Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 19:23:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084888.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_SRR3084888 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084888.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 19:23:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084888.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,476,485
Mapped reads	2,203,449 / 88.97%
Unmapped reads	273,036 / 11.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,179 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	93,485 / 3.77%
Duplication rate	3.49%
Clipped reads	727,274 / 29.37%

2.2. ACGT Content

Number/percentage of A's	44,562,506 / 29.12%
Number/percentage of C's	28,164,597 / 18.4%
Number/percentage of T's	48,672,448 / 31.8%
Number/percentage of G's	31,618,216 / 20.66%
Number/percentage of N's	23,720 / 0.02%
GC Percentage	39.06%

2.3. Coverage

Mean	0.0495

Standard Deviation	0.4145

2.4. Mapping Quality

Mean Mapping Quality	47.33

2.5. Mismatches and indels

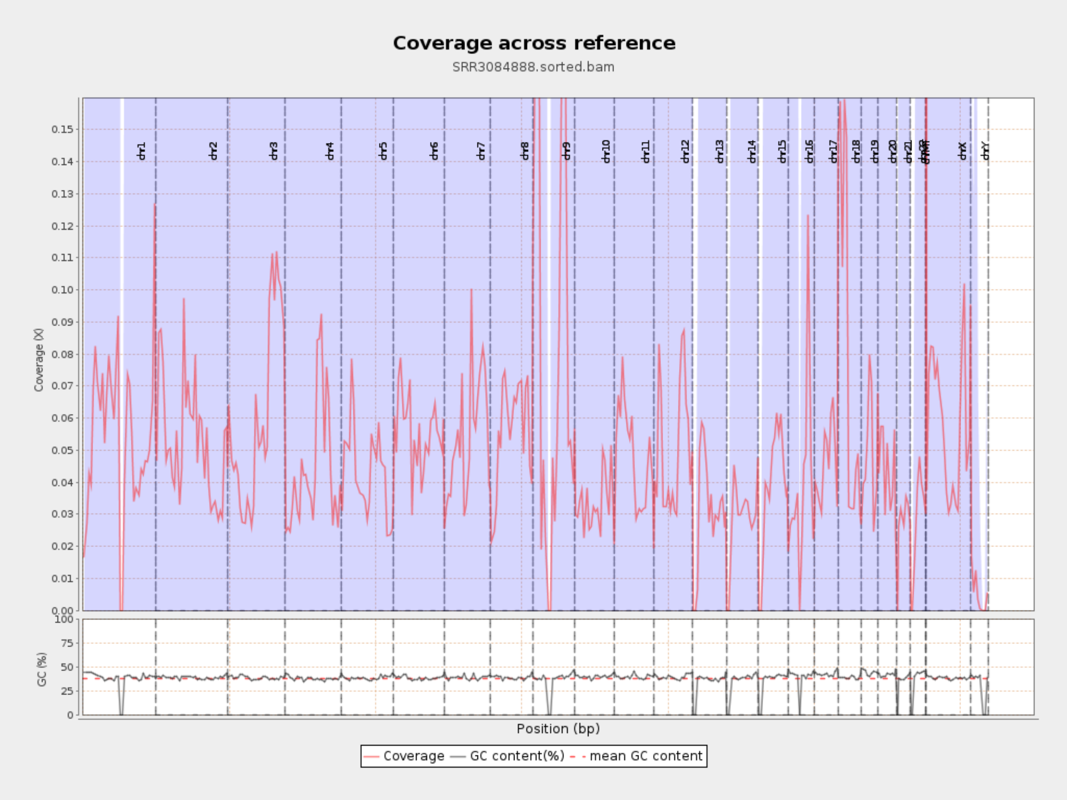
General error rate	0.85%
Mismatches	1,273,960
Insertions	12,046
Mapped reads with at least one insertion	0.54%
Deletions	34,390
Mapped reads with at least one deletion	1.54%
Homopolymer indels	48.9%

2.6. Chromosome stats

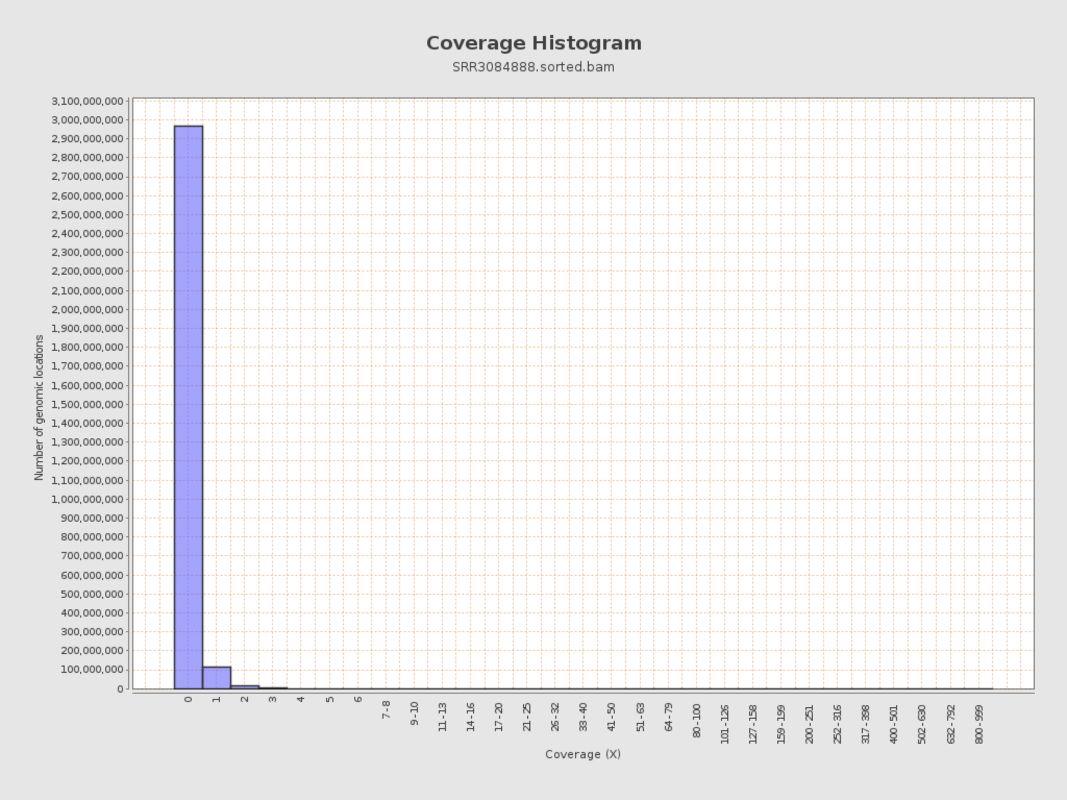
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13658196	0.0548	0.8764
chr2	243199373	12882755	0.053	0.4796
chr3	198022430	11782038	0.0595	0.2737
chr4	191154276	8497987	0.0445	0.2383
chr5	180915260	7850029	0.0434	0.2397
chr6	171115067	9560708	0.0559	0.2736
chr7	159138663	8678408	0.0545	0.433

chr8	146364022	8154760	0.0557	0.5571
chr9	141213431	11901675	0.0843	0.461
chr10	135534747	4595868	0.0339	0.2631
chr11	135006516	6524046	0.0483	0.3525
chr12	133851895	6841264	0.0511	0.2575
chr13	115169878	3583276	0.0311	0.1959
chr14	107349540	3026013	0.0282	0.1954
chr15	102531392	3920946	0.0382	0.2177
chr16	90354753	3395027	0.0376	0.2341
chr17	81195210	3788485	0.0467	0.2542
chr18	78077248	6572322	0.0842	0.6354
chr19	59128983	2922205	0.0494	0.5393
chr20	63025520	2796853	0.0444	0.2386
chr21	48129895	1325009	0.0275	0.1944
chr22	51304566	1418262	0.0276	0.1834
chrMT	16571	17372	1.0483	1.2049
chrX	155270560	9107674	0.0587	0.3021
chrY	59373566	300528	0.0051	0.1199

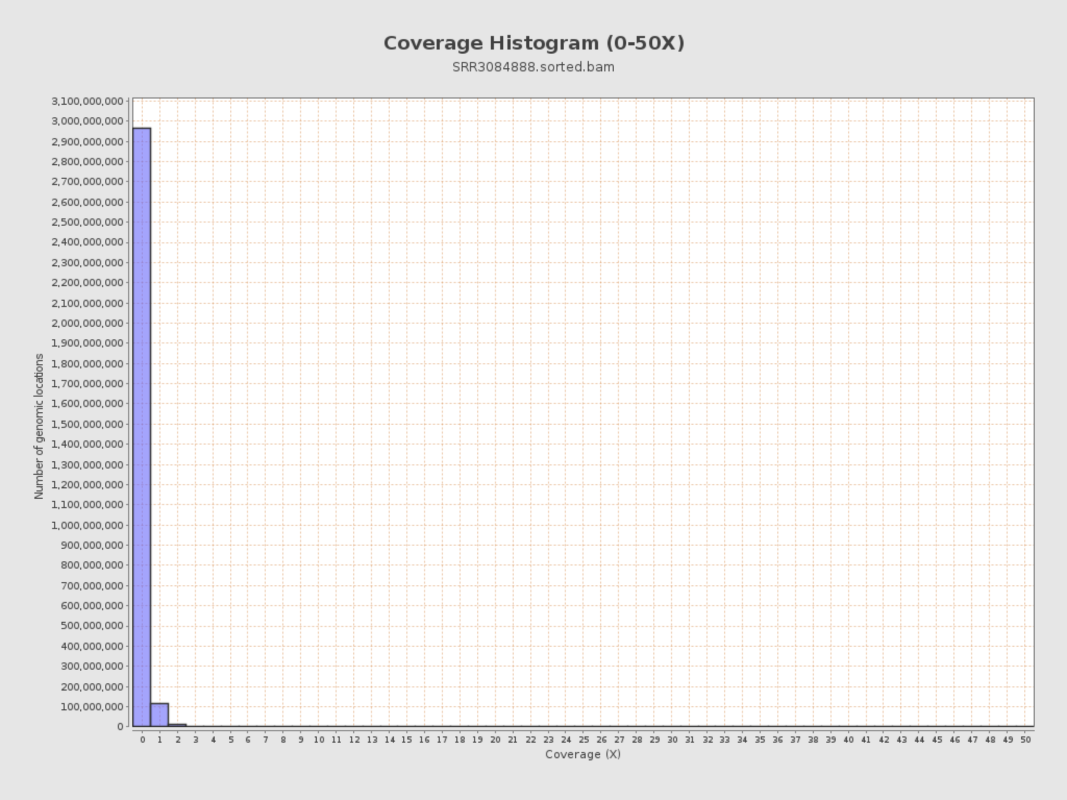
3. Results : Coverage across reference



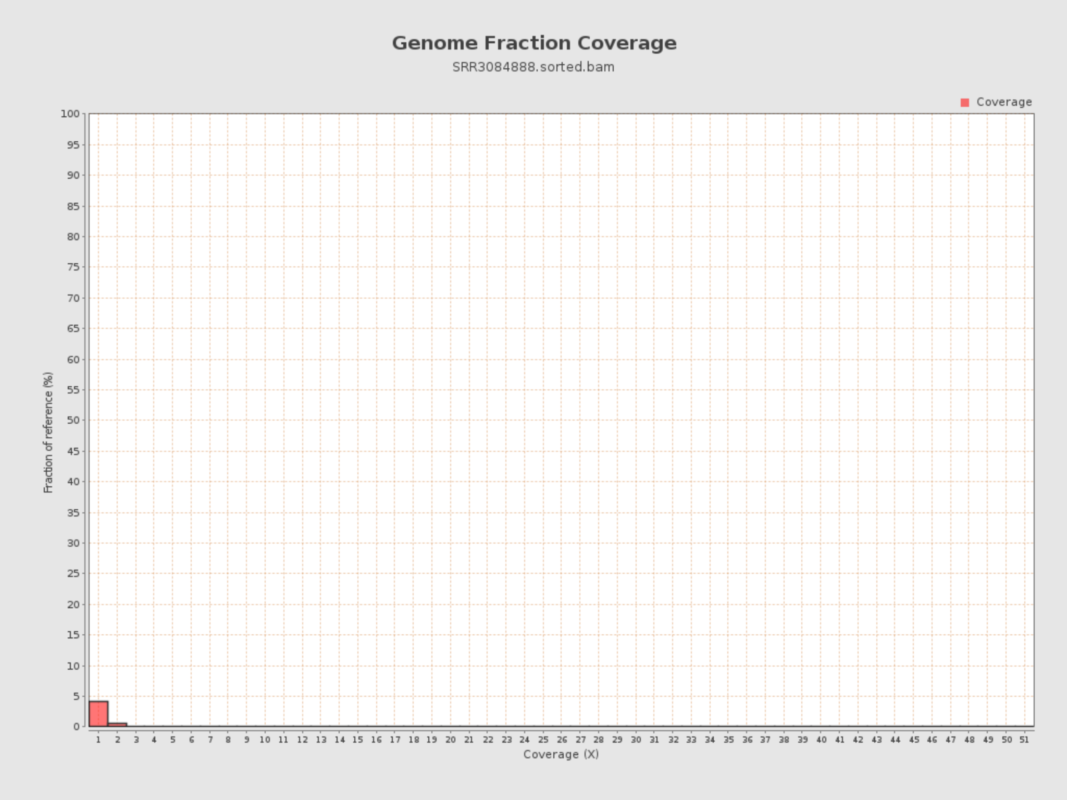
4. Results : Coverage Histogram



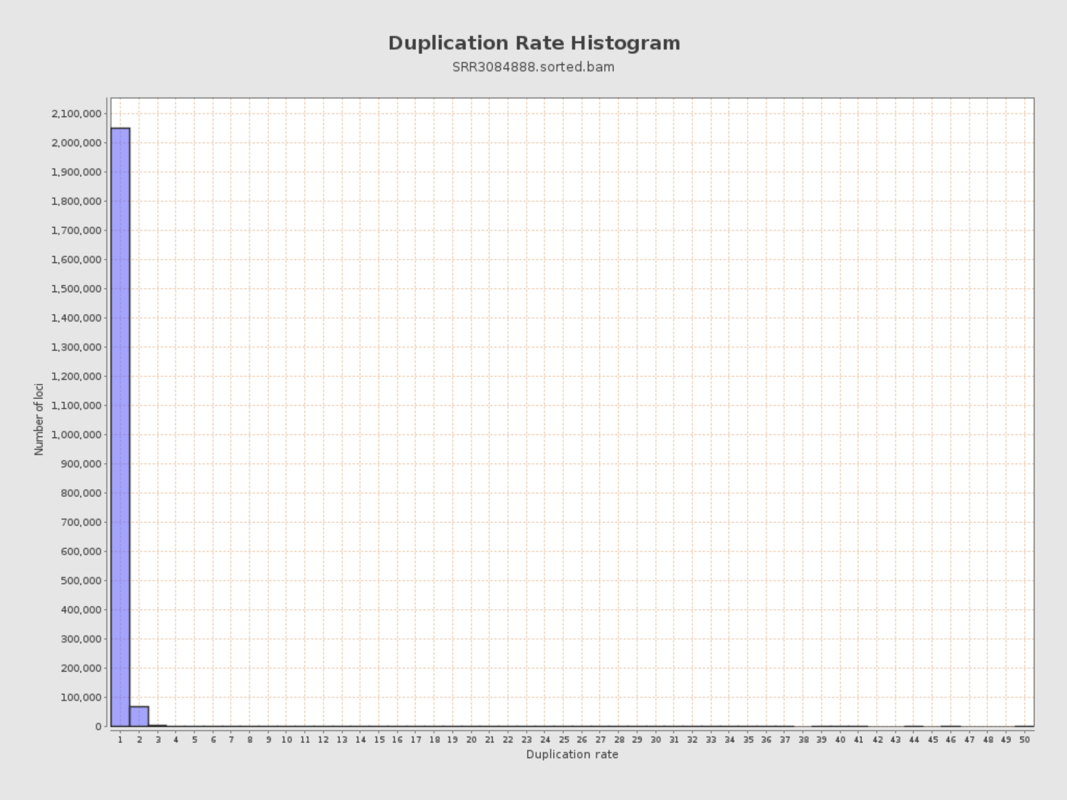
5. Results : Coverage Histogram (0-50X)



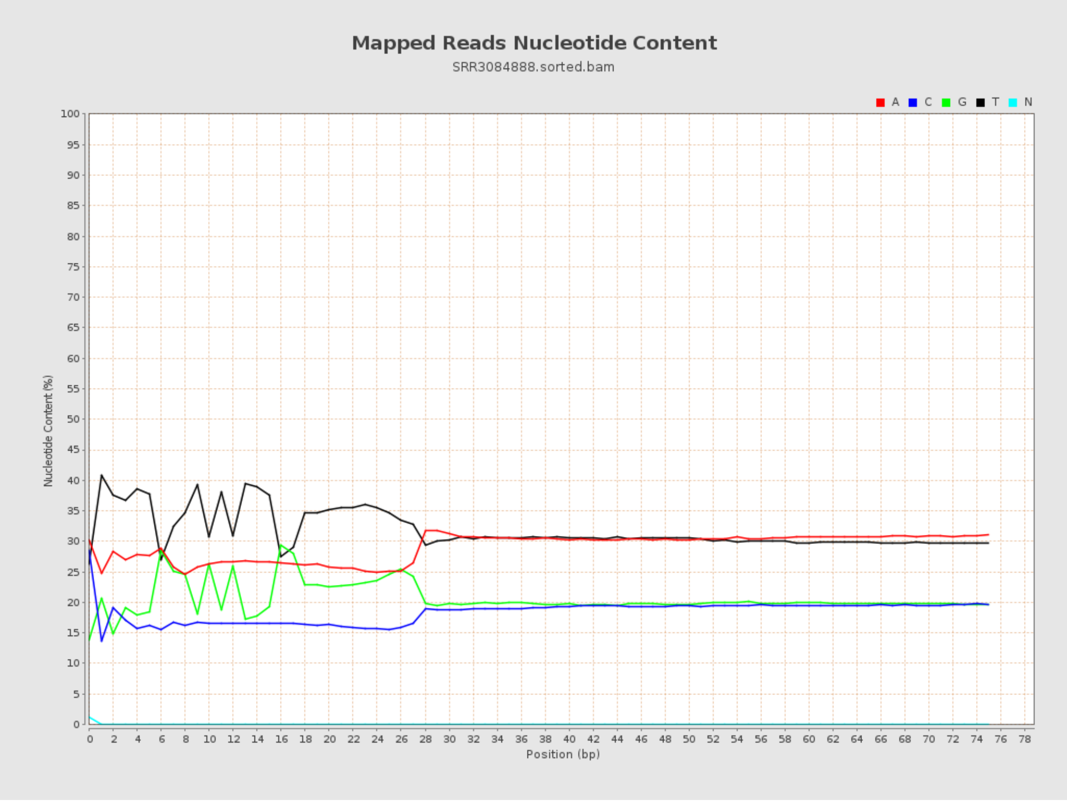
6. Results : Genome Fraction Coverage



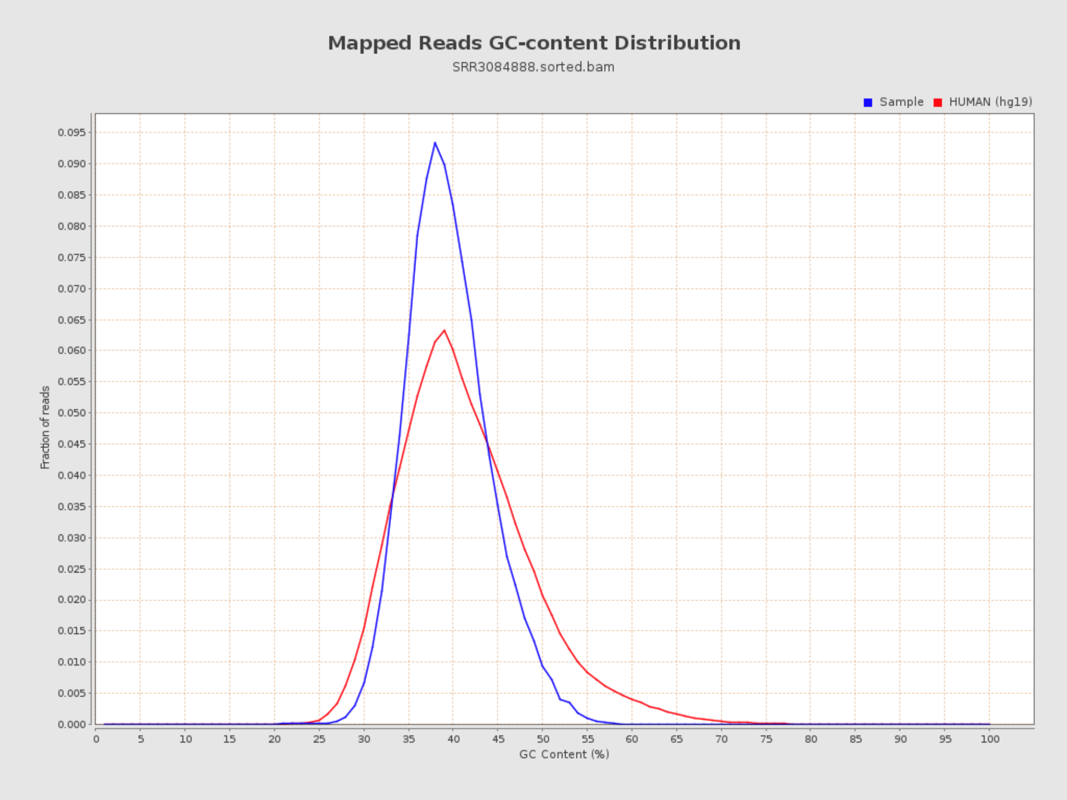
7. Results : Duplication Rate Histogram



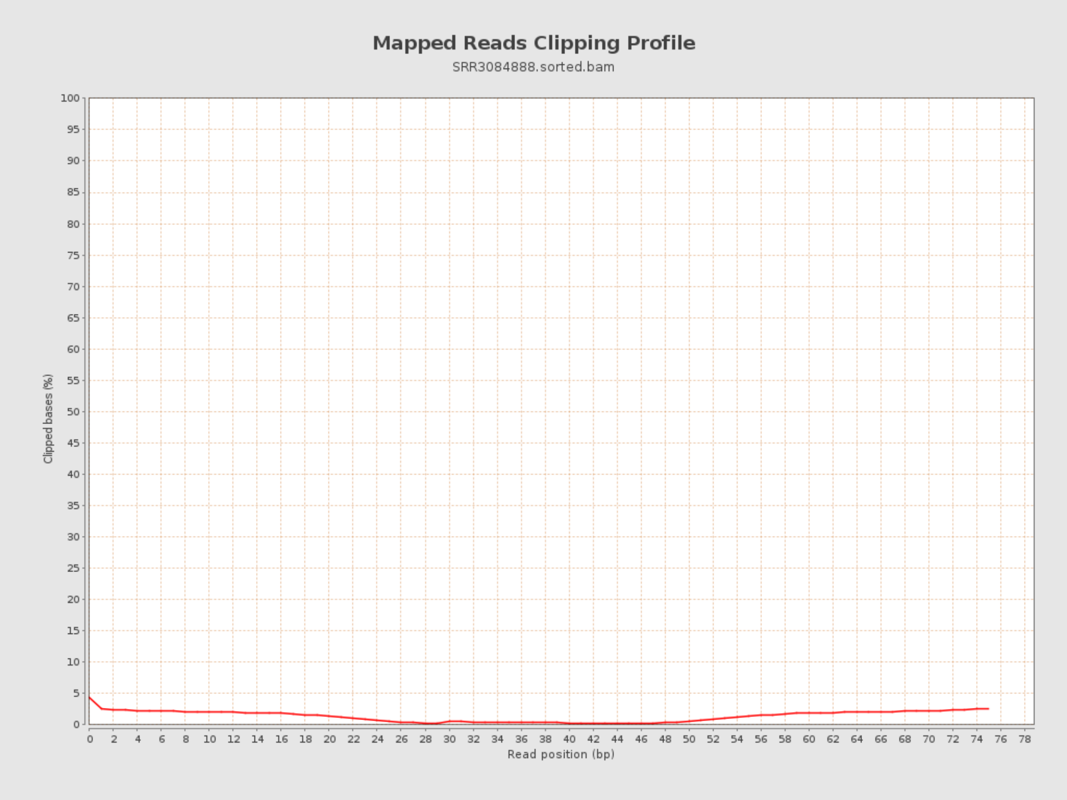
8. Results : Mapped Reads Nucleotide Content



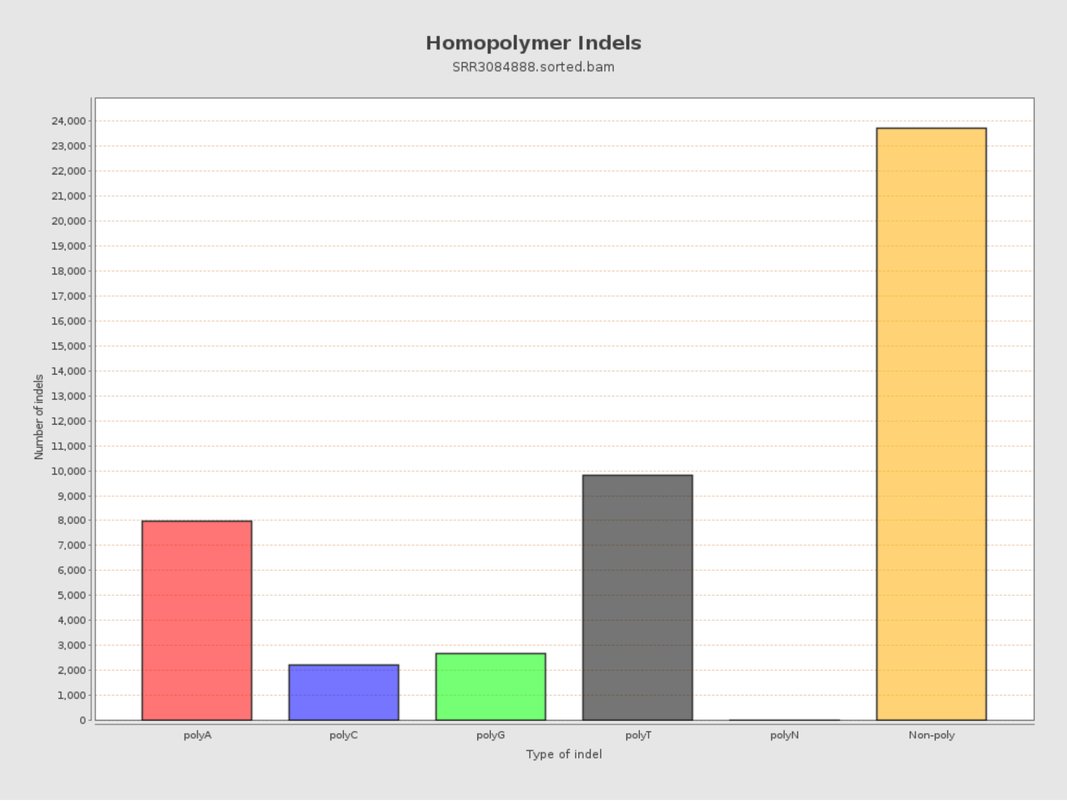
9. Results : Mapped Reads GC-content Distribution



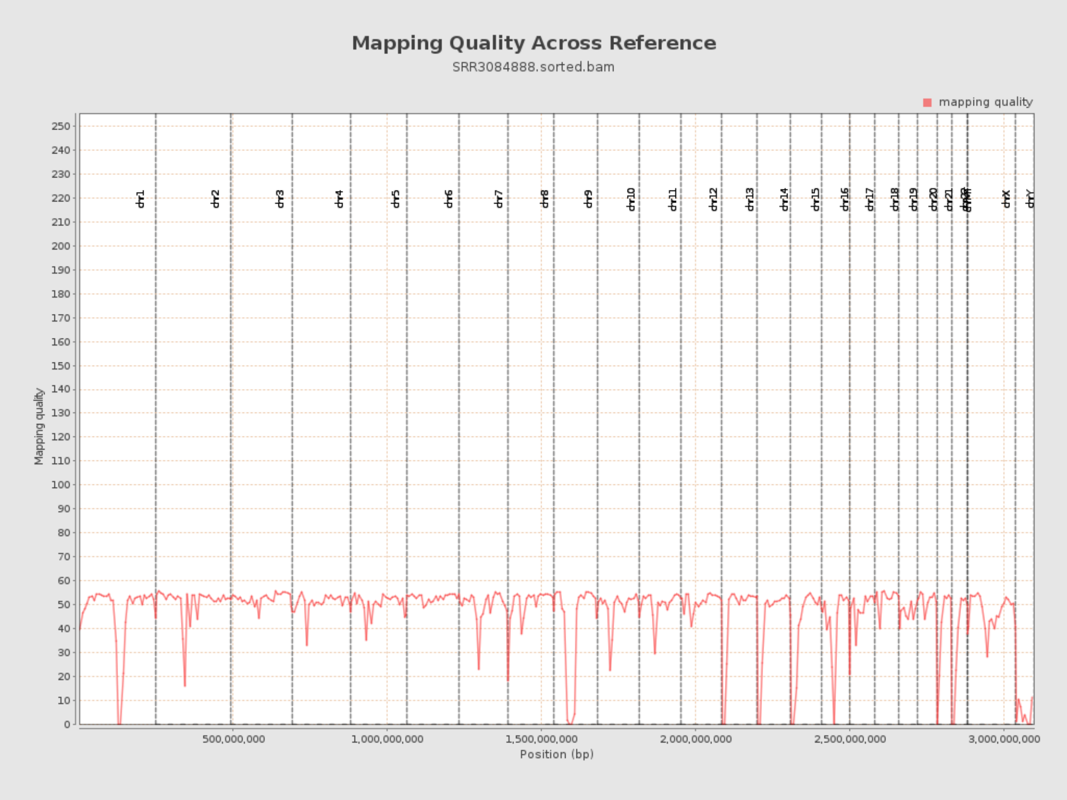
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram