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**Supplementary Data**

**Vagal-mAChR4 signaling promotes Friend virus complex (FV)-induced acute erythroleukemia**

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**Supplementary Table S1** Primers used in this study.

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| Primers | Primer sequence (5′-3′) |
| *Epor* | F-GGGCTCCGAAGAACTTCTGTG |
|  | R-ATGACTTTCGTGACTCACCCT |
| *Nfe2* | F-TCCTCAGCAGAACAGGAACAG |
|  | R-GGCTCAAAAGATGTCTCACTTGG |
| *Klf1* | F-AGACTGTCTTACCCTCCATCAG |
|  | R-GGTCCTCCGATTTCAGACTCAC |
| *Gata1* | F-TGGGGACCTCAGAACCCTTG |
|  | R-GGCTGCATTTGGGGAAGTG |
| *Gapdh* | F-AGGTCGGTGTGAACGGATTTG |
|  | R-TGTAGACCATGTAGTTGAGGTCA |
| *Chrna1* | F-TCATCAACACACACCACCGT |
|  | R-TGCAATGTACTTCACGCCCT |
| *Chrna2* | F-CCATGGGTGTCCTCTATGGC |
|  | R-TCCCCAGGAAGCAGACGATA |
| *Chrna3* | F-TGTCCCTGTCTGCTCTGTCA |
|  | R-GCCATCAAGGGTTGCAGAAA |
| *Chrna4* | F-GGCGTCCAGTACATTGCAGA |
|  | R-CCGGTTTGGAAGATGTGGGT |
| *Chrna5* | F-AGAAGCCGAGAAAGACGGTG |
|  | R-ATCCGATCGAGAACTTGGGC |
| *Chrna6* | F-GGACCCCAAAAGCCATACCA |
|  | R-CTCTGTCCACCACCATAGCC |
| *Chrna7* | F-CCCTGATGGTGGCAAAATGC |
|  | R-ATCATGTGTTGGGGAGCAGG |
| *Chrna9* | F-GCCTCAGAAAACGTCCCTCT |
|  | R-TCAGGTTGGACCCTGGAAGT |
| *Chrna10* | F-GGGTTTCTGCTCCTGCTCTT |
|  | R-TGTAGGTAGGCGTCTGTCCA |
| *Chrnb1* | F-GTGGTCCTCAACCTGCATCA |
|  | R-GATAAATCGTCGCAGGTCCG |
| *Chrnb2* | F-GTGTACGCTTCATTGCGGAC |
|  | R-GGTCACGGGATGAGTAGCTG |
| *Chrnb3* | F-ACGGAGAGTAAGGGAACCGT |
|  | R-CCAGAGGAAGATGCGGTCAA |
| *Chrnb4* | F-TCGCACAGCATTTGGAGAGT |
|  | R-TAGCCTAGAGGCCCTTGGAG |
| *Chrm1* | F-TCCCATGGAAACCCTGAATCC |
|  | R-AGACGGTGATGTTGGGACTG |
| *Chrm2* | F-CTAATTACTACTTCCCCGGCAC |
|  | R-AGTCAAGTGGCCAAAGAAACA |
| *Chrm3* | F-CTGCAGCCGGGAGCC |
|  | R-CCACAGTCCACTGAGCAAGT |
| *Chrm4* | F-CTCTGGCTAGTTCCGCCGTC |
|  | R-CTCAGGGAACCAGTCACTGTC |
| *Chrm5* | F-ATCCTCCCGTAGAAGCACCT |
|  | R-TTTTCAGTCCGAGGGCTCAC |
| *ChrnD* | F-GTTCCTGCTTTTCGGCATGG |
|  | R-CAAACATGAGGTCACTGCGG |
| *ChrnE* | F-GGTTCCACAGAAGGTCCTGG |
|  | R-TGGCAACCACCATGACGAAT |
| *ChrnG* | F-CCCCTTCGATTGGCAGAACT |
|  | R-CACGGAGTCCAGGAGCATTT |
| *Fli1* | F-ATGGACGGGACTATTAAGGAGG |
|  | R-GAAGCAGTCATATCTGCCTTGG |
| *Spi1* | F-ATGTTACAGGCGTGCAAAATGG |
|  | R-TGATCGCTATGGCTTTCTCCA |
| *Gp 1* | F-ATGGGACAGACCGTAACCACCC |
|  | R-GACACTATGGGAGAGGGGGCA |
| *Gp2/3* | F-ATGTCATTCATCTGGCAGTCCGC |
|  | R-GACCTCCCTAATCGTCTAAGGTCAGG |
| *Gp4* | F-GGGGACAATGACAGATGCCTTTCC |
|  | R-TATTGAGGACCTGGCGGGTCAAA |

**Supplementary Table S2** Sequence alignment between the FV strain adopted in this study (OQ718806) and NC\_001362.1 friend mouse leukemia virus FB29 (<https://www.ncbi.nlm.nih.gov/nuccore/NC_001362.1>) and X02794|X02794.1 Friend murine leukemia virus FB-57 (<https://www.ncbi.nlm.nih.gov/nuccore/X02794>).

|  |  |  |  |
| --- | --- | --- | --- |
| Sequence alignment | FB29 | | FB-57 |
| Matrix | | EDNAFULL | EDNAFULL |
| Gap penalty | | 2 | 2 |
| Extend penalty | | 2 | 2 |
| Score | | 36447 | 36186 |
| OQ718806 length | | 7610 | 7610 |
| NC\_001362.1 length | | 8323 | 8359 |
| Alignment length | | 8328 | 8361 |
| Identity | | 7441/8328 (89.35%) | 7420/8361 (88.75%) |
| Similarity | | 7441/8328 (89.35%) | 7420/8361 (88.75%) |
| Gaps | | 723/8328 (8.68%) | 753/8361 (9.01%) |

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**Supplementary Fig. S1** Viral identification **A** Gene structure of SFFV. **B** Gene products of SFFV detected by electrophoresis amplified with SFFV primers and our viral template. **C** Blast comparison our sequencing results with the SFFV reference sequence.