

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 12:18:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008805.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_SRR6008805 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008805.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 12:18:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008805.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,527,159
Mapped reads	1,290,099 / 84.48%
Unmapped reads	237,060 / 15.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,550 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	103,946 / 6.81%
Duplication rate	6.47%
Clipped reads	642,605 / 42.08%

2.2. ACGT Content

Number/percentage of A's	22,534,925 / 26.79%
Number/percentage of C's	16,412,156 / 19.51%
Number/percentage of T's	25,811,289 / 30.68%
Number/percentage of G's	19,244,101 / 22.87%
Number/percentage of N's	126,075 / 0.15%
GC Percentage	42.38%

2.3. Coverage

Mean	0.0272

Standard Deviation	0.3111
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2.4. Mapping Quality

Mean Mapping Quality	44.58
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2.5. Mismatches and indels

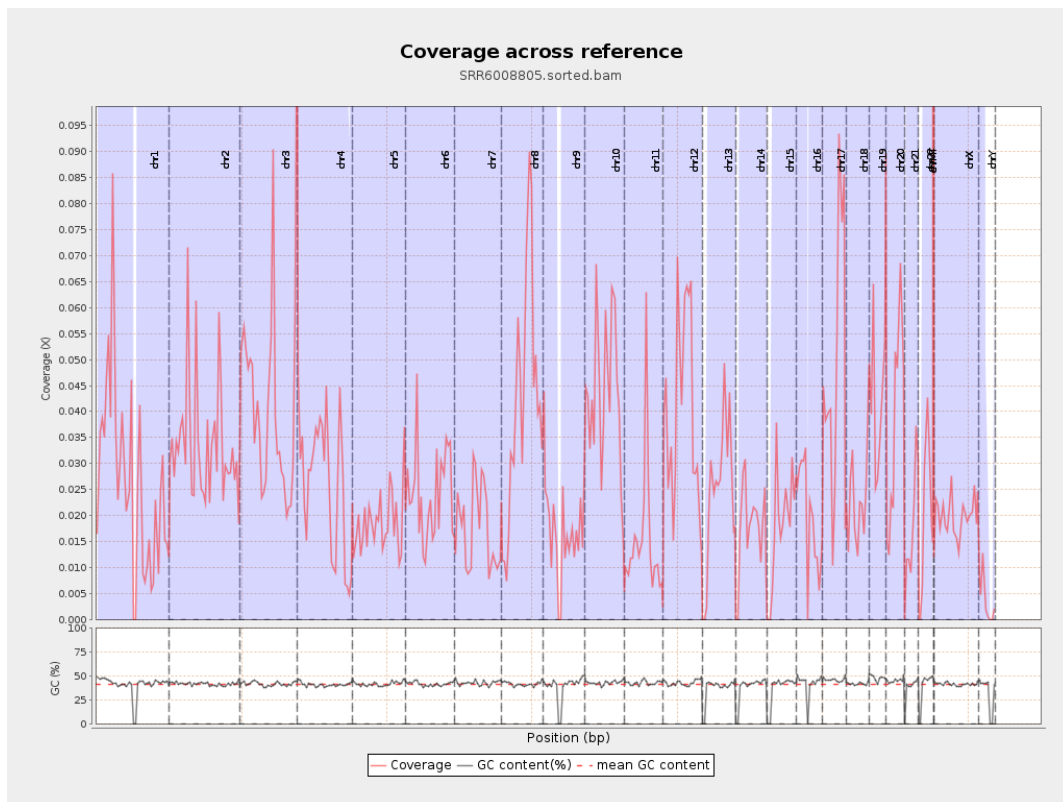
General error rate	0.88%
Mismatches	730,579
Insertions	6,114
Mapped reads with at least one insertion	0.47%
Deletions	26,293
Mapped reads with at least one deletion	2.01%
Homopolymer indels	45.43%

2.6. Chromosome stats

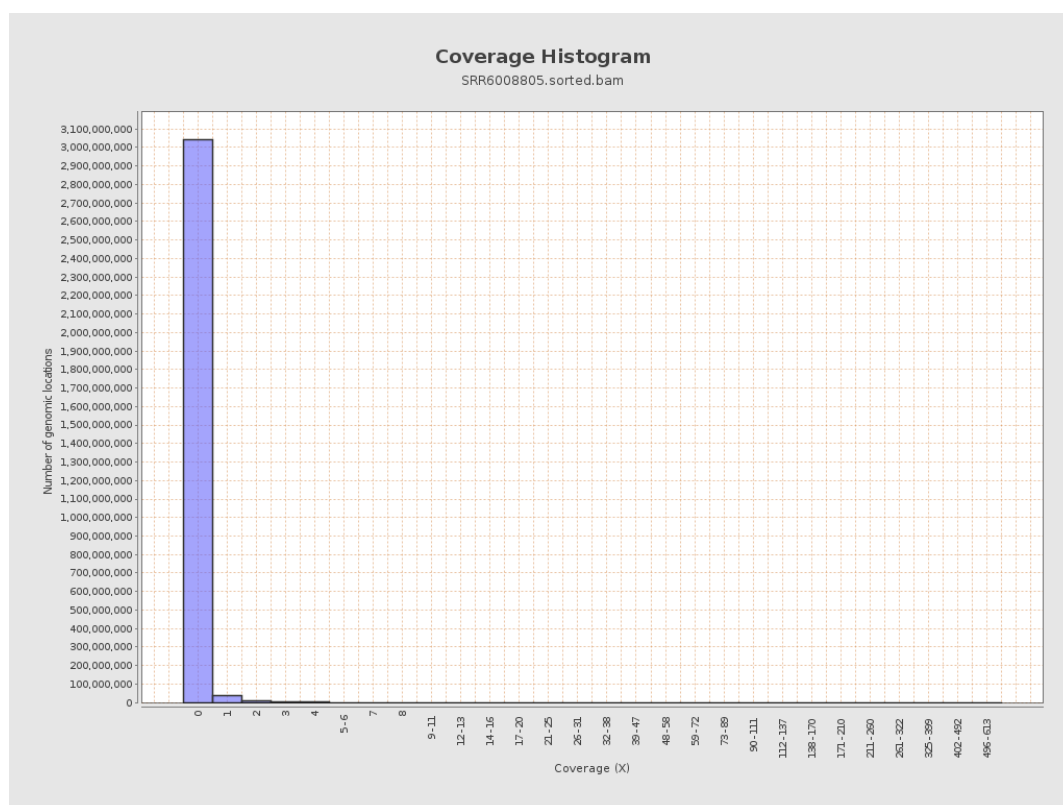
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6536969	0.0262	0.5236
chr2	243199373	8225804	0.0338	0.4101
chr3	198022430	7970766	0.0403	0.2838
chr4	191154276	4903362	0.0257	0.2256
chr5	180915260	3380717	0.0187	0.1908
chr6	171115067	4145844	0.0242	0.2341
chr7	159138663	2839743	0.0178	0.2257

chr8	146364022	6094714	0.0416	0.4165
chr9	141213431	2232599	0.0158	0.2229
chr10	135534747	5890313	0.0435	0.393
chr11	135006516	2072487	0.0154	0.1904
chr12	133851895	5507537	0.0411	0.2886
chr13	115169878	2831947	0.0246	0.2207
chr14	107349540	1894257	0.0176	0.1923
chr15	102531392	1868512	0.0182	0.1864
chr16	90354753	1730996	0.0192	0.2571
chr17	81195210	3982685	0.0491	0.3264
chr18	78077248	1753493	0.0225	0.3534
chr19	59128983	2532370	0.0428	0.4605
chr20	63025520	2420097	0.0384	0.2817
chr21	48129895	858050	0.0178	0.1946
chr22	51304566	1013767	0.0198	0.1966
chrMT	16571	218844	13.2064	8.6553
chrX	155270560	3061127	0.0197	0.2022
chrY	59373566	208528	0.0035	0.1606

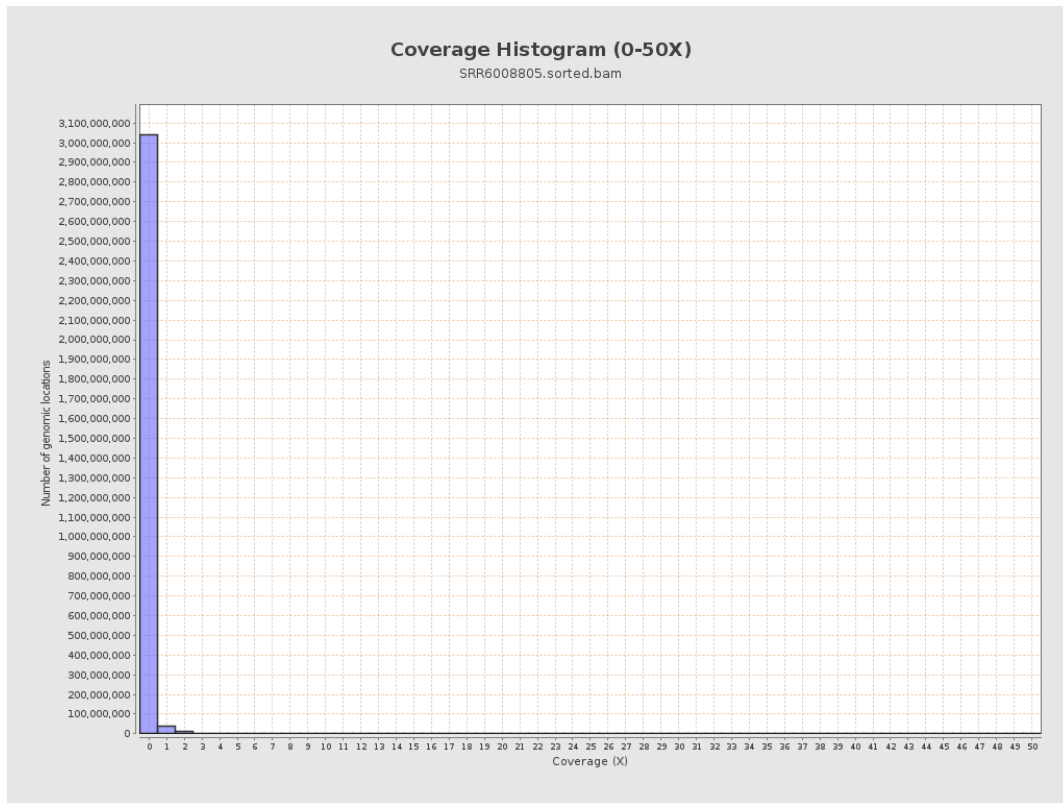
3. Results : Coverage across reference



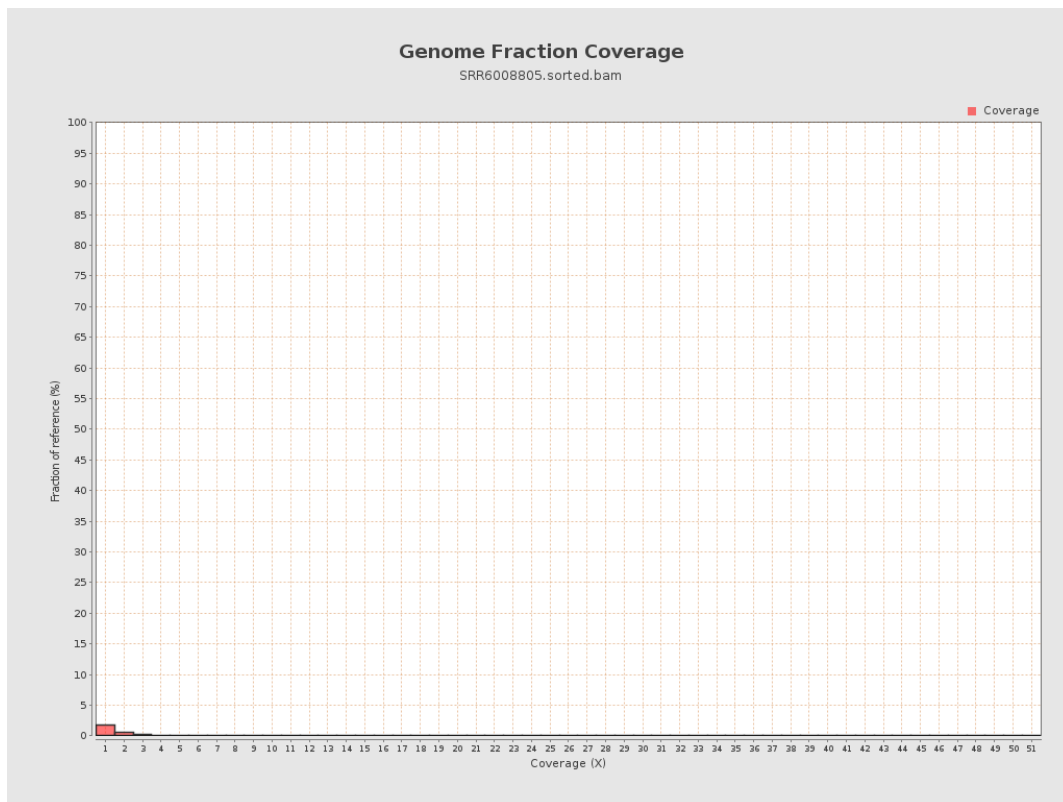
4. Results : Coverage Histogram



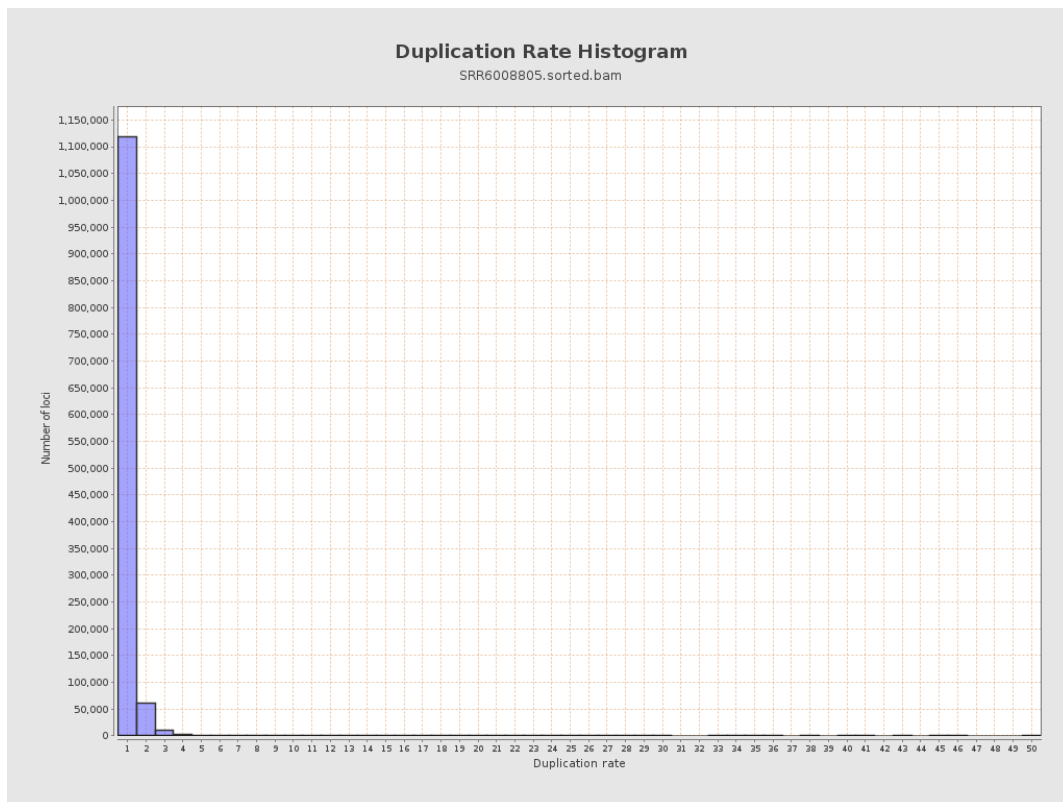
5. Results : Coverage Histogram (0-50X)



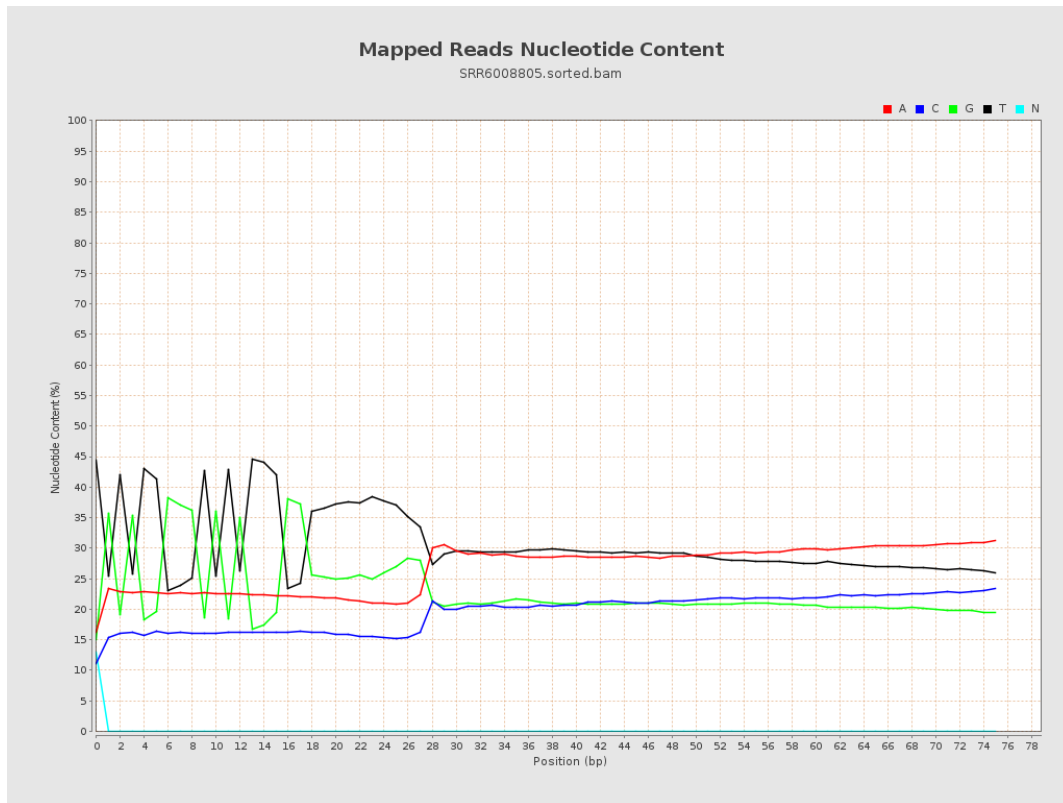
6. Results : Genome Fraction Coverage



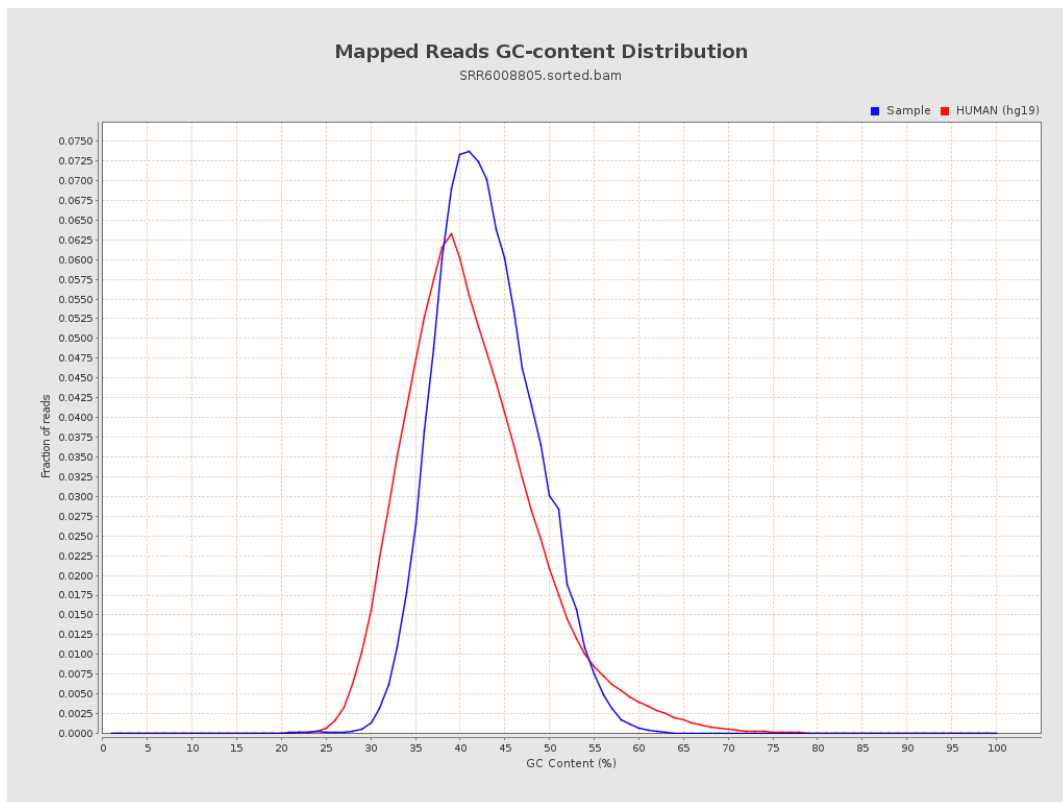
7. Results : Duplication Rate Histogram



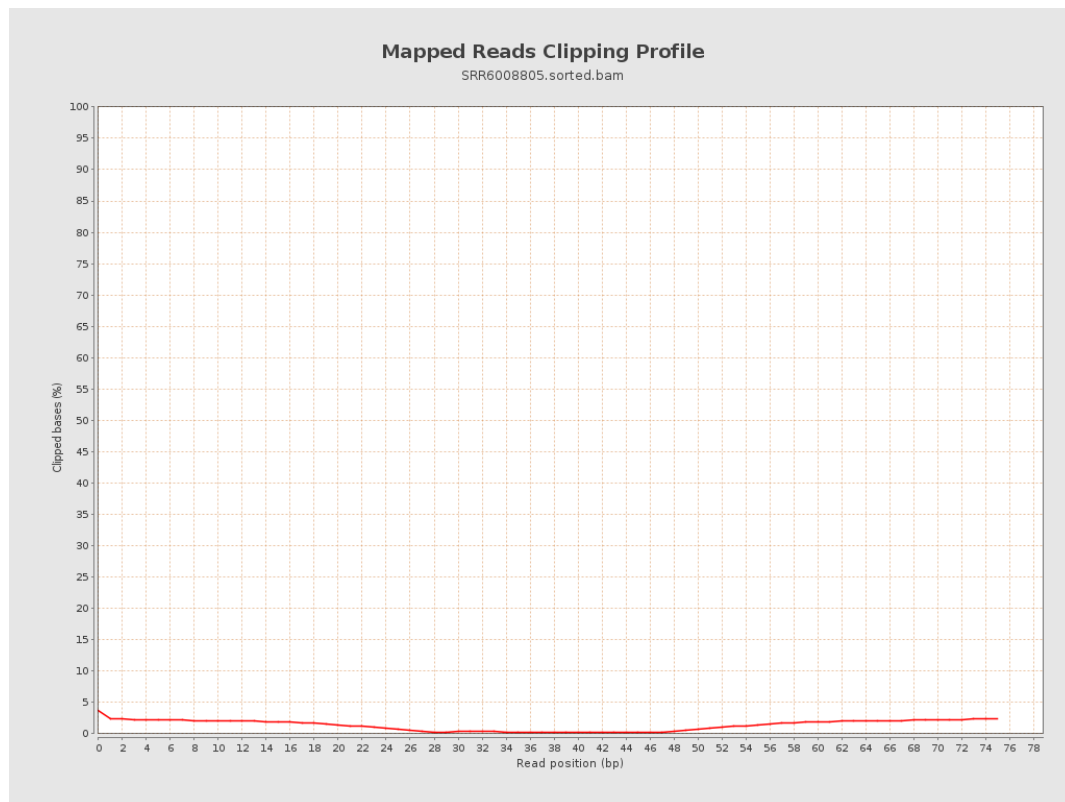
8. Results : Mapped Reads Nucleotide Content



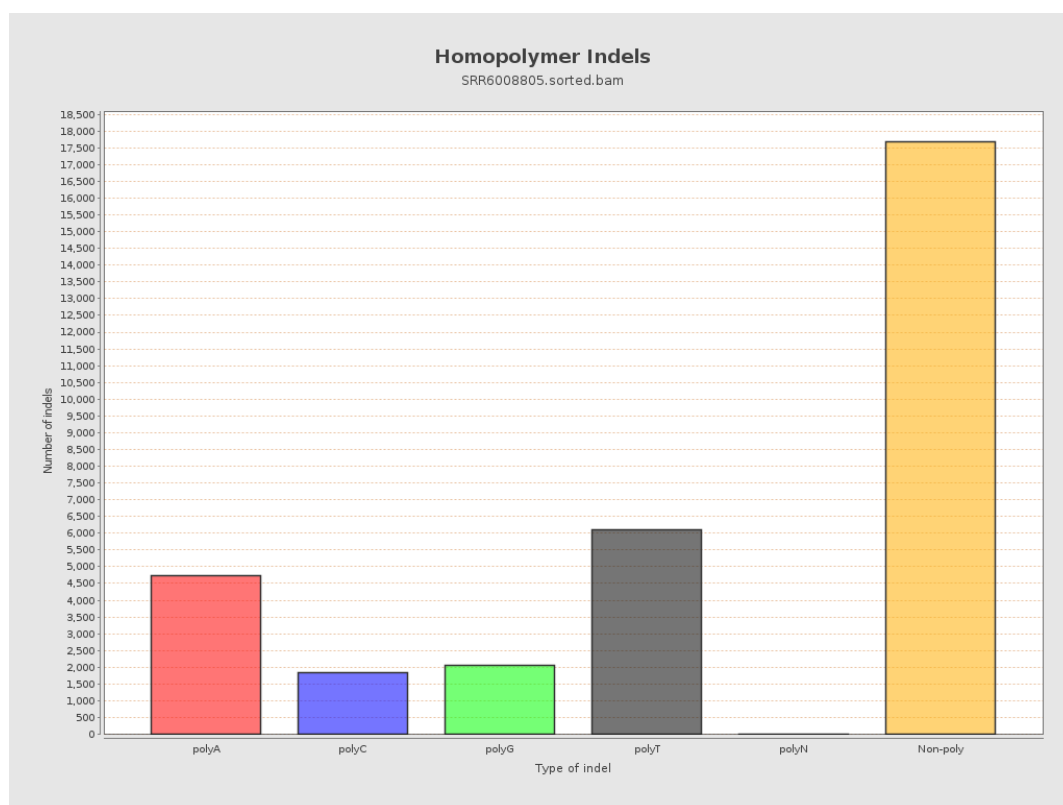
9. Results : Mapped Reads GC-content Distribution



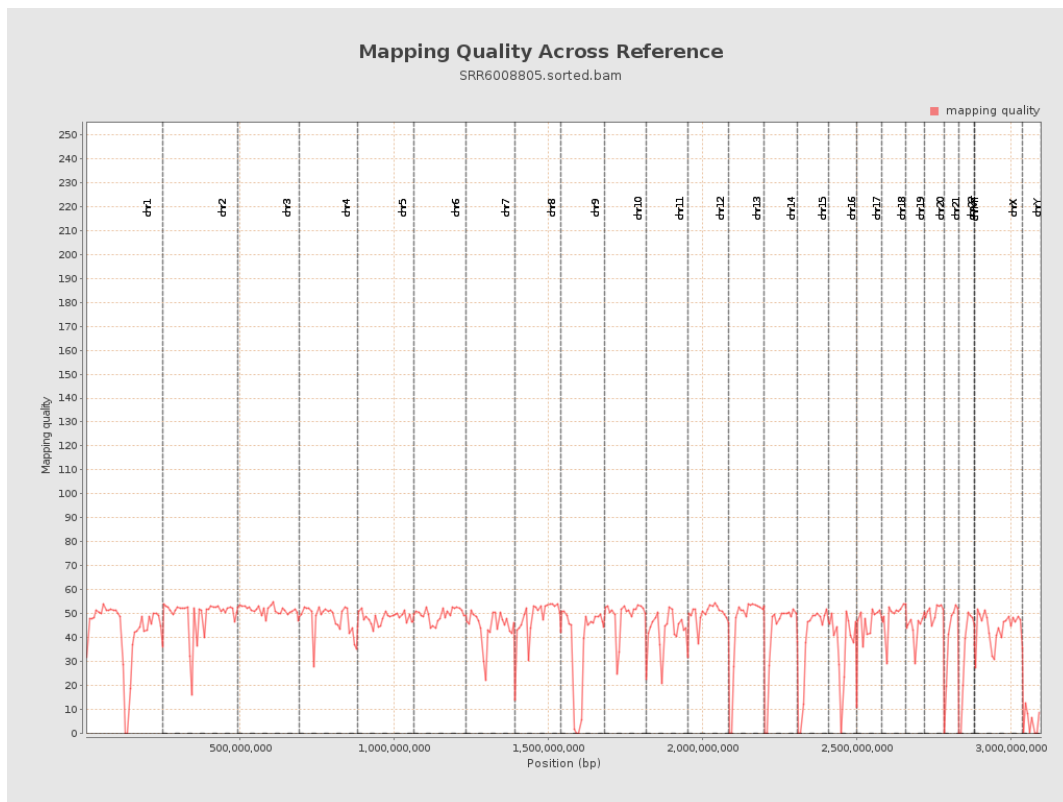
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

