## First test of MAb:

	Mab concentration						
	1	0.5	0.1				
	1 µg/ 50 Taq	0.5 μg/ 50 Taq	0.1 μg/ 50 Taq				
10xBuffer	4	4	4	μl			
Taq 40U/µl	1	1	1	μl			
MAb	9	4,5	0,1	μl			
H2O	26	30,5	34,1	μl			
Incubate for 10 min at room temp.							

Mixes of Taq and MAb made before the setup of the PCR reaction.

## Master Mix without Taq

Fragment:	Covid19 #7		A56C	Date	19.05.2021		
PCR volum, μl	10		# of reactions		100		
	Working						
	solutions		Total volume 1000 μl		Desired		
	concentration		Volum		concentration		
H2O			820,00				
10X Thermopol #1	0	mM MgCl	100,00				
MgCl	200	mM	10,00		2,00001	mМ	
Primer forward	100	μM	3,00		0,3	μM	
Primer reverse	100	μM	3,00		0,3	μM	94C-2min
Fam GC-Clamp	100	μM	0,00		0,00001	μM	94C-20sec
dNTP	100	mM	4,00		400	μM	A 56C-20sec 45cycles
cDNA covid-19	100	ng	10,00		1	ng/µl	72C-40sec
EVA green 20X			40,00		0,8	Х	Melting
BSA	100	%	10,00		1	%	
Таq	40	U/µl	0,00		0	U/µl	

19 $\mu$ l of the different Taq/MAb mixes where added to 250 $\mu$ l of the master mix above. 0.5  $\mu$ l Taq (without MAb) was added to the control.

Derivative of the melting curve and the amplification curves are depicted below in the following order. 1µg MAb, 0,5µg MAb, 0,1µg MAb and only Taq (no MAb).

The data show that there are more impurities with reduced MAb concentration. Which also corresponds with the Cq values. The PCR was started with 2 minute incubation at 94°C. This is most likely not enough to denature all the MAb at the highest concentration which is reflected in a high Cq value (needs a few more cycles to get going). This can also increase the variation between the 24 replicates.

Data summarized in table below.

	Mean Cq	1 STD
1µg	26,1	0,57
0,5µg	25,8	0,33
0,1µg	25,0	0,07
0µg	24,4	0,12







## 0,1µg MAb





