



Request form for rhAmpSeq assay design

Please complete one form for each rhAmpSeq panel.

First and last name:

Organization:

Email:

NGS application type (Please select one):

SNP hotspots

CRISPR on-target/off-target analysis

Input type (Please select one):

(Option 1) Target in BED file with genome information (preferred)

(Option 2a) Target SNP embedded in FASTA sequences + genome information

(Option 2b) Target SNP embedded in FASTA sequences (no genome information)

(Option 3) Target in BED file + reference sequence (no genome information)

Other (requires special processing)

Panel name (This will be printed on tube and plate labels. Maximum number of characters = 30.):

Genome information (Please specify genus and species):

Genus and species: (e.g., Homo sapiens)

Genome build: (e.g., GRCh38)

Other:

Sequencing platform

Paired-end reads: Yes No

Minimum insert size (≥ 50 bp, default = 70):

Maximum insert size (≤ 200 bp, default = 120):

See what more we can do for you at www.idtdna.com.

Please refer to document “Input data formats for rhAmpSeq assay design” (Step 1) for data format.

Please specify names of submitted files:

Target BED file (4- or 6-column BED file only):

Filename:

If target SNP embedded in FASTA file, FASTA target file:

Filename:

If reference sequence in FASTA format:

Filename:

If genome or reference sequence is not publicly available:

Data/file transfer method (FTP site, USB drive, etc.):

Additional files: