KY706330 (Sv)	AGTTTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCA	60
KY706327 (Sv)	AGTTTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCA	60
KY706326 (Sv)	AGTTTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCA	60
KY706329 (Sv)	AGTCTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCG	60
KY706324 (Sv)	AGTCTTGTCCTCACAGCCCTCACATCCACAACCAACAAATTTCCCATCTTGTCTGTTGCG	60
KY706332 (Sv)	AGTCTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCT-GTCTGTTGCG	60
KY706331 (Sv)	AGTCTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCG	60
KY706328 (Sv)	AGTCTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCG	60
KY706325 (Sv)	AGTCTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCG	60
KY706323 (Sv)	AGTCTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCG	60
LS999505 (Sv)	AGTCTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCG	60
LS999504 (Sv	AGTCTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCG	60
LS999503 (Sv)	AGTCTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCG	60
LS999502 (Sv)	AGTCTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCG	60
MH554418 (Svv)*	AGTTTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCA	60
MH554402 (Svv)	AGTCTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCG	60
MN862448 (Svv)	AGTTTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCA	60
MN862451 (Svv)	AGTCTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCG	60
MN862450 (Svv)	AGTCTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCG	60
MN862447 (Svv)	AGTCTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCG	60
MN862446 (Svv)	AGTCTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCG	60
MN862449 (Svv)	AGTCTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCG	60
MN862445 (Svv)	AGTCTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCG	60
ON863777 (Svv)	AGTTTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATGTTGTCTGTTGCA	60
ON863778 (Svv)	AGTTTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCA	60
ON863779 (Svv)	AGTTTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCA	60
ON863780 (Svv)	AGTTTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCA	60
ON863776 (Svv)	AGTTTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCA	60
ON863781 (Svv)	AGTTTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCA	60
ON863782 (Svv)	AGTCTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCG	60
ON863783 (Svv)	AGTCTTGTCCTCACAGCCCTCACATCCACAACCATCAAATTTCCCATCTTGTCTGTTGCG	60
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KY706327 (Sv)	GACAGAGTATTGCTCCATATCTATCTGCCTCCCG-CGTCCTGTGACGACGCGGGGCAATG	120
KY706326 (Sv)	GACAGAGTATTGCTCCATATCTATCTGCCTCCCG-CGTCCTGTGACGACGCGGGGCAATG	120
KY706329 (Sv)	GACAGAGTATTGCTCCATATCTATCTGCCTCCCGTCGTCCTGTGACGACGCGGGGCAATG	120
KY706324 (Sv)	GACAGAGTATTGCTCCATATCTATCTGCCTCCCGTCGTCCTGTGACGACGCGGGGCAATG	120
KY706332 (Sv)	GACAGAGTATTGCTCCATATCTATCTGCCTCCCGTCGTCCTGTGACGACGCGGGGCAATG	120
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KY706325 (Sv)	GACAGAGTATTGCTCCATATCTATCTGCCTCCCGTCGTCCTGTGACGACGCGGGGCAATG	120
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LS999505 (Sv)	GACAGAGTATTGCTCCATATCTATCTGCCTCCCGTCGTCCTGTGACGACGCGGGGCAATG	120
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MH554418 (Svv)*	GACAGAGTATTGCTCCATATCTATCTGCCTCCCG-CGTCCTGTGACGACGCGGGGCAATG	120
MH554402 (Svv)	GACAGAGTATTGCTCCATATCTATCTGCCTCCCGTCGTCCTGTGACGACGCGGGGCAATG	120
MN862448 (Svv)	GACAGAGTATTGCTCCATATCTATCTGCCTCCCG-CGTCCTGTGACGACGCGGGGCAATG	120
MN862451 (Svv)	GACAGAGTATTGCTCCATATCTATCTGCCTCCCGTCGTCCTGTGACGACGCGGGGCAATG	120
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MN862449 (Svv)	GACAGAGTATTGCTCCATATCTATCTGCCTCCCGTCGTCCTGTGACGACGCGGGGCAATG	120
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ON863777 (Svv)	GACAGAGTATTGCTCCATATCTATCTGCCTCCCG-CGTCCTGTGACGACGCGGGGCAATG	120
ON863778 (Svv)	GACAGAGTATTGCTCCATATCTATCTGCCTCCCG-CGTCCTGTGACGACGCGGGGCAATG	120
ON863779 (Svv)	GACAGAGTATTGCTCCATATCTATCTGCCTCCCG-CGTCCTGTGACGACGCGGGGCAATG	120
ON863780 (Svv)	GACAGAGTATTGCTCCATATCTATCTGCCTCCCG-CGTCCTGTGACGACGCGGGGCAATG	120
ON863776 (Svv)	GACAGAGTATTGCTCCATATCTATCTGCCTCCCG-CGTCCTGTGACGACGCGGGGCAATG	120
ON863781 (Svv)	GACAGAGTATTGCTCCATATCTATCTGCCTCCCG-CGTCCTGTGACGACGCGGGGCAATG	120
ON863782 (Svv)	GACAGAGTATTGCTCCATATCTATCTGCCTCCCGTCGTCCTGTGACGACGCGGGGCAATG	120

ON863783 (Svv)	GACAGAGTATTGCTCCATATCTATCTGCCTCCCG**T**CGTCCTGTGACGACGCGGGGCAATG	120
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KY706329 (Sv)	AAAATTGTTACCCCTCCTTTCA**T**AAAAAGTCGTGCACAGACCACGAACAACCCCACCGAC	180
KY706324 (Sv)	AAAATTGTTACCCCTCCTTTCA**C**AAAAAGTCGTGCACAGACCACGAACAACCCCACCGAC	180
KY706332 (Sv)	AAAATTGTTACCCCTCCTTTCA**C**AAAAAGTCGTGCACAGACCACGAACAACCCCACCGAC	180
KY706331 (Sv)	AAAATTGTTACCCCTCCTTTCA**C**AAAAAGTCGTGCACAGACCACGAACAACCCCACCGAC	180
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MH554402 (Svv)	AAAATTGTTACCCCTCCTTTCA**C**AAAAAGTCGTGCACAGACCACGAACAACCCCACCGAC	180
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MN862451 (Svv)	AAAATTGTTACCCCTCCTTTCA**C**AAAAAGTCGTGCACAGACCACGAACAACCCCACCGAC	180
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ON863777 (Svv)	AAAATTGTTACCCCTCCTTTCA**C**AAAAAGTCGTGCACAGACCACGAACAACCCCACCGAC	180
ON863778 (Svv)	AAAATTGTTACCCCTCCTTTCA**C**AAAAAGTCGTGCACAGACCACGAACAACCCCACCGAC	180
ON863779 (Svv)	AAAATTGTTACCCCTCCTTTCA**C**AAAAAGTCGTGCACAGACCACGAACAACCCCACCGAC	180
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ON863776 (Svv)	AAAATTGTTACCCCTCCTTTCA**C**AAAAAGTCGTGCACAGACCACGAACAACCCCACCGAC	180
ON863781 (Svv)	AAAATTGTTACCCCTCCTTTCA**C**AAAAAGTCGTGCACAGACCACGAACAACCCCACCGAC	180
ON863782 (Svv)	AAAATTGTTACCCCTCCTTTCA**C**AAAAAGTCGTGCACAGACCACGAACAACCCCACCGAC	180
ON863783 (Svv)	AAAATTGTTACCCCTCCTTTCA**C**AAAAAGTCGTGCACAGACCACGAACAACCCCACCGAC	180
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KY706327 (Sv)	ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCA**C**AAAGGAAGCCGCC**G**	240
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KY706329 (Sv)	ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCA**T**AAAGGAAGCCGCC**C**	240
KY706324 (Sv)	ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCA**C**AAAGGAAGCCGCC**G**	240
KY706332 (Sv)	ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCA**C**AAAGGAAGCCGCC**G**	240
KY706331 (Sv)	ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCA**C**AAAGGAAGCCGCC**G**	240
KY706328 (Sv)	ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCA**C**AAAGGAAGCCGCC**G**	240
KY706325 (Sv)	ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCA**C**AAAGGAAGCCGCC**G**	240
KY706323 (Sv)	ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCA**C**AAAGGAAGCCGCC**G**	240
LS999505 (Sv)	ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCA**C**AAAGGAAGCCGCC**G**	240
LS999504 (Sv)	ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCA**C**AAAGGAAGCCGCC**G**	240
LS999503 (Sv)	ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCA**C**AAAGGAAGCCGCC**G**	240
LS999502 (Sv)	ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCA**C**AAAGGAAGCCGCC**G**	240
MH554418 (Svv)*	ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCA**C**AAAGGAAGCCGCC**G**	240
MH554402 (Svv)	ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCA**C**AAAGGAAGCCGCC**G**	240
MN862448 (Svv)	ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCA**C**AAAGGAAGCCGCC**G**	240
MN862451 (Svv)	ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCA**C**AAAGGAAGCCGCC**G**	240
MN862450 (Svv)	ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCA**C**AAAGGAAGCCGCC**G**	240
MN862447 (Svv)	ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCA**C**AAAGGAAGCCGCC**G**	240
MN862446 (Svv)	ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCA**C**AAAGGAAGCCGCC**G**	240
MN862449 (Svv)	ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCA**T**AAAGGAAGCCGCC**G**	240
MN862445 (Svv)	ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCA**T**AAAGGAAGCCGCC**G**	240
ON863777 (Svv)	ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCA**C**AAAGGAAGCCGCC**G**	240
ON863778 (Svv)	ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCA**C**AAAGGAAGCCGCC**G**	240
ON863779 (Svv)	ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCA**C**AAAGGAAGCCGCC**G**	240
ON863780 (Svv)	ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCA**C**AAAGGAAGCCGCC**G**	240
ON863776 (Svv)	ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCA**C**AAAGGAAGCCGCC**G**	240

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ON863781 (Svv)      ATGCCTCTTATCGCACGCCTGCCTCGAATTGATTACTGACCCTCACAAAGGAAGCCGCCG      240
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KY706330 (Sv)       AACTCGGTAAGGGTTCTTTCAA      262
KY706327 (Sv)       AACTCGGTAAGGGTTCTTTCAA      262
KY706326 (Sv)       AACTCGGTAAGGGTTCTTTCAA      262
KY706329 (Sv)       AACTCGGTAAGGGTTCTTTCAA      262
KY706324 (Sv)       AACTCGGTAAGGGTTCTTTCAA      262
KY706332 (Sv)       AACTCGGTAAGGGTTCTTTCAA      262
KY706331 (Sv)       AACTCGGTAAGGGTTCTTTCAA      262
KY706328 (Sv)       AACTCGGTAAGGGTTCTTTCAA      262
KY706325 (Sv)       AACTCGGTAAGGGTTCTTTCAA      262
KY706323 (Sv)       AACTCGGTAAGGGTTCTTTCAA      262
LS999505 (Sv)       AACTCGGTAAGGGTTCTTTCAA      262
LS999504 (Sv)       AACTCGGTAAGGGTTCTTTCAA      262
LS999503 (Sv)       AACTCGGTAAGGGTTCTTTCAA      262
LS999502 (Sv)       AACTCGGTAAGGGTTCTTTCAA      262
MH554418 (Svv)*     AACTCGGTAAGGGTTCCTTCAA      262
MH554402 (Svv)      AACTCGGTAAGGGTTCCTTCAA      262
MN862448 (Svv)      AACTCGGTAAGGGTTCCTTCAA      262
MN862451 (Svv)      AACTCGGTAAGGGTTCCTTCAA      262
MN862450 (Svv)      AACTCGGTAAGGGTTCCTTCAA      262
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ON863776 (Svv)      AACTCGGTAAGGGTTCCTTCAA      262
ON863781 (Svv)      AACTCGGTAAGGGTTCCTTCAA      262
ON863782 (Svv)      AACTCGGTAAGGGTTCCTTCAA      262
ON863783 (Svv)      AACTCGGTAAGGGTTCCTTCAA      262
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Supplementary Figure S5. Alignment of *Seimatosporium vitis* (Sv) and *Sei. vitis-viniferae* (Svv) *tef1-a* sequence data obtained in this study and currently available in the NCBI database. Base differences (substitutions: 8 and insertions/deletions: 2) are shown in color. Highlighted alignment position 252 depicts a T/C nucleotide substitution that is consisted among (Sv)/(Svv) isolates, respectively. All other nucleotide differences appear to be variably distributed between species. *tef1-a* sequence data of the (Svv) ex-type specimen (CBS 123004). This information is not available for the ex-type of (Sv) (MFLUCC 14-0051).