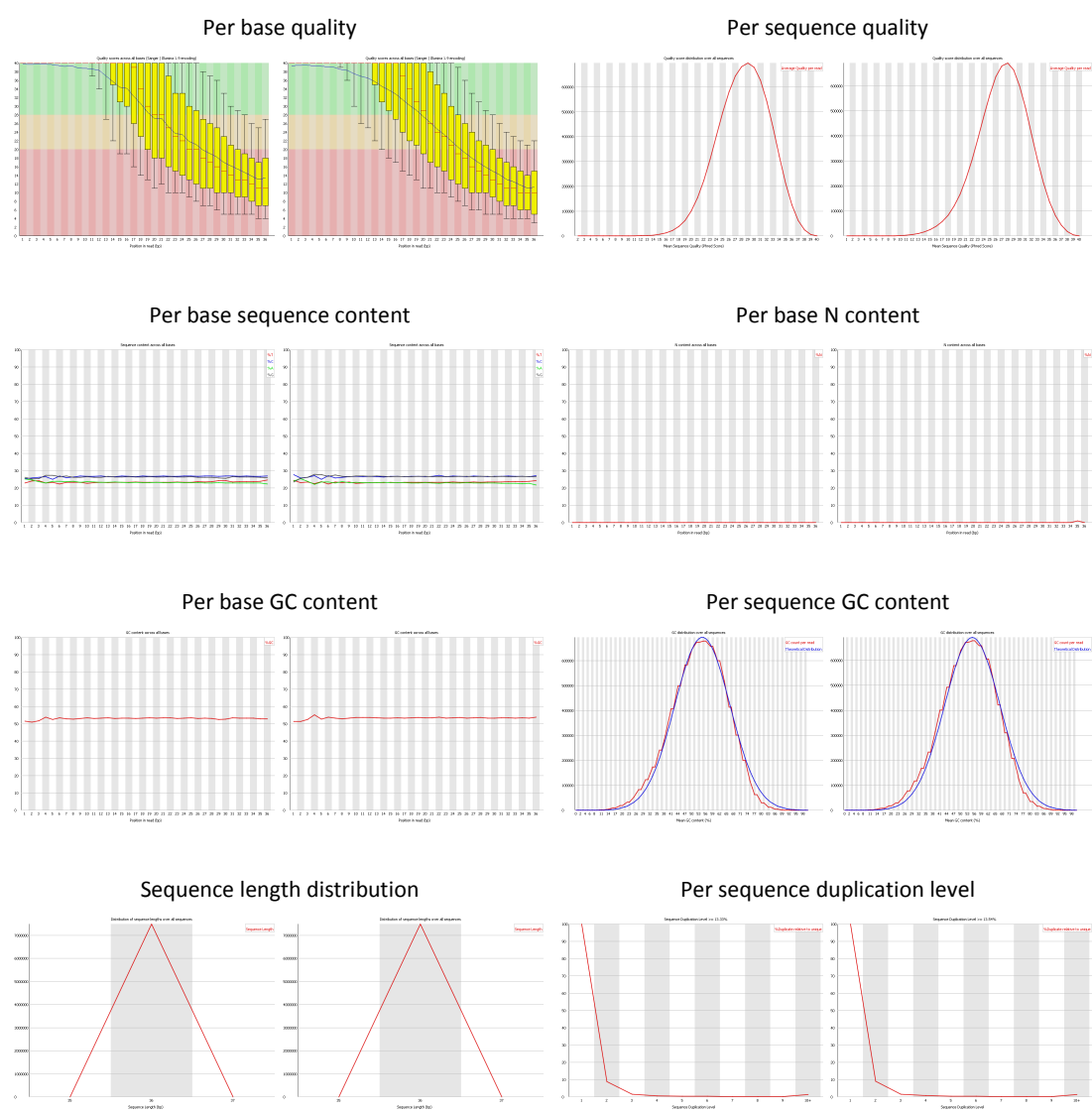


No overrepresented sequences

id69_6.fastq - 7479444 reads, 36 nt, 53% GC (pair 1), 53% GC (pair 2)



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

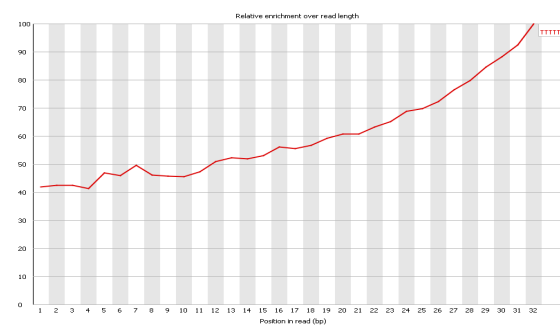
Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

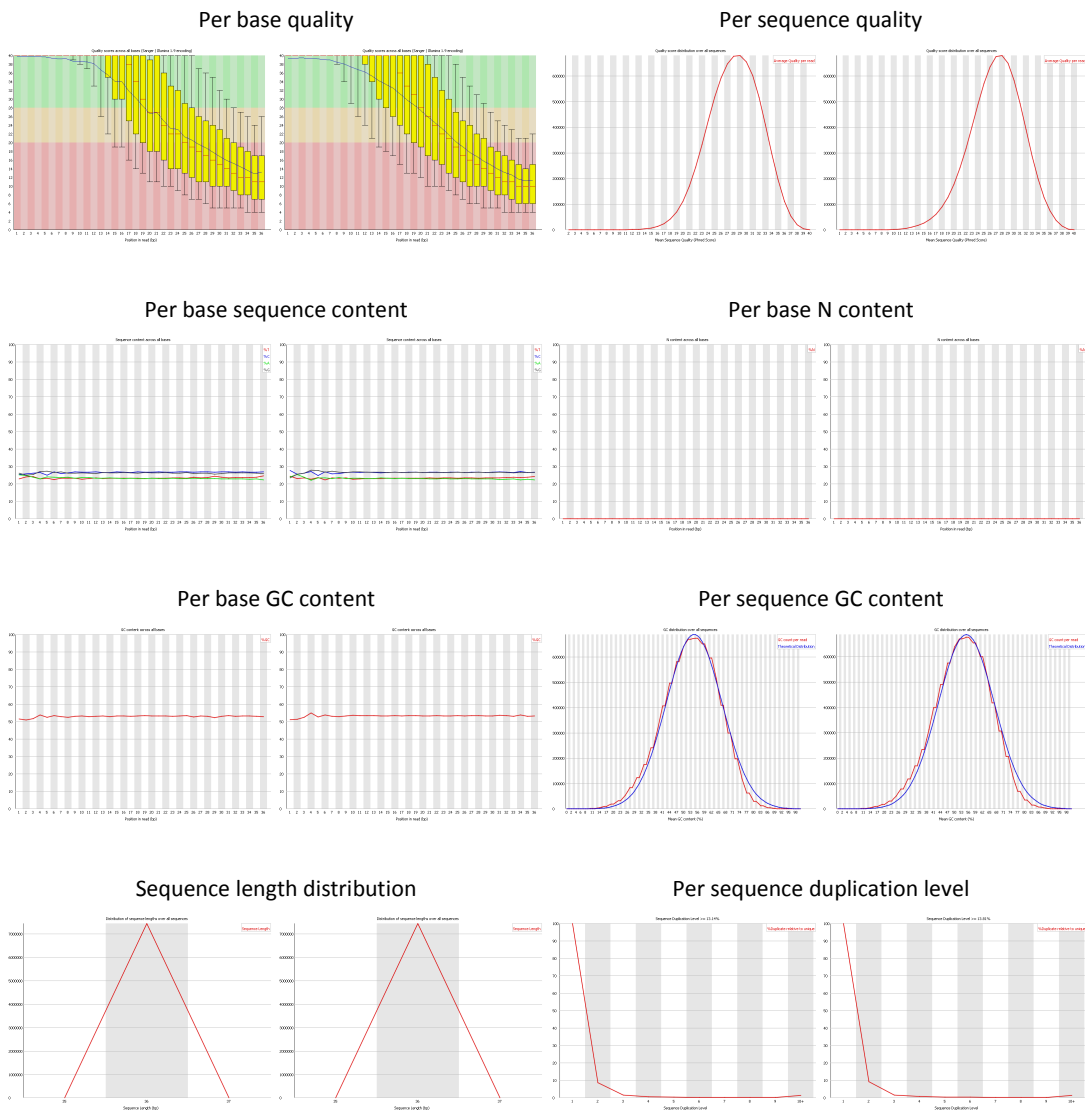
Overrepresented Kmers (pair 1)

Overrepresented Kmers (pair 2)

No overrepresented sequences



id69_7.fastq - 7442889 reads, 36 nt, 53% GC (pair 1), 53% GC (pair 2)



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

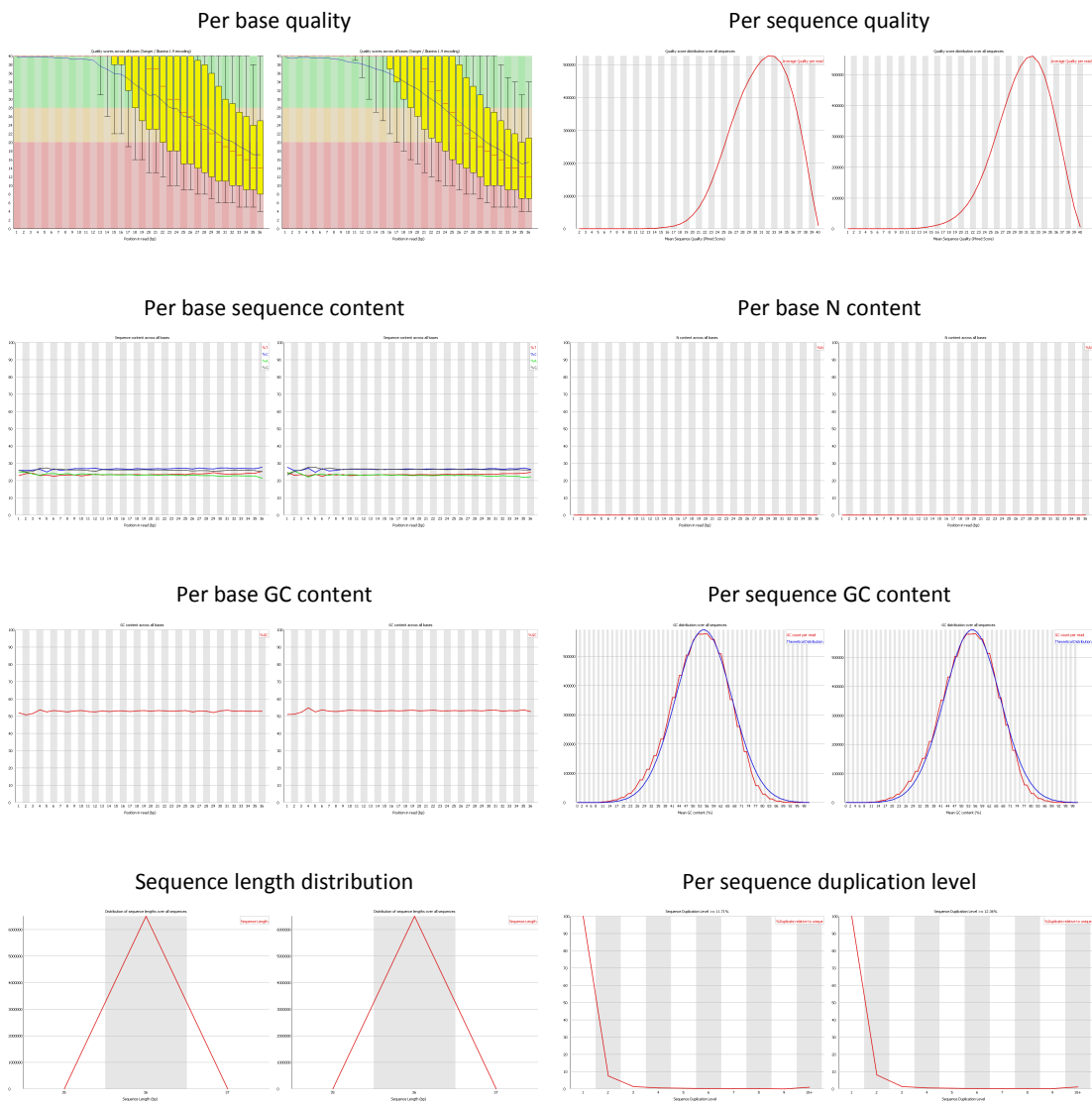
Overrepresented Kmers (pair 1)

No overrepresented sequences

Overrepresented Kmers (pair 2)

No overrepresented sequences

id69_8.fastq - 6491737 reads, 36 nt, 52% GC (pair 1), 53% GC (pair 2)

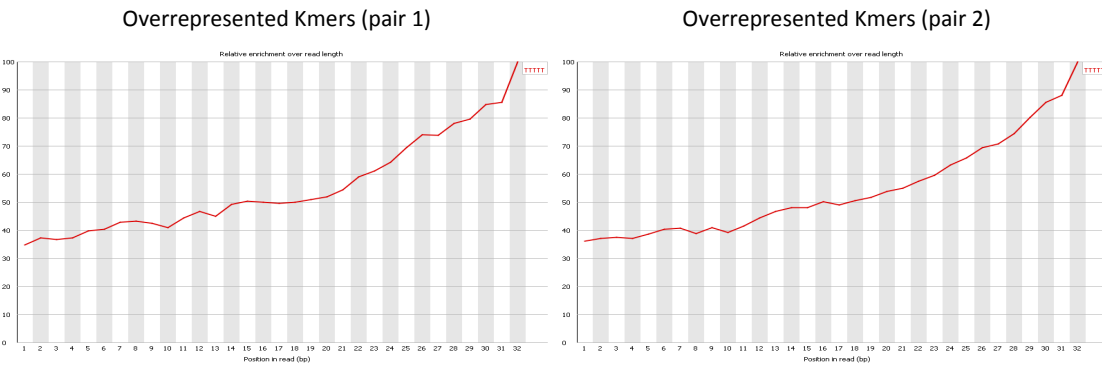


Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

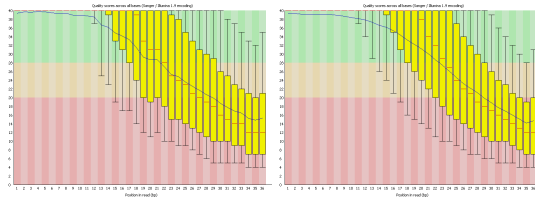
Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

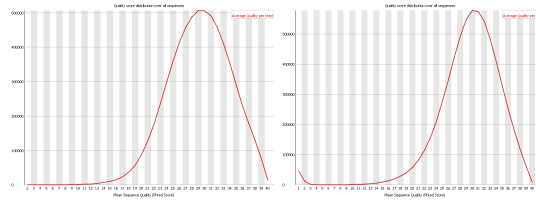


id71_1.fastq - 6447580 reads, 36 nt, 52% GC (pair 1), 52% GC (pair 2)

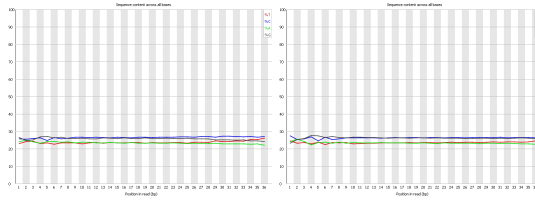
Per base quality



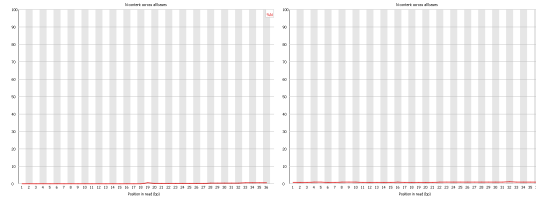
Per sequence quality



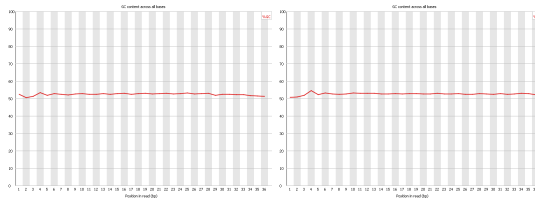
Per base sequence content



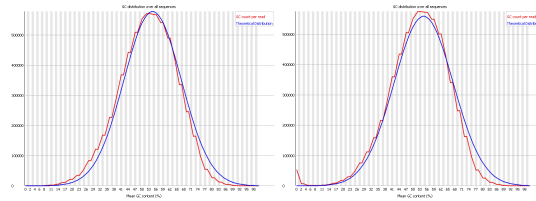
Per base N content



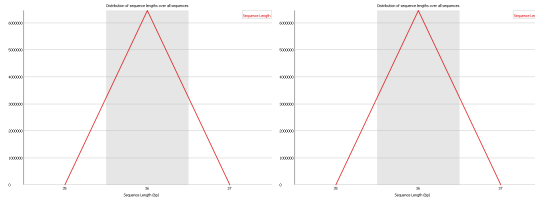
Per base GC content



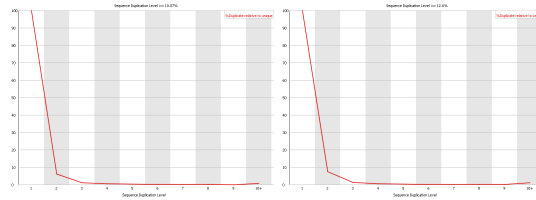
Per sequence GC content



Sequence length distribution



Per sequence duplication level



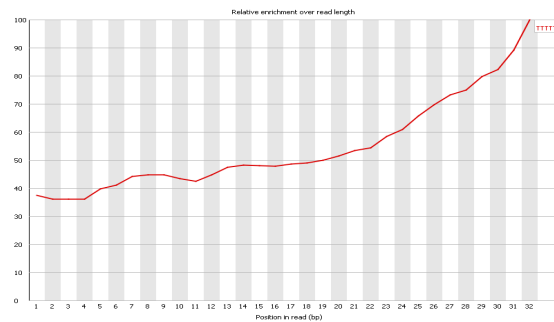
Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

[illegible]

Overrepresented Kmers (pair 1)

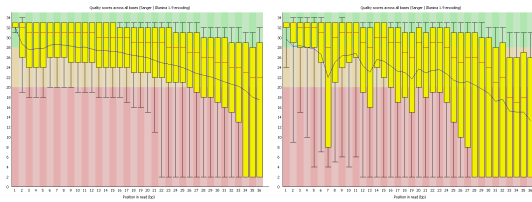


Overrepresented Kmers (pair 2)

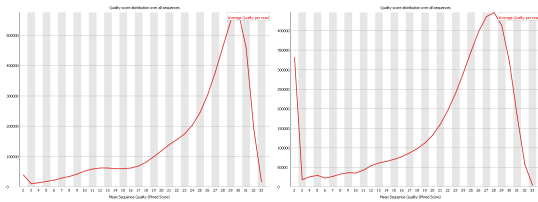
No overrepresented sequences

id80_3.fastq - 4857581 reads, 36 nt, 53% GC (pair 1), 52% GC (pair 2)

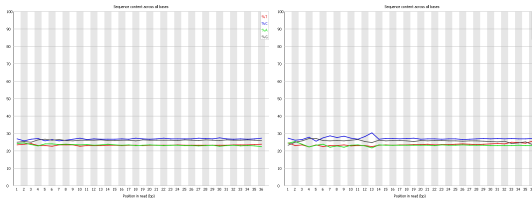
Per base quality



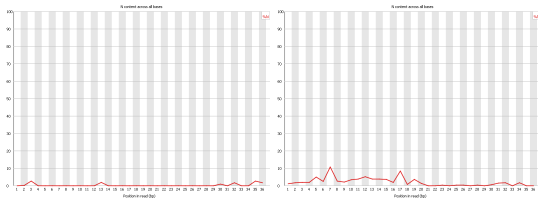
Per sequence quality



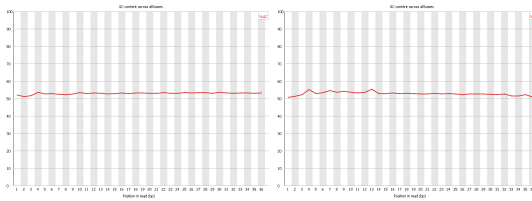
Per base sequence content



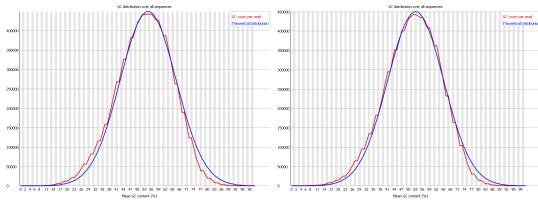
Per base N content



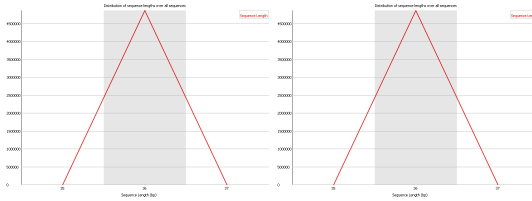
Per base GC content



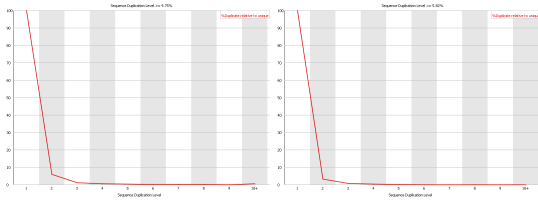
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

No overrepresented sequences

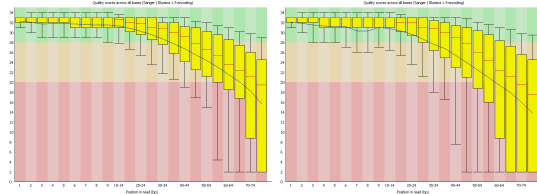
Overrepresented Kmers (pair 2)

No overrepresented sequences

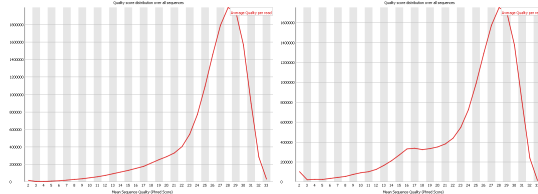
Emco5

id106_4.fastq - 14875367 reads, 76 nt, 49% GC (pair 1), 49% GC (pair 2)

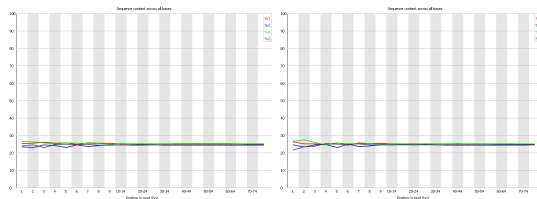
Per base quality



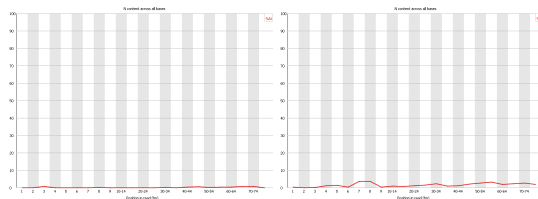
Per sequence quality



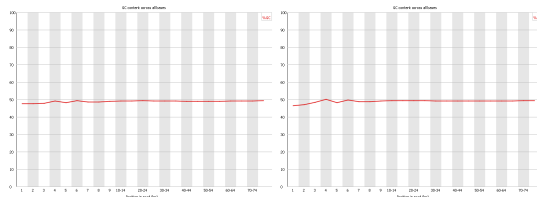
Per base sequence content



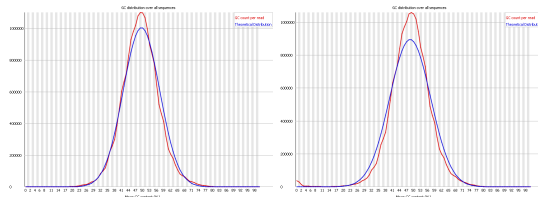
Per base N content



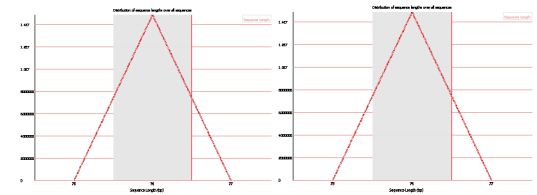
Per base GC content



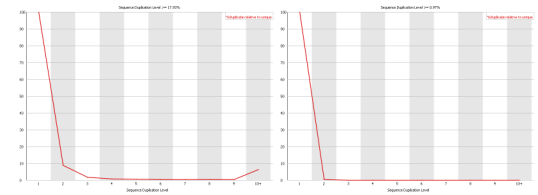
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

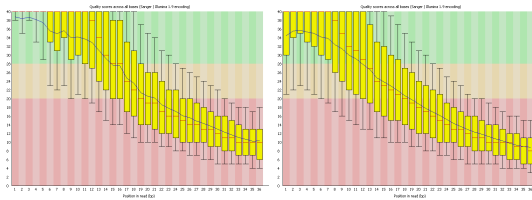
No overrepresented sequences

Overrepresented Kmers (pair 2)

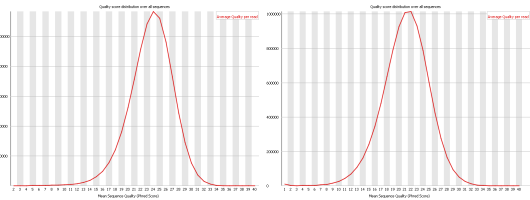
No overrepresented sequences

id62_3.fastq - 9298549 reads, 36 nt, 48% GC (pair 1), 48% GC (pair 2)

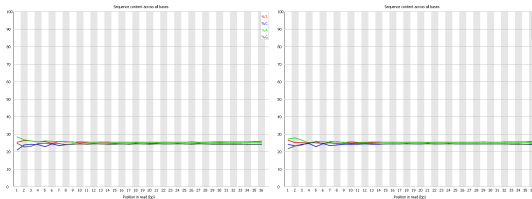
Per base quality



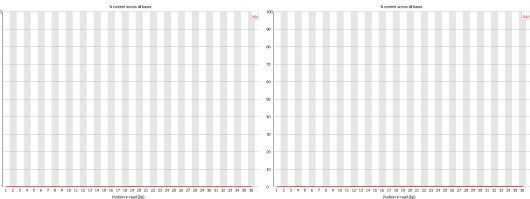
Per sequence quality



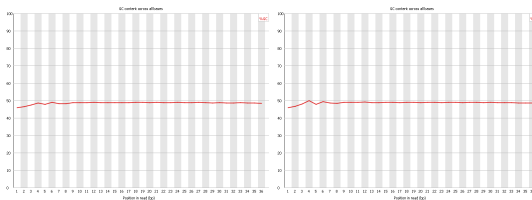
Per base sequence content



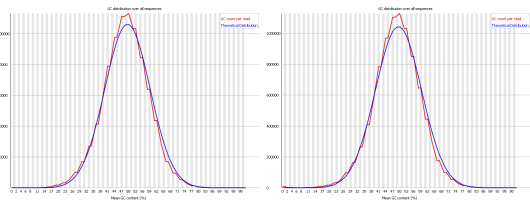
Per base N content



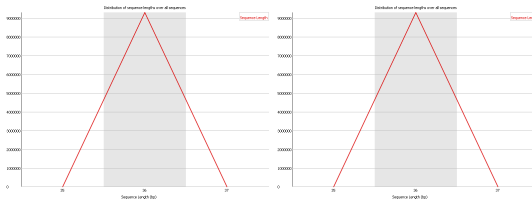
Per base GC content



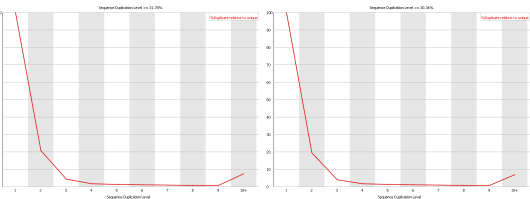
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

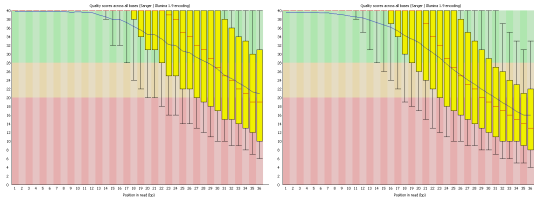
No overrepresented sequences

Overrepresented Kmers (pair 2)

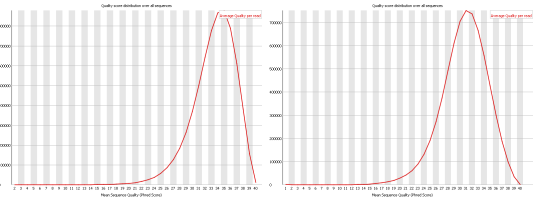
No overrepresented sequences

id64_5.fastq - 6829216 reads, 36 nt, 48% GC (pair 1), 48% GC (pair 2)

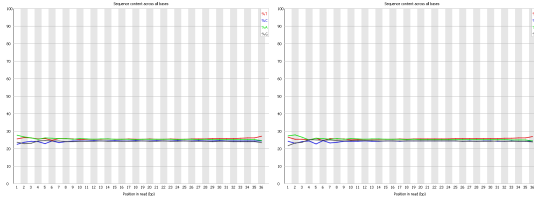
Per base quality



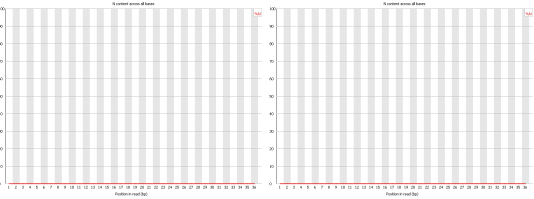
Per sequence quality



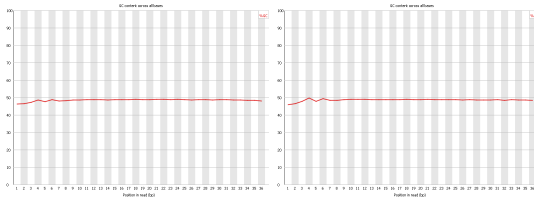
Per base sequence content



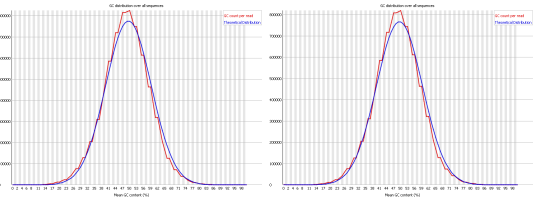
Per base N content



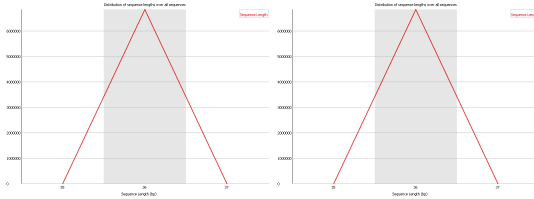
Per base GC content



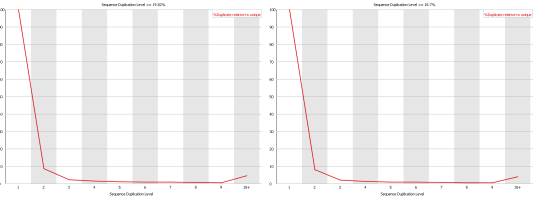
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

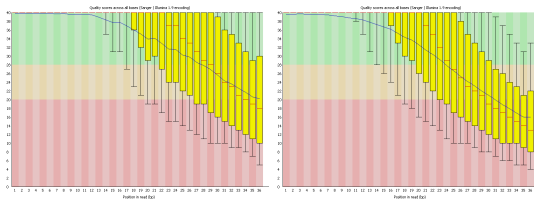
No overrepresented sequences

Overrepresented Kmers (pair 2)

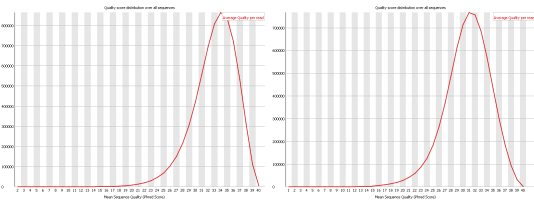
No overrepresented sequences

id64_6.fastq - 6859266 reads, 36 nt, 48% GC (pair 1), 48% GC (pair 2)

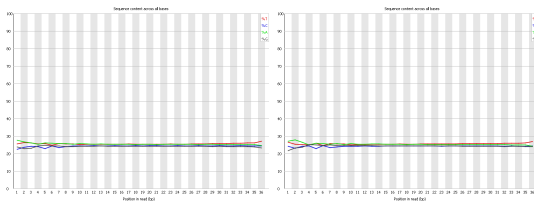
Per base quality



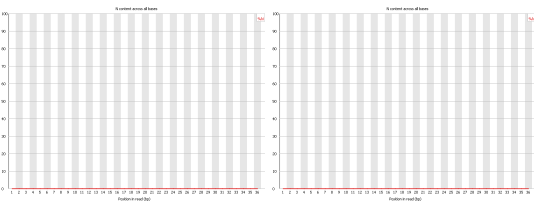
Per sequence quality



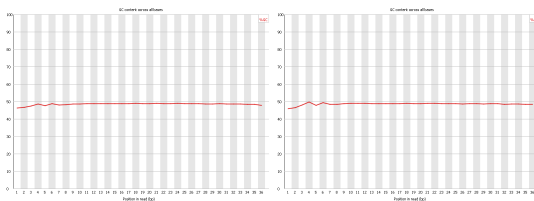
Per base sequence content



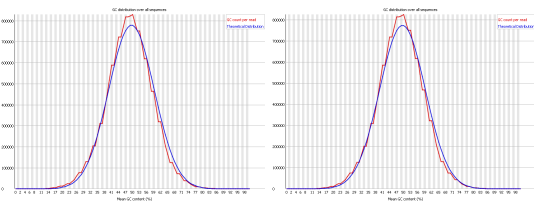
Per base N content



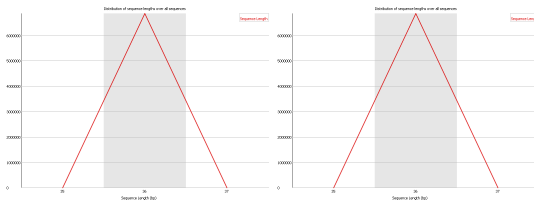
Per base GC content



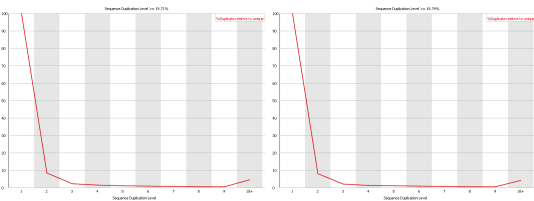
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

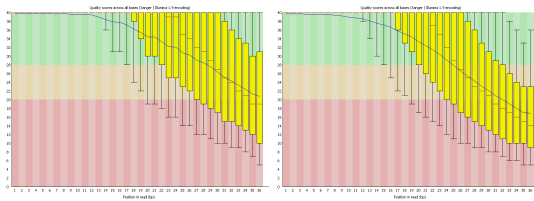
No overrepresented sequences

Overrepresented Kmers (pair 2)

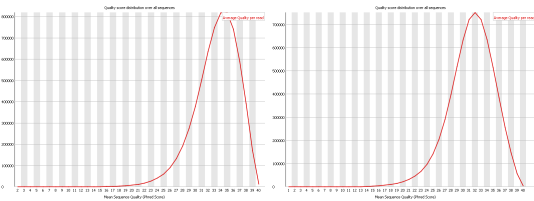
No overrepresented sequences

id64_7.fastq - 6693301 reads, 36 nt, 48% GC (pair 1), 48% GC (pair 2)

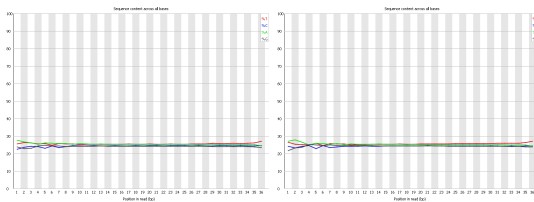
Per base quality



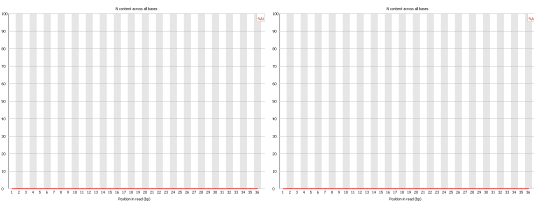
Per sequence quality



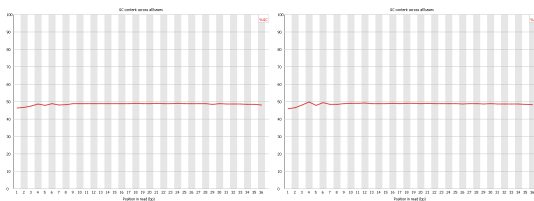
Per base sequence content



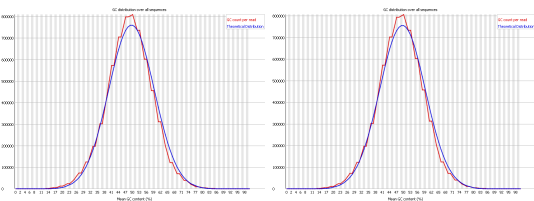
Per base N content



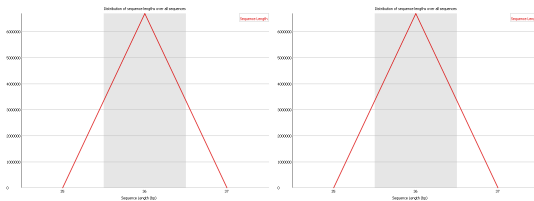
Per base GC content



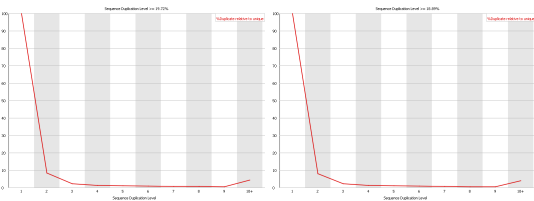
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

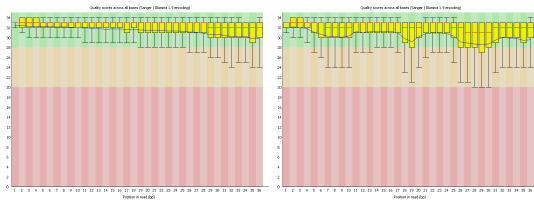
No overrepresented sequences

Overrepresented Kmers (pair 2)

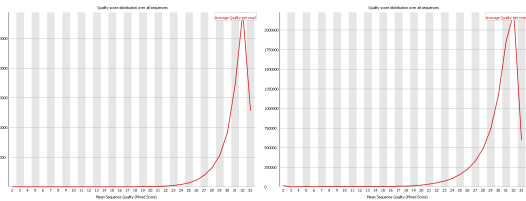
No overrepresented sequences

id88_1.fastq - 8220407 reads, 36 nt, 49% GC (pair 1), 49% GC (pair 2)

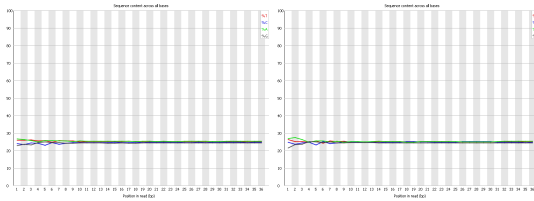
Per base quality



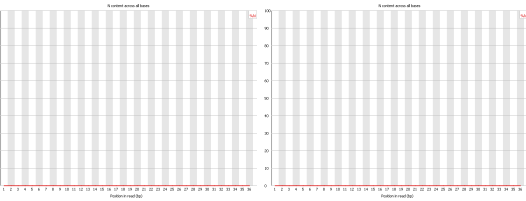
Per sequence quality



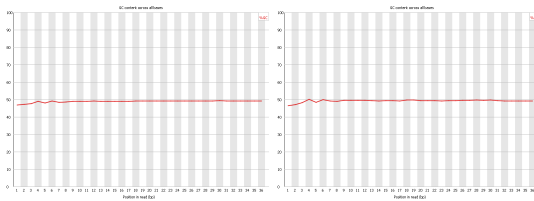
Per base sequence content



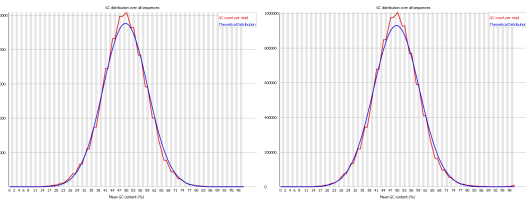
Per base N content



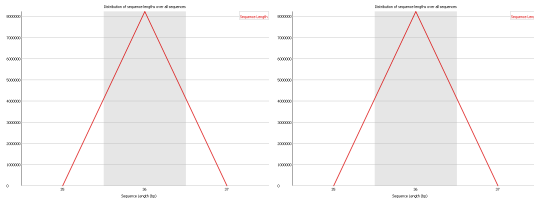
Per base GC content



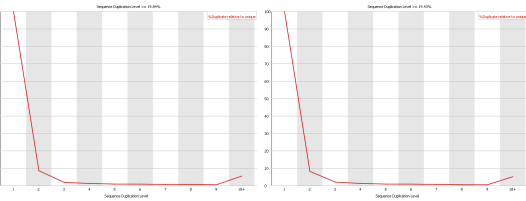
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

CC occurs 10166 times (0.12%) - Source: No Hit

Overrepresented Kmers (pair 1)

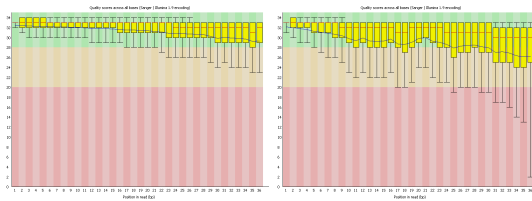
No overrepresented sequences

Overrepresented Kmers (pair 2)

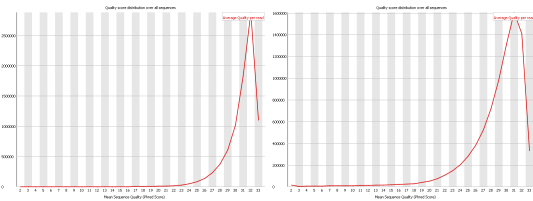
No overrepresented sequences

id88_2.fastq - 8450470 reads, 36 nt, 49% GC (pair 1), 49% GC (pair 2)

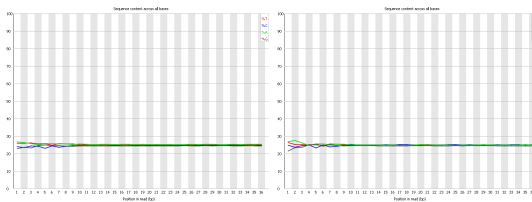
Per base quality



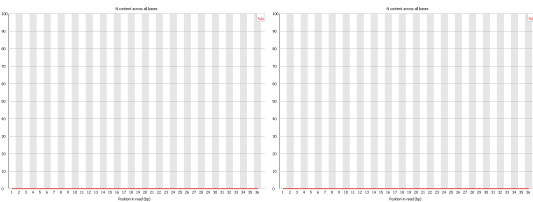
Per sequence quality



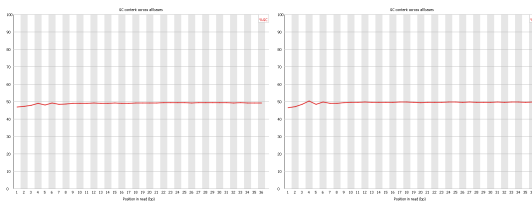
Per base sequence content



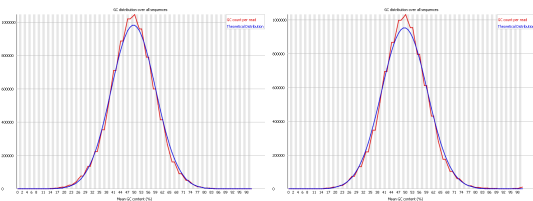
Per base N content



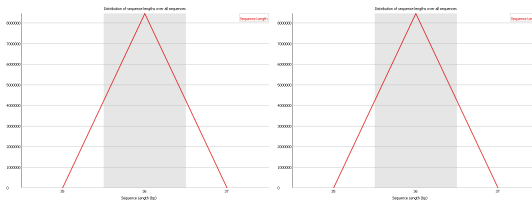
Per base GC content



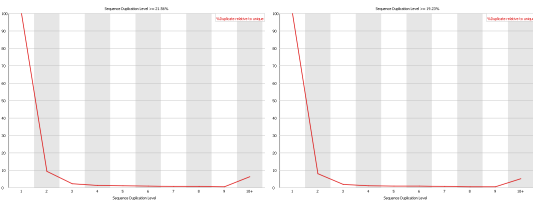
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC occurs 10230 times (0.12%) - Source: No Hit

Overrepresented Kmers (pair 1)

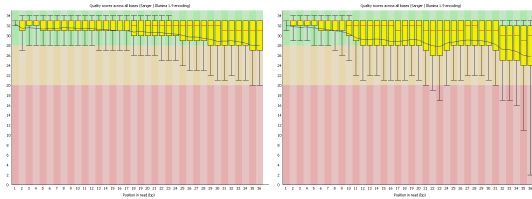
No overrepresented sequences

Overrepresented Kmers (pair 2)

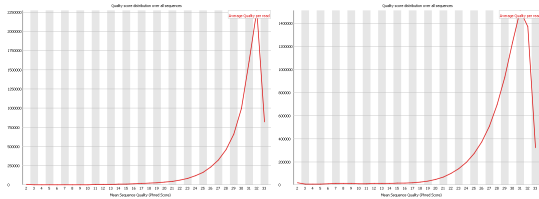
No overrepresented sequences

id88_3.fastq - 8019255 reads, 36 nt, 49% GC (pair 1), 49% GC (pair 2)

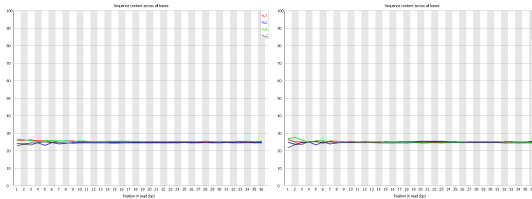
Per base quality



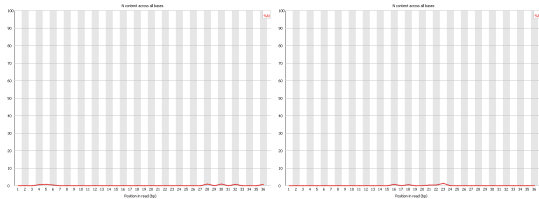
Per sequence quality



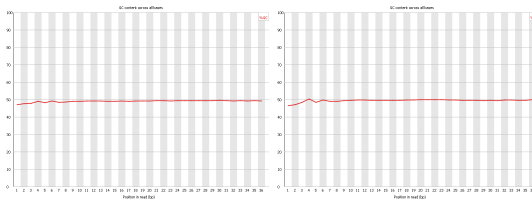
Per base sequence content



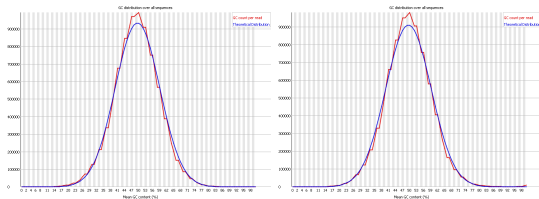
Per base N content



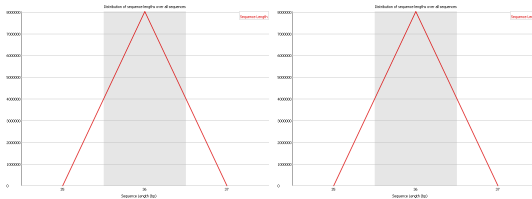
Per base GC content



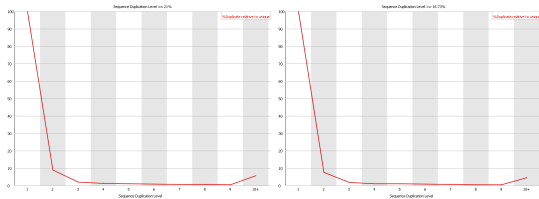
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC occurs 8820 times (0.10%) - Source: No Hit

Overrepresented Kmers (pair 1)

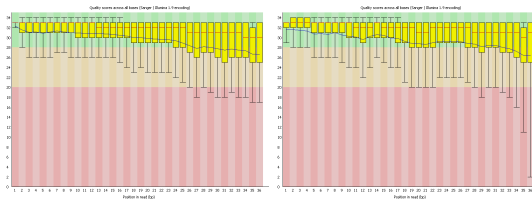
No overrepresented sequences

Overrepresented Kmers (pair 2)

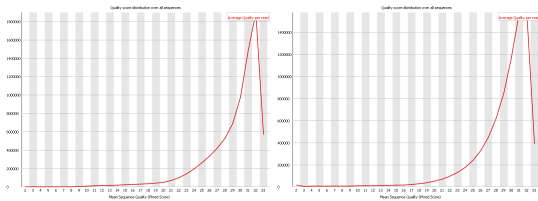
No overrepresented sequences

id88_4.fastq - 7984802 reads, 36 nt, 49% GC (pair 1), 49% GC (pair 2)

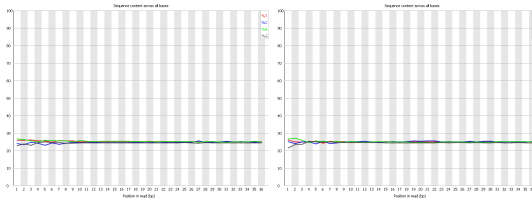
Per base quality



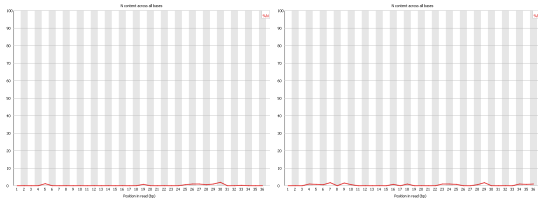
Per sequence quality



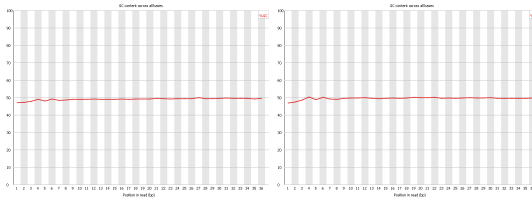
Per base sequence content



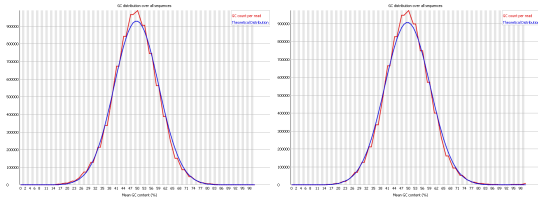
Per base N content



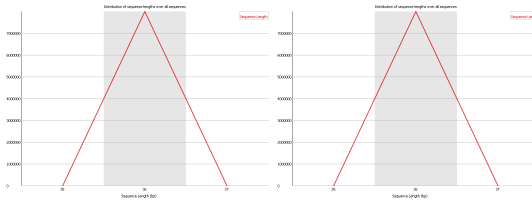
Per base GC content



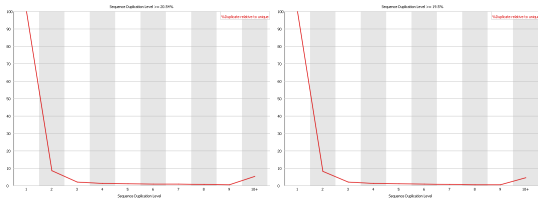
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

CC occurs 8162 times (0.10%) - Source: No Hit

Overrepresented Kmers (pair 1)

No overrepresented sequences

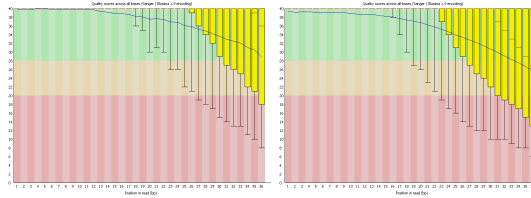
Overrepresented Kmers (pair 2)

No overrepresented sequences

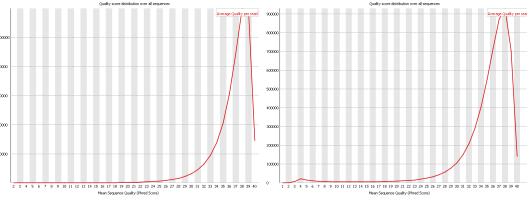
Emoy2

id64_8.fastq - 5522389 reads, 36 nt, 48% GC (pair 1), 48% GC (pair 2)

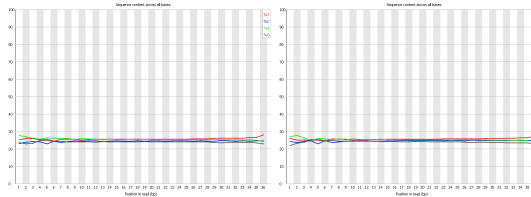
Per base quality



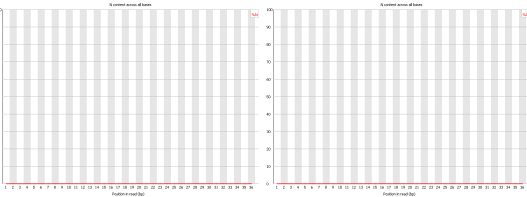
Per sequence quality



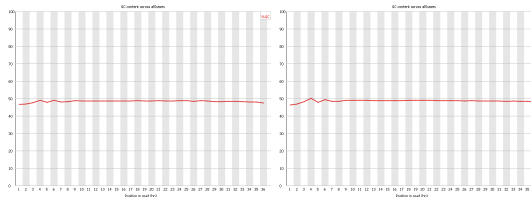
Per base sequence content



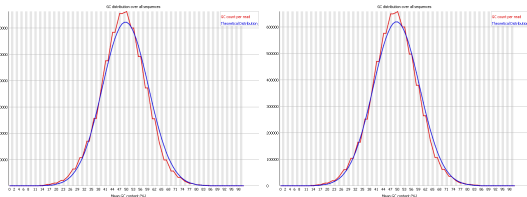
Per base N content



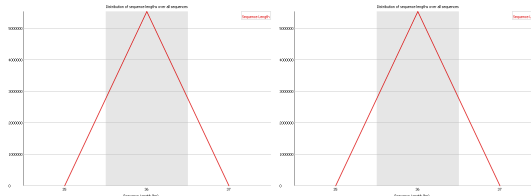
Per base GC content



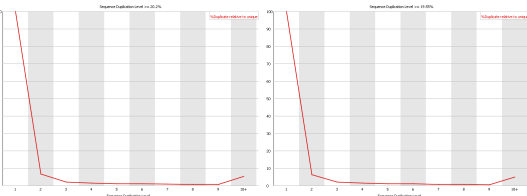
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

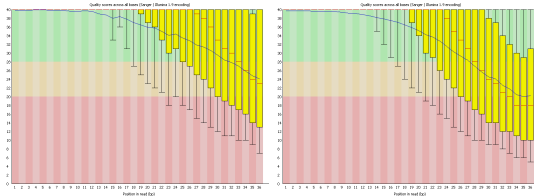
No overrepresented sequences

Overrepresented Kmers (pair 2)

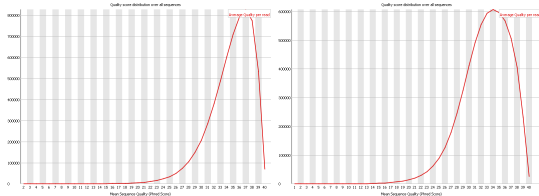
No overrepresented sequences

id66_3.fastq - 6170273 reads, 36 nt, 48% GC (pair 1), 48% GC (pair 2)

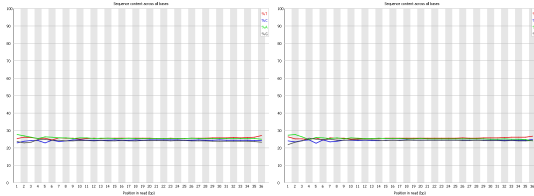
Per base quality



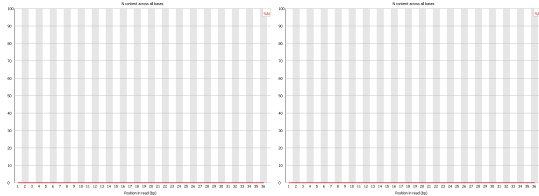
Per sequence quality



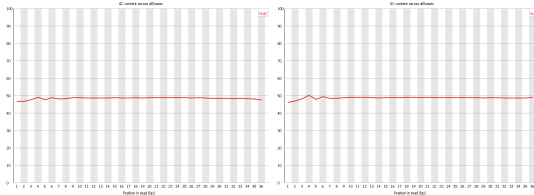
Per base sequence content



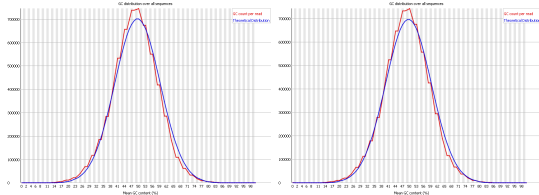
Per base N content



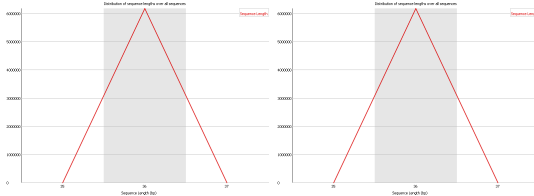
Per base GC content



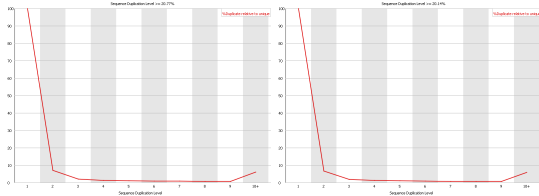
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

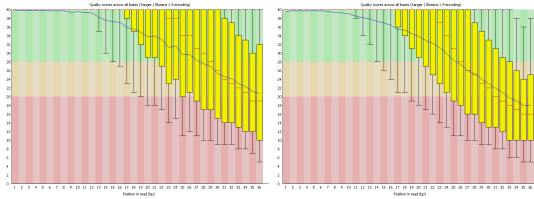
No overrepresented sequences

Overrepresented Kmers (pair 2)

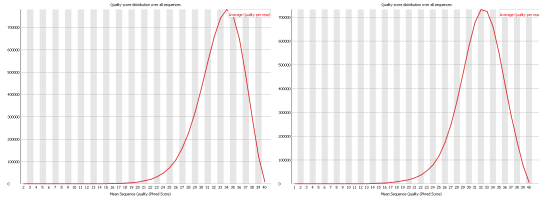
No overrepresented sequences

id69_1.fastq - 6498911 reads, 36 nt, 48% GC (pair 1), 48% GC (pair 2)

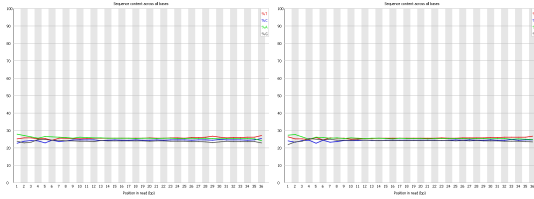
Per base quality



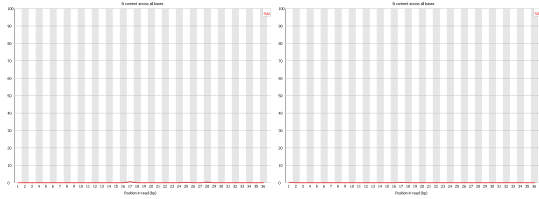
Per sequence quality



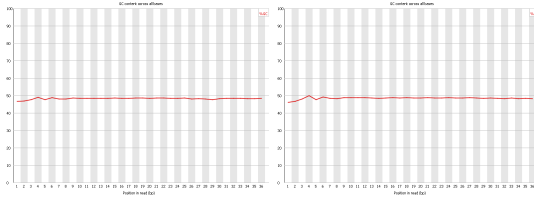
Per base sequence content



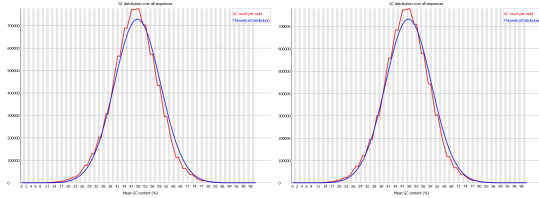
Per base N content



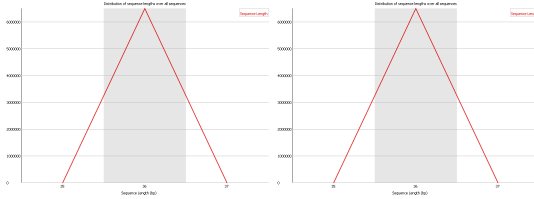
Per base GC content



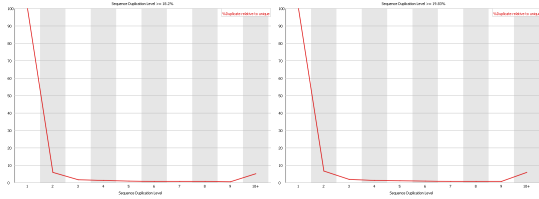
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

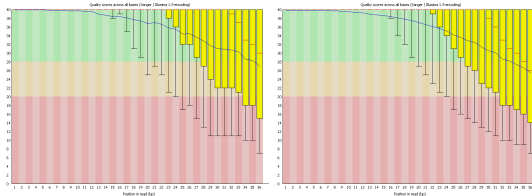
No overrepresented sequences

Overrepresented Kmers (pair 2)

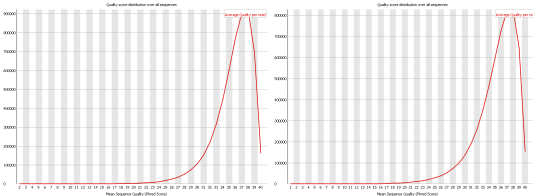
No overrepresented sequences

id69_2.fastq - 5553597 reads, 36 nt, 48% GC (pair 1), 48% GC (pair 2)

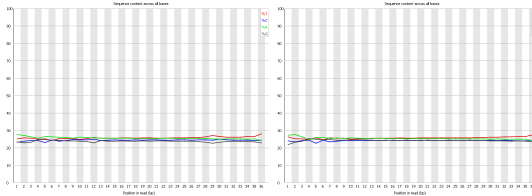
Per base quality



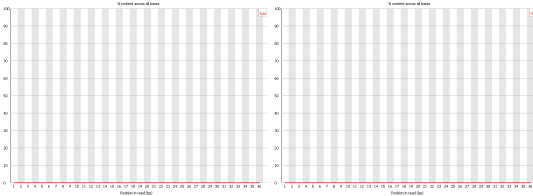
Per sequence quality



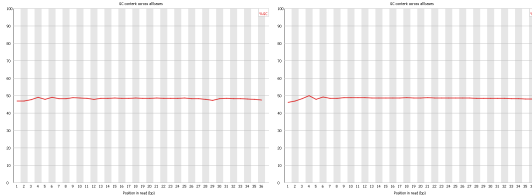
Per base sequence content



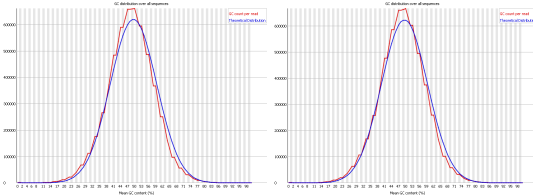
Per base N content



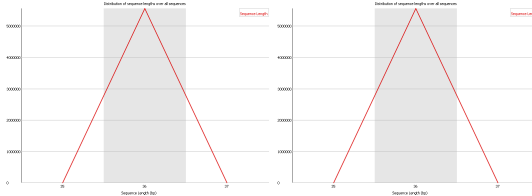
Per base GC content



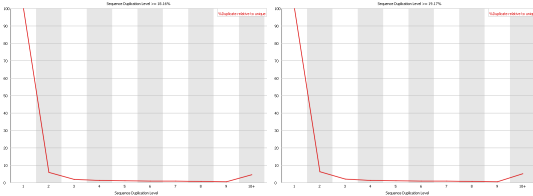
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

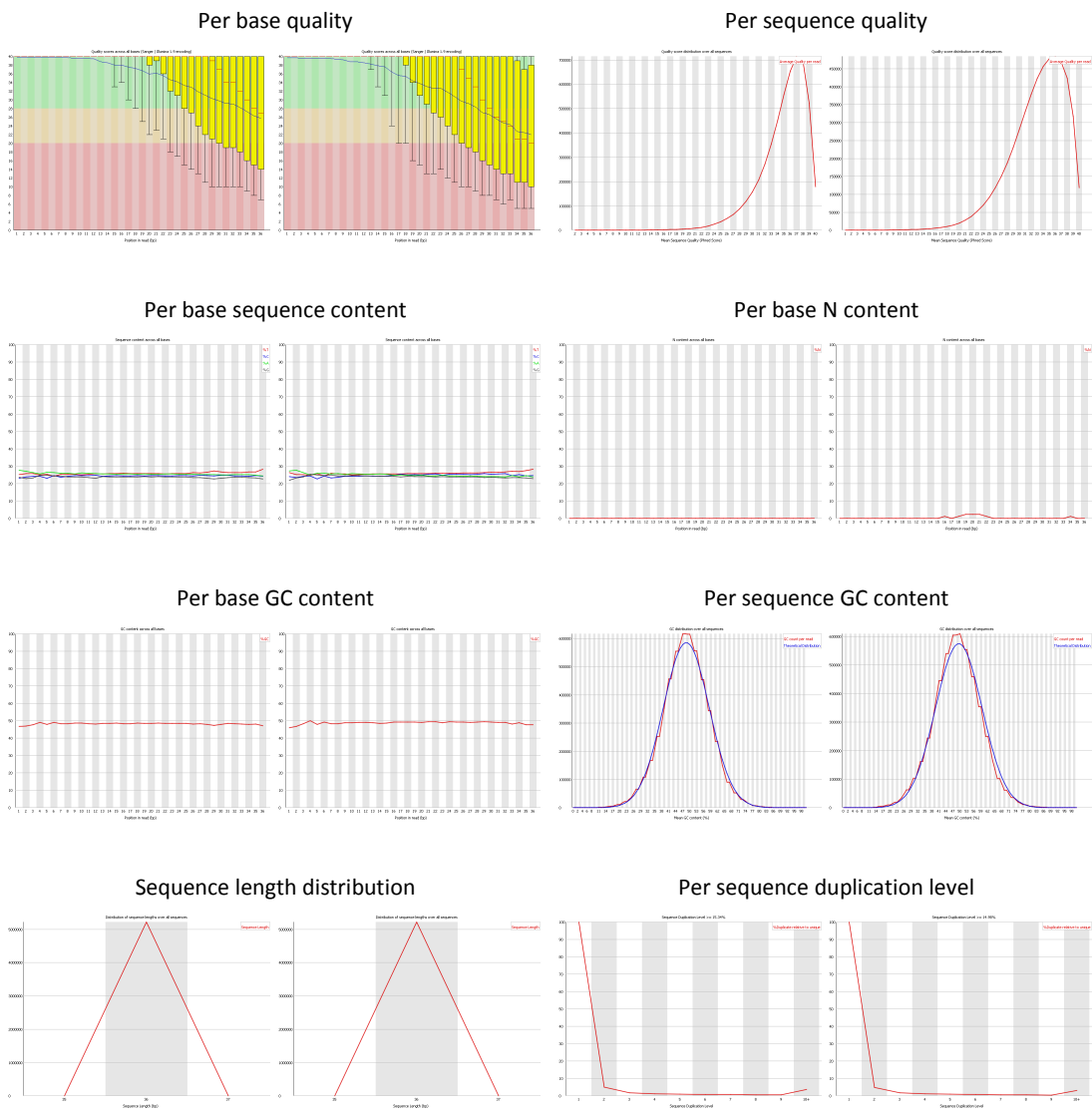
Overrepresented Kmers (pair 1)

No overrepresented sequences

Overrepresented Kmers (pair 2)

No overrepresented sequences

id69_3.fastq - 5212403 reads, 36 nt, 48% GC (pair 1), 48% GC (pair 2)



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

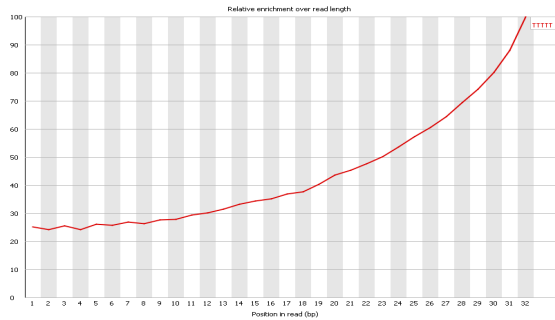
Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

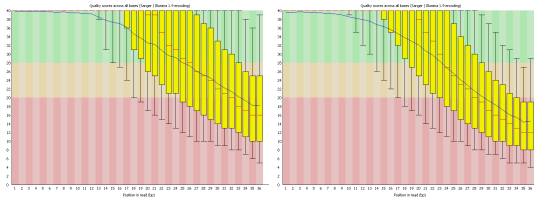
Overrepresented Kmers (pair 2)

No overrepresented sequences

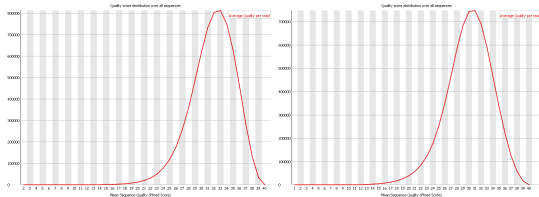


id69_5.fastq - 6895867 reads, 36 nt, 48% GC (pair 1), 48% GC (pair 2)

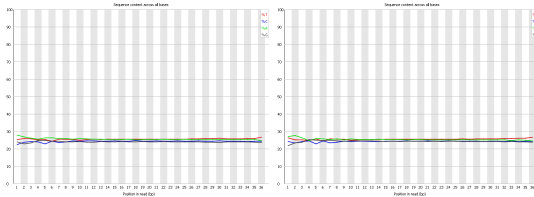
Per base quality



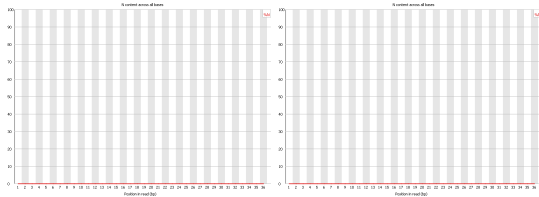
Per sequence quality



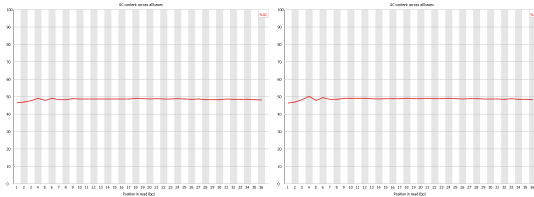
Per base sequence content



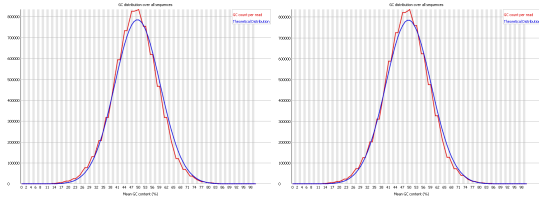
Per base N content



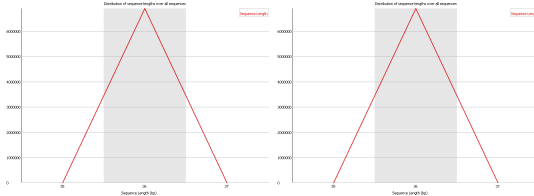
Per base GC content



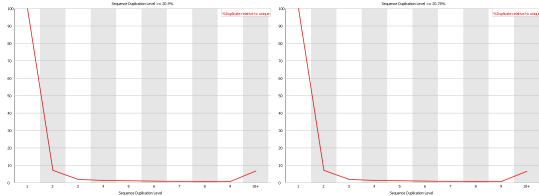
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

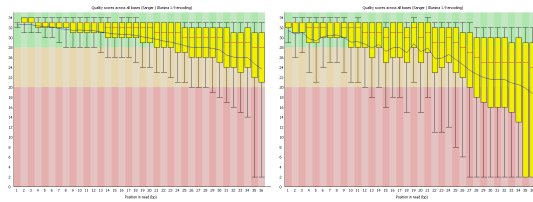
No overrepresented sequences

Overrepresented Kmers (pair 2)

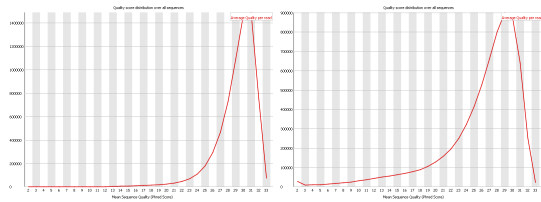
No overrepresented sequences

id79_2.fastq - 6924796 reads, 36 nt, 48% GC (pair 1), 48% GC (pair 2)

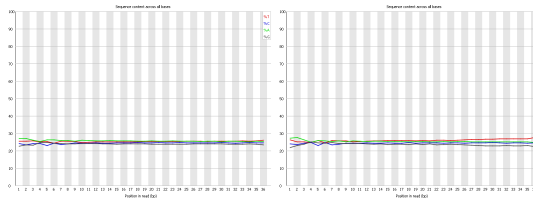
Per base quality



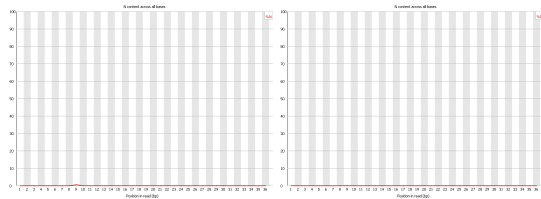
Per sequence quality



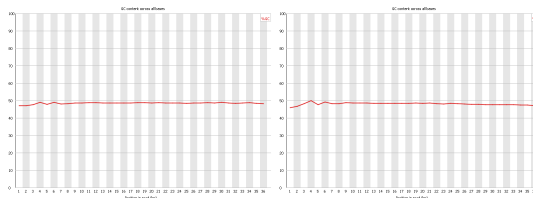
Per base sequence content



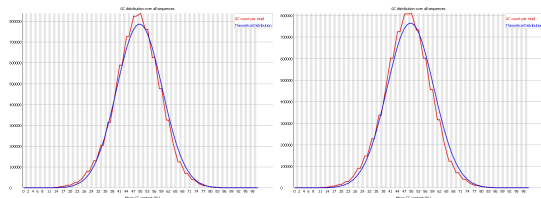
Per base N content



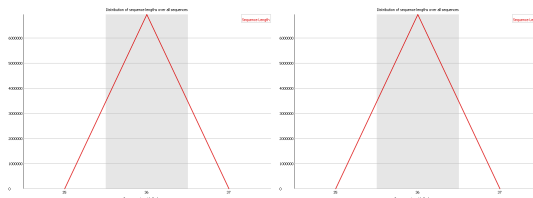
Per base GC content



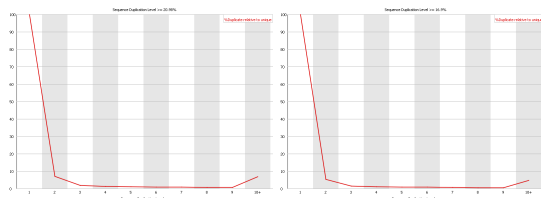
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

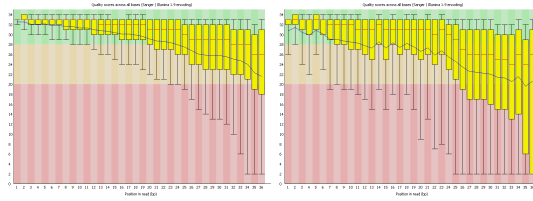
No overrepresented sequences

Overrepresented Kmers (pair 2)

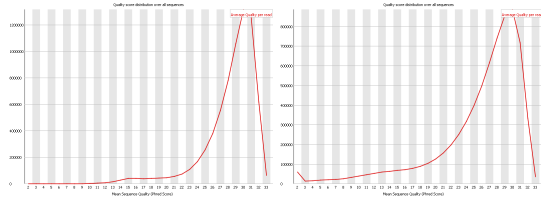
No overrepresented sequences

id79_3.fastq - 7029825 reads, 36 nt, 48% GC (pair 1), 48% GC (pair 2)

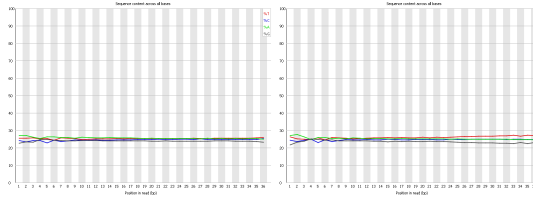
Per base quality



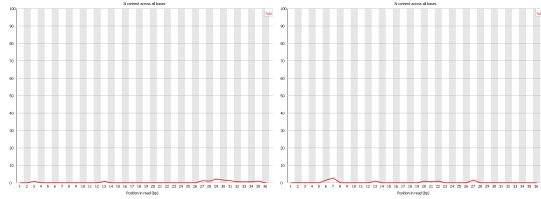
Per sequence quality



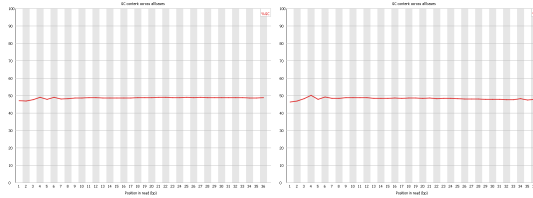
Per base sequence content



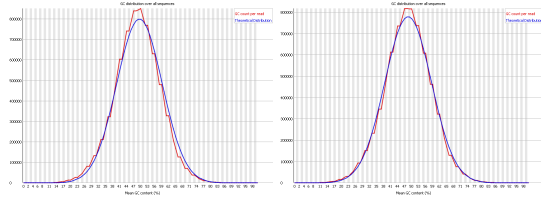
Per base N content



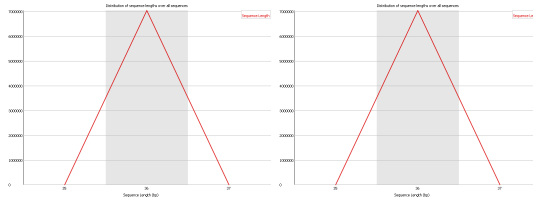
Per base GC content



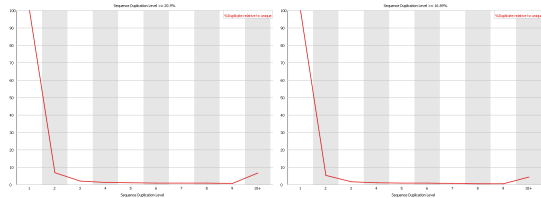
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

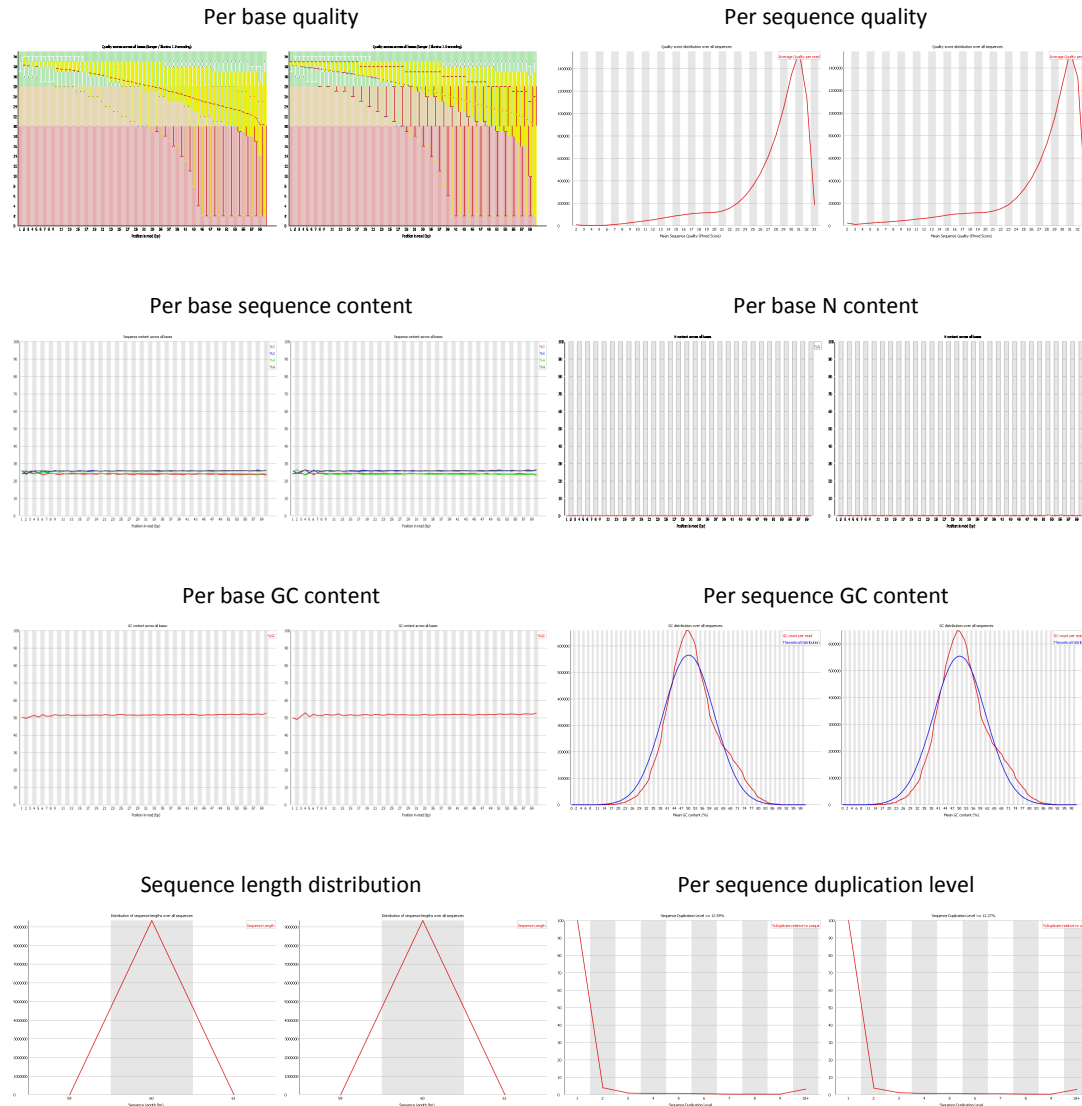
No overrepresented sequences

Overrepresented Kmers (pair 2)

No overrepresented sequences

Emwa1

042009_5.fastq - 9331001 reads, 60 nt, 51% GC (pair 1), 51% GC (pair 2)



Overrepresented sequences (top 5 for pair 1)

GATCTCATGGTGATGATTCTGCTGCTTGATAAAATTTTCAGGTATTCTGTCAGCCGTAAGTC occurs 10788 times (0.11%) - Source: No Hit
GATCTCCGAGGAGCAAAATTAAGCAATAAGGAGGGTCTGCTGATGCTCCACTTGAA occurs 9414 times (0.10%) - Source: No Hit

Overrepresented sequences (top 5 for pair 2)

GATCTCATGGTGATGATTCTGCTGCTTGATAAAATTTTCAGGTATTCTGTCAGCCGTAAGTC occurs 14374 times (0.15%) - Source: No Hit

Overrepresented Kmers (pair 1)

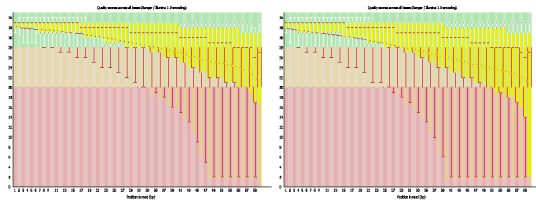
No overrepresented sequences

Overrepresented Kmers (pair 2)

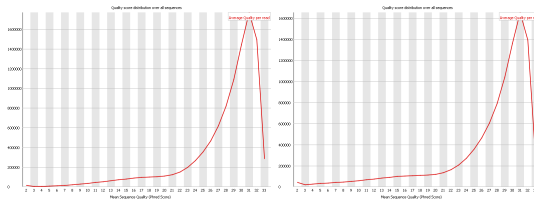
No overrepresented sequences

042009_6.fastq - 10052856 reads, 60 nt, 51% GC (pair 1), 51% GC (pair 2)

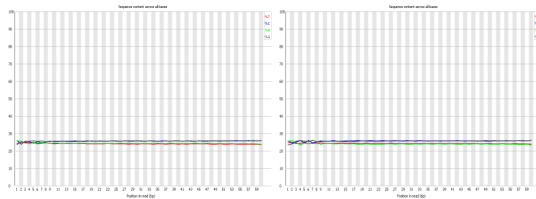
Per base quality



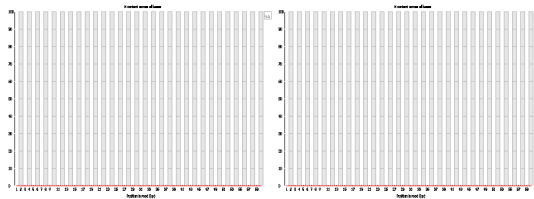
Per sequence quality



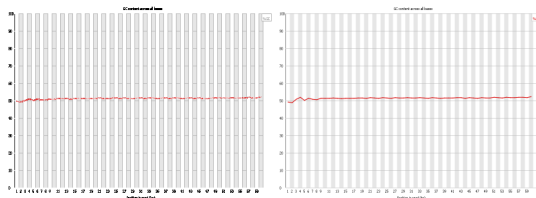
Per base sequence content



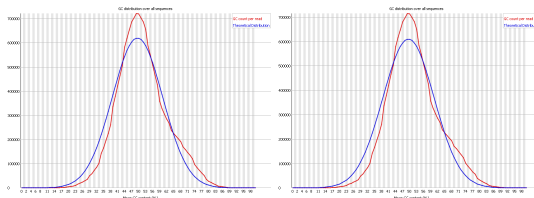
Per base N content



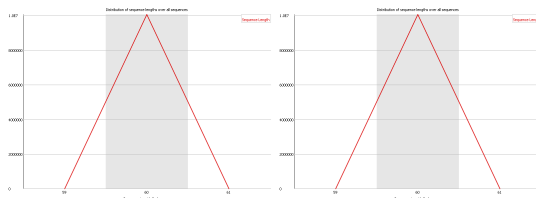
Per base GC content



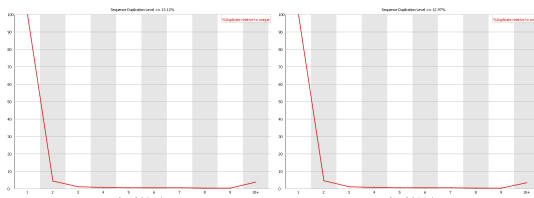
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

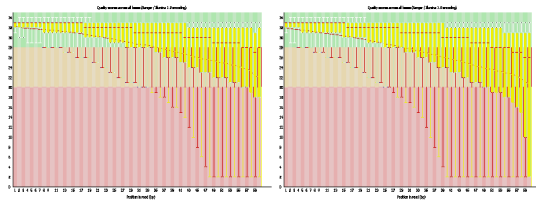
No overrepresented sequences

Overrepresented Kmers (pair 2)

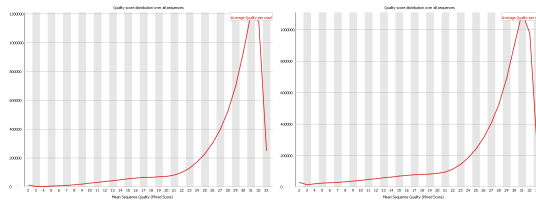
No overrepresented sequences

042009_7.fastq - 6864697 reads, 60 nt, 51% GC (pair 1), 51% GC (pair 2)

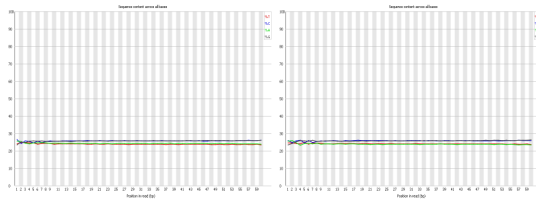
Per base quality



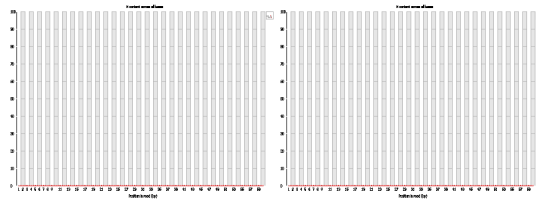
Per sequence quality



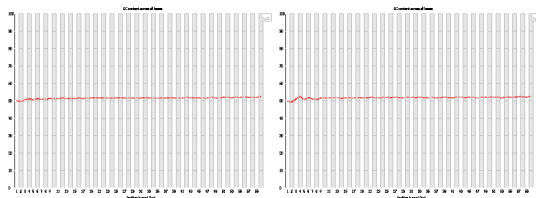
Per base sequence content



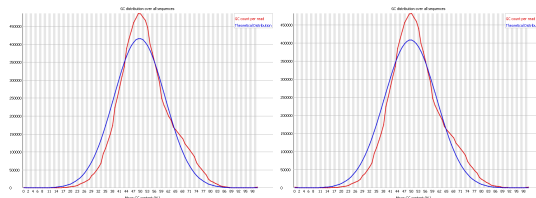
Per base N content



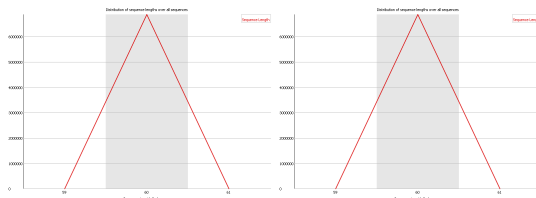
Per base GC content



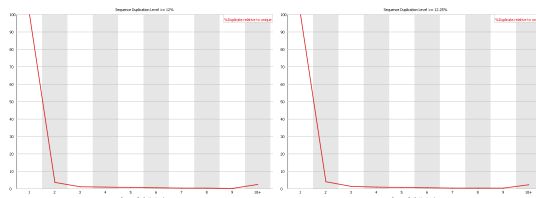
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

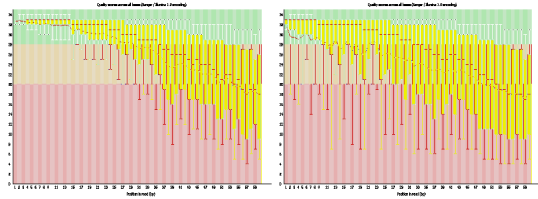
No overrepresented sequences

Overrepresented Kmers (pair 2)

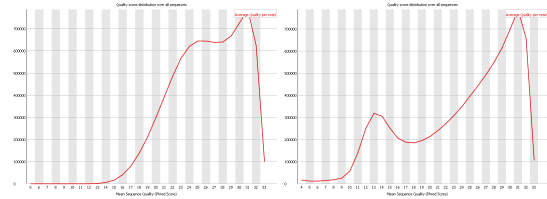
No overrepresented sequences

102009_6.fastq - 8342846 reads, 60 nt, 57% GC (pair 1), 59% GC (pair 2)

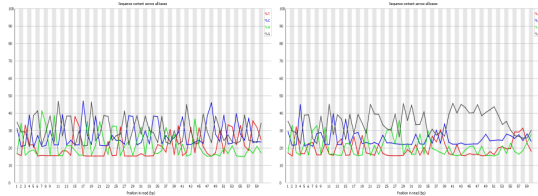
Per base quality



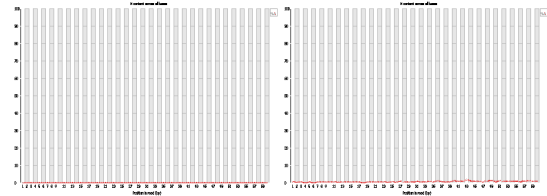
Per sequence quality



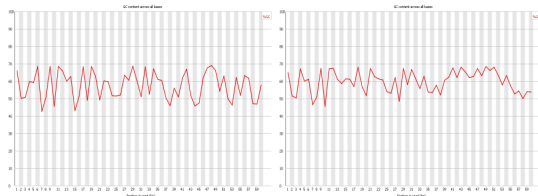
Per base sequence content



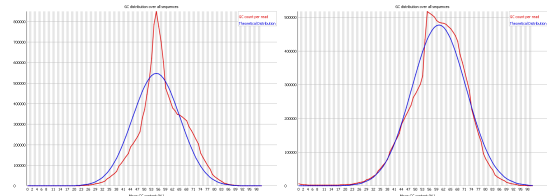
Per base N content



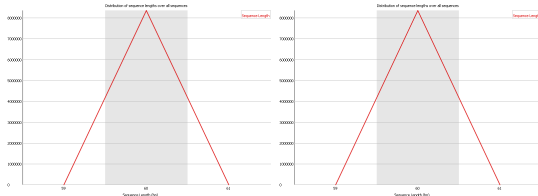
Per base GC content



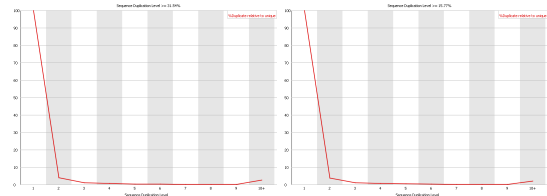
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

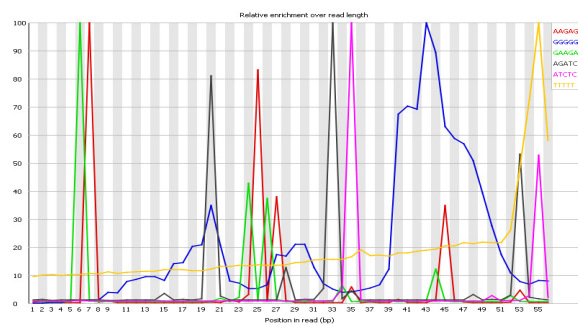
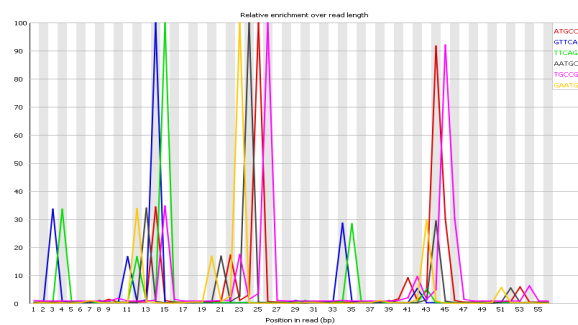
GATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATATCGTATGCCGCTTCTGCTTG occurs 300631 times (3.60%) - Source: Illumina Paired End PCR Primer 2 (98% over 60bp)
CGGTTTCAGCAGGAATGCCGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATAT occurs 153771 times (1.84%) - Source: Illumina Paired End PCR Primer 2 (97% over 41bp)
GATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGCTTCTGCTTG occurs 94770 times (1.13%) - Source: Illumina Paired End PCR Primer 2 (100% over 60bp)
GATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATATCGTATGCCGCTTCTGCTTG occurs 71579 times (0.85%) - Source: Illumina Paired End PCR Primer 2 (98% over 53bp)
GATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATATCGTATGCCGCTTCTGCTTG occurs 70810 times (0.84%) - Source: Illumina Paired End PCR Primer 2 (98% over 59bp)

Overrepresented sequences (top 5 for pair 2)

CGGCATTCTGCTGAACCGAGATCGGAAGAGCGTCGTAGGGAAAGAGTGTAGATCTCG occurs 113983 times (1.36%) - Source: Illumina Single End PCR Primer 1 (100% over 41bp)
CGGCATTCTGCTGAACCGAGATCGGAAGAGCGTCGTAGGGAAAGAGGTGTAGATCTCG occurs 31196 times (0.37%) - Source: Illumina Single End PCR Primer 1 (97% over 41bp)
CGGCATTCTGCTGAACCGAGATCGGAAGAGCGTCGTAGGGAAAGAGTGTAGATCTCG occurs 14025 times (0.16%) - Source: Illumina Single End PCR Primer 1 (97% over 41bp)
CGGCATTCTGCTGAACCGAGATCGGAAGAGCGTCGTAGGGAAAGAGGGGAGATCTCG occurs 11729 times (0.14%) - Source: Illumina Single End PCR Primer 1 (96% over 32bp)
CGGCATTCTGCTGAACCGAGATCGGAAGAGCGTCGTAGGGAAAGAGTGTAGATCTCG occurs 8939 times (0.10%) - Source: Illumina Single End PCR Primer 1 (97% over 41bp)

Overrepresented Kmers (pair 1)

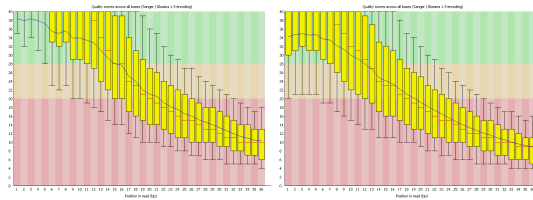
Overrepresented Kmers (pair 2)



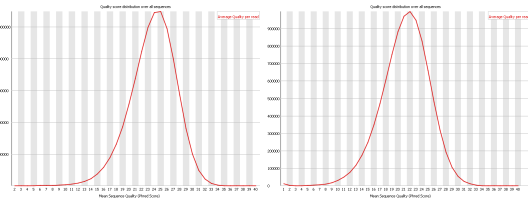
Hind2

id62_2.fastq - 9427603 reads, 36 nt, 48% GC (pair 1), 48% GC (pair 2)

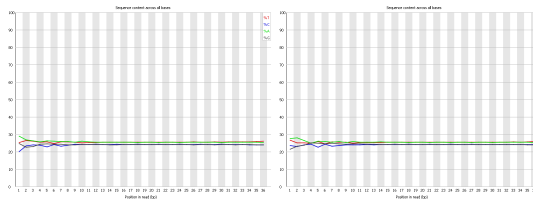
Per base quality



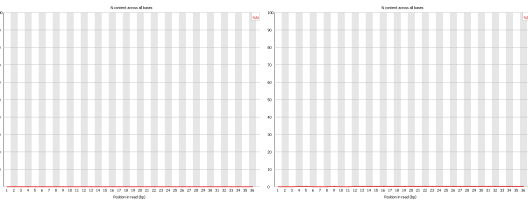
Per sequence quality



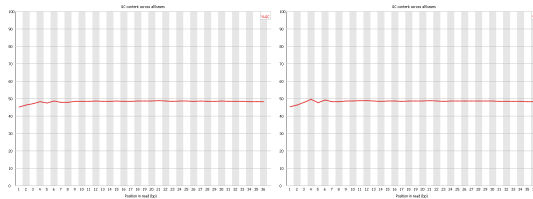
Per base sequence content



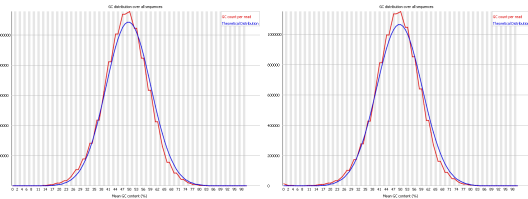
Per base N content



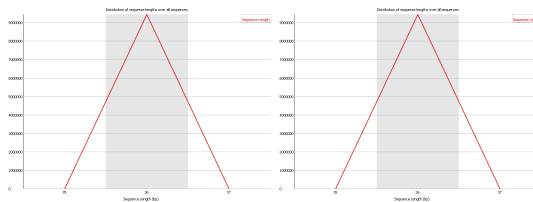
Per base GC content



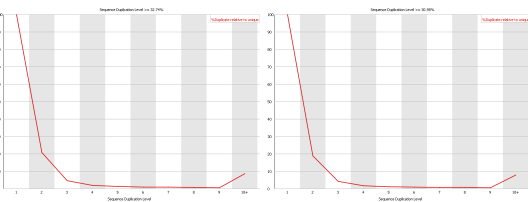
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

[illegible]

Overrepresented Kmers (pair 1)

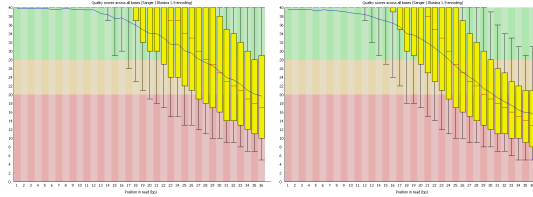
No overrepresented sequences

Overrepresented Kmers (pair 2)

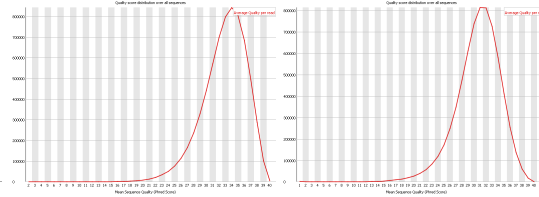
No overrepresented sequences

id64_1.fastq - 6811355 reads, 36 nt, 48% GC (pair 1), 48% GC (pair 2)

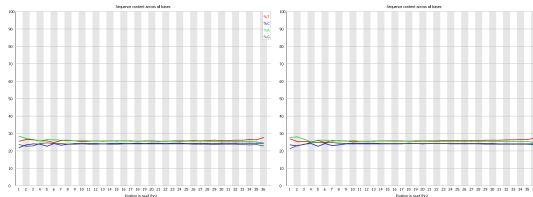
Per base quality



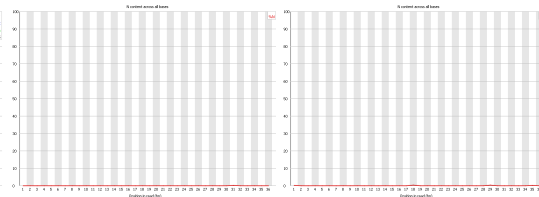
Per sequence quality



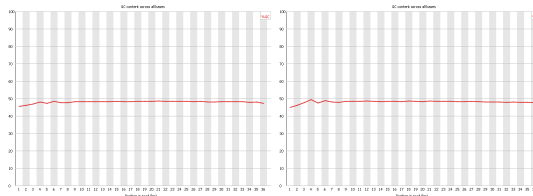
Per base sequence content



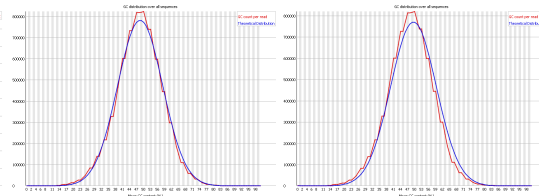
Per base N content



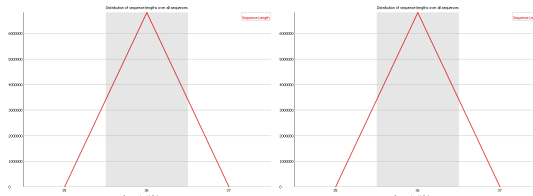
Per base GC content



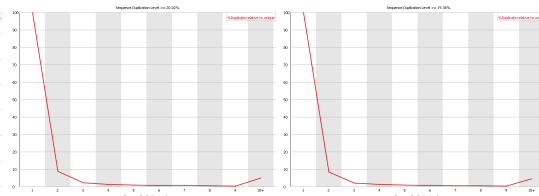
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

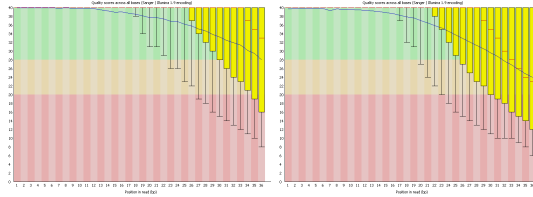
No overrepresented sequences

Overrepresented Kmers (pair 2)

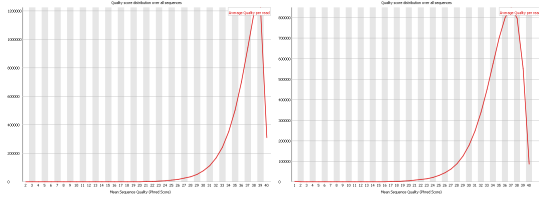
No overrepresented sequences

id64_2.fastq - 6019458 reads, 36 nt, 48% GC (pair 1), 48% GC (pair 2)

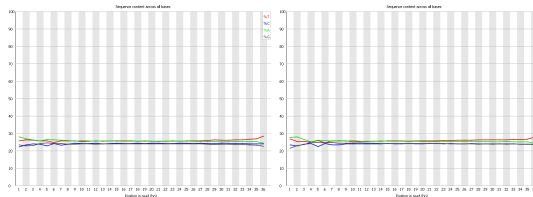
Per base quality



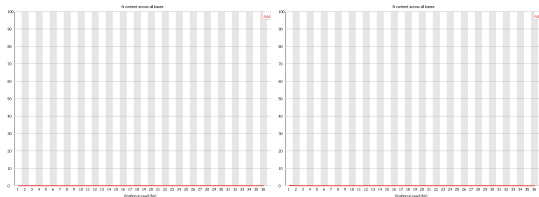
Per sequence quality



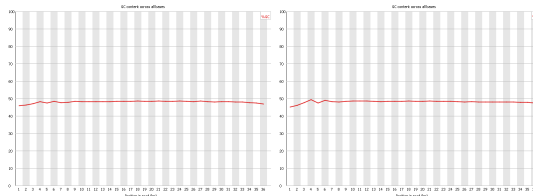
Per base sequence content



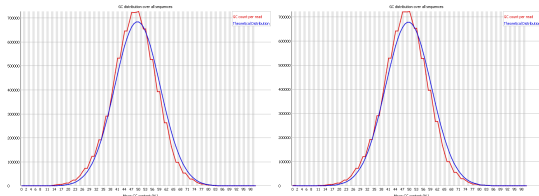
Per base N content



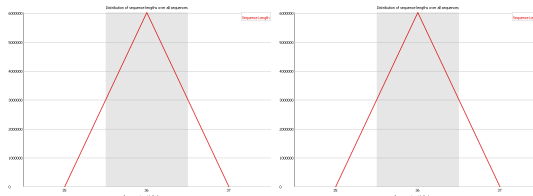
Per base GC content



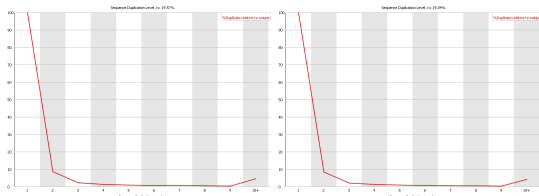
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

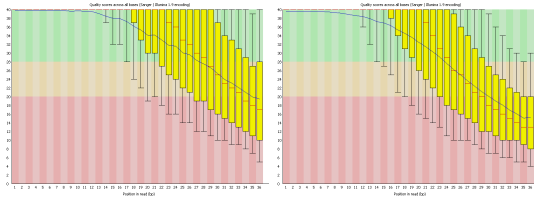
No overrepresented sequences

Overrepresented Kmers (pair 2)

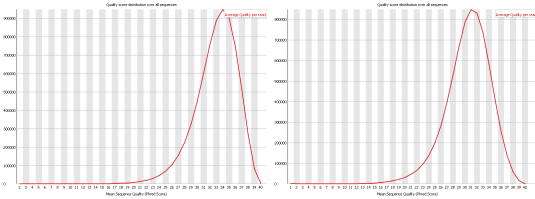
No overrepresented sequences

id64_3.fastq - 7185077 reads, 36 nt, 48% GC (pair 1), 48% GC (pair 2)

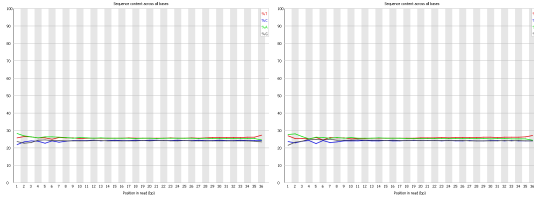
Per base quality



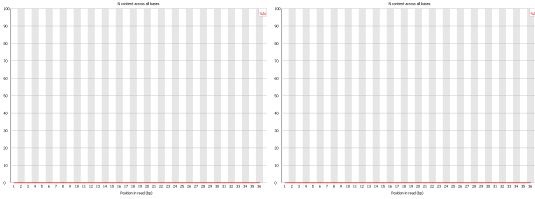
Per sequence quality



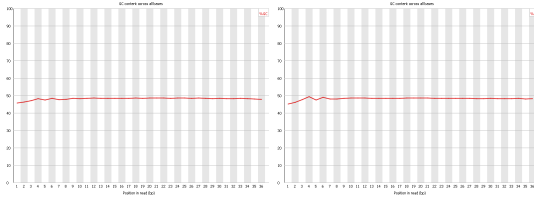
Per base sequence content



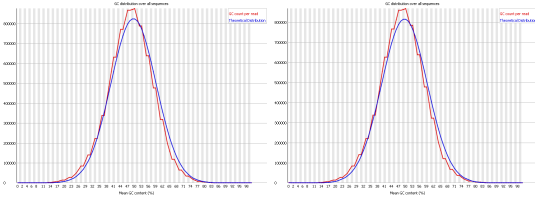
Per base N content



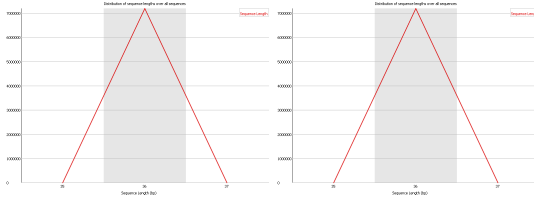
Per base GC content



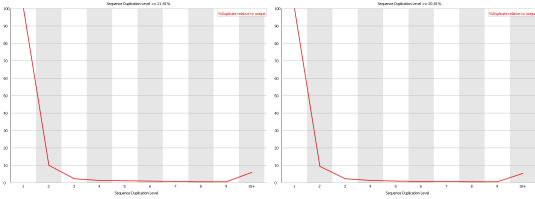
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

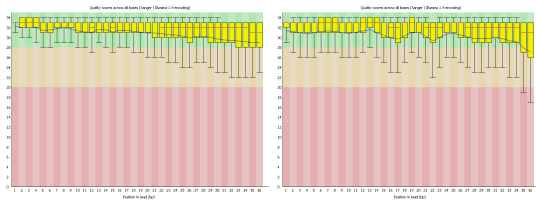
No overrepresented sequences

Overrepresented Kmers (pair 2)

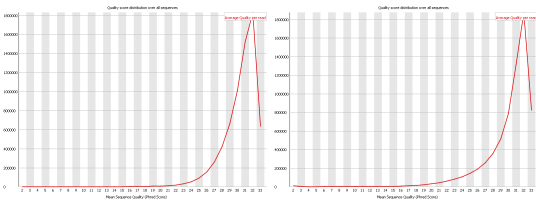
No overrepresented sequences

id87_5.fastq - 6759050 reads, 36 nt, 49% GC (pair 1), 49% GC (pair 2)

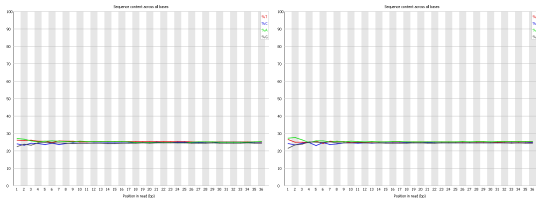
Per base quality



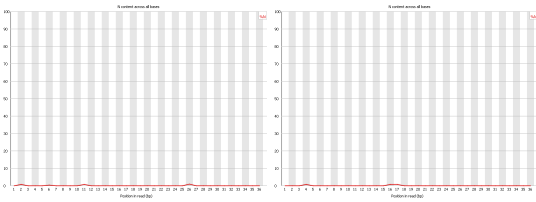
Per sequence quality



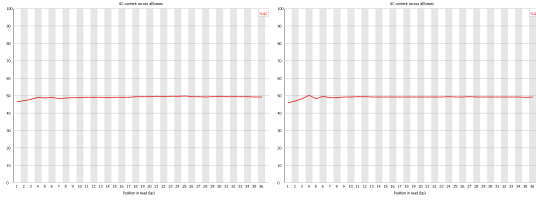
Per base sequence content



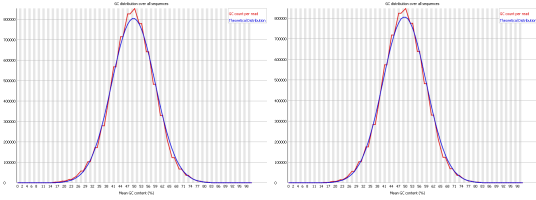
Per base N content



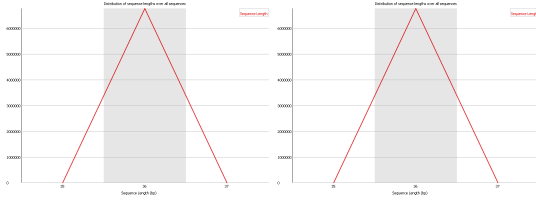
Per base GC content



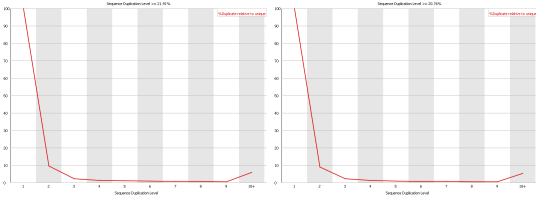
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

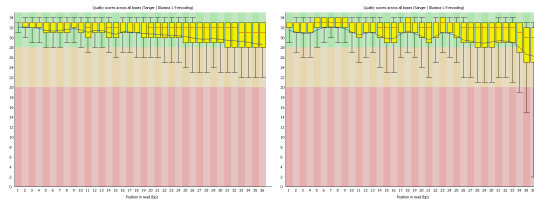
No overrepresented sequences

Overrepresented Kmers (pair 2)

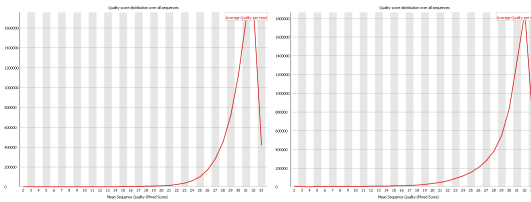
No overrepresented sequences

id87_6.fastq - 6919355 reads, 36 nt, 49% GC (pair 1), 49% GC (pair 2)

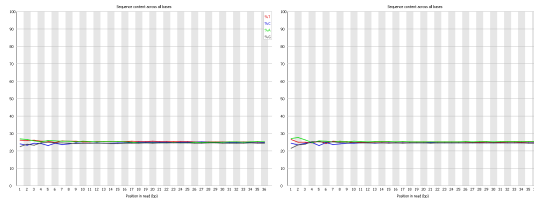
Per base quality



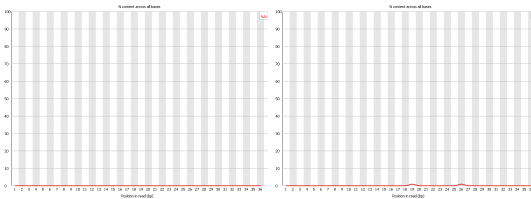
Per sequence quality



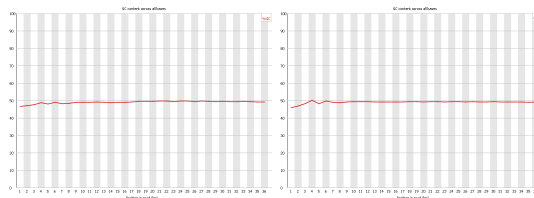
Per base sequence content



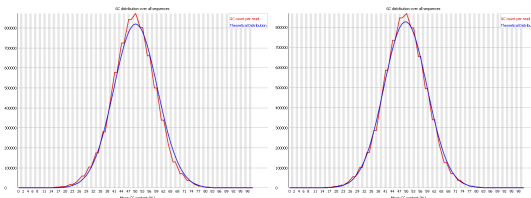
Per base N content



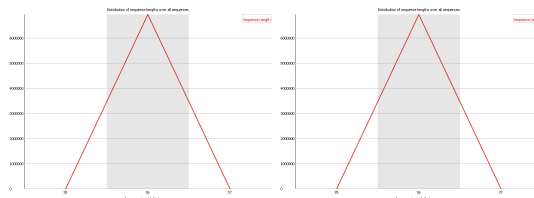
Per base GC content



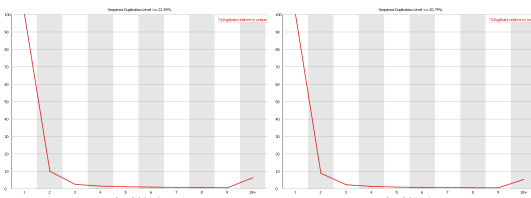
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

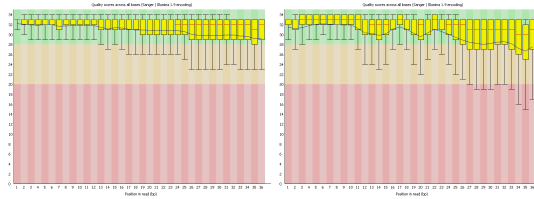
No overrepresented sequences

Overrepresented Kmers (pair 2)

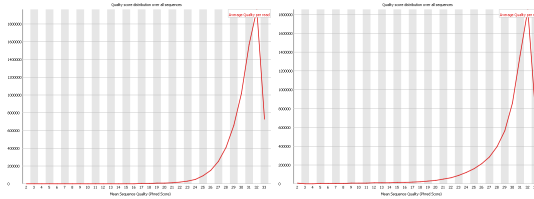
No overrepresented sequences

id87_7.fastq - 7017475 reads, 36 nt, 49% GC (pair 1), 49% GC (pair 2)

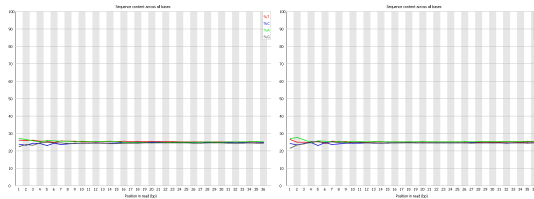
Per base quality



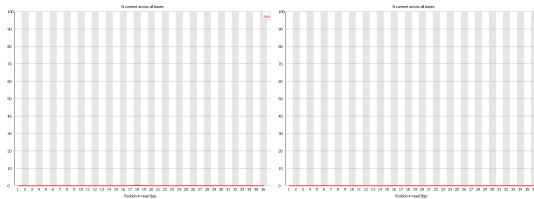
Per sequence quality



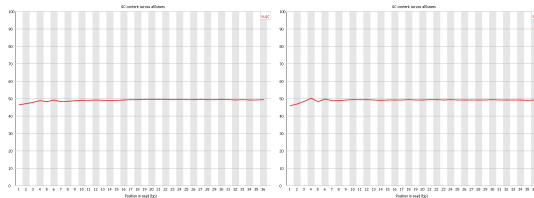
Per base sequence content



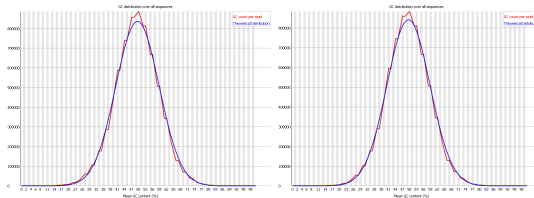
Per base N content



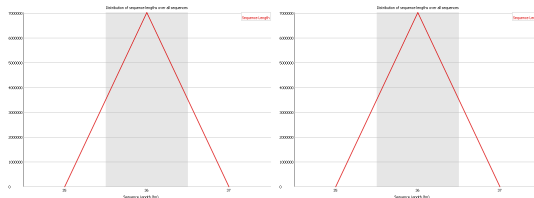
Per base GC content



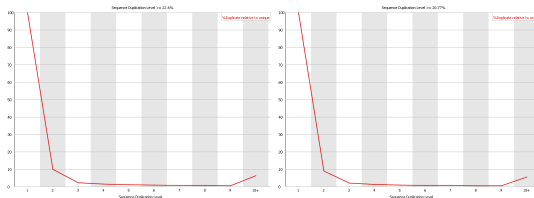
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

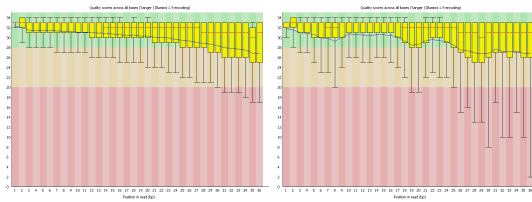
No overrepresented sequences

Overrepresented Kmers (pair 2)

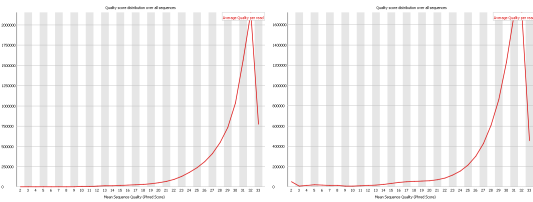
No overrepresented sequences

id88_5.fastq - 8489136 reads, 36 nt, 48% GC (pair 1), 49% GC (pair 2)

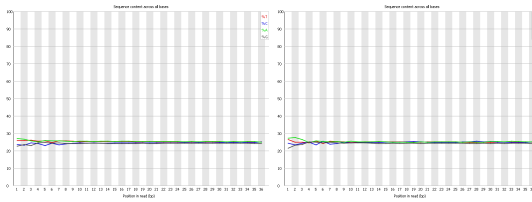
Per base quality



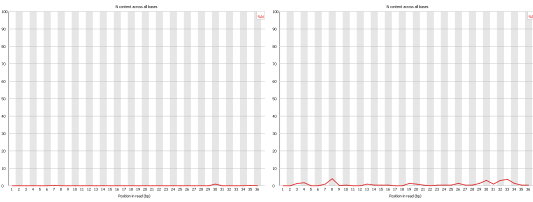
Per sequence quality



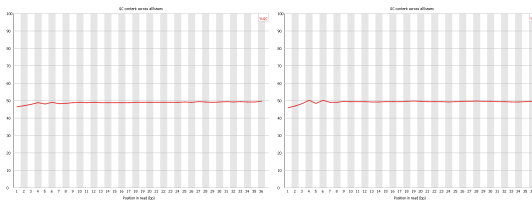
Per base sequence content



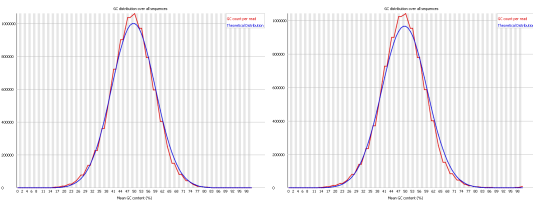
Per base N content



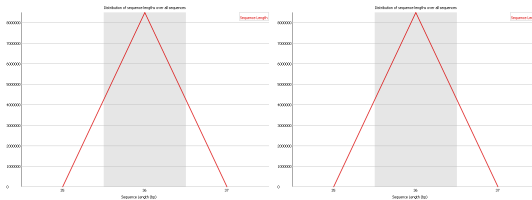
Per base GC content



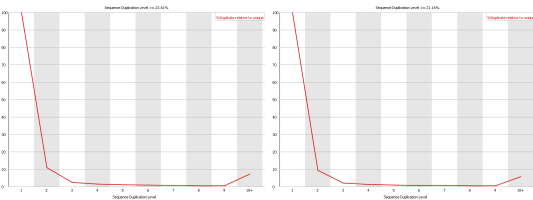
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

No overrepresented sequences

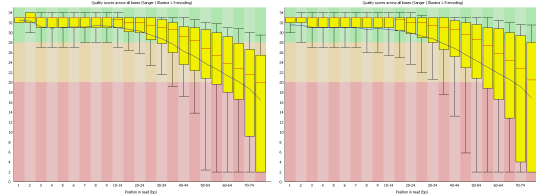
Overrepresented Kmers (pair 2)

No overrepresented sequences

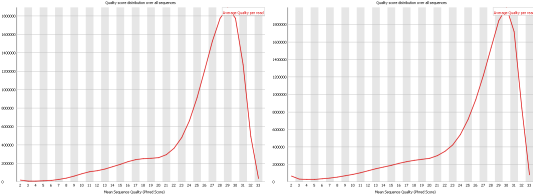
Maks9

id108_3.fastq - 14928614 reads, 76 nt, 50% GC (pair 1), 50% GC (pair 2)

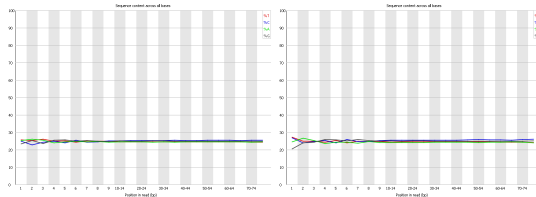
Per base quality



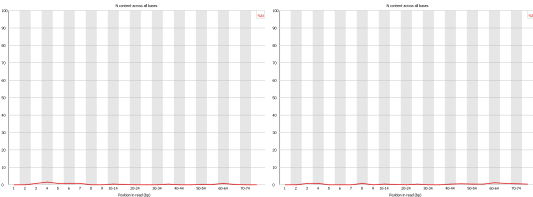
Per sequence quality



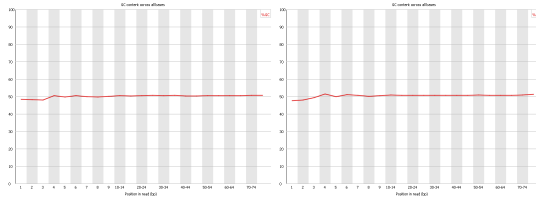
Per base sequence content



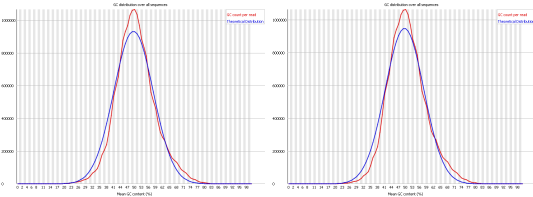
Per base N content



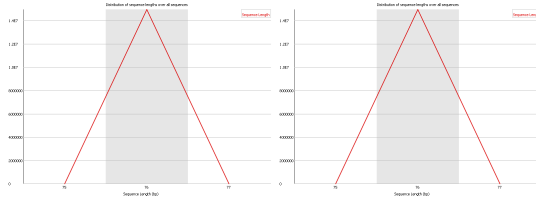
Per base GC content



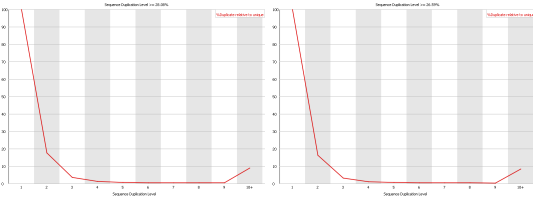
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

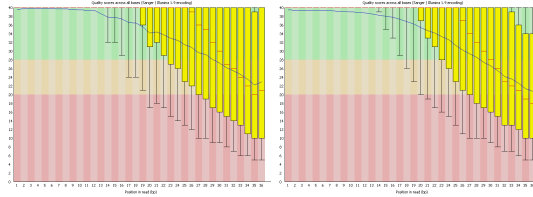
No overrepresented sequences

Overrepresented Kmers (pair 2)

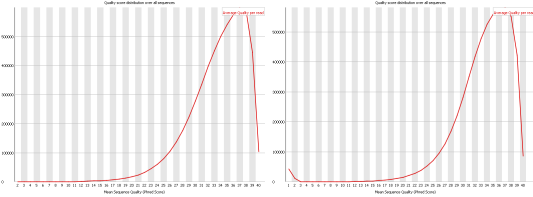
No overrepresented sequences

id71_2.fastq - 5771643 reads, 36 nt, 48% GC (pair 1), 48% GC (pair 2)

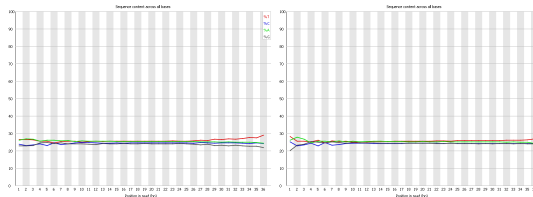
Per base quality



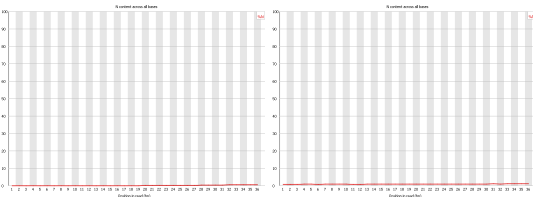
Per sequence quality



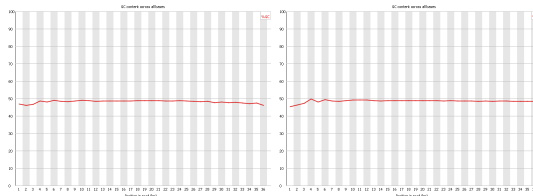
Per base sequence content



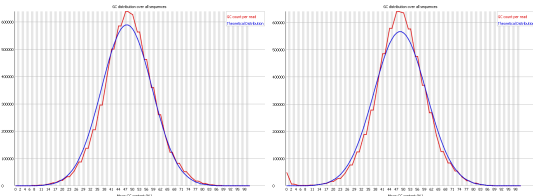
Per base N content



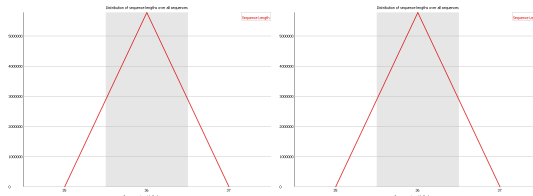
Per base GC content



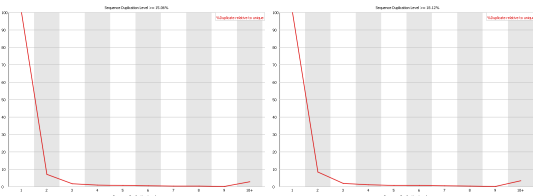
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

[illegible]

Overrepresented Kmers (pair 1)

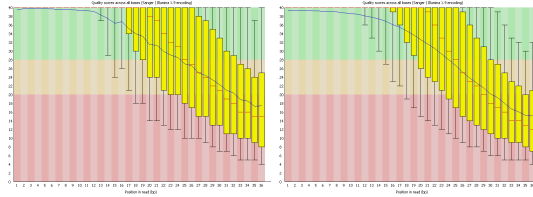
No overrepresented sequences

Overrepresented Kmers (pair 2)

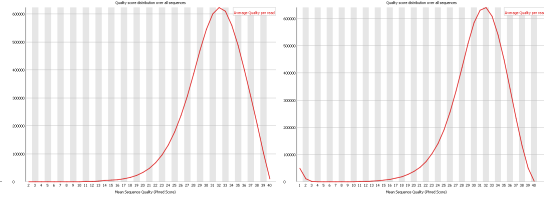
No overrepresented sequences

id71_3.fastq - 6487059 reads, 36 nt, 48% GC (pair 1), 48% GC (pair 2)

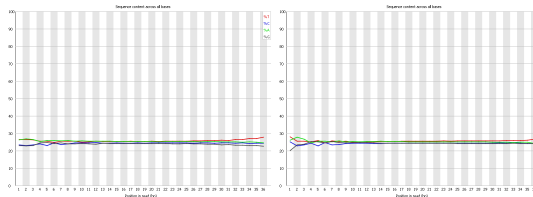
Per base quality



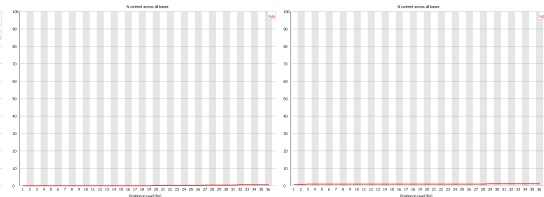
Per sequence quality



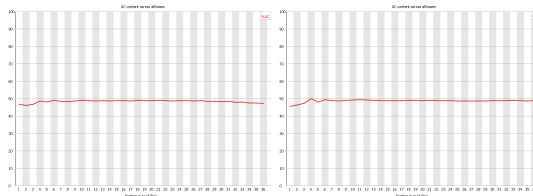
Per base sequence content



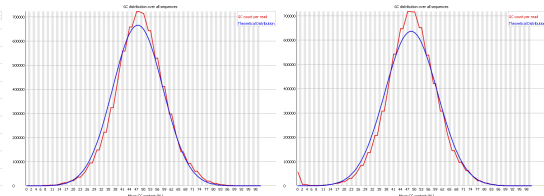
Per base N content



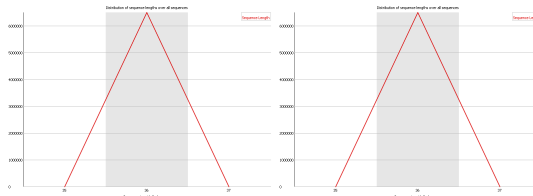
Per base GC content



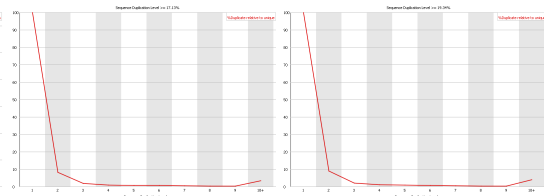
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

[illegible]

Overrepresented Kmers (pair 1)

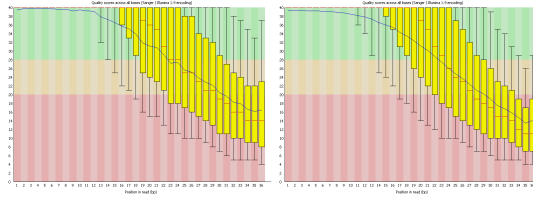
No overrepresented sequences

Overrepresented Kmers (pair 2)

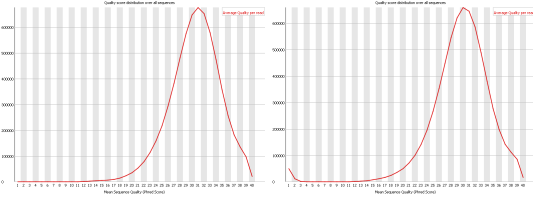
No overrepresented sequences

id71_5.fastq - 6555660 reads, 36 nt, 48% GC (pair 1), 48% GC (pair 2)

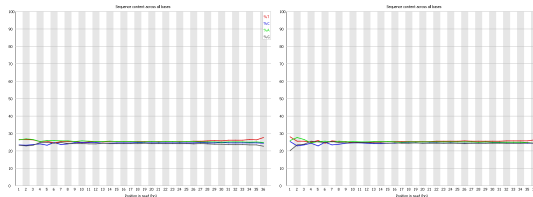
Per base quality



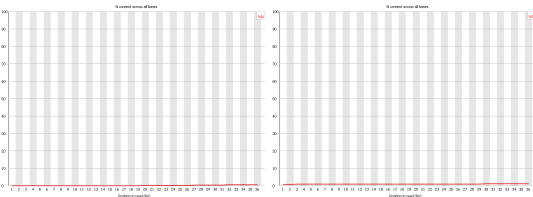
Per sequence quality



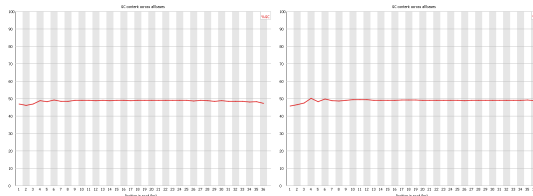
Per base sequence content



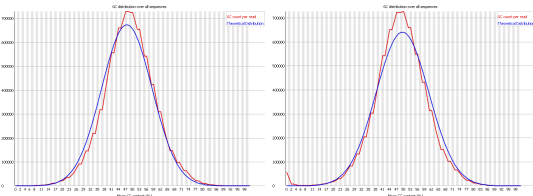
Per base N content



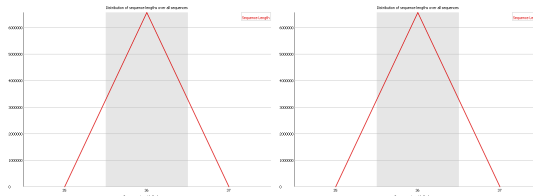
Per base GC content



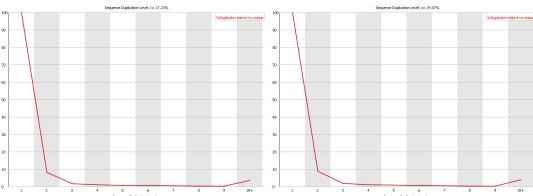
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

[illegible]

Overrepresented Kmers (pair 1)

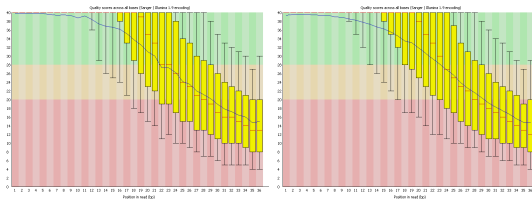
No overrepresented sequences

Overrepresented Kmers (pair 2)

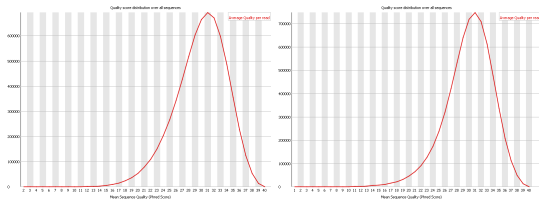
No overrepresented sequences

id74_8.fastq - 6748036 reads, 36 nt, 48% GC (pair 1), 48% GC (pair 2)

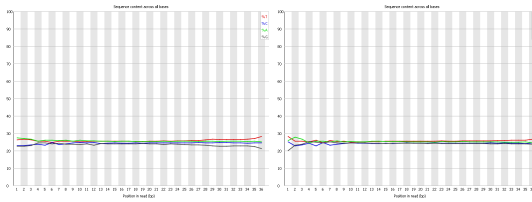
Per base quality



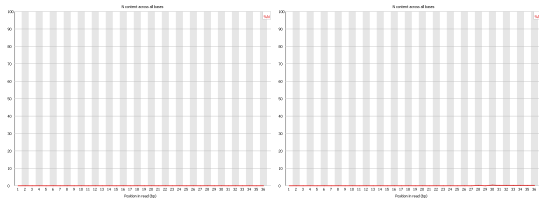
Per sequence quality



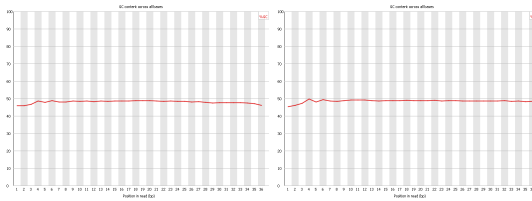
Per base sequence content



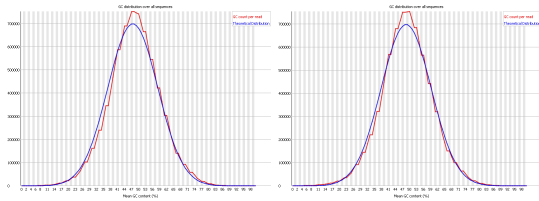
Per base N content



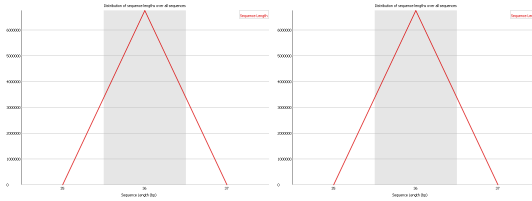
Per base GC content



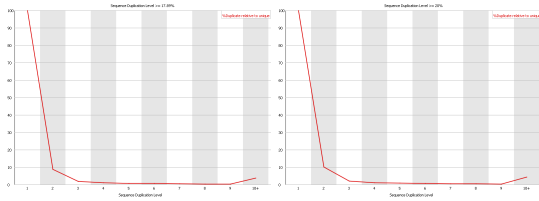
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

No overrepresented sequences

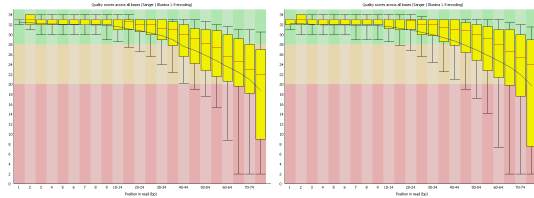
Overrepresented Kmers (pair 2)

No overrepresented sequences

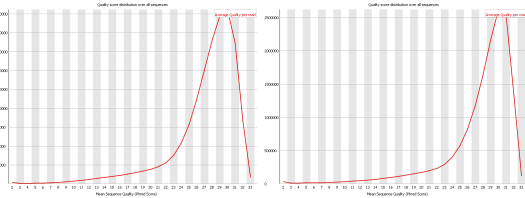
Noco2

id108_2.fastq - 15334521 reads, 76 nt, 49% GC (pair 1), 49% GC (pair 2)

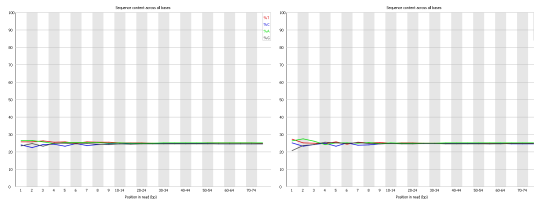
Per base quality



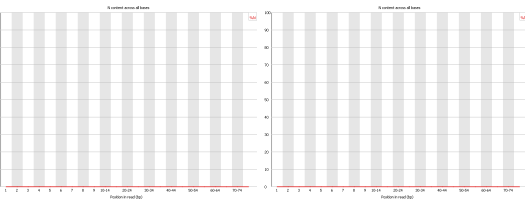
Per sequence quality



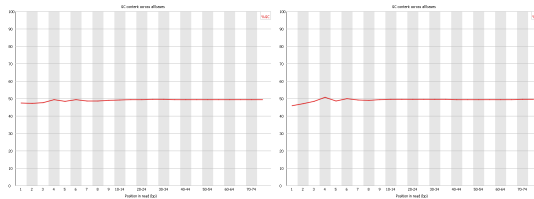
Per base sequence content



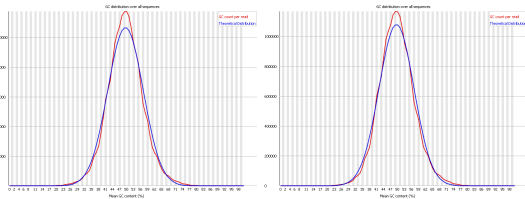
Per base N content



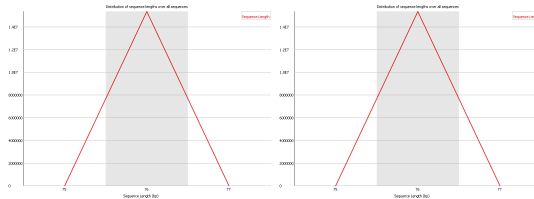
Per base GC content



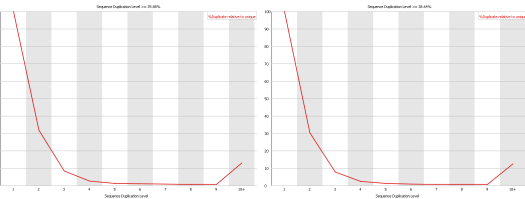
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

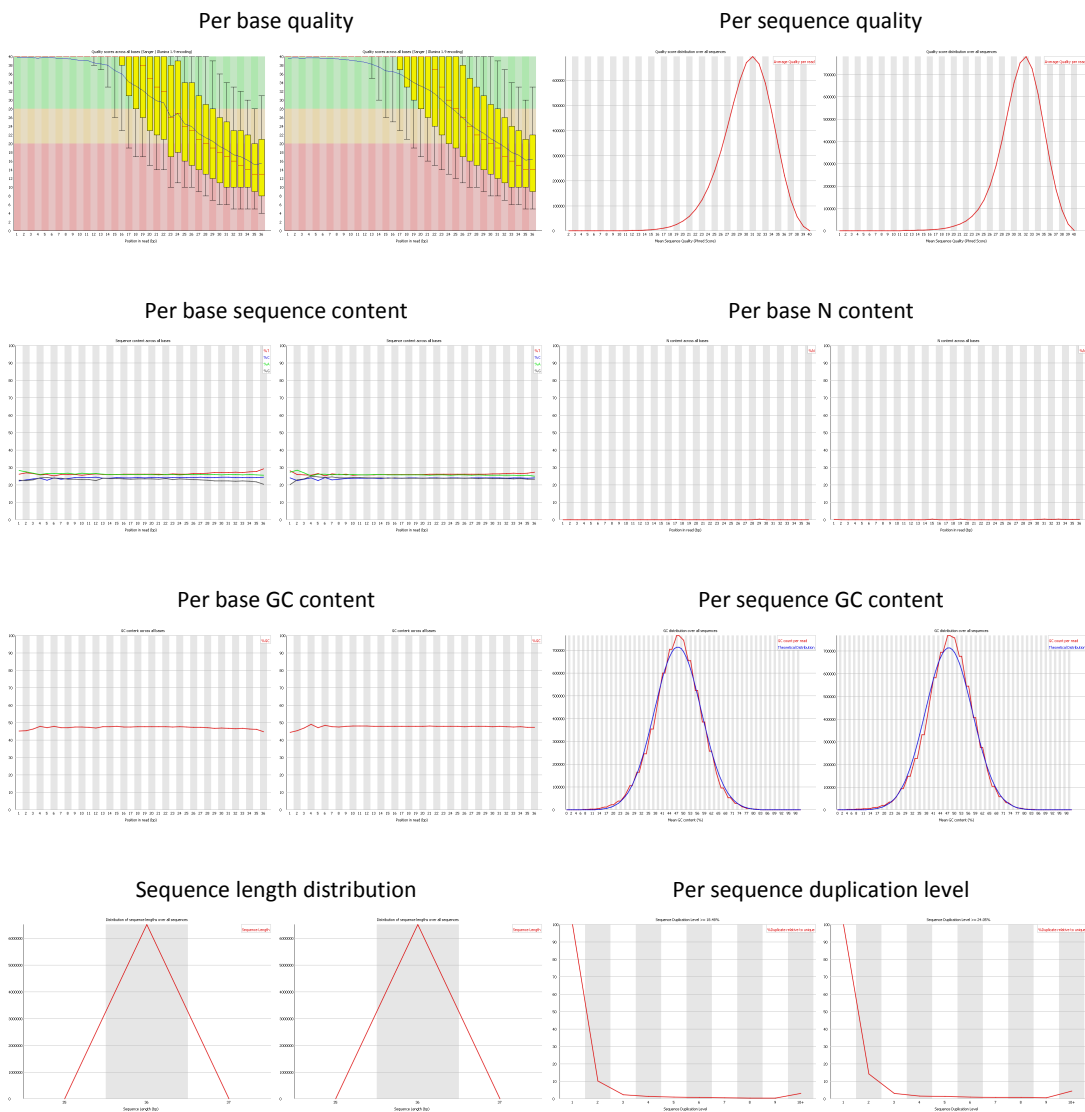
Overrepresented Kmers (pair 1)

No overrepresented sequences

Overrepresented Kmers (pair 2)

No overrepresented sequences

id74_1.fastq - 6505077 reads, 36 nt, 47% GC (pair 1), 47% GC (pair 2)



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

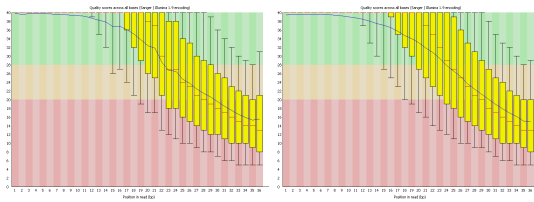
No overrepresented sequences

Overrepresented Kmers (pair 2)

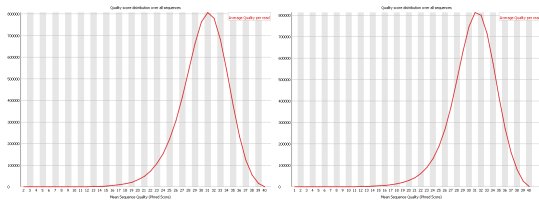
No overrepresented sequences

id74_2.fastq - 7012353 reads, 36 nt, 47% GC (pair 1), 47% GC (pair 2)

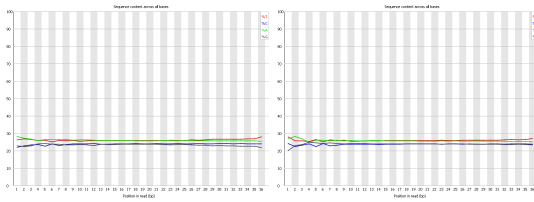
Per base quality



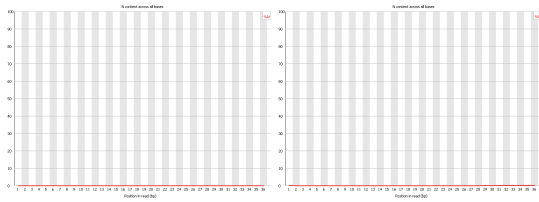
Per sequence quality



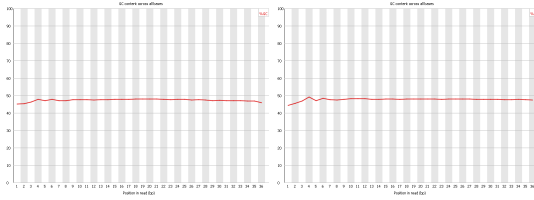
Per base sequence content



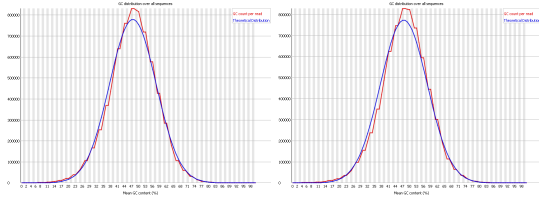
Per base N content



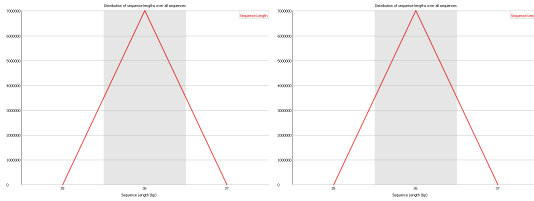
Per base GC content



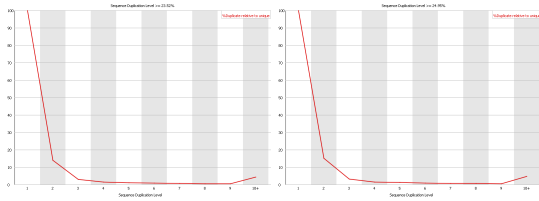
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

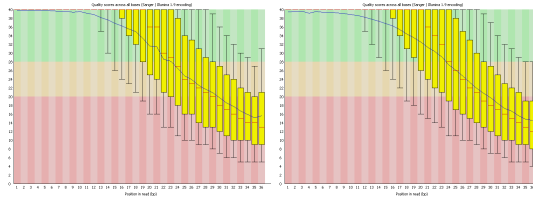
No overrepresented sequences

Overrepresented Kmers (pair 2)

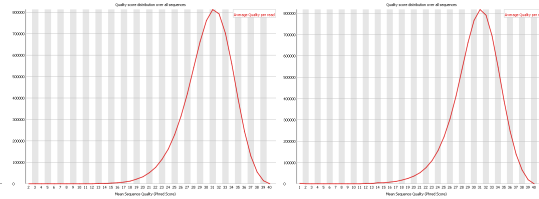
No overrepresented sequences

id74_3.fastq - 7141259 reads, 36 nt, 47% GC (pair 1), 47% GC (pair 2)

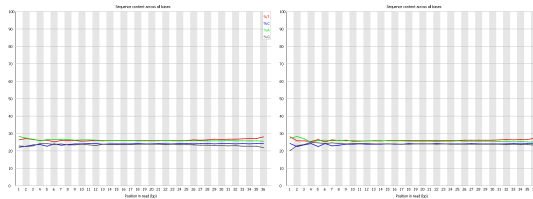
Per base quality



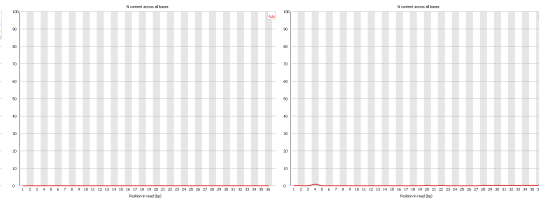
Per sequence quality



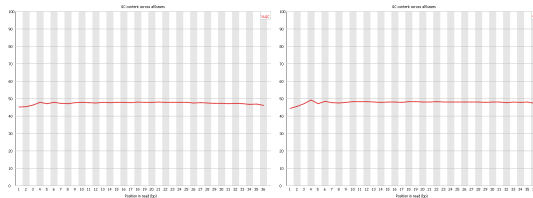
Per base sequence content



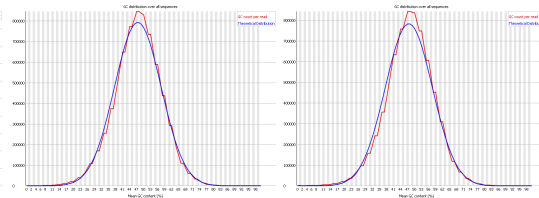
Per base N content



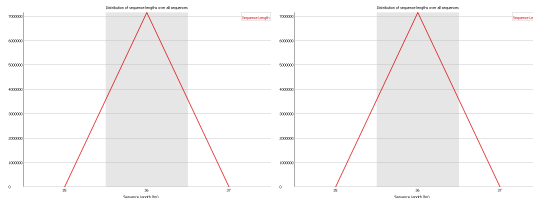
Per base GC content



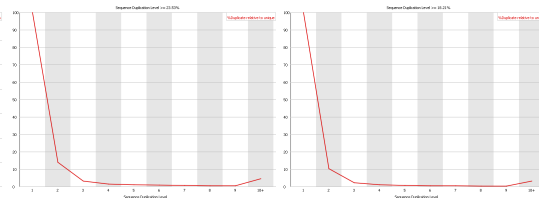
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

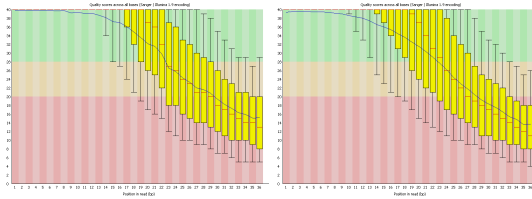
No overrepresented sequences

Overrepresented Kmers (pair 2)

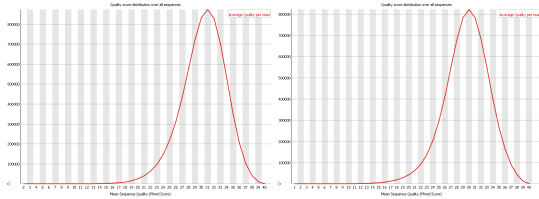
No overrepresented sequences

id74_5.fastq - 7170441 reads, 36 nt, 47% GC (pair 1), 48% GC (pair 2)

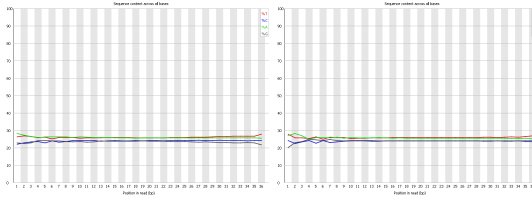
Per base quality



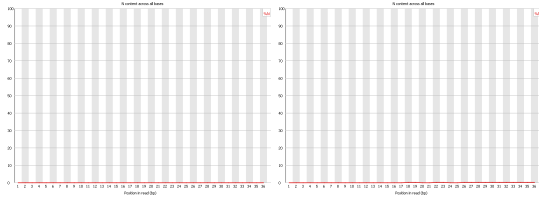
Per sequence quality



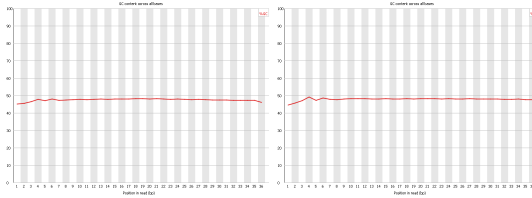
Per base sequence content



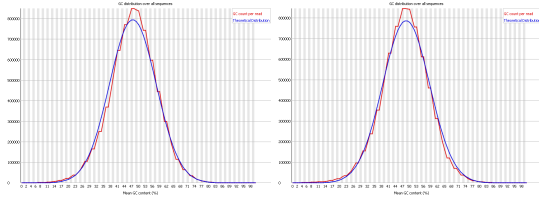
Per base N content



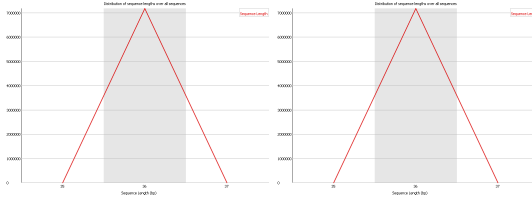
Per base GC content



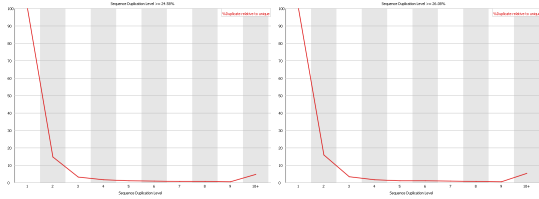
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

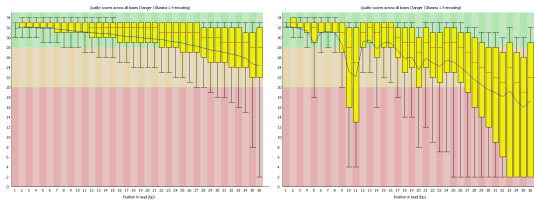
No overrepresented sequences

Overrepresented Kmers (pair 2)

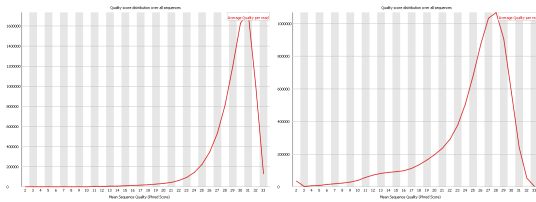
No overrepresented sequences

id80_1.fastq - 8137378 reads, 36 nt, 48% GC (pair 1), 47% GC (pair 2)

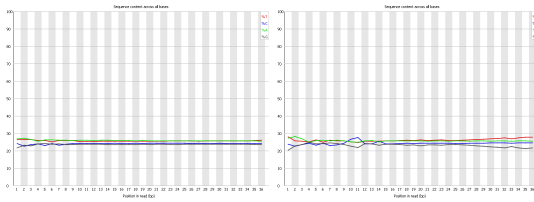
Per base quality



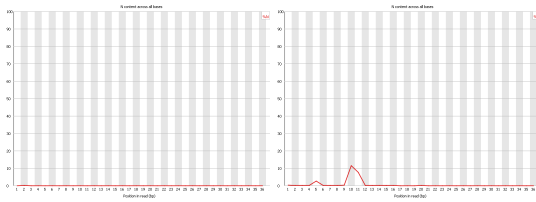
Per sequence quality



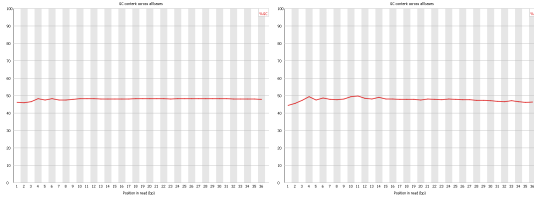
Per base sequence content



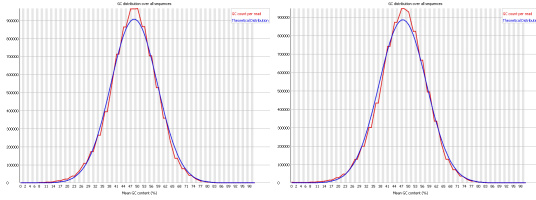
Per base N content



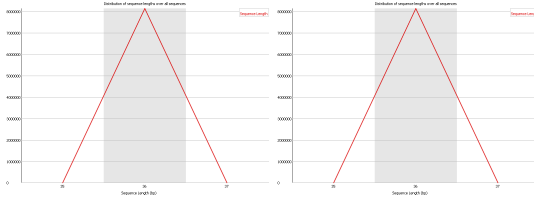
Per base GC content



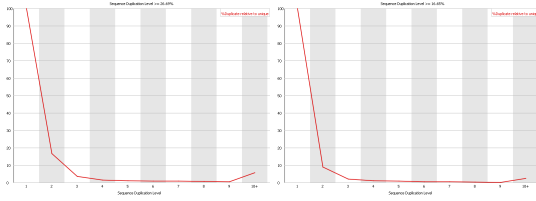
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

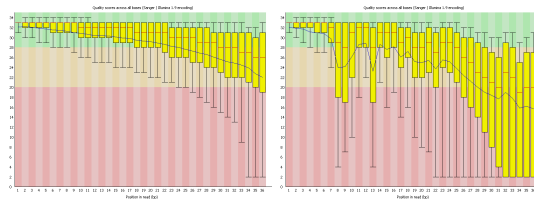
No overrepresented sequences

Overrepresented Kmers (pair 2)

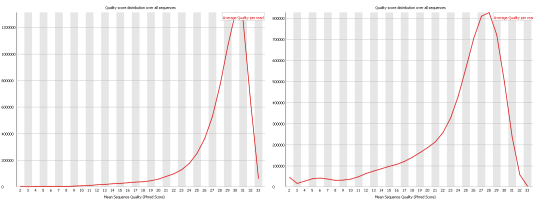
No overrepresented sequences

id80_2.fastq - 7058507 reads, 36 nt, 48% GC (pair 1), 47% GC (pair 2)

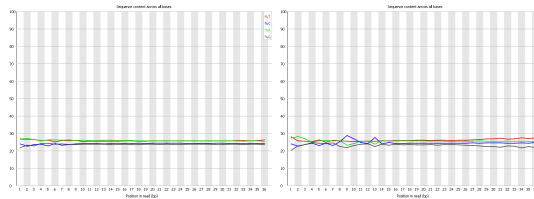
Per base quality



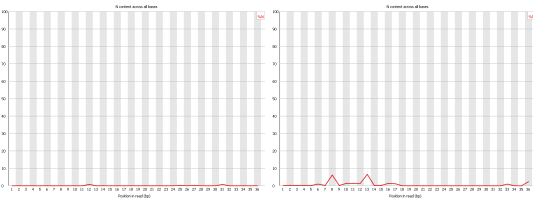
Per sequence quality



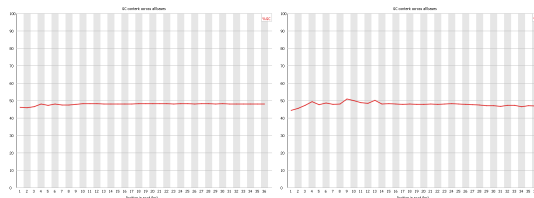
Per base sequence content



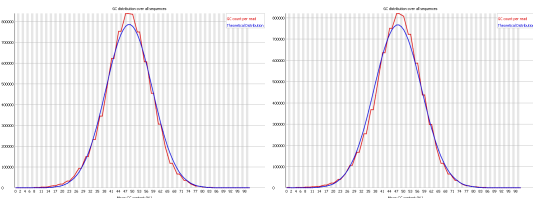
Per base N content



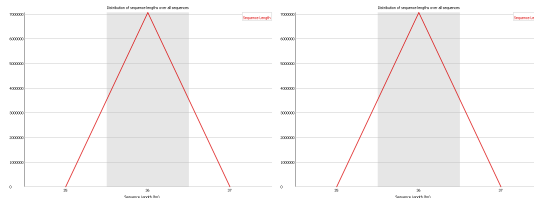
Per base GC content



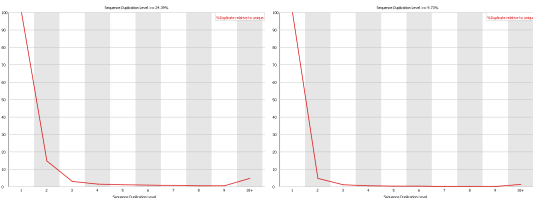
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

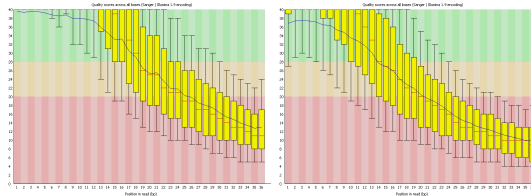
No overrepresented sequences

Overrepresented Kmers (pair 2)

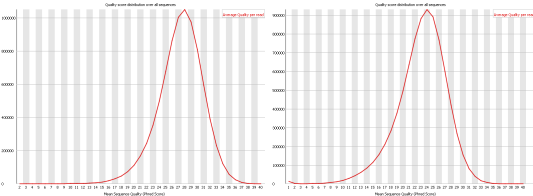
No overrepresented sequences

id62_1.fastq - 8406786 reads, 36 nt, 48% GC (pair 1), 48% GC (pair 2)

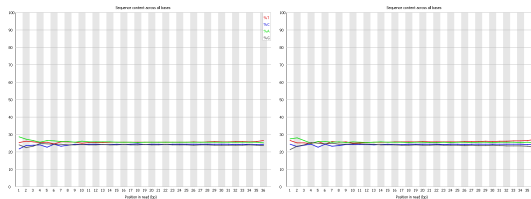
Per base quality



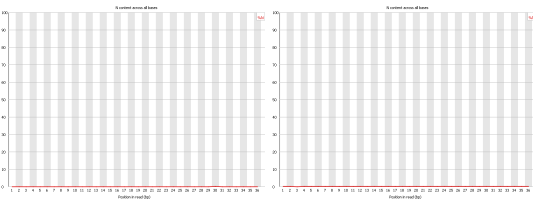
Per sequence quality



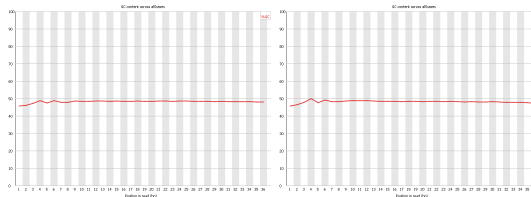
Per base sequence content



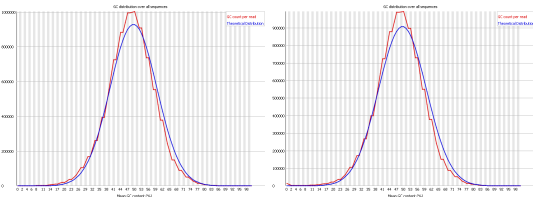
Per base N content



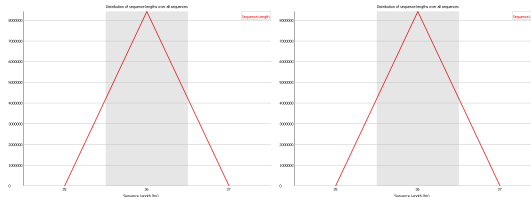
Per base GC content



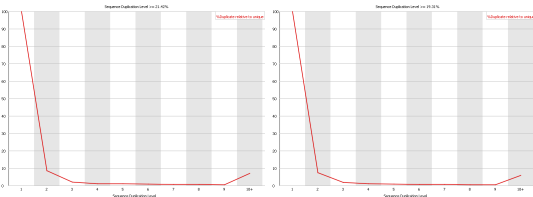
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

[illegible]

Overrepresented Kmers (pair 1)

No overrepresented sequences

Overrepresented Kmers (pair 2)

No overrepresented sequences

The figure displays eight rows of plots, each representing a different genomic metric. Each row contains two plots: the left plot is for the HBB gene and the right plot is for the whole genome.

- Per base quality:** The left plot shows quality scores across the HBB gene (1-36 bp) with a yellow histogram and a black line. The right plot shows the quality score distribution for the whole genome as a red bell curve.
- Per sequence quality:** The left plot shows quality scores across the HBB gene. The right plot shows the quality score distribution for the whole genome as a red bell curve.
- Per base sequence content:** The left plot shows sequence content across the HBB gene (1-36 bp) with a yellow histogram and a black line. The right plot shows the sequence content distribution for the whole genome as a red bell curve.
- Per base N content:** The left plot shows N content across the HBB gene (1-36 bp) with a yellow histogram and a black line. The right plot shows the N content distribution for the whole genome as a red bell curve.
- Per base GC content:** The left plot shows GC content across the HBB gene (1-36 bp) with a yellow histogram and a black line. The right plot shows the GC content distribution for the whole genome as a red bell curve.
- Per sequence GC content:** The left plot shows GC content across the HBB gene (1-36 bp) with a yellow histogram and a black line. The right plot shows the GC content distribution for the whole genome as a red bell curve.
- Sequence length distribution:** The left plot shows sequence length distribution for the HBB gene (1-36 bp) with a yellow histogram and a black line. The right plot shows the sequence length distribution for the whole genome as a red bell curve.
- Per sequence duplication level:** The left plot shows duplication level across the HBB gene (1-36 bp) with a yellow histogram and a black line. The right plot shows the duplication level distribution for the whole genome as a red bell curve.

No overrepresented sequences

[illegible]

No overrepresented sequences

No overrepresented sequences

The figure displays a series of plots comparing genomic metrics for the HBB gene (left column) and the whole genome (right column). The metrics are organized into four rows:

- Per base quality:** Shows quality scores across the HBB gene and whole genome. The HBB gene plot shows a significant drop in quality towards the end of the gene, while the whole genome plot shows a more stable quality profile.
- Per sequence quality:** Displays the distribution of sequence quality scores. Both plots show a similar distribution, peaking around a quality score of 30.
- Per base sequence content:** Shows the distribution of sequence content across the HBB gene and whole genome. The HBB gene plot shows a significant drop in content towards the end of the gene, while the whole genome plot shows a more stable content profile.
- Per base N content:** Displays the distribution of N content across the HBB gene and whole genome. Both plots show a similar distribution, with N content being very low across the entire region.
- Per base GC content:** Shows the distribution of GC content across the HBB gene and whole genome. The HBB gene plot shows a significant drop in GC content towards the end of the gene, while the whole genome plot shows a more stable GC content profile.
- Per sequence GC content:** Displays the distribution of sequence GC content. Both plots show a similar distribution, peaking around a GC content of 40%.
- Sequence length distribution:** Shows the distribution of sequence lengths. Both plots show a similar distribution, peaking around a length of 1000.
- Per sequence duplication level:** Displays the distribution of duplication levels. Both plots show a similar distribution, peaking around a duplication level of 1.0.

No overrepresented sequences

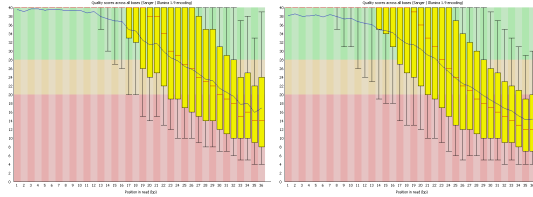
[illegible]

No overrepresented sequences

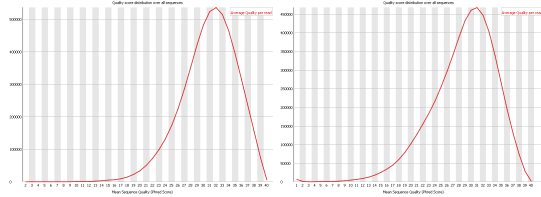
No overrepresented sequences

id75_3.fastq - 5628839 reads, 36 nt, 48% GC (pair 1), 48% GC (pair 2)

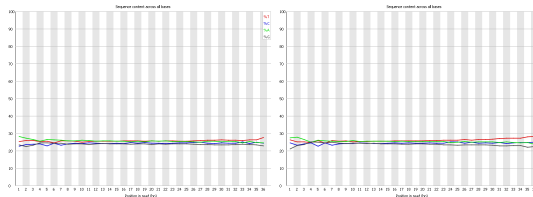
Per base quality



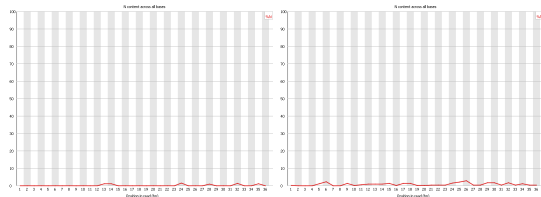
Per sequence quality



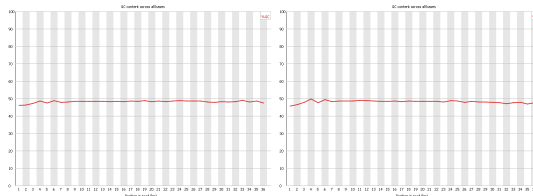
Per base sequence content



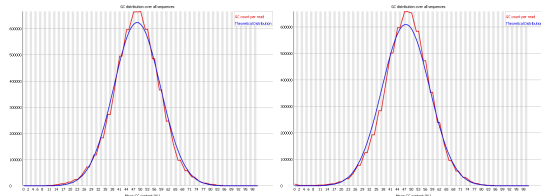
Per base N content



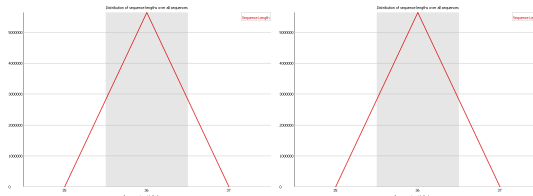
Per base GC content



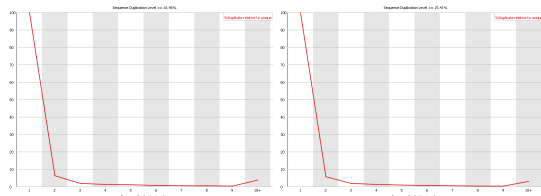
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

[illegible]

Overrepresented Kmers (pair 1)

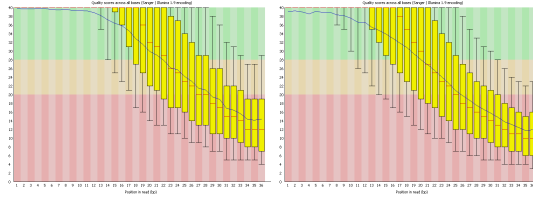
No overrepresented sequences

Overrepresented Kmers (pair 2)

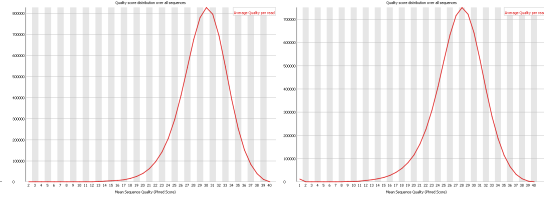
No overrepresented sequences

id75_5.fastq - 7118701 reads, 36 nt, 48% GC (pair 1), 48% GC (pair 2)

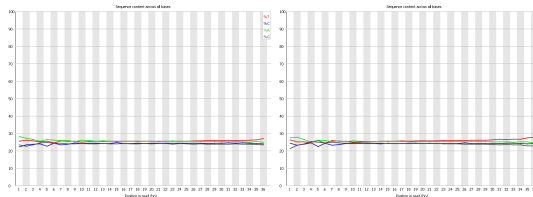
Per base quality



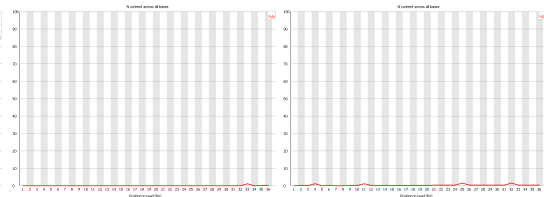
Per sequence quality



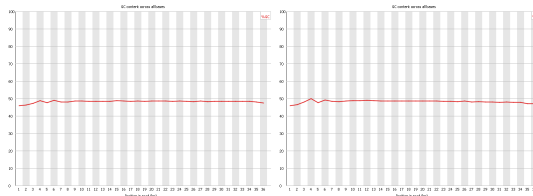
Per base sequence content



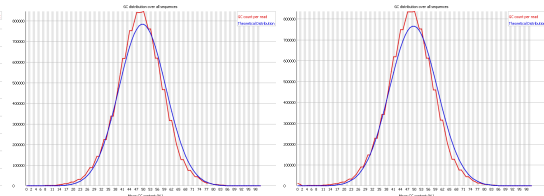
Per base N content



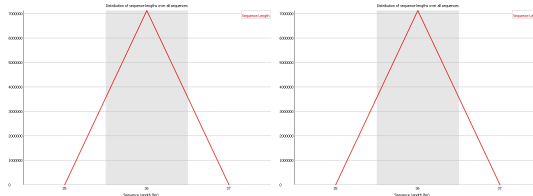
Per base GC content



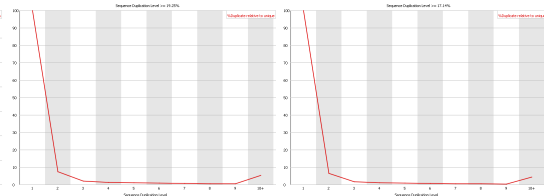
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

[illegible]

Overrepresented Kmers (pair 1)

No overrepresented sequences

Overrepresented Kmers (pair 2)

No overrepresented sequences

The figure displays a comparison of genomic metrics between the reference genome (left column) and the assembled contigs (right column). The metrics are organized into four rows:

- Per base quality:** Shows quality scores across the genome. The reference genome (left) shows a high quality score (mostly above 30), while the assembled contigs (right) show a lower quality score (mostly below 20).
- Per sequence quality:** Shows the distribution of sequence quality. The reference genome (left) has a peak around 30, while the assembled contigs (right) have a peak around 20.
- Per base sequence content:** Shows the distribution of sequence content. The reference genome (left) has a peak around 30, while the assembled contigs (right) have a peak around 20.
- Per sequence sequence content:** Shows the distribution of sequence content. The reference genome (left) has a peak around 30, while the assembled contigs (right) have a peak around 20.

The plots are arranged in a 4x2 grid, with the reference genome on the left and the assembled contigs on the right. The x-axis for all plots represents the genome position (1 to 250,000,000). The y-axis represents the quality score or sequence content. The reference genome plots show a high quality score (mostly above 30), while the assembled contigs plots show a lower quality score (mostly below 20).

No overrepresented sequences

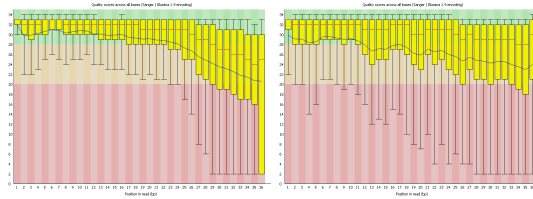
[illegible]

No overrepresented sequences

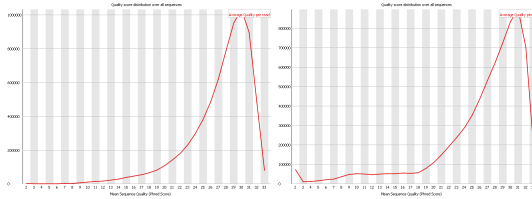
No overrepresented sequences

id87_3.fastq - 7076768 reads, 36 nt, 49% GC (pair 1), 50% GC (pair 2)

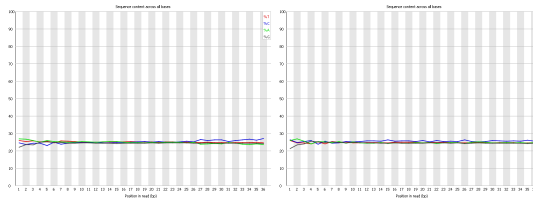
Per base quality



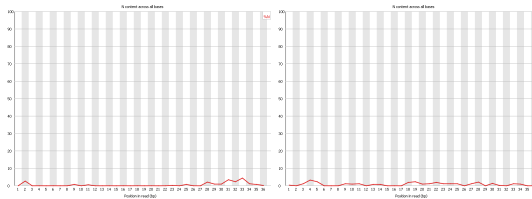
Per sequence quality



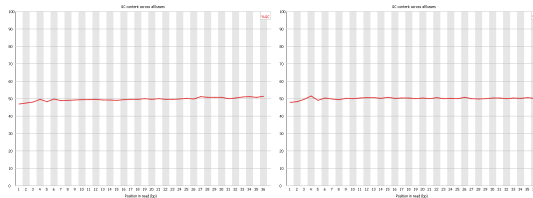
Per base sequence content



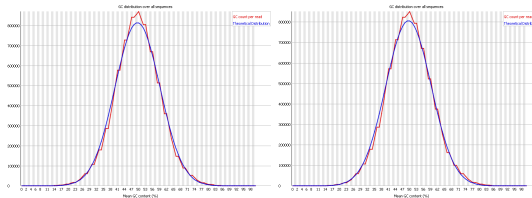
Per base N content



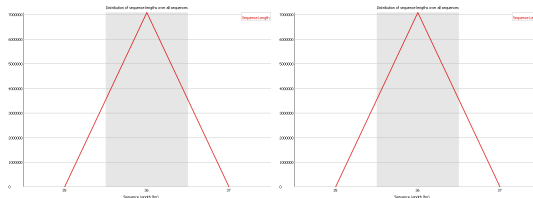
Per base GC content



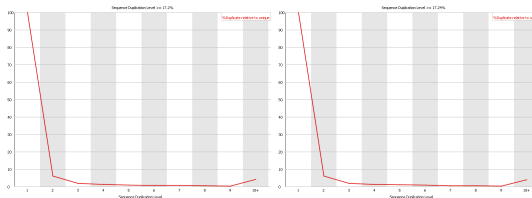
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

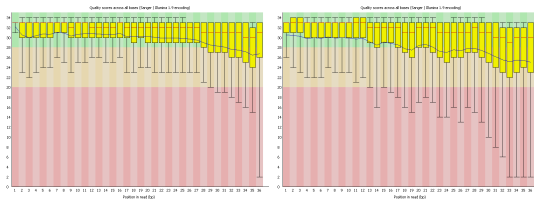
No overrepresented sequences

Overrepresented Kmers (pair 2)

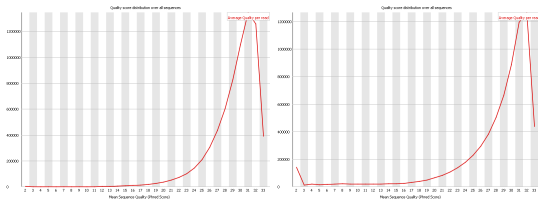
No overrepresented sequences

id87_4.fastq - 6988412 reads, 36 nt, 49% GC (pair 1), 49% GC (pair 2)

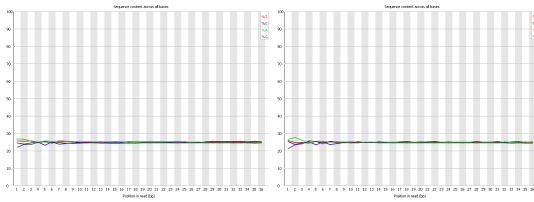
Per base quality



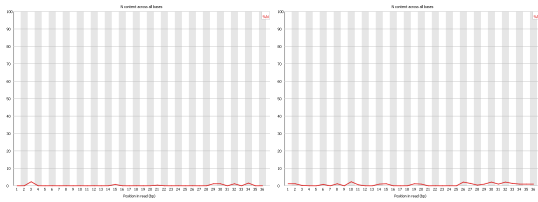
Per sequence quality



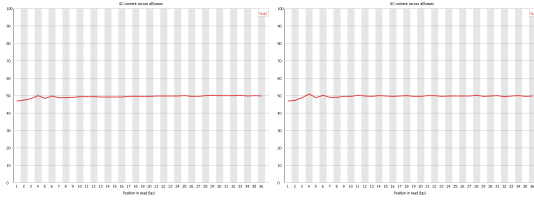
Per base sequence content



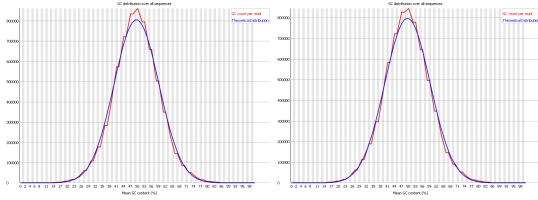
Per base N content



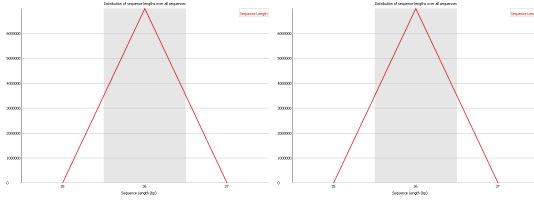
Per base GC content



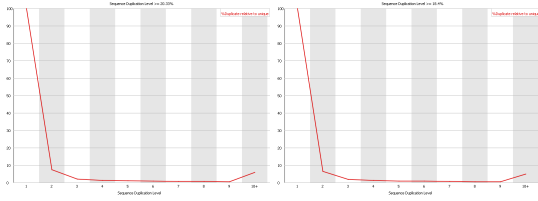
Per sequence GC content



Sequence length distribution



Per sequence duplication level



Overrepresented sequences (top 5 for pair 1)

No overrepresented sequences

Overrepresented sequences (top 5 for pair 2)

No overrepresented sequences

Overrepresented Kmers (pair 1)

No overrepresented sequences

Overrepresented Kmers (pair 2)

No overrepresented sequences