Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 11:02:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068115.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_SRR6068115 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068115.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 11:02:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068115.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,562,668
Mapped reads	1,189,686 / 76.13%
Unmapped reads	372,982 / 23.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,012 / 0.7%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	229,941 / 14.71%
Duplication rate	13.17%
Clipped reads	448,360 / 28.69%

2.2. ACGT Content

Number/percentage of A's	22,985,437 / 28.42%
Number/percentage of C's	14,748,401 / 18.23%
Number/percentage of T's	26,029,866 / 32.18%
Number/percentage of G's	17,033,798 / 21.06%
Number/percentage of N's	87,946 / 0.11%
GC Percentage	39.29%

2.3. Coverage

Mean	0.0261

Standard Deviation	0.5138

2.4. Mapping Quality

Mean Mapping Quality	47.03

2.5. Mismatches and indels

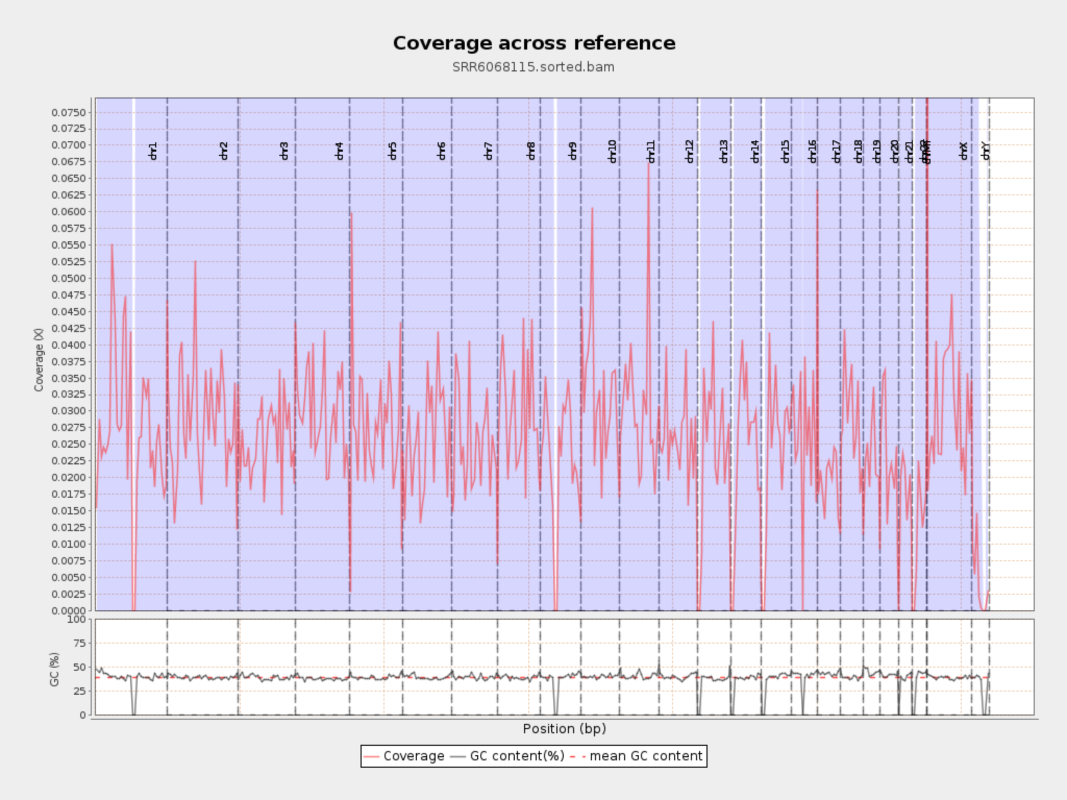
General error rate	0.88%
Mismatches	701,587
Insertions	6,278
Mapped reads with at least one insertion	0.52%
Deletions	19,061
Mapped reads with at least one deletion	1.58%
Homopolymer indels	47.72%

2.6. Chromosome stats

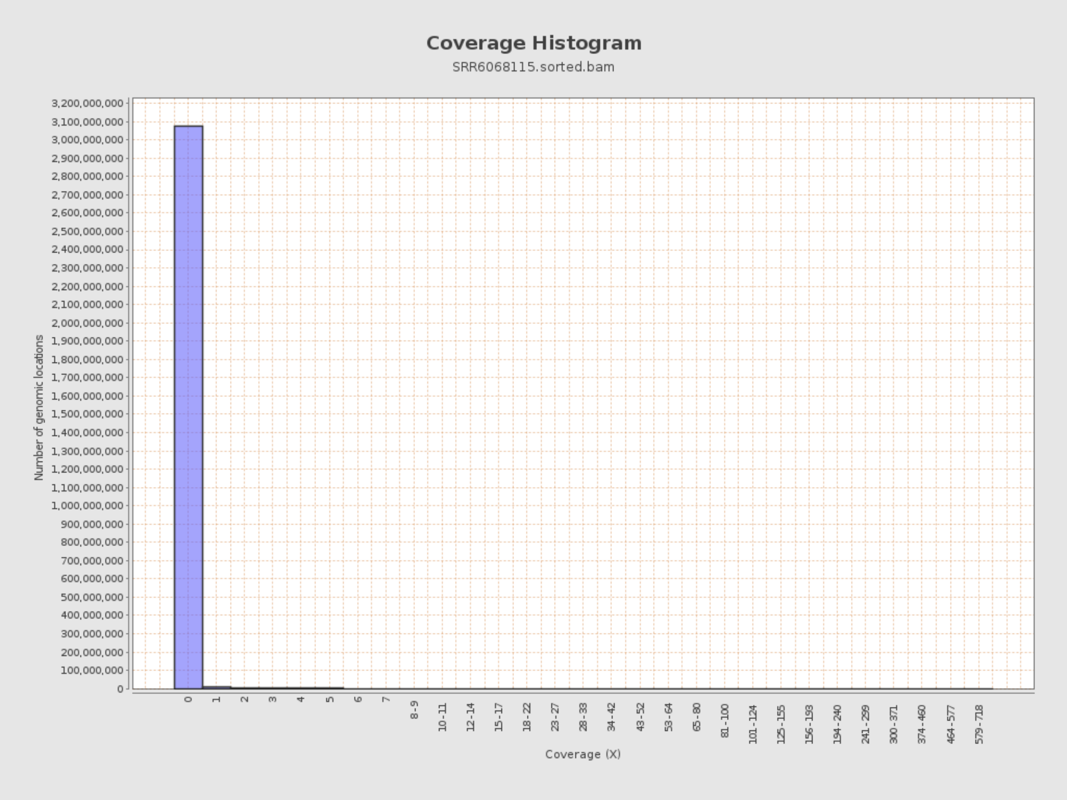
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6660166	0.0267	0.7046
chr2	243199373	6953663	0.0286	0.5267
chr3	198022430	5051457	0.0255	0.4611
chr4	191154276	5751841	0.0301	0.5189
chr5	180915260	5242446	0.029	0.4989
chr6	171115067	4413375	0.0258	0.479
chr7	159138663	3973273	0.025	0.4776

chr8	146364022	4363877	0.0298	0.5597
chr9	141213431	3208126	0.0227	0.4621
chr10	135534747	4448472	0.0328	0.5985
chr11	135006516	4129832	0.0306	0.5361
chr12	133851895	3512914	0.0262	0.4651
chr13	115169878	2708605	0.0235	0.4607
chr14	107349540	2564846	0.0239	0.4755
chr15	102531392	2437743	0.0238	0.4616
chr16	90354753	2343812	0.0259	0.474
chr17	81195210	1559256	0.0192	0.3703
chr18	78077248	2282070	0.0292	0.6691
chr19	59128983	1354929	0.0229	0.4776
chr20	63025520	1494794	0.0237	0.4558
chr21	48129895	842932	0.0175	0.3538
chr22	51304566	642072	0.0125	0.3054
chrMT	16571	14605	0.8814	2.1932
chrX	155270560	4712687	0.0304	0.5281
chrY	59373566	249539	0.0042	0.1637

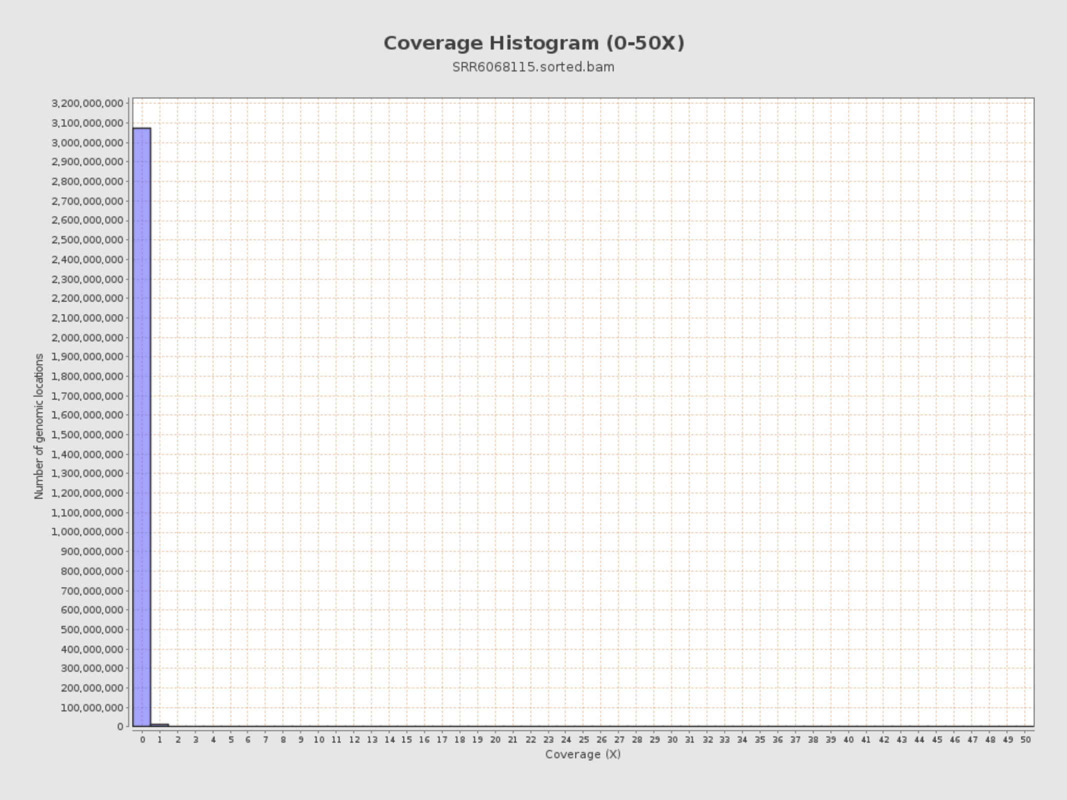
3. Results : Coverage across reference



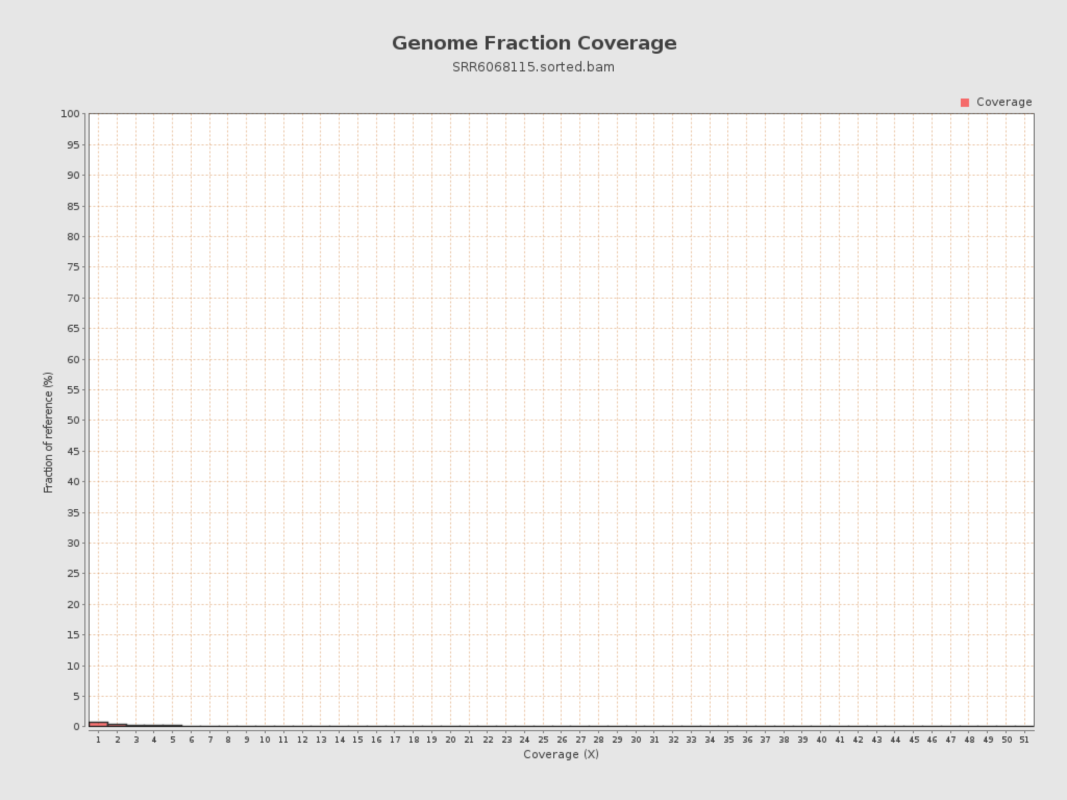
4. Results : Coverage Histogram



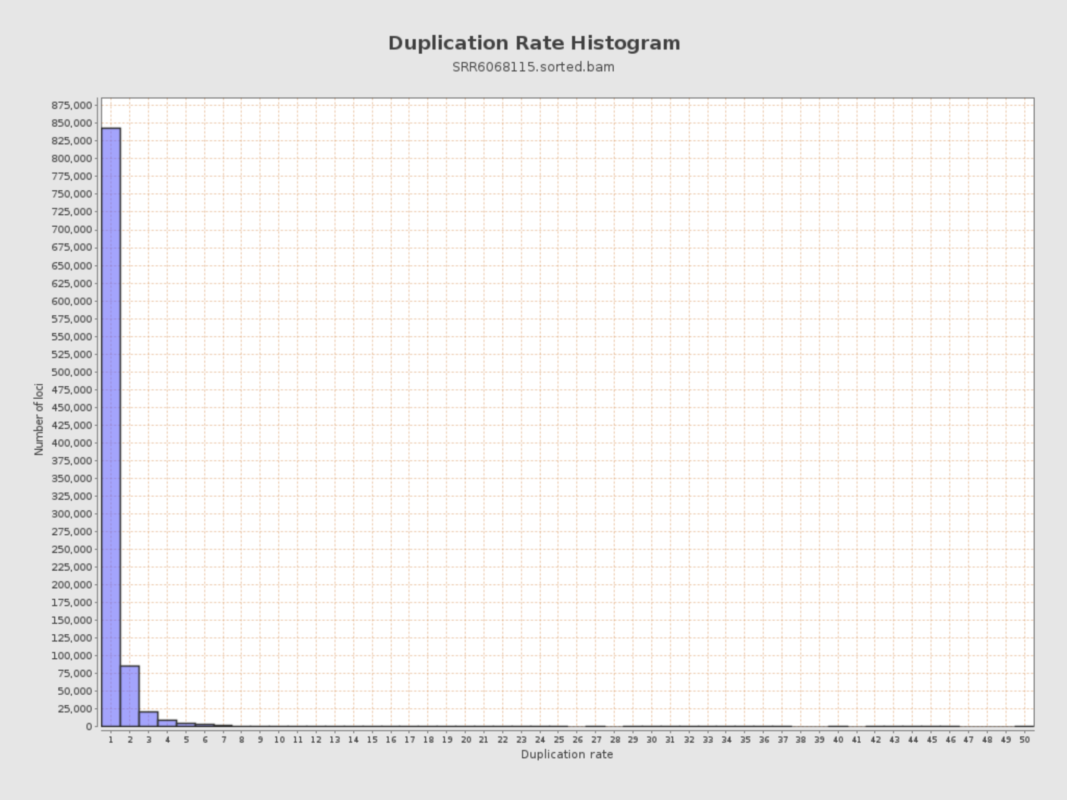
5. Results : Coverage Histogram (0-50X)



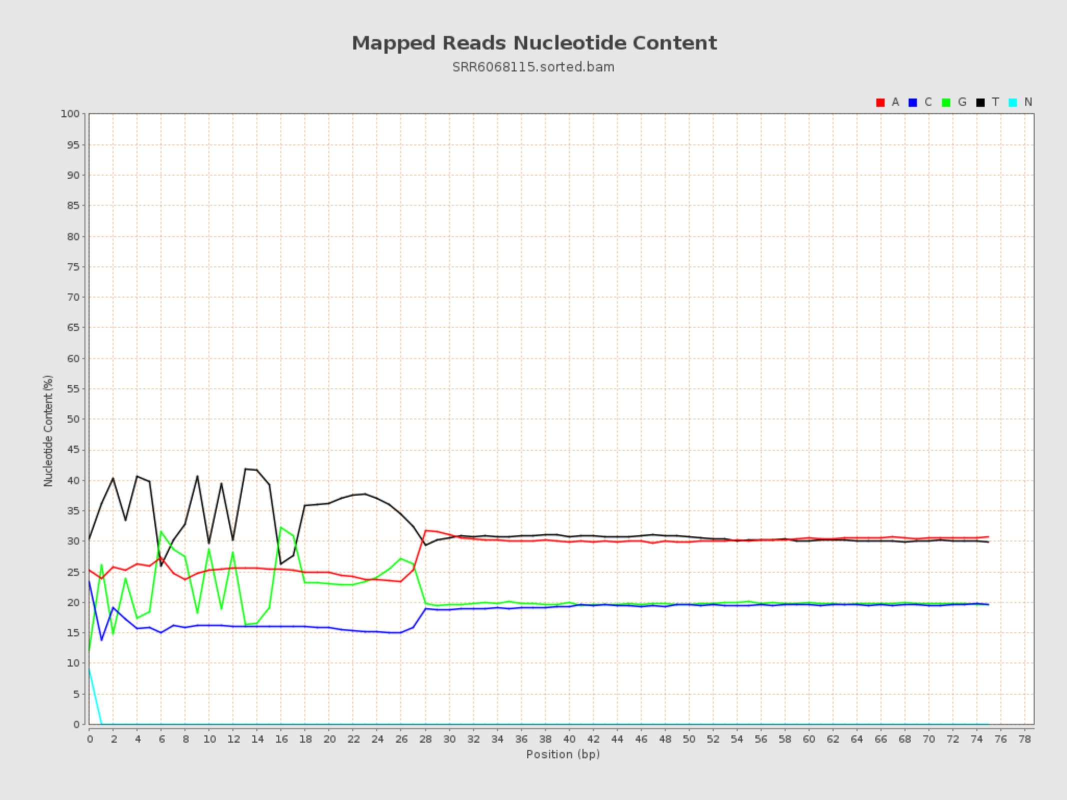
6. Results : Genome Fraction Coverage



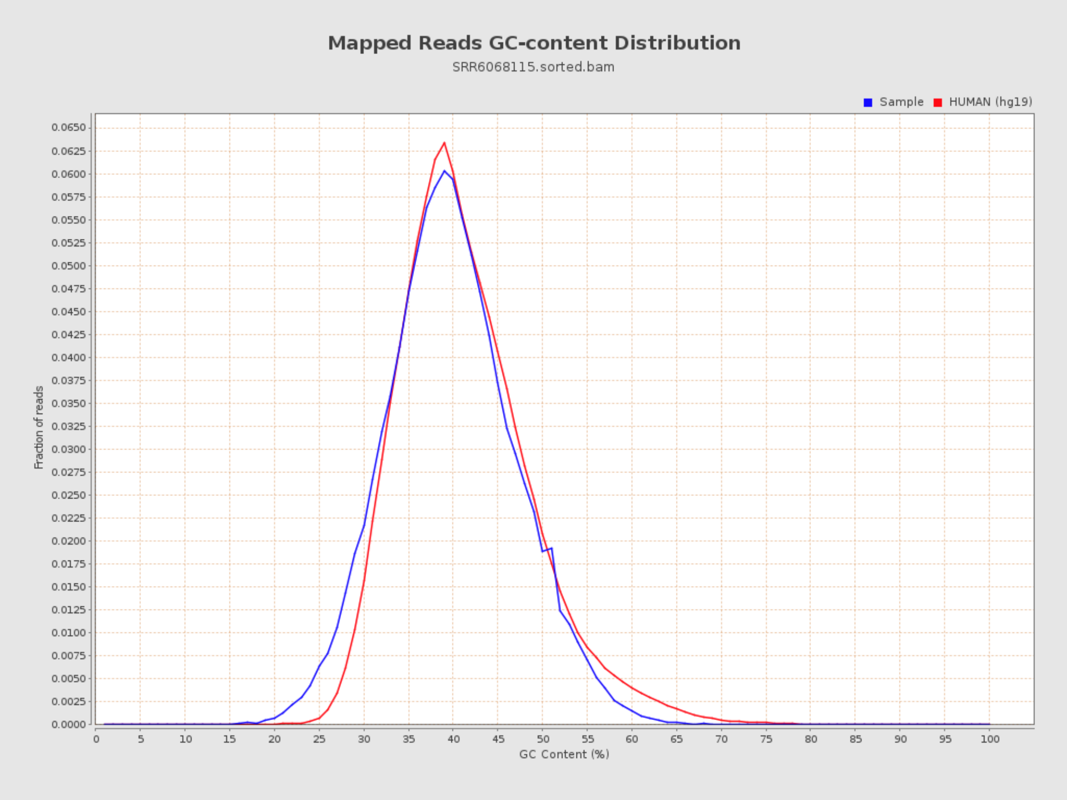
7. Results : Duplication Rate Histogram



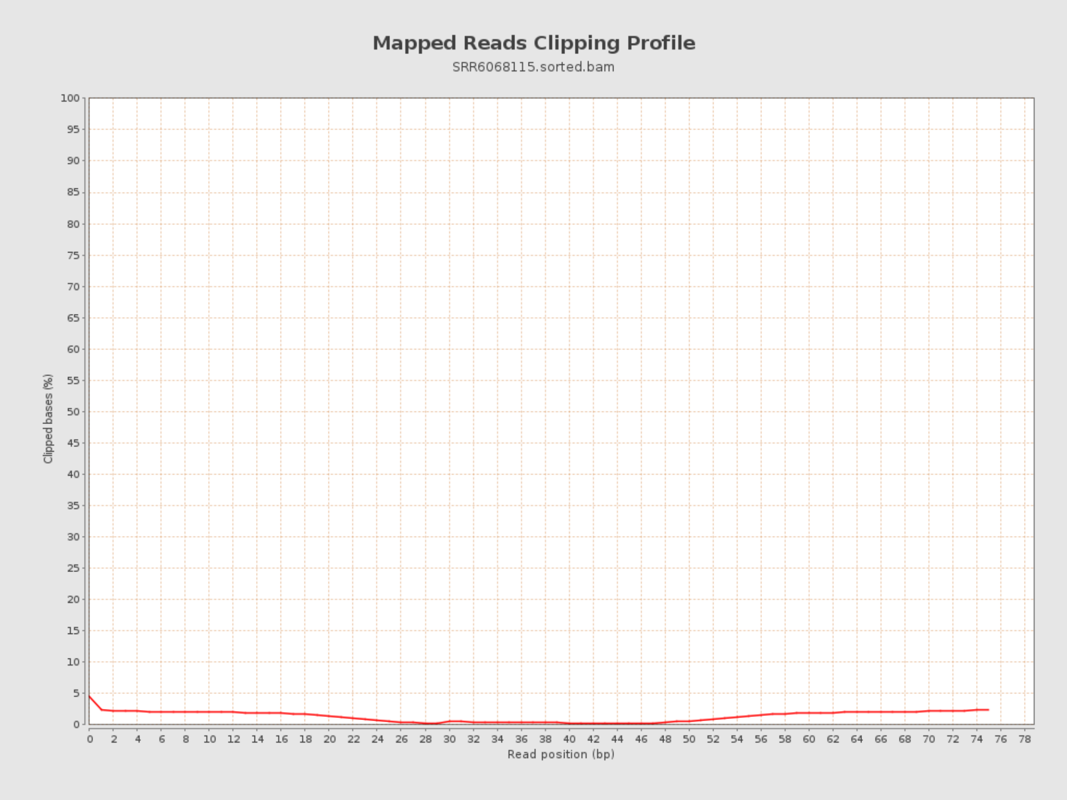
8. Results : Mapped Reads Nucleotide Content



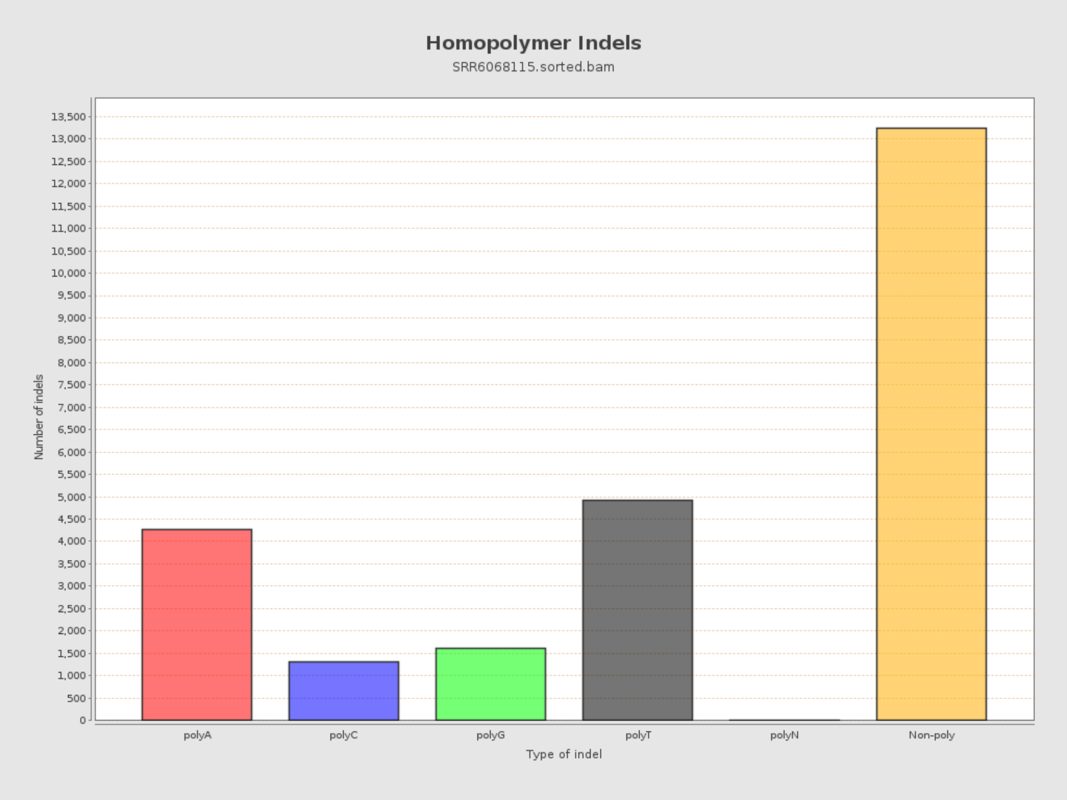
9. Results : Mapped Reads GC-content Distribution



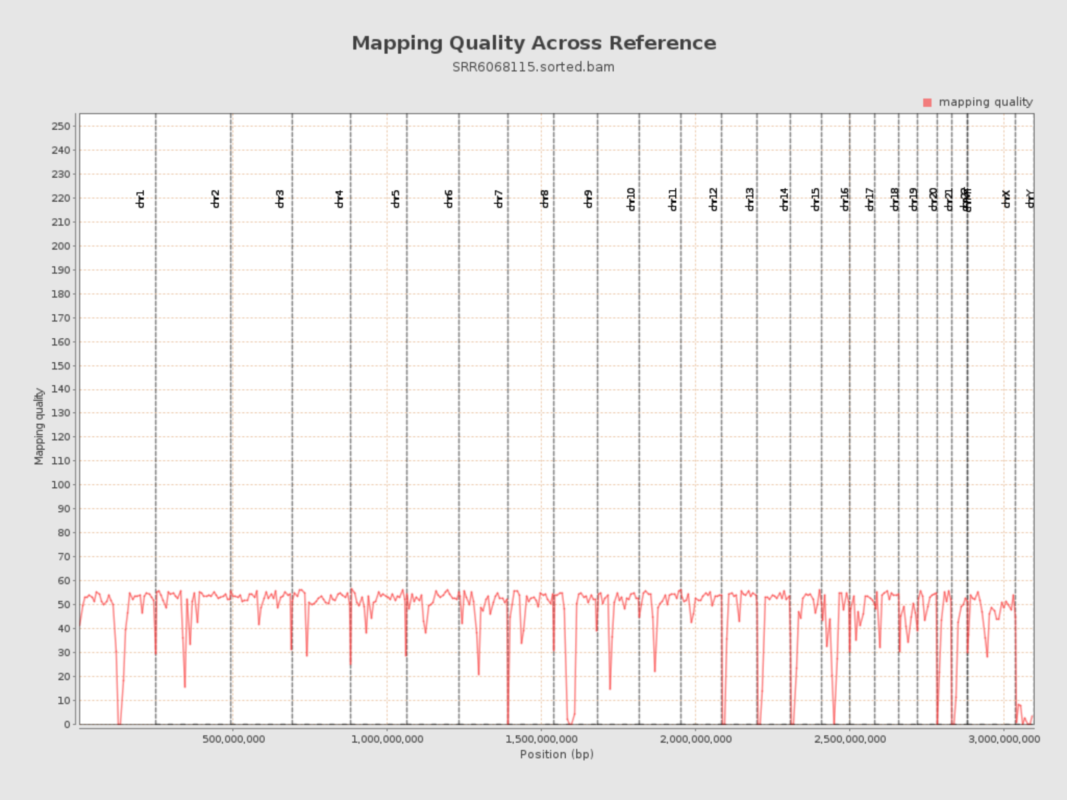
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram