Normalization Protocol for Sørensen *et al.*

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Data Acquisition

Data were downloaded from Gene Expression Omnibus (GEO) as raw Affymetrix .CEL files under the accession id, GSE5147:
http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE5147

All data are referenced in:
> Sørensen JG, Nielsen MM, Kruhøffer M, Justesen J et al. *Full genome gene expression analysis of the heat stress response in Drosophila melanogaster.* Cell Stress Chaperones. 2005.10(4):312-28.

Affymetrix Normalization Protocol

Data for this dataset were normalized by the authors with GCRMA [1].

Affymetrix Presence/Absence calls

No presence/absence call information or raw data files were supplied with the dataset and therefore presence/absence calls are not included.

Mapping Affymetrix Probe Sets to FlyBase Annotated Genes

Drosophila melanogaster sequences were downloaded from FlyBase[1].   All sequences associated with the printed probes were searched against the version 5 genome assembly of the *D. melanogaster* genome using BLASTn (E-value $< 10^{-3}$). BLAST results were processed with custom Perl scripts. The physical coordinates of transcripts associated with a FlyBase annotated gene were from version 5.10 of the *D. melanogaster* genome annotation. An Affymetrix probe set was mapped to a FlyBase gene ID if the BLAST results mapped to transcripts from a unique gene and only one gene. Strandedness was also considered.

Merging Probe Sets Across Replicate Arrays

There are multiple hybridizations done for the same condition and the intensity values are merged by simply taking the average for a particular probe set across the arrays under the same condition.

References

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[1] ftp://www.flybase.net/genomes/Drosophila_melanogaster/

1. Wu, Z. and R.A. Irizarry, *Preprocessing of oligonucleotide array data.* Nature Biotechnol. 2004. **22**(6):656-658.