Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 00:05:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004075.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_SRR6004075 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004075.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 00:05:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004075.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,111,548
Mapped reads	1,919,541 / 90.91%
Unmapped reads	192,007 / 9.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,177 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	69,829 / 3.31%
Duplication rate	2.82%
Clipped reads	833,561 / 39.48%

2.2. ACGT Content

Number/percentage of A's	36,738,916 / 28.48%
Number/percentage of C's	23,910,132 / 18.54%
Number/percentage of T's	40,455,413 / 31.37%
Number/percentage of G's	27,849,418 / 21.59%
Number/percentage of N's	23,200 / 0.02%
GC Percentage	40.13%

2.3. Coverage

Mean	0.0417

Standard Deviation	0.3574

2.4. Mapping Quality

Mean Mapping Quality	45.99

2.5. Mismatches and indels

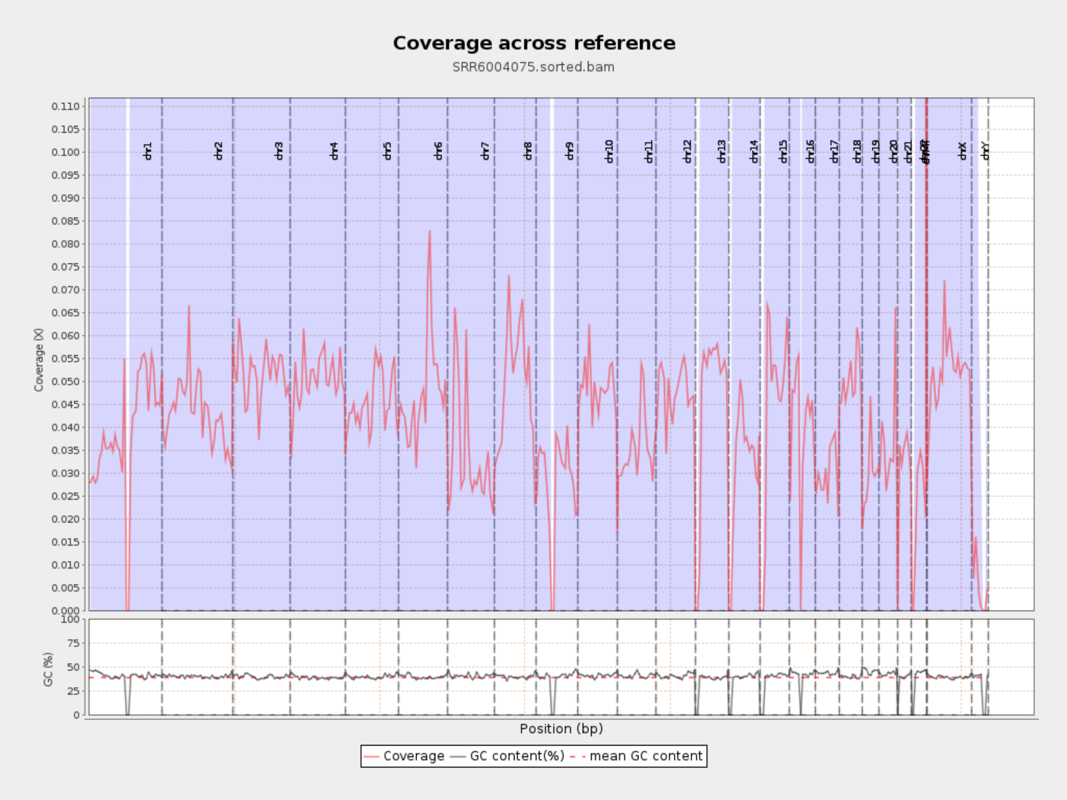
General error rate	0.89%
Mismatches	1,132,408
Insertions	9,547
Mapped reads with at least one insertion	0.49%
Deletions	33,523
Mapped reads with at least one deletion	1.73%
Homopolymer indels	46.38%

2.6. Chromosome stats

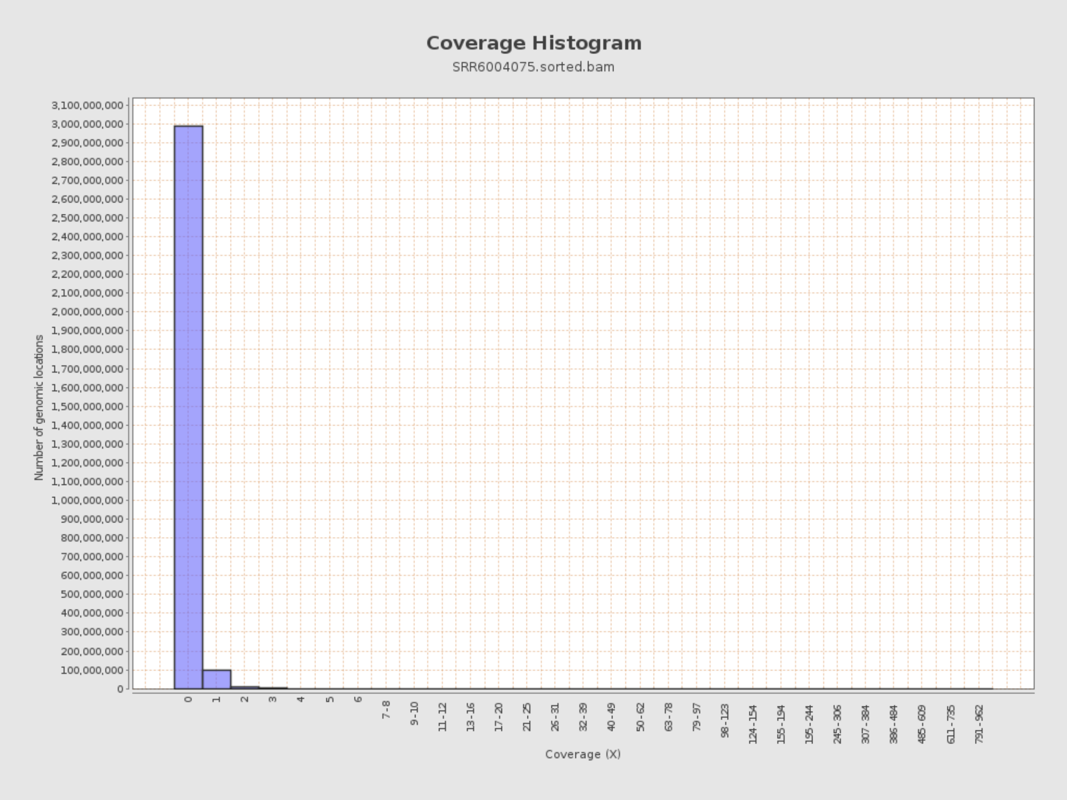
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9645104	0.0387	0.5919
chr2	243199373	10510269	0.0432	0.3863
chr3	198022430	10299105	0.052	0.2562
chr4	191154276	9639557	0.0504	0.2692
chr5	180915260	8249639	0.0456	0.2417
chr6	171115067	8168804	0.0477	0.2645
chr7	159138663	5482146	0.0344	0.4482

chr8	146364022	7238848	0.0495	0.6307
chr9	141213431	3962382	0.0281	0.2844
chr10	135534747	6611485	0.0488	0.3283
chr11	135006516	4776021	0.0354	0.3189
chr12	133851895	6366022	0.0476	0.2503
chr13	115169878	5207011	0.0452	0.2471
chr14	107349540	3369309	0.0314	0.2133
chr15	102531392	4481426	0.0437	0.2425
chr16	90354753	3614097	0.04	0.2486
chr17	81195210	2422495	0.0298	0.215
chr18	78077248	3944073	0.0505	0.581
chr19	59128983	1764835	0.0298	0.4161
chr20	63025520	2336519	0.0371	0.2294
chr21	48129895	1506098	0.0313	0.2168
chr22	51304566	1075198	0.021	0.1604
chrMT	16571	22950	1.3849	1.5338
chrX	155270560	8014465	0.0516	0.2791
chrY	59373566	327535	0.0055	0.118

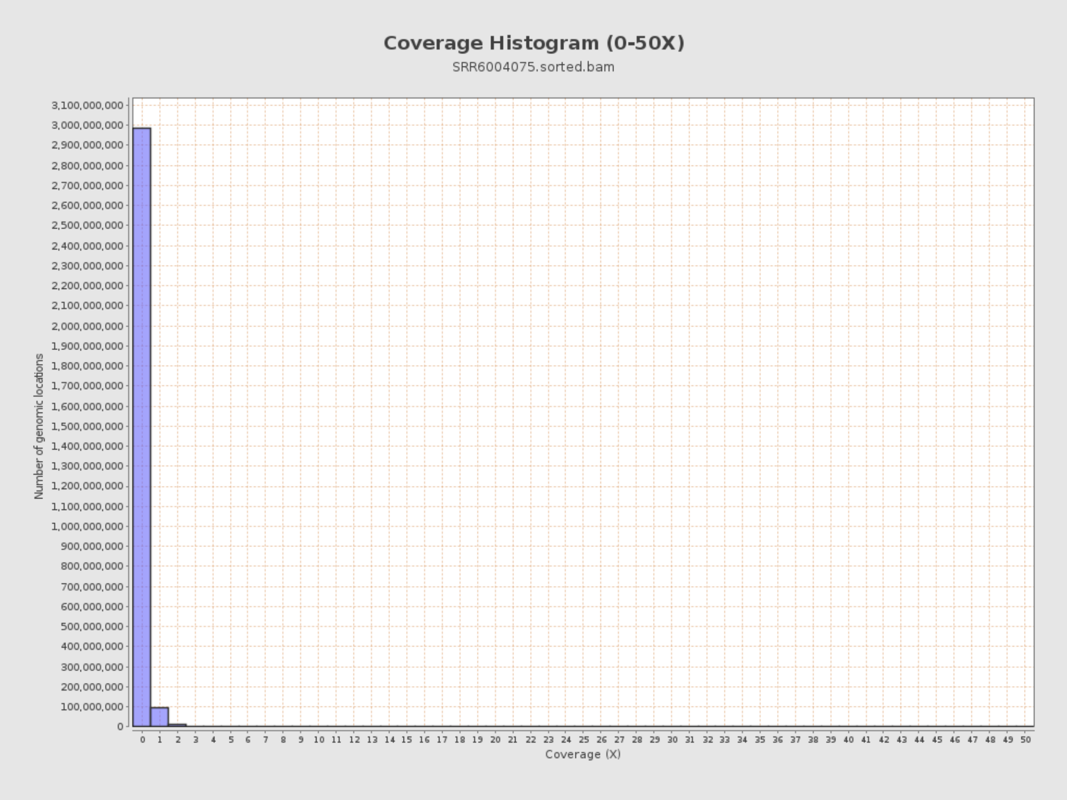
3. Results : Coverage across reference



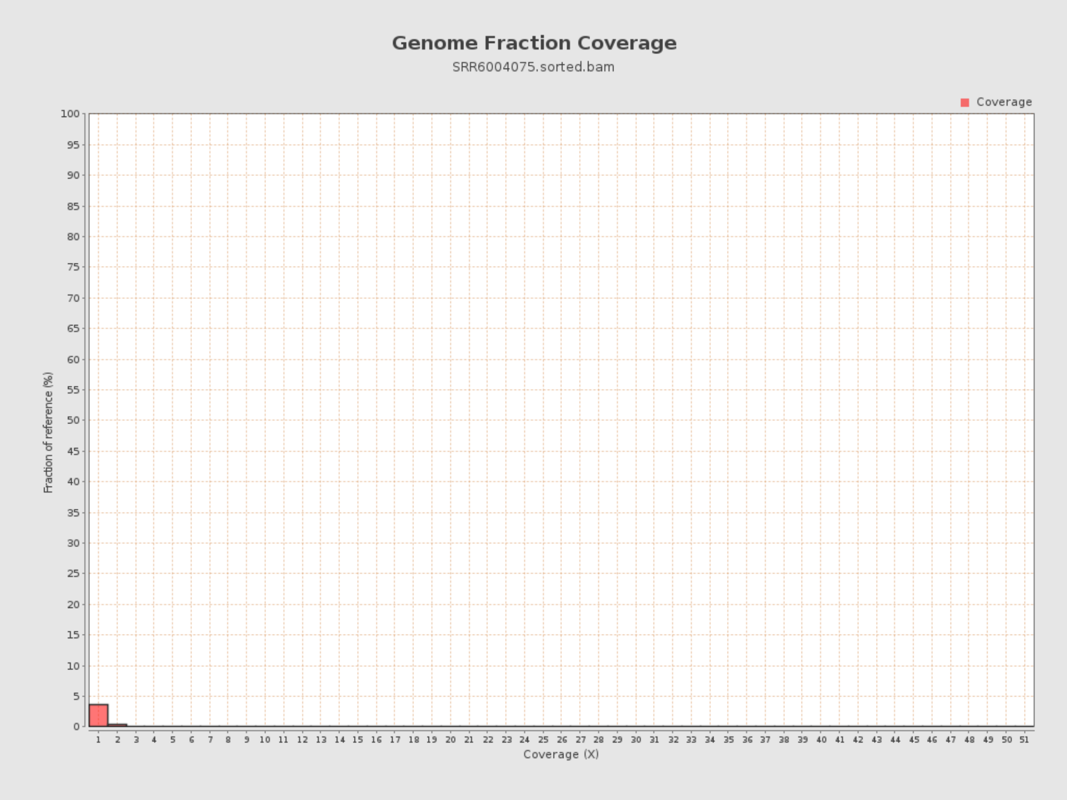
4. Results : Coverage Histogram



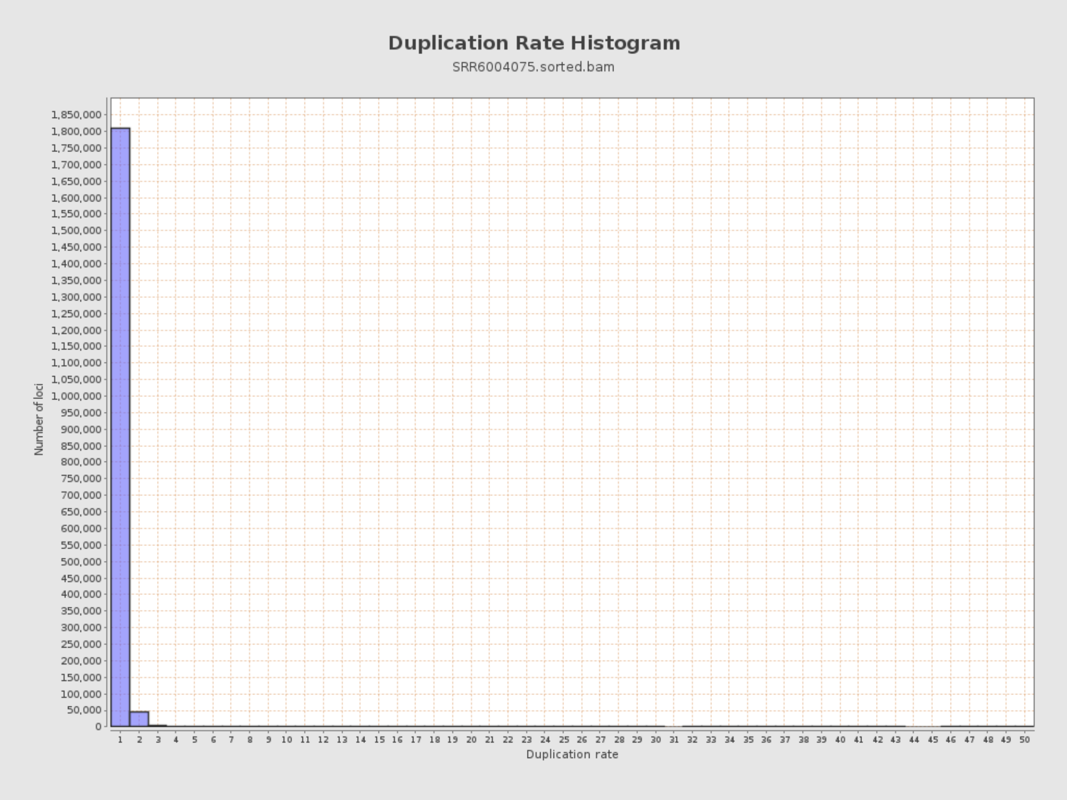
5. Results : Coverage Histogram (0-50X)



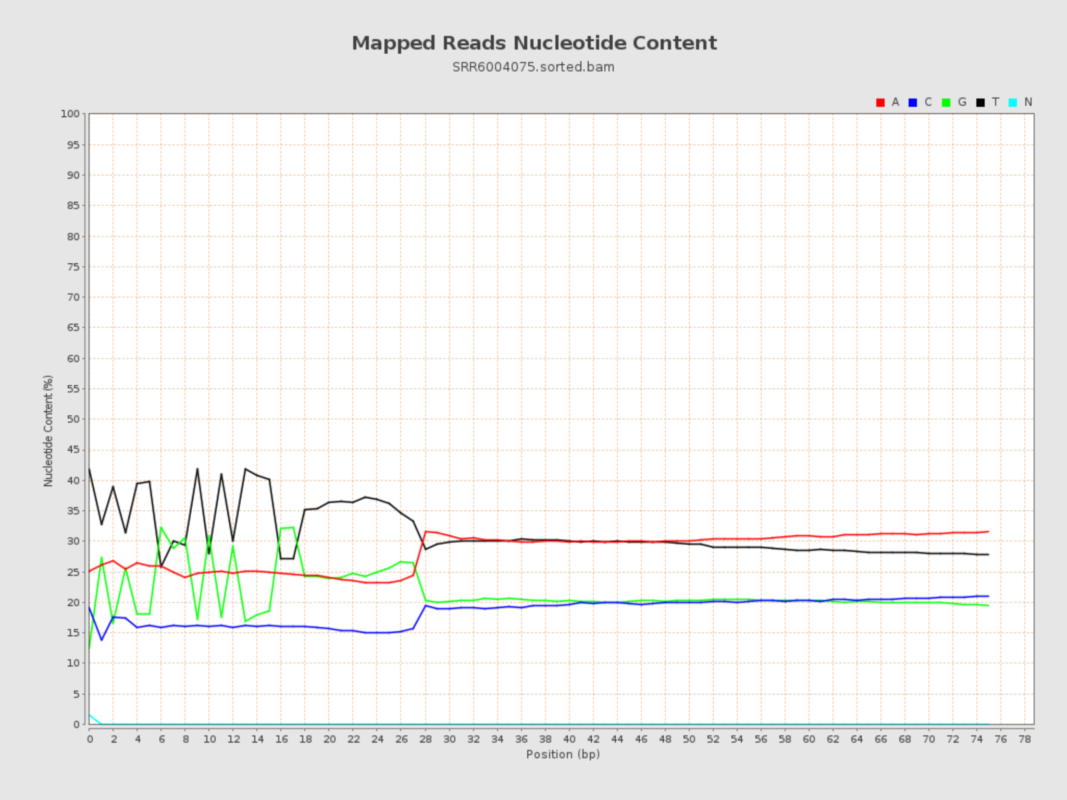
6. Results : Genome Fraction Coverage



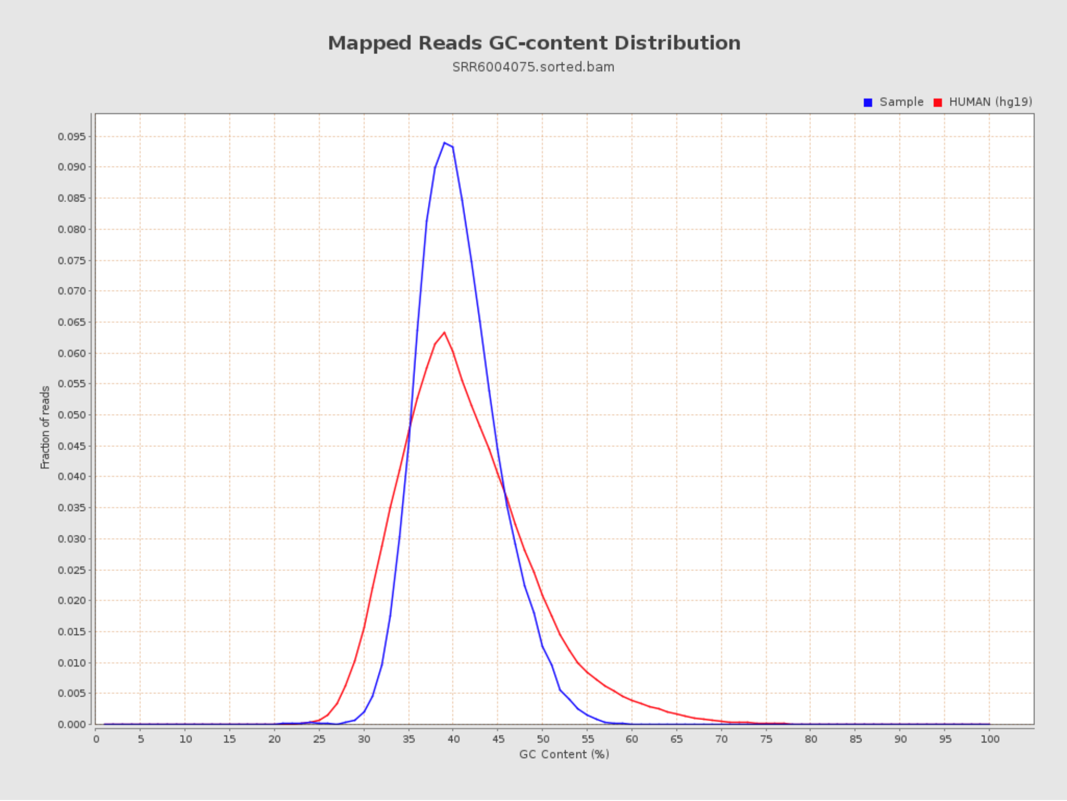
7. Results : Duplication Rate Histogram



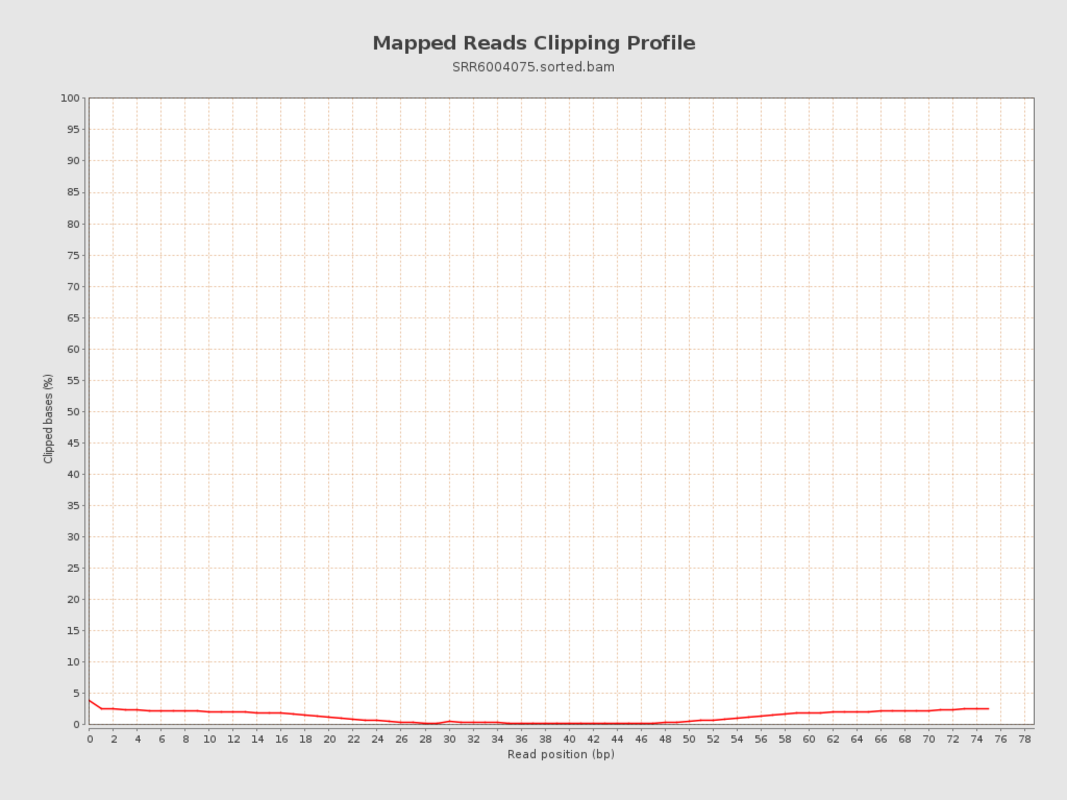
8. Results : Mapped Reads Nucleotide Content



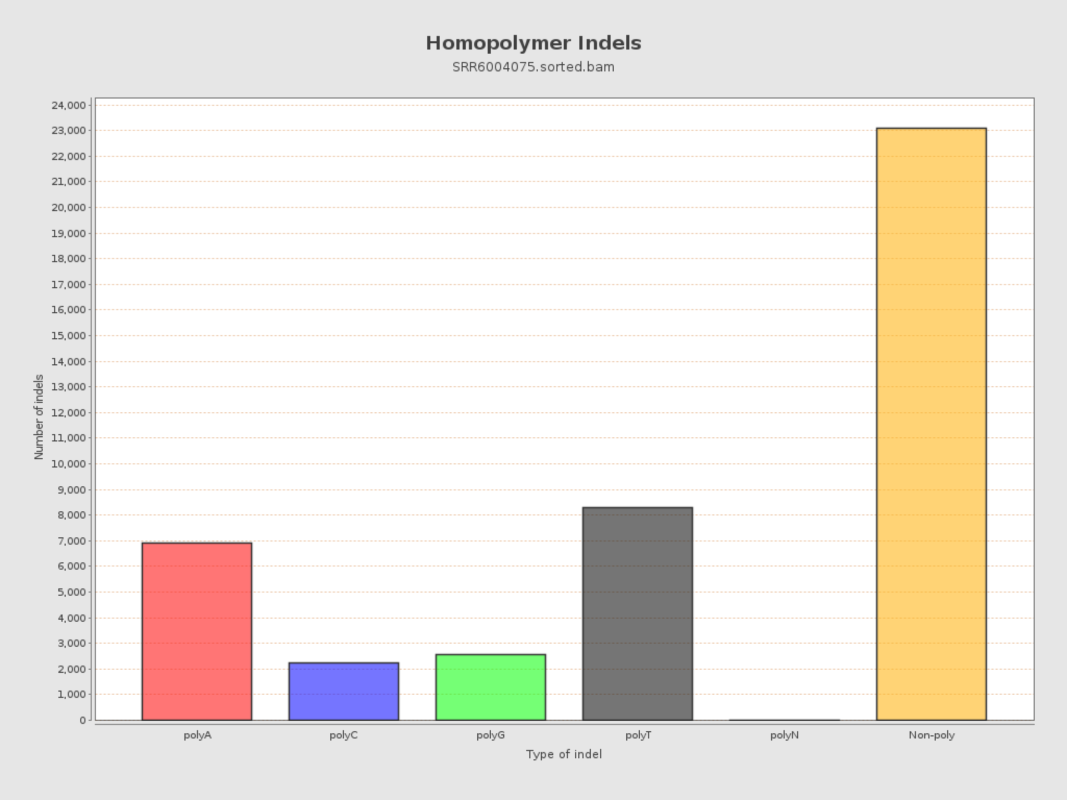
9. Results : Mapped Reads GC-content Distribution



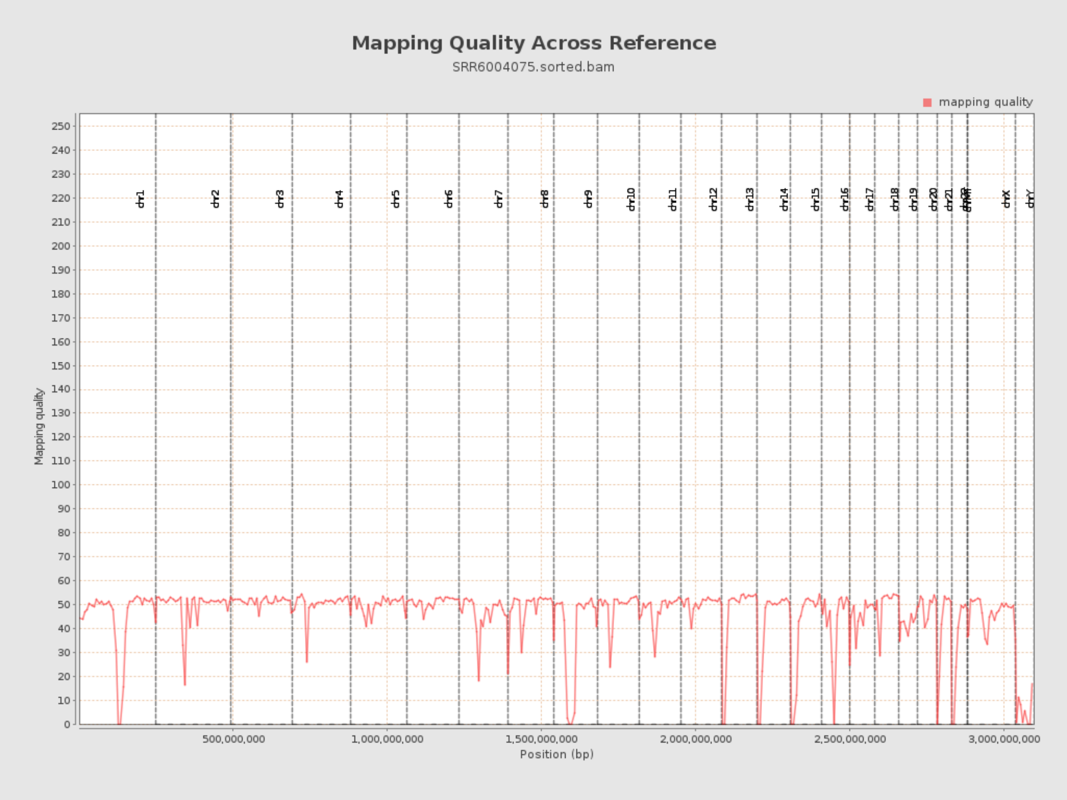
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram