Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/25 02:33:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617725.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_SRR8617725 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617725_1.fastq.gz SRR8617725_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 25 02:33:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617725.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,383,146
Mapped reads	31,102,766 / 96.05%
Unmapped reads	1,280,380 / 3.95%
Mapped paired reads	31,102,766 / 96.05%
Mapped reads, first in pair	15,856,305 / 48.96%
Mapped reads, second in pair	15,246,461 / 47.08%
Mapped reads, both in pair	30,268,994 / 93.47%
Mapped reads, singletons	833,772 / 2.57%
Secondary alignments	0
Supplementary alignments	2,153,976 / 6.65%
Read min/max/mean length	30 / 150 / 153.38
Duplicated reads (estimated)	7,855,626 / 24.26%
Duplication rate	14.84%
Clipped reads	19,304,285 / 59.61%

2.2. ACGT Content

Number/percentage of A's	1,181,096,556 / 28.67%
Number/percentage of C's	809,438,610 / 19.65%
Number/percentage of T's	1,201,446,106 / 29.16%
Number/percentage of G's	928,028,924 / 22.52%
Number/percentage of N's	15,881 / 0%

GC Percentage	42.17%

2.3. Coverage

Mean	1.3321
Standard Deviation	24.2585

2.4. Mapping Quality

Mean Mapping Quality	51.64

2.5. Insert size

Mean	566,043.51
Standard Deviation	7,237,776.39
P25/Median/P75	204 / 271 / 351

2.6. Mismatches and indels

General error rate	1.54%
Mismatches	60,554,258
Insertions	900,568
Mapped reads with at least one insertion	2.64%
Deletions	1,623,708
Mapped reads with at least one deletion	4.94%
Homopolymer indels	41.38%

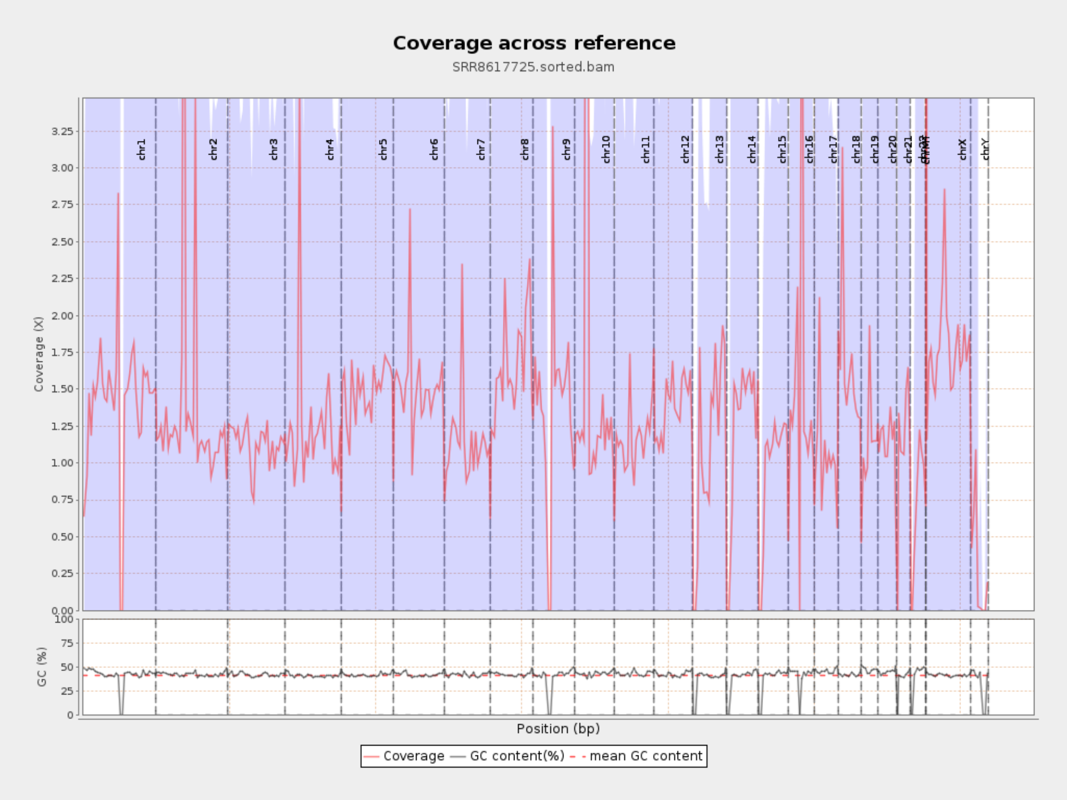
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

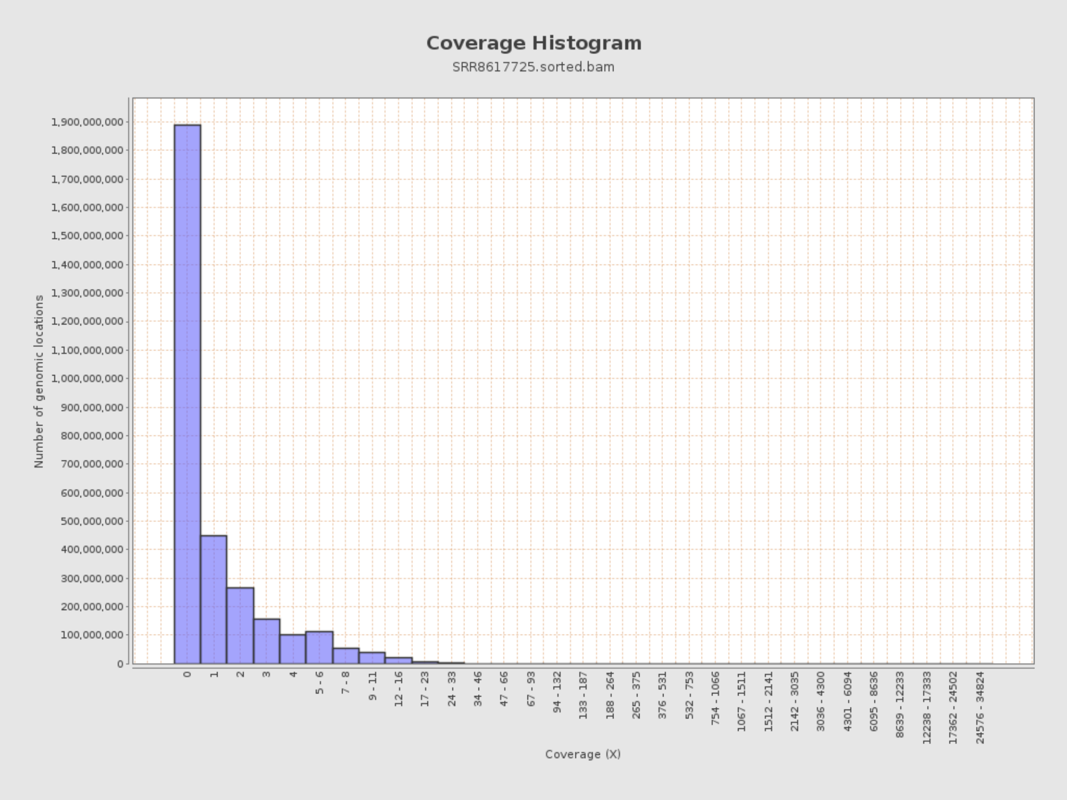
		bases	coverage	deviation
chr1	249250621	352389755	1.4138	21.4321
chr2	243199373	340196000	1.3988	34.8822
chr3	198022430	223354742	1.1279	3.8021
chr4	191154276	240816855	1.2598	15.8214
chr5	180915260	268995080	1.4869	3.9836
chr6	171115067	260691949	1.5235	14.213
chr7	159138663	182371813	1.146	18.6233
chr8	146364022	243825872	1.6659	7.8432
chr9	141213431	196792391	1.3936	36.249
chr10	135534747	222500045	1.6416	75.7107
chr11	135006516	157423061	1.166	13.5791
chr12	133851895	185412554	1.3852	7.1885
chr13	115169878	131162175	1.1389	2.6738
chr14	107349540	132977459	1.2387	4.1456
chr15	102531392	96679835	0.9429	4.2428
chr16	90354753	140608047	1.5562	32.363
chr17	81195210	88034500	1.0842	16.8745
chr18	78077248	130060320	1.6658	34.7915
chr19	59128983	68019580	1.1504	11.3866
chr20	63025520	73008866	1.1584	5.3658
chr21	48129895	56264189	1.169	8.0879
chr22	51304566	37057780	0.7223	4.0724
chrMT	16571	965801	58.2826	29.0474
chrX	155270560	276464228	1.7805	7.4827

chrY	59373566	17574950	0.296	20.7161

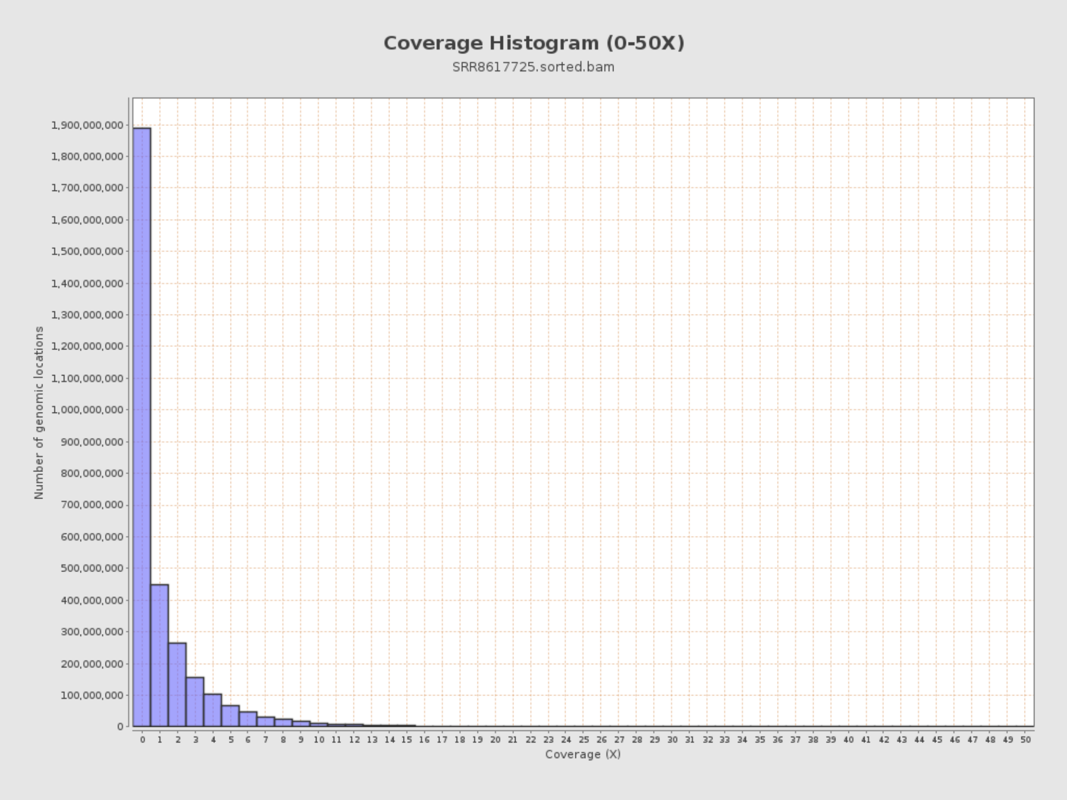
3. Results : Coverage across reference



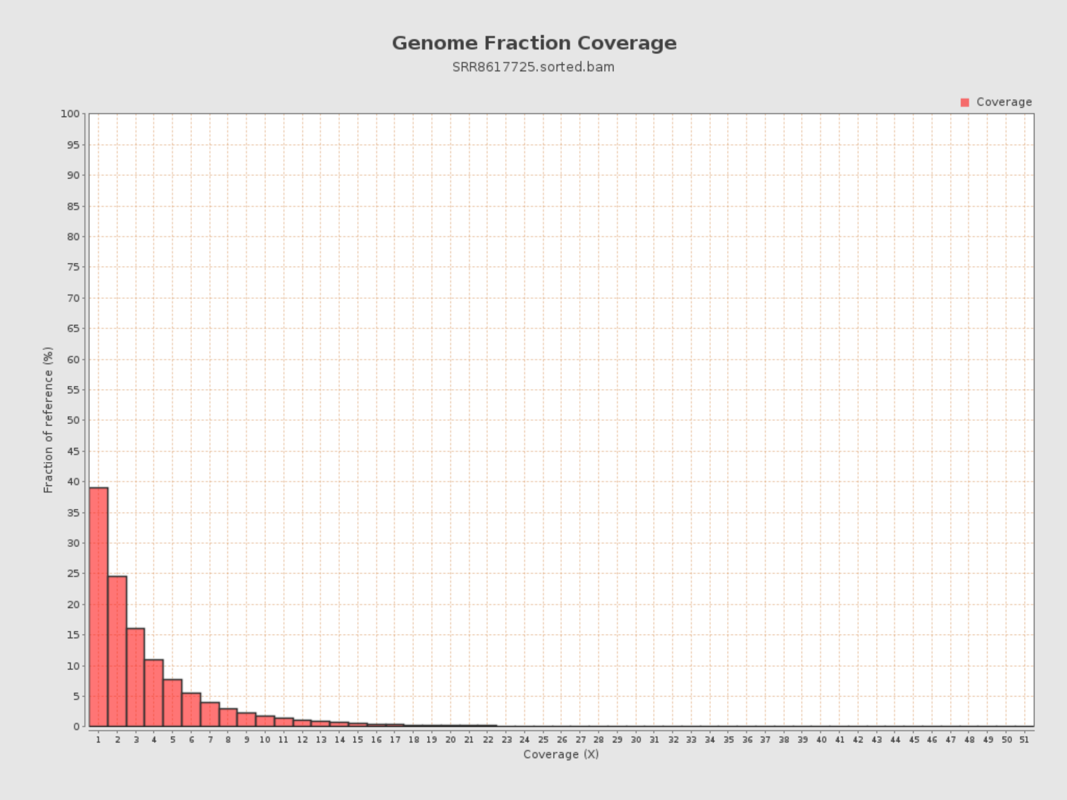
4. Results : Coverage Histogram



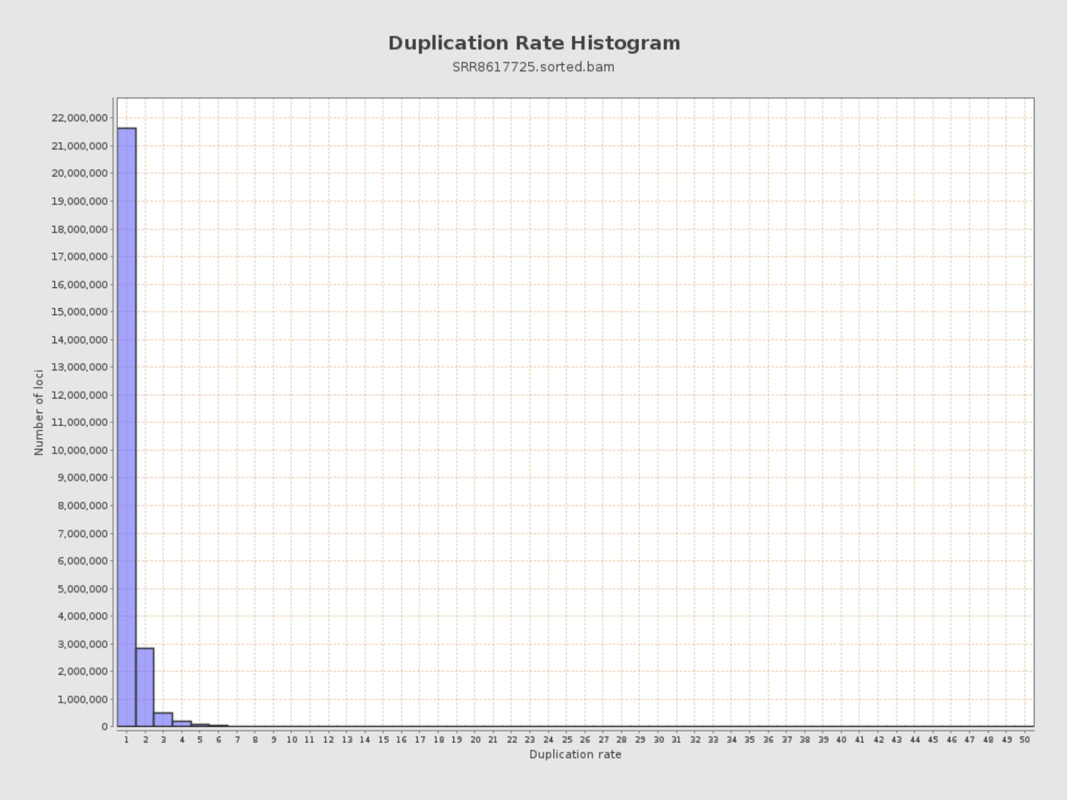
5. Results : Coverage Histogram (0-50X)



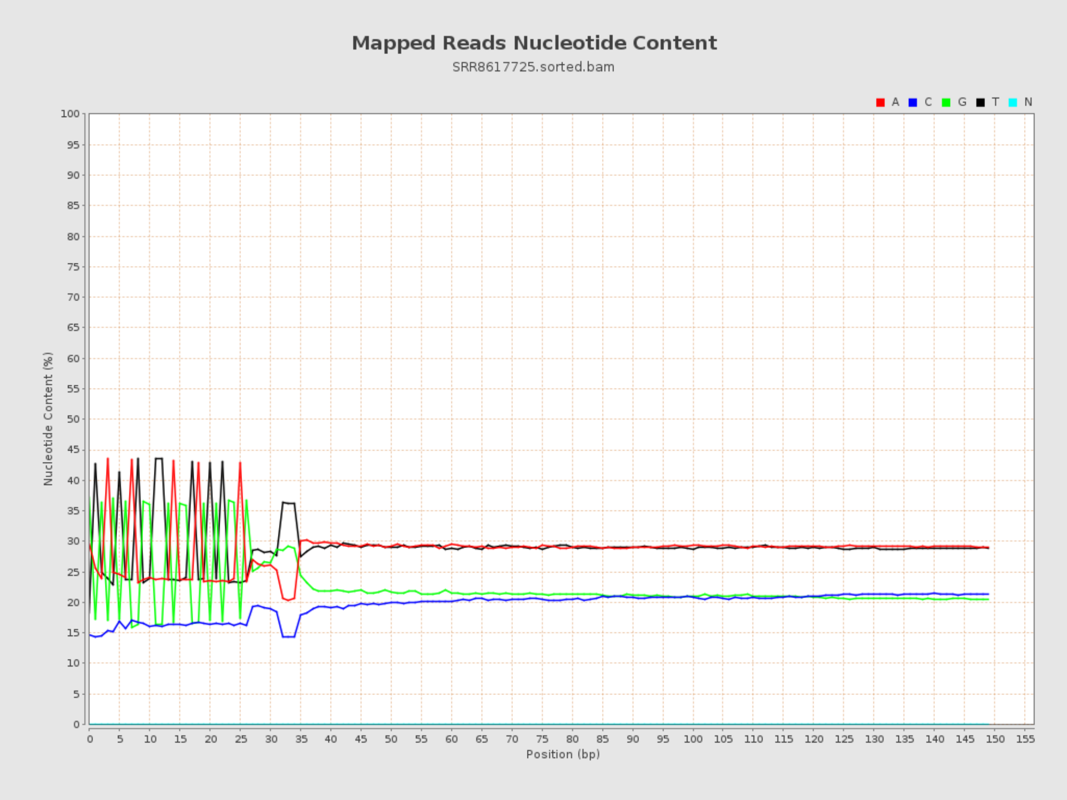
6. Results : Genome Fraction Coverage



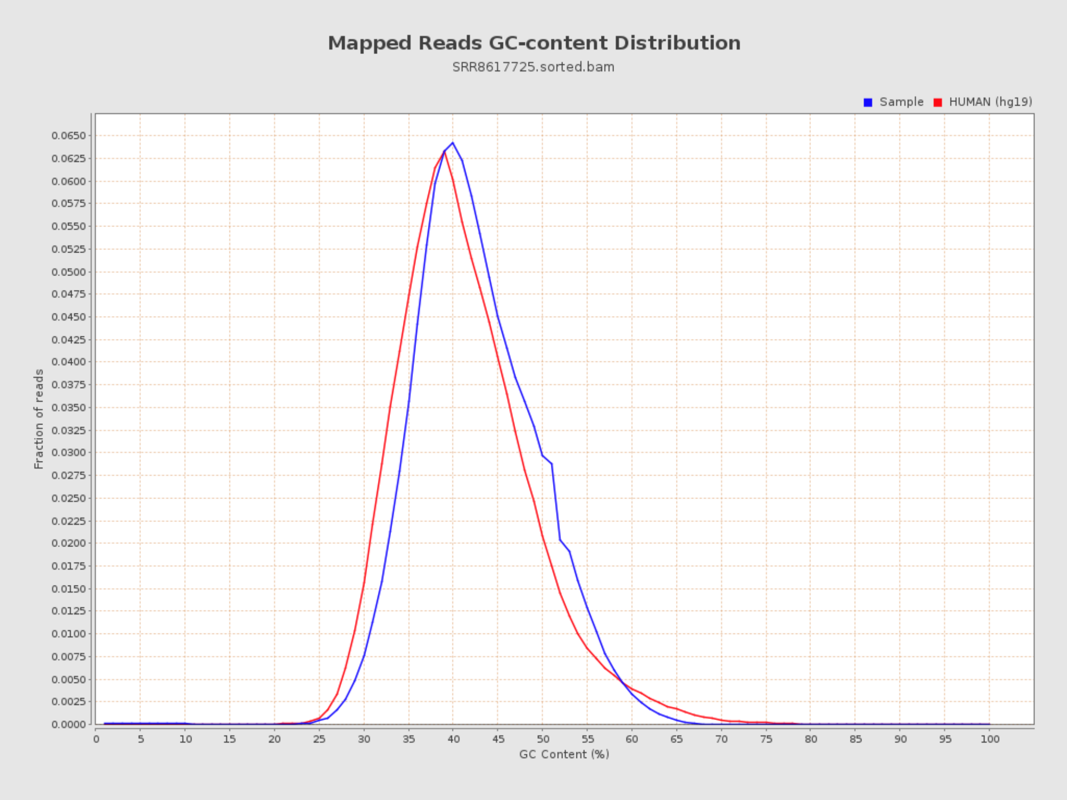
7. Results : Duplication Rate Histogram



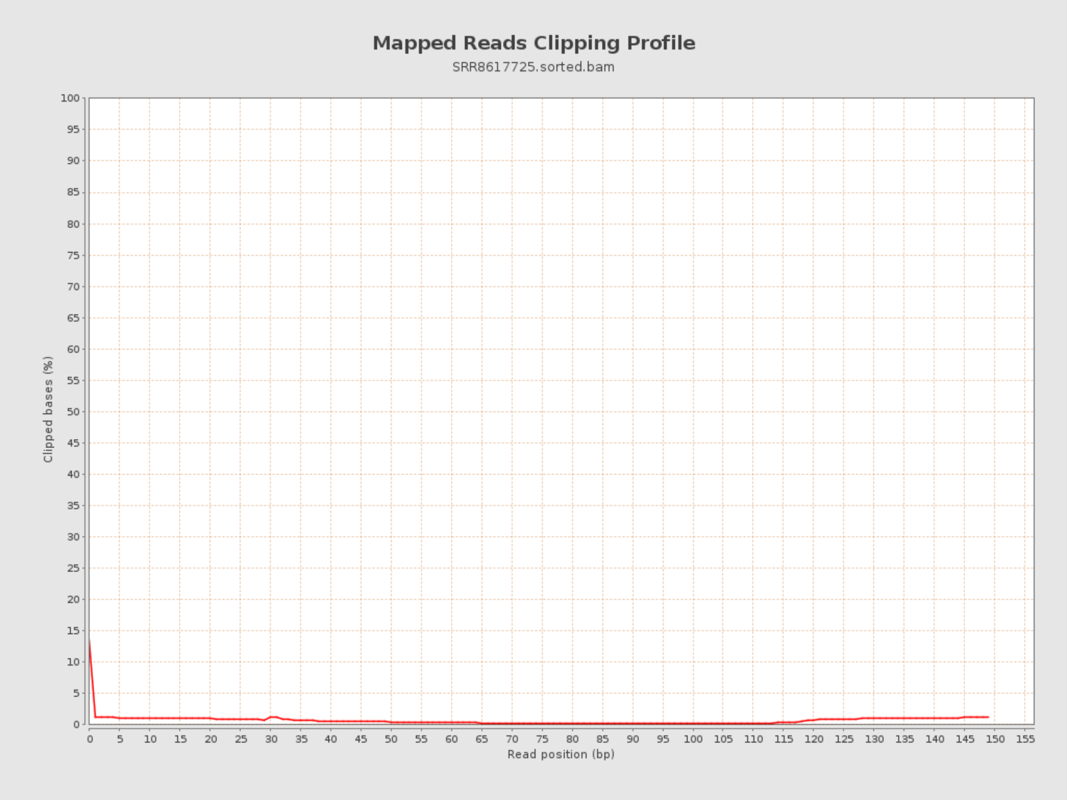
8. Results : Mapped Reads Nucleotide Content



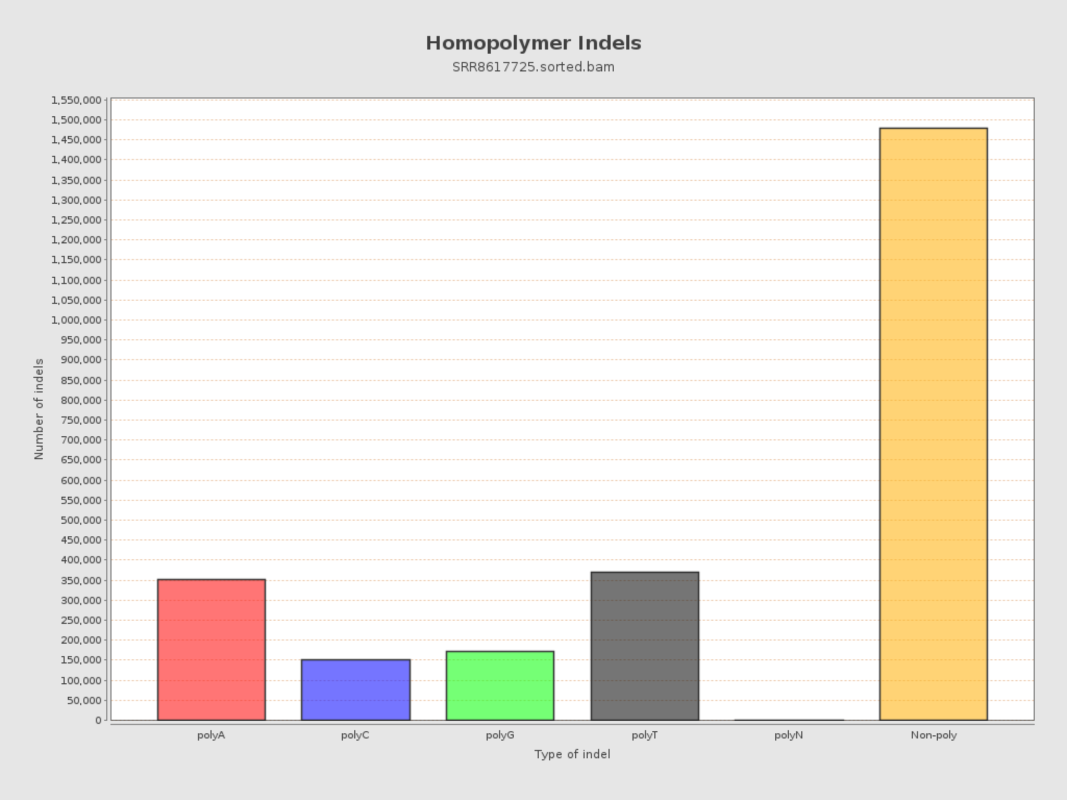
9. Results : Mapped Reads GC-content Distribution



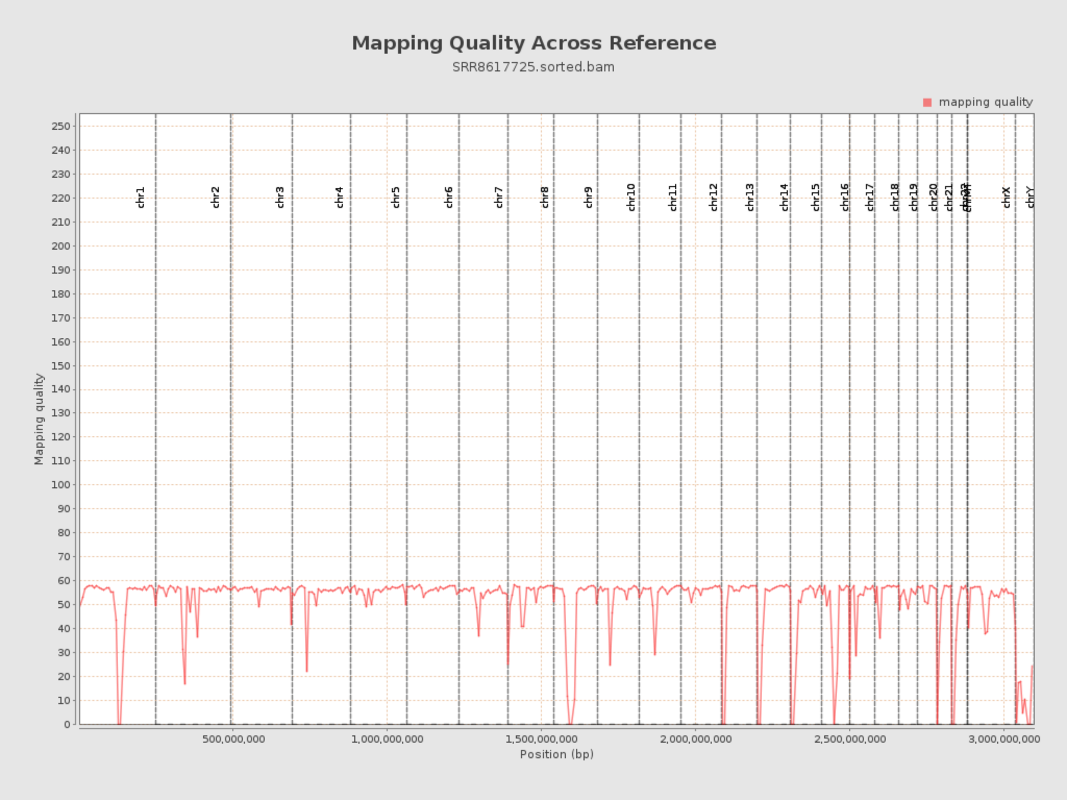
10. Results : Mapped Reads Clipping Profile



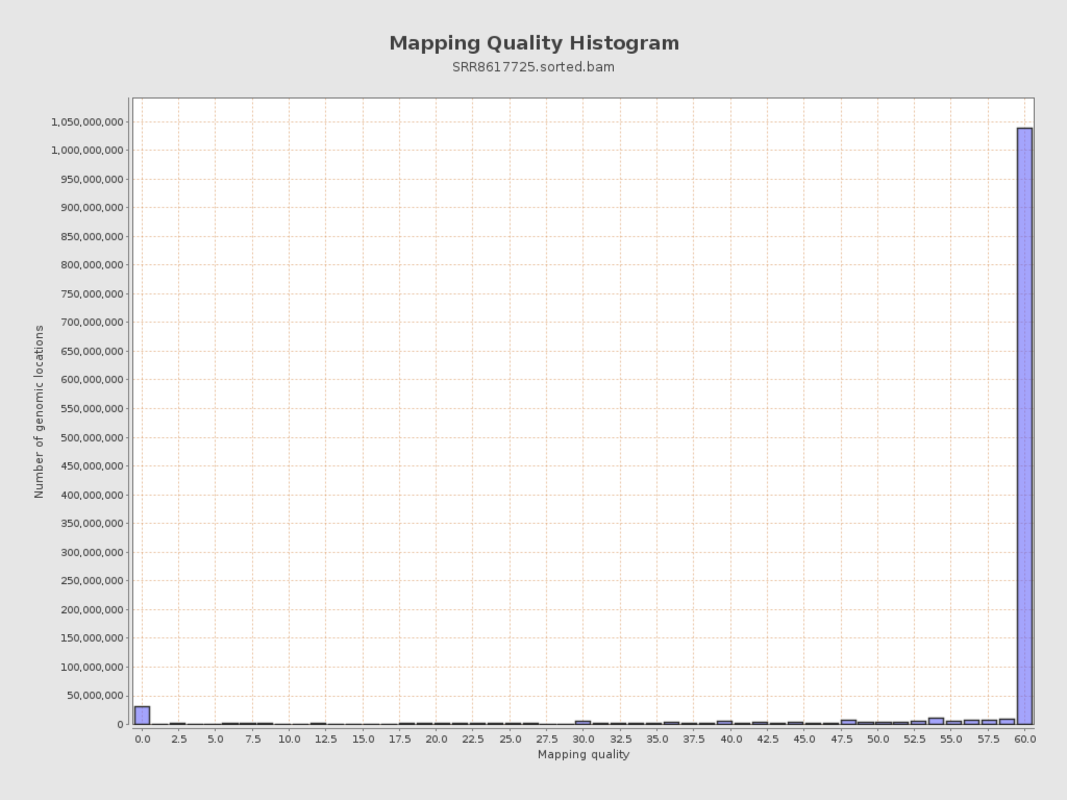
11. Results : Homopolymer Indels



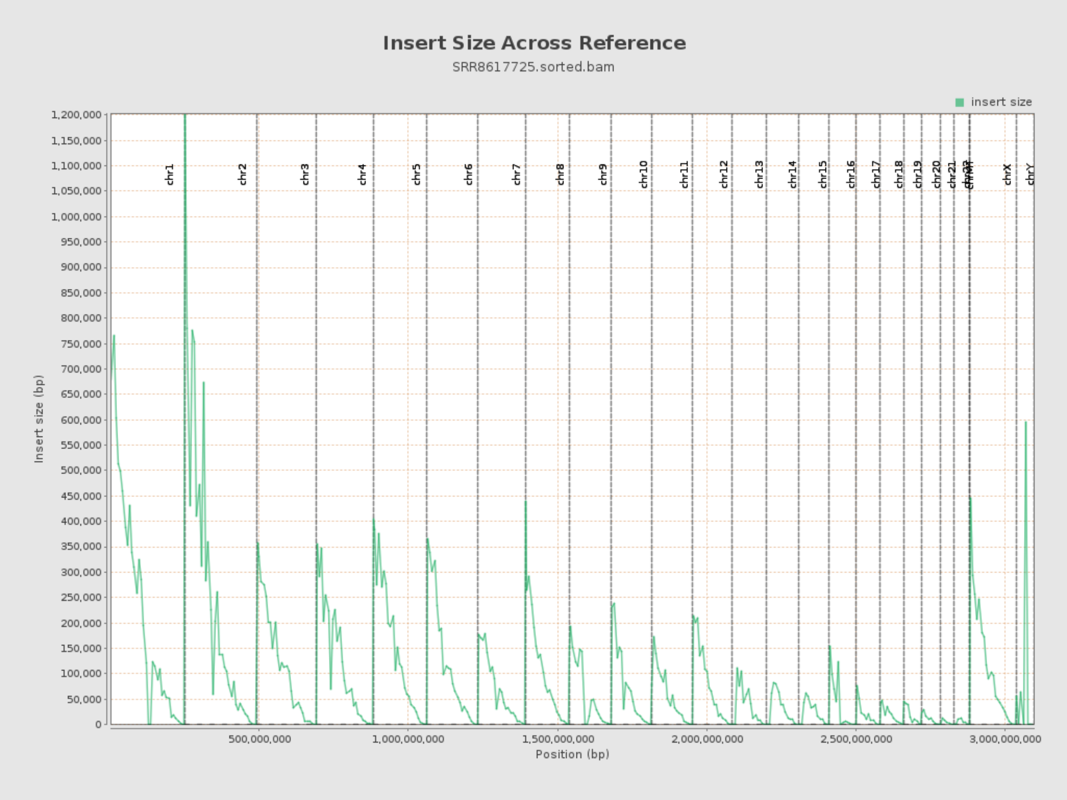
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram