

S3 Table. RepeatExplorer2 identified repetitive DNA elements with at least one high confidence call amongst four Illumina generated mite sequences

Cluster	Consensus Sequence	Probability Confidence Score (Genome Proportion Score)			
		Human 1	Human 2	Pig 1	Pig 2
606bp LTR (SSR6)	<p>ATTGGTGACTATGAGAAGCCTAGAAA GACTGGTGAAACAATAACAAAATG AGAGATCCAACCTGGTAAAACCTGTGAC AAGGATTGTGAAACGAAAACCTGATG GCACTGAAACTGTTGAAGAGCATATT GAAGAACGTAAATCCGTTCCAAGATC ATTGAGCAGAGACGATAAACCTGAGC AGTCGAAAATATTCGATGCCAAAAAA CCGAGAAAGATCGTCAGAATCATTCT GAAGAAACCCAATGGTGATGAATCA GTTGAAGAGCTATTGCTAGACCCTGA <u>TACCAAAC</u>¹AGGAAGATATCGATAAA GTGTTGAAAGACGAGATACAGAATGC <u>TCTTGCTAAGAGTGATGAT</u>²CCGGATG CTAAGATAATTGCCAATATTGTGTCA <u>ACAACTCCTGGT</u>³GTAGAAGAGACGG TTGAAGAATTTCGAGACGGATCCTCAA ACTGTGAAAAAGAATATTGATGATGT ACTGAAAAAAGCTCCAAGGACCAAA ACCTCGAGAAAGAAAGATCCTCTCGG TAAAATTGTTACTAAGGTATTTAAAC GCAAACCTGATGGCAAAGAAACAGTT GAAGAGAAAGTCGAAGATCCTCAAG TGACCGGAAAG</p>	0.889 (0.018%)	0.976 (0.021%)	0.959 (0.027%)	0.933 (0.023%)
201bp Microsatellite	<p>TCGTAACCTGATATCGAACTGGCAAA AAGAAAATTGTGAAGAAGAAGAAAC CGAAACAAGGTGTAGATGCAGAAAC ACCTATTGAACAAGAAACAAAAGCA AAAGATGAATCTAAACCAGATGAGTC TGTGCCTGAGATCAGTGAGGTGGTTC CTGAATCACTCGACAAAGATGAAACT AGAGAGGAATTCATCACTGAAG</p>	0.986 (0.057%)	0.994 (0.073%)	0.979 (0.086%)	0.994 (0.086%)
93bp Microsatellite	<p>TACACTTGCTCCTGTTGGTGCAACTG GTCCAACCTGAGAAAGAACCATTCA ACTGAATATCCATCGACTTCGACAAT CTCAGACAAAGATAGAACCACTTATG AACCTGGAACCAG</p>	0.994 (0.026%)	0.993 (0.032%)	0.979 (0.039%)	0.965 (0.037%)

375bp Microsatellite (SSR5)	GTTGGTTTCTCCATTCCACCATCGATT GGTTTTTCGGACTCTTCATCGATTGGT ATC ¹ TTGCGATCTTCATCTCCTGGTCTG CTTCATCTCAACGA ² TTTCCTCACTAA TCTCAGTAGTCACAGATTCAGTTCTAT CTTTGTCTCCACCTTCGAC ³ CAGTGTT GGTTTCGAATCTTTGCGTTTGGTCAAT TTACTTTTCTCTTAGTTTCAATTCG ACTGTTGATTCTGTTTTAGGAACTTCT TCTTGTCTTCTGGAGCGATAGATTCT CTTCGCTTGAGATCTATAGAGTCTTCA GTGATTTGCTTTTCTTCTTCAACTGGT TTCTTATGAGAATCTTTTCGTTTGATT TTTCTAGGTTTCTTCGTTTCTTCATCA	0.767 (0.024%)	0.853 (0.034%)	N/A	0.928 (0.044%)
117bp Microsatellite	TACACTTGCTCCTGTTGGTGCAACTG GTCCAAGTGAAGAAAGAACCATTCACA ACTGAATATCCATCGACTTCGACAAT CTCAGACAAAGATAGAACCACTTATG AACCTGGAACCAG	0.986 (0.057%)	0.981 (0.018%)	0.994 (0.023%)	0.986 (0.030%)
333bp Microsatellite	TTTCGCCTTCCACTTTGGGAATATCAA CATCAACATCTACTTCAGGACCAGAC ACTTTTGGTCCTTTGAACCCAAATTTA GGCATAGAGAACTCCCAATCTTTTCC ATCTTTCTCTTTCGATTTTTTGTCCTTC TTCTTCTTCAGAGATAGATTCACATCA CCTTCAACCTTCGGTAATTCTACATCT GGCATATCAACTTCAGCCTTTCCTAA ATCTACATCTGGTCCGCTTATTTTCGG ACCTTTGAAACCGAATTTGGGCATAT GTAATCCCCATCCTTTGCCATCTTTGT CTCCCATATCTGGTGATTTTCTATCTA AACTCAGATCGA	0.955 (0.013%)	0.981 (0.013%)	0.959 (0.018%)	0.985 (0.018%)
40bp Microsatellite	GGCAAAGAAGCTCCAACCAAGCCTG ATGACAAGAAAGAACCA	0.487 (0.026%)	0.781 (0.012%)	0.056 (0.094%)	0.908 (0.026%)
315bp Microsatellite	TTACAAGAATTGCAAGATGTTGTAGT GTCAAAAGGTCAACCTGTAGCAAAAC TTGAAGCACAAATTGCTGGAAATCCG AAACCAAAGGTCGAATGGTTCAAAG ATAATCAAAAACCTGAAGAATCGCCA CATTGGAAGATGGTCAGCGATGGCAA AGACAAATACTCATTGACTATTCAA ACGTGAATAGTGAAGACGTTGGACAA TACAAAATTCTGGCCACCAATGATCT TGGTAAAACCTGAATCAAAGGCCAAAT TATCAATCGGTGATGGATCAAACCA GATGATGCAAAGAAACACTCTCCTGA AATT	N/A	N/A	0.959 (0.010%)	0.976 (0.014%)

75bp Microsatellite	GATGGTTGCAATGATGATGTCGGAAC ACCAGCCAAAGCGCTAGGATCTCTTG CTGATGGTTCTCTGCCTAATTCT	N/A	N/A	0.644 (0.013%)	0.915 (0.014%)
336bp Microsatellite	GGTGGGTCCCTCCCTAGCTGGCGAAG GGTGGGGTGGTGGGGCCAGTGCACAC AAGGCCTTTTCAGGCCCATCCGCCT TCTCCCTGAAGTAGAGCACGTTTGGA GTTGGTTTCCAGCTCCAGCGACGACC TGCAAAGCACCAGTGCACAGGGAGC AGGAGGCAGCCCAGAACCTCCTTGTT CCTATGGCGAGCAATGGGCTAGGGGA GAAACCAGAAAGCGCTGCTTTCCTGA GCAAACACGCATTGGGGCTGAGCTTG GTTTCCCGAGGAGAGTTTCACTTTCG CGAATGCAGCTCCCAGAAGCTAGTTT TGTGCCTTTTCTGAGATGGGCCCTA	N/A	N/A	0.868 (0.050%)	0.071 (0.026%)
84bp Microsatellite	GAGCTTCTTTGCCTGGTTCTTTCTTGT CTTCAGGCTTGGTTGGAGCATCTTTGC CTGGTTCTTTCTTGTTCATCAGGCTTGG TTG	N/A	N/A	0.819 (0.024%)	N/A

N/A - not available

¹Forward primer binding site

²Probe binding site

³Reverse primer binding site