Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 01:56:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548967.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_SRR1548967 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548967.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 01:56:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548967.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,177,201
Mapped reads	6,289,585 / 87.63%
Unmapped reads	887,616 / 12.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	279,304 / 3.89%
Duplication rate	2.84%
Clipped reads	479,183 / 6.68%

2.2. ACGT Content

Number/percentage of A's	70,555,067 / 28.36%
Number/percentage of C's	52,916,098 / 21.27%
Number/percentage of T's	72,027,797 / 28.95%
Number/percentage of G's	53,298,836 / 21.42%
Number/percentage of N's	354 / 0%
GC Percentage	42.69%

2.3. Coverage

Mean	0.0804
Standard Deviation	0.7327

2.4. Mapping Quality

Mean Mapping Quality	38

2.5. Mismatches and indels

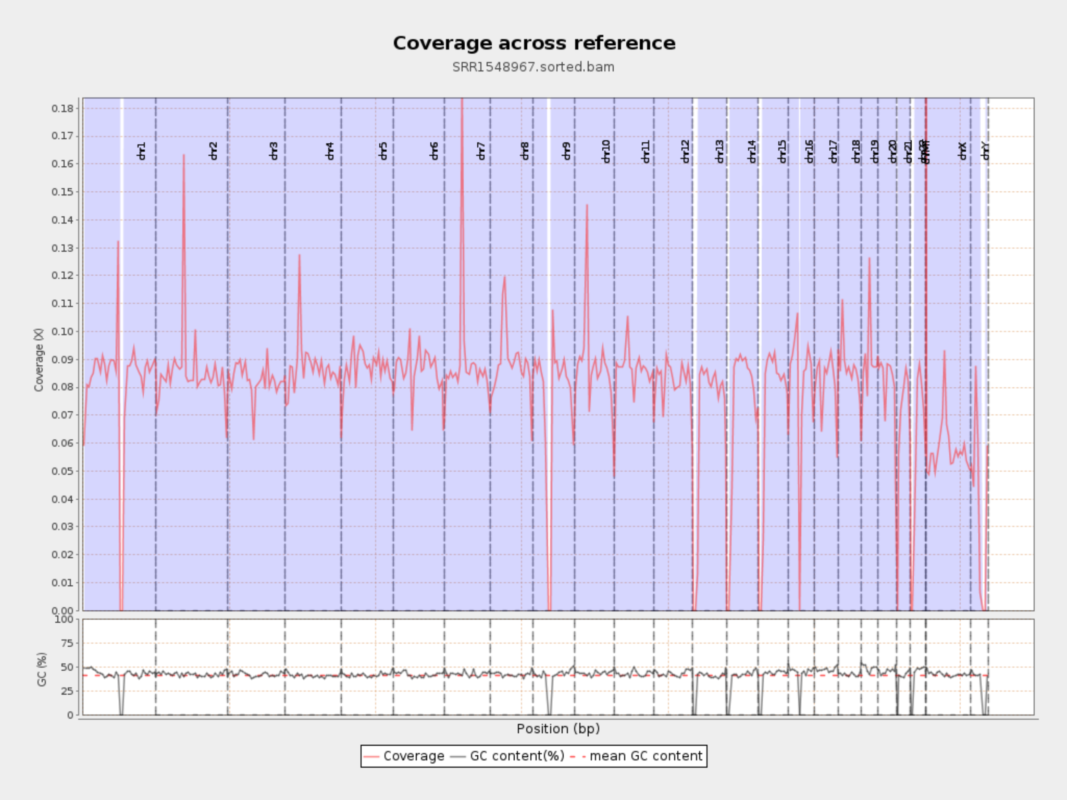
General error rate	0.3%
Mismatches	734,616
Insertions	7,961
Mapped reads with at least one insertion	0.13%
Deletions	18,074
Mapped reads with at least one deletion	0.29%
Homopolymer indels	39.69%

2.6. Chromosome stats

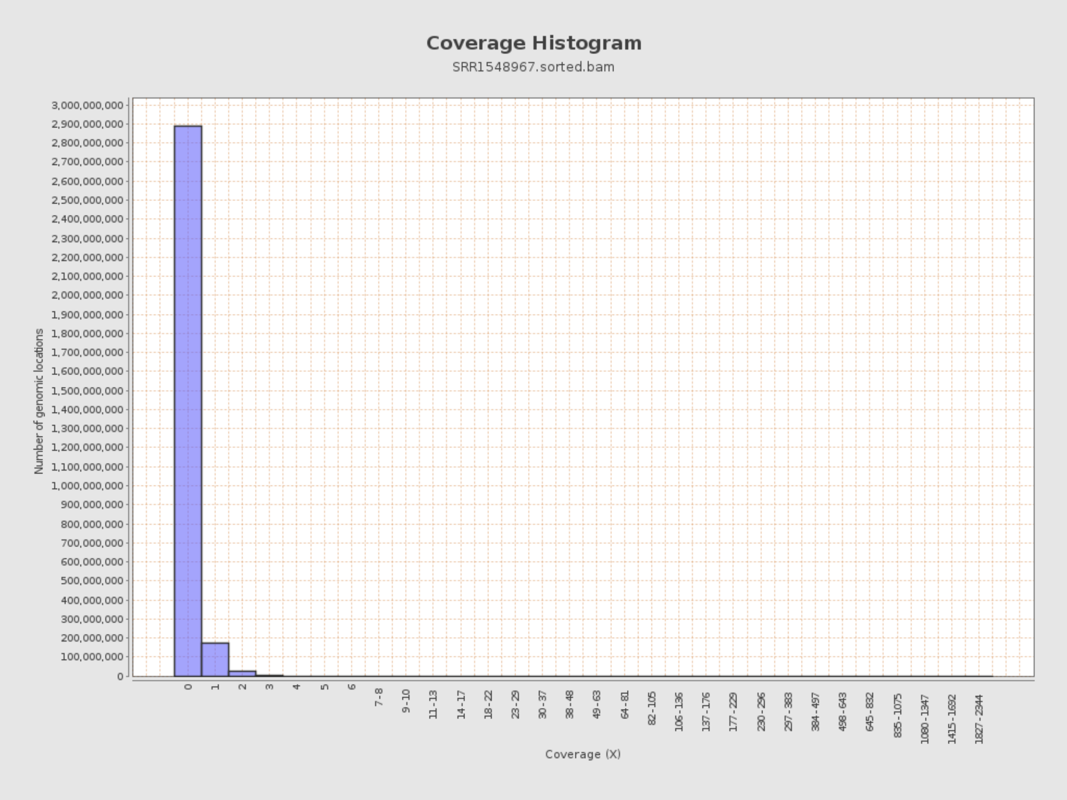
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20308702	0.0815	1.1956
chr2	243199373	20924166	0.086	0.7671
chr3	198022430	16388721	0.0828	0.3371
chr4	191154276	16722060	0.0875	0.3976
chr5	180915260	15740561	0.087	0.3621
chr6	171115067	14836717	0.0867	0.3779
chr7	159138663	14289296	0.0898	1.2013
chr8	146364022	12980135	0.0887	1.2436

chr9	141213431	10556437	0.0748	0.7985
chr10	135534747	12013570	0.0886	0.5958
chr11	135006516	11666358	0.0864	0.5704
chr12	133851895	11095842	0.0829	0.3725
chr13	115169878	7867682	0.0683	0.2987
chr14	107349540	7708590	0.0718	0.4631
chr15	102531392	7124456	0.0695	0.3106
chr16	90354753	7115460	0.0788	0.4228
chr17	81195210	6714025	0.0827	0.3688
chr18	78077248	6876734	0.0881	1.5393
chr19	59128983	5343471	0.0904	1.1877
chr20	63025520	5158886	0.0819	0.3697
chr21	48129895	3229036	0.0671	0.4559
chr22	51304566	2847250	0.0555	0.3614
chrMT	16571	6600	0.3983	0.752
chrX	155270560	9032619	0.0582	0.4557
chrY	59373566	2274266	0.0383	0.3742

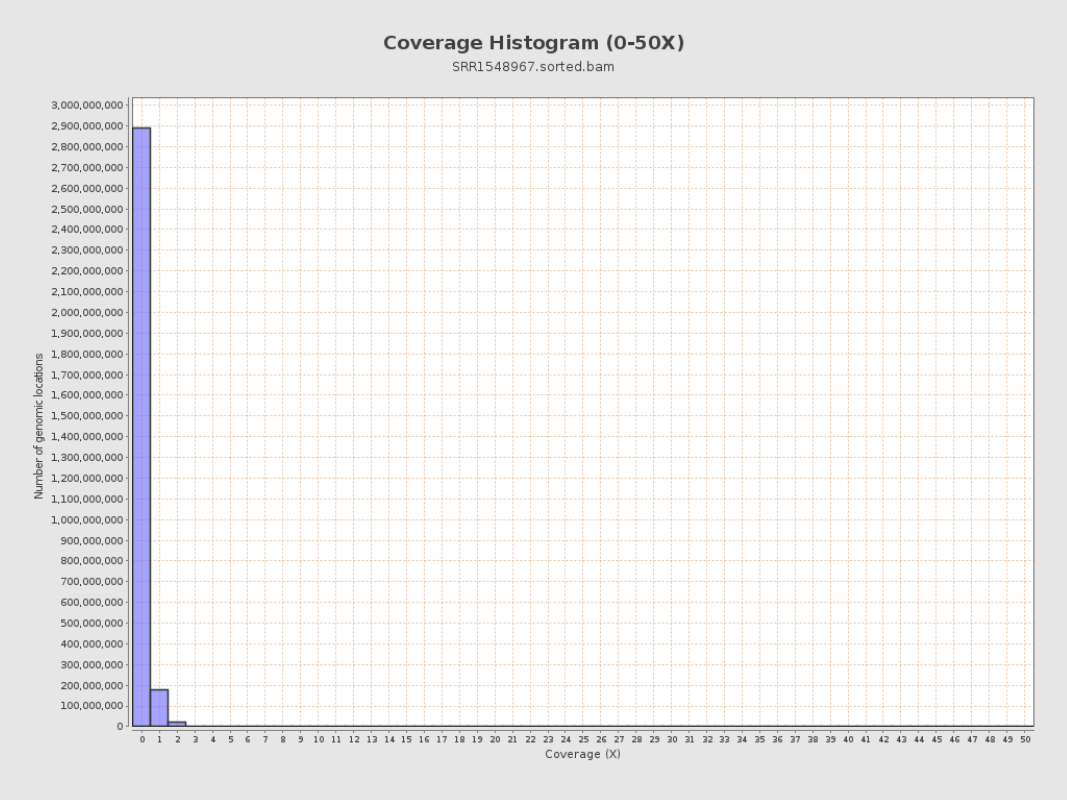
3. Results : Coverage across reference



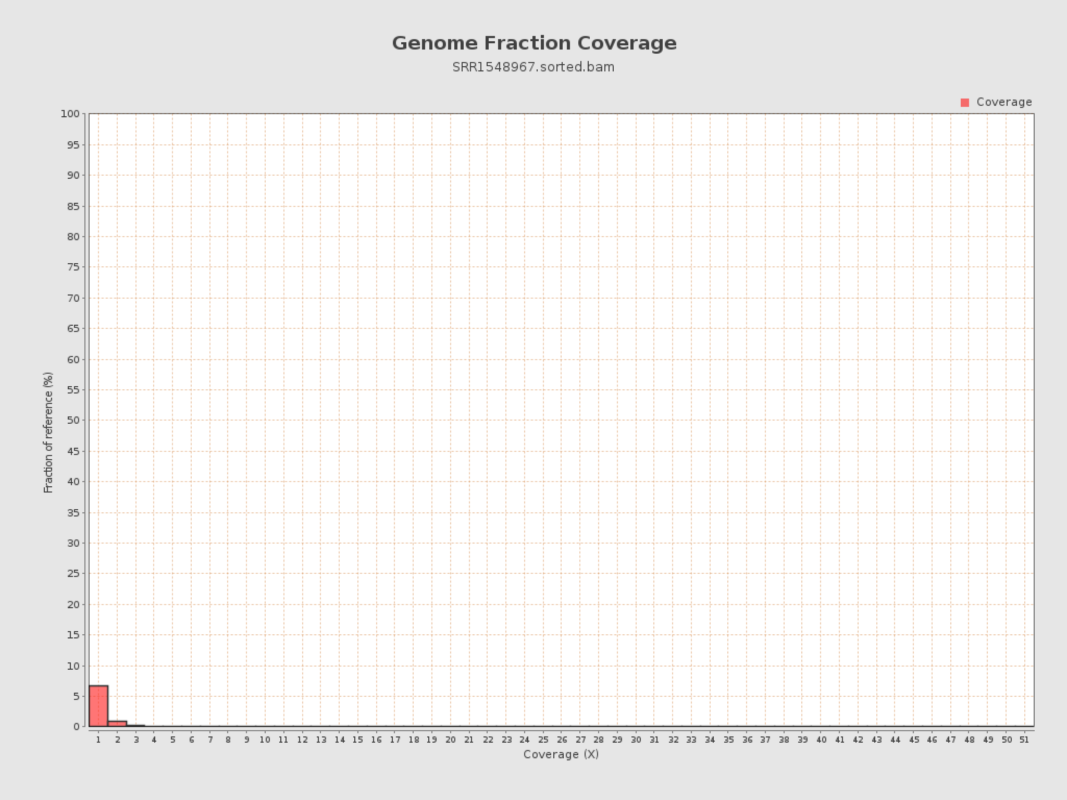
4. Results : Coverage Histogram



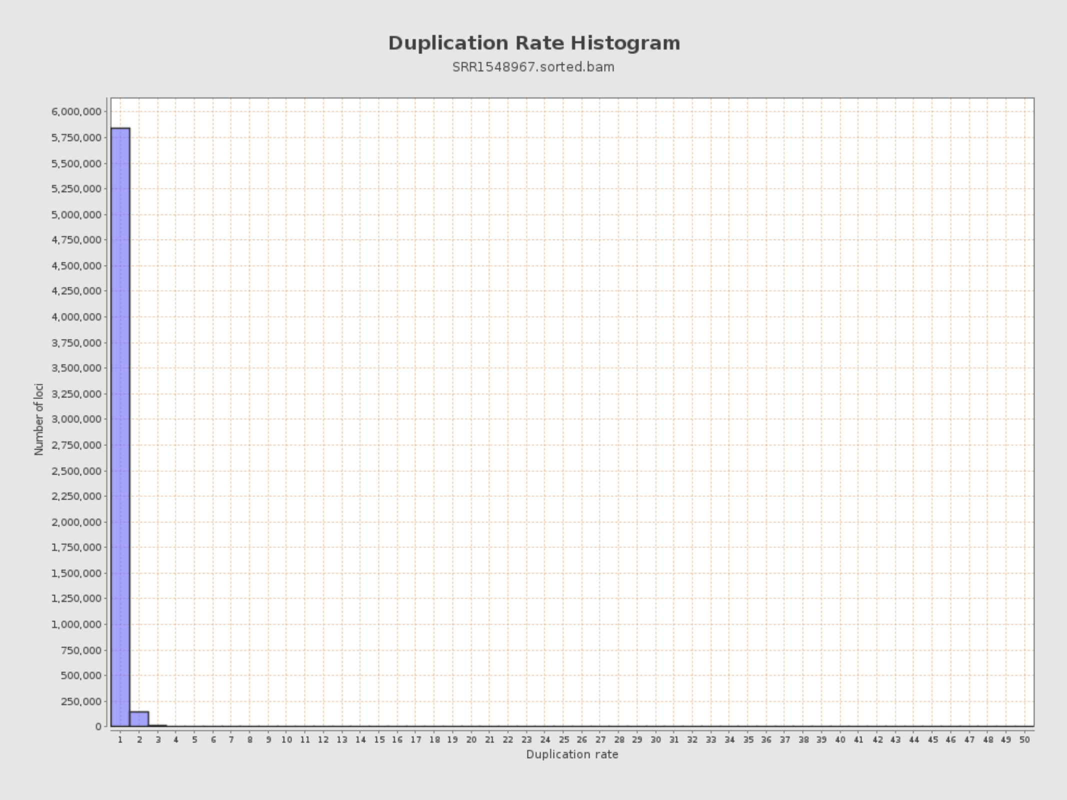
5. Results : Coverage Histogram (0-50X)



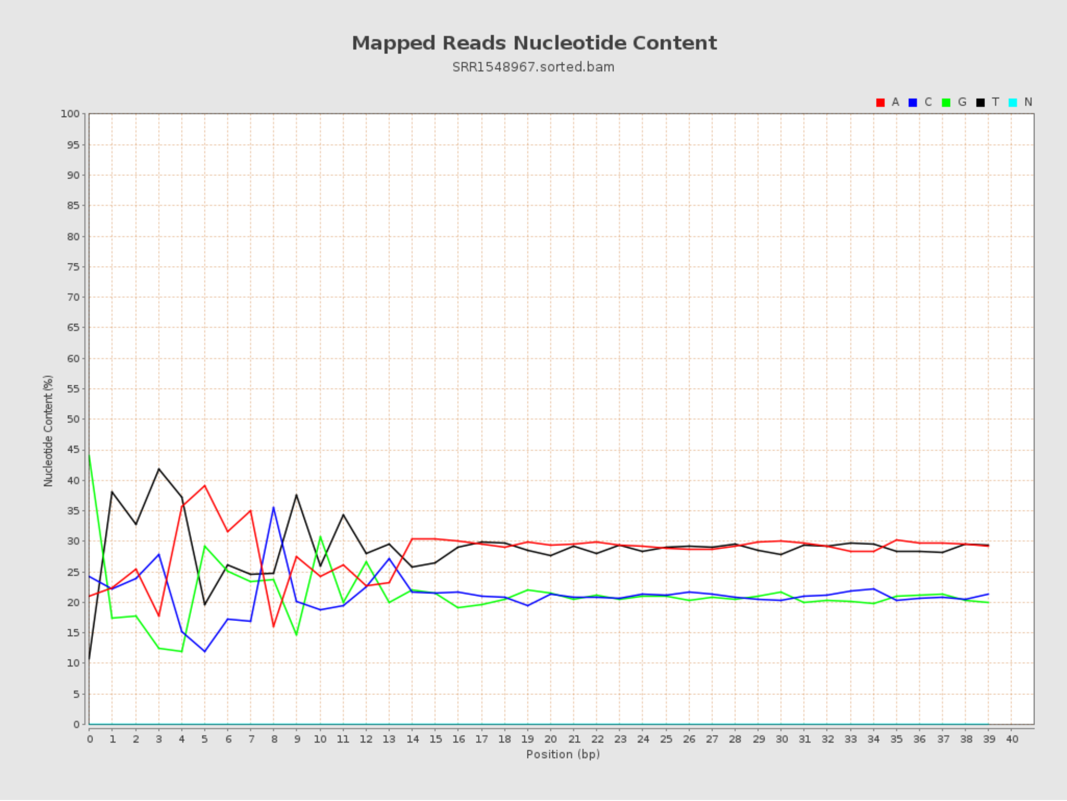
6. Results : Genome Fraction Coverage



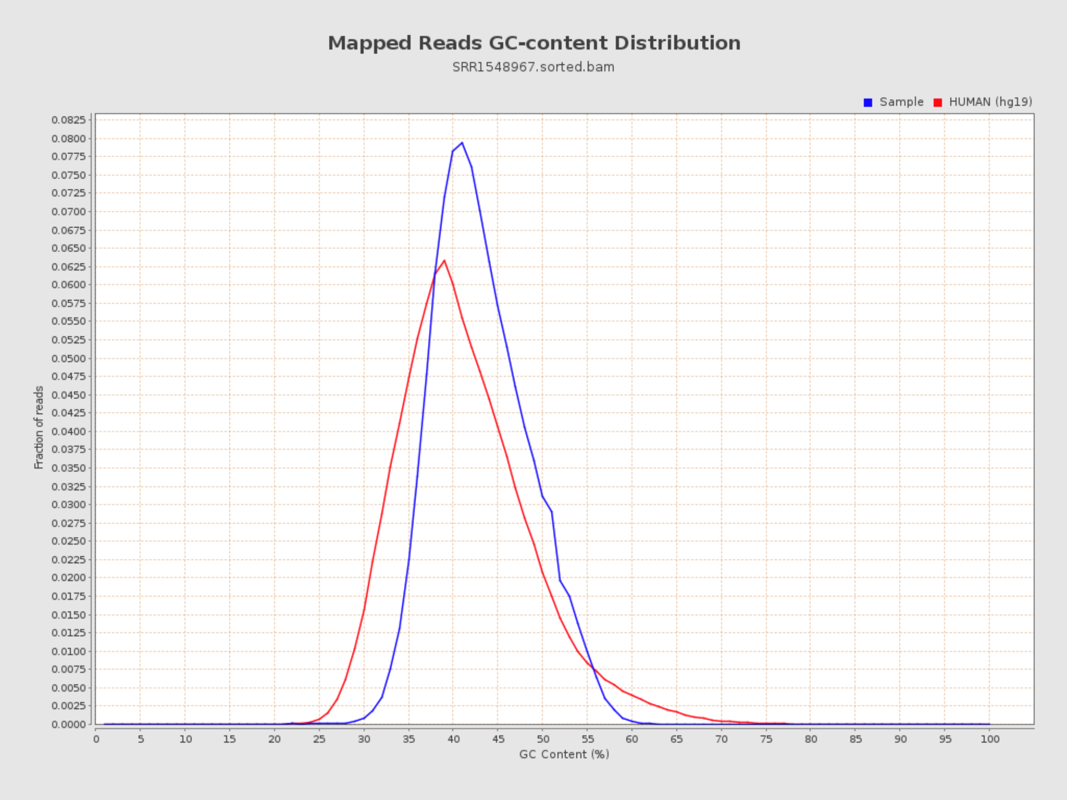
7. Results : Duplication Rate Histogram



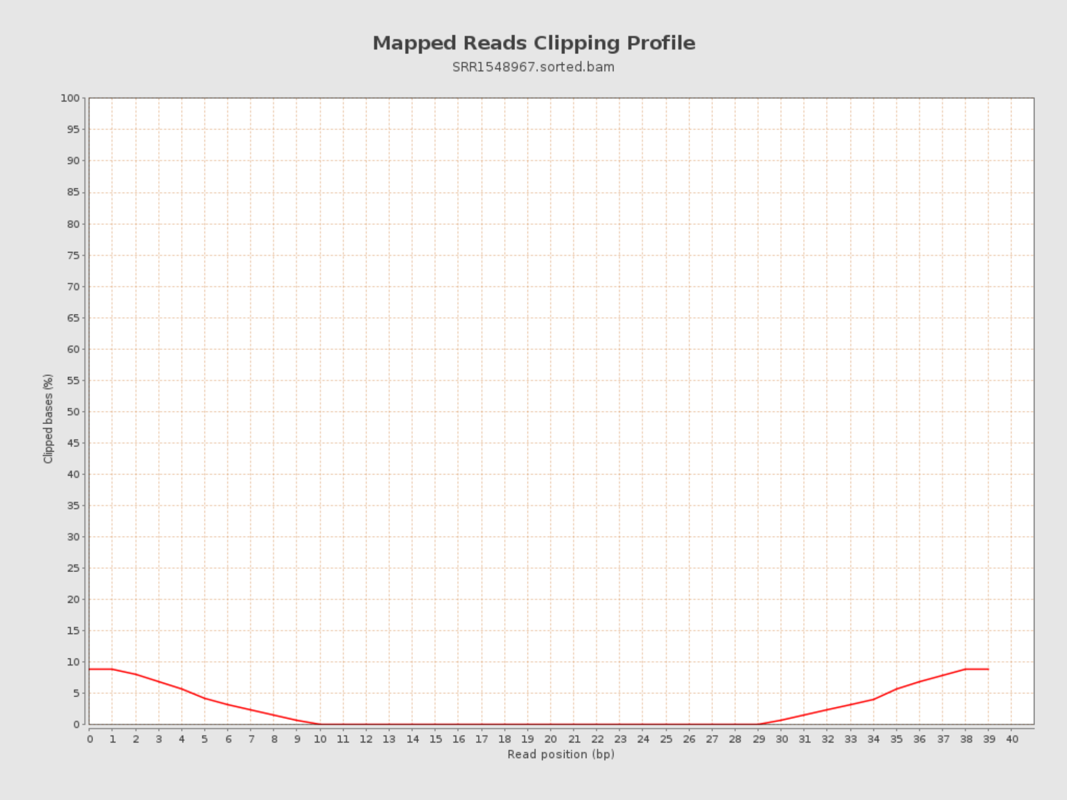
8. Results : Mapped Reads Nucleotide Content



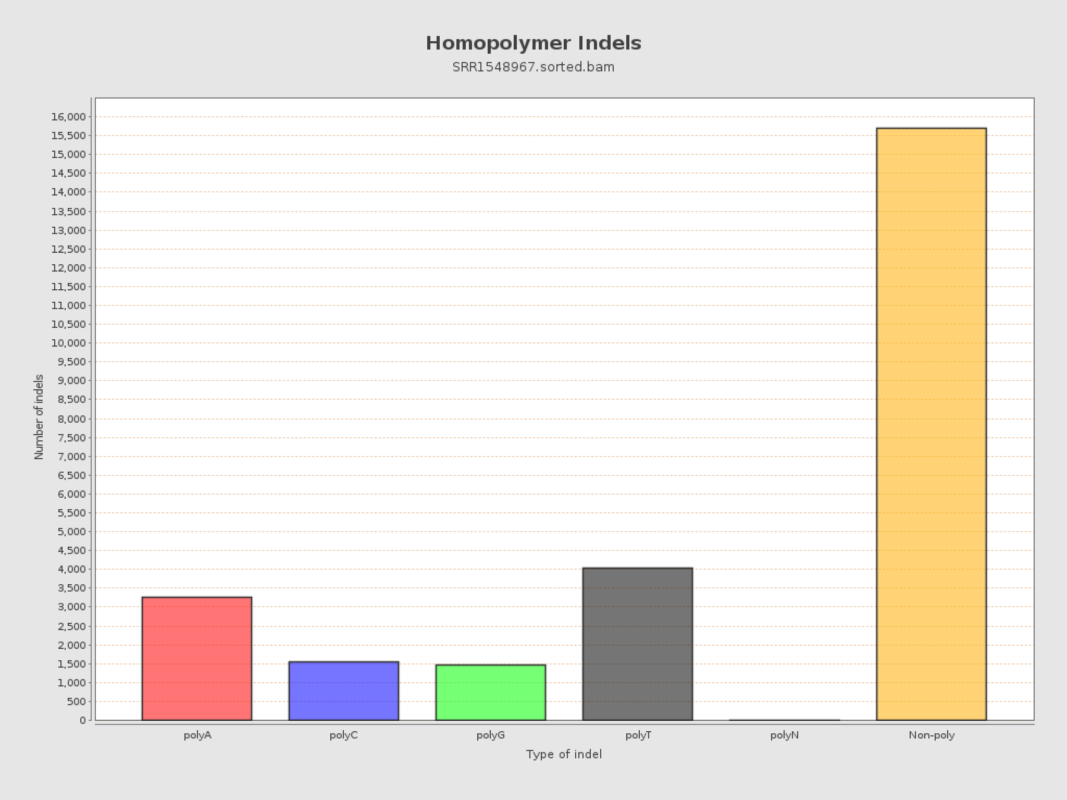
9. Results : Mapped Reads GC-content Distribution



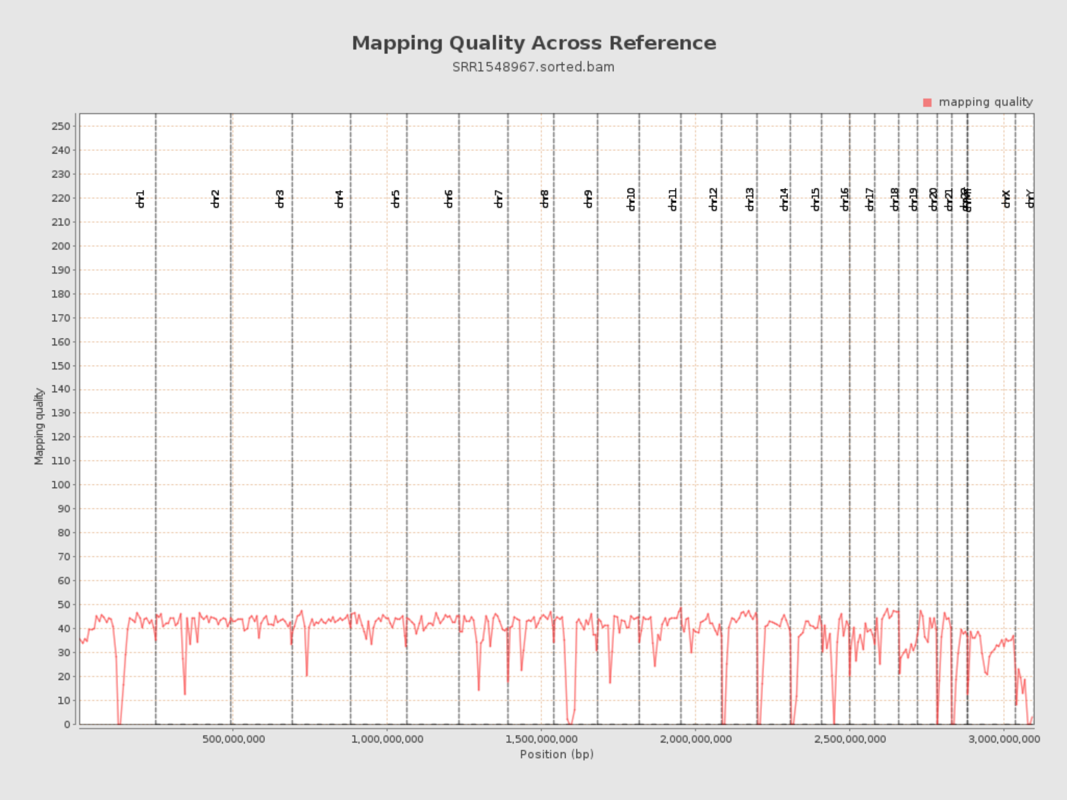
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram