

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 22:25:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505986.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1505986 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505986.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 22:25:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505986.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,997,537
Mapped reads	6,471,322 / 71.92%
Unmapped reads	2,526,215 / 28.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	237 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	417,453 / 4.64%
Duplication rate	4.66%
Clipped reads	864,780 / 9.61%

2.2. ACGT Content

Number/percentage of A's	92,679,854 / 30.68%
Number/percentage of C's	58,932,162 / 19.51%
Number/percentage of T's	90,634,157 / 30%
Number/percentage of G's	59,872,125 / 19.82%
Number/percentage of N's	1,204 / 0%
GC Percentage	39.32%

2.3. Coverage

Mean	0.0976

Standard Deviation	1.0154
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2.4. Mapping Quality

Mean Mapping Quality	46.08
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2.5. Mismatches and indels

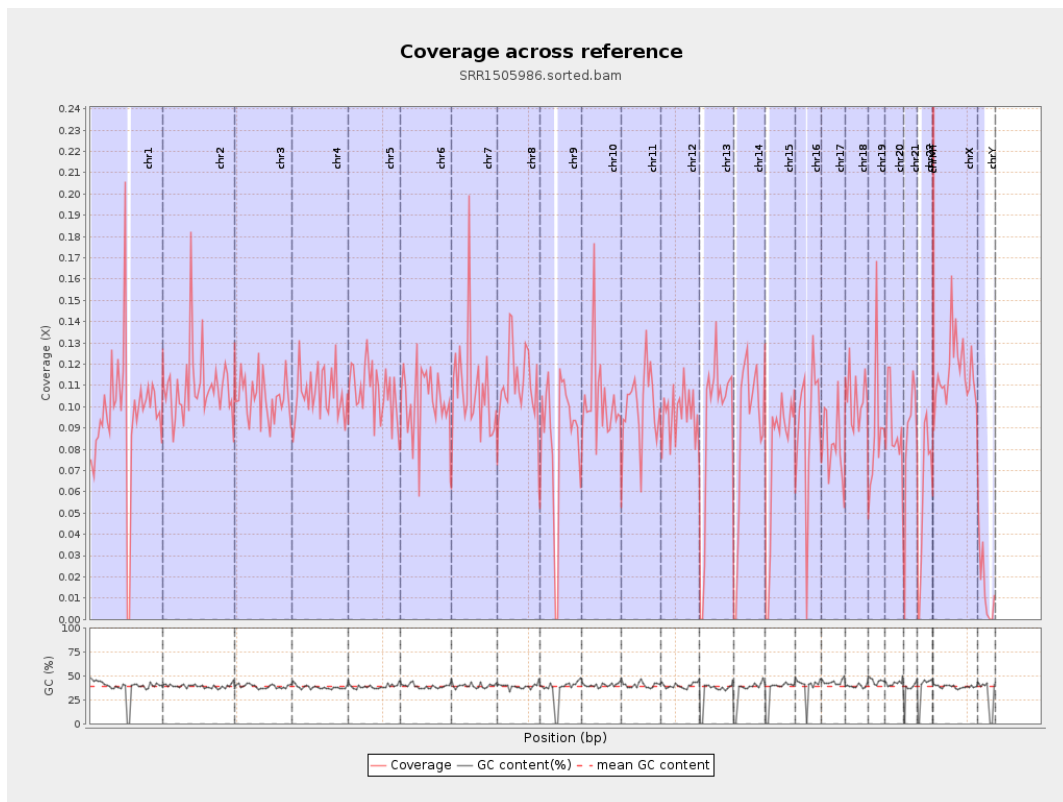
General error rate	0.47%
Mismatches	1,403,874
Insertions	14,293
Mapped reads with at least one insertion	0.22%
Deletions	42,167
Mapped reads with at least one deletion	0.65%
Homopolymer indels	47.55%

2.6. Chromosome stats

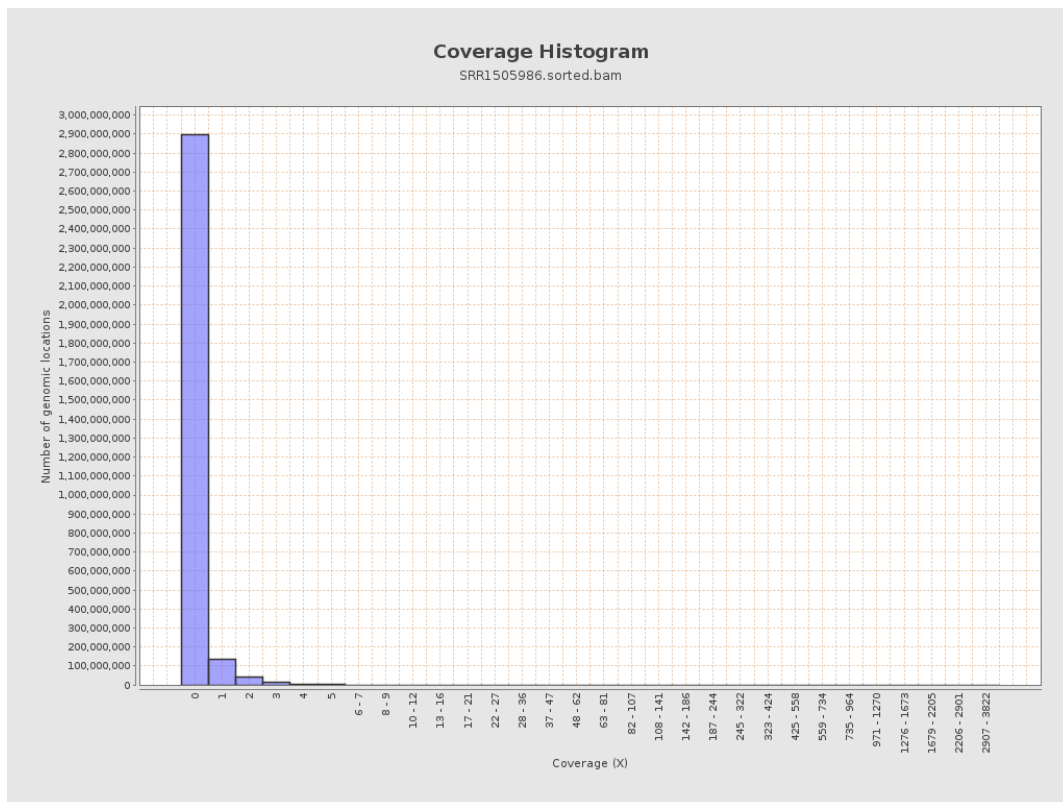
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	23807686	0.0955	2.1844
chr2	243199373	26566760	0.1092	0.7347
chr3	198022430	20639416	0.1042	0.4707
chr4	191154276	20286334	0.1061	0.4737
chr5	180915260	19257636	0.1064	0.4765
chr6	171115067	17618647	0.103	0.536
chr7	159138663	17080169	0.1073	1.1506

chr8	146364022	16124401	0.1102	2.0947
chr9	141213431	12192746	0.0863	0.6664
chr10	135534747	13902369	0.1026	0.9211
chr11	135006516	13600308	0.1007	0.7407
chr12	133851895	12888026	0.0963	0.4908
chr13	115169878	10688967	0.0928	0.4247
chr14	107349540	9665161	0.09	0.6534
chr15	102531392	7827833	0.0763	0.3822
chr16	90354753	8189862	0.0906	0.5099
chr17	81195210	6695133	0.0825	0.4857
chr18	78077248	8109838	0.1039	1.6428
chr19	59128983	5281343	0.0893	1.4728
chr20	63025520	5663080	0.0899	0.4331
chr21	48129895	4165256	0.0865	0.4631
chr22	51304566	3029962	0.0591	0.3259
chrMT	16571	39731	2.3976	2.5593
chrX	155270560	17995259	0.1159	0.6339
chrY	59373566	860746	0.0145	0.2151

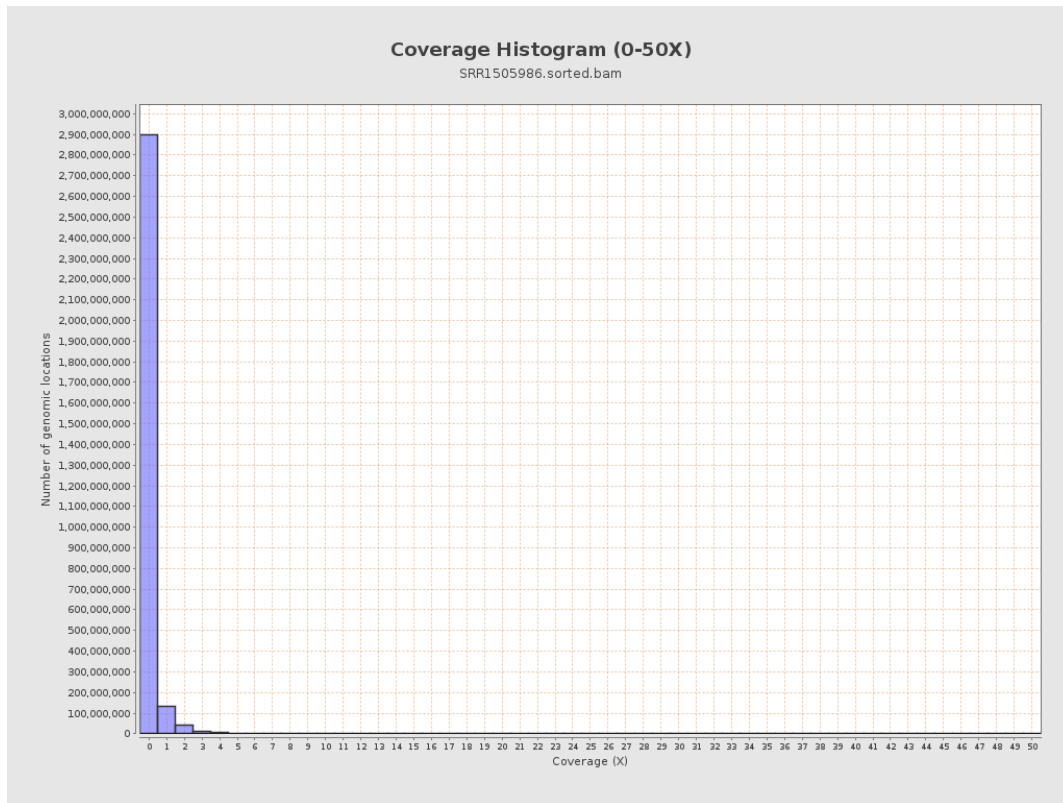
3. Results : Coverage across reference



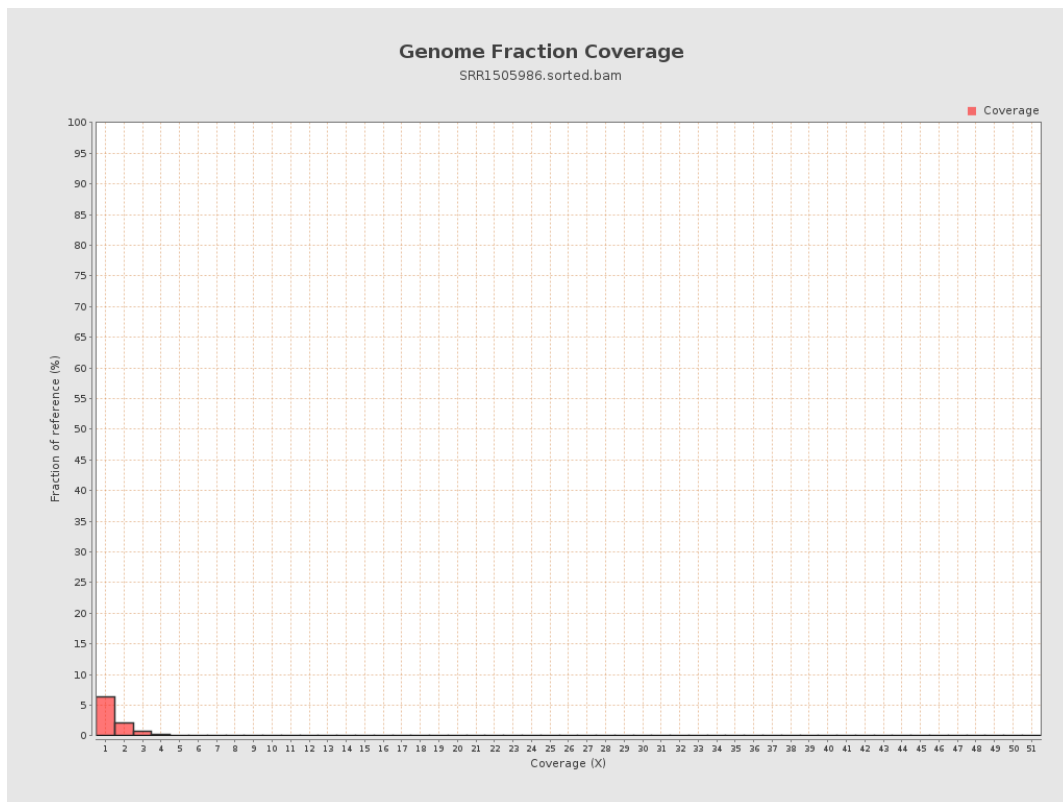
4. Results : Coverage Histogram



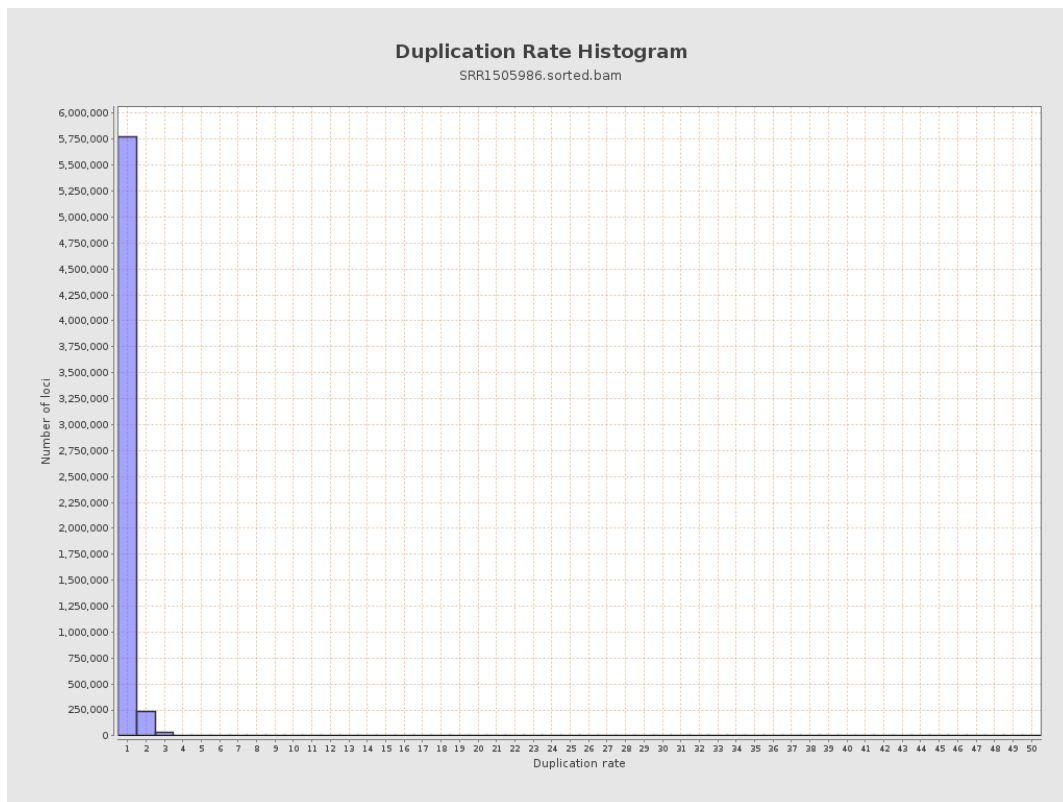
5. Results : Coverage Histogram (0-50X)



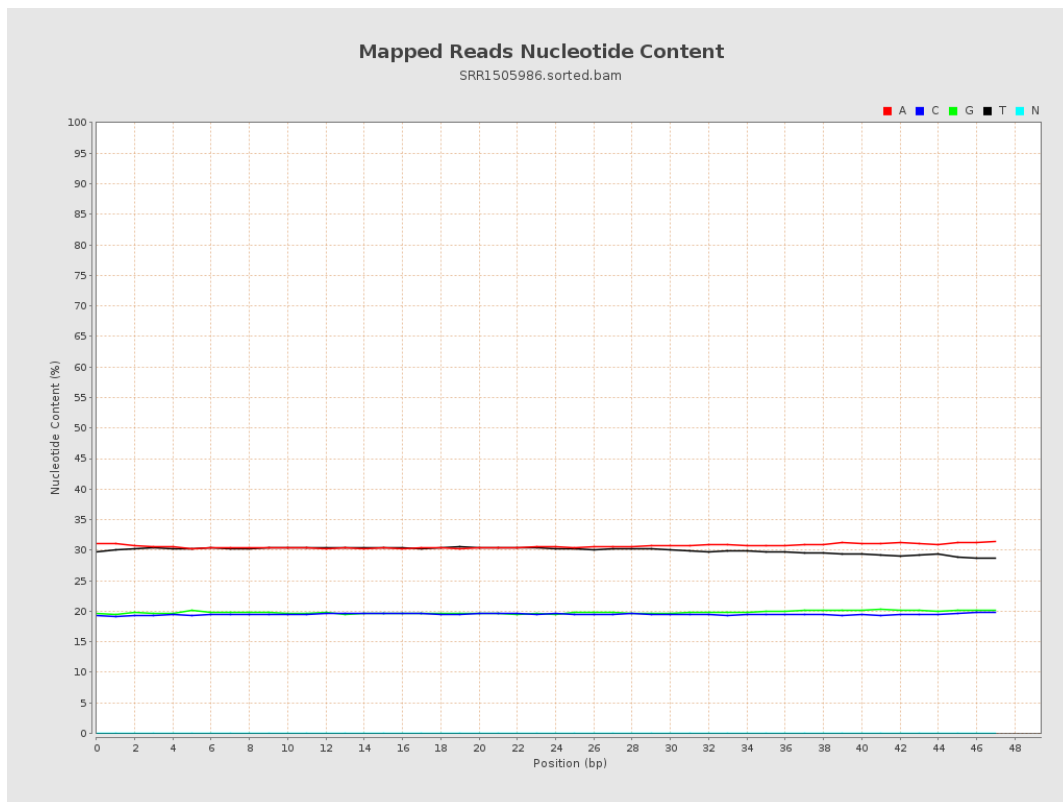
6. Results : Genome Fraction Coverage



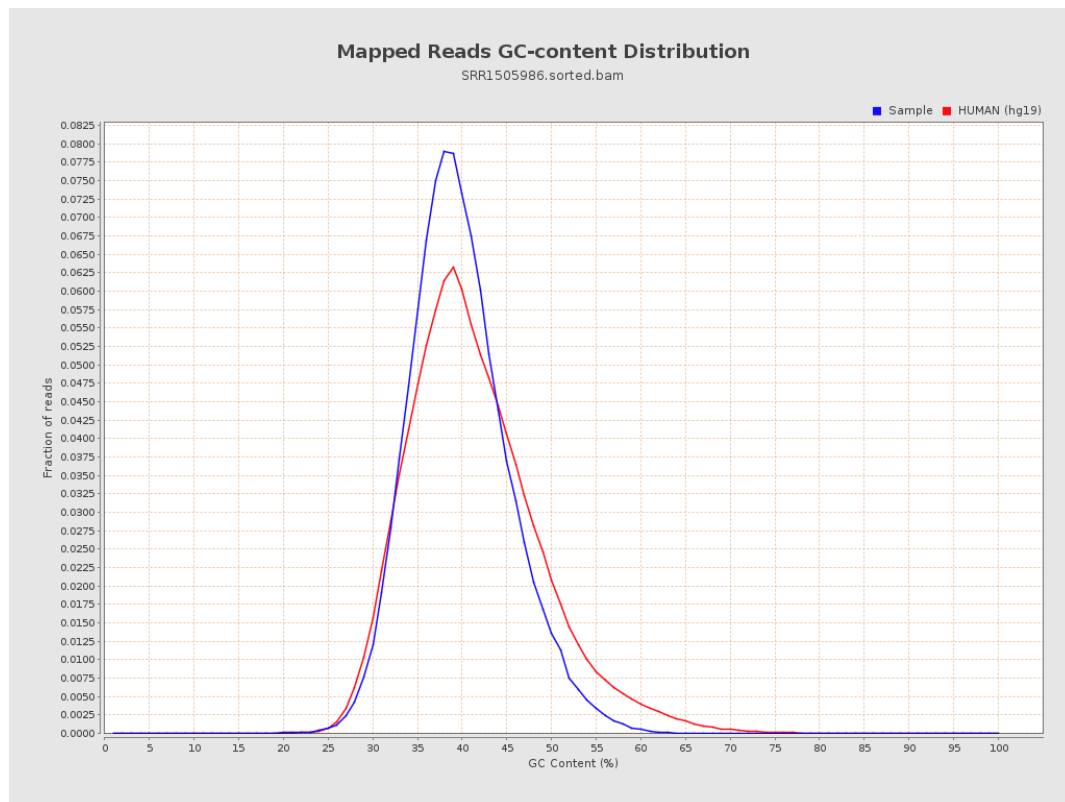
7. Results : Duplication Rate Histogram



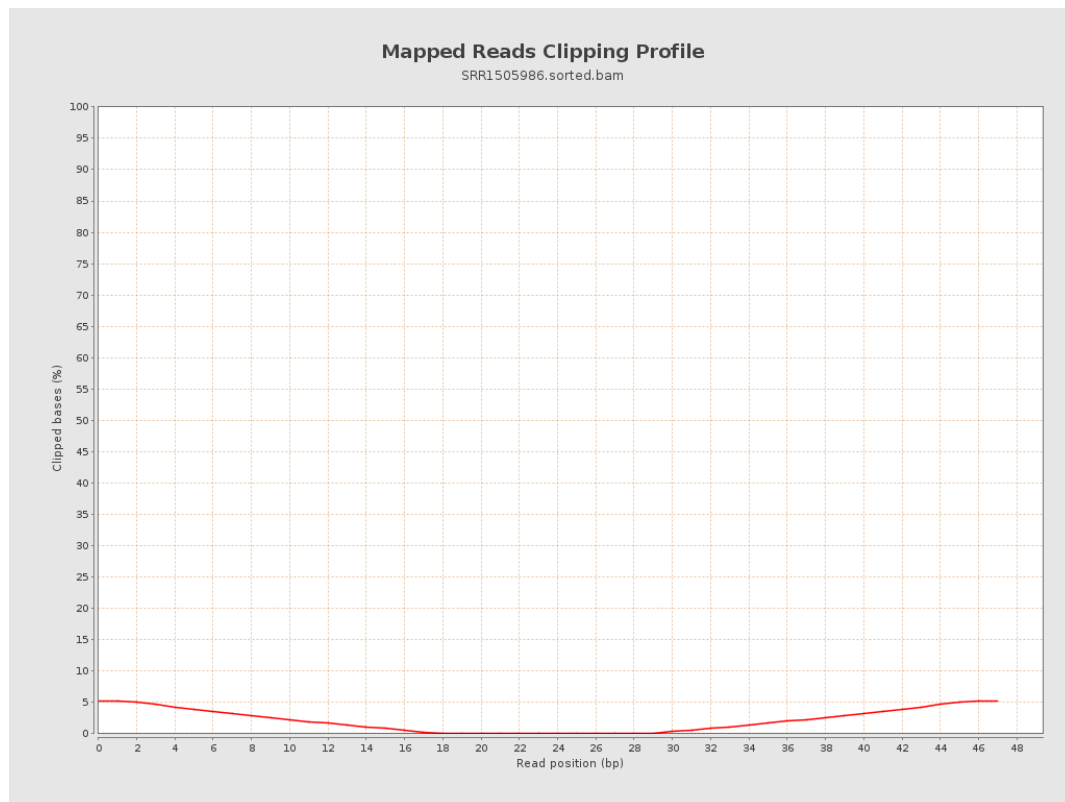
8. Results : Mapped Reads Nucleotide Content



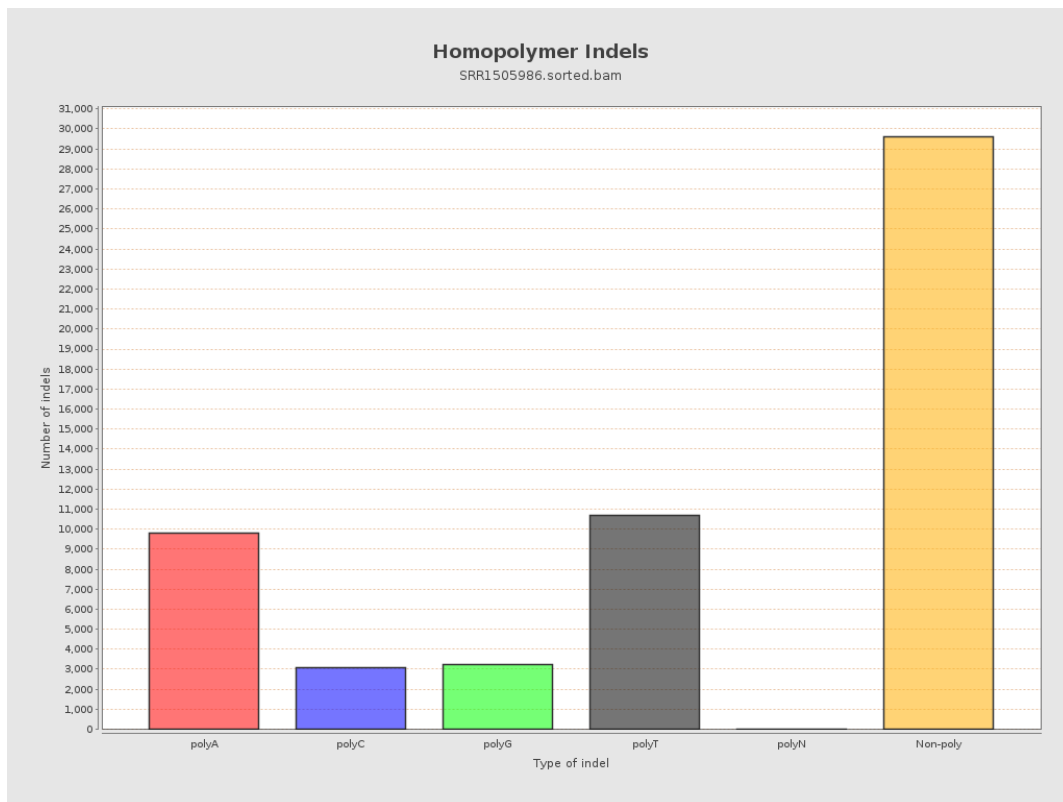
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

