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# 1. Summary mapping report

## 1.1 Summary statistics

	Count	Average length	Total bases
Reads	10,960,956	75	822,071,700
Matched	1,942,551	75	145,691,325
Not matched	9,018,405	75	676,380,375
Contigs	56	50,179	2,810,035
Reads in pairs	1,528,216	215.83	
Broken paired reads	414,335	75	

## 1.2 General algorithm parameters

Parameter	Value
Conflict resolution	Vote (A, C, G, T)
Non specific matches	ignore

## 1.3 Reads parameters

Reads	Length	Type	Parameters
MMLabsCulture2_CTCTCT AC- AAGGAGTA_L001_R1_001 (paired)	Long	Paired	Length=0.9,Similarity=0.98

## 1.4 Quality measurement

Length	
N75	65,015
N50	140,709
N25	265,480

## 1.5 Distribution of read length

Length	Count
75	10,960,956

## 1.6 Distribution of matched read length

Length	Count
75	1,942,551

## 1.7 Distribution of non-matched read length

Length	Count
75	9,018,405

## 1.8 Paired reads distance distribution

