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1 **Development of SNP for the deep-sea fish blue ling, *Molva dypterygia* (Pennant,**
2 **1784) from ddRAD sequencing data**

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15 **ABSTRACT**

16 Blue ling is a deep-water species that has been severely fished upon in to coastal and offshore
17 fisheries since the early seventies, thus causing the collapse of the populations in the last two
18 decades. Genetic information is scarce in this species, and molecular markers are therefore
19 needed to provide advice both for management and for rebuilding the stocks.

20 A suite of 103 SNP markers was identified from ddRADsequencing data. From those, 81 were
21 organized in three multiplex reactions, and tested on 150 individuals from three different
22 sampling locations. Good-quality amplification products were successfully obtained from 70 of
23 the markers.

24 All SNP loci were biallelic, with averaged H_e per locus ranging between 0.101 and 0.500.

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26 **Keywords:** blue ling, *Molva dypterygia*, SNP, ddRAD, management advice, stock
27 rebuilding, fisheries depletion

28 Blue ling (*Molva dipterygia*) are distributed across the Northeast Atlantic (Large et al. 2010);
29 inhabiting depths between 200 and 1500 m (Gordon & Hunter 1994). This species spawns in
30 very dense aggregations throughout its entire geographic range (Magnússon et al. 1997; Large
31 et al. 2010). Blue ling stocks in the NE Atlantic were moderately exploited until the 1960s and
32 1970s. Subsequently, more intensive fishing across its range, mainly in the spawning grounds
33 led to the collapse of the populations during the late 1990ies (Large et al. 2010). Different
34 regulations were enacted to rebuild the stocks, with varying success (ICES 2018).
35 The genetic population structure of this species has barely been investigated (Reiss et al.
36 2009), and, hence, genetic information is needed to develop appropriate management
37 strategies to rebuild the fishing stocks.

38

39 Genomic DNA was extracted from sixteen blue ling ethanol-preserved fin samples (eight from
40 Faroe Islands and eight from Norwegian offshore - Eggakanten) using the Qiagen DNeasy
41 Blood & Tissue Kit. A ddRAD library for SNP discovery was constructed following Manousaki
42 et al. (2016) and employed a *Sbf* I - *Sph* I restriction enzyme combination. The library was
43 sequenced as part of an Illumina MiSeq run (v2 chemistry, 160 base paired end reads). Stacks
44 software v1.27 (Catchen et al. 2013) was used to demultiplex samples and identify / call
45 genotypes (de novo assembly; key STACKS parameters m=6, M=2, n=1). A total of 956
46 polymorphic RAD loci containing one or two SNPs and scored for at least 12 of the 16 samples.
47 Initially a subset of 103 polymorphic RADtags was identified for Sequenom MassARRAY
48 individual SNP assay (i.e., minor allele frequency > 0.1; > 35 bases available flanking DNA
49 either side of SNP, absence of repetitive DNA close to the SNP). Three multiplex assays were
50 successfully designed for 81 of these loci; which were then test screened on 150 individuals
51 collected in three different sampling sites (i.e. Eggakanten, Yrkefjorden and Faroe Islands).
52 After purging bad quality markers, a set of 70 SNPs loci were retained for further analyses.

53

54 Observed (H_o) and expected heterozygosity (H_e) as well as the inbreeding coefficient (F_{IS}) were
55 computed with GenAlEx (Peakall & Smouse 2006). The genotype distribution of each locus

56 was compared with the expected Hardy-Weinberg distribution (HWE) as was the departure
57 from Linkage Disequilibrium (LD), using the program GENEPOP 7 (Rousset 2008). Analyses
58 were conducted both at population level and pooling the 150 individuals.

59

60 In the pooled set of individuals, deviations from Hardy Weinberg expectations were detected
61 at $P < 0.05$ at two loci (Mdy_015 and Mdy_038) whereas loci Mdy_021, Mdy_027, Mdy_041
62 showed deviations at $P < 0.001$ that remained significant after Bonferroni sequential correction.
63 The individual analyses conducted on the population basis showed that 7.6% of the tests
64 departed from HWE; percentage that dropped to half after correction for multiple tests. Loci
65 Mdy_021 and Mdy_41 were out of HWE in the three sampling sites and continued to be so
66 after Bonferroni correction. Departures from LD were detected in 5% of tests dealing with
67 pooled data (0.1% after multiple test correction) and in 4.4% across the three populations
68 (0.05% after correction). Observed heterozygosity per locus (H_o) ranged between 0.107 and
69 0.947 (**Table 1**), with averaged (\pm SE) over all loci in the pooled set of individuals of $0.362 \pm$
70 0.017 ; whereas H_e ranged from 0.101 to 0.500, with an average of 0.354 ± 0.014 . The range
71 of the inbreeding coefficient (F_{IS}) per locus was -0.896 to 0.152, with an average of $-0.018 \pm$
72 0.018 . Locus Mdy_41, showing $H_o=0.947$, was heterozygote CT for 94.7% of the individuals.

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78 also thank the Directorate of Fisheries and the Norwegian Fishermen's Association for
79 financing this project.

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81 **CONFLICTS OF INTEREST**

82 The authors declare that they do not have conflicts of interests.

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Table 1.- Summary table for the 70 SNP markers distributed in three multiplex reactions. Sequence and [SNP], number de individuals tested (N), minor allele frequency (MAF); observed (H_o) and expected (H_e) heterozygosity; inbreeding coefficient (F_{is}); and probability for Hardy-Weinberg equilibrium tests (ns = non-significant, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$).

M	SNP_ID	Sequence	Alleles	N	MAF	Ho	He	F _{is}	HWEP
M1	Mdy_001	CATGCAGTCAGGACACAGCAATGGAAGATGCTCTTCTTAAAATCGGAATATTGCAAAGCTGTTTCGACATGATTTATGTTGAGCTGTATTGACCATA[C/T]CATAACAGCATGTTAAATCATGAGGTGACCRGCCATT	C/T	150	0.403	0.540	0.481	-0.122	ns
M1	Mdy_009	CATGCTGAGCAGCGGGGAGAAGGTCAAGGTGGACCTGCACCCCTCAGTGGCTGACCCGGGAGAGAGCTCTGGTCTACATGGTCCCATGGCAGCGTCC[C/T]GGGGGCACACGGCCATCAGCTCCACGAGAACCCTCC	C/T	150	0.460	0.453	0.497	0.087	ns
M1	Mdy_015	TGCAGGGGGTCTGTTCCAGGTCAAAGGTCAAGGTGAT[A/G]TCCATCGGGGGCGGGCCATGATCATATAGGAGCACTCCAGATTGTGGGGTACTTGTCCGGGAACCCGGGGAATCGATCATCCCG	A/G	150	0.410	0.580	0.484	-0.199	*
M1	Mdy_020	CATGCACAGCACAACCTGCGTGAGGTAAAACCATGATGTAGAGAACACATTGAAATAGATG[G/T]AGACAGGAGGTTATGATAGTTTATTCTTAATACAAAGTGGCTGCACATAAACCAACCTGTAACCCACCTTCATT	G/T	150	0.487	0.480	0.500	0.039	ns
M1	Mdy_023	CATGCTGAAGTAGGATCAGATCATCACGTTACATAAAGAAGGCTGTCATTAGTCTTAAACATAGAC[A/C]ATATACCTGCCTCCCTTATACATGGATSSGGGCTTACCAGAAGCACTCATATGTGAATCAACATATAT	A/C	150	0.253	0.400	0.378	-0.057	ns
M1	Mdy_025	TGCAGGAGAATCCGAGGACGACAAGAAGCGAGGCCGGTGCAGCGACAGCGAGGTGAGCCAGGTGAGGGAGAGCTGCAGAACCCTCCTCCTG[C/T]GGAGGAGGAGGTCCATGTTCTCCTCKCCTCCCGTGAAGGAT	C/T	150	0.220	0.293	0.343	0.145	ns
M1	Mdy_027	TGCAGGTGGAGGGCTGAGGGGGCTGCGTTCAACGGCACAC[A/G]GTGTTGTTGAATGAGGGAGGGGGCGTGGCGACGCCAGGCACAGCCCTCACTCTGCGTGAATACCCGAGTACCGCCGAACCTAATGTGCTTTG	A/G	150	0.433	0.627	0.491	-0.276	***
M1	Mdy_029	TGCAGGTTCACTGCGGCCATTGGCTGTTGCAACCCAGATTCTTT[C/G]GGCTGGGAGGCGAAACACCTCGAAACTAGACTATACTGACTGTTGTGTGATCCAGGGTTTGGTCCCTCCATCTTACCATGACGTGGAA	C/G	150	0.383	0.487	0.473	-0.029	ns
M1	Mdy_031	TGCAGGACGAGCAGCGTACGGTTACATACCCGAGTTACCAGGTTACGCTTCATTTAGC[C/G]TTTACATGGTCAACAGGTTACCAGGTCAGTGTCAAGTAAAGTGTGCTTCATTTACAACTTACAATAGAACCA	C/G	150	0.177	0.287	0.291	0.015	ns
M1	Mdy_032	CATGCAGATTCGAGCTTCAACACTAATTGGCAACACTGACAGACAGCGCAGTGTACTGTCAAATGCGC[A/C]CCAATTACCAGAGGTTGTTCCTTTTGTAATCTTCCAATAGAATGCCTAATTAGCATT	A/C	150	0.413	0.507	0.485	-0.045	ns
M1	Mdy_034	TGCAGGAGAGCTTTGTTGCCCTCCATAGGCTTAGCTTAGGGGTCGCGCTGAGAAGTGCAGTCAACCGAGACATAAAGATC[A/G]TCGTTTTGTTCTCGTGGTGTACACCTTAAAGTAGAGGTATGGGTGATACCA	A/G	150	0.283	0.407	0.406	-0.001	ns
M1	Mdy_035	CATGCATTTGTTTCGGTGGTGTTCATATGAATGAAGTCAAACGTCTGTAATGTGTATGTATGTGTTGCATGGCGGTGCA[C/T]GTAATTTAAAGCTAGAGTAGGCAATTTATTTAGAAGAATCTTTGTCATA	C/T	150	0.337	0.447	0.447	0.000	ns
M1	Mdy_045	CATGCAGCCATACATGCCACCTATTCTCCTTGAAGGCGTCCGTCGCTTTTATTGTGATTGTGCAACTTTTTGTAATAACAGTAAAGTCTT[A/C]TGGGGCGTTGATTGCCTTTCAATATCAGTCAGTGCATGAA	A/C	150	0.403	0.513	0.481	-0.067	ns
M1	Mdy_050	CATGCTAACACTGTTACAGCAGACAGAGGGAGAGAATGTGCTTGGTTTTCTAGTGATAATGTCAGTCTGATAAT[A/G]TTACATAGCGCAATCATTGTTGCTGTTTGGTTTTCTAGGCTTTTCTGTAAGAAAAGTTA	A/G	150	0.247	0.360	0.372	0.031	ns
M1	Mdy_056	TGCAGGGGCTCAGGCCTCAGCAGATCCGCTCCCGTAGGAGATGCGCTCAACAGTGGTCCCGGTTCTGCGAATAAAA[C/T]GAATATACGCACGAGATTGGGCAGTGTAGTGGGGGTGATGTTGCGTCAAGAT	C/T	150	0.300	0.400	0.420	0.048	ns
M1	Mdy_067	CATGCTGAACTTAAAGGGGTAATTGCTCAAATTGCCATGAGATTTGCACCTT[A/G]CTTAGTGTCTGTTACGTAATAAAAAAAGAAAGAAAGAAACGACTGATGGTCTATTCCGACCCAGAAAGCAAAATAGATTGA	A/G	150	0.097	0.180	0.175	-0.031	ns
M1	Mdy_068	TGCAGGTTGCCGCGGAAACACACCCCAACAACCAATACAGGACAAGGCCAGGGGCGGAGTAGCCCGTAAATACAAGA[C/T]ATCCAGAGGGGCGATCCCTGACAAGTTACACTGTAAGAAAAGAGTGCATATATG	C/T	150	0.127	0.213	0.221	0.036	ns
M1	Mdy_070	TGCAGGCCCTCCCTCATCCACCTGCCTCCTCCAGGAGCATCAGGCTCCGTGGCTGGCCAGTGTGATCTGTGCAGTA[C/T]CTCTTCTCATAGCCTGTCTGGGCTTACAACCGAGGTTAGAGGGCTAGCT	C/T	150	0.177	0.247	0.291	0.152	ns
M1	Mdy_078	TGCAGGTGTCTTACACTGGGTAATATTTCTAGCAGTAAACATATTAATGTGGAGCCCTGTCAGGCTGTCCCTGCTGCCTCAGTAAACACTTCCAG[C/T]CATAATCAGAATGTAAACCTGGCACAGAGCAGGG	C/T	150	0.077	0.140	0.142	0.011	ns
M1	Mdy_080	TGCAGGATATTTCTATGCTAATACAGTTCATCAGTATGGGCAATGAAGGACGGCTCCAGCATTAGCCAGAAACTGAAC[A/G]TGCTGTTGGAATGTTGGACCATGGACGTTTCTACTTGTACTTTAAAGGGCTAGT	A/G	150	0.133	0.213	0.231	0.077	ns
M1	Mdy_085	TGCAGGAAAGGCGAGCAGGTGGATCCGGCTCTGGGGTGGACCGGGAGTCTCAGTGGTGGAGCGGAGCTCCCTATGCCCGGACAGTACC[C/G]GTGTTGGAGCGGTAAGGCAGGAAGGCCCTGGTAACATTCTC	A/G	150	0.187	0.307	0.304	-0.010	ns
M1	Mdy_086	CATGCACGATGTGACACTTCCACTGCAGGCTTCACTTGAATTTGAAATGGATTTTCTCCACAGACTAGTTATGTTTTAG[A/C]GAAAGAAATCATTGGGCTGATGGTTTTACYTCTTACACTTGCACATCCC	A/C	149	0.117	0.221	0.207	-0.068	ns
M1	Mdy_088	CATGCACCTGAGGGCAGYCTATTATTGGTTATGCAATTTGGATCAATGAACCGAACCCACACCATGC[G/T]TAGTCAGCGTTGACTTTAGTGCATAACAGACTTCCCTTATTAGGCAAAACGTTATTAATCCAAAAAC	G/T	150	0.090	0.180	0.164	-0.099	ns
M1	Mdy_096	TGCAGGCAGACCGGTACACTGGGCGTCGAAACCCAGTACCTTTGGCTGGGAGTCAAACCCCTATAGCCACTGCACCTAACCCT[A/G]CACTGCTTGGTTACCTTACTATATCTTTAGAAAAACAAATGCATGTG	A/G	150	0.053	0.107	0.101	-0.056	ns
M1	Mdy_098	CATGCTCCTTTGCTTAAAGAGAAGCCCATTTCTCCTCACTCGTTGTAAGATACG[C/T]GTTTTGTCTGAAAGTGGTGGCAAGCCCTTTCAAAGTACTTTGTTTTAGGCTGAGACWATAGTTGGGCCAACATAA	C/T	150	0.187	0.280	0.304	0.078	ns
M2	Mdy_002	TGCAGGTAGAGCTCGGCCACGCTGGCCAGGTCCATGTCCAGCGCCCTGCAGCCCGCCACGGCCTCAA[A/C]CCACGTGAGTTCGCGCATCAACAGCTGCACCGTGTGATTGTTGAAGTGGAGGAGCTCCGTCGGAGCC	A/C	150	0.393	0.480	0.477	-0.006	ns
M2	Mdy_012	TGCAGGACCAGGTCAAATTTGAATTATACCTCTGCACTGAGCCGCGTACTAGTAGGTACATCATTGGCTCT[A/C]TCCGGTGCTTGCATGTATTCTCCGCTTCACTGATTCTGAGCTTCRTCTGCCAAATGTTTT	A/C	150	0.350	0.447	0.455	0.018	ns
M2	Mdy_019	CATGCAGCCCCAGCCACAGTCAAGTGGTGGAGACTGGATCCCTCCAGCTGGGGAACTCTCCTCTGAGTGCAGCCACAGCCTGGAGACGAACGCTCC[A/G]TGGAAACGCTTACCTCGTCTGAAATAGAGAGAGAAAT	A/G	150	0.330	0.393	0.442	0.111	ns
M2	Mdy_026	TGCAGGATGGTTGCGACAGCGCAAAGAGAGGAAGAAGACGGTCTCCTCAGCAGCATGCCACGGAGAAGAAGATCAGCAG[C/T]GCCAGCGACTGCATAAACGCCATGGTGGATGGCTCGGAGCTGAAGAAGGTGC	C/T	150	0.423	0.447	0.488	0.085	ns
M2	Mdy_028	TGCAGGCGTCTCTGTTTTGACAGTCCCGGTTAGTTTGAATAAACGCC[A/T]TTTACTGATTTTTGTGTACACATGACATTCTGCTTTGGCACAAGGACAGCGCCCTGAGTCCCGAGTGAAGCTGTGTGTC	A/T	149	0.460	0.477	0.497	0.041	ns
M2	Mdy_030	TGCAGGATGAGGAGATGCTGTGGATTCCAGTTGGACTGGCGGCTTACGCTTCTGTGACAGGGATATGTCATCCATCT[C/A]TCTCGTGGCCACCTCAATGTCGGGCGTTCACACAGGCTGGTGGGTGGAG	A/C	150	0.467	0.453	0.498	0.089	ns
M2	Mdy_037	TGCAGGATGTTGCTTACATTTGTGAGGAATTAGTTTCAATTTTCAATTTTGTGATGTTCTTGGGAAACAAATGAACTGAATTACACAAGAA[C/T]GAAATAATGACCAATAATGATACAGTGGACTTTCTTT	C/T	150	0.297	0.367	0.417	0.121	ns
M2	Mdy_042	TGCAGGTTAAAAACATTGTGCTTACGCAACATGACCATGGTGAATAATTGGTCAAATGATCTGAATTGACTTGTAT[C/T]AGGAATGCCTTGGAGTGCAAAAGTTGCTAAACCAACACATGCTAGCGATGTAT	C/T	150	0.243	0.367	0.368	0.004	ns
M2	Mdy_046	CATGCTCAGCAGGATGCTCATTATCTGCATCTAAAAATATATGTATTCAAATTCAGGGCAGTCGGATTATCTTTGATAAAAAAACCATCA[G/T]TGCTAAAAATGACAMGTGCCTACATGTCAAATGGGAT	G/T	150	0.317	0.420	0.433	0.030	ns

M2	Mdy_048	TGCAGGGTTAAACCATCGTCACAGAAGTGTGATTATTCATTT[C/T]GCTTAATCCCACTATGAAGAATGGAGCCTGATTAATGAACGTAAGGATATTTATTGATTCTGTGTCCAATTGGAAAATCTATTACATTTA	C/T	150	0.447	0.467	0.494	0.056	ns
M2	Mdy_049	TGCAGGCGCTTGTGTACCCGCTAAACATTCAGAGGGGGCCAGCAGGAGCTGCTCCTCCTACCTCCTCGGCTGCCGCCTC[C/T]GACAGGAGCCCTCCTCCTGAGCGCAGGTGACGTGGAAGTAGGAGCGGCACATGC	C/T	150	0.277	0.340	0.400	0.151	ns
M2	Mdy_051	TGCAGGGTAAGAAAATAATGACCTTCAGCCCAAAGCAGATTCCCGGGTTAGATTATCTACTCTGATATTT[C/G]TTTTATTTGTGAGTAAAGTTGACATGGGGTTTTCTCCGGTGCAGCTGTCTGATGCAACACG	C/G	150	0.113	0.213	0.201	-0.061	ns
M2	Mdy_054	TGCAGGTATCGACCCTAATGTGCTCAGACTGGAGCTTGACAGATCTGTGGCACAATAAAGAGTCGACCGAGGTGAGTCAAGATGACGCGAGA[C/G]GGTCAATCATGTCAAGATGTGTTGATTCTCATCCTGCATCAAA	G/T	150	0.190	0.287	0.308	0.069	ns
M2	Mdy_059	TGCAGGACTCCTGCACCAAGCTGCAGACGCTCAACACCCAGCTACAGGTGAGCCACCGCGCTTTACACACAAGCTGCGGCT[A/T]ACTGAAGAGTGTATCGTGGCTGGAACACAGCTAGCACGTAGCTATTACTG	A/T	150	0.250	0.367	0.375	0.022	ns
M2	Mdy_063	TGCAGGAAGCCACCTCCTCAGACTCTTGTGGGAGTTCAGCAGATTCTAGACCAGAGCGGTGCATGACATCTGC[A/G]TCAAAAACCTAGATCTTACGAGCGCCCTAATGCATGTTAATAACATTACTTTATTGTGA	A/G	150	0.240	0.400	0.365	-0.096	ns
M2	Mdy_064	CATGCTAAATGCTTCCCGAGCATTAAATTTCCGATACCTGCGGAACGTGGCACACACATAAT[G/T]CCATGAAATCACCGTACATCCAAGCGATTGAATTTAAAGATTTACGGCAACAGTCCAGTGGGTTTTGTT	G/T	150	0.127	0.240	0.221	-0.085	ns
M2	Mdy_073	CATGCTTAACATAGATGCTTATATACTGCATATGCACACAGTACCGTACATAAATACATATGTGTTACATACAGACACATG[A/C]AGTTTGGAGTGTGAGAGCAGAGCTGGGCCAGGACACAGTAAAGTGGTCAGAGTC	A/C	150	0.170	0.247	0.282	0.126	ns
M2	Mdy_074	TGCAGGTGAGTGCAGCTCATGGGTGAAAGGCCACAGCACCCTGAACCTCAGCTACACGGG[C/T]GTCCCTGAGACCCGTTGCTTATCTTTGGGACAGTCGTTTGGAAAGAACTAGAGTAAAGGAACTGTTTGG	C/T	150	0.143	0.260	0.246	-0.059	ns
M2	Mdy_077	CATGCCTGAAACCCCGAAAAACCCAGGTATAAATTAGGCTTT[C/T]GATGTTTTATTGATTCAAACCAATGTGACGAGGGCCAACAGCATCCATTGTTCCCTCTGTAAACGACCTCCTAATGAACCCACAGCC	C/T	150	0.263	0.353	0.388	0.089	ns
M2	Mdy_087	CATGCCTGTATATGTAATTAGGTCATCATTTATTTAGTTTTATTTCACTGGCATATTTACTCAGTCCCTTAAGGTGGTTTTCTTAGGGAAGG[C/G]CCACTGTAGTGAAGAAGTTCGCTTTCCACAGCTAGAA	A/G	150	0.113	0.227	0.201	-0.128	ns
M2	Mdy_094	CATGCAGAGTCAGCTAGAAATACAATACATGCCACAGATGATTTGCATTGCA[C/T]TGCCAGAGTGTCTTATGATGGACAATTAGCAAGGTTTGGGAAGTTTAGTTWAAAAAAGGTTATATAACATCCATGT	C/T	150	0.743	0.353	0.382	0.074	ns
M2	Mdy_099	CATGCAGACCCAGCTGTAAGGAGCAGTTTGCAGTGCATGCTGGG[A/C]TTGTAGTGCCGTGCATCGCTGGCGATGCAGGCCAAAATTGATTGAAAACCTCAAATGATAGATTGGATGGAATTGGTCCAAGTCCGGGA	A/C	150	0.127	0.213	0.221	0.036	ns
M2	Mdy_101	TGCAGGAGCCCTTTCACCCGCTCAACTCCTGGCTAACAGGGGCCGAGAAAACAGAACGGTCCCTACTTCAACCCG[C/G]TGGATTACACTCACATCAACCAACATTAAMATATAGAGAAGAAACCAACCAAT	A/G	150	0.253	0.333	0.378	0.119	ns
M3	Mdy_004	TGCAGGAAATGATTTTTGTTGGATGCATCATGTTTTGCCAAAAAGGACACACCACAAGAGATGTGTGCGCC[C/T]GCAACCATACTAAAACTTAAATTTAAAAATGCCAACGTCCTGTTTCAATTAGCGGTCTG	C/T	150	0.380	0.467	0.471	0.010	ns
M3	Mdy_006	TGCAGGGGACCCATCCAATCAACTCCAGTTCACAGGTTAGTCTCCCAACACAGCCGTGTTCTGGGAAAG[A/C]AACACAAACATTAACWTGATGCATAACAATGGGTTGGGACACACAAGAGACTTAGTTGGCAC	A/C	150	0.483	0.553	0.499	-0.108	ns
M3	Mdy_010	TGCAGGTCAAATGTTGCTTCTTATAAAAAATKGGTGTGTATGTATGTGTGGCTTTCATAGGTCTGTTT[A/G]ATTTTTGTTCCAAAAACTACTTTAGGAAGTTAATACAGCGATTATTACGAGTTTGGTCGTTATTTATG	A/G	150	0.477	0.447	0.499	0.105	ns
M3	Mdy_018	TGCAGGCTACCCTGTAGGCATTCTTGTAGTAAAGTGTCCAACACCTAGATGACC[A/G]TGGCACATCTCAAAAATCCTGGTACGTCCTTAAAAAGTAAACATGTTCAACTCATTACTTATGTTGCTTGGCTTAGGTGT	A/G	150	0.433	0.520	0.491	-0.059	ns
M3	Mdy_021	CATGCTGAATTACAGTATTGTTGAAAGGTCTGTTATTTGATTTTTGTGTTGGTTGAAGGG[C/T]TCAATTAAMTTTTGATTAATAAGTGTATCAGTAAACTAAATAGGATGTGGTGCCTTGTCTGCTTCTTTGAA	C/T	149	0.322	0.644	0.437	-0.475	***
M3	Mdy_024	TGCAGGCTGTGTACCTAAATGAACAAAAATAAATCCTCCAGTCCAGGAGATTTGTGCRGGTCTGTTGATGATAGAATGTTCTCGTGTATATT[A/G]GTGATGATGACCCATGTGTGTGACACATTGTCACAATATT	A/G	150	0.207	0.307	0.328	0.065	ns
M3	Mdy_038	TGCAGGCTGTGGGATCCCTCGGGGTCCAAACGCTCTCTCTCACAGACC[C/T]GCGGTCTGAGTCAGCGCCGACGCCGAGGACCAGCAGATGAAGTCTGAAGTGGGCGGTGGCATACTTGTGATTTGTGAAAATGT	C/T	150	0.480	0.587	0.499	-0.175	*
M3	Mdy_039	TGCAGGGGAATCACTGCTGACTGACGAGAGATAGGAAGTCCAGGAGATGG[C/G]GGAGAGGGAAAAGGACAGGAGAGAGGTGGAATTAAGACGTATAAGATGGCCGGTGGGAGATAGGTTAAGACAATTATTATA	C/G	150	0.307	0.440	0.425	-0.035	ns
M3	Mdy_041	TGCAGGGACACAGCAGAGACCTTATGCTCTGGAAGGGCACTGCAGACGTGCGG[C/T]GTTTGAGTTTAAAGGTGCAGTACGTAACGTTGACCGGAGGTTCAATACGGTCTGCAGACGTGCGGTGTTTGAATTTAAA	C/T	150	0.480	0.947	0.499	-0.896	***
M3	Mdy_047	CATGCTAAACGCTTTTCATGGCTGTGCTGTTGTCAAAATGGTGGGTTATTGTTTGGTCCATGTT[C/T]ATCTCCTTATAACATATCTGTCTTATCTGTGTTGGCAGCTGGACTTCTCTGATATGCCATGTGCGCGCT	A/T	150	0.433	0.480	0.491	0.023	ns
M3	Mdy_052	TGCAGGTAGGATATTATAGAGCTGGGTAATCATTGTAAGTCTTTCAATAGGAAGTGGAAAGGGGTTTGTGGATATGTGGATCTTGAAGATAAAGAGG[A/G]ACGAATCGTACTGGACAATGCAACATCAGACGCC	A/G	150	0.210	0.327	0.332	0.015	ns
M3	Mdy_058	TGCAGGTGGGTTGGGACGTTGTTGGTGGTGGTGGTGGGTTGTTGGGTTGTGTGAGGAACACTT[A/G]GGCAGTGCATTCTAATCTGCCGAGAAATAAGATGTGTAATTTACTTTAAAGCTTTTGAC	A/G	150	0.137	0.233	0.236	0.011	ns
M3	Mdy_060	TGCAGGTAAAGATACAAGTGCACCAATTGAAGGCAAAAATAATTTTTGTGTCATGAAATTAACCACATCTCAGTATT[C/T]CTTGTTCATTGGTTACCATAGATCTTTTACTGTGACAAACTCTATCACAGCCCAT	C/T	150	0.127	0.213	0.221	0.036	ns
M3	Mdy_061	TGCAGGTACTCACACTATGGGTTAGCACTGCGGCTAGCGCTGTTGCTAACCACGTCTAGGTTTTAAACCGACTGTT[C/T]GTGAGTTTGTATGTTCTCCGTGTTGATGTTGTTGATCTCTCCYATACCAAAGACATACA	C/T	150	0.207	0.293	0.328	0.105	ns
M3	Mdy_069	CATGCTTCAAAACAACAAATATCCCTCCTGATTGAAACCAAGTTCAACGCTCCATACCAAACCAACTCAATCGGGCAAAACATTGACCGCTAG[A/G]GGGGGGGGGAAACAGGAAACCCCGCGCTGAAC	A/G	150	0.183	0.287	0.299	0.043	ns
M3	Mdy_071	TGCAGGTCCGTCAGTGGCCCCACTGGATCTTAAACCTCTAAGGCACTCCATTTCCACACGGACTAAACCGCTA[C/T]GAGCGGTTGTTATTTGCGGGGTAATACCCACCGCTTAAAGCAGGTGACCTTCAG	C/T	150	0.100	0.200	0.180	-0.111	ns
M3	Mdy_075	TGCAGGTTAAAGACCGCATTCTAAAAGATAATTTGTACCCTGAGTACAGAGATACAATAAGATGAAAG[G/T]ATACCATCTACACCAACAAGAAAATCCAAAATGTTAACCGAATTCACGGTCCAAATCTCA	G/T	150	0.130	0.247	0.226	-0.090	ns
M3	Mdy_081	CATGCAAGCTCCTTTCTTCTGTGCTGACTTTGGTGGTGGTGGTGGTGGGTTGTTGGGTTGTGTGAGGAACACTT[A/G]GGCAGTGCATTCTAATCTGCCGAGAAATAAGATGTGTAATTTACTTTAAAGCTTTTGAC	A/T	149	0.114	0.228	0.202	-0.129	ns
M3	Mdy_083	CATGCAGGCAGATAGAAAGTGAACAAAAGAGTCTGTTCACTGCTTTTGTGTTCTGAGAGACT[C/G]GTGGATGATGATTCATAACATCACAAATGCTAATACCAAAAAGAGAGCTTGTCCCCACAATCTTAAAAAC	C/G	150	0.107	0.187	0.191	0.021	ns
M3	Mdy_084	TGCAGGTACCAGCCCTCCTGGACCCCTGACACCTCAATCATTCTCAGACCACCGTACATT[C/T]GTATCGCATTGTTGAGAAAGCCCTCCAGGTTGCTGAGCCTGAGAACGGCTGCGTATTGCTRGCCG	C/T	150	0.100	0.187	0.180	-0.037	ns
M3	Mdy_089	CATGCTGCAGTGTACGCAACGACCCACGCGCTGAATCAGCAGCCAC[C/T]GCCAGACGTTATGGAGGCTTAGCGGACACAACACATGGTCCAATCGTGACAACACTACTGGGTTCCAAAAAACGAAATGAGGT	C/T	150	0.170	0.300	0.282	-0.063	ns
M3	Mdy_092	CATGCATTTCACTTGTGTAAGACAAAACCTAAAGGCAGAAAGACCCACGAACAACAGCAACTGAAGAC[A/C]RCTGCAGTAAAGCCCTGGCAAGCATCACAAAGGAGGAAACCGAGCATTGGTGTGATGCCATGGT	A/C	150	0.120	0.200	0.211	0.053	ns