

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 08:33:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008724.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_SRR6008724 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008724.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 08:33:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008724.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,655,960
Mapped reads	1,094,911 / 66.12%
Unmapped reads	561,049 / 33.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,369 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	41,853 / 2.53%
Duplication rate	3.13%
Clipped reads	680,160 / 41.07%

2.2. ACGT Content

Number/percentage of A's	18,269,389 / 26.95%
Number/percentage of C's	11,569,498 / 17.06%
Number/percentage of T's	21,210,410 / 31.28%
Number/percentage of G's	16,729,004 / 24.67%
Number/percentage of N's	20,506 / 0.03%
GC Percentage	41.74%

2.3. Coverage

Mean	0.0219

Standard Deviation	0.2126
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2.4. Mapping Quality

Mean Mapping Quality	44.28
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2.5. Mismatches and indels

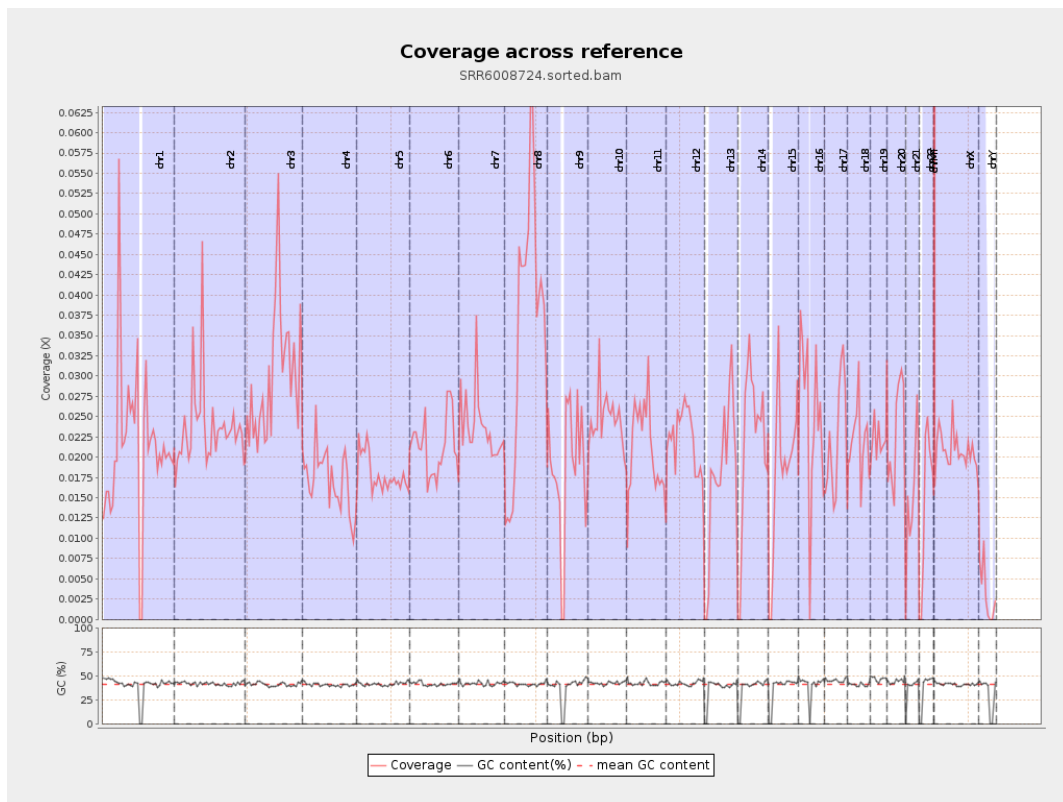
General error rate	1%
Mismatches	668,515
Insertions	5,339
Mapped reads with at least one insertion	0.48%
Deletions	22,969
Mapped reads with at least one deletion	2.07%
Homopolymer indels	47.23%

2.6. Chromosome stats

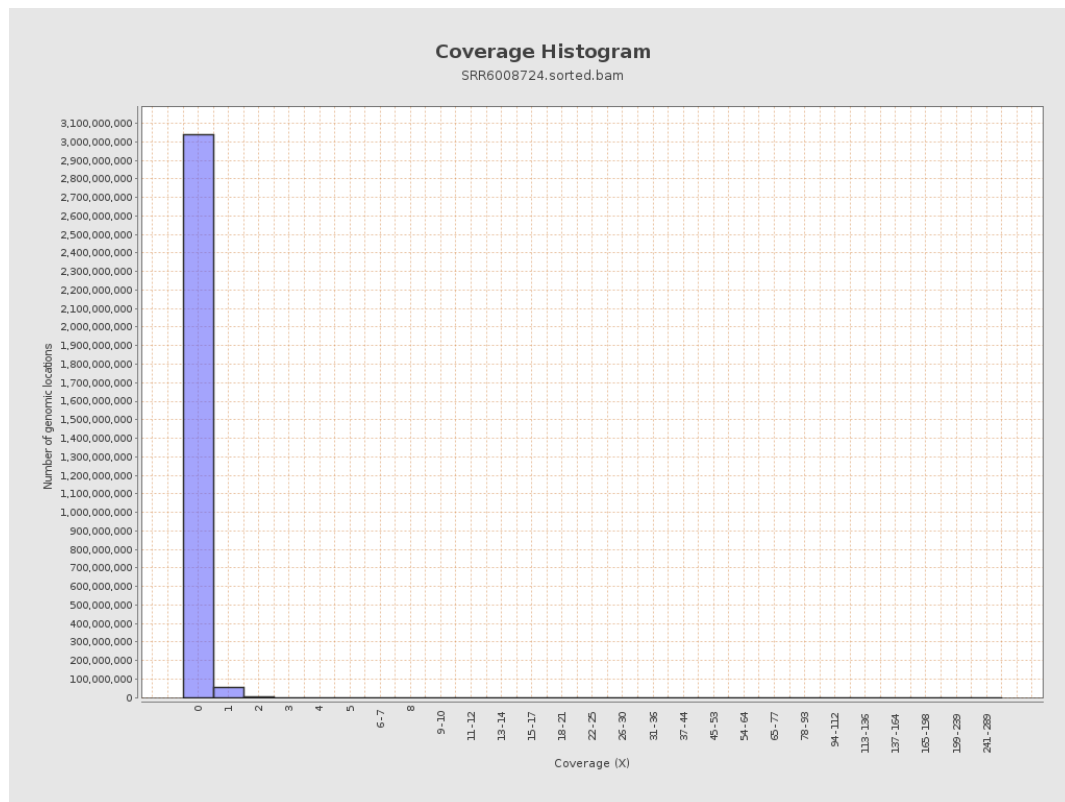
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5274833	0.0212	0.2779
chr2	243199373	5767428	0.0237	0.266
chr3	198022430	5893149	0.0298	0.1938
chr4	191154276	3287161	0.0172	0.1525
chr5	180915260	3249686	0.018	0.1484
chr6	171115067	3645316	0.0213	0.1807
chr7	159138663	3800643	0.0239	0.2932

chr8	146364022	5300822	0.0362	0.2829
chr9	141213431	2646806	0.0187	0.213
chr10	135534747	3322252	0.0245	0.2081
chr11	135006516	2880659	0.0213	0.204
chr12	133851895	2975354	0.0222	0.1674
chr13	115169878	2055274	0.0178	0.1478
chr14	107349540	2365041	0.022	0.1709
chr15	102531392	1881390	0.0183	0.1532
chr16	90354753	2229853	0.0247	0.1889
chr17	81195210	1802303	0.0222	0.1852
chr18	78077248	1729252	0.0221	0.3204
chr19	59128983	1327136	0.0224	0.2494
chr20	63025520	1434762	0.0228	0.1731
chr21	48129895	742790	0.0154	0.1453
chr22	51304566	763658	0.0149	0.1346
chrMT	16571	31664	1.9108	2.027
chrX	155270560	3242224	0.0209	0.176
chrY	59373566	187074	0.0032	0.0794

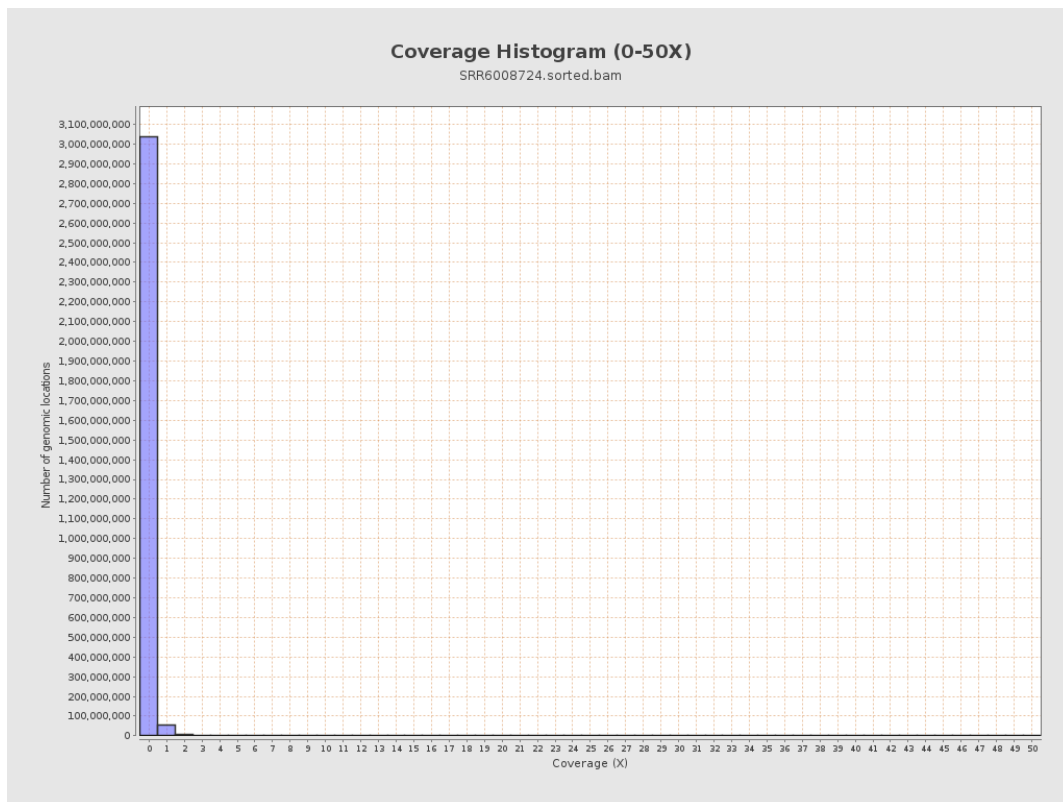
3. Results : Coverage across reference



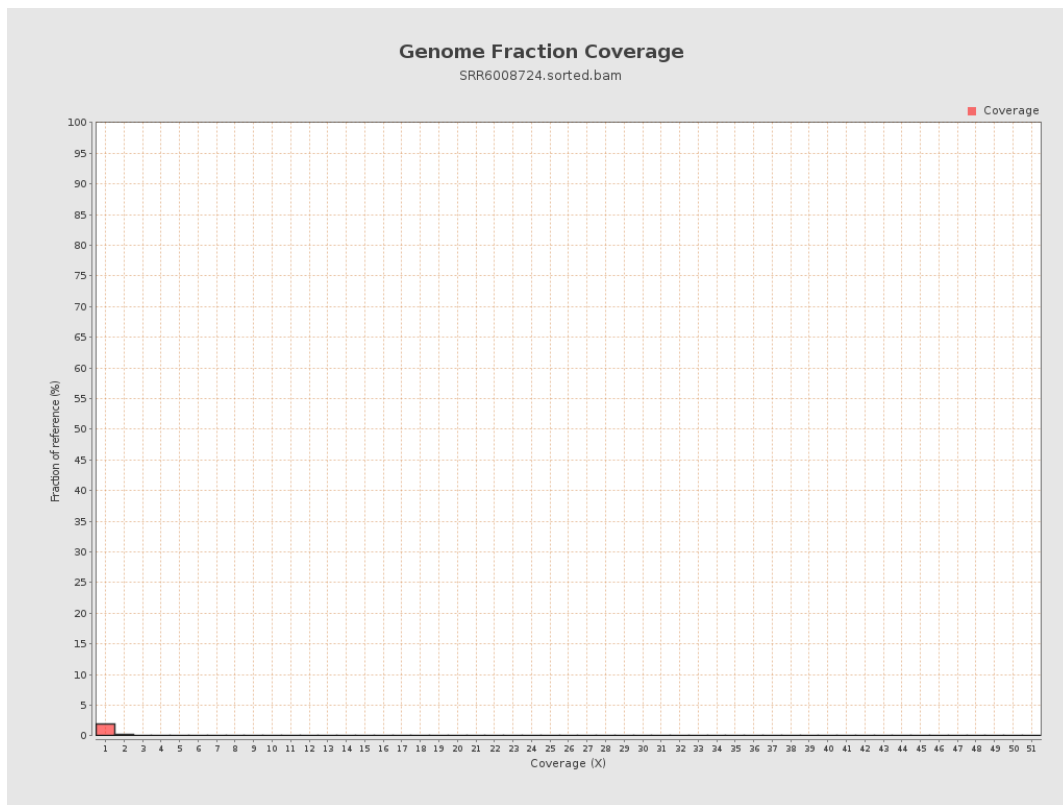
4. Results : Coverage Histogram



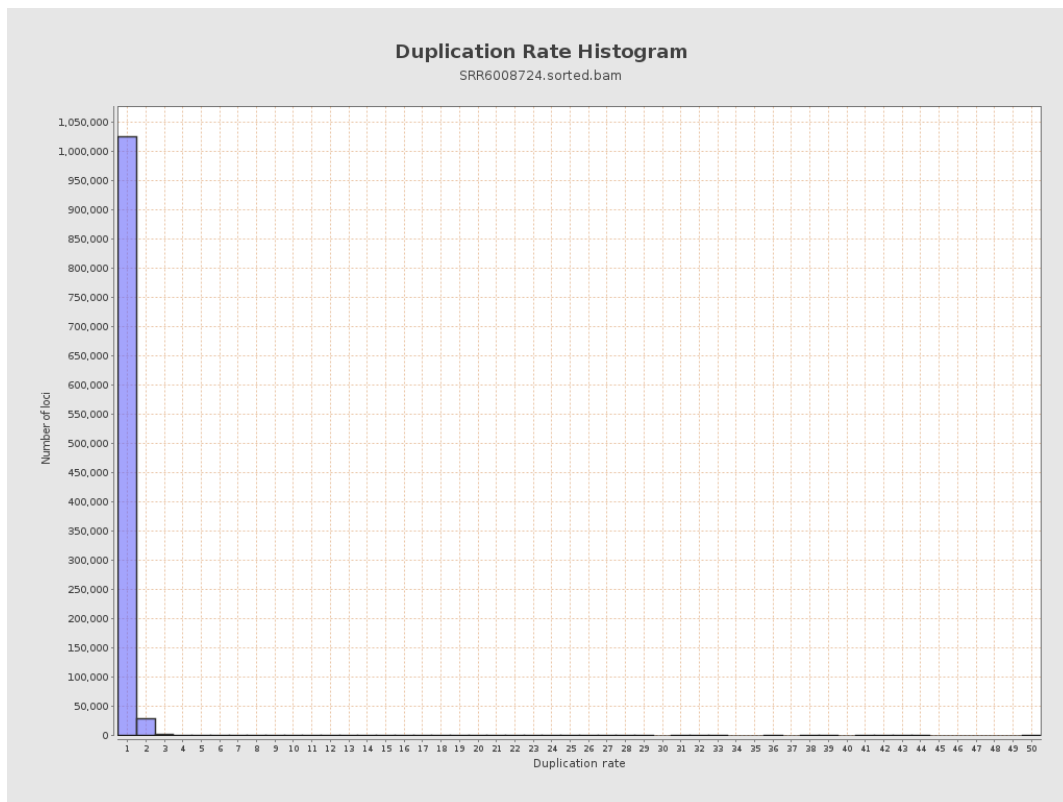
5. Results : Coverage Histogram (0-50X)



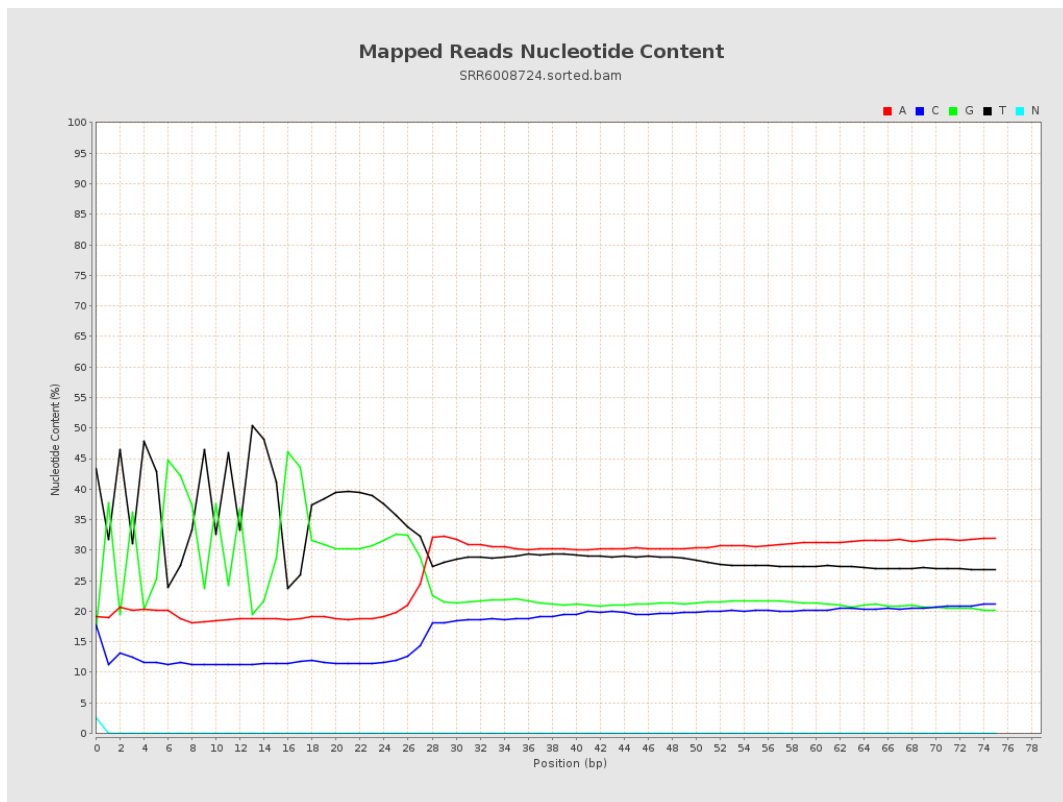
6. Results : Genome Fraction Coverage



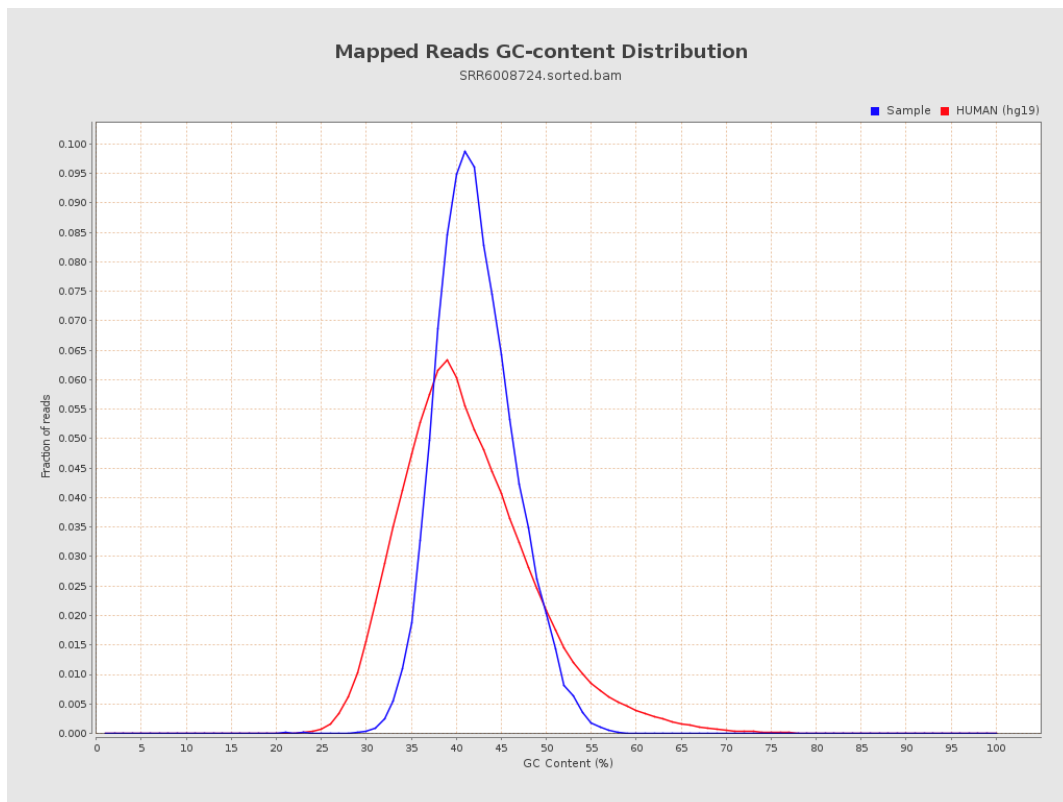
7. Results : Duplication Rate Histogram



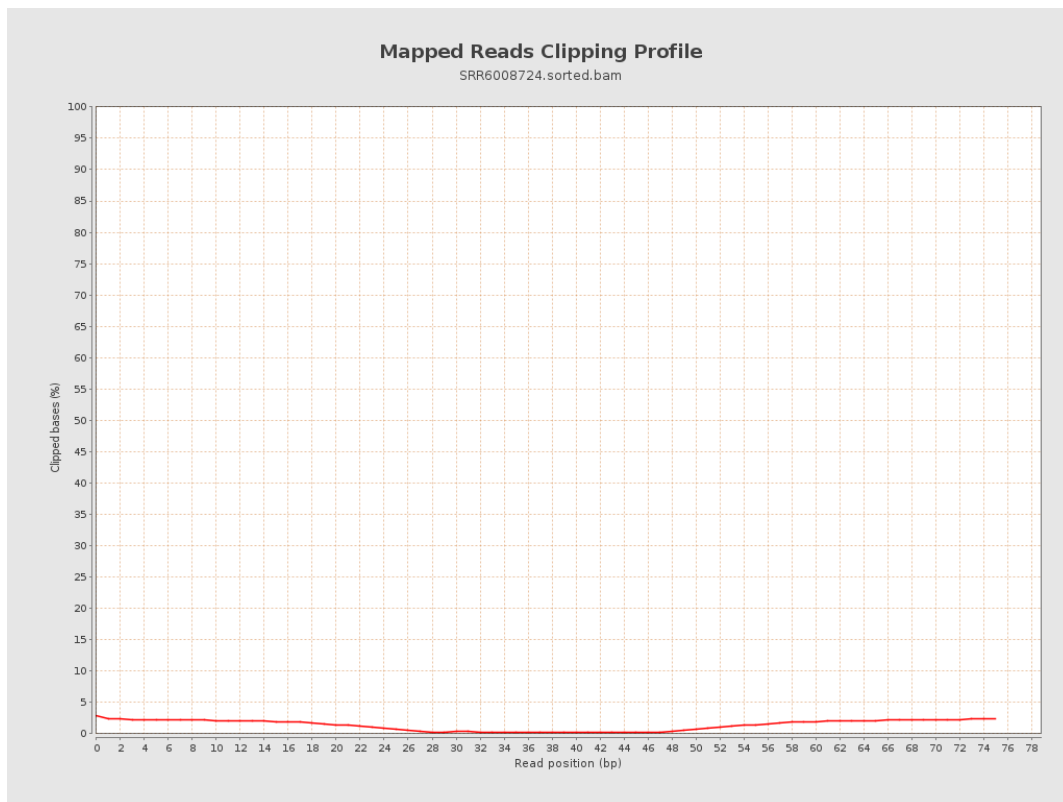
8. Results : Mapped Reads Nucleotide Content



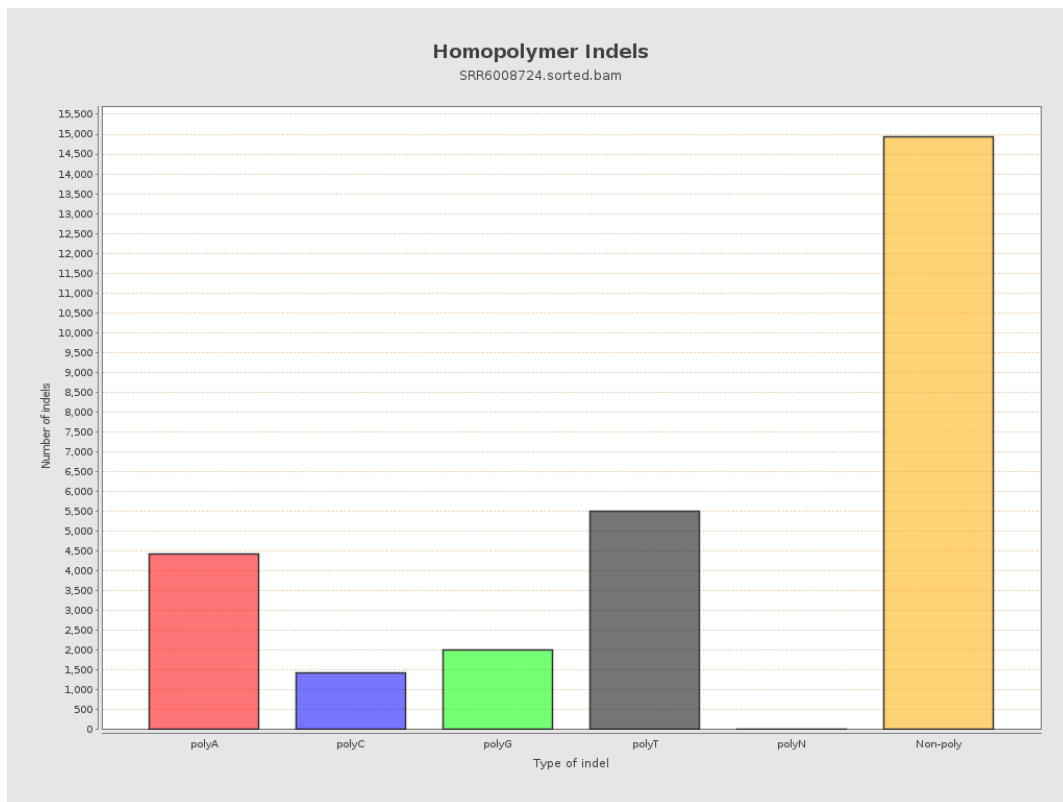
9. Results : Mapped Reads GC-content Distribution



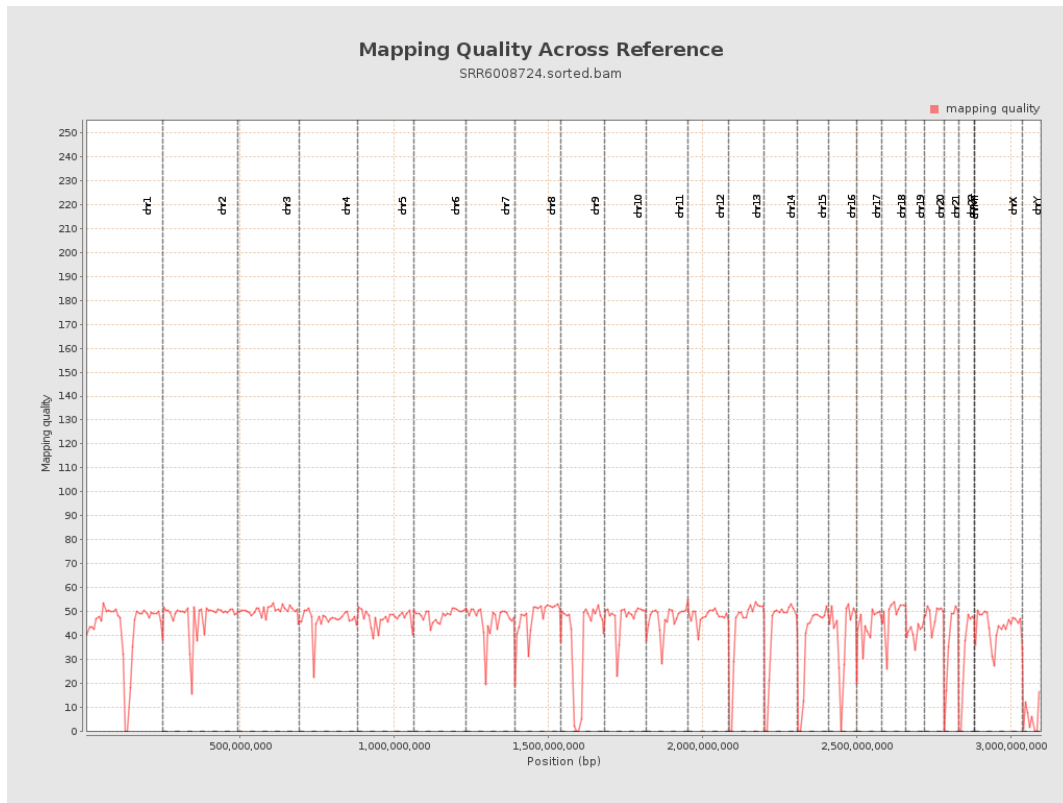
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

