

Supplemental Materials

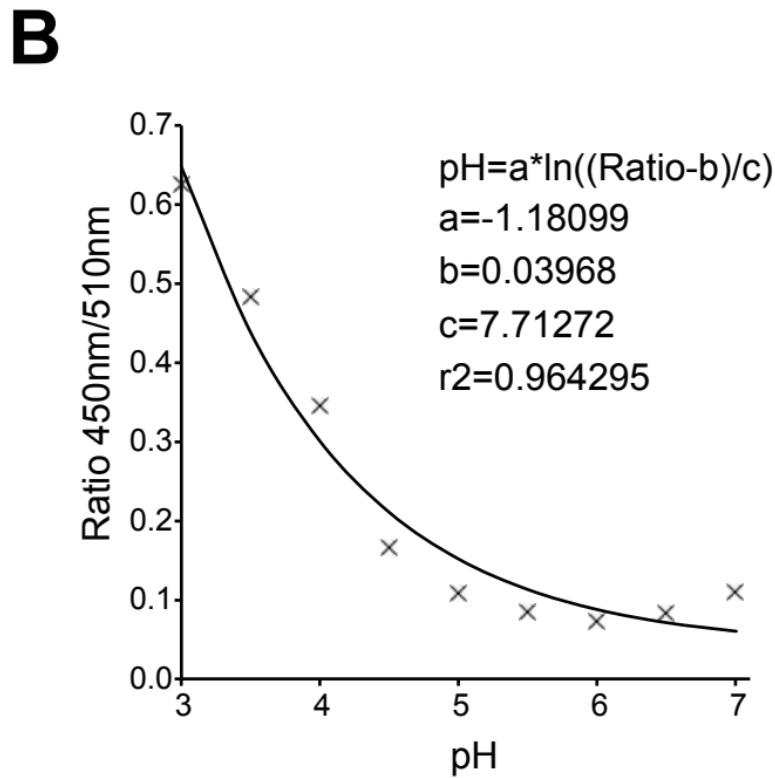
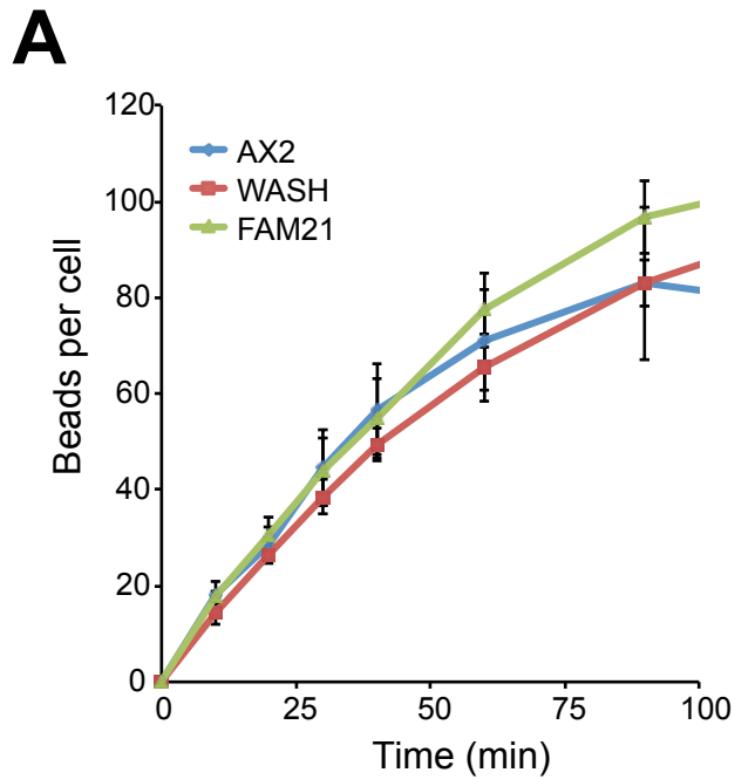
Molecular Biology of the Cell

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Supplementary Figure 1. (A) Normal phagocytosis of beads in WASH complex mutants. (B) Calibration curve of lysosensor blue/green fluorescence at different pH's. The ratio of emission at 450nm/510nm at each pH is plotted. A best fit curve was then fitted using the least squares method, and the equation, and R^2 value are indicated on the graph.

Supplementary table 1. Full list of proteins reduced by at least 30% in both *WASH* and *FAM21* mutants. Proteins are grouped by subcellular compartment. *P<0.05, **P<0.005, ***P<0.001 (T-test).

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Accession no.	UniProt	Description	Compartment	WASH/ax2	Sig.	Fam21/ax2	Sig
DDB_G0293376	Q54BW4	Circularly permuted Ras protein 2 (DdiCPRas2)	Transmembrane	0.47	***	0.33	***
DDB_G0289157	Q9U641	Conditioned medium factor receptor 1	Transmembrane	0.56	***	0.52	***
DDB_G0269160	P24639_ISOFORM_Short	Annexin A7 [ISOFORM Short]	Transmembrane, Endosomal	0.64	***	0.42	***
DDB_G0267430	Q8T674	ABC transporter G family member 20	Transmembrane, Endosomal	0.66	***	0.64	**
DDB_G0287297	Q7YXD4_CHAIN_0	Protein P80 [CHAIN 0]	Transmembrane, Endosomal	0.70	***	0.50	***
DDB_G0295683	B0G198	LIM-type zinc finger-containing protein;	Cytoskeleton	0.30	***	0.18	***
DDB_G0267382	P27133	Coronin	Cytoskeleton	0.47	***	0.56	***
DDB_G0274575	Q9XXV8	Myosin-K heavy chain	Cytoskeleton	0.61	*	0.44	*
DDB_G0289553	P07830_CHAIN_0	Major actin [CHAIN 0]	Cytoskeleton	0.62	***	0.73	***
DDB_G0267374	P13021	F-actin-capping protein subunit beta	Cytoskeleton	0.64	***	0.56	**
DDB_G0275759	Q86H36	DNA-directed RNA polymerase I subunit rpa1 (RNA polymerase I subunit A1)	Nucleus	0.41	***	0.36	***
DDB_G0288455	Q54IS9	Nucleoporin 210;	Nucleus	0.43	**	0.34	*
DDB_G0290331	Q54G78	FACT complex subunit SSRP1	Nucleus	0.51	***	0.49	***
DDB_G0291636	Q54EH2	DNA-directed RNA polymerases I, II, and III subunit rpabc1 (RNA polymerases I, II, and III subunit rpabc1)	Nucleus	0.53	*	0.58	*
DDB_G0282677	Q54S43	FACT complex subunit SPT16	Nucleus	0.54	***	0.60	***
DDB_G0286509	Q54LP8	Histone H2B.v3	Nucleus	0.63	***	0.50	***
DDB_G0283539	Q23858_CHAIN_0	Calreticulin [CHAIN 0]	ER	0.55	***	0.33	***
DDB_G0283497	Q54R45_CHAIN_0	Translocon-associated protein subunit alpha (TRAP-alpha) (SSR-alpha) [CHAIN 0]	ER	0.58	*	0.56	*
DDB_G0276141	Q86IA3_CHAIN_0	Protein disulfide-isomerase 1 (PDI1) [CHAIN 0]	ER	0.61	***	0.69	***
DDB_G0280057	Q9NKX1_CHAIN_0	Endoplasmic reticulum homolog [CHAIN 0]	ER	0.61	*	0.46	**
DDB_G0275025	Q86Z90_CHAIN_0	Putative protein disulfide-isomerase DDB_G0275025 [CHAIN 0]	ER	0.62	*	0.55	*
DDB_G0291434	Q54EN4_CHAIN_0	Protein disulfide-isomerase 2 (PDI2) [CHAIN 0]	ER	0.64	***	0.46	**
DDB_G0276445	Q8T869_CHAIN_0	Luminal-binding protein 2 (BiP 2) [CHAIN 0]	ER	0.66	***	0.59	***
DDB_G0274181	Q86KC1_CHAIN_0	Lysozyme	Lysosomal	0.65	***	0.47	***
DDB_G0283401	Q54R55	Cathepsin Z;	Lysosomal	0.44	***	0.37	**
DDB_G0282539	P13723_CHAIN_0	Beta-hexosaminidase subunit A1 [CHAIN 0]	Lysosomal	0.60	*	0.45	**
DDB_G0291191	Q54F16	Cysteine protease;	Lysosomal	0.57	***	0.45	**
DDB_G0281823	Q23857	Vegetative stage specific V4-7;	Lysosomal	0.39	**	0.36	*
DDB_G0279059	Q54XB6	Mannose-6-phosphate receptor domain-containing protein;	Lysosomal	0.62	***	0.62	**
DDB_G0292206	P34098	Alpha-mannosidase 58 kDa subunit	Lysosomal	0.72	***	0.52	***
DDB_G0267406	Q9XYS8	Lysosomal membrane protein 2-A	Lysosomal	0.76	**	0.40	***
DDB_G0281663	Q5XM24_CHAIN_0	Autocrine proliferation repressor protein A [CHAIN 0]	Secreted	0.56	***	0.39	***
DDB_G0270834	Q55C09_CHAIN_0	Sphingomyelin phosphodiesterase A (aSMase A) [CHAIN 0]	Secreted	0.64	*	0.66	**
DDB_G0279717	Q54WD8	Carboxylesterase, type B family protein;	Secreted	0.57	***	0.38	***
DDB_G0281153	Q54UD0	Eukaryotic translation initiation factor 3 subunit H (eIF3h)	Ribosomal	0.34	**	0.27	**
DDB_G0279109	Q54X97	Eukaryotic translation initiation factor 3 subunit C (eIF3c)	Ribosomal	0.36	**	0.45	*
DDB_G0293560	Q54BM1	DNA-directed RNA polymerase I subunit rpa2 (RNA polymerase I subunit 2)	Ribosomal	0.46	*	0.49	*
DDB_G0285683	Q54MT0	Eukaryotic translation initiation factor 3 subunit I (eIF3i)	Ribosomal	0.47	***	0.41	**
DDB_G0287005	Q54KZ8	Eukaryotic translation initiation factor 3 subunit M (eIF3m)	Ribosomal	0.49	***	0.39	***
DDB_G0274627	Q55U49	Eukaryotic translation initiation factor 3 subunit D (eIF3d)	Ribosomal	0.51	***	0.61	***
DDB_G0283597	Q54QW1	Eukaryotic translation initiation factor 3 subunit B (eIF3b)	Ribosomal	0.53	***	0.41	***
DDB_G0278815	Q54XP6	Eukaryotic translation initiation factor 5B (eIF-5B)	Ribosomal	0.54	***	0.28	***
DDB_G0293052	Q54CC5	Eukaryotic translation initiation factor 3 subunit E (eIF3e)	Ribosomal	0.63	***	0.59	**
DDB_G0291788	Q54E42	Putative uncharacterized protein adprt3;	Cytoplasmic	0.57	***	0.63	***
DDB_G0283419	Q54R41_CHAIN_0	Guanine nucleotide-binding protein alpha-9 subunit (G alpha-9) [CHAIN 0]	Cytoplasmic	0.59	**	0.52	*
DDB_G0274775	Q86IV4	PH domain-containing protein DDB_G0274775	Cytoplasmic	0.61	**	0.37	***
DDB_G0293730	Q54BH5	PI-PLC X-box domain-containing protein DDB_G0293730	Cytoplasmic	0.64	***	0.28	***
DDB_G0271750	Q55AR6	Neurofibromin-A (DdNF1)	Cytoplasmic	0.66	***	0.65	***
DDB_G0269926	Q55CS2	RNA-binding region RNP-1 domain-containing protein;	Cytoplasmic	0.69	***	0.71	**
DDB_G0269016	Q55EK2	Probable cytochrome P450 524A1	Cytoplasmic	0.67	**	0.55	*
DDB_G0275227	Q55J43	FK506-binding protein 1 (PP1ase) (Rotamase)	Cytoplasmic	0.61	***	0.80	*
DDB_G0285357	Q54NB6	FK506-binding protein 4 (PP1ase) (Rotamase)	Cytoplasmic	0.42	***	0.67	***
DDB_G0293008	Q7YXU4	Copine-A	Cytoplasmic and endosome membrane	0.60	***	0.32	***
DDB_G0272875	Q86K21	Copine-B	Cytoplasmic and endosome membrane	0.51	*	0.23	***
DDB_G0284693	Q54P95	Probable cytochrome c oxidase subunit 6B	Mitochondrial	0.47	***	0.43	**
DDB_G0277213	Q86K89	Putative uncharacterized protein;	Mitochondrial	0.52	***	0.48	***
DDB_G0271848	Q01501	Mitochondrial outer membrane protein porin (VDAC)	Mitochondrial	0.52	***	0.41	***
DDB_G0293874	Q54B67	Mitochondrial substrate carrier family protein Z	Mitochondrial	0.52	**	0.47	***
DDB_G0288247	Q9GRX6_CHAIN_0	Apoptosis-inducing factor 1, mitochondrial [CHAIN 0]	Mitochondrial	0.53	***	0.46	**
DDB_G0294092	O21049	Cytochrome c oxidase subunit 3	Mitochondrial	0.55	**	0.52	***
DDB_G0292306	Q54DF1_CHAIN_0	ATP synthase subunit gamma, mitochondrial [CHAIN 0]	Mitochondrial	0.55	*	0.50	*
DDB_G0290997	Q54F93	Mitochondrial-processing peptidase subunit alpha	Mitochondrial	0.56	***	0.50	***
DDB_G0292250	Q54DK1	Sulfide:quione oxidoreductase, mitochondrial	Mitochondrial	0.56	***	0.35	***
DDB_G0278095	Q54YT4_CHAIN_0	Trans-2-enoyl-CoA reductase, mitochondrial [CHAIN 0]	Mitochondrial	0.56	**	0.62	*
DDB_G0288777	Q4W6B5	Beta subunit of mitochondrial processing peptidase;	Mitochondrial	0.57	***	0.46	***
DDB_G0293646	Q54BF6	Mitochondrial substrate carrier family protein N	Mitochondrial	0.57	***	0.46	***
DDB_G0294012	Q9XPJ9	ATP synthase subunit alpha, mitochondrial	Mitochondrial	0.59	***	0.50	***
DDB_G0283283	Q54RA8	ATP synthase subunit O, mitochondrial (OSCP)	Mitochondrial	0.61	***	0.60	***
DDB_G0267454	O97470	Mitochondrial substrate carrier family protein ancA (ANT)	Mitochondrial	0.61	***	0.51	***
DDB_G0269916	Q55CS9_CHAIN_0	ATP synthase subunit beta, mitochondrial [CHAIN 0]	Mitochondrial	0.62	***	0.58	***
DDB_G0280535	Q9U3X4_CHAIN_0	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (FP)	Mitochondrial	0.63	**	0.54	***
DDB_G0271774	Q1ZP3	Probable cytochrome b-c1 complex subunit 6	Mitochondrial	0.63	**	0.47	**
DDB_G0285399	Q54NC1	NADH-cytochrome b5 reductase 1	Mitochondrial	0.64	**	0.47	**
DDB_G0290333	Q54G77	Putative uncharacterized protein;	Unknown	0.37	**	0.22	**
DDB_G0291464	Q54EL0	Putative uncharacterized protein;	Unknown	0.39	*	0.45	**
DDB_G0286079	Q54MA4	Putative uncharacterized protein;	Unknown	0.47	*	0.51	*
DDB_G0285359	Q54NB5	Putative uncharacterized protein;	Unknown	0.48	***	0.26	***
DDB_G0285079	Q54NS5	Putative uncharacterized protein;	Unknown	0.53	**	0.63	*
DDB_G0268496	Q55GH1	Putative uncharacterized protein;	Unknown	0.54	*	0.53	*
DDB_G0268646	B0G0Y7	Putative uncharacterized protein;	Unknown	0.56	***	0.79	*
DDB_G0286131	Q54M91	Putative uncharacterized protein;	Unknown	0.56	*	0.54	*
DDB_G0289345	Q54HN1	Putative uncharacterized protein;	Unknown	0.58	*	0.70	*
DDB_G0287257	Q54KM5	Putative uncharacterized protein;	Unknown	0.66	***	0.69	**
DDB_G0289715	Q54H42	Putative uncharacterized protein;	Unknown	0.67	*	0.48	*
DDB_G0269976	Q55CN9	Putative uncharacterized protein;	Unknown	0.68	**	0.47	**