

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 07:31:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240229.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_SRR6240229 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240229.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 07:31:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240229.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,794,064
Mapped reads	1,379,571 / 76.9%
Unmapped reads	414,493 / 23.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,546 / 0.42%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	148,437 / 8.27%
Duplication rate	9.04%
Clipped reads	934,811 / 52.11%

2.2. ACGT Content

Number/percentage of A's	22,038,681 / 26.28%
Number/percentage of C's	14,735,219 / 17.57%
Number/percentage of T's	27,308,467 / 32.56%
Number/percentage of G's	19,768,228 / 23.57%
Number/percentage of N's	20,387 / 0.02%
GC Percentage	41.14%

2.3. Coverage

Mean	0.0271

Standard Deviation	0.2711
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2.4. Mapping Quality

Mean Mapping Quality	44.77
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2.5. Mismatches and indels

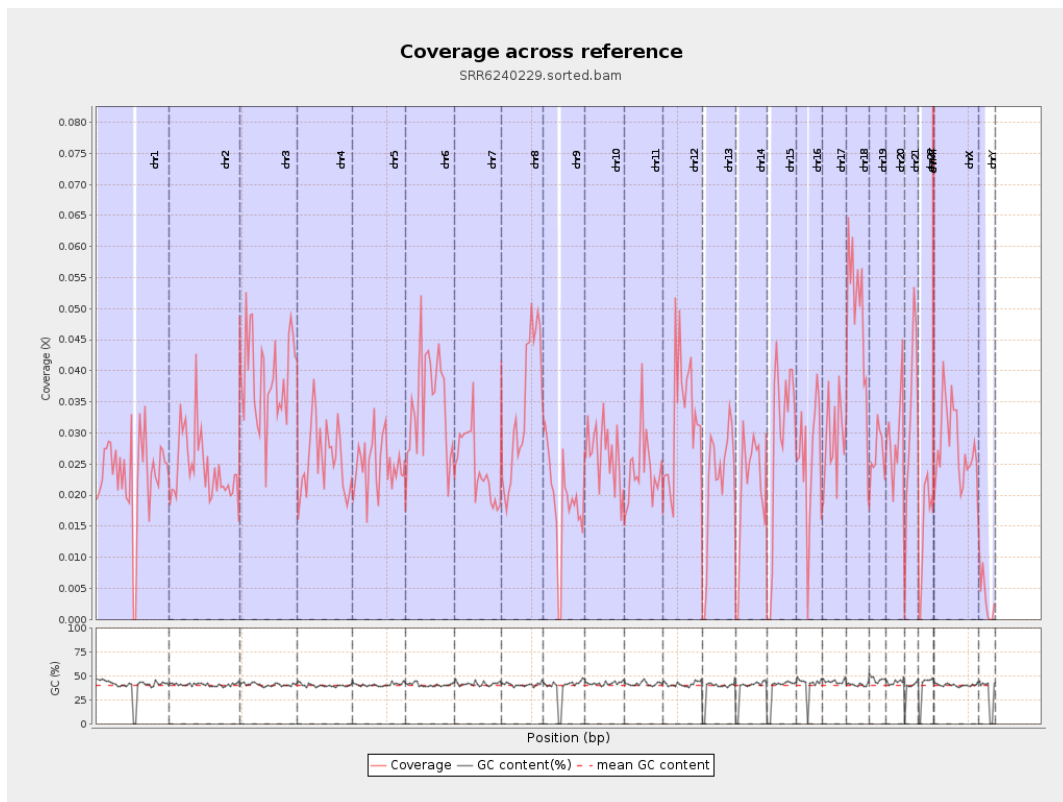
General error rate	0.9%
Mismatches	745,471
Insertions	5,460
Mapped reads with at least one insertion	0.39%
Deletions	23,939
Mapped reads with at least one deletion	1.72%
Homopolymer indels	48.62%

2.6. Chromosome stats

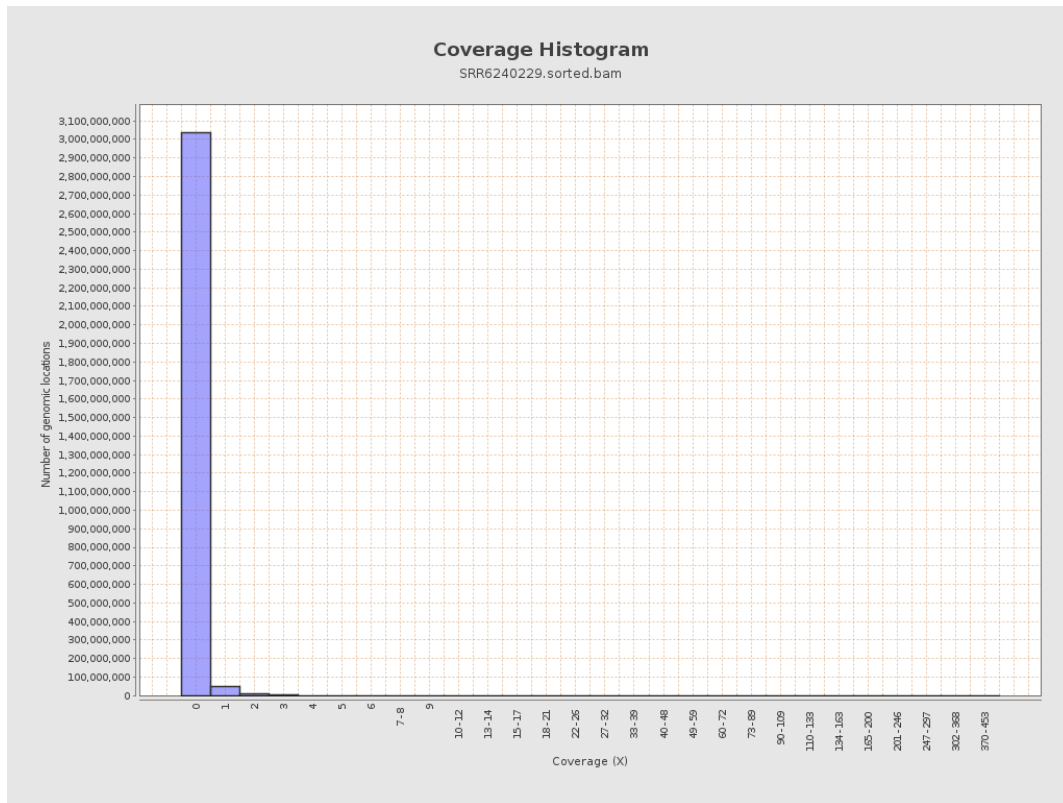
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5800825	0.0233	0.3607
chr2	243199373	5902973	0.0243	0.3579
chr3	198022430	7765055	0.0392	0.2614
chr4	191154276	4865885	0.0255	0.2127
chr5	180915260	4500466	0.0249	0.207
chr6	171115067	5848252	0.0342	0.3038
chr7	159138663	3901246	0.0245	0.3085

chr8	146364022	4944125	0.0338	0.3314
chr9	141213431	2647219	0.0187	0.2429
chr10	135534747	3631351	0.0268	0.2413
chr11	135006516	3245007	0.024	0.222
chr12	133851895	4363394	0.0326	0.2379
chr13	115169878	2540469	0.0221	0.1943
chr14	107349540	2236096	0.0208	0.1947
chr15	102531392	2959886	0.0289	0.2311
chr16	90354753	2323260	0.0257	0.2128
chr17	81195210	2322070	0.0286	0.2354
chr18	78077248	3826935	0.049	0.3869
chr19	59128983	1576740	0.0267	0.3044
chr20	63025520	1850890	0.0294	0.2271
chr21	48129895	1546440	0.0321	0.2392
chr22	51304566	746990	0.0146	0.1553
chrMT	16571	37360	2.2545	2.8988
chrX	155270560	4324945	0.0279	0.2381
chrY	59373566	204230	0.0034	0.0832

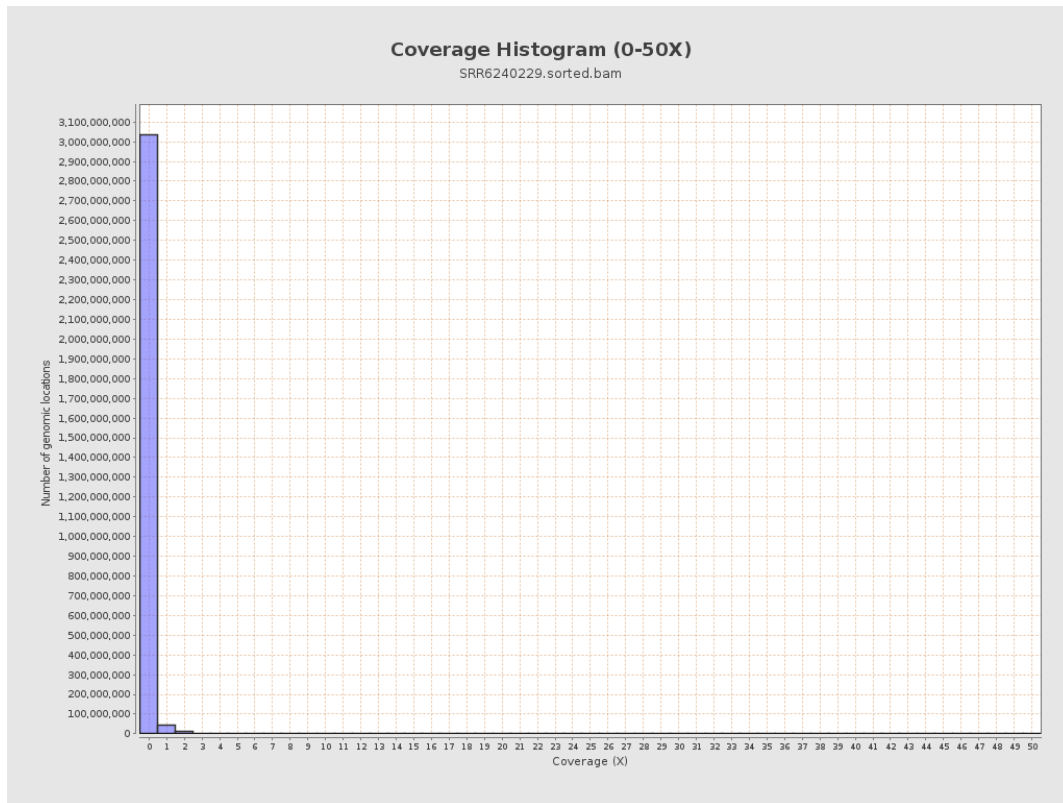
3. Results : Coverage across reference



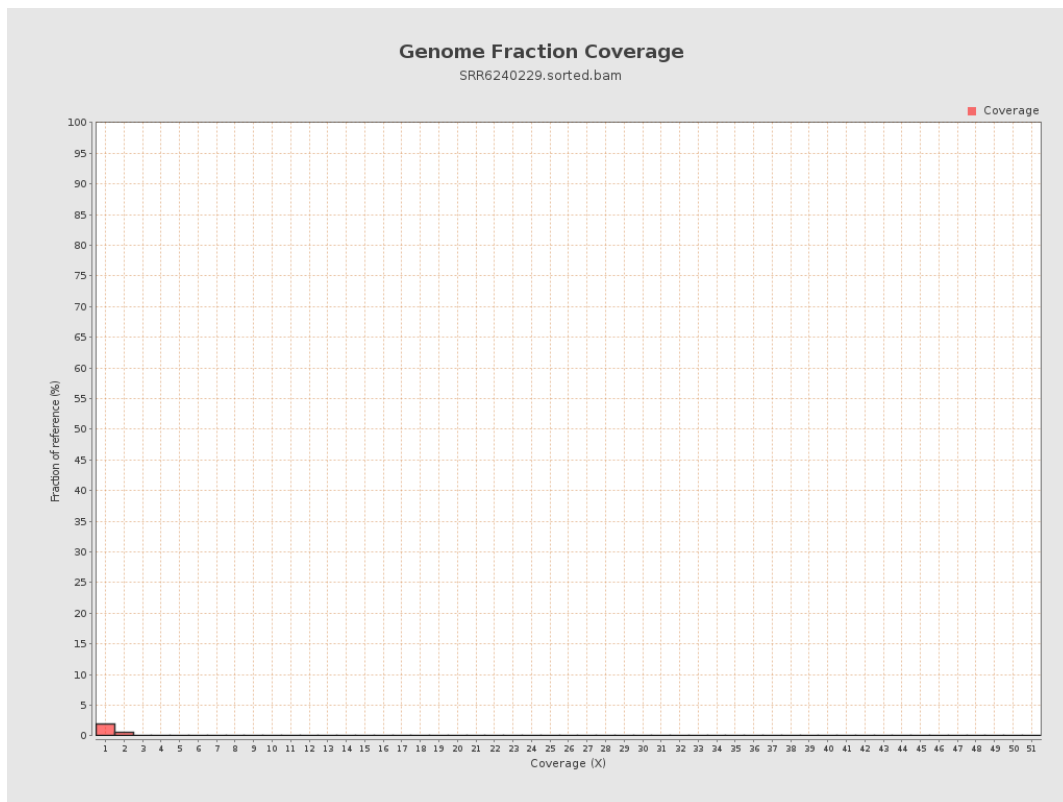
4. Results : Coverage Histogram



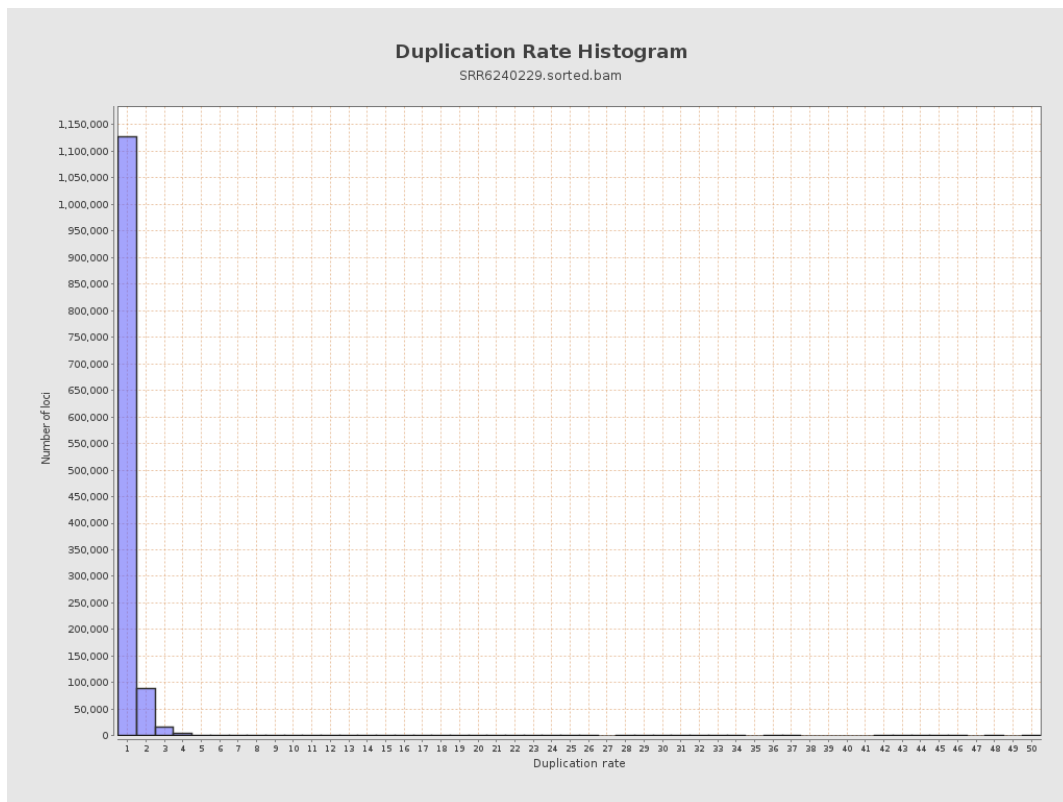
5. Results : Coverage Histogram (0-50X)



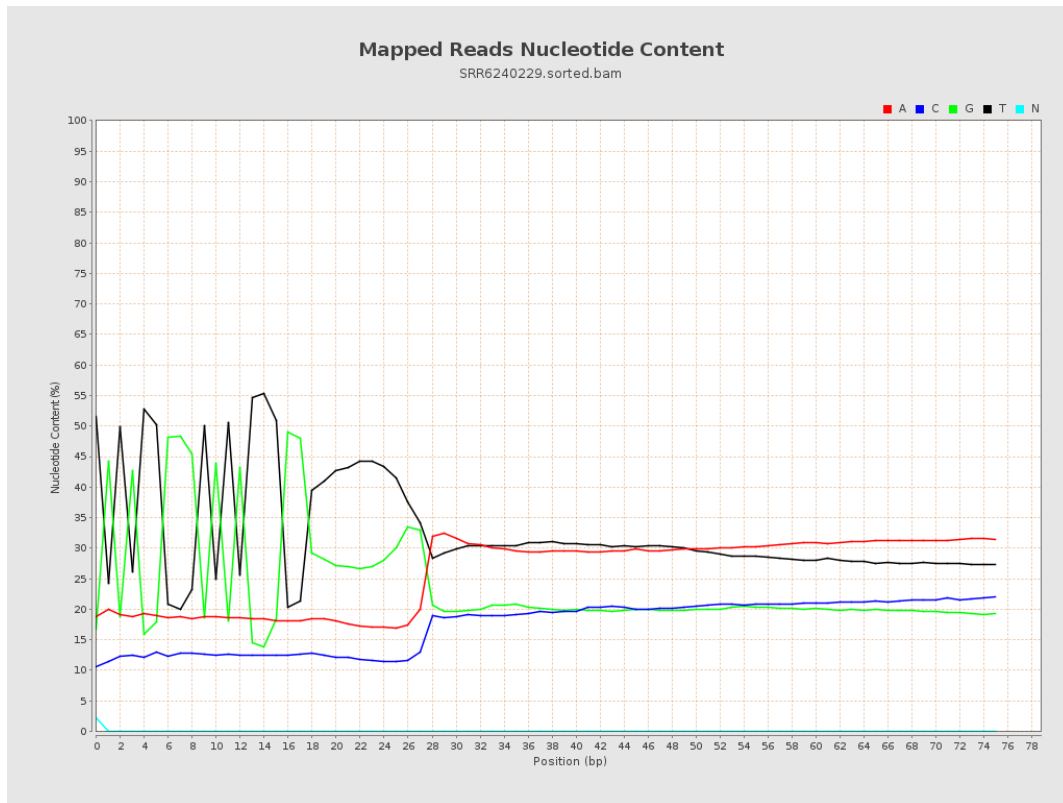
6. Results : Genome Fraction Coverage



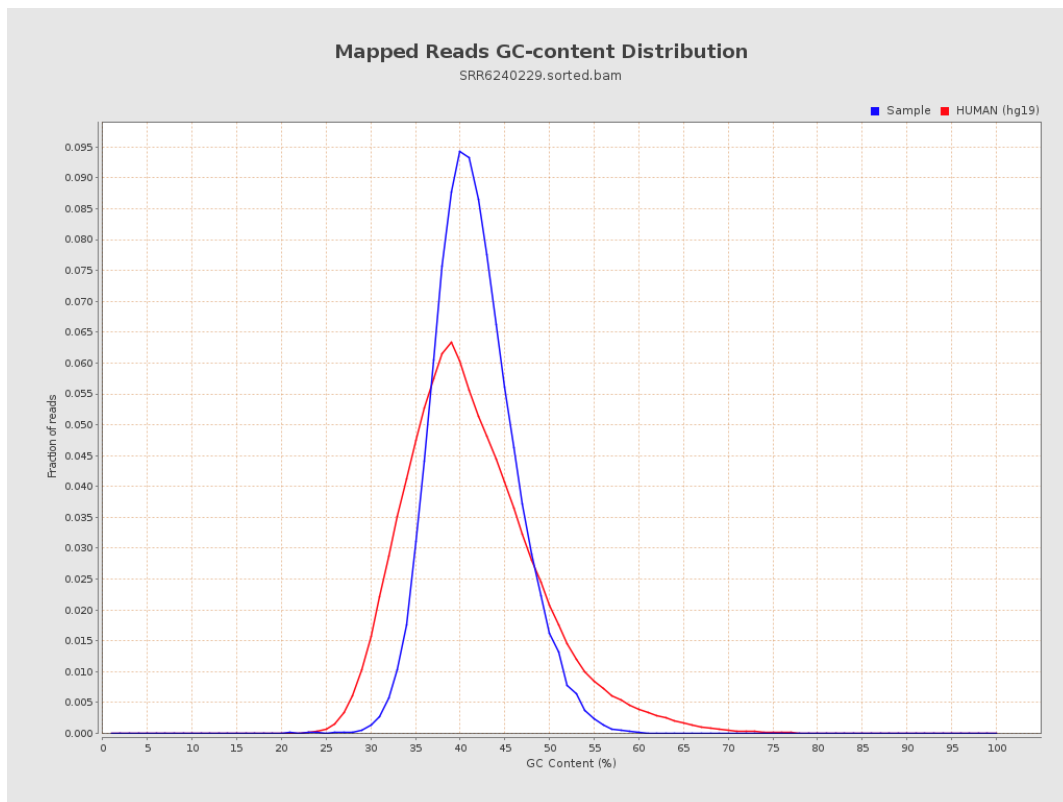
7. Results : Duplication Rate Histogram



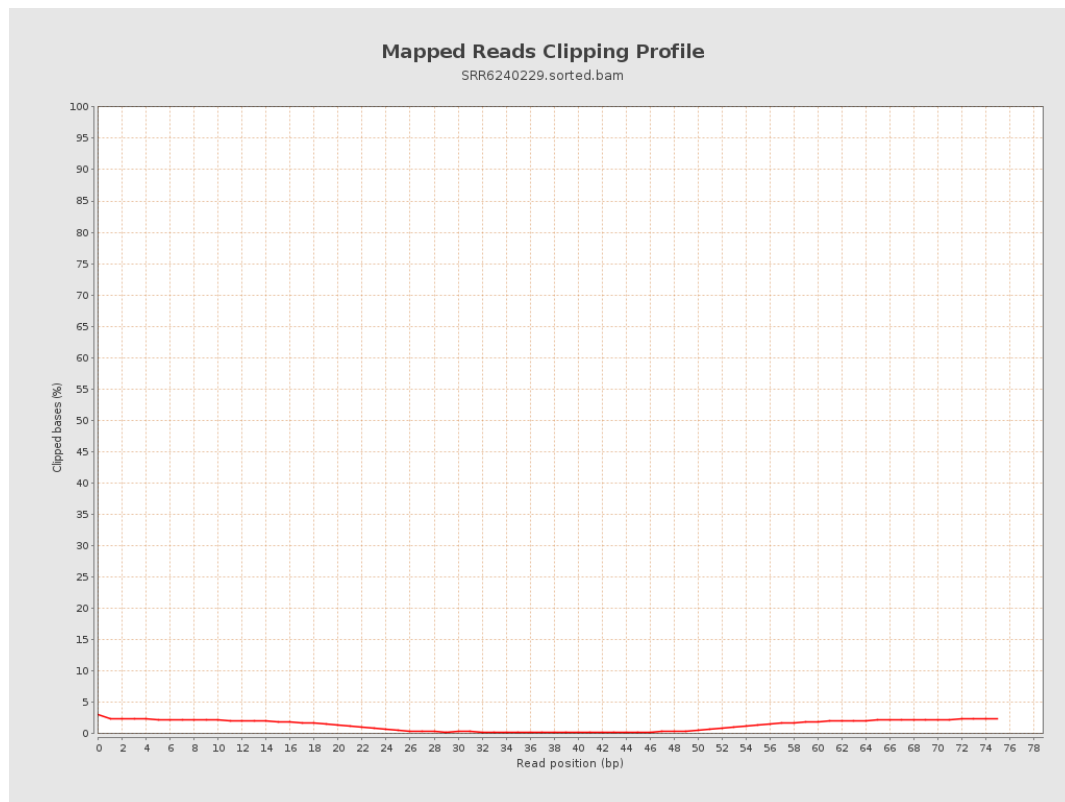
8. Results : Mapped Reads Nucleotide Content



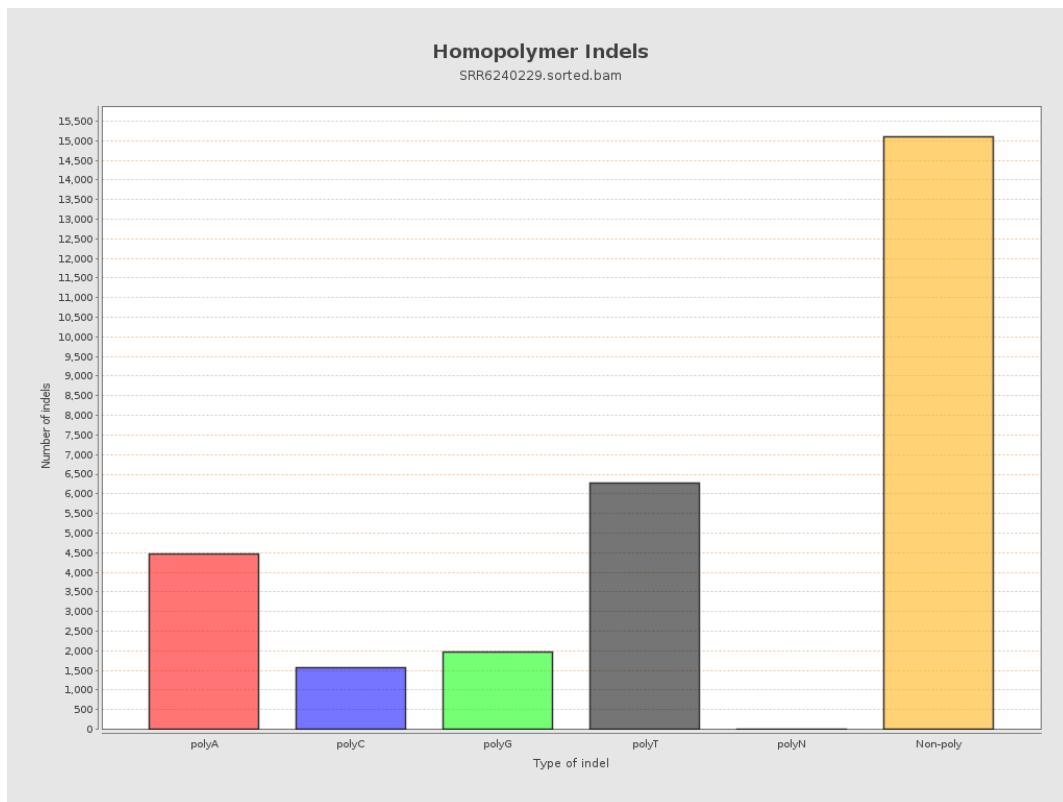
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

