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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.