

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 10:16:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008762.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_SRR6008762 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008762.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 10:16:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008762.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,724,958
Mapped reads	1,538,274 / 89.18%
Unmapped reads	186,684 / 10.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,705 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	98,300 / 5.7%
Duplication rate	5.04%
Clipped reads	691,410 / 40.08%

2.2. ACGT Content

Number/percentage of A's	27,469,415 / 26.89%
Number/percentage of C's	19,936,192 / 19.51%
Number/percentage of T's	31,316,553 / 30.65%
Number/percentage of G's	23,313,796 / 22.82%
Number/percentage of N's	130,404 / 0.13%
GC Percentage	42.33%

2.3. Coverage

Mean	0.033

Standard Deviation	0.3477
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2.4. Mapping Quality

Mean Mapping Quality	44.81
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2.5. Mismatches and indels

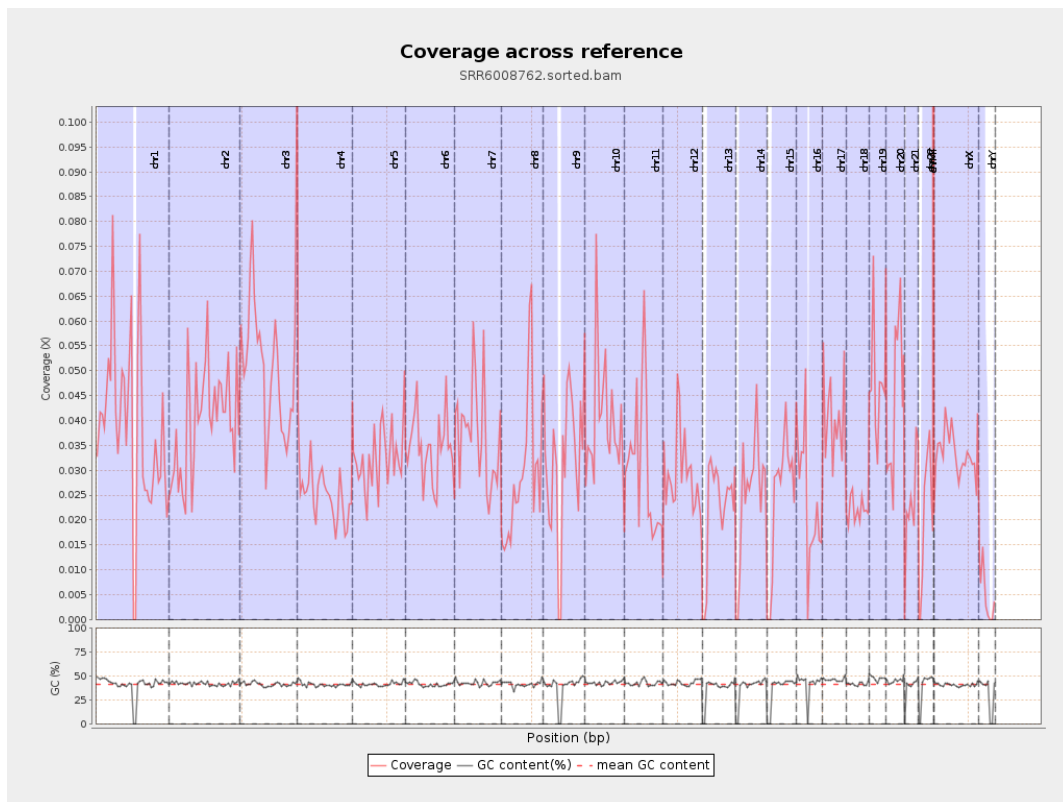
General error rate	0.84%
Mismatches	842,729
Insertions	7,979
Mapped reads with at least one insertion	0.51%
Deletions	28,063
Mapped reads with at least one deletion	1.81%
Homopolymer indels	44.85%

2.6. Chromosome stats

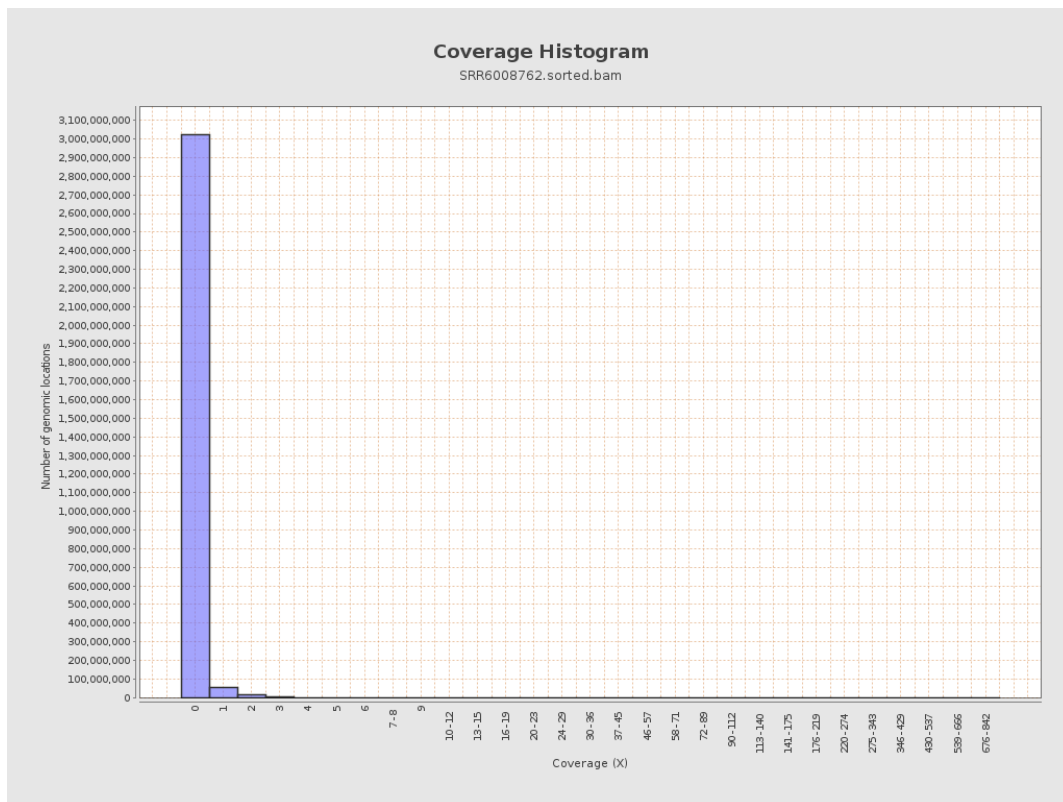
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9510333	0.0382	0.5594
chr2	243199373	9712080	0.0399	0.4743
chr3	198022430	10082244	0.0509	0.301
chr4	191154276	4784918	0.025	0.2159
chr5	180915260	5859744	0.0324	0.234
chr6	171115067	5866552	0.0343	0.2614
chr7	159138663	5897745	0.0371	0.3625

chr8	146364022	4255470	0.0291	0.5334
chr9	141213431	4287740	0.0304	0.263
chr10	135534747	5351769	0.0395	0.4359
chr11	135006516	4142335	0.0307	0.245
chr12	133851895	3942743	0.0295	0.2266
chr13	115169878	2518324	0.0219	0.1922
chr14	107349540	2677072	0.0249	0.2147
chr15	102531392	2581105	0.0252	0.2049
chr16	90354753	2118666	0.0234	0.3058
chr17	81195210	3323079	0.0409	0.283
chr18	78077248	1728650	0.0221	0.3388
chr19	59128983	2833403	0.0479	0.4167
chr20	63025520	2747798	0.0436	0.2776
chr21	48129895	1134104	0.0236	0.2137
chr22	51304566	1044885	0.0204	0.1842
chrMT	16571	402971	24.3178	13.6189
chrX	155270560	5130876	0.033	0.2415
chrY	59373566	281991	0.0047	0.1531

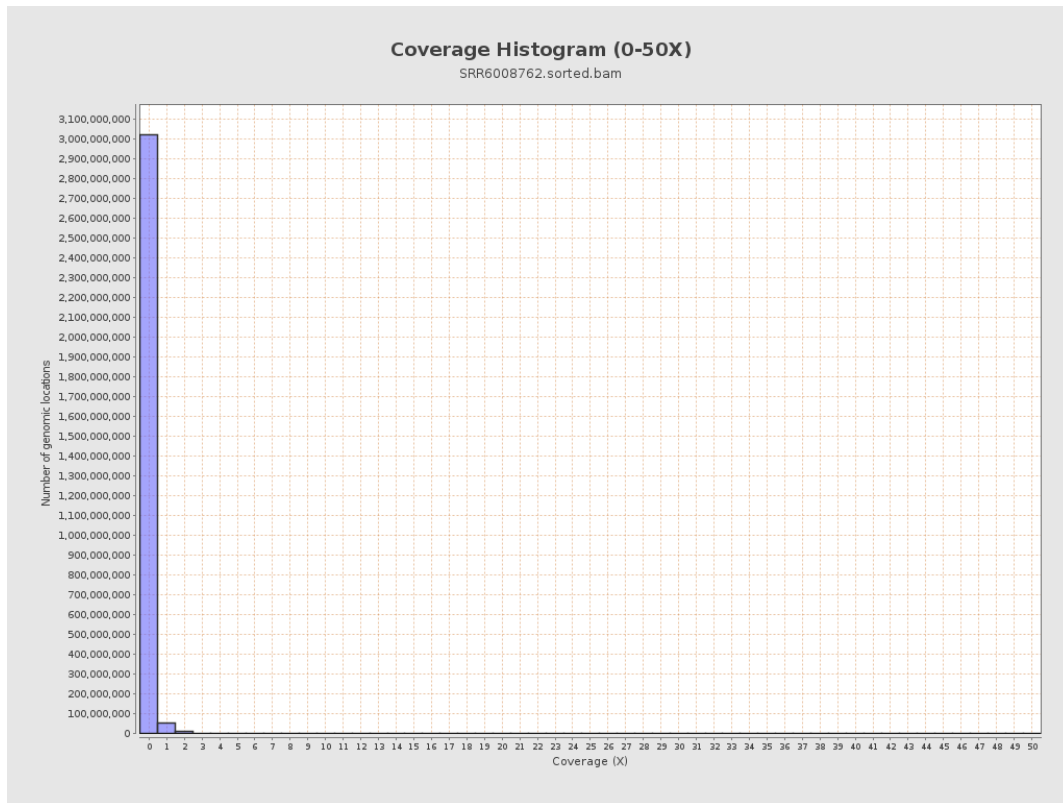
3. Results : Coverage across reference



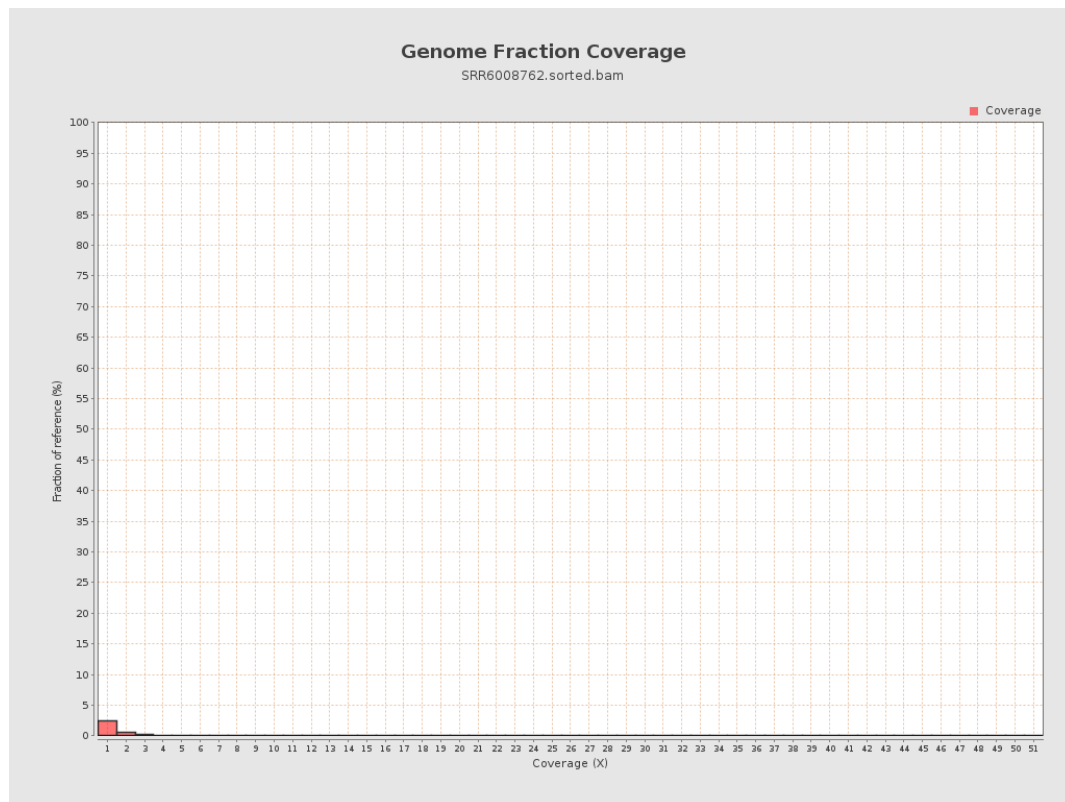
4. Results : Coverage Histogram



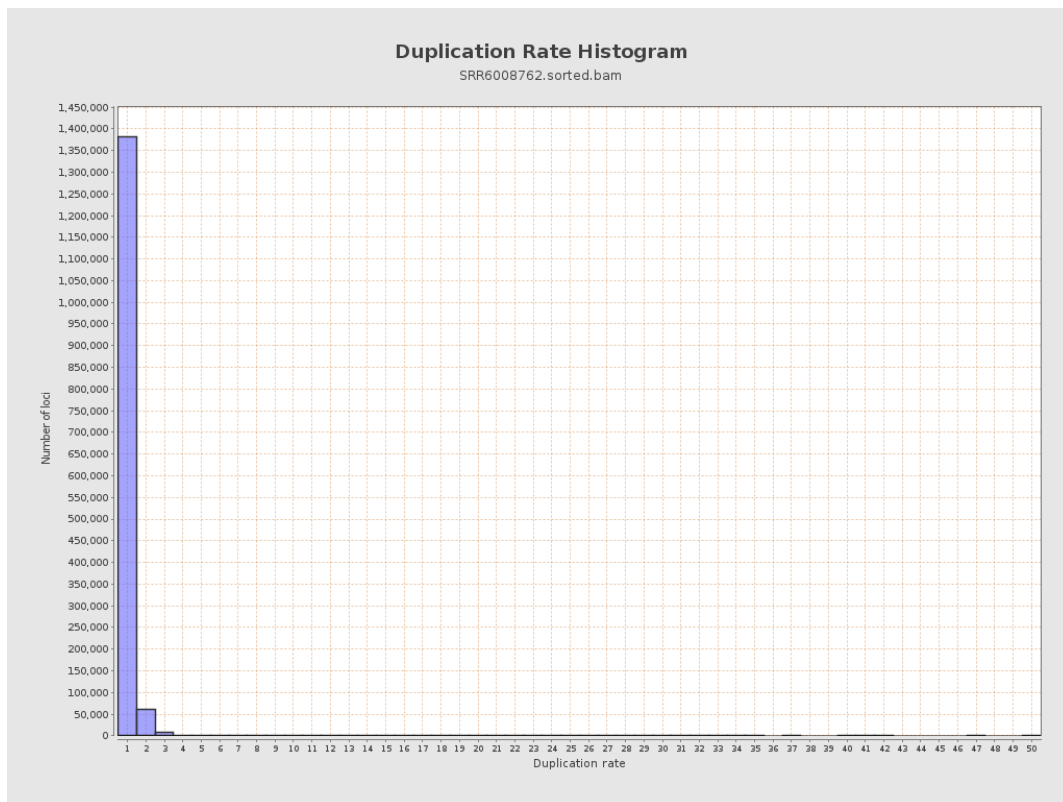
5. Results : Coverage Histogram (0-50X)



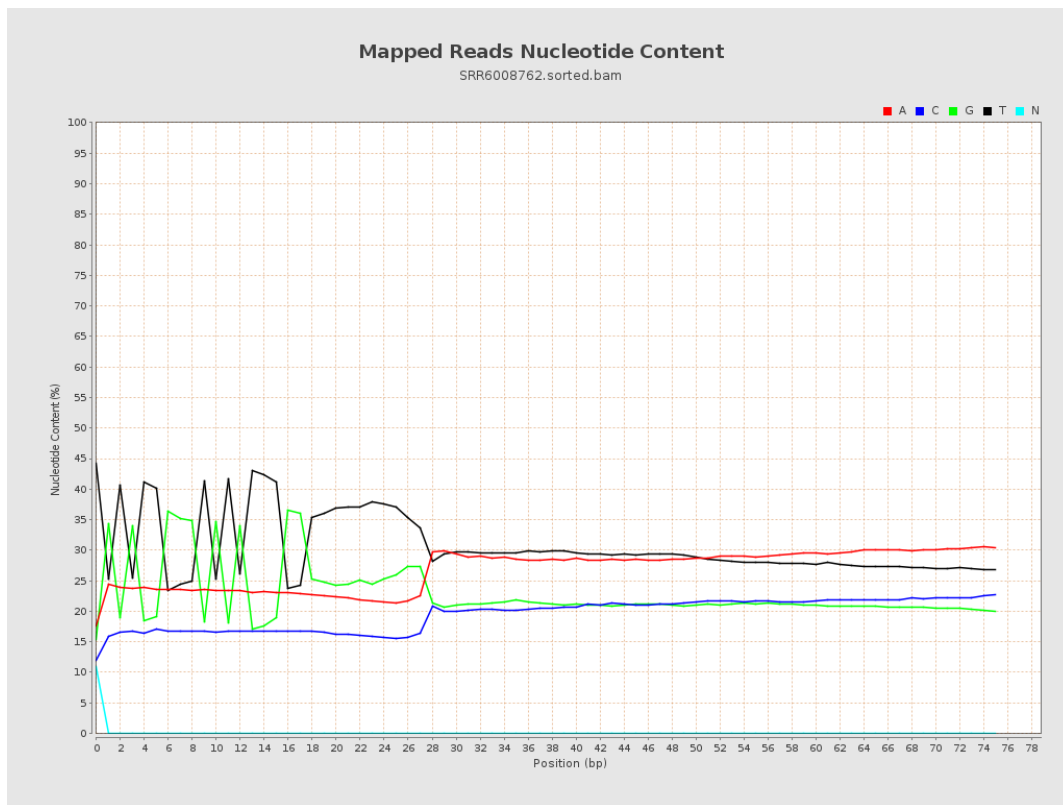
6. Results : Genome Fraction Coverage



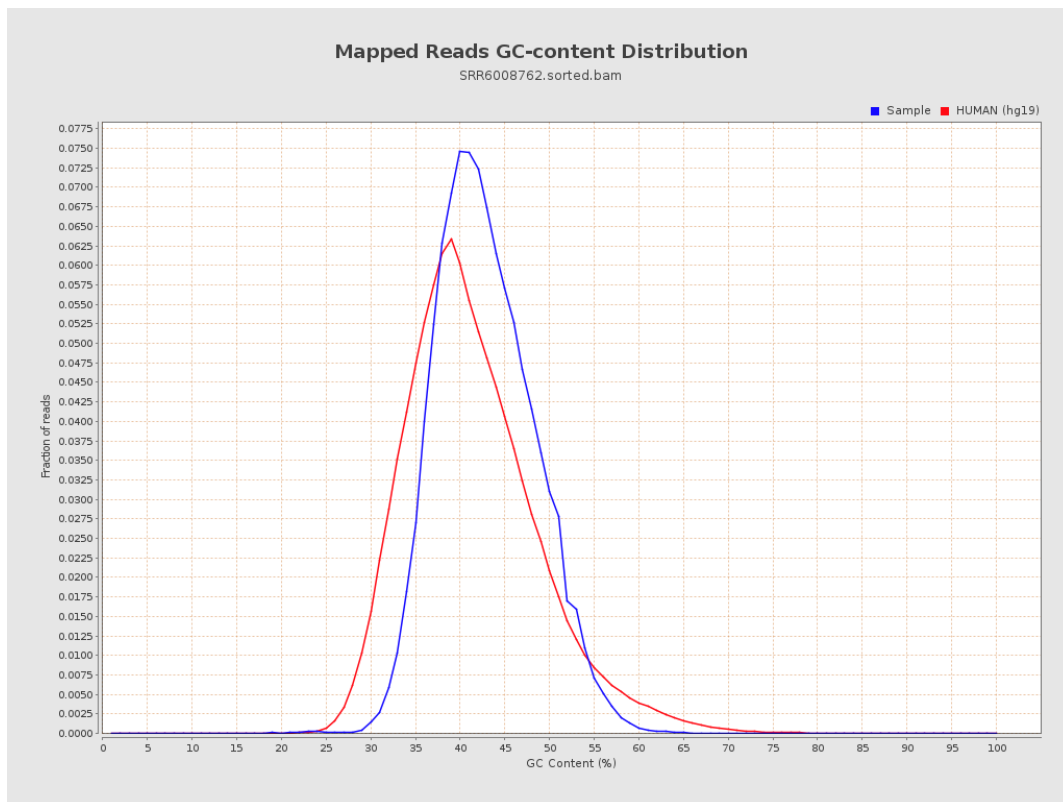
7. Results : Duplication Rate Histogram



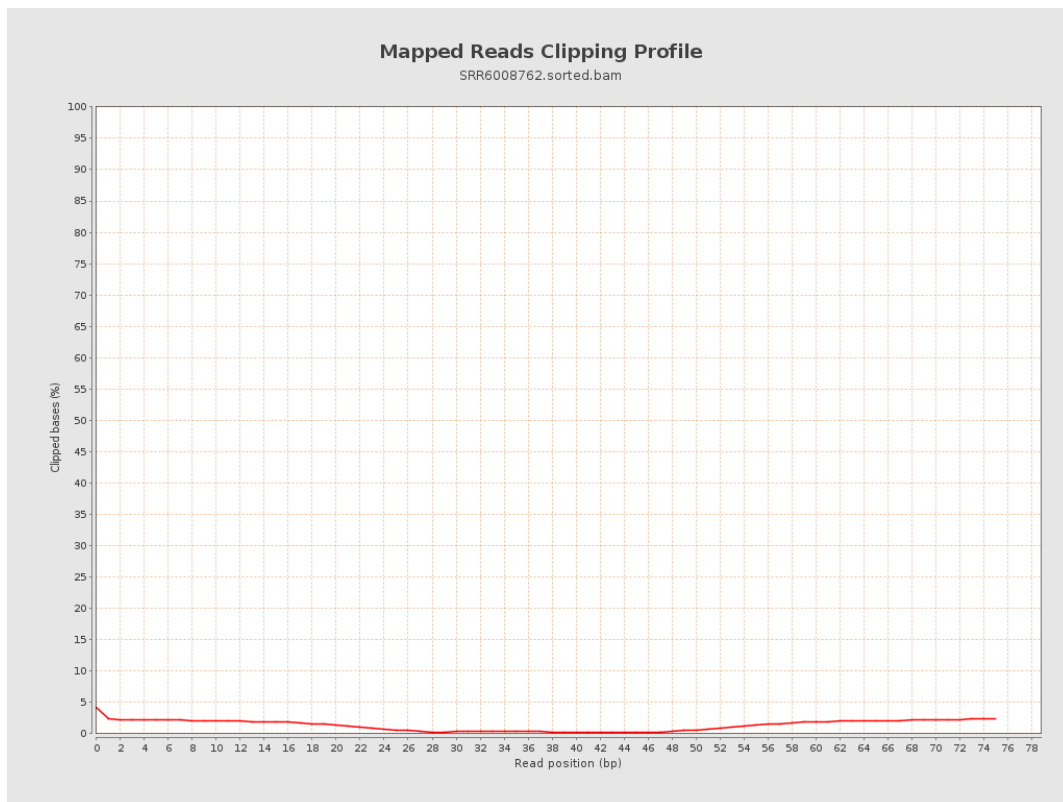
8. Results : Mapped Reads Nucleotide Content



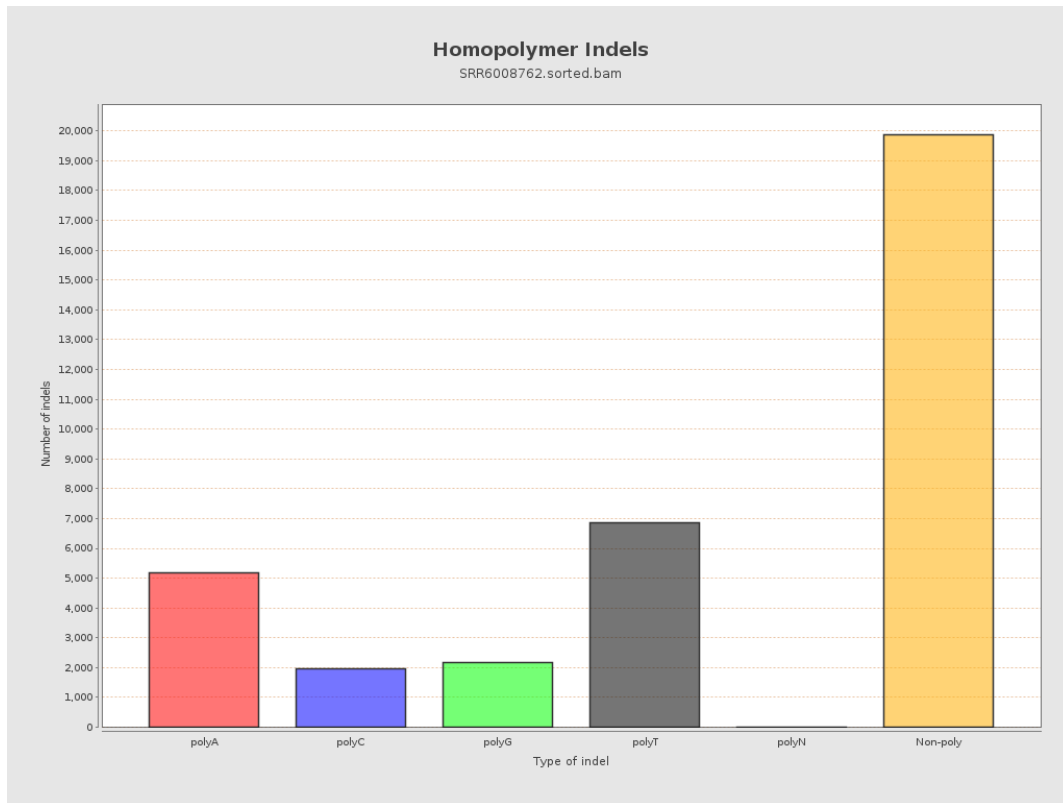
9. Results : Mapped Reads GC-content Distribution



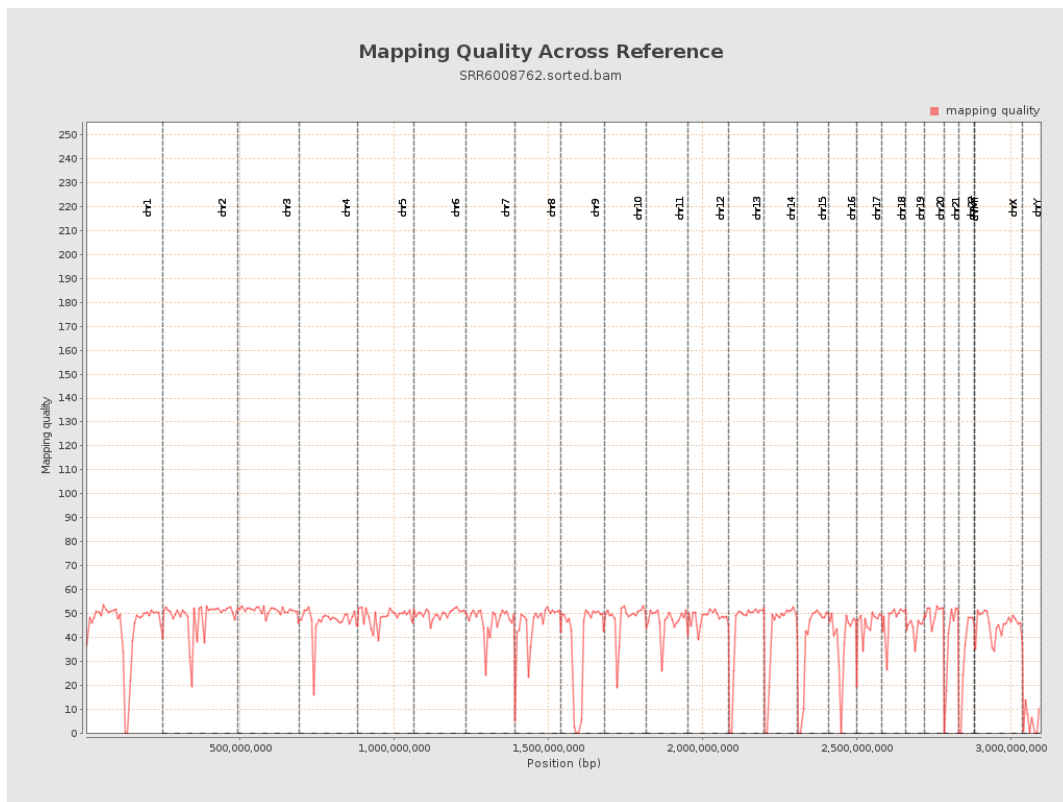
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

