

Table S1. List of genes tested and dsRNAs used for screening for endocytic regulators of JAK–STAT signalling

<i>Drosophila</i> genes		CG Nr.	Forward primer	Reverse primer	Molecular function	Human homologues	Evidence
rh5	Rh5	CG5279	gaattaatacactactatagggTAA TACGACTACTATAGGG AGAAGGGCTTCC	gaattaatacactactatagggTAA TACGACTACTATAGGG AGAGCTGACACT		OPN5 opsin 5 isoform 1	Best Blast
z	LacZ		gaattaatacactactatagggTAA TACGACTACTATAGGG AGACAGTGGCGTCTGGC GGAAAA	gaattaatacactactatagggTAA TACGACTACTATAGGG AGATCCGAGCCAGTTTA CCCCGT		-	-
stat	STAT92E	CG4257	taatacactactatagggTAATA CGACTACTATAGGGAG AAGCTGCTTGCCCA	taatacactactatagggTAATA CGACTACTATAGGGAG CAGCTGAGAACCGA		STAT5B signal transducer and activator of transcription 5B	Homologue
socs	SOCS36E	CG15154	gaattaatacactactatagggTAA TACGACTACTATAGGG AGAAACGTGCC	gaattaatacactactatagggTAA TACGACTACTATAGGG AGACCCCATCCA		SOCS5 suppressor of cytokine signaling 5	UCSC
1	Rab5	CG3664	taatacactactatagggGCTCG TTTCGTTTCGTTTCT	taatacactactatagggCTATC TTAGGCTTGCAGACC	GTP binding. GTPase activity	RAB5A RAB5A, member RAS oncogene family	Homologue
	Rab5	CG3664	taatacactactatagggGGCAA CCACTCCACGCA	taatacactactatagggTCCTG GCCAGCCGTGT			
	Rab5	CG3664	taatacactactatagggGCTCT CCTGGTACTCGTGGGA	taatacactactatagggCATCC ACACTCAGCAGCAAT			
2	TSG101	CG9712	taatacactactatagggTCCCTA TTTGTATTTGGTTGATGG A	taatacactactatagggATATG GGGCTGCGATTTGT	protein binding, small conjugating protein ligase activity	TSG101 tumor susceptibility gene 101	Homologue
	TSG101	CG9712	taatacactactatagggATCCC TCAAATCCCAGTTCC	taatacactactatagggAAAGT GGCGCTGTGGTG			
3	Rab11	CG5771	taatacactactatagggGCAAA ACAATTAAGCGCAA	taatacactactatagggATGTT CTGGAATGCCGTTTC	GTP binding. GTPase activity,	RAB11A RAB11A, member RAS oncogene family	Homologue
4	Rab7	CG5915	taatacactactatagggGGACA CTGCTGGTCAGGAAC	taatacactactatagggACTTG AAACGCCATCTCCAC	GTP binding. GTPase activity	RAB7A RAB7A, member RAS oncogene family	Homologue
5	Hrs	CG2903	taatacactactatagggTCCCA AGAATGCCTTTGC	taatacactactatagggCTGGT ACTTGTCCGAGGAGC	protein binding, zinc ion binding	HGS hepatocyte growth factor-regulated tyrosine kinase substrate	Homologue
	Hrs	CG2903	taatacactactatagggCAGCA GATCATGCCCTG	taatacactactatagggGGCGC AGCTGCATCTC			
6	Chc	CG9012	taatacactactatagggTTGCC ACCAAGTATCACGAA	taatacactactatagggCCAGT TCGTGCGTTGAGAAT	protein binding, structural molecule activity	CLTC clathrin, heavy chain (Hc)	Homologue
	Chc	CG9012	taatacactactatagggCCGGA ACGGGTGAAGAAC	taatacactactatagggCACAA TCCACGCTCGTAG			
7	Clc	CG6948	taatacactactatagggATCCT CCACTGGCAGTTTGT	taatacactactatagggTCAAT GTGGTTAGGCGAGTG	protein binding, structural molecule activity	CLTA clathrin, light chain (Lca)	Homologue
	Clc	CG6948	taatacactactatagggAGTCA GCTCTCGGGGAC	taatacactactatagggTTTCCC GCCTTGTTCACC			
8	α -adaptin	CG4260	taatacactactatagggCCATG GCTATCGGTGAAACT	taatacactactatagggGGCCG TCTCCAGATAGTTGA	protein binding, protein transporter activity	AP2A2 adaptor-related protein complex 2, alpha 2 subunit	Homologue
	α -adaptin	CG4260	taatacactactatagggGTGGA CGTTATCCTCAATCTA	taatacactactatagggAAAAT TGAGCTCTCGCGTT			
9	α -adaptin / CG31654	CG31654	taatacactactatagggCCTTTT CATCTCAGTGTGGTG	taatacactactatagggTGTTA CGATCCGGGATAAGC	protein binding, protein transporter activity	AP2A2 adaptor-related protein complex 2, alpha 2 subunit	Homologue
10	α -adaptin	CG31654	taatacactactatagggGCCCT GCGCAACATCAA	taatacactactatagggGAATC CTTCAAGGAAGCTGT	protein binding, protein transporter activity	AP1B1 adaptor-related protein complex 1, beta 1 subunit	Homologue
	Bap	CG12532	taatacactactatagggCCAGA CATTCTCAAGCACGA	TaatacactactatagggTTCAA GGAAGCTGTCAAGCA			
11	AP47	CG9388	taatacactactatagggGCTAC GCCATCAAGTGCTATC	taatacactactatagggACCGG GAAGAAGTCTGGAG	protein binding	AP1M1 adaptor-related protein complex 1, mu 1 subunit	Homologue
12	orange	CG3029	taatacactactatagggGATTG GCGGATCGGATTAC	taatacactactatagggGCGTG GAATATCAGGTCCAG	protein binding, protein transporter activity	APS2 AP-3 complex subunit sigma-1	Best Blast

13	<i>Eps15</i>	<i>CG1693</i> 2	taatacgaactactatagggTCCGA TCAATGGTCACACAG	TaatacgaactactatagggGGAGT AATGGCGTTGCTCTT	<i>calcium ion binding</i>	<i>EPS15</i> <i>L1</i>	<i>epidermal growth factor receptor pathway substrate 15-like 1</i>	<i>Homologone</i>
14	<i>lqf</i>	<i>CG8532</i>	taatacgaactactatagggCCTAC AATGTGGTGGCCTTT	taatacgaactactatagggCAGTT GAAGTTCCTCCTCGC		<i>EPN1</i>	<i>epsin 1</i>	<i>Homologone</i>
	<i>lqf</i>	<i>CG8532</i>	TGCCATCATGAGCGAGA TAGtaatacgaactactataggg	taatacgaactactatagggGCTGC AGTTGAAGTTCCTCC				
15	<i>corn</i>	<i>CG3238</i> 6	taatacgaactactatagggGCTGA GCGAATCTGTTGTCA	taatacgaactactatagggAGTGT GTCCGTTTTTGAGG	<i>microtubule binding, protein binding</i>	?	?	
16	<i>shibire</i>	<i>CG1810</i> 2	taatacgaactactatagggATCGA AGATGAAACGGATCG	taatacgaactactatagggATGCC TGGTGATATCCTTG	<i>GTP binding, GTPase activity, actin binding, metarhodopsin binding, protein binding</i>	<i>DNM1</i>	<i>dynamain 1</i>	<i>Best Blast</i>
17	<i>Arr2</i>	<i>CG5962</i>	taatacgaactactatagggCCTGG ATGGTCACTTGAAGG	taatacgaactactatagggCGGTT GGAGTAGCTTGAAGG		<i>ARRB</i> 2	<i>arrestin, beta 2 isoform 2</i>	<i>Best Blast</i>
18	<i>kurtz</i>	<i>CG1487</i>	taatacgaactactatagggGTGAG CATGAGTGACGGAGA	taatacgaactactatagggAACTT TTACAGGTGTGGCCG		<i>ARRB</i> 1	<i>arrestin, beta 1</i>	<i>Best Blast</i>
	<i>kurtz</i>	<i>CG1487</i>	taatacgaactactatagggAAGTA TTTCGGCCACACCTG	taatacgaactactatagggTAGGG TCGGACTCGCTTCTA				
19	<i>cenB1A</i>	<i>CG6742</i>	taatacgaactactatagggTGCGT GACCTATTACCACCA	taatacgaactactatagggTTGTC GCTGAGGTAGAACCA	<i>ARF GTPase activator activity, protein binding, zinc ion binding</i>	<i>CENT</i> B2	<i>centaurin, beta 2</i>	<i>Homologone</i>
20	<i>Dor</i>	<i>CG3093</i>	taatacgaactactatagggTCTCT GGCTCCGGCTATAAA	taatacgaactactatagggTCTGC CTTAAGCGTCTCCTG		<i>VPS18</i>	<i>vacuolar protein sorting 18 homolog (S. cerevisiae)</i>	<i>Homologone</i>
	<i>Dor</i>	<i>CG3093</i>	taatacgaactactatagggGTGTT TAACCTCAGGGTGAC	taatacgaactactatagggGCGTG CTCGGCTATCA				
21	<i>CG3393</i> 6	<i>CG3393</i> 6	taatacgaactactatagggGGGCA AGGGCAAGTACATAG	taatacgaactactatagggTTGAT CAGCTGACTCTGCGT		<i>ZFAN</i> D6	<i>zinc finger, AN1-type domain 6</i>	<i>Homologone</i>
22	<i>CG6637</i>	<i>CG6637</i>	taatacgaactactatagggGGGCA AGGGCAAGTACATAG	taatacgaactactatagggTTGAT CAGCTGACTCTGCGT		<i>SNF8</i>	<i>SNF8, ESCRT-II complex subunit homologue (S. cerevisiae)</i>	<i>Homologone</i>
23	<i>CG9779</i>	<i>CG9779</i>	taatacgaactactatagggGCAGG AGTGGACGCATAAGA	taatacgaactactatagggTCTGA ATGGAGTTGAGGTGC		<i>VPS24</i>	<i>vacuolar protein sorting 24 homolog (S. cerevisiae)</i>	<i>Homologone</i>
	<i>CG9779</i>	<i>CG9779</i>	taatacgaactactatagggGGCAA CCAGCTGGATCG	taatacgaactactatagggCGCAG CAGACGCAGAC				
24	<i>Uba1</i>	<i>CG1782</i>	taatacgaactactatagggCCTTCT GTACCAGCTCTGCG	taatacgaactactatagggCTCTG ATCGACGACAAACCC	<i>binding, ubiquitin activating enzyme activity, ubiquitin-protein ligase activity</i>	<i>UBE1</i>	<i>ubiquitin-activating enzyme E1</i>	<i>Homologone</i>
	<i>Uba1</i>	<i>CG1782</i>	taatacgaactactatagggTAAGG CCTGCAGTGGAAAGTTT ACA	taatacgaactactatagggGATCC ATATATATGCGAGCATC CAC				
25	<i>Uba2</i>	<i>CG9086</i>	taatacgaactactatagggCTTGA AGAAGGTGAGGCTGG	taatacgaactactatagggGAAGA CGTTCTCCGAGTTGG	<i>protein binding, ubiquitin-protein ligase activity, zinc ion binding</i>	<i>UBR2</i>	<i>ubiquitin protein ligase E3 component n-recogin 2</i>	<i>Homologone</i>
	<i>Uba2</i>	<i>CG9086</i>	taatacgaactactatagggATAGG TTCAACACGATCCCC	taatacgaactactatagggGAAGG CTGGTGTAGTTTGG				
26	<i>Uba2</i>	<i>CG7528</i>	taatacgaactactatagggCAGAC AATGCAGTGAATCGG	taatacgaactactatagggACTGA TTATGGCGTCAACTCTT	<i>SUMO activating enzyme activity, protein binding</i>	<i>SAE2</i>	<i>SUMO1 activating enzyme subunit 2</i>	<i>Homologone</i>
	<i>Uba2</i>	<i>CG7528</i>	taatacgaactactatagggAACAT TATTCTGCTATTGCCAC CA	taatacgaactactatagggGCTAC GACTTCGAACAAGTTTTC AT				
27	<i>CG1435</i> 4	<i>CG1435</i> 4	taatacgaactactatagggAATGT CAATGTGCGTGTGG	taatacgaactactatagggCGTAG GATCTTCGGTCCCTT	<i>SUMO activating enzyme activity,</i>	<i>GRIPA</i> P1	<i>GRIP1 associated protein 1 coatomer protein complex, subunit beta 2 (beta prime)</i>	<i>Best Blast</i>
28	<i>b'Cop</i>	<i>CG6699</i>	taatacgaactactatagggAGACC ATTGCTCACAAATCCC	taatacgaactactatagggAGCAG ACCAGACTGCCACTT	<i>protein binding, structural molecule activity,</i>	<i>COPB</i> 2		<i>Homologone</i>
	<i>b'Cop</i>	<i>CG6699</i>	taatacgaactactatagggTTTCG GAGTGCCTCAAAC	taatacgaactactatagggCTCTTT AACCAGAGACATGTTG				
29	<i>Amph</i>	<i>CG8604</i>	taatacgaactactatagggTAAGG AAGGTGGCAAACAGC	taatacgaactactatagggGTCGT CATCTCAAACGGAT	<i>protein binding,</i>	<i>BIN1</i>	<i>bridging integrator 1</i>	<i>Homologone</i>
30	<i>AnnX</i>	<i>CG9579</i>	taatacgaactactatagggCGTGG	taatacgaactactatagggAGTTG	<i>actin binding,</i>	<i>ANXA</i>	<i>annexin A6</i>	<i>Homologone</i>

			CCAATACTTACGTCC	AGTGCGTCCAGTCAC	calcium ion binding, phospholipid binding	6		ne
31	<i>Arr1</i>	<i>CG5711</i>	taatacgaactactatagggGAGCTCGAACTGGAGGTCAC	taatacgaactactatagggAGAGCTGTGTCTTTGCGCCTT	metarhodopsin binding,	<i>ARRB2</i>	<i>arrestin, beta 2 isoform 2</i>	<i>Best Blast</i>
32	<i>CG2774</i>	<i>CG2774</i>	taatacgaactactatagggCATCCATGATCTGCTTGTTGG	taatacgaactactatagggACCTCGGTGATCTTGTGCTC	phosphoinositide binding, protein binding	<i>SNX2</i>	<i>sorting nexin 2</i>	<i>Homologone</i>
		<i>CG2774</i>	taatacgaactactatagggTCCAA	taatacgaactactatagggGTAGCTCTATCTTCTCCTCC				
33	<i>opa1-like</i>	<i>CG8479</i>	taatacgaactactatagggGTCAGGTACTGCCAGTGGGT	taatacgaactactatagggTGCCAGGAATTCATATCG	GTP binding, GTPase activity	<i>OPAI</i>	<i>optic atrophy 1 (autosomal dominant)</i>	<i>Homologone</i>
		<i>CG8479</i>	taatacgaactactatagggGAGAA	taatacgaactactatagggTTATTC				
34	<i>CG9139</i>	<i>CG9139</i>	GATGGAGAAGGAGAAAC taatacgaactactatagggTACCC AACAGCGTGGTCAT	CTGGCAAATCGACTA taatacgaactactatagggTTGTG GTTCTGCGTCATCA	DNA binding, guanyl-nucleotide	<i>RABGEF1</i>	<i>RAB guanine nucleotide exchange factor (GEF) 1</i>	<i>Homologone</i>
35	<i>CG9318</i>	<i>CG9318</i>	taatacgaactactatagggGCAAA CGATCGAGGTAAGGA	taatacgaactactatagggGCATG GTGGCAATGATAATG		<i>TM9SF2</i>	<i>transmembrane 9 superfamily member 2</i>	<i>Best Blast</i>
36	<i>CG10971</i>	<i>CG10971</i>	taatacgaactactatagggATTTT GCAGTCTTCGGTTG	taatacgaactactatagggGGTCA GCGTAACGAGGATTT		<i>HIP1</i>	<i>huntingtin interacting protein 1</i>	<i>Homologone</i>
37	<i>CG2774</i>	<i>CG2774</i>	taatacgaactactatagggGGAAC TTTGAGGCGGAAGAC	taatacgaactactatagggCATTT AGATCAGCGGCACCT	phosphoinositide binding, protein binding	<i>SNX2</i>	<i>sorting nexin 2</i>	<i>Homologone</i>
		<i>CG31048</i>	taatacgaactactatagggGCAAG TACCAGGAGGCTTTCTCTC T	taatacgaactactatagggTTCTG CGAGCGAGGACGATTGT GTA				
38	<i>CG31064</i>	<i>CG31064</i>	taatacgaactactatagggATGCG GCTCCAGAAGAC	taatacgaactactatagggTTTCG GTACATCTCCAGGTT	zinc ion binding	<i>RUFY2</i>	<i>RUN and FYVE domain containing 2</i>	<i>Homologone</i>
		<i>CG31064</i>	taatacgaactactatagggTTGAG CGCAGTAATCTGGTG	taatacgaactactatagggCGCTC ATCATCAGAGCATGT				
39	<i>epsin-like</i>	<i>CG31170</i>	taatacgaactactatagggGCAGC GGCACTATATGTTGA	taatacgaactactatagggCATTC TTTTATCAGCCCGGA	molecular function	<i>CLINT1</i>	<i>clathrin interactor 1</i>	<i>Homologone</i>
40	<i>Rab9Fb</i>	<i>CG32670</i>	taatacgaactactatagggTATTG CTGTCTTTGGCCCTC	taatacgaactactatagggGAGAT ACGGCGCATGTCTTC	GTP binding, GTPase activity	<i>RAB26</i>	<i>RAB26, member RAS oncogene family</i>	<i>Best Blast</i>
41	<i>Rab9D</i>	<i>CG32678</i>	taatacgaactactatagggGAGCC AATACGACAATCCGT	taatacgaactactatagggACGAT GGGCATAGTTGAACC	ATP binding, GTP binding, GTPase activity	<i>RAB26</i>	<i>RAB26, member RAS oncogene family</i>	<i>Best Blast</i>
42	<i>aCop</i>	<i>CG7961</i>	taatacgaactactatagggGGACG AGTCTGGAGTGTTT	taatacgaactactatagggAGGAA GCTAAGCTTGTCAAA	protein binding, structural molecule activity	<i>COPA</i>	<i>coatamer protein complex, subunit alpha</i>	<i>Homologone</i>
43	<i>opa1-like</i>	<i>CG8479</i>	taatacgaactactatagggTCTTTT TGCTTTTCGACACA	taatacgaactactatagggAGCAA GATAGACCAAGCCACA		<i>OPAI</i>	<i>optic atrophy 1 (autosomal dominant)</i>	<i>Homologone</i>
44	<i>faf</i>	<i>CG1945</i>	taatacgaactactatagggGCCAA CTAAAGGTTTCTGCG	taatacgaactactatagggCAGAG ACCACGTGGAACGTA	ubiquitin thiolesterase activity, ubiquitin-specific protease activity	<i>USP9X</i>	<i>ubiquitin specific peptidase 9, X-linked</i>	<i>Homologone</i>
		<i>CG1945</i>	taatacgaactactatagggAACTT AAGTCAGCGATGGATG GGT	taatacgaactactatagggGATGC GGATCAAGTTGCAGGAT GTT				
45	<i>gig</i>	<i>CG6975</i>	taatacgaactactatagggCAACA CGCTCCTCAAGATCA	taatacgaactactatagggCAGAA ATTCCAGAACCGGAG	GTPase activator activity, kinase binding	<i>TSC2</i>	<i>tuberous sclerosis 2</i>	<i>Homologone</i>
		<i>CG6975</i>	taatacgaactactatagggTACAG CACCAAGGATATGCGTG TGA	taatacgaactactatagggGTTCA TGCACAGCTTGGTGTG ATG				
46	<i>hk</i>	<i>CG10653</i>	taatacgaactactatagggAATTG TCCGCATTTACAGCTC	taatacgaactactatagggTTAAG ATATGCGAGGCCAG	microtubule binding	<i>HOOK3</i>	<i>golgi-associated microtubule-binding protein HOOK3</i>	<i>Best Blast</i>
47	<i>Mer</i>	<i>CG14228</i>	taatacgaactactatagggACACC AGGTGCAACAGATCC	taatacgaactactatagggCACTA GATGGCACAGGAGCA	cytoskeletal protein binding, protein binding	<i>NF2</i>	<i>neurofibromin 2 (bilateral acoustic neuroma)</i>	<i>Homologone</i>
48	<i>Drp1</i>	<i>CG3210</i>	taatacgaactactatagggAGCTT GAGTGCCCTACTGGT	taatacgaactactatagggTTCCCT GCACACCAAGAAAGTG	GTP binding, GTPase activity	<i>DNM1L</i>	<i>dynamain 1-like</i>	<i>Homologone</i>
49	<i>Past1</i>	<i>CG6148</i>	taatacgaactactatagggACGTT	taatacgaactactatagggGTCTG	GTP binding,	<i>SRL</i>	<i>sarcalumenin</i>	<i>Best Blast</i>

			GATTGGTCCGCTATC	GATCCTCGAGCTTTG	<i>GTPase activity, calcium ion binding</i>			
50	<i>Pi3K59 F</i>	<i>CG5373</i>	taatacgaactactatagggGGCAC CTCCATCTCAATGTT	taatacgaactactatagggACATG TCATCCACCACGATG	<i>1-phosphatidylinositol-3-kinase activity,</i>	<i>PIK3C 3</i>	<i>phosphoinositide-3-kinase, class 3</i>	<i>Homologous</i>
51	<i>Pi3K68 D</i>	<i>CG1162 1</i>	taatacgaactactatagggCTCTC CTGATCCCTCGTCTG	taatacgaactactatagggAAGCC CTCCACAGACTTTCA	<i>1-phosphatidylinositol-3-kinase activity,</i>	<i>PIK3C 2A</i>	<i>phosphoinositide-3-kinase, class 2, alpha polypeptide</i>	<i>Homologous</i>
52	<i>Rab-RP3</i>	<i>CG7062</i>	taatacgaactactatagggCTTAT CAGCGGGGTGTTTGT	taatacgaactactatagggTTTAA GTTCTGTGGCCAGG	<i>GTP binding, GTPase activity</i>	<i>RAB43</i>	<i>RAB43, member RAS oncogene family</i>	<i>Homologous</i>
53	<i>RabX2</i>	<i>CG2885</i>	taatacgaactactatagggTAAGG TTCTGTCCTGGGTG	taatacgaactactatagggTCCTC CTCTTCTGCTCAGA	<i>ATP binding, GTP binding, GTPase activity</i>	<i>RAB12</i>	<i>RAB12, member RAS oncogene family</i>	<i>Best Blast</i>
	<i>RabX2</i>	<i>CG2885</i>	taatacgaactactatagggCTTCG ACTATCTGTTTAAGGTTCTC	taatacgaactactatagggGTTGT GAAGTACATAACGATGGTAT				
54	<i>RabX4</i>	<i>CG3111 8</i>	taatacgaactactatagggGACAG GAAGGCATCTTCGAT	taatacgaactactatagggAAGCT GCAAATCTGGGACAC	<i>GTP binding, GTPase activity</i>	<i>RAB26</i>	<i>RAB26, member RAS oncogene family</i>	<i>Best Blast</i>
	<i>RabX4</i>	<i>CG3111 8</i>	taatacgaactactatagggccagAT TGCCGAAAACCTTC	taatacgaactactatagggAGCCC AGTCCCTTAACTGGT				
55	<i>Rab1</i>	<i>CG3320</i>	taatacgaactactatagggTTCCG GATTCACAGATGACA	taatacgaactactatagggATTTTC CAACACTGCCGCTA	<i>GTP binding, GTPase activity,</i>	<i>RAB1 A</i>	<i>RAB1A, member RAS oncogene family</i>	<i>Homologous</i>
	<i>Rab1</i>	<i>CG3320</i>	taatacgaactactatagggGTTAT ATCAGCACAATCGGAGT GGA	taatacgaactactatagggTCAGC AGCAACCGGATTTGGTG TTT				
56	<i>Rab3</i>	<i>CG7576</i>	taatacgaactactatagggTGACG TTGACGTTCTCCTTG	taatacgaactactatagggGGACA GGAGCGGTACAGAAC	<i>GTP binding, GTPase activity</i>	<i>RAB12</i>	<i>RAB12, member RAS oncogene family</i>	<i>Best Blast</i>
57	<i>Rab4</i>	<i>CG4921</i>	taatacgaactactatagggACACC ATCGGAGTGGAGTTC	taatacgaactactatagggAAGGT GCTTGCTTCCAGAAA	<i>GTP binding, GTPase activity</i>	<i>RAB4 B</i>	<i>RAB4B, member RAS oncogene family</i>	<i>Homologous</i>
58	<i>Rab8</i>	<i>CG8287</i>	taatacgaactactatagggCTTCG ATTTTCGCTATCGCT	taatacgaactactatagggCATGG TGGCAACGACTACAC	<i>ATP binding, GTP binding, GTPase activity</i>	<i>RAB8 A</i>	<i>RAB8A, member RAS oncogene family</i>	<i>Homologous</i>
59	<i>Rab10</i>	<i>CG1706 0</i>	taatacgaactactatagggTGAAC ATGGCATTGCGTTTA	taatacgaactactatagggATCCA TCGTTGCGAGTTTTG	<i>ATP binding, GTP binding, GTPase activity</i>	<i>RAB10</i>	<i>RAB10, member RAS oncogene family</i>	<i>Homologous</i>
60	<i>Rab26</i>	<i>CG7605</i>	taatacgaactactatagggACTGC TGCTGTACGACGTGA	taatacgaactactatagggTGAAG GACAGCTCCACATTG	<i>ATP binding, GTP binding, GTPase activity,</i>	<i>RAB37</i>	<i>RAB37, member RAS oncogene family</i>	<i>Homologous</i>
61	<i>Rab27</i>	<i>CG1479 1</i>	taatacgaactactatagggGGATG ATTAGCCGCTTGAAC	taatacgaactactatagggACAAC CATTGCTTGGGAGAG	<i>ATP binding, GTP binding, GTPase activity</i>	<i>RAB27 A</i>	<i>RAB27A, member RAS oncogene family</i>	<i>Homologous</i>
62	<i>Rab30</i>	<i>CG9100</i>	taatacgaactactatagggTACTG CCATCCTTGCTCCTT	taatacgaactactatagggACACC CAGCGACTCAAAAAC	<i>GTP binding, GTPase activity</i>	<i>RAB30</i>	<i>RAB30, member RAS oncogene family</i>	<i>Homologous</i>
	<i>Rab30</i>	<i>CG9100</i>	taatacgaactactatagggTCAGC CGCCTTGACTAGAGTTG GA	taatacgaactactatagggTCAGC CGCCTTGACTAGAGTTG GA				
63	<i>Rab35</i>	<i>CG9575</i>	taatacgaactactatagggTGTTG GTTGTTTGGTGGTGT	taatacgaactactatagggGGAAG GTGGTCATTACCGAA	<i>ATP binding, GTP binding, GTPase activity,</i>	<i>RAB35</i>	<i>RAB35, member RAS oncogene family</i>	<i>Homologous</i>
64	<i>Rab40</i>	<i>CG1900</i>	taatacgaactactatagggGATCG ATACCGTCGAAGCTC	taatacgaactactatagggACATG GGAACCATGACCAAG	<i>GTP binding, GTPase activity, Protein ubiquitination</i>	<i>RAB40 C</i>	<i>RAB40C, member RAS oncogene family</i>	<i>Homologous</i>
65	<i>Scamp</i>	<i>CG9195</i>	taatacgaactactatagggTGTGT GGTGTGGTCCATTTCT	taatacgaactactatagggGCCCT TGCTCTCTTGGAGAT	<i>phosphatidylethanolamine binding,</i>	<i>SCAMP1</i>	<i>secretory carrier membrane protein 1</i>	<i>Homologous</i>
66	<i>Spri</i>	<i>CG3317 5</i>	taatacgaactactatagggCAACA ACAACGGCCAACC	taatacgaactactatagggGTGGC AACCGCTGGACT	<i>Ras GTPase binding</i>	<i>RIN2</i>	<i>Ras and Rab interactor 2</i>	<i>Homologous</i>
78	<i>Ubp64E</i>	<i>CG5486</i>	taatacgaactactatagggAAGAG GCTCAGCTGCGTAAG	taatacgaactactatagggATACG CAAGGCAGTTTGGAC	<i>ubiquitin thiolesterase activity,</i>	<i>USP47</i>	<i>ubiquitin specific peptidase 47</i>	<i>Homologous</i>