Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 11:28:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008785.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_SRR6008785 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008785.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 11:28:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008785.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,171,058
Mapped reads	966,064 / 82.49%
Unmapped reads	204,994 / 17.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,649 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	22,678 / 1.94%
Duplication rate	1.73%
Clipped reads	498,164 / 42.54%

2.2. ACGT Content

Number/percentage of A's	17,760,670 / 28.4%
Number/percentage of C's	11,170,329 / 17.86%
Number/percentage of T's	19,179,382 / 30.67%
Number/percentage of G's	14,417,083 / 23.05%
Number/percentage of N's	10,507 / 0.02%
GC Percentage	40.92%

2.3. Coverage

Mean	0.0202

Standard Deviation	0.1999

2.4. Mapping Quality

Mean Mapping Quality	45.25

2.5. Mismatches and indels

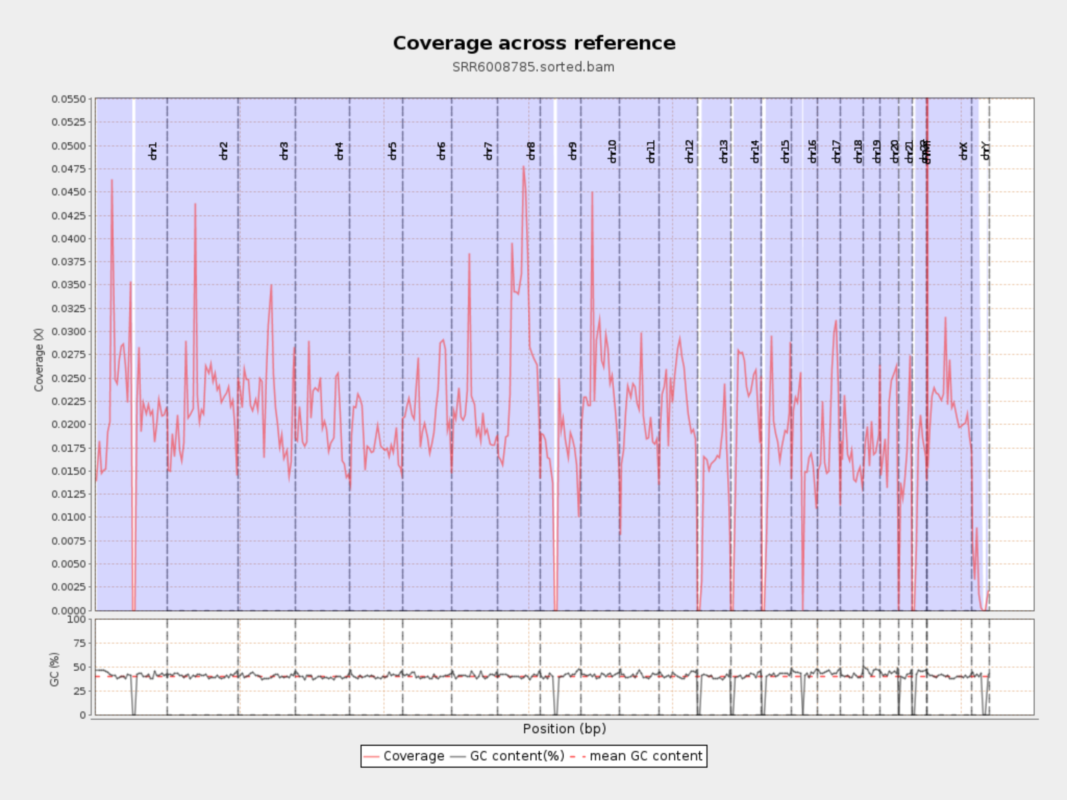
General error rate	0.81%
Mismatches	493,593
Insertions	5,587
Mapped reads with at least one insertion	0.57%
Deletions	16,666
Mapped reads with at least one deletion	1.71%
Homopolymer indels	46.66%

2.6. Chromosome stats

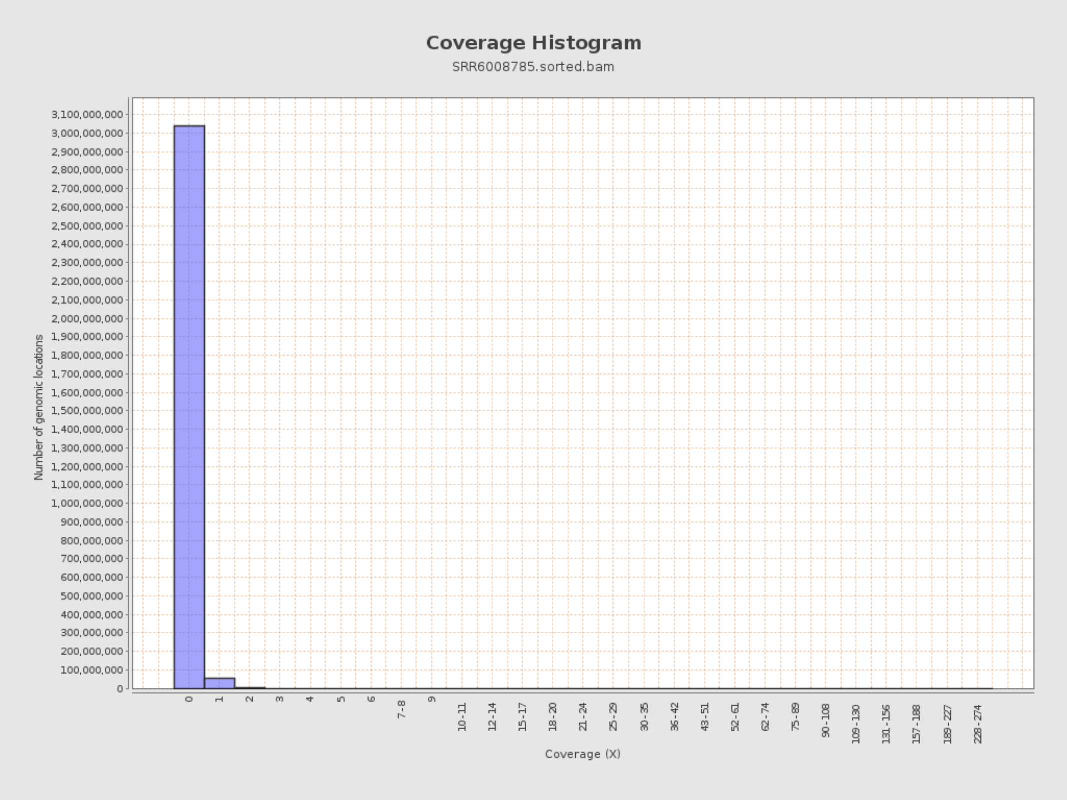
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5323084	0.0214	0.2827
chr2	243199373	5417261	0.0223	0.2364
chr3	198022430	4445612	0.0225	0.1579
chr4	191154276	3865212	0.0202	0.1554
chr5	180915260	3336143	0.0184	0.1422
chr6	171115067	3714076	0.0217	0.1736
chr7	159138663	3360230	0.0211	0.2678

chr8	146364022	4234596	0.0289	0.2319
chr9	141213431	2221145	0.0157	0.1952
chr10	135534747	3452781	0.0255	0.242
chr11	135006516	2794284	0.0207	0.1992
chr12	133851895	3084226	0.023	0.1591
chr13	115169878	1606836	0.014	0.1217
chr14	107349540	2212793	0.0206	0.1581
chr15	102531392	1698180	0.0166	0.1337
chr16	90354753	1482010	0.0164	0.15
chr17	81195210	1668876	0.0206	0.167
chr18	78077248	1273780	0.0163	0.3373
chr19	59128983	1075910	0.0182	0.2228
chr20	63025520	1267310	0.0201	0.1503
chr21	48129895	746966	0.0155	0.1383
chr22	51304566	657878	0.0128	0.1173
chrMT	16571	47868	2.8887	2.5142
chrX	155270560	3415454	0.022	0.1689
chrY	59373566	163028	0.0027	0.08

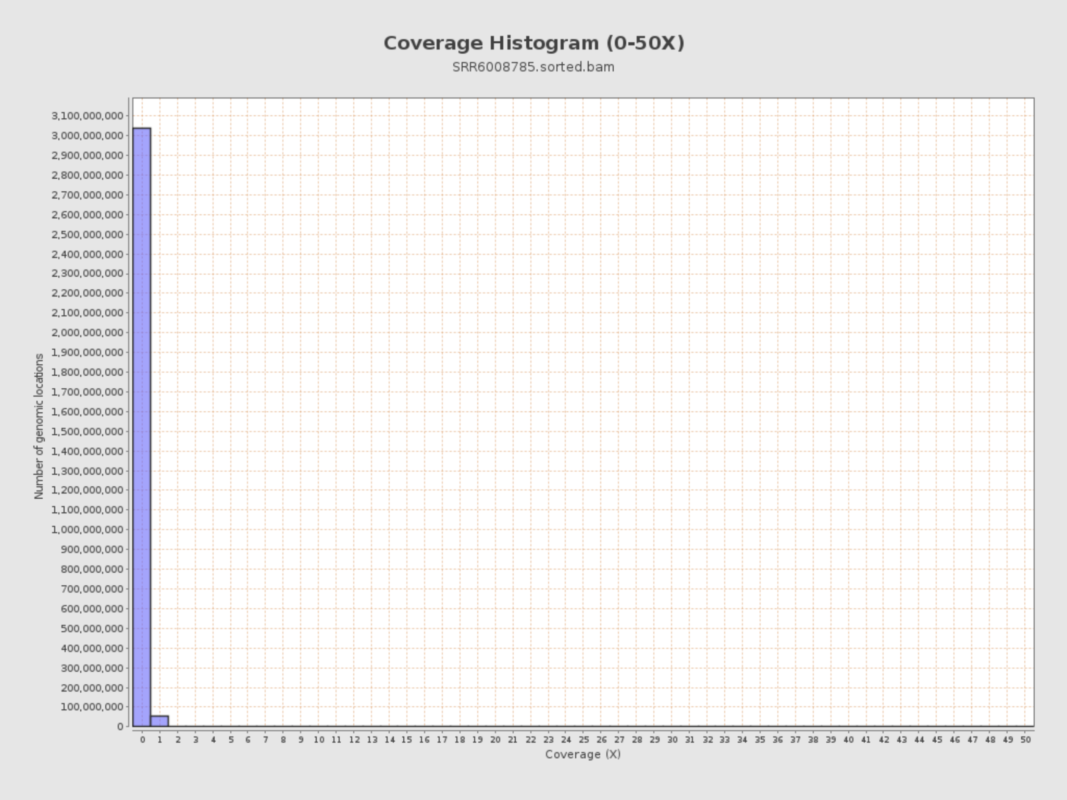
3. Results : Coverage across reference



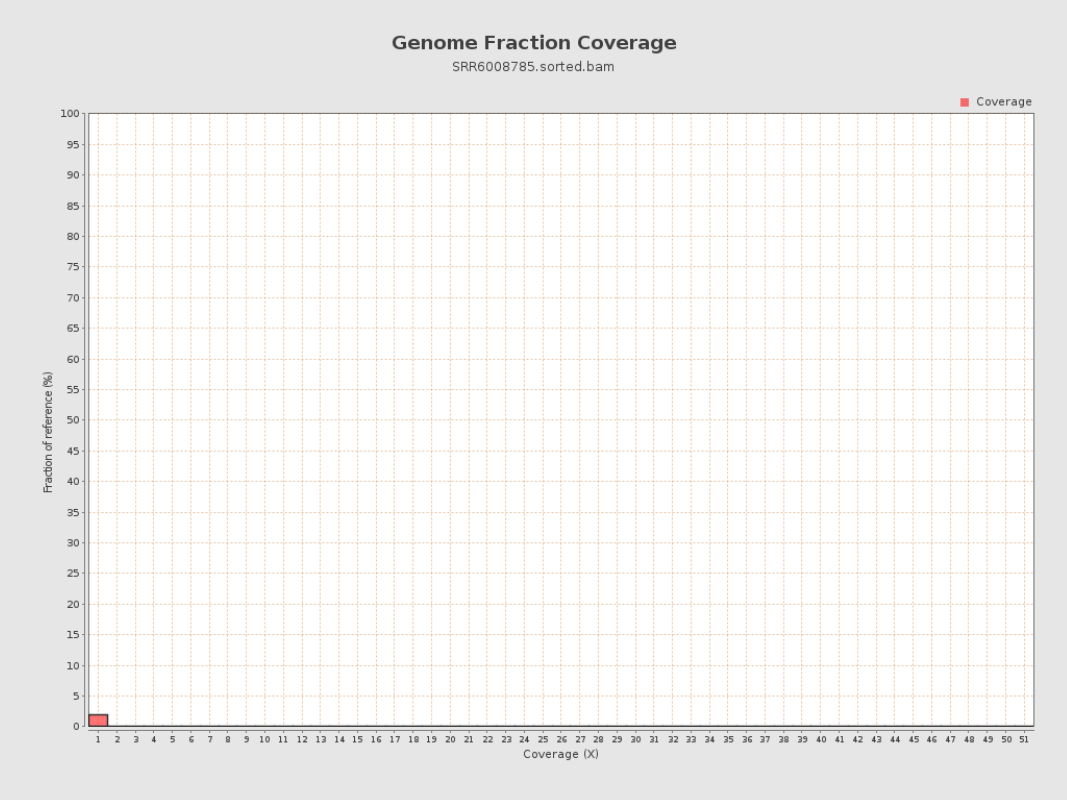
4. Results : Coverage Histogram



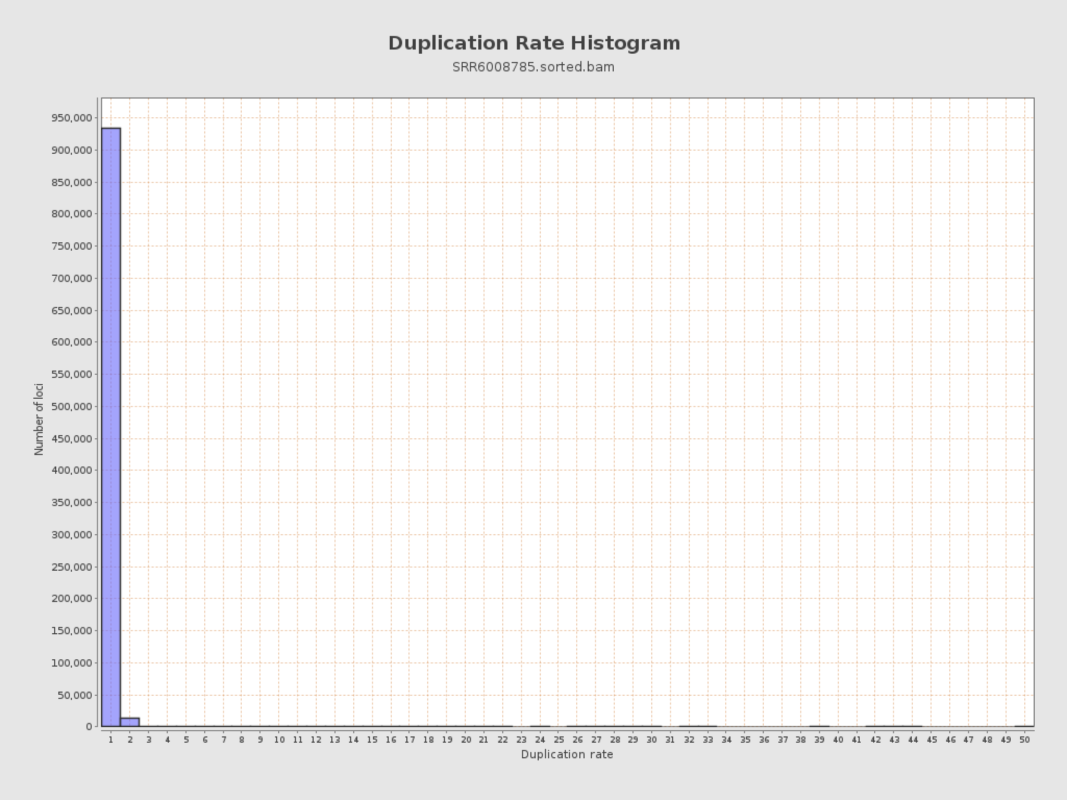
5. Results : Coverage Histogram (0-50X)



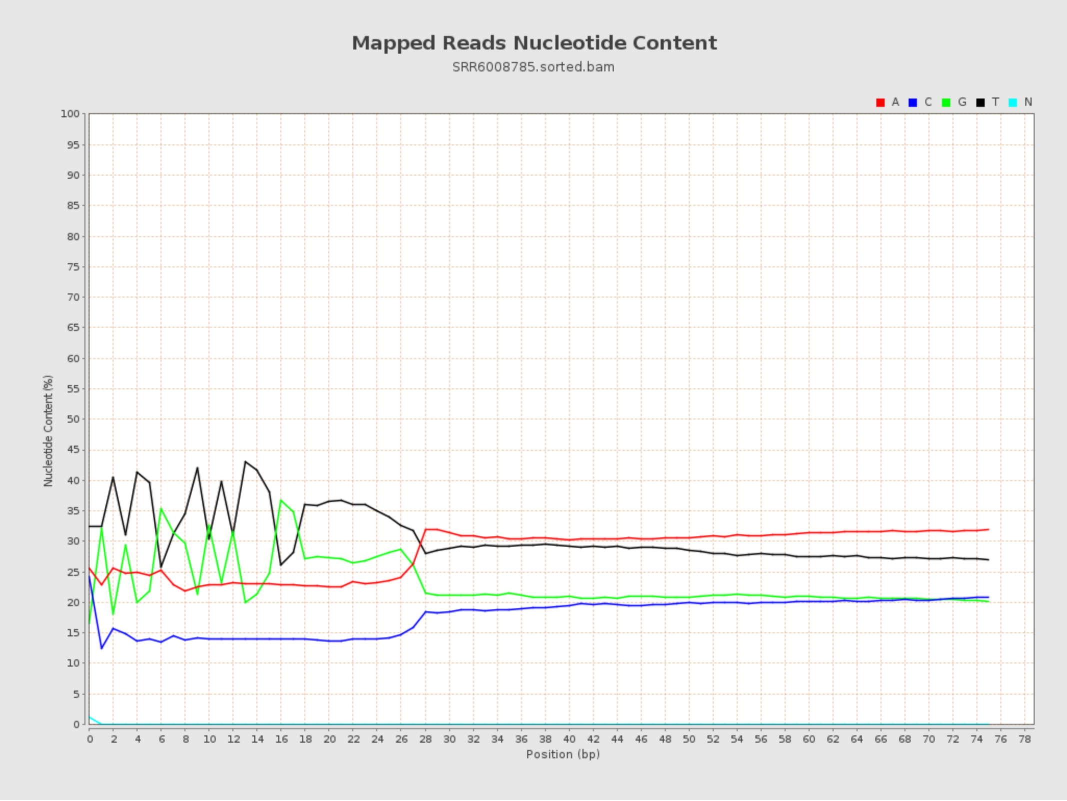
6. Results : Genome Fraction Coverage



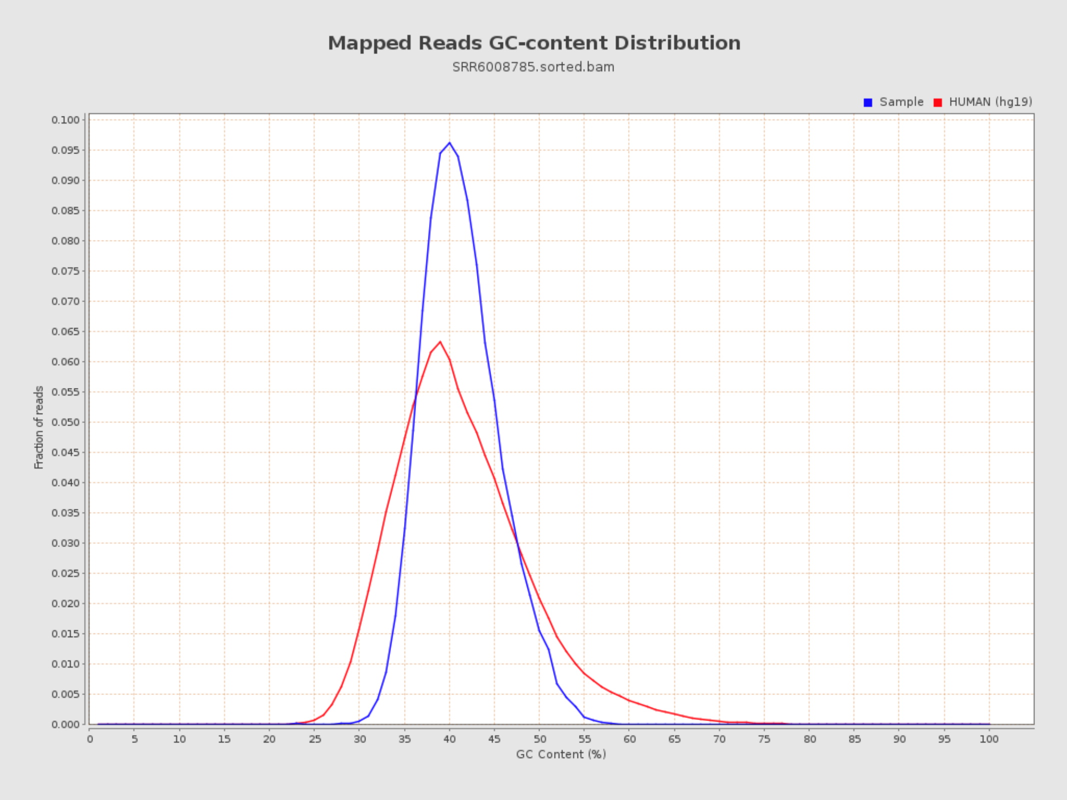
7. Results : Duplication Rate Histogram



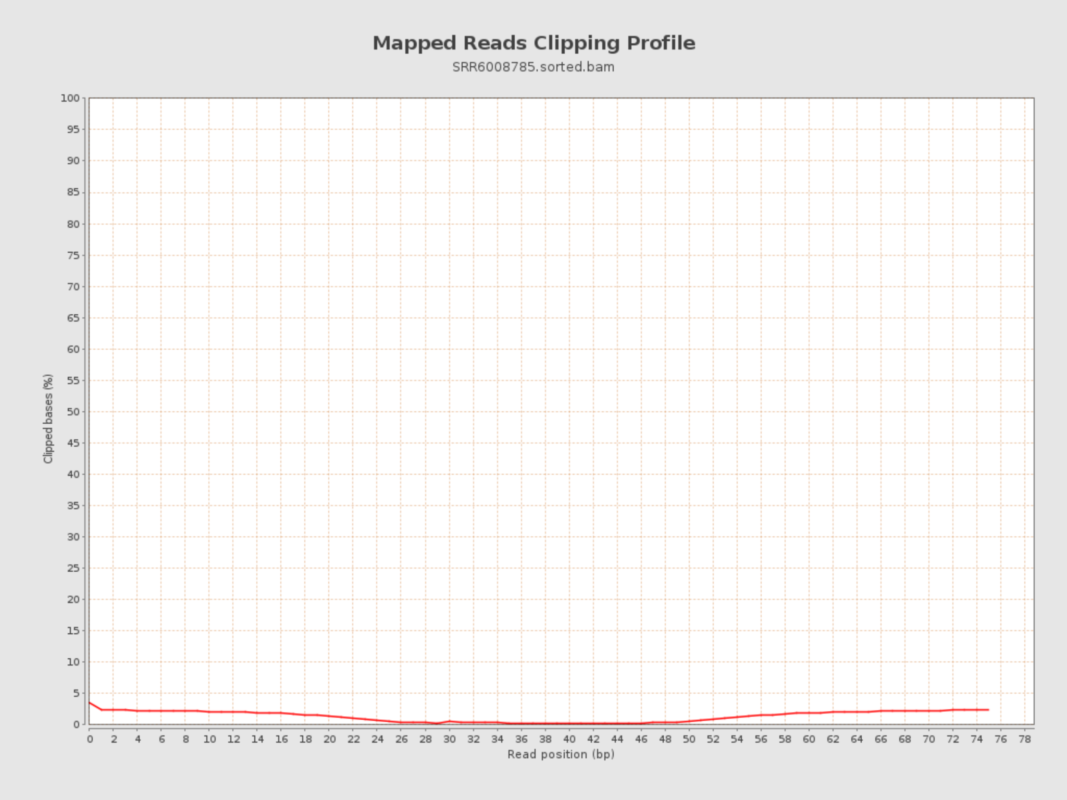
8. Results : Mapped Reads Nucleotide Content



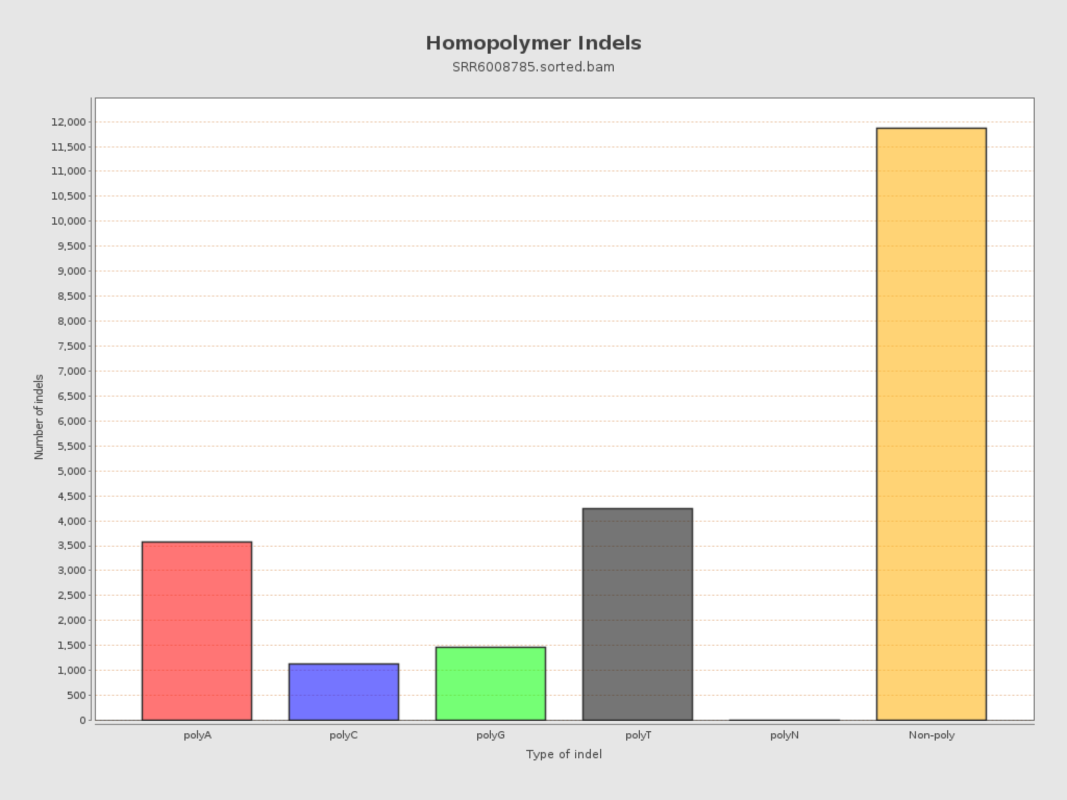
9. Results : Mapped Reads GC-content Distribution



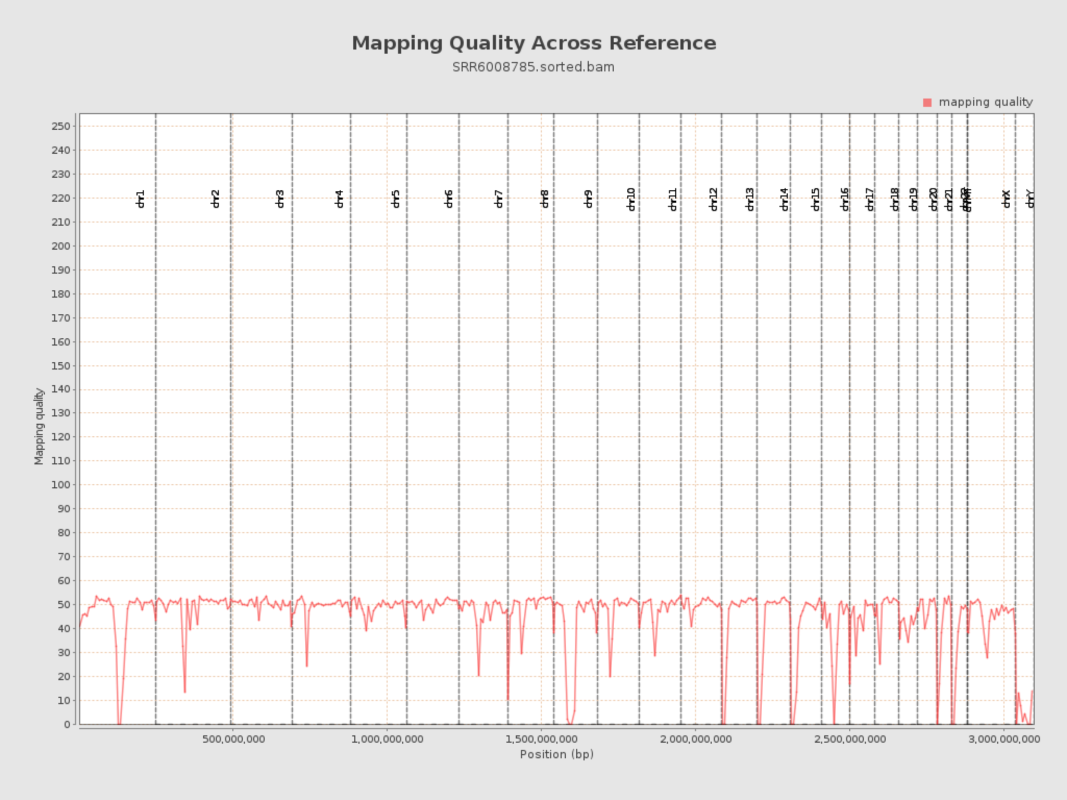
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram