Supporting material (Appendix) for the thesis:

The analysis of high-throughput biological datasets utilising distributed computing

Submitted by

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Appendix 1

Testing the Protein Databank (Chapter 5)

1.1 PDB file accessions used for benchmarking

Data used from the Protein Databank for benchmarking PDB-Hadoop (chapter 5 section 5.6) is listed below, by PDB entry (accession):

```
pdb1a30, pdb1a31, pdb1a32, pdb1a33, pdb1a34, pdb1a35, pdb1a36, pdb1a37, pdb1a38,
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pdb1a3i, pdb1a3j, pdb1a3k, pdb1a3l, pdb1a3m, pdb1a3n, pdb1a3o, pdb1a3p, pdb1a3q,
pdb1a3r, pdb1a3s, pdb1a3t, pdb1a3u, pdb1a3v, pdb1a3w, pdb1a3x, pdb1a3y, pdb1a3z,
pdb1dk0, pdb1dk1, pdb1dk2, pdb1dk3, pdb1dk4, pdb1dk5, pdb1dk6, pdb1dk7, pdb1dk8,
pdb1dk9, pdb1dka, pdb1dkc, pdb1dkd, pdb1dke, pdb1dkf, pdb1dkg, pdb1dkh, pdb1dki,
pdb1dkj, pdb1dkk, pdb1dkl, pdb1dkm, pdb1dkn, pdb1dko, pdb1dkp, pdb1dkq, pdb1dkr,
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pdb7a3h

1.2 Sample PDB-Hadoop job output

1.2.1 Dihedrals job output

A sample of the output from PDB-Hadoop during the computation of torsional (dihedral) angles on the PDB macro-molecular structure entries listed in section 1.1 above (discussed in chapter 5, section 5.5.1). NB: Only the first 20 records in the PDB is shown for two entries.

```
Extracted/writing file /tmp/pdb3gax.ent
pdb3gax.ent-0000000001 Phi,Psi,Omega,Chain,Residue
pdb3gax.ent-0000000002 1, 0.00, 164.35, 179.04, "A", "GLY12"
pdb3gax.ent-0000000003 2, -71.04, 145.47, -179.55, "A", "PRO13"
pdb3gax.ent-0000000004 3, -107.27, 154.17, 175.62, "A", "MET14"
pdb3gax.ent-0000000005 4, -58.21, 144.81, 175.34, "A", "ASP15"
pdb3gax.ent-0000000006 5, -141.64, 175.10, -178.81, "A", "ALA16"
pdb3gax.ent-0000000007 6, -143.17, 162.72, 177.07, "A", "SER17"
pdb3gax.ent-0000000008 7, -68.77, -13.42, 167.40, "A", "VAL18"
pdb3gax.ent-0000000009 8, -63.05, -22.24, -179.18, "A", "GLU19"
pdb3gax.ent-0000000010 9, -76.13, 128.76, -179.80, "A", "GLU20"
pdb3gax.ent-0000000011 10, -53.96, -43.56, 179.65, "A", "GLU21"
pdb3gax.ent-0000000012 11, -62.53, -44.40, 172.47, "A", "GLY22"
pdb3gax.ent-0000000013 12, -55.75, -47.94, 177.52, "A", "VAL23"
pdb3gax.ent-0000000014 13, -59.85, -41.82, 179.37, "A", "ARG24"
pdb3gax.ent-0000000015 14, -64.57, -44.26, 177.91, "A", "ARG25"
pdb3gax.ent-0000000016 15, -64.42, -39.67, 176.43, "A", "ALA26"
```

```
pdb3gax.ent-0000000017 16, -59.85, -49.39, -179.06, "A", "LEU27"
pdb3gax.ent-0000000018 17, -66.68, -41.04, 173.57, "A", "ASP28"
pdb3gax.ent-0000000019 18, -55.45, -52.34, -176.12, "A", "PHE29"
pdb3gax.ent-0000000020 19, -62.26, -45.43, 178.14, "A", "ALA30"
pdb3gax.ent-0000000021 20, -65.31, -41.39, 172.49, "A", "VAL31"
......
......
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pdb3ga3.ent-0000000001 Phi,Psi,Omega,Chain,Residue
pdb3ga3.ent-0000000002 1, 0.00, -25.54, -177.36, "A", "ALA893"
pdb3ga3.ent-0000000003 2, -63.68, -21.97, 178.11, "A", "LYS894"
pdb3ga3.ent-0000000004 3, -103.02, 7.32, 178.37, "A", "HIS895"
pdb3ga3.ent-0000000005 4, -68.56, 160.12, 177.24, "A", "TYR896"
pdb3ga3.ent-0000000006 5, -92.42, 128.71, 179.37, "A", "LYS897"
pdb3ga3.ent-0000000007 6, -94.55, 50.91, -178.00, "A", "ASN898"
pdb3ga3.ent-0000000008 7, -133.32, 78.56, -179.84, "A", "ASN899"
pdb3ga3.ent-0000000009 8, -60.43, -21.70, 179.64, "A", "PRO900"
pdb3ga3.ent-0000000010 9, -63.02, -13.94, 179.82, "A", "SER901"
pdb3ga3.ent-0000000011 10, -70.68, -17.54, -176.86, "A", "LEU902"
pdb3ga3.ent-0000000012 11, -122.34, 157.51, 175.84, "A", "ILE903"
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pdb3ga3.ent-0000000014 13, -111.26, 126.57, 178.44, "A", "PHE905"
pdb3ga3.ent-0000000015 14, -113.43, 144.65, 175.13, "A", "LEU906"
pdb3ga3.ent-0000000016 15, -58.98, 131.57, -177.90, "A", "CYS907"
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pdb3ga3.ent-0000000018 17, -89.35, -53.63, -176.44, "A", "ASN909"
pdb3ga3.ent-0000000019 18, -101.81, -4.60, 178.96, "A", "CYS910"
pdb3ga3.ent-0000000020 19, 69.58, 7.36, 179.63, "A", "SER911"
pdb3ga3.ent-0000000021 20, -68.24, 147.11, 177.33, "A", "VAL912"
......
......
```

1.2.2 Docking job output

Below is a sample of the output from PDB-Hadoop during the docking of a small oligo-peptide (discussed in chapter 5, section 5.5.2) against the PDB macro-molecular entries listed in section 1.1 above. The output employs the *post-processing* step of PDB-Hadoop to extract docking scores from Vina AutoDock and summarise them in order of best (lowest energy) docking score.

```
Extracted/writing file /tmp/pdb1a3q.ent
Initiating post-processing...
pdb1a3q.ent-0000000001     1         -4.6      0.000      0.000
pdb1a3q.ent-0000000002     2         -4.4     22.399     23.769
pdb1a3q.ent-0000000003     3         -4.2     22.208     22.970
pdb1a3q.ent-0000000004     4         -4.2     19.226     21.204
pdb1a3q.ent-0000000005     5         -4.1     34.622     36.402
pdb1a3q.ent-0000000006     6         -4.0     20.313     22.641
pdb1a3q.ent-0000000007     7         -4.0     34.348     35.354
pdb1a3q.ent-0000000008     8         -4.0     27.283     29.148
pdb1a3q.ent-0000000009     9         -3.9     26.239     27.588
Extracted/writing file /tmp/pdb2dkr.ent
Initiating post-processing...
pdb2dkr.ent-0000000001     1         -5.0      0.000      0.000
```

```
pdb2dkr.ent-0000000002     2         -4.7      3.496      5.931
pdb2dkr.ent-0000000003     3         -4.6      3.759      4.530
pdb2dkr.ent-0000000004     4         -4.6      5.178      6.929
pdb2dkr.ent-0000000005     5         -4.4     24.758     26.165
pdb2dkr.ent-0000000006     6         -4.3      2.661      3.299
pdb2dkr.ent-0000000007     7         -4.2     21.788     22.757
pdb2dkr.ent-0000000008     8         -4.0     17.432     19.035
pdb2dkr.ent-0000000009     9         -4.0     14.814     15.540
......
......
```

Appendix 2

Transcriptomics analysis (Chapter 6)

2.1 Wild-type *D. melanogaster* results

Motif spacing: **10bp**								
Exon GC%	**30-40%**		**40-50%**		**50-60%**		**60-70%**	
Motif GC%	50	0	50	0	50	0	50	0
#Correlations	16	96	16	96	16	96	8	96
p(t-test)	$4.83\text{x}10^{-4}(1.54\text{x}10^{-3})$*		$9.91\text{x}10^{-1}(9.91\text{x}10^{-1})$		$6.56\text{x}10^{-1}(7.50\text{x}10^{-1})$		$3.50\text{x}10^{-1}(4.38\text{x}10^{-1})$	
p(Wilcoxon)	$8.79\text{x}10^{-2}(1.41\text{x}10^{-1})$		$1.96\text{x}10^{-1}(2.61\text{x}10^{-1})$		$4.69\text{x}10^{-1}(5.36\text{x}10^{-1})$		1.00(1.00)	
Exon GC%	**30-40%**		**40-50%**		**50-60%**		**60-70%**	
Motif GC%	50	25	50	25	50	25	50	25
#Correlations	64	96	64	96	64	96	54	96
p(t-test)	$7.66\text{x}10^{-3}(1.53\text{x}10^{-2})$*		$8.53\text{x}10^{-1}(9.10\text{x}10^{-1})$		$3.31\text{x}10^{-1}(4.38\text{x}10^{-1})$		$4.81\text{x}10^{-2}(8.55\text{x}10^{-2})$	
p(Wilcoxon)	$5.40\text{x}10^{-3}(1.73\text{x}10^{-2})$*		$9.52\text{x}10^{-1}(1.00)$		$1.83\text{x}10^{-1}(2.61\text{x}10^{-1})$		$8.58\text{x}10^{-2}(1.41\text{x}10^{-1})$	
Exon GC%	**30-40%**		**40-50%**		**50-60%**		**60-70%**	
Motif GC%	50	75	50	75	50	75	50	75
#Correlations	64	96	64	96	64	96	64	96
p(t-test)	$1.40\text{x}10^{-1}(2.25\text{x}10^{-1})$		$3.55\text{x}10^{-1}(4.38\text{x}10^{-1})$		$6.26\text{x}10^{-3}(1.43\text{x}10^{-2})$*		$9.88\text{x}10^{-5}(3.95\text{x}10^{-4})$*	
p(Wilcoxon)	$2.30\text{x}10^{-2}(4.60\text{x}10^{-2})$*		$4.11\text{x}10^{-1}(5.06\text{x}10^{-1})$		$1.00\text{x}10^{-2}(2.68\text{x}10^{-2})$*		$8.07\text{x}10^{-4}(1.28\text{x}10^{-2})$*	
Exon GC%	**30-40%**		**40-50%**		**50-60%**		**60-70%**	
Motif GC%	50	100	50	100	50	100	50	100
#Correlations	16	96	16	96	16	96	16	96
p(t-test)	$1.08\text{x}10^{-3}(2.89\text{x}10^{-3})$*		$4.82\text{x}10^{-6}(2.57\text{x}10^{-5})$*		$2.28\text{x}10^{-6}(1.82\text{x}10^{-5})$*		$3.45\text{x}10^{-8}(5.52\text{x}10^{-7})$*	
p(Wilcoxon)	$1.31\text{x}10^{-2}(2.99\text{x}10^{-2})$*		$2.71\text{x}10^{-3}(1.28\text{x}10^{-2})$*		$1.92\text{x}10^{-3}(1.28\text{x}10^{-2})$*		$3.20\text{x}10^{-3}(1.28\text{x}10^{-2})$*	

Table 2.1: T-test and Wilcoxon-test comparisons of Pearson correlations for motif-pairs at 10bp spacing for varying motif GC and mean exon GC content in Wild-type *D. melanogaster*. FDR corrected p-values in parenthesis, using a False positive rate of 5% ($\alpha = 0.05$). * suggests rejection of the null hypothesis.

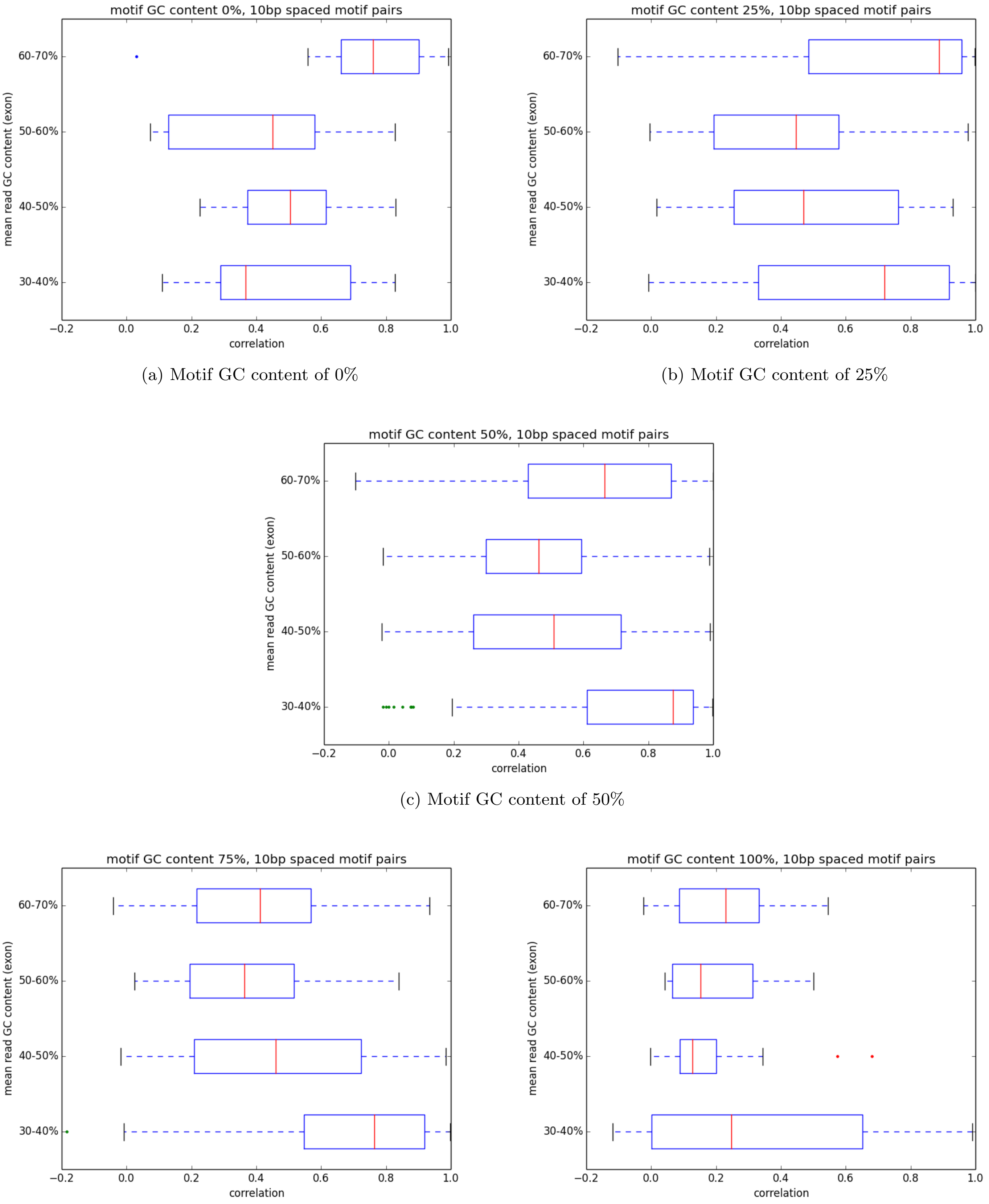
Motif spacing: **50bp**								
Exon GC%	**30-40%**		**40-50%**		**50-60%**		**60-70%**	
Motif GC%	50	0	50	0	50	0	50	0
#Correlations	16	96	16	96	16	96	4	96
p(t-test)	2.87x10^{-2}(7.07x10^{-2})		4.94x10^{-1}(6.32x10^{-1})		9.91x10^{-1}(9.91x10^{-1})		5.58x10^{-1}(6.87x10^{-1})	
p(Wilcoxon)	5.23x10^{-3}(2.47x10^{-2})*		4.38x10^{-1}(5.84x10^{-1})		5.35x10^{-1}(6.58x10^{-1})		1.00(1.00)	
Exon GC%	**30-40%**		**40-50%**		**50-60%**		**60-70%**	
Motif GC%	50	25	50	25	50	25	50	25
#Correlations	64	96	64	96	64	96	46	96
p(t-test)	3.89x10^{-1}(5.42x10^{-1})		4.87x10^{-1}(6.32x10^{-1})		8.69x10^{-1}(9.31x10^{-1})		1.63x10^{-1}(2.75x10^{-1})	
p(Wilcoxon)	1.58x10^{-1}(2.81x10^{-1})		3.29x10^{-1}(4.78x10^{-1})		8.94x10^{-1}(9.86x10^{-1})		7.97x10^{-1}(9.11x10^{-1})	
Exon GC%	**30-40%**		**40-50%**		**50-60%**		**60-70%**	
Motif GC%	50	75	50	75	50	75	50	75
#Correlations	61	96	64	96	64	96	64	96
p(t-test)	8.73x10^{-1}(9.31x10^{-1})		1.15x10^{-1}(2.17x10^{-1})		7.15x10^{-2}(1.51x10^{-1})		7.53x10^{-2}(1.51x10^{-1})	
p(Wilcoxon)	7.82x10^{-1}(9.11x10^{-1})		5.49x10^{-2}(1.17x10^{-1})		2.04x10^{-1}(3.11x10^{-1})		4.30x10^{-3}(2.47x10^{-2})*	
Exon GC%	**30-40%**		**40-50%**		**50-60%**		**60-70%**	
Motif GC%	50	100	50	100	50	100	50	100
#Correlations	16	96	16	96	16	96	16	96
p(t-test)	5.69x10^{-3}(2.00x10^{-2})*		1.06x10^{-2}(2.82x10^{-2})*		1.36x10^{-3}(5.42x10^{-3})*		7.23x10^{-5}(5.78x10^{-4})*	
p(Wilcoxon)	9.73x10^{-3}(3.21x10^{-2})*		1.74x10^{-2}(4.63x10^{-2})*		8.36x10^{-3}(3.21x10^{-2})*		2.00x10^{-2}(4.92x10^{-2})*	

Table 2.2: T-test and Wilcoxon-test comparisons of Pearson correlations for motif-pairs at 50bp spacing for varying motif GC and mean exon GC content in Wild-type *D. melanogaster*. FDR corrected p-values in parenthesis, using a False positive rate of 5% ($\alpha = 0.05$). * suggests rejection of the null hypothesis.

Motif spacing: **100bp**								
Exon GC%	**30-40%**		**40-50%**		**50-60%**		**60-70%**	
Motif GC%	50	0	50	0	50	0	50	0
#Correlations	16	96	16	96	16	96	3	96
p(t-test)	1.31x10^{-2}(3.14x10^{-2})*		2.03x10^{-2}(4.64x10^{-2})*		4.54x10^{-1}(5.73x10^{-1})		1.06x10^{-4}(5.66x10^{-4})*	
p(Wilcoxon)	8.79x10^{-2}(1.62x10^{-1})		2.78x10^{-1}(3.92x10^{-1})		6.05x10^{-1}(6.92x10^{-1})		1.09x10^{-1}(1.87x10^{-1})	
Exon GC%	**30-40%**		**40-50%**		**50-60%**		**60-70%**	
Motif GC%	50	25	50	25	50	25	50	25
#Correlations	64	96	64	96	64	96	52	96
p(t-test)	1.31x10^{-1}(2.17x10^{-1})		4.58x10^{-2}(9.16x10^{-2})		4.51x10^{-2}(9.16x10^{-2})		5.57x10^{-1}(6.38x10^{-1})	
p(Wilcoxon)	8.09x10^{-2}(1.62x10^{-1})		1.73x10^{-2}(4.63x10^{-2})*		1.06x10^{-1}(1.87x10^{-1})		4.39x10^{-1}(5.40x10^{-1})	
Exon GC%	**30-40%**		**40-50%**		**50-60%**		**60-70%**	
Motif GC%	50	75	50	75	50	75	50	75
#Correlations	64	96	64	96	64	96	64	96
p(t-test)	3.23x10^{-1}(4.68x10^{-1})		6.12x10^{-3}(1.77x10^{-2})*		3.11x10^{-1}(4.67x10^{-1})		1.28x10^{-3}(4.65x10^{-3})*	
p(Wilcoxon)	1.45x10^{-1}(2.40x10^{-1})		3.46x10^{-2}(7.90x10^{-2})		3.99x10^{-1}(5.33x10^{-1})		3.26x10^{-3}(2.23x10^{-2})*	
Exon GC%	**30-40%**		**40-50%**		**50-60%**		**60-70%**	
Motif GC%	50	100	50	100	50	100	50	100
#Correlations	16	96	16	96	16	96	16	96
p(t-test)	5.91x10^{-4}(2.58x10^{-3})*		2.93x10^{-9}(7.03x10^{-8})*		1.84x10^{-6}(2.19x10^{-5})*		4.67E-11(2.24x10^{-9})*	
p(Wilcoxon)	1.51x10^{-2}(4.53x10^{-2})*		1.12x10^{-3}(1.80x10^{-2})*		1.31x10^{-2}(4.18x10^{-2})*		7.76x10^{-4}(1.80x10^{-2})*	

Table 2.3: T-test and Wilcoxon-test comparisons of Pearson correlations for motif-pairs at 100bp spacing for varying motif GC and mean exon GC content in Wild-type *D. melanogaster*. FDR corrected p-values in parenthesis, using a False positive rate of 5% ($\alpha = 0.05$). * suggests rejection of the null hypothesis.

Wild type *D. melanogaster* - motif-pair correlations at 10bp apart



(a) Motif GC content of 0%

(b) Motif GC content of 25%

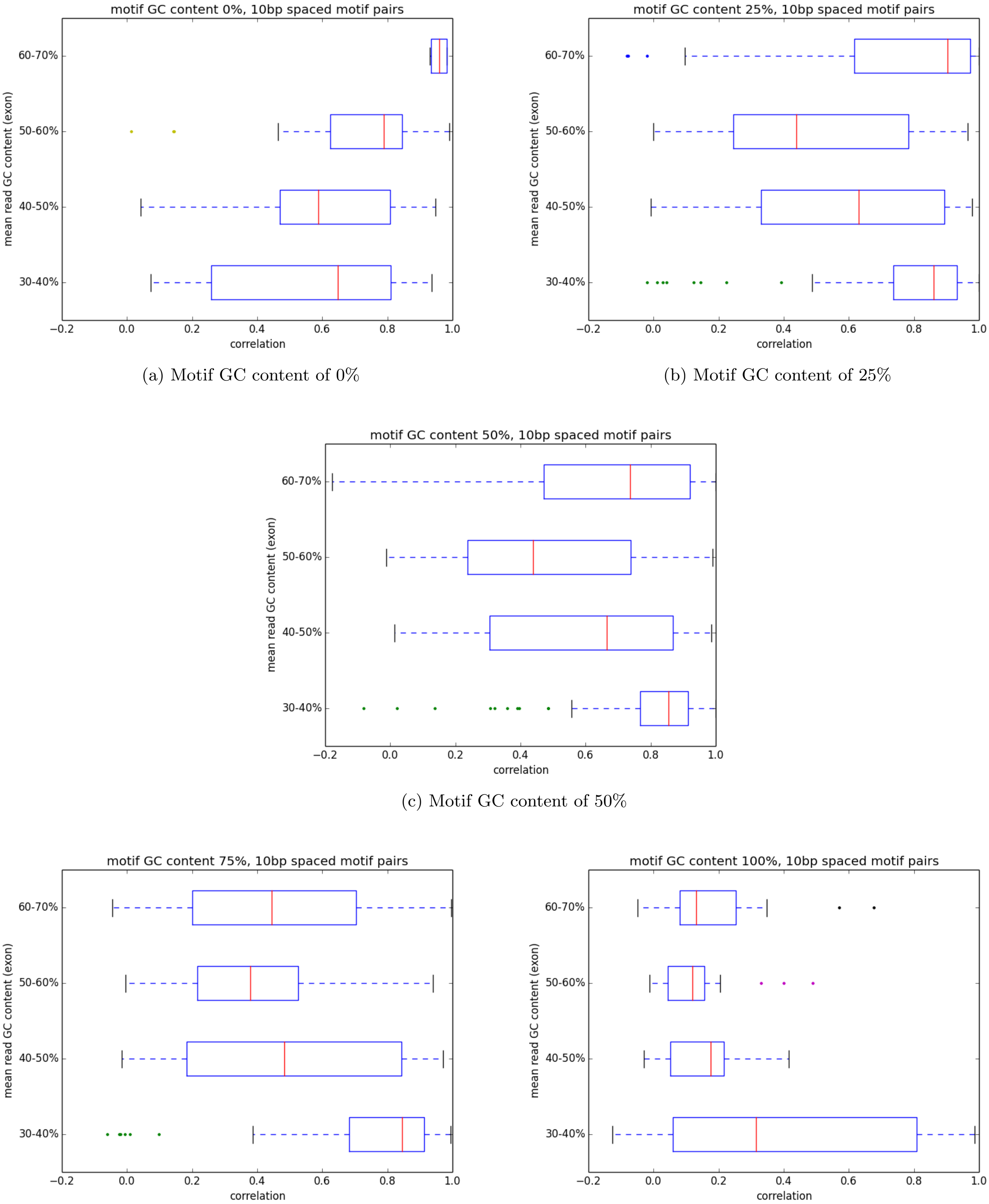
(c) Motif GC content of 50%

(d) Motif GC content of 75%

(e) Motif GC content of 100%

Figure 2.1: Box and whisker plots of motif-pair correlations at a distance of 10bp for Wild-type *D. melanogaster*

Wild type *D. melanogaster* - motif pair correlations at 10bp apart (excluding hexamer primers)



(a) Motif GC content of 0%

(b) Motif GC content of 25%

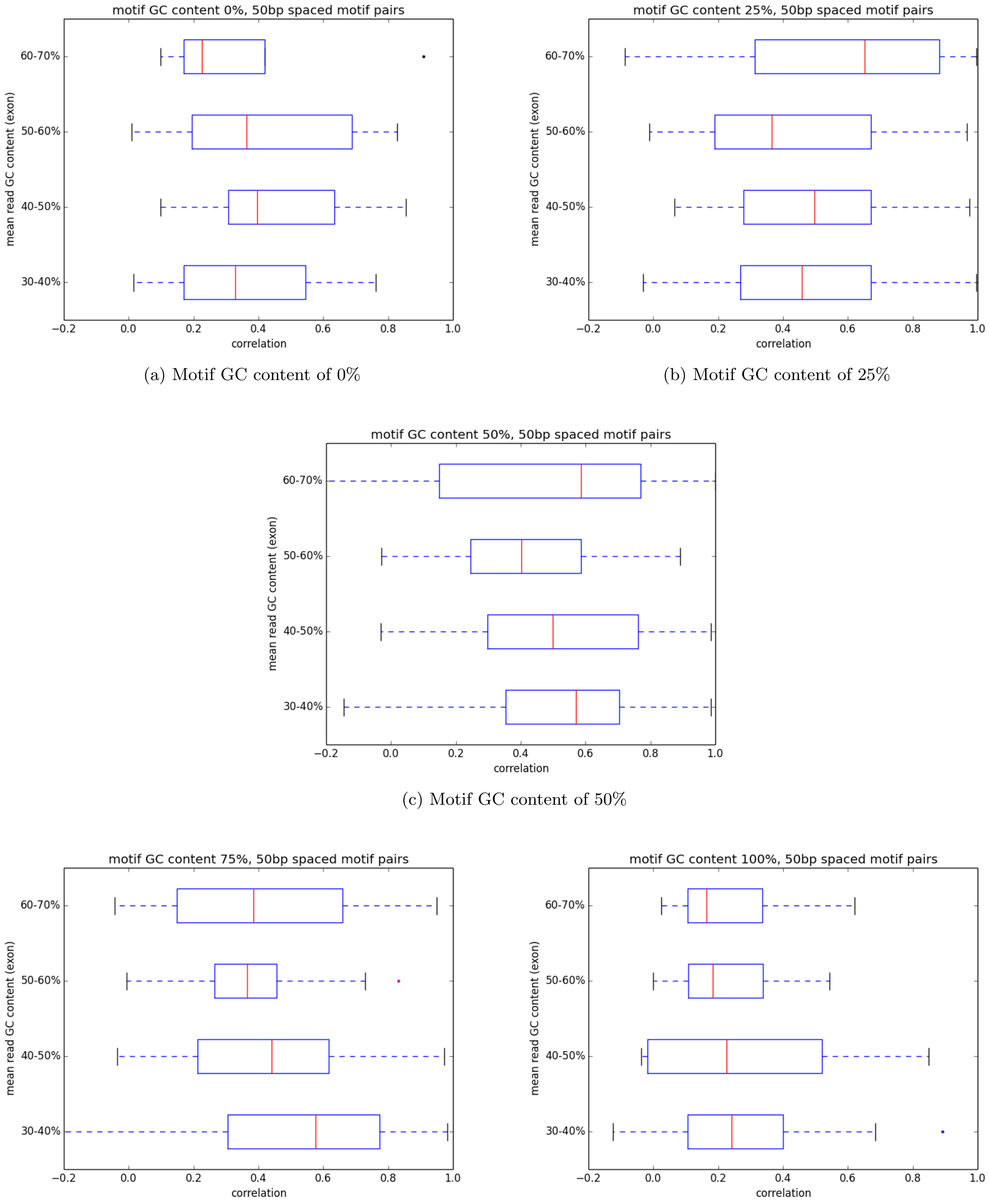
(c) Motif GC content of 50%

(d) Motif GC content of 75%

(e) Motif GC content of 100%

Figure 2.2: Box and whisker plots of motif pair correlations at a distance of 10bp for Wild-type *D. melanogaster* (Excluding hexamer regions)

Wild type *D. melanogaster* - motif-pair correlations at 50bp apart



(a) Motif GC content of 0%

(b) Motif GC content of 25%

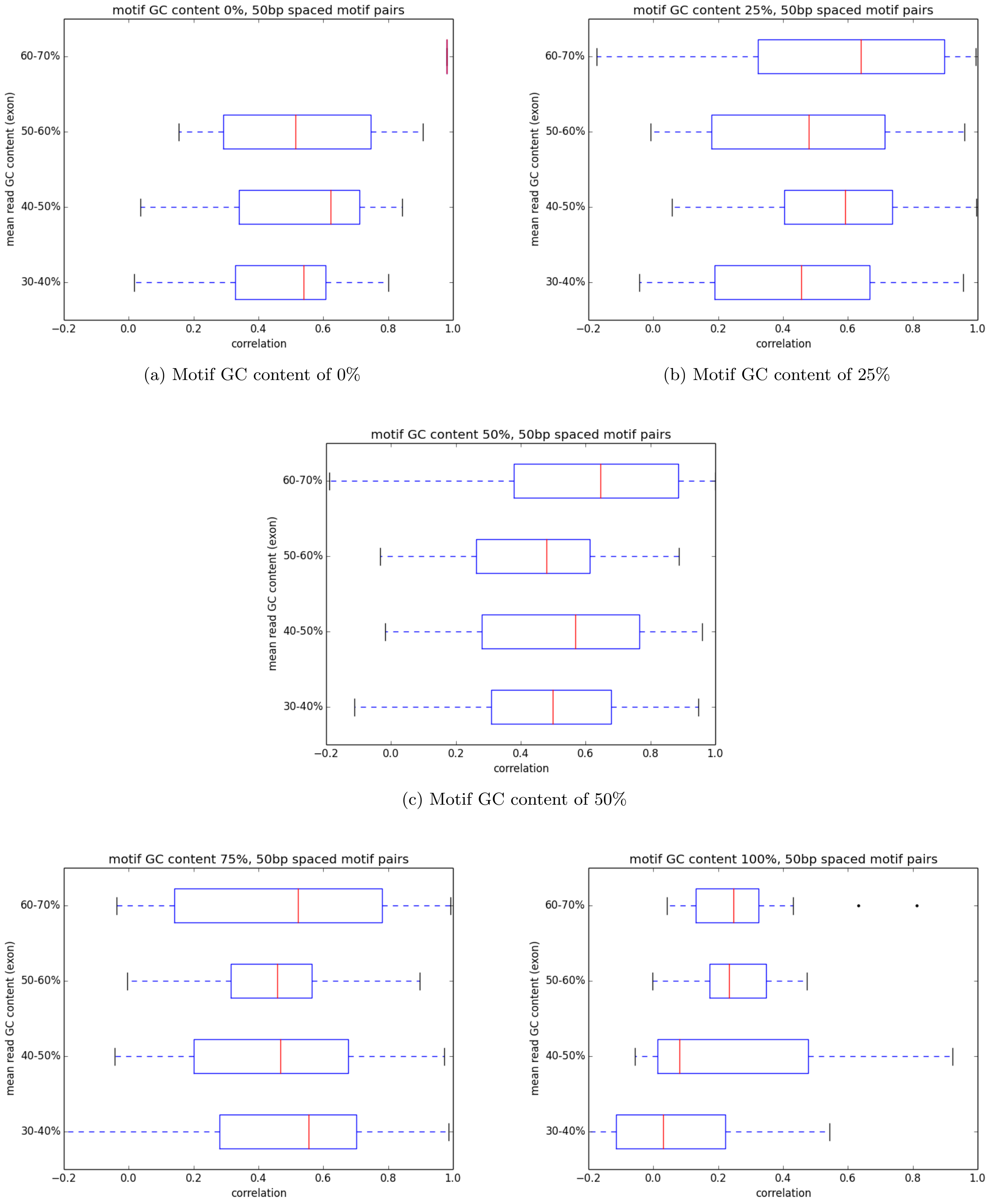
(c) Motif GC content of 50%

(d) Motif GC content of 75%

(e) Motif GC content of 100%

Figure 2.3: Box and whisker plots of motif-pair correlations at a distance of 50bp for Wild-type *D. melanogaster*

Wild type *D. melanogaster* - motif pair correlations at 50bp apart (excluding hexamer primers)



(a) Motif GC content of 0%

(b) Motif GC content of 25%

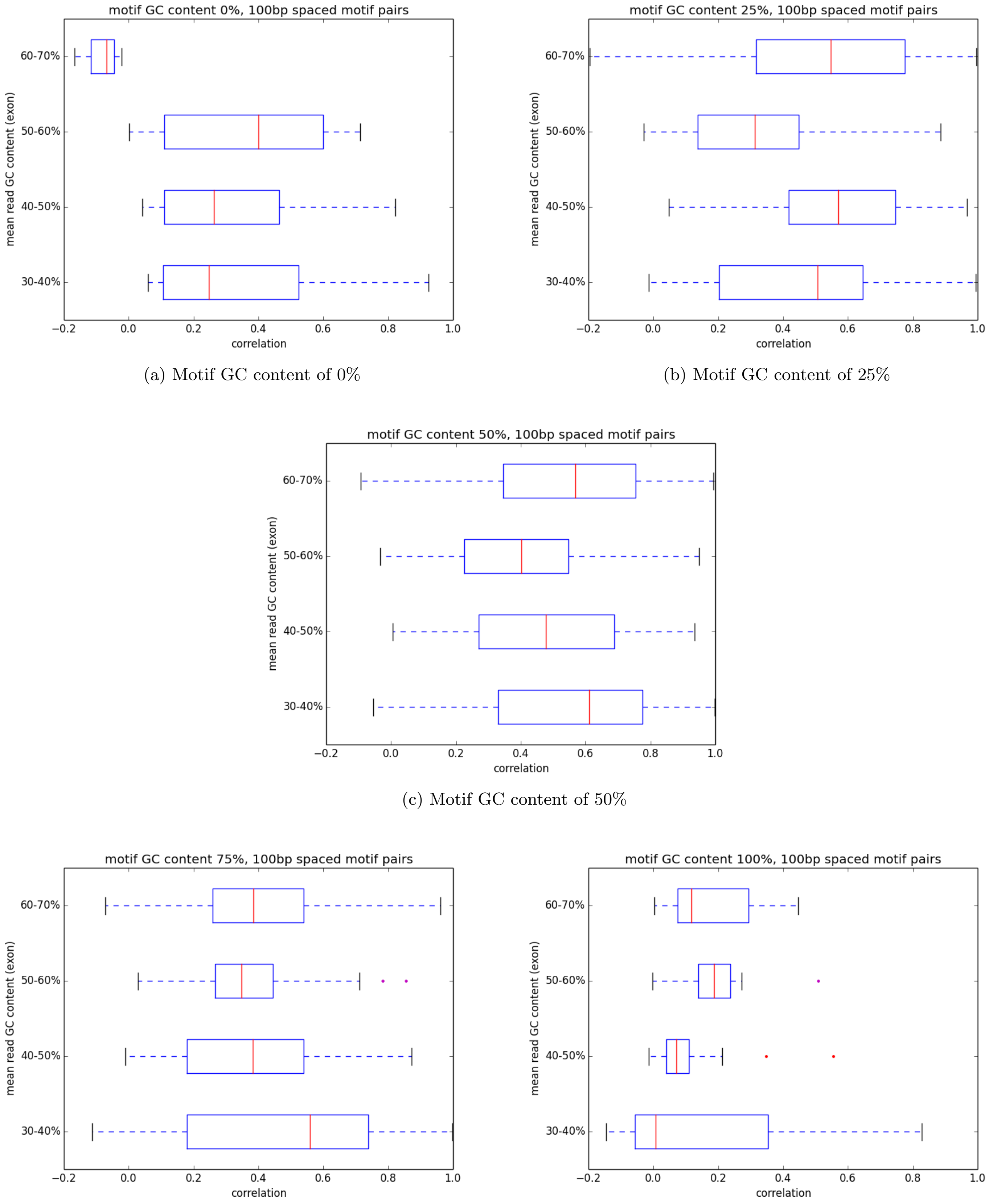
(c) Motif GC content of 50%

(d) Motif GC content of 75%

(e) Motif GC content of 100%

Figure 2.4: Box and whisker plots of motif pair correlations at a distance of 50bp for Wild-type *D. melanogaster* (Excluding hexamer regions)

Wild type *D. melanogaster* - motif-pair correlations at 100bp apart



(a) Motif GC content of 0%

(b) Motif GC content of 25%

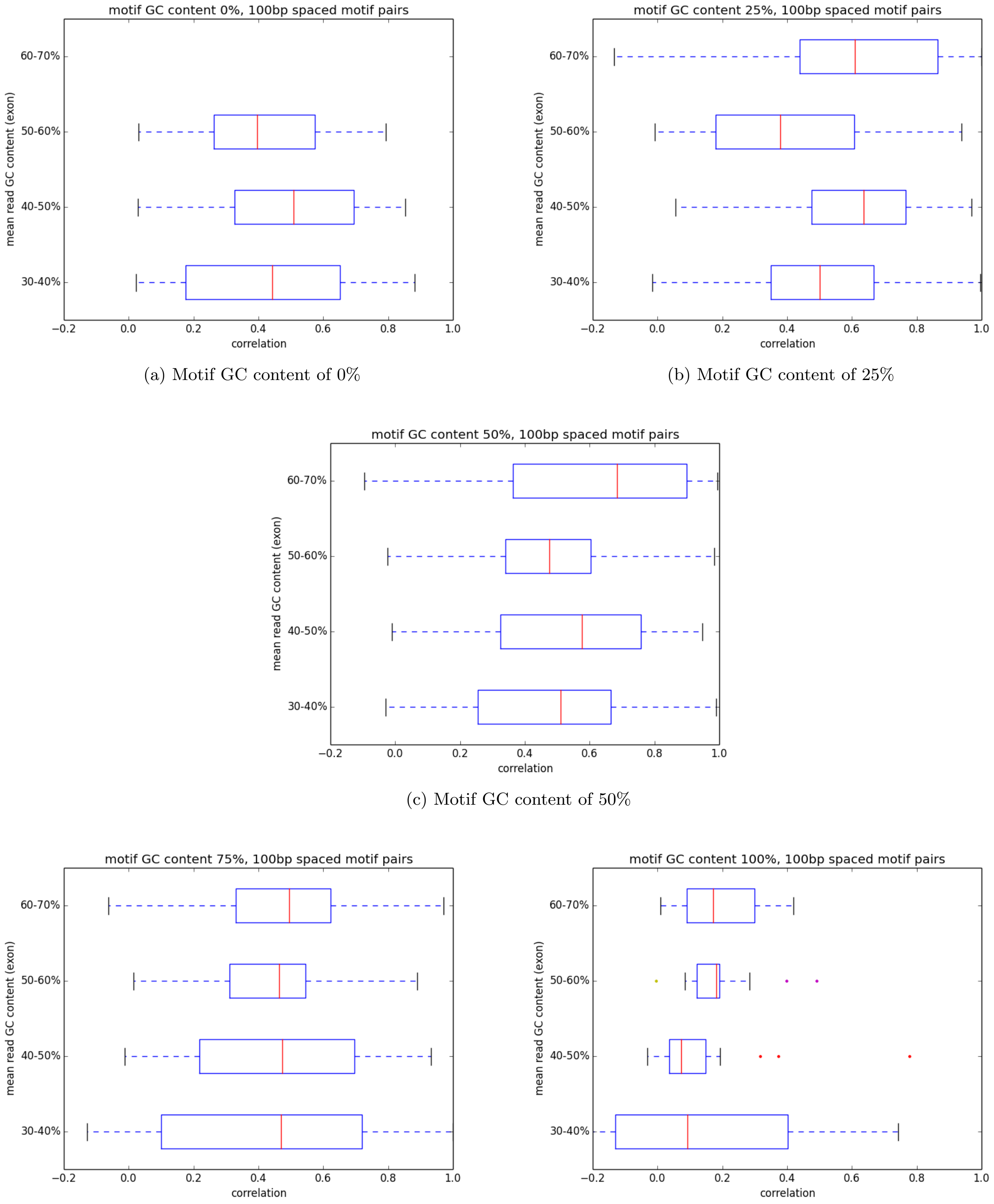
(c) Motif GC content of 50%

(d) Motif GC content of 75%

(e) Motif GC content of 100%

Figure 2.5: Box and whisker plots of motif-pair correlations at a distance of 100bp for Wild-type *D. melanogaster*.

Wild type *D. melanogaster* - motif pair correlations at 100bp apart (excluding hexamer primers)



(a) Motif GC content of 0%

(b) Motif GC content of 25%

(c) Motif GC content of 50%

(d) Motif GC content of 75%

(e) Motif GC content of 100%

Figure 2.6: Box and whisker plots of motif pair correlations at a distance of 100bp for Wild-type *D. melanogaster* (Excluding hexamer regions)

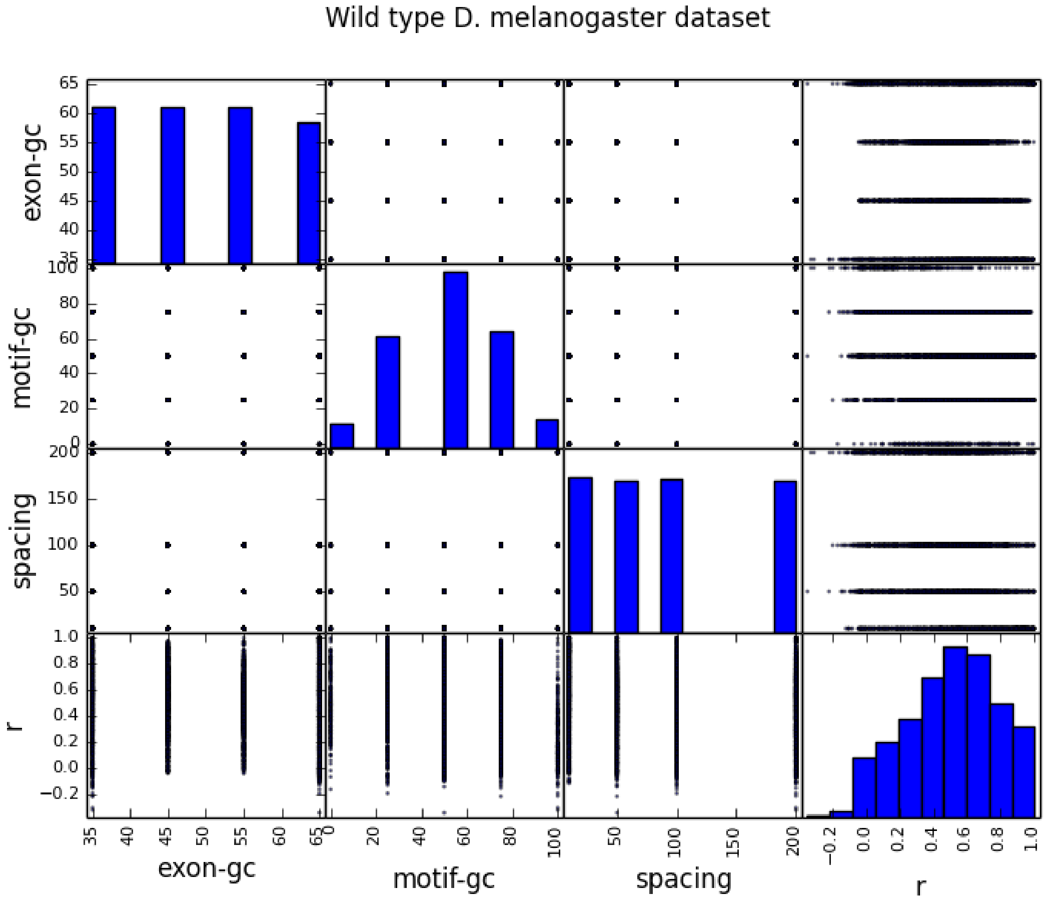


Figure 2.7: Scatter-matrix plot of correlation as a function of *4-mer* motif and exon GC content in wild type *D. melanogaster*.

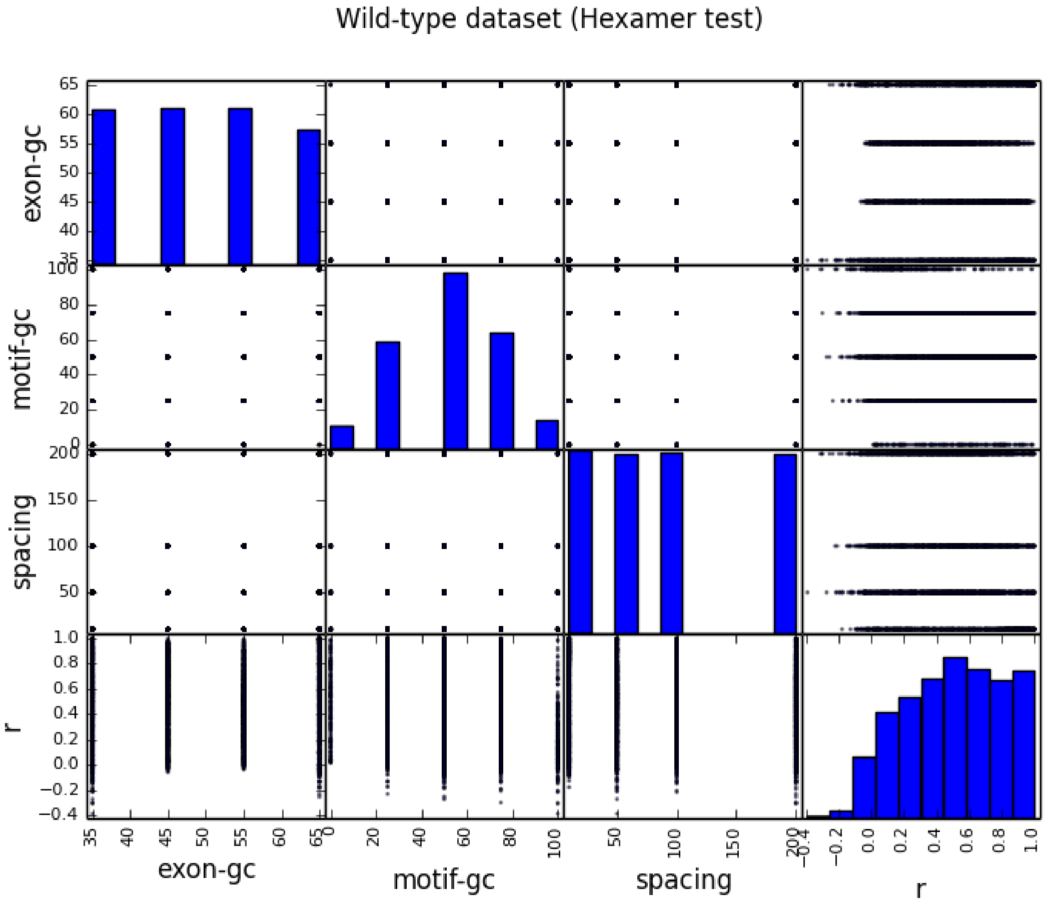


Figure 2.8: Scatter-matrix plot of correlation as a function of *4-mer* motif and exon GC content in wild type *D. melanogaster*. Random hexamer priming region has been excluded.

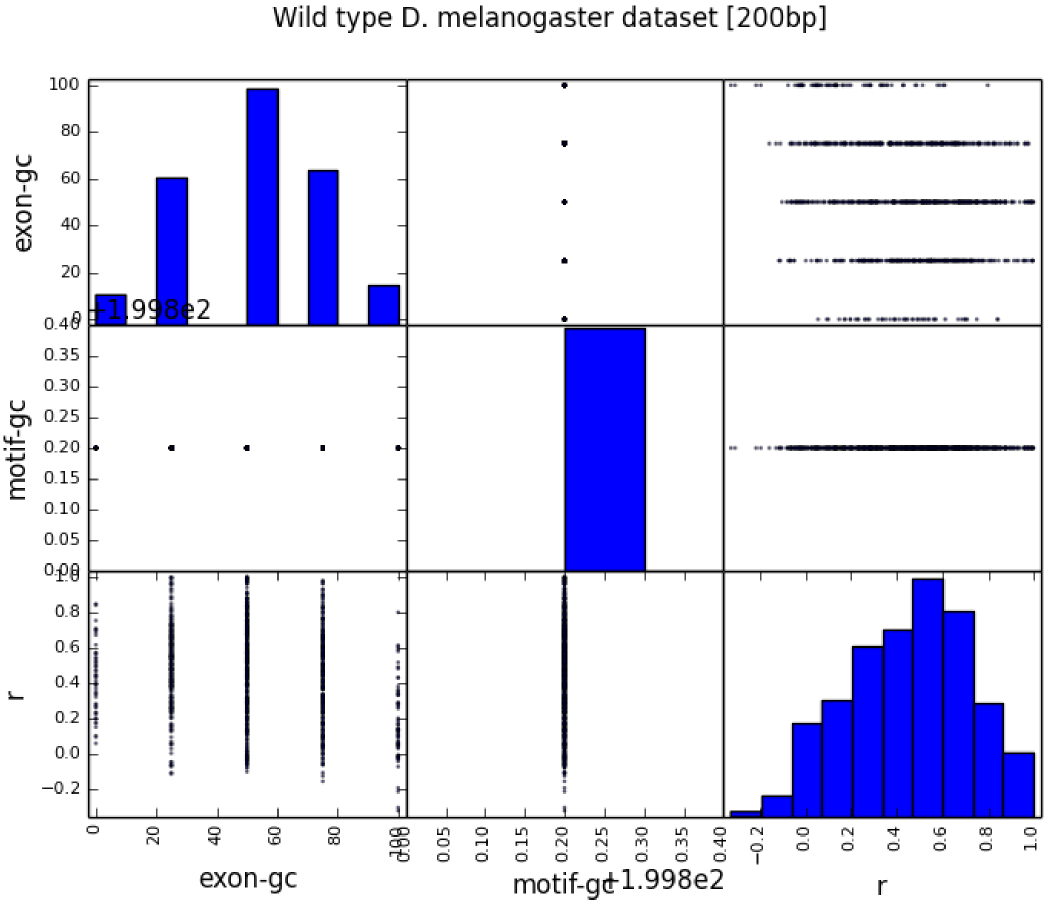


Figure 2.9: Scatter-matrix plot of correlation as a function of *4-mer* motif and exon GC content in wild type *D. melanogaster* at a motif-pair spacing of 200bp.

2.2 Mutant-r2-type *D. melanogaster* results

Motif spacing: **10bp**								
Exon GC%	**30-40%**		**40-50%**		**50-60%**		**60-70%**	
Motif GC%	50	0	50	0	50	0	50	0
#Correlations	16	96	16	96	16	96	16	96
p(t-test)	$2.15\text{x}10^{-3}(1.15\text{x}10^{-2})$*		$3.94\text{x}10^{-1}(5.25\text{x}10^{-1})$		$2.02\text{x}10^{-1}(3.90\text{x}10^{-1})$		$9.55\text{x}10^{-1}(9.55\text{x}10^{-1})$	
p(Wilcoxon)	$6.05\text{x}10^{-1}(6.45\text{x}10^{-1})$		$5.69\text{x}10^{-1}(6.45\text{x}10^{-1})$		$3.26\text{x}10^{-1}(4.74\text{x}10^{-1})$		$1.48\text{x}10^{-1}(3.38\text{x}10^{-1})$	
Exon GC%	**30-40%**		**40-50%**		**50-60%**		**60-70%**	
Motif GC%	50	25	50	25	50	25	50	25
#Correlations	64	96	64	96	64	96	64	96
p(t-test)	$2.19\text{x}10^{-1}(3.90\text{x}10^{-1})$		$9.51\text{x}10^{-1}(9.55\text{x}10^{-1})$		$5.28\text{x}10^{-2}(1.41\text{x}10^{-1})$		$2.93\text{x}10^{-1}(4.69\text{x}10^{-1})$	
p(Wilcoxon)	$3.09\text{x}10^{-1}(4.74\text{x}10^{-1})$		$5.74\text{x}10^{-1}(6.45\text{x}10^{-1})$		$5.25\text{x}10^{-2}(1.88\text{x}10^{-1})$		$2.83\text{x}10^{-2}(1.51\text{x}10^{-1})$	
Exon GC%	**30-40%**		**40-50%**		**50-60%**		**60-70%**	
Motif GC%	50	75	50	75	50	75	50	75
#Correlations	64	96	64	96	64	96	64	96
p(t-test)	$3.26\text{x}10^{-1}(4.75\text{x}10^{-1})$		$8.44\text{x}10^{-1}(9.55\text{x}10^{-1})$		$4.35\text{x}10^{-3}(1.39\text{x}10^{-2})$*		$4.50\text{x}10^{-1}(5.54\text{x}10^{-1})$	
p(Wilcoxon)	$2.47\text{x}10^{-1}(4.40\text{x}10^{-1})$		$5.43\text{x}10^{-1}(6.45\text{x}10^{-1})$		$6.11\text{x}10^{-3}(9.77\text{x}10^{-2})$		$9.15\text{x}10^{-1}(9.15\text{x}10^{-1})$	
Exon GC%	**30-40%**		**40-50%**		**50-60%**		**60-70%**	
Motif GC%	50	100	50	100	50	100	50	100
#Correlations	16	96	16	96	16	96	16	96
p(t-test)	$1.06\text{x}10^{-5}(1.69\text{x}10^{-4})$*		$3.16\text{x}10^{-3}(1.26\text{x}10^{-2})$*		$7.19\text{x}10^{-4}(5.75\text{x}10^{-3})$*		$6.88\text{x}10^{-2}(1.57\text{x}10^{-1})$	
p(Wilcoxon)	$2.62\text{x}10^{-2}(1.51\text{x}10^{-1})$		$7.03\text{x}10^{-2}(1.88\text{x}10^{-1})$		$6.27\text{x}10^{-2}(1.88\text{x}10^{-1})$		$1.79\text{x}10^{-1}(3.58\text{x}10^{-1})$	

Table 2.4: T-test and Wilcoxon-test comparisons of Pearson correlations for motif-pairs at 10bp spacing for varying motif GC and mean exon GC content in Mutant-r2 type *D. melanogaster*. FDR corrected p-values in parenthesis, using a False positive rate of 5% ($\alpha = 0.05$). * suggests rejection of the null hypothesis.

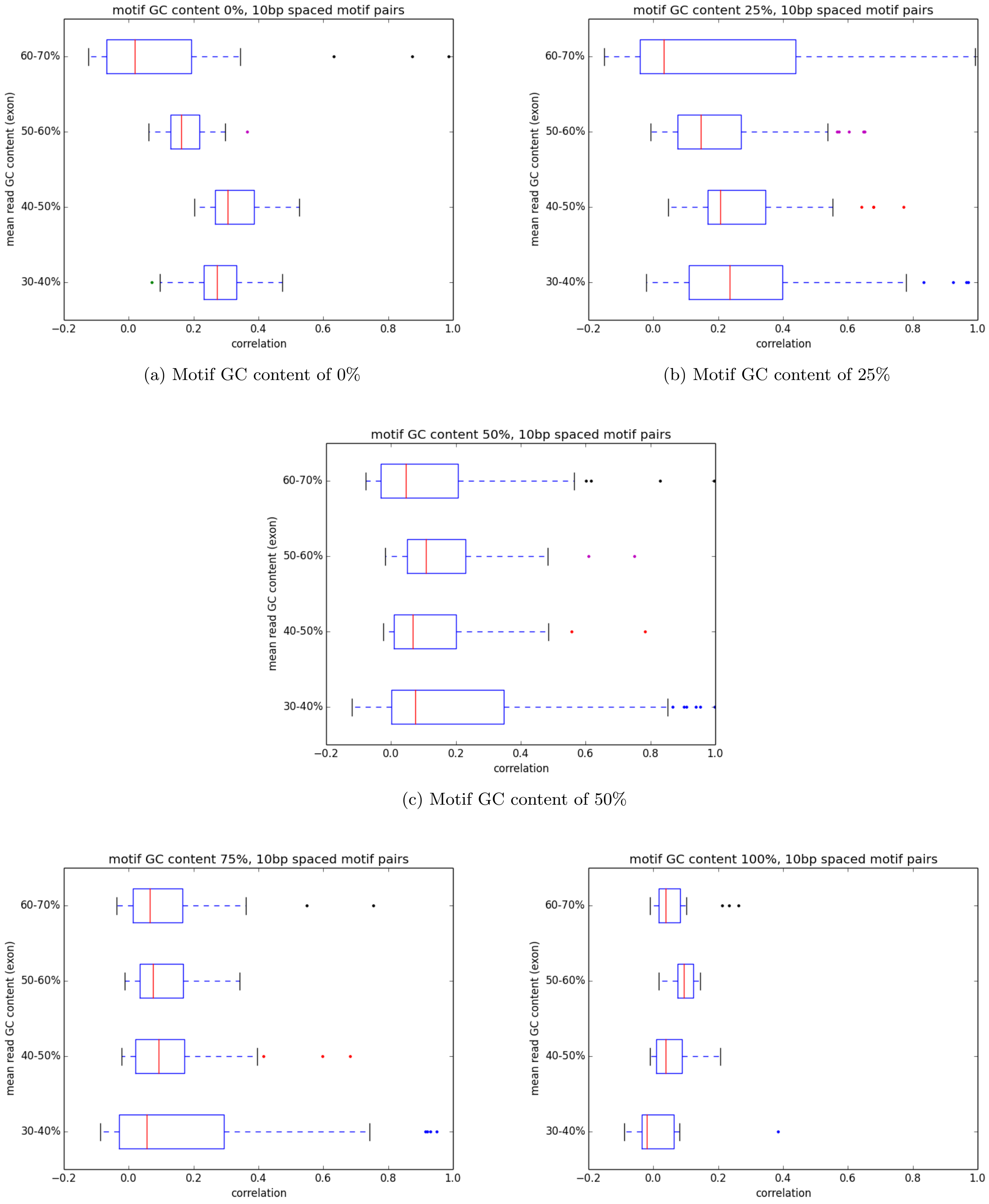
Motif spacing: **50bp**								
Exon GC%	**30-40%**		**40-50%**		**50-60%**		**60-70%**	
Motif GC%	50	0	50	0	50	0	50	0
#Correlations	16	96	16	96	16	96	13	96
p(t-test)	9.09x10^{-1}(9.65x10^{-1})		8.87x10^{-1}(9.65x10^{-1})		2.40x10^{-1}(4.53x10^{-1})		9.65x10^{-1}(9.65x10^{-1})	
p(Wilcoxon)	8.79x10^{-2}(3.13x10^{-1})		5.35x10^{-1}(7.35x10^{-1})		1.79x10^{-1}(4.09x10^{-1})		8.07x10^{-1}(8.61x10^{-1})	
Exon GC%	**30-40%**		**40-50%**		**50-60%**		**60-70%**	
Motif GC%	50	25	50	25	50	25	50	25
#Correlations	64	96	64	96	64	96	64	96
p(t-test)	2.31x10^{-1}(4.53x10^{-1})		7.02x10^{-1}(8.99x10^{-1})		2.30x10^{-1}(4.53x10^{-1})		2.62x10^{-3}(2.02x10^{-2})*	
p(Wilcoxon)	4.85x10^{-2}(2.80x10^{-1})		2.11x10^{-1}(4.40x10^{-1})		1.11x10^{-1}(3.57x10^{-1})		1.63x10^{-3}(5.23x10^{-2})	
Exon GC%	**30-40%**		**40-50%**		**50-60%**		**60-70%**	
Motif GC%	50	75	50	75	50	75	50	75
#Correlations	64	96	64	96	64	96	64	96
p(t-test)	8.67x10^{-1}(9.65x10^{-1})		6.63x10^{-1}(8.85x10^{-1})		2.96x10^{-1}(4.99x10^{-1})		1.24x10^{-1}(3.98x10^{-1})	
p(Wilcoxon)	5.47x10^{-1}(7.35x10^{-1})		7.99x10^{-1}(8.61x10^{-1})		6.78x10^{-1}(7.75x10^{-1})		2.34x10^{-1}(4.40x10^{-1})	
Exon GC%	**30-40%**		**40-50%**		**50-60%**		**60-70%**	
Motif GC%	50	100	50	100	50	100	50	100
#Correlations	16	96	16	96	16	96	16	96
p(t-test)	4.76x10^{-2}(2.11x10^{-1})		6.06x10^{-1}(8.43x10^{-1})		1.42x10^{-1}(4.13x10^{-1})		2.07x10^{-1}(4.53x10^{-1})	
p(Wilcoxon)	6.42x10^{-1}(7.60x10^{-1})		9.59x10^{-1}(9.59x10^{-1})		1.63x10^{-1}(4.09x10^{-1})		2.34x10^{-1}(4.40x10^{-1})	

Table 2.5: T-test and Wilcoxon-test comparisons of Pearson correlations for motif-pairs at 50bp spacing for varying motif GC and mean exon GC content in Mutant-r2 type *D. melanogaster*. FDR corrected p-values in parenthesis, using a False positive rate of 5% ($\alpha = 0.05$). * suggests rejection of the null hypothesis.

Motif spacing: **100bp**								
Exon GC%	**30-40%**		**40-50%**		**50-60%**		**60-70%**	
Motif GC%	50	0	50	0	50	0	50	0
#Correlations	16	96	16	96	16	96	15	96
p(t-test)	7.05x10^{-1}(8.67x10^{-1})		1.84x10^{-1}(4.81x10^{-1})		4.86x10^{-1}(6.86x10^{-1})		2.26x10^{-1}(4.81x10^{-1})	
p(Wilcoxon)	7.56x10^{-1}(8.44x10^{-1})		1.63x10^{-1}(3.90x10^{-1})		4.69x10^{-1}(6.82x10^{-1})		1.06x10^{-2}(1.27x10^{-1})	
Exon GC%	**30-40%**		**40-50%**		**50-60%**		**60-70%**	
Motif GC%	50	25	50	25	50	25	50	25
#Correlations	64	96	64	96	64	96	64	96
p(t-test)	4.70x10^{-1}(6.86x10^{-1})		7.37x10^{-1}(8.85x10^{-1})		3.07x10^{-2}(1.47x10^{-1})		5.19x10^{-1}(7.12x10^{-1})	
p(Wilcoxon)	5.74x10^{-1}(7.07x10^{-1})		3.92x10^{-1}(6.07x10^{-1})		5.93x10^{-2}(2.73x10^{-1})		9.09x10^{-1}(9.34x10^{-1})	
Exon GC%	**30-40%**		**40-50%**		**50-60%**		**60-70%**	
Motif GC%	50	75	50	75	50	75	50	75
#Correlations	64	96	64	96	64	96	64	96
p(t-test)	2.98x10^{-1}(5.10x10^{-1})		5.60x10^{-3}(3.36x10^{-2})*		4.78x10^{-1}(6.86x10^{-1})		9.54x10^{-1}(9.65x10^{-1})	
p(Wilcoxon)	2.83x10^{-2}(1.94x10^{-1})		8.69x10^{-2}(3.01x10^{-1})		3.00x10^{-1}(5.12x10^{-1})		3.00x10^{-1}(5.12x10^{-1})	
Exon GC%	**30-40%**		**40-50%**		**50-60%**		**60-70%**	
Motif GC%	50	100	50	100	50	100	50	100
#Correlations	16	96	16	96	16	96	16	96
p(t-test)	8.31x10^{-3}(4.43x10^{-2})*		1.86x10^{-5}(4.47x10^{-4})*		2.92x10^{-1}(5.10x10^{-1})		1.10x10^{-1}(3.76x10^{-1})	
p(Wilcoxon)	1.09x10^{-1}(3.34x10^{-1})		4.46x10^{-3}(9.77x10^{-2})		4.69x10^{-1}(6.82x10^{-1})		1.63x10^{-1}(3.90x10^{-1})	

Table 2.6: T-test and Wilcoxon-test comparisons of Pearson correlations for motif-pairs at 100bp spacing for varying motif GC and mean exon GC content in Mutant-r2 type *D. melanogaster*. FDR corrected p-values in parenthesis, using a False positive rate of 5% ($\alpha = 0.05$). * suggests rejection of the null hypothesis.

Mutant-r2 type *D. melanogaster* - motif-pair correlations at 10bp apart



(a) Motif GC content of 0%

(b) Motif GC content of 25%

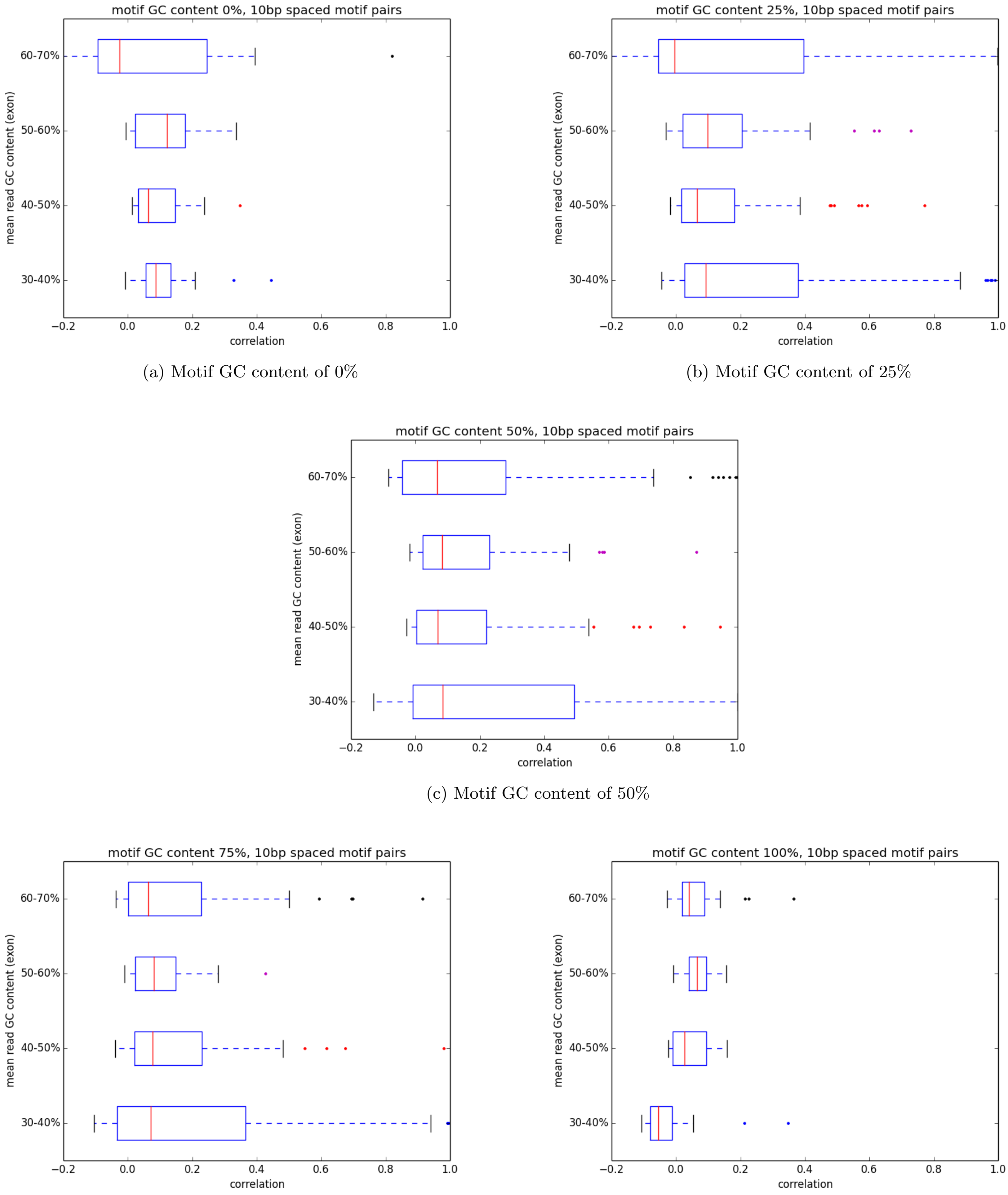
(c) Motif GC content of 50%

(d) Motif GC content of 75%

(e) Motif GC content of 100%

Figure 2.10: Box and whisker plots of motif-pair correlations at a distance of 10bp for Mutant-r2-type *D. melanogaster*

Mutant-r2 type *D. melanogaster* - motif pair correlations at 10bp apart (excluding hexamer primers)



(a) Motif GC content of 0%

(b) Motif GC content of 25%

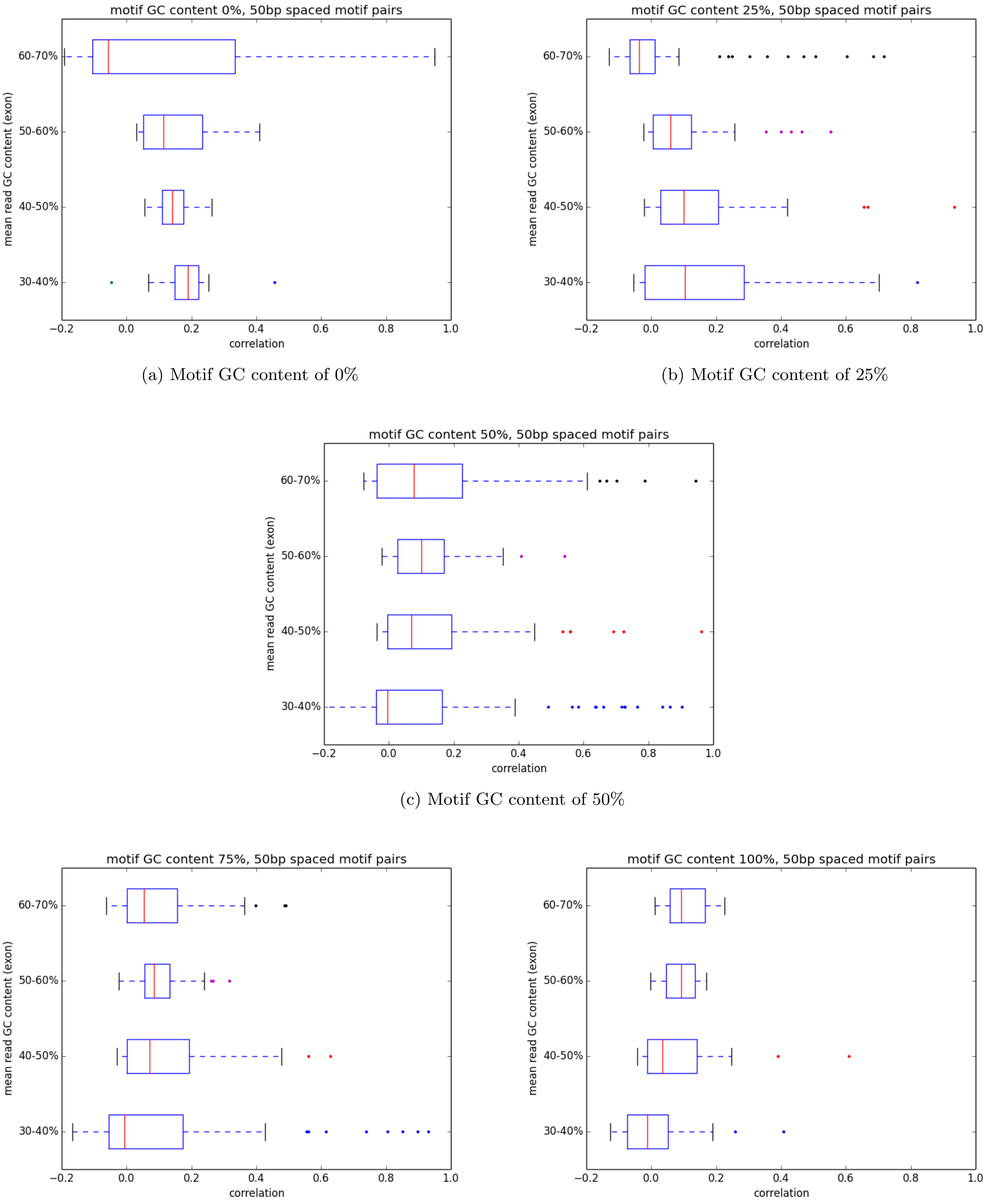
(c) Motif GC content of 50%

(d) Motif GC content of 75%

(e) Motif GC content of 100%

Figure 2.11: Box and whisker plots of motif pair correlations at a distance of 10bp for Mutant-r2-type *D. melanogaster* (Excluding hexamer regions)

Mutant-r2 type *D. melanogaster* - motif-pair correlations at 50bp apart



(a) Motif GC content of 0%

(b) Motif GC content of 25%

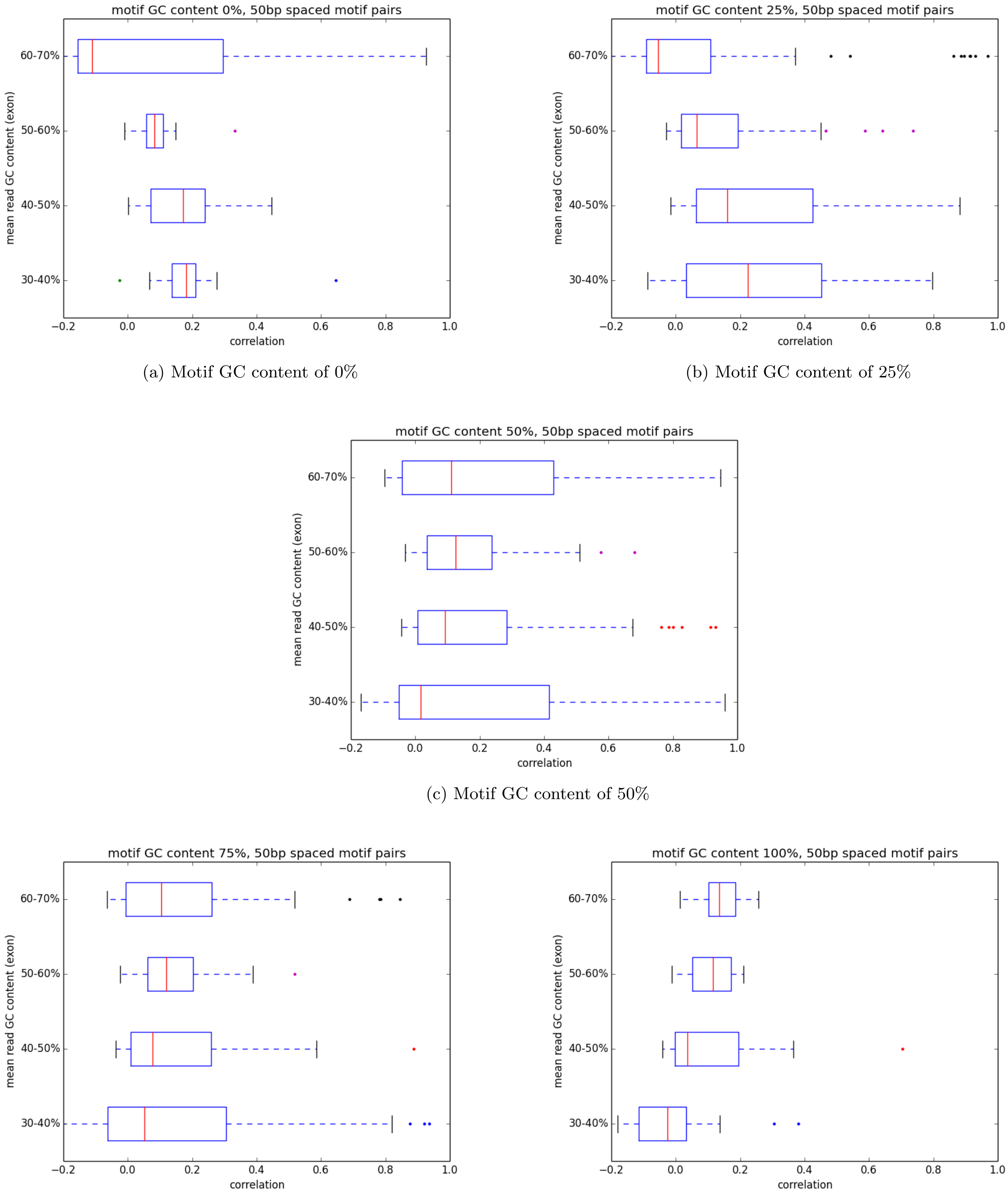
(c) Motif GC content of 50%

(d) Motif GC content of 75%

(e) Motif GC content of 100%

Figure 2.12: Box and whisker plots of motif-pair correlations at a distance of 50bp for Mutant-r2-type *D. melanogaster*

Mutant-r2 type *D. melanogaster* - motif pair correlations at 50bp apart (excluding hexamer primers)



(a) Motif GC content of 0%

(b) Motif GC content of 25%

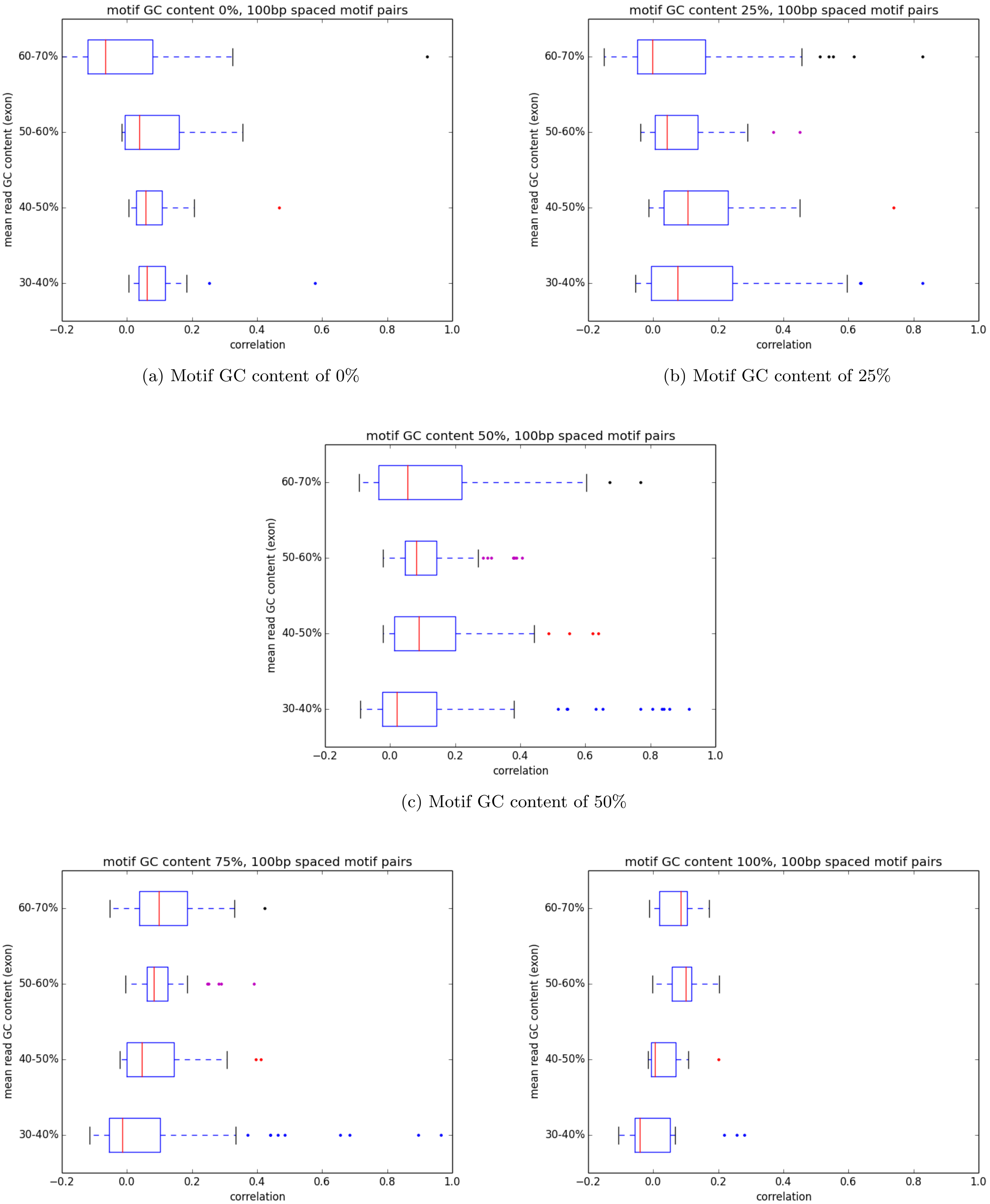
(c) Motif GC content of 50%

(d) Motif GC content of 75%

(e) Motif GC content of 100%

Figure 2.13: Box and whisker plots of motif pair correlations at a distance of 50bp for Mutant-r2-type *D. melanogaster* (Excluding hexamer regions)

Mutant-r2 type *D. melanogaster* - motif-pair correlations at 100bp apart



(a) Motif GC content of 0%

(b) Motif GC content of 25%

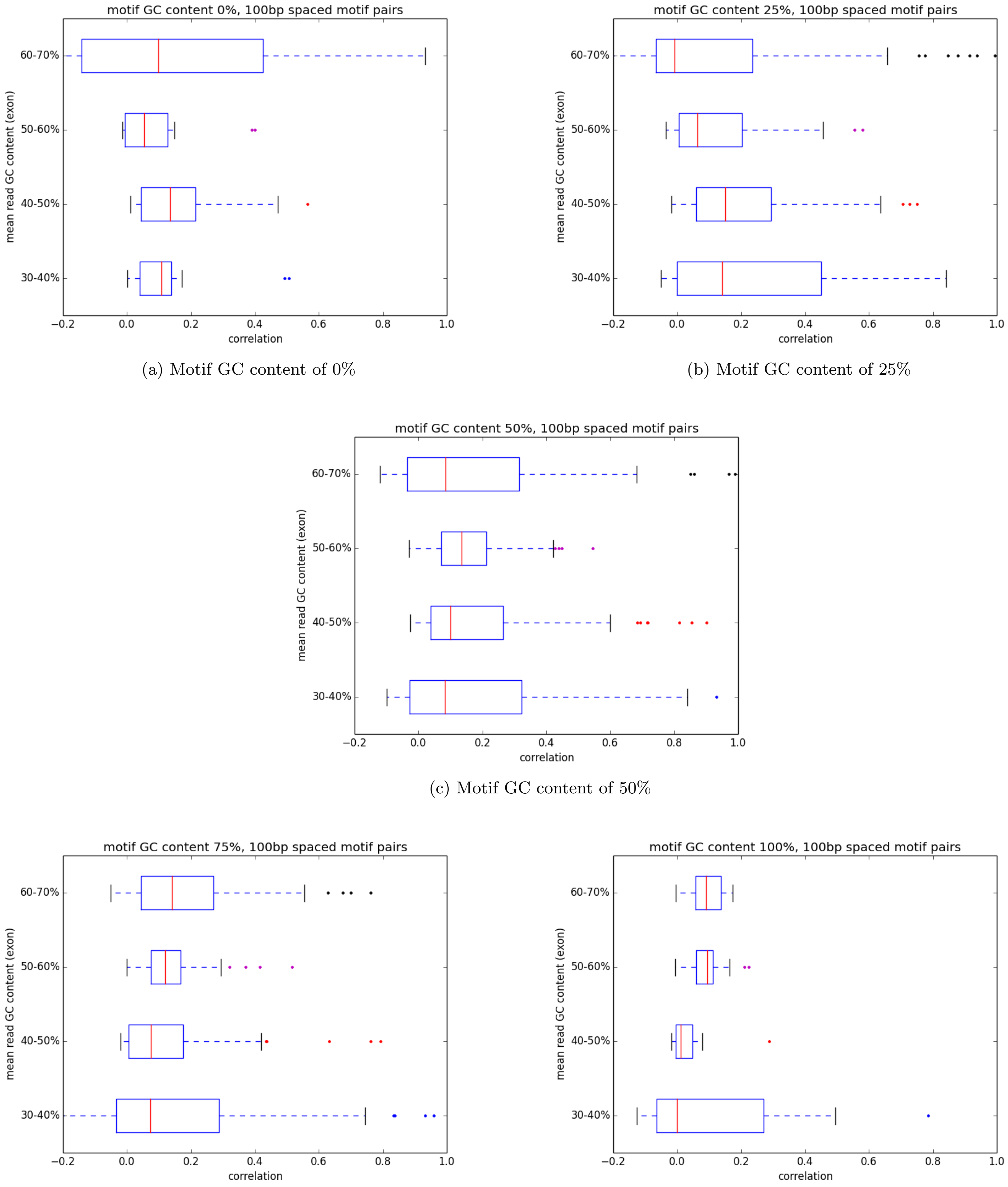
(c) Motif GC content of 50%

(d) Motif GC content of 75%

(e) Motif GC content of 100%

Figure 2.14: Box and whisker plots of motif-pair correlations at a distance of 100bp for Mutant-r2-type *D. melanogaster*.

Mutant-r2 type *D. melanogaster* - motif pair correlations at 100bp apart (excluding hexamer primers)



(a) Motif GC content of 0%

(b) Motif GC content of 25%

(c) Motif GC content of 50%

(d) Motif GC content of 75%

(e) Motif GC content of 100%

Figure 2.15: Box and whisker plots of motif pair correlations at a distance of 100bp for Mutant-r2-type *D. melanogaster* (Excluding hexamer regions)

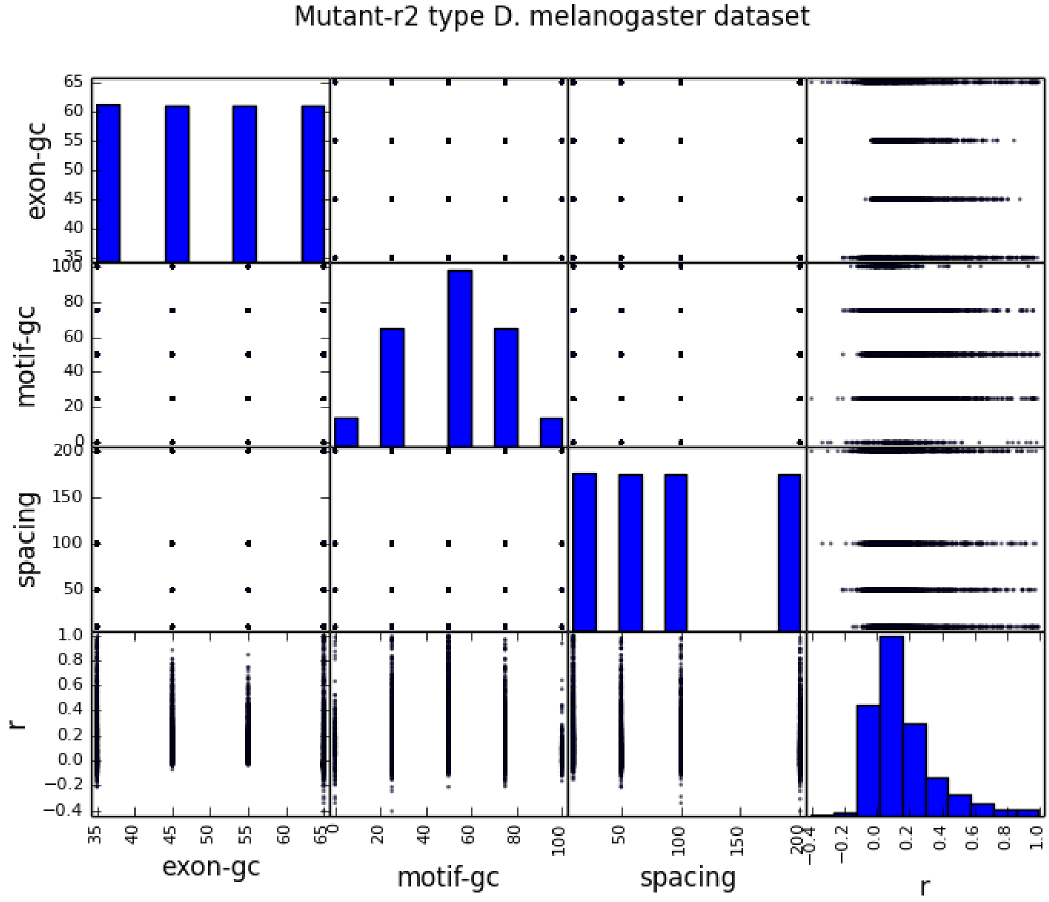


Figure 2.16: Scatter-matrix plot of correlation as a function of *4-mer* motif and exon GC content in mutant-r2 *D. melanogaster*.

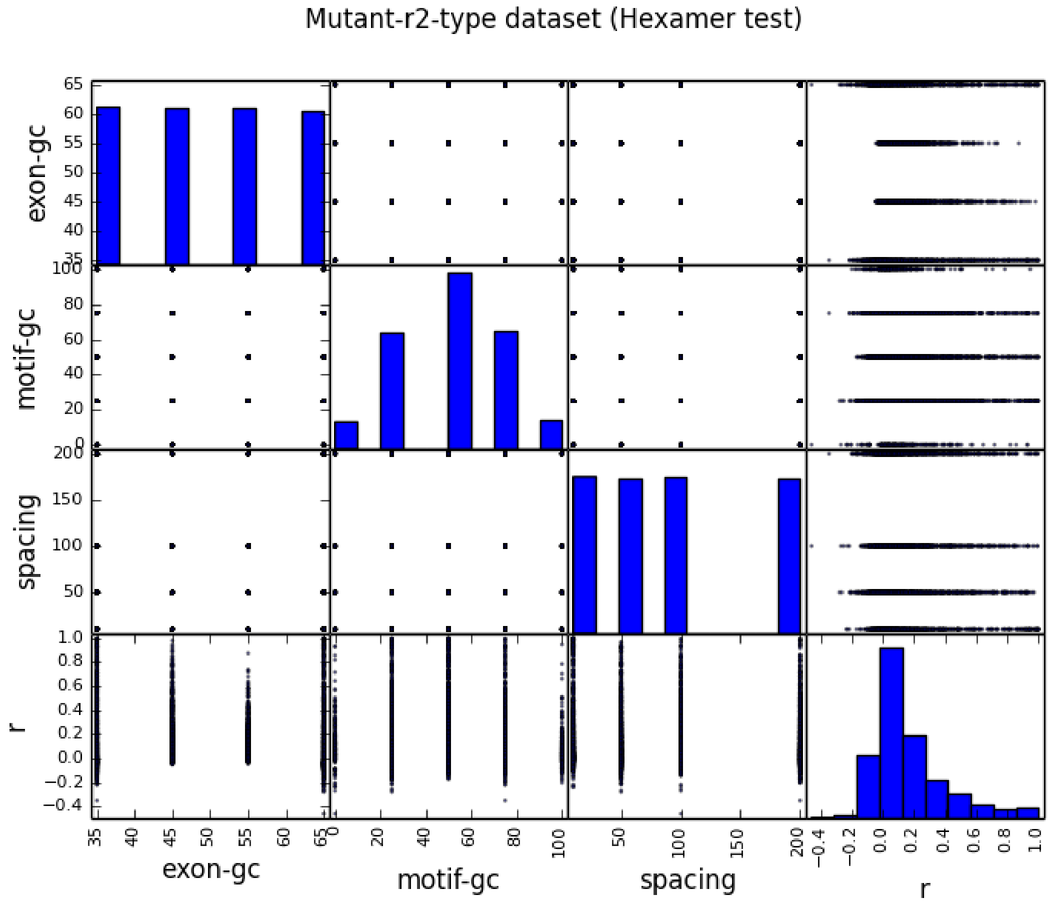


Figure 2.17: Scatter-matrix plot of correlation as a function of *4-mer* motif and exon GC content in mutant-r2 *D. melanogaster*. Random hexamer priming region has been excluded.

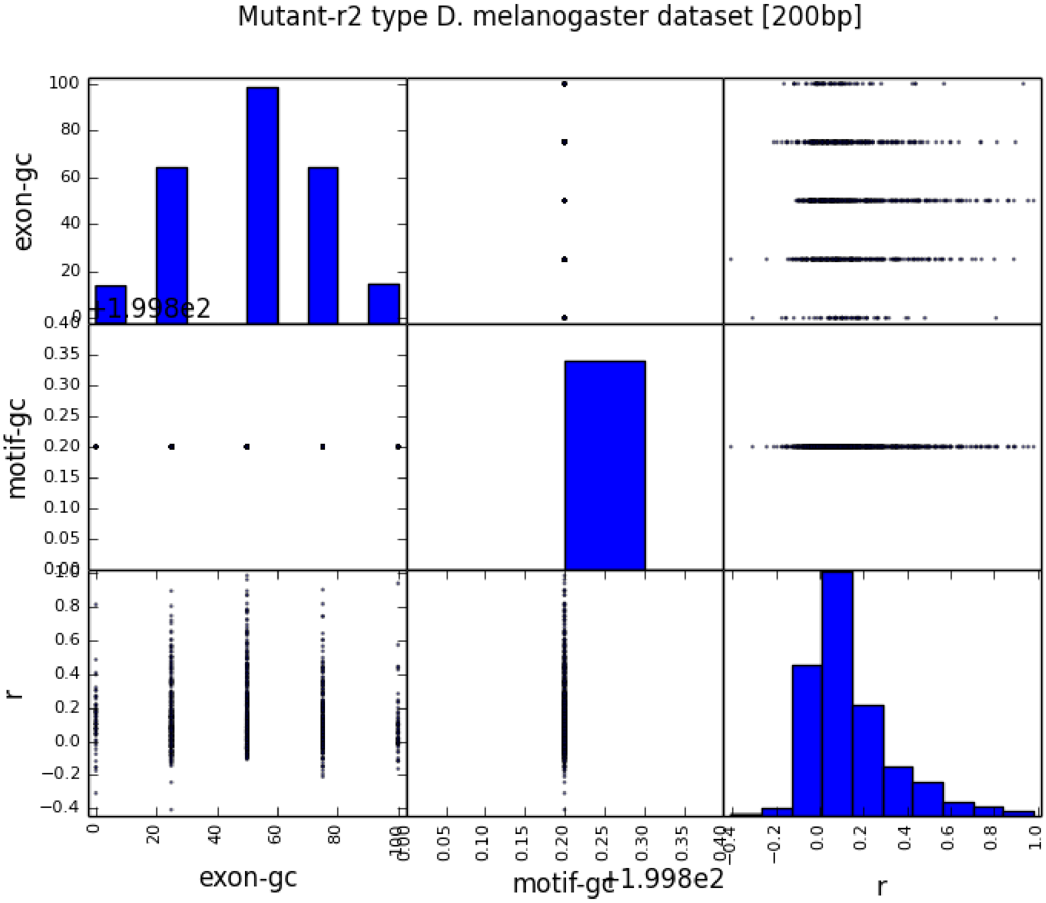


Figure 2.18: Scatter-matrix plot of correlation as a function of *4-mer* motif and exon GC content in mutant-r2 *D. melanogaster* at a motif-pair spacing of 200bp.