Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 03:01:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004121.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_SRR6004121 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004121.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 03:01:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004121.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,727,572
Mapped reads	3,892,601 / 82.34%
Unmapped reads	834,971 / 17.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,164 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	298,797 / 6.32%
Duplication rate	5.92%
Clipped reads	1,841,918 / 38.96%

2.2. ACGT Content

Number/percentage of A's	71,099,033 / 27.62%
Number/percentage of C's	45,408,414 / 17.64%
Number/percentage of T's	84,641,496 / 32.88%
Number/percentage of G's	56,209,310 / 21.84%
Number/percentage of N's	28,119 / 0.01%
GC Percentage	39.48%

2.3. Coverage

Mean	0.0832

Standard Deviation	0.8181

2.4. Mapping Quality

Mean Mapping Quality	45.55

2.5. Mismatches and indels

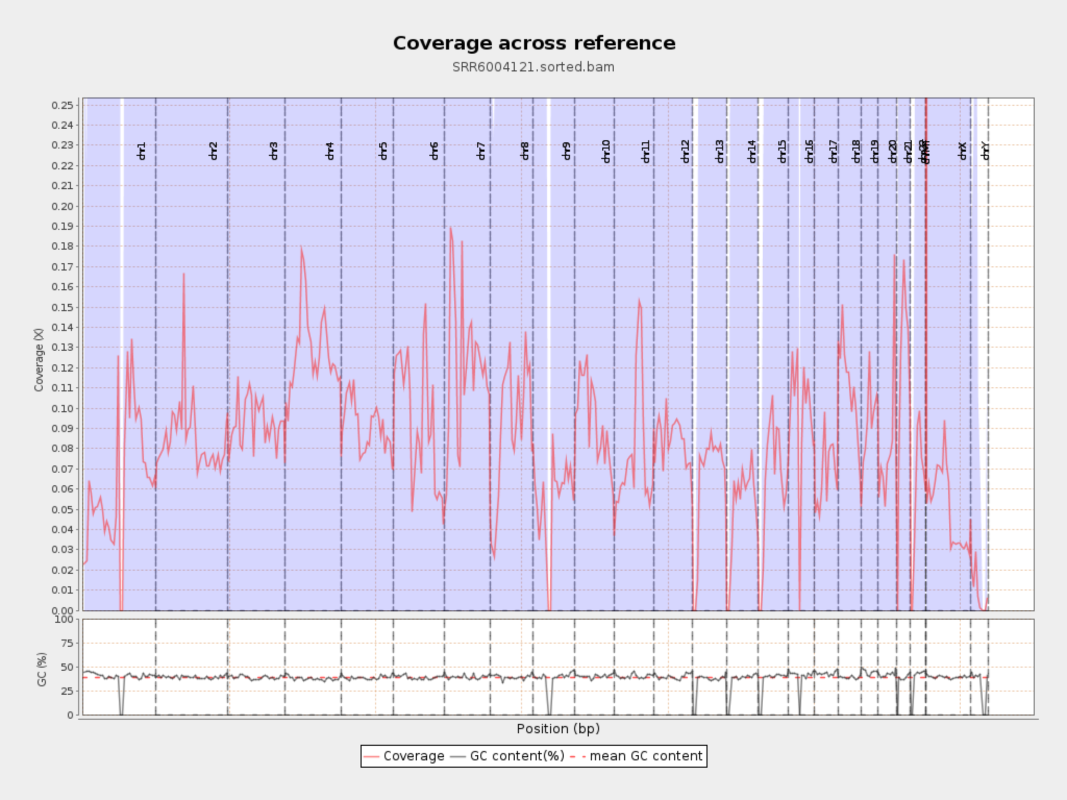
General error rate	1%
Mismatches	2,542,384
Insertions	22,943
Mapped reads with at least one insertion	0.58%
Deletions	75,816
Mapped reads with at least one deletion	1.93%
Homopolymer indels	48.15%

2.6. Chromosome stats

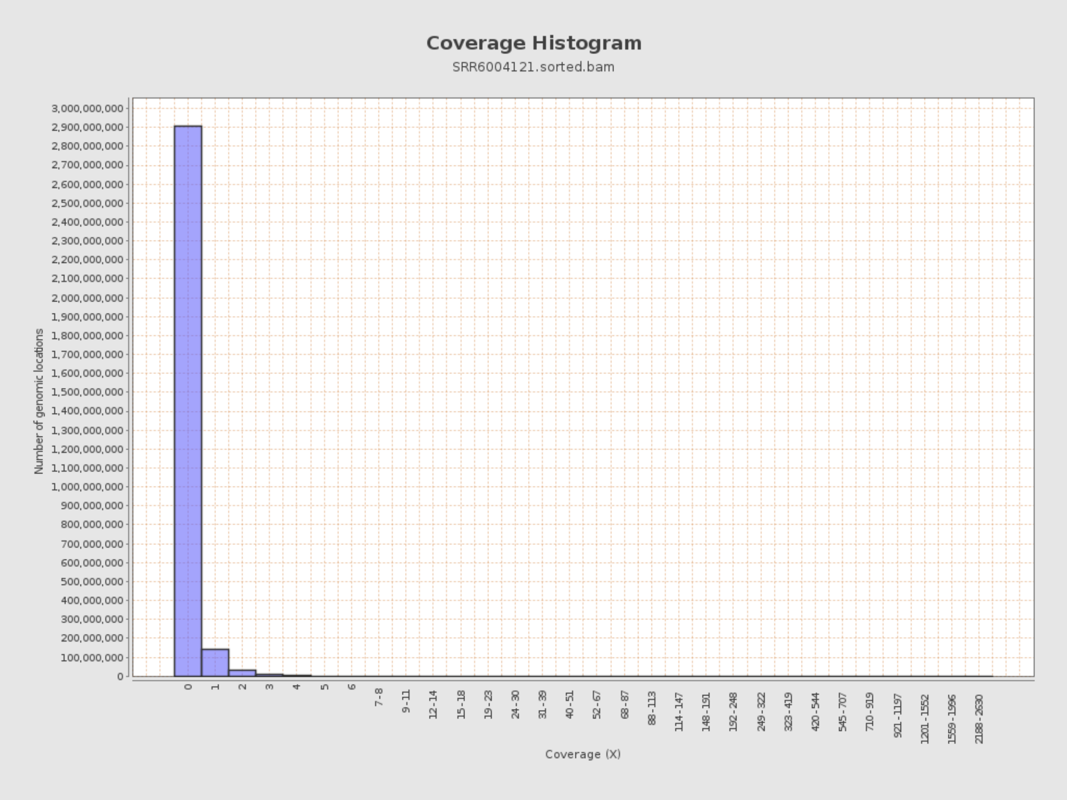
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15855183	0.0636	1.4918
chr2	243199373	20652927	0.0849	0.9247
chr3	198022430	18488536	0.0934	0.394
chr4	191154276	24651873	0.129	0.4741
chr5	180915260	16452581	0.0909	0.3992
chr6	171115067	16268225	0.0951	0.4831
chr7	159138663	19215080	0.1207	1.2995

chr8	146364022	13434670	0.0918	1.5813
chr9	141213431	7583199	0.0537	0.6665
chr10	135534747	12872017	0.095	0.6112
chr11	135006516	10496214	0.0777	0.5662
chr12	133851895	11265648	0.0842	0.3846
chr13	115169878	7456221	0.0647	0.3262
chr14	107349540	5614014	0.0523	0.3578
chr15	102531392	6313784	0.0616	0.3241
chr16	90354753	8588514	0.0951	0.4621
chr17	81195210	5439435	0.067	0.3834
chr18	78077248	8759999	0.1122	1.4606
chr19	59128983	5546988	0.0938	0.9965
chr20	63025520	5259710	0.0835	0.4166
chr21	48129895	5594367	0.1162	0.469
chr22	51304566	2943753	0.0574	0.3034
chrMT	16571	323538	19.5243	11.579
chrX	155270560	7899846	0.0509	0.3924
chrY	59373566	535332	0.009	0.1836

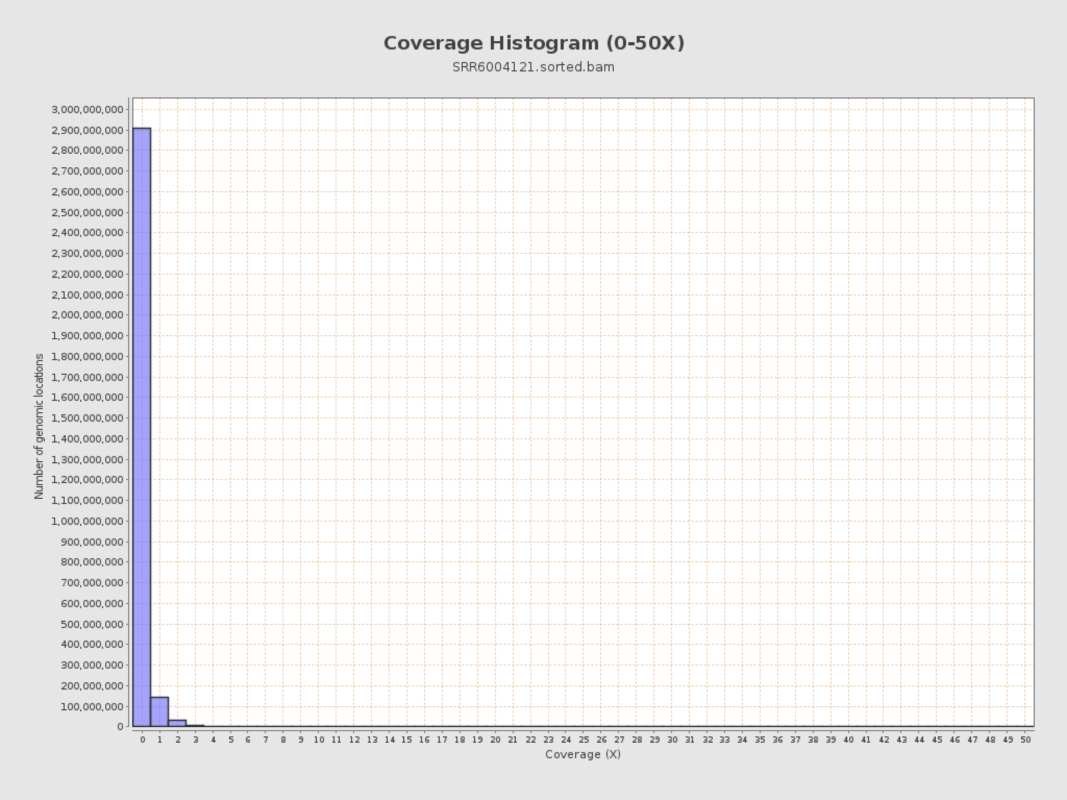
3. Results : Coverage across reference



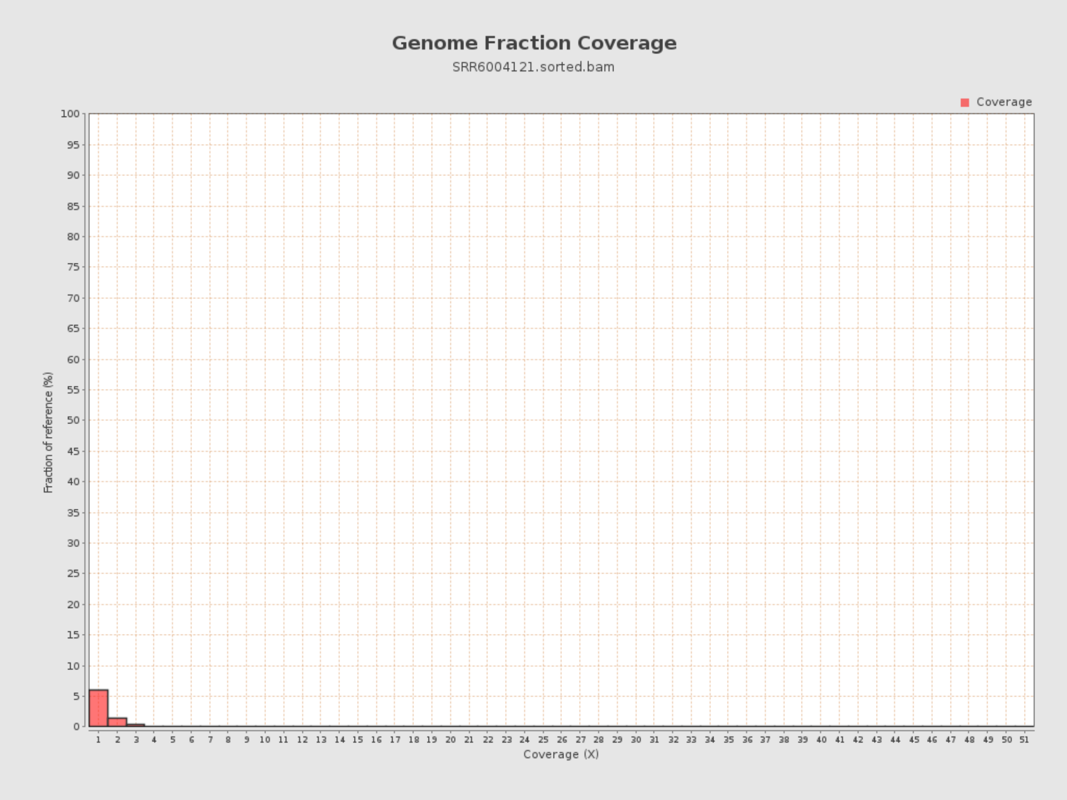
4. Results : Coverage Histogram



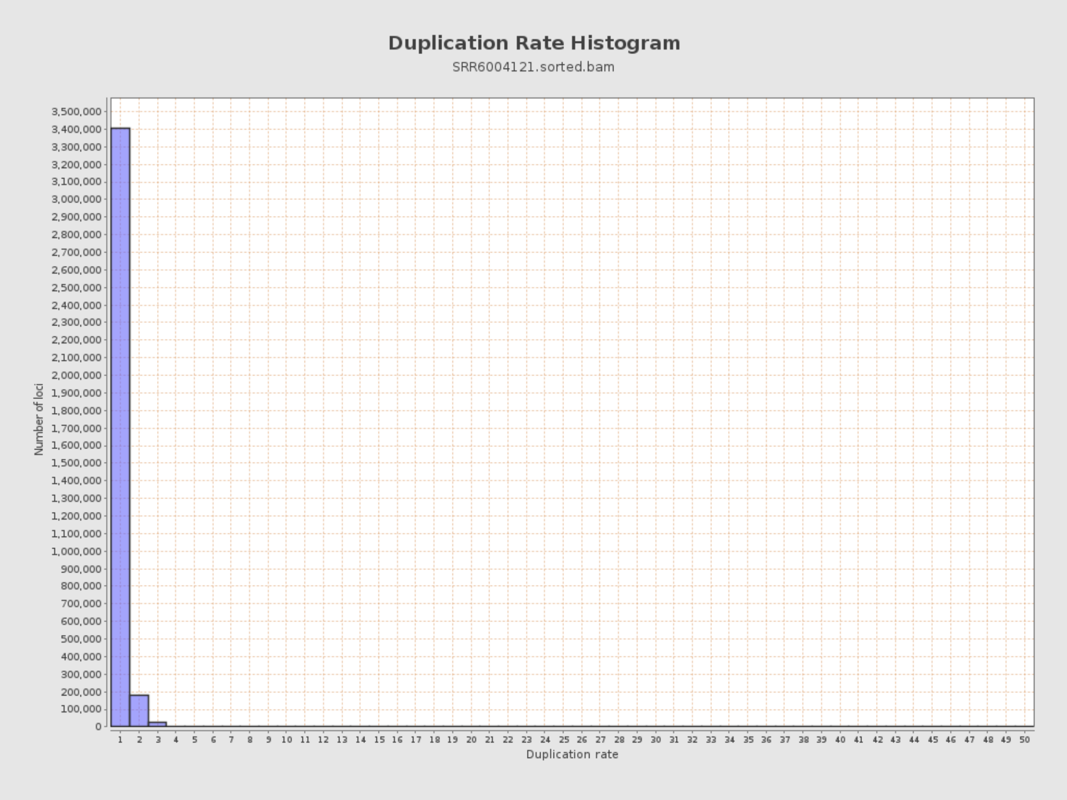
5. Results : Coverage Histogram (0-50X)



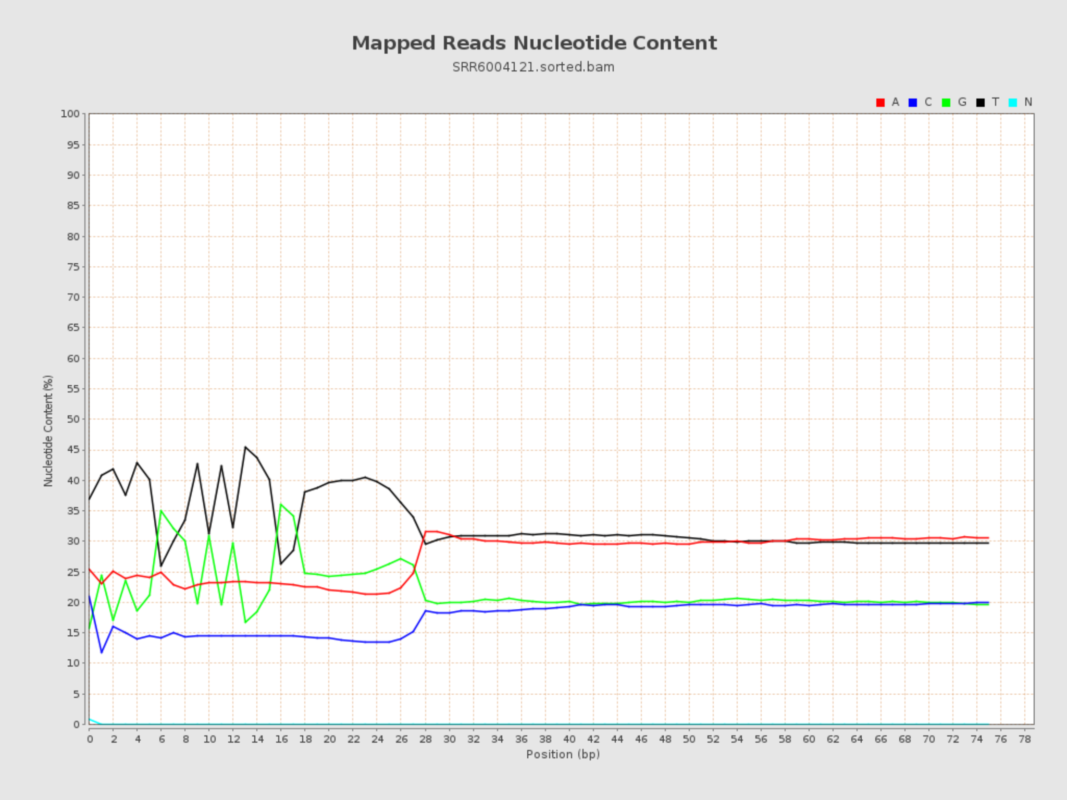
6. Results : Genome Fraction Coverage



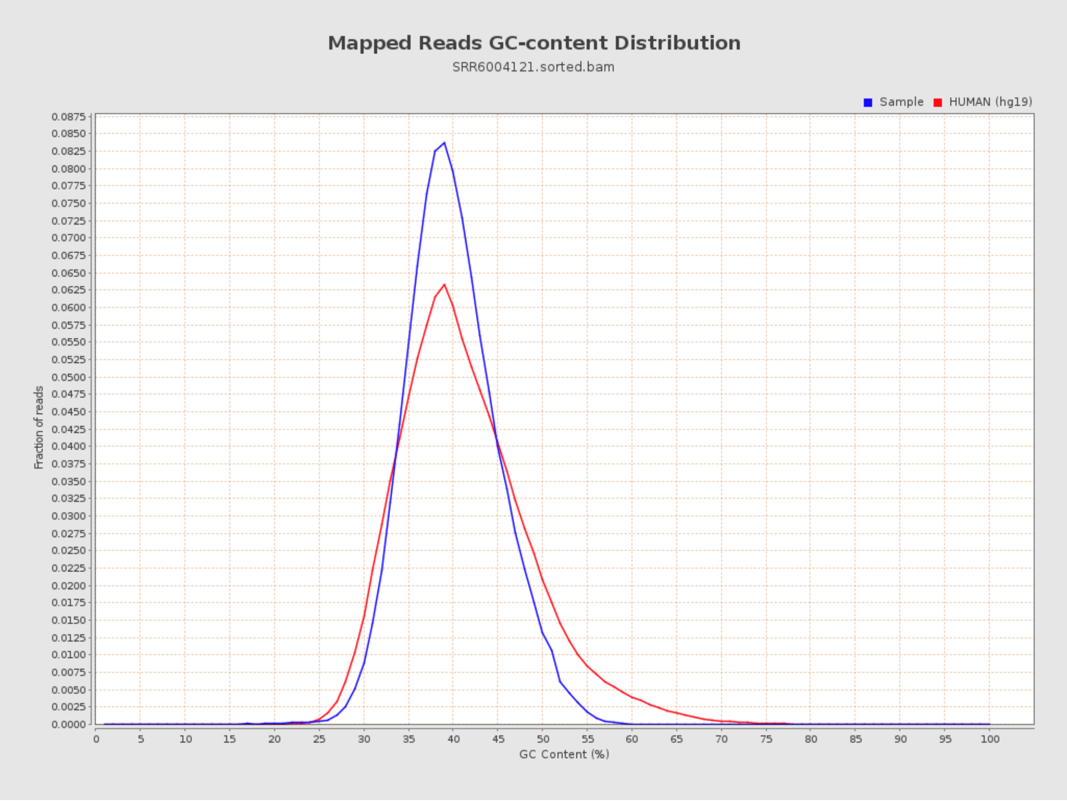
7. Results : Duplication Rate Histogram



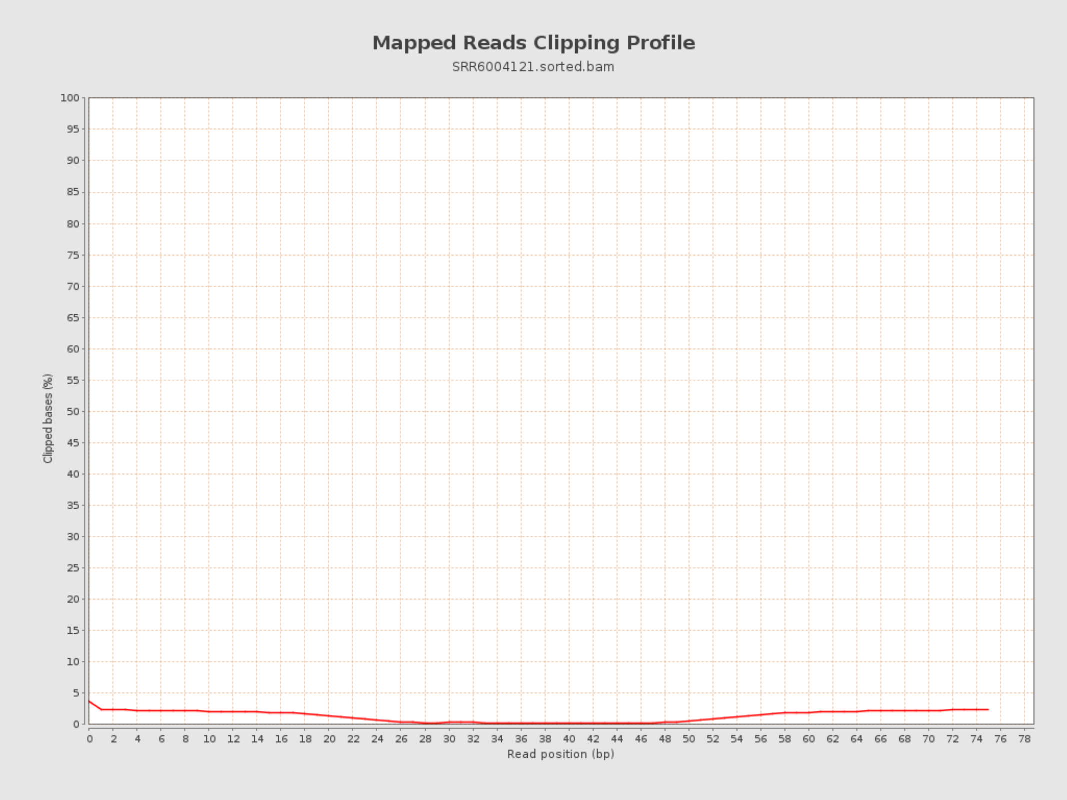
8. Results : Mapped Reads Nucleotide Content



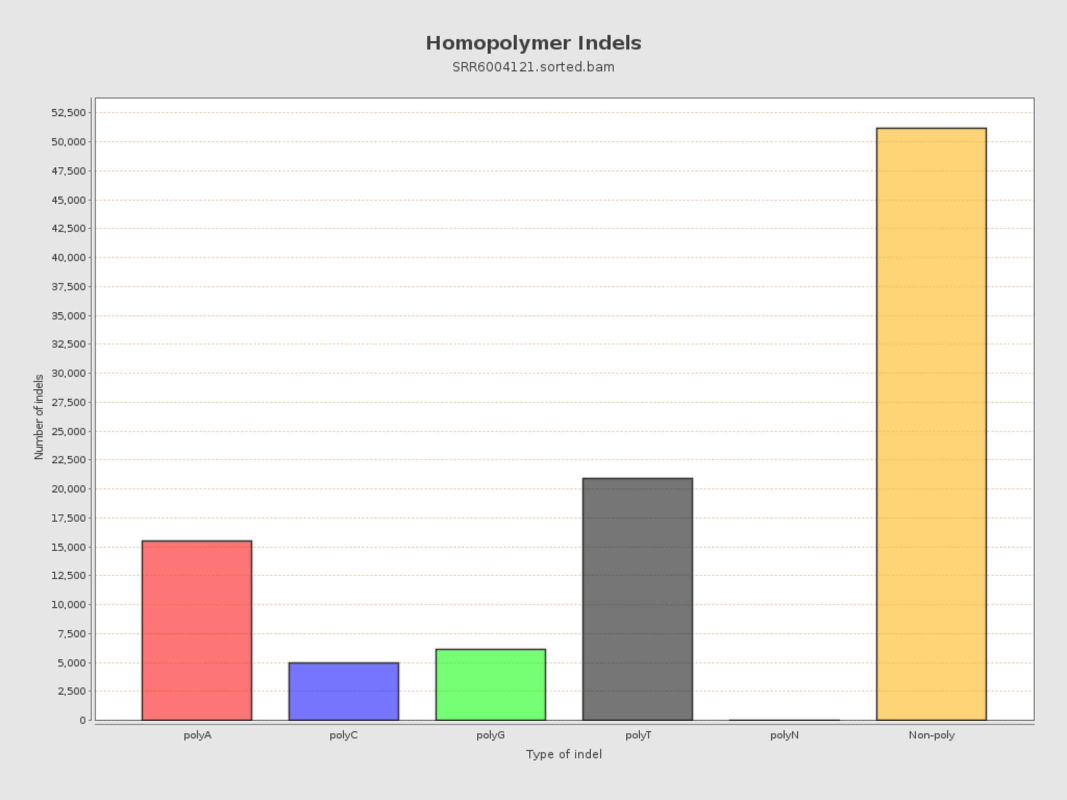
9. Results : Mapped Reads GC-content Distribution



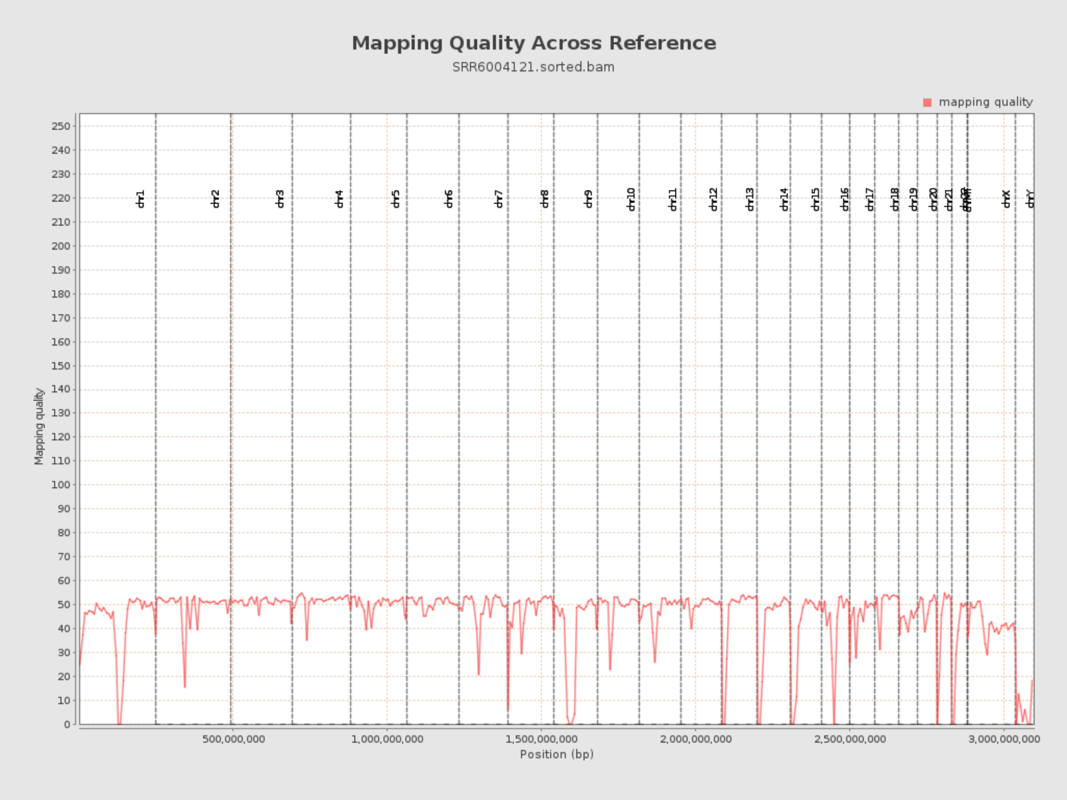
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram