Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 08:16:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008717.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_SRR6008717 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008717.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 08:16:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008717.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,028,909
Mapped reads	1,623,130 / 80%
Unmapped reads	405,779 / 20%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,683 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	44,789 / 2.21%
Duplication rate	2.18%
Clipped reads	716,077 / 35.29%

2.2. ACGT Content

Number/percentage of A's	33,214,463 / 30.53%
Number/percentage of C's	19,001,434 / 17.47%
Number/percentage of T's	32,667,922 / 30.03%
Number/percentage of G's	23,880,285 / 21.95%
Number/percentage of N's	15,483 / 0.01%
GC Percentage	39.42%

2.3. Coverage

Mean	0.0352

Standard Deviation	0.2714

2.4. Mapping Quality

Mean Mapping Quality	47.37

2.5. Mismatches and indels

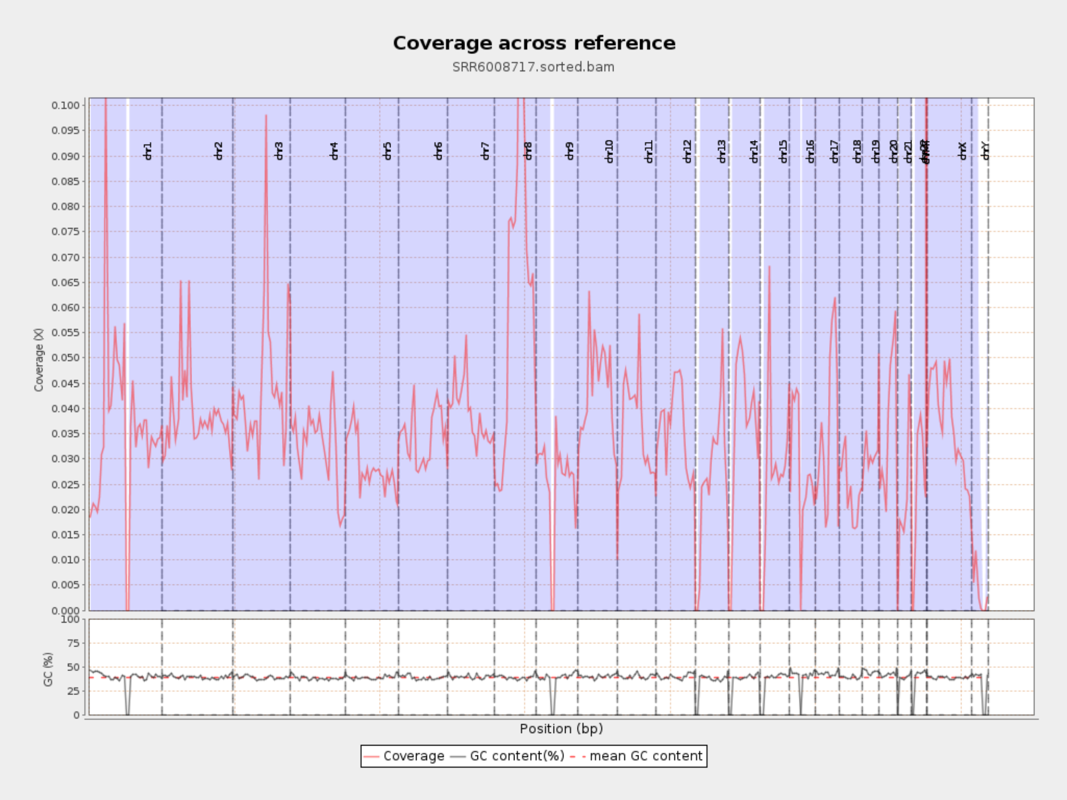
General error rate	0.89%
Mismatches	949,556
Insertions	8,532
Mapped reads with at least one insertion	0.52%
Deletions	30,195
Mapped reads with at least one deletion	1.84%
Homopolymer indels	48.21%

2.6. Chromosome stats

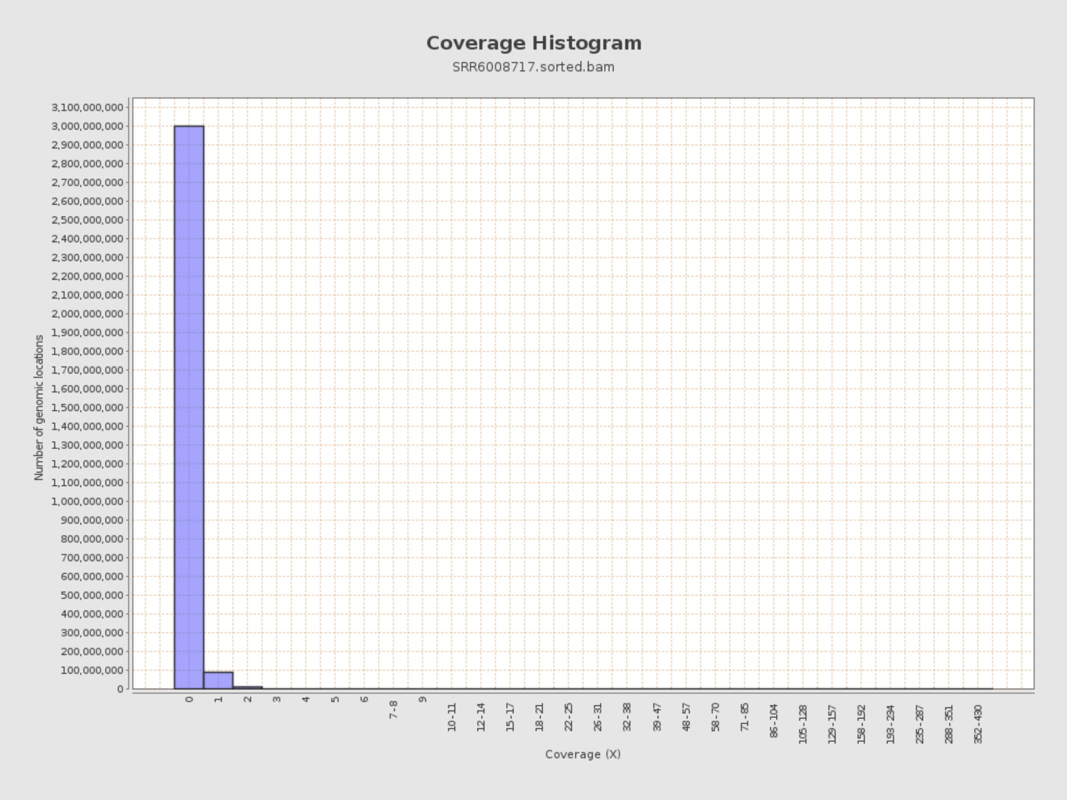
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8919442	0.0358	0.3877
chr2	243199373	9502049	0.0391	0.3286
chr3	198022430	8740666	0.0441	0.236
chr4	191154276	6159820	0.0322	0.202
chr5	180915260	5202297	0.0288	0.186
chr6	171115067	5905908	0.0345	0.2325
chr7	159138663	6260473	0.0393	0.3302

chr8	146364022	9298718	0.0635	0.4015
chr9	141213431	3572731	0.0253	0.2362
chr10	135534747	5981140	0.0441	0.3152
chr11	135006516	4881551	0.0362	0.2707
chr12	133851895	4857120	0.0363	0.211
chr13	115169878	3040067	0.0264	0.1785
chr14	107349540	3909501	0.0364	0.2174
chr15	102531392	2791287	0.0272	0.1825
chr16	90354753	2550518	0.0282	0.205
chr17	81195210	2904974	0.0358	0.2464
chr18	78077248	1854870	0.0238	0.3898
chr19	59128983	1853138	0.0313	0.2511
chr20	63025520	2354478	0.0374	0.2151
chr21	48129895	1090024	0.0226	0.1753
chr22	51304566	1171893	0.0228	0.1653
chrMT	16571	32485	1.9604	2.367
chrX	155270560	5750235	0.037	0.2338
chrY	59373566	243171	0.0041	0.1047

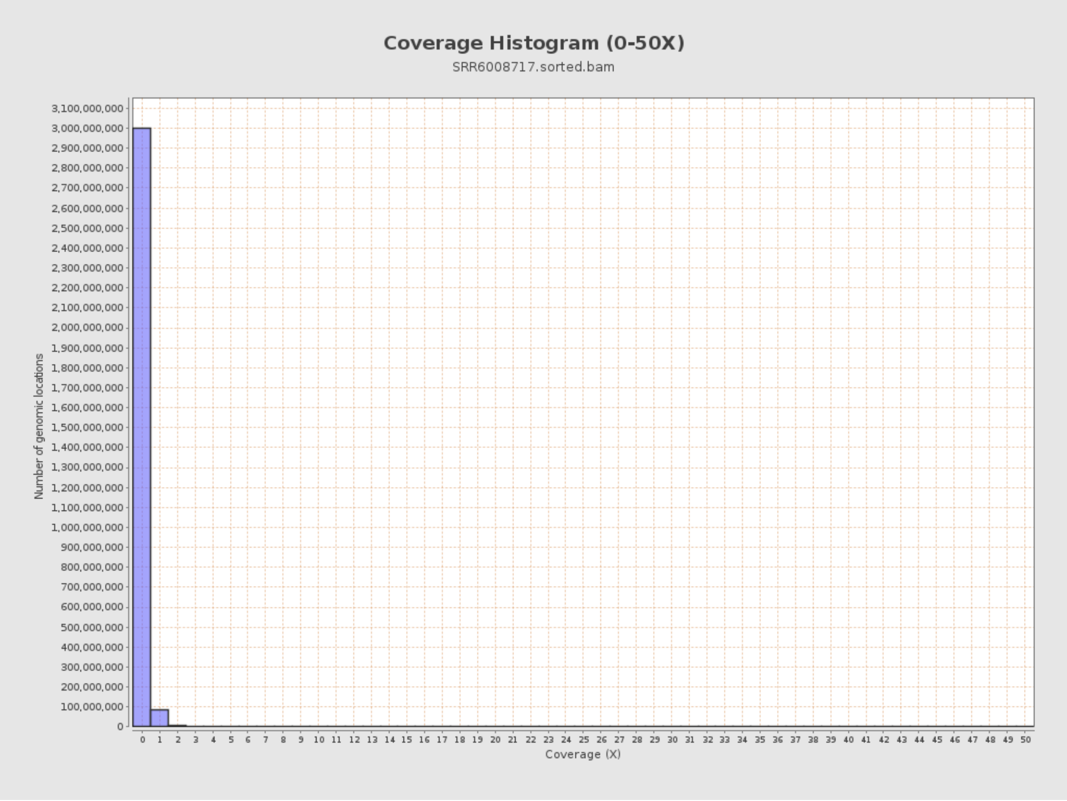
3. Results : Coverage across reference



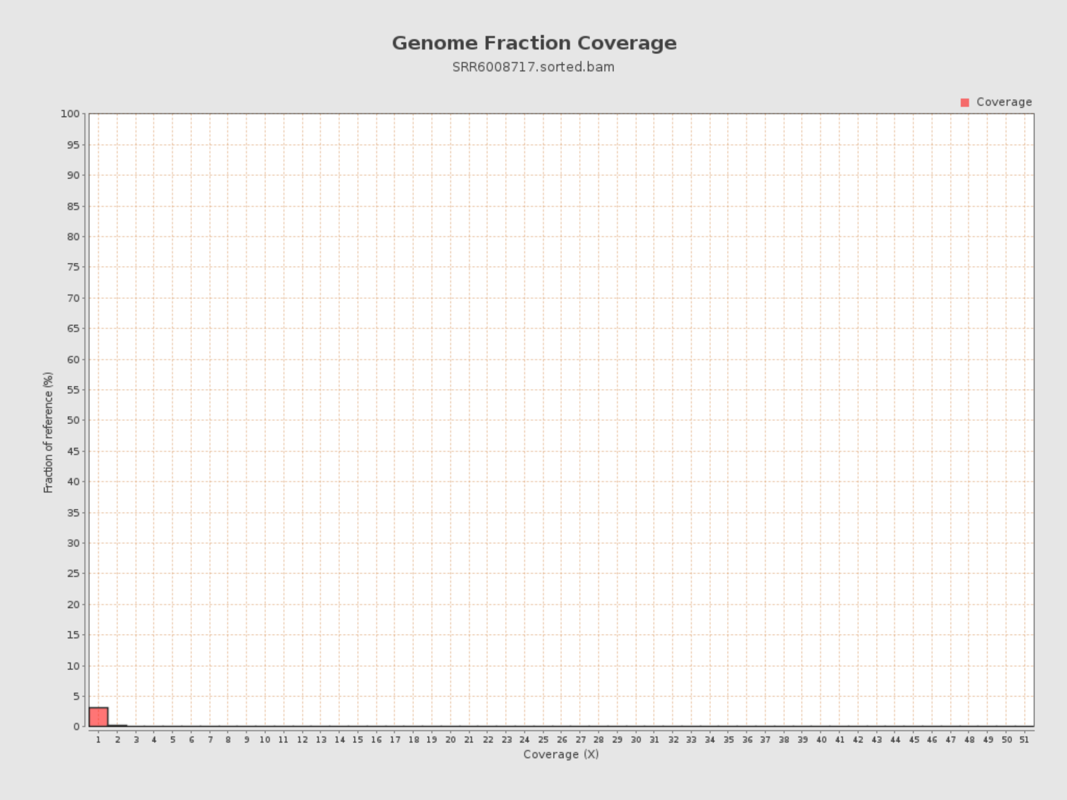
4. Results : Coverage Histogram



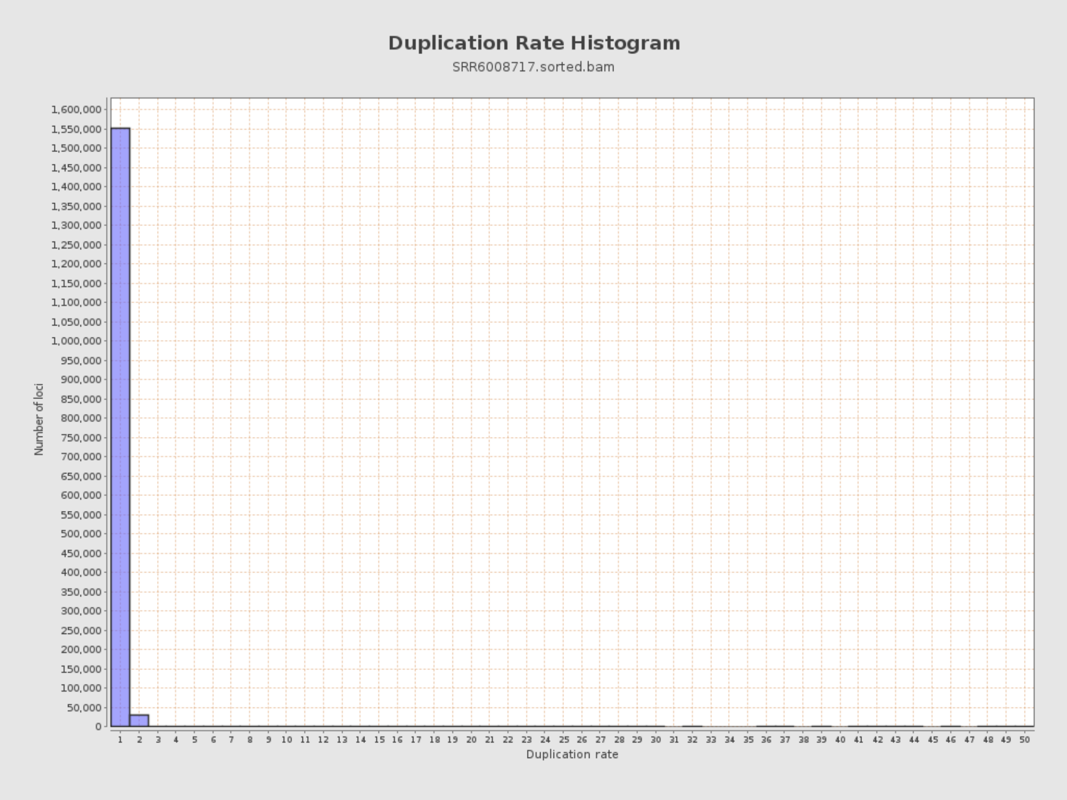
5. Results : Coverage Histogram (0-50X)



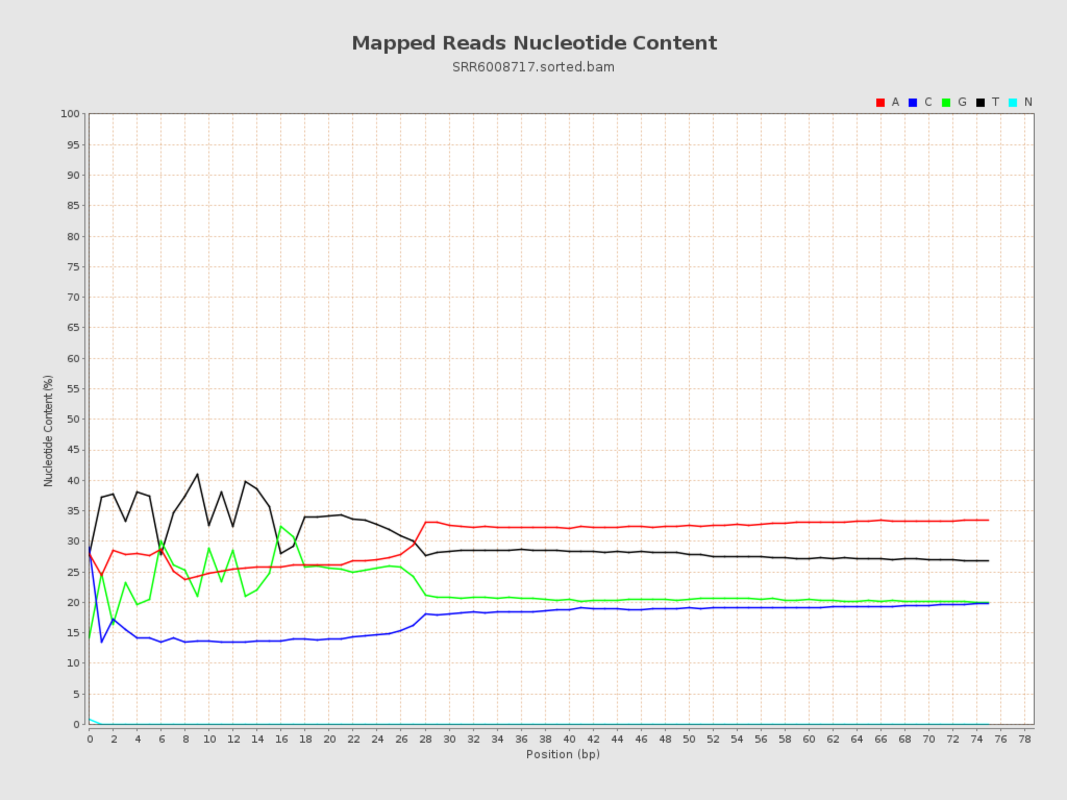
6. Results : Genome Fraction Coverage



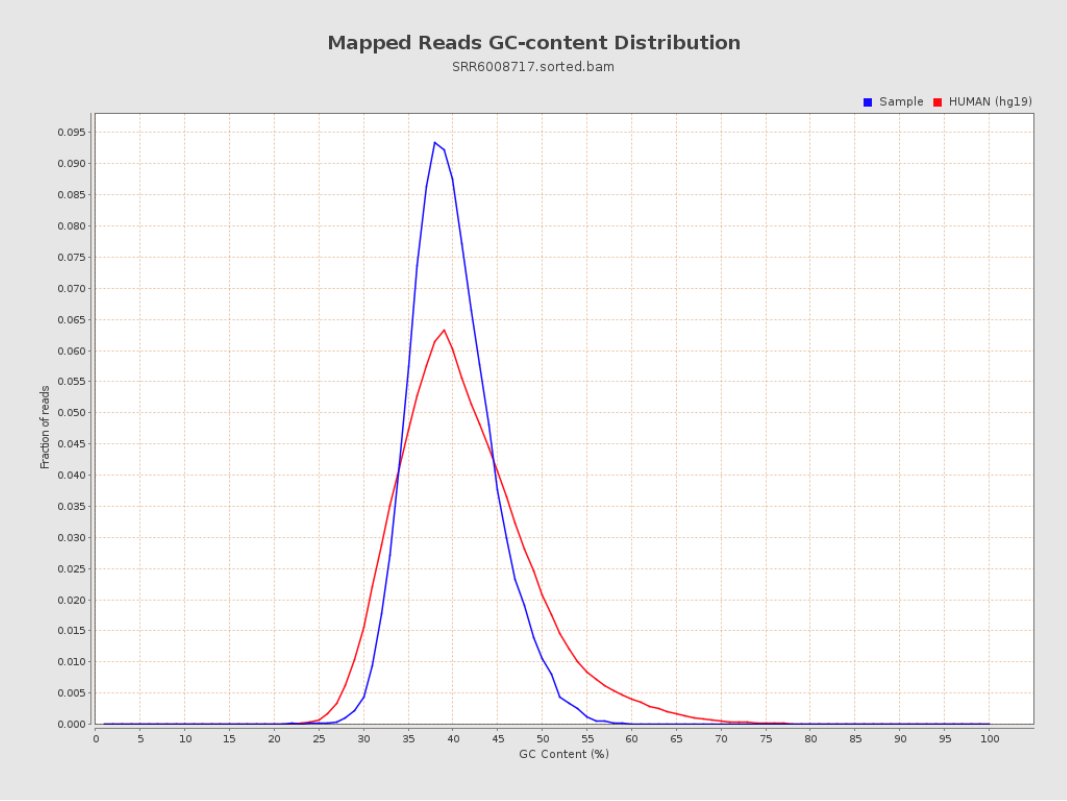
7. Results : Duplication Rate Histogram



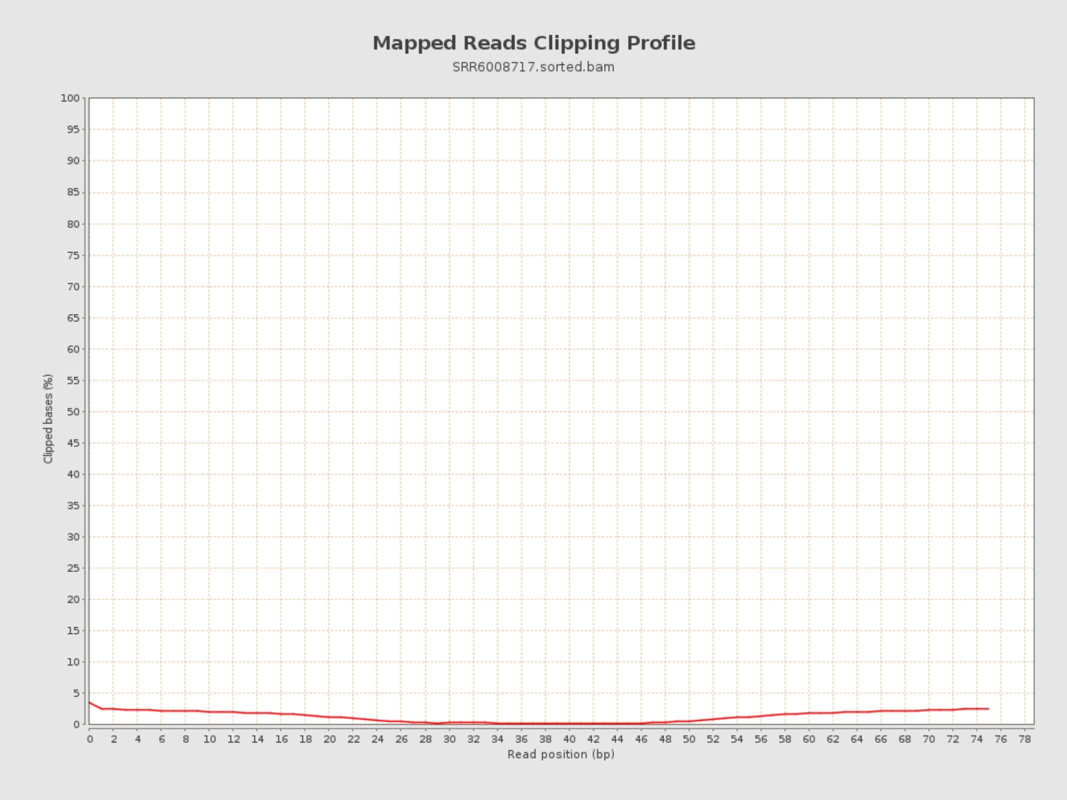
8. Results : Mapped Reads Nucleotide Content



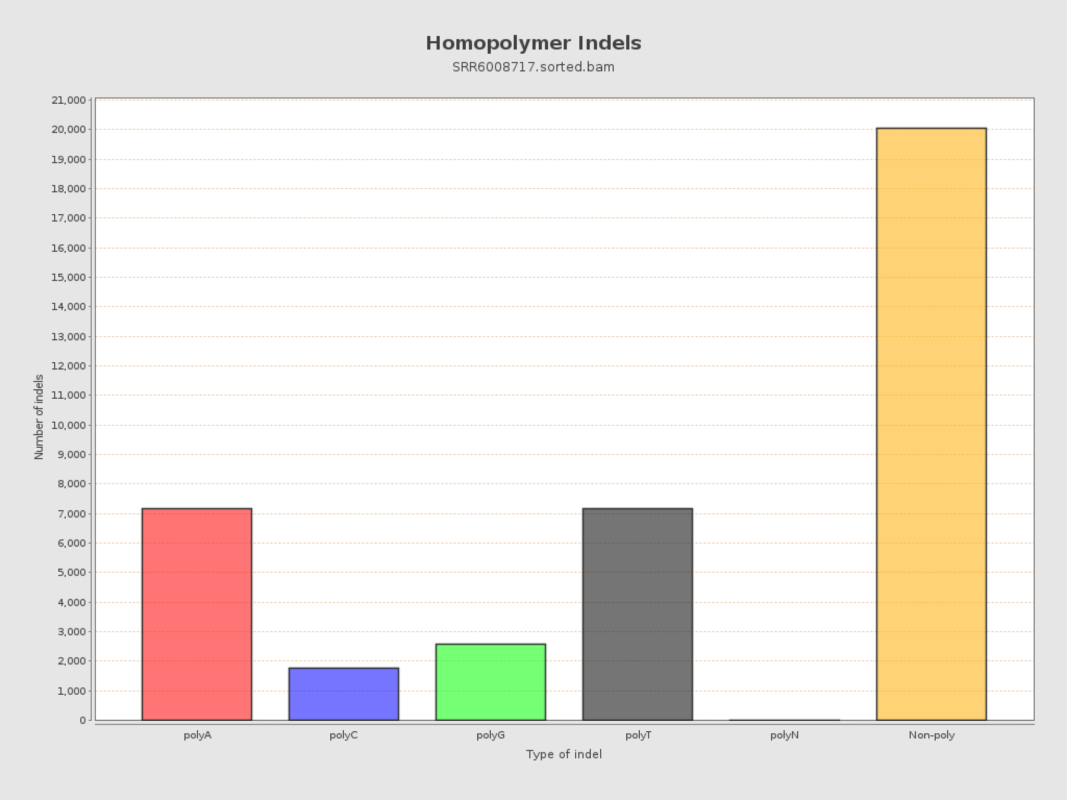
9. Results : Mapped Reads GC-content Distribution



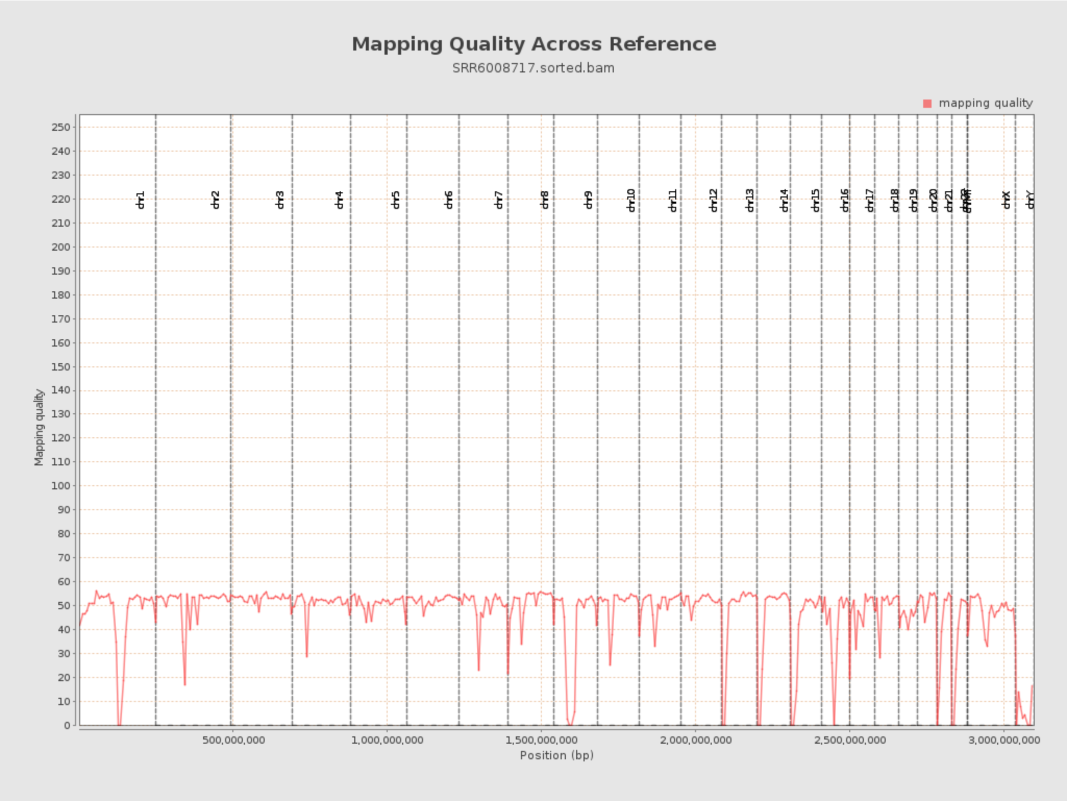
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram