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Supplementary Information for

Crtc Modulates Fasting Programs Associated with 1-C Metabolism and Inhibition of Insulin Signaling

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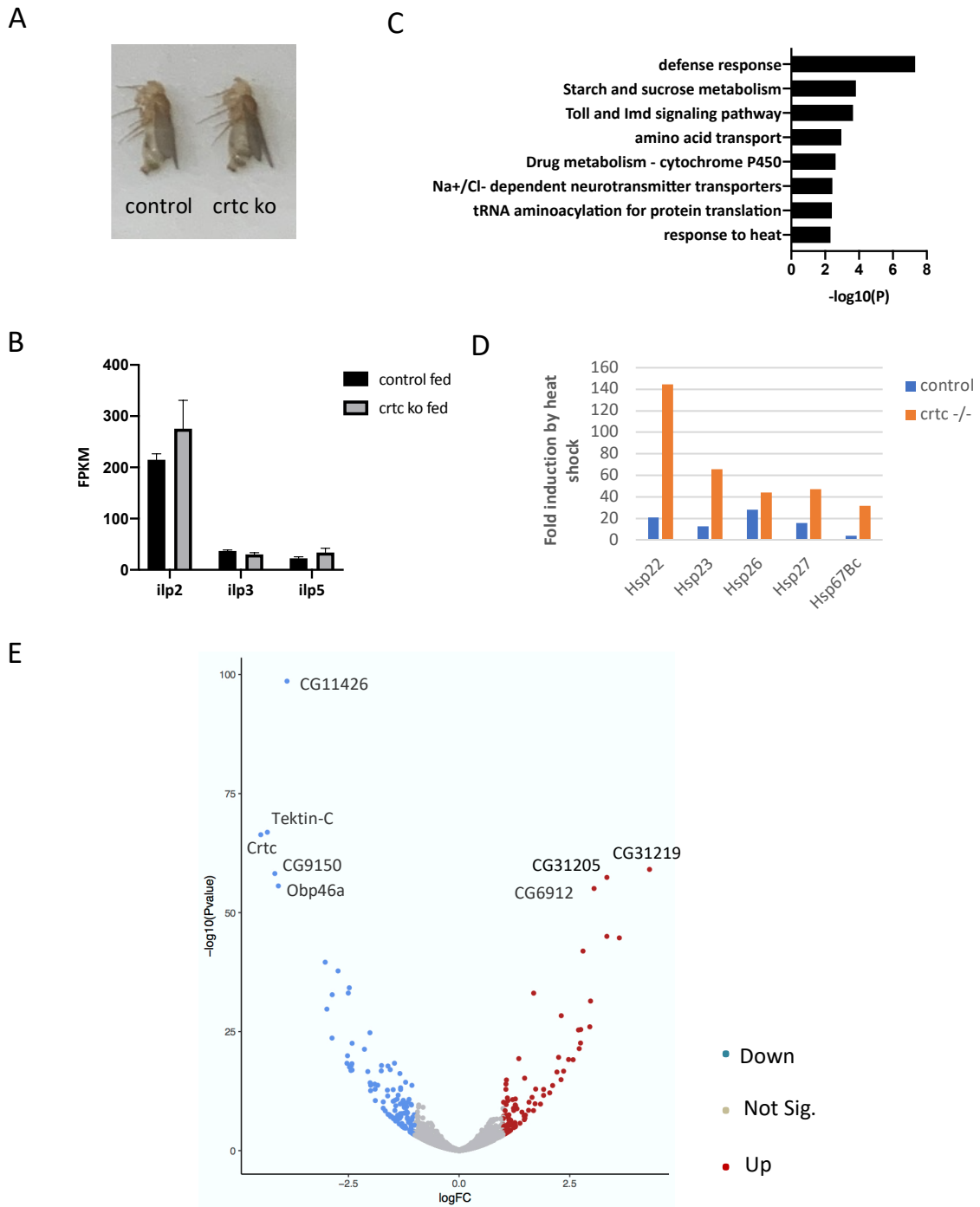


Fig. S1. CRTC promotes starvation resistance. (A) Comparison of body sizes between control and Crtc KO adult flies. (B) Comparison of Dilp expression in control and Crtc KO flies in the fed state. (C) Gene ontology enrichment analysis with the list of down-regulated genes in Crtc KO in the fed state. (D) Fold change of several small heat shock mRNAs in response to thermal stress in control and Crtc KO. (E) Volcano plot showing significantly altered genes in the absence of Crtc in the fed state in fly heads; Blue and red dots in the volcano plot indicate genes fulfilling the

following criteria, fold change > 2 and adjusted p value < 0.05; Blue dots are down-regulated genes and red dots are up-regulated genes in Crtc KO.

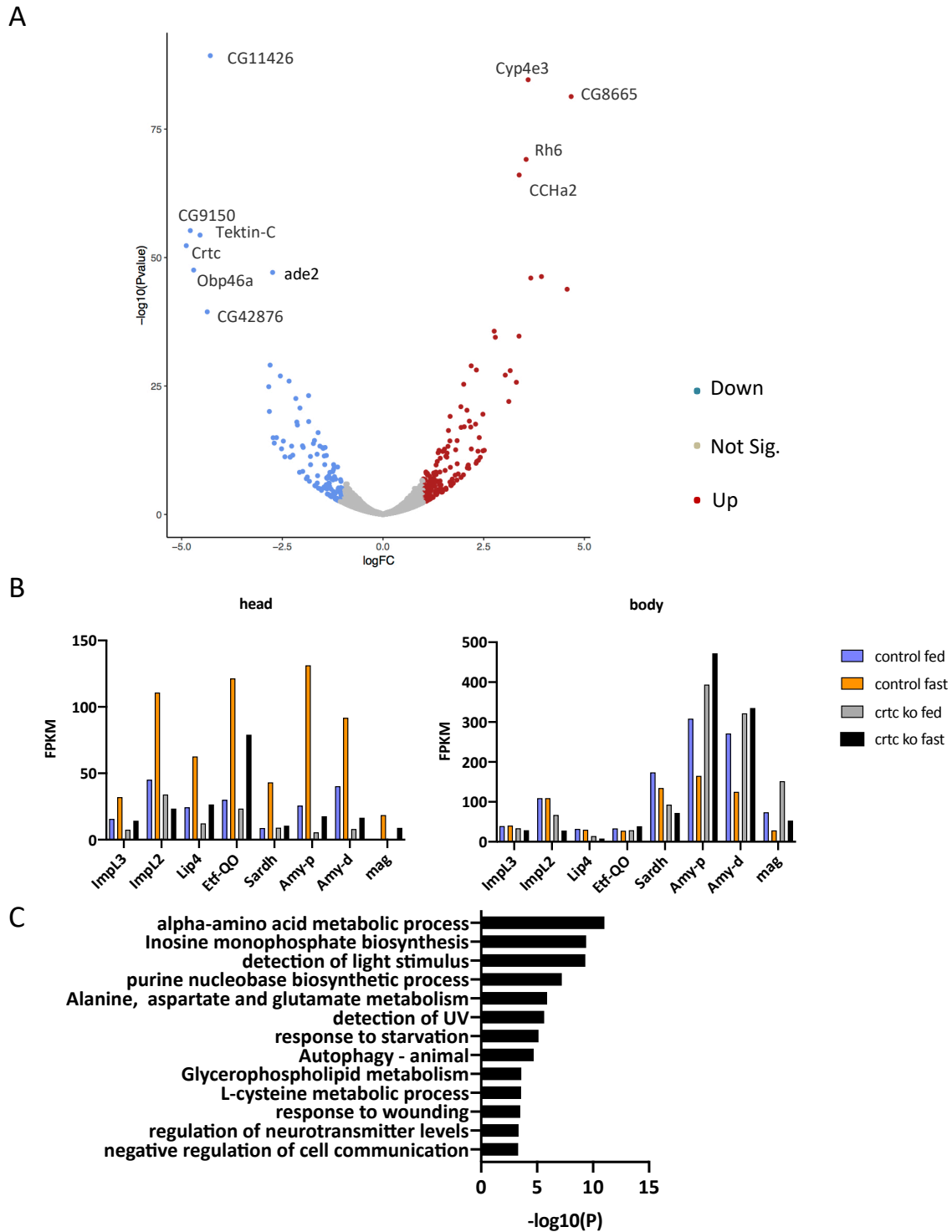


Fig. S2. CRTC promotes fasting-inducible gene expression. (A) Volcano plot showing significantly altered genes in Crtc KO fly heads in the fasted state compared with control; The blue and red dots in the volcano plot indicate genes fulfilling the following criteria, fold change > 2 and adjusted p value < 0.05; Blue dots correspond to down-regulated genes and red dots are up-regulated genes in Crtc KO. (B) Examples of fasting-inducible genes in the fly head but not in the

body from RNA-seq studies. (C) Gene ontology enrichment analysis with fasting-inducible genes in the fly body.

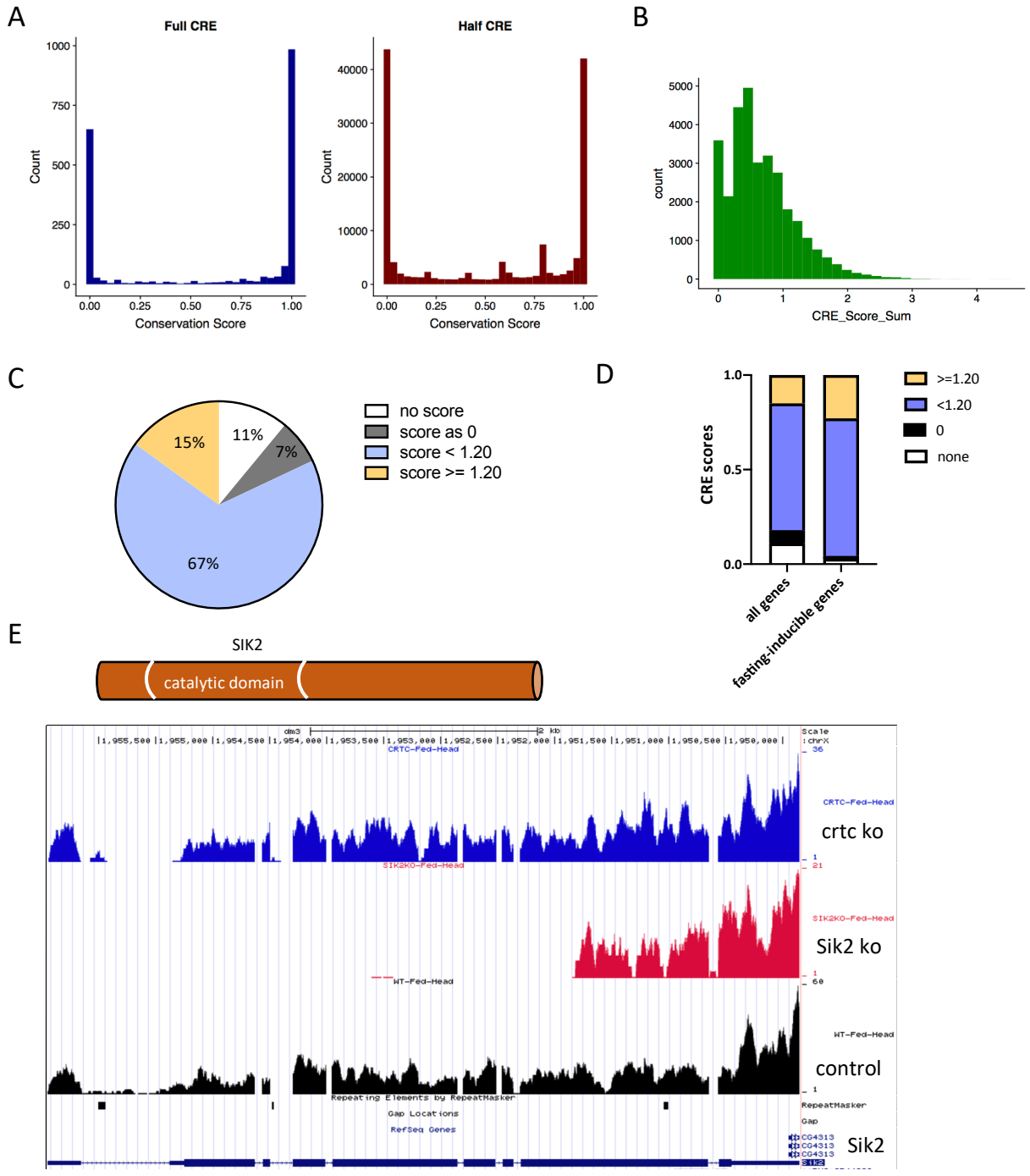


Fig. S3. CREB binding sites in the fly genome. (A) Conservation score distribution for all full CRE sites and half CRE sites in the fly genome. (B) CRE score distribution for all fly genes. (C) Percentage of fly genes with no CRE score, score as 0, score less than 1.2, score equals to or higher than 1.20. (D) Enrichment of genes having greater CRE scores among fasting-inducible genes compared with all genes in the fly genome. (E) Schematic diagram showing deletion of the

catalytic domain in Sik2 mutant, UCSC genome browser view showing no transcripts of the catalytic domain in Sik2 KO.

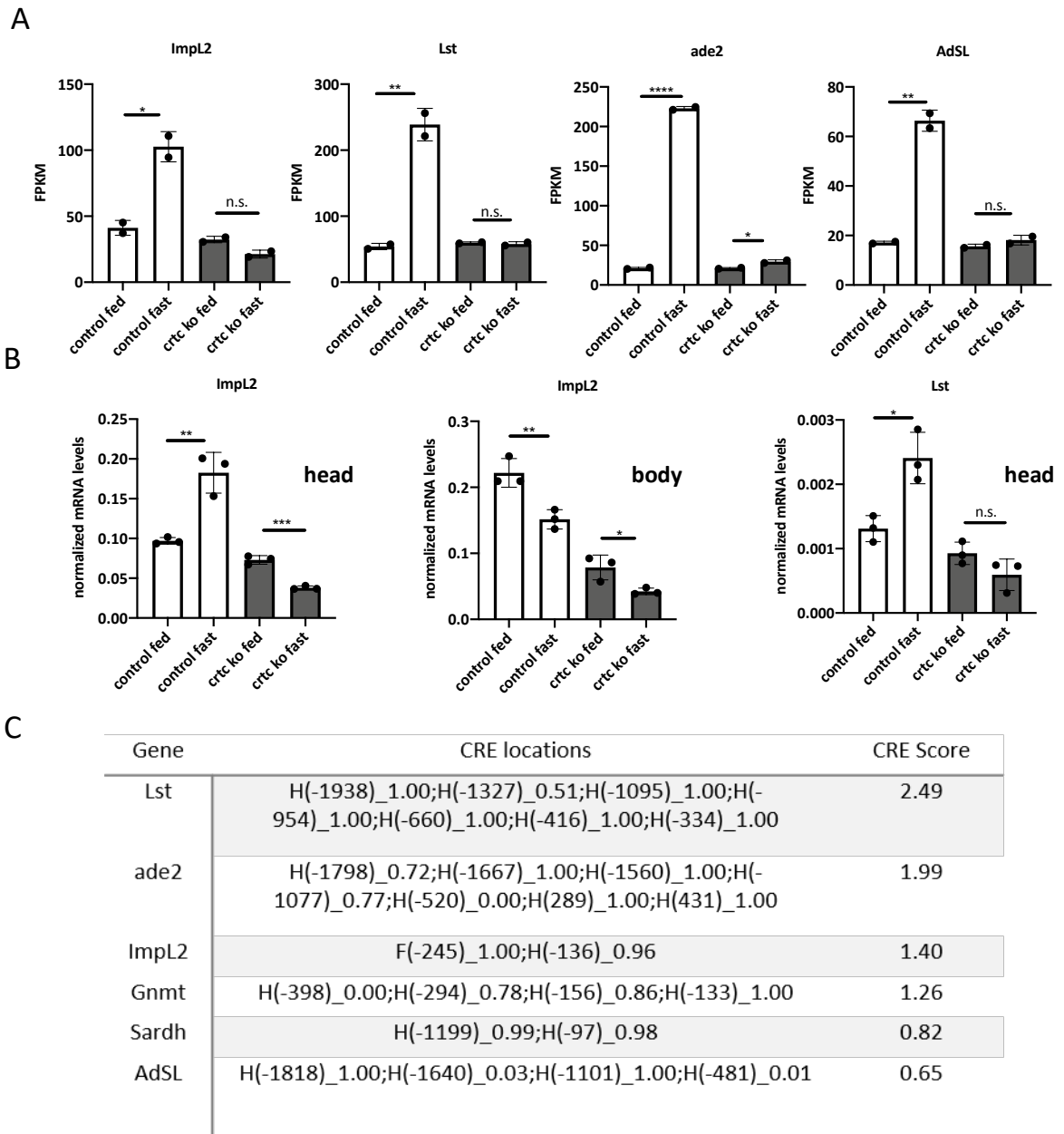


Fig. S4. CRTC stimulates expression of genes involved in one carbon metabolism and inhibition of insulin signaling. (A) Impl2, Lst, Ade2 and AdSL mRNA levels in adult fly head, genotypes and conditions as indicated. (B) Impl2 mRNA levels in adult fly head and fly body, Lst mRNA levels in adult fly head. (C) CRE information for CRTC target genes, Gnmt, Sardh, ade2, AdSL, Impl2 and Lst; The CREs are listed in the following format: {Full or Half site}(distance to transcription start site)_(conservation score). The listed CRE sites are within 2kb upstream and 500 bp downstream of transcription start site (TSS).

Table S1. FKPM of the 91 fasting-inducible genes shown in the heatmap in Figure 2A.

Gene	white fed-1	white fasted-1	crtc ko fed-1	crtc ko fasted-1	white fed-2	white fasted-2	crtc ko fed-2	crtc ko fasted-2
AdSL	16.7971	63.3695	16.2366	16.7526	17.5305	69.3623	15.0338	19.542
Adgf-D	35.0991	93.7841	19.738	44.6331	39.3781	98.0226	20.8751	51.2627
Ahcy13	40.163	186.488	48.1101	124.307	45.5154	232.735	62.0369	176.734
Amy-d	40.3109	91.8234	8.05947	16.5523	39.1519	106.73	8.07528	19.0611
Amy-p	25.6619	131.343	5.59577	17.6509	41.997	249.488	7.18074	30.6622
CG10361	9.26351	23.1892	11.4537	16.5109	10.0192	20.1996	8.66629	19.6257
CG10383	11.5323	116.572	14.7199	115.8	11.6033	98.0487	13.8337	131.567
CG10924	1.19038	9.03302	14.7855	309.861	0.662564	10.1542	15.4561	314.401
CG11089	47.0503	473.121	44.5705	352.171	51.666	551.476	49.047	493.115
CG11425	13.6814	65.9586	9.14394	15.0363	16.2685	88.0609	9.95437	19.2099
CG11899	56.3361	236.515	43.0674	147.884	75.0046	297.224	63.9936	223.879
CG12262	91.9173	229.803	57.5061	241.92	98.9623	285.442	76.6946	302.765
CG12428	15.1111	32.3386	13.9302	68.4965	12.1667	27.6657	14.0539	72.1496
CG12825	2.87892	7.61335	5.86584	6.49136	2.96372	10.2605	7.28814	14.6437
CG14022	18.3206	43.2952	21.1198	40.9702	21.6653	52.169	16.5563	50.3155
CG1441	11.2366	42.2186	11.7915	61.5	16.814	47.3026	15.5292	80.8113
CG1673	20.5933	168.432	11.2326	125.789	20.6106	168.451	12.1991	160.781
CG16758	130.513	399.878	174.847	508.291	135.253	430.516	225.579	683.829
CG17597	9.4166	22.6449	9.38089	21.3864	10.671	22.2608	11.1607	28.015
CG18547	5.26581	10.9306	9.19137	14.0241	6.57959	13.7309	8.31962	16.2807
CG3011	59.6602	267.124	49.6518	135.65	78.7801	351.644	66.6977	202.676
CG3036	103.006	283.831	106.605	266.424	95.4978	264.654	99.8258	276.428
CG32687	39.3269	79.6463	43.1923	101.627	42.066	98.0134	49.4429	135.222
CG34136	23.3956	90.5076	11.9213	145.929	25.957	80.5056	23.2731	185.232
CG3999	4.33155	11.1878	3.11073	2.90627	3.22242	10.3202	2.96295	4.03465
CG42675	3.17485	8.53324	9.0937	13.6906	7.16253	15.4732	12.0222	17.5704
CG42708	24.0167	51.4001	24.4375	68.1889	26.8587	56.6871	26.3892	78.1702
CG42751	11.3258	26.3296	3.34603	10.1142	4.07687	18.414	0.937289	6.80403
CG42806	43.7838	106.207	40.379	129.546	42.8982	123.312	53.2167	158.784
CG42876	14.4527	63.011	0.556784	0	12.4367	51.4113	0	0
CG45087	128.411	1015.95	170.918	959.988	125.211	1022.95	189.98	1137.27
CG5321	15.3759	34.7839	17.4786	72.1809	18.6831	39.6896	24.2854	87.7037
CG5953	8.87284	31.2392	6.4661	28.838	7.90384	28.366	6.64343	26.7738
CG5955	21.9575	98.4232	24.4062	92.0661	28.6872	133.199	30.0838	132.185
CG5966	6.92595	191.985	2.81093	152.721	6.98767	186.364	2.4971	159.758
CG6188	161.718	441.55	80.8978	134.305	170.253	485.444	112.259	171.064
CG6287	186.093	438.146	190.196	342.784	243.751	605.924	255.212	521.919
CG6385	8.79331	43.2456	9.08925	10.5644	10.5677	41.6326	8.95202	11.514
CG6767	182.024	480.635	161.533	274.463	147.959	335.927	128.185	237.604
CG7059	14.7528	61.7184	11.9323	44.8833	15.7302	70.4568	17.592	56.3298
CG7530	36.4632	81.3763	33.9732	100.197	33.9104	84.2234	33.0662	118.953

Continued. Gene	white fed-1	white fasted-1	crtc ko fed-1	crtc ko fasted-1	white fed-2	white fasted-2	crtc ko fed-2	crtc ko fasted-2
CG7763	2.42172	40.6286	0.443598	0.968973	1.41435	28.0125	0.385946	1.6204
CG8112	20.6586	54.3355	22.3891	63.2502	24.6903	68.2208	42.0931	97.0992
CG8129	9.18211	39.4921	6.99164	64.7438	8.42901	40.6992	10.3804	69.8552
CG8249	2.9306	12.7243	4.36089	8.96511	3.896	12.0974	5.3103	11.3701
CG8317	57.4598	256.195	60.7098	60.3549	50.6727	221.342	58.879	55.5653
CG8468	24.6931	50.7867	42.6062	78.4221	26.4319	59.1348	47.7428	90.8028
CG8654	10.5881	40.2272	7.24561	56.4715	9.24608	41.9767	10.1829	63.6345
CG9547	13.7822	39.9601	16.0278	29.6957	15.8721	47.2664	15.2245	35.5381
CG9757	1.50756	10.6237	1.36311	3.77781	2.57607	15.1652	4.09725	1.83356
CR44138	5.7076	13.3512	3.41157	16.2284	3.17872	11.0231	7.98604	24.1834
CR44816	4.63352	31.5846	14.25	15.8337	8.6506	24.2578	21.2199	17.6342
CR45018,IP3K2	10.904	26.6712	3.3112	4.0368	8.94743	30.7661	6.71452	4.91237
Cyp4ac3	7.90791	18.9149	6.98494	16.7448	6.95096	16.1381	4.90868	17.8907
Cyp4e2	32.6891	79.5329	36.273	97.6722	28.533	62.8803	35.4863	99.975
Cyp4e3	5.56986	105.237	7.0611	1478.5	6.10292	98.0905	8.33451	1620.98
Cyp4p1	26.191	61.8988	12.4212	18.2753	25.0887	54.4007	13.2449	18.4404
Cyp6a2	13.4251	32.9618	14.1802	31.9297	18.1469	36.8792	22.2143	36.0711
Cyp6a8	3.59867	21.093	2.70798	26.159	2.27537	18.2994	2.25592	22.6416
Cyp6w1	46.9063	104.962	45.1286	101.444	38.8924	101.928	43.401	111.949
Etf-QO	30.0868	121.487	23.435	79.078	34.7504	137.687	31.3663	102.634
Fuca	4.59449	10.3243	4.78042	12.103	5.14272	13.7622	5.88957	15.1525
Gillspla2	26.0755	236.607	16.1738	141.684	33.0719	299.733	20.8027	185.632
ldgf1	32.2723	83.9368	24.8749	25.8994	28.6079	72.6051	20.1755	28.8307
ImpL2	45.175	110.759	34.0735	23.3999	37.1806	94.5664	30.6086	19.1425
ImpL3	15.7376	32.0953	7.61076	14.3405	20.696	44.4639	8.95344	30.3095
InR	7.30988	16.4978	8.43799	19.6895	4.21841	9.00552	4.95771	9.94683
Lip4	24.4435	62.6641	12.3448	26.5589	23.9901	52.4195	11.4374	29.3778
Mal-B2	96.3998	669.68	48.6989	269.2	100.094	638.215	49.4414	310.585
Nmdmc	61.4896	265.04	16.6023	103.112	64.8414	290.859	20.2344	169.627
Reg-2	35.2561	90.3193	32.7774	82.0982	33.8022	96.2059	44.1083	124.562
SCOT	15.9249	32.0679	26.6161	51.5792	18.7956	40.3409	36.1338	64.4257
Scfp	13.4221	28.8431	16.1177	54.5939	11.2739	31.6172	13.6986	45.8278
Sirup	165.943	491.735	154.79	658.011	204.041	688.781	247.796	1024.06
Spat	48.7003	146.76	29.5468	159.048	54.0694	182.198	43.5224	224.986
Spn27A	25.7639	52.6072	28.1447	40.9363	35.2433	73.049	36.5791	65.7402
Spn88Eb	21.1737	68.585	10.431	94.2221	14.8672	69.6537	8.66629	98.1283
T3dh	4.4633	12.0849	7.30253	22.2623	5.00744	10.3933	7.84543	30.6558
Thor	389.102	1046.23	215.175	1139.52	290.12	870.693	186.779	1146.56
Tsp42Ed	29.5065	106.539	21.9967	60.5994	36.51	150.441	26.925	97.0388
aay	152.296	596.289	146.836	805.379	152.313	589.869	157.188	938.596
ade2	21.9207	224.684	21.7226	31.0683	20.24	221.158	20.5704	27.9121
ade3	21.7572	172.647	23.5168	148.232	23.5109	188.468	20.9603	177.27
ade5	135.1	624.706	106.359	392.273	120.563	580.371	97.526	403.77
atk	2.04769	26.4547	0.94025	9.31988	1.15279	22.9189	0.886715	10.6438
bmm	31.9207	157.38	23.2108	107.7	29.0347	140.446	22.0193	112.554
fbp	62.3036	188.27	51.8783	143.613	69.9337	221.455	65.7054	183.645

Continued. Gene	white fed-1	white fasted-1	crtc ko fed-1	crtc ko fasted-1	white fed-2	white fasted-2	crtc ko fed-2	crtc ko fasted-2
mag	0.212542	18.5618	0.197171	8.90934	0.311792	18.4102	0	11.5792
pug	61.2127	173.727	65.5517	80.8201	69.2697	186.508	67.7489	100.522
rost	6.22428	17.0486	4.69874	4.01136	4.88496	15.5597	3.20835	3.38676
yip2	87.568	191.979	96.6058	356.691	75.1095	199.15	95.5022	440.876

Table S2. FKPM of the 92 fasting-downregulated genes shown in the heatmap in Figure 2A.

Gene	white fed-1	white fasted-1	crtc ko fed-1	crtc ko fasted-1	white fed-2	white fasted-2	crtc ko fed-2	crtc ko fasted-2
AQP	15.2232	7.25833	6.29179	8.14339	18.8018	9.3815	11.5136	10.7339
CCHa2	140.416	46.2777	385.545	558.026	113.34	39.6834	384.548	584.052
CG10026	24.9056	9.50822	22.411	13.0759	24.1495	10.1281	21.5111	16.0761
CG10516	20.4593	4.71609	20.0686	12.4948	21.1041	8.03656	33.2291	15.7635
CG10657	14.4725	4.74895	27.6141	25.5457	17.5231	5.3308	38.2009	25.269
CG11458	34.6403	16.6845	19.3294	55.4152	35.7804	12.5905	34.3643	57.0793
CG11741	30.9492	7.65818	7.72299	10.4719	34.0929	12.4575	6.21418	5.25529
CG13026	18.7348	9.16835	4.4036	5.56189	13.8514	6.6203	3.79254	5.66331
CG13360	14.5398	6.37356	13.7721	14.836	17.4926	6.98326	21.615	17.2556
CG13422	189.98	53.5589	104.078	173.738	173.731	58.7743	147.188	69.9701
CG13607	50.774	8.63793	44.5269	29.0999	57.9817	13.9641	53.9516	41.6156
CG14246	10.3756	2.126	6.48226	8.80269	8.38832	3.28978	6.17281	9.01711
CG14298	28.3306	9.81222	41.7565	27.4726	30.7157	10.0406	47.1893	31.008
CG14419	56.6704	16.1095	132.105	114.968	51.9591	14.8621	153.157	106.94
CG14439	18.7015	8.02454	26.1052	18.2527	20.6159	7.64653	27.6736	24.6569
CG14567	29.8658	5.56581	5.74566	2.09715	29.1166	7.64445	8.73327	1.30835
CG14687	246.401	110.896	94.0404	75.3832	278.43	128.358	100.762	83.6248
CG14688	51.0619	18.3249	37.2978	34.9336	41.8128	20.8604	44.0583	36.7613
CG15021	30.0545	12.6703	26.1978	21.8873	33.1099	14.9118	22.6485	23.5594
CG15096	125.249	62.0822	75.8772	48.0592	116.53	56.1353	82.5477	57.051
CG15282	50.2254	2.64061	96.25	18.2479	52.9552	1.67601	108.99	14.9618
CG15353	49.7162	6.34945	121.47	85.1264	32.9278	9.78859	111.764	72.0832
CG15394	29.3528	12.6228	18.2449	17.2183	13.751	6.40118	14.9884	10.4921
CG16756	84.0774	29.7057	85.0088	66.0768	79.5237	34.4511	102.614	56.9479
CG16772	128.505	41.4856	111.351	55.6516	115.555	46.2701	115.391	55.9641
CG18302	21.989	10.186	25.1367	12.9099	18.8709	8.08367	22.2889	12.8753
CG18522	32.4063	16.0412	37.7849	22.9602	32.5735	13.4603	38.1503	24.7106
CG1887	35.7074	16.9701	45.9201	21.8488	40.3738	14.7799	45.3963	22.0278
CG2781	47.4576	16.0672	51.9637	43.0795	30.81	13.029	39.7523	33.2394
CG3348	55.8917	6.41403	27.0327	8.12234	57.7512	7.62169	20.652	10.4457
CG34165	19.387	9.3146	57.9329	21.2433	25.5837	4.12451	64.3377	19.716
CG34291	25.2508	12.0932	29.9572	32.4891	25.9761	6.69029	18.8637	45.9715
CG3630	25.6285	9.41675	20.1687	13.8155	32.1443	9.45962	23.4741	22.1312
CG4000	160.892	71.9392	103.913	196.926	209.479	91.9745	143.325	277.324
CG42821	21.3985	1.96881	17.0468	3.39313	22.1715	2.56589	18.6426	2.64016
CG4288	22.8723	11.0093	10.7106	6.89487	29.5952	13.3997	16.1225	9.16197
CG4461	84.1111	36.9514	18.5612	26.3799	84.1825	40.6637	16.5473	21.5666
CG4462	12.2094	4.23832	10.9902	6.63022	11.5652	4.24489	9.97103	6.39652
CG4797	32.2584	15.2468	29.2712	25.435	39.5536	19.3254	34.3817	32.0683
CG5023	71.2803	29.3173	102.46	61.5055	92.4631	39.0797	142.82	72.6316
CG5162	42.1312	18.5046	39.2905	21.9242	45.593	21.9213	46.3991	36.1221
CG5707	33.5828	15.783	29.0956	41.3019	36.7705	16.3587	34.382	49.9529
CG5773	232.81	70.0822	271.893	310.504	260.181	82.7332	361.379	444.955
CG5991	101.696	36.8407	121.946	106.184	109.167	33.3414	132.389	123.799

Continued. Gene	white fed-1	white fasted-1	crtc ko fed-1	crtc ko fasted-1	white fed-2	white fasted-2	crtc ko fed-2	crtc ko fasted-2
CG6126	47.9035	17.6791	40.0189	32.6486	55.0532	21.1578	44.7589	30.892
CG7203	90.3285	23.041	84.4486	100.391	94.3532	35.578	99.9855	140.18
CG7300	15.5972	6.44102	4.73044	7.6	14.8168	5.79956	10.1964	6.74069
CG8147	10.592	0.145372	20.4574	0.97542	10.3496	0.207383	26.9725	0.850778
CG9238	70.8084	15.9584	81.2319	63.5909	56.1193	11.0646	70.6845	62.5247
CG9416	10.6749	4.05979	12.2991	7.31655	11.1208	3.61188	13.744	8.42306
CG9436	48.0543	17.3364	44.0492	23.618	68.3684	24.2006	60.9599	37.9846
CG9497	25.4737	11.4569	16.7037	20.8565	26.2701	13.0388	19.5281	25.3562
CG9498	26.6387	6.99384	25.4862	13.1897	28.8025	9.27717	29.1172	16.62
CG9747	19.9634	8.5947	32.6213	22.5583	20.5823	8.90891	37.4528	24.9766
CG9837	36.9363	18.1992	41.9736	18.087	40.7903	13.9633	39.6555	19.1714
CR43995	17.0737	7.09405	20.9975	17.0508	16.0577	6.05433	8.15335	5.57368
CR44095	11.637	5.1848	17.5275	12.7111	11.6401	4.23156	15.8486	10.3301
CR44772	20.6884	8.49755	20.8705	25.7425	16.0693	4.72352	6.38173	13.072
Cg25C	15.4871	5.62379	19.3425	13.8735	17.173	4.86822	17.8155	9.70451
Clect27	98.5889	28.4933	99.9697	57.6085	94.3551	28.8485	110.61	67.4332
Cyp313a1	218.182	92.7605	217.309	158.772	161.92	61.2559	187.293	166.393
Cyp6t1	14.8709	5.03121	15.0947	17.2244	10.2137	4.67213	13.0798	16.6418
DNasell	72.7705	28.7374	33.3012	29.064	73.8104	35.5655	29.7572	35.2394
Dat	133.295	64.6395	128.16	96.2054	169.633	80.2083	174.671	115.186
DptB	242.283	54.9087	197.777	100.254	149.488	45.3797	200.935	10.5223
Drsl4	649.489	230.811	94.9012	24.4116	517.34	201.535	105.174	19.1165
IM14	6133.76	2509.58	2064.56	2310.86	2812.28	1363.26	1556.72	1239.87
Listericin	279.291	92.7818	316.417	163.797	319.187	120.364	377.682	159.884
Lsd-1	76.654	28.2794	69.7814	248.4	91.5707	38.9727	102.121	371.935
Lsp1beta	83.5976	24.3847	329.017	106.897	74.3742	22.5976	331.058	101.255
Lsp2	47.4257	15.3759	201.669	54.8567	39.2925	12.5692	212.438	70.0923
Mlp60A	316.382	113.929	576.347	513.47	344.658	154.264	726.915	478.285
Nplp2	5996.57	1954.5	4220.11	2930.23	4796.04	1552.87	4535.82	3230.15
Nplp3	1081.29	401.409	1055.57	1513.93	946.7	353.979	982.982	1529.6
Nplp4	20.0303	2.6821	45.6445	38.8696	6.83707	1.69982	34.7257	22.3083
Obp99b	759.943	281.551	419.883	577.386	661.787	275.894	459.361	442.442
Ork1	11.7987	4.08261	9.98325	3.5679	15.5876	6.67938	13.877	5.7834
PGRP-SB1	243.79	81.9286	239.241	102.129	248.266	93.1065	288.921	106.638
RabX5	7.57274	3.02597	5.57491	0.756836	11.9473	3.98451	7.01408	2.88684
Rfabg	331.949	128.42	355.521	225.736	238.236	88.0808	269.447	177.903
Tig	17.2134	6.47626	19.126	14.451	16.8029	5.62085	19.0724	15.3973
TotX	74.3668	20.0439	81.1758	44.8433	51.7063	12.3143	75.8463	55.6714
babos	49.9648	23.547	38.755	32.0789	57.7871	22.32	46.362	35.1156
cbt	77.8371	28.4433	49.1792	29.7931	68.7781	22.6021	45.1511	34.9748
fit	194.051	3.69306	117.29	27.8022	127.328	0.492414	120.396	24.2975
fusl	19.7608	9.53204	14.7973	7.02418	22.6042	10.1612	15.7498	9.99844
pncr008:3L	4.79922	2.04831	6.15255	9.63875	21.3405	7.46	9.97386	11.9751
sug	38.6377	8.68087	25.911	24.2051	50.391	10.487	31.6625	30.1239
sxe2	142.572	48.9513	173.881	125.249	161.47	52.1874	202.785	157.193
tobi	14.7797	5.32715	0.661454	0.567016	16.5253	5.34981	0.703703	0.619935
vkg	10.1989	2.77024	10.0382	6.95671	11.2359	3.16846	10.6213	5.89651

Continued. Gene	white fed-1	white fasted-1	crtc ko fed-1	crtc ko fasted-1	white fed-2	white fasted-2	crtc ko fed-2	crtc ko fasted-2
yellow-c	36.7338	14.5286	30.4778	19.7912	33.6554	13.344	22.6949	17.3511

Table S3. 85 fasting-inducible genes shown in the volcano plot in Figure 2B.

GeneID	log2(FC)	StdErr	Wald-Stats	P-value	P-adj
CG5966	4.33079299	0.17712939	24.4498839	5.05E-132	4.72E-128
ade2	3.16077359	0.1523123	20.7519266	1.18E-95	5.51E-92
CG11089	3.13749236	0.15537531	20.1929912	1.13E-90	3.52E-87
Cyp4e3	3.593549	0.19461764	18.4646619	3.98E-76	9.30E-73
ade3	2.9366143	0.16958987	17.3159769	3.56E-67	6.67E-64
CG1673	2.70535658	0.16406354	16.4896877	4.35E-61	6.79E-58
CG10383	2.9115558	0.17705937	16.4439517	9.27E-61	1.24E-57
Gllspla2	2.85526943	0.19327914	14.7727756	2.19E-49	2.57E-46
Mal-B2	2.59325423	0.18375692	14.1124165	3.18E-45	3.31E-42
atk	3.19370404	0.22681261	14.0808043	4.98E-45	4.67E-42
bmm	2.08366935	0.16480268	12.6434195	1.22E-36	9.49E-34
Nmdmc	1.98490694	0.15922078	12.4663808	1.14E-35	8.20E-33
ade5	2.12263631	0.17082649	12.4256861	1.90E-35	1.27E-32
aay	1.77895646	0.14795327	12.0237724	2.67E-33	1.66E-30
Etf-QO	1.842308	0.16378618	11.2482506	2.36E-29	1.38E-26
Amy-p	2.17460228	0.20346958	10.6876038	1.16E-26	6.41E-24
mag	2.95757382	0.2770273	10.6761096	1.32E-26	6.85E-24
CG10924	2.71639513	0.26326238	10.3182049	5.83E-25	2.87E-22
Sardh	1.85483228	0.18678915	9.93008557	3.08E-23	1.44E-20
AdSL	1.71774905	0.17408628	9.86722827	5.77E-23	2.57E-20
Lst	1.97544546	0.20180764	9.78875451	1.26E-22	5.35E-20
CG8654	1.79637847	0.18929724	9.48972369	2.32E-21	8.03E-19
CG3011	1.95558284	0.20602234	9.49209124	2.26E-21	8.03E-19
CG8129	1.94770285	0.21516241	9.05224494	1.40E-19	4.52E-17
CG7763	2.48990131	0.27596993	9.02236466	1.84E-19	5.74E-17
CG11899	1.846077	0.20543006	8.98640153	2.55E-19	7.47E-17
CG16758	1.3974266	0.1575668	8.86878849	7.39E-19	2.10E-16
CG3036	1.32327848	0.14964033	8.84306057	9.31E-19	2.56E-16
Ahcy	1.95358643	0.22157011	8.81701258	1.18E-18	3.14E-16
CG5955	1.78528845	0.20283793	8.80155115	1.35E-18	3.51E-16
CG5953	1.60724911	0.18579688	8.65057091	5.12E-18	1.30E-15
CG7059	1.77785989	0.20600059	8.63036307	6.12E-18	1.51E-15
Gnmt	1.45487565	0.17176301	8.47024999	2.45E-17	5.73E-15
CG11425	1.84642097	0.2222947	8.30618542	9.88E-17	2.26E-14
Cyp6a8	2.07779933	0.25373857	8.18874067	2.64E-16	5.75E-14
fbp	1.5321324	0.18844424	8.13042837	4.28E-16	8.90E-14
Thor	1.38110854	0.17109593	8.07212986	6.91E-16	1.41E-13
hll	2.2705306	0.28429927	7.98641025	1.39E-15	2.77E-13
pug	1.42499161	0.18376887	7.75425999	8.89E-15	1.60E-12

Continued. GeneID	log2(FC)	StdErr	Wald-Stats	P-value	P-adj
CG42876	1.66647501	0.21636842	7.70202528	1.34E-14	2.37E-12
Tsp42Ed	1.72925756	0.22504991	7.68388464	1.54E-14	2.68E-12
yip2	1.21904335	0.1660707	7.34050845	2.13E-13	3.50E-11
Spat	1.56204135	0.2134938	7.3165655	2.54E-13	4.04E-11
CG15337	2.05897188	0.28494763	7.22579042	4.98E-13	7.77E-11
Spn88Eb	1.5063443	0.2104895	7.15638687	8.28E-13	1.27E-10
Cyp6w1	1.1926009	0.17401244	6.85353834	7.20E-12	1.07E-09
Sirup	1.47496422	0.21863887	6.74612073	1.52E-11	2.18E-09
wb	1.46438027	0.22094105	6.62792303	3.40E-11	4.69E-09
GLS	1.11991827	0.17037028	6.57343698	4.92E-11	6.67E-09
ldgf1	1.19032549	0.18178714	6.5479082	5.83E-11	7.80E-09
Reg-2	1.40074435	0.21901437	6.39567335	1.60E-10	2.11E-08
Amy-d	1.06778749	0.16794455	6.35797627	2.04E-10	2.66E-08
CG9547	1.33179256	0.21094019	6.31360268	2.73E-10	3.50E-08
CG1441	1.31857834	0.20893322	6.31100369	2.77E-10	3.51E-08
CG7530	1.04288769	0.16785713	6.21294824	5.20E-10	6.32E-08
CG32687	1.080355	0.17551157	6.15546301	7.49E-10	8.92E-08
CG42806	1.27776132	0.2096659	6.09427332	1.10E-09	1.29E-07
CG3902	1.04470894	0.17309614	6.03542588	1.59E-09	1.75E-07
ImpL2	1.13115728	0.19020856	5.94693163	2.73E-09	2.84E-07
CG8468	1.08106829	0.18473655	5.85194575	4.86E-09	4.84E-07
Cyp4p1	1.03219536	0.17823578	5.79117919	6.99E-09	6.81E-07
Lip4	1.12438199	0.19420442	5.78968286	7.05E-09	6.81E-07
CG6287	1.22829181	0.21210893	5.79085388	7.00E-09	6.81E-07
Adgf-D	1.29481189	0.22451342	5.7671914	8.06E-09	7.70E-07
Cyp4e2	1.07176156	0.18747147	5.71693158	1.08E-08	1.01E-06
CG6767	1.06999887	0.19510008	5.48435891	4.15E-08	3.53E-06
CG31075	1.06054354	0.19422808	5.46029972	4.75E-08	4.01E-06
CG3999	1.27818047	0.23706709	5.39164037	6.98E-08	5.80E-06
Grip	1.25588634	0.2335603	5.37713957	7.57E-08	6.21E-06
CG18003	1.00841335	0.1882051	5.35805547	8.41E-08	6.79E-06
CG8249	1.23900556	0.23904013	5.18325339	2.18E-07	1.67E-05
CG34136	1.18369621	0.23197432	5.10270369	3.35E-07	2.51E-05
CG12262	1.33599523	0.26764259	4.99171395	5.98E-07	4.39E-05
Cyp6a2	1.01493967	0.21266842	4.77240431	1.82E-06	0.00011917
CG42751	1.32047186	0.27951238	4.72419813	2.31E-06	0.00014322
Sclp	1.08502127	0.23018223	4.71374904	2.43E-06	0.00014978
Cyp6g1	1.00198998	0.21651273	4.62785714	3.69E-06	0.00021616
CG5321	1.05681301	0.23451585	4.50636069	6.59E-06	0.00035129
CG14022	1.0624592	0.25178017	4.21978911	2.45E-05	0.00115609
Cyp4ac3	1.06923614	0.2544187	4.20266328	2.64E-05	0.00123468

Continued. GeneID	log2(FC)	StdErr	Wald-Stats	P-value	P-adj
CG13283	1.11248683	0.26641264	4.17580342	2.97E-05	0.00136927
CG11125	1.15135585	0.27753604	4.14849129	3.35E-05	0.00151608
CG9757	1.08221961	0.27631559	3.91660715	8.98E-05	0.00367098
CG18858	1.01207884	0.26581804	3.80741222	0.00014043	0.00545457
CG1942	1.00509407	0.27973988	3.59295956	0.00032694	0.0112519

Table S4. 60 fasting-downregulated genes shown in the volcano plot in Figure 2B.

GeneID	log2(FC)	StdErr	Wald-Stats	P-value	P-adj
fit	-3.5762559	0.26512446	-13.48897	1.82E-41	1.55E-38
Gbs-70E	-1.9196215	0.19697233	-9.7456405	1.93E-22	7.84E-20
Nplp2	-1.5266688	0.15691936	-9.7290022	2.27E-22	8.85E-20
Lsp1beta	-1.6273616	0.17098354	-9.5176507	1.77E-21	6.63E-19
sxe2	-1.4312305	0.15719376	-9.104881	8.64E-20	2.89E-17
Root	-2.2780153	0.25349418	-8.98646	2.55E-19	7.47E-17
Clect27	-1.484961	0.1727634	-8.5953444	8.30E-18	1.99E-15
CG5991	-1.3391342	0.16188923	-8.2719165	1.32E-16	2.94E-14
Obp99b	-1.2729592	0.15587903	-8.166328	3.18E-16	6.76E-14
cbt	-1.3773248	0.17391483	-7.9195365	2.38E-15	4.65E-13
Nplp3	-1.3905998	0.17687821	-7.8619056	3.78E-15	7.23E-13
CCHa2	-1.3857296	0.17795735	-7.7868636	6.87E-15	1.29E-12
Col4a1	-1.4196454	0.18298442	-7.7582855	8.61E-15	1.58E-12
CG5773	-1.4731574	0.19314917	-7.6270449	2.40E-14	4.09E-12
vkg	-1.4492649	0.19744278	-7.3401769	2.13E-13	3.50E-11
GNBP-like3	-1.4389712	0.19638398	-7.3273348	2.35E-13	3.79E-11
sug	-1.6214829	0.22874152	-7.0887125	1.35E-12	2.04E-10
CG13607	-1.5944815	0.23343529	-6.8305076	8.46E-12	1.24E-09
CG3348	-1.7081441	0.25328017	-6.7440895	1.54E-11	2.18E-09
CG6126	-1.2143637	0.18111205	-6.7050412	2.01E-11	2.81E-09
PGRP-SB1	-1.4232389	0.22655293	-6.2821477	3.34E-10	4.17E-08
CG9498	-1.3841018	0.22039792	-6.2800131	3.39E-10	4.17E-08
CG15096	-1.0011913	0.16444303	-6.0883777	1.14E-09	1.32E-07
CG16772	-1.1618649	0.19159853	-6.0640592	1.33E-09	1.52E-07
Listericin	-1.2267676	0.20258241	-6.0556475	1.40E-09	1.58E-07
CG7203	-1.435104	0.23846328	-6.018134	1.76E-09	1.92E-07
CG3630	-1.2729309	0.21173961	-6.011775	1.84E-09	1.97E-07
apolpp	-1.2223505	0.20348011	-6.0072235	1.89E-09	2.01E-07
Lsp2	-1.6441519	0.27566933	-5.9642179	2.46E-09	2.59E-07
CG15282	-1.6941467	0.2850756	-5.942798	2.80E-09	2.88E-07
Cyp313a1	-1.1865224	0.2010501	-5.9016256	3.60E-09	3.66E-07
phu	-1.6716687	0.28431462	-5.8796438	4.11E-09	4.14E-07
tobi	-1.2873143	0.22373805	-5.7536674	8.73E-09	8.26E-07
TotX	-1.4398967	0.25067511	-5.7440752	9.24E-09	8.65E-07
Tig	-1.1478994	0.20428546	-5.6190948	1.92E-08	1.74E-06
CG14688	-1.1872298	0.21415973	-5.5436649	2.96E-08	2.64E-06

Continued. GeneID	log2(FC)	StdErr	Wald-Stats	P-value	P-adj
CG5162	-1.0595514	0.1920967	-5.515719	3.47E-08	3.04E-06
CG4000	-1.0964477	0.1990289	-5.5089872	3.61E-08	3.13E-06
CG14439	-1.1879716	0.21633764	-5.491285	3.99E-08	3.43E-06
IM14	-1.1223813	0.20907532	-5.3683107	7.95E-08	6.47E-06
CG2781	-1.1429309	0.21539913	-5.3061075	1.12E-07	8.88E-06
Ork1	-1.1338305	0.21540529	-5.2637076	1.41E-07	1.10E-05
CG14567	-1.3241685	0.26559819	-4.9856084	6.18E-07	4.48E-05
Hml	-1.2258845	0.2466466	-4.9702061	6.69E-07	4.78E-05
CG4462	-1.1532905	0.23343686	-4.9404818	7.79E-07	5.53E-05
CG18302	-1.0744436	0.22143903	-4.8520969	1.22E-06	8.47E-05
CG9436	-1.0864491	0.22693458	-4.787499	1.69E-06	0.00011292
CG9416	-1.1058789	0.2332915	-4.7403312	2.13E-06	0.00013587
CG10516	-1.1615496	0.25001378	-4.6459425	3.39E-06	0.00020314
MFS9	-1.07104	0.23400655	-4.5769658	4.72E-06	0.00026765
CG10026	-1.0382808	0.22873108	-4.5393078	5.64E-06	0.00030539
Cpr49Ae	-1.0021296	0.22374828	-4.4788261	7.51E-06	0.00039033
CG4797	-1.067875	0.24858567	-4.2958027	1.74E-05	0.00084864
CG14298	-1.0553688	0.25283507	-4.1741393	2.99E-05	0.00137256
CG42821	-1.1611169	0.28471349	-4.078194	4.54E-05	0.00199468
Cdk4	-1.0334038	0.26145659	-3.9524872	7.73E-05	0.0032613
CG16978	-1.0134907	0.25761029	-3.9342013	8.35E-05	0.00345299
caix	-1.1009349	0.28402448	-3.8761973	0.0001061	0.00426274
CG9400	-1.0885597	0.284925	-3.8205133	0.00013317	0.00521608
CG11741	-1.0147853	0.2817239	-3.6020561	0.00031571	0.01094579

Table S5. KEGG pathway analysis for genes in Table 1.

PathwayName	#Gene	Statistics
Metabolic pathways	29	C=892;O=29;E=2.22;R=13.08;rawP=4.39e-26;adjP=5.71e-25
Limonene and pinene degradation	7	C=68;O=7;E=0.17;R=41.41;rawP=3.45e-10;adjP=2.24e-09
Glycine, serine and threonine metabolism	5	C=27;O=5;E=0.07;R=74.50;rawP=6.14e-09;adjP=2.66e-08
One carbon pool by folate	3	C=11;O=3;E=0.03;R=109.71;rawP=2.37e-06;adjP=7.70e-06
Purine metabolism	5	C=120;O=5;E=0.30;R=16.76;rawP=1.22e-05;adjP=3.17e-05
Starch and sucrose metabolism	3	C=55;O=3;E=0.14;R=21.94;rawP=0.0003;adjP=0.0006
Pentose phosphate pathway	2	C=22;O=2;E=0.05;R=36.57;rawP=0.0014;adjP=0.0024
Ether lipid metabolism	2	C=23;O=2;E=0.06;R=34.98;rawP=0.0015;adjP=0.0024
Lysine degradation	2	C=26;O=2;E=0.06;R=30.94;rawP=0.0019;adjP=0.0027
Fatty acid metabolism	2	C=28;O=2;E=0.07;R=28.73;rawP=0.0022;adjP=0.0029
Valine, leucine and isoleucine degradation	2	C=31;O=2;E=0.08;R=25.95;rawP=0.0027;adjP=0.0032
Glycerolipid metabolism	2	C=43;O=2;E=0.11;R=18.71;rawP=0.0051;adjP=0.0055
Glycerophospholipid metabolism	2	C=55;O=2;E=0.14;R=14.63;rawP=0.0083;adjP=0.0083

C: the number of reference genes in the category

O: the number of genes in the gene set and also in the category

E: the expected number in the category

R: ratio of enrichment rawP: p value from hypergeometric test

adjP: p value adjusted by the multiple test adjustment

Table S6. CRTC-dependent fasting-inducible genes shown in Figure 2C.

Gene	white fed-1	white fasted-1	crtc ko fed-1	crtc ko fasted-1	white fed-2	white fasted-2	crtc ko fed-2	crtc ko fasted-2
ade2	21.9207	224.684	21.7226	31.0683	20.24	221.158	20.5704	27.9121
CR45018,IP3K2	10.904	26.6712	3.3112	4.0368	8.94743	30.7661	6.71452	4.91237
ImpL2	45.175	110.759	34.0735	23.3999	37.1806	94.5664	30.6086	19.1425
CG11425	13.6814	65.9586	9.14394	15.0363	16.2685	88.0609	9.95437	19.2099
rost	6.22428	17.0486	4.69874	4.01136	4.88496	15.5597	3.20835	3.38676
CG8317(Lst)	57.4598	256.195	60.7098	60.3549	50.6727	221.342	58.879	55.5653
CG6385(Sardh)	8.79331	43.2456	9.08925	10.5644	10.5677	41.6326	8.95202	11.514
CG3999	4.33155	11.1878	3.11073	2.90627	3.22242	10.3202	2.96295	4.03465
AdSL	16.7971	63.3695	16.2366	16.7526	17.5305	69.3623	15.0338	19.542
Cyp4p1	26.191	61.8988	12.4212	18.2753	25.0887	54.4007	13.2449	18.4404
CG6188(Gnmt)	161.718	441.55	80.8978	134.305	170.253	485.444	112.259	171.064
ldgf1	32.2723	83.9368	24.8749	25.8994	28.6079	72.6051	20.1755	28.8307

Table S7. CRE sites and scores for genes shown in Figure 2C.

Gene	All_CREs	CRE_Score_Sum
CR45018	H(-1653)_1.00;H(-1638)_1.00;H(-1513)_1.00;H(-1489)_1.00;F(-1110)_1.00;H(-981)_0.30;H(-639)_0.99;H(-424)_0.00;H(183)_1.00	2.94
Lst	H(-1938)_1.00;H(-1327)_0.51;H(-1095)_1.00;H(-954)_1.00;H(-660)_1.00;H(-416)_1.00;H(-334)_1.00	2.49
ade2	H(-1798)_0.72;H(-1667)_1.00;H(-1560)_1.00;H(-1077)_0.77;H(-520)_0.00;H(289)_1.00;H(431)_1.00	1.99
ImpL2	F(-245)_1.00;H(-136)_0.96	1.40
CG11425	H(-636)_1.00;H(-163)_1.00;H(175)_0.87	1.31
Gnmt	H(-398)_0.00;H(-294)_0.78;H(-156)_0.86;H(-133)_1.00	1.26
ldgf1	H(-776)_1.00;H(-544)_0.89;H(-532)_0.70	1.09
Sardh	H(-1199)_0.99;H(-97)_0.98	0.82
AdSL	H(-1818)_1.00;H(-1640)_0.03;H(-1101)_1.00;H(-481)_0.01	0.65
CG3999	H(-1890)_0.00;H(-372)_0.01;H(-51)_0.05;H(179)_0.80	0.41
Cyp4p1	H(-1289)_0.38;H(-833)_0.46;H(20)_0.00	0.31

Table S8. Genes lower expressed in *crtc* ko under both feeding and fasting condition.

Aats-lys	lr75a	phr	CG10514	CG31954	CG5646
Acp65Aa	lr75b	plx	CG11426	CG32364	CG5791
Amy-d	Jhl-1	RnrL	CG11842	CG32368	CG6639
Amy-p	Jhl-21	Skeletor	CG11892	CG33123	CG6910
c-cup	lig3	Spn55B	CG1246	CG33296	CG9119
Cyp9f3Psi	Mis12	ssx	CG12512	CG34138	CG9121
Dgp-1	noe	Tektin-C	CG13794	CG3513	CG9150
Drsl4	Oat	tobi	CG14186	CG3699	CG9305
dtr	Obp46a	TpnC41C	CG15539	CG42260	CG9505
Hsp67Bc	PGRP-SD	w	CG1667	CG42876	CR13130
	Crtc		CG17264	CG43064	CR44283
			CG2233	CG4757	CR44506
			CG30424	CG5535	CR44922

Table S9. Genes lower expressed in crtc ko uniquely after fasting treatment.

ade2	ImpL2	CG11170	CG3999
AdSL	Lst	CG11425	CG4269
atk	Mal-B2	CG12716	CG5793
CecA2	nesd	CG15093	CG7763
Cyp4p1	ninaG	CG15337	CG7829
Desat1	PGRP-LB	CG15725	CG9279
dob	qin	CG18003	CG9766
edin	rost	CG31974	CR31032
Galk	Rpb12	CG32052	CR45018
Gnmt	Sardh	CG34166	CR45299
Got2	shop		
hll	slam		
ldgf1	TotC		

Table S10. Genes lost fasting-induction in both crtc ko and creb ko.

Gene	white fasted	creb ko fasted	white fast/creb ko fast
ade2	224.684	47.3793	4.74224
ImpL2	110.759	32.6851	3.388669
CG8317(Lst)	256.195	87.9635	2.912515
CG6385(Sardh)	43.2456	19.179	2.254841
CR45018,IP3K2	26.6712	12.5504	2.125127
AdSL	63.3695	34.9441	1.813453

Table S11. Genes having CRE scores greater than 2.50.

Genes	All_CREs	CRE_Score_Sum
CG14185	H(-1837)_1.00;H(-1825)_0.48;H(-1813)_0.01;F(-1693)_1.00;H(-1372)_0.00;F(-1192)_1.00;H(-1078)_1.00;H(-661)_1.00;F(-647)_1.00;F(-636)_1.00;H(380)_0.00;H(434)_0.65	4.43
CG14186	F(-1630)_1.00;F(-1619)_1.00;H(-1605)_1.00;H(-1188)_1.00;F(-1074)_1.00;H(-894)_0.00;F(-573)_1.00;H(-453)_0.01;H(-441)_0.48;H(-429)_1.00;H(-72)_0.41	4.29
CG30456	H(-1785)_1.00;H(-1017)_1.00;F(-931)_1.00;H(-546)_0.00;H(-484)_0.99;H(-434)_1.00;H(-392)_1.00;H(42)_0.31;H(157)_0.97;H(364)_0.97	3.81
Ets21C	H(-1991)_0.48;H(-1282)_0.79;H(-1067)_0.80;H(-1051)_1.00;H(-1039)_0.97;H(-566)_0.85;H(-344)_0.00;H(-335)_0.01;H(6)_1.00;H(211)_1.00;H(411)_1.00;H(453)_1.00	3.65
CG1764	H(-1772)_1.00;H(-1165)_0.00;H(-950)_0.99;H(-608)_0.30;F(-479)_1.00;H(-100)_1.00;H(-76)_1.00;H(49)_1.00;H(64)_1.00	3.63
CG45060	H(-1834)_0.00;H(-1683)_0.00;H(-1214)_0.99;H(-1165)_0.83;H(-1017)_0.94;H(-455)_1.00;H(-415)_1.00;H(-356)_0.91;H(-301)_1.00;H(360)_0.78;H(476)_1.00	3.55
CR44217	H(-1868)_1.00;H(-1743)_1.00;H(-813)_1.00;H(-375)_0.93;H(-325)_0.06;H(-176)_1.00;H(-111)_0.00;H(-3)_1.00;H(101)_1.00;H(304)_1.00	3.32
jbug	H(-1894)_1.00;H(-1695)_1.00;H(-939)_0.00;H(-630)_1.00;F(-66)_1.00;H(194)_1.00;H(211)_1.00;H(240)_0.80	3.28
Hsc70-3	H(-1806)_1.00;H(-1075)_1.00;H(-990)_0.92;H(-612)_0.94;H(-363)_1.00;H(-287)_1.00;H(169)_1.00;H(258)_1.00	3.25
CG5065	H(-1832)_1.00;H(-1826)_1.00;F(-763)_1.00;H(-154)_1.00;H(242)_1.00;H(291)_1.00;H(372)_1.00	3.22
CR44474	H(-1940)_1.00;H(-879)_1.00;H(-853)_1.00;H(-693)_1.00;H(-235)_1.00;H(148)_1.00;H(216)_1.00;H(222)_0.66	3.19
CG15040	H(-1758)_0.98;H(-837)_0.00;H(-322)_0.84;H(-246)_1.00;H(-235)_1.00;H(227)_0.05;H(237)_1.00;H(371)_0.41;H(447)_1.00;H(458)_1.00	3.17
CR45540	H(-1818)_1.00;H(-1582)_0.95;H(-1395)_0.53;H(-312)_1.00;F(29)_1.00;H(44)_1.00;H(222)_1.00	3.15
CG44774	H(-1872)_1.00;H(-1651)_1.00;H(-1642)_0.97;H(-1275)_0.02;H(-1054)_1.00;H(-1045)_1.00;H(-833)_0.58;H(-610)_0.00;H(-601)_0.05;H(-234)_0.66;H(-11)_1.00;H(-2)_0.94;H(365)_0.05	3.14
CG17724	H(-1916)_0.80;H(-1882)_1.00;H(-1876)_0.70;H(-1575)_0.80;H(-1316)_0.77;H(-1284)_0.68;H(-1169)_0.99;H(-974)_1.00;H(-71)_1.00;H(105)_1.00	3.09
CR44262	H(-1362)_0.77;F(-692)_0.96;H(-591)_0.00;H(-72)_1.00;H(1)_0.84;H(108)_1.00;H(138)_0.00;H(160)_1.00;H(400)_0.32	3.07
thoc7	H(-1918)_0.98;H(-1847)_0.00;H(-1735)_0.72;H(-1525)_0.74;H(-1444)_0.86;H(-940)_0.84;H(-174)_0.67;H(-167)_0.94;H(70)_1.00;H(161)_1.00	3.03

Continued. Genes	All_CREs	CRE_Score_Sum
chb	H(-1874)_1.00;H(-1204)_1.00;H(-942)_0.02;H(-660)_0.85;H(-539)_1.00;H(-297)_0.73;H(-119)_1.00;H(427)_0.97;H(447)_0.77	3.01
CG3770	H(-1097)_1.00;H(-491)_1.00;H(-323)_0.98;H(-47)_0.95;H(32)_1.00;H(377)_0.96;H(475)_0.80	3.01
CG4880	H(-1169)_1.00;F(-1112)_0.75;H(-1097)_0.79;H(-752)_0.92;H(-710)_0.82;H(-698)_0.75;H(-447)_0.78;H(-386)_0.99	3.00
CR45170	F(-1940)_1.00;H(-1287)_0.42;H(-786)_0.99;H(-305)_1.00;F(-104)_1.00;H(154)_1.00	2.97
CR45018	H(-1653)_1.00;H(-1638)_1.00;H(-1513)_1.00;H(-1489)_1.00;F(-1110)_1.00;H(-981)_0.30;H(-639)_0.99;H(-424)_0.00;H(183)_1.00	2.94
CR45203	H(-1642)_0.60;H(-1633)_1.00;H(-1205)_0.53;H(-1174)_1.00;F(-1135)_1.00;H(-1024)_1.00;H(-673)_1.00;H(-598)_1.00	2.94
CG8314	H(-678)_0.64;H(-600)_0.66;H(-321)_0.61;H(-78)_0.95;H(-21)_0.40;H(99)_0.99;H(110)_1.00;H(237)_0.98	2.92
C3G	H(-1576)_0.93;H(-878)_1.00;H(-849)_0.98;H(-843)_0.99;H(-372)_0.20;H(-31)_1.00;F(456)_1.00	2.92
shot	H(-975)_1.00;H(-397)_0.40;H(-367)_1.00;H(-207)_0.99;H(-195)_0.97;H(-189)_0.06;H(-55)_1.00;H(460)_1.00	2.91
SmydA-3	H(-1716)_1.00;H(-1668)_0.96;H(-1207)_0.00;F(-496)_1.00;H(-122)_0.00;F(33)_1.00;H(180)_0.96;H(431)_0.00	2.90
CR45402	H(-1932)_0.01;H(-1593)_1.00;H(-1587)_1.00;H(-1550)_1.00;H(-1538)_1.00;F(-1293)_1.00;H(-1188)_0.69;H(-1179)_1.00;H(-875)_0.00;H(-823)_0.99	2.88
CR44803	H(-1456)_1.00;H(-1018)_0.93;H(-968)_0.06;H(-819)_1.00;H(-754)_0.00;H(-646)_1.00;H(-542)_1.00;H(-339)_1.00;H(125)_1.00	2.88
CG17734	H(-1936)_1.00;H(-1868)_0.68;H(-1686)_0.57;H(-1256)_0.60;H(-1157)_0.80;H(-999)_0.60;H(-729)_0.00;H(-561)_0.00;H(-446)_1.00;H(-261)_0.31;F(265)_1.00;H(388)_0.07	2.88
CG7191	H(-1474)_1.00;H(-494)_1.00;H(-385)_1.00;H(-326)_1.00;H(-88)_0.22;H(216)_1.00;H(244)_1.00;H(262)_0.33	2.87
CG9331	F(-1355)_1.00;H(-871)_1.00;H(-833)_0.93;H(99)_1.00;H(114)_1.00;H(272)_1.00	2.86
Cct1	H(-1286)_0.00;H(-932)_1.00;H(-699)_0.99;H(-607)_0.98;H(-605)_1.00;H(-551)_0.54;F(-108)_1.00	2.84
CR44184	H(-1068)_0.00;H(-697)_1.00;H(-251)_1.00;H(-59)_1.00;H(-35)_1.00;H(155)_1.00;H(272)_1.00	2.82
Gp93	H(-1898)_0.95;H(-1512)_0.76;H(-1457)_0.95;H(-768)_1.00;H(23)_0.82;H(91)_1.00;H(298)_0.61;H(411)_1.00	2.81
CR45144	H(-819)_0.08;H(-635)_0.80;H(-510)_0.80;H(-429)_1.00;H(-310)_1.00;H(-162)_0.80;H(-143)_1.00;H(71)_0.66	2.81
Dh44	H(-1633)_1.00;H(-1154)_1.00;H(-620)_1.00;H(-515)_0.72;H(-437)_0.00;H(-331)_1.00;H(-106)_0.00;H(5)_1.00;H(240)_0.98	2.81

Continued. Genes	All_CREs	CRE_Score_Sum
IP3K2	H(-1281)_1.00;H(-1266)_1.00;H(-1141)_1.00;H(-1117)_1.00;F(-738)_1.00;H(-609)_0.30;H(-267)_0.99;H(-52)_0.00	2.80
CG14280	H(-1565)_1.00;H(-1204)_1.00;H(-906)_0.98;H(-807)_1.00;H(-388)_0.00;H(-374)_0.00;H(-172)_0.99;H(76)_1.00;H(217)_0.84	2.80
trc	H(-1479)_0.87;H(-1413)_1.00;H(-1241)_1.00;H(-1060)_0.77;H(-747)_0.81;H(-464)_0.75;H(302)_1.00;H(332)_0.98	2.80
CG7365	H(-1934)_0.00;H(-1706)_1.00;H(-1644)_1.00;H(-1008)_1.00;H(182)_1.00;F(358)_1.00;H(370)_1.00	2.80
LamC	F(-1396)_1.00;F(-1273)_1.00;H(20)_1.00;H(162)_1.00;H(227)_0.38;H(399)_0.66	2.79
CR44920	H(-1829)_1.00;H(-1780)_1.00;H(-1567)_1.00;H(-1339)_1.00;H(-1291)_1.00;H(-1213)_1.00;H(325)_1.00;H(453)_1.00	2.78
betaTub56D	H(-1770)_0.90;H(-1273)_0.00;F(-1142)_1.00;H(-659)_1.00;H(-428)_0.98;H(-299)_1.00;H(117)_1.00	2.77
IP3K1	F(-1915)_1.00;F(-1562)_1.00;H(-975)_0.91;H(-808)_1.00;H(-723)_1.00;H(-240)_1.00	2.75
CR44679	H(-603)_0.41;H(-246)_1.00;H(-234)_0.48;H(-222)_0.01;F(-102)_1.00;H(219)_0.00;F(399)_1.00	2.75
beat-11b	H(-1924)_1.00;H(-1056)_0.85;H(-339)_1.00;H(-158)_1.00;H(-38)_0.11;H(17)_1.00;H(28)_1.00;H(114)_0.39	2.75
CR45135	H(-930)_1.00;H(-522)_1.00;H(-222)_1.00;H(67)_1.00;H(74)_1.00;H(219)_1.00;H(403)_0.00	2.75
CR45306	F(-1867)_1.00;H(-1819)_1.00;H(-1593)_1.00;F(-1554)_1.00;H(-1538)_0.00;F(-1495)_1.00;H(-816)_1.00	2.74
CR45703	H(-1649)_1.00;H(-1421)_0.44;H(-1369)_1.00;H(-1349)_1.00;H(-40)_1.00;H(37)_0.40;H(176)_1.00;H(223)_1.00	2.74
CG13594	H(-1579)_0.05;H(-726)_1.00;H(-566)_1.00;H(-238)_1.00;H(175)_1.00;H(244)_1.00;H(278)_1.00	2.73
svr	H(-883)_1.00;H(-819)_1.00;H(-761)_0.00;H(-91)_0.27;H(-44)_0.66;F(20)_1.00;H(73)_1.00	2.73
GLS	H(-1925)_0.22;H(-1874)_0.60;H(-1629)_0.36;H(-658)_0.14;F(-238)_1.00;H(-209)_1.00;H(151)_0.97;H(242)_1.00	2.73
CR45376	F(-1352)_1.00;F(-1296)_1.00;H(-1144)_0.02;H(-676)_1.00;H(-1)_0.99;H(196)_0.99	2.73
CG8713	H(-1816)_0.19;H(-1040)_0.81;F(-56)_1.00;H(-42)_1.00;F(409)_1.00	2.72
CR44661	H(-1439)_1.00;H(-1391)_0.97;H(79)_1.00;H(154)_0.99;H(201)_1.00;H(353)_1.00;H(422)_0.41	2.72
Pak	H(-1933)_0.00;H(-1821)_0.00;H(-1676)_1.00;H(-1484)_0.98;H(-771)_1.00;H(-764)_1.00;H(37)_0.82;H(247)_1.00;H(420)_0.97	2.72
Glut4EF	H(-1751)_0.98;H(-1337)_0.69;H(-610)_1.00;H(-438)_1.00;H(-427)_1.00;H(392)_0.98;H(430)_1.00	2.71

Continued. Genes	All_CREs	CRE_Score_Sum
Rab1	H(-1785)_0.93;H(-1592)_0.80;H(-1319)_0.80;H(-1034)_0.34;H(-761)_1.00;H(16)_1.00;H(298)_1.00;H(400)_1.00	2.71
CG3408	H(-1775)_0.17;H(-1556)_0.81;H(-1158)_1.00;H(-896)_1.00;H(-890)_1.00;H(-465)_0.81;H(70)_0.03;H(171)_0.97;H(475)_1.00	2.71
CR43440	H(-1500)_1.00;H(-1495)_0.85;H(-1484)_1.00;H(-1267)_1.00;H(-211)_1.00;H(-2)_1.00;H(9)_1.00	2.71
AP-2alpha	H(-1911)_0.80;H(-1689)_0.96;H(-1451)_0.13;H(-607)_0.83;F(-240)_0.99;H(426)_1.00;H(451)_1.00	2.70
mir-988	H(-1962)_0.99;H(-1534)_0.80;H(-1241)_0.80;H(-997)_1.00;H(-982)_1.00;H(-322)_1.00;H(4)_0.00;H(288)_0.73;H(345)_0.80	2.69
l(2)efl	H(-1926)_0.89;F(-1514)_0.95;H(-1309)_0.16;H(-703)_1.00;H(-568)_1.00;H(-104)_1.00;H(444)_0.60;H(465)_0.48	2.68
CG5214	H(-918)_0.99;F(-840)_0.98;H(-690)_0.07;F(-567)_1.00;H(-41)_0.31;H(144)_1.00;H(259)_0.00;H(427)_0.00	2.68
CR45658	H(-897)_1.00;H(-544)_1.00;H(-481)_0.97;H(112)_0.02;H(192)_1.00;H(241)_1.00;H(250)_1.00	2.67
ort	H(-2000)_0.87;H(-1898)_1.00;F(-764)_1.00;H(-376)_1.00;H(-87)_0.94;H(203)_0.99	2.67
mir-9a	H(-1733)_1.00;H(-1681)_1.00;H(-1167)_1.00;H(-687)_0.79;H(-259)_1.00;H(43)_1.00;H(427)_1.00	2.66
E2f1	H(-1211)_1.00;H(-447)_0.97;H(-351)_1.00;H(-132)_0.99;F(215)_1.00	2.66
CR45650	H(-1179)_0.99;H(-226)_1.00;H(-60)_0.97;H(281)_1.00;F(414)_1.00	2.66
CG42321	H(-848)_0.99;H(-700)_0.95;H(-113)_0.99;H(157)_1.00;H(280)_1.00;H(394)_1.00	2.66
CR45371	H(-1538)_1.00;H(-1251)_0.44;H(-1050)_0.52;H(-384)_0.48;H(-348)_1.00;H(-127)_1.00;H(-90)_0.80;H(326)_0.99	2.65
CR46055	H(-1332)_1.00;H(-1248)_0.00;H(-993)_0.00;F(-226)_1.00;H(121)_0.99;H(340)_1.00;H(436)_0.97	2.65
CG10948	H(-1943)_0.03;H(-968)_0.79;H(-289)_0.99;F(-268)_1.00;H(-71)_1.00;H(408)_1.00	2.64
CR44269	H(-1601)_1.00;H(-535)_1.00;H(-326)_1.00;H(-193)_1.00;H(-156)_1.00;H(-132)_1.00	2.63
CG13919	H(-1580)_0.80;H(-1140)_0.77;H(-905)_0.60;H(-603)_0.86;H(-442)_0.60;H(-277)_1.00;H(-93)_0.06;H(176)_0.80;H(271)_0.79	2.63
CR45606	H(-1913)_1.00;F(-1821)_1.00;H(-1801)_1.00;H(-1281)_1.00;H(-1070)_1.00;H(-1012)_1.00;H(130)_0.94	2.61
Nmdar2	H(-1691)_0.00;H(-705)_1.00;H(-602)_0.82;H(-265)_0.82;H(1)_0.98;F(96)_1.00	2.60
Proc	H(-1379)_0.00;H(-1006)_0.94;H(-774)_1.00;H(-744)_1.00;H(-256)_1.00;H(32)_1.00;H(183)_1.00	2.60
Wbp2	H(-1478)_0.80;H(-455)_1.00;H(24)_1.00;F(221)_1.00;H(242)_0.99	2.60

Continued. Genes	All_CREs	CRE_Score_Sum
CR45579	H(-1128)_0.09;H(-1015)_1.00;H(-1009)_1.00;H(-533)_1.00;H(-426)_1.00;H(189)_1.00;H(270)_0.99	2.60
CR45874	H(-1728)_0.68;H(-1408)_0.95;H(-908)_1.00;H(-604)_0.97;H(-503)_0.03;H(32)_0.81;H(457)_1.00;H(463)_1.00	2.60
CG15861	H(-1539)_0.80;H(-1441)_0.96;H(-1096)_1.00;H(-1017)_0.95;H(-741)_0.98;H(-573)_1.00;H(33)_1.00	2.60
CG44038	H(-1008)_1.00;H(-943)_1.00;H(-600)_1.00;H(-508)_1.00;H(37)_1.00;H(176)_1.00	2.59
CG7550	H(-1566)_0.80;H(-1461)_0.72;H(-1149)_1.00;H(-987)_0.73;H(-333)_0.20;H(-153)_0.60;H(78)_0.82;H(167)_0.82;H(177)_0.66	2.59
Dak1	H(-1790)_0.59;H(-1138)_0.44;H(-968)_0.64;H(-471)_0.20;F(-3)_1.00;H(99)_1.00;H(192)_0.93	2.58
CG13982	H(-1940)_0.03;H(-1460)_0.04;H(-1315)_0.90;H(-773)_0.78;H(-79)_0.00;H(75)_1.00;H(118)_0.99;H(124)_1.00;H(137)_1.00;H(316)_0.01	2.58
Nplp1	H(-1212)_0.99;H(-1177)_1.00;F(-156)_1.00;H(-78)_0.97;H(422)_0.98	2.58
caix	H(-1522)_0.01;H(-968)_0.61;H(-788)_0.07;H(-549)_1.00;H(-419)_1.00;H(-373)_1.00;H(-334)_0.49;H(-4)_1.00;H(27)_0.52	2.57
CG1607	H(-1786)_0.97;H(-780)_0.00;H(-2)_0.95;H(285)_0.99;F(307)_1.00;H(454)_1.00	2.57
CG32812	H(-1410)_1.00;H(-1173)_0.71;H(-650)_0.00;H(-523)_0.44;H(-451)_0.92;H(-402)_1.00;H(98)_0.95;H(219)_1.00	2.56
CR45501	H(-1210)_0.81;H(-858)_0.80;H(-585)_0.60;H(-471)_1.00;H(-342)_0.61;H(-92)_1.00;H(-17)_0.99	2.55
REPTOR	H(-1458)_1.00;H(-782)_1.00;F(-509)_1.00;H(26)_1.00;H(354)_0.99	2.54
Pal2	H(-1965)_1.00;H(-1830)_1.00;H(-1224)_0.16;F(-1019)_0.95;H(-607)_0.89;F(-494)_1.00	2.54
CG10737	H(-1795)_1.00;H(-1719)_0.97;H(-287)_1.00;F(-244)_1.00;H(406)_0.86;H(412)_0.42	2.53
Sras	H(-1588)_0.80;H(-1408)_0.79;H(-1382)_0.80;H(-1366)_1.00;H(-496)_0.54;H(-265)_0.97;H(70)_0.93;H(427)_0.66	2.52
CG34135	H(-1922)_0.80;H(-867)_0.65;H(-564)_0.95;H(-120)_0.94;H(-108)_0.15;H(147)_0.80;H(168)_0.78;H(421)_0.80	2.52
CG32425	H(-1448)_0.57;H(-1355)_0.61;H(-1189)_0.81;H(-1087)_0.50;H(-939)_0.98;H(-895)_0.60;H(-488)_0.79;H(-275)_0.58;H(429)_0.99	2.51