

**Table S9. mRNA expression levels of T. ni homologs associated with endocytosis.**

Complex / Category	Gene*	T. ni Ortholog	RPKM								STDEV								
			C	0	6	12	18	24	36	48	C	0	6	12	18	24	36	48	
Nucleation	FCHO2	UN040353	18.87	20.95	20.38	12.41	8.08	6.43	3.32	2.00	0.39	1.28	1.04	0.98	0.43	0.11	0.28	0.1	
		UN009494	1.39	0.89	1.20	0.75	0.24	0.22	0.31	0.14	0.33	0.31	0.25	0.08	0.25	0.19	0.11	0.07	
	Eps15	UN011157	1.10	1.08	1.45	0.68	0.19	0.27	0.16	0.12	0.66	0.45	0.32	0.43	0.17	0.23	0.18	0.11	
		UN013798	1.03	0.83	1.09	0.70	0.37	0.22	0.05	0.08	0.56	0.24	0.13	0.45	0.14	0.11	0.09	0.08	
		UN002595	6.81	3.09	4.68	2.57	1.34	0.81	0.34	0.11	0.56	0.18	0.58	0.28	0.33	0.04	0.15	0.06	
		UN003280	2.94	2.95	2.96	2.44	1.27	0.73	0.37	0.21	0.78	0.79	0.72	0.4	0.17	0.11	0.11	0.08	
Intersectin	UN005672	3.44	2.58	3.97	2.11	1.30	0.66	0.24	0.07	1.50	0.79	0.7	0.55	0.59	0.26	0.13	0.11		
	UN060218	12.21	7.82	15.33	5.70	3.65	3.16	0.60	0.31	0.34	0.18	0.95	0.75	0.38	0.99	0.14	0.06		
Cargo selection	AP2A2	UN047885	7.37	7.32	13.00	8.25	5.10	4.62	2.63	1.65	0.28	0.51	1.1	0.5	0.21	0.09	0.39	0.04	
		UN014947	44.00	53.90	54.16	25.95	14.18	8.62	3.00	1.14	0.89	2.21	1.02	1.46	0.84	0.75	0.58	0.24	
	AP2B1	UN011341	26.64	46.90	59.71	33.70	17.69	10.86	4.88	2.00	1.43	1.03	2.8	0.98	1.19	0.4	0.59	0.21	
		UN063500	86.79	89.01	116.07	85.00	54.28	39.01	18.69	11.62	2.03	0.77	4.53	0.25	1.89	1.03	0.65	0.28	
	AP2S1	UN007037	30.41	41.94	82.27	46.00	28.14	22.62	8.76	3.28	1.14	1.82	4.6	3.15	0.83	1.79	0.18	0.27	
	Epsin1	UN027037	29.28	32.32	22.83	9.46	5.81	4.17	2.44	1.17	2.83	2.80	1.12	0.58	0.6	0.57	0.4	0.27	
	Epsin2	UN027034	28.38	32.70	21.63	8.81	5.39	4.13	2.27	1.18	2.70	2.78	1.24	0.28	0.53	0.77	0.42	0.23	
	Epsin2	UN027035	30.85	35.79	23.81	9.65	5.95	4.28	2.39	1.33	3.03	3.12	1.32	0.41	0.61	0.72	0.35	0.21	
	Epsin2	UN027036	29.85	31.75	22.87	10.18	6.28	4.51	2.44	1.16	3.33	2.54	1.56	0.69	0.63	0.45	0.3	0.31	
	AP180	UN026112	46.47	26.29	24.58	12.66	8.15	5.40	2.52	1.12	1.62	1.23	1.3	0.53	1.02	0.67	0.51	0.41	
		UN048726	30.95	21.33	22.85	11.29	6.34	3.98	2.70	0.99	1.10	2.24	2.47	0.48	1.99	0.75	0.08	0.26	
	HIP1	UN063828	12.95	12.10	4.89	2.15	1.23	0.88	0.73	0.27	2.29	0.78	0.77	0.63	0.89	0.46	0.43	0.34	
		UN046737	29.67	26.02	14.19	7.32	4.59	2.19	1.44	0.57	1.11	1.04	0.4	0.22	0.4	0.36	0.07	0.12	
	UN046738	9.15	10.99	4.86	2.83	1.76	0.80	0.61	0.30	0.93	0.38	0.41	0.17	0.31	0.12	0.04	0.11		
	Coat assembly	Clathrin heavy chain	UN005722	43.72	51.20	47.67	30.94	17.75	12.99	8.27	4.57	0.84	1.71	1.1	1.42	1.11	0.51	0.23	0.57
			UN005723	43.87	51.47	48.01	31.14	17.88	13.09	8.32	4.58	0.90	1.72	1.07	1.44	1.11	0.51	0.22	0.58
Clathrin heavy chain		UN014999	1.20	0.11	0.42	0.72	0.53	0.17	0.24	0.29	0.23	0.14	0.32	0.2	0.13	0.2	0.24	0.18	
Clathrin heavy chain		UN015987	0.68	0.43	0.25	0.52	0.30	0.41	0.28	0.10	0.20	0.35	0.14	0.08	0.14	0.07	0.17	0.08	
Clathrin heavy chain		UN063236	0.99	0.87	1.18	1.22	0.93	0.53	0.48	0.45	0.48	0.08	0.18	0.22	0.29	0.33	0.08	0.25	
Clathrin light chain		UN033438	189.69	185.45	263.24	175.03	106.40	81.06	30.97	11.30	6.09	7.50	9.19	6.69	3.82	3.74	1.15	0.24	
		UN033439	94.76	141.19	233.60	120.85	77.03	55.84	19.80	8.17	4.16	8.06	4.39	13.64	7.07	6.88	0.43	2.63	
Scission	SNX9	UN016210	32.19	35.65	39.26	18.52	13.67	11.64	4.98	2.12	1.02	1.36	1.06	1.02	1.29	0.51	0.43	0.03	
		UN016211	34.69	38.60	42.40	19.98	14.70	12.59	5.39	2.32	1.08	1.43	1.13	1.16	1.39	0.54	0.44	0.04	
	Amphiphysin2	UN069370	5.91	5.44	6.21	4.19	3.27	1.91	0.49	0.42	0.26	0.79	0.26	0.61	0.7	0.6	0.13	0.25	
	Amphiphysin2	UN002455	3.55	4.19	4.08	3.01	2.29	1.27	0.62	0.39	0.92	0.35	0.57	0.54	0.41	0.33	0.39	0.25	
	Dynamitin	UN031377	31.61	39.53	26.20	13.02	7.25	5.33	3.04	1.30	0.89	1.24	0.9	0.57	0.57	0.5	0.36	0.13	
Uncoating	HSC70	UN059101	4220.74	6035.30	3956.62	3208.57	1995.66	1249.91	702.51	265.29	50.53	113.26	34	85.52	6.95	30.06	24.69	15.41	
		UN065667	4.48	4.03	5.57	3.21	1.77	1.30	0.65	0.24	0.40	0.59	0.26	0.19	0.4	0.3	0.08	0.12	
	Synaptojanin1	UN002448	3.90	2.49	4.09	2.40	1.43	1.21	0.36	0.35	0.21	0.40	0.36	0.21	0.09	0.05	0.11	0.22	
	N-WASP	UN066639	10.39	8.41	8.30	3.36	2.48	1.58	1.46	0.66	0.35	1.13	1.22	0.57	0.55	0.31	0.39	0.28	
	N-WASP	UN006410	1.61	1.95	2.77	1.36	0.92	0.73	0.36	0.34	0.17	0.57	1.19	0.4	0.95	0.27	0.32	0.3	
	Arp2	UN012801	30.58	51.55	55.70	39.47	18.80	12.42	5.32	2.98	1.34	1.99	3.05	0.92	0.29	0.82	0.15	0.28	
	Arp3	UN064270	48.23	126.36	179.84	70.99	40.36	27.52	9.62	3.52	1.27	1.25	2.16	3.45	0.9	1.5	0.65	0.3	
Other	lipophorin receptor	UN005188	66.88	39.04	5.39	4.94	3.62	5.58	3.56	1.90	1.33	0.61	0.25	0.18	0.11	0.31	0.31	0.09	
		UN005189	63.63	38.20	5.79	5.07	3.50	5.34	3.46	1.87	0.43	0.37	0.24	0.3	0.29	0.35	0.41	0.05	
	lipophorin receptor	UN005190	77.26	45.72	5.42	6.47	4.96	8.51	5.28	2.87	1.10	1.89	0.51	0.38	0.19	0.1	0.36	0.3	
	lipophorin receptor	UN005191	73.39	45.42	6.11	6.94	5.00	8.67	5.40	2.99	0.68	1.57	0.59	0.64	0.48	0.32	0.53	0.14	
	nonclathrin coat protein gamma1-COP	UN022302	32.02	33.45	37.22	21.92	11.96	7.92	2.86	1.27	2.66	2.12	0.84	1.08	0.45	0.19	0.56	0.31	
	nonclathrin coat protein gamma1-COP	UN023807	20.94	33.52	36.03	25.34	13.06	8.95	4.07	1.81	1.53	0.54	1.31	0.85	1.08	0.33	0.51	0.53	
	nonclathrin coat protein gamma2-COP	UN044805	14.60	13.99	18.82	10.20	5.75	3.26	1.21	0.62	0.71	0.67	0.46	0.15	0.3	0.05	0.19	0.18	

\* Grey color indicates unigenes with expression level less than 5 RPKM at all time points



**Table S11. mRNA expression levels of T. ni homologs associated with PIK3.**

Complex / Category		Gene*	T. ni Ortholog	RPKM								STDEV								
				C	0	6	12	18	24	36	48	C	0	6	12	18	24	36	48	
PIK3	Class I	Catalytic subunits	Dp110	UN002968	17.28	5.17	3.16	1.57	0.95	0.77	0.49	0.30	0.39	0.76	0.49	0.41	0.36	0.35	0.33	0.24
		Regulatory subunits	p60	UN067526	4.90	4.08	4.26	2.86	2.07	1.93	1.41	0.94	0.17	0.46	0.5	0.12	0.22	0.06	0.16	0.2
	Class II	Catalytic subunits	p60	UN067527	5.00	4.27	4.38	2.90	2.03	1.96	1.45	0.95	0.26	0.51	0.45	0.18	0.22	0.08	0.2	0.23
		Regulatory subunits	pi3k_68D	UN060409	7.48	8.62	8.67	6.49	3.71	2.68	1.77	1.13	0.27	0.11	0.47	0.25	0.17	0.21	0.26	0.13
	Class III	Catalytic subunits	Vps34	UN063291	6.22	10.81	9.03	5.45	3.25	2.06	1.26	0.80	0.27	0.49	0.63	0.21	0.39	0.07	0.27	0.21
			Ird1	UN066671	8.84	7.52	6.35	3.24	1.93	0.83	0.63	0.28	1.32	0.46	0.38	0.32	0.22	0.2	0.39	0.15
		Regulatory subunits	Ird1	UN041295	3.99	3.33	3.74	3.04	1.90	1.31	0.75	0.44	0.14	0.22	0.25	0.22	0.21	0.04	0.08	0.04
			Ird1	UN041381	5.17	4.46	5.63	8.55	3.51	2.86	1.41	1.10	0.25	0.34	0.34	0.48	0.12	0.38	0.16	0.14
			beclin 1	UN064841	7.62	6.90	7.98	4.40	3.24	2.51	0.92	0.53	1.67	0.40	0.38	0.18	0.53	0.24	0.16	0.04
			UVRAG	UN068281	3.64	2.10	2.35	1.62	1.08	0.75	0.51	0.41	0.12	0.36	0.07	0.24	0.13	0.09	0.09	0.03
	BIF1	UN047139	9.22	11.84	11.86	10.08	7.33	6.41	2.84	1.66	0.82	0.90	0.52	0.46	0.62	0.15	0.04	0.2		
	Akt/PKB	Akt/PKB	UN018533	25.72	43.50	55.07	36.72	19.26	14.30	6.27	2.63	0.44	1.40	1.94	0.19	0.97	0.86	0.79	0.36	

\* Grey color indicates unigenes with expression level less than 5 RPKM at all time points

Abbreviation: ATG14L, autophagy-related protein 14-like protein UVRAG, BIF1, Bax-interaction factor 1, Dp110, Drosophila melanogaster p110, PI3K, Phosphoinositide 3-kinases, PKB, protein kinase B, Vps, vacuolar protein sorting, UVRAG, ultraviolet radiation resistance-associated protein

**Table S12. mRNA expression levels of T. ni homologs associated with MAP kinase signaling pathways.**

Complex / Category	Gene*	T. ni Ortholog	RPKM								STDEV							
			C	0	6	12	18	24	36	48	C	0	6	12	18	24	36	48
MAP kinase	MAP kinase kinase (hep)	UN020647	28.03	30.08	30.68	33.30	16.96	10.51	5.86	4.08	0.93	0.28	1.41	0.56	0.89	0.51	0.59	0.14
	MAP kinase kinase 3/4/6	UN023339	22.97	28.57	57.32	26.06	17.03	14.21	5.89	2.31	0.83	0.70	1.98	0.7	0.62	0.64	0.53	0.36
	MAP kinase kinase 3/4/6	UN066938	3.46	3.86	4.96	4.03	2.59	1.67	0.98	0.58	0.50	0.40	0.44	0.5	0.2	0.15	0.12	0.02
	MAP kinase kinase 4	UN028639	2.52	5.08	6.63	4.18	3.68	3.54	2.23	1.24	0.28	0.52	0.54	0.76	0.24	0.23	0.38	0.2
	MAP kinase kinase 4	UN028641	8.31	12.48	21.50	11.57	9.84	9.51	5.89	2.24	0.40	0.97	1.08	1.38	0.34	0.33	0.55	0.17
	MAP kinase kinase 4	UN049071	5.51	6.01	14.98	7.63	5.10	3.35	1.07	0.63	0.22	0.38	1	0.52	0.18	0.39	0.22	0.05
	MAP kinase kinase 4	UN066579	58.29	78.32	130.34	58.97	35.36	28.64	10.90	3.25	0.68	1.60	4.73	2.43	0.98	0.7	0.63	0.59
	MAP kinase kinase 4	UN066580	71.48	89.34	153.92	69.88	41.47	34.57	13.13	3.70	0.16	2.20	5.5	3.15	1.55	0.9	0.9	0.62
	MAP kinase kinase 4	UN069980	9.40	4.79	6.31	3.55	1.71	1.24	0.53	0.39	1.07	0.86	0.74	0.5	0.71	0.24	0.09	0.19
	MAP kinase phosphatase-1 (Dmkp-1)	UN062932	5.98	5.54	11.14	8.98	5.28	3.25	1.30	0.62	0.16	0.39	1	0.7	0.37	0.19	0.13	0.04
	MAP kinase phosphatase-1 (Dmkp-1)	UN062933	6.14	5.70	11.59	9.26	5.46	3.36	1.31	0.62	0.19	0.50	0.98	0.67	0.43	0.22	0.13	0.02
	MAP kinase phosphatase-1 (Dmkp-1)	UN063348	5.70	7.60	10.85	5.07	3.56	2.69	1.30	0.71	0.21	0.36	0.3	0.43	0.27	0.05	0.1	0.24
	MAP kinase phosphatase-1 (Dmkp-1)	UN063349	6.35	8.02	11.70	5.41	3.74	2.78	1.35	0.73	0.33	0.41	0.43	0.46	0.28	0.05	0.09	0.22
	Ras85D	UN067243	41.39	49.22	55.50	38.27	23.25	18.25	9.24	6.28	0.61	2.36	1.91	1.33	0.79	0.42	0.27	0.38
	Ras85D	UN031780	13.06	17.37	21.51	13.54	8.65	5.50	3.00	1.85	0.44	0.70	0.85	0.62	0.36	0.27	0.52	0.11
	Ras85D	UN050418	98.63	161.30	180.69	95.76	50.46	37.34	15.11	7.67	2.57	6.20	3.15	4.9	1.42	1.03	1.44	0.62
	phl (Dsim\phl)	UN067576	4.97	5.45	5.17	3.77	2.25	1.26	1.10	0.67	0.65	0.38	0.26	0.14	0.28	0.19	0.24	0.08
	phl (Dsim\phl)	UN067577	5.22	5.30	4.97	3.66	2.15	1.30	1.09	0.73	0.54	0.39	0.38	0.25	0.31	0.18	0.25	0.13
	phl (Dsim\phl)	UN067579	4.27	5.12	4.98	3.65	2.05	1.06	1.07	0.50	0.75	0.33	0.25	0.24	0.33	0.23	0.32	0.13
	phl (Dsim\phl)	UN067578	5.45	5.40	5.05	3.62	2.08	1.37	1.09	0.77	0.57	0.41	0.47	0.23	0.33	0.09	0.2	0.19
	phl (Dsim\phl)	UN067580	5.46	5.21	4.85	3.50	1.99	1.30	1.05	0.75	0.50	0.48	0.53	0.3	0.25	0.14	0.18	0.2
	phl (Dsim\phl)	UN067581	4.45	4.83	4.66	3.47	1.86	1.06	1.04	0.55	0.63	0.36	0.36	0.44	0.42	0.21	0.33	0.14
	phl (Dsim\phl)	UN067582	4.67	4.90	4.74	3.38	1.71	1.12	1.05	0.58	0.66	0.35	0.47	0.45	0.48	0.09	0.27	0.2
	phl (Dsim\phl)	UN067583	4.66	4.62	4.43	3.21	1.57	1.02	0.99	0.54	0.51	0.45	0.53	0.55	0.37	0.17	0.25	0.26
	stress-activated p38a/p38b MAP kinase	UN006627	2.54	3.53	1.51	1.22	0.41	0.52	0.39	0.17	0.63	0.05	0.34	0.14	0.02	0.24	0.2	0.09
	stress-activated p38a/p38b MAP kinase	UN015143	32.14	32.84	48.66	35.10	20.89	16.20	8.41	4.23	0.77	1.08	2.95	0.97	0.4	1.21	0.21	0.4
	stress-activated p38a/p38b MAP kinase	UN015144	28.43	29.99	45.49	33.59	19.99	15.56	8.18	4.15	0.68	1.04	2.98	1.12	0.47	1.16	0.29	0.45
	stress-activated p38a/p38b MAP kinase	UN015145	20.57	23.73	37.71	29.71	17.72	13.42	7.55	4.16	0.83	1.00	2.66	1.28	0.29	1.08	0.24	0.4
	stress-activated p38a/p38b MAP kinase	UN015146	17.57	15.62	20.43	11.78	6.97	6.01	2.39	0.98	0.13	1.31	1.32	0.17	0.48	1.46	0.14	0.23
	stress-activated p38a/p38b MAP kinase	UN019909	23.95	29.11	26.37	17.86	10.12	9.22	4.94	3.37	0.58	1.06	0.74	0.24	0.45	0.73	0.46	0.27
	stress-activated p38a/p38b MAP kinase	UN022961	10.97	27.66	25.89	17.47	10.41	8.83	4.30	3.10	0.65	0.63	0.43	0.96	0.27	0.42	0.33	0.27
	stress-activated p38a/p38b MAP kinase	UN022962	11.60	28.79	26.98	18.16	10.80	9.11	4.41	3.16	0.68	0.63	0.43	0.99	0.35	0.43	0.35	0.23
	stress-activated p38a/p38b MAP kinase	UN022963	11.33	28.82	26.61	17.98	10.78	9.14	4.43	3.24	0.69	0.66	0.55	1	0.29	0.38	0.33	0.29
stress-activated p38a/p38b MAP kinase	UN022964	11.99	30.02	27.77	18.70	11.20	9.44	4.55	3.30	0.72	0.66	0.56	1.04	0.36	0.39	0.35	0.25	

\* Grey color indicates unigenes with expression level less than 5 RPKM at all time points

**Table S13. mRNA expression levels of T. ni homologs associated with the Nuclear Pore Complex (NPC).**

Complex / Category	Gene*	T. ni Ortholog	RPKM								STDEV							
			C	0	6	12	18	24	36	48	C	0	6	12	18	24	36	48
Central FG-Nups	Nup54-like	UN037243	18.66	21.70	25.74	15.14	8.65	5.05	1.54	0.93	2.47	1.46	1.8	0.68	0.41	0.26	0.21	0.23
	Nup54-like	UN045238	10.21	17.14	20.98	13.78	7.27	4.87	2.31	0.90	2.81	1.49	0.86	1.29	0.7	0.78	0.2	0.13
	Nup58-like	UN042519	6.31	9.73	13.00	6.86	3.53	2.53	1.01	0.40	1.18	1.01	0.66	0.57	0.31	0.08	0.05	0.22
	Nup58-like	UN042520	8.06	11.94	15.80	8.41	4.31	3.17	1.21	0.46	1.53	1.18	0.72	0.63	0.37	0.12	0.09	0.24
	Nup58-like	UN044794	15.68	21.21	24.39	11.87	7.85	4.90	1.59	0.80	2.23	1.47	1.37	0.53	0.58	0.49	0.52	0.34
	Nup58-like	UN057197	0.51	0.16	0.00	0.00	0.00	0.00	0.00	0.05	0.24	0.17	0	0	0	0	0	0.09
Inner-ring Nups	Nup155-like	UN039075	18.48	17.15	22.49	14.83	6.99	4.59	1.69	0.69	0.93	0.29	1.04	0.82	0.47	0.53	0.16	0.13
	Nup155-like	UN039076	18.98	17.68	23.16	15.06	7.11	4.70	1.75	0.71	0.90	0.35	1	0.92	0.48	0.54	0.19	0.11
	Nup155-like	UN044744	10.79	15.56	14.96	11.14	5.33	3.47	1.48	0.33	1.25	1.52	1.97	0.25	0.75	1.29	0.64	0.14
	Nup188-like	UN044117	9.07	17.40	23.24	14.73	9.12	6.37	3.93	1.90	0.71	0.96	1.83	1.06	0.88	0.55	0.72	0.04
	Nup188-like	UN049566	14.20	15.44	18.75	11.12	6.75	4.39	2.38	1.05	0.56	0.57	0.3	0.25	0.42	0.34	0.25	0.05
	Nup188-like	UN049567	13.89	14.82	17.90	10.55	6.51	4.20	2.30	1.05	0.63	0.72	0.47	0.26	0.33	0.36	0.18	0.05
Nuclear Basket	Nup153-like	UN065879	5.58	3.63	5.48	4.27	2.98	2.61	1.71	1.16	0.36	0.11	0.41	0.26	0.29	0.05	0.05	0.16
	Tpr	UN044650	24.27	10.41	16.16	6.88	4.46	3.25	1.54	0.63	1.30	0.42	0.42	0.57	0.32	0.24	0.24	0.2
	Rae1	UN003227	40.25	67.16	127.77	58.24	40.04	27.24	16.87	6.31	2.78	2.74	2.04	2.83	2.37	1.84	1.14	0.89
	Rae1	UN070808	30.18	84.66	156.53	82.16	51.82	33.44	23.14	9.64	3.27	0.63	3.65	5.98	4.92	1.61	0.61	0.95
	Nup50-like	UN007020	39.07	38.53	75.39	39.72	27.72	19.82	7.58	2.81	2.55	2.25	2.33	2.68	0.41	0.5	0.39	0.24
Outer-ring Nups	Nup160-like	UN022888	12.42	24.40	35.75	19.73	11.61	7.59	4.76	1.80	0.50	0.76	0.36	0.55	1.35	1.23	0.46	0.12
	Nup160-like	UN024938	19.27	22.73	30.61	15.48	11.12	7.14	3.81	1.28	1.69	0.96	0.69	0.34	0.52	0.82	0.12	0.13
	Nup160-like	UN049466	6.12	12.06	15.37	8.94	4.84	4.01	2.32	0.91	0.57	0.98	1.3	1.35	0.51	0.94	0.35	0.24
	Nup43-like	UN067119	51.08	98.54	120.88	71.55	43.65	32.40	13.75	5.51	1.55	0.28	0.9	4.37	0.67	1.7	0.65	0.33
Outer-ring Nups/central FG-Nups	Nup98-Nup96-like	UN064454	7.91	5.12	4.98	4.01	2.23	1.63	1.46	0.93	1.10	0.13	0.54	0.69	0.55	0.41	0.34	0.32
	Nup98-Nup96-like	UN064455	7.65	4.79	5.04	4.04	2.67	1.90	1.80	1.25	1.13	0.22	0.37	0.54	0.56	0.34	0.28	0.43
	Nup98-Nup96-like	UN068053	8.62	4.40	4.45	3.32	1.88	1.28	0.94	0.64	0.35	0.28	0.31	0.25	0.36	0.21	0.04	0.07
	Nup98-Nup96-like	UN068054	6.34	3.49	3.67	2.75	1.74	1.30	0.76	0.67	0.29	0.32	0.34	0.21	0.29	0.17	0.08	0.05
	Nup98-Nup96-like	UN068453	6.34	4.93	4.20	3.42	1.89	0.90	0.65	0.52	0.67	0.29	0.42	0.24	0.28	0.12	0.04	0.19
	Nup98-Nup96-like	UN070747	8.48	4.79	2.92	2.88	1.51	1.41	0.35	0.60	1.13	0.17	0.55	0.5	0.34	0.48	0.26	0.36
Transmembrane Nups	NDC1-like	UN021885	19.03	28.18	29.89	21.14	10.40	9.73	2.58	1.04	0.99	2.24	0.85	2.92	0.72	0.18	0.68	0.16
	GLE1-like	UN047960	14.51	13.57	18.14	10.08	6.66	5.18	2.08	1.15	0.88	1.30	0.73	1.11	0.42	0.37	0.21	0.13
	Nup53-like	UN006036	0.78	0.89	1.14	1.46	0.80	0.59	0.37	0.23	0.41	0.24	0.26	0.48	0.21	0.25	0.14	0.21
	Nup53-like	UN006037	1.41	1.24	1.75	2.33	0.93	0.77	0.46	0.31	0.55	0.28	0.44	0.71	0.24	0.54	0.12	0.3
	Nup53-like	UN021120	21.08	27.91	35.91	27.92	17.15	13.11	5.30	2.41	0.78	1.16	0.71	2.7	0.31	0.41	0.37	0.06
	Nup53-like	UN056272	0.00	0.09	0.02	0.28	0.04	0.07	0.07	0.14	0.00	0.16	0.04	0.12	0.08	0.12	0.12	0.15
	Nup85-like	UN045474	6.82	13.45	13.03	13.42	7.21	5.47	3.48	1.92	0.05	2.33	1.75	0.67	1.03	0.48	0.68	0.49
	Nup85-like	UN049654	10.30	18.79	17.88	13.02	6.83	5.24	2.24	0.91	0.45	1.45	0.81	0.39	0.55	0.25	0.38	0.18
	Nup85-like	UN056742	0.00	0.00	0.03	0.09	0.27	0.20	0.16	0.07	0.00	0.00	0.06	0.1	0.32	0.18	0.27	0.12

\* Grey color indicates unigenes with expression level less than 5 RPKM at all time points

**Table S14.mRNA expression levels of T. ni homologs associated with the TREX (transcription-export) pathway.**

Complex / Category	Gene*	T. ni Ortholog	RPKM								STDEV							
			C	0	6	12	18	24	36	48	C	0	6	12	18	24	36	48
TREX	ALYREF	UN063917	73.16	104.20	84.45	29.36	21.57	18.76	10.40	3.93	1.44	1.35	1.32	2.27	0.83	0.44	1.15	0.77
	ALYREF	UN063918	126.26	184.81	126.38	45.28	30.94	25.88	14.05	5.09	2.14	2.65	2.23	4	1.93	1.21	1.56	1.07
	DDX39A	UN010528	44.22	32.27	43.85	27.76	17.83	16.79	8.33	3.64	1.71	2.47	1.26	0.21	0.6	0.14	0.4	0.5
	DDX39A/DDX39B	UN007276	747.82	1152.22	820.10	397.81	207.42	167.57	75.34	32.20	13.35	22.60	28.44	22.14	4.87	4.72	3.65	1.03
	DDX39A/DDX39B	UN007277	874.91	1309.79	872.07	412.38	217.71	176.33	79.09	33.50	14.43	35.92	31.2	23.32	4.32	6.08	3.08	1.73
	DDX39A/DDX39B	UN017599	0.15	0.13	0.21	0.29	0.23	0.00	0.31	0.26	0.25	0.16	0.13	0.28	0.17	0	0.25	0.45
	DDX39A/DDX39B	UN035530	167.98	304.23	383.19	221.89	118.84	93.41	37.78	14.57	3.60	2.77	6.56	9.85	4.73	1.13	0.96	0.16
	DDX39A/DDX39B	UN063722	145.16	121.00	158.81	79.02	52.69	41.12	23.69	10.11	3.08	0.61	2.61	4.46	1.33	1.23	2.05	0.71
	DDX39B	UN070500	86.88	73.96	149.12	47.62	38.08	22.58	13.00	5.00	2.48	5.81	6.44	4.02	1.69	1.57	1.05	0.12
	POLDIP3	UN015446	25.28	29.10	39.08	27.33	16.74	11.83	5.63	2.55	1.23	2.94	3.06	0.92	1.23	0.44	0.47	0.12
	POLDIP3	UN015447	29.59	33.82	43.58	30.63	18.16	12.52	6.10	2.80	1.35	3.59	3.32	1.13	1.27	0.34	0.48	0.15
	RBM39	UN014629	47.85	52.33	46.55	19.18	13.79	9.50	5.65	2.91	1.99	2.19	1.77	0.77	0.35	0.78	0.19	0.15
	RBM39	UN014630	59.58	67.16	57.42	23.69	17.27	11.75	7.14	3.60	2.57	2.66	1.96	1.04	0.24	0.97	0.4	0.18
	RBM39	UN014631	21.95	34.32	28.93	12.35	9.05	6.86	4.00	1.89	1.38	0.40	0.85	0.54	0.7	0.23	0.69	0.2
	RBM39	UN017155	0.21	0.22	0.26	0.46	0.27	0.26	0.52	0.39	0.36	0.19	0.27	0.24	0.26	0.06	0.24	0.14
	RBM39	UN021342	0.24	0.22	0.25	0.29	0.36	0.35	0.46	0.50	0.12	0.21	0.06	0.11	0.17	0.06	0.09	0.15
	SARNP	UN006330	29.06	25.84	50.93	25.74	16.71	14.88	6.12	2.24	0.40	1.79	0.55	1.54	0.57	1.16	1.05	0.24
	SARNP	UN006331	29.84	26.51	52.37	26.36	17.14	15.23	6.26	2.31	0.41	1.87	0.61	1.55	0.6	1.21	1.07	0.27
	Thoc 1	UN027216	2.77	4.33	6.41	3.07	2.23	1.39	0.78	0.30	0.36	0.61	1.06	0.15	0.47	0.36	0.15	0.19
	Thoc 1	UN027217	31.18	28.59	31.94	13.13	10.64	8.07	4.25	2.14	3.80	0.63	2.79	0.88	0.86	0.33	0.38	0.78
	Thoc 1	UN027624	23.31	24.63	34.33	12.14	10.34	8.40	4.00	1.53	0.39	1.19	1.47	0.35	1.07	0.79	0.39	0.36
	Thoc 2	UN022316	30.92	31.68	25.17	9.72	6.92	4.17	2.28	1.05	0.10	1.54	0.73	0.63	0.31	0.23	0.16	0.33
	Thoc 6	UN035293	19.20	19.73	38.32	14.96	10.67	7.48	4.09	1.91	1.87	0.99	1.66	1.33	0.76	0.69	0.08	0.27
	Thoc 6	UN044917	9.53	13.27	24.21	7.91	6.05	4.30	2.43	0.84	1.11	1.05	1.71	0.47	0.78	0.55	0.51	0.34
	Thoc 7	UN014434	35.04	31.66	55.65	24.35	17.75	14.44	7.82	2.96	1.32	0.91	3.74	2.93	1.84	0.43	0.66	0.09
	Thoc3	UN004477	11.30	18.92	26.25	17.16	10.65	7.73	3.10	1.66	0.36	0.58	0.55	1.11	0.57	0.38	0.32	0.3
	Thoc3	UN004480	11.74	19.25	25.82	17.57	10.91	7.30	3.24	1.83	0.38	0.25	0.51	1.02	0.47	0.49	0.18	0.66
	Thoc3	UN004482	12.88	20.99	28.73	18.94	11.71	7.54	3.30	1.55	0.57	0.37	0.45	0.95	0.48	0.27	0.31	0.48
	Thoc3	UN004486	13.77	22.65	30.50	20.43	12.70	8.30	3.57	1.67	0.60	0.44	0.42	1.36	0.52	0.33	0.09	0.45
	Thoc3	UN048114	14.53	9.79	16.41	7.48	5.10	4.12	1.68	0.77	0.95	0.62	0.57	0.43	0.51	0.32	0.23	0.08
ZC3H11A	UN068727	0.73	0.99	1.99	1.02	0.76	1.02	0.55	0.29	0.21	0.37	0.48	0.26	0.27	0.66	0.04	0.15	
ZC3H11A	UN068728	2.28	2.66	4.71	2.48	1.87	1.63	0.59	0.44	0.13	0.91	0.82	0.7	0.42	0.69	0.28	0.37	
ZC3H11A	UN068729	0.78	1.42	3.99	2.31	1.70	1.33	0.87	0.36	0.23	0.35	0.64	0.52	0.42	0.72	0.45	0.18	
ZC3H11A	UN068730	2.72	3.51	7.40	4.14	3.09	2.10	0.92	0.55	0.26	1.02	0.97	1	0.24	0.76	0.34	0.46	

\* Grey color indicates unigenes with expression level less than 5 RPKM at all time points

**Table S15. mRNA expression levels of T. ni homologs associated with small RNA generating pathway.**

Complex / Category	Gene*	T. ni Ortholog	RPKM								STDEV							
			C	0	6	12	18	24	36	48	C	0	6	12	18	24	36	48
			Arg 1	UN047527	17.57	18.98	22.74	10.39	7.29	4.17	1.75	1.05	1.41	0.68	0.78	0.68	0.3	0.67
Arg 1	UN064364	12.06	18.35	15.97	9.15	4.78	3.15	1.39	0.83	1.26	1.35	1.09	0.8	0.73	0.81	0.42	0.28	
Arg 2	UN049184	198.60	166.57	131.04	50.79	33.46	22.60	14.73	7.44	5.41	4.89	2.07	0.59	1.29	0.7	0.84	0.33	
Arg 3 / Bm piwi	UN063569	93.22	91.60	114.19	56.40	28.07	21.08	7.59	2.83	1.34	0.87	2.1	2.75	1.09	0.73	0.75	0.33	
Arg 3 / Bm piwi	UN070631	4.50	3.12	4.00	2.81	1.73	1.24	0.79	0.52	0.29	0.16	0.29	0.25	0.06	0.15	0.06	0.17	
Arg 3 / Bm piwi	UN070632	4.53	3.12	4.03	2.84	1.74	1.26	0.79	0.51	0.31	0.16	0.29	0.24	0.06	0.17	0.06	0.17	
Ago-Aub	UN063569	93.22	91.60	114.19	56.40266	28.06745	21.0755	7.592289	2.83	1.34	0.87	2.1	2.75	1.09	0.73	0.75	0.33	
R2D2	UN034727	14.16	13.23	24.99	11.52686	5.58322	4.66343	1.687366	0.60	1.68	0.46	1.93	0.65	1.02	0.46	1.06	0.29	
R2D2	UN034726	8.01	6.80	13.98	6.6099	3.037442	2.599077	0.844967	0.35	0.87	0.19	1.23	0.43	0.43	0.38	0.58	0.21	
R3D1	UN069998	18.66	34.85	46.60	33.74212	16.90344	11.99221	5.476954	1.25	1.41	1.96	3.68	0.63	1.83	1.67	1.19	0.4	
R3D1	UN069997	13.71	25.80	31.52	23.38806	11.39307	8.326638	3.920268	0.94	0.76	1.12	2.1	0.09	1.01	1.54	0.74	0.26	
R3D1	UN069996	29.14	60.56	97.34	76.80119	41.49592	30.12166	14.54886	5.49	1.80	1.40	1.31	1.8	1.05	1.83	0.79	0.58	
R3D1	UN069995	27.11	56.43	89.97	71.23328	38.42907	27.97211	13.55114	5.15	1.53	1.21	1.1	1.85	0.87	1.78	0.71	0.49	
Drosha	UN066532	7.10	3.71	4.98	2.62483	1.444257	1.143077	0.45159	0.26	0.31	0.11	0.4	0.1	0.27	0.09	0.12	0.09	
Pasha	UN010331	2.05	0.66	1.17	0.40	0.36	0.25	0.15	0.03	0.28	0.25	0.17	0.09	0.19	0.13	0.16	0.03	
Pasha	UN010332	1.99	0.61	1.08	0.44	0.41	0.25	0.22	0.05	0.32	0.23	0.08	0.1	0.16	0.16	0.13	0.04	
Pasha	UN011902	1.35	0.71	1.46	0.55	0.60	0.37	0.21	0.14	0.24	0.22	0.19	0.14	0.16	0.19	0.04	0.05	
Pasha	UN011903	1.34	0.54	1.46	0.61	0.60	0.45	0.23	0.17	0.22	0.27	0.18	0.15	0.19	0.23	0.05	0.15	
Dicer-1	UN008847	4.29	1.02	1.32	0.73	0.42	0.53	0.32	0.20	0.42	0.05	0.13	0.09	0.11	0.12	0.09	0.12	
Dicer-1	UN008848	2.39	0.90	1.11	0.58	0.46	0.32	0.21	0.23	0.55	0.23	0.14	0.25	0.33	0.08	0.16	0.2	
Dicer-2	UN036750	0.36	0.09	0.03	0.05	0.06	0.48	0.48	0.07	0.31	0.15	0.06	0.09	0.13	0.2	0.49	0.12	
Dicer-2	UN048573	0.21	0.09	0.00	0.06	0.24	0.27	0.16	0.17	0.36	0.08	0	0.13	0.17	0.07	0.14	0.15	
Dicer-2	UN066277	104.89	40.75	28.79	8.76	5.02	3.55	2.62	1.46	1.77	2.21	0.76	0.43	0.35	0.33	0.14	0.21	
Dicer-2	UN066287	107.23	41.61	29.68	8.98	5.16	3.69	2.68	1.49	1.83	2.19	0.73	0.47	0.42	0.33	0.13	0.19	
endoribonuclease Dcr-1	UN068521	3.71	0.83	1.28	0.66	0.46	0.51	0.28	0.19	0.35	0.16	0.2	0.12	0.17	0.06	0.11	0.13	
endoribonuclease Dcr-1	UN068522	4.75	0.67	1.06	0.51	0.43	0.43	0.27	0.18	0.42	0.10	0.21	0.12	0.13	0.03	0.11	0.16	

\* Grey color indicates unigenes with expression level less than 5 RPKM at all time points





hsp family	hsp60	UN014211	0.56	0.68	0.46	0.28	0.36	0.26	0.23	0.23	0.24	0.21	0.13	0.16	0.07	0.06	0.02	0.05
	hsp60	UN015254	628.12	684.35	701.64	280.20	179.61	148.18	62.30	19.82	20.32	14.94	12.4	20.33	1.57	2.5	2.7	0.70
	hsp70	UN000527	151.19	168.50	125.86	83.77	50.23	34.16	17.94	8.43	5.44	9.86	4.08	1.98	0.73	2.65	1.78	0.33
	hsp70	UN001769	27.55	3.03	7.05	13.83	40.66	5.05	19.10	6.04	3.72	0.3	1.05	0.9	1.73	1.08	3.47	0.58
	hsp70	UN001910	28.15	4.19	9.25	19.76	52.31	7.17	22.03	9.04	2.39	0.22	0.2	1.96	0.77	0.62	0.98	1.03
	hsp70	UN002604	4.58	0.32	0.47	2.35	6.10	1.28	3.20	1.86	0.14	0.07	0.18	0.21	0.55	0.06	0.08	0.08
	hsp70	UN002605	4.80	0.30	0.47	2.39	6.13	1.29	3.29	1.93	0.25	0.04	0.18	0.2	0.53	0.04	0.07	0.04
	hsp70	UN025820	0.22	0.31	0.13	0.36	0.43	0.36	0.23	0.19	0.13	0.17	0.07	0.1	0.2	0.34	0.18	0.07
	hsp70	UN033115	0.13	0.22	0.09	0.44	0.34	0.26	0.47	0.11	0.22	0.2	0.11	0.24	0.3	0.07	0.41	0.20
	hsp70	UN033766	0.08	0.18	0.10	0.41	0.03	0.32	0.30	0.13	0.14	0.17	0.12	0.13	0.06	0.39	0.1	0.11
	hsp70	UN045506	7.70	0.98	1.18	2.16	6.51	0.78	3.16	0.76	1.02	0.66	0.35	0.45	1.91	0.51	0.94	0.66
	hsp70	UN049959	308.75	317.56	185.89	79.55	49.11	32.01	15.03	5.16	8.69	3.12	5.91	4.46	3.36	3.69	1.63	0.23
	hsp70	UN059101	4220.74	6035.30	3956.62	3208.57	1995.66	1249.91	702.51	265.29	50.53	113.26	34	85.52	6.95	30.06	24.69	15.41
	hsp70	UN060321	0.00	0.00	0.07	0.16	0.05	0.25	0.20	0.12	0	0	0.13	0.31	0.09	0.22	0.18	0.20
	hsp70-2	UN016518	674.30	565.26	436.90	276.77	193.91	139.11	53.29	21.88	19.61	10.79	7.62	8.5	4.73	2.5	0.57	1.18
	hsp90	UN009070	1070.57	893.61	1044.44	745.83	522.85	219.35	100.09	28.23	19.09	24.61	23.75	23.77	9.24	6.35	6.86	2.16
	hsp90 35140899 miss su	UN046602	161.68	170.81	193.25	190.24	112.68	62.10	34.72	13.25	6.48	6.69	18.83	10.02	1.9	1.47	1.65	1.05
	small heat shock protein 19.7	UN063826	17.85	0.59	1.32	6.56	11.83	3.10	6.58	2.27	1.2	0.18	0.43	0.81	0.42	0.9	0.77	0.50
	small heat shock protein 22.2	UN062469	10.41	1.60	1.71	8.14	12.63	2.95	9.13	5.02	1.32	0.53	0.6	0.98	1.04	0.62	2.05	0.87
	small heat shock protein 22.2	UN064082	12.71	1.93	1.29	6.94	11.57	2.41	8.54	4.15	1.08	0.41	0.11	0.88	1.17	0.66	1.1	1.40
	small heat shock protien	UN002579	7.15	0.09	0.60	1.82	2.56	0.75	1.72	0.25	0.54	0.1	0.22	0.37	0.97	0.24	0.29	0.22
	small heat shock protien	UN023968	259.74	442.90	268.46	81.91	36.19	25.98	11.06	7.53	6.46	9.93	4.92	4.38	3.24	2.41	0.45	1.21
	small heat shock protien	UN026941	0.83	0.04	0.25	0.19	0.38	0.25	0.28	0.00	0.39	0.07	0.05	0.13	0.19	0.28	0.27	0.00
	small heat shock protien	UN029422	14.76	7.57	11.93	25.52	30.71	5.88	14.53	4.14	2.74	0.71	0.98	1.66	1.76	0.13	1.87	1.16
	small heat shock protien	UN047293	22.97	37.78	20.78	7.08	2.70	2.06	1.50	1.48	0.84	1.34	2.39	0.8	0.5	0.33	0.27	0.15
	small heat shock protien	UN054228	16.63	14.93	13.47	5.21	4.53	2.76	2.24	0.94	2.54	1.53	0.94	0.47	0.28	0.39	0.31	0.39

\* Grey color indicates unigenes with expression level less than 5 RPKM at all time points

**Table S17. mRNA expression levels of T. ni homologs associated with ROS (Response to Oxidative Stress).**

Complex / Category	Gene*	T. ni Ortholog	RPKM									STDEV								
			C	0	6	12	18	24	36	48	C	0	6	12	18	24	36	48		
Response to Oxidative Stress (ROS)	Catalase (Cat)	UN006553	135.55	108.35	72.13	28.82	19.29	13.33	7.16	4.44	3.68	1.95	1.44	1.16	0.82	0.61	0.64	0.22		
	Superoxide dismutase (Sod)	UN067329	101.06	111.65	126.34	87.58416	55.20862	44.28785	22.36421	5.53	7.09	1.43	4.95	2.88	3.39	0.62	2.01	0.56		
	Superoxide dismutase (Sod)	UN059002	7.39	4.41	5.77	8.93535	12.87558	5.757411	7.750131	3.96	1.68	0.94	0.92	0.62	0.8	0.26	0.55	0.64		
	Superoxide dismutase (Sod)	UN059001	7.32	4.40	6.98	12.92635	18.04469	8.091656	11.83632	5.56	1.60	0.48	0.62	1.11	0.76	0.19	1.8	0.72		
	Superoxide dismutase 2 (Mn)	UN064375	61.82	82.30	134.99	75.88046	50.83795	37.82841	18.74022	4.91	5.06	2.40	2.26	3.57	1.9	2.68	2.01	0.5		
	oxidative stress responsive 1	UN023676	20.24	29.26	28.37	14.92765	9.418093	6.75948	2.89714	1.54	0.76	0.96	0.21	0.8	0.34	0.15	0.18	0.04		
	oxidative stress responsive 1	UN005844	2.11	1.63	2.60	1.37	0.87	0.74	0.33	0.10	0.25	0.23	0.27	0.06	0.14	0.19	0.11	0.05		
	Glutathione peroxidase (Gpx)	UN034134	31.61	41.25	42.42	28.39655	21.83728	23.76671	11.70197	4.52	1.07	0.89	0.49	1.26	0.47	1.24	0.97	0.39		
	Glutathione peroxidase (Gpx)	UN034135	125.94	152.80	168.75	114.4644	89.22505	98.43038	48.79471	18.80	4.87	2.96	0.88	5.51	1.48	7.51	3.73	1.43		
	Glutathione peroxidase (Gpx)	UN056254	4.03	15.71	18.49	13.12899	7.506068	4.165343	2.437845	1.05	0.12	0.50	0.83	0.48	0.43	0.29	0.29	0.21		
	Glutathione peroxidase (Gpx)	UN056255	4.18	16.33	19.13	13.4623	7.714708	4.236106	2.48764	1.07	0.15	0.56	0.73	0.48	0.51	0.25	0.27	0.24		
	Glutathione peroxidase (Gpx)	UN070028	3.26	1.74	3.34	2.564754	1.800751	1.699263	1.103247	0.64	0.23	0.33	0.32	0.36	0.26	0.13	0.16	0.18		
	Cytochrome P-450	UN034682	4.01	2.07	2.86	1.872326	1.189273	1.051006	0.772079	0.36	0.39	0.13	0.27	0.31	0.12	0.31	0.21	0.14		
	Cytochrome P-450	UN034680	12.32	7.51	6.78	3.744029	2.645622	1.994642	1.289785	0.61	0.46	0.15	0.55	0.42	0.31	0.23	0.24	0.07		
	Cytochrome P-450	UN024318	1.21	0.08	0.11	0.021262	0.031966	0.024853	0.033447	0.02	0.49	0.02	0.05	0.02	0.04	0.04	0.06	0.03		
	Cytochrome P-450	UN016751	3.95	0.17	0.30	0.17	0.06	0.00	0.03	0.01	0.21	0.09	0.12	0.04	0.07	0	0.04	0.02		

\* Grey color indicates unigenes with expression level less than 5 RPKM at all time points

**Table S18. mRNA expression levels of T. ni homologs associated with NFkB-IkB (Nuclear Factor kB- and I kB).**

Complex / Category	Gene*	T. ni Ortholog	RPKM								STDEV							
			C	0	6	12	18	24	36	48	C	0	6	12	18	24	36	48
IkB family	IkBa/IkBβ/IkBε/IkBγ	UN043702	35.57	21.62	24.12	14.42	10.14	7.94	3.72	2.70	2.19	0.84	1	1.89	1.38	1.32	1.34	0.18
	NF-kB1 (p105/p50)/NF-kB2 (p100/p52)	UN022266	75.35	36.64	30.78	15.91	8.72	6.29	2.68	1.19	6.65	1.54	1.22	0.91	1.47	0.33	0.68	0.06
NFkB family	p65/RelB/c-Rel	UN058651	16.87	13.36	12.05	8.75	5.23	3.66	2.46	1.19	0.46	0.84	0.66	0.17	0.74	0.37	0.26	0.13
	p65/RelB/c-Rel	UN058652	15.67	11.04	8.92	6.36	3.76	2.43	1.74	0.95	0.68	0.64	0.62	0.34	0.4	0.38	0.09	0.07
IKK complex	Ikkα/IKKβ	UN065352	8.05	4.75	5.91	2.45	1.69	1.41	0.57	0.34	0.23	0.53	0.49	0.14	0.2	0.1	0.09	0.15
	NEMO (IKKγ)	UN000226	14.61	3.82	3.34	2.05	1.14	1.03	0.25	0.39	0.30	0.47	0.63	0.3	0.16	0.3	0.13	0.07
	NEMO (IKKγ)	UN068267	15.98	4.27	3.54	2.27	1.32	1.07	0.27	0.44	0.35	0.48	0.77	0.3	0.24	0.27	0.14	0.12
	NEMO (IKKγ)	UN068268	17.11	4.43	3.69	2.26	1.33	1.14	0.30	0.45	0.49	0.56	0.75	0.33	0.23	0.32	0.15	0.09

\* Grey color indicates unigenes with expression level less than 5 RPKM at all time points

Abbreviation: Bcl-3, B-cell lymphoma 3 protein, Dif, dorsal-related immunity factor, Ird5, immune response deficient protein 5, IkB, inhibitor of NF-kappa-B, IKK, IkB kinase, NEMO, NF-kappa-B essential modulator, NFkB, nuclear factor kappa B.



LPR2	UN005188	66.88	39.04	5.39	4.94	3.62	5.58	3.56	1.90	1.33	0.61	0.25	0.18	0.11	0.31	0.31	0.09
LPR2	UN005189	63.63	38.20	5.79	5.07	3.50	5.34	3.46	1.87	0.43	0.37	0.24	0.3	0.29	0.35	0.41	0.05
NFAT	UN067086	11.96	3.61	1.88	1.19	0.86	0.80	0.23	0.18	0.46	0.30	0.25	0.2	0.22	0.25	0.05	0.06
NFAT	UN068064	9.90	4.45	2.34	2.01	1.19	1.03	0.58	0.43	0.29	0.67	0.25	0.54	0.41	0.14	0.36	0.13
PELLE	UN035304	24.66	31.58	24.12	17.03	10.07	5.69	3.03	1.43	0.62	0.56	1.09	0.56	0.4	0.43	0.31	0.07
PELLE	UN035305	24.09	31.97	23.59	16.90	9.95	5.70	2.88	1.49	0.38	1.33	1.75	0.69	0.49	0.5	0.5	0.18
PELLINO	UN040918	15.80	23.72	14.82	11.59	7.22	6.20	4.47	3.73	0.44	1.17	0.45	0.49	0.56	0.96	0.31	0.36
PGRP-SA/PGRP-SC2/PRGP-SC1A/PRGP-SC1B	UN007389	2.78	0.95	1.76	0.54	0.34	0.07	0.05	0.04	0.46	0.16	0.22	0.06	0.2	0.12	0.08	0.07
PGRP-SA/PGRP-SC2/PRGP-SC1A/PRGP-SC1B	UN014065	1.28	1.06	0.80	0.44	0.37	0.10	0.00	0.11	0.89	0.26	0.49	0.18	0.29	0.09	0	0.15
PGRP-SA/PGRP-SC2/PRGP-SC1A/PRGP-SC1B	UN014066	1.24	1.09	0.76	0.35	0.37	0.08	0.00	0.13	0.8	0.29	0.52	0.1	0.27	0.08	0	0.16
POSH	UN063975	13.98	11.84	7.55	4.43	2.21	1.92	1.29	0.67	1.01	0.67	0.65	0.5	0.38	0.24	0.15	0.21
POSH	UN063976	12.43	9.56	5.52	3.25	1.54	1.52	1.00	0.44	1.8	0.72	0.65	0.15	0.26	0.26	0.34	0.23
SERPIN-27A	UN032437	30.80	31.30	28.67	11.12	5.49	5.13	2.61	0.69	2.34	0.87	0.63	0.7	0.43	0.17	0.09	0.18
SKPA	UN059632	72.56	70.36	124.69	67.53	53.17	40.52	15.94	5.00	5.64	2.07	4	6.17	2.22	2.63	1.95	0.68
SPN4	UN067625	93.52	103.25	105.01	41.43	23.35	18.33	8.62	3.44	2.72	6.76	1.62	2.31	1.21	0.74	0.64	0.21
SPN4	UN067626	102.46	110.67	113.81	44.69	25.26	19.81	9.38	3.70	2.75	6.54	2.33	2.87	1.32	0.76	0.7	0.24
SPN4	UN067627	104.69	118.11	119.09	47.16	26.37	20.82	9.77	3.87	2.99	6.98	2.02	2.9	1.34	0.92	0.76	0.19
SPN4	UN067628	116.13	128.17	130.66	51.50	28.87	22.78	10.76	4.20	3.03	6.74	2.84	3.6	1.49	0.94	0.85	0.23
TOLL-8/TOLLO/TOLL 6	UN065961	8.43	5.05	2.16	1.33	0.29	0.26	0.15	0.08	0.35	0.22	0.22	0.08	0.06	0.03	0.02	0.04
TRAF1	UN042308	13.29	13.35	7.54	6.91	3.35	2.73	1.51	1.37	0.98	1.32	0.65	0.38	0.37	0.41	0.03	0.08
TRAF2	UN004752	2.75	2.93	3.94	1.73	1.12	0.95	0.53	0.43	0.56	0.28	0.48	0.31	0.32	0.31	0.27	0.23
UEV1A	UN049742	41.92	98.87	137.08	125.26	67.22	49.57	20.45	7.44	1.79	8.13	10.68	9.4	1.67	3.29	0.29	0.52

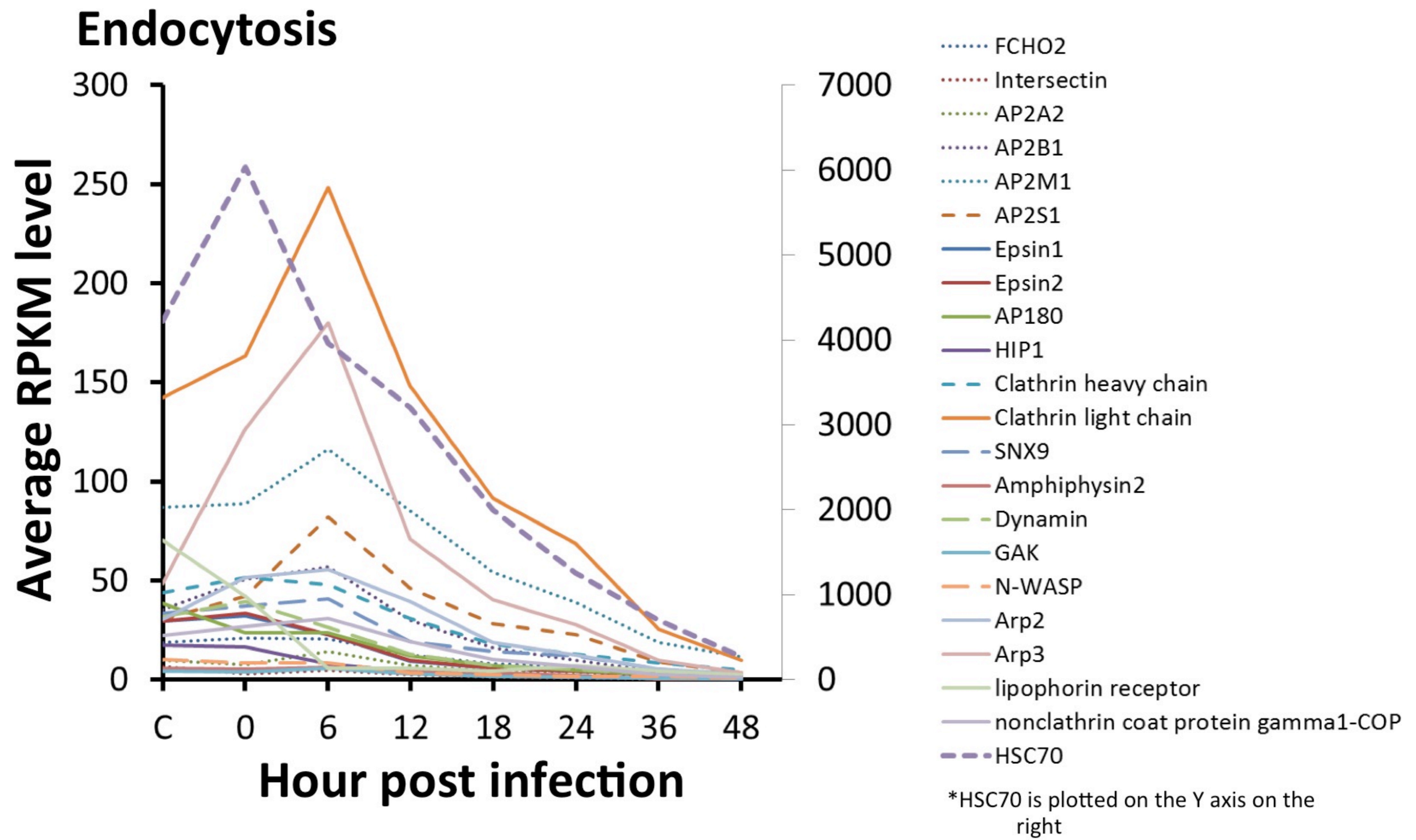
\* Grey color indicates unigenes with expression level less than 5 RPKM at all time points

**Table S20. mRNA expression levels of T. ni homologs associated with histone deacetylase (HDAC) and Sirtuin genes.**

Complex / Category	Gene*	T. ni Ortholog	RPKM								STDEV								
			C	0	6	12	18	24	36	48	C	0	6	12	18	24	36	48	
Class I	HDAC1 (Rpd3) HDAC3	UN068617	63.86	54.33	91.61	48.81	28.10	18.54	7.57	3.84		1.79	1.61	3.47	1.04	0.88	0.59	0.24	0.49
		UN067194	7.49	6.28	5.11	3.69	2.17	1.93	0.89	0.56		0.20	0.37	0.24	0.26	0.34	0.30	0.09	0.03
Class II	HDAC4 / HDAC6	UN065394	4.73	4.64	5.94	5.08	3.13	2.40	1.80	1.19		0.13	0.15	0.45	0.49	0.21	0.14	0.11	0.1
Class III	Sirt1 / Sirt2	UN001946	12.38	8.71	16.38	11.64	7.15	5.53	2.82	1.46		0.26	0.65	0.3	0.26	0.56	0.26	0.14	0.27
		UN003285	2.10	1.81	3.62	0.86	0.99	1.44	0.64	0.30		0.07	0.14	0.12	0.28	0.12	0.47	0.18	0.11
	Sirt4 isoform A	UN003284	1.75	1.26	3.01	0.73	0.85	1.23	0.48	0.29		0.10	0.23	0.07	0.21	0.03	0.37	0.29	0.05
		UN003286	1.64	1.04	3.52	0.83	1.06	1.11	0.61	0.24		0.29	0.48	0.21	0.36	0.41	0.55	0.41	0.12
	Sirt6	UN034256	16.71	21.78	28.30	14.43	10.49	8.21	3.10	1.42		1.06	0.38	1.78	0.69	1.01	0.83	0.31	0.33
Sirt7	UN068768	3.33	5.23	4.33	3.19	2.07	0.94	0.44	0.16		0.56	0.32	0.67	0.73	0.2	0.36	0.18	0.14	
Class IV	HDAC11	UN010002	1.32	0.46	1.59	0.78	0.68	0.43	0.22	0.12		0.11	0.19	0.15	0.17	0.1	0.18	0.08	0.03

\* Grey color indicates unigenes with expression level less than 5 RPKM at all time points

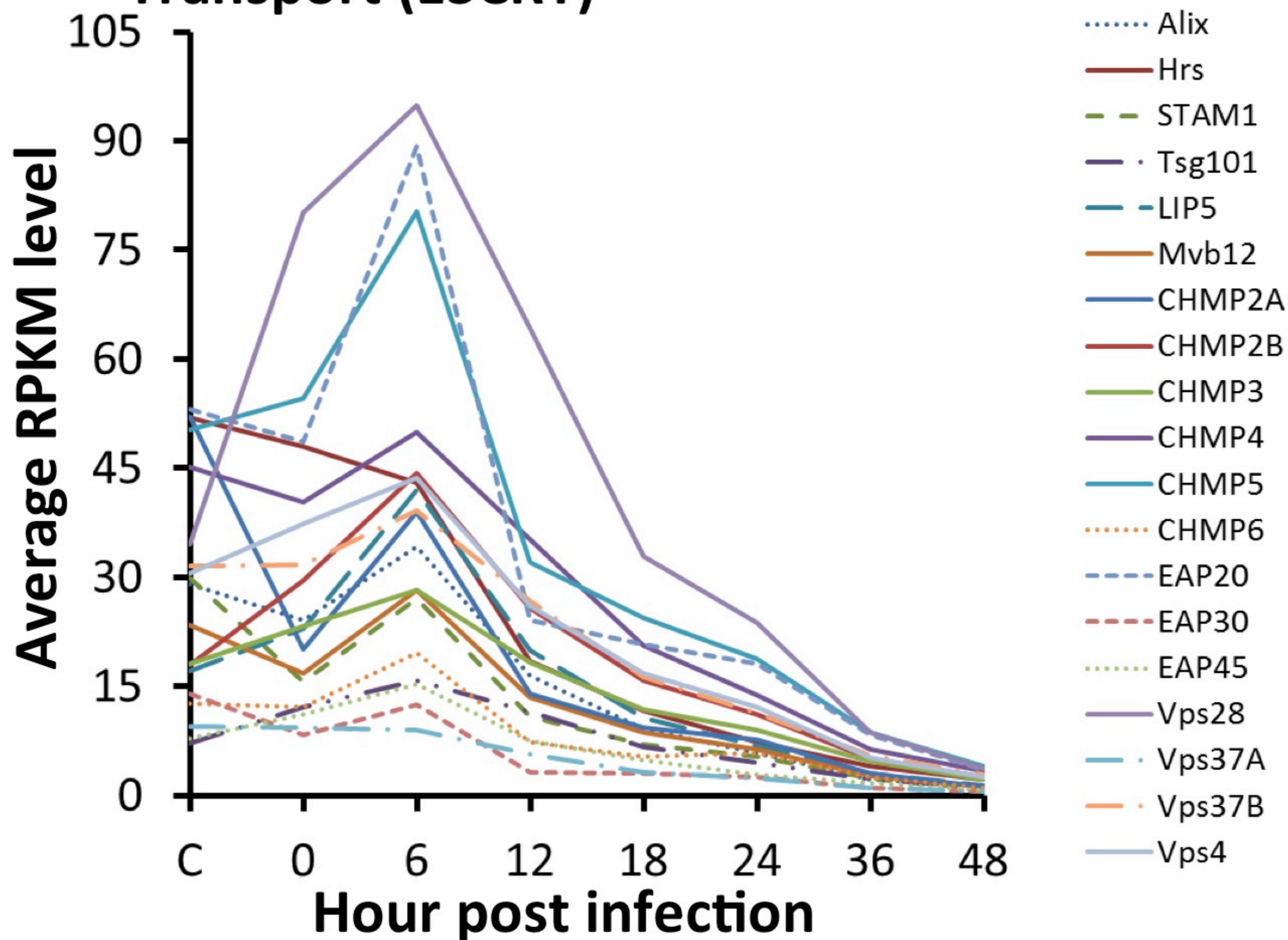
Fig. S1



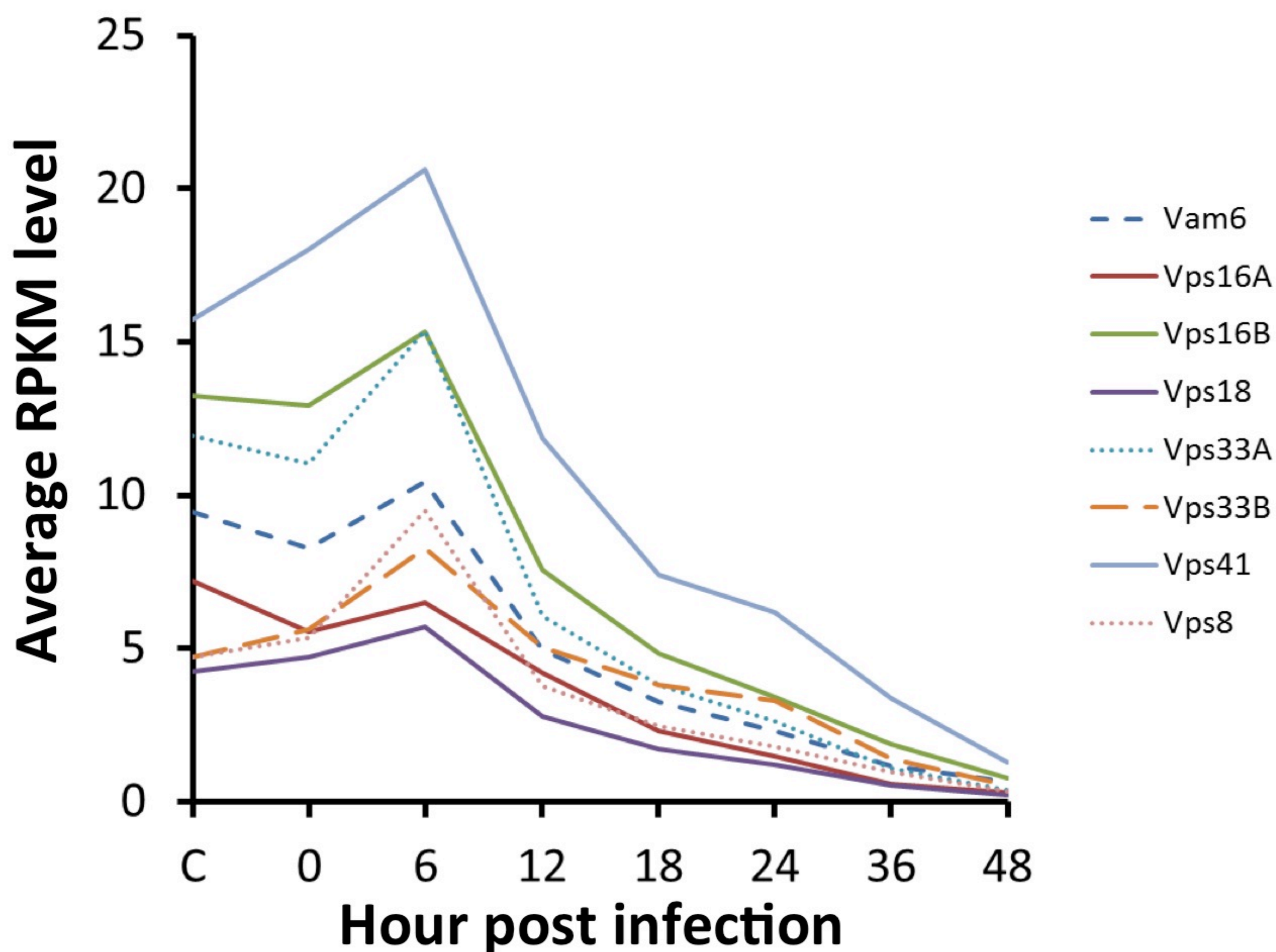


**Fig. S2**

**(A) Endosomal Sorting Complex Required for Transport (ESCRT)**



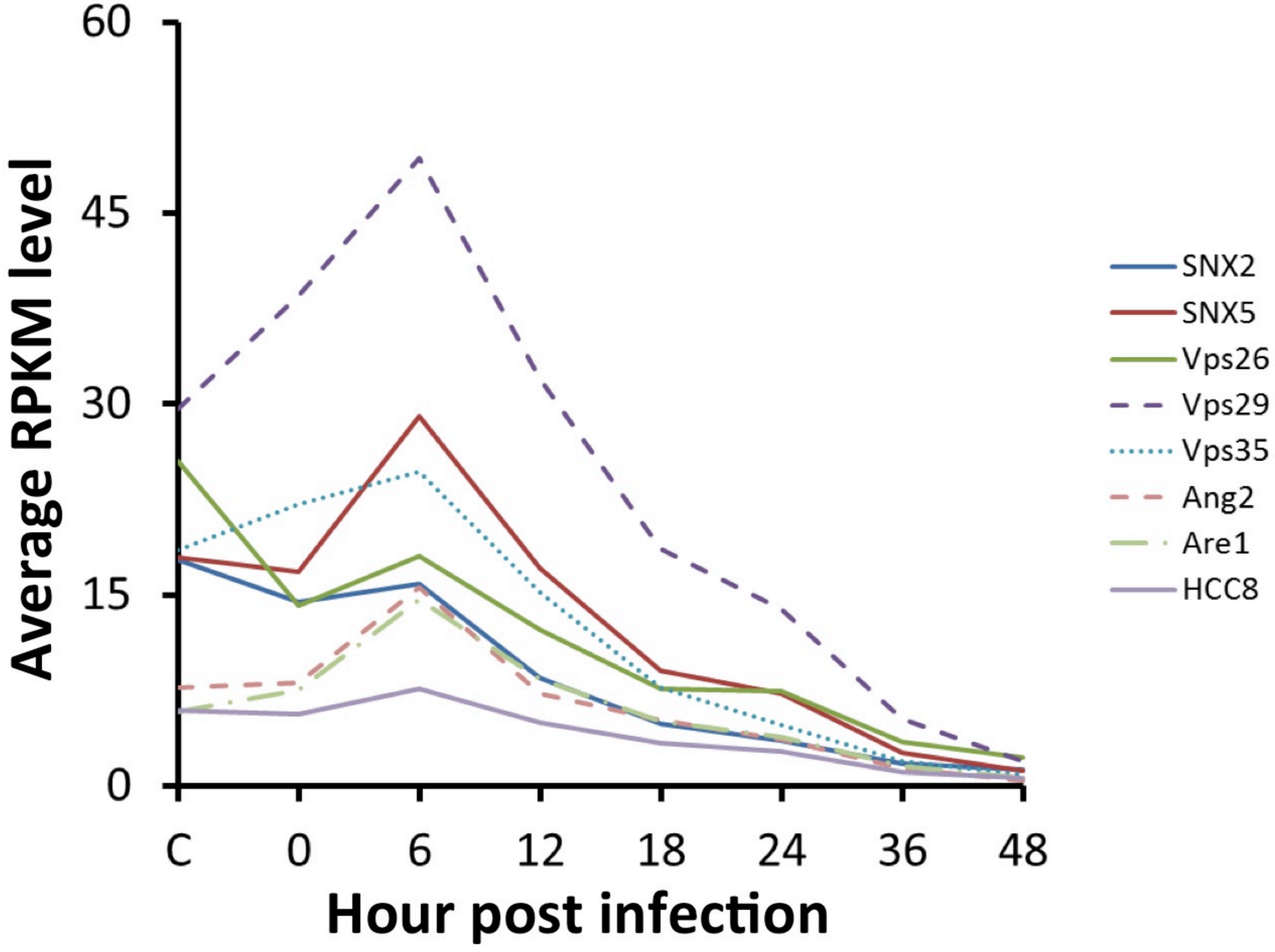
**(B) Vacuolar Protein Sorting complex C (VPS-C)**



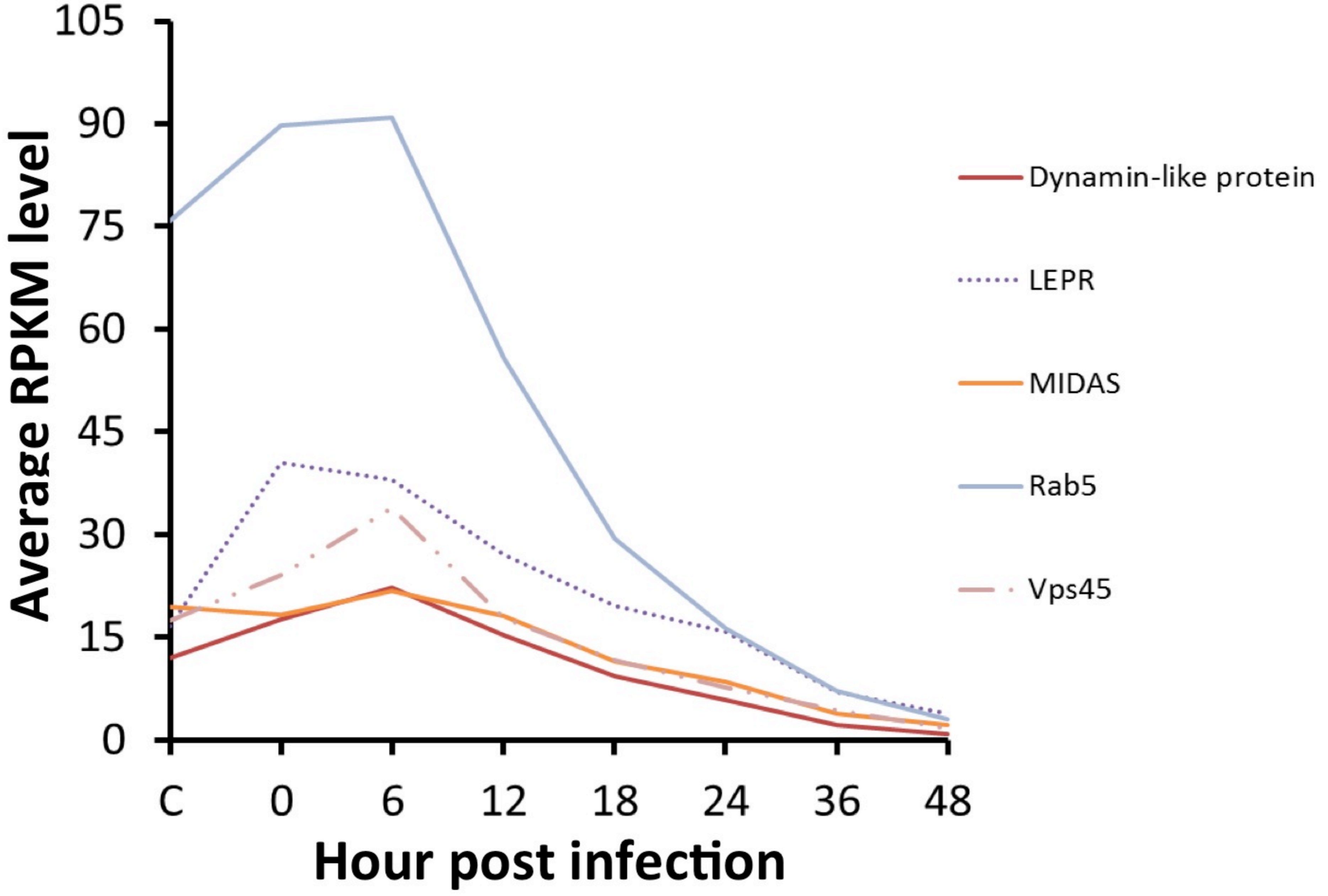


**Fig. S3**

**(A) Retromer & GARP**



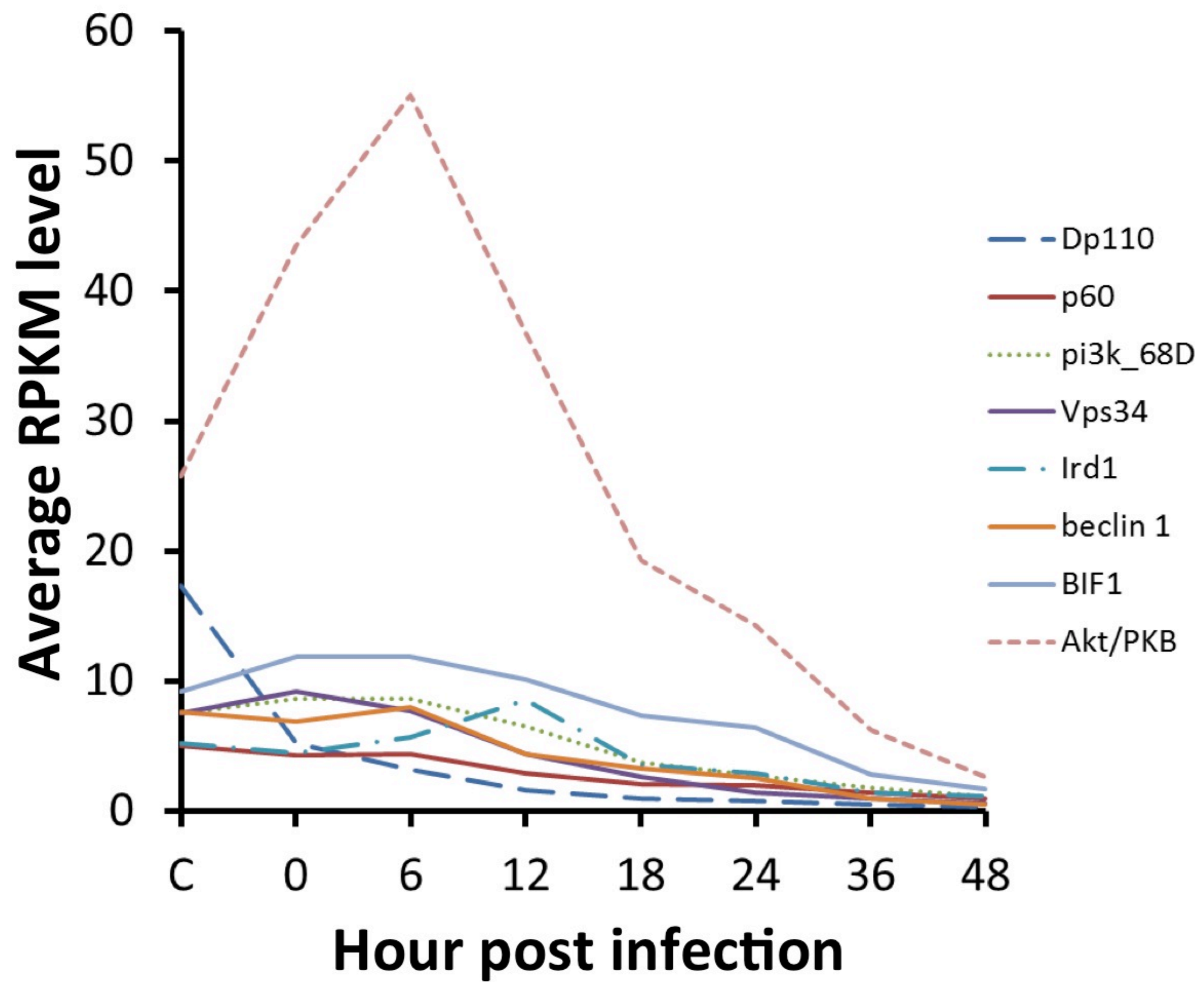
**(B) Other characterized Vps genes**



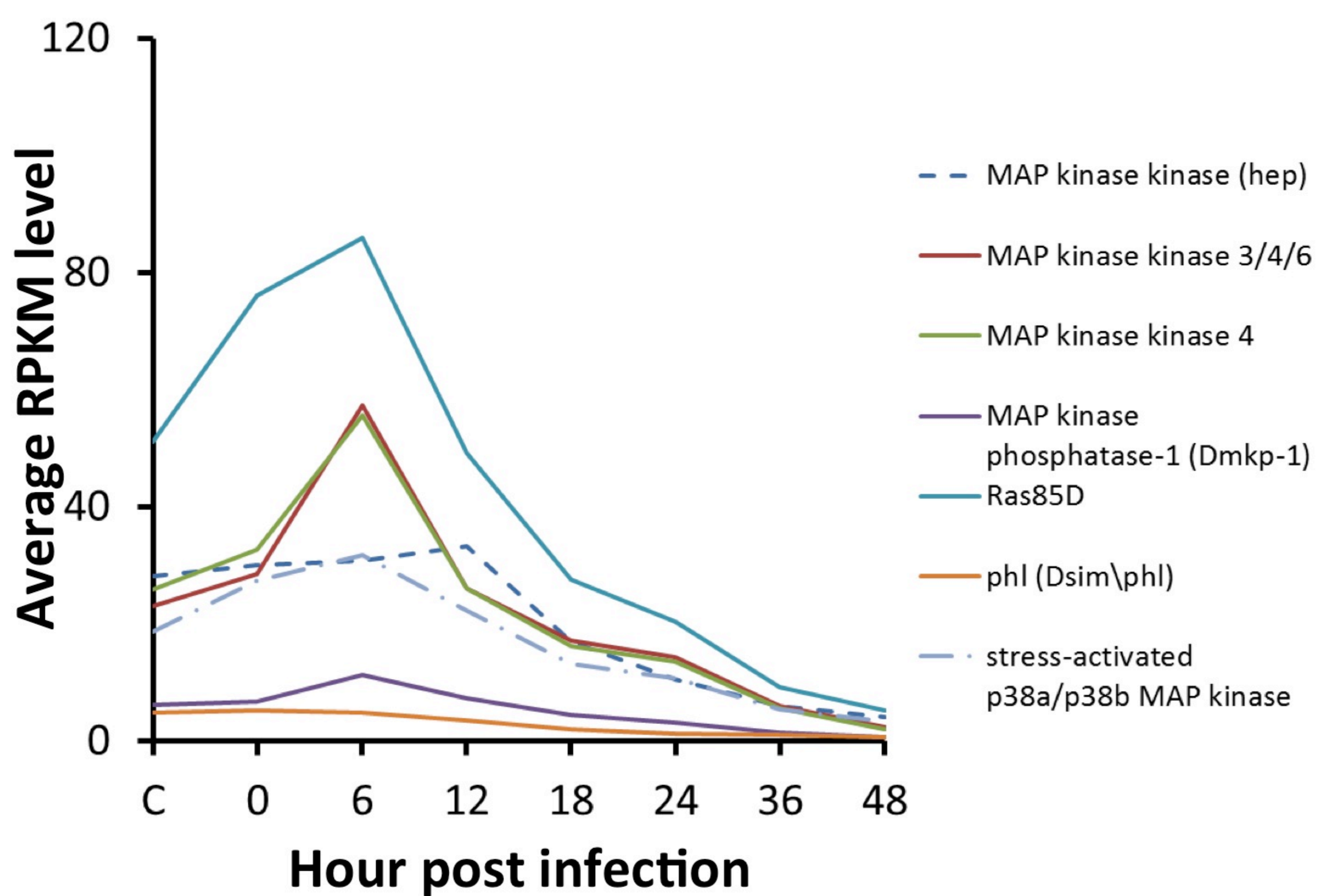


**Fig. S4**

**(A) PI3K**



**(B) MAP Kinase Signaling pathway**



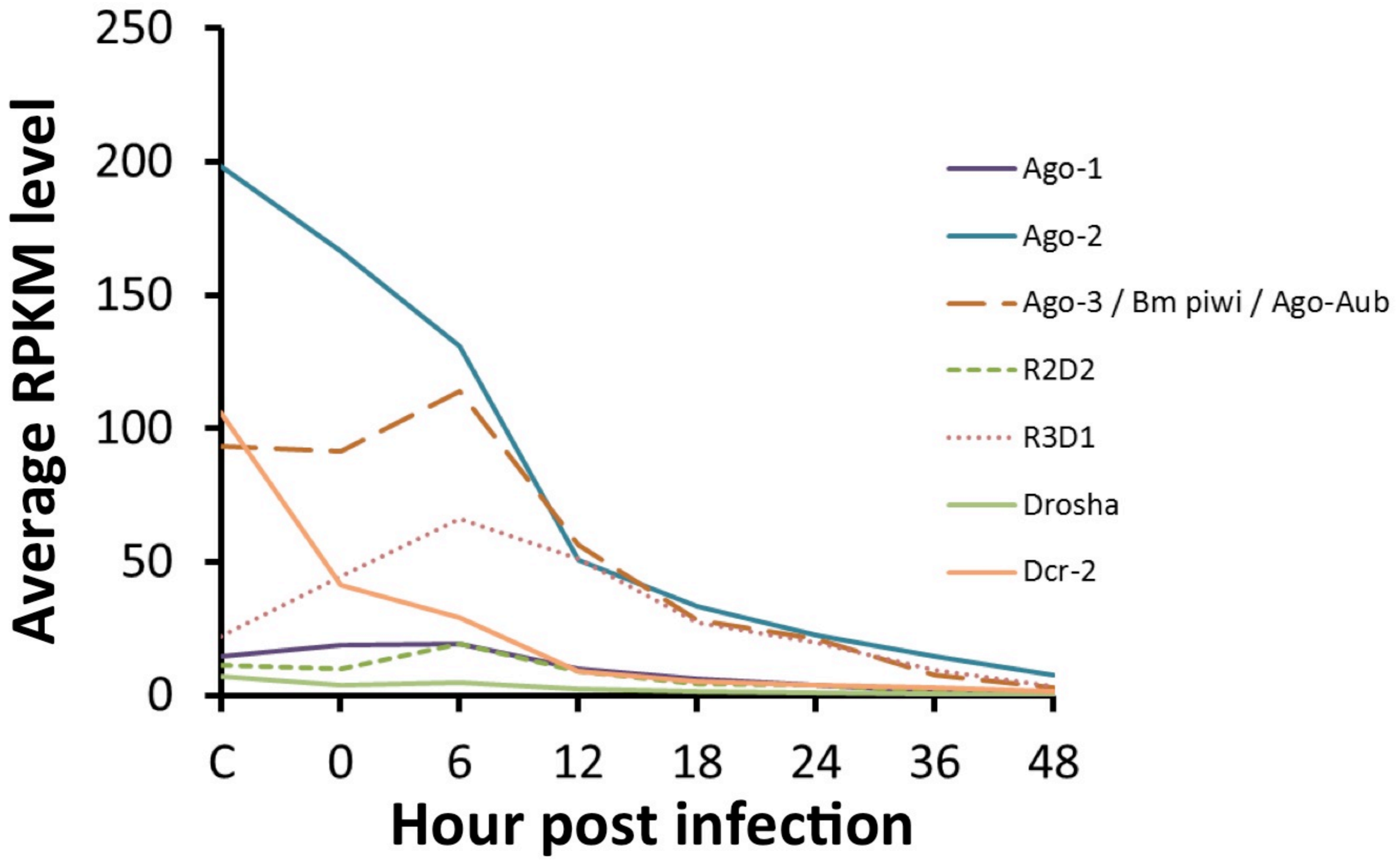






**Fig. S6**

### Small RNA

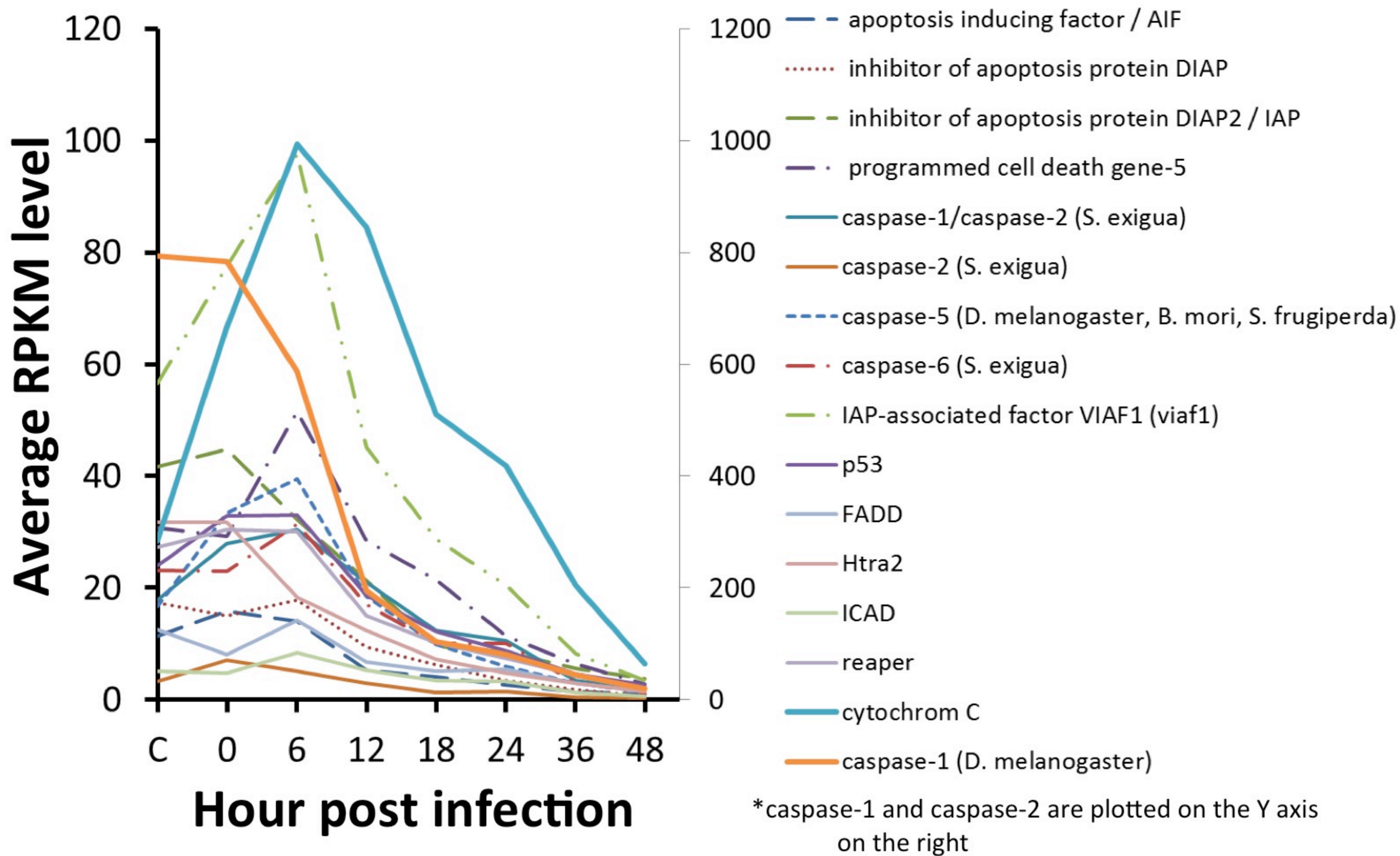


Note: Although we identified homologs of Dicer 1 (UN008847) and Pasha (UN010331) (see Table S15), RPKM values were below 5 and were therefore not included on the graph.



**Fig. S7**

**(A) Apoptosis**



**(B) HSP family**

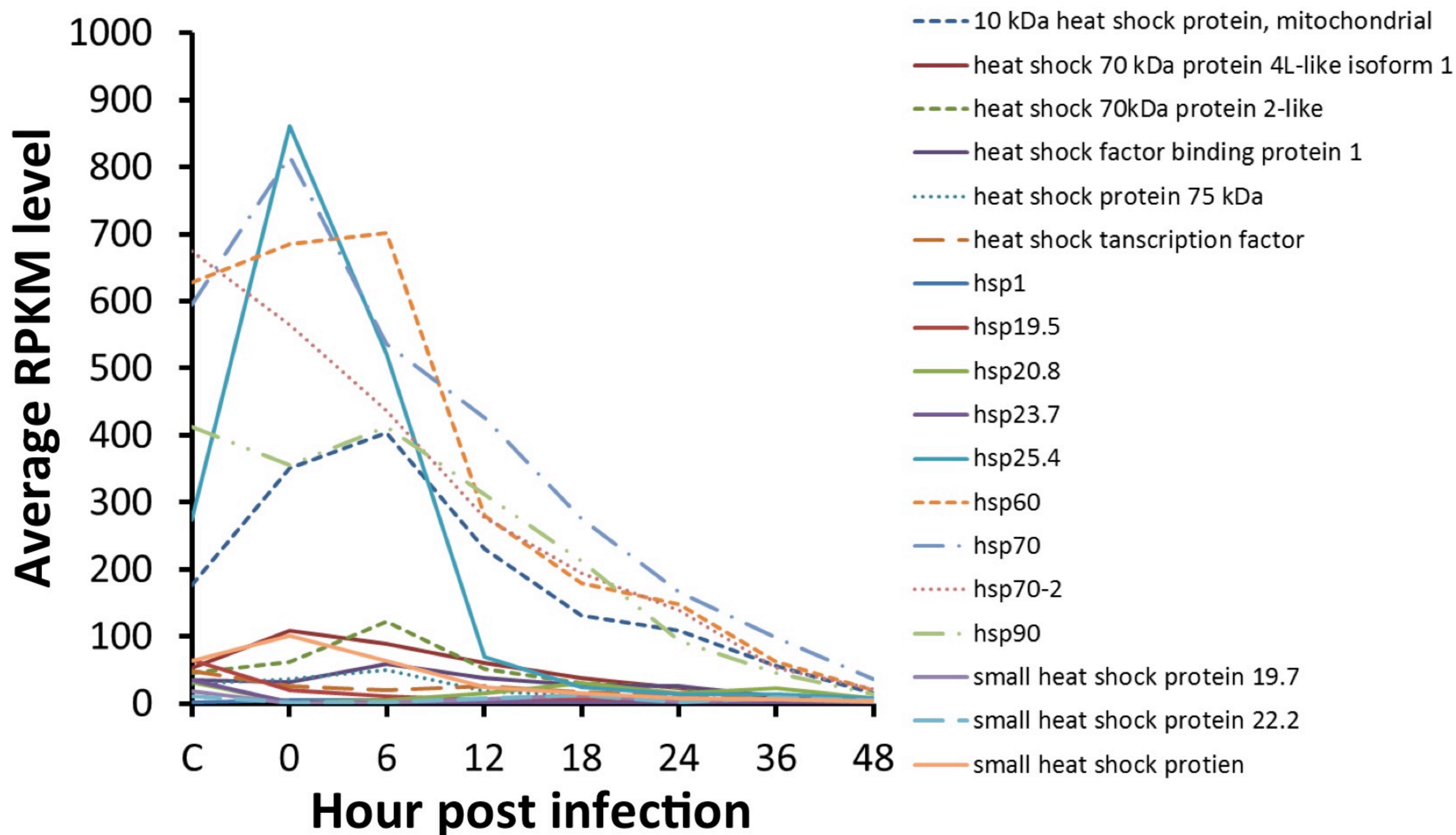
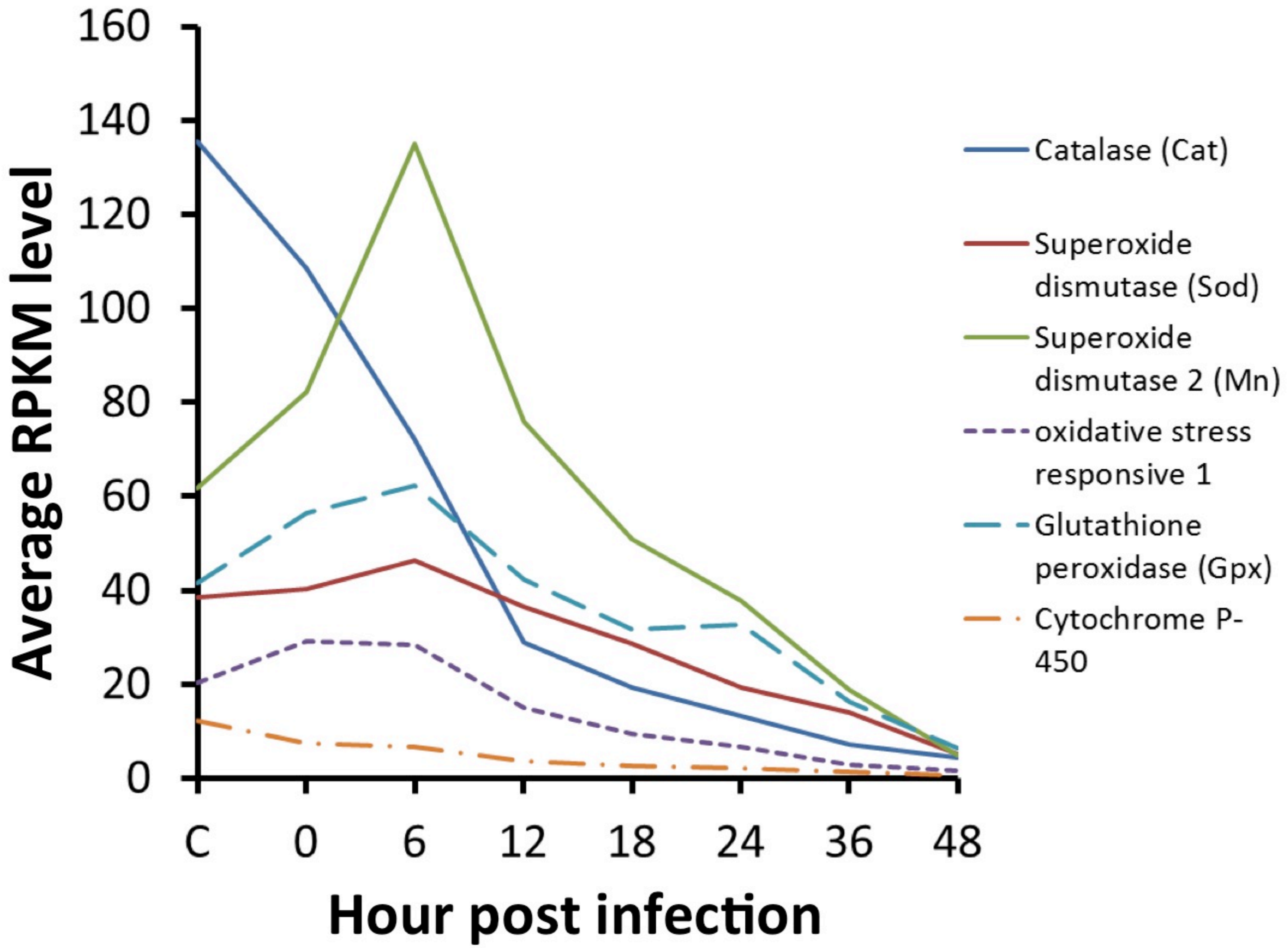




Fig. S8

### (A) Reactive Oxygen Species (ROS)



### (B) NFkB-IkB

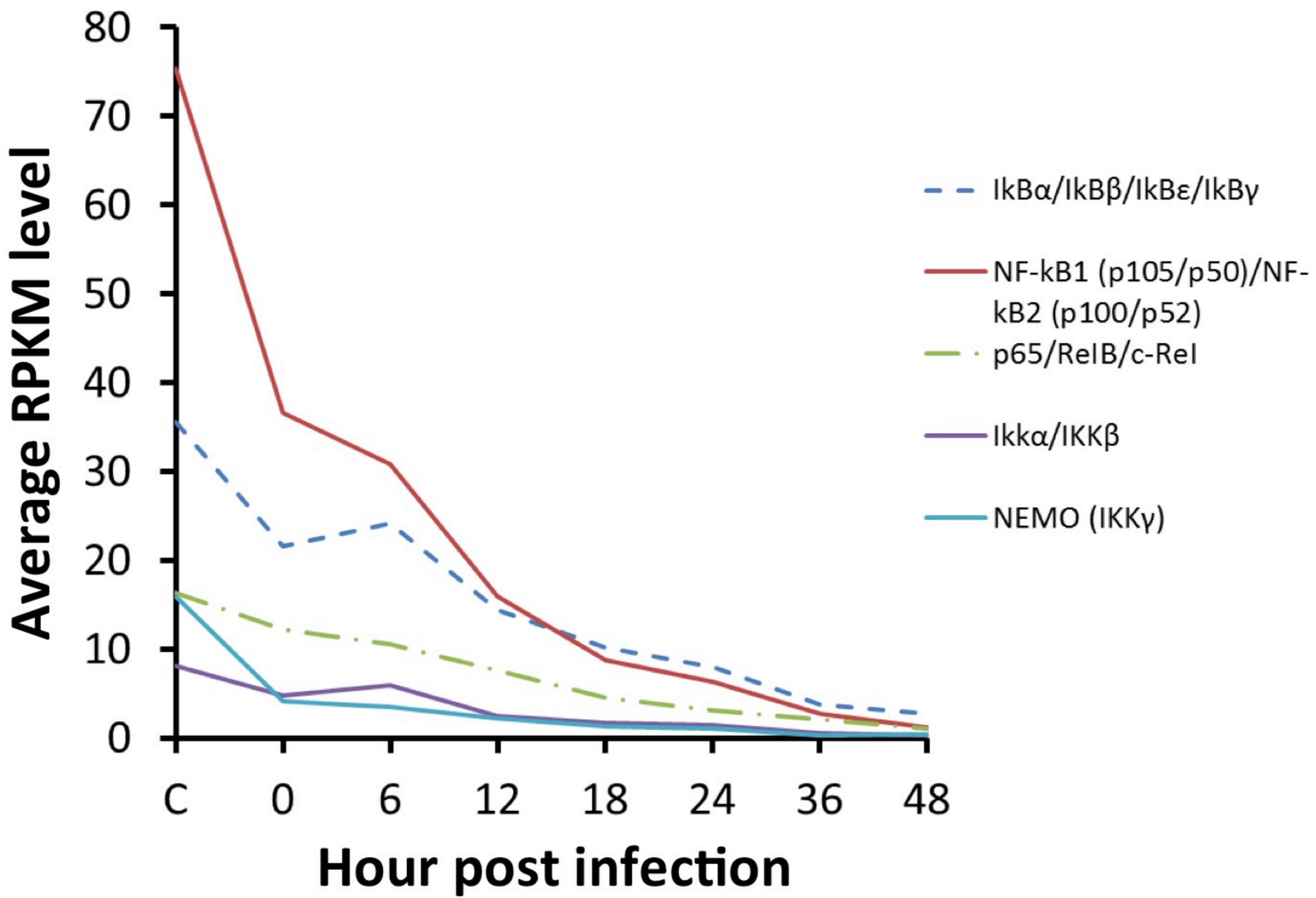
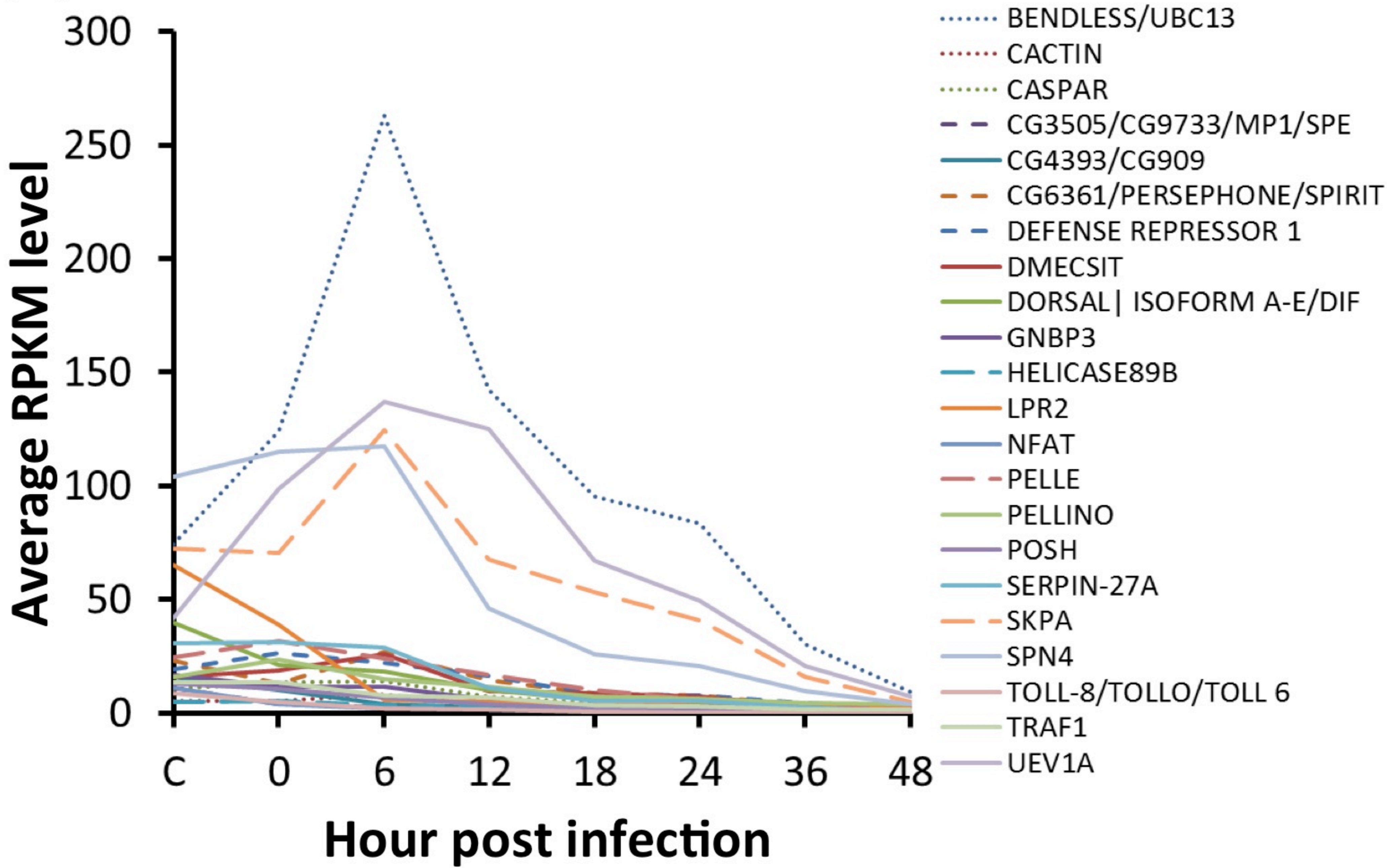




Fig. S9

### (A) IMD and Toll



### (B) JAK/STAT

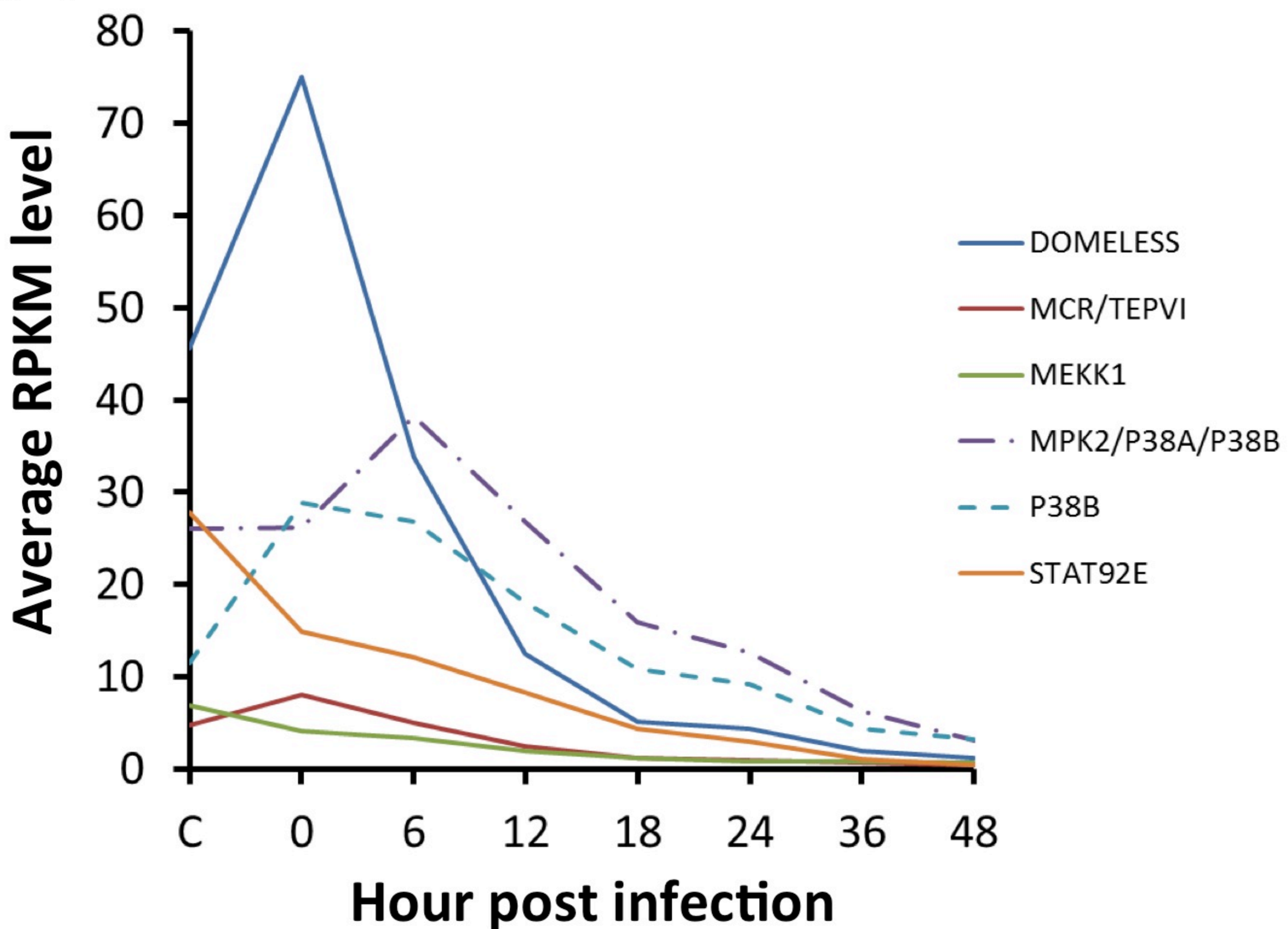
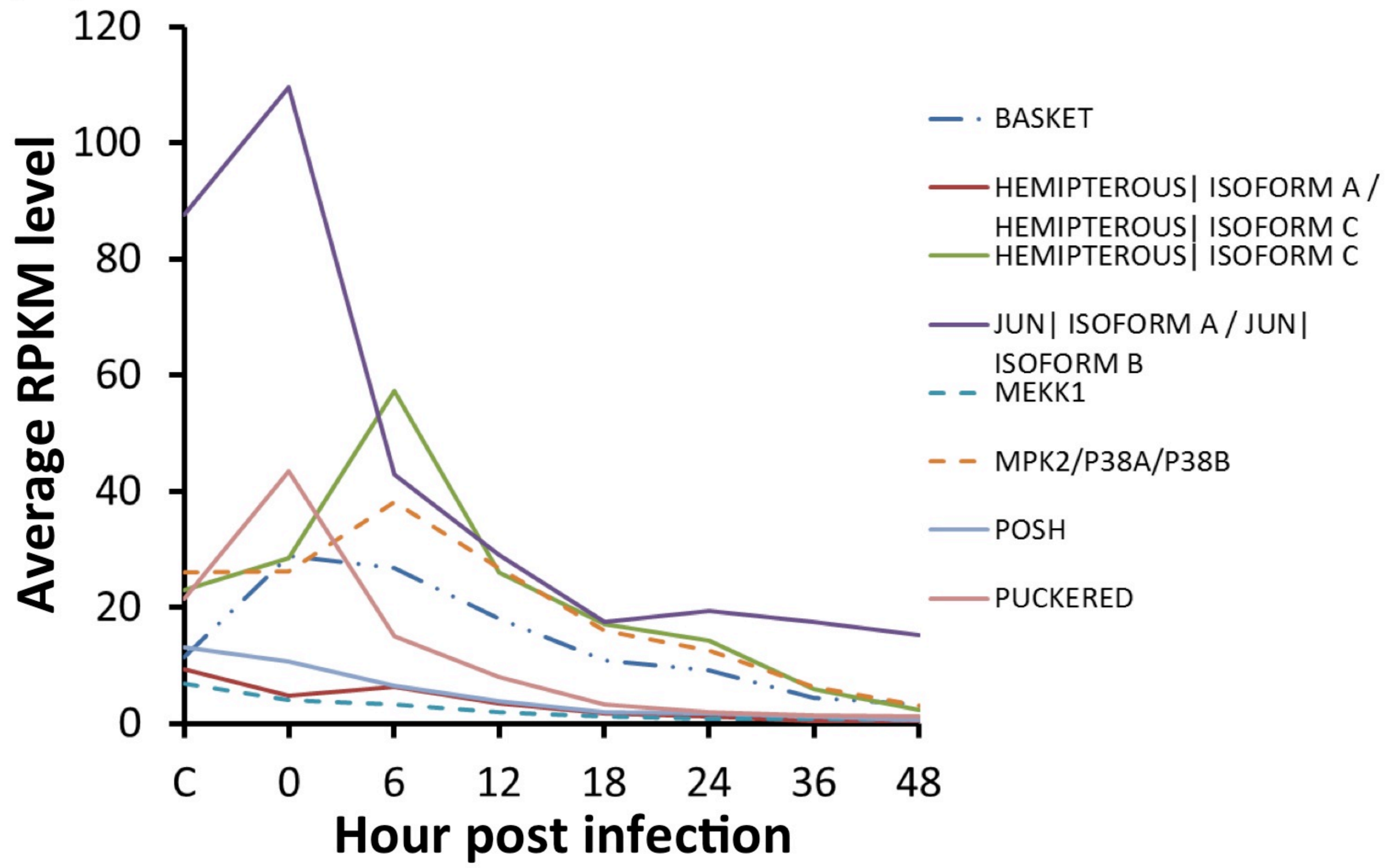




Fig. S10

**(A) JNK**



**(B) HDAC and Sirtuins**

