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### References

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## Abstract

# Functional Annotation of RIKEN Mouse cDNA Clones Using GNF Expression Atlas

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Annotation of novel cDNAs relies on multiple lines of evidence, including gene structure, predicted ORFs, and predicted protein motifs. Insight into function also relies on expression profiling, through querying EST databases of direct experimentation.

High-throughput gene expression profiling, by use of spotted arrays or oligo chip methods, has become an important tool for investigating transcriptional activity. Among cDNAs predicted to encode related proteins, different expression patterns can suggest functional specialization. Additionally, common expression patterns can serve to group otherwise unrelated cDNAs. Expression profiling may be particularly useful for difficult to annotate clones, for which other lines of evidence are not available.

GNF has generated and analyzed gene expression previously from a set of 45 murine samples across a diverse list of normal tissues, organs, and cell lines probed with the Affymetrix MG-U74A chip. These data have been published (Su et al. 2002) and are available at the GNF's free and publicly accessible Web site (Gene Expression Atlas, <http://expression.gnf.org>), which integrates data visualization and curation of current gene annotations.

We identified the relationship between the RIKEN collection and MG-U74A/B/C targets by SIM4-polished BLAST alignments between 60,770 RIKEN clone sequences and 36,701 target sequences arrayed on the U74A/B/C chips. The results of this analysis are summarized in Table 1. There are 25,831 RIKEN clones represented on this array set. Of these, 2994 have lower quality similarity hits at the DNA or protein level (i.e., are not automatically or easily annotated by homology).

Ten additional tissues were profiled using the Affymetrix MG-U74Bv2 and MG-U74Cv2 chips to allow for inferred functional annotation in the absence of other evidence. These tissues were chosen to give the greatest representation of gene expression by extrapolation from the results obtained with U74A. Five of the tissues are also in common with those used to probe the RIKEN microarray. The combined resources should provide an extremely comprehensive characterization of the expression data.

Figure 1 shows just two arbitrarily taken cases in which tentative annotation may be inferred from the expression profile.

**Table 1.** The Counts of RIKEN Clones Represented on MG-U74 A, B, and C Chips

Chip	Probe sets	RIKEN hits	and not U74A	and not U74B	and not easy to annotate <sup>a</sup>
U74A	12,422	12,199	–	–	454
U74B	12,411	11,165	9,965	–	1,669
U74C	11,868	4,138	3,667	2,926	821

<sup>a</sup>Not counting clones with evidence class 0–4 (The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I and II Team 2002).

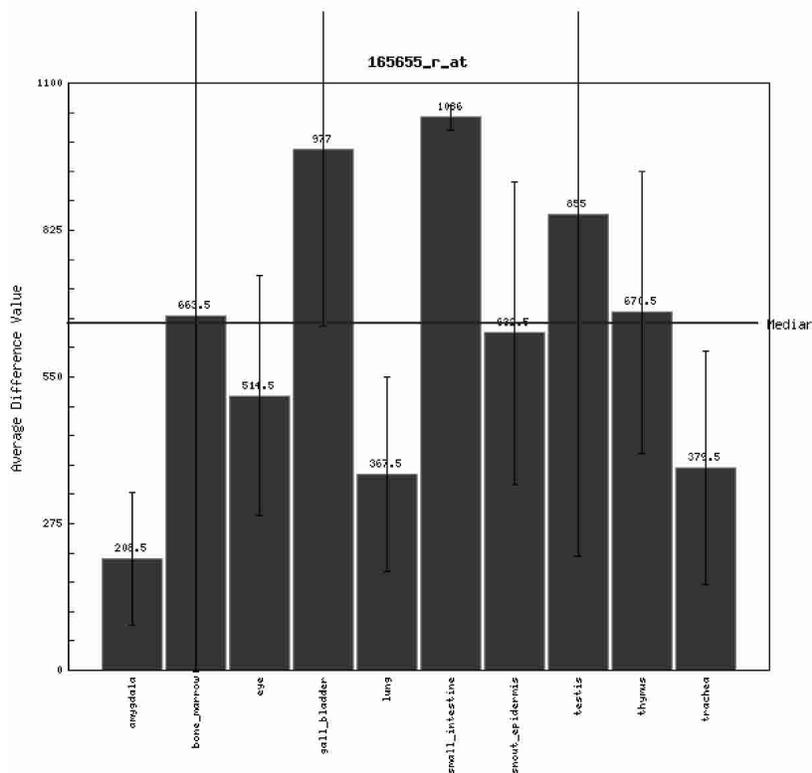
## REFERENCES

- The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I and Phase II Team. 2002. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. *Nature* **420**: 563–573.
- Su, A.I., Cooke, M.P., Ching, K.A., Hakak, Y., Walker, J.R., Wiltshire, T., Orth, A.P., Vega, R.G., Sapinoso, L.M., Moqrich, A., et al. 2002. Large-scale analysis of the human and mouse transcriptomes. *Proc. Natl. Acad. Sci.* **99**: 4465–4470.

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Article and publication are at <http://www.genome.org/cgi/doi/10.1101/gr.1457103>.

**A**

**165655\_r\_at** Original Affymetrix Annotation  
AI448459:mq40a07.x1 Mus musculus cDNA, 3 end

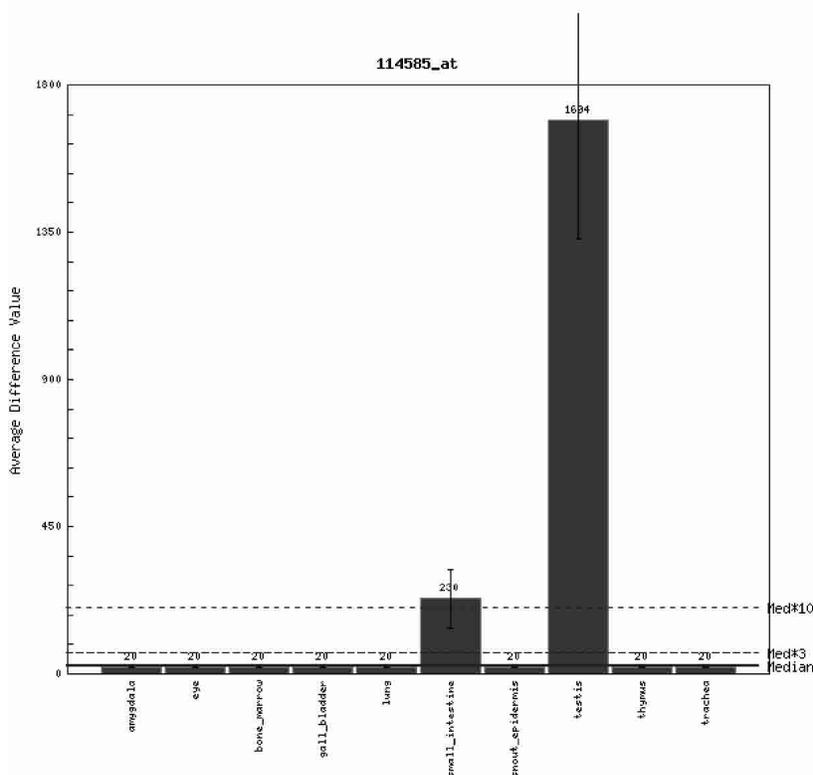
Current Annotation Thu Apr 24 19:15:04 PDT 2003

**Locuslink\_id** 56226  
**name** espin  
**symbol** Espn  
**product** espin  
**sumfunc** none  
**summary** none  
**go** actin bundling activity;ATP binding activity;cilium;brush border;actin cytoskeleton;parallel actin filament bundle formation;  
**extannot** none  
**phenotype** none  
**map** 4 80.1 cM|MGD|G|4 E1  
**maplink** MGD  
**nm** NM\_019585 Notes  
**np** NP\_062531  
**pubmed** [12207892](#) [11217851](#) [11076861](#)  
[11042159](#) [10975527](#) [10588661](#)  
[10349636](#)

**NCBI\_MGD Human-Mouse Synteny**

h_chr	h_id	h_sym	m_chr	m_id	m_sym
1	7161	TP73	4	22062	Trp73
1	49856	WDR8	4	59002	Wdr8
1	83715	DKFZP454A196	4	56226	Espn
1	11392	HBACH	4	70025	2410041A17Rk
1	8514	KCNAB2	4	16498	Kcnab2

**Unigene Expect** 5e-55 **identity** 100%  
137 bases  
**ug** Mm.32006  
**name** Espn  
**title** espin  
**cytoband** 4 80.1 cM  
**chromosome** 4  
**expression** eyeball colon lung ...

**B**

**114585\_at** Original Affymetrix Annotation  
AW046432:UI-M-BH1-akp-d-05-0-UI.s1  
Mus musculus cDNA, 3 end

Current Annotation Thu Apr 24 19:32:17 PDT 2003

**Locuslink\_id** 207175  
**name** centrin 4  
**symbol** LOC207175  
**product** centrin 4  
**sumfunc** none  
**summary** none  
**go** none  
**extannot** none  
**phenotype** none  
**map** none  
**maplink** none  
**nm** NM\_145825 Notes  
**np** NP\_665824  
**pubmed** none

**Unigene Expect** 2e-90 **identity** 100%  
**matchlength** 181 bases **Query size** 181 bases  
**ug** Mm.25493  
**name** LOC207175  
**title** centrin 4  
**cytoband** 3 B  
**chromosome** 3  
**expression** visual cortex fetus testis spermatocytes, pooled from multiple mice 18-day leptotene and zygotene spermatocytes Testicles mammary gland bladder olfactory brain bone marrow heart

**Figure 1** (A) RIKEN clone 0610007F01 is interrogated by the probe set 165655\_r\_at. (B) RIKEN clones 6430560A18 and G430087M20 are associated with the probe set 114585\_at with testis-specific pattern.