Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 09:20:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068088.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_SRR6068088 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068088.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 09:20:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068088.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,278,529
Mapped reads	4,037,342 / 94.36%
Unmapped reads	241,187 / 5.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,663 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	679,788 / 15.89%
Duplication rate	13.57%
Clipped reads	2,097,713 / 49.03%

2.2. ACGT Content

Number/percentage of A's	67,660,496 / 26.01%
Number/percentage of C's	46,308,434 / 17.8%
Number/percentage of T's	85,683,477 / 32.93%
Number/percentage of G's	60,490,144 / 23.25%
Number/percentage of N's	28,238 / 0.01%
GC Percentage	41.05%

2.3. Coverage

Mean	0.0841

Standard Deviation	0.8587

2.4. Mapping Quality

Mean Mapping Quality	45.71

2.5. Mismatches and indels

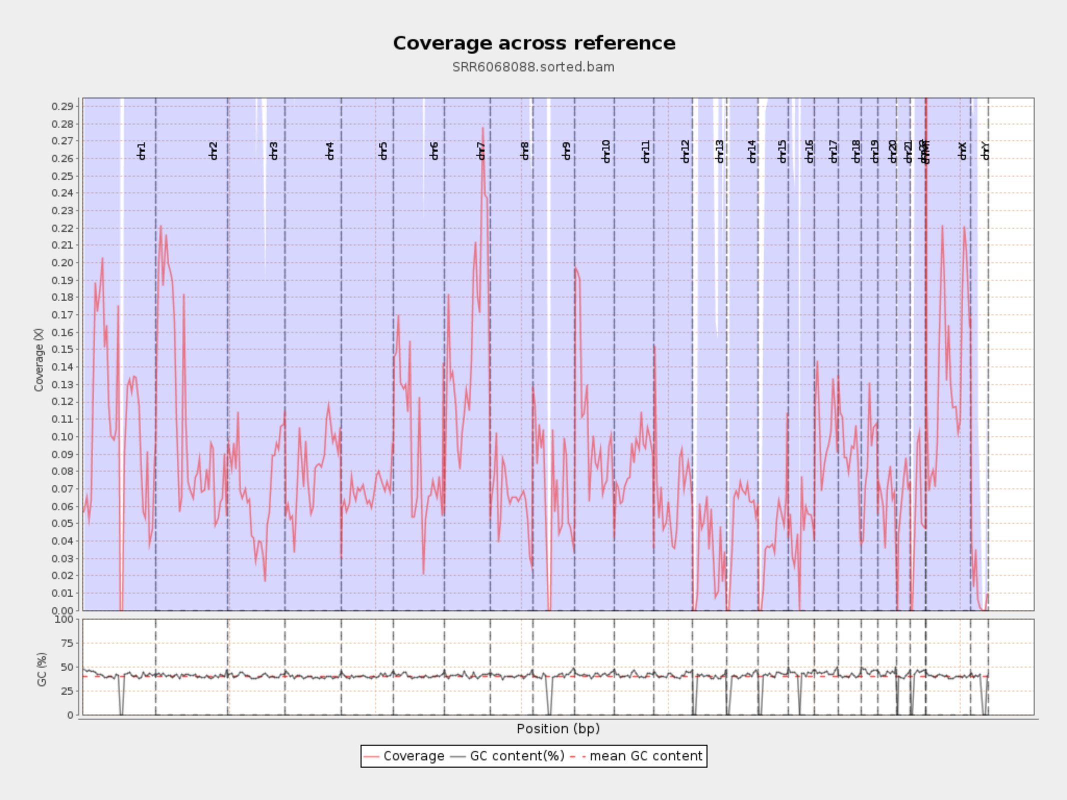
General error rate	0.55%
Mismatches	1,398,250
Insertions	17,117
Mapped reads with at least one insertion	0.42%
Deletions	55,971
Mapped reads with at least one deletion	1.37%
Homopolymer indels	44.96%

2.6. Chromosome stats

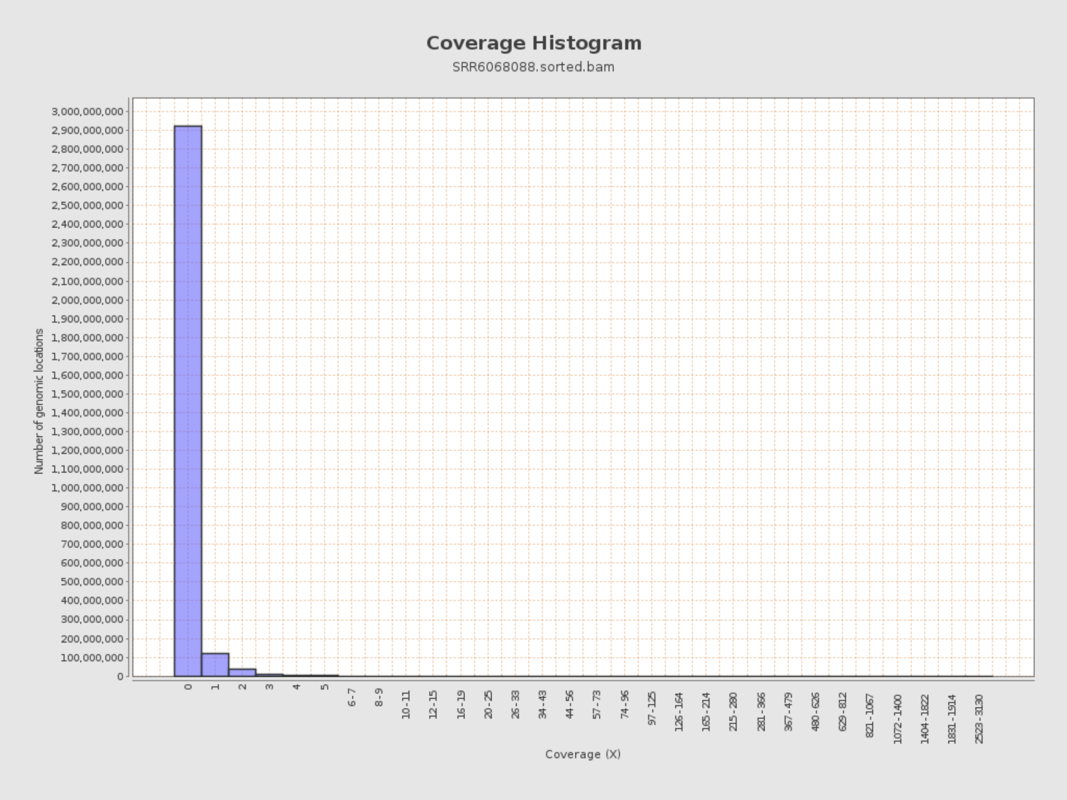
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26089535	0.1047	1.6047
chr2	243199373	27032911	0.1112	1.5297
chr3	198022430	13808091	0.0697	0.3771
chr4	191154276	15576123	0.0815	0.4606
chr5	180915260	12503472	0.0691	0.3787
chr6	171115067	15829112	0.0925	0.6011
chr7	159138663	24388763	0.1533	0.8452

chr8	146364022	9281705	0.0634	0.9801
chr9	141213431	9608438	0.068	0.8577
chr10	135534747	14504501	0.107	0.644
chr11	135006516	11462142	0.0849	0.5543
chr12	133851895	9126370	0.0682	0.4677
chr13	115169878	3748174	0.0325	0.3297
chr14	107349540	5928594	0.0552	0.4182
chr15	102531392	4044182	0.0394	0.3155
chr16	90354753	4060195	0.0449	0.3921
chr17	81195210	8577940	0.1056	0.5205
chr18	78077248	7337899	0.094	1.4423
chr19	59128983	5127634	0.0867	1.0557
chr20	63025520	4024958	0.0639	0.3856
chr21	48129895	2962581	0.0616	0.3995
chr22	51304566	2686200	0.0524	0.3151
chrMT	16571	549797	33.1783	20.4162
chrX	155270560	21288183	0.1371	0.6694
chrY	59373566	720634	0.0121	0.2825

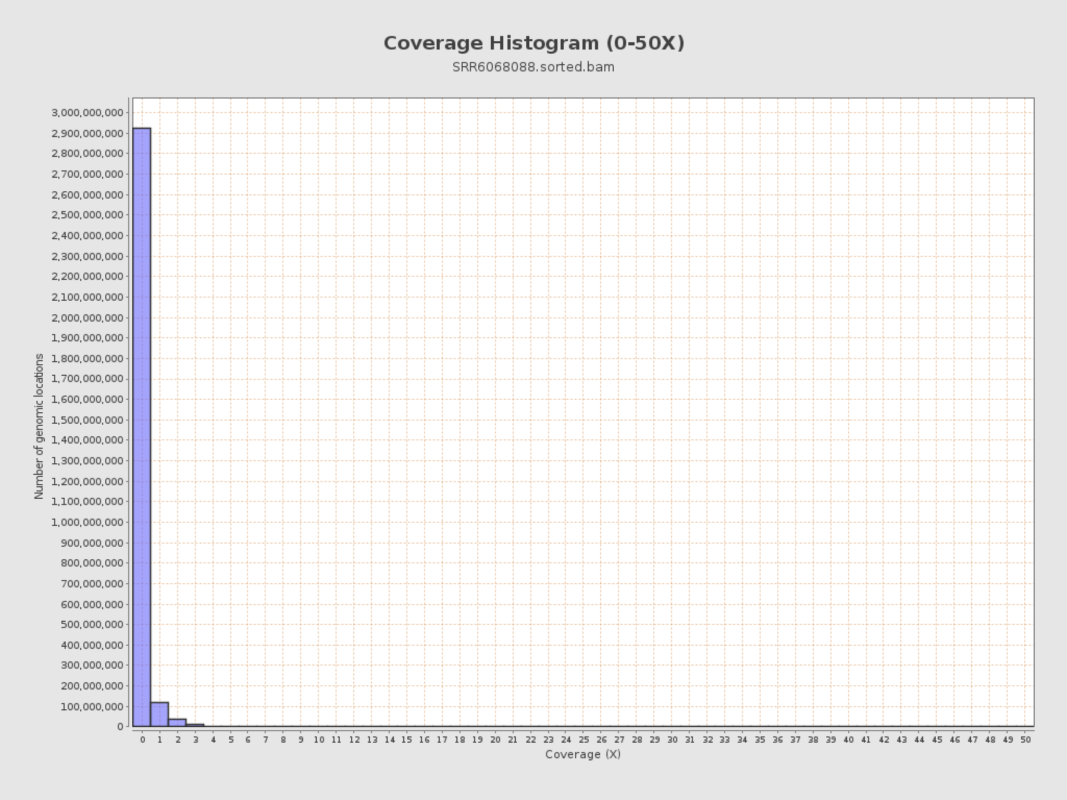
3. Results : Coverage across reference



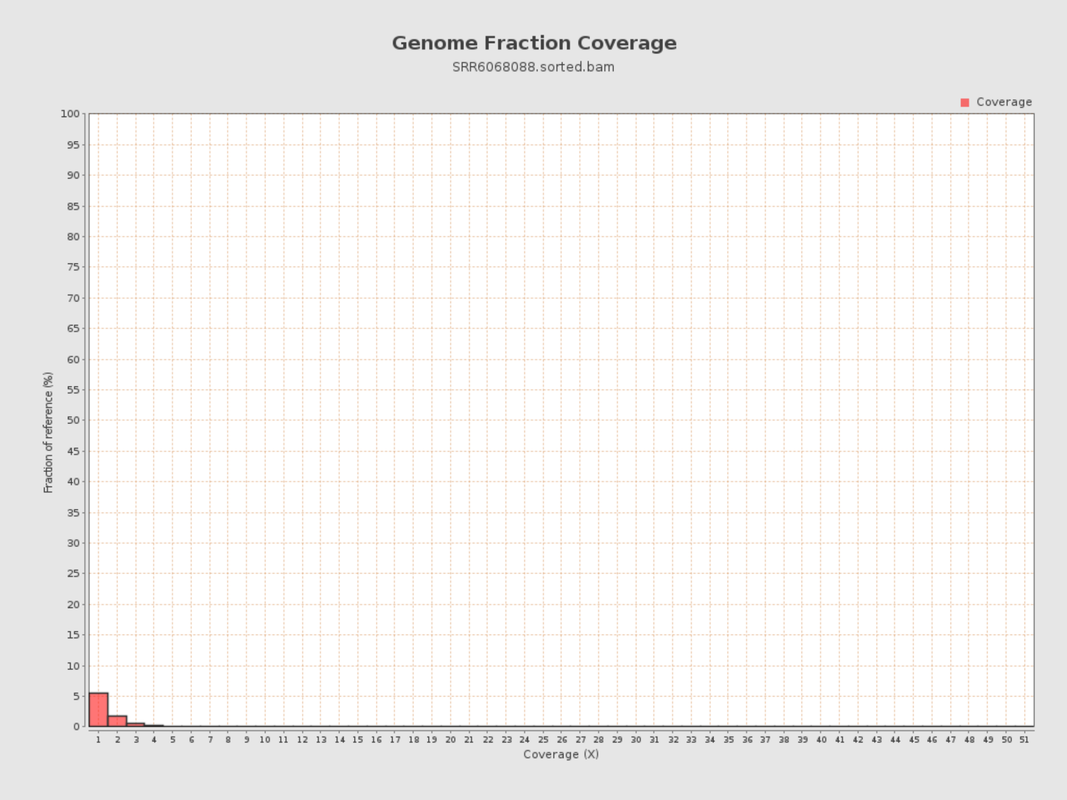
4. Results : Coverage Histogram



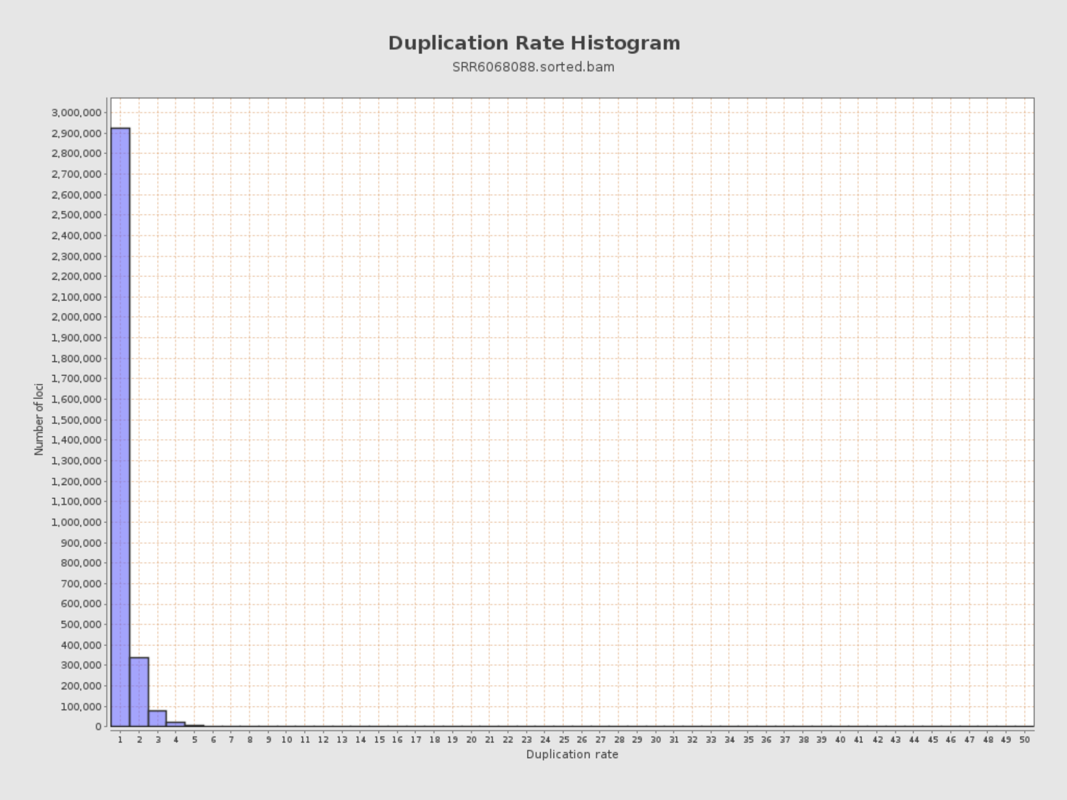
5. Results : Coverage Histogram (0-50X)



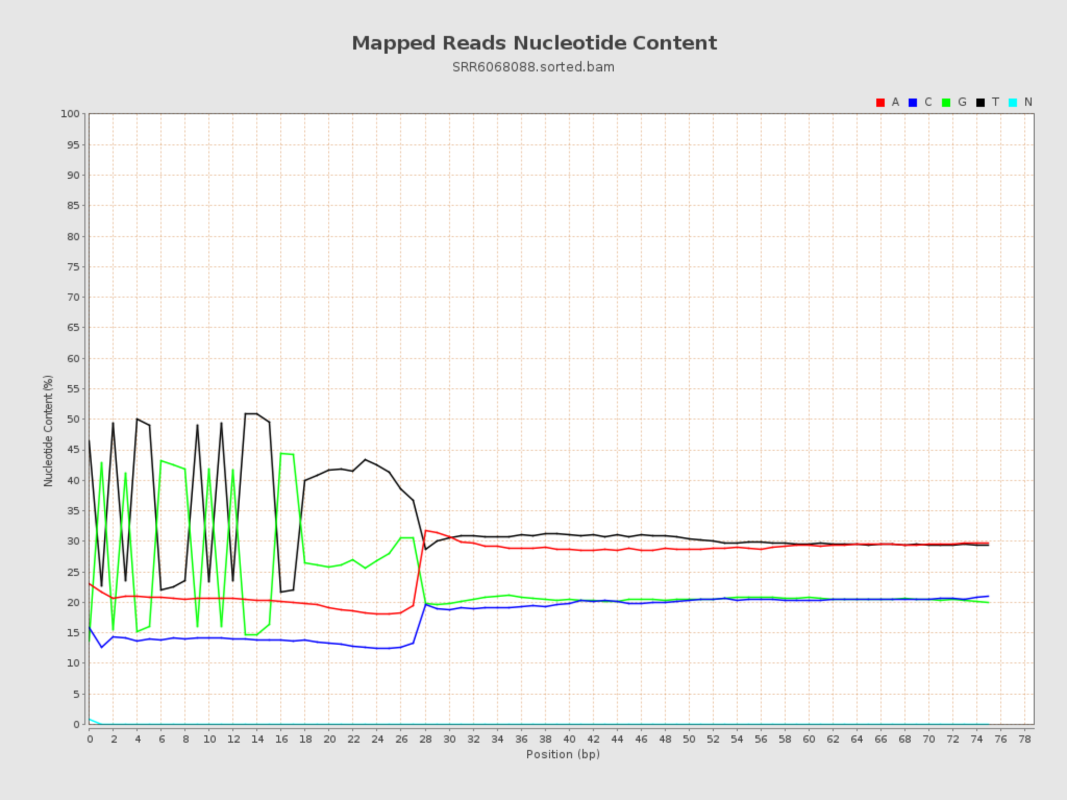
6. Results : Genome Fraction Coverage



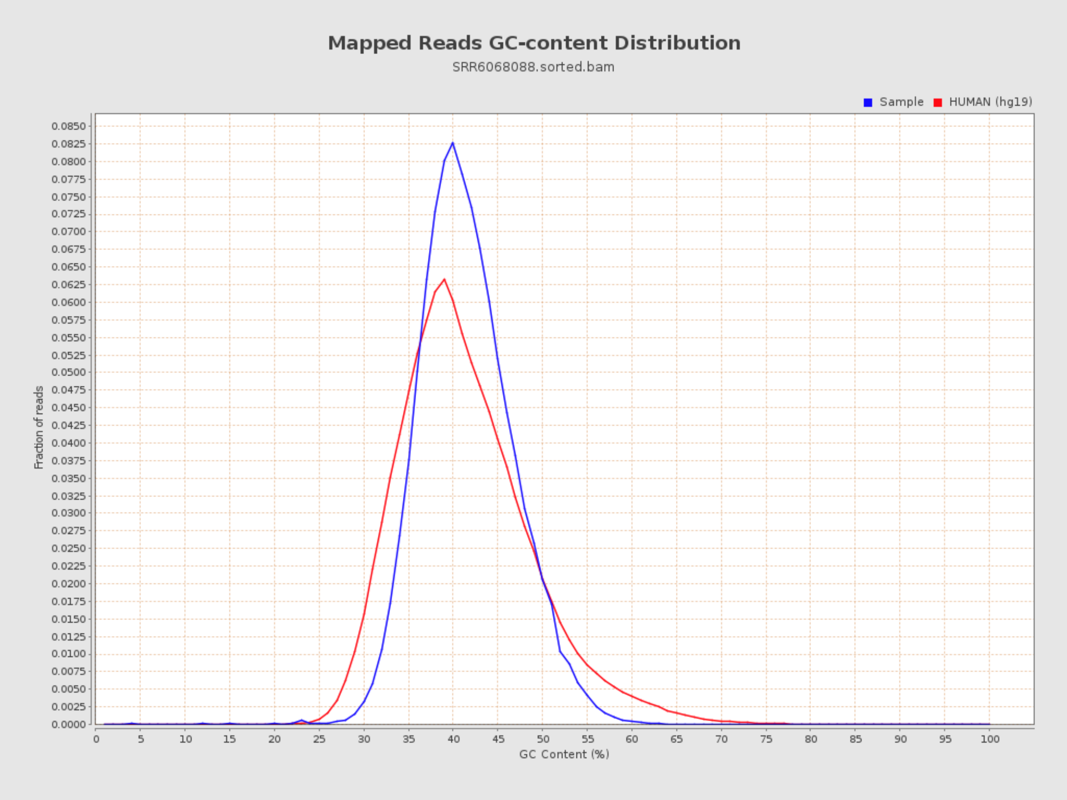
7. Results : Duplication Rate Histogram



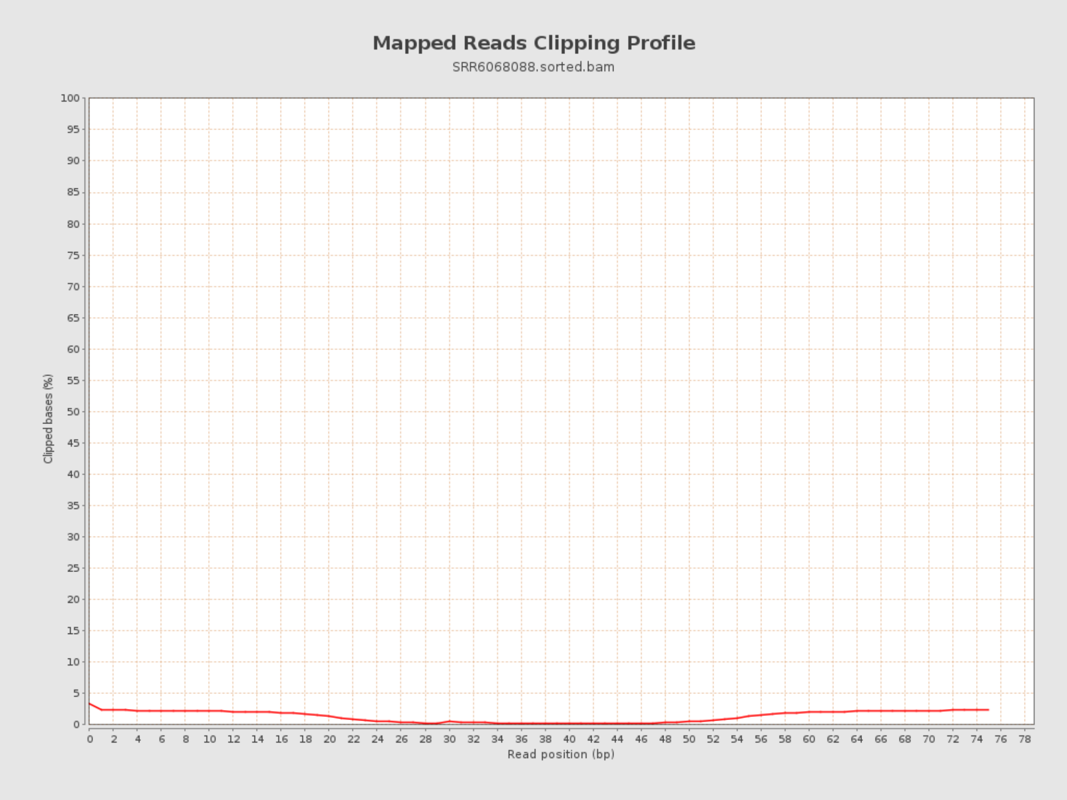
8. Results : Mapped Reads Nucleotide Content



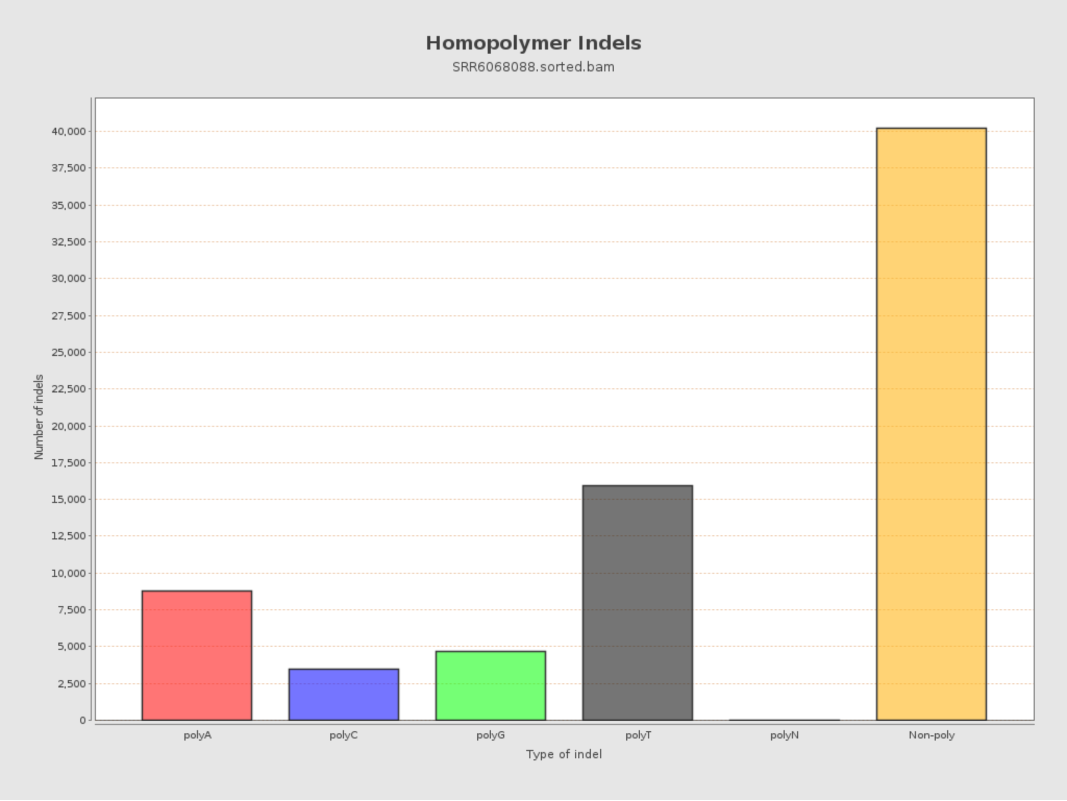
9. Results : Mapped Reads GC-content Distribution



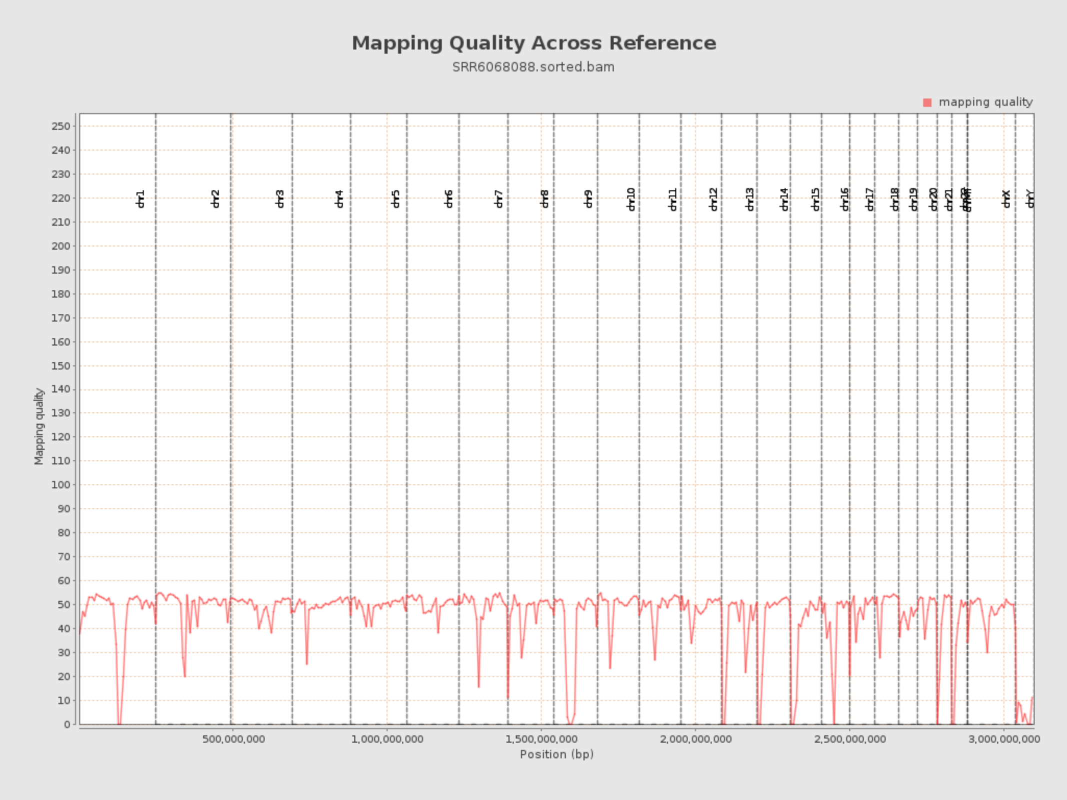
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram