

Claims:**1. A kit comprising:**

(1) an RNA linker comprising:

(i) a first polynucleotide, and,

(ii) a second polynucleotide,

wherein the first and the second polynucleotides form a first double stranded region flanked by a first ligation compatible end, and a 3'-overhang at the 3'-end of the first polynucleotide, wherein the 3'-overhang comprises a random-sequence primer; and,

(2) a DNA linker comprising:

(iii) a third polynucleotide, and,

(iv) a fourth polynucleotide,

wherein the third and the fourth polynucleotides form a second double stranded region flanked by a blunt end and a second ligation compatible end, wherein the first and the second ligation compatible ends ligate to each other, or are adaptable to ligate to each other.

2. The kit of claim 1, wherein the first ligation compatible end is a 3'-overhang at the 3'-end of the second polynucleotide, and the second ligation compatible end is a 3'-overhang at the 3'-end of the third polynucleotide, wherein both 3'-overhangs anneal to each other for ligation.

3. The kit of claim 1, wherein the first double stranded region comprises a first recognition site for a first restriction enzyme (RE) that cleaves 3' to the random-sequence primer, or, wherein the second double stranded region comprises a second recognition site for a second restriction enzyme (RE) that cleaves 5' to the third polynucleotide.

4. The kit of claim 1, wherein one or more of said first, second, third, and fourth polynucleotides are DNA, or, wherein one or more of said first, second, third, and fourth polynucleotides comprise a modified nucleotide, such as a biotinylated T (Thymidine).

5. The kit of claim 1, wherein said first polynucleotide comprises a plurality of polynucleotides, each differing only at the random-sequence primer region, or, wherein said first polynucleotide

comprises a homogeneous population of polynucleotides having identical random-sequence primer, or, wherein said random-sequence primer comprises 4, 5, 6, 7, 8, or more nucleotides.

6. The kit of claim 1, wherein the first double stranded region comprises a unique sequence that distinguishes the RNA linker from the DNA linker, or, wherein the second double stranded region comprises a unique sequence that distinguishes the RNA linker from the DNA linker, or, wherein the last nucleotide of the first recognition site is the last base-paired nucleotide 5' to the random sequence primer, or, wherein the last nucleotide of the second recognition site is a base-paired nucleotide at the blunt end.

7. The kit of claim 1, wherein the first and the second restriction enzymes are the same, or, wherein the first or the second restriction enzyme is independently selected from:

AarI, AceIII, AfoI, BaeI, Bbr7I, BbvI, BbvII, BccI, Bce83I, BceAI, BceFI, BcgI, BciVI, BfiI, BinI, BpII, BsaXI, BscAI, BseMII, BseRI, BsgI, BsmI, BsmAI, BsmFI, Bsp24I, BspCNI, BspMI, BsrI, BsrDI, BstF5I, BtgZI, BtsI, CjeI, CjePI, EciI, Eco31I, Eco57I, Eco57MI, EcoP15I, Esp3I, FaeI, FauI, FokI, GsuI, HaeIV, HgaI, Hin4I, HphI, HpyAV, Ksp632I, MboII, MlyI, MmeI, MnlI, PfiI, PpiI, PstI, RleAI, SapI, SfaNI, SspD5I, Sth132I, StsI, TaqII, TspDTI, TspGWI, TspRI or Tth111II, or,

wherein the cleavage site of the first or the second restriction enzyme is at least about 10, 12, 14, 16, 18, 20, or more nucleotides 3' to the last nucleotide of the recognition site, or, wherein the first and the fourth polynucleotides are dephosphorylated.

8. The kit of claim 1, further comprising a reagent that cross-links protein and polynucleotide, such as a reagent comprising formaldehyde, or, further comprising an affinity reagent (*e.g.*, an antibody, or a monoclonal antibody) that specifically or selectively bind a component of chromatin (*e.g.*, histone), or, further comprising an end-repairing mixture that converts DNA containing damaged or incompatible 5'- and/or 3'-protruding ends to 5'-phosphorylated, blunt-ended DNA, or, further comprising a DNA ligase (*e.g.*, T4 ligase), or, further comprising a reagent that reverses cross-linking of protein and polynucleotide (*e.g.*, Proteinase K), or, further comprising the first and/or the second restriction enzyme(s), or, further comprising a pair of concatenating adapters for PCR amplification of blunt-ended double stranded DNA,

or, further comprising a Taq DNA polymerase, or, further comprising a reverse transcriptase.

9. A paired-end tag (PET) polynucleotide comprising a central region comprising the first and second double stranded regions of claim 1, said central region being flanked by:

(1) at a site proximal to said first double stranded region, a sequence tag of a non-coding RNA (ncRNA); and

(2) at a site proximal to said second double stranded region, a sequence tag of a genomic DNA.

10. The PET polynucleotide of claim 9, wherein the sequence tag of the non-coding RNA (ncRNA) has a free end resulting from digestion by said first restriction enzyme, or, wherein the sequence tag of the non-coding RNA (ncRNA) uniquely identifies a genomic region from which the ncRNA is transcribed, or, wherein said sequence tag of the non-coding RNA (ncRNA) is about 8-30 base pairs in length, or, wherein the sequence tag of the genomic DNA has a free end resulting from digestion by said second restriction enzyme, or, wherein the sequence tag of the genomic DNA uniquely identifies a genomic region at which the genomic DNA is located, or, wherein said sequence tag of the genomic DNA is about 8-30 base pairs in length.

11. A paired-end tag (PET) library comprising two or more members of the PET polynucleotide of claim 9, wherein each member of the PET library comprises the same said central region, and different said sequence tag of the noncoding RNA (ncRNA) of claim 9 or different said sequence tag of the genomic DNA of claim 9 or both.

12. A vector comprising a PET polynucleotide of claim 9, optionally further comprising a plurality of concatenated PET polynucleotide of claim 9.

13. A concatemer of two or more PET polynucleotides of claim 9.

14. A method of identifying functional interaction loci within a genome for non-coding RNAs (ncRNAs) of the genome, the method comprising:

(1) providing chromatin fragments comprising cross-linked genomic DNA fragments and cross-linked ncRNAs;

(2) using the RNA linker and the DNA linker of claim 1, ligating an end of a cross-linked genomic DNA fragment to an end of a cDNA of a cross-linked ncRNA, under a condition for proximity ligation, wherein said end of the cross-linked genomic DNA fragment is ligated to the DNA linker, and said end of the cDNA of the cross-linked ncRNA comprises the RNA linker;

(3) isolating a PET polynucleotide of claim 9 for sequencing analysis; and,

(4) mapping the sequence tag of the genomic DNA and the sequence tag of the ncRNA within each said PET polynucleotide to a reference genome, thereby identifying functional interaction loci within the reference genome for said non-coding RNAs (ncRNAs) of the reference genome.

15. The method of claim 14, wherein the ncRNAs and the genomic DNA are cross-linked in live cells through formaldehyde-mediated cross-linking, or, wherein chromatin fragments are generated by sonication, or, wherein the cDNA of the cross-linked ncRNA comprises a first strand cDNA reverse transcribed from the random sequence primer of the RNA linker, and the ncRNA template, or, wherein 2nd strand cDNA synthesis is carried out after proximity ligation but before step (3), or, further comprising repairing the ends of the cross-linked genomic DNA fragments to 5'-phosphorylated, blunt ended DNA prior to step (2), or, wherein the third polynucleotide of the DNA linker is dephosphorylated and the DNA linker does not self-ligate, or, further comprising identifying clusters of two or more PET polynucleotides having overlapping sequence tags of the genomic DNA and overlapping sequence tags of the ncRNA, optionally, further comprising excluding PET polynucleotides comprising sequence tags of rRNA, or, further comprising isolating or enriching a subset of chromatin fragments prior to step (2), optionally, the subset of chromatin fragments is isolated or enriched by immunoprecipitation using an antibody specific for a protein component of the subset of chromatin fragments and further optionally, wherein the protein component is a histone, a transcription factor, a polycomb-group (PcG) family protein; a recombination involved factor; a chromatin insulator or chromatin waver; a methyl-CpG-binding protein; or an RNA binding protein.