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Supporting information for article:

The use of local structural similarity of distant homologues for crystallographic model building from a molecular-replacement solution

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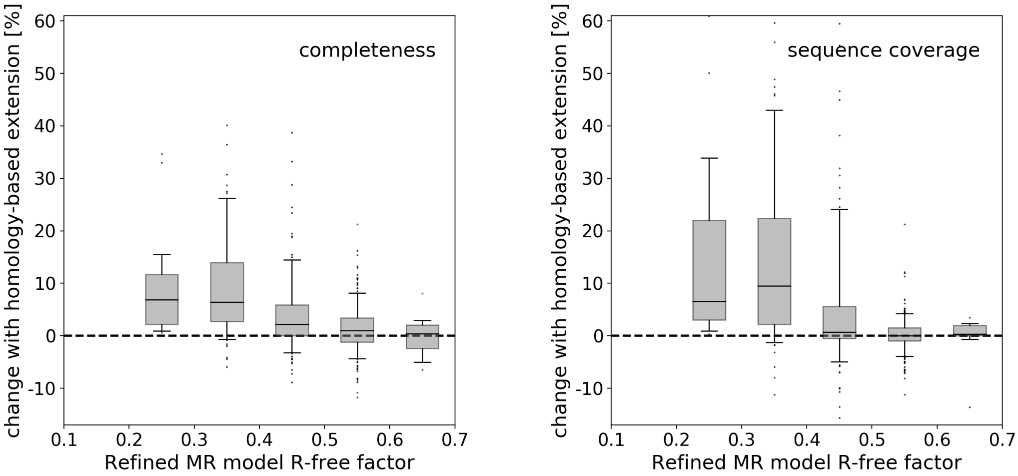
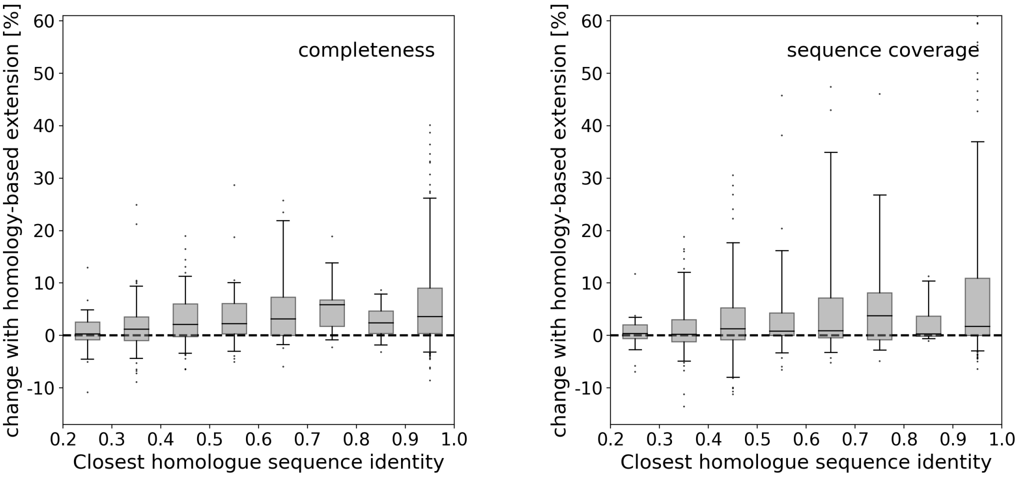


a) *b)*

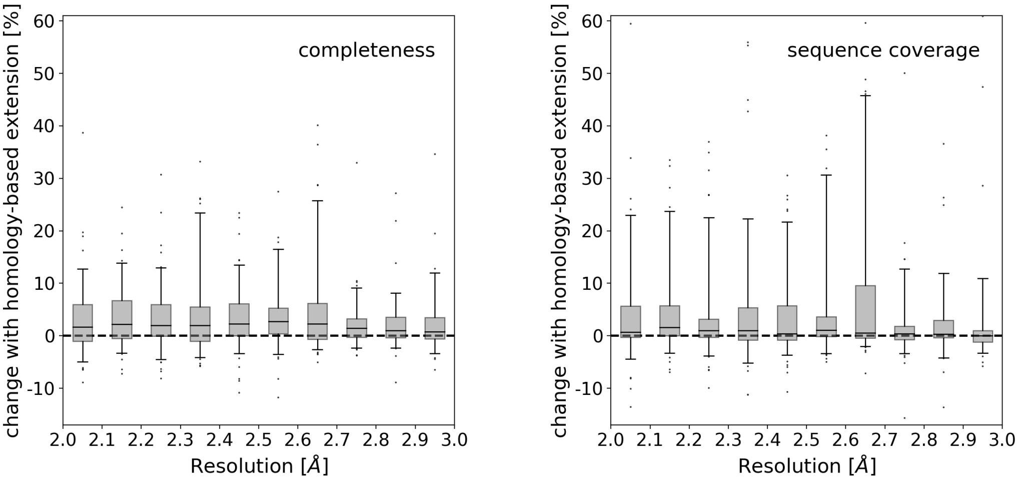
Figure S1 The improvement in model building for test set II at a resolution between 2 and 3 Å as a function of refined MR model R-free factor. a) the fraction of residues built; b) sequence coverage. Box plot whiskers correspond to the 5th and 95th percentile.



a)

b)

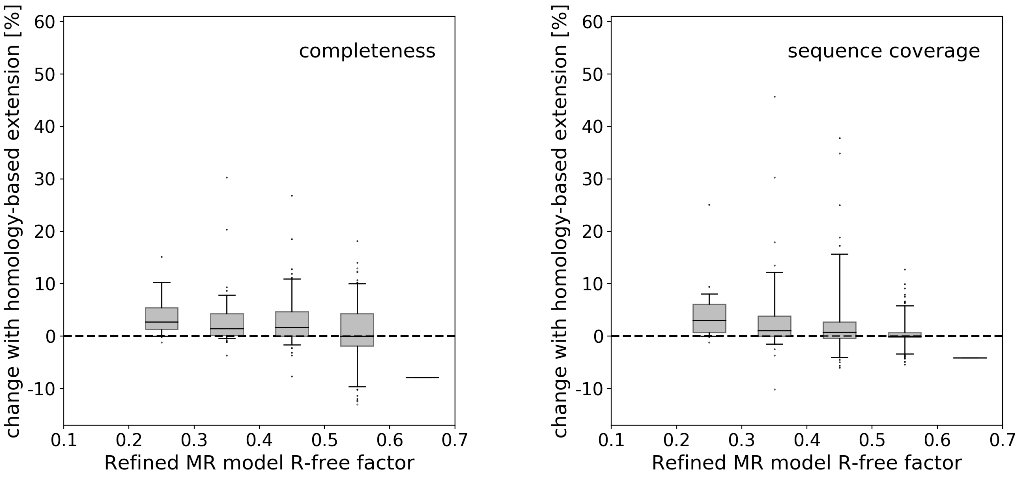
Figure S2 The improvement in model building for test set II at a resolution between 2 and 3 Å as a function of sequence identity to a closest homologue used for model extension. a) the fraction of residues built; b) sequence coverage. Box plot whiskers correspond to the 5th and 95th percentile.



a)

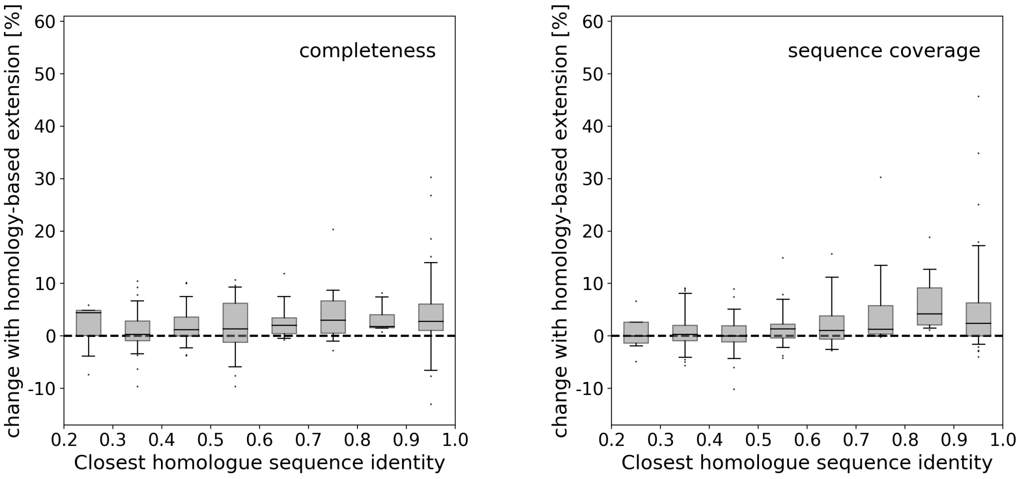
b)

Figure S3 The improvement in model building for test set II at a resolution between 2 and 3 Å as a function of resolution. a) the fraction of residues built; b) sequence coverage. Box plot whiskers correspond to the 5th and 95th percentile.



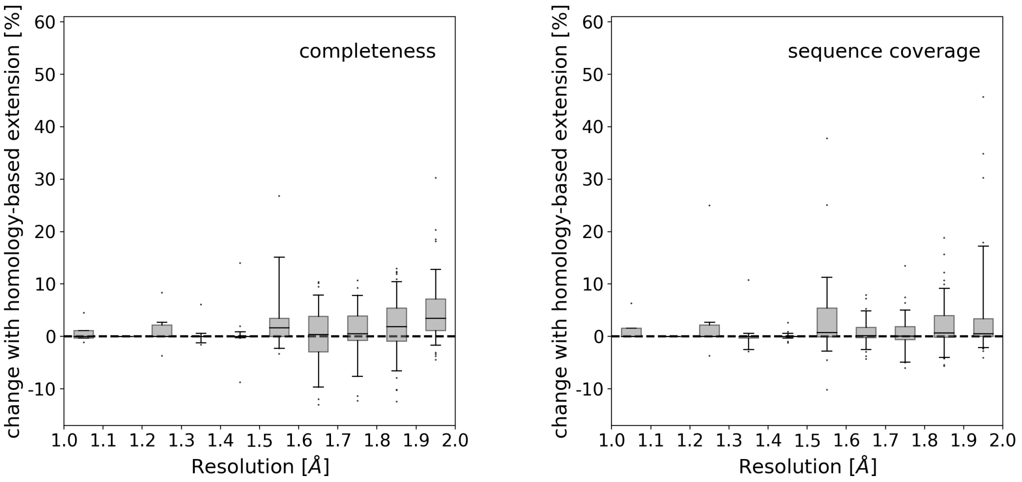
a) *b)*

Figure S4 The improvement in model building for test set II at a resolution between 1 and 2 Å as a function of refined MR model R-free factor. a) the fraction of residues built; b) sequence coverage. Box plot whiskers correspond to the 5th and 95th percentile.



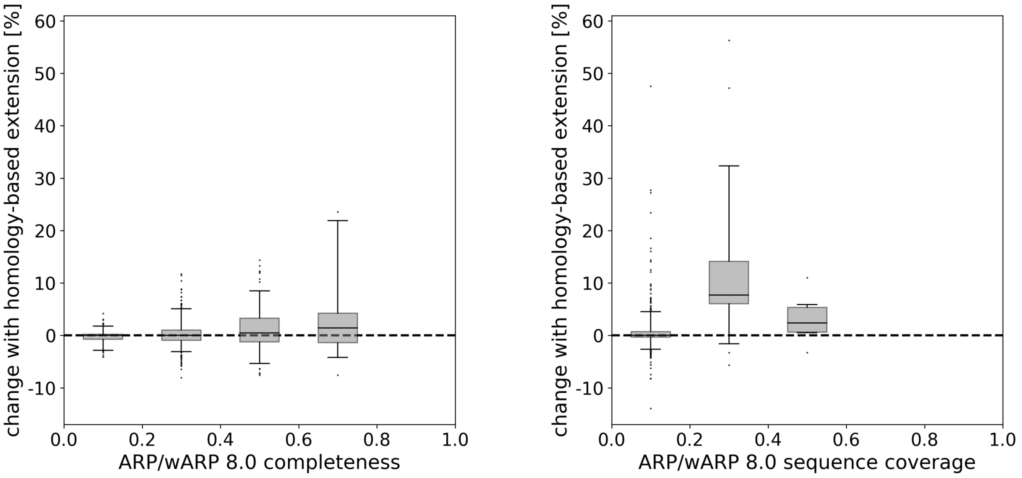
a) *b)*

Figure S5 The improvement in model building for test set II at a resolution between 1 and 2 Å as a function of of sequence identity to a closest homologue used for model extension. a) the fraction of residues built; b) sequence coverage. Box plot whiskers correspond to the 5th and 95th percentile.



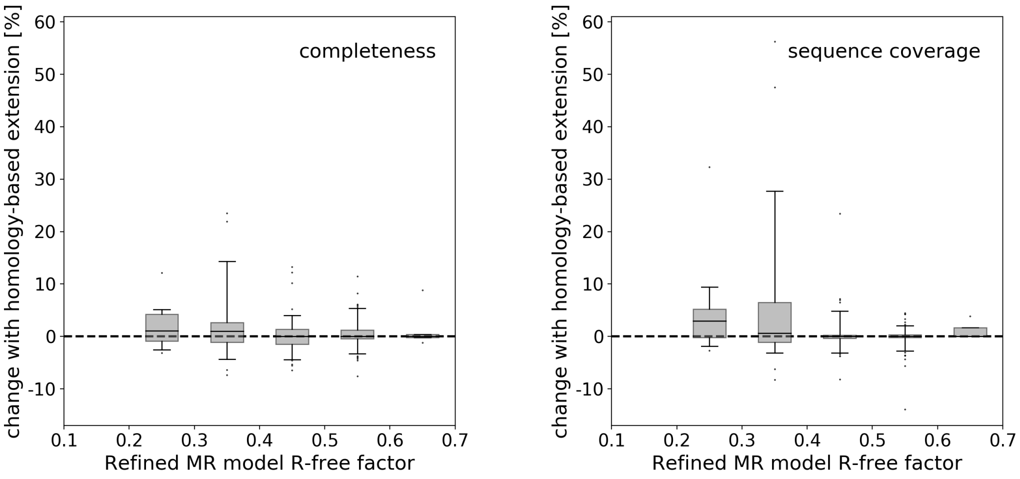
a) *b)*

Figure S6 The improvement in model building for test set II at a resolution between 1 and 2 Å as a function of resolution. a) the fraction of residues built; b) sequence coverage. Box plot whiskers correspond to the 5th and 95th percentile.



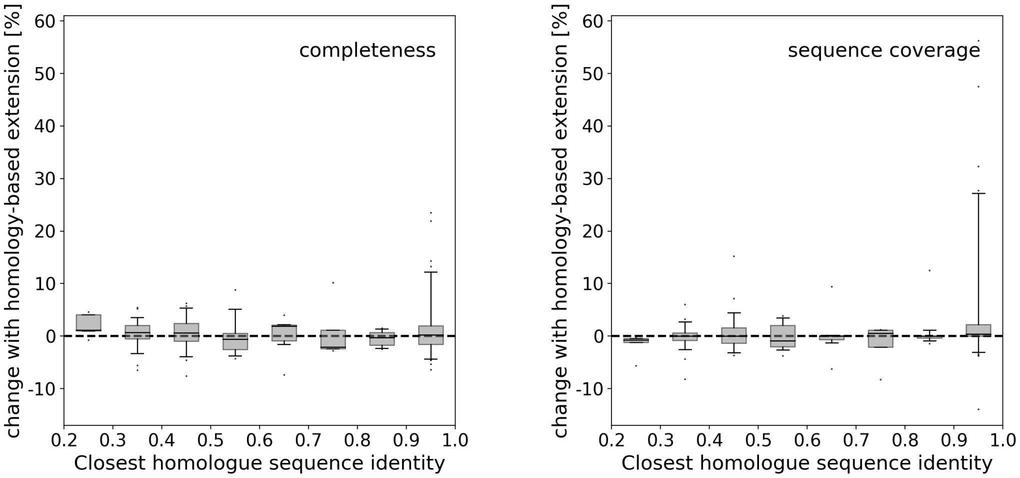
a) *b)*

Figure S7 The improvement in model building for test set II at a resolution between 3 and 4 Å as a function of a) model completeness and b) sequence coverage. Box plot whiskers correspond to the 5th and 95th percentile.



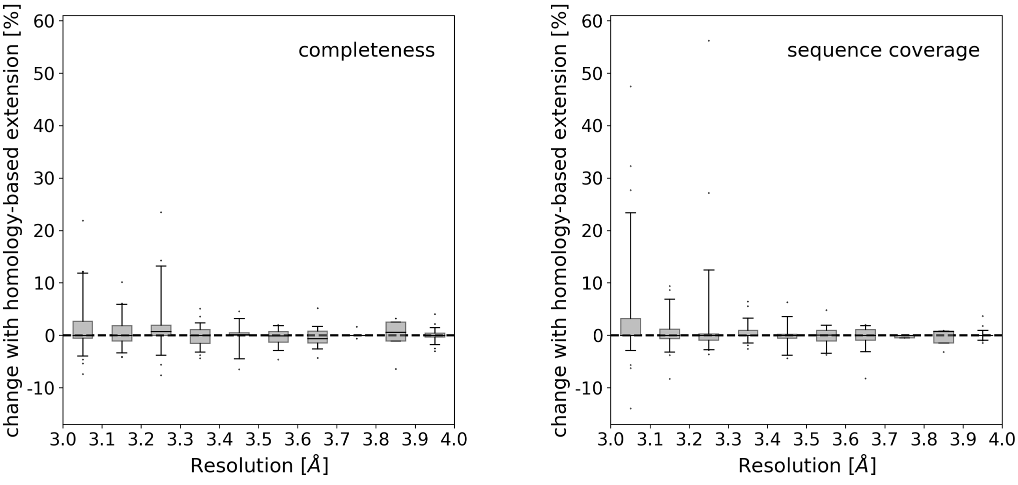
a) *b)*

Figure S8 The improvement in model building for test set II at a resolution between 3 and 4 Å as a function of refined MR model R-free factor. a) the fraction of residues built; b) sequence coverage. Box plot whiskers correspond to the 5th and 95th percentile.



a) *b)*

Figure S9 The improvement in model building for test set II at a resolution between 3 and 4 Å as a function of of sequence identity to a closest homologue used for model extension. a) the fraction of residues built; b) sequence coverage. Box plot whiskers correspond to the 5th and 95th percentile.



a) *b)*

Figure S10 The improvement in model building for test set II at a resolution between 3 and 4 Å as a function of resolution. a) the fraction of residues built; b) sequence coverage. Box plot whiskers correspond to the 5th and 95th percentile.