FlyNet: a versatile network prioritization server for the Drosophila community

Junha Shin, Sunmo Yang, Eiru Kim, Chan Yeong Kim, Hongseok Shim, Ara Cho, Hyojin Kim, Sohyun Hwang, Jung Eun Shim and Insuk Lee*

Department of Biotechnology, College of Life Science and Biotechnology, Yonsei University, Seoul, Korea

Received February 23, 2015; Revised April 08, 2015; Accepted April 24, 2015

ABSTRACT

Drosophila melanogaster (fruit fly) has been a popular model organism in animal genetics due to the high accessibility of reverse-genetics tools. In addition, the close relationship between the Drosophila and human genomes rationalizes the use of Drosophila as an invertebrate model for human neurobiology and disease research. A platform technology for predicting candidate genes or functions would further enhance the usefulness of this long-established model organism for gene-to-phenotype mapping. Recently, the power of network prioritization for gene-to-phenotype mapping has been demonstrated in many organisms. Here we present a network prioritization server dedicated to Drosophila that covers approximately half of the coding genome. This server, dubbed FlyNet, has several distinctive features, including (i) prioritization for both genes and functions; (ii) two complementary network algorithms: direct neighborhood and network diffusion; (iii) spatiotemporal-specific networks as an additional prioritization strategy for traits associated with a specific developmental stage or tissue and (iv) prioritization for human disease genes. FlyNet is expected to serve as a versatile hypothesis-generation platform for genes and functions in the study of basic animal genetics, developmental biology and human disease. FlyNet is available for free at http://www.inetbio.org/flynet.

INTRODUCTION

Drosophila remains an important model organism even after a century of research. Numerous biological processes that have been evolutionary conserved across species, such as embryogenesis and canonical cell signalling pathways, have been genetically dissected in Drosophila. Approximately half of Drosophila protein sequences have mammalian homologs (1), and ∼75% of known human disease genes have Drosophila orthologs (2). Drosophila therefore is expected to be an effective model for human disease research. Indeed, several recent studies have utilized Drosophila to identify genes associated with human diseases and traits (3–5).

Several reverse-genetics resources are available for Drosophila. These resources are based on the transposon insertion mutant libraries and RNA interference (RNAi) of both cell-based and organismal systems (6–9). However, unbiased genome-wide screens are costly and suffer from high false discovery rates. Reverse-genetics screens for Drosophila phenotypes become more efficient through systematic gene prioritization. One increasingly popular approach for gene prioritization is network prioritization, which is based on the functional closeness to the known phenotype genes within the gene networks. The concepts underlying network prioritization as well as its efficacy for gene-to-function and gene-to-phenotype mapping have recently been reviewed (10–12).

Here we present a network prioritization server for Drosophila dubbed FlyNet. Although network prioritization servers exist for multiple organisms, to the best of our knowledge FlyNet represents the first network prioritization server dedicated to Drosophila. FlyNet is highly accurate and can effectively predict gene-to-phenotype associations. This Drosophila-specific server further benefits from using Drosophila-specific information, such as the gene expression atlas, across cell types and developmental stages. Such information can help users generate more reliable hypotheses relevant to the spatiotemporal context and select more confident candidates. FlyNet also can prioritize Drosophila genes for human diseases with an option for the integration of human genetic evidence, such as genome-wide association studies (GWAS) and de novo mutation screens.

NETWORK CONSTRUCTION

The procedure that we used to construct our network consists of three major steps: (i) inferring co-functional gene pairs from various data sources; (ii) benchmarking networks inferred from individual data sources to assign likelihood scores for network links and (iii) integrating all com-

*To whom correspondence should be addressed. Tel: +82 2 2123 5559; Fax: +82 2 369 7265; Email: insuklee@yonsei.ac.kr

© The Author(s) 2015. Published by Oxford University Press on behalf of Nucleic Acids Research.
This is an Open Access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/4.0/), which permits unrestricted reuse, distribution, and reproduction in any medium, provided the original work is properly cited.
component networks using a modified naive Bayesian approach. The FlyNet gene network was constructed based on genome build release 5.54 from FlyBase (13). A set of gold-standard functional gene pairs was generated based on the Gene Ontology Biological Process (GO-BP) (14) and MetaCyc pathway terms (15). The co-functional links in FlyNet were inferred from *Drosophila*-derived data with the following computational algorithms: co-citation (CC) of gene names among PubMed abstracts; co-expression (CX) of genes in 53 experimental series comprising 1873 microarray samples in the Gene Expression Omnibus ( GEO) database (16); domain co-occurrence (DC) between proteins (17); functional links by genomic context based on gene neighborhood (GN) (18) and phylogenetic profile similarity (PG); protein-protein interactions via high-throughput assays (HT) and literature-based links (LC) from the iRefWeb meta-database version 13 (19). Additional links were inferred from published (17,20,21) and unpublished networks for other organisms. A total of 21 component networks were incorporated into FlyNet, and are summarized in Table 1 and Supplementary Table S1. These networks were benchmarked against the gold-standard gene pairs using a log-likelihood score scheme and then integrated into a single network, FlyNet, using a weighted sum method, as has been described for other published networks (17,20,21). Detailed information and methodologies are described in the Supplementary Online Methods. The integrated FlyNet gene network contains 13 119 genes (~95% of the coding genes) and 779 484 links.

NETWORK ASSESSMENT

To assess the compatibility of the fly gene networks with fly biological pathways, we employed the FlyReactome database (22), which is independent from the gold-standard data set that was used for the network training. FlyReactome contains only expert-curated *Drosophila* core pathways and reactions. Gene pairs that share pathway terms and those that do not share pathway terms generated 1305 positive and 14 365 negative gene pairs, respectively, for validation. The accuracy of the networks for the given coverage of the positive gene pairs was analyzed by a precision-recall curve. The performance of FlyNet in the retrieval of core pathway links was superior to other fly gene networks from STRING (23), FunCoup (24) and GeneMANIA (25) (Figure 1A).

Because functionally associated genes tend to share loss-of-function phenotypes, we expected that the more accurate networks would include a higher percentage of gene pairs that share RNAi phenotypes. We generated 316 924 positive and 7 107 807 negative gene pairs that share or do not share, respectively, RNAi phenotypes from the GenomeRNAi database (26). Compared with other network servers, FlyNet contained a higher percentage of gene pairs that share RNAi phenotypes for the given genome coverage of the network nodes (Figure 1B). Among the 21 component networks, the highest percentage of gene pairs in FlyNet originated from the co-expression network of fly genes (DM-CX) (Supplementary Figure S1). To determine the possibility of circular reasoning when predicting published RNAi phenotypes, we also assessed FlyNet with the co-citation links (DM-CC) excluded. We found that links derived from the DM-CC have no significant effect on the performance of FlyNet, as assessed by the RNAi phenotype data (Supplementary Figure S2). We measured the overlap between the FlyNet training data and the two validation data sets to confirm their independence. We found that only 33.5% of the FlyReactome and 1.2% of the GenomeRNAi positive gene pairs overlapped with the network training data. Therefore, the higher accuracy of FlyNet compared with other fly gene networks may be attributed, at least in part, to the network construction procedure, which is maximally optimized to the *Drosophila* biology. Taken together, we conclude that FlyNet is a highly accurate and comprehensive functional gene network that can effectively reconstruct both core pathways and phenotypes in *Drosophila*.

NETWORK PRIORITIZATION OPTIONS

Distinctive features of the FlyNet web server

In addition to FlyNet, there are currently two other publicly available fly network prioritization servers: GeneMANIA and FunCoup. However, these two servers are not dedicated to *Drosophila*. In addition, compared with these servers, FlyNet has several distinctive features that enable more versatile hypothesis generation for *Drosophila*-based studies: (i) FlyNet can prioritize both genes (gene prioritization) and functional annotations (function prioritization); (ii) FlyNet can use two complementary network prioritization algorithms, direct neighborhood and network diffusion, compared with other publicly available network prioritization servers, which provide only one or the other algorithm for use; (iii) FlyNet can utilize a spatiotemporal-specific network (STN) as an additional prioritization strategy for traits associated with a specific developmental stage or tissue and (iv) FlyNet can prioritize *Drosophila* genes not only for *Drosophila* traits (Fly prioritizer) but also for human disease (Human prioritizer).

Fly prioritizer—function prioritization

This option prioritizes functional annotations based on GO-BP terms and GenomeRNAi phenotypic terms for a query gene. The functional annotation terms are ranked by the sum of the network edge weight scores (i.e. the sum of the log-likelihood scores in FlyNet) from the query gene to all neighbor genes annotated by each annotation term. We used all 5434 Kyoto Encyclopaedia of Genes and Genomes (KEGG) (27) pathway terms for 2690 fly genes to assess the predictive power of the function prioritization option in FlyNet. The KEGG pathway database was chosen, because the data are well structured and highly curated, and was not used to train FlyNet. We prioritized the KEGG terms for the 2690 genes and counted the number of retrieved terms that were correct among the top-ranked predictions. We found that 4510 (83.0%) KEGG terms were correctly retrieved within the top 10 candidates and 4812 (88.6%) were retrieved within the top 20 candidates, whereas only 1460 (26.9%) and 1953 (35.9%) terms, respectively (Figure 2A), were retrieved by random prediction. These results indicate that FlyNet can effectively predict novel functional annotations for a query gene.
Table 1. Summary of the 21 component networks for FlyNet

| Code     | Description                                                                 | # Genes | # Links  |
|----------|-----------------------------------------------------------------------------|---------|---------|
| DM-CC    | Co-citation of two fly genes across Medline and PubMed Central               | 6027    | 503 475 |
| DM-CX    | Co-expression of two fly genes in high-dimensional gene expression data from the GEO database (16) | 11 718 | 275 033 |
| DM-DC    | Co-occurrence of protein domains between two fly genes (17)                 | 4407    | 7604    |
| DM-GN    | Chromosomal proximity between bacterial orthologs of two fly genes in bacterial genomes (18) | 1979    | 15 820  |
| DM-HT    | Protein–protein interactions (PPIs) identified by high-throughput assays in iRefWeb database (19) | 7759    | 25 519  |
| DM-LC    | Protein–protein interactions (PPIs) identified by small-scale experiments collected via literature curation in iRefWeb database (19) | 1202    | 2226    |
| DM-PG    | Phylogenetic profile similarity between two fly genes                       | 3557    | 80 506  |
| AT-CC    | Orthology transfer of co-citation links in an A. thaliana network (21)       | 1747    | 17 501  |
| AT-CX    | Orthology transfer of co-expression links in an A. thaliana network (21)     | 1105    | 9455    |
| AT-HT    | Orthology transfer of high-throughput PPI in an A. thaliana network (21)     | 1013    | 2823    |
| AT-LC    | Orthology transfer of literature curated PPI in an A. thaliana network (21)  | 856     | 1977    |
| CE-CX    | Orthology transfer of co-expression links in a C. elegans network (20)       | 1434    | 17 497  |
| DR-CX    | Orthology transfer of co-expression links in a D. rerio network              | 3223    | 55 515  |
| HS-CX    | Orthology transfer of co-expression links in a H. sapiens network            | 3366    | 32 482  |
| HS-HT    | Orthology transfer of literature curated PPI in a H. sapiens network         | 2741    | 12 520  |
| HS-LC    | Orthology transfer of literature curated PPI in a H. sapiens network         | 5254    | 50 488  |
| SC-CC    | Orthology transfer of co-citation links in a S. cerevisiae network (17)      | 2449    | 48 473  |
| SC-CX    | Orthology transfer of co-expression links in a S. cerevisiae network (17)    | 1674    | 18 488  |
| SC-GT    | Orthology transfer of genetic interactions in a S. cerevisiae network (17)   | 1254    | 6482    |
| SC-HT    | Orthology transfer of high-throughput PPI in a S. cerevisiae network (17)    | 1622    | 18 300  |
| SC-LC    | Orthology transfer of literature-curated PPI in a S. cerevisiae network (17) | 2016    | 16 481  |
| FlyNet   | Integrated network                                                          | 13 119  | 779 484 |

Figure 1. The assessment of FlyNet using gene pairs derived from (A) FlyReactome annotations and (B) GenomeRNAi phenotype terms. The precision of the gene pairs was measured every 1000 pairs, which were sorted by the network edge weight scores. For the assessment by GenomeRNAi, the coverage of the fly genome was used, because the number of gene pairs by the RNAi phenotype is so large (316 924) that the recall for the majority of the gene pairs is not feasible.

Fly prioritizer–gene prioritization

This option prioritizes fly genes for a given function, pathway and phenotype that are specified by user-input genes. Because these user-input genes guide the search for new candidates in the network, these genes are called guide genes. Upon prioritization, the rank of each fly gene is determined from its association with the guide genes. FlyNet can use two complementary network algorithms to measure the association of each fly gene with the guide gene: direct neighborhood and network diffusion. Network diffusion algorithms propagate guide gene information throughout the entire network, whereas direct neighborhood algorithms propagate guide gene information only to directly connected neighbours. These algorithms are complementary, and therefore it is advantageous to use both algorithms for prioritization. FlyNet uses the sum of the edge weight
scores for the direct neighborhood algorithm and Gaussian smoothing for the network diffusion algorithm, the latter of which is also used in GeneMANIA (25). Based on the prioritized genes, FlyNet first measures the retrieval power for the guide genes to estimate the prediction power of FlyNet for the given traits depicted by these guide genes. The prediction power is assessed by receiver operating characteristic (ROC) analyses and summarized as an area under the ROC curve (AUC) score. The traits with high AUC scores are more likely to benefit from network prioritization.

One distinctive feature of FlyNet is the use of STN as an additional strategy to predict genes for traits associated with a specific developmental stage or tissue. If the known genes for a trait (i.e. guide genes) generally have more network neighbors in a specific developmental stage or tissue type, then novel candidate genes with the same spatiotemporal specificity in network neighbors are more likely to be confident candidates. For this analysis, we first constructed networks for each of the four developmental stages and 10 tissue types in *Drosophila* by filtering the FlyNet edges for genes with a BPKM (i.e. bases per kilobase per million mapped bases) > 1, based on the recent *Drosophila* transcriptome data from the modENCODE project (28). We then compared the networks to identify specific network links for each of four developmental stages. We also compared the networks to identify specific network links for
each of 10 tissue types. The resultant 14 STNs are summarized in Supplementary Table S2, and their edge information can be downloaded from the FlyNet server. To measure the functional spatiotemporal specificity for each gene, we counted the number of network neighbors across the 14 STNs. This method provides an opportunity to further select candidate genes based on the STN neighbors. For example, genes annotated by the GO-BP terms 'compound eye development', 'sensory perception of smell' and 'spermatogenesis' exhibit the highest number of STN neighbors for the central nervous system (CN), head (HD) and accessory gland (AG), respectively (Figure 2B). Users also can visualize a heat map that displays the number of STN neighbors across the 14 spatiotemporal contexts for guide genes and candidate genes; an example for spermatogenesis is shown in Figure 2C. If users click the tissue most enriched for STN neighbours (e.g. the AG for spermatogenesis), all the genes are sorted by the number of STN neighbours. As expected, the top-ranked genes are highly enriched for guide genes (highlighted in red), which have many AG-specific network neighbours.

The gene prioritization module also provides several additional analysis results: (i) the visualization of a network of guide genes and a network of a combined set of guide genes and candidate genes using Cytoscape web (29); (ii) the lists of guide genes and candidate genes and (iii) a gene set analysis for guide genes, candidate genes or their combined set with GO-BP, KEGG, BioCyc and GenomeRNAi terms using the hypergeometric test. In particular, we adapted REVIGO (30) to effectively summarize and visualize redundant information in the GO-BP terms.

To assess the predictive power of FlyNet for fly gene prioritization, we performed an ROC analysis for 389 RNAi phenotypes from the GenomeRNAi database (31). We confirmed that the predictive power of FlyNet is significantly higher than random models \(P = 8.08e-34\), Wilcoxon signed-rank test (Figure 2D). We also assessed the predictive power of FlyNet using multiple guide gene sets for the same pathway derived from independent RNAi screens. We collected three gene sets for the ‘Imd pathway’, which were derived from three independent screens by Gesellechen et al. (32) (21 genes), Kleino et al. (33) (eight genes) and Valanne et al. (34) (30 genes), and submitted each of these three sets for gene prioritization. The validation of the three prediction results by the 22 ‘Imd pathway’ genes annotated in FlyReactome demonstrated discovery rates of 14–22% and 9–12% for the top 50 and 100 candidates, respectively (Figure 2E). These results represent 88–138 fold and 56–75 fold enrichment, respectively, compared with the expected discovery rate by random chance (i.e. 22 Imd pathway genes represent \(\sim 0.16%\) of the 13,942 genes in the fly genome).

### Human prioritizer–human disease prioritization

*Drosophila* models have been used for the study of neurodevelopmental disorders, cancer and other human diseases (5,35,36). Fly genes and fly mutants are valuable resources in human disease research studies. Therefore, we developed FlyNet to prioritize *Drosophila* genes not only for fly traits (*Fly prioritizer*) but also for human diseases (*Human prioritizer*). The human prioritizer attempts to identify novel human disease genes that can be used to construct a human disease model in the fly, which may allow for genetic screens of disease gene modulators and may identify new therapeutic targets. The human prioritizer option uses the same methods as the fly prioritizer, including the direct neighborhood algorithm, with an additional step for orthology mapping between fly and human genes. Users may submit either fly genes or human genes as guide genes. For example, disease-associated fly genes derived from ‘FlyBase human disease alleles’ or human disease genes from ‘OMIM morbidmap’ (37) can be used as guide genes. These genes are available from the web server, and users can submit these genes with a simple click.

To assess the predictive power of the human prioritizer for disease genes, we tested various neurodevelopmental disease genes derived from the OMIM database. We submitted human OMIM genes for autism, epilepsy and schizophrenia as guide genes. To validate the resultant novel candidate genes for each neurodevelopmental disease, we used 138 human orthologs of X-chromosome fly genes whose associations with human neurological diseases were reported by a recent mutagenesis screen (5). By random chance, the discovery rate for identifying these 138 genes out of 1710 human orthologs of X-chromosome fly genes is 8.1%. In contrast, we observed a discovery rate of 32–64% for the top 50 candidate genes for the diseases, which represents a 4–8-fold enrichment due to the network prioritization (Figure 3A). We also used *de novo* mutations in autism (480 human genes), epilepsy (204 human genes) or schizophrenia (695 human genes) collected from various studies (see Supplementary Online Methods) to assess the network prioritization for the same three neurodevelopmental disorders. Because there is a significant overlap of genes between these neurological diseases (38), we used the union of these three gene sets (800 genes) to assess the prediction for each disorder. We observed a discovery rate of 34–45% for the top 100 candidate genes for these three disorders, which represents a 4.2–5.6-fold enrichment due to the network prioritization compared with random expectation (i.e. 800 genes represent 8.1% of the 9857 human orthologs in the fly genome) (Figure 3B).

Human genetics studies have revealed that human disease is associated with multiple genes. In particular, thousands of genes associated with heritable disorders have been identified via GWAS and *de novo* mutation screens. We hypothesized that the integration of genetic evidence with network evidence may give rise to more confident candidate genes, which then could be validated experimentally. Therefore, the FlyNet server implements an option to filter novel candidates with network prioritization using support genes, which generally are derived from human genetics studies. FlyNet currently provides support genes derived from many human GWAS and *de novo* mutation screens, and these genes can be submitted as support genes with a simple click. Users also can submit their own support genes. If a user chooses this option, then the report page will display two separate lists of candidate genes: (i) *first-tier candidate genes*, which represent the intersection of support genes with the neighbors of guide genes (i.e. the intersection of candidates by human genetic evidence with candidates by network evidence) and (ii) *second-tier candidate genes*.
which include all candidates from the network prioritization. The first-tier candidates, which are supported by both network and genetic evidence, are more likely to be promising candidates than those supported by network evidence only. If users need only a handful of candidates with high confidence, then this option may be useful.

CONCLUSIONS
FlyNet is a freely available network prioritization server dedicated to the Drosophila community. A functional gene network of Drosophila genes was constructed with machine learning procedures optimized for the Drosophila biology. We demonstrated that FlyNet can effectively predict gene functional links, function/pathways, genes for pathways/phenotypes and human disease genes. FlyNet is a distinctive network prioritization server because it prioritizes genes as well as functions, uses two complementary network algorithms and STN and can predict human disease genes. Therefore, FlyNet is a versatile hypothesis-generation server for Drosophila biologists who study basic animal genetics as well as human diseases.

SUPPLEMENTARY DATA
Supplementary Data are available at NAR Online.

FUNDING
National Research Foundation of Korea (2012M3A9B4028641, 2012M3A9C7050151). Funding for open access charge: National Research Foundation of Korea (2012M3A9C7050151).

Conflict of interest statement. None declared.

REFERENCES
1. Friedman, R. and Hughes, A.L. (2001) Pattern and timing of gene duplication in animal genomes. Genome Res., 11, 1842–1847.
2. Bier, E. (2005) Drosophila, the golden bug, emerges as a tool for human genetics. Nat. Rev. Genet., 6, 9–23.
3. Bayat, V., Thiffault, I., Jaiswal, M., Tetreault, M., Doni, T., Sasaarman, F., Bernard, G., Demers-Lamarche, J., Dicaire, M. J., Mathieu, J. et al. (2012) Mutations in the mitochondrial methionyl-tRNA synthetase cause a neurodegenerative phenotype in flies and a recessive ataxia (ARSAL) in humans. PLoS Biol., 10, e1001288.
4. Neely, G. G., Hess, A., Costigan, M., Keene, A. C., Goulas, S., Langeslag, M., Griffin, R. S., Belfer, I., Dai, F., Smith, S. B. et al. (2010) A genome-wide Drosophila screen for heat nociception identifies alpha2delta3 as an evolutionarily conserved pain gene. Cell, 143, 628–638.
5. Yamamoto, S., Jaiswal, M., Charrn, W. L., Gambin, T., Karaca, E., Mizraa, G., Wiszniowski, W., Sandoval, H., Haelterman, N. A., Xiong, B. et al. (2014) A drosophila genetic resource of mutants to study mechanisms underlying human genetic diseases. Cell, 159, 200–214.
6. Boutros, M., Kiger, A. A., Armknecht, S., Kerr, K., Hild, M., Koch, B., Haas, S. A., Paro, R., Perrimon, N. and Heidelberg Fly Array, C. (2004) Genome-wide RNAi analysis of growth and viability in Drosophila cells. Science, 303, 832–835.
7. Dietzl, G., Chen, D., Schnorrer, F., Su, K. C., Barinova, Y., Fellner, M., Gasser, B., Kinsey, K., Oppel, S., Scheiblauer, S. et al. (2007) A genome-wide transgenic RNAi library for conditional gene inactivation in Drosophila. Nature, 448, 151–156.
8. Parks, A. L., Cook, K. R., Belvin, M., Dompe, N. A., Fawcett, R., Huppert, K., Tan, L. R., Winter, C. G., Bogart, K. P., Deal, J. E. et al.
10. Lee, I. (2013) Network approaches to the genetic dissection of phenotypes in animals and humans. *Anim. Cells Syst.*, 17, 75–79.

11. Ideker, T. and Sharan, R. (2008) Protein networks in disease. *Genome Res.*, 18, 644–652.

12. Lehner, B. (2013) Genotype to phenotype: lessons from model organisms for human genetics. *Nat. Rev. Genet.*, 14, 168–178.

13. Dos Santos, G., Schroeder, A.J., Goodman, J.L., Strelets, V.B., Crosby, M.A., Thurmond, J., Emmert, D.B., Gelbart, W.M. and FlyBase. (2015) FlyBase: introduction of the Drosophila melanogaster Release 6 reference genome assembly and large-scale migration of genome annotations. *Nucleic Acids Res.*, 43, D690–D697.

14. Gene Ontology annotations and resources. Blake, A., Dolan, M., Drabkin, H., Hill, D.P., Li, N., Sitnikov, D., Bridges, S., Burgess, S., Buza, T. et al. (2013) Gene Ontology annotations and resources. *Nucleic Acids Res.*, 41, D530–D533.

15. Caspi, R., Altman, R., Billington, R., Dreher, K., Foerster, H., Fulcher, C.A., Holland, T.A., Keesler, I.M., Kothari, A., Kubo, A. et al. (2014) The MetaCyc database of metabolic pathways and enzymes and the BioCyc collection of Pathway/Genome Databases. *Nucleic Acids Res.*, 42, D459–D471.

16. Barrett, T., Wilhite, S.E., Ledoux, P., Evangelista, C., Kim, I.F., Tomashevsky, M., Marshall, K.A., Philippy, K.H., Sherman, P.M., Holko, M. et al. (2013) NCBI GEO: archive for functional genomics data sets–update. *Nucleic Acids Res.*, 41, D991–D995.

17. Kim, H., Shin, J., Kim, E., Kim, H., Hwang, S., Shim, J.E. and Lee, J. (2014) YeastNet v3: a public database of data-specific and integrated functional gene networks for Saccharomyces cerevisiae. *Nucleic Acids Res.*, 42, D731–D736.

18. Shin, J., Lee, T., Kim, H. and Lee, J. (2014) Complementarity between distance- and probability-based methods of gene neighbourhood identification for pathway reconstruction. *Mol. Biosyst.*, 10, 24–29.

19. Turner, B., Razick, S., Turinsky, A.L., Vlasblom, J., Crowdy, E.K., Cho, E., Morrison, K., Donaldson, I.M. and Wodak, S.J. (2010) iRefWeb: interactive analysis of consolidated protein interaction data and their supporting evidence. *Database (Oxford)*, 2010, baq023.

20. Cho, A., Shin, J., Hwang, S., Kim, C., Shim, H., Kim, H., Kim, H. and Lee, J. (2014) WormNet v3: a network-assisted hypothesis-generating server for Caenorhabditis elegans. *Nucleic Acids Res.*, 42, W76–W82.

21. Lee, T., Yang, S., Kim, E., Ko, Y., Hwang, S., Shin, J., Shim, J.E., Shim, H., Kim, H. and Kim, C. et al. (2015) AraNet v2: an improved database of co-functional gene networks for the study of Arabidopsis thaliana and 27 other nonmodel plant species. *Nucleic Acids Res.*, 43, D996–D1002.

22. Matthews, L., Gopinath, G., Gillespie, M., Caudy, M., Croft, D., de Bono, B., Garapati, P., Hemish, J., Hermjakob, H., Jassal, B. et al. (2009) Reactome knowledgebase of human biological pathways and processes. *Nucleic Acids Res.*, 37, D619–D622.

23. Franceschini, A., Szklarczyk, D., Frankild, S., Kuhn, M., Simonovic, M., Roth, A., Lin, J., Minguez, P., Bork, P., von Mering, C. et al. (2013) STRING v9.1: protein–protein interaction networks, with increased coverage and integration. *Nucleic Acids Res.*, 41, D808–D815.

24. Schmitt, T., Ogris, C. and Sonnhammer, E.L. (2014) FunCoup 3.0: database of genome-wide functional coupling networks. *Nucleic Acids Res.*, 42, D380–D388.

25. Warde-Farley, D., Donaldson, S.L., Comes, O., Zuberi, K., Budruki, R., Chao, P., Franz, M., Grouios, C., Kazi, F., Lopes, C.T. et al. (2010) The GeneMANIA prediction server: biological network integration for gene prioritization and predicting gene function. *Nucleic Acids Res.*, 38, W214–W220.

26. Schmitt, E.E., Pelz, O., Buhlmann, S., Kerr, G., Horn, T. and Boutilier, M. (2013) GenomeRNAi: a database for cell-based and in vivo RNAi phenotypes, 2013 update. *Nucleic Acids Res.*, 41, D1021–D1026.

27. Kanehisa, M., Goto, S., Sato, Y., Kawashima, M., Furumichi, M. and Tanabe, M. (2014) Data, information, knowledge and principle: back to metabolism in KEGG. *Nucleic Acids Res.*, 42, D199–D205.

28. Brown, J.B., Boley, N., Eisman, R., May, G.E., Stoiber, M.H., Duf, M.O., Booth, B.W., Wen, J., Park, S., Suzuki, A.M. et al. (2014) Diversity and dynamics of the Drosophila transcriptome. *Nature*, 512, 393–399.

29. Lopes, C.T., Franz, M., Kazi, F., Donaldson, S.L., Morris, Q. and Bader, G.D. (2010) Cytoscape Web: an interactive web-based network browser. *Bioinformatics*, 26, 2347–2348.

30. Supf, F., Bosnjak, M., Skuca, N. and Smuc, T. (2011) REVIGO summarizes and visualizes long lists of gene ontology terms. *PLoS One*, 6, e21800.

31. McGarry, K.L., Lee, I. and Marcotte, E.M. (2007) Broad network-based predictability of Saccharomyces cerevisiae gene loss-of-function phenotypes. *Genome Biol.*, 8, R258.

32. Gesellchen, V., Kutterneuker, D., Stekel, M., Polte, N. and Boutsos, M. (2005) An RNA interference screen identifies Inhibitor of Apoptosis Protein 2 as a regulator of innate immune signalling in *Drosophila*. *EMBO Rep.*, 6, 979–984.

33. Kleino, A., Valanne, S., Ulvila, J., Kallio, J., Myllymaki, H., Enwald, H., Stoven, S., Poisdevin, M., Ueda, R., Hultmark, D. et al. (2005) Inhibitor of apoptosis 2 and TAK1-binding protein are components of the Drosophila *ipd* pathway. *EMBO J.*, 24, 3432–3434.

34. Valanne, S., Myllymaki, H., Kallio, J., Schmid, M.R., Kleino, A., Murumagi, A., Airaksinen, L., Kotipelto, T., Kaustio, M., Ulvila, J. et al. (2010) Genome-wide RNA interference in *Drosophila* cells identifies G proteincoupled receptor kinase 2 as a conserved regulator of NF-kappaB signalling. *J. Immunol.*, 184, 6188–6198.

35. Bellen, H.J., Tong, C. and Tsuda, H. (2010) 100 years of *Drosophila* research and its impact on vertebrate neuroscience: a history lesson for the future. *Nat. Rev. Neurosci.*, 11, 514–522.

36. Rudrapatna, V.A., Cagan, R.L. and Das, T.K. (2012) *Drosophila* cancer models. *Dev. Dyn.*, 241, 107–118.

37. Amberger, J.S., Bocchini, C.A., Schiettecatte, F., Scott, A.F. and Hamosh, A. (2015) OMIM.org: Online Mendelian Inheritance in Man (OMIM(R)), an online catalog of human genes and genetic disorders. *Nucleic Acids Res.*, 43, D789–D798.

38. Fromer, M., Pocklington, A.J., Kavanagh, D.H., Williams, H.J., Dwyer, S., Gormley, P., Georgieva, L., Rees, E., Palta, F., Ruderfer, D.M. et al. (2014) De novo mutations in schizophrenia implicate synaptic networks. *Nature*, 506, 179–184.