

CPOS Genomics Core

NGS platform Sequencing Run only service guideline

User have to provide the information prior sample submission:

1. Libraries information via Library Submission Form (in excel format)
2. Official library preparation protocol
3. Index i7 and i5 sequences
4. Index i7 and i5 sequences with full adapter sequences (if customized protocol or custom ordered adapter oligo used)

The job request will be on-hold until all information are available.

For user using custom protocol, use blast search for index checking, at least pick the first and the last one for the check:

Adapter sequence of i7:

CAAGCAGAAGACGGCATAACGAGAT**i7**GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG

Template sequence for i7 blast:

5'- AGATCGGAAGAGCACACGTCTGAACTCCAGTCACATCTCGTATGCCGTCTTCTGCTTG -3'

The screenshot shows the NCBI BLAST web interface. The 'Enter Query Sequence' field contains the template sequence: AGATCGGAAGAGCACACGTCTGAACTCCAGTCACATCTCGTATGCCGTCTTCTGCTTG. The 'Enter Subject Sequence' field contains the adapter sequence: CAAGCAGAAGACGGCATAACGAGATGTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG. The 'Program Selection' section is set to 'Highly similar sequences (megablast)'. The 'BLAST' button is visible at the bottom.

Subject Descr: None
Subject Length: 76
Other reports: [MSA View](#)

Descriptions | Graphic Summary | **Alignments** | Dot Plot

Alignment view: Pairwise | CDS feature

2 sequences selected

Download | Graphics

Sequence ID: Query_50429 Length: 76 Number of Matches: 1

Range 1: 1 to 66

Score	Expect	Identities	Gaps	Strand
71.3 bits(30)	1e-18	58/66(88%)	8/66(12%)	Plus/Minus

Query 1: AGATGGGAGGACACAGCTGAACTCCAGTCAC-----ATCTGGATGCGGCTCTC 52
 Subject 66: AGATGGGAGGACACAGCTGAACTCCAGTCACAACTCTTTCCCTACACGACGCTCTTCCGATCT 7

Query 53: TCTTGG 58
 Subject 6: TCTTGG 1

Index sequence

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Adapter sequence of i5:

5'- AATGATACGGCGACCACCGAGATCTACAC **i5** TCGTCGGCAGCGTC-3'

Template sequence for i5 blast:

5' AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT