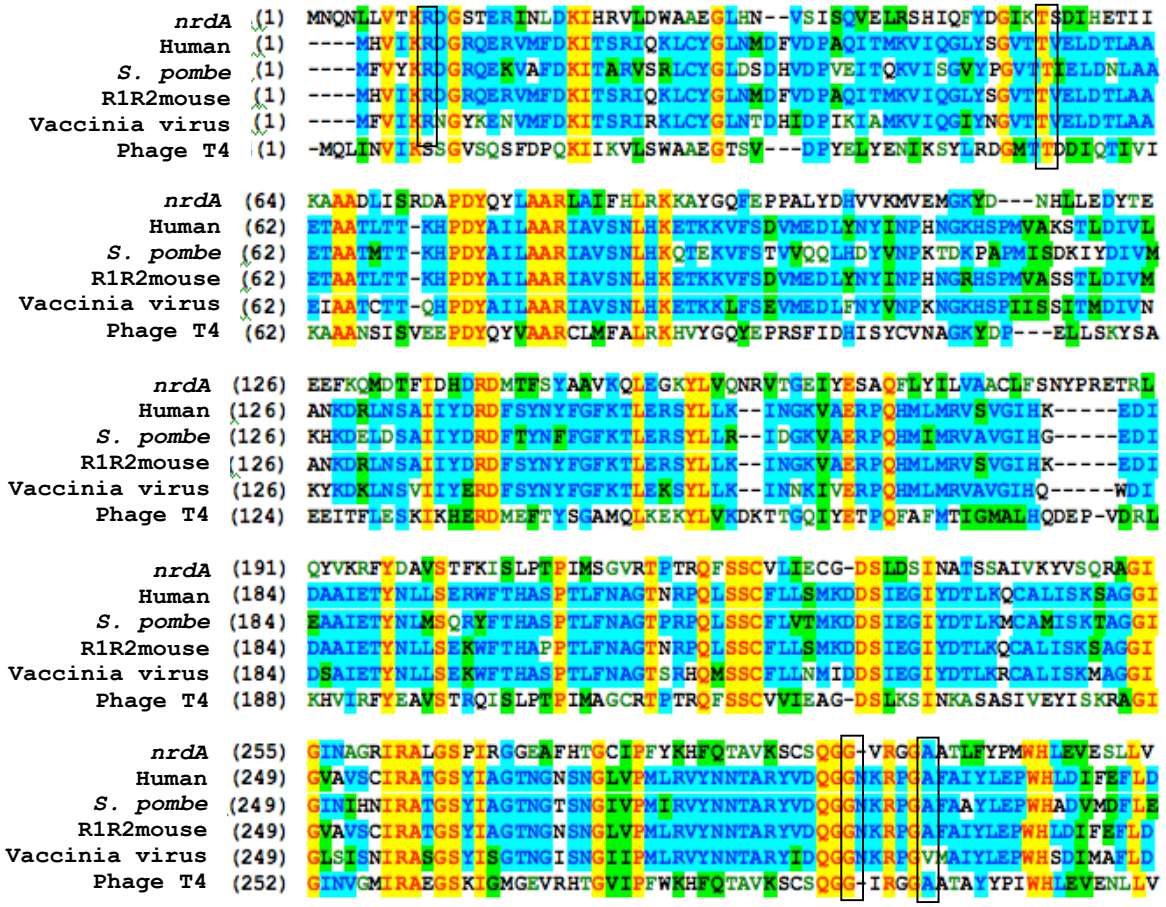
A.


nrdA (1) MNQNLLVTKRDGSTERINLDKIHRVLDWAAEGLHN--VSISQVELRSHIQFYDGIKTSDIHETII
Human (1) ----MHVIKRDGRQERVMFDKITSRIQKLCYGLNMDFVDPAQITMKVIQGLYSGVTTVELDTLAA
S. pombe (1) ----MFVYKRDGRQEKVAFDKITARVSRLCYGLDSDHVDPVEITQKVISGVYPGVTTIELDNLAA
R1R2mouse (1) ----MHVIKRDGRQERVMFDKITSRIQKLCYGLNMDFVDPAQITMKVIQGLYSGVTTVELDTLAA
Vaccinia virus (1) ----MFVIKRNGYKENVMFDKITSRIRKLCYGLNTDHIDPIKIAMKVIQGIYNGVTTVELDTLAA
Phage T4 (1) -MQLINVIKSSGVSQSFDPQKIIKVLSWAAEGTSV---DPYELYENIKSYLRDGMTTDDIQTIVI
nrdA (64) KAAADLISRDAPDYQYLAARLAIFHLRKKAYGQFEPPALYDHVVKMVEMGKYD---NHLLEDYTE
Human (62) ETAATLTT-KHPDYAILAARIAVSNLHKETKKVFSDVMEDLYNYINPHNGKHSPMVAKSTLDIVL
S. pombe (62) ETAATMTT-KHPDYAILAARIAVSNLHKQTEKVFSTVVQQLHDYVNPKTDKPAPMISDKIYDIVM
R1R2mouse (62) ETAATLTT-KHPDYAILAARIAVSNLHKETKKVFSDVMEDLYNYINPHNGRHSPMVASSTLDIVM
Vaccinia virus (62) EIAATCTT-QHPDYAILAARIAVSNLHKETKKLFSEVMEDLFNYVNPKNGKHSPIISSITMDIVN
Phage T4 (62) KAAANSISVEEPDYQYVAARCLMFALRKHVYGQYEPRSFIDHISYCVNAGKYDP---ELLSKYSA
nrdA (126) EEFKQMDTFIDHDRDMTFSYAAVKQLEGKYLVQNRVTGEIYESAQFLYILVAACLFSNYPRETRL
Human (126) ANKDRLNSAIIYDRDFSYNYFGFKTLERSYLLK--INGKVAERPQHMLMRVSVGIHK-----EDI
S. pombe (126) KHKDELDSAIIYDRDFTYNFFGFKTLERSYLLR--IDGKVAERPQHMIMRVAVGIHG-----EDI
R1R2mouse (126) ANKDRLNSAIIYDRDFSYNYFGFKTLERSYLLK--INGKVAERPQHMLMRVSVGIHK-----EDI
Vaccinia virus (126) KYKDKLNSVIIYERDFSYNYFGFKTLEKSYLLK--INNKIVERPQHMLMRVAVGIHQ-----WDI
Phage T4 (124) EEITFLESKIKHERDMEFTYSGAMQLKEKYLVKDKTTGQIYETPQFAFMTIGMALHQDEP-VDRL
nrdA (191) QYVKRFYDAVSTFKISLPTPIMSGVRTPTRQFSSCVLIECG-DSLDSINATSSAIVKYVSQRAGI
Human (184) DAAIETYNLLSERWFTHASPTLFNAGTNRPQLSSCFLLSMKDDSIEGIYDTLKQCALISKSAGGI
S. pombe (184) EAAIETYNLMSQRYFTHASPTLFNAGTPRPQLSSCFLVTMKDDSIEGIYDTLKMCAMISKTAGGI
R1R2mouse (184) DAAIETYNLLSEKWFTHAPPTLFNAGTNRPQLSSCFLLSMKDDSIEGIYDTLKQCALISKSAGGI
Vaccinia virus (184) DSAIETYNLLSEKWFTHASPTLFNAGTSRHQMSSCFLLNMIDDSIEGIYDTLKRCALISKMAGGI
Phage T4 (188) KHVIRFYEAVSTRQISLPTPIMAGCRTPTRQFSSCVVIEAG-DSLKSINKASASIVEYISKRAGI
nrdA (255) GINAGRIRALGSPIRGGEAFHTGCIPFYKHFQTAVKSCSQGG-VRGGAATLFYPMWHLEVESLLV
Human (249) GVAVSCIRATGSYIAGTNGNSNGLVPMLRVYNNTARYVDQGGNKRPGAFAIYLEPWHLDIFEFLD
S. pombe (249) GINIHNIRATGSYIAGTNGTSNGIVPMIRVYNNTARYVDQGGNKRPGAFAAYLEPWHADVMDFLE
R1R2mouse (249) GVAVSCIRATGSYIAGTNGNSNGLVPMLRVYNNTARYVDQGGNKRPGAFAIYLEPWHLDIFEFLD
Vaccinia virus (249) GLSISNIRASGSYISGTNGISNGIIPMLRVYNNTARYIDQGGNKRPGVMAIYLEPWHSDIMAFLD
Phage T4 (252) GINVGMIRAEGSKIGMGEVRHTGVIPFWKHFQTAVKSCSQGG-IRGGAATAYYPIWHLEVENLLV

B.

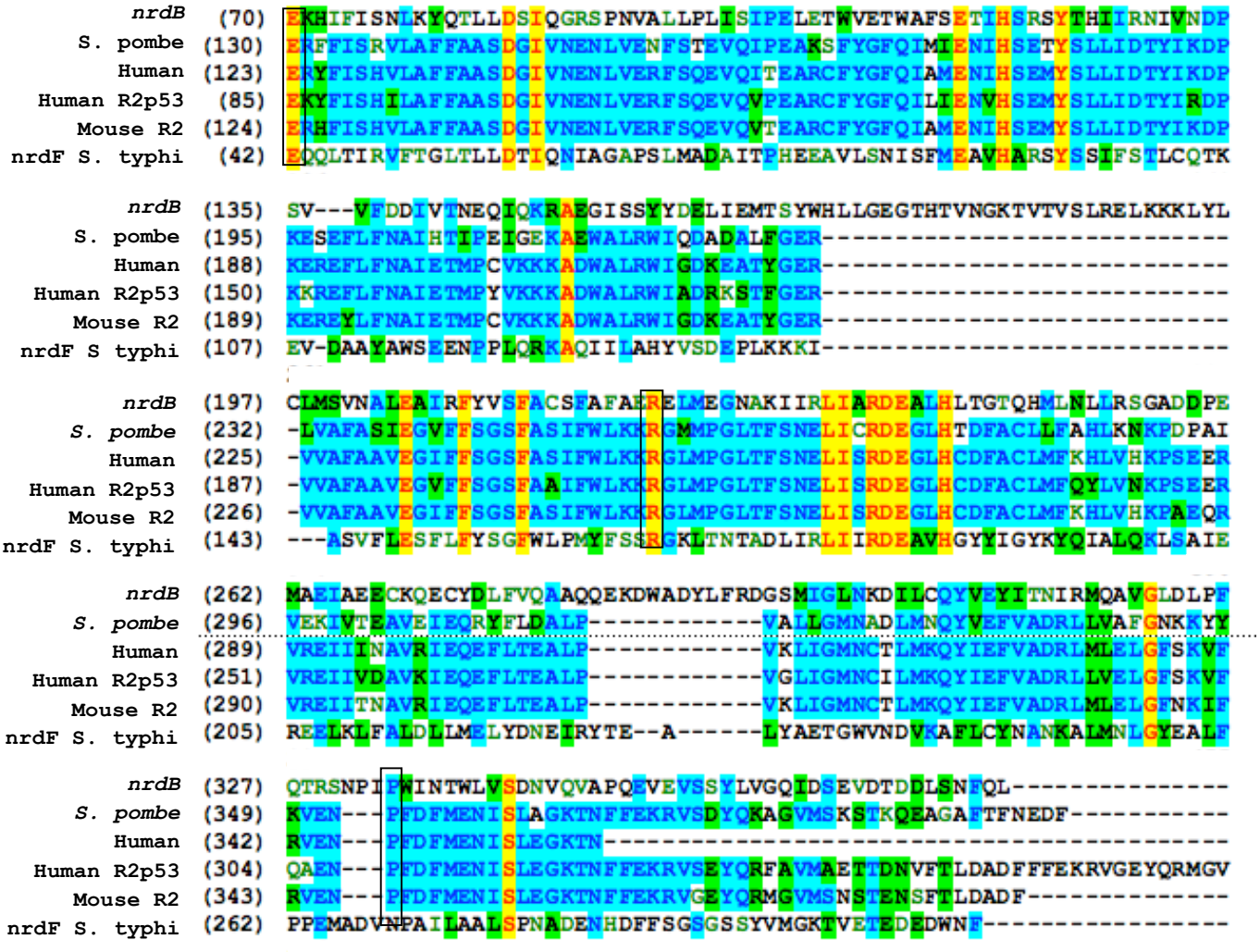


Figure S1. Alignment of RNR R1 (A) and R2 (B) sequences from different species. Different colors indicate different degrees of conservation. Rectangles indicate the residues that were found to yield mutator phenotype when altered. Sequences were obtained from GenBank (NCBI) and alignments were generated using the program VectorNTI (Invitrogen). *nrdA* and *nrdB* represent the *E. coli* ribonucleotide reductase gene.