Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 07:04:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008688.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_SRR6008688 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008688.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 07:04:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008688.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	880,013
Mapped reads	745,104 / 84.67%
Unmapped reads	134,909 / 15.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,387 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	20,839 / 2.37%
Duplication rate	1.79%
Clipped reads	368,646 / 41.89%

2.2. ACGT Content

Number/percentage of A's	13,488,848 / 27.72%
Number/percentage of C's	8,995,838 / 18.48%
Number/percentage of T's	15,060,595 / 30.94%
Number/percentage of G's	11,112,050 / 22.83%
Number/percentage of N's	12,310 / 0.03%
GC Percentage	41.32%

2.3. Coverage

Mean	0.0157

Standard Deviation	0.237

2.4. Mapping Quality

Mean Mapping Quality	43.53

2.5. Mismatches and indels

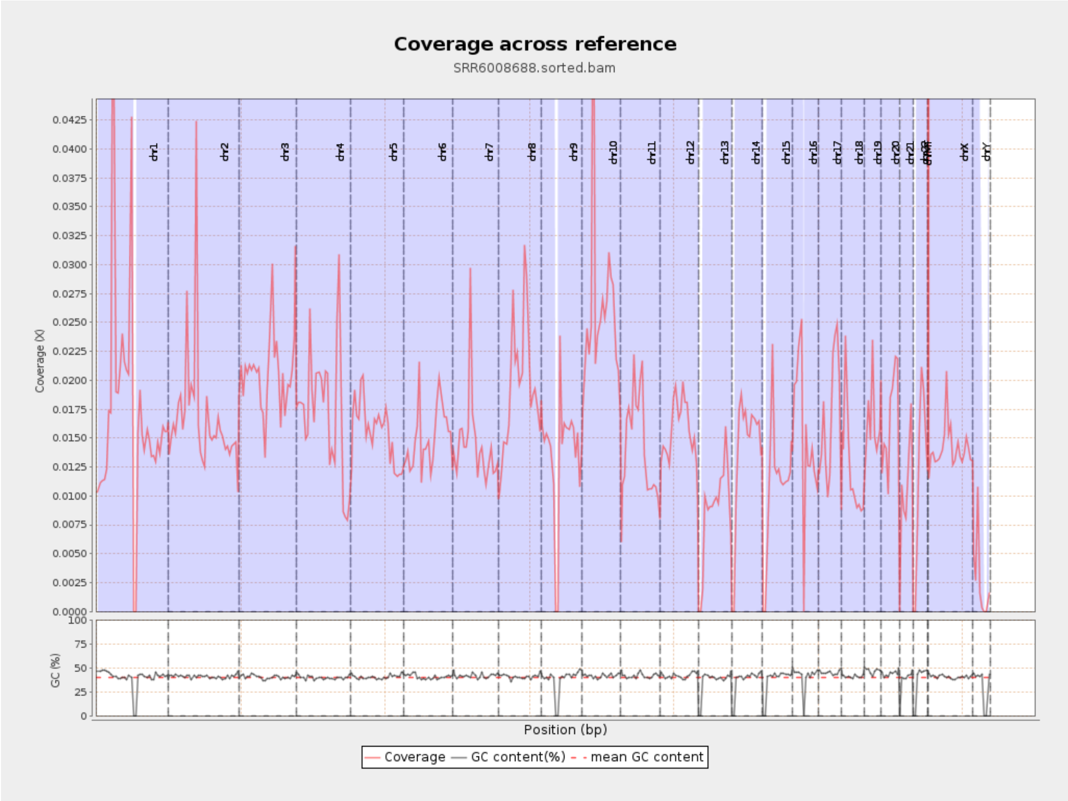
General error rate	1%
Mismatches	476,824
Insertions	3,918
Mapped reads with at least one insertion	0.52%
Deletions	23,376
Mapped reads with at least one deletion	3.08%
Homopolymer indels	42.47%

2.6. Chromosome stats

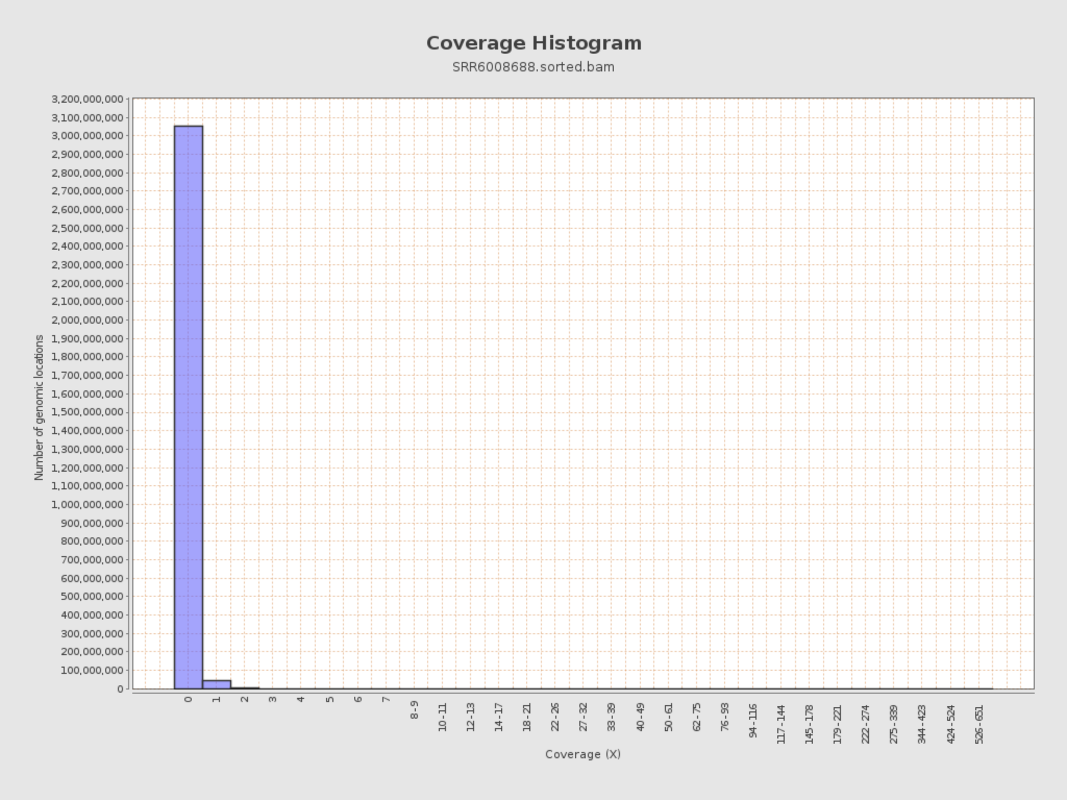
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4272486	0.0171	0.5105
chr2	243199373	4082270	0.0168	0.2291
chr3	198022430	4059461	0.0205	0.1549
chr4	191154276	3323873	0.0174	0.1476
chr5	180915260	2838734	0.0157	0.1315
chr6	171115067	2587915	0.0151	0.1421
chr7	159138663	2297479	0.0144	0.2094

chr8	146364022	2882854	0.0197	0.3274
chr9	141213431	1925351	0.0136	0.1988
chr10	135534747	3564436	0.0263	0.3424
chr11	135006516	1949063	0.0144	0.1581
chr12	133851895	2098169	0.0157	0.1327
chr13	115169878	1005242	0.0087	0.0966
chr14	107349540	1486249	0.0138	0.1306
chr15	102531392	1104235	0.0108	0.1077
chr16	90354753	1356581	0.015	0.155
chr17	81195210	1348576	0.0166	0.1483
chr18	78077248	954352	0.0122	0.346
chr19	59128983	968942	0.0164	0.3384
chr20	63025520	1040521	0.0165	0.1371
chr21	48129895	511125	0.0106	0.1193
chr22	51304566	619255	0.0121	0.1144
chrMT	16571	79590	4.803	3.3154
chrX	155270560	2196397	0.0141	0.1359
chrY	59373566	157811	0.0027	0.1029

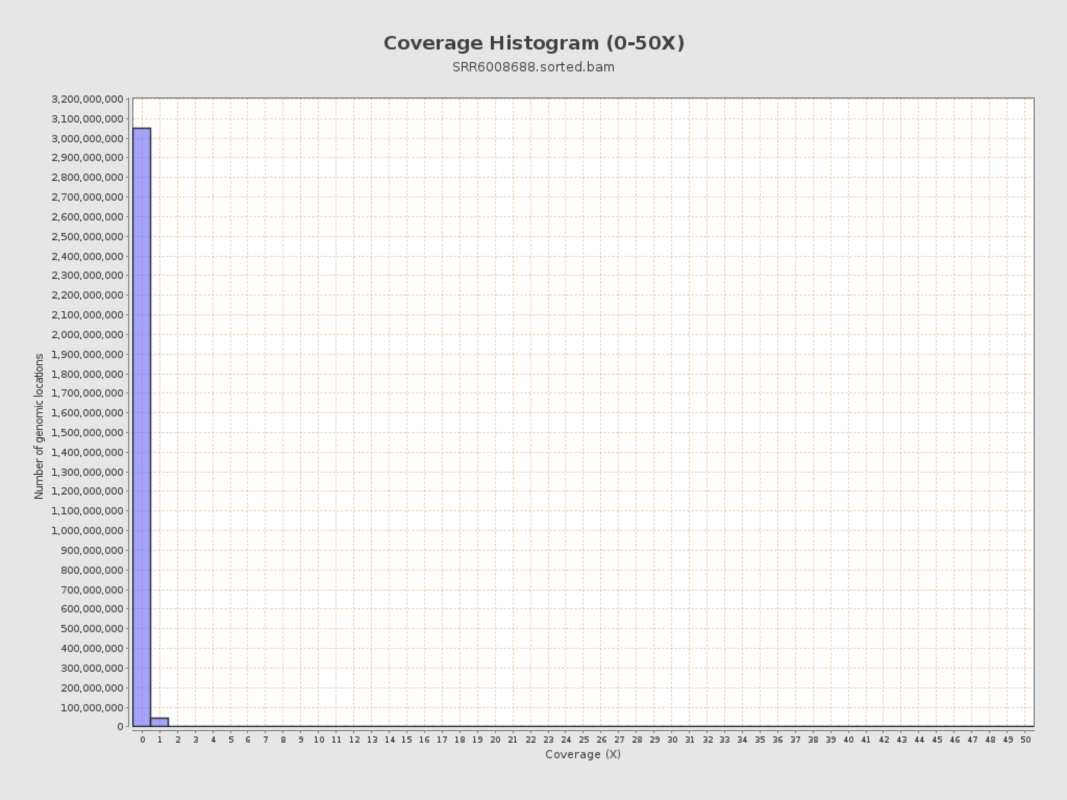
3. Results : Coverage across reference



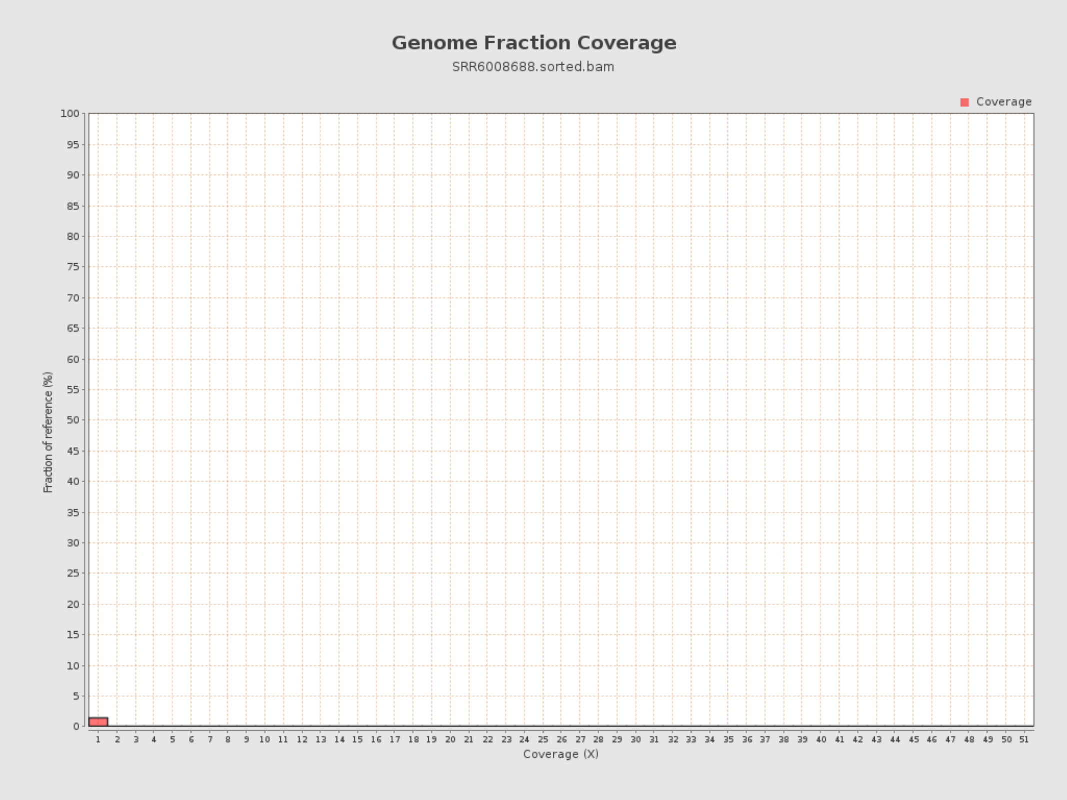
4. Results : Coverage Histogram



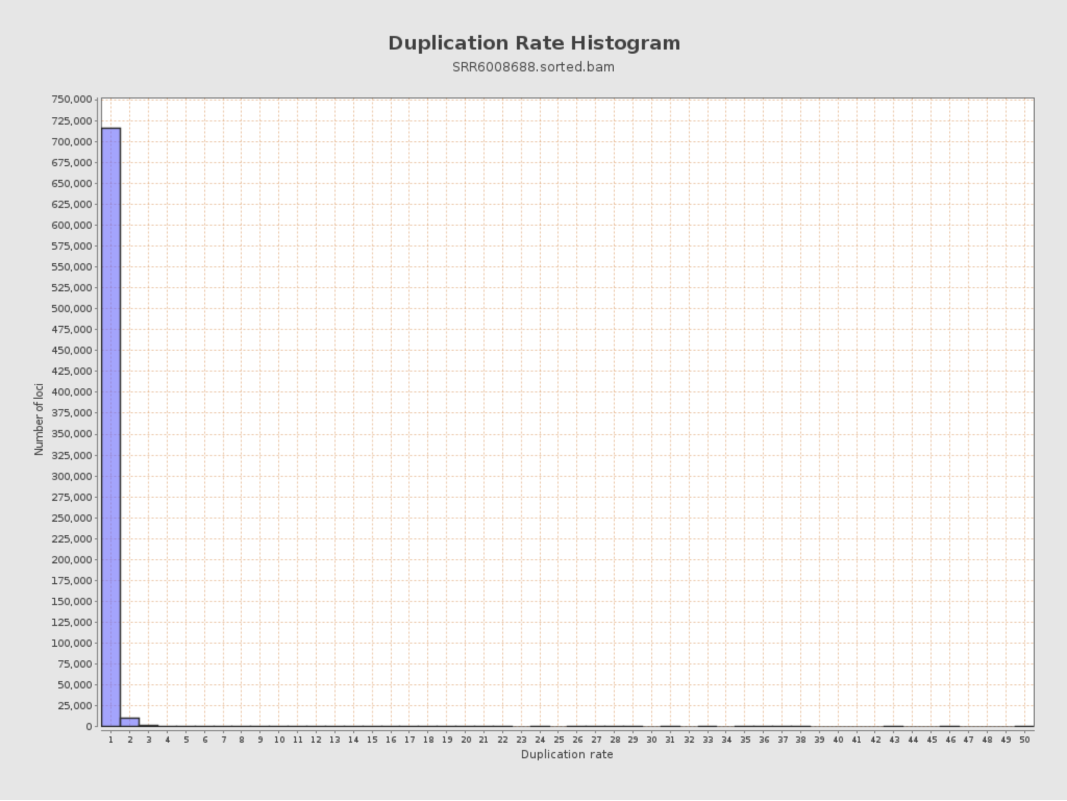
5. Results : Coverage Histogram (0-50X)



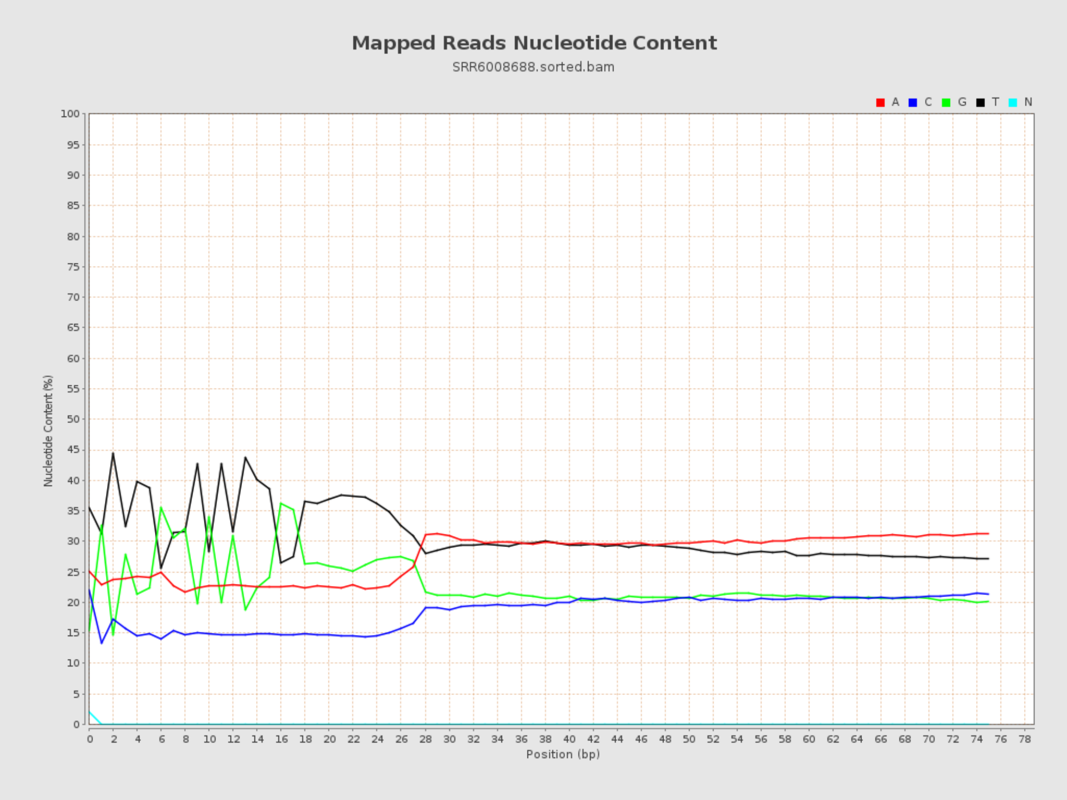
6. Results : Genome Fraction Coverage



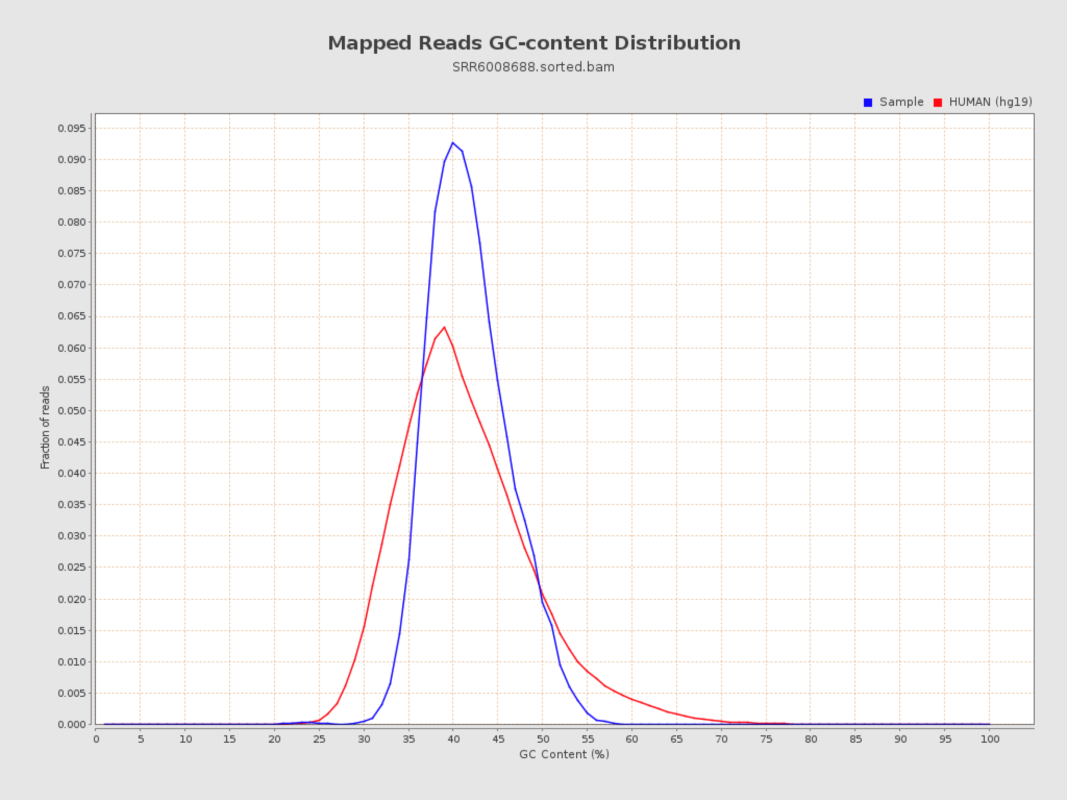
7. Results : Duplication Rate Histogram



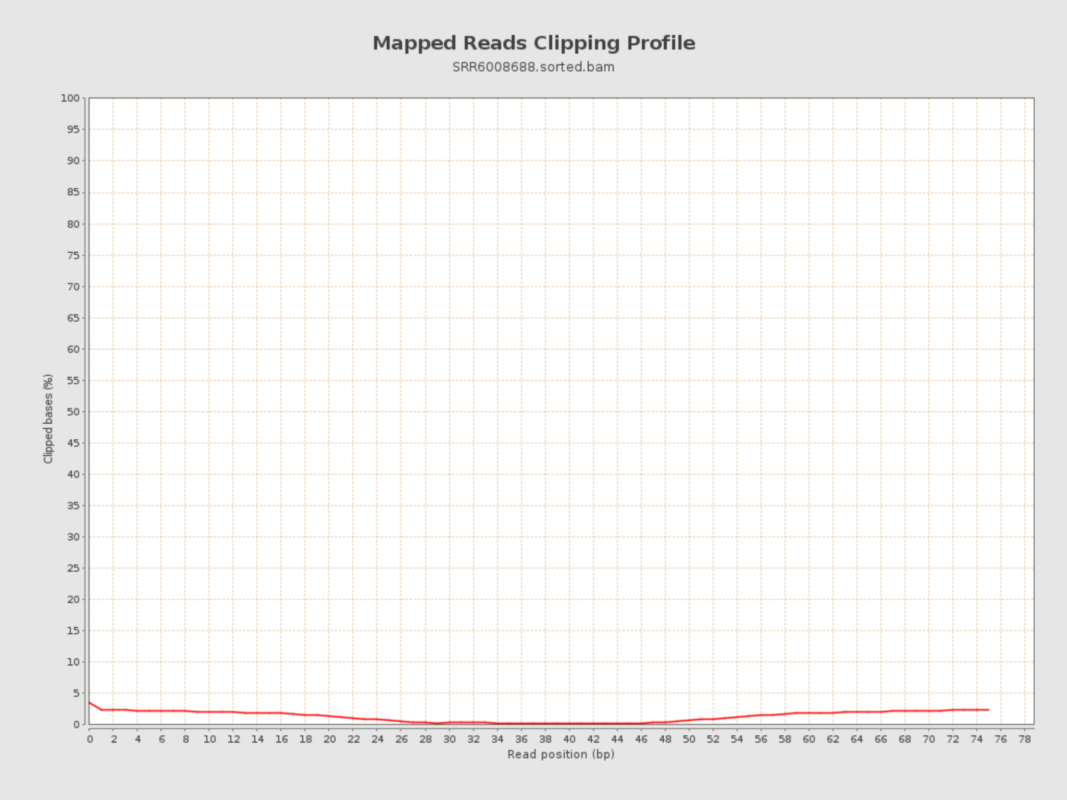
8. Results : Mapped Reads Nucleotide Content



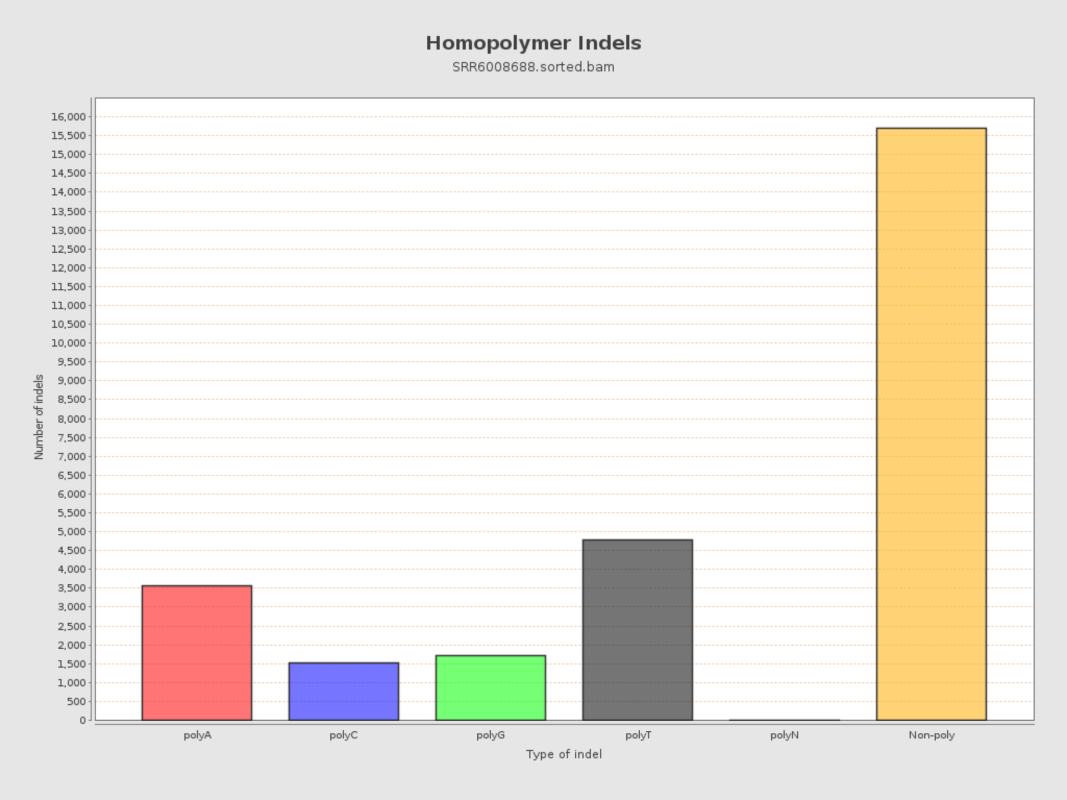
9. Results : Mapped Reads GC-content Distribution



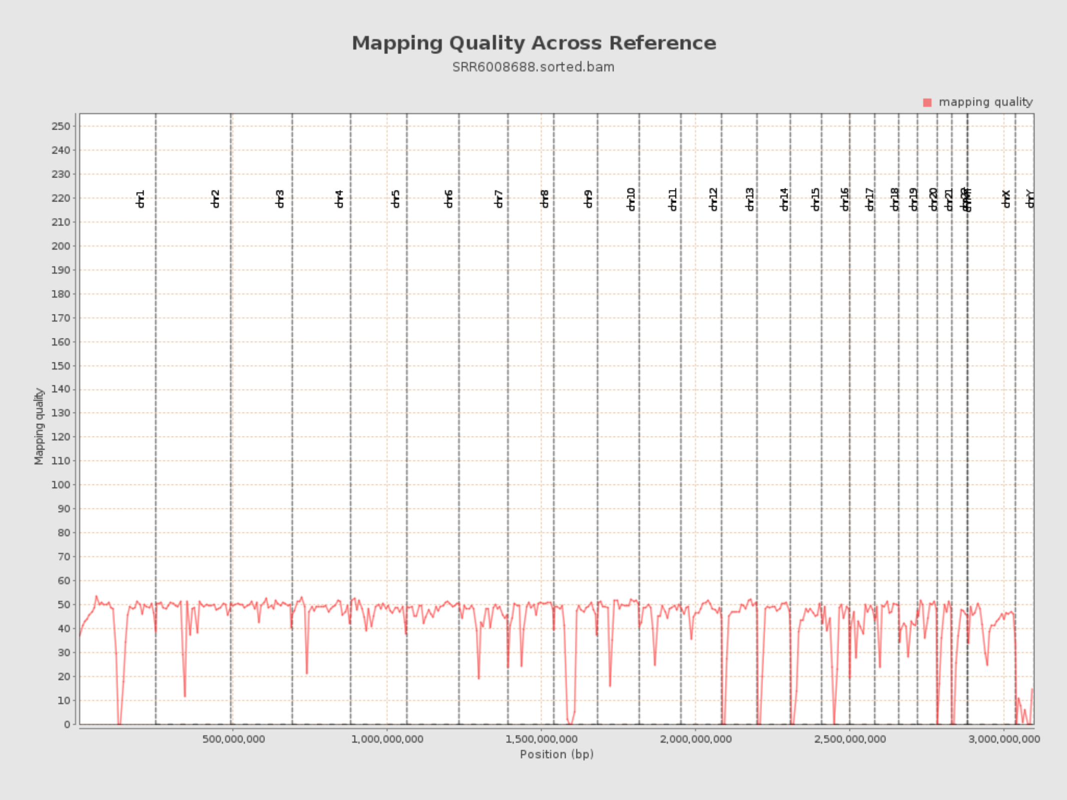
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram