Deconvolute

Compiling and Boost libraries

This program requires the C++ Boost libraries to be installed on the server.
Compiling with g++ (all on one line)

```
g++ Deconvoluted.cpp Engine.cpp DataStore.cpp -I <path to boost installation> -L <path to boost libraries> -lboost_iostreams -o Deconvolute.exe 2> errors.txt
```

Any errors in the compiling will be saved to the errors.txt file. If this file has zero size the build as worked. If not look in the file and resolve the first error and then rebuild until it works.

Command line arguments

Read one filename with path,
Read two filename with path,
Primer file with path,
Index file with path,
Path to folder to save data in,
Minimum PCR length,
Maximum PCR length.

Example primer file

CGTGCCAGCCACCGCG
GGGTATCTAATCCYAGTTTG

These sequences can contain degenerate bases: S, W, R or Y.

Example index file

AACTGTAG
ACACTAAG
ACAGGCGC
ACTCGTGT
AGTACTCC
ATTGTGAA
CAATTAAC
CATAGAGT
CCATTCGA
CCTTCACC
GACGTCTT
GCCACAGG
GTCTACAC
GTGAATAT
GTGTCGGA

TAAGGTCA
TGCGAGAC
TGGCCGGT
TTCCTGTT
TTGCCTAG

These sequences can only contain standard bases: A, C, G or T.

Library production

The Sequence is PCR amplified with the primers of interest and the product cleaned up to remove primer dimer and primers. The amplicon is then used to make a whole genome library with a kit like the NEB NextUltra.

Example of reads with Primers

Sequence	**Comment**
1)	Forward sequence
GGGACTCGTGTGGATTGCGCTGTTATCCCTAGGGTA	Start of read with forward primer
----------GGATTGCGCTGTTATCC	Target primer sequence which is 14 to 17 bp from start
----ACTCGTGT	Index sequence which before the target sequence
NNNN	Unique id and stagger to create difference offset to aid base calling
2)	Reverse complement
ATTCGTACACTAAGAGACGAGAAGACCCTATGGAGCTTT	Start of read with reverse prime
----------AGACGAGAAGACCCTAT	
----ACACTAAG	
NNNNNN	