

Table S3. Results of GARD analysis.

| domain | search nr sites | c-AIC BP0 | c-AIC BP1 | delta c-AIC | position | lnL      |
|--------|-----------------|-----------|-----------|-------------|----------|----------|
| B30.2  | 2               | 15941.80  | 15898.9   | 42.96       | 285      | -7874,11 |
|        | 20              | 15870.80  | 15842.1   | 28.67       | 285      | -7819,98 |
| RBB    | 2               | 17847.00  | 17592.3   | 254.63      | 236      | -8773,79 |
|        | 20              | 17808.60  | 17545.4   | 263.22      | 236      | -8732,86 |

The c-AIC, Akaike`s information criterium indicates which model fits the data best.

The positions of detected breakage points correspond with the nucleotide position in the alignment that we used for the GARD analysis. They correspond with the Valine<sub>484</sub> of zebrafish finTRIM13 in the B30.2 domain and Glycine<sub>107</sub> in the RBB domain