Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 11:05:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068116.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_SRR6068116 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068116.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 11:05:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068116.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,976,536
Mapped reads	1,496,045 / 75.69%
Unmapped reads	480,491 / 24.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,696 / 0.79%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	239,468 / 12.12%
Duplication rate	11.31%
Clipped reads	657,639 / 33.27%

2.2. ACGT Content

Number/percentage of A's	27,839,844 / 27.87%
Number/percentage of C's	18,045,962 / 18.07%
Number/percentage of T's	32,122,999 / 32.16%
Number/percentage of G's	21,779,825 / 21.8%
Number/percentage of N's	103,364 / 0.1%
GC Percentage	39.87%

2.3. Coverage

Mean	0.0323

Standard Deviation	0.4617

2.4. Mapping Quality

Mean Mapping Quality	46.78

2.5. Mismatches and indels

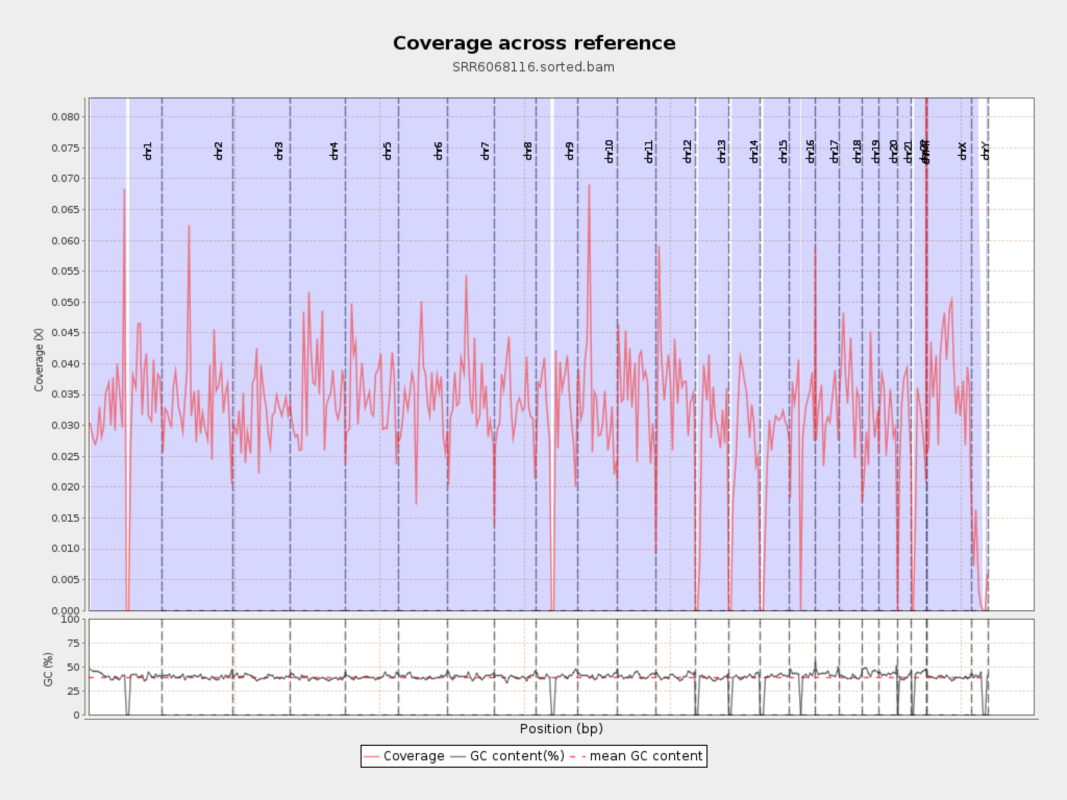
General error rate	0.9%
Mismatches	880,261
Insertions	8,030
Mapped reads with at least one insertion	0.53%
Deletions	23,294
Mapped reads with at least one deletion	1.54%
Homopolymer indels	48%

2.6. Chromosome stats

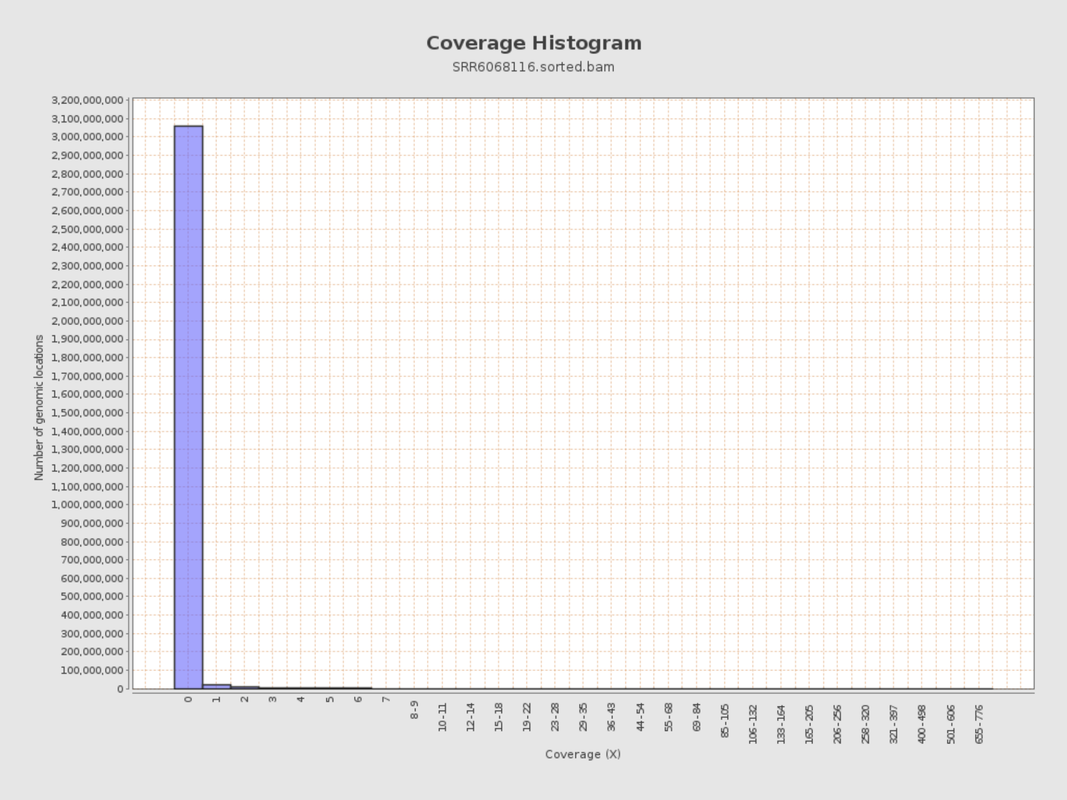
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8290587	0.0333	0.6121
chr2	243199373	8256608	0.0339	0.4947
chr3	198022430	6287636	0.0318	0.403
chr4	191154276	6745178	0.0353	0.4338
chr5	180915260	6347564	0.0351	0.4284
chr6	171115067	5822164	0.034	0.4263
chr7	159138663	5599419	0.0352	0.5088

chr8	146364022	4850104	0.0331	0.6135
chr9	141213431	4333754	0.0307	0.4327
chr10	135534747	4600426	0.0339	0.4859
chr11	135006516	4787706	0.0355	0.4525
chr12	133851895	4933989	0.0369	0.4288
chr13	115169878	3134904	0.0272	0.3735
chr14	107349540	2883404	0.0269	0.3733
chr15	102531392	2478807	0.0242	0.3489
chr16	90354753	2781908	0.0308	0.3929
chr17	81195210	2556671	0.0315	0.3855
chr18	78077248	2834660	0.0363	0.6253
chr19	59128983	1760016	0.0298	0.4672
chr20	63025520	1976830	0.0314	0.3882
chr21	48129895	1397908	0.029	0.3751
chr22	51304566	1099788	0.0214	0.303
chrMT	16571	18683	1.1275	2.0885
chrX	155270560	5830429	0.0376	0.453
chrY	59373566	321225	0.0054	0.1597

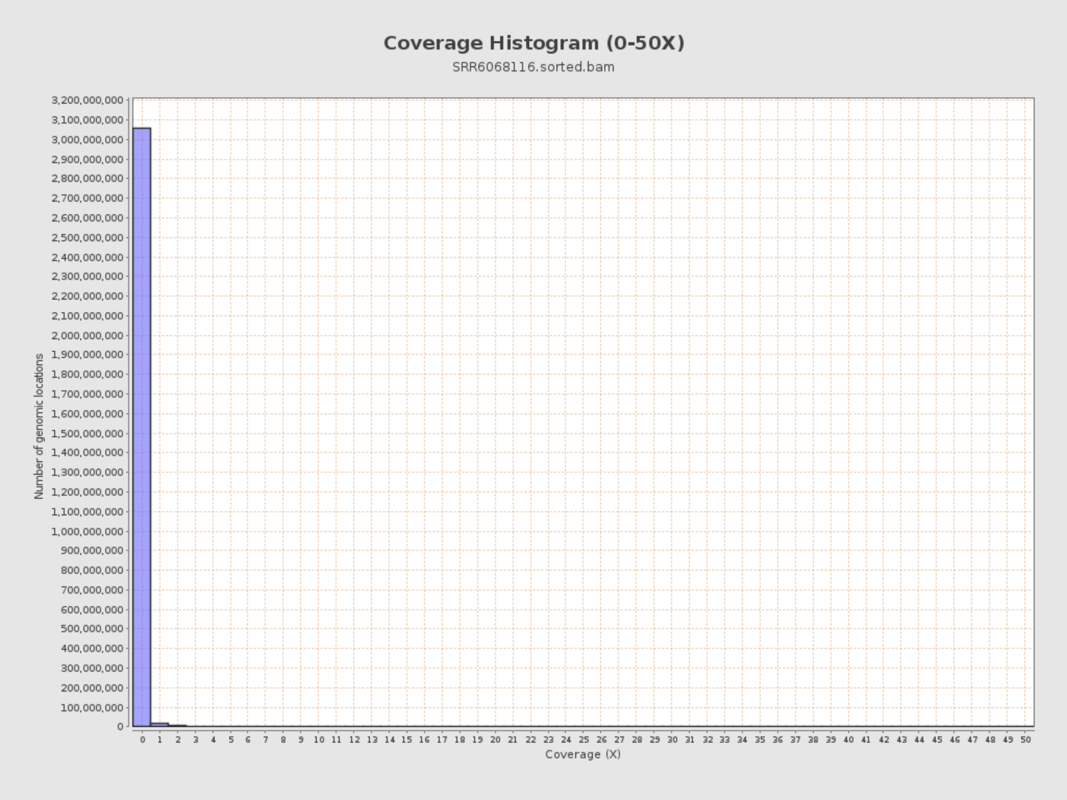
3. Results : Coverage across reference



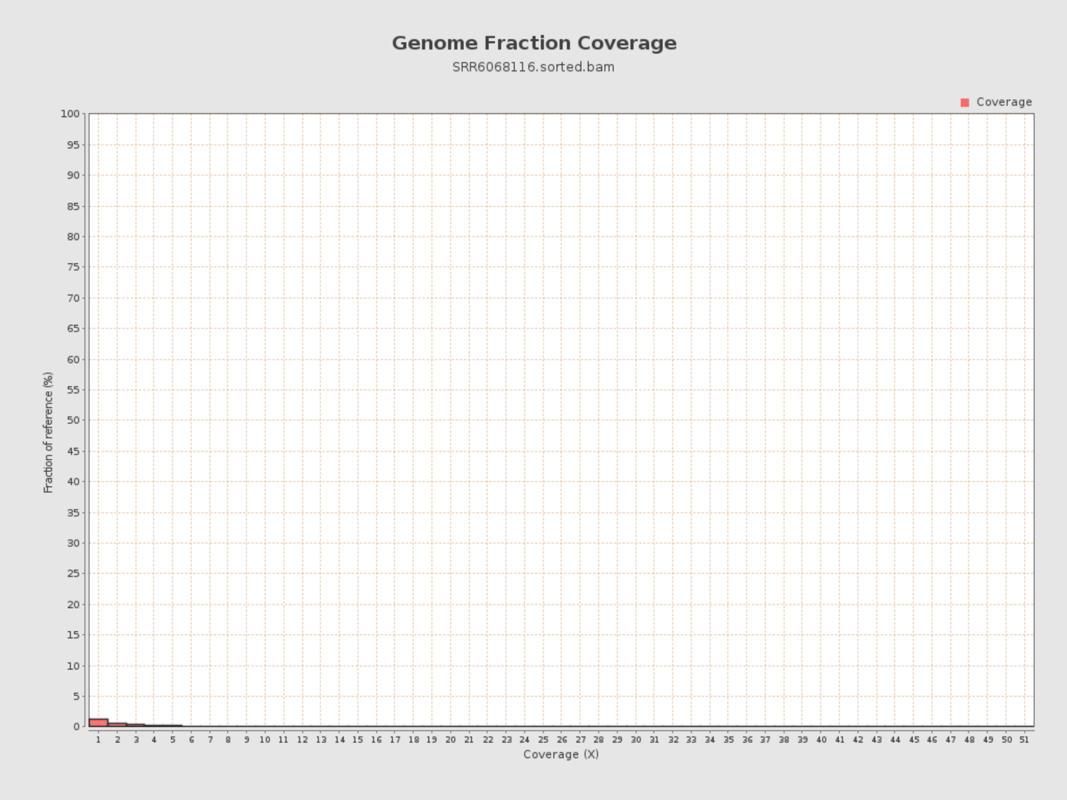
4. Results : Coverage Histogram



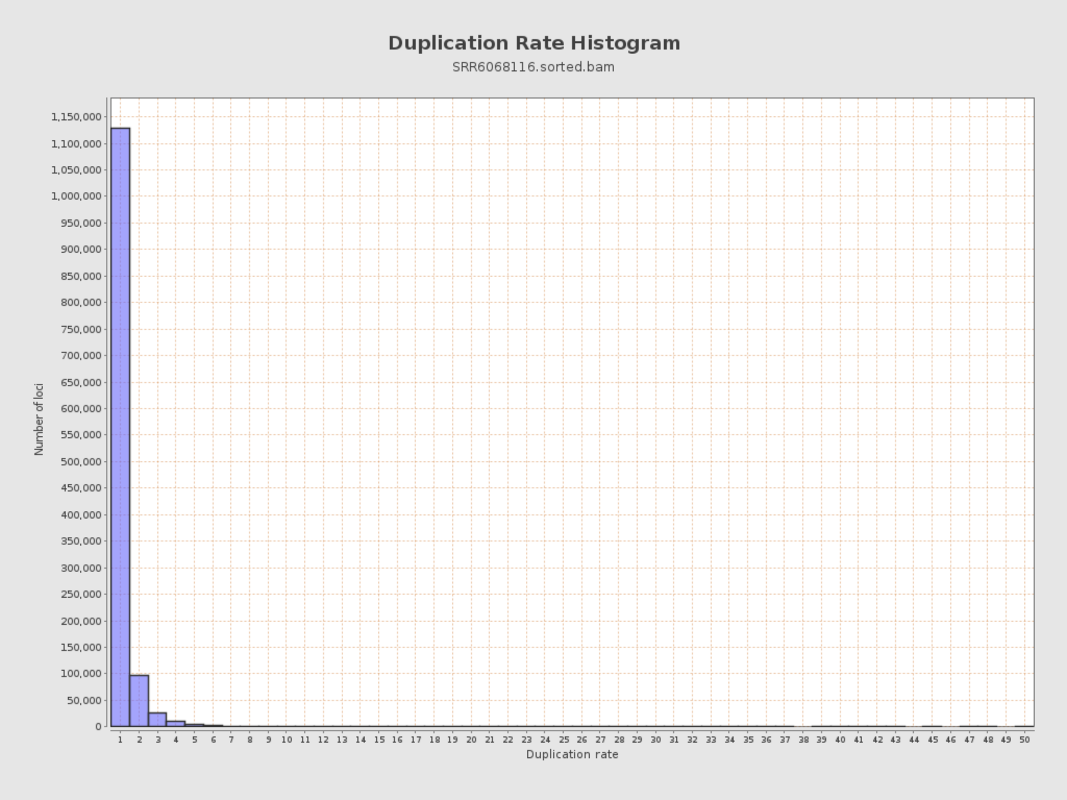
5. Results : Coverage Histogram (0-50X)



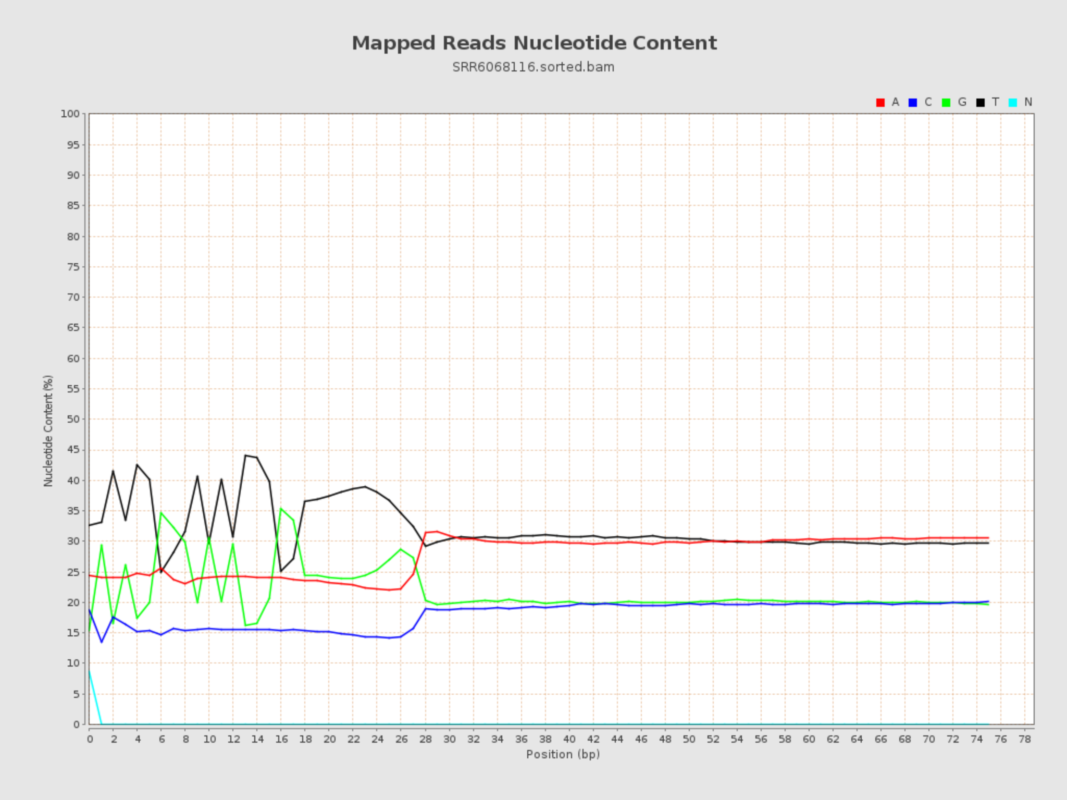
6. Results : Genome Fraction Coverage



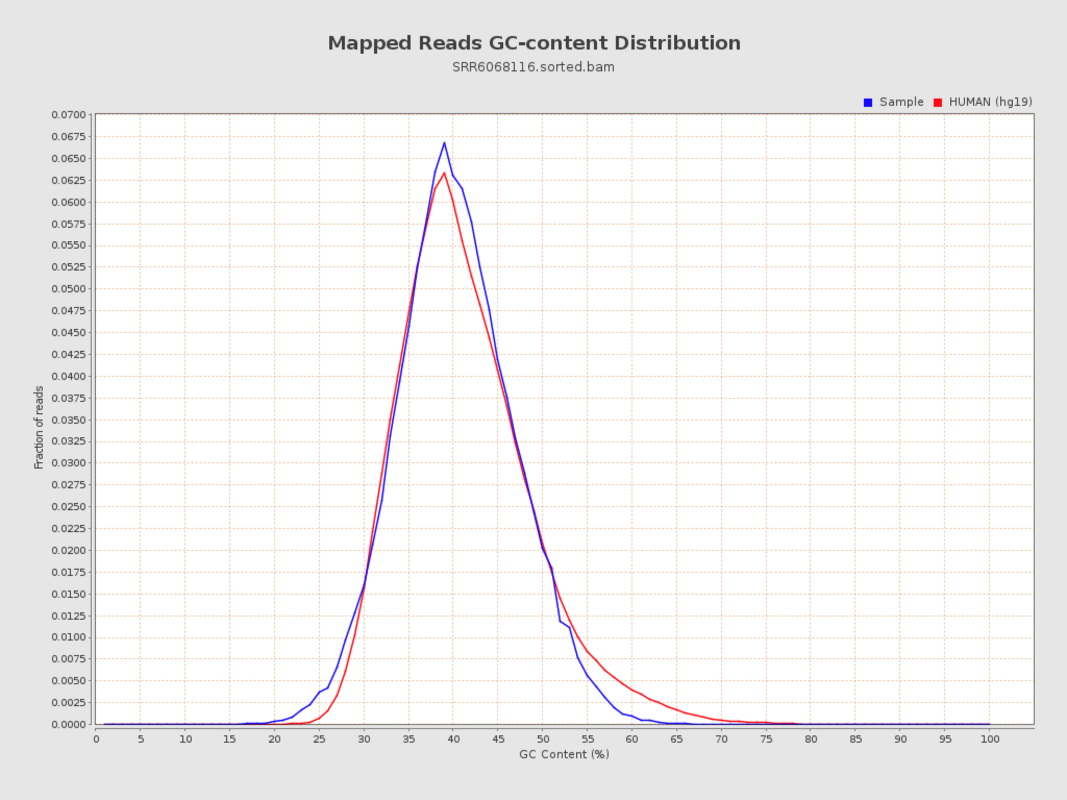
7. Results : Duplication Rate Histogram



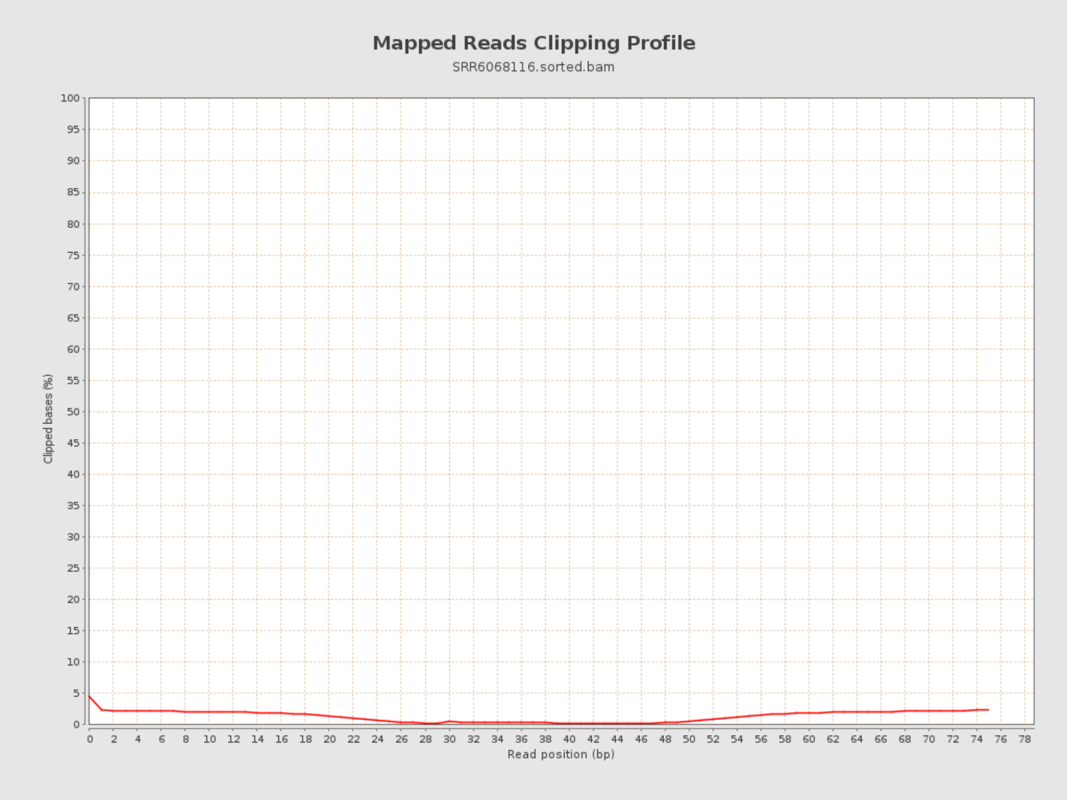
8. Results : Mapped Reads Nucleotide Content



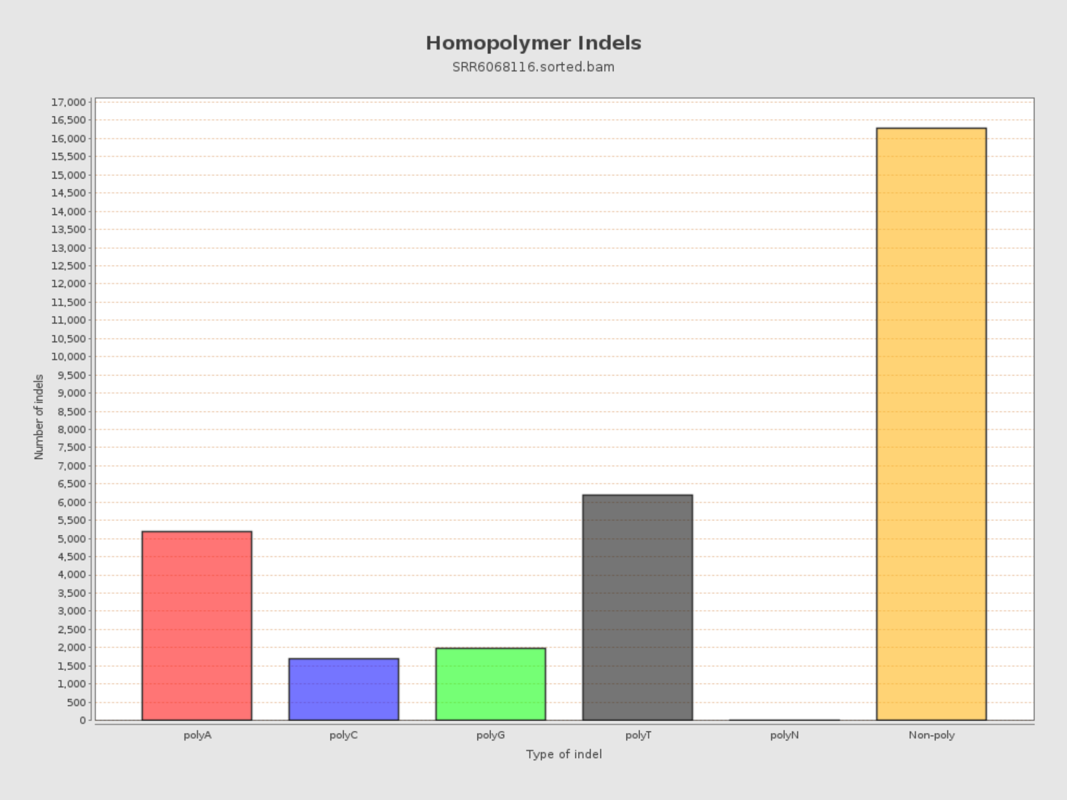
9. Results : Mapped Reads GC-content Distribution



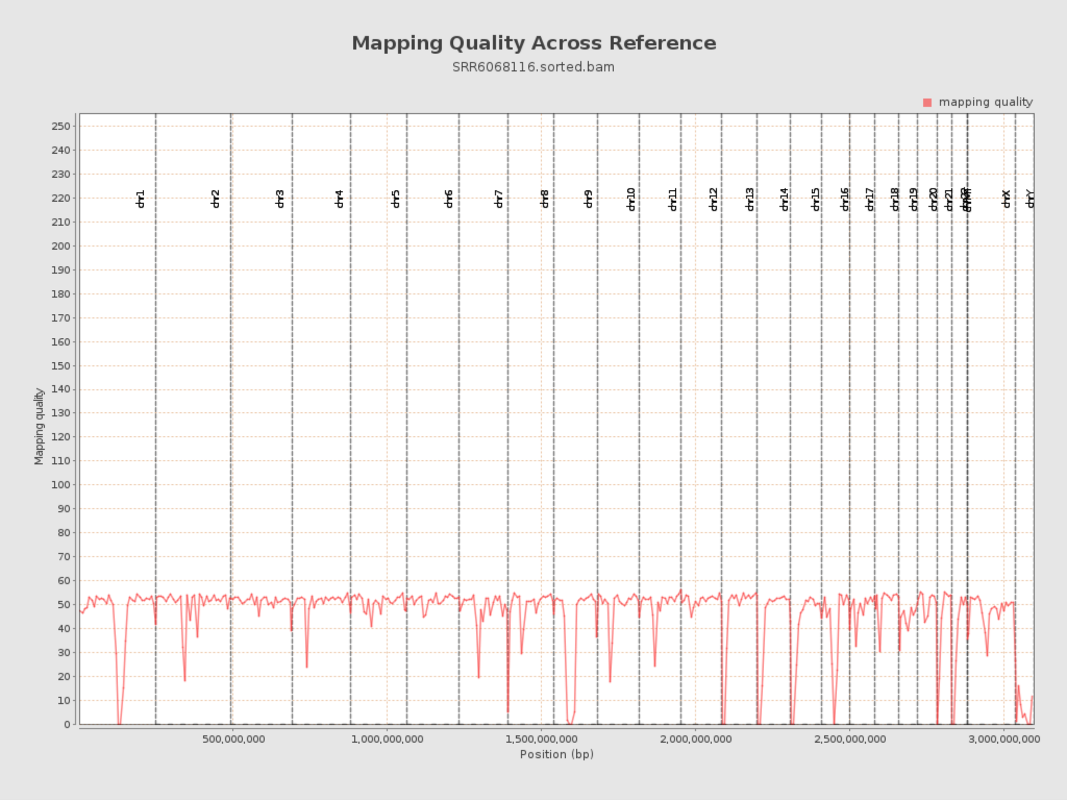
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram