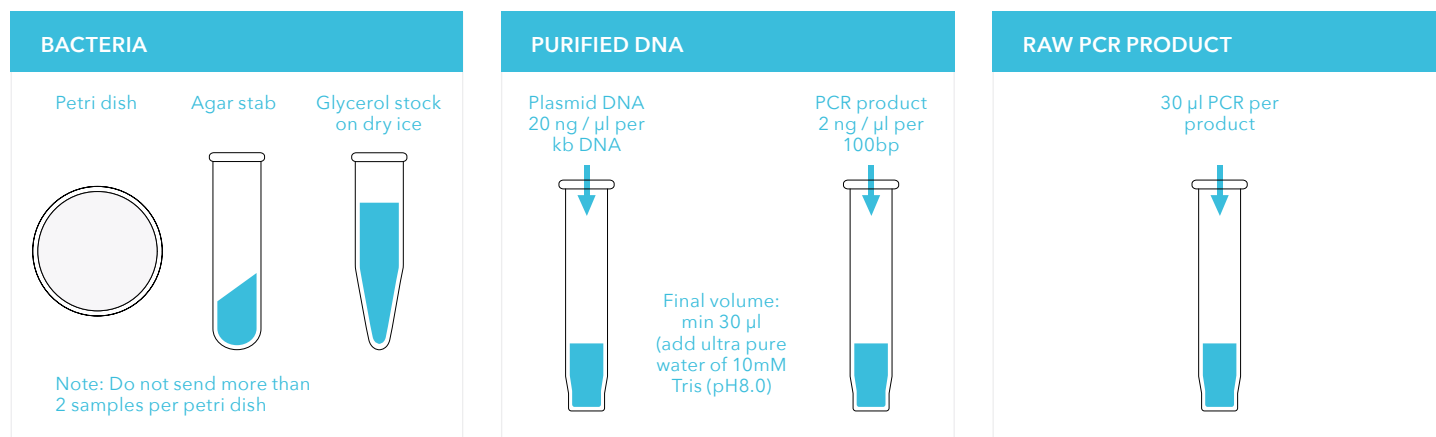


Order instructions full 24H sequencing

SAMPLE PREPARATION

1. SAMPLES



Notes

- Samples can be send in using our free BaseBox service
- DNA preferably column purified dissolved in water or 10mM Tris pH8.0.
- DNA samples should be free of EDTA and ethanol since trace amounts of these compounds will inhibit the sequence reaction.
- 2 μ L of the PCR product on agarose gel should give a single clear and sharp band.

2. PRIMERS

STANDARD PRIMER	CUSTOM PRIMER	CLIENT-SPECIFIC PRIMER	TO BE SYNTHESISED
Provided by BaseClear free of charge	Sent with your order, 10 pmol/ μ L in minimal volume of 20 μ L	Your custom primer, already stored at BaseClear	Submit primer sequence, additional costs and one day extra delivery time

CREATE ONLINE ORDER

Create your order using our convenient online portal <https://orders.baseclear.com>. Print the generated order form to send with your samples

WE PERFORM

- Optional plasmid isolation (miniprep) or PCR product purification
- DNA concentration measurement (using fluorescence method) for optimal results
- Sequencing run on ABI 3730(XL) DNA Analyzer
- Data analysis by KB caller, for superior base calling and sequence data interpretation

YOU RECEIVE

- Data within 1 working day (results sent before 10 a.m.)
- Results provided via our secure online portal
- E-mail notification when results are ready to download
- Full report, including sequence data in FASTA, SCF and ABI format.
- Sequence length of up to 1.100 bp (long run) or 550 bp (short run)
- Sequence runs are reviewed manually by our specialists
- Multiple re-runs (if needed) included

STANDARD PRIMER LIST

NAME	PRIMER SEQUENCE
3-AOX1	GCAAATGGCATTCTGACATCC
5-AOX1	GACTGGTTCCAATTGACAAGC
AmpL1	ACAGTCCAGTTACGCTGGAGTC
AmpR1	CTTTCTGCTATGGAGGTCAGGTATG
attL1-Fw	ACTTAAGCTCGGGCCCCAAA
attL2-Rv	TGTAACATCAGAGATTTTGAGACA
BGH2	GAACTAGAAGGCACAGTCGAGG
CMV-fw2	CGGTACGGTGGGAGGTCT
MF	TTTCCCAGTACGACGTTG
MF (-47)	CGCCAGGGTTTTCCCAGTCACGAC
MF-20i	GTA AACGACGCGCCAG
MR	GGATAACAATTCACACAGG
MR-invitrogen	CAGGAACAGCTATGACC

NAME	PRIMER SEQUENCE
pBAD Forward	ATGCCATAGCATTTTTATCC
pBAD Reverse	GATTTAATCTGTATCAGG
pDonR F1T	CGCGTTAACGCTAGCATGGATCTC
pDonR R1	GTAACATCAGAGATTTTGAGACAC
pECFP-C1-FW	CAAAGACCCCAACGAGAAGC
pECFP-C1-RV	CATTCATTTTATGTTTCAGGTTC
pGEX forward	ATAGCATGGCCTTTGACAGG
pGEX reverse	GAGCTGCATGTGTCAGAGG
poly-A	TTTTTTTTTTTTTTTTTTTTT
pQE60-FW	CCCGAAAAGTGCCACCTG
pQE60-Rv	GTTCTGAGGTCATTACTGG
pRSforward	CCCTGAACCTCCTCGTTTCGACC
pRSReverse	GAGACGTGCTACTTCCATTGTC

NAME	PRIMER SEQUENCE
pRSeq	GCTGACGTCATCAACCCGCT
pTrcHis Forw.	GAGGTATATATTAATGTATCG
pTrcHis Rev.	GATTTAATCTGTATCAGGCTG
SL1C	AGTCCAGTTACGCTGGAGTC
Sp6i	GATTTAGGTGACACTATAG
SR2	GGTCAGGTATGATTTAAATGGTCAGT
T3ext.	AATTAACCCCTCACTAAAGGG
T3i	AATTAACCCCTCACTAAAG
T7	TAATACGACTCACTATAGGG
T7-R	GCTAGTTATTGCTCAGCGG
Tk PolyA Rev	CTTCCGTTTTCAGTTAGC

ABBREVIATIONS SANGER SEQUENCING

HS	High signal	EC	Echo signal after a stretch
LS	Low signal	BP	Broad peaks at the end
NO	No signal	BG	Background signal
SD	Signal drop	SP	Spike in the sequence
SS	Signal stop	ST	Stretch in the sequence
DS	Double signal	R	Reaction will be repeated
DB	Double signal at the start	X	Reaction will not be repeated
DE	Double signal at the end		