

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 06:53:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240216.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_SRR6240216 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240216.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 06:53:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240216.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,797,095
Mapped reads	1,364,321 / 75.92%
Unmapped reads	432,774 / 24.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,246 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	130,370 / 7.25%
Duplication rate	7.84%
Clipped reads	725,358 / 40.36%

2.2. ACGT Content

Number/percentage of A's	24,436,816 / 27.7%
Number/percentage of C's	15,962,401 / 18.09%
Number/percentage of T's	28,469,609 / 32.27%
Number/percentage of G's	19,357,310 / 21.94%
Number/percentage of N's	7,756 / 0.01%
GC Percentage	40.03%

2.3. Coverage

Mean	0.0285

Standard Deviation	0.3243
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2.4. Mapping Quality

Mean Mapping Quality	46.7
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2.5. Mismatches and indels

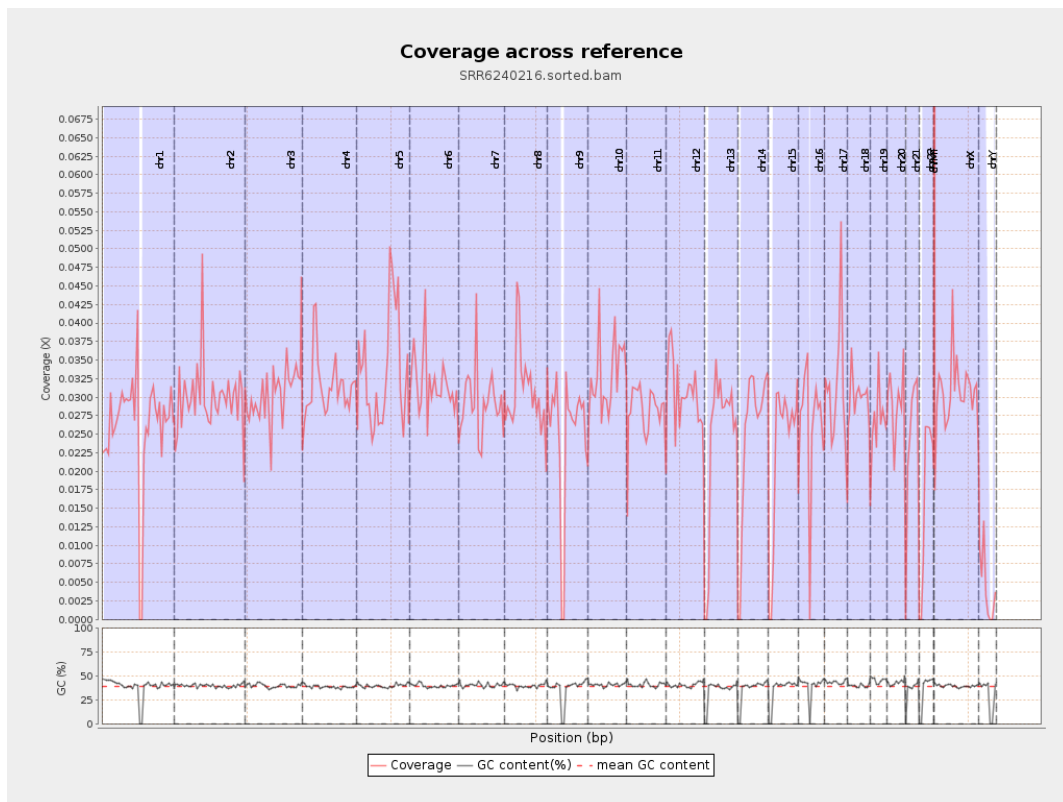
General error rate	0.83%
Mismatches	721,876
Insertions	6,395
Mapped reads with at least one insertion	0.47%
Deletions	22,670
Mapped reads with at least one deletion	1.65%
Homopolymer indels	47.91%

2.6. Chromosome stats

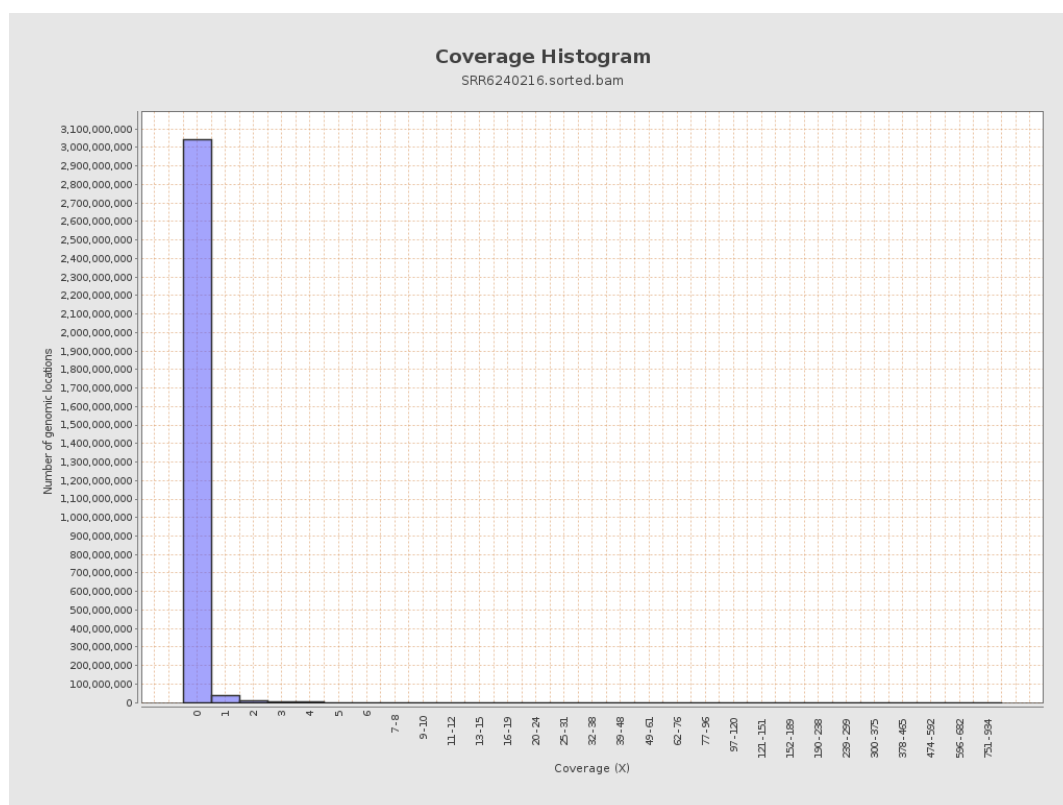
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6521598	0.0262	0.442
chr2	243199373	7281359	0.0299	0.3371
chr3	198022430	6017266	0.0304	0.2553
chr4	191154276	6000232	0.0314	0.2666
chr5	180915260	6116421	0.0338	0.2743
chr6	171115067	5442812	0.0318	0.2898
chr7	159138663	4666292	0.0293	0.3457

chr8	146364022	4496006	0.0307	0.6073
chr9	141213431	3547470	0.0251	0.2857
chr10	135534747	4459528	0.0329	0.3095
chr11	135006516	3827190	0.0283	0.2923
chr12	133851895	4106947	0.0307	0.2596
chr13	115169878	2802930	0.0243	0.2335
chr14	107349540	2701018	0.0252	0.24
chr15	102531392	2342883	0.0229	0.2259
chr16	90354753	2343190	0.0259	0.2443
chr17	81195210	2517068	0.031	0.2675
chr18	78077248	2351993	0.0301	0.47
chr19	59128983	1593490	0.0269	0.3159
chr20	63025520	1833627	0.0291	0.253
chr21	48129895	1176441	0.0244	0.2338
chr22	51304566	891910	0.0174	0.1869
chrMT	16571	197738	11.9328	9.9236
chrX	155270560	4780962	0.0308	0.2721
chrY	59373566	256708	0.0043	0.1035

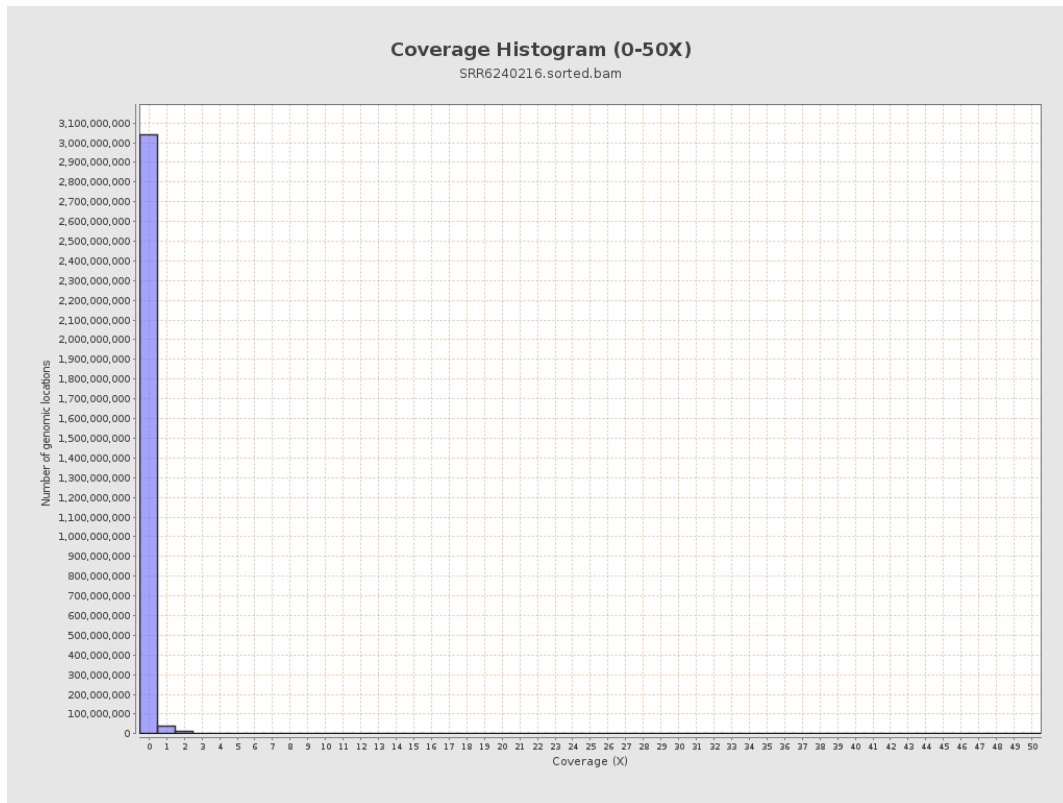
3. Results : Coverage across reference



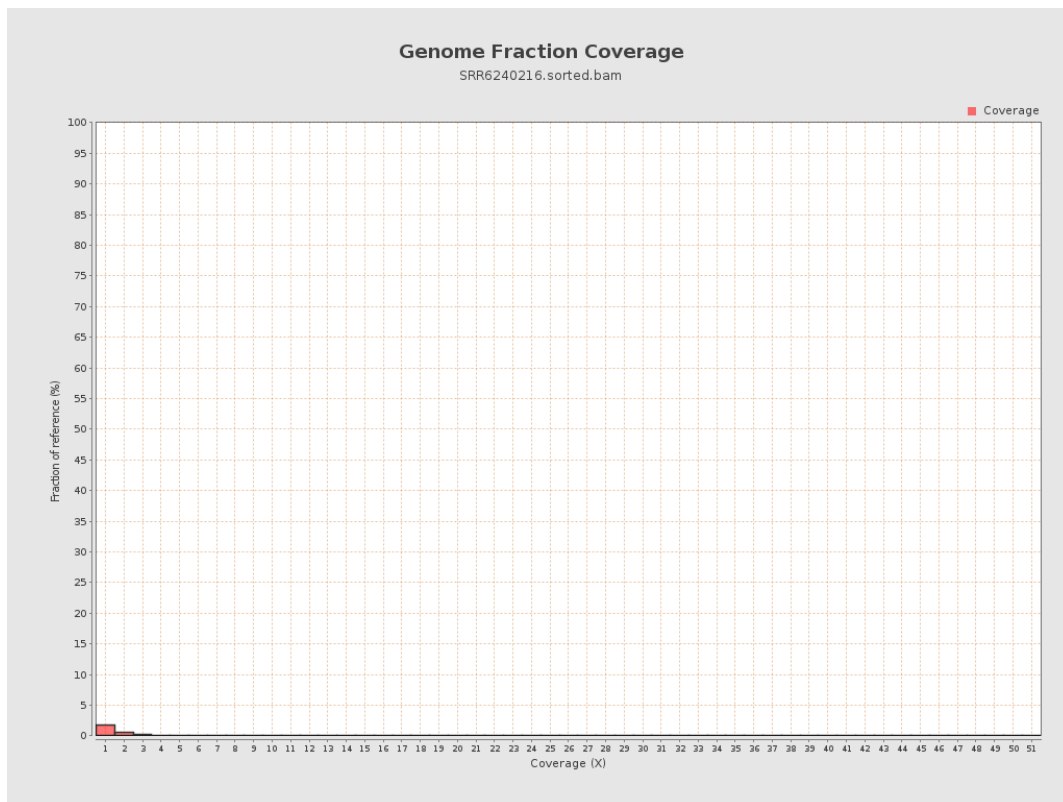
4. Results : Coverage Histogram



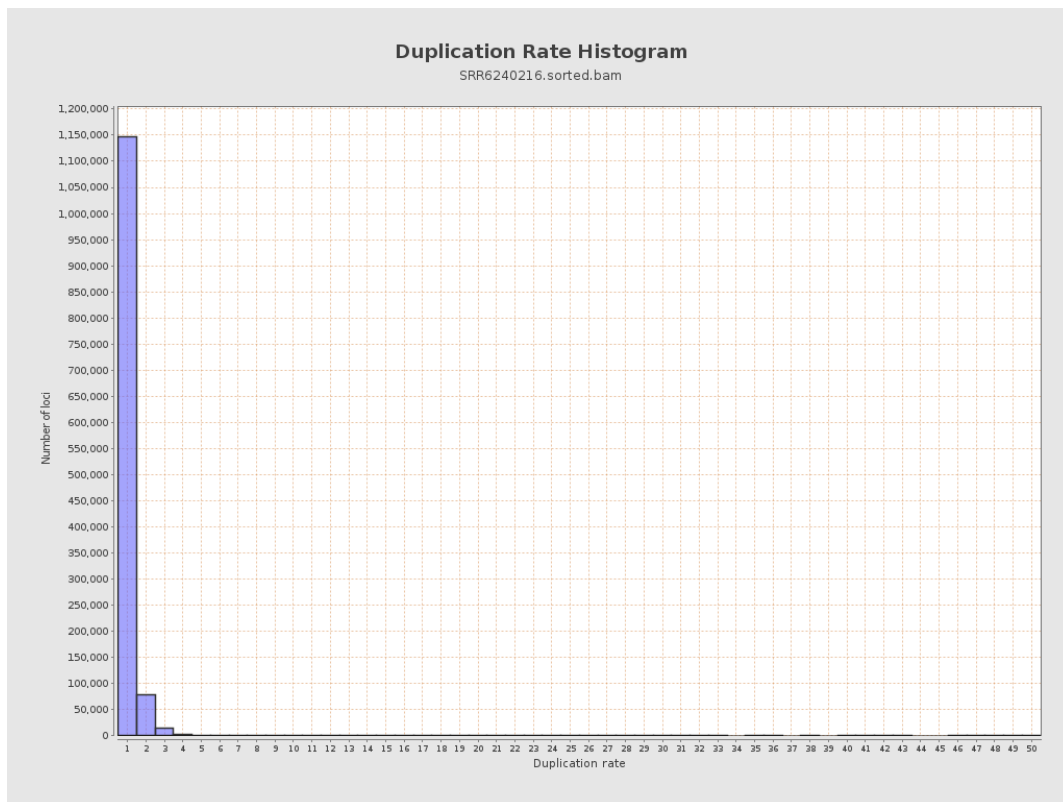
5. Results : Coverage Histogram (0-50X)



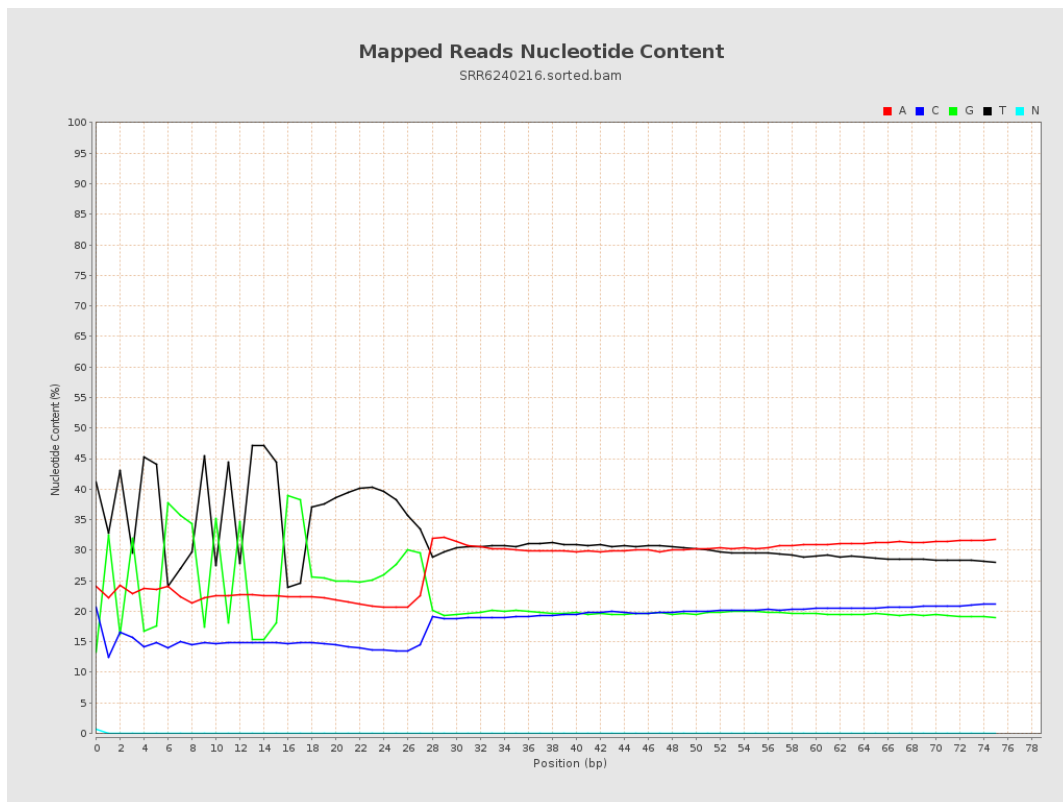
6. Results : Genome Fraction Coverage



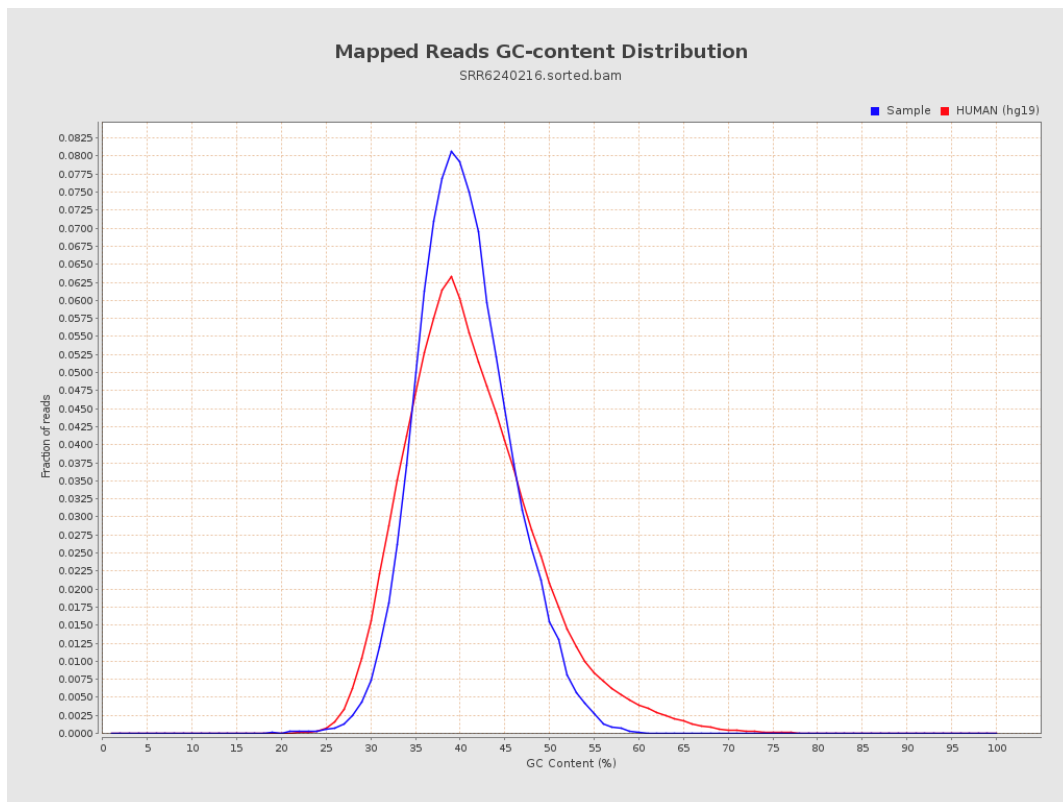
7. Results : Duplication Rate Histogram



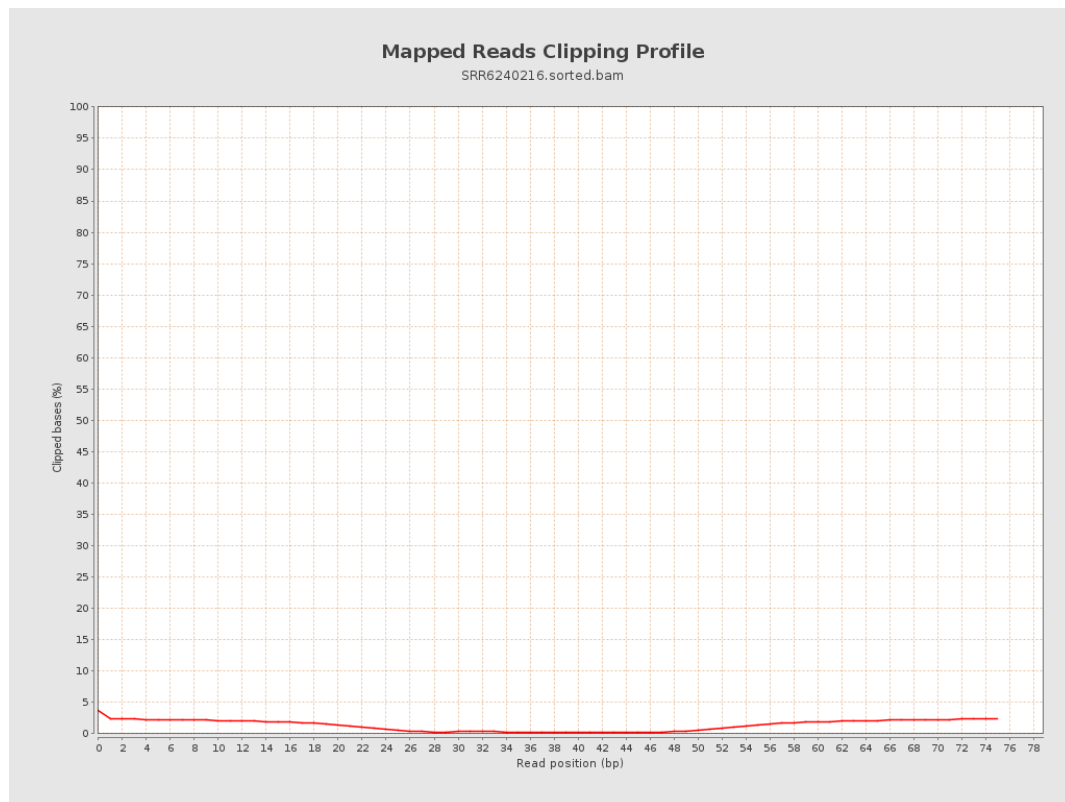
8. Results : Mapped Reads Nucleotide Content



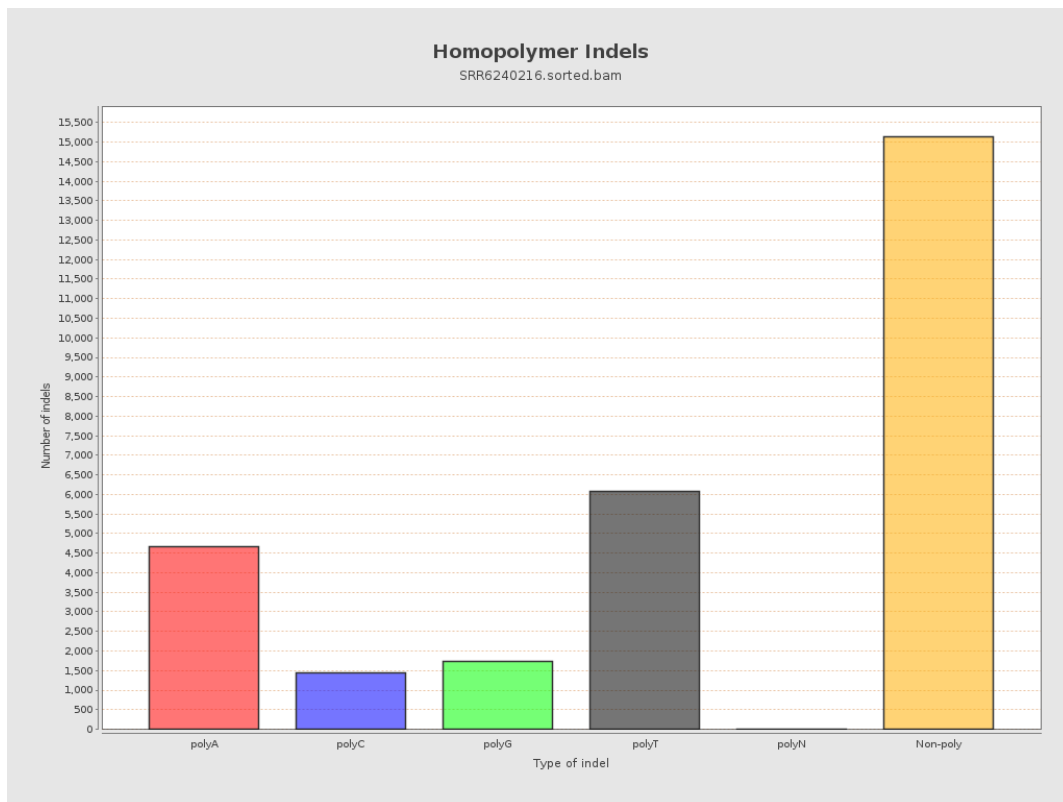
9. Results : Mapped Reads GC-content Distribution



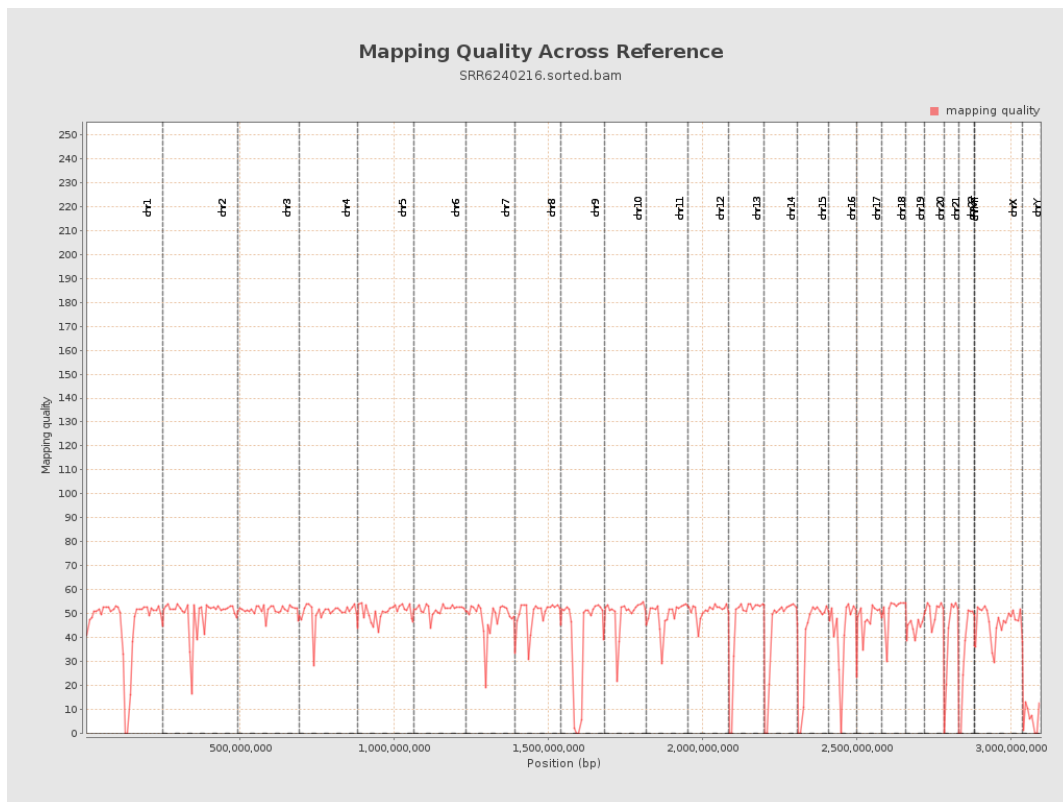
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

