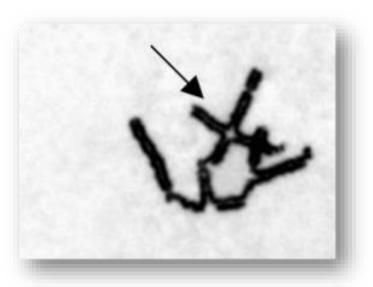
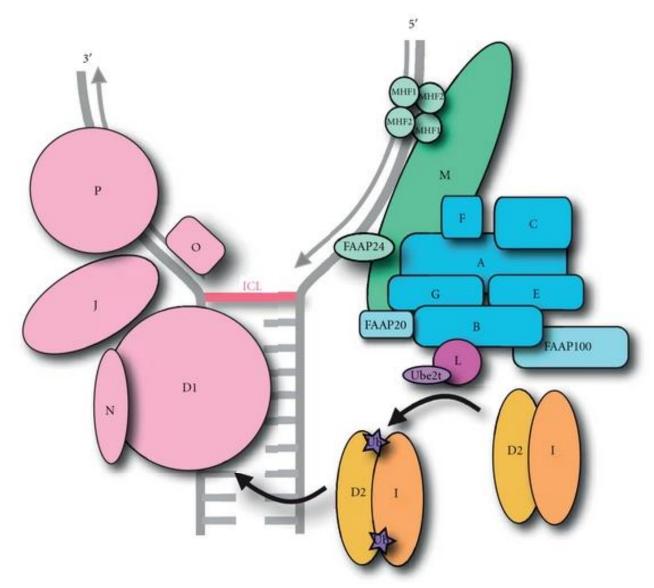


What is Fanconi Anemia?

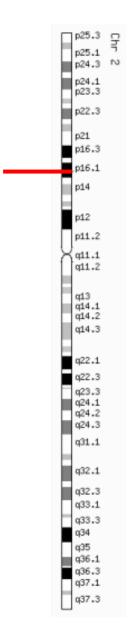


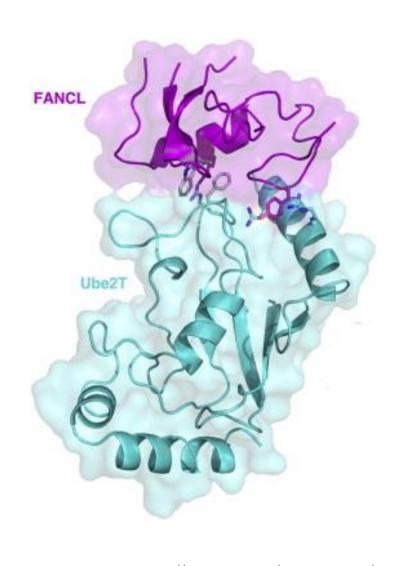


What is the Fanconi Anemia pathway?

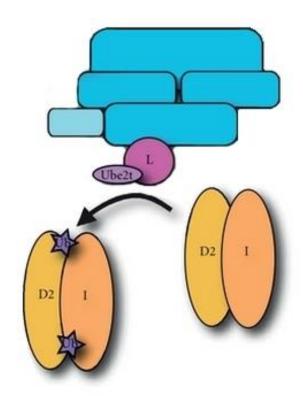


What is Fanconi Anemia Complementation Group L?





What role does FANCL play?



Cellular Components

Fanconi Anemia nuclear complex

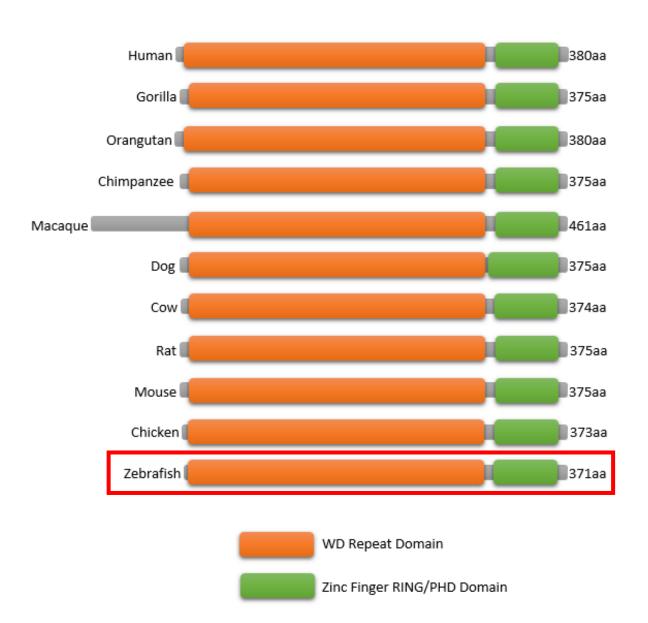
Molecular Function

Ubiquitin-protein transferase activity

Biological Processes

Protein ubiquitination DNA Repair

How well conserved is FANCL?

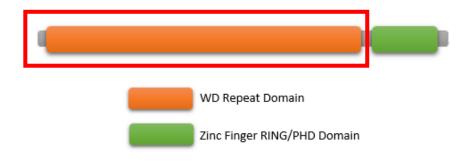


Knowledge Gap: Why do FANCL-caused FA patients have such varying phenotypes?



Understand how different mutations affect phenotype and ID complex ubiquitination.

Hypothesis



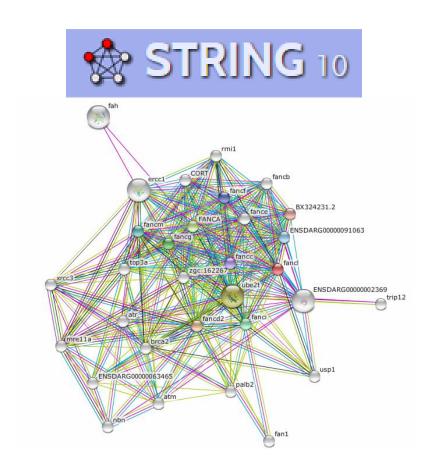
Mutations occurring in the WD40 domain will have a greater effect on phenotype than mutations to the RING finger domain.

Aim II Aim III

Identify binding partners of FANCL that have a role in skin pigmentation

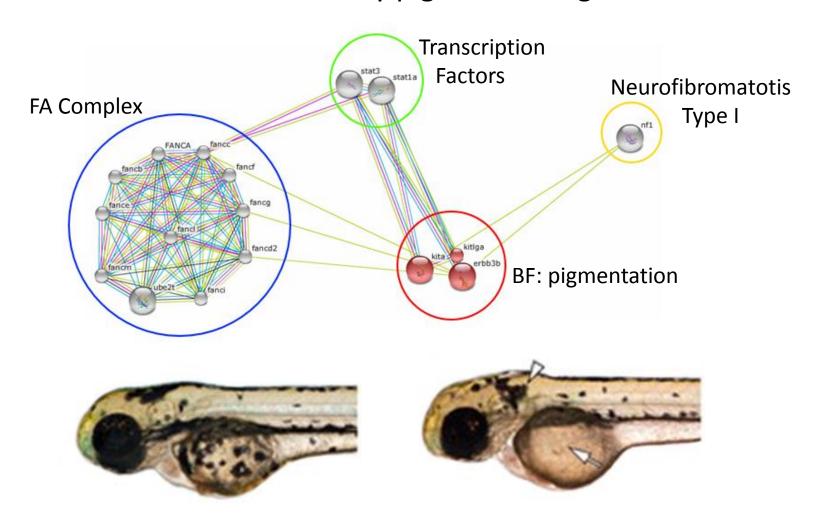
Aim I: Approach

Find binding partners in STRING related to skin pigmentation



Utilize the CRISPER/Cas9 system to mutate these genes to confirm

Aim I: Results kita identified as key pigmentation gene



Mills et al., 2007 - Deconstructing evolution of adult phenotypes: genetic analyses of kit reveal homology and evolutionary novelty during adult pigment pattern development of Danio fishes. Development 134(6):1081-1090

Aim II Aim III

Determine which domain plays a more prominent role in pigmentation

Aim II: Approach

Identify conserved regions in the WD40 and RING domains.

WD-Repeat <u>Domain</u>

	200	210	, 220	230	240	250	260
Zebrafish/1-371	YYSQLITEME	TLG <mark>WD</mark> KLLF	IDAEFRTLQL	KAEDSAGRQHA	ITVKLKSKYP	AEAPEFSADLF	PIPLVITWT
Chicken/1-373	YYSCLIRDLE	TEG <mark>WN</mark> KVAY	VDTGLTTVKLK	KAEDSRGRQHL	LTEKENAKYP	TEPPDCVVDFF	PVQFAISWM
Brown_Rat/1-375	FCKDLLTEIG	A I G <mark>WD</mark> KLAC	VDTSFTTIKL	KADDASGRKHL	LTVKLKAKYP	VEPPDCLVDFF	PIPFSVSWT
House_Mouse/1-375	FCKDLLTEIG	A I G <mark>WD</mark> KLAC	VESSFSTIKL	KADDASGRKHL	LTVKLKAKYP	VEPPDCVVDFF	PVPFSVSWT
Cattle/1-374	FYSSLIGEIR	TLG <mark>WD</mark> KLVF	VDPCFSTIKL	(A-DVSGREHL	LIVKLKAKYP	AESPDCVVDFF	PVPFSVSWT
Dog/1-375	FYSSLMEEIG	TLG <mark>WD</mark> KLVY	VDTCLSTIKLK	KAEDASGRKHL	LTLKLKTKYP	TESPDCVVDFF	PVSFSVSWT
Macaque/1-461	FYSSLIEEIG	TLG <mark>WD</mark> RLVY	VDTCFSTIKL	KAEDASGREHL	LTLKLKAKYP	AESPDCFVDFF	PVPFSASWT
Orangutan/1-380	FYSSLIEEIG	TLG <mark>wd</mark> klvy.	ADTCFSTIKL	KAEDASGREHL	LTEKEKAKYP	AESPDYFVDFF	PVPFCASWT
Chimpanzee/1-375	FYSSLIEEIG	TLG <mark>wd</mark> klvy.	ADTCFSTIKL	KAEDASGREHL	LTEKEKAKYP	AESPDYFVDFF	PVPFCASRT
Human/1-380	FYSSLIEEIG	TLG <mark>wd</mark> klvy.	ADTCFSTIKL	KAEDASGREHL	LTLKLKAKYP	AESPDYFVDFF	PVPFCASWT
Gorilla/1-375	FYSSLIEEIG	TLG <mark>wd</mark> klvy.	ADTCFSTIKL	KAEDASGREHL	LTEKEKAKYP	AESPDYFVDFF	PVPFCASWT

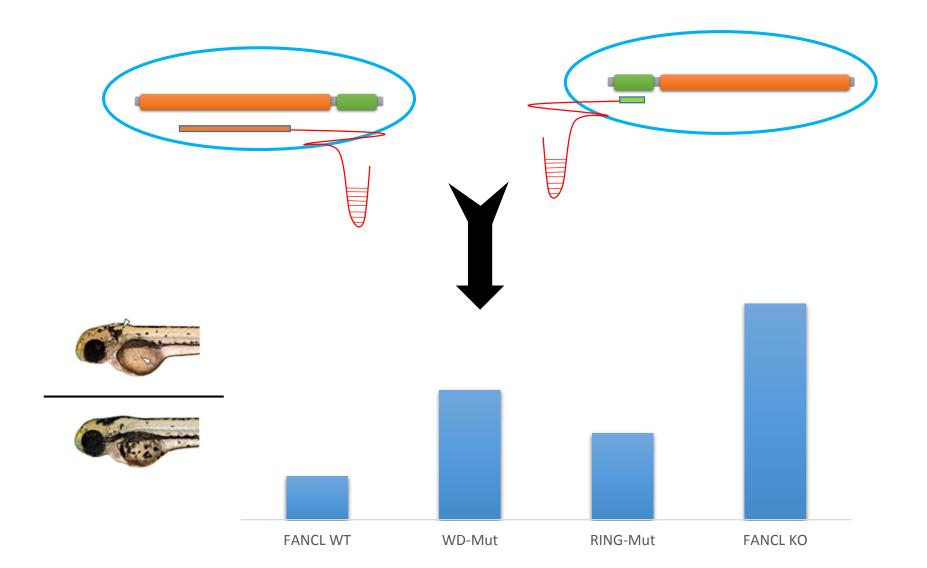
RING Domain

	400	0 410	420	430	440	450	460
Zebrafish/1-371	FSVECG <mark>I</mark> (C <mark>y</mark> syrlesaipd	QVCNDPRCGQPF	HQVCLYE <mark>W</mark> LR	GLPTSRQSFNI	VFGECPYCSKP	TVKMV
Chicken/1-373	F T K D C G <mark>I</mark> (C <mark>y</mark> ayrlngttpd	QVCNEPRCGQPF	HQACLYE <mark>w</mark> lQ:	GLPSSRQSFNV	/IFGECPYCNKPI	TVKSS
Brown_Rat/1-375	FSMDCG <mark>I</mark> (C <mark>y</mark> arhlngaipd	QVCNNPQCGQLF	HQMCLYE <mark>w</mark> lr:	GLSSSRQSFNV	FFGECPYCSKP	ITLKMS
House_Mouse/1-375	FSMDCG <mark>I</mark> (C <mark>y</mark> arhlngaipd	QVCNNPQCGQPF	HEICLYE <mark>w</mark> lr:	GLSTSRQSFNV	FFGDCPYCSKP	ITLKMS
Cattle/1-374	FSMDCG <mark>I</mark> (C <mark>y</mark> ayqldgaipd	QVCDNSQCGQSF	HYTCLYE <mark>w</mark> lr:	GLLTSRQSFNI	IFGECPYCSKP	ITLKMS
Dog/1-375	FSMDCG <mark>I</mark> (C <mark>y</mark> ayqldgaipd	QVCDNLQCGQPF	HQICLYE <mark>w</mark> vr	GLLTSRQSFXI	IFGECPYCSKP	ITLKMS
Macaque/1-461	F T M D C G <mark>I</mark> (C <mark>y</mark> ayqldgaipd	QVCDNSQCEQPF	HQICLYE <mark>w</mark> lr:	GLLTSRQSFNI	IFGECPYCSKP	ITLKMS
Orangutan/1-380	F T M D C G <mark>I</mark> (C <mark>y</mark> ayqldgtipd	QVCDNSQCGQPF	HQICLYE <mark>w</mark> lr:	GLLTSRQSFNI	IFGECPYCSKP	ITLKMS
Chimpanzee/1-375	F T M D C G <mark>I</mark> (C <mark>y</mark> ayqldgtipd	QVCDNSQCGQPF	HQICLYE <mark>w</mark> lr:	GLLTSRQSFNI	IFGECPYCSKP	ITLKMS
Human/1-380	F T M D C G <mark>I</mark> (C <mark>y</mark> ayqldgtipd	QVCDNSQCGQPF	HQICLYE <mark>w</mark> lr:	GLLTSRQSFNI	IFGECPYCSKP	ITLKMS
Gorilla/1-375	F T M D C G I (C <mark>y</mark> ayqldgtipd	<u>QVCDNSQCGQPF</u>	HQICLYE <mark>w</mark> lr	<u>GLLTSRQSFNI</u>	IFGECPYCSKP	TLKMS

Utilize the CRISPER/Cas9 system to induce site specific mutations

Aim II: Expected Results

WD40-mutant transgenic lines will have more mutant Zebrafish

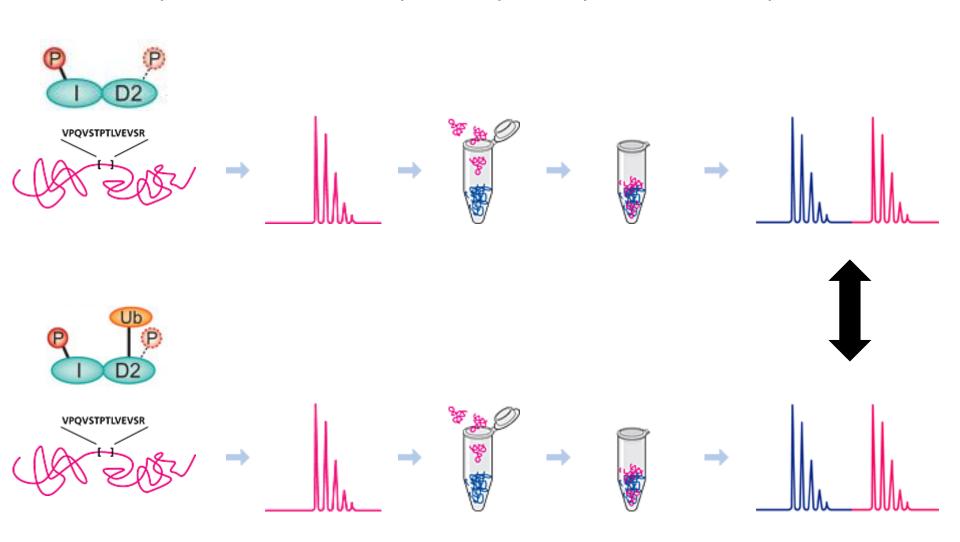


Aim I Aim III

Quantify the level of ubiquitination in each transgenic line

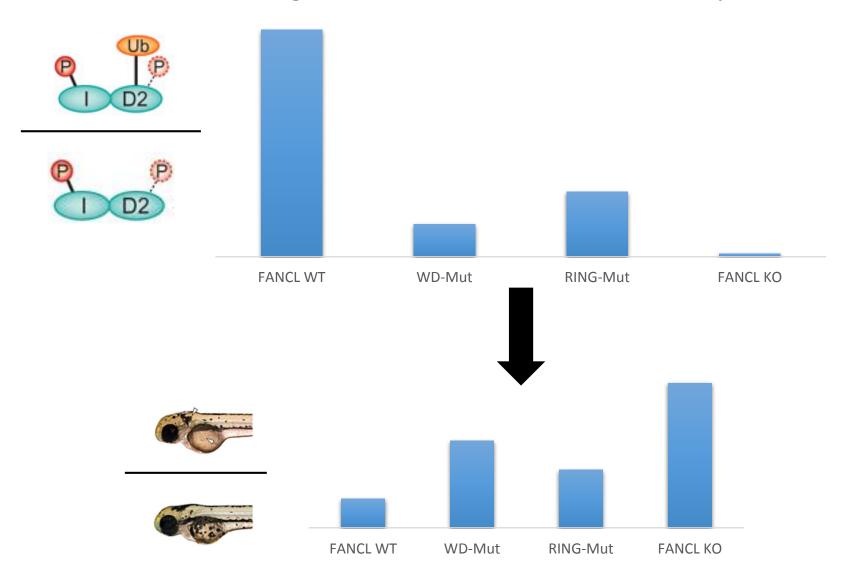
Aim III: Approach

Utilize quantitative mass spec to quantify levels of ubiquitination



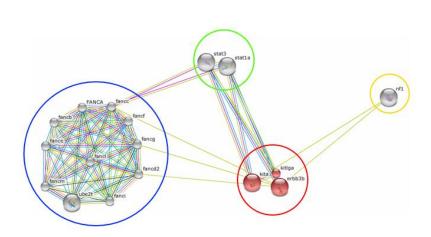
Aim III: Expected Results

WD40-mutant transgenic lines will have reduced ubiquitination



Future Directions

Relationship between FA, KIT, and pigmentation



Binding between core complex proteins

