

S1A

G G G T C T C G G T G G G G G T C A C T G G G T T G C G G G C T T G G

G4Hunter_translate

3 3 3 0 -1 0 -1 2 2 0 4 4 4 4 4 0 -1 0 -1 0 3 3 3 0 0 1 -1 3 3 3 -1 0 0 2 2

G4Hscoring

$$\text{G4Hscore} = (3+3+3+0-1+0-1+2+2+0+4+4+4+4+4+0-1+0-1+0+3+3+3+0+0+1-1+3+3+3-1+0+0+2+2)/35$$

G4Hscore=1.43

Classical examples:

21g	GGGTTAGGGTTAGGGTTAGGG	1.71
A22g	AGGGTTAGGGTTAGGGTTAGGG	1.64
cMYC	TGAGGGTGGGTAGGGTGGGTAA	1.68
27Kras	GGGCGGTGTGGAAGAGGGAAGAGGGG	1.81
cKit1	GGGAGGGCGCTGGGAGGAGGG	1.86
cKit2GG	GGGCGGGCGCGAGGGAGGGG	2.1
Oxy28	GGGGTTTTGGGGTTTTGGGGTTTTGGGG	2.29
22Agm4	ATGGTTAGTGTTAGGTTTAGTG	0.55
CGG12	(CGG)12	1
ds26	CAATCGGATCGAATTCGATCCGATTG	0
21Ctel	CCCTAACCTAACCTAACCC	-1.71

S1B

G4Hunter on a long sequence

GAGGACAAGGAGGTGCGAGGAAAGGGGTTGGGGGATGGTCCCACAGGCAGCCACACCTGAGGCGTGGGCGGCCGGTAGGAGCTGGGGGAGGGCGG
GGAGAAGAGGGGTTTCTGTGTGTAGA

(1) G4Hunter_translate

1 0 2 2 0 -1 0 0 2 2 0 2 2 0 1 -1 1 0 2 2 0 0 0 4 4 4 4 0 0 4 4 4 4 0 0 2 2 0 -3 -3 -3 0 -1 0 2 2 -1 0 1 -2 -2 0 -1 0 -2 -2 0
1 0 2 2 -1 1 0 3 3 3 -1 2 2 -2 -2 2 2 0 0 2 2 0 1 -1 0 4 4 4 4 0 3 3 3 -1 4 4 4 4 0 1 0 0 1 0 4 4 4 4 0 0 0 -1 0 1 0 1 0 1
0 0 1 0

(2) G4Hscore_windowed (k=25)

1.00 1.12 1.28 1.20 1.12 1.28 1.48 **1.64 1.80 1.88 1.80 1.80 1.80 1.80 1.64 1.56** 1.40 1.40 1.28 1.20 1.28 1.36 1.32 1.16
1.04 0.80 0.56 0.56 0.52 0.36 0.12 -0.12 -0.28 -0.40 -0.40 -0.32 -0.32 -0.44 -0.40 -0.28 -0.04 0.20 0.32 0.32 0.40 0.40 0.24 0.20 0.28
0.32 0.40 0.48 0.56 0.68 0.68 0.80 0.84 0.84 0.96 1.12 1.20 1.28 1.48 1.44 **1.56 1.56 1.56** 1.40 **1.60 1.68 1.76 2.00 2.04**
1.96 1.96 2.00 1.92 2.00 2.16 2.28 2.48 2.48 2.32 2.16 1.96 1.80 1.68 1.68 1.60 1.48 1.40 1.44 1.28 1.16 1.00

(3) Window extraction (threshold=1.5)

	start	end	width	G4Hscore (window=25)
[1]	8	17	10	[1.64 1.80 1.88 1.80 1.80 1.80 1.80 1.80 1.64 1.56]
[2]	66	68	3	[1.56 1.56 1.56]
[3]	70	91	22	[1.60 1.68 1.76 2.00 2.08 2.04 1.96 1.96 2.00 1.92 2.00 2.16 2.28 2.48 2.48 2.32 2.16 1.96 1.80 1.68 1.68 1.60]

(4) Sequence extraction

	start	end	width	sequence	G4Hscore
[1]	8	41	34	[AGGAGGTGCGAGGAAAGGGGTTGGGGGATGGTCC]	1.44
[2]	66	92	27	[GGGCGGCCGGTAGGAGCTGGGGGAGGG]	1.67
[3]	70	115	46	[GGCCGGTAGGAGCTGGGGGAGGGCGGGGAGAAGAGGGGTTTCTGTG]	1.54

(5) Fusion of overlapping sequences

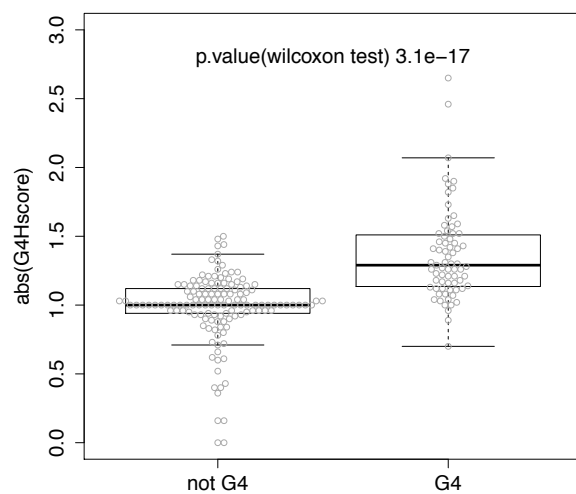
	start	end	width	sequence	G4Hscore
[1]	8	41	34	[AGGAGGTGCGAGGAAAGGGGTTGGGGGATGGTCC]	1.44
[2]	66	115	50	[GGGCGGCCGGTAGGAGCTGGGGGAGGGCGGGGAGAAGAGGGGTTTCTGTG]	1.58

(6) Extremity repair and final G4Hscore computation

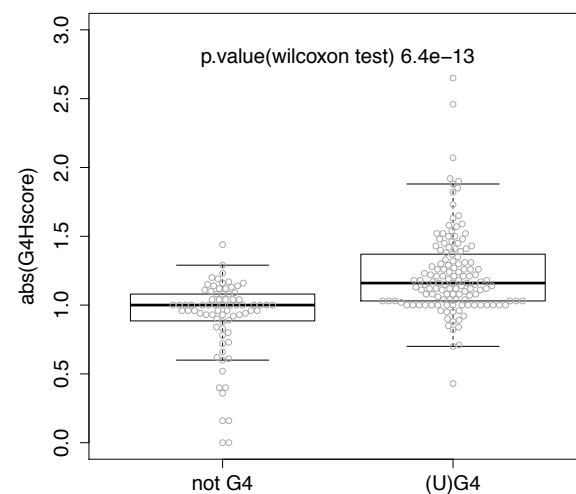
	start	end	sequence	G4Hscore
[1]	9	38	GGAGGTGCGAGGAAAGGGGTTGGGGGATGG	1.77
[2]	66	115	GGGCGGCCGGTAGGAGCTGGGGGAGGGCGGGGAGAAGAGGGGTTTCTGTG	1.58

GAGGACAAGGAGGTGCGAGGAAAGGGGTTGGGGGATGGTCCACAGGCAGCCACACCTGAGGCGTGGGCGGCCGGTAGGAGCTGGGGGAGGGCGGGGAGAAGAGGGGTTCTGTGTGTGTAGA

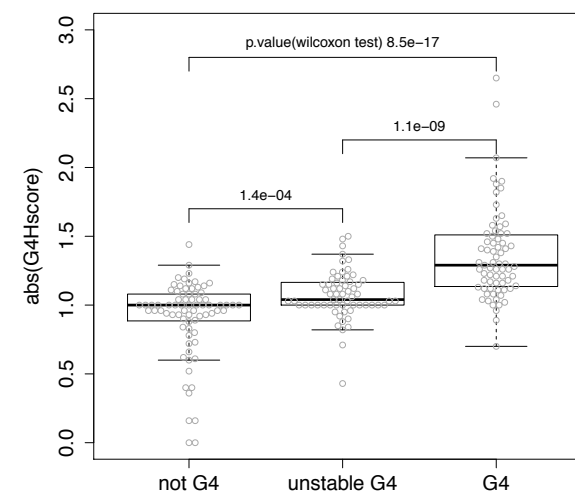
S2A



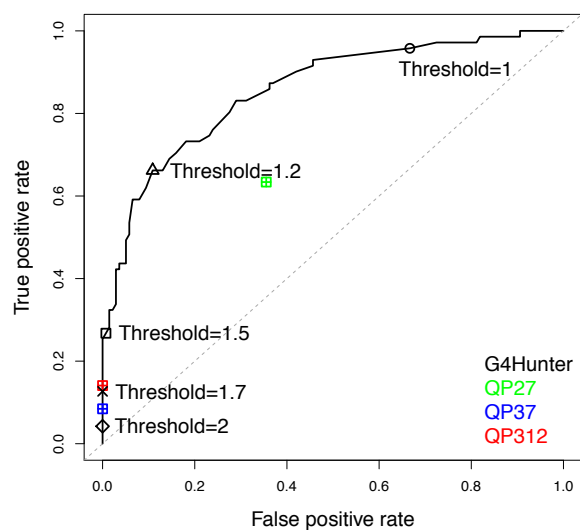
S2B



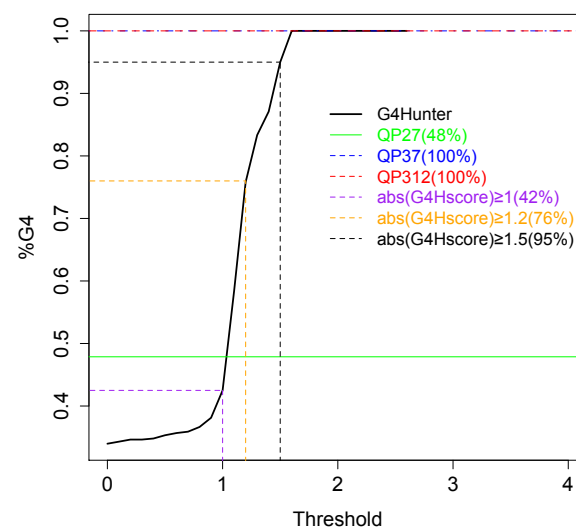
S2C



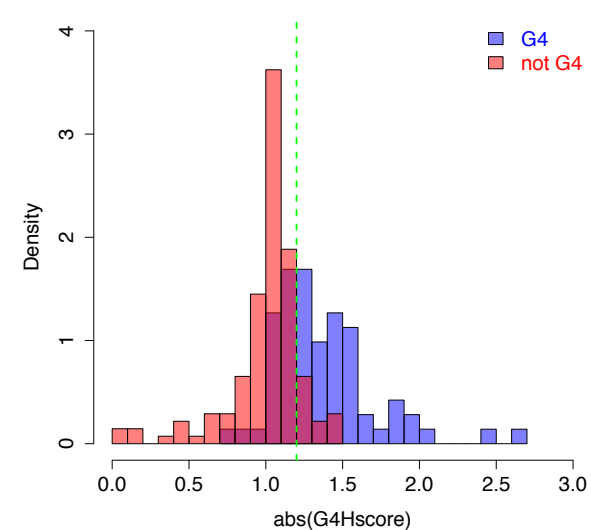
S2D



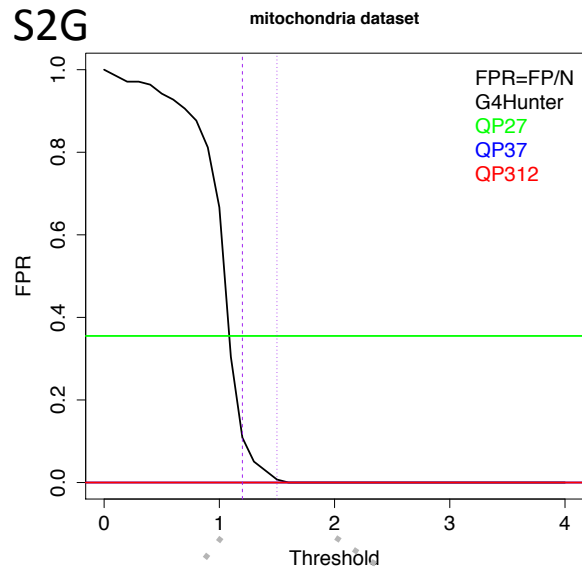
S2E



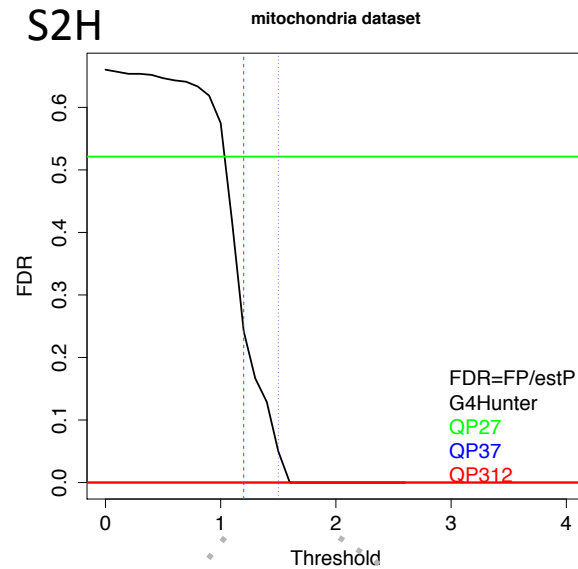
S2F



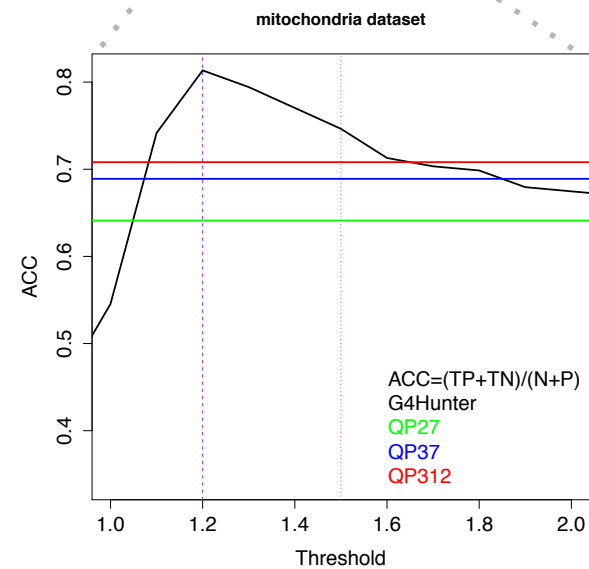
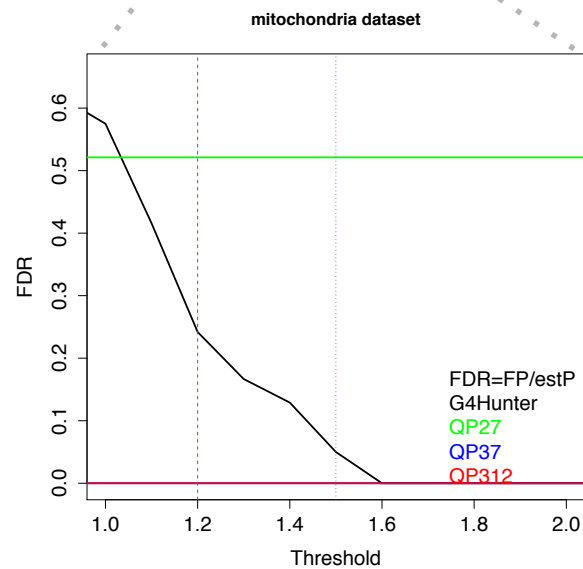
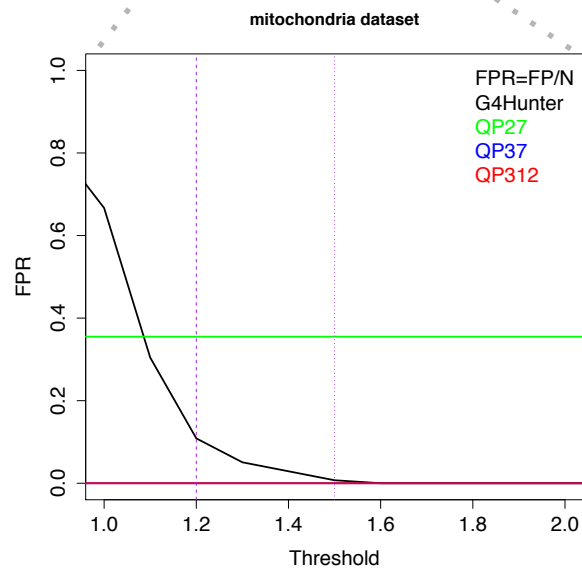
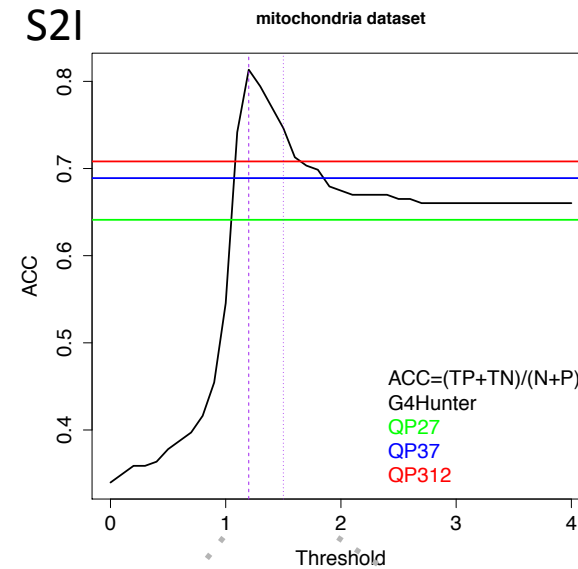
S2G



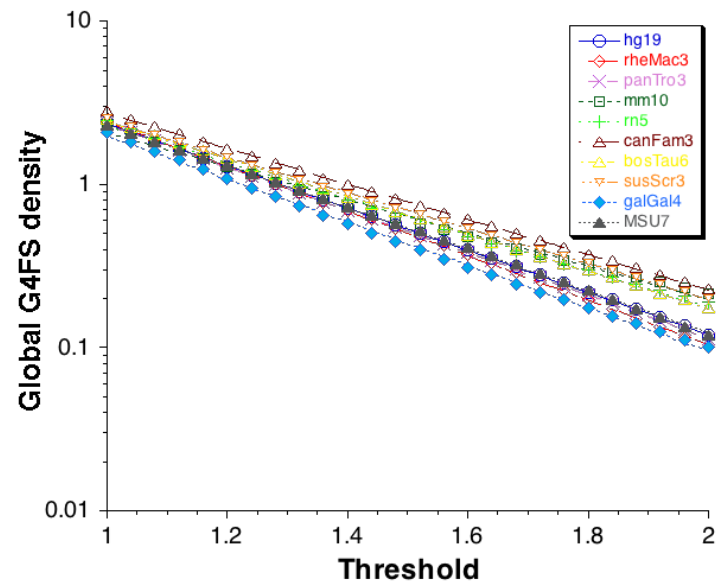
S2H



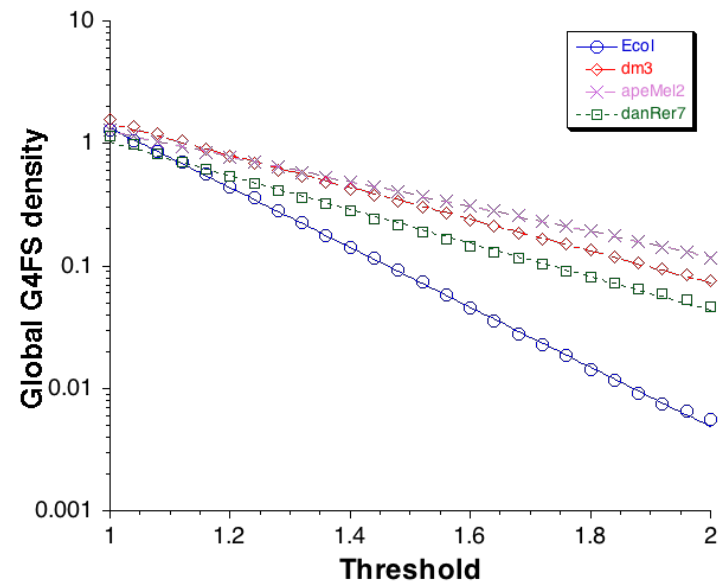
S2I



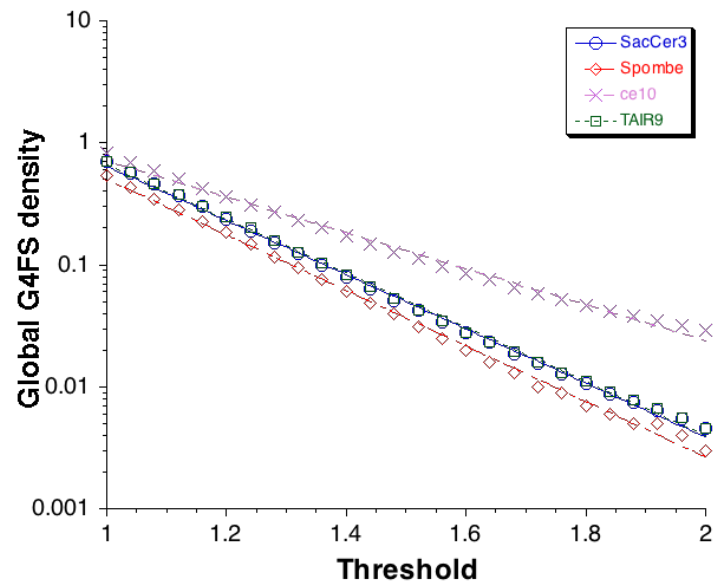
S3A



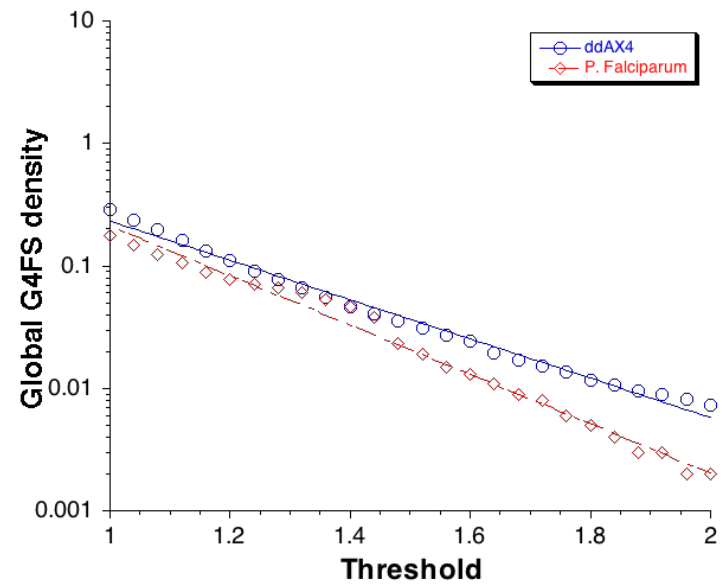
S3B



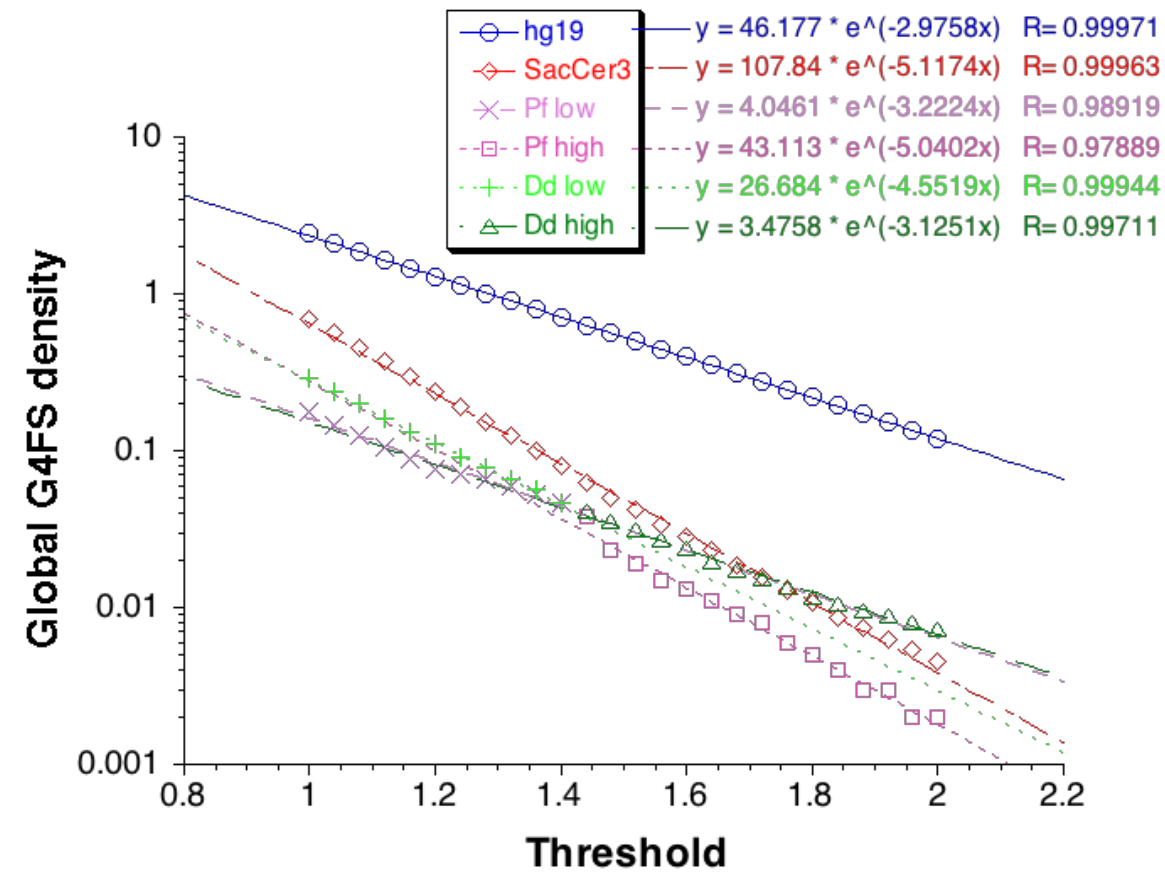
S3C



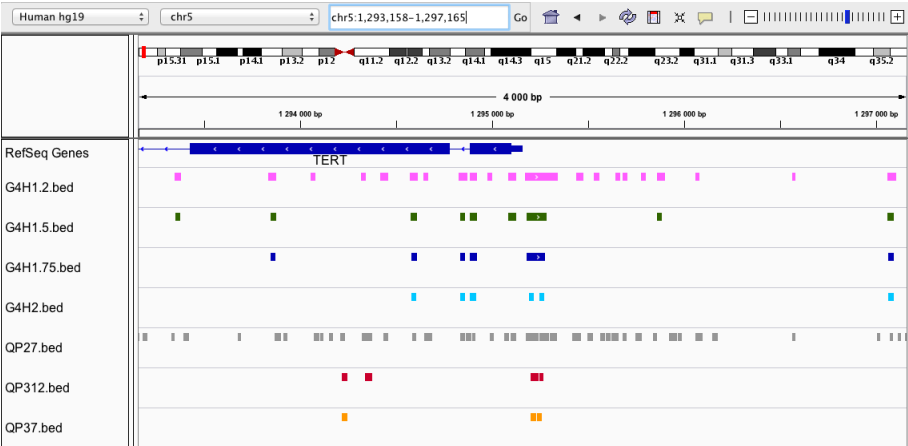
S3D



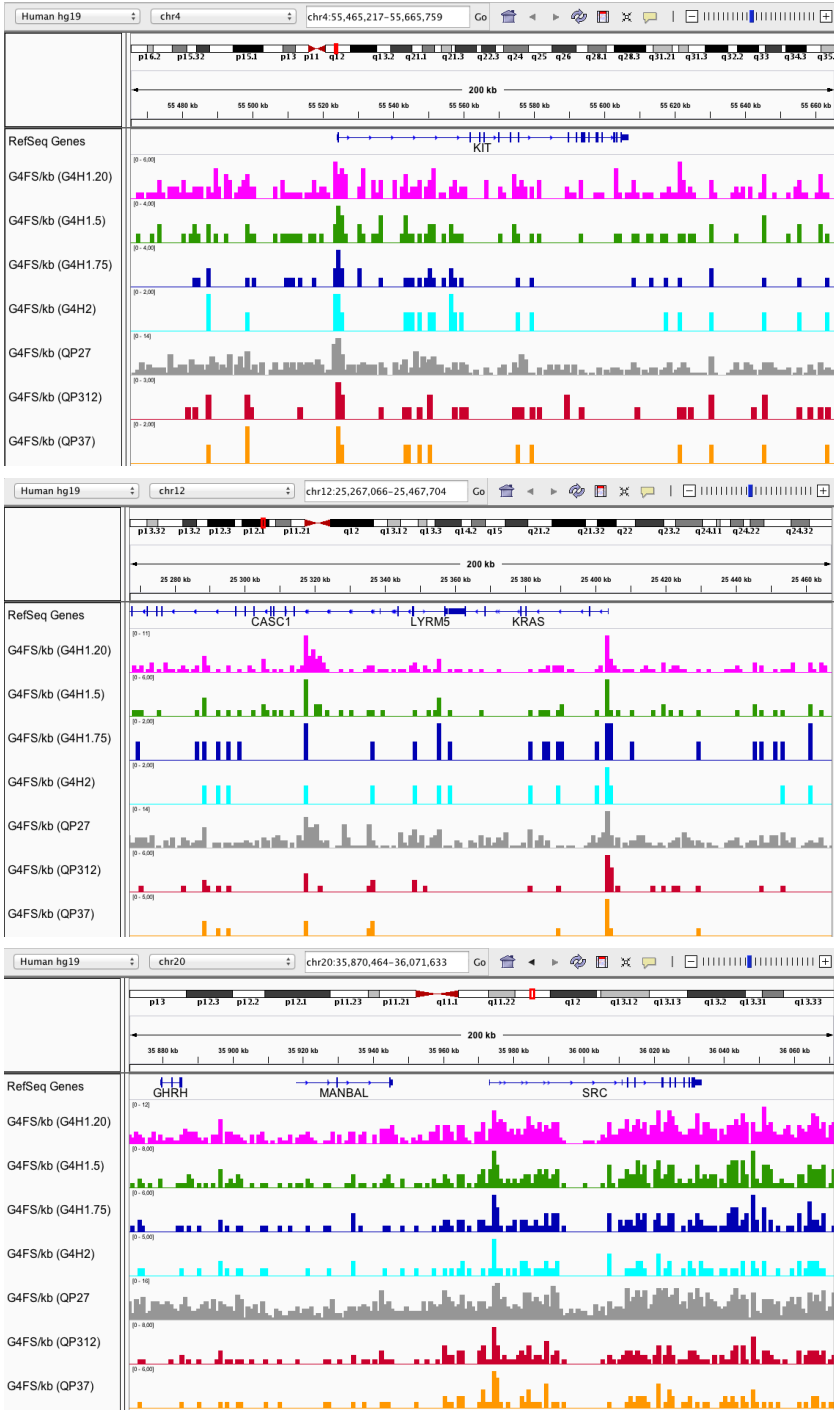
S3E



S4A



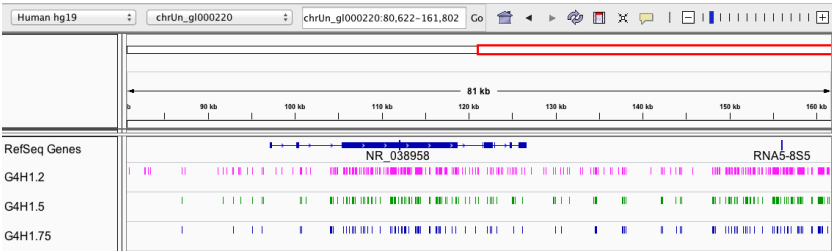
S4B



S4C



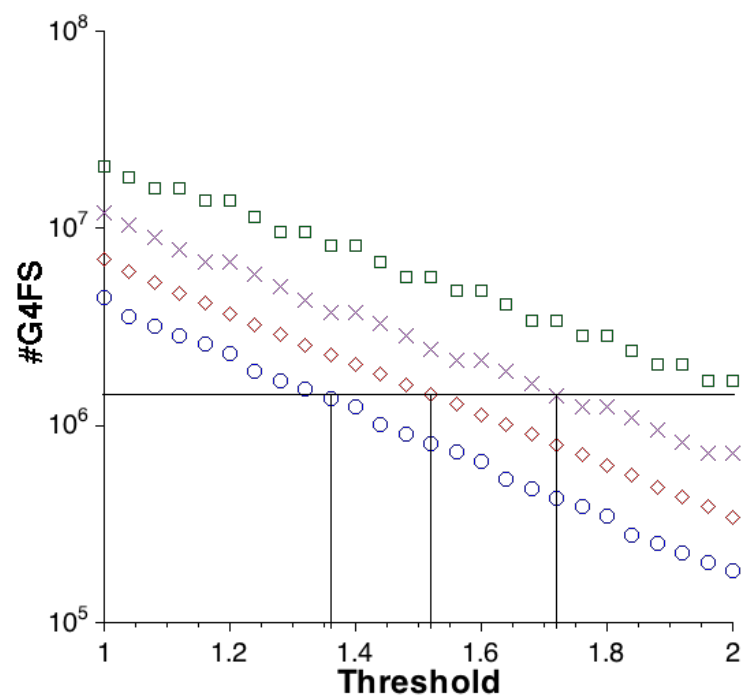
dm3



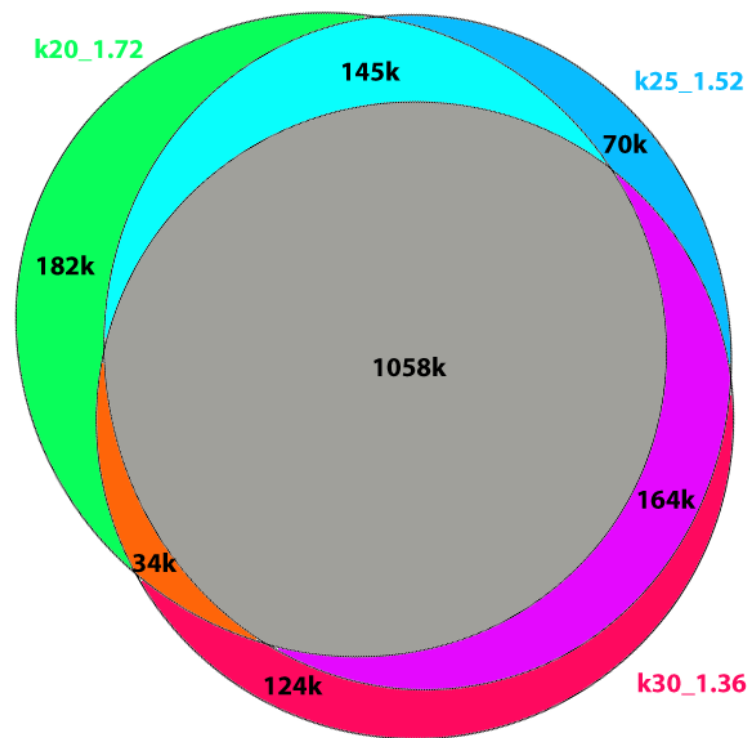
rDNA(hg19)

SacCer3

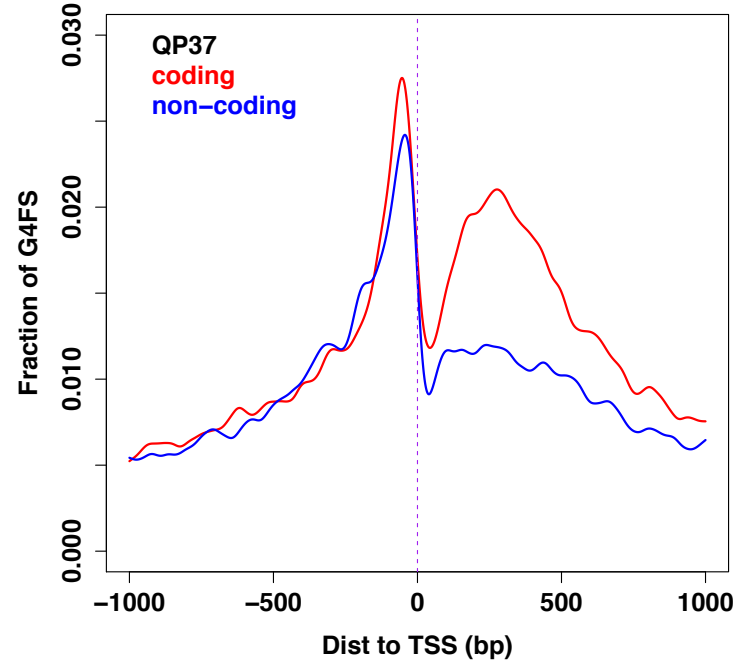
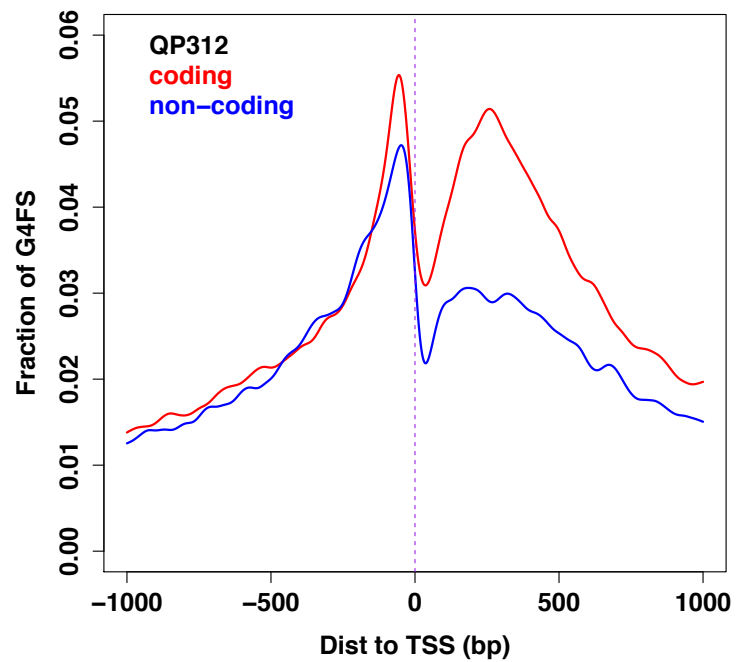
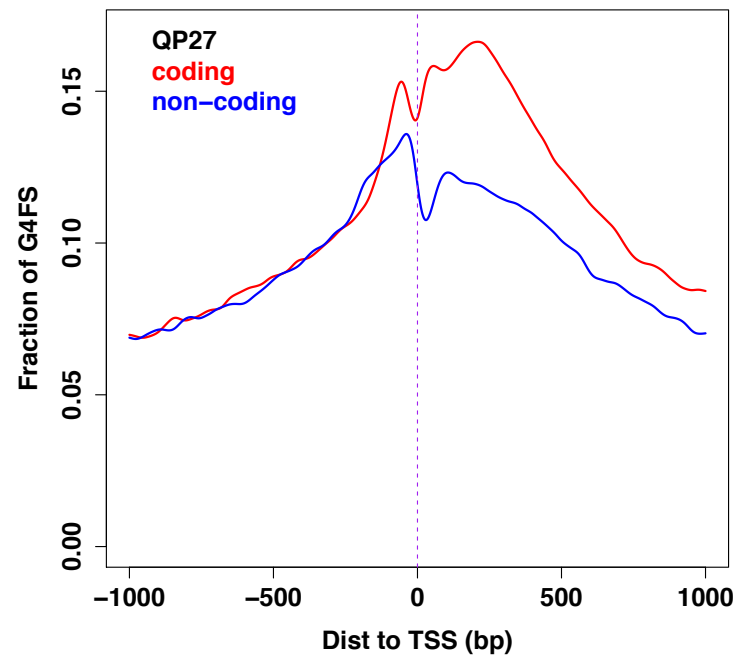
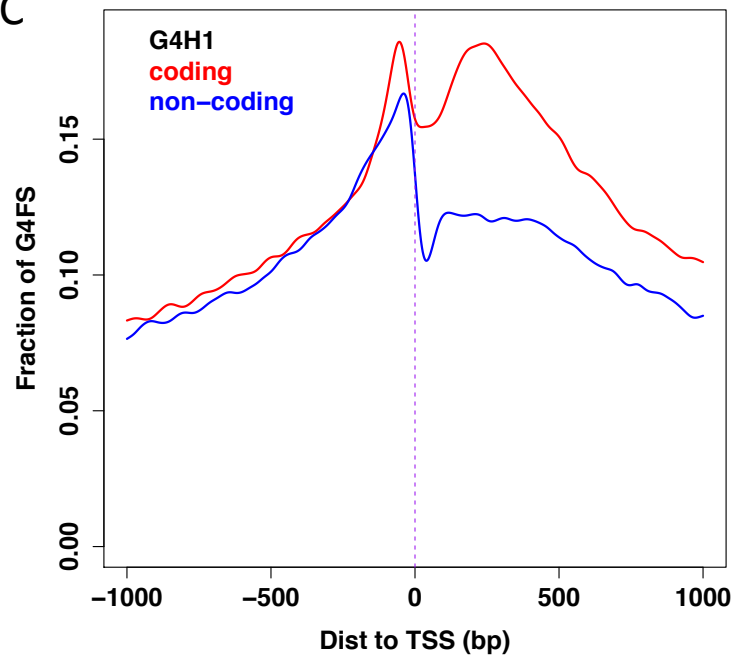
S5A



S5B



S5C



S6

