Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 07:58:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548933.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_SRR1548933 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548933.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 07:58:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548933.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,070,153
Mapped reads	6,160,803 / 87.14%
Unmapped reads	909,350 / 12.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	212,125 / 3%
Duplication rate	2.53%
Clipped reads	421,292 / 5.96%

2.2. ACGT Content

Number/percentage of A's	71,798,405 / 29.42%
Number/percentage of C's	50,061,446 / 20.51%
Number/percentage of T's	72,069,191 / 29.53%
Number/percentage of G's	50,127,026 / 20.54%
Number/percentage of N's	2,204 / 0%
GC Percentage	41.05%

2.3. Coverage

Mean	0.0788
Standard Deviation	0.9385

2.4. Mapping Quality

Mean Mapping Quality	42.94

2.5. Mismatches and indels

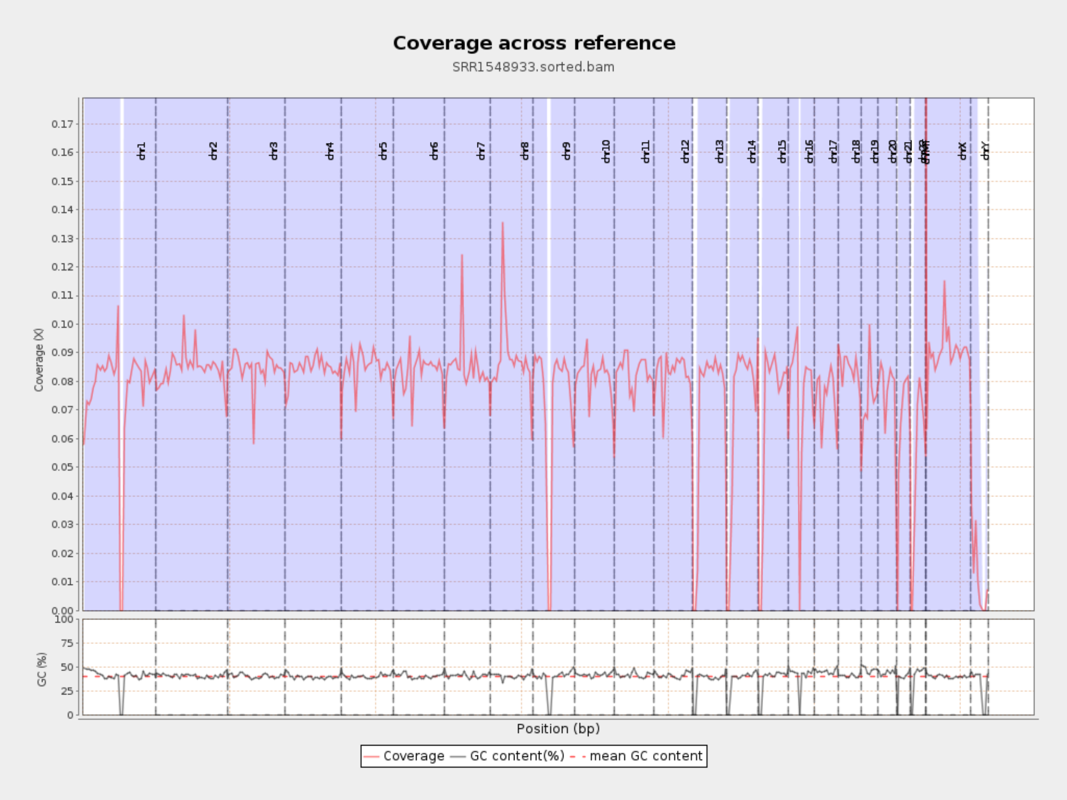
General error rate	0.26%
Mismatches	637,346
Insertions	7,467
Mapped reads with at least one insertion	0.12%
Deletions	19,706
Mapped reads with at least one deletion	0.32%
Homopolymer indels	41.43%

2.6. Chromosome stats

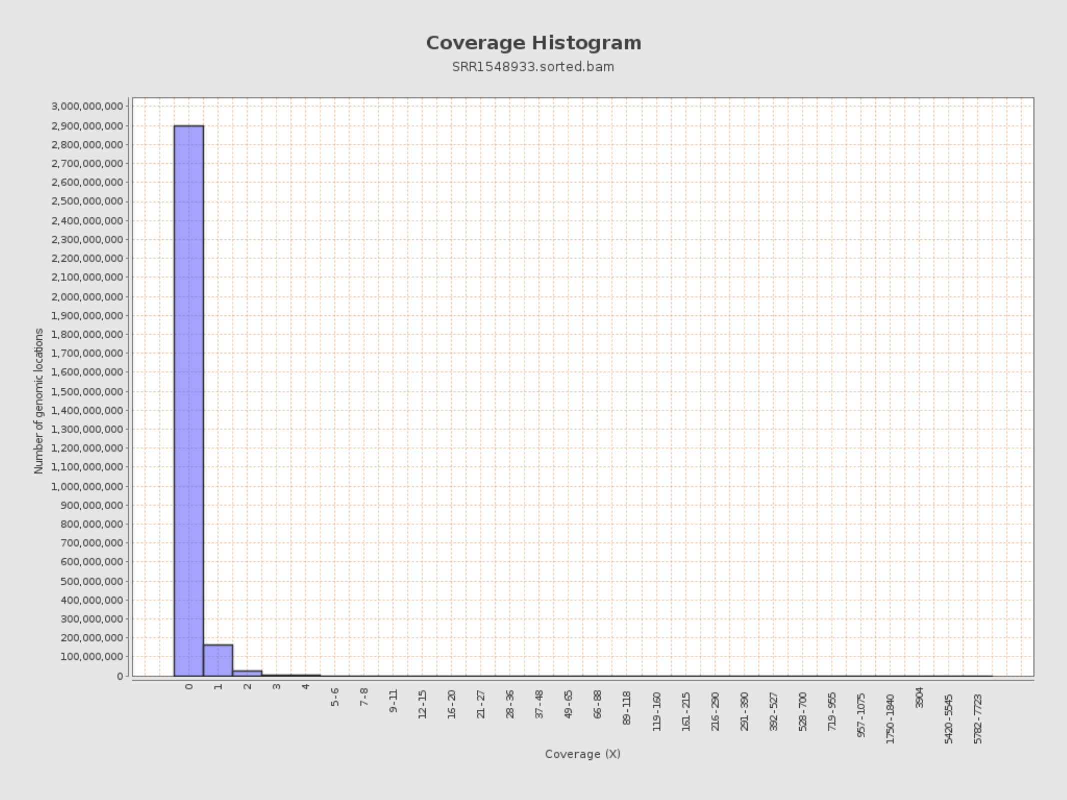
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19079051	0.0765	0.8288
chr2	243199373	20628856	0.0848	0.4475
chr3	198022430	16751355	0.0846	0.3467
chr4	191154276	16208436	0.0848	0.3562
chr5	180915260	15292770	0.0845	0.3507
chr6	171115067	14372622	0.084	0.3774
chr7	159138663	13565662	0.0852	0.6851
chr8	146364022	12919463	0.0883	3.7464

chr9	141213431	10260386	0.0727	0.4359
chr10	135534747	11133304	0.0821	0.4191
chr11	135006516	11160928	0.0827	0.5228
chr12	133851895	11089156	0.0828	0.3519
chr13	115169878	8019226	0.0696	0.3126
chr14	107349540	7542079	0.0703	0.3629
chr15	102531392	7024835	0.0685	0.3105
chr16	90354753	6650573	0.0736	0.3432
chr17	81195210	6101339	0.0751	0.3546
chr18	78077248	6616408	0.0847	0.7575
chr19	59128983	4394491	0.0743	0.7378
chr20	63025520	4913564	0.078	0.3449
chr21	48129895	3053894	0.0635	0.3285
chr22	51304566	2610429	0.0509	0.2937
chrMT	16571	4923	0.2971	0.6545
chrX	155270560	14009510	0.0902	0.4156
chrY	59373566	681367	0.0115	0.1655

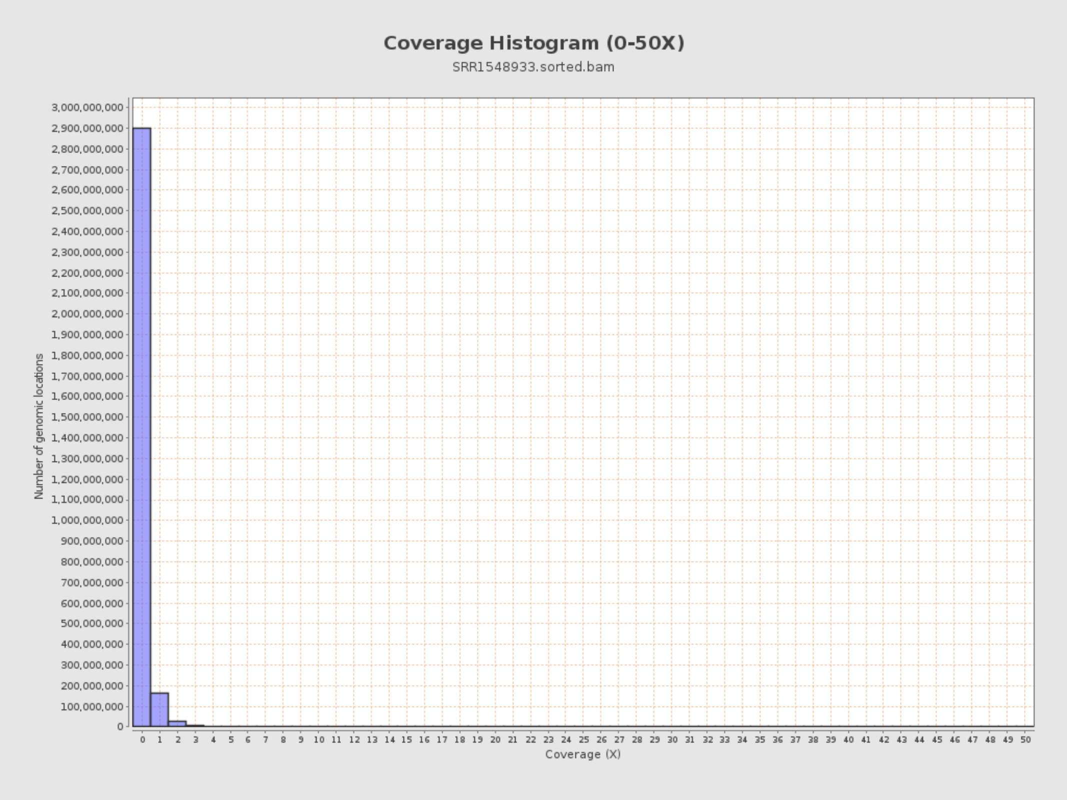
3. Results : Coverage across reference



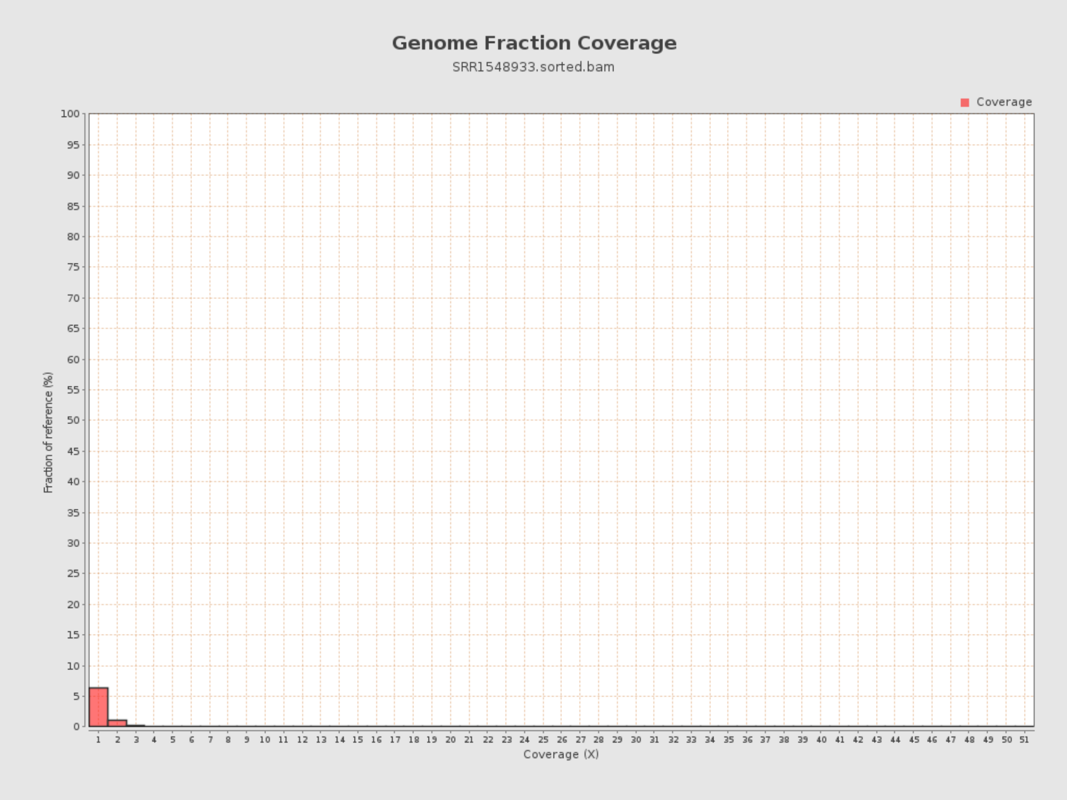
4. Results : Coverage Histogram



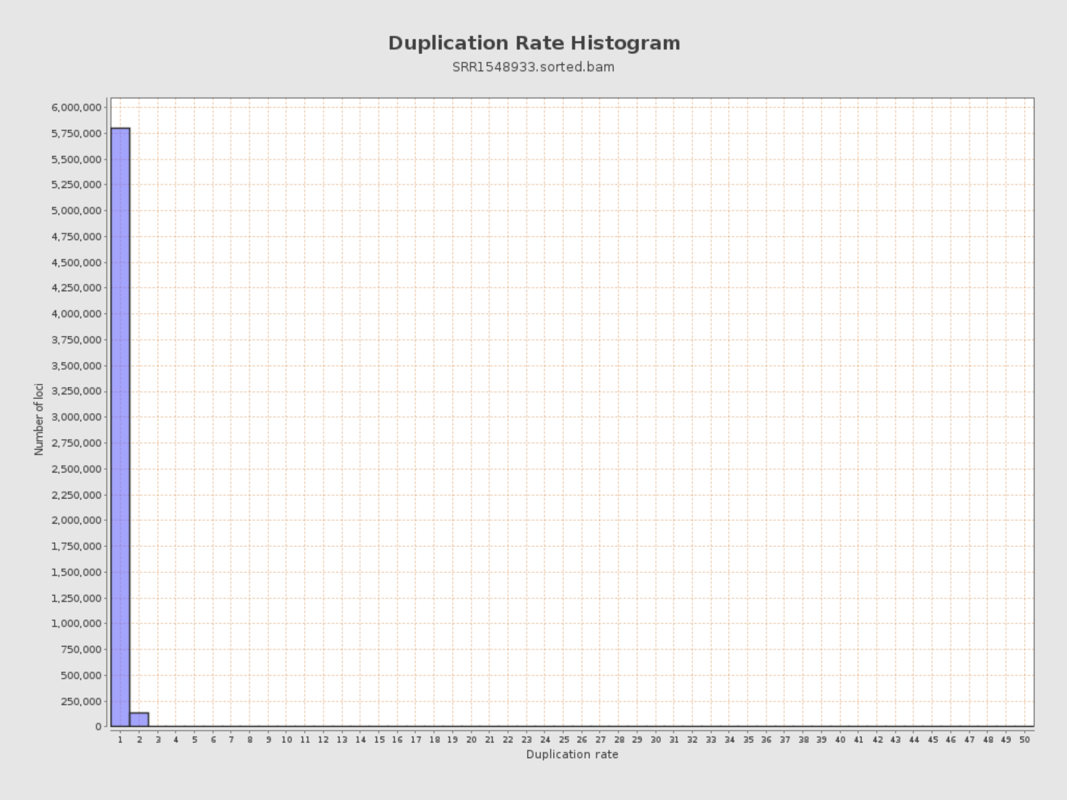
5. Results : Coverage Histogram (0-50X)



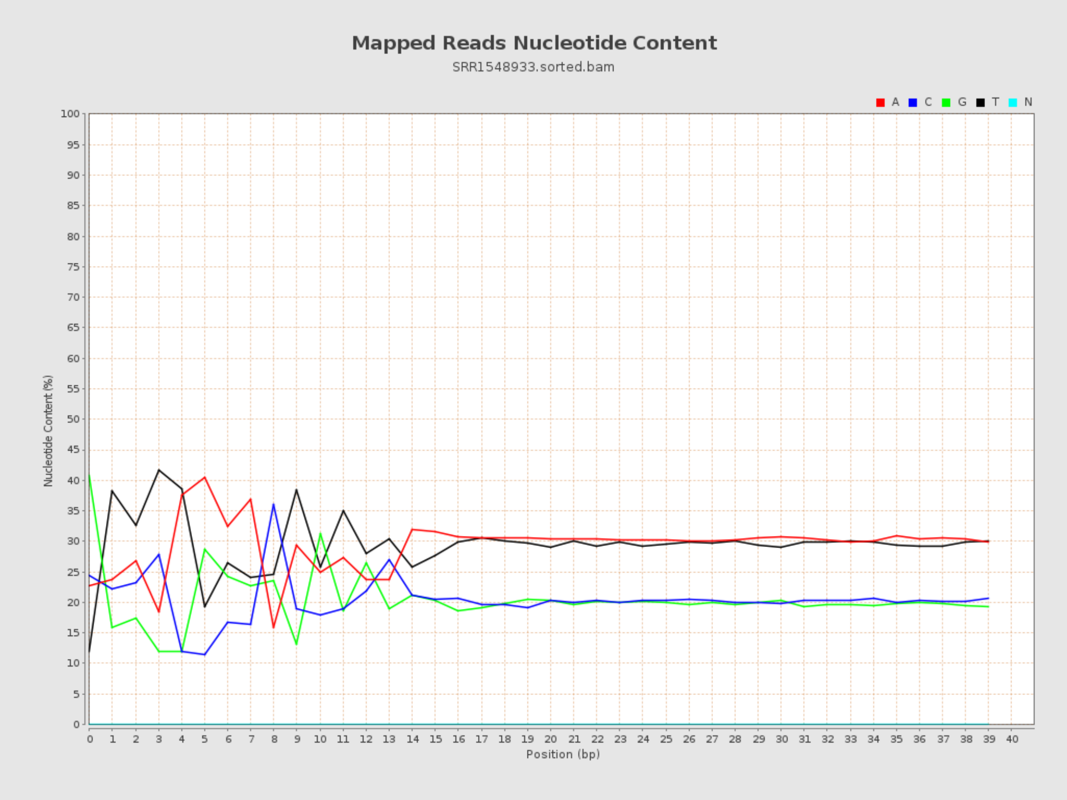
6. Results : Genome Fraction Coverage



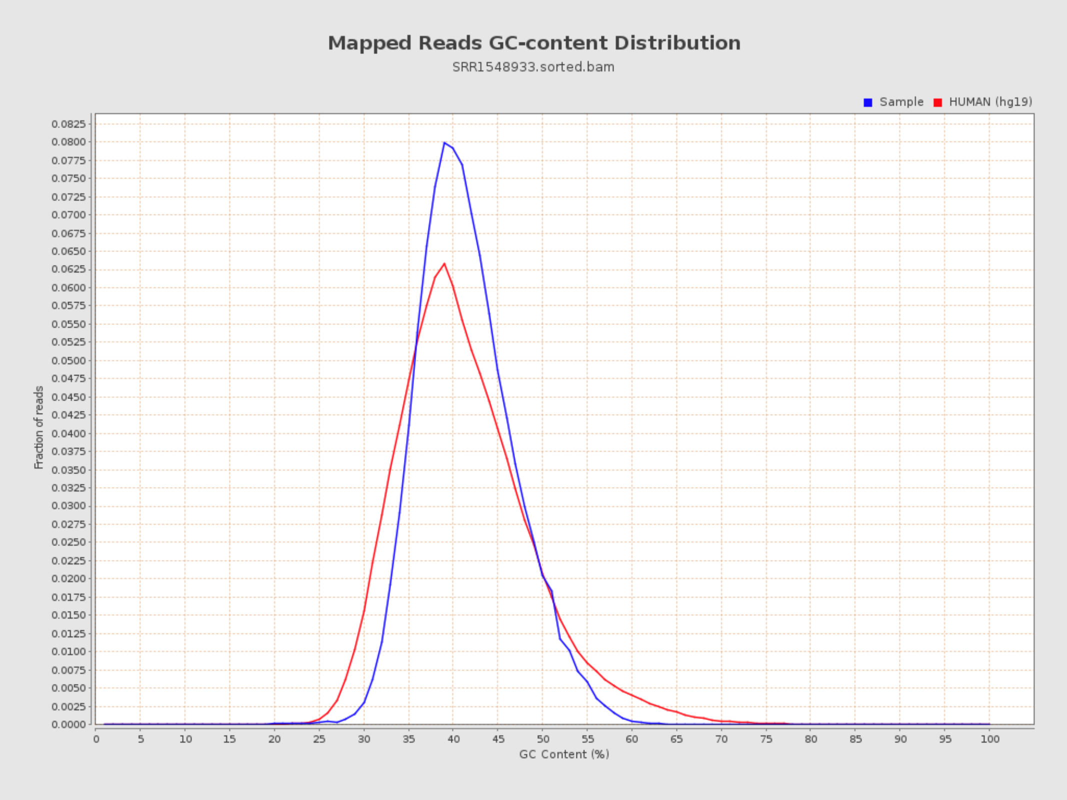
7. Results : Duplication Rate Histogram



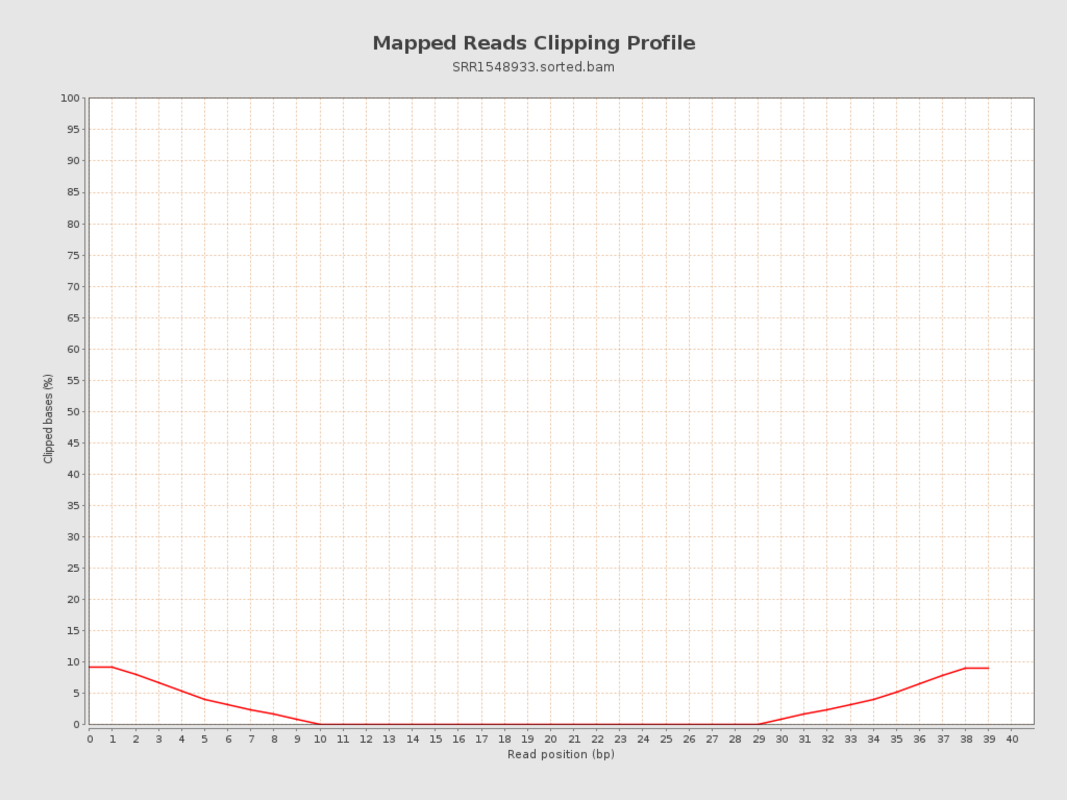
8. Results : Mapped Reads Nucleotide Content



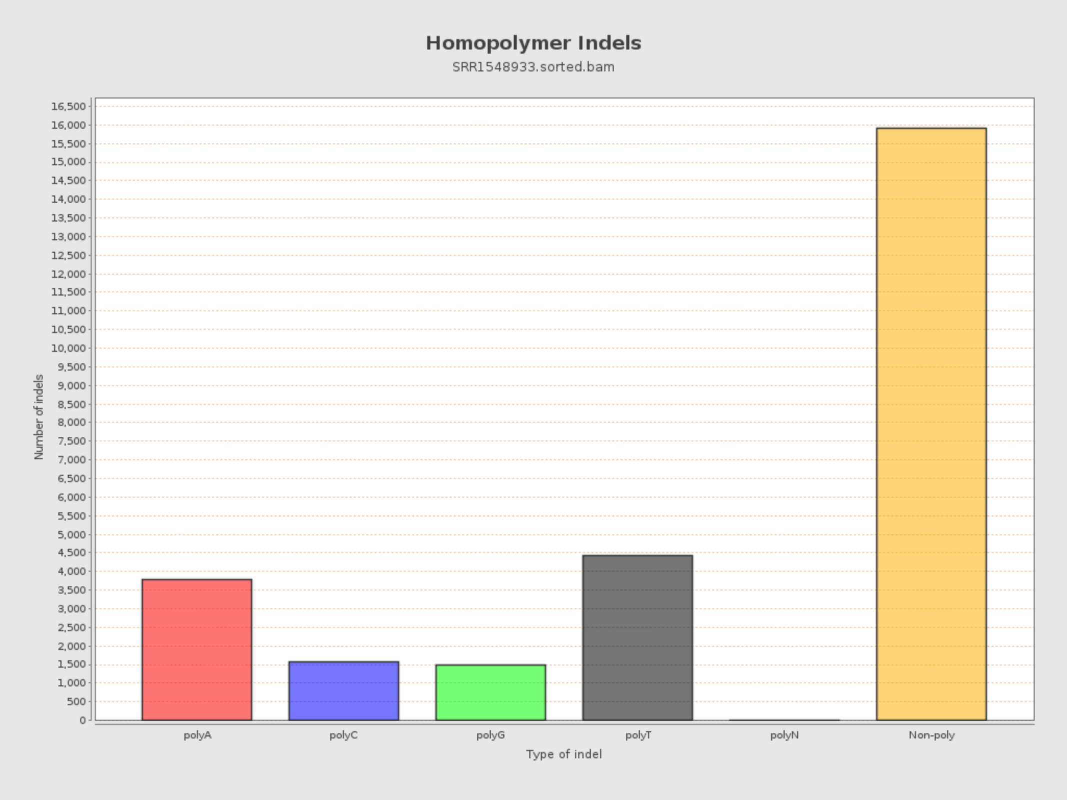
9. Results : Mapped Reads GC-content Distribution



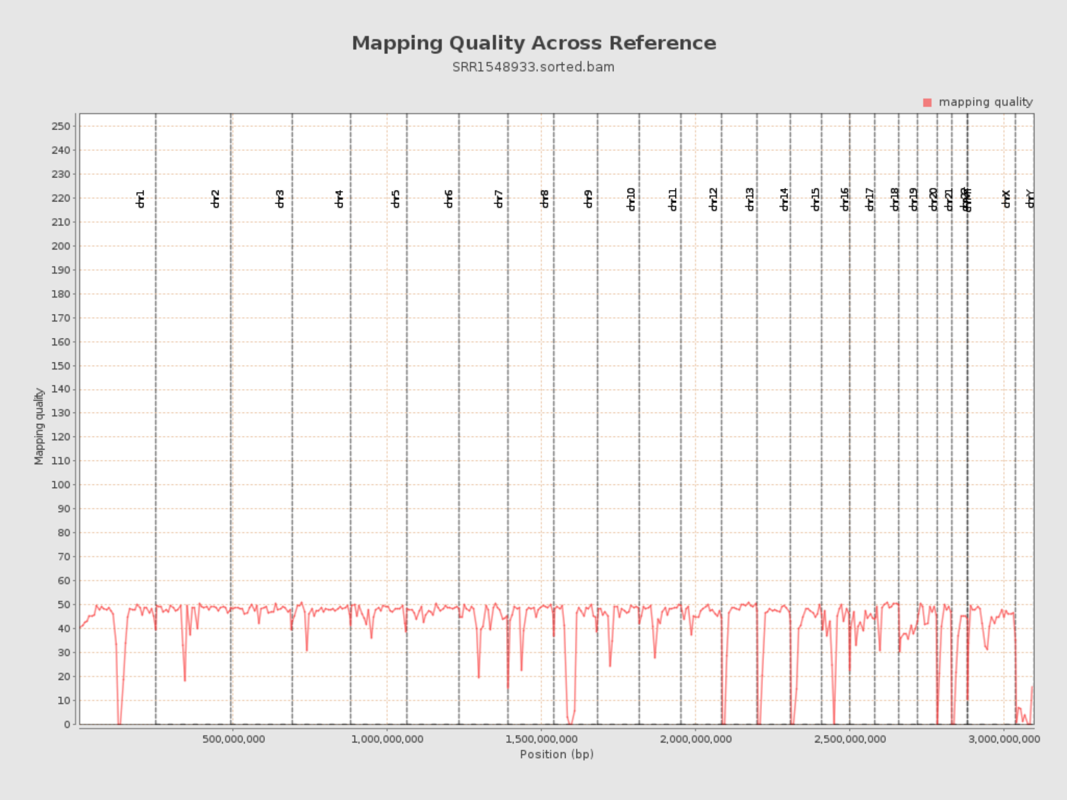
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram