Sequence: SEQ10013054_A1_F06_0

		Quality:	0 - 9	
Samples:	15199		10 - 19	
Bases:	1251		20 - 29	
Average spacing:	13.0		>= 30	
Average quality >=	10: 89, 20: 142, 30: 981			

16.09.2022

CC KGSWMGG GMMKGG CTGAATG MMGYRWYACTAGCRAATCYAGCTWCAYGAAGTCKGGTTRCWKACWTCSATCCKRACTGAGAGAGGT

TKTTRGGATYAGCATSYYGYCRCBWGGYMGCYKYCTKCWGTACCCCYYATTGYAACACGTGTGTAGCCCCRGACGTAAGGGCC

GTGCWGATKWGACGTCATCCCCAYYTTCCTCACATCWYAMGASGGCWSTCTCTAGASYCCTCARYRWGAYSTGWTARTMWC

TAAAKATARGGKKYGCKCKCKWTRTGGCWYTTAMSCMSACAYCTCRSGGCRMGAKSWGAMSACMACYRTGCMRCAYCTTCACMW

SWGYCTYRCSGMTAYWSTGTYCCWATATATTCWGWTGCWATTTAAGCSCGGRTRAGGYTCCTCGCRTAWYMTCGAATTAAAM

CAYRTGTTCCTCCGCKTGTGCGGGCCCCCGWCWATTCCTTTGAGTTWCACCGTTGCCGGCGYACTCCCCAGGTGGAATACWTA

Sequence: SEQ10013054_A1_F06_0

ATGCTTTCGCTTGGCCGCTTRCTGTATATCGCAAACAGCGAGTATTCATCGTTTACTGTGTGGACTACCAGGGTATCTAATCCT

GTTTGATACCCACACTTTCGAGYATCAGTGTCAGTKACAGTCYAGTRAGCTGCCTTCGCAATCGGAGTTCTTCGTGATATCTA

AGCATTTCACCGCTACACCACGAATTCCGCCYACCTCTACTGTACTCAAGACTRCCAGTTTCAACTGCAATTTTACGGTTGA

GCCGCAAACTTTCACAACTGACTTAACAATCCACCTACGCTCCCTTTAAACCCAATAAATCCGGATAACGCTCGGATCCTC

CRATTACCGCGGCTGCTGGCACRGAGTTAGCCGATCCTTATTCATATGGTACATACAAAATTCCACACGTGGAAYACTT

TATTCCCATATAAAGAAGTTTACGACCCATAGAGCCTTCATCCTTCACGCTACTTGGCTGGTTCAGRCTCTCGCCCATTG