

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 15:36:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068188.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_SRR6068188 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068188.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 15:36:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068188.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,248,551
Mapped reads	1,139,837 / 91.29%
Unmapped reads	108,714 / 8.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,486 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	39,899 / 3.2%
Duplication rate	2.87%
Clipped reads	450,393 / 36.07%

2.2. ACGT Content

Number/percentage of A's	22,573,676 / 29.12%
Number/percentage of C's	14,375,687 / 18.54%
Number/percentage of T's	24,431,457 / 31.52%
Number/percentage of G's	16,061,748 / 20.72%
Number/percentage of N's	75,482 / 0.1%
GC Percentage	39.26%

2.3. Coverage

Mean	0.0251

Standard Deviation	0.2734
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2.4. Mapping Quality

Mean Mapping Quality	45.65
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2.5. Mismatches and indels

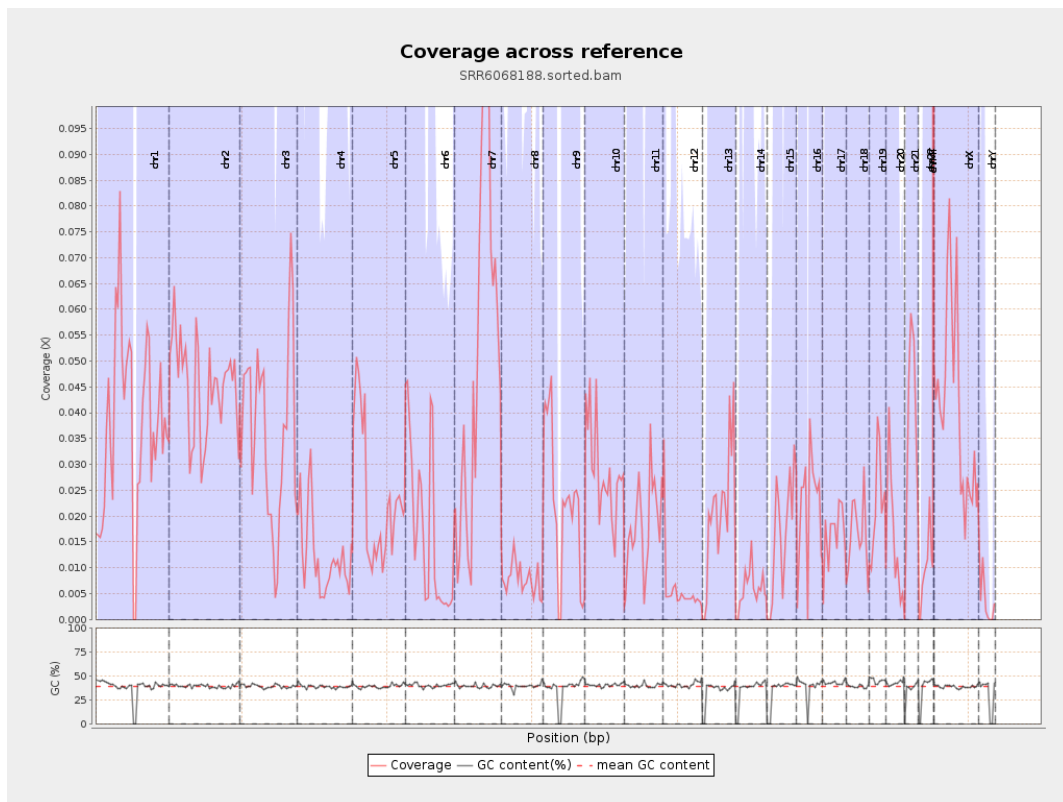
General error rate	0.84%
Mismatches	644,066
Insertions	5,407
Mapped reads with at least one insertion	0.47%
Deletions	20,228
Mapped reads with at least one deletion	1.75%
Homopolymer indels	46.87%

2.6. Chromosome stats

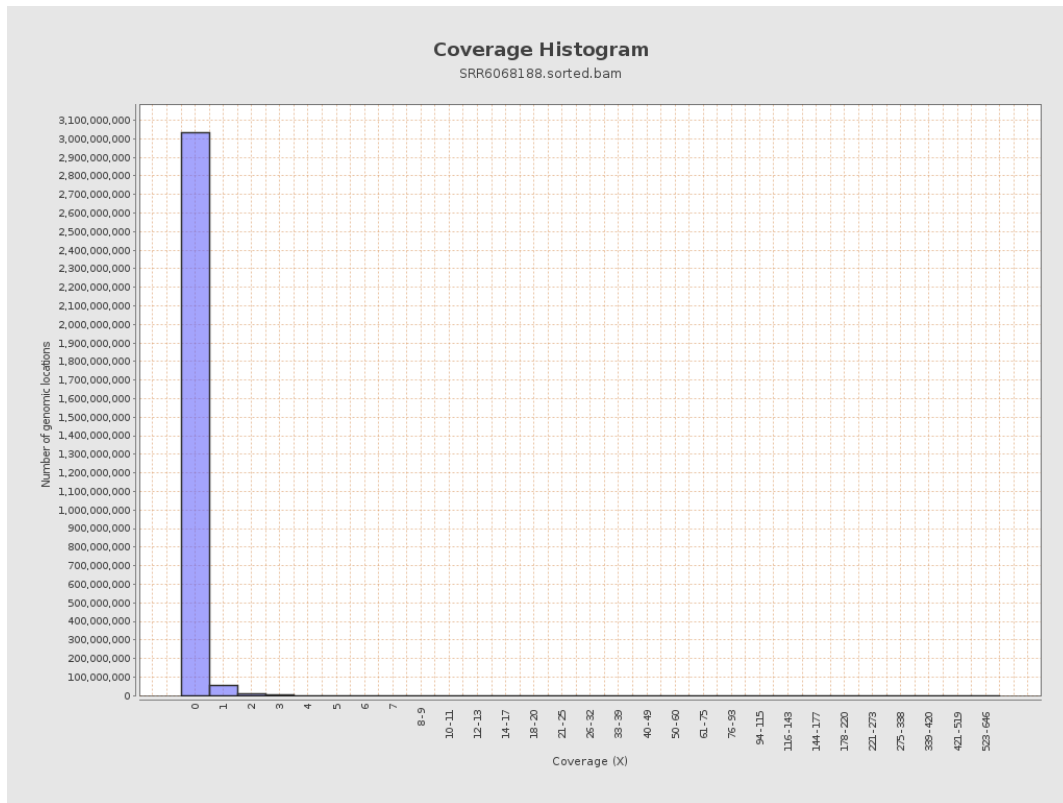
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9436165	0.0379	0.5597
chr2	243199373	10941085	0.045	0.2757
chr3	198022430	7218535	0.0365	0.2203
chr4	191154276	2315697	0.0121	0.1329
chr5	180915260	4243529	0.0235	0.1745
chr6	171115067	2969577	0.0174	0.1746
chr7	159138663	8308903	0.0522	0.4393

chr8	146364022	1128363	0.0077	0.3571
chr9	141213431	3168054	0.0224	0.1918
chr10	135534747	3898691	0.0288	0.2648
chr11	135006516	2447814	0.0181	0.1994
chr12	133851895	795274	0.0059	0.0937
chr13	115169878	2431181	0.0211	0.1652
chr14	107349540	651755	0.0061	0.0974
chr15	102531392	1714616	0.0167	0.1467
chr16	90354753	1968048	0.0218	0.1836
chr17	81195210	1313116	0.0162	0.151
chr18	78077248	1295667	0.0166	0.2307
chr19	59128983	1328487	0.0225	0.3799
chr20	63025520	1026929	0.0163	0.1491
chr21	48129895	1768052	0.0367	0.2326
chr22	51304566	503607	0.0098	0.1119
chrMT	16571	17509	1.0566	1.2652
chrX	155270560	6441902	0.0415	0.2624
chrY	59373566	220644	0.0037	0.1025

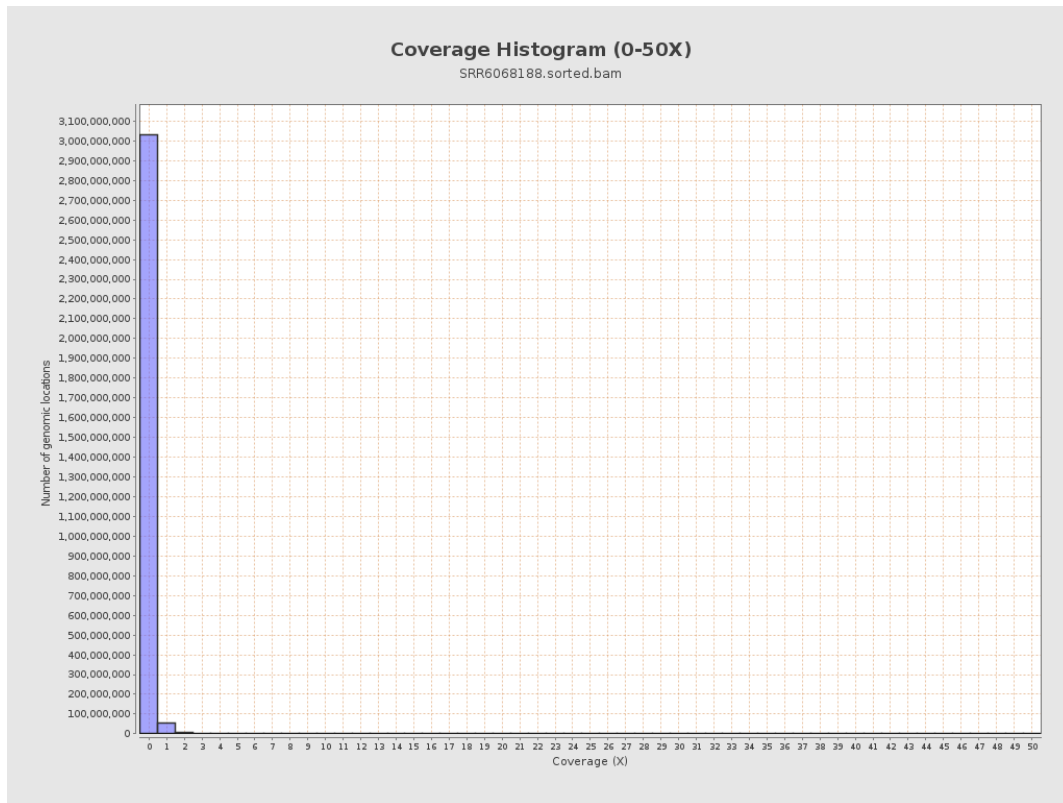
3. Results : Coverage across reference



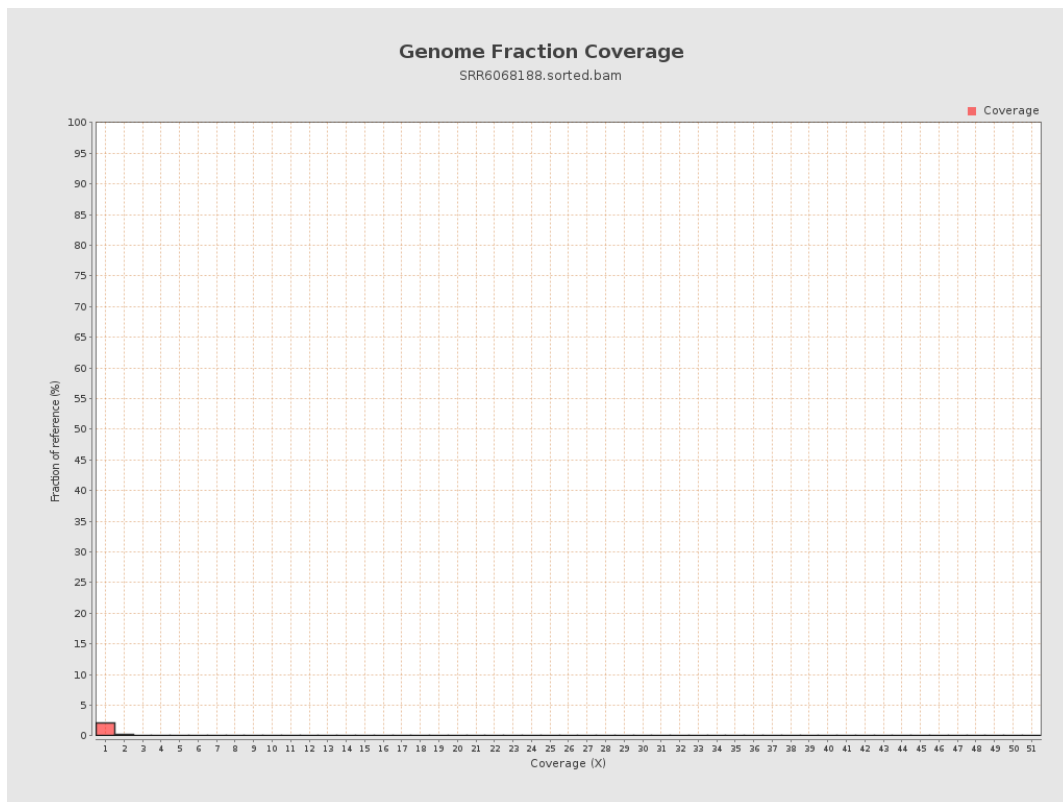
4. Results : Coverage Histogram



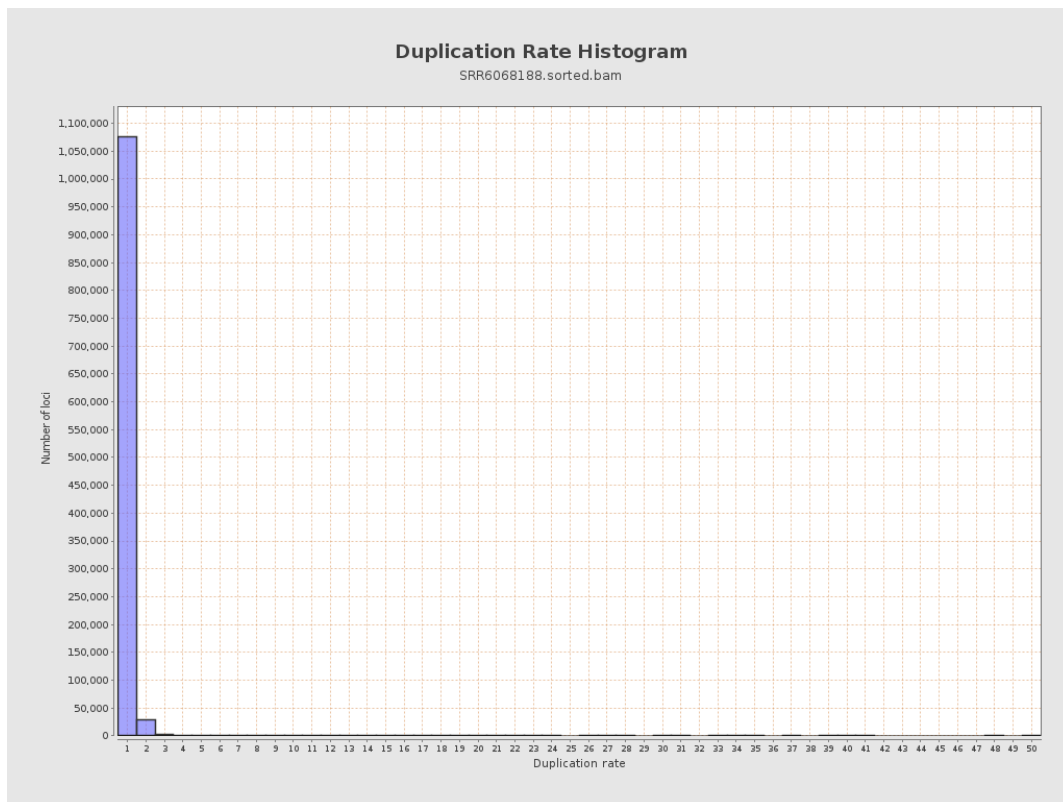
5. Results : Coverage Histogram (0-50X)



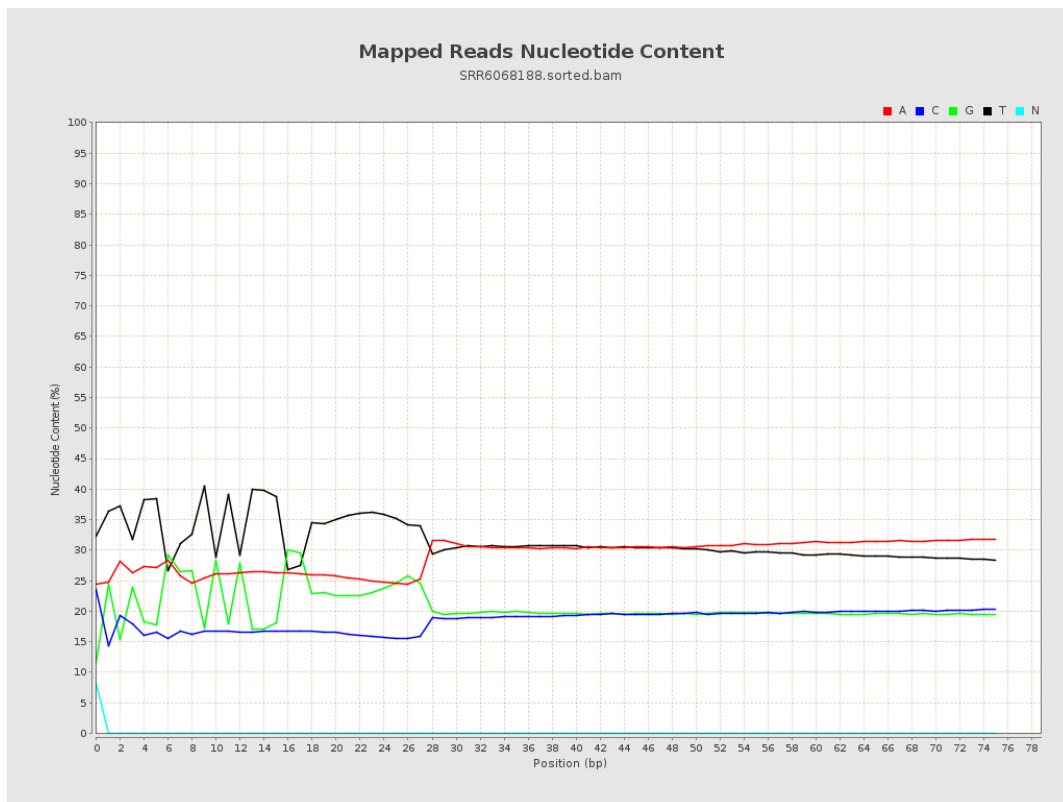
6. Results : Genome Fraction Coverage



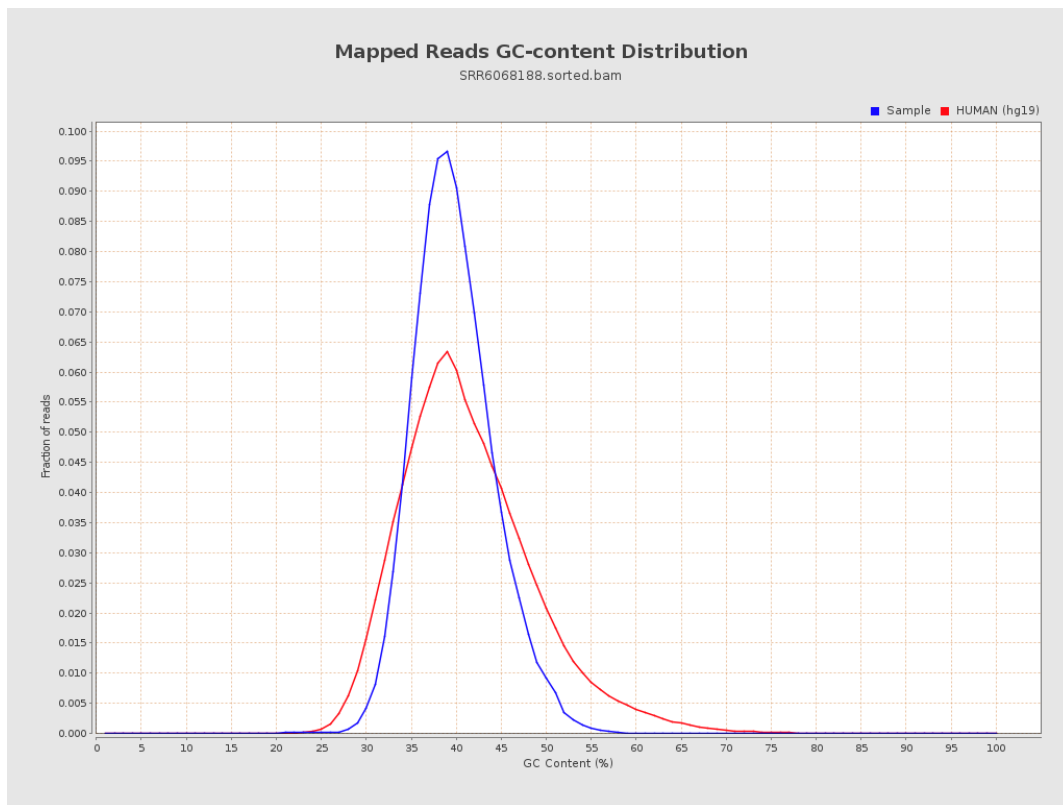
7. Results : Duplication Rate Histogram



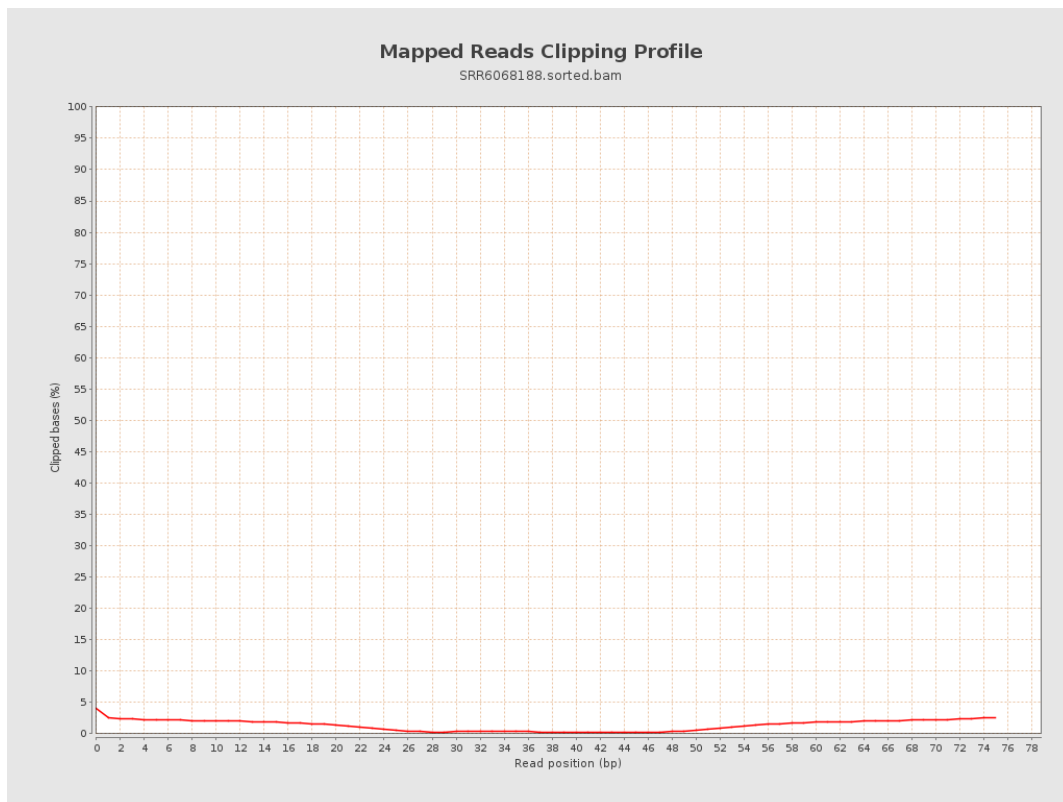
8. Results : Mapped Reads Nucleotide Content



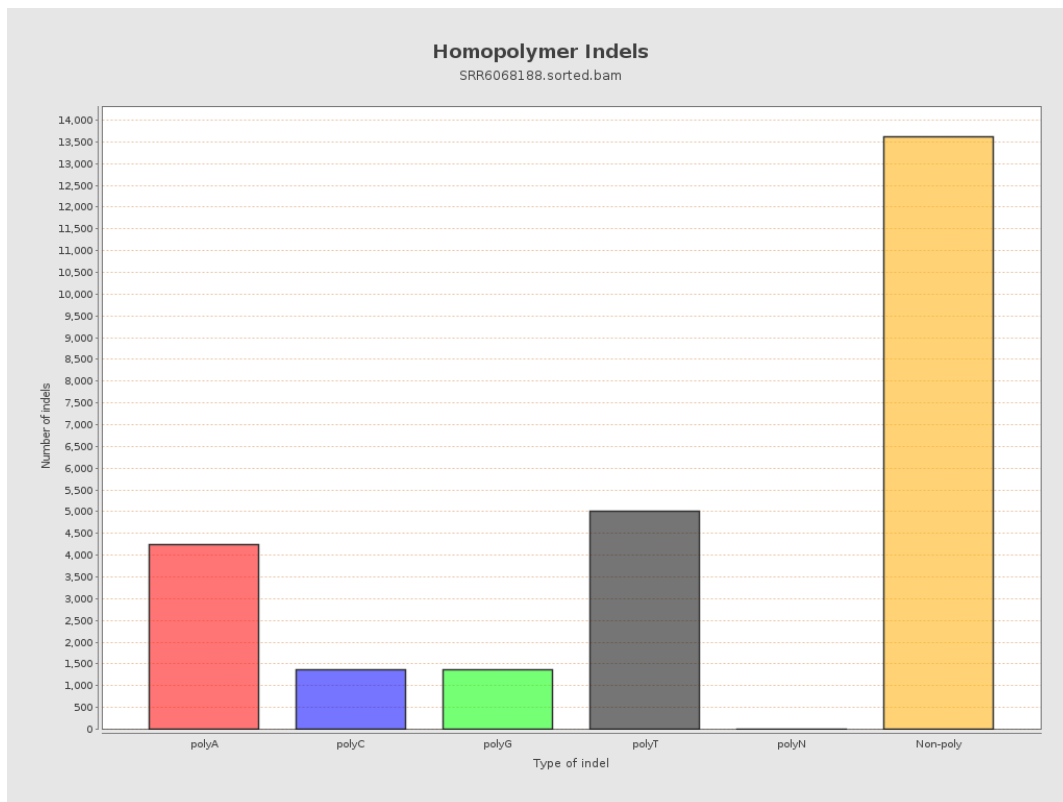
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

