

Table S1A. Genes more dependent on *topi* than *achi/vis*

Gene	Function	topi-v- achi/vis	aly-v-wild -type	comr-v-wild type	topi-v-wild type	achi/vis-v- wild type	can-v-wild type	Wild-type rank	Map
CG11591	Unknown	-4.61	-3.80	-2.98	-7.70	-3.09	-1.96	8	64A
CG4439	Leucyl aminopeptidase	-3.46	-1.73	-1.97	-7.17	-3.70	-2.33	46	53C
CG7046	DNA binding	-3.48	-0.67	-0.88	-5.15	-1.66	-1.07	50	94B
CG3213	Cytoskeleton	-6.55	-10.02	-10.15	-10.21	-3.66	-2.39	74	23F
CG5017	Nucleosome assembly	-3.18	-4.24	-5.27	-6.55	-3.37	-1.74	96	98B
CG7164	Cytoskeleton	-3.77	-8.07	-7.95	-7.48	-3.72	-2.40	170	28C
TrxT	Thioredoxin	-6.06	-1.37	-1.33	-6.05	0.02	0.61	174	4F
Menl-2	Malate dehydrogenase	-3.01	-5.31	-5.28	-5.80	-2.79	-2.03	272	53C
CG6790	Unknown	-3.28	-2.80	-1.92	-5.73	-2.45	-0.38	320	86E
CG15177	Unknown	-3.45	-6.08	-5.84	-6.41	-2.96	-1.10	342	84A
CG11601	Unknown	-3.13	-0.93	-0.96	-3.94	-0.81	-0.65	399	21B
CG9875	5-Formyltetrahydrofolate cyclo-ligase	-4.21	-5.78	-6.78	-7.00	-2.78	-1.76	424	59D
CG13473	Pyridoxamine-phosphate oxidase	-3.52	-1.76	-3.37	-6.69	-3.17	-1.47	510	84E
CG15742	Cell adhesion	-4.26	-0.42	-1.33	-6.19	-1.93	-0.31	521	11E
CG4198	Cytoskeleton	-4.10	-2.15	-2.46	-7.23	-3.14	-1.24	537	4F
CG13186	Unknown	-4.62	-6.70	-6.15	-7.14	-2.51	-3.24	706	48E
CG3994	Metal ion transporter	-3.21	-3.52	-2.45	-5.66	-2.44	-0.37	731	35C
CG3121	Cytoskeleton	-4.87	-1.86	-4.91	-7.33	-2.46	-0.92	809	60B
CG11068@	Unknown	-4.37	-2.81	-2.38	-7.20	-2.83	-1.12	1090	12C
CG11700S	DNA metabolism	-7.24	0.70	0.92	-4.79	2.45	2.94	1342	5E
CG16781	Unknown	-4.73	-1.32	-1.71	-5.68	-0.95	-0.28	1563	3D
CG10881	Translational initiation	-4.44	-6.79	-7.11	-6.57	-2.13	-0.53	1639	92E
I-+	Protein phosphatase inhibitor	-4.27	-5.19	-3.63	-6.48	-2.21	-0.92	1826	86E
CG14708	Defense response	-5.37	0.43	0.70	-6.06	-0.69	0.99	1829	86E
CG11700S		-8.96	0.79	1.02	-6.35	2.61	3.23	1866	5E
CG13829	Oxidative phosphorylation	-3.65	-3.33	-2.98	-5.06	-1.41	0.24	1964	94E
CG6301	Cytoskeleton	-3.68	0.24	-1.46	-4.84	-1.17	-1.44	2122	53D
CG14811	Unknown	-3.48	2.07	1.44	-1.80	1.68	0.40	2124	2B
CG18472	Chaperone	-3.89	-2.89	-0.79	-5.49	-1.60	0.08	2364	97D
CG15296	Unknown	-3.57	-5.78	-5.24	-5.31	-1.74	-0.55	2416	9D
CG10459	Receptor kinase	-4.69	0.23	-0.36	-5.93	-1.24	0.06	2708	46B
CG10513	Unknown	-3.74	0.66	0.86	-2.11	1.63	1.29	3001	96C
CG5065	Unknown	-4.97	1.39	1.43	-4.43	0.54	1.72	3090	53C
CG10748	Tricarboxylic acid cycle	-4.61	2.03	2.56	-4.46	0.15	0.58	3362	69F
GstD5	Glutathione S-transferase	-3.34	0.77	3.40	0.30	3.64	-0.03	3598	87B
CG1924	Chaperone	-4.14	-1.74	-2.28	-4.30	-0.16	0.29	4079	11A
CG5342	Unknown	-5.64	0.76	1.54	-3.83	1.81	1.73	4273	86E
CG1494	ABC transporter	-3.74	-3.65	-3.87	-3.76	-0.02	0.77	4307	19F
CG18518	RNA polymerase	-4.05	2.00	2.47	-3.49	0.56	0.17	4717	35D
CG12725	Ubiquitin-like	-5.14	-0.19	0.68	-4.43	0.71	1.03	5179	11F
Cyp4p3	Cytochrome P450	-3.07	0.35	2.89	0.35	3.42	0.70	5200	45B
CG1268	Hydrogen-exporting ATPase	-3.03	-0.58	1.88	-0.56	2.47	0.25	5781	64A
Arc-p34	Cytoskeleton	-3.50	1.75	2.10	-1.13	2.37	1.83	5850	38C
CG15730	Unknown	-3.60	2.17	0.14	-3.18	0.42	0.39	6076	11A
CG6704	Aryl sulfotransferase/ retinoid dehydratase	-3.71	0.67	1.55	-0.93	2.78	1.47	6629	50C

Table S1B. Genes more dependent on *achi/vis* than *topi*

Gene	Function	topi-v- achi/vis	aly-v-wild type	comr-v- wild type	topi-v-wild type	achi/vis-v- wild type	can-v-wild type	Wild- type rank	Map
Mst84Dc	Unknown	3.12	-0.65	-0.99	-3.16	-6.27	-1.64	1	84D
CR32658	Non-coding RNA	3.33	-0.82	-1.01	-3.14	-6.47	-1.61	30	11A
CG15219	Unknown	3.76	-1.12	-1.92	-1.79	-5.54	-2.37	33	40E
CG12816	Unknown	5.68	-0.32	-0.55	-2.30	-7.97	-0.87	85	86A
CG17736	Unknown	4.48	-2.86	-2.73	-3.77	-8.24	-3.26	87	76D
CG10396	Cytochrome-c oxidase	3.55	-1.98	-2.14	-4.16	-7.72	-2.39	132	41F
CG7211	Hydrogen-exporting ATPase	4.19	0.59	0.11	0.44	-3.75	0.08	193	28C
Mst57Db @ψ	Oviposition	3.23	-1.10	-1.46	0.72	-2.51	0.22	289	96F
CG9222	Protein kinase	4.22	-0.01	-1.68	-2.87	-7.09	-2.07	386	26B
CR32661	Non-coding RNA	3.12	-0.83	-1.57	-3.65	-6.77	-2.83	427	10F
CG16825	Amino acid transport	3.70	-0.23	-0.96	-0.51	-4.21	-1.39	462	34B
Arp53D	Cytoskeleton	3.53	-0.16	0.22	-3.62	-7.15	0.11	497	53D
CG8349	Cytidine deaminase	5.60	-2.63	-2.62	-2.20	-7.80	-3.04	575	28F
CG7570	Unknown	3.96	-1.31	-1.91	-1.47	-5.44	-1.86	588	76D
CG32316-ORFB	Tricarboxylic acid cycle	3.21	-1.45	-2.88	-2.67	-5.88	-1.93	798	62A
Mst57Da @ψ	Oviposition	3.27	-0.90	-1.13	1.26	-2.02	0.47	811	96F
CG14757	Unknown	4.02	0.20	0.08	-0.54	-4.56	-0.47	882	44B
CG5103	Transketolase	3.42	-3.12	-2.78	-2.83	-6.25	-2.80	909	75C
CG13032	Cytoskeleton	3.09	-0.15	-0.52	-0.63	-3.71	-1.38	967	73B
CG12376	Unknown	4.18	-0.79	-1.93	-2.90	-7.08	-0.58	1196	44E
GstE1	Glutathione S-transferase	3.87	0.18	-3.89	0.70	-3.17	0.11	1232	55C
CG1950	Unknown	5.52	-2.72	-0.91	-0.70	-6.23	-1.29	1297	11A
CG7257	Proteasome regulation	3.58	0.95	0.88	1.49	-2.08	0.57	1391	68E
Acp70A @	Hormone, female mating / oviposition	3.07	-1.44	-2.26	0.04	-3.02	-0.79	1454	70A
CG31872 @##	Triacylglycerol lipase	3.25	-0.90	-1.94	0.73	-2.52	0.62	1875	32A
CG13501	Unknown	5.39	0.99	0.00	-0.86	-6.24	-1.82	2658	58B
CG12817	Unknown	5.77	3.04	2.17	2.16	-3.60	0.78	2681	86A
CG9227	Unknown	3.43	2.46	2.36	1.20	-2.23	1.28	2737	26B
CG10694	Base-excision repair	3.53	-0.03	0.04	-0.19	-3.71	-0.92	2858	95E
vis	Transcription factor	3.47	3.19	2.71	2.51	-0.96	2.06	2951	49A
msopa @	Unknown	3.52	-0.68	-1.09	1.48	-2.04	0.48	3077	79B
CG17097 @*	Triacylglycerol lipase	3.53	-1.22	-2.33	-0.05	-3.58	0.27	3113	32A
CG14838	Cytoskeleton	4.89	0.49	0.85	0.78	-4.11	0.09	3190	66A
CG14839	Cytoskeleton	5.18	-0.51	-0.31	0.14	-5.05	-1.32	3196	88B
CG11052	Unknown	5.08	1.70	1.62	1.69	-3.39	1.10	3758	84E
Cyp4p1	Cytochrome P450	5.87	-1.61	-6.67	0.72	-5.15	-2.38	4000	45B
CG2667	Diacylglycerol kinase	3.14	-2.16	-1.78	-0.52	-3.67	-1.92	4177	84E
CG9777	mRNA processing	4.27	2.75	2.46	1.16	-3.11	0.34	4557	14F
CG31872 @##	Triacylglycerol lipase	3.12	-0.54	-1.97	0.95	-2.17	0.41	4967	32A
CG14087	Unknown	6.59	2.71	2.58	3.05	-3.54	1.59	5011	76B
CG1442	Translation initiation	3.49	3.73	3.53	3.41	-0.08	2.99	5139	98F
CG6244	Unknown	5.79	2.66	2.08	1.83	-3.97	2.26	5229	72A
CG31633	Unknown	3.22	2.84	2.98	3.06	-0.16	2.51	5409	26F
Acp33A @	Hormone, regulation of female mating	3.19	-1.43	-3.16	0.86	-2.33	-0.03	5534	33A
CG18284 @*	Lipase	3.20	-1.10	-0.73	0.97	-2.23	0.19	6463	32A
CG18240	Unknown	4.47	-1.39	-1.69	3.06	-1.41	3.49	6981	47D
CG2467	Cell communication	3.35	1.32	0.87	1.50	-1.86	0.01	7027	10F
Obp56d	Pheromone response	3.96	-0.39	-1.70	1.70	-2.26	-0.03	7386	56E
CG13617	Unknown	3.75	3.58	3.03	3.61	-0.14	1.64	7961	96A

Table S1C. Genes whose relative expression in wild-type and mutant testes has previously been determined by northern blotting or RNA in situ hybridisation (White-Cooper et al., 1998)

Gene	Function	aly-v-wild type	comr-v-wild type	topi-v-wild type	achi/vis-v-wild type	can-v-wild type	Wild-type rank	Map
Reduced in aly and can class on northern or by RNA in situ								
Mst84Dc	Unknown	-0.65	-0.99	-3.16	-6.27	-1.64	1	84D
Mst84Dd	Unknown	-1.35	-2.53	-4.42	-4.30	-2.09	3	84D
Mst84Da	Unknown	-0.72	-1.03	-2.88	-4.37	-1.40	4	84D
Mst84Db	Unknown	-1.03	-1.59	-4.04	-5.05	-1.86	9	84D
Mst98Ca	Unknown	-1.17	-2.14	-5.20	-6.34	-1.78	16	98C
Mst87F	Unknown	-2.12	-4.00	-4.97	-5.92	-2.06	26	87F
Mst98Cb	Unknown	-0.76	-1.07	-5.62	-6.38	-2.21	34	98C
dj	Sperm tail	-6.39	-6.82	-8.65	-9.45	-2.36	124	84C
janB	Unknown	-3.74	-4.50	-7.94	-7.89	-2.95	152	99D
gdl	Unknown	-3.84	-3.58	-3.51	-3.89	-2.44	407	71C
fzo	Mitochondrial fusion	-6.75	-6.98	-6.24	-6.56	-2.41	2647	94E
Reduced in aly-class specifically by RNA in situ								
bol	Cell cycle	-2.13	-2.71	-3.41	-3.57	-1.38	345	66F
twe	Cell cycle	-1.06	-1.40	-1.67	-2.65	0.18	2711	35F
CycB	Cell cycle	-0.88	-1.03	-0.84	-0.47	1.16	2944	59A
Expression detected in mutants at similar levels to wild-type by RNA in situ								
rux	Cell cycle	0.11	-0.38	-0.79	-1.19	0.17	972	5D
polo	Cell cycle	0.89	1.38	0.47	0.28	0.47	2174	77B
neb	Cytoskeleton	-1.04	-0.97	-0.76	-1.34	0.02	2267	38B
pelo	Cell cycle	1.20	1.34	0.68	0.93	1.09	2965	30C
CycA	Cell cycle	1.82	1.37	1.45	1.09	1.50	4695	68D

Fold-change expression differences between testis RNA samples analysed on the Affymetrix chips. Fold changes are expressed as the \log_2 of the expression ratio for each genotype pair. **Bright green** indicates at least an eightfold reduction ($\log_2 \leq -3$); **Dark green** indicates at least a twofold reduction ($\log_2 \leq -1$); **yellow** indicates at least a twofold increase ($\log_2 \geq 1$); **red** indicates at least an eightfold increase ($\log_2 \geq 3$). Wild-type rank is the rank order of the signal intensity for the wild-type samples (so CG11591 was the eighth most intense signal on the wild-type arrays). Predicted function and cytogenetic map position were taken from FlyBase. Genes chosen for further analysis by RT-PCR and in situ are shown in bold.

@, genes for which the one-tailed *t*-test *P*-value for *achi/vis*>*topi* (A) or *topi*>*achi/vis* (B) was greater than 0.005 but less than 0.05. For all other genes *P*<0.005.

\$ and # indicate genes with two probes on the array

* and ψ indicate pairs (or more) of homologous genes from the same chromosomal region (i.e. recent duplications).

