Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 04:51:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548982.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_SRR1548982 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548982.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 04:51:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548982.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,082,255
Mapped reads	4,479,168 / 44.43%
Unmapped reads	5,603,087 / 55.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	110,301 / 1.09%
Duplication rate	1.68%
Clipped reads	305,797 / 3.03%

2.2. ACGT Content

Number/percentage of A's	52,771,901 / 29.74%
Number/percentage of C's	35,374,694 / 19.94%
Number/percentage of T's	53,432,006 / 30.12%
Number/percentage of G's	35,835,193 / 20.2%
Number/percentage of N's	9,725 / 0.01%
GC Percentage	40.14%

2.3. Coverage

Mean	0.0573
Standard Deviation	0.3982

2.4. Mapping Quality

Mean Mapping Quality	43.6

2.5. Mismatches and indels

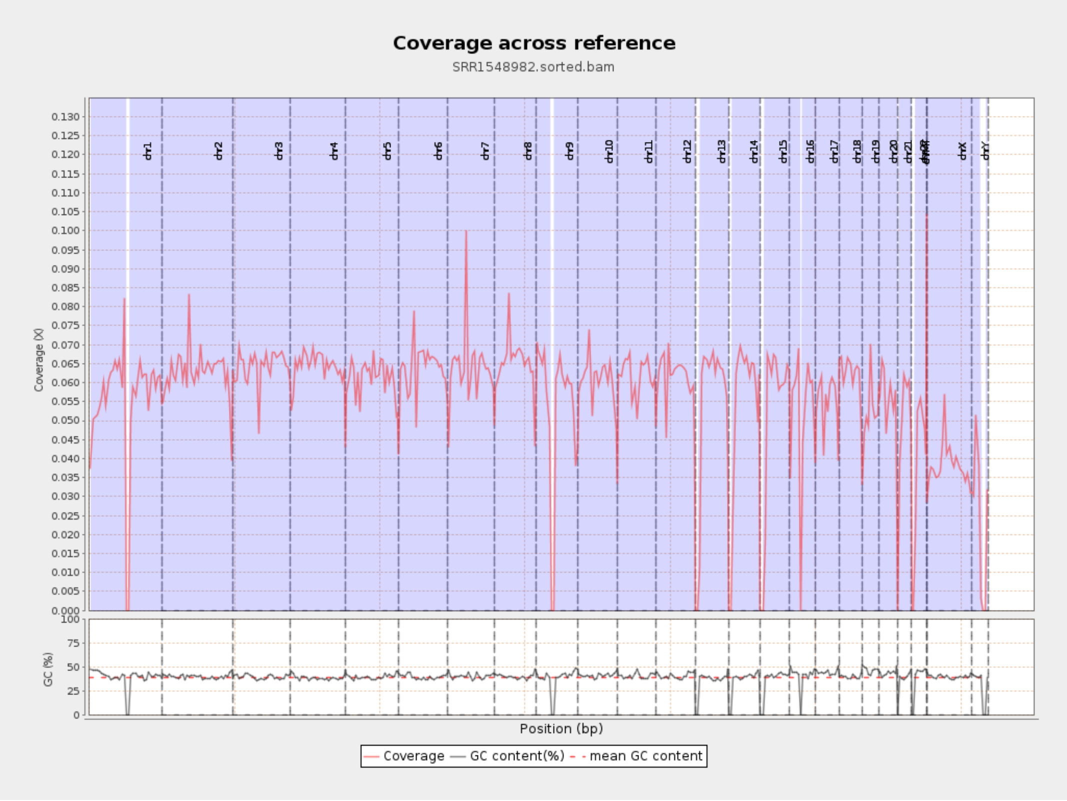
General error rate	0.28%
Mismatches	495,450
Insertions	5,819
Mapped reads with at least one insertion	0.13%
Deletions	16,991
Mapped reads with at least one deletion	0.38%
Homopolymer indels	45.25%

2.6. Chromosome stats

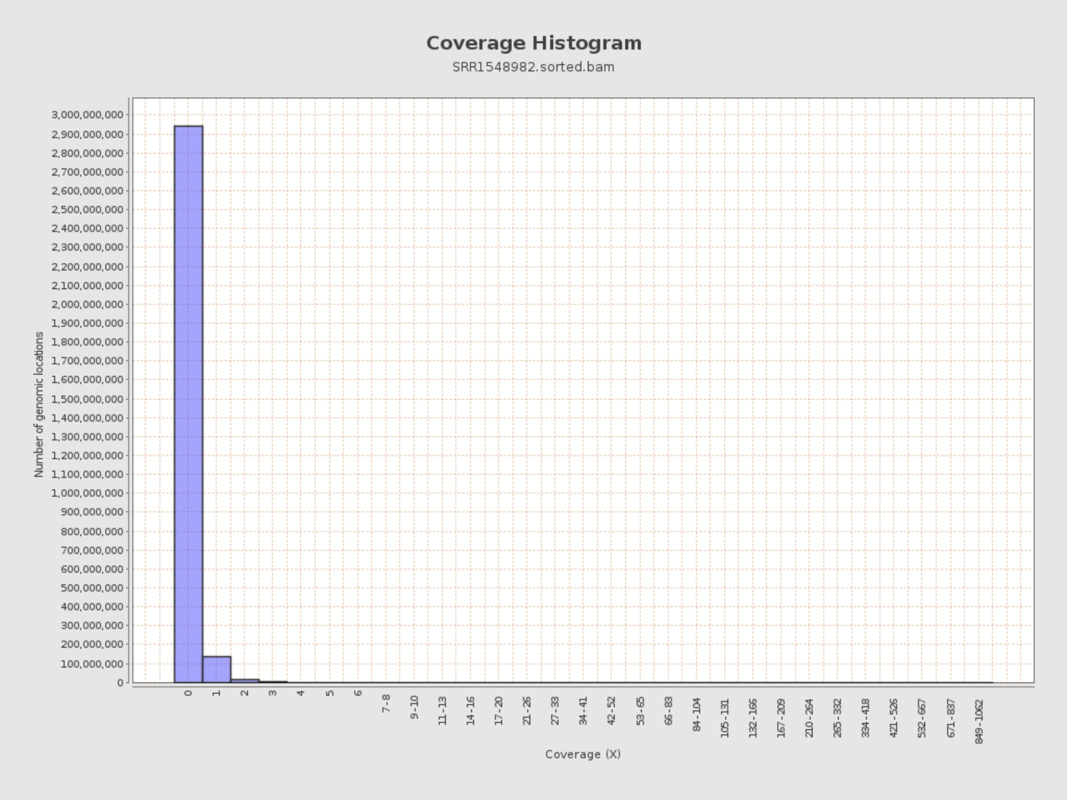
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13829230	0.0555	0.6668
chr2	243199373	15298527	0.0629	0.3718
chr3	198022430	12754166	0.0644	0.2819
chr4	191154276	12301465	0.0644	0.288
chr5	180915260	11094393	0.0613	0.2795
chr6	171115067	10891616	0.0637	0.3403
chr7	159138663	10275269	0.0646	0.6097
chr8	146364022	9528170	0.0651	0.6105

chr9	141213431	7530928	0.0533	0.3464
chr10	135534747	8283987	0.0611	0.3316
chr11	135006516	8287113	0.0614	0.3609
chr12	133851895	8252138	0.0617	0.2839
chr13	115169878	6106071	0.053	0.2541
chr14	107349540	5672726	0.0528	0.2971
chr15	102531392	5208681	0.0508	0.2506
chr16	90354753	4704624	0.0521	0.2711
chr17	81195210	4429752	0.0546	0.2818
chr18	78077248	4901747	0.0628	0.5814
chr19	59128983	3105833	0.0525	0.5677
chr20	63025520	3538065	0.0561	0.2716
chr21	48129895	2318525	0.0482	0.2772
chr22	51304566	1843217	0.0359	0.2407
chrMT	16571	1731	0.1045	0.3517
chrX	155270560	5925671	0.0382	0.2617
chrY	59373566	1361261	0.0229	0.2207

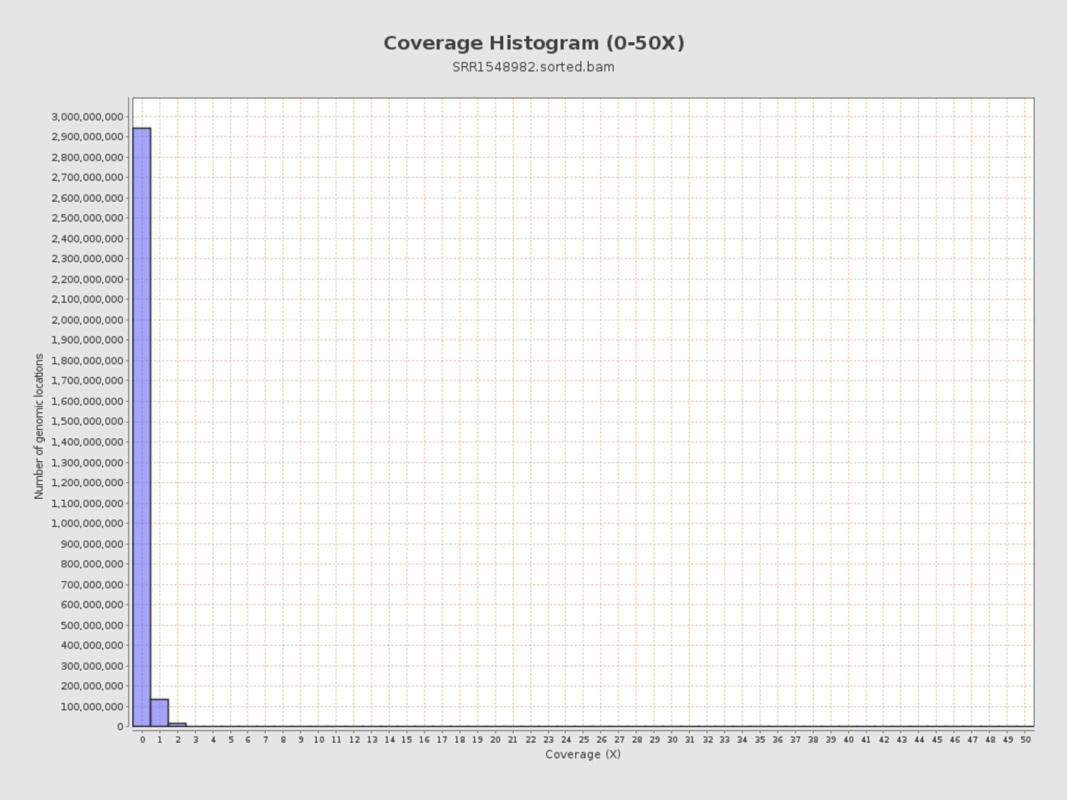
3. Results : Coverage across reference



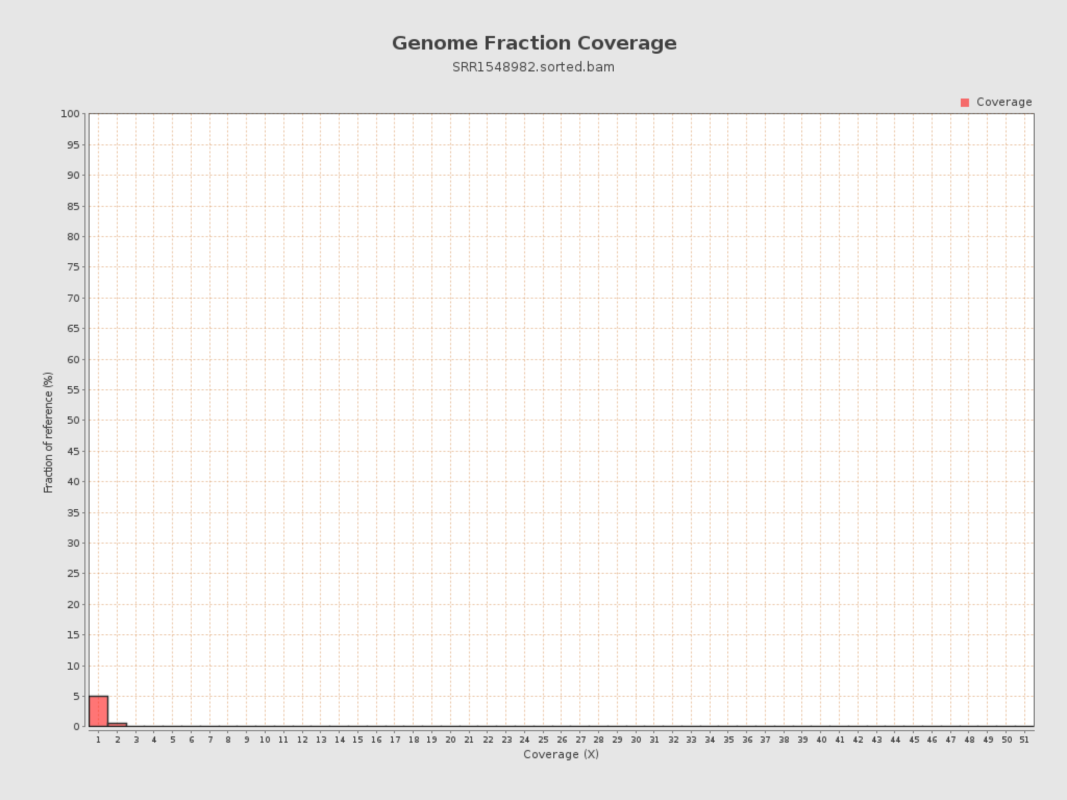
4. Results : Coverage Histogram



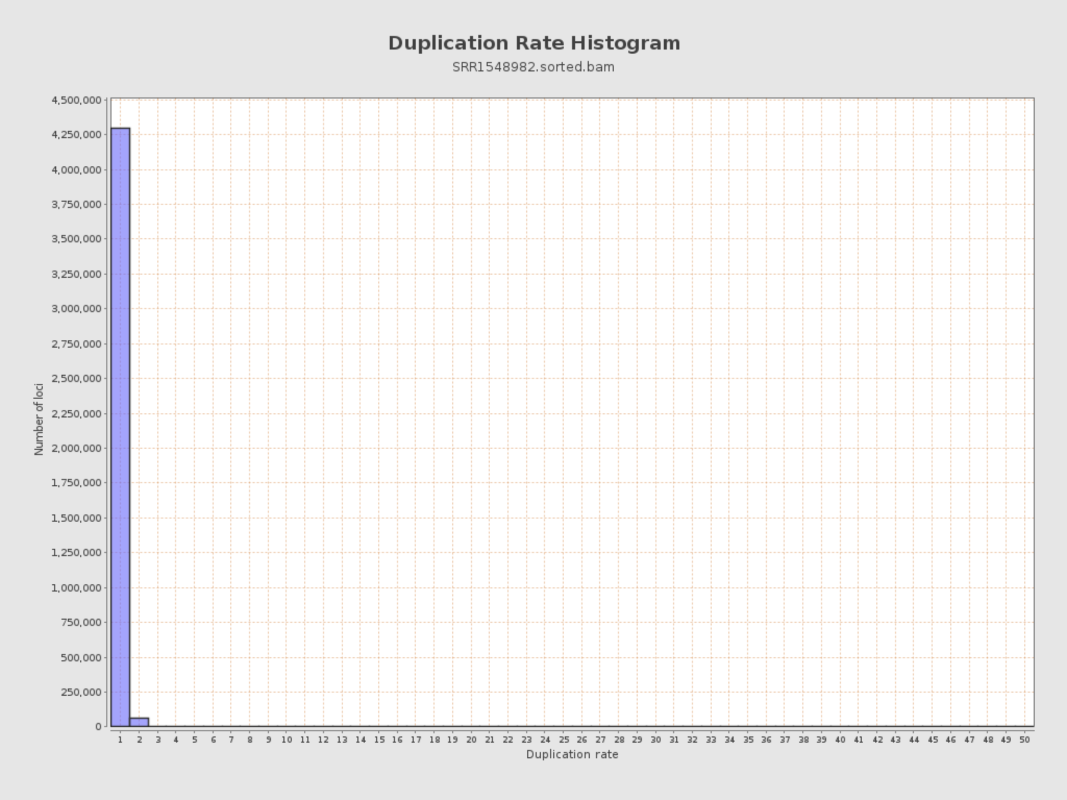
5. Results : Coverage Histogram (0-50X)



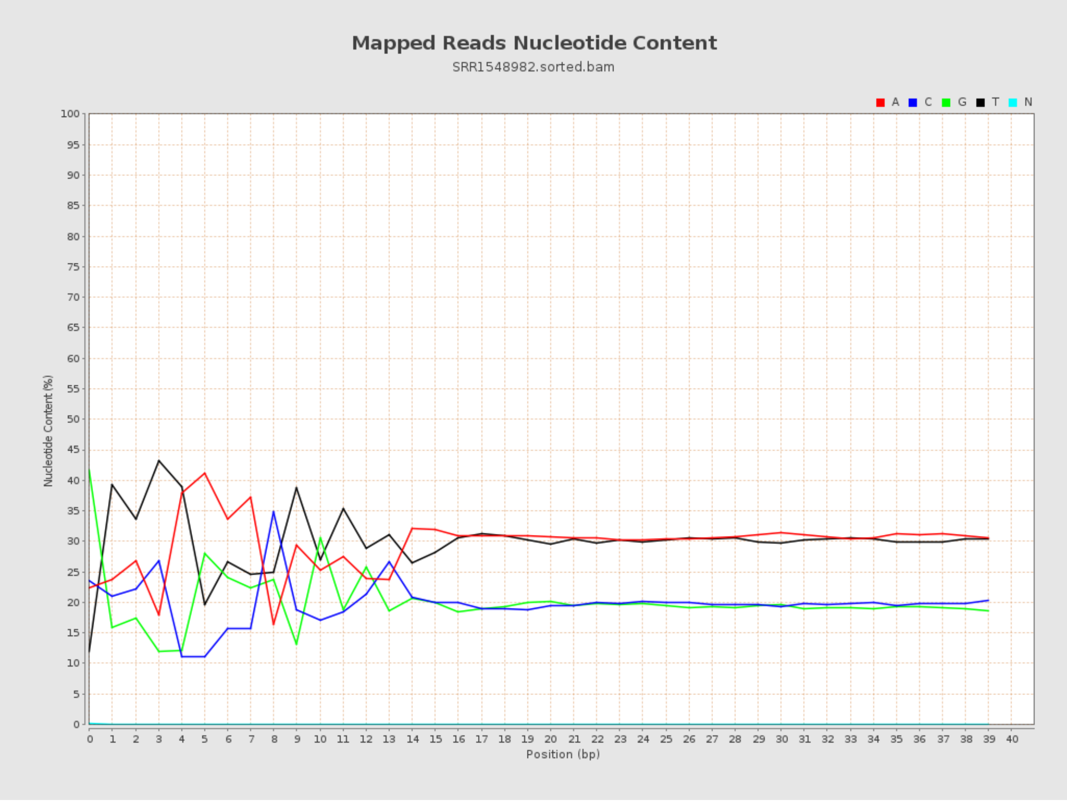
6. Results : Genome Fraction Coverage



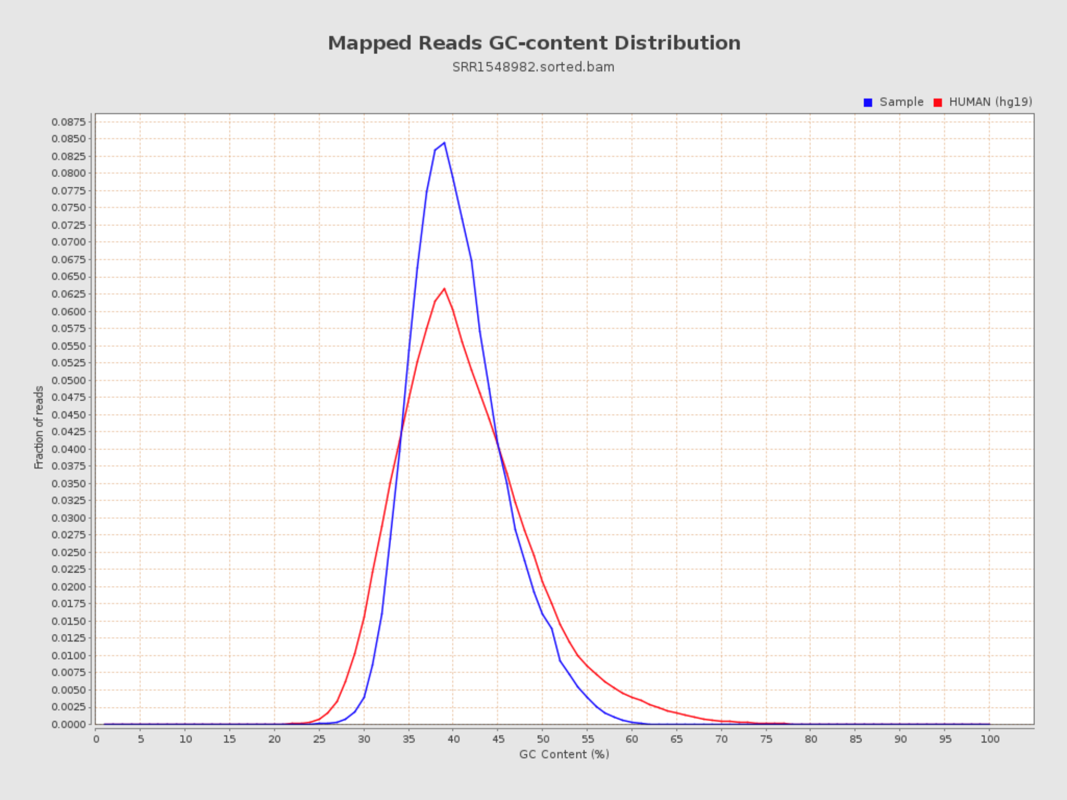
7. Results : Duplication Rate Histogram



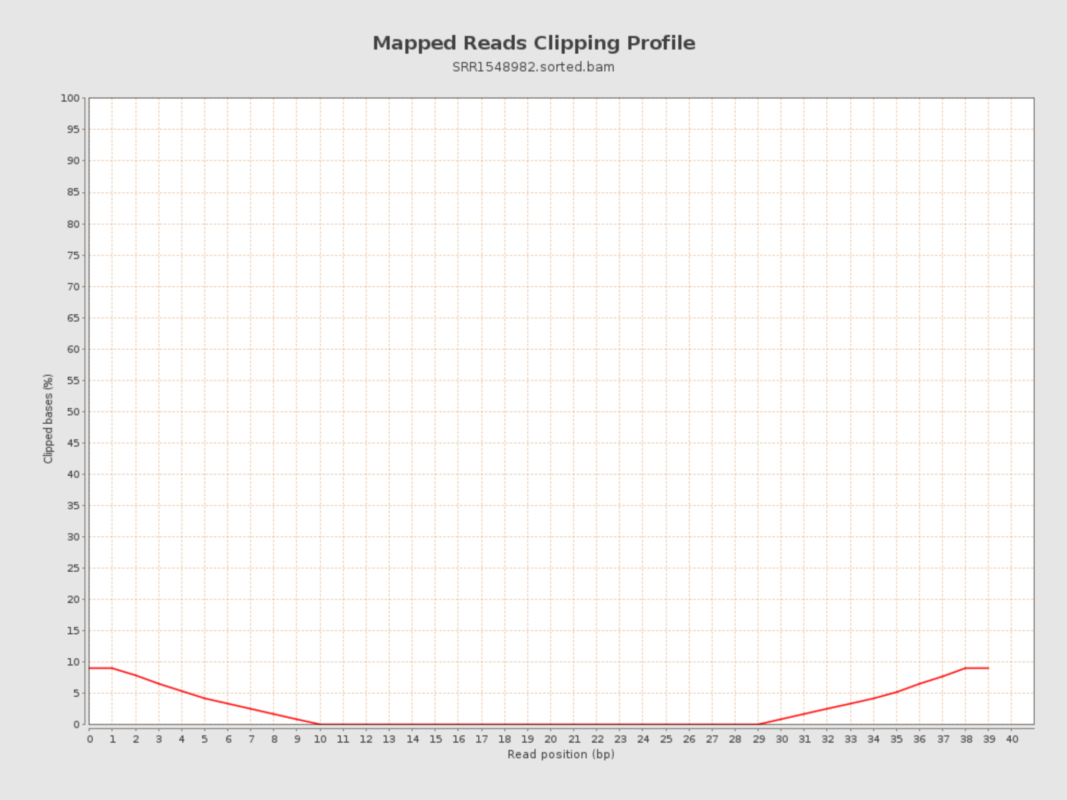
8. Results : Mapped Reads Nucleotide Content



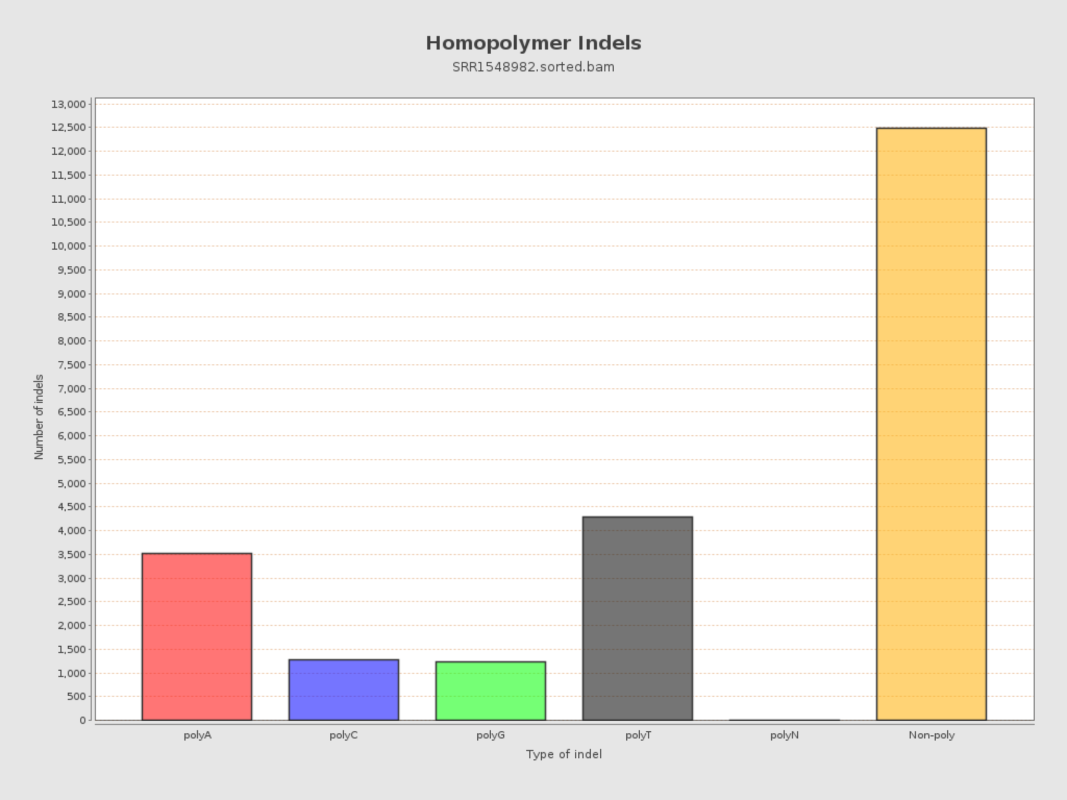
9. Results : Mapped Reads GC-content Distribution



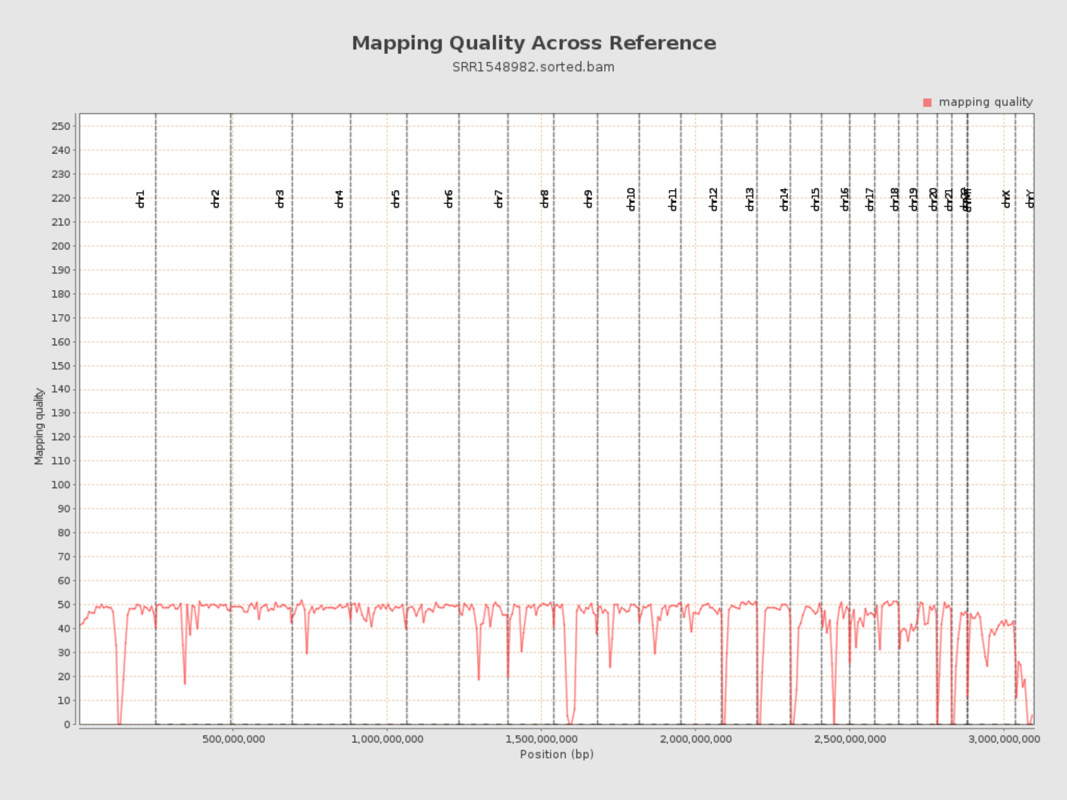
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram