

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 05:27:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240184.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_SRR6240184 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240184.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 05:27:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240184.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,468,637
Mapped reads	1,137,215 / 77.43%
Unmapped reads	331,422 / 22.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,947 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	106,636 / 7.26%
Duplication rate	7.51%
Clipped reads	597,783 / 40.7%

2.2. ACGT Content

Number/percentage of A's	21,297,540 / 28.75%
Number/percentage of C's	13,706,704 / 18.5%
Number/percentage of T's	23,351,005 / 31.52%
Number/percentage of G's	15,661,868 / 21.14%
Number/percentage of N's	56,799 / 0.08%
GC Percentage	39.65%

2.3. Coverage

Mean	0.0239

Standard Deviation	0.2889
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2.4. Mapping Quality

Mean Mapping Quality	46.62
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2.5. Mismatches and indels

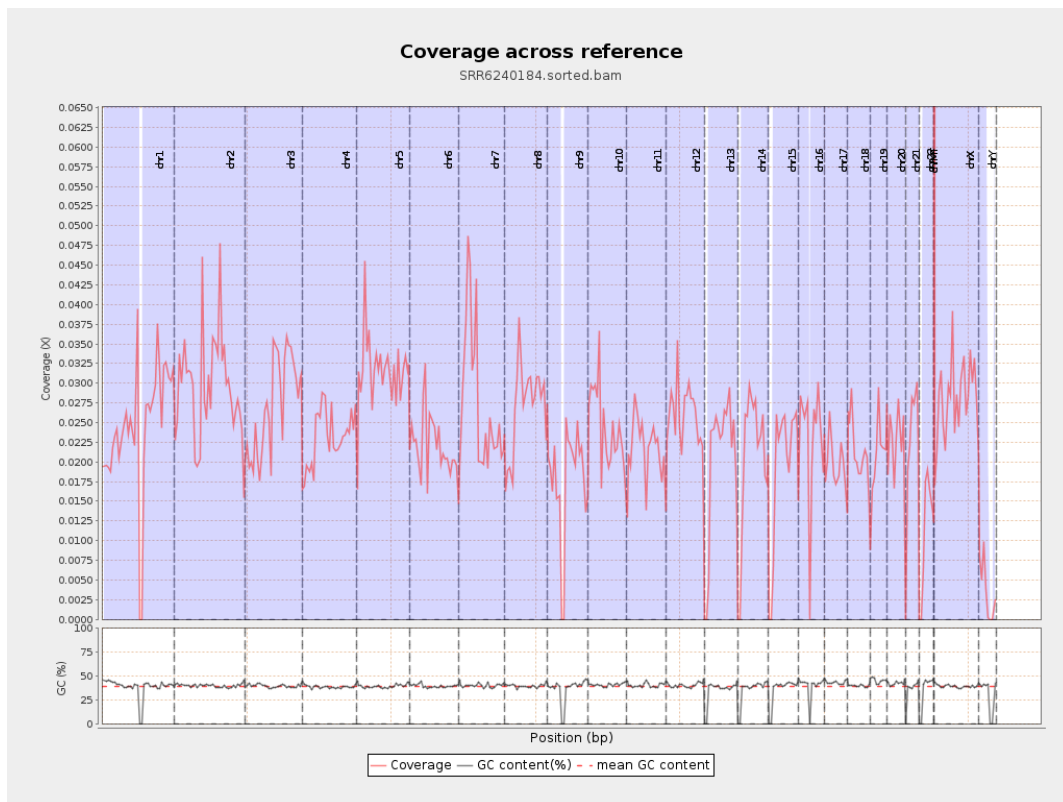
General error rate	0.93%
Mismatches	679,985
Insertions	5,280
Mapped reads with at least one insertion	0.46%
Deletions	20,927
Mapped reads with at least one deletion	1.82%
Homopolymer indels	48.19%

2.6. Chromosome stats

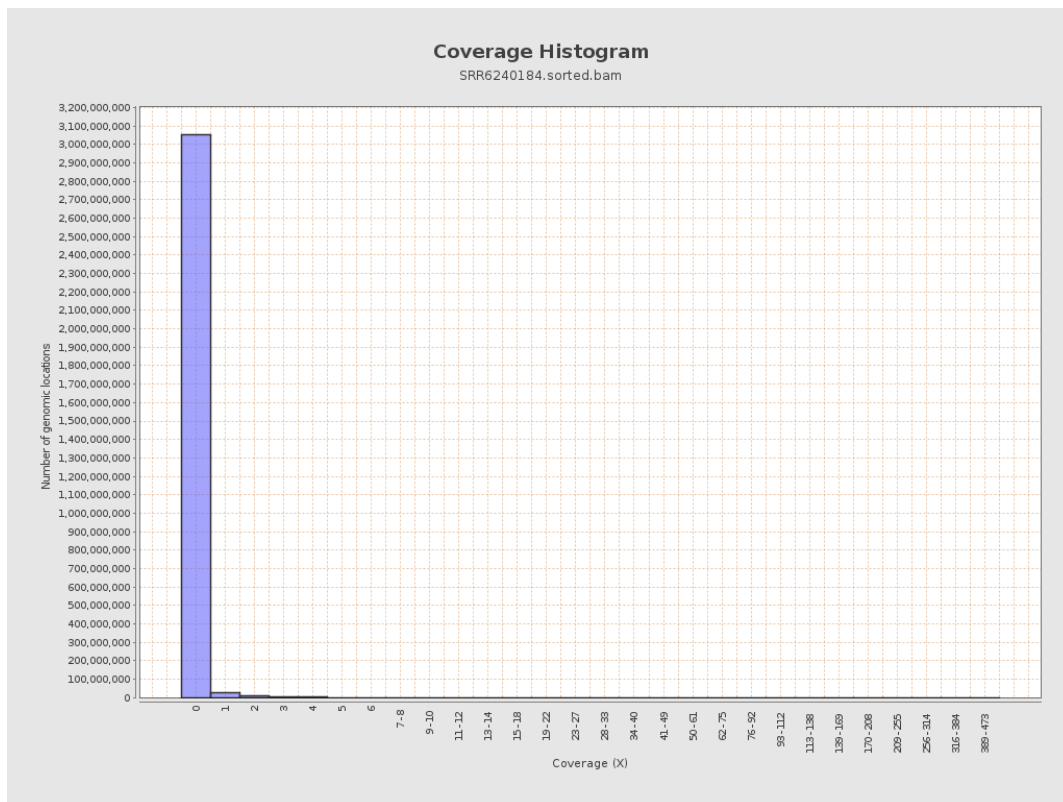
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6135571	0.0246	0.4397
chr2	243199373	7205151	0.0296	0.3133
chr3	198022430	5383157	0.0272	0.249
chr4	191154276	4417998	0.0231	0.235
chr5	180915260	5798322	0.032	0.2713
chr6	171115067	3773913	0.0221	0.2487
chr7	159138663	4381016	0.0275	0.3739

chr8	146364022	3970906	0.0271	0.3766
chr9	141213431	2523864	0.0179	0.2381
chr10	135534747	3284981	0.0242	0.2765
chr11	135006516	2951843	0.0219	0.2613
chr12	133851895	3483427	0.026	0.2567
chr13	115169878	2332352	0.0203	0.218
chr14	107349540	2210467	0.0206	0.2295
chr15	102531392	1985195	0.0194	0.2162
chr16	90354753	2045054	0.0226	0.2326
chr17	81195210	1604657	0.0198	0.2236
chr18	78077248	1666847	0.0213	0.3658
chr19	59128983	1254089	0.0212	0.3193
chr20	63025520	1416511	0.0225	0.2282
chr21	48129895	1090218	0.0227	0.2326
chr22	51304566	591657	0.0115	0.1562
chrMT	16571	19307	1.1651	1.6627
chrX	155270560	4374569	0.0282	0.2661
chrY	59373566	209309	0.0035	0.0981

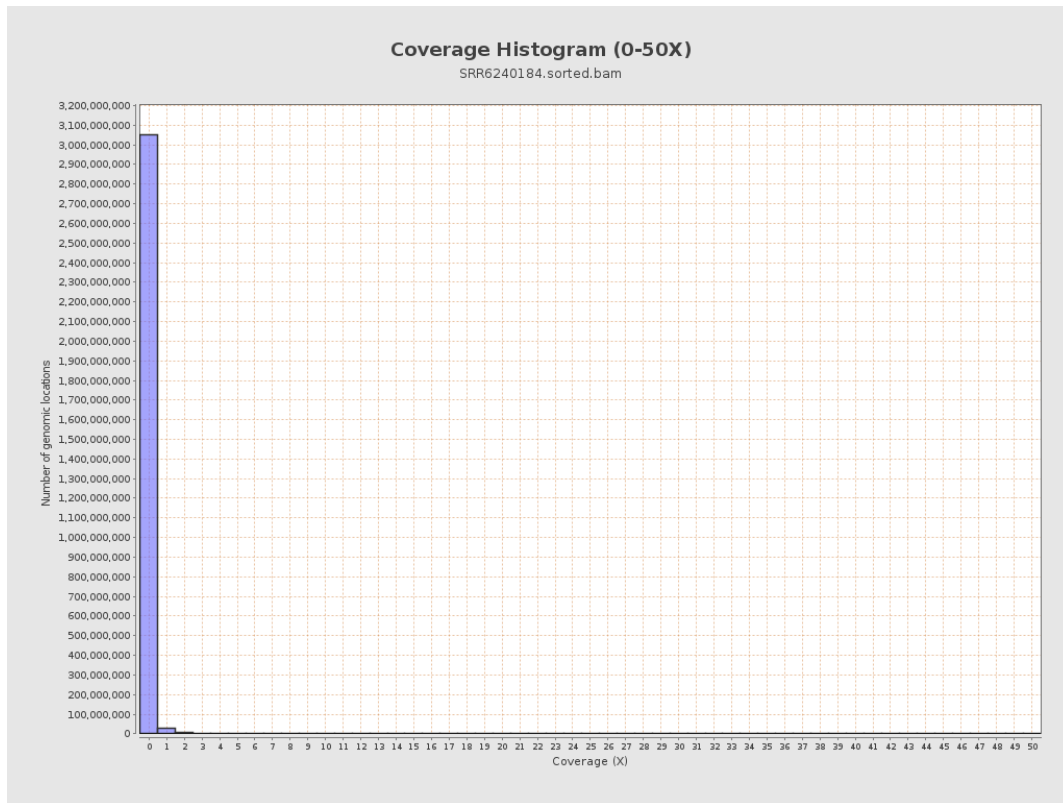
3. Results : Coverage across reference



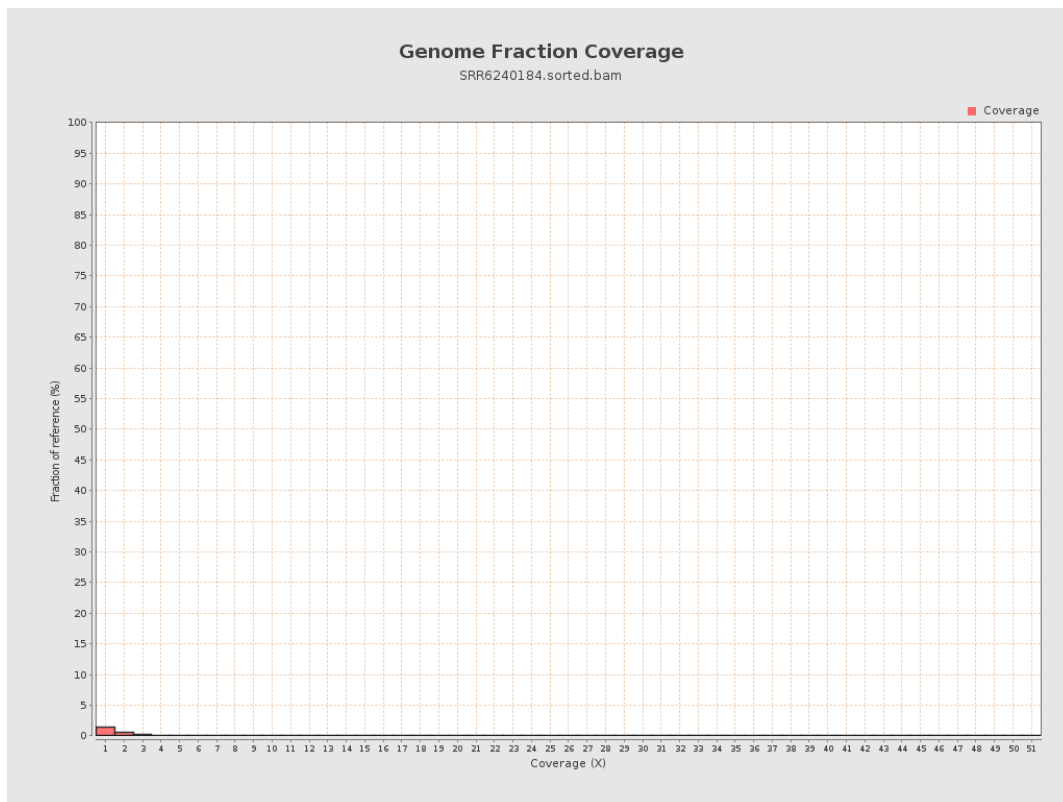
4. Results : Coverage Histogram



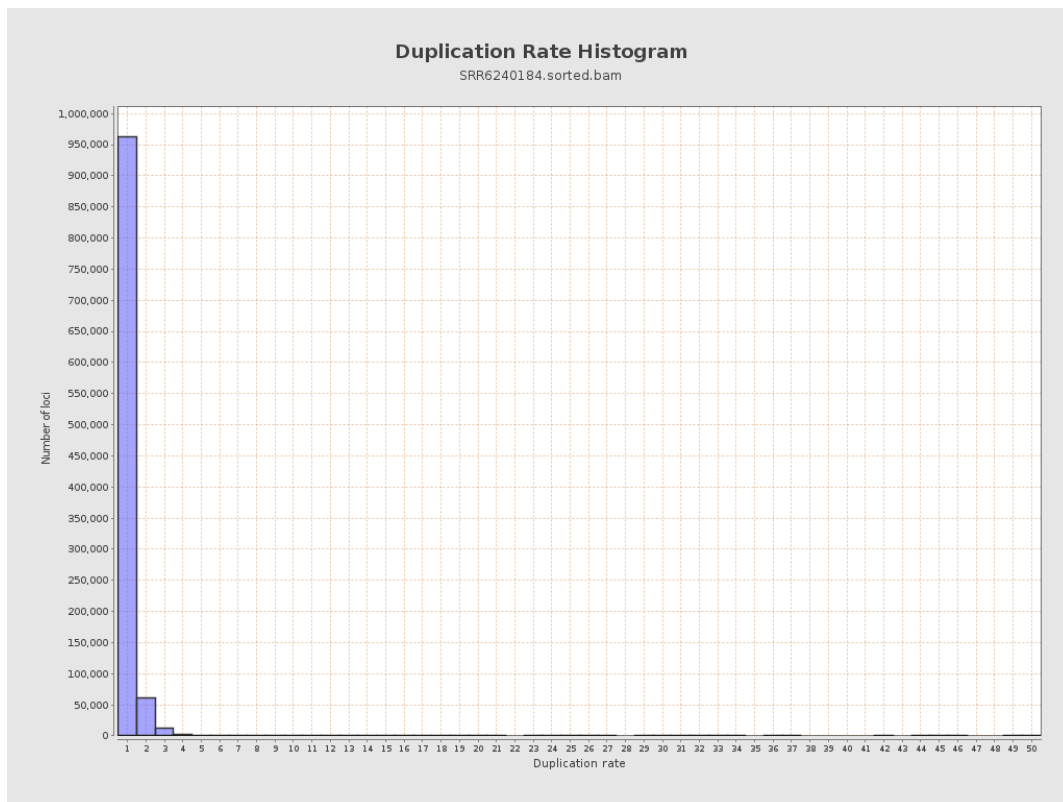
5. Results : Coverage Histogram (0-50X)



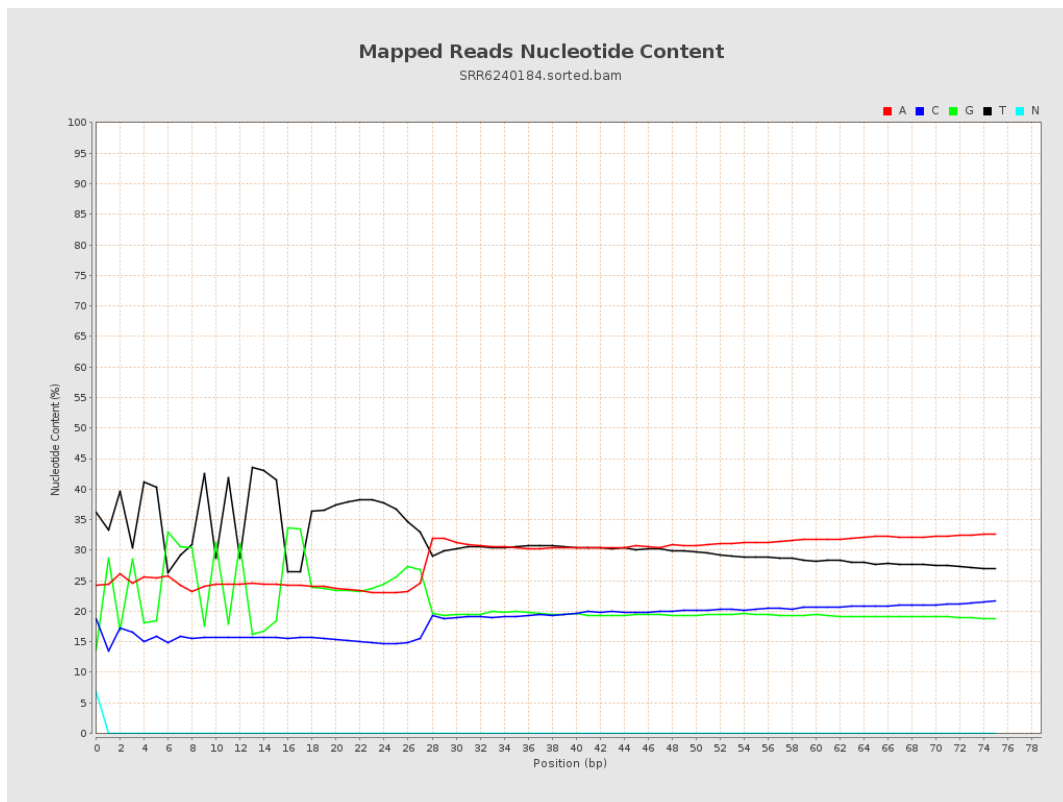
6. Results : Genome Fraction Coverage



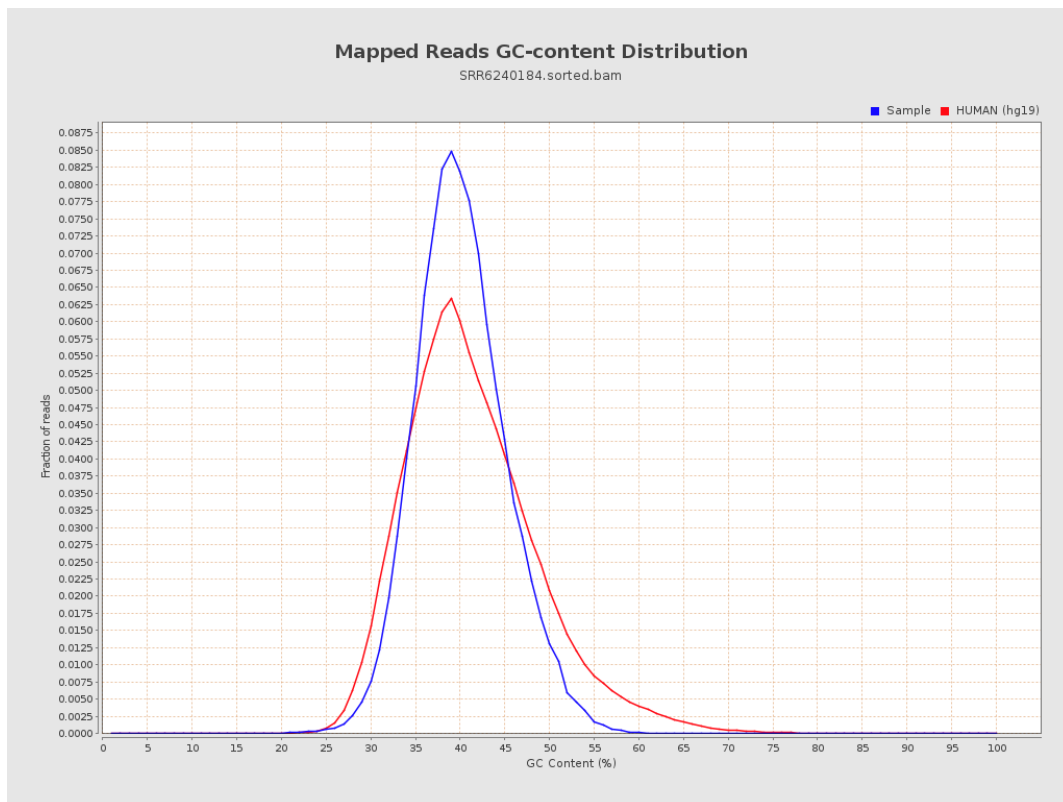
7. Results : Duplication Rate Histogram



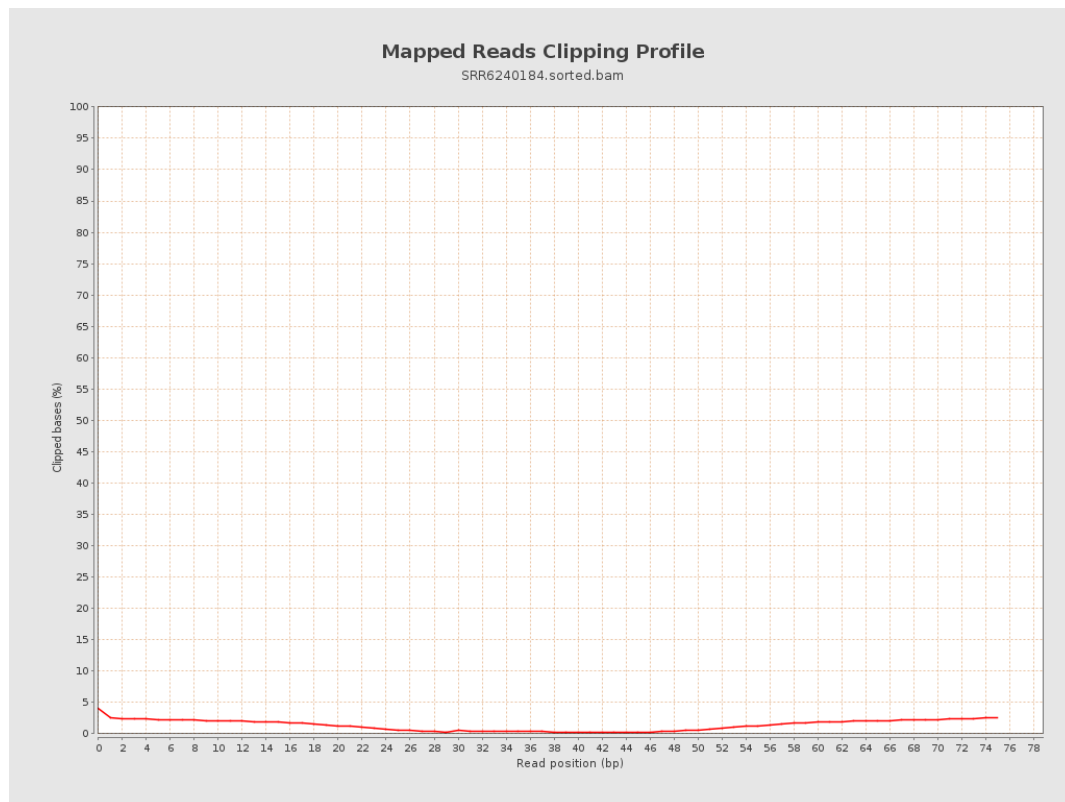
8. Results : Mapped Reads Nucleotide Content



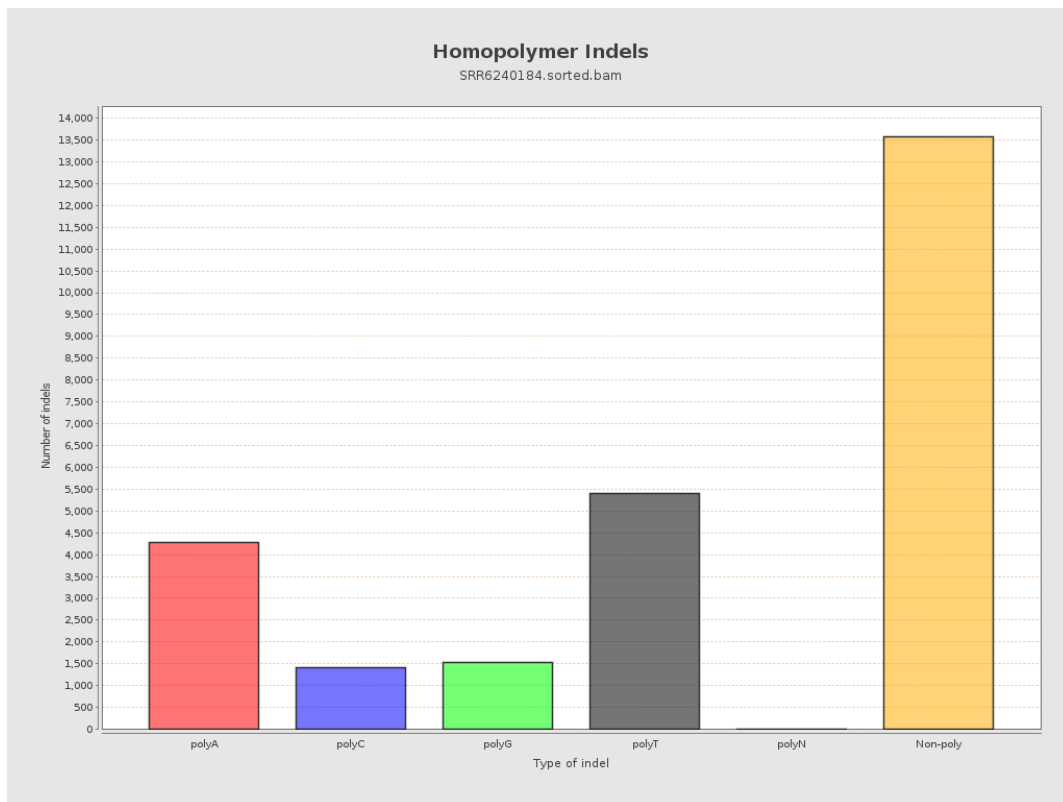
9. Results : Mapped Reads GC-content Distribution



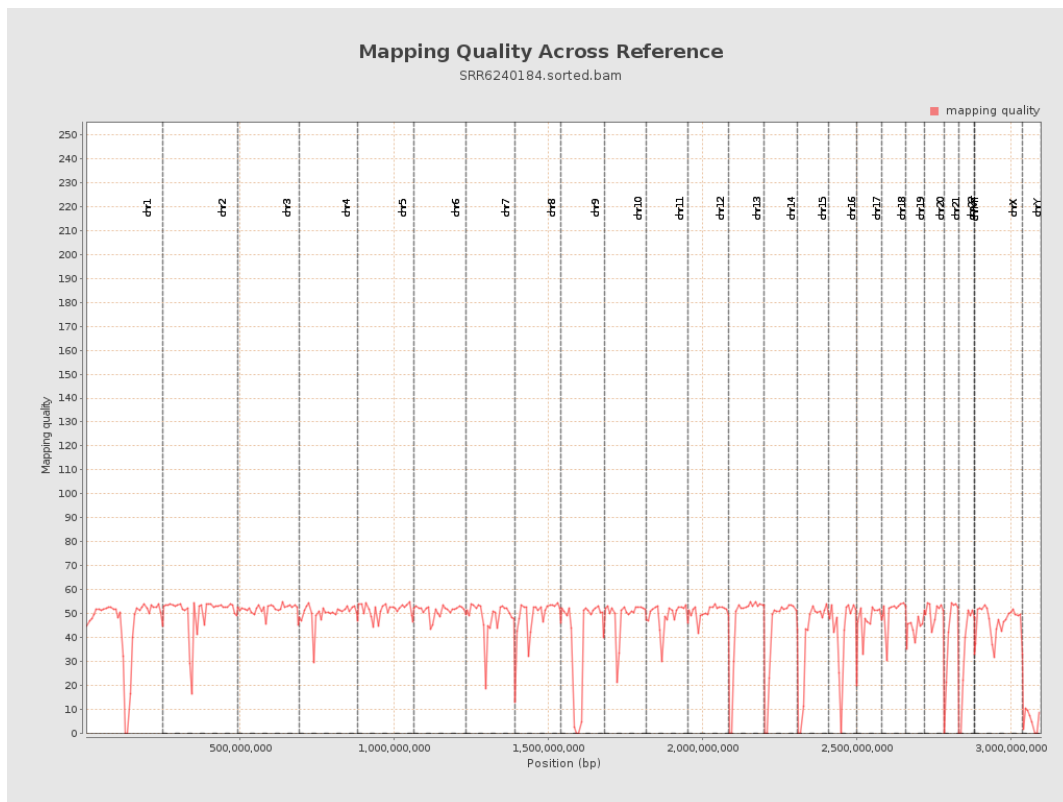
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

