Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 20:24:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089696.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_SRR089696 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089696.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 20:24:44 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089696.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	24,404,189
Mapped reads	19,569,747 / 80.19%
Unmapped reads	4,834,442 / 19.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	866 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,646,259 / 10.84%
Duplication rate	10%
Clipped reads	3,307,982 / 13.55%

2.2. ACGT Content

Number/percentage of A's	293,305,753 / 32.3%
Number/percentage of C's	180,728,984 / 19.9%
Number/percentage of T's	242,269,670 / 26.68%
Number/percentage of G's	191,810,441 / 21.12%
Number/percentage of N's	29,089 / 0%
GC Percentage	41.02%

2.3. Coverage

Mean	0.2934

Standard Deviation	1.597

2.4. Mapping Quality

Mean Mapping Quality	42.98

2.5. Mismatches and indels

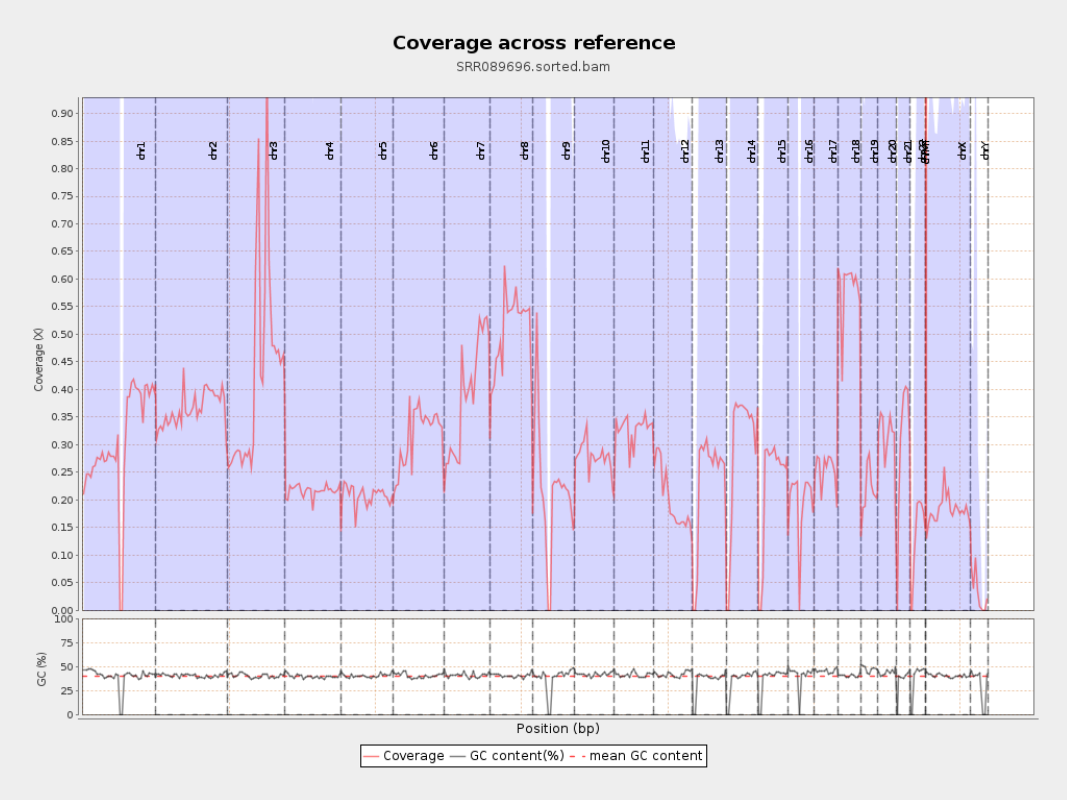
General error rate	0.57%
Mismatches	5,073,294
Insertions	43,540
Mapped reads with at least one insertion	0.22%
Deletions	132,522
Mapped reads with at least one deletion	0.68%
Homopolymer indels	44.09%

2.6. Chromosome stats

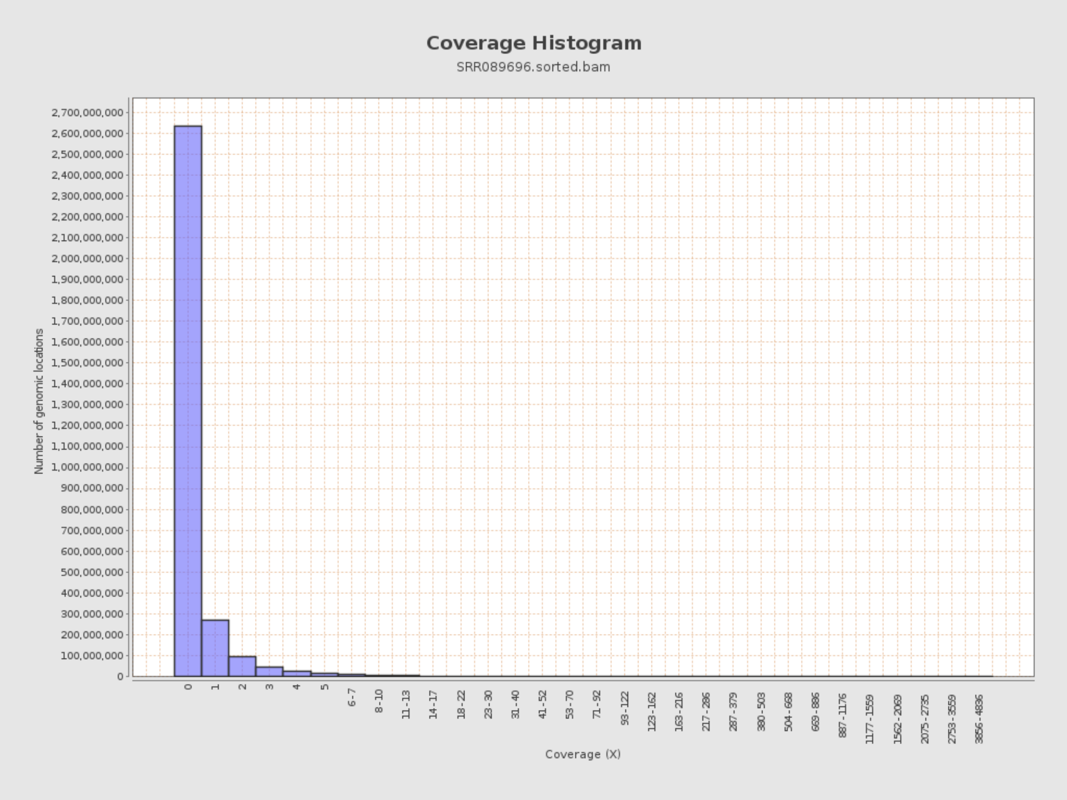
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	75625008	0.3034	1.8154
chr2	243199373	88893593	0.3655	2.323
chr3	198022430	83996905	0.4242	1.2989
chr4	191154276	41413681	0.2167	0.8566
chr5	180915260	37450476	0.207	0.8206
chr6	171115067	54188541	0.3167	1.3685
chr7	159138663	61989312	0.3895	2.5956

chr8	146364022	74461424	0.5087	3.1056
chr9	141213431	31232667	0.2212	1.3613
chr10	135534747	37838368	0.2792	1.3635
chr11	135006516	44078799	0.3265	1.4023
chr12	133851895	26841331	0.2005	0.8445
chr13	115169878	26828139	0.2329	0.886
chr14	107349540	31801945	0.2962	1.1306
chr15	102531392	22800872	0.2224	0.8466
chr16	90354753	17233820	0.1907	0.8737
chr17	81195210	20878754	0.2571	1.0683
chr18	78077248	45432534	0.5819	2.1599
chr19	59128983	13016636	0.2201	1.7759
chr20	63025520	19968712	0.3168	1.0857
chr21	48129895	14480645	0.3009	1.1198
chr22	51304566	6935051	0.1352	0.6509
chrMT	16571	786827	47.4822	42.7589
chrX	155270560	28220839	0.1818	1.142
chrY	59373566	1945099	0.0328	0.4665

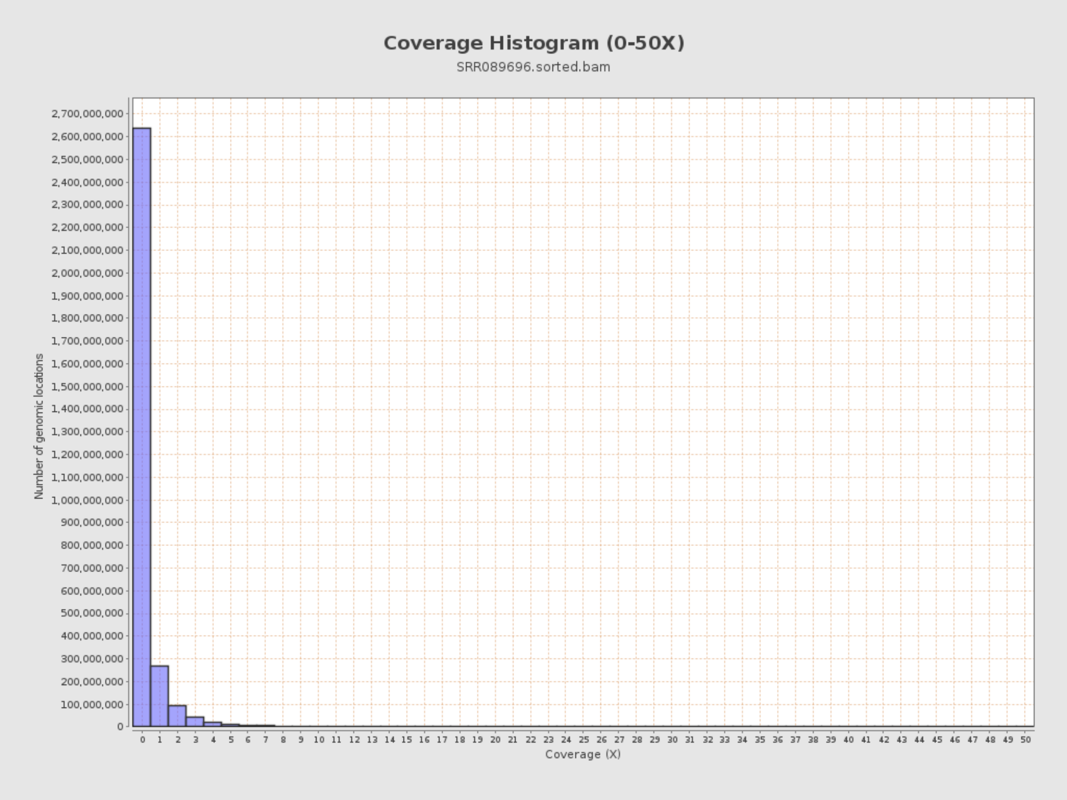
3. Results : Coverage across reference



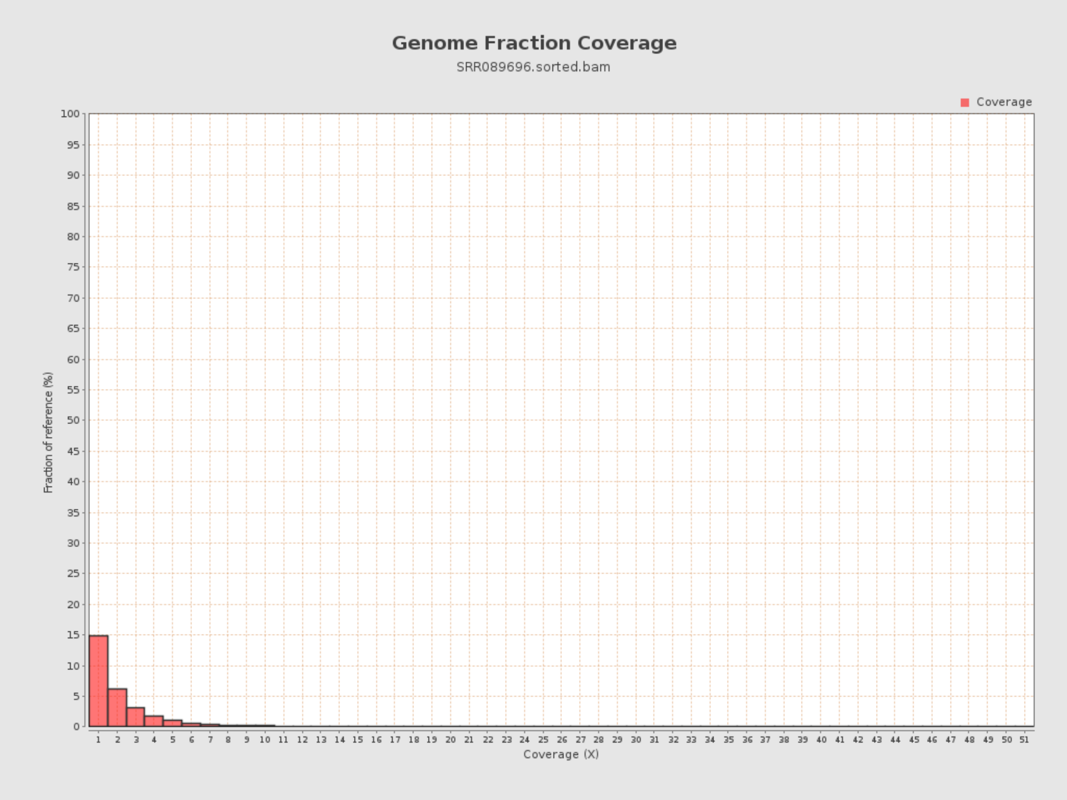
4. Results : Coverage Histogram



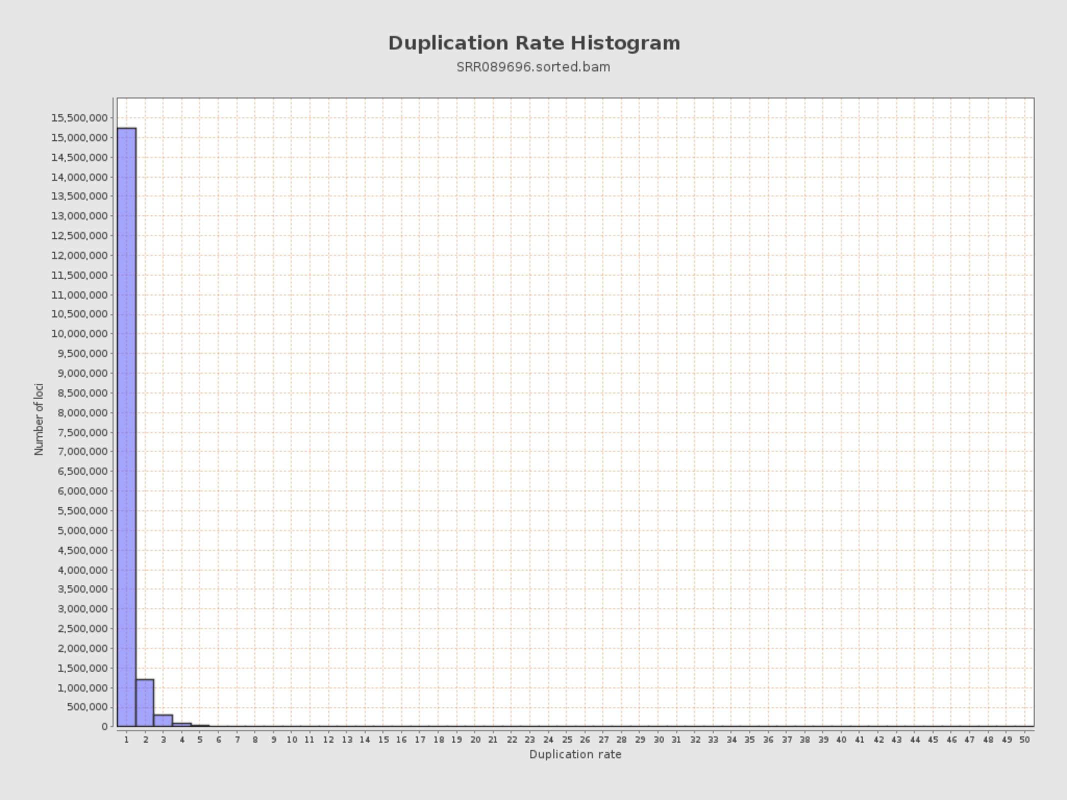
5. Results : Coverage Histogram (0-50X)



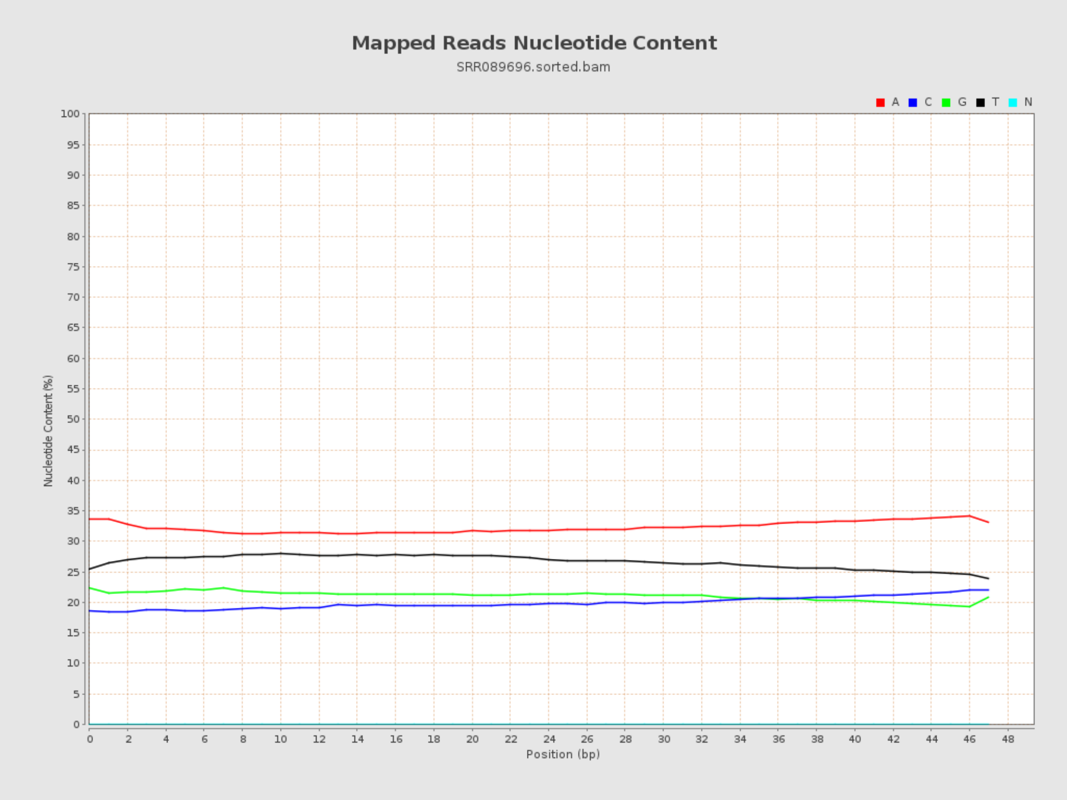
6. Results : Genome Fraction Coverage



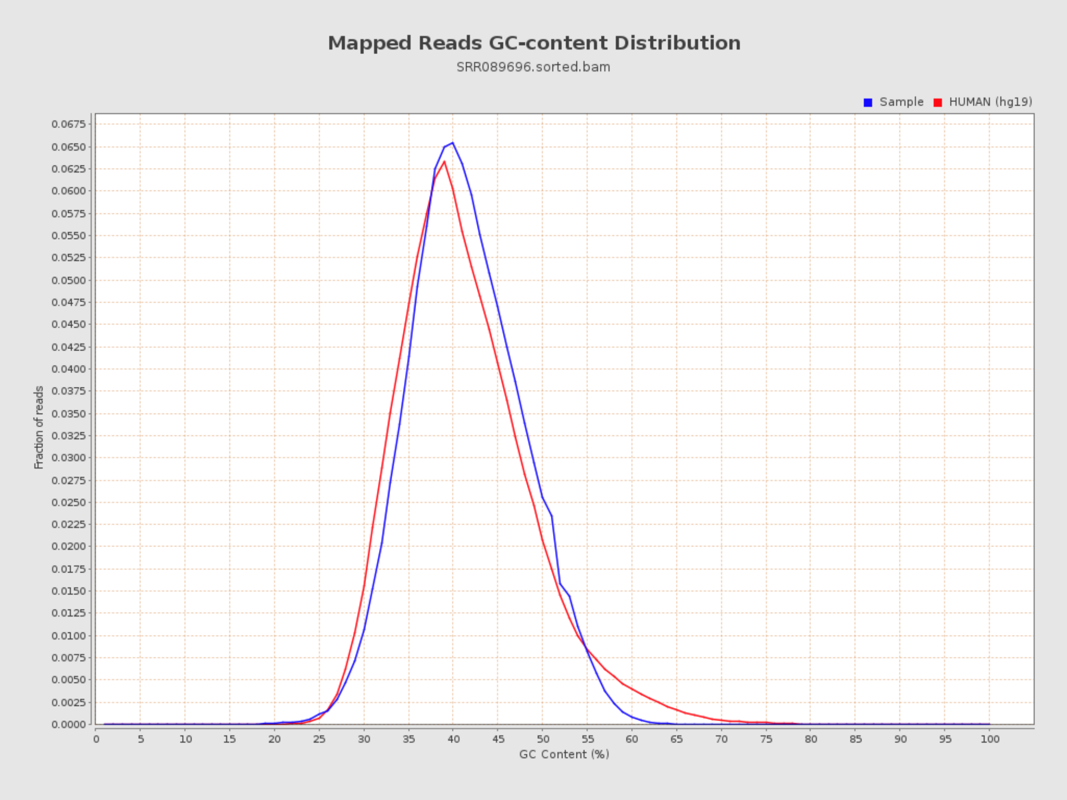
7. Results : Duplication Rate Histogram



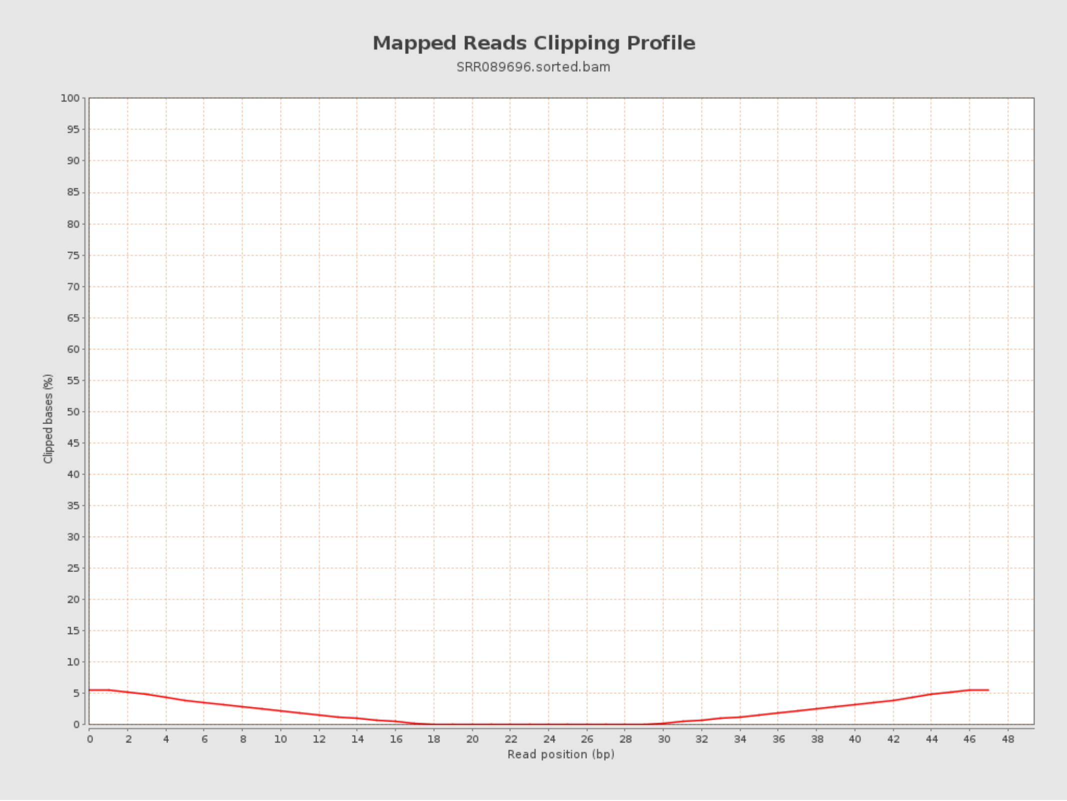
8. Results : Mapped Reads Nucleotide Content



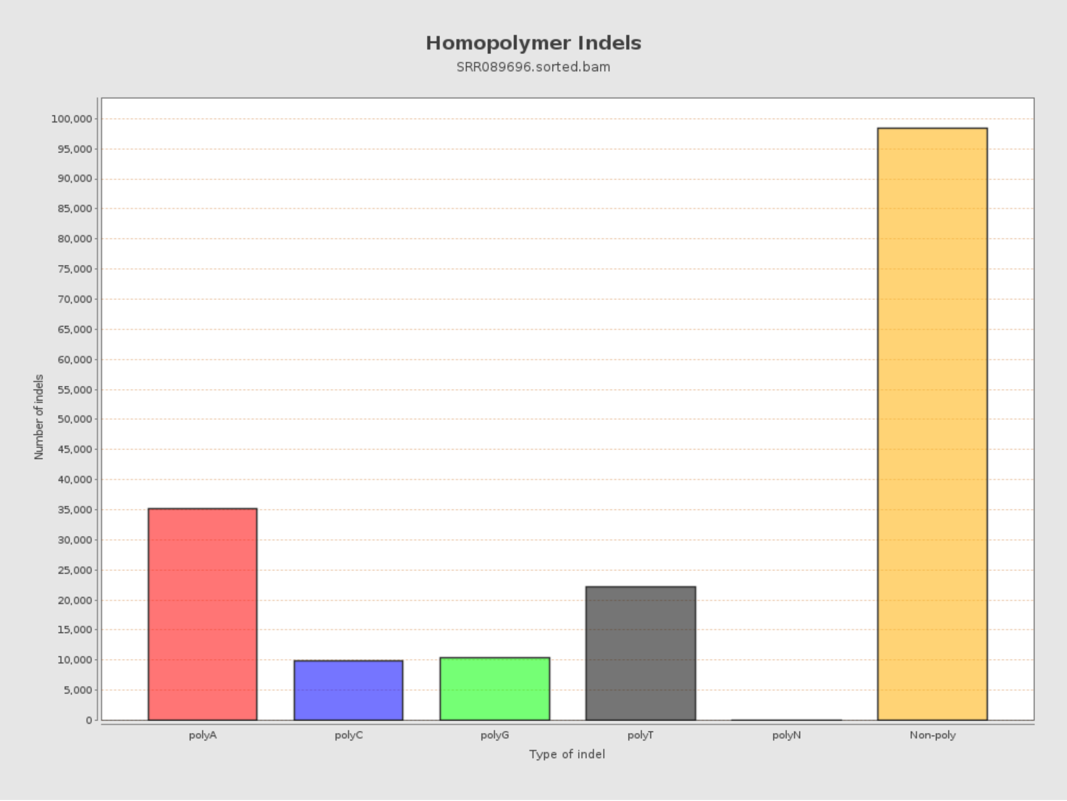
9. Results : Mapped Reads GC-content Distribution



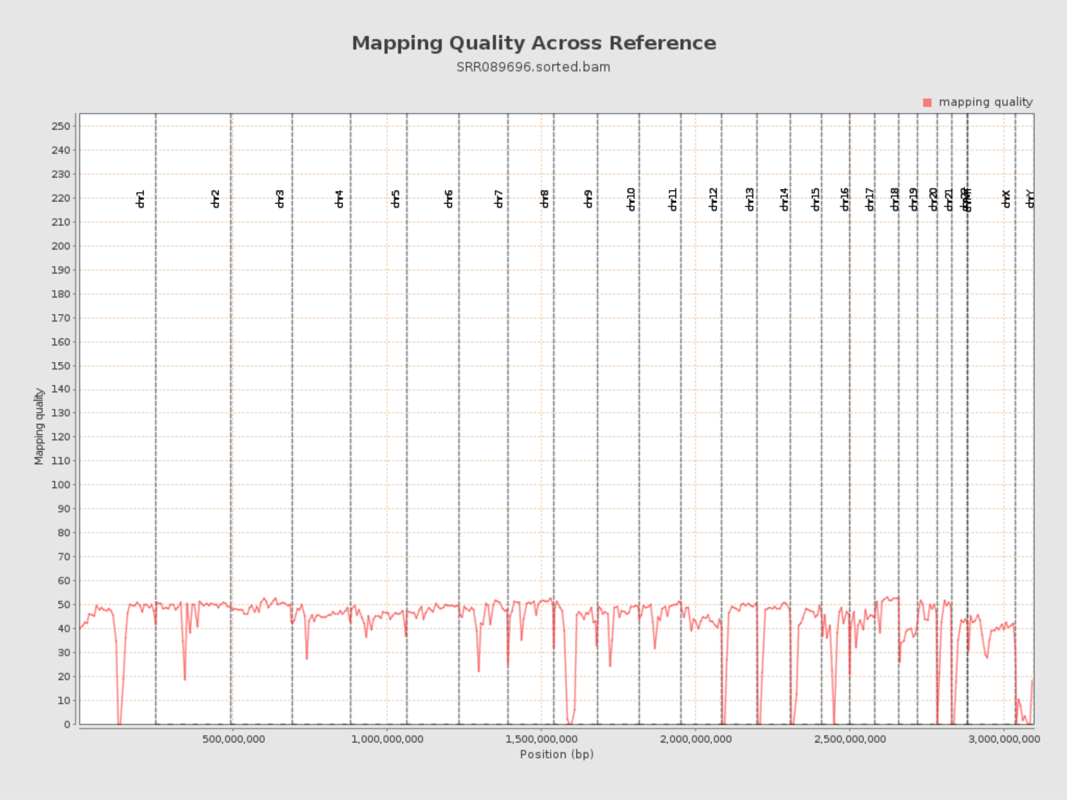
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram