Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 14:37:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082425.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_SRR3082425 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082425.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 14:37:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082425.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,062,896
Mapped reads	2,761,860 / 90.17%
Unmapped reads	301,036 / 9.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,941 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	112,765 / 3.68%
Duplication rate	3.08%
Clipped reads	1,207,666 / 39.43%

2.2. ACGT Content

Number/percentage of A's	52,196,887 / 28.1%
Number/percentage of C's	34,699,765 / 18.68%
Number/percentage of T's	58,060,056 / 31.25%
Number/percentage of G's	40,814,951 / 21.97%
Number/percentage of N's	3,935 / 0%
GC Percentage	40.65%

2.3. Coverage

Mean	0.06

Standard Deviation	0.4837

2.4. Mapping Quality

Mean Mapping Quality	46.12

2.5. Mismatches and indels

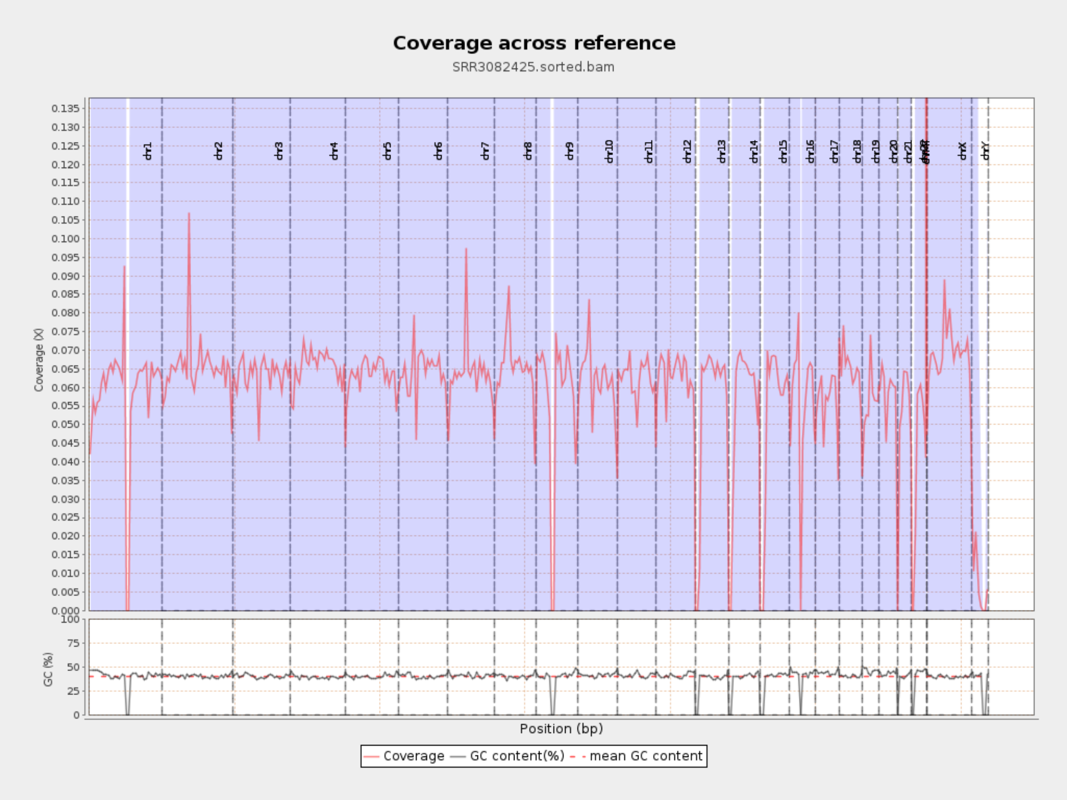
General error rate	0.84%
Mismatches	1,540,326
Insertions	14,943
Mapped reads with at least one insertion	0.54%
Deletions	42,376
Mapped reads with at least one deletion	1.52%
Homopolymer indels	47.51%

2.6. Chromosome stats

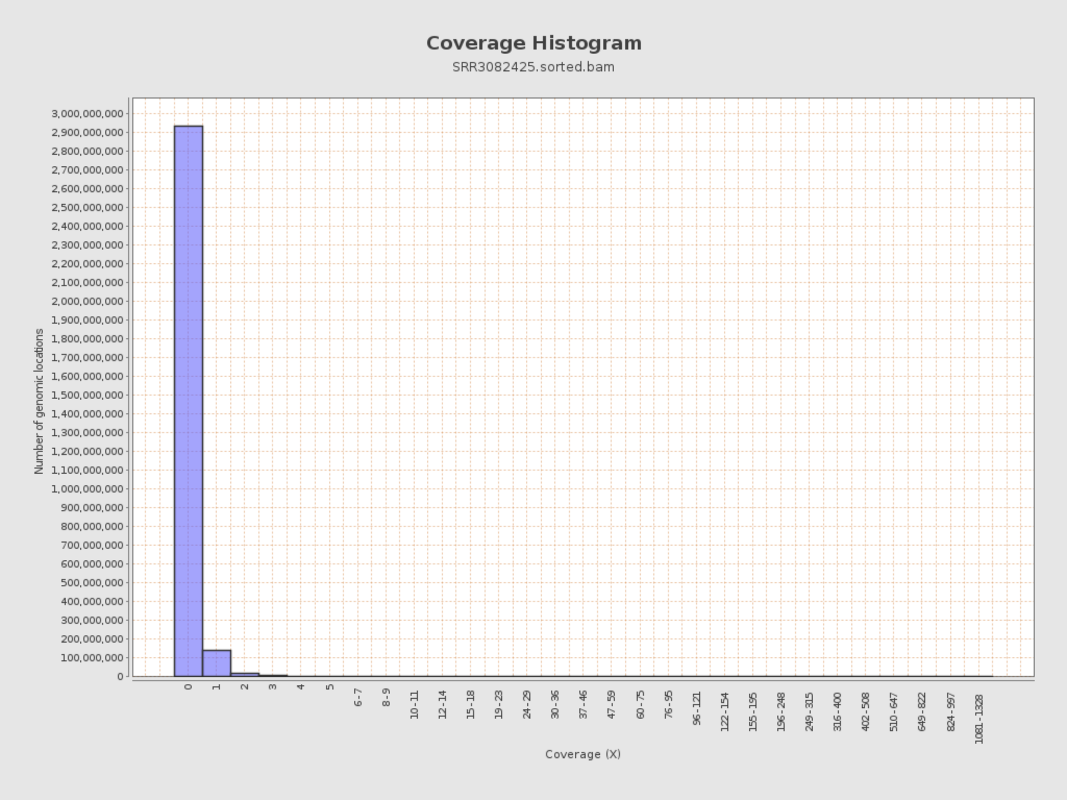
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14584335	0.0585	0.8027
chr2	243199373	15988692	0.0657	0.6189
chr3	198022430	12586400	0.0636	0.2831
chr4	191154276	12545785	0.0656	0.3029
chr5	180915260	11475170	0.0634	0.2849
chr6	171115067	10963265	0.0641	0.3472
chr7	159138663	10225835	0.0643	0.6233

chr8	146364022	9532766	0.0651	0.8545
chr9	141213431	7991654	0.0566	0.4465
chr10	135534747	8477887	0.0626	0.4107
chr11	135006516	8383078	0.0621	0.4041
chr12	133851895	8457625	0.0632	0.2886
chr13	115169878	6193495	0.0538	0.2603
chr14	107349540	5717977	0.0533	0.2824
chr15	102531392	5317684	0.0519	0.2711
chr16	90354753	5062010	0.056	0.3027
chr17	81195210	4509583	0.0555	0.2937
chr18	78077248	5098811	0.0653	0.8524
chr19	59128983	3328347	0.0563	0.6091
chr20	63025520	3669227	0.0582	0.2801
chr21	48129895	2460719	0.0511	0.2749
chr22	51304566	1981585	0.0386	0.2187
chrMT	16571	107597	6.4931	3.9667
chrX	155270560	10743991	0.0692	0.3361
chrY	59373566	440208	0.0074	0.1487

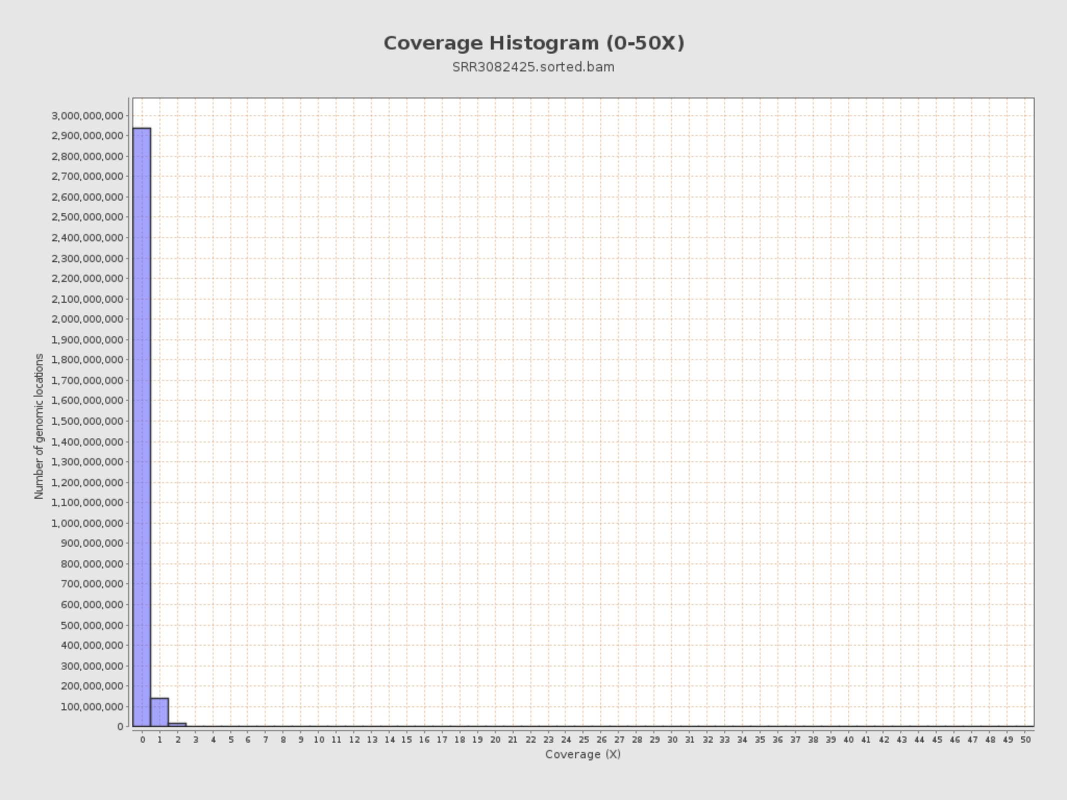
3. Results : Coverage across reference



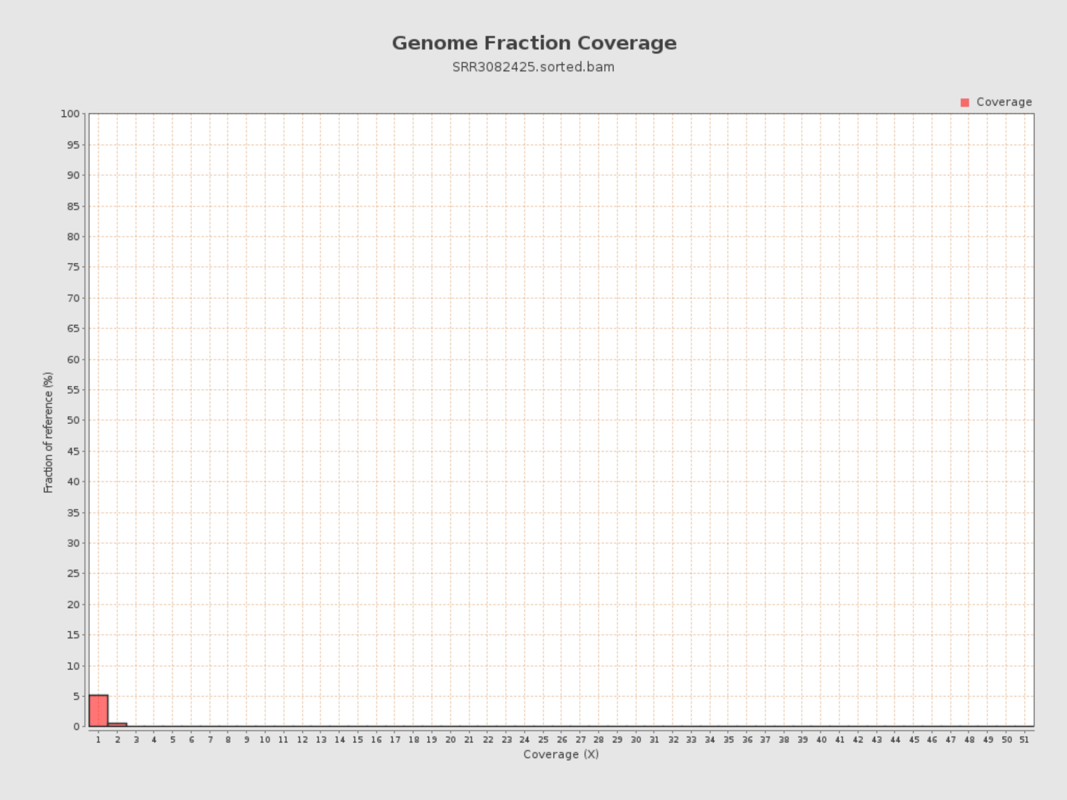
4. Results : Coverage Histogram



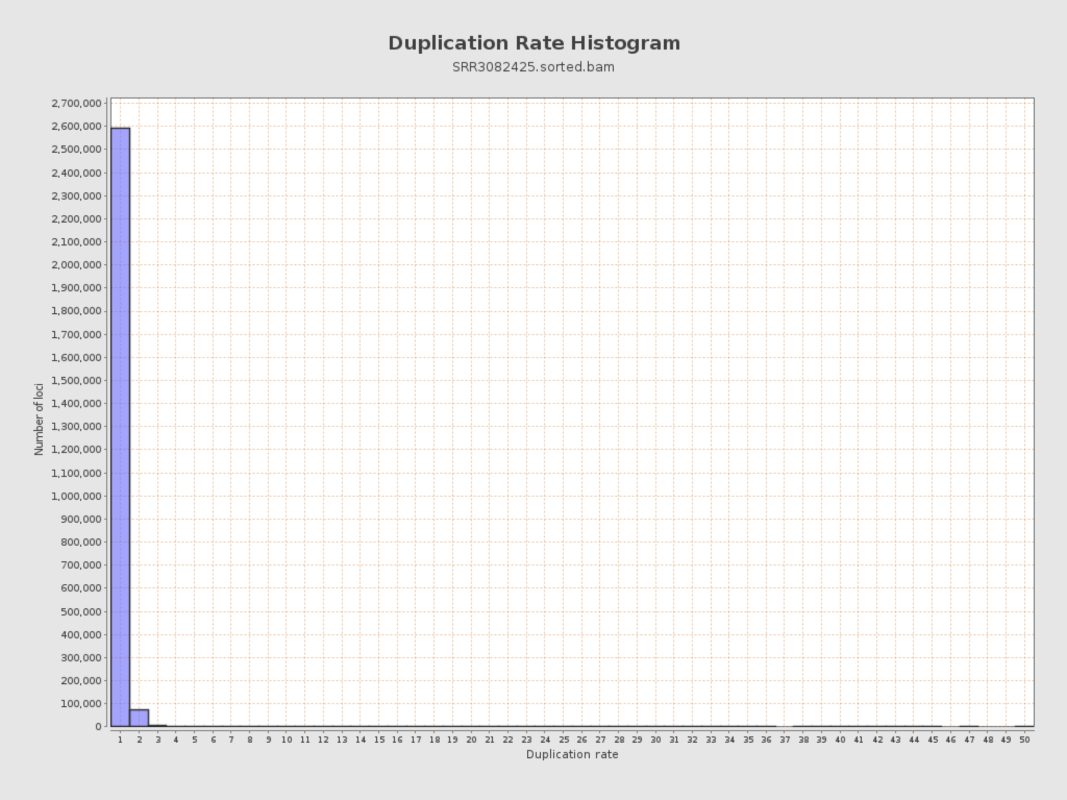
5. Results : Coverage Histogram (0-50X)



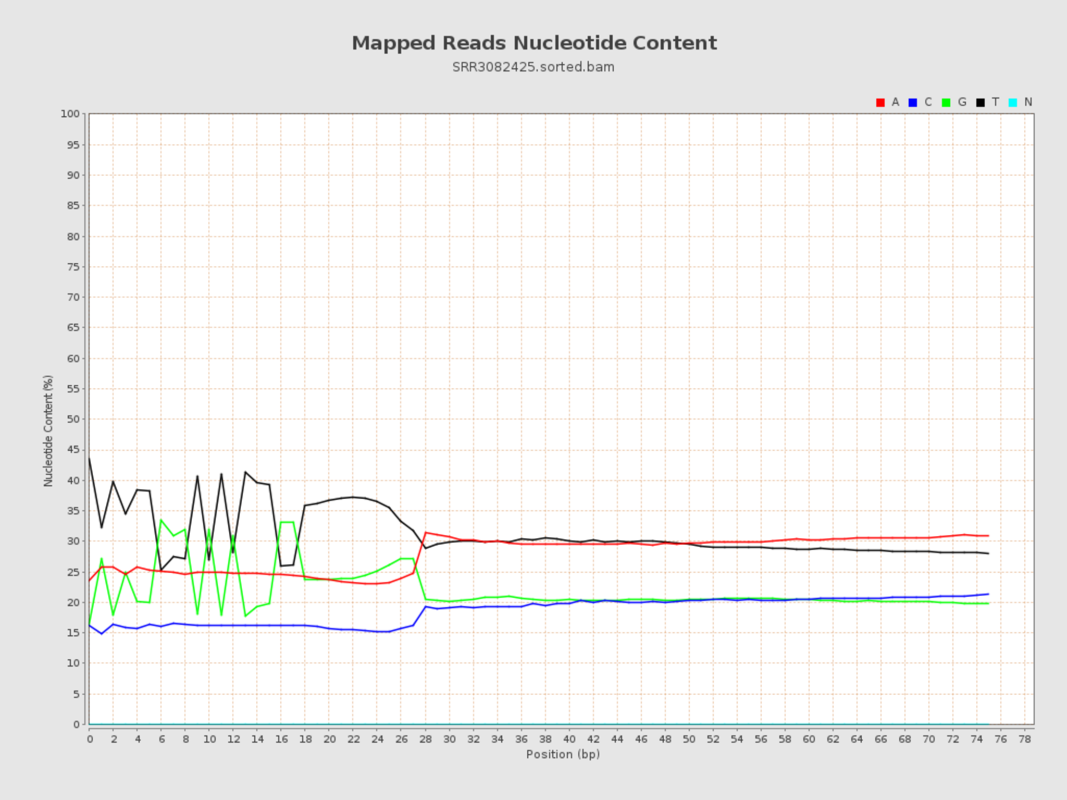
6. Results : Genome Fraction Coverage



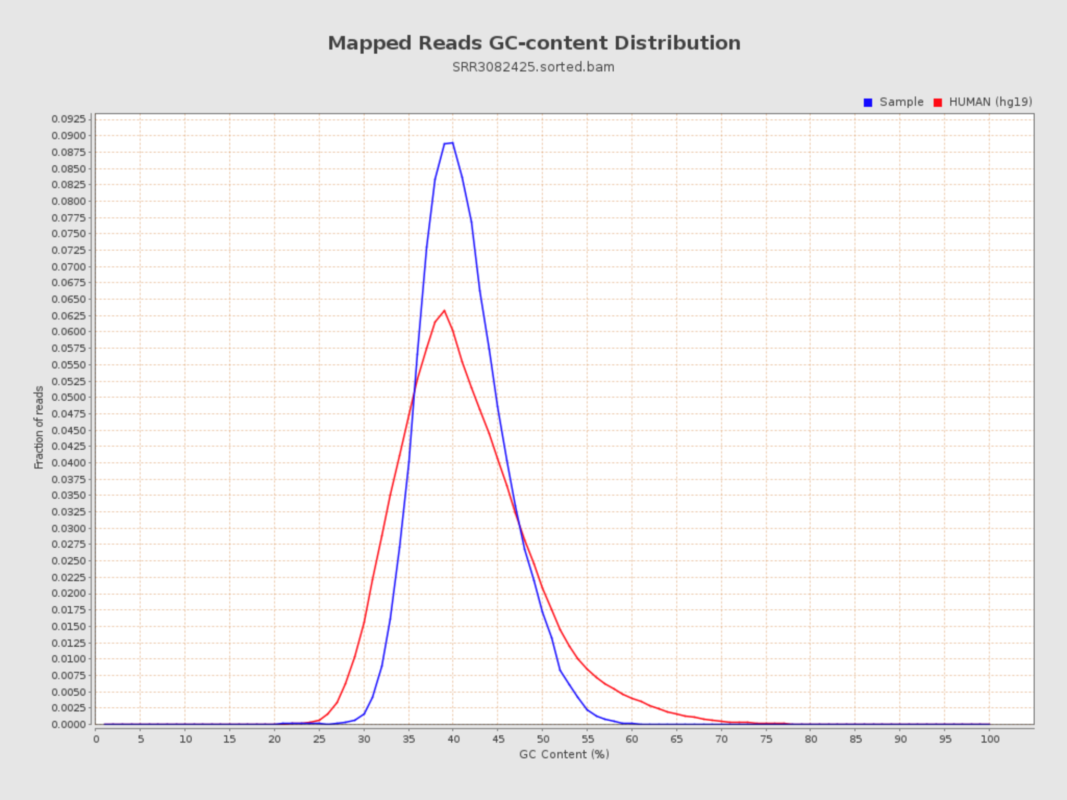
7. Results : Duplication Rate Histogram



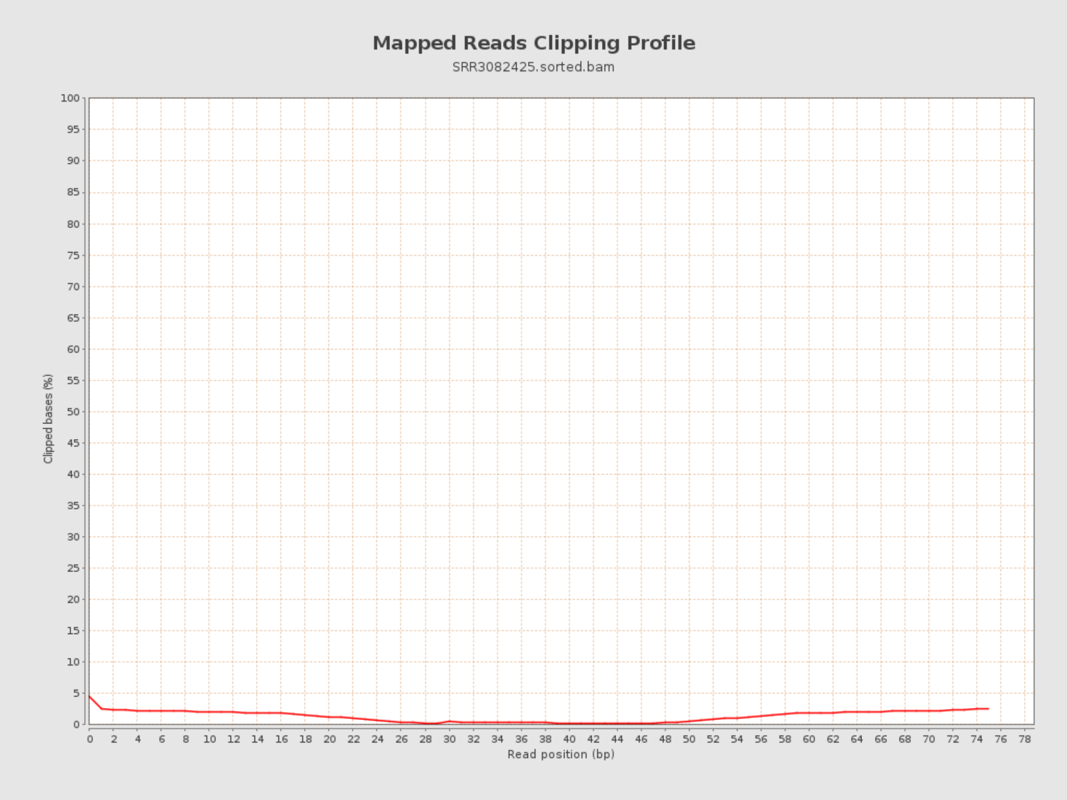
8. Results : Mapped Reads Nucleotide Content



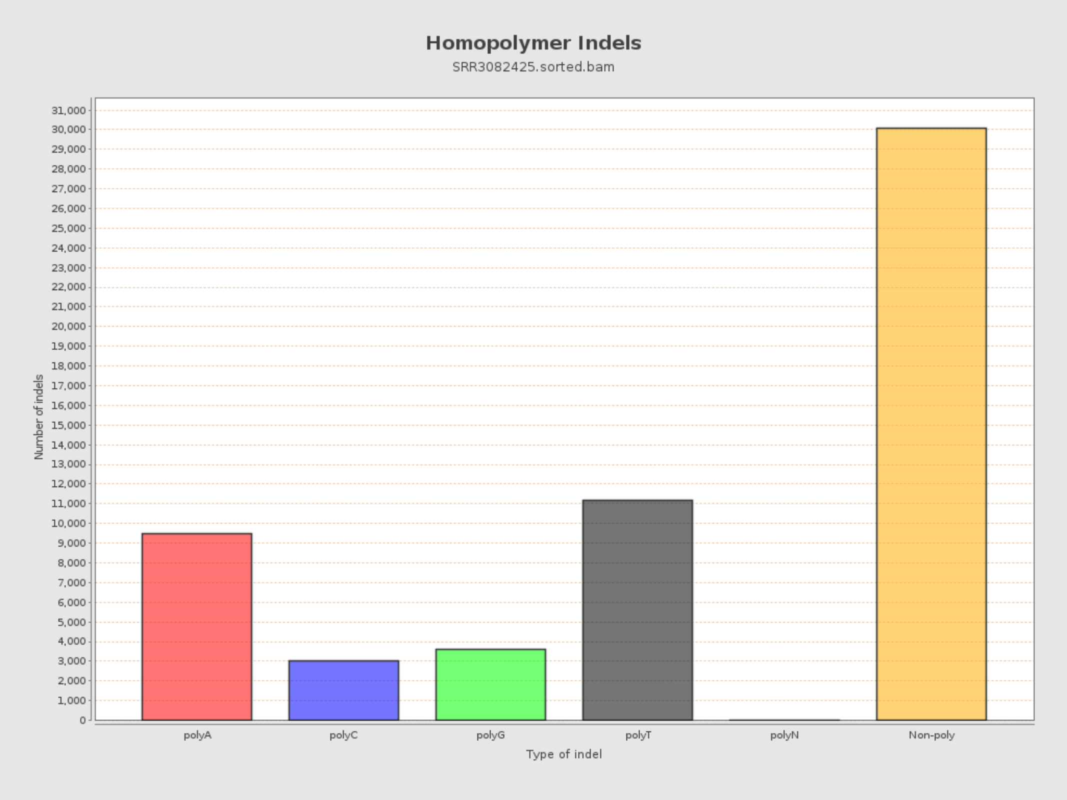
9. Results : Mapped Reads GC-content Distribution



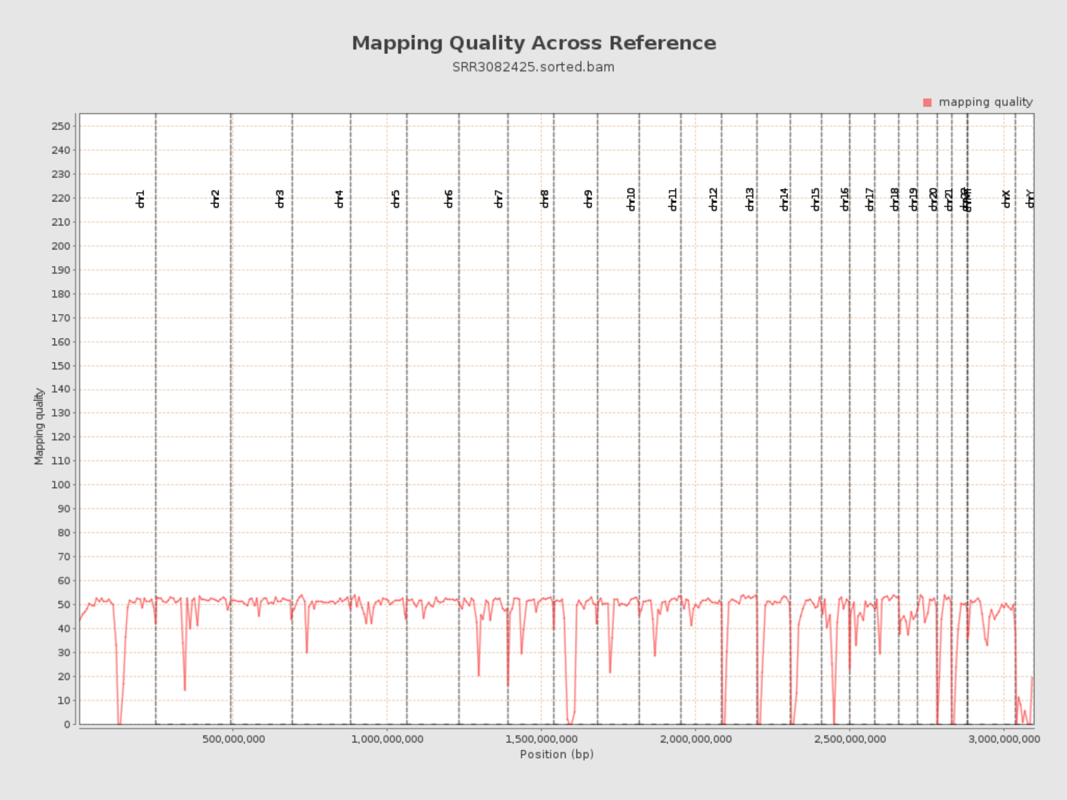
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram