

# MiSeq Metagenomics Results

## Next-Generation Sequencing Service

**WESTERN SYDNEY**  
UNIVERSITY



Research

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### Sequencing Information

Sequencing date	16.08.16
Target region	ITS FITS7-ITS4
Read length	2 x 281 bp
Total PF reads for sequencing run	25,298,208

Sample ID	Customer ID	Index Number	Index 1 (I7)	Index 2 (I5)	% Reads Identified (PF)	Number of reads
ROH1	1	165	TGCAGCTA	TCGACTAG	0.5282	133,625
ROH2	2	166	TGCAGCTA	TTCTAGCT	0.4229	106,986
ROH3	3	167	TGCAGCTA	CCTAGAGT	0.3718	94,059
ROH4	4	168	TGCAGCTA	GCGTAAGA	0.2847	72,024
ROH5	5	169	TGCAGCTA	CTATTAAG	0.3864	97,752
ROH6	6	170	TGCAGCTA	AAGGCTAT	0.3542	89,606
ROH7	7	171	TGCAGCTA	GAGCCTTA	0.4596	116,271
ROH8	8	172	TGCAGCTA	TTATGCGA	0.489	123,708
ROH9	9	173	TCGACGTC	TCGACTAG	0.5155	130,412
ROH10	10	174	TCGACGTC	TTCTAGCT	0.5245	132,689
ROH11	11	175	TCGACGTC	CCTAGAGT	0.2919	73,845
ROH12	12	176	TCGACGTC	GCGTAAGA	0.5864	148,349
ROH13	13	177	TCGACGTC	CTATTAAG	0.5486	138,786
ROH14	14	178	TCGACGTC	AAGGCTAT	0.8581	217,084
ROH15	15	179	TCGACGTC	GAGCCTTA	0.4955	125,353
ROH16	16	180	TCGACGTC	TTATGCGA	0.6078	153,763
ROH17	17	181	AAGAGGCA	CTCTCTAT	0.3219	81,435
ROH18	18	182	AAGAGGCA	TATCCTCT	0.4488	113,538
ROH19	19	183	AAGAGGCA	GTAAGGAG	0.4924	124,568
ROH20	20	184	AAGAGGCA	ACTGCATA	0.3265	82,599
ROH21	21	185	AAGAGGCA	AAGGAGTA	0.3057	77,337
ROH22	22	186	AAGAGGCA	CTAAGCCT	0.481	121,684
ROH23	23	187	AAGAGGCA	CGTCTAAT	0.2581	65,295
ROH24	24	188	AAGAGGCA	TCTCTCCG	0.3496	88,443

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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