Simulation Results

February 17, 2018

Values given are average values of AVGRE (AVerage Relative Error) metric with standard deviations given in parenthesis:

$$AVGRE = \frac{1}{1000} \sum_{i \in M_a \cup M_e} \left| T_{i,e} * \frac{\sum_{i \in M_a} T_{i,a}}{\sum_{i \in M_a \cup M_e} T_{i,e}} - T_{i,a} \right| \tag{1}$$

Where M_a as the set of actual haploid reference sequences contributing to a pooled sample and M_e as the set of additional references a method classifies as having a non-zero number of reads that are not truly present. Also, let $T_{i,e}$ be the count of reads estimated for reference i and $T_{i,a}$ is the actual number of simulated reads from reference i present in the sample.

Table 1: **Per reference error rates, 1,000,000 reads**

Read Length	Region	Samples	Method	Shannon Diversity									
				[0,0.7)	[0.7,1.4)	[1.4,2)	[2,2.7)	[2.7,3.4)	[3.4,4.1)	[4.1,4.8)	[4.8,5.5)	[5.5,6.2)	[6.2,6.9]
75bp SE	Full gene	110	Karp	439.3 (262.1)	372.3 (178.9)	379.3 (111.4)	304.4 (90.7)	268.4 (41.2)	260.8 (39)	236.2 (21.6)	252 (28.4)	254.7 (15.5)	261.5 (12.2)
			UCLUST	1229.1 (376.1)	1218.9 (246.3)	1207.1 (168.5)	1054.1 (209.2)	1008.2 (55.7)	1002.1 (72)	894.4 (33.7)	874.6 (38.5)	827.6 (29)	808 (30.8)
			SortMeRNA	1267.3 (367)	1275.8 (216.7)	1257.6 (144.9)	1112.7 (193.6)	1039.5 (72)	1041 (84.6)	942.5 (47.3)	928.3 (28.6)	880.5 (34.4)	883.2 (130.5)
			Kallisto	575.3 (283)	548.9 (206.1)	553.3 (93.5)	439.9 (106.7)	393 (38.3)	391.9 (49.7)	363.4 (23.7)	384.3 (31.2)	389.4 (21.6)	400.5 (15.5)
			USEARCH61	1276.9 (367.9)	1264.4 (191.7)	1231.9 (149.3)	1092 (202.6)	1021.1 (74)	1021.3 (85.1)	917.2 (46.4)	895 (29.3)	848.3 (33.4)	828.4 (31.7)
	V4	130	Karp	309.3 (227.7)	321.2 (224.5)	345.9 (121.2)	306.3 (121.6)	241.6 (54.5)	222.1 (45.4)	191.3 (19.8)	195.4 (16.4)	175.2 (8.3)	176.9 (5.4)
			UCLUST	1083.5 (517.4)	1013.1 (368.4)	1115.6 (203.2)	1018 (136.9)	919 (197.1)	867.5 (83.7)	831.1 (41.1)	818.8 (49.1)	755.9 (27.6)	713.9 (13.7)
			SortMeRNA	1014.8 (505.2)	880.1 (345.4)	1073.2 (179.1)	944.3 (143.4)	874.6 (197.3)	846.3 (90)	860 (52.4)	845.7 (54.1)	805.1 (29.5)	762 (10.6)
			Kallisto	449.8 (262.1)	496.3 (267.7)	520.4 (160.2)	476.2 (113.3)	417.9 (155.1)	383.6 (93.7)	325.5 (29.5)	350.6 (24.3)	339.8 (8.5)	352 (9.4)
			USEARCH61	1086.5 (447.6)	957 (357.6)	1100.7 (166.1)	995.5 (176.2)	885.4 (205.6)	852.6 (93.4)	855.9 (47.6)	832.2 (55.5)	778.3 (29.9)	726.1 (8.6)
151bp PE	Full gene	130	Karp	93.6 (118.9)	50.9 (35)	75.2 (43.8)	74.7 (37.7)	89.4 (55)	63.5 (20.8)	73.5 (12.2)	65.2 (13.1)	60.8 (4.7)	57.6 (3.8)
			UCLUST	572.3 (484.7)	552.4 (388.9)	541.7 (313.8)	473.8 (264.9)	419.9 (124.4)	405.3 (82.4)	468.6 (59.1)	430.3 (51.2)	433 (22.3)	419.2 (9.9)
			SortMeRNA	929.2 (540)	726.5 (343.7)	676.1 (281.3)	680.9 (266.3)	648.4 (173.2)	607.8 (125.3)	619.8 (73.1)	593.6 (46.1)	569.6 (35.4)	523 (11.1)
			Kallisto	15.9 (12.6)	46.8 (24.4)	52.6 (21.4)	71.3 (19.4)	77.6 (17.1)	72.8 (11.1)	76.7 (7.3)	75.3 (5.3)	76.5 (5.2)	77.1 (2.9)
			USEARCH61	598.1 (591.3)	630.4 (436.8)	666.3 (354.2)	502 (225.4)	539.5 (162.3)	419.1 (106.6)	480 (65.3)	439.8 (35.3)	461.7 (22)	458 (17.2)
	V4	190	Karp	1.2 (2.2)	5.5 (16.7)	6.2 (18.5)	1.9 (1.4)	3.2 (4.3)	3.5 (2.2)	5.5 (3.1)	4.7 (1.2)	6 (2)	6.9 (0.8)
			UCLUST	48.5 (262.1)	56.4 (140.8)	77.9 (194.9)	21.7 (39)	65.1 (91.1)	97 (137.6)	64.4 (25.9)	72 (30.9)	80.1 (22.7)	101.3 (10.8)
			SortMeRNA	70.6 (264.4)	119.5 (278.2)	114.3 (207.8)	85.8 (72.4)	117.7 (137.5)	209.8 (144.6)	152.1 (68)	140.7 (42.6)	150.9 (31)	147.5 (22.1)
			Kallisto	65.2 (270.8)	93.9 (189.5)	83.3 (87.4)	70.1 (14)	89.6 (46.8)	122.5 (53.5)	118.8 (21)	96.7 (14)	95.7 (9.6)	101.2 (6.2)
			USEARCH61	89.8 (348.2)	155.6 (320)	101.8 (161)	56.4 (102.4)	119.2 (138.1)	125.6 (51.3)	151.1 (69.3)	121.7 (31.2)	110.9 (32.3)	135.3 (17.4)
301bp PE	Full gene	170	Karp	97.7 (129.6)	149.4 (228.2)	105.7 (73.1)	97 (59.1)	101.7 (63.4)	98.8 (27.3)	112.7 (27.1)	131.7 (33.7)	117 (16.9)	116.6 (8.2)
			UCLUST	275.6 (356.4)	285.1 (334.8)	310.7 (237.5)	242.3 (137.1)	281.6 (150.3)	293.2 (51.4)	287.6 (79.4)	312.2 (38.5)	294.7 (31)	301.3 (16.2)
			SortMeRNA	356.6 (407.6)	566.2 (457.5)	531.9 (246.7)	427.6 (151.1)	460.8 (145.7)	471.9 (63.3)	485.6 (81.3)	505.2 (47.6)	456.1 (36.3)	444.8 (19.4)
			Kallisto	449.5 (376.7)	800.7 (304.1)	908.6 (253.7)	985.8 (249.8)	1059.5 (128.8)	1045.4 (117.6)	1082.2 (110.4)	1083.8 (41.3)	1100.3 (25.2)	1095.2 (17.5)
			USEARCH	196.1 (238.5)	380 (389.1)	269 (187)	245.3 (121.1)	299.2 (138.6)	260.7 (42.7)	334.5 (58.3)	344.5 (51.5)	376.7 (43)	371.7 (25.6)
	V4	190	Karp	12.6 (54.5)	29.5 (139.3)	10.1 (10.3)	48.8 (61.9)	16 (20)	14.9 (13.4)	12.2 (4.3)	16.8 (9.6)	15.9 (5.4)	17.6 (3.3)
			UCLUST	63.3 (288.8)	72.5 (269.5)	54.2 (148.8)	15.7 (20.4)	39.3 (56.8)	19.1 (28.5)	38.8 (28.7)	56.6 (24)	56.5 (16.5)	73.3 (18.1)
			SortMeRNA	110.4 (389.9)	161.8 (393.1)	51.1 (108.5)	217.1 (235.3)	128.4 (73.3)	126.4 (106.9)	97.4 (65.2)	105 (53.4)	104.8 (19.5)	101.9 (11.4)
			Kallisto	484.1 (366.5)	873.8 (372.9)	990.5 (281.5)	1143.9 (205.7)	1251.8 (174.9)	1236.2 (97.9)	1257.4 (89.1)	1255.3 (51.2)	1243.3 (41.6)	1272.6 (29.5)
			USEARCH61	54.9 (194.6)	66 (243.9)	95.6 (177.7)	129.8 (141)	68.4 (54.8)	108.9 (86.2)	53.4 (29.7)	81.6 (25.2)	85.4 (29.9)	98.6 (10.5)

SE=Single-end, PE=Paired-end

Table 2: **Per reference error rates, 100,000 reads**

Read Length	Region	Samples	Method	Shannon Diversity									
				[0,0.7)	[0.7,1.4)	[1.4,2)	[2,2.7)	[2.7,3.4)	[3.4,4.1)	[4.1,4.8)	[4.8,5.5)	[5.5,6.2)	[6.2,6.9]
75bp SE	Full gene	130	Karp	39.7 (21)	41.1 (14.3)	41.5 (15.2)	37.5 (8.3)	34.7 (6.8)	32.9 (2.9)	32.5 (1.7)	31.7 (1.7)	32.3 (1.4)	33.7 (0.8)
			UCLUST	105.9 (45.4)	118.1 (18.4)	113.2 (16.3)	108.4 (14.7)	102.6 (10)	98.8 (3.3)	92.9 (5.2)	86.7 (3.6)	82.8 (1.8)	78.1 (1.1)
			SortMeRNA	113.7 (41.4)	122.8 (18.1)	118.7 (16.6)	117.5 (12.2)	109.1 (6.4)	103.5 (4.7)	100 (3.9)	93.9 (1.5)	90 (1.7)	85.9 (1)
			Kallisto	55.2 (22.9)	53.8 (16.2)	53.2 (15.4)	48.1 (8.5)	44.8 (6.4)	42.8 (3.5)	42.6 (1.8)	41.4 (1.7)	42.5 (1.4)	44.1 (0.9)
			USEARCH61	111.2 (41.7)	123 (17.6)	117.4 (17.5)	113.9 (14.2)	105.4 (6.8)	98.7 (5.7)	94.9 (4.5)	88.7 (1.9)	84.2 (1.9)	79.5 (0.9)
	V4	130	Karp	34 (25.5)	31.9 (19.3)	34.2 (13.9)	37.5 (12.8)	29.9 (9)	24.9 (5.3)	23.8 (3.5)	22.5 (2)	22.6 (1.5)	23.2 (0.8)
			UCLUST	104.3 (49.1)	101.5 (43.4)	105 (25.1)	111.2 (27.1)	102.2 (13.9)	91.7 (11.8)	88 (6.1)	80.6 (4.8)	78.6 (3.5)	72.5 (1.7)
			SortMeRNA	114.3 (47.2)	110.5 (44)	106.2 (20.1)	110.2 (22.1)	98.9 (13.2)	91.3 (7)	89.6 (5.4)	88.3 (4.6)	84.7 (2.3)	80.7 (1.2)
			Kallisto	48.8 (28.8)	49.5 (27)	55.4 (26.6)	52.9 (13.9)	45.7 (10.3)	40.5 (10.9)	37.8 (4.6)	36.2 (3.5)	37.2 (2.4)	37.4 (1.2)
			USEARCH61	121.1 (48.4)	113.9 (42.4)	108.6 (21)	110.3 (22.5)	99.8 (13.5)	88.6 (7.3)	87 (6.1)	84.6 (5.4)	78.9 (2.3)	73.4 (1.4)
151bp PE	Full gene	130	Karp	7.3 (8.8)	7 (7.3)	9 (5.6)	7.4 (2.8)	6.5 (2)	6.4 (1.2)	7.1 (1.5)	7 (1.3)	6.4 (0.6)	5.9 (0.5)
			UCLUST	45.5 (40.8)	43.1 (31.5)	53.5 (30.9)	50.6 (23.2)	39.5 (7.7)	43.9 (8.6)	46.4 (5.9)	44.9 (4.8)	46.5 (3.1)	44.8 (2.7)
			SortMeRNA	65.1 (43.2)	45.4 (27.3)	75.1 (28.4)	73.2 (20)	54.9 (10.8)	65.4 (5.5)	63.1 (3.9)	63.5 (4.7)	63.1 (3)	56.4 (1.9)
			Kallisto	2.6 (2.4)	4.1 (2.2)	5.3 (2.4)	6.6 (1.6)	6.4 (1)	6.7 (1)	7.7 (0.6)	7.6 (0.5)	7.9 (0.4)	8.8 (0.2)
			USEARCH61	55.9 (50)	44.2 (34)	52.9 (23.9)	52.8 (20.3)	44.8 (12.4)	45.5 (5.2)	50.3 (4.4)	48.8 (5.7)	49.2 (2.6)	49.1 (2.6)
	V4	190	Karp	0.1 (0.1)	0.3 (0.5)	0.7 (2.2)	0.3 (0.1)	0.8 (0.5)	0.8 (0.9)	0.9 (0.4)	0.9 (0.2)	1.2 (0.2)	1.6 (0.1)
			UCLUST	5.1 (25.3)	4.8 (20)	7 (15.1)	11.5 (11.7)	8.1 (6.9)	8.5 (8.1)	10 (5.6)	7.2 (2.9)	8.2 (2.2)	10.5 (1.3)
			SortMeRNA	3.8 (12.4)	18.4 (33.2)	16.6 (27.3)	19.2 (20.2)	11.9 (8.3)	16.7 (10.4)	16.4 (7)	14.6 (4.1)	13.8 (3.1)	15.4 (1.5)
			Kallisto	2.3 (1.7)	5.5 (2.9)	8.3 (5.2)	11.1 (9.4)	10.1 (4.9)	9 (1.8)	10.4 (2.3)	10.8 (2.3)	10.1 (0.6)	11.5 (0.6)
			USEARCH61	5 (25.2)	12.4 (36.8)	8.4 (15.7)	18.5 (15.5)	9.9 (7.6)	9.5 (8.1)	14.9 (8.4)	14.7 (5.4)	11.3 (3.3)	14.2 (1.2)
301bp PE	Full gene	130	Karp	5.5 (7.7)	8.7 (11.5)	12 (11.4)	13.5 (10.4)	9 (3.1)	11.7 (4.8)	11.1 (1.7)	11.7 (1.5)	11.4 (1.5)	11.5 (0.6)
			UCLUST	18.7 (20.5)	25.4 (29)	37.2 (27.6)	34.2 (23.5)	23.6 (9.8)	32.4 (6.8)	31.6 (4.6)	32.2 (5.9)	33.2 (4.3)	31.5 (1.7)
			SortMeRNA	40 (35.3)	39.8 (30.7)	47.6 (22)	56.5 (20.9)	43.6 (12.8)	52.7 (12.4)	49.6 (6.1)	49.3 (4.9)	49.3 (3.8)	46.5 (2.1)
			Kallisto	43.1 (36.3)	68.6 (35.7)	89.6 (27.3)	89.9 (20.8)	98.8 (19.4)	100.5 (11.7)	110.9 (13)	106 (5.2)	111.6 (5.4)	113.1 (2.3)
			USEARCH61	29.1 (47.3)	27.5 (34.6)	32.4 (28.4)	35.5 (25.7)	26.4 (9)	34.3 (10.3)	31.6 (4.5)	32.3 (2.6)	32.6 (4)	32.7 (2.3)
	V4	190	Karp	0.6 (1.9)	0.9 (1)	1.5 (2.2)	1.8 (1.7)	2 (2.9)	1.7 (0.9)	1.9 (0.3)	2.5 (0.5)	2.9 (0.6)	3.9 (0.3)
			UCLUST	0.5 (1)	4 (20)	11.6 (23.1)	1.9 (2.7)	2.8 (3.6)	4.4 (4.1)	3.9 (2.3)	5.2 (2.7)	6.4 (2)	7.3 (1.1)
			SortMeRNA	5.2 (27)	5.3 (15.1)	11.5 (21.8)	7.9 (12.3)	9.4 (10.9)	15.7 (7.1)	10.2 (5.4)	10.5 (4)	10.9 (3.2)	10.6 (1.5)
			Kallisto	62.2 (48.3)	100.3 (38.1)	90.2 (27.9)	113.5 (14.4)	112.3 (17.9)	118.5 (10.5)	121.2 (11.8)	129.2 (6.5)	128.5 (3.7)	132.7 (2.2)
			USEARCH61	9.2 (39)	6.7 (21.3)	6.1 (14.8)	5.1 (7.2)	6.2 (9.1)	4 (2)	7 (2.5)	8.1 (3.6)	8.1 (1.8)	11.2 (1.3)

SE=Single-end, PE=Paired-end

Table 3: **Per species error rates, 1,000,000 reads**

Read Length	Region	Samples	Method	Shannon Diversity									
				[0,0.7)	[0.7,1.4)	[1.4,2)	[2,2.7)	[2.7,3.4)	[3.4,4.1)	[4.1,4.8)	[4.8,5.5)	[5.5,6.2)	[6.2,6.9]
75bp SE	Full gene	110	Karp	28.6 (41.4)	74.6 (67.4)	103.2 (72.5)	91.7 (37.2)	59.7 (21.4)	67.6 (32.8)	63.5 (19.4)	71.2 (23.4)	72.9 (17.7)	71.1 (13.7)
			Karp-Collapse	39.3 (62.1)	111.9 (102.9)	141.4 (68.6)	131.9 (88.9)	99.3 (30.6)	91.1 (29.8)	87.1 (15.3)	89.8 (20.2)	88.6 (14.1)	84.3 (12.1)
			UCLUST	90 (142.5)	265.3 (308.5)	281.6 (259.6)	267.7 (158.4)	210.6 (102.1)	181.2 (78.9)	176.2 (48.3)	176 (50.9)	178.3 (40.9)	170 (40)
			SortMeRNA	78.9 (120.8)	295.5 (368.3)	291.1 (240.6)	265.4 (168.6)	231.4 (109.6)	193.8 (76.6)	182.2 (52.5)	185.7 (48.1)	185.8 (38.5)	199.6 (105.4)
			Kallisto	49.2 (65.3)	119.5 (104.7)	157.6 (106.1)	141.5 (56.2)	96 (30.1)	113.2 (49.9)	103.2 (28.4)	113.9 (32.7)	117.7 (25.1)	111.1 (20.4)
			USEARCH61	82 (122)	297 (361)	297.6 (261.9)	274 (168.9)	230.2 (101.3)	203.5 (90.4)	181.8 (49.2)	187.9 (49.6)	185.3 (40.7)	176.8 (41)
			Mothur NB	102.1 (183.2)	302.5 (329.3)	326.5 (234.5)	351.1 (182.2)	256.4 (86)	288.3 (125.5)	243.9 (60.9)	251.9 (54.6)	243 (46.5)	282 (205.3)
			16S Classifier	204.9 (365.4)	289.7 (330.9)	299.6 (283.8)	383.8 (144.3)	306.5 (141.3)	319.4 (152.4)	297.2 (58)	297.6 (83.2)	305.7 (68.1)	296.5 (60.6)
			SINTAX	49.2 (79.6)	241.3 (312.3)	245.6 (227.6)	241.9 (187.7)	186.0 (116.8)	205.2 (103.4)	199.1 (41.0)	196.2 (58.2)	208.3 (51.5)	203.9 (40.7)
	V4	130	Karp	5.8 (8.2)	32 (53.2)	15.2 (20.5)	15.8 (15.1)	30.2 (22.6)	23.8 (6.8)	18.3 (6)	18.9 (6.5)	15.1 (4)	15.5 (2.3)
			Karp-Collapse	16.4 (18.6)	65.1 (80.9)	30.3 (37.4)	30.3 (24.1)	59.7 (38.8)	59 (13.1)	52.9 (12.1)	54.1 (13.1)	48.1 (5)	41.5 (3.5)
			UCLUST	11.4 (14.4)	70.9 (132.5)	23.1 (29.8)	32.5 (37.9)	68.5 (55.4)	53.6 (21.6)	44.9 (9.7)	47 (18.3)	44.8 (10.4)	41 (4.8)
			SortMeRNA	15.1 (22.9)	65.6 (114.8)	24.2 (31.7)	33.3 (35.7)	74.5 (66.5)	52.1 (13.4)	49.3 (20.2)	50.7 (19.6)	44.3 (8.3)	46.1 (4.3)
			Kallisto	16.2 (19.3)	64.1 (115.8)	20.1 (23.3)	22.9 (18.8)	57.4 (71.1)	38.1 (13.5)	31.1 (8.4)	33.4 (11.8)	30.5 (7.2)	30.9 (3.9)
			USEARCH61	18 (26.8)	78.4 (122.7)	25.6 (33.6)	38.5 (44.4)	77.1 (67.5)	52.5 (13.8)	47.2 (15)	50.4 (20.8)	45.1 (9.9)	44.3 (4.6)
			Mothur NB	13.6 (15.7)	96 (133.4)	55.6 (102.3)	70.8 (76.4)	111.5 (73.5)	94.9 (40.2)	93.4 (32.7)	97.8 (16.2)	98.3 (15.2)	96.8 (4.3)
			16S Classifier	28.1 (38.2)	171.7 (276.1)	51.8 (97.6)	68.4 (92.8)	108.1 (98.9)	68.6 (35.3)	66.9 (30.5)	69.5 (11.6)	78.5 (15.4)	82.8 (5.5)
			SINTAX	1.8 (<0.1)	31.3 (<0.1)	10.0 (<0.1)	32.5 (53.8)	65.8 (52.7)	43.9 (27.5)	40.4 (16.7)	46.3 (19.8)	48.0 (16.5)	49.9 (6.0)
151bp PE	Full gene	130	Karp	2.8 (4.5)	3.7 (6.8)	4.3 (8.4)	7 (8.1)	9.5 (7)	8.9 (5)	8.1 (3.3)	9.9 (2.7)	10 (1.5)	9.4 (0.8)
			Karp-Collapse	13.8 (18.8)	22.2 (40.4)	13.2 (20.9)	46.5 (53.5)	31.1 (25.8)	40.6 (20.5)	35.2 (15.8)	41 (14.8)	40.4 (9.5)	39 (3.6)
			UCLUST	15.2 (21.3)	33.8 (74.6)	43.6 (75.9)	35.6 (32.9)	42 (24.8)	48.6 (27.6)	54.7 (17.1)	55.2 (11.8)	59.7 (10.7)	59.3 (7)
			SortMeRNA	24 (32.9)	48 (86.3)	55.5 (73.2)	59.6 (28.3)	86.3 (45.4)	80 (40.7)	87.3 (33.8)	75 (18.9)	81.5 (13.1)	74.7 (3.6)
			Kallisto	1.7 (2.2)	7 (15.4)	13 (23.1)	11.6 (11.3)	13.8 (9)	16.7 (8)	21.5 (8.7)	17.4 (4.4)	19.9 (3.8)	19.1 (1.4)
			USEARCH61	17 (18.7)	56.4 (133.8)	69.4 (88.7)	39.7 (45)	59.1 (38.3)	52.4 (27.7)	56.2 (20)	55 (12.7)	67 (12.7)	67.3 (3.4)
			Mothur NB	48.4 (49.3)	108.1 (102.9)	113.8 (103.6)	120.6 (48.4)	161.1 (33.8)	175.2 (59.6)	180.5 (32.6)	168.6 (20.9)	162.7 (14.9)	140.9 (6.9)
			16S Classifier	213.6 (354.9)	247.2 (317.4)	292.2 (259.4)	213 (95.8)	273.5 (108.9)	270.8 (101.5)	276 (52)	240.6 (34)	267.9 (32)	254.9 (9)
			SINTAX	20.1 (28.9)	32.3 (64.6)	61.6 (81.9)	51.8 (49.6)	79.0 (32.0)	96.2 (52.9)	98.6 (37.4)	97.2 (22.3)	102.3 (19.0)	99.1 (6.2)
	V4	190	Karp	<0.1 (<0.1)	0.1 (0.5)	2.1 (11.3)	0.1 (0.2)	1.2 (3.3)	0.4 (0.7)	0.4 (0.8)	1.1 (1.2)	0.9 (0.7)	1.5 (0.7)
			Karp-Collapse	<0.1 (<0.1)	0.1 (0.2)	2.2 (11.4)	0.1 (0.3)	1.2 (3.4)	0.9 (1.6)	0.6 (0.9)	1.5 (1.7)	0.8 (0.7)	1.3 (0.9)
			UCLUST	1.1 (4.3)	0.2 (0.5)	0.4 (0.9)	15.7 (44.2)	15 (44.9)	6.5 (12.2)	3.6 (7.5)	3.6 (6.1)	5.7 (5.5)	7.5 (2.4)
			SortMeRNA	1.1 (3.9)	2.6 (7)	0.5 (1.3)	17.1 (45.9)	13 (26.8)	14 (25.1)	7.5 (9.7)	9.5 (11.4)	10.7 (8.8)	9.7 (4.7)
			Kallisto	0.5 (0.9)	29.5 (155.7)	2.1 (5.7)	1.5 (3.1)	12.7 (28.1)	24.5 (45.9)	8.7 (10.3)	6.6 (5)	6.9 (3.8)	7.3 (1.8)
			USEARCH61	0.8 (3.9)	67.8 (251.7)	1.9 (5.3)	0.2 (0.5)	17.2 (49.9)	15 (26.1)	12.3 (14.6)	7.8 (8.7)	9.6 (6.5)	8.4 (2.2)
			Mothur NB	61.7 (81)	54.8 (78.7)	89.9 (104.7)	112.2 (132.3)	99.3 (77.2)	132.6 (49.2)	102.8 (38.1)	94.4 (18.5)	99.2 (13.2)	103.9 (11.7)
			16S Classifier	165.2 (335.8)	133.2 (242.7)	123.2 (123.9)	82.5 (107)	67.1 (42)	126.7 (87.2)	79.2 (34.3)	69.4 (16.4)	73.2 (13.3)	81.8 (12.5)
			SINTAX	2.4 (5.2)	21.7 (60.5)	35.4 (86.0)	18.2 (45.5)	47.3 (61.9)	80.8 (100.7)	28.9 (24.6)	26.3 (16.5)	20.8 (10.3)	29.1 (6.6)

SE=Single-end, PE=Paired-end

Table 4: **Per species error rates, 1,000,000 reads**

Read Length	Region	Samples	Method	Shannon Diversity									
				[0,0.7)	[0.7,1.4)	[1.4,2)	[2,2.7)	[2.7,3.4)	[3.4,4.1)	[4.1,4.8)	[4.8,5.5)	[5.5,6.2)	[6.2,6.9]
301bp PE	Full gene	170	Karp	0.7 (1)	2.3 (2.5)	9.3 (19.9)	13.3 (20.7)	13.3 (11.7)	8.6 (6.5)	14.4 (4.7)	13.7 (3.2)	16.1 (4.4)	14.8 (2.9)
			Karp-Collapse	2.9 (5)	14.9 (27.6)	17.6 (41.2)	12.5 (18.6)	17.1 (18)	14.5 (7.3)	21.7 (12.5)	19 (5.7)	18.6 (5)	16.5 (2.4)
			UCLUST	6.3 (13.3)	16 (33)	23.5 (63.1)	26.6 (40.2)	54.7 (78.7)	34.5 (31.6)	37.3 (17.2)	39.9 (9.7)	43.8 (12.2)	42.3 (5.9)
			SortMeRNA	15.1 (31.7)	48 (85.1)	43.7 (47.4)	53.6 (54.9)	73.1 (73.7)	60.6 (31.6)	66.2 (24.3)	75.2 (14.3)	72.9 (12.9)	71.4 (10.1)
			Kallisto	27.8 (54.7)	112.9 (228.6)	60.8 (74.3)	194.6 (181.1)	254.9 (165.4)	255.8 (68.4)	256.1 (100)	275.4 (29.4)	310.1 (61.8)	307.6 (19.4)
			USEARCH61	6.8 (16.7)	16.1 (28.8)	40.7 (100.2)	29.5 (33.2)	36.4 (27)	24.8 (12.9)	38.7 (17.5)	38.1 (8.2)	49.3 (12)	52 (10.9)
			Mothur NB	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)
			16S Classifier	203.8 (354.4)	291.8 (291.1)	240 (216.8)	249.6 (150.8)	251.7 (144.5)	241.7 (59.8)	238.9 (79.5)	252.9 (27.2)	251.4 (39.3)	251 (16.5)
			SINTAX	7.7 (16.1)	40.7 (81.1)	48.7 (117.2)	80.7 (84.4)	106.8 (120.5)	101.5 (50.6)	87.1 (35.5)	94.9 (16.7)	103.2 (21.2)	100.4 (17.4)
	V4	190	Karp	0.5 (1.9)	0.3 (1.1)	0.9 (4.2)	3.8 (10.2)	0.5 (0.6)	0.9 (1.4)	1.4 (1.2)	2.3 (1.8)	1.5 (1.3)	1.3 (0.3)
			Karp-Collapse	0.5 (2)	0.1 (0.2)	0.1 (0.3)	0.8 (2.1)	0.4 (0.6)	0.3 (0.3)	0.4 (0.4)	1.1 (2.7)	1 (1.5)	0.5 (0.3)
			UCLUST	<0.1 (0.1)	3.8 (18.2)	0.1 (0.6)	<0.1 (0.1)	5.1 (11.1)	0.8 (1.2)	2.7 (6.5)	3.4 (5.2)	4.7 (4.8)	6 (3)
			SortMeRNA	2 (6.6)	4.2 (18)	2.5 (11.4)	7.2 (19.1)	9.8 (15.3)	3.7 (8.6)	10.8 (17.7)	7.4 (7)	8.4 (10.7)	5.7 (2.5)
			Kallisto	5.4 (7.5)	14.5 (30)	20.9 (75.6)	28 (42.2)	66.8 (74.3)	79.4 (82.1)	106 (54)	107.2 (45.8)	101.6 (35.4)	107.6 (18.3)
			USEARCH61	0.6 (2.4)	0.1 (0.2)	0.1 (0.3)	3.3 (5.6)	1.8 (3.5)	2.3 (3.3)	2.6 (4)	3.6 (5.8)	5.7 (3.4)	6.2 (2.9)
			Mothur NB	303 (706.3)	48.3 (80.4)	68.8 (90.3)	43.4 (65.9)	109.6 (83.1)	99.2 (63.2)	126.5 (45.2)	108.3 (23.4)	115.5 (24.4)	98.1 (6.6)
			16S Classifier	160 (363.6)	152.5 (265.7)	111.2 (168.6)	60.8 (93.5)	84.7 (78.3)	81.6 (72.3)	101.3 (43.2)	85.5 (25.1)	93.6 (26)	79.5 (9)
			SINTAX	<0.1 (0.1)	72.1 (218.4)	0.2 (0.6)	58.3 (182.3)	10.2 (12.0)	36.6 (52.6)	35.2 (34.6)	23.8 (9.1)	33.2 (11.1)	28.7 (6.8)

SE=Single-end, PE=Paired-end

Table 5: **Per genus error rates, 1,000,000 reads**

Read Length	Region	Samples	Method	Shannon Diversity									
				[0,0.7)	[0.7,1.4)	[1.4,2)	[2,2.7)	[2.7,3.4)	[3.4,4.1)	[4.1,4.8)	[4.8,5.5)	[5.5,6.2)	[6.2,6.9]
75bp SE	Full gene	110	Karp	120.3 (97.5)	201.7 (165.9)	228.2 (46.5)	229.9 (63.1)	170.9 (32.5)	165.5 (35.2)	166.2 (35.3)	166.3 (27.7)	153.3 (19.4)	135.3 (23.6)
			Karp-Collapse	134 (116.8)	207.7 (164.1)	262.5 (64.8)	231.9 (69.7)	193.3 (29.6)	179.4 (37.4)	184.2 (35.6)	174.7 (21)	161.1 (14.4)	142.2 (18.4)
			UCLUST	374 (309.4)	488 (409.6)	557.2 (171.4)	503.8 (151.8)	430.7 (60.5)	402.9 (93)	386.3 (64.5)	362.1 (60.8)	330 (39.3)	279 (45.3)
			SortMeRNA	366.9 (296.9)	505 (426.9)	536.7 (141)	503.5 (136.2)	436.2 (54.8)	421.9 (77.5)	407.3 (68.4)	387.8 (57.5)	357.6 (36)	354 (220.2)
			Kallisto	246.1 (148.5)	324.4 (227.7)	388.9 (72.4)	379.1 (92.4)	297.5 (48.4)	291.7 (51.1)	281.7 (47)	274.8 (39.3)	251.7 (28.7)	218.9 (36.4)
			USEARCH61	400.7 (317.7)	517.9 (432.1)	562.4 (156.6)	513.7 (147.3)	441 (60.3)	419 (83.9)	399.5 (65.7)	374.5 (58.6)	338.5 (36.9)	288.2 (46.1)
			Mothur NB	409.9 (378.6)	454.2 (348.5)	529.2 (215.6)	596.1 (163.6)	553.9 (99.1)	586.4 (124.7)	540.2 (64.2)	544.1 (62)	533.5 (54.8)	536.6 (136.9)
			16S Classifier	1722 (648.2)	1190.5 (884.1)	1550.5 (424.4)	1799 (221.8)	1704.5 (220.7)	1679.8 (297.9)	1663 (202.4)	1654 (227.7)	1636.6 (236.6)	1595.3 (242.3)
			SINTAX	169.4 (210.8)	345.1 (324.9)	389.4 (163.4)	440.7 (123.4)	413.2 (81.9)	399.0 (115.0)	405.0 (49.9)	403.4 (71.7)	393.8 (59.2)	373.2 (62.2)
	V4	130	Karp	31.3 (32.9)	81 (77.5)	84.9 (49.9)	84.2 (37.9)	70.9 (29.5)	68.2 (13.6)	65.1 (16.5)	64.5 (11.5)	53.6 (4.8)	44.9 (3.9)
			Karp-Collapse	125 (201)	176.5 (125.3)	193.6 (81.4)	177.6 (60.8)	179.6 (52.9)	166.3 (20.7)	172.4 (28)	162.1 (24)	129.9 (12.7)	101.4 (4.8)
			UCLUST	112.2 (221.8)	161.9 (173)	155.2 (85)	158.2 (77.2)	152.9 (55.5)	141.2 (30)	147.3 (29.7)	144.9 (29.6)	116.7 (14)	91.9 (6)
			SortMeRNA	100.9 (209.6)	144.7 (149.2)	159.3 (103.1)	160.3 (87.3)	145.1 (57.4)	137.5 (18.5)	153.8 (35.2)	151.4 (22.3)	123.3 (13.2)	102.2 (6.8)
			Kallisto	71.3 (70.4)	156 (145.1)	141.2 (61.2)	145 (41.2)	135.1 (43.1)	126.8 (22.1)	124.6 (24.7)	122.1 (15.8)	102.3 (7.4)	85.7 (5.3)
			USEARCH61	114.5 (217.1)	170 (171.7)	175.2 (109.4)	172 (89.5)	154 (55.1)	148.7 (26.3)	152 (34.3)	151 (24.9)	120.4 (14.1)	96.6 (6.3)
			Mothur NB	198.2 (441.1)	225.9 (178.4)	325 (146.9)	321.6 (118.9)	330.6 (53.3)	325.4 (51.3)	332.6 (45.4)	316.9 (34.2)	310.9 (32.7)	285.7 (10.3)
			16S Classifier	613.6 (798.1)	652.4 (595.8)	658.2 (407.7)	691.6 (256.6)	669.5 (167)	677.7 (173.9)	680.6 (108.2)	663.1 (93.6)	714.5 (36.7)	693.3 (22.4)
			SINTAX	41.5 (54.0)	89.2 (79.9)	106.6 (71.8)	139.4 (64.7)	179.1 (62.3)	173.6 (37.9)	161.5 (40.8)	177.5 (33.6)	182.5 (17.9)	170.6 (7.9)
151bp PE	Full gene	130	Karp	4.5 (7.6)	8.8 (10)	8.3 (10.2)	9.5 (9.5)	12.4 (7.5)	12.6 (7.3)	12.6 (3.2)	14.8 (3.4)	15.3 (1.7)	14.6 (1.2)
			Karp-Collapse	17.7 (36.3)	57.5 (107.3)	17.6 (19.5)	51.7 (66.4)	40.8 (29.8)	36.2 (10.3)	43 (14.6)	45 (13.3)	48.3 (10.6)	49.7 (5.6)
			UCLUST	38.5 (63.6)	87.1 (132.5)	52 (86.4)	66.5 (83.2)	51.4 (28.5)	63.1 (33.5)	65.9 (16.6)	59.6 (13.4)	70.1 (10.7)	66.9 (4.3)
			SortMeRNA	53.1 (58.6)	110.7 (123.3)	87.5 (101.4)	113.9 (52.3)	105.3 (53.4)	116.4 (61.7)	100.5 (31)	102.6 (19.5)	99.4 (14.4)	87.7 (5.6)
			Kallisto	8.3 (11.5)	25.4 (21.8)	37.3 (25.9)	44.6 (27.7)	51.9 (11.8)	53.3 (8.4)	54.2 (11.9)	53.3 (5.2)	55.6 (4.5)	55.2 (2.8)
			USEARCH61	24 (28.9)	101 (122.2)	73.3 (89)	49.8 (39.7)	68.9 (48.8)	62.4 (24.6)	71.7 (17)	70.2 (15)	78 (12.5)	76.2 (5.9)
			Mothur NB	121.7 (90.7)	201.9 (139.5)	212.8 (94.8)	264.6 (92.3)	247.2 (95.3)	251.3 (95.2)	218.3 (53.1)	210.3 (19.5)	199.9 (24)	167.8 (13.7)
			16S Classifier	1393 (844.9)	1240.4 (645)	1306.4 (531.2)	1184.9 (346.1)	1345.6 (159.5)	1385.8 (130.9)	1352.3 (99.9)	1326 (45.9)	1347.4 (59.8)	1347.5 (15.5)
			SINTAX	37.9 (47.4)	99.2 (149.6)	87.0 (98.4)	113.1 (56.8)	118.8 (44.5)	133.6 (57.1)	130.5 (33.9)	126.8 (27.1)	136.3 (18.0)	126.4 (5.7)
	V4	190	Karp	0.2 (0.3)	2.4 (12)	4.2 (16.3)	0.7 (1.1)	2.1 (4.2)	1.6 (1.5)	3.1 (2.5)	2.5 (1)	2.4 (0.7)	3 (0.8)
			Karp-Collapse	0.2 (0.7)	0.4 (1.2)	4.2 (16.6)	0.6 (1.3)	1.9 (4.3)	2.5 (3.1)	1.7 (1.6)	1.8 (1.2)	1.3 (0.9)	2 (1)
			UCLUST	0.7 (2.1)	0.2 (0.3)	36.7 (174.8)	4.6 (7.8)	21.2 (46.4)	14.9 (25.4)	13.2 (19.1)	11.8 (12.9)	11.8 (7.9)	15.1 (4.6)
			SortMeRNA	7.8 (35.9)	14.7 (56.7)	19.4 (65.3)	15.6 (27.6)	18.3 (40.9)	33.8 (40.2)	25.6 (19.3)	27.1 (12.9)	29.1 (13.2)	31.7 (12.9)
			Kallisto	5.9 (7.3)	8.7 (10.2)	29.3 (26.3)	33 (19.1)	35.6 (41.5)	49 (39.2)	42.8 (8.6)	37.2 (8.2)	35.9 (3.8)	36.9 (2.4)
			USEARCH61	11.2 (62)	37 (173.1)	13.4 (62.1)	5.6 (9.1)	24.1 (46.6)	31.1 (47.2)	24.3 (16)	20.7 (18.6)	23.1 (9.7)	24.1 (7.3)
			Mothur NB	93.3 (86.2)	129.4 (95.4)	246 (196.5)	305.5 (117.4)	242.4 (47.3)	319.5 (38.1)	311.5 (41.2)	297 (36.2)	277.4 (16.7)	251.1 (11.4)
			16S Classifier	299.2 (653.9)	277.4 (402.6)	348.3 (365.4)	422.7 (396.9)	247.8 (118.7)	366.5 (193.1)	329.2 (84)	342.1 (83.2)	320 (56.8)	317.9 (33.6)
			SINTAX	3.7 (8.7)	14.6 (55.4)	87.9 (258.9)	60.7 (127.4)	36.1 (59.6)	80.9 (77.9)	60.2 (39.3)	50.8 (47.8)	36.6 (14.9)	40.1 (8.9)

SE=Single-end, PE=Paired-end

Table 6: **Per genus error rates, 1,000,000 reads**

Read Length	Region	Samples	Method	Shannon Diversity									
				[0,0.7)	[0.7,1.4)	[1.4,2)	[2,2.7)	[2.7,3.4)	[3.4,4.1)	[4.1,4.8)	[4.8,5.5)	[5.5,6.2)	[6.2,6.9]
301bp PE	Full gene	170	Karp	7.1 (20.1)	6 (11.2)	14.4 (17.4)	19.6 (23.7)	16.8 (16.2)	12.1 (4.4)	21.6 (9.1)	19.4 (2.2)	22.5 (2.7)	24.8 (2.5)
			Karp-Collapse	9.2 (10.2)	15.7 (28.5)	26.3 (37.5)	20.9 (20.6)	21.8 (23.3)	19.4 (9.3)	22 (11)	20.1 (4.5)	21.4 (3.6)	19.8 (2.3)
			UCLUST	23 (59)	15.9 (33)	30.3 (43.2)	27.8 (38)	42.3 (49.8)	38.3 (37.6)	42 (22.4)	37.7 (10.8)	47.7 (10.7)	40.5 (5.6)
			SortMeRNA	42.2 (88.1)	46.7 (64.8)	93.4 (85.5)	71.1 (55.1)	75.3 (71.8)	76.3 (35.1)	79.5 (24.4)	81.5 (20.9)	79.4 (10.1)	72.9 (7.5)
			Kallisto	313.5 (368.4)	468 (380)	636.5 (277.7)	688 (218.7)	782 (175.3)	741.7 (174.4)	816.1 (142.6)	792.6 (61.3)	825.7 (55)	814.9 (25)
			USEARCH61	21.2 (50.3)	18.7 (34.4)	41.8 (48)	27.4 (34.8)	34.4 (35.9)	24.2 (8.9)	44.1 (26)	44 (11.2)	48.5 (9)	50 (9)
			Mothur NB	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)
			16S Classifier	1049.8 (861.4)	1272.6 (572.3)	1328.5 (462.9)	1188.2 (210.2)	1277.6 (279)	1168.9 (190)	1264.5 (178.9)	1232 (87.2)	1231.3 (39.9)	1223 (20.6)
			SINTAX	25.9 (36.1)	53.3 (97.8)	93.2 (91.2)	87.3 (59.1)	109.6 (88.6)	109.7 (68.9)	103.8 (48.5)	104.0 (13.8)	118.7 (18.0)	105.7 (11.3)
	V4	190	Karp	4.2 (20.9)	1.1 (1.4)	5.2 (8)	24 (41.4)	6.6 (7.7)	4.7 (2.6)	4.3 (1.3)	6.3 (3.3)	5.6 (1.3)	5.4 (1)
			Karp-Collapse	0.7 (2.5)	0.2 (0.8)	0.8 (1.8)	4.4 (13.3)	0.6 (0.7)	1 (1.5)	0.5 (0.4)	1.3 (2.9)	0.8 (0.5)	0.7 (0.5)
			UCLUST	0.1 (0.4)	2.9 (14.5)	1.5 (9.4)	5.3 (16)	3.8 (10.6)	4.8 (13.7)	2.7 (6.6)	1.2 (1)	6.4 (5)	7.9 (2.8)
			SortMeRNA	1.8 (5.7)	8.7 (31.1)	4.4 (15.4)	2.7 (3.1)	6.4 (15.9)	17.2 (41.6)	17.2 (28)	7.1 (7)	18.3 (12.1)	12.2 (3.7)
			Kallisto	69.8 (117.7)	207.2 (264.6)	430.5 (318.3)	565.1 (199.5)	533 (175.4)	592.3 (112.4)	561.6 (103.2)	550.4 (57.3)	570.4 (41.2)	558 (30.5)
			USEARCH61	0.8 (3.4)	1 (3.8)	3.5 (14.5)	0.5 (1)	4.7 (12.3)	10.1 (17.6)	5.8 (9.3)	6 (9.4)	7.2 (3.9)	9.4 (3.9)
			Mothur NB	133.2 (387.6)	207.9 (155.1)	393.5 (262.2)	308.4 (76.4)	317.8 (73.1)	309.4 (28.7)	306.9 (29.1)	292.3 (26.3)	275.6 (12.7)	242.1 (9.6)
			16S Classifier	28.4 (39.5)	342.1 (518.5)	433.8 (405.3)	396.7 (294.1)	344.8 (242.8)	367.7 (72.8)	329 (85.5)	324.3 (24.9)	353.1 (41.3)	329.6 (23.8)
			SINTAX	2.7 (7.1)	100.4 (363.6)	47.8 (118.9)	26.8 (44.0)	28.8 (51.7)	74.6 (125.3)	58.3 (38.8)	39.4 (21.0)	48.6 (16.9)	40.9 (8.0)

SE=Single-end, PE=Paired-end

Table 7: **Per family error rates, 1,000,000 reads**

Read Length	Region	Samples	Method	Shannon Diversity									
				[0,0.7)	[0.7,1.4)	[1.4,2)	[2,2.7)	[2.7,3.4)	[3.4,4.1)	[4.1,4.8)	[4.8,5.5)	[5.5,6.2)	[6.2,6.9]
75bp SE	Full gene	110	Karp	110.6 (113.4)	224.3 (142.9)	181 (73.5)	206.8 (84.7)	148.6 (28.3)	132.6 (16.7)	119.7 (9.1)	118.4 (10)	96 (10.8)	82 (6.9)
			Karp-Collapse	107 (112.6)	215.7 (137.3)	165.3 (69.9)	198.8 (83.6)	132.9 (18.9)	126.9 (15.5)	113.5 (8.1)	112.2 (11.7)	93.9 (11.1)	77.1 (7)
			UCLUST	279.5 (218)	467.2 (256.4)	390 (176.4)	388.7 (166.9)	293.5 (51.2)	265.6 (33)	233.4 (17.7)	216.2 (23.1)	167.6 (18.3)	132.7 (11.7)
			SortMeRNA	254.4 (195.7)	467.4 (273.8)	377.2 (179.3)	391.3 (149.9)	308.9 (52.1)	292.3 (35)	263.7 (17.9)	247.5 (24.2)	198.4 (21)	190 (114.3)
			Kallisto	271.7 (167.3)	415.9 (182.5)	354.8 (124)	366.2 (125.1)	290.2 (31.1)	260.1 (20.5)	224.5 (10.9)	208.9 (17.6)	166.6 (18.6)	140.6 (12.1)
			USEARCH61	287.7 (224.9)	497.8 (276.8)	399.7 (179.8)	402.7 (170.3)	306.5 (45.7)	282.6 (30.5)	244.7 (17.8)	227.2 (24.5)	175.1 (21.3)	138.3 (12.4)
			Mothur NB	327.3 (341.2)	433.9 (261.7)	433.9 (199.8)	510.9 (181.8)	392.8 (110.9)	416.4 (99.2)	405.4 (50.3)	404.8 (40.2)	382.7 (49.5)	382.5 (34)
			16S Classifier	1992.7 (44.6)	1941.3 (106.7)	1866.6 (267.6)	1946.1 (108.2)	1843.5 (148.6)	1912.7 (68.7)	1846.3 (57.8)	1834.4 (57.1)	1837.6 (57.9)	1853.3 (57.3)
			SINTAX	98.1 (99.2)	269.1 (177.0)	238.0 (100.9)	368.7 (140.5)	257.9 (53.1)	250.5 (43.5)	247.1 (26.8)	278.4 (21.1)	253.1 (22.3)	252.9 (10.2)
	V4	130	Karp	40.9 (55.3)	86.7 (92.1)	96.5 (63.2)	79.1 (23.1)	72 (25.3)	63.4 (14.4)	63.9 (15.4)	58.1 (4.4)	46.8 (5.6)	38.8 (2.7)
			Karp-Collapse	165.2 (270.1)	241.1 (173.6)	231 (104.8)	199.5 (54)	181.9 (40.6)	145.9 (27)	160.9 (43)	130.6 (10.6)	103.9 (15.5)	74.2 (4.8)
			UCLUST	130.2 (295.7)	166.8 (186.9)	157 (97.1)	146.3 (78.7)	124.5 (50.9)	99.4 (26.5)	119.5 (49.1)	95 (10.3)	75.6 (9.7)	51.2 (4.6)
			SortMeRNA	157.1 (341.8)	139.6 (167.5)	150.6 (101.1)	133.6 (61.5)	123.6 (49.5)	105.2 (22)	125.9 (40)	110.3 (10)	91.3 (14.7)	66.7 (5.2)
			Kallisto	104.1 (80.9)	205 (135.8)	201 (78.8)	180.8 (46.8)	165.3 (35.7)	144 (18.3)	142.4 (25.2)	126.6 (11)	101.6 (9.5)	79.6 (2.2)
			USEARCH61	149 (300.8)	172 (182.2)	175.9 (111.8)	142.1 (60.7)	130.6 (51.2)	105.1 (21.6)	122.5 (43.8)	103.3 (10.2)	78.5 (13.3)	55.3 (3.6)
			Mothur NB	311.4 (491.2)	404.8 (345.2)	498.2 (210.2)	399.5 (188.6)	397.4 (171.5)	423.9 (54)	433.3 (63.8)	408.8 (41.3)	374.4 (50.9)	344 (13.1)
			16S Classifier	1045.6 (710.8)	1440.5 (395.3)	1230.8 (400.5)	1266.7 (294.5)	1289.4 (179)	1100.4 (149.2)	1151.3 (98.8)	1130.1 (64.3)	1129.6 (61.3)	1113.8 (19.5)
			SINTAX	60.8 (57.0)	86.4 (41.1)	163.5 (100.3)	194.9 (96.5)	185.1 (48.4)	178.8 (32.9)	200.3 (41.8)	185.1 (19.2)	166.7 (10.6)	163.5 (6.1)
151bp PE	Full gene	130	Karp	2 (3.2)	5.3 (7.6)	7.4 (10.9)	8.4 (9.1)	9.3 (5.1)	10.4 (7.3)	9.4 (3.1)	11.1 (2.3)	11.7 (2.1)	10.5 (0.9)
			Karp-Collapse	6.3 (3.6)	20.8 (22.4)	17.8 (13.1)	26.8 (25)	28.6 (11.7)	27.3 (8.8)	27 (7.6)	24.7 (3.2)	23.6 (4.2)	22.1 (1.5)
			UCLUST	3.9 (3.5)	19.1 (31.3)	27.6 (45.9)	26.1 (20.7)	28.9 (18.6)	25.3 (14.5)	21.6 (5.3)	24.7 (3.8)	27.1 (6)	24.1 (2.8)
			SortMeRNA	7 (9.3)	31.2 (39.4)	39.1 (50.4)	41.2 (30.2)	40.9 (26.8)	38 (17.9)	31.2 (8.8)	35.3 (5.8)	33.8 (5.4)	28.8 (2.1)
			Kallisto	14.1 (12.1)	46.1 (24.1)	51.8 (22)	70.6 (19.3)	76.2 (16.9)	71.2 (10.8)	74.7 (7.4)	72.3 (4.9)	71.9 (5)	70.4 (2.7)
			USEARCH61	9.2 (5.2)	26.7 (37.6)	43.8 (57.7)	35.5 (26.9)	40.5 (25.5)	35.4 (13.3)	31.7 (5.6)	33.9 (4.6)	34.9 (7.3)	31.5 (2.2)
			Mothur NB	135.1 (52.8)	168.5 (59.9)	207 (108.5)	169.8 (72)	157.3 (48.2)	146.2 (57.7)	89.2 (21)	83.9 (17.9)	76.5 (11.7)	59.8 (6.3)
			16S Classifier	1873.9 (215.5)	1821.7 (284.1)	1821.5 (278.6)	1799.6 (172.9)	1675.5 (168.9)	1663.9 (85.2)	1625.2 (83)	1666.5 (24.1)	1645.3 (32.9)	1646.5 (6.8)
			SINTAX	9.9 (10.8)	51.8 (191.6)	36.2 (60.1)	45.5 (32.3)	42.4 (29.2)	34.7 (18.1)	30.6 (11.8)	29.9 (5.2)	32.5 (6.2)	28.0 (2.7)
	V4	190	Karp	0.5 (0.9)	2.9 (12.9)	5.2 (18.4)	1.3 (1.5)	2.5 (4.3)	2.1 (1.5)	3.7 (2.5)	3 (1)	3 (0.7)	3.7 (0.8)
			Karp-Collapse	0.2 (0.7)	0.5 (1.6)	5.1 (18.7)	1 (1.8)	2.1 (4.7)	1.3 (1.6)	1.7 (1.5)	2 (1.3)	1.6 (1)	2.4 (1.1)
			UCLUST	0.9 (2.4)	1.2 (3.1)	41.4 (174.9)	5.7 (7.5)	9.3 (17.7)	23.8 (35.5)	23.9 (24.8)	25.9 (32.4)	13.6 (6.3)	16.2 (4)
			SortMeRNA	2.7 (5.8)	10.5 (52.9)	21.9 (76)	17.2 (30)	10.1 (17.8)	31.2 (46.9)	30.4 (22.9)	39.5 (32.2)	35.1 (12.7)	30.6 (5.8)
			Kallisto	14.9 (16.9)	28.4 (23)	54 (26.4)	58.7 (15.6)	53.6 (11.7)	61.2 (11.1)	66 (8.2)	60.9 (6.8)	59.4 (5.2)	59.2 (2.2)
			USEARCH61	38.5 (227.6)	10.3 (53)	21.7 (76.1)	16.9 (30.2)	10.4 (17.2)	35.1 (49.3)	29.2 (23.1)	34.1 (35.3)	27.4 (8.9)	26.4 (4.8)
			Mothur NB	192.6 (337.3)	212.8 (171.7)	288.2 (267)	310.4 (201)	319 (88.7)	276.7 (53.4)	309.4 (35.4)	254.1 (36.3)	206.5 (18.5)	138.2 (12.5)
			16S Classifier	555.2 (799.3)	204.1 (349.5)	385.9 (434.3)	368.2 (250.2)	335.6 (214.1)	326.9 (111.0)	296.2 (81.7)	263.3 (48.9)	279.3 (26.2)	247.5 (22.7)
			SINTAX	3.3 (9.4)	0.8 (1.9)	48.1 (213.0)	0.5 (0.7)	56.1 (101.6)	17.8 (30.4)	9.6 (9.9)	16.9 (11.4)	9.7 (6.1)	13.5 (3.4)

SE=Single-end, PE=Paired-end

Table 8: **Per family error rates, 1,000,000 reads**

Read Length	Region	Samples	Method	Shannon Diversity									
				[0,0.7)	[0.7,1.4)	[1.4,2)	[2,2.7)	[2.7,3.4)	[3.4,4.1)	[4.1,4.8)	[4.8,5.5)	[5.5,6.2)	[6.2,6.9]
301bp PE	Full gene	170	Karp	7.2 (20.6)	5.3 (11.1)	9.2 (15.8)	11.7 (15.3)	11 (14.6)	12.6 (6)	12.2 (2.6)	14.4 (4.3)	15.9 (2.5)	17.3 (1.3)
			Karp-Collapse	8.7 (11)	7.3 (5.1)	8.6 (4)	13.1 (13.5)	12.2 (13.2)	16.3 (16.5)	10.6 (2.9)	10.8 (1.7)	12.1 (2.4)	11.7 (2.1)
			UCLUST	16.1 (54.8)	3.7 (8.1)	7.9 (18.9)	2.6 (6.1)	5.4 (7.4)	7 (8.8)	9.1 (9.7)	9.5 (4)	7.9 (2.6)	9.6 (2.7)
			SortMeRNA	9.6 (22.9)	16.6 (29.9)	16.8 (25.6)	12.2 (16.1)	19.9 (19.6)	20.6 (15.5)	18.4 (7.8)	23 (8.2)	16.2 (4.5)	16.3 (2.6)
			Kallisto	448.6 (375.8)	796.4 (302)	908.1 (253.8)	981.1 (252.7)	1053.6 (128.8)	1037.5 (123.2)	1067.3 (108.7)	1039 (56.3)	1055.4 (31)	1008.5 (23.7)
			USEARCH61	10 (40.1)	4.8 (10.7)	12.8 (30.4)	6.8 (13.2)	10.6 (14.4)	13.3 (15)	10.3 (11.6)	12.3 (9)	11.1 (4.3)	12.1 (2.1)
			Mothur NB	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)
			16S Classifier	1545.3 (609.4)	1550.6 (460.4)	1602.6 (296.6)	1502.9 (266.1)	1534.1 (148.4)	1506 (113.6)	1507.8 (43.9)	1431.6 (69.8)	1419.6 (31.1)	1404.9 (13.7)
			SINTAX	4.9 (13.0)	10.1 (20.7)	12.9 (25.0)	10.9 (23.8)	19.9 (19.9)	18.8 (15.2)	17.3 (10.0)	22.3 (6.5)	16.7 (4.7)	18.1 (3.2)
	V4	190	Karp	10.4 (53.9)	2.8 (2.7)	6.9 (8.3)	28.2 (46.2)	8.5 (7.8)	6.3 (2.8)	6.5 (2.2)	8.1 (4.2)	7 (1.4)	6.7 (1.1)
			Karp-Collapse	0.7 (3.2)	0.3 (0.7)	0.3 (0.6)	5.4 (16.3)	0.4 (0.4)	0.4 (0.2)	0.4 (0.2)	0.5 (0.1)	0.6 (0.4)	0.4 (0.1)
			UCLUST	0.1 (0.6)	0.4 (2.6)	9.9 (62.6)	<0.1 (<0.1)	<0.1 (<0.1)	0.2 (0.4)	0.6 (0.9)	0.4 (0.5)	1.4 (1.4)	2.8 (3.1)
			SortMeRNA	0.9 (3.3)	0.3 (0.9)	1.2 (5.7)	29.9 (91.3)	15.7 (47.6)	9.6 (28)	4.6 (6.3)	4.3 (4.8)	3.9 (3.2)	3.5 (2.4)
			Kallisto	238.4 (274)	536.3 (426.2)	774.3 (317.3)	989.2 (211.7)	958.5 (207.2)	1032.7 (110.9)	997.7 (142.1)	975.5 (82.1)	978.7 (58.5)	968.1 (25)
			USEARCH61	<0.1 (0.1)	<0.1 (<0.1)	<0.1 (<0.1)	0.1 (0.3)	4.1 (13)	4.9 (14.9)	2.8 (8.5)	1.1 (2)	3.8 (4.1)	3.2 (2.2)
			Mothur NB	325.2 (516.6)	196.8 (80.5)	364.2 (291)	298.3 (117.3)	313.7 (56.7)	260.9 (54.5)	265.5 (29.4)	238.3 (21.4)	212.7 (24)	147.6 (11.7)
			16S Classifier	281.0 (555.8)	325.1 (528.0)	345.1 (342.8)	395.3 (304.7)	245.2 (163.2)	311.6 (118.9)	299.0 (82.9)	271.8 (56.3)	264.8 (34.6)	255.0 (18.2)
			SINTAX	0.6 (2.3)	39.6 (122.7)	1.0 (2.8)	0.4 (0.7)	26.1 (61.2)	11.9 (35.2)	9.4 (14.6)	13.9 (8.2)	14.7 (12.6)	10.0 (3.7)

SE=Single-end, PE=Paired-end

Table 9: **Per order error rates, 1,000,000 reads**

Read Length	Region	Samples	Method	Shannon Diversity									
				[0,0.7)	[0.7,1.4)	[1.4,2)	[2,2.7)	[2.7,3.4)	[3.4,4.1)	[4.1,4.8)	[4.8,5.5)	[5.5,6.2)	[6.2,6.9]
75bp SE	Full gene	110	Karp	64.3 (48)	99.4 (57.8)	122.2 (51.2)	124.4 (43.9)	97.8 (14)	79 (12.7)	64.2 (8.8)	64.3 (4.6)	56.2 (4.6)	49.4 (3.6)
			Karp-Collapse	63.2 (46.2)	93.3 (54.3)	117 (52.5)	114.4 (38.8)	89.5 (13.8)	76 (13.1)	60.7 (10.2)	57.5 (5.8)	54.2 (4)	44.6 (3)
			UCLUST	161.7 (93.4)	222.9 (116.5)	258.1 (117.9)	211.1 (89.2)	193.1 (36.3)	149.8 (30.3)	117.2 (15.4)	108.4 (11.6)	84.1 (7.8)	69.2 (7.6)
			SortMeRNA	164.7 (88.6)	223.2 (119.5)	251.7 (113.9)	218.9 (79.7)	213.5 (34.2)	171.1 (32.5)	144.5 (23.3)	131.1 (16.4)	106.6 (8.7)	106.7 (69.1)
			Kallisto	194.9 (80.2)	256.4 (95.2)	269.1 (103)	236.3 (69.9)	212.5 (29.4)	166.9 (15.3)	135.3 (15.7)	124.9 (13.9)	102.3 (7.8)	89.8 (9.2)
			USEARCH61	175 (95.4)	246.1 (127)	274.9 (123.8)	223 (97.4)	204.7 (31.5)	161.8 (31.8)	127.4 (16.3)	117.7 (14)	91.7 (6.9)	74.8 (8.6)
			Mothur NB	269.2 (309)	313.1 (247.7)	412.6 (235.6)	318.6 (74.9)	301.3 (72.2)	298.6 (96.1)	304 (44.6)	282.1 (47.5)	279.9 (42.2)	289.3 (24.5)
			16S Classifier	1861.1 (80.4)	1661 (240.2)	1533.3 (369.8)	1509.2 (209.8)	1535.3 (232.4)	1438 (136.6)	1351 (102.1)	1332.7 (83.4)	1317.6 (70.8)	1357.9 (54.4)
			SINTAX	44.2 (28.5)	131.4 (63.8)	209.3 (107.3)	229.0 (89.1)	212.7 (42.6)	187.0 (36.5)	202.1 (23.9)	210.8 (11.4)	199.2 (15.2)	204.1 (9.0)
	V4	130	Karp	34.2 (51.4)	60.5 (74.3)	61.8 (46)	61.5 (25.2)	50.3 (14.4)	52.3 (12.5)	48.6 (13.7)	43.3 (9.2)	37 (5.1)	33.5 (1.7)
			Karp-Collapse	166.9 (273.6)	176.7 (116.8)	159.8 (91.7)	135.9 (54.2)	125.3 (37.6)	104.3 (25.9)	102.5 (40.4)	83.7 (10.4)	68.9 (7.7)	51 (3.9)
			UCLUST	124 (307.2)	99.1 (138.9)	87.7 (83.7)	66 (53.3)	59.8 (28.4)	50.4 (12.3)	57.3 (42.1)	46.3 (4.4)	37.5 (4.5)	28.5 (3.7)
			SortMeRNA	143.8 (344.9)	82.6 (104.6)	80 (67.4)	68.6 (49)	72.2 (27.1)	66.4 (15.7)	72.6 (35.2)	62.6 (4.2)	59.3 (7.6)	49.9 (4.2)
			Kallisto	99.2 (84.1)	165.2 (117.8)	159.9 (87.7)	130.7 (46.1)	118.7 (34.4)	114 (18.1)	111.9 (19.8)	100.9 (6)	85.3 (6.2)	74.6 (1.5)
			USEARCH61	133.4 (310.3)	104 (138.3)	99 (94.2)	71.9 (57.2)	67.4 (30.2)	57.1 (13.3)	60.5 (34.2)	54.1 (5.9)	42.7 (6.2)	32.7 (3.7)
			Mothur NB	372.8 (484.3)	369.9 (277.3)	487.4 (250.4)	435.3 (81)	415.5 (129.2)	462.6 (134.4)	410.9 (46.2)	393.5 (45.5)	356.1 (43.7)	333.2 (11)
			16S Classifier	1374 (578.8)	1459.5 (400.8)	1277.8 (381.3)	1155.3 (265)	1164.7 (216.7)	1140.2 (113.3)	1060.4 (85.6)	1068 (118.3)	1038.7 (50.7)	1023.9 (23.6)
			SINTAX	62.6 (64.7)	115.3 (67.7)	180.3 (151.7)	174.7 (92.1)	159.3 (51.1)	159.3 (27.2)	173.7 (43.7)	173.6 (16.8)	166.1 (15.4)	165.0 (5.1)
151bp PE	Full gene	130	Karp	1.4 (2)	5.2 (7.6)	6 (9.9)	4.6 (2.8)	8.1 (4.9)	8.8 (7)	7.5 (2.8)	8.5 (1.6)	8.4 (1.6)	7.1 (0.8)
			Karp-Collapse	5.9 (3.9)	18.7 (21.2)	16 (11.6)	16.6 (7.7)	25.7 (11)	22.7 (7.2)	21.7 (6.3)	18.1 (3.6)	15.7 (3.3)	13.9 (1)
			UCLUST	3.1 (3.7)	15.4 (29.5)	9.8 (12.4)	18.4 (14)	16 (5.4)	16.3 (12.9)	15.9 (5.2)	14.2 (3.9)	13.9 (4.2)	13.2 (1.1)
			SortMeRNA	3.5 (3.7)	27.2 (59.5)	15.6 (16.1)	24.1 (23.3)	26.9 (19.6)	17.7 (7.1)	18.1 (6.6)	18.7 (3)	17.1 (3.2)	15 (1.3)
			Kallisto	14 (12.1)	45.8 (24.5)	49.4 (23.4)	69.6 (20.2)	74.6 (17.6)	68.5 (11.4)	69.4 (8.7)	68.4 (5.5)	68 (5)	67.3 (3.3)
			USEARCH61	8.6 (5)	20.3 (35.5)	19.3 (25.8)	17.8 (5.3)	30.7 (16.3)	25.9 (11)	22.5 (7.4)	21.7 (4.8)	19.3 (5.6)	16.9 (2.4)
			Mothur NB	124.1 (49)	158.7 (38.5)	181.6 (100.1)	138 (61.4)	124.3 (26.8)	101.7 (63.1)	56.6 (11.6)	45.6 (10.5)	38 (7.4)	31.2 (3.9)
			16S Classifier	1463.4 (501.1)	1595.9 (330.7)	1315.6 (343.1)	1423.4 (275.3)	1179 (270)	1280.7 (169.5)	1260.5 (117.9)	1250.6 (54.6)	1189.3 (50.9)	1206.5 (20.7)
			SINTAX	4.6 (5.5)	48.2 (190.4)	10.7 (16.3)	19.9 (21.2)	22.5 (23.0)	12.9 (12.4)	15.0 (6.7)	11.5 (3.0)	11.8 (3.0)	11.7 (1.2)
	V4	190	Karp	0.5 (0.9)	3.1 (13.5)	5.4 (18.7)	1.4 (1.5)	2.6 (4.3)	2.2 (1.8)	3.8 (2.2)	2.8 (1.1)	2.9 (1.1)	3.4 (0.9)
			Karp-Collapse	0.1 (0.3)	0.5 (1.5)	5.3 (19)	1.1 (1.8)	2.1 (4.7)	1.2 (1.6)	1.6 (1.4)	1.8 (1.2)	1.4 (0.9)	2.1 (1)
			UCLUST	2.6 (6.8)	19.6 (84.2)	51 (177.6)	5.9 (7.5)	22.4 (37.7)	33.6 (38)	29.4 (19.3)	27.8 (26.4)	20.9 (10.4)	17.7 (3.2)
			SortMeRNA	4.3 (8.2)	28.9 (98.2)	31.7 (84.5)	15.2 (23.7)	29.1 (38.9)	41.8 (46.9)	35.4 (16.8)	39.9 (28.2)	35.5 (8.5)	28.8 (4.5)
			Kallisto	21.5 (19.7)	51.5 (37.4)	62.9 (28.2)	67.3 (13.6)	70.1 (16.5)	80 (13.8)	78.6 (9.2)	71.9 (5.9)	70.5 (3.6)	72.4 (2.6)
			USEARCH61	4.1 (8.1)	28.9 (98.2)	31.4 (84.6)	15 (23.9)	29.1 (38.8)	41.7 (47.2)	34.6 (17.4)	36.3 (29.4)	29.6 (8.3)	25.4 (3.4)
			Mothur NB	186.7 (338)	220 (308.9)	188 (240.4)	277.6 (219.4)	335.7 (140.9)	252.4 (63.6)	262.4 (49.6)	203.5 (24.8)	148.6 (14)	93.4 (10.6)
			16S Classifier	421.7 (719.2)	128.1 (296)	179.8 (298.2)	347 (246.2)	259.3 (229.1)	299 (110.6)	195.2 (56.1)	231.5 (55.5)	239.6 (34.2)	219.7 (17.2)
			SINTAX	0.2 (0.4)	0.1 (0.3)	47.9 (213.3)	0.3 (0.5)	22.3 (69.3)	1.7 (1.9)	4.4 (7.1)	6.6 (10.2)	3.2 (1.6)	5.4 (3.3)

SE=Single-end, PE=Paired-end

Table 10: **Per order error rates, 1,000,000 reads**

Read Length	Region	Samples	Method	Shannon Diversity									
				[0,0.7)	[0.7,1.4)	[1.4,2)	[2,2.7)	[2.7,3.4)	[3.4,4.1)	[4.1,4.8)	[4.8,5.5)	[5.5,6.2)	[6.2,6.9]
301bp PE	Full gene	170	Karp	2.5 (4)	5.1 (11.1)	4 (4.6)	10.2 (14.5)	6.8 (5.1)	10.3 (7.2)	9.1 (2.2)	9.5 (3)	10.6 (2.4)	10 (0.6)
			Karp-Collapse	7.7 (9.4)	7 (5.2)	7.7 (3.7)	12.4 (13.3)	8.2 (3.3)	13.9 (16.6)	8.4 (3.1)	7.9 (1.3)	9.2 (3.5)	7.8 (1.2)
			UCLUST	0.6 (0.6)	3.1 (7.2)	3.6 (10)	0.7 (0.7)	1.7 (3.9)	0.6 (0.5)	3.5 (6.8)	4.3 (4.3)	2.7 (1.9)	3.3 (0.9)
			SortMeRNA	1.9 (4.2)	14.5 (29.2)	9.8 (20.1)	6.4 (14)	7.7 (9)	10 (13.1)	8.1 (5.3)	11.9 (9.8)	8 (4)	6.9 (1.5)
			Kallisto	424.4 (355.2)	778.8 (311.9)	883.6 (263.2)	972.5 (260)	1034.9 (139.8)	1022.5 (125.7)	1028.7 (118)	982 (63.5)	1006.9 (44.8)	961.9 (28.8)
			USEARCH61	0.4 (0.4)	3.8 (10.5)	3.4 (12.7)	5.1 (12.5)	3.7 (4.1)	8 (14.6)	7.1 (11.3)	6.4 (7.6)	5.3 (3.9)	4.8 (2)
			Mothur NB	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)
			16S Classifier	1450.8 (557.7)	1246 (555.4)	1445.1 (305.4)	1268.7 (292.5)	1244.6 (190.6)	1218.4 (169.2)	1162.5 (110.2)	1070.7 (139)	1103.1 (60.3)	1090.2 (14)
			SINTAX	0.5 (1.1)	8.5 (20.4)	6.1 (15.1)	3.4 (5.9)	7.9 (9.5)	7.3 (13.0)	5.8 (7.3)	10.1 (7.9)	6.0 (2.4)	6.7 (1.5)
	V4	190	Karp	10.8 (54)	6 (11.3)	8.4 (8.9)	29.5 (49)	8.6 (7.8)	7 (3.9)	6.3 (1.9)	7.4 (3.5)	6.5 (1.4)	5.5 (1)
			Karp-Collapse	0.3 (1.9)	0.3 (0.9)	0.3 (0.5)	5.8 (17.6)	0.4 (0.4)	0.4 (0.3)	0.3 (0.2)	0.3 (0.1)	0.4 (0.2)	0.3 (0.1)
			UCLUST	<0.1 (<0.1)	0.4 (2.6)	14.1 (89.3)	<0.1 (<0.1)	<0.1 (<0.1)	0.1 (0.4)	0.2 (0.7)	<0.1 (<0.1)	0.1 (0.4)	0.9 (1.6)
			SortMeRNA	0.1 (0.1)	0.1 (0.2)	0.1 (<0.1)	32 (99.7)	15.3 (47.7)	9.2 (28.1)	0.8 (1)	1.8 (3.3)	0.9 (1.1)	1.6 (1.2)
			Kallisto	433.9 (358)	829.3 (396.8)	942.4 (299.1)	1117.8 (212.9)	1226.9 (192.2)	1186.1 (114.5)	1199.5 (107.4)	1171.1 (76.2)	1129.7 (72.7)	1159.8 (28.7)
			USEARCH61	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	0.1 (0.3)	<0.1 (<0.1)	4.7 (14.9)	2.7 (8.5)	<0.1 (<0.1)	0.7 (2.1)	1.4 (1.8)
			Mothur NB	453.4 (590.8)	268 (140.8)	321.1 (250.6)	267.8 (116.2)	211.2 (70.8)	230.8 (56.7)	181.6 (16.7)	157.2 (22.9)	145.4 (22.5)	84.9 (12.9)
			16S Classifier	264.4 (624.3)	141.4 (361.1)	182.8 (297.6)	155.1 (194.5)	163.1 (99.7)	212.9 (80.2)	201.3 (79)	214.3 (45.4)	211.3 (54.8)	203.6 (11.2)
			SINTAX	<0.1 (0.2)	<0.1 (0.1)	28.2 (126.3)	0.3 (0.5)	20.6 (61.1)	11.2 (35.4)	3.0 (7.3)	1.9 (3.0)	1.7 (2.4)	3.4 (2.3)

SE=Single-end, PE=Paired-end

Table 11: **Per class error rates, 1,000,000 reads**

Read Length	Region	Samples	Method	Shannon Diversity									
				[0,0.7)	[0.7,1.4)	[1.4,2)	[2,2.7)	[2.7,3.4)	[3.4,4.1)	[4.1,4.8)	[4.8,5.5)	[5.5,6.2)	[6.2,6.9]
75bp SE	Full gene	110	Karp	44.5 (22.4)	51 (18.5)	60.1 (27.4)	71.6 (22.5)	46.5 (11)	44.4 (11.5)	36.7 (5.4)	38.4 (4)	35.5 (3.6)	34.8 (2.7)
			Karp-Collapse	44 (23.4)	48.2 (16.7)	62.4 (26.2)	60.8 (15.8)	40.5 (12.1)	41.3 (11.2)	33.6 (5.2)	33.8 (4.2)	31.6 (3)	29.2 (2.1)
			UCLUST	109.1 (46.6)	121.5 (50.7)	124.2 (60.1)	94.5 (39)	82.4 (16.3)	70.1 (16.9)	53.8 (8)	50.1 (8.5)	39.2 (3.9)	34.5 (5.5)
			SortMeRNA	119.1 (58.1)	127 (56.6)	123.5 (49.7)	107.1 (40.6)	102.5 (18.7)	90.3 (26.9)	76.6 (11.1)	68.7 (12.2)	57.1 (5.5)	62.6 (43.4)
			Kallisto	161.9 (48.5)	160.1 (41.8)	150.8 (50.5)	147.2 (43.5)	113.4 (21)	99.9 (16.7)	83.2 (10.3)	79.1 (7.5)	67.7 (5.9)	64.8 (7.5)
			USEARCH61	118.2 (48.3)	136.9 (63.9)	132.7 (59.4)	99.7 (40.5)	91.3 (19.7)	78.7 (17.2)	60.7 (10.9)	57.1 (9.8)	46.9 (4.9)	41.1 (6.2)
			Mothur NB	271 (288.5)	256.4 (208.2)	228.4 (119.4)	196 (78)	215.3 (62)	231.4 (101.4)	233.8 (39)	221.7 (45)	217.7 (40.9)	229.2 (26.9)
			16S Classifier	1804.8 (125.8)	1479.4 (314.9)	1336 (450.7)	1339.5 (294.4)	1292.2 (290.4)	1177.6 (177.8)	1156.4 (112.3)	1092.8 (91.3)	1112.8 (71.6)	1155.5 (52.3
			SINTAX	33.7 (26.3)	91.8 (40.9)	104.6 (35.6)	100.0 (29.3)	86.9 (35.9)	97.4 (21.7)	94.3 (17.1)	92.1 (10.7)	81.7 (14.7)	85.8 (6.4)
	V4	130	Karp	25.7 (31.4)	26 (18.8)	30.1 (20)	44.6 (12.5)	34.1 (9.7)	38.1 (9.9)	32.8 (4)	31.8 (7)	26.9 (3.9)	26.4 (1.9)
			Karp-Collapse	136.3 (203.8)	86.1 (63.9)	85.8 (23.8)	78.7 (27.5)	67.1 (20.1)	59.7 (16.1)	47.4 (4.9)	44.4 (11.7)	37.7 (4.7)	29.2 (2.9)
			UCLUST	76.9 (194)	26.8 (42.8)	26.4 (11.4)	26 (12.7)	23 (6.8)	20.9 (4.7)	17.4 (4.5)	16 (4.3)	13.4 (1.9)	11.5 (1.5)
			SortMeRNA	107.8 (282.9)	28.5 (35.4)	33.2 (14.7)	32.6 (12.4)	37.2 (10.1)	38.7 (9.8)	33.8 (6)	33.3 (5.3)	36.3 (5.7)	30.7 (2.2)
			Kallisto	78.3 (61.8)	82.8 (48.3)	91.5 (27.3)	81.3 (23.4)	75.7 (13.6)	76.1 (13.3)	74.7 (6.7)	69.3 (8)	64 (5.1)	62 (1.9)
			USEARCH61	94.9 (240.5)	29.9 (41.6)	33.7 (24.5)	30.4 (12.4)	25.5 (8.8)	21.5 (6.1)	18.3 (4.7)	19.2 (4)	16.4 (2.9)	12.7 (1.9)
			Mothur NB	331.1 (341.6)	279.9 (208.2)	328.4 (165.6)	353.7 (95.6)	318 (72.7)	345.9 (81.7)	324.9 (60.2)	339.4 (29.5)	332 (25.7)	310.7 (10.6)
			16S Classifier	1339 (559.1)	1317.8 (386)	1160.2 (344.3)	1066.2 (243.3)	1050.8 (202.2)	1041.2 (99.2)	944.7 (77.1)	976.5 (115.2)	950.2 (44.6)	931.7 (27.2)
			SINTAX	69.1 (96.6)	77.3 (62.0)	72.5 (38.5)	87.4 (32.2)	67.8 (14.5)	64.4 (12.6)	61.8 (13.8)	66.6 (9.4)	67.9 (8.0)	63.0 (5.4)
151bp PE	Full gene	130	Karp	1.6 (2.5)	4.8 (7.6)	5.6 (9.6)	3.7 (2.5)	6.4 (4)	6.7 (5.9)	5.4 (2.7)	5.8 (1.4)	6 (1.4)	5 (0.5)
			Karp-Collapse	4.9 (3.5)	17.9 (21.2)	15.4 (11.3)	14.8 (8.2)	17.1 (5.9)	19.7 (6.5)	16.3 (6.2)	14 (3)	10.1 (1.9)	9.3 (0.8)
			UCLUST	1.9 (1.7)	3.8 (6.5)	4.4 (5.1)	9.9 (3.8)	10.1 (4.1)	9 (1.8)	9.2 (2.6)	7.7 (1.1)	6.9 (1)	7.1 (0.8)
			SortMeRNA	2.1 (1.4)	3.9 (3.3)	5.6 (3.7)	9.1 (3.4)	10.3 (4.1)	11.3 (6.5)	9.7 (2.2)	9.5 (2.8)	9.2 (1)	8.5 (0.9)
			Kallisto	14 (12.1)	45.5 (24.6)	48.4 (23.6)	67.4 (21.5)	69.5 (16.1)	63.6 (14.2)	62.1 (8.1)	63.7 (6.2)	61.3 (4.2)	62.1 (2.6)
			USEARCH61	7.5 (4.6)	12.1 (30.6)	10.5 (9.3)	15.8 (5.6)	20.2 (4.8)	18.8 (7.7)	13.5 (3.8)	12.2 (2.3)	11.3 (1.9)	9.5 (1.5)
			Mothur NB	123.4 (49.5)	148.7 (32.1)	132 (34.7)	129 (66)	94.4 (25.9)	80.6 (52.7)	34.2 (10)	25.7 (4.1)	18.7 (3.9)	14.1 (1.9)
			16S Classifier	1378.1 (455)	1479.9 (322.6)	1194.7 (367.4)	1250.5 (299.2)	1000.7 (262.9)	1111.1 (163.7)	1092.7 (99.3)	1082.8 (43.8)	1033.2 (49.4)	1042.6 (22.1)
			SINTAX	1.0 (1.6)	35.7 (190.9)	1.9 (1.8)	2.6 (1.0)	2.3 (1.0)	2.3 (0.7)	3.8 (1.9)	2.3 (0.4)	2.4 (0.8)	2.2 (0.4)
	V4	190	Karp	0.5 (0.9)	3.1 (13.5)	5.4 (18.7)	1.3 (1.5)	2.4 (4.3)	1.9 (1.8)	3.3 (2.1)	2.3 (1)	2.4 (1.2)	2.7 (0.9)
			Karp-Collapse	0.1 (0.3)	0.5 (1.5)	5.2 (19)	1 (1.8)	2 (4.6)	1.1 (1.5)	1.4 (1.3)	1.6 (1.1)	1.3 (0.8)	2 (1)
			UCLUST	2.4 (6.7)	19.6 (84.2)	23.3 (67.7)	5.6 (7.3)	21.9 (37.3)	31.6 (36.9)	27.6 (19.2)	24.2 (20.9)	18.2 (8.5)	14.8 (3.2)
			SortMeRNA	4 (8.2)	28.9 (98.2)	30 (78.7)	12.9 (17.5)	28.5 (38.6)	39.6 (45.5)	32.7 (17.2)	32.8 (22)	29.6 (5.9)	24.6 (5.6)
			Kallisto	21.3 (19.8)	51 (37.6)	61.2 (27.7)	63.4 (16.7)	67.7 (16.2)	74.9 (12)	74.1 (9.3)	67.5 (5.9)	66 (3.5)	68.3 (1.9)
			USEARCH61	3.9 (8.2)	28.9 (98.3)	29.6 (78.8)	12.8 (17.6)	28.6 (38.6)	38.9 (46)	32.1 (17.6)	31.1 (21.8)	23.8 (6.5)	21.6 (4.5)
			Mothur NB	99.6 (28)	152.7 (170.3)	168.6 (244.7)	224.2 (180.7)	235.9 (89.6)	196.8 (56.9)	186.7 (39.9)	137.4 (28.9)	95.1 (17)	53.8 (12.8)
			16S Classifier	299.9 (653.2)	117.2 (283.8)	83.3 (188.1)	285.5 (228.6)	229.3 (231.7)	178.8 (68)	152.1 (49.2)	159.3 (47.6)	171.7 (31.7)	154.8 (20.6)
			SINTAX	<0.1 (0.1)	0.1 (0.3)	0.1 (0.3)	<0.1 (0.1)	0.3 (0.3)	0.7 (0.8)	0.9 (1.4)	1.4 (2.6)	0.7 (0.6)	1.7 (1.7)

SE=Single-end, PE=Paired-end

Table 12: **Per class error rates, 1,000,000 reads**

Read Length	Region	Samples	Method	Shannon Diversity									
				[0,0.7)	[0.7,1.4)	[1.4,2)	[2,2.7)	[2.7,3.4)	[3.4,4.1)	[4.1,4.8)	[4.8,5.5)	[5.5,6.2)	[6.2,6.9]
301bp PE	Full gene	170	Karp	2.4 (4)	5.4 (11.2)	2.9 (2.7)	5.8 (7.4)	5.1 (4.4)	5.1 (1.5)	6.4 (1.8)	5.8 (1.2)	6.7 (1.5)	6.1 (1)
			Karp-Collapse	7.4 (9.5)	6.2 (4.5)	7.4 (3.8)	8.9 (3.9)	6.7 (2.2)	7.3 (2.4)	5.6 (1)	5.5 (1)	5.1 (1)	4.7 (0.3)
			UCLUST	0.5 (0.4)	0.7 (0.7)	0.7 (1.1)	0.3 (0.2)	0.3 (0.2)	0.1 (0.1)	0.1 (0.1)	0.1 (0.2)	0.1 (<0.1)	0.3 (0.3)
			SortMeRNA	0.9 (1.9)	2.1 (4.8)	1.8 (1.8)	2 (1.7)	2 (1.5)	3.8 (4.2)	2.2 (1)	2.9 (3.4)	2.7 (1.5)	2.3 (0.5)
			Kallisto	422.7 (354.9)	765 (324.1)	875 (270)	934.6 (272.6)	1001 (133.8)	991.9 (146.7)	953.9 (165.3)	910.8 (83.5)	875.5 (62.5)	860.7 (33.1)
			USEARCH61	0.4 (0.4)	0.8 (0.9)	0.7 (0.4)	0.8 (0.5)	0.7 (0.5)	0.5 (0.2)	0.6 (0.6)	0.8 (1)	0.6 (0.5)	0.5 (0.4)
			Mothur NB	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)	NA (NA)
			16S Classifier	1253.5 (573.7)	1152.9 (532.1)	1245.4 (311.4)	1082.1 (302.1)	1056.5 (189.9)	1007.4 (142.9)	964.2 (74.9)	876.1 (95.4)	933.3 (67.4)	908.8 (13.2)
			SINTAX	<0.1 (<0.1)	0.2 (1.1)	0.1 (0.3)	0.1 (0.2)	0.6 (1.6)	0.2 (0.2)	0.3 (0.4)	0.5 (1.2)	0.7 (0.6)	0.5 (0.4)
	V4	190	Karp	10.1 (49.9)	6 (11.3)	8.4 (8.9)	29.1 (49.1)	8.1 (7.7)	6.2 (4.1)	5.2 (1.7)	6.1 (3.5)	5 (1.6)	3.8 (0.8)
			Karp-Collapse	0.3 (1.7)	0.3 (0.8)	0.3 (0.5)	5.7 (17.3)	0.3 (0.3)	0.3 (0.2)	0.3 (0.2)	0.3 (0.1)	0.3 (0.2)	0.2 (0.1)
			UCLUST	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	0.2 (0.6)
			SortMeRNA	0.1 (<0.1)	0.1 (<0.1)	0.1 (<0.1)	0.1 (<0.1)	0.2 (<0.1)	0.2 (0.1)	0.3 (0.1)	0.4 (0.1)	0.4 (0.1)	0.7 (0.6)
			Kallisto	433 (357.9)	815.4 (401.5)	922.9 (303.1)	1101.6 (207.4)	1167.7 (216.8)	1148.7 (133.4)	1155.1 (167.4)	1121.2 (111.8)	1066.4 (95.6)	1107.7 (39.1)
			USEARCH61	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	0.2 (0.6)
			Mothur NB	354.1 (485)	222.7 (108.1)	227.1 (182.4)	201.7 (79.5)	140.5 (41.1)	152 (17)	136.7 (33.8)	109.8 (15.9)	91.1 (17.5)	51.2 (13.5)
			16S Classifier	171.8 (510)	71.9 (122.7)	97.2 (214.6)	141.2 (195.1)	102.9 (64.3)	115.9 (63.8)	132.9 (67.9)	165 (37.9)	151 (46.6)	144.4 (13)
			SINTAX	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	0.7 (1.8)	0.1 (0.2)	0.2 (0.6)

SE=Single-end, PE=Paired-end

Table 13: **Per species error rates, 100,000 reads**

Read Length	Region	Samples	Method	Shannon Diversity									
				[0,0.7)	[0.7,1.4)	[1.4,2)	[2,2.7)	[2.7,3.4)	[3.4,4.1)	[4.1,4.8)	[4.8,5.5)	[5.5,6.2)	[6.2,6.9]
75bp SE	Full gene	130	Karp	1.6 (2.5)	2.1 (3.4)	4.1 (4.8)	4.1 (3.1)	4.8 (2.7)	4.3 (1.3)	4.4 (0.9)	4.2 (0.9)	3.7 (0.7)	3.4 (0.3)
			Karp-Collapse	2.9 (4.4)	3.8 (7.1)	6.3 (6.4)	8.8 (6.2)	9.2 (5.2)	8.7 (2.6)	8.6 (1.4)	8.6 (1.2)	6.7 (1)	5.5 (0.3)
			UCLUST	2.9 (6)	5.3 (11.9)	7.4 (9.3)	7.8 (6.7)	9.8 (6.3)	7.8 (2.9)	8.2 (2.2)	8.1 (1.5)	6.5 (1.1)	5.9 (0.4)
			SortMeRNA	4.1 (10.5)	5.6 (12.6)	7.7 (9.2)	9.4 (8)	11 (7.2)	9.2 (3.6)	9.9 (3.2)	9.7 (1.5)	8 (1.3)	7 (0.4)
			Kallisto	2.4 (3.4)	2.9 (5.1)	5.5 (6)	5.9 (4.2)	6.8 (4)	5.9 (1.7)	5.9 (1.4)	5.9 (1)	5.1 (0.9)	4.7 (0.3)
			USEARCH61	3.5 (8.2)	6.1 (14.5)	7.5 (8.9)	8.5 (7.3)	10.1 (6.3)	8 (2.6)	8.6 (2.5)	8.7 (1.5)	7 (1.4)	6.1 (0.4)
			Mothur NB	5.6 (14.4)	8.1 (18.6)	12.5 (17.8)	13.3 (9.5)	17.5 (15.4)	14.6 (8)	14 (3.5)	14.5 (1.1)	12.8 (1.6)	12 (0.9)
			16S Classifier	7.9 (24.2)	12.4 (25.7)	12.5 (20.3)	11.9 (10.4)	12.4 (11.4)	10.5 (7.2)	11.1 (4.7)	11.2 (1.3)	10.3 (1.4)	10.8 (0.7)
			SINTAX	0.9 (2.5)	1.5 (3.5)	4.8 (10.5)	3.5 (5.2)	6.2 (4.1)	5.0 (2.5)	5.9 (3.0)	6.7 (1.7)	6.0 (1.1)	6.6 (0.6)
	V4	130	Karp	0.9 (1.6)	1.5 (2.3)	2.2 (2.1)	2 (1.9)	2.6 (1.7)	2.6 (1.4)	2.1 (0.7)	2.3 (0.6)	2 (0.3)	1.9 (0.3)
			Karp-Collapse	2 (3.6)	3.6 (4.5)	4 (4)	4.5 (4.8)	5.3 (3.4)	5.7 (2.6)	6.1 (1.4)	5.2 (1.2)	5 (0.6)	4.1 (0.4)
			UCLUST	2.2 (4.2)	2.9 (3.6)	4.5 (5.1)	4.9 (5.9)	5.3 (4.1)	5.1 (2.4)	5 (1.4)	5.1 (1.8)	4.4 (0.6)	4.2 (0.4)
			SortMeRNA	1.8 (3.1)	3 (3.9)	4.6 (5.5)	4.5 (4.7)	5.5 (4)	5.5 (2.6)	5.4 (1.2)	5.6 (1.6)	5.3 (0.8)	4.9 (0.5)
			Kallisto	1.6 (2.8)	2.4 (3.2)	3.3 (3.3)	3.1 (3)	3.9 (2.5)	3.5 (1.8)	3.2 (0.9)	3.7 (1.1)	3.1 (0.5)	3.1 (0.4)
			USEARCH61	2.8 (6.2)	3 (3.9)	4.7 (5.5)	4.6 (5.4)	5.2 (3.8)	4.9 (2.2)	4.7 (1.2)	5.1 (1.7)	4.6 (0.8)	4.1 (0.5)
			Mothur NB	8.9 (19.3)	7.6 (13)	8.6 (11.3)	9.6 (10.9)	8 (4.7)	9.4 (5)	9.8 (3.1)	9.6 (2.4)	9.3 (1)	9.4 (0.8)
			16S Classifier	14.5 (33)	12.2 (21)	10.9 (18.7)	8.2 (10.9)	6.9 (5.5)	7.3 (5)	7.7 (2.6)	7.6 (2.2)	7.1 (0.9)	7.9 (0.7)
			SINTAX	0.5 (0.6)	1.3 (2.2)	2.7 (5.3)	5.7 (7.5)	4.6 (5.7)	3.9 (2.7)	4.2 (1.5)	5.2 (2.4)	4.4 (0.7)	4.9 (0.6)
151bp PE	Full gene	130	Karp	0.1 (0.4)	0.1 (0.1)	0.7 (1.5)	0.1 (0.1)	0.4 (0.3)	0.5 (0.3)	0.5 (0.3)	0.4 (0.1)	0.5 (0.1)	0.4 (<0.1)
			Karp-Collapse	0.3 (0.4)	0.2 (0.4)	1.4 (3.5)	1.1 (1.3)	1.9 (1.6)	2 (1.1)	2.7 (1.8)	2.3 (0.7)	1.9 (0.5)	1.2 (0.2)
			UCLUST	0.1 (0.1)	0.3 (0.5)	3.3 (11.8)	1.2 (1.3)	3.5 (4.1)	2.3 (0.9)	3.5 (1.4)	2.5 (0.8)	3 (0.7)	2.3 (0.3)
			SortMeRNA	0.3 (0.3)	0.5 (0.9)	3.3 (9.9)	2 (2.1)	3 (1.5)	4 (2)	4.4 (2)	4.1 (1.2)	4.3 (0.9)	3.3 (0.3)
			Kallisto	0.2 (0.6)	<0.1 (0.1)	0.2 (0.7)	0.3 (0.4)	0.5 (0.5)	0.4 (0.3)	0.6 (0.5)	0.6 (0.2)	0.8 (0.2)	0.8 (0.1)
			USEARCH61	0.2 (0.2)	0.2 (0.3)	5.4 (18.3)	1.1 (1.7)	2.8 (2.1)	3 (1.6)	3.4 (2)	2.2 (0.6)	2.9 (0.8)	2.5 (0.3)
			Mothur NB	3.3 (5.4)	2.9 (5.2)	6.4 (8.3)	8.9 (8.1)	13.9 (6.7)	10.4 (4)	11.5 (3.7)	12.5 (2.2)	13.6 (1.6)	12.5 (0.5)
			16S Classifier	10.3 (24.3)	2.5 (4.5)	8.7 (15.8)	7.6 (9.8)	13.5 (9.5)	8.1 (4.9)	8.2 (3.2)	9.9 (2)	11.4 (1.9)	10.7 (0.7)
			SINTAX	0.1 (0.1)	0.3 (0.5)	4.9 (18.5)	0.9 (1.4)	4.0 (3.7)	3.0 (2.2)	3.5 (2.4)	3.5 (1.0)	4.2 (1.1)	3.4 (0.4)
	V4	190	Karp	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	0.3 (0.7)	0.1 (0.2)	0.1 (<0.1)	0.1 (<0.1)	0.2 (0.1)
			Karp-Collapse	<0.1 (<0.1)	<0.1 (0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	0.2 (0.4)	0.1 (0.2)	0.1 (0.2)	0.1 (0.1)	0.1 (0.1)
			UCLUST	7.2 (33.9)	0.2 (0.9)	<0.1 (0.1)	3.7 (10.6)	0.1 (0.2)	0.6 (1.1)	0.5 (0.6)	0.5 (0.7)	0.4 (0.4)	0.6 (0.4)
			SortMeRNA	0.4 (1.4)	1.6 (6.9)	0.7 (2)	6.4 (18.8)	0.3 (0.4)	1.3 (1.3)	1.1 (1.3)	2.1 (1.3)	1.1 (0.6)	1.2 (0.6)
			Kallisto	<0.1 (0.1)	0.1 (0.2)	0.1 (0.1)	0.3 (0.6)	0.4 (0.7)	0.9 (1.5)	0.8 (0.5)	0.8 (0.7)	0.7 (0.1)	0.8 (0.2)
			USEARCH61	7.7 (33.8)	0.2 (0.9)	0.3 (1)	3.7 (10.7)	1.8 (4.9)	0.7 (1.6)	1.3 (1.6)	0.9 (0.9)	0.7 (0.4)	0.9 (0.5)
			Mothur NB	3.5 (10.7)	11.4 (13.1)	6 (8.9)	9.8 (11.7)	10.5 (5.9)	10 (5.3)	9.4 (2.9)	9.7 (2.5)	10.4 (0.9)	10.3 (0.8)
			16S Classifier	23.1 (7.4)	22.7 (19.8)	12.3 (8.1)	9.8 (8.3)	9.2 (9.4)	6 (8.8)	2.9 (7.1)	2.1 (6.8)	0.7 (7.7)	0.8 (8.2)
			SINTAX	0.1 (0.2)	3.7 (11.1)	7.4 (23.1)	3.7 (8.6)	1.1 (1.7)	4.9 (7.0)	2.5 (2.2)	2.9 (2.6)	2.5 (1.3)	2.9 (0.9)

SE=Single-end, PE=Paired-end

Table 14: **Per species error rates, 100,000 reads**

Read Length	Region	Samples	Method	Shannon Diversity									
				[0,0.7)	[0.7,1.4)	[1.4,2)	[2,2.7)	[2.7,3.4)	[3.4,4.1)	[4.1,4.8)	[4.8,5.5)	[5.5,6.2)	[6.2,6.9]
301bp PE	Full gene	170	Karp	0.1 (0.2)	0.5 (1.2)	0.4 (0.7)	<0.1 (0.1)	0.5 (0.5)	0.6 (0.6)	0.8 (0.4)	0.7 (0.3)	0.7 (0.3)	0.7 (0.1)
			Karp-Collapse	0.2 (0.3)	0.6 (1.4)	2 (3.7)	0.1 (0.3)	0.7 (0.7)	1 (0.7)	1.4 (1.1)	1.4 (0.9)	0.9 (0.4)	0.7 (0.2)
			UCLUST	0.5 (0.9)	1.8 (5.2)	1.6 (3.4)	0.3 (0.6)	0.7 (0.6)	2 (2.5)	1.7 (1.1)	1.7 (0.8)	1.8 (0.6)	1.6 (0.4)
			SortMeRNA	0.5 (0.8)	2 (4)	2.2 (3.7)	1.7 (1.6)	1.5 (1.5)	4.3 (5.4)	3 (1.2)	3.1 (1.1)	2.9 (0.9)	2.6 (0.4)
			Kallisto	0.8 (1.3)	5.2 (10.4)	1.4 (2)	4.1 (6.6)	6.1 (7.1)	10.7 (8.2)	11 (5.9)	11.2 (3.4)	12.7 (2.5)	13.1 (1.6)
			USEARCH61	0.4 (0.8)	1.2 (3.3)	1.6 (2.2)	0.5 (0.9)	1.1 (1.2)	1.7 (1.3)	1.8 (0.9)	2.1 (0.9)	2 (0.8)	1.6 (0.2)
			Mothur NB	3.6 (3.3)	10.7 (14.8)	10.9 (9.5)	5.2 (3.5)	10.4 (4)	12.6 (8)	13.9 (3.6)	12.9 (2)	13.9 (1.8)	12.9 (0.6)
			16S Classifier	20.4 (36.4)	16.8 (24.5)	12.3 (12.1)	4.6 (4.5)	8.4 (4.7)	9.1 (5.7)	11.7 (4.8)	10 (1.9)	11.7 (2.3)	11.2 (1)
			SINTAX	0.5 (1.0)	1.4 (3.3)	1.3 (3.3)	0.3 (0.7)	1.8 (2.1)	3.5 (3.8)	2.7 (1.4)	3.1 (0.9)	3.2 (1.0)	3.2 (0.4)
	V4	190	Karp	<0.1 (<0.1)	<0.1 (0.1)	0.1 (0.1)	0.1 (0.2)	0.5 (1.6)	0.1 (<0.1)	0.1 (0.1)	0.2 (0.1)	0.2 (0.1)	0.3 (0.1)
			Karp-Collapse	<0.1 (<0.1)	<0.1 (0.1)	<0.1 (<0.1)	0.1 (0.3)	0.4 (1.3)	<0.1 (<0.1)	0.1 (0.1)	0.1 (0.1)	<0.1 (<0.1)	0.1 (0.1)
			UCLUST	<0.1 (<0.1)	0.6 (3.2)	<0.1 (<0.1)	<0.1 (0.1)	0.1 (0.4)	0.2 (0.6)	0.2 (0.4)	0.5 (0.9)	0.3 (0.3)	0.7 (0.2)
			SortMeRNA	<0.1 (<0.1)	0.1 (0.2)	<0.1 (0.1)	0.3 (0.5)	1.2 (3.5)	0.8 (1.2)	0.8 (0.8)	0.9 (0.8)	0.6 (0.6)	0.6 (0.3)
			Kallisto	0.1 (0.2)	3.3 (7.7)	2.4 (4.1)	5.3 (10.2)	3 (2.6)	5.6 (2.6)	7.6 (4.8)	9.4 (2.6)	9 (2.6)	11 (1.4)
			USEARCH61	<0.1 (<0.1)	<0.1 (0.1)	0.1 (0.4)	0.1 (0.4)	1.7 (5.2)	0.6 (0.8)	0.7 (1.1)	0.5 (0.3)	0.6 (0.4)	0.7 (0.3)
			Mothur NB	2 (4)	3.3 (5.1)	7.2 (9.9)	5.5 (5.3)	6.3 (5.9)	9.1 (5.1)	9.2 (3.5)	10.9 (2.4)	9.4 (1.9)	10 (0.8)
			16S Classifier	14.9 (33.5)	5.6 (9.3)	12 (18.9)	6.8 (9.2)	4.9 (4.6)	7.1 (4.6)	7 (3.5)	7.9 (2)	7.1 (1.8)	8 (1)
			SINTAX	<0.1 (0.2)	<0.1 (<0.1)	4.9 (11.9)	0.3 (0.7)	0.5 (1.0)	3.6 (5.4)	3.0 (2.3)	2.5 (1.3)	2.3 (1.0)	2.9 (0.6)

SE=Single-end, PE=Paired-end

Table 15: **Per genus error rates, 100,000 reads**

Read Length	Region	Samples	Method	Shannon Diversity									
				[0,0.7)	[0.7,1.4)	[1.4,2)	[2,2.7)	[2.7,3.4)	[3.4,4.1)	[4.1,4.8)	[4.8,5.5)	[5.5,6.2)	[6.2,6.9]
75bp SE	Full gene	130	Karp	8.8 (9.7)	11.6 (7.5)	14.2 (5.5)	14.8 (4.2)	13.8 (2)	14 (1.8)	12.9 (1.2)	10.8 (0.8)	10.1 (1)	8.3 (0.4)
			Karp-Collapse	17.3 (18)	20.2 (13.3)	27.7 (9.9)	29.7 (6.1)	27.6 (3.2)	26.6 (2.2)	24.3 (2.7)	20.9 (1.6)	18.2 (1.2)	13.8 (0.4)
			UCLUST	15.3 (17.5)	20.1 (15.3)	26.5 (10.1)	27.3 (6.5)	26.4 (3.6)	25.9 (3.2)	24.2 (3)	19.9 (1.4)	18.1 (1.4)	13.8 (0.5)
			SortMeRNA	16.7 (19)	21.3 (15.5)	30.5 (10.9)	32 (8.3)	31.2 (4.9)	30.5 (3.5)	29 (3.2)	25 (1.7)	22.7 (2.1)	17.2 (0.7)
			Kallisto	14.4 (15.1)	16.9 (11)	21.6 (7.8)	22.2 (5.4)	21.2 (3.2)	20.1 (2.4)	18.6 (1.8)	15.8 (1.2)	14.4 (1.4)	11.7 (0.5)
			USEARCH61	16.3 (19)	20.7 (15.3)	28.2 (10.7)	28.3 (6.6)	27.5 (3.6)	26.8 (2.4)	25 (2.6)	20.9 (1.4)	18.8 (1.5)	14.2 (0.5)
			Mothur NB	20.6 (30.4)	22.1 (18.2)	43.6 (25.6)	37.4 (15.2)	40.8 (11)	39.7 (4.5)	37.6 (6.3)	36.6 (2.3)	34 (1.7)	31.8 (1.9)
			16S Classifier	89.3 (93.6)	86.4 (77.6)	113 (49.8)	99.4 (47.6)	90.9 (28.9)	89.1 (24.7)	86.1 (12.6)	89 (5.6)	86.4 (6.3)	86.5 (2.5)
			SINTAX	5.2 (5.6)	12.7 (15.0)	19.0 (13.4)	19.4 (7.6)	18.2 (6.7)	22.0 (6.5)	20.3 (3.1)	19.3 (1.6)	19.7 (2.0)	19.2 (0.7)
	V4	130	Karp	4.7 (6)	8.1 (8.7)	10.1 (8.3)	10.3 (3.8)	9.2 (4.1)	8.6 (2.8)	6.8 (1.6)	7.3 (1.2)	6.5 (0.9)	5.6 (0.5)
			Karp-Collapse	11.3 (11.3)	16.7 (13.7)	21.6 (14)	20.9 (6.7)	19.3 (6.2)	20.3 (5)	16.1 (3.2)	15.2 (1.7)	13.8 (1.6)	10.4 (0.8)
			UCLUST	7.7 (7.9)	15 (17.8)	19.6 (16.4)	19.5 (8.6)	17.6 (6.5)	16.9 (4.7)	13.4 (3.6)	13.9 (1.7)	12 (1.7)	9.8 (0.8)
			SortMeRNA	7.1 (7.9)	16.8 (20)	20.6 (15.1)	19.1 (7.7)	19.4 (6.7)	19.9 (4.6)	16.1 (3.3)	16.9 (1.5)	15.9 (1.7)	12.7 (0.7)
			Kallisto	9.4 (9.4)	13.6 (12.2)	18.7 (14.5)	16.5 (6.3)	15 (4.5)	15 (4.1)	12.2 (2.3)	12.5 (2.1)	11 (1.3)	9.3 (0.7)
			USEARCH61	8.7 (11.2)	17.2 (21.4)	20.9 (16.4)	19 (9.3)	18.6 (6.3)	17.5 (4.1)	14 (3.1)	14.1 (1.6)	12.7 (1.8)	10.1 (0.8)
			Mothur NB	11.5 (10.7)	25.7 (25.6)	34.1 (22.4)	39.2 (20.6)	36.8 (9.5)	35.4 (8.4)	32.2 (5.5)	33.2 (3.1)	30.7 (2.5)	28.7 (0.9)
			16S Classifier	79.2 (79.9)	86.7 (63)	77.2 (48.1)	80.6 (33.6)	80.9 (14.7)	76.2 (19.7)	68 (14.8)	72.8 (8.5)	69 (5.1)	70.2 (2.3)
			SINTAX	4.4 (4.5)	11.5 (17.8)	18.8 (21.6)	17.4 (13.5)	19.0 (8.4)	18.3 (4.9)	16.1 (4.5)	18.6 (3.2)	17.3 (2.7)	17.3 (0.8)
151bp PE	Full gene	130	Karp	0.5 (1.4)	0.5 (0.6)	0.7 (0.9)	1 (0.7)	1.1 (0.6)	0.8 (0.3)	1.2 (0.3)	1.1 (0.3)	1.1 (0.2)	1.1 (0.1)
			Karp-Collapse	1.4 (4)	2.3 (4.3)	2.1 (3)	4.2 (4.7)	3 (2.4)	2.4 (1.8)	4.5 (3.1)	2.6 (0.8)	2 (0.5)	1.8 (0.2)
			UCLUST	1 (2)	1.5 (1.7)	5.1 (11.5)	2.9 (2.2)	3.8 (2.3)	3.9 (2)	6.2 (2.5)	4 (0.7)	3.8 (0.7)	3.8 (0.5)
			SortMeRNA	2.7 (4.3)	3 (3.8)	7.1 (9.6)	7.1 (4.3)	5.9 (2.5)	6 (2.4)	8.3 (2.8)	6.7 (1.2)	6.4 (0.7)	5.6 (0.3)
			Kallisto	0.9 (1.1)	1.9 (2)	1.6 (1.2)	2.7 (1.4)	2.7 (1)	3.1 (0.8)	3.3 (0.6)	3.3 (0.3)	3.4 (0.3)	3.6 (0.1)
			USEARCH61	2.1 (5.3)	1.7 (1.6)	3.8 (5)	6.5 (6.4)	4.6 (4)	4.4 (2.8)	6 (2.5)	4.6 (0.9)	4.2 (0.8)	4.2 (0.4)
			Mothur NB	11.4 (20.5)	19.8 (17.4)	26.3 (10.3)	31.1 (7.6)	29.3 (6.6)	29.4 (5.2)	29.6 (2.6)	27.7 (3)	27.5 (1.2)	24.7 (1.1)
			16S Classifier	84.3 (85.7)	83.7 (67.3)	62.9 (38.2)	71.1 (18.5)	77.6 (28.2)	79.4 (10.9)	73.6 (7.9)	77.3 (9.9)	77.1 (7)	75.4 (3.1)
			SINTAX	1.3 (2.5)	2.5 (3.9)	6.7 (17.0)	5.5 (3.6)	4.9 (2.0)	6.1 (2.8)	7.5 (3.3)	6.4 (1.4)	6.0 (1.4)	5.7 (0.7)
	V4	190	Karp	<0.1 (<0.1)	0.1 (0.3)	0.3 (1)	0.1 (<0.1)	0.4 (0.6)	0.3 (0.1)	0.5 (0.5)	0.4 (0.2)	0.5 (0.2)	0.6 (0.1)
			Karp-Collapse	<0.1 (0.1)	0.1 (0.3)	0.3 (1)	<0.1 (<0.1)	0.3 (0.6)	0.1 (0.2)	0.4 (0.5)	0.2 (0.3)	0.2 (0.2)	0.2 (0.1)
			UCLUST	4 (25)	0.4 (1.6)	0.8 (2.9)	3.6 (10.1)	0.6 (1.1)	0.4 (0.6)	1.5 (3.4)	0.9 (0.5)	1.1 (0.8)	1.5 (0.5)
			SortMeRNA	2.3 (11)	6.6 (21)	2.3 (8.2)	6.5 (17.6)	1.5 (1.6)	1.6 (1.6)	3.4 (4.2)	3.4 (2.4)	2.9 (1.5)	3 (0.8)
			Kallisto	0.6 (0.8)	1.5 (1.8)	2.8 (2.8)	2.7 (0.8)	3.6 (1.8)	3.5 (0.9)	3.6 (0.6)	3.9 (0.9)	4 (0.4)	3.9 (0.3)
			USEARCH61	4.5 (24.8)	0.8 (2.5)	0.7 (2.8)	4.9 (10.3)	1 (1.5)	0.8 (1)	3.5 (4.4)	1.8 (1.1)	2.4 (1.3)	2.4 (0.5)
			Mothur NB	14.7 (11.2)	24.3 (10.4)	25.8 (17.3)	30.9 (10.5)	29.9 (6.7)	28.1 (6.2)	28.1 (3.1)	28.9 (2.3)	27.4 (2.4)	24.9 (1.1)
			16S Classifier	39.1 (70.6)	55.6 (65.4)	37.6 (33.4)	26.6 (21.1)	33.2 (24.4)	32.4 (9.1)	30 (9.2)	34.2 (8.3)	31.1 (2.7)	33.2 (3.1)
			SINTAX	7.7 (34.0)	8.0 (21.7)	11.0 (24.7)	4.5 (9.4)	2.0 (2.4)	3.7 (2.5)	5.3 (5.4)	3.9 (2.2)	5.3 (1.3)	4.2 (1.0)

SE=Single-end, PE=Paired-end

Table 16: **Per genus error rates, 100,000 reads**

Read Length	Region	Samples	Method	Shannon Diversity									
				[0,0.7)	[0.7,1.4)	[1.4,2)	[2,2.7)	[2.7,3.4)	[3.4,4.1)	[4.1,4.8)	[4.8,5.5)	[5.5,6.2)	[6.2,6.9]
301bp PE	Full gene	170	Karp	0.2 (0.4)	0.8 (1.8)	0.3 (0.3)	1 (2.1)	0.9 (0.7)	1.4 (1)	1.6 (0.8)	1.4 (0.3)	1.5 (0.3)	1.7 (0.1)
			Karp-Collapse	0.2 (0.5)	0.7 (1.3)	1.9 (4.1)	1.4 (3.2)	1.4 (1.5)	1.4 (0.9)	1.8 (1.4)	1.4 (0.8)	1.3 (0.3)	0.9 (0.2)
			UCLUST	0.3 (0.4)	1.5 (3.4)	2.8 (6.1)	2.9 (5.2)	1.7 (1.3)	3.7 (3.3)	3.1 (2.5)	2.2 (0.7)	2.1 (0.5)	2 (0.3)
			SortMeRNA	0.9 (1.5)	2.9 (3.8)	4.8 (6.2)	4 (4.4)	5.5 (3)	7.8 (6.1)	6.1 (1.6)	4.8 (1.2)	4.4 (0.7)	4 (0.3)
			Kallisto	15.5 (27.7)	26.5 (34.9)	28.1 (23.7)	34.9 (26.1)	37.1 (14.8)	47.2 (9.2)	51.2 (9.2)	51.4 (6)	53.7 (6)	52.1 (2.2)
			USEARCH61	0.2 (0.4)	1.8 (4.9)	1.7 (2.2)	2.4 (5.3)	2.3 (2.4)	2.4 (1.6)	2.8 (1.6)	2.6 (0.7)	2.1 (0.5)	2.1 (0.3)
			Mothur NB	9.7 (20)	25.8 (24.2)	26.9 (18.3)	25.4 (12.1)	30.9 (4.6)	31.1 (9.8)	30.2 (3.6)	28.8 (2.6)	28.2 (1.4)	26.2 (1.3)
			16S Classifier	62.5 (79.6)	51.3 (54.8)	77.7 (50.1)	60.1 (30.2)	67.2 (9.7)	71.6 (15.1)	70.2 (12.7)	65.9 (10.1)	67 (7.3)	67.2 (4)
			SINTAX	0.7 (1.1)	3.9 (8.7)	4.0 (6.8)	3.0 (3.3)	3.5 (3.5)	6.4 (4.8)	4.8 (2.6)	4.1 (1.0)	4.4 (0.9)	4.3 (0.7)
	V4	190	Karp	0.1 (0.2)	0.3 (0.5)	0.6 (1)	0.8 (1)	1.3 (2.8)	0.6 (0.2)	0.6 (0.1)	0.7 (0.2)	1 (0.2)	1.1 (0.1)
			Karp-Collapse	<0.1 (<0.1)	0.1 (0.4)	<0.1 (0.1)	0.2 (0.4)	<0.1 (0.1)	0.2 (0.3)	0.1 (0.1)	0.1 (0.1)	0.1 (<0.1)	0.1 (<0.1)
			UCLUST	<0.1 (<0.1)	<0.1 (0.1)	0.6 (2.5)	<0.1 (<0.1)	<0.1 (0.1)	0.4 (0.8)	0.3 (0.4)	0.9 (0.9)	0.4 (0.3)	0.7 (0.4)
			SortMeRNA	0.1 (0.5)	0.7 (2.4)	0.4 (2)	0.8 (1.6)	0.8 (1.5)	2 (2.1)	1.7 (1.8)	2.3 (1.3)	1.2 (0.6)	1 (0.3)
			Kallisto	14.6 (28.4)	38.1 (43)	37.7 (24)	41.4 (22.5)	41.7 (16.7)	52.6 (17.7)	47.9 (10.9)	55.7 (7.3)	55.6 (6.9)	57.5 (2.7)
			USEARCH61	<0.1 (0.2)	0.2 (0.8)	<0.1 (<0.1)	0.2 (0.5)	0.1 (0.3)	1 (1.2)	1 (1.3)	0.9 (0.7)	1 (0.7)	0.9 (0.3)
			Mothur NB	28.1 (55)	27.3 (33.2)	29.3 (12.6)	28 (10.5)	29.7 (5)	30 (3.5)	27.3 (3.6)	29.7 (3)	26.8 (2.2)	24.7 (1.1)
			16S Classifier	38.4 (74.8)	30.4 (42.4)	52.5 (44.8)	25 (20.9)	32.2 (20.6)	32.6 (12.2)	32.9 (10.1)	31.2 (7.8)	32.2 (5.6)	31.6 (2.4)
			SINTAX	0.5 (1.3)	4.2 (14.6)	5.1 (17.2)	0.7 (1.1)	1.8 (4.9)	5.9 (4.8)	3.4 (2.0)	4.3 (2.8)	4.0 (2.1)	4.1 (0.8)

SE=Single-end, PE=Paired-end

Table 17: **Per family error rates, 100,000 reads**

Read Length	Region	Samples	Method	Shannon Diversity									
				[0,0.7)	[0.7,1.4)	[1.4,2)	[2,2.7)	[2.7,3.4)	[3.4,4.1)	[4.1,4.8)	[4.8,5.5)	[5.5,6.2)	[6.2,6.9]
75bp SE	Full gene	130	Karp	15 (8.3)	16.8 (8.4)	15.9 (6.3)	16.6 (3.8)	15.7 (3)	13.9 (2.2)	13.1 (2)	10 (0.7)	8.7 (1)	6.4 (0.3)
			Karp-Collapse	34.6 (15.2)	31 (13.3)	33 (9.5)	36.2 (5.9)	32.3 (6.5)	26.9 (3)	25 (3.7)	18.9 (1.2)	15.4 (1.7)	10.7 (0.5)
			UCLUST	28.6 (13.5)	27.7 (13)	28.9 (8.8)	30 (6.2)	28.6 (6.2)	23.9 (3)	22.3 (3.1)	17 (1.4)	13.6 (1.7)	9.2 (0.5)
			SortMeRNA	29.7 (14.3)	29.1 (13.2)	32.9 (10.6)	34.9 (5.5)	34.5 (7.1)	30.1 (3)	28.9 (3.7)	22.3 (1.5)	18.4 (1.9)	12.8 (0.5)
			Kallisto	27.2 (12.8)	26.3 (11.6)	26.9 (8.2)	27.6 (5)	25.7 (3.5)	21.8 (2.4)	20.5 (2.7)	15.8 (1.3)	13.2 (1.3)	9.5 (0.3)
			USEARCH61	30.7 (14.6)	28.6 (13.7)	30.5 (10)	31 (5.9)	29.7 (6.3)	24.7 (2.6)	23.4 (3.6)	17.8 (1.4)	14.2 (1.9)	9.6 (0.5)
			Mothur NB	45.3 (56.4)	34.1 (21.2)	39.1 (21.8)	38 (11.1)	45.5 (9.6)	40.2 (7.4)	39.3 (4.2)	37.4 (3.2)	35.4 (2.1)	34.2 (1.8)
			16S Classifier	173.5 (57.9)	131.8 (71.1)	151.9 (40.2)	172 (19.3)	147.3 (10.6)	156.1 (12.4)	149.8 (10.7)	144.3 (6.9)	146.4 (4.6)	145.7 (1.6)
			SINTAX	7.7 (4.1)	16.4 (10.6)	17.2 (9.4)	21.7 (4.7)	22.6 (7.3)	21.8 (3.3)	21.4 (2.7)	18.6 (1.5)	18.8 (1.7)	17.8 (0.7)
	V4	130	Karp	6.1 (7.9)	8.6 (7.8)	9 (3.9)	7.5 (3.9)	8.7 (4.2)	8.1 (2.1)	7 (1.1)	6.1 (0.9)	5.7 (0.6)	4.5 (0.3)
			Karp-Collapse	17.8 (13.4)	20 (12.8)	21 (7.3)	18.9 (8.1)	20.1 (6)	18.6 (5.9)	16 (2.9)	12.8 (1.7)	11.1 (0.9)	7.9 (0.8)
			UCLUST	9.3 (11)	15.4 (13.7)	16.6 (7.9)	14.1 (7.9)	14.5 (5.9)	14.6 (6.7)	11.6 (2.3)	9.5 (2)	8.5 (1)	6.1 (0.7)
			SortMeRNA	9.3 (10.2)	15.6 (15.2)	17.1 (7.2)	14.7 (7.6)	17.4 (6.1)	18 (5.9)	16.2 (3)	13.9 (1.9)	13.7 (0.7)	10.5 (0.8)
			Kallisto	15.3 (12.1)	17.4 (12)	20 (10.3)	16.6 (6.3)	17.3 (5.2)	17.2 (5.2)	14.8 (1.9)	12 (1.1)	10.9 (0.6)	8.6 (0.4)
			USEARCH61	11.6 (15)	17.9 (17.4)	17.2 (7)	14.9 (8.2)	14.8 (5.8)	14.7 (5.6)	12.6 (2.5)	9.9 (1.8)	9 (0.7)	6.3 (0.6)
			Mothur NB	25.9 (29)	38 (26.3)	38.2 (15.4)	44.6 (16)	36.4 (9.8)	48.3 (13.2)	39.7 (5)	39.7 (5)	36.9 (2.6)	35.5 (1.4)
			16S Classifier	136.5 (69.9)	129 (46.1)	121.5 (44.5)	130.7 (19.5)	117.7 (18.2)	125 (17.3)	114.7 (10.9)	115.6 (7.7)	113.2 (2.7)	112 (3.4)
			SINTAX	6.3 (6.3)	14.2 (12.8)	18.8 (10.9)	16.7 (8.7)	16.9 (4.9)	22.2 (7.2)	18.1 (2.7)	18.5 (2.8)	18.3 (1.0)	16.6 (0.9)
151bp PE	Full gene	130	Karp	0.5 (1.1)	0.8 (1.2)	1.1 (1.2)	1.4 (0.7)	1.4 (0.9)	0.9 (0.2)	1.4 (0.4)	1.1 (0.3)	1.2 (0.2)	1.1 (0.1)
			Karp-Collapse	0.6 (1.2)	1.7 (2.9)	3.8 (5.2)	2 (1.9)	2.2 (2.5)	1.2 (0.5)	2.1 (1)	1.3 (0.3)	1.5 (0.2)	1.3 (0.2)
			UCLUST	2 (5.7)	2 (2.5)	4.3 (5.6)	3.9 (4.6)	3.3 (2.9)	3.3 (1.4)	3.4 (1.8)	2.5 (0.5)	2.4 (0.5)	2.3 (0.3)
			SortMeRNA	2.3 (4.5)	3.3 (4.8)	5.5 (6)	6.5 (5.5)	4.1 (3.1)	4.3 (2.3)	4.4 (1.9)	4.5 (0.5)	4.1 (0.6)	3.9 (0.3)
			Kallisto	1.9 (2.2)	3.3 (2.4)	3.8 (1.7)	5.2 (1.8)	5.3 (1.1)	4.9 (1)	5.6 (1.1)	5.6 (0.5)	5.4 (0.4)	5.5 (0.2)
			USEARCH61	0.9 (1.2)	2.1 (2.8)	3.9 (4.9)	4.7 (3.5)	4 (3.3)	3.5 (1.5)	3.2 (0.8)	2.9 (0.4)	3 (0.3)	2.9 (0.2)
			Mothur NB	9.9 (14.1)	17.1 (10.7)	24.6 (17.6)	20.7 (10.8)	18.4 (8.5)	15.2 (5.4)	15.7 (3.7)	13.7 (2.3)	14.3 (1.9)	12.2 (1.3)
			16S Classifier	135.5 (71.3)	135.4 (53.5)	118.7 (39.8)	123.9 (18.3)	118.3 (18.9)	127 (10)	113.5 (13)	121.8 (9.6)	114.7 (7)	116.3 (3.1)
			SINTAX	2.1 (5.8)	2.2 (3.0)	4.7 (5.7)	4.5 (5.2)	3.7 (4.3)	3.3 (1.6)	3.7 (2.0)	2.7 (0.8)	2.3 (0.5)	2.2 (0.2)
	V4	190	Karp	0.1 (0.1)	0.1 (0.3)	0.5 (1.9)	0.2 (<0.1)	0.5 (0.5)	0.4 (0.1)	0.6 (0.5)	0.5 (0.2)	0.6 (0.2)	0.6 (0.1)
			Karp-Collapse	<0.1 (0.1)	0.1 (0.3)	0.4 (1.9)	<0.1 (<0.1)	0.3 (0.6)	0.3 (0.3)	0.4 (0.6)	0.2 (0.2)	0.3 (0.2)	0.2 (0.1)
			UCLUST	4.1 (25)	0.3 (1)	0.9 (3.7)	4.6 (10.2)	1.5 (1.8)	0.5 (0.8)	2.3 (4.1)	1.7 (1)	1.5 (0.8)	1.7 (0.5)
			SortMeRNA	2.2 (11.1)	0.4 (1)	1.3 (3.8)	7.6 (17.5)	1.6 (1.7)	1.6 (1.6)	4.4 (5)	3.1 (1.6)	2.9 (1)	3 (0.5)
			Kallisto	1.7 (1.6)	3.9 (2.7)	5.1 (3.2)	4.8 (1.2)	5.9 (1.3)	5.7 (1.1)	6.3 (0.9)	6.3 (0.6)	6.1 (0.7)	6.3 (0.2)
			USEARCH61	4.4 (24.8)	0.3 (1)	1 (3.7)	5.1 (10.1)	1.4 (1.8)	0.7 (0.9)	3.9 (5.1)	2.7 (1.3)	2.8 (1.1)	2.6 (0.5)
			Mothur NB	20.4 (10.5)	30.9 (25.5)	27.5 (9.8)	31.2 (11.8)	27.3 (5.2)	26 (6.2)	21.3 (5.6)	19.7 (2.9)	16.5 (2.6)	14.1 (1.3)
			16S Classifier	46.6 (18.2)	63.7 (48.9)	27.4 (26)	29.2 (30.5)	19 (24.2)	9.4 (31.3)	6.8 (27)	4 (29.1)	4.1 (27.3)	1.9 (26.9)
			SINTAX	0.3 (1.2)	0.2 (0.8)	0.1 (0.1)	3.2 (9.2)	1.1 (1.8)	0.3 (0.4)	2.9 (5.0)	1.2 (1.2)	1.8 (0.9)	1.4 (0.4)

SE=Single-end, PE=Paired-end

Table 18: **Per family error rates, 100,000 reads**

Read Length	Region	Samples	Method	Shannon Diversity									
				[0,0.7)	[0.7,1.4)	[1.4,2)	[2,2.7)	[2.7,3.4)	[3.4,4.1)	[4.1,4.8)	[4.8,5.5)	[5.5,6.2)	[6.2,6.9]
301bp PE	Full gene	170	Karp	0.2 (0.3)	0.7 (1.2)	0.5 (0.3)	0.7 (0.7)	1 (0.7)	1.3 (0.9)	1.6 (0.5)	1.3 (0.2)	1.4 (0.1)	1.6 (0.1)
			Karp-Collapse	0.1 (0.2)	0.4 (0.9)	0.2 (0.2)	0.5 (0.7)	1 (1.4)	0.6 (1)	1 (0.8)	0.6 (0.3)	0.5 (0.1)	0.5 (0.1)
			UCLUST	<0.1 (0.1)	0.2 (0.4)	1.5 (4.9)	1.6 (3.3)	1.7 (1.8)	1.6 (2)	1.5 (1.4)	0.7 (0.4)	1 (0.5)	0.7 (0.2)
			SortMeRNA	0.8 (1.7)	1.7 (4.2)	2.1 (4.8)	2.3 (3)	3.2 (2.4)	2.8 (1.8)	3.4 (2)	3 (1.1)	2.5 (0.4)	2.2 (0.3)
			Kallisto	28.2 (35.2)	55.7 (39.3)	73.3 (33.7)	71.9 (17.7)	71.2 (12.4)	84.9 (15.5)	83.7 (9.7)	82.1 (5.5)	81.4 (7)	79.2 (3)
			USEARCH61	<0.1 (0.1)	0.2 (0.2)	0.2 (0.4)	0.6 (1.1)	1.5 (2)	0.8 (1.1)	1.5 (1.1)	0.8 (0.4)	0.7 (0.2)	0.9 (0.2)
			Mothur NB	6.8 (13.2)	14.1 (12.5)	12 (9.8)	17.6 (11.4)	23.4 (8.1)	15.5 (6.9)	19.2 (4.9)	14.1 (3.8)	15.1 (1.9)	12.6 (1.1)
			16S Classifier	94.4 (76.4)	109.3 (60.1)	128.3 (30.1)	105.9 (33)	105.8 (16.5)	101.6 (15.4)	96.7 (5.4)	93.3 (7.4)	90.9 (3.8)	93.4 (2.4)
			SINTAX	0.1 (0.1)	0.4 (1.2)	1.5 (4.8)	2.8 (4.4)	2.6 (3.6)	2.2 (2.1)	2.0 (1.3)	1.4 (0.8)	1.5 (0.6)	1.2 (0.2)
	V4	190	Karp	0.3 (0.6)	0.6 (0.6)	0.9 (1.1)	1 (1)	1.7 (3)	0.8 (0.2)	0.9 (0.2)	1 (0.2)	1.2 (0.2)	1.4 (0.1)
			Karp-Collapse	<0.1 (<0.1)	<0.1 (0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (0.1)	0.1 (0.3)	<0.1 (<0.1)	0.1 (0.1)	<0.1 (<0.1)	0.1 (<0.1)
			UCLUST	<0.1 (<0.1)	<0.1 (0.1)	0.3 (2)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	0.5 (1.6)	0.1 (0.1)	0.2 (0.2)
			SortMeRNA	<0.1 (<0.1)	0.5 (2.1)	<0.1 (0.1)	0.1 (0.1)	0.5 (1.4)	0.6 (1.1)	1.7 (1.8)	1.1 (1.1)	0.6 (0.2)	0.5 (0.2)
			Kallisto	43.8 (44.7)	72.1 (43.5)	73.5 (26.6)	84.2 (25.6)	90 (22.8)	92.7 (17.2)	88.5 (13.6)	103.5 (11.4)	98.7 (5.2)	99.1 (3.9)
			USEARCH61	3.3 (20.9)	0.1 (0.3)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	0.5 (0.9)	<0.1 (0.1)	0.5 (0.5)	0.5 (0.6)	0.3 (0.2)
			Mothur NB	39.9 (61.6)	42.6 (46.9)	26.6 (9.8)	28.2 (8.8)	27.4 (8.3)	23.5 (4.6)	23.9 (6.3)	22 (4.4)	17.3 (2.6)	15 (1.4)
			16S Classifier	19.3 (52)	33.2 (52.9)	36.1 (39.2)	33.8 (22.5)	31.7 (19.2)	26.6 (14.7)	29.4 (5.1)	29.9 (6.5)	26.9 (3.1)	25.1 (1.9)
			SINTAX	<0.1 (<0.1)	6.2 (24.7)	0.4 (1.7)	0.8 (2.3)	1.5 (3.3)	0.5 (1.1)	0.7 (1.3)	1.1 (0.9)	1.4 (0.9)	1.1 (0.4)

SE=Single-end, PE=Paired-end

Table 19: **Per order error rates, 100,000 reads**

Read Length	Region	Samples	Method	Shannon Diversity									
				[0,0.7)	[0.7,1.4)	[1.4,2)	[2,2.7)	[2.7,3.4)	[3.4,4.1)	[4.1,4.8)	[4.8,5.5)	[5.5,6.2)	[6.2,6.9]
75bp SE	Full gene	130	Karp	15.4 (11.2)	13.1 (10.8)	10.2 (4.4)	11.2 (3.1)	12.1 (3.9)	8.7 (2.2)	8.4 (1.6)	5.4 (0.6)	5.2 (0.5)	4.1 (0.4)
			Karp-Collapse	36.1 (17.9)	29.4 (16.5)	23.4 (7.2)	26.1 (7.4)	25.6 (8.5)	18.5 (3.5)	17 (3)	11.2 (1)	9.9 (1)	7.4 (0.5)
			UCLUST	28.9 (21.3)	23.1 (17.8)	17.1 (7.4)	19.7 (7.4)	20.4 (8.2)	14.1 (3.3)	13.5 (2.8)	8.9 (1)	7.7 (0.9)	5.7 (0.3)
			SortMeRNA	32.1 (23.6)	26.6 (18.9)	22.1 (7.9)	24.4 (6.8)	27.4 (9.3)	20.4 (3.7)	20 (2.8)	13.6 (1.3)	12.8 (1)	10.1 (0.7)
			Kallisto	28.4 (15.3)	24.5 (14.2)	19.3 (6)	21.1 (5.1)	19.9 (5.2)	15.4 (2.9)	14.7 (2.5)	10 (0.9)	9.4 (0.7)	7.4 (0.3)
			USEARCH61	30.4 (22.6)	24.8 (19.3)	19 (8.3)	20.3 (7.1)	21.2 (8.3)	14.8 (3.3)	14.3 (3)	9.5 (1)	8.1 (0.9)	6.1 (0.4)
			Mothur NB	46 (52.8)	43.3 (28.7)	39.3 (20.9)	33.2 (13.1)	49.5 (10.8)	37.2 (4.6)	36.3 (4.8)	35.6 (2.3)	34.4 (2.5)	33.7 (1.5)
			16S Classifier	178.7 (24.8)	174 (16.1)	153.3 (18.7)	151.9 (26.1)	152.7 (10.7)	144.4 (8.1)	141.2 (13.7)	139 (7.5)	141.7 (3.2)	142.5 (1.7)
			SINTAX	12.3 (14.1)	20.0 (12.1)	15.1 (7.6)	19.5 (7.9)	24.2 (8.6)	20.9 (4.2)	22.3 (2.9)	20.0 (1.0)	20.1 (0.9)	20.6 (0.6)
	V4	130	Karp	3.8 (4.7)	5.4 (4.5)	5.5 (3.2)	5.5 (3.4)	5.9 (1.4)	5.7 (1.4)	4.6 (0.8)	4.3 (0.5)	3.8 (0.4)	3.3 (0.2)
			Karp-Collapse	16.8 (12.9)	14.9 (12.1)	16.1 (8.4)	12.5 (4.8)	14.4 (2.4)	13.8 (3.7)	10.4 (2)	9.2 (2.1)	7.1 (0.6)	5.2 (0.4)
			UCLUST	6.5 (9)	8.2 (7.9)	7.7 (5.8)	6.1 (4.9)	8.2 (2)	8.5 (4.4)	5.5 (1.2)	6 (1.4)	4.4 (0.6)	3.5 (0.3)
			SortMeRNA	7.4 (9.6)	8.4 (7.1)	10.5 (6)	9.7 (5)	12.3 (1.6)	13.5 (3.2)	11.5 (2.6)	11.4 (2.1)	10.3 (0.6)	9.2 (0.6)
			Kallisto	14 (11.7)	13.8 (10.6)	14.5 (7.4)	12.6 (4.9)	13.6 (1.9)	13.1 (3.9)	11.1 (1.5)	10.1 (0.8)	9.1 (0.7)	7.8 (0.4)
			USEARCH61	9 (14.2)	9 (9.5)	8.7 (6.8)	7.5 (5.8)	8.6 (1.9)	8.6 (3.9)	6.5 (1.8)	6.4 (1.6)	4.9 (0.5)	3.8 (0.4)
			Mothur NB	31.4 (31.7)	41 (39.3)	48.5 (25)	42.3 (15)	46.9 (13.2)	47.5 (6)	39.7 (6.2)	40.1 (6.1)	35.6 (2)	34.1 (1.2)
			16S Classifier	148.1 (61.4)	126.5 (44.3)	130.9 (37.7)	112.6 (29.9)	118.5 (12.5)	116 (14.4)	106 (17.6)	108.1 (12.9)	103.8 (4.9)	102.4 (2.8)
			SINTAX	6.7 (6.0)	14.2 (10.4)	14.9 (8.1)	14.5 (7.2)	19.4 (3.2)	18.9 (4.8)	17.7 (1.9)	18.4 (2.8)	17.1 (0.5)	16.6 (0.5)
151bp PE	Full gene	130	Karp	0.5 (1.1)	0.6 (1)	0.8 (0.7)	1.2 (0.8)	1.2 (0.9)	0.8 (0.4)	1.2 (0.3)	1 (0.2)	1 (0.1)	1 (0.1)
			Karp-Collapse	0.5 (1.1)	0.6 (1)	0.9 (1)	1.1 (0.8)	1.8 (2.5)	0.8 (0.5)	1.4 (0.6)	1 (0.3)	1 (0.2)	1 (0.1)
			UCLUST	0.4 (0.3)	1 (1)	1.3 (1.1)	2.8 (3.8)	2.3 (2.9)	1.6 (0.9)	1.8 (0.5)	1.6 (0.4)	1.5 (0.2)	1.5 (0.2)
			SortMeRNA	2.2 (4.2)	1.1 (0.8)	2.3 (1.9)	3.6 (4.2)	2.5 (2.9)	2.4 (1)	2.4 (0.4)	3.1 (0.6)	3 (0.4)	3.2 (0.3)
			Kallisto	2.2 (2.1)	3.9 (2.3)	5 (2.4)	6.1 (1.8)	5.8 (1.3)	5.7 (0.9)	6.6 (0.8)	6 (0.6)	6.1 (0.5)	6.4 (0.2)
			USEARCH61	1.4 (2.1)	1.4 (0.8)	2.2 (1.6)	3.7 (3.6)	3.2 (3.8)	2.1 (0.5)	2.4 (0.5)	2.1 (0.3)	2.2 (0.3)	2.1 (0.3)
			Mothur NB	6.3 (9.5)	8.3 (7.1)	13.7 (15.2)	10 (7.5)	11.2 (7.3)	8 (3.1)	6.5 (2.8)	6.9 (2.9)	6.1 (1.3)	5.4 (1.1)
			16S Classifier	145.4 (60.4)	122.3 (49.7)	111.6 (48.1)	103.4 (35.7)	111.8 (16.8)	110 (19.6)	100.7 (14.8)	105.4 (9.8)	96.7 (6.3)	99.8 (1.8)
			SINTAX	0.3 (0.5)	1.0 (1.8)	1.0 (1.4)	2.5 (4.2)	2.2 (4.5)	1.2 (1.1)	1.1 (0.4)	1.3 (0.8)	1.1 (0.3)	1.2 (0.3)
	V4	190	Karp	0.1 (<0.1)	0.2 (0.3)	0.6 (2.2)	0.2 (<0.1)	0.5 (0.5)	0.4 (0.1)	0.6 (0.4)	0.5 (0.2)	0.5 (0.1)	0.6 (0.1)
			Karp-Collapse	<0.1 (0.1)	0.1 (0.4)	0.5 (2.3)	<0.1 (<0.1)	0.3 (0.6)	0.2 (0.2)	0.3 (0.5)	0.2 (0.2)	0.2 (0.2)	0.2 (0.1)
			UCLUST	2 (11.2)	0.4 (1.2)	1 (3.3)	5.7 (11.1)	2.7 (2.2)	2.6 (3.1)	2.9 (3.7)	2.2 (1.1)	2 (1.2)	2.1 (0.4)
			SortMeRNA	2.4 (11.2)	0.5 (1.2)	2.4 (6.7)	8.5 (17.9)	2.6 (1.5)	3 (2.9)	4.3 (4.4)	3.3 (1.4)	3 (1.2)	3 (0.3)
			Kallisto	2.1 (1.7)	5.3 (2.8)	7.1 (3.5)	5.7 (1.4)	6.9 (1.3)	7.5 (1.9)	7.5 (1.2)	7.4 (0.8)	7.3 (0.5)	7.5 (0.4)
			USEARCH61	2.3 (11.2)	0.5 (1.2)	2.4 (6.7)	6.1 (11)	2.6 (1.5)	2.7 (3)	4.1 (4.1)	3 (1.3)	3 (1.3)	2.7 (0.2)
			Mothur NB	30 (32.7)	33.9 (24.7)	32.3 (22)	32.7 (8)	27.3 (9.2)	22.6 (4.3)	17.3 (4.9)	14.2 (2.8)	11.1 (1.9)	9.4 (0.7)
			16S Classifier	23.2 (55.8)	26.5 (40.5)	14.1 (21.7)	23.7 (30.5)	17.5 (12.3)	23.7 (9.7)	24.7 (5.9)	23.2 (5)	23.7 (4)	22.3 (2.1)
			SINTAX	0.3 (1.2)	<0.1 (<0.1)	<0.1 (0.1)	3.0 (9.2)	2.2 (4.9)	0.4 (0.6)	1.2 (3.2)	0.7 (1.1)	0.7 (0.8)	0.4 (0.2)

SE=Single-end, PE=Paired-end

Table 20: **Per order error rates, 100,000 reads**

Read Length	Region	Samples	Method	Shannon Diversity									
				[0,0.7)	[0.7,1.4)	[1.4,2)	[2,2.7)	[2.7,3.4)	[3.4,4.1)	[4.1,4.8)	[4.8,5.5)	[5.5,6.2)	[6.2,6.9]
301bp PE	Full gene	170	Karp	0.3 (0.3)	0.7 (1.2)	0.5 (0.6)	0.6 (0.6)	1 (0.7)	1.1 (0.8)	1.2 (0.5)	1.1 (0.2)	1.2 (0.2)	1.3 (0.1)
			Karp-Collapse	0.1 (0.3)	0.4 (0.9)	0.1 (0.1)	0.3 (0.7)	0.7 (1.4)	0.2 (0.2)	0.6 (0.8)	0.3 (0.2)	0.3 (0.1)	0.3 (0.1)
			UCLUST	<0.1 (0.1)	<0.1 (0.1)	0.2 (0.4)	0.1 (0.1)	0.7 (1.7)	0.1 (0.2)	0.6 (1.1)	0.2 (0.2)	0.5 (0.6)	0.3 (0.1)
			SortMeRNA	0.3 (0.6)	0.4 (0.7)	0.6 (0.8)	0.4 (0.4)	1.2 (1.8)	1.2 (1)	2 (1.8)	1.4 (0.3)	1.7 (0.3)	1.7 (0.1)
			Kallisto	42.3 (36)	67.4 (36.1)	81.8 (32.3)	84.9 (17.8)	96.7 (21)	92 (16.2)	97.9 (17.3)	92.2 (4)	92.3 (8)	88.6 (2.7)
			USEARCH61	<0.1 (0.1)	<0.1 (0.2)	<0.1 (0.1)	<0.1 (<0.1)	0.9 (2)	0.2 (0.2)	0.8 (1.1)	0.3 (0.2)	0.3 (0.2)	0.4 (0.1)
			Mothur NB	4.1 (13.1)	9.6 (14.1)	5.9 (6.7)	5.3 (6.5)	13.2 (11.2)	8.8 (3.7)	8.1 (2.3)	7 (2.3)	6.4 (0.9)	5.1 (0.7)
			16S Classifier	91.3 (66.2)	107.7 (65.1)	108.4 (38)	90 (39.3)	98.2 (23.3)	99.2 (16.9)	90.3 (6.4)	89.8 (11.6)	86.7 (4.4)	86.8 (2.7)
			SINTAX	<0.1 (<0.1)	0.1 (0.3)	0.2 (0.5)	0.6 (1.5)	1.4 (3.4)	0.6 (0.6)	1.1 (1.1)	0.6 (0.4)	0.7 (0.7)	0.6 (0.2)
	V4	190	Karp	0.3 (0.7)	0.7 (0.6)	1 (1.1)	1.1 (1.1)	1.6 (3)	0.9 (0.5)	0.9 (0.2)	1 (0.2)	1.1 (0.1)	1.2 (0.1)
			Karp-Collapse	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	0.1 (<0.1)
			UCLUST	<0.1 (<0.1)	<0.1 (0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (0.1)	0.1 (0.1)
			SortMeRNA	<0.1 (<0.1)	<0.1 (0.1)	<0.1 (<0.1)	0.1 (0.1)	1.2 (3.5)	0.2 (0.1)	0.5 (0.7)	0.5 (0.2)	0.4 (0.1)	0.2 (0.1)
			Kallisto	59.1 (48.6)	98.6 (39.5)	84.3 (30.2)	110.3 (17.5)	105.9 (21.4)	114.4 (10.4)	113.3 (13.4)	120.4 (10.8)	117.4 (6.1)	117.2 (4.3)
			USEARCH61	<0.1 (<0.1)	<0.1 (0.3)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	0.1 (0.3)	0.1 (0.2)	0.1 (0.1)
			Mothur NB	40.3 (58.1)	38.3 (41.9)	22 (11.8)	25.9 (11.6)	21.5 (8.8)	21 (4.6)	16.9 (3.9)	15.6 (4.6)	11.3 (1.9)	8.4 (1.5)
			16S Classifier	2.5 (4.8)	25.6 (42.5)	18.2 (31.1)	26 (31.1)	22.9 (26.2)	20.3 (11.4)	26.1 (7.3)	23 (5.3)	20.2 (4.4)	20.4 (2.7)
			SINTAX	<0.1 (<0.1)	0.4 (1.8)	<0.1 (<0.1)	0.1 (0.3)	<0.1 (<0.1)	<0.1 (<0.1)	0.2 (0.5)	0.3 (0.5)	0.6 (0.7)	0.4 (0.2)

SE=Single-end, PE=Paired-end

Table 21: **Per class error rates, 100,000 reads**

Read Length	Region	Samples	Method	Shannon Diversity									
				[0,0.7)	[0.7,1.4)	[1.4,2)	[2,2.7)	[2.7,3.4)	[3.4,4.1)	[4.1,4.8)	[4.8,5.5)	[5.5,6.2)	[6.2,6.9]
75bp SE	Full gene	130	Karp	10.2 (6.3)	6.2 (4.3)	6 (2)	7 (2.5)	5.3 (1.3)	4.3 (0.9)	3.5 (0.9)	2.5 (0.3)	2.6 (0.3)	2.1 (0.3)
			Karp-Collapse	26.6 (12.5)	18 (8.9)	16.2 (4)	17.1 (5.1)	12.8 (2)	10.9 (2)	8.6 (1.5)	6.2 (0.6)	5.7 (0.7)	4.2 (0.4)
			UCLUST	19 (18.1)	10.4 (7.6)	9.7 (3.3)	11.2 (4.6)	7.8 (2.2)	6.4 (1.6)	5.1 (1.1)	3.5 (0.5)	3.2 (0.3)	2.3 (0.2)
			SortMeRNA	22.2 (19.7)	14.3 (8.2)	14.6 (4.4)	16.4 (5.7)	13 (3)	12.1 (1.9)	10.9 (1.4)	8 (0.8)	8.2 (1)	6.8 (0.5)
			Kallisto	20.8 (9.4)	15 (6.1)	13.4 (3.7)	14.5 (4.5)	10.7 (1.6)	9.3 (1.7)	8.2 (1.6)	5.9 (0.5)	5.9 (0.2)	5.2 (0.2)
			USEARCH61	20 (18.7)	11.4 (8.1)	11.1 (3.7)	11.7 (4.4)	8.3 (1.9)	7 (1.5)	5.6 (1.3)	3.8 (0.5)	3.5 (0.3)	2.5 (0.3)
			Mothur NB	35.6 (47.1)	33.6 (24.1)	34 (20.5)	29.8 (12.7)	38.4 (5.7)	30.8 (4.4)	30.6 (4.3)	34.4 (2.7)	34.5 (2.3)	33.1 (1.1)
			16S Classifier	165.6 (33.8)	158.3 (24.1)	137.5 (28.4)	131.5 (35.1)	146 (11.4)	129.8 (11.7)	123.7 (14)	122.9 (8.7)	125.4 (3.1)	125.5 (2.8)
			SINTAX	8.6 (14.3)	7.3 (6.2)	7.8 (3.9)	11.0 (5.2)	9.9 (2.7)	9.8 (2.8)	9.4 (2.0)	8.7 (0.8)	8.9 (0.6)	8.8 (0.5)
	V4	130	Karp	1.4 (1.5)	2.5 (1.5)	3.8 (2)	3.3 (2.7)	3 (1)	2.9 (0.9)	2.7 (0.4)	2.4 (0.6)	2.2 (0.2)	2.2 (0.3)
			Karp-Collapse	9.9 (7.2)	7.9 (4.6)	10.7 (5.7)	7.5 (3.2)	7.6 (1.3)	6.9 (2.2)	5.3 (1.1)	5 (1.7)	3.6 (0.4)	3 (0.3)
			UCLUST	2 (2.3)	2.4 (2.1)	3.9 (3)	2.3 (0.4)	2.7 (0.8)	3.2 (1.2)	2 (0.2)	2.6 (1.1)	1.7 (0.3)	1.6 (0.2)
			SortMeRNA	2.8 (1.8)	3.8 (2.4)	6.7 (2.7)	6.1 (2.1)	6.8 (1.2)	7.7 (2.4)	7.3 (1.5)	7.2 (1.8)	6.9 (0.6)	6.8 (0.5)
			Kallisto	7.9 (6.1)	7.5 (3.1)	9.9 (4.7)	7.9 (2)	7.9 (1)	7.4 (1)	7 (0.7)	6.7 (0.7)	6.8 (0.3)	6.4 (0.4)
			USEARCH61	2.3 (3.2)	2.5 (2)	4.4 (3.7)	2.8 (0.6)	3 (0.7)	3.2 (1.4)	2.5 (0.5)	2.8 (1)	1.9 (0.2)	1.7 (0.2)
			Mothur NB	27.7 (39.5)	23.3 (15.4)	36.3 (20.4)	35.7 (13.4)	35 (11.2)	36.5 (7.4)	33.9 (5.3)	34.1 (3)	32.3 (2.5)	32 (0.9)
			16S Classifier	138.8 (59.2)	119.1 (42.7)	120.8 (33.7)	105 (28.9)	108.9 (13.3)	106.2 (12.8)	94.3 (16)	96.6 (11.2)	94 (3.3)	93.3 (2.1)
			SINTAX	3.4 (3.3)	6.0 (5.0)	9.7 (5.2)	6.7 (2.7)	9.0 (2.0)	8.2 (1.9)	7.1 (1.4)	8.0 (2.0)	6.3 (0.5)	6.3 (0.4)
151bp PE	Full gene	130	Karp	0.5 (1.1)	0.6 (1)	0.7 (0.7)	1 (0.8)	0.9 (0.6)	0.7 (0.3)	1 (0.3)	0.8 (0.2)	0.7 (0.1)	0.7 (0.1)
			Karp-Collapse	0.5 (1.1)	0.6 (1)	0.7 (0.7)	0.8 (0.7)	0.9 (0.7)	0.5 (0.2)	1 (0.4)	0.8 (0.3)	0.7 (0.1)	0.7 (0.1)
			UCLUST	0.4 (0.3)	0.7 (0.4)	0.9 (0.5)	0.9 (0.2)	1.2 (0.3)	1.1 (0.2)	1 (0.2)	1.1 (0.4)	0.9 (0.1)	0.9 (0.1)
			SortMeRNA	1.1 (3)	0.8 (0.5)	1.1 (0.5)	1.2 (0.3)	1.2 (0.4)	1.6 (0.4)	1.7 (0.2)	2 (0.6)	1.9 (0.4)	2.3 (0.2)
			Kallisto	2.2 (2.1)	3.5 (2.2)	4.9 (2.4)	5.9 (1.8)	5.4 (1.4)	5.3 (0.8)	6.1 (1)	5.5 (0.8)	5.5 (0.5)	5.8 (0.2)
			USEARCH61	0.7 (0.7)	1.3 (0.7)	1.6 (0.9)	2.1 (0.7)	1.6 (0.5)	1.6 (0.4)	1.6 (0.4)	1.4 (0.3)	1.3 (0.2)	1.3 (0.2)
			Mothur NB	5.5 (6.2)	7 (6.6)	7.6 (6)	5.8 (5.3)	5.3 (3.3)	4.1 (1.5)	4.4 (1.8)	3.7 (1.2)	3.2 (0.9)	2.7 (0.5)
			16S Classifier	139.2 (59.7)	107.7 (49.1)	97.5 (43.2)	90.9 (34.2)	98 (17.6)	98.8 (17.4)	87.9 (14)	90.9 (9.1)	83.4 (6.8)	86.4 (1.8)
			SINTAX	0.2 (0.3)	0.2 (0.2)	0.3 (0.3)	0.3 (0.1)	0.3 (0.1)	0.3 (0.1)	0.3 (0.1)	0.3 (0.4)	0.2 (0.1)	0.2 (<0.1)
	V4	190	Karp	0.1 (<0.1)	0.2 (0.3)	0.6 (2.2)	0.2 (<0.1)	0.5 (0.5)	0.3 (0.1)	0.5 (0.5)	0.4 (0.2)	0.4 (0.1)	0.4 (0.1)
			Karp-Collapse	<0.1 (0.1)	0.1 (0.4)	0.5 (2.3)	<0.1 (<0.1)	0.3 (0.6)	0.1 (0.1)	0.3 (0.5)	0.2 (0.2)	0.2 (0.1)	0.2 (0.1)
			UCLUST	0.3 (0.9)	0.4 (1.2)	1 (3.3)	5.7 (11.1)	2.1 (1.5)	2.5 (3)	2.6 (2.9)	2 (1.1)	1.8 (1.1)	1.7 (0.4)
			SortMeRNA	0.7 (1.4)	0.5 (1.2)	2.4 (6.7)	8.4 (17.8)	2.6 (1.5)	3 (2.9)	3.9 (3.7)	3 (1.2)	2.6 (1.1)	2.5 (0.3)
			Kallisto	2 (1.7)	5.2 (2.8)	7 (3.5)	5.6 (1.4)	6.6 (1.4)	6.9 (1.7)	7.1 (1.3)	7 (0.8)	6.8 (0.4)	7 (0.3)
			USEARCH61	0.6 (1.4)	0.5 (1.2)	2.3 (6.7)	6 (11)	2.6 (1.5)	2.7 (3)	3.7 (3.5)	2.7 (1.1)	2.5 (1.2)	2.3 (0.3)
			Mothur NB	29.3 (32.6)	25.5 (7)	25.3 (10.8)	29.9 (8.1)	21.6 (8.2)	16.6 (4.2)	12.6 (3.7)	9.1 (1.9)	7.2 (1.5)	5.8 (0.7)
			16S Classifier	22.1 (56)	21.1 (41.2)	10.7 (19.4)	13.4 (14.5)	13.1 (12.3)	19.8 (8.9)	17.8 (6.2)	18 (4.4)	16.4 (3.1)	16.1 (1.8)
			SINTAX	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	2.9 (8.9)	1.5 (4.3)	0.3 (0.5)	0.6 (1.3)	0.1 (0.1)	0.3 (0.4)	0.2 (0.1)

SE=Single-end, PE=Paired-end

Table 22: **Per class error rates, 100,000 reads**

Read Length	Region	Samples	Method	Shannon Diversity									
				[0,0.7)	[0.7,1.4)	[1.4,2)	[2,2.7)	[2.7,3.4)	[3.4,4.1)	[4.1,4.8)	[4.8,5.5)	[5.5,6.2)	[6.2,6.9]
301bp PE	Full gene	170	Karp	0.3 (0.3)	0.7 (1.2)	0.5 (0.6)	0.6 (0.5)	0.7 (0.4)	0.9 (0.7)	0.7 (0.2)	0.8 (0.1)	0.8 (0.2)	0.8 (0.1)
			Karp-Collapse	0.1 (0.2)	0.3 (0.9)	0.1 (0.1)	0.3 (0.6)	0.1 (0.1)	0.2 (0.2)	0.1 (0.1)	0.2 (0.1)	0.2 (0.1)	0.1 (<0.1)
			UCLUST	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)
			SortMeRNA	0.2 (0.2)	0.3 (0.6)	0.4 (0.7)	0.2 (0.2)	0.4 (0.1)	0.8 (0.9)	0.7 (0.1)	0.9 (0.2)	1 (0.2)	1.3 (0.1)
			Kallisto	42 (36)	66.4 (37.6)	79.9 (32.1)	83.3 (17.9)	91.8 (23.1)	87.5 (16.9)	91.5 (19.1)	84.8 (7.7)	85.7 (7.6)	82.2 (5.4)
			USEARCH61	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (0.1)	<0.1 (<0.1)	<0.1 (<0.1)
			Mothur NB	4.1 (13.1)	7.4 (13.6)	4.4 (6.6)	3.4 (4.9)	7.9 (10.6)	6.2 (2.8)	4.4 (1.5)	4 (2.1)	3.6 (0.8)	2.9 (0.6)
			16S Classifier	86.1 (65.9)	96.4 (63.8)	97.5 (33.9)	75.5 (32)	84.9 (19.8)	84.9 (15)	74.5 (8.2)	75.1 (10.3)	72.4 (3.8)	72.4 (2.6)
			SINTAX	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	0.1 (0.4)	0.1 (0.3)	0.1 (0.1)	<0.1 (0.1)	<0.1 (<0.1)
	V4	190	Karp	0.3 (0.7)	0.6 (0.6)	0.9 (1.1)	1 (1.1)	1.6 (3)	0.8 (0.5)	0.7 (0.2)	0.7 (0.2)	0.8 (0.2)	0.8 (0.1)
			Karp-Collapse	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)
			UCLUST	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)
			SortMeRNA	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	0.1 (<0.1)	1.2 (3.5)	0.2 (<0.1)	0.2 (<0.1)	0.3 (0.1)	0.3 (0.1)	0.2 (<0.1)
			Kallisto	58.9 (48.5)	95.1 (42.1)	81.9 (31.7)	107.7 (16)	103.4 (23.8)	110.3 (13.7)	109.6 (14.7)	114.6 (14.8)	113.5 (7.3)	111.5 (5.3)
			USEARCH61	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)
			Mothur NB	39.2 (57.3)	35.5 (38.5)	17.4 (9.9)	21.3 (8.6)	19.1 (7.8)	16.3 (4.5)	12.1 (2.5)	10.1 (3)	6.8 (1.5)	4.8 (1.1)
			16S Classifier	1.8 (4.9)	11.4 (31.7)	13.6 (28.7)	18.2 (28.6)	14.8 (24.3)	13.1 (10.7)	16 (7.6)	15.7 (4.5)	13.8 (3.9)	14.3 (1.7)
			SINTAX	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	<0.1 (<0.1)	0.2 (0.5)	<0.1 (<0.1)	0.2 (0.3)	0.1 (0.1)

SE=Single-end, PE=Paired-end