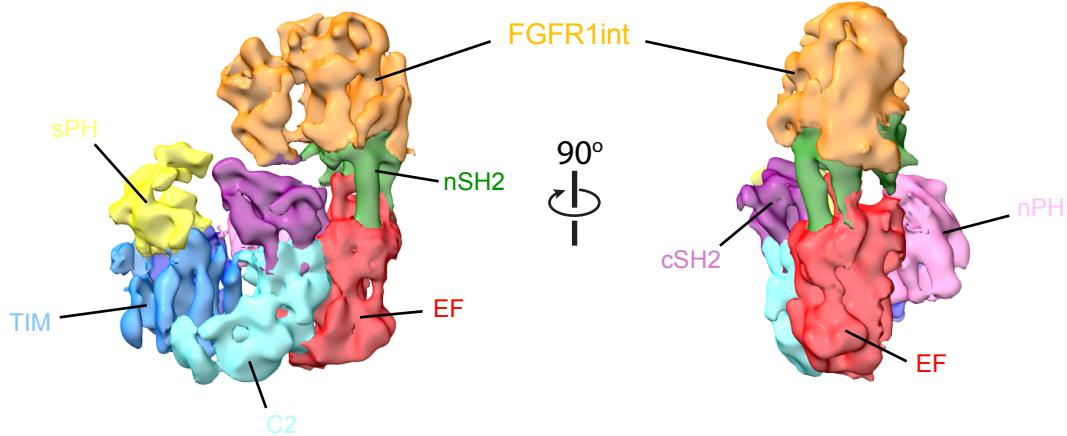
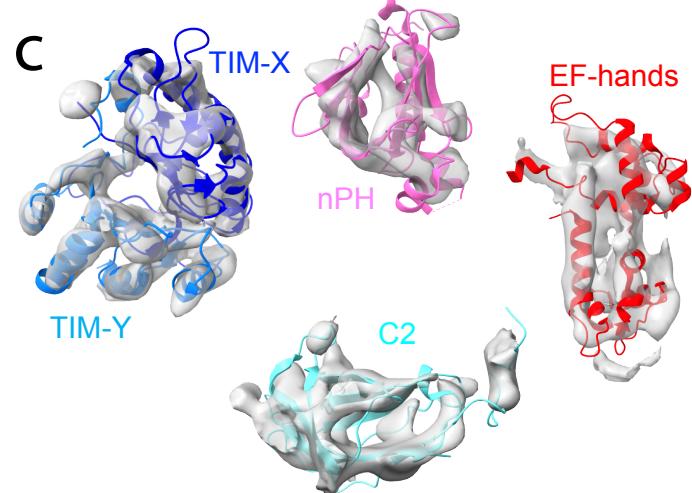
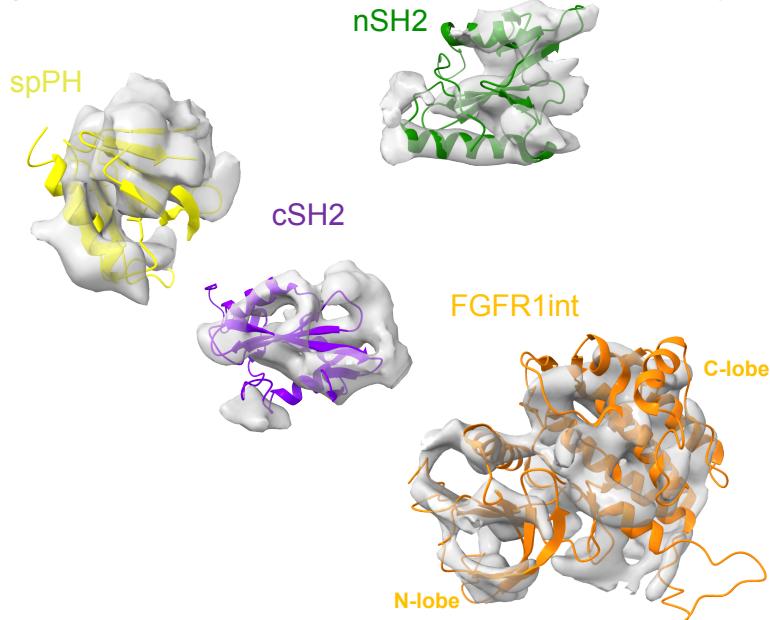
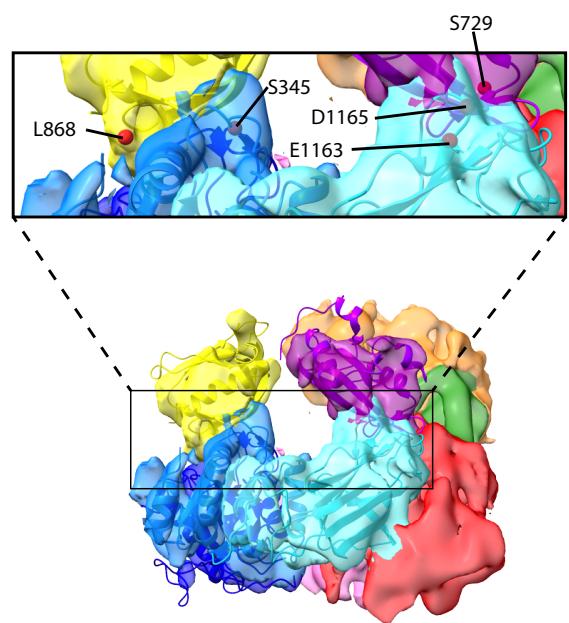
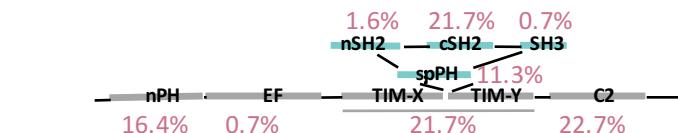


Figure S1

a**b**

Domain	σ level	CC value
nPH	0.025	0.8066
EF	0.025	0.7768
TIM-X	0.03	0.8329
sPH	0.02	0.8230
nSH2	0.025	0.8647
cSH2	0.02	0.8173
TIM-Y	0.03	0.8476
C2	0.025	0.8472
FGFR1int	0.02	0.8092

**d****e****Figure S2**

a

Total number of observations = 432

		nPH	
PLCG1	MAGAASPANCAGCGPGAPSDAEVLHLCRSLEVGTVMTLFYSSKKSQRP	60	
PLCG2	-----MSTTVNVDLAEYEKSQIKRAELGTVM	52	
PLCG1	TWSRGADKIEGAIDIKEIRPDKTSRDFDRYQEDPAFPRPDQSHCFVILYGMFRLKTL	120	
PLCG2	AWSKTADKIEGFLDIMEIKEIRPDKNSKDFERA---KAVRQKEDCCFTILYGTQFLSTL	109	
	EF		
PLCG1	SLOATSEDEVNMWIKGLTWLMEDTLQAPTPLQIERWLRKOFYSVDRRNREDRISAKDLKNM	180	
PLCG2	SLAADSKEDAVNWLSGLKLILHQEAMNASTPTIIESWLRKQIYSVQDQTRRRNSISLRELTKI	169	
PLCG1	LSQVNYRVNPVNMRFLRERLTDLEQRSGDITYGQFAQLYRSLMYSAQKTMMDLPFLEAS---T	237	
PLCG2	LPLINFKVSSAKFLKDKFVEIGAHKDELSFEQPHFLFYKKLMFEQOKSILDEFKKDSSVF	229	
PLCG1	LRAGERPELCRVSLPESQOFLLDYQGELWAVDRLQVQEFMLSFLRDPPLREIEEPYFFLDE	297	
PLCG2	LGNTDRPDASAVYLHDQFQRFILHEQQEHWAQDNLNVKVERMTKFIDDMRTEAEPFLVDE	289	
	TIM-X		
PLCG1	FVTFLFSKENSVWNSQLDAVCPTDMNNPLSHYWISSHNTYLTGQFSSSESSLEAYARCL	357	
PLCG2	FLTYLFSRENSIWDEKYDAVDMQDMNNPLSHYWISSHNTYLTGQFLRSSESSPEAYIRCL	349	
PLCG1	RMGCRCIELDCWDGPDPGMPVIIHGHTLTTKIKFSDVLHTIKEHAFVASEYPVILSIEDHC	417	
PLCG2	RMGCRCIELDCWDGPDPGKPVIIHGWTTRTTKIKFDDVVQAIKDHAFVTSSFPVILSIEEH	409	

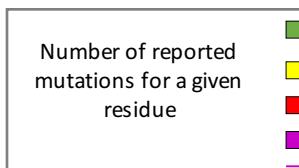
PLCG1	SIAQQRNMAQYFKVVLGDTLLTKPVEISADGLPSPNQLKRKILIKHKKLAEGSAVEEVP	477	
PLCG2	SVEQQRHMAKAFKEVFGDQLLTKPTEASADQLPSPSQLREKIIIKHKKLGPRGDV	466	
	spPH-p1		
PLCG1	SMMYSENDISNIKNGILYLEDPVNHEWYPHYFVLTSSKIIYSSEETSSDQGNEDEEKP	537	
PLCG2	---NMEDKQDEHKQOGLYMWDSIDQKWTRHCAIADAKLSFSDDIEQTM---EEVPQ	519	
	nSH2		
PLCG1	VSSSTELHSNEKWFGKGLAGRDRHIAERLLTEYCIETGAPDGSLVRESETFVGDTY	597	
PLCG2	DIPPTELHFGEKWFHKVKE----RTSAEKLLQEYCMETGGKDGTFLVRESETFPNDY	575	
PLCG1	SFWRNQKVQHCRISRQDAGTPKFFLTDLNLFDSLQYDLYTHQVQVPLRCNEFMRSLSEP	657	
PLCG2	SFWRSGRVQHCRIRSTMEGGTLKYYLTDNLTFSSYIALQHYRETHLRCAEFLRLTDV	635	
	cSH2		
PLCG1	PQTNAHESKENYHASLTRAQAEHMLMRVPRDGAFLVRKRNEPNSYAISSRAEGKIKHCRV	717	
PLCG2	PNPNPHESKPNYYDSLRSRGEAEDMLMRIPRDGAFLRKREGSDSYAITFRARGKVKHCR	695	

PLCG1	QQEGQTVMGLNSE-FDSLVLDISYYEKHPLYRKMKLRYPIINEALEKIGTAEPDYGALYE	776	
PLCG2	NRDGRHFVLTGSAYFESLVELVSYYEKHSLYRKMLRLRYPTPELLERYNME-RDINSLYD	754	
	SH3		
PLCG1	GRNPGFYVEANP--MPTFKCAVKALFDYKAQREDELTIFIKSAIIQVNVEQEGGNWRGDYG	834	
PLCG2	VS--RMYVDPSEINPSMPQRTVKALYDYKAKRSDELSCFCRGALIHNVSKEPGGNWKGDY	812	
	SPDH-p2		
PLCG1	GKKQLWPSNYVEEMNPVALEPEREHDENSPLGDLRQGVLDVPACQIAIRPEGKNNRL	894	
PLCG2	TRIQQYFSPSNYVEDISTAD-FEELEKQITIEDNPLGSLCRGILDLNNTYNVVKAPQGKQKS	871	

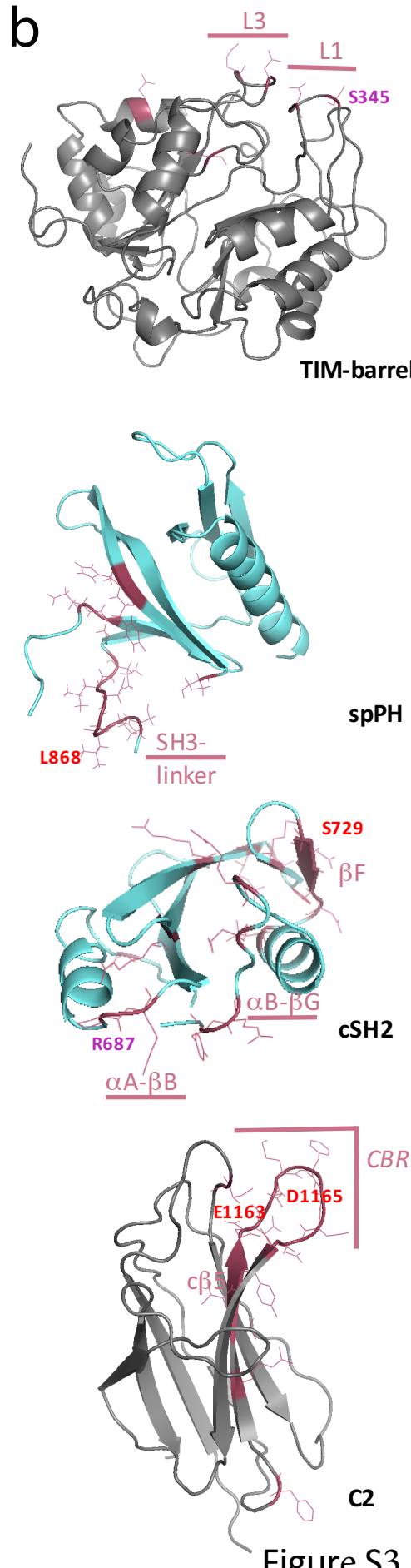
PLCG1	PFVFSISMASVAHSLDVAADSQEELQDWVKKIREVAQTADARLTGKIMERRKKIALELS	954	
PLCG2	PFVFILEPKQGDPPVFEATDRVEELFEWFQSIREITWKIDTKENNMKYWEKNQSIATELS	931	
	TIM-Y		
PLCG1	ELVVYCRPVPFDEEKIGTERACYRDMSSFPETKAEKYVNKAKGKKFLQYNRQLQSRIPK	1014	
PLCG2	DLVVYCKPTSKTKDN--LENPDFREIRSFTVETKADSIIR-QKPVDLLKYNQKGLTRVY	988	
	C2		
PLCG1	GORLSSNYDPLPMWICGSQIQLVALNFQTPDKPMQMNCQALFMTGRHCGYVLOPSTMREAF	1074	
PLCG2	GORVSSNYDFFRLWLCCSQMVALNFQTAGKYMQMNHALFSLNGRTGYVLOPESMRTEKY	1048	

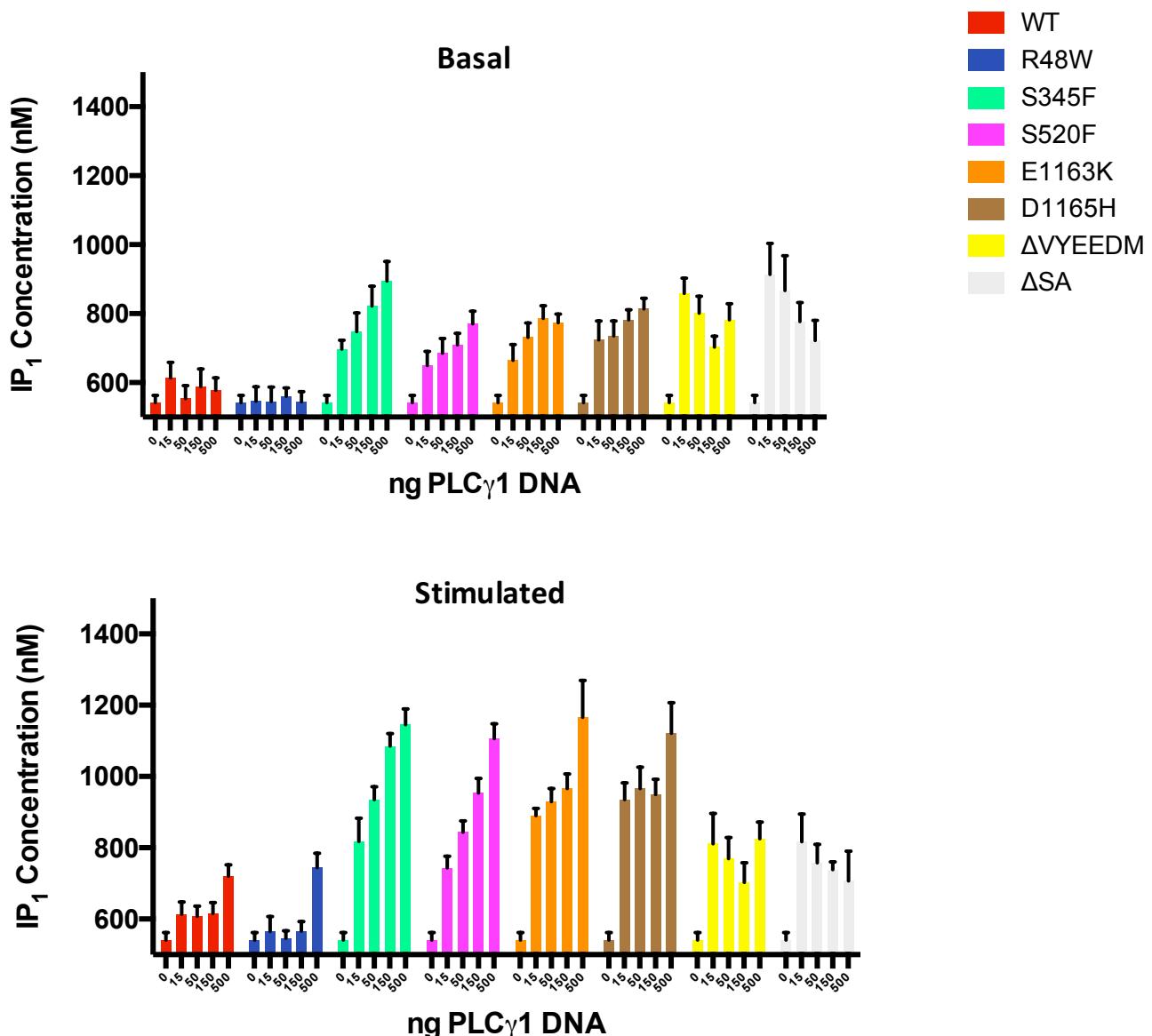
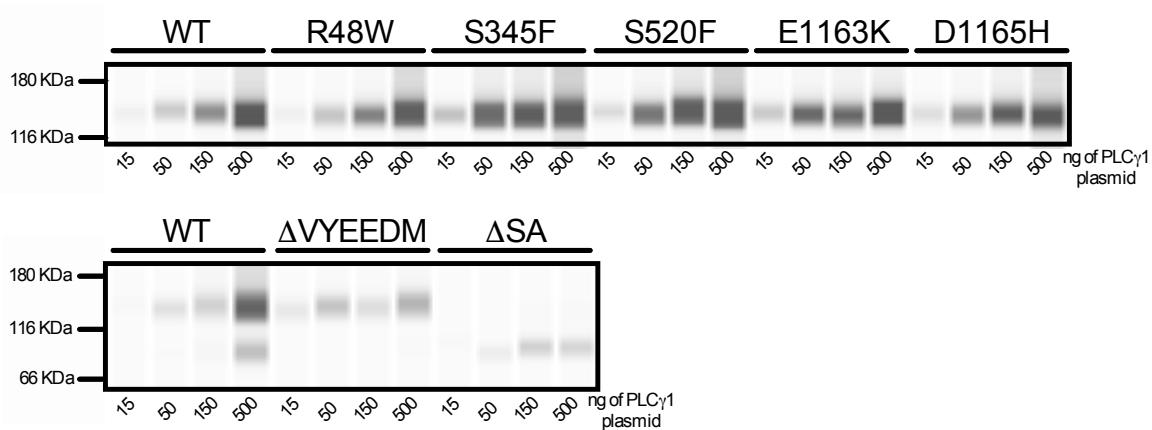
PLCG1	DPFDKSSLRGLLEPCAIISIEVLGARHLPKNGRGIVCPFVEIEVAGAEYDSTKQKTEFVVDN	1134	
PLCG2	DPMPPEQSQRKIL-MTLLTVKVLGARHLPKLGRIACPFVVEICGAEYDNNKFKTTVVDN	1107	
	C2		
PLCG1	GLNPVWPWPK--PFHFQISNPEFAFLRFVYEEEDMFSDQFLAQATFPVGLKTGYRAVPL	1192	
PLCG2	GLSPIWAPTQEKVTFIYDPNLAFLRFVYEEEDMFSDPNFLAHATYPIKAVKSGFRSVPL	1167	

PLCG1	KNNYSEDLELASLLIKIDIFPAKENGDLSPFGSTSRLRERGSDASGQLFHGRAREGSFESR	1252	
PLCG2	KNGYSEDIELASLLVFCMRPVLESEEELYSSCQLRRQEEELNNQFLYDTHQNLRNAN	1227	
	C2		
PLCG1	YQQPFFEDFRISQEHHLADHFDSRERRAPRTRVNGDNRL-	1290	
PLCG2	RDALVKEFVNENQQLQ-YQEKCNKRLREKRVSNNSKFYS	1265	



Rare variants



a**b****Figure S4**

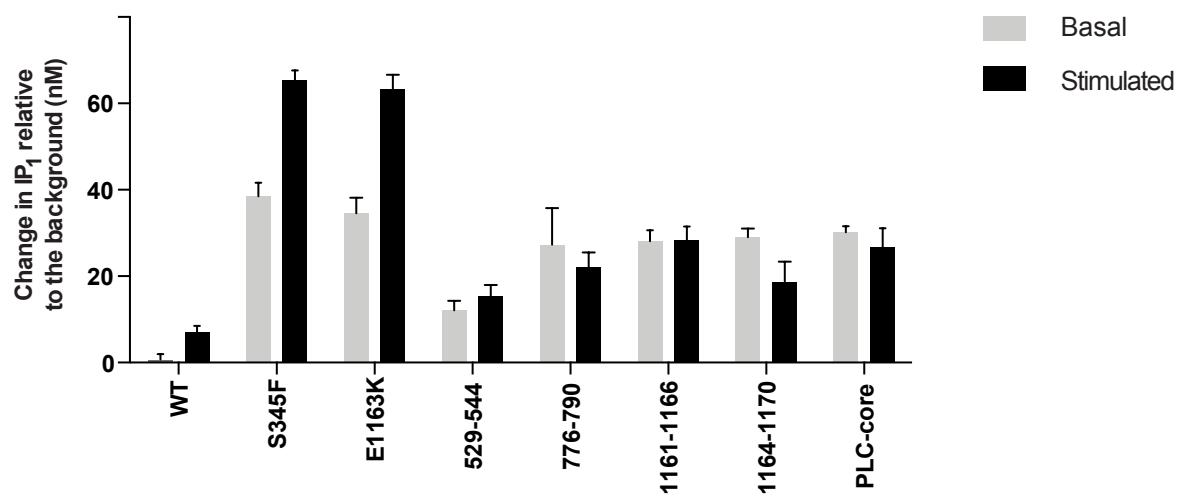
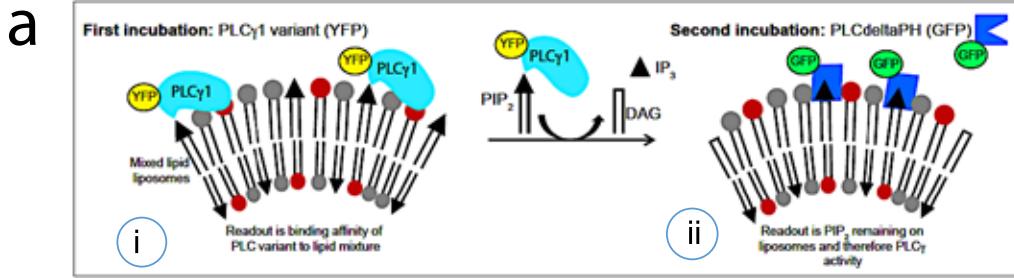


Figure S5



b

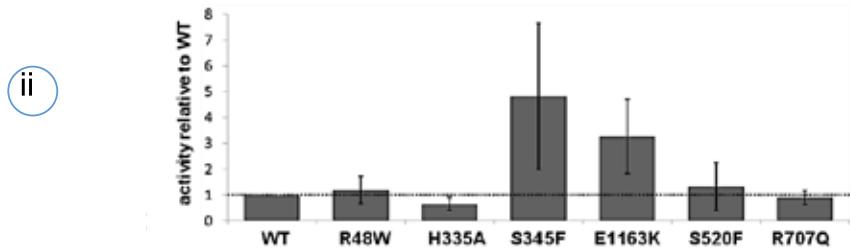


Figure S6

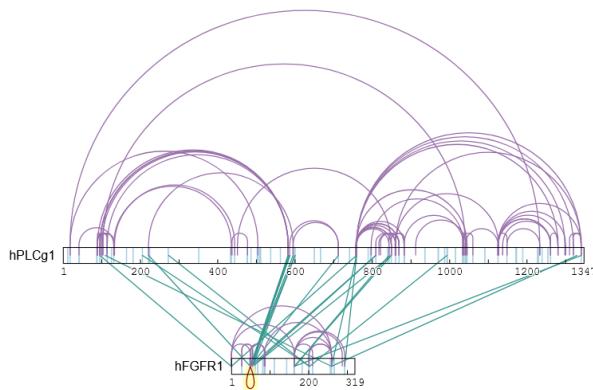
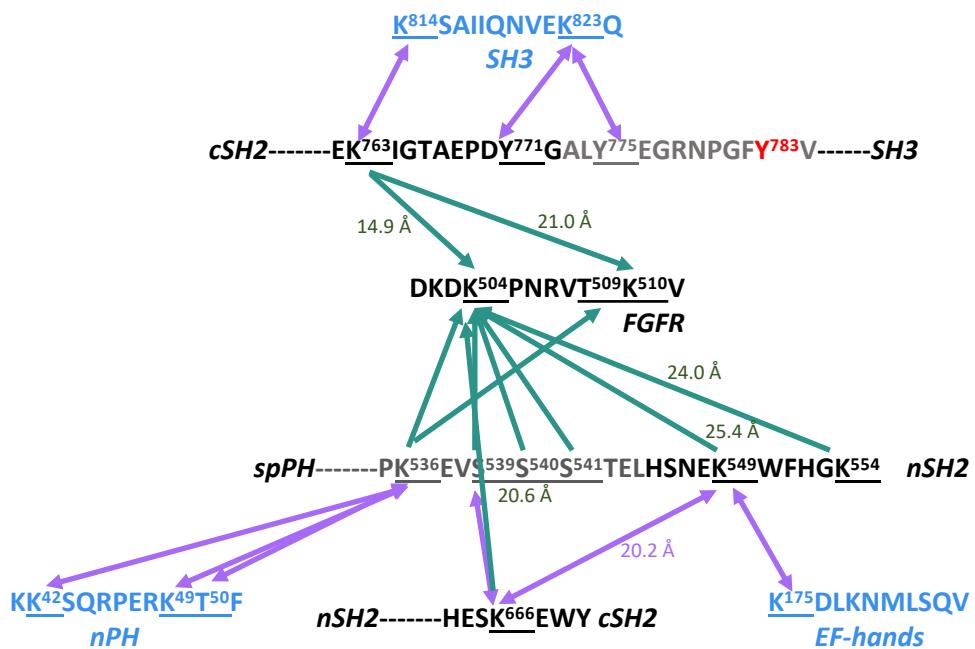
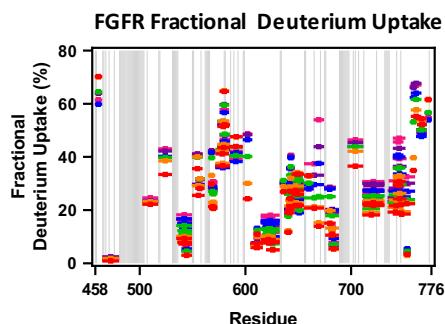
a**b**

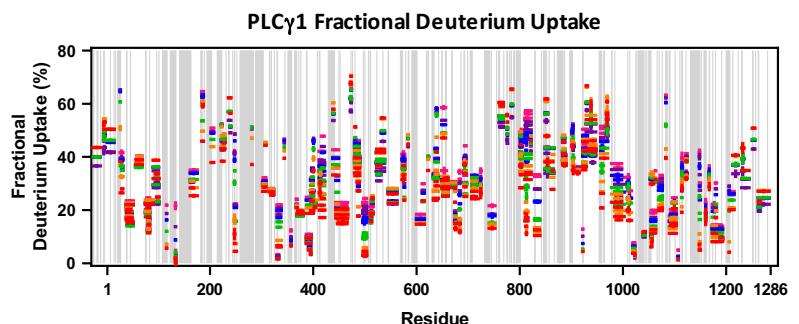
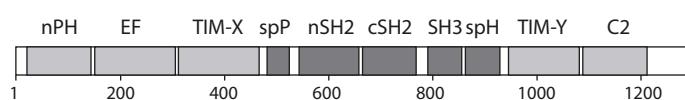
Figure S7

a

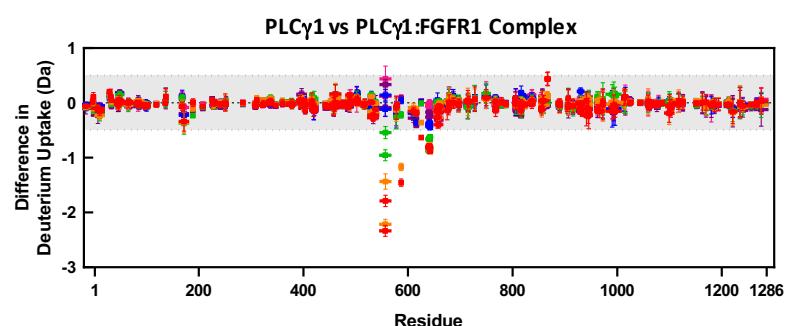
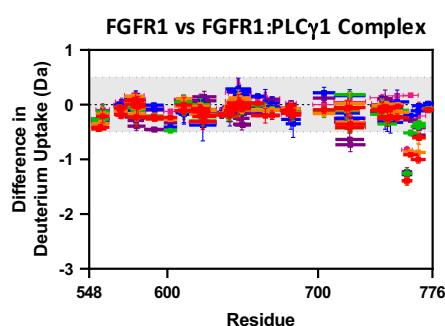
FGFR1int



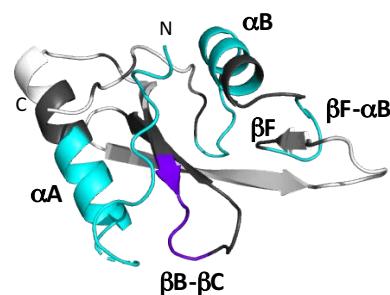
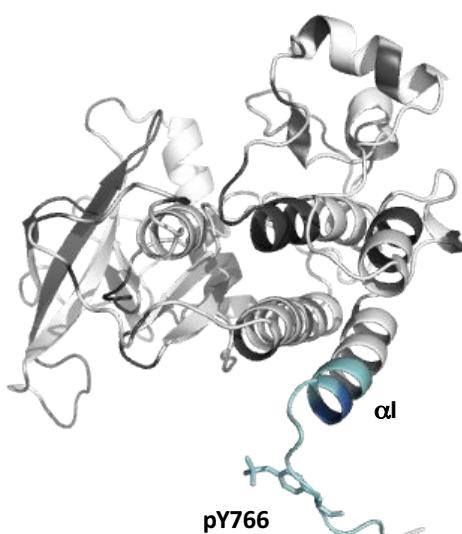
PLC γ 1



b



C



- Not covered
 - > -1.5
 - $-1.5 \text{ to } -2$
 - < -2

Figure S8