Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 05:48:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008661.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_SRR6008661 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008661.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 05:48:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008661.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,649,981
Mapped reads	1,441,051 / 87.34%
Unmapped reads	208,930 / 12.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,613 / 0.76%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	93,443 / 5.66%
Duplication rate	5.43%
Clipped reads	728,779 / 44.17%

2.2. ACGT Content

Number/percentage of A's	25,107,406 / 26.82%
Number/percentage of C's	17,155,567 / 18.32%
Number/percentage of T's	29,705,717 / 31.73%
Number/percentage of G's	21,625,664 / 23.1%
Number/percentage of N's	36,242 / 0.04%
GC Percentage	41.42%

2.3. Coverage

Mean	0.0303

Standard Deviation	0.289

2.4. Mapping Quality

Mean Mapping Quality	44.65

2.5. Mismatches and indels

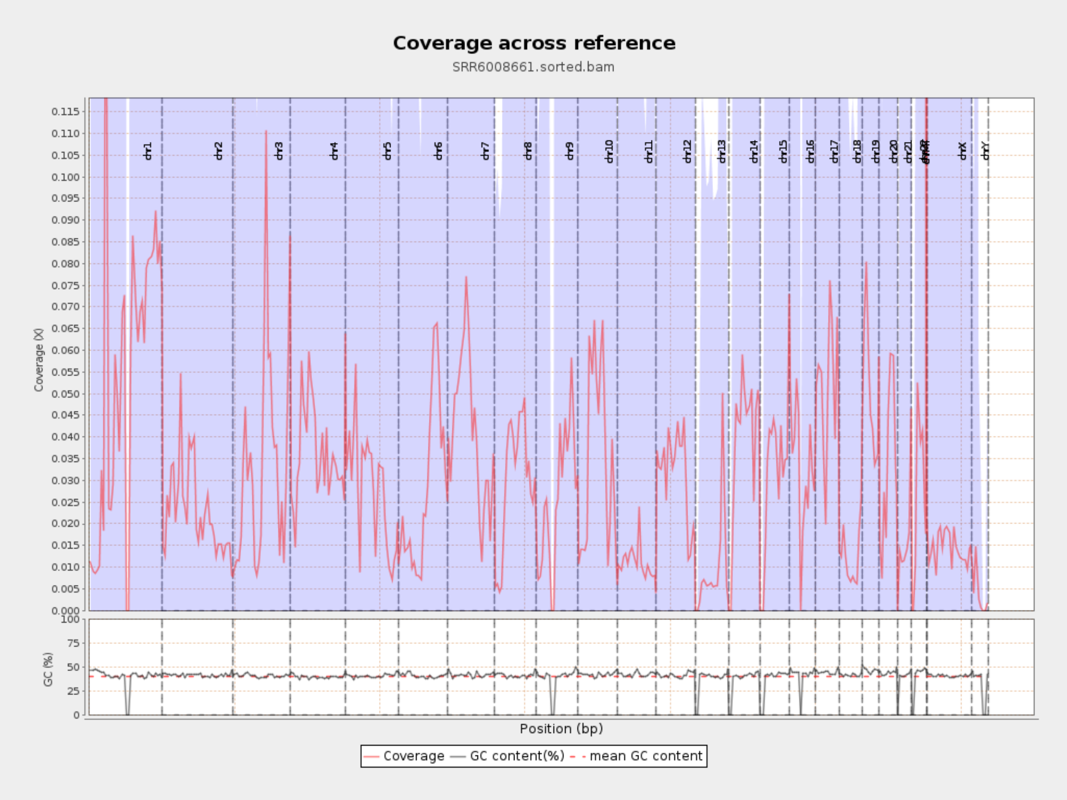
General error rate	0.83%
Mismatches	768,173
Insertions	6,850
Mapped reads with at least one insertion	0.47%
Deletions	28,093
Mapped reads with at least one deletion	1.93%
Homopolymer indels	46.51%

2.6. Chromosome stats

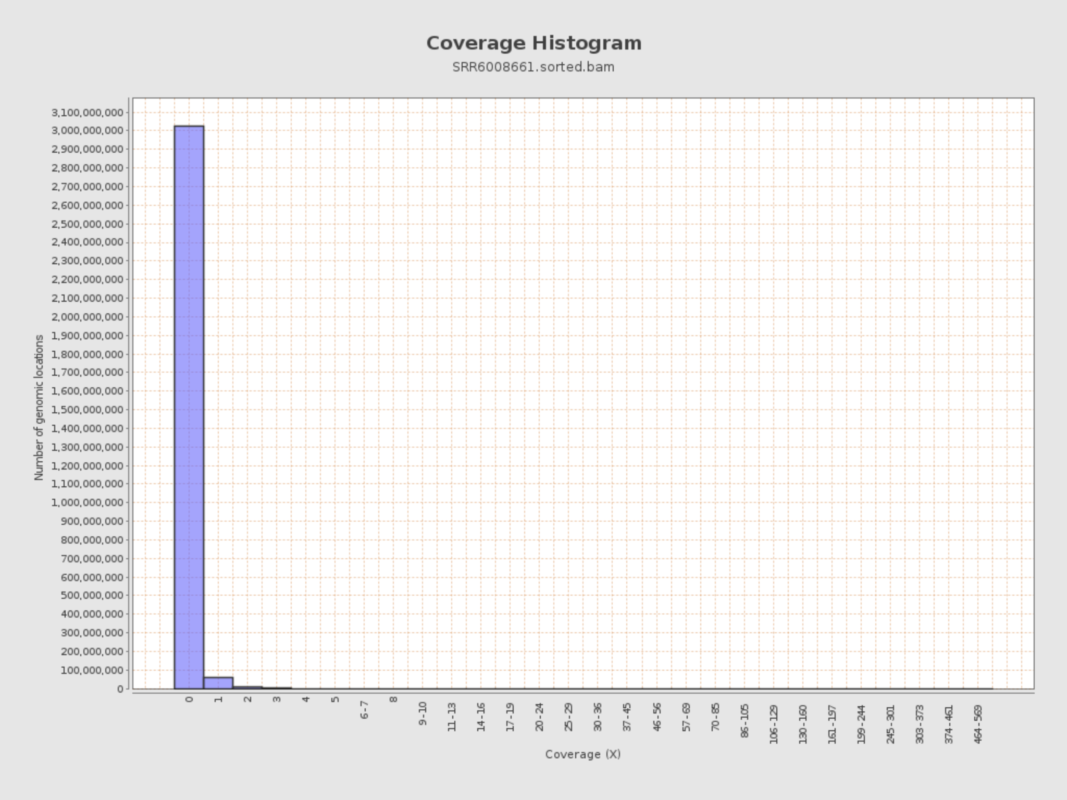
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13258155	0.0532	0.5619
chr2	243199373	5553775	0.0228	0.2787
chr3	198022430	6488643	0.0328	0.2238
chr4	191154276	6863340	0.0359	0.2434
chr5	180915260	5058128	0.028	0.2061
chr6	171115067	4706737	0.0275	0.2142
chr7	159138663	6662043	0.0419	0.3974

chr8	146364022	4347480	0.0297	0.3226
chr9	141213431	3646077	0.0258	0.2378
chr10	135534747	4836470	0.0357	0.2877
chr11	135006516	1501643	0.0111	0.1533
chr12	133851895	4294399	0.0321	0.223
chr13	115169878	1146118	0.01	0.1233
chr14	107349540	4165380	0.0388	0.248
chr15	102531392	3193352	0.0311	0.2185
chr16	90354753	2961013	0.0328	0.2298
chr17	81195210	4229927	0.0521	0.3007
chr18	78077248	940644	0.012	0.3057
chr19	59128983	3066949	0.0519	0.3964
chr20	63025520	2104271	0.0334	0.2285
chr21	48129895	758669	0.0158	0.1655
chr22	51304566	1325293	0.0258	0.1948
chrMT	16571	67918	4.0986	3.6918
chrX	155270560	2271765	0.0146	0.1559
chrY	59373566	229560	0.0039	0.1576

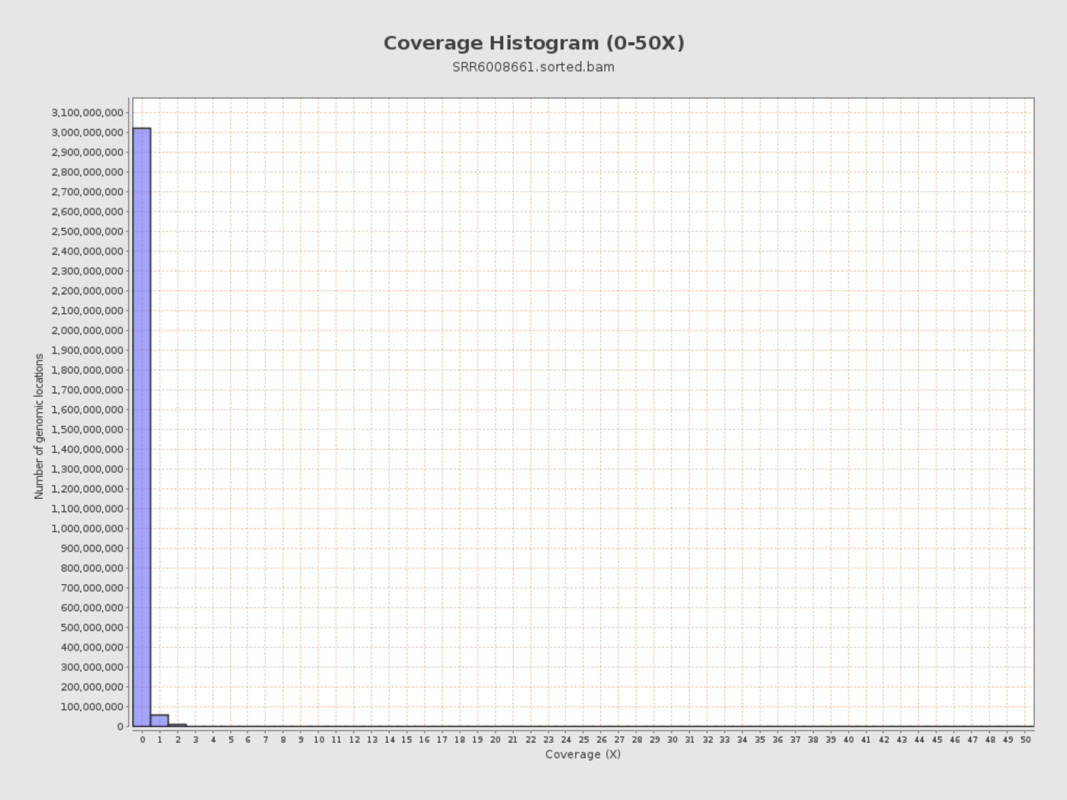
3. Results : Coverage across reference



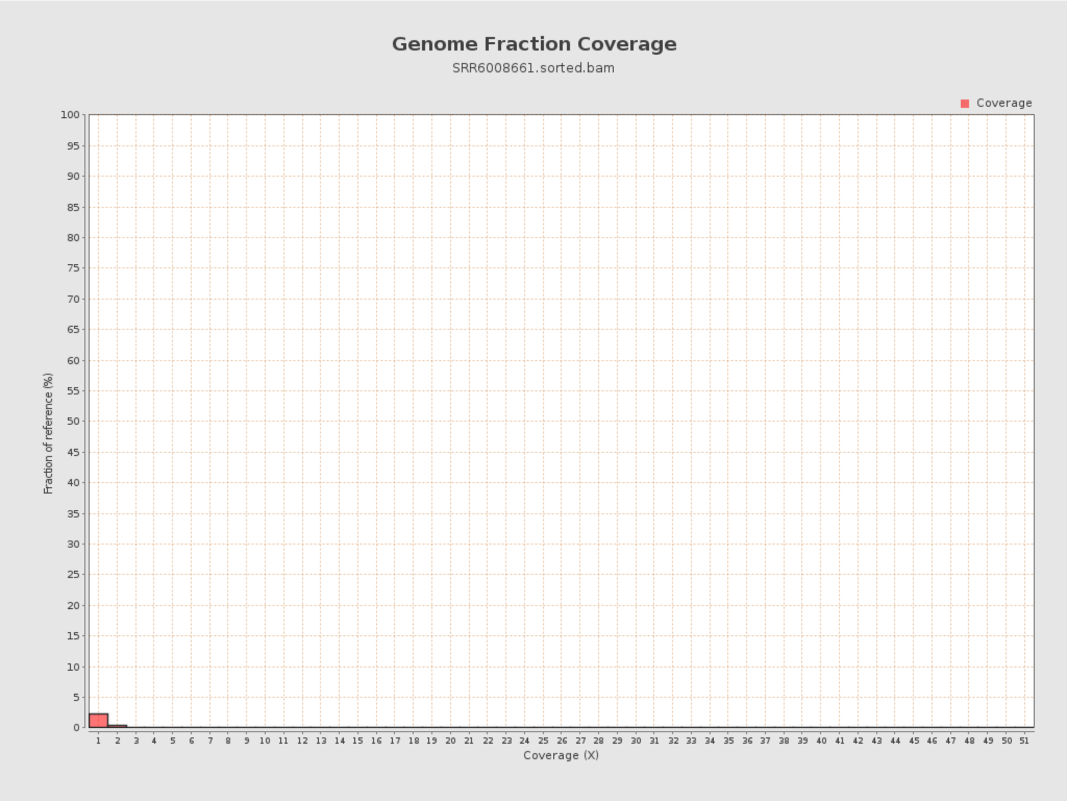
4. Results : Coverage Histogram



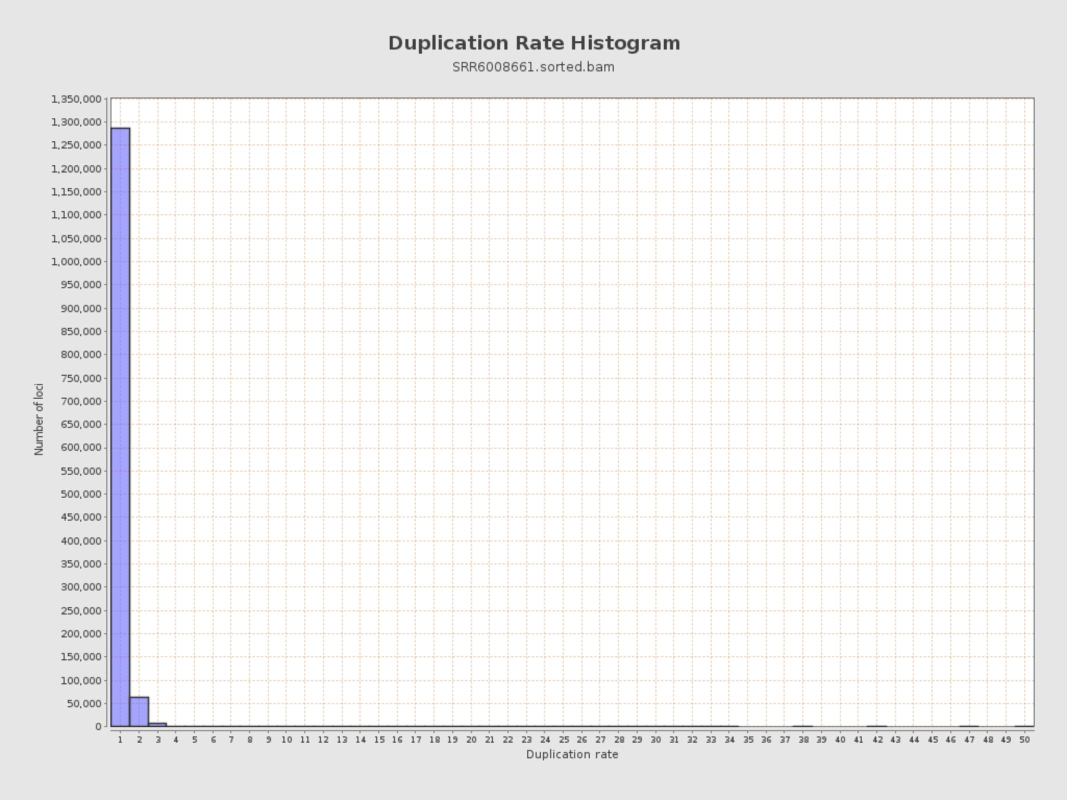
5. Results : Coverage Histogram (0-50X)



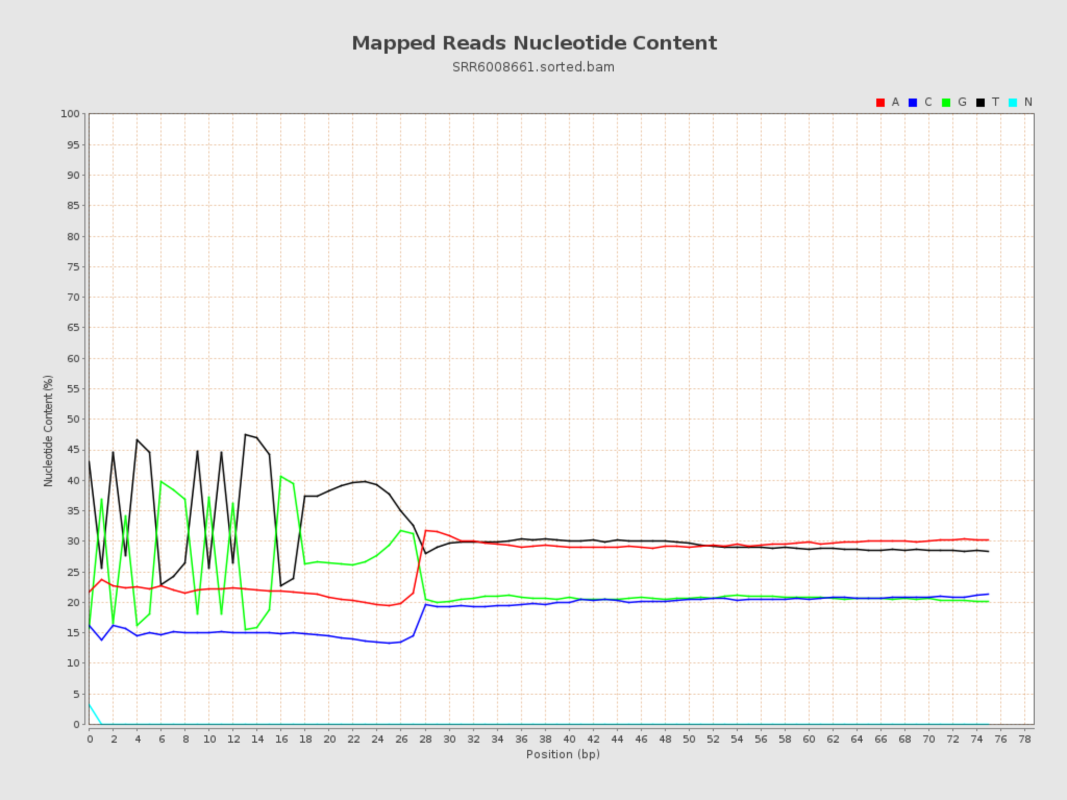
6. Results : Genome Fraction Coverage



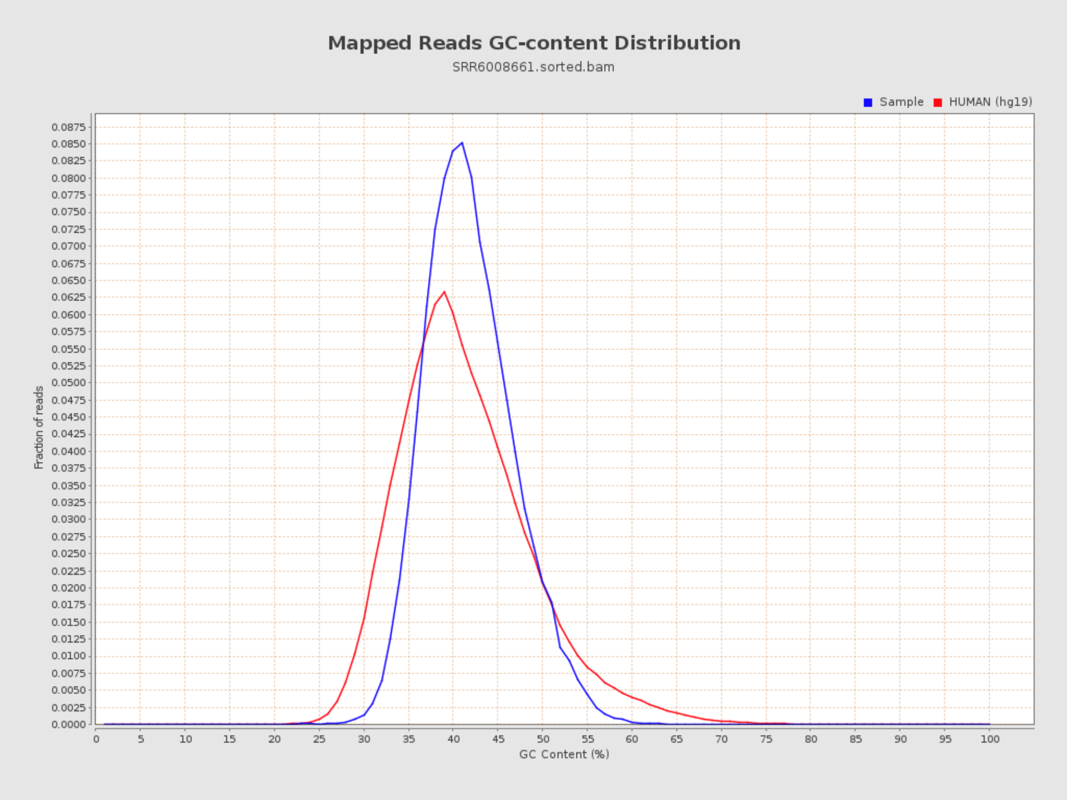
7. Results : Duplication Rate Histogram



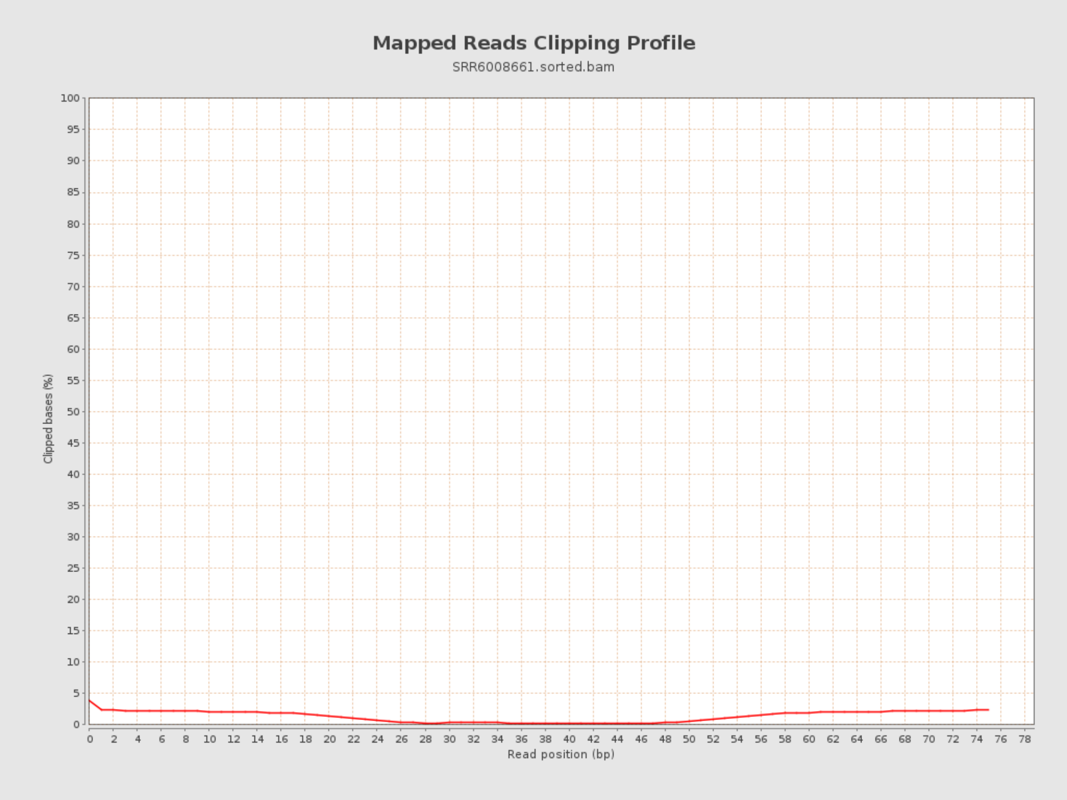
8. Results : Mapped Reads Nucleotide Content



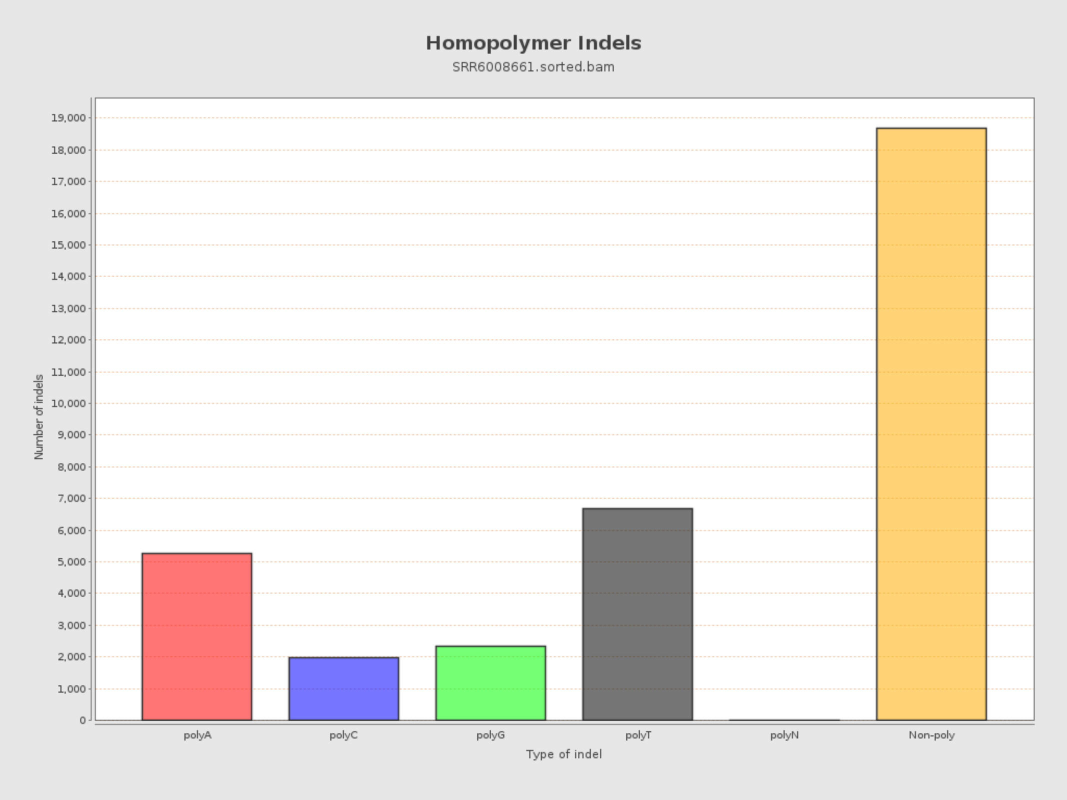
9. Results : Mapped Reads GC-content Distribution



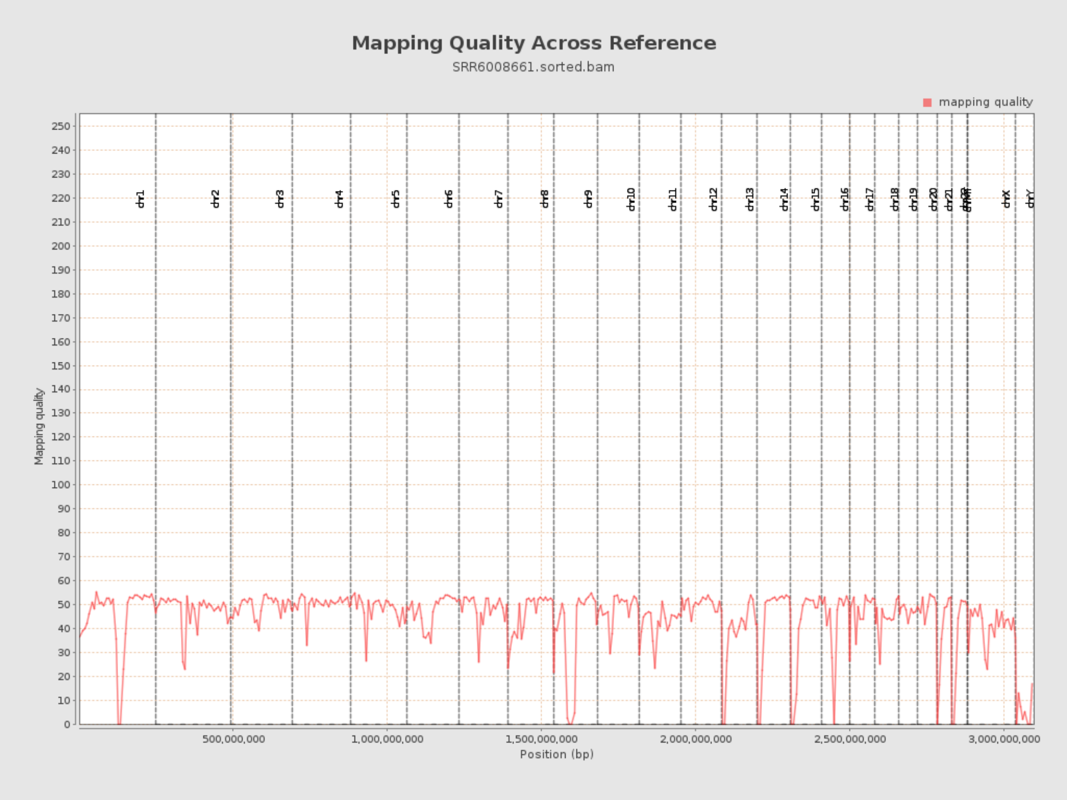
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram