

• **gi|941349837|gb|LJCH0100007.1| Genome - MsatB -158bp**

TCCCTCGCTAATTTTTTCATGCTTTCTTCTTTTAGATTTTTTTTTTATGATTTTCGTTTAATCAGTCGAGGTT
GCTCCGTGGAAGGCC**TTTGTTCGGTTGTTTGG**AGCGACGGCTTTACCGTTTGTAGTATGTGTGTGT
GTGCAGCAGAAGCATGTCTCATTACAGAA**ACACACACACACACACAC**AACACATATACATGGTGAGTGTGTG
TTAGTGTCTGT**TTACCGCCGTTTAACTTCGAA**AGGGCCGTTGAAACGAGAAGAGAAGCCCGGAACGAC
TCCAGGGCCGACCTCGCAGGCAGCAGAGCAACCCTCCTCCGCTCTAATATACAGTCTCAAAGCGACGGGA

• **gi|941348343|gb|LJCH01001501.1| Genome - MsatF -216bp**

ATGACATAAAAAATGATTAATAACGTTTACGCGAGGTCCGACACGGCGCTGCACAAAATATATCGGAAGGGT
TAAAACCCCGCACACCGAGGGGGCGGCAGCTCGCATTCTTTTTTT**TAAAGGGTTGGGAGGTTGGC**AGCA
GTGGTAGATTTAAATGCGTTACGTTGTGCCGTTGTTGTTGATGTAGCAGAAGTGCCTTCAAATAAATTT
GCAAAACACCACAAACAAAAATAAATAAATAAATAAATCGCGTGCATCAAAAC**ACACACACACACACAC**
ACAAATTCACATGTTTTTGTCTTTGTGATTT**GTGCACGTGTATGGATCGTG**TTTGTCTCACGGTCGCA
TCATCCAACCCCCACCCCTGAGCCCAATTATTTATACAACAATAAATTGATTGGAAAAATAATGG

• **gi|919344888|gb|GDKQ01000971.1| Transcriptome - MsatI -286bp**

GCACGCCTTAACACCGGCATCGGATGAGGCGTAGATC**CTGATCACCGGAACCCTCTC**GACCACCTCACCC
CTGAACTCGGAATTGAAGACGTCCAAGTCGTGCACGGGTTTGGCGGTGTAAGAGTCCATGCAGTTTATGC
GAAAGCTCGCCA**TCTCTCTCTCTCTCT**NCTTACCAGGCTCTCCTTAAACATGTTGTTTCAGAAATTCCTCG
AAGCCGTAAACAAACAACACCGACAACAACAACAACGAAACATTGTCAAAAAATTTGCTTGTTCG
CACTGGANCCAGTCTGCCAAC**CGGCATAAACCCGGGAATTC**GCACAAGCAAAAAAAAAAAGGAAATTC
GTTGGATGAGCGGGGATTTTCTCTCGTACGATTGGTAGAACCGTTTGTATTTTTTTCTTGAACGTTN

• **gi|941349386|gb|LJCH01000458.1| Genome - MsatP -410bp**

ACCATAGAAGTTTTTATGTCATATGTCACGTATAGTGCAGTAAACCATTAGGAATAATGAAG
AAAAATAAATGCAGATACTATAAAATGTT**TTGGTATGCAATTGTGAGGC**GATTGCAGCCCTTAGCGTATC
ATTTACGTGGTGGTTCCGCCGGAAGATCTGAAGTTGCGCAACTCACTTACGGATTAAAGGTGGAATCG
TGCAGGAATTTATGACCCGACATTAGTACGTGCAGTTGCGCCTGGCGCAGGATTAGGACTTCGAGGAA
GAGAAGAAGCGAGCAGCAGATTGAGATCGGGGATGAATGTGGACGATGCAGCGCTGAAAAATTTGCAC
GTTTCGAATCATTTCGTTCTTGT**ATGATGATGATGATGATGATGATG**GTTGTGATGATCTTGCCGTGCG
TTTTCTTTTGATAAGACCGTCAACAAAAACAACCTTCGGTTGGGATTAATAATAGCGGCCGCGTATGATG
TTACATCGTCTGCCAACCGGAGAGACTATATGCATGTTTGTGCATGTATATACATATGGATGGATGAATG
TGTACGTGCCGCTTCGTTGCGGCGTTTATGCTTGTAGCAGAGGCGAGAGCATCTGGCCTGGCCTAGAA

• **gi|919338980|gb|GDKQ01004844.1| Transcriptome - MsatE -201bp**

NN
NN
TGAATGCGGTGGTCTCGTCGGTCTGGATGGTCCG**AT**
GGATGGATGGAGAGTGGCCTGCAAAAAAGGGGGAGCCGAAGACGCAGACTCCGCACGCTCTCCGCTACAG
TCCGNC**ACACACACACACACACAC**GCACACGTCTCTGTGCCGTTTTCGCGGGCGGCCGCGCAAGAGATA
CATAAATGATCGGGCGTCGCGACGCCCTCGCTCGCTCGC**CGCCCTTTCGAAACCATCAA**CCACCCGACG
TATCCACACATTTAATTCACCTCCGAATGAGGAGGGCGTCAATCGTAAATCTCAATTACGGTAATCAA

• **gi|919330077|gb|GDKQ01010587.1| Transcriptome - MsatG -224bp**

CAGCAGCTTCGCGCCGTTTCGCCATCCTCGTACCGCTTCGCAGTGCAGTGGGACGCTCCGAATCGTT
CGTGTGCGTGTCTTCTACCTCAGTTTGATCCGGAACGAGTCCGAGTGTGGTTCGTTGCGCTCTATCTCACAC
GTGTGTGTAATAGTGT**ATATATATATATAT**NGGAGAGGAAGTTGTGTGTACAGCGCGCATAGTGT
TCCATATACGAATCGCACGCTCTATGCTAATGGACGTCTAAATTTTCAAATGGCTGCCGATTC**GGGTAT**
GGATACGTGCCATCACCAGAGATCGCGGACTCCAGGAAGAGCCGCTCGACGGGGACACCGAGAACGGA
GACACGAAGCGCTCGCACTTACAGCACAGGTGGTGTGATGGAACATACCACTTCANTCGCACAACCTGCAGAAG

• **gi|941349834|gb|LJCH01000010.1| Genome - MsatH -283bp**

CGAGTAATCCTGGATAAAGAAAGAGAAGAAAAAAGCAAACCCAATTTACGAACATCTTATGGGGGAA
ATGTACAAAAGTCTTACGTGCGTGTGCCGAGAGAAGCTCCTTCATGATGAAGTTG**TCGTAGATGTCTCGTG**
CCTGCTTCATCCGTTTCGTCGCTCGTTCCAGTTTCTCGTACTGTTTATCTGTGAGAAGCAAAAACGGAC
AATGAGAGCGCATCTTGTCCGAGAATCGTTAAAACCCGACGCGCACGTACAACATCCGGTGCAAAGAC
AGACAGTAAGTG**AGAGAGAGAGAGAGAGAG**ATACAGAGCGTATTATTACGCTCATCTAGCAAACGTCAGC
GAATCCTGGACAATCATCATATTATTGTTGTTATGC**CAGCCACCCTTCAAACCTG**GGTCACACACAAC
AAACACACACAAACATAACAACAACCCCATCTCTCTCATCTGTGCGCGCGCGAAATTCATTT

• **gi|941349831|gb|LJCH01000013.1| Genome - MsatK -334bp**

CCTCTTAAATAGAGATTTAGTTTATGTTTATCCAGGAAGTGGCATTTAGGACCCATAAAATAATTTCTCC
AT**GCTCTCATTCTCCCAAACGC**AATTACGAAAATAAATAACGGTTTATGCATTAATAATTATATAAATGTC
TCGTAACGCCCGGATTATTGCGCTCGGTTAGAGACCAAAAAGAAGAGATAGAAAAAAAAACGATCAAGA
GTAAAAGATAAGTTTTGGGCTGTAAGGGCCGTGATATCCATAAAAATGATTCCAAGTGCATTCATATTGT
ATCATGGGTAGGGGTG**AGGAGGAGGAGGAGGAGGAGGAGG**AACAGGAGGCGGGAAGCGATATAATCCTTC
GGCTATTCAAGCCAAGGGCAATAATTCACTTTTATG**GACAACCTTATGCGCGTCCAC**GGGAACGGGAGCCA
TCGCTGTGCTACTCATAGGGGAACCCCTGTCCTTTATACACCGGTATGAATTTTAATTCGGGCCGGGCG

• **gi|941349840|gb|LJCH01000004.1| Genome - MsatO -395bp**

TTAATCGGTTATAGTTGAGTCCACCCAGCTATCTTCGATCAATGAATCAGTTATGCCTT**ATGCCAATTAA**
CGCGTCGAGGATTAATTGATTTTCAGTGTAAAGTCTAATTAATTTTCGCGCACTCCTTC**TTCTTCTTCTT**
CTTCTTCTTCGACGGCGACGAAGGGGAAAAAGTGCATTGCACCATTCAATACCGGGAGGAAACTGTTGTT
TTTTTTGCTTGCTTGTCTGTTTGTTCAGTTTTCGCTTCTTTCTGTTCTTGTTCATATTGTAAATACGAT
TTCGCGTATAATTAATGGACTTTTAAATGCTCCGGTTGGGAGCGGTCGTAAGCAGAAGGAGGAGGAAGCG
GAATAATGAATACGACGACCTACACAACTGAAAACCCGTCCTCGTGAGGTAAAGAGTCCAAAAAATGTA
TCATCGGAATCCAC**CAGTCGCACAGGTAACGATG**ATGATAATATCGATGCATTCGATACGTTTCCGGATC
GGGTAACGTTGGAAACCGTACCGGATCGAATCCGAAATCGGAAAGGCACGGTTCTTCTTCTGCTGTCAAC

2. BLAST annotation

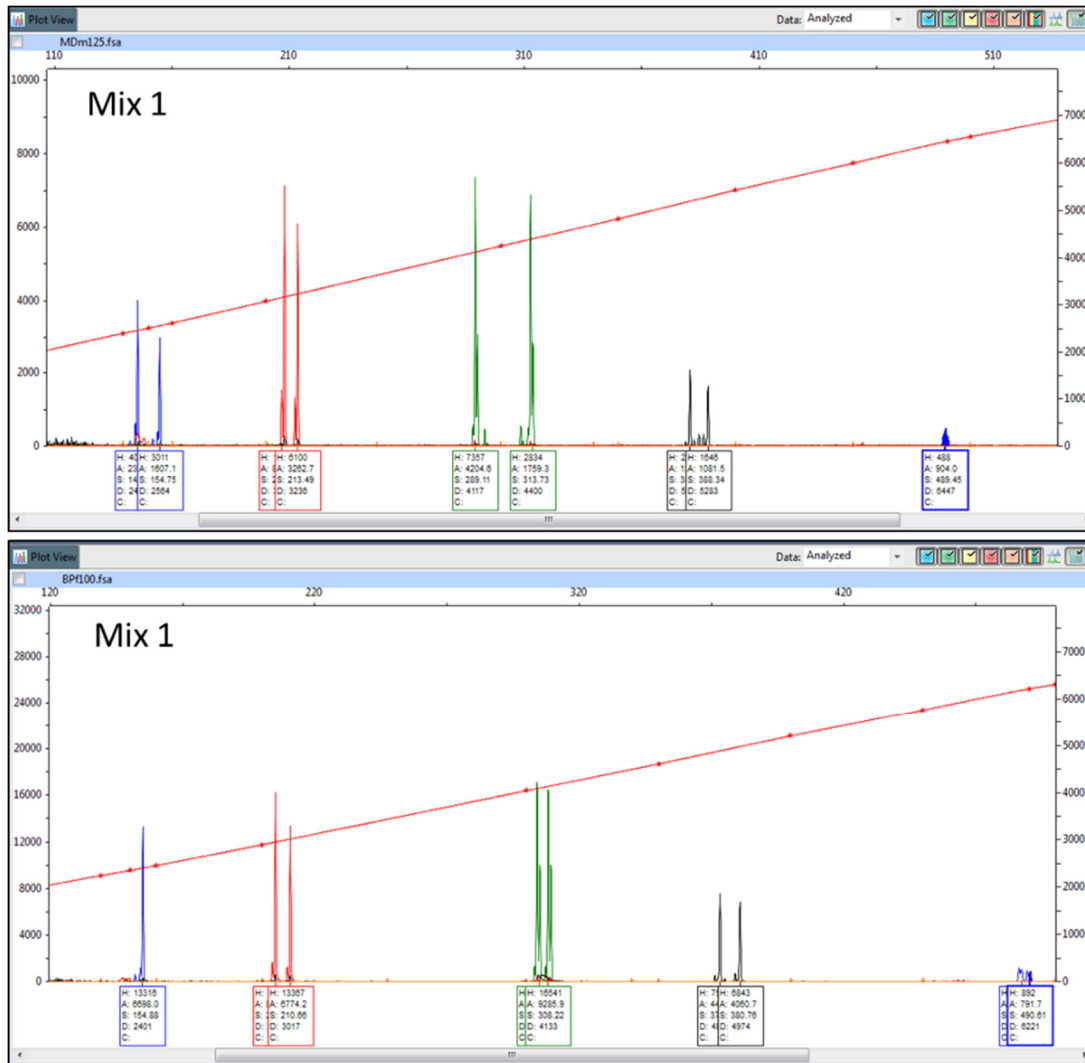
Table S1. Summary of the BLASTx searches using the sequences containing the microsatellite markers against the NCBI nr database.

	BLASTx	Bit-score	e-value	Query cover	Identity
Nvesp_A	PREDICTED: putative transcription factor SOX-15 [Nicrophorus vespilloides]	170	3e-47	99%	100%
Nvesp_D	No significant similarity found				
Nvesp_J	No significant similarity found				
Nvesp_M	PREDICTED: broad-complex core protein isoforms 1/2/3/4/5-like [Bombus terrestris]	121	5e-32	26%	98%
Nvesp_Q	No significant similarity found				
Nvesp_B	No significant similarity found				
Nvesp_F	No significant similarity found				
Nvesp_I	PREDICTED: DNA polymerase zeta catalytic subunit [Nicrophorus vespilloides]	110	2e-25	36%	100%
Nvesp_P	No significant similarity found				
Nvesp_E	No significant similarity found				
Nvesp_G	PREDICTED: RNA-binding protein Nova-1 isoform X1 [Nicrophorus vespilloides]	100	7e-22	33%	100%
Nvesp_H	PREDICTED: G protein-coupled receptor kinase 1 [Nicrophorus vespilloides]	74.7	1e-12	25%	88%
Nvesp_K	No significant similarity found				
Nvesp_O	No significant similarity found				

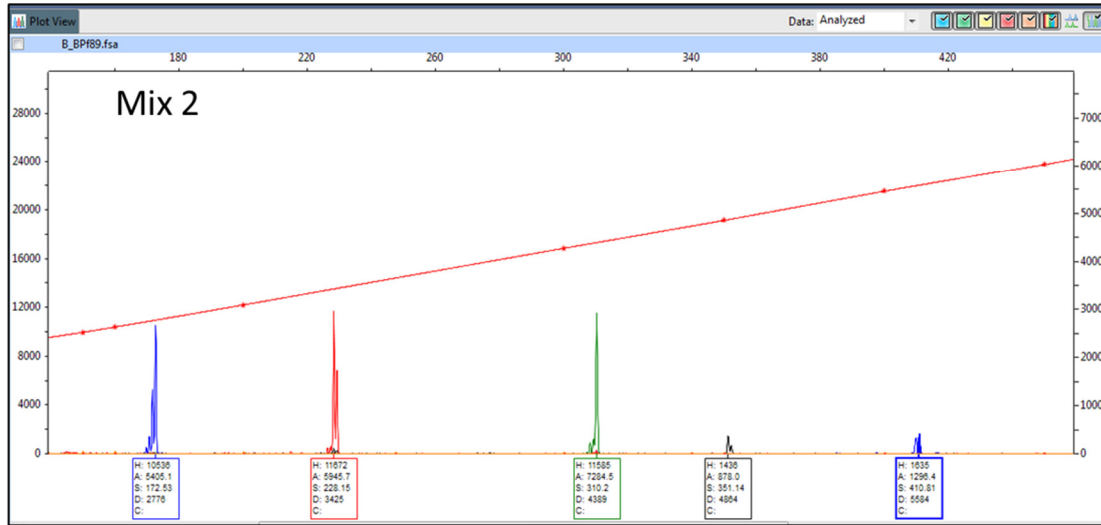
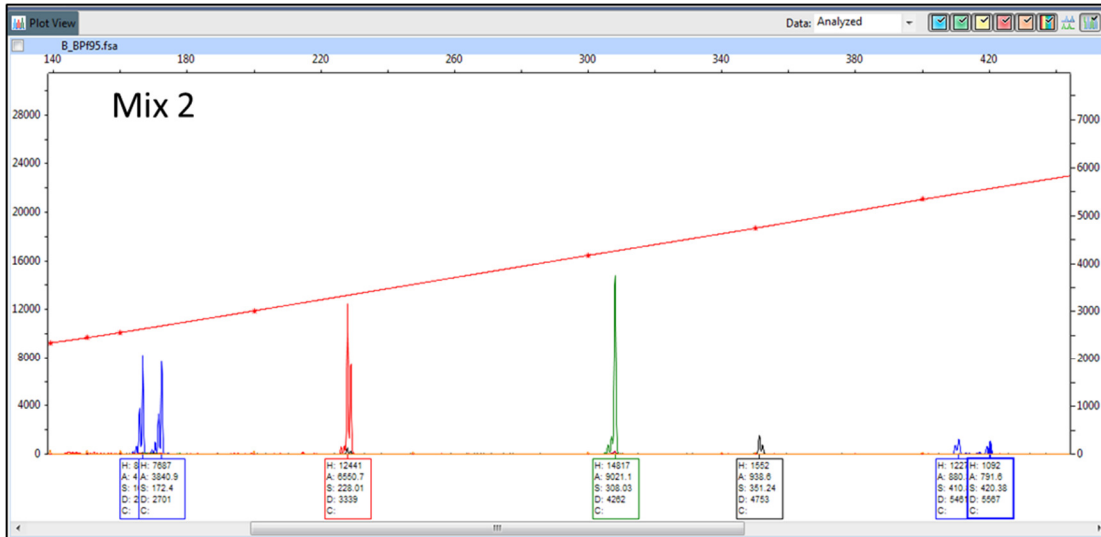
Pink: alignment score 80-200; Green: alignment score 50-80

3. Chromatographs

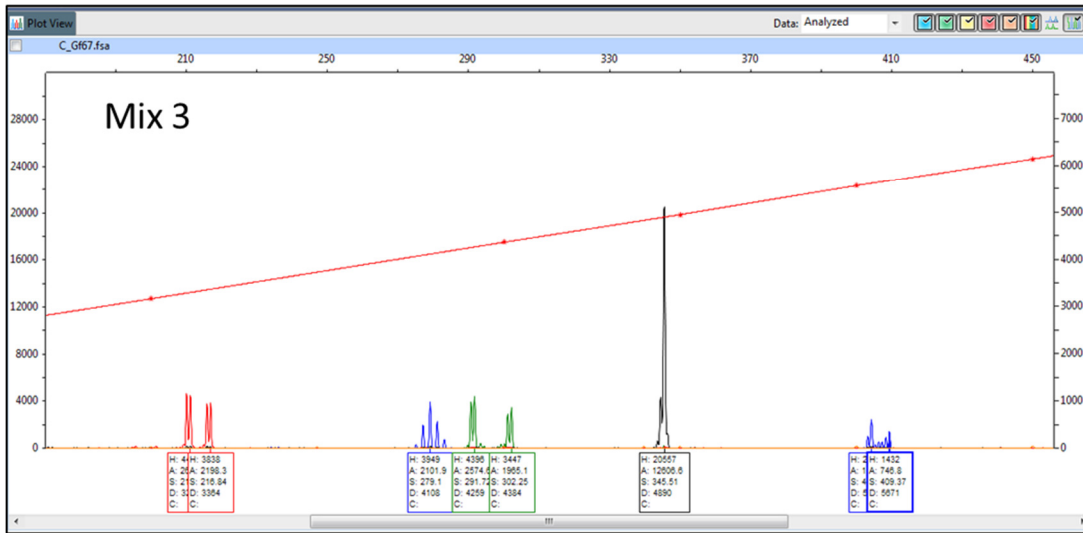
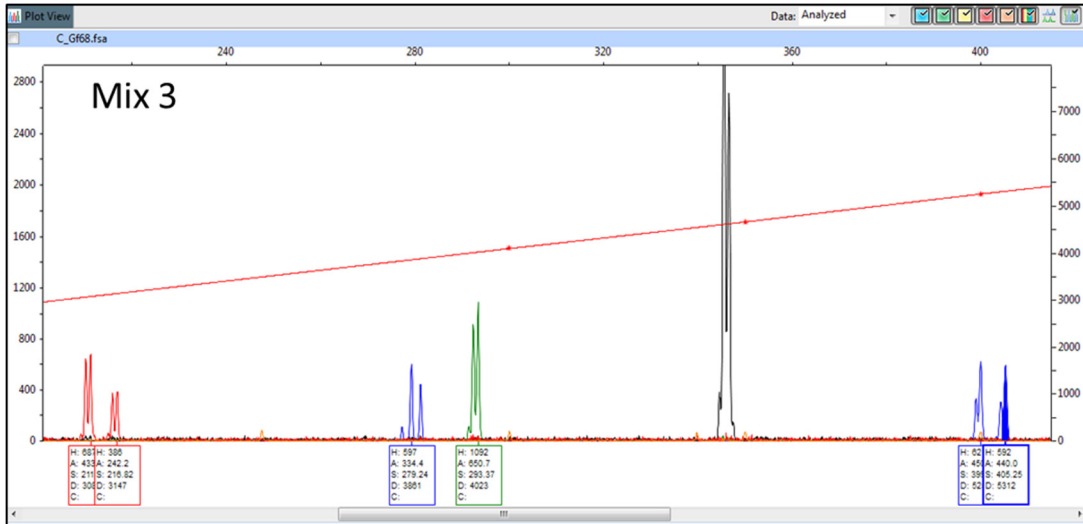
Representation of two random Peak Scanner v.1.0 (Applied Biosystems) chromatographs per genotyped multiplex.



Mix 1: Blue: Nvesp_A; Red: Nvesp_D; Green: Nvesp_J; Black: Nvesp_M; Blue2: Nvesp_Q



Mix 2: Blue: Nvesp_B; Red: Nvesp_F; Green: Nvesp_I; Black: not used; Blue2: Nvesp_P



Mix 3: Red: Nresp_E; Blue: Nresp_G; Green: Nresp_H; Black: Nresp_K; Blue2: Nresp_O