

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 15:07:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234092.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_SRR6234092 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234092.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 15:07:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234092.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,339,925
Mapped reads	5,066,567 / 94.88%
Unmapped reads	273,358 / 5.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,215 / 0.62%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	677,797 / 12.69%
Duplication rate	11.18%
Clipped reads	2,589,825 / 48.5%

2.2. ACGT Content

Number/percentage of A's	84,575,589 / 25.78%
Number/percentage of C's	59,245,650 / 18.06%
Number/percentage of T's	106,746,878 / 32.54%
Number/percentage of G's	77,481,540 / 23.62%
Number/percentage of N's	31,432 / 0.01%
GC Percentage	41.67%

2.3. Coverage

Mean	0.106

Standard Deviation	1.0805
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2.4. Mapping Quality

Mean Mapping Quality	45.73
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2.5. Mismatches and indels

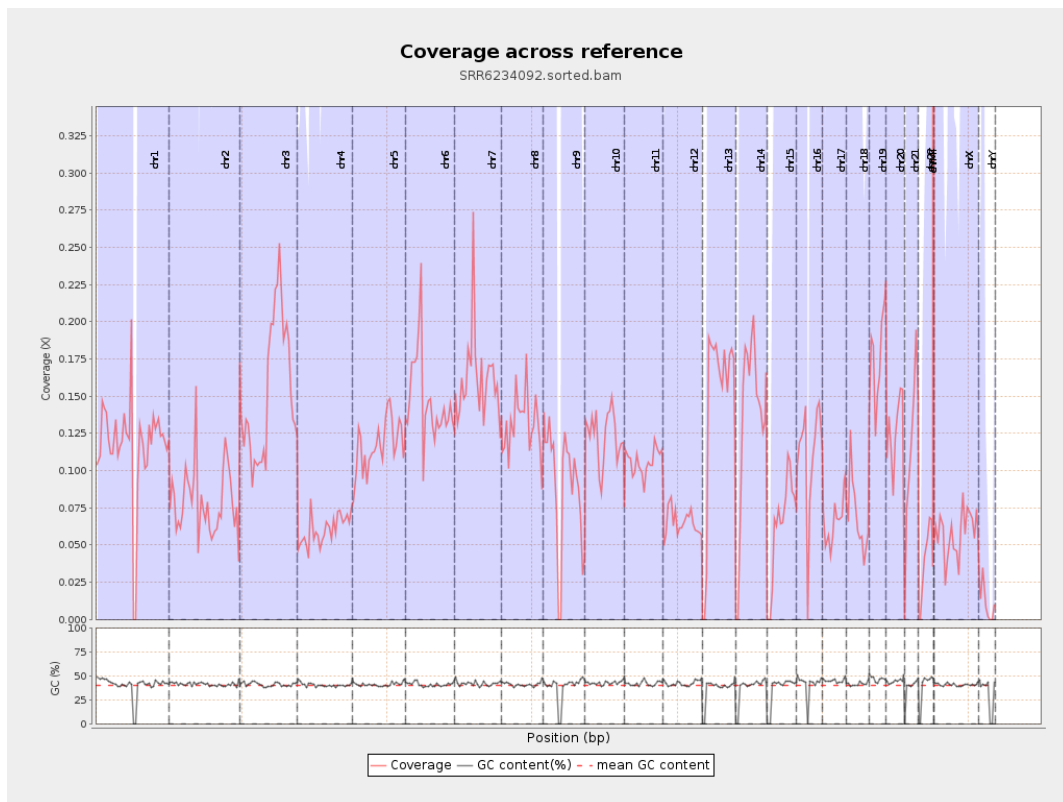
General error rate	0.54%
Mismatches	1,720,390
Insertions	20,831
Mapped reads with at least one insertion	0.41%
Deletions	72,580
Mapped reads with at least one deletion	1.42%
Homopolymer indels	44.42%

2.6. Chromosome stats

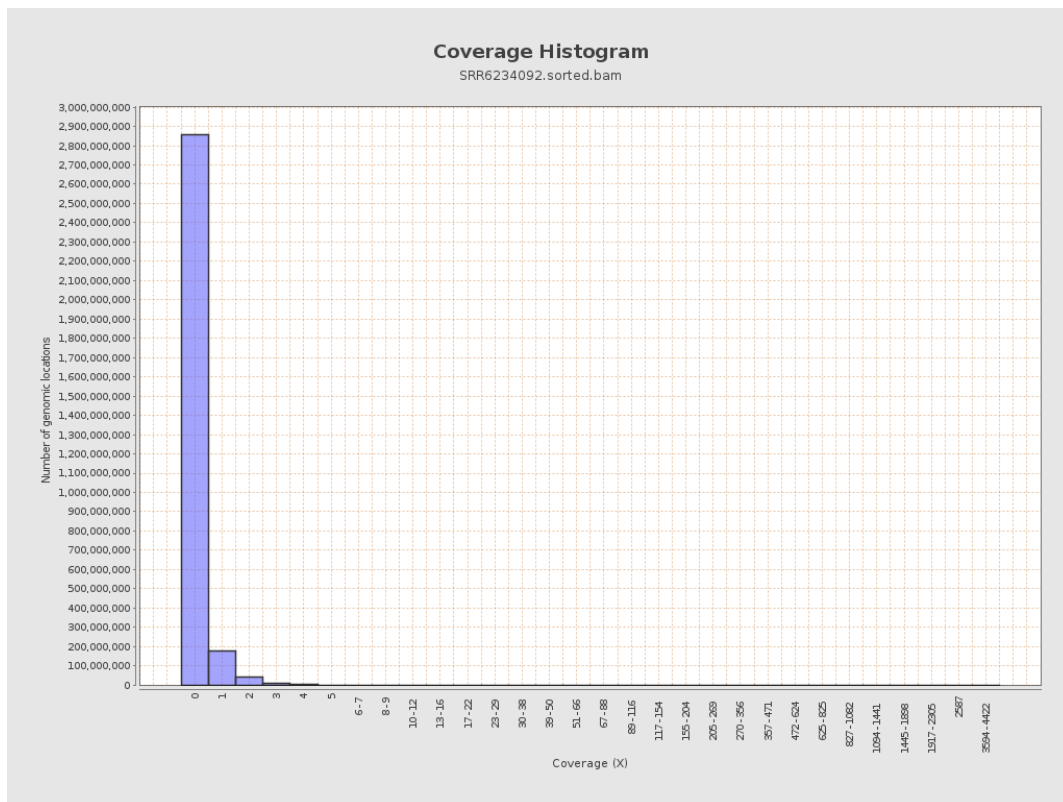
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	29049437	0.1165	1.9049
chr2	243199373	19324746	0.0795	2.019
chr3	198022430	30460613	0.1538	0.5211
chr4	191154276	11470335	0.06	0.3825
chr5	180915260	21180746	0.1171	0.4608
chr6	171115067	25100539	0.1467	0.8737
chr7	159138663	25789970	0.1621	1.8156

chr8	146364022	19173239	0.131	1.0419
chr9	141213431	12676170	0.0898	0.7159
chr10	135534747	16689485	0.1231	0.7378
chr11	135006516	14205456	0.1052	0.7776
chr12	133851895	8696264	0.065	0.381
chr13	115169878	16759240	0.1455	0.5604
chr14	107349540	14356558	0.1337	0.5569
chr15	102531392	6593763	0.0643	0.3797
chr16	90354753	10145555	0.1123	0.5455
chr17	81195210	5430420	0.0669	0.422
chr18	78077248	5394872	0.0691	1.7991
chr19	59128983	10373129	0.1754	1.169
chr20	63025520	7838952	0.1244	0.5338
chr21	48129895	5582929	0.116	0.4706
chr22	51304566	2034650	0.0397	0.2495
chrMT	16571	306414	18.491	10.9463
chrX	155270560	8929396	0.0575	0.4409
chrY	59373566	644369	0.0109	0.2459

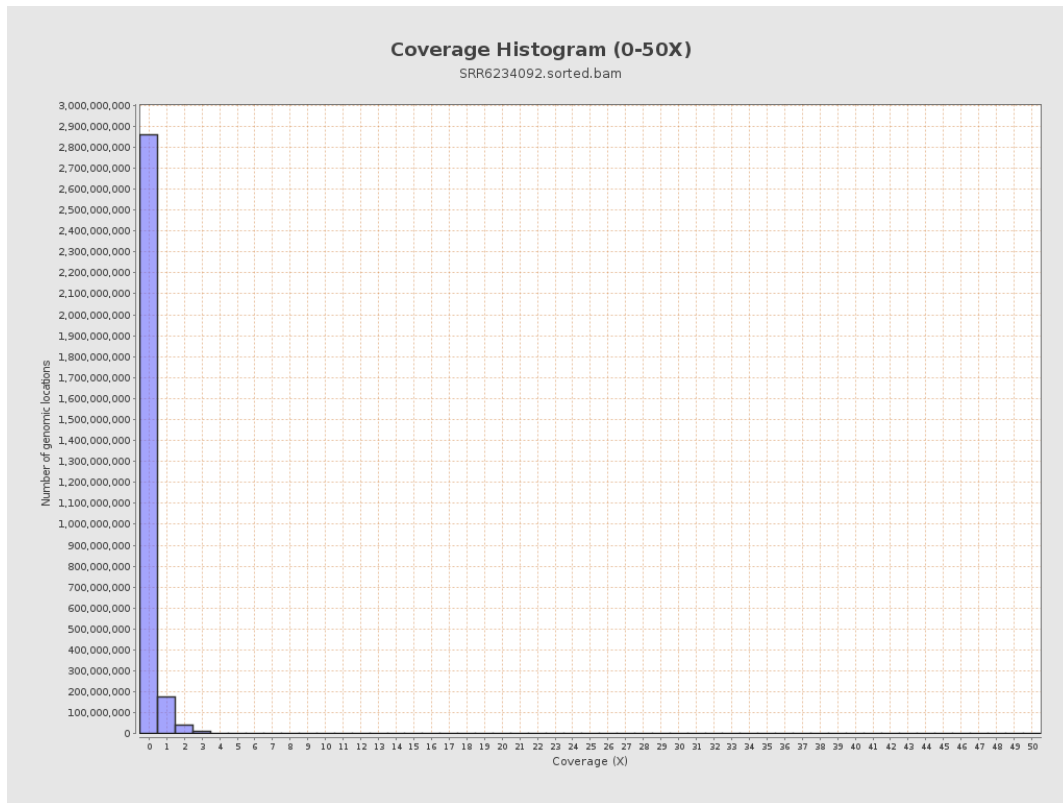
3. Results : Coverage across reference



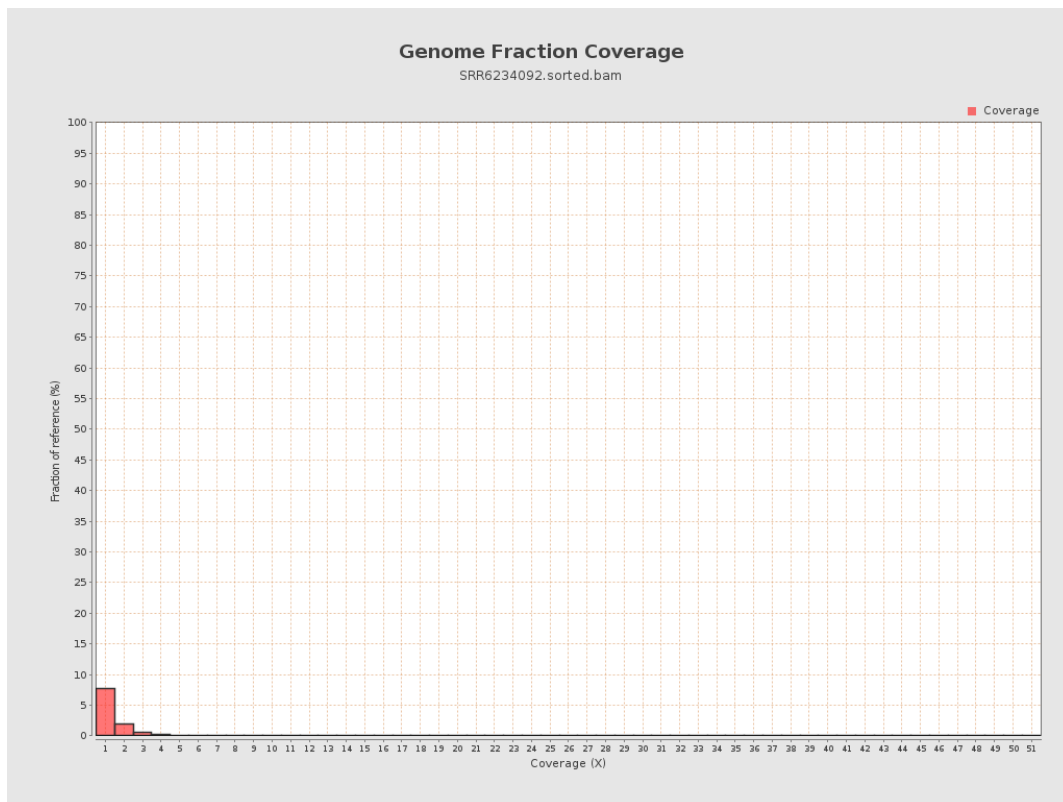
4. Results : Coverage Histogram



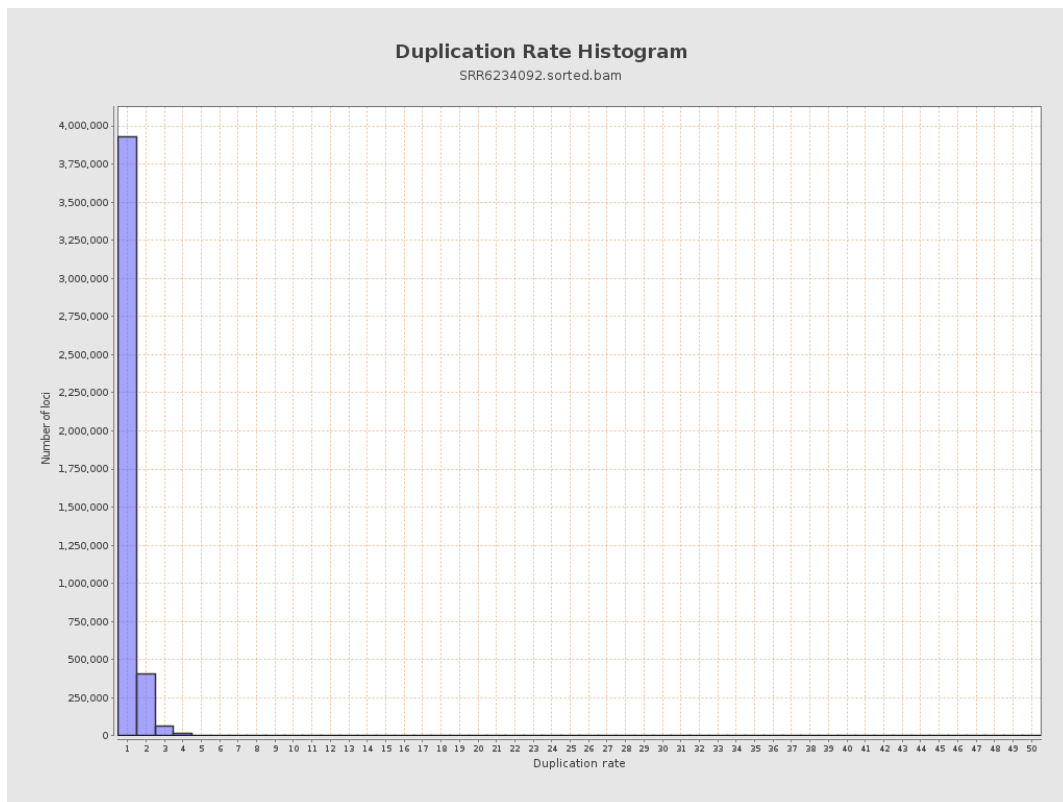
5. Results : Coverage Histogram (0-50X)



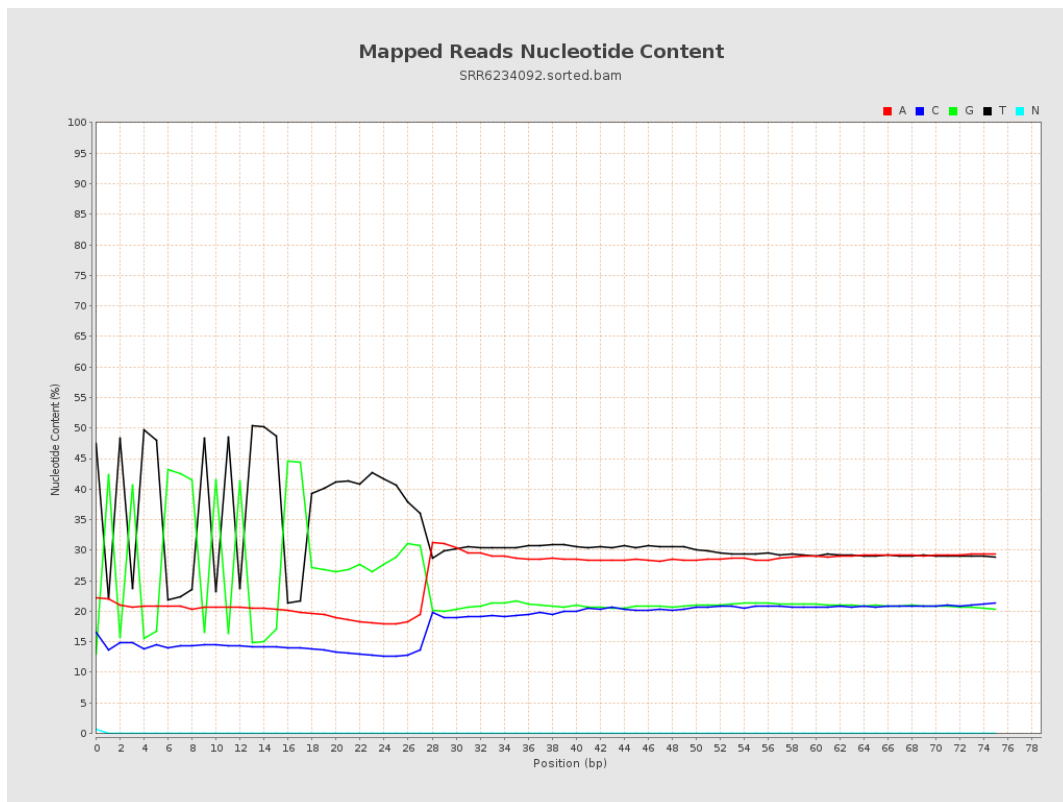
6. Results : Genome Fraction Coverage



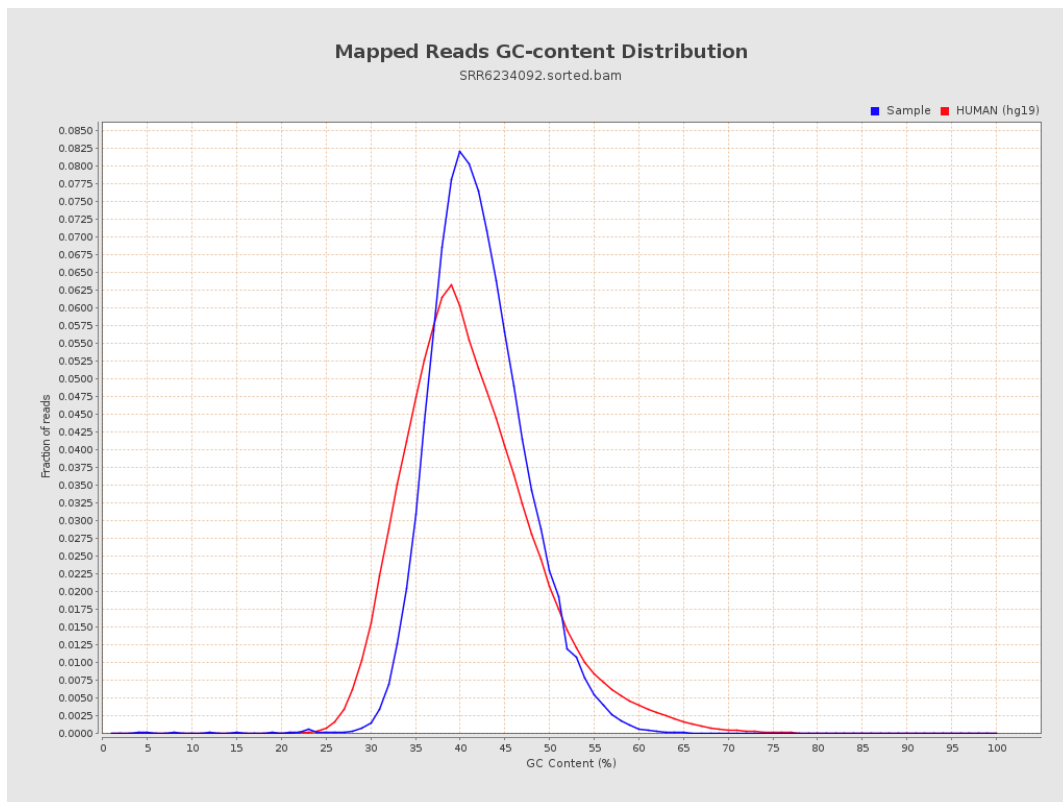
7. Results : Duplication Rate Histogram



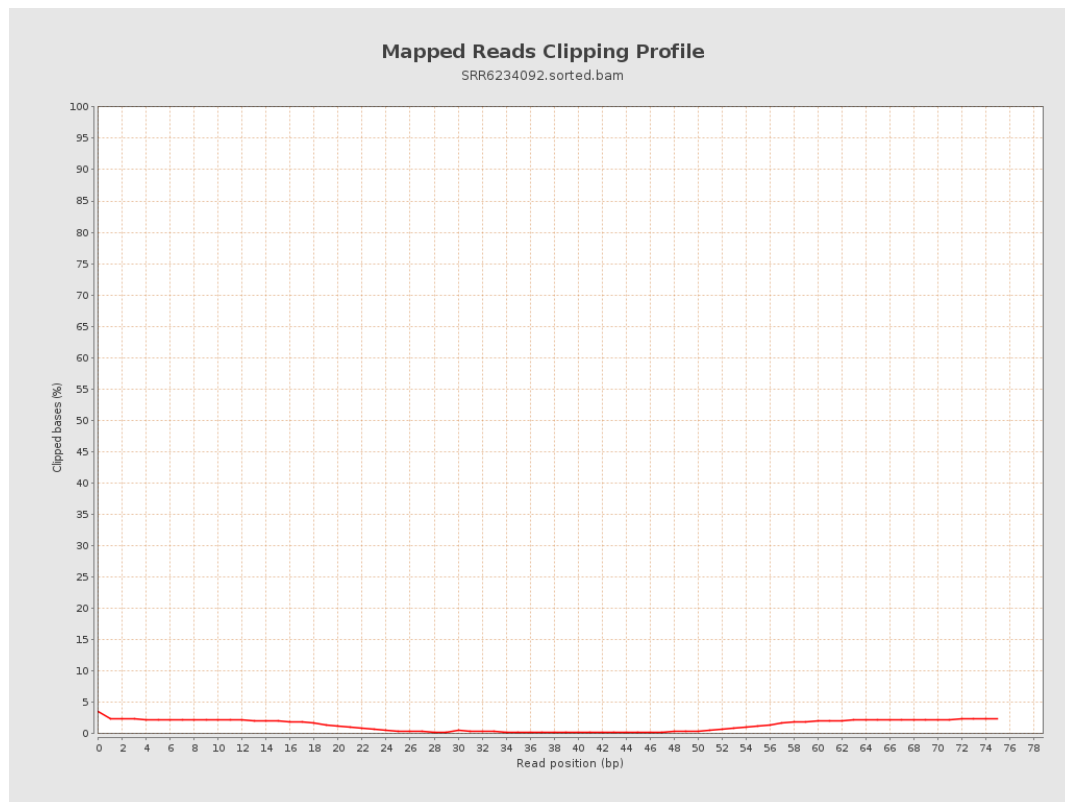
8. Results : Mapped Reads Nucleotide Content



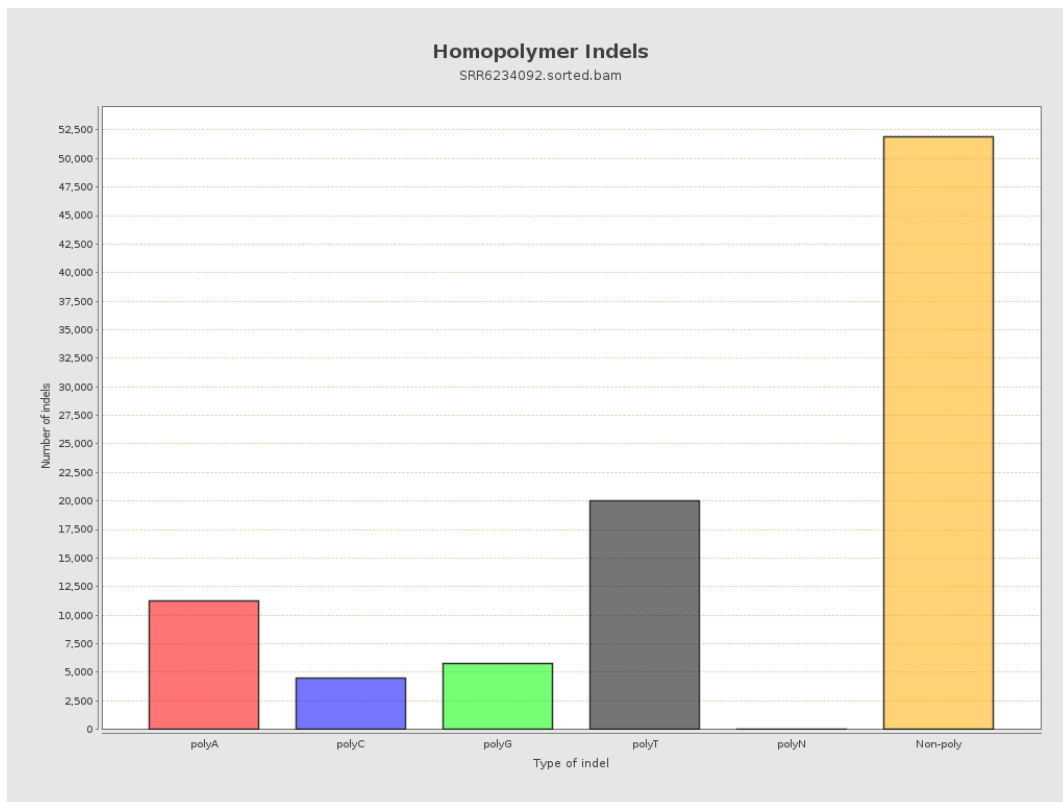
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

