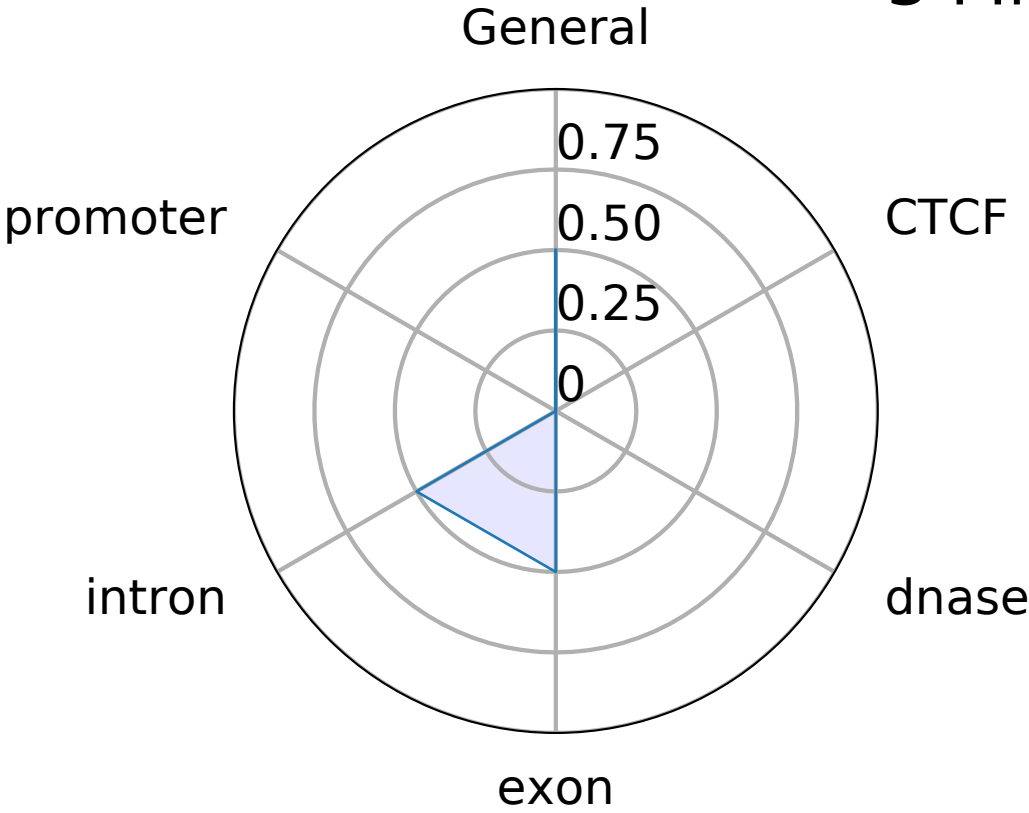


# 3 Mismatches



	Position	# Targets
General	0.5	3.0
CTCF	0.0	0.0
dnase	0.0	0.0
exon	0.5	1.0
intron	0.5	1.0
promoter	0.0	0.0

