Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 13:50:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068158.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_SRR6068158 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068158.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 13:50:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068158.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,691,165
Mapped reads	4,431,513 / 94.47%
Unmapped reads	259,652 / 5.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,537 / 0.74%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	531,314 / 11.33%
Duplication rate	9.85%
Clipped reads	2,341,406 / 49.91%

2.2. ACGT Content

Number/percentage of A's	74,495,747 / 26.15%
Number/percentage of C's	50,898,167 / 17.87%
Number/percentage of T's	93,181,935 / 32.72%
Number/percentage of G's	66,218,116 / 23.25%
Number/percentage of N's	32,017 / 0.01%
GC Percentage	41.12%

2.3. Coverage

Mean	0.092

Standard Deviation	0.9762

2.4. Mapping Quality

Mean Mapping Quality	45.93

2.5. Mismatches and indels

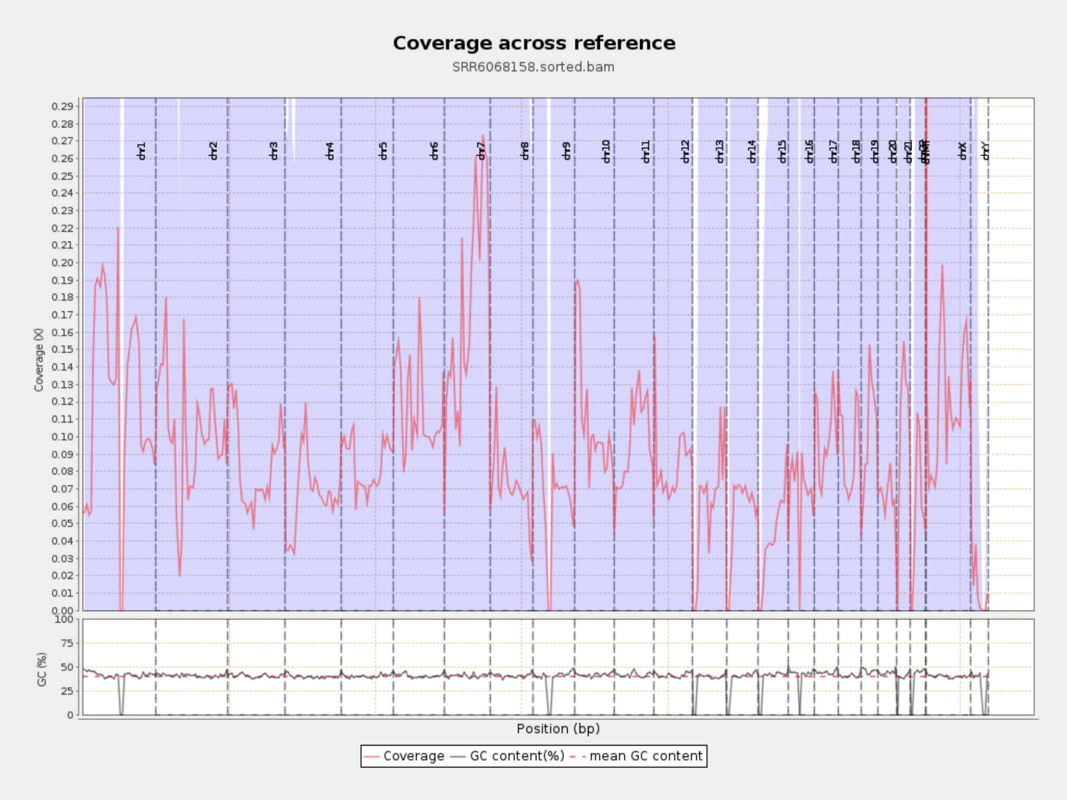
General error rate	0.59%
Mismatches	1,632,818
Insertions	18,000
Mapped reads with at least one insertion	0.4%
Deletions	68,063
Mapped reads with at least one deletion	1.52%
Homopolymer indels	44.71%

2.6. Chromosome stats

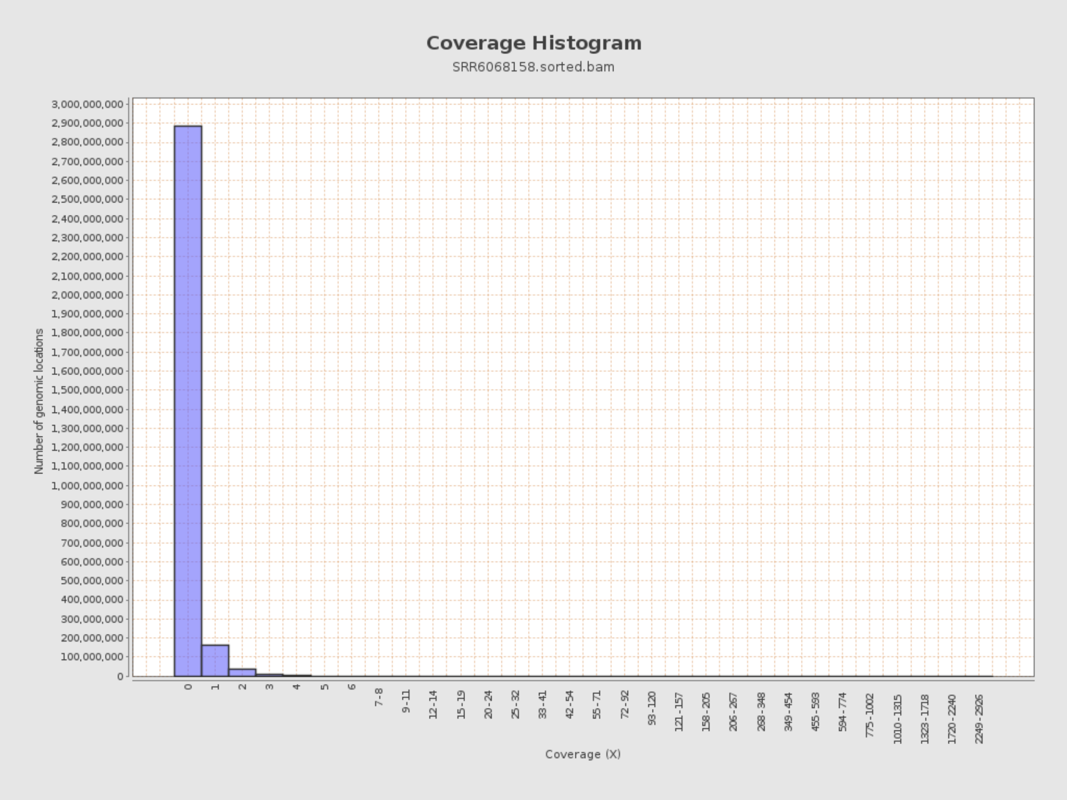
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30733237	0.1233	2.2761
chr2	243199373	24741134	0.1017	1.3413
chr3	198022430	16769204	0.0847	0.3803
chr4	191154276	12809995	0.067	0.3726
chr5	180915260	15171223	0.0839	0.3787
chr6	171115067	20016262	0.117	0.6173
chr7	159138663	28116672	0.1767	1.5283

chr8	146364022	10466681	0.0715	0.946
chr9	141213431	9662407	0.0684	0.6342
chr10	135534747	14970586	0.1105	0.6429
chr11	135006516	13224366	0.098	0.5582
chr12	133851895	11318626	0.0846	0.4188
chr13	115169878	7125909	0.0619	0.36
chr14	107349540	6045396	0.0563	0.3742
chr15	102531392	4354914	0.0425	0.3088
chr16	90354753	6105398	0.0676	0.393
chr17	81195210	8267963	0.1018	0.459
chr18	78077248	7312226	0.0937	1.2231
chr19	59128983	6095359	0.1031	1.4042
chr20	63025520	4155516	0.0659	0.363
chr21	48129895	5011974	0.1041	0.4418
chr22	51304566	2927535	0.0571	0.3003
chrMT	16571	357287	21.561	12.4843
chrX	155270560	18403621	0.1185	0.5512
chrY	59373566	781910	0.0132	0.3393

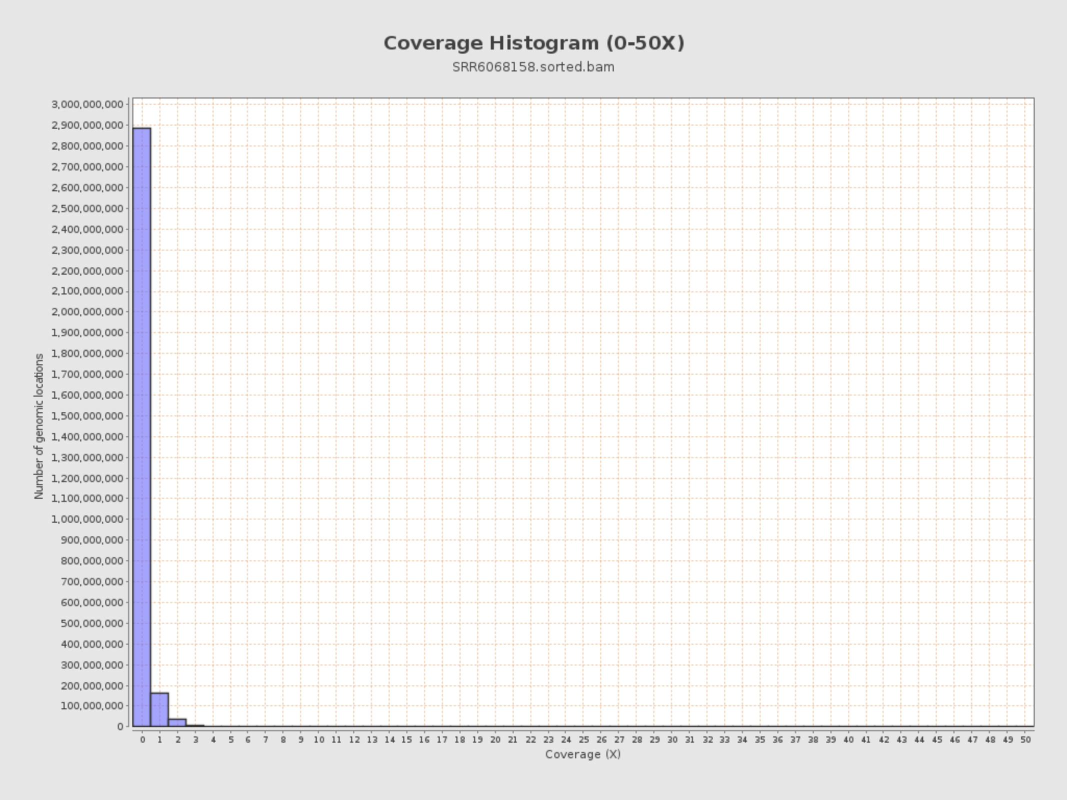
3. Results : Coverage across reference



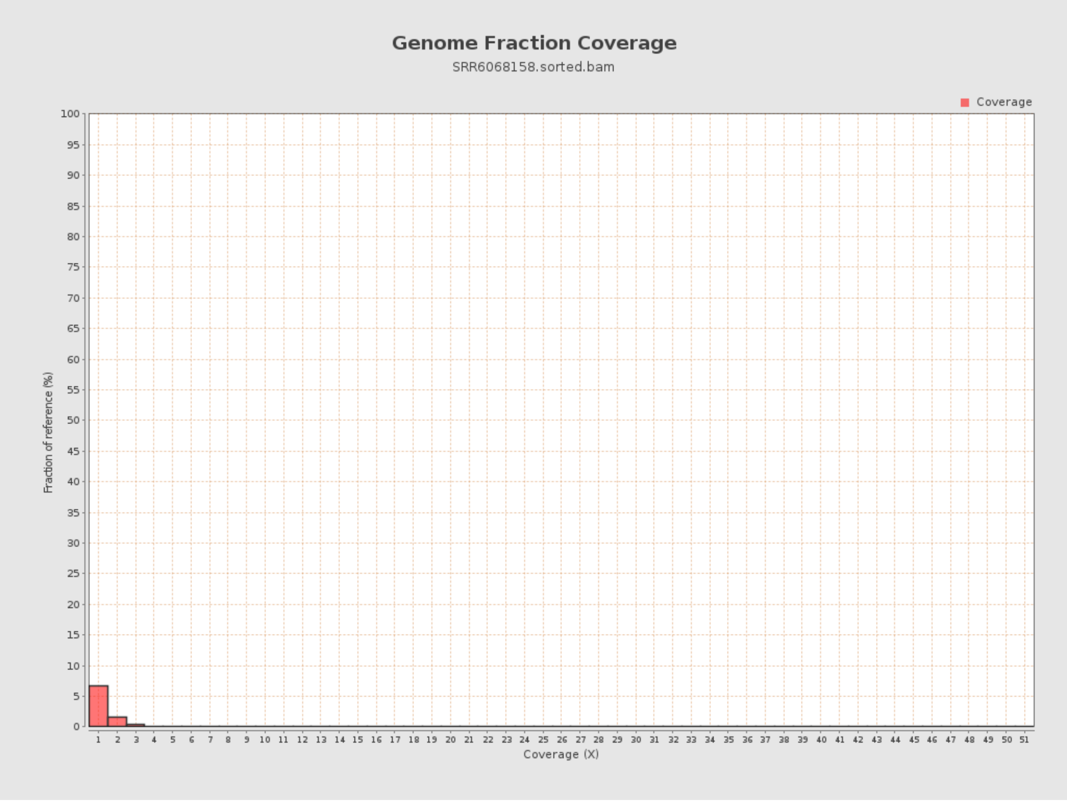
4. Results : Coverage Histogram



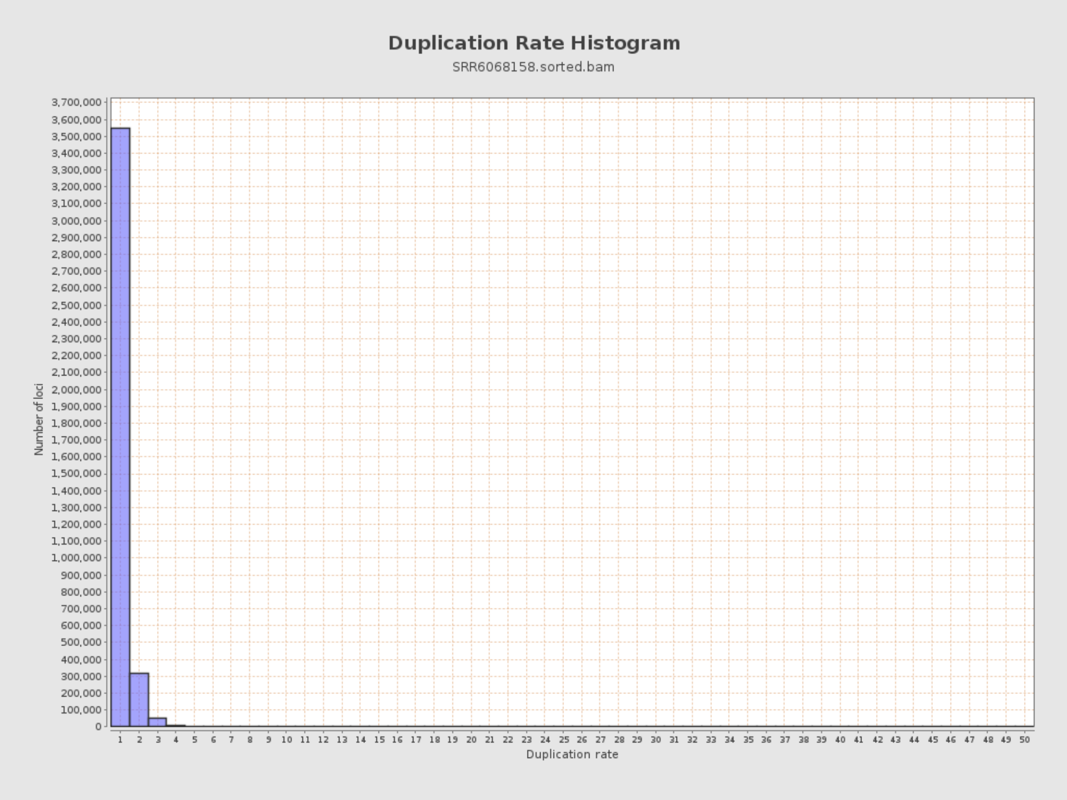
5. Results : Coverage Histogram (0-50X)



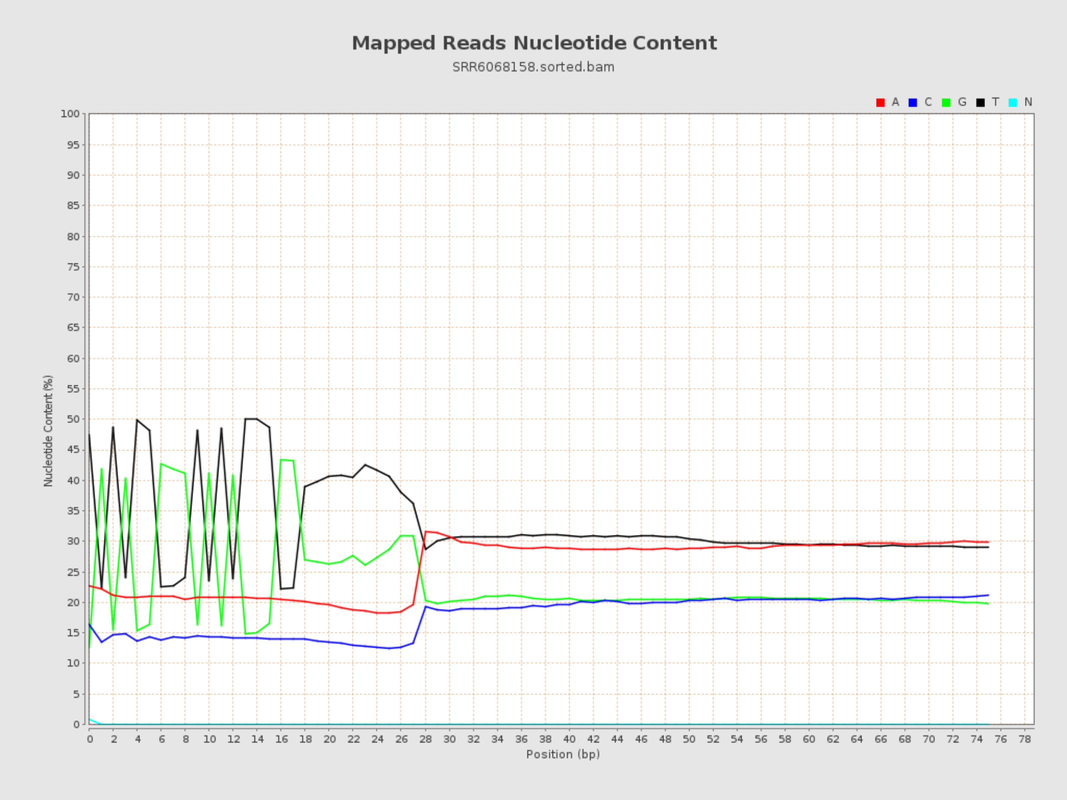
6. Results : Genome Fraction Coverage



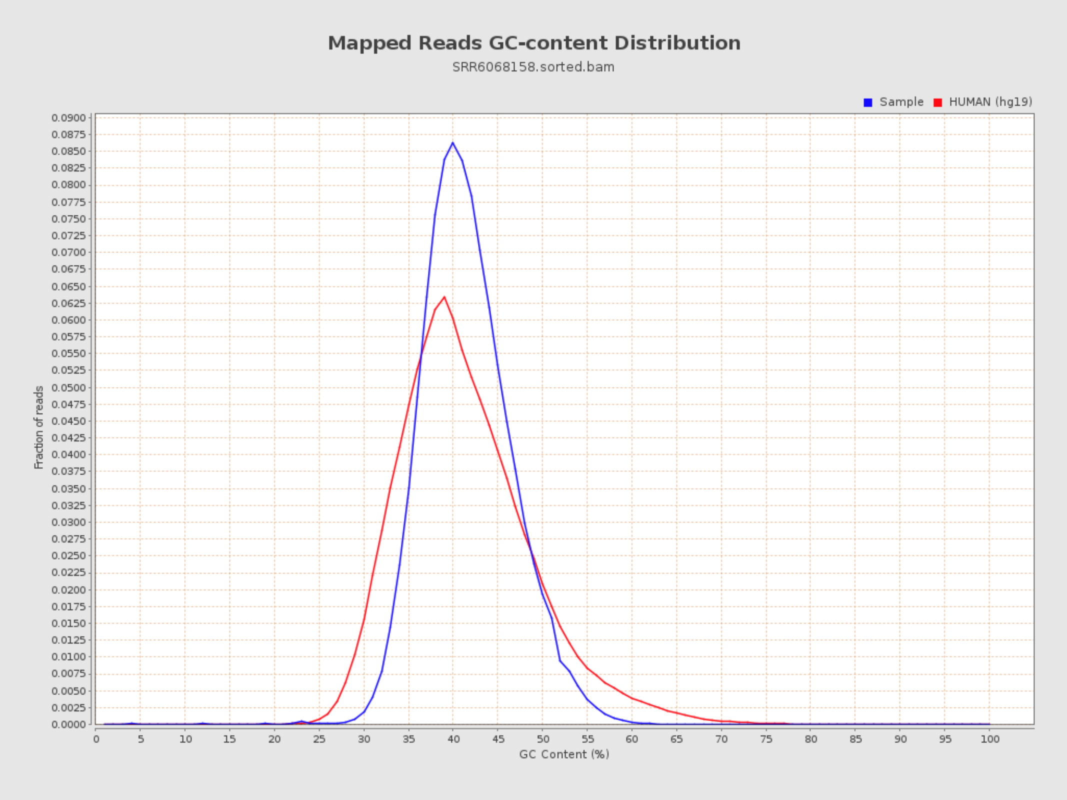
7. Results : Duplication Rate Histogram



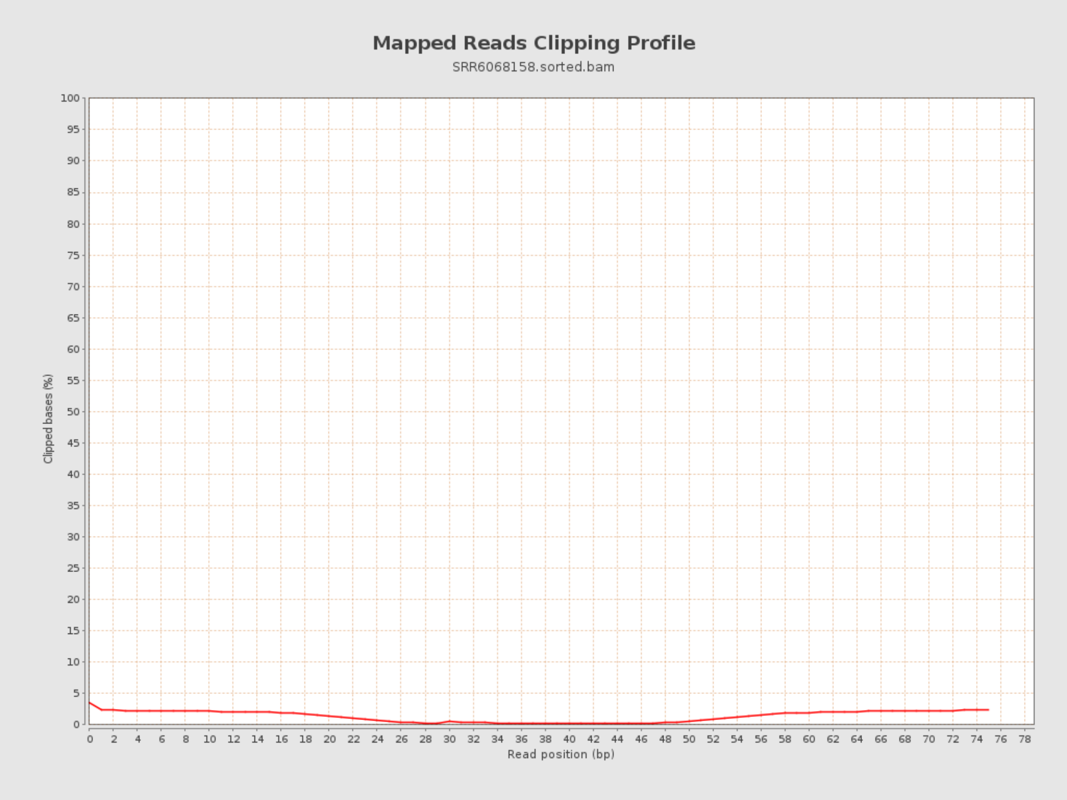
8. Results : Mapped Reads Nucleotide Content



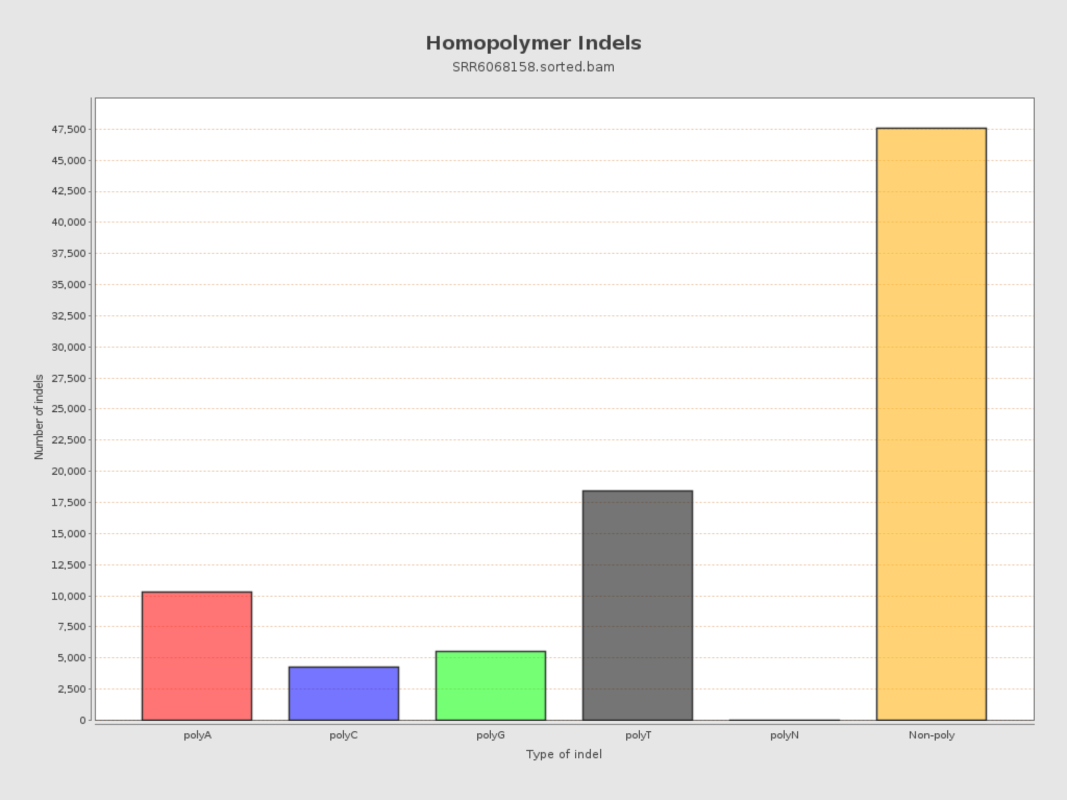
9. Results : Mapped Reads GC-content Distribution



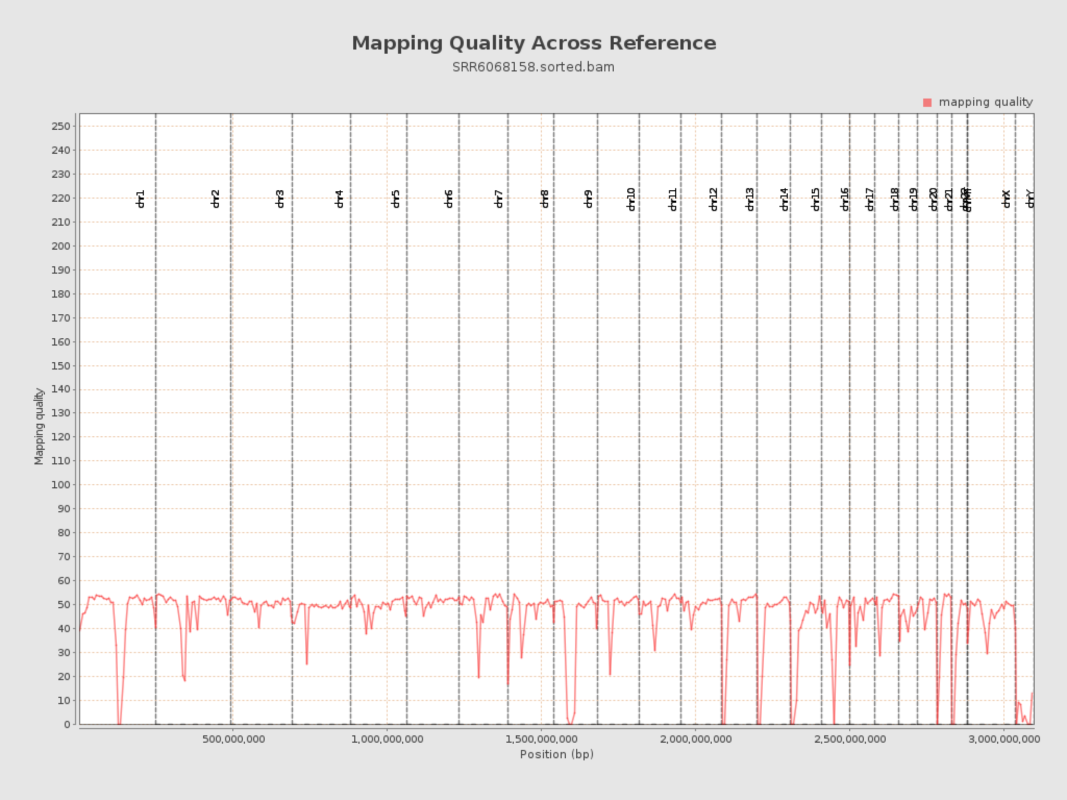
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram