

Amplicon Diversity Assay List

At RTL Genomics, we are able to use almost any amplicon assay for your project. Illumina projects should use amplicons with a length less than 550 bp. Longer assays may be used if desired, but will make our denoising and analysis process unavailable for your data. We may also be unable to perform taxonomic analysis for some functional genes.

Our recommended assays are listed below, but you can choose to combine forward and reverse primers in a different configuration to target the variable region of interest. Recommended assays have the best historical performance and are commonly used regions. All primers have different amplification bias for certain organisms, and that information is not always known for all primers. Primers marked as “universal” show amplification of multiple kingdoms with the same primer. Other primers preferentially amplify only their listed kingdom organism.

If the primer you are looking for is not listed, we still may have it, but if that is not the case it can easily be ordered. Please inquire and we will be happy to assist you.

Recommended assays:

Assay	Forward Primer	Reverse Primer	Notes
28F	28F - GAGTTTGATCNTGGCTCAG	519R - GTNTTACNGCGGCKGCTG	Default 16S, V1-V3
357wF	357wF - CCTACGGGNGGCWGCAG	806R GGACTACHVGGGTWTCTAAT	V3-V4
515F	515F - GTGCCAGCMGCCGCGGTAA	806R GGACTACHVGGGTWTCTAAT	Earth Microbiome, V4
515yF	515yF - GTGYCAGCMGCCGCGGTAA	926pF - CCGYCAATTYMTTTRAGTTT	Earth Microbiome, V4-5
Arch517F	Arch517F - GCYTAAAGSRNCCGTAGC	Arch909R TTTCAGYCTTGCRCCGTAC	Default Archaea 16S, V4-5
ITS1	ITS1F CTTGGTCATTTAGAGGAAGTAA	ITS2aR GCTGCGTTCTTCATCGATGC	Default Fungal ITS, ITS1

Bold are from Earth Microbiome Project, *Italicized are default primers for RTLGenomics*

** Bacterial & Archaeal “universal”

*** Bacterial & Archaeal & Eukaryotic “universal”

Bacterial Primers

16S

27F AGAGTTTGATCCTGGCTCAG

338R GCTGCCTCCCGTAGGAGT

27-YMF AGAGTTTGATYMTGGCTCAG

533R TTACCGCGGCTGCTGGCAC

27mF AGRGTTYGATYMTGGCTCAG

534R TYACCGCGGCTGCTGG

28F-YM GAGTTTGATYMTGGCTCAG

These primers
are mixed at a
4:1:1:1 ratio
(28F-YM is at
4 parts)

28F-Borrellia GAGTTTGATCCTGGCTTAG

28F-Chloroflex GAATTTGATCTTGGTTT CAG

28F-Bifdo GGGTTCGATTCTGGCTCAG

28F GAGTTTGATCNTGGCTCAG

519R *GTNTTACNGCGGCKGCTG*

63F CAGGCCTAACACATGCAAGTC

388R *TGCTGCCTCCCGTAGGAGT*

104F GGCGVACGGGTGAGTAA

530aR GTATTACCGCGGCTGCTG

338F TCCTACGGGAGGCAGCAGT

530R CCGCNGCNGCTGGCAC

338aF ACTCCTACGGGAGGCAGCAG

797R GGACTACCAGGGTATCTAATCCTGTT

338bF ACWCCTACGGGWGGCWGC

518R ATTACCGCGGCTGCTGG

Firm350F GGCAGCAGTRGGGAATCTTC

Firm814R ACACYTAGYACTCATCGTTT

Cyan359F GGGGAATYTTCCGCAATGGG

Cyan781R GACTACWGGGGTATCTAATCCCWTT

AMX368F TTCGCAATGCCCGAAAGG

AMX821R AAAACCCCTCTACTTAGTGCCC

357F (341F) CCTACGGGAGGCAGCAG *

907R CCGTCAATTCMTTTGAGTTT

926wR CCGTCAATTYMTTTRAGTTT

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** Bacterial & Archaeal “universal”

*** Bacterial & Archaeal & Eukaryotic “universal”

357wF CCTACGGGNGGCWGCAG

515F GTGCCAGCMGCCGCGGTAA

515yF GTGYCAGCMGCCGCGGTAA

515wF GTGYCAGCMGCCGCGGTA

530F GTGCCAGCMGCNGCGG

926wF AAACYAAAKGAATTGRCGG

939F TTGACGGGGGCCCGCACAAAG

785R GACTACHVGGGTATCTAATCC

806R GGACTACHVGGGTWTCTAAT**

806bR GGACTACNVGGGTWTCTAAT

909R CCCCGYCAATTCMTTTRAGT

926R CCGTCAATTCMTTTRAGTTT

926pfR CCGYCAATTYMTTTRAGTTT

1392R ACGGGCGGTGTGTRC***

1492R TACCTTGTTACGACTT

Archaeal Assays

16S

Arch340wF CCCTAYGGGGYGASCAG

Arch517F GCYTAAAGSRNCCGTAGC

Arch519wF CAGCMGCCGCGGTAA

Arch806R GGACTACVSGGGTATCTAAT

Arch909R TTTCAGYCTTGCGRCCGTAC

Arch1017R GGCCATGCACCWCCTCTC

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** Bacterial & Archaeal “universal”

*** Bacterial & Archaeal & Eukaryotic “universal”

Eukaryote/Fungi Assays

18S

Euk1AF CTGGTTGATCCTGCCAG

Euk516R ACCAGATTGCCCTCC

EukA7F AACCTGGTTGATCCTGCCAGT

Euk570R GCTATTGGAGCTGGAATTAC

Euk300F AGGGTTCGATTCCGGAG

Euk555R GCTGCTGGCACCAGACT

Euk515F GTGYCAGCMGCCGCGGTA

EukNSR951R TTGGYRAATGCTTTTCGC

Euk516F GGAGGGCAAGTCTGGT

Euk1052R TGCATGGYYGYCGYCAGYTC

Euk1055R CGGCCATGCACCACC

Euk1560F TGGTGCATGGCCGTTCTTAGT

Euk2035R CATCTAAGGGCATCACAGACC

Euk1391F GTACACACCGCCCGTC

EukBR TGATCCTTCTGCAGGTTACCTAC

TAReukF CCAGCASCYGCGGTAATTCC

TAReukR ACTTTCGTTCTTGATYRA

EukBaIR ACTTTCGTTCTTGATYRR

EukSto2R ACTTTCGTTCTTGAT

TAReukR3mR ACTTTCGTTCTTGATYRATGA

ITS

ITS1F CTTGGTCATTTAGAGGAAGTAA

ITS2aR GCTGCGTTCTTCATCGATGC

ITS3F GCATCGATGAAGAACGCAGC

ITS4R TCCTCCGCTTATTGATATGC

ITS9F GAACGCAGCRAAIIGYGA

23S

AlgaeF GGACAGAAAGACCCTATGAA

AlgaeR TCAGCCTGTTATCCCTAGAG

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** Bacterial & Archaeal “universal”

*** Bacterial & Archaeal & Eukaryotic “universal”



Arthropod COI

mICOLintF **GGWACWGGWTGAACWGTWTAYCCYCC**

HCO2198R **TAAACTTCAGGGTGACCAAAAAATCA**

Plant trnL

trnLcF **CGAAATCGGTAGACGCTACG**

trnLdR **GGGGATAGAGGGACTTGAAC**

trnLgF **GGGCAATCCTGAGCCAA**

trnLhR **CGCGCATGGTGGATTACAATCC**

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**** Bacterial & Archaeal “universal”**

***** Bacterial & Archaeal & Eukaryotic “universal”**