Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 00:52:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004088.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_SRR6004088 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004088.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 00:52:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004088.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,055,198
Mapped reads	2,735,834 / 89.55%
Unmapped reads	319,364 / 10.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,410 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	116,427 / 3.81%
Duplication rate	3.03%
Clipped reads	1,255,380 / 41.09%

2.2. ACGT Content

Number/percentage of A's	51,674,158 / 28.36%
Number/percentage of C's	32,821,199 / 18.01%
Number/percentage of T's	57,500,569 / 31.56%
Number/percentage of G's	40,027,930 / 21.97%
Number/percentage of N's	193,706 / 0.11%
GC Percentage	39.98%

2.3. Coverage

Mean	0.0589

Standard Deviation	0.5467

2.4. Mapping Quality

Mean Mapping Quality	44.82

2.5. Mismatches and indels

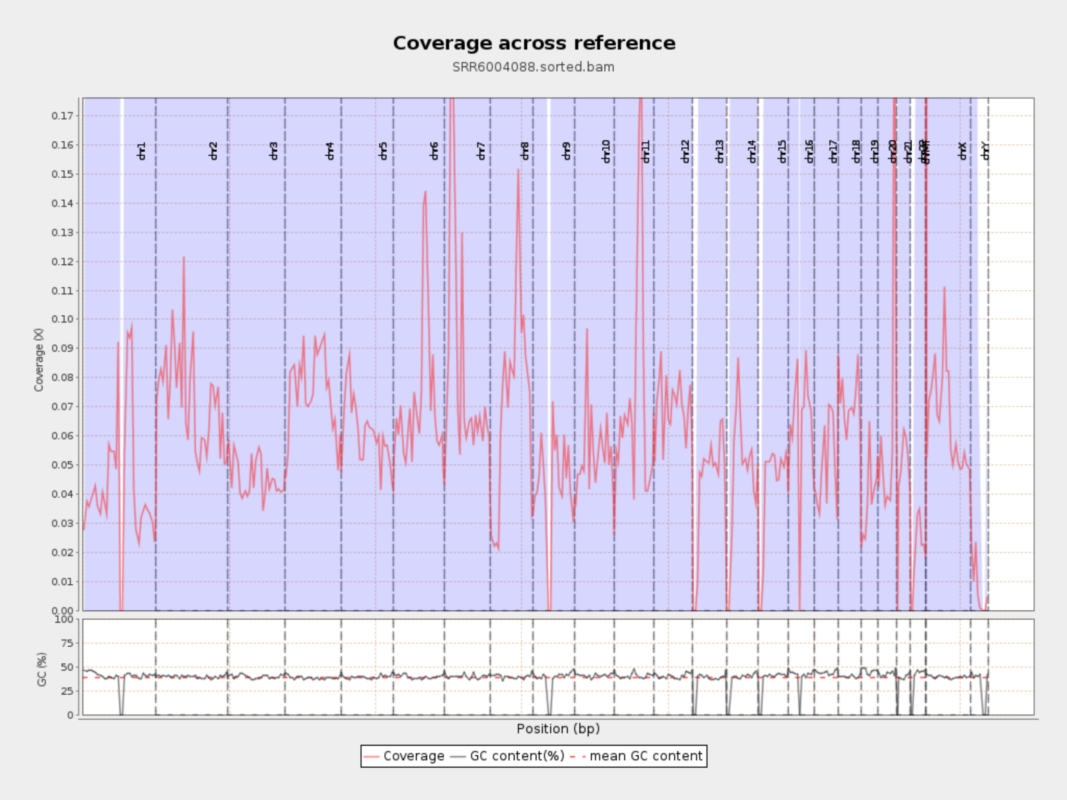
General error rate	0.96%
Mismatches	1,715,033
Insertions	15,071
Mapped reads with at least one insertion	0.55%
Deletions	67,274
Mapped reads with at least one deletion	2.42%
Homopolymer indels	44.65%

2.6. Chromosome stats

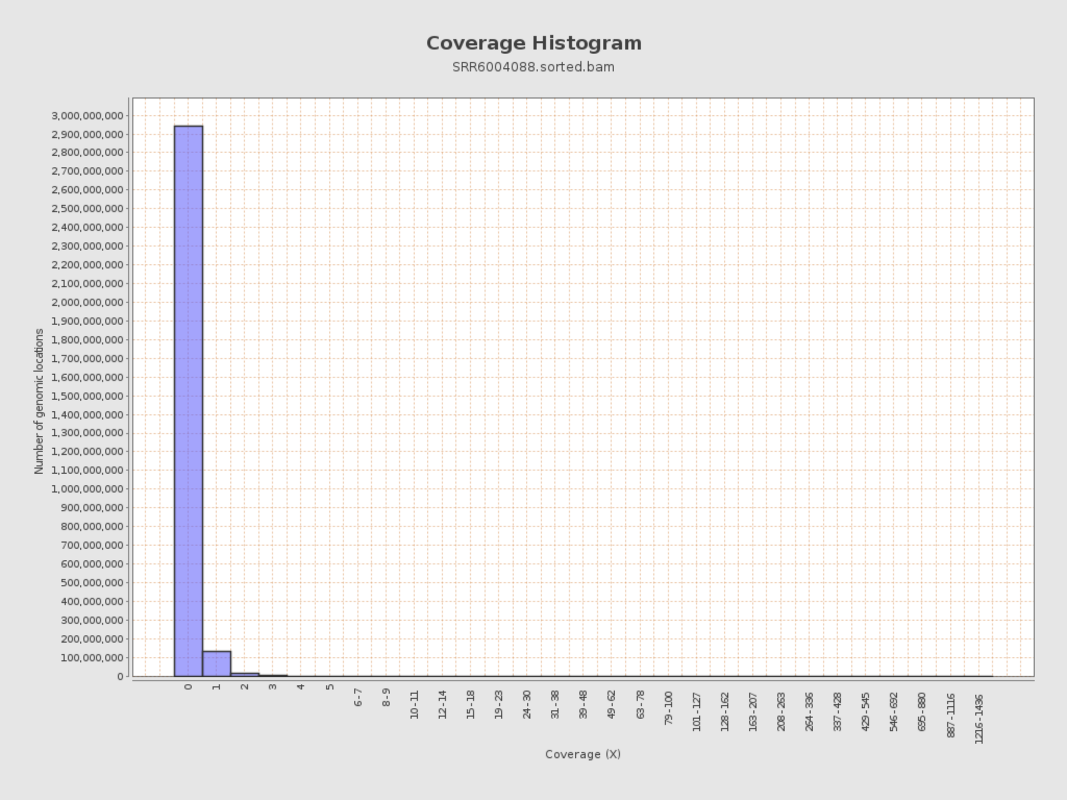
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10639179	0.0427	0.9353
chr2	243199373	17652383	0.0726	0.6287
chr3	198022430	9068350	0.0458	0.2475
chr4	191154276	14506069	0.0759	0.3283
chr5	180915260	11085834	0.0613	0.2899
chr6	171115067	12382154	0.0724	0.3525
chr7	159138663	13043616	0.082	0.9149

chr8	146364022	10687574	0.073	0.9058
chr9	141213431	6093911	0.0432	0.5013
chr10	135534747	7364979	0.0543	0.4735
chr11	135006516	9909307	0.0734	0.5244
chr12	133851895	9393633	0.0702	0.315
chr13	115169878	5017235	0.0436	0.2368
chr14	107349540	5042655	0.047	0.3049
chr15	102531392	4165081	0.0406	0.236
chr16	90354753	5634427	0.0624	0.3742
chr17	81195210	4108073	0.0506	0.3101
chr18	78077248	5616009	0.0719	0.9049
chr19	59128983	2302982	0.0389	0.7236
chr20	63025520	4623294	0.0734	0.3394
chr21	48129895	2249313	0.0467	0.2726
chr22	51304566	1029598	0.0201	0.1571
chrMT	16571	30841	1.8611	1.8078
chrX	155270560	10219856	0.0658	0.3594
chrY	59373566	463965	0.0078	0.1651

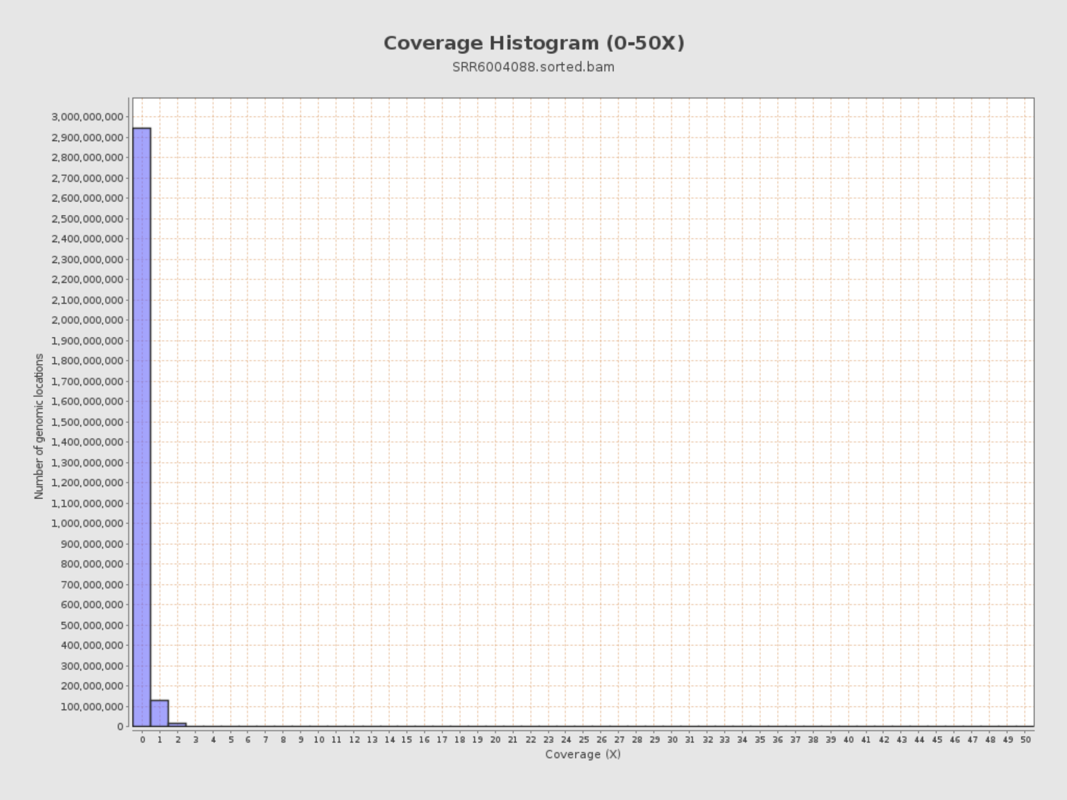
3. Results : Coverage across reference



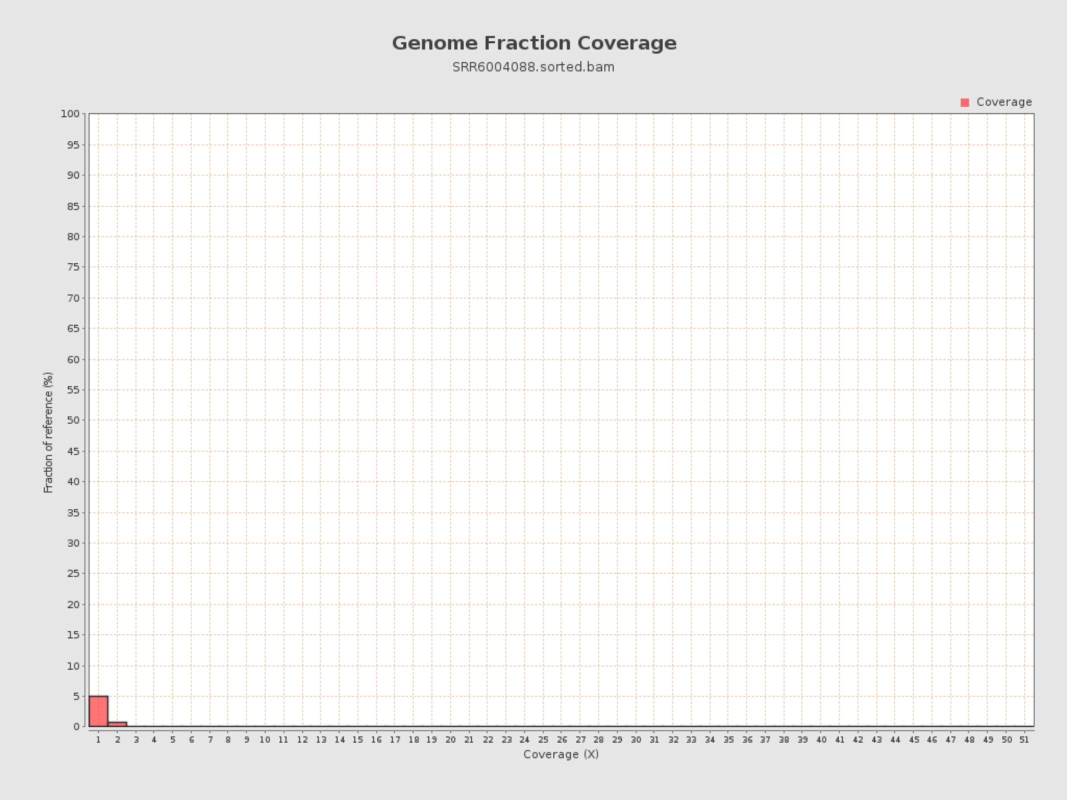
4. Results : Coverage Histogram



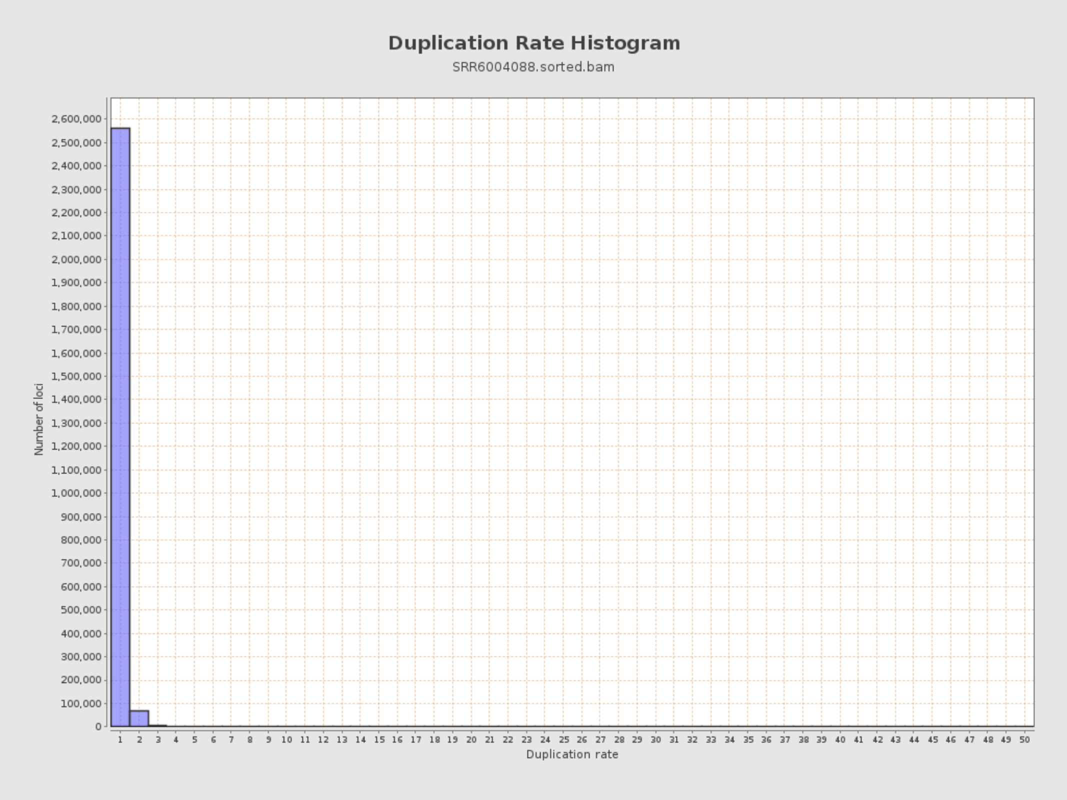
5. Results : Coverage Histogram (0-50X)



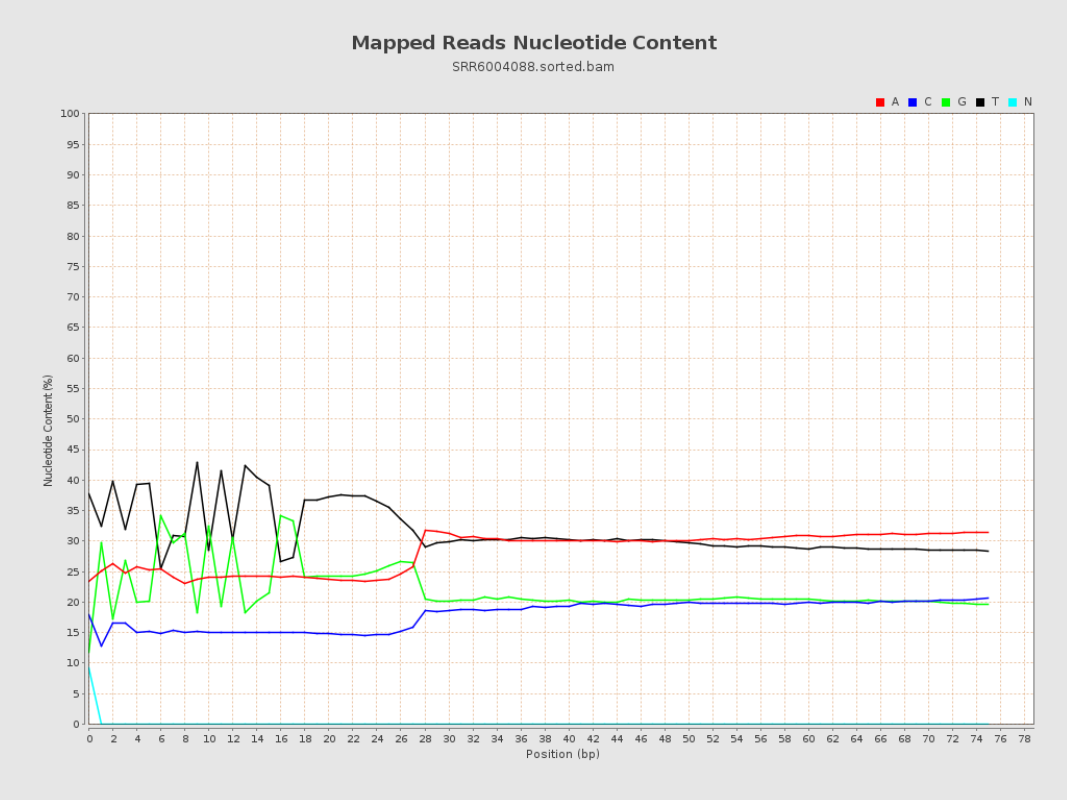
6. Results : Genome Fraction Coverage



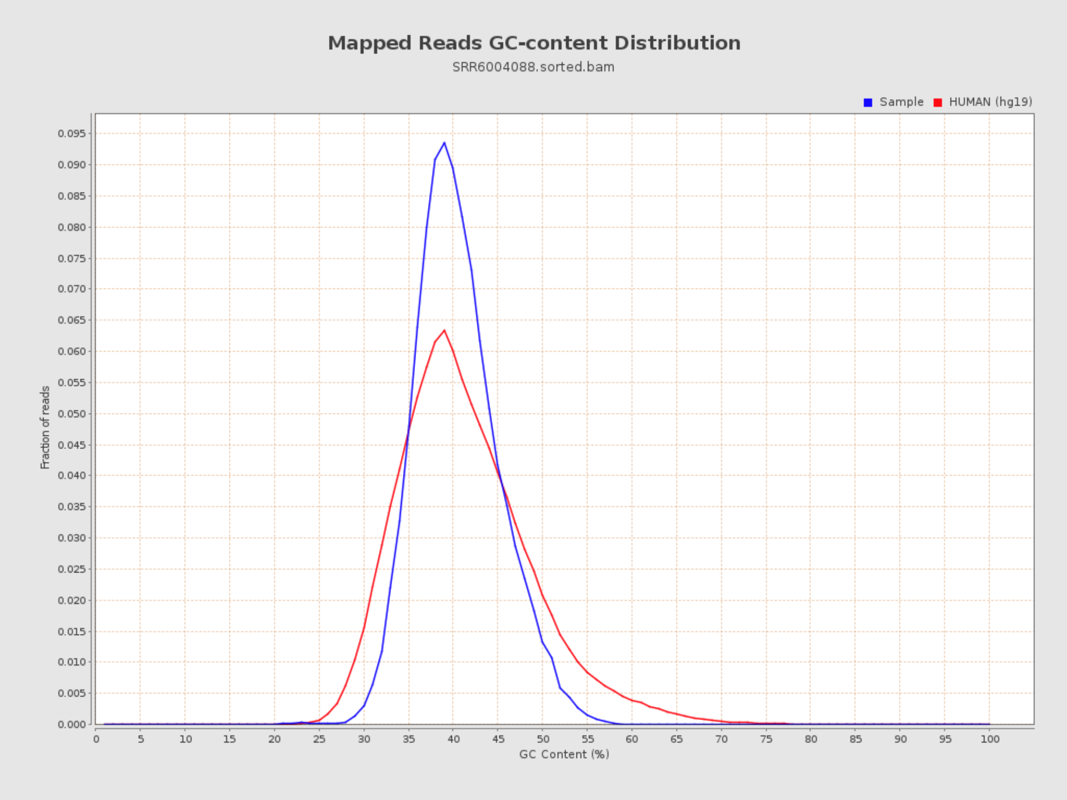
7. Results : Duplication Rate Histogram



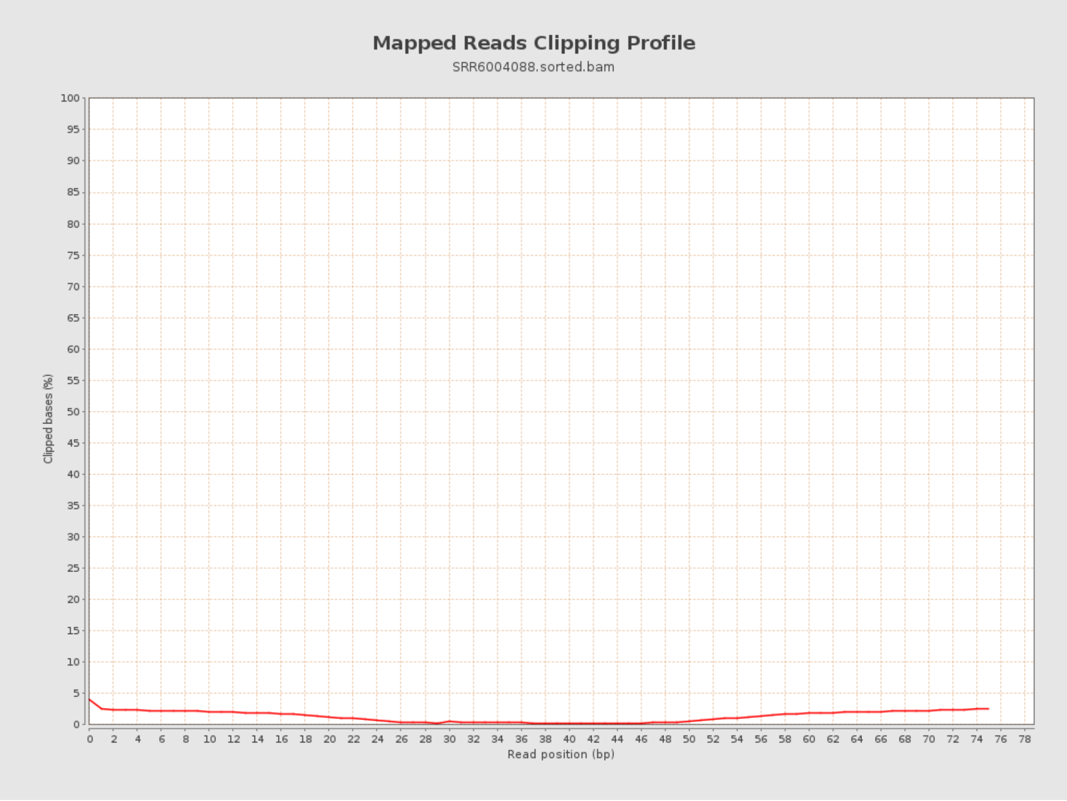
8. Results : Mapped Reads Nucleotide Content



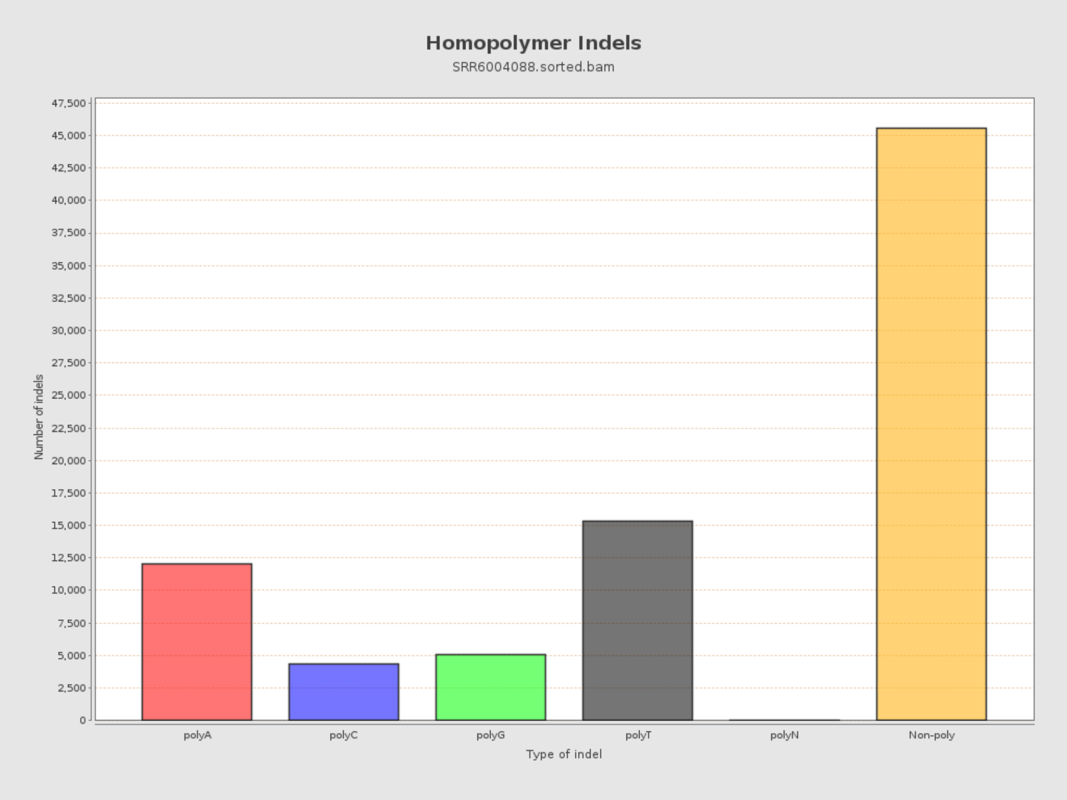
9. Results : Mapped Reads GC-content Distribution



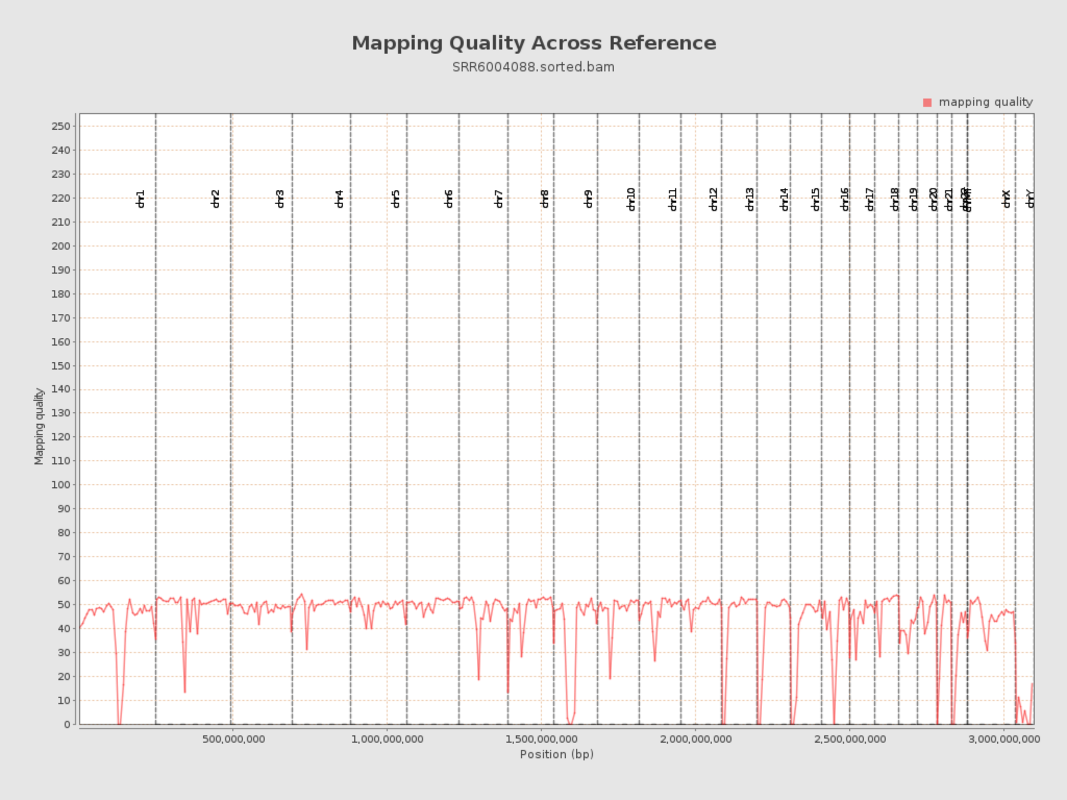
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram