**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 translocations, then (a) in (4) holds for such an ending gene. Otherwise, (b) in (4) holds for such an ending gene.

**Proof:** 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 $x$, $x_2$, ..., $x_n$ and $-x_n$, $-x_{n-1}$, ..., $-x_1$ 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 1 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 1 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 1 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 $X=x_1, x_2$, ..., $x_n$ such that $x_1 \leq i$ and $x_n$ is the right ending gene that is the biggest satisfying $x_n \leq i$. 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 $X_1=x_1, x_2$, ..., $x_{i-1}$ and $X_2=x_i$. Let $Y=Y_1Y_2$, where $Y_1=x_j, x_{j+1}$, ..., $i$, is the segment of genes in the correct positions with positive sign. Then we can extend the segment $Y_1$ into $j, j+1$, ..., $i$, $i+1$ 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. $\square$