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:

NGS • CRISPR • Functional Genomics • Synthetic Biology • PCR & qPCR • Custom Oligos • Contract Manufacturing