

# **Gene-edited murine cell lines for propagation of chronic wasting disease prions**

Rupali Walia, Cheng Ching Ho, Chi Lee, Sabine Gilch and Hermann M. Schatzl

**Supplementary Data**

CAD5_WT	CCTGGAGGGTGGAACACCGGTGGAAGCCGGTATCCCAGGGCAGGGAAAGCCCTGGAGGCAAC
CAD5_KO2A	CCTGGAGGGTGGAACACCGGTG-----
CAD5_KO2B	CCTGGAGGGTGGAACACCGGTAT-----CGGTATCCCAGGGCAGGGAAAGCCCTGGAGGCAAC
CAD5_KO2C	CCTGGAGGGTGGAACACCGGTAT-----CCCAGGGCAGGGAAAGCCCTGGAGGCAAC *****.
CAD5_WT	CGTTACCCACCTCAGGGTGGCACCTGGGGCAGCCCCACGGTGGCTGGGACAACCC
CAD5_KO2A	-----
CAD5_KO2B	CGTTACCCACCTCAGGGTGGCACCTGGGGCAGCCCCACGGTGGCTGGGACAACCC
CAD5_KO2C	CGTTACCCACCTCAGGGTGGCACCTGGGGCAGCCCCACGGTGGCTGGGACAACCC
CAD5_WT	CATGGGGGCAGCTGGGACAACCTCATGGTGGTAGTTGGGTCAAGCCCCATGGCGGTGGA
CAD5_KO2A	-----
CAD5_KO2B	CATGGGGGCAGCTGGGACAACCTCATGGTGGTAGTTG-----
CAD5_KO2C	CATGGGGGCAGCTGGGACAACCTCATGGTGGTAGTTG-----
CAD5_WT	TGGGGCCAAGGAGGGGGTACCCATAATCAGTGGAACAGCCCAGCAAACCA
CAD5_KO2A	-----GAAGGGGGTACCCATAATCAGTGGAACAGCCCAGCAAACCA
CAD5_KO2B	-----GGGTCAAGCCCCATGGCGGTGGAACAGCCCAGCAAACCA
CAD5_KO2C	-----GGGTCAAGCCCCATGGCGGTGGAACAGCCCAGCAAACCA *** : . *** . : . * *****

**Supplementary Figure S1a: Indel signatures in CAD5-KO2 clone.**

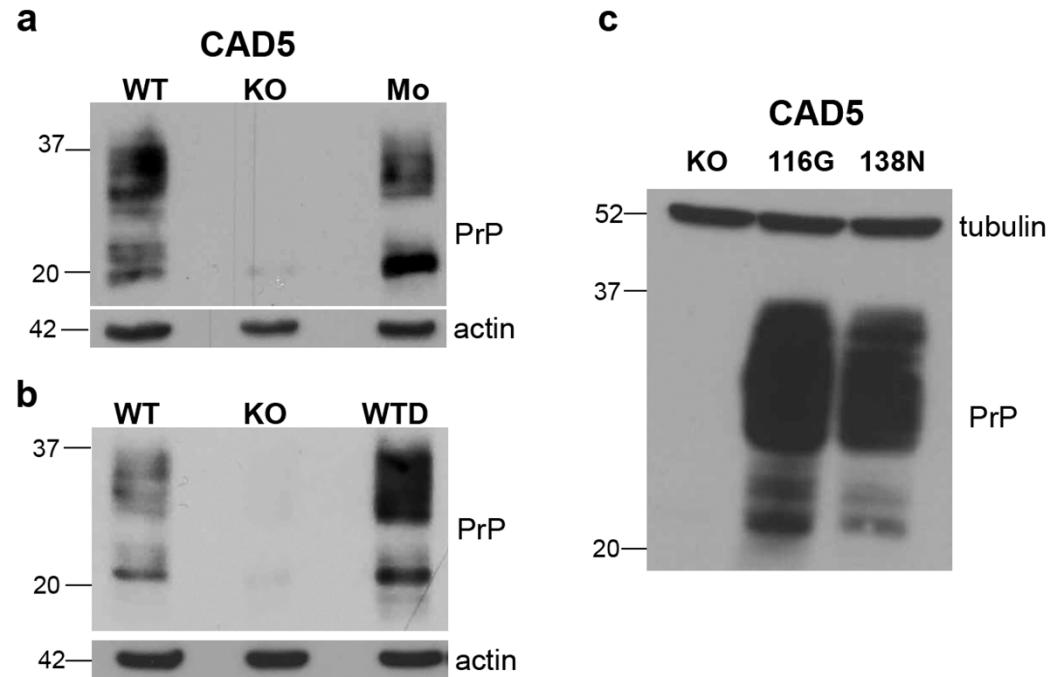
Genomic PCR was done from CAD5-KO2 cell clone using PrP-F and PrP-R primers and cloned into a bacterial mini library. Sequence comparison of ten bacterial inserts with the wild type control (CAD5\_WT) shows: CAD5\_KO2A having a large deletion between gRNA1 and gRNA2 (the same sequence appeared in 7/10 bacterial clones) while CAD5\_KO2B and CAD5\_KO2C had disruptions/smaller deletions at the gRNA1 and gRNA 2 site and appeared in 2/10 and 1/10 sequences respectively. Yellow and blue regions represent the gRNA1 and gRNA2 sites, respectively. Sequence in red represents indels.

CLUSTAL 2.1 multiple sequence alignment

MEF_KO1	CCTGGAGGGTGGAACACCGGTGGAAGCCGGTATCCCAGGGCAGGGAAAGCCCTGGAGGCAAC
MEF_KO2	CCTGGAGGGTGGAACACCGGTGGAAGCCGGTATCCCAGGGCAGGGAAAGCCCTGGAGGCAAC
MEF_WT	CCTGGAGGGTGGAACACCGGTGGAAGCCGGTATCCCAGGGCAGGGAAAGCCCTGGAGGCAAC
	*****
MEF_KO1	CGTTACCCACCTCAGGGTGGCACCTGGGGCAGCCCCACGGTGGTGGCTGGGACAACCC
MEF_KO2	CGTTACCCACCTCAGGGTGGCACCTGGGGCAGCCCCACGGTGGTGGCTGGGACAACCC
MEF_WT	CGTTACCCACCTCAGGGTGGCACCTGGGGCAGCCCCACGGTGGTGGCTGGGACAACCC
	*****
MEF_KO1	CATGGGGCAGCTGGGACAACCTCATGGTGGTAGTTGGGTCAAGCCCCATGGCGGTGGA
MEF_KO2	CATGGGGCAGCTGGGACAACCTCATGGTGGTAGTTGGGTCAAGCCCCATGGCGGTGGA
MEF_WT	CATGGGGCAGCTGGGACAACCTCATGGTGGTAGTTGGGTCAAGCCCCATGGCGGTGGA
	*****
MEF_KO1	TGGGGCCAAGGAAGGGGGTACCCATAATCAGTGGAACAAAGCCCAGCAAACCAAAACCAA
MEF_KO2	TGGGGCCAAGG-----GGGTACCCATAATCAGTGGAACAAAGCCCAGCAAACCAAAACCAA
MEF_WT	TGGGGCCAAGG-AAGGGGGTACCCATAATCAGTGGAACAAAGCCCAGCAAACCAAAACCAA
	*****

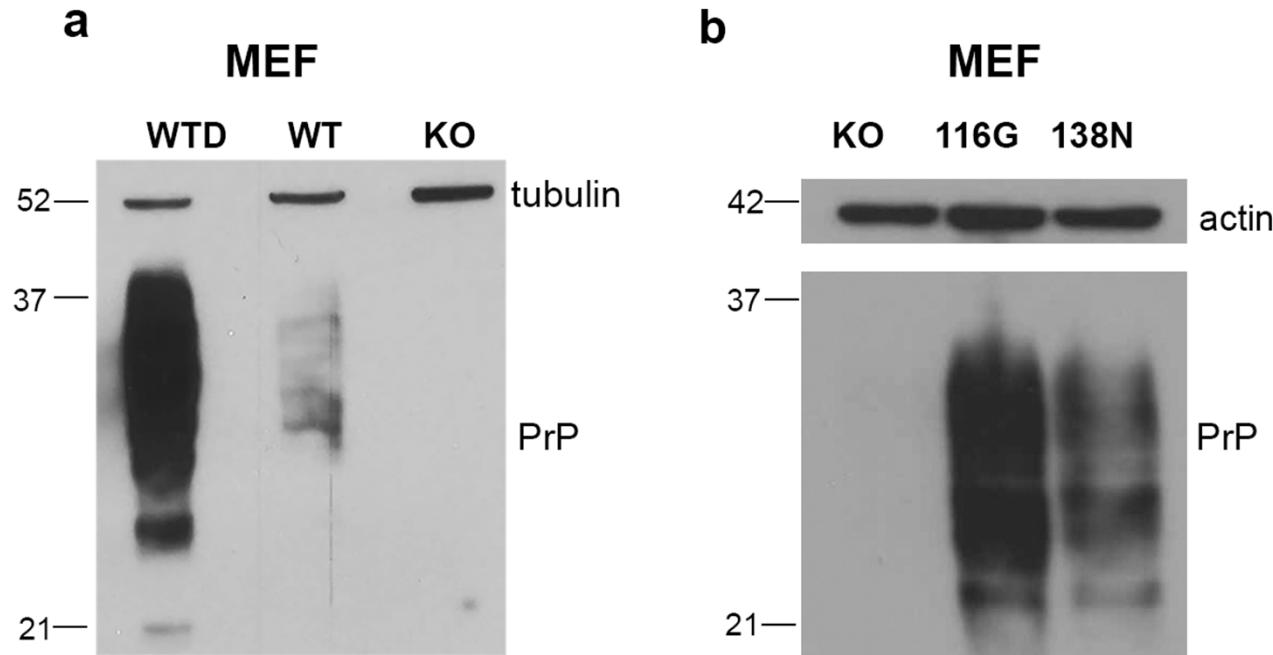
**Supplementary Figure S1b: *Indel* signature in MEF-KO clones.**

Genomic PCR was done from a representative CC9 clonal isolate of MEF cells using PrP-F and PrP-R primers. Sequence comparison of PCR amplicons (cloned into a bacterial mini library - KO1 and KO2) with the wild type (MEF\_WT) shows *indels* at the gRNA2 target site. Yellow and blue regions represent the gRNA1 and gRNA2 sites, respectively. Sequence in red represents *indels*.



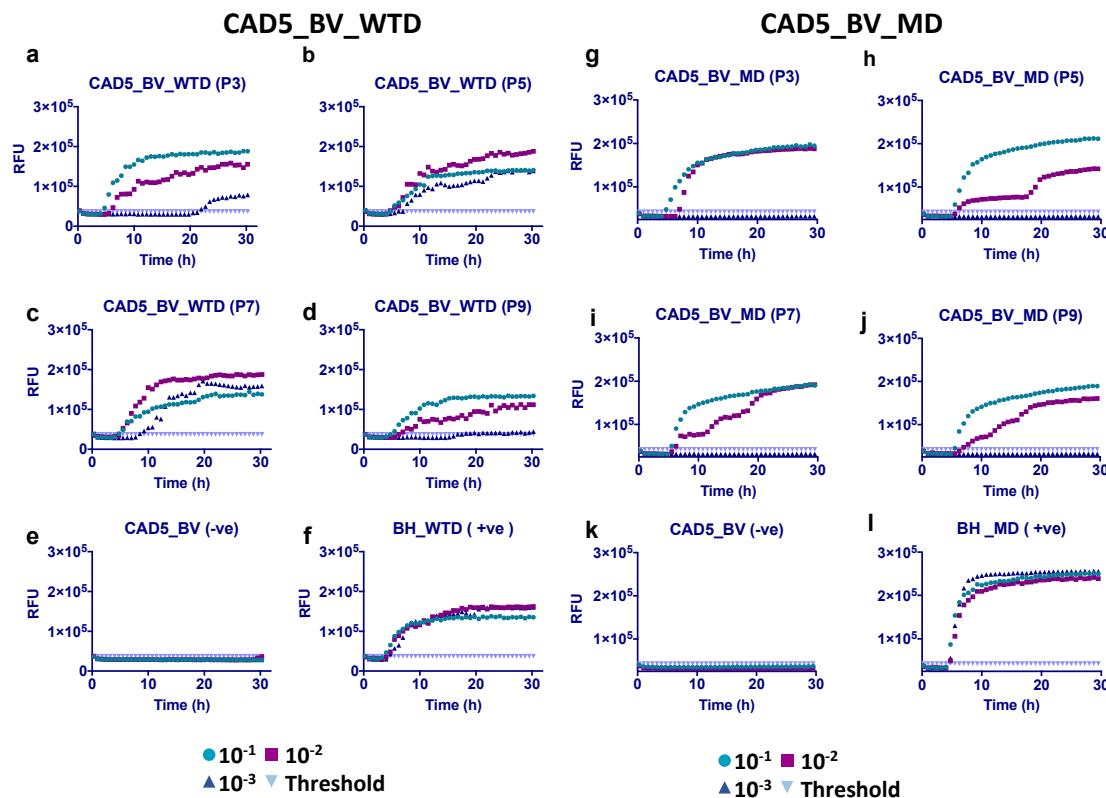
**Supplementary Figure S2: Stable reconstitution of CAD5 PrP<sup>-/-</sup> cells (KO2) with MoPrP and cervid WTD, 116G, and 138N PrP using lentiviral transduction.**

**(a)** Western blot analysis showing expression of Mo-PrP in transduced cells. **(b)** Western blot showing the expression of wild-type WTD-PrP (white-tailed deer) in transduced cells. **(c)** Western blot showing expression of 116G and 138N-PrP in transduced cells. WT represents the parental wild-type CAD5 cells expressing murine PrP and KO represents the CAD5 knock-out background (KO2). The blots were probed with anti-PrP mAb 4H11 and actin or tubulin was used as a loading control



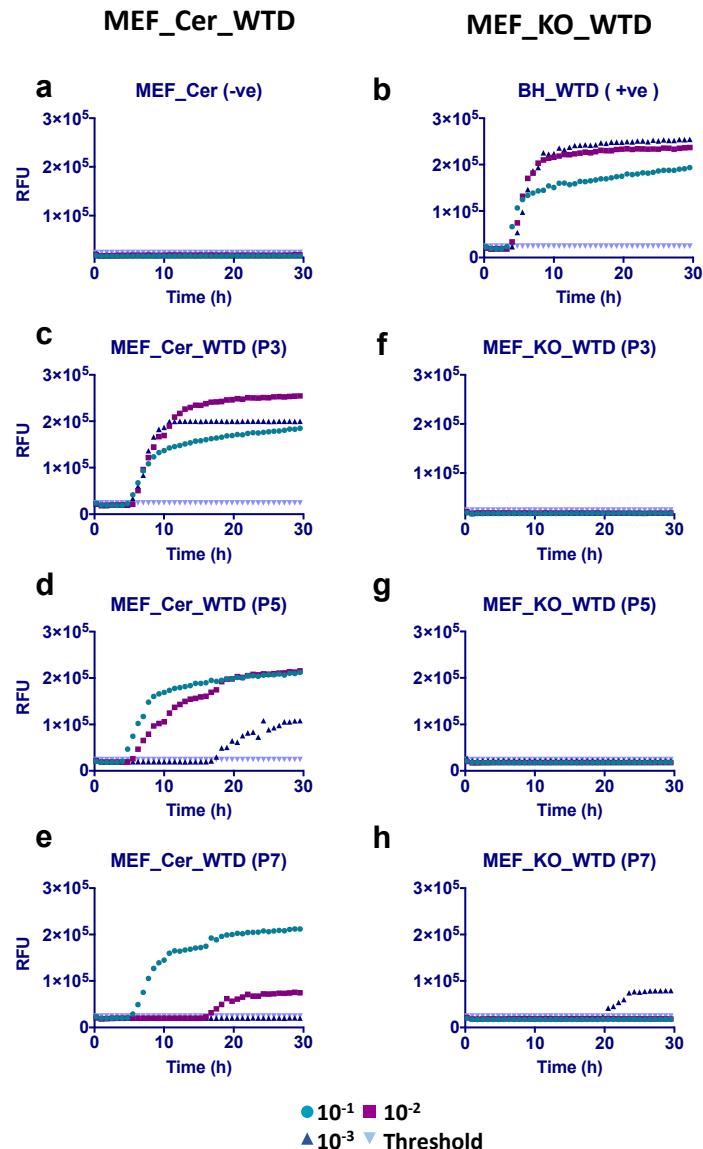
**Supplementary Figure S3: Stable reconstitution of MEF PrP<sup>-/-</sup> cells (KO1) with cervid WTD, 116G and 138N polymorphic PrP variants using lentiviral transduction.**

**(a)** Western blot analysis showing the expression of wild type WTD-PrP (white-tailed deer) in transduced cells. **(b)** Western blot showing expression of 116G and 138N-PrP in transduced cells. WT represents the parental MEF wild-type cells expressing murine PrP and KO represents the MEF knock out cells (KO1). The blots were probed with anti-PrP mAb 4H11 and tubulin was used as a loading control.



**Supplementary Figure S4: RT-QuIC analysis showing positive prion seeding activity in CAD5\_BV cells with white-tailed deer (WTD) and mule deer (MD) CWD prions.**

RT-QuIC assay was setup as done in Fig. 5. A positive seeding activity was seen up to passage P9 in cells infected with white-tailed deer (CAD5\_BV\_WTD) prions (**a-d**) as well as with mule deer (CAD5\_BV\_MD) CWD prions (**g-j**). (**e, k**) represent uninfected cell lysate at passage 3 (negative control). (**f, l**) 1% WTD- and MD-brain homogenate (BH) was used as positive control for the assay.



**Supplementary Figure S5: RT-QuIC analysis showing positive prion seeding activity in MEF\_Cer cells infected with WTD CWD prions and absence of seeding activity in infected knock out cells (MEF\_KO\_WTD).**

RT-QuIC assay was setup as done in Fig. 5. A positive seeding activity was seen in passage P3-P7 in cells infected with white-tailed deer (MEF\_Cer\_WTD) prions (c-e). No seeding activity was observed in infected non-reconstituted knock out (MEF\_KO\_WTD) cells (f-h\*). (a) represents uninfected cell lysate at passage 3 (negative control). (b) 1% WTD-brain homogenate (BH) was used as positive control for the assay.

\* Sample h is negative as only one out of four replicates showed a weak signal. Samples are scored positive when at least 50% of the replicates ( $\geq 2$  out of 4) reached a ThT fluorescence cut-off.

**Supplementary Table S1: Oligonucleotides and primers used in this study**

No.	Oligo/ Primer	Sequence
1	gRNA1	GGTGGAACACCGCTGGAAGC
2	gRNA2	GATTATGGGTACCCCTCCT
3	PrPF	ATGGCGAACCTGGCTACTGGCTG
4	PrPR	TCATCCCACGATCAGGAAGATG
5	LV- Mo-PrPF	TTTTGAATTGCCACCATGGCGAACCTGGCTACTGGCTG
6	LV- Mo-PrPR	TTTTGGATCCTCATCCCACGATCAGGAAGATG
7	LV- BV-PrPF	GATGATGGATCCATGGCGAACCTCAGCTACTG
8	LV- BV-PrPR	ACCGGTTCATCCCACGATCAGGAAGA
9	LV- Cer-PrPF	GATGATGGATCCATGGTAAAAGCCACATAGGC
10	LV- Cer-PrPR	ACCGGTCTATCCTACTATGAGAAAAAT

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**Supplementary: Original Blots**

**Figure 2d, 2e, 2f**

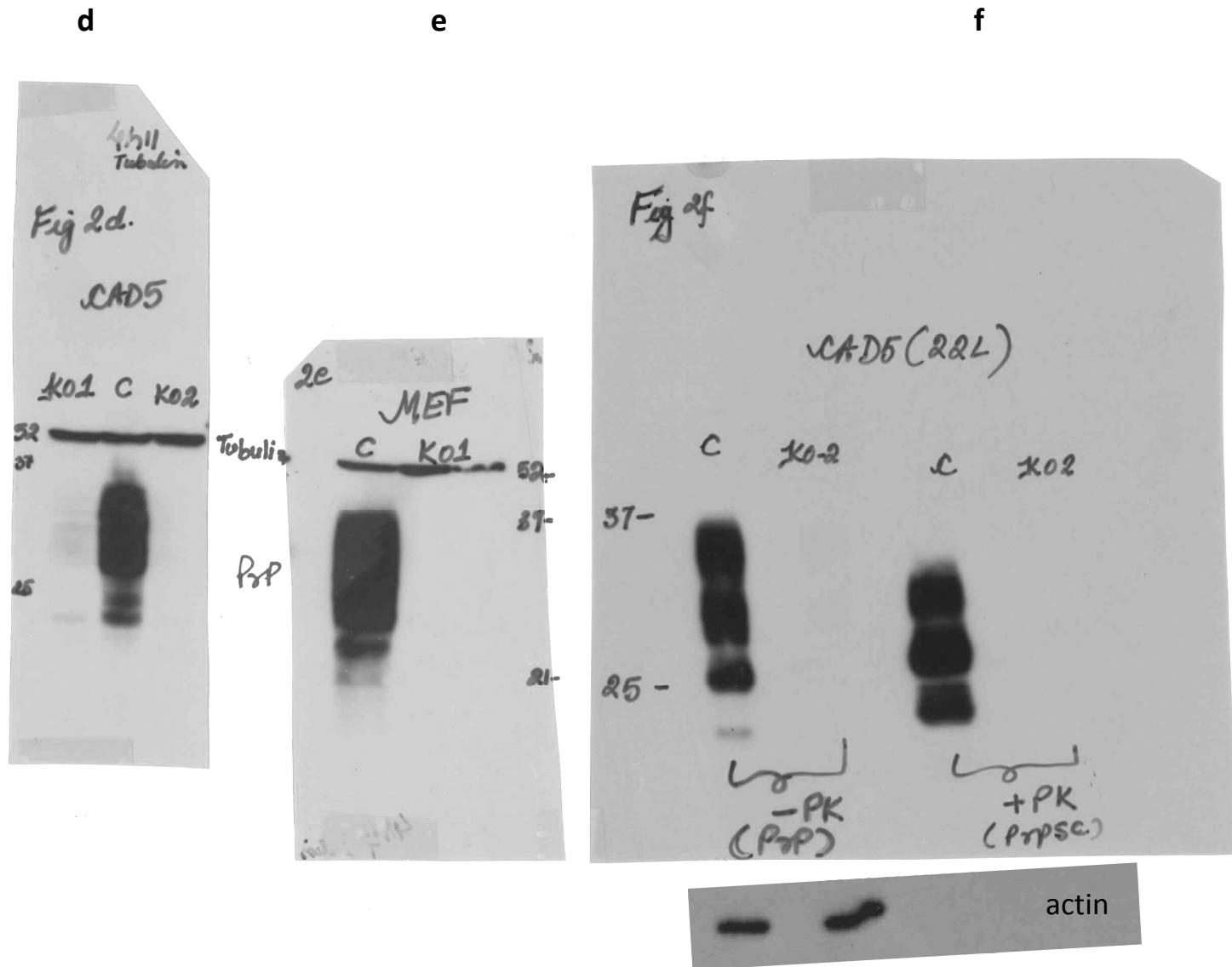
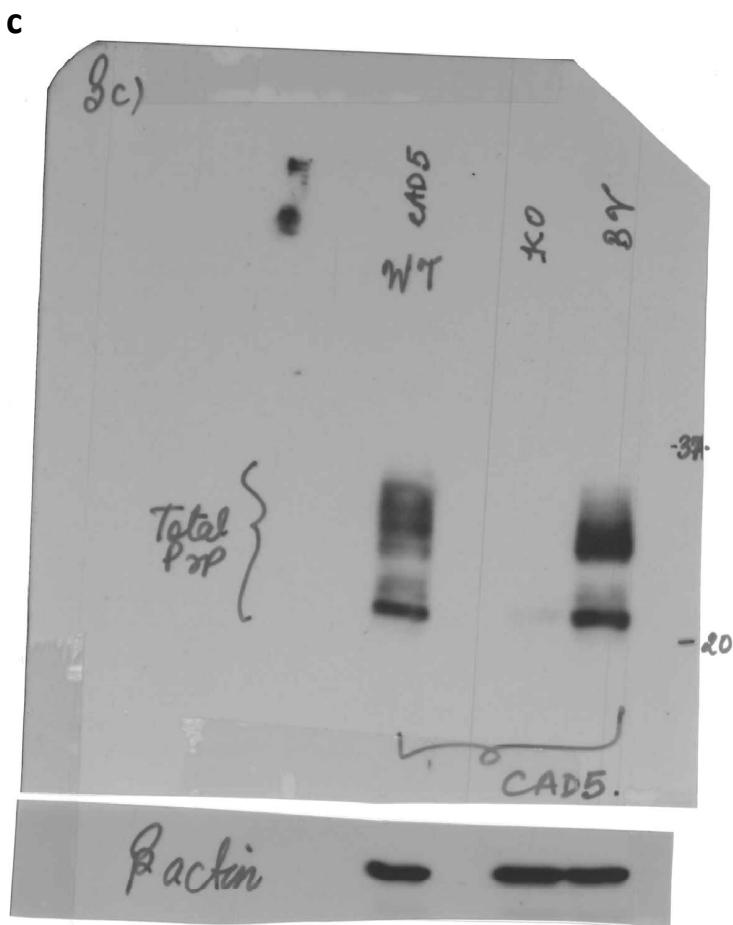
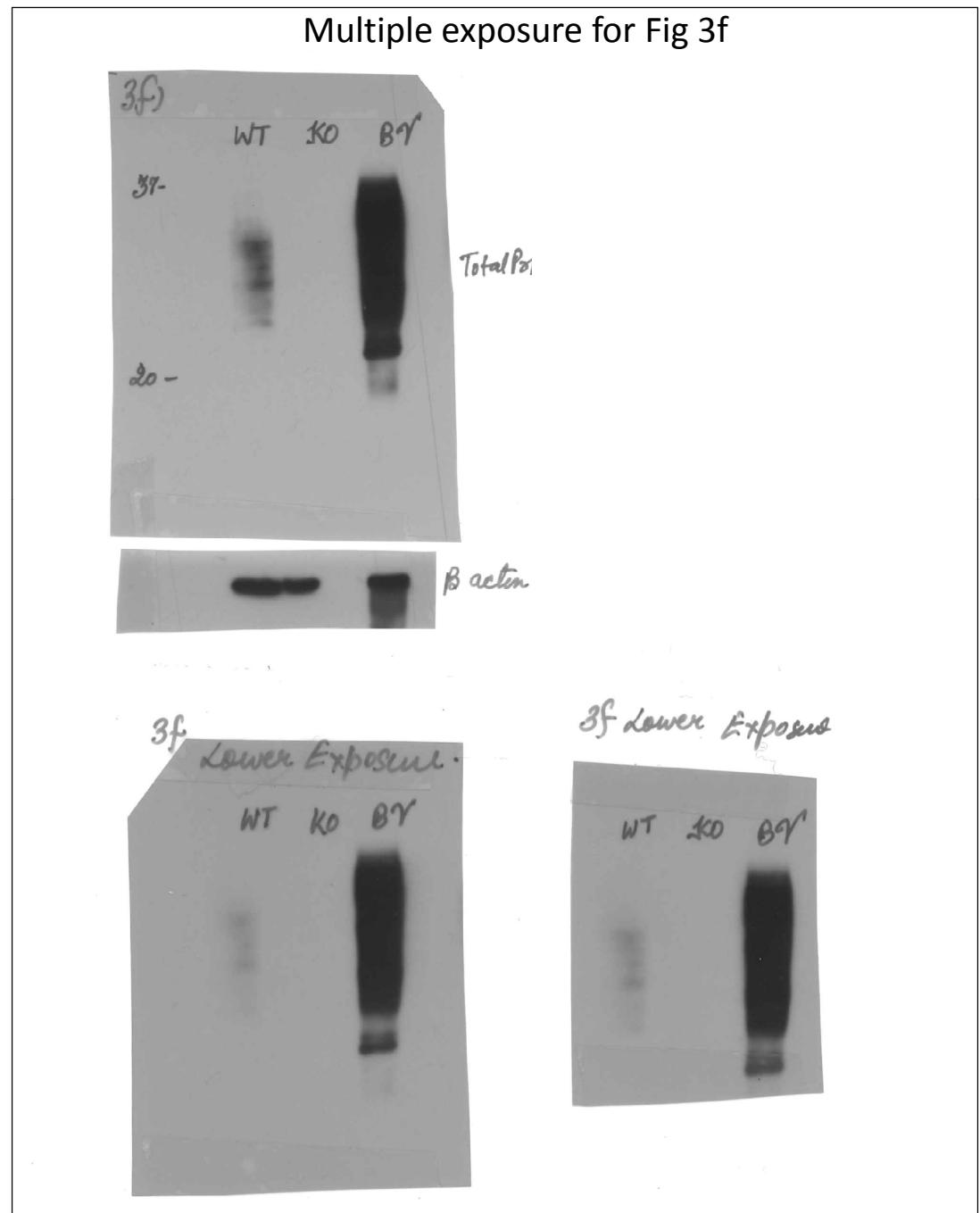


Figure 3c , 3f



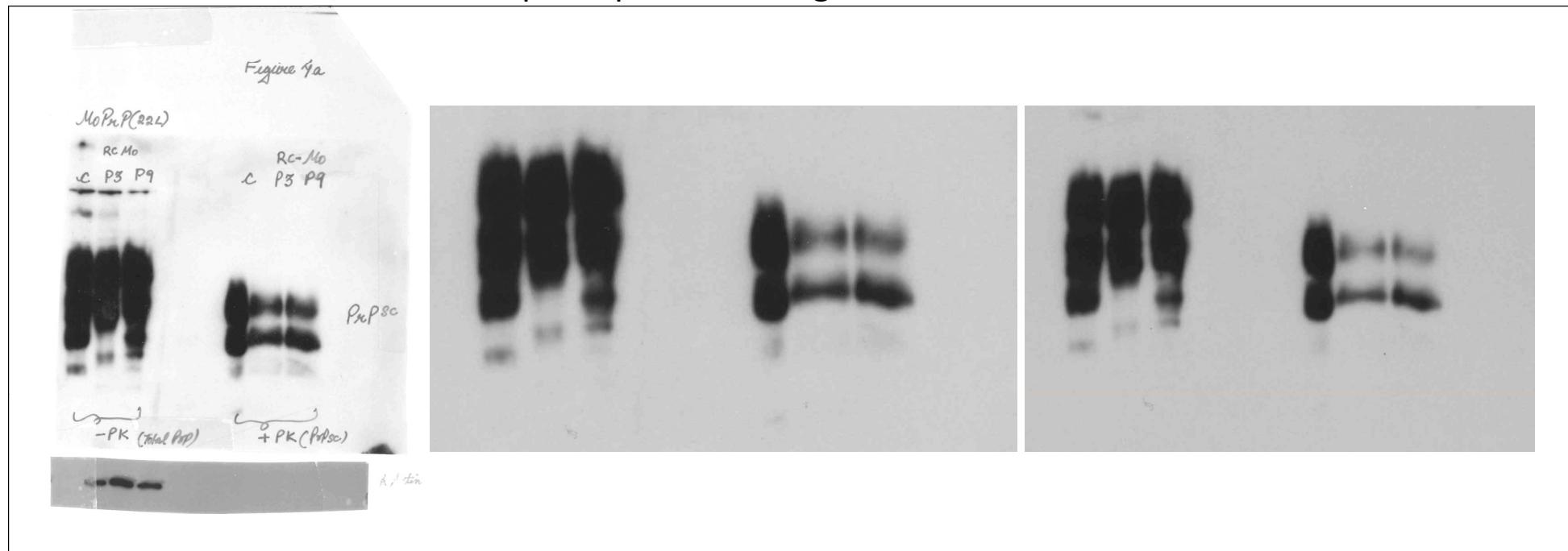
f



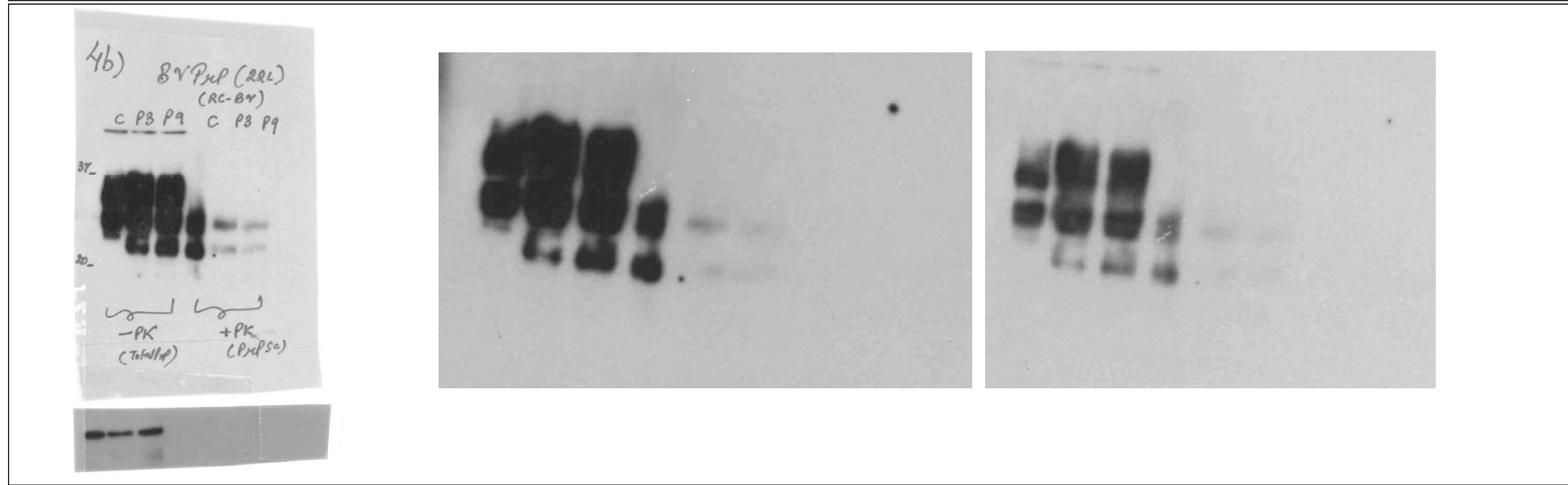
**Figure 4a , 4b**

Multiple exposure for Fig 4a and 4b

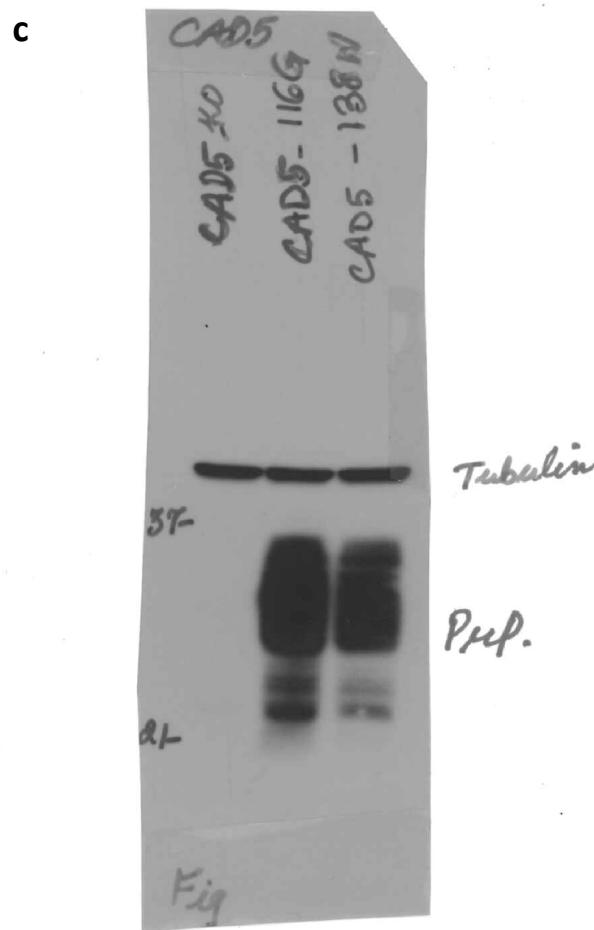
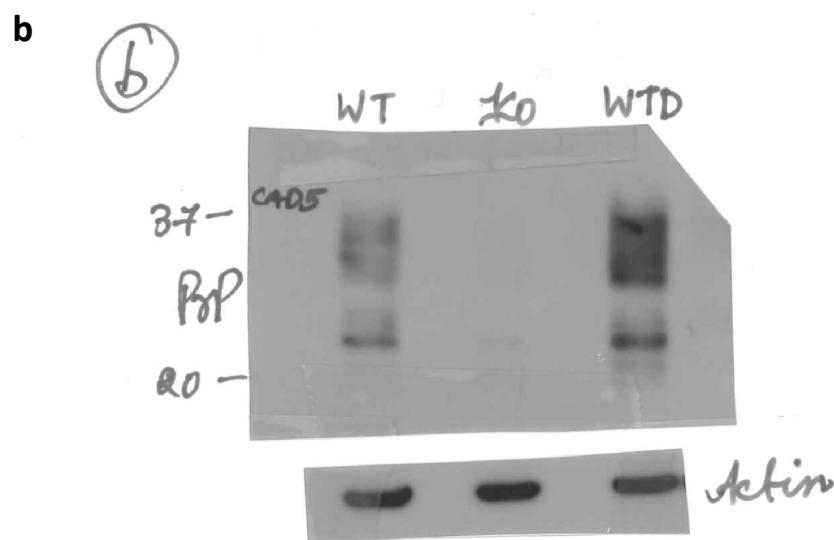
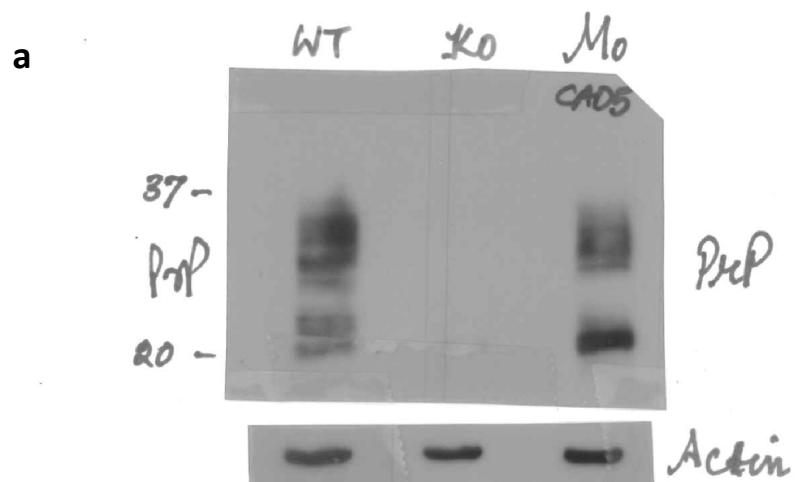
**a**



**b**

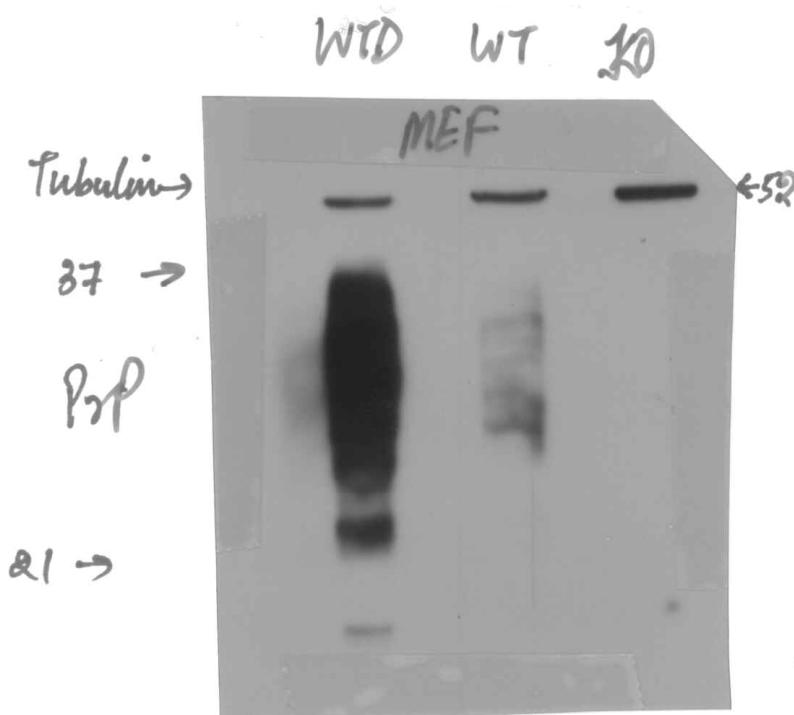


**Figure S2 a, b, c**



**Figure S3 a, b**

**a**



**b**

