Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 13:01:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008823.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_SRR6008823 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008823.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 13:01:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008823.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,842,022
Mapped reads	1,518,401 / 82.43%
Unmapped reads	323,621 / 17.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,031 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	149,177 / 8.1%
Duplication rate	7.73%
Clipped reads	839,654 / 45.58%

2.2. ACGT Content

Number/percentage of A's	26,543,169 / 27.45%
Number/percentage of C's	17,933,334 / 18.55%
Number/percentage of T's	30,523,175 / 31.57%
Number/percentage of G's	21,542,002 / 22.28%
Number/percentage of N's	142,135 / 0.15%
GC Percentage	40.83%

2.3. Coverage

Mean	0.0313

Standard Deviation	0.4139

2.4. Mapping Quality

Mean Mapping Quality	40.11

2.5. Mismatches and indels

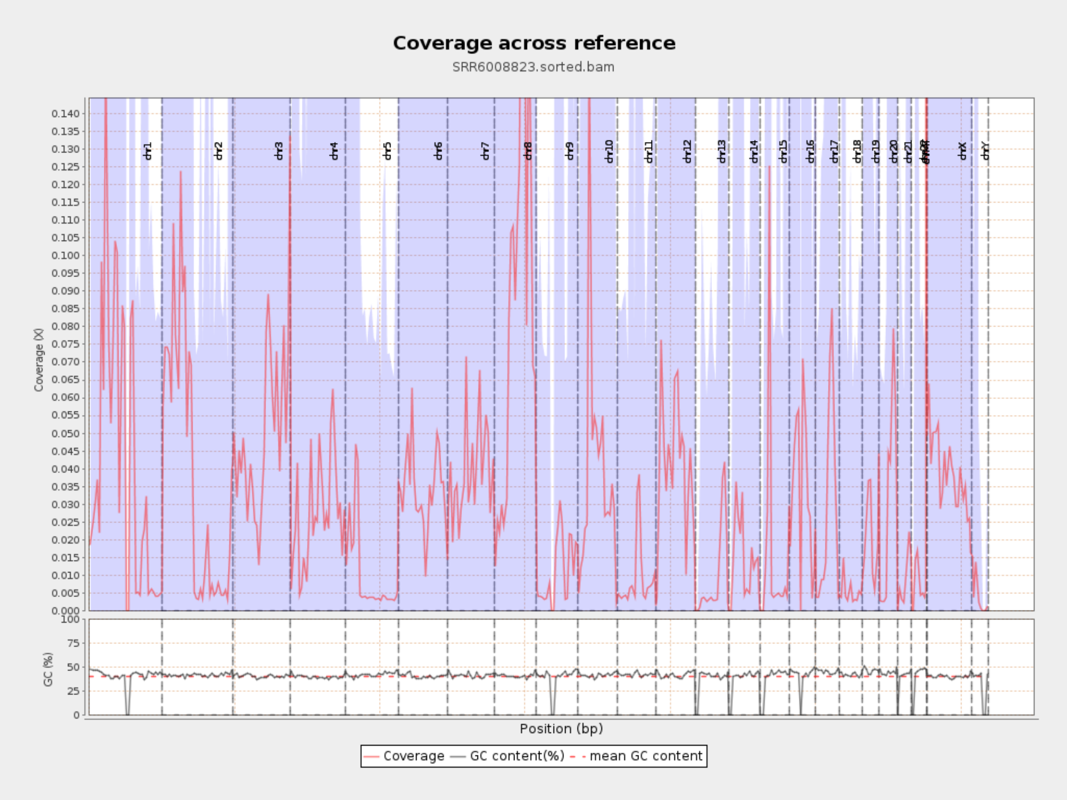
General error rate	0.89%
Mismatches	851,020
Insertions	6,000
Mapped reads with at least one insertion	0.39%
Deletions	34,448
Mapped reads with at least one deletion	2.24%
Homopolymer indels	45%

2.6. Chromosome stats

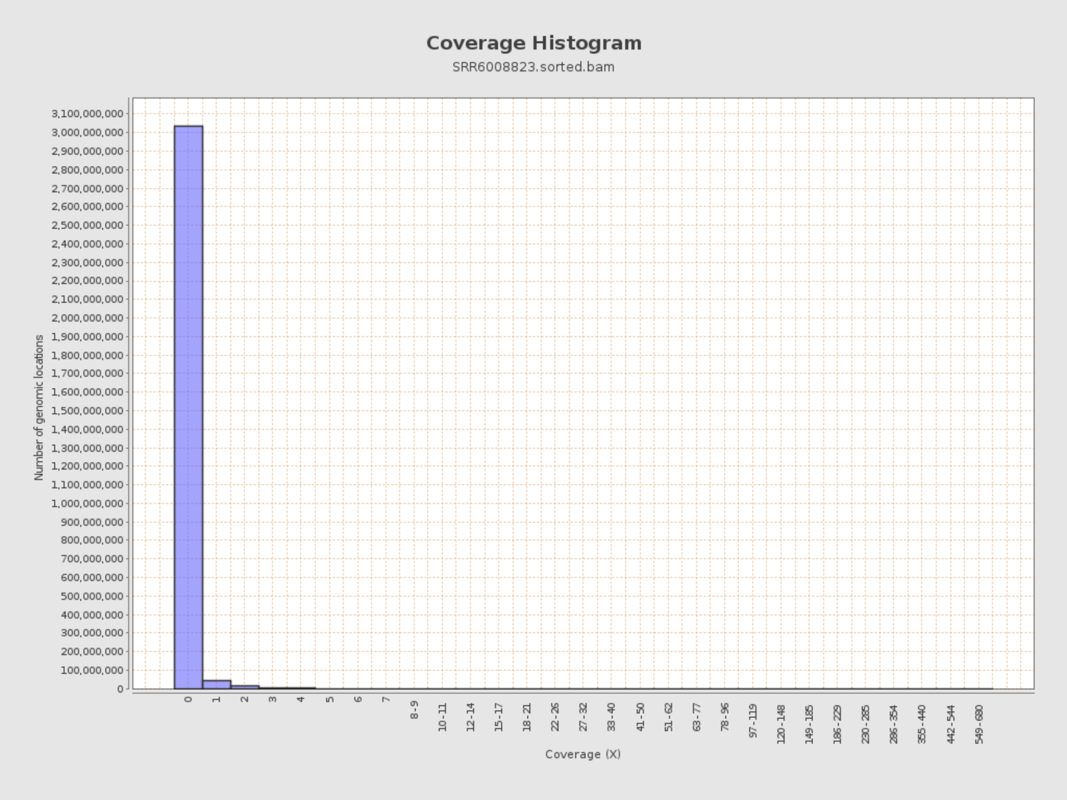
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10385635	0.0417	0.5618
chr2	243199373	9439540	0.0388	0.3652
chr3	198022430	9756358	0.0493	0.3784
chr4	191154276	5206786	0.0272	0.3115
chr5	180915260	1810863	0.01	0.1417
chr6	171115067	5836301	0.0341	0.2842
chr7	159138663	6297938	0.0396	0.5009

chr8	146364022	13493858	0.0922	0.4843
chr9	141213431	1593034	0.0113	0.1845
chr10	135534747	5314582	0.0392	1.1382
chr11	135006516	1267524	0.0094	0.1575
chr12	133851895	5466151	0.0408	0.2884
chr13	115169878	1168060	0.0101	0.1461
chr14	107349540	1584667	0.0148	0.1823
chr15	102531392	1631630	0.0159	0.3036
chr16	90354753	3074934	0.034	0.3912
chr17	81195210	2310667	0.0285	0.2355
chr18	78077248	405340	0.0052	0.3045
chr19	59128983	1256582	0.0213	0.3825
chr20	63025520	1931875	0.0307	0.2455
chr21	48129895	443608	0.0092	0.1366
chr22	51304566	355396	0.0069	0.1087
chrMT	16571	398781	24.065	15.2688
chrX	155270560	6068093	0.0391	0.2906
chrY	59373566	245425	0.0041	0.2248

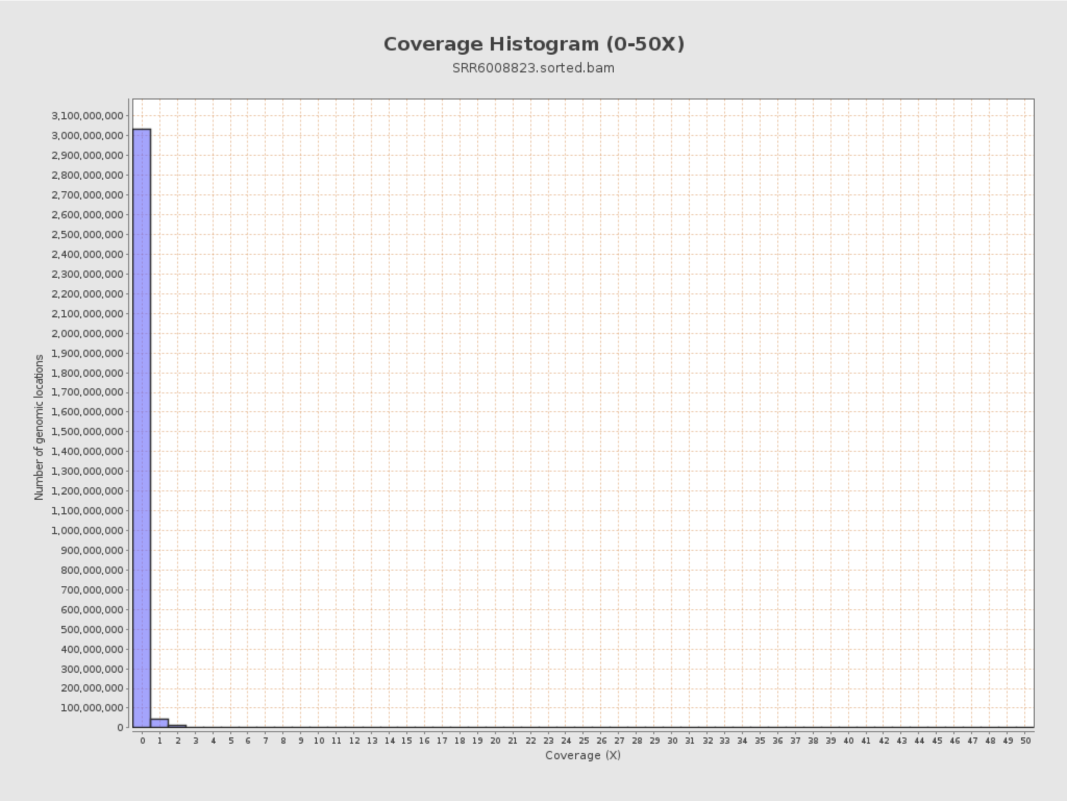
3. Results : Coverage across reference



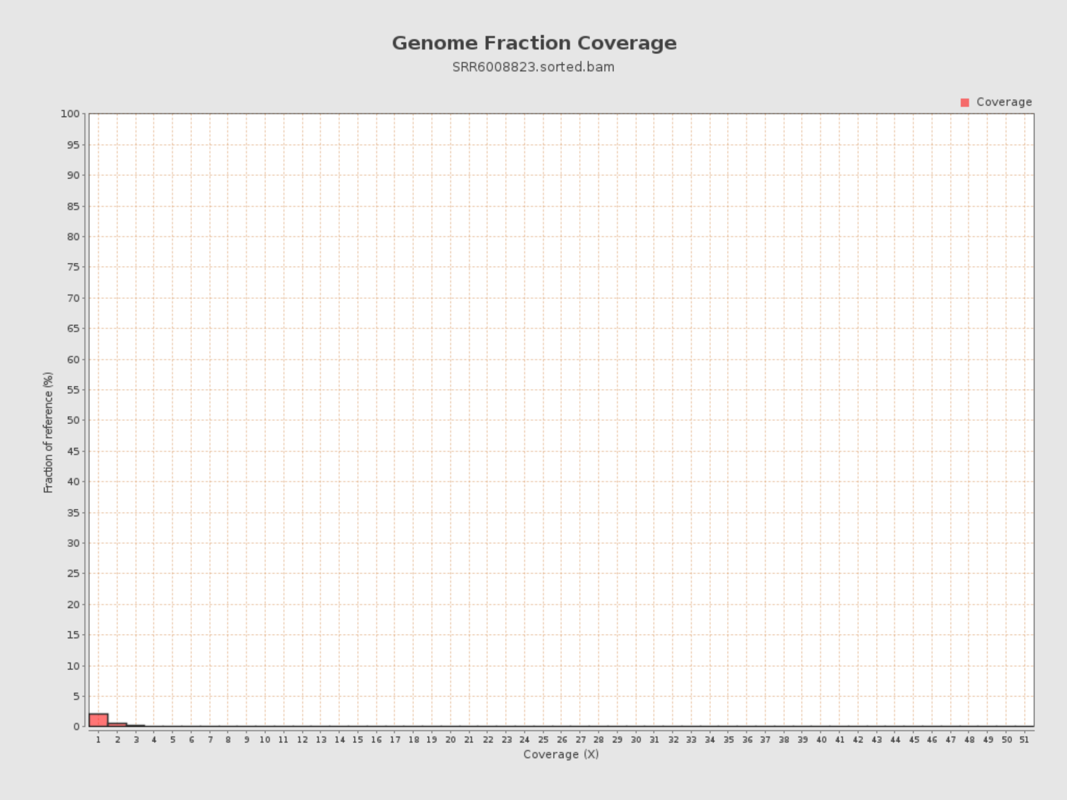
4. Results : Coverage Histogram



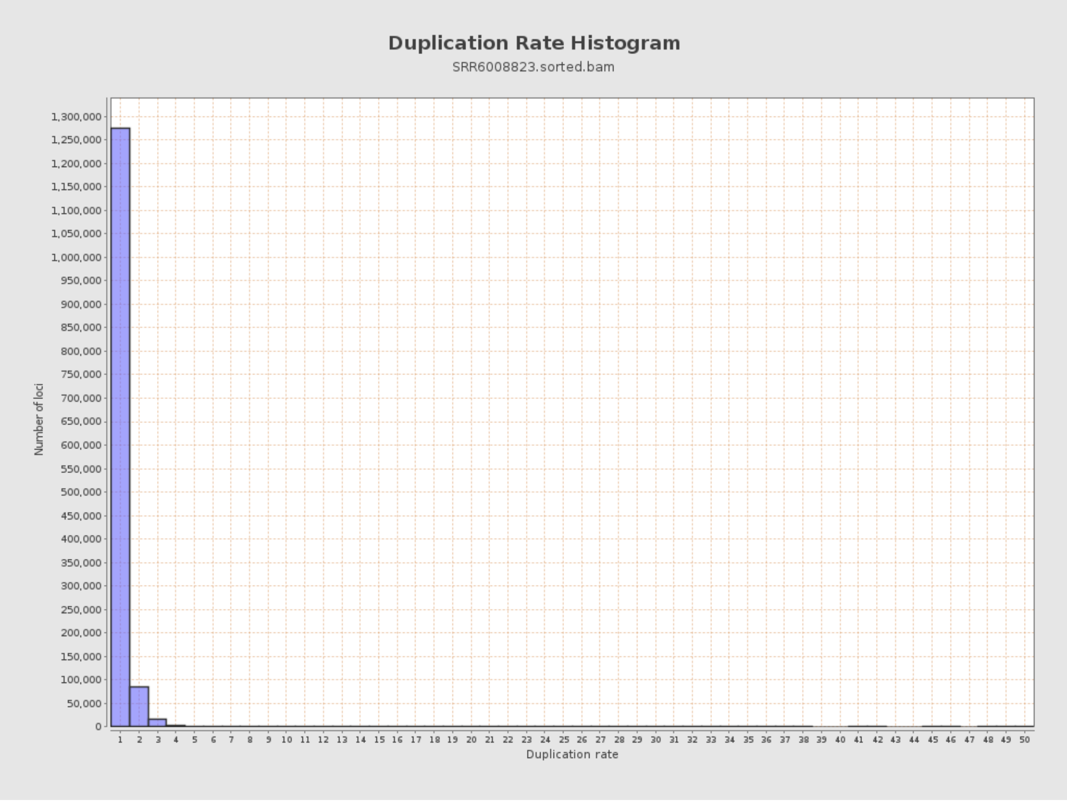
5. Results : Coverage Histogram (0-50X)



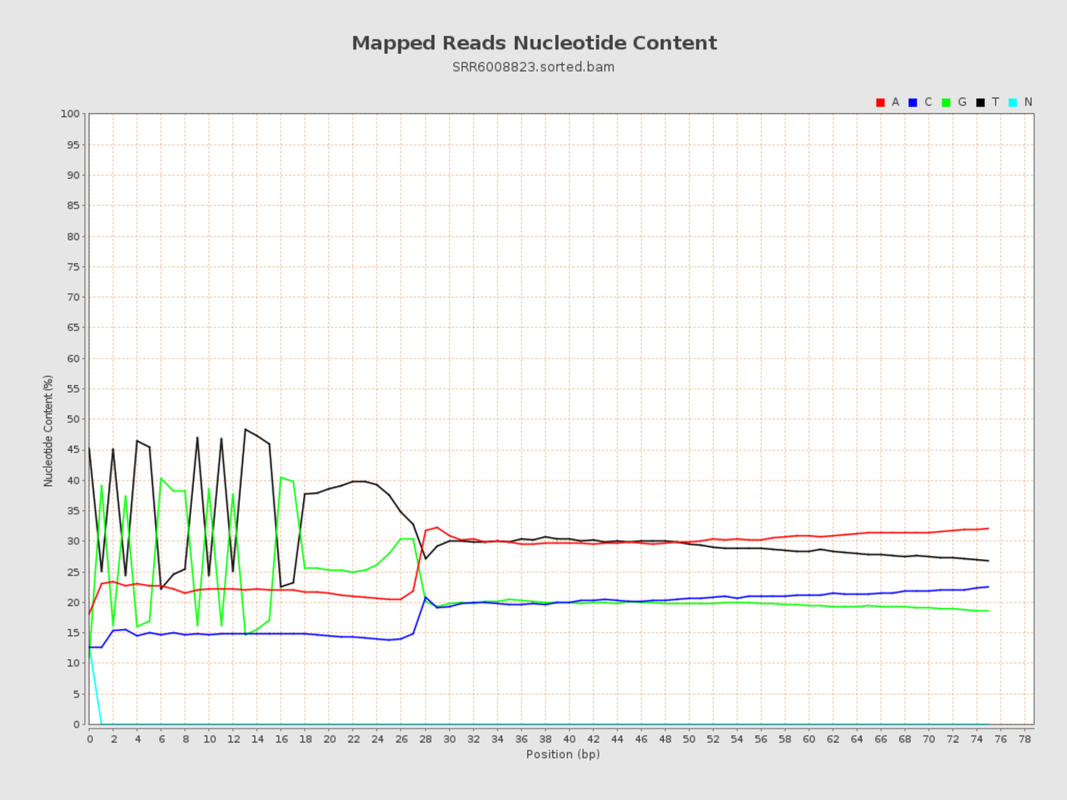
6. Results : Genome Fraction Coverage



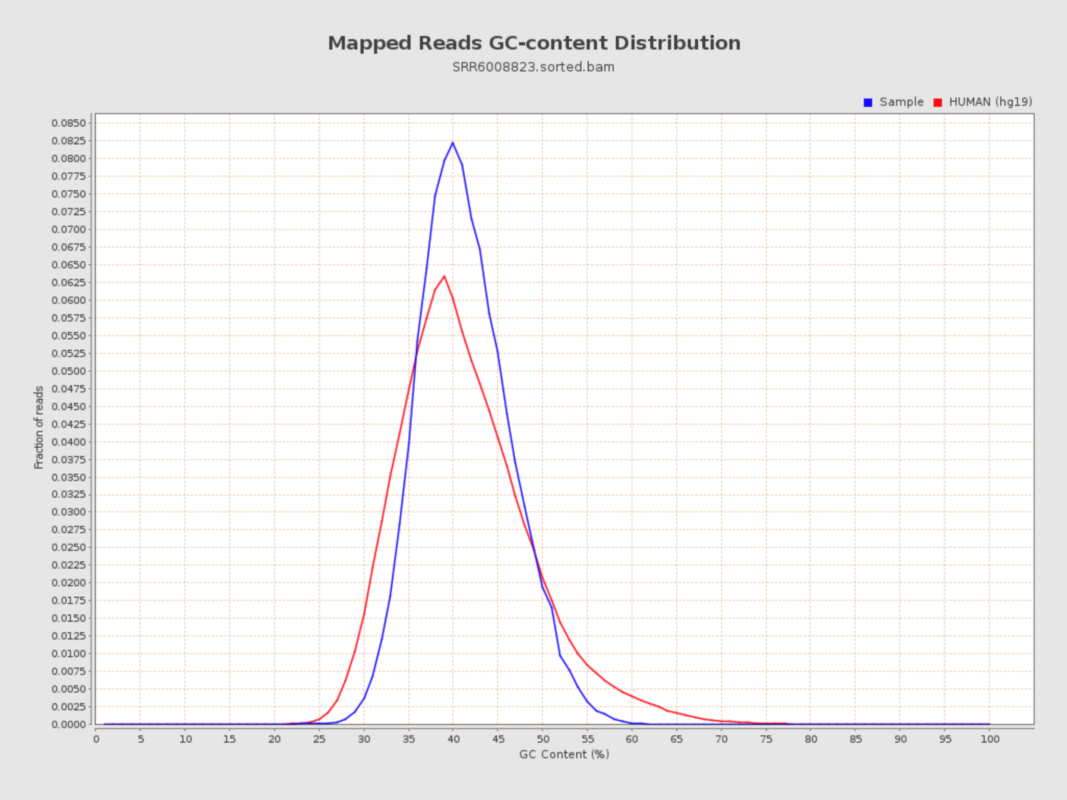
7. Results : Duplication Rate Histogram



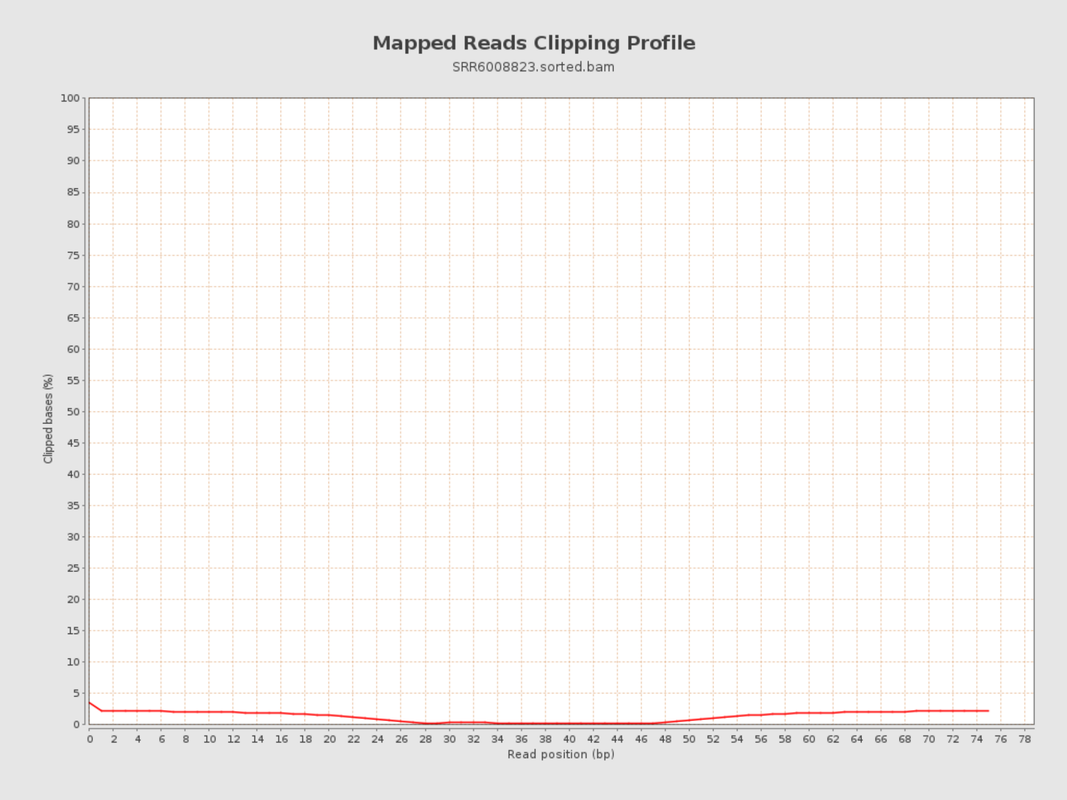
8. Results : Mapped Reads Nucleotide Content



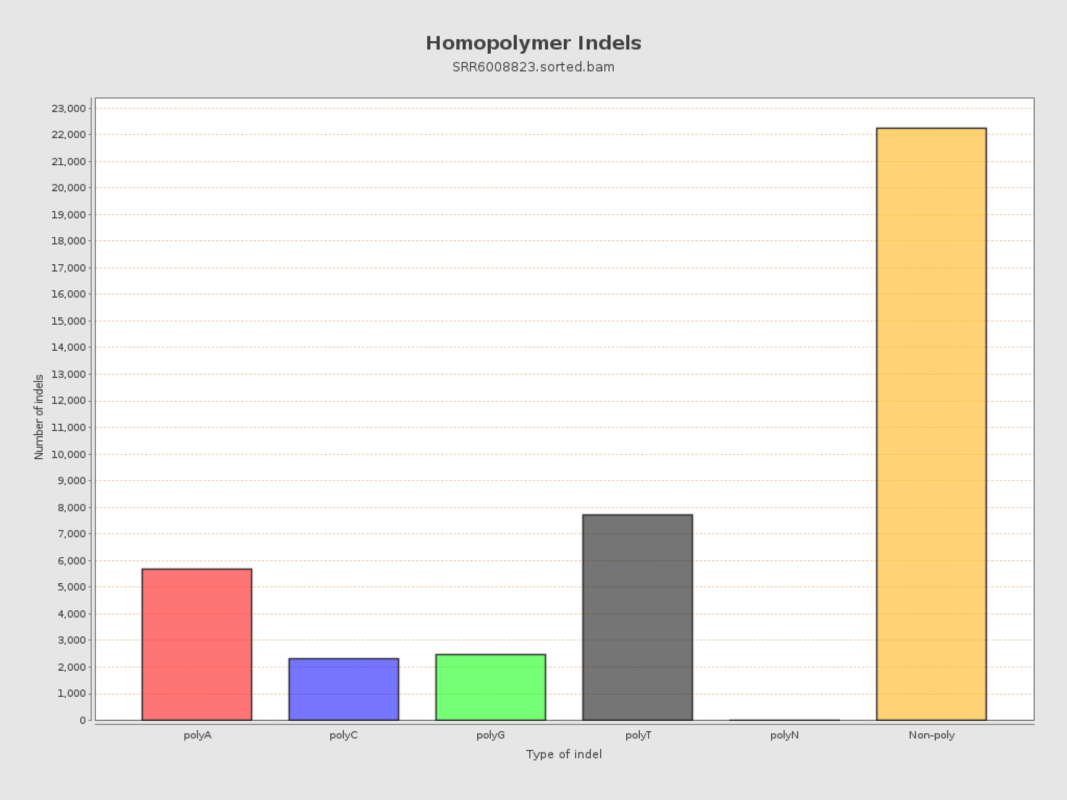
9. Results : Mapped Reads GC-content Distribution



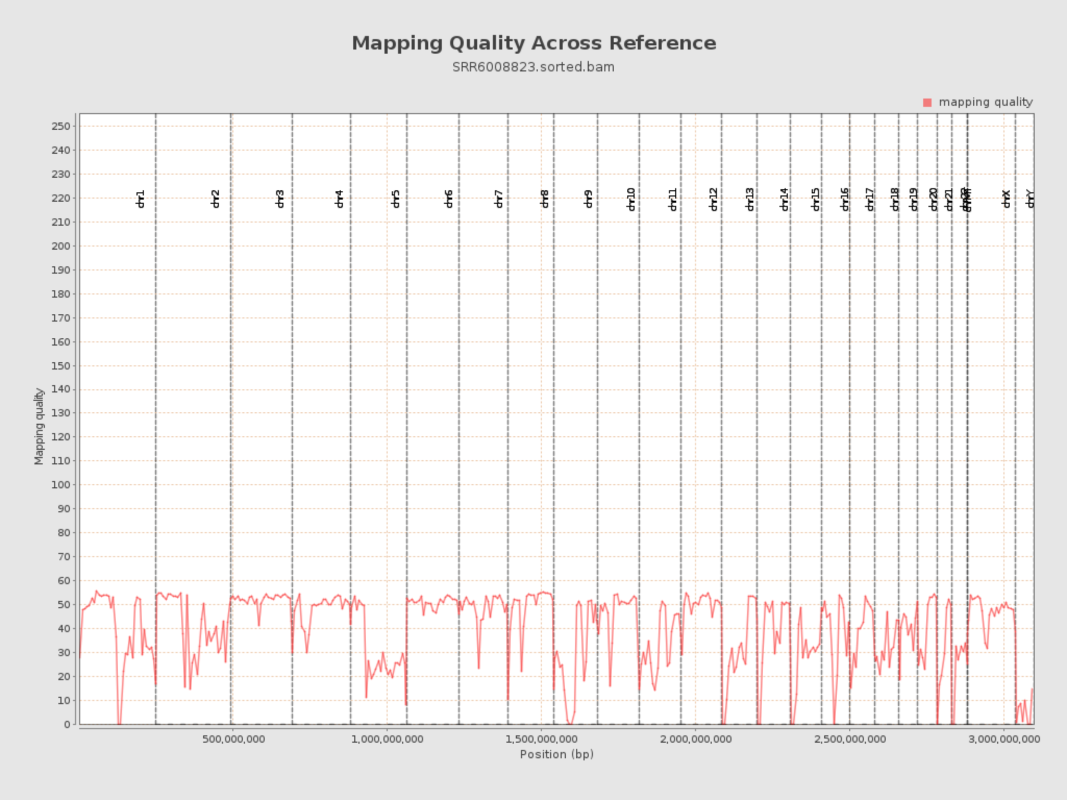
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram