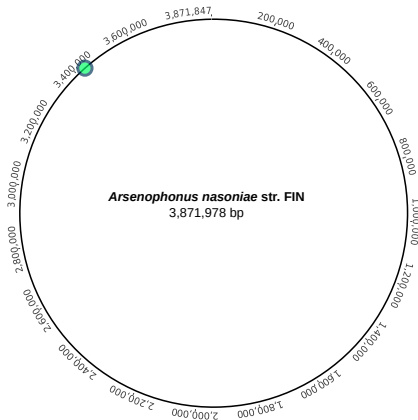
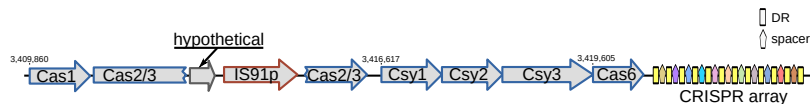


A)



B)



C)

Position	Repeat	%id	Repeat_Sequence	Spacer_Sequence
3420432	28	100.0	GTTCACCTGCCACATAGGCAGCTTAGAAA	CGTTCATCAATTTCTGGCGTAATACGAAAGGT
3420492	28	100.0		CTAAGGAGTCGAATGACCGCACTGCGCCAGAC
3420552	28	100.0		TGCTTCGGGGGTGTTCAATGATTAACTACTGTG
3420613	28	100.0		GATAACTGGGCTGACGAATCTGACAATTTCTG
3420673	28	100.0		GAAACGTTTTATGATCTCTCTCCACCCGAAA
3420733	28	100.0		TTAAGCAACGGTACCAATGTGACGGTAAATGA
3420793	28	100.0		ACCAAAAACGTGGAATTCGCCAATGACAGGCT
3420853	28	100.0		GAATTACAAACCATGAATAACATCTACACCAA
3420913	28	100.0		CCCAACGCCCCACGATGCGGTATTCAAGCAGT
3420973	28	100.0		ATCAACATCTTTGAGTGTGGAACACAAAAGA
3421033	28	92.9	T.....G	TTTTGTTATAACATAAAGATATAAATTAAATTG
3421093	27	78.6	T.A...C....C.....G	
12	28	97.6	GTTCACCTGCCACATAGGCAGCTTAGAAA	DR consensus

D)

	Chr.	pArsFIN2	pArsFIN3	pArsFIN4	pArsFIN5	pArsFIN6	pArsFIN7	pArsFIN8	pArsFIN9	pArsFIN10	pArsFIN11	pArsFIN12	pArsFIN13	pArsFIN14	pArsFIN15	pArsFIN16	pArsFIN17	pArsFIN18
spacer_1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
spacer_2	1	1	1	1	1	0	0	1	1	1	0	0	0	0	0	0	0	0
spacer_3	1	1	1	1	4	1	2	3	2	2	1	1	0	1	0	0	0	0
spacer_4	11	21	5	5	6	6	4	3	7	7	1	1	0	1	0	0	0	0
spacer_5	9	19	3	5	7	6	4	5	6	5	1	1	0	1	0	0	0	0
spacer_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
spacer_7	0	0	1	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0
spacer_8	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
spacer_9	0	1	0	0	1	1	1	2	1	1	1	1	0	0	0	0	0	0
spacer_10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
spacer_11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
total hits	23	43	11	12	20	15	11	14	17	16	6	4	0	3	0	0	0	0