Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 09:37:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068092.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_SRR6068092 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068092.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 09:37:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068092.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,313,573
Mapped reads	2,051,645 / 88.68%
Unmapped reads	261,928 / 11.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,012 / 0.95%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	146,082 / 6.31%
Duplication rate	5.73%
Clipped reads	1,083,838 / 46.85%

2.2. ACGT Content

Number/percentage of A's	37,148,348 / 27.85%
Number/percentage of C's	24,865,718 / 18.64%
Number/percentage of T's	41,914,470 / 31.42%
Number/percentage of G's	29,471,770 / 22.09%
Number/percentage of N's	2,762 / 0%
GC Percentage	40.73%

2.3. Coverage

Mean	0.0431

Standard Deviation	0.4045

2.4. Mapping Quality

Mean Mapping Quality	42.74

2.5. Mismatches and indels

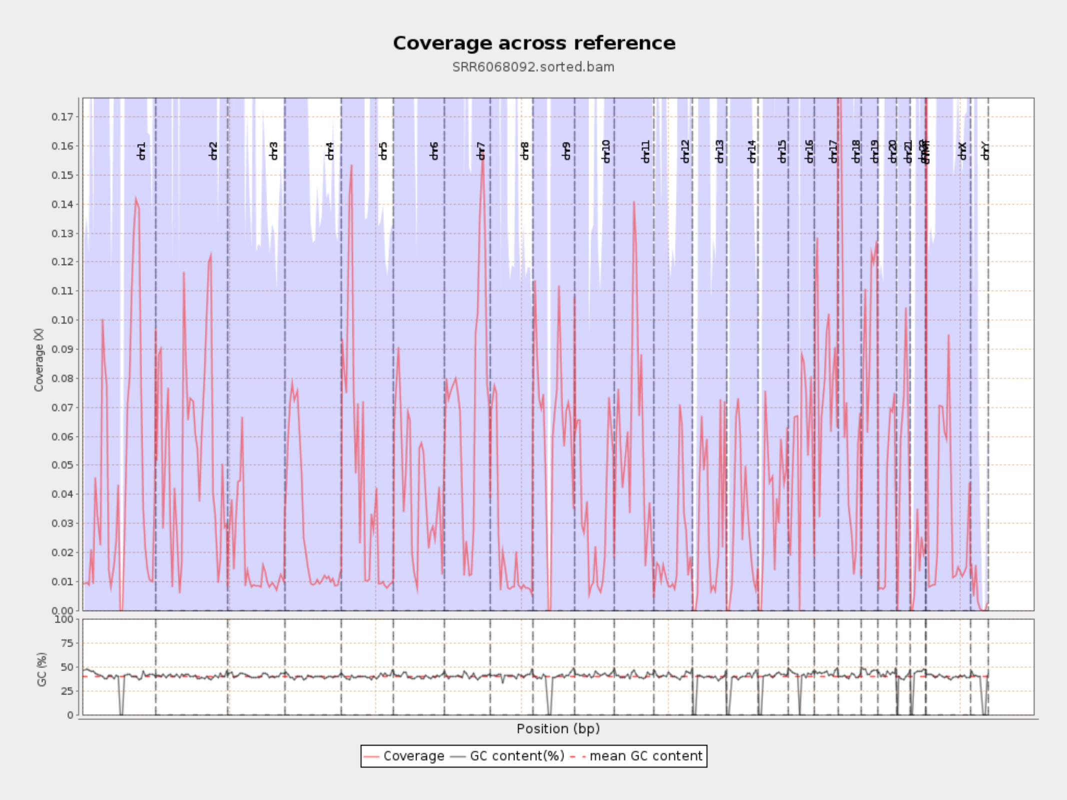
General error rate	0.8%
Mismatches	1,044,950
Insertions	10,646
Mapped reads with at least one insertion	0.51%
Deletions	35,903
Mapped reads with at least one deletion	1.73%
Homopolymer indels	45.93%

2.6. Chromosome stats

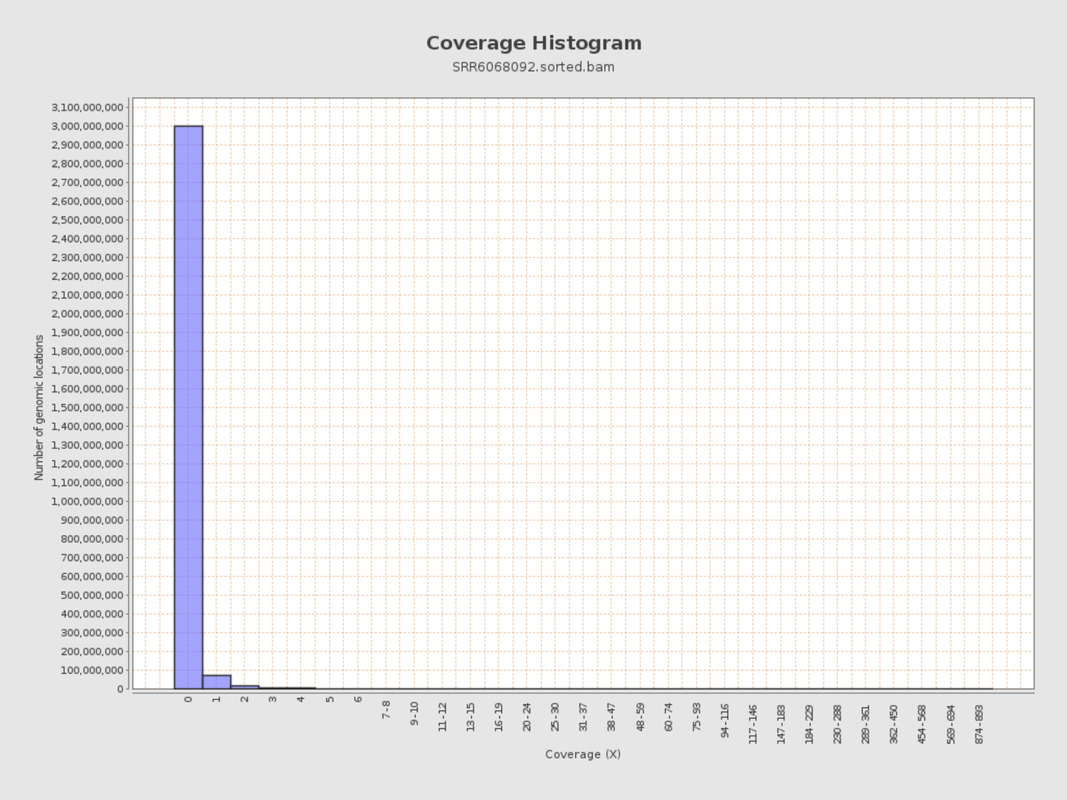
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11246372	0.0451	0.6664
chr2	243199373	13706709	0.0564	0.5933
chr3	198022430	3524829	0.0178	0.1786
chr4	191154276	5420711	0.0284	0.2312
chr5	180915260	8037827	0.0444	0.2857
chr6	171115067	7413836	0.0433	0.327
chr7	159138663	11292950	0.071	0.376

chr8	146364022	3065243	0.0209	0.4506
chr9	141213431	9082753	0.0643	0.4963
chr10	135534747	4545746	0.0335	0.3086
chr11	135006516	8059911	0.0597	0.3461
chr12	133851895	2728065	0.0204	0.2108
chr13	115169878	3599770	0.0313	0.2355
chr14	107349540	3206628	0.0299	0.2704
chr15	102531392	3898658	0.038	0.2589
chr16	90354753	4961863	0.0549	0.3502
chr17	81195210	6786227	0.0836	0.3938
chr18	78077248	5933866	0.076	0.7724
chr19	59128983	5678347	0.096	0.6109
chr20	63025520	2386455	0.0379	0.2594
chr21	48129895	2668792	0.0554	0.3275
chr22	51304566	802477	0.0156	0.1566
chrMT	16571	30861	1.8623	2.0393
chrX	155270560	5093407	0.0328	0.2744
chrY	59373566	289319	0.0049	0.1592

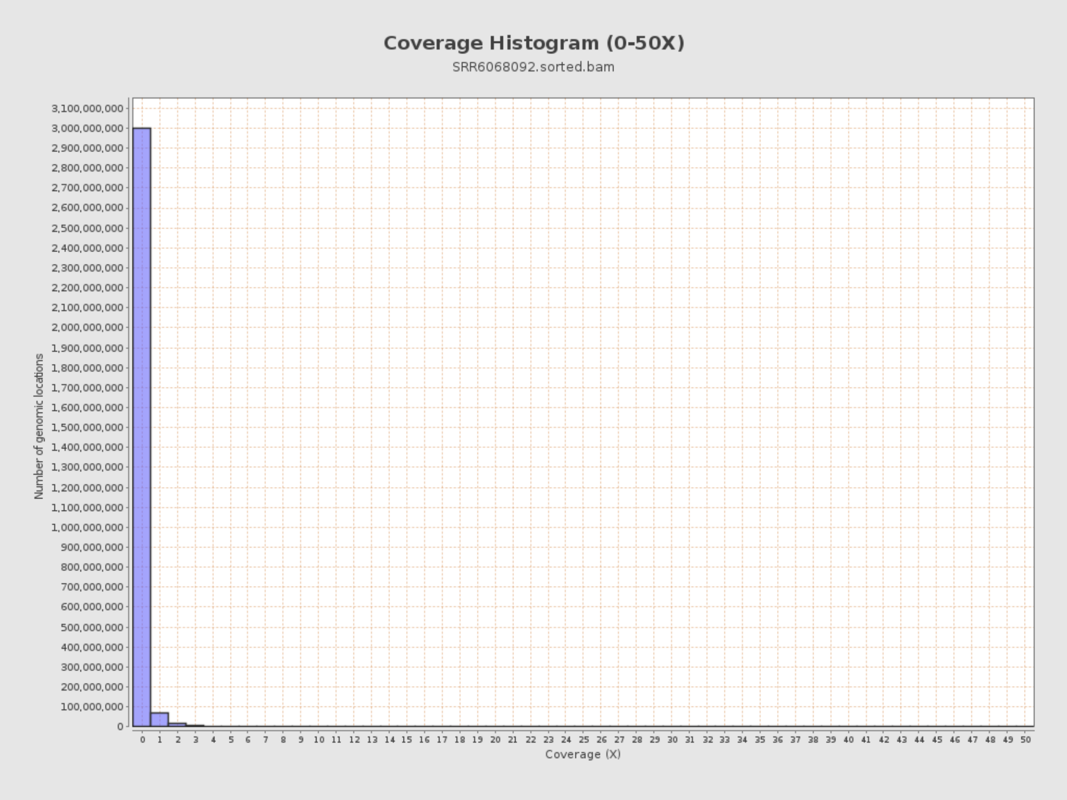
3. Results : Coverage across reference



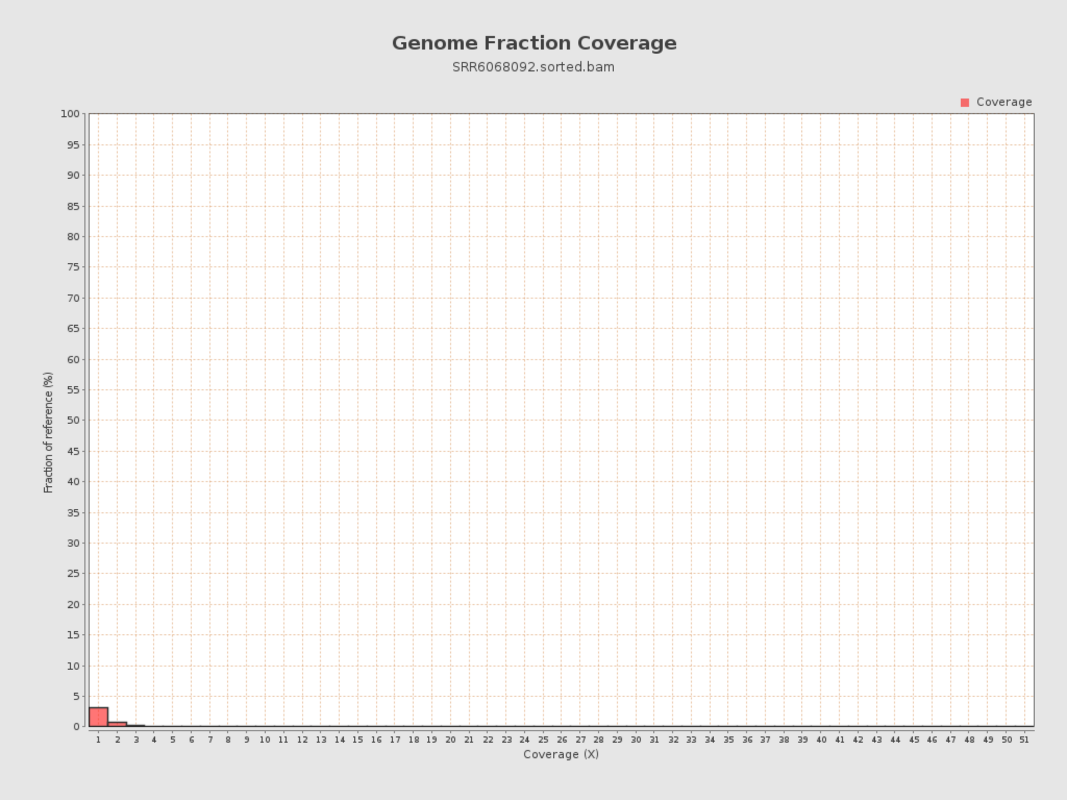
4. Results : Coverage Histogram



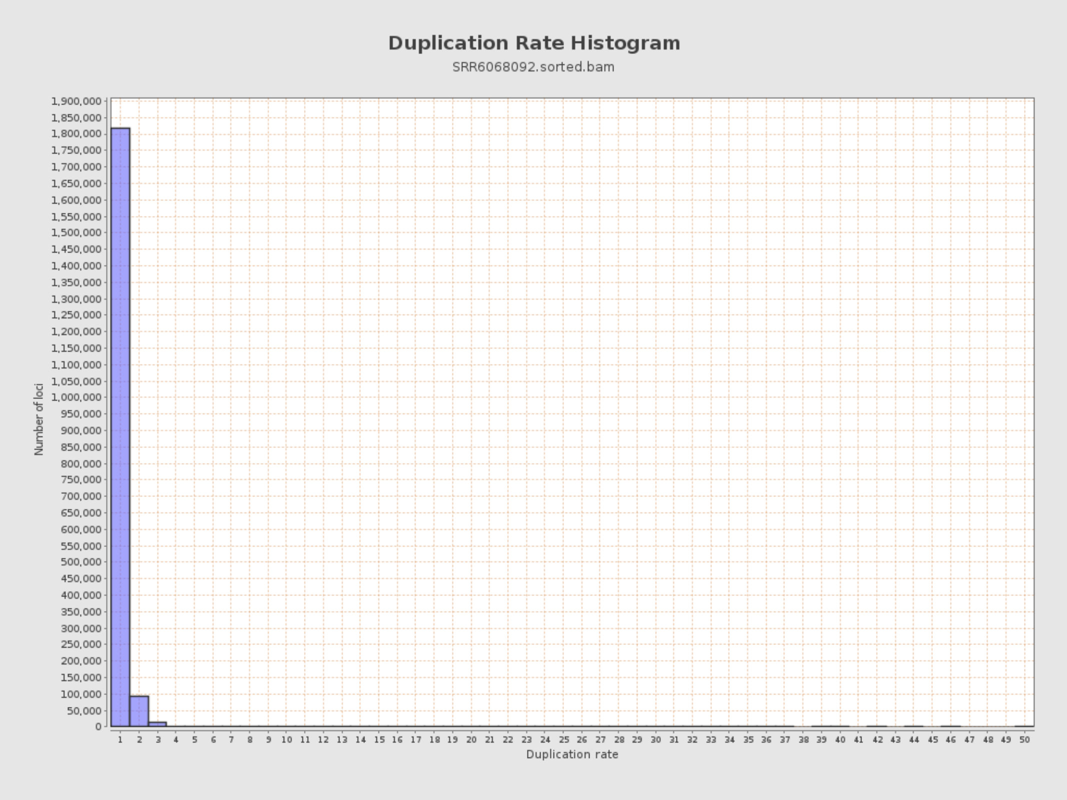
5. Results : Coverage Histogram (0-50X)



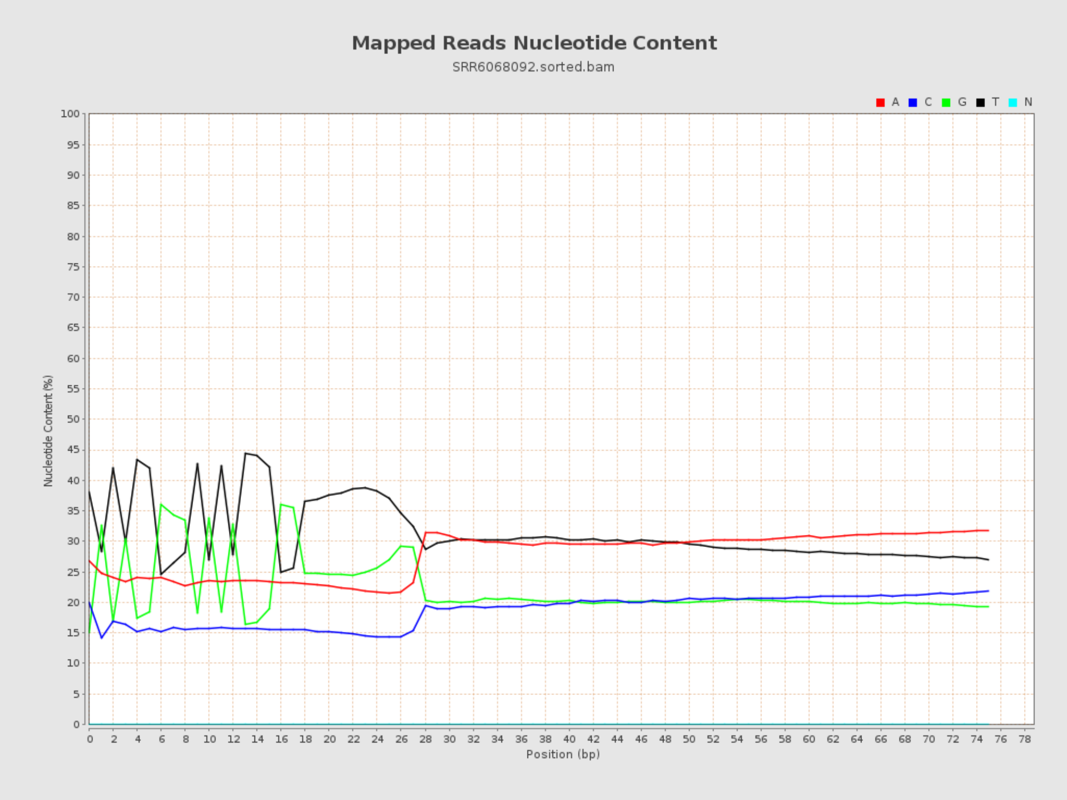
6. Results : Genome Fraction Coverage



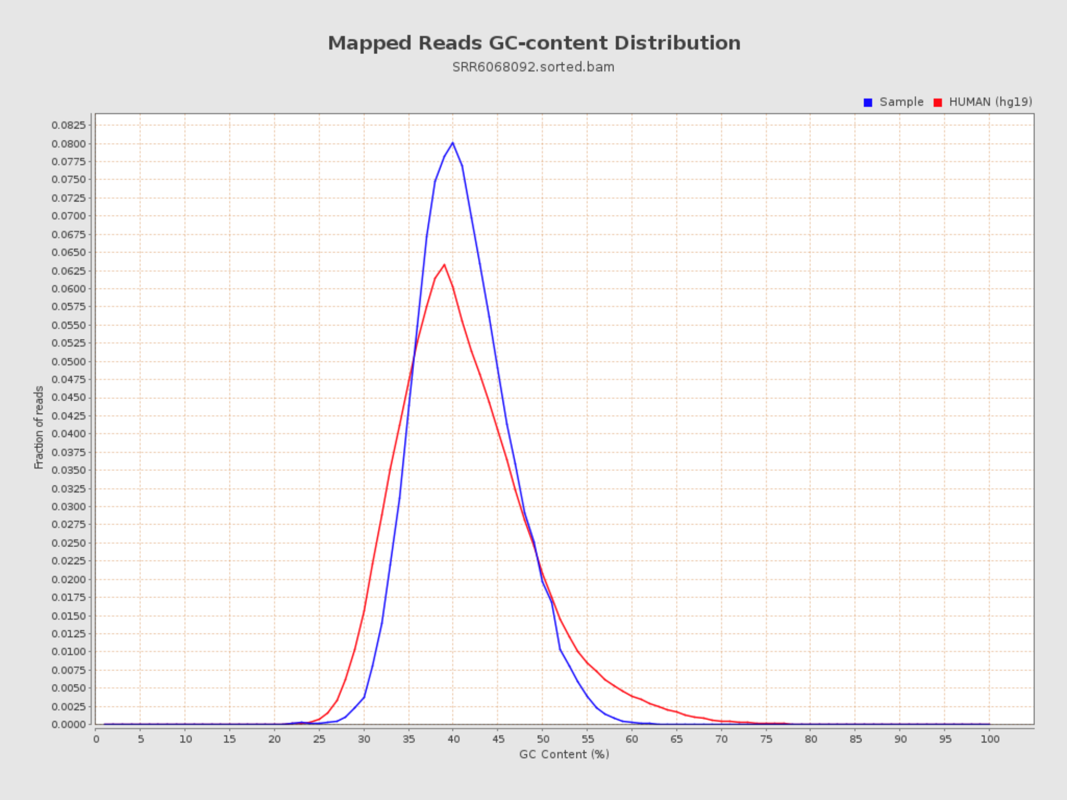
7. Results : Duplication Rate Histogram



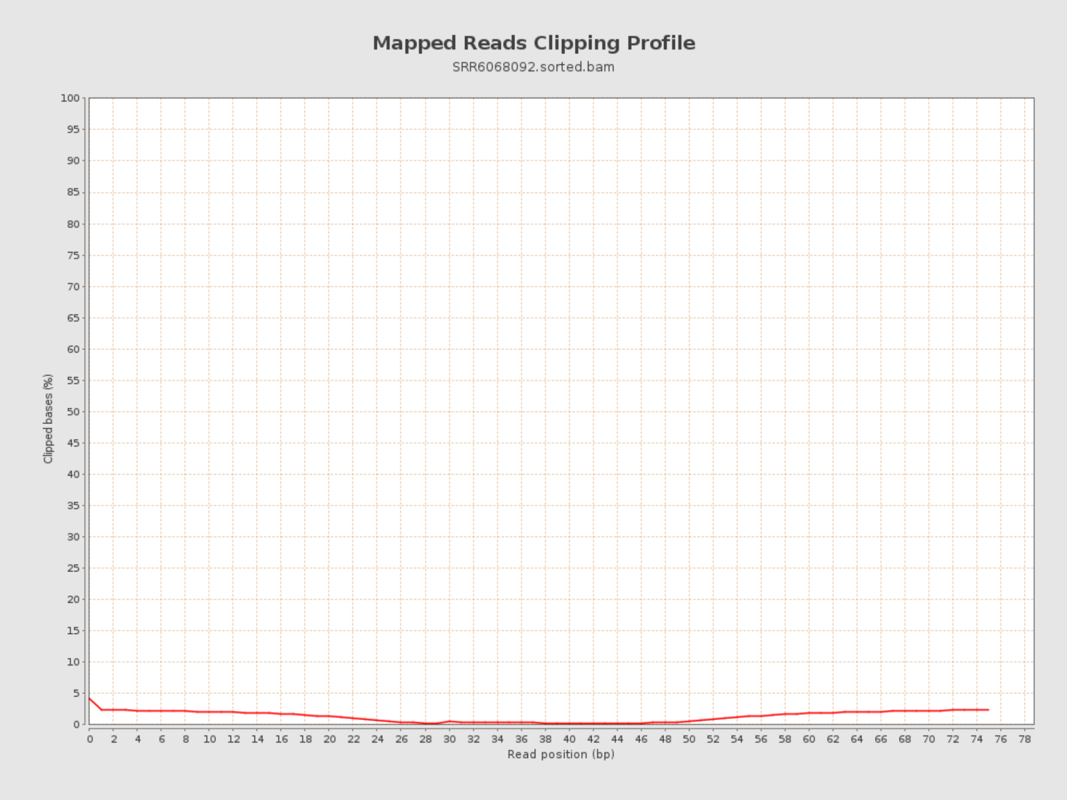
8. Results : Mapped Reads Nucleotide Content



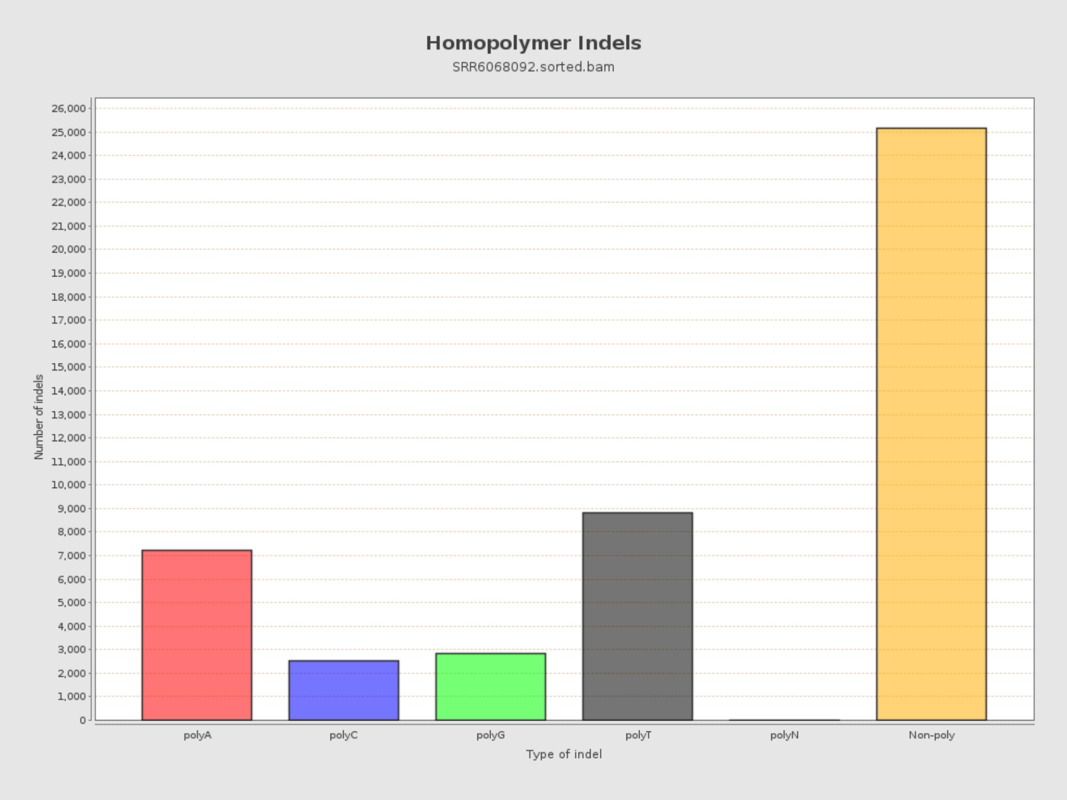
9. Results : Mapped Reads GC-content Distribution



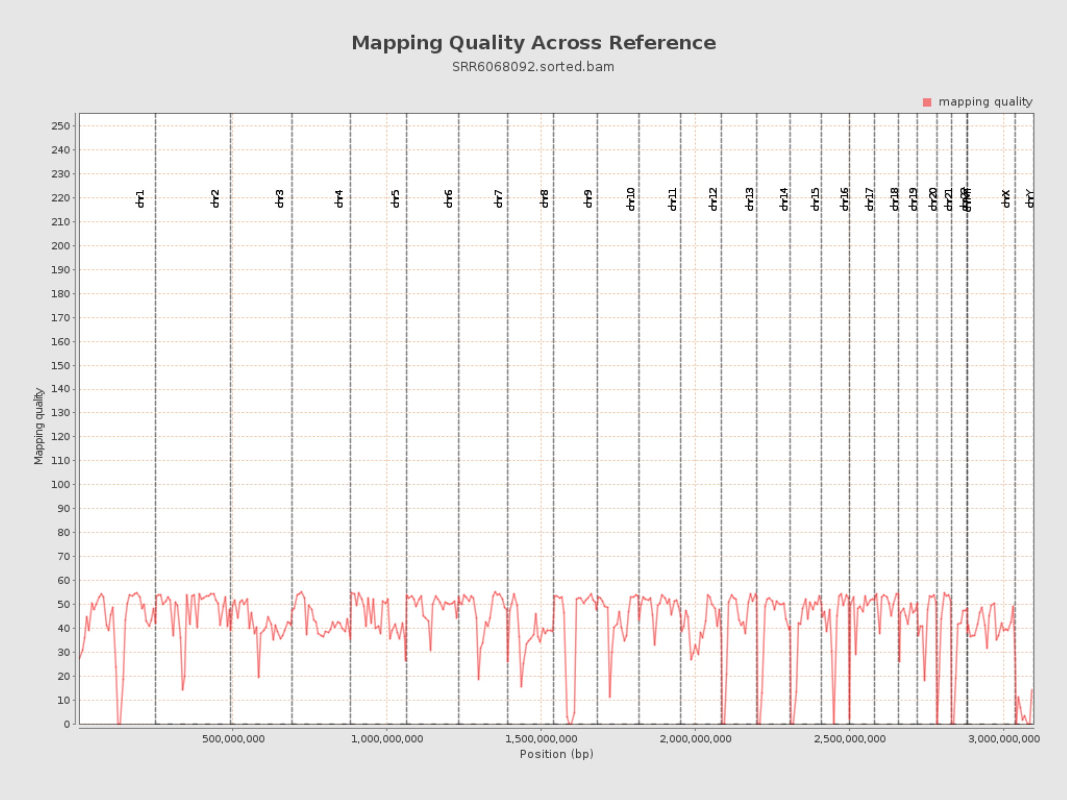
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram