


Additional file 3: Conserved motif in the intracellular domain of tartan, capricious and Lrrn1

```

462 CRHKIRETIKGLWGNSALGRKEREY-QKTFCDEDYMSRHQHFPCSLGTHSTFPNTYTAPHPGATHHYGMC 535 ICD TRN-Dm
474 CRHRIREMLKG----HSALGRKEREY-QKTFSDEEYMSRPP--PGGGGVHPAAGGYPIAGNSRMIPVTEL 540-stop ICD CAPS-Dm
654 KRKNYH-----HSLKK-----YMQKTSSIPLNELYPPLINLWEGDSDKDKDGSAETKPTQVDTSRSYY 716-stop ICD Lrrn1-Gg

```



Clustal alignment of the intracellular domains (ICD) of tartan, capricious and chick Lrrn1. The entire intracellular domains of CAPS and Lrrn1 are shown. The ICD of TRN is truncated at residue 535. Dashed lines represent gaps introduced by the alignment algorithm to produce an optimal alignment. Residues identical across two sequences are highlighted in black. Sequence positions are numbered on the left and right. *Dm* = *Drosophila melanogaster* (TRN =NP_524055; CAPS = NP_729880, Gg = *Gallus gallus*.). Red arrow indicates the position of a hypomorphic allele of CAPS (T501I) within a short motif (QKT) conserved between all three proteins.

Alignment was generated using the DNASTAR software module MegAlign