CONTENTS

SUPPLEMENTARY MATERIALS AND METHODS

Primers used for ChIP-qPCR

U6
GGCGCCAGTGCTCACTACTT
GGGCCATGCTAATCTTCTCTG
amplify - 87 to +61 from snRNA:U6:96Ac transcript start

InR
P1
CATTCAGTGTTTCACGCGAT
GGCAATTCACTGTGGCCTCT
amplify -38844 to -38720 relative to translational start
P3
GCCGCTGACAATTATTGTTGT
GCCCGTGATTCGTGTGAGTGA
amplify -9830 to - 9696
CDS
GCGATGATCGCTGGAAGGTT
GCGTTTGTCAATTCCGAGGAT
amplify +2979 to +3105

Akt
GCAAGGGCACCTTTGGTAAG
GTGGACTTGAGCACACGACTC
amplify +885 to +1029

Cat-Indy
GCTTAGCCTACCGCTATTTG
CTAGACTGAGAGAACTTAC
amplify 3' past Cat and in the 3' end of Indy
+17340 to +17219 relative to Indy start

TOR
ACGGATTCCTCGGACTTGGA
TTTGGCCTCTGTACCGAAGT
amplify from +4966 to + 5088

Su(Hw)
CACCCGCTCGTACCACTTGAA
TACTCCGGCTTTTTAACCACCTGT
amplify +1136 to +1304

Aldh-III
AAAATAATAATGGGTGTGGCTAAA
GCGAAACGGGGGAATAAT
amplify +7477 to 7665

CG14131/Pi3K68D
CAGGCCGTTCTTGTTGTTGG
ACGTGGCGGCGGTTGTT
amplify from +93 to + 263. This (as well as the whole CG14131) is within the Pi3K68D (Phosphotidylinositol 3 kinase 68D; CG11621) gene.

CPTI
ATCTTGTATCGGACGGGTAATGA
TGGGACAATGGGTGATAGGTG

from +1954 to +2057

4E-BP (Thor)
CGGCAATAACAACAAGAACCAG
CGCCTGATTATTCTGCTTGGTC
amplify -367 to -267

SUPPLEMENTARY FIGURES

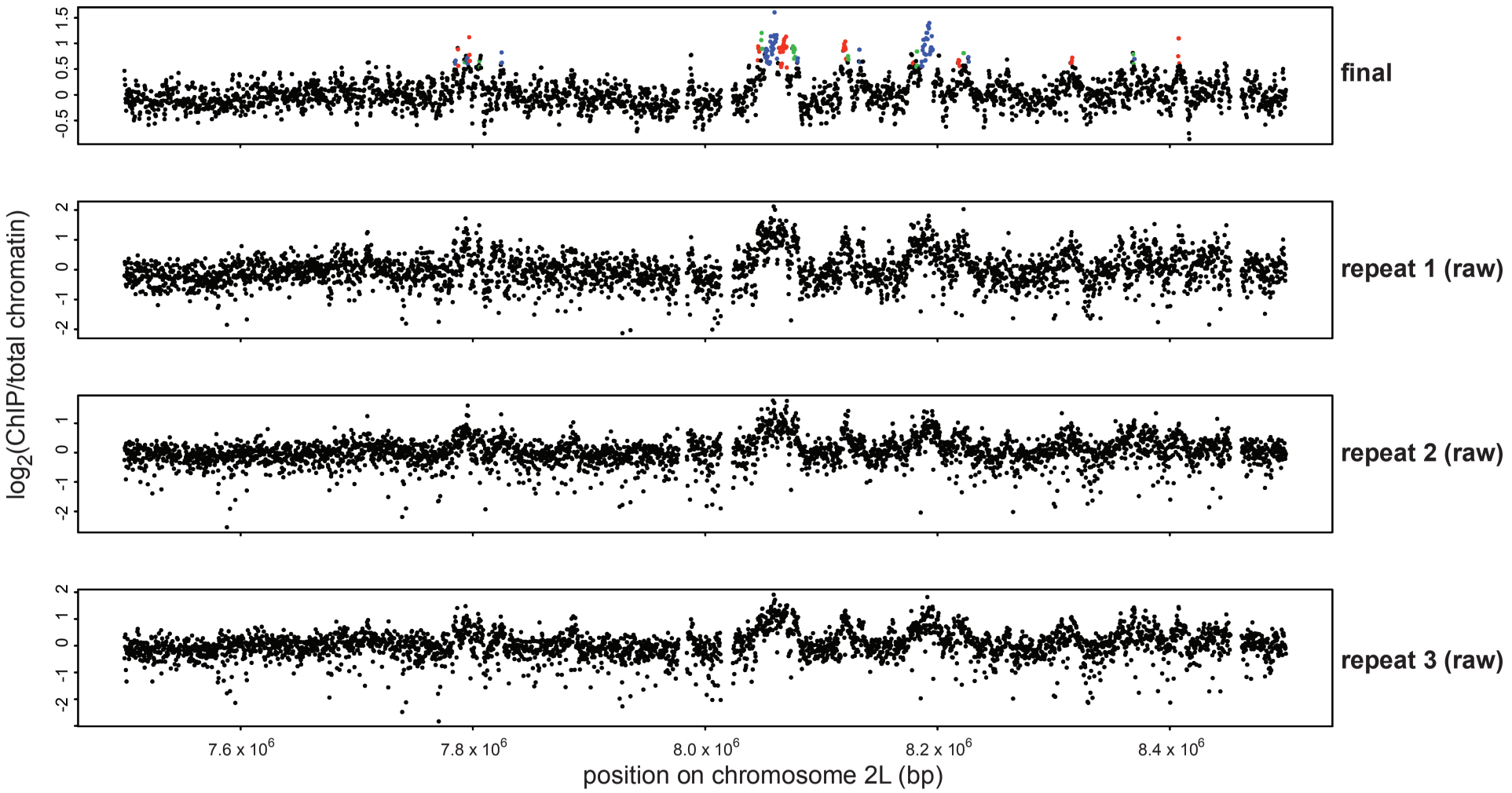
CAPTIONS

Supplementary Figure 1 Example of signal reproducibility in the three independent biological repeats of ChIP-chip on wild-type untreated females. The top panel shows the processed combined data with the peaks called indicated in colour, the lower three panels show raw (scaled log 2 Cy5/Cy3 ratios) data for the individual repeats.

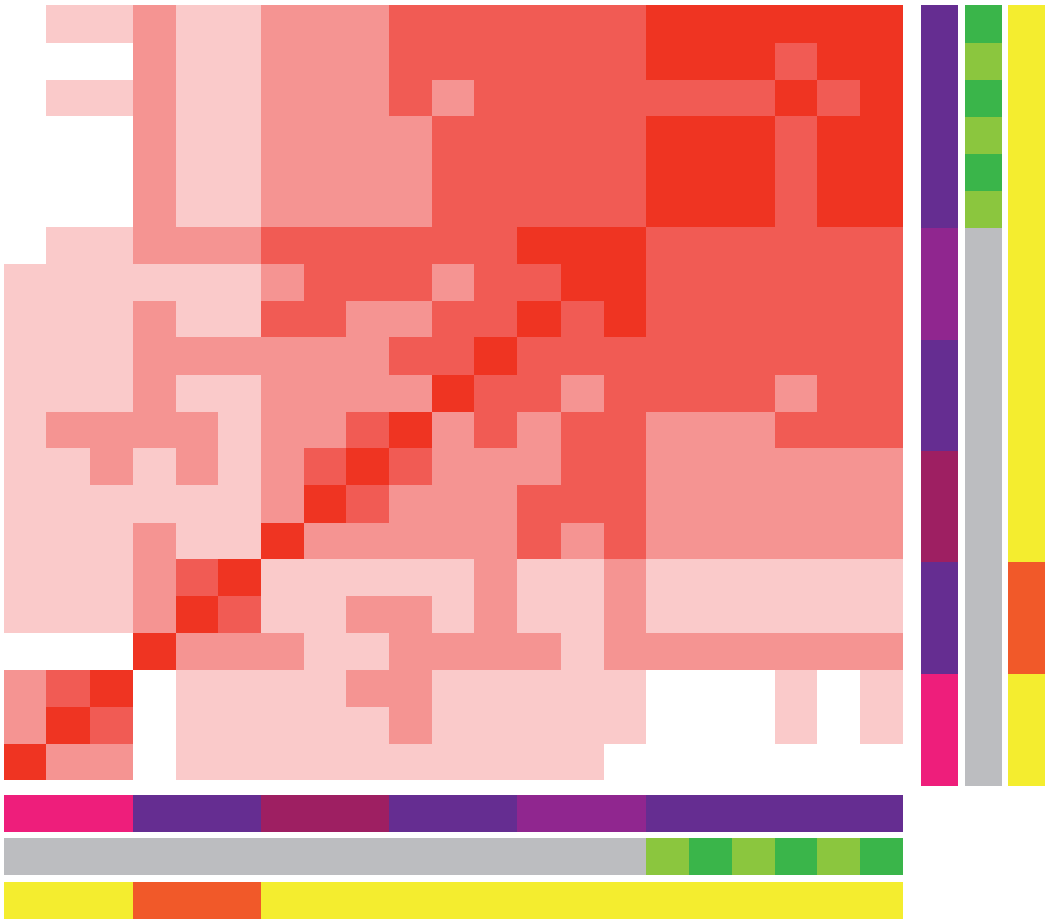
Supplementary Figure 2 Pearson correlation coefficients for all the ChIP-chip experiments. The raw scaled data for all ChIP-chip experiments were compared to each other and the Pearson correlation coefficients determined. The values of the Pearson correlation coefficients are indicated by the intensity of red (see scale). The experiments are coded in the legend. The mock-controls (IP with pre-immune serum on wild-type chromatin and anti-dFOXO IP on *dfoxo* null chromatin) are less similar to the experimental samples than the experimental samples are amongst themselves. Unstressed wild-type, stressed wild-type and *daGAL4>UAS-dInR*^{DN} samples are all highly similar.

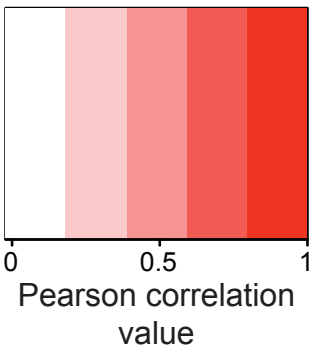
Supplemental Figure 3 Analysis of dFOXO distribution with respect to gene features on a genome-wide scale. Upstream/downstream refer to 1 kb from the 5'/3' UTR. Z-score represents the number of standard deviations each observation is from the mean of the distribution of 10^3 random peak sets, of identical size, length and chromosomal distribution. dFOXO bound regions are over-represented in genic regions, and tend to localise to the 3'-end of genes ($p<10^{-15}$), are not enriched in 5' UTR, and are under-represented in 5' upstream region ($p=1.5x10^{-4}$).

Supplementary Figure 1



Supplementary Figure 2



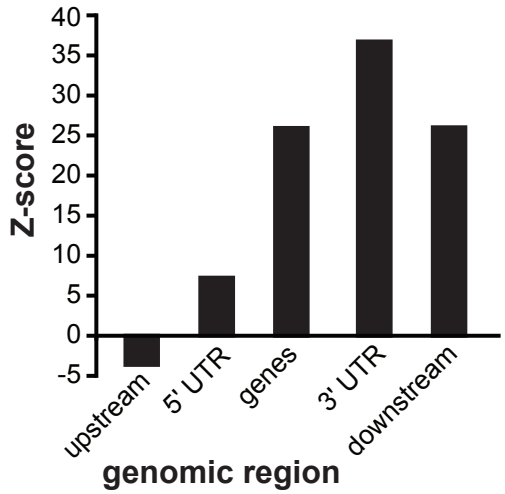


genotype
- *foxoΔ/foxoΔ*
- wt
- *daG4*
- *daG4>UAS-InR^{DN}*

condition
- standard
- paraquat
- starvation

antibody
- anti-dFOXO
- preimmune serum

Supplementary Figure 3



SUPPLEMENTARY TABLES

Supplementary Table 1 *De novo* motif identification from peaks (MEME)

Motif consensus	p
GCTGCTGCTG	$1.3x10^{-27}$
CTGCTGCTGC	$1.2x10^{-14}$
CTCCTCCTCC	$1.3x10^{-15}$
C[T/A]CCGCCGCC	$5.1x10^{-13}$
CAGC[A/T]CTGC	$1.9x10^{-8}$

Supplementary Table 2 Overlap in dFOXO binding locations under standard conditions, compared to those under stress and dFOXO binding locations in *daGAL4 UAS-InR^{DN}* flies compared to *daGAL4* controls. For each comparison the overlap is given per set. The counts of peak overlaps suggest that there are unique peaks between the sets, however visual inspection of 'unique' treatment peaks in the control data shows in the great majority of cases that a peak of smaller magnitude exists at a level below the peak-calling threshold. For Pearson correlations amongst these experiments see Supplemental Figure 2.

Comparison	**Peak set**	**Total peaks that directly overlap other peak set**	**Total peaks in set**
Untreated vs Paraquat	Untreated	1017	1423
	Paraquat	957	1439
Untreated vs Starvation	Untreated	1098	1423
	Starvation	1078	1528
daGAL4 vs *daGAL4 UAS-InR^{DN}*	*daGAL4*	993	1455
	daGAL4 UAS-InR^{DN}	1076	1643