## Additional file 3: Figure S2.

| RCC1 Repeat | From | To | Fragment |
|---|---|---|---|
| RCC1-Rep_1 | 317 | 355 | LSSVYAWGGGLSIPLRLPMMPNTEVVQVAAGRTQKAGVTR |
| Non_Canonical_2 | 357 | 414 | GRLILWEAPPLGTGGGTLLPGAVELPQPQFVSRFLEGQSGVTIKHVACGDLFTACLTD |
| RCC1-Rep_3 | 415 | 466 | RGIIMTFGSGSNGCLGHGSLTDISQPTIVEALLGYEMVQVACGASHVLALSA |
| RCC1_Rep_4 | 467 | 518 | DGELFAWGRGDGGRLGLGTRESHNCPQQVPMVPGQEAQRVVCGIDCSMILTS |
| RCC1_Rep_5 | 520 | 571 | GRVLACGSNRFNKLGLDCLSLEEEPVPHPQQVEEALSFTPLGSAPLDRETLLC |
| RCC1_Rep_6 | 585 | 636 | SGACYTFGSNQHGQLGTSSRRVSRAPCRVQGLEGIKMVMVACGDAFTVAIGA |
| RCC1_Rep_7 | 638 | 689 | GEVYSWGKGARGRLGRRDEDAGLPRPVQLDETHPYTVTSVSCCHGNTLLAVR |

### RCC1 domains.

Figure illustrates predicted RCC1 domains as defined by the web based program REP (RCC1 repeat, left column) and their alignment around the RCC1 motif (red text), which was used as the basis for three dimensional protein folding predictions. Amino acid positions in the protein are indicated as starting (from) and end (to) positions based on the rat sequence (NP_001099274). Orange bold text highlights the G[QRC]LG motifs, and are also conserved amino acids. An additional RCC1-like repeat domain was annotated as a non-canonical domain as it did not contain the typical repeat motif. Bold green text with box indicates position of the known mutations in Nek8 from human (RCC1-Rep-1,(P), Rcc1-Rep-3 (H) and RCC1-4 (A) ) and mouse (RCC1-Rep-3 (G*), jck* and the red square highlight the R650C Nek8 LPK mutation (RCC1-Rep-7 (R).

### References


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