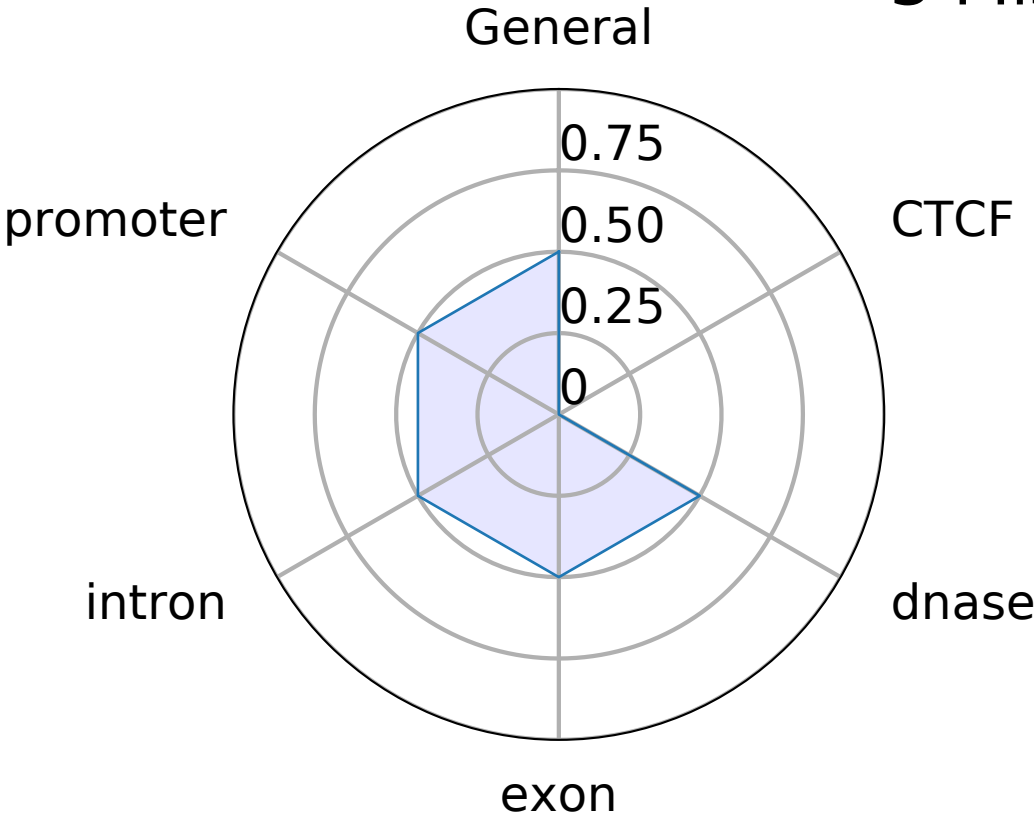


3 Mismatches



	Position	# Targets
General	0.5	35.0
CTCF	0.0	0.0
dnase	0.5	4.0
exon	0.5	2.0
intron	0.5	11.0
promoter	0.5	13.0

