

Supplementary Information

Table

Table S1a. List of genes of which spatially close cis-regulatory elements neighbored MLV integration sites (bare glass substrate, curvature = 0.00 μm^{-1}).

LIST
CDK13, AMD1, LCORL, SNX17, RMDN2, ADPRHL1, GNL3, RPRM

The genes of which spatially close cis-regulatory elements as well as TSSs are located within 5 kb from MLV integration sites (“Cis-TSS group”) are shown in black, and the genes of which spatially close cis-regulatory elements only are located near MLV integration sites (“Cis-only group”) are shown in green and bold.

Table S1b. List of genes of which spatially close cis-regulatory elements neighbored MLV integration sites (1200-nm bead substrate, curvature = 1.67 μm^{-1}).

LIST
<p>SLC25A13, POMT2, TBC1D23, NEO1, PTPN21, RFX3, ATRX, DNAJA1, TGDS, SEMA6A, CBX5, DSP, ADNP, RS1, FZD3, PPP1R13L, SGTA, SYNGR4, PHF14, SLC1A1, GATA3, SNX25, NUP98, ARMC8, EEF1B2, STAG1, TST, JUND, ZNF304, TRAFD1, SCYL2, RSAD1, MRPL47, CCDC115, MAPK8IP3, FN3KRP, CETN2, RGS10, LAMTOR1, RNF219, GTF3C6, ELK4, LYSMD1, CWC22, FBXW12, ZNF143, MAPK7, MCM7, SRRM2, ANKS3, LRRC45, THOP1, MBOAT1, KCTD13, INHBC, TBL1XR1, EGR3, TOB2, POU3F1, ZNF397, ZSCAN30, C19orf54, HN1, WDR5, ARHGEF12, METTL9, SND1, C5AR1, ZNF583, PRKDC, RUND2A, CYBASC3, MUTED, Q6RUI8, Q9BUK0, HOXA11, AP2B1, CLK1, POLA2, RNH1, NDUFS1, FNIP2, POU1F1, SEMA3C, SNRPA, DDHD2, PEBP1, GANAB, MAEA, THOC5, RBM23, GSTZ1, GSS, PRELID3B, MRGBP, TBL1X, ARL2BP, MCM4, CCDC94, PLGRKT, PALD1, NDUFC1, SNX15, ANAPC15, COQ5, NAA25, RWDD1, FAM120B, PTK7, SLC9A2, RGS2, PIK3R3, STMN1, CD3EAP, HOXB3, ETF1, BICC1, NRN1, MKKS, NCLN, MPST, PARP2, KRBA1, PRPF38A, COL4A2, UBQLN1, BORA, IMP4, APTX, HDGF, C1orf43, GATAD2B, C1orf35, PARP1, RPS27A, CTDSPL, ADAMTS19, NSDHL, SYBU, HAUS6, SLX4IP, TMEM138, INCENP, COMM7, SPATA4, SEC24D, DCP1B, NPAS3, GPR180, ZDHHC7, TRIP12, FBXO36, TRIM11, SLC25A28, PAFAH2, ADIPOR1, RECQL4, LRRC14, TMEM143, CLHC1, SCNM1, ZMYM6, RFC4, GNL3, HNF4G, DEPDC4, C16orf71, PPIB, LMAN2, STRA13, SNTB1, HOXC5, CHRNA7, RPRM, CHID1, C9orf50, CALR, DCTPP1, PLAG1, LCK, AP2A2, LHFP, IRAK1, ZFP36L1, DRG1, HEXIM1, ZNF395, COL4A1, COL25A1, NDUFA4, SF3B3, ADA, HOXA4, FAM114A1, S100A10, MRPS18B, STK19, DXO, PPP1R10, MZT1, AP4M1, ARPC1A, DDOST, MRPS21, CAMKKA, ORC1L, TNRC9, THRAP1, SYBL1, HNRPA1, ATBF1, NLIIF, HNRPU, PB1, UBXD7, C1orf190, GNB2L1, Q9P2B7</p>

The genes of which spatially close cis-regulatory elements as well as TSSs are located within 5 kb from MLV integration sites (“Cis-TSS group”) are shown in black, and the genes of which spatially close cis-regulatory elements only are located near MLV integration sites (“Cis-only group”) are shown in green and bold.

Table S1c. List of genes of which spatially close cis-regulatory elements neighbored MLV integration sites (600-nm bead substrate, curvature = 3.33 μm^{-1}).

LIST
OSGEP, P2RX3, CUTA, ECT2, BCAS2, MBOAT1, KIAA1274, APEX1, NDUFC1, IGF1R, SSRP1, AP3S2, KLHL14

The genes of which spatially close cis-regulatory elements as well as TSSs located are within 5 kb from MLV integration sites (“Cis-TSS group”) are shown in black, and the genes of which spatially close cis-regulatory elements only are located near MLV integration sites (“Cis-only group”) are shown in green and bold.

Table S1d. List of genes of which spatially close cis-regulatory elements neighbored MLV integration sites (300-nm bead substrate, curvature = 6.67 μm^{-1}).

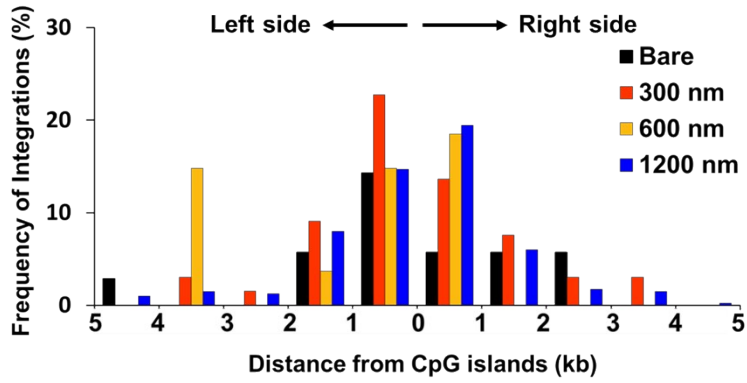
LIST
CDK13, PLOD1, CBX5, DSP, MED13, COPS7A, CUTA, ARMC8, ATG14, UTP3, PIGC, RSAD1, NMRAL1, CWC22, LRR1, ARL4C, GPAA1, ZNF583, MUTED, POLA2, MCM2, RANGAP1, ZC3H7B, HMOX2, FBXW4, RWDD1, RGS2, TMEM138, PAFAH2, ADIPOR1, ISL2, ZNF333, CYB561A3, OSR2, PSIP1, RUVBL1, RPRM, EXOSC4, C9orf50, PPARA, HDAC2, KLHL14, HNRPA1

The genes of which spatially close cis-regulatory elements as well as TSSs are located within 5 kb from MLV integration sites (“Cis-TSS group”) are shown in black, and the genes of which spatially close cis-regulatory elements only are located near MLV integration sites (“Cis-only group”) are shown in green and bold.

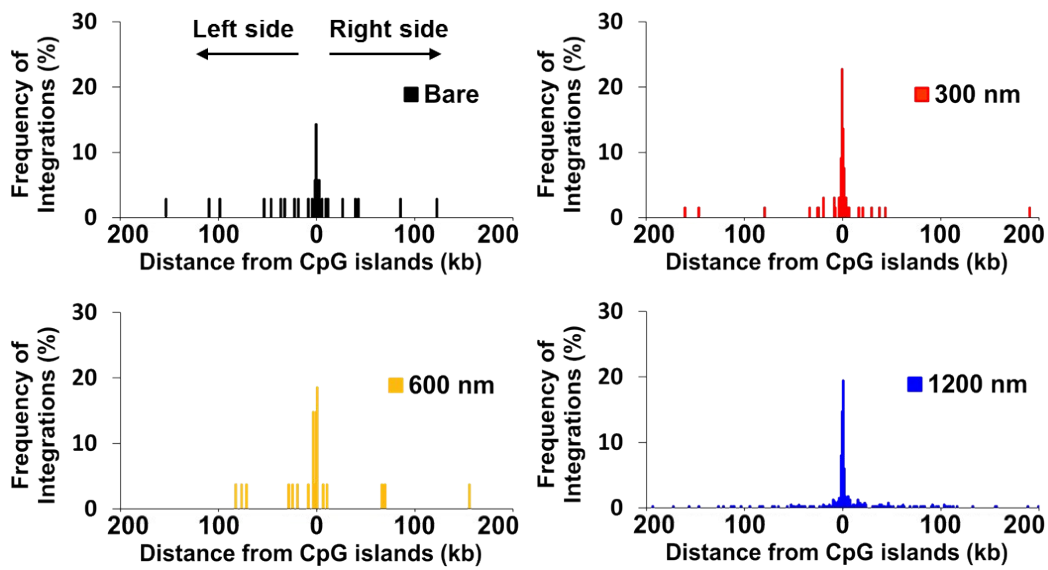
Figures

Figure S1.

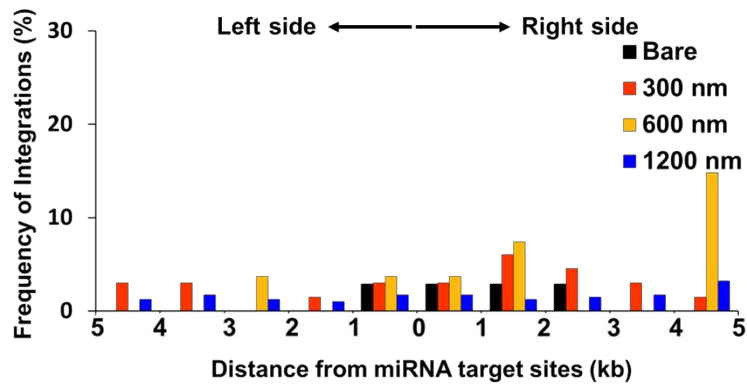
a



b



c



d

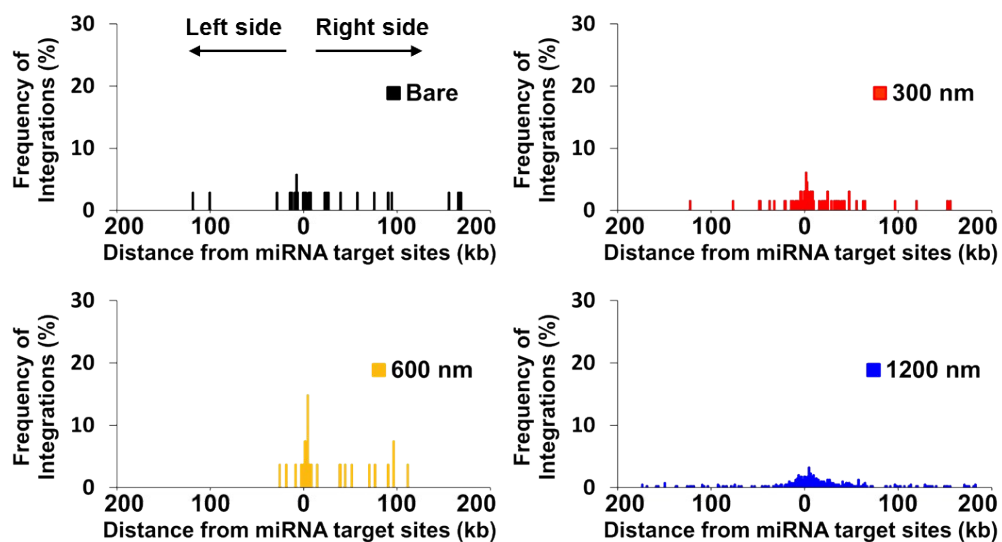
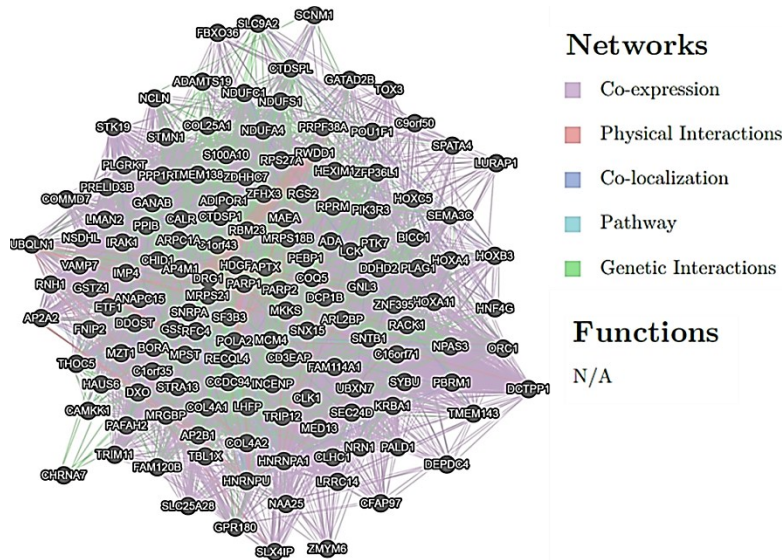


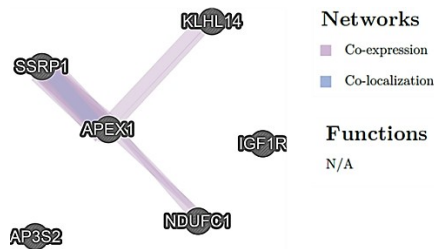
Figure S1. Spatial distribution of MLV integrations around CpG islands and miRNA target sites. (a) Within a 5-kb window of CpG islands. (b) Within a 200-kb window of CpG islands. (c) Within a 5-kb window of miRNA target sites. (d) Within a 200-kb window of miRNA target sites.

Figure S2.

a



b



c

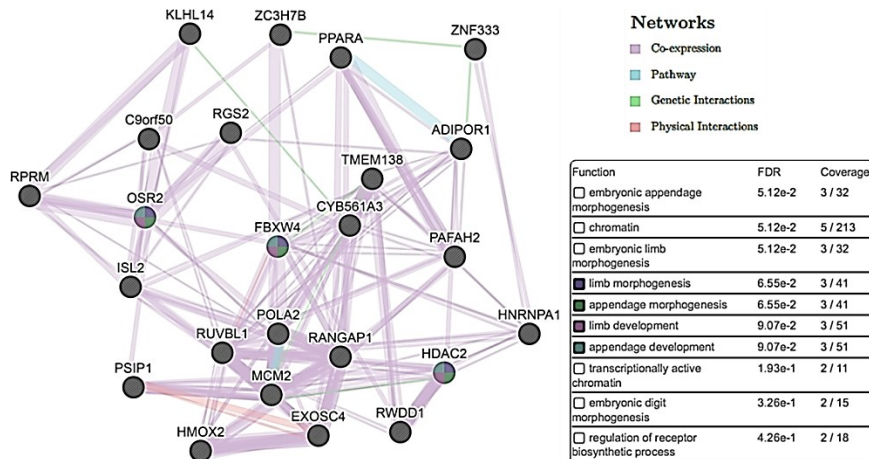


Figure S2. Genetic networks and biological functions for the genes of which spatially close cis-regulatory elements are located within 5 kb from MLV integration sites. Genes shown as nodes are connected when the

corresponding genes are related based on co-expression, co-localization, physical and genetic interactions between them, and involvement in common biological pathways^{1, 2}. The nodes for specific genes that are involved in a common biological function are labelled with the corresponding color shown in the box that lists the relevant functions. If a certain gene is involved in multiple biological functions, the gene node is filled with multiple colors corresponding to these functions. (a) For the “Cis-only group” of the 1200-nm bead case (curvature = $1.67 \mu\text{m}^{-1}$). (b) For the “Cis-only group” of the 600-nm bead case (curvature = $3.33 \mu\text{m}^{-1}$). (c) For the “Cis-only group” of the 300-nm bead case (curvature = $6.67 \mu\text{m}^{-1}$).

References

1. D. Warde-Farley, S. L. Donaldson, O. Comes, K. Zuberi, R. Badrawi, P. Chao, M. Franz, C. Grouios, F. Kazi, C. T. Lopes, A. Maitland, S. Mostafavi, J. Montojo, Q. Shao, G. Wright, G. D. Bader and Q. Morris, *Nucleic Acids Res.*, 2010, **38**, W214-220.
2. K. Zuberi, M. Franz, H. Rodriguez, J. Montojo, C. T. Lopes, G. D. Bader and Q. Morris, *Nucleic Acids Res.*, 2013, **41**, W115-122.