Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 13:17:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008829.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_SRR6008829 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008829.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 13:17:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008829.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,546,895
Mapped reads	1,165,942 / 75.37%
Unmapped reads	380,953 / 24.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,305 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	136,263 / 8.81%
Duplication rate	9.16%
Clipped reads	588,619 / 38.05%

2.2. ACGT Content

Number/percentage of A's	21,163,338 / 27.87%
Number/percentage of C's	14,174,839 / 18.67%
Number/percentage of T's	23,914,604 / 31.5%
Number/percentage of G's	16,578,653 / 21.83%
Number/percentage of N's	99,598 / 0.13%
GC Percentage	40.5%

2.3. Coverage

Mean	0.0245

Standard Deviation	0.3042

2.4. Mapping Quality

Mean Mapping Quality	44.35

2.5. Mismatches and indels

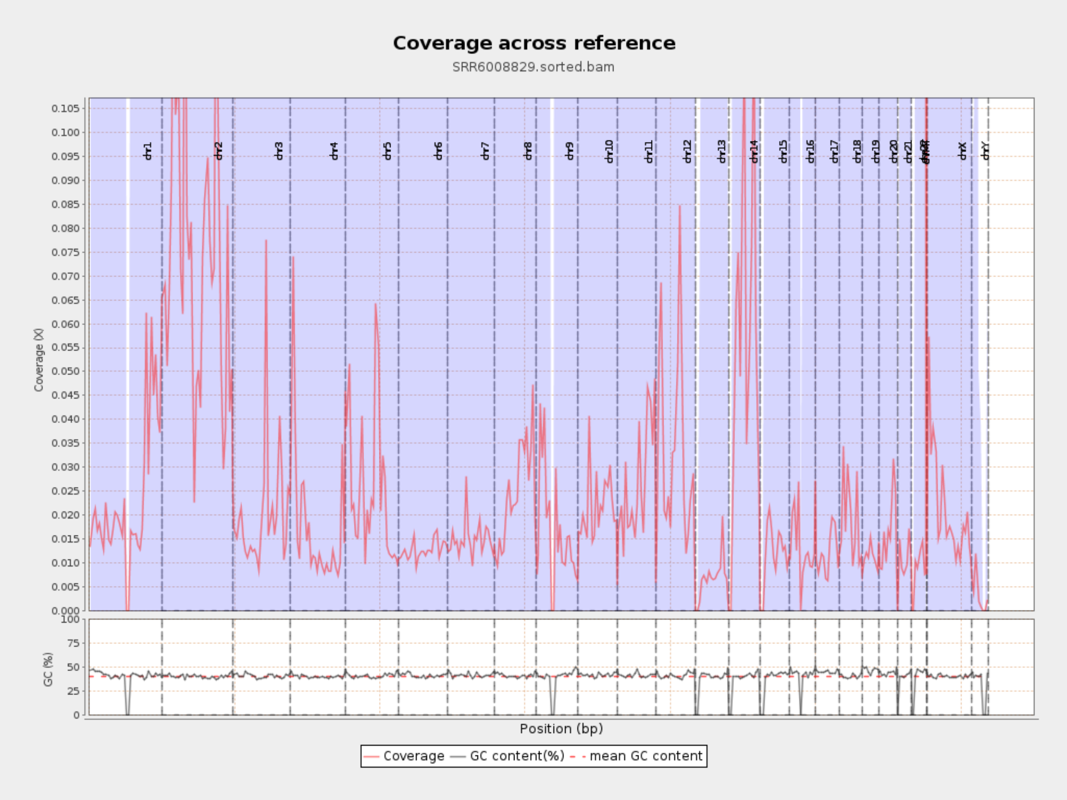
General error rate	0.84%
Mismatches	630,994
Insertions	5,082
Mapped reads with at least one insertion	0.43%
Deletions	20,264
Mapped reads with at least one deletion	1.72%
Homopolymer indels	46.53%

2.6. Chromosome stats

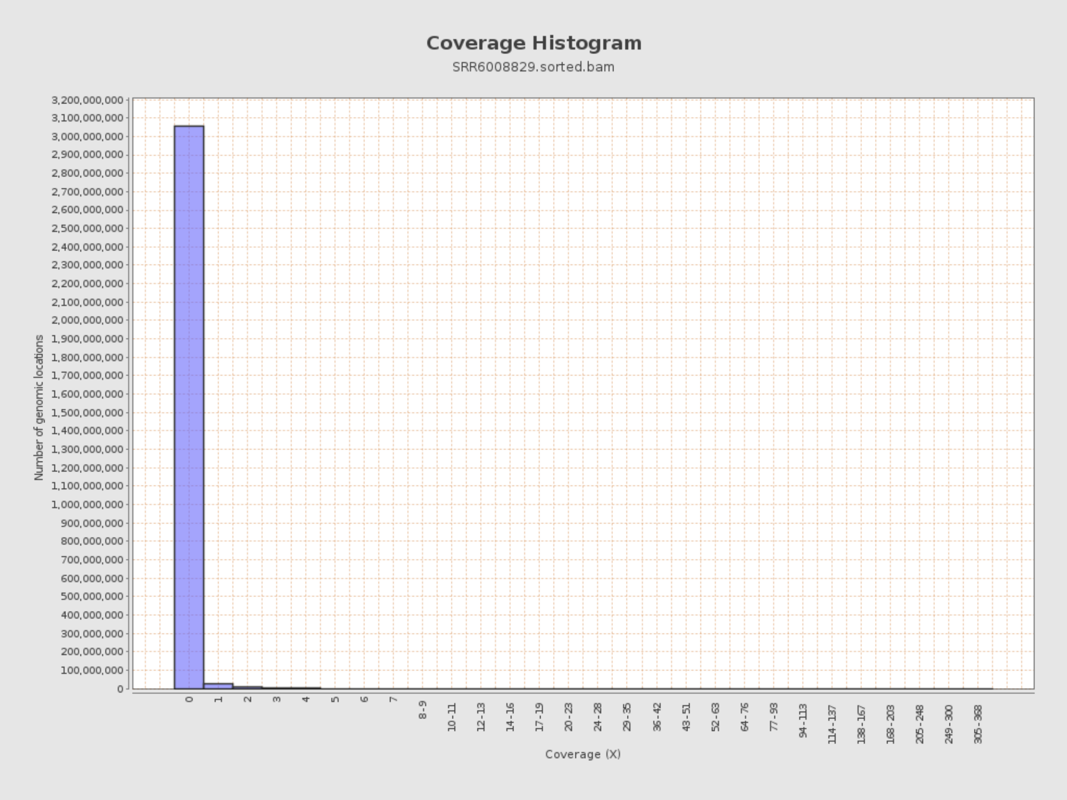
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5789034	0.0232	0.3273
chr2	243199373	18288952	0.0752	0.5319
chr3	198022430	4000003	0.0202	0.2305
chr4	191154276	3356146	0.0176	0.2341
chr5	180915260	4566690	0.0252	0.2695
chr6	171115067	2161144	0.0126	0.1943
chr7	159138663	2384264	0.015	0.2265

chr8	146364022	3611044	0.0247	0.3038
chr9	141213431	2408794	0.0171	0.2745
chr10	135534747	2950505	0.0218	0.2913
chr11	135006516	3572706	0.0265	0.3086
chr12	133851895	4487379	0.0335	0.2976
chr13	115169878	784889	0.0068	0.1378
chr14	107349540	6315333	0.0588	0.422
chr15	102531392	1229916	0.012	0.2232
chr16	90354753	1186475	0.0131	0.1975
chr17	81195210	962873	0.0119	0.1752
chr18	78077248	1484892	0.019	0.5042
chr19	59128983	670939	0.0113	0.2412
chr20	63025520	1038359	0.0165	0.2061
chr21	48129895	500392	0.0104	0.159
chr22	51304566	437617	0.0085	0.142
chrMT	16571	316126	19.0771	13.9981
chrX	155270560	3276507	0.0211	0.2534
chrY	59373566	185225	0.0031	0.1318

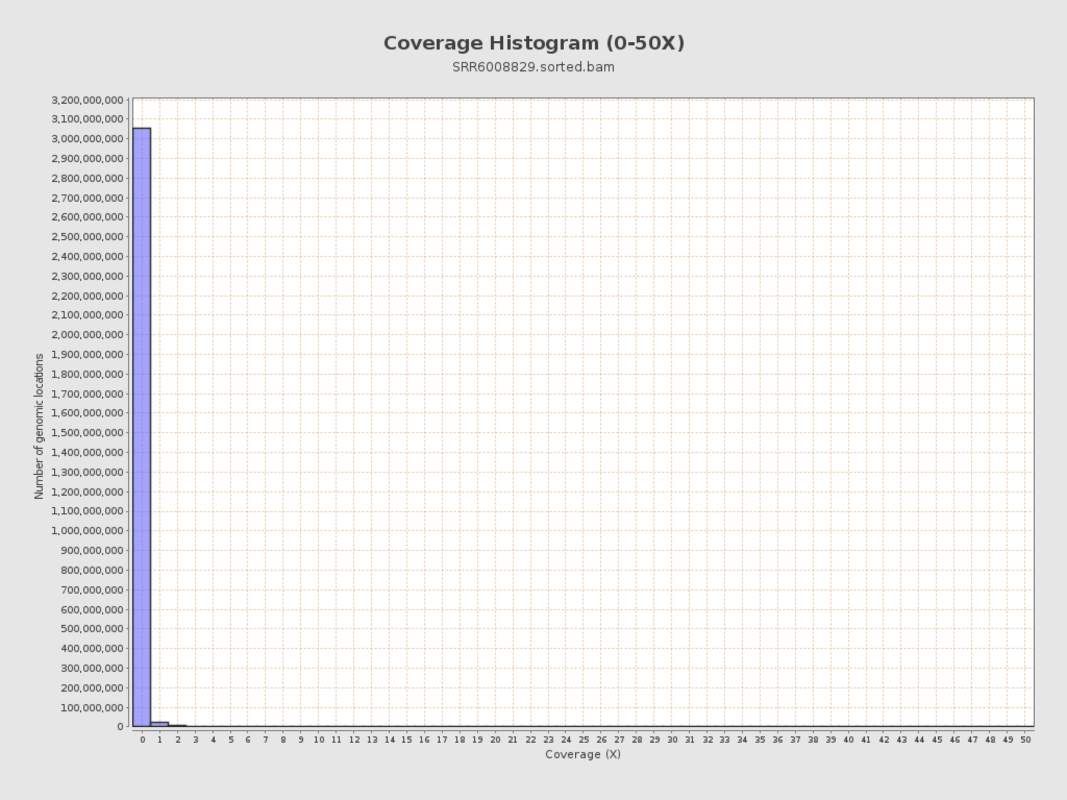
3. Results : Coverage across reference



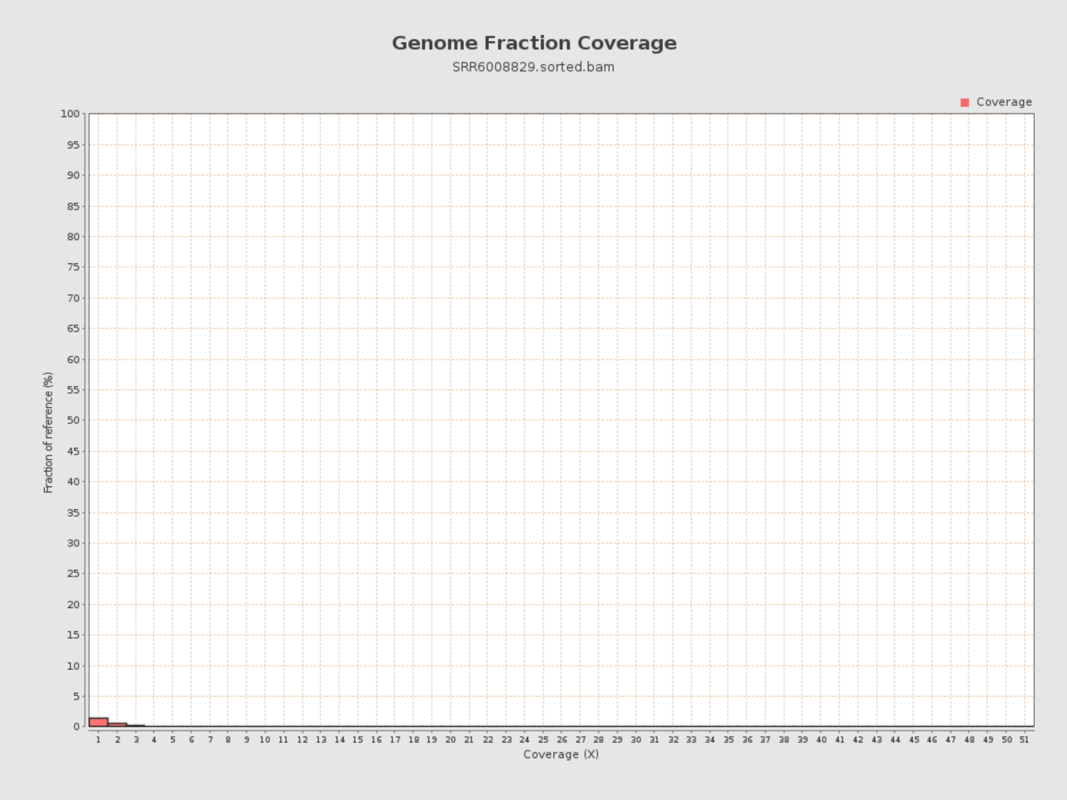
4. Results : Coverage Histogram



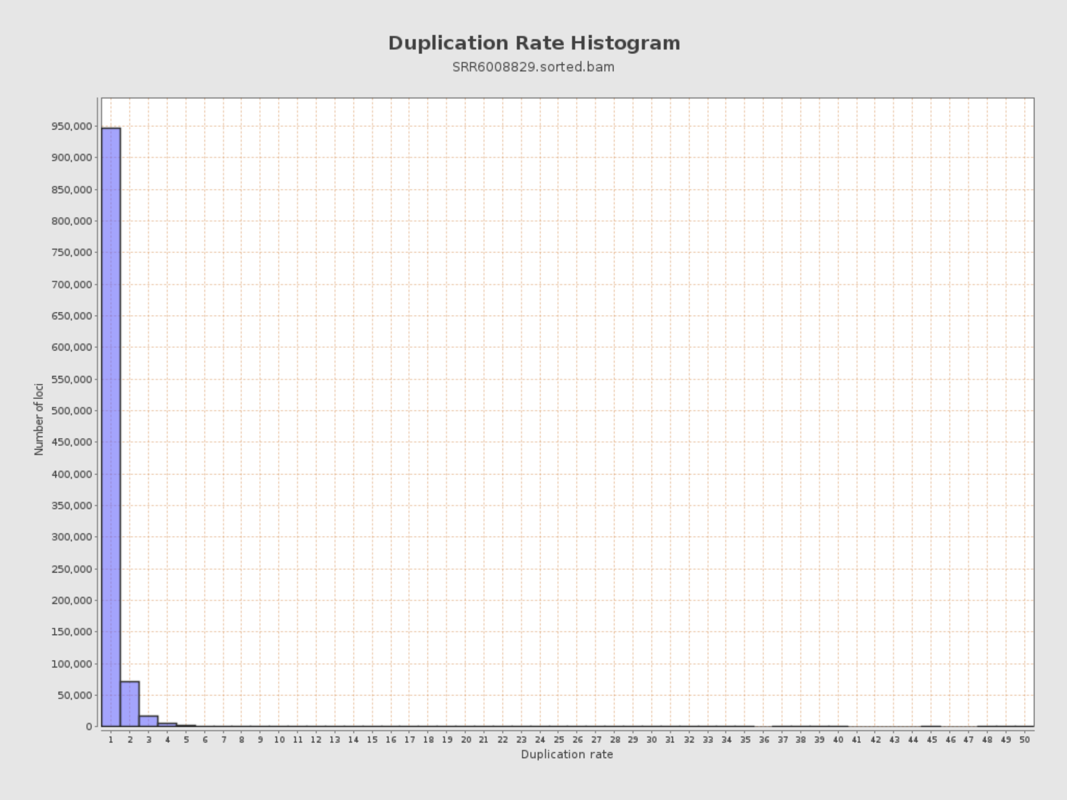
5. Results : Coverage Histogram (0-50X)



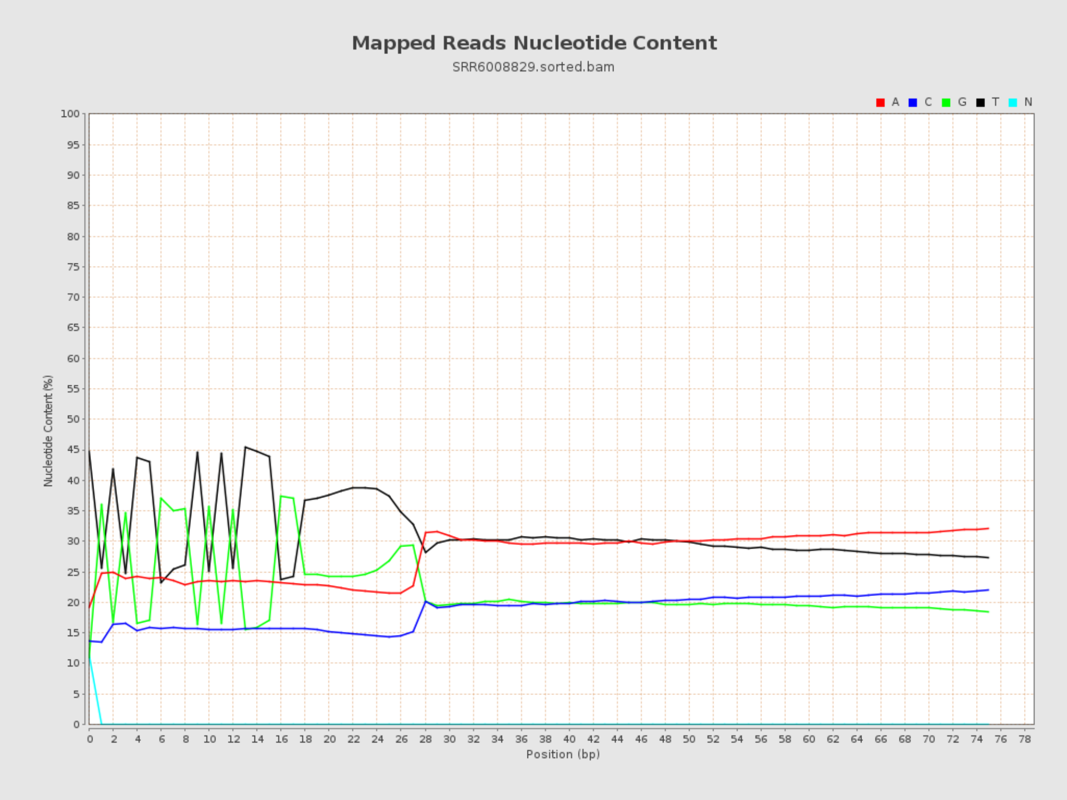
6. Results : Genome Fraction Coverage



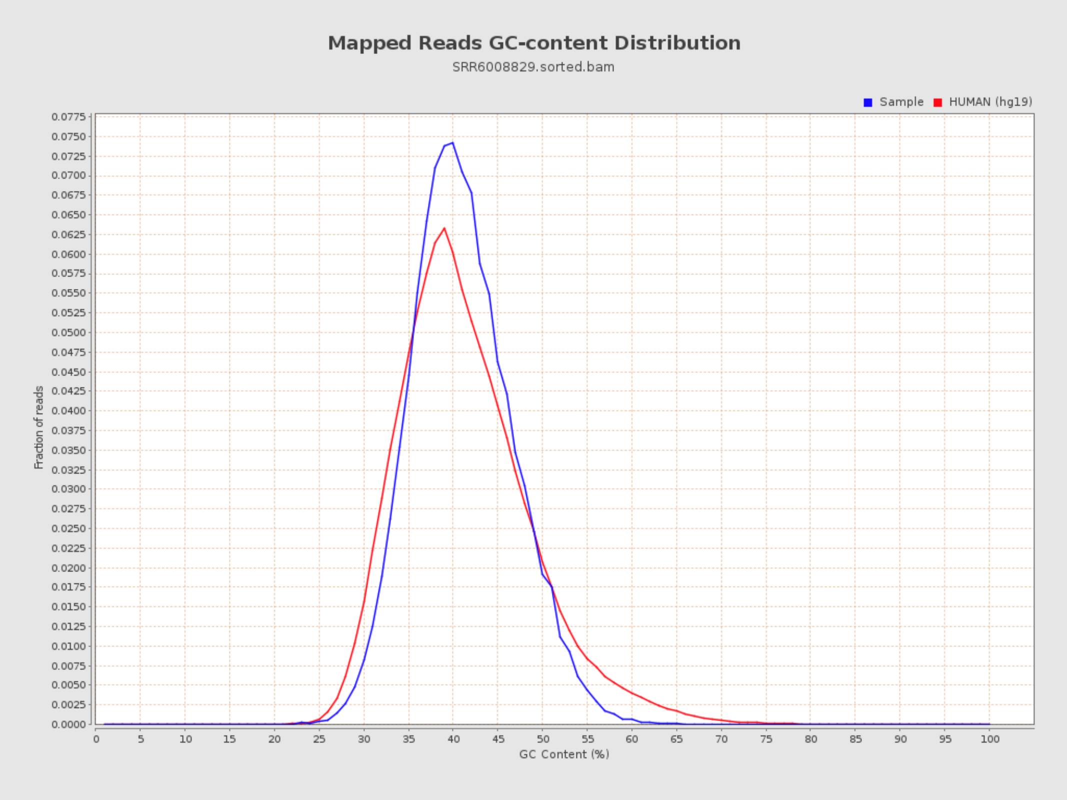
7. Results : Duplication Rate Histogram



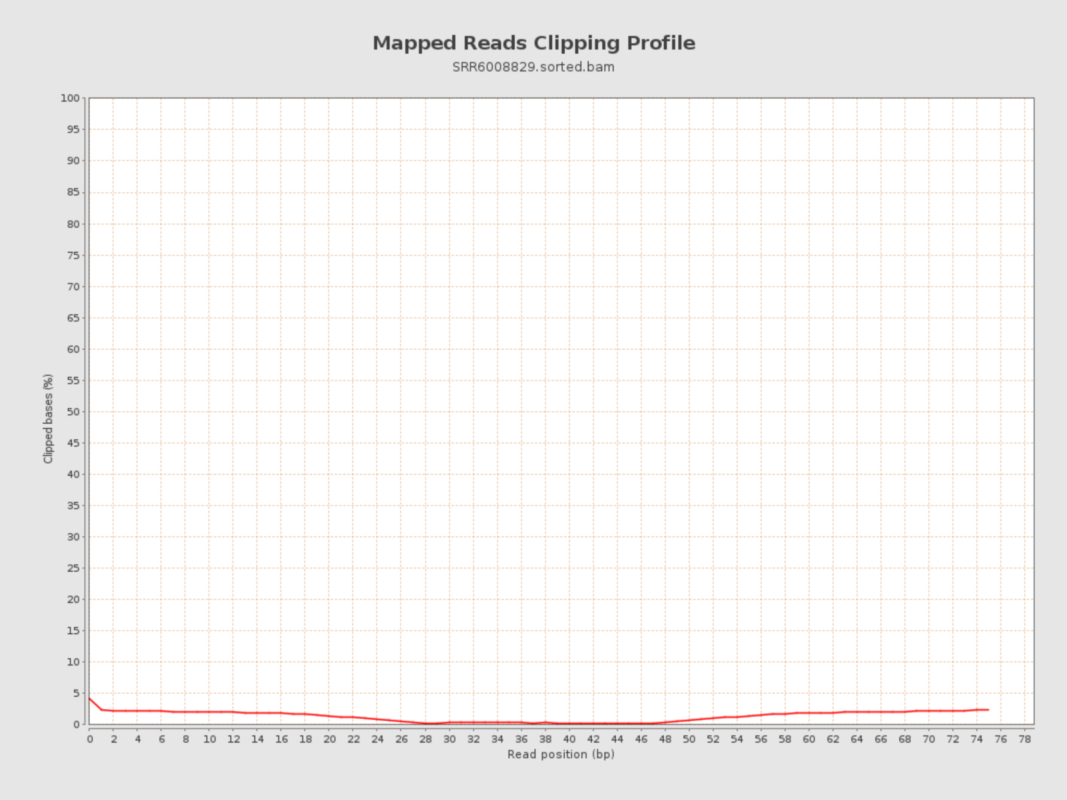
8. Results : Mapped Reads Nucleotide Content



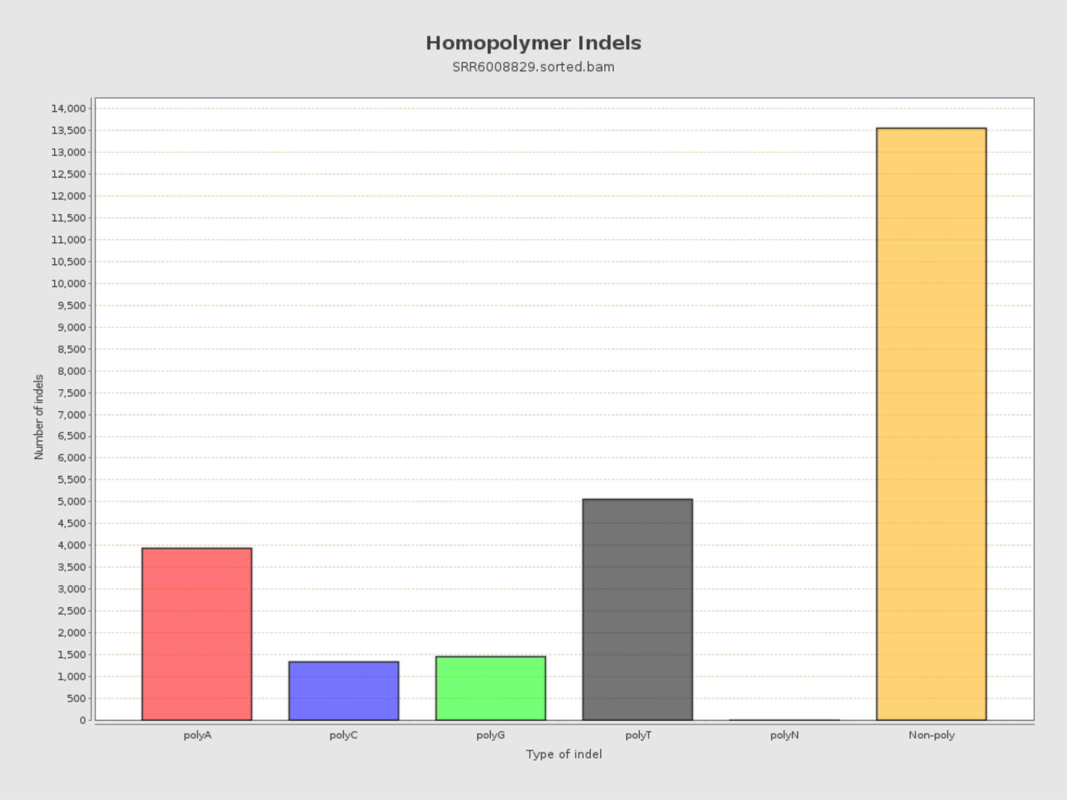
9. Results : Mapped Reads GC-content Distribution



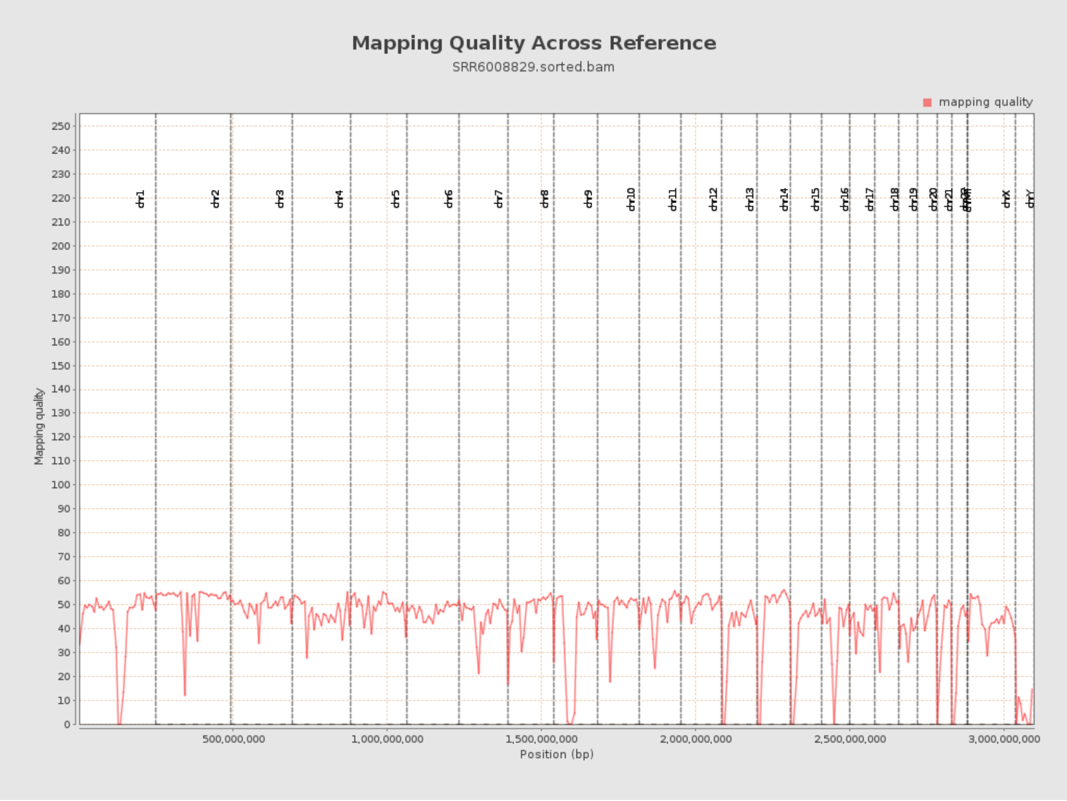
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram