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# 1. Summary mapping report

## 1.1 Summary statistics

	Count	Average length	Total bases
Reads	8,358,458	75	626,884,350
Matched	2,578,763	75	193,407,225
Not matched	5,779,695	75	433,477,125
Contigs	42	66,987	2,813,485
Reads in pairs	2,107,630	217.23	
Broken paired reads	471,133	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
MMLabsCulture1_TAGGCA TG- AAGGAGTA_L001_R1_001 (paired)	Long	Paired	Length=0.9,Similarity=0.98

## 1.4 Quality measurement

N75	99,263
N50	365,415
N25	533,982

## 1.5 Distribution of read length

Length	Count
75	8,358,458

## 1.6 Distribution of matched read length

Length	Count
75	2,578,763

## 1.7 Distribution of non-matched read length

Length	Count
75	5,779,695

## 1.8 Paired reads distance distribution

