Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 15:25:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068183.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_SRR6068183 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068183.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 15:25:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068183.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,707,015
Mapped reads	1,526,128 / 89.4%
Unmapped reads	180,887 / 10.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,039 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	125,622 / 7.36%
Duplication rate	6.83%
Clipped reads	613,068 / 35.91%

2.2. ACGT Content

Number/percentage of A's	29,700,887 / 28.67%
Number/percentage of C's	19,552,038 / 18.87%
Number/percentage of T's	32,377,737 / 31.25%
Number/percentage of G's	21,847,488 / 21.09%
Number/percentage of N's	118,665 / 0.11%
GC Percentage	39.96%

2.3. Coverage

Mean	0.0335

Standard Deviation	0.3761

2.4. Mapping Quality

Mean Mapping Quality	45.95

2.5. Mismatches and indels

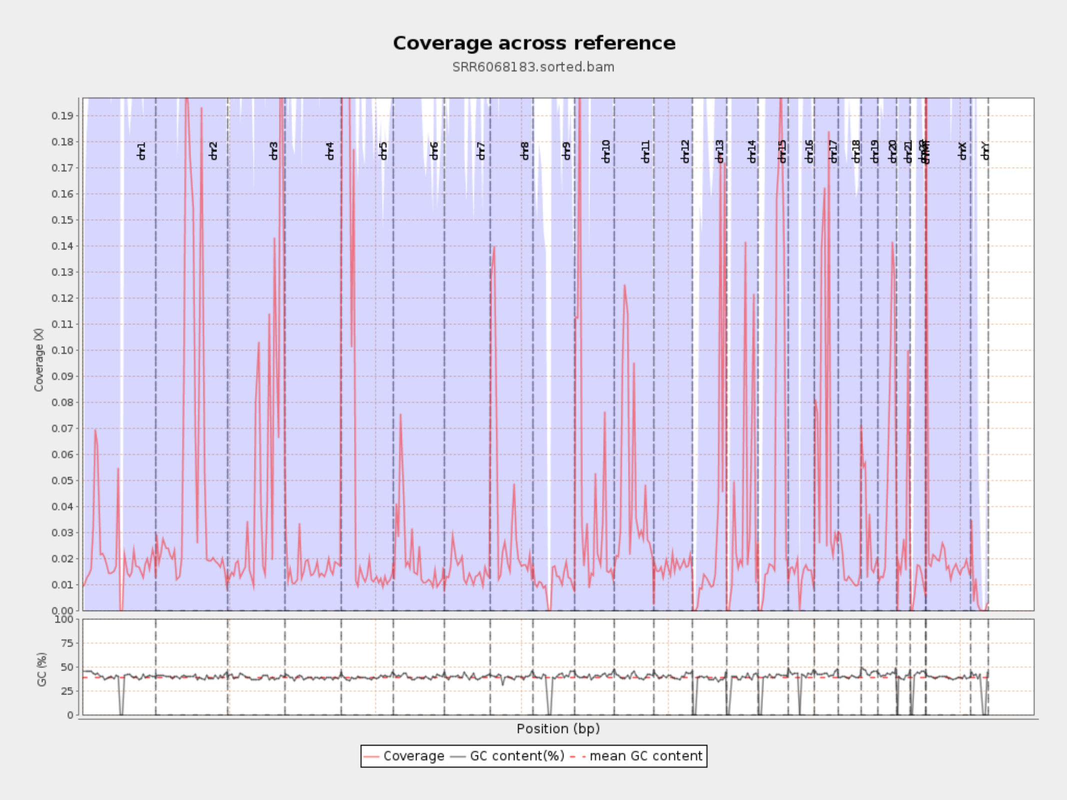
General error rate	0.84%
Mismatches	857,167
Insertions	7,377
Mapped reads with at least one insertion	0.48%
Deletions	26,845
Mapped reads with at least one deletion	1.74%
Homopolymer indels	48.24%

2.6. Chromosome stats

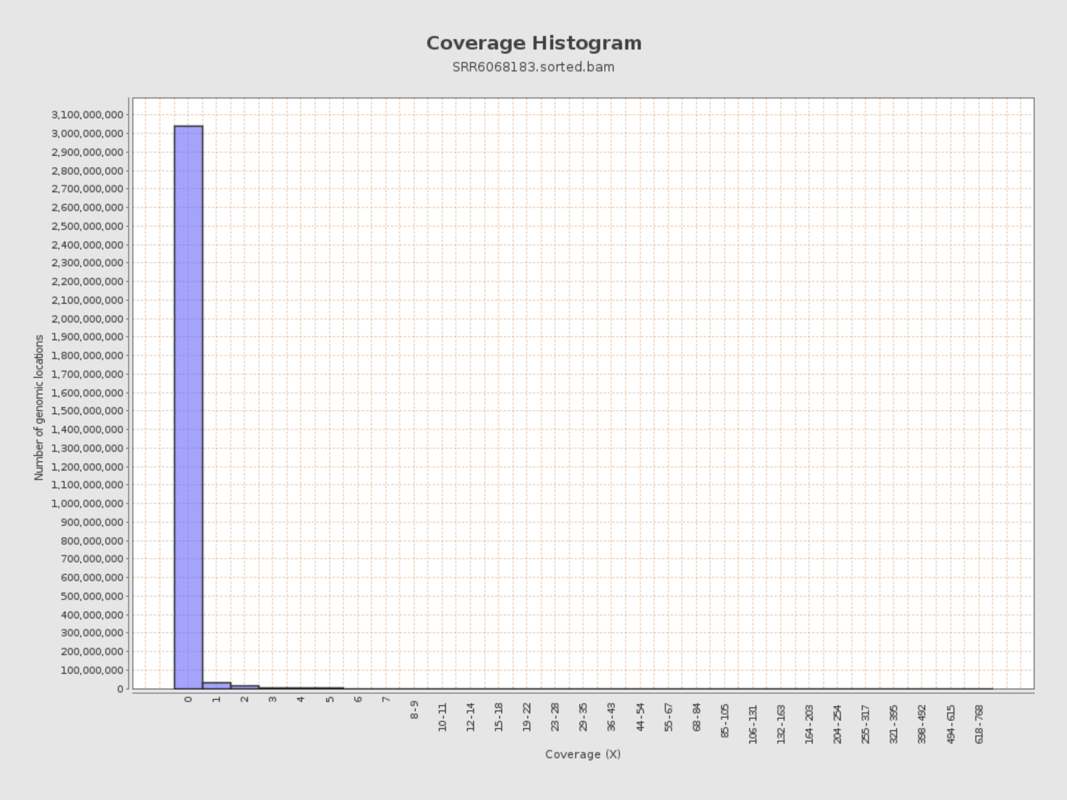
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5116286	0.0205	0.6732
chr2	243199373	12968698	0.0533	0.4023
chr3	198022430	10323396	0.0521	0.3803
chr4	191154276	3106657	0.0163	0.2157
chr5	180915260	10268676	0.0568	0.4022
chr6	171115067	3514574	0.0205	0.2384
chr7	159138663	2367258	0.0149	0.2289

chr8	146364022	5297825	0.0362	0.5036
chr9	141213431	1542590	0.0109	0.1779
chr10	135534747	6228820	0.046	0.3703
chr11	135006516	6263833	0.0464	0.3672
chr12	133851895	2288853	0.0171	0.2131
chr13	115169878	4267328	0.0371	0.3298
chr14	107349540	4060589	0.0378	0.3251
chr15	102531392	6076005	0.0593	0.4108
chr16	90354753	1234517	0.0137	0.2062
chr17	81195210	6036844	0.0743	0.5131
chr18	78077248	1180169	0.0151	0.2463
chr19	59128983	1879742	0.0318	0.5523
chr20	63025520	3791392	0.0602	0.4022
chr21	48129895	1481911	0.0308	0.2905
chr22	51304566	499419	0.0097	0.1525
chrMT	16571	43427	2.6207	2.9026
chrX	155270560	3463930	0.0223	0.2455
chrY	59373566	342482	0.0058	0.1325

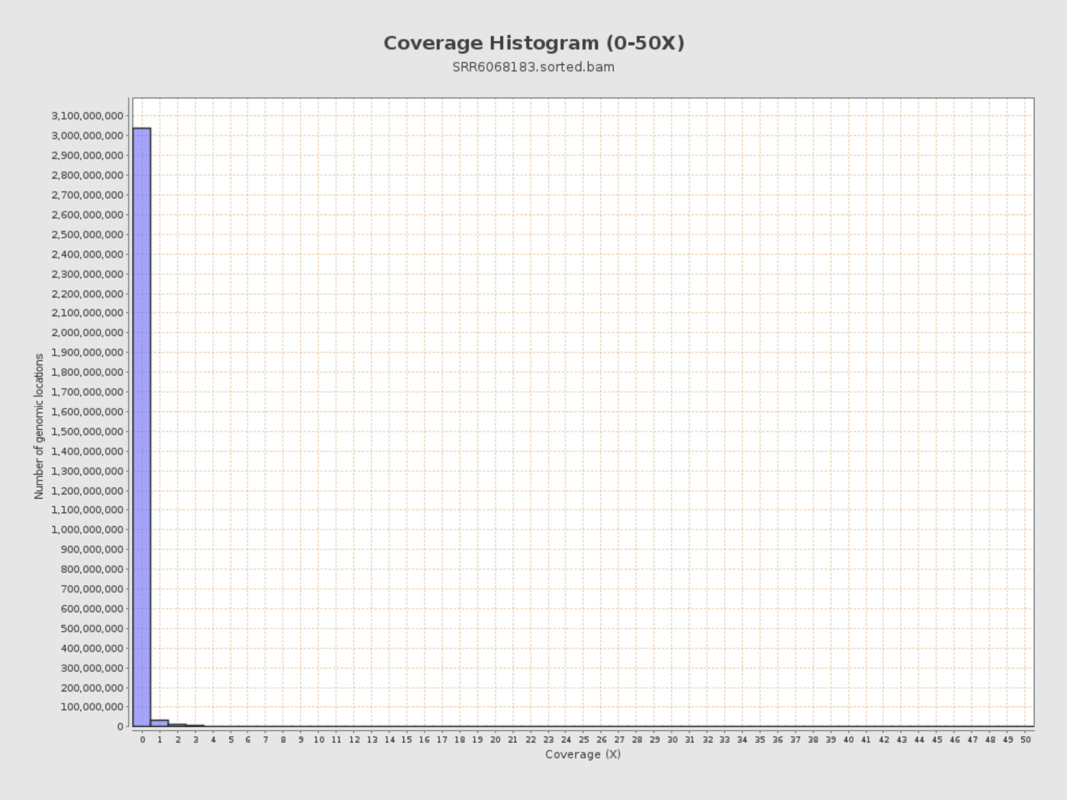
3. Results : Coverage across reference



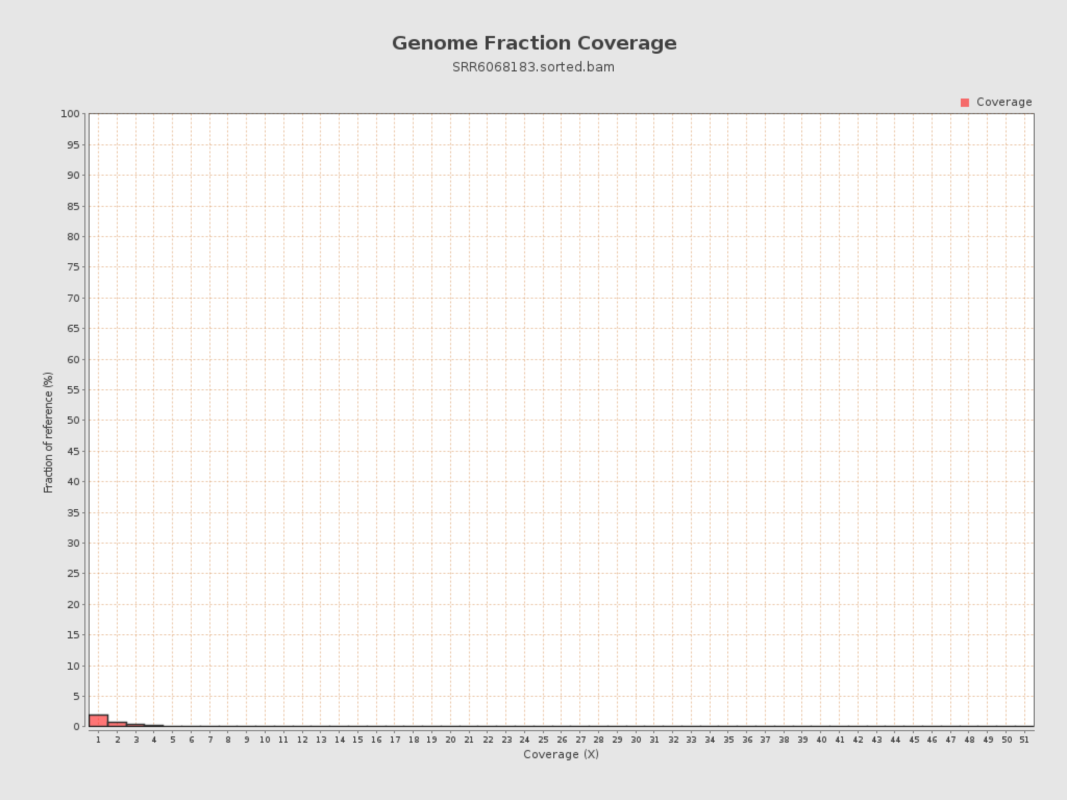
4. Results : Coverage Histogram



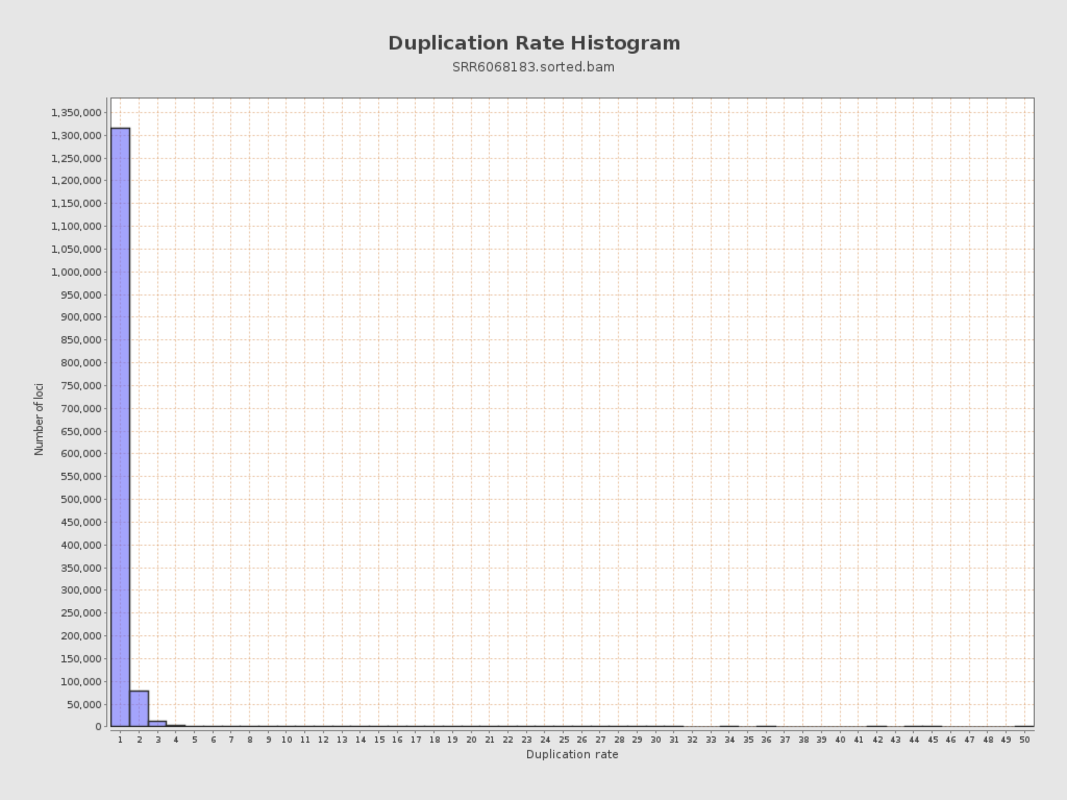
5. Results : Coverage Histogram (0-50X)



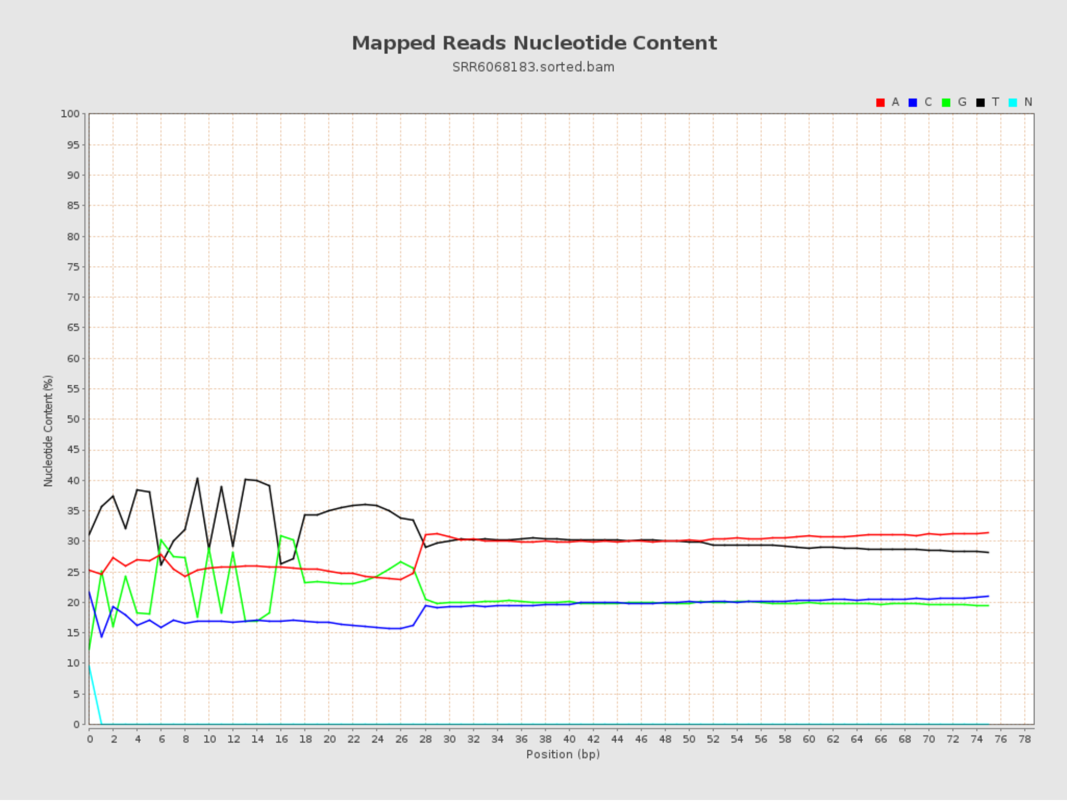
6. Results : Genome Fraction Coverage



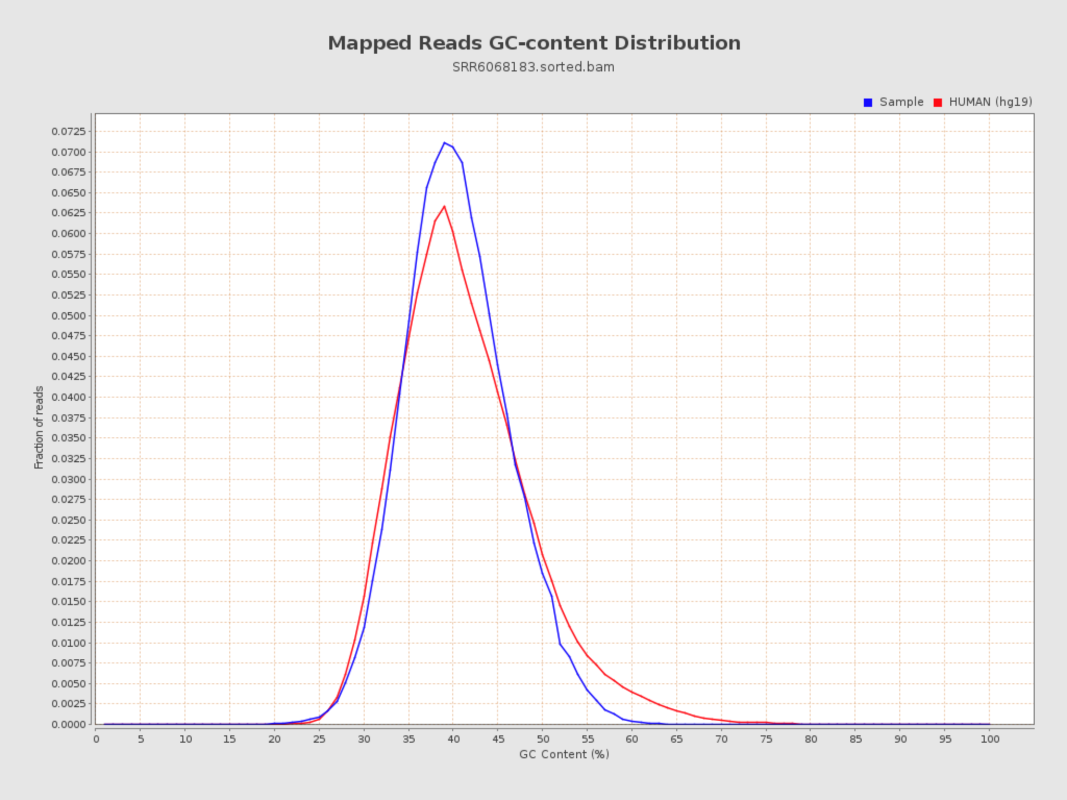
7. Results : Duplication Rate Histogram



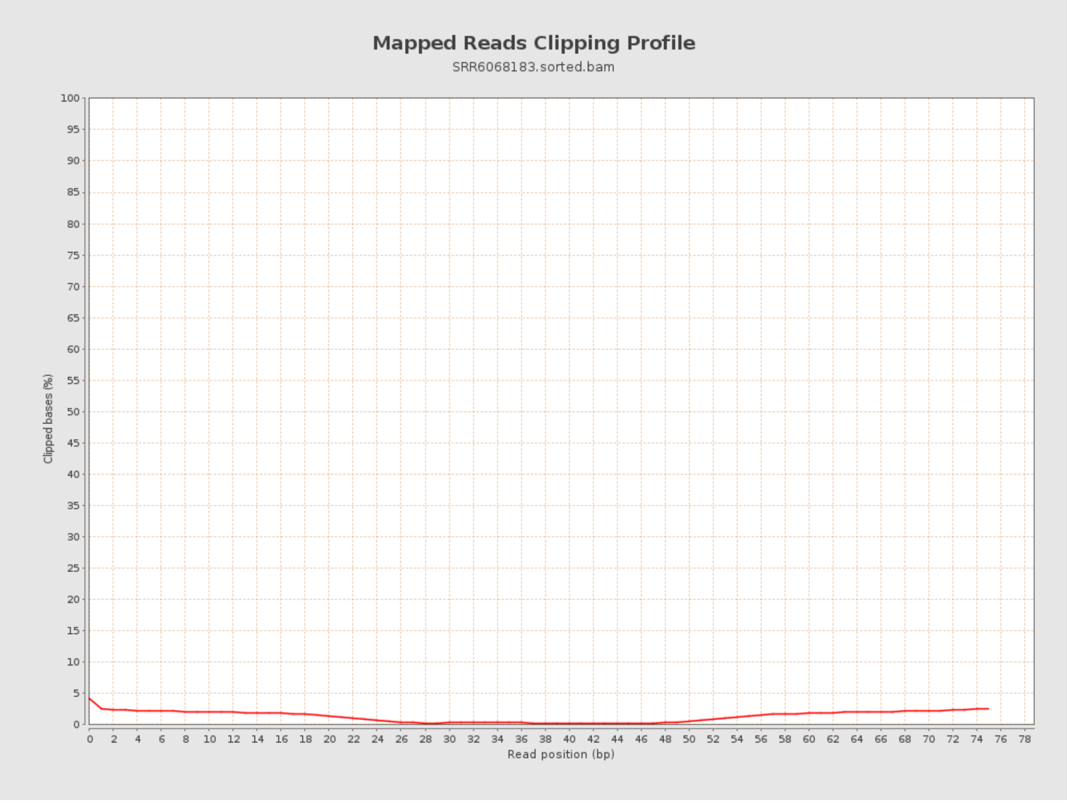
8. Results : Mapped Reads Nucleotide Content



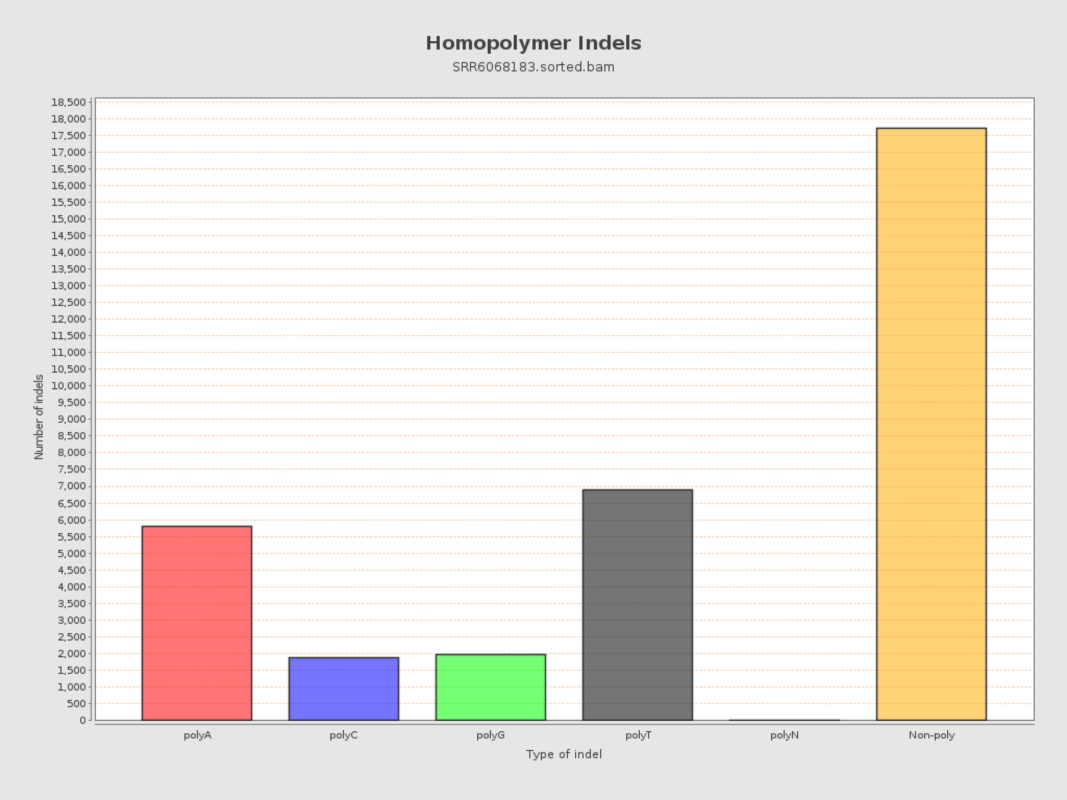
9. Results : Mapped Reads GC-content Distribution



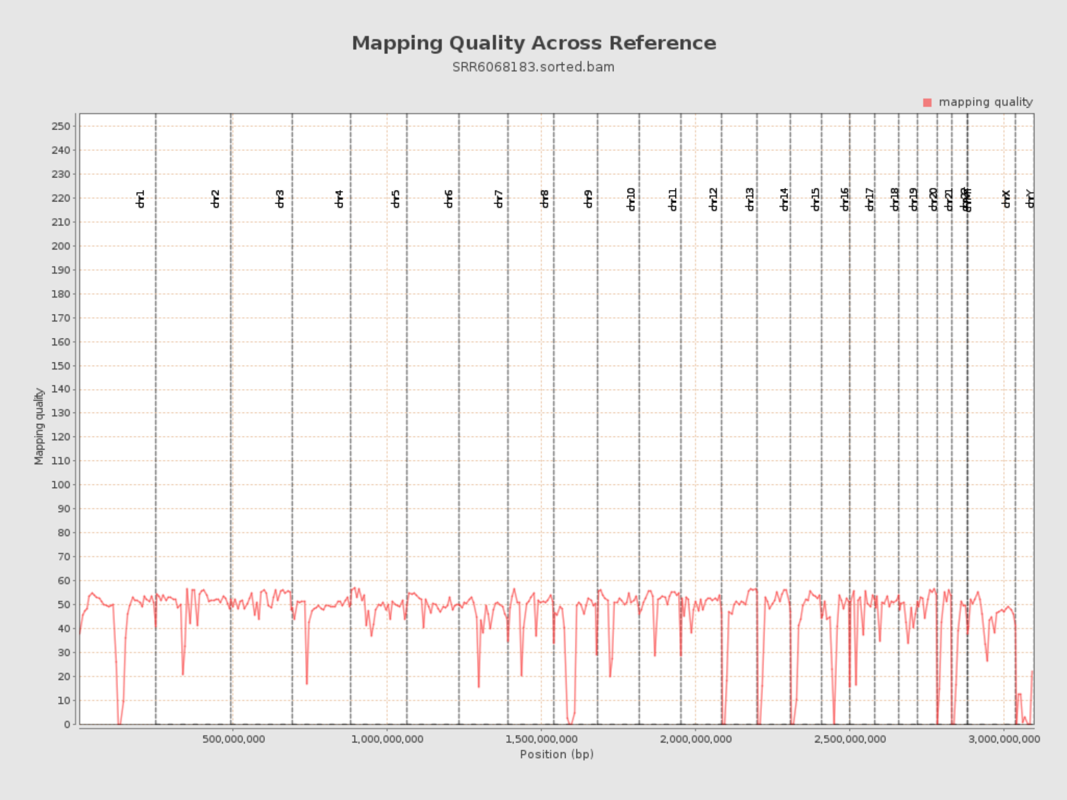
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram