

WHAT IS CLAIMED IS:

1. A method for selectively amplifying target nucleic acid fragments having an overlapping region, comprising the steps of:
 - (a) obtaining a first nucleic acid sequence comprising a first tag (t2) and a first forward primer (F1) complementary to a first target nucleic acid fragment,
 - (b) obtaining a second nucleic acid sequence comprising a second tag (t1) and a first reverse primer (R1) complementary to the first target nucleic acid fragment,
 - (c) obtaining a third nucleic acid sequence comprising the second tag (t1) and a second forward primer (F2) complementary to a second target nucleic acid fragment,
 - (d) obtaining a fourth nucleic acid sequence comprising a third tag (t3), and a second reverse primer (R2) complementary to the second nucleic acid fragment, wherein the first and the second target nucleic acid fragments have an overlapping region,
 - (e) mixing the first and the second target nucleic acid fragments, the first, the second, the third, and the fourth nucleic acid sequences, and an effective amount of reagents necessary for performing a polymerase chain reaction (PCR);
 - (f) cycling the mixture of (e) through denaturing, annealing and primer extension steps of PCR for at least two times, and
 - (g) cycling the mixture of (f) through denaturing, annealing and primer extension steps of PCR at an annealing temperature higher than that in step (f) to obtain amplification products.
2. The method according to claim 1, wherein the second nucleic acid sequence further comprises a full sequence of the second forward primer (F2), in between the second tag (t1) and the first reverse primer (R1).
3. The method according to claim 1, wherein the second nucleic acid sequence further comprises F2[^], which is a 5'-end partial sequence of the second forward primer (F2), in between the second tag (t1) and the first reverse primer (R1).
4. The method according to claim 3, wherein the 5'-end partial sequence of the second forward primer contains 10-90% of the F2 sequence.

5. The method according to claim 1, wherein the annealing temperature in step (g) is 2-35° C. higher than the annealing temperature in step (f).

6. The method according to claim 1, wherein the PCR cycling in step (f) is repeated 2-10 times.

7. The method according to claim 1, wherein the third tag is the same as the second tag.

8. The method according to claim 6, further comprising the steps of:

(h) mixing the amplification products from step (g), either treated or untreated, with a first and a second universal PCR primers that bind to t1 and t2 respectively, but do not bind to the first and the second target nucleic acid fragments, and an effective amount of reagents necessary for performing a PCR, and

(i) cycling the mixture of step (h) through denaturing, annealing and primer extension steps of PCR to obtain second amplification products.

9. The method of claim 8, wherein the products from step (g) are pre-treated by dilution, single-strand exonuclease digestion, purification, or adaptor ligation.

10. The method of claim 3, wherein F2[^] contains 2-40 nucleotides.

11. The method of claim 3, wherein F2[^] contains 4-40 nucleotides.

12. The method of claim 3, wherein F2[^] is 1-5 nucleotides shorter than F2.