Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 13:55:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068159.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_SRR6068159 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068159.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 13:55:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068159.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,530,643
Mapped reads	4,333,770 / 95.65%
Unmapped reads	196,873 / 4.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,916 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	461,613 / 10.19%
Duplication rate	8.86%
Clipped reads	2,092,029 / 46.18%

2.2. ACGT Content

Number/percentage of A's	77,140,915 / 27.18%
Number/percentage of C's	51,049,596 / 17.99%
Number/percentage of T's	92,232,960 / 32.5%
Number/percentage of G's	63,365,269 / 22.33%
Number/percentage of N's	33,120 / 0.01%
GC Percentage	40.31%

2.3. Coverage

Mean	0.0917

Standard Deviation	0.8735

2.4. Mapping Quality

Mean Mapping Quality	46.17

2.5. Mismatches and indels

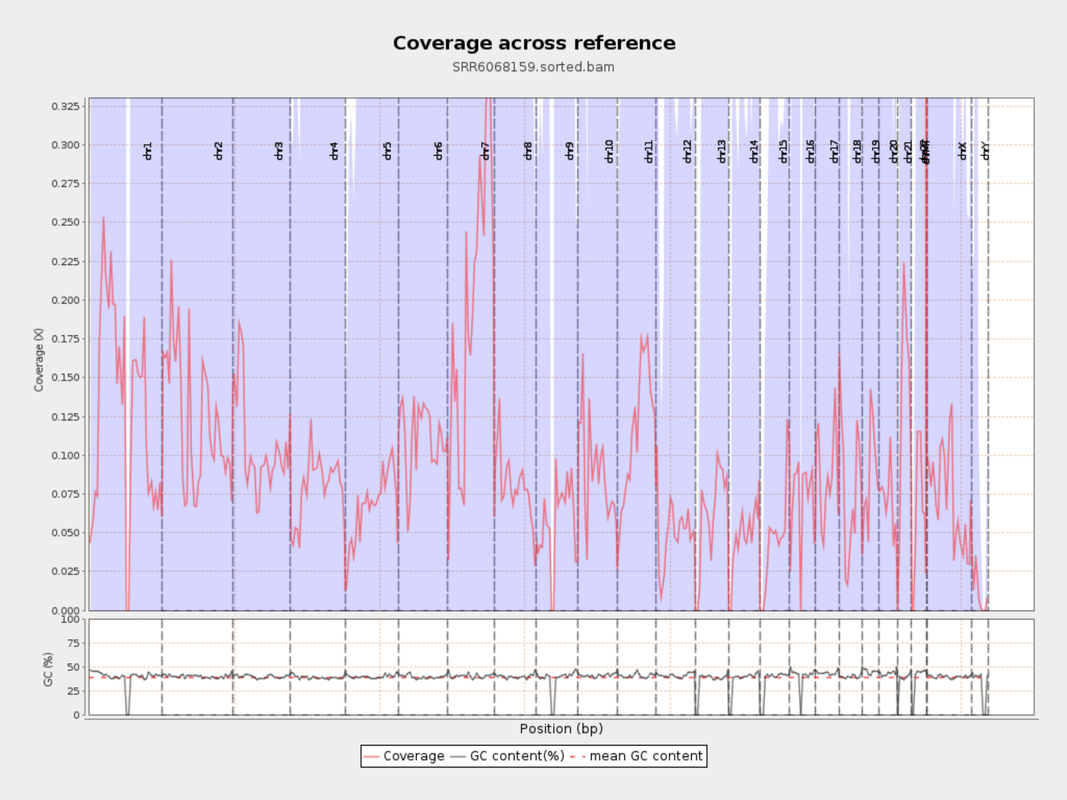
General error rate	0.57%
Mismatches	1,579,941
Insertions	18,135
Mapped reads with at least one insertion	0.42%
Deletions	68,156
Mapped reads with at least one deletion	1.56%
Homopolymer indels	44.92%

2.6. Chromosome stats

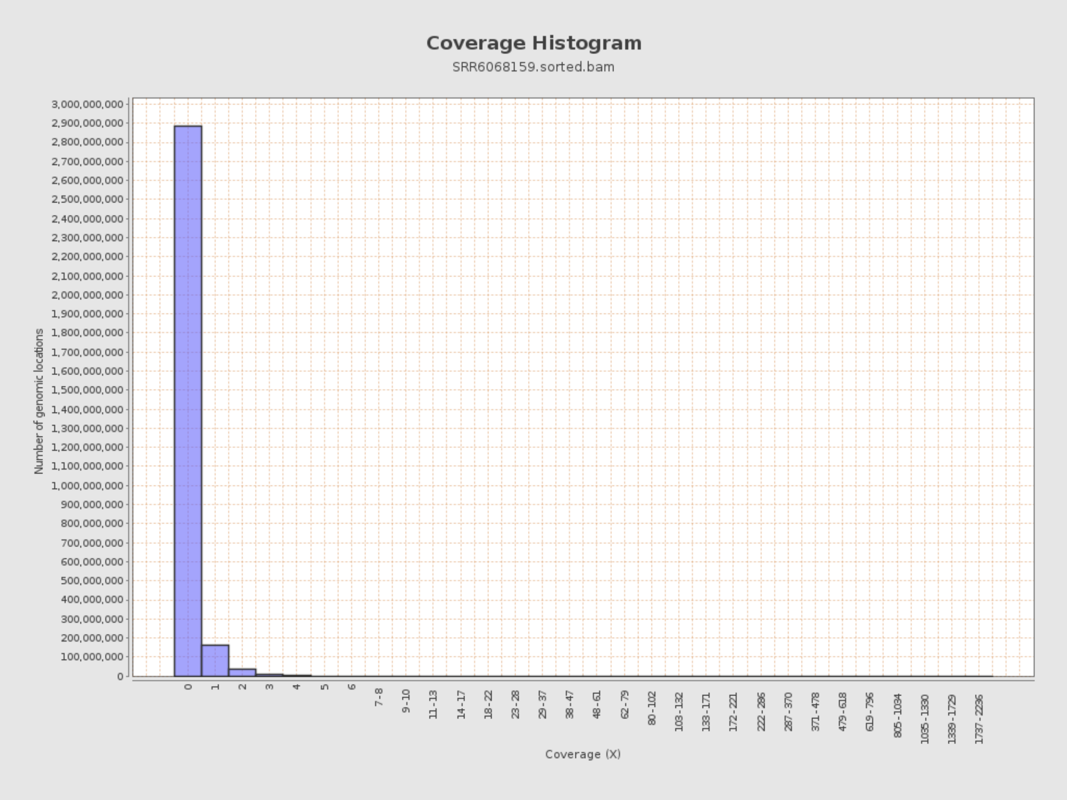
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	32509691	0.1304	1.9305
chr2	243199373	30121854	0.1239	0.9403
chr3	198022430	21026100	0.1062	0.4209
chr4	191154276	15195274	0.0795	0.3803
chr5	180915260	12240853	0.0677	0.3391
chr6	171115067	19172647	0.112	0.5357
chr7	159138663	31585710	0.1985	1.6037

chr8	146364022	11785462	0.0805	0.947
chr9	141213431	8095533	0.0573	0.6709
chr10	135534747	12261032	0.0905	0.6784
chr11	135006516	15611429	0.1156	0.6289
chr12	133851895	6865482	0.0513	0.3383
chr13	115169878	7034944	0.0611	0.3248
chr14	107349540	4898634	0.0456	0.3652
chr15	102531392	4622251	0.0451	0.3015
chr16	90354753	6350338	0.0703	0.4098
chr17	81195210	7036878	0.0867	0.4123
chr18	78077248	6119160	0.0784	1.3187
chr19	59128983	5220477	0.0883	1.1738
chr20	63025520	4443989	0.0705	0.3772
chr21	48129895	6428973	0.1336	0.495
chr22	51304566	3111011	0.0606	0.3089
chrMT	16571	242493	14.6336	8.6459
chrX	155270560	11319235	0.0729	0.4246
chrY	59373566	641901	0.0108	0.3072

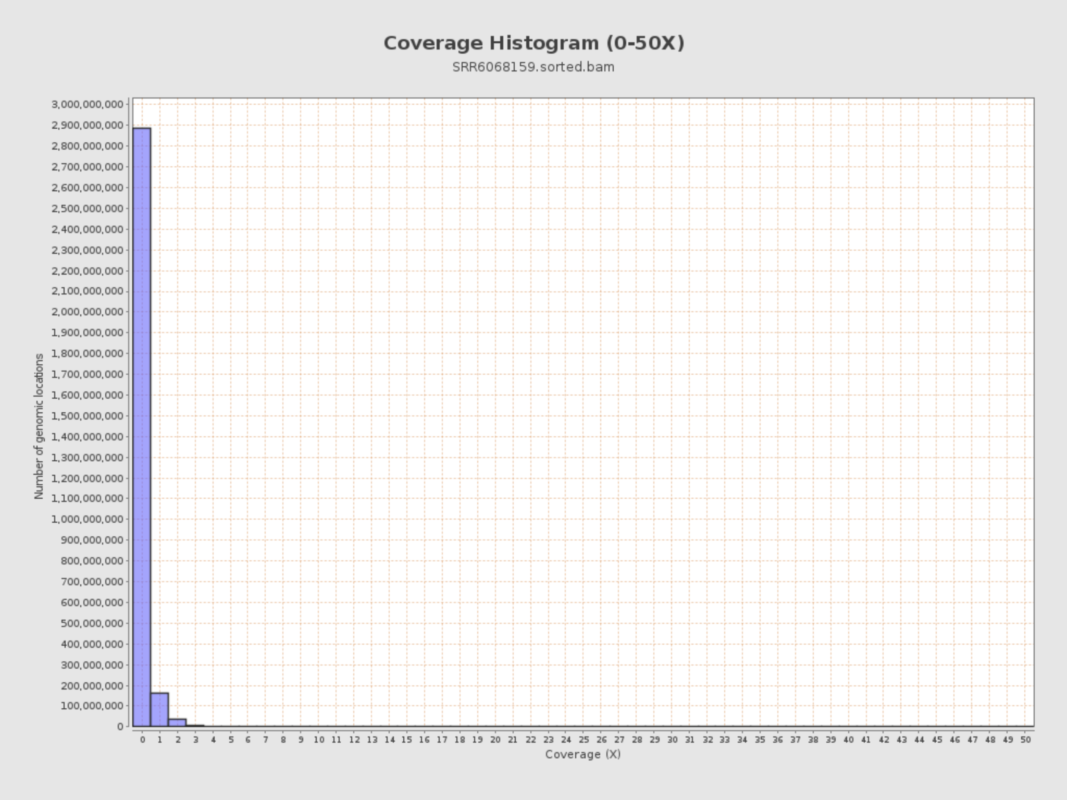
3. Results : Coverage across reference



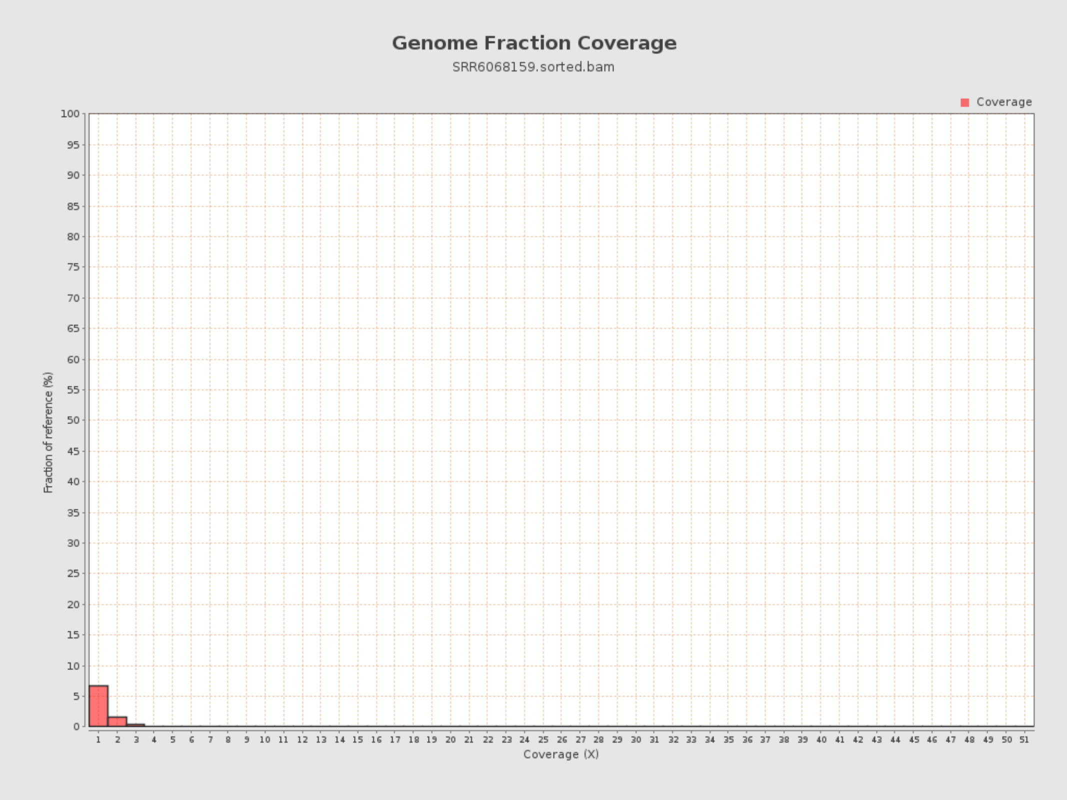
4. Results : Coverage Histogram



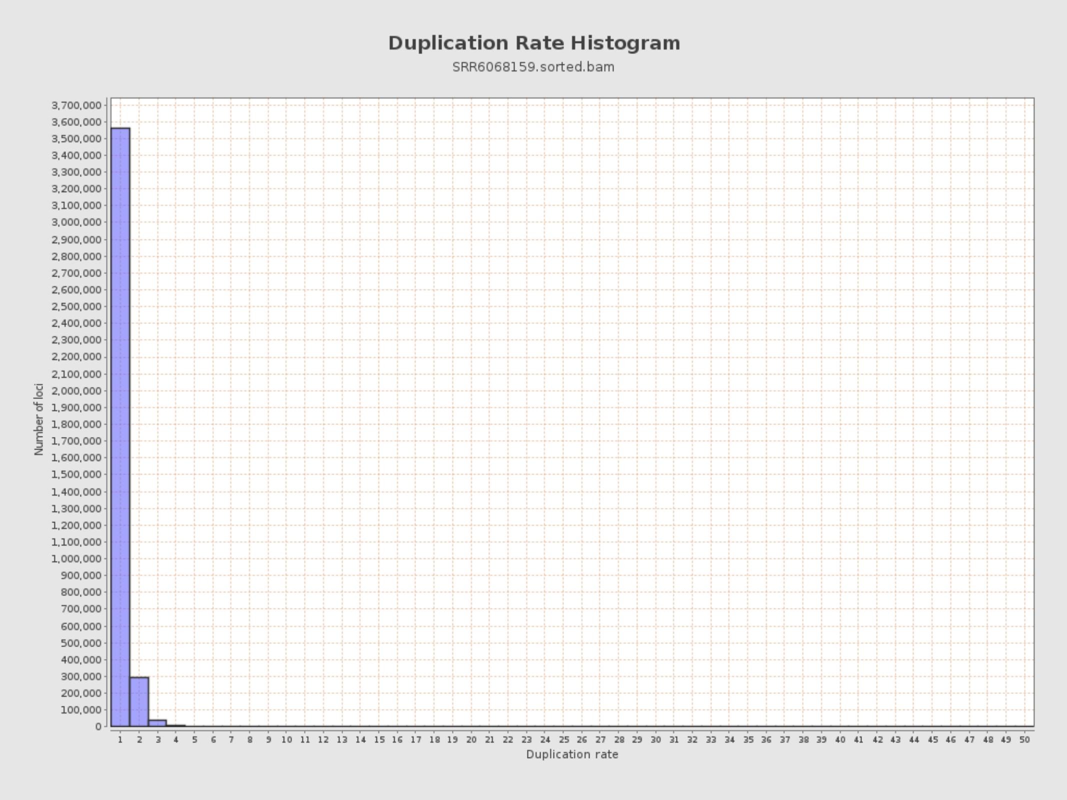
5. Results : Coverage Histogram (0-50X)



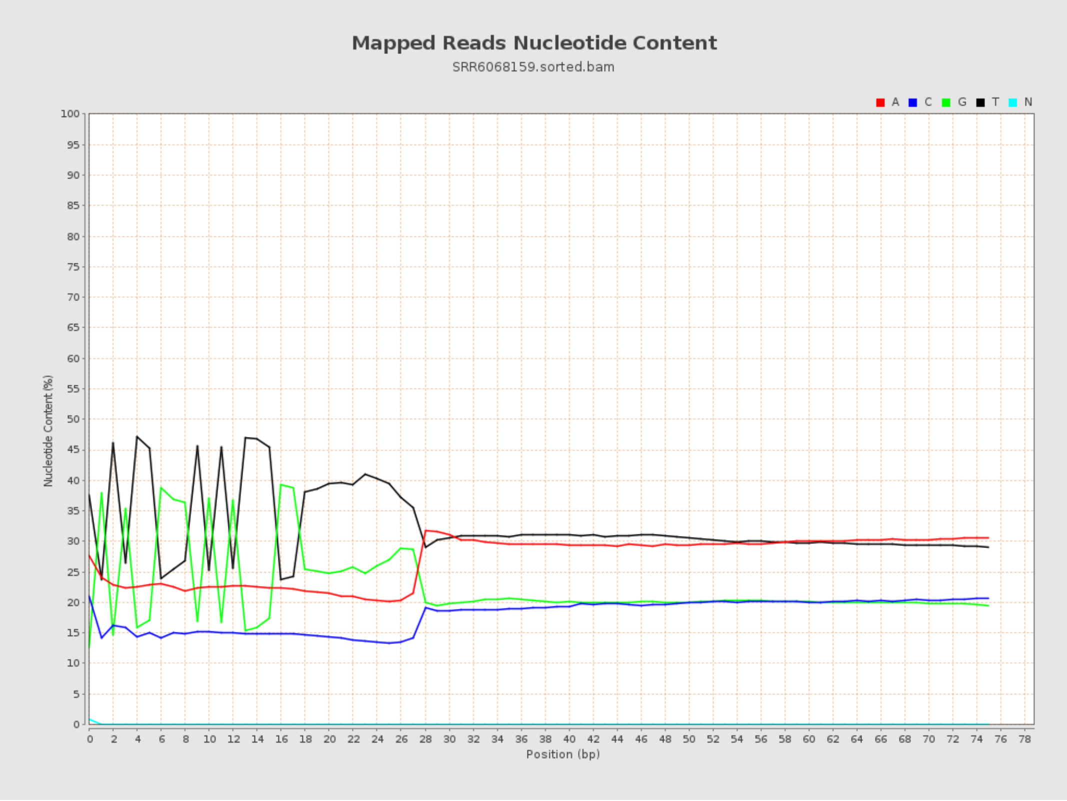
6. Results : Genome Fraction Coverage



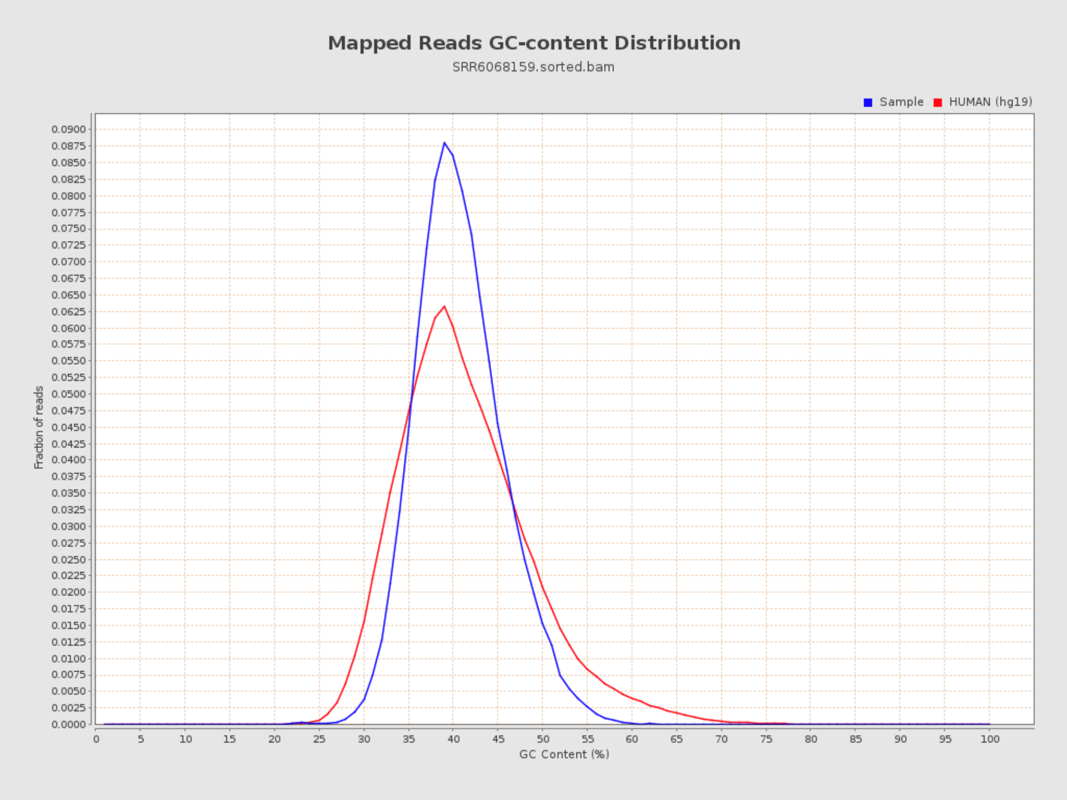
7. Results : Duplication Rate Histogram



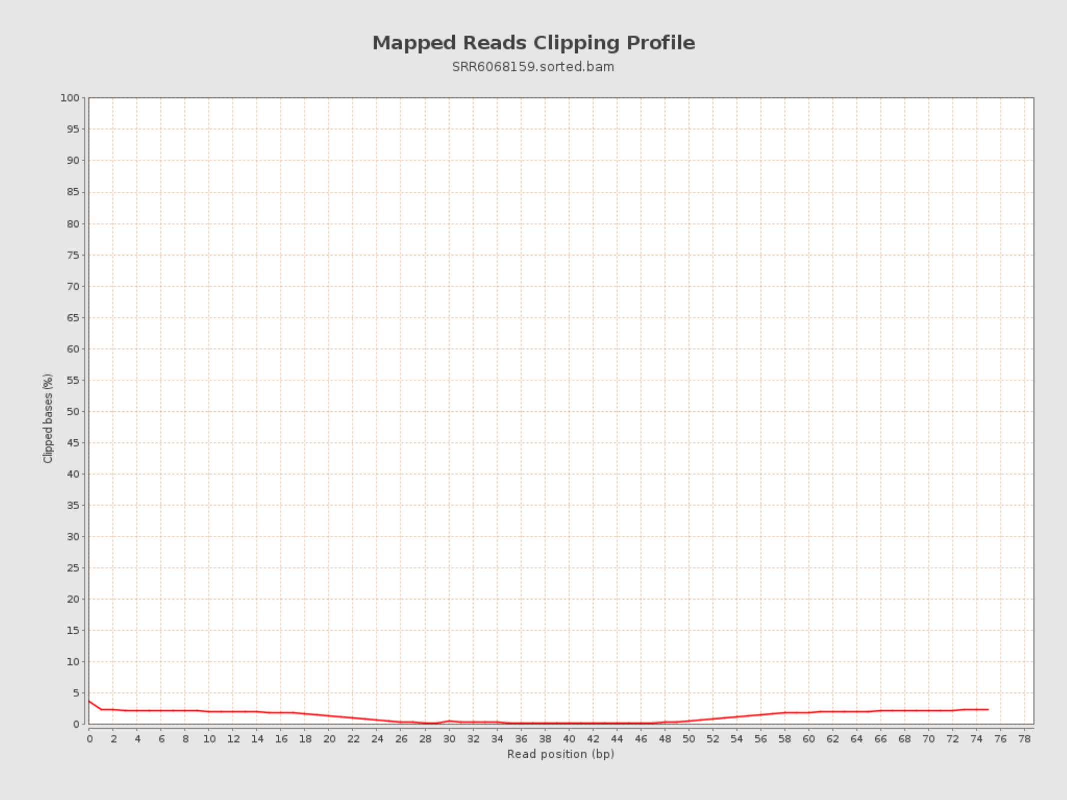
8. Results : Mapped Reads Nucleotide Content



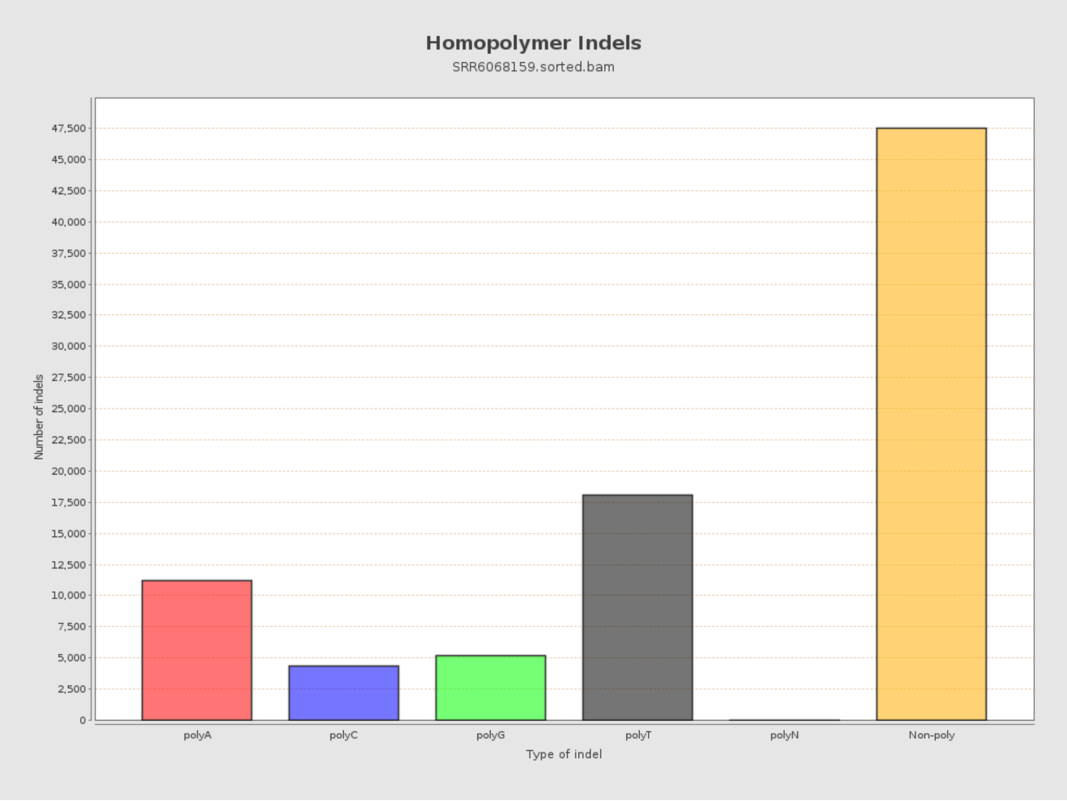
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



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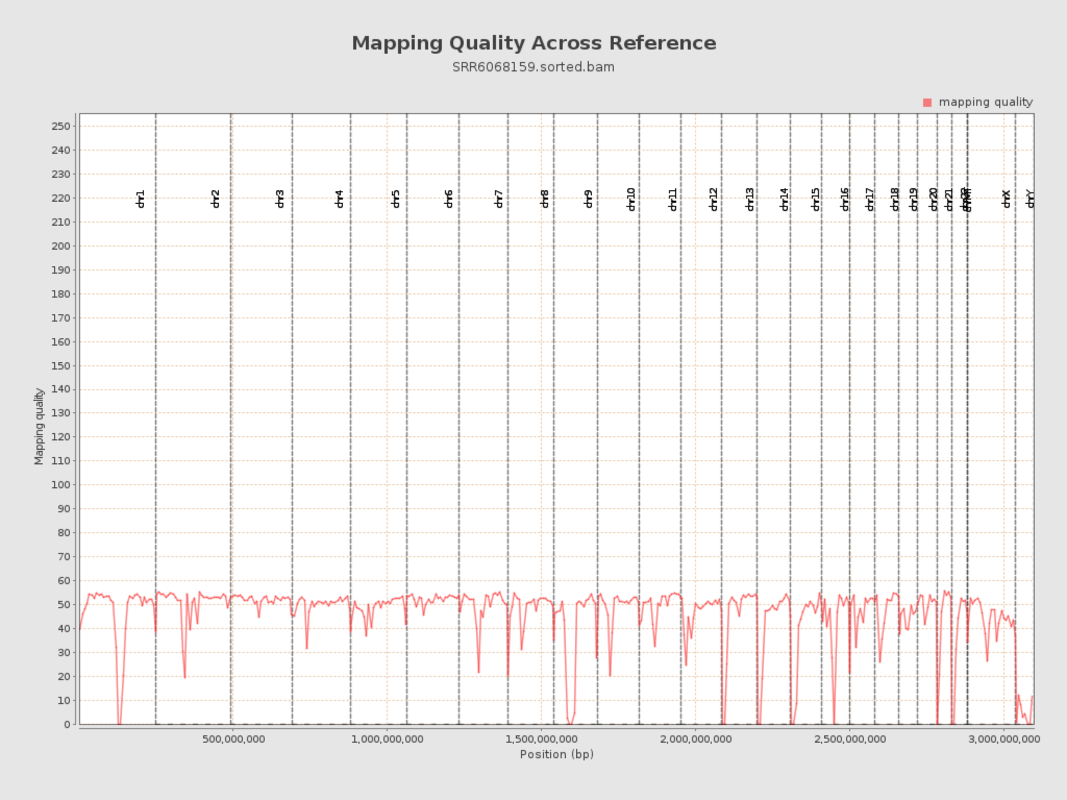
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram