Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 11:08:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068117.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_SRR6068117 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068117.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 11:08:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068117.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,320,545
Mapped reads	2,039,655 / 87.9%
Unmapped reads	280,890 / 12.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,212 / 0.96%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	149,352 / 6.44%
Duplication rate	5.94%
Clipped reads	886,677 / 38.21%

2.2. ACGT Content

Number/percentage of A's	38,704,873 / 28.36%
Number/percentage of C's	24,373,679 / 17.86%
Number/percentage of T's	44,179,885 / 32.37%
Number/percentage of G's	29,080,199 / 21.31%
Number/percentage of N's	145,993 / 0.11%
GC Percentage	39.16%

2.3. Coverage

Mean	0.0441

Standard Deviation	0.3966

2.4. Mapping Quality

Mean Mapping Quality	37.08

2.5. Mismatches and indels

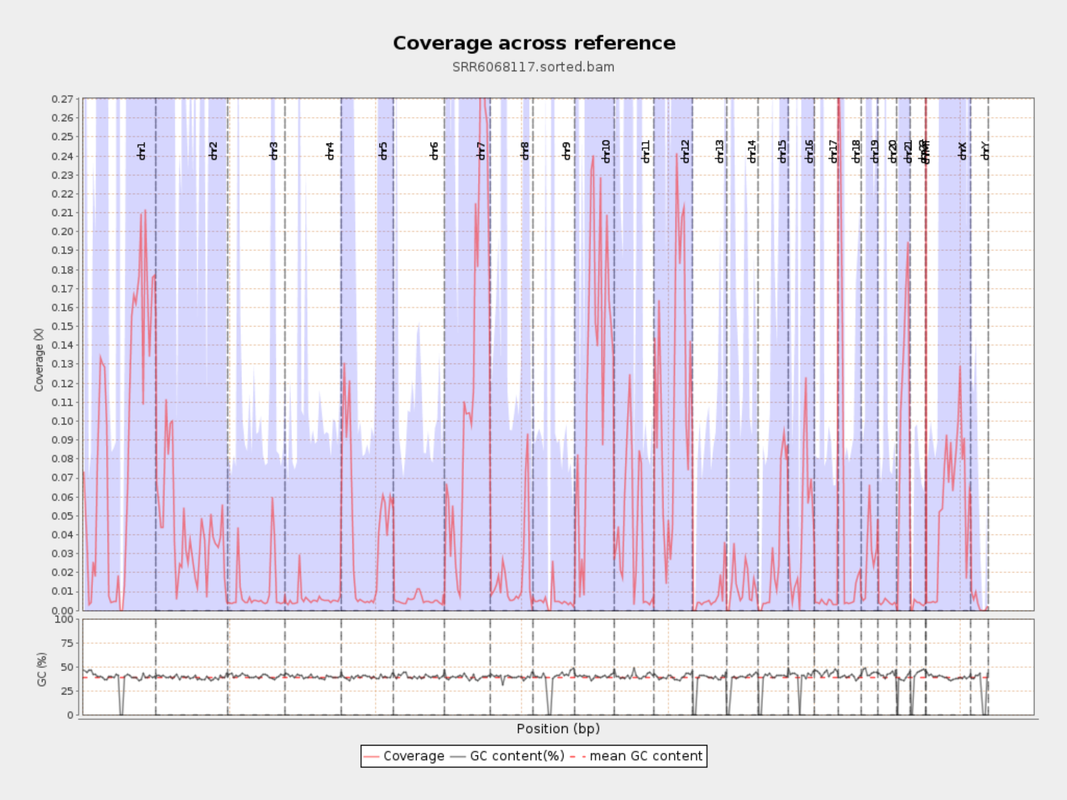
General error rate	0.91%
Mismatches	1,227,462
Insertions	10,083
Mapped reads with at least one insertion	0.49%
Deletions	44,833
Mapped reads with at least one deletion	2.17%
Homopolymer indels	45.61%

2.6. Chromosome stats

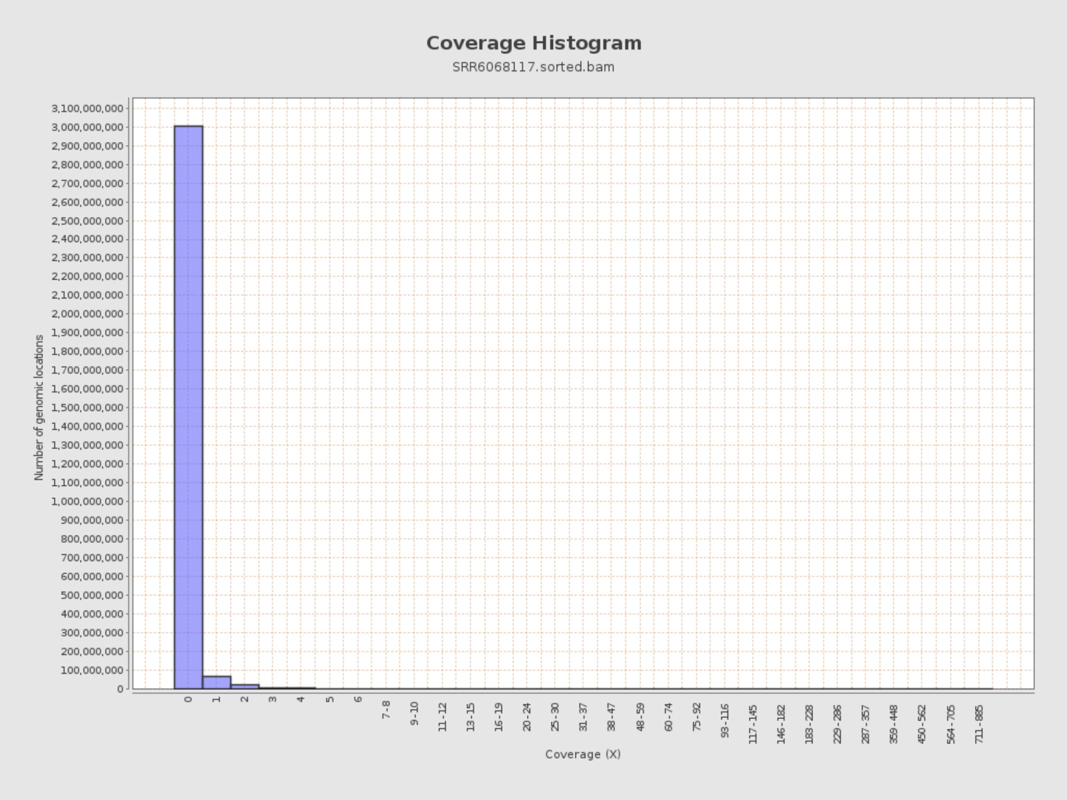
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22008439	0.0883	0.4586
chr2	243199373	10156115	0.0418	0.4956
chr3	198022430	2004961	0.0101	0.1298
chr4	191154276	1185897	0.0062	0.1232
chr5	180915260	7507125	0.0415	0.2756
chr6	171115067	954511	0.0056	0.1136
chr7	159138663	20001445	0.1257	0.5414

chr8	146364022	2852136	0.0195	0.5195
chr9	141213431	740609	0.0052	0.2325
chr10	135534747	17824167	0.1315	0.6076
chr11	135006516	5475577	0.0406	0.736
chr12	133851895	15537725	0.1161	0.4677
chr13	115169878	876766	0.0076	0.1145
chr14	107349540	1361917	0.0127	0.165
chr15	102531392	3001373	0.0293	0.2271
chr16	90354753	3919720	0.0434	0.2834
chr17	81195210	342211	0.0042	0.2444
chr18	78077248	4667080	0.0598	0.6773
chr19	59128983	1702387	0.0288	0.3535
chr20	63025520	268178	0.0043	0.139
chr21	48129895	5233629	0.1087	0.4682
chr22	51304566	164666	0.0032	0.069
chrMT	16571	5415	0.3268	0.7464
chrX	155270560	8541124	0.055	0.3904
chrY	59373566	224761	0.0038	0.0794

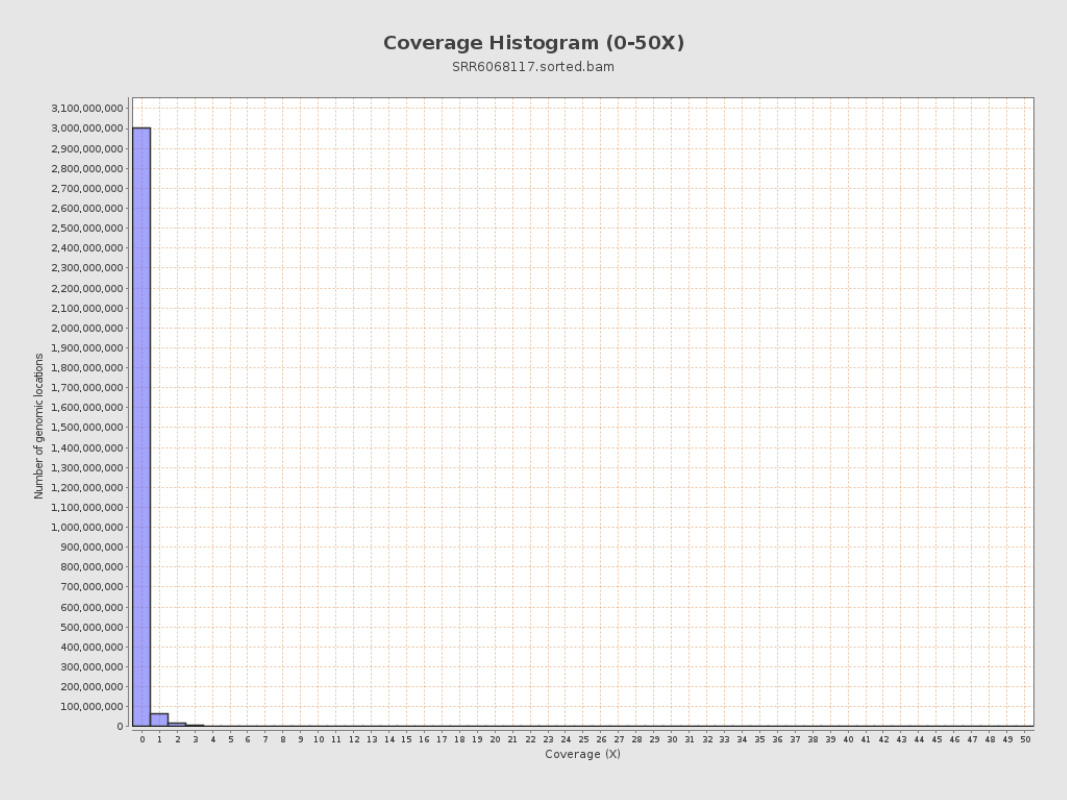
3. Results : Coverage across reference



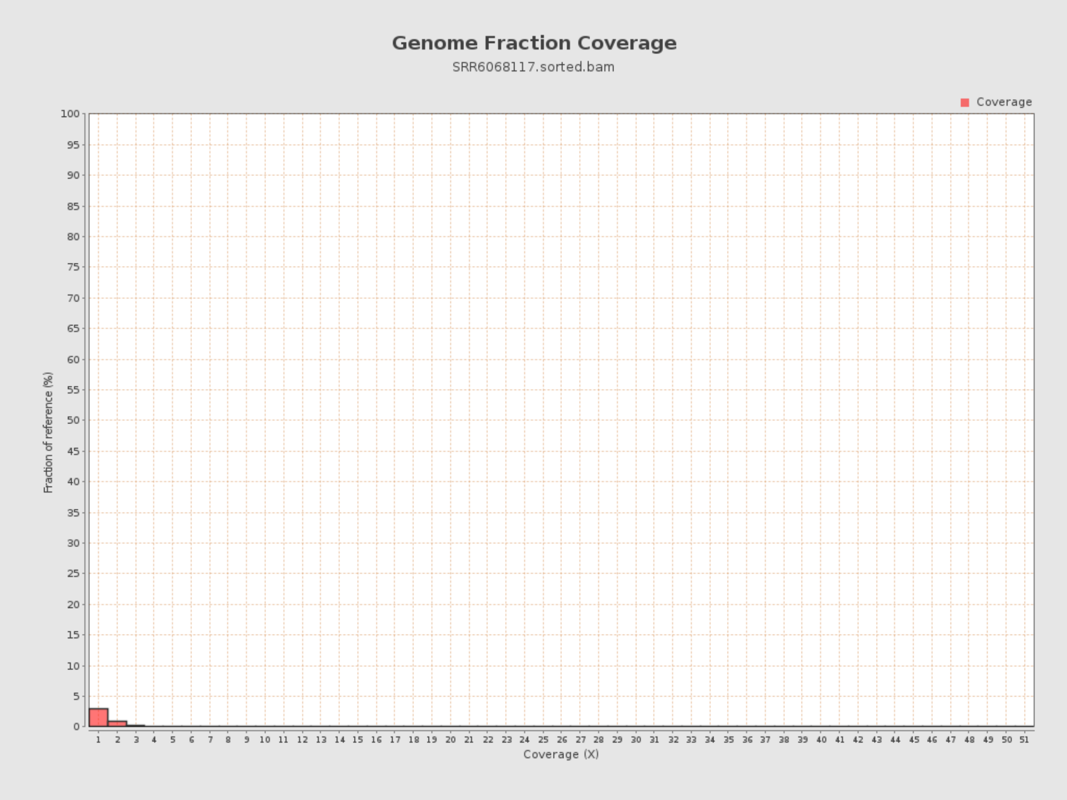
4. Results : Coverage Histogram



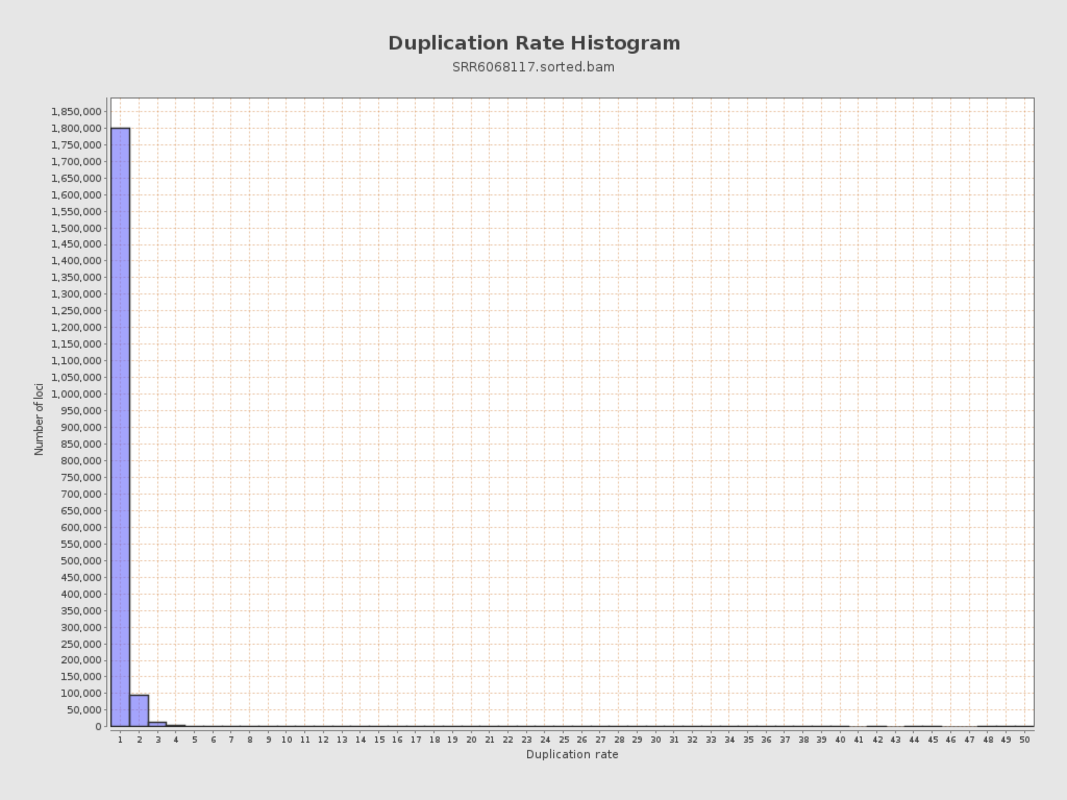
5. Results : Coverage Histogram (0-50X)



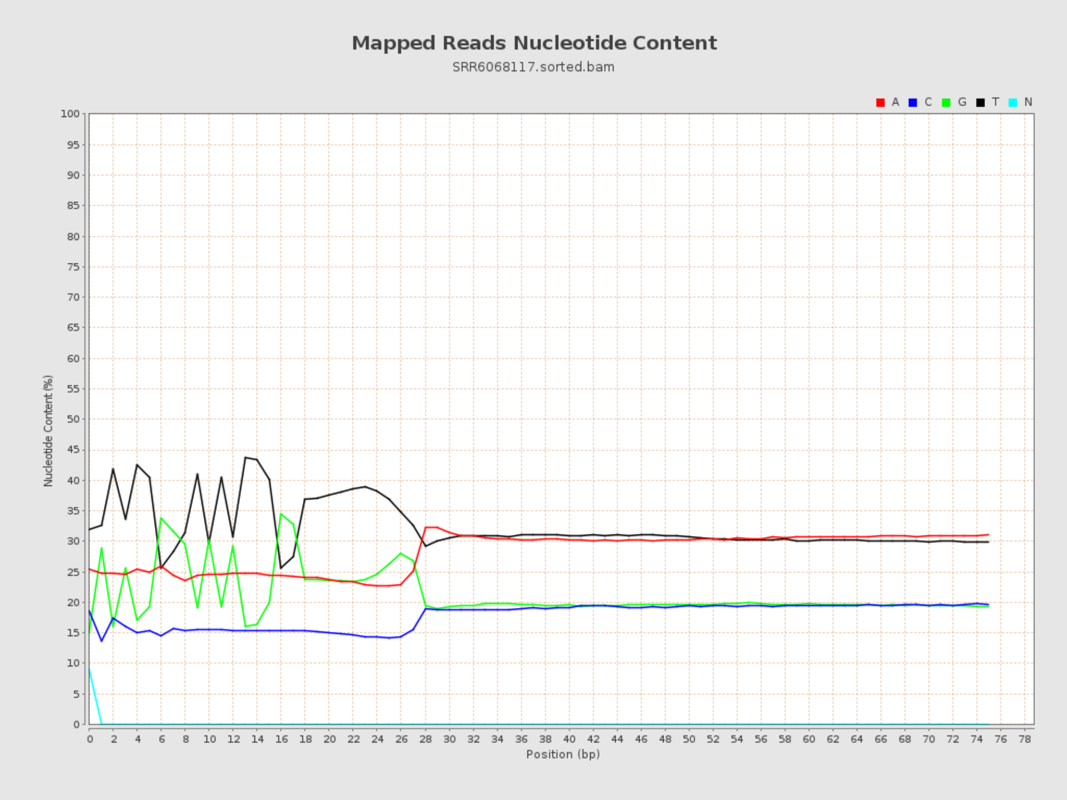
6. Results : Genome Fraction Coverage



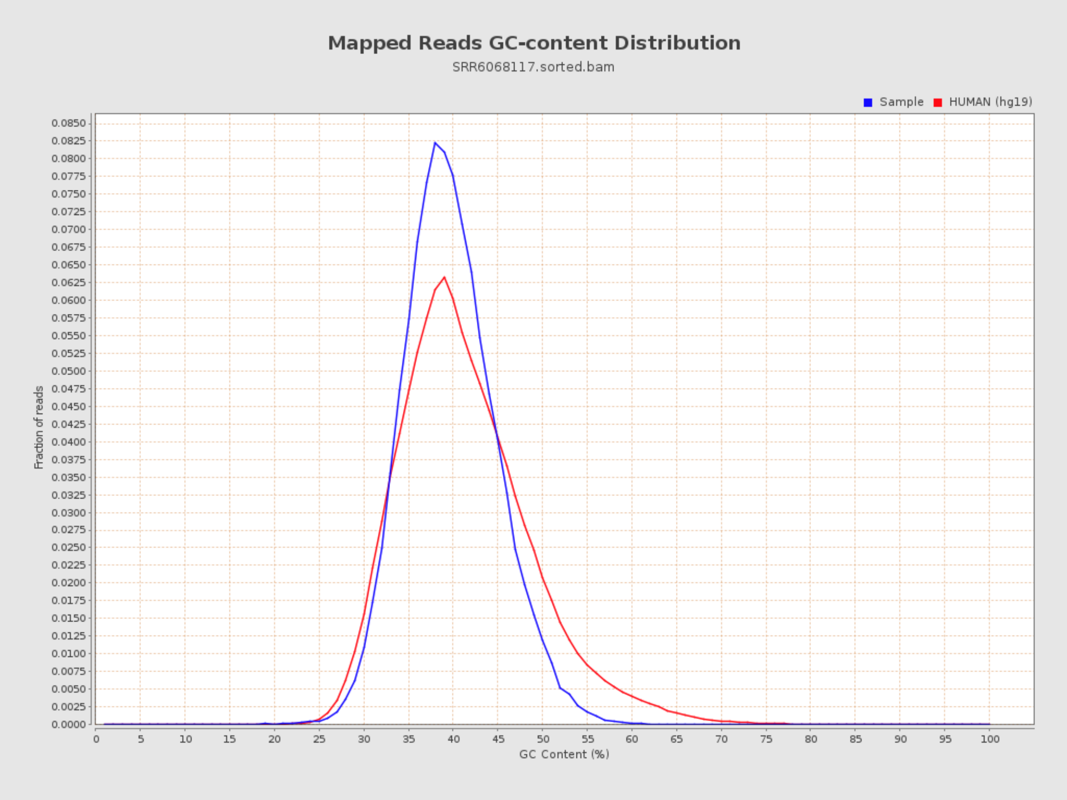
7. Results : Duplication Rate Histogram



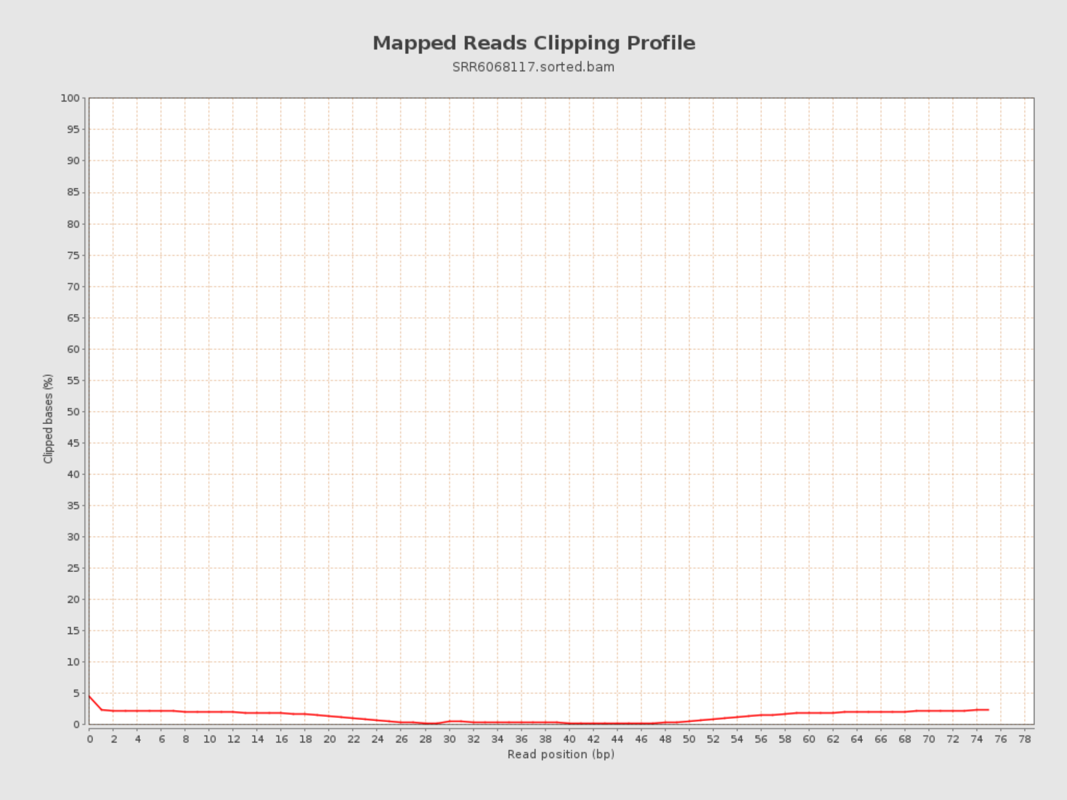
8. Results : Mapped Reads Nucleotide Content



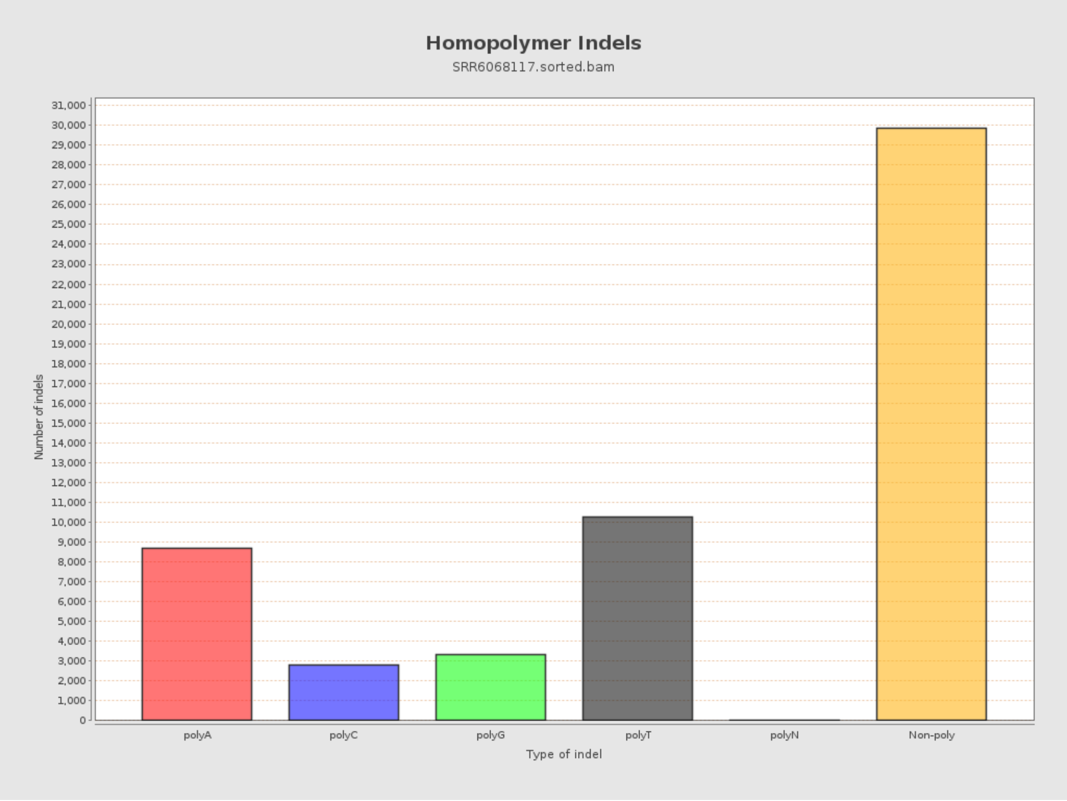
9. Results : Mapped Reads GC-content Distribution



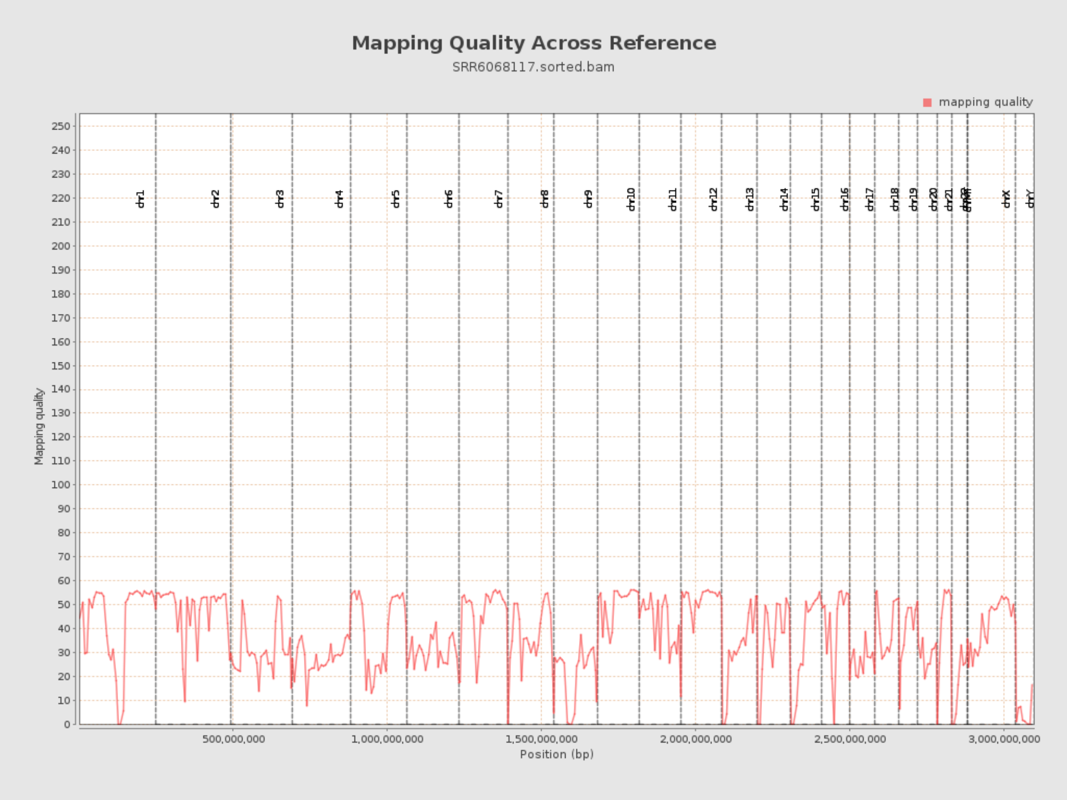
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram