

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 09:24:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008742.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_SRR6008742 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008742.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 09:24:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008742.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,369,866
Mapped reads	1,118,515 / 81.65%
Unmapped reads	251,351 / 18.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,326 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	19,968 / 1.46%
Duplication rate	1.41%
Clipped reads	458,265 / 33.45%

2.2. ACGT Content

Number/percentage of A's	23,039,579 / 30.43%
Number/percentage of C's	13,585,711 / 17.94%
Number/percentage of T's	22,560,728 / 29.8%
Number/percentage of G's	16,523,697 / 21.82%
Number/percentage of N's	7,248 / 0.01%
GC Percentage	39.77%

2.3. Coverage

Mean	0.0245

Standard Deviation	0.1962
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2.4. Mapping Quality

Mean Mapping Quality	46.61
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2.5. Mismatches and indels

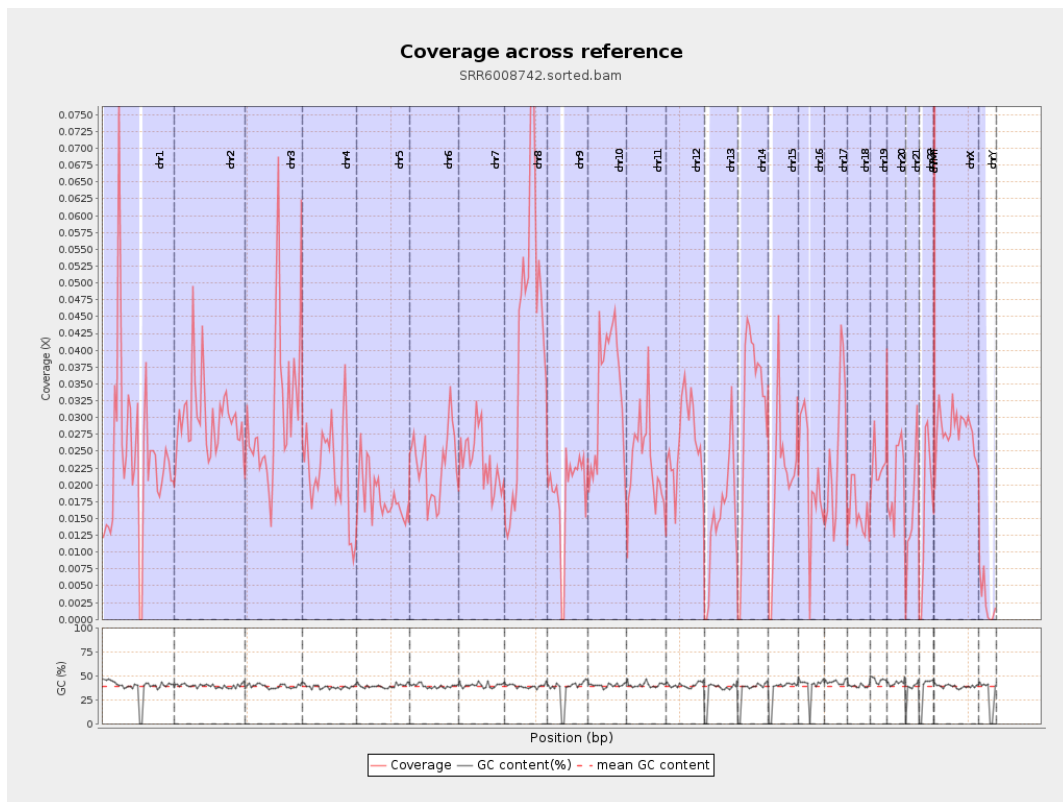
General error rate	0.87%
Mismatches	646,196
Insertions	6,321
Mapped reads with at least one insertion	0.56%
Deletions	24,386
Mapped reads with at least one deletion	2.15%
Homopolymer indels	46.15%

2.6. Chromosome stats

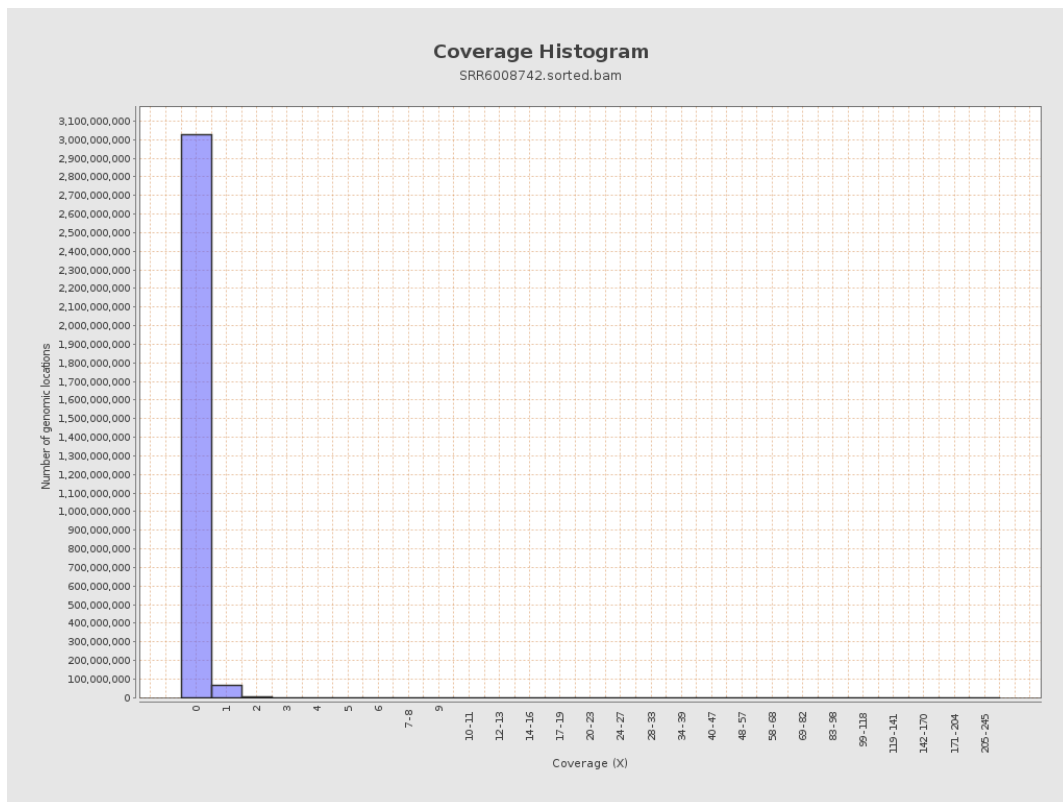
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5855109	0.0235	0.2623
chr2	243199373	7318586	0.0301	0.228
chr3	198022430	6024331	0.0304	0.1821
chr4	191154276	4221142	0.0221	0.157
chr5	180915260	3322637	0.0184	0.1407
chr6	171115067	3928656	0.023	0.1677
chr7	159138663	3755454	0.0236	0.2106

chr8	146364022	6160779	0.0421	0.2587
chr9	141213431	2650123	0.0188	0.1774
chr10	135534747	4534495	0.0335	0.2339
chr11	135006516	3181953	0.0236	0.2074
chr12	133851895	3533489	0.0264	0.1689
chr13	115169878	1747678	0.0152	0.1274
chr14	107349540	3363280	0.0313	0.1859
chr15	102531392	2136361	0.0208	0.15
chr16	90354753	1904983	0.0211	0.1631
chr17	81195210	2003015	0.0247	0.1828
chr18	78077248	1233585	0.0158	0.2939
chr19	59128983	1378017	0.0233	0.2044
chr20	63025520	1281936	0.0203	0.1506
chr21	48129895	799237	0.0166	0.1383
chr22	51304566	873938	0.017	0.1354
chrMT	16571	20229	1.2207	1.3703
chrX	155270560	4368165	0.0281	0.1844
chrY	59373566	159986	0.0027	0.0755

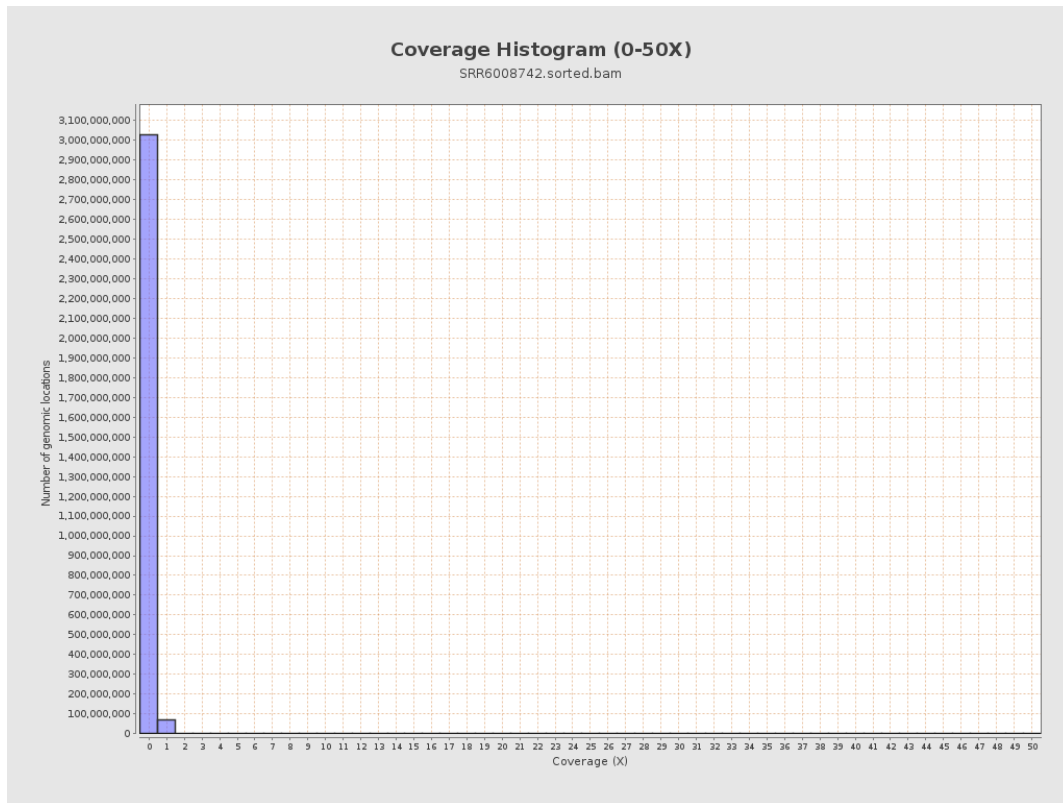
3. Results : Coverage across reference



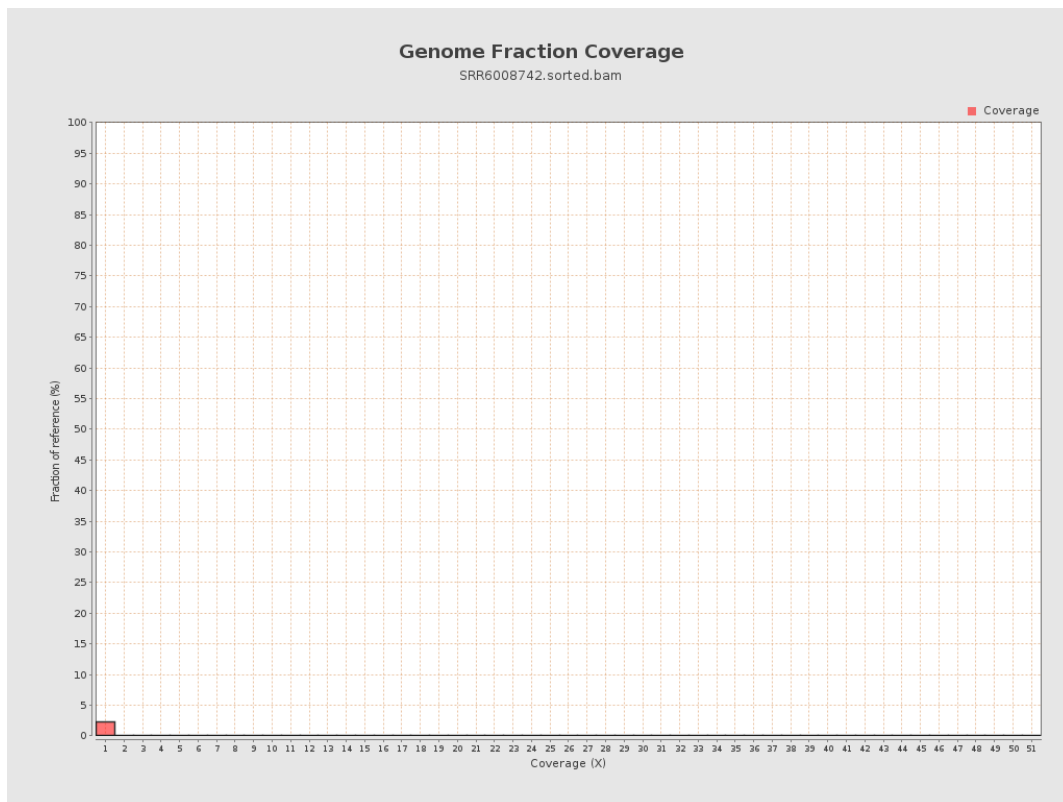
4. Results : Coverage Histogram



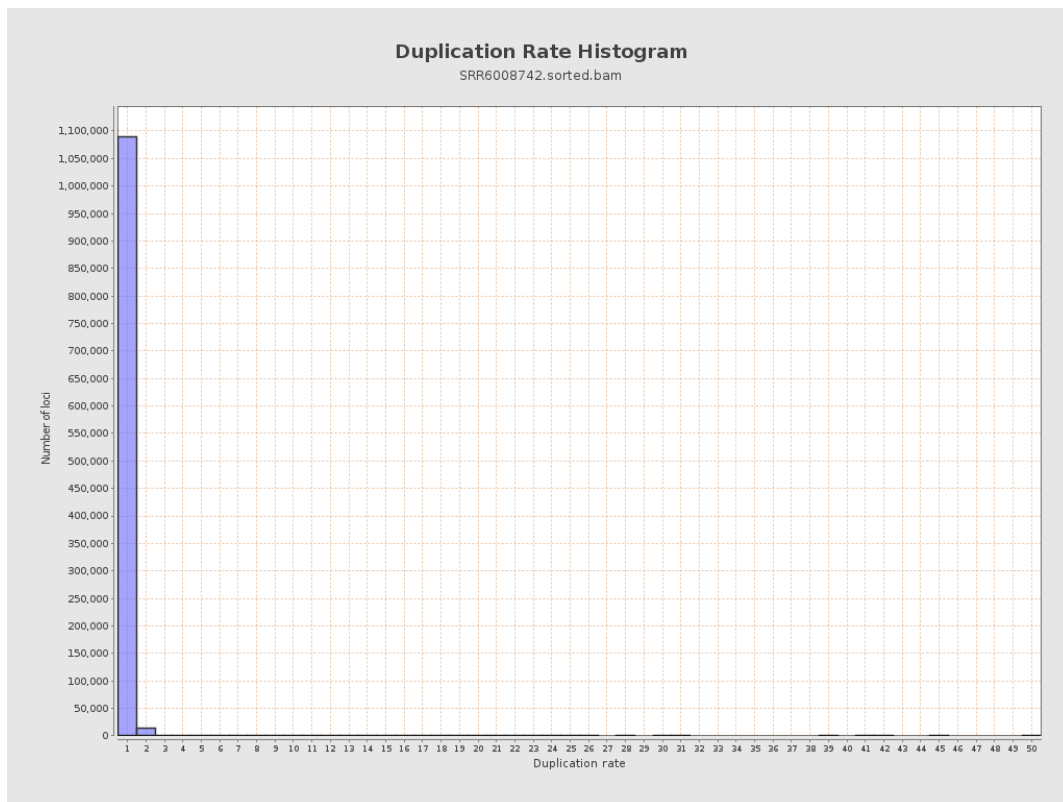
5. Results : Coverage Histogram (0-50X)



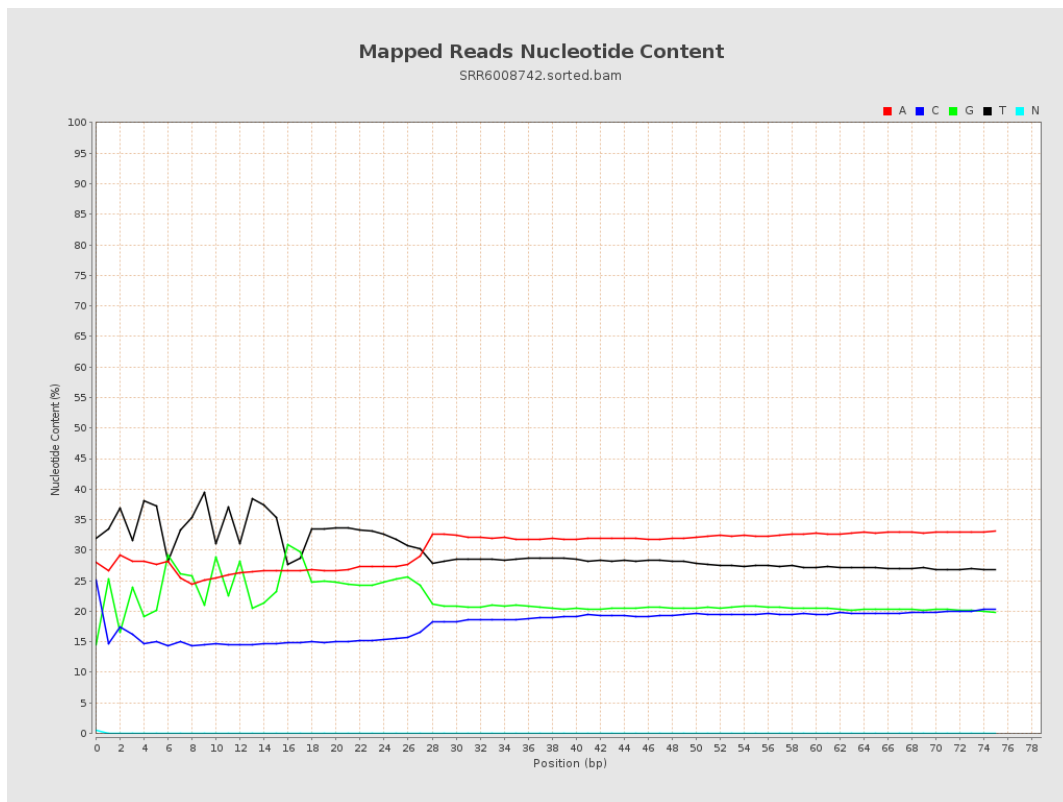
6. Results : Genome Fraction Coverage



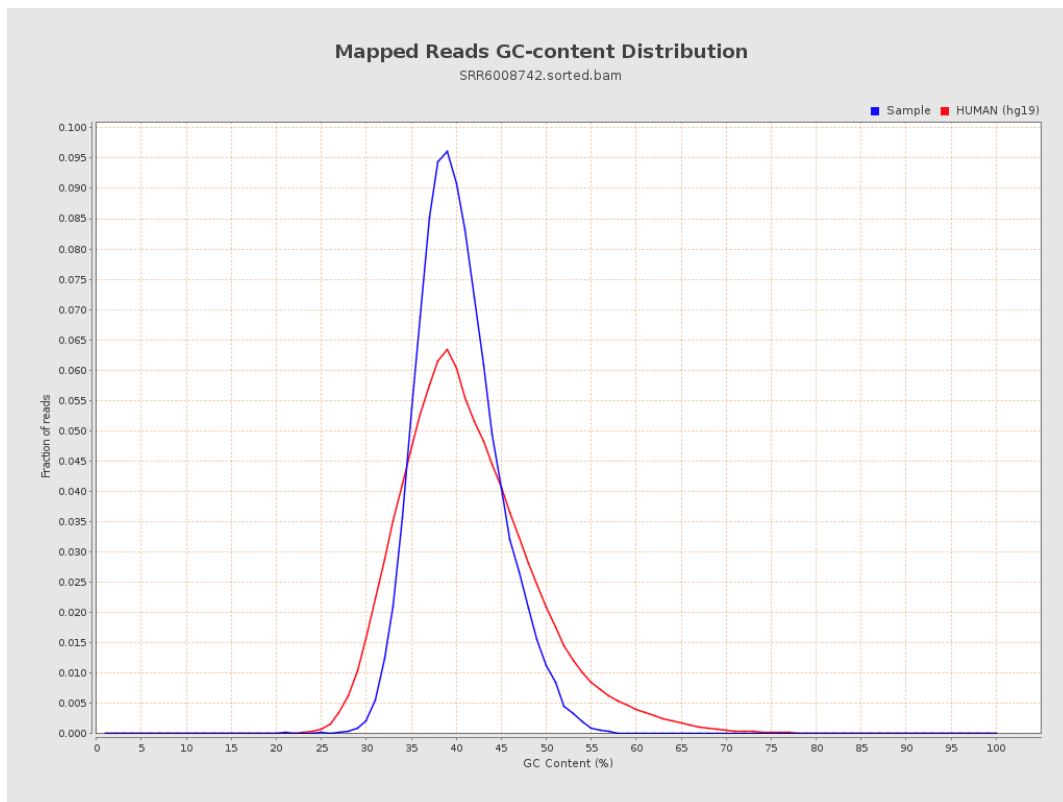
7. Results : Duplication Rate Histogram



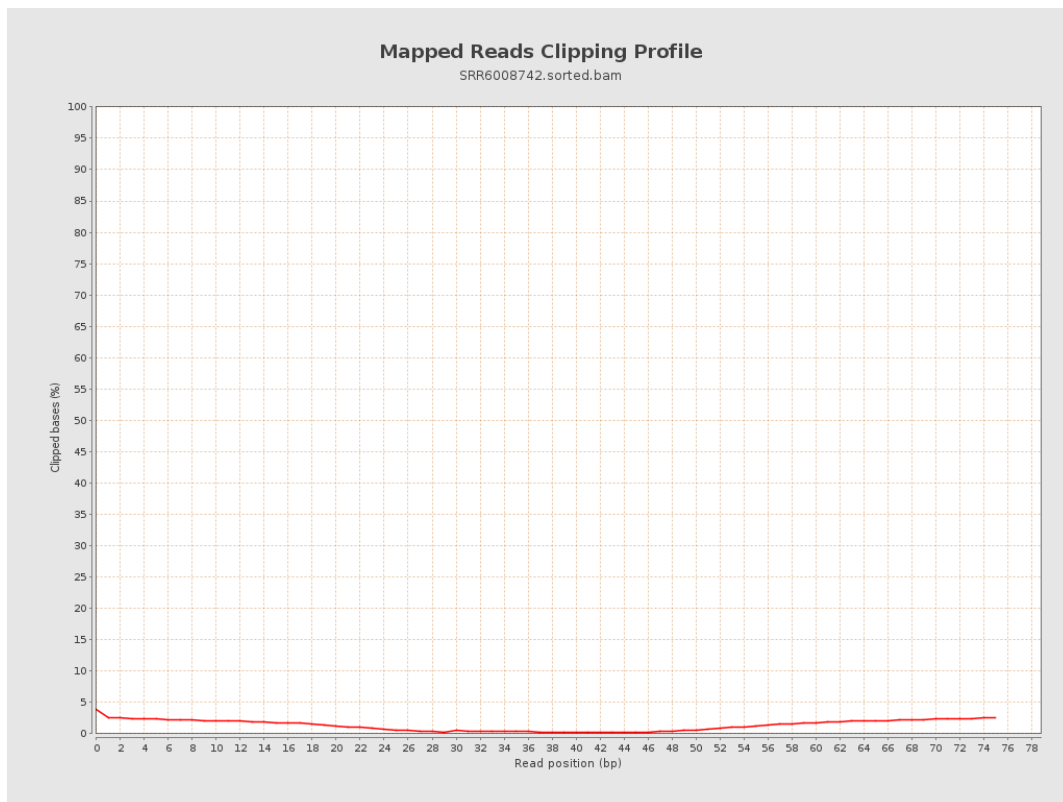
8. Results : Mapped Reads Nucleotide Content



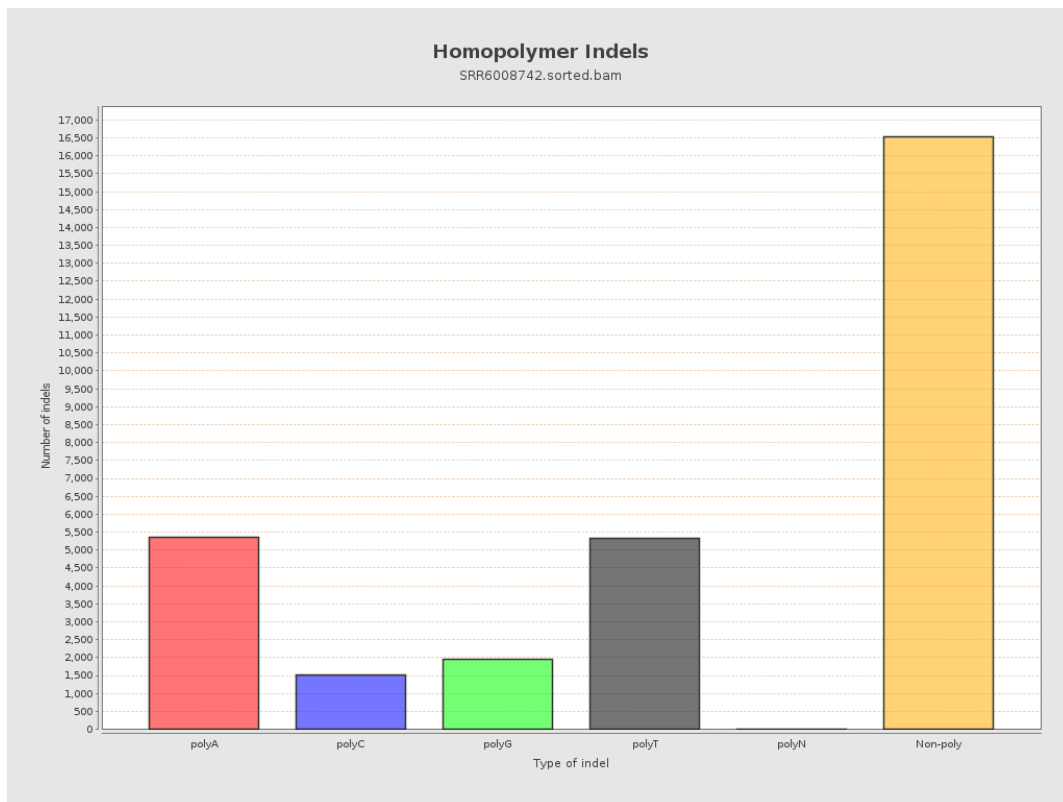
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

