Figure S1

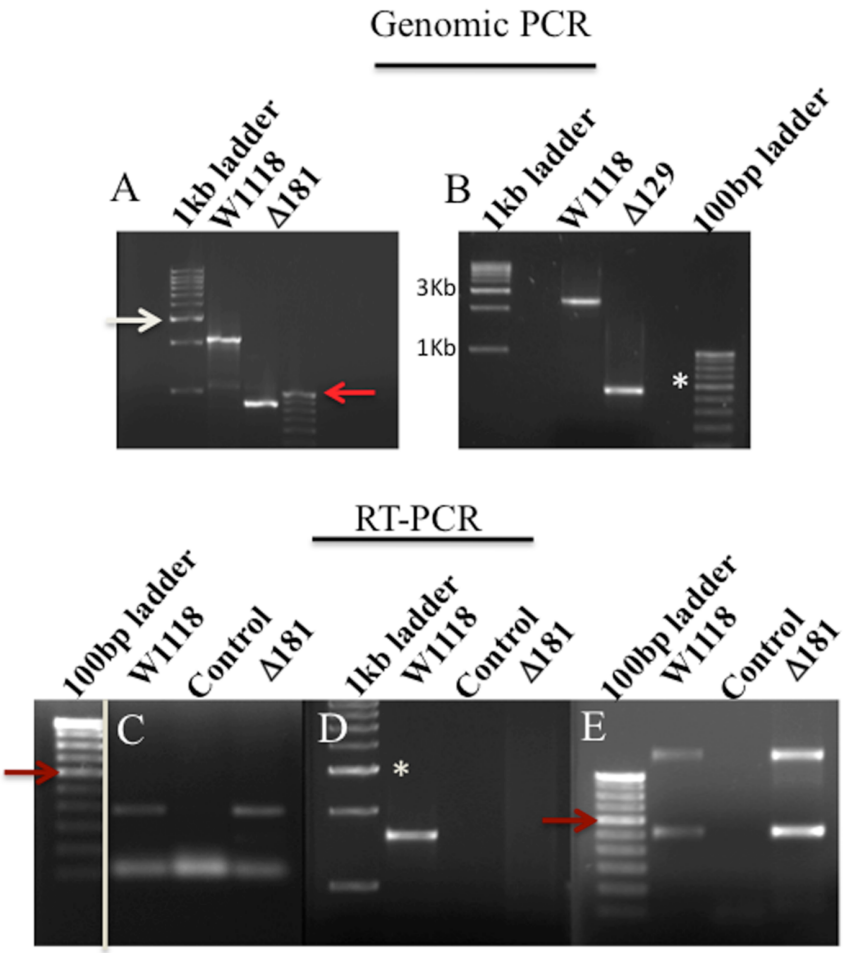

Figure S1: (A) Genomic PCR analysis of D181 mutants. Primers 2F and 31660_Ex2R (Fig1, gray arrows), amplify a 2128 base pair product with wildtype DNA. A band of approximately 850bp is seen with D181 DNA indicating a deletion between these primer sites. White arrow points to the 3kb band; the red arrow indicates 1kb.
(B) Genomic PCR analysis of D129 mutant. PCR with primers 3F and Int2_R2 (Fig1, red arrows) amplify a 2.4 kb region from wildtype DNA. In the D129 mutant, a smaller region of approximately 500bp is seen. The 600bp bright band (asterisk; 100bp ladder, Bangalore Genei, India) is spiked for easy identification.
(C-E) RT-PCR analysis of *Dmon1*$^{\Delta 181}$ mutants. (C) RT-PCR using primers 1F and 2R. The expected 340bp size band was amplified from cDNA derived from wildtype and *Dmon1*$^{\Delta 181}$ animals. The red arrow marks the 600bp band in the DNA ladder. The white line after the lane showing the DNA ladder and RT-PCR product denotes cropping of the lanes in the middle (D) PCR with primers 1F and 4R, amplified the full length *Dmon1*cDNA from wildtype but not *Dmon1*$^{\Delta 181}$ mutant indicating the absence of a full length transcript. The asterisk denotes a 3kb band. (E) PCR using primers designed to the 3' coding region of *CG31660/pog*. The two bands observed in each case correspond to different splice variants of *pog*. The red arrow marks the 600bp band. The middle lane in panels C,D and, and E is the no DNA RT-PCR control.