Supplementary Table S1 | Mock community construction.

Strain	**Size (bp)**	**GC content (%)**
Roseobacter denitrificans OCh114	4,330,000	58.9
Staphylococcus epidermidis ATCC 12228	2,560,000	32.1
Polaromonas naphthalenivorans CJ2	5,370,000	61.7
Chromobacterium violaceum ATCC 12472	4,750,000	64.8
Corynebacterium glutamicum ATCC 13032	3,310,000	53.8
Klebsiella pneumoniae KCTC 2242	5,460,000	57.3
Pseudomonas stutzeri ATCC 17588	4,550,000	63.9
Arthrobacter chlorophenolicus A6	4,980,000	66.0
Escherichia coli Strain W	5,010,000	50.8
Escherichia coli KCTC 2571	4,750,000	50.9
Total : 10 strains		

Supplementary Table S2 | The highest/lowest Z values and frequent sequences flanking substitution errors. <S> denotes substitution errors.

Substitution error	**NGS system**	**Highest Z value**	**Most frequent sequence**	**Lowest Z value**	**Least frequent sequence**
Mono-nucleotides	GS junior	C<S>G	C<S>G	C<S>C	C<S>C
	FLX+	C<S>G	C<S>G	C<S>C	G<S>G
	PGM	T<S>A	C<S>T	C<S>C	G<S>G
	MiSeq	C<S>G	G<S>G	T<S>G	A<S>T
	GAII	C<S>G	G<S>T	A<S>T	C<S>C
	HiSeq	G<S>G	G<S>G	T<S>G	T<S>G
Di-nucleotides	GS junior	TG<S>CG	TT<S>AT	AT<S>AT	CT<S>AG
	FLX+	TG<S>CG	TT<S>CA	AT<S>AT	CT<S>AG
	PGM	TC<S>CC	CC<S>TC	CC<S>CC	CT<S>AG
	MiSeq	GG<S>GA	GG<S>GA	GG<S>CC	TA<S>TA
	GAII	AG<S>TG	GG<S>TT	CC<S>CG	AC<S>CG
	HiSeq	AC<S>GT	GG<S>GG	TA<S>AG	TA<S>CG
Tri-nucleotides	GS junior	CCG<S>ATC, ACA<S>CCG	TTT<S>ATC, TTT<S>CAG	ACA<S>CCC, GGG<S>CCT	TAT<S>ACG, ACA<S>GTG, etc
	FLX+	CAC<S>AAT, ATT<S>GTG	CAC<S>AAT, GGG<S>TGA	ACA<S>CCC, AAA<S>CCC	CTC<S>TAG, TCT<S>AGT, etc
	PGM	TGC<S>CCA, ATT<S>GTG	GCC<S>TCA, ACC<S>TCA	GCA<S>CGA, AAA<S>TTT	CTA<S>ATG, TGT<S>TAG
	MiSeq	CGG<S>CAA, GTG<S>TCC	GGG<S>GAA, GGG<S>TCA	GGG<S>GAT, GTG<S>TCT	CTA<S>GAG, TAC<S>TAG
	GAII	ATT<S>TAC, GTA<S>AAT	TTT<S>TTT, TTT<S>TAA	TTT<S>TAC, GTA<S>AAA	CGT<S>GGG, GAC<S>CTA
	HiSeq	TGG<S>CCA, CAC<S>GTG	ATG<S>TCA, TGA<S>CAT	AGA<S>CAT, TGG<S>CCT	TTA<S>GCG, CGT<S>ACG
Tetra-nucleotides	GS junior	ACCG<S>CCTC, CAAT<S>TATT	TCCG<S>CCTA, GTGG<S>CCTG	GAAT<S>TATT, AATA<S>ATTC	GCCG<S>CCTA, TCGG<S>CCTG, etc

	FLX+	TCAC<S>AATA, TATT<S>GTGA	TCAC<S>AATA, TATT<S>GTGA	GTGG<S>GCAA, TTGC<S>CCAC	ATAC<S>GTAT, ACTG<S>TGTC, etc
	PGM	ACAG<S>TCCC, TAGG<S>CGGA	TATT<S>AATA, TCAC<S>AATA	TCCG<S>CCTG, TATT<S>GTGC	TAGG<S>CGGT, TAGA<S>CATG, etc
	MiSeq	GGGG<S>GAAG, CTTC<S>CCCC	GGGG<S>GAAG, CGGG<S>TCAC	GTTC<S>CCCC, CTTC<S>CCCA	AGGG<S>CCCT, GTCT<S>CTAG, etc
	GAII	ACAG<S>TGTG, GATC<S>CGTG	GATC<S>CGTG, ACAG<S>TGTG	CACC<S>AAGG, ATAA<S>GGCT	CCTT<S>GGTG, GCCT<S>GGGT, etc
	HiSeq	ACAC<S>GTGA, TCAC<S>GTGT	GATG<S>TCAC, GTGA<S>CATC	TCAC<S>GTGA, CAGG<S>CCTG	GGCG<S>TCGT, AGCG<S>TCGG

Supplementary Table S3 | Error rates and lengths of the longest homopolymers.

NGS system	All reads	Length of a homopolymer				
		<4 bp	≥4 bp & ≤5 bp	≥6 bp & ≤7 bp	≥8 bp & ≤9 bp	>9 bp
GS junior	0.50%	0.72%	0.51%	0.75%	1.02%	1.67%
FLX+	0.72%	0.86%	0.78%	0.90%	1.01%	1.26%
PGM	2.67%	2.64%	2.68%	2.95%	3.71%	4.05%
MiSeq	0.95%	0.73%	0.87%	0.96%	1.78%	2.08%
GAII	0.60%	0.58%	0.57%	0.55%	1.55%	5.08%
HiSeq	0.67%	1.31%	0.59%	0.49%	0.55%	0.97%

“Length of a homopolymer” indicates the length of the longest homopolymer in each read.