

MiSeq Metagenomics Results

Next-Generation Sequencing Service

WESTERN SYDNEY
UNIVERSITY



Research

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Sequencing Information

Sequencing date	10.08.16
Target region	16S 341F-805R
Read length	2 x 301 bp
Total PF reads for sequencing run	21,173,186

Sample ID	Customer ID	Index Number	Index 1 (I7)	Index 2 (I5)	% Reads Identified (PF)	Number of reads
ROH1	1	165	TGCAGCTA	CTCTCTAT	0.38	80,818
ROH2	2	166	TGCAGCTA	TATCCTCT	0.31	64,832
ROH3	3	167	TGCAGCTA	GTAAGGAG	0.36	76,668
ROH4	4	168	TGCAGCTA	ACTGCATA	0.29	62,270
ROH5	5	169	TGCAGCTA	AAGGAGTA	0.36	75,355
ROH6	6	170	TGCAGCTA	CTAAGCCT	0.37	78,955
ROH7	7	171	TGCAGCTA	CGTCTAAT	0.42	88,906
ROH8	8	172	TGCAGCTA	TCTCTCCG	0.38	80,649
ROH9	9	173	TCGACGTC	CTCTCTAT	0.49	102,817
ROH10	10	174	TCGACGTC	TATCCTCT	0.89	188,335
ROH11	11	175	TCGACGTC	GTAAGGAG	0.45	96,296
ROH12	12	176	TCGACGTC	ACTGCATA	0.65	137,774
ROH13	13	177	TCGACGTC	AAGGAGTA	0.77	162,229
ROH14	14	178	TCGACGTC	CTAAGCCT	0.45	96,063
ROH15	15	179	TCGACGTC	CGTCTAAT	0.43	90,325
ROH16	16	180	TCGACGTC	TCTCTCCG	0.44	92,633
ROH17	17	181	TAAGGCGA	TCGACTAG	0.34	72,306
ROH18	18	182	TAAGGCGA	TTCTAGCT	0.26	54,288
ROH19	19	183	TAAGGCGA	CCTAGAGT	0.28	58,713
ROH20	20	184	TAAGGCGA	GCGTAAGA	0.38	81,072
ROH21	21	185	TAAGGCGA	CTATTAAG	0.46	97,524
ROH22	22	186	TAAGGCGA	AAGGCTAT	0.37	77,282
ROH23	23	187	TAAGGCGA	GAGCCTTA	0.39	83,105
ROH24	24	188	TAAGGCGA	TTATGCGA	0.34	72,772

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Illumina overhang adapter*

Forward overhang 5' TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG-[locus-specific sequence]

Reverse overhang 5' GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG-[locus-specific sequence]

**Sequences have undergone adapter trimming*

Bacterial primers (16S)

341F – 5' CCTACGGGNGGCWGCAG

805R – 5' GACTACHVGGGTATCTAATCC

27F – 5' AGAGTTTGATCMTGGCTCAG

519R – 5' GWATTACCGCGGCKGCTG

515F – 5' GTGCCAGCMGCCGCGGTAA

806R – 5' GGACTACHVGGGTWTCTAAT

Fungal primers (ITS)

FITS7 – 5' GTGARTCATCGAATCTTTG

ITS4 – 5' TCCTCCGCTTATTGATATGC