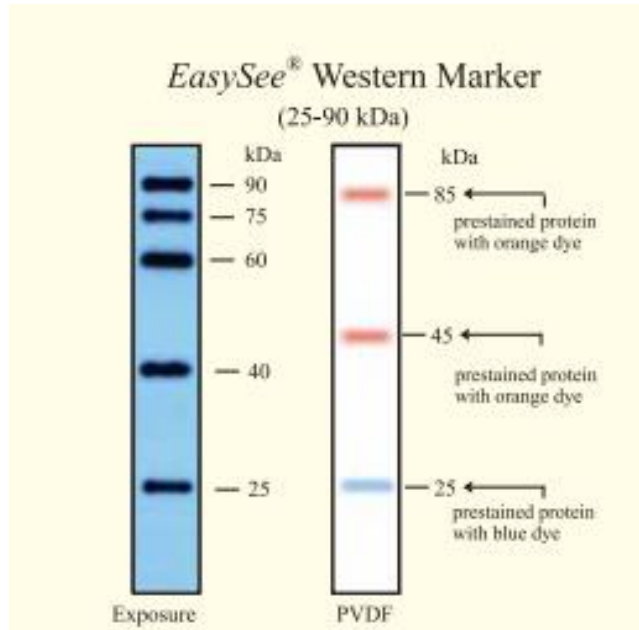


Marker-1 (M1)



Marker-2 (M2)

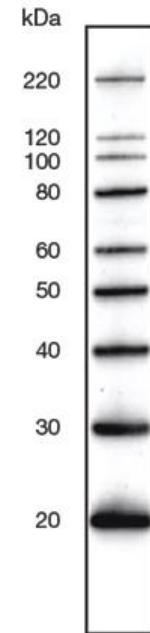


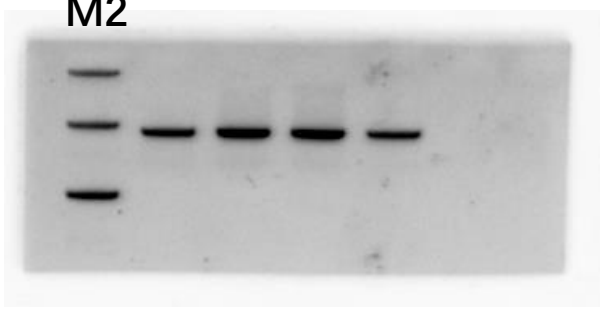
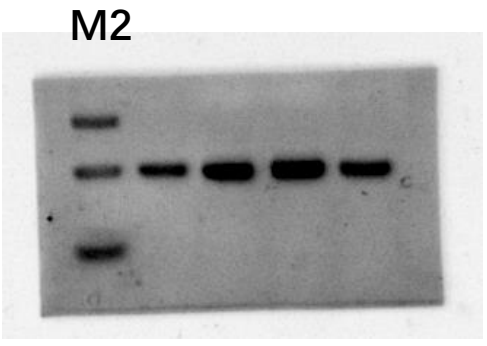
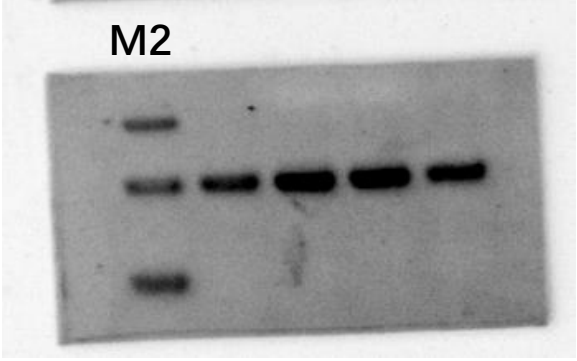
Fig2 D

1

2

3

PCNA
(30 KD)



GAPDH
(36 KD)

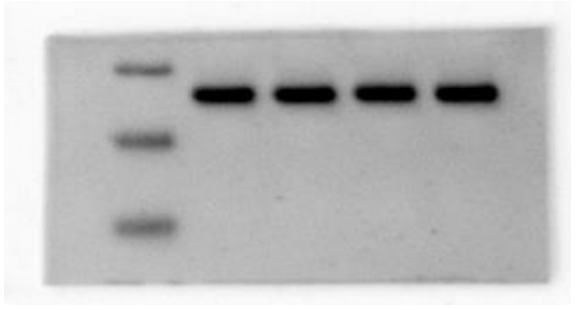
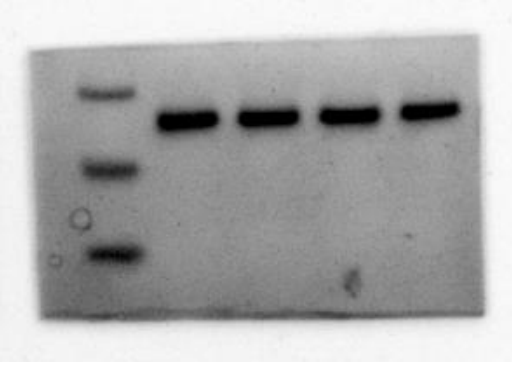
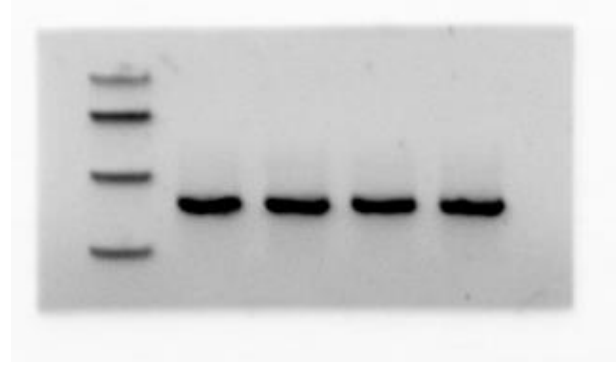


Fig2 E

1

2

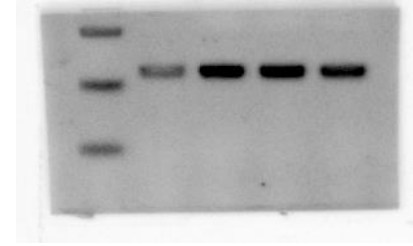
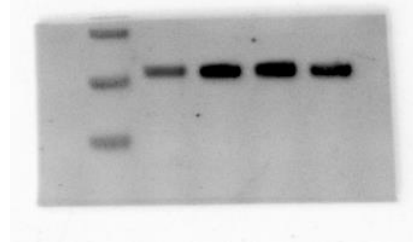
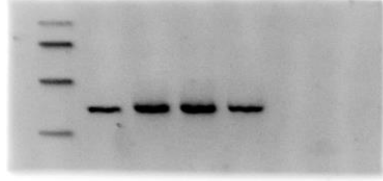
3

M1

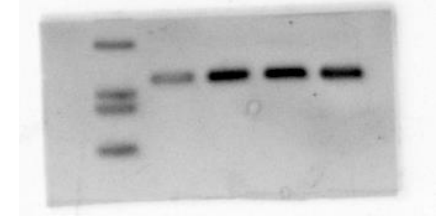
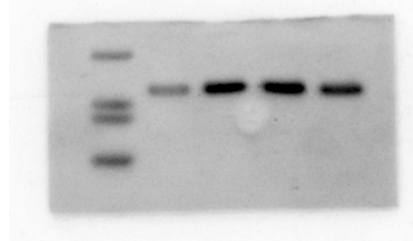
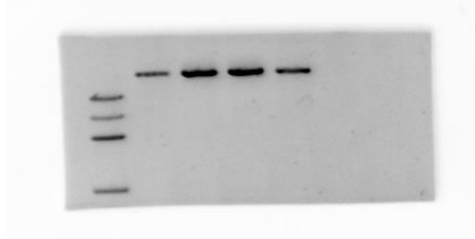
M2

M2

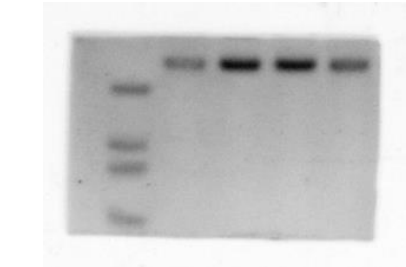
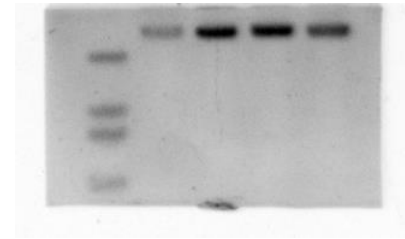
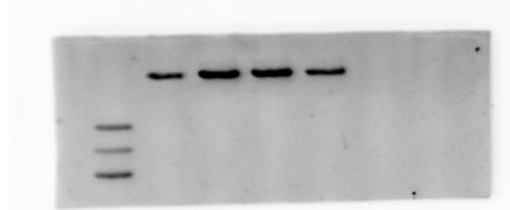
α -SMA
(33 KD)



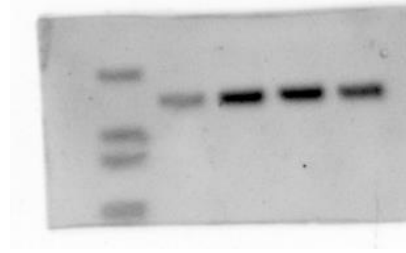
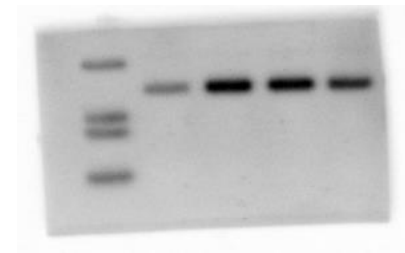
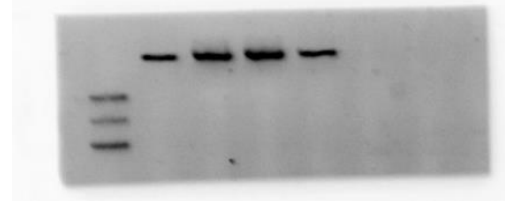
Col I
(139 KD)



FN
(285 KD)



Col IV
(163 KD)



GAPDH
(36 KD)

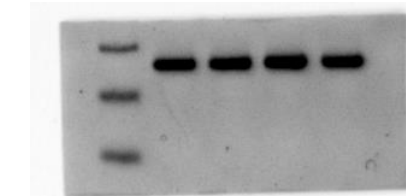
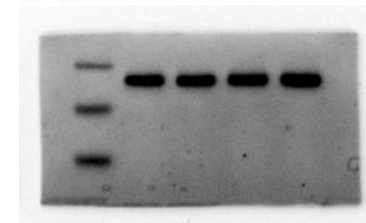
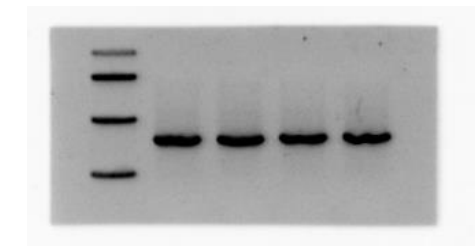


Fig4 D

1

2

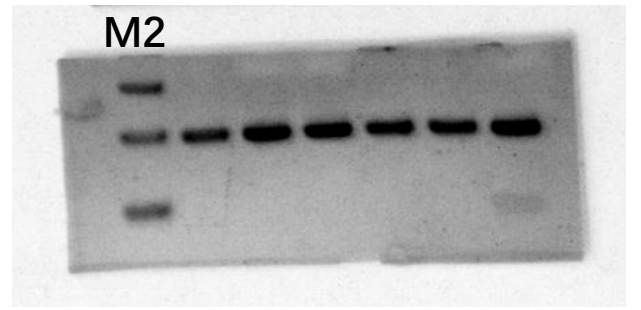
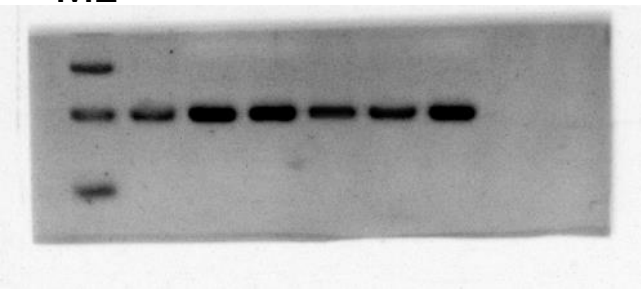
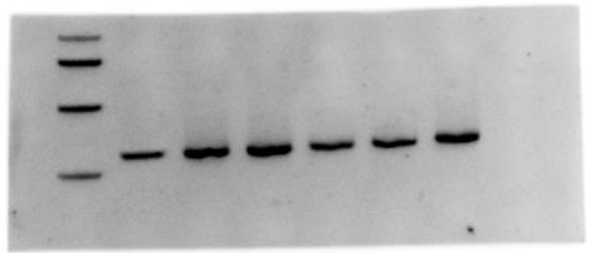
3

M1

M2

M2

PCNA
(30 KD)



GAPDH
(36 KD)

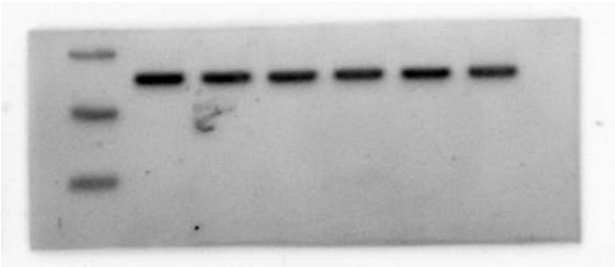
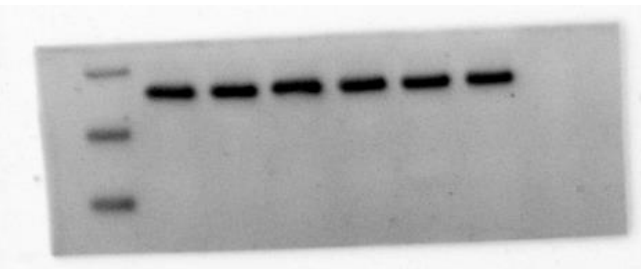
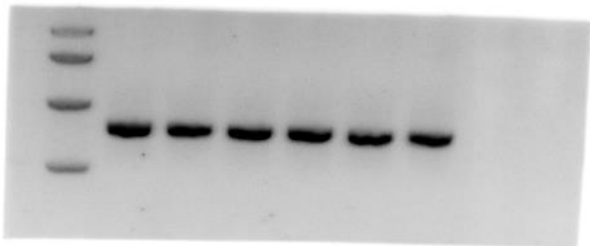


Fig4 E

1

2

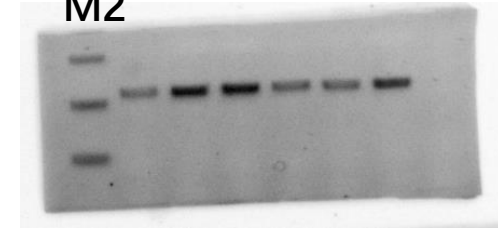
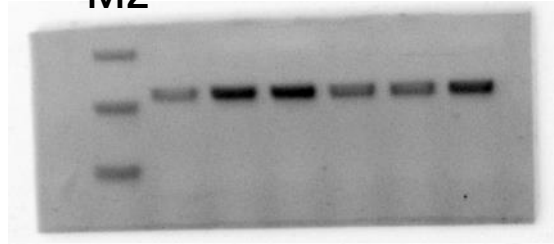
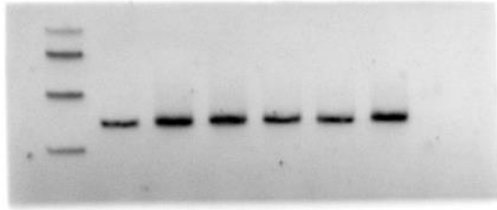
3

M1

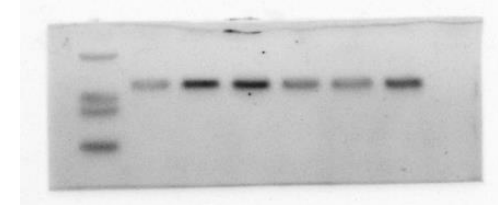
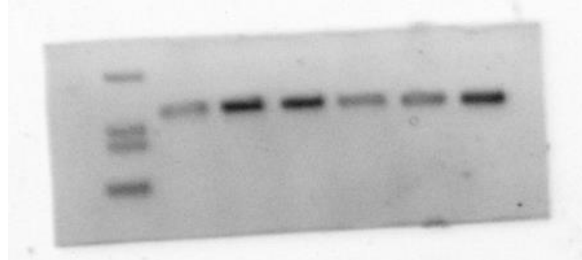
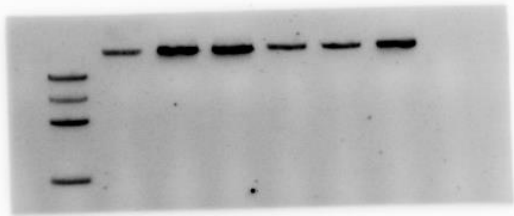
M2

M2

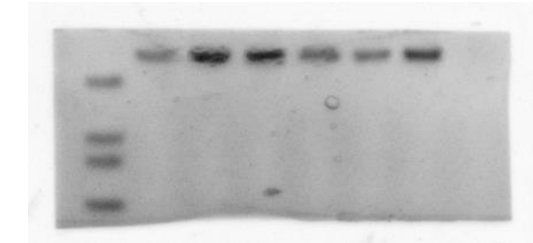
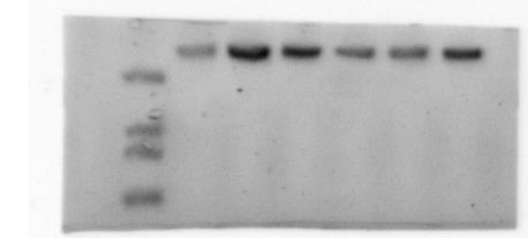
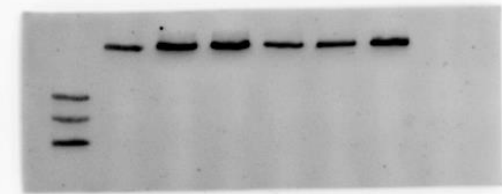
α -SMA
(33 KD)



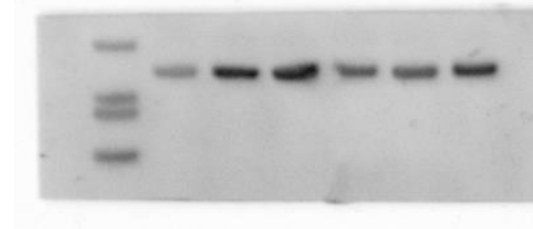
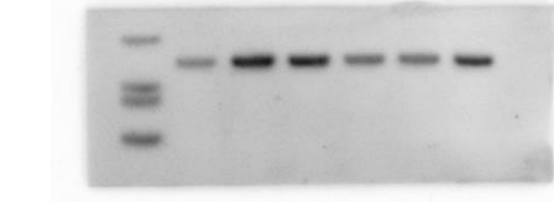
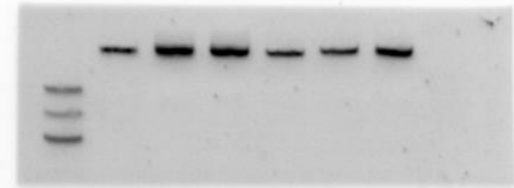
Col I
(139 KD)



FN
(285 KD)



Col IV
(163 KD)



GAPDH
(36 KD)

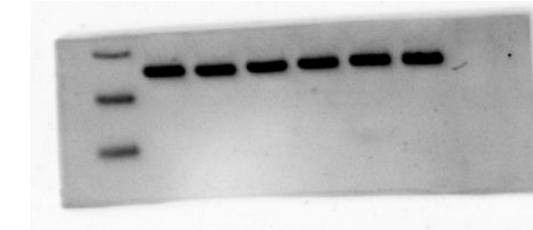
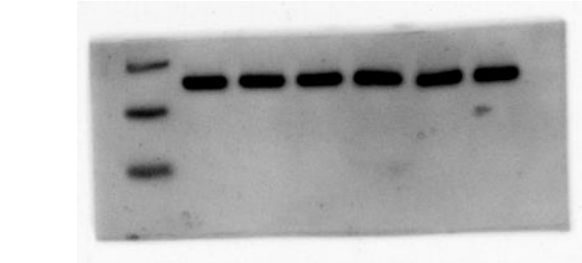
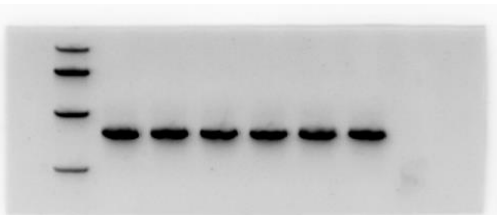


Fig5 F

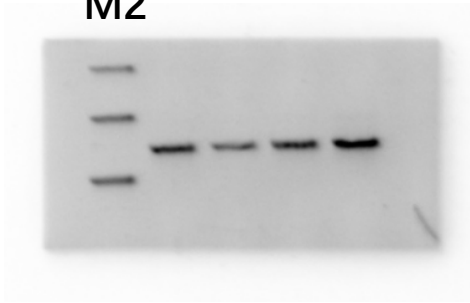
1

2

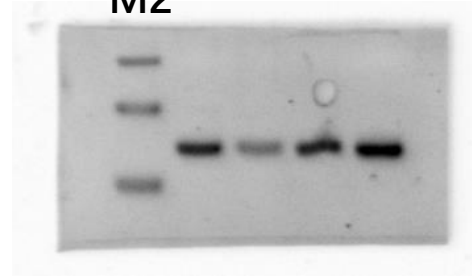
3

Tmbim6
(24 KD)

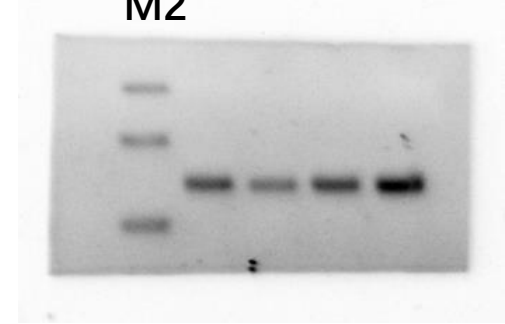
M2



M2



M2



GAPDH
(36 KD)

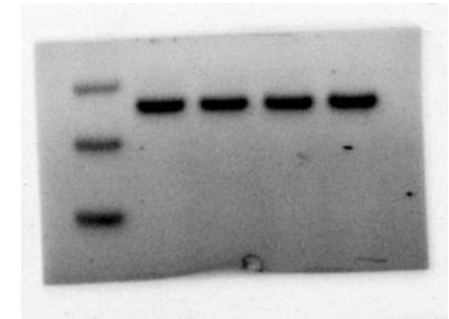
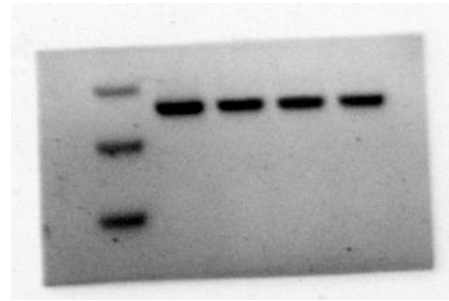
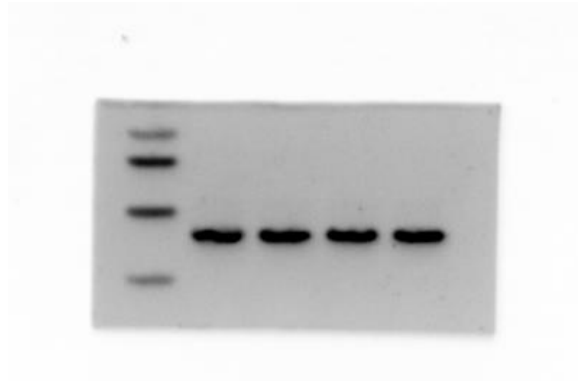


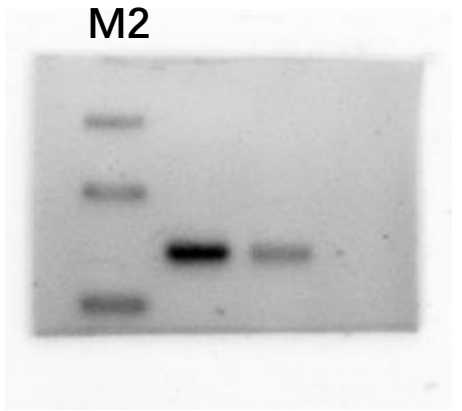
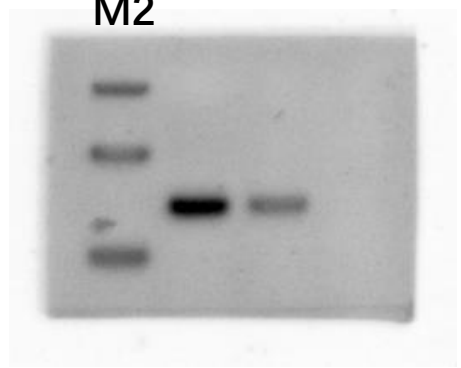
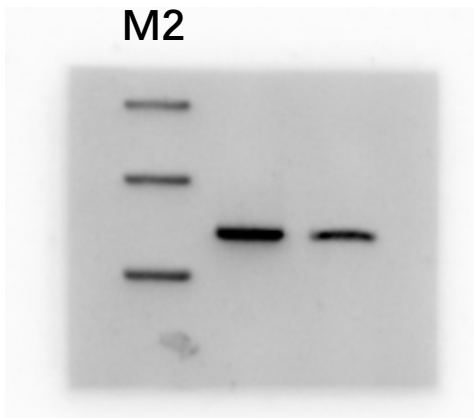
Fig5 H

1

2

3

Tmbim6
(24 KD)



GAPDH
(36 KD)

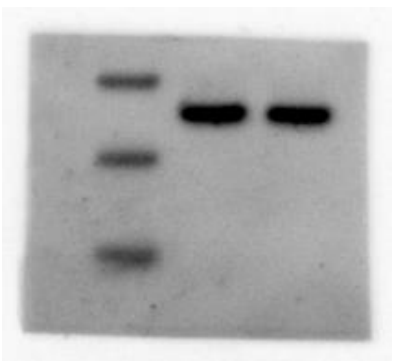
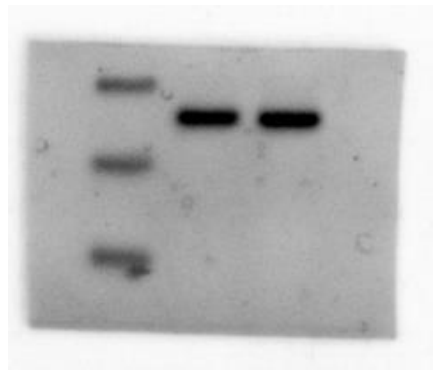
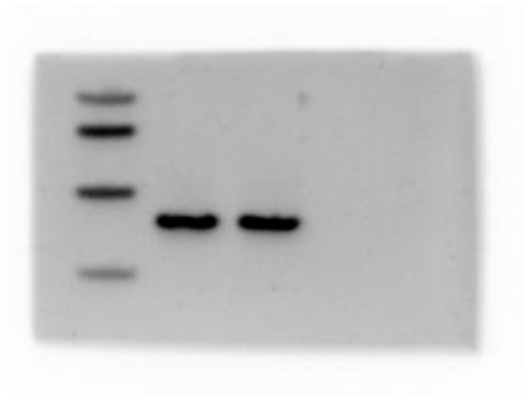


Fig5 I

1

2

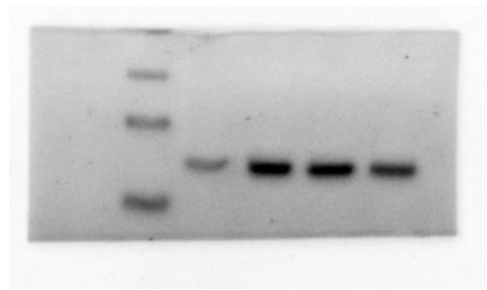
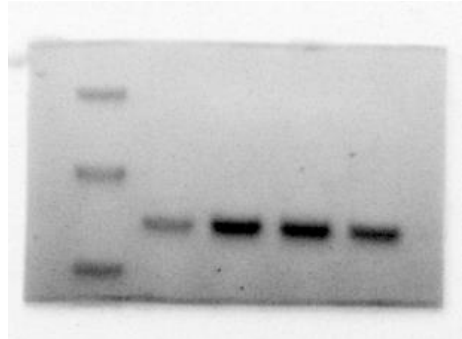
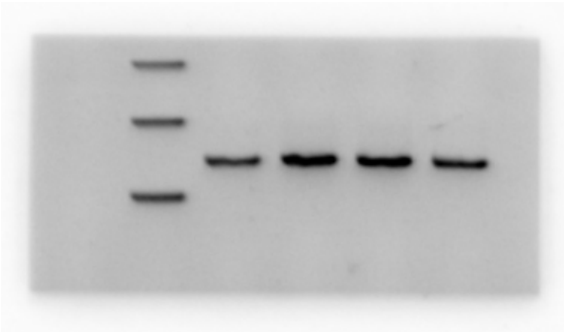
3

M2

M2

M2

Tmbim6
(24 KD)



GAPDH
(36 KD)

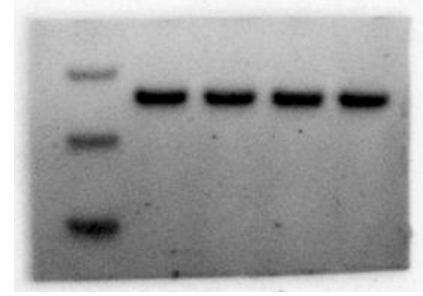
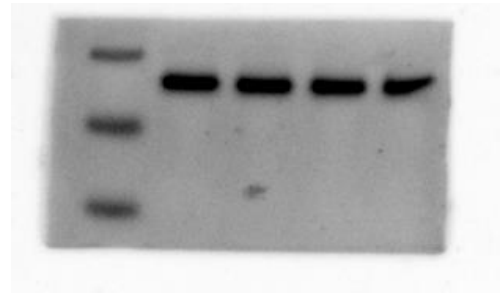
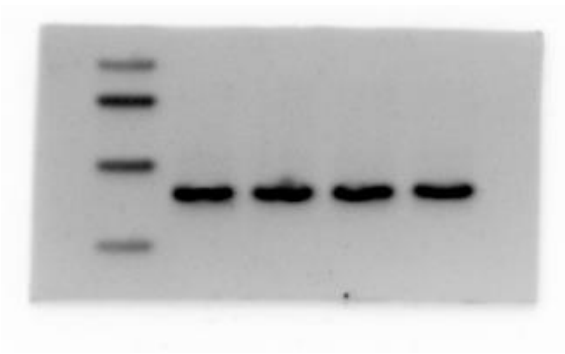


Fig6 B

1

2

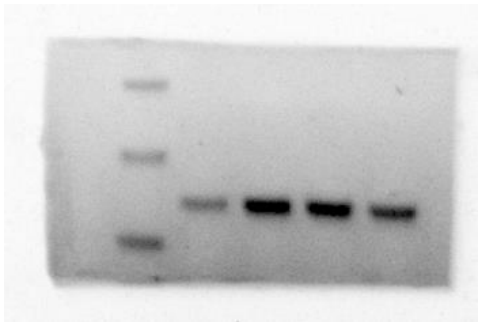
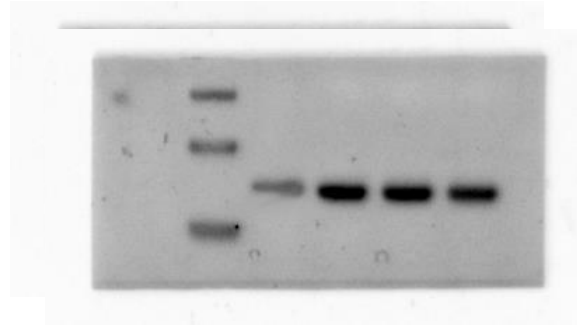
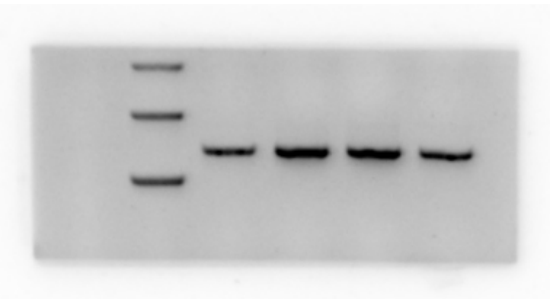
3

M2

M2

M2

Tmbim6
(24 KD)



GAPDH
(36 KD)

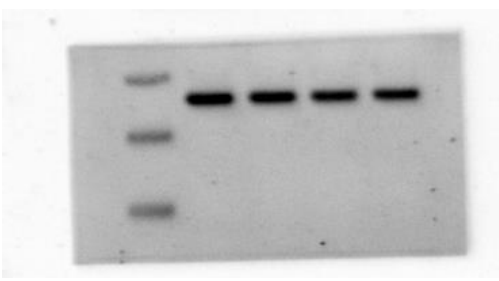
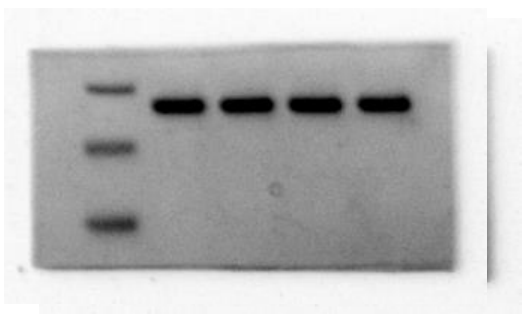
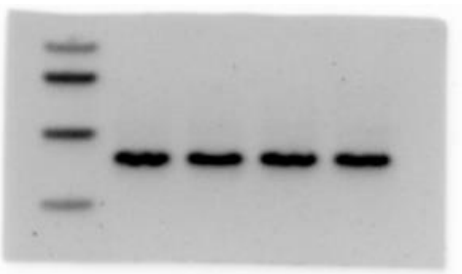


Fig6 E

1

2

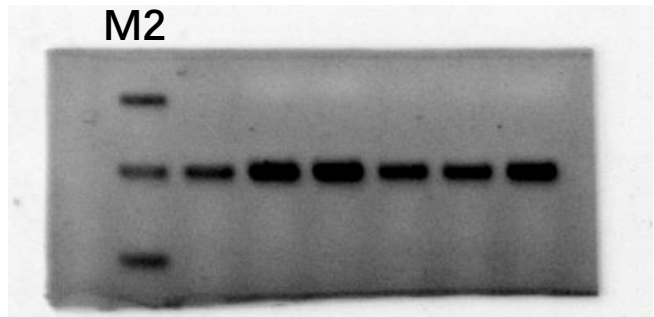
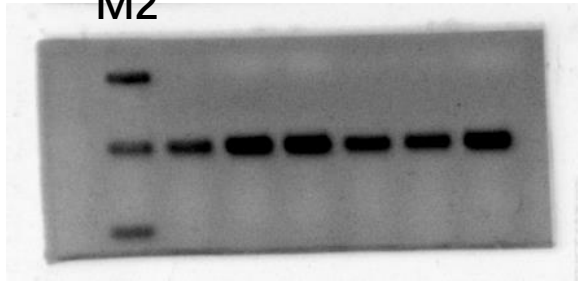
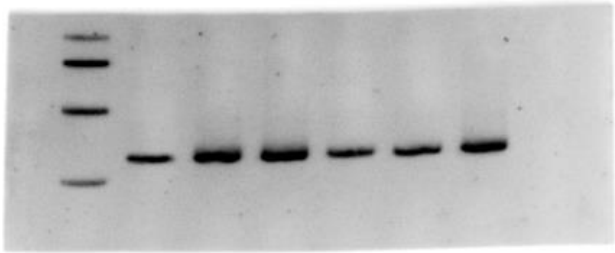
3

M1

M2

M2

PCNA
(30 KD)



GAPDH
(36 KD)

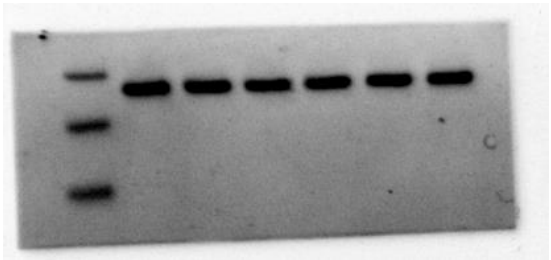
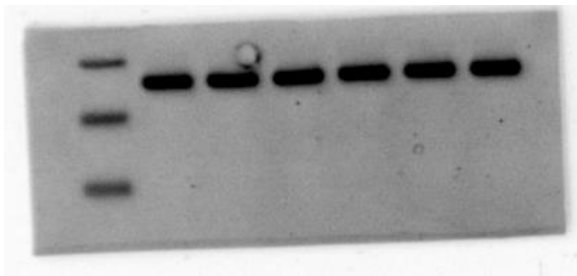
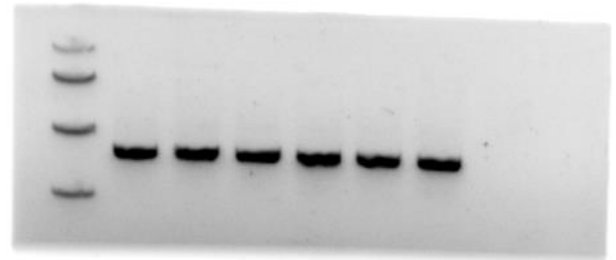


Fig6 F

1

2

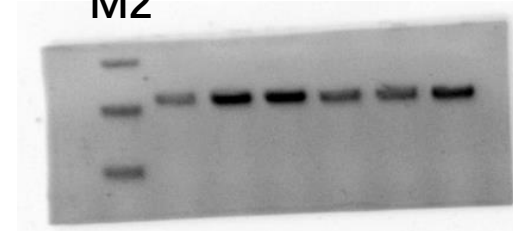
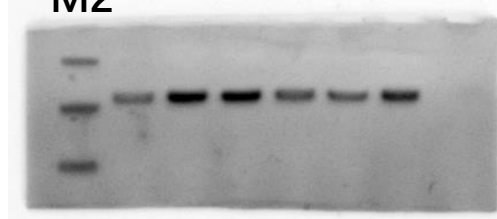
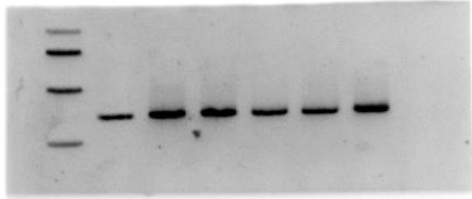
3

M1

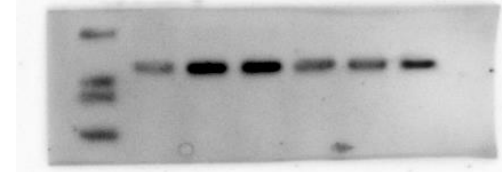
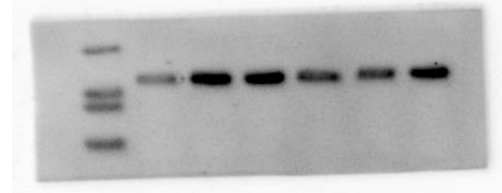
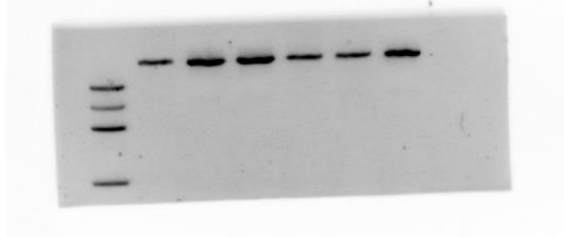
M2

M2

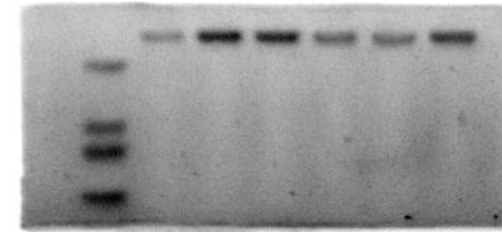
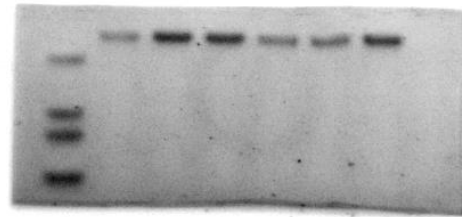
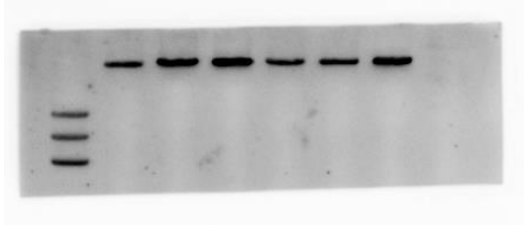
α -SMA
(33 KD)



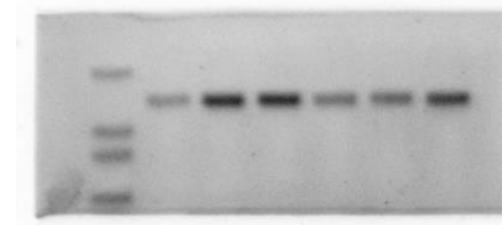
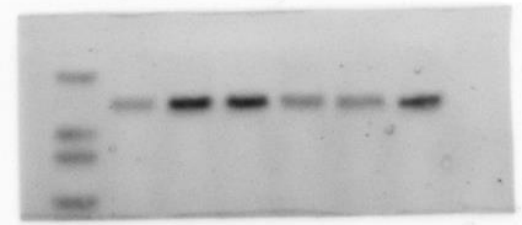
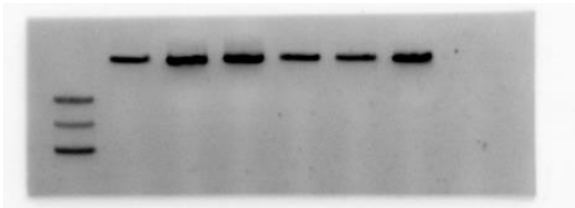
Col I
(139 KD)



FN
(285 KD)



Col IV
(163 KD)



GAPDH
(36 KD)

