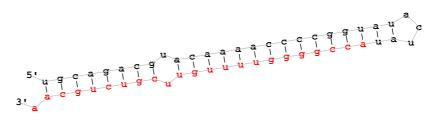
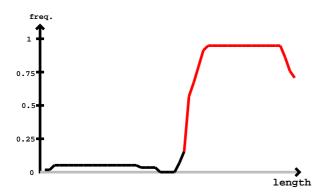
miRBase precursor : chromosome\_12\_63573

Total read count : 58 chromosome\_12\_63573 read 55 unt remaining reads : 3





5 '

## chromosome\_12\_63573

٠-	$ugcagacguacaaaaccccgguauacuau \\ \underbrace{accgggguuuuguucgucugcaa}$	-3'	exp	
	(((((((((((((((((((((((((((((((((((((((	reads	mm.	sample
	ugcagacguacaaaacccc	1	0	seq
	.gcagacgGacaaaaccccggua	2	1	seq
	auaccgggguuuuguucgucuCc	3	1	seq
	auaccgggguuuuguucgucugc	1	0	seq
	uaccgggguuuuguCcgucugc	2	1	seq
	Aaccgggguuuuguucgucugca.	1	1	seq
	uaccgggguuuuguucgucugcaa	2	0	seq
	accgggguuuuguucgucug	1	0	seq
	accgggguuuuguucgAcugca.	1	1	seq
	accgggguuuuguucgucugcaa	17	0	seq
	Cccgggguuuuguucgucugcaa	2	1	seq
	Gccgggguuuuguucgucugcaa	3	1	seq
	Gegggguuuuguuegueug	1	1	seq
	ccgggguuuuguucgucug	2	0	seq
	Ucgggguuuuguucgucug	1	1	seq
	ccgggguuuuguucgucugcaa	1	0	seq
	ccgggguuuuguucguAugcaa	1	1	seq
	Ugggguuuuguucgucugcaa	3	1	seq
	Agggguuuuguucgucugcaa	1	1	seq
	cgggguuuuguucgucugcaa	3	0	seq
	Aggguuuuguucgucugcaa	1	1	seq
	gggguuuuguucgucugcaa	1	0	seq
	Uggguuuuguucgucugcaa	5	1	seq
	ggguuuuguucgucugca.	1	0	seq
	ggguuuuguucAucugcaa	1	1	seq