Table S1: Quantification of patterning defects in genetic interaction assays with moderate cindrRNAi

	per Hexagon [2.]															
GENOTYPE [1.]	**# cone cell defects**		**# 1° cell defects**		**ommatidia orientation errors**		**# of bristle defects**		**# of 3° defects**		**IPC #**		**OMS** [3.]			**p-value** [4.]
	Mean	**SD**	**Mean**	**SD**	**Mean**	**SD**	**Mean**	**SD**	**Mean**	**SD**	**Mean**	**SD**	**Mean**	**SD**	**SE**	
GMR-Gal4/+; UAS-cindr^{RNAi}*/+*	**0.08**	0.27	**0.37**	0.56	**0.13**	0.34	**1.19**	0.85	**2.27**	0.64	**10.57**	1.38	**5.68**	1.63	0.19	
GMR-Gal4/+; UAS-cindr^{RNAi}*/ Cbl*^{F165}	**0.07**	0.25	**0.51**	0.83	**0.28**	0.83	**1.91**	0.84	**2.56**	0.72	**10.67**	1.93	**7.37**	1.79	0.21	1.16×10^{-8}
shi^{FL54}*/+; GMR-Gal4/+; UAS-cindr*^{RNAi}*/+*	**0.17**	0.38	**0.45**	0.62	**0.16**	0.37	**1.28**	0.75	**2.37**	0.69	**11.08**	1.84	**6.19**	1.96	0.23	0.0869771
GMR-Gal4/Rab5^{2}*; UAS-cindr*^{RNAi}*/ +*	**0.11**	0.31	**0.36**	0.78	**0.16**	0.37	**1.73**	0.89	**2.49**	0.70	**11.85**	2.14	**6.49**	2.36	0.27	0.0153886
control genotypes:																
GMR-Gal4/+; UAS-lacZ / +	**0.03**	0.23	**0.00**	0.00	**0.03**	0.16	**0.31**	0.46	**0.13**	0.34	**12.28**	0.80	**0.93**	1.08	0.12	
GMR-Gal4/+; Cbl^{F165} */ +*	**0.01**	0.12	**0.03**	0.16	**0.03**	0.16	**0.39**	0.66	**0.39**	0.67	**12.03**	0.54	**1.05**	1.58	0.18	
shi^{FL54}*/+; GMR-Gal4/+*	**0.01**	0.12	**0.00**	0.00	**0.00**	0.00	**0.37**	0.51	**0.36**	0.61	**12.24**	0.59	**1.07**	1.40	0.16	
GMR-Gal4/Rab5^{2}	**0.00**	0.00	**0.03**	0.23	**0.01**	0.12	**0.07**	0.25	**0.27**	0.60	**12.28**	0.75	**0.79**	1.38	0.17	

Notes:

1. *Cbl*^{F165}, *shi*^{FL54} and *Rab5*^{2} are loss of function alleles.
2. 75 hexagonal fields of each genotype were analyzed.
3. The Ommatidial Mispatterning Score (OMS) is the mean number of errors observed in each hexagonal field; SD = standard deviation, SE = standard error.
4. Student T-tests compared total patterning errors in experimental and *GMR>Cindr*^{RNAi} datasets. P-values below 0.01 are statistically significant at the 1% confidence level.