

Table: A profile of 172 microsatellite markers developed for the musk shrew, *Suncus murinus*.

Locus name ^a	Clone ID	Clone size (bp)	Accession number	Primer pair sequence (5' - 3') ^b	Tandem repeat array ^b	T _A ^c	Product size (bp) ^d
<i>NGA8</i>	1-4-2	404	AB276109	F: tgagatgccacttaggggattacc R: ccgatgggcgaggacggcggtcc	(TG) ₁₉	50.0	386
<i>NGA9</i>	1A3	295	AB277375	F: cctgtgtgtacgtgtgtaggac R: acctcaccacttgcggacactc	(TG) ₅	61.6	256
<i>NGA10</i>	1A11	244	AB277376	F: cgccagcctgattctgggtccaac R: tgaagtgacaatgcgtgtggtacc	(CT) ₅ (TC) ₇ (TG) ₃ (GT) ₆	59.3	174
<i>NGA11</i>	1B3	435	AB277377	F: agccaatatgatgttctccagg R: cctatgacatggactctgccggtg	(CA) ₈	59.7	256
<i>NGA12</i>	1B5	691	AB277378	F: acatggtcgcattcacagacac R: tgctggtgccagaaggtcagcagg	(CA) ₄ (TA) ₄ (CA) ₄	59.7	331
<i>NGA13</i>	1C8	350	AB277379	F: tgttgctgccttggctgtgtg R: agaatttccatctgcaaggtgc	(GT) ₅	59.4	181
<i>NGA14</i>	1C12	350	AB277380	F: acagaagcagcaagcaggccag R: agaacttgaacatcaggtaggctg	(CA) ₁₇	58.3	310
<i>NGA15</i>	1D1	263	AB277381	F: atttctcccactcagtgggagac R: tgagctctccatggtgtaggacc	(CA) ₅	59.8	259
<i>NGA16</i>	1D4	433	AB277382	F: cccacaggaaggctagcagtc R: actgctagacagggtgtcatg	(TACA) ₉	60.5	355
<i>NGA17</i>	1H12	364	AB277383	F: ccatgcaggctgaacctggga R: tgaataagcattgagcatcccag	(CTT) ₃ (CTGA) ₃	60.8	251
<i>NGA18</i>	5A2	158	AB277384	F: tggaaaaggcgaaggacctgggtg R: tgggcttgatcctggctcccaagg	(TC) ₁₅	61.3	136
<i>NGA19</i>	5C5	277	AB277385	F: ccttgttctgtgttcaggagcca R: acccctgagcatcaccagttgtgg	(CA) ₂₁	59.4	238
<i>NGA20</i>	5D7	163	AB277386	F: aggtcatttcaggatctgacc R: acttgctgctgacacgtgtggaca	(TG) ₁₃	58.5	117
<i>NGA21</i>	5H5	399	AB277387	F: tggaaacaaccagatgctgac R: tcagaactggttgctgcatgc	(GA) ₅ A(AG) ₇ (GA) ₆ (AG) ₆	59.4	310

Table continued

Locus name ^a	Clone ID	Clone size (bp)	Accession number	Primer pair sequence (5' - 3') ^b	Tandem repeat array ^b	T _A ^c	Product size (bp) ^d
<i>NGA22</i>	5H7	355	AB277388	F: tcatacattcgcaccatcgggac R: actgctggtgggaatgccacatgg	(TC) ₁₀	59.5	266
<i>NGA23</i>	6A2	415	AB277389	F: acagtagtgcaagccagtgtc R: tctgggaccattaggcgaccct	(GA) ₇	59.4	376
<u><i>NGA24</i></u>	6A5	260	AB277390	F: tcaaccaggatctcaccatggggt R: agactttgagtcaaccccaggct	(GT) ₁₅	60.0	99
<i>NGA25</i>	6A12	557	AB277391	F: ccatggagagatttctgagtgcag R: gaatccccacctttgggcctgatc	(TG) ₁₆	58.6	329
<i>NGA26</i>	12A8	639	AB277392	F: ccacatctggcagggctcaga R: agacatagtcataccagcctggac	(TC) ₁₉	61.6	570
<i>NGA27</i>	1A6	252	AB277393	F: ccaagcaagtgtcactgcccgt R: tctgcaaaccaacacgctcacac	(GT) ₅	62.4	242
<i>NGA28</i>	2A6	193	AB277394	F: actgctacagacacgtgtgctg R: accggcgtgcatgctggtgc	(AC) ₄ (CA) ₆	61.0	193
<i>NGA29</i>	2B1	186	AB277395	F: ccttcacgctcaaaccaatgacg R: tctcctttaaccgggaggcagt	(TC) ₅	58.5	145
<i>NGA30</i>	6B6	580	AB277396	F: tgaatcgggggaattccctcaagc R: ggctcttaggtctcagcctccagg	(ATT) ₆	61.9	373
<u><i>NGA31</i></u>	6B9	330	AB277397	F: aggttgcaactggtgaagtggagg R: tgaggaggcagtgctggaagag	(AC) ₂₃	61.6	160
<i>NGA32</i>	6B10	468	AB277398	F: agttaatcctgacagtgccggga R: caatgtccttatgctgccagtagg	(CA) ₁₃	60.7	339
<u><i>NGA33</i></u>	6B12	510	AB277399	F: acaaaacaagttctcaggtgccctg R: gctttgcacgtgtgaggctgtgga	(TC) ₂₃	59.4	179
<u><i>NGA34</i></u>	6C9	276	AB277400	F: agaagaccatatgtggtgccag R: acgatcccctggacctgccatgag	(TG) ₂₃	60.7	203
<i>NGA35</i>	12A11	349	AB277401	F: gccgtcagtcacagcagcac R: agaagcacctccttgctcctcatg	(CA) ₂₃	63.4	339

Table continued

Locus name ^a	Clone ID	Clone size (bp)	Accession number	Primer pair sequence (5' - 3') ^b	Tandem repeat array ^b	T _A ^c	Product size (bp) ^d
<i>NGA36</i>	2A2	186	AB277402	F: gctcaaaccaatgacgagagcctc R: tcctccttaaccgggaggcagt	(TC) ₆	58.6	137
<i>NGA37</i>	5A6	323	AB277403	F: ggttctggaaggcacctccgca R: acaagcatgagattgccacactgg	(TC) ₇	61.2	236
<i>NGA38</i>	3-2-1	279	AB277404	F: tgactccttgagtctgtgtgtgg R: agtagtgccttagtccttgggctc	(AC) ₂₄	59.1	193
<i>NGA39</i>	3-2-2	229	AB277405	F: tgtgtgcaaatcccaatgccagg R: tggctctctgaggaccagacag	(CA) ₂₁	60.2	146
<i>NGA40</i>	3-3-1	342	AB277406	F: ggccaaagcactaagcctatgc R: ctccagtccttagaggaaccagc	(CA) ₄ T(AC) ₁₈	60.9	328
<i>NGA41</i>	I-A02	330	AB277407	F: actacaagcctcaggccagtctg R: agagctgtaaggactgagcactgc	(TC) ₃₃	61.1	282
<i>NGA42</i>	I-B06	201	AB277408	F: acccttcccatcagtgggtctc R: tggaggaactaacaggctaggcac	(TC) ₃₀	60.5	166
<i>NGA43</i>	I-B10	238	AB277409	F: tggctccccgaattatgggcatg R: tggctaaagtcagaggccagactc	(GT) ₂₁	61.7	152
<i>NGA44</i>	I-C03	146	AB277410	F: gcagaagttattgcctgaagcag R: actggtcagacataccagaggcct	(TC) ₈	58.7	104
<i>NGA45</i>	1-C04	206	AB277411	F: agtcttgagatgcagcagaagg R: agaagttctggatagggctgagg	(TC) ₇	59.3	161
<i>NGA46</i>	I-D05	187	AB277412	F: agtgtttaagtgagccctggtc R: agaagctcaccttcatgcgcacag	(TG) ₂₄	58.5	119
<i>NGA47</i>	I-D10	380	AB277413	F: cgattgccacaagggcggagagtg R: accagtgtacatttctgccacca	(GA) ₄ (GT) ₂ (GA) ₄	60.1	244
<i>NGA48</i>	I-F01	240	AB277414	F: tcatgaggtgagctggaagtcc R: acatggaatcagccatgctgag	(TC) ₆	58.4	138
<i>NGA49</i>	I-G02	342	AB277415	F: acagcaggeccaggctccatc R: agcaatcacaagatgccaaccac	(TG) ₇	62.1	296

Table continued

Locus name ^a	Clone ID	Clone size (bp)	Accession number	Primer pair sequence (5' - 3') ^b	Tandem repeat array ^b	T _A ^c	Product size (bp) ^d
<i>NGA50</i>	I-G03	284	AB277416	F: acataccccagcatgtccacagac R: tcttgccctgccttagggaagtgg	(CA) ₇	61.0	182
<i>NGA51</i>	I-H03	218	AB277417	F: cccttgagcacagagccaaaggga R: actgcctattgatttcttgggggtg	(CT) ₅	57.5	098
<i>NGA52</i>	I-H09	575	AB277418	F: ccctgtcattgggtagtggct R: tcagccctctgtacgagtcagg	(TC) ₁₀	60.2	172
<i>NGA53</i>	II-B05	180	AB277419	F: cagcccacaagataagggtcttcc R: tctcagtgcagtagtaggtgcagc	(CA) ₇ (AC) ₆ A ₂ (CA) ₅	59.3	160
<i>NGA54</i>	II-C06	245	AB277420	F: cctgggtttgaaattaggagcctc R: ccaatacacatttctctggcaccag	(GA) ₇ (GATA) ₃ (GA) ₁₇	60.6	202
<i>NGA55</i>	II-C07	217	AB277421	F: aggcattgtcattgccatgtgagc R: attcgtccctcagcagtcagg	(CT) ₂₂	61.9	182
<i>NGA56</i>	II-C11	271	AB277422	F: acatcagagagatcctgggggtc R: agcatcctctggaaggtcagcagg	(GA) ₃₁	62.2	266
<i>NGA57</i>	II-D05	373	AB277423	F: caatggcctgaattgtgcgtgtg R: accccagtttgaacctgagcac	(GA) ₅ A ₂ (GA) ₈ A(GA) ₅	59.1	126
<i>NGA58</i>	II-E06	240	AB277424	F: tcaccactcttgtggtgagc R: acatggaatcagccatgctgag	(TC) ₆	58.8	160
<i>NGA59</i>	II-E09	462	AB277425	F: actgggttcaatccctggcatcc R: tgatccctgagcacaagcaggag	(TG) ₁₄ (AG) ₁₇	60.7	386
<i>NGA60</i>	II-F02	534	AB277426	F: gtgatttctaagcacagagccagg R: tgeatcagctttgagagtgcctg	T ₃ (CT) ₃ (TC) ₂₂ T ₃	59.6	407
<i>NGA61</i>	II-F04	264	AB277427	F: agctaggagtaacctgagcacc R: ttcacccatctgcctctggggca	(GA) ₄₃	62.1	196
<i>NGA62</i>	II-F11	329	AB277428	F: acaacgccctcaccagggea R: actgtcctgtctggggagcaggag	(TC) ₁₀ ...(TC) ₆ ...(CA) ₂₀	63.7	292
<i>NGA63</i>	II-G03	586	AB277429	F: agtgaatccatctgggcctaggct R: caggaaggaataaggggccacctg	(TC) ₂₄	60.2	543

Table continued

Locus name ^a	Clone ID	Clone size (bp)	Accession number	Primer pair sequence (5' - 3') ^b	Tandem repeat array ^b	T _A ^c	Product size (bp) ^d
<i>NGA64</i>	II-H02	226	AB277430	F: tcacccctgactctggaacagac R: agtgcacacatggaggagagtg	(CT) ₄ T(TC) ₇	58.2	111
<i>NGA65</i>	II-H10	334	AB277431	F: agcactgaactaggagtagcctc R: ggctagttagccttcaggctgtgg	(TC) ₉	59.8	280
<i>NGA66</i>	III-A02	485	AB277432	F: cattccctccaccagccaactgc R: tgaatagtctgtggggcagg	A ₂ (CA) ₂₁ A ₂	61.1	307
<i>NGA67</i>	III-C11	209	AB277433	F: tcatgcgacatgaagcttgacacc R: tgcctttgacaggcattctgg	(GA) ₁₆	58.5	135
<i>NGA68</i>	III-D01	283	AB277434	F: atctgaggccttgacagatacc R: cctgaatggagaaatggcctgcac	(GA) ₂₀	57.3	233
<i>NGA69</i>	III-D09	511	AB277595	F: cagagagagattccaggcaggtgg R: cctcagaggactcactgtggcagc	(GT) ₇ AT(GT) ₂ (GTAT) ₆	61.4	223
<i>NGA71</i>	III-E03	409	AB277436	F: agcccaatagtgtccagcacac R: tctgcccaagaatgcctttggggac	(CT) ₉	59.7	372
<i>NGA72</i>	III-E07	379	AB277437	F: ttcccaagcttacctgggag R: agagcactcatctccccacagagg	T ₃ (GT) ₆ T ₃	60.6	286
<i>NGA73</i>	III-E12	375	AB277438	F: cctctcttctgtggaagggtgtgc R: tgtgttgcatggcgtggtgtg	(AC) ₅	62.3	287
<i>NGA74</i>	III-H02	327	AB277439	F: atgtagacgctgagagccctc R: tgggagtatcactgagccctctgc	(TC) ₅ C ₂ (CT) ₃	60.9	224
<i>NGA75</i>	IV-B05	231	AB277440	F: tcaactcaacacaagtgtggacac R: tgcctcaaccctagagcaggggtg	(CT) ₆ TTCTT(TC) ₁₁	59.8	169
<i>NGA76</i>	IV-C10	479	AB277441	F: gagggggaggtacaatttcc R: ccctgcaaataggagcaaga	(CT) ₃₂	55.0	239
<i>NGA77</i>	IV-C11	595	AB277442	F: tgcactactgcactcctcaggcgt R: acaatatccttcaccagtgcac	(GA) ₁₉	59.6	472
<i>NGA78</i>	IV-D01	418	AB277443	F: acacgcagctgcagcacatcctg R: aggggtggcttgcttcagtgc	(TG) ₂₂	61.6	381

Table continued

Locus name ^a	Clone ID	Clone size (bp)	Accession number	Primer pair sequence (5' - 3') ^b	Tandem repeat array ^b	T _A ^c	Product size (bp) ^d
<i>NGA79</i>	IV-D04	154	AB277444	F: tccagagcccctgagaactgc R: aggttgactcaaaggaccatgctc	(CA) ₂₉	54.5	146
<i>NGA80</i>	IV-D05	233	AB277445	F: ccagaccaggtgggagtcgtg R: gttaggtcctgcctccagctccag	G ₂ (CT) ₉ G ₂	63.7	161
<i>NGA81</i>	IV-D10	261	AB277446	F: accaattccaataaccaggaggct R: tcaagtcagacgtgtggcccaac	(GA) ₂₇	59.5	173
<i>NGA82</i>	IV-E04	400	AB277447	F: acctctatctcggatgggcac R: ttgcagacatccagctgggcggag	(CA) ₂₃	60.7	325
<i>NGA83</i>	IV-E09	413	AB277448	F: caatgaaggctcccagegcacc R: gggtggctctgtatcctgggcac	(GA) ₂₉	62.1	396
<i>NGA84</i>	IV-G05	322	AB277449	F: agctcagctgttgatggatgtgc R: aggaacatggctcctgtacctgc	(AG) ₄ (GA) ₄ (AG) ₄	62.0	288
<i>NGA85</i>	IV-G07	241	AB277450	F: tgtagaattgctgctggacctg R: tgatctactgcatgggactggtc	C ₂ (CT) ₇ G ₄	59.4	213
<i>NGA86</i>	IV-H08	253	AB277451	F: tcaacccccttaggtctgggct R: agcagtccccagcatgaagcctac	(CACAAA) ₃ (CA) ₇ A ₉	58.6	246
<i>NGA87</i>	V-A07	503	AB277452	F: tcacagtctctggaccattgagg R: tggcattgttactcagtctgacc	(GA) ₄₅	57.1	208
<i>NGA88</i>	V-B12	216	AB277453	F: accatacccagggtgctcaggac R: aggcctagctagcagaatcac	(AC) ₆	60.0	210
<i>NGA89</i>	V-C01	207	AB277454	F: tgttggagcaggaaggtagtcct R: agagcaggagctctgggccacatc	(CA) ₂₁	61.5	183
<i>NGA90</i>	V-C04	193	AB277455	F: ccagtttgaagtctgctactgtgg R: ggctggaccagagataaagcctgc	(GA) ₄₁	60.7	141
<i>NGA91</i>	V-D05	180	AB277456	F: ccagcctgtactggctagctga R: cctcacctggaccacactgc	(CACT) ₁₀	61.2	180
<i>NGA92</i>	V-D08	503	AB277457	F: agatacaatgtttgtcccagcag R: tgaagacatacccgggtgggggga	(TC) ₅ T ₄ (CT) ₂₃	60.9	498

Table continued

Locus name ^a	Clone ID	Clone size (bp)	Accession number	Primer pair sequence (5' - 3') ^b	Tandem repeat array ^b	T _A ^c	Product size (bp) ^d
<u>NGA93</u>	V-E09	197	AB277458	F: tctctcagaaaccctgcctgcag R: tggggtctcatgaccaccaagg	T ₃ (CT) ₁₀ (TC) ₇	61.7	157
<u>NGA94</u>	V-E10	380	AB277459	F: cctcatccagccagatgactgagc R: atatgtgggaactgccacccac	(GT) ₁₄	62.5	346
<u>NGA95</u>	V-F01	274	AB277460	F: tcctgggtgctatggtccaagc R: tgggagcccaaagccaggggaag	G ₃ (GA) ₄ (AG) ₃ G ₃	63.6	213
<u>NGA96</u>	V-F05	177	AB277461	F: cctcagaggtaaatcctggtcac R: acccagacctatcacggtcaatgc	(GT) ₁₈	60.1	166
<u>NGA97</u>	V-G01	312	AB277462	F: ccagttgtcccgcgagccacc R: aaacgacacagtgccagggcggt	(AC) ₆ C ₃ ACTA(CA) ₆	62.1	308
<u>NGA98</u>	V-G09	440	AB277463	F: acttgggcaaatgcaaggtcag R: tegtactctgagtgtgagcctgg	(TG) ₇ (AG) ₁₀	59.7	398
<u>NGA99</u>	V-H08	441	AB277464	F: tgctgctctatgccaaccctc R: tcagggaccactactgcagagtgg	(TCTCTG) ₇ (TC) ₄₅	63.3	276
<u>NGA100</u>	VI-B08	326	AB277465	F: gcccttgacagatcaaccaggct R: gcttggagaatatccgatgtgcag	(GA) ₂₁	59.1	196
<u>NGA101</u>	VI-B12	369	AB277466	F: acagagacagagatatgggctgc R: cacagctggagttgttgcgtctc	(GA) ₄₆	62.6	264
<u>NGA102</u>	VI-C04	310	AB277467	F: tgtcctgaaatctgggagcagg R: tgatcgacagcatcagcaagatgc	(GA) ₃₅	60.4	193
<u>NGA103</u>	VI-C05	221	AB277468	F: agctagctcttaggctgagag R: agcagaagagctggggacactgc	(GA) ₂₈	60.9	211
<u>NGA104</u>	VI-D02	483	AB277496	F: aactgtgaatctctggggtcg R: acgcagactcacacagaggctcac	(GT) ₁₇	60.7	363
<u>NGA105</u>	VI-D05	205	AB277469	F: acacagtgtcccagagctgt R: agtaactctgagcacctgcag	(TC) ₃₈ A ₄	58.6	164
<u>NGA106</u>	VI-D08	444	AB277470	F: agaccatgtactctcagccac R: tgtgccaggcaggtcatggtgg	(TC) ₁₀ (CT) ₅	59.5	351

Table continued

Locus name ^a	Clone ID	Clone size (bp)	Accession number	Primer pair sequence (5' - 3') ^b	Tandem repeat array ^b	T _A ^c	Product size (bp) ^d
<i>NGA107</i>	VI-D11	561	AB277471	F: tgatctcagttgaggatgccag R: gctcagcagtgctggggcttactc	(TC) ₄₇	60.2	429
<i>NGA108</i>	VI-D12	579	AB277472	F: ttcgccagcctgcctctgtag R: tcaagtgaatagcctgagacc	(TCTG) ₁₁ (TC) ₁₁ (AC) ₁₇	58.7	349
<i>NGA109</i>	VI-E01	520	AB277473	F: aggaaggactgaagtgacggatgg R: tccaggactcagatatccaccagg	(TG) ₁₀	61.3	471
<i>NGA110</i>	VI-E02	343	AB277474	F: acctgtactctctgcctcgagc R: atcaatgcgcgccctgtgtgcagc	(GA) ₃₁ G(GA) ₁₁	62.0	317
<i>NGA111</i>	VI-E05	301	AB277475	F: cccgagatgittggtgctgggcga R: tgagttggcattggagggcgtagg	(GA) ₂₂ A ₂	62.0	256
<i>NGA112</i>	VI-E10	284	AB277476	F: ccaatgaaggctcccagcgcga R: agctaggagtgcacccaggacc	(AG) ₅₄	64.2	276
<i>NGA113</i>	VI-F08	187	AB277477	F: acctaaaactccccagggagac R: cctgaggtctgtgacaggaccag	(TG) ₈ (GT) ₃	61.1	145
<i>NGA114</i>	VI-F12	436	AB277478	F: tcaactgactcctaaagctgggggt R: cagtgccccatgtactgtgggcac	(TC) ₃₂ C ₃ (TC) ₁₁	62.3	282
<i>NGA115</i>	VI-G04	382	AB277479	F: ccatgtcacagaaaagcagctgag R: agcacattggatgcagtgctc	(GT) ₅ A(TG) ₈	59.7	354
<i>NGA116</i>	VI-H02	335	AB277480	F: tctggcagattctagccaggag R: agagccaggaataaccctgagcag	(CA) ₂₆	58.8	252
<i>NGA117</i>	VI-H10	352	AB277481	F: ggctggaggttgtgtaaacccca R: teggctgttcaccaaccctgtgg	(CT) ₉ (CCCT) ₂	62.1	313
<i>NGA118</i>	VI-H12	455	AB277482	F: tgcaagagcgcacctagcagcctgg R: acacttgggaagcaggacctctc	(GA) ₁₀₈	61.3	416
<i>NGA119</i>	VII-A08	448	AB277483	F: tccccctgattgcctctgtggcag R: gcttgccctgaaatagcaggagtg	(TC) ₂₇	59.9	286
<i>NGA120</i>	VII-B02	194	AB277484	F: acaccagtggtactctgggggtg R: tgtcccttgagttagaccttcagg	C ₂ (TC) ₁₀ (CT) ₁₄ G ₃	61.1	138

Table continued

Locus name ^a	Clone ID	Clone size (bp)	Accession number	Primer pair sequence (5' - 3') ^b	Tandem repeat array ^b	T _A ^c	Product size (bp) ^d
<i>NGA170</i>	VII-B04	315	AB277485	F: gtttgctcaaagtctctgggcag R: tgtgctattgtagagcagtc	(GT) ₈	59.2	249
<i>NGA121</i>	VII-B05	297	AB277486	F: agcatggaggtaagggtgttgc R: cctggatgtcagggtcggggagac	(AC) ₁₄	61.8	287
<i>NGA122</i>	VII-B06	384	AB277487	F: tcctcccgtgtgtgtgtgtg R: tgggtctgaatgctgaggctttgc	(TG) ₂₃	61.3	263
<i>NGA123</i>	VII-B07	367	AB277488	F: aggctgatcatgggactagggagg R: tctcatagcaagacggactttgg	(GA) ₂₆	60.6	268
<i>NGA124</i>	VII-B09	328	AB277489	F: tcctccacctgttcccagcatgc R: agcaggatcaattcagggtctgg	(TC) ₆ C ₃ A(TC) ₅	60.3	300
<i>NGA125</i>	VII-B11	344	AB277490	F: agtttctccaccgctcccacag R: tgcagtcaggagtaacttctgagc	(CA) ₁₆	60.7	293
<i>NGA126</i>	VII-C01	393	AB277491	F: tgaggcttccacagtgtagctcc R: ccagatctctgagcactgctgc	(CT) ₂₁	59.2	337
<u><i>NGA127</i></u>	VII-C02	393	AB277492	F: tgatgacctggggctctggtc R: agctagtgatagagccagagggac	(TC) ₈ TGA(TC) ₈	61.7	259
<i>NGA128</i>	VII-C03	431	AB277493	F: agcacaataactctggaggcttc R: agccggcacttggccagatttgc	G ₃ (GA) ₅ A ₈ GAAG ₇	60.1	212
<i>NGA129</i>	VII-C04	137	AB277494	F: accacactccagttgtaggggtg R: aggaagagtccccaacaccctc	(GA) ₃₀	60.8	130
<u><i>NGA130</i></u>	VII-C07	331	AB277497	F: cgggagaaggtcagaggcagagca R: gtaaccctgagcatagccgggtg	(TC) ₂₀	62.7	187
<u><i>NGA131</i></u>	VII-D01	560	AB277498	F: gactcttaatcaccagcctgatg R: agtggattccagccctgatgc	(TC) ₅ (CT) ₄ T(TC) ₂₅	58.8	285
<i>NGA132</i>	VII-G05	205	AB277499	F: acacagtgtcccagagctgt R: gagtaactctgagcacctgc	(TC) ₃₈	58.4	165
<i>NGA133</i>	VII-H03	461	AB277500	F: agatattgcacaagccacctgc R: tcagaaatcacattccctgagctg	G ₄ T ₂ (TC) ₉	57.8	250

Table continued

Locus name ^a	Clone ID	Clone size (bp)	Accession number	Primer pair sequence (5' - 3') ^b	Tandem repeat array ^b	T _A ^c	Product size (bp) ^d
<i>NGA134</i>	VII-H10	314	AB277501	F: tgcgagagtgtgtgagcgcgtg R: tcagatgctcaagtacagctgg	(GT) ₅ A(TG) ₃	57.2	160
<u><i>NGA135</i></u>	VIII-A05	553	AB277502	F: gttgagagggttggcgggagt R: actagaaggtgcatcgaggaccac	(GT) ₂₅	61.4	256
<i>NGA136</i>	VIII-A12	242	AB277503	F: ccatcgtcttcttggtctggatgc R: tgacagcacctcctactggcagg	(TC) ₂₂	62.5	232
<i>NGA137</i>	VIII-B12	382	AB277504	F: catgtcacagaaaagcagctgagc R: tggacttgcatccccgactcac	(GT) ₅ A(TG) ₈	60.0	230
<u><i>NGA138</i></u>	VIII-C02	368	AB277505	F: gaaaggtctgctacccacctcag R: tgtagccaaattgacacaacggag	(AC) ₁₇	60.3	232
<i>NGA139</i>	VIII-C07	345	AB277506	F: accactaagaaccagggtcagc R: agacacgtgactgctgagctc	(CT) ₂₆ (CA) ₁₄	60.4	257
<i>NGA140</i>	VIII-D02	263	AB277507	F: cctgcaccctaacagccccgag R: acttagcagagtagcctggtg	(AC) ₅	60.6	190
<i>NGA141</i>	VIII-D07	157	AB277508	F: actgccgctatcatcggaagcctc R: caccatctctctgggagcaagagc	(TC) ₂₅	59.0	123
<u><i>NGA142</i></u>	VIII-F01	196	AB277509	F: agcgggaactgtatcttggggcac R: ccccagtgagatcagtggtggct	(GA) ₃₅	63.0	145
<u><i>NGA143</i></u>	VIII-F07	559	AB277510	F: ccatgtggctggctgggtctg R: tccaaagattgcatcatggcagc	(GA) ₃₃	59.0	373
<i>NGA144</i>	VIII-F10	503	AB277511	F: tcgtttgtcagagttcagggaagc R: actgcttctctagtgggtggagg	(CT) ₆ (TC) ₂₈	60.6	227
<u><i>NGA145</i></u>	VIII-G01	378	AB277512	F: tccaggagtagatctttgcacgct R: agaacctttaagtcgtgggtgag	(AC) ₂₂ C(CCA) ₇	60.1	197
<u><i>NGA146</i></u>	VIII-H01	219	AB277513	F: cctgcagctggattctcaaccgga R: tggggtgctcgaaccctagtcagc	(GT) ₁₇	63.3	174
<i>NGA147</i>	VIII-H05	438	AB277514	F: acaagctgccttgagcacacag R: tgaatacctcacatgtgtgggacc	(GT) ₁₃	59.7	408

Table continued

Locus name ^a	Clone ID	Clone size (bp)	Accession number	Primer pair sequence (5' - 3') ^b	Tandem repeat array ^b	T _A ^c	Product size (bp) ^d
<i>NGA148</i>	VIII-H10	299	AB277515	F: cctgtatgagctatgcacaagcca R: tcctatcagtatgatctggtgc	(CT) ₁₀	59.7	272
<i>NGA149</i>	IX-A02	263	AB277516	F: cctgacatgcaagcactgcct R: tgagcccagcagctgtcactggca	(GA) ₆₃	62.9	253
<i>NGA150</i>	IX-A07	209	AB277517	F: agaaataatgagcaccctcaggtg R: actccctgggatagcagatgtg	(GA) ₁₁	58.2	156
<i>NGA151</i>	IX-B11	518	AB277518	F: tgtccctgtgcttgttctgggctg R: aggtcgacaatcagctgggctg	(GT) ₂₁ (GA) ₃₁	62.3	416
<i>NGA152</i>	IX-C01	584	AB277519	F: cctggtggctttatgggaagcttg R: cagtgcacacaatagccaacggtc	(AT) ₄ (TC) ₁₁	60.7	366
<i>NGA153</i>	IX-D02	286	AB277520	F: cctacaaggttcgacctcactgc R: aacctggaggggtgccgactact	(TC) ₆	61.9	275
<i>NGA154</i>	IX-D07	162	AB277521	F: tcacacttagcttgttggcagg R: ccatttgcggtattctgggaagg	(GA) ₅ (CA) ₉	60.3	155
<u><i>NGA155</i></u>	IX-D11	586	AB277522	F: cctaactggcttcaggctgac R: atgggagtgtagaggagccggcag	(TC) ₁₆	62.1	212
<i>NGA156</i>	IX-E02	346	AB277523	F: tggttcctcgaaactgccaag R: tggactgtctgtcccagaagag	(TC) ₉ T ₃ C(CT) ₁₄	60.8	307
<i>NGA157</i>	IX-E03	285	AB277524	F: tgccttgtatgaagcttgcaccac R: actccttggagacaagctcc	(GA) ₆	59.9	228
<i>NGA158</i>	IX-E05	357	AB277525	F: aggagtcaggactctgtcctagc R: acctagtactctgtcctcgagc	(TC) ₂₉	61.4	344
<i>NGA159</i>	IX-E10	293	AB277526	F: tcagacacttactggcttgggag R: accactctcgaatacccctccag	(GA) ₄₆	61.6	230
<i>NGA160</i>	IX-F05	184	AB277527	F: acaggaagcaaaaggcgcactc R: ccagaaggcacctctcaggcag	(GT) ₁₇	60.9	165
<u><i>NGA161</i></u>	IX-G06	397	AB277528	F: acatgtgacctgcttgcagaagc R: agaggctgtgtcagtcaggggct	A ₈ (GA) ₃₁ T ₇	60.5	303

Table continued

Locus name ^a	Clone ID	Clone size (bp)	Accession number	Primer pair sequence (5' - 3') ^b	Tandem repeat array ^b	T _A ^c	Product size (bp) ^d
<i>NGA162</i>	IX-H02	497	AB277529	F: cccttactctggtccaagcccac R: agctcccacagtctgggcaagacc	(CT) ₃₂	62.4	479
<i>NGA163</i>	IX-H07	273	AB277530	F: gcacacagaccaggaaggcttgctc R: tgccaagaatggtggaagtcacg	(GA) ₃₀	59.5	251
<i>NGA164</i>	X-A02	203	AB277531	F: cccattctggatgaccaccagtc R: ggctggtgttcaggtccagctc	(GA) ₉	61.5	187
<i>NGA165</i>	X-A04	298	AB277532	F: acccctagcattttggcgactac R: agtaaccctgtagtgacgccagg	(TC) ₃₂	61.8	247
<i>NGA166</i>	X-B06	609	AB277533	F: agatagggttaaaccacagtgtctg R: agtacctgcgtagatccccagc	(GT) ₁₈	57.3	282
<i>NGA167</i>	X-C06	572	AB277534	F: tctttactctaggcatgctagc R: tggaaaccctccaccagtgcagg	(TC) ₂₆ (CA) ₂₀	59.5	243
<i>NGA168</i>	X-C11	281	AB277535	F: agcaggctgggtgtaggagcattg R: tgaacagggttagagcccatgcag	(TC) ₁₀	62.7	241
<i>NGA169</i>	X-C12	481	AB277536	F: tgggttagggactgcccctgca R: tcctgcaattctgcatggggacc	(GA) ₂₄	64.4	394
<i>NGA170</i>	X-D03	170	AB277537	F: tcgggatcacctaaggatgccaaag R: ccacagaaggtgaagaccccagac	T ₂ (GA) ₁₀	59.7	123
<i>NGA171</i>	X-D05	402	AB277538	F: ccttctgtgaagcaccgagt R: tctgtaccacgttattgggggag	(TC) ₅ (CT) ₃	60.7	244
<i>NGA172</i>	X-D08	393	AB277539	F: tgaggctttccacagtgtagctcc R: ccagatataccttgagcactgctgc	(CT) ₂₁	59.2	337
<i>NGA173</i>	X-D12	463	AB277540	F: ccagaggtctagactagctggctg R: agaccctggagtctgtggtg	(AC) ₁₉	57.3	207
<i>NGA174</i>	X-E06	154	AB277541	F: agagcccctgagaactgccaggtg R: aggtgtactcaaaggaccatgctc	(AC) ₂₅	59.6	143
<i>NGA175</i>	X-E09	354	AB277542	F: acctgagcacaagtccagcttg R: tcaatgcgtgccctgtgtgcagc	(GA) ₃₇	61.9	290

Table continued

Locus name ^a	Clone ID	Clone size (bp)	Accession number	Primer pair sequence (5' - 3') ^b	Tandem repeat array ^b	T _A ^c	Product size (bp) ^d
<u>NGA176</u>	X-F10	214	AB277543	F: ccaacacctcctcaccctcagagc R: tgctcaggcttattcatggctcag	(GA) ₁₉	60.3	186
<u>NGA177</u>	X-G10	477	AB277544	F: gggtagagcccaccctaagc R: gagagcgagggaaagagaca	(TC) ₁₉	59.0	238
<u>NGA178</u>	X-H06	313	AB277545	F: tgggttggtgtgtctgagc R: tgcttgagattgtcaagagcctc	(TG) ₆ (AG) ₂₁	60.1	273
<u>NGA179</u>	X-H08	261	AB277546	F: agtgatagcacaacaggtctgc R: tggttctgcttcaggggatcagg	(GA) ₂₀	61.0	251

These marker data were published in **Experimental Animals 57(2): 129-134, 2008**.

^aThe underlined loci were polymorphic with distinguishable alleles in a F₂ mapping population developed from BAN-*kc, oeb* and WZ strains of the house musk shrew, *Suncus murinus*. Segregation of alleles of each of these loci on electrophoretic gels is shown in the Figure below. Locus names were based on the Laboratory of Animal Genetics code, NGA, followed by Arabic numerals in serial order.

^bBased on the sequence obtained from the cloned allele (TKU strain of *S. murinus*) amplified with universal M13 forward primer. F and R represent forward and reverse primer sequences, respectively.

^cOptimal annealing temperature as determined using DNA from the TKU strain of *S. murinus*. The PCR was carried out in a 14 µl reaction volume containing approximately 50 ng of genomic DNA, 10 mM Tris-HCl (pH8.3), 50 mM KCl, 1.5 mM MgCl₂, 1.0 mM dNTPs, 0.54 µM of each primer and 0.35 unit Taq DNA polymerase (Takara Bio Inc., Seta, Japan). Thermal profiles of GeneAmp® PCR System 9700 thermal cycler (Applied Biosystems, Tokyo, Japan) were as follows: initial denaturation at 94°C for 5 min, followed by 35 cycles at 94°C for 30 s; annealing at optimal primer temperature for 1 min and polymerization at 72°C for 1 min. Final polymerization step was for 10 min at 72°C.

^dSize of the PCR product, including the primer sequences, obtained from the clone used to develop the loci.