Supplementary Data

FlyAtlas 2: A new version of the *Drosophila melanogaster* expression atlas with RNA-Seq, miRNA-Seq and sex-specific data

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Table S1. Number of flies used and yields of total RNA for different tissues

	Adult		**Larvae**	
Tissue	**No. flies**	**RNA (ng/µl)**	**No. flies**	**RNA (ng/µl)**
Whole	10	830	10	1220
Carcass	35	310	15	415
Midgut	80	480	15	310
Hindgut	1100	330	100	220
Anal Pad	1690	202	—	—
Malpighian Tubules	210	430	75	380
Head	10	130*	—	—
Ovary	16	1620	—	—
Testis	60	275	—	—
Accessory Gland	118	310	—	—
Brain	320	210	55	445
Salivary Gland			50	480
Trachea	—	—	230	230
Fat Body	—	—	12	245

*Although this is less than the 200 ng/µl normally required, the RNA passed quality control and yielded satisfactory RNA-Seq data.

Table S2. Tables in the MySQL relational database, FlyAtlas 2

Gene

```
+-------------+--------------+------+-----+---------+-------+
| Field       | Type         | Null | Key | Default | Extra |
+-------------+--------------+------+-----+---------+-------+
| FBgn        | char(11)     | NO   | PRI | NULL    |       |
| CGNum       | varchar(10)  | YES  |     | NULL    |       |
| Symbol      | varchar(40)  | YES  |     | NULL    |       |
| Name        | varchar(100) | YES  |     | NULL    |       |
| RomanSymbol | varchar(100) | YES  |     | NULL    |       |
| RomanName   | varchar(200) | YES  |     | NULL    |       |
| Locus       | varchar(40)  | NO   |     | NULL    |       |
| BioType     | varchar(25)  | NO   |     | NULL    |       |
+-------------+--------------+------+-----+---------+-------+
```

Ambiguity

```
+-------------+----------+------+-----+---------+-------+
| Field       | Type     | Null | Key | Default | Extra |
+-------------+----------+------+-----+---------+-------+
| MaskedFBgn  | char(11) | NO   | PRI | NULL    |       |
| MaskingFBgn | char(11) | NO   | PRI | NULL    |       |
+-------------+----------+------+-----+---------+-------+
```

GeneWithOntol

```
+-------+----------+------+-----+---------+-------+
| Field | Type     | Null | Key | Default | Extra |
+-------+----------+------+-----+---------+-------+
| FBgn  | char(11) | NO   | PRI | NULL    |       |
| GOid  | char(7)  | NO   | PRI | NULL    |       |
+-------+----------+------+-----+---------+-------+
```

Ontology

```
+--------+--------------+------+-----+---------+-------+
| Field  | Type         | Null | Key | Default | Extra |
+--------+--------------+------+-----+---------+-------+
| GOid   | char(7)      | NO   | PRI | NULL    |       |
| GOname | varchar(250) | NO   |     | NULL    |       |
| GOtype | varchar(18)  | NO   |     | NULL    |       |
+--------+--------------+------+-----+---------+-------+
```

Transcript

```
+----------------+---------------+------+-----+---------+-------+
| Field          | Type          | Null | Key | Default | Extra |
+----------------+---------------+------+-----+---------+-------+
| FBgn           | char(11)      | NO   | MUL | NULL    |       |
| FBtr           | char(11)      | NO   | PRI | NULL    |       |
| TranscriptName | varchar(50)   | NO   |     | NULL    |       |
| Strand         | enum('+','-') | NO   |     | NULL    |       |
| ExonCount      | int(3)        | NO   |     | NULL    |       |
| ExonStarts     | varchar(1000) | NO   |     | NULL    |       |
| ExonEnds       | varchar(1000) | NO   |     | NULL    |       |
+----------------+---------------+------+-----+---------+-------+
```

Tissue

```
+--------------+------------------------------+------+-----+---------+-------+
| Field        | Type                         | Null | Key | Default | Extra |
+--------------+------------------------------+------+-----+---------+-------+
| TissueID     | int(3)                       | NO   | PRI | NULL    |       |
| Stage        | enum('Adult','Larval')       | YES  |     | NULL    |       |
| Sex          | enum('Male','Female','Both') | YES  |     | NULL    |       |
| TissueName   | varchar(30)                  | NO   |     | NULL    |       |
| Abbreviation | char(2)                      | NO   |     | NULL    |       |
| UniTissueID  | int(2)                       | NO   | MUL | NULL    |       |
| Reference    | enum('Yes','No')             | NO   |     | NULL    |       |
| Replicates   | int(11)                      | NO   |     | 0       |       |
+--------------+------------------------------+------+-----+---------+-------+
```

UniTissue

```
+---------------+-------------+------+-----+---------+-------+
| Field         | Type        | Null | Key | Default | Extra |
+---------------+-------------+------+-----+---------+-------+
| UniTissueID   | int(2)      | NO   | PRI | NULL    |       |
| UniTissueName | varchar(30) | NO   |     | NULL    |       |
+---------------+-------------+------+-----+---------+-------+
```

GeneFPKM

```
+-----------+--------------------------------------+------+-----+---------+-------+
| Field     | Type                                 | Null | Key | Default | Extra |
+-----------+--------------------------------------+------+-----+---------+-------+
| FBgn      | char(11)                             | NO   | PRI | NULL    |       |
| TissueID  | int(3)                               | NO   | PRI | NULL    |       |
| FPKM      | double(8,2)                          | NO   |     | NULL    |       |
| Replicate1| double(8,2)                          | NO   |     | NULL    |       |
| Replicate2| double(8,2)                          | NO   |     | NULL    |       |
| Replicate3| double(8,2)                          | NO   |     | NULL    |       |
| SD        | double(8,2)                          | NO   |     | NULL    |       |
+-----------+--------------------------------------+------+-----+---------+-------+
```

TranscriptFPKM

```
+-----------+--------------------------------------+------+-----+---------+-------+
| Field     | Type                                 | Null | Key | Default | Extra |
+-----------+--------------------------------------+------+-----+---------+-------+
| FBtr      | char(11)                             | NO   | PRI | NULL    |       |
| TissueID  | int(3)                               | NO   | PRI | NULL    |       |
| FPKM      | double(8,2)                          | NO   |     | NULL    |       |
| Replicate1| double(8,2)                          | NO   |     | NULL    |       |
| Replicate2| double(8,2)                          | NO   |     | NULL    |       |
| Replicate3| double(8,2)                          | NO   |     | NULL    |       |
| SD        | double(8,2)                          | NO   |     | NULL    |       |
+-----------+--------------------------------------+------+-----+---------+-------+
```

GeneRPM

```
+------------+----------+------+-----+---------+-------+
| Field      | Type     | Null | Key | Default | Extra |
+------------+----------+------+-----+---------+-------+
| FBgn       | char(11) | NO   | PRI | NULL    |       |
| TissueID   | int(3)   | NO   | PRI | NULL    |       |
| RPM        | int(11)  | NO   |     | NULL    |       |
| Replicate1 | int(11)  | NO   |     | NULL    |       |
| Replicate2 | int(11)  | NO   |     | NULL    |       |
| Replicate3 | int(11)  | NO   |     | NULL    |       |
| SD         | int(11)  | NO   |     | NULL    |       |
+------------+----------+------+-----+---------+-------+
```

TranscriptRPM

```
+------------+----------+------+-----+---------+-------+
| Field      | Type     | Null | Key | Default | Extra |
+------------+----------+------+-----+---------+-------+
| FBtr       | char(11) | NO   | PRI | NULL    |       |
| TissueID   | int(3)   | NO   | PRI | NULL    |       |
| RPM        | int(11)  | NO   |     | NULL    |       |
| Replicate1 | int(11)  | NO   |     | NULL    |       |
| Replicate2 | int(11)  | NO   |     | NULL    |       |
| Replicate3 | int(11)  | NO   |     | NULL    |       |
| SD         | int(11)  | NO   |     | NULL    |       |
+------------+----------+------+-----+---------+-------+
```

Table S3. Validation of FlyAtlas 2 data set by reference to genes with extreme specificity of expression in particular tissues

Gene	Head	Midgut	Malpighian Tubules	Hindgut	Ovary	Testis
trp	**134** **2650**	0.1 0	0 0	0 0	0 0	0 0
Jon99Ci	0 12	**1998** **6335**	11.4 0	7.6 0	0 0	0.4 11
CG15408	0 0	0.6 0	**597** **4338**	0.1 0	0 0	2.2 7
CG9993	0 0	0.2 0.1	2.4 1	**595** **2648**	0.1 0	0.2 0
otu	0 0	0.2 8	0.8 0	0.5 0	**59** **1353**	1.4 6
Mst84Dd	1.1 0	0.1 0	0.3 0	13 0	1 0	**4997** **2526**

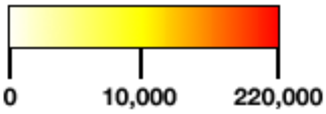
Red: FlyAtlas 2; **Blue**: FlyAtlas 1 (1)

Units are arbitrary signal units in the case of FlyAtlas 1, and FPKM in the case of FlyAtlas 2.

Table S4. Validation of FlyAtlas 2 data set by comparison with results of Fagegaltier *et al.*(2) for the most highly enriched microRNAs in testis and ovary

	Fagegaltier *et al.*			**This study**		
mir	**Testis**	**Testis/Total**	**Rank**	**Testis**	**Testis/Total**	**Rank**
mir-975	7469	1.00	1	2218	0.98	na
mir-310	11746	1.00	2	7931	0.97	8
mir-311	12537	0.99	3	56554	0.98	5
mir-959	60382	0.99	4	7035	0.98	7
mir-978	29600	0.99	5	495	0.99	na
mir-964	35403	0.99	6	5035	0.98	na
mir-976	26338	0.99	7	13366	0.98	3
mir-312	5964	0.98	8	46104	0.98	4
mir-977	28350	0.98	9	294	0.98	na
mir-983	23562	0.97	10	1367	0.97	na
mir-988	23055	0.96	11	546	0.84	na
mir-984	7704	0.93	12	1643	0.98	na
mir-960	19026	0.92	13	20604	0.99	2
mir-12	217798	0.91	14	27109	0.83	11
mir-274	27748	0.89	15	4689	0.63	na
mir-317	15712	0.87	16	74325	0.57	22
mir-9b	23545	0.85	17	3956	0.89	na
mir-305	65041	0.82	18	11126	0.65	na
mir-34	40124	0.81	19	13599	0.46	24
mir-316	15460	0.74	20	4022	0.79	na
mir-11	32372	0.69	21	20971	0.61	21
mir-125	11659	0.69	22	2108	0.62	na

	Fagegaltier *et al.*			**This study**		
mir	**Ovary**	**Ovary/Total**	**Rank**	**Ovary**	**Ovary/Total**	**Rank**
mir-318	34886	1.00	1	122908	0.76	13
mir-994	14463	0.99	2	18545	0.82	12
mir-275	12586	0.94	3	10347	0.83	10
mir-989	88414	0.87	4	20745	0.88	1
mir-9b	10570	0.87	5	9038	0.85	4
mir-184	30821	0.80	6	152506	0.65	18
mir-996	28482	0.78	7	3193	0.73	na
mir-79	6723	0.75	8	90	0.79	na
mir-33	4025	0.67	9	12173	0.59	22
mir-34	6344	0.66	10	1744	0.16	na



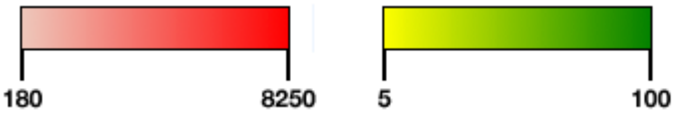
na = not applicable as signal < 5% max

The absolute values for expression of transcripts are not comparable between the two studies although each employs the three-colour scale, shown.

Table S5. Comparison of FlyAtlas 2 and FlyAtlas 1 data for 60 most highly expressed genes in the Malpighian tubules
(i) Ordered by most enriched genes in FlyAtlas 1

	FlyAtlas 1			FlyAtlas 2		
Gene	Abundance	Whole	Enrich.	FPKM	Whole	Enrich.
CG4314	4177	45	93	190	4.7	40
CG9270	1106	13	81	54	1.3	42
CG33282	798	10	73	103	1.3	79
CG15088	918	13	68	95	5.1	19
CG18095	980	14	68	271	4.6	59
CG13905	1534	22	67	289	3.7	78
CG3212	281	4	64	40	0.7	57
CG15408	4337	67	64	597	13	46
CG13311	1876	29	63	428	9.3	46
CG8837	1088	17	61	101	3.7	27
CG10207	2613	43	60	946	17.9	53
CG8028	2008	34	59	212	5	42
CG8620	979	16	59	156	2.4	65
CG17751	1859	31	58	196	3.4	58
CG31792	218	3	58	13	0.3	43
CG1139	1727	30	58	116	7.8	15
CG18473	4250	75	56	297	7.1	42
CG16727	2501	44	56	283	4.6	62
CG9717	1989	37	53	113	5.4	21
CG3285	3501	67	52	364	8.9	41
CG33281	1936	39	49	131	6	22
CG42235	1425	29	49	1542	29.5	52
CG13977	2635	54	49	437	10.2	43
CG6465	3646	78	46	226	5.8	39
CG15221	594	13	45	62	1.7	36
CG34043	4207	94	44	825	11.1	74
CG15155	5291	120	44	1695	33	51
CG10369	4932	115	43	418	10	42
CG3270	6215	147	42	903	22.5	40
CG14606	1468	34	42	276	5.6	49
CG14575	512	12	42	49	1.1	45
CG6602	3426	81	42	805	15	54
CG17752	6340	156	40	1131	18	63
CG17110	1174	29	40	91	1.6	57
CG2759	1571	39	40	127	4.3	30
CG31272	6019	151	40	533	8.4	63
CG30277	1637	42	39	212	4.3	49
CG31106	5145	133	38	710	12.2	58
CG31663	1365	36	38	210	5.8	36
CG34456	303	8	38	67	2	34
CG32024	2491	67	37	593	10.3	58
CG6125	4530	122	37	319	8.3	38
CG17027	1526	41	37	210	6.8	31
CG5697	3029	82	37	302	8.3	36
CG32024	2492	67	37	593	10.3	58
CG10626	348	9	36	22	0.8	28

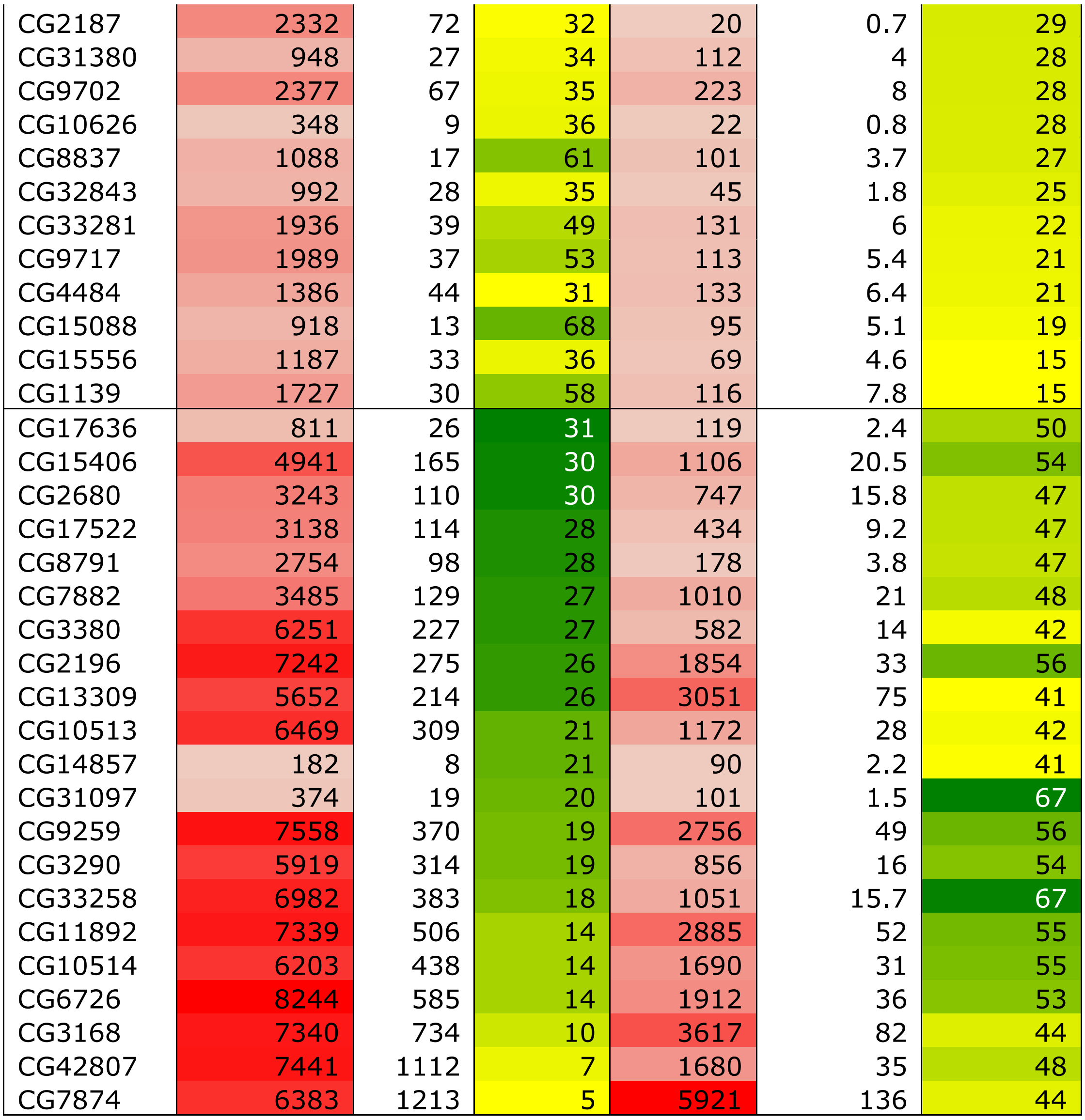
CG32023	4818	133	36	1000	21	48
CG15556	1187	33	36	69	4.6	15
CG7171	6590	183	36	940	9.4	100
CG10006	902	25	36	365	7.3	50
CG32843	992	28	35	45	1.8	25
CG9702	2377	67	35	223	8	28
CG30016	3945	112	35	1503	45	33
CG31380	948	27	34	112	4	28
CG3690	566	16	34	356	6.7	53
CG14957	1989	60	33	312	5.2	60
CG2187	2332	72	32	20	0.7	29
CG9444	398	12	32	31	0.7	44
CG5361	535	16	32	49	0.8	61
CG4484	1386	44	31	133	6.4	21
CG31097	374	19	20	101	1.5	67
CG33258	6982	383	18	1051	15.7	67
CG9259	7558	370	19	2756	49	56
CG2196	7242	275	26	1854	33	56
CG11892	7339	506	14	2885	52	55
CG10514	6203	438	14	1690	31	55
CG15406	4941	165	30	1106	20.5	54
CG3290	5919	314	19	856	16	54
CG6726	8244	585	14	1912	36	53
CG17636	811	26	31	119	2.4	50
CG7882	3485	129	27	1010	21	48
CG42807	7441	1112	7	1680	35	48
CG2680	3243	110	30	747	15.8	47
CG17522	3138	114	28	434	9.2	47
CG8791	2754	98	28	178	3.8	47
CG3168	7340	734	10	3617	82	44
CG7874	6383	1213	5	5921	136	44
CG10513	6469	309	21	1172	28	42
CG3380	6251	227	27	582	14	42
CG14857	182	8	21	90	2.2	41
CG13309	5652	214	26	3051	75	41



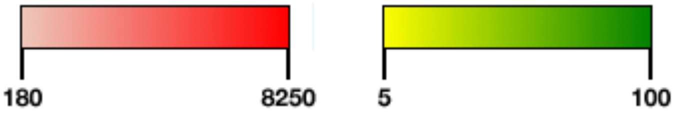
The abundance values for FlyAtlas 1 are in arbitrary units. The ‘Enrich.’ column is the enrichment calculated by dividing the absolute value of expression in Malpighian tubules by that in whole flies.

(ii) Ordered by most enriched genes in FlyAtlas 2

	FlyAtlas 1			FlyAtlas 2		
Gene	Abundance	Whole	Enrich.	FPKM	Whole	Enrich.
CG7171	6590	183	36	940	9.4	100
CG33282	798	10	73	103	1.3	79
CG13905	1534	22	67	289	3.7	78
CG34043	4207	94	44	825	11.1	74
CG8620	979	16	59	156	2.4	65
CG31272	6019	151	40	533	8.4	63
CG17752	6340	156	40	1131	18	63
CG16727	2501	44	56	283	4.6	62
CG5361	535	16	32	49	0.8	61
CG14957	1989	60	33	312	5.2	60
CG18095	980	14	68	271	4.6	59
CG31106	5145	133	38	710	12.2	58
CG17751	1859	31	58	196	3.4	58
CG32024	2491	67	37	593	10.3	58
CG32024	2492	67	37	593	10.3	58
CG3212	281	4	64	40	0.7	57
CG17110	1174	29	40	91	1.6	57
CG6602	3426	81	42	805	15	54
CG3690	566	16	34	356	6.7	53
CG10207	2613	43	60	946	17.9	53
CG42235	1425	29	49	1542	29.5	52
CG15155	5291	120	44	1695	33	51
CG10006	902	25	36	365	7.3	50
CG30277	1637	42	39	212	4.3	49
CG14606	1468	34	42	276	5.6	49
CG32023	4818	133	36	1000	21	48
CG13311	1876	29	63	428	9.3	46
CG15408	4337	67	64	597	13	46
CG14575	512	12	42	49	1.1	45
CG9444	398	12	32	31	0.7	44
CG31792	218	3	58	13	0.3	43
CG13977	2635	54	49	437	10.2	43
CG8028	2008	34	59	212	5	42
CG18473	4250	75	56	297	7.1	42
CG10369	4932	115	43	418	10	42
CG9270	1106	13	81	54	1.3	42
CG3285	3501	67	52	364	8.9	41
CG4314	4177	45	93	190	4.7	40
CG3270	6215	147	42	903	22.5	40
CG6465	3646	78	46	226	5.8	39
CG6125	4530	122	37	319	8.3	38
CG15221	594	13	45	62	1.7	36
CG5697	3029	82	37	302	8.3	36
CG31663	1365	36	38	210	5.8	36
CG34456	303	8	38	67	2	34
CG30016	3945	112	35	1503	45	33
CG17027	1526	41	37	210	6.8	31
CG2759	1571	39	40	127	4.3	30



CG2187	2332	72	32	20	0.7	29
CG31380	948	27	34	112	4	28
CG9702	2377	67	35	223	8	28
CG10626	348	9	36	22	0.8	28
CG8837	1088	17	61	101	3.7	27
CG32843	992	28	35	45	1.8	25
CG33281	1936	39	49	131	6	22
CG9717	1989	37	53	113	5.4	21
CG4484	1386	44	31	133	6.4	21
CG15088	918	13	68	95	5.1	19
CG15556	1187	33	36	69	4.6	15
CG1139	1727	30	58	116	7.8	15
CG17636	811	26	31	119	2.4	50
CG15406	4941	165	30	1106	20.5	54
CG2680	3243	110	30	747	15.8	47
CG17522	3138	114	28	434	9.2	47
CG8791	2754	98	28	178	3.8	47
CG7882	3485	129	27	1010	21	48
CG3380	6251	227	27	582	14	42
CG2196	7242	275	26	1854	33	56
CG13309	5652	214	26	3051	75	41
CG10513	6469	309	21	1172	28	42
CG14857	182	8	21	90	2.2	41
CG31097	374	19	20	101	1.5	67
CG9259	7558	370	19	2756	49	56
CG3290	5919	314	19	856	16	54
CG33258	6982	383	18	1051	15.7	67
CG11892	7339	506	14	2885	52	55
CG10514	6203	438	14	1690	31	55
CG6726	8244	585	14	1912	36	53
CG3168	7340	734	10	3617	82	44
CG42807	7441	1112	7	1680	35	48
CG7874	6383	1213	5	5921	136	44



The abundance values for FlyAtlas 1 are in arbitrary units. The 'Enrich.' column is the enrichment calculated by dividing the absolute value of expression in Malpighian tubules by that in whole flies.

Table S6. Genes for which there are no data in FlyAtlas 2 because their transcripts are indistinguishable from those of other genes

Masked Gene	**Symbol**	**Masking Gene**	**Symbol**
FBgn0003067	Pepck	FBgn0266488	CG45087
FBgn0004407	DNApol-γ35	FBgn0064115	GatC
FBgn0024182	waw	FBgn0024251	bbx
FBgn0025355	SuUR	FBgn0266540	CG45101
FBgn0025825	HDAC3	FBgn0266539	CG45100
FBgn0026778	Rad1	FBgn0085343	Sws1
FBgn0027358	Tim9b	FBgn0031041	CG12788
FBgn0028581	mei-217	FBgn0002709	mei-218
FBgn0029154	Menl-1	FBgn0029153	Menl-2
FBgn0030298	Or10a	FBgn0045502	Gr10a
FBgn0031159	CG11566	FBgn0064123	stg1
FBgn0031454	CG9960	FBgn0031455	Snapin
FBgn0032755	CG17344	FBgn0263982	CG43731
FBgn0033693	CG13175	FBgn0053964	CG33964
FBgn0034649	PIG-M	FBgn0259726	CG42380
FBgn0039367	CG17197	FBgn0039366	CG17198
FBgn0040715	CG15386	FBgn0259717	CG42371
FBgn0042182	CG18749	FBgn0064126	CG33722
FBgn0050072	Obp50c	FBgn0050073	Obp50b
FBgn0050080	CG30080	FBgn0261538	CG42662
FBgn0050100	CG30100	FBgn0259718	CG42372
FBgn0050481	mRpL53	FBgn0053155	CG33155
FBgn0052298	CG32298	FBgn0052299	CG32299
FBgn0061361	CG33786	FBgn0061362	CG33785
FBgn0085206	CG34177	FBgn0085207	CG34178
FBgn0085344	CG34315	FBgn0005654	lat
FBgn0085346	CG34317	FBgn0260468	CG7950
FBgn0250911	CG42245	FBgn0035357	MEP-1
FBgn0259199	Snup	FBgn0259200	CG42304
FBgn0259202	CG42306	FBgn0034372	Gint3
FBgn0259709	CG42363	FBgn0259708	CG42362
FBgn0259721	CG42375	FBgn0260464	CG9288
FBgn0259725	CG42379	FBgn0259726	CG42380
FBgn0259727	CG42381	FBgn0259726	CG42380
FBgn0259730	tal-1A	FBgn0259733	tal-AA
FBgn0259731	tal-2A	FBgn0259733	tal-AA
FBgn0259732	tal-3A	FBgn0259733	tal-AA
FBgn0259933	CG42456	FBgn0035436	CG12016
FBgn0259990	CG42487	FBgn0039565	CG4884
FBgn0259991	CG42488	FBgn0039339	CG5116
FBgn0260222	CG42496	FBgn0050290	Ppcdc
FBgn0260223	CG42497	FBgn0027360	Tim10

FBgn0260224	CG42498	FBgn0039405	PIG-P
FBgn0260228	CG42502	FBgn0040992	CG10570
FBgn0260229	CG42503	FBgn0039280	Mocs2
FBgn0260231	CG42505	FBgn0260230	CG42504
FBgn0260237	CG42511	FBgn0037689	CG8135
FBgn0260401	MED9	FBgn0260392	CG42518
FBgn0260454	CG17139	FBgn0260453	CG17140
FBgn0260759	CG42557	FBgn0260760	CG42558
FBgn0261353	Ccdc56	FBgn0261381	mtTFB1
FBgn0261357	CG42634	FBgn0261358	CG42635
FBgn0261536	CG42660	FBgn0261537	CG42661
FBgn0261679	CG42726	FBgn0261680	CG42727
FBgn0261683	B9d2	FBgn0261697	tectonic
FBgn0261704	CG42740	FBgn0027544	CG2217
FBgn0261837	pre-mod(mdg4)-T	FBgn0261838	pre-mod(mdg4)-Z
FBgn0262837	CG43201	FBgn0262807	CG43178
FBgn0263387	CG43439	FBgn0250849	CG32388
FBgn0264298	CG43776	FBgn0264297	CG43775
FBgn0264364	CG43816	FBgn0045827	CG13245
FBgn0265083	CG44194	FBgn0038107	CG17327
FBgn0265968	Tfb5	FBgn0031668	CG31917
FBgn0266195	Tgs1	FBgn0261019	moi
FBgn0266435	CG45065	FBgn0266434	CG45064
FBgn0266438	PIG-Z	FBgn0266439	CG45069
FBgn0266445	CG45075	FBgn0266450	Kr-h1
FBgn0266489	CG45088	FBgn0027581	CG6191
FBgn0266525	CG45092	FBgn0033095	CG3409
FBgn0266526	CG45093	FBgn0050497	CG30497
FBgn0266538	CG45099	FBgn0038927	CG6015

‘Masked’ Genes are those that were absent from the FPKM or RPM output of the computational analysis of the sequence reads. In each case an overlapping gene was identified with an identical transcript and this is referred to as a ‘masking’ gene and is listed in the second half of the table.

Table S7. Transcripts for which there are no data in FlyAtlas 2

FBtr0070244
FBtr0070691
FBtr0070742
FBtr0071008
FBtr0071052
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FBtr0071681
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FBtr0347349

Table S8. RNA genes detected in FlyAtlas 2

Type	Total	Signal
All RNA genes	3603	1828
pseudogene	232	74
ncRNA	549	370
snRNA	31	24
tRNA	314	8
rRNA	151	6
snoRNA	288	214
lincRNA	1800	1003
pre miRNA	238	129

A signal was regarded as an FPKM greater than 2 or an RPM (microRNAs) greater than 100 in at least one tissue.

Figure S1. Relational database schema for FlyAtlas 2

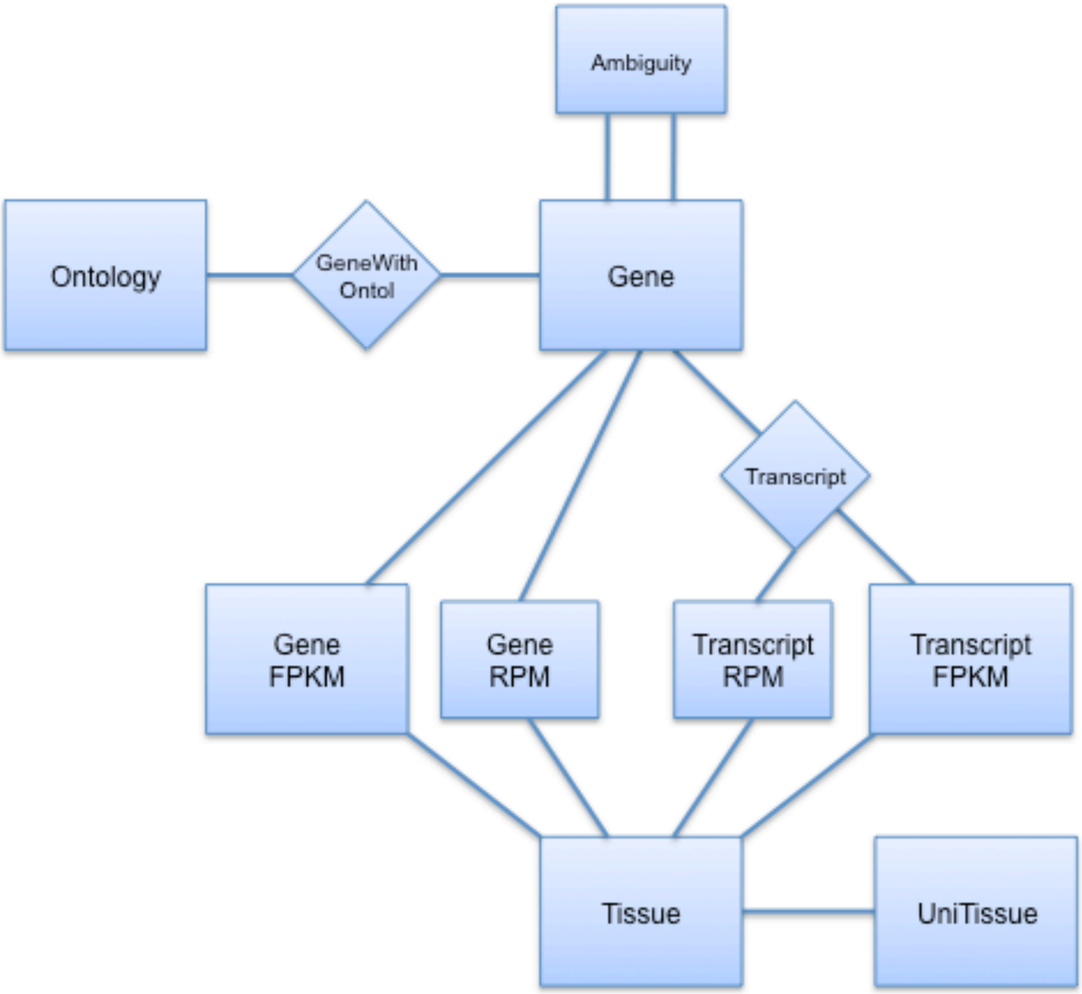
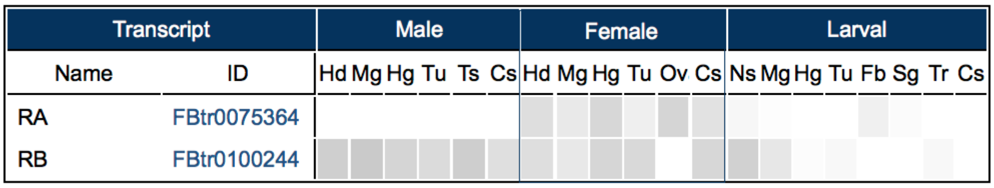


Figure S2. Validation of FlyAtlas 2 data set by reference to genes the transcripts of which show well-characterized sexual dimorphism in soma

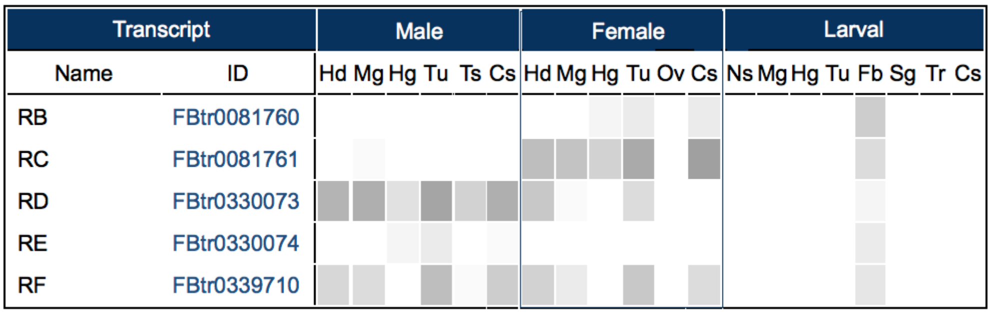
tra



Transcript		Male						Female						Larval							
Name	ID	Hd	Mg	Hg	Tu	Ts	Cs	Hd	Mg	Hg	Tu	Ov	Cs	Ns	Mg	Hg	Tu	Fb	Sg	Tr	Cs
RA	FBtr0075364							▨	▨	▨	▨	▨	▨	▨	▨			▨	▨		
RB	FBtr0100244	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨		▨	▨	▨	▨	▨			▨	

The isoform FBtr0075364, expressed only in females, is the key factor allowing splicing of exon 4 of *dsx* in females to produce *dsx* transcript FBtr008176 (3).

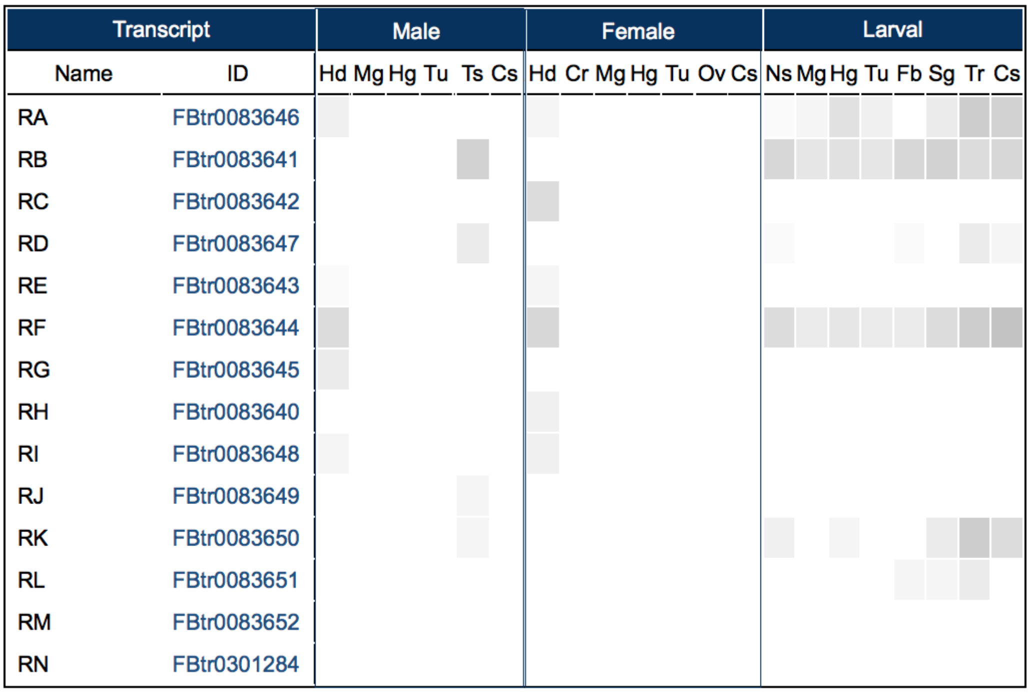
dsx



Transcript		Male						Female						Larval							
Name	ID	Hd	Mg	Hg	Tu	Ts	Cs	Hd	Mg	Hg	Tu	Ov	Cs	Ns	Mg	Hg	Tu	Fb	Sg	Tr	Cs
RB	FBtr0081760									▨	▨		▨					▨			
RC	FBtr0081761		▨					▨	▨	▨	▨		▨					▨			
RD	FBtr0330073	▨	▨	▨	▨	▨	▨	▨	▨		▨							▨			
RE	FBtr0330074			▨	▨		▨											▨			
RF	FBtr0339710	▨	▨		▨	▨	▨	▨	▨		▨		▨					▨			

The differential splicing of exon 4 causes FBtr0081761 to be expressed only in females, and FBtr0330073 in males, as explained in the main text.

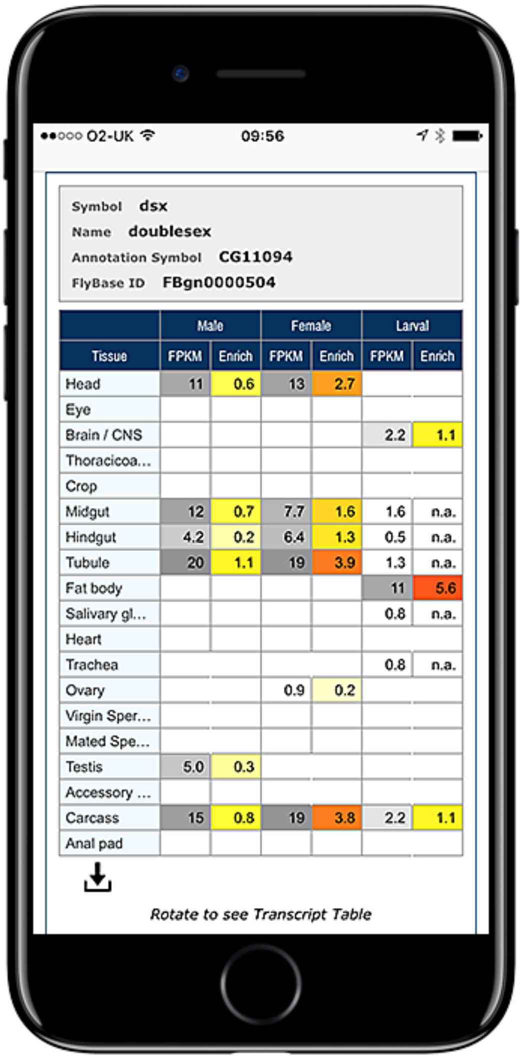
fru



Transcript		Male						Female							Larval							
Name	ID	Hd	Mg	Hg	Tu	Ts	Cs	Hd	Cr	Mg	Hg	Tu	Ov	Cs	Ns	Mg	Hg	Tu	Fb	Sg	Tr	Cs
RA	FBtr0083646	▨						▨							▨	▨	▨	▨		▨	▨	▨
RB	FBtr0083641					▨									▨	▨	▨	▨	▨	▨	▨	▨
RC	FBtr0083642							▨														
RD	FBtr0083647					▨									▨				▨		▨	▨
RE	FBtr0083643	▨						▨														
RF	FBtr0083644	▨						▨							▨	▨	▨	▨	▨	▨	▨	▨
RG	FBtr0083645	▨																				
RH	FBtr0083640							▨														
RI	FBtr0083648	▨						▨														
RJ	FBtr0083649					▨																
RK	FBtr0083650					▨									▨		▨			▨	▨	▨
RL	FBtr0083651																		▨	▨	▨	
RM	FBtr0083652																					
RN	FBtr0301284																					

Differences in exons 2 and 3 resulting from alternative splicing results in male-specific and female-specific forms of *fru*, the male-specific ones being implicated in control of courtship behaviour (4). The isoform here found only in the heads of males, FBtr0083645, shows the male-specific splice, whereas FBtr0083642, here found only in females, shows the female-specific splice.

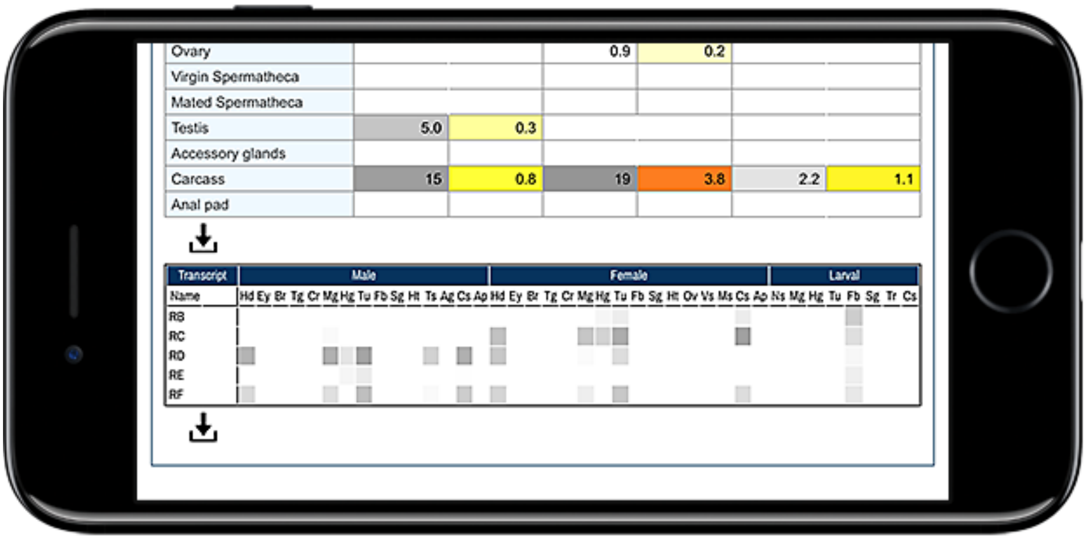
Figure S3. Responsive adaptation of FlyAtlas 2 search output to mobile devices



Symbol **dsx**
Name **doublesex**
Annotation Symbol **CG11094**
FlyBase ID **FBgn0000504**

	Male		Female		Larval	
Tissue	FPKM	Enrich	FPKM	Enrich	FPKM	Enrich
Head	11	0.6	13	2.7		
Eye						
Brain / CNS					2.2	1.1
Thoracicoa...						
Crop						
Midgut	12	0.7	7.7	1.6	1.6	n.a.
Hindgut	4.2	0.2	6.4	1.3	0.5	n.a.
Tubule	20	1.1	19	3.9	1.3	n.a.
Fat body					11	5.6
Salivary gl...					0.8	n.a.
Heart						
Trachea					0.8	n.a.
Ovary			0.9	0.2		
Virgin Sper...						
Mated Spe...						
Testis	5.0	0.3				
Accessory ...						
Carcass	15	0.8	19	3.8	2.2	1.1
Anal pad						

Rotate to see Transcript Table



Ovary			0.9	0.2		
Virgin Spermatheca						
Mated Spermatheca						
Testis	5.0	0.3				
Accessory glands						
Carcass	15	0.8	19	3.8	2.2	1.1
Anal pad						

Transcript	Male															Female																Larval							
Name	Hd	Ey	Br	Tg	Cr	Mg	Hg	Tu	Fb	Sg	Ht	Ts	Ag	Cs	Ap	Hd	Ey	Br	Tg	Cr	Mg	Hg	Tu	Fb	Sg	Ht	Ov	Vs	Ms	Cs	Ap	Ns	Mg	Hg	Tu	Fb	Sg	Tr	Cs
RB																																							
RC																																							
RD																																							
RE																																							
RF																																							

An iPhone 7 (375×667 px) is illustrated. On an iPhone 5 (320×568 px) in portrait view the table is visible, but not the area below it.

References for Supplementary Data

1. Chintapalli, V.R., Wang, J. and Dow, J.A.T. (2007) Using FlyAtlas to identify better Drosophila melanogaster models of human disease. *Nat Genet*, **39**, 715-720.
2. Fagegaltier, D., König, A., Gordon, A., Lai, E.C., Gingeras, T.R., Hannon, G.J. and Shcherbata, H.R. (2014) A genome-wide survey of sexually dimorphic expression of Drosophila miRNAs identifies the steroid hormone-induced miRNA let-7 as a regulator of sexual identity. *Genetics*, **198**, 647-668.
3. Lynch, K.W. and Maniatis, T. (1996) Assembly of specific SR protein complexes on distinct regulatory elements of the Drosophila doublesex splicing enhancer. *Genes & Development*, **10**, 2089-2101.
4. Ryner, L.C., Goodwin, S.F., Castrillon, D.H., Anand, A., Villella, A., Baker, B.S., Hall, J.C., Taylor, B.J. and Wasserman, S.A. (1996) Control of male sexual behavior and sexual orientation in Drosophila by the fruitless gene. *Cell*, **87**, 1079-1089.