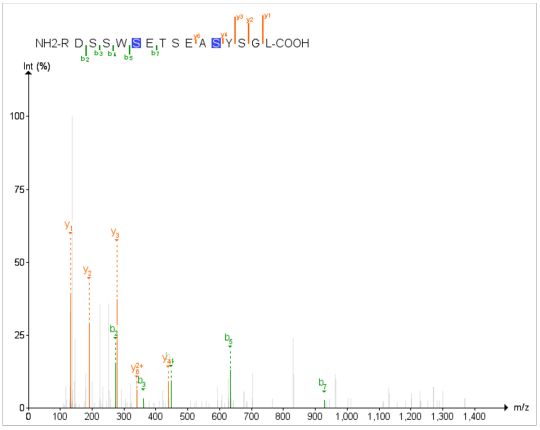
SUPPLEMENTAL FIGURE 1

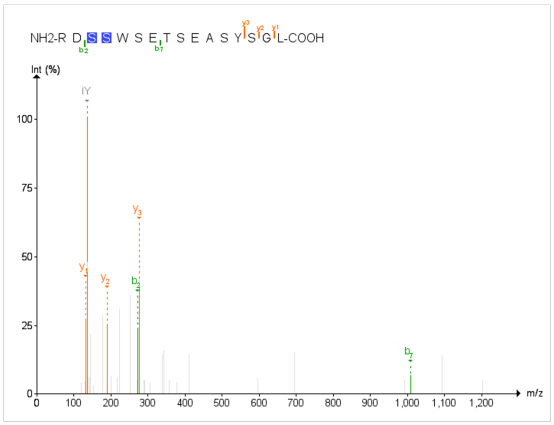
A

RDSSWS*ETSEAS*YSGL



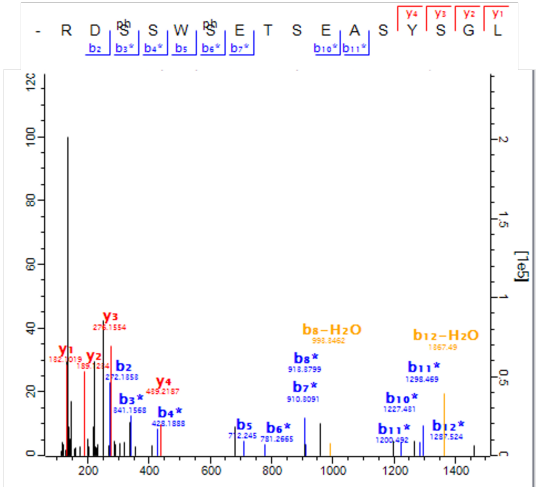
B

RDS*S*WSETSEASYSGL



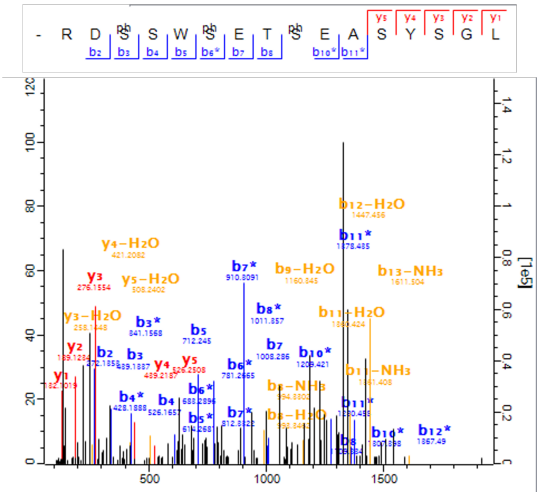
C

RDS*SWS*ETSEASYSGL



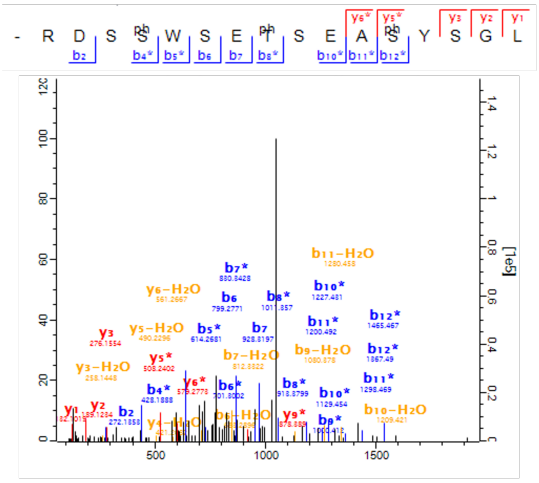
D

RDS*SWS*ETS*EASYSGL



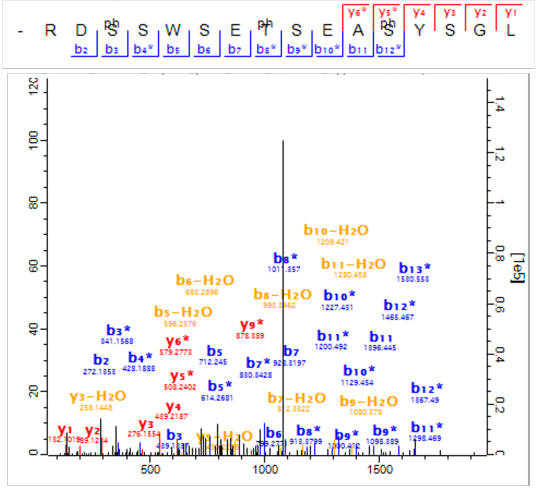
E

RDSS*WSET*SEAS*YSGL

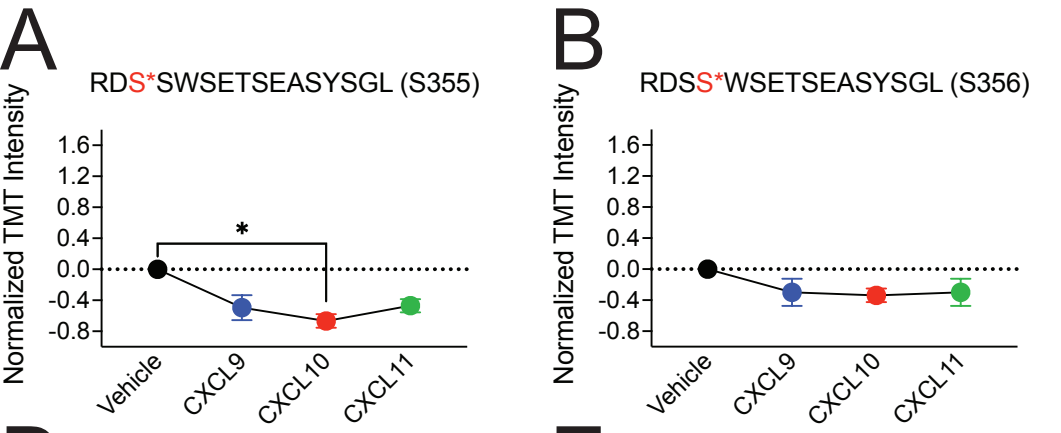


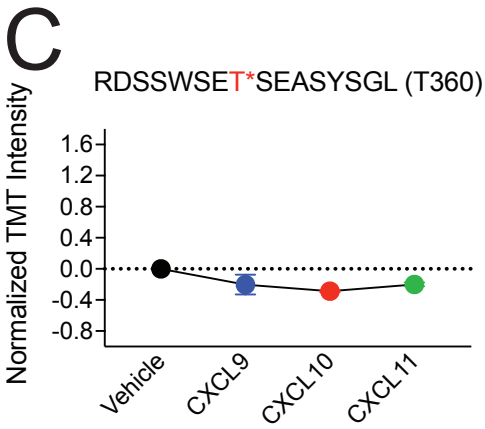
F

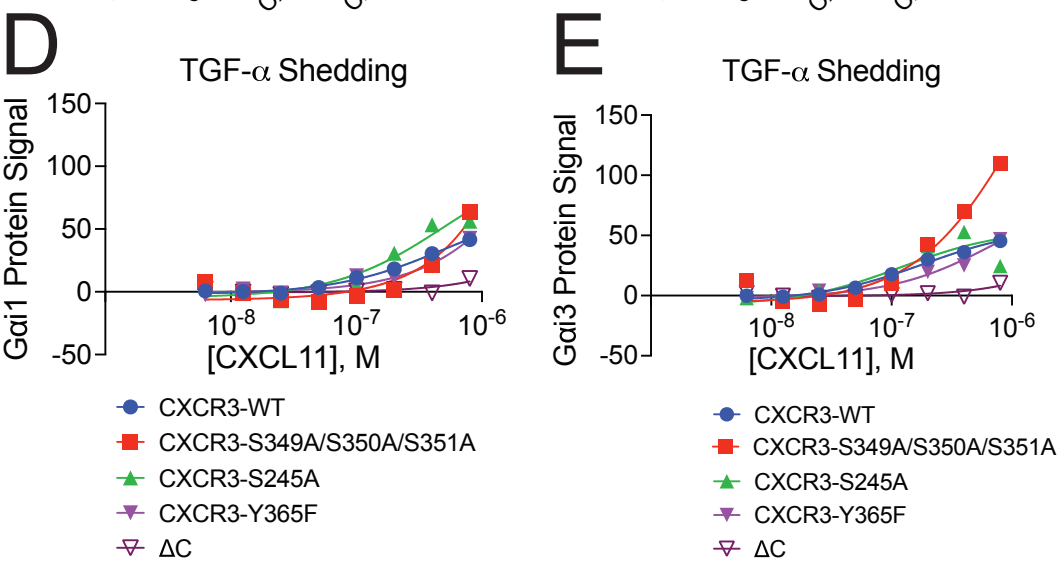
RDS*SWSET*SEAS*YSGL

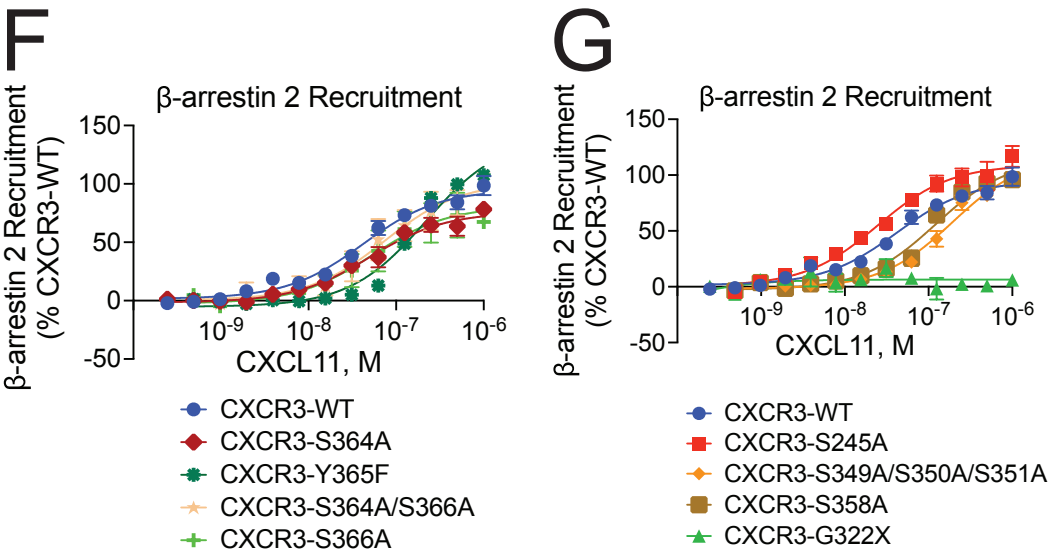


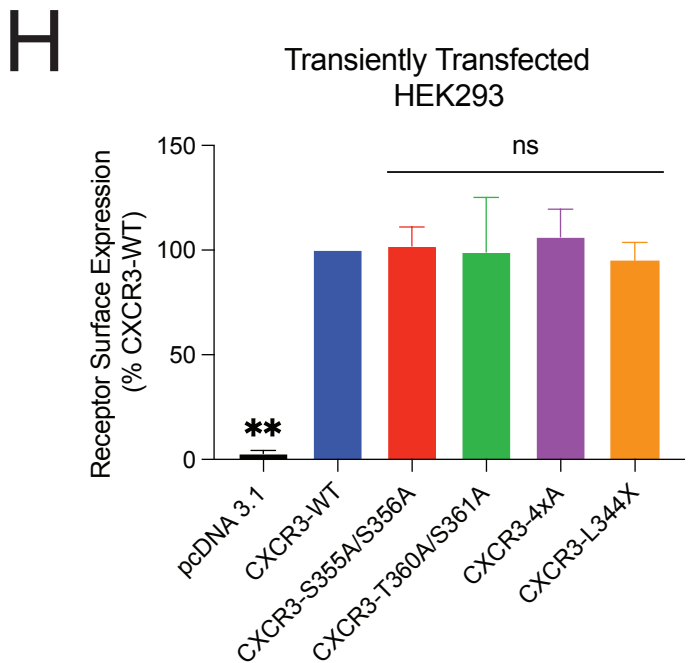
SUPPLEMENTAL FIGURE 2



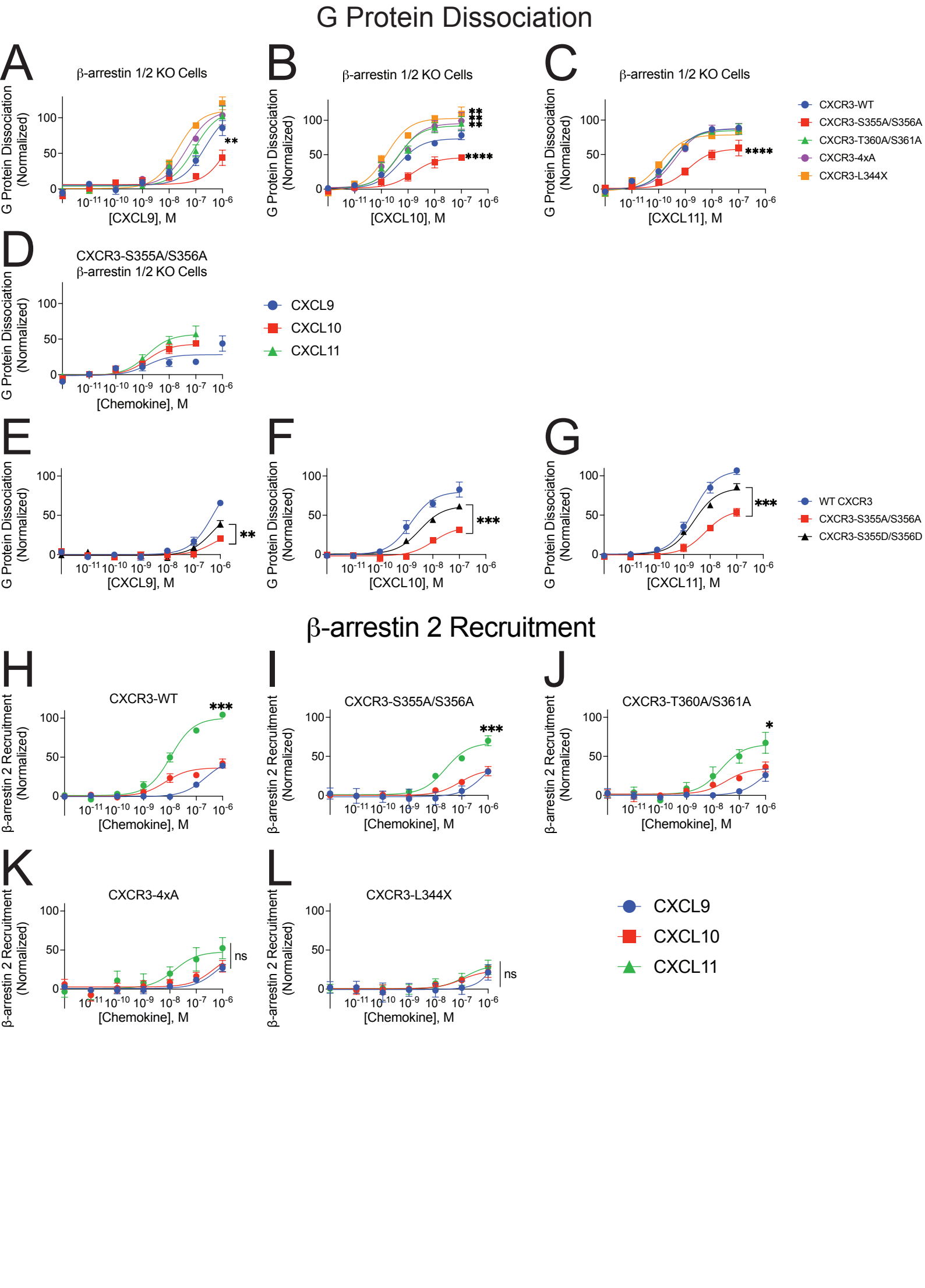






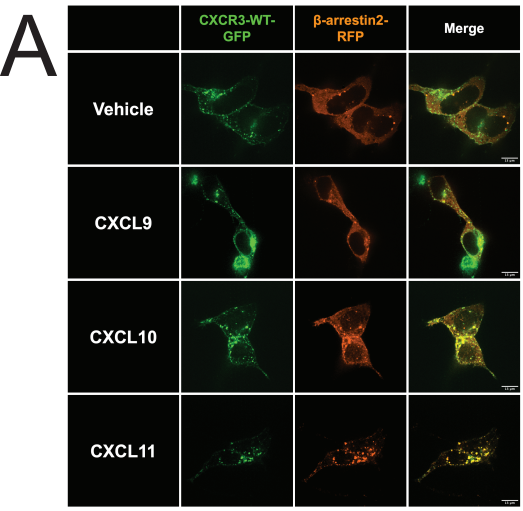


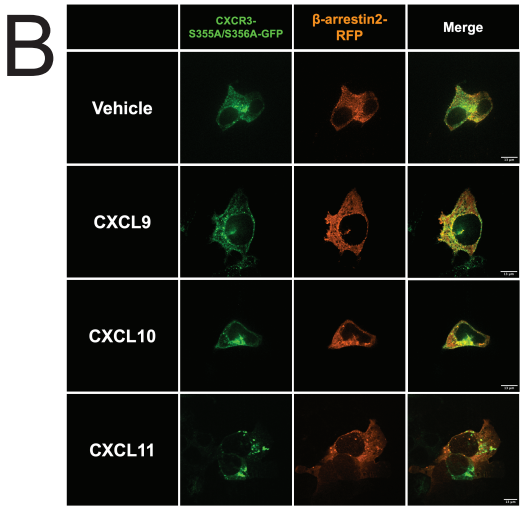
SUPPLEMENTAL FIGURE 3

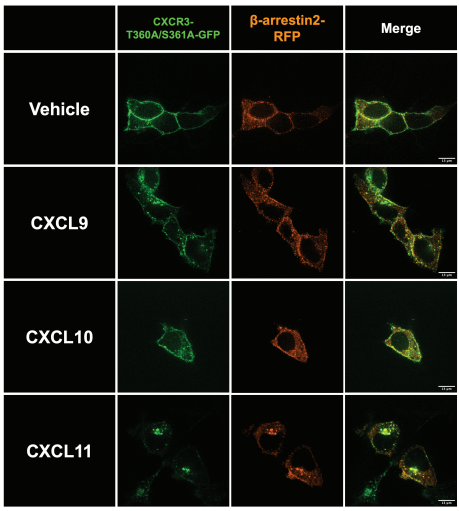


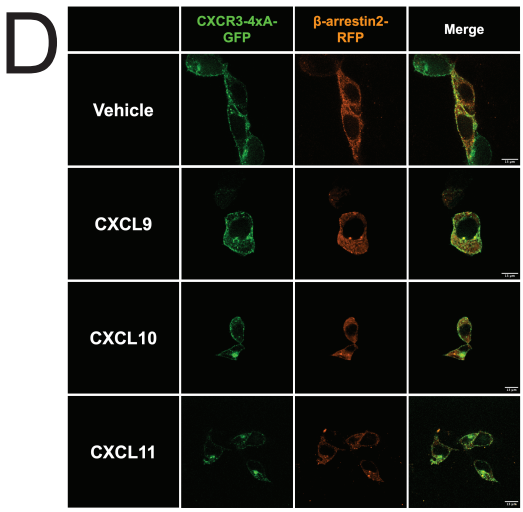
SUPPLEMENTAL FIGURE 4

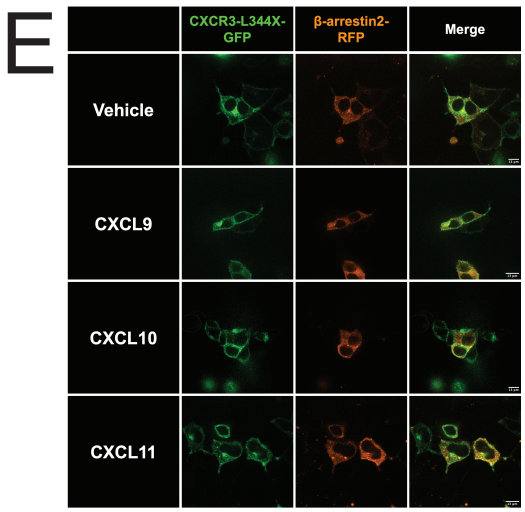
Receptor Internalization

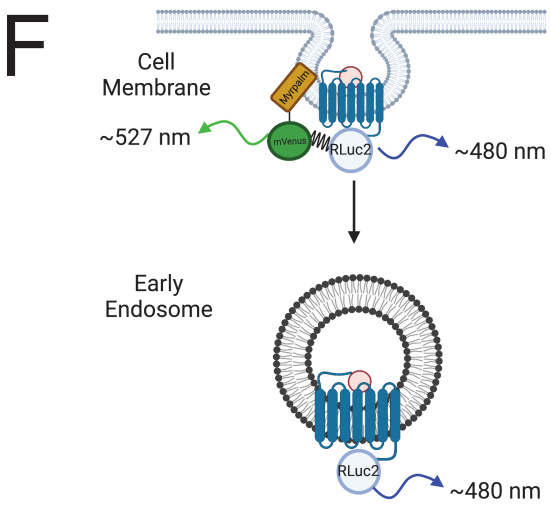


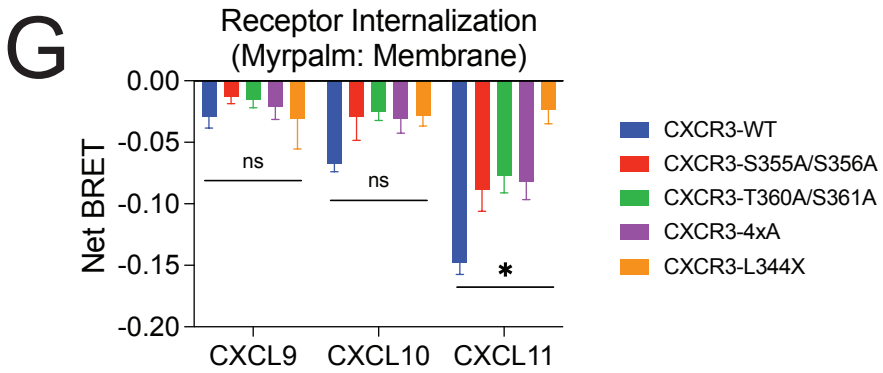


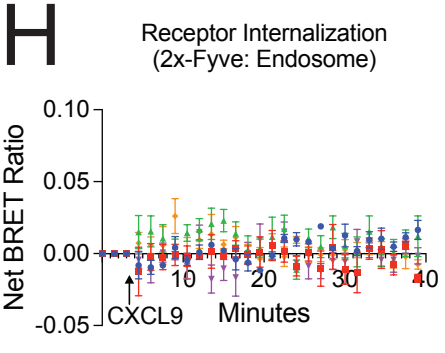


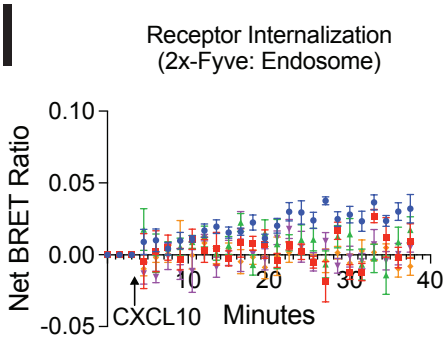


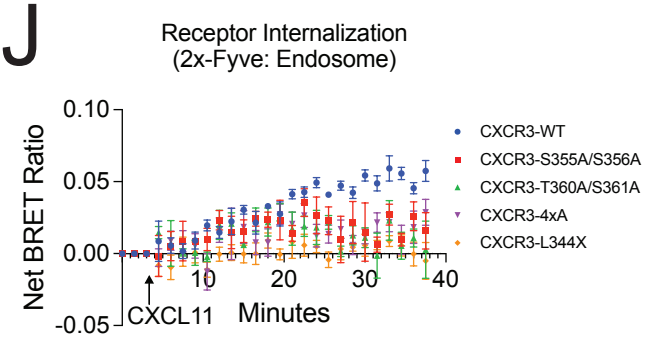




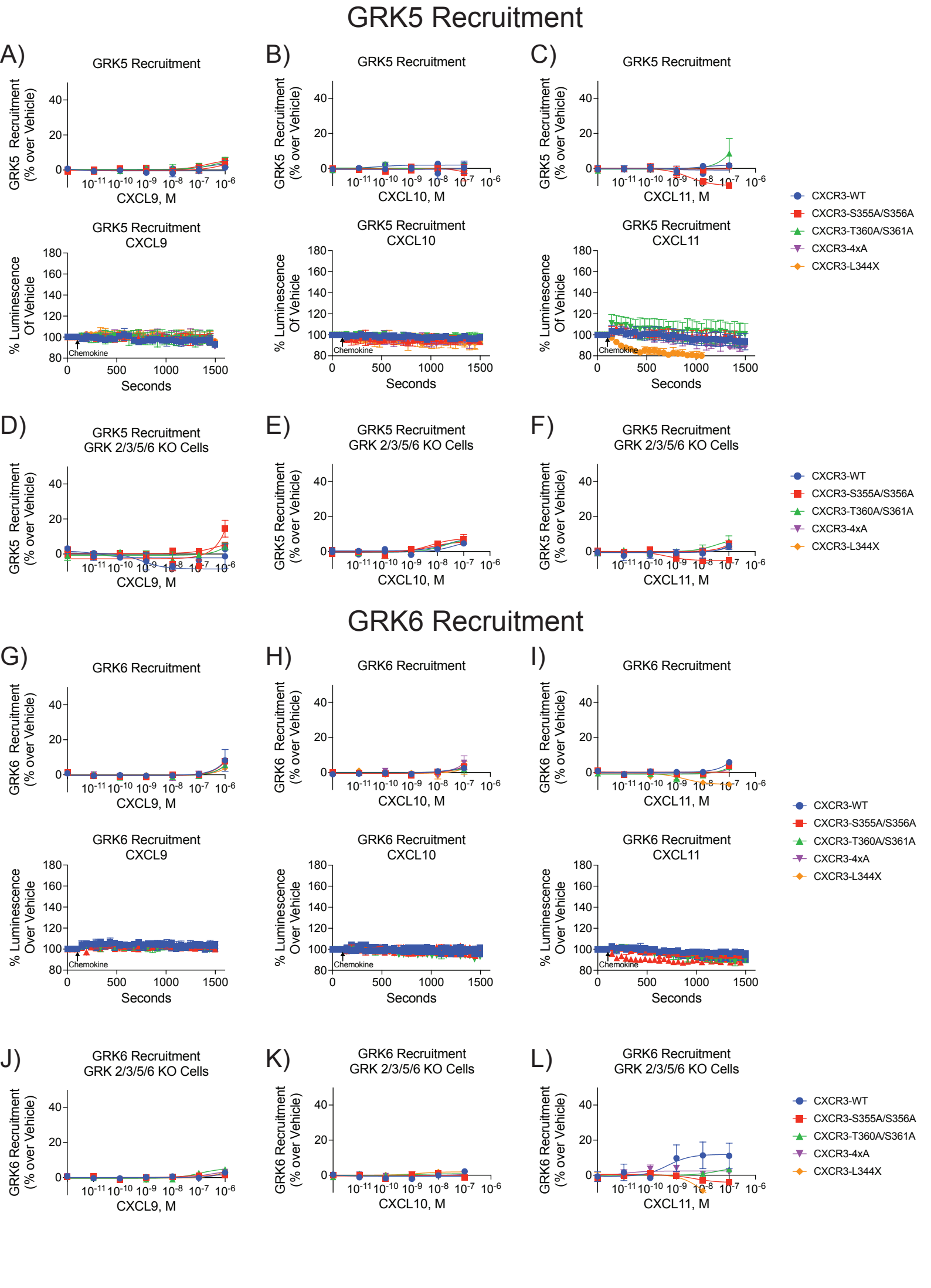




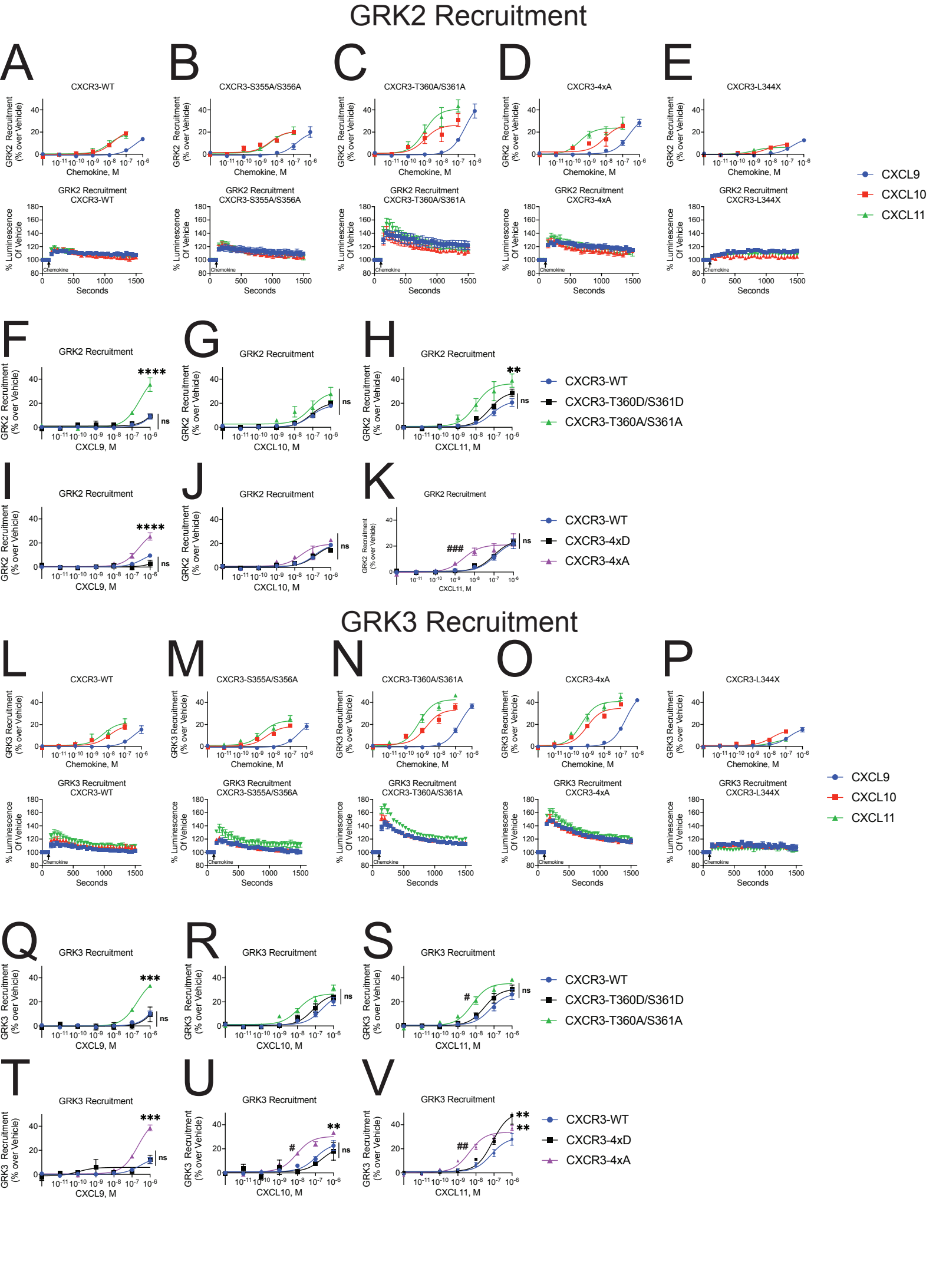




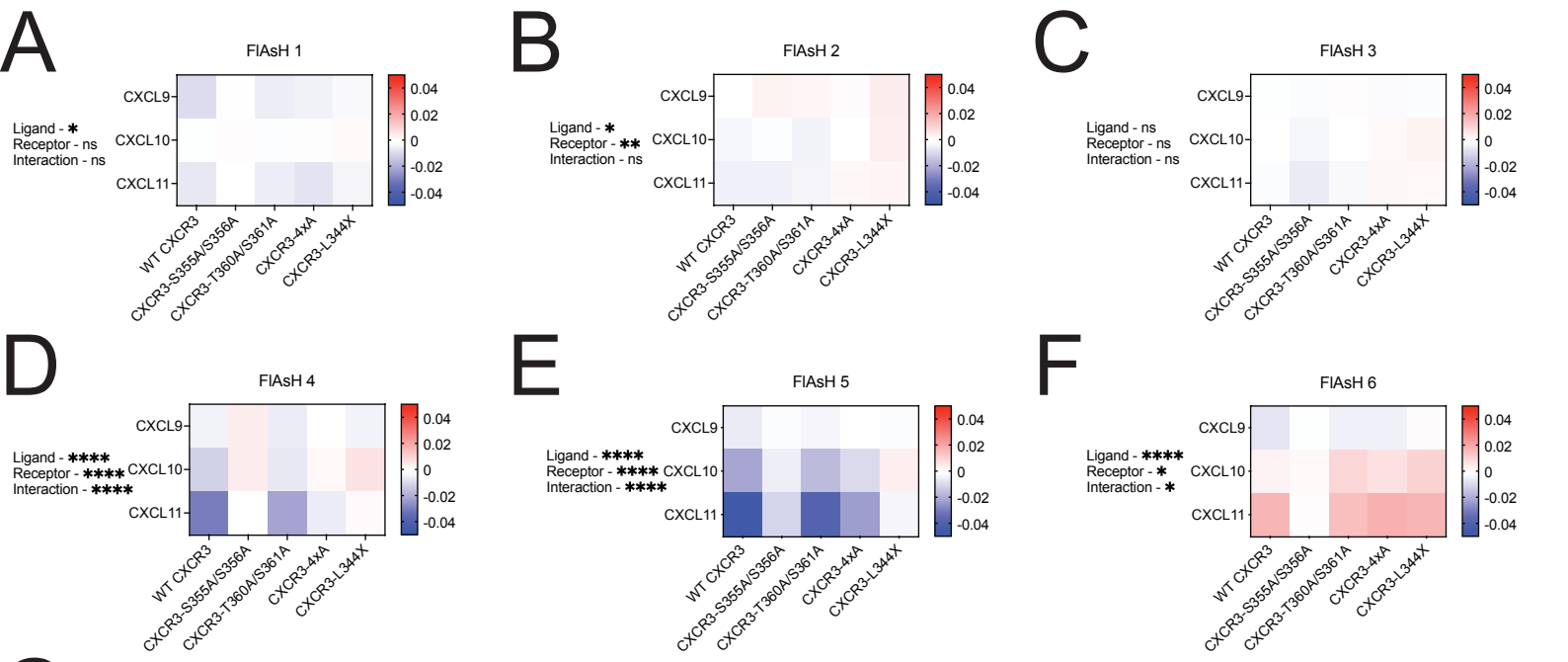
SUPPLEMENTAL FIGURE 5

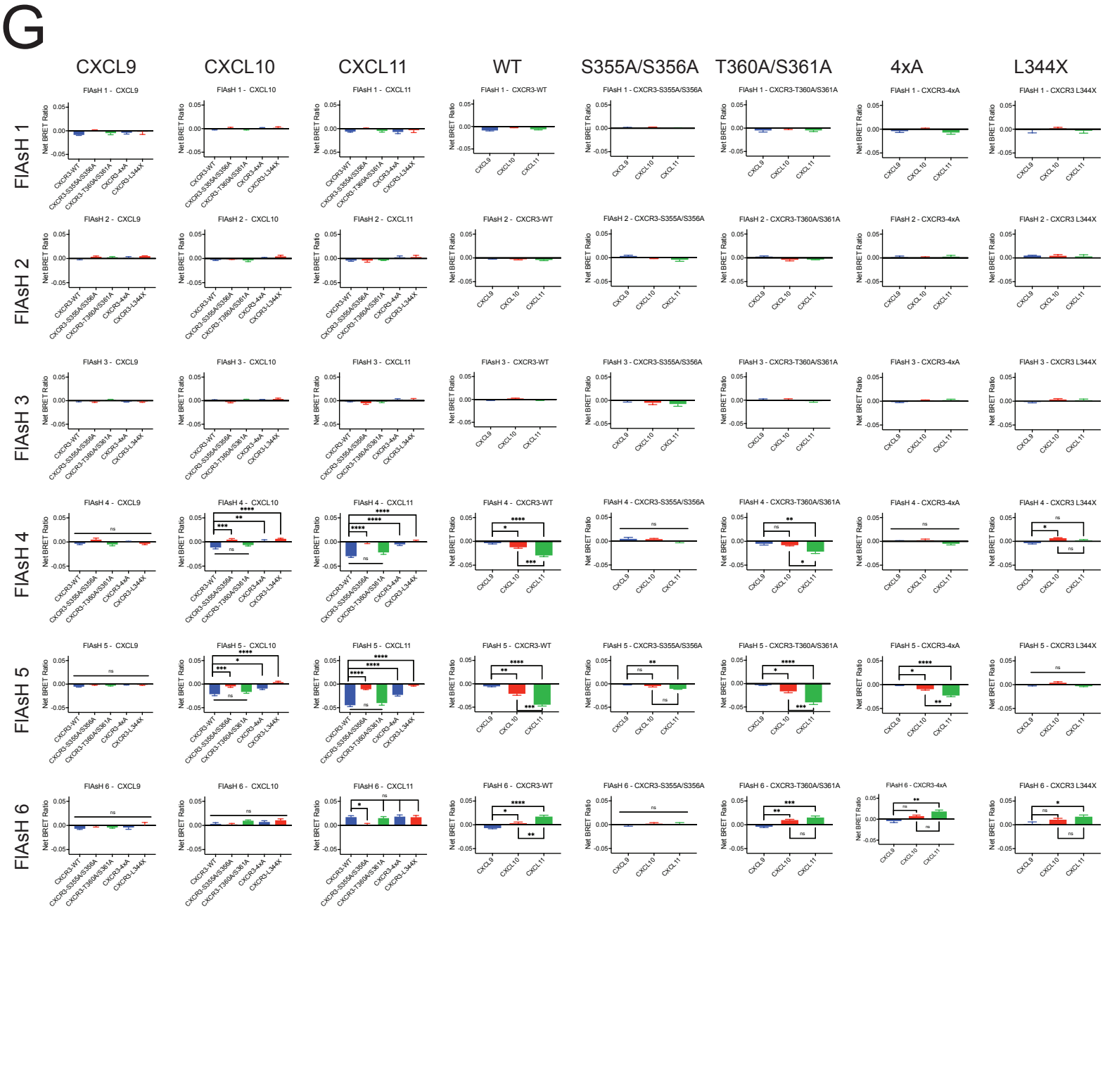


SUPPLEMENTAL FIGURE 6

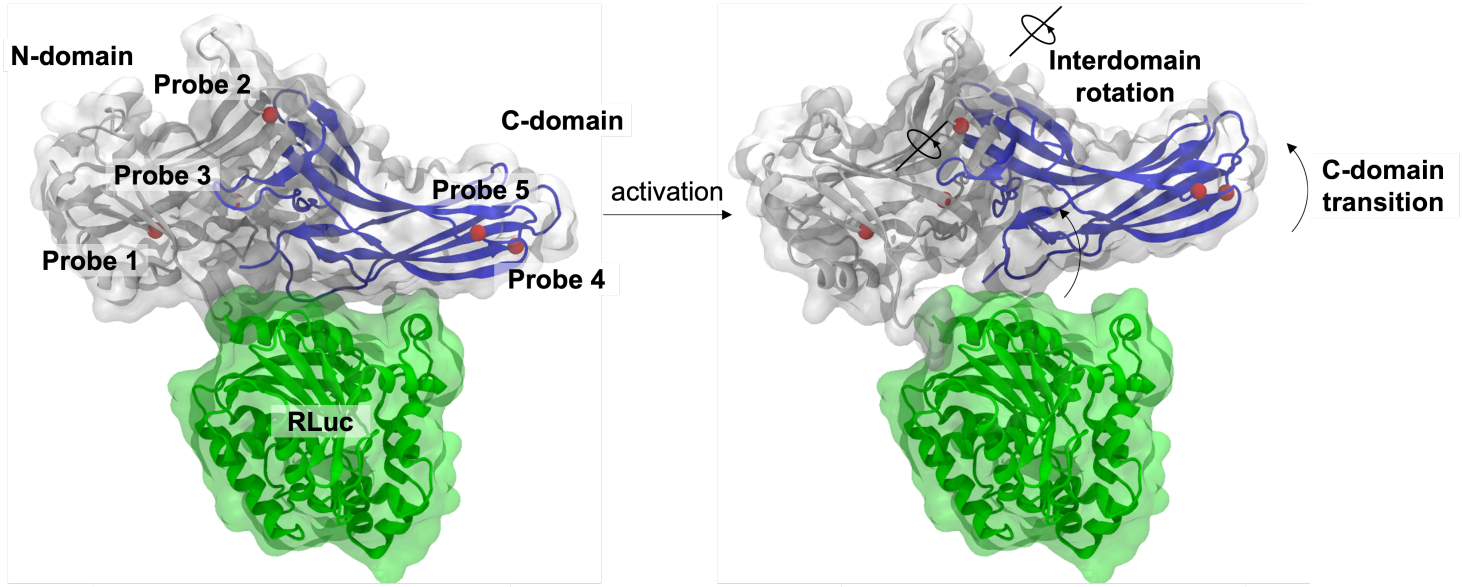


SUPPLEMENTAL FIGURE 7





SUPPLEMENTAL FIGURE 8

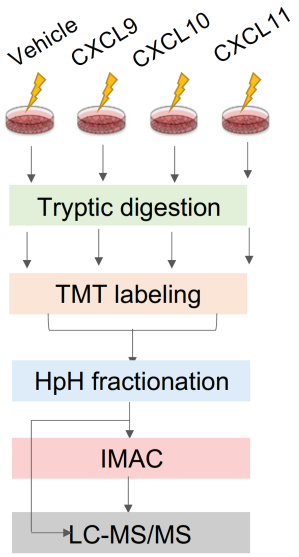


Inactive State
(low interdomain rotation angle)

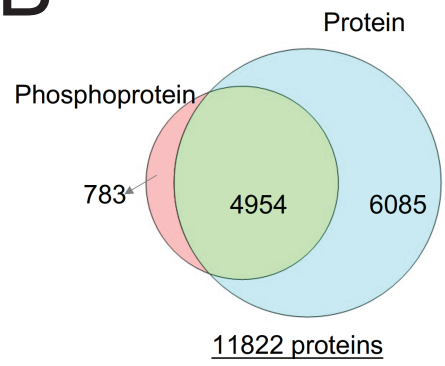
Active State
(high interdomain rotation angle)

SUPPLEMENTAL FIGURE 9

A



B

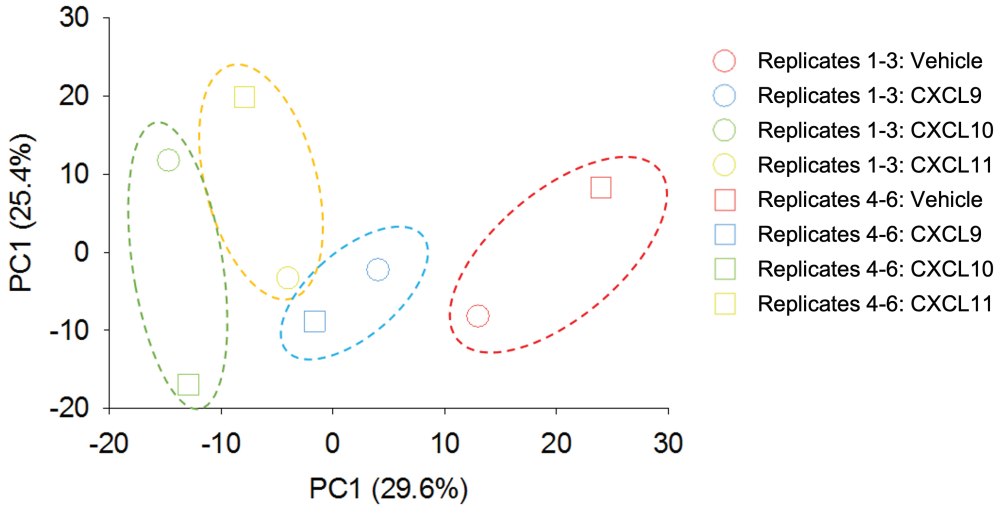


C

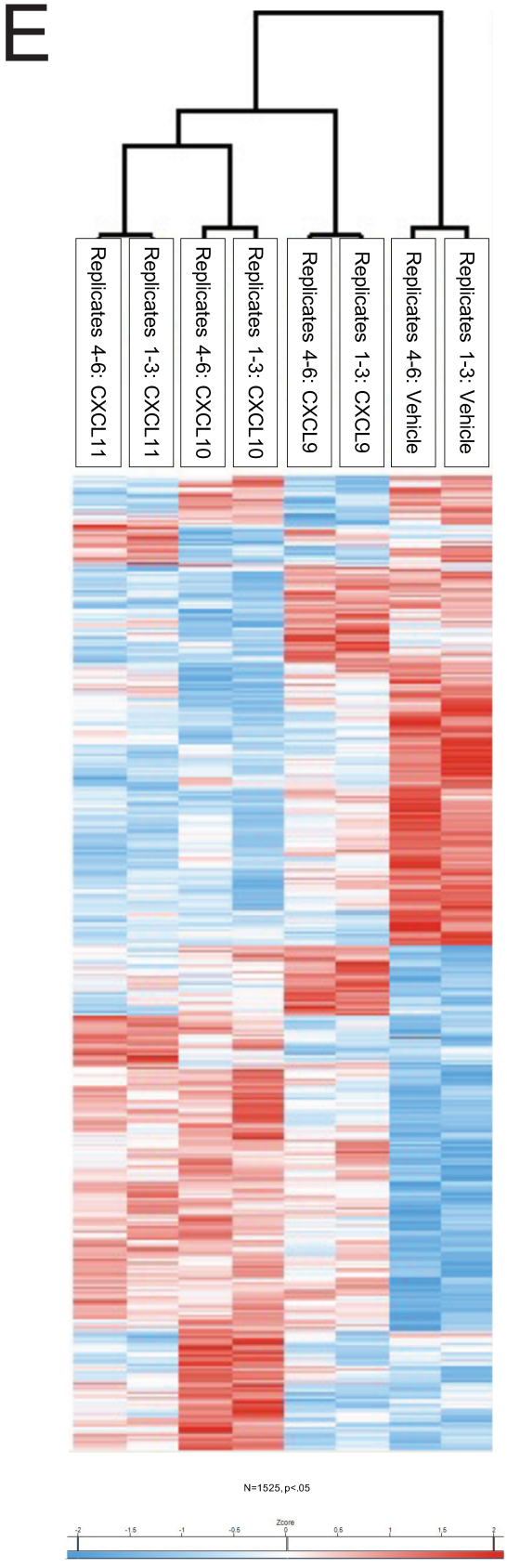
Proteome	
Total Peptides	159739
Proteins	11038

Phosphoproteome	
Total Peptides	29992
Phosphopeptides	26556
Phosphorylation Sites	22620
Phosphoproteins	5736
Class 1 Phosphorylation Sites	16448
S	18388
T	4112
Y	120

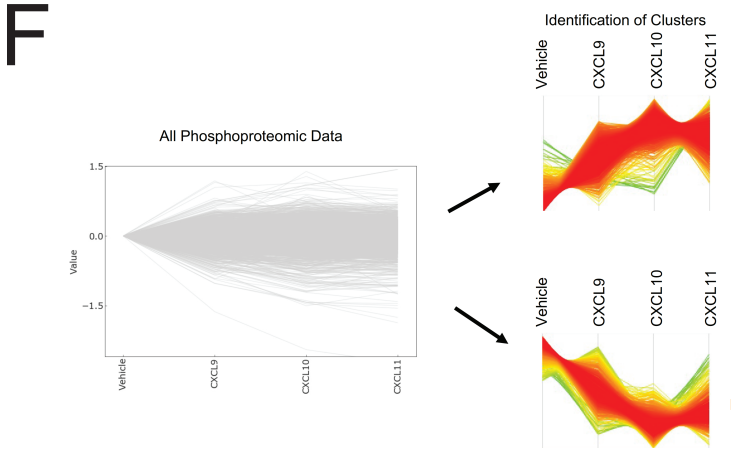
D



E



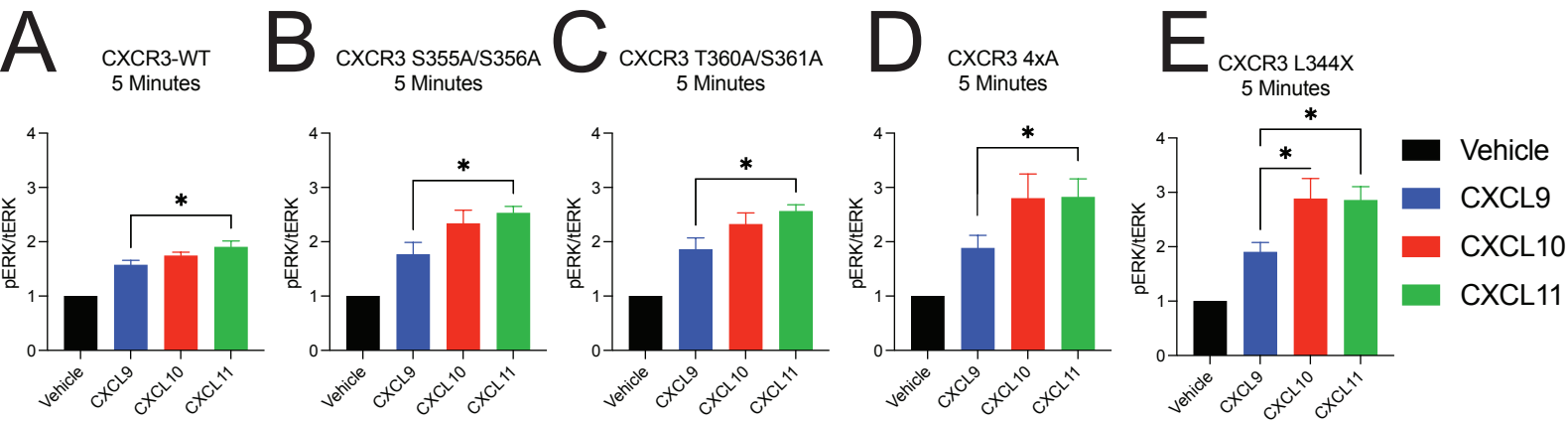
F

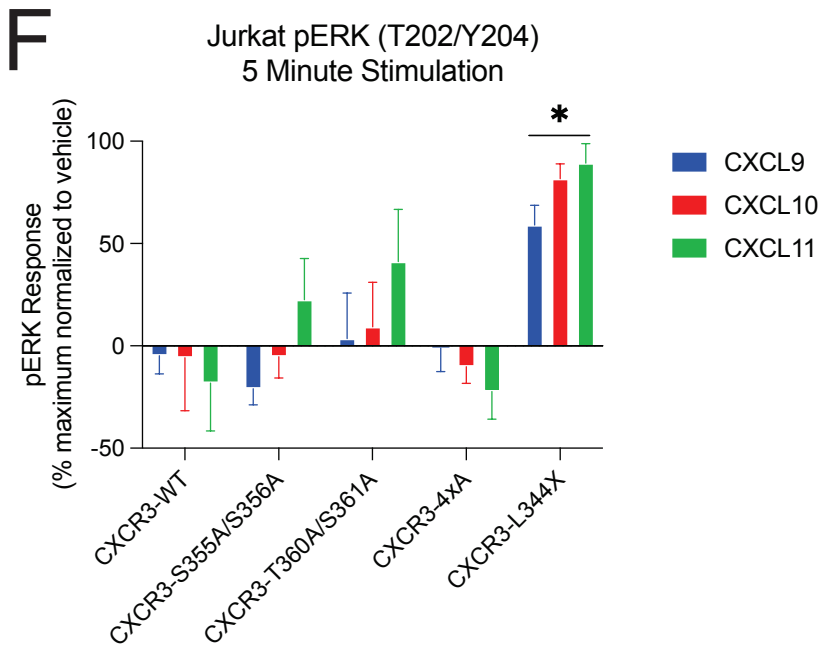


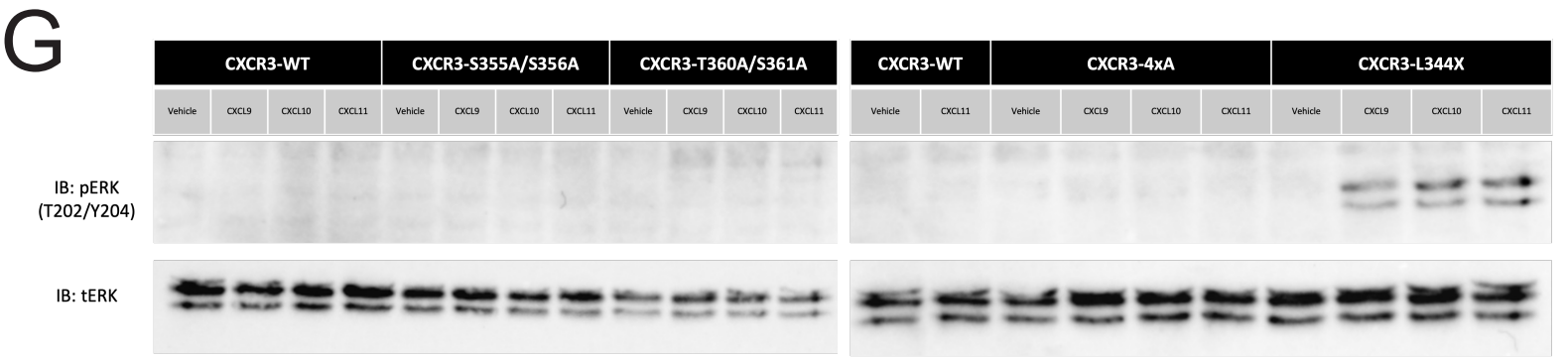
G

Cellular Comparment	Percentage	Biological Process	Percentage	Molecular Function	Percentage
Cytoplasm	19.4%	Transcription, DNA-Templated	20.4%	Protein Binding	40.6%
Nucleus	18.9%	Negative Regulation Of Transcription From RNA Polymerase II Promoter	9.2%	Poly(A) RNA Binding	10.8%
Nucleoplasm	14.5%	Negative Regulation Of Transcription, DNA-Templated	7.8%	ATP Binding	8.7%
Cytosol	12.8%	Protein Phosphorylation	7.0%	DNA Binding	8.2%
Membrane	7.9%	Cell-Cell Adhesion	6.9%	RNA Binding	4.2%
Nucleolus	4.1%	Cell Division	6.3%	Chromatin Binding	3.5%
Perinuclear Region Of Cytoplasm	2.6%	Viral Process	6.2%	Cadherin Binding Involved In Cell-Cell Adhesion	3.4%
Centrosome	2.5%	mRNA Splicing, Via Spliceosome	5.1%	Protein Serine/Threonine Kinase Activity	3.1%
Cell-Cell Adherens Junction	2.5%	Mitotic Nuclear Division	4.4%	Protein Kinase Binding	2.8%
Microtubule	2.4%	Cellular Response To DNA Damage Stimulus	4.0%	Nucleotide Binding	2.7%
Cytoskeleton	2.2%	mRNA Processing	3.8%	Protein Kinase Activity	2.7%
Protein Complex	2.0%	RNA Splicing	3.5%	Actin Binding	2.0%
Focal Adhesion	2.0%	Peptidyl-Serine Phosphorylation	3.1%	Microtubule Binding	1.8%
Nuclear Speck	1.8%	Protein Sumoylation	3.0%	Kinase Activity	1.8%
Midbody	1.1%	Covalent Chromatin Modification	2.8%	SH3 Domain Binding	1.2%
Intracellular Ribonucleoprotein Complex	1.1%	mRNA Export From Nucleus	2.7%	Structural Constituent Of Cytoskeleton	1.1%
Lamellipodium	1.0%	Microtubule Cytoskeleton Organization	2.4%	Helicase Activity	1.0%
Spindle	0.9%	Mitotic Cytokinesis	1.4%	ATP-Dependent Dna Helicase Activity	0.6%

SUPPLEMENTAL FIGURE 10







SUPPLEMENTAL FIGURE 11