Theorem 1: Considering the source genome A and the destination genome B, A can be transformed into B by translocations if and only if:
(1) The two genomes contain the same set of genes;
(2) The two genomes contain the same number (must be at least 2) of chromosomes;
(3) The two genomes have the same set of ending (either head or tail) genes;
(4) For any gene g that is an ending gene in A, (a) if g's sign in A is different from that in B, then g must be a head in one genome and a tail in the other; (b) if g has the same sign in both A and B, then g must be either a head in both genomes or a tail in both genomes.

Proof: (*only if*) Since a translocation never creates or destroys any gene, (1) holds. Since a translocation never changes the number of chromosomes nor the set of ending genes, (2) and (3) hold. Note that, a prefix-prefix translocation never changes the sign of any gene, whereas a prefix-suffix can change the signs of genes. If an ending gene is involved in even number of prefix-suffix translocations, then (a) in (4) holds for such an ending gene. Otherwise, (b) in (4) holds for such an ending gene.

(*if*) Now we show that if conditions (1)–(4) hold, we can transform A into B.

By changing the sign and re-naming the genes, we can assume that all the genes in B are positive and gene $i+1$ is on the right of gene i if gene $i+1$ is not an ending gene on the left of a chromosome. If gene $i+1$ is the ending gene on the left of a chromosome, then gene i is an ending gene on the right of a chromosome. For example, B=((1, 2, 3), (4, 5, 6), (7, 8, 9, 10)).

Our strategy to transform A into B is (1) to put gene 1 in the correct position with positive sign, (2) after having put genes 1 to i to the correct positions with positive sign, we put gene $i+1$ in the correct position with positive sign.

Note that the prefix-prefix and prefix-suffix operations allow us to treat $x_1,x_2,\ldots, x_n$ and $-x_n,-x_{n-1}, \ldots, -x_1$ as the same chromosome. Thus, we can assume that gene 1 in A is always the left ending gene and the sign is always positive. (Otherwise, we can simply reverse the chromosome to fit our assumption.) Suppose that genes 1 to i have been put in the correct positions with positive sign and there exists a chromosome whose genes are all greater than i. If gene i and gene $i+1$ are not in the same chromosome, we can use one translocation operation to put gene $i+1$ in the correct position with positive sign and keep genes 1 to i "unchanged". If gene i and gene $i+1$ are in the same chromosome, then we can put gene $i+1$ in the correct position with positive sign and keep genes 1 to i "unchanged" by using two translocations. This process can continue until genes 1 to i are in the correct positions with positive sign, gene i and gene $i+1$ are in the same chromosome, say, Y, and there does not exist a chromosome whose genes are all greater than i. Let X be the chromosome $X=x_1,x_2,\ldots x_n$ such that $x_i \le i$ and x_n is the right ending gene that is the biggest satisfying $x_n \le i$. In this case, condition (4) ensures that the four ending genes in X and Y are in the correct positions with positive sign.

We decompose X into two segment $X=X_1X_2$, where $X_1=x_1,x_2, \ldots, x_{n-1}$ and $X2=x_n$. Let $Y=Y_1Y_2$, where $Y_1=j, j+1, \ldots, i$, is the segment of genes in the correct positions with positive sign. Then we can extend the segment Y_1 into $j, j+1, \ldots, i, i+1$ by two translocations, where the first translocation acts on X and Y and cuts X into X_1 and X_2. In the process, we will never further cut X_1 and X_2. This process can go on until all genes in Y are in the correct positions with positive sign. During the process, even number of prefix-suffix translocations must be used since the right and left ending genes in Y are transformed back as the right ending gene in Y. Thus, X is also recovered. This completes the proof. □