Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 10:25:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548937.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_SRR1548937 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548937.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 10:25:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548937.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,024,579
Mapped reads	7,027,746 / 87.58%
Unmapped reads	996,833 / 12.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	283,277 / 3.53%
Duplication rate	2.49%
Clipped reads	642,442 / 8.01%

2.2. ACGT Content

Number/percentage of A's	81,113,262 / 29.22%
Number/percentage of C's	57,613,565 / 20.76%
Number/percentage of T's	81,442,710 / 29.34%
Number/percentage of G's	57,416,403 / 20.68%
Number/percentage of N's	2,393 / 0%
GC Percentage	41.44%

2.3. Coverage

Mean	0.0897
Standard Deviation	1.1713

2.4. Mapping Quality

Mean Mapping Quality	37.78

2.5. Mismatches and indels

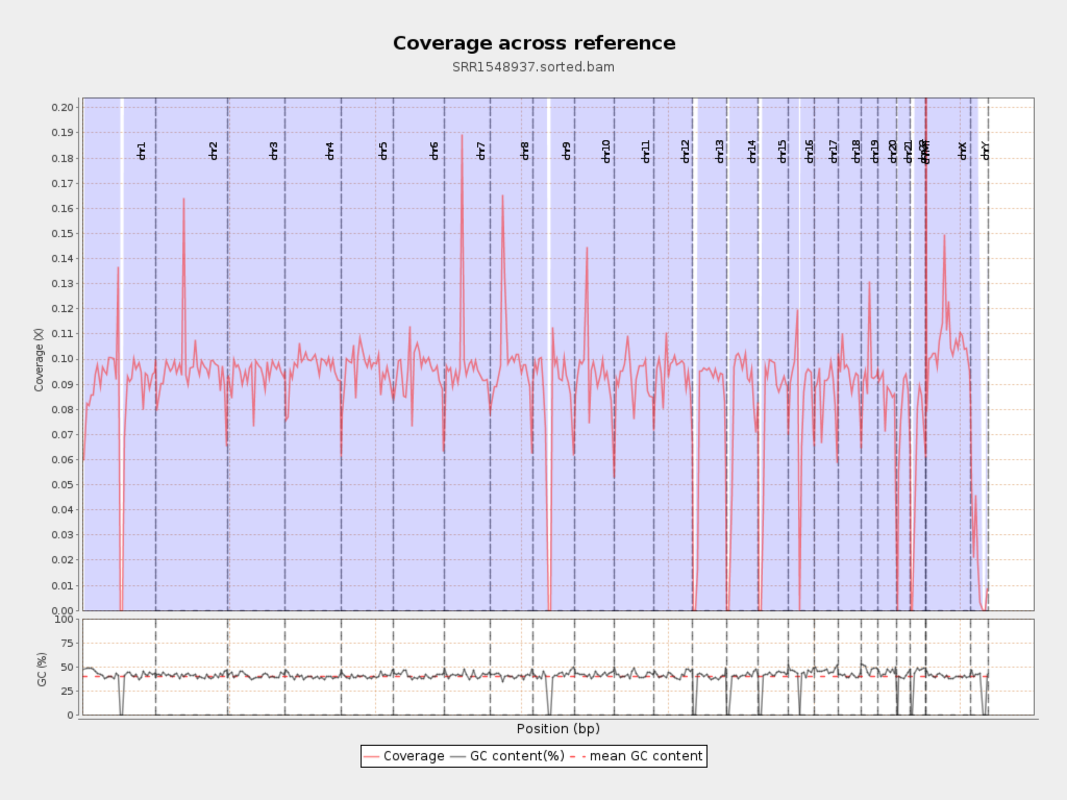
General error rate	0.34%
Mismatches	925,734
Insertions	10,742
Mapped reads with at least one insertion	0.15%
Deletions	23,447
Mapped reads with at least one deletion	0.33%
Homopolymer indels	38.81%

2.6. Chromosome stats

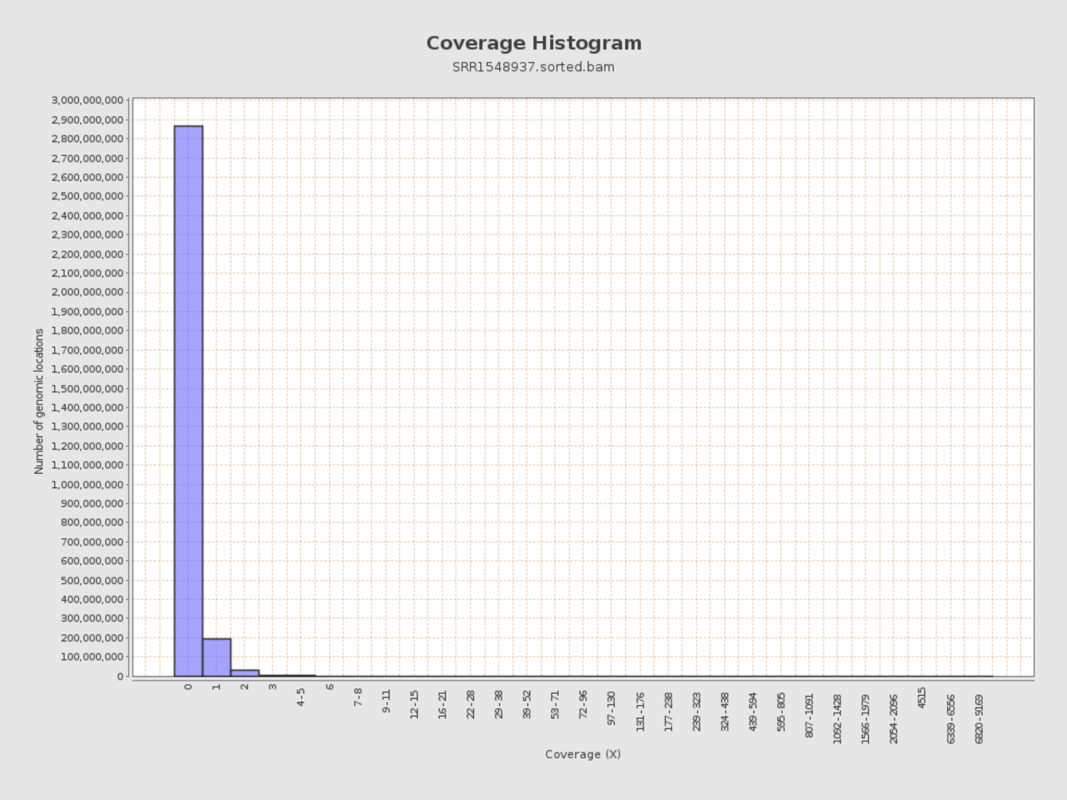
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21619011	0.0867	1.1961
chr2	243199373	23500053	0.0966	0.7083
chr3	198022430	18655412	0.0942	0.3604
chr4	191154276	18459988	0.0966	0.3876
chr5	180915260	17281095	0.0955	0.3772
chr6	171115067	16270130	0.0951	0.4235
chr7	159138663	15643063	0.0983	1.1043
chr8	146364022	14550661	0.0994	4.4327

chr9	141213431	11633409	0.0824	0.7209
chr10	135534747	12825981	0.0946	0.592
chr11	135006516	12471906	0.0924	0.7125
chr12	133851895	12677120	0.0947	0.3921
chr13	115169878	8953356	0.0777	0.3203
chr14	107349540	8407678	0.0783	0.456
chr15	102531392	7803357	0.0761	0.3262
chr16	90354753	7434046	0.0823	0.4154
chr17	81195210	7105856	0.0875	0.3927
chr18	78077248	7403813	0.0948	1.394
chr19	59128983	5660469	0.0957	1.1981
chr20	63025520	5361147	0.0851	0.3663
chr21	48129895	3455979	0.0718	0.408
chr22	51304566	2906332	0.0566	0.3249
chrMT	16571	6340	0.3826	0.7082
chrX	155270560	16516790	0.1064	0.5244
chrY	59373566	1015768	0.0171	0.2189

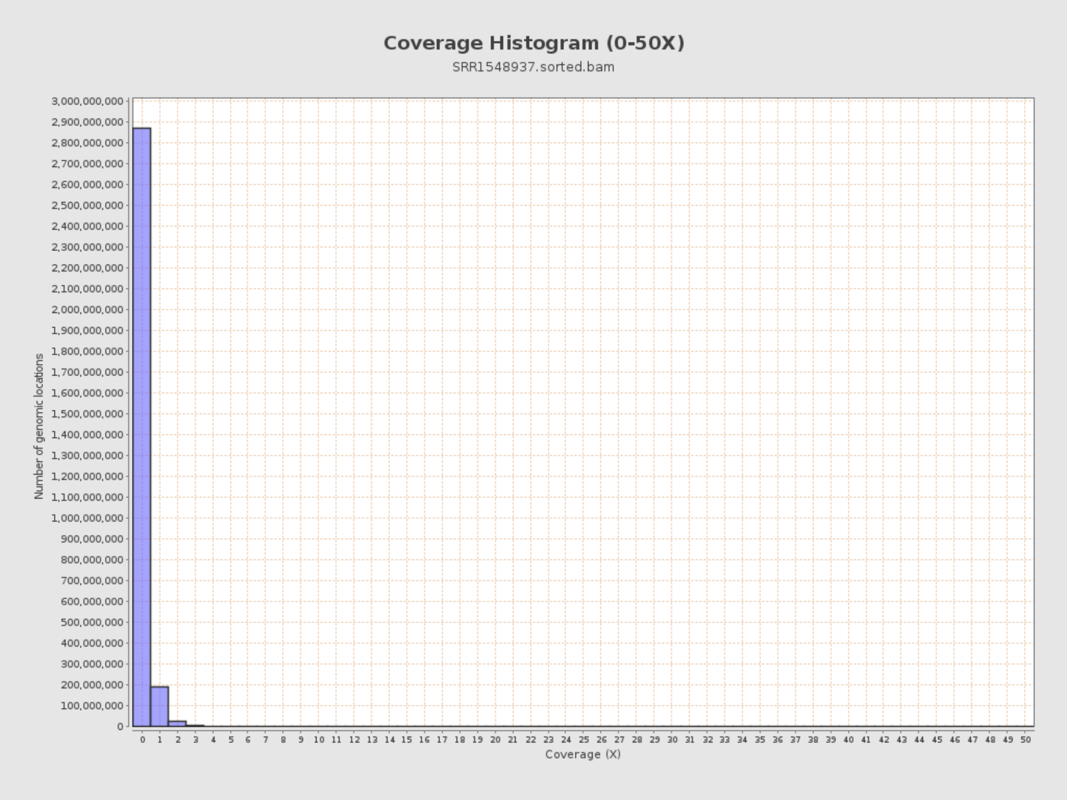
3. Results : Coverage across reference



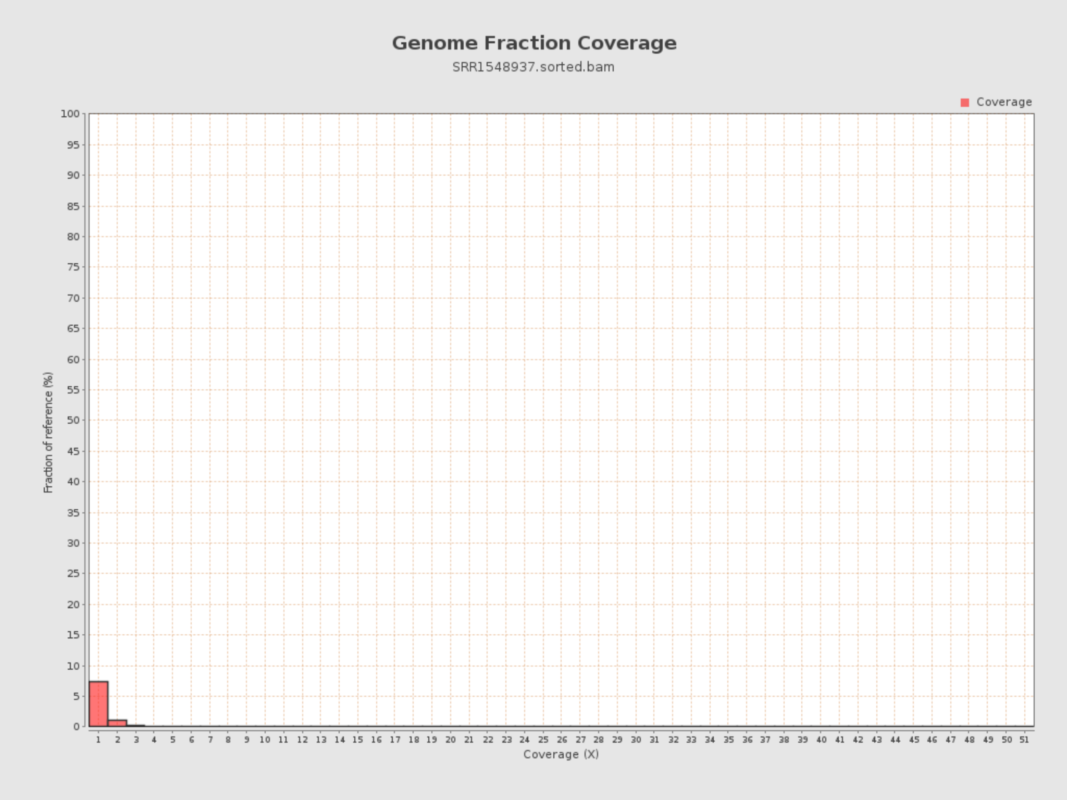
4. Results : Coverage Histogram



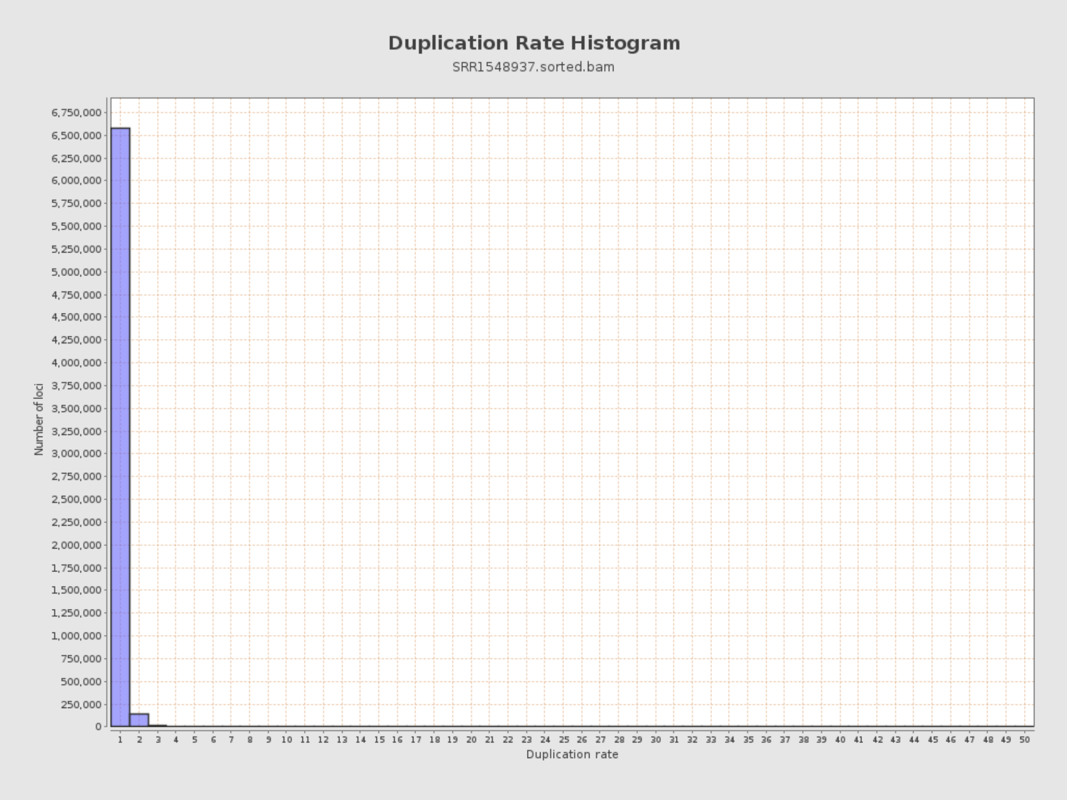
5. Results : Coverage Histogram (0-50X)



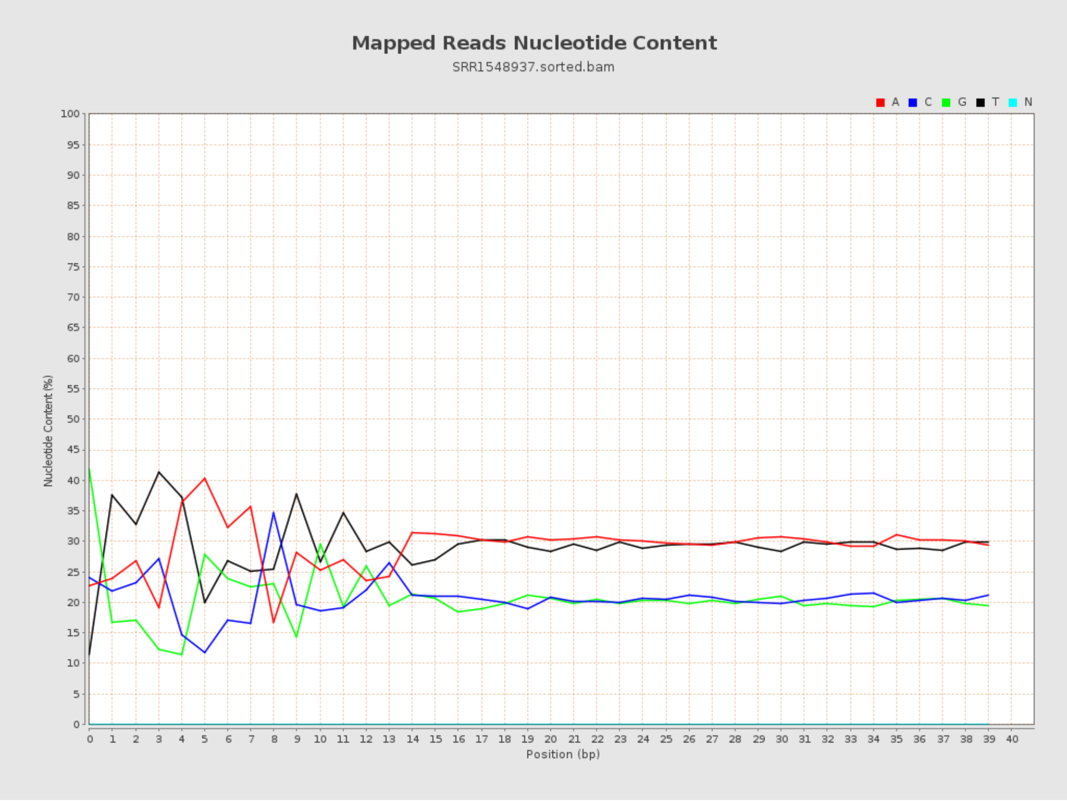
6. Results : Genome Fraction Coverage



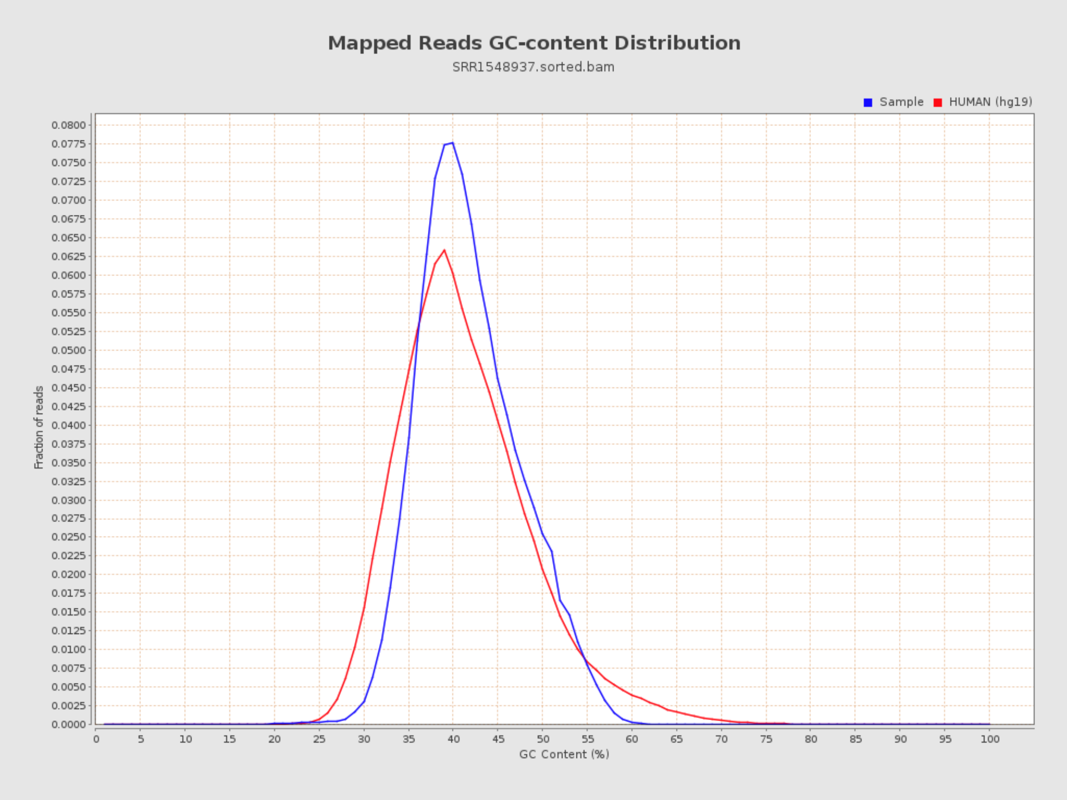
7. Results : Duplication Rate Histogram



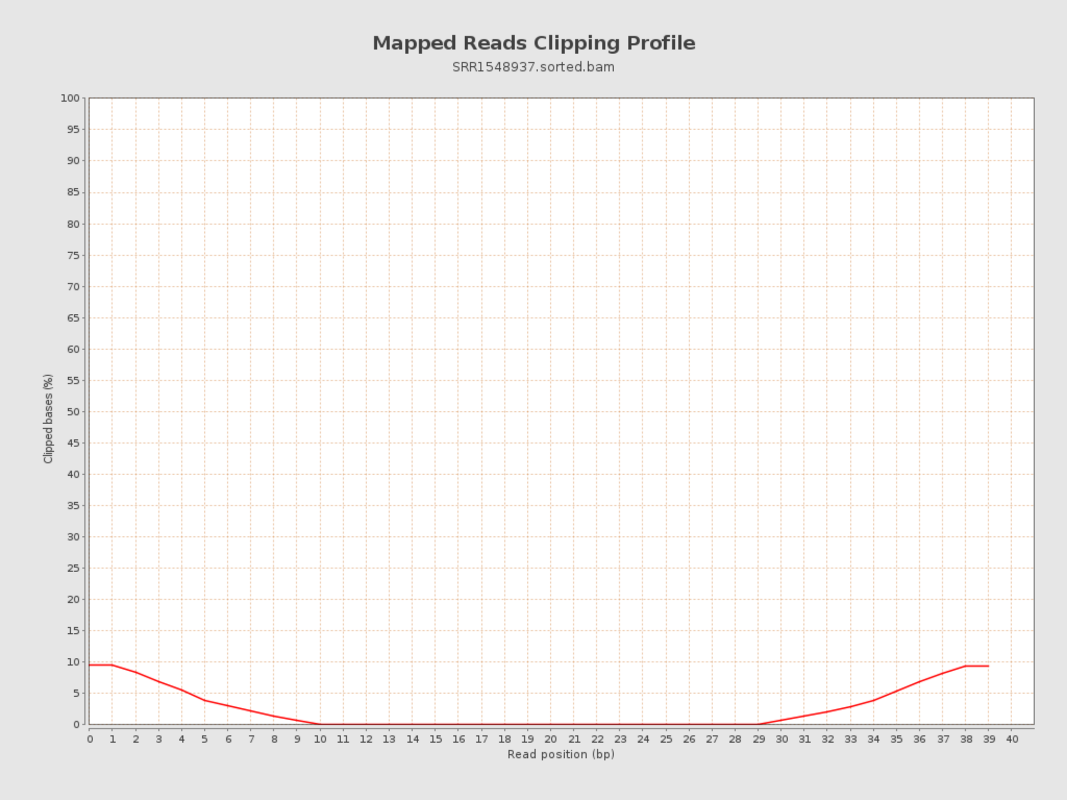
8. Results : Mapped Reads Nucleotide Content



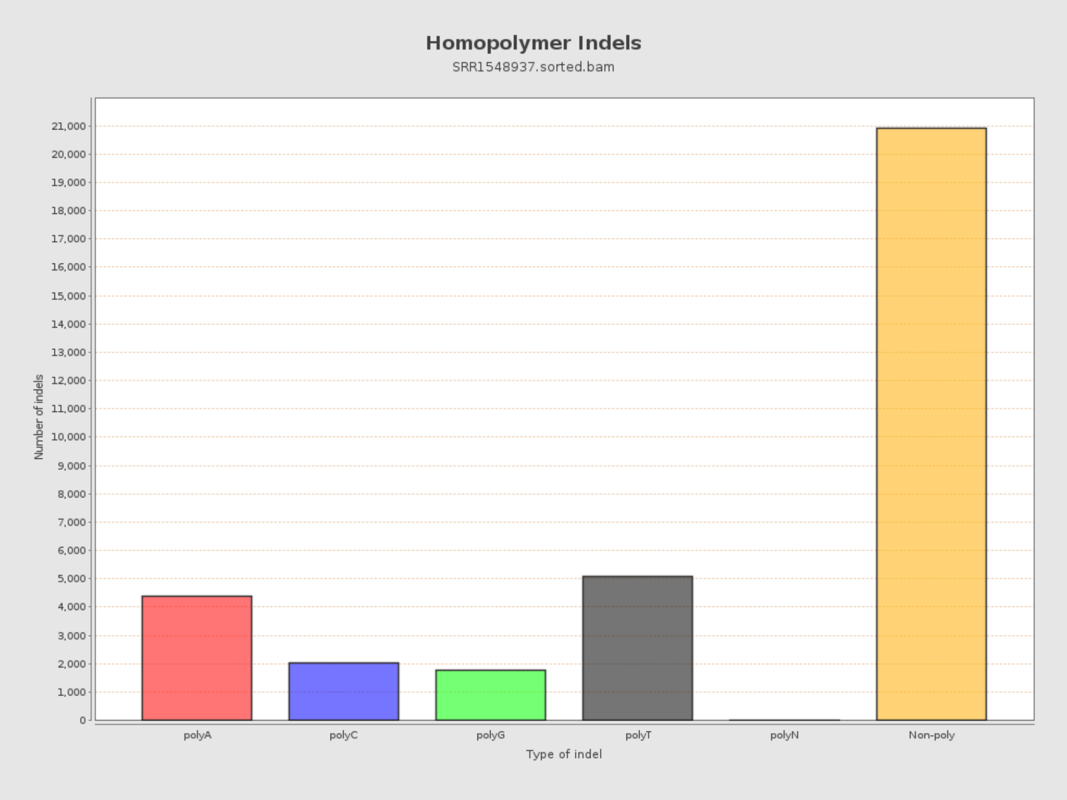
9. Results : Mapped Reads GC-content Distribution



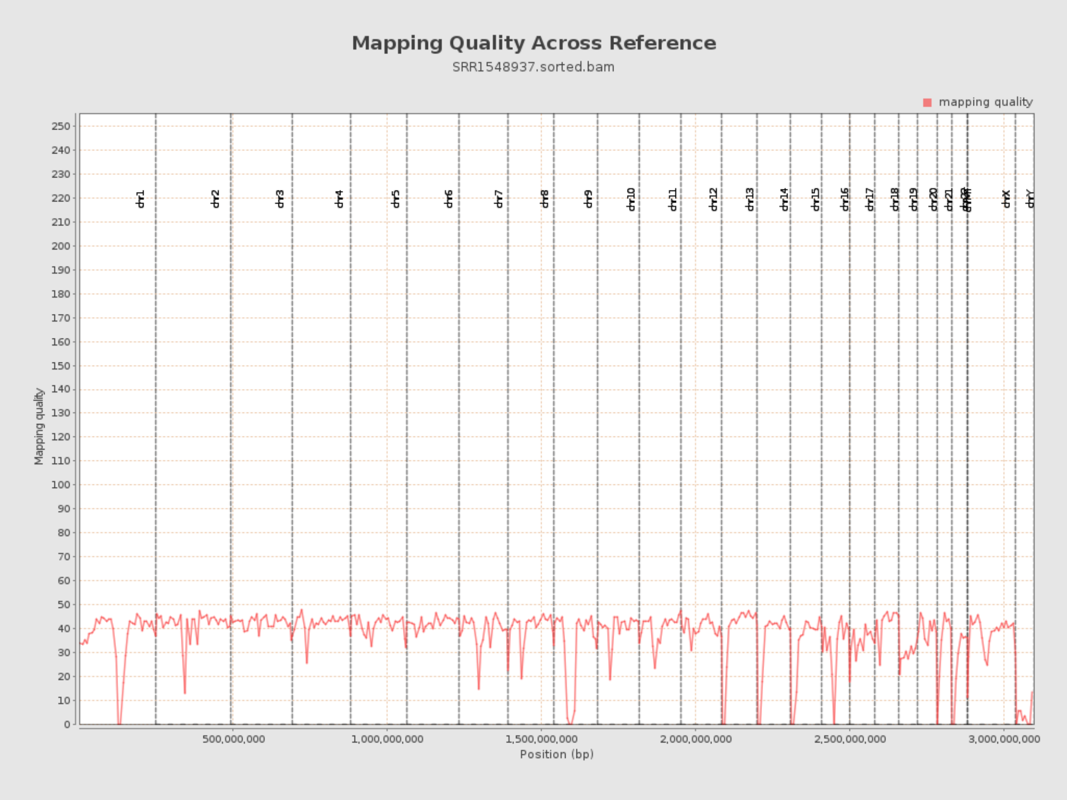
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram