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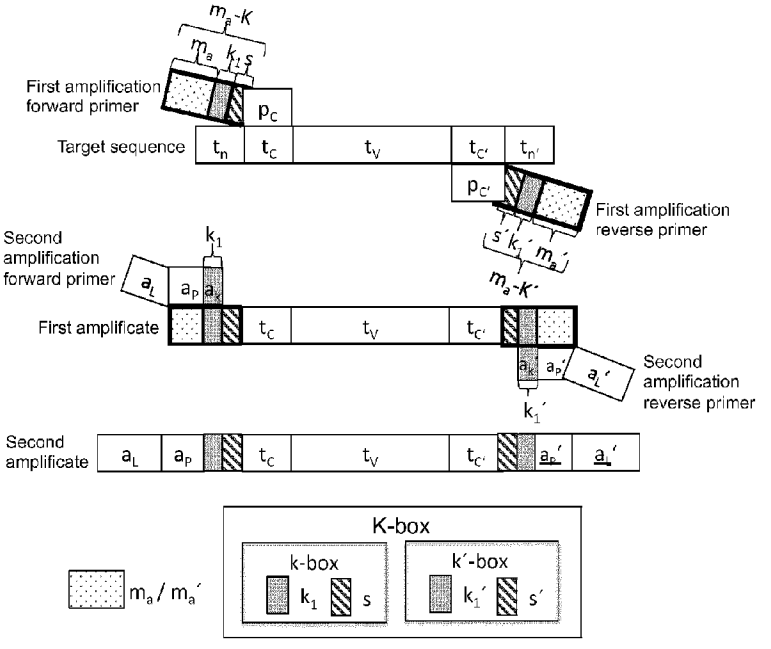

(57) Abrégé/Abstract:
The invention relates to a method for amplifying a target nucleic acid sequence t_n-t_C-t_V-$t_{C'}$-t_n' comprising a first amplification using a first primer pair with sequence m_a-K-p_C and m_a-K'-p_C', and a subsequent second amplification using a second primer pair with sequence a_L-a_P-a_K and a_L'-a_P'-a_K', wherein p_C is the same sequence as sequence element t_C. p_C and p_C' are 8 to 40 nucleotides in length, K comprises a 3'-terminal sequence k1-k2-s, s is a mismatch sequences preventing PCR bias, a_k is the same sequence as sequence element k_1, a_P-a_K hybridize to a contiguous sequence on sequence element m_a-K, k_1 is 2 to 9 nucleotides in length, a_L and a_L' can be any sequence, and t_V is a variable region within said target nucleic acid sequence. The invention further relates to collections of primer sets for use in the method of the invention.

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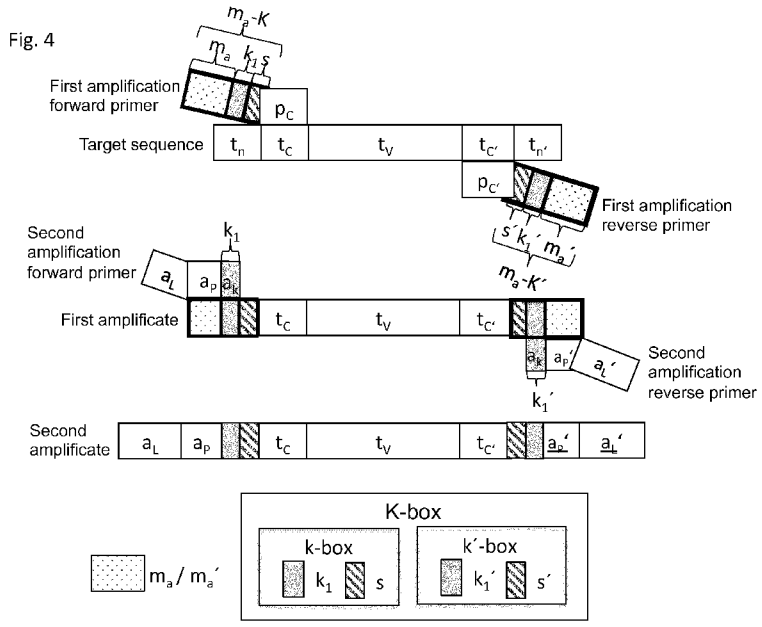
[Continued on next page]

(54) Title: METHODS AND PRIMER SETS FOR HIGH THROUGHPUT PCR SEQUENCING

Fig. 4



(57) Abstract: The invention relates to a method for amplifying a target nucleic acid sequence t_n-t_C-t_V-$t_{C'}$-t_n' comprising a first amplification using a first primer pair with sequence m_a-K-p_C and m_a-K'-p_C', and a subsequent second amplification using a second primer pair with sequence a_L-a_P-a_K and a_L'-a_P'-a_K', wherein p_C is the same sequence as sequence element t_C. p_C and p_C' are 8 to 40 nucleotides in length, K comprises a 3'-terminal sequence k1-k2-s, s is a mismatch sequences preventing PCR bias, a_k is the same sequence as sequence element k_1, a_P-a_K hybridize to a contiguous sequence on sequence element m_a-K, k_1 is 2 to 9 nucleotides in length, a_L and a_L' can be any sequence, and t_V is a variable region within said target nucleic acid sequence. The invention further relates to collections of primer sets for use in the method of the invention.

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Methods and primer sets for high throughput PCR sequencing

Description

Innovative techniques have been recently developed that allow the parallel generation of millions of sequence reads in a single run. High-dimensional data derived from this "next generation" or high throughput sequencing (NGS or HTS) may be used to resolve the biological variability within a single individual or within a population to a hitherto unknown precision and depth. Very sensitive techniques, however, bear the high risk of (cross-) contaminations from various sources. In order to avoid misinterpretation of NGS/HTS data, methods are needed that (i) prevent the amplification of potentially contaminating sequences and/or (ii) allow detecting the presence of contaminating sequences. The prevention of contaminations, in cooperation with identification of potential residual contaminations, is crucial for sensitive and reliable NGS diagnostics.

One major source for contamination is a two-step PCR amplification strategy, which is frequently used to generate PCR libraries suitable for NGS sequencing (Baetens et al., Human Mutation 32, 1053-1062 (2011)). In the first amplification reaction, the target nucleic acid sequence is amplified using specific primers flanked by a tail sequence (designated as m_a in the context of the present specification; e.g. a M13 or T7 tail). Subsequently, a second (adaptor) primer pair amplifies the first amplificate producing the second amplificate, which can be used for sequencing. In the second amplification reaction, nucleic acid sequences required for NGS sequencing are introduced, employing primers complementary at their 3´ end to the tail sequence of the first amplification primers. To make this approach more cost-efficient, multiplexing of several samples for NGS sequencing can be performed (Baetens, ibid.) by introducing so-called barcodes or multiplex-identifiers in the middle or close to the 5´ end of the second amplification primers.

An overview showing potential sources of contamination is given in the table overleaf. Fields C and D are of most relevance for the present invention. A two-step amplification strategy shows a high probability for cross-contamination by carry-over of amplicons from the first PCR to the re-amplification (C) due to the high number of amplicons generated in the first amplification reaction. Furthermore, PCR products of a second amplification may contaminate other second amplification reactions (D). In the case of amplicon isolation by gel extraction or PCR-purification kits, the risk of contamination is even higher.

Type of contamination	Timepoint of contamination	
	First amplification PCR mix	Second amplification PCR mix
1st amplification PCR product	(A) Prevention: UTP/UNG System Detection: PCR with first. amplification tail-specific primers	(C) Prevention and detection: Double contamination protection (this invention)
2nd amplification PCR product	(B) Detection: PCR with first or second amplification tail- or adaptor-specific primers. Prevention: UTP/UNG System	(D) Prevention and detection: Double contamination protection (this invention)

Table 1: Sources of cross-contamination and its prevention in a two-step PCR setting for NGS library generation. A & B: Contaminations of the first amplification by PCR products derived from another first or second amplification can be prevented by the UTP/UNG system and detected by tail- or adaptor-specific primers (US5035996, also published as EP0401037, US6844155B2, US7914986B2). C & D: Contaminations of the second amplification by PCR products derived from another first or second amplification can be prevented and detected by the "double contamination protection" described in the present invention.

The objective of the present invention is to (i) avoid and/or to (ii) detect PCR-based contamination in applications employing massive parallel sequencing (NGS/HTS) techniques. This objective is attained by the subject matter of the independent claims.

Terms and definitions

Nucleic acid sequences are given from 5' to 3' end. A sequence tract in the context used herein refers to a contiguous sequence; a sequence tract designator is a letter, optionally having a subscript or superscript, representing a sequence tract. k_1, k_1', k_2, k_2', s and s´ are examples for sequence tract designators. Where sequences are given as a sequence of sequence tract designators, such sequences are understood to be ordered similarly in 5' to 3' order. A sequence tract is also called a sequence element.

Nucleic acid target sequences may be DNA or RNA; in case of RNA being the target sequence for amplification and sequencing, RNA is transcribed into cDNA (by reverse transcriptase) prior to amplification.

A "primer" in the context of the present specification refers to a single stranded DNA -or nucleic acid analogue building block- oligomer having a length between 8 and 100 nucleotides.

"Capable of forming a hybrid" in the context of the present invention relates to sequences that are able to bind selectively to their target sequence under the conditions of a PCR or sequencing reaction (for example, 10 mmol/l Tris-HCl pH 8.3; 100 mmol/l KCl; 1.5 mmol/l $MgCl_2$; 0.2 mmol/l dNTP, each; primer annealing temperature of 40°C to 68°C). Such hybridizing sequences may be contiguously reverse-complimentary to the target sequence, or may comprise gaps, mismatches or additional non-matching nucleotides. The minimal length for a sequence to be capable of forming a hybrid depends on its composition, with C or G nucleotides contributing more to the energy of binding than A or T/U nucleotides, and on the backbone chemistry, with some modifications such as LNA having significantly higher binding energy and thus, shorter minimal lengths, compared to DNA.

"Nucleotide" in the context of the present invention is a nucleic acid or nucleic acid analogue building block, an oligomer of which is capable of forming selective hybrids with an RNA or DNA sequence on the basis of base pairing. The term *nucleotides* in this context includes the classic ribonucleotide building blocks adenosine, guanosine, uridine (and ribosylthymine), cytidine, and the classic deoxyribonucleotides deoxyadenosine, deoxyguanosine, thymidine, deoxyuridine and deoxycytidine. The term *nucleotides* further includes analogues of nucleic acids, such as phosphorotioates, 2'O-methylphosphothioates, peptide nucleic acids (PNA; N-(2-aminoethyl)-glycine units linked by peptide linkage, with the nucleobase attached to the alpha-carbon of the glycine) or *locked nucleic acids* (LNA; 2'O, 4'C methylene bridged RNA building blocks). A *primer sequence* as used in the context of the present specification may be composed of any of the above nucleotides, or mixtures thereof. In some embodiments, a primer sequence is composed of deoxynucleotides, with the last (from the 3' position) 1, 2, 3 or 4 internucleotide bonds being phosporothioates. In certain embodiments, the last 4, 3, 2 or 1 nucleotides (counting from the 3´position) are LNA nucleotide analogues. In certain embodiments, the second nucleotide from the 3´position is a LNA nucleotide analogue. In certain embodiments, the second and third nucleotide from the 3´position is a LNA nucleotide analogue.

Summary of the invention

The present invention provides guidelines for the design of three synergistically acting primer elements (designated generally as K-box with a capital "K", subdivided into a k-box (written with a lower case "k") for the forward primers and a k´-box for the reverse primers respectively) which in combination greatly improves the accuracy of PCR library preparations that can be analysed by methods including, but not restricted to, next generation sequencing (NGS).

The method of the invention makes use of two primer pairs. The first or initial primer pair amplifies the target sequence generating a first amplificate. Subsequently, a nested second (adaptor) primer pair amplifies the first amplificate producing the second amplificate, which can be used for sequencing.

For the analysis of a plurality of samples in parallel, the invention introduces the use of "sets" of individualized primer pairs for the first and second amplification to avoid cross-contamination, i.e. for each individual sample a different set is used. Thereby, a specific second primer pair is designed to only work together with a specific first primer pair within an individual set. The first and second primer pairs of an individualized primer set comprise a specially designed sequence tract referred to as K-box (K). Each K-box is specific for an individual primer set. The K-box of the (initial) primers for the first amplification step can comprise different elements k_1, k_1', k_2, k_2', s and s´. As explained in detail below, s/s´ prevent PCR bias, k_2/k_2' serve to detect contaminations and k_1/k_1', which are also present in the K-box of the second amplification primers, prevent contamination. Importantly, matching k_1/k_1' sequences enable the second primer pair to amplify the first amplificate only if the matching k_1/k_1' sequences were comprised in the first primer of the same set that was used to generate the first amplificate. Primer pairs are arranged in corresponding and matching sets. A number of sets (e.g. set 1 - 300) represent a collection. A collection with N sets will allow processing N different samples without cross-contaminations in the second amplification reactions.

All initial primers of the first amplification step of a collection amplify the same target sequence. Different collections, amplifying different target sequences (i.e. in a multiplex PCR), may be combined as a multiplex-collection.

Definition of frequently used terms

Term	Description
Set	Within an individual set, a specific second primer pair is designed to work only together with a specific first primer pair.
Collection	A number of sets represent a collection.
Multiplex collection	A combination of different collections amplifying different target sequences.

Detailed description of the invention

Overview of the target and primer sequence tracts

Short description of primer and sequence tract abbreviations

Abbreviation	Description
Target sequence tracts	
t_n-t_C-t_V-t_C'-t_n'	Different sequence tracts of the target nucleic acid sequence.
t_C/t_C'	Target sequence tract used for target-specific primer binding
t_V	Target nucleic acid sequence of interest.
t_n/t_n'	Sequence tracts of the target gene located in 5' and 3' position of t_C/t_C', respectively.
Sequence tracts of the primers used for first amplification	
m_a/m_a´	Tail sequence (e.g. M13) of first amplification primer.
m_a-K/m_a-K´	Tail sequence + K-box of first amplification primer.
p_C/p_C'	First amplification primer sequence tracts which provide target specificity.

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Sequence tracts of the primers used for second amplification	
a_P/a_P'	Second amplification primer sequence tracts which hybridize to m_a/m_a'.
a_L/a_L'	Second amplification primer sequence tracts for NGS sequencing.
K-box	
K-box	Comprises the sequence tracts k_1/k_1', k_2/k_2', s/s'.
k-box	K-box of the left (up-stream) first and second amplification primer.
k'-box	K-box of the right (down-stream) first and second amplification primer.
k_1/k_1'	K-box elements of first and second amplification primers for suppression of contaminations.
k_2/k_2'	K-box element of first amplification primers for detection of contaminations.
s/s'	K-box element present in first amplification primers to avoid a PCR bias possibly introduced by k_1/k_1', k_2/k_2'.

In general, the "prime" or apostrophe (') indicates that a sequence tract or element has a similar functional characteristic as its non-prime counterpart, but is located on a primer on the other side of the target sequence, and is understood to work in reverse direction.

The target nucleic acid sequences subject to amplification are described as t_C-t_V-t_C'. Therein, t_C/t_C' are the sequence tracts to which the forward (left) and reverse (right) primary amplification primer hybridizes, respectively. t_V is a region of interest (the sequenced part likely to contain the variability that the sequencing seeks to elucidate) within a target nucleic acid sequence. Furthermore the target nucleic acid sequence elements t_n and t_n' are located in 5' and 3' position, respectively, of t_C-t_V-t_C'. The target structure can also be described as t_n-t_C-t_V-t_C'-t_n'.

A primer for use in a method or collection of primers according to the invention is composed of at least two sequence tracts.

A left first or initial primer used in the first round of amplification comprises (from 5' to 3' OH-end) a sequence tract m_a-k-box (also designated as m_a-K) and a sequence tract p_C (Fig. 1). Sequence tract p_C provides target specificity, while m_a-K provides a non-target-specific sequence tract, parts or all of which can be used for hybridization of a second "adaptor" primer. Within m_a-K the sequence tract m_a can comprise sequence elements necessary for sequencing purposes or consist of sequences such as M13, whereas the K-box comprises the K-box elements (k_1/k_1', k_2/k_2', s/s´).

The left adaptor (second) primer comprises distinct sequence tracts, designated a_L and a_P-a_K, which are used for the second amplification. a_L and a_P confer functional features for high throughput sequencing, e.g. template sequences for sequencing primers and/or for attachment of the amplificate to a solid surface such as a slide or a bead. Furthermore, a_P can consist of a sequence such as M13. The sequence tract a_K comprises k_1, which is a sequence element of the K-box.

The reverse or right primers, of both the initial and adaptor primers, comprise sequence tracts of similar characteristics, designated m_a´-k´-box (also designated as m_a-K') and p_C' for the right initial (first) primer. The right adaptor (second) primer comprises the sequence tracts a_L' and a_P'-a_K' (Fig. 1).

Sequence elements a_L and a_P are used for sequencing purposes, such as, by way of non-limiting example, sequencing primer hybridization sites and/or solid support attachment sites. Methods for high-throughput sequencing are well known in the art and include so called "Illumina" bridge PCR-sequencing methods, shown inter alia in US2011045541A1, US2005100900A1, US2002055100A1; pyrosequencing, shown inter alia in US6,274,320, US 7,244,567, US 7,264,929; US 7,323,305 and US 7,575,865; "2 base encoding" technology (US4883750, US5750341) and others. Further relevant methods for high-throughput sequencing and applications are described in the following manuscripts:

Robustness of Amplicon Deep Sequencing Underlines Its Utility in Clinical Applications. Grossmann et al. J Mol Diagn. 2013 May 14. doi:pii: S1525-1578(13)00057-3. PMID:23680131; Solid-State and Biological Nanopore for Real-Time Sensing of Single Chemical and Sequencing of DNA. Haque et al. Nano Today. 2013 Feb;8(1):56-74. PMID:23504223; Next-generation sequencing - feasibility and practicality in haematology. Kohlmann et al. Br J Haematol. 2013 Mar;160(6):736-53. doi: 10.1111/bjh.12194. Epub 2013 Jan 7. PMID:23294427; Progress in ion torrent semiconductor chip based sequencing.

Merriman et al. Electrophoresis. 2012 Dec;33(23):3397-417. doi: 10.1002/elps.201200424. Erratum in: Electrophoresis. 2013 Feb;34(4):619. PMID:23208921; Comparison of next-generation sequencing systems. Liu et al. J Biomed Biotechnol. 2012;2012:251364. doi: 10.1155/2012/251364. PMID:22829749; Current state-of-art of sequencing technologies for plant genomics research. Thudi M et al. Brief Funct Genomics. 2012 Jan;11(1):3-11. doi: 10.1093/bfgp/elr045. PMID:22345601; Integration of next-generation sequencing into clinical practice: are we there yet? Kohlmann A et al. Semin Oncol. 2012 Feb;39(1):26-36. doi: 10.1053/j.seminoncol.2011.11.008. PMID:22289489.

The primers of the invention provide particular sequence elements (K-boxes), which greatly reduce the likelihood that such contaminations occur and enable the recognition of amplicon contaminations within the sequencing results. The K-box elements are designated k_1, k_1', k_2, k_2', s and s', and are selected by bioinformatics methods as one single K-box, the selection being made not to perform mismatches with the 3´ends of the primers employed. For clarification of their mode of action, however, the three K-box elements are outlined in the following in detail separately:

Role of k_1 and k_1´ K-box elements and mode of action:

The k_1/k_1' sequences are designed to prevent contamination from previous amplification reactions. As outlined in Fig. 1 the forward primer of the first PCR is composed of (i) a target-specific proportion p_C, (ii) and the K-box sequence element k_1, which is specific for each primer set and (iii) and a sequence element m_a. The reverse primer of the first PCR is composed in the same way but in reverse-complement fashion.

A specific k_1 and/or k_1´ element is used for a particular reaction and is varied when the amplification reaction is performed repeatedly. In other words, if a routine diagnostic amplification reaction (e.g. the analysis of T-cell receptor beta (TCRß) rearrangements or the analysis of cancer genes) is performed a plurality of times in the same laboratory, primers using different k_1/k_1´ elements may be used for each individual experiment until all variations of k_1 and k_1' have been consumed. The 3' end of the second (or adaptor) primer is chosen to hybridize to k_1 or k_1', respectively, along the entire length of k_1 (or k_1'). Thus, pairs of first and second primers are formed, where the "left" adaptor primer hybridizes to sequence tract k_1 that was generated by the "left" initial primer, and the "right" adaptor primer hybridizes to the sequence tract k_1´ that was generated by the "right" initial primer. In order to allow full hybridization, the adaptor primer will hybridize not necessarily only to the tract generated by

k_1 (or k_1'), but - if k_1 (or k_1') does not provide sufficient length of hybridization tract - for the hybridization temperature selected for the reaction - also to a sequence tract adjacent to k_1 (or k_1') on its 5' end, namely m_a and m_a' (see Fig. 1).

As example, five samples are processed in parallel with five different sets of first (initial) and second (adaptor) primers with a k_1/k_1' element combination specific for each of the five samples. In the case of contamination of the second PCR of sample 2 with PCR products derived from the primary PCR of sample 1, the mismatch between the k_1 and/or k_1' element of the PCR product of sample 1 and the different k_1 and/or k_1' elements of the sample 2 primers will prevent the amplification of the contaminating material.

Both, k_1 and k_1' can be of 1, 2, 3, 4, 5, 6, 7, 8, 9 or more bases in length. As shown in the proof of principle example below (Table 4) even a k_1/k_1' sequence of one base reduces contamination. However since the number of permutations is relatively low and the discriminatory power (in the sense of contamination suppression) of a one-base mismatch not as great as that of longer mismatches, k_1 and k_1' elements of greater length, for example 2, 3, 4, 5, 6, 7, 8 or 9 have broader utility (Examples are given in Tables 16-19).

Role of k_2 and k_2' K-box elements and mode of action:

A further K-box element is a sequence element k_2 or k_2', comprised in the sequence tract m_a-K or m_a-K', respectively, of the initial primer, but not in the corresponding sequence tract in the second amplification (adaptor) primer (Fig. 2). Hence, k_2 and k_2' are characteristic of the initial primer only. In embodiments where k_2 (or k_2') and k_1 (or k_1') sequences are comprised in the initial primer, the k_2 (or k_2') element is downstream (towards the 3' end) from the k_1 (or k_1') sequence element (Fig. 2).

While k_1 and k_1' lead to suppression of contaminations, the k_2/k_2' sequences are designed to detect contamination from previous amplification reactions.

Therefore, as in the case of k_1 (or k_1'), the presence of k_2 (or k_2') in specific variation (Examples are provided in Table 20) over a plurality of primer sets used at different times or for different samples in the same routine setting helps to detect contaminations and synergistically control the contamination suppression efficacy of k_1 / k_1'.

Role of S and S' K-box elements and mode of action:

The K-box elements S/S' prevent a possible PCR bias dependent on k_1/k_1' and k_2/k_2' sequences as outlined below.

s separates the target-specific left initial primer sequence p_C from the sequence tracts k_2 and/or k_1. s' separates the target-specific right initial primer sequence p_C' from k_2' and/or k_1' (see Fig. 3-4). Since k_1/k_1' and k_2/k_2' vary among different primers used in subsequent amplifications, some variations of k_2/k_2' and/or k_1/k_1' may coincidentally match in their 3' end nucleotides the sequence of the target next to the hybridizing part of the initial primers p_C or p_C'. The target sequence-matching tract of the initial primer would be longer for some targets than for others, leading to PCR bias resulting from higher annealing temperatures.

This problem is amplified if – as provided in some embodiments of the present invention - multiplex-collections are employed. A set within a multiplex collection addresses different target sequences for use in a multiplex PCR, but carries the same k_1 (and k_1') and, optionally, k_2 (and k_2') elements. Here, different annealing temperatures might introduce a PCR bias that may significantly skew any quantitative interpretation of the results.

Hence, in some embodiments a short (1, 2, 3 or 4 nucleotides) separator sequence s (s') is introduced into the k/k' sequence tract, immediately upstream of the p_C/p_C' sequence tract, i.e., at the 3' terminal end of k/k'. s and s' are thus designed to prevent a hybrid formation with the template (target) sequence t_n/t_n' adjacent to the primer-hybridizing sequence tract t_C/t_C', as outlined in Fig. 3-4.

Advantages of using combined k_1, k_2, s and k_1', k_2', s' sequence elements:

The three K-box elements work synergistically to achieve the overall goal of preventing PCR-based contamination in applications employing NGS/HTS techniques.

Since the k_2/k_2' elements are only present in the first amplification primers an eventual contamination can still be identified in the second amplification product. Thus, k_2/k_2' elements determine and therefore control the contamination suppression efficiency of k_1/k_1'.

Furthermore, s/s' is the K-box family member that solves the problem of a possible PCR bias dependent on k_1/k_1' and k_2/k_2' sequences.

Finally, all three K-box elements together must be designed bioinformatically as one unit and optimized not to form hybrids (e.g. more than 6 bp match within 10 bp) that might lead to mispriming with any primer sequence but especially at the 3'ends of the primers employed.

Different aspects of the invention:

According to a first aspect of the invention, a method for amplifying a target nucleic acid sequence t_C-t_V-t_C' comprised within a sequence tract t_n-t_C-t_V-t_C'-t_n' is provided, said

method comprising conducting a plurality of polymerase chain reaction (PCR) amplification reactions. In other words, the invention is directed toward a method of repeatedly amplifying or sequencing the same target sequence (albeit in variation that may occur within a sequence tract of interest designated t_V). Each reaction comprises two PCR amplification steps: a first amplification step, in which a target nucleic acid sequence is amplified using a first ("initial") primer pair, and includes the reactants known to the skilled artisan as necessary for conducting a PCR reaction, i.e. nucleoside triphosphates (ATP, GTP, TTP, CTP), a suitable buffer and thermostable polymerase such as Taq polymerase. This initial primer pair is composed of a left (forward) first ("initial") PCR primer having a sequence m_a-K-p_C composed of two sequence elements m_a-K and p_C in 5'-3' orientation, and a right (reverse) initial primer having a sequence m_a-K'-p_C', similarly oriented from 5' to 3'. The product of the first amplification set is a first amplificate, comprising the target nucleic acid sequence flanked on either side by sequence tracts m_a-K and m_a-K', respectively (Fig. 1).

The sequence t_C-t_V-t_C' constitutes the amplified region of the target, whereas the short sequence elements t_n and t_n' are flanking regions that define the selection of sequence elements s and s' in the primer set.

The method of the invention further comprises a second PCR amplification step, whereby a first amplificate is re-amplified using a second ("adaptor") primer pair composed of a left (forward) second ("adaptor") PCR primer having a sequence a_L-a_P-a_K composed of the sequence elements a_L, a_P and a_K in 5'-3' orientation and a right (reverse) second ("adaptor") PCR primer having a sequence a_L'-a_P'-a_K'. Again, the reactants necessary for conducting a PCR reaction, i.e. nucleoside triphosphates, a suitable buffer and thermostable polymerase are present. The product of the second amplification is a second amplificate (Fig. 1).

Within the first primer pair, p_C displays the same sequence as the target sequence element t_C, p_C' is the reverse complimentary sequence to t_C'. In other words, p_C and p_C' are the target-specific primer sequences that hybridize to the target and effect amplification. p_C and p_C' each independently from one another are 8 to 40 nucleotides in length.

Within the first primer pair, m_a-K comprises a k-box with the sequence element k_1, and m_a-K' comprises a k'-box with a sequence element k_1'. k_1 and k_1' each independently from one another are a sequence 2, 3, 4, 5, 6, 7, 8 or 9 nucleotides in length. k_1 and k_1' are not meant to hybridize to the target sequence. A first primer pair and a second primer pair with

identical k_1 and k_1' form a set. k_1 and k_1' are the sequence elements that individualize different primer sets from one another. k_1 and k_1' match the first "initial" and the second "adaptor" PCR primer pairs to one another within a set. Thus, k_1 and k_1' of the first initial primer pair correspond to the sequence elements a_k (k_1) and a_K' (k_1'), respectively, in the second primer pair (Fig. 1).

Furthermore, m_a-K comprises a sequence element s on its 3' terminus and m_a-K' comprises a sequence element s' on its 3' terminus. s and s' are mismatch sequences selected not to form a continuous hybrid sequence with sequence element t_n and t_n' and s and s' are independently 1, 2, 3, 4 or 5 nucleotides in length. As described in detail above, the effect of this element is to avoid an inadvertent rise of the annealing temperature of p_C and p_C' on the target in some primers dependent on m_a-K and/or m_a-K´ sequences. This element helps to avoid PCR bias (Fig. 3-4).

Sequence tract a_P-a_K hybridizes to a contiguous sequence on sequence element m_a-K, and a_P'-a_K' hybridizes to a contiguous sequence on sequence element m_a-K'. In other words, a_P-a_K (and its analogue a_P'-a_K') is the sequence tract on the 3' terminal end of the adaptor primer that recognizes the initial primer.

m_a-K and m_a-K' can be of any length that fits their general purpose, but will generally be within the usual length of a primer target sequence, i.e. m_a-K and m_a-K' will be generally each independently from one another a sequence 10 to 40 nucleotides in length, in certain embodiments from about 15 to 30 nucleotides in length.

a_L and a_L' and also a_P and a_P´ independently from one another can be any sequence that fits the general purpose of providing a sequence useful for sequencing the second amplificate, for example by providing a sequencing primer annealing target and/or a sequence for attaching the second amplificate to a chip or bead or any other surface-bound structure as may be useful in NGS/HTS sequencing.

t_V is a variable region within said target nucleic acid sequence.

Additionally, according to this first aspect of the invention, a particular set of primers for each one of said plurality of amplification reactions is provided, for each of which the sequence of one of k_1 and k_1' is different from the sequence of any other k_1 and k_1', respectively, in any other set of the sets of primers. In other words, no particular sequence of k_1 and/or k_1' occurs more than once in any set.

In some embodiments, a_L and a_L' are 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65 or 70 nucleotides in length. In some embodiments, p_C and p_C' each independently from one another are 8, 10, 12, 14, 16, 18, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 32, 34, 36, 38 or 40 nucleotides in length.

Thus, in certain embodiments, m_a-K comprises a 3'-terminal sequence k_1-s, and m_a-K' comprises a 3'-terminal sequence k_1'-s'.

In certain embodiments, m_a-K comprises a sequence element k_2 3'-terminal to sequence element k_1, and m_a-K' comprises a sequence element k_2' 3'-terminal to sequence element k_1' (Fig. 2). k_2 and k_2' each independently from one another are 2, 3, 4, 5, 6 or 7 nucleotides in length. k_2 and k_2' serve to individualize the first primer pair of the set from other first (initial) primers. k_2 and k_2' have no complementary sequence elements on the second ("adaptor") primers. The second primers k_1 and k_1' have complementary sequences to the first primers within one primer set.

In some embodiments, the primer set uses all three elements k_1/k_1', k_2/k_2' and s/s' (Fig. 3). Thus m_a-K comprises a 3'-terminal sequence k_1-k_2-s, and m_a-K' comprises a 3'-terminal sequence k_1'-k_2'-s'. In some embodiments, m_a-K comprises a 3'-terminal sequence k_1-k_2-s, and m_a-K' comprises a 3'-terminal sequence k_1'-k_2'-s' and the first and/or second primer pairs have phosphorothiolated moieties on the last 1, 2, 3 or 4 internucleotide linkages at their 3'terminal end.

In certain embodiments, K comprises a 3'-terminal sequence k_1-k_2-s, and K' comprises a 3'-terminal sequence k_1'-k_2'-s', wherein

- k_1 and k_1' each independently from one another are a sequence 2 to 9 nucleotides in length,
- k_2 and k_2' each independently from one another are a sequence 2 to 7 nucleotides in length;
- s and s' are mismatch sequences selected not to form a continuous hybrid sequence with sequence element t_n and t_n', and s and s' are independently 1, 2, 3, 4 or 5 nucleotides in length,

- a_k is the same sequence as sequence element k_1 and a_K' is the same sequence as sequence element k_1',
- a_k and a_K' are selected not to hybridize to k_2 and k_2', respectively;

- a_P-a_K hybridizes to a contiguous sequence on m_a-K and a_P'-a_K' hybridizes to a contiguous sequence on m_a-K'
- p_C, p_C', m_a-K and m_a-K' each independently from one another are a sequence 10 to 40 nucleotides in length, and a_L and a_L' independently from one another can be any sequence.

In certain embodiments, k_1 and k_1' each independently from one another are a sequence 5, 6, 7, 8 or 9 nucleotides in length, s and s' are each independently 2, 3, or 4 nucleotides in length, and /or k_2 and k_2' each independently from one another are a sequence 2, 3, 4, 5 or 6 nucleotides in length.

In certain embodiments, for each particular set of primers,

- each k_1 is different from of any other k_1 and each k_1' is different from any other k_1', resulting in a specific combination of k_1 and k_1' for each set, and/or
- each k_2 is different from of any other k_2 and each k_2' is different from any other k_2' resulting in a specific combination of k_2 and k_2' for each set.

In some embodiments, the sets of primers comprise

- a left (forward) initial primer comprising a sequence element p_C selected from any one of SEQ ID NO 001 to SEQ ID NO 045 and a right (reverse) initial primer comprising a sequence element p_C' selected from any one of SEQ ID NO 046 to SEQ ID NO 058; and/or
- a left (forward) initial primer comprising a sequence element p_C selected from any one of SEQ ID NO 189 to SEQ ID NO 232 and a right (reverse) initial primer comprising a sequence element p_C' selected from any one of SEQ ID NO 233 to SEQ ID NO 246; and/or
- a left (forward) initial primer comprising a sequence element m_a selected from any one of SEQ ID NO 059 to SEQ ID NO 085 and a right (reverse) initial primer comprising a sequence element m_a selected from any one of SEQ ID NO 086 to SEQ ID NO 117; and/or
- a left (forward) adaptor primer comprising a sequence element a_L-a_P selected from any one of SEQ ID NO 118 to SEQ ID NO 149 and a right (reverse) adaptor primer

comprising a sequence element m_a selected from any one of SEQ ID NO 150 to SEQ ID NO 182.

In certain embodiments, k_1 and k_1' and/or k_2 and k_2' (where k_2 and k_2' are contained in the sequence) are selected not to hybridize to the sequence elements t_n and t_n' adjacent to the amplified sequence tract. In other words, k_1 and k_1' and k_2 and k_2' (where k_2 and k_2' are contained in the sequence) are separate and distinct from a primer sequence directed toward target amplification. All k-box components solely and exclusively have the purpose of distinguishing the primer set, and thus preventing erroneous amplification of amplicon contaminations, as set forth above.

In some embodiments, the left initial primer, the right initial primer, the left adaptor primer and/or the right adaptor primer are characterized by one or several nuclease resistant nucleotide(s) or nuclease resistant internucleosidic bond(s) on or near (at position 1, 2, 3 and /or 4 counting from) the 3' terminus of the primers. In other words, the 3' end of the primer is protected against 3' exonuclease digestion by providing bonds that inhibit or resist the exonuclease activity.

In some embodiments, the nuclease resistant internucleosidic bond is a phosphorothioate bond. In some embodiments, the nuclease resistant nucleotide is a 2-O-methylated ribonucleotide. In some embodiments, the nuclease resistant nucleotide is an LNA building block (a 2'O, 4'C-methylene bridged RNA building block). In some embodiments, the nuclease resistant nucleotide is a 2-F-deoxyribonucleotide. In some embodiments, the nuclease resistant nucleotide is a 2-propyne-deoxyribonucleotide.

In some embodiments, the nuclease resistant nucleotide or nuclease resistant internucleosidic bond is the last internucleosidic bond counting from the 3' terminus of said primer(s). In some embodiments, the nuclease resistant nucleotide or nuclease resistant internucleosidic bond is located on position -1, -2, -3, and/or -4 counting from the 3' terminus of said primer(s). In some embodiments, the nuclease resistant nucleotide or nuclease resistant internucleosidic bond are located at position – 1 and – 2, in some embodiments at position -1 and -2 and – 3, or in some embodiments at position -1 and -2 and – 3 and -4.

For avoidance of doubt, in the sequence 5' GpApTxGyC 3', y marks the -1 position, x marks the -2 position, p marks the -3 and -4 position of the internucleosidic bonds, and C marks the position -1 and G marks the position -2 of the nucleotide counting from the 3' end.

According to one alternative of this first aspect of the invention, a method for sequencing a target sequence t_C-t_V-t_C' comprised within a sequence tract t_n-t_C-t_V-t_C'-t_n' is provided, said method comprising the steps of

a. amplifying said target sequence by a method as outlined above in any of the aspects and embodiments provided, and

b. sequencing said second amplificate including sequence elements m_a-K and/or m_a-K', yielding a set of readout sequences.

Methods of sequencing are known to the skilled artisan and include (but are not limited to) the methods described in the publications referenced above.

In some embodiments, the method for sequencing a target sequence further comprises the steps of

c. aligning each member of said set of readout sequences to sequence element m_a-K and/or m_a-K' comprised in said initial primer, respectively, and

d. assigning a value of 0 or 1 as a measure of contamination to each sequence of said set of readout sequences (e.g. the results of NGS sequencing of one sample), wherein complete alignment of a member of said set of readout sequences (i.e. a particular readout sequence) to said sequence element m_a-K or m_a-K' corresponds to the value of 0 (signifying no contamination for that particular set member), and incomplete alignment of a member of said set of readout sequences to said sequence element m_a-K or m_a-K' corresponds to 1 (signifying that this particular read was caused by a contamination); and

(i) determining a percentage of contamination by adding all values assigned in step d), resulting in a value sum, and dividing said value sum by the total number of reads; and / or

(ii) removing the sequences having a value of "1" from the sequence set.

Thus, if the set of readout sequences consists of 10.000 sequences, for 32 of which the sequence tract corresponding to m_a-K or m_a-K' does not align with the particular sequence expected (chosen) for the particular run, then a percentage of contamination of 32/10.000, resulting in 0,0032 or 0,32% is computed.

In other words, the method for sequencing a target sequence includes a step of validation or quality control, wherein all sequences obtained are checked for the presence of identifier

sequences k_2, k_2' and/or k_1, k_1' (k_1, k_1' can be relevant as identifier of the first amplification reaction, since k_1, k_1' of the second amplification primer can be partially degraded in the second PCR by proof reading polymerases as outlined in detail in the proof of principle examples). Unexpected identifier sequences, or unexpected combinations thereof, are regarded as contamination.

For each amplification reaction, a different set of primers is used, the difference being in different sequence elements k_1, k_1', k_2 and k_2' or combinations thereof. In other words, the method comprises the steps of providing a set of primers for each sample of said plurality of samples, each set of primers comprising a pair of initial PCR primers comprising a left initial PCR primer having a sequence m_a-K-p_C and a right initial primer having a sequence and m_a-K'-p_C', and a pair of adaptor PCR primers comprising a left adaptor PCR primer having a sequence a_L-a_P-a_K and a right adaptor PCR primer having a sequence a_L'-a_P'-a_K'.

According to another aspect of the invention, a set of primers for use in a method for amplifying or sequencing a target nucleic acid sequence according to the invention is provided, wherein each set of primers of said collection comprises

i. a pair of initial PCR primers comprising a left (forward) initial PCR primer having a sequence m_a-K-p_C and a right (reverse) initial primer having a sequence and m_a-K'-p_C', and

ii. a pair of adaptor PCR primers comprising a left adaptor PCR primer having a sequence a_L-a_P-a_K and a right adaptor PCR primer having a sequence a_L'- a_P'-a_K',

wherein all sequence designators have the meaning outlined above, namely:

- p_C is the same sequence as sequence element t_C and p_C' is the reverse complimentary sequence to t_C',
- K comprises a sequence element k_1 and a 3'-terminal sequence element s, and K' comprises a sequence element k_1' and a 3'-terminal sequence element s', wherein
  - k_1 and k_1' each independently from one another are a sequence 2 to 9 nucleotides in length,
  - s and s' are mismatch sequences selected not to form a continuous hybrid sequence with sequence element t_n and t_n', and s and s' are each independently 1, 2, 3, 4 or 5 nucleotides in length,

- a_k is the same sequence as sequence element k_1 and a_K' is the same sequence as sequence element k_1',
- a_P-a_K hybridizes to a contiguous sequence on m_a-K and a_P'-a_K' hybridizes to a contiguous sequence on m_a-K'
- p_C, p_C', m_a-K and m_a-K' each independently from one another are a sequence 10 to 40 nucleotides in length, and a_L and a_L' independently from one another can be any sequence.

In some embodiments, K comprises a 3'-terminal sequence k_1-k_2-s, and K' comprises a 3'-terminal sequence k_1'-k_2'-s', wherein k_2 and k_2' each independently from one another are a sequence 2 to 7 nucleotides in length, and a_k and a_K' are selected not to hybridize to k_2 and k_2', respectively.

In certain embodiments, all sequence elements a_P are the same and all sequence elements a_P' are the same for a collection.

In one embodiment, a set of primers according to the invention (and intended for use in a method of the invention) comprises:

- a left (forward) initial primer comprising a sequence element p_C selected from any one of SEQ ID NO 001 to SEQ ID NO 045 and a right (reverse) initial primer comprising a sequence element p_C' selected from any one of SEQ ID NO 046 to SEQ ID NO 058; and/or
- a left (forward) initial primer comprising a sequence element p_C selected from any one of SEQ ID NO 189 to SEQ ID NO 232 and a right (reverse) initial primer comprising a sequence element p_C' selected from any one of SEQ ID NO 233 to SEQ ID NO 246; and/or
- a left (forward) initial primer comprising a sequence element m_a selected from any one of SEQ ID NO 059 to SEQ ID NO 085 and a right (reverse) initial primer comprising a sequence element m_a selected from any one of SEQ ID NO 086 to SEQ ID NO 117; and/or
- a left (forward) adaptor primer comprising a sequence element a_L-a_P selected from any one of SEQ ID NO 118 to SEQ ID NO 149 and a right (reverse) adaptor primer comprising a sequence element m_a selected from any one of SEQ ID NO 150 to SEQ ID NO 182.

According to another aspect of the invention, a collection of sets of primers for use in a method for amplifying or sequencing a target nucleic acid sequence according to any of the preceding aspects and embodiments is provided, wherein each set adheres to the definition given for the previously defined aspect of the invention (a set of primers according to the invention), and wherein for all sets of primers comprised within said collection, all sequence elements p_C are the same and all sequence elements p_C' are the same. Furthermore, each set of primers is characterized by a different combination of k_1 and k_1' from any other set of primers.

In other words: in each of these sets of primers, k_1 is different from one of any other k_1 and/or k_1' is different from one of any other k_1' in each of the other sets. In other words, each set has a unique K1/K1´combination.

In some embodiments of this aspect of the invention, where k_2 and k_2' are present, for each said particular set of primers, one of k_2 and k_2' are different from of any other k_2 and k_2', respectively. In other words: each set of primers is characterized by a different combination of k_1, k_1', k_2 and k_2' from any other set of primers.

In certain embodiments, the collection of sets of primers according to the invention comprise 4, 8, 16, 24, 32, 40, 48, 56, 64, 72, 80, 160, 200, 256 or 1024 different sets of primers.

According to yet another aspect of the invention, a multiplex-collection (primer library) comprising a plurality of collections of sets of primers according to the invention is provided, whereby each collection is characterized by a different combination of p_C and p_C'.

A multiplex set within a multiplex collection is defined as a multiplex collection member (primer library member). In other words, a multiplex set is a plurality of sets of primers for employment in a method of the invention, wherein the plurality is characterized in that each member set differs from any other member set in their combination of p_C and p_C', but for all member sets, k_1 and k_1' (and, where applicable, k_2 and k_2') are the same. The multiplex collection members can thus be used together, within the same multiplex PCR, and different multiplex collection members (discriminated by different K-boxes) will be used in repeated PCR/sequencing rounds.

To demonstrate the validity and power of the present invention, a PCR-based analysis of T-cell receptor beta (TCRß) gene rearrangements was performed.

In general, the use of a two-step PCR strategy for TCR analyses has the advantage that the initial PCR with gene-specific TCR primers requires only a few PCR cycles minimizing PCR-generated bias, and thereafter the first amplificate is amplified evenly with the adaptor specific primers by a further PCR step. Furthermore, different adaptors suitable for different NGS platforms can be added by the second PCR.

In one embodiment, sequences for the target-binding tract of left (p_C) initial primer are those given as SEQ ID NO 001-045, and right (p_C') initial primer sequences are those given as SEQ ID NO 046-058. In another embodiment for the target-binding tract of left (p_C) initial primer are those given as SEQ ID NO 189-232 , and right (p_C') initial primer sequences are those given as SEQ ID NO 233-246. The primers given as SEQ ID NO 001-058 and as SEQ ID NO 189-246 were optimized in two aspects: 1) to have a similar annealing temperature and 2) to minimize self priming.

The methods, sets of primers, collections and multiplex collections provided herein are of particular use in methods for analysing *in vitro* the TCRß repertoire of a human patient.

Wherever alternatives for single separable features are laid out herein as "embodiments", it is to be understood that such alternatives may be combined freely to form discrete embodiments of the invention disclosed herein.

The invention is further illustrated by the following examples and figures, from which further embodiments and advantages can be drawn. These examples are meant to illustrate the invention but not to limit its scope.

Short description of the figures

Fig. 1 shows the primers, target and first and second amplificate of the method of the invention, wherein the sequence tract m_a-K comprises a sequence element k_1 and the sequence tract m_a-K´ comprises a sequence element k_1´. Reverse complementary sequence tracts are underlined.

Fig. 2 shows the primers, target and first and second amplificate of the method of the invention, wherein the sequence tract m_a-K, in addition to k_1, comprises a sequence element k_2 and the sequence tract m_a-K´, in addition to k_1´, comprises a sequence element k_2´ Reverse complementary sequence tracts are underlined.

Fig. 3 shows the primers, target and first and second amplificate of the method of the invention, wherein the sequence tract m_a-K, in addition to k_1 and k_2 comprises a sequence element s and the sequence tract m_a-K´, in addition to k_1´and k_2´, comprises a sequence element s´. Reverse complementary sequence tracts are underlined.

Fig. 4 shows the primers, target and first and second amplificate of the method of the invention, wherein the sequence tract m_a-K, in addition to k_1, comprises a sequence element s and the sequence tract m_a-K´, in addition to k_1´ comprises a sequence element s´. Reverse complementary sequence tracts are underlined.

Examples

In the proof of principle experiments k_1/k_1' (with a lower case k) are together also termed K_1 with a capital letter and k_2/k_2' sequence tracts are thereafter also termed K_2. Furthermore, s_1/s_1' sequence tracts are thereafter also termed S. In general, the "prime" or apostrophe (') indicates that a sequence tract or element has a similar functional characteristic as its non-prime counterpart, but is located on a primer on the other side of the target sequence.

Example 1: Proof of principle experiments for K_1 function.

The basic experimental layout to demonstrate contamination suppression is outlined below:

1) PCR products of the first amplification were defined as a 100% contamination and were used as template for the second amplification. In order to demonstrate the function and effectiveness of K_1 sequence tracts to suppress this contamination, K_1 mismatches of different length (N = 1, 2, 3, 4, 6 bp) between primers of the first and second PCR amplification were investigated. Furthermore, effects on contamination suppression, (i) employing polymerases with and without proofreading activity and (ii) primers with and without phosphorothioate bonds or LNAs were analysed.

2) For comparison and to simulate the situation without contamination suppression, simultaneous PCRs employing primers with completely matching K_1 sequences were performed.

3) The amount of the PCR products generated by the PCRs under (1) and (2) were quantified and normalized as described more detailed below. Replicates were

performed for all experiments and the mean and standard deviation of PCR product quantity was calculated to obtain statistical reliable results.

If a reamplification with K_1 sequence tracts that mismatch between the first and the second amplification primers showed no PCR product after the second amplification, this was regarded as a complete suppression of the contamination from the primary amplification.

If a reamplification with K_1 sequence tracts that mismatch between the first and the second amplification primers showed PCR products after the second amplification, this was regarded as an incomplete suppression of the contamination from the primary amplification.

Detailed description of the methods:

PCR was performed using a DNA thermal cycler (PE 9700, Perkin Elmer, Rodgau, Germany). As template for first amplification reactions 100 ng DNA from the T-cell lymphoma cell line Peer was applied, which carries a known TCRß gene rearrangement employing the V-4 and J-2-.1 segments.

The initial primers used for the first round of amplification comprised in order from 5' to 3' end a sequence tract m_a-K and a sequence tract p_C (Fig. 1). Sequence tract p_C provided target specificity, while m_a-K provided a non-target-specific sequence tract, parts or all of which can be used for hybridization of a second "adaptor" primer. The left initial PCR primers had a sequence m_a-K-p_C with the matching sequence p_C to the V-4 segment (SEQ 183; TTATTCCTTCACCTACACACCCTGC), whereas the right initial primers which had the sequence and m_a-K'-p_C' with the matching sequence p_C' (SEQ ID NO 184; AGCACTGTCAGCCGGGTGCCTGG) to the J-2.1 segment.

The 3' end of the k–box of forward initial primers had the sequence element s with the two nucleotides "GG", whereas the 3' end of the k'-box of the initial reverse primer had a sequence element s' with two nucleotides "TA".

Furthermore, the k–box of the forward initial primers had a sequence element m_a (SEQ ID NO 185; CGCTCTTCCGATCT) on the 5' end and the k'-box of the initial reverse primers had a sequence element m_a' (SEQ ID NO 186; TGCTCTTCCGATCT) on the 5' end (See Fig. 3 for the overview of the sequence tract names).

As listed in Table 2, the k-box of the initial forward primers harboured different k_1 and k_2 sequences and the k'-box of the initial reverse primers harboured different k_1' and k_2' sequences.

k-box name	k_1 sequence	k_2 sequence	k´-box name	k_1'sequence	k_2'sequence
1bpV1	G	G	1bJ1	C	C
1bpV2	A	C	1bpJ2	T	G
2bpV1	AC	G	2bpJ1	TG	C
2bpV2	CA	C	2bpJ2	GT	G
3bpV1	ACC	G	3bpJ1	TGG	C
3bpV2	CAG	C	3bpJ2	GTC	G

Table 2: k-box and k´-box element sequences are listed as present in 5´-3´orientation of the forward or reverse primers.

First amplification steps were performed in a final volume of 50 µl with final concentrations of 1 x PCR Buffer containing 3 mM $MgCl_2$, 0.2 mM of each dNTP, 1.0 µM forward primer and 1.0 µM reverse primer and 1 unit AmpliTaq Gold DNA Polymerase (Applied Biosystems, Foster City, CA, USA) and the following cycling conditions: 1 cycle at 95°C for 15 min, 34 cycles at 95°C for 30 s, 65°C for 45 s and 72°C for 45 sec respectively, and a final 10 min elongation step at 72°C. Primary PCR products were purified using the QIAquick PCR Purification Kit (Qiagen, Hilden, Germany) according to the manufacturer's instructions. DNA concentration was determined via the Qubit® 1.0 Fluorometer (Invitrogen, Darmstadt, Germany). As template for the second amplification 500 pg from the purified first amplification product was used.

For second amplification a pair of adaptor PCR primers comprising a left adaptor PCR primer having a sequence a_L-a_P-a_K and a right adaptor PCR primer having a sequence a_L'- a_P'-a_K' was employed.

The left adaptor primers had the sequence element a_L-a_P (SEQ ID NO 187) whereas the right adaptor primers had the sequence element a_L'-a_P' (SEQ ID NO 188).

Furthermore, the k-box of the forward adaptor primer harbored different k_1 sequences and the k´-box of the reverse adaptor primers harbored different k_1' (listed in Table 2).

Since K_1 mismatches of the second amplification primer can be removed at the 3´ end by the 3´-5´ exonuclease-activity of a proofreading polymerase during the second amplification, the strength of a protective effect of phosphorothioates at (i) the first, (ii) the first and second (iii) and at the first to third position from the 3´ end of the k-box and k´-box from the left

(forward) and right (reverse) second amplification primer, respectively, was analysed in comparison to primers without protective phosphorothioate bonds.

The second amplification steps were performed (i) with a proofreading polymerase (Phusion High-Fidelity DNA Polymerase (Finnzymes, Espoo, Finland)) or (ii) a polymerase without proofreading activity (AmpliTaq Gold).

For PCRs with proofreading polymerase the second amplification step was performed in a final volume of 50 µl including final concentrations of 1 x Phusion HF Buffer with 1.5 mM $MgCL_2$, 0.05 mM of each dNTP, 1.0 µM forward primer, 1.0 µM reverse primer and 1 unit Phusion High-Fidelity DNA Polymerase. The following thermal cycling conditions were used for the second amplification: 1 cycle at 98°C for 30 s, 12 cycles at 98°C for 10 s, 58°C for 30 s and 72°C for 30s respectively, and a final 5 min elongation at 72°C.

For PCRs with AmpliTaq-Gold the second amplification step was performed in a final volume of 50 µl with final concentrations of 1 x PCR Buffer, 3 mM $MgCl_2$, 0.2 mM of each dNTP, 1.0 µM forward primer and 1.0 µM reverse primer and 1 unit AmpliTaq Gold DNA Polymerase. The following thermal cycling conditions were used for the second amplification: 1 cycle at 95°C for 15 min, 23 cycles at 98°C for 10 s, 54°C for 30 s and 72°C for 30 s, respectively, and a final 5 min elongation step at 72°C.

PCR products were analysed on a 6% acrylamide gels and Tif files were produced with Biorad Geldoc 2000 (München, Germany) using default conditions. PCR bands were further quantified with the FusionCapt Advance software (Vilber Lourmat, Eberhardzell, Germany). For quantification of the PCR products, equal areas (= gates) were analysed from (i) a gel quantification standard (= a Peer PCR product, 8 µl) which was set to 100% for each analysis, (ii) the PCR products (iii) a no template control (NTC) and (iv) the background gate. As FusionCapt Advance software parameters linear background subtraction was set for each gel in the middle of the background band and a rolling ball background subtraction (size = 11) was employed. With the help of Microsoft Excel the mean and standard derivation (SDN) of replicated experiments was determined.

Results

The results for the experiments regarding the K_1-mediated suppression of contamination by mismatches in the K-boxes including the impact of the number of phosphorothioate bonds are given as single values in Table 3. A summary of Table 3 is given in Table 4. The second amplification primers in the experiments had 0-3 phosphorothioate bonds. A 100%

contamination was simulated (a PCR product amplified with the Peer specific first amplification primers described above, employing Peer DNA as template) by adding a PCR product generated in a first PCR round into the second PCR. The second PCR was performed with matching second amplification primers (K_1 = 0 bp mismatch) and second amplification primers with 1 bp and 2 bp K_1 mismatches (summing up the K_1 mismatches of the forward and reverse primer).

The usage of mismatched K-boxes leads to a strong reduction of amplification, which was more pronounced when using 2 bases as compared to only one base. This demonstrates the validity our concept (Table 3 and 4).

Analysed sample / FA primer combination	SA primer combination	K_1 mis-match (bp)	Vol. % (3 PT)	Vol. % (2 PT)	Vol. % (1 PT)	Vol. % (0 PT)
Gel quant standard			100.0	100.0	100.0	100.0
Peer 1bpV1 1bpJ1	1bpV1 1bpJ1	0	136.7	163.1	152.4	176.9
Peer 1bpV1 1bpJ1	1bpV1 1bpJ2	1	28.7	38.4	63.6	171.8
Peer 1bpV1 1bpJ1	1bpV2 1bpJ1	1	41.6	40.9	69.6	169.9
Peer 1bpV1 1bpJ1	1bpV2 1bpJ2	2	17.0	12.2	28.7	127.7
NTC 1bpV1 1bpJ1	1bpV1 1bpJ1	0	13.7	10.8	11.6	14.0
Background			12.0	9.7	8.8	15.7
Gel quant standard			100.0	100.0	100.0	100.0
Peer 1bpV1 1bpJ2	1bpV1 1bpJ1	1	8.9	20.1	18.6	109.3
Peer 1bpV1 1bpJ2	1bpV1 1bpJ2	0	84.8	119.5	100.5	122.0
Peer 1bpV1 1bpJ2	1bpV2 1bpJ1	2	7.8	12.7	10.8	76.7
Peer 1bpV1 1bpJ2	1bpV2 1bpJ1	1	13.9	22.0	25.8	104.3
NTC 1bpV1 1bpJ2	1bpV1 1bpJ1	1	9.5	12.0	7.5	9.6
Background			7.7	11.0	8.0	7.9
Gel quant standard			100.0	100.0	100.0	100.0
Peer 1bpV2 1bpJ1	1bpV1 1bpJ1	1	19.3	28.2	45.1	87.0
Peer 1bpV2 1bpJ1	1bpV1 1bpJ2	2	10.6	11.9	14.2	80.5
Peer 1bpV2 1bpJ1	1bpV2 1bpJ1	0	82.4	83.9	86.8	101.3
Peer 1bpV2 1bpJ1	1bpV2 1bpJ2	1	11.7	16.8	21.3	78.0
NTC 1bpV2 1bpJ1	1bpV1 1bpJ1	1	9.2	8.5	8.9	7.8
Background			7.0	12.0	6.8	8.2
Gel quant standard			100.0	100.0	100.0	100.0

Peer 1bpV2 1bpJ2	1bpV1 1bpJ1	2	10.1	10.2	11.8	81.7
Peer 1bpV2 1bpJ2	1bpV1 1bpJ2	1	22.7	22.5	38.2	113.8
Peer 1bpV2 1bpJ2	1bpV2 1bpJ1	1	11.4	11.3	13.1	103.0
Peer 1bpV2 1bpJ2	1bpV2 1bpJ2	0	94.0	81.1	78.7	96.9
NTC 1bpV2 1bpJ2	1bpV1 1bpJ1	2	9.3	8.2	8.1	10.0
Background			9.7	7.9	8.2	10.2

Table 3: Effect of the number of K_1 mismatches (1 and 2 bp) on contamination suppression employing second amplification primers with 3, 2, 1 and 0 phosphorothioate (PT) bonds at their 3´end and proofreading polymerase. As gel quantification (quant) standard the same Peer TCR PCR product was used on each gel for normalization of the PCR product quantities and was set to 100%. Therefore, Vol. % larger than 100% can be achieved. Relevant for the effect of contamination suppression are the summary statistics (Table 4). (FA = first amplification, SA = second amplification, NTC no template control, bp = base pair, Vol. % volume percent as determined by FusionCapt Advance software, PT = phosphorothioate bond).

K_1 mismatch (bp)	Vol. % (3 PT) Mean	Vol. % (3 PT) SDN	Vol. % (2 PT) Mean	Vol. % (2 PT) SDN	Vol. % (1 PT) Mean	Vol. % (1 PT) SDN	Vol. % (0 PT) Mean	Vol. % (0 PT) SDN
0	99.5	21.9	111.9	33.2	104.6	28.7	124.3	31.8
1	19.8	10.3	25.0	9.6	36.9	19.7	117.1	32.9
2	11.4	3.4	11.8	0.9	16.4	7.2	91.7	20.9

Table 4: Summary statistics of Table 3 (bp = base pair, Vol. % volume percent, SDN = standard deviation, PT = phosphorothioate bond). Quantities around 100% Vol. mean that there is no suppression of contamination. A lower Vol. % is the result of contamination suppression.

The mean of all NTCs in Table 3 was 9.7 (SDN: 1.9) and the mean of background was 9.4 (SDN: 2.3).

Taken together, Table 3 and 4 demonstrate that in a setting with a proofreading polymerase employed in the second amplification, contamination suppression is much more effective with phosphorothioate bonds at the 3´end of the k-box and k´-box of reamplification primers. Furthermore, an increasing number of K_1 mismatches leads to improved contamination suppression. For example with 2 bp K_1 mismatches and 2 phophorothioate bonds the contamination (mean of 11.8, SDN: 0.9) is almost suppressed to NTC or background level.

Further experiments with longer K_1 mismatches revealed a complete suppression of contamination. The effectiveness of K_1 mismatches of 2, 3, 4, and 6 bp total length, to suppress contaminations was analysed in comparison to controls without K_1 mismatches. The second amplification primers in these experiments had 3 phosphorothioate bonds. The results are given in Table 5. A summary statistic with mean and standard deviation of the results in Table 5 is given in Table 6.

Analysed sample / FA primer combination	**SA primer combination**	**Vol. % (3 PT)**	**K_1 mismatch (bp)**
Gel quant standard		100.0	
Peer 2bpV1 2bpJ1	2bpV1 2bpJ1	113.8	0
Peer 2bpV1 2bpJ1	2bpV1 2bpJ2	11.5	2
Peer 2bpV1 2bpJ1	2bpV2 2bpJ1	10.4	2
Peer 2bpV1 2bpJ1	2bpV2 2bpJ2	10.9	4
NTC 2bpV1 2bpJ1	2bpV1 2bpJ1	10.6	0
Background		9.5	
Gel quant standard		100.0	
Peer 2bpV1 2bpJ2	2bpV1 2bpJ1	9.8	2
Peer 2bpV1 2bpJ2	2bpV1 2bpJ2	99.3	0
Peer 2bpV1 2bpJ2	2bpV2 2bpJ1	8.5	4
Peer 2bpV1 2bpJ2	2bpV2 2bpJ2	8.9	2
NTC 2bpV1 2bpJ2	2bpV1 2bpJ1	7.6	2
Background		8.0	
Gel quant standard		100.0	
Peer 2bpV2 2bpJ1	2bpV1 2bpJ1	11.2	2
Peer 2bpV2 2bpJ1	2bpV1 2bpJ2	8.1	4
Peer 2bpV2 2bpJ1	2bpV2 2bpJ1	88.9	0
Peer 2bpV2 2bpJ1	2bpV2 2bpJ2	8.5	2
NTC 2bpV2 2bpJ1	2bpV1 2bpJ1	7.7	2
Background		9.4	
Gel quant standard		100.0	
Peer 2bpV2 2bpJ2	2bpV1 2bpJ1	10.8	4
Peer 2bpV2 2bpJ2	2bpV1 2bpJ2	13.1	2
Peer 2bpV2 2bpJ2	2bpV2 2bpJ1	9.6	2
Peer 2bpV2 2bpJ2	2bpV2 2bpJ2	98.5	0

NTC 2bpV2 2bpJ2	2bpV1 2bpJ1	11.8	4
Background		11.1	
Gel quant standard		100.0	
Peer 3bpV1 3bpJ1	3bpV1 3bpJ1	70.1	0
Peer 3bpV1 3bpJ1	3bpV1 3bpJ2	12.1	3
Peer 3bpV1 3bpJ1	3bpV2 3bpJ1	22.4	3
Peer 3bpV1 3bpJ1	3bpV2 3bpJ2	12.8	6
NTC 3bpV1 3bpJ1	3bpV1 3bPJ1	19.0	0
Background		9.9	
Gel quant standard		100.0	
Peer 3bpV1 3bpJ2	3bpV1 3bpJ1	10.0	3
Peer 3bpV1 3bpJ2	3bpV1 3bpJ2	79.8	0
Peer 3bpV1 3bpJ2	3bpV2 3bpJ1	9.2	6
Peer 3bpV1 3bpJ2	3bpV2 3bpJ2	17.5	3
NTC 3bpV1 3bpJ2	3bpV1 3bpJ1	8.4	3
Background		8.2	
Gel quant standard		100.0	
Peer 3bpV2 3bpJ1	3bpV1 3bpJ1	8.6	3
Peer 3bpV2 3bpJ1	3bpV1 3bpJ2	7.0	6
Peer 3bpV2 3bpJ1	3bpV2 3bpJ1	71.5	0
Peer 3bpV2 3bpJ1	3bpV2 3bpJ2	7.6	3
NTC 3bpV2 3bpJ1	3bpV1 3bpJ1	6.8	3
Background		7.8	
Gel quant standard		100.0	
Peer 3bpV2 3bpJ2	3bpV1 3bpJ1	7.2	6
Peer 3bpV2 3bpJ2	3bpV1 3bpJ2	7.4	3
Peer 3bpV2 3bpJ2	3bpV2 3bpJ1	9.2	3
Peer 3bpV2 3bpJ2	3bpV2 3bpJ2	61.4	0
NTC 3bpV2 3bpJ2	3bpV1 3bpJ1	8.0	6
Background		8.8	

Table 5 Effect of the number of K_1 mismatches (2, 3 4 and 6 bp total length) on contamination suppression employing second amplification primers with 3 phosphorothioate bonds at their 3´end and proofreading polymerase. As gel quantification (quant) standard the same Peer TCR PCR product was used on each gel for normalization of the PCR product quantities and was set to 100%. Therefore, Vol. % larger than 100% can be achieved. Quantities around 100% Vol. mean that there is no contaminations suppression. A lower Vol. % is a result of contamination suppression. (FA = first amplification, SA = second

amplification, NTC = no template control, bp = base pair, Vol. % volume percent, PT = phosphorothioate bond).

K_1 mismatch	Vol. % Mean	Vol. % SDN
0	85.4	16.7
2	10.4	1.4
3	11.9	5.0
4	9.6	1.3
6	9.1	2.3

Table 6: Summary statistics of Table 5. Quantities around 100% Vol. means that there is no contamination suppression. A lower Vol. % is a result of the contamination suppression. (bp = base pair, Vol. % volume percent, SDN = standard deviation).

In Table 5 the mean of all NTCs was 10.0 (SDN: 3.7) and the mean of background was 9.1 (SDN: 1.0).

In summary, Table 5 and 6 show that in a setting with a proofreading polymerase employed in second amplification and 3 phosphorothioate bonds at the 3´end of the k-box and k´-box of the second amplification primers K_1 mismatches of 4 bp (mean 9.6, SDN 1.3) and 6 bp (mean 9.1, SDN 2.3) lead to complete suppression of contaminations comparable to NTCs and background.

In another experiment the effect of the number of K_1 mismatches (1 and 2 bp) on contamination suppression employing second amplification primers without phosphorothioate bonds and a polymerase without proofreading activity (AmpliTaq Gold) was analysed (Table 7). Summary statistics for Table 7 are provided in Table 8.

Analysed sample /FA primer combination	SA primer combination	Vol. %	K_1 mismatch
Gel quant standard	-	100	
Peer 1bpV1 1bpJ1	1bpV1 1bpJ1	155.7	0
Peer 1bpV1 1bpJ1	1bpV2 1bpJ1	92.1	1
Peer 1bpV1 1bpJ1	1bpV2 1bpJ2	54.9	2

NTC 1bpV1 1bpJ1	1bpV1 1bpJ1	13.8	0
NTC 1bpV1 1bpJ1	1bpV2 1bpJ1	14.2	1
NTC 1bpV1 1bpJ1	1bpV2 1bpJ2	11.9	2
Background	-	13.2	
Gel quant standard	-	100	
Peer 1bpV1 1bpJ2	1bpV2 1bpJ1	51.0	2
Peer 1bpV1 1bpJ2	1bpV1 1bpJ2	115.0	0
Peer 1bpV1 1bpJ2	1bpV2 1bpJ2	84.7	1
NTC 1bpV1 1bpJ2	1bpV2 1bpJ1	10.3	2
NTC 1bpV1 1bpJ2	1bpV1 1bpJ2	10.8	0
NTC 1bpV1 1bpJ2	1bpV2 1bpJ2	9.4	1
Background	-	9.8	
Gel quant standard	-	100	
Peer 1bpV2 1bpJ1	1bpV1 1bpJ1	104.6	1
Peer 1bpV2 1bpJ1	1bpV2 1bpJ1	120.3	0
Peer 1bpV2 1bpJ1	1bpV1 1bpJ2	77.8	2
NTC 1bpV2 1bpJ1	1bpV1 1bpJ1	38.0	1
NTC 1bpV2 1bpJ1	1bpV2 1bpJ1	30.2	0
NTC 1bpV2 1bpJ1	1bpV1 1bpJ2	20.3	2
Background	-	14.5	
Gel quant standard	-	100	
Peer 1bpV2 1bpJ2	1bpV1 1bpJ1	50.1	2
Peer 1bpV2 1bpJ2	1bpV2 1bpJ1	62.7	1
Peer 1bpV2 1bpJ2	1bpV2 1bpJ2	89.1	0
NTC 1bpV2 1bpJ2	1bpV1 1bpJ1	12.5	2
NTC 1bpV2 1bpJ2	1bpV2 1bpJ1	16.5	1
NTC 1bpV2 1bpJ2	1bpV2 1bpJ2	15.0	0
Background	-	11.2	

Table 7: Effect of the number of K_1 mismatches (1 and 2 bp total length) on contamination suppression employing second amplification primers without phosphorothioate bonds and a polymerase without proofreading activity. As gel quantification (quant) standard the same Peer TCR PCR product was used on each gel for normalization of the PCR product quantities and was set to 100%. Therefore, Vol. % larger than 100% can be achieved. Quantities around 100% Vol. mean that there is no contaminations suppression. A lower Vol. % is a result of contamination suppression. (FA = first amplification, SA = second amplification, bp = base pair, Vol. % volume percent)

K_1 mismatches	Vol. % Mean	Vol. % SDN
0	120.0	23.7
1	86.0	15.2
2	58.5	11.3

Table 8: A summary statistics of Table 7 is provided. Quantities around 100% Vol. mean that there is no contamination suppression. A lower Vol. % is a result of contamination suppression. (bp = base pair, Vol. % volume percent, SDN = standard deviation).

The mean of all NTCs in Table 7 was 16.9 (SDN: 8.0) and the mean of background was 12.2 (SDN: 1.8).

In summary, Table 7 and 8 show that also in a setting with a polymerase without proofreading activity and second amplification primers without phosphorothioate bonds at the 3´end of the k-box and k´-box contamination suppression increases with an increasing number of K_1 mismatches.

Contamination suppression by K_1 employing a TCRß multiplex-collection

To demonstrate that K_1 is able to suppress contaminations employing a multiplex collection (referred to as TCRß multiplex collection) with 44 TCRß V segment specific primers (p_C, SEQ ID NO 189 - 232) and 14 TCRß J segment specific primers (p_C´, SEQ ID NO 233 - 246) was used in the first PCR amplification. Each of these primers had a 5´ S sequence of two nucleotides in length (For the SEQ ID NO 189-193, 195, 197, 198, 201-211, 213-221, 223-229, 231, 233-241 and 243-246 the S sequence was “GG”, for the SEQ ID NO 194, 200 and 230, the S sequence was “TG”, for the SEQ ID NO 196, 199, 212, 222, 242 the S sequence was “GT”, for the SEQ ID NO 232 the S sequence was “TT”. The orientation of these S sequences is in 5´- 3´direction of the primer.

Furthermore, in this TCRß multiplex collection the k–box of the forward initial primers had the tail sequence element m_a (SEQ ID NO 247 GCTCTTCCGATCT) on their 5' end and the k'-box of the initial reverse primers had a sequence element m_a´ (SEQ ID NO 247; GCTCTTCCGATCT) on their 5' end.

Second amplification primers were employed (i) with 2 phosphorothioate bonds at their 3´ end and in another experiment with (ii) an LNA at the second position from the 3´ end. Three primer sets (Set 1-3) were used with the set specific K_1 and K_2 sequences given in Table 9.

Name	k_1 sequence	k_2 sequence	k_1'sequence	k_2'sequence
Set1	CACCCAA	GAC	GTTGGTT	CGT
Set2	AGTTTTG	CGG	GGTCATG	TGG
Set3	CTTTAGA	GTG	GCCATTT	TAA

Table 9: k-box and k´-box element sequences are listed as present in 5´-3´orientation of the forward or reverse primers.

The first PCRs (with AmpliTaq-Gold) and second PCRs (with the proofreading Phusion High-Fidelity DNA Polymerase) were performed as described above, with 100 ng of tonsillar DNA as template. The PCR results were quantified with the FusionCapt Advance software as described above.

The performed PCR reactions (all nine K_1 match and mismatch combinations possible for Set 1-3) and the results are given in Table 10.

Analysed sample / FA primer set	SA primer set	Vol. % (PT)	Vol. % (LNA)	K_1 match/ mismatch
Gel quant standard	-	100	100	-
Set1	Set 1	113.6	62.8	match
Set1	Set 2	29.5	28.6	mismatch
Set1	Set 3	28.8	34.3	mismatch
NTC Set1	NTC Set1	24.1	26.9	match
NTC Set1	NTC Set2	24.1	31.0	mismatch
NTC Set1	NTC Set2	22.1	31.3	mismatch
Background	-	25.5	34.0	-
Gel quant standard	-	100	100	-
Set2	Set2	83.5	102.1	match
Set2	Set1	25.1	21.7	mismatch
Set2	Set3	23.5	24.2	mismatch
NTC Set2	NTCSet2	21.0	19.0	match
NTC Set2	NTCSet1	23.9	20.4	mismatch

NTC Set2	NTCSet3	29.0	23.0	mismatch
Background	-	23.6	20.7	-
Gel quant standard	-	100	100	-
Set3	Set3	104.8	50.9	match
Set3	Set1	28.7	14.4	mismatch
Set3	Set2	23.8	18.1	mismatch
NTCSet3	NTCSet3	26.8	18.3	match
NTCSet3	NTCSet1	21.3	20.0	mismatch
NTCSet3	NTCSet2	22.0	17.1	Mismatch
Background	-	26.8	21.5	-

Table 10 Analysis of contamination suppression by K_1 employing a TCRß multiplex-collection. As gel quantification (quant) standard the same Peer TCR PCR product was used on each gel for normalization of the PCR product quantities and was set to 100%. Therefore, Vol. % larger than 100% can be achieved. Quantities around 100% Vol. mean that there is no contaminations suppression. A lower Vol. % is a result of contamination suppression. (FA = first amplification, SA = second amplification, Vol. % volume percent, PT = phosphorothioate bonds; LNA = locked nucleic acid)

A summary statistics of Table 10 is provided in Table 11. These results show, that in a K_1 match situation the contamination is amplified, whereas in the K_1 mismatch situation the contamination is not amplified (being comparable to background, considering the SDN).

	Vol. % Mean (PT)	**Vol. % SDN (PT)**	**Vol. % Mean (LNA)**	**Vol. % SDN (LNA)**
Match	100.6	12.6	71.9	21.9
Mismatch	26.6	2,5	23.6	6.6
NTC	23.8	2.5	23.0	5.1
Background	25.3	1.3	25.4	6.1

Table 11: Summary statistics of Table 10. Quantities around 100% Vol. mean that there is no contaminations suppression. A lower Vol. % is a result of the contamination suppression. (Vol. % volume percent, SDN = standard deviation, PT = phosphorothioate bonds; LNA = locked nucleic acid).

Example 2: Proof of principle for k_2 and k_2' function:

As a short sequence element, k_2 is located at the 3´-end of the sequence element k_1 and k_2' is a sequence element located at the 3'-end of the sequence element k_1' (Fig. 2-3). K_2 serves to individualize the first primer pair of the set and have no complementary sequence

elements on the second ("adaptor") primers. K_2 sequences are designed to detect contamination from previous amplification reactions and therefore control the suppression efficiency of K_1.

For this example, it is assumed that five samples are processed in parallel in a stripe with 5 PCR tubes for the first amplification and another stripe with 5 PCR tubes for the second amplification using five different primer sets. In this example for "Tube Nr. 1" one specific k_2 and/or k_2' sequence in the first amplification primer is employed as well as a k_1 and k_1' sequence matching the first and second amplification primer. In this setting a contamination can be clearly identified by a mismatched k_2 (or k_2') element if a "Tube Nr. 2" second amplification product contains k_2/k_2' elements of the "Tube Nr. 1" amplification product but k_1 and k_1' sequences of the "Tube Nr. 2" second amplification primers. In this case the contamination is caused by nonspecific priming of "Tube Nr. 2" k_1 and k_1' element of the second amplification primers to the "Tube Nr.1" k_1 and k_1' element in the first amplification product. Furthermore the contamination amplification could be caused by partial or full degradation of the "Tube Nr. 2" k_1 and k_1' element by polymerases with proofreading activity. Since the k_2/k_2' elements are only present in the first amplification primers the contamination can still be identified in the second amplification product. Therefore, k_2/k_2' elements can be seen as a valuable safe lock mechanism to detect contaminations, complementing the already significant contribution of k_1/k_1' sequences to avoid such contaminations. There is a synergistic control function of k_2/k_2' that ensures the k_1/k_1' contamination suppression works 100%.

In order to demonstrate the function and effectiveness of k_2/k_2' sequence tracts to detect contaminations a first and second amplification with primers specific for the Peer TCR as described above were used with the following k-box and k´-box elements for the first forward amplification primer given in Table 2:

"Tube Nr. 1" (Set1) first amplification: forward primer 1bpV1 and reverse primer 1bpJ1

"Tube Nr. 2" (Set 2) second amplification: forward primer 1bpV2 and reverse primer 1bpJ1

Therefore, there is 1 bp k_1 mismatch between the "Tube Nr. 1" first amplification primer (k_1 = "G") and the "Tube Nr. 2" second amplification primer (k_1 = "A"). Furthermore, the "Tube Nr. 1" first amplification primer had the k_2 = "G" (Table 2).

The first "Tube Nr. 1" amplification was regarded to be a "100% contamination" ("Tube Nr.1" primary amplification product) of "Tube Nr. 2" second amplification. Therefore, a second

amplification was performed with "Tube Nr. 2" second amplification primers and the "Tube Nr. 1" first amplification product as template. In the gel analysis of the resulting second amplification PCR product there was a PCR product detectable, since due to the only 1 bp long k_1 mismatch this "Tube Nr. 1" contamination was not completely suppressed during second amplification (with "Tube Nr. 2" second amplification primers). This PCR product was sequenced.

Sanger sequencing of the amplicon identified the k_2 sequence of the amplicon as identifier of the "Tube Nr. 1" primary amplification forward primer (k_2 = "G"). Therefore, in this case the "Tube Nr. 1" specific k_2' sequence (k_2 = "G") identified the contamination from the "Tube Nr. 1" primary amplification product in the "Tube Nr. 2" second amplification (The "Tube Nr. 2" k_2 sequence would have been "C" for the "Tube Nr. 2" k-box 1bpV2 Table 2).

To gain a deeper understanding of this contamination detection and prevention system the second amplification in this experiment was performed independently with proofreading polymerase and with a polymerase without proofreading activity, with the PCR conditions described above for these reactions. As a result, in both experiments the contamination ("Tube Nr. 1" sample) could be identified by Sanger sequencing due to the contamination specific k_2 sequence (k_2 = "G").

The sequencing results revealed that with proofreading polymerase the k_1 sequence from the contaminating ("Tube Nr. 1") sample was found, whereas in the second amplification employing a polymerase without proofreading activity k_1 sequences from the second amplification primers ("Tube Nr. 2" amplification) were present. This is due to fact that there was a k_1 mismatch between the first and second amplification reverse primer and the k_1 element of the second amplification primer was removed (degraded) at the 3´ end by the exonuclease-activity of a proofreading polymerase during the second amplification, despite the second amplification primers harbouring two phosphorothioate bonds. In contrast, the k_1 element of the second amplification primer was not removed using a polymerase without proofreading activity.

Taken together, the Sanger sequencing demonstrated the k_2/k_2' function to detect contamination. Thereby polymerase with or without proofreading polymerase can be used in second amplification. Importantly k_2/k_2' elements help to understand and control the function of k_1/k_1'. Another important result of this experiment is that if proofreading polymerase is employed, unexpected k_1/k_1' hybrids can be detected in the resulting

sequence reads by bioinformatics methods and these sequences can be removed as contaminations.

Example 3: Proof of principle for S function

A feature that improves on the performance of the above elements k_1 (and k_1') and k_2 (and k_2') is the introduction of short separator sequences s and s' (Fig. 3-4). s separates the constant initial primer sequence p_C from the sequence tracts k_1 and k_2 and s' separates the constant initial primer sequence p_C´ from k_1´ and k_2´ respectively. Since k_1 /k_1´ and k_2/k_2´ vary among different primers used in subsequent reactions, it may well be that some variations of k_1/k_1' and / or k_2/k_2' coincidentally match in their last nucleotides on the 3' terminal end the sequence of the target next to the hybridizing part of the initial primer, p_C or p_C´. Therefore, the target sequence-matching tract of the initial primer would be elongated, leading to higher annealing temperatures and thus, possibly, PCR bias.

As a proof of principle that S reduces PCR bias a simulation of an incidentally match of 6 bp length of the k-box and k´-box in the first amplification primers to the target sequence was analysed with S of 1, 2 and 3 bp length and no S sequence for comparison.

The first amplification was performed as described above with 100 ng template DNA from the T-cell lymphoma cell line Peer and the following cycle conditions. 1 cycle at 95°C for 15 min, 29 cycles at 95°C for 30 s, 68 °C for 45 s and 72°C for 45 sec respectively, and a final 10 min elongation at 72°C.

The first amplification PCR primers had a sequence m_aK-p_C with the matching sequence p_C to the V-4 segment (SEQ ID NO 248; ACCTACACACCCTGC), whereas the right first amplification primers which had the sequence and m_aK'-p_C' had the matching sequence p_C' (SEQ ID NO 249; AGCCGGGTGCCTGG) to the J-2.1 segment. Furthermore, the k–box of the left first amplification primers had a sequence element m_a (SEQ ID NO 250; CGCTCTTCCGATCT) on the 5' terminus and the k'-box of the right first amplification primers had a sequence element m_a´ (SEQ ID NO 251; TGCTCTTCCGATCT) on the 5' terminus.

An overview of the 6bp matching K-box sequences to the V-4 segment and J-2.1 segment together with the s sequences of different length are given in Table 12.

Primer	K-box sequence	Template sequence match	S sequence
VKM	TCCTTC	Yes	none
VKMS1	TTCCTT	Yes	G
VKMS2	ATTCCT	Yes	GG
VKMS3	TATTCC	Yes	AGG
VKMM	CAACGT	No	none
VKMMS1	GGTTCA	No	G
VKMMS2	GGAGTA	No	GG
VKMMS3	GCACTT	No	AGG
JKM	ACTGTC	yes	none
JKMS1	CACTGT	yes	T
JKMS2	GCACTG	yes	GT
JKMS3	AGCACT	yes	CGT
JKMM	TGACGA	No	none
JKMMS1	GTTGAC	No	T
JKMMS2	ATGACT	No	GT
JKMMS3	GTTGAG	No	CGT

Table 12: Overview of S sequences and 6 bp K-box sequences. Some of the K-box sequences have a full-match to the V-4 segment and J-2.1 segment to simulate an incidentally matched K-box to the template sequence. In the first column (Primer) the first letter "V" or "J" stands for the V- or J- TCR Primer in which the respective K-box is comprised, "KM" stands for K-box match to template sequence; "KMM" stand for K-box mismatch to template sequence and S1-3 gives the length of a separator sequence S (1-3 nucleotides).

Nr.	Sample	Primer	Vol. % E1	Vol. % E2	Vol. % E3	Vol. % E4	Vol. % E5	Mean	SDN
1	Gel-St.	-	100	100	100	100	100	100.0	0.0
2	Peer	VKM JKM	67.1	56.4	54.2	48.9	65.8	58.5	7.0
3	Peer	VKMM JKMM	27.6	13.6	15.1	14.9	16.7	17.6	5.1
4	Peer	VKMS1 JKMS1	30.7	24.5	27.7	22.0	29.2	26.8	3.2
5	Peer	VKMS2 JKMS2	39.8	20.5	19.5	26.6	14.9	24.3	8.6
6	Peer	VKMS3 JKMS3	27.1	14.5	16.9	16.2	17.3	18.4	4.5
7	Peer	VKMMS1 JKMMS1	16.6	11.4	14.6	13.4	13.7	13.9	1.7

8	Peer	VKMMS2 JKMMS2	24.2	14.3	13.6	13.4	12.9	15.7	4.3
9	Peer	VKMMS3 JKMMS3	21.0	9.6	21.3	14.4	21.4	17.5	4.8
10	Back-ground	-	11.3	8.5	10.9	10	11.1	10.4	1.0
11	Gel-St.	-	100	100	100	100	100	100.0	0.0
12	NTC	VKM JKM	7.2	8	9.3	6.3	7.3	7.6	0.9
13	NTC	VKMM JKMM	9.5	7.8	9.4	6.8	6.9	8.1	1.1
14	NTC	VKMS1 JKMS1	9.5	8.5	9.7	7.8	8.7	8.8	0.6
15	NTC	VKMS2 JKMS2	9.2	9.1	10.8	6.8	7.7	8.7	1.3
16	NTC	VKMS3 JKMS3	8.6	8.2	9.2	6.7	7.1	8.0	0.8
17	NTC	VKMMS1 JKMMS1	9.1	9.1	9.7	6.9	7.9	8.5	0.9
18	NTC	VKMMS2 JKMMS2	7.3	7.2	9.7	7.6	7.7	7.9	0.8
19	NTC	VKMMS3 JKMMS3	7.7	9.1	9.5	6.7	7.7	8.1	0.9
20	Back-ground	-	8	9.1	8.6	5.8	7.5	7.8	1.0

Table 13: Experiment Nr. and results of proof of principle experiments to show that S can help to avoid a PCR bias by preventing K-box matches to the DNA template and therefore preventing unequal primer annealing temperatures and different amplification rates. Gel-St. (Gel quantification standard) = the same Peer TCR PCR product was used on each gel as standard for normalization of PCR product quantity and was set to 100%. Vol. % = volume percent, E1-5 = Experiment 1-5 (Replicates), SDN = standard deviation). In the third column (Primer) the primer pairs employed in the PCR are given. Thereby the first letter "V" or "J" stands for the V- or J- TCR Primer in which the respective K-box is comprised, "KM" stands for K-box match to template sequence; "KMM" stand for K-box mismatch to template sequence and S1-3 gives the length of a separator sequence S (1-3 nucleotides).

Table 13 shows that S sequences lead to a similar amplification despite of coincidentally template matching k-box and k´-box sequences. For example in Table 13 line 6 the amplification (Vol. %) with primers harbouring a S sequence of 3 bp length and template matching k-box and k´-box sequences have a mean of 18.4 (SDN 4.5) which is comparable to the amplification without template matching k-box and k´-box sequences in Table 13 line 3 with a mean of 17.6 (SDN 5.1).

This is the proof of the principle that S functions in a synergistic way to avoid PCR bias, due to altered primer annealing temperatures in the case of coincidentally template matching variations of some K-box sequences.

Example 4: Contamination suppression by K_1 and detection by K_2 employing a TCRß multiplex collection and NGS analysis

We employed the TCRß multiplex collection (SEQ ID NO 189-246) with the related S sequences as described above, to analyse the effectiveness of K_1 to suppress contaminations and K_2 to detect residual contaminations. The K_1 and K_2 elements employed in Set 1-3 are described in Table 9).

Two analyses listed in Table 14 were performed in duplicates. In these experiments tonsillar DNA was used as template for the first amplification as well as the DNA of two T-cell lines (Jurkat and Karpas299). As template for the second amplification a total of 500 pg from the purified first amplification products was used as product mix.

In the first duplicate (Sample Nr. 1 and 2, Table 14) the first amplificate mix used as template for second amplification comprised 50% tonsillar amplificate (Set1), 25% Jurkat amplificate (Set1) and 25% Karpas299 amplificate (Set1). The second amplification primers were from Set1.

In the second duplicate (Sample 3 and 4, Table 14) the amplificate mix was used as template for second amplification comprised 50% tonsillar amplificate (Set1), 25% Jurkat amplificate (Set2) and 25% Karpas299 amplificate (Set3). The second amplification primers were from Set1.

Therefore In the first duplicate tonsillar TCRs were amplified without contamination protection and two spiked in contaminations (Jurkat, Karpas299 TCRs) and in the second duplicate tonsillar TCRs are amplified with contamination protection and the same spiked in contaminations (Jurkat, Karpas299)..

Sample Nr (Barcode)	Template for second amplification	Function
1	50% First amplification with tonsillar DNA (Set 1) 25% First amplification of Jurkat DNA (Set1) 25% First amplification of Karpas299 DNA (Set1)	Contamination with Jurkat and Karpas 299 (no contamination protection)
2		
3	50% First amplification with tonsillar DNA (Set 1) 25% First amplification of Jurkat DNA (Set2) 25% First amplification of Karpas299 DNA (Set3)	Contamination with Jurkat and Karpas 299 (contamination protection)
4		

Table 14: Experimental design to analyse contamination suppression by K_1 and detection by K_2 employing a TCRß multiplex-collection and NGS analysis. For each of the 4 samples an individual standard Illumina barcodes was introduced into the amplification product by the right second amplification primer to allow NGS multiplexing.

The resulting 4 NGS libraries were sequenced with MISEQ (Illumina) in the paired end modus (2 x 150 bp). By a tailored bioinformatics algorithm resulting reads were clustered and classified with respect to the K-box elements and the templates used. Frequencies of the respective tonsil and cell line reads and respective primer elements (Set 1-3) were counted and tabulated (Table 15).

The results given in Table 15 demonstrate that (i) without contamination protection (sample 1 and 2) the 2 cell line contaminations were detected with the expected percentage of approximately 25 %. Strikingly in sample 3 and 4 due to the contamination protection by K_1 the 2 cell line contaminations were supressed totally (cell line 1) and down to a percentage of 0.01 in (cell line 2). The residual cell line 2 contamination could be detected by K_2.

Sample	SET	Tonsil	Cell line 1 (Jurkat)	Cell line 2 (Karpas299)	Total read number
1	(1/1/1)	48,79%	23,70%	27,51%	180226
2	(1/1/1)	49,74%	23,30%	26,96%	272669
3	(1/2/3)	99,99%	0,00%	0,01%	314388
4	(1/2/3)	99,99%	0,00%	0,01%	311956

Table 15 NGS results of contamination suppression analysis described in Table 14. The Set information of the related reads refers always to the triplet (Tonsil/cell line 1/cell line 2).

Design of suitable k_1 /k_1' and k_2 /k_2' sequences.

To provide examples for suitable k_1 and k_1' sequences, they were designed in a way to (a) optimally avoid cross-hybridization between all k_1 and k_1' sequences given in one of the Tables 16-19 below, (b) adjust the melting temperatures of k_1 and k_1' sequences in a narrow range and (c) to avoid low complex base compositions with > 2/3 of the bases being the same nucleotide (A,C,G,T),

Each of the Tables 16-19 consists of an equal number of k_1 and k_1' sequences for the forward and reverse primers and a specific length (4, 5,r 6, 7 or 8 nucleotides).

In detail, features a)-c) were established by comparing all potential k_1 and k_1' sequences of one specific length (4, 5, 6, 7 or 8 bp) against each other and excluded all those which were reverse-complements to any other k_1 and k_1' sequences of this specific length. To further refine the k_1 and k_1' sequences the design algorithm compared in a further step all k_1 and k_1' sequences of one specific length (4, 5, 6, 7 or 8 bp) against all other reverse complement k_1 and k_1' sequences of this specific length and excluded all k_1 and k_1' sequences which either had >2 common bases at the 3' terminal end of the k_1 and k_1' sequences or had >60% bases in common with another k_1 and k_1' sequence.

The final results of this optimized k_1 and k_1' sequences are given in Tables 16-19. It is understood that this are examples and that other optimized K_1-boxes with different selection criteria are possible.

Furthermore, examples of suitable k_2/k_2' sequences are provided (Table 20), which were designed in a way to exclude all respective reverse complement sequences from the set of k_2/k_2' sequences. As an example, if ATC is chosen as one possible k_2 element, GAT is automatically excluded from the set of k_2' elements.

For final incorporation into the primer design, the K-boxes are designed as one unit being selected to form a minimum of cross-hybridization with the 3´ends of the primes employed.

Primer side	k_1 – or k_1' sequence	Melting temperature
A	CTGA	12
A	AGTG	12
A	CAAC	12
A	GGAA	12
A	GTCA	12
A	AAGC	12
A	ATTA	8
A	AGCC	14
A	CGAG	14
A	AGGA	12
A	TAGA	10
B	GCGA	14
B	ACGG	14
B	CGTA	12
B	ACTC	12
B	CTTC	12
B	ACCA	12
B	GCAC	14
B	GACC	14
B	ATAC	10
B	CGGC	16
B	GATA	10

Table 16: Optimized k_1 and k_1' sequences of 4 bp length. For example the segment side A can be employed in the right primers and B in the left primers. Furthermore, the segment side B can be employed in the right primers and A in the left primers.

Primer side	k_1 – or k_1' sequence	Melting temperature
A	CTCTA	14
A	ATCAG	14
A	ATTGG	14
A	ATACG	14
A	ACGCA	16
A	ACCAA	14
A	AATGC	14
A	AAGGA	14
A	TCACA	14
A	ATATA	10
A	ATGTC	14
A	AGCTG	16
A	CAACC	16
B	GTTTA	12
B	GCTCC	18
B	CTTAA	12
B	GAGGC	18
B	ACACT	14
B	AATCG	14
B	CATCA	14
B	GTAGA	14
B	CTTTC	14
B	AAGCC	16
B	AAAGT	12
B	CGGAA	16
B	CTCAC	16
B	CGGAA	16
B	CTCAC	16

Table 17: Optimized k_1 and k_1' sequences of 5 bp length. For example the segment side A can be employed in the right primers and B in the left primers. Furthermore, the segment side B can be employed in the right primers and A in the left primers.

5

Primer side	k_1 – or k_1' sequence	Melting temperature [°C]
A	CTCTGA	18
A	GGTTAA	16
A	GCCTTA	18
A	CGGACG	22
A	GTCAAA	16
A	GATCGA	18
A	CTTGTA	16
A	AACTTG	16
A	AATCAT	14
A	ACTATG	16
A	GCAACA	18
A	CGAAGC	20
A	GAGTCC	20
A	GGCAAC	20
A	AAATGT	14
A	CTATCA	16
B	AAGCTG	18
B	GCCCAA	20
B	ATCAGA	16
B	ACTCAG	18
B	GGTATA	16
B	AAAGGG	18
B	AATGCT	16
B	CCAAGG	20
B	ACGCGG	22
B	GACGGA	20
B	GCGCAC	22
B	GTAGAA	16
B	ACCGCA	20
B	AAACCC	18
B	AGAACT	16
B	GAGCTA	18

Table 18: Optimized k_1 and k_1' sequence of 6 bp length. For example the segment side A can be employed in the right primers and B in the left primers. Furthermore, the segment side B can be employed in the right primers and A in the left primers.

K1 "A 7 nt"	K1 "B 7 nt"	K1 "A 8 nt"	K1 "B 8 nt"
AACCAAC	GAGCACA	CGTGTCGC	AGGCACCA
CATGACC	CACCCAA	ATGATGAC	GCTTCTTA
CATGACC	CACCCAA	ATGATGAC	GCTTCTTA
AAATGGC	CTTCCTA	AAACCTGT	ATACTTCG
AGGTAGC	AGTTTTG	GAATGATA	ACGATTGG
TATGTCA	CTGTTAA	ATCGGTGC	GGCAGCGA
CTATGTA	CTTTAGA	GATGTTCA	ATGTTCGG
CATTGCG	AAGACGG	CTGCGACA	GGTGGCTA
AGAAGGA	AGCGGCC	CATCTAGA	CAATACCC
GATCTCC	CAGTAGG	AACGCTGA	CTATTTAC
ACTATGC	AGTGCCA	ATGCTGTG	TGCGAAAA
GACGCAC	GAGCACA	GAACACAA	CAAGCGAG
ACTTGAA	GAGCACA	CTTAAGTC	CAGCCGAA
CGGTGAC	CACCCAA	GAGAAGGC	CCCAAAAC
GAACTGA	AGTTTTG	GGATGTAA	AGGCACCA
CGGATTA	AGTTTTG	AGCAAGGA	AGGCACCA
GTATAAA	CTGTTAA	ACTCAGTA	GCTTCTTA

Table 19: Optimized k_1 and k_1' sequence of 7 and 8 nucleotide (nt) length. For example the segment side A can be employed in the right primers and B in the left primers. Furthermore, the segment side B can be employed in the right primers and A in the left primers.

5

Primer side	k_2 – or k_2' sequence		Primer side	k_2 – or k_2' sequence
A	ACG		B	GAC
A	CCA		B	CGG
A	TTA		B	GTG
A	TCG		B	TGT
A	GGT		B	AAG

Table 20: Examples for k_2 and k_2' sequence of 3 bp length. For example the segment side A can be employed in the right primers and B in the left primers. Furthermore, the segment side B can be employed in the right primers and A in the left primers.

What is claimed is:

1. A method for amplifying a target nucleic acid sequence t_C-t_V-t_C' comprised within a sequence tract t_n-t_C-t_V-t_C'-t_n', said method comprising conducting a plurality of amplification reactions, each reaction comprising

- a first amplification step, whereby said target nucleic acid sequence is amplified using
    i. a left (forward) initial PCR primer having a sequence m_a-K-p_C and
    ii. a right (reverse) initial primer having a sequence and m_a-K'-p_C',

  yielding a first amplificate,
- a second amplification step, whereby said first amplificate is amplified using
    iii. a left (forward) adaptor PCR primer consisting of a sequence a_L-a_P-a_K and
    iv. a right (reverse) adaptor PCR primer consisting of a sequence a_L'-a_P'-a_K',

  yielding a second amplificate,

wherein

- t_V is a variable region within said target nucleic acid sequence,
- p_C is the same sequence as sequence element t_C and p_C' is the reverse complementary sequence to t_C',
- K comprises a sequence element k_1 and a 3'-terminal sequence element S, and K' comprises a sequence element k_1' and a 3'-terminal sequence element S', wherein
    - k_1 and k_1' each independently from one another are a sequence 2 to 9 nucleotides in length,
    - S and S' are mismatch sequences selected not to form a continuous hybrid sequence with sequence element t_n and t_n', and S and S' are each independently 1, 2, 3, 4 or 5 nucleotides in length,

- a_k is the same sequence as sequence element k_1 and a_K' is the same sequence as sequence element k_1',
- a_P-a_K hybridizes to a contiguous sequence on m_a-K and a_P'-a_K' hybridizes to a contiguous sequence on m_a-K',
- p_C, p_C', m_a-K and m_a-K' each independently from one another are a sequence 10 to 40 nucleotides in length, and a_L and a_L' independently from one another can be any sequence, and wherein

a particular set of primers for each one of said plurality of amplification reactions is provided, wherein in each of these sets of primers

- k_1 of said particular set is different from any other k_1 in any of the other sets and/or
- k_1' of said particular set is different from any other k_1' in any of the other sets.

2. The method according to claim 1, wherein K comprises a 3'-terminal sequence k_1-k_2-s, and K' comprises a 3'-terminal sequence k_1'-k_2'-s', wherein
   - k_2 and k_2' each independently from one another are a sequence 2 to 7 nucleotides in length,
   - a_k and a_K' are selected not to hybridize to k_2 and k_2', respectively;
   - for each said particular set of primers, one of k_2 and k_2' are different from of any other k_2 and k_2', respectively

   and k_1, k_1', s and s' are as defined in claim 1.

3. The method according to any one of claims 1-2, wherein said particular sets of primers comprise
   - a left (forward) initial primer comprising a sequence element p_C selected from any one of SEQ ID NO 001 to SEQ ID NO 045 and a right (reverse) initial primer comprising a sequence element p_C' selected from any one of SEQ ID NO 046 to SEQ ID NO 058; and/or
   - a left (forward) initial primer comprising a sequence element p_C selected from any one of SEQ ID NO 189 to SEQ ID NO 232 and a right (reverse) initial primer comprising a sequence element p_C' selected from any one of SEQ ID NO 233 to SEQ ID NO 246; and/or

- a left (forward) initial primer comprising a sequence element m_a selected from any one of SEQ ID NO 059 to SEQ ID NO 085 and a right (reverse) initial primer comprising a sequence element m_a selected from any one of SEQ ID NO 086 to SEQ ID NO 117.

4. The method for amplifying a target nucleic acid sequence according to any one of claims 1-3, wherein in the first and/or second amplification step, a DNA polymerase having a 3'-5' exonuclease proofreading activity is used.

5. A method for sequencing a target sequence t_C-t_V-t_C' comprised within a sequence tract t_n-t_C-t_V-t_C'-t_n', comprising the steps of

   a) amplifying said target sequence by a method according to claim 1, 3 or 4; and

   b) sequencing said second amplificate including sequence elements m_a-K and / or m_a-K', yielding a set of readout sequences.

6. The method of claim 5, further comprising the steps of

   c) aligning each member of said set of readout sequences to sequence element m_a-K and/or m_a-K' comprised in said initial primer, respectively, and

   d) assigning a value of 0 or 1 as a measure of contamination to each sequence of said set of readout sequences, wherein complete alignment of a member of said set of readout sequences to said sequence element m_a-K or m_a-K' corresponds to a value of 0, and incomplete alignment of a member of said set of readout sequences to said sequence element m_a-K or m_a-K' corresponds to a value of 1; and

      (i) determining a percentage of contamination by adding all values assigned in step d), resulting in a value sum, and dividing said value sum by the total number of reads; and / or

      (ii) removing the sequences having a value of "1" from the sequence set.

7. A collection of sets of primers for use in a method for amplifying or sequencing a target nucleic acid sequence t_C-t_V-t_C' comprised within a sequence tract t_n-t_C-t_V-t_C'-t_n' according to any one of claims 1 to 6, wherein each set of primers comprises

i. a pair of initial PCR primers comprising a left (forward) initial PCR primer having a sequence m_a-K-p_C and a right (reverse) initial primer having a sequence and m_a-K'-p_C', and

ii. a pair of adaptor PCR primers comprising a left adaptor PCR primer consisting of a sequence a_L-a_P-a_K and a right adaptor PCR primer consisting of a sequence a_L'- a_P'-a_K',

wherein

- p_C is the same sequence as sequence element t_C and p_C' is the reverse complementary sequence to t_C',
- K comprises a sequence element k_1 and a 3'-terminal sequence element s, and K' comprises a sequence element k_1' and a 3'-terminal sequence element s', wherein
  - k_1 and k_1' each independently from one another are a sequence 2 to 9 nucleotides in length,
  - s and s' are mismatch sequences selected not to form a continuous hybrid sequence with sequence element t_n and t_n', and s and s' are each independently 1, 2, 3, 4 or 5 nucleotides in length,
- a_k is the same sequence as sequence element k_1 and a_K' is the same sequence as sequence element k_1',
- a_P-a_K hybridizes to a contiguous sequence on m_a-K and a_P'-a_K' hybridizes to a contiguous sequence on m_a-K', and

p_C, p_C', m_a-K and m_a-K' each independently from one another are a sequence 10 to 40 nucleotides in length, and a_L and a_L' independently from one another can be any sequence,

and wherein

- for all sets of primers comprised within said collection, all sequence elements p_C are the same and all sequence elements p_C' are the same; and

in each of these sets of primers

- k_1 is different from one of any other k_1 and/or

- k_1' is different from one of any other k_1'

in each of the other sets.

8. A collection of sets of primers according to claim 7, wherein
   - - sequence element p_C of said left (forward) initial primer is selected from any one of SEQ ID NO 001 to SEQ ID NO 045 and sequence element p_C' of said right (reverse) initial primer is selected from any one of SEQ ID NO 046 to SEQ ID NO 058; and/or
   - sequence element p_C of said left (forward) initial primer is selected from any one of SEQ ID NO 189 to SEQ ID NO 232 and sequence element p_C' of said right (reverse) initial primer is selected from any one of SEQ ID NO 233 to SEQ ID NO 246; and/or
   - sequence element m_a of said left (forward) initial primer is selected from any one of SEQ ID NO 059 to SEQ ID NO 085 and sequence element m_a of said right (reverse) initial primer is selected from any one of SEQ ID NO 086 to SEQ ID NO 117.
9. The collection of sets of primers according to claim 8, wherein K comprises a 3'-terminal sequence k_1-k_2-s, and K' comprises a 3'-terminal sequence k_1'-k_2'-s', wherein
   - k_2 and k_2' each independently from one another are a sequence 2 to 7 nucleotides in length,
   - a_k and a_K' are selected not to hybridize to k_2 and k_2', respectively;

   in each of these sets of primers
   - k_2 is different from one of any other k_2 and/or
   - k_2' is different from one of any other k_2'

   in each of the other sets, and k_1, k_1', s and s' are as defined in claim 7.
10. The collection of sets of primers according to any one of claims 7 to 9, comprising 4, 8, 16, 24, 32, 40, 48, 56, 64, 72, 80, 160, 200, 256 or 1024 different sets of primers.
11. The collection of sets of primers according to any one of claims 7 to 10, wherein

- k_1 and k_1' and/or k_2 and k_2' are selected not to hybridize to the sequence elements t_n and t_n';
- all sequence elements a_P are the same and all sequence elements a_P' are the same; and /or
- a_k and a_K' are selected not to hybridize to k_2 and k_2', respectively.

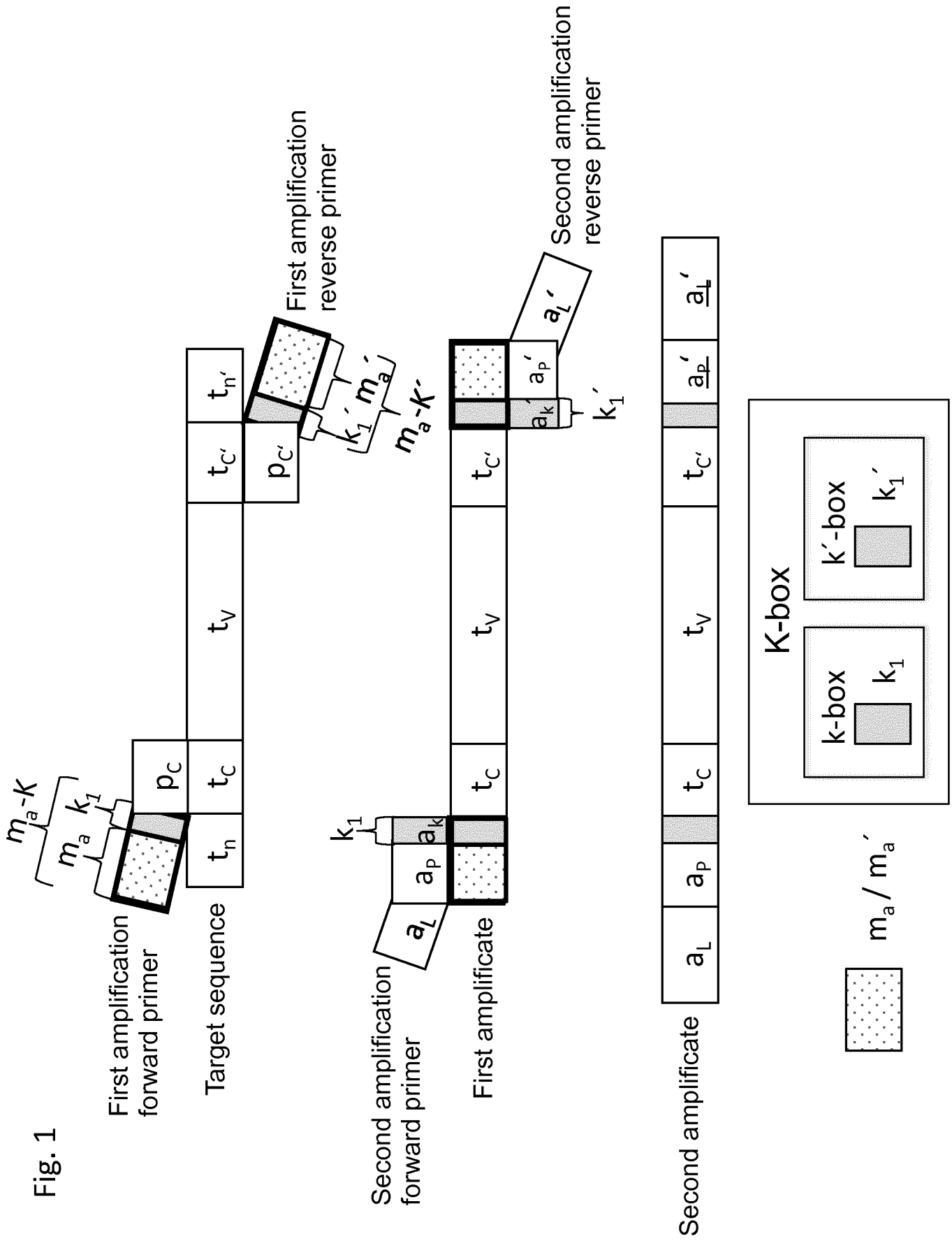
12. A multiplex collection comprising a plurality of collections of sets of primers according to any one of claims 7 to 11, wherein each collection is characterized by a different combination of p_C and p_C'.

13. The multiplex collection according to claim 12, wherein

- each p_C comprises, or is, a sequence selected from any one of SEQ ID NO 001 to SEQ ID NO 045, and wherein each p_C' comprises, or is, a sequence selected from any one of SEQ ID NO 046 to SEQ ID NO 058, or
- wherein each p_C comprises, or is, a sequence selected from any one of SEQ ID NO 189 to SEQ ID NO 232, and wherein each p_C' comprises, or is, a sequence selected from any one of SEQ ID NO 233 to SEQ ID NO 246.

14. A method for ex-vivo analysis of the T cell receptor ß chain repertoire of a patient, comprising the use of a method according to any one of claims 1 to 6, or of a collection of sets of primers according to any one of claims 7 to 11 or a multiplex collection according to claim 12 or 13.

Fig. 1


First amplification forward primer
Target sequence
First amplification reverse primer
Second amplification forward primer
First amplificate
Second amplification reverse primer
Second amplificate
K-box
k-box
k'-box
m_a / m_a'

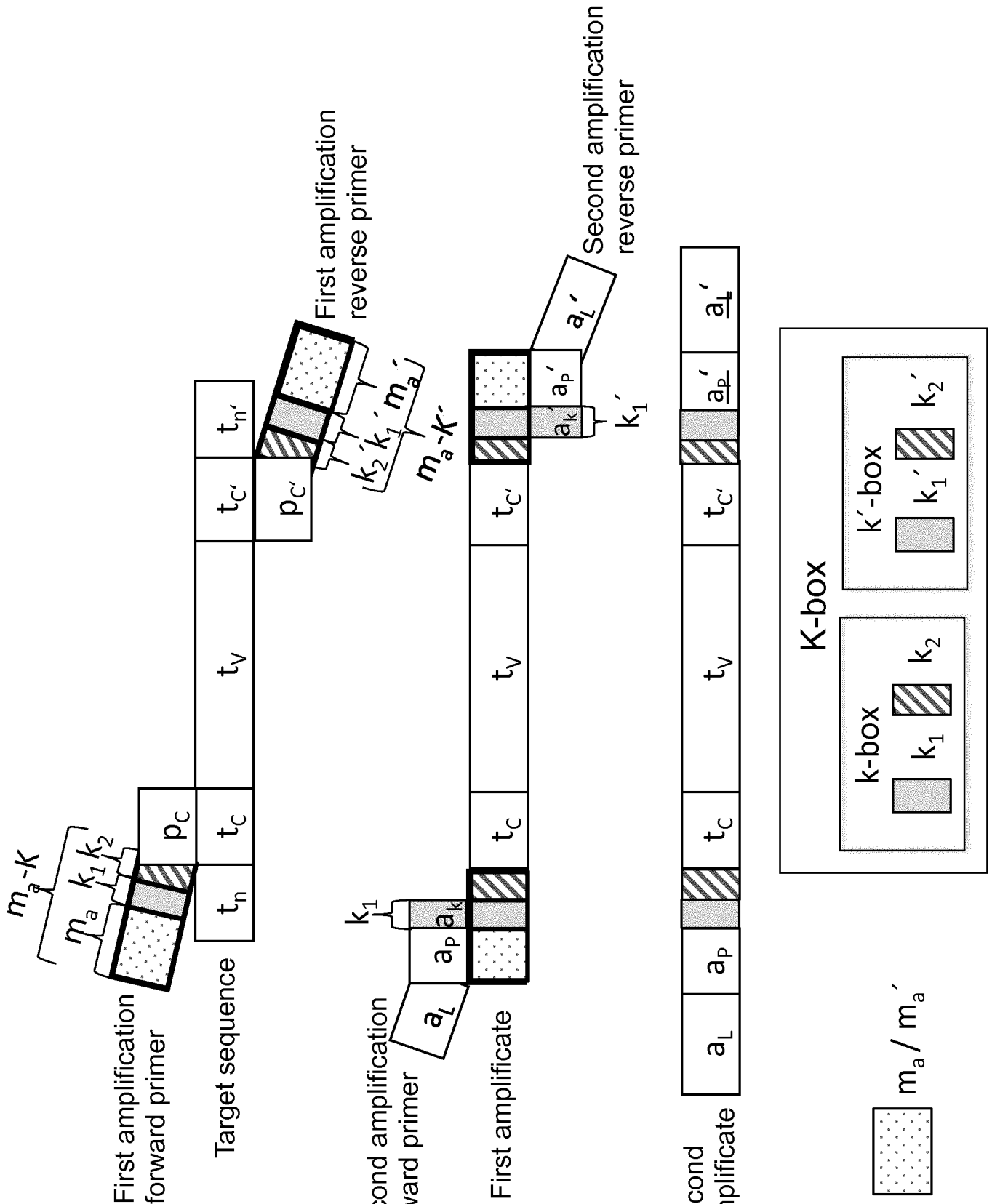

First amplification forward primer
Target sequence
First amplification reverse primer
Second amplification forward primer
First amplificate
Second amplification reverse primer
Second amplificate
K-box
k-box
k´-box
m_a / m_a´

Fig. 2

Fig. 3

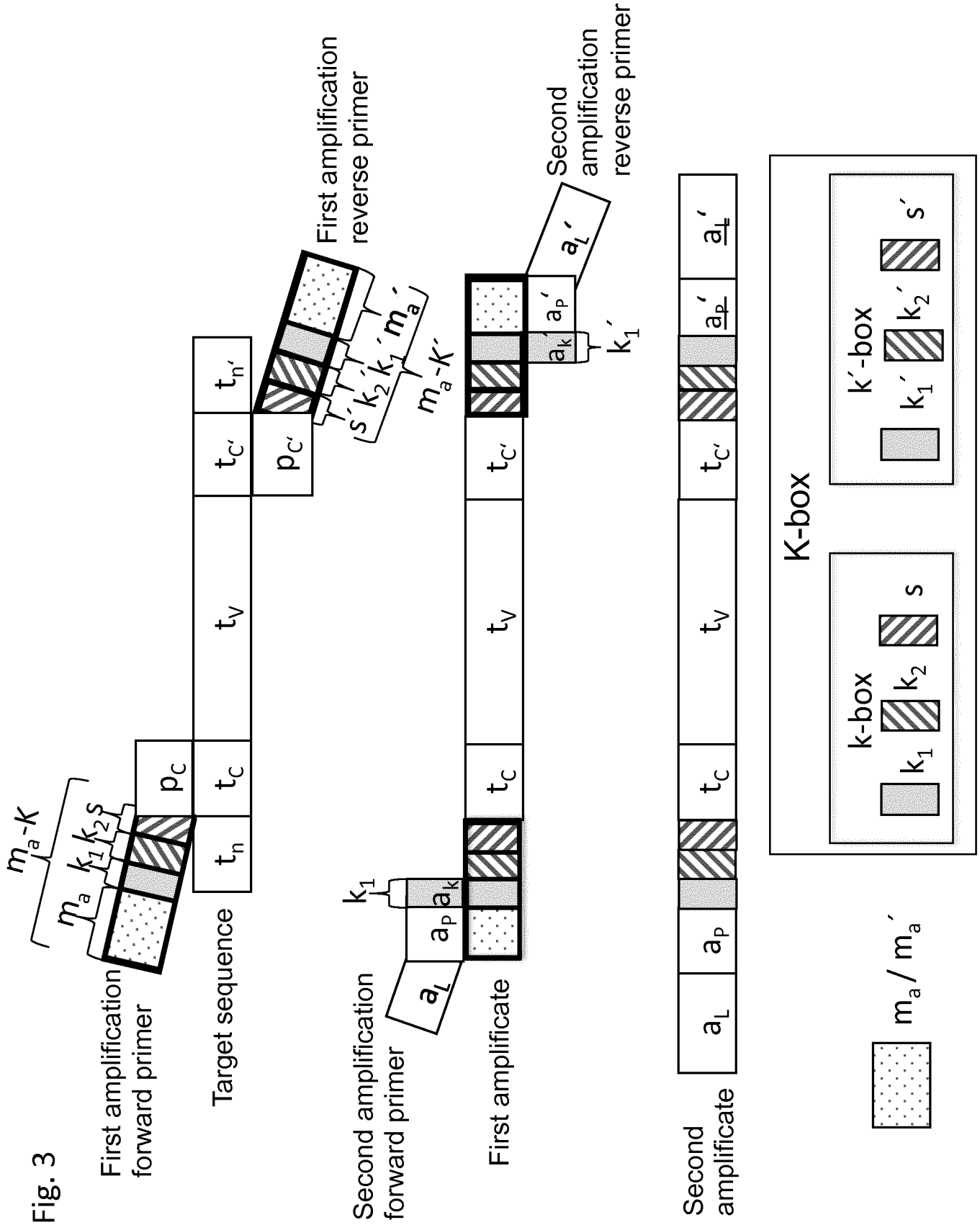
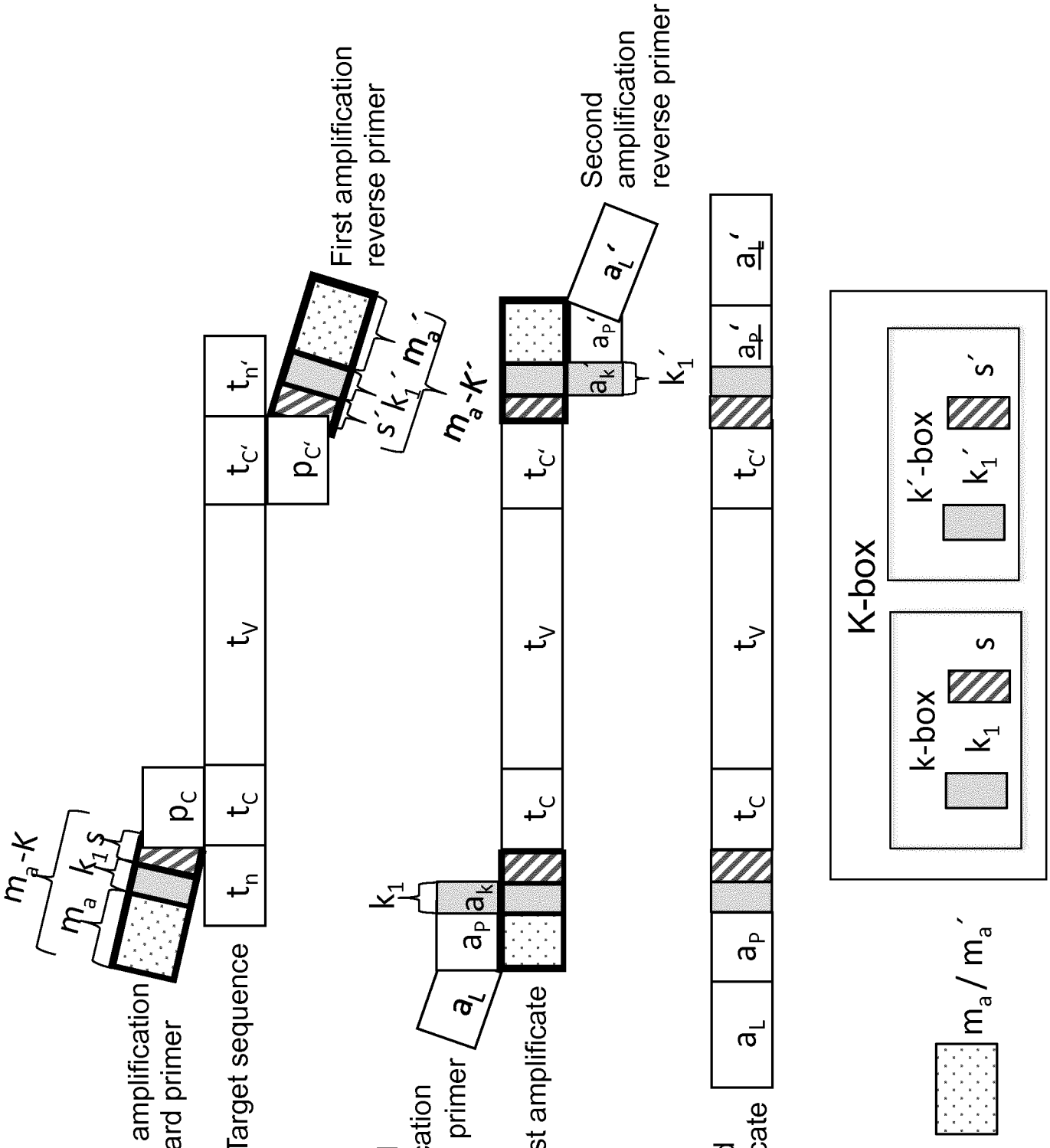
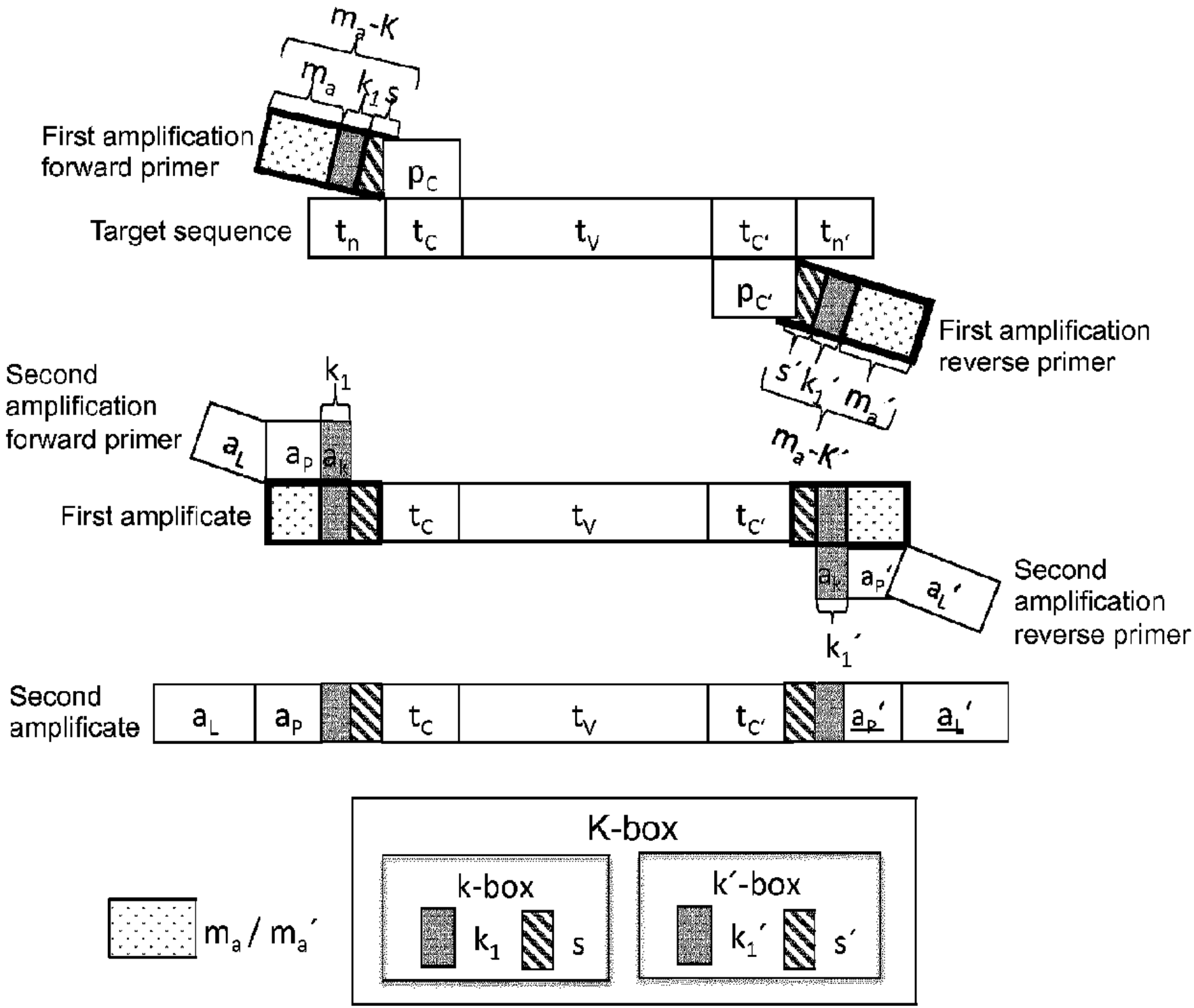

First amplification forward primer
Target sequence
First amplification reverse primer
Second amplification forward primer
First amplificate
Second amplification reverse primer
Second amplificate
K-box
k-box
k´-box
m_a / m_a´

Fig. 4


First amplification forward primer
Target sequence
First amplification reverse primer
Second amplification forward primer
First amplificate
Second amplification reverse primer
Second amplificate
K-box
k-box
k´-box
s
s´
m_a / m_a´


m_a-K
m_a k_1 s
First amplification forward primer
p_C
Target sequence
t_n t_C t_V $t_{C'}$ $t_{n'}$
$p_{C'}$
First amplification reverse primer
s´ k_1´ m_a´
m_a-K´
Second amplification forward primer
k_1
a_L a_P a_k
First amplificate
t_C t_V $t_{C'}$
a_k´ a_P´ a_L´
Second amplification reverse primer
k_1´
Second amplificate
a_L a_P t_C t_V $t_{C'}$ a_P´ a_L´
m_a / m_a´
K-box
k-box
k_1 s
k´-box
k_1´ s´