Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 02:56:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063569.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_SRR6063569 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063569.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 02:56:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063569.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,951,902
Mapped reads	1,398,502 / 71.65%
Unmapped reads	553,400 / 28.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,509 / 0.79%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	92,966 / 4.76%
Duplication rate	5.24%
Clipped reads	769,704 / 39.43%

2.2. ACGT Content

Number/percentage of A's	26,057,255 / 28.77%
Number/percentage of C's	16,855,593 / 18.61%
Number/percentage of T's	29,645,257 / 32.73%
Number/percentage of G's	18,018,568 / 19.89%
Number/percentage of N's	1,655 / 0%
GC Percentage	38.5%

2.3. Coverage

Mean	0.0293

Standard Deviation	0.3442

2.4. Mapping Quality

Mean Mapping Quality	44.97

2.5. Mismatches and indels

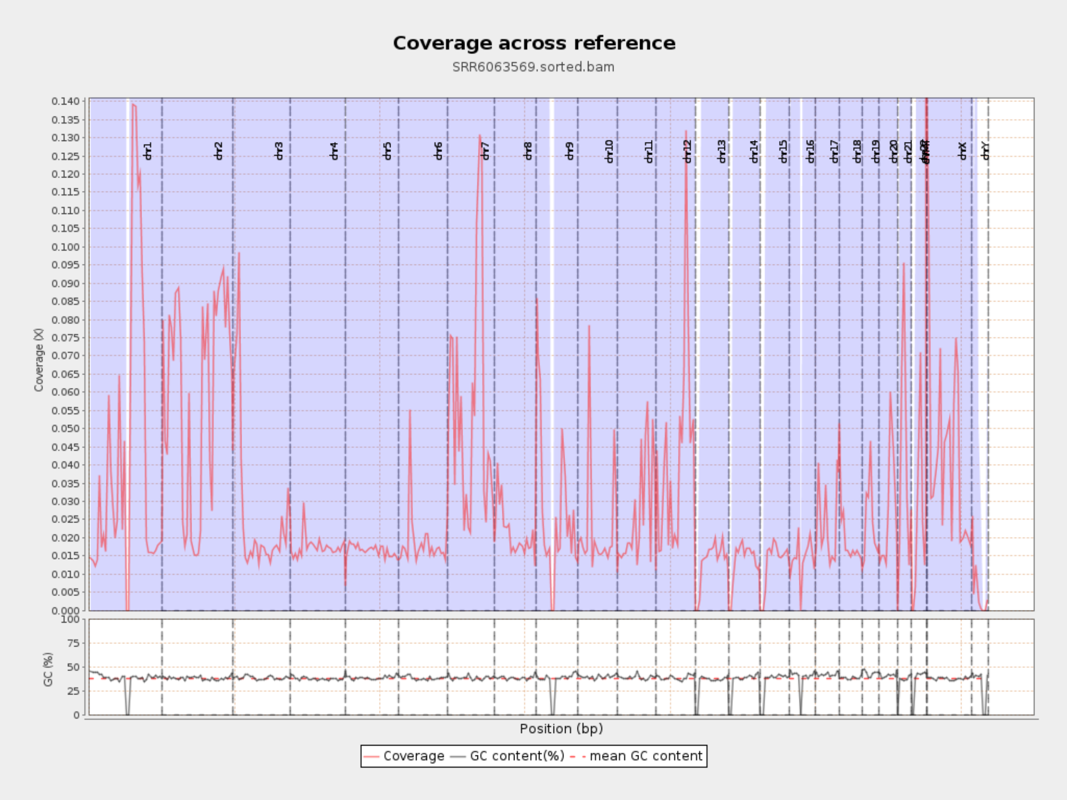
General error rate	0.87%
Mismatches	771,617
Insertions	8,071
Mapped reads with at least one insertion	0.57%
Deletions	24,511
Mapped reads with at least one deletion	1.73%
Homopolymer indels	47.31%

2.6. Chromosome stats

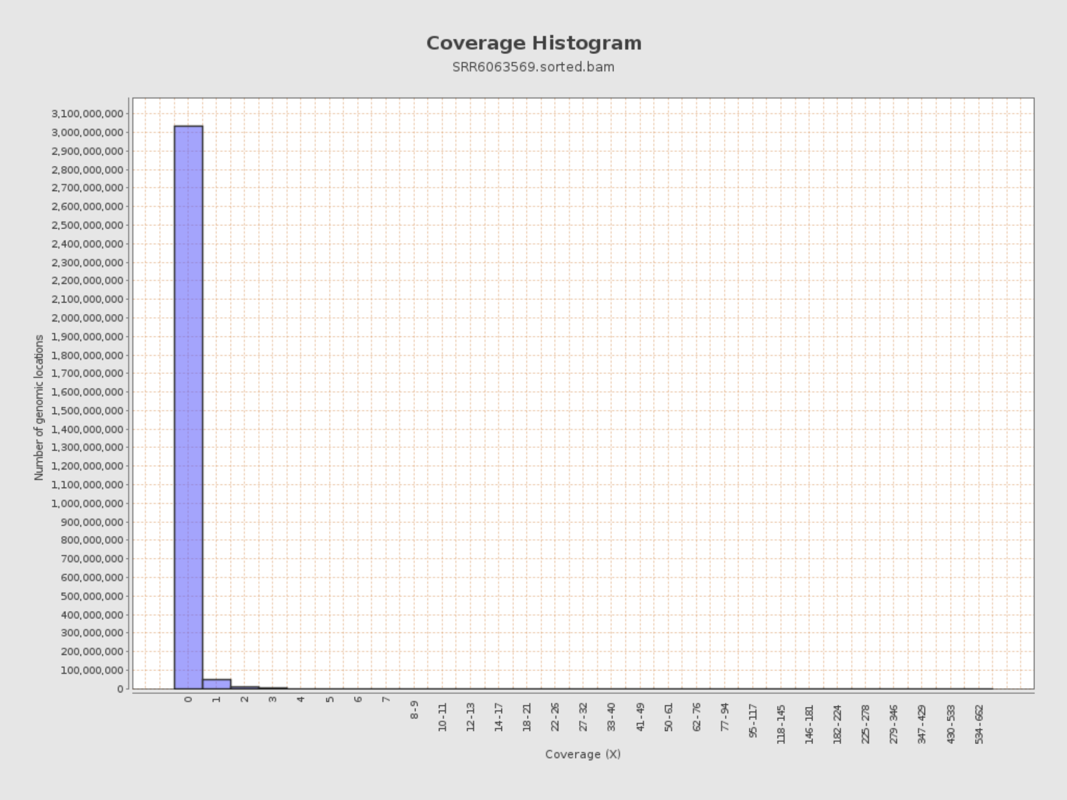
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10263822	0.0412	0.64
chr2	243199373	14519160	0.0597	0.4606
chr3	198022430	5273994	0.0266	0.2509
chr4	191154276	3332999	0.0174	0.1935
chr5	180915260	2998736	0.0166	0.225
chr6	171115067	3231287	0.0189	0.2184
chr7	159138663	8832810	0.0555	0.3695

chr8	146364022	3120228	0.0213	0.2951
chr9	141213431	3669346	0.026	0.256
chr10	135534747	3064102	0.0226	0.6284
chr11	135006516	3591608	0.0266	0.2489
chr12	133851895	5892354	0.044	0.2852
chr13	115169878	1550131	0.0135	0.161
chr14	107349540	1426275	0.0133	0.1718
chr15	102531392	1351625	0.0132	0.1686
chr16	90354753	1297038	0.0144	0.1817
chr17	81195210	1953394	0.0241	0.2177
chr18	78077248	1525576	0.0195	0.4016
chr19	59128983	1484968	0.0251	0.3336
chr20	63025520	1736184	0.0275	0.2274
chr21	48129895	1880862	0.0391	0.2728
chr22	51304566	1161611	0.0226	0.1979
chrMT	16571	48966	2.9549	3.0623
chrX	155270560	7102591	0.0457	0.3003
chrY	59373566	309212	0.0052	0.1039

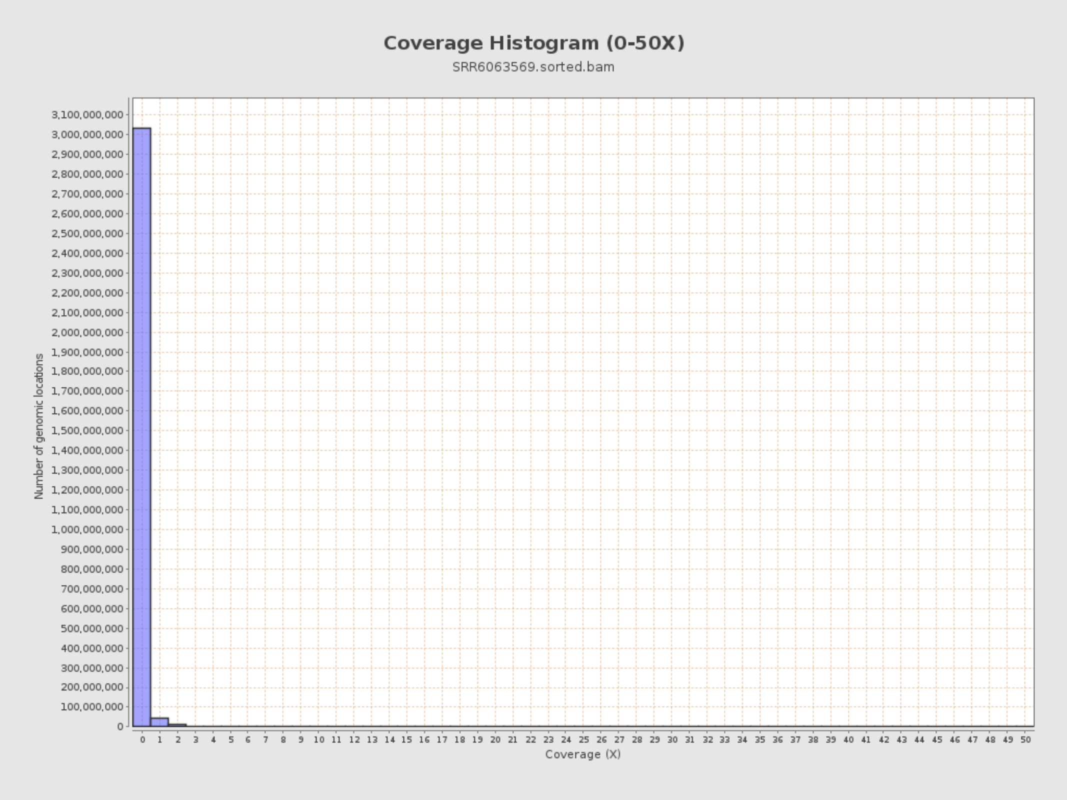
3. Results : Coverage across reference



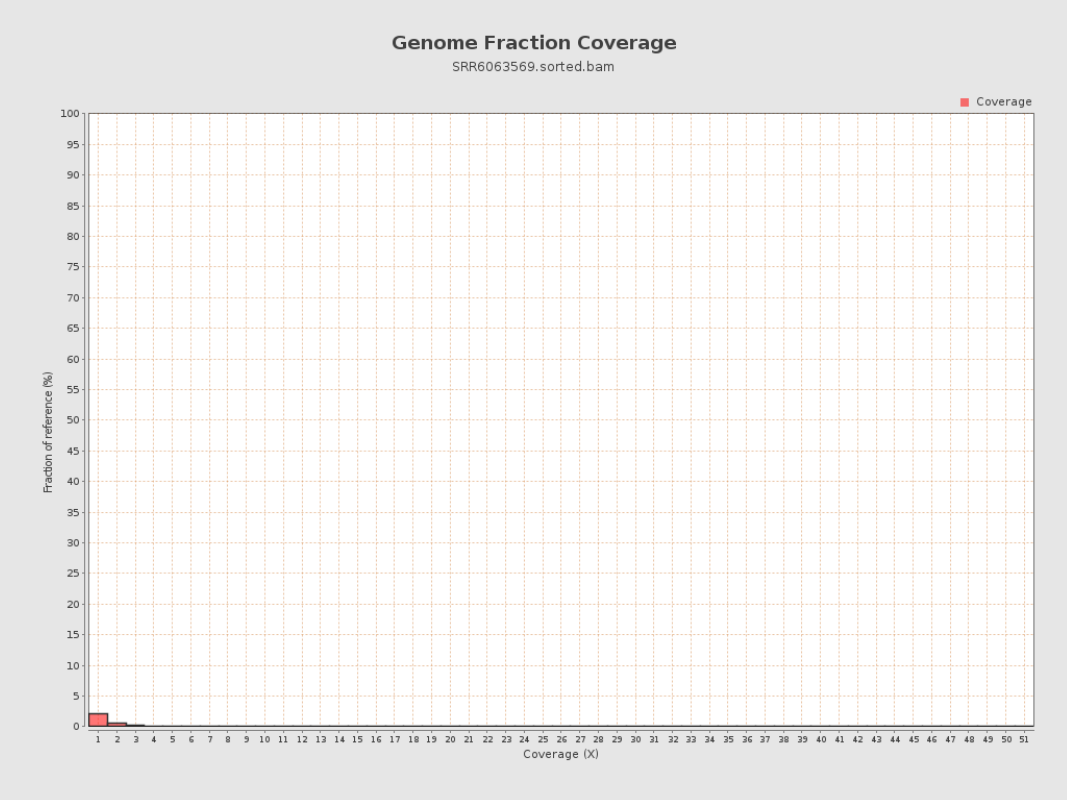
4. Results : Coverage Histogram



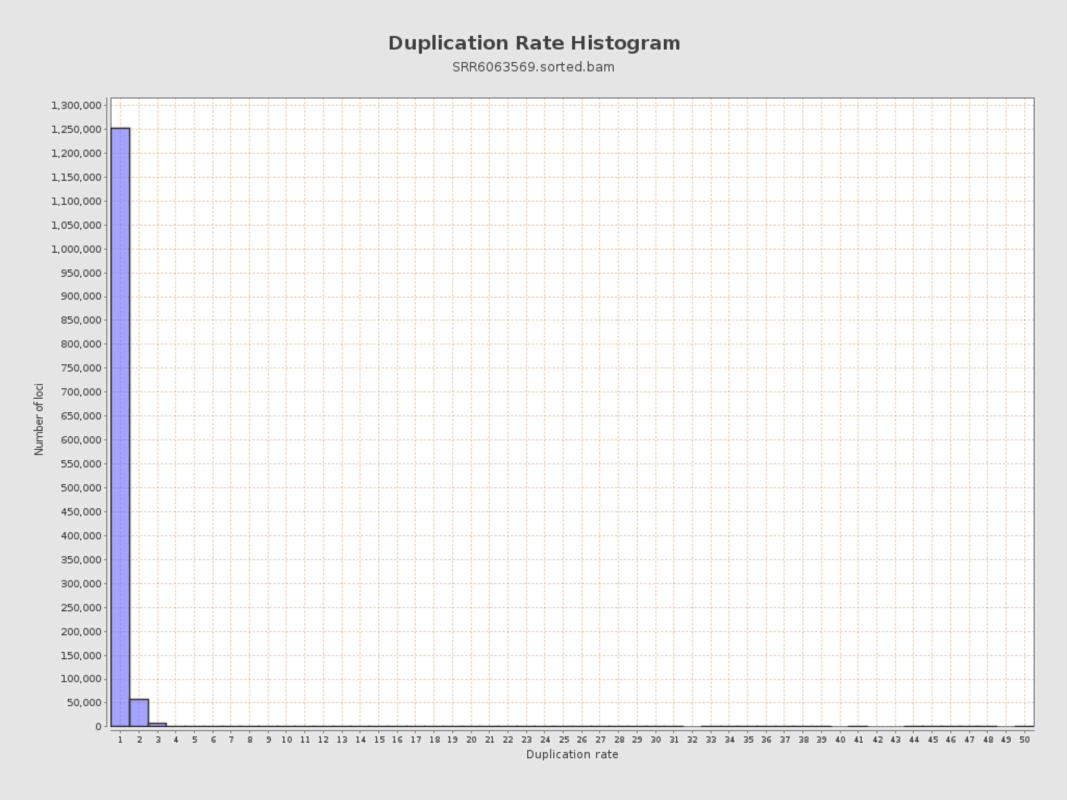
5. Results : Coverage Histogram (0-50X)



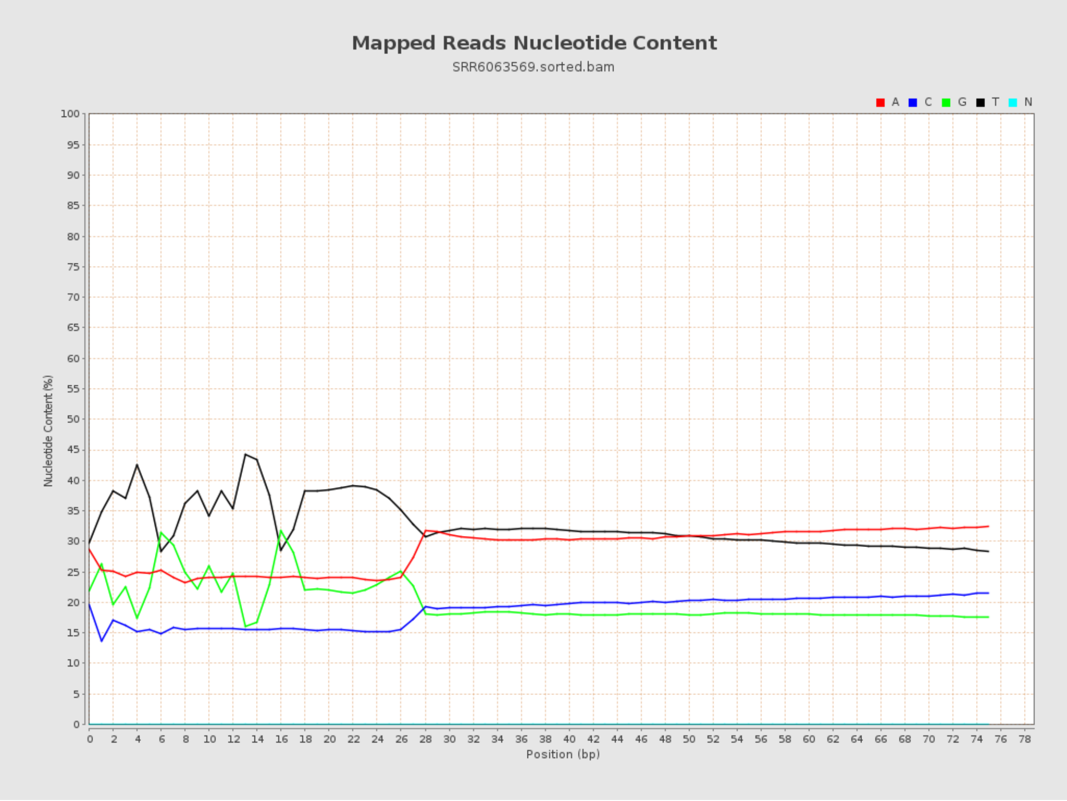
6. Results : Genome Fraction Coverage



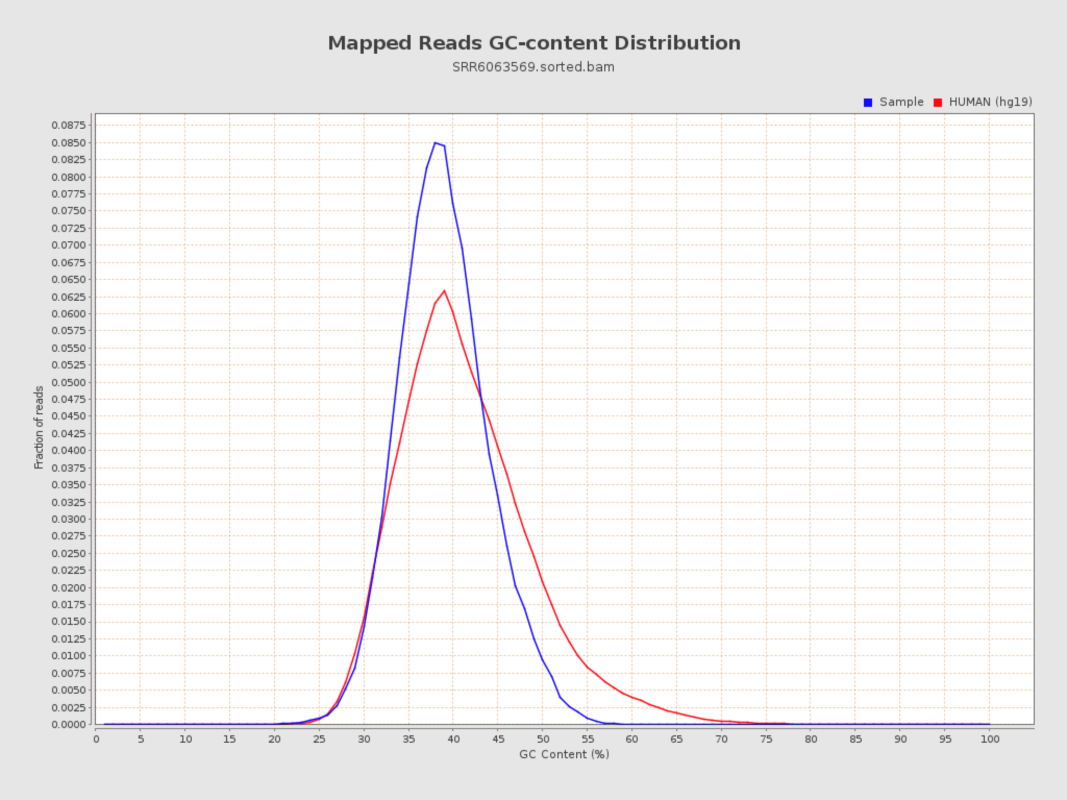
7. Results : Duplication Rate Histogram



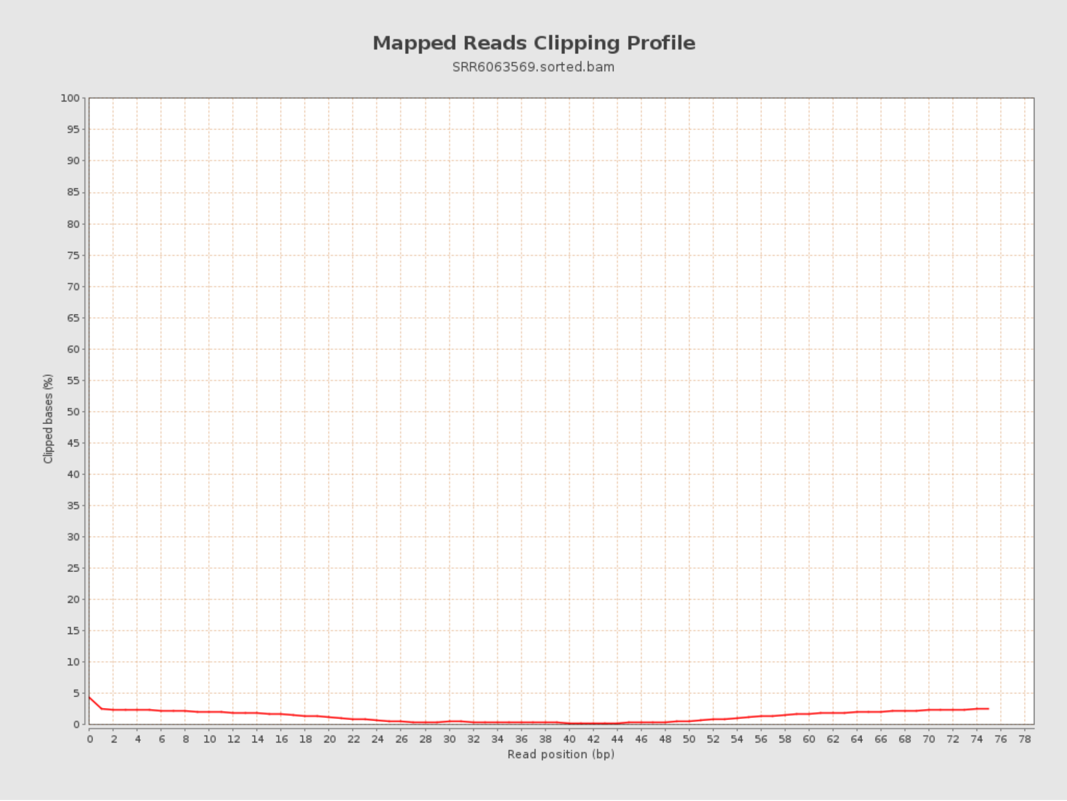
8. Results : Mapped Reads Nucleotide Content



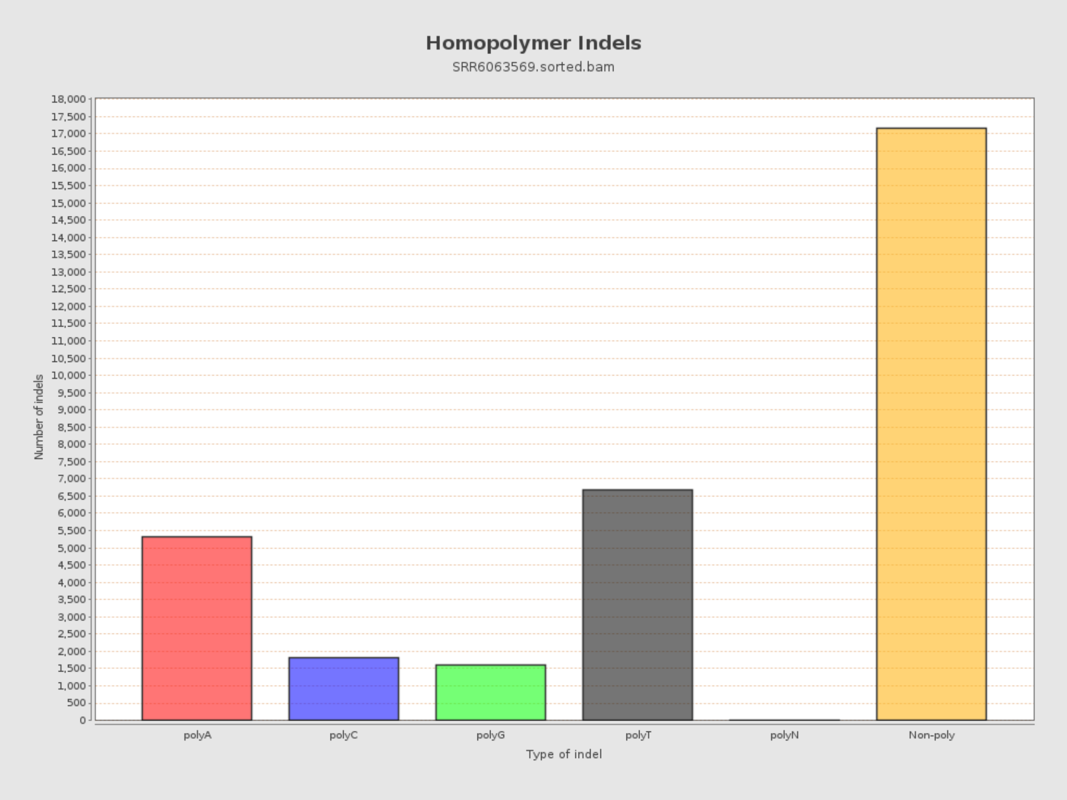
9. Results : Mapped Reads GC-content Distribution



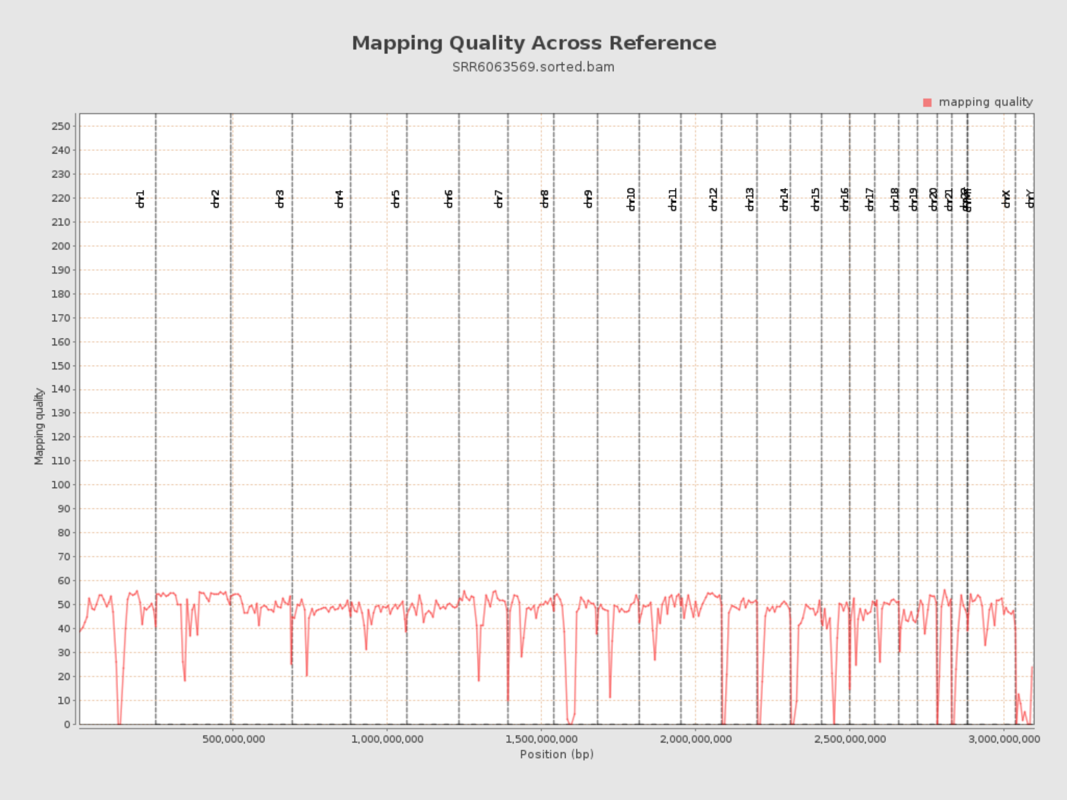
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram