Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 19:37:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013284.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_SRR6013284 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013284.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 19:37:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013284.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,410,828
Mapped reads	2,011,172 / 83.42%
Unmapped reads	399,656 / 16.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,276 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	224,755 / 9.32%
Duplication rate	8.86%
Clipped reads	1,288,213 / 53.43%

2.2. ACGT Content

Number/percentage of A's	36,203,238 / 28.86%
Number/percentage of C's	23,593,332 / 18.81%
Number/percentage of T's	38,546,200 / 30.73%
Number/percentage of G's	27,059,771 / 21.57%
Number/percentage of N's	43,340 / 0.03%
GC Percentage	40.38%

2.3. Coverage

Mean	0.0405

Standard Deviation	0.4307

2.4. Mapping Quality

Mean Mapping Quality	44.74

2.5. Mismatches and indels

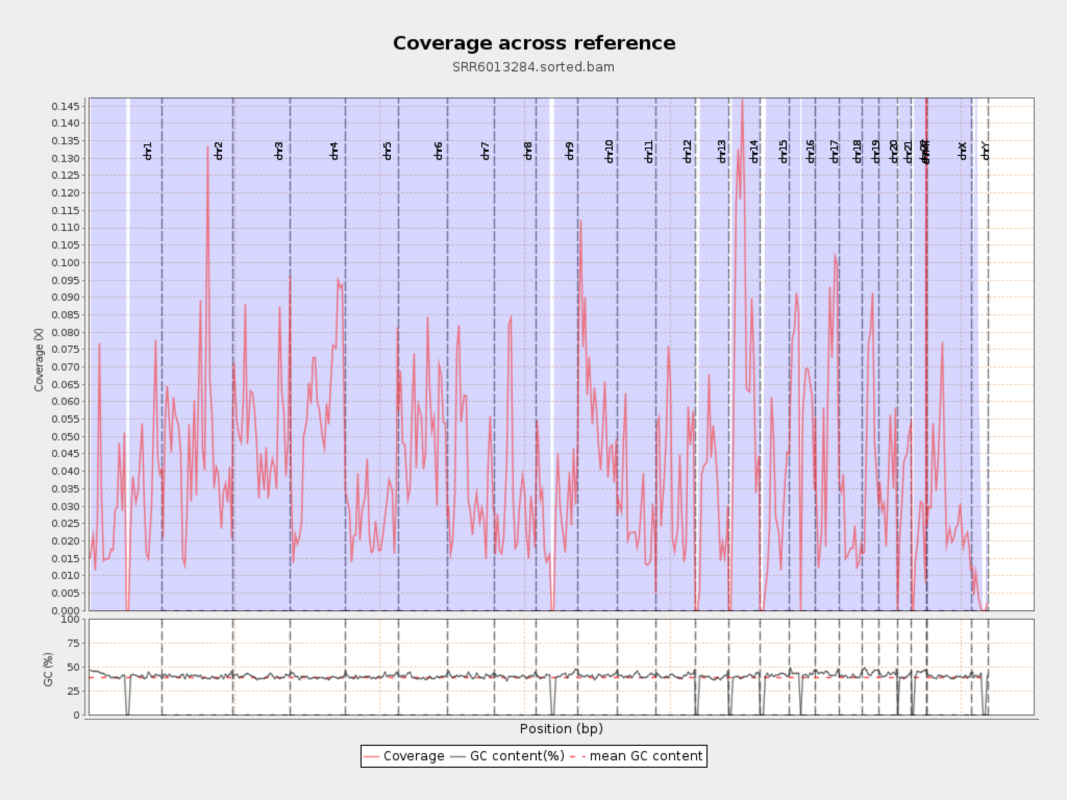
General error rate	0.87%
Mismatches	1,073,555
Insertions	8,332
Mapped reads with at least one insertion	0.41%
Deletions	36,456
Mapped reads with at least one deletion	1.79%
Homopolymer indels	44.69%

2.6. Chromosome stats

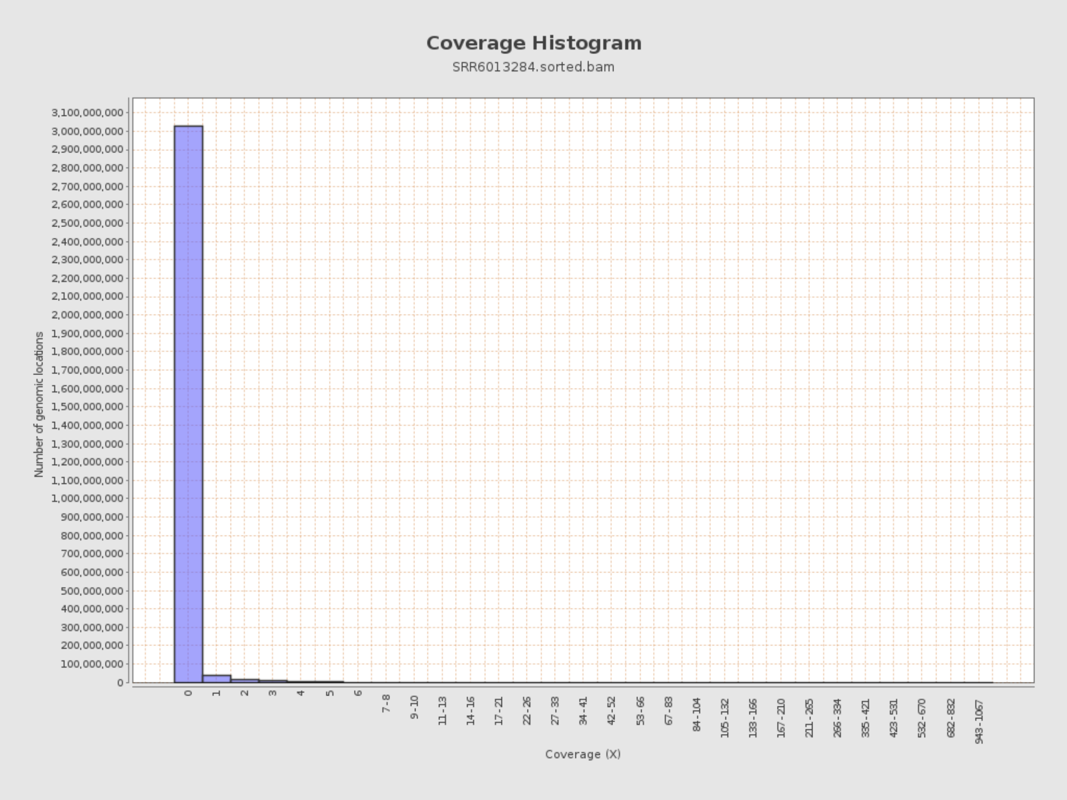
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7660993	0.0307	0.6839
chr2	243199373	11413235	0.0469	0.4233
chr3	198022430	10347369	0.0523	0.3874
chr4	191154276	10686687	0.0559	0.3941
chr5	180915260	4877154	0.027	0.2675
chr6	171115067	9195990	0.0537	0.4254
chr7	159138663	6095313	0.0383	0.5009

chr8	146364022	4598177	0.0314	0.6539
chr9	141213431	3817879	0.027	0.305
chr10	135534747	8256580	0.0609	0.5075
chr11	135006516	3653778	0.0271	0.2953
chr12	133851895	5378653	0.0402	0.329
chr13	115169878	3543613	0.0308	0.287
chr14	107349540	8106931	0.0755	0.462
chr15	102531392	2615778	0.0255	0.2663
chr16	90354753	5669351	0.0627	0.4067
chr17	81195210	4650376	0.0573	0.3911
chr18	78077248	1694506	0.0217	0.4756
chr19	59128983	3141917	0.0531	0.5681
chr20	63025520	2337495	0.0371	0.3204
chr21	48129895	1734994	0.036	0.3054
chr22	51304566	855845	0.0167	0.27
chrMT	16571	12603	0.7605	1.2796
chrX	155270560	4932708	0.0318	0.3018
chrY	59373566	229795	0.0039	0.0913

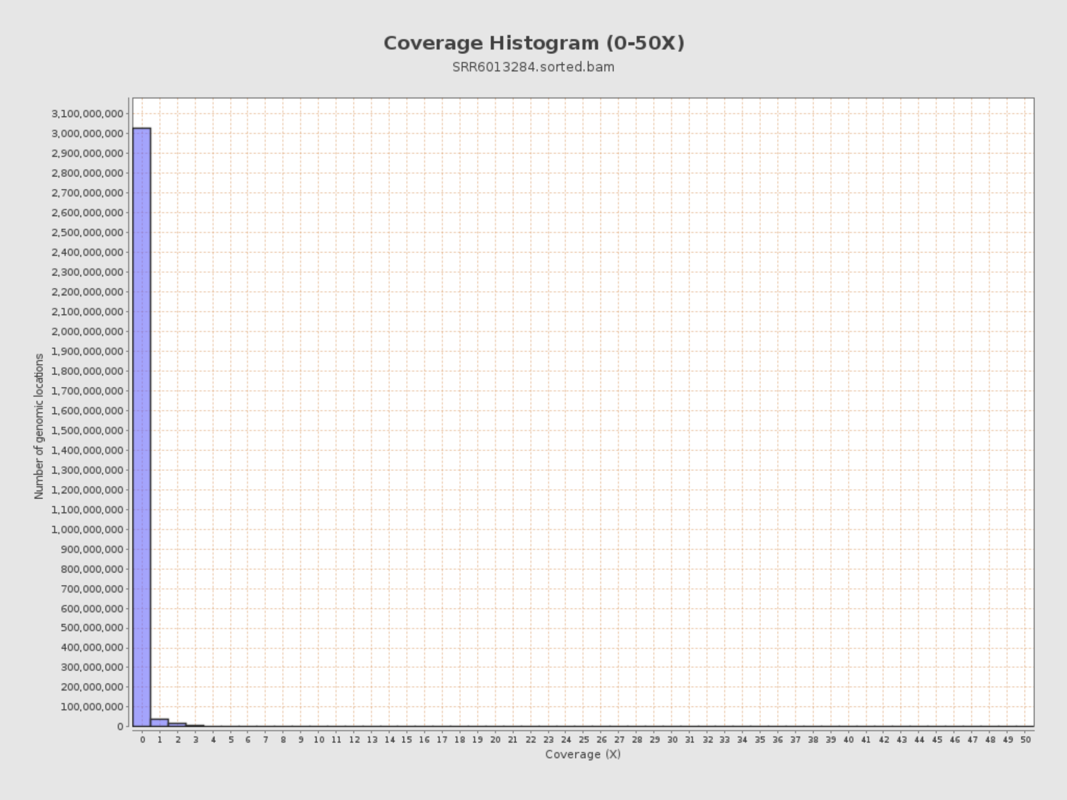
3. Results : Coverage across reference



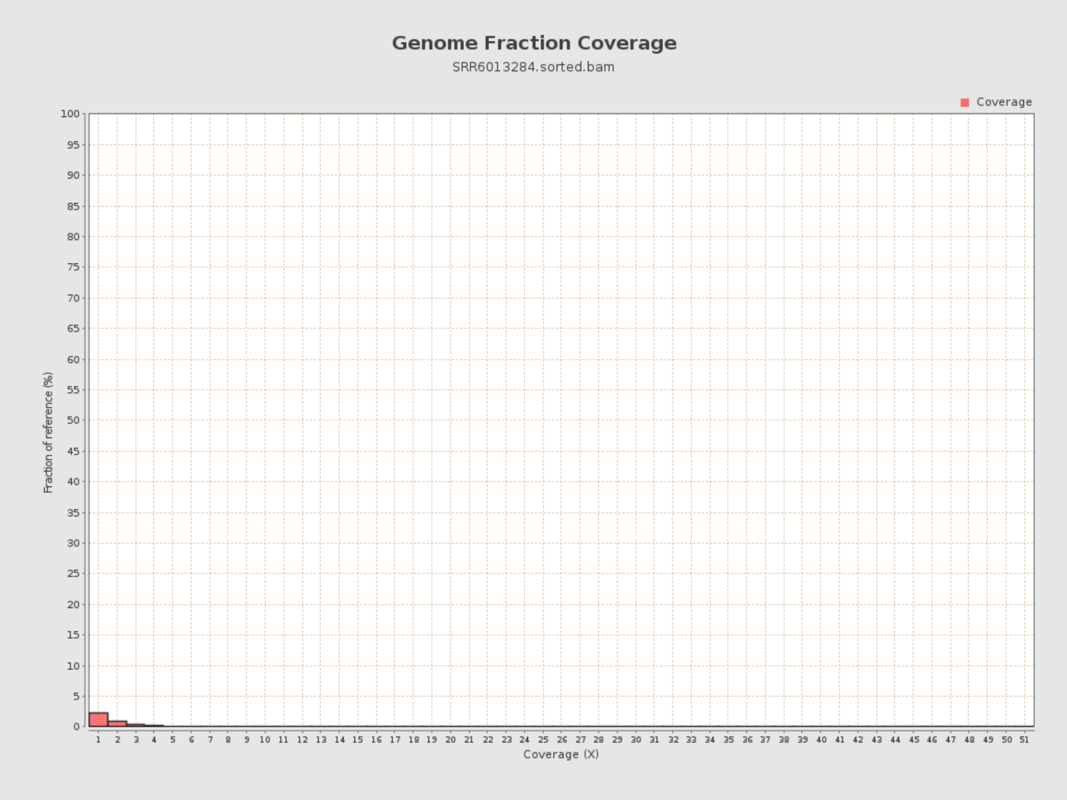
4. Results : Coverage Histogram



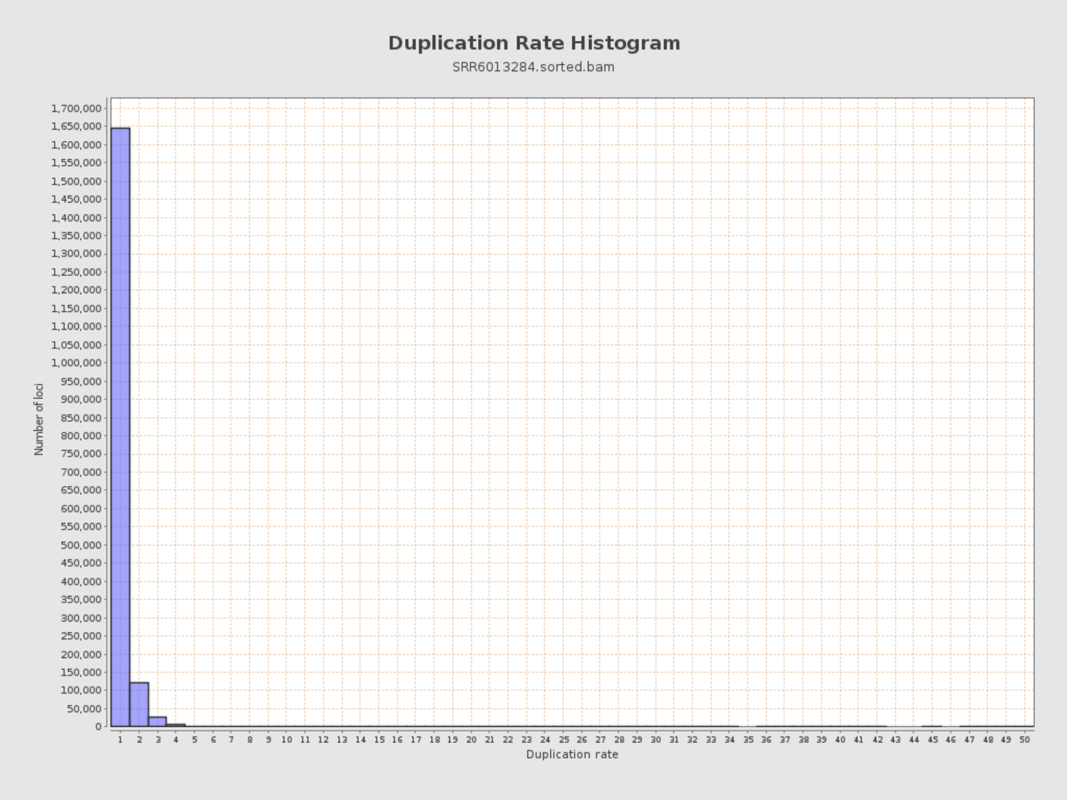
5. Results : Coverage Histogram (0-50X)



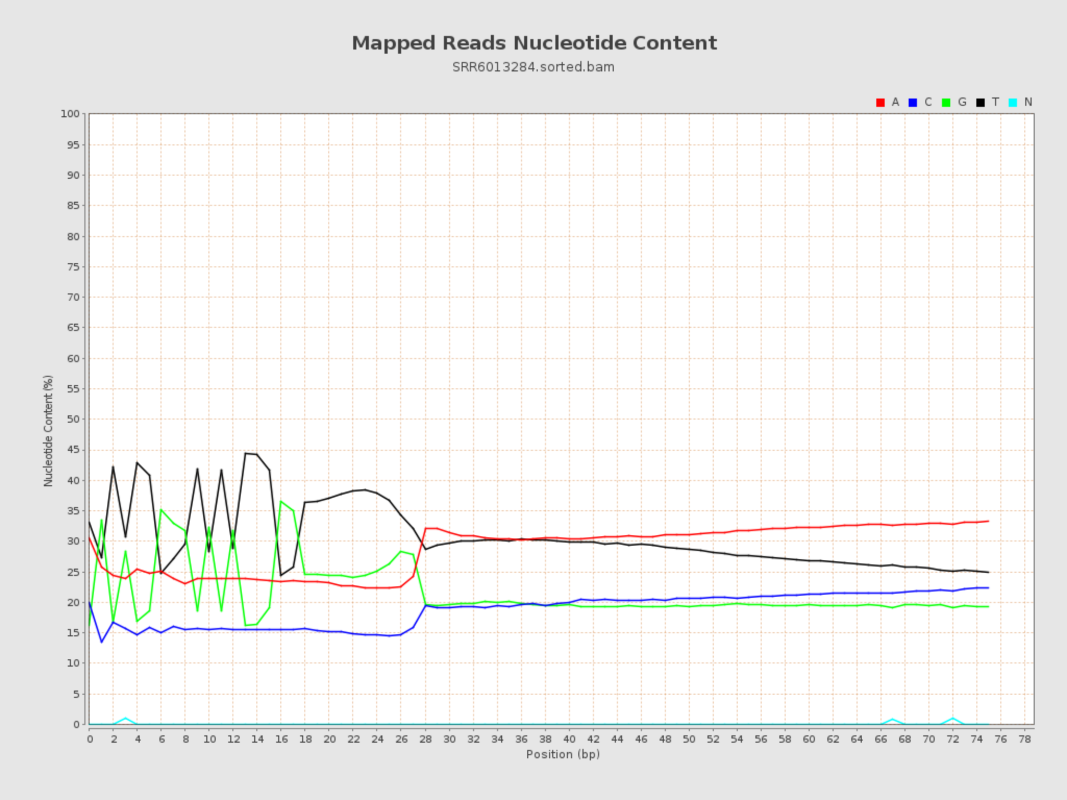
6. Results : Genome Fraction Coverage



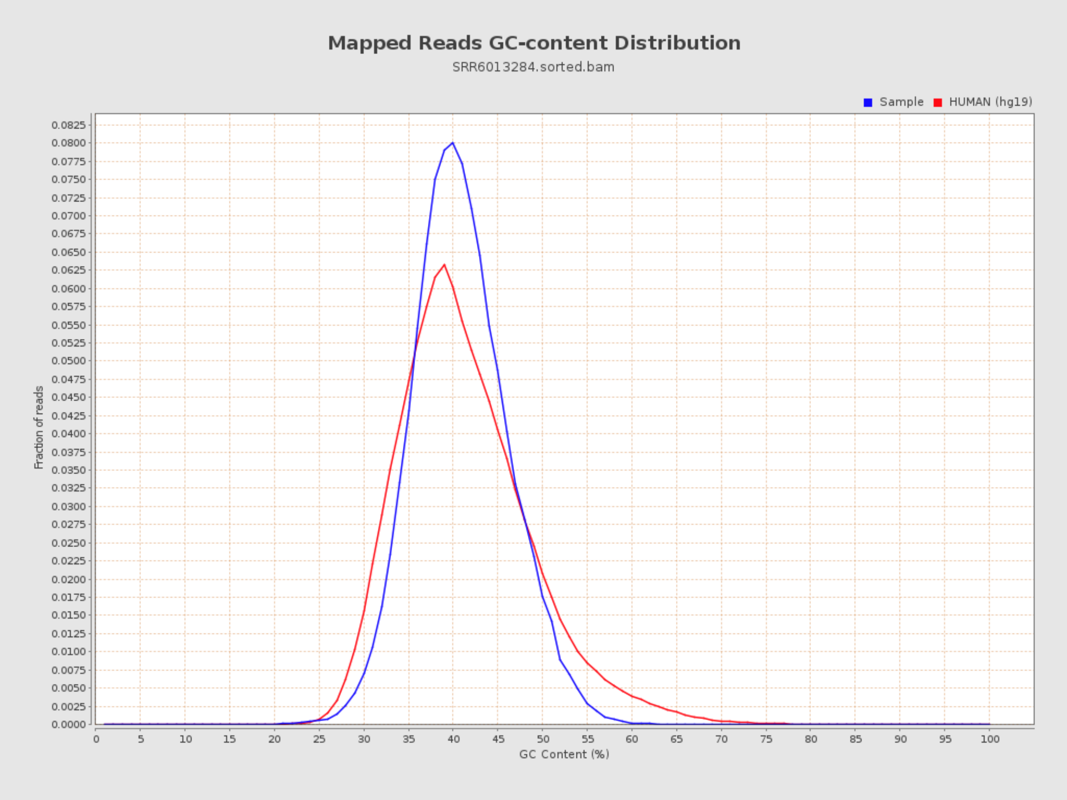
7. Results : Duplication Rate Histogram



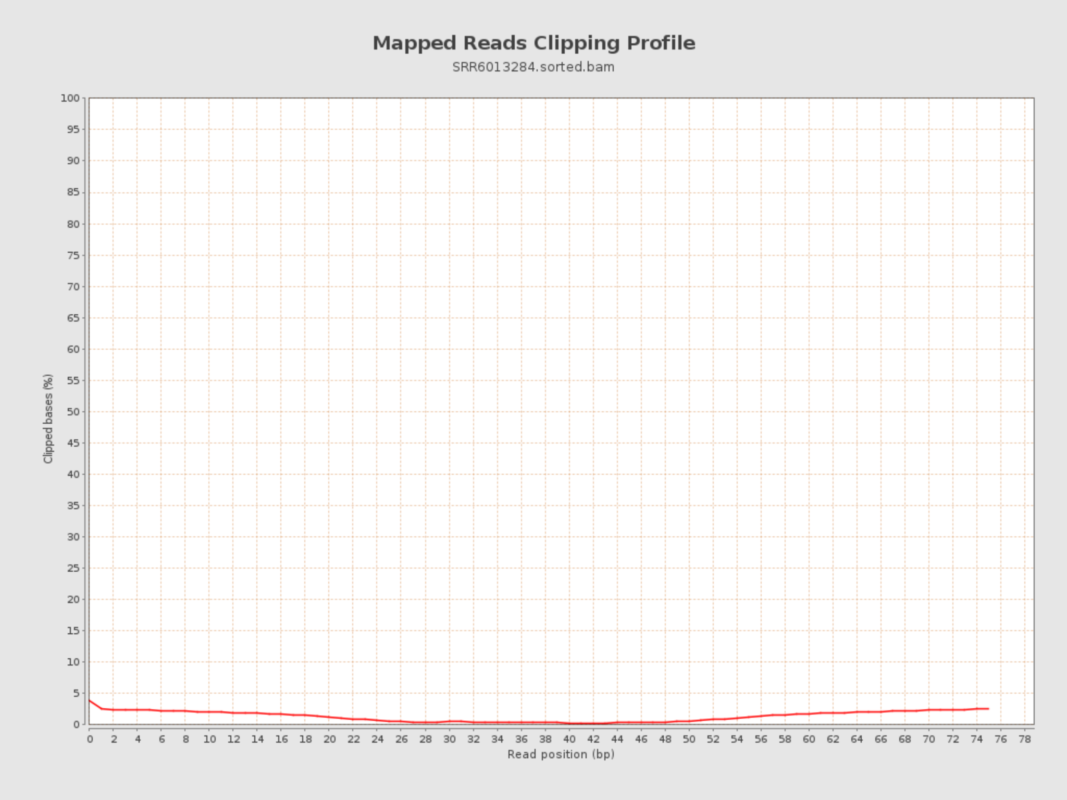
8. Results : Mapped Reads Nucleotide Content



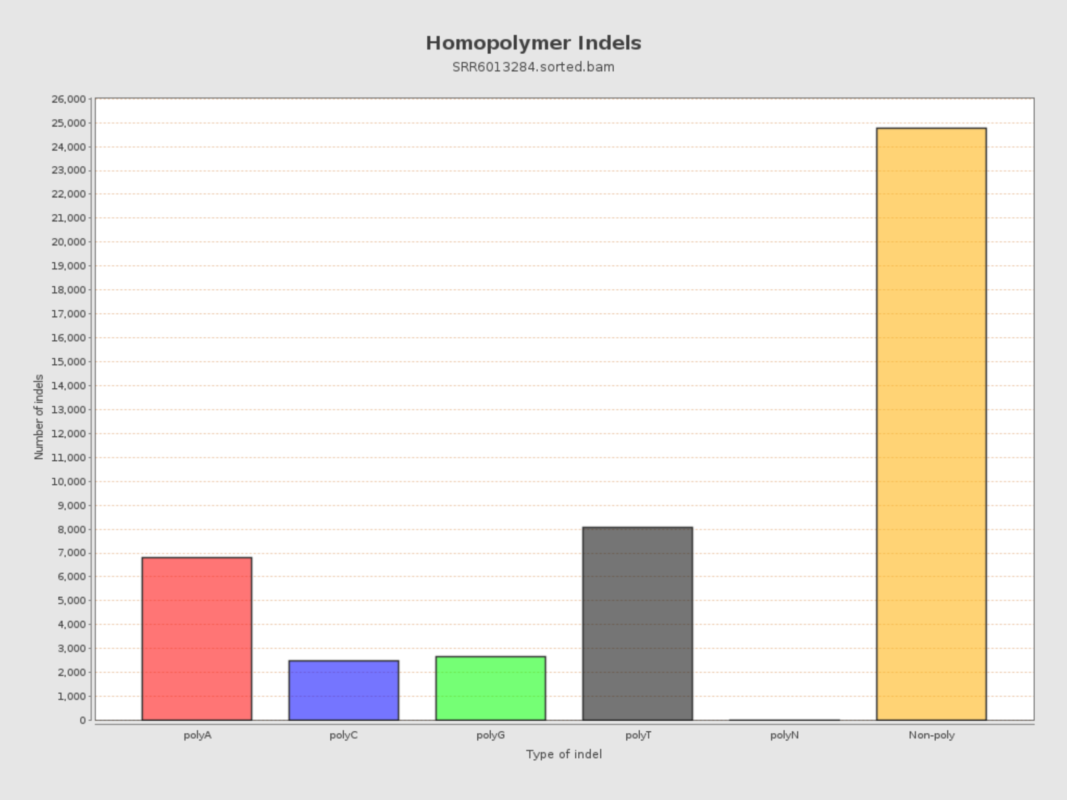
9. Results : Mapped Reads GC-content Distribution



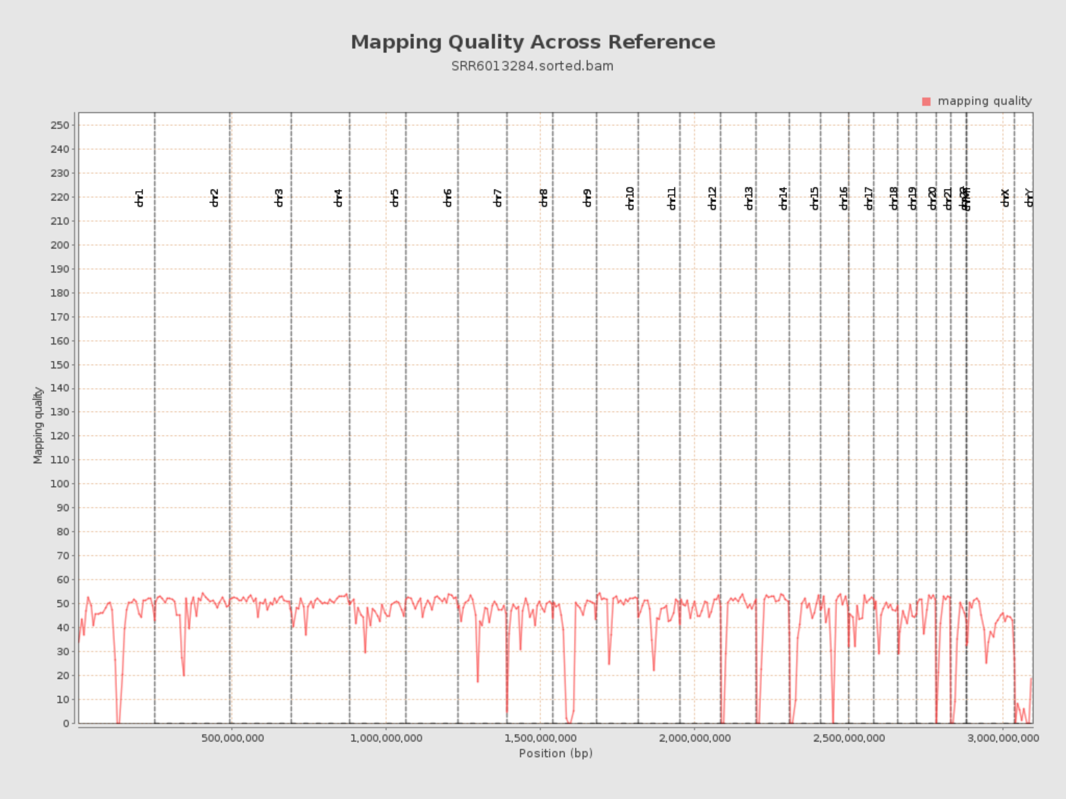
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram