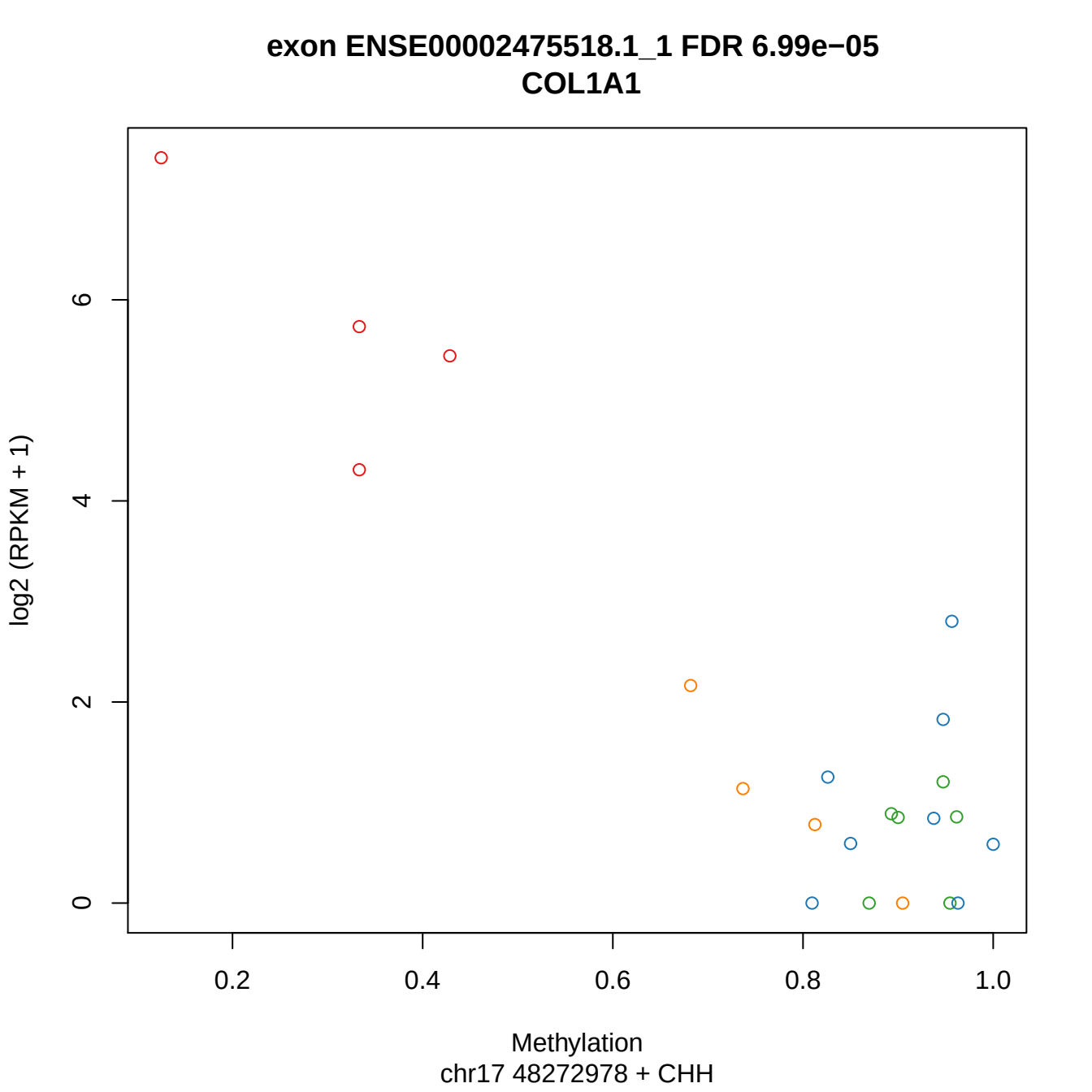

exon ENSE00001301933.3_1 FDR 6.95e−05
ADAMTS17
log2 (RPKM + 1)
0.4
0.6
0.8
1.0
1.2
1.4
1.6
0.0
0.2
0.4
0.6
0.8
Methylation
chr15 100510945 − CHH


exon ENSE00001154898.1_1 FDR 0.000205
FBN3
log2 (RPKM + 1)
0.0
0.5
1.0
1.5
2.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Methylation
chr19 8151123 + CHH


exon ENSE00001753313.1_1 FDR 0.000599
DCHS1
log2 (RPKM + 1)
0.5
1.0
1.5
2.0
2.5
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Methylation
chr11 6648467 + CHH


exon ENSE00003482623.1_1 FDR 0.00013
STRA6
log2 (RPKM + 1)
0.0
0.5
1.0
1.5
0.2
0.4
0.6
0.8
1.0
Methylation
chr15 74483519 − CHH


exon ENSE00003353543.1_1 FDR 0.000649
C16orf74
log2 (RPKM + 1)
0.5
1.0
1.5
2.0
0.0
0.1
0.2
0.3
0.4
0.5
Methylation
chr16 85742521 − CHG


exon ENSE00002475518.1_1 FDR 6.99e−05
COL1A1
log2 (RPKM + 1)
0
2
4
6
0.2
0.4
0.6
0.8
1.0
Methylation
chr17 48272978 + CHH