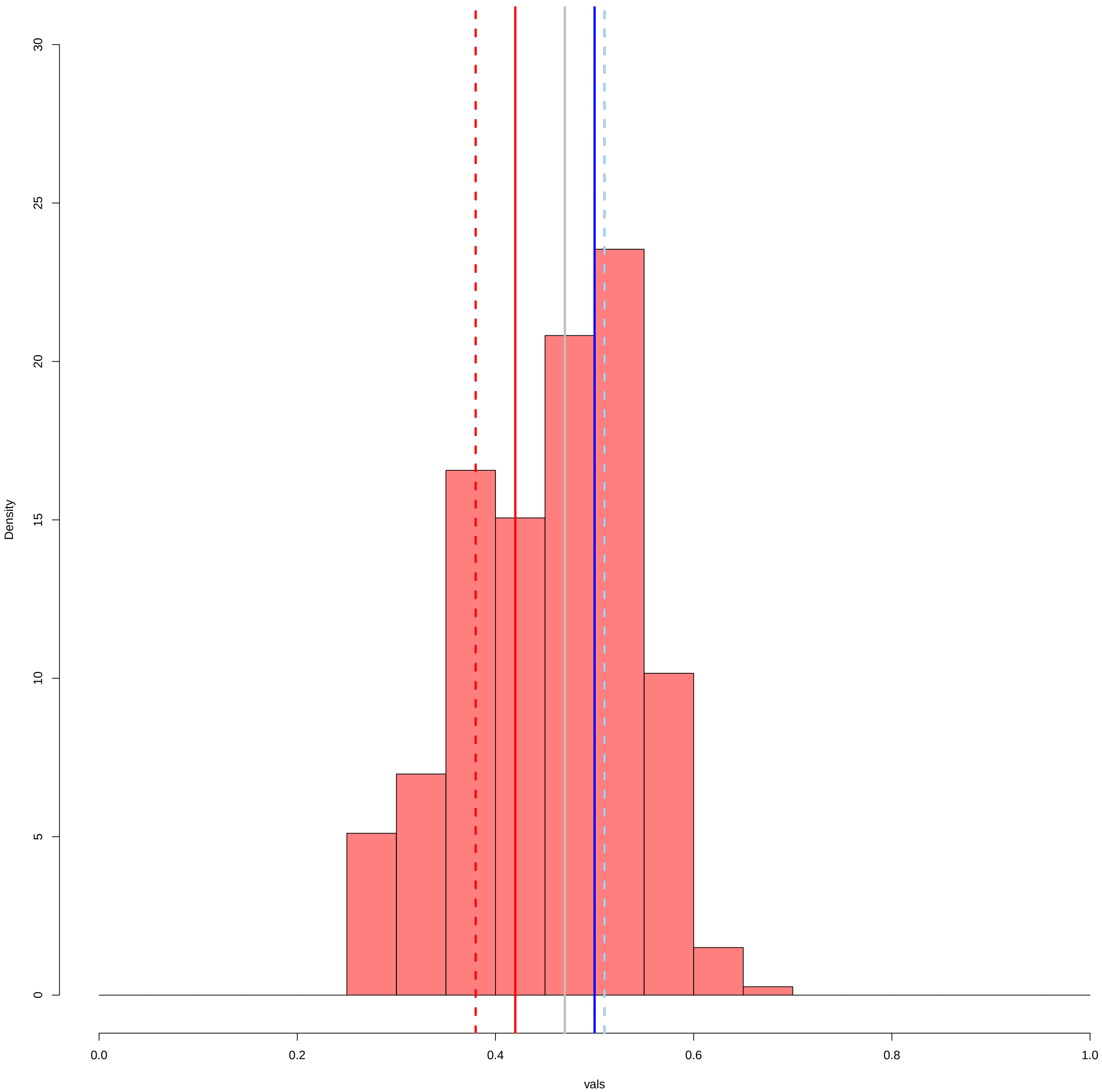
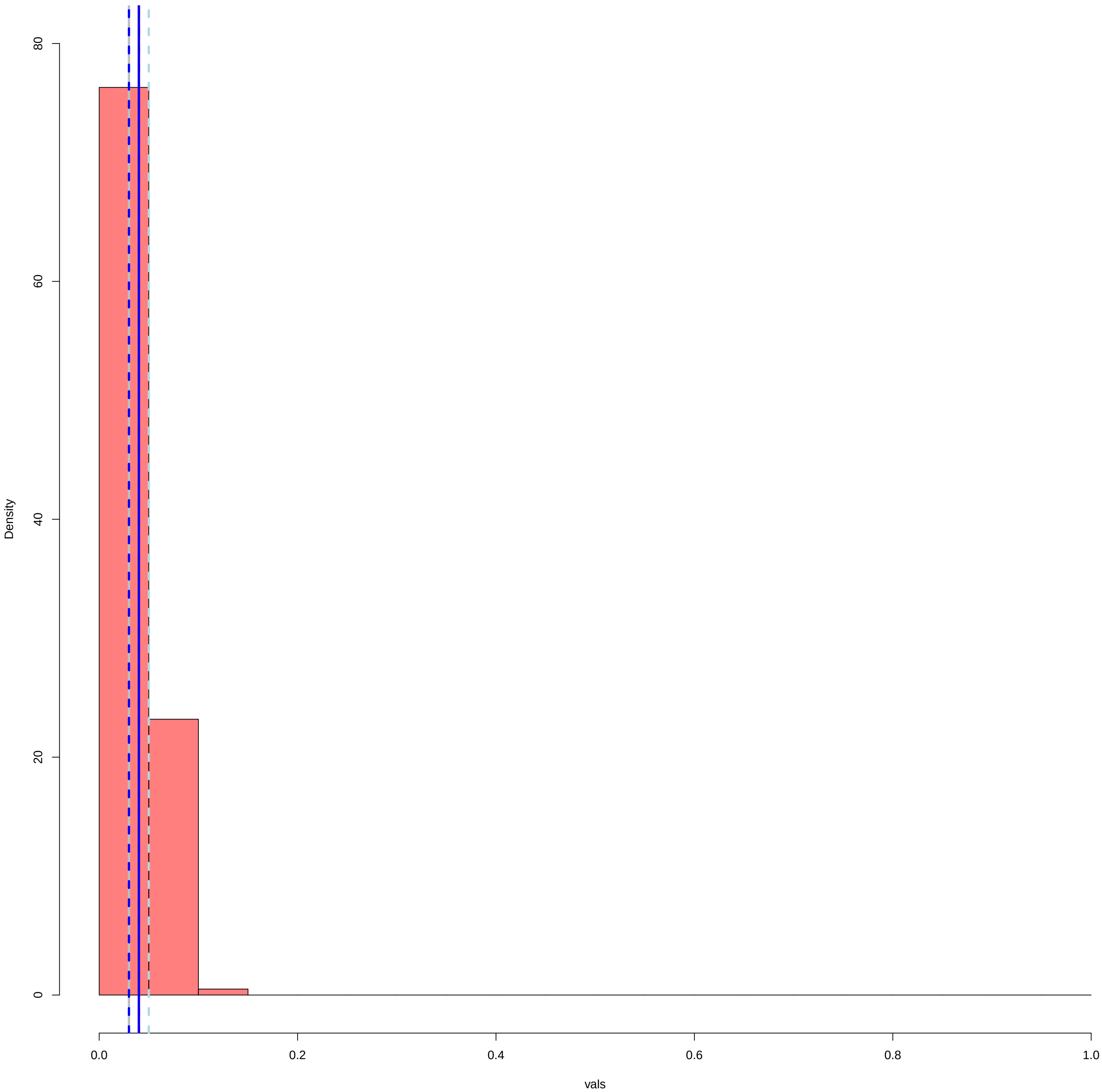


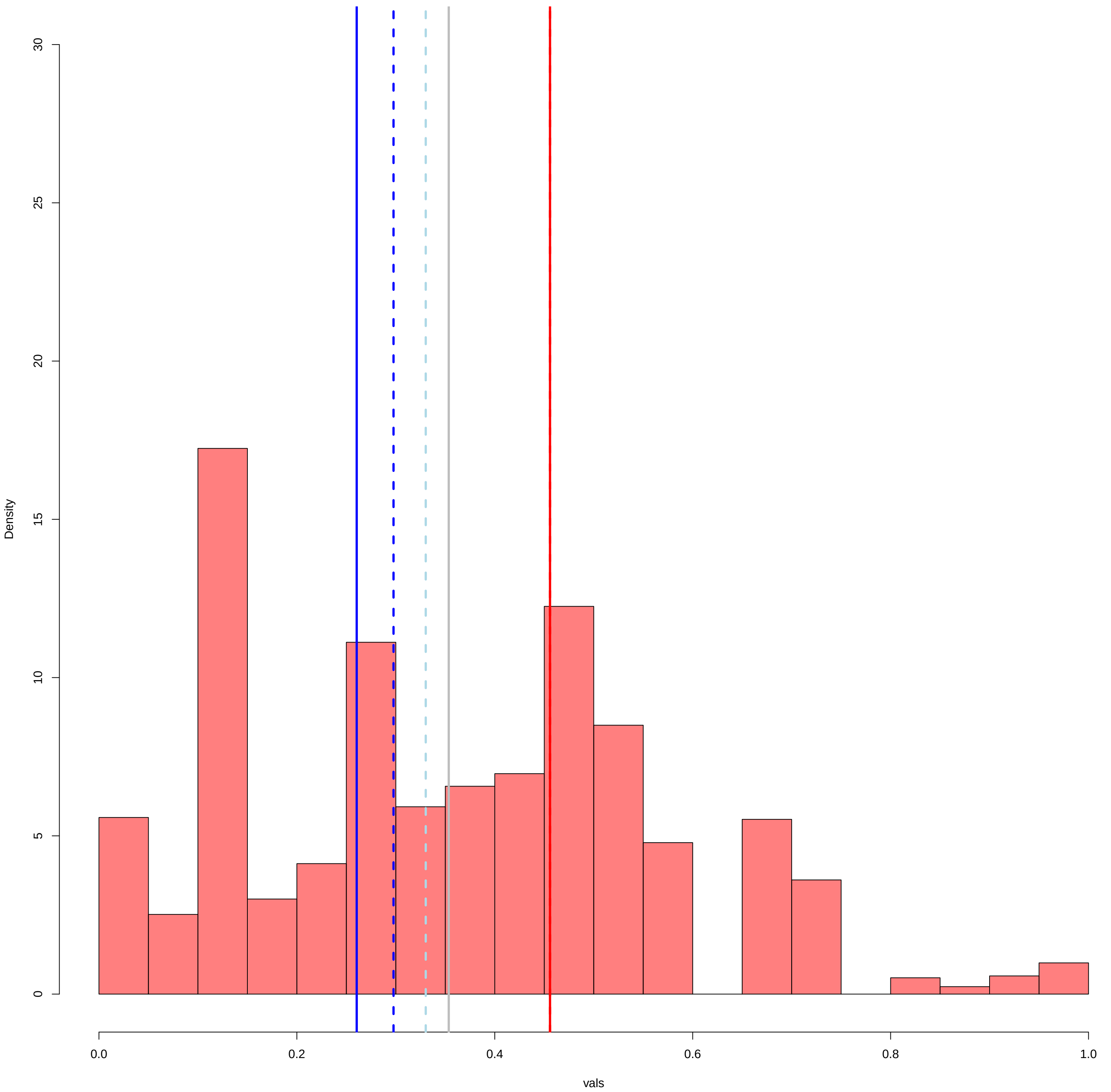
CDKL5: GC (Percent GC content in a window of +/-75bp)



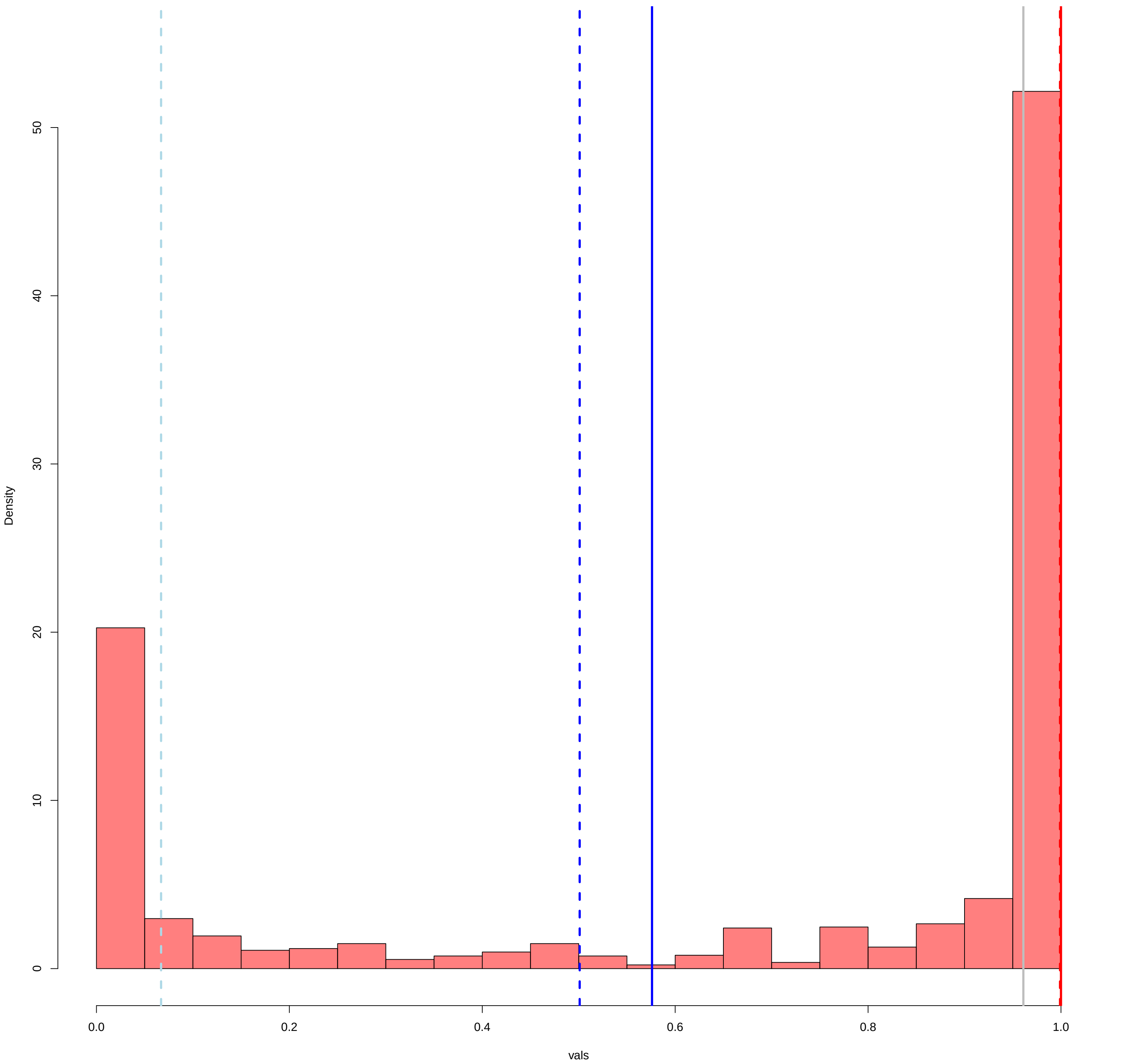
CDKL5: CpG (Percent CpG in a window of +/-75bp)



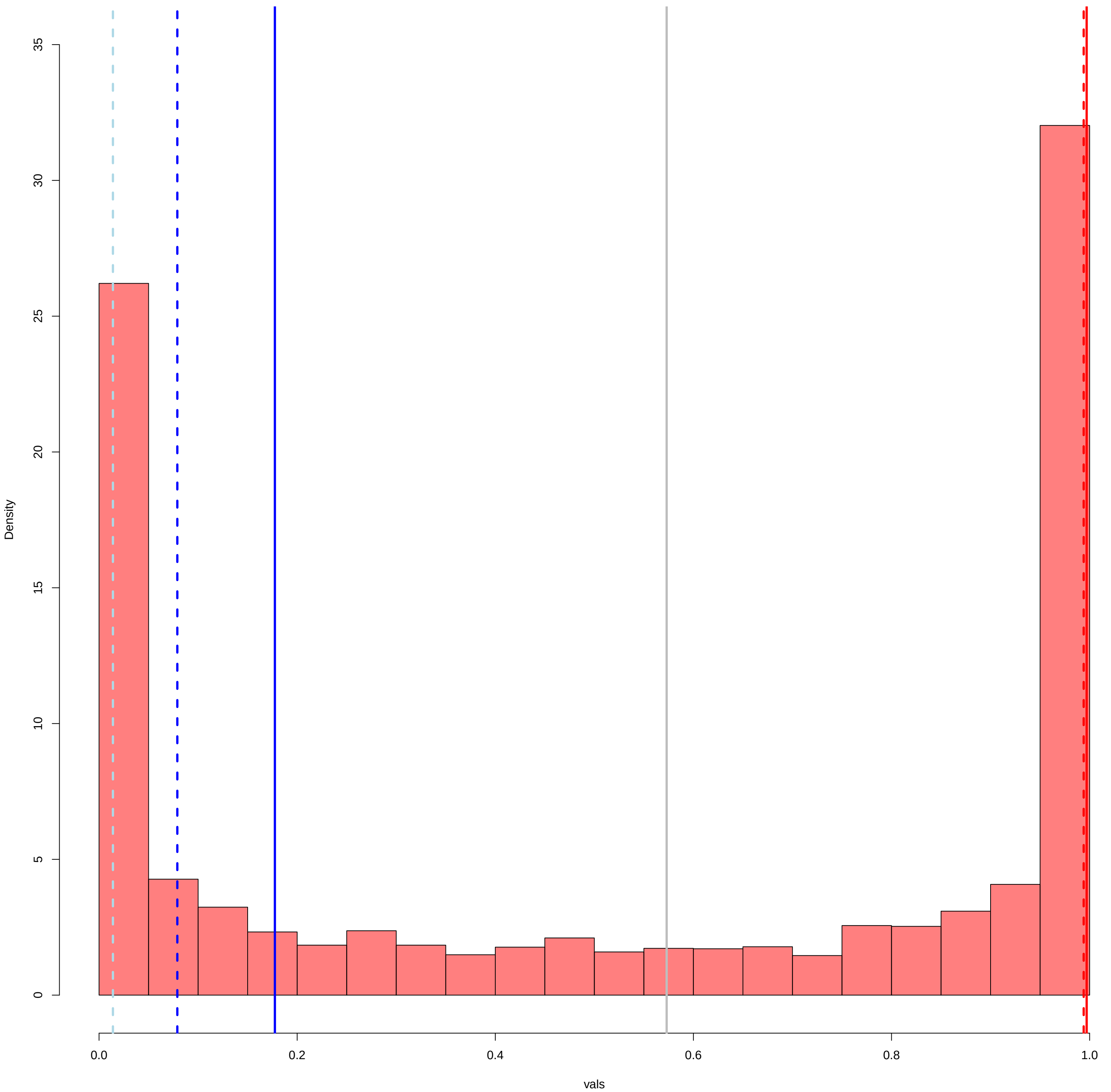
CDKL5: Grantham



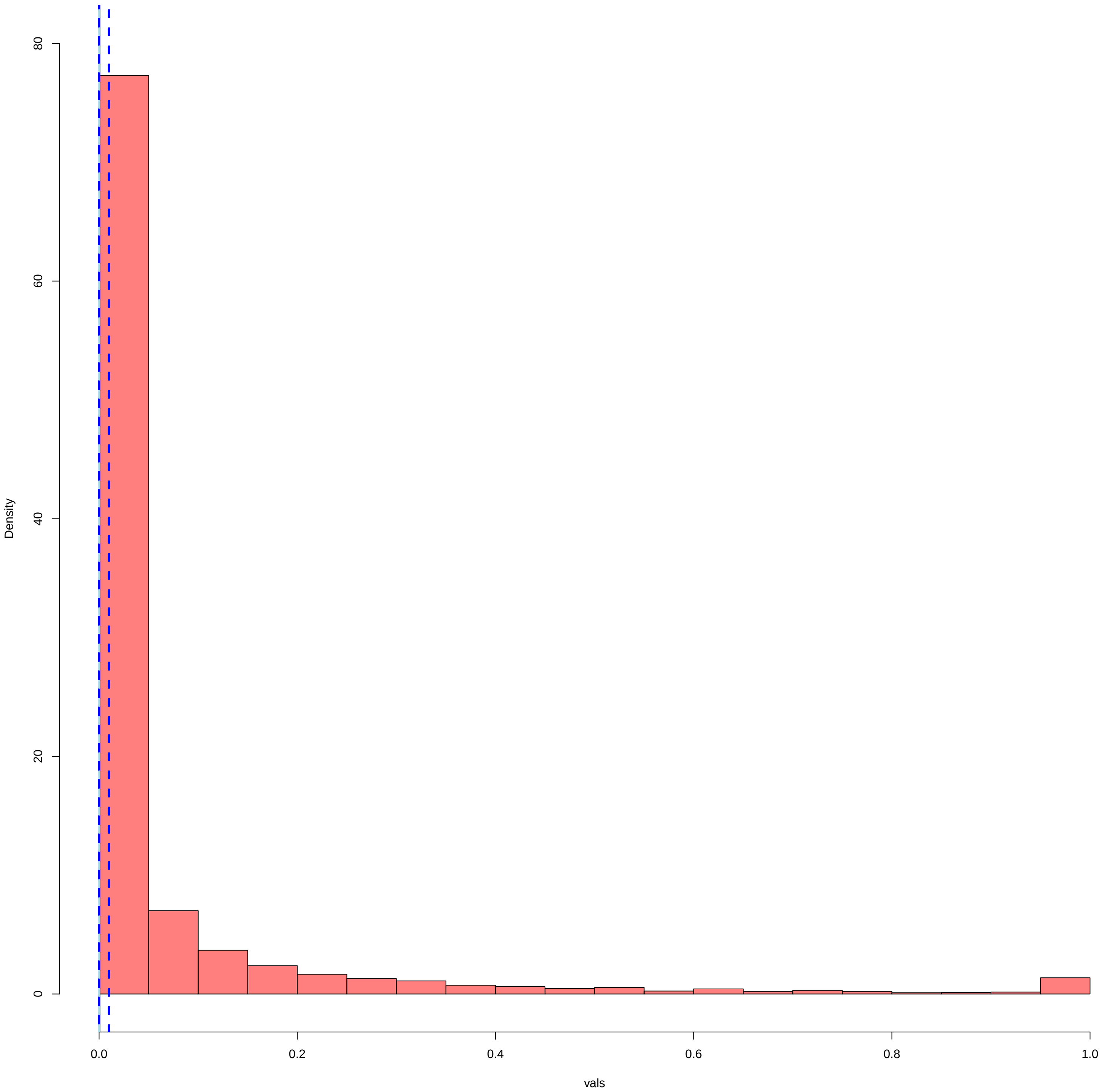
CDKL5: Hdiv quan



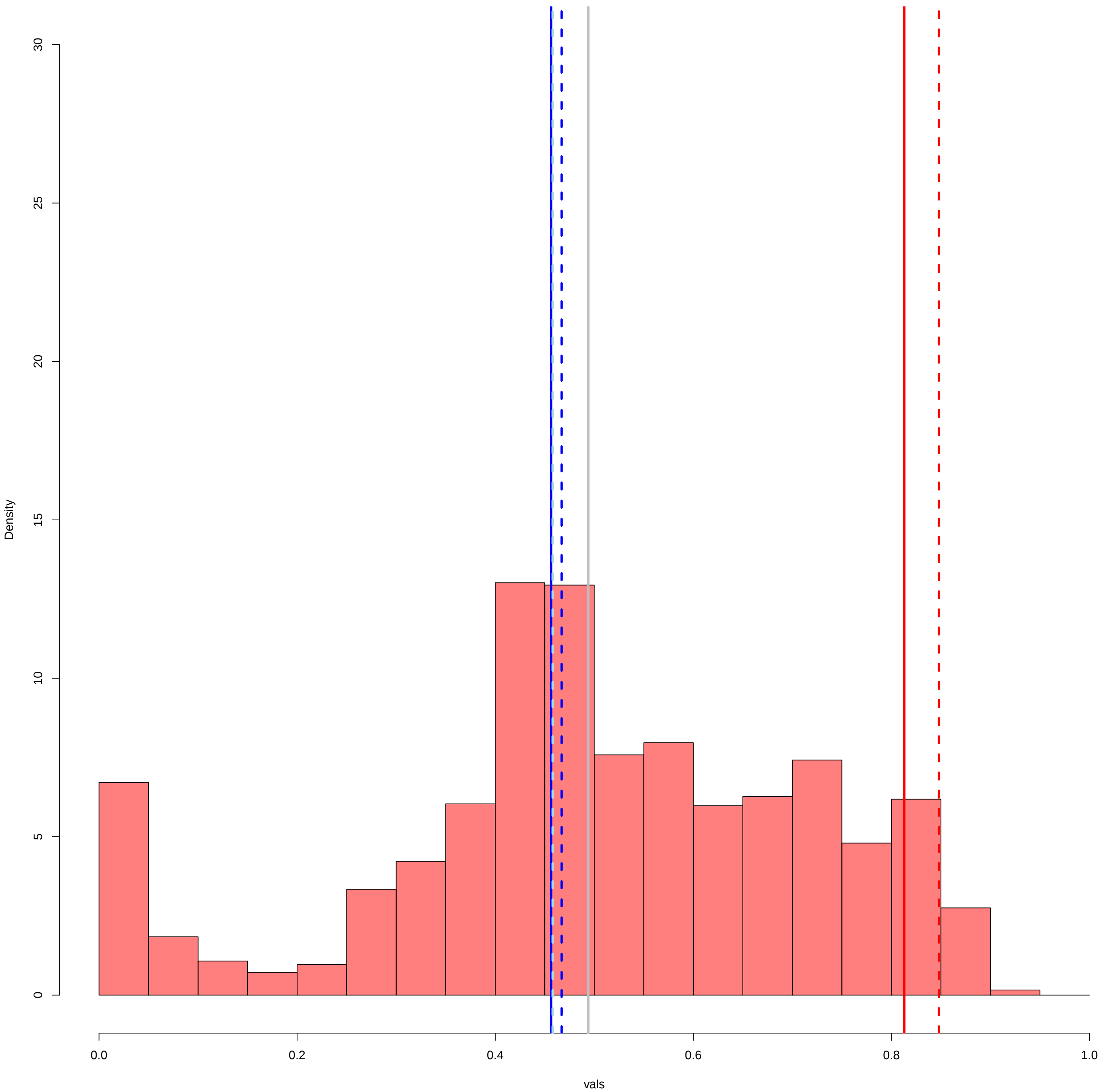
CDKL5: Hvar quan



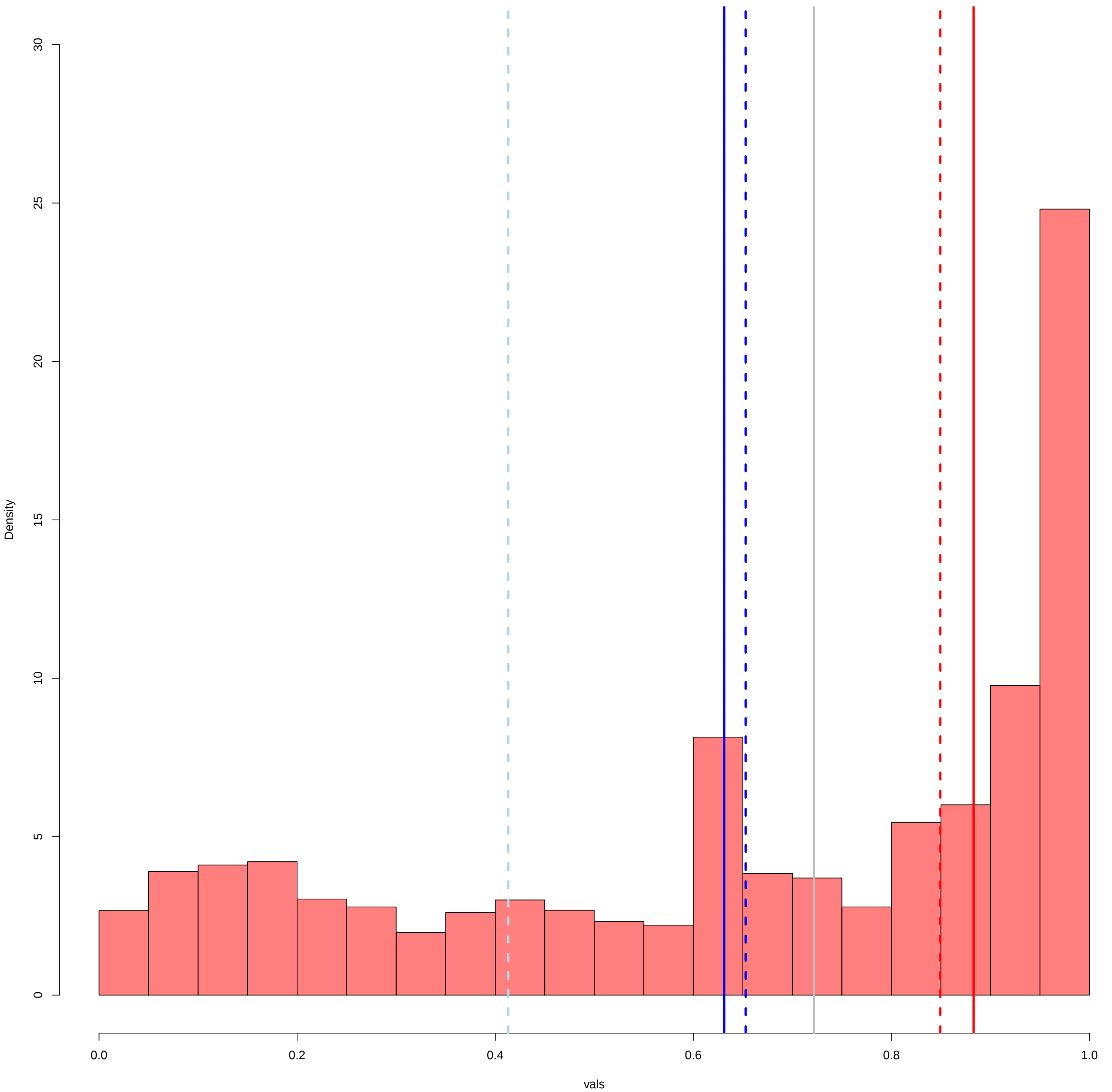
CDKL5: SIFT



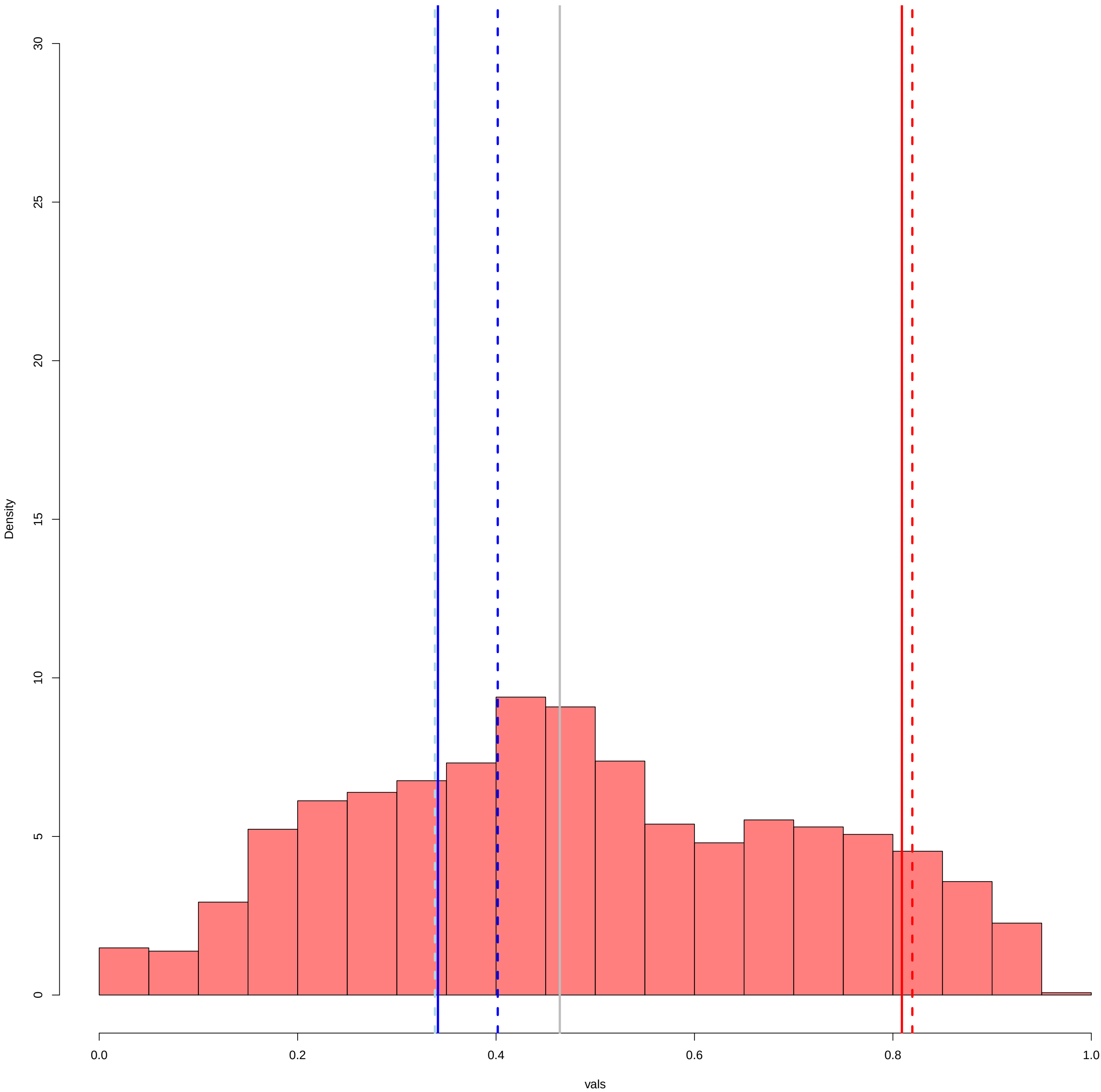
CDKL5: Condel



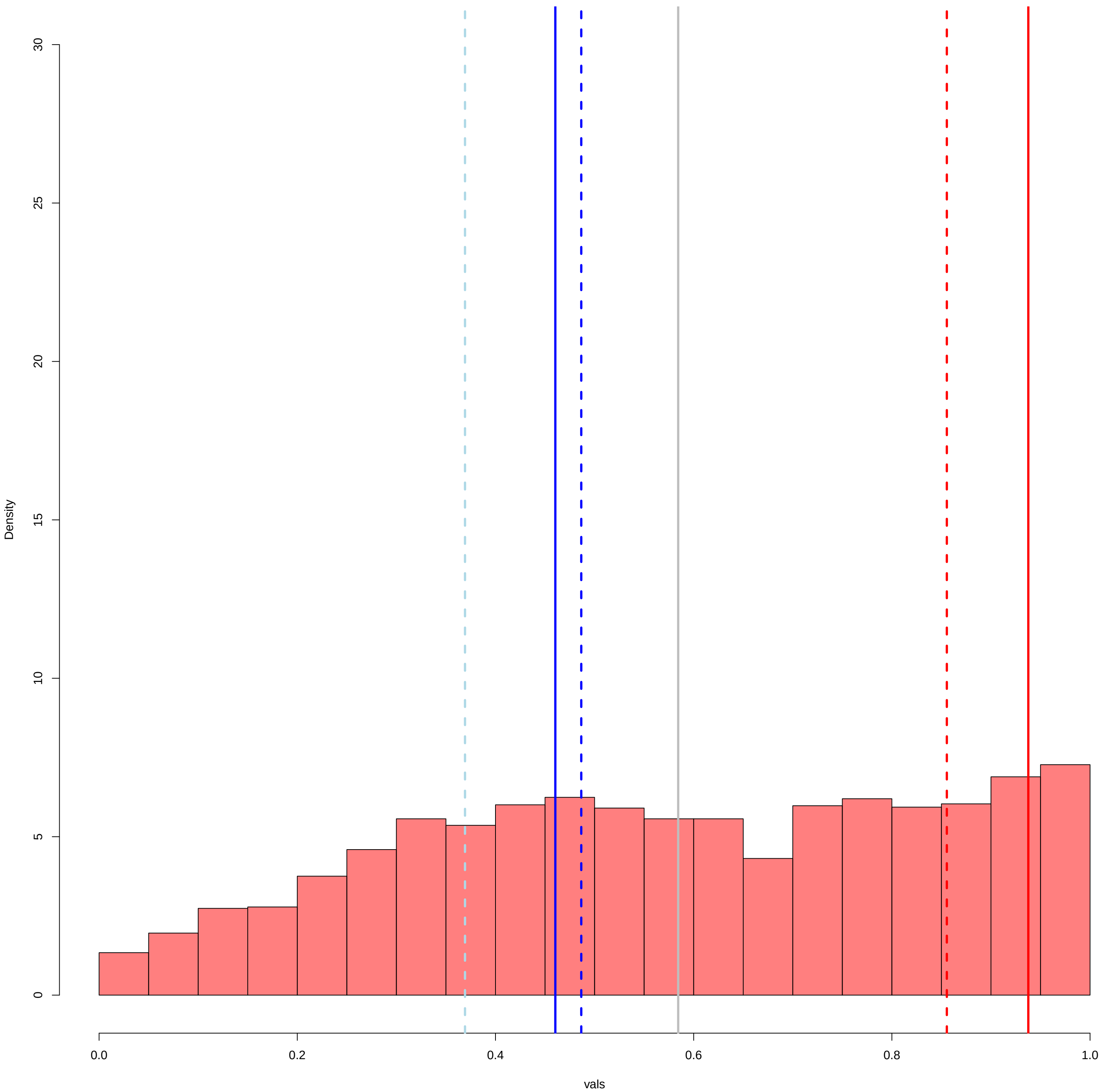
CDKL5: GERP++_RS_rankscore



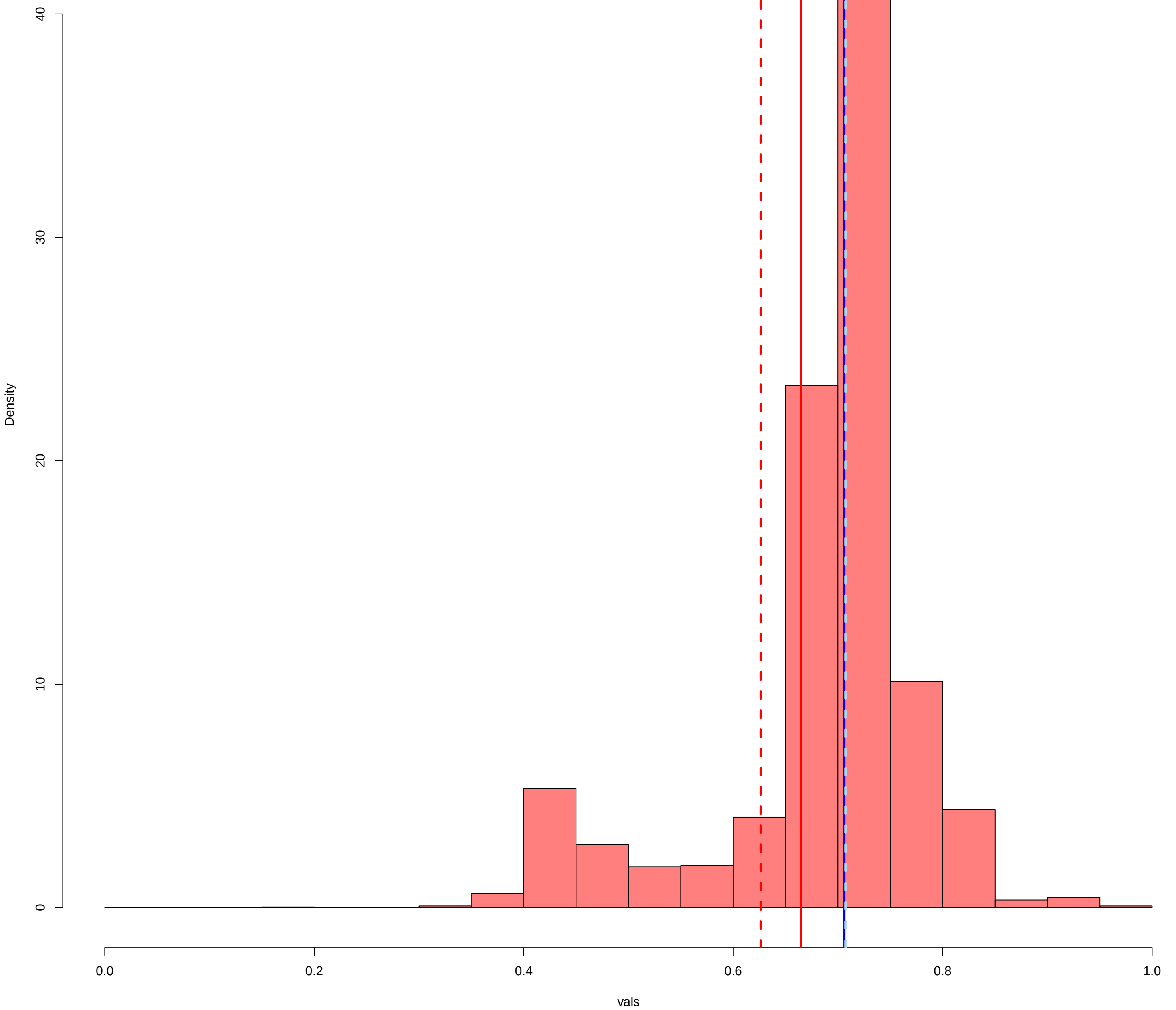
CDKL5: CADD_raw_rankscore



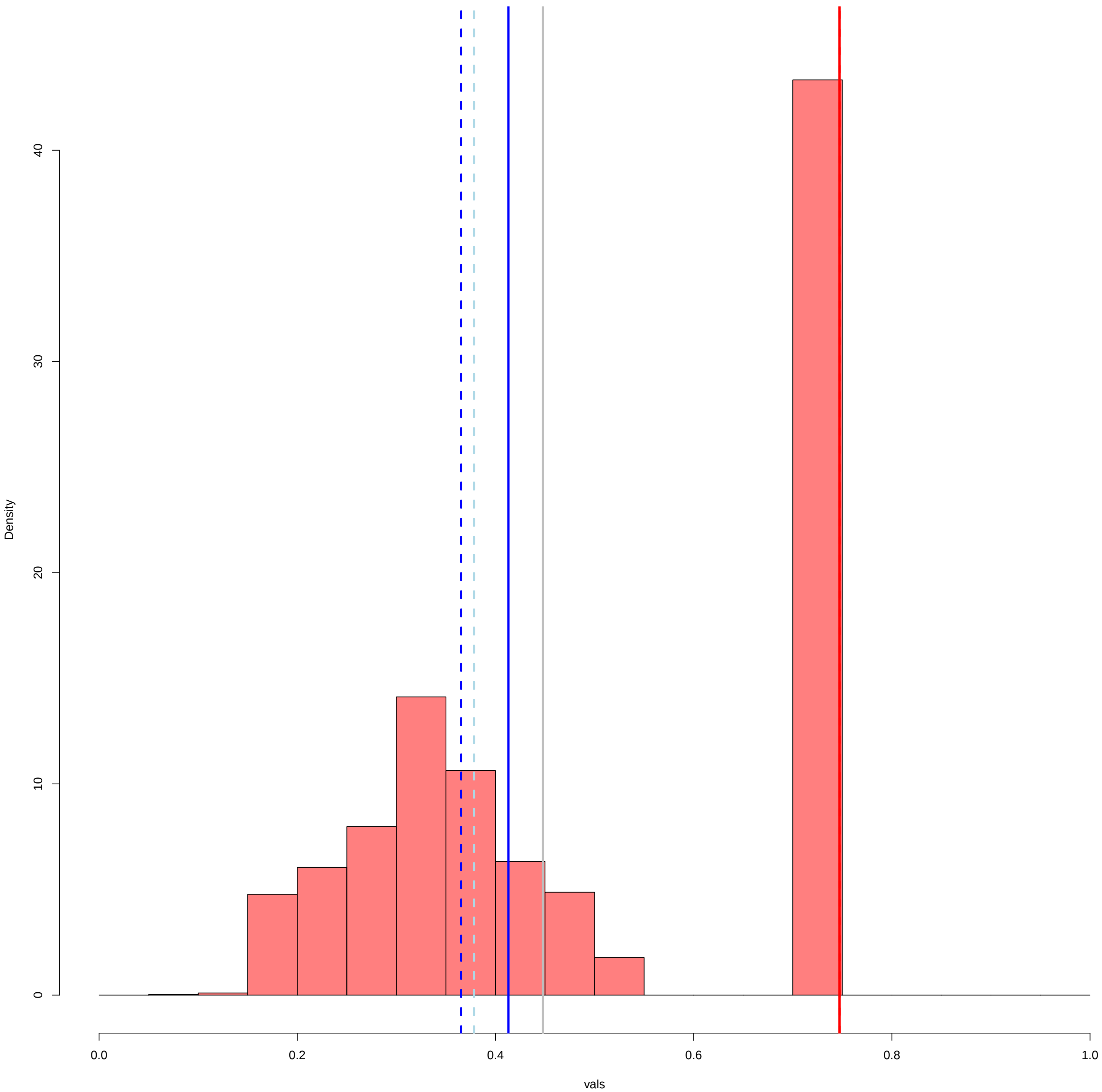
CDKL5: DANN_rankscore



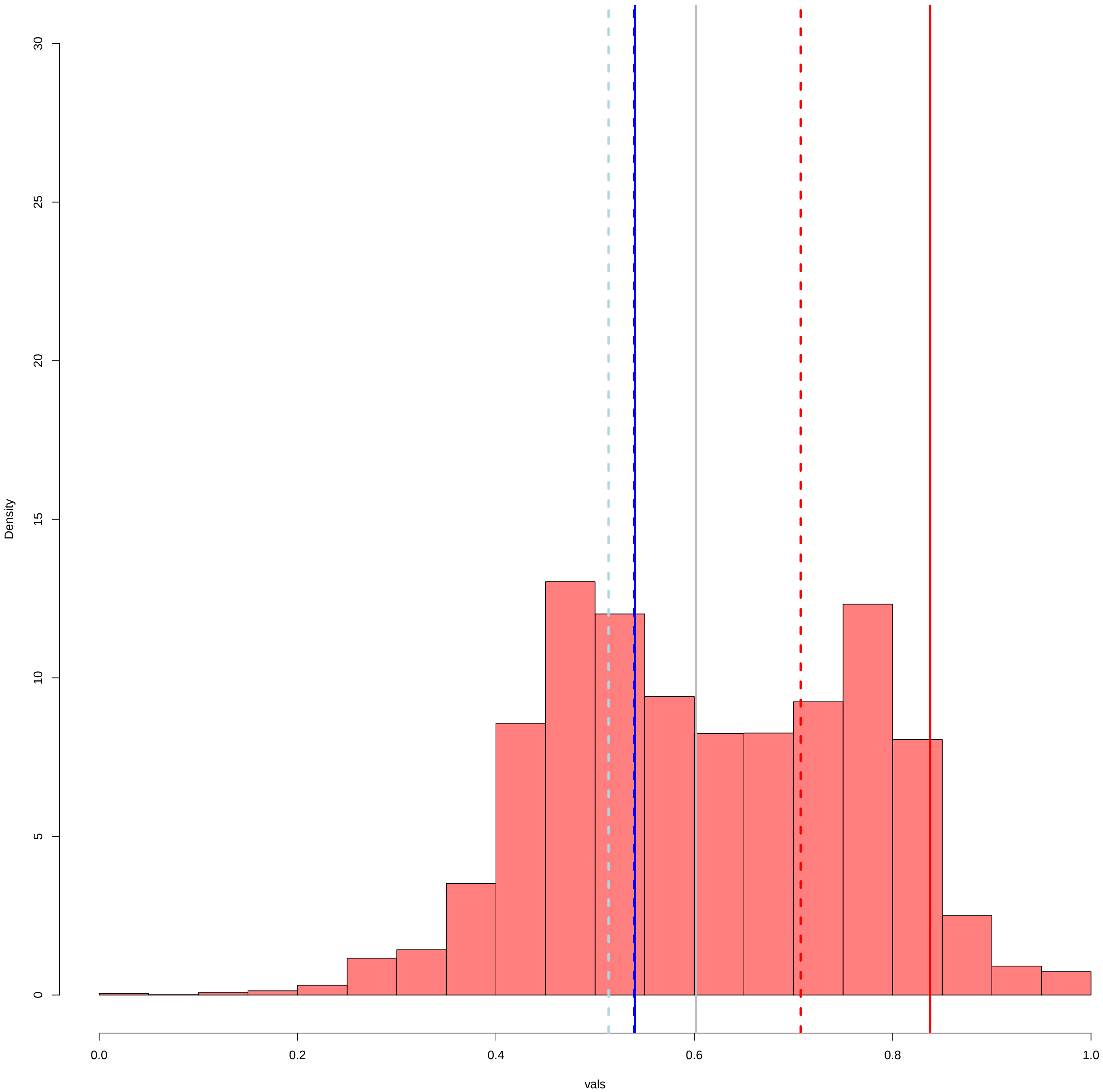
CDKL5: FATHMM_converted_rankscore



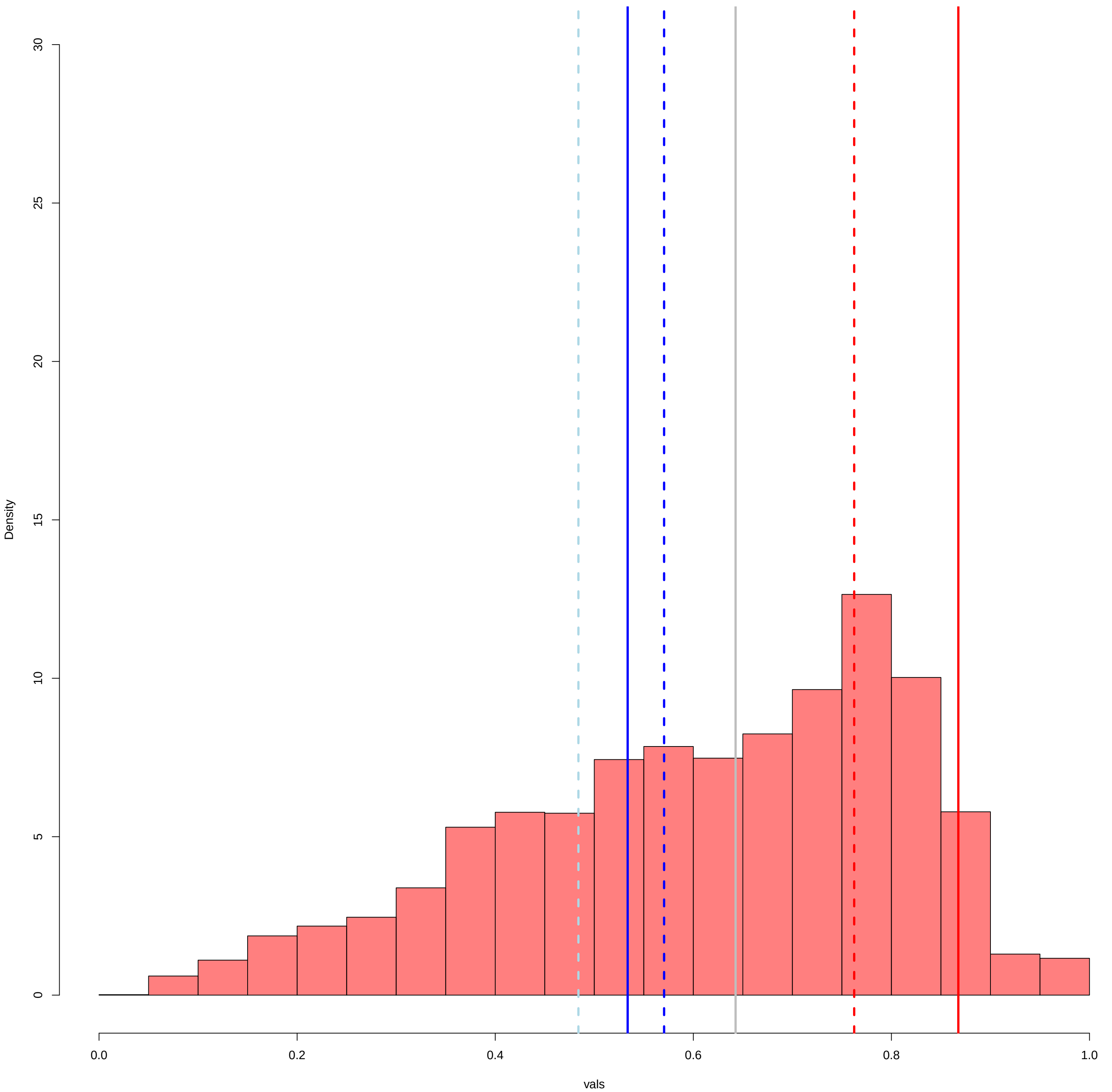
CDKL5: GenoCanyon_score_rankscore



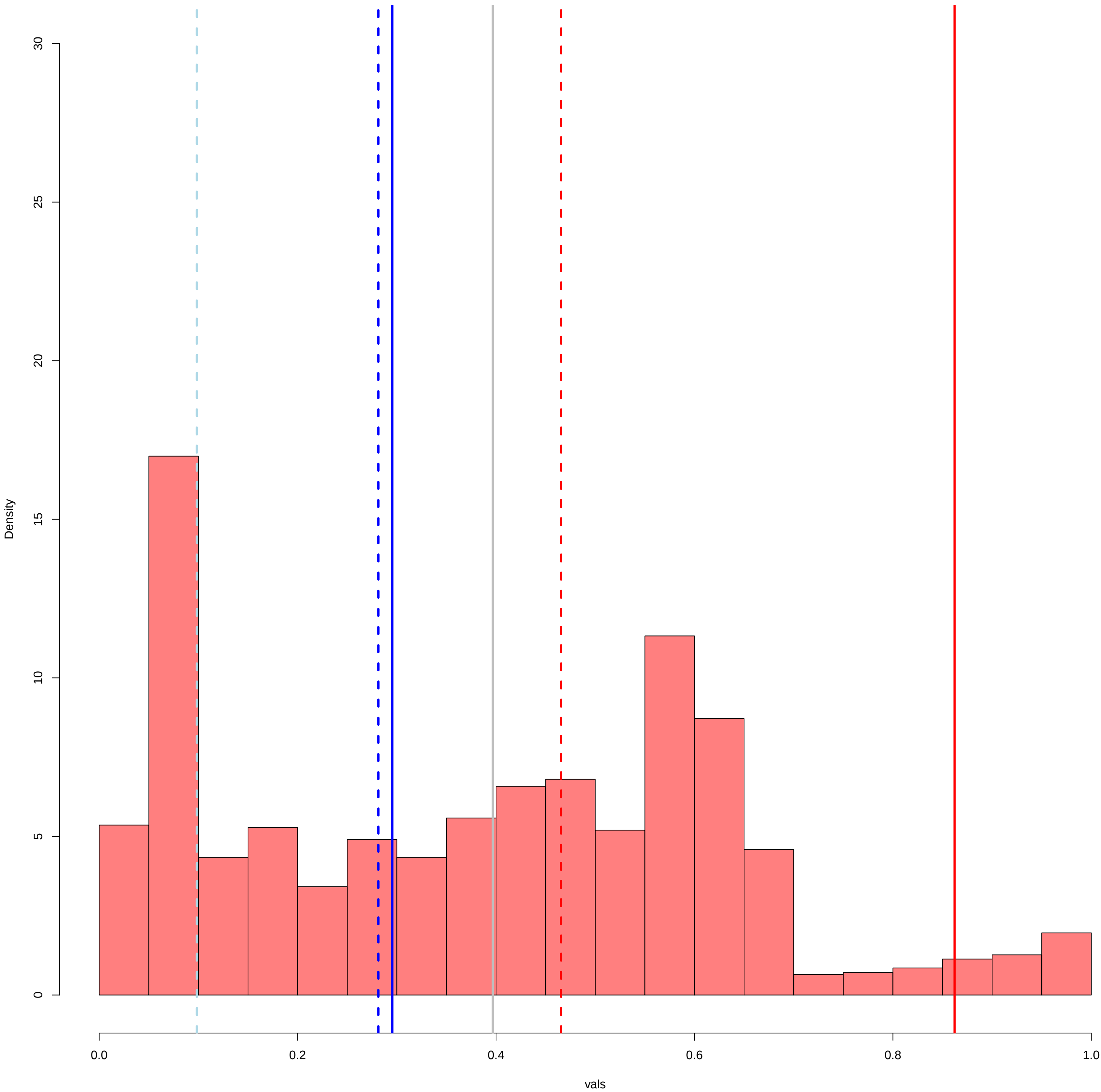
CDKL5: MetaLR_rankscore



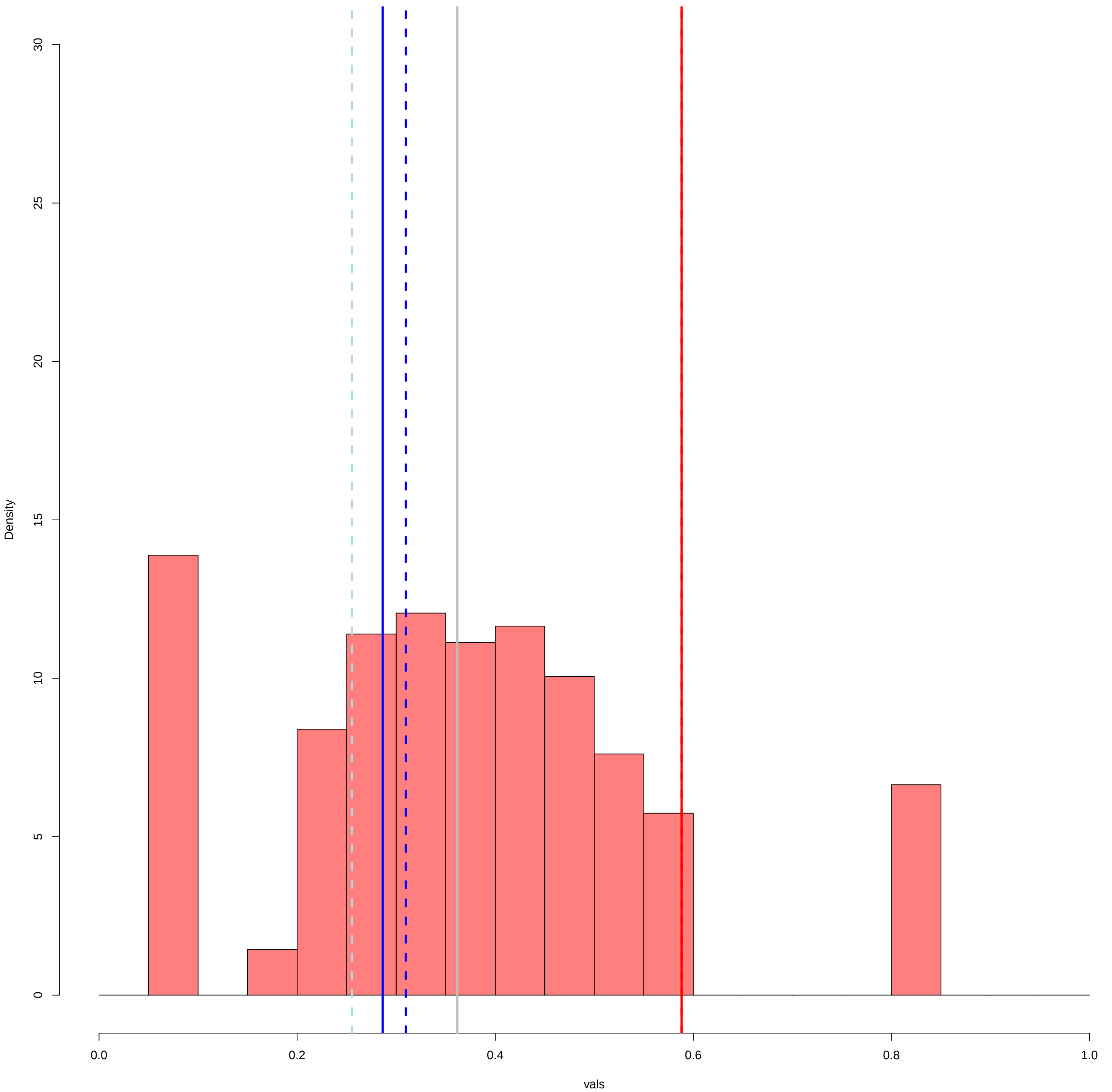
CDKL5: MetaSVM_rankscore



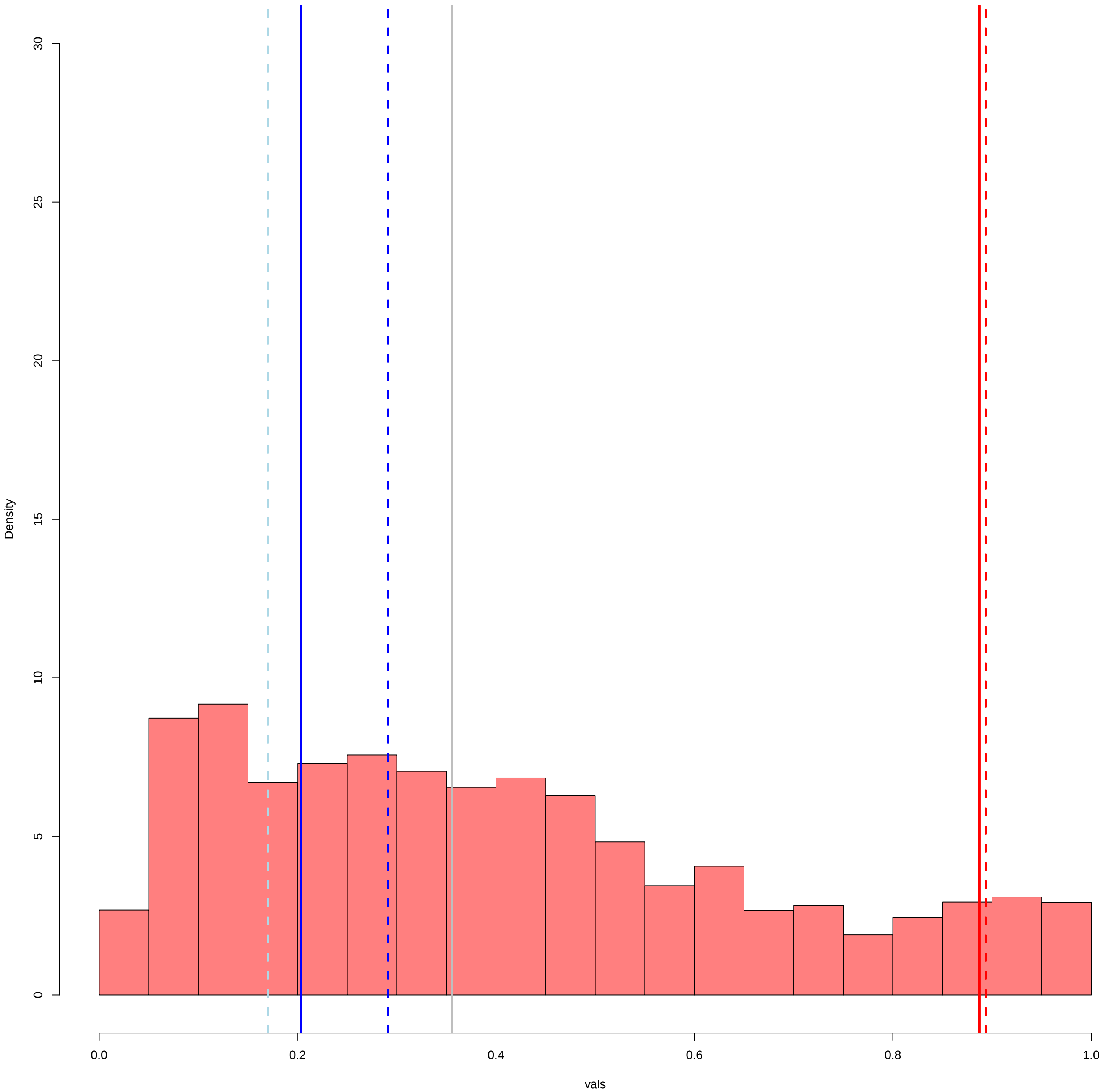
CDKL5: MutationAssessor_score_rankscore



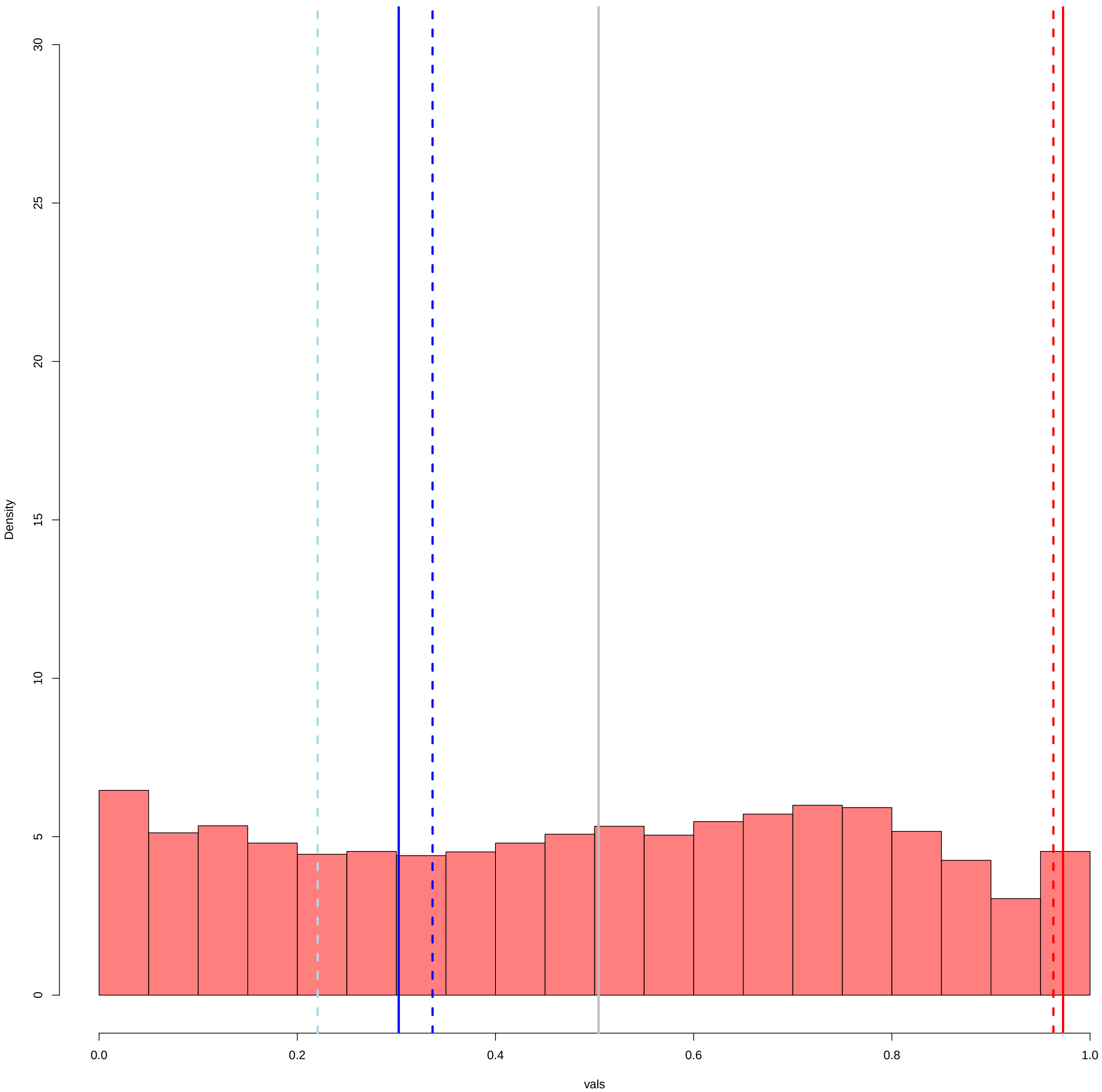
CDKL5: MutationTaster_converted_rankscore



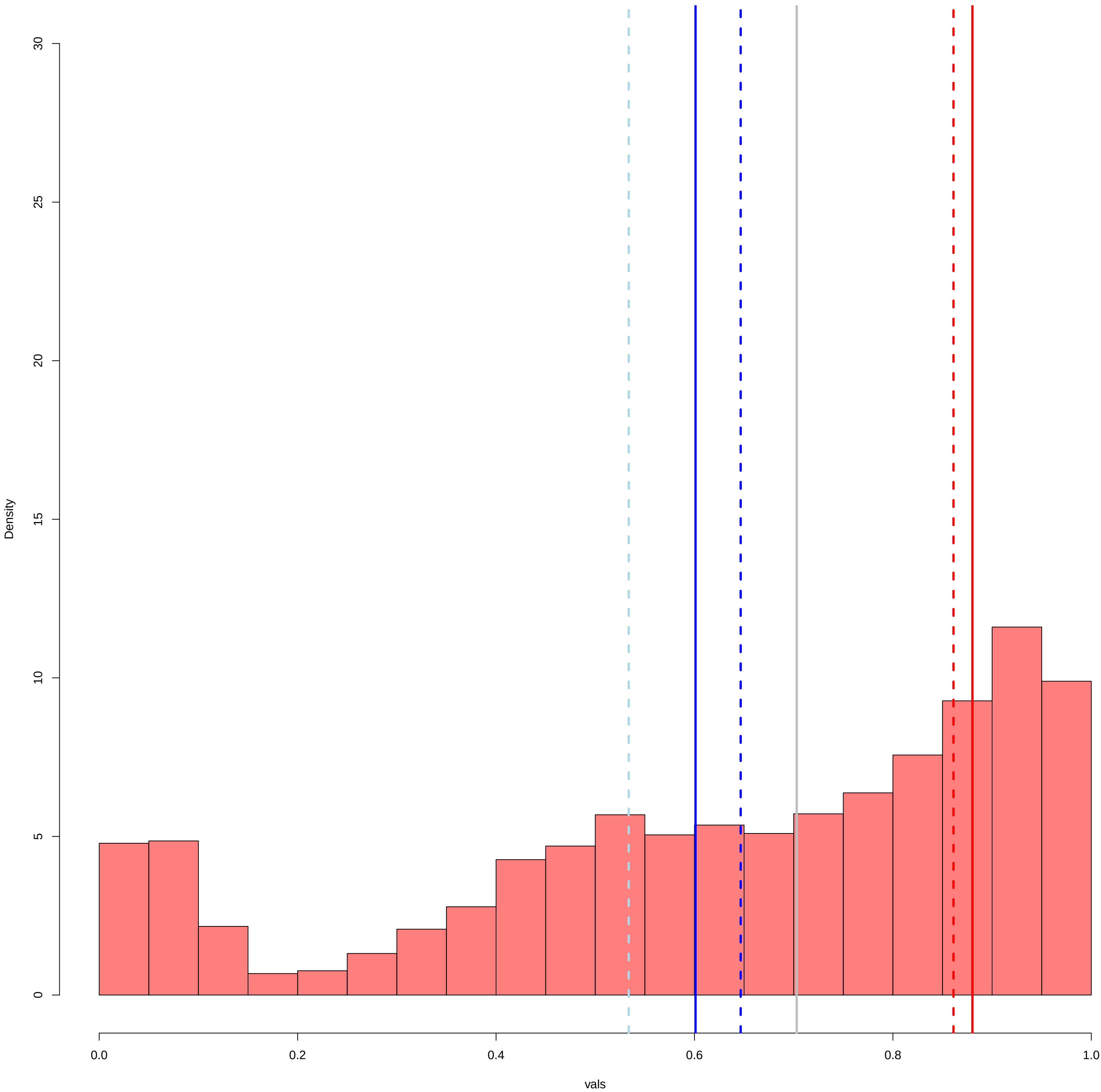
CDKL5: PROVEAN_converted_rankscore



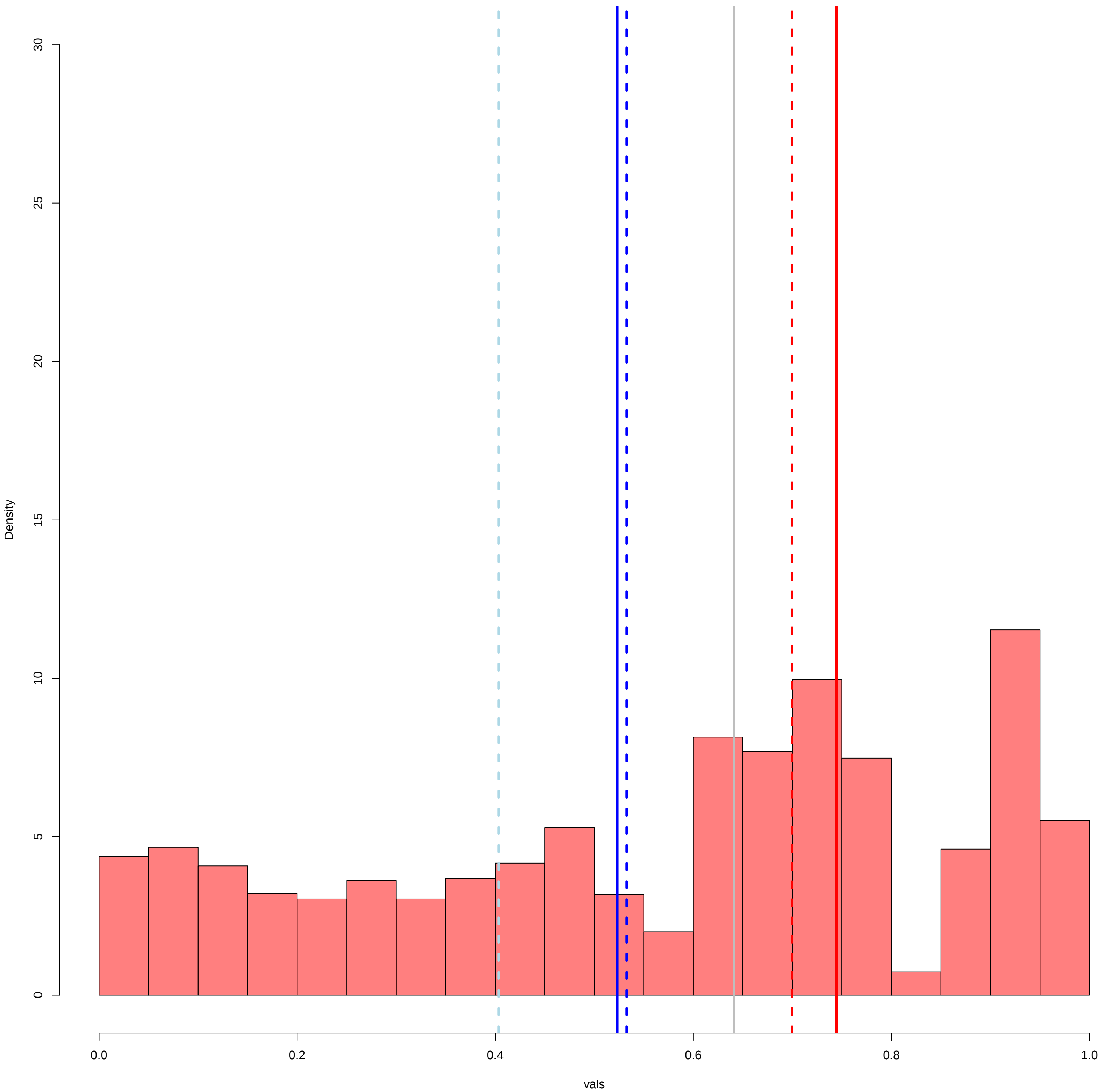
CDKL5: VEST3_rankscore



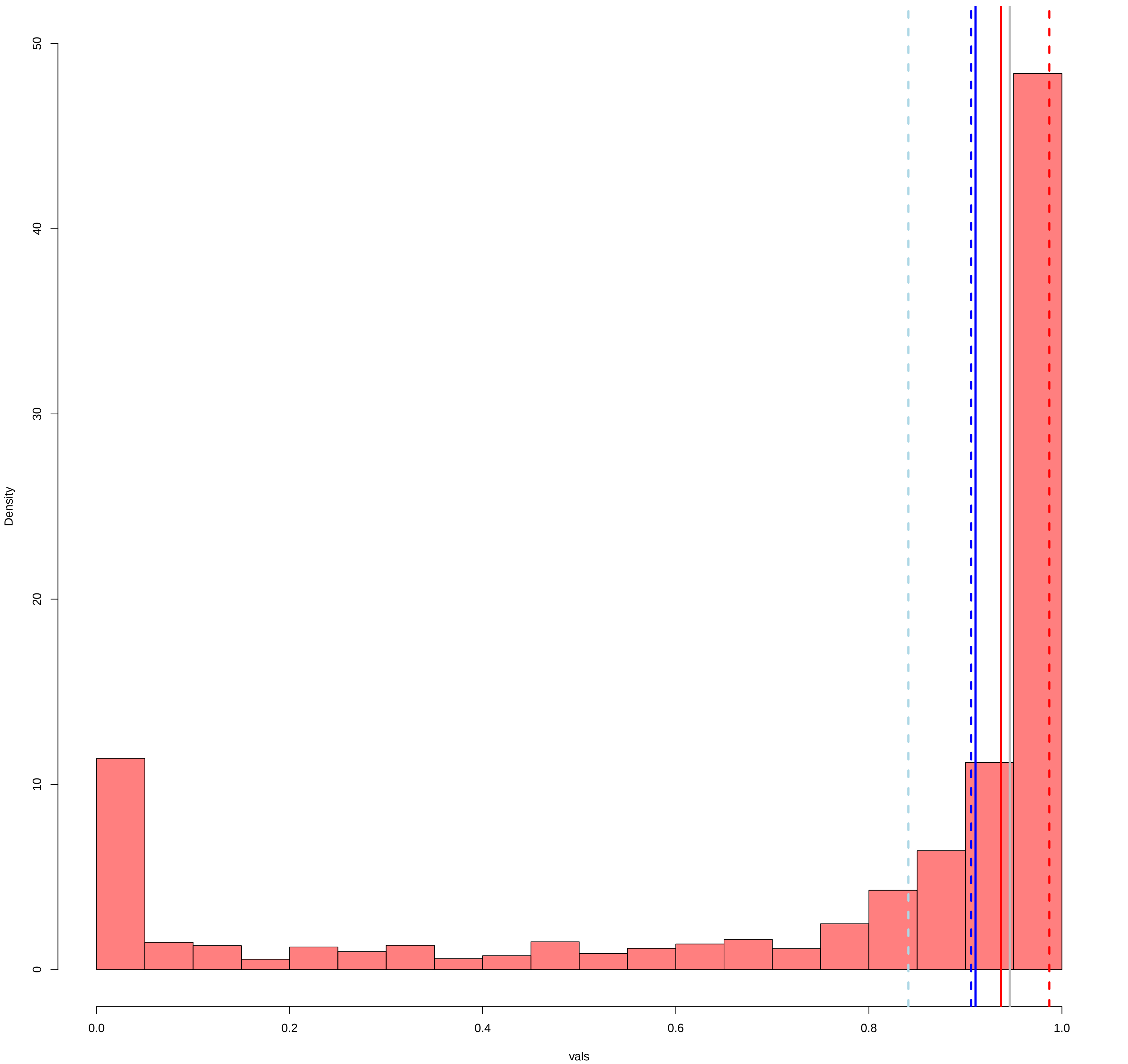
CDKL5: fathmm-MKL_coding_rankscore



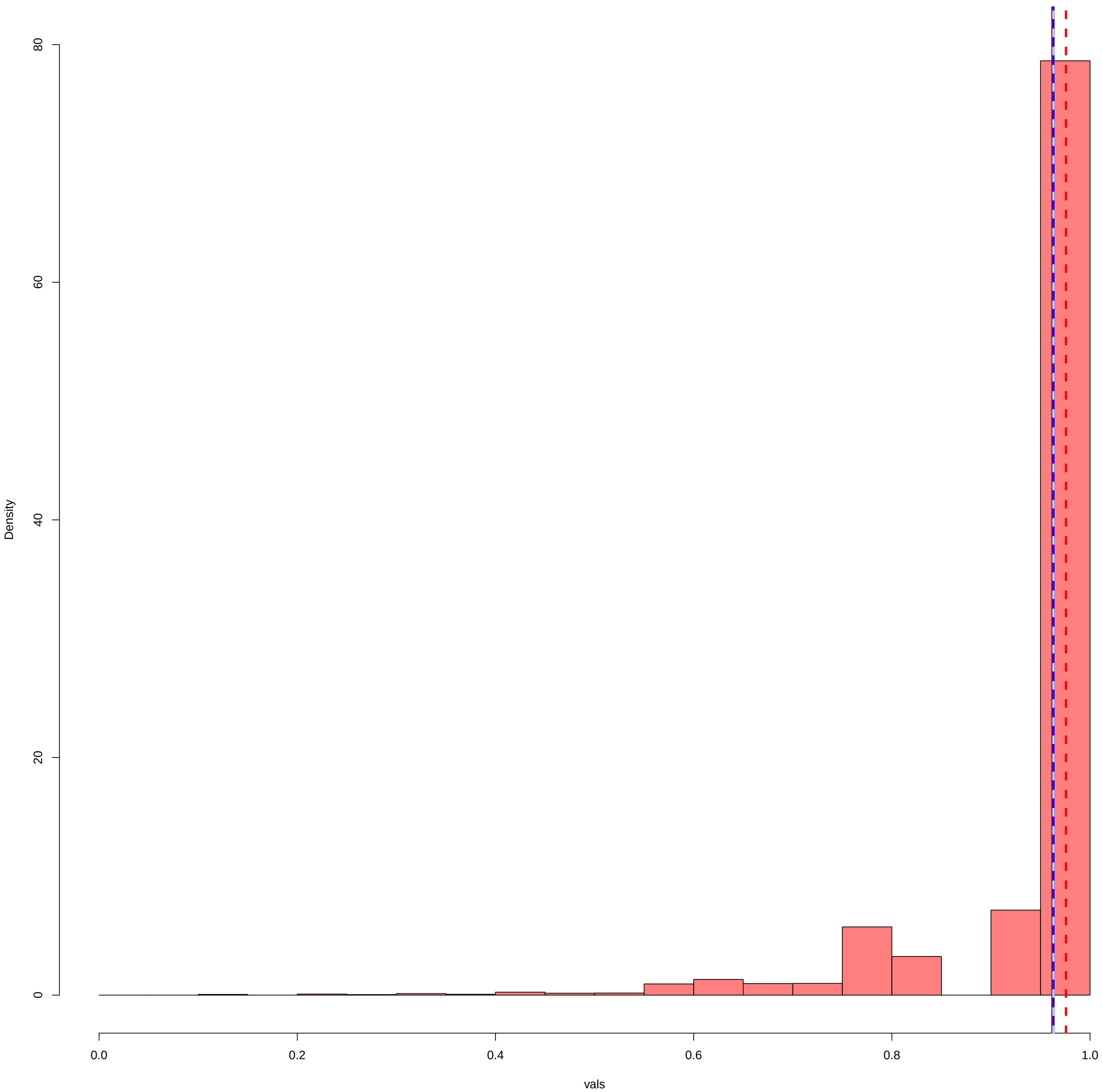
CDKL5: SiPhy_29way_logOdds_rankscore



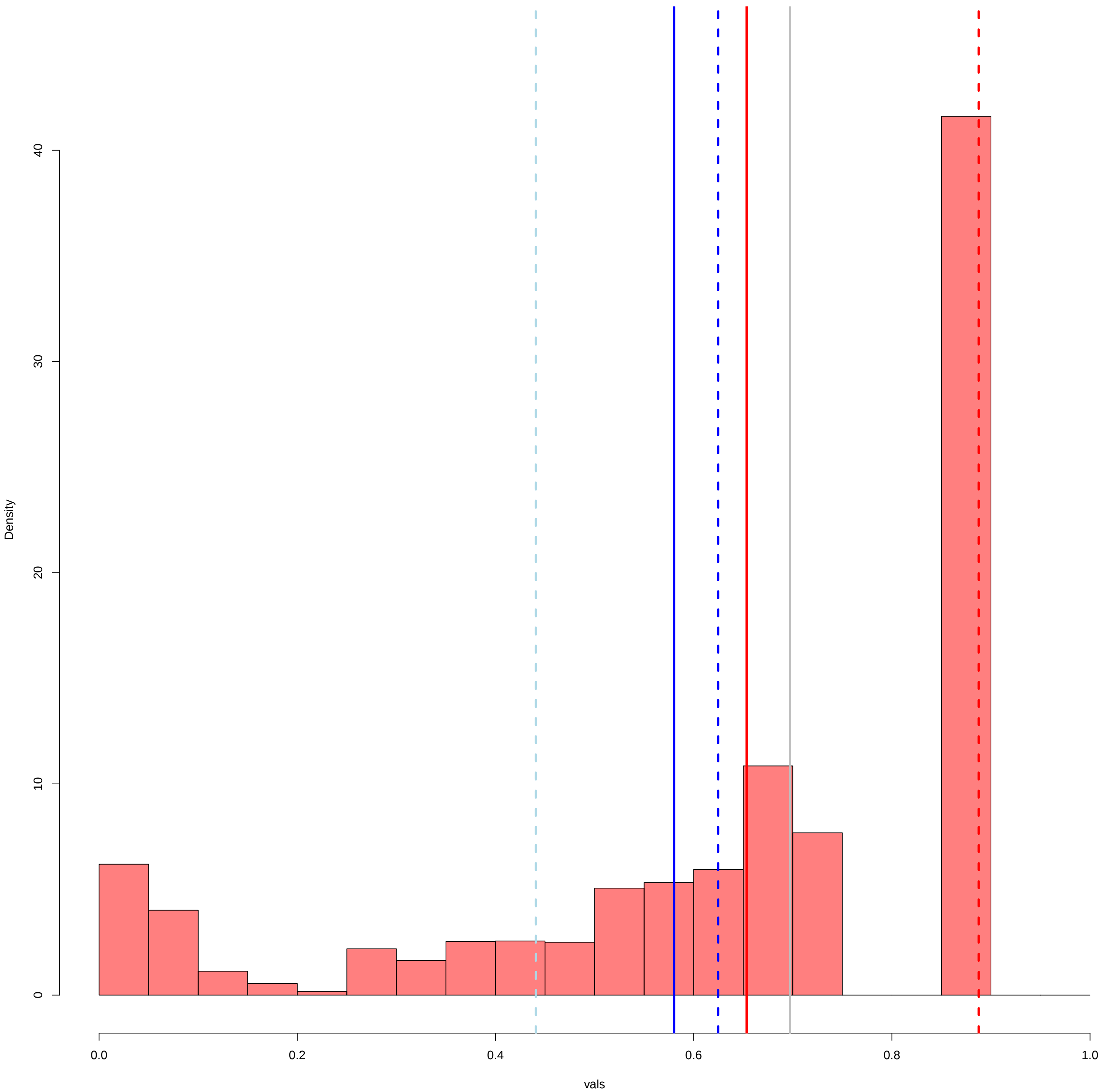
CDKL5: priPhCons



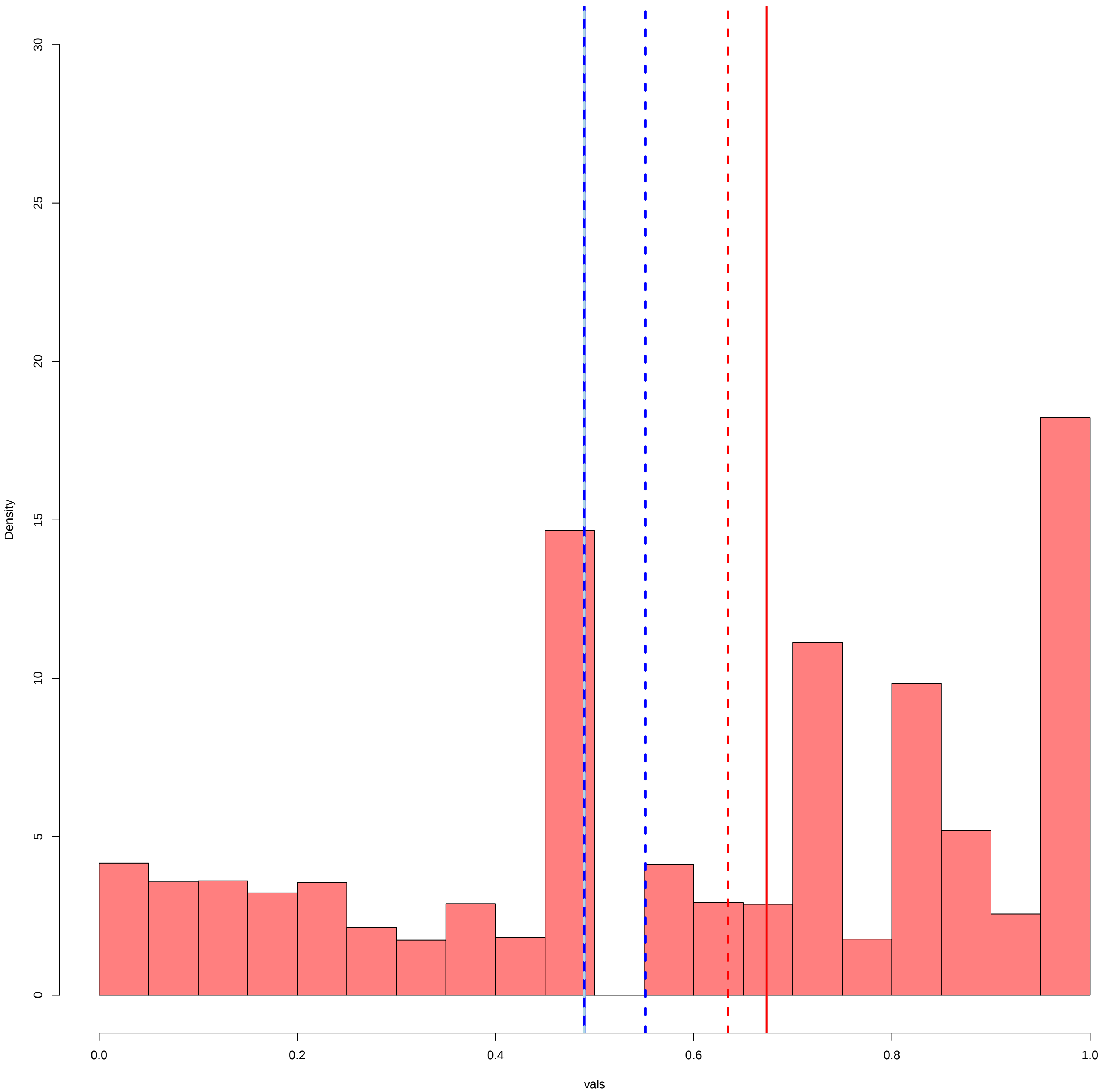
CDKL5: priPhyloP



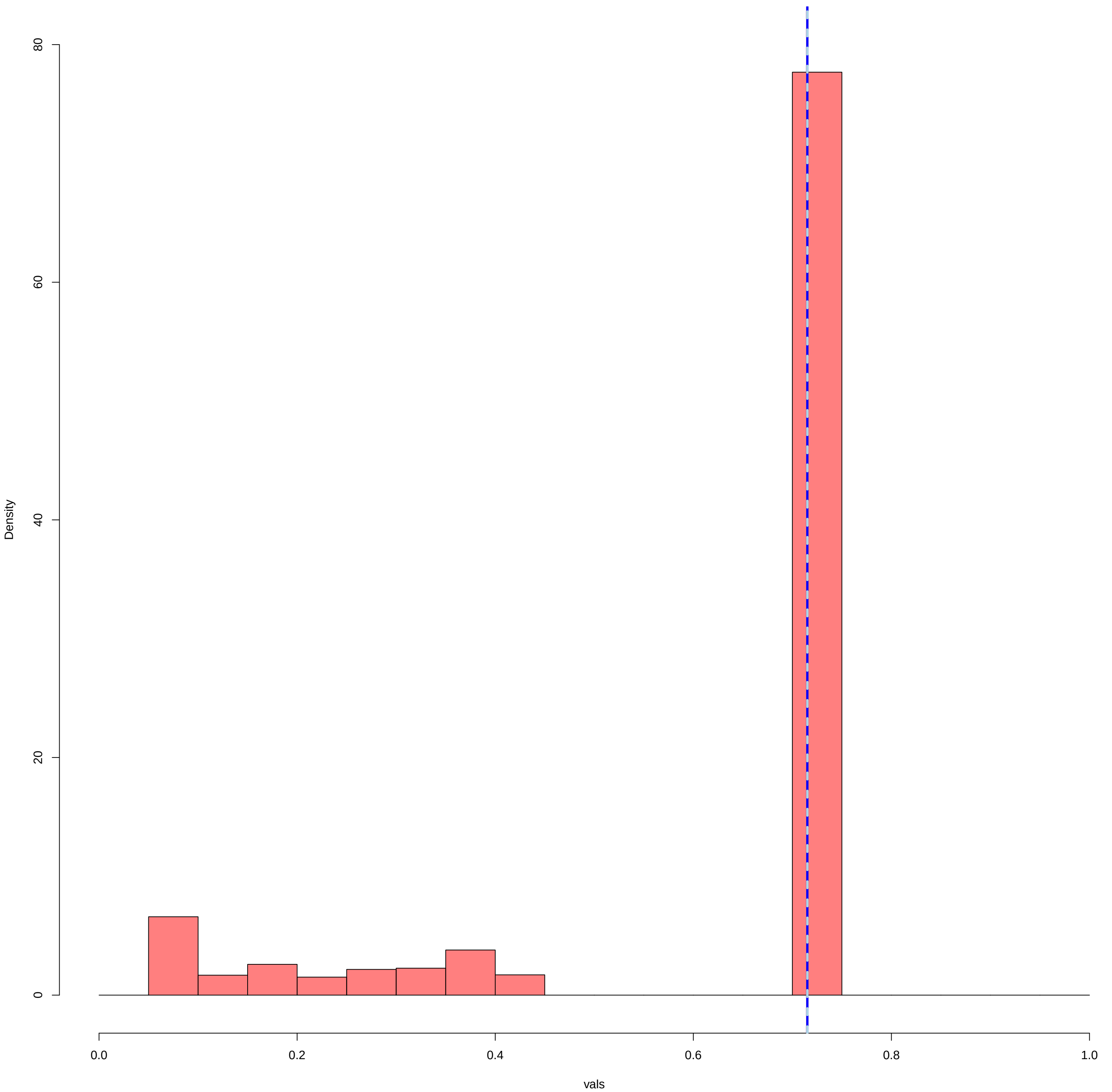
CDKL5: phastCons20way_mammalian_rankscore



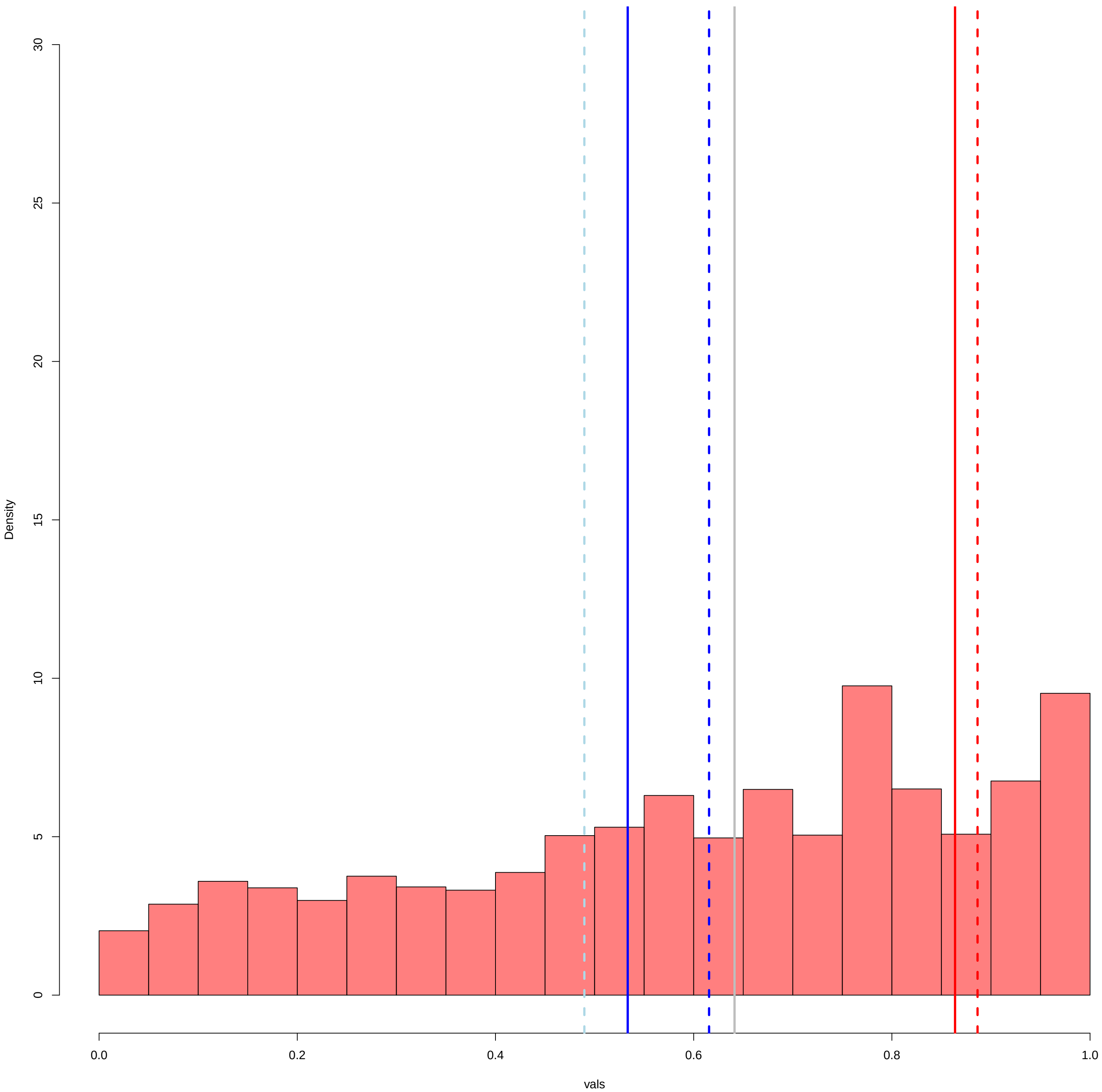
CDKL5: phyloP20way_mammalian_rankscore



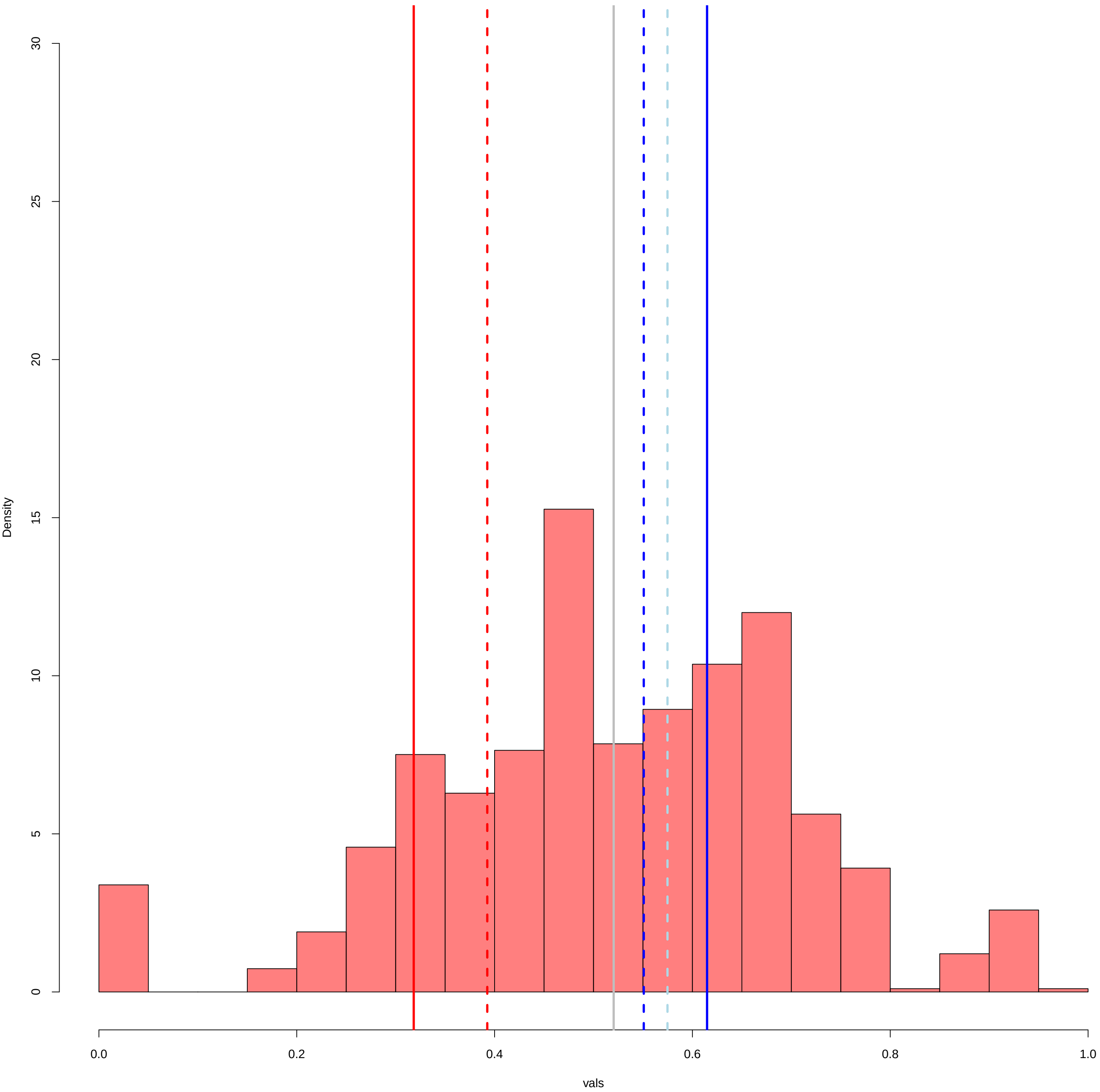
CDKL5: phastCons100way_vertebrate_rankscore



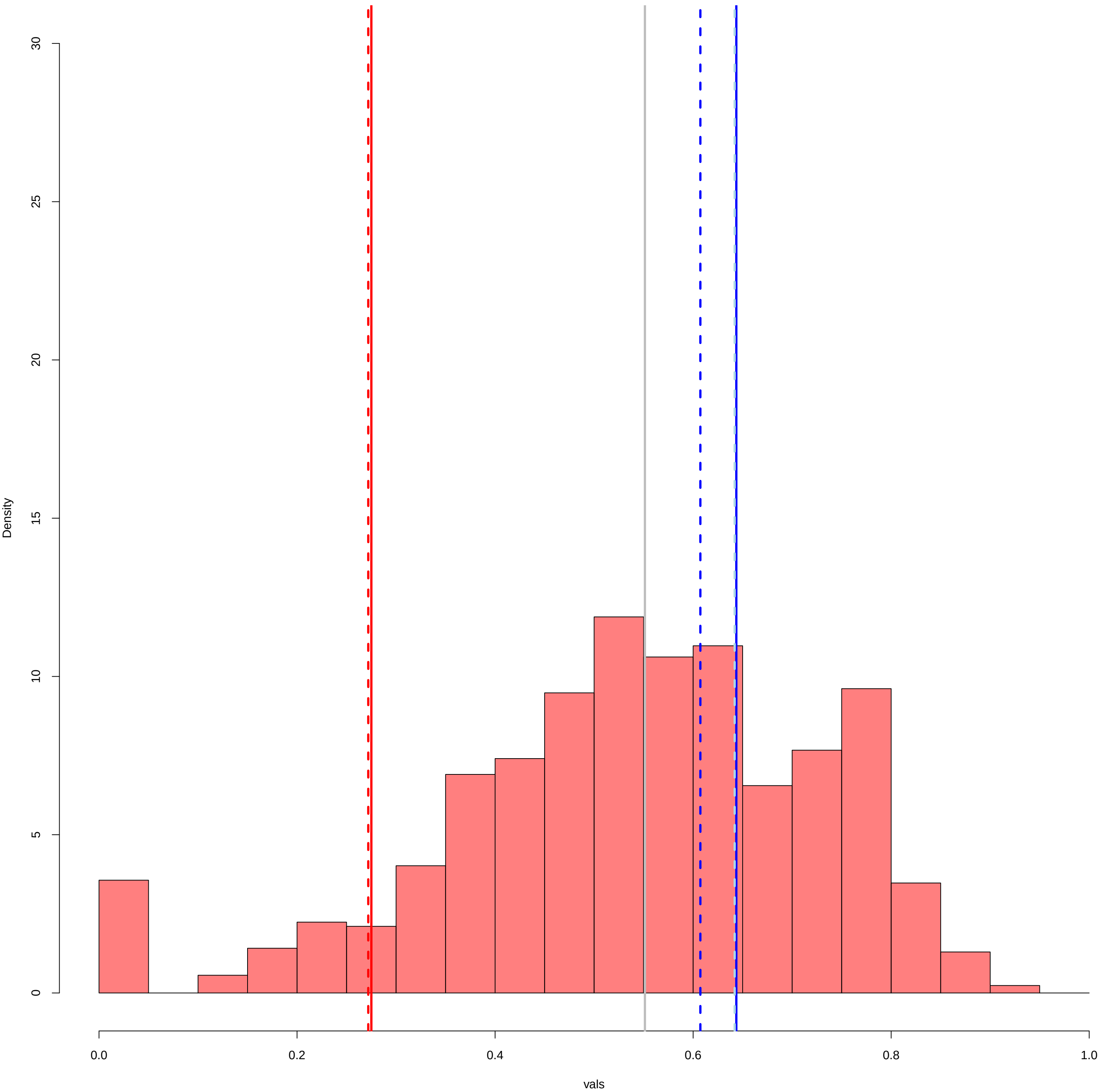
CDKL5: phyloP100way_vertebrate_rankscore



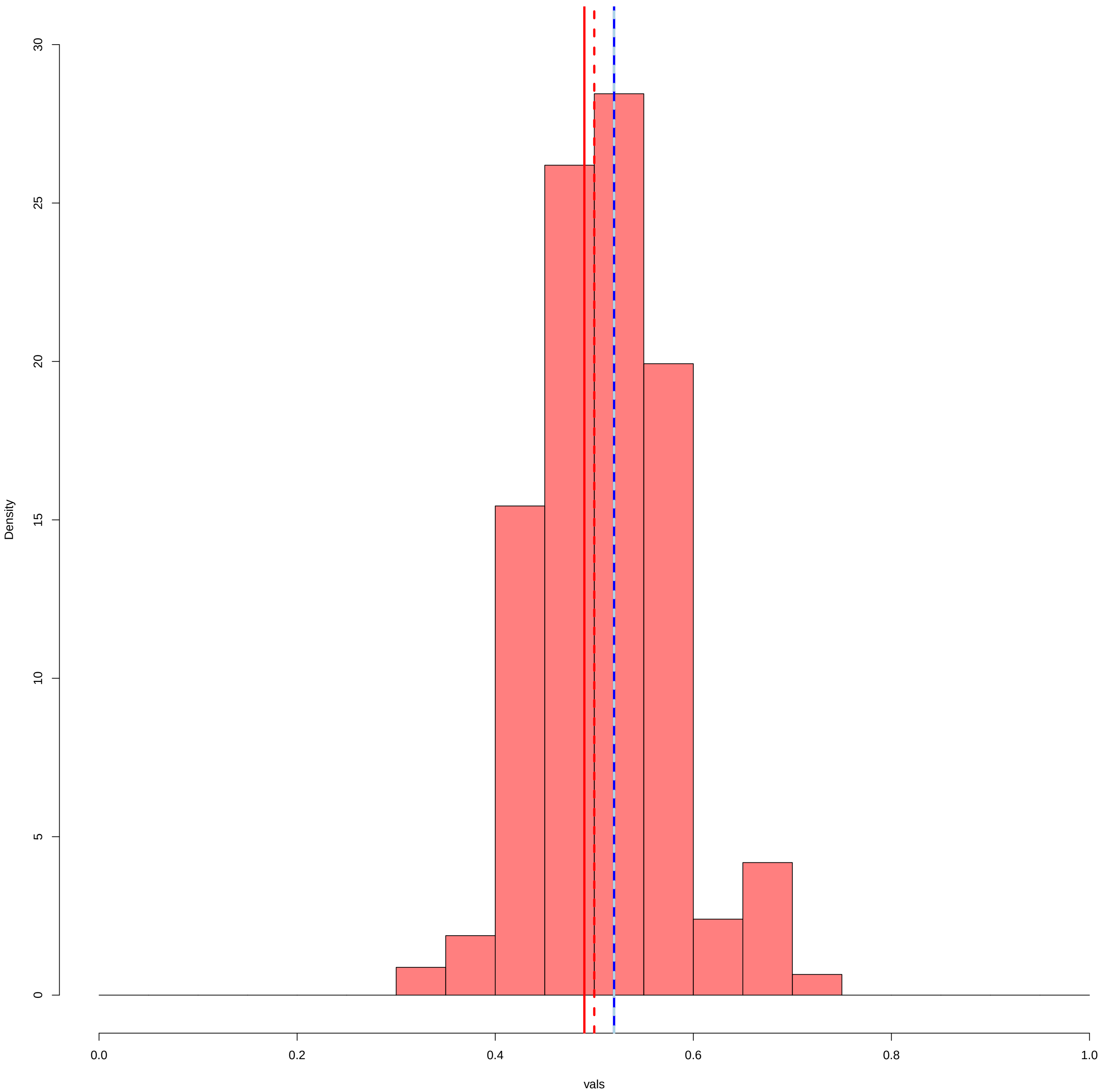
CDKL5: ExAC v1 MTR



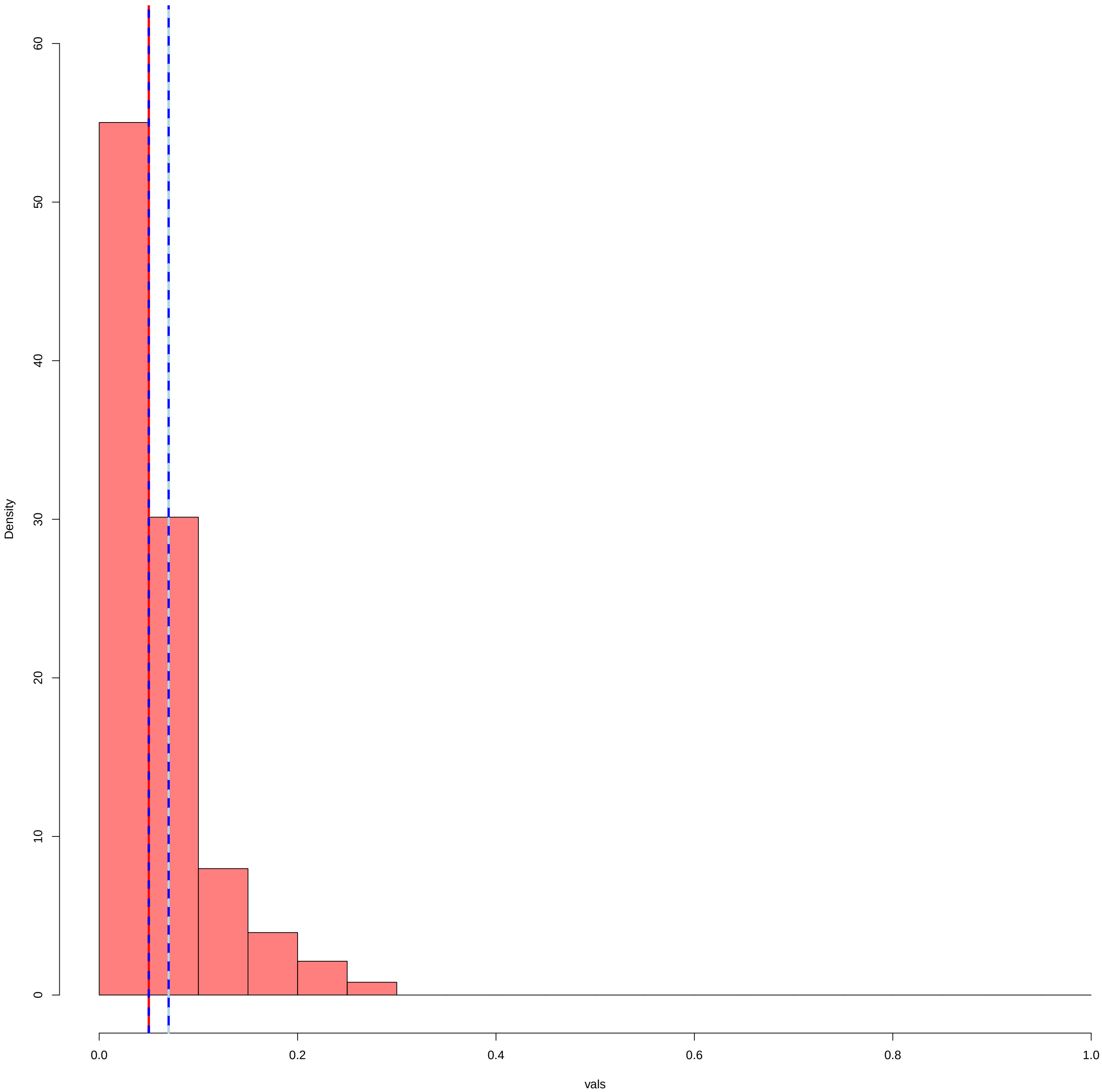
CDKL5: ExAC v2 & gnomAD MTR



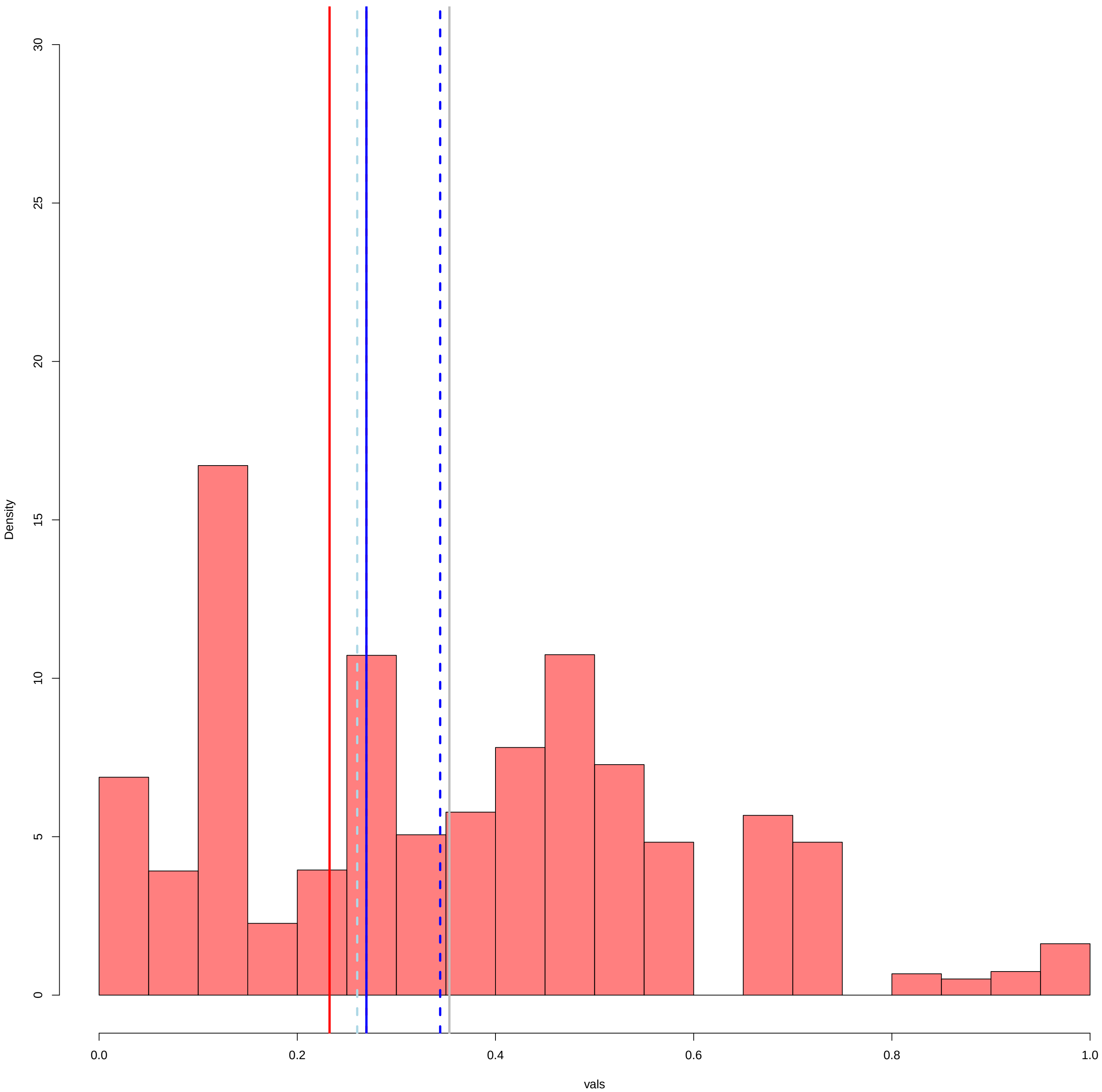
GRIN2A: GC (Percent GC content in a window of ± 75 bp)



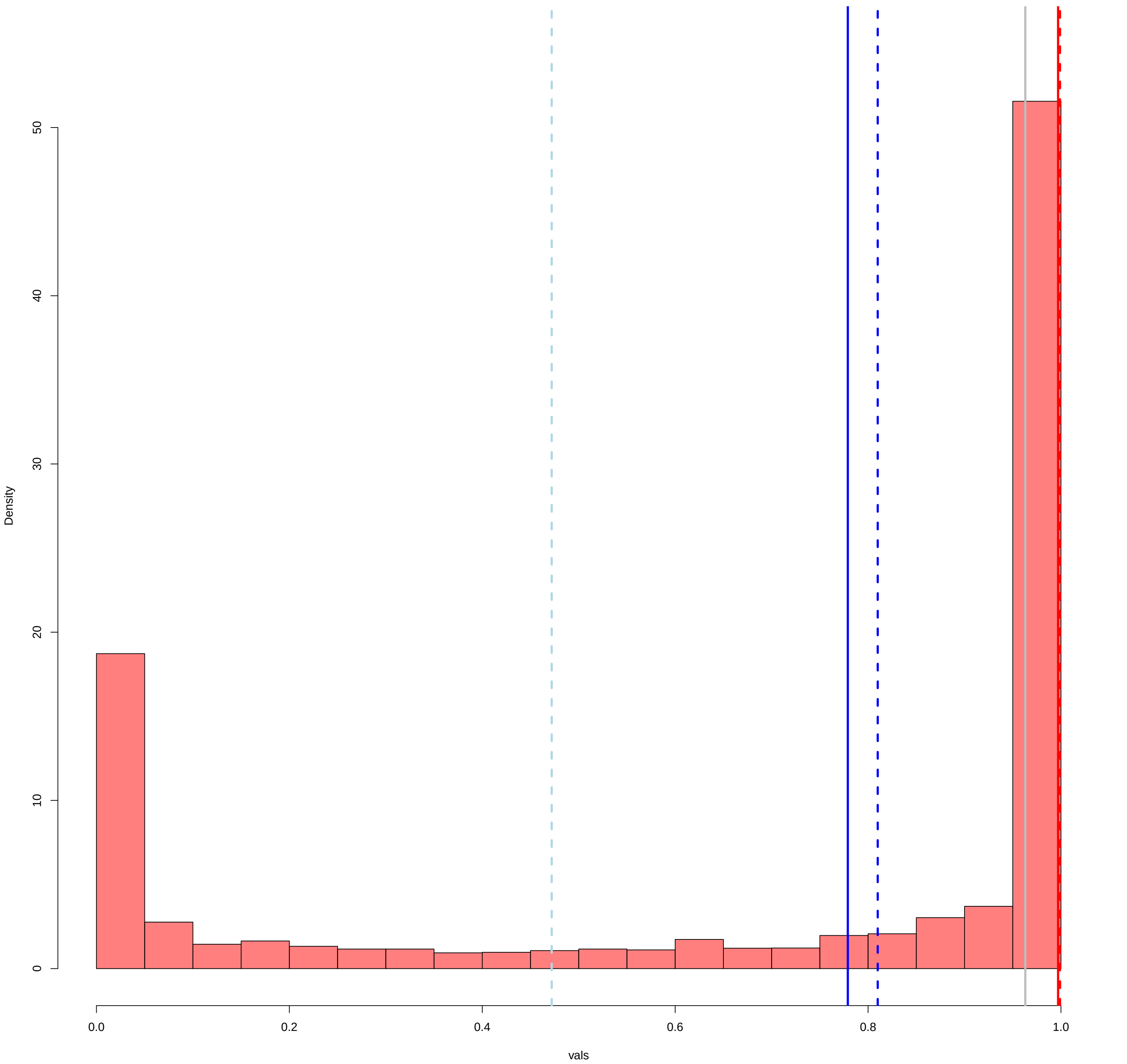
GRIN2A: CpG (Percent CpG in a window of +/-75bp)



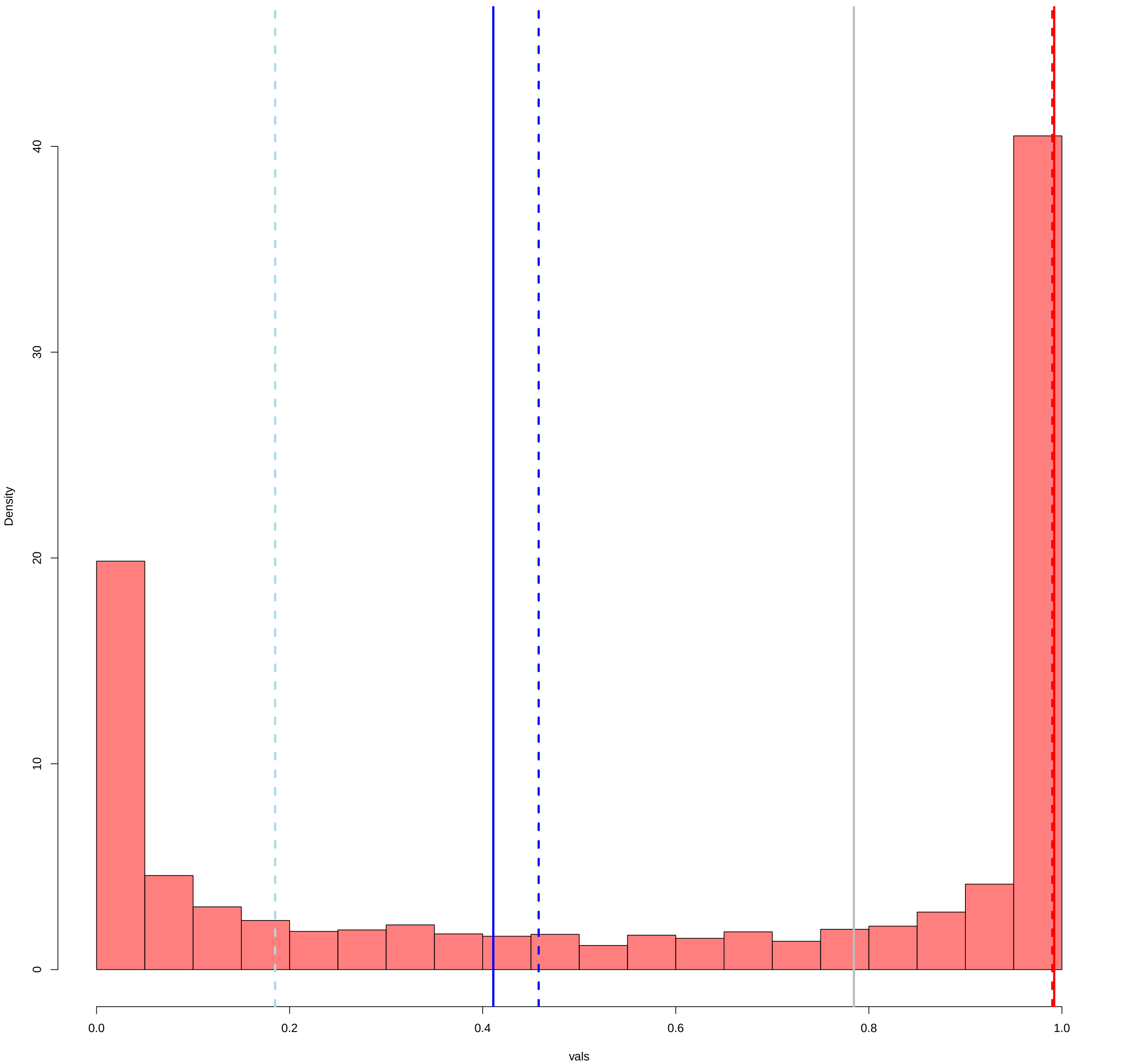
GRIN2A: Grantham



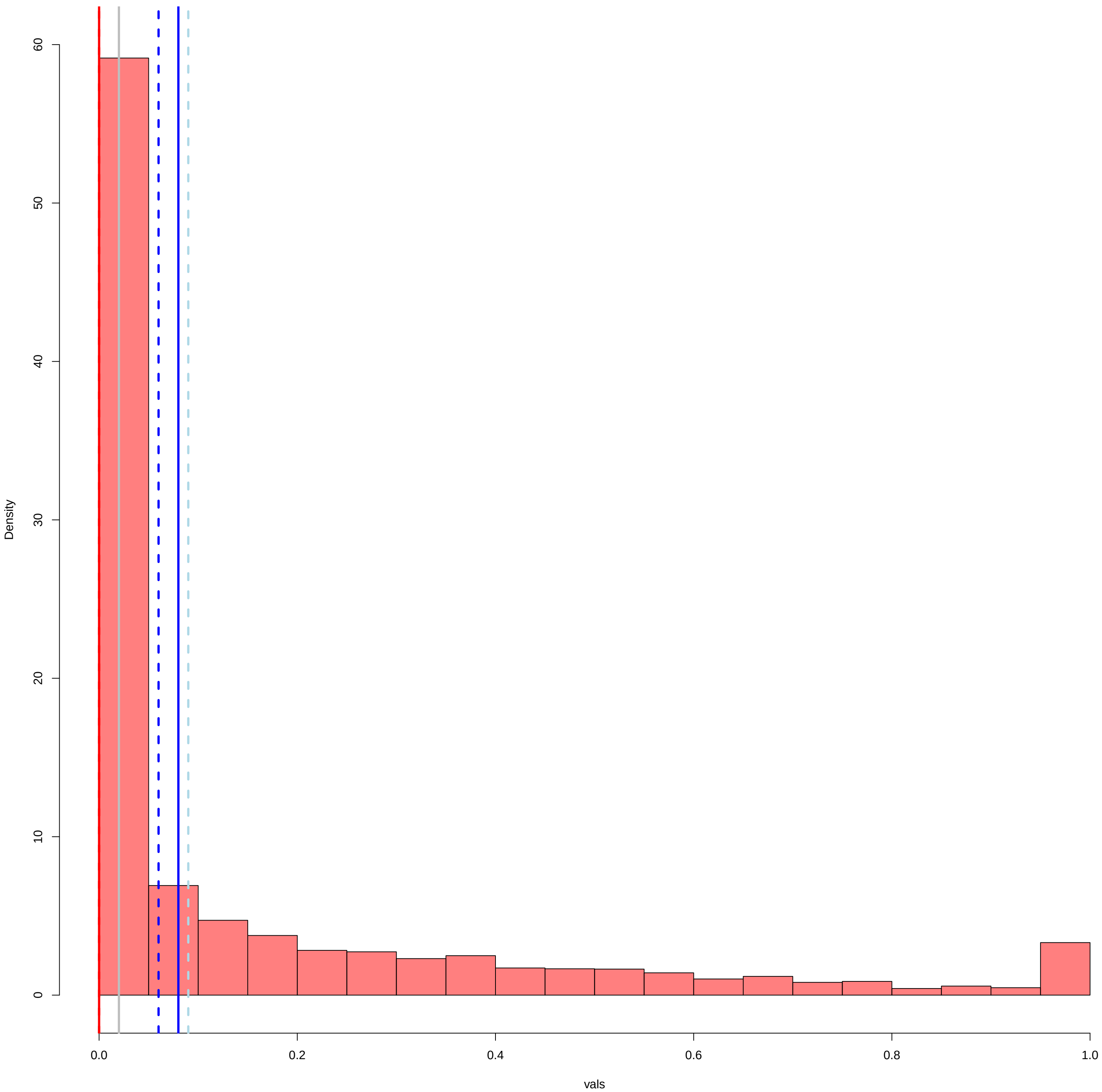
GRIN2A: Hdiv quan



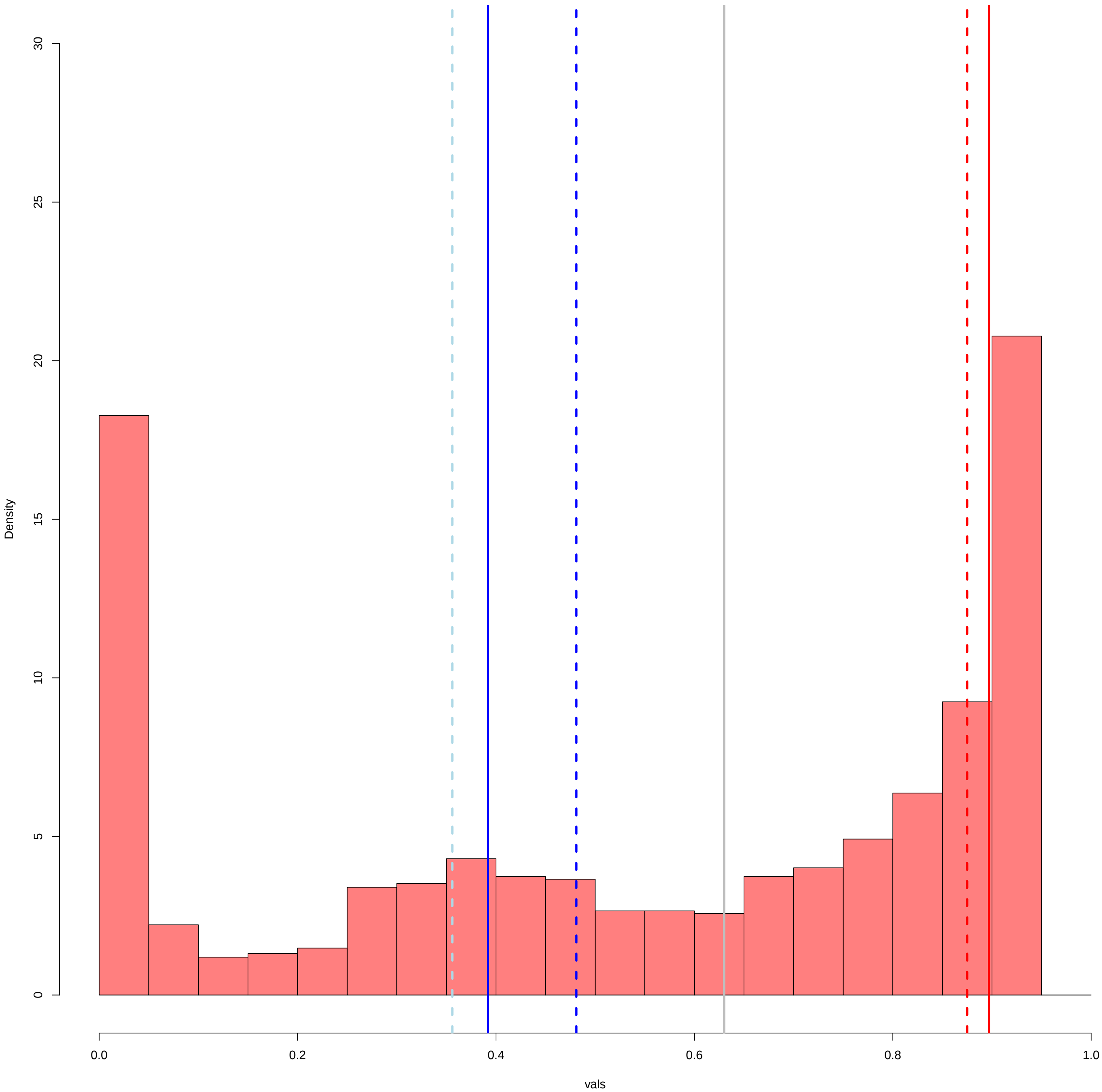
GRIN2A: Hvar quan



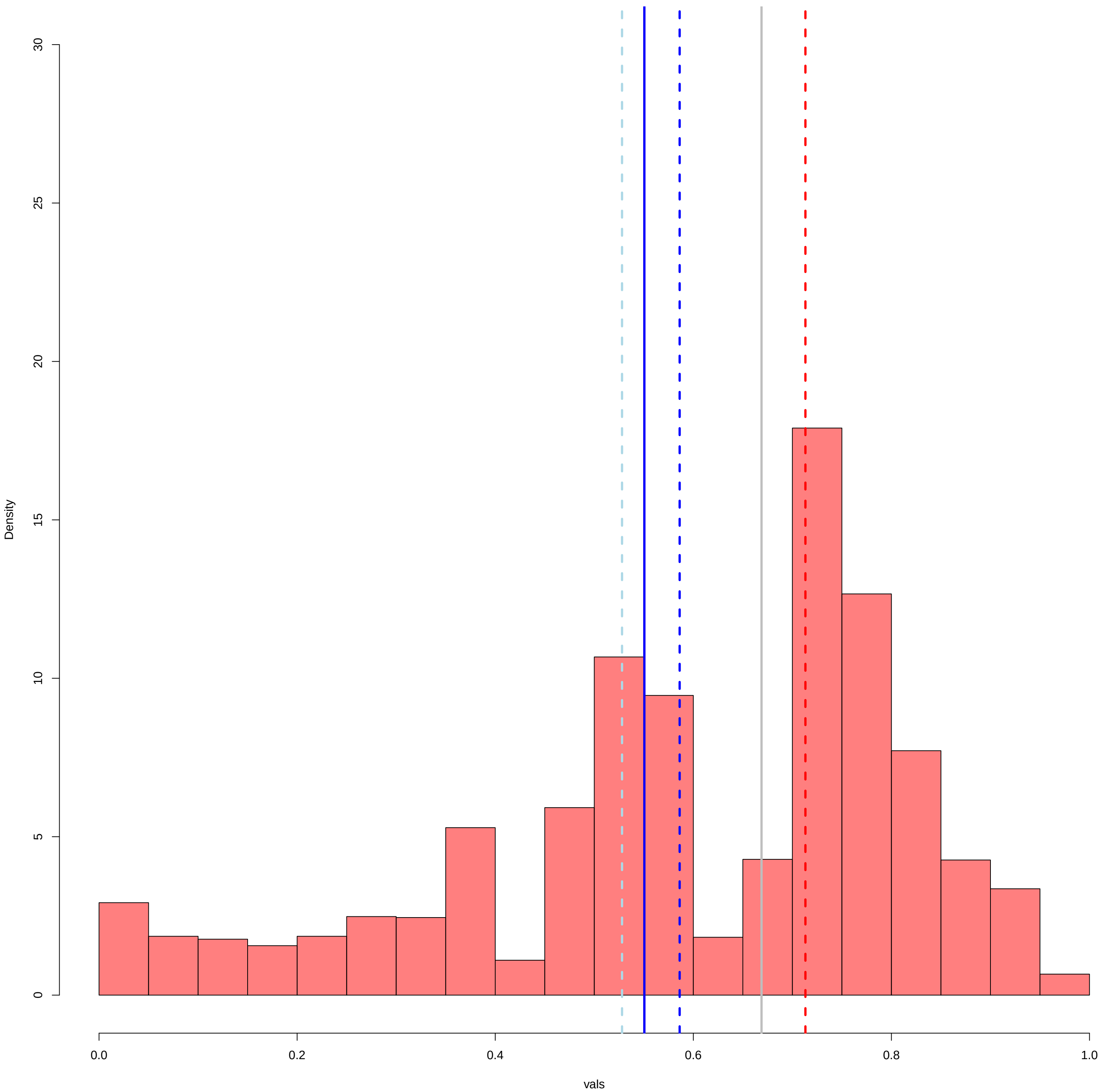
GRIN2A: SIFT



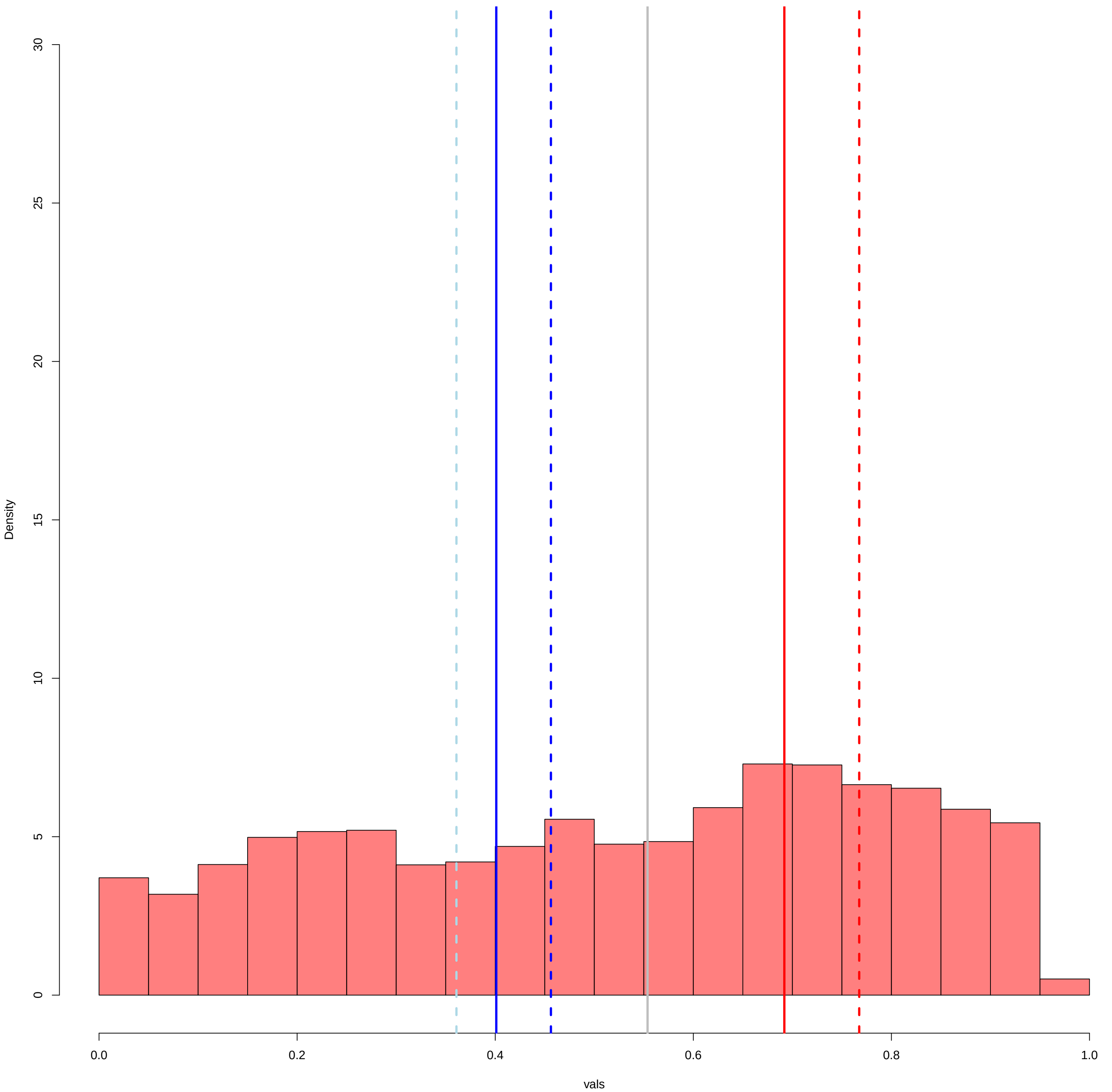
GRIN2A: Condel



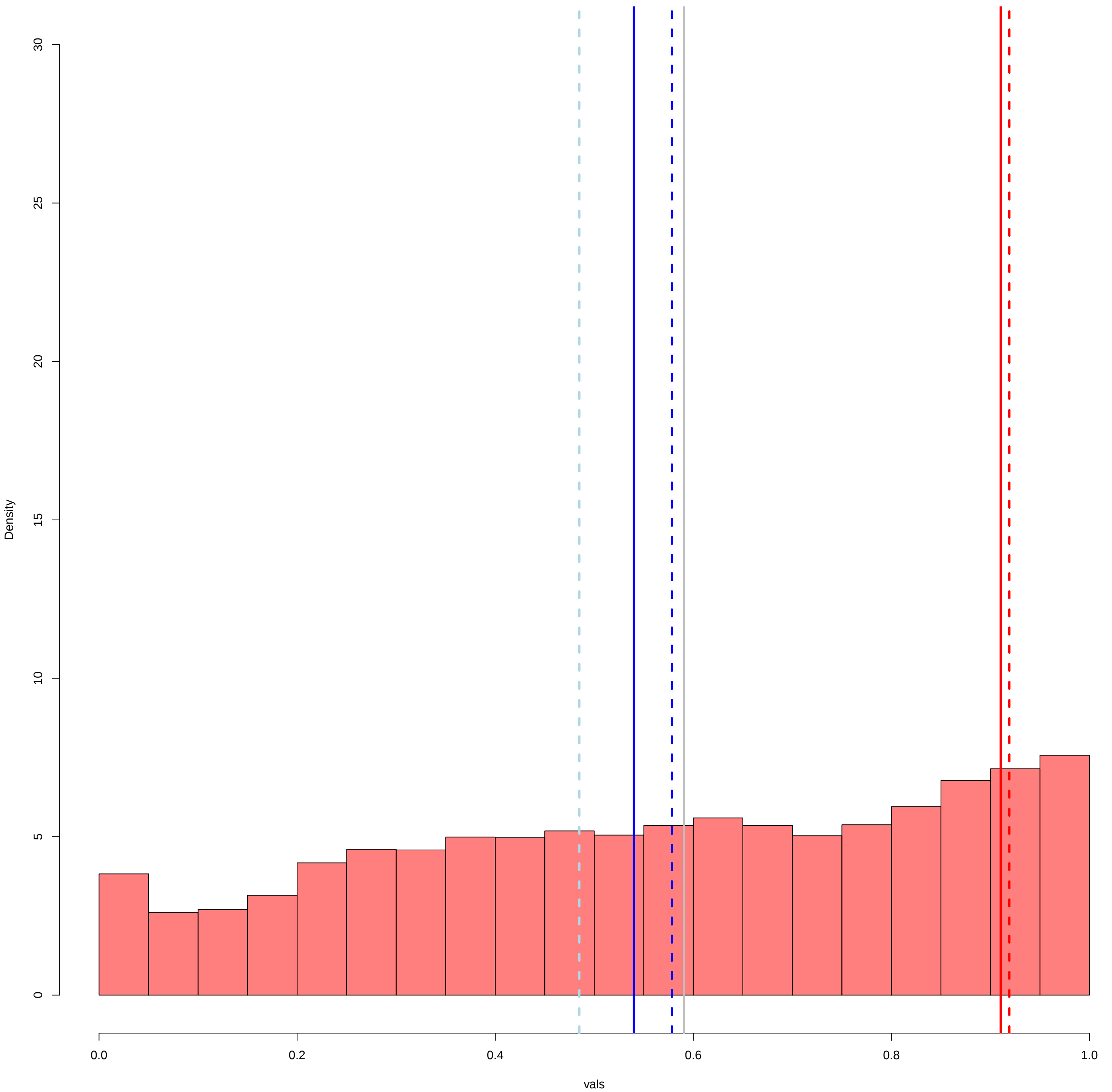
GRIN2A: GERP++_RS_rankscore



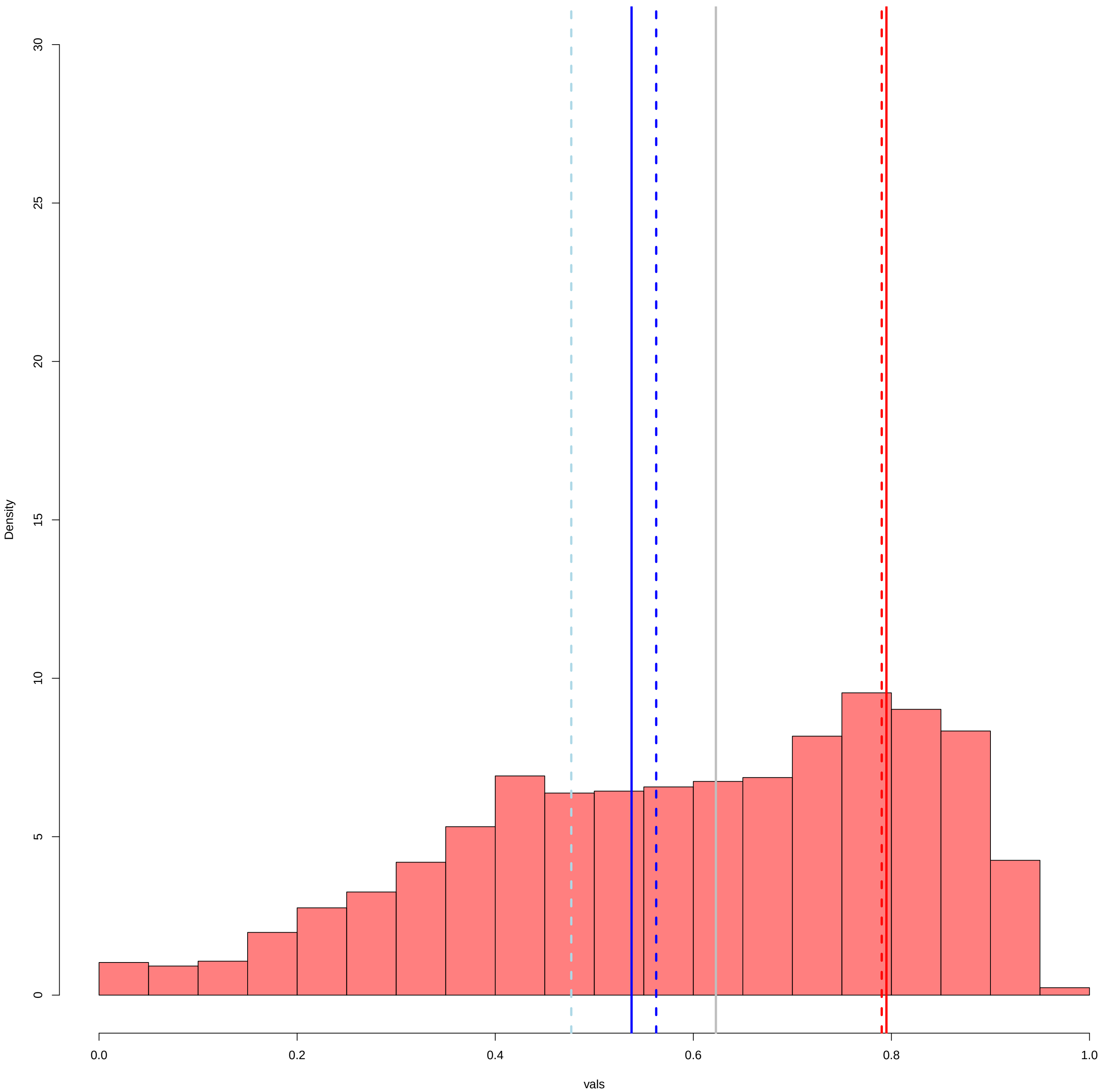
GRIN2A: CADD_raw_rankscore



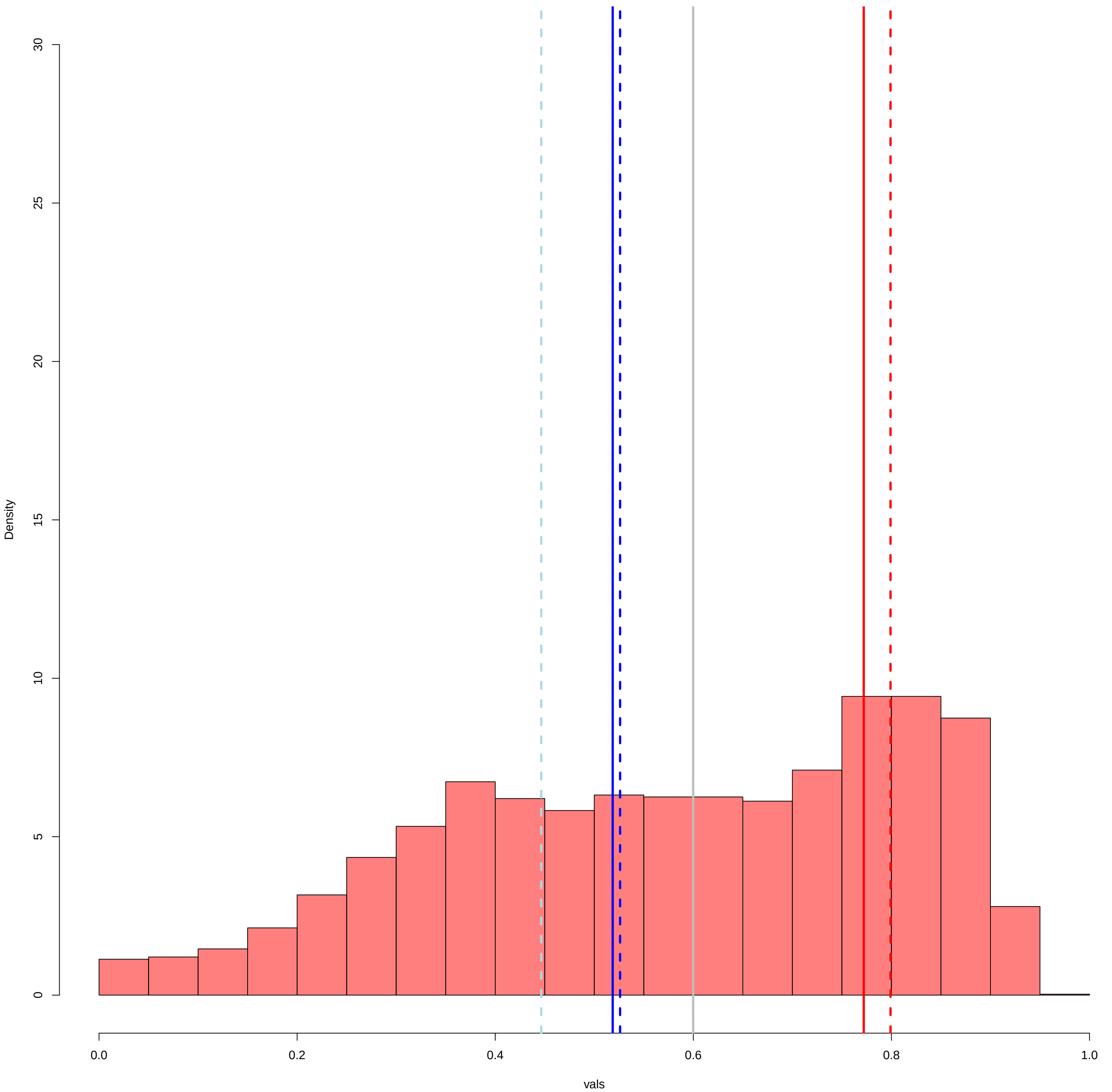
GRIN2A: DANN_rankscore



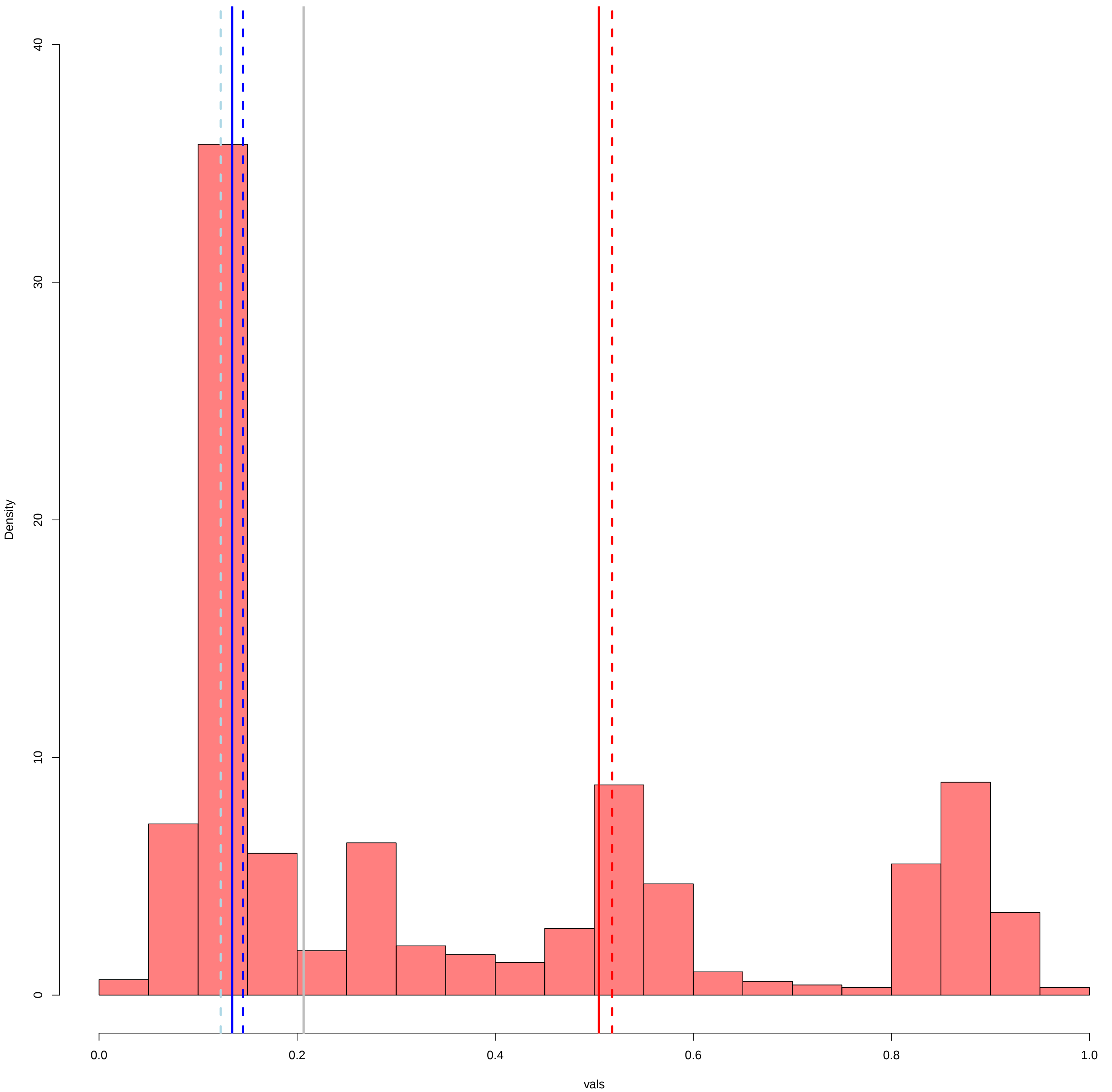
GRIN2A: Eigen-PC-raw_rankscore



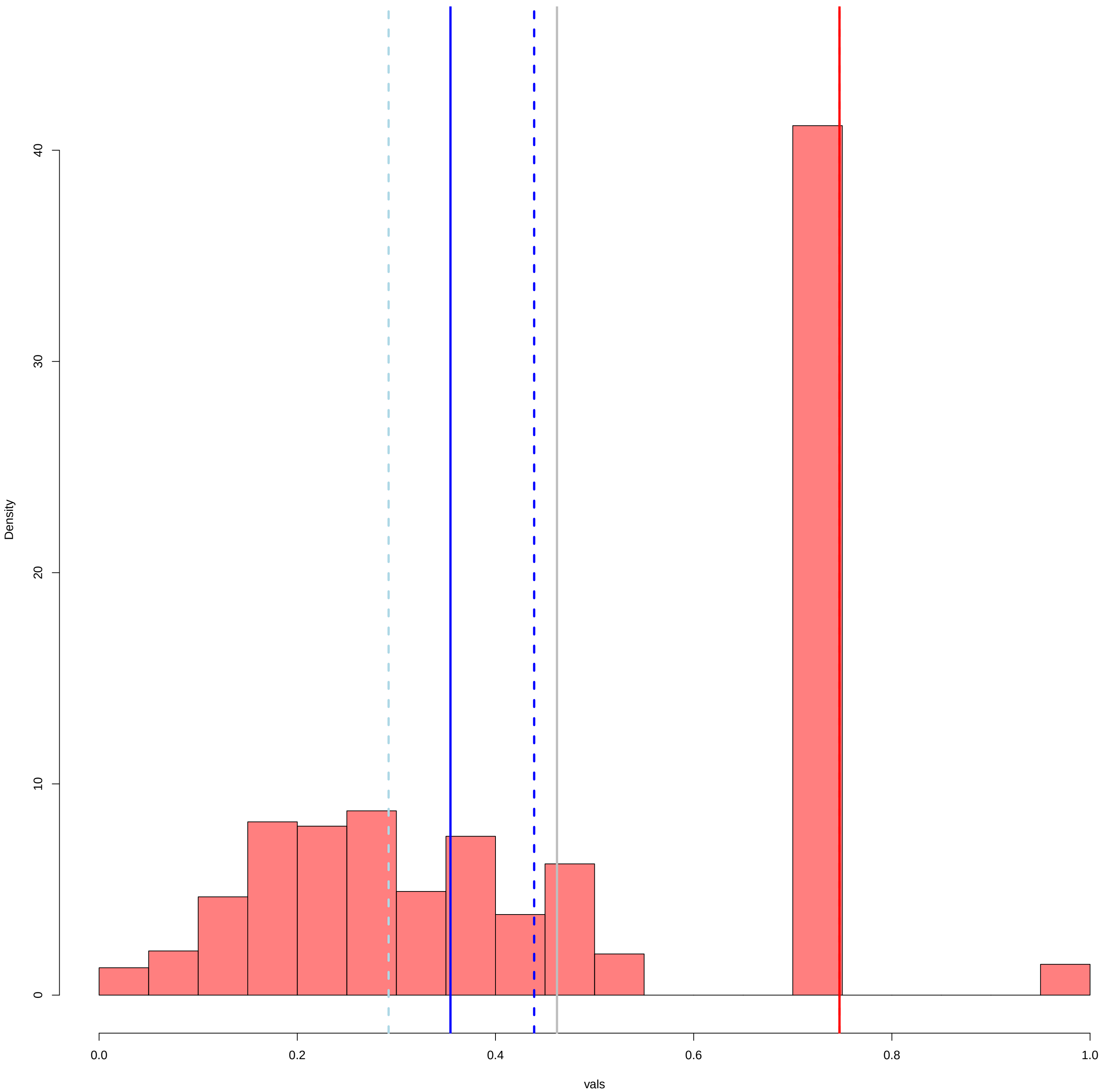
GRIN2A: Eigen-raw_rankscore



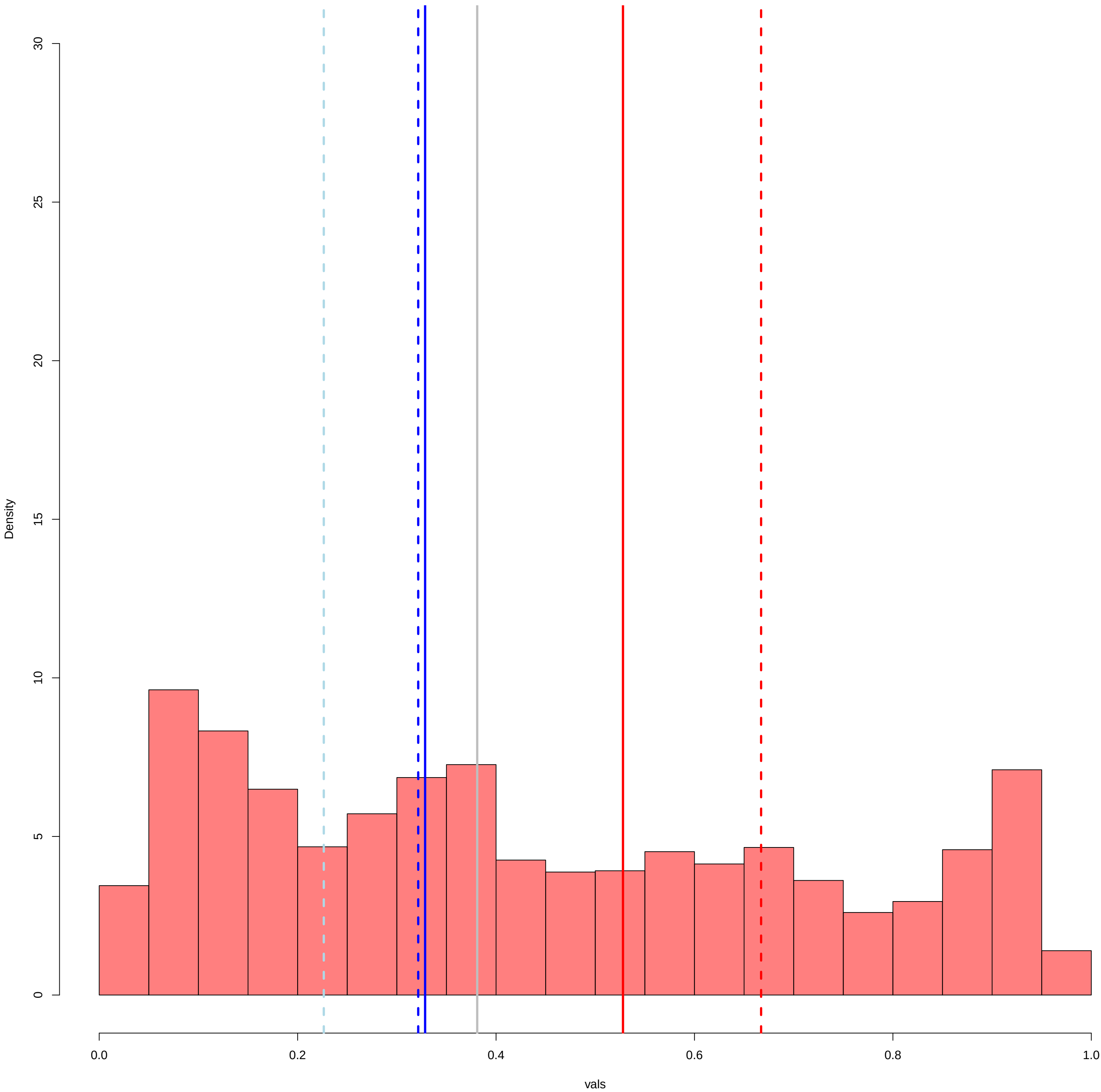
GRIN2A: FATHMM_converted_rankscore



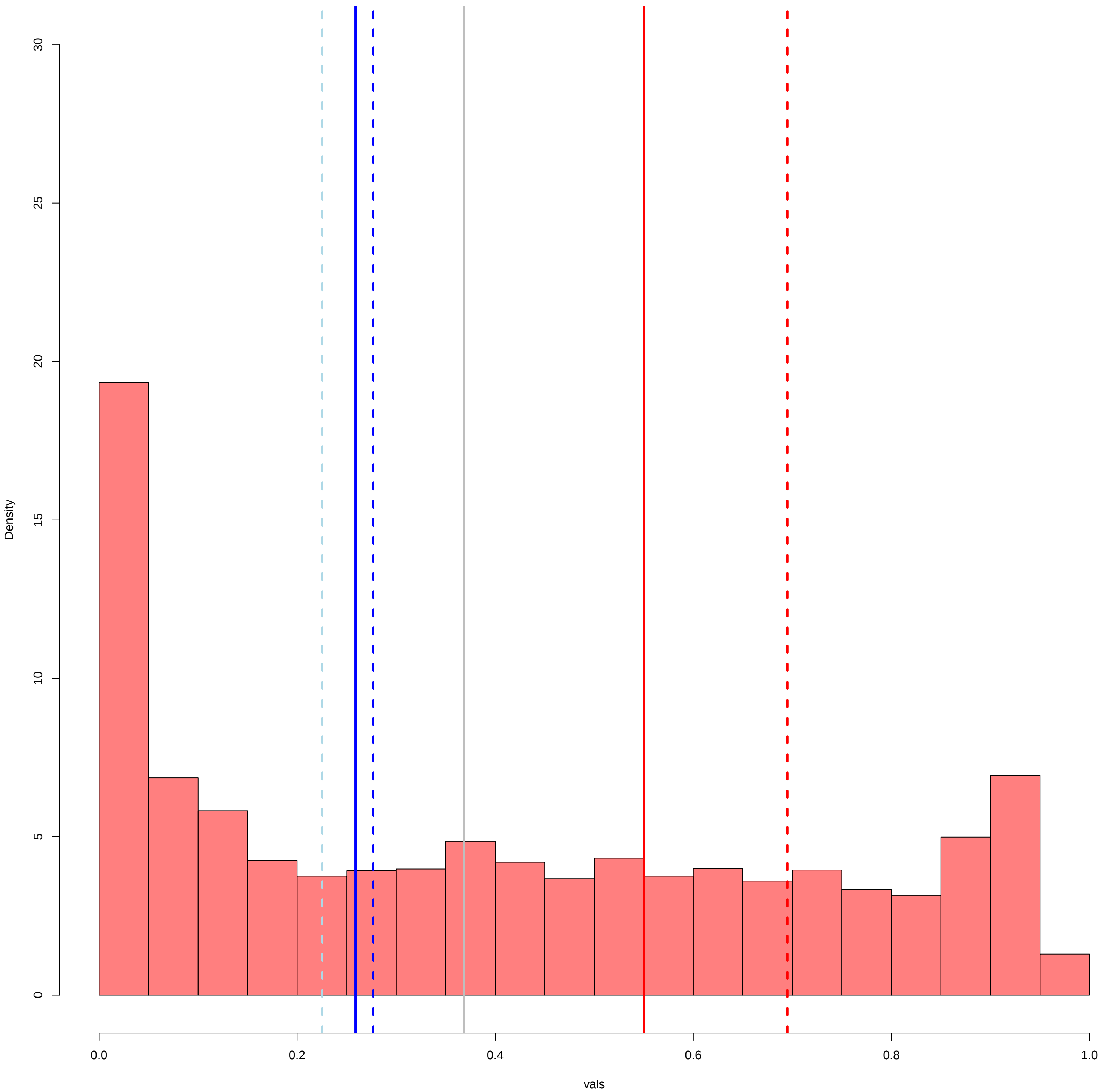
GRIN2A: GenoCanyon_score_rankscore



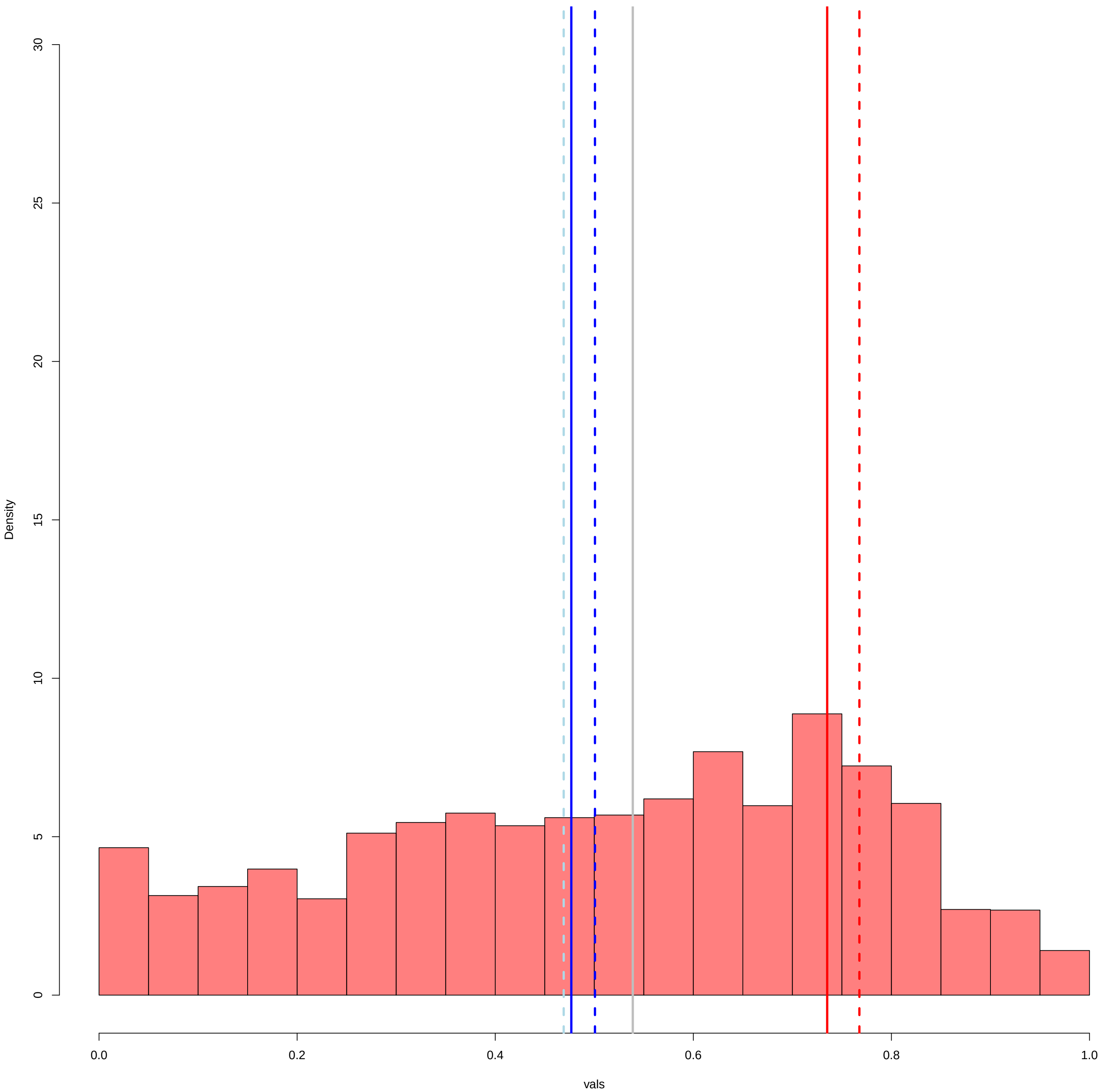
GRIN2A: MetaLR_rankscore



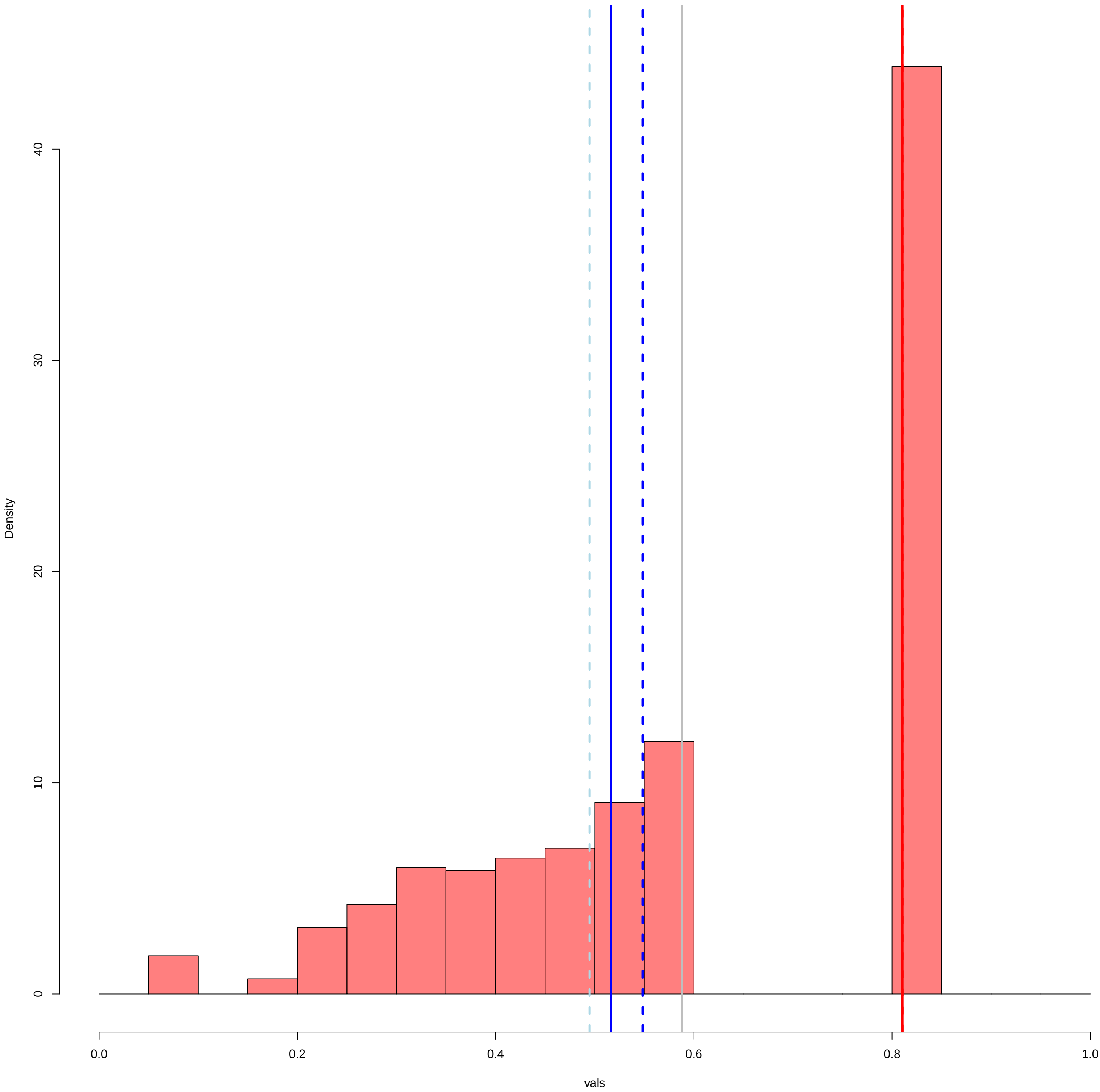
GRIN2A: MetaSVM_rankscore



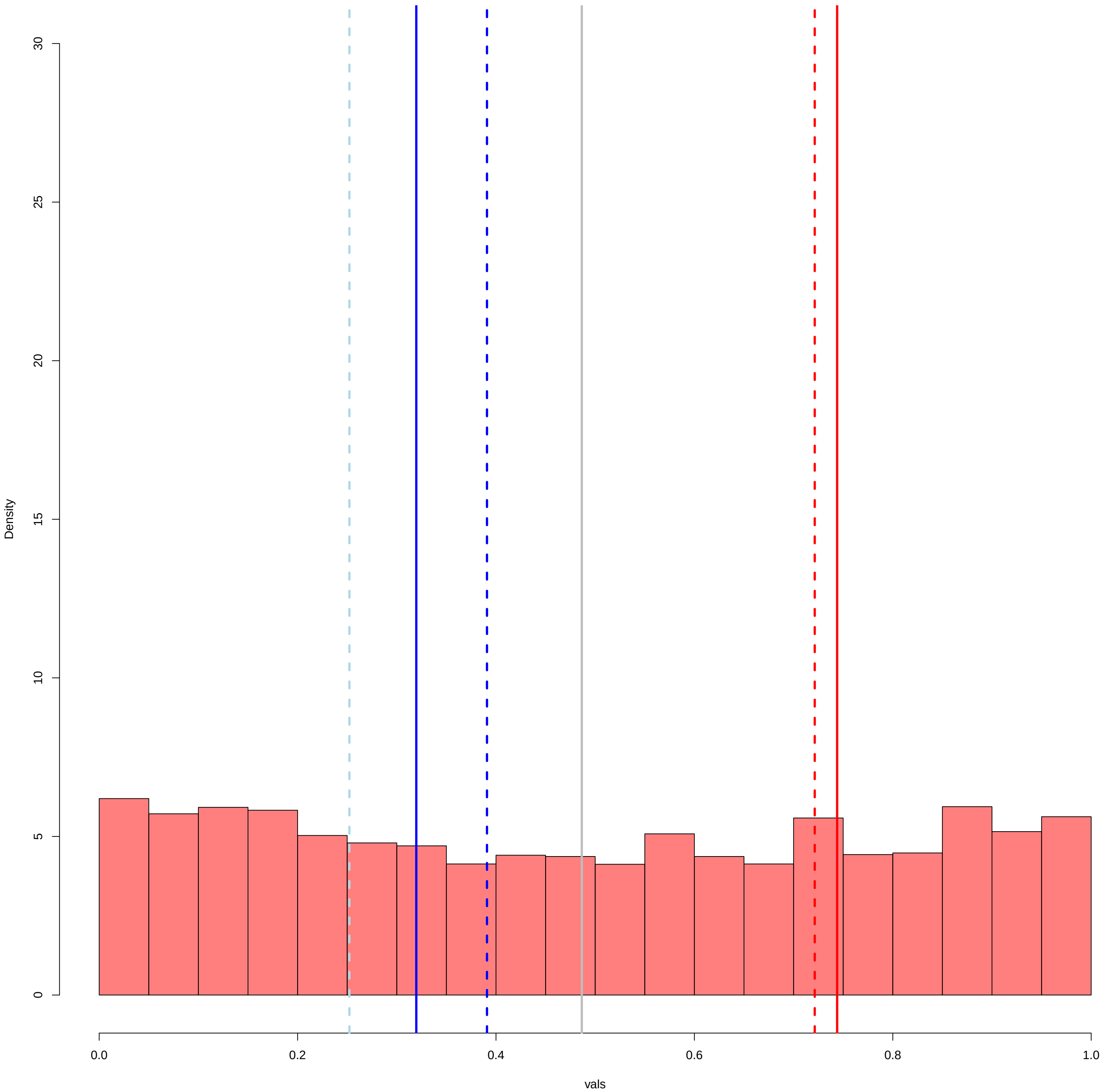
GRIN2A: MutationAssessor_score_rankscore



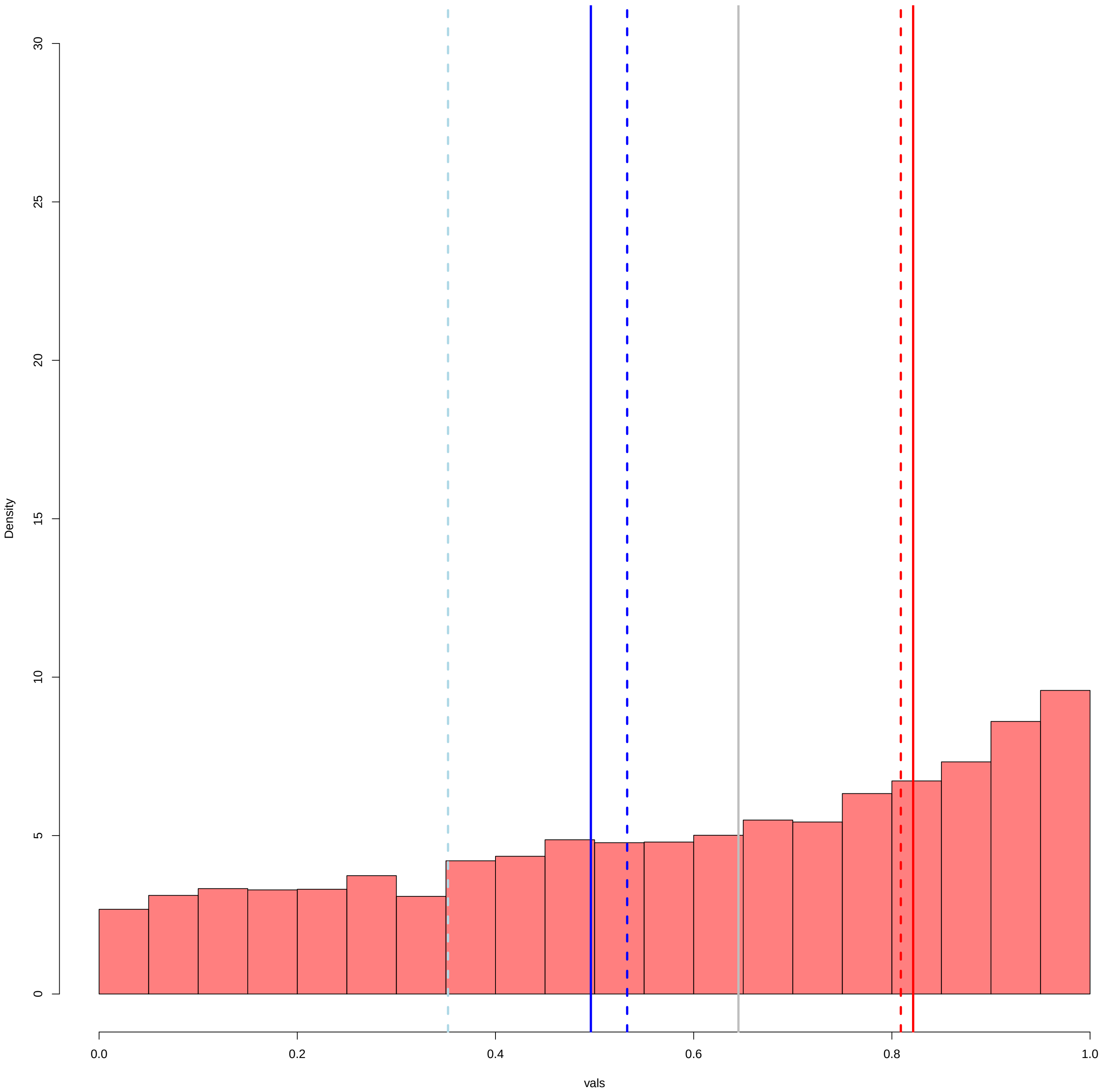
GRIN2A: MutationTaster_converted_rankscore



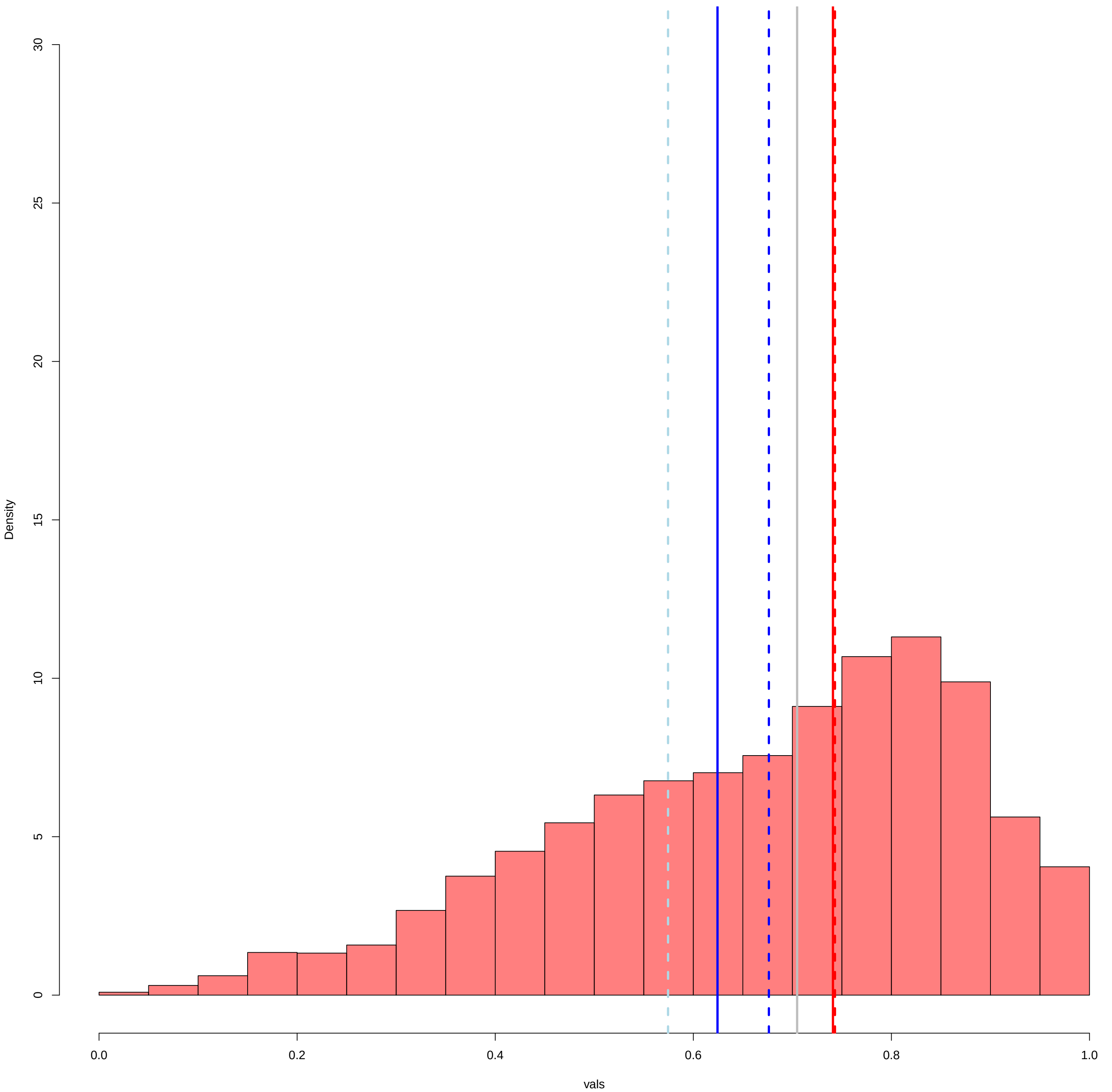
GRIN2A: PROVEAN_converted_rankscore



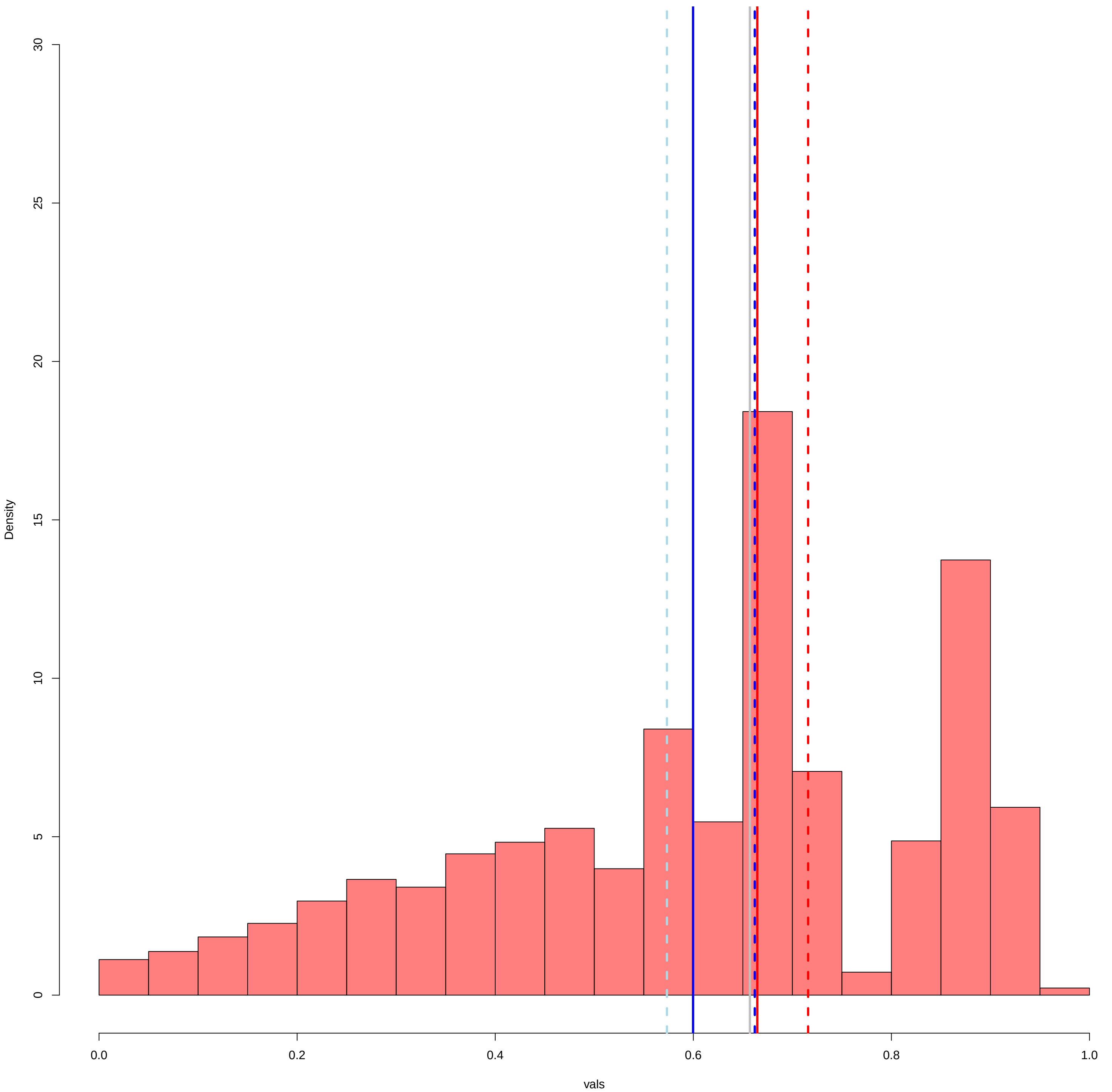
GRIN2A: VEST3_rankscore



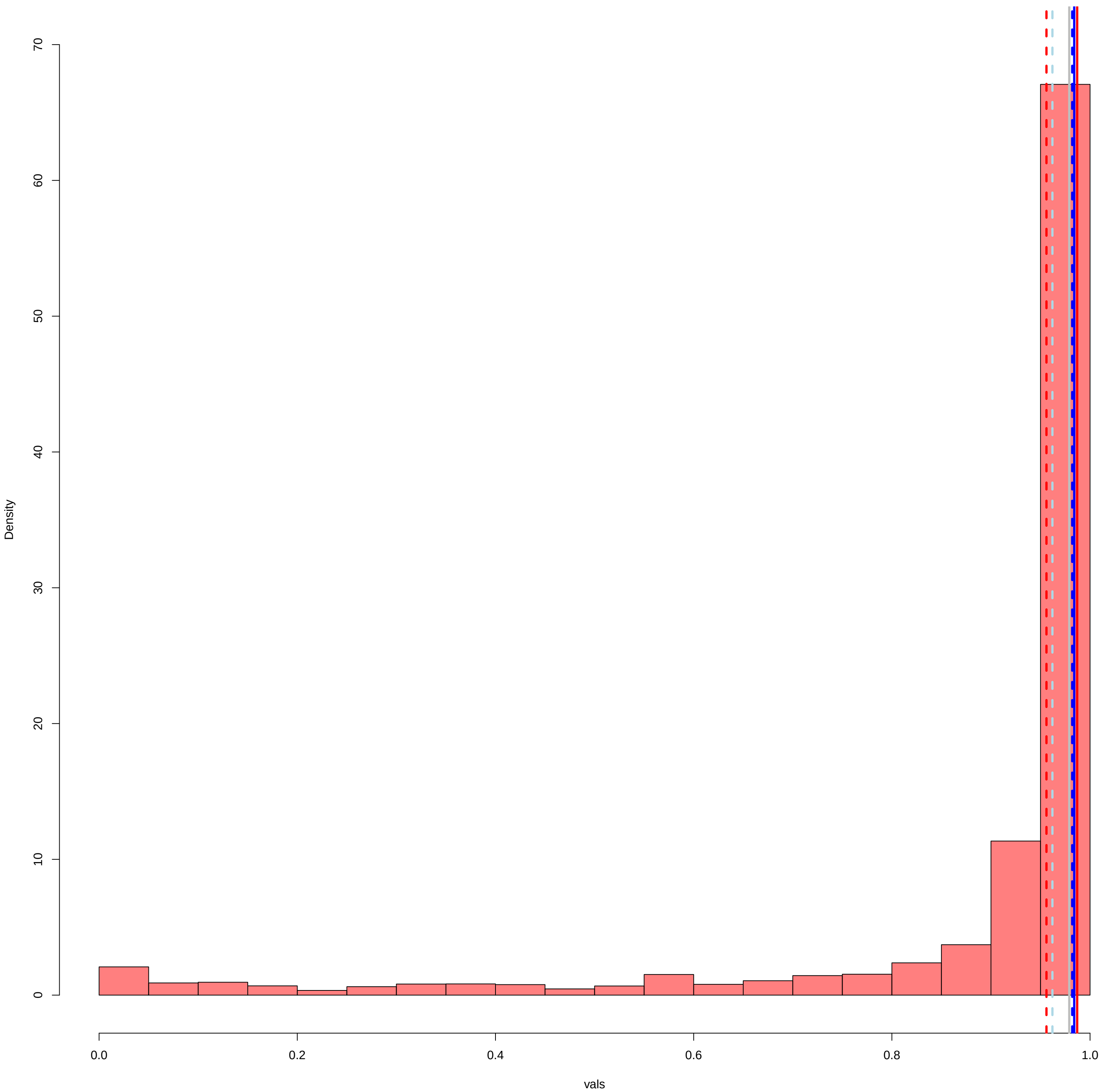
GRIN2A: fathmm-MKL_coding_rankscore



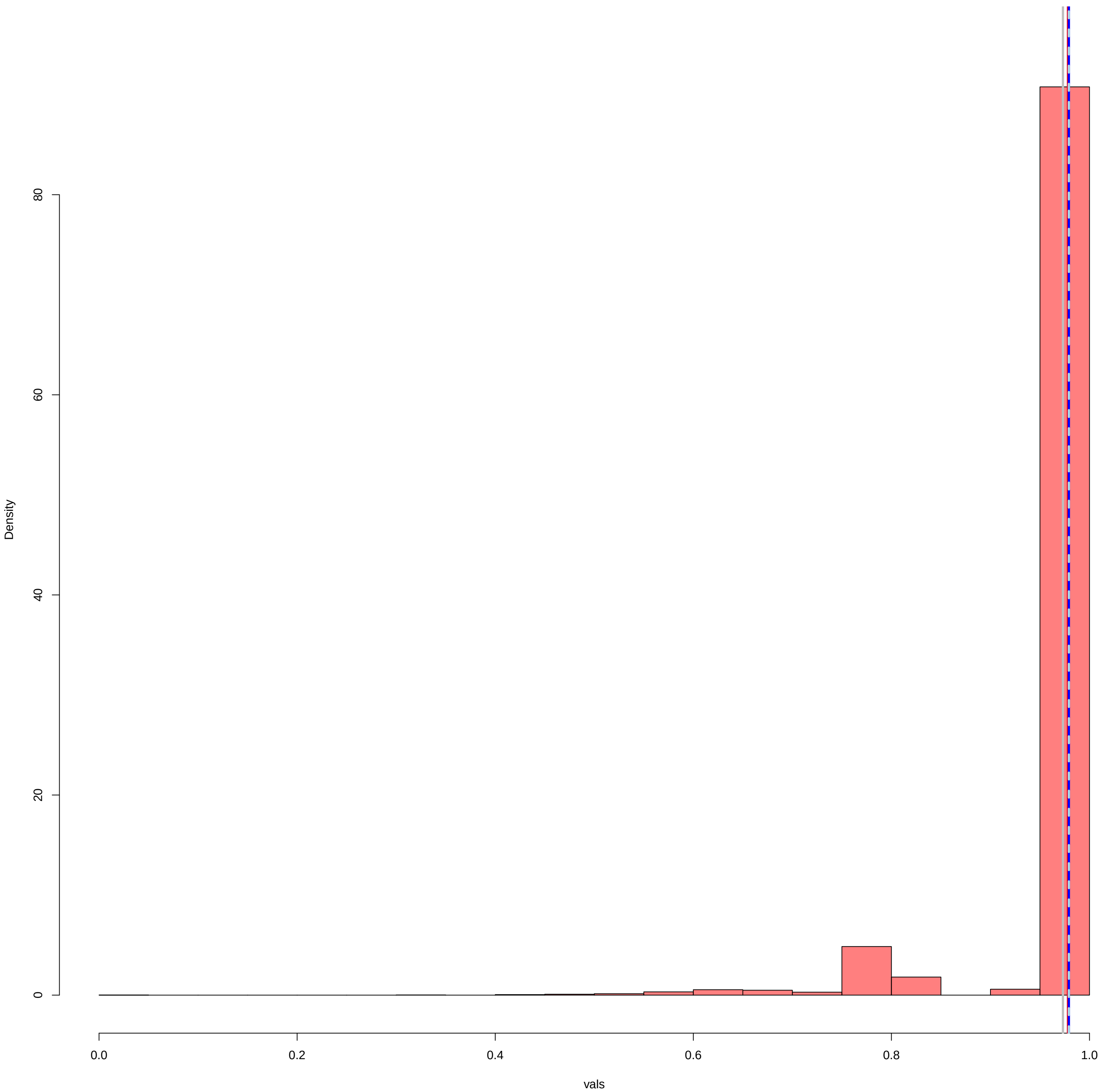
GRIN2A: SiPhy_29way_logOdds_rankscore



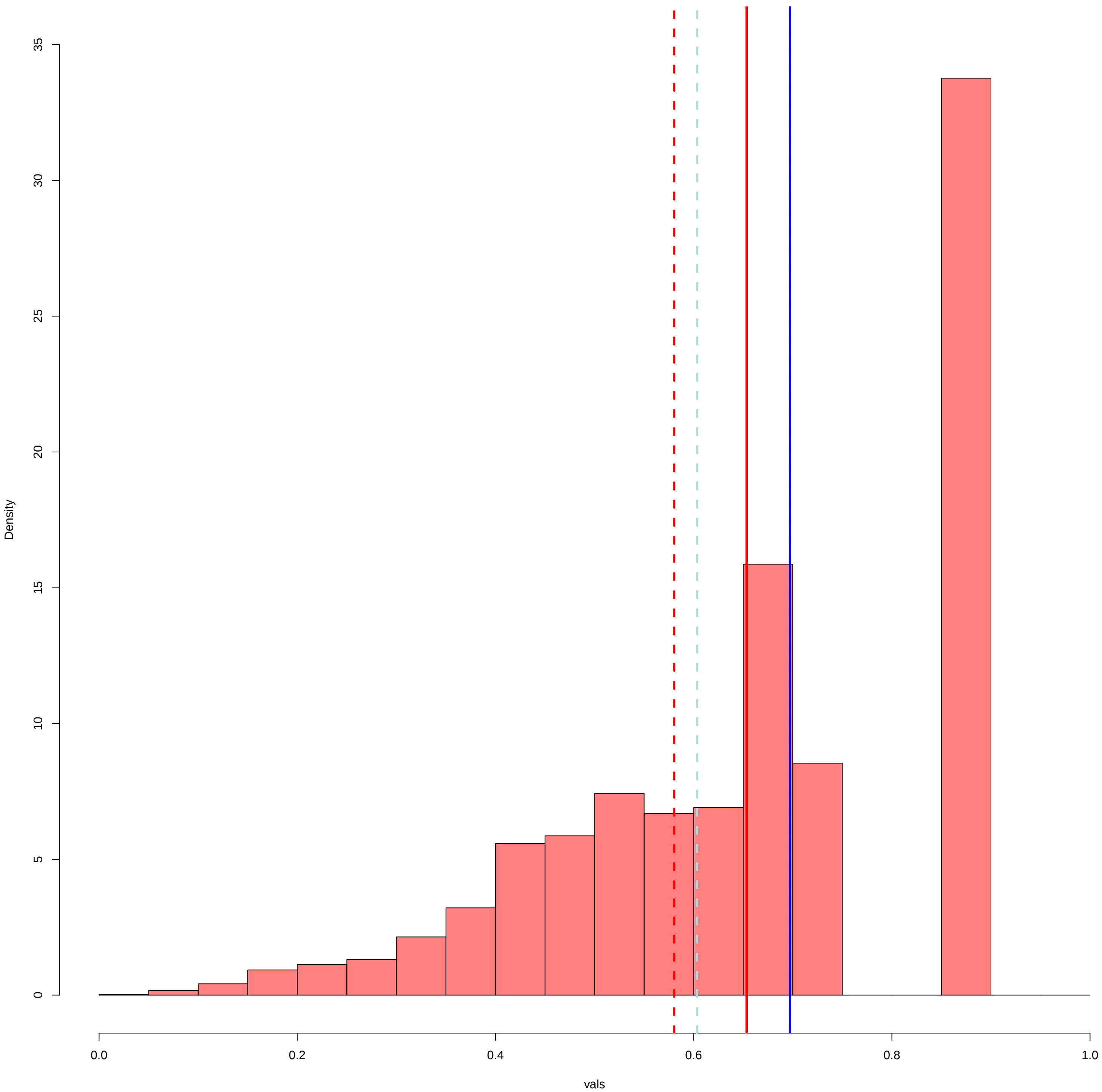
GRIN2A: priPhCons



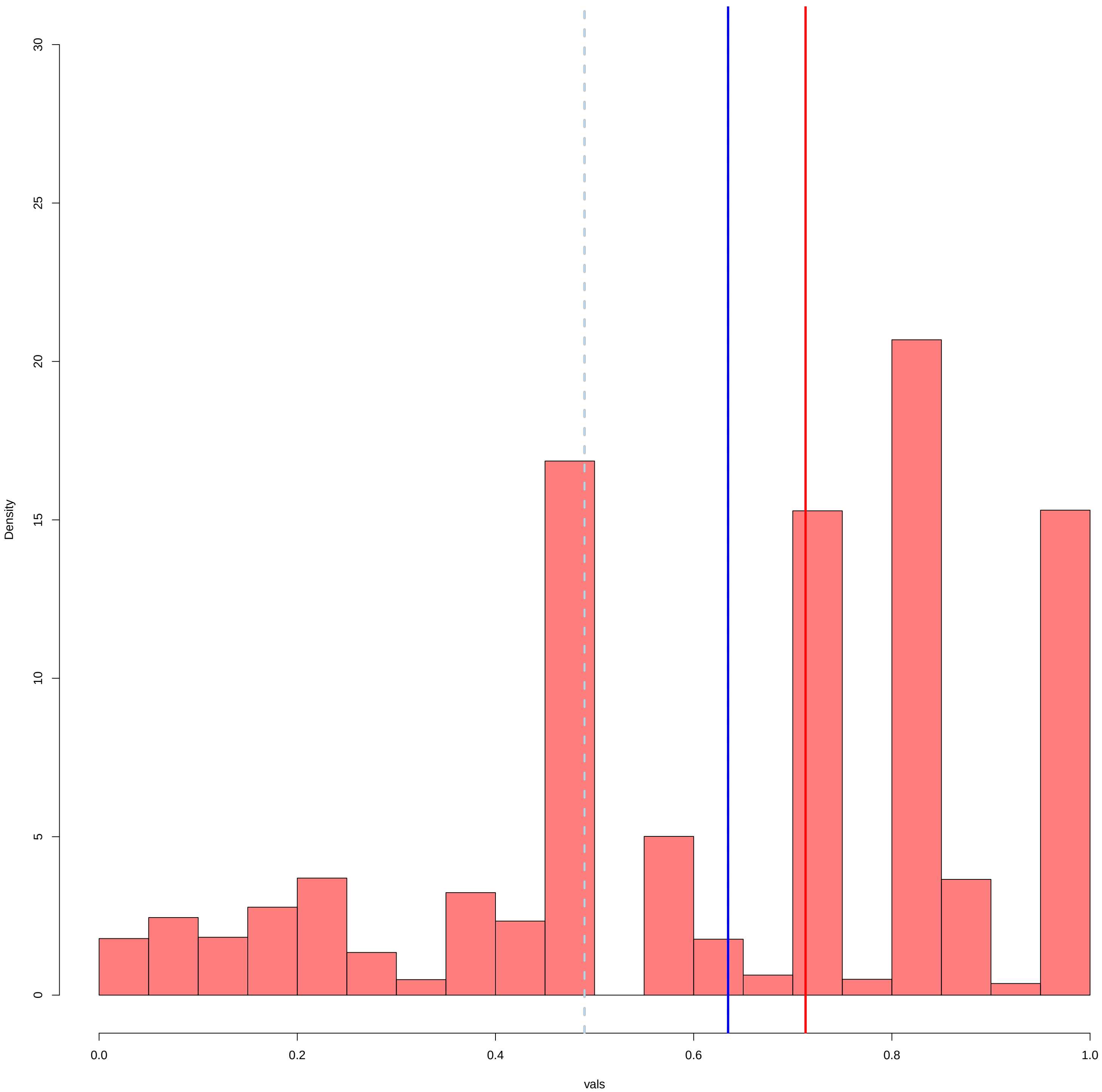
GRIN2A: priPhyloP



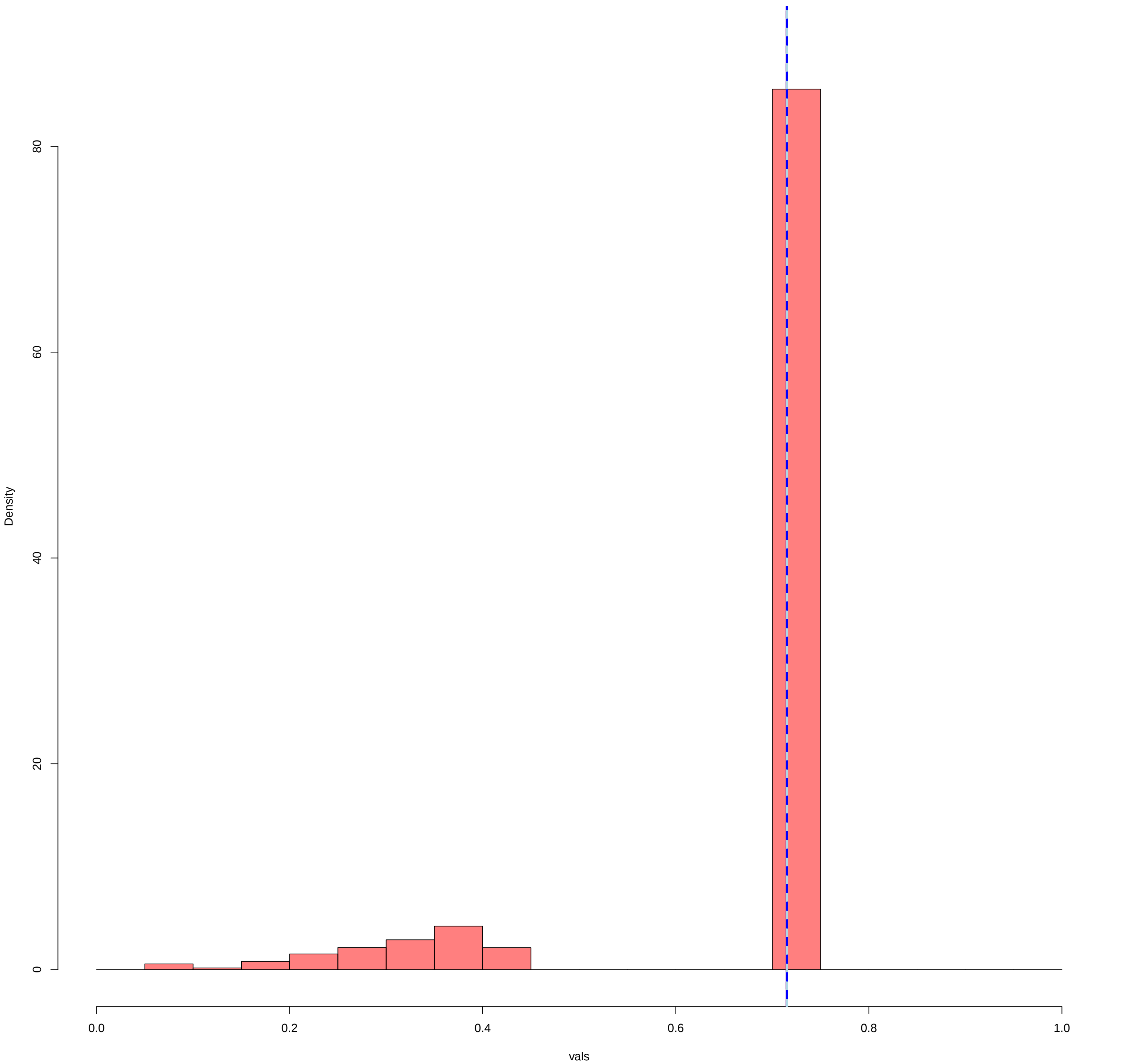
GRIN2A: phastCons20way_mammalian_rankscore



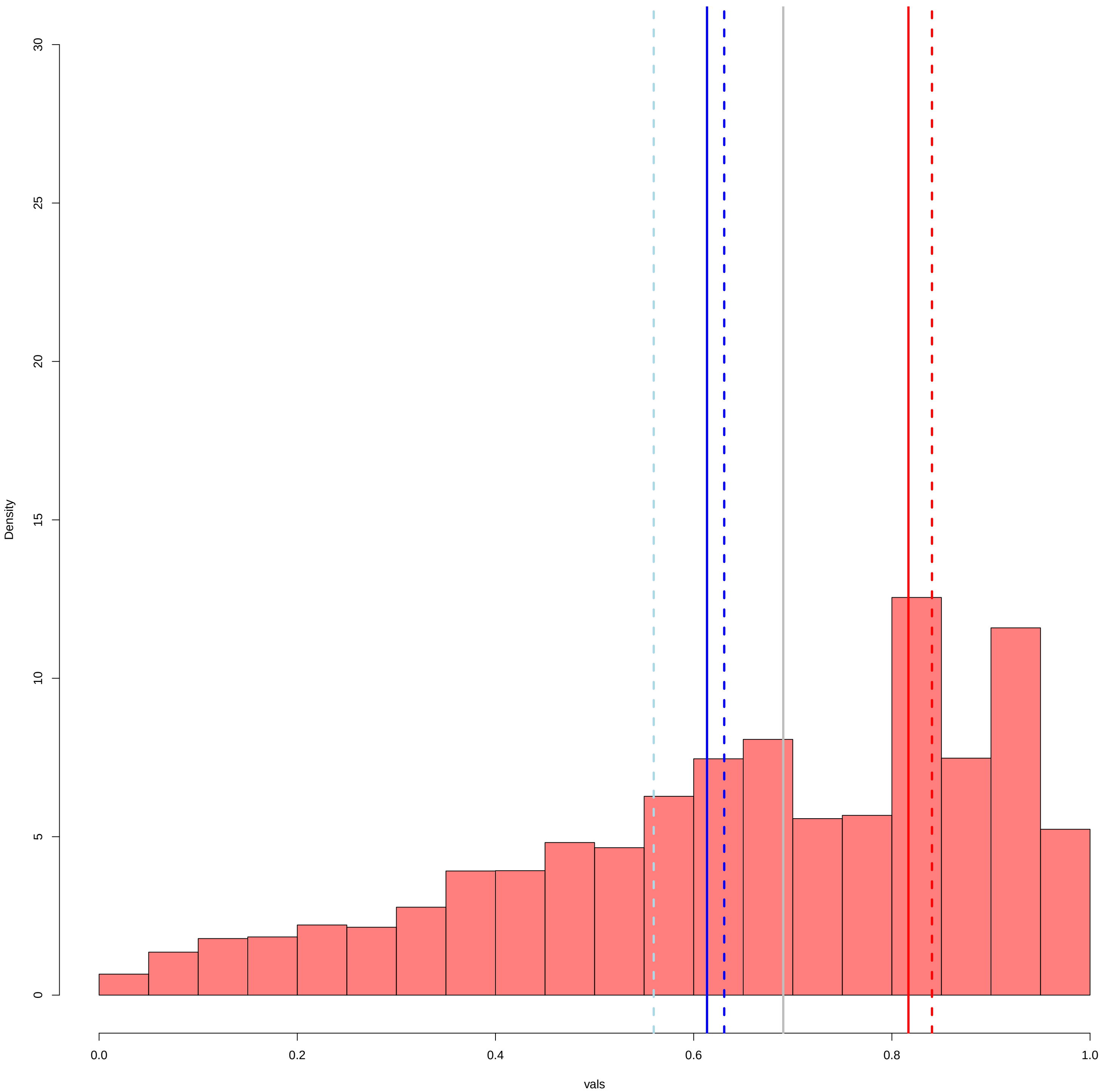
GRIN2A: phyloP20way_mammalian_rankscore



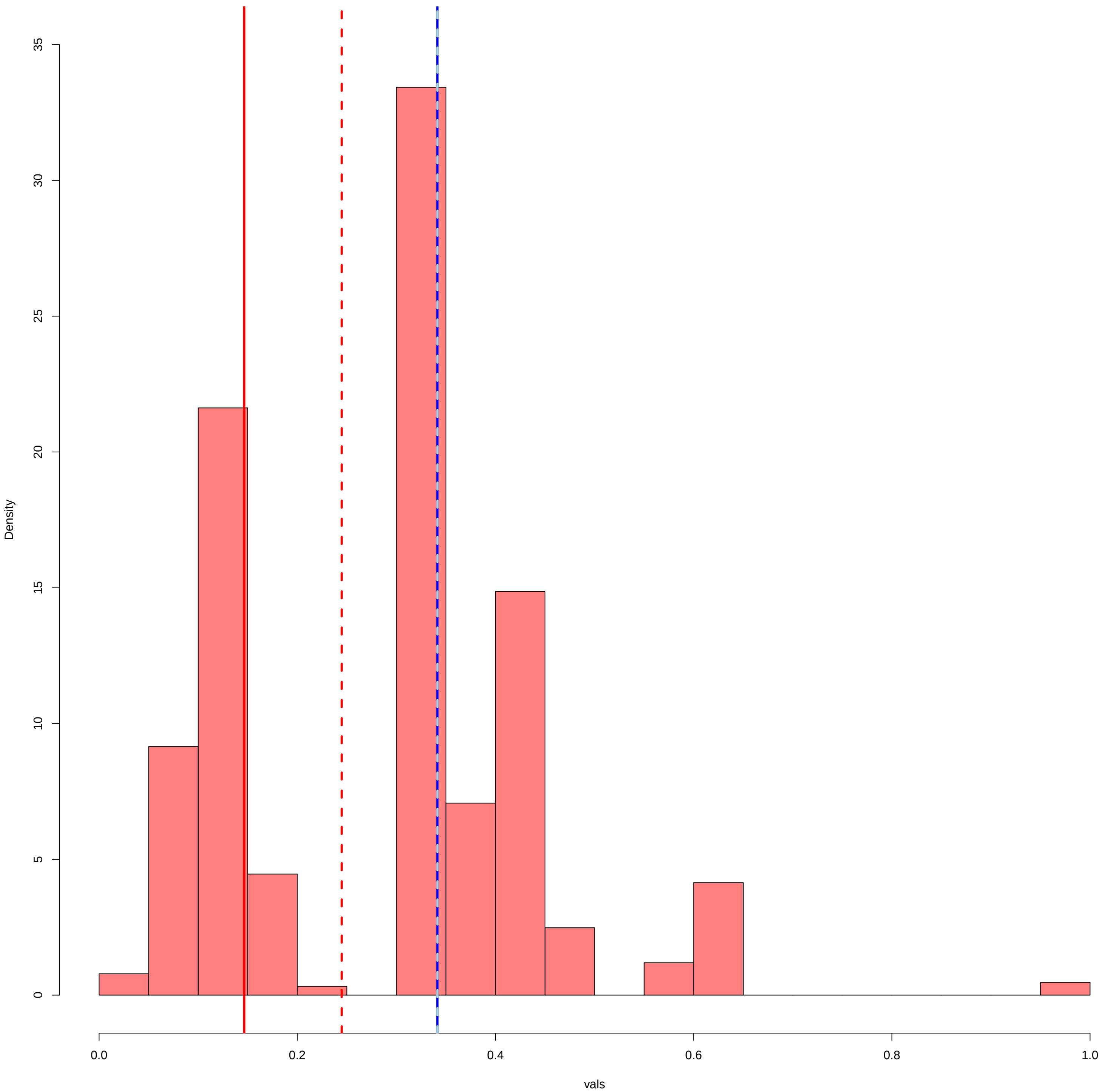
GRIN2A: phastCons100way_vertebrate_rankscore



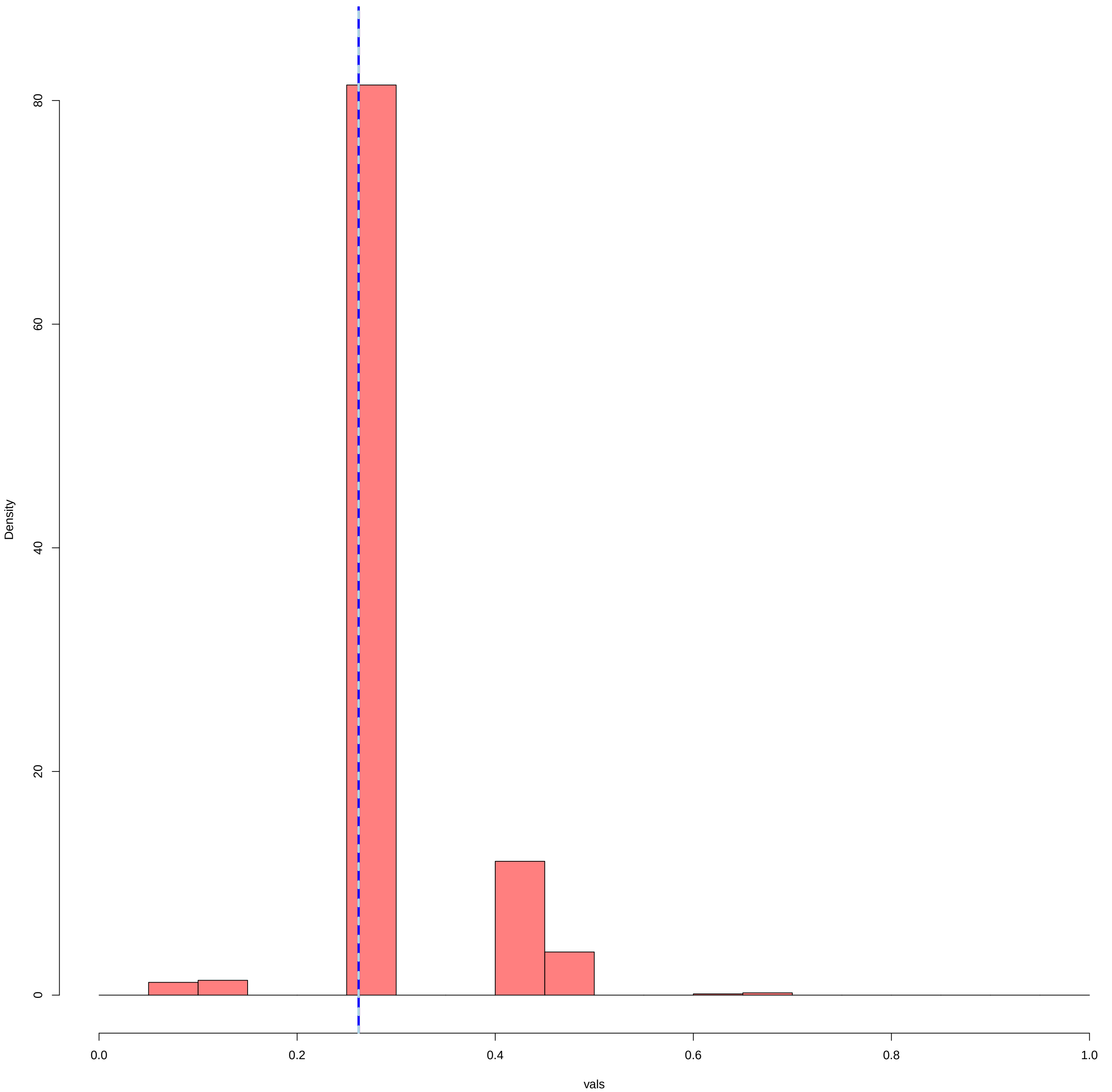
GRIN2A: phyloP100way_vertibrate_rankscore



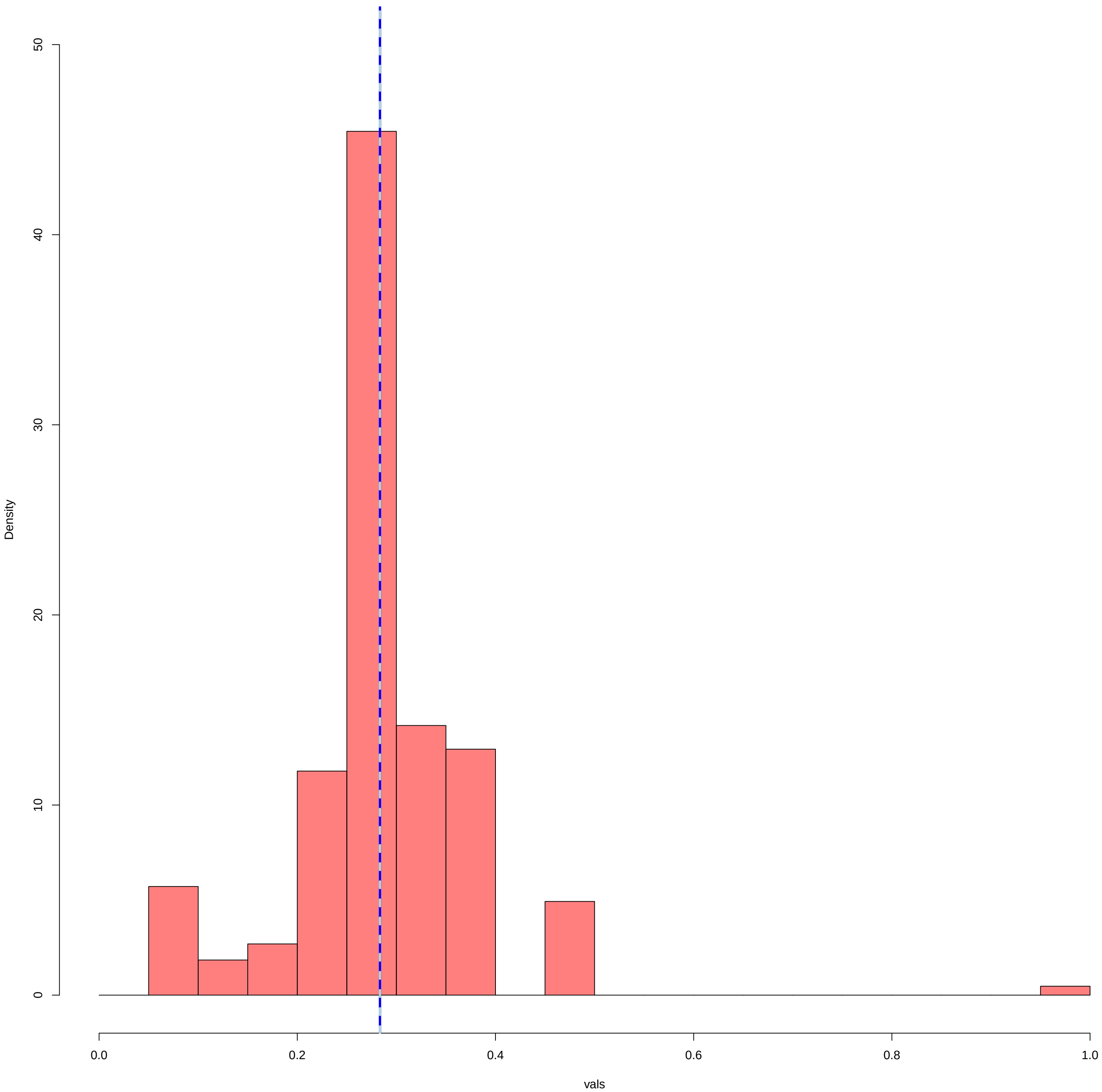
GRIN2A: H1-hESC_fitCons_score_rankscore



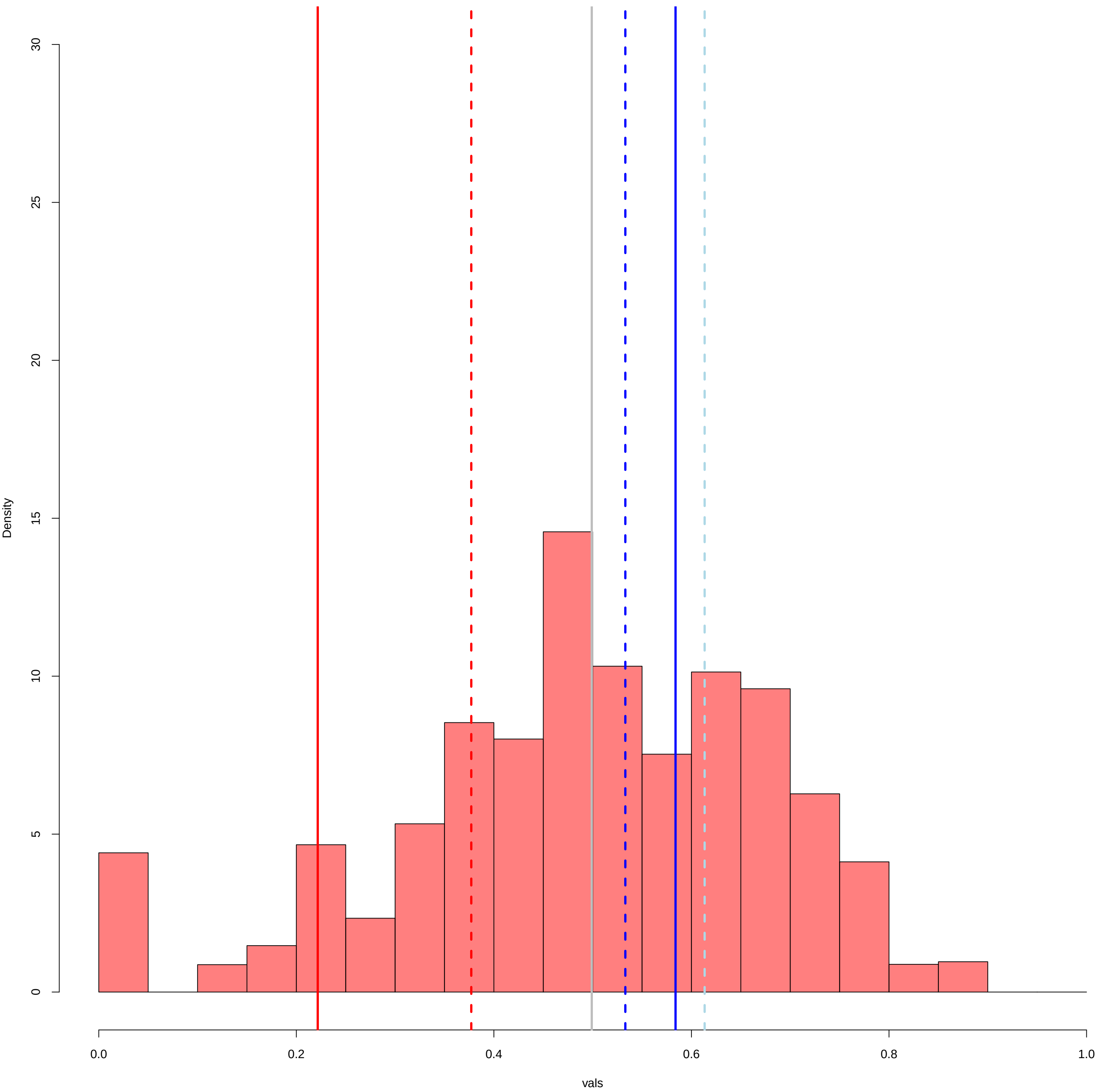
GRIN2A: HUVEC_fitCons_score_rankscore



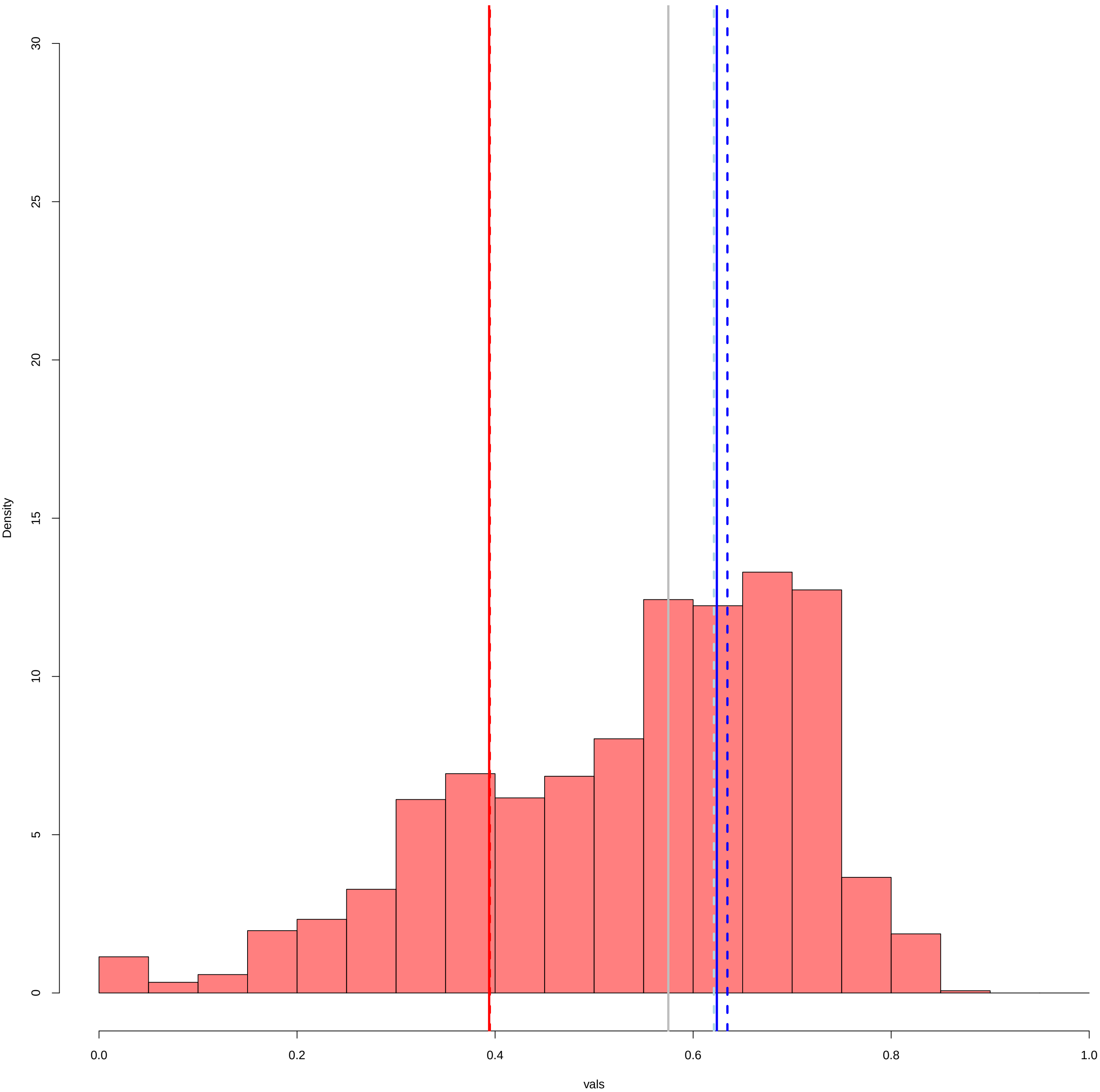
GRIN2A: integrated_fitCons_score_rankscore



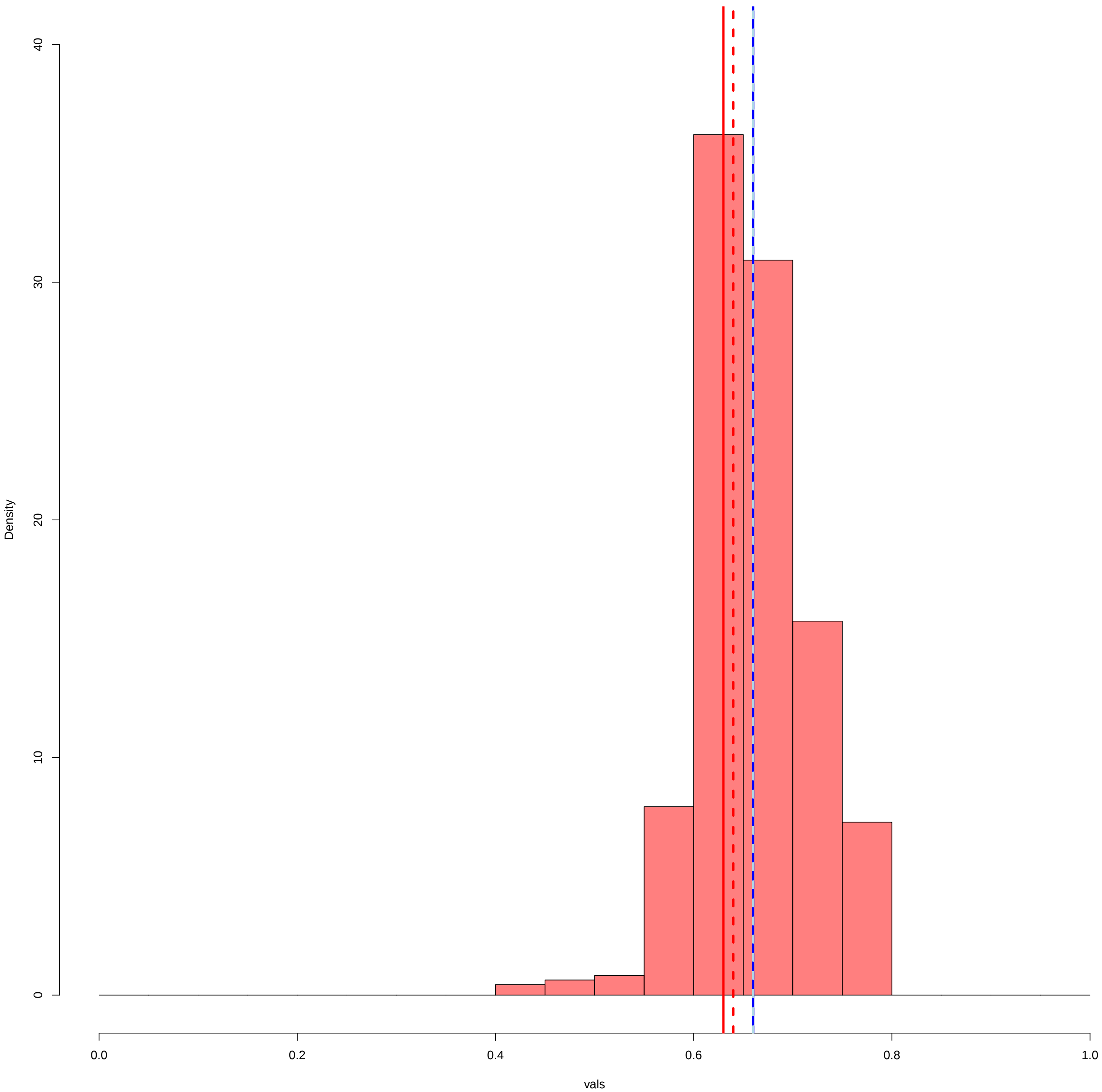
GRIN2A: ExAC v1 MTR



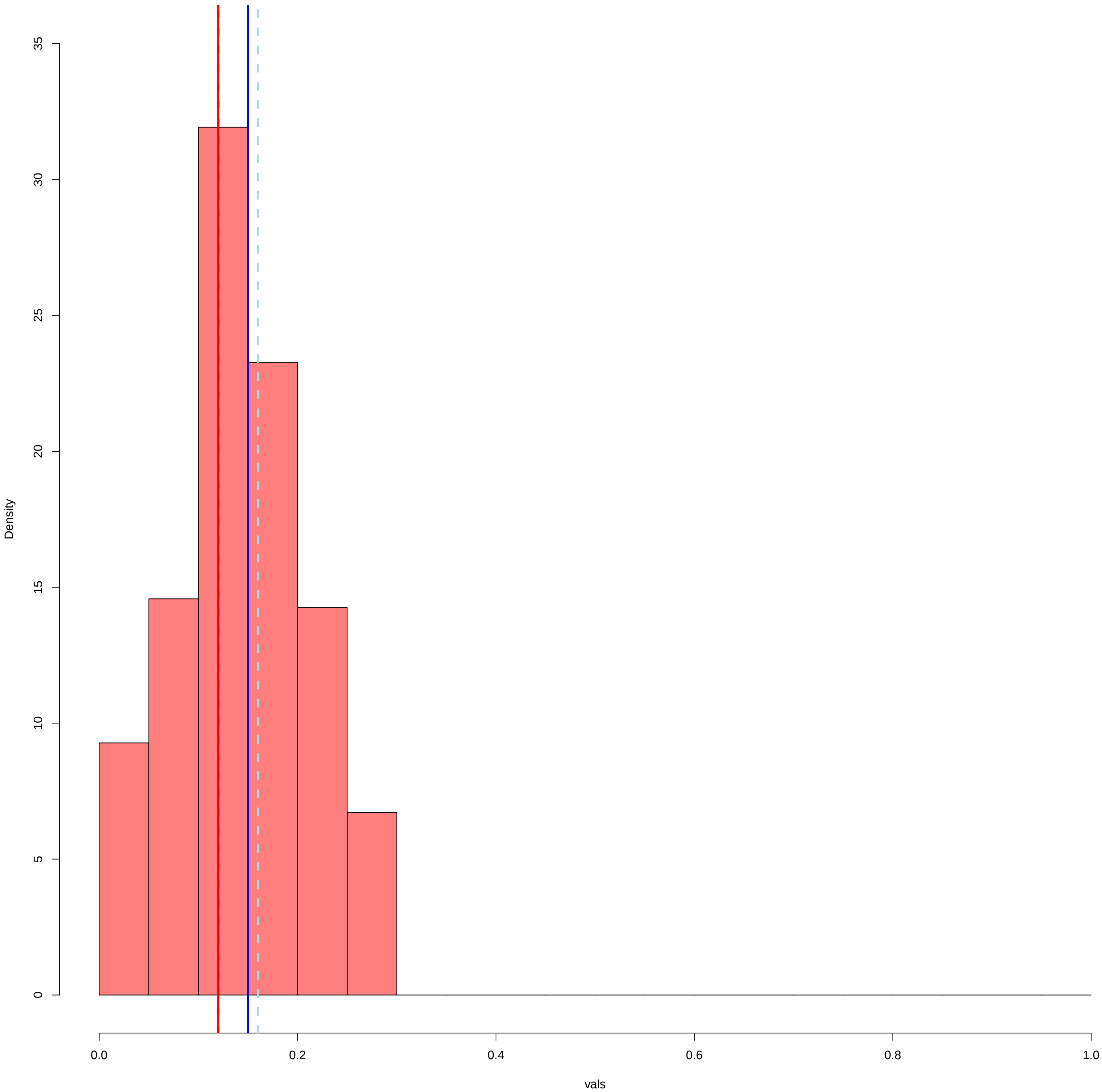
GRIN2A: ExAC v2 & gnomAD MTR



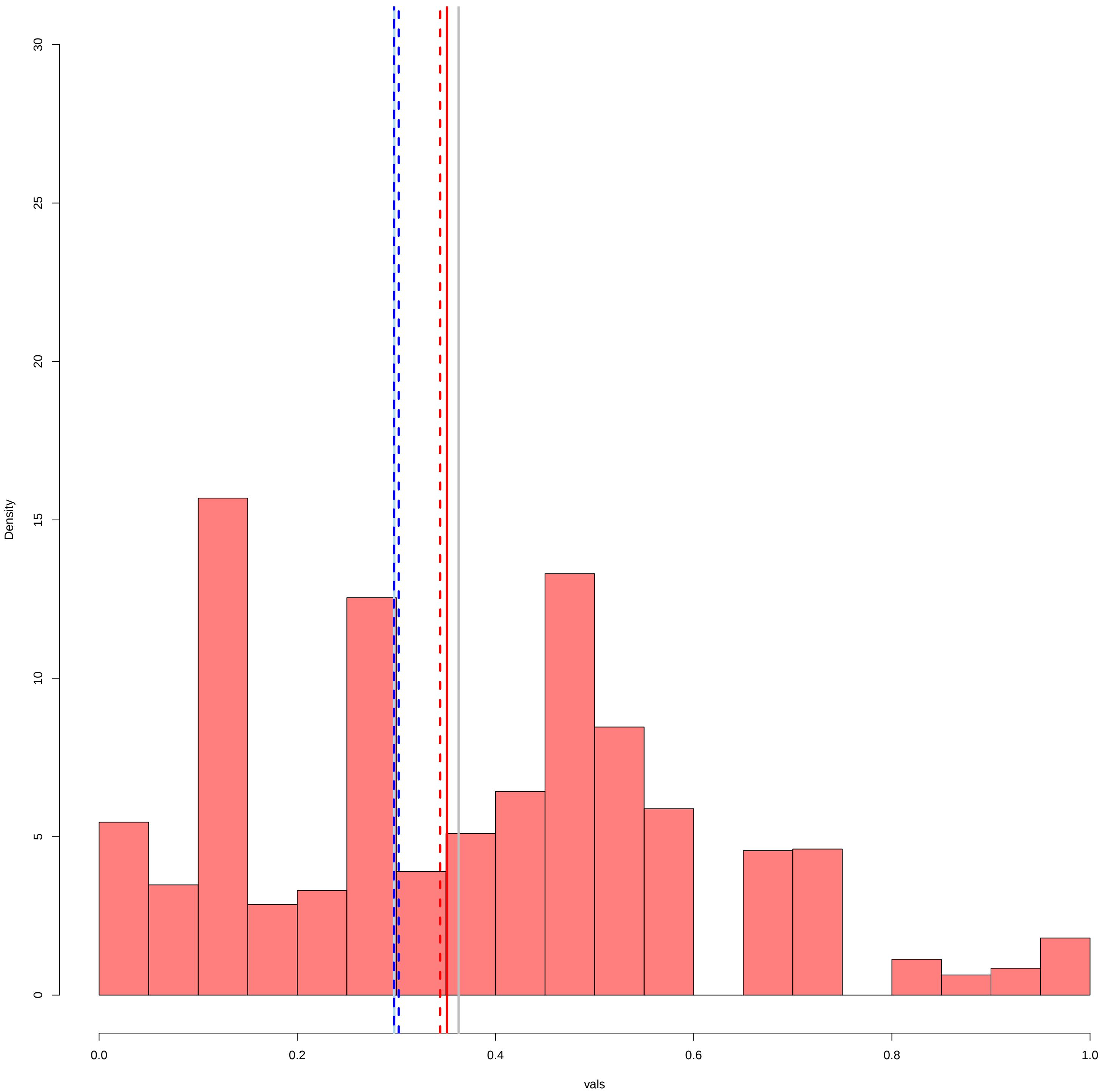
KCNQ2: GC (Percent GC content in a window of ± 75 bp)



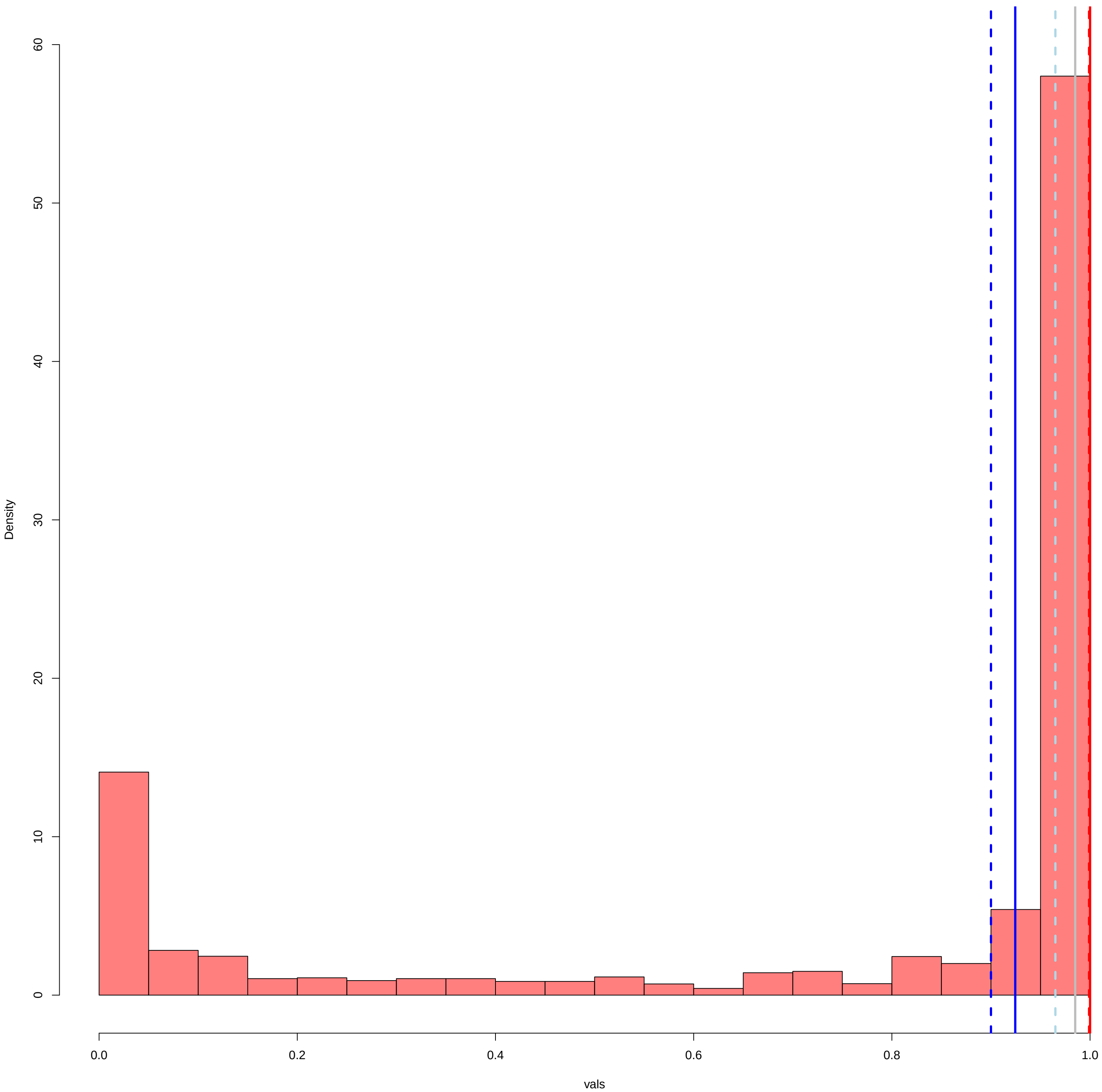
KCNQ2: CpG (Percent CpG in a window of +/-75bp)



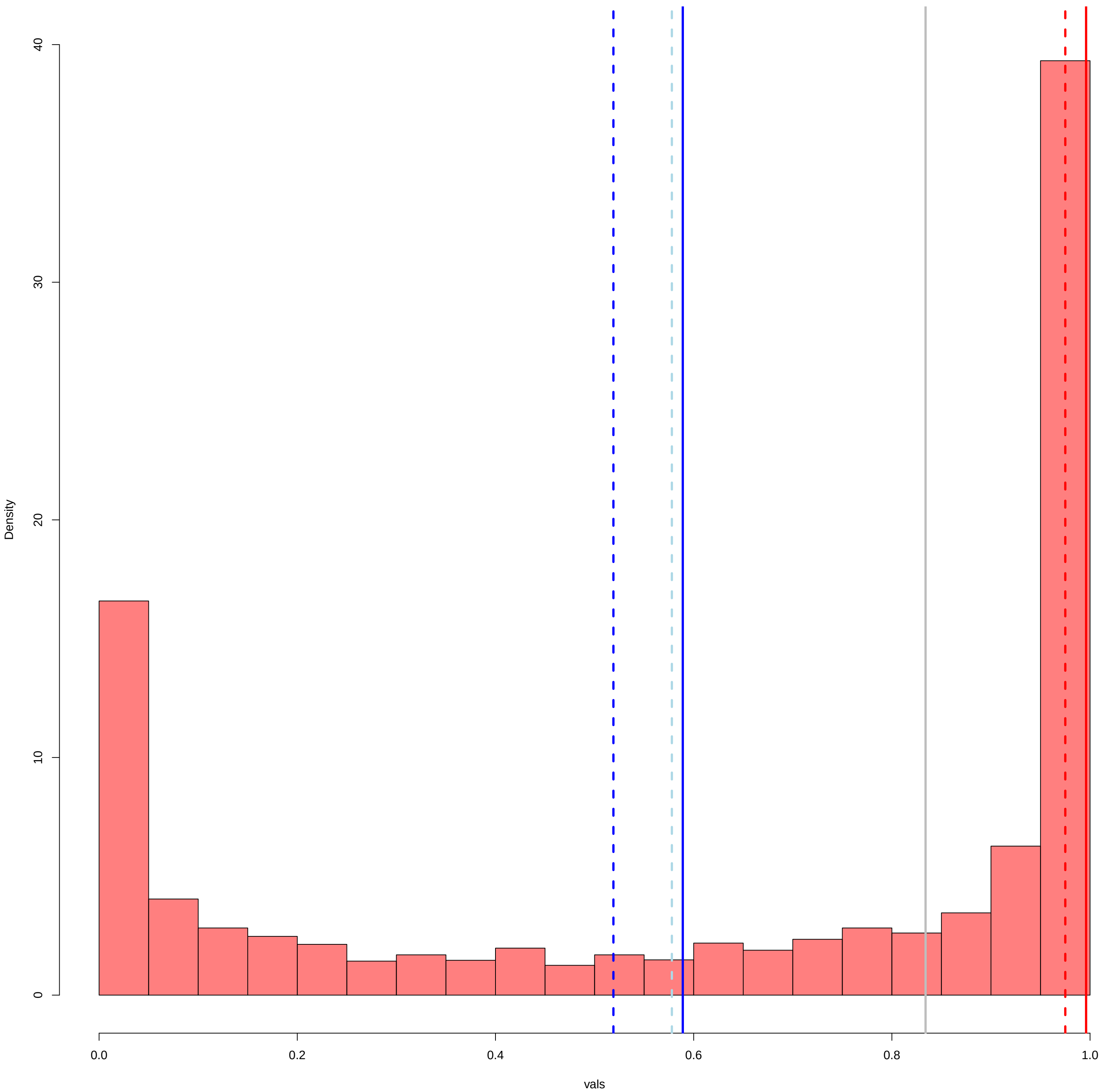
KCNQ2: Grantham



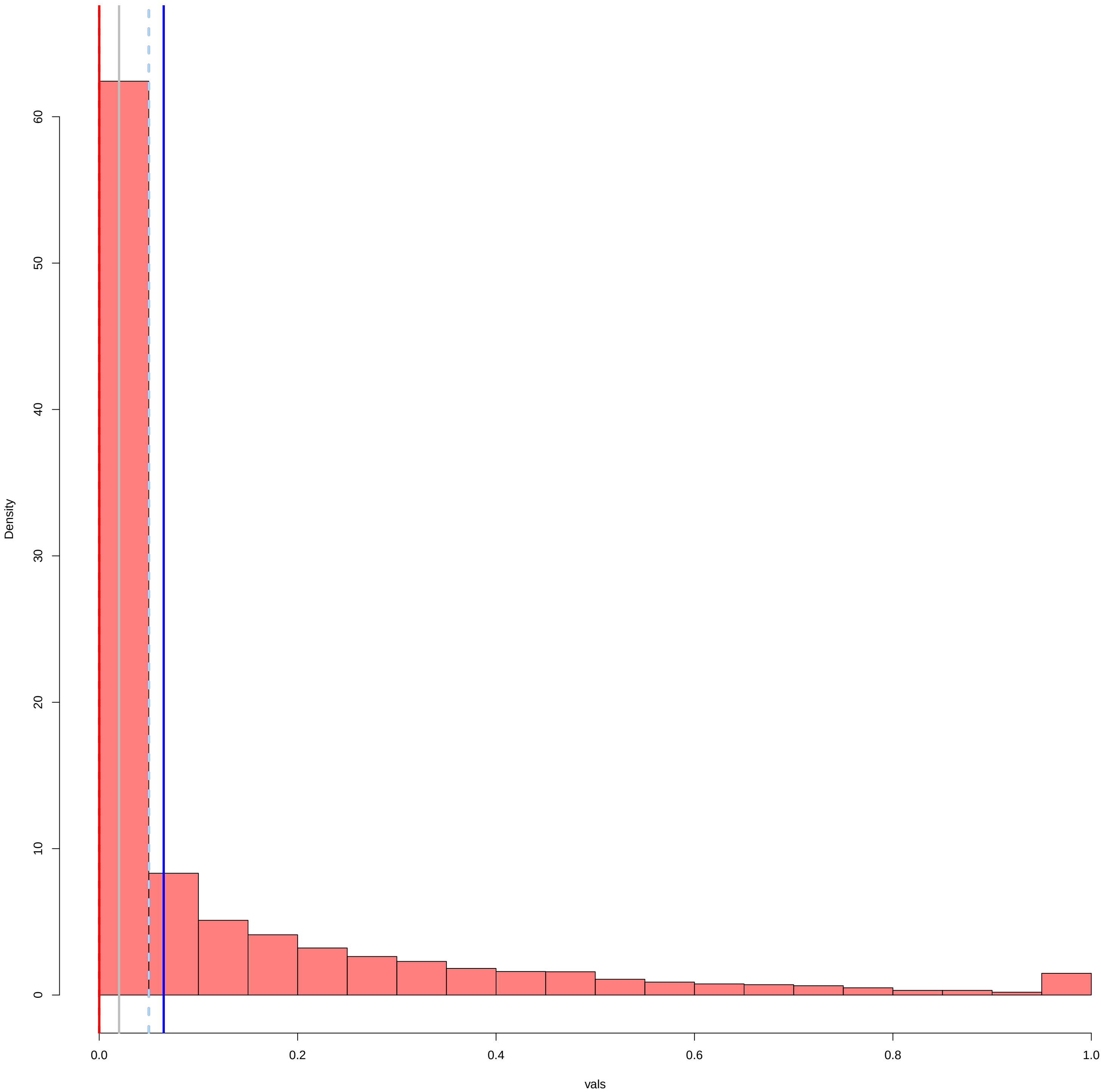
KCNQ2: Hdiv quan



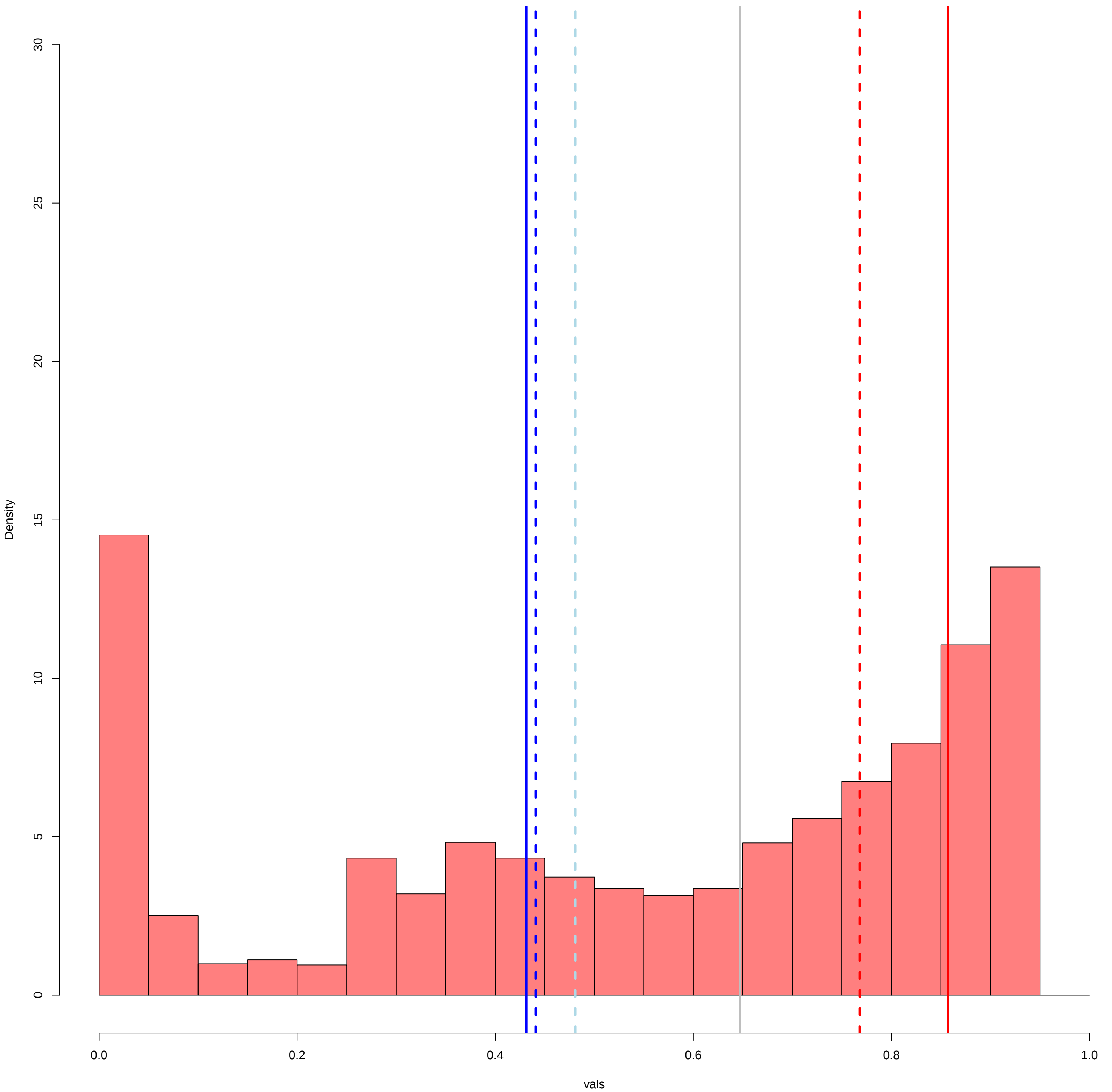
KCNQ2: Hvar quan



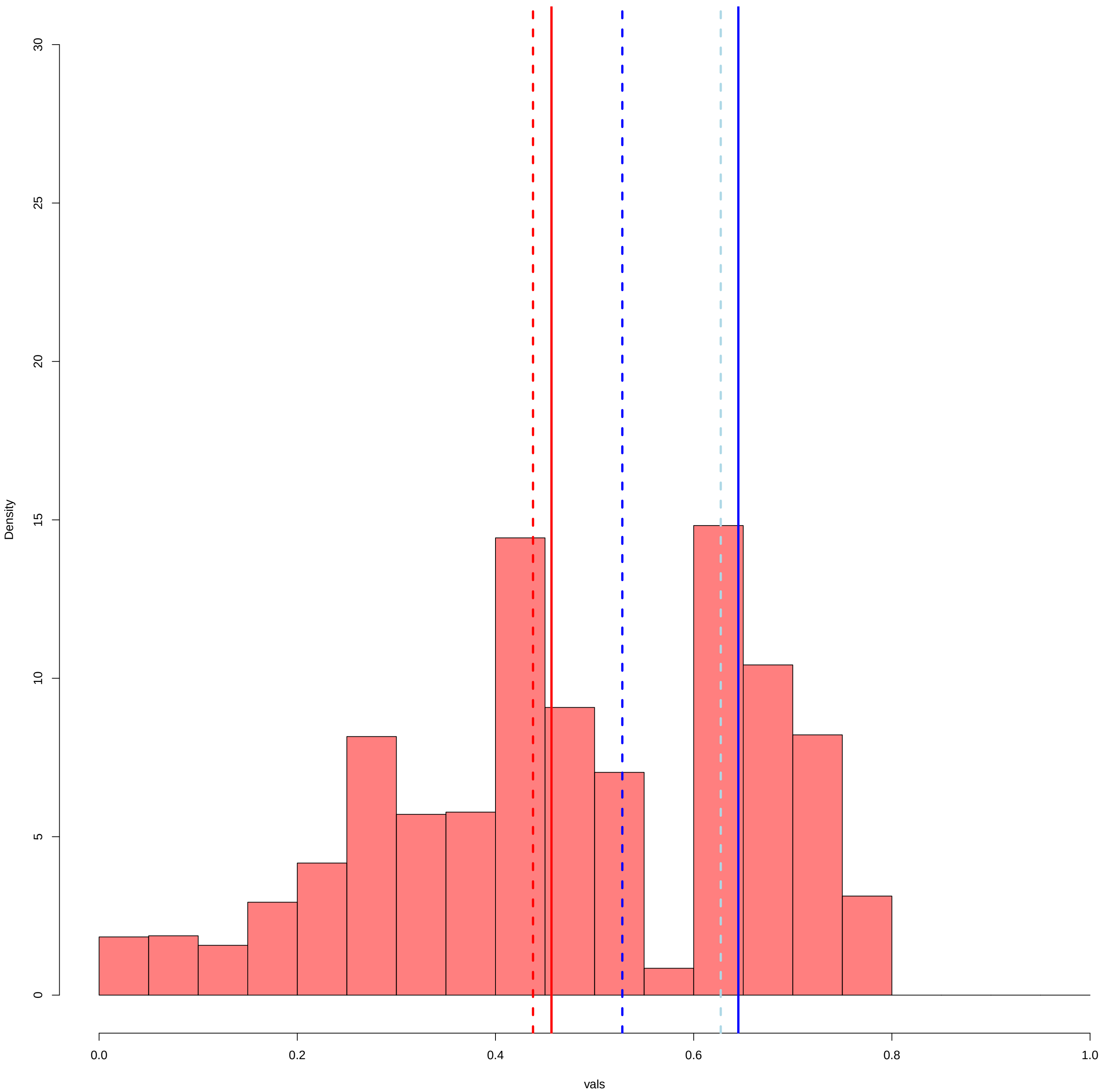
KCNQ2: SIFT



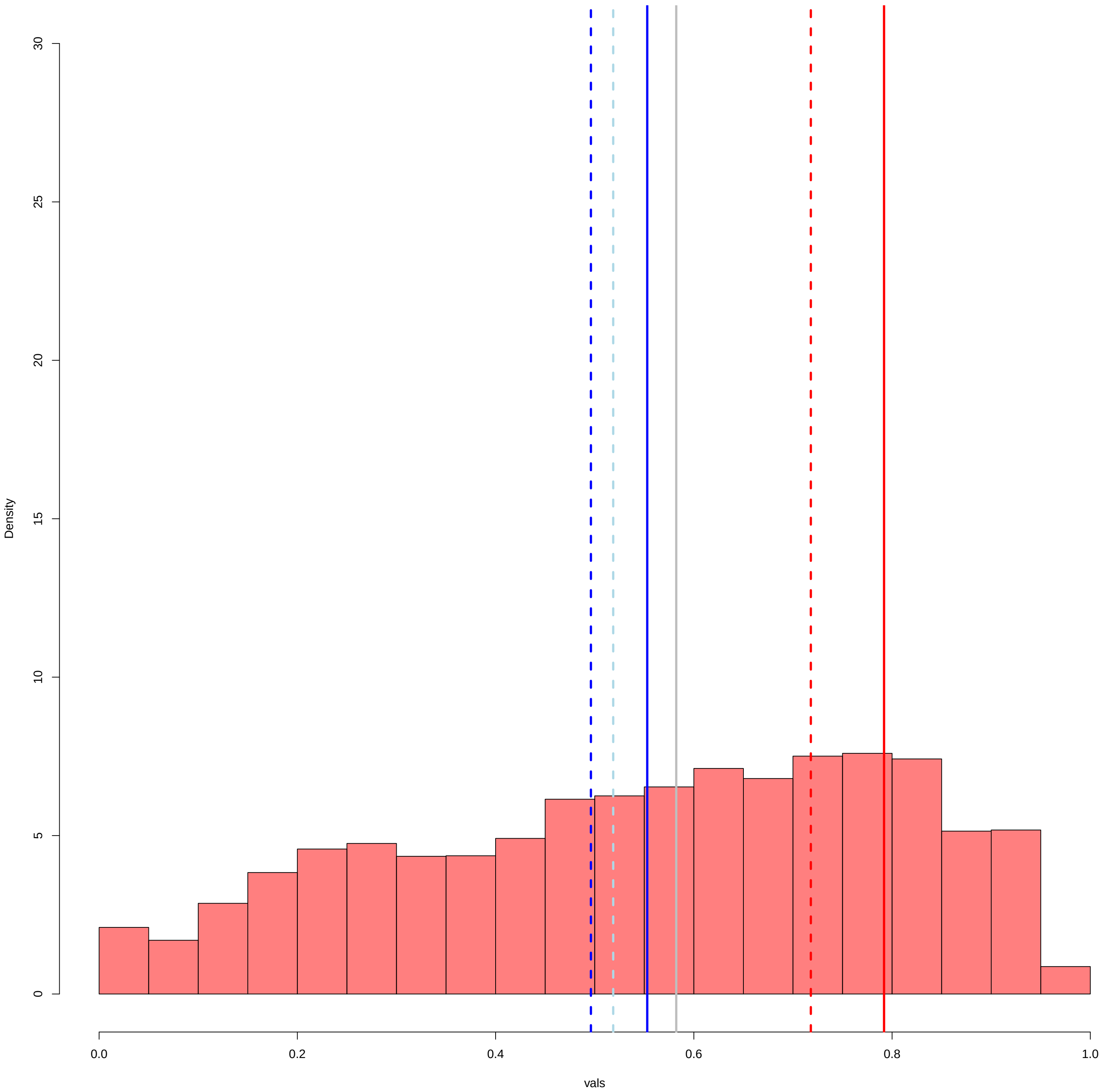
KCNQ2: Condel



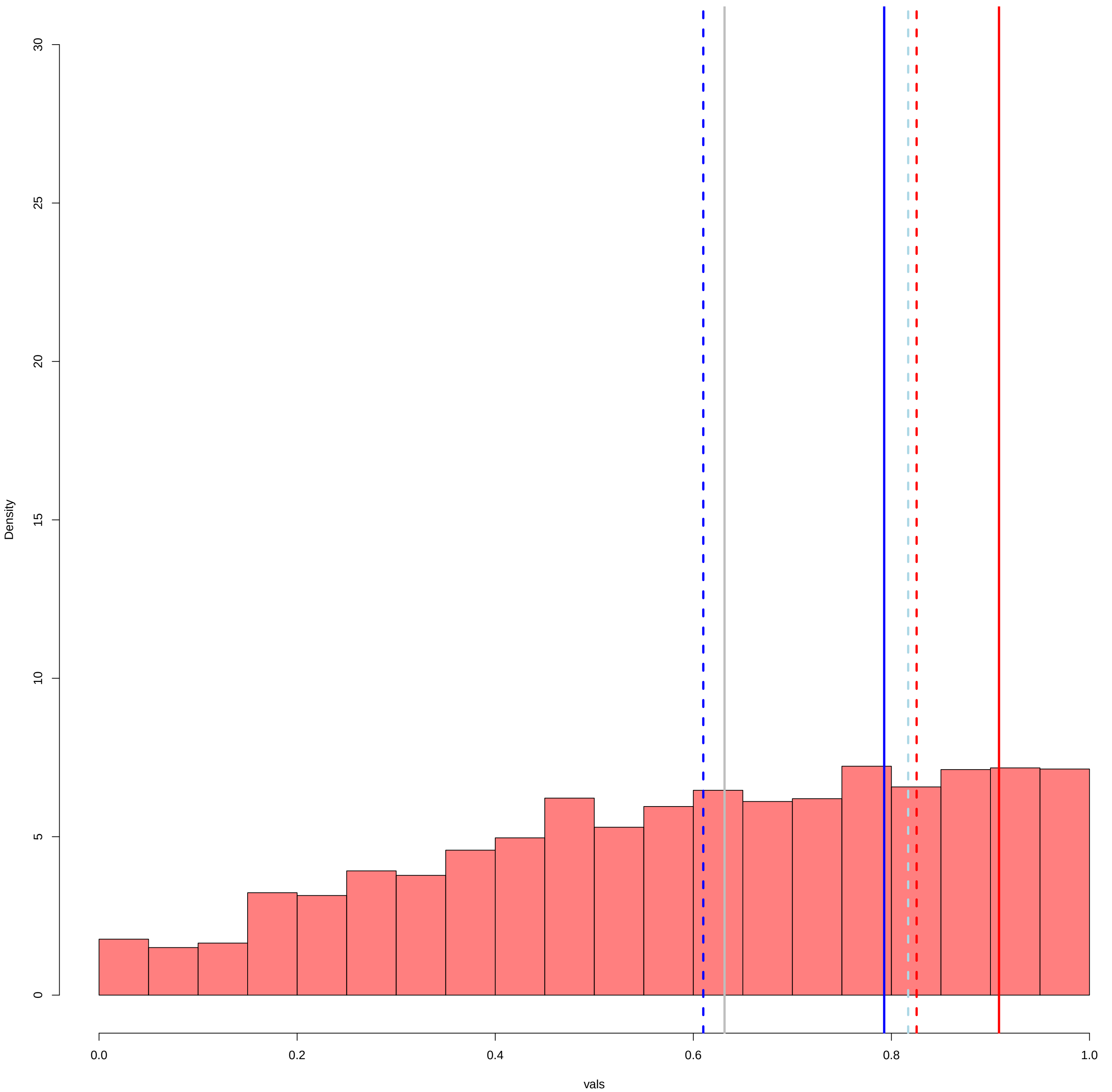
KCNQ2: GERP++_RS_rankscore



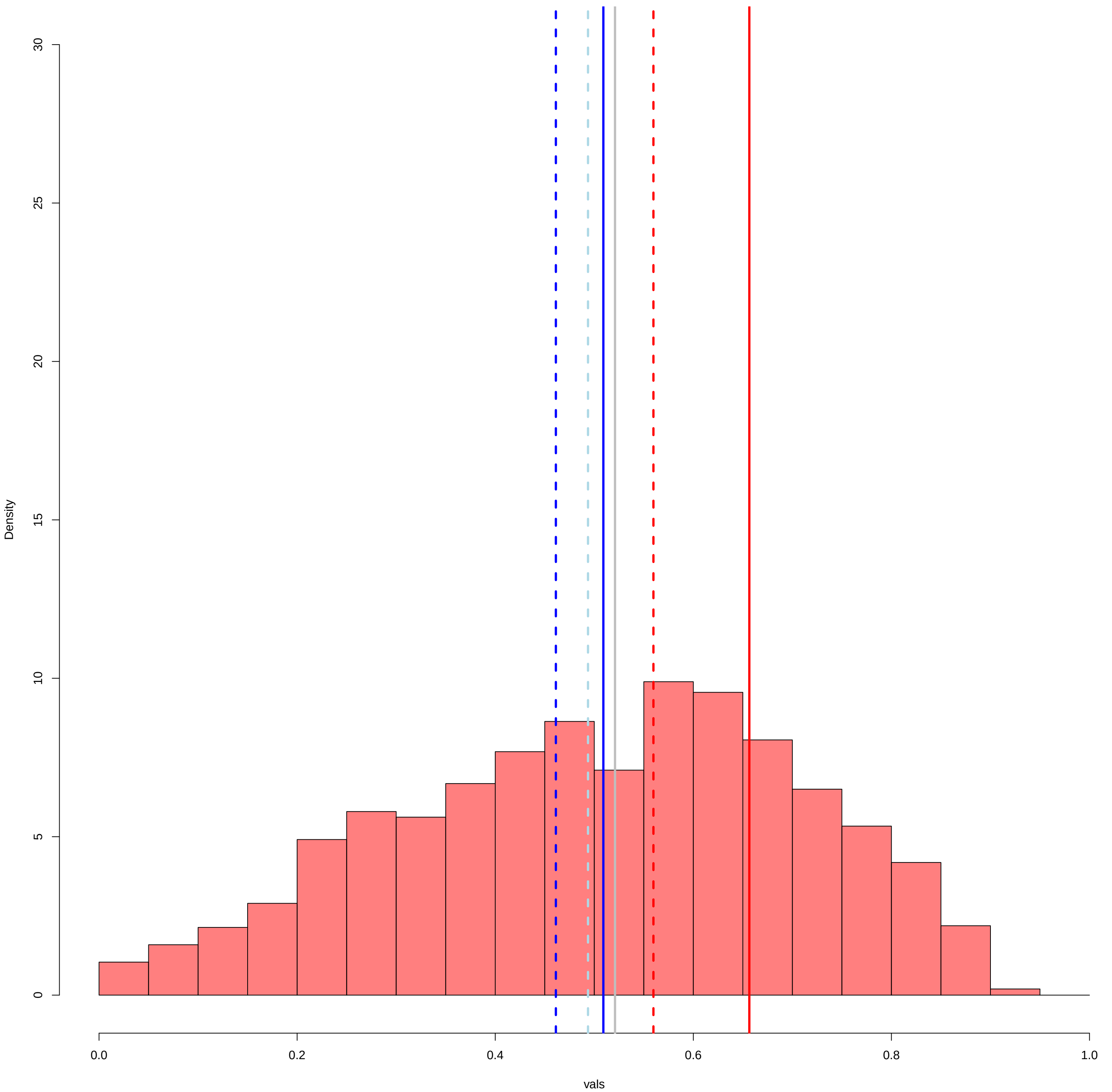
KCNQ2: CADD_raw_rankscore



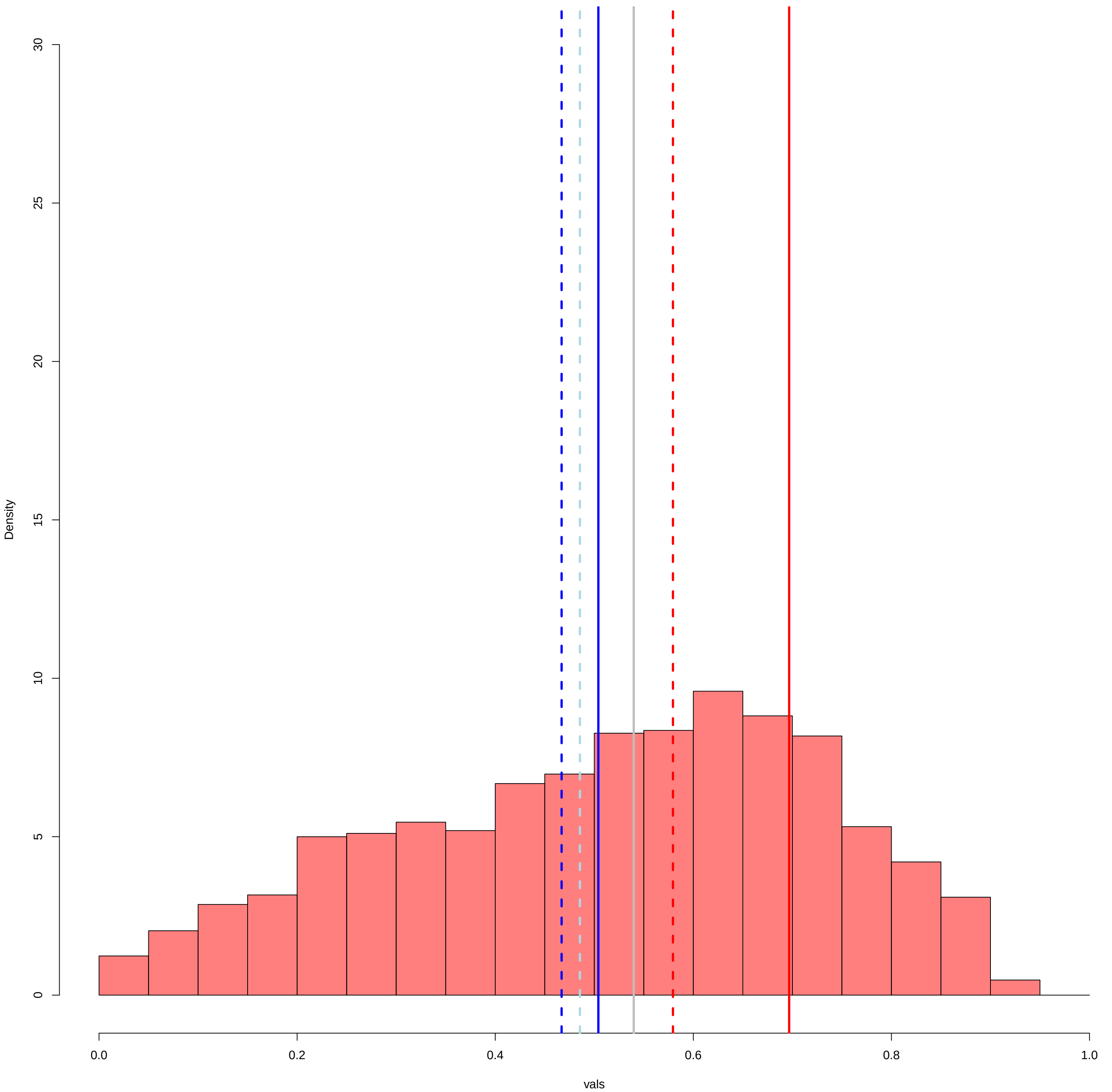
KCNQ2: DANN_rankscore



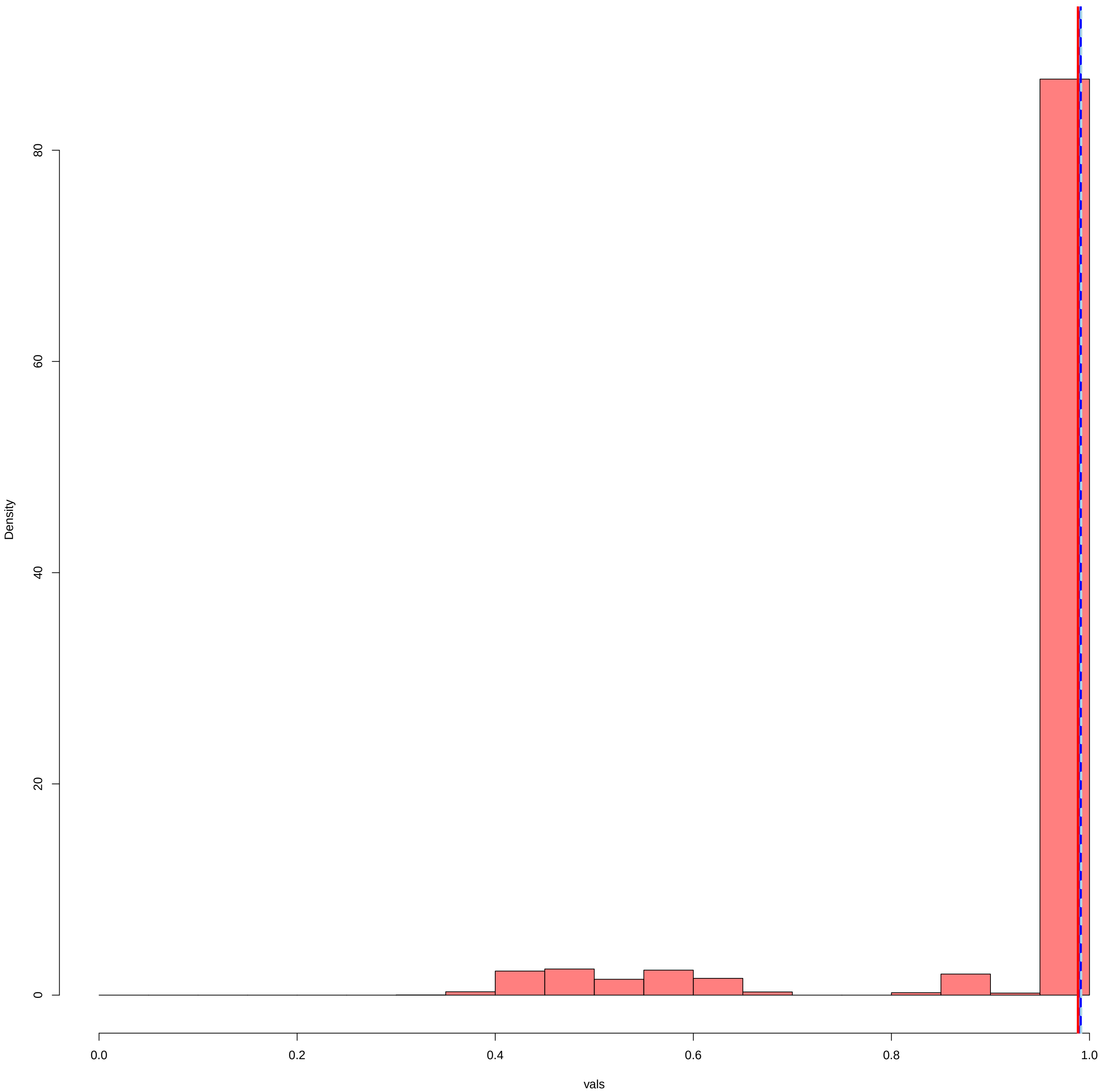
KCNQ2: Eigen-PC-raw_rankscore



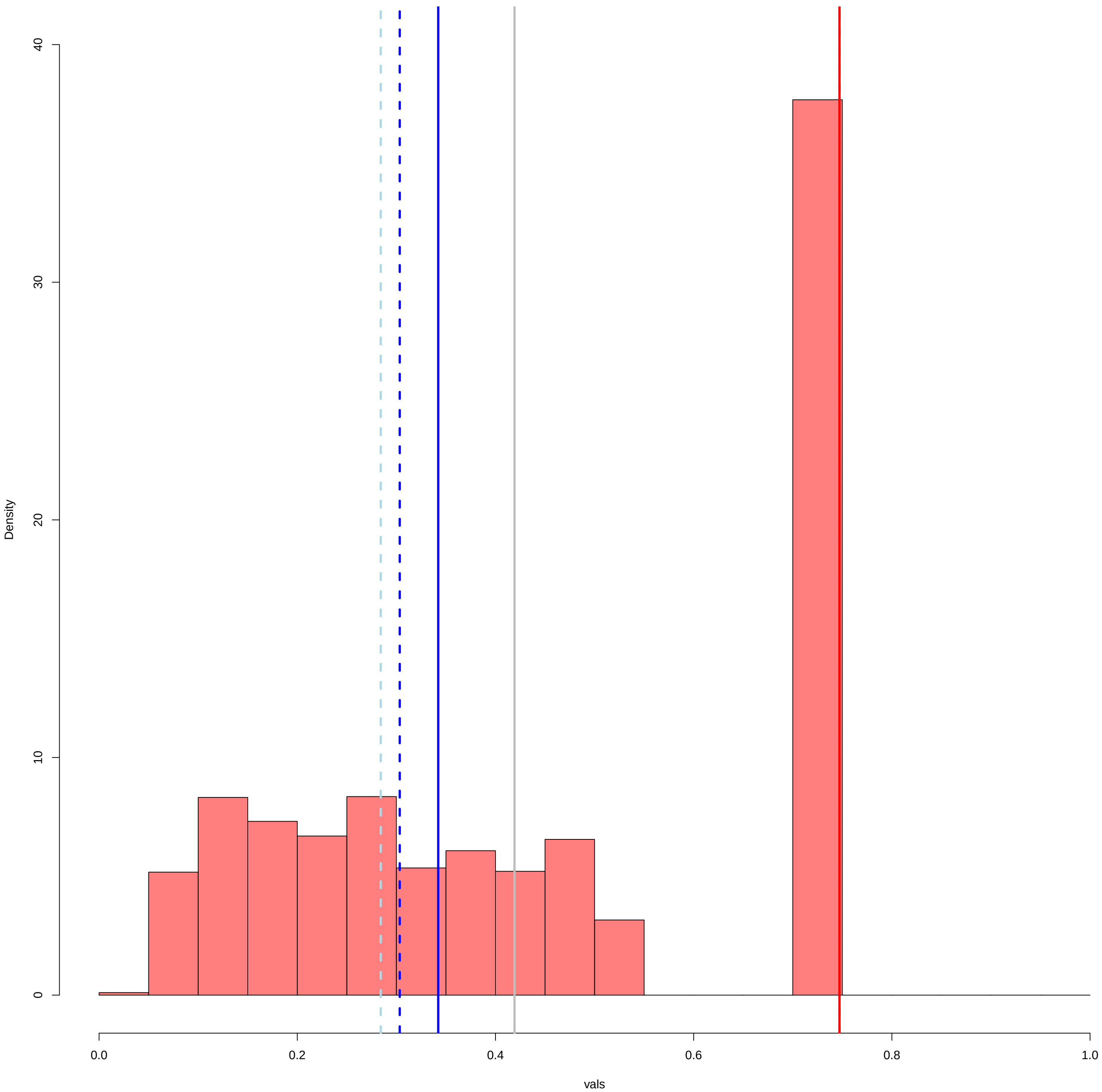
KCNQ2: Eigen-row_rankscore



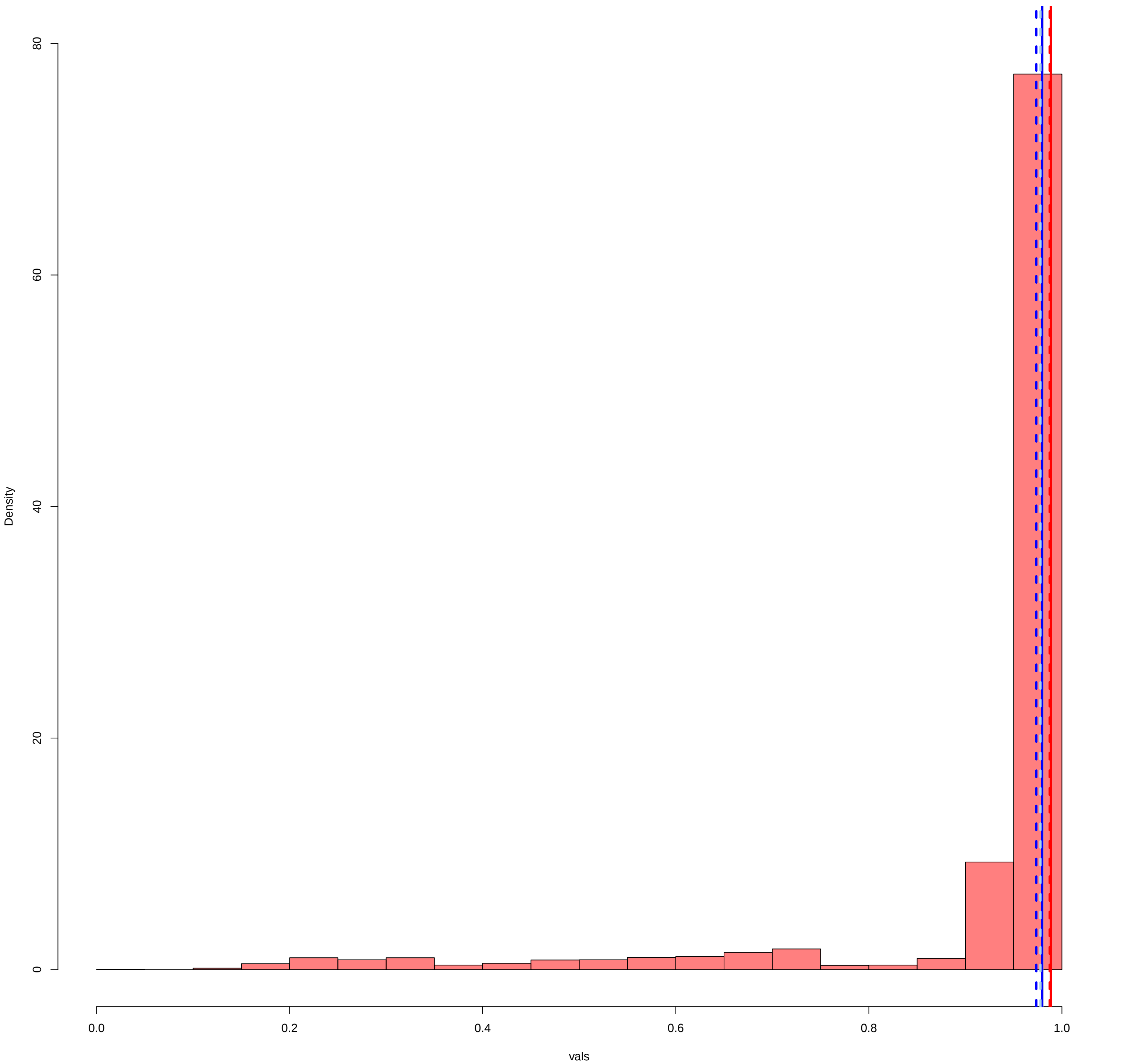
KCNQ2: FATHMM_converted_rankscore



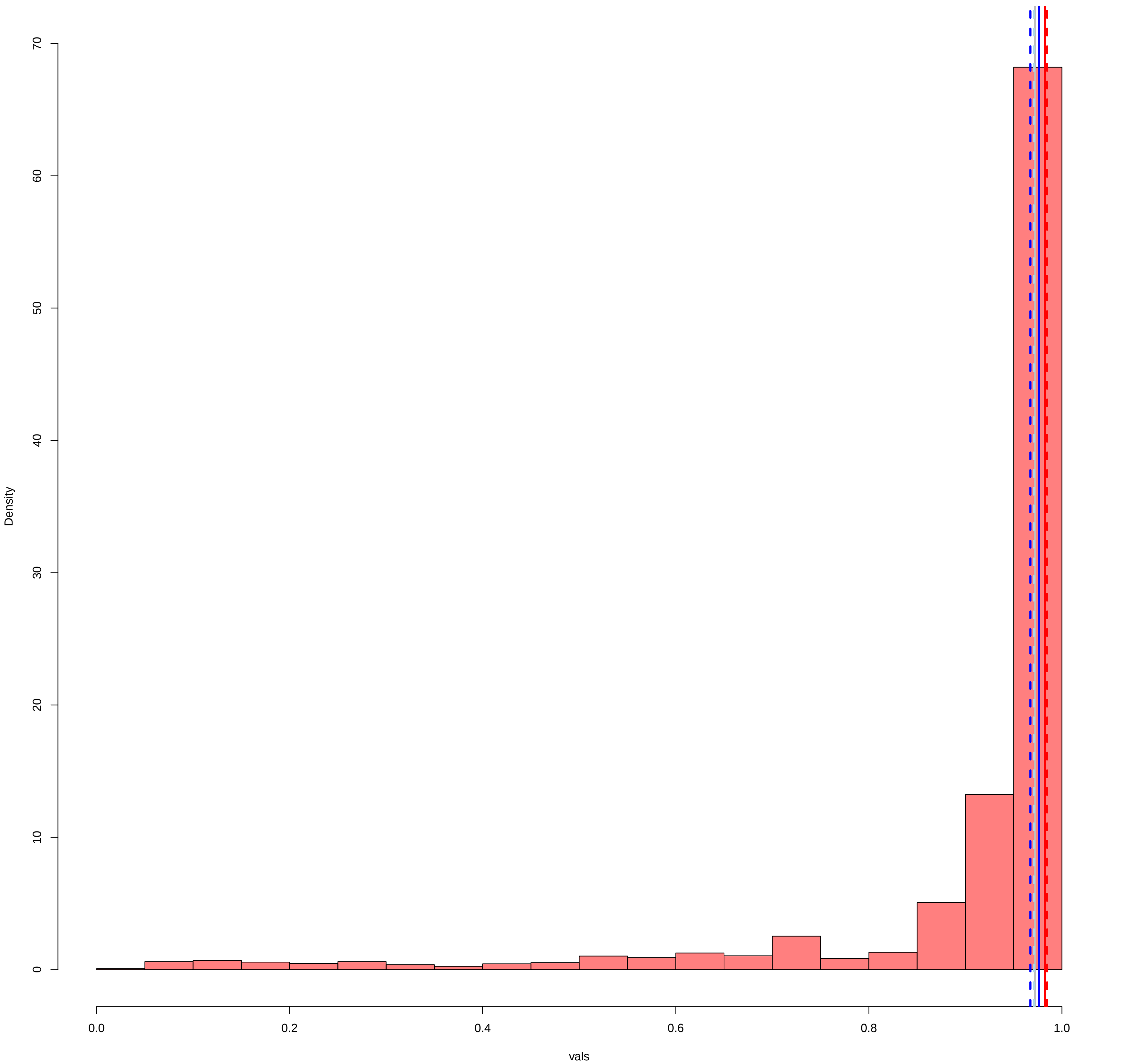
KCNQ2: GenoCanyon_score_rankscore



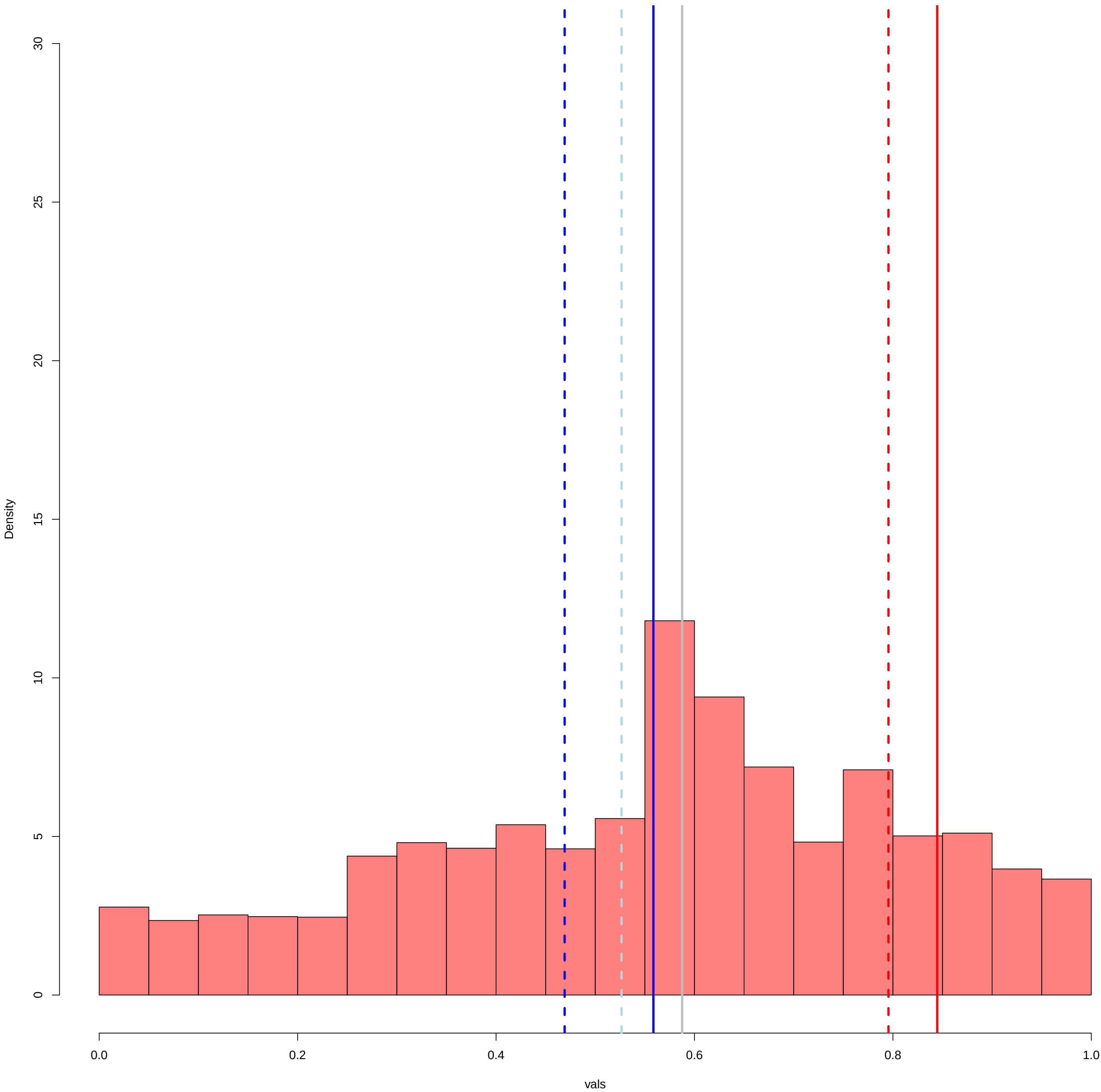
KCNQ2: MetaLR_rankscore



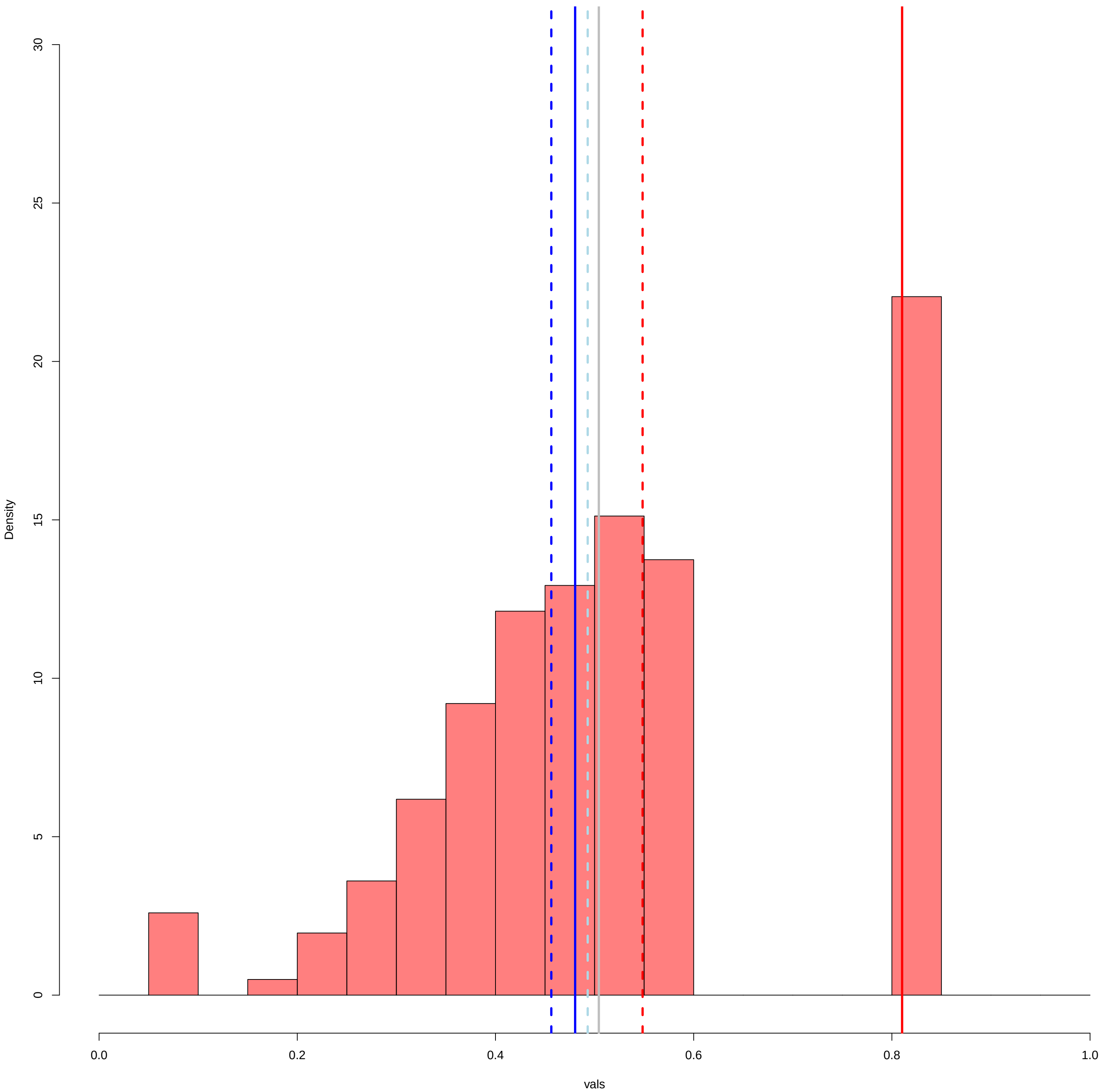
KCNQ2: MetaSVM_rankscore



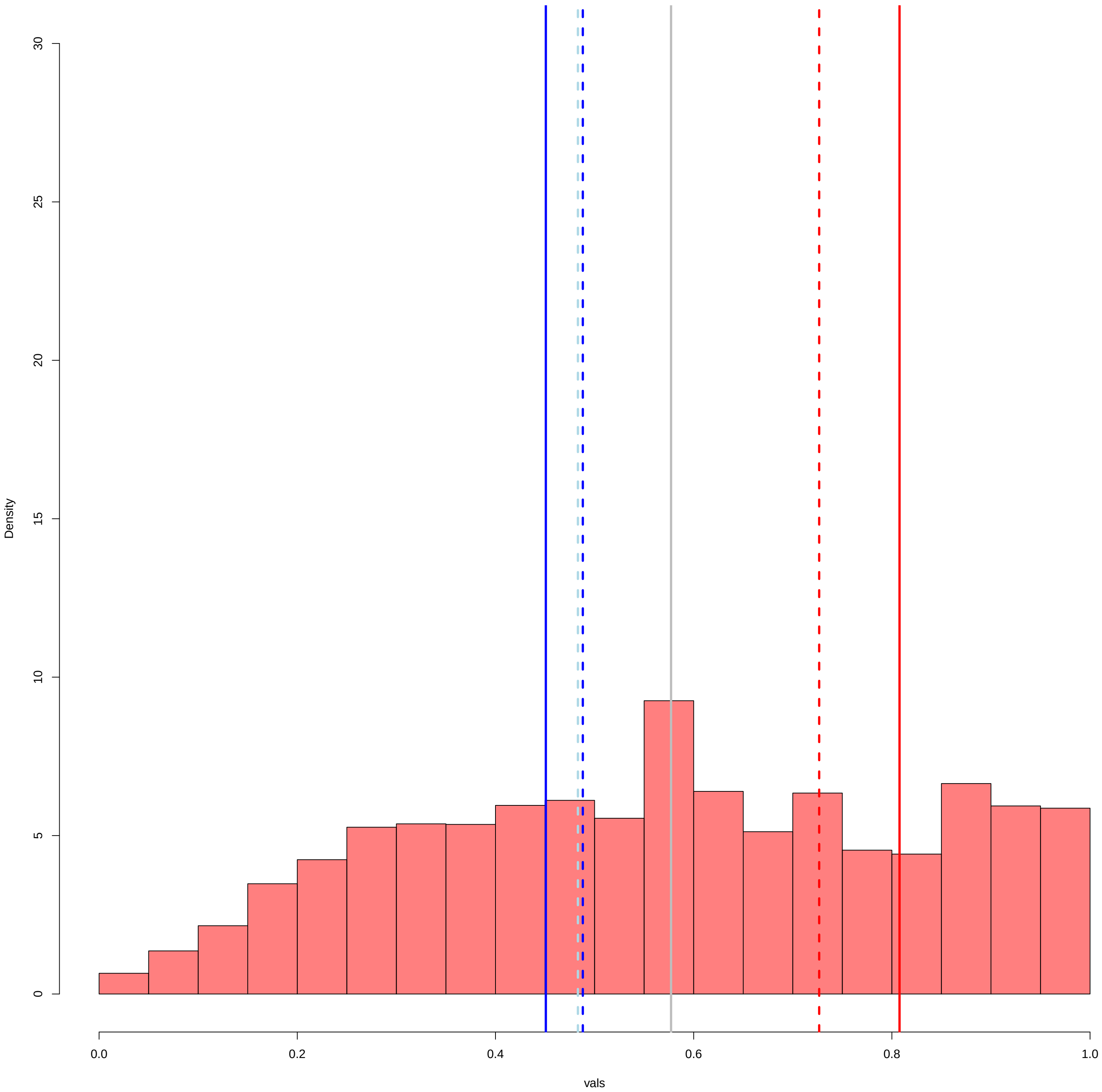
KCNQ2: MutationAssessor_score_rankscore



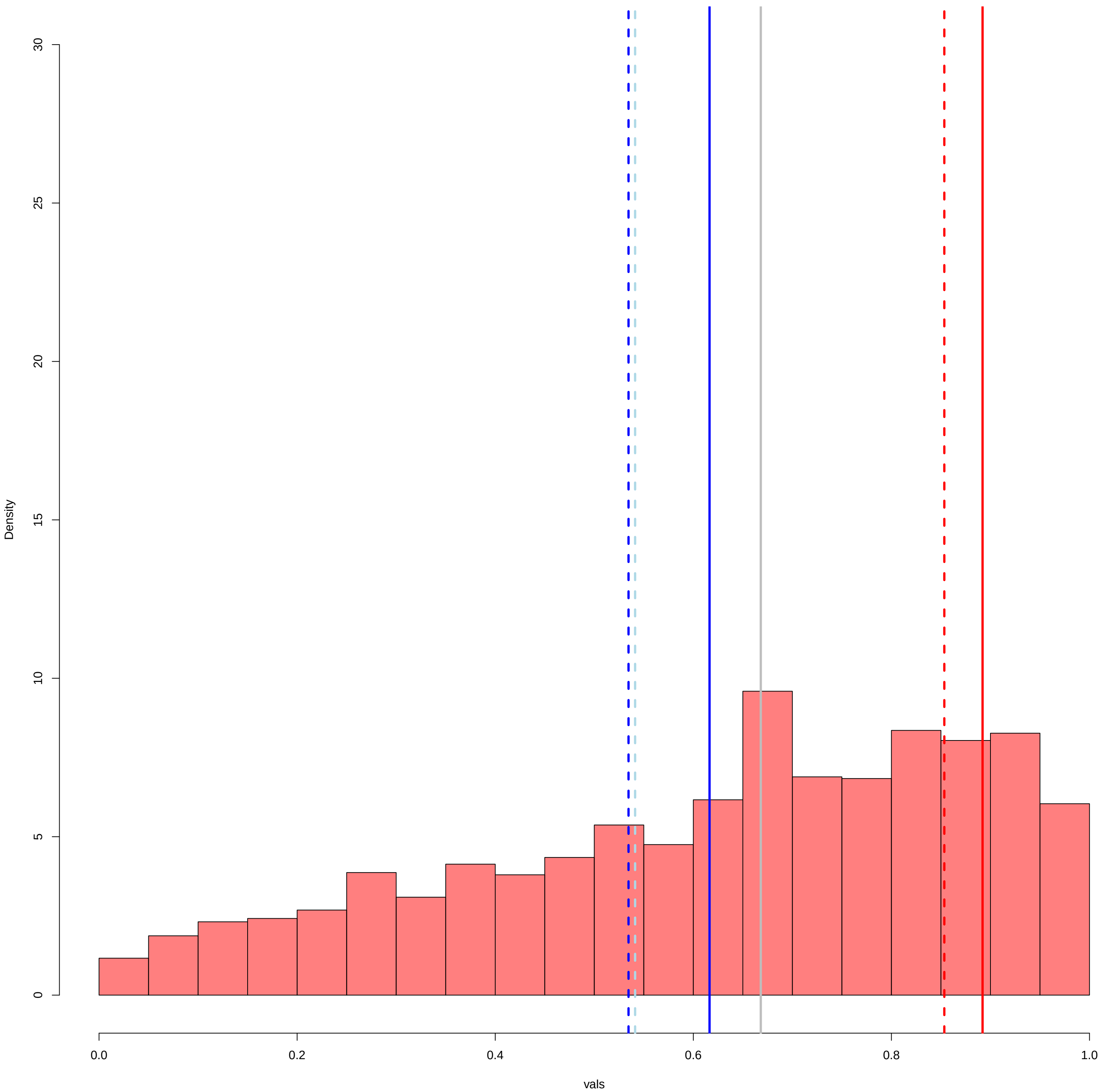
KCNQ2: MutationTaster_converted_rankscore



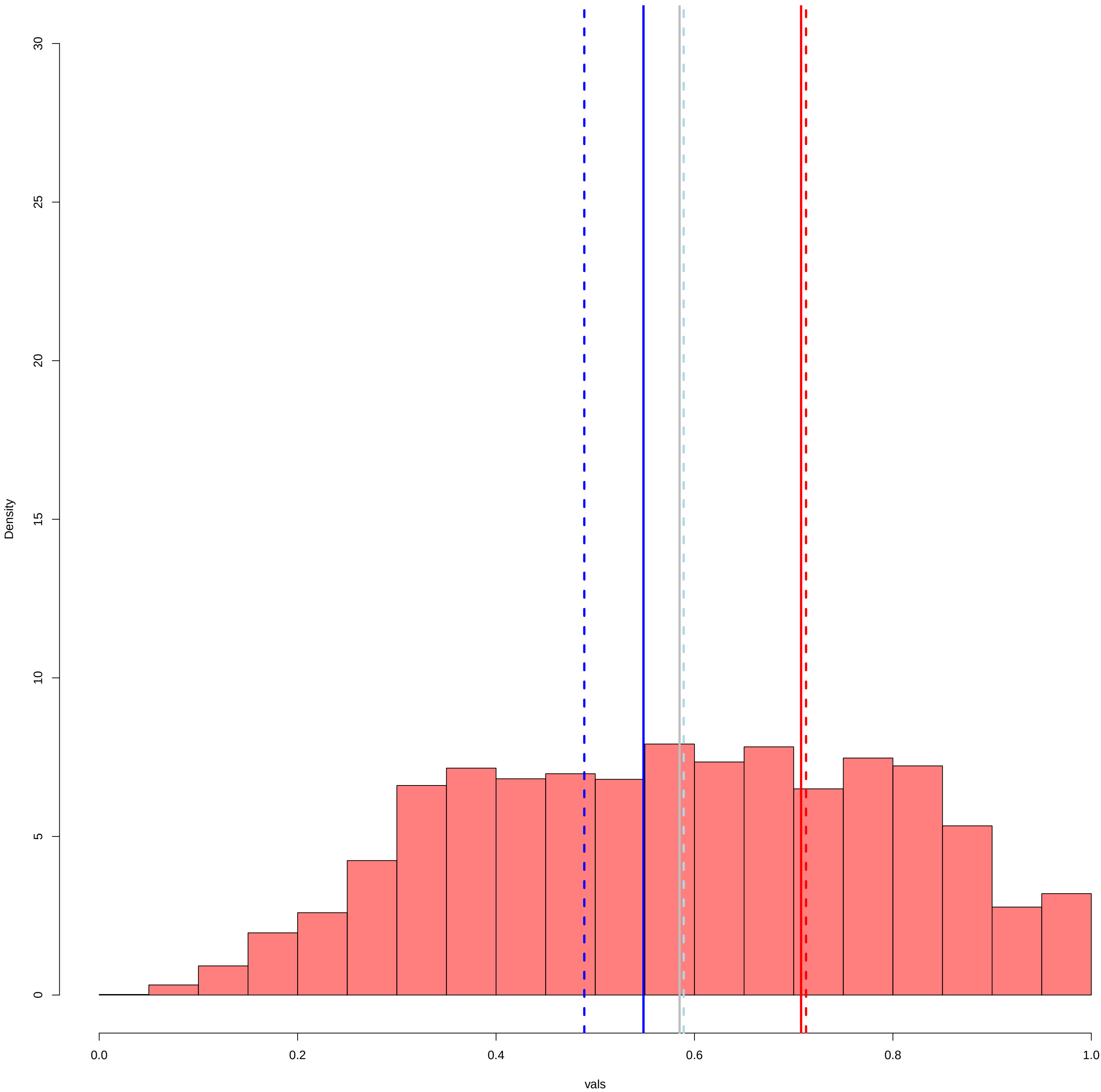
KCNQ2: PROVEAN_converted_rankscore



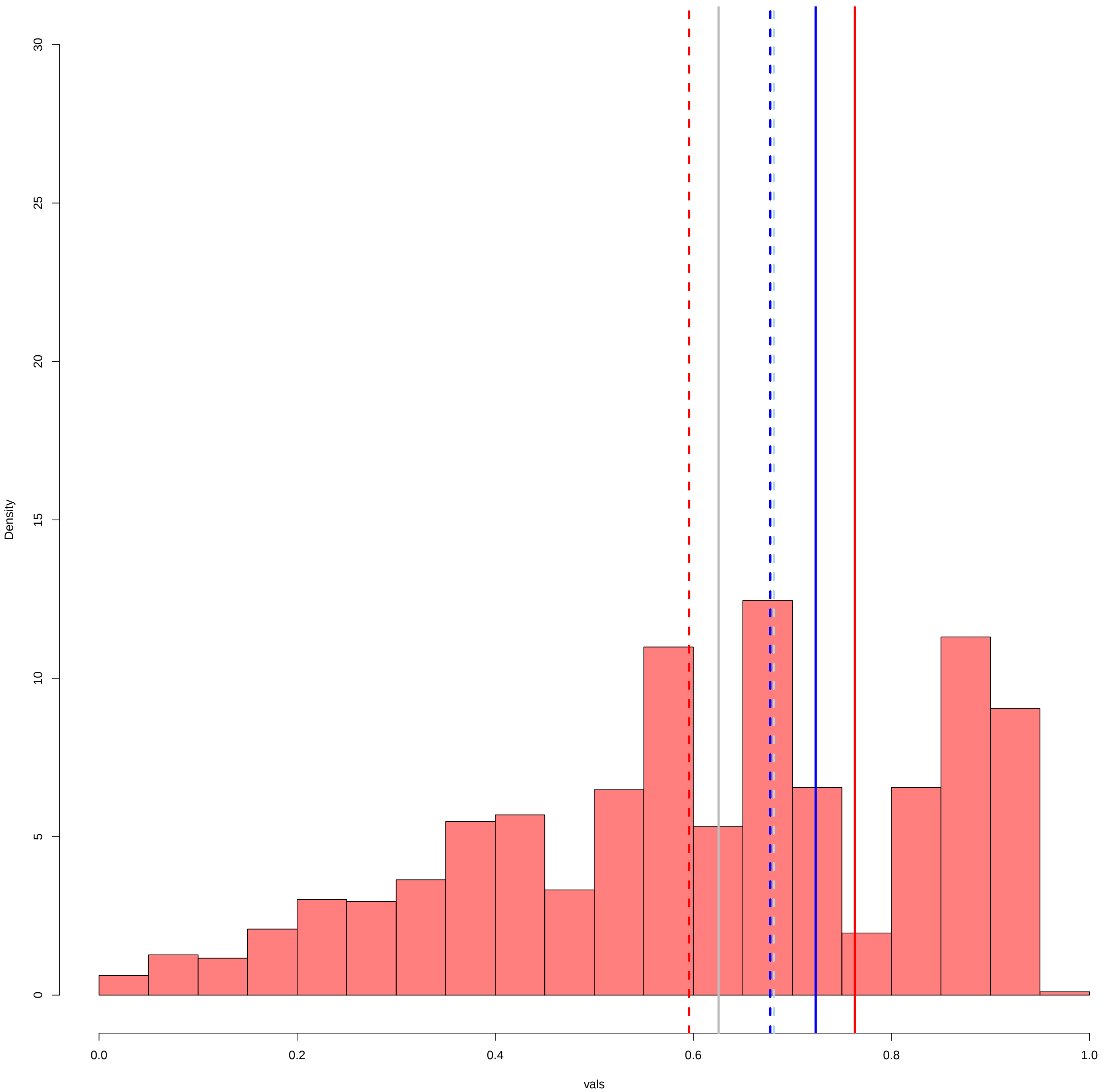
KCNQ2: VEST3_rankscore



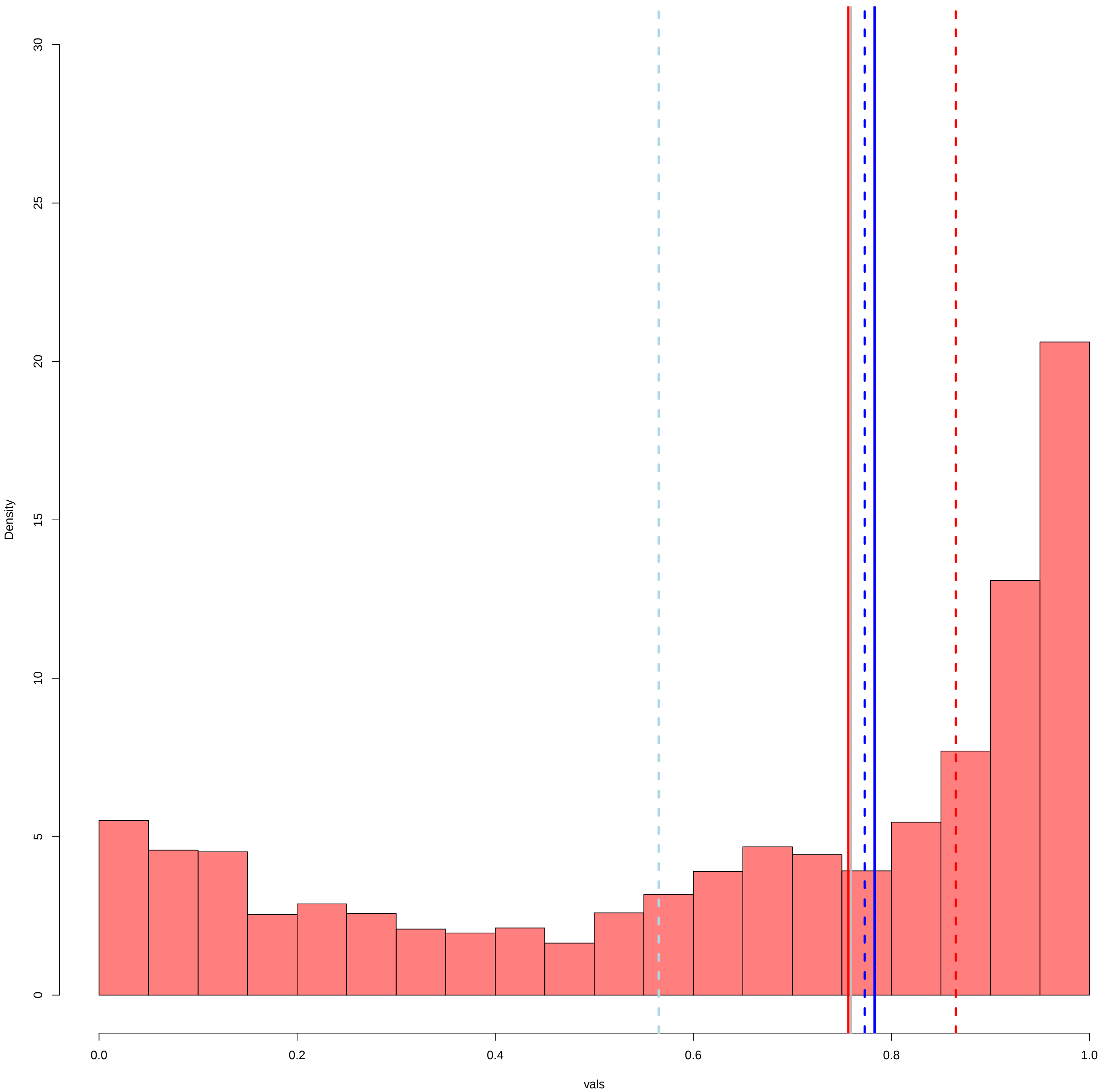
KCNQ2: fathmm-MKL_coding_rankscore



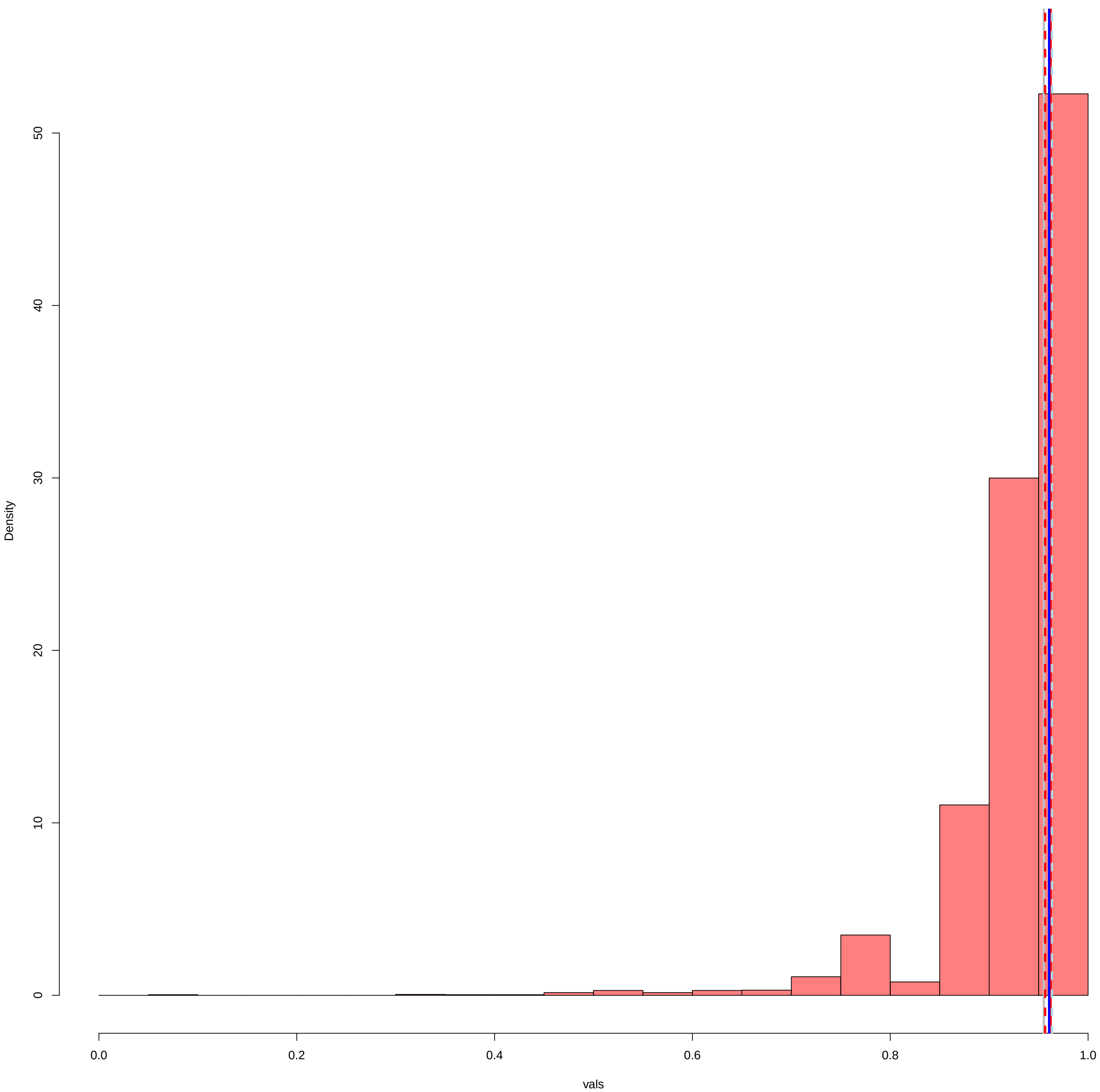
KCNQ2: SiPhy_29way_logOdds_rankscore



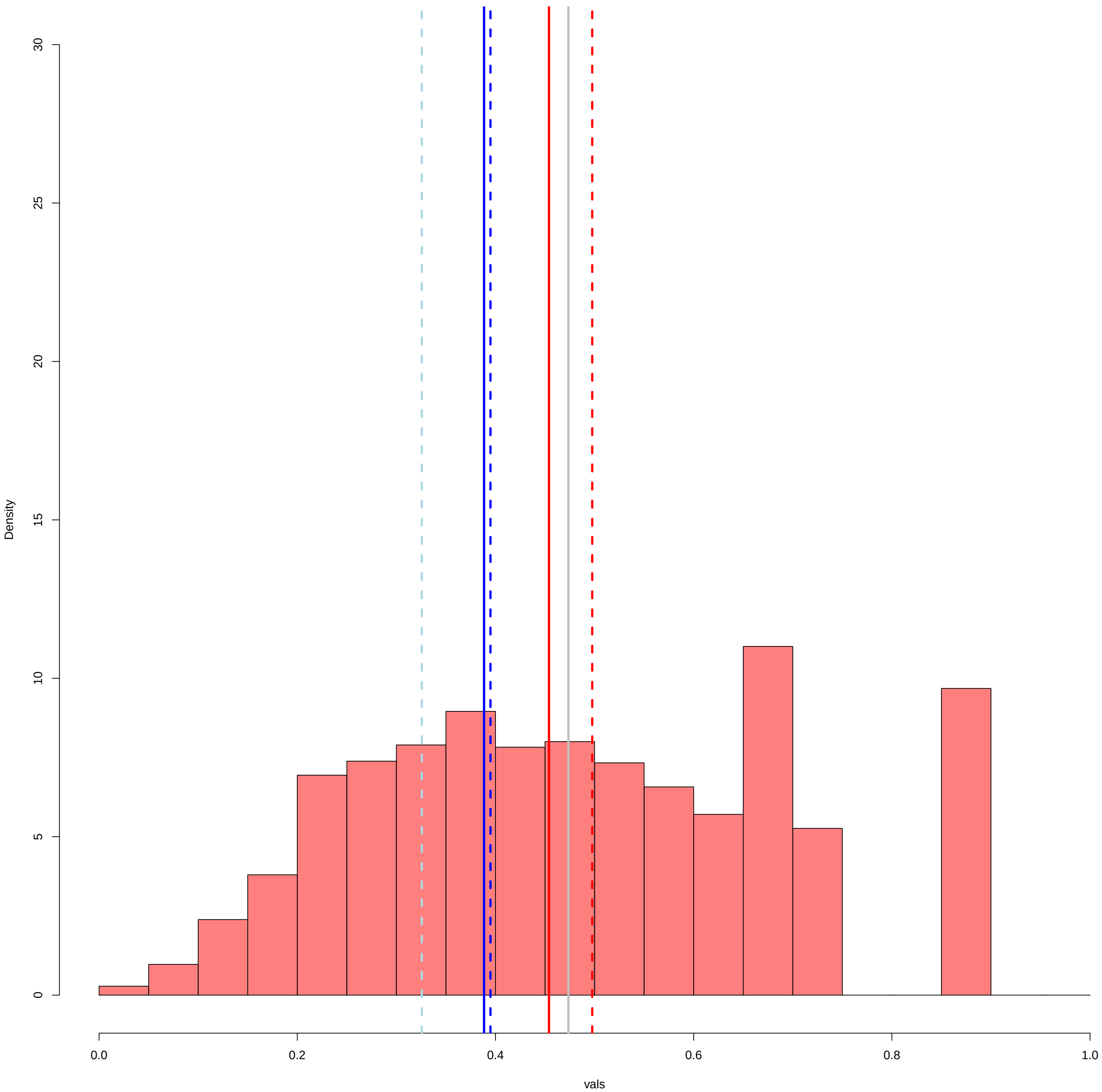
KCNQ2: priPhCons



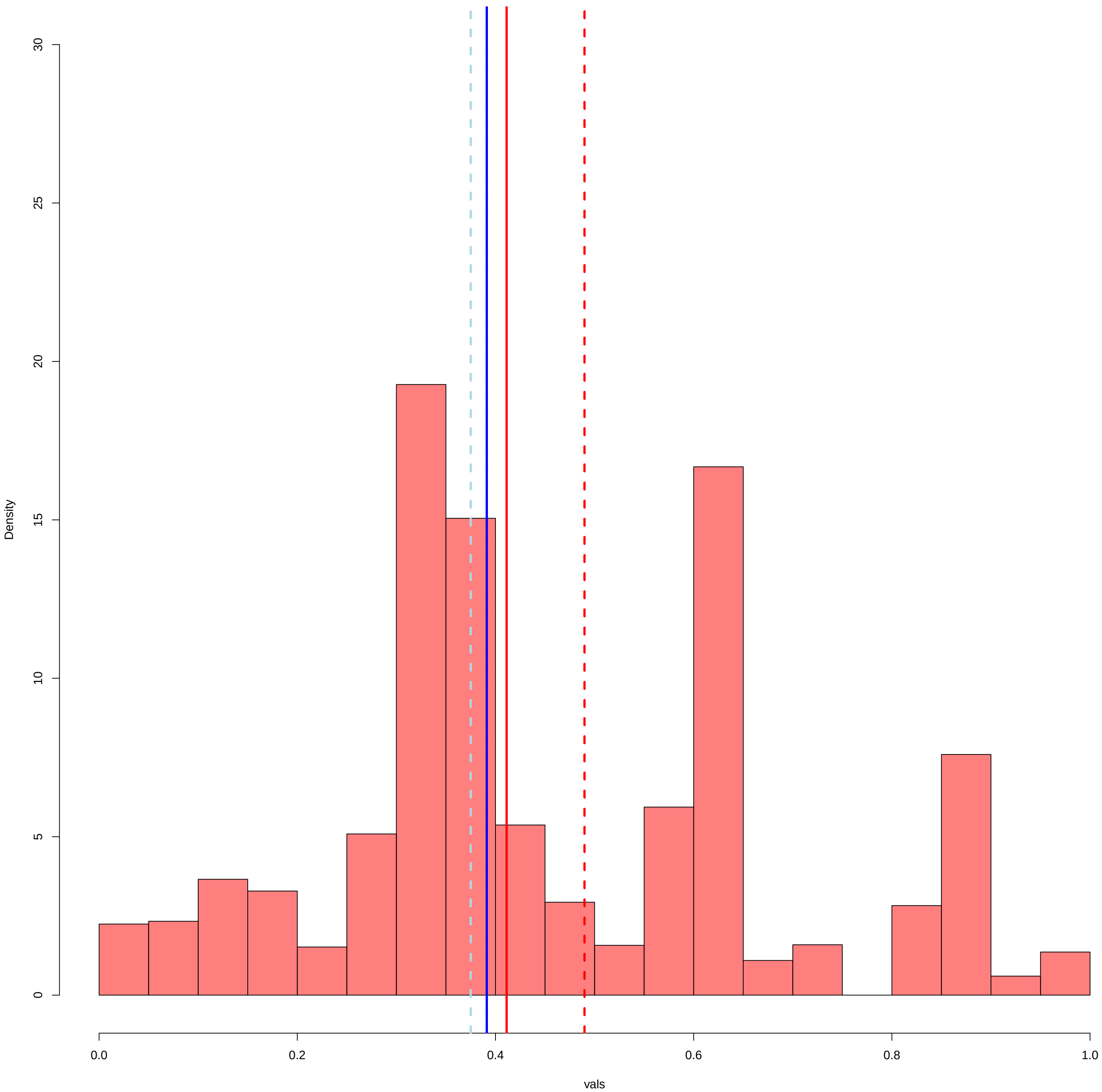
KCNQ2: priPhyloP



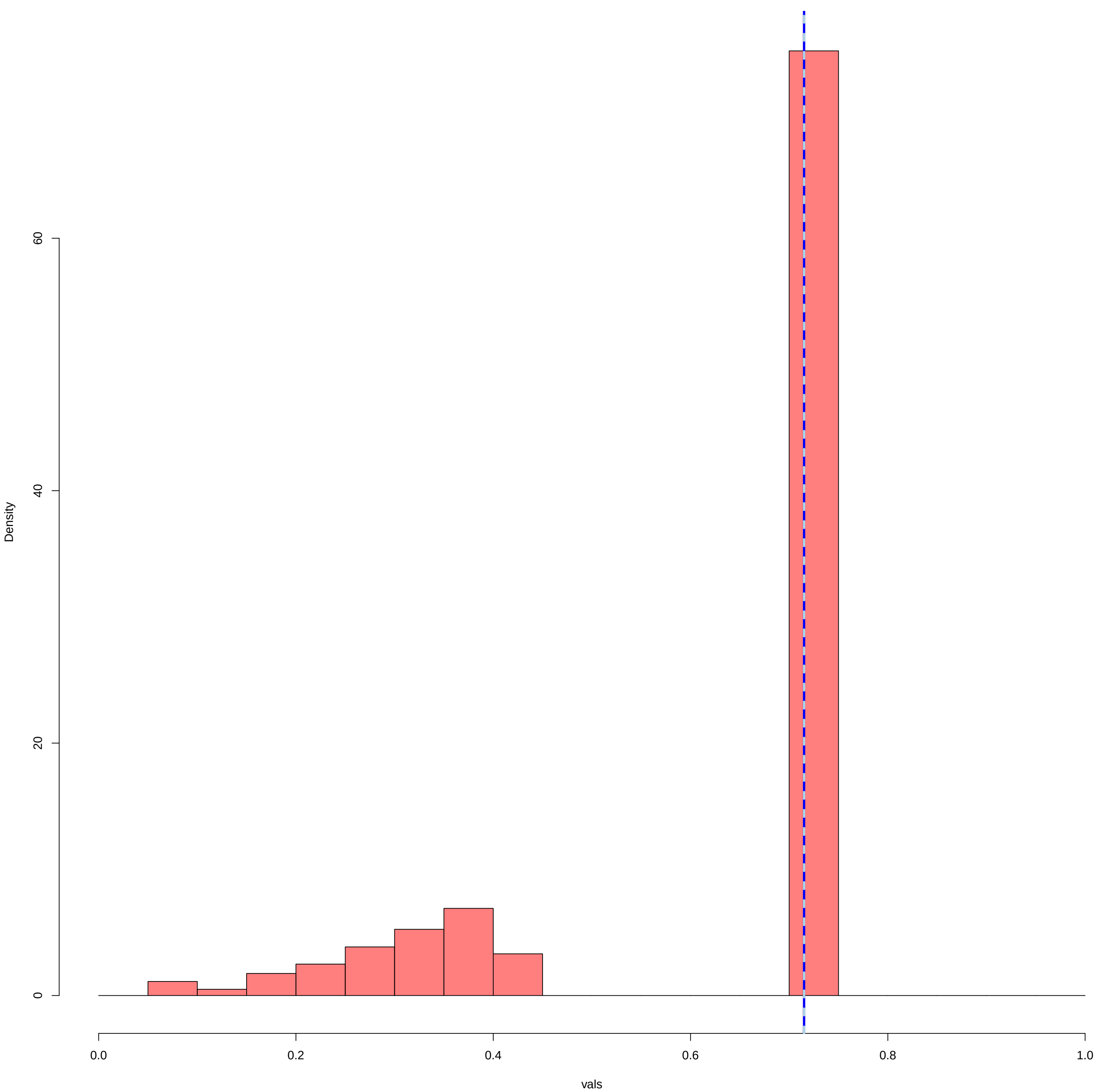
KCNQ2: phastCons20way_mammalian_rankscore



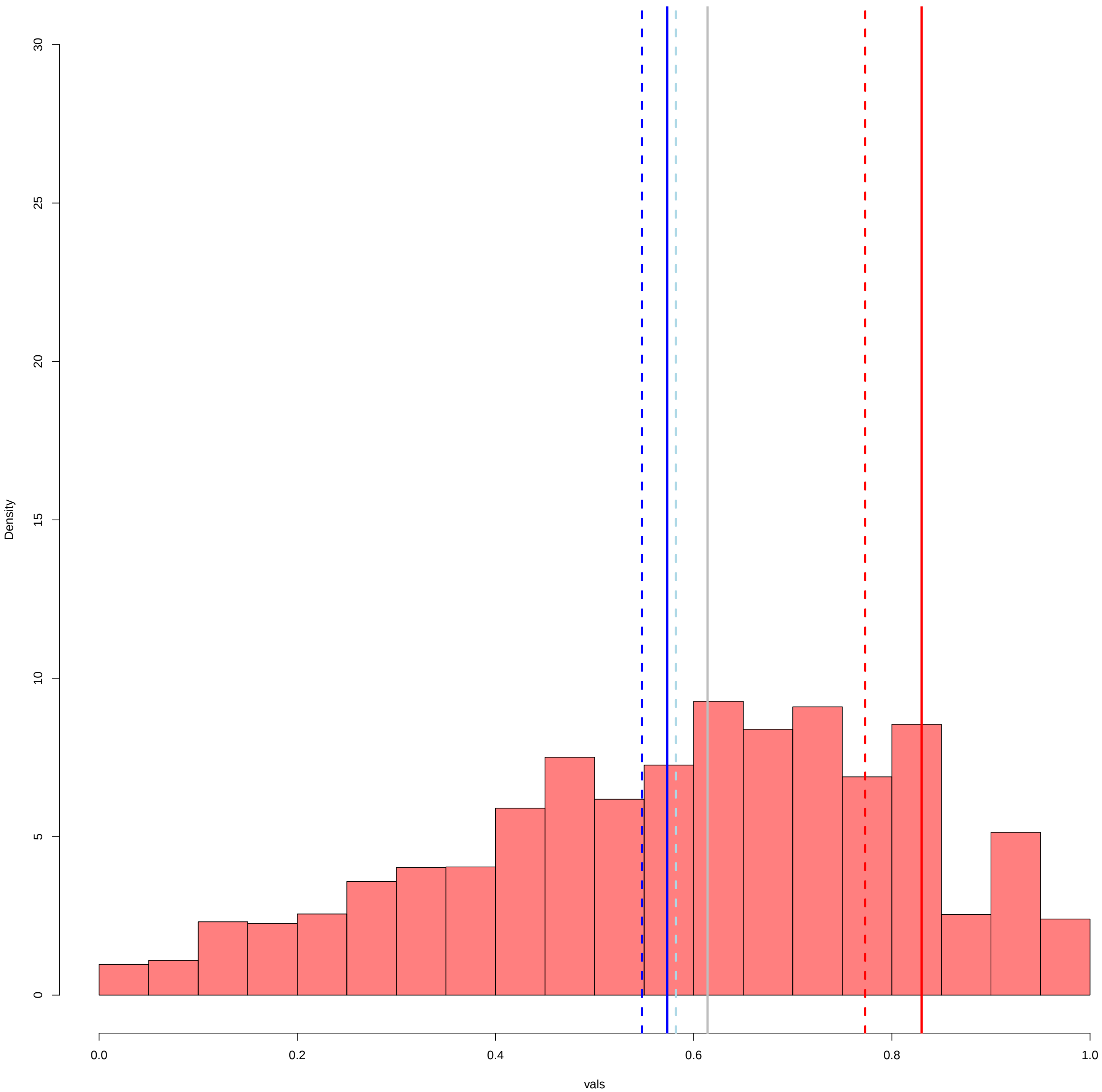
KCNQ2: phyloP20way_mammalian_rankscore



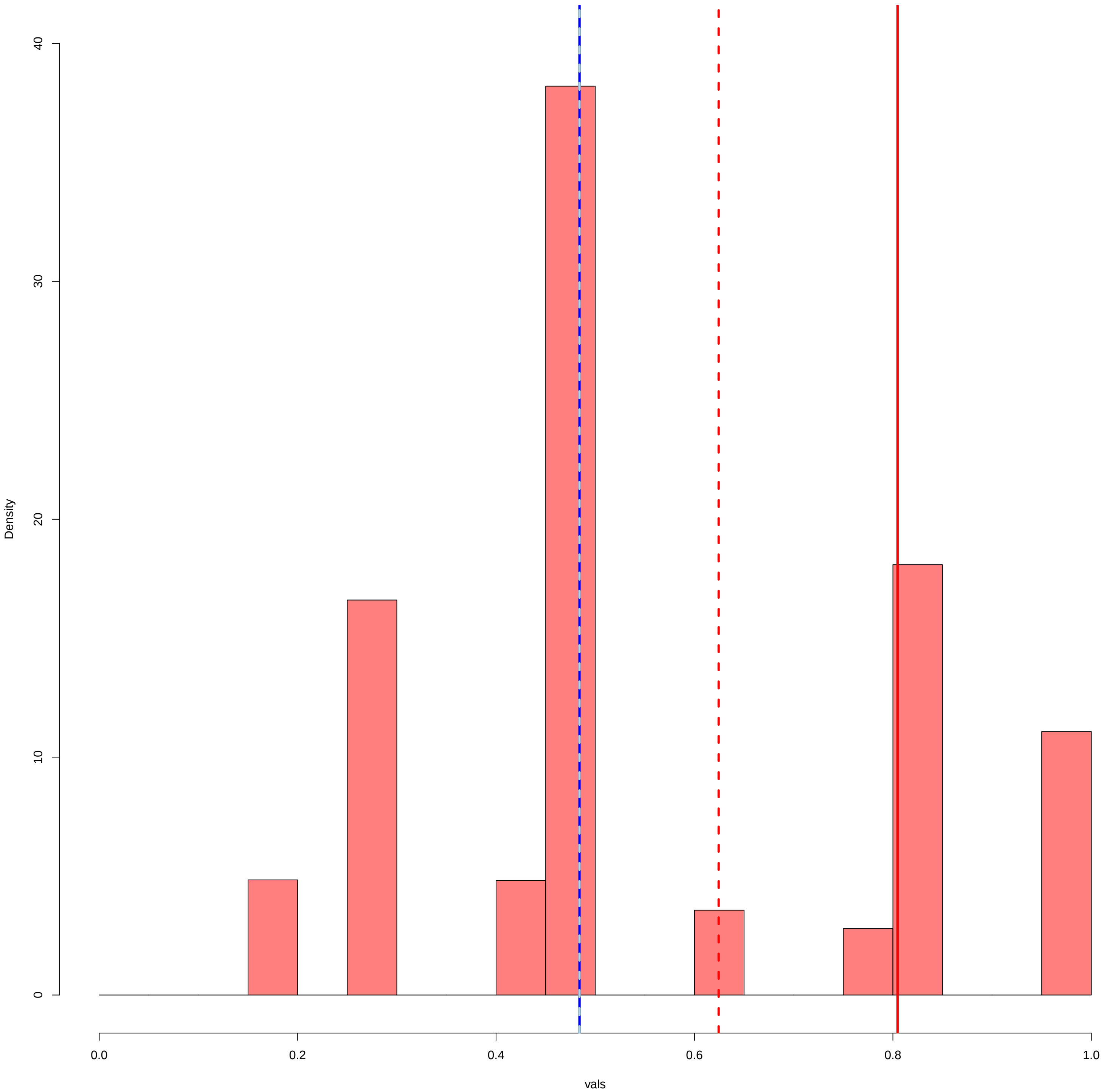
KCNQ2: phastCons100way_vertebrate_rankscore



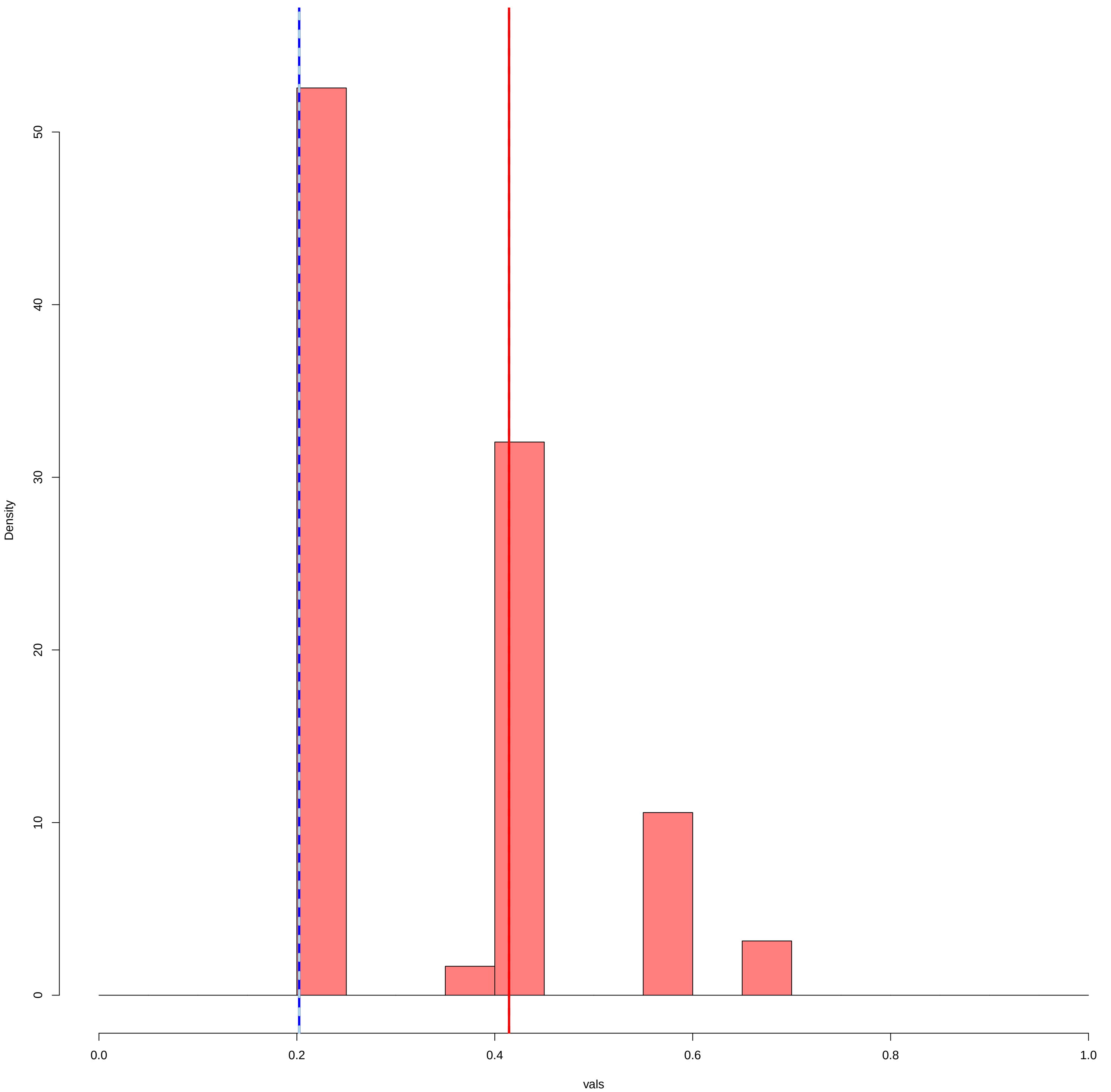
KCNQ2: phyloP100way_vertebrate_rankscore



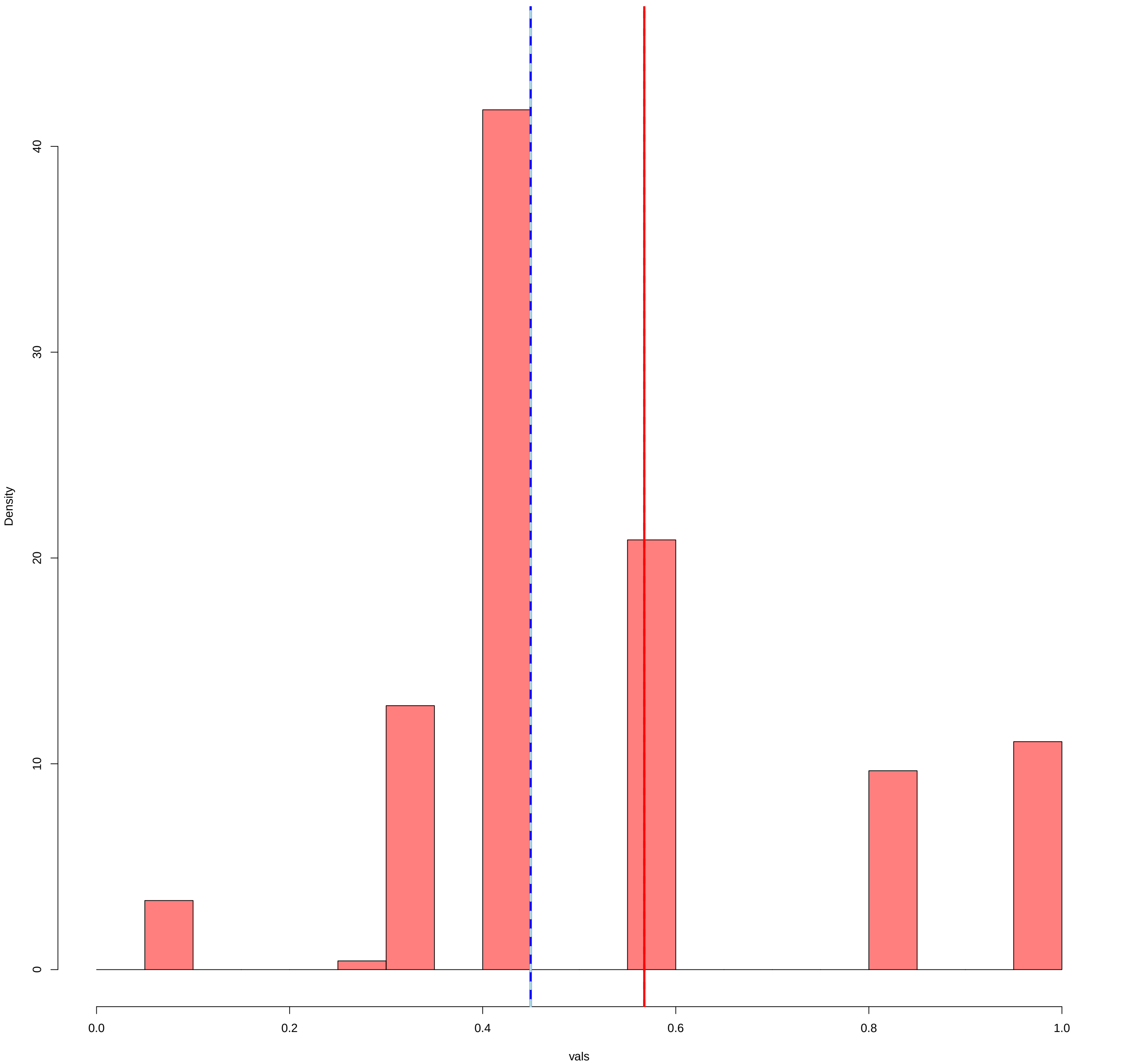
KCNQ2: H1-hESC_fitCons_score_rankscore



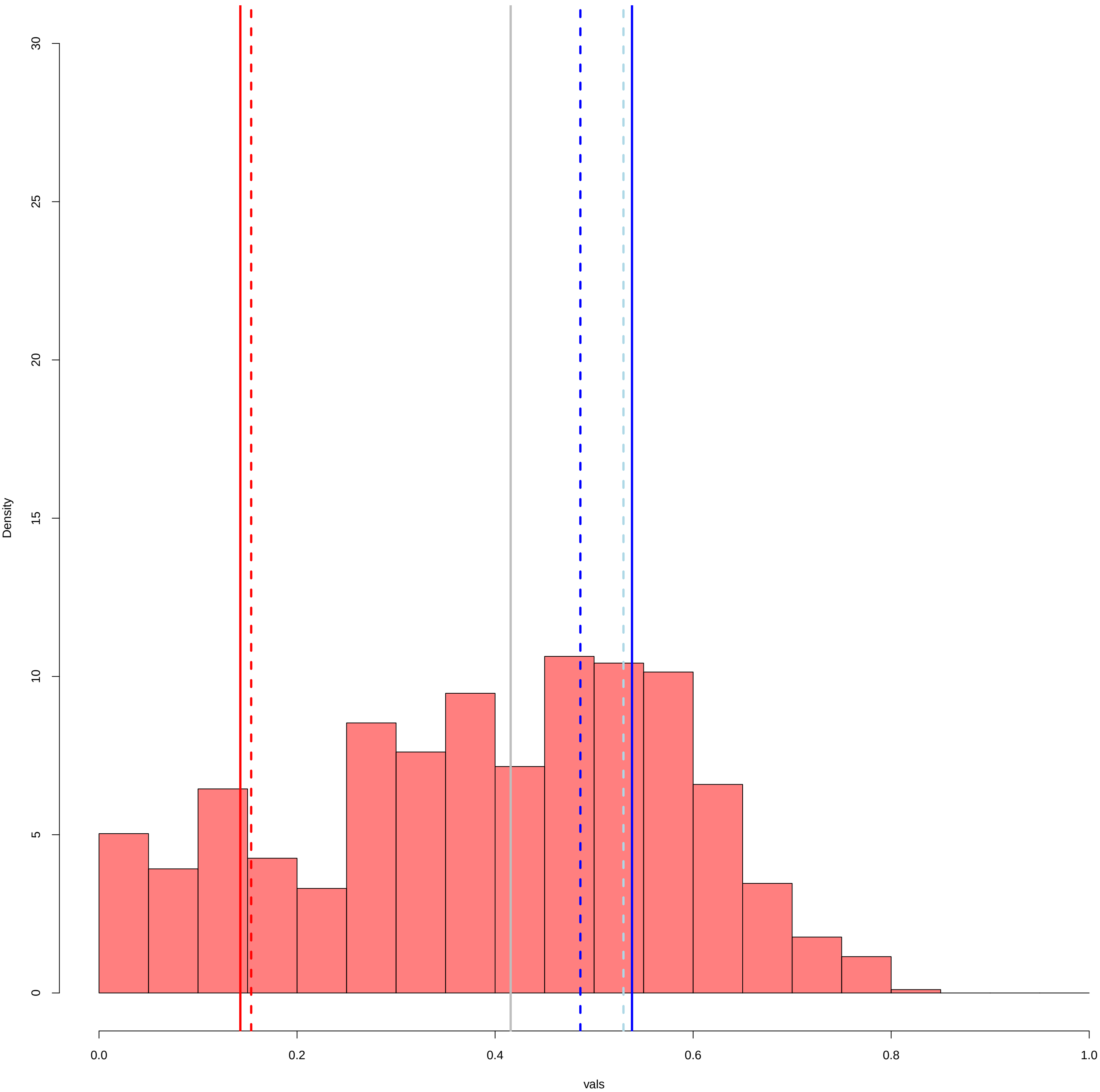
KCNQ2: HUVEC_fitCons_score_rankscore



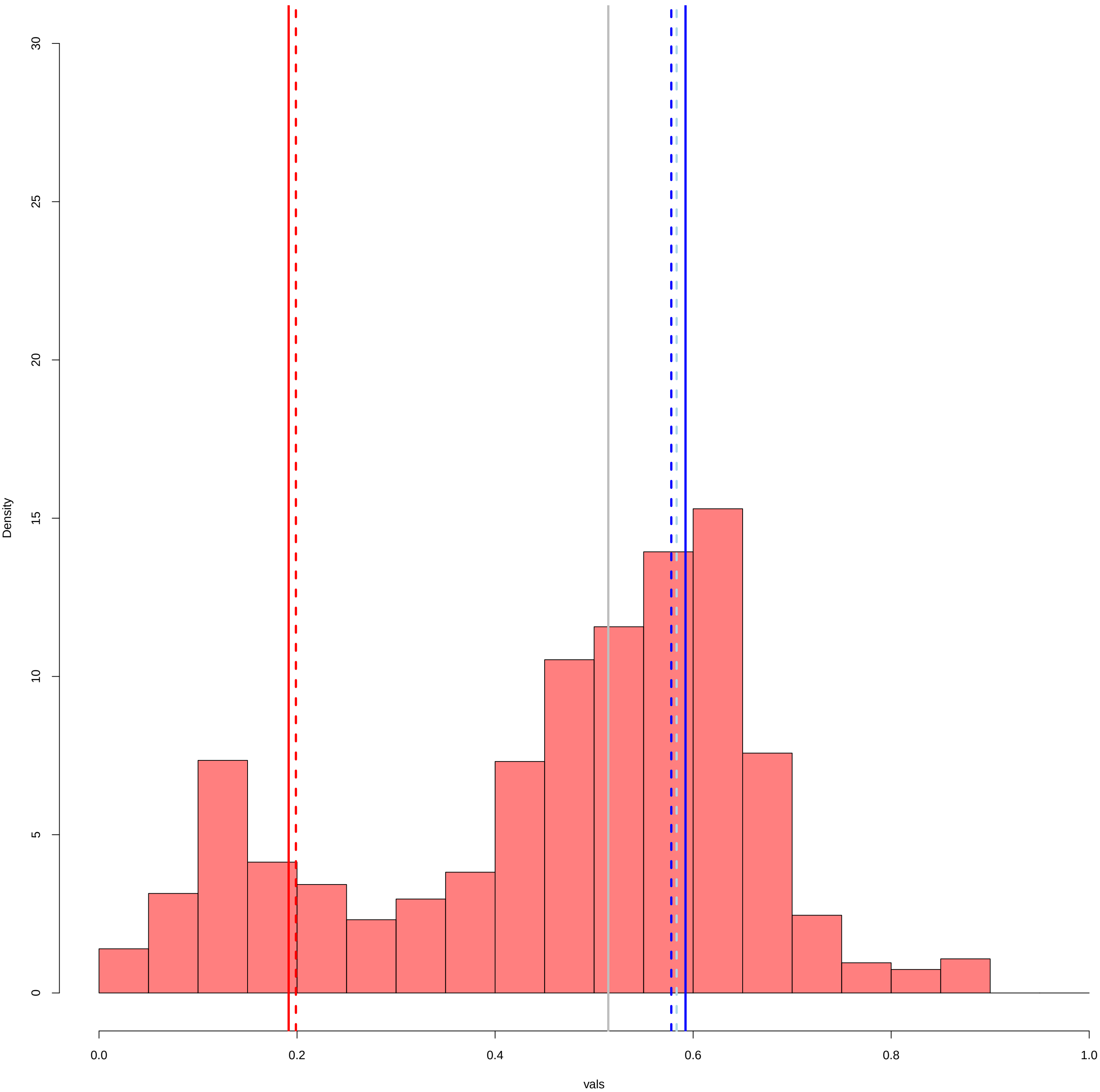
KCNQ2: integrated_fitCons_score_rankscore



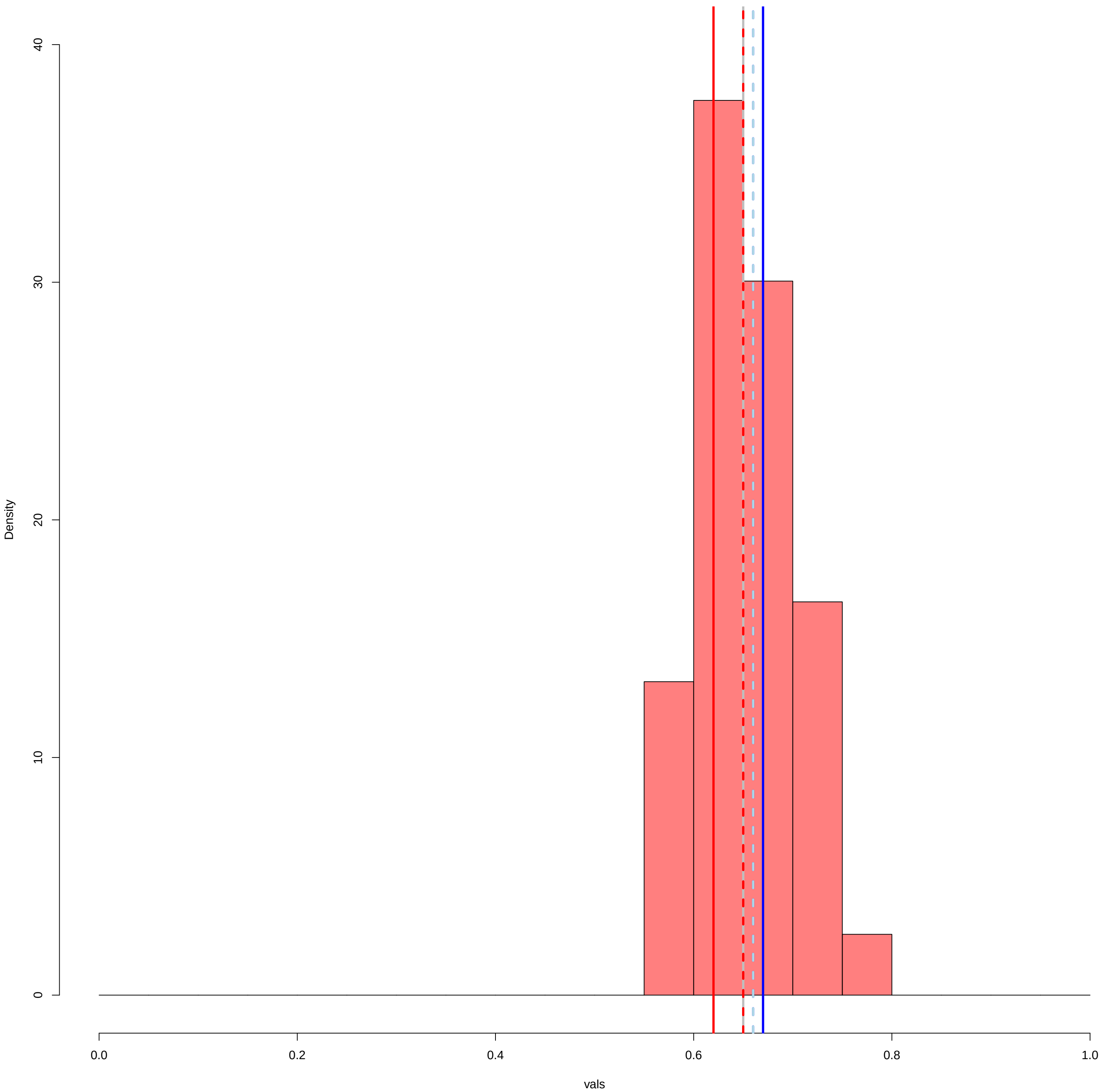
KCNQ2: ExAC v1 MTR



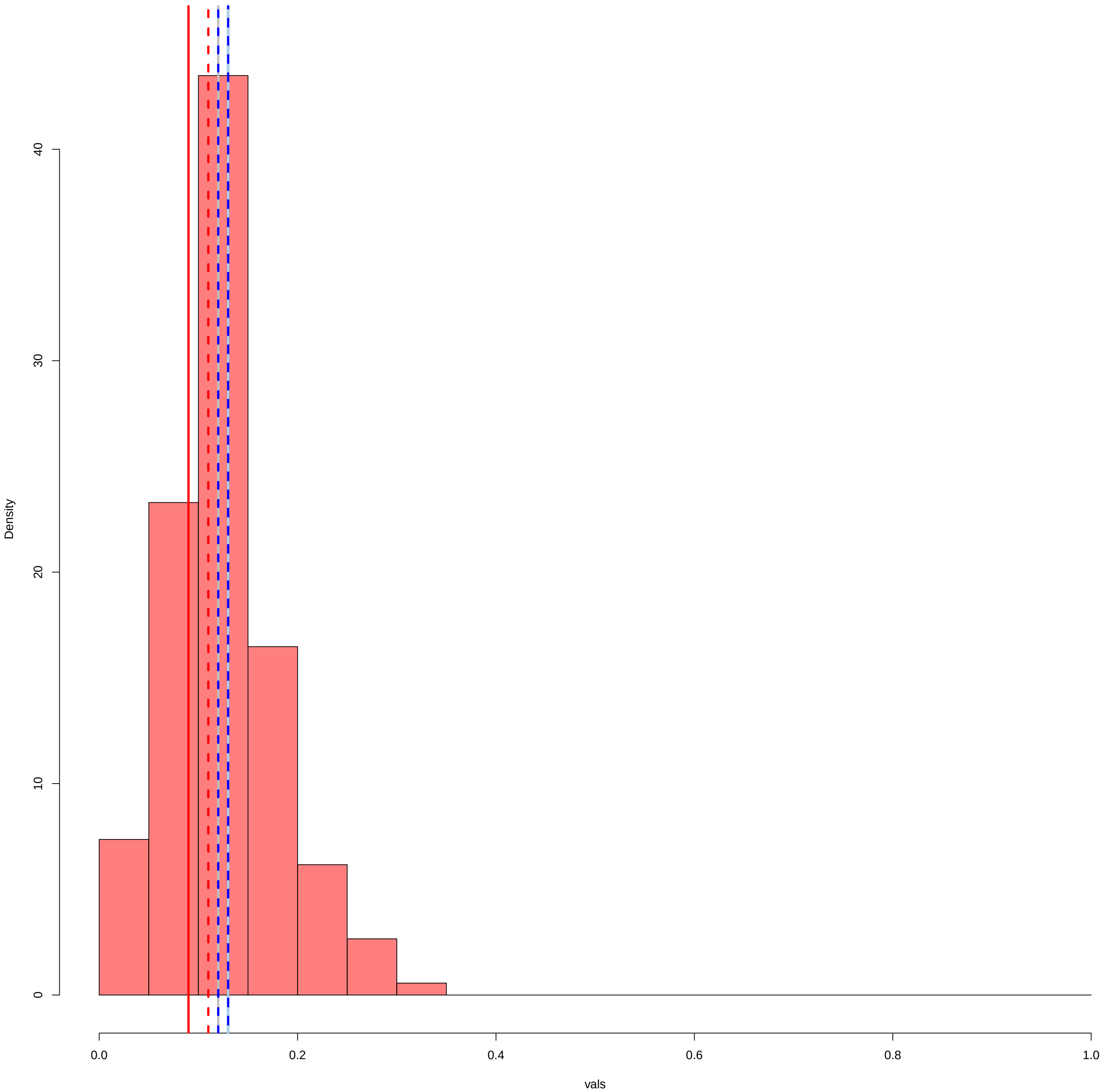
KCNQ2: ExAC v2 & gnomAD MTR



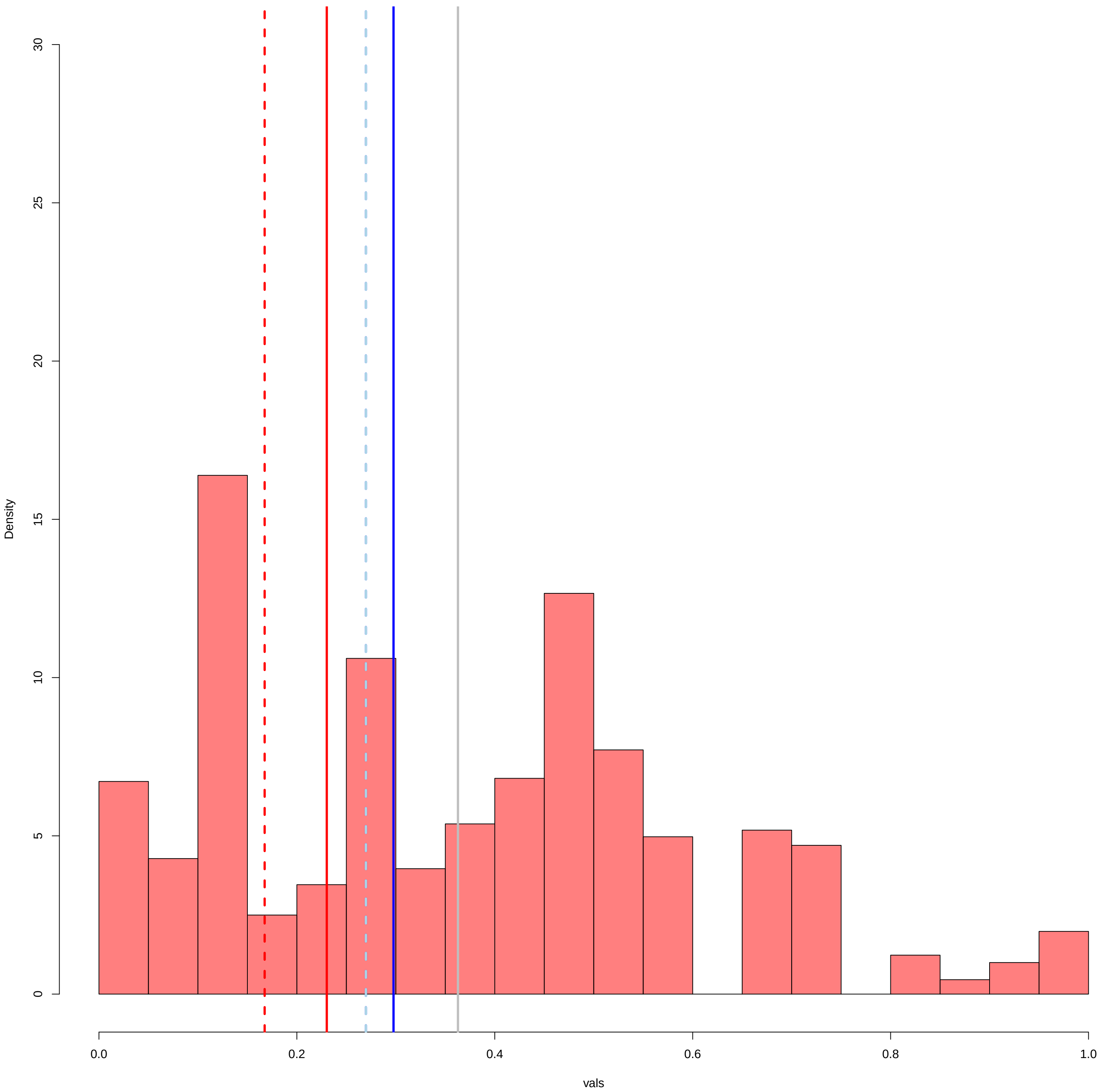
KCNT1: GC (Percent GC content in a window of +/-75bp)



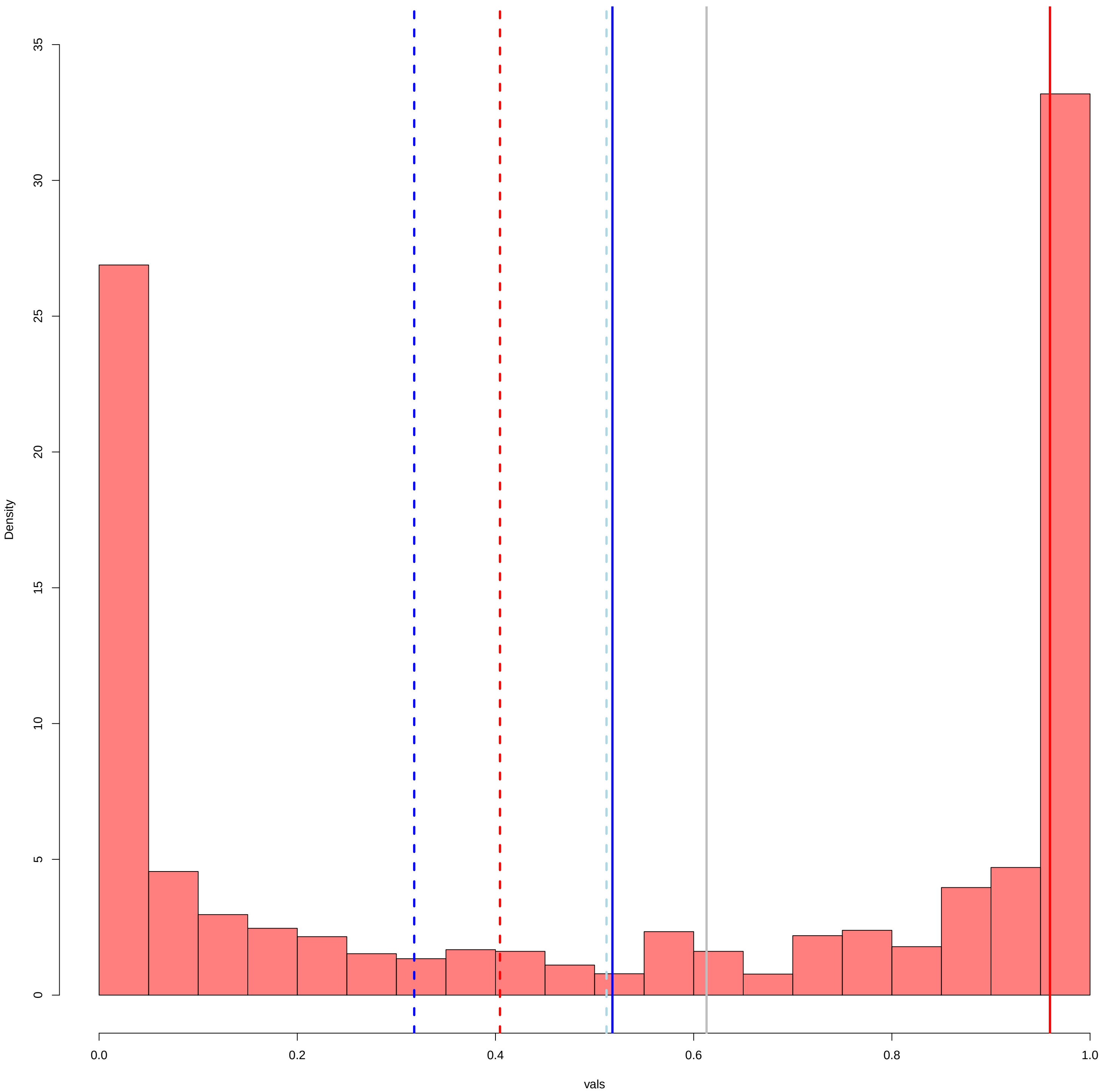
KCNT1: CpG (Percent CpG in a window of +/-75bp)



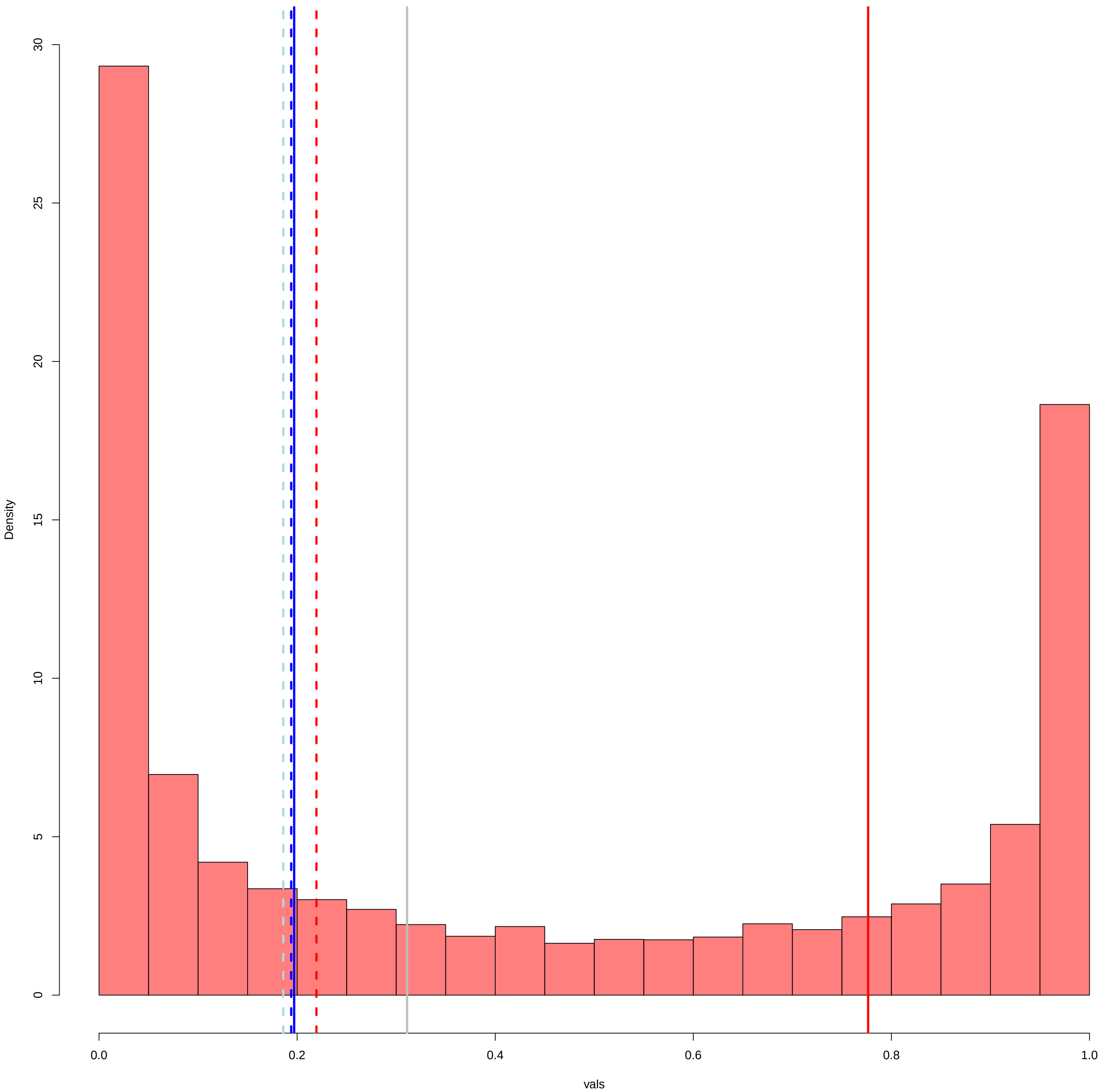
KCNT1: Grantham



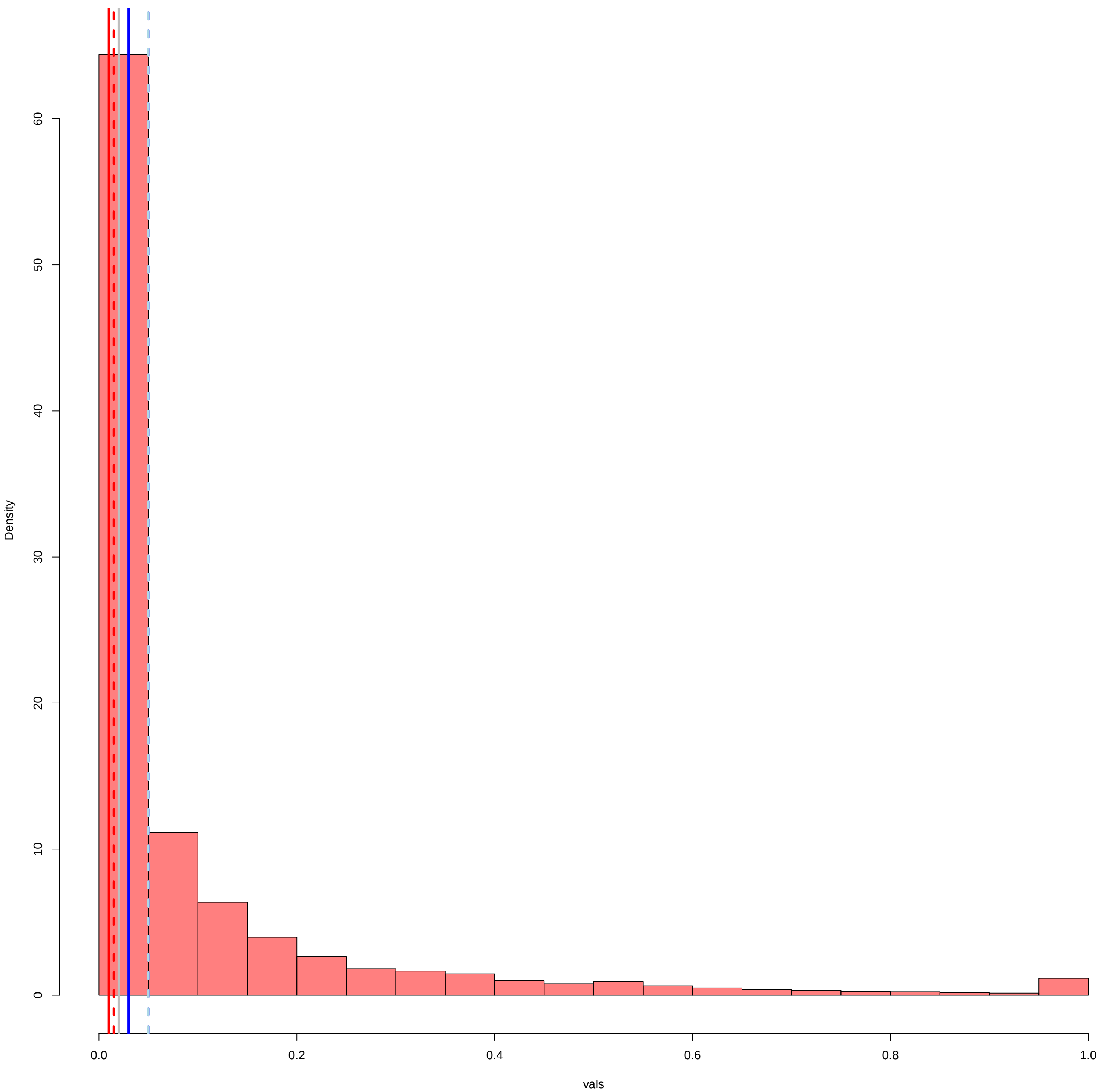
KCNT1: Hdiv quan



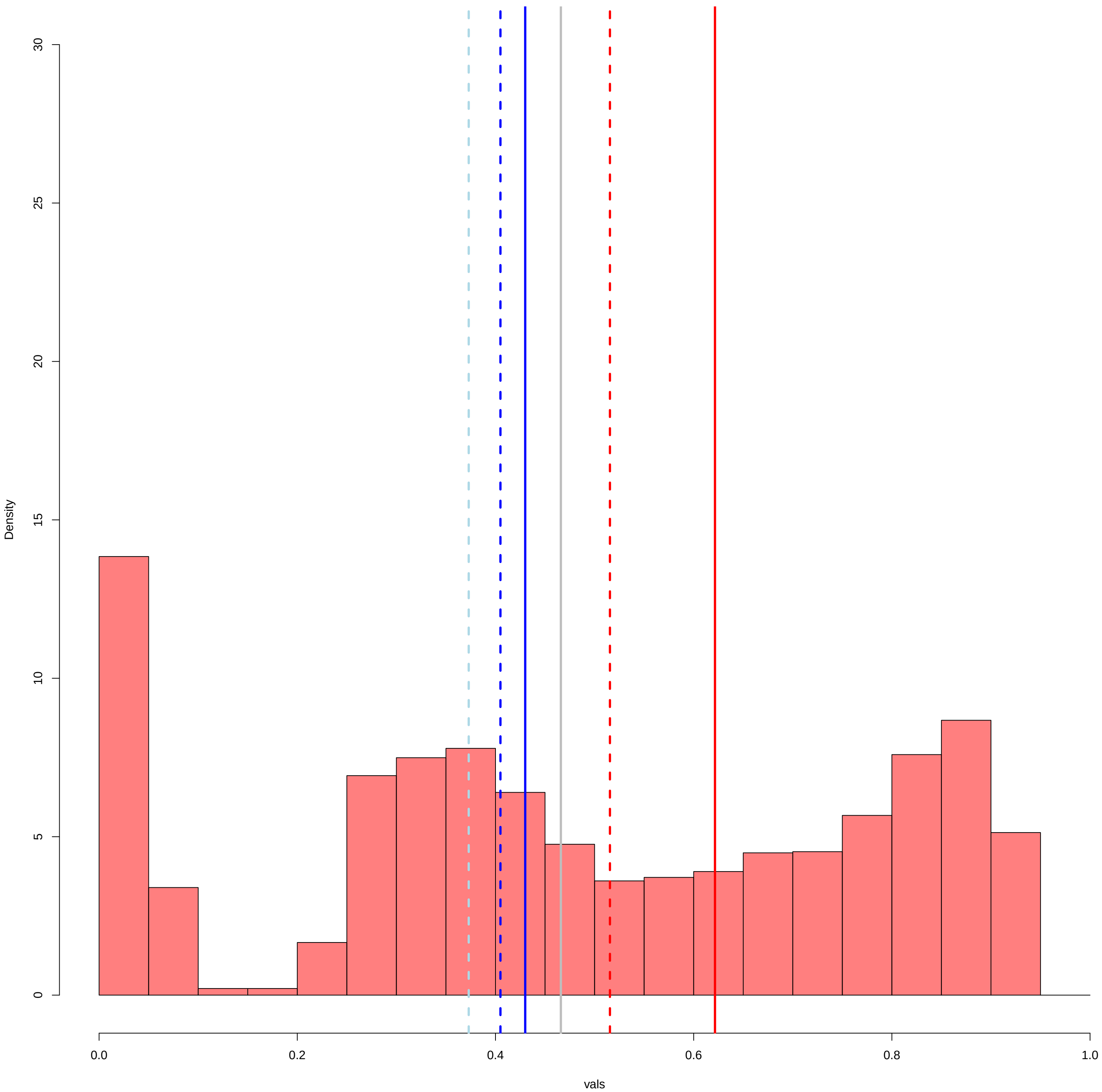
KCNT1: Hvar quan



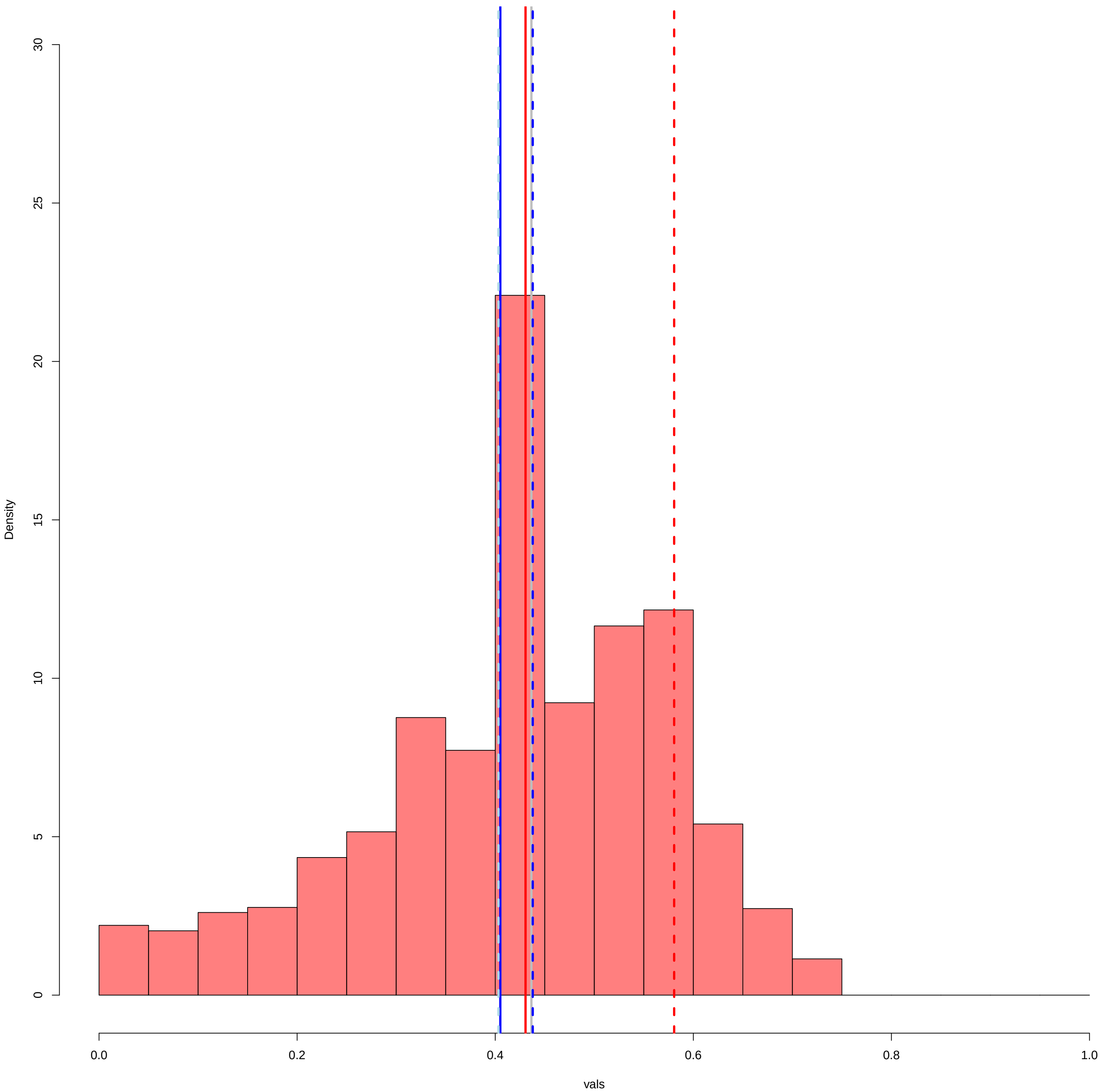
KCNT1: SIFT



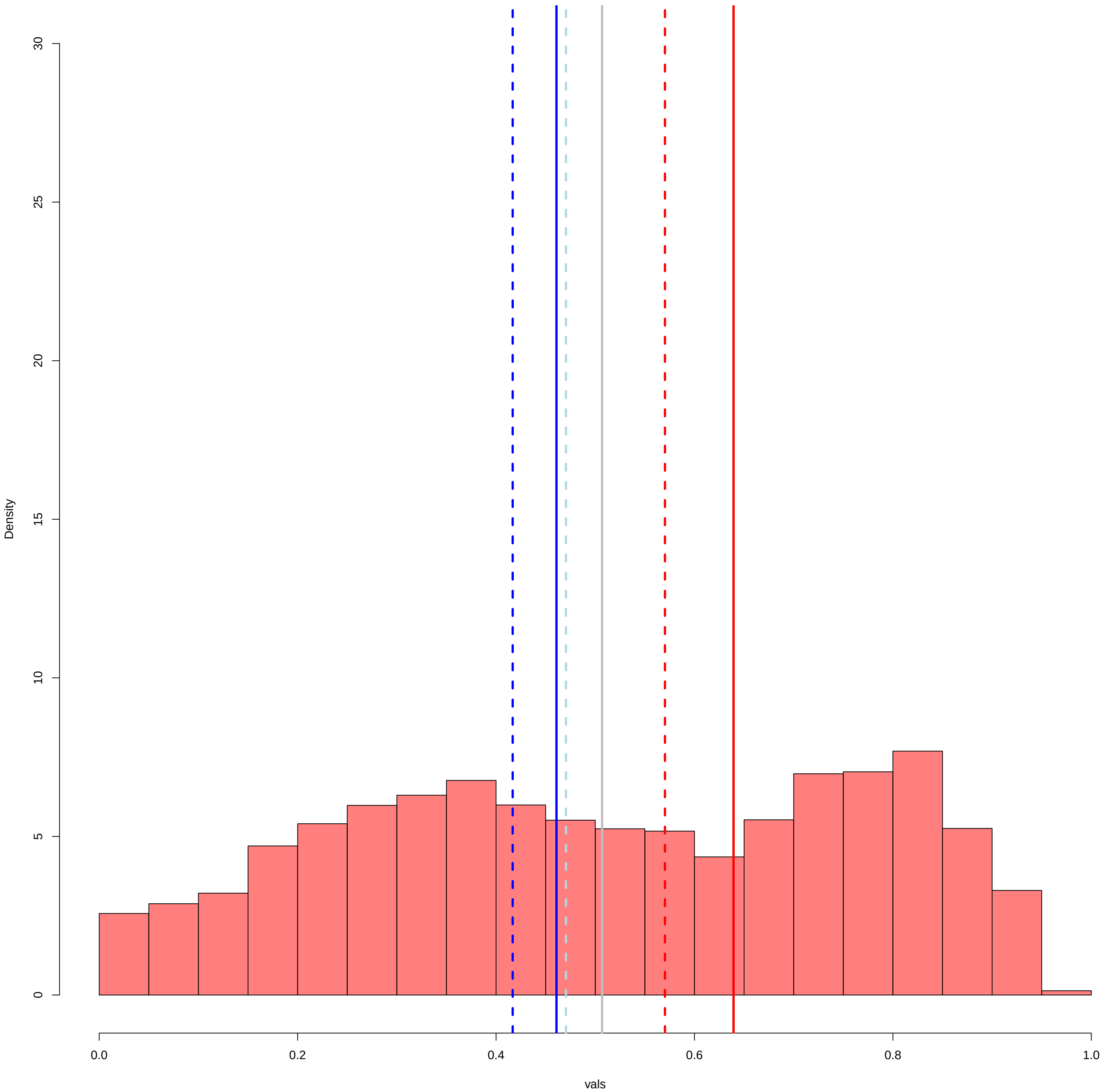
KCNT1: Condel



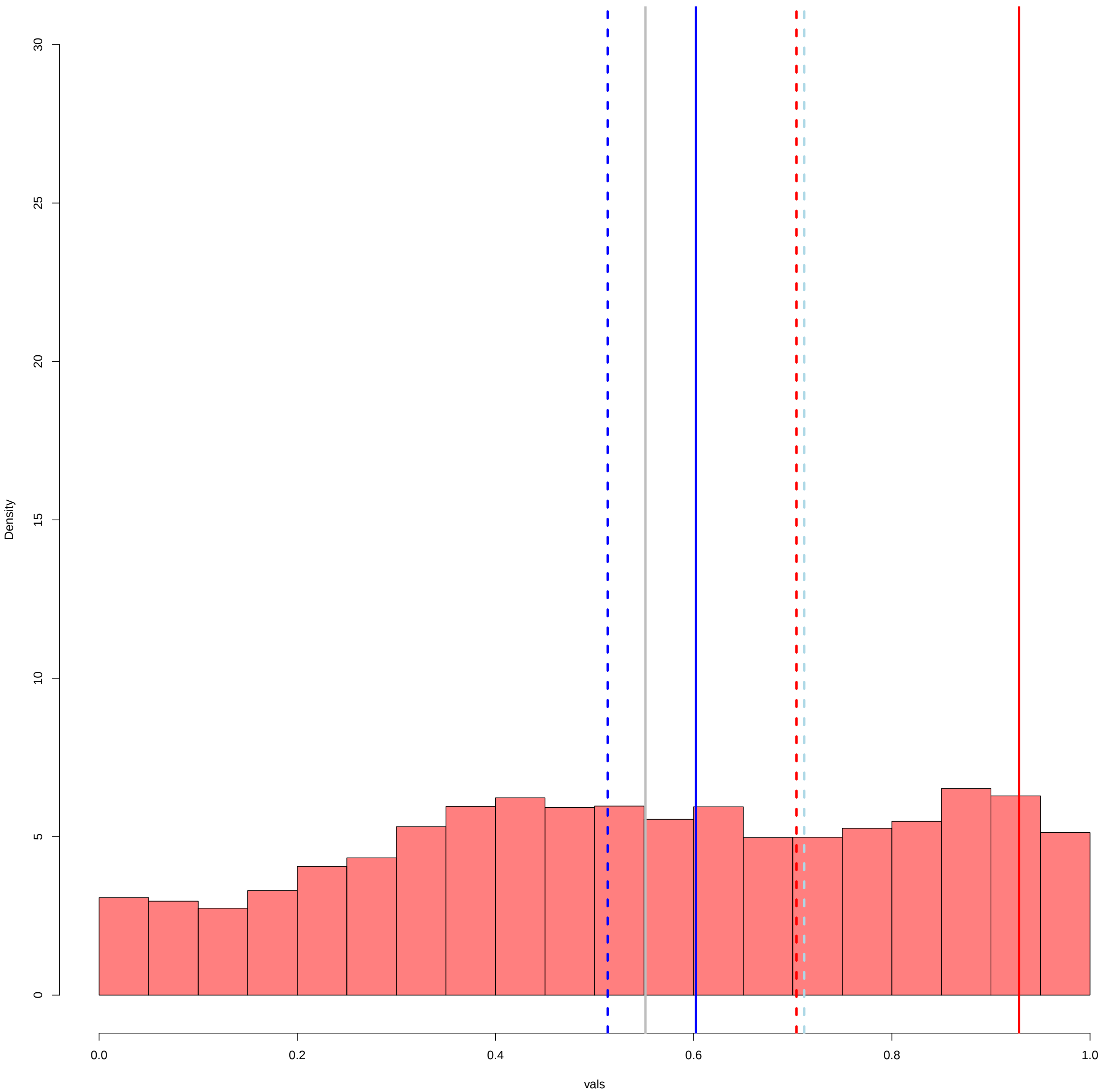
KCNT1: GERP++_RS_rankscore



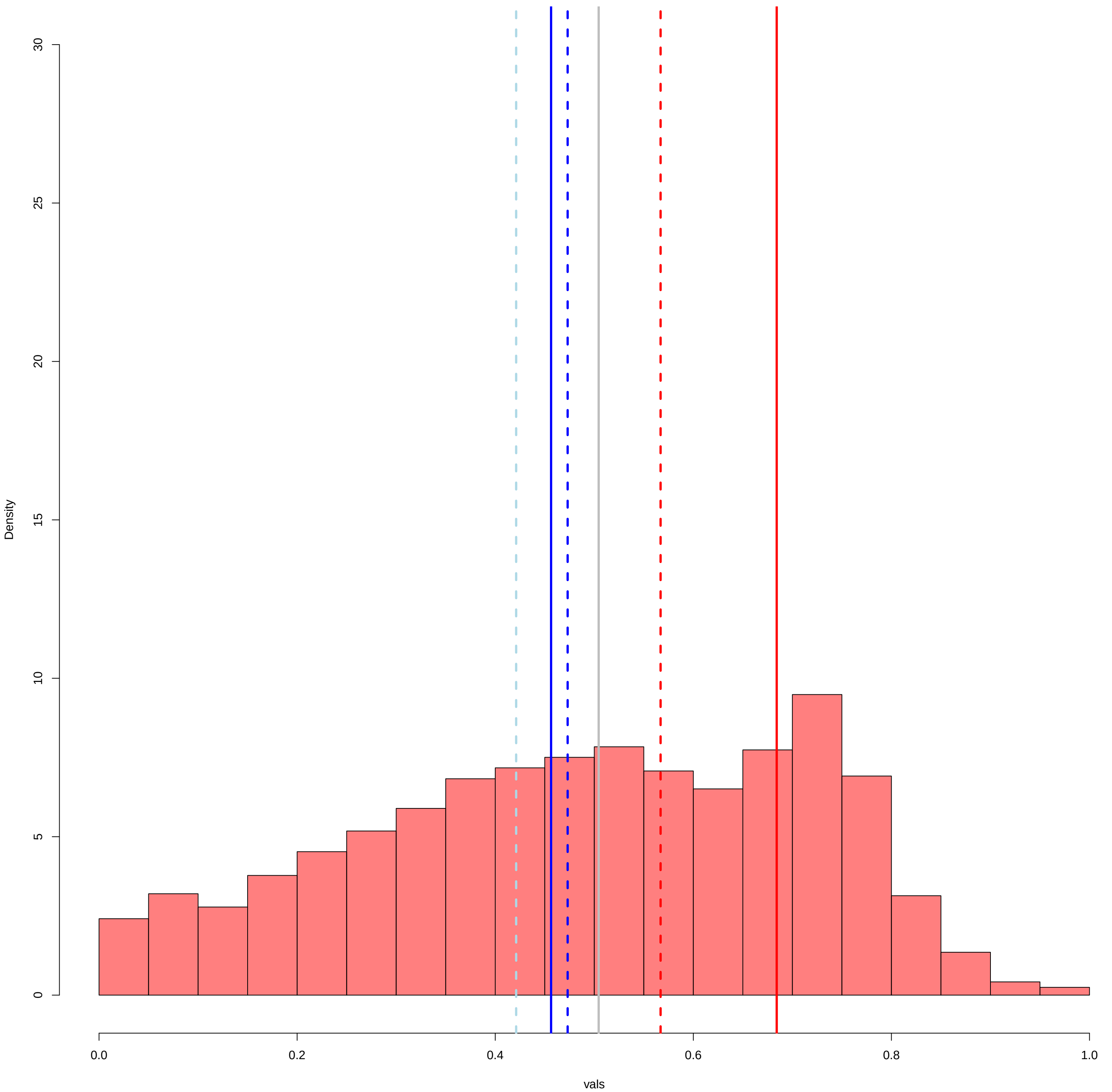
KCNT1: CADD_raw_rankscore



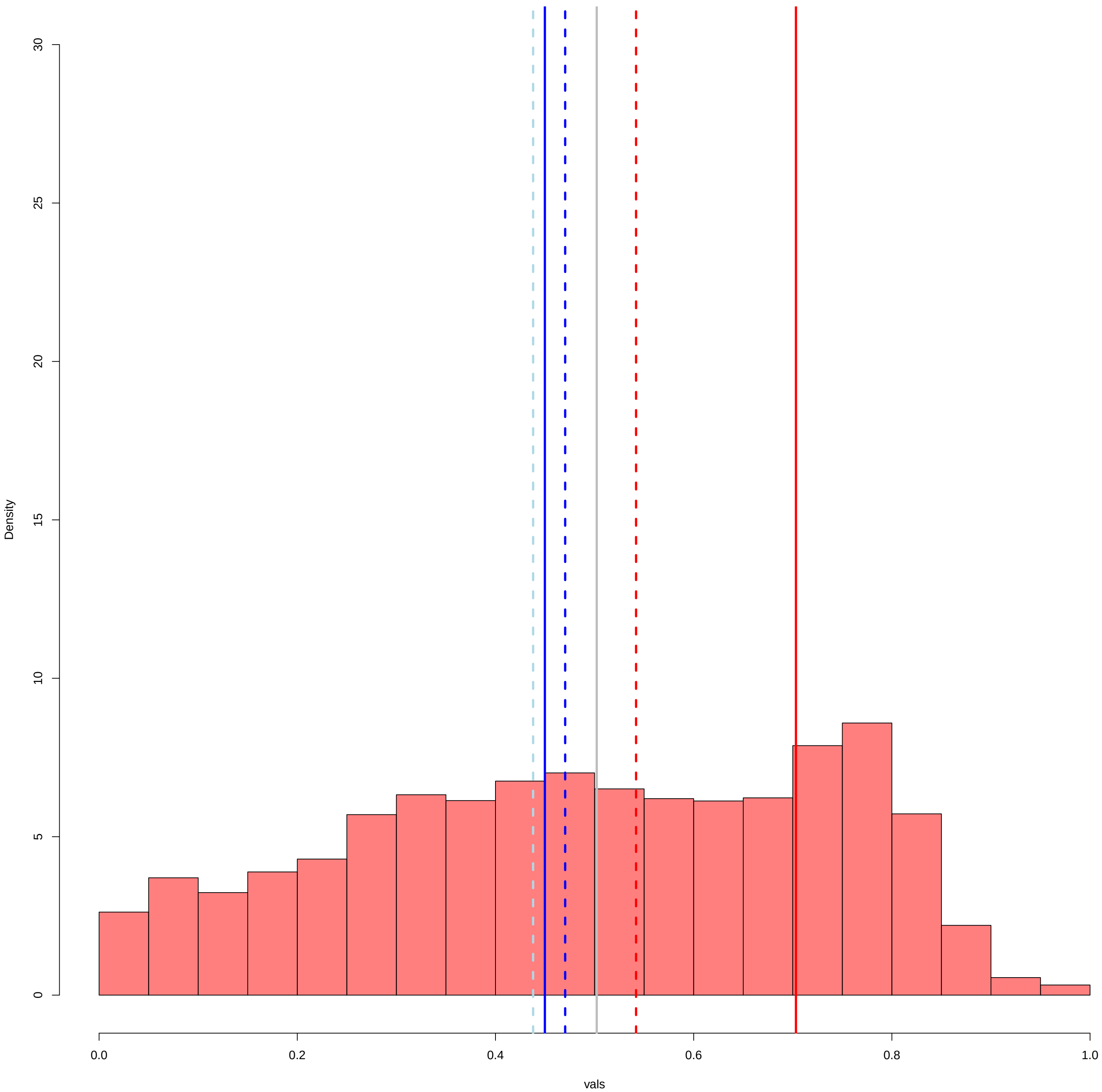
KCNT1: DANN_rankscore



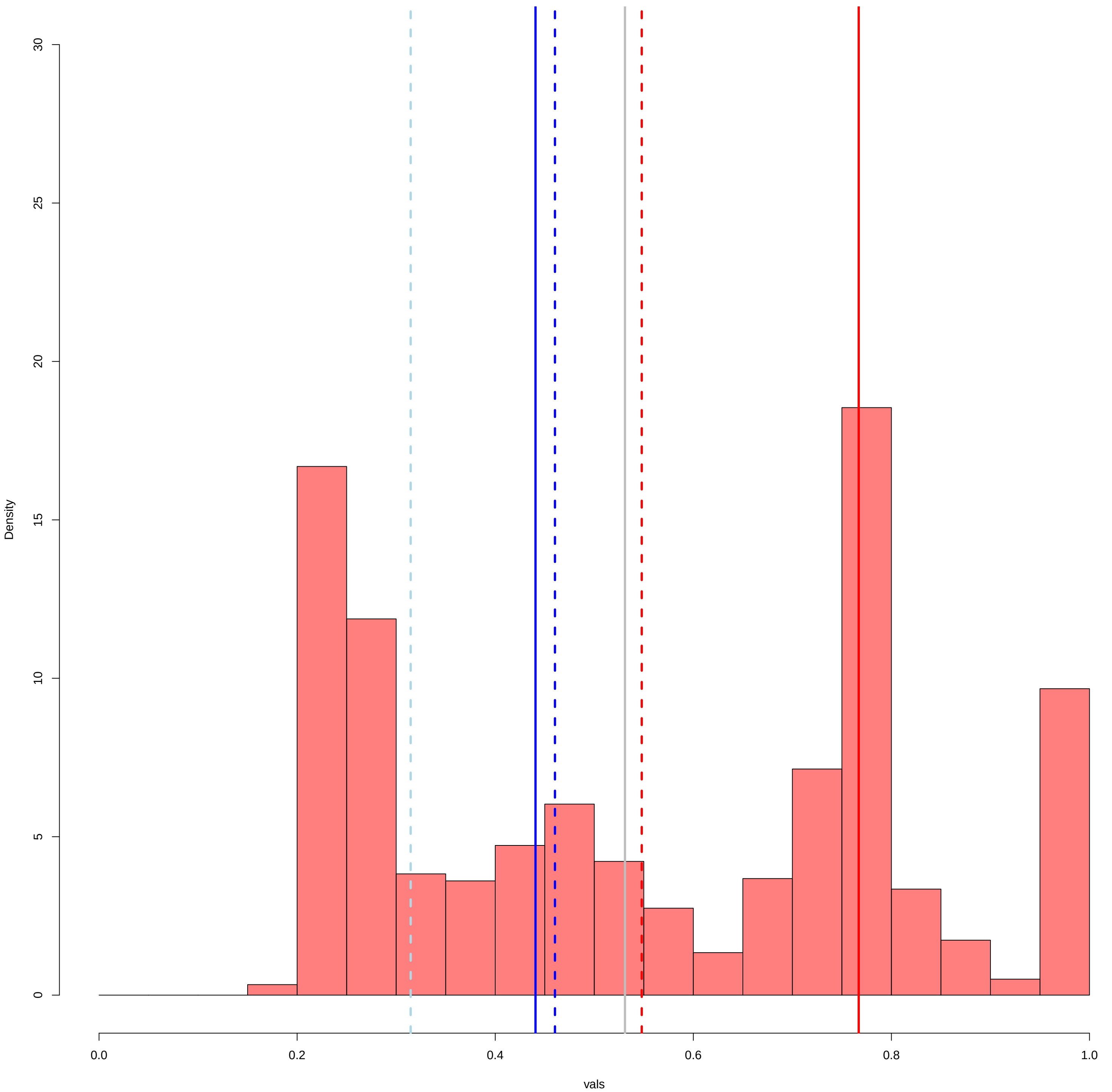
KCNT1: Eigen-PC-raw_rankscore



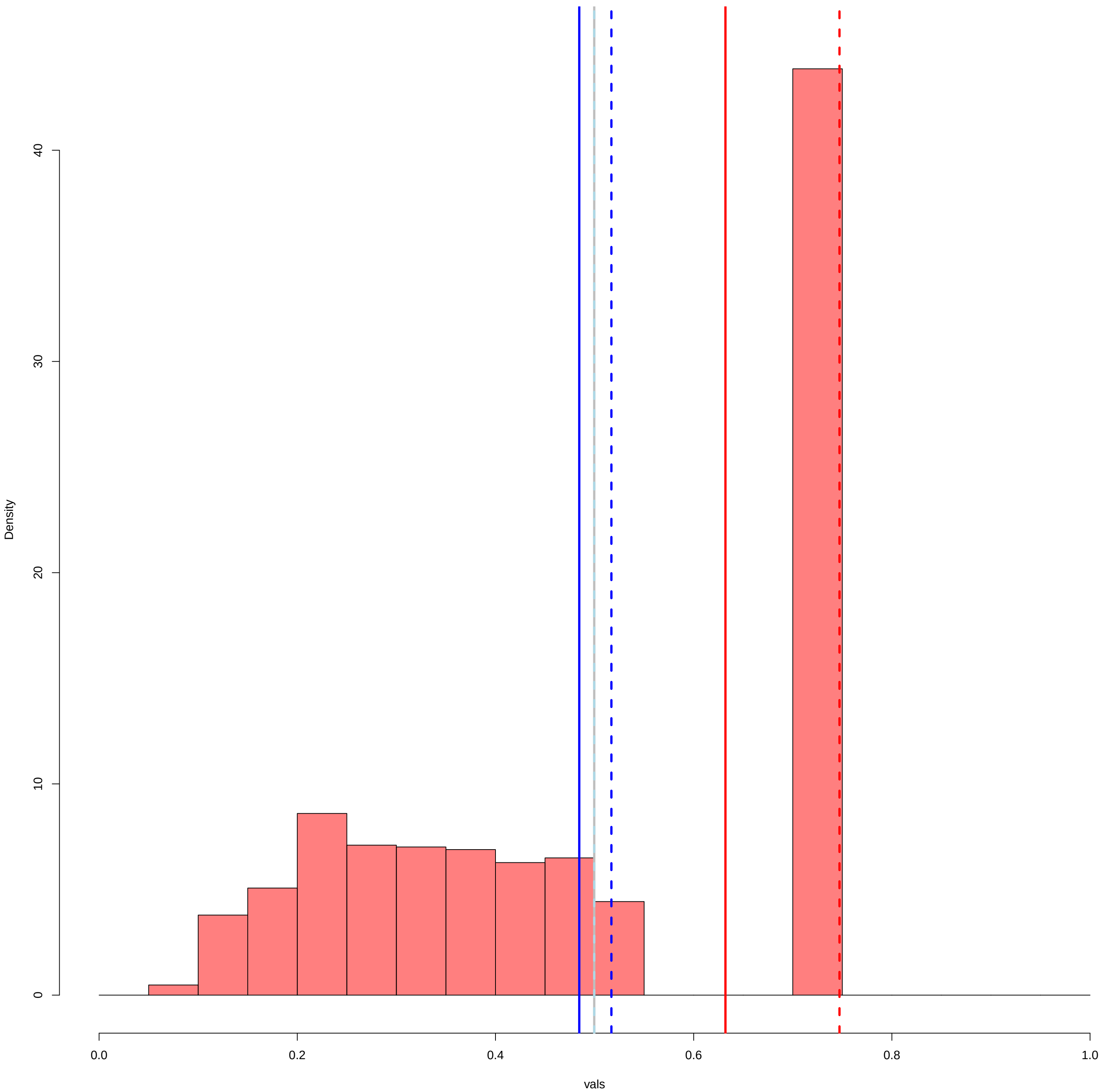
KCNT1: Eigen-row_rankscore



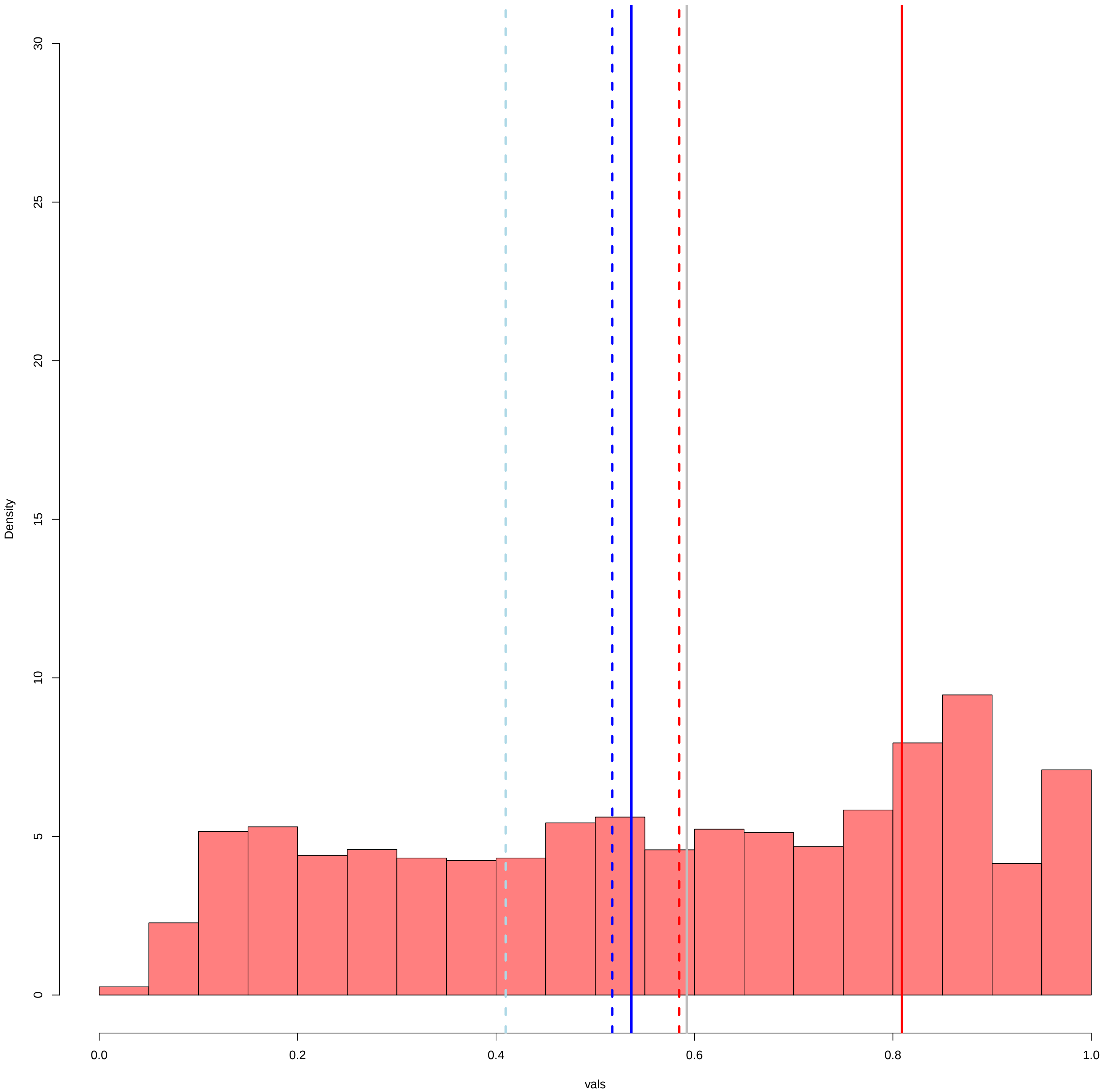
KCNT1: FATHMM_converted_rankscore



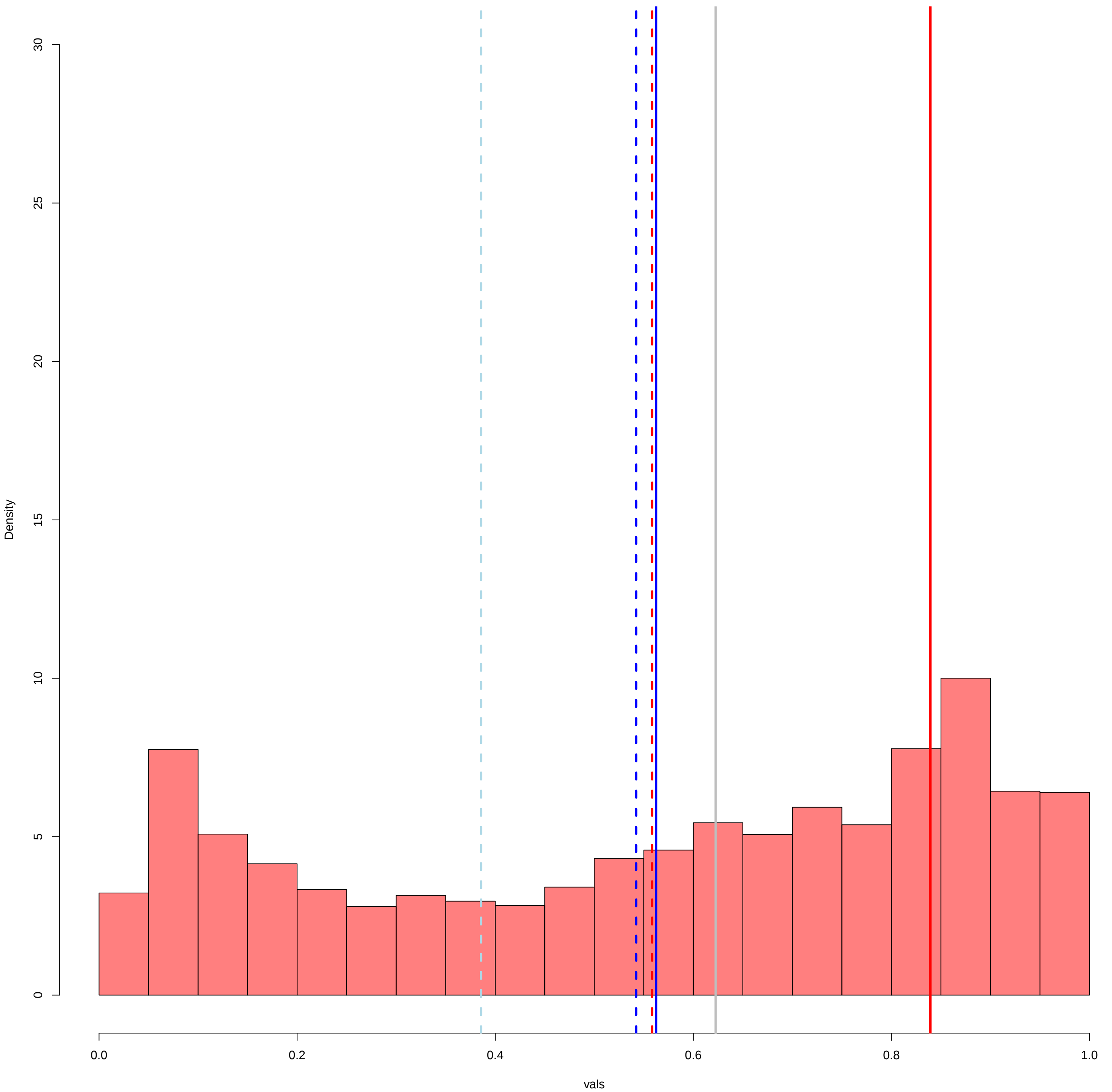
KCNT1: GenoCanyon_score_rankscore



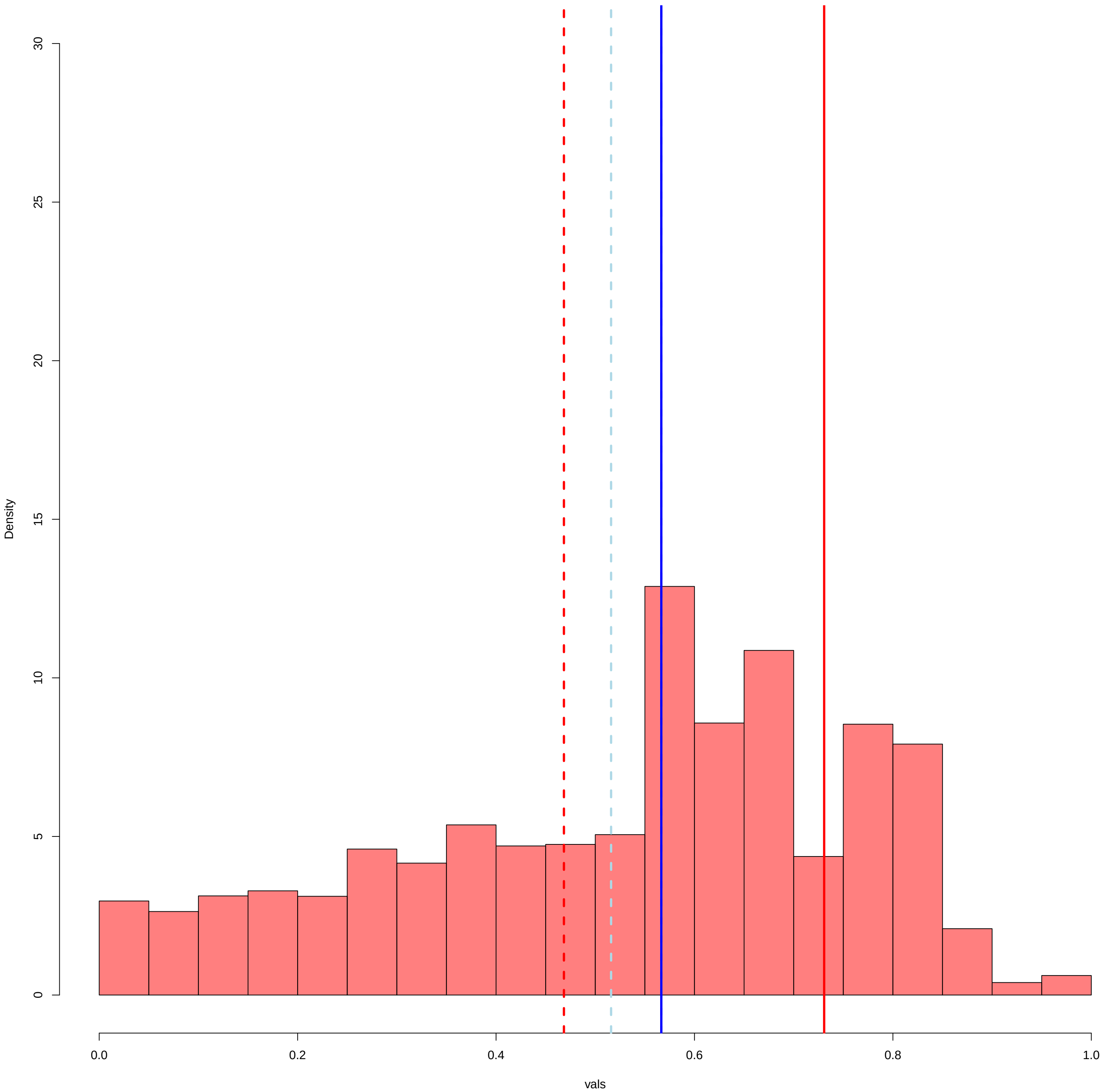
KCNT1: MetaLR_rankscore



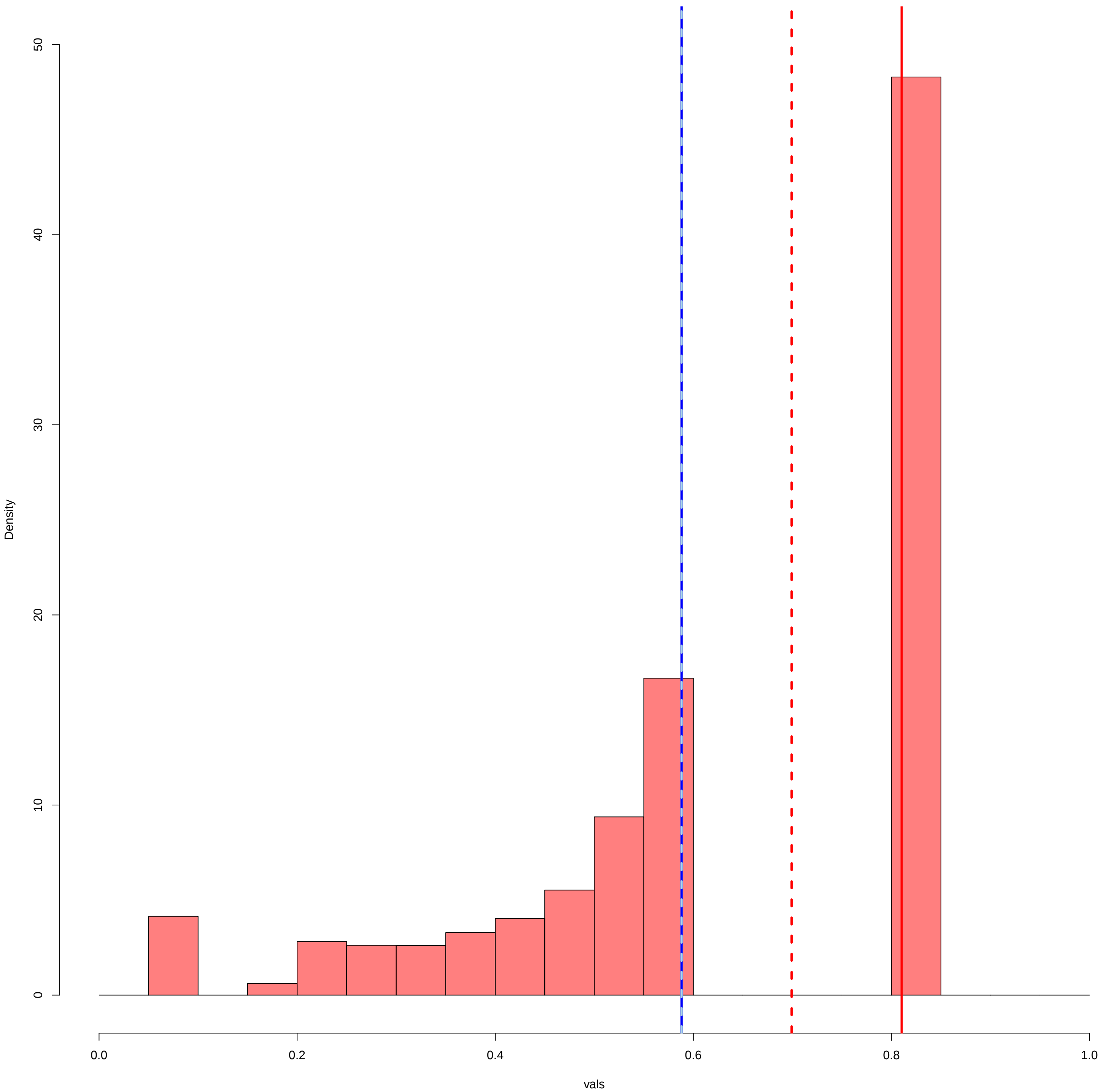
KCNT1: MetaSVM_rankscore



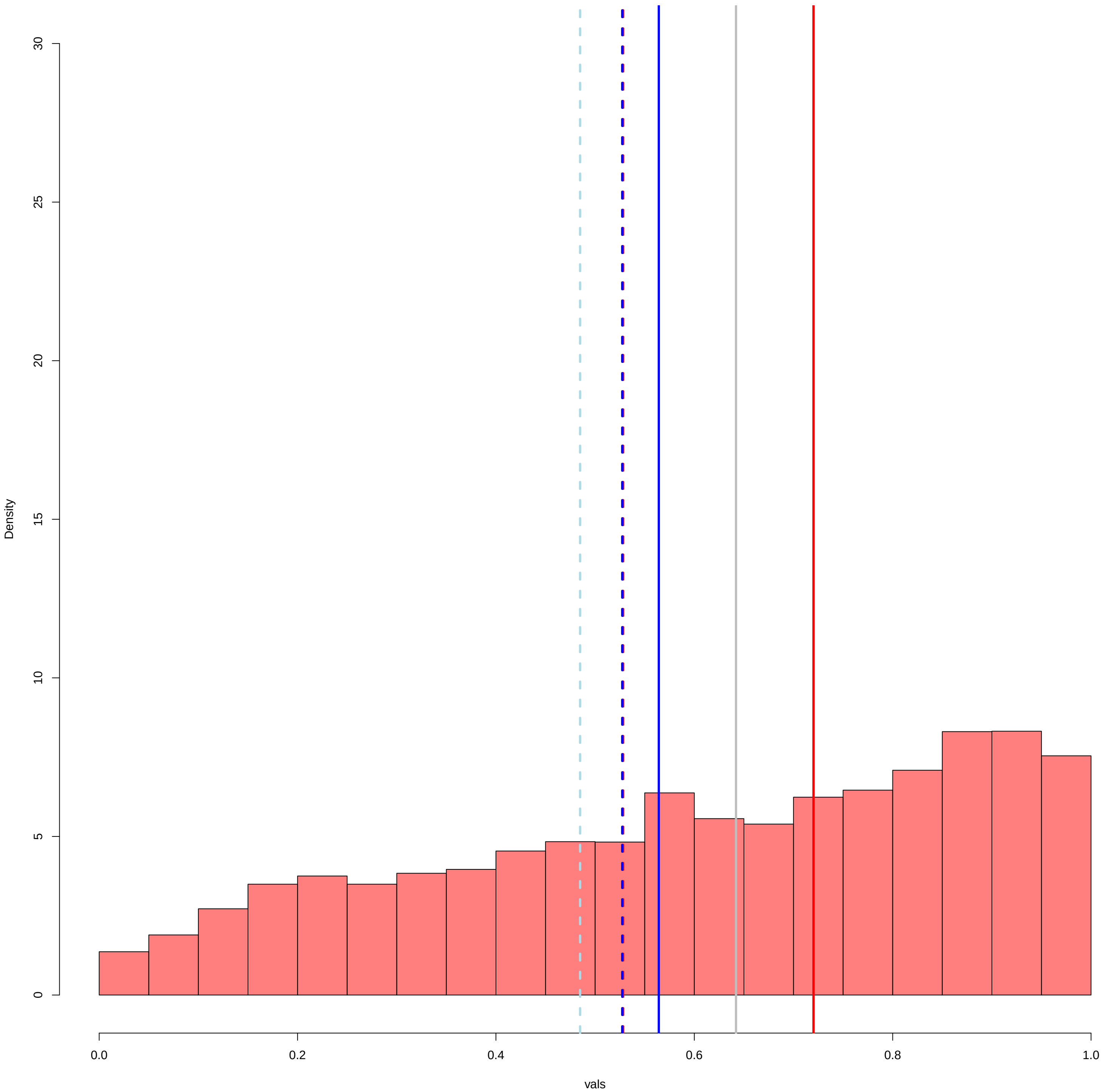
KCNT1: MutationAssessor_score_rankscore



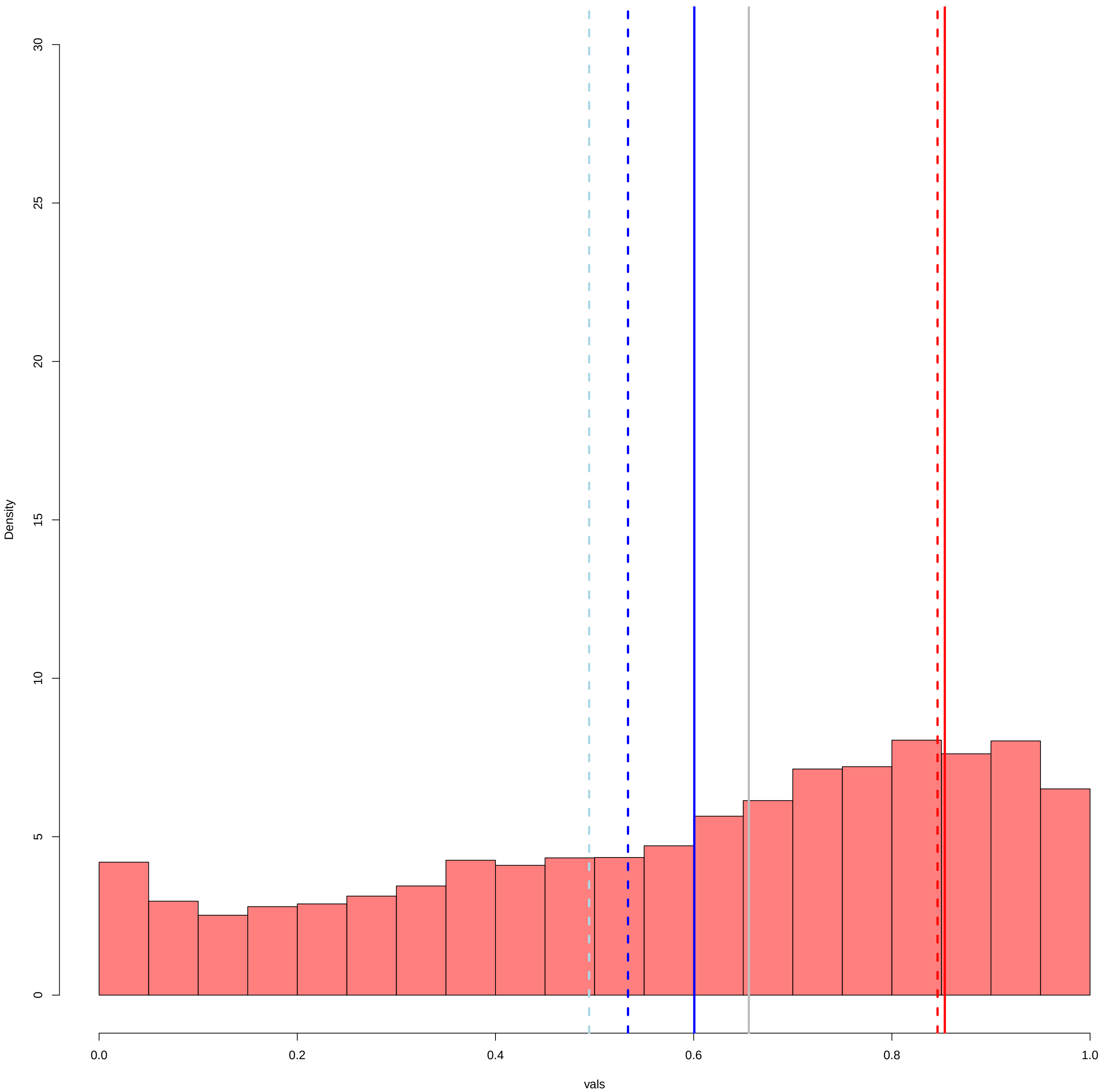
KCNT1: MutationTaster_converted_rankscore



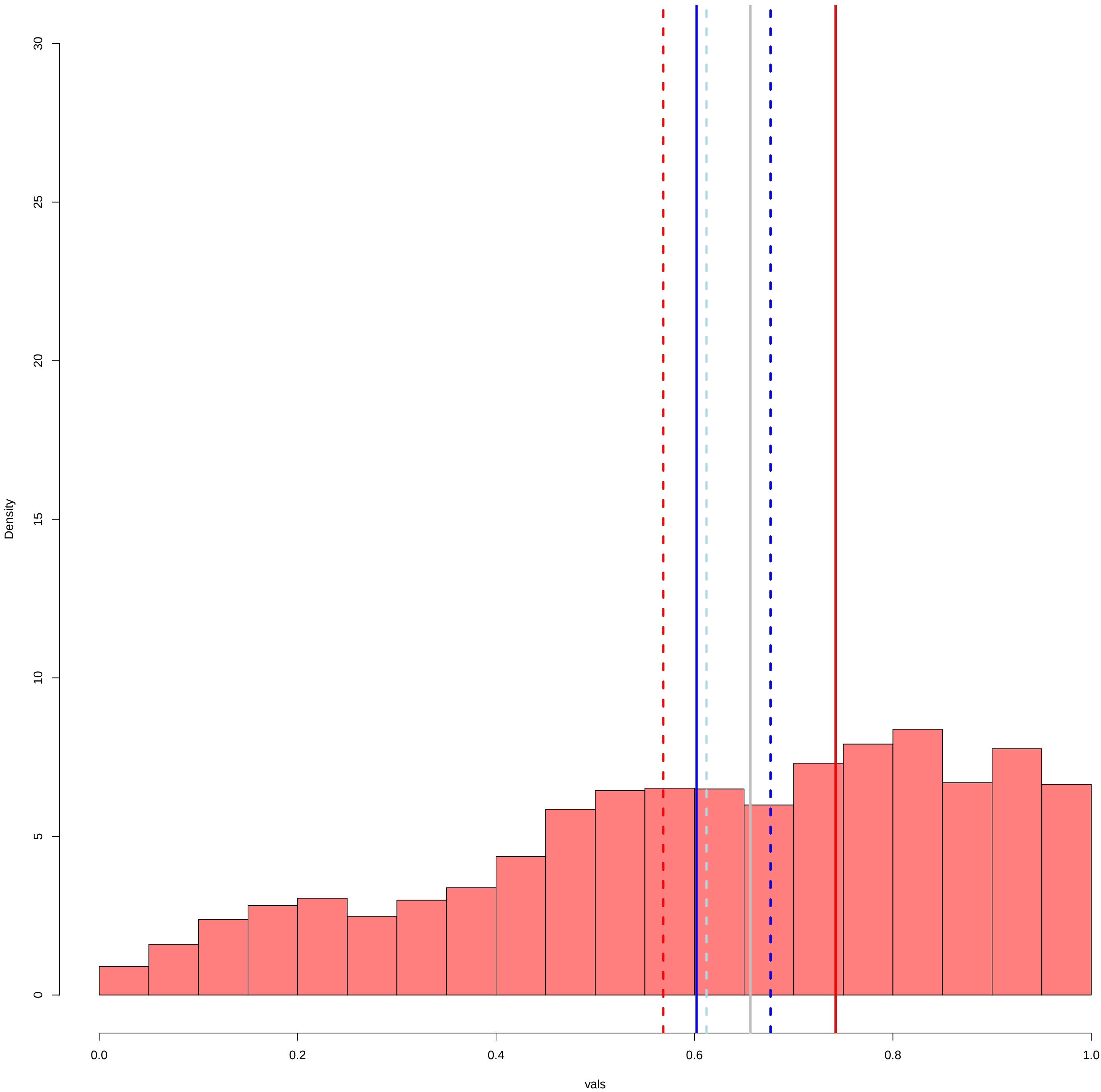
KCNT1: PROVEAN_converted_rankscore



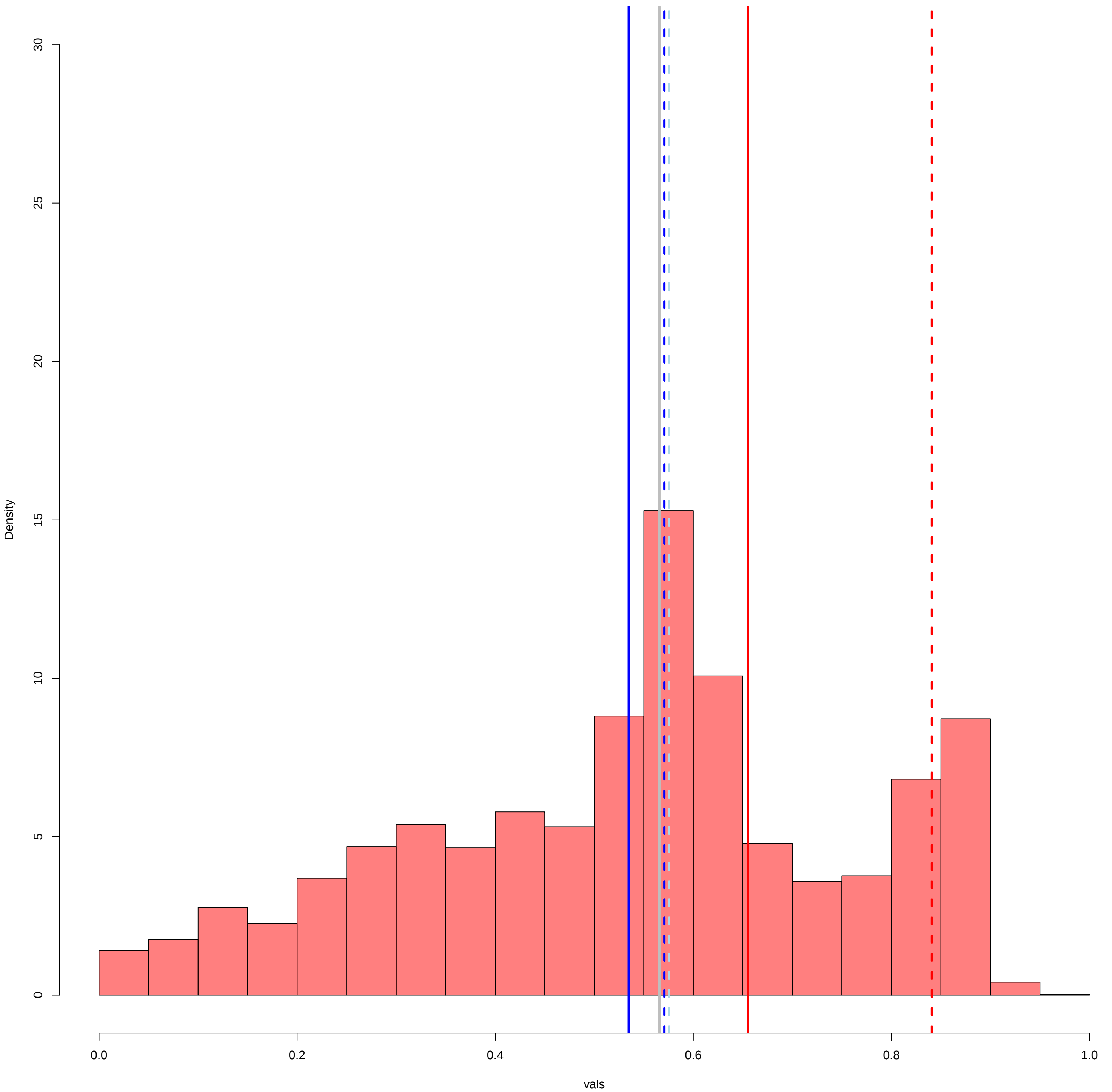
KCNT1: VEST3_rankscore



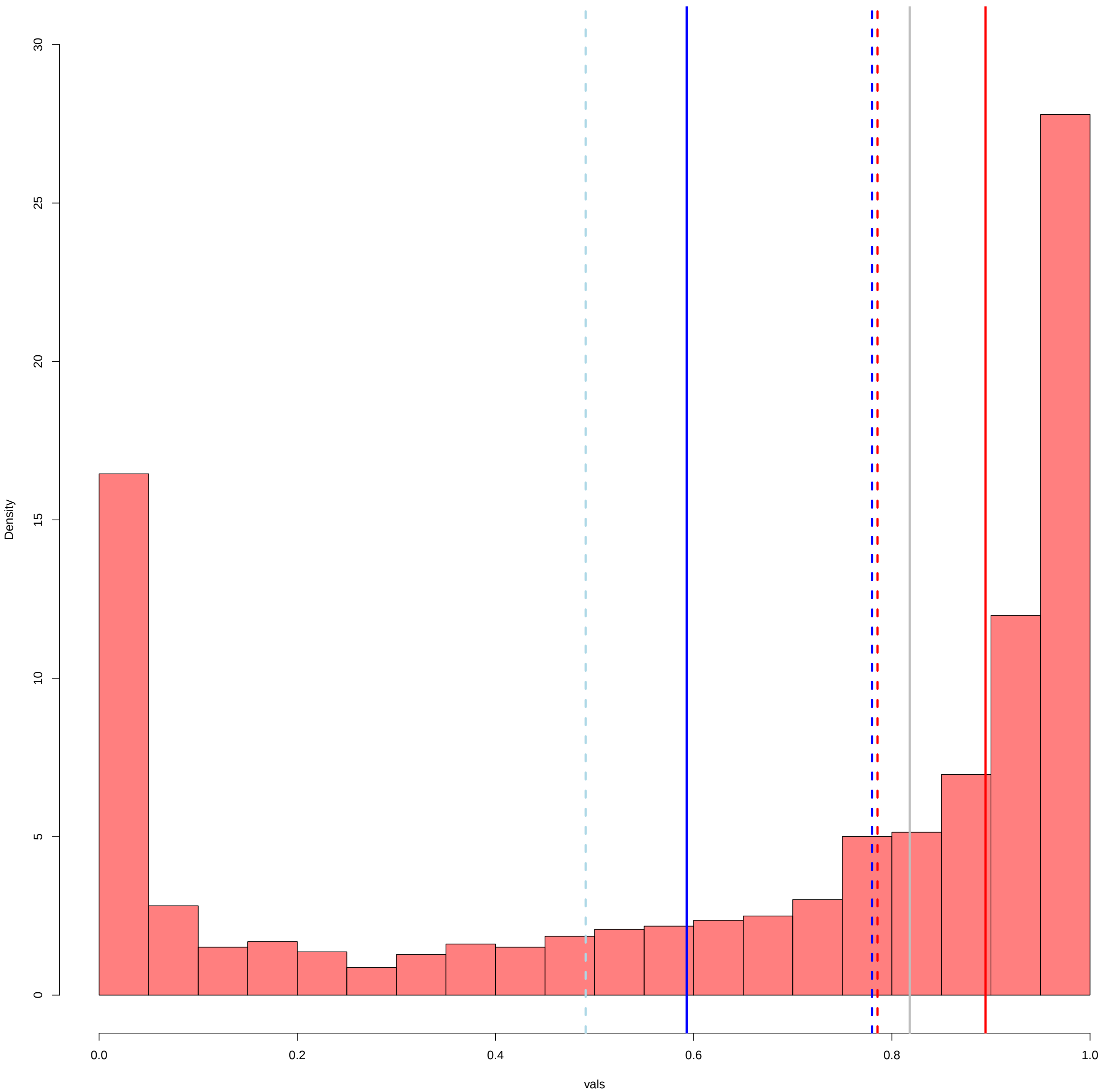
KCNT1: fathmm-MKL_coding_rankscore



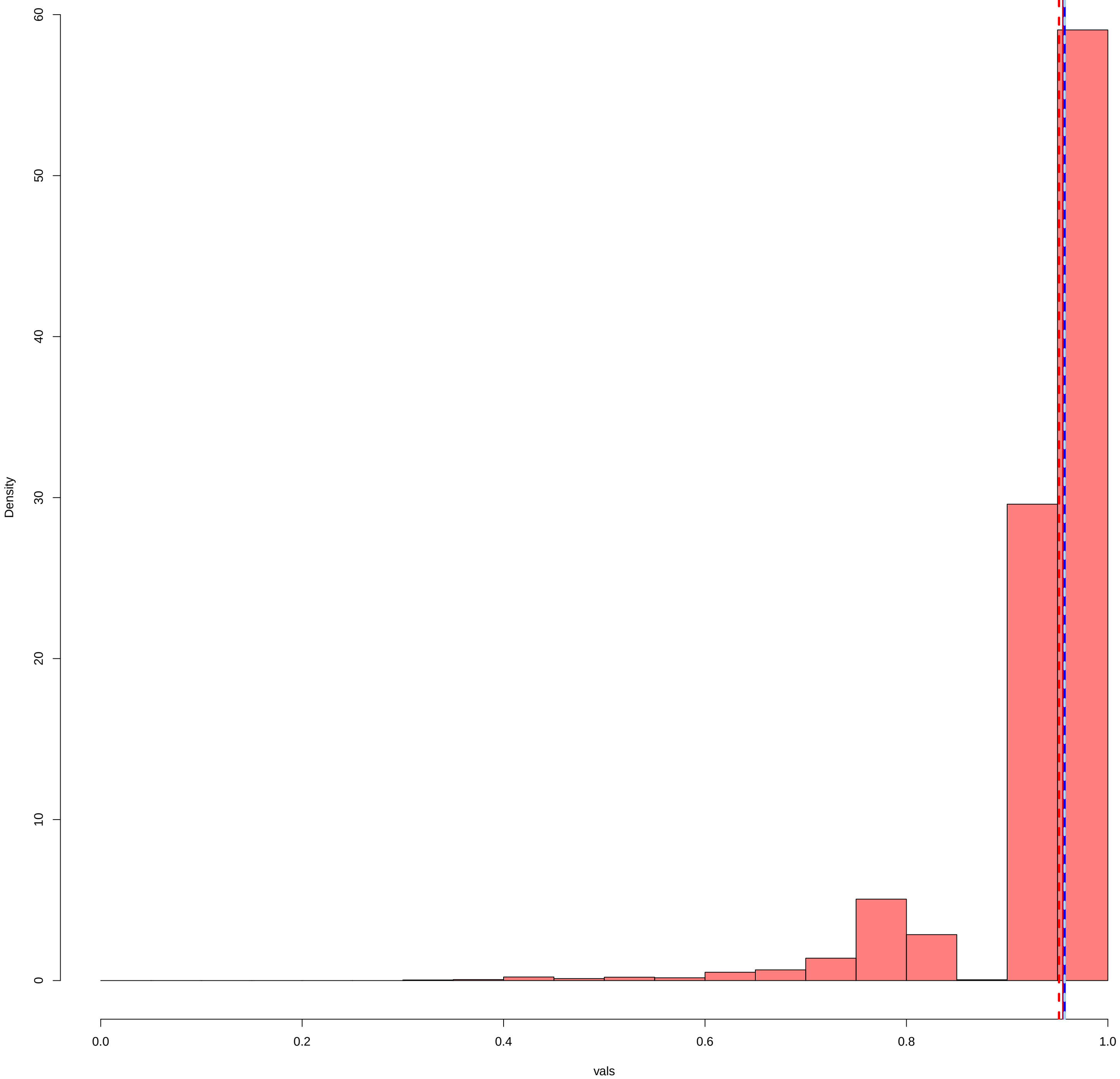
KCNT1: SiPhy_29way_logOdds_rankscore



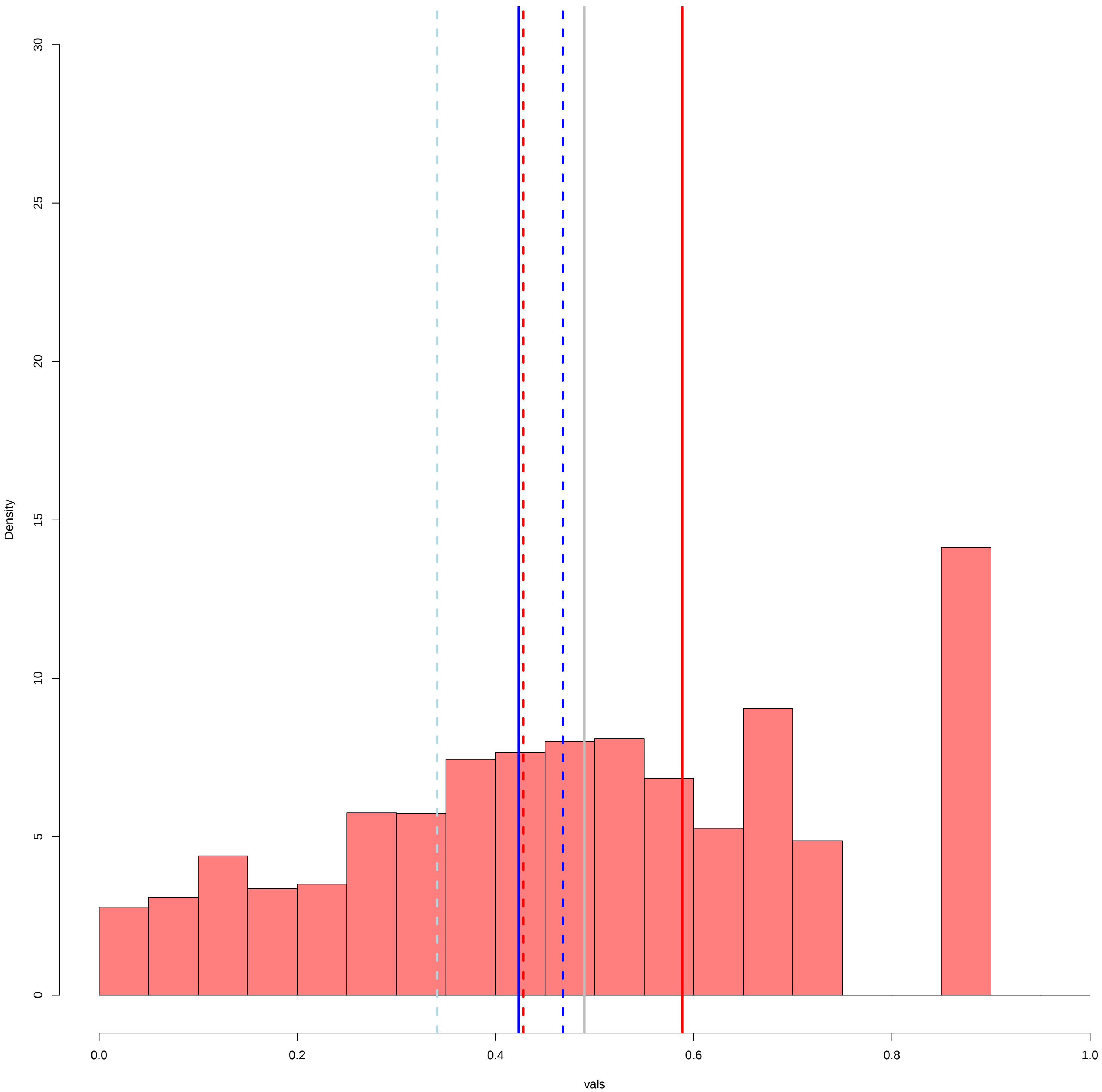
KCNT1: priPhCons



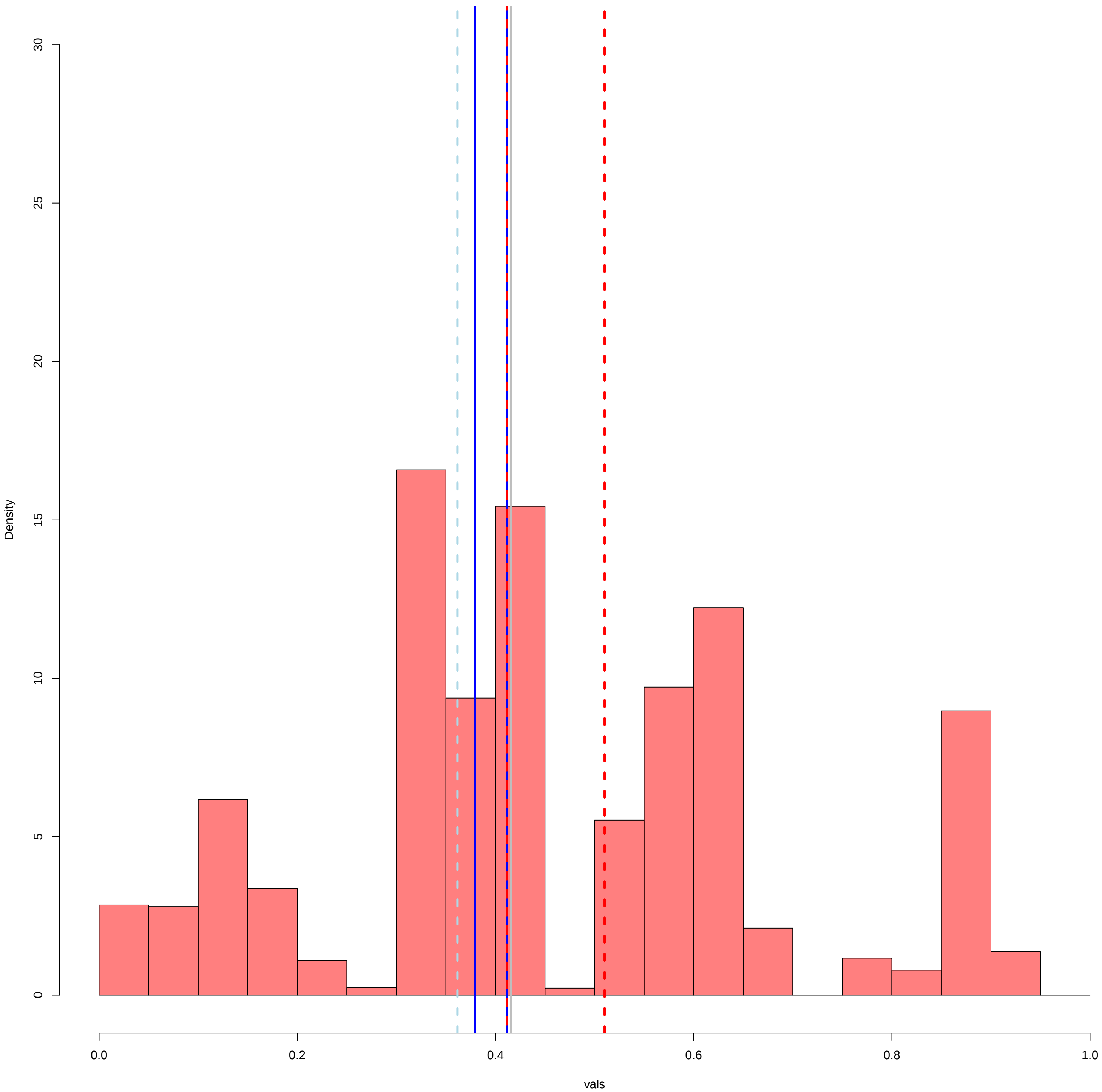
KCNT1: priPhyloP



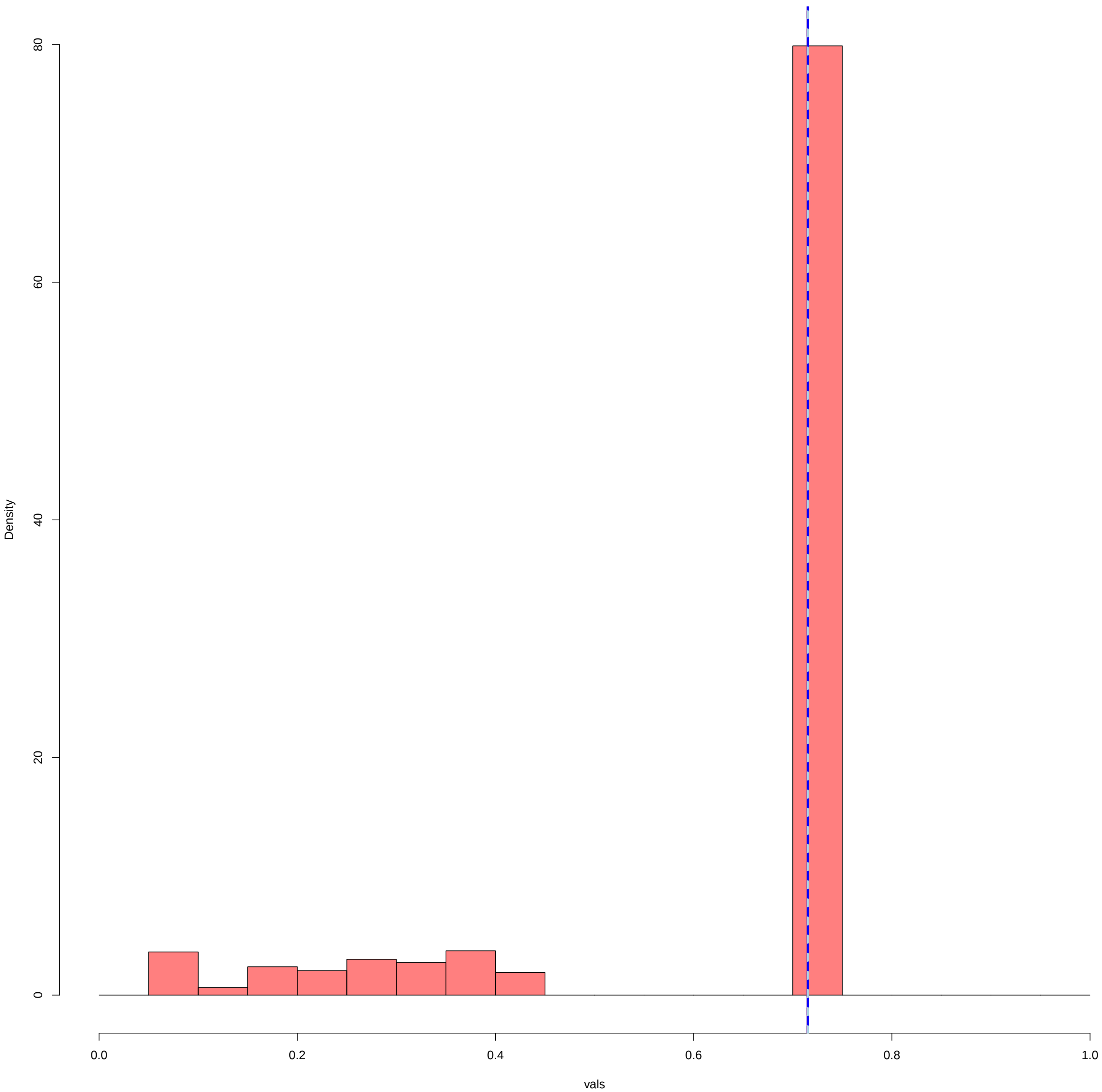
KCNT1: phastCons20way_mammalian_rankscore



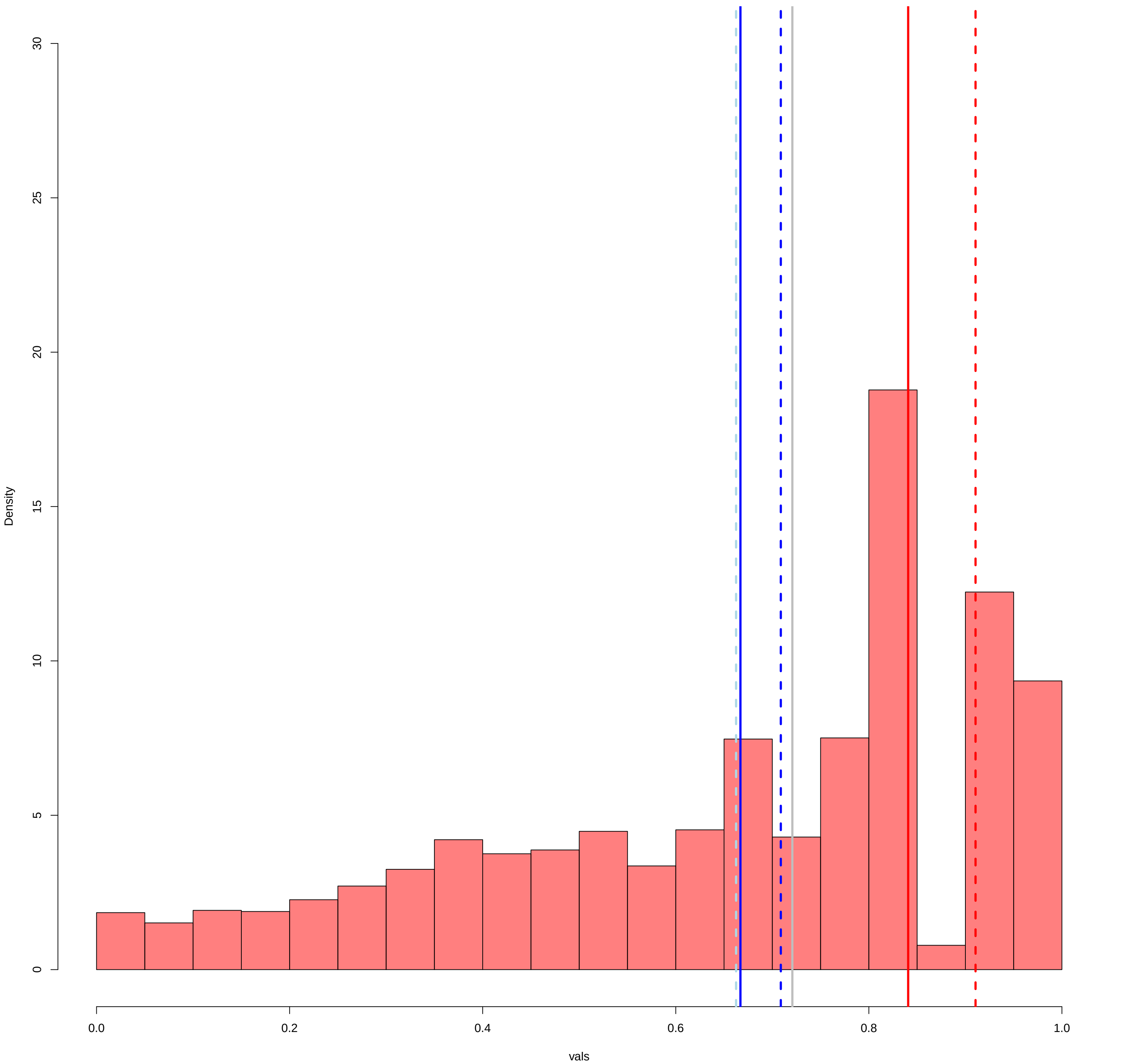
KCNT1: phyloP20way_mammalian_rankscore



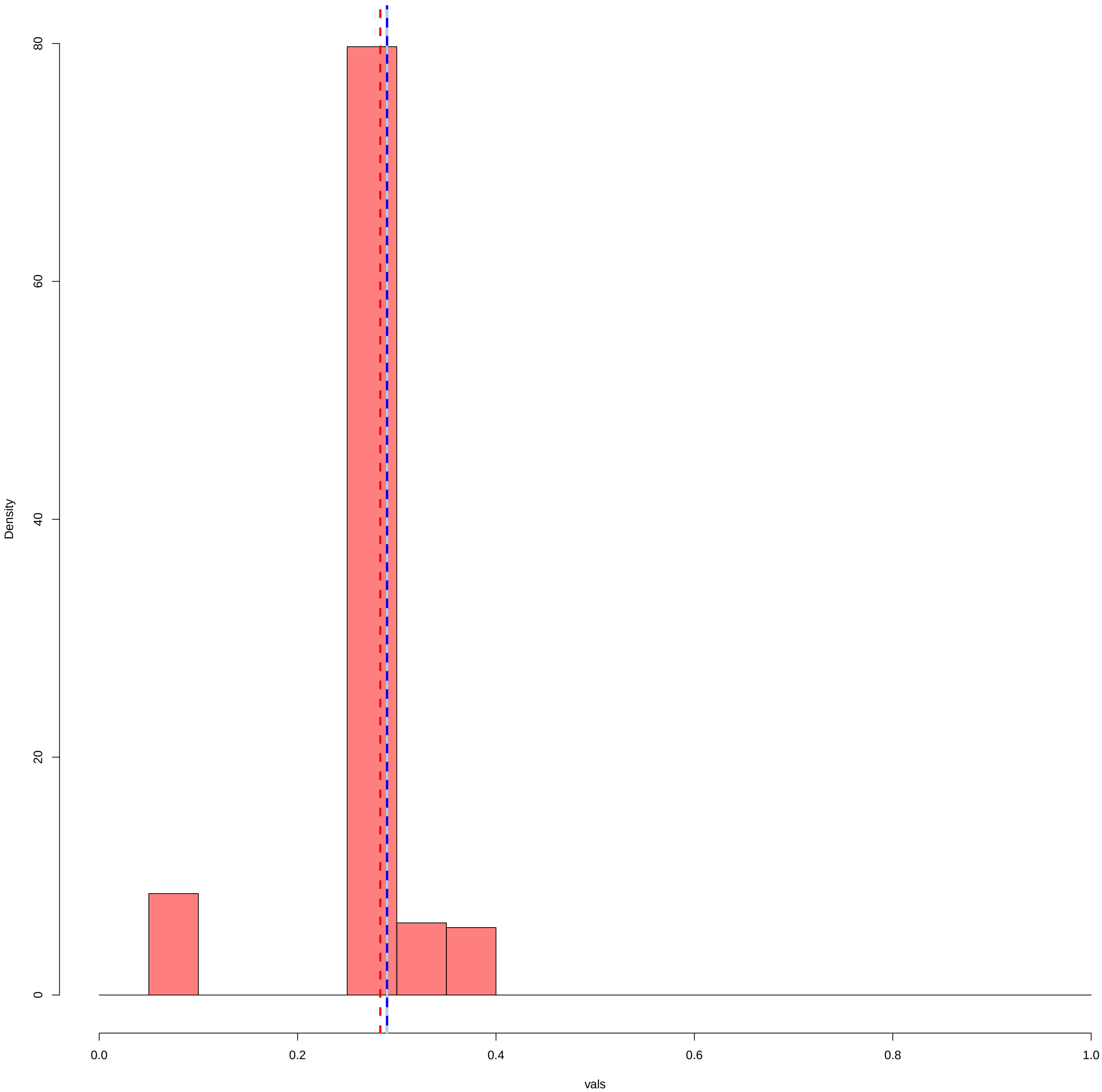
KCNT1: phastCons100way Vertebrate RankScore



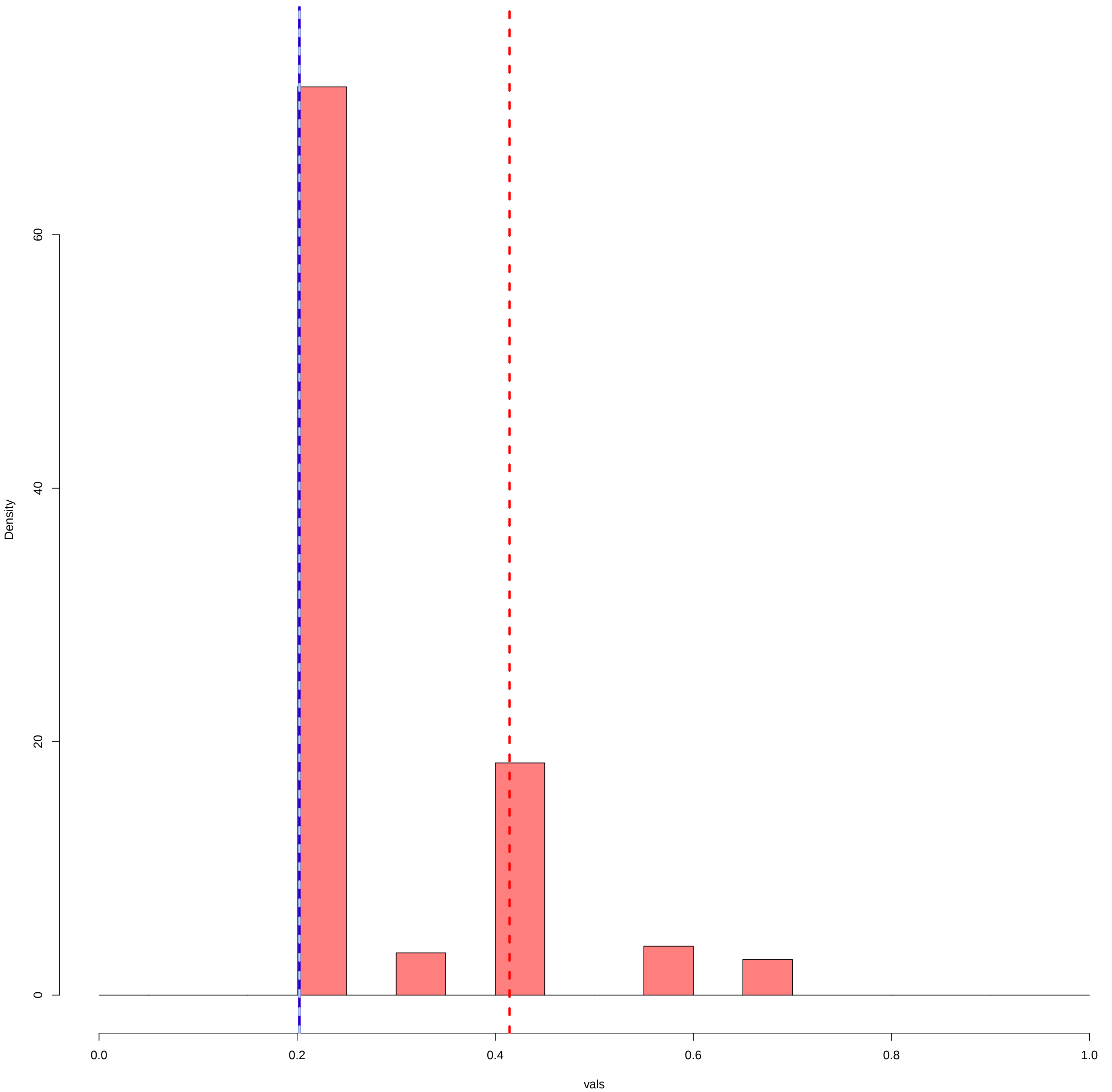
KCNT1: phyloP100way_vertebrate_rankscore



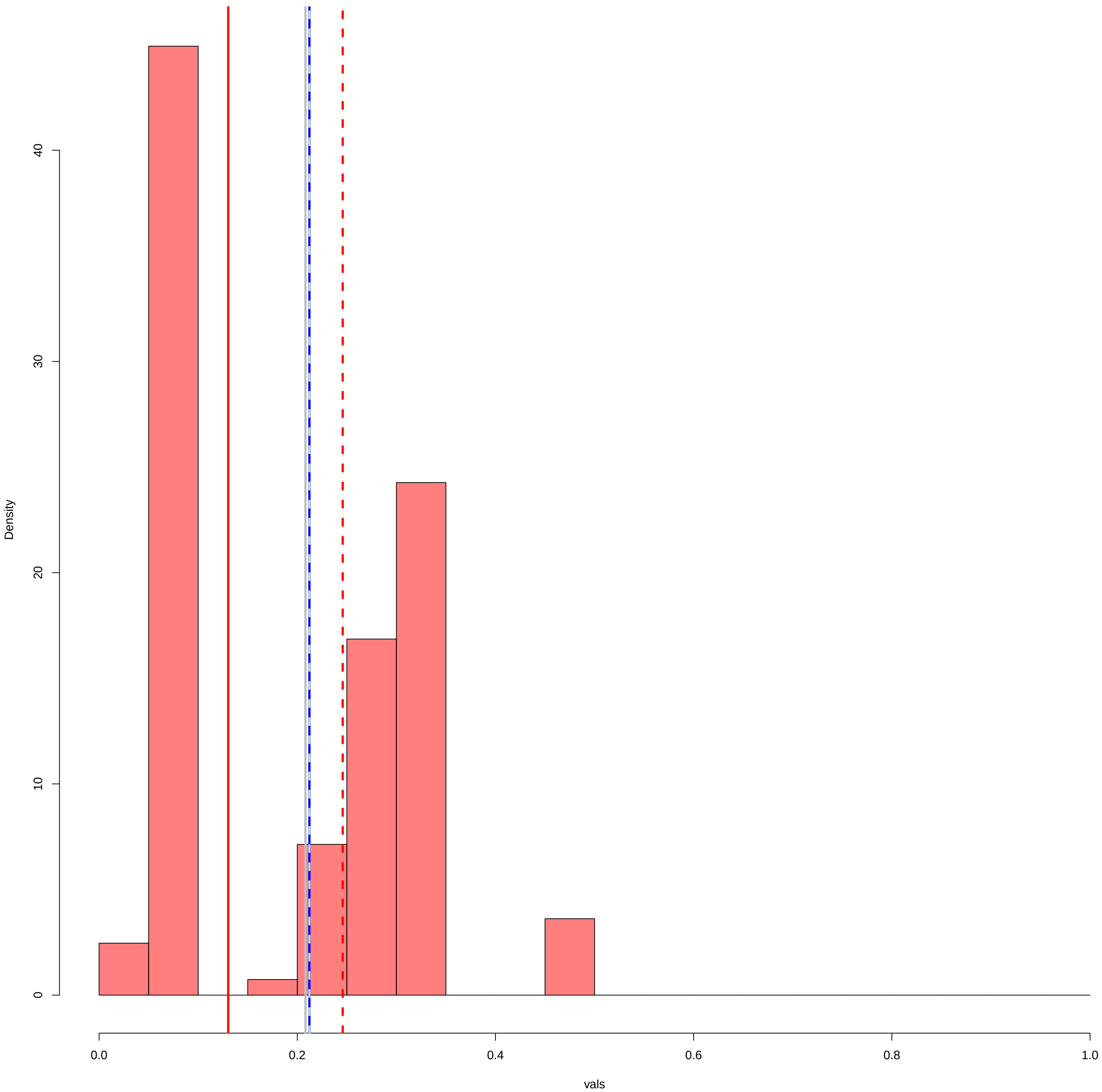
KCNT1: H1-hESC_fitCons_score_rankscore



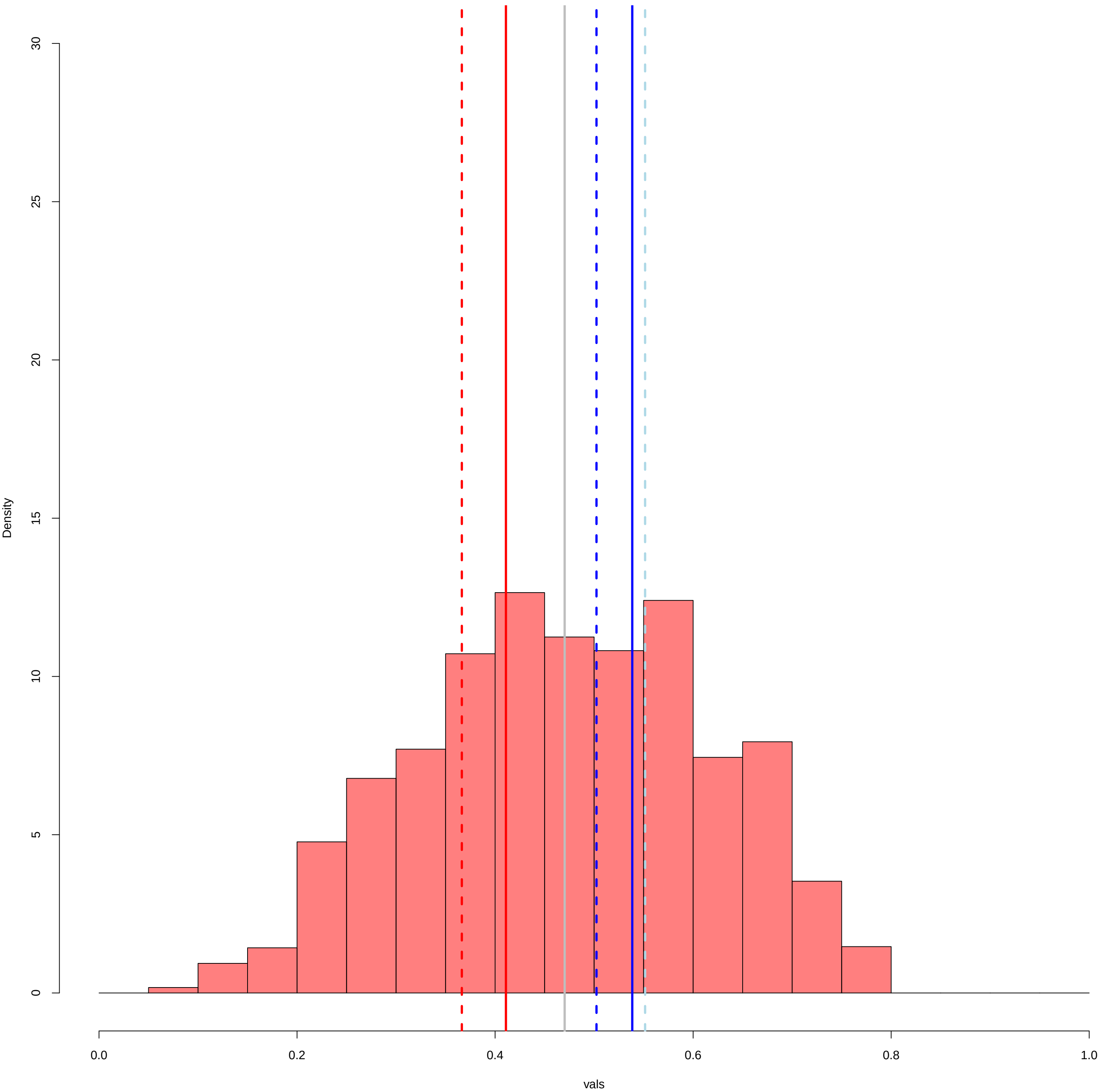
KCNT1: HUVEC_fitCons_score_rankscore



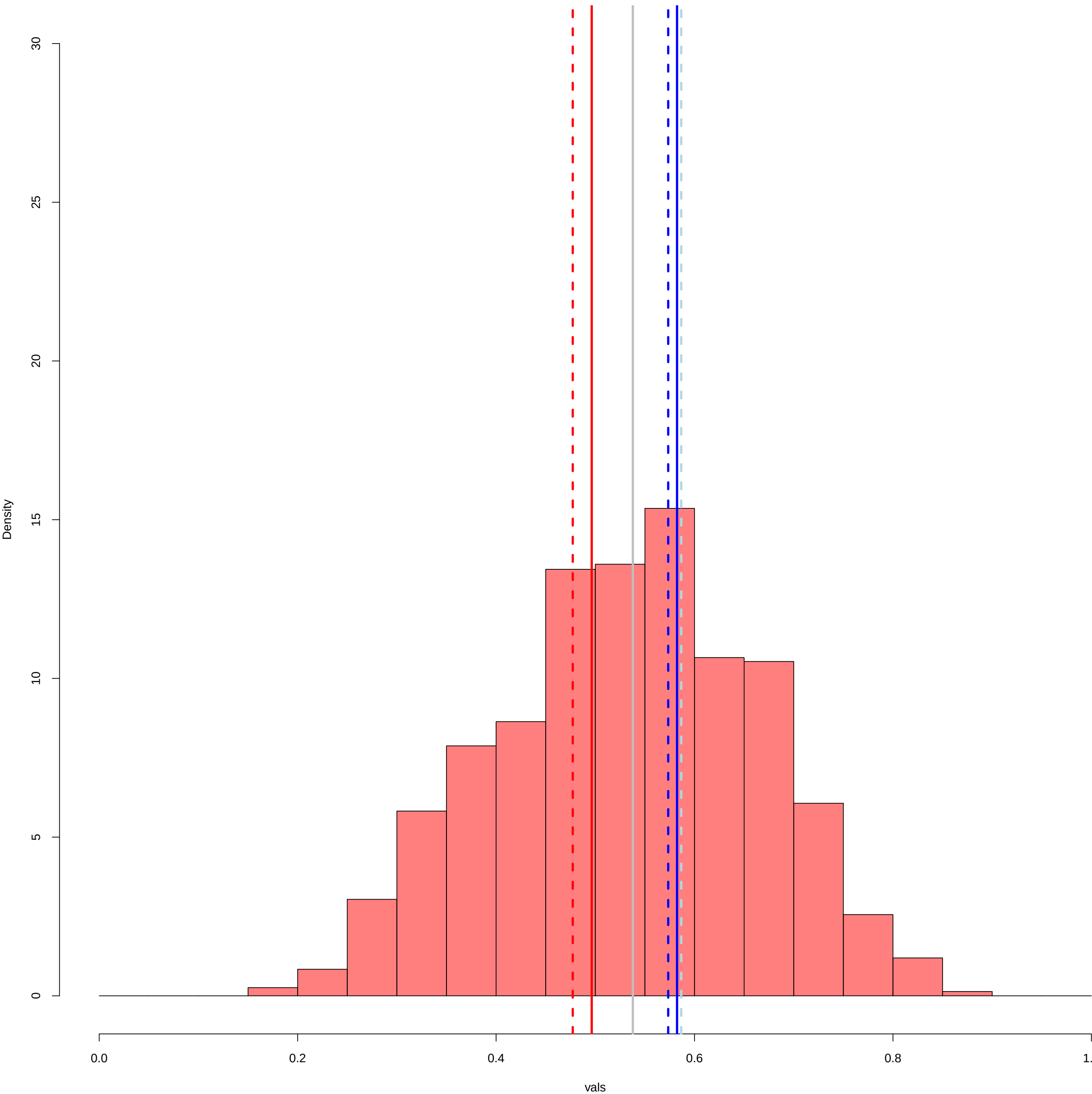
KCNT1: integrated_fitCons_score_rankscore



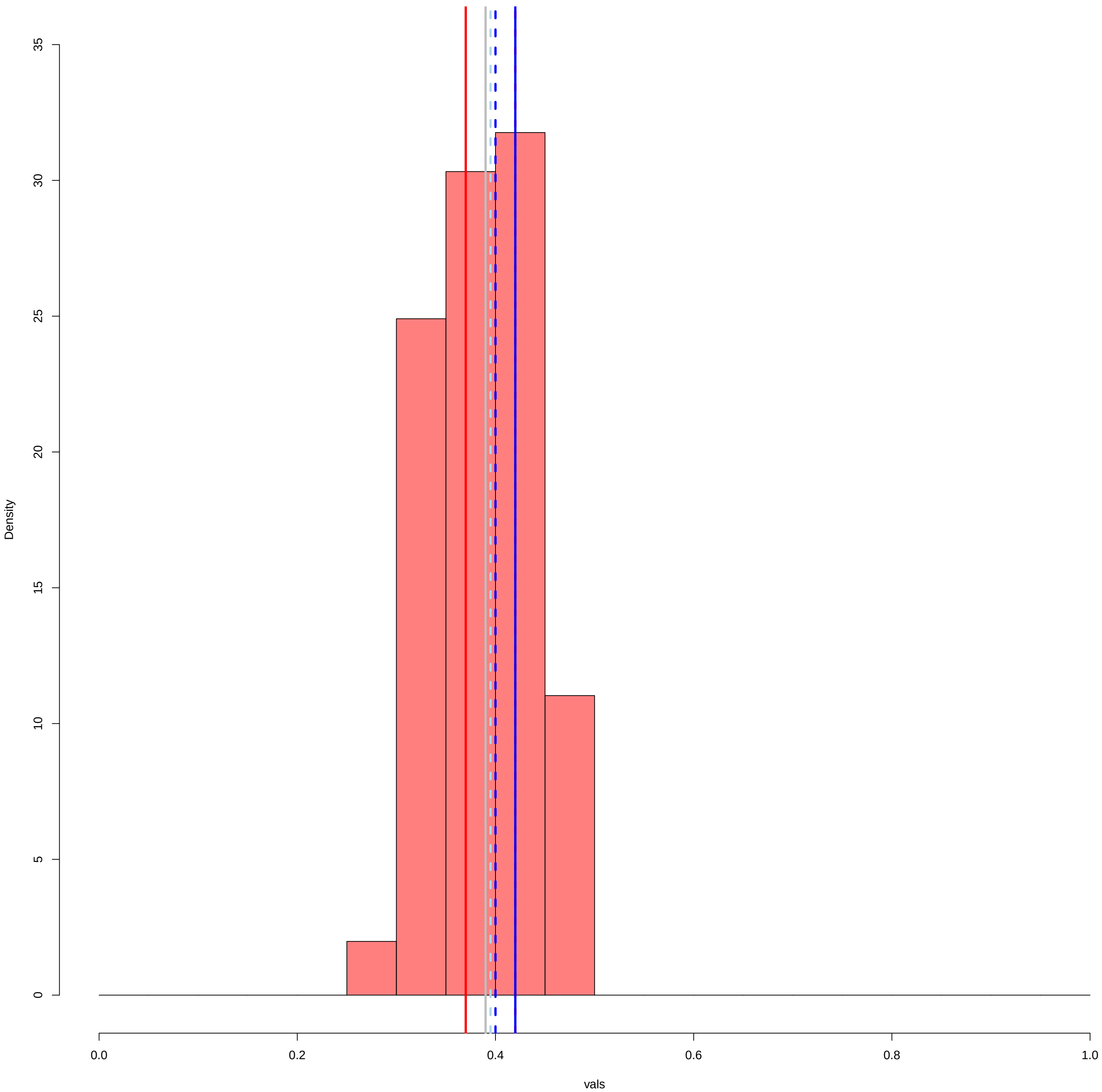
KCNT1: ExAC v1 MTR



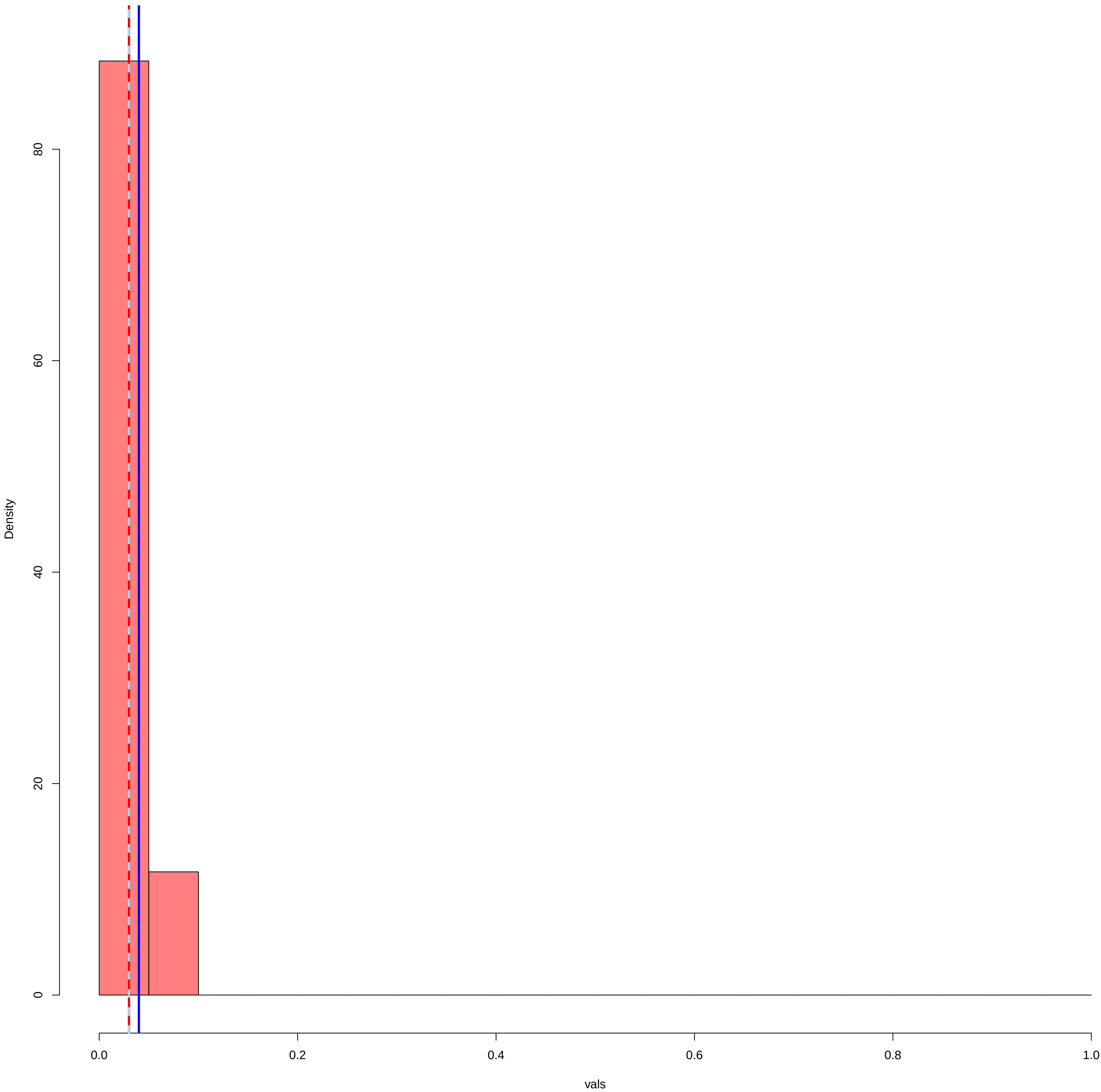
KCNT1: ExAC v2 & gnomAD MTR



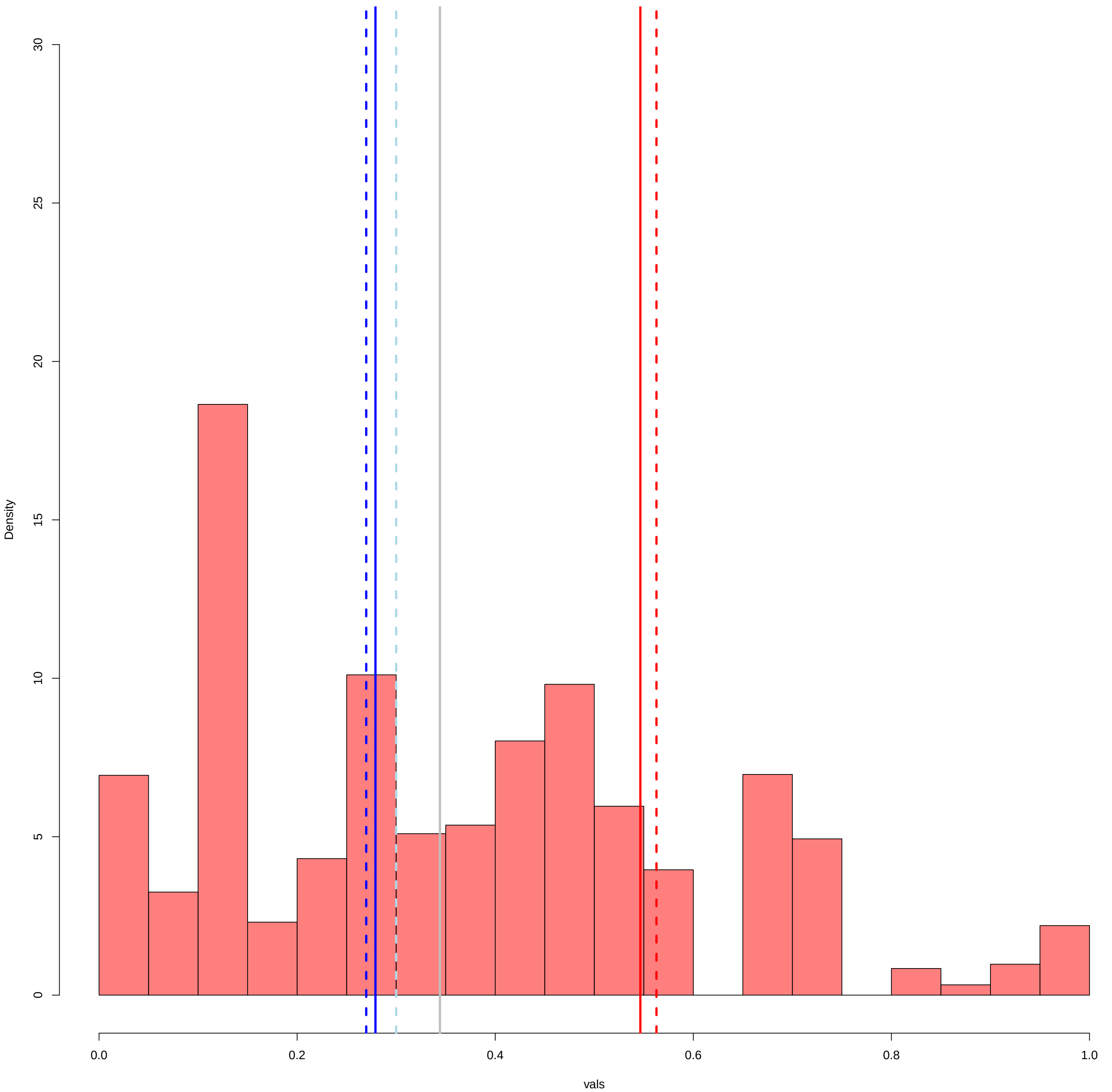
LGI1: GC (Percent GC content in a window of ± 75 bp)



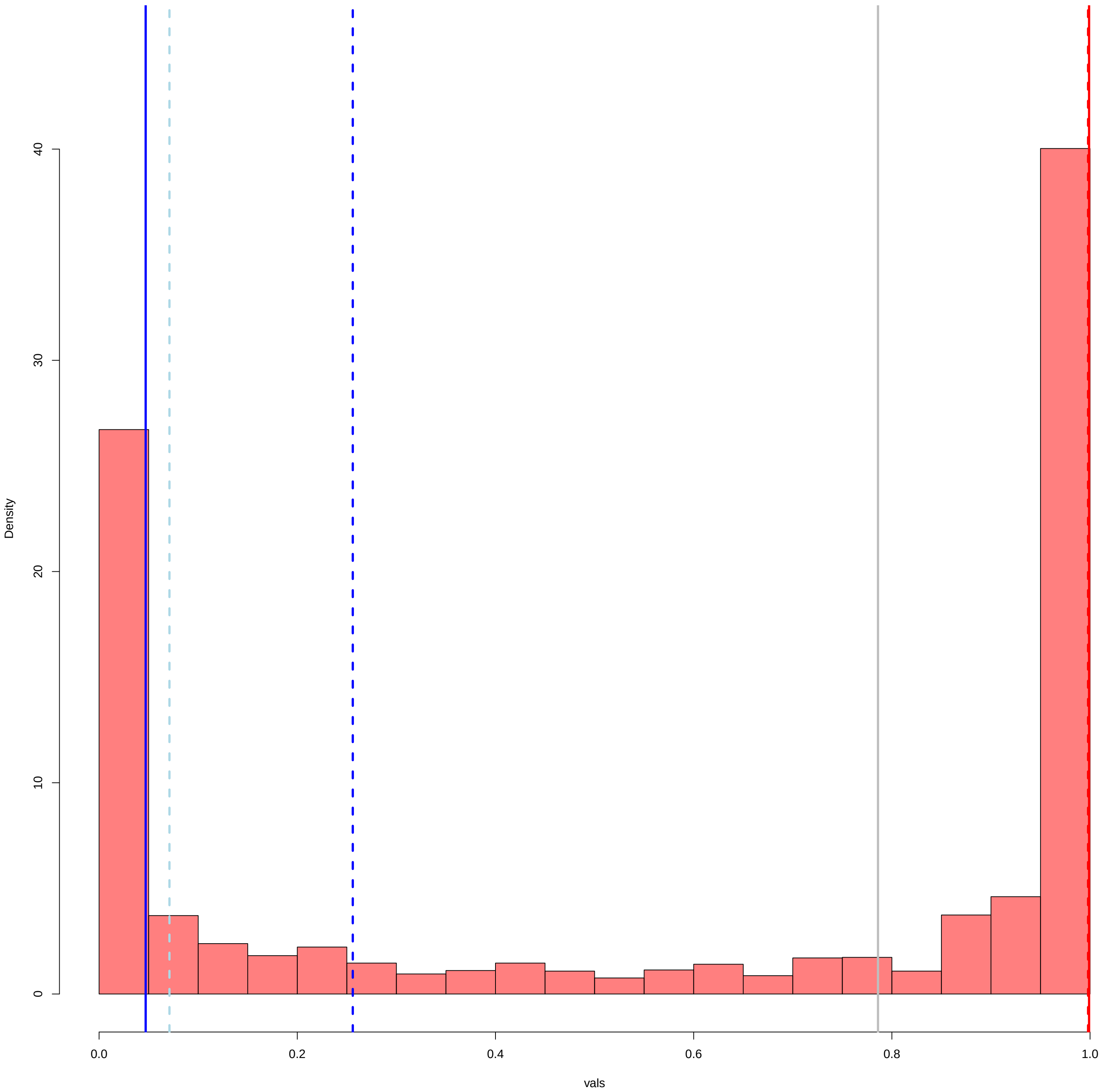
LGI1: CpG (Percent CpG in a window of +/-75bp)



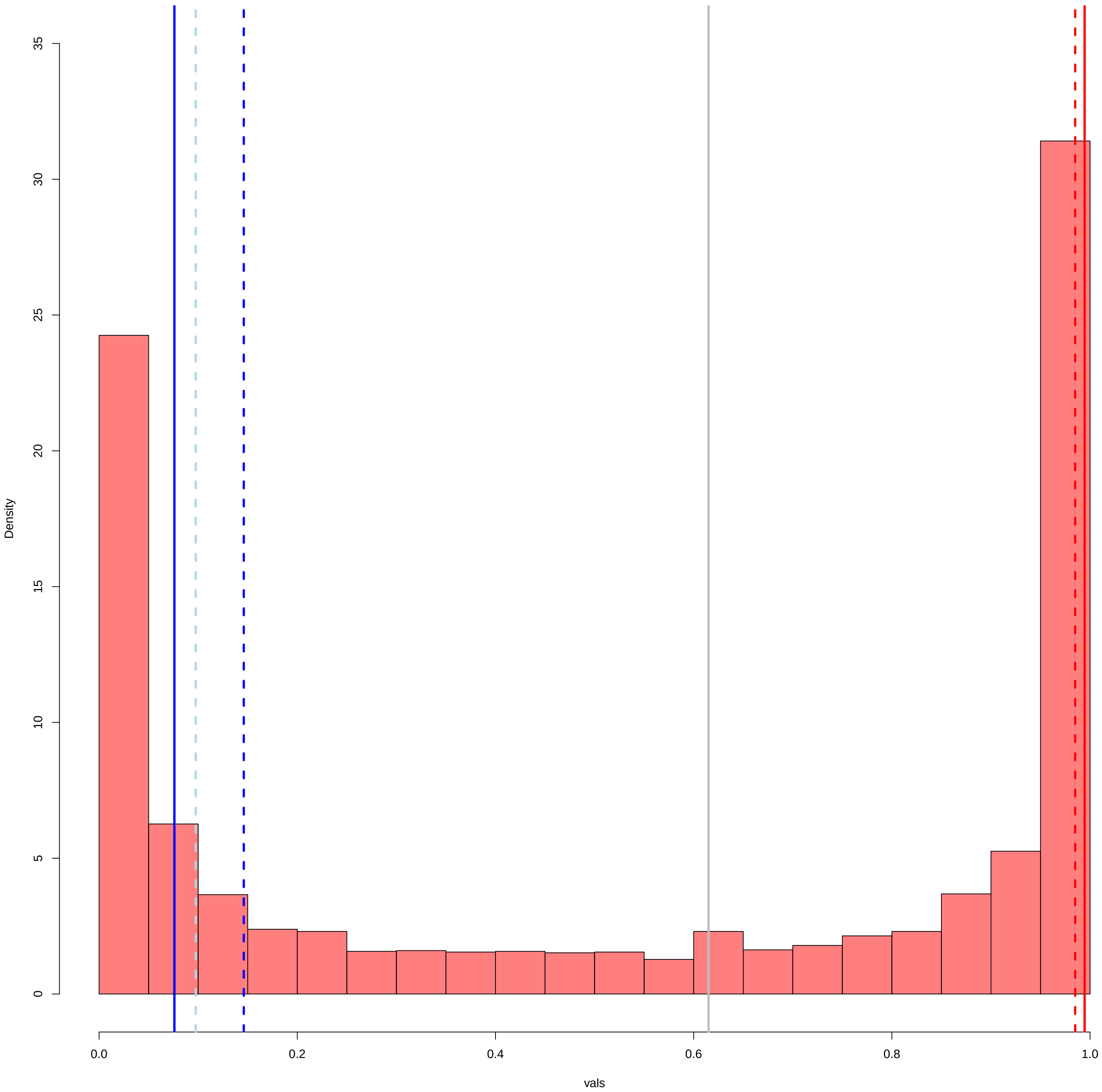
LGI1: Grantham



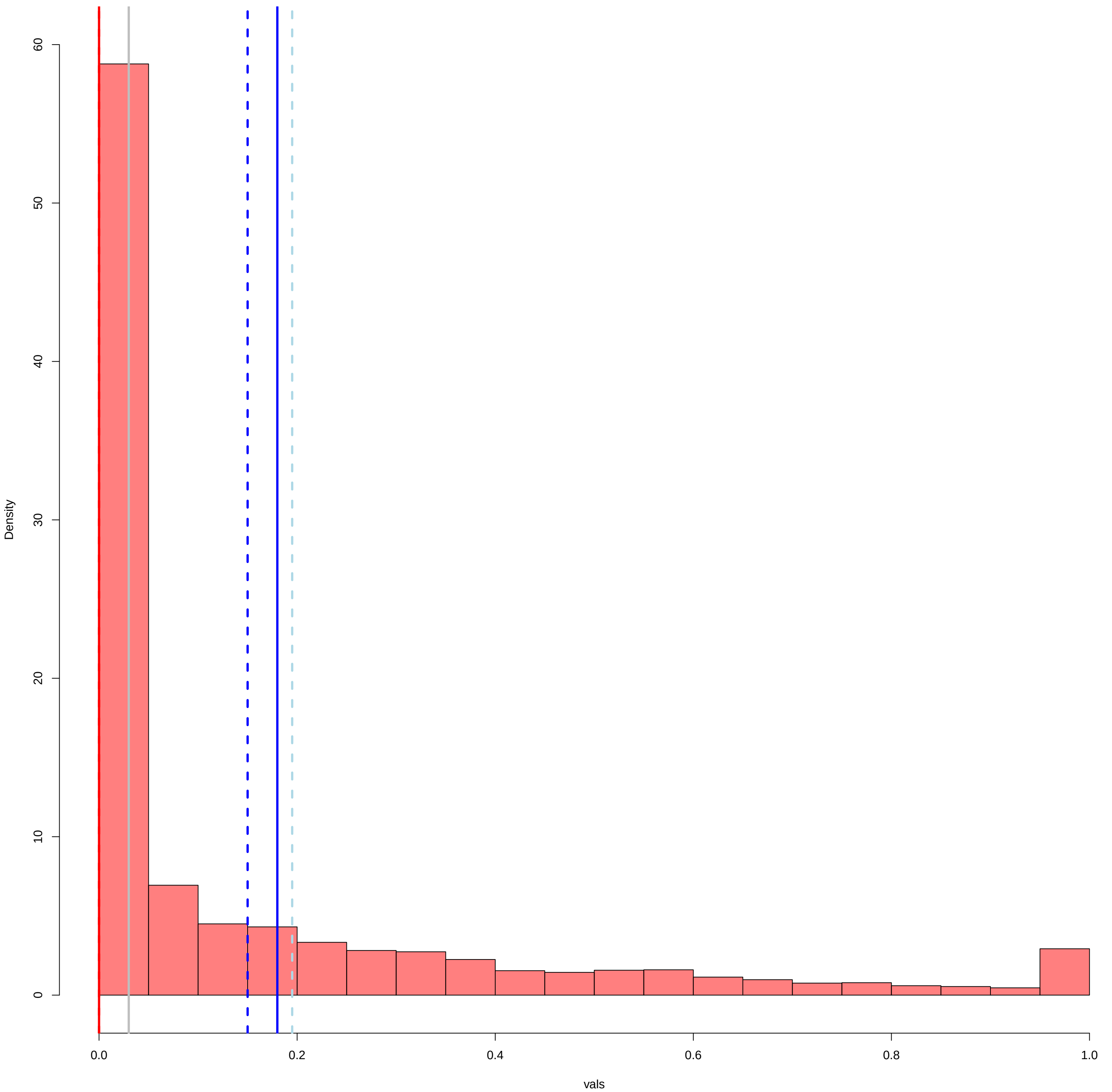
LGI1: Hdiv quan



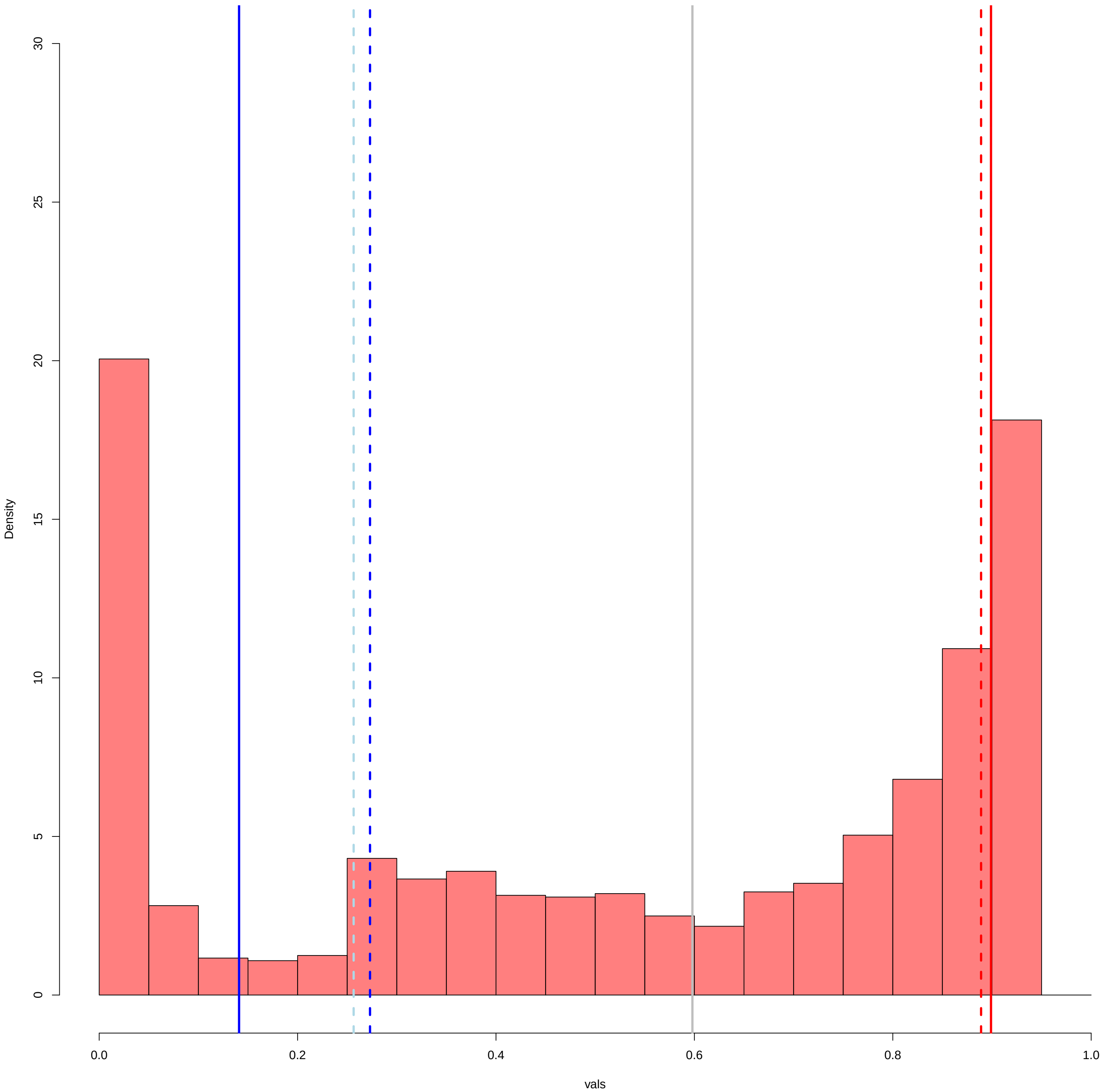
LGI1: Hvar quan



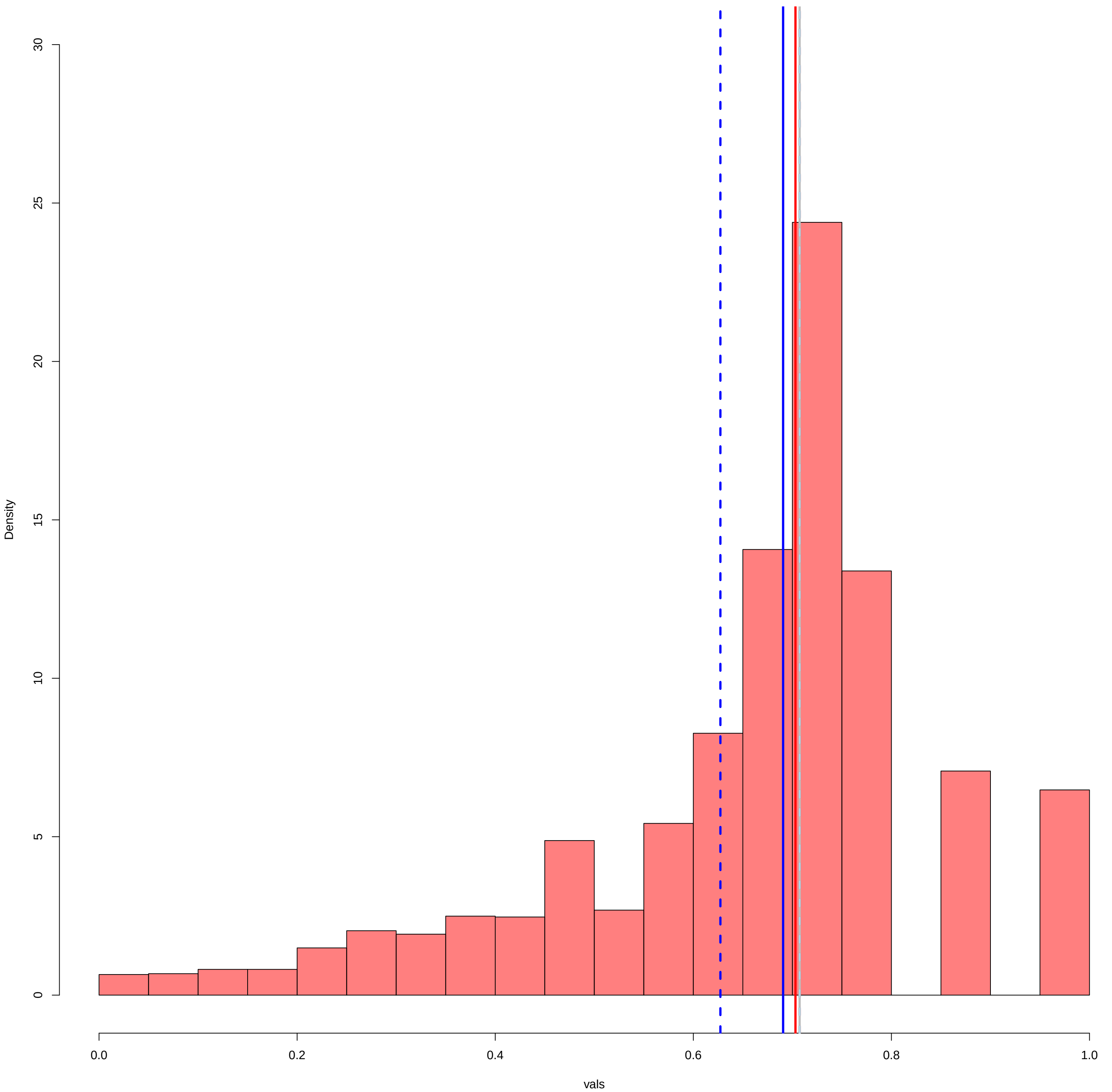
LGI1: SIFT



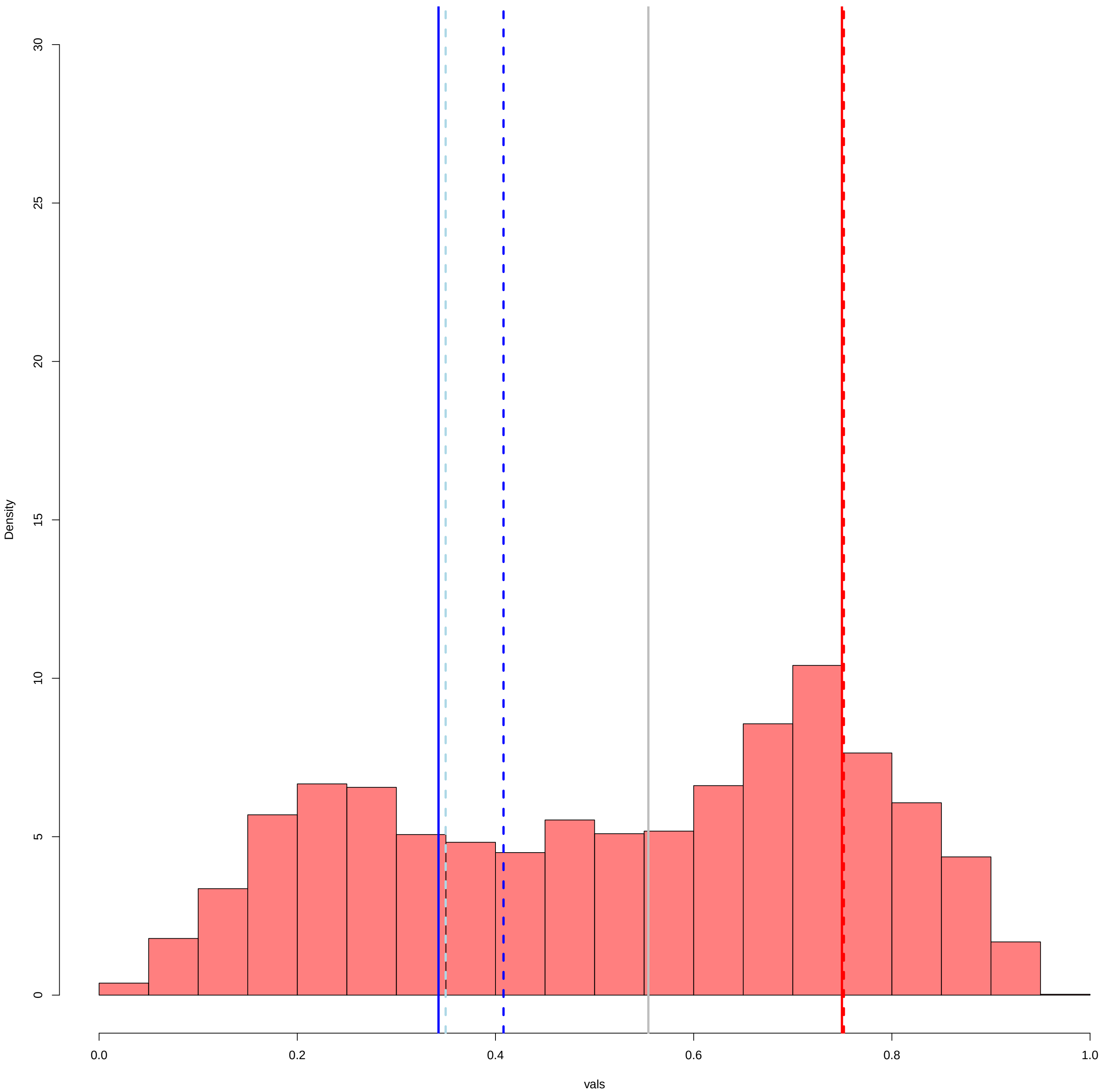
LGI1: Condel



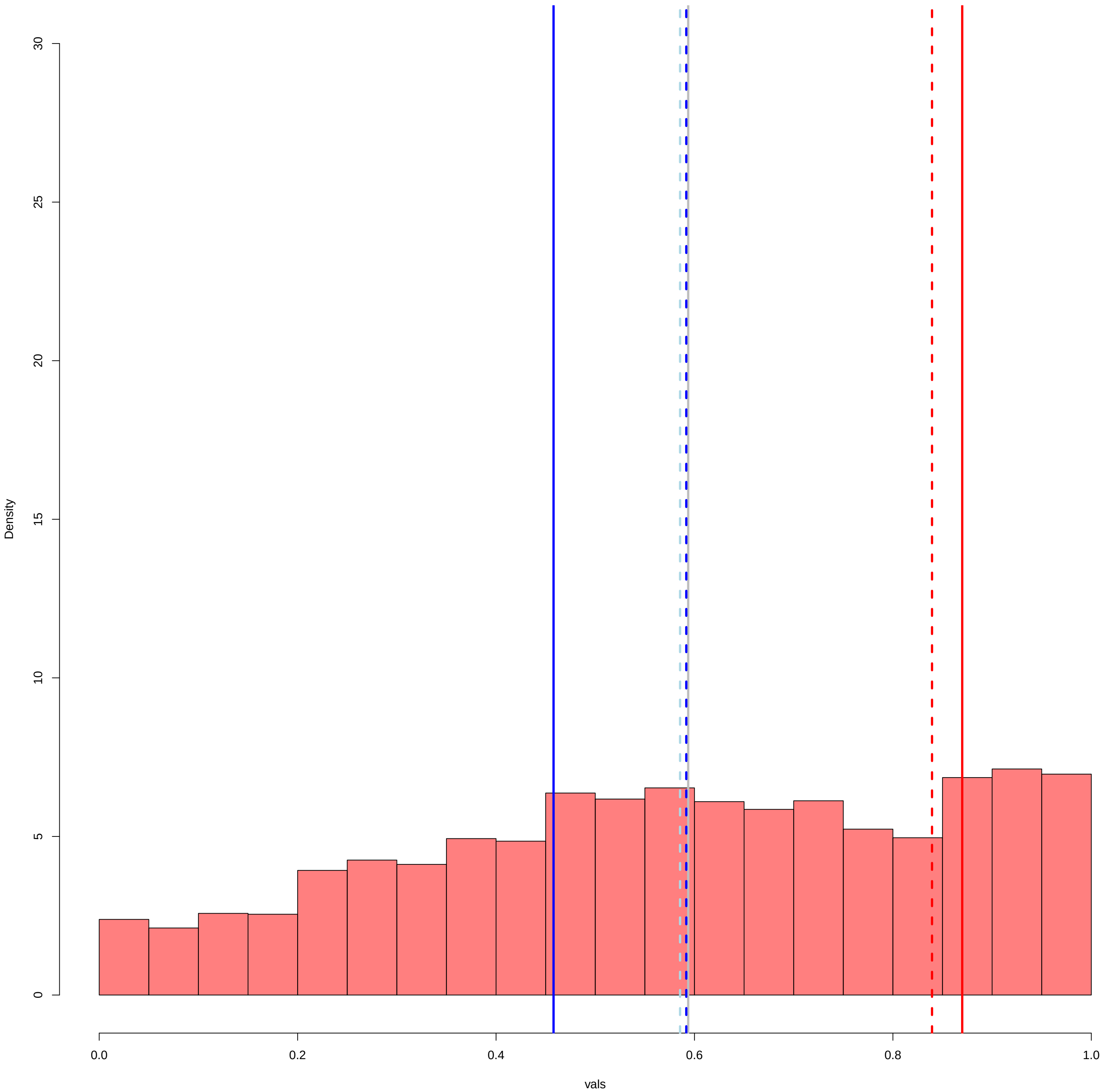
LGI1: GERP++_RS_rankscore



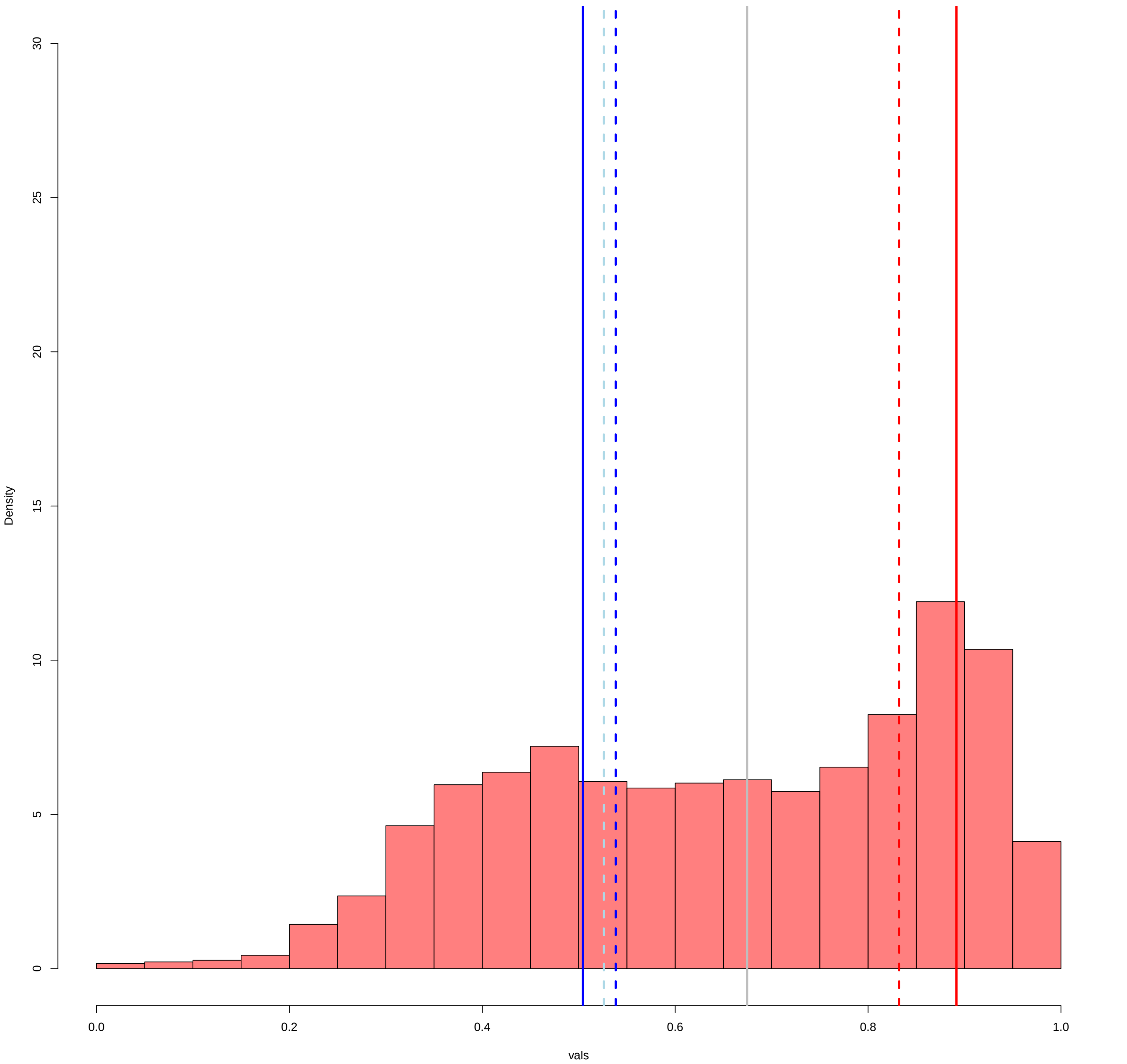
LG11: CADD_raw_rankscore



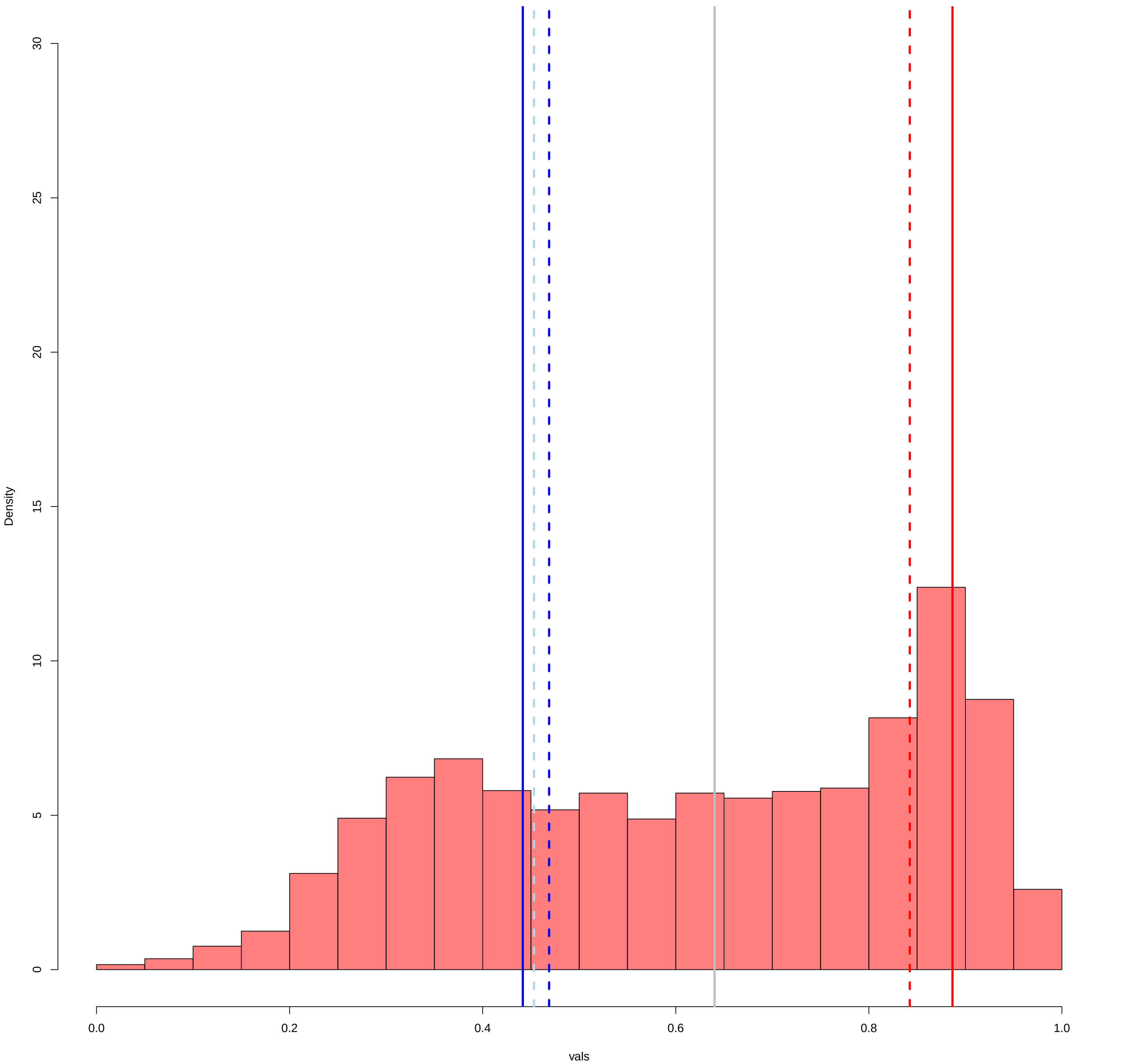
LGI1: DANN_rankscore



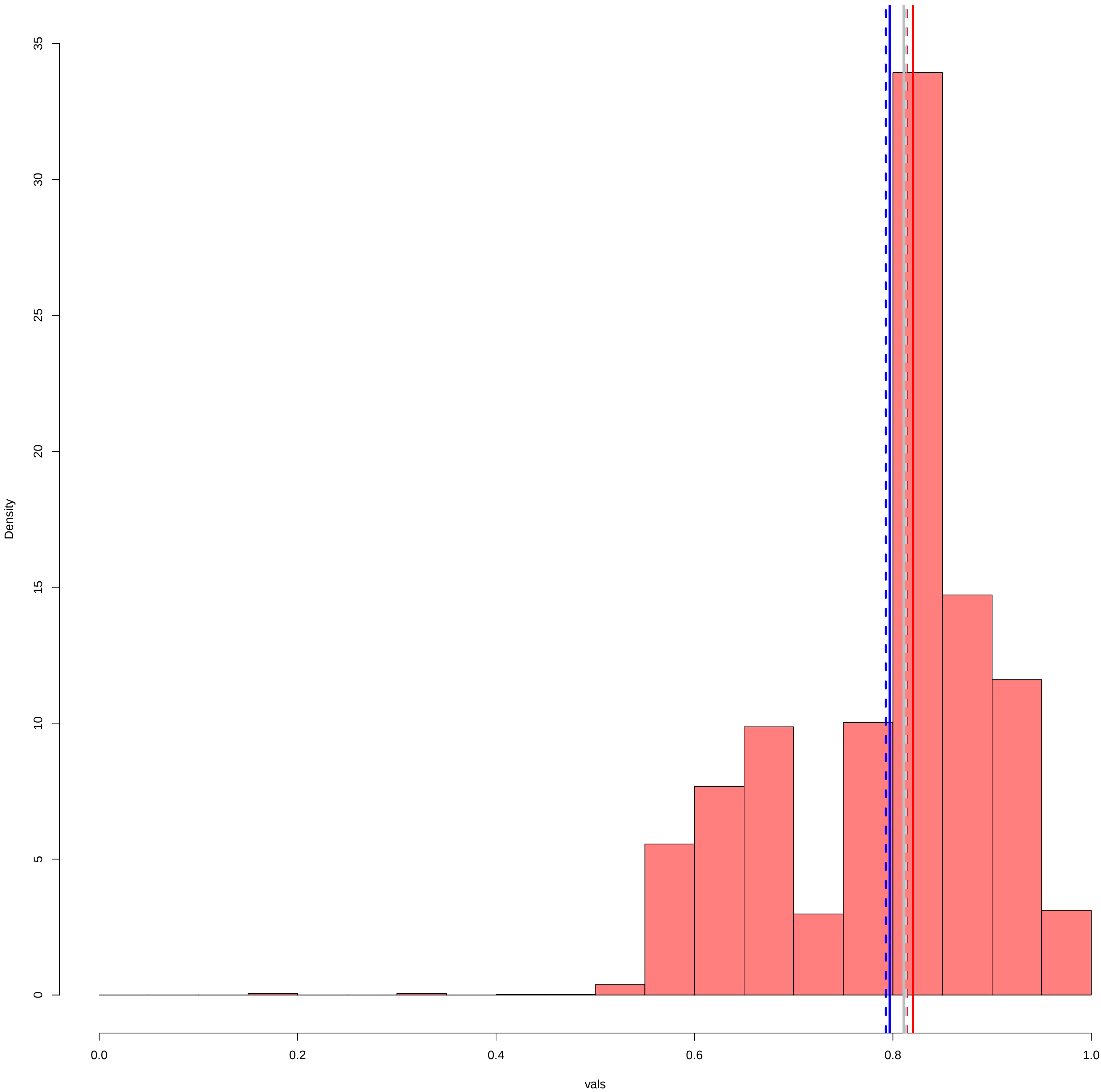
LGI1: Eigen-PC-raw_rankscore



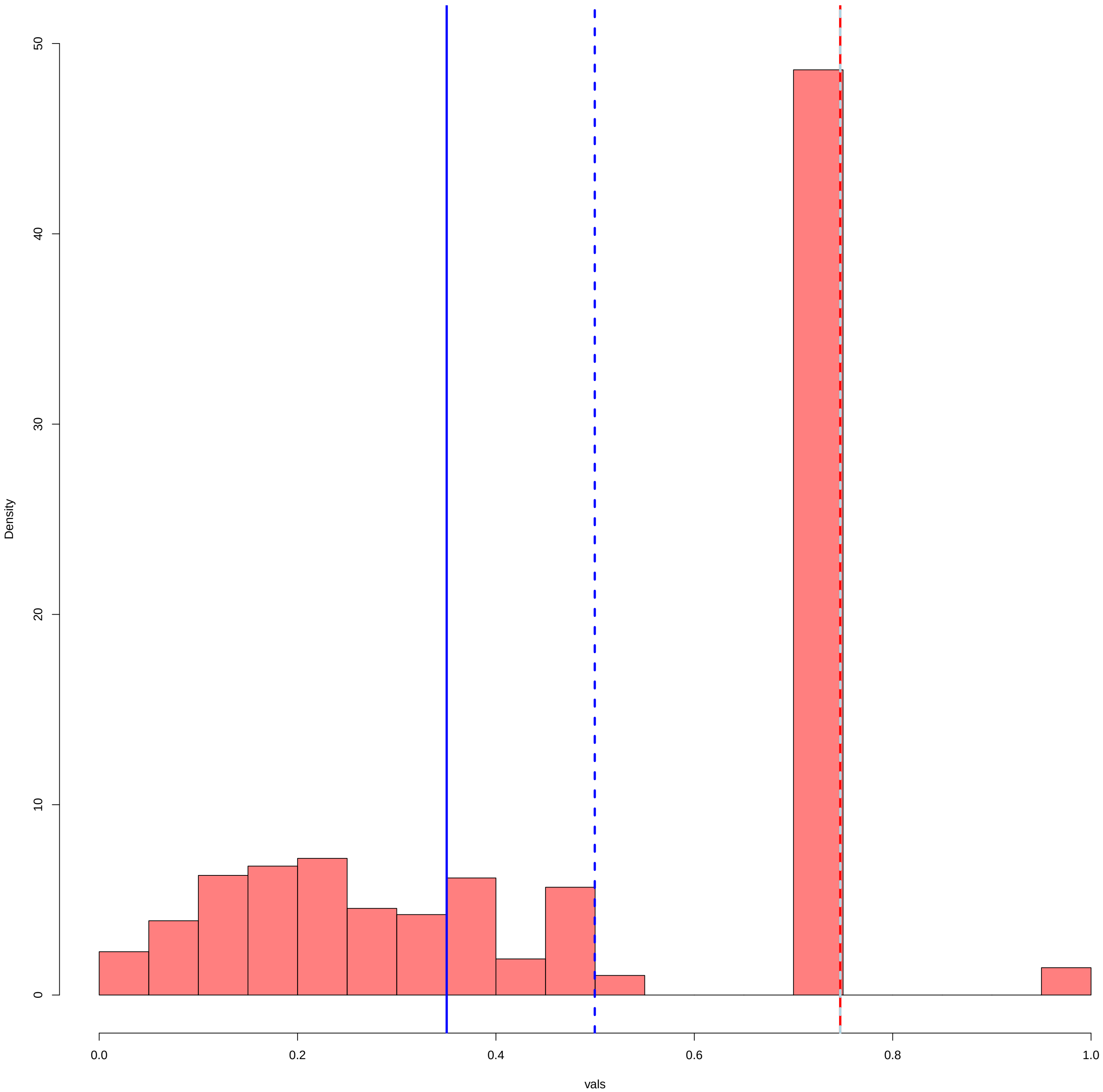
LGI1: Eigen-row_rankscore



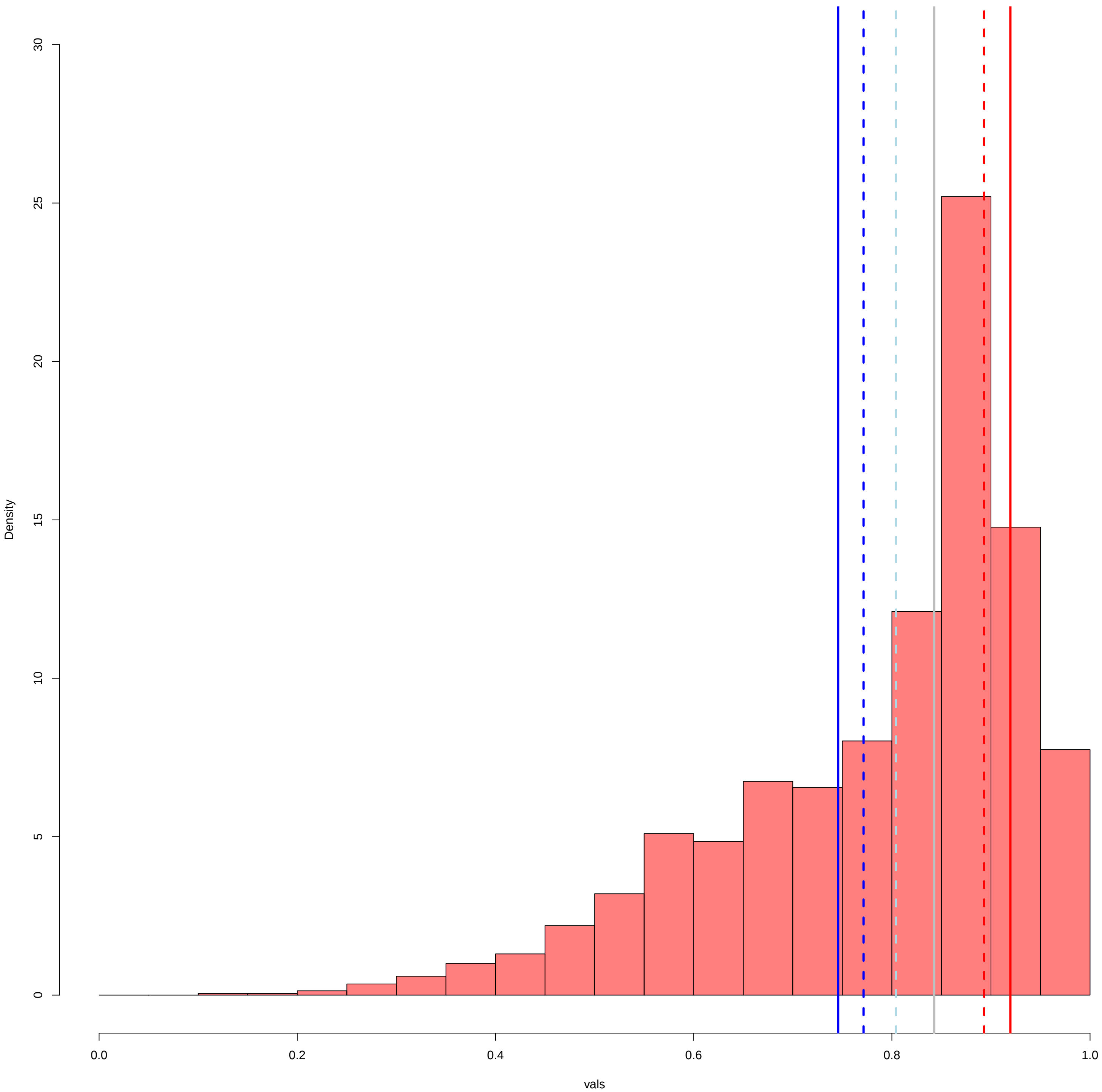
LGI1: FATHMM_converted_rankscore



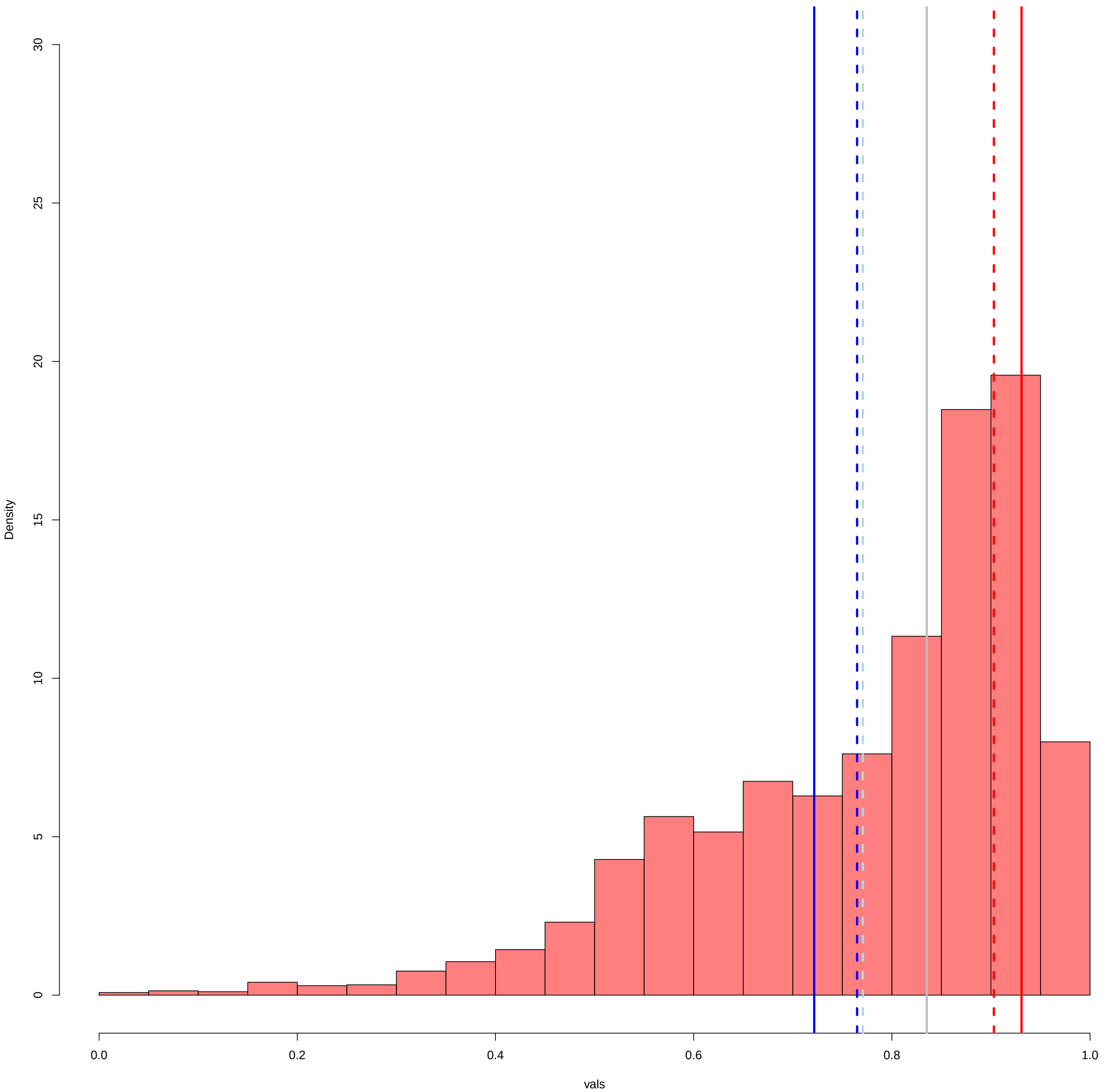
LGI1: GenoCanyon_score_rankscore



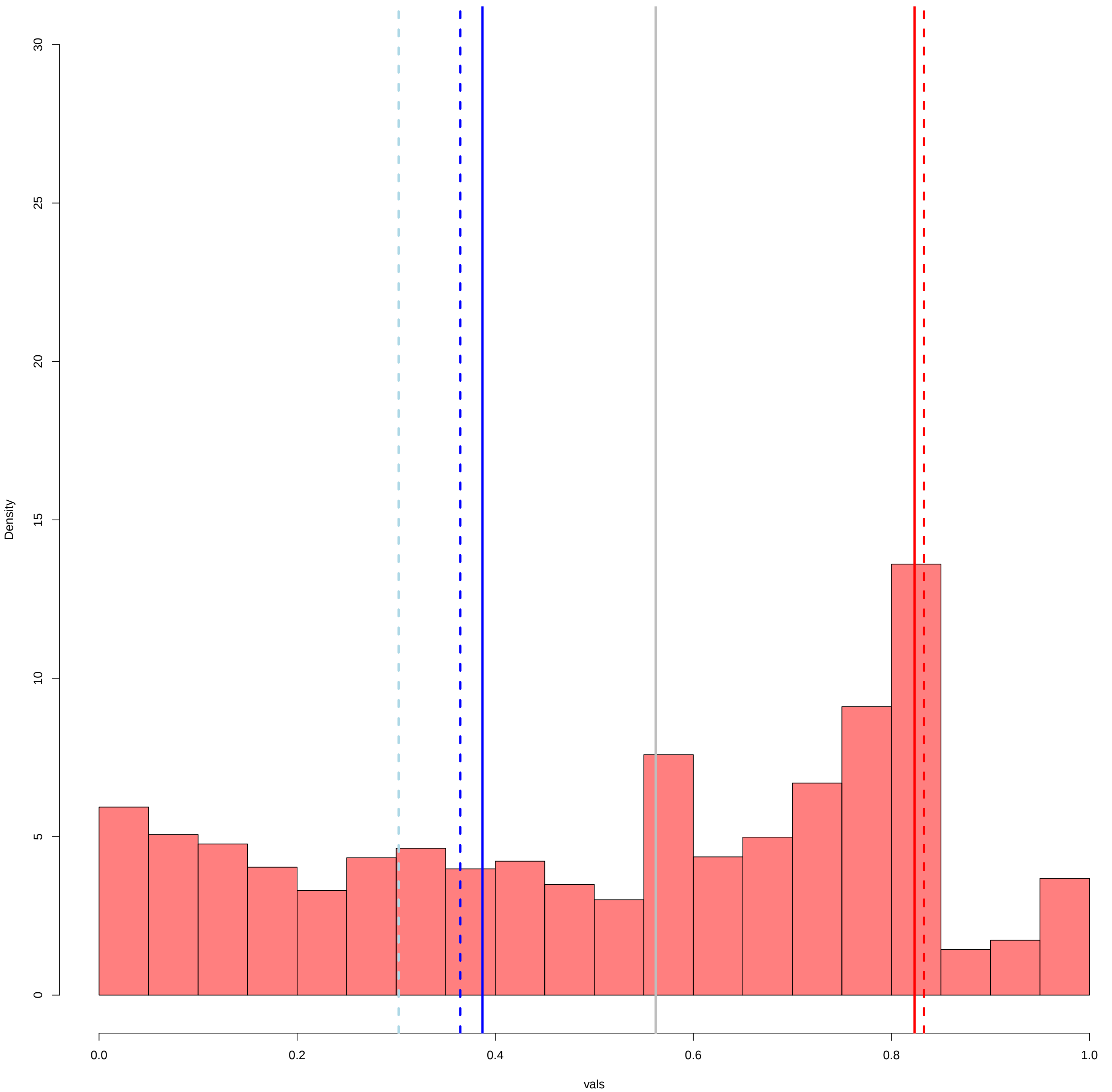
LGI1: MetaLR_rankscore



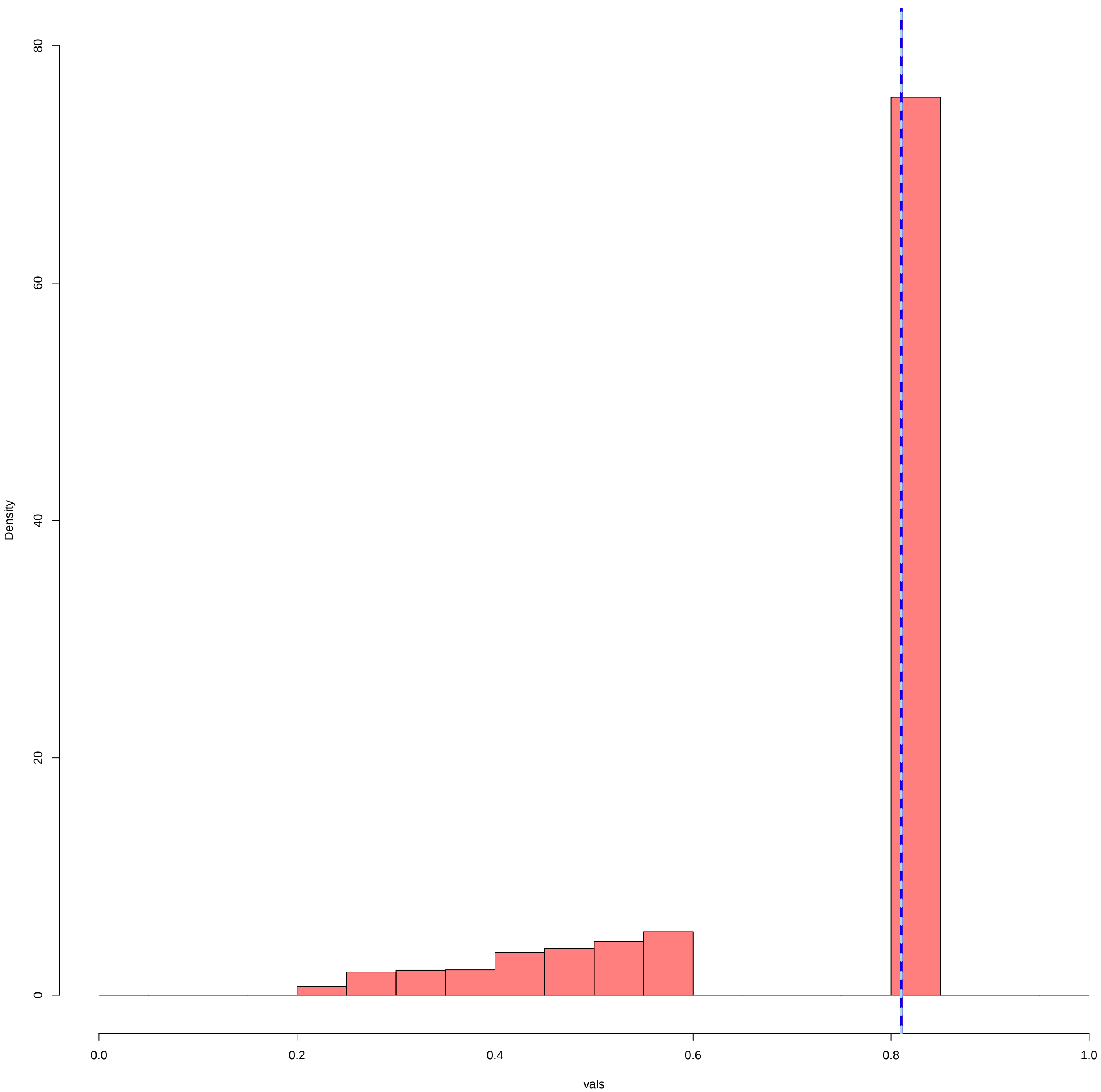
LGI1: MetaSVM_rankscore



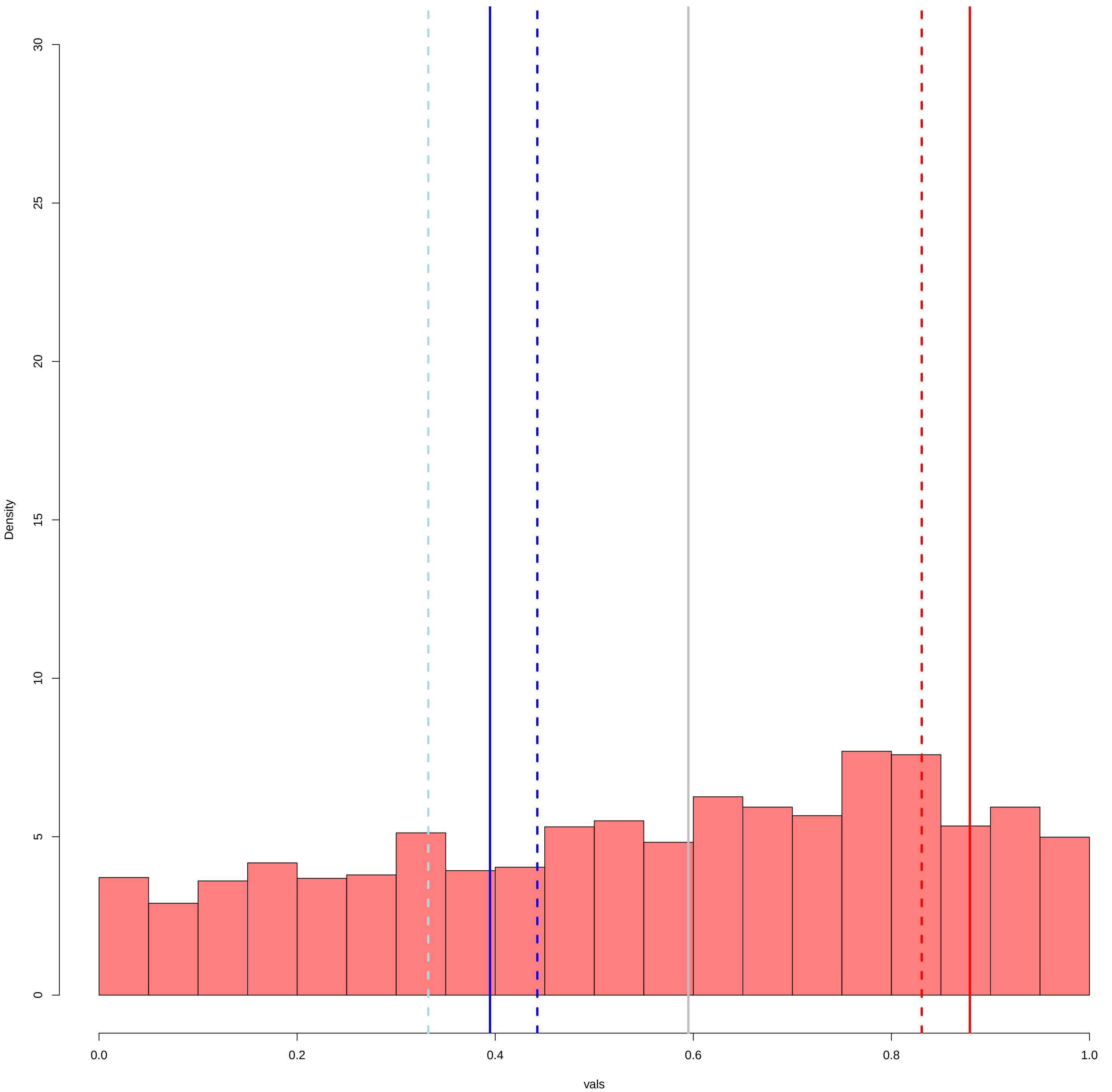
LGI1: MutationAssessor_score_rankscore



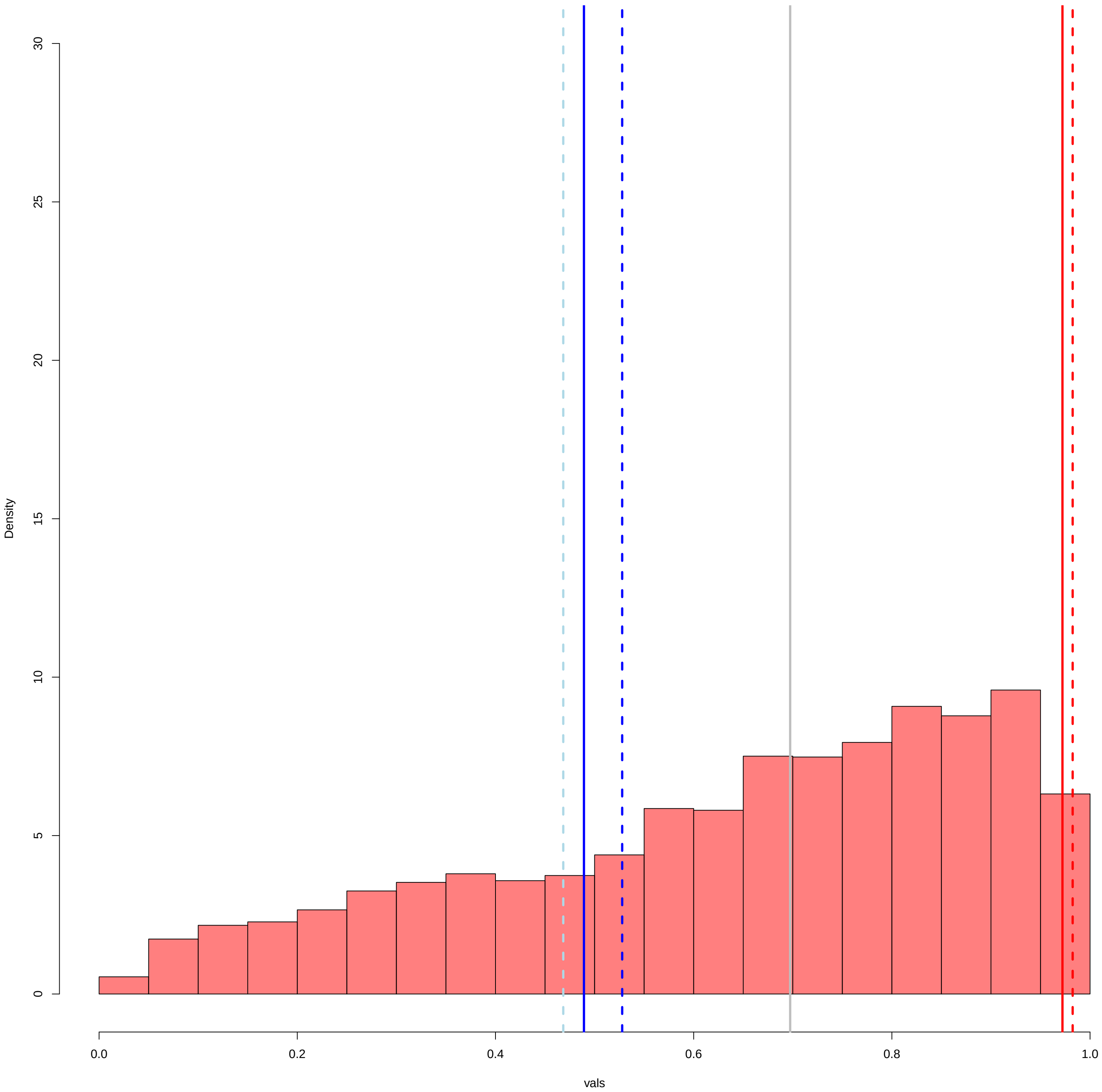
LGI1: MutationTaster_converted_rankscore



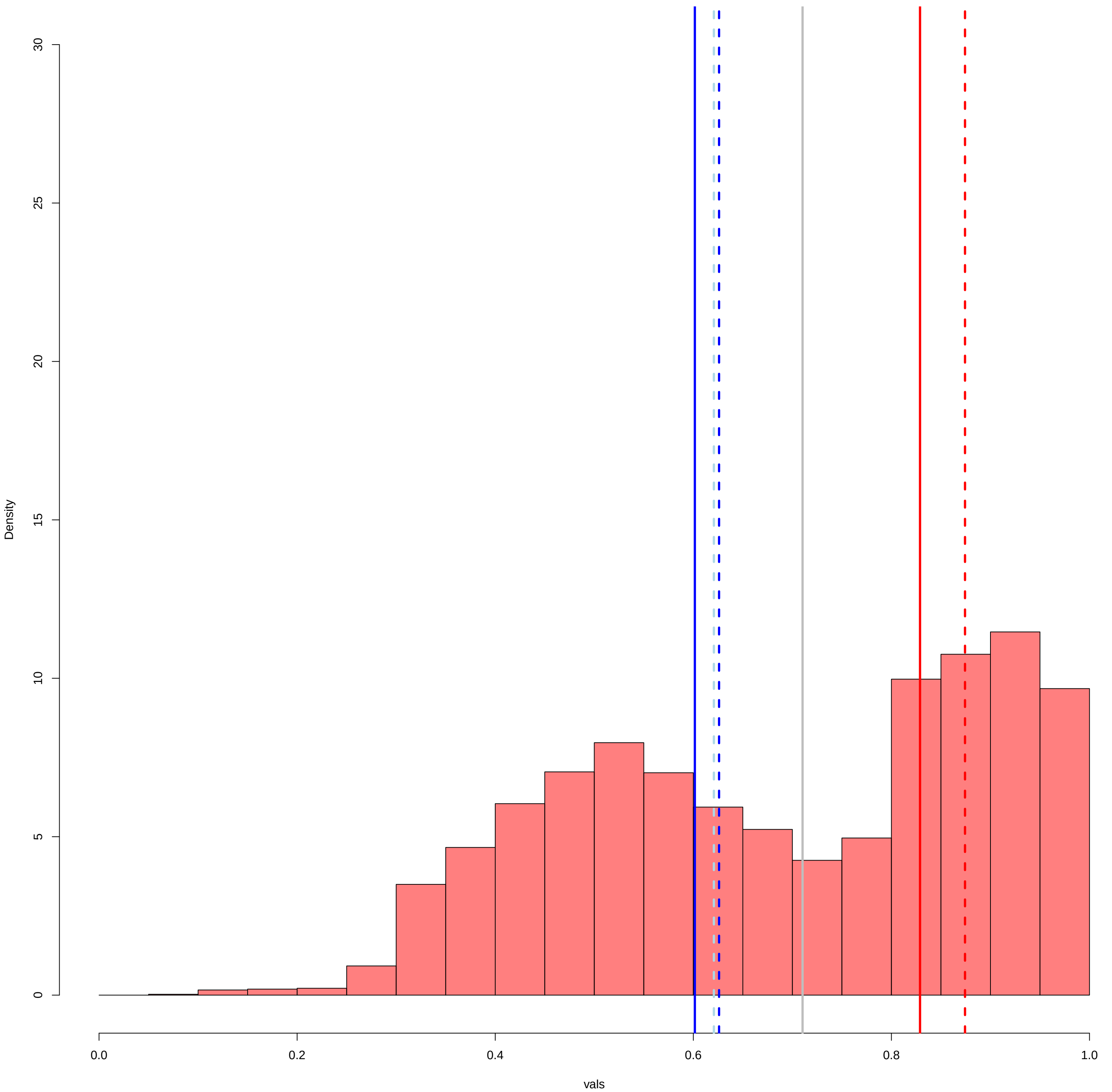
LGI1: PROVEAN_converted_rankscore



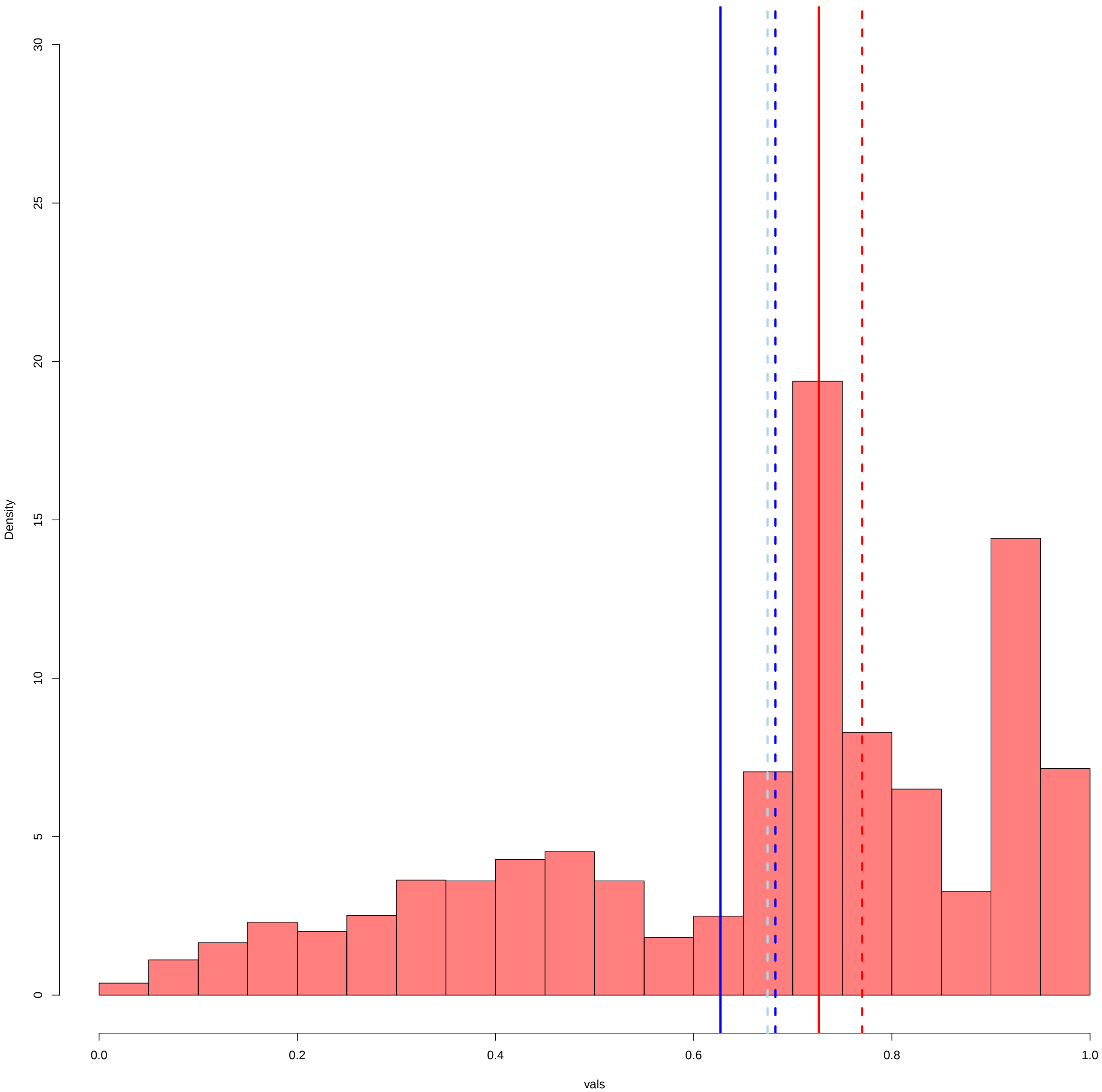
LGI1: VEST3_rankscore



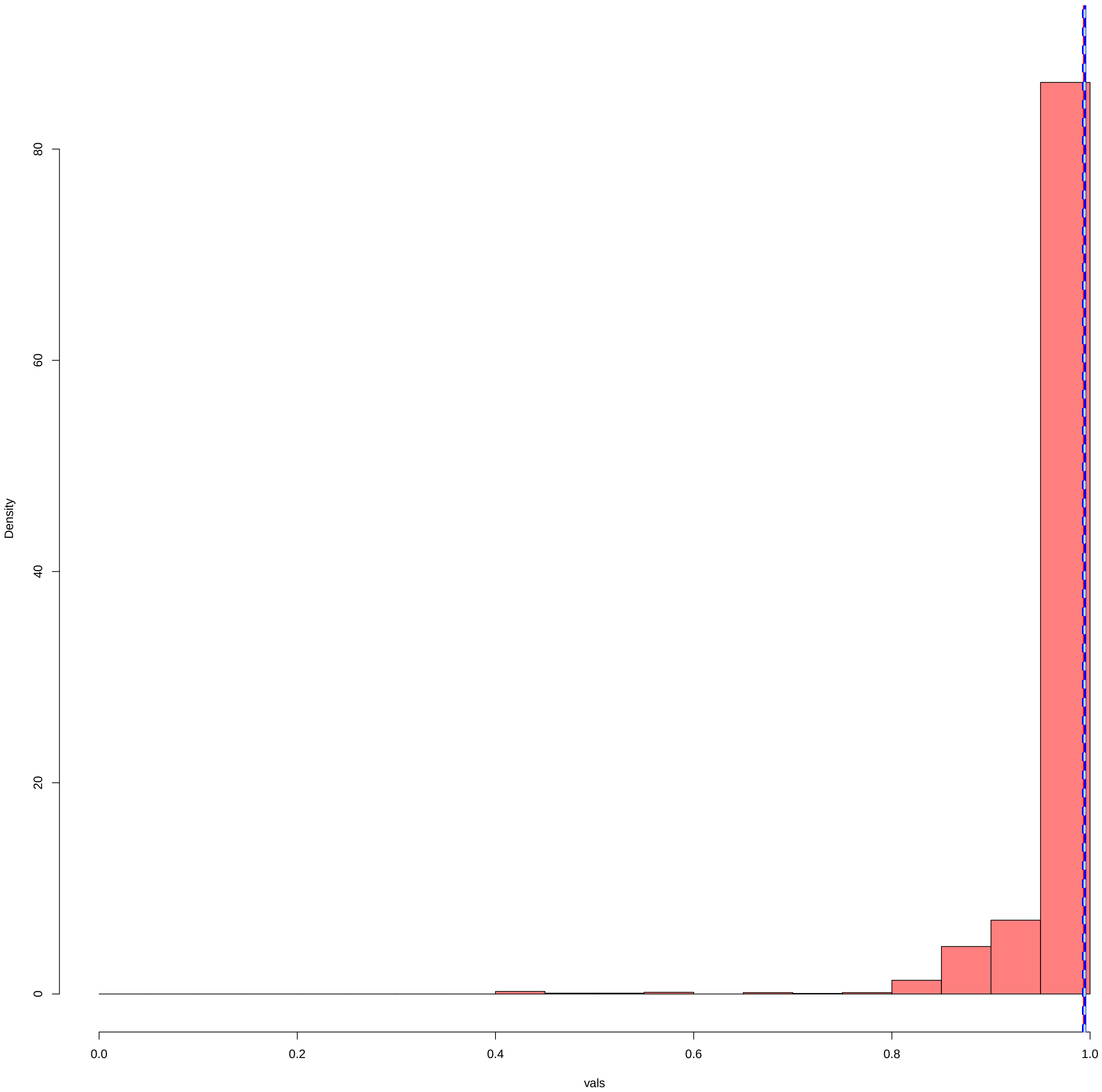
LGI1: fathmm-MKL_coding_rankscore



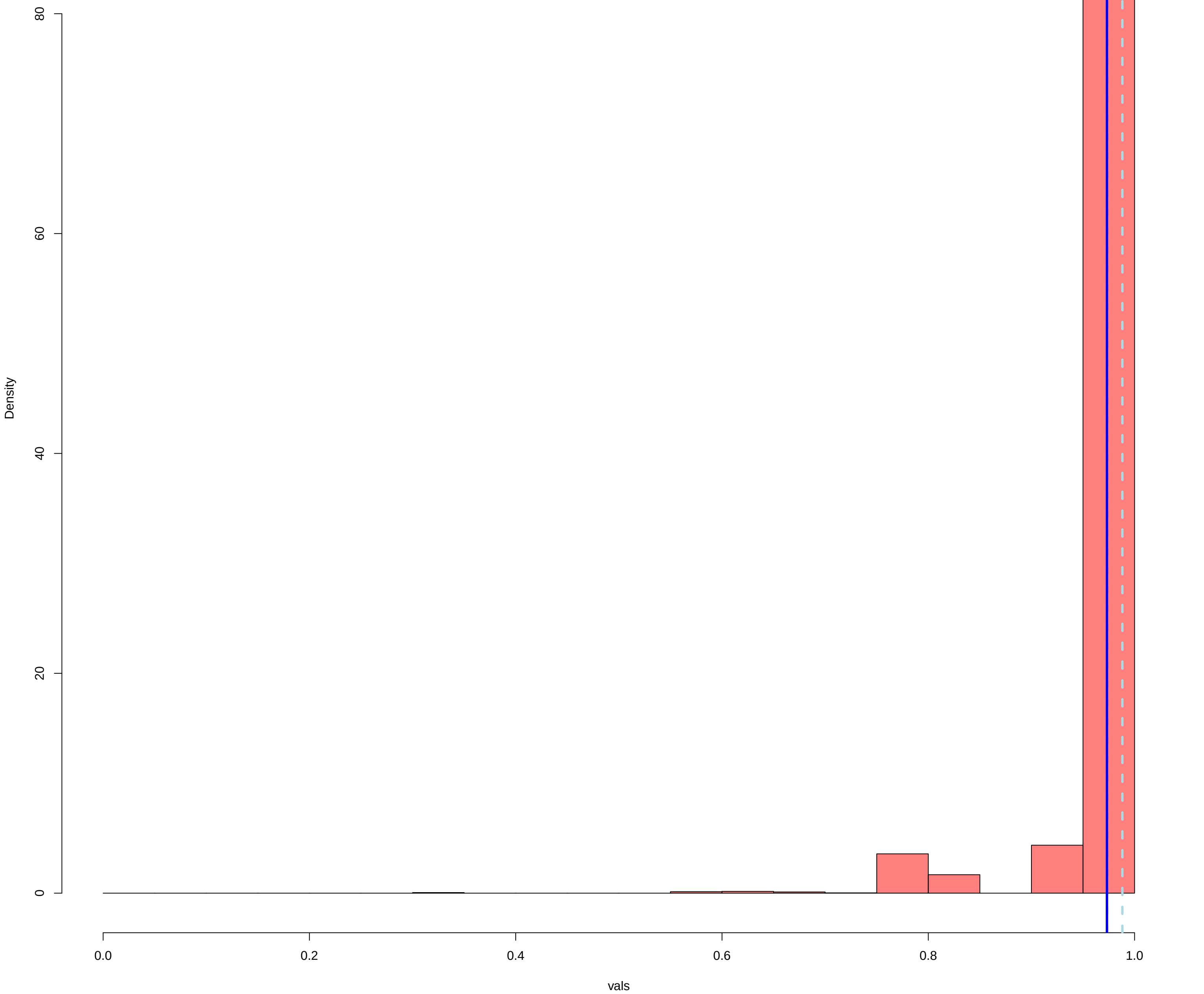
LGI1: SiPhy_29way_logOdds_rankscore



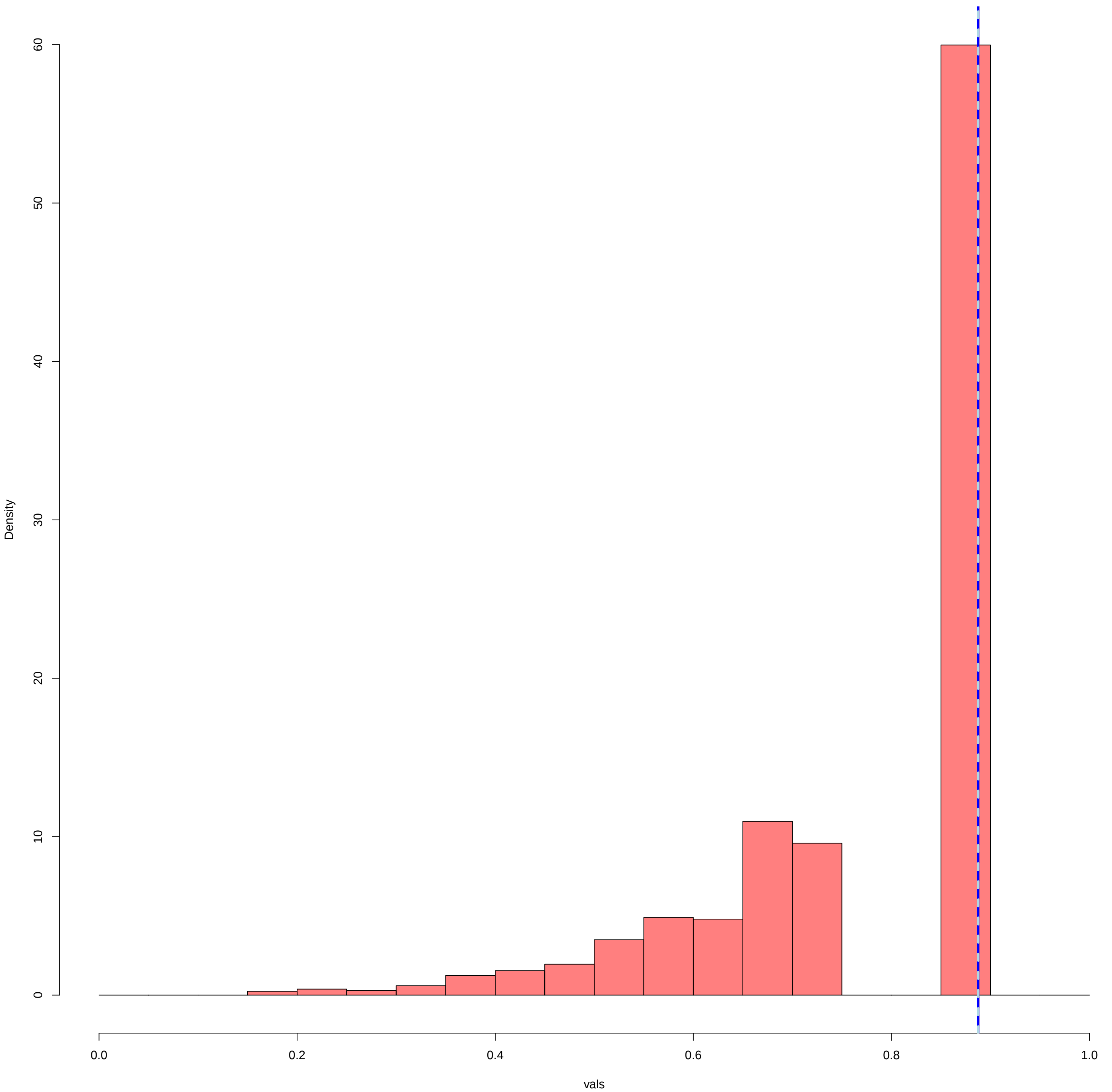
LGI1: priPhCons



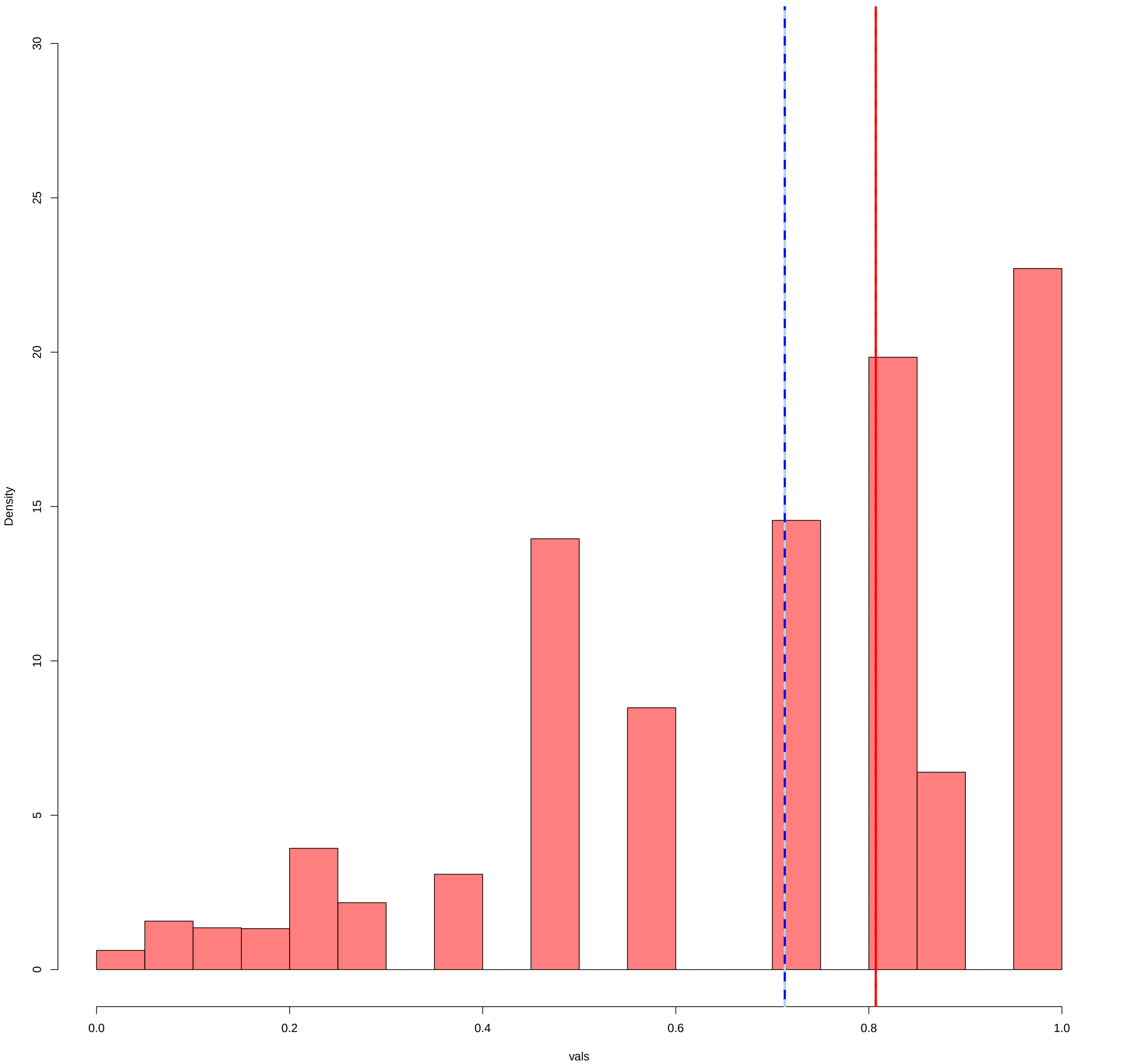
LGI1: priPhyloP



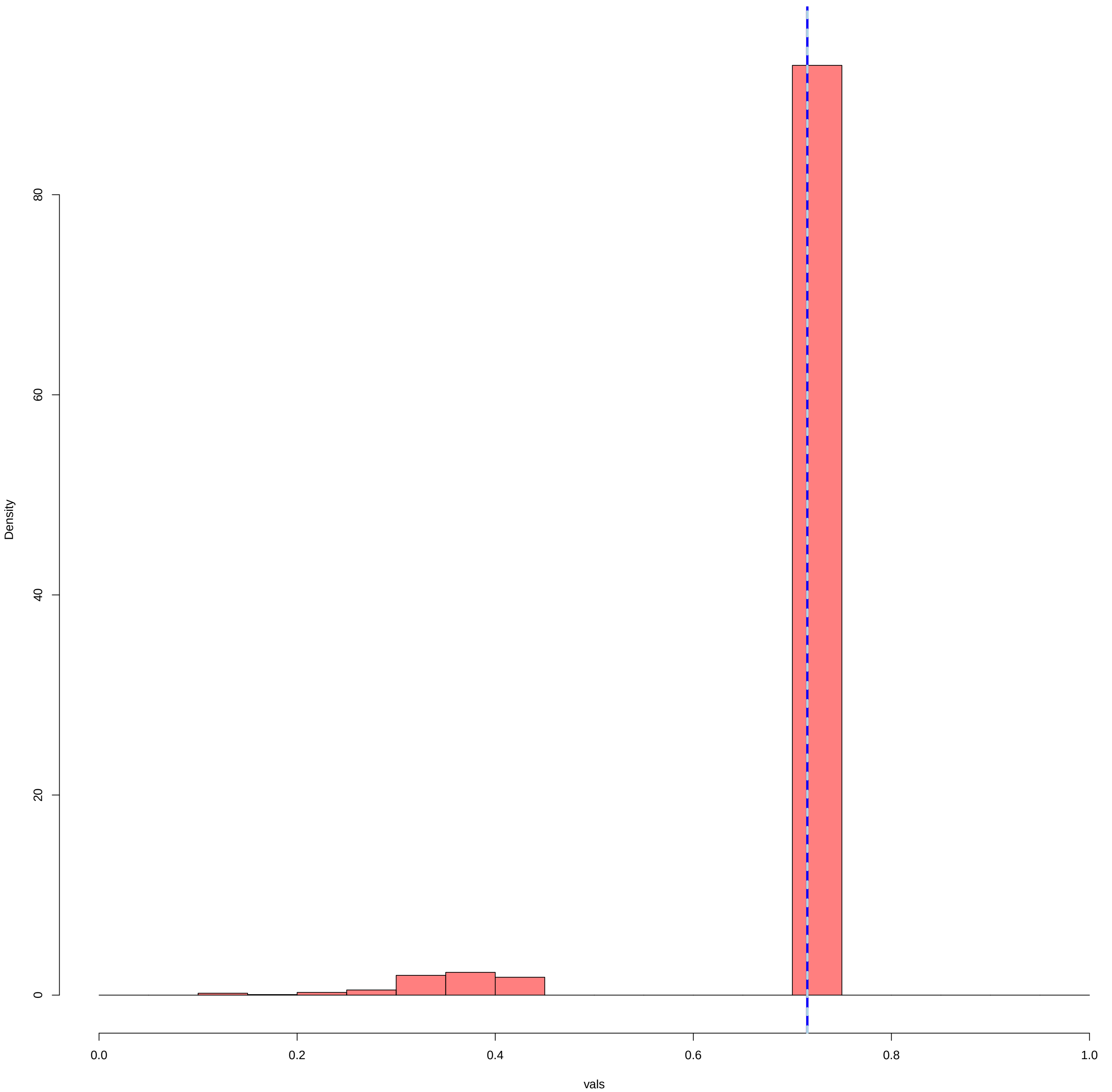
LGI1: phastCons20way_mammalian_rankscore



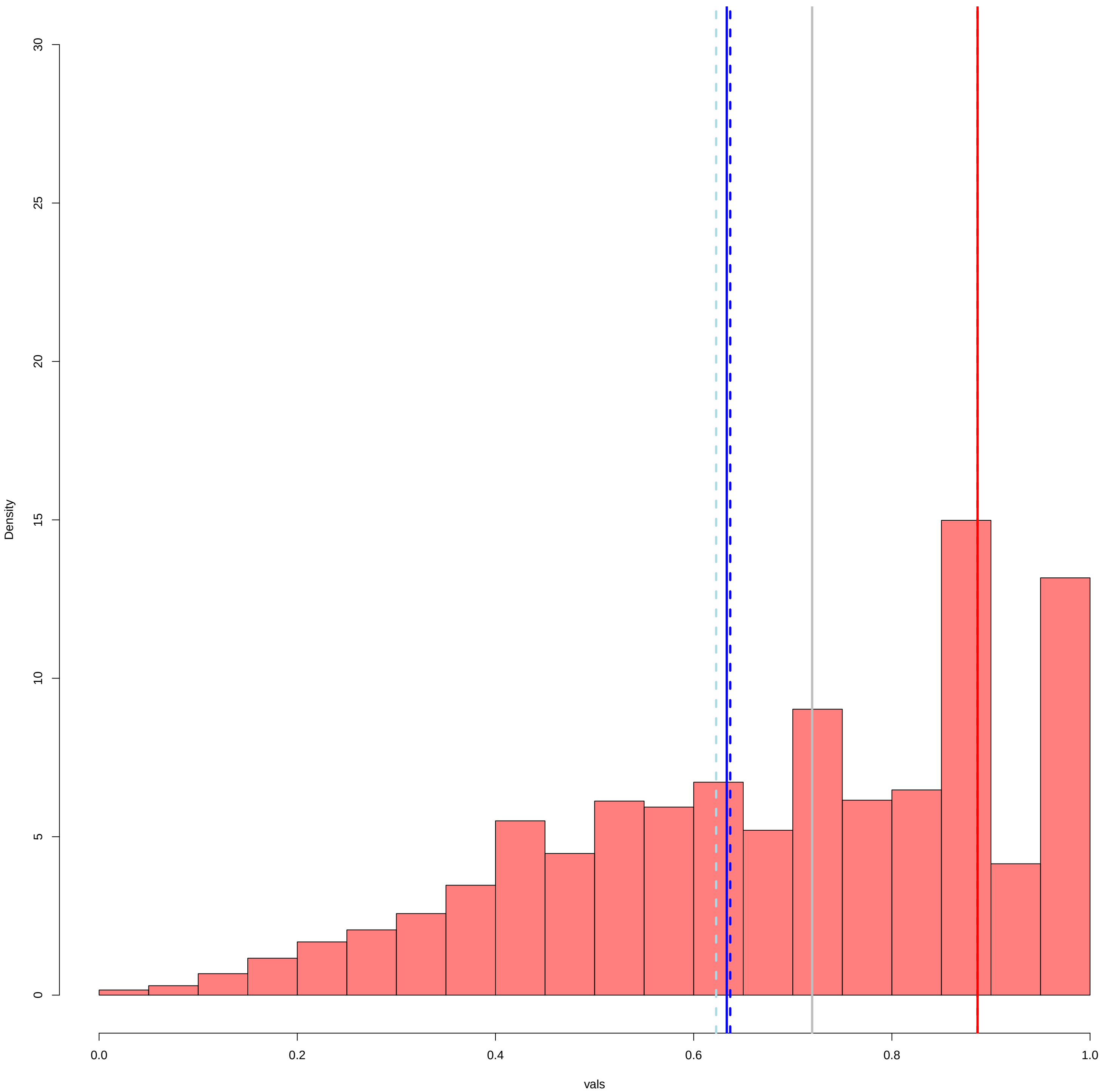
LGI1: phyloP20way_mammalian_rankscore



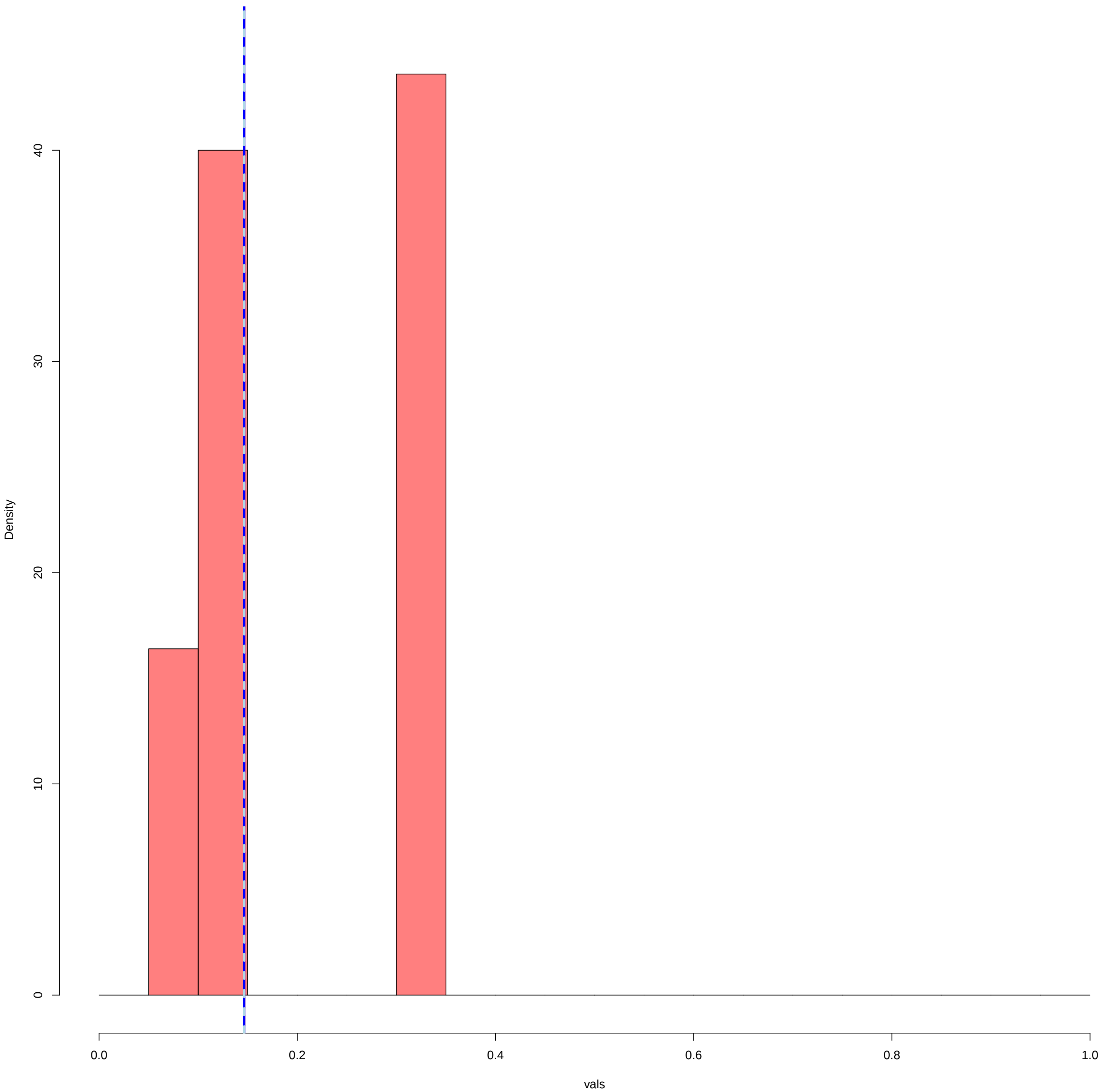
LGI1: phastCons100way Vertebrate RankScore



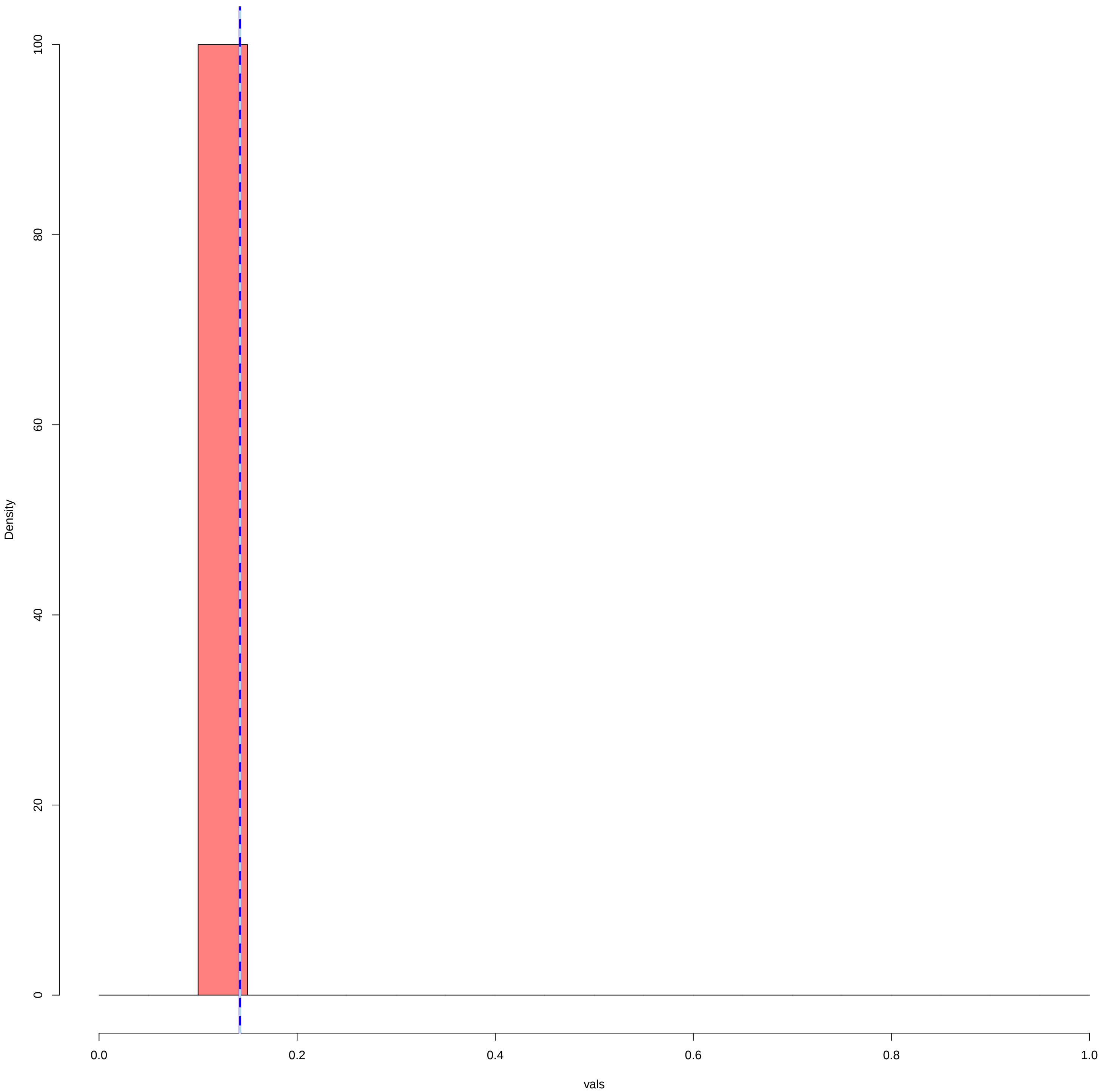
LGI1: phyloP100way_vertebrate_rankscore



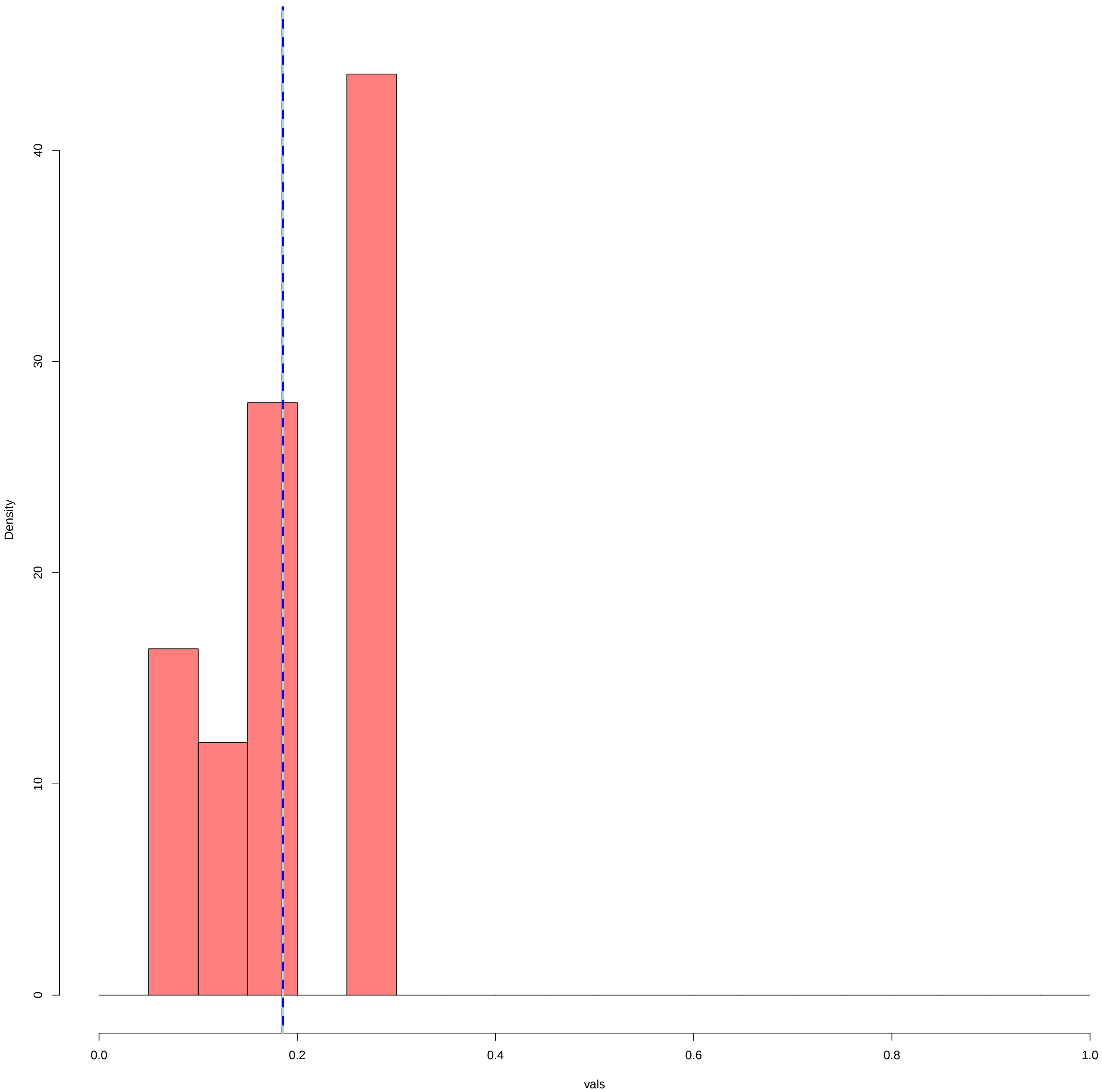
LGI1: H1-hESC_fitCons_score_rankscore



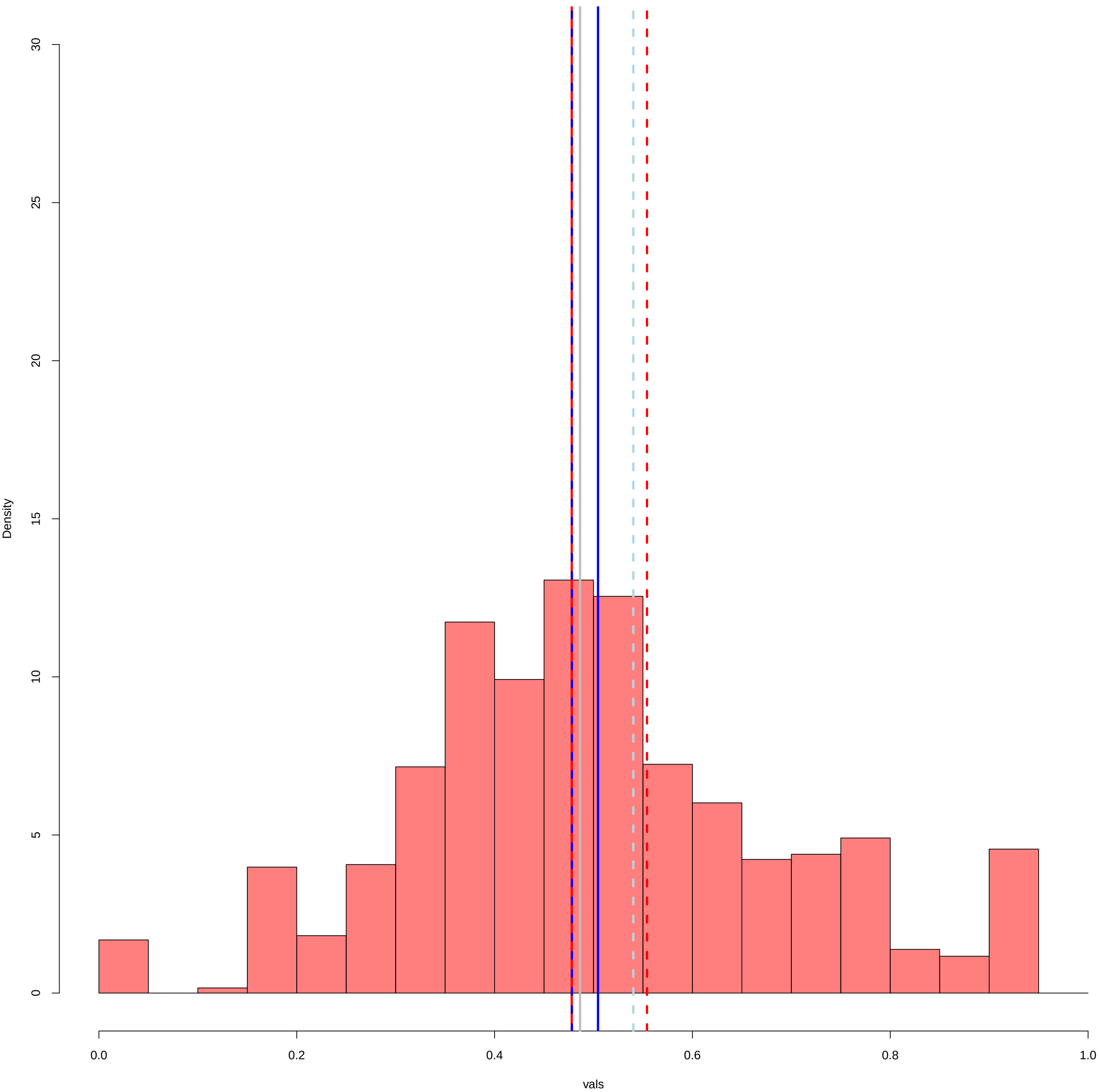
LGI1: HUVEC_fitCons_score_rankscore



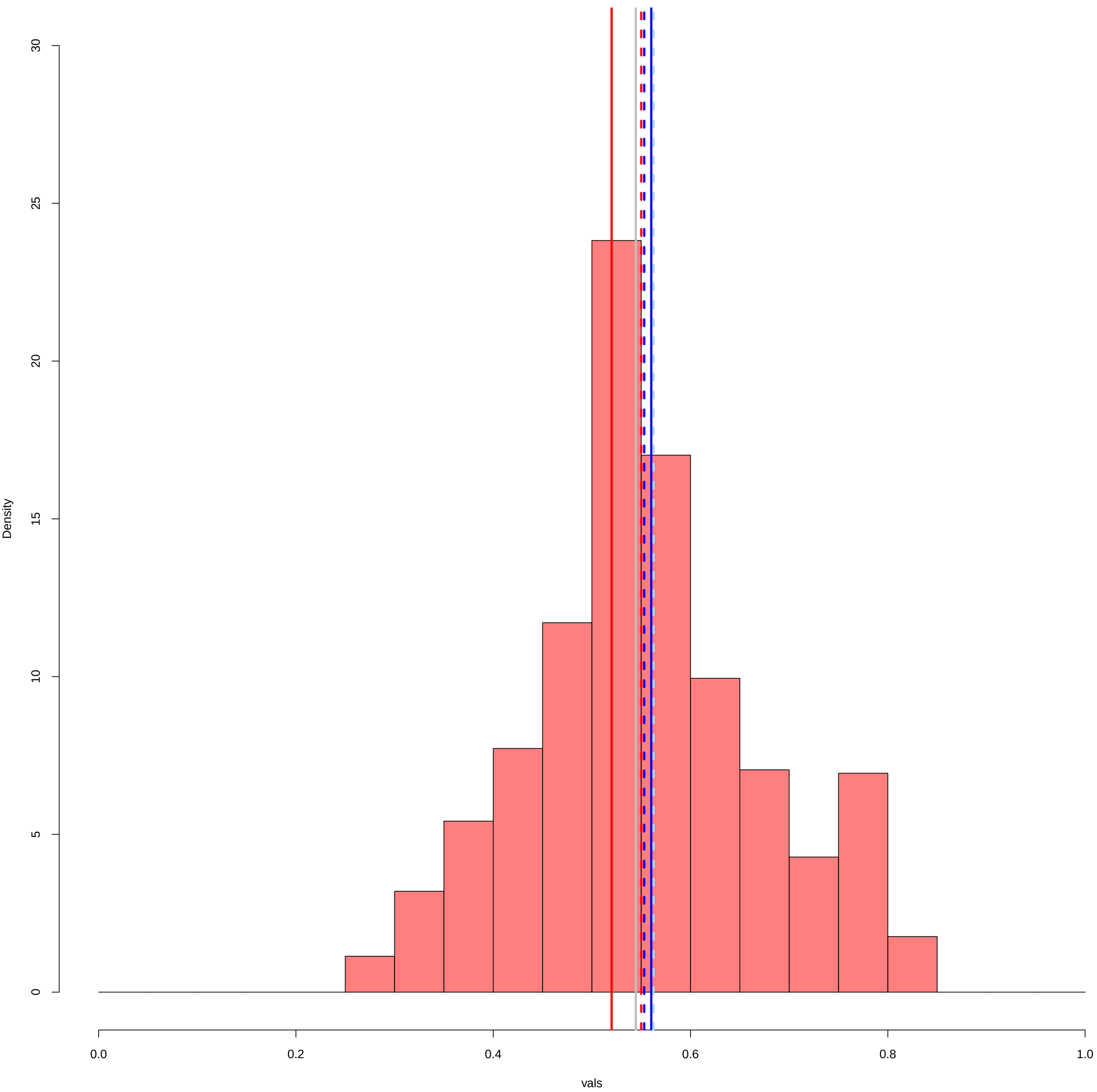
LGI1: integrated_fitCons_score_rankscore



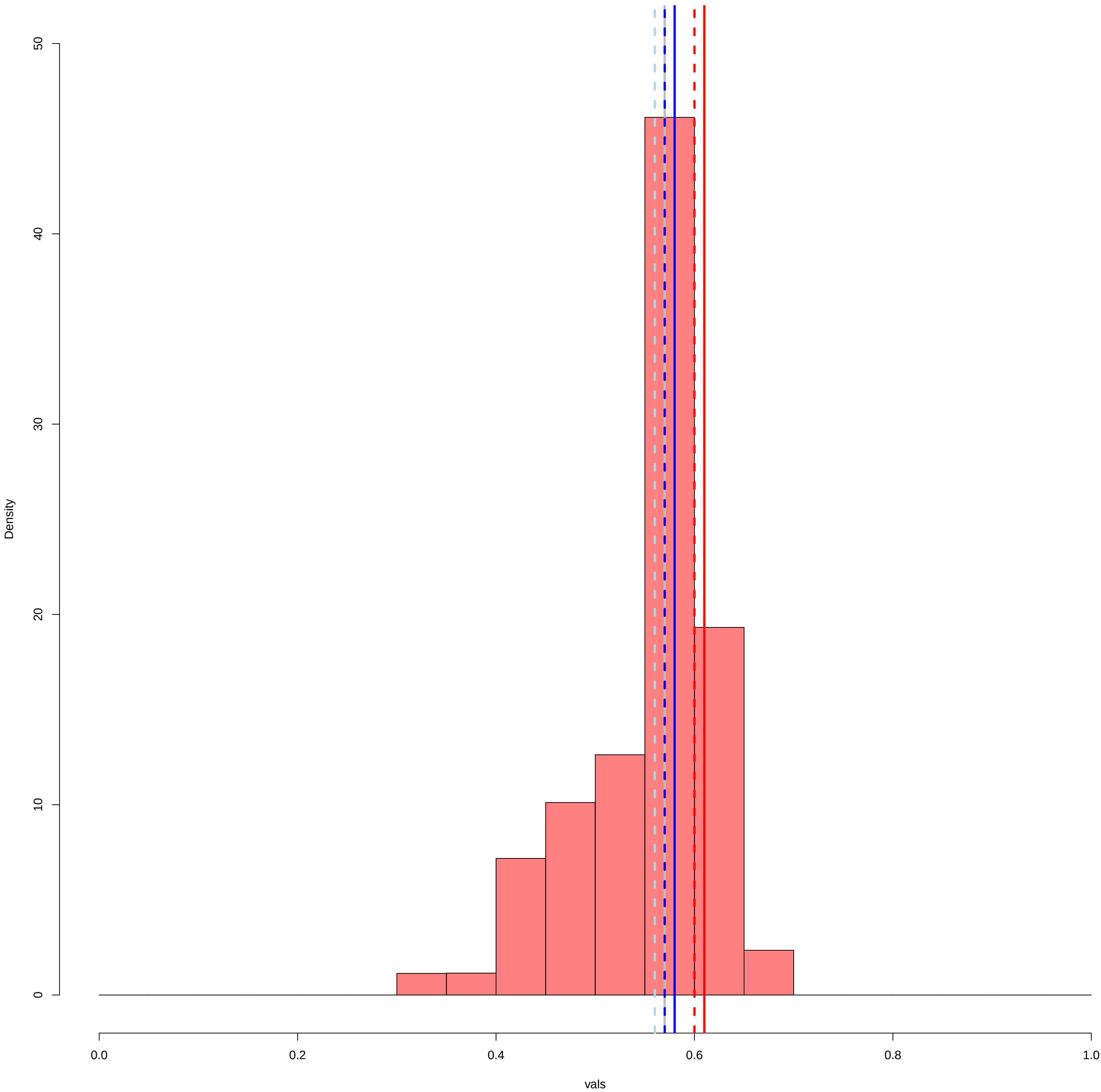
LGI1: ExAC v1 MTR



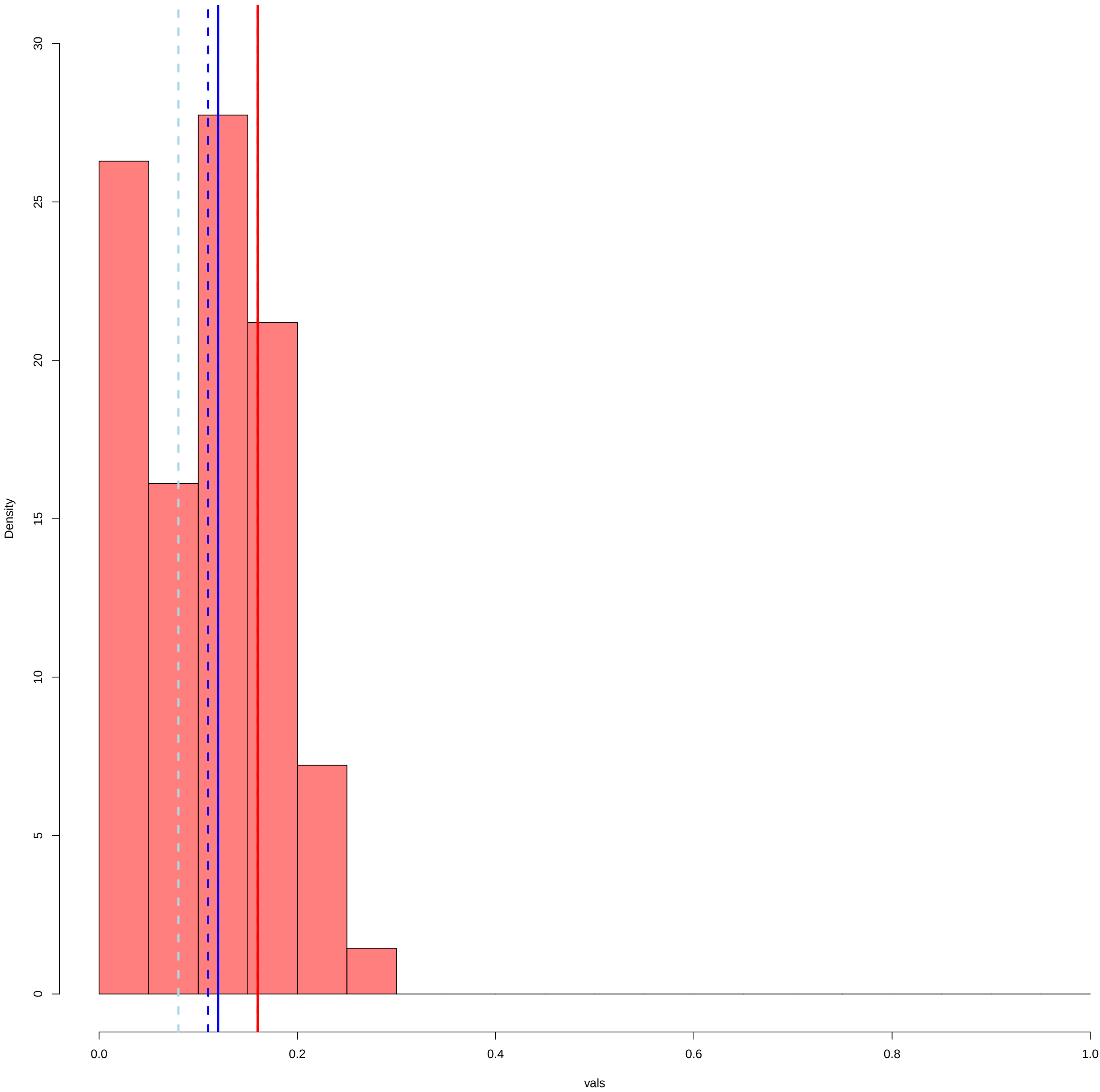
LGI1: ExAC v2 & gnomAD MTR



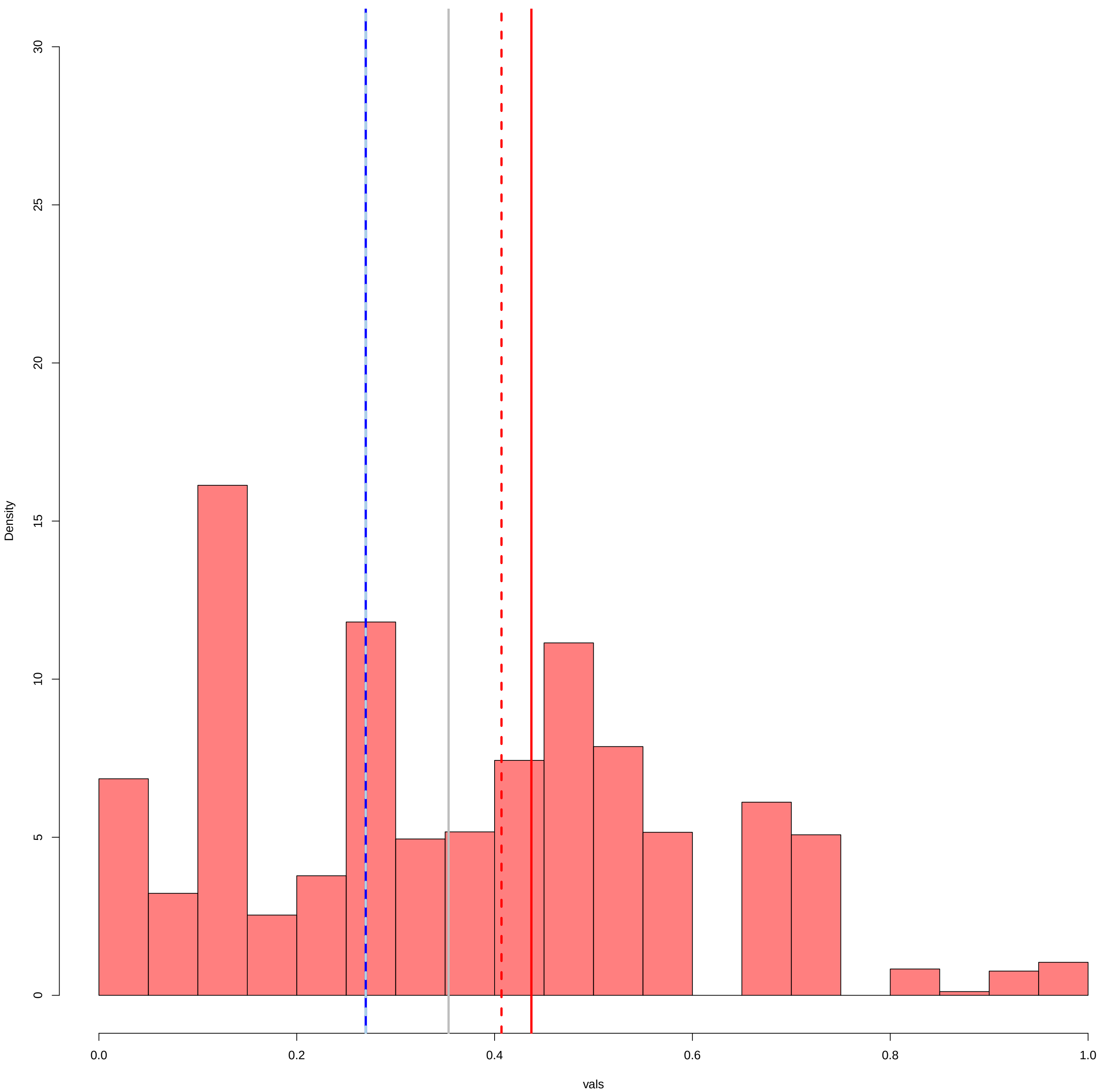
PCDH19: GC (Percent GC content in a window of +/-75bp)



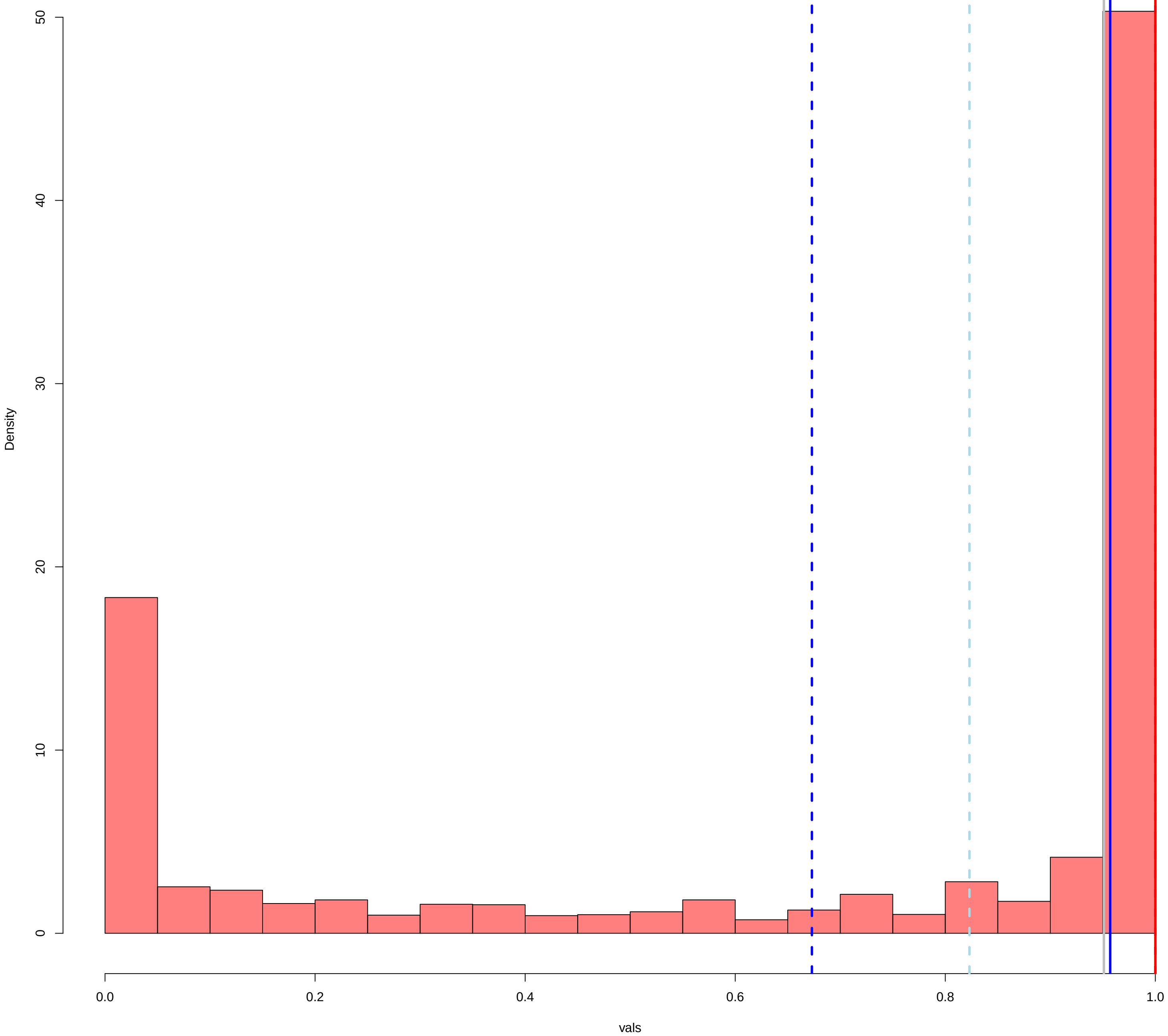
PCDH19: CpG (Percent CpG in a window of +/-75bp)



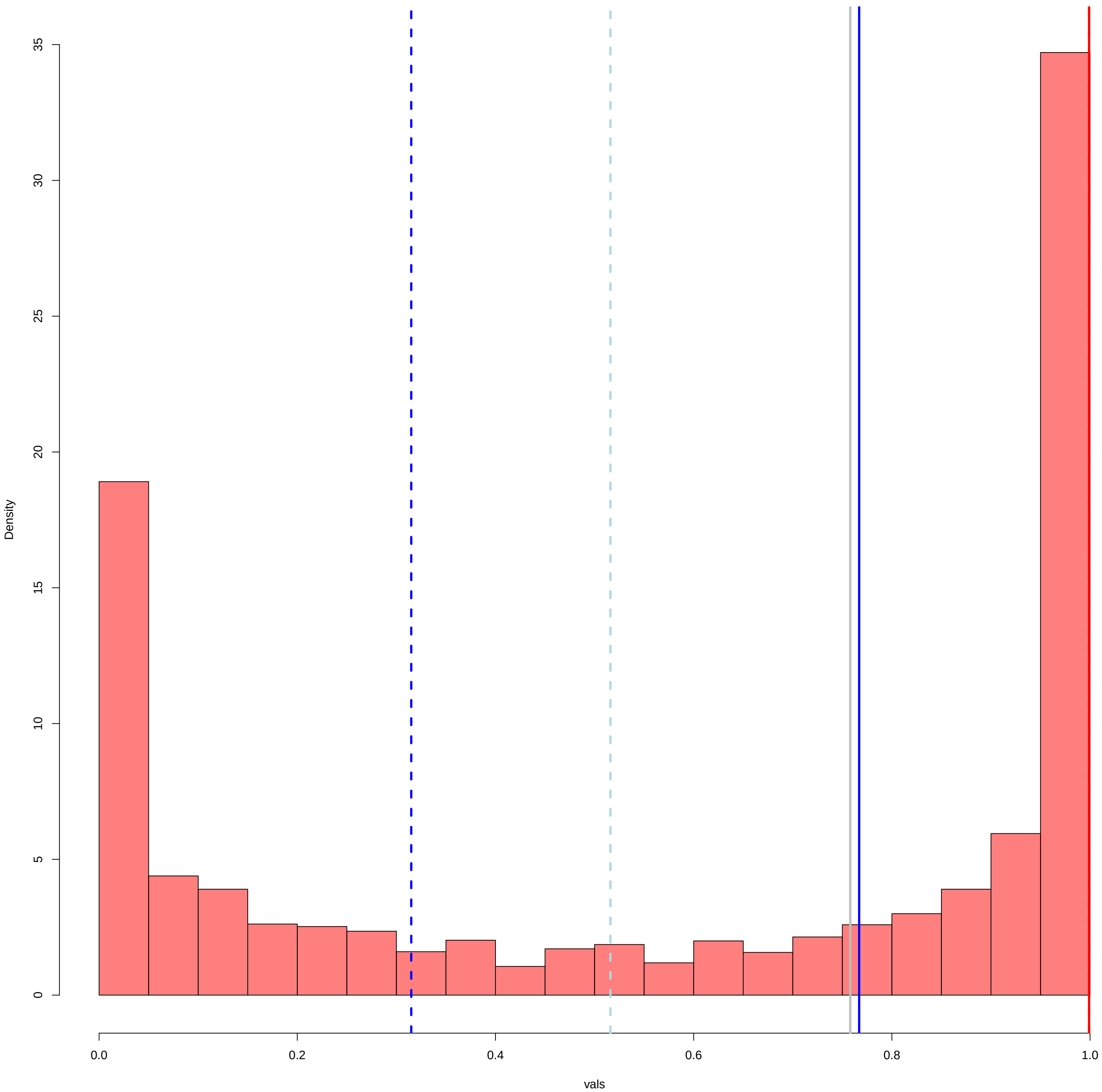
PCDH19: Grantham



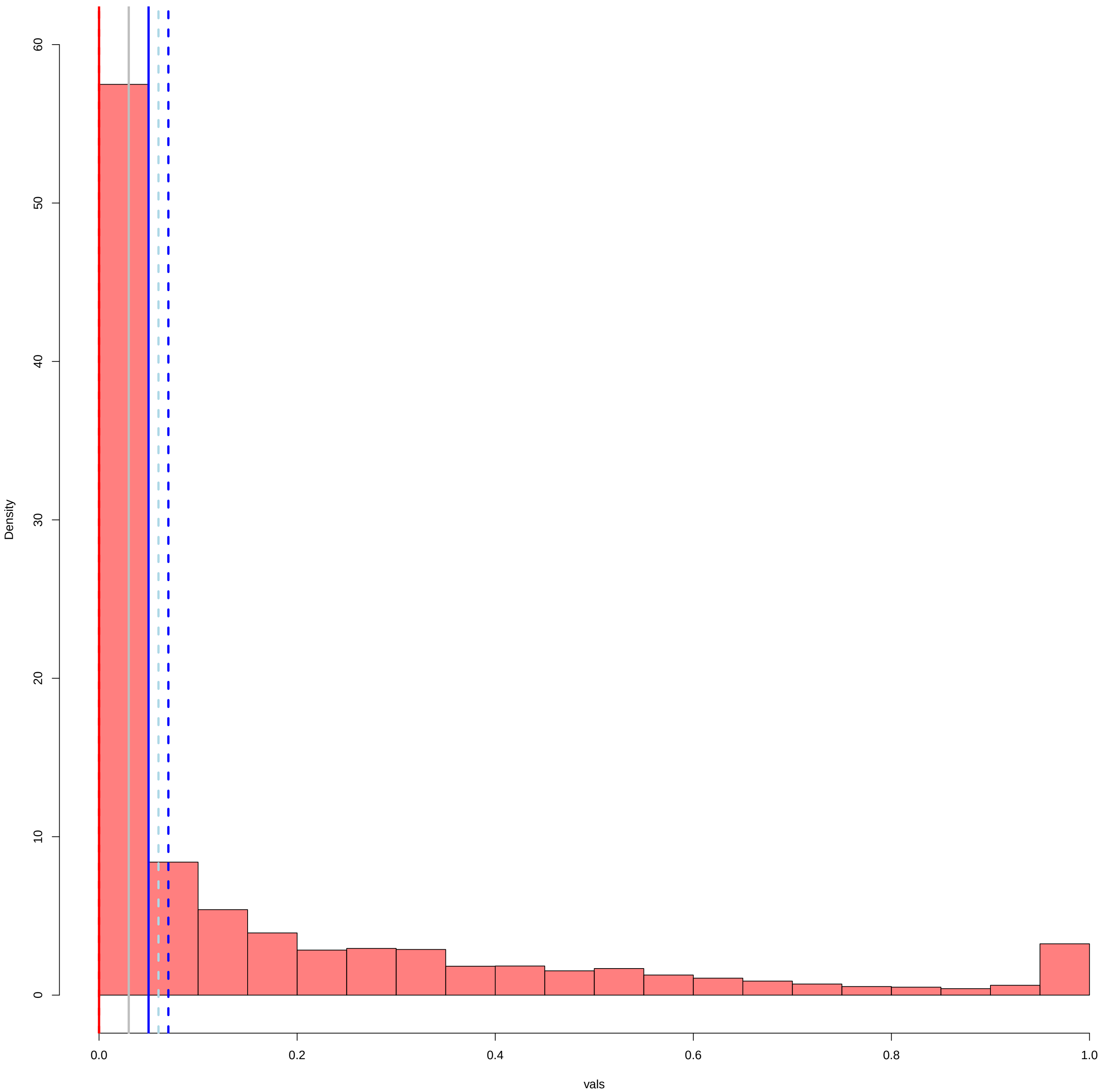
PCDH19: Hdiv quan



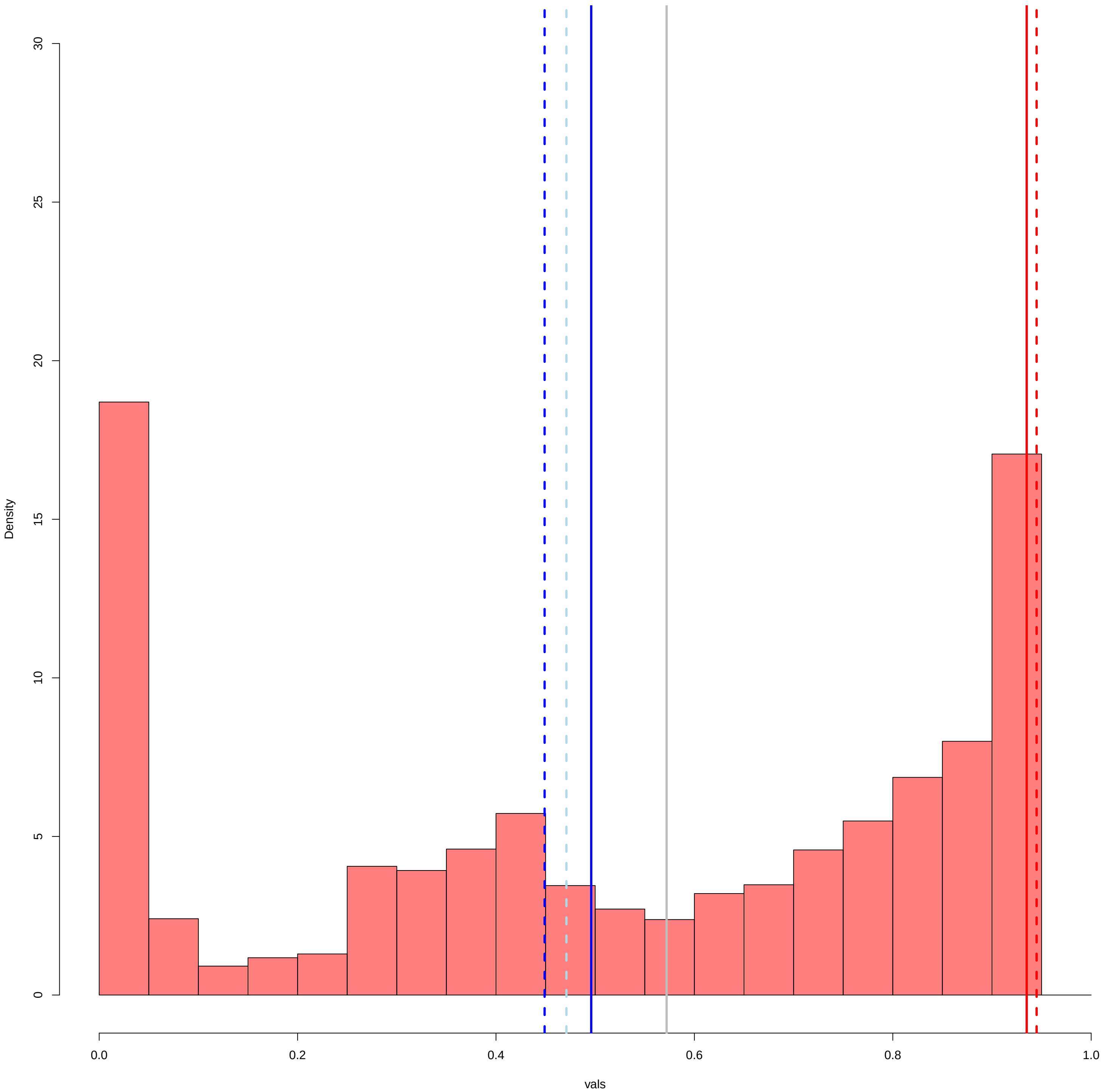
PCDH19: Hvar quan



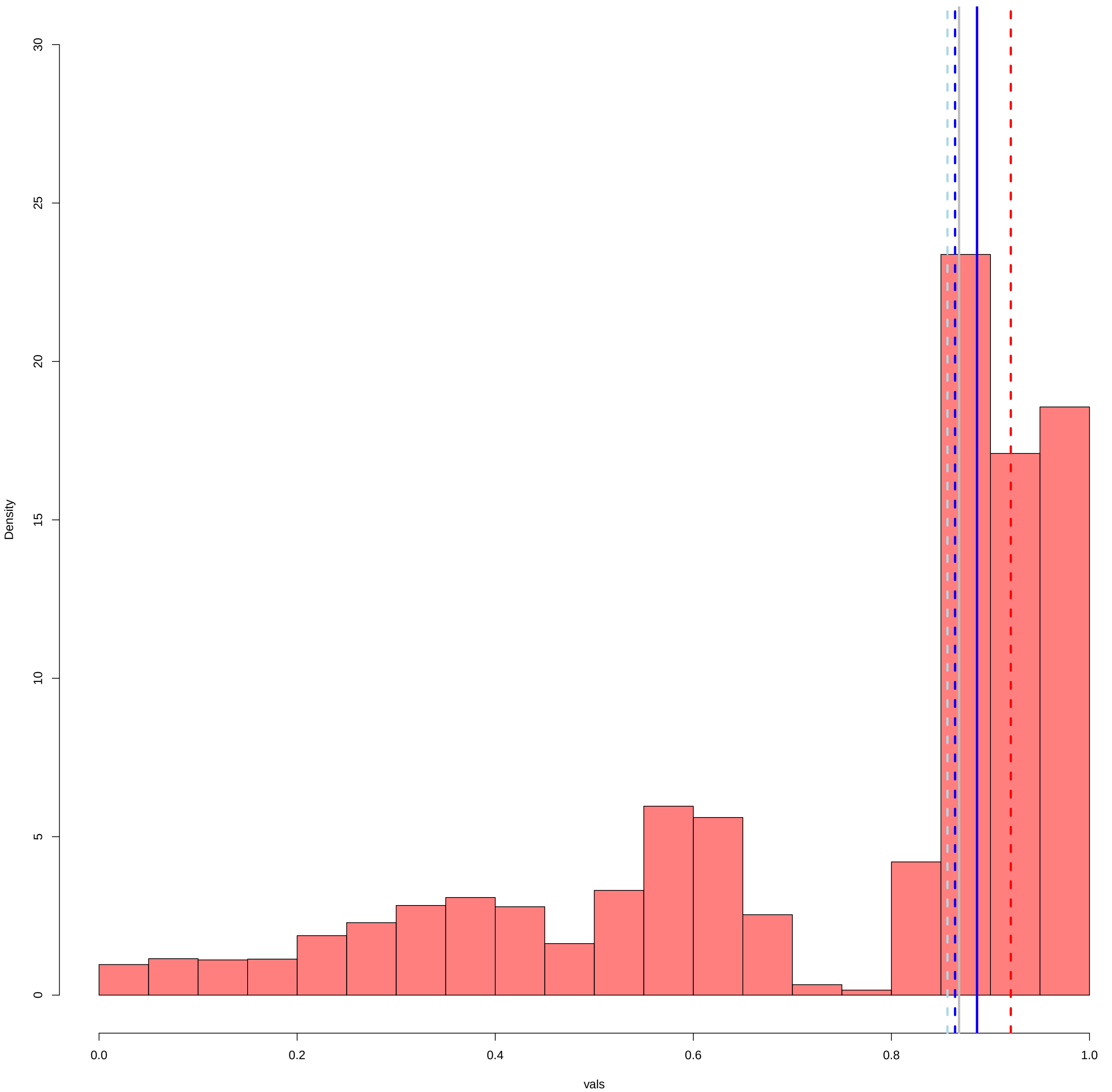
PCDH19: SIFT



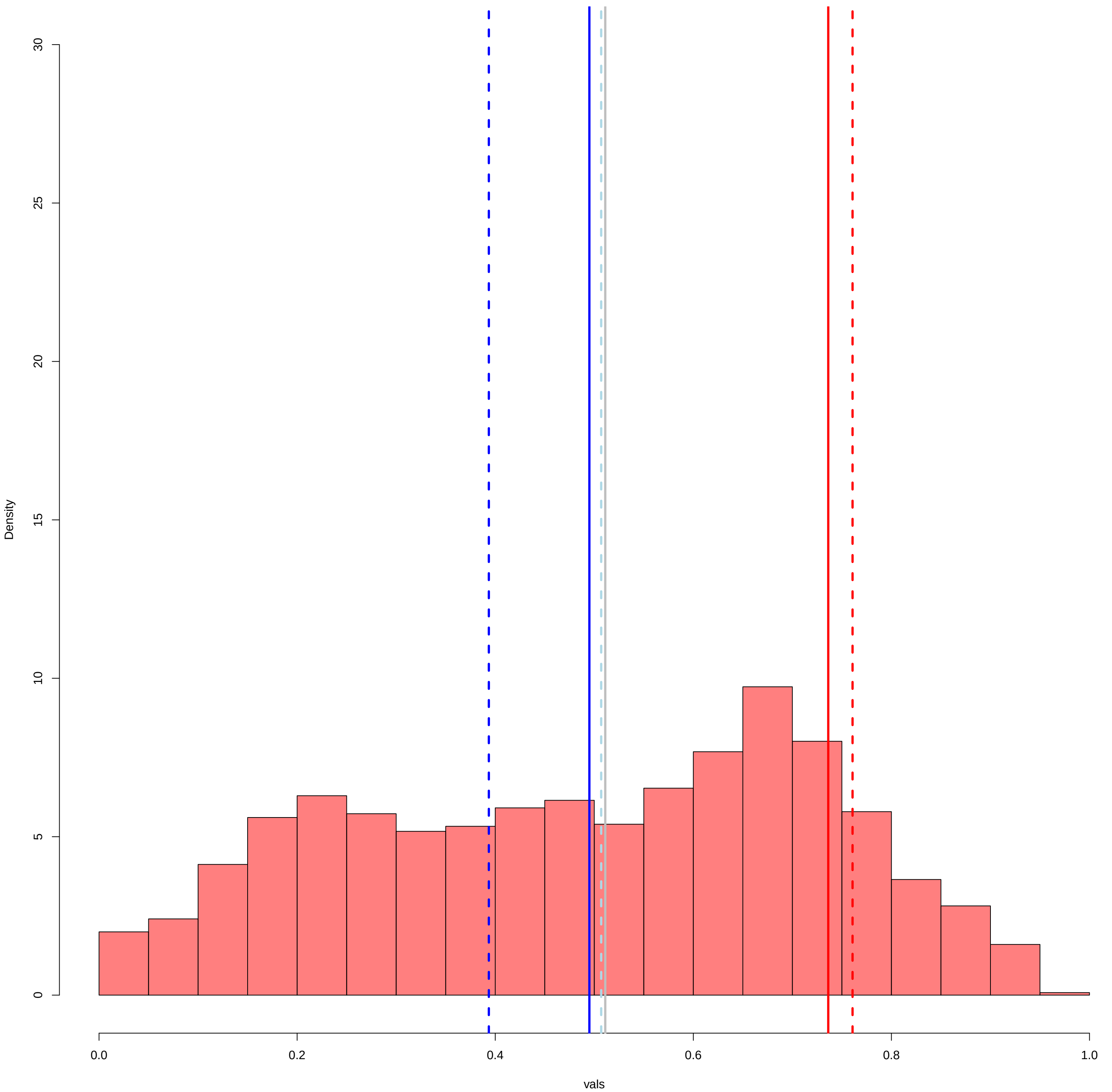
PCDH19: Condel



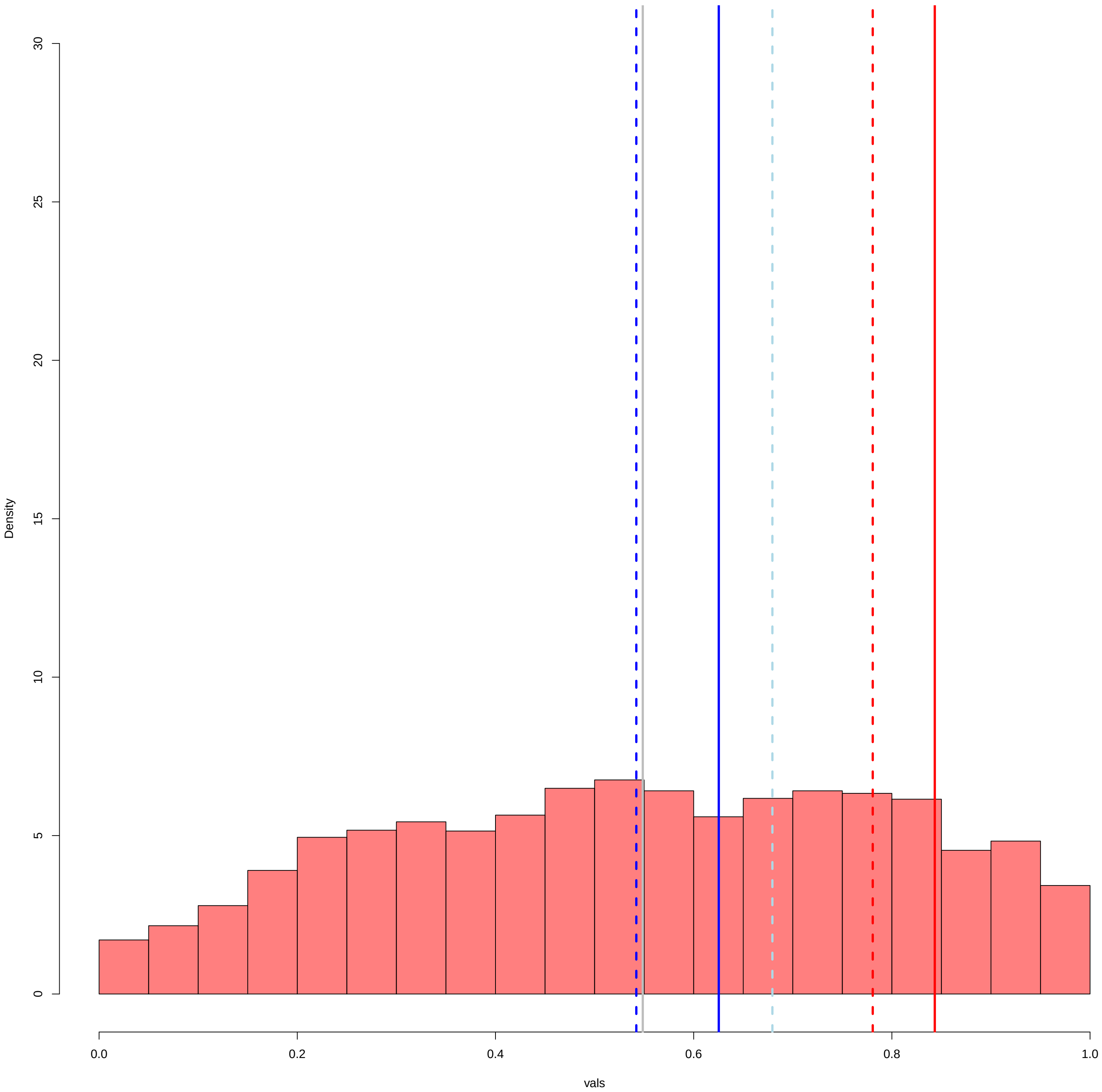
PCDH19: GERP++_RS_rankscore



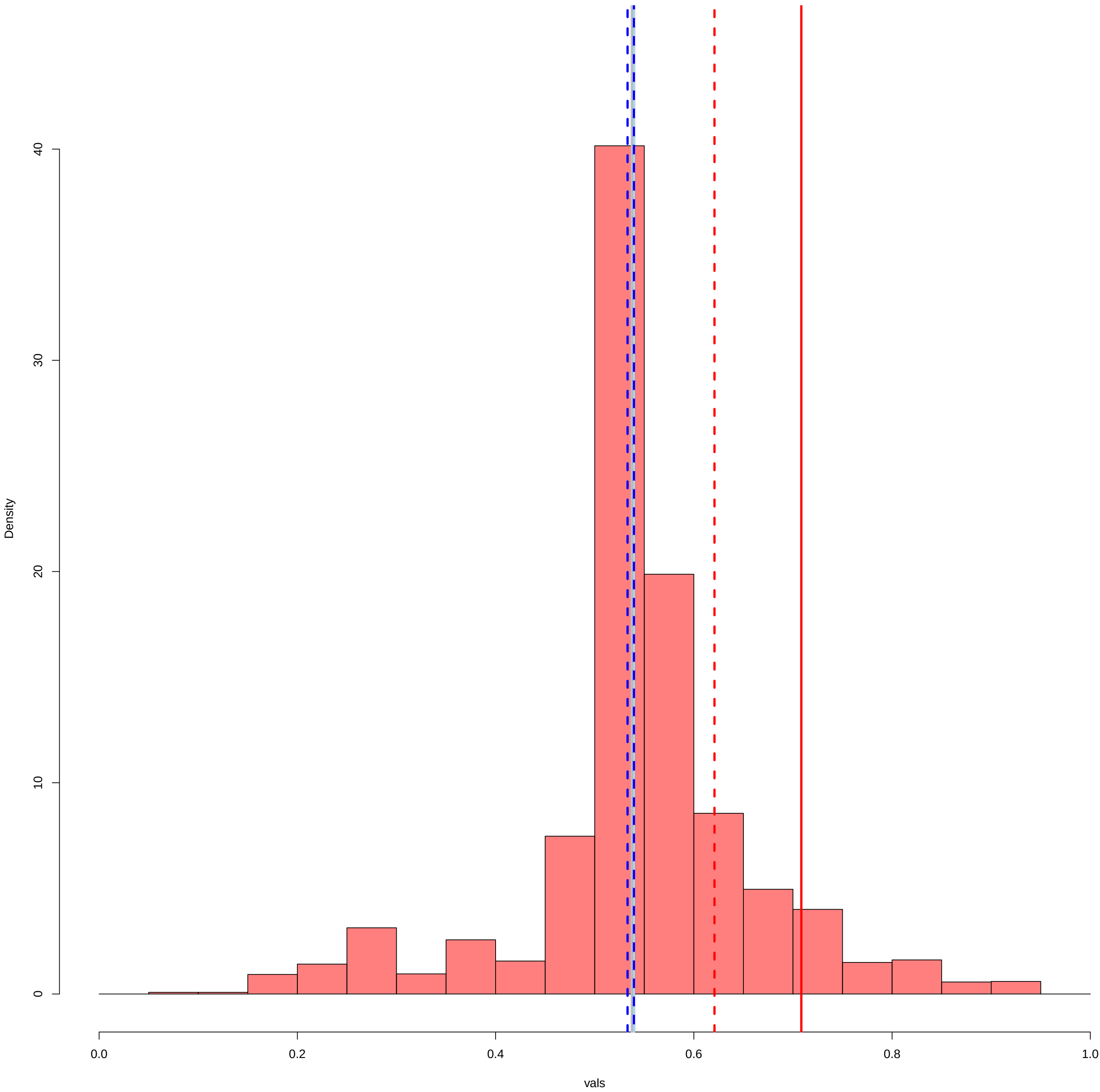
PCDH19: CADD_raw_rankscore



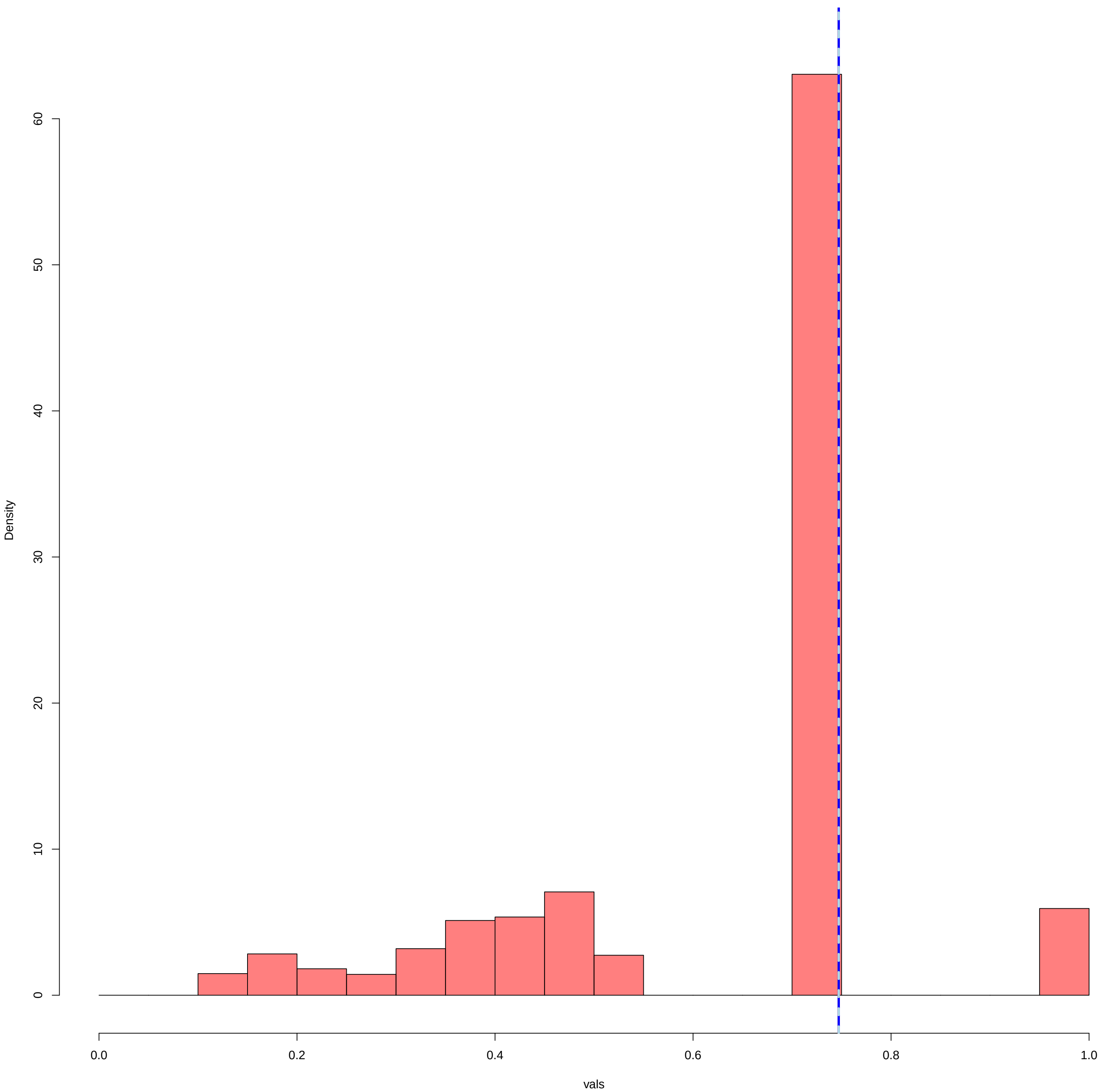
PCDH19: DANN_rankscore



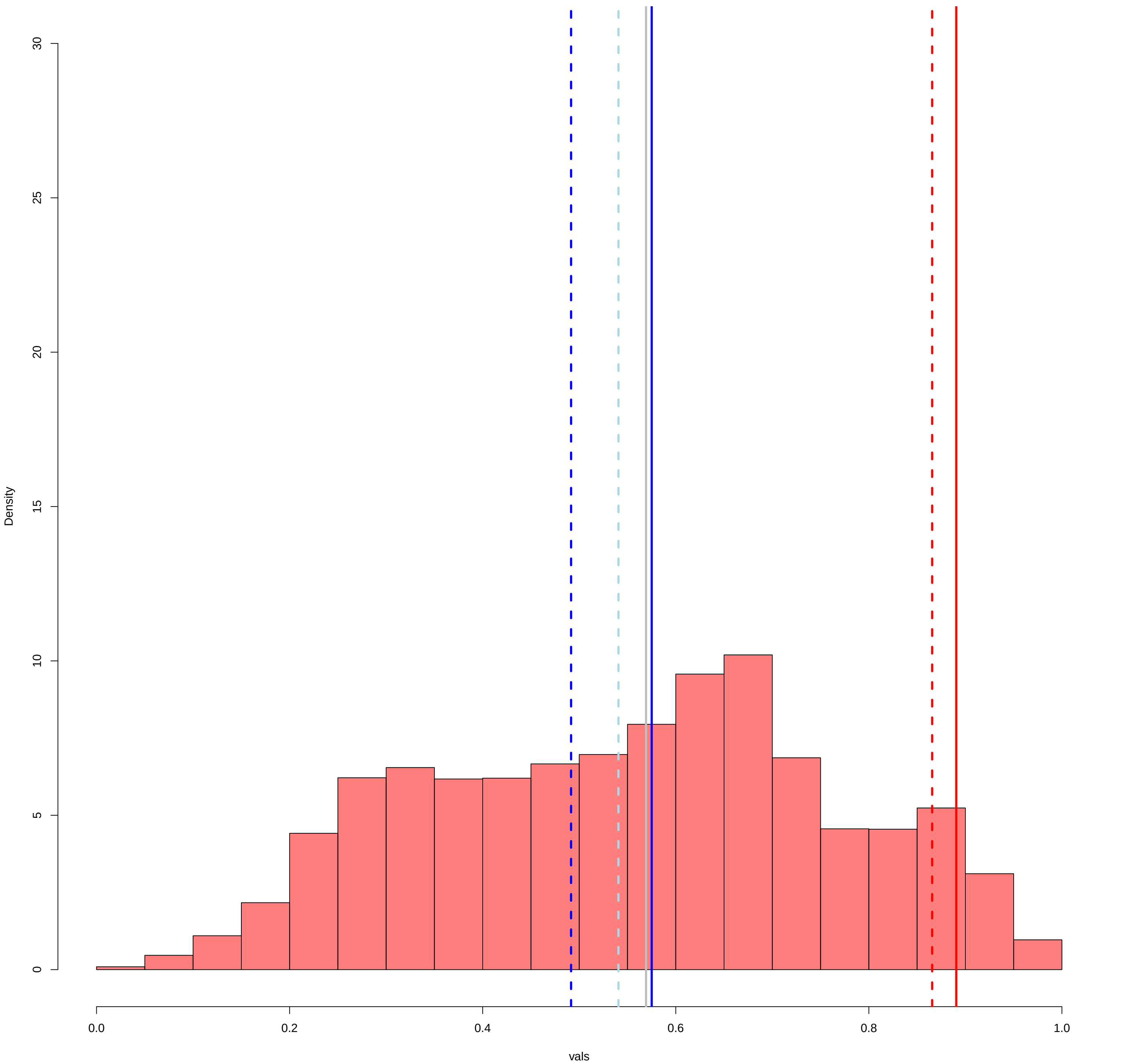
PCDH19: FATHMM_converted_rankscore



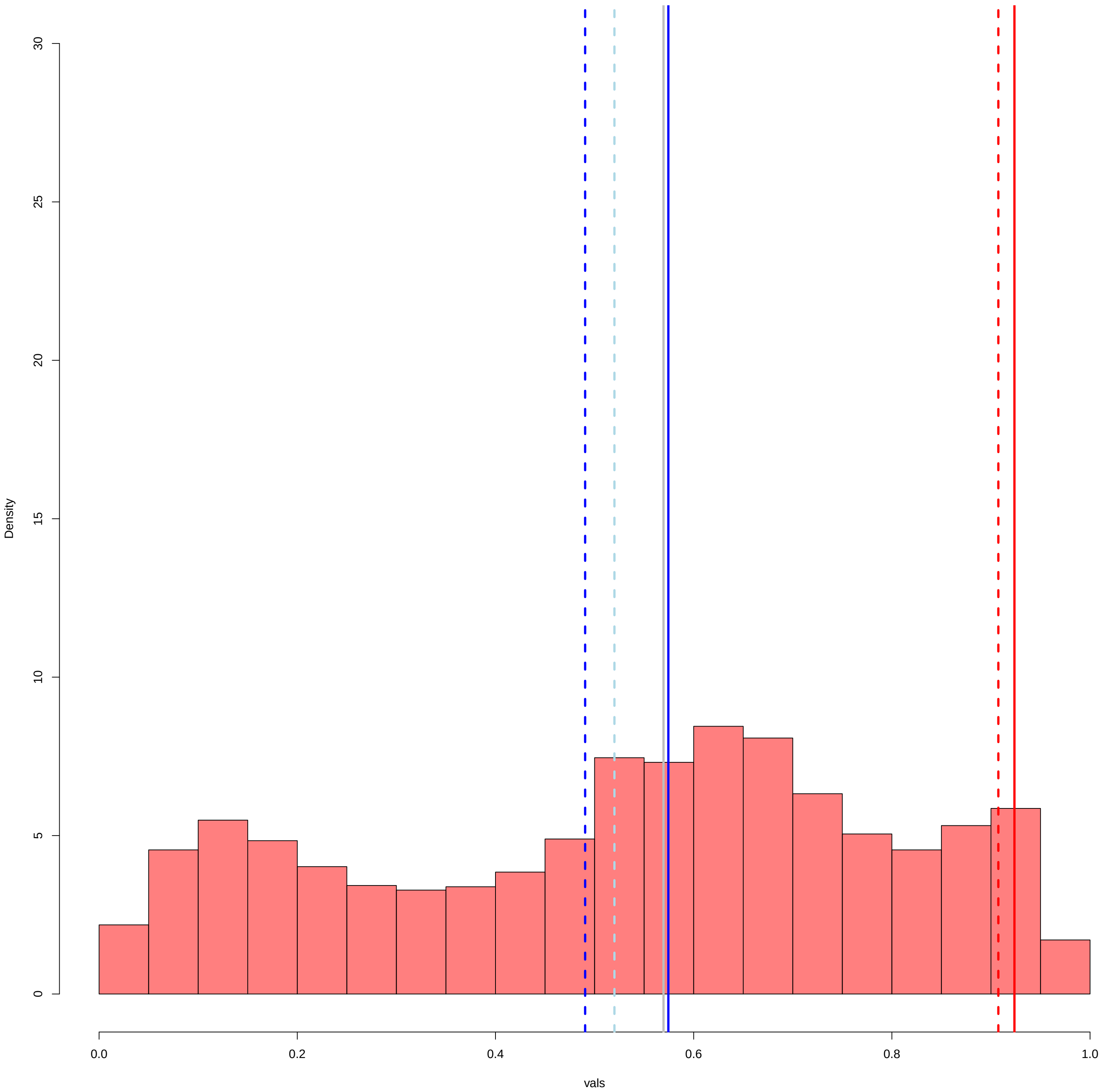
PCDH19: GenoCanyon_score_rankscore



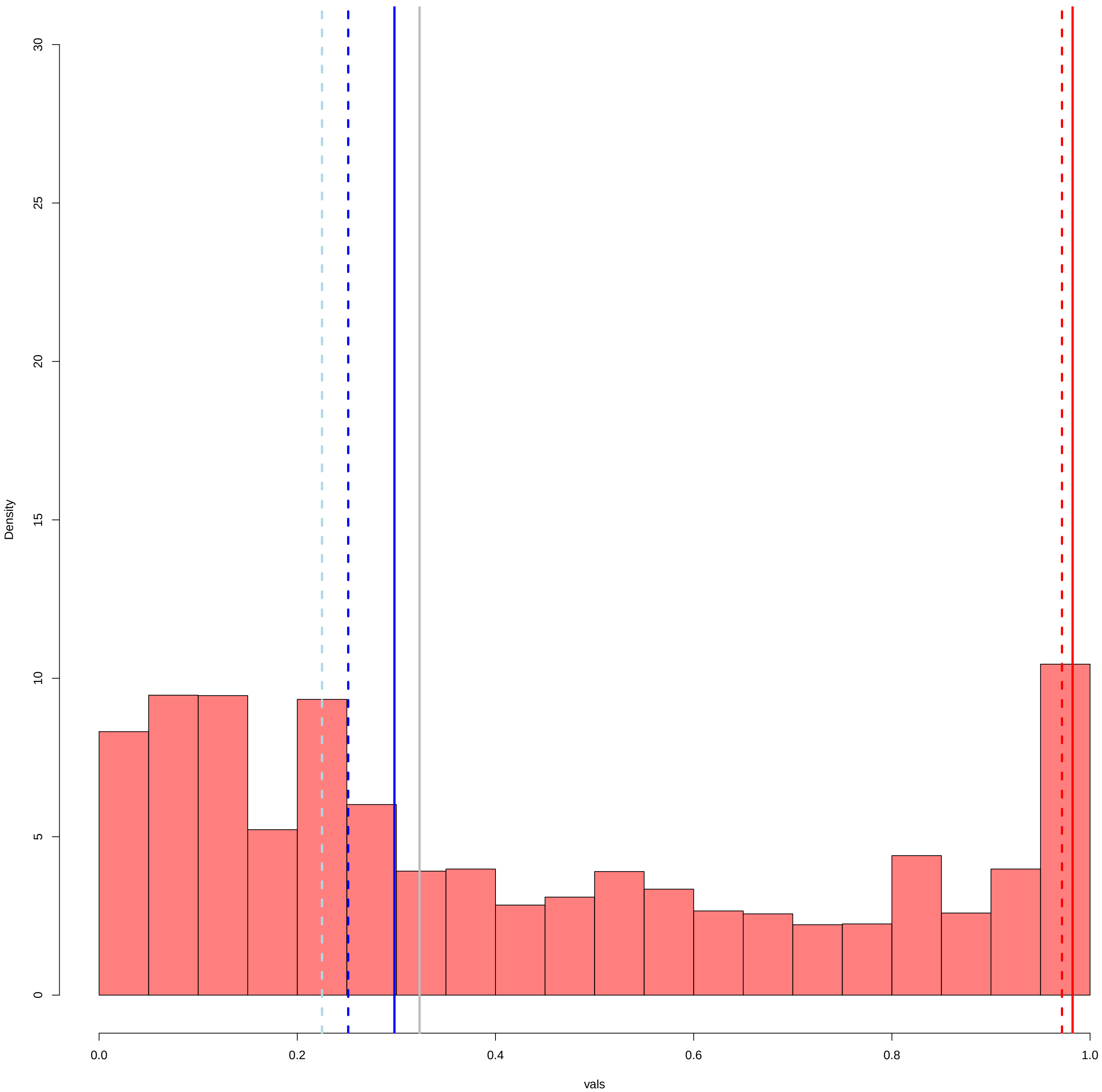
PCDH19: MetaLR_rankscore



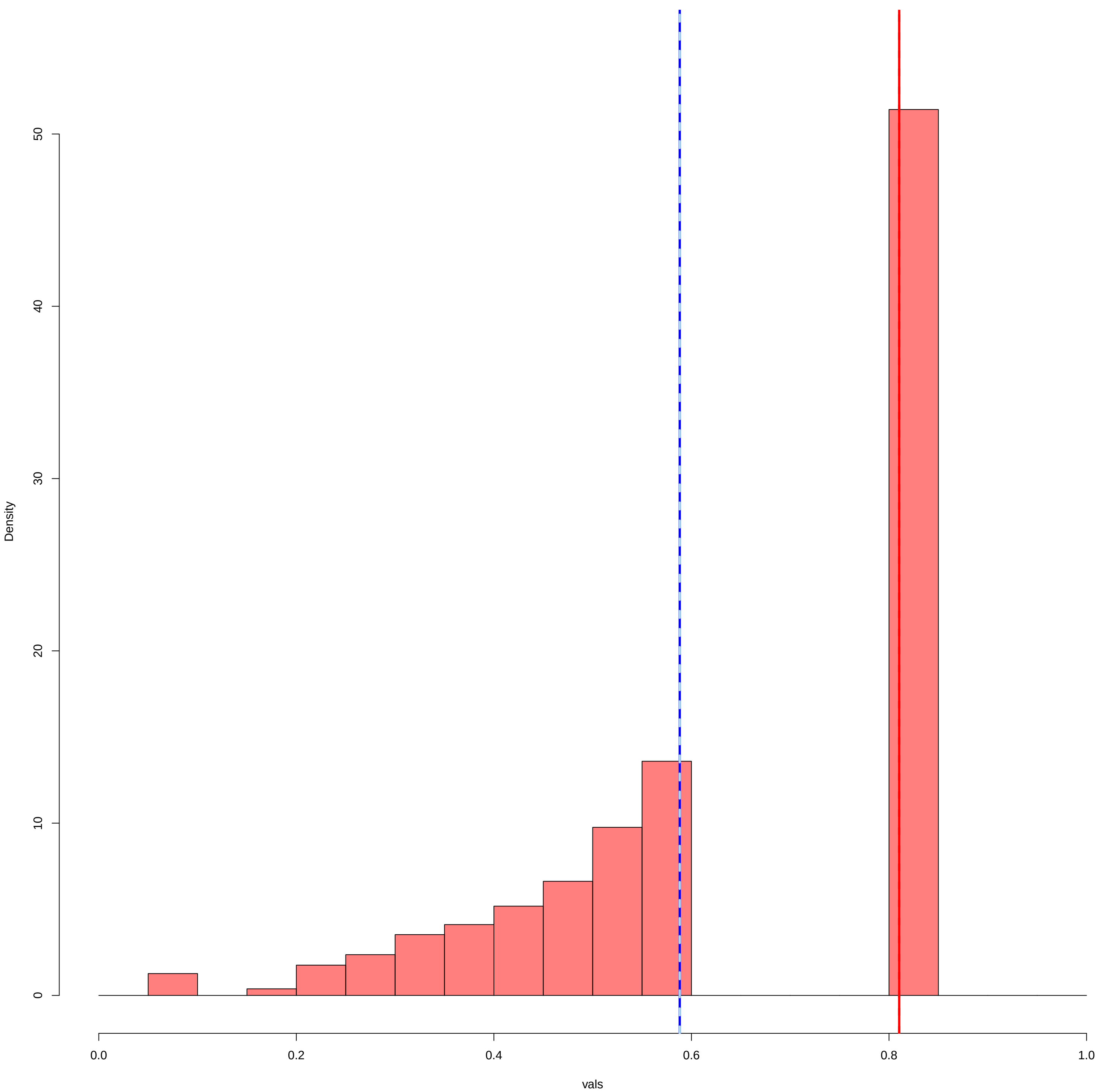
PCDH19: MetaSVM_rankscore



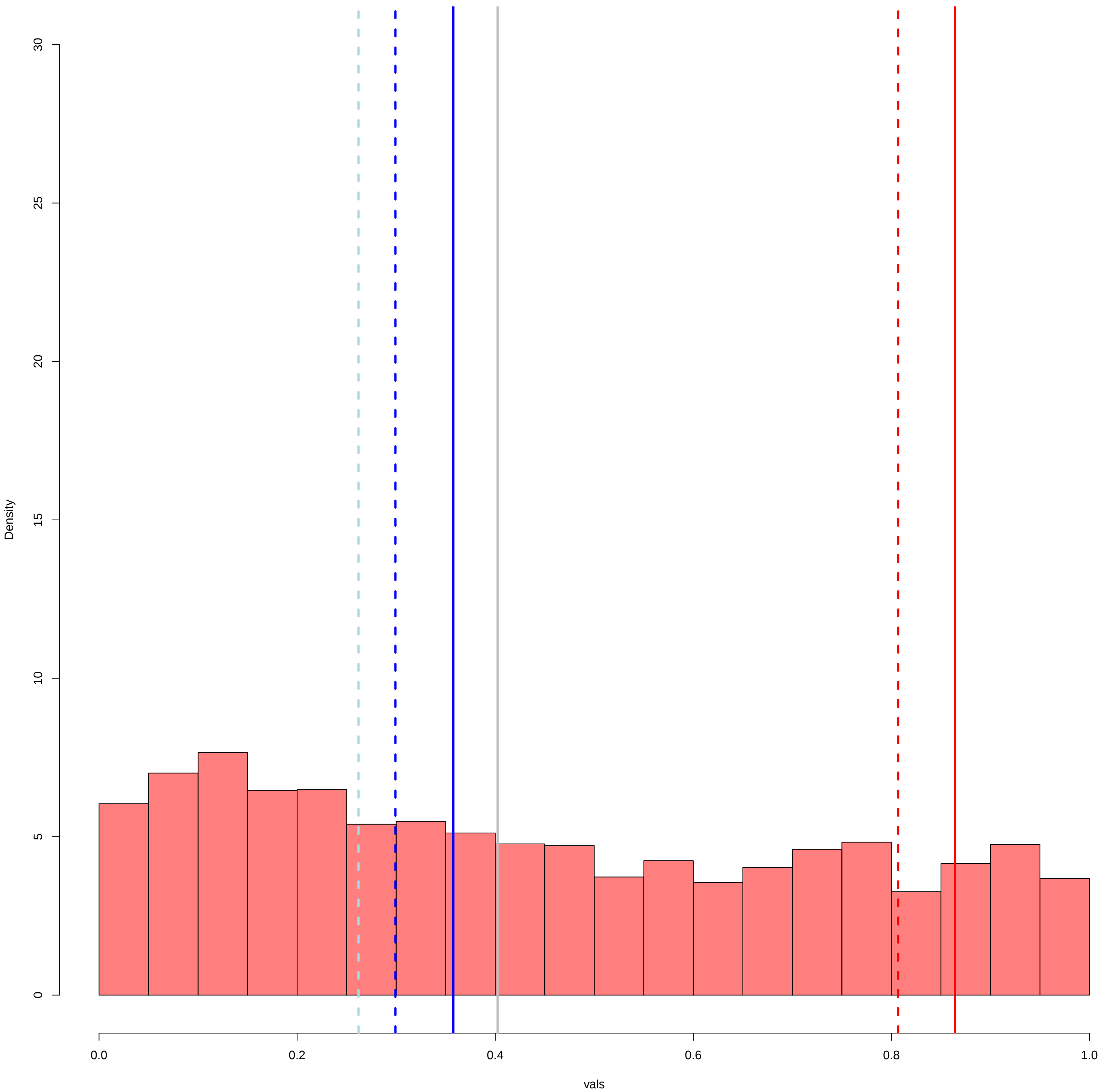
PCDH19: MutationAssessor_score_rankscore



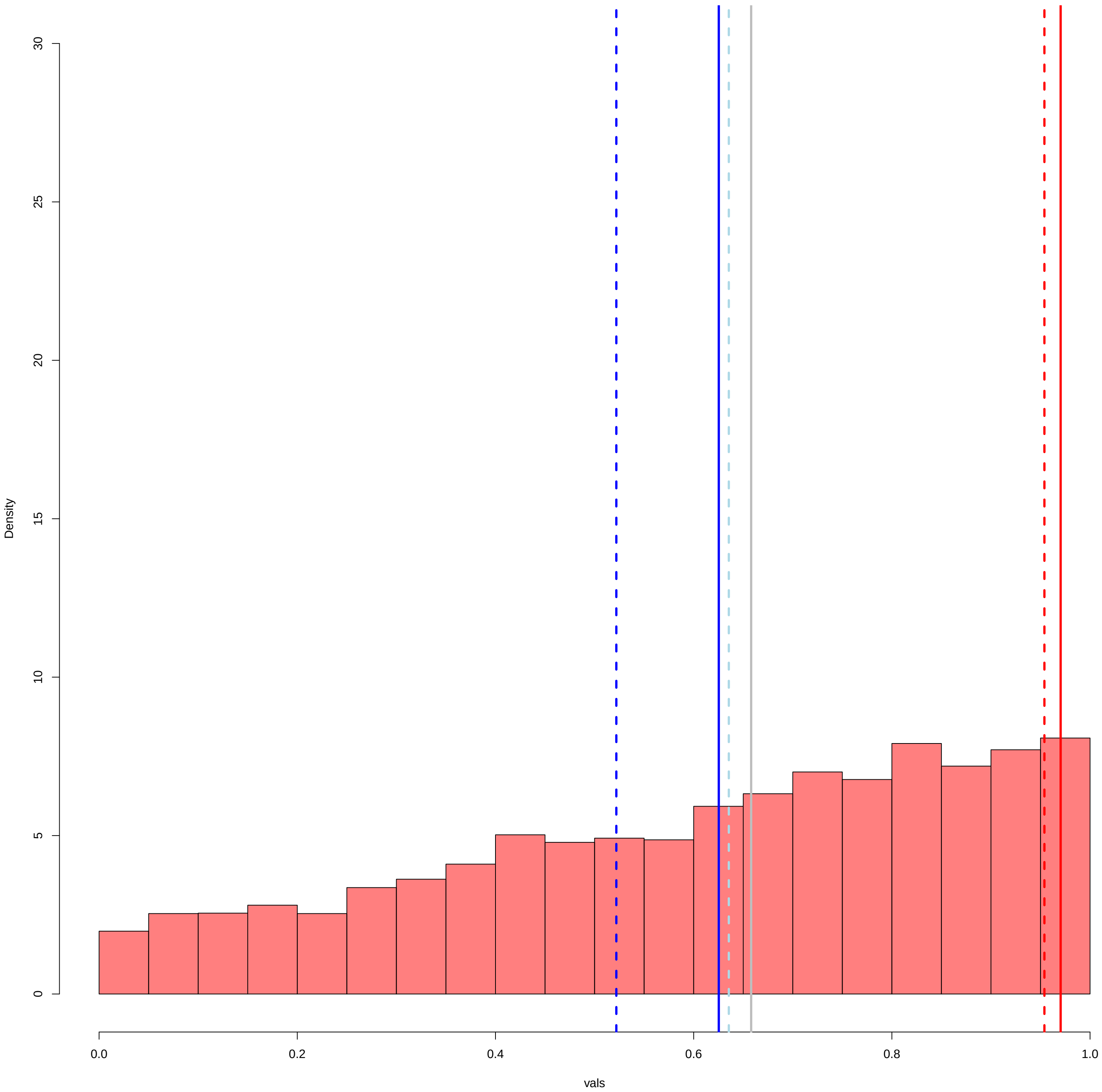
PCDH19: MutationTaster_converted_rankscore



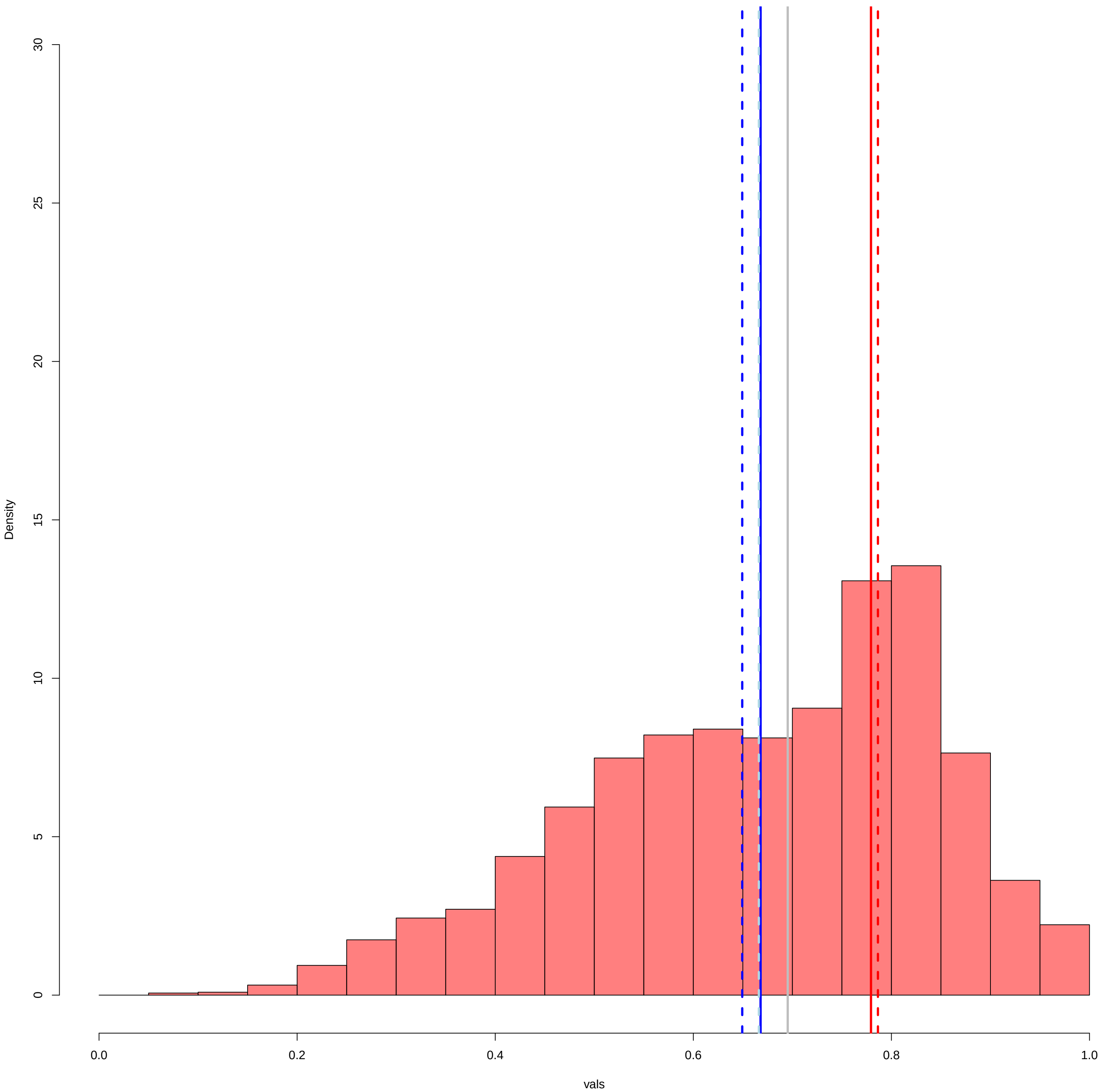
PCDH19: PROVEAN_converted_rankscore



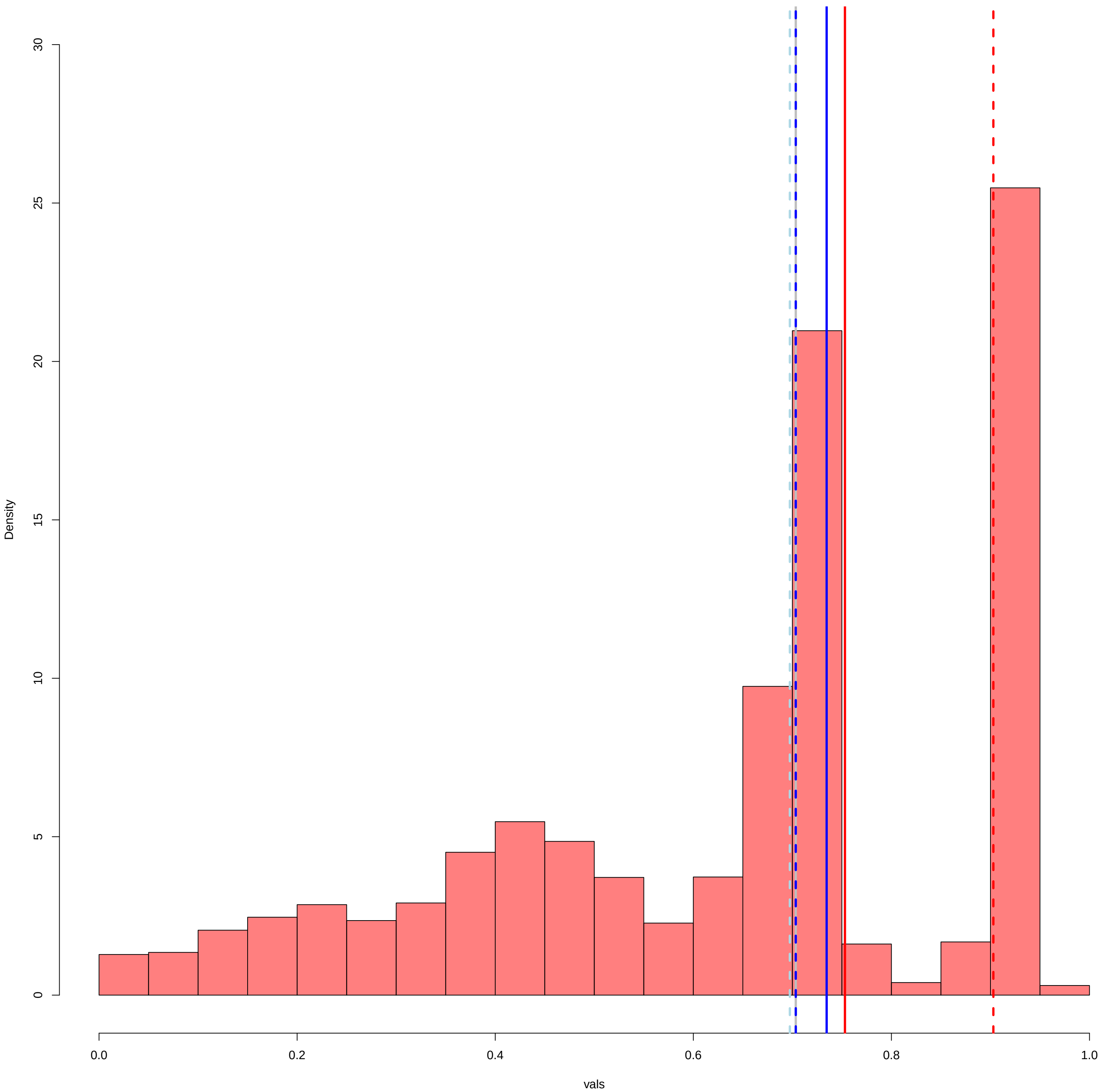
PCDH19: VEST3_rankscore



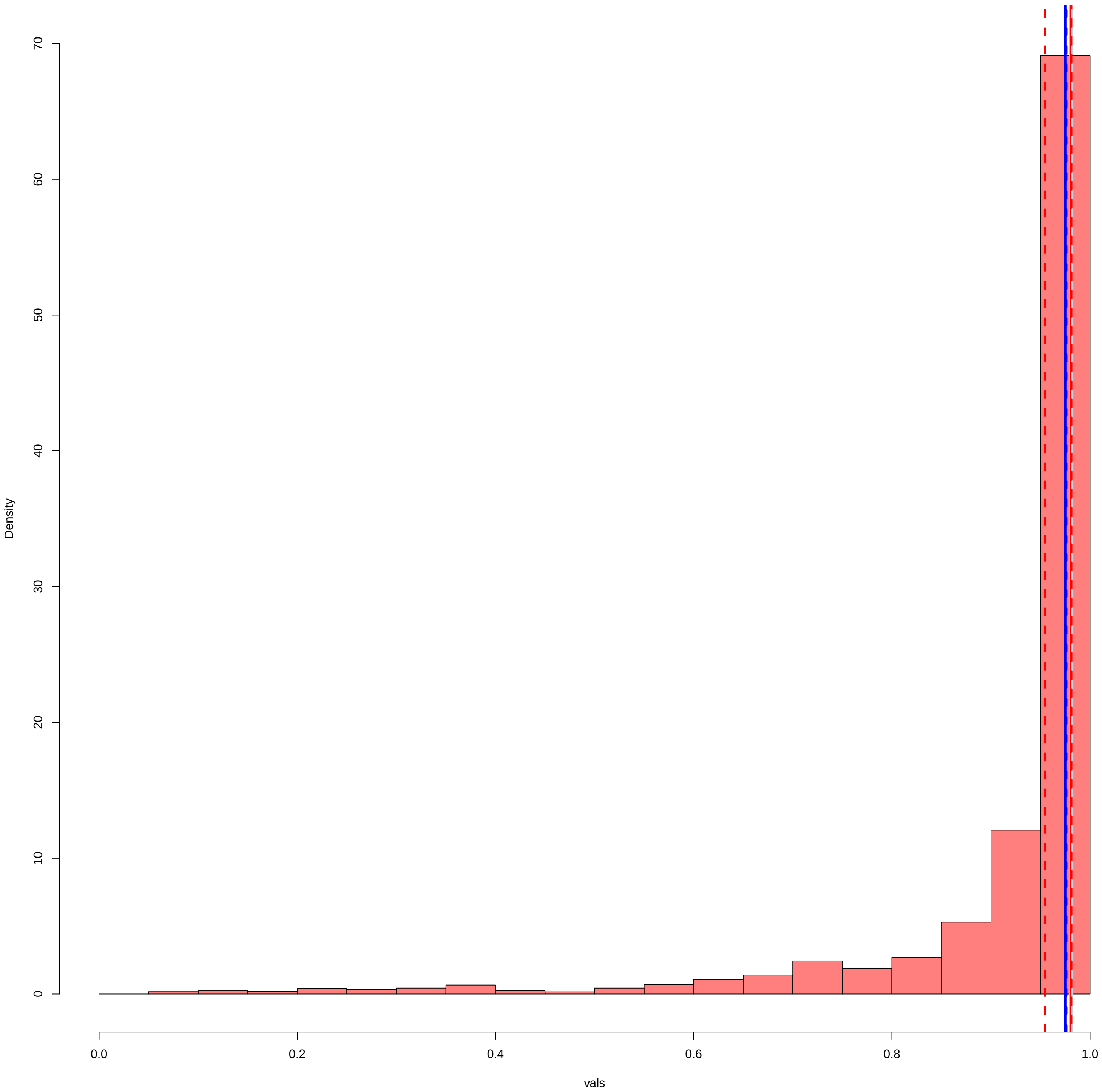
PCDH19: fathmm-MKL_coding_rankscore



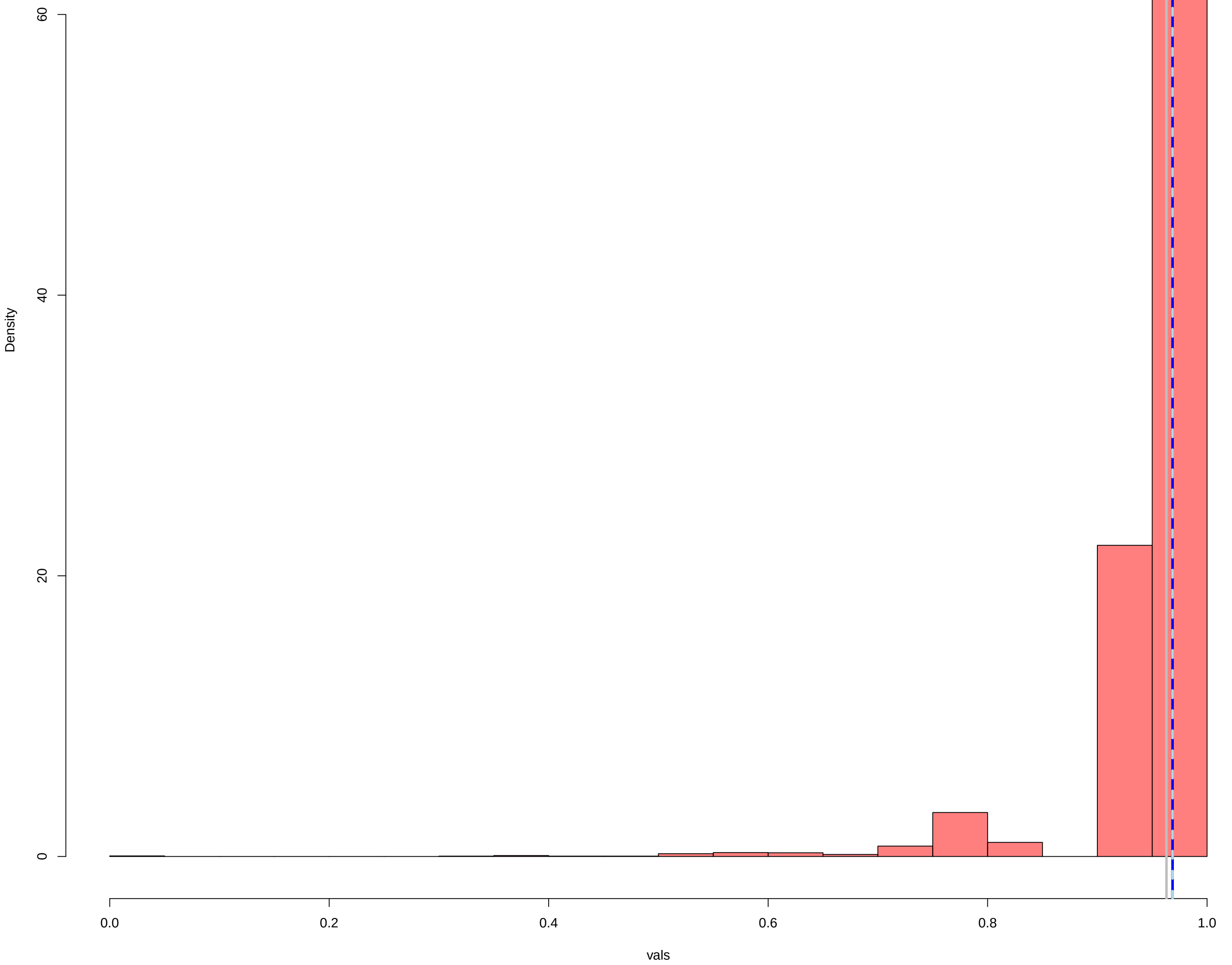
PCDH19: SiPhy_29way_logOdds_rankscore



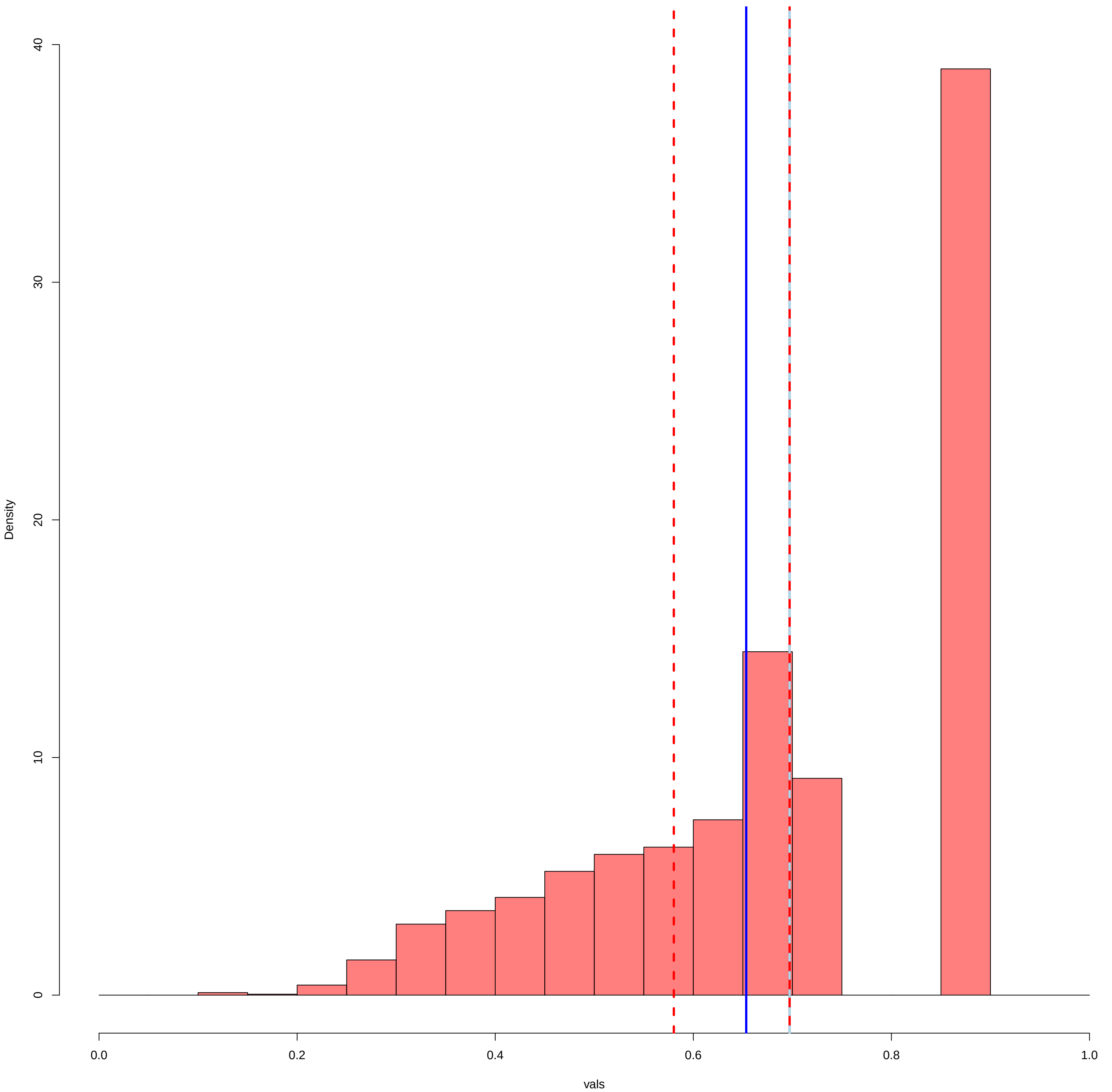
PCDH19: priPhCons



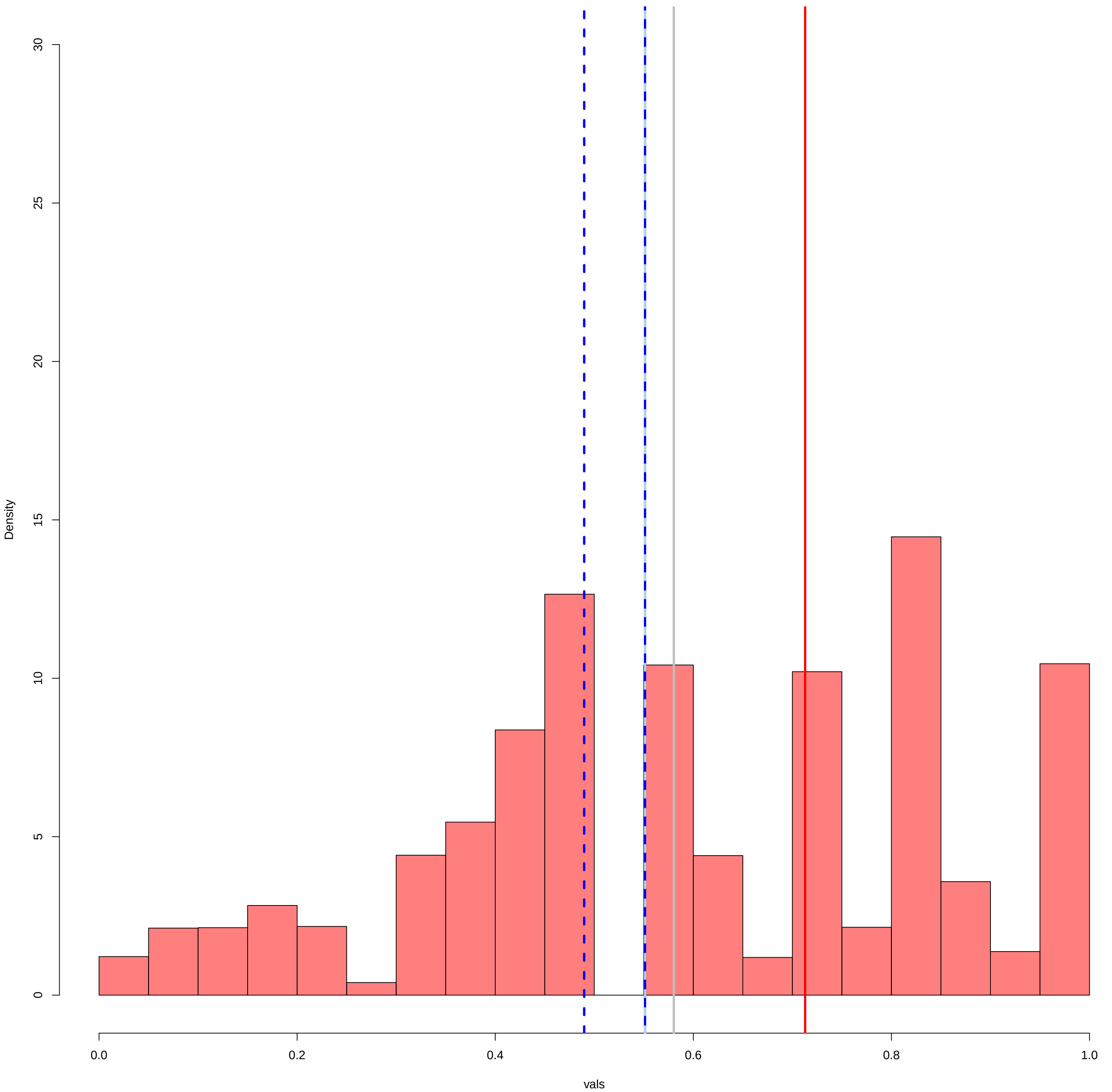
PCDH19: priPhyloP



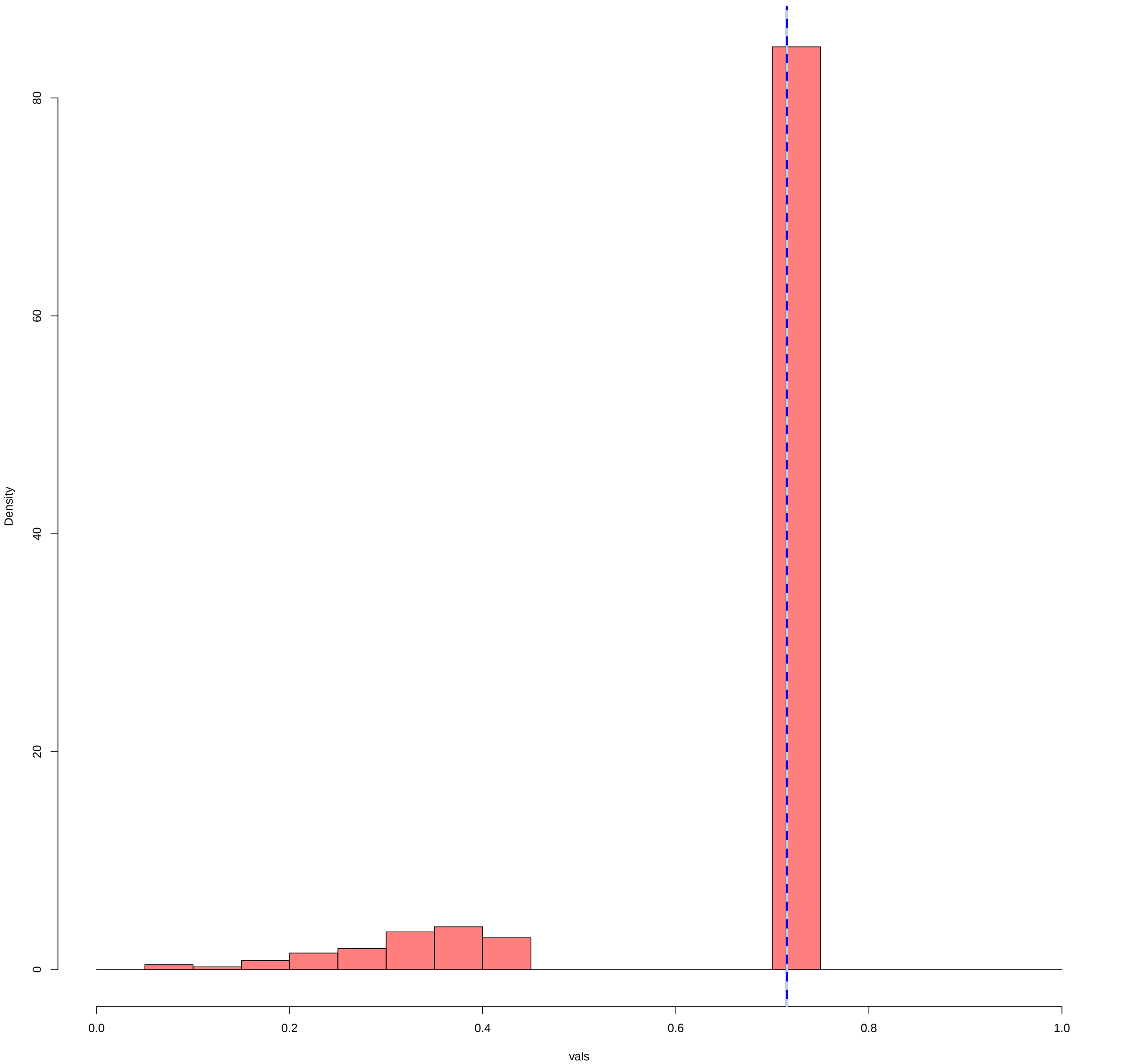
PCDH19: phastCons20way_mammalian_rankscore



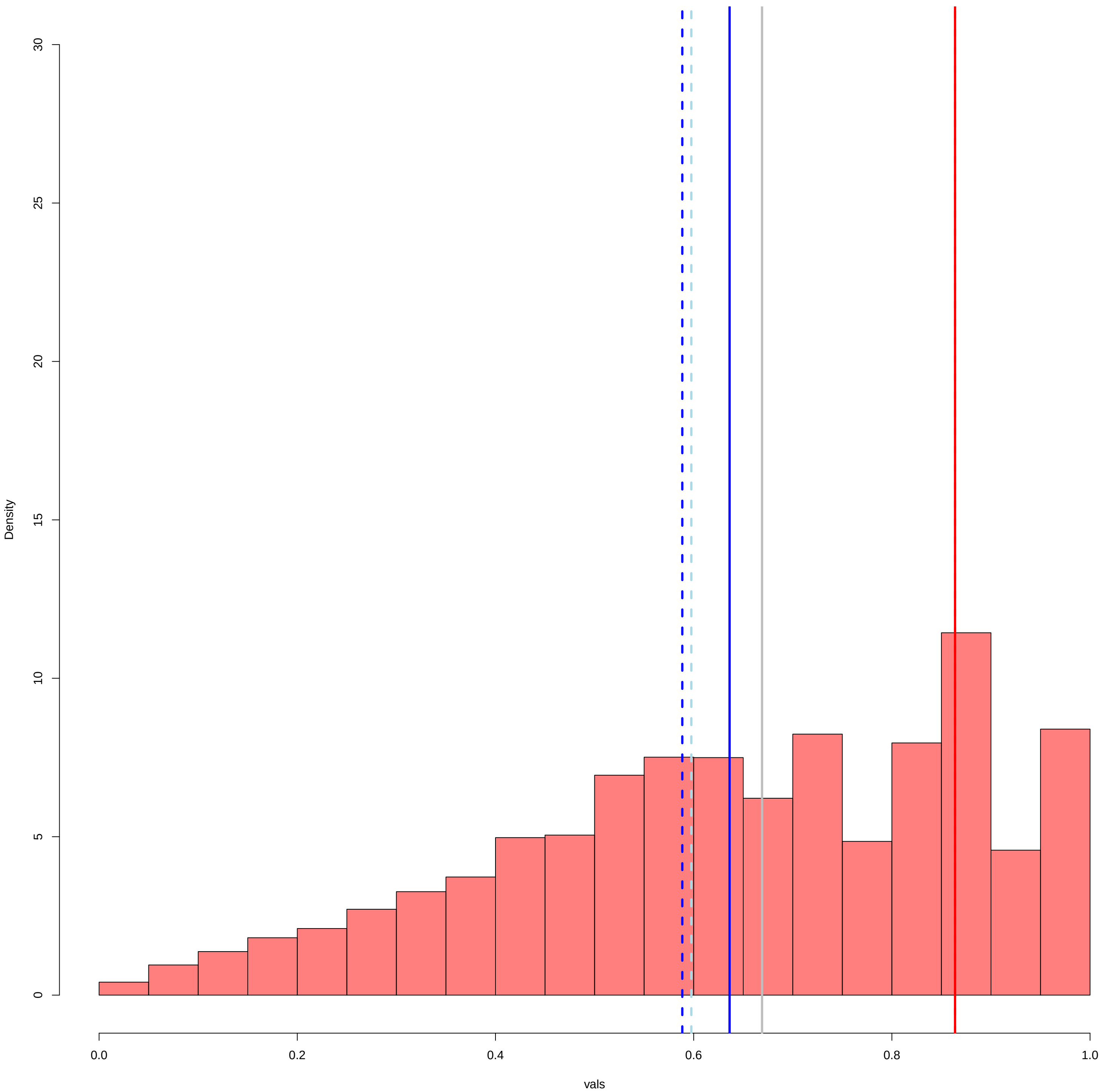
PCDH19: phyloP20way_mammalian_rankscore



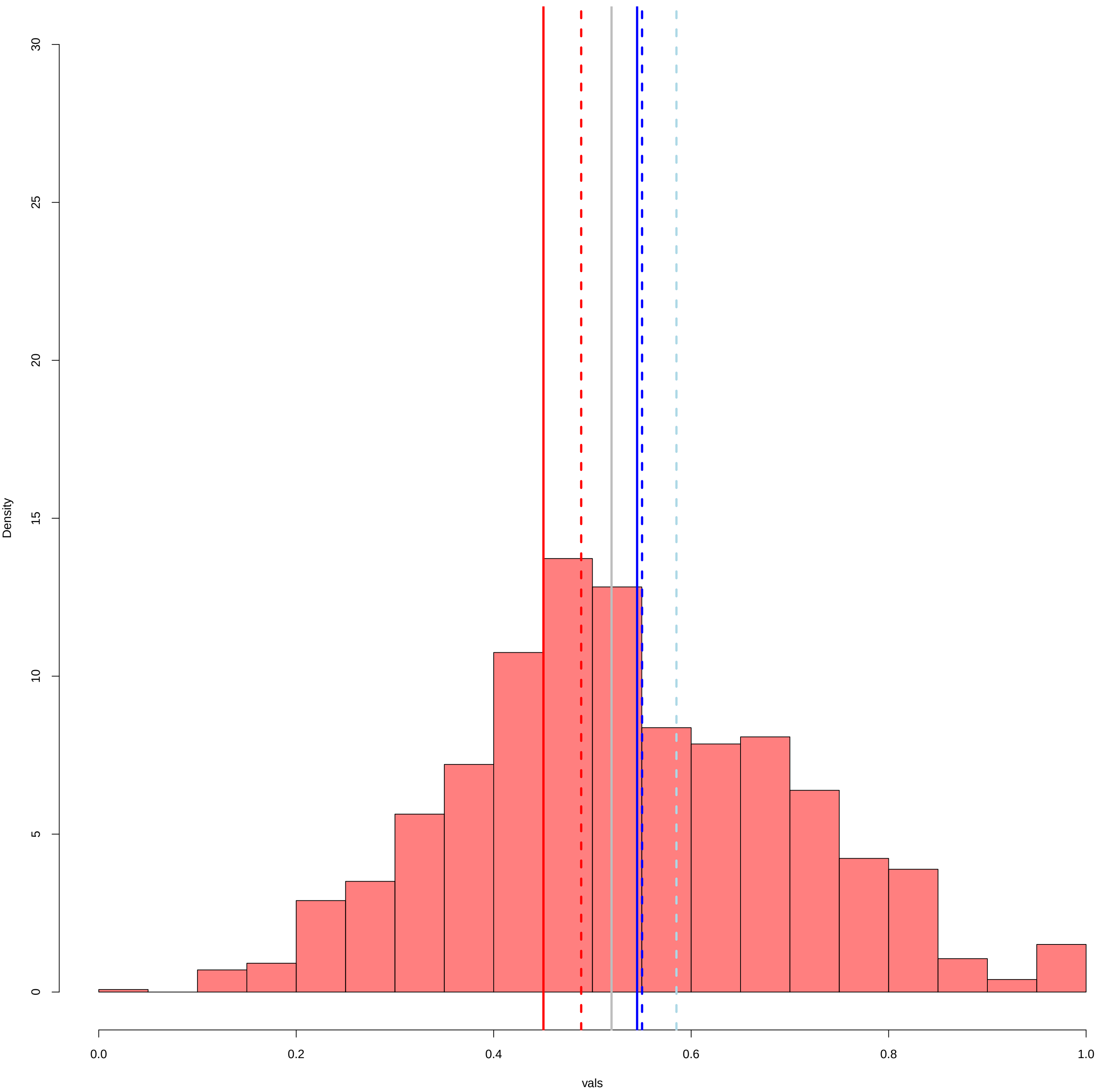
PCDH19: phastCons100way_vertebrate_rankscore



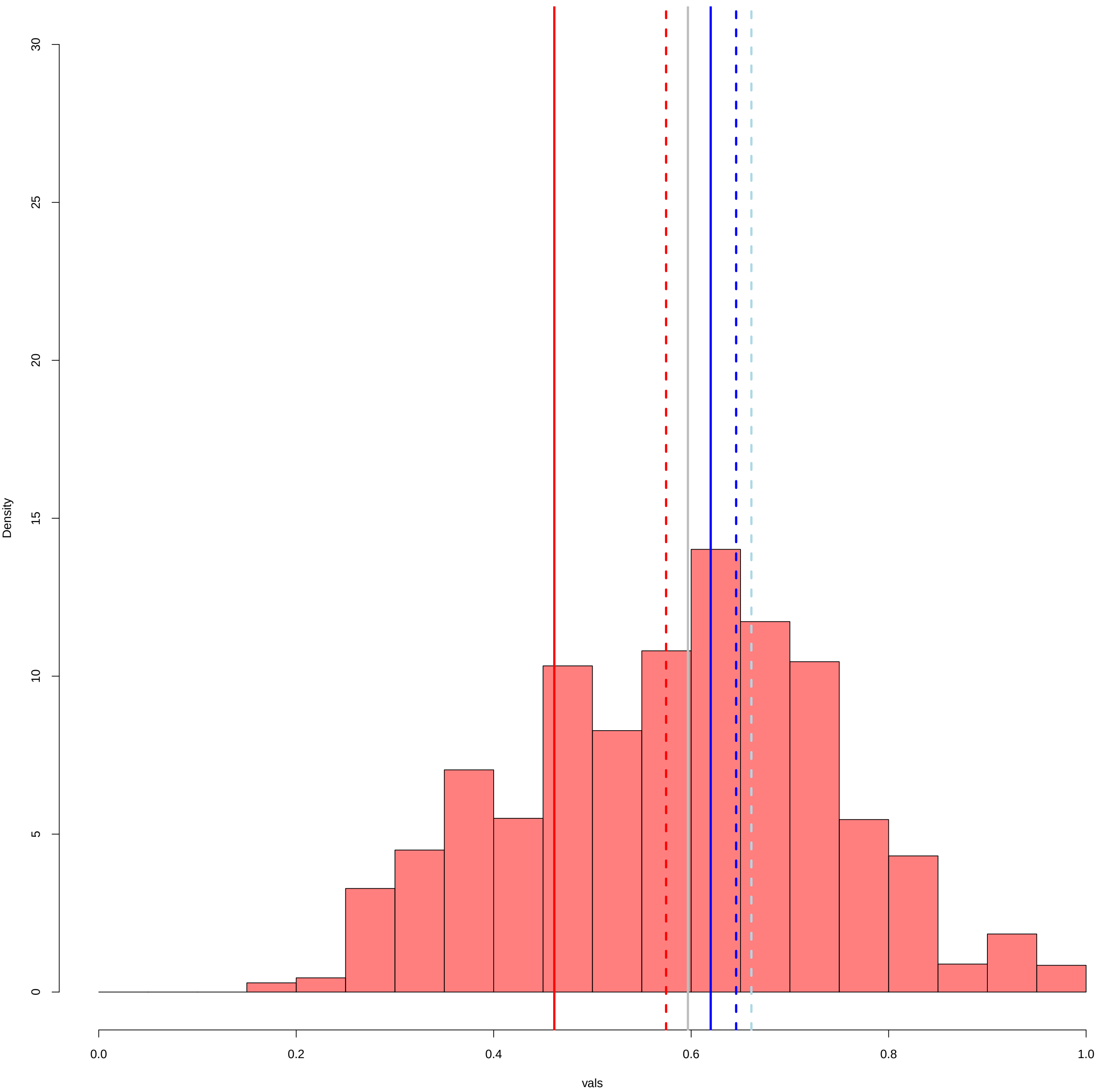
PCDH19: phyloP100way_vertebrate_rankscore



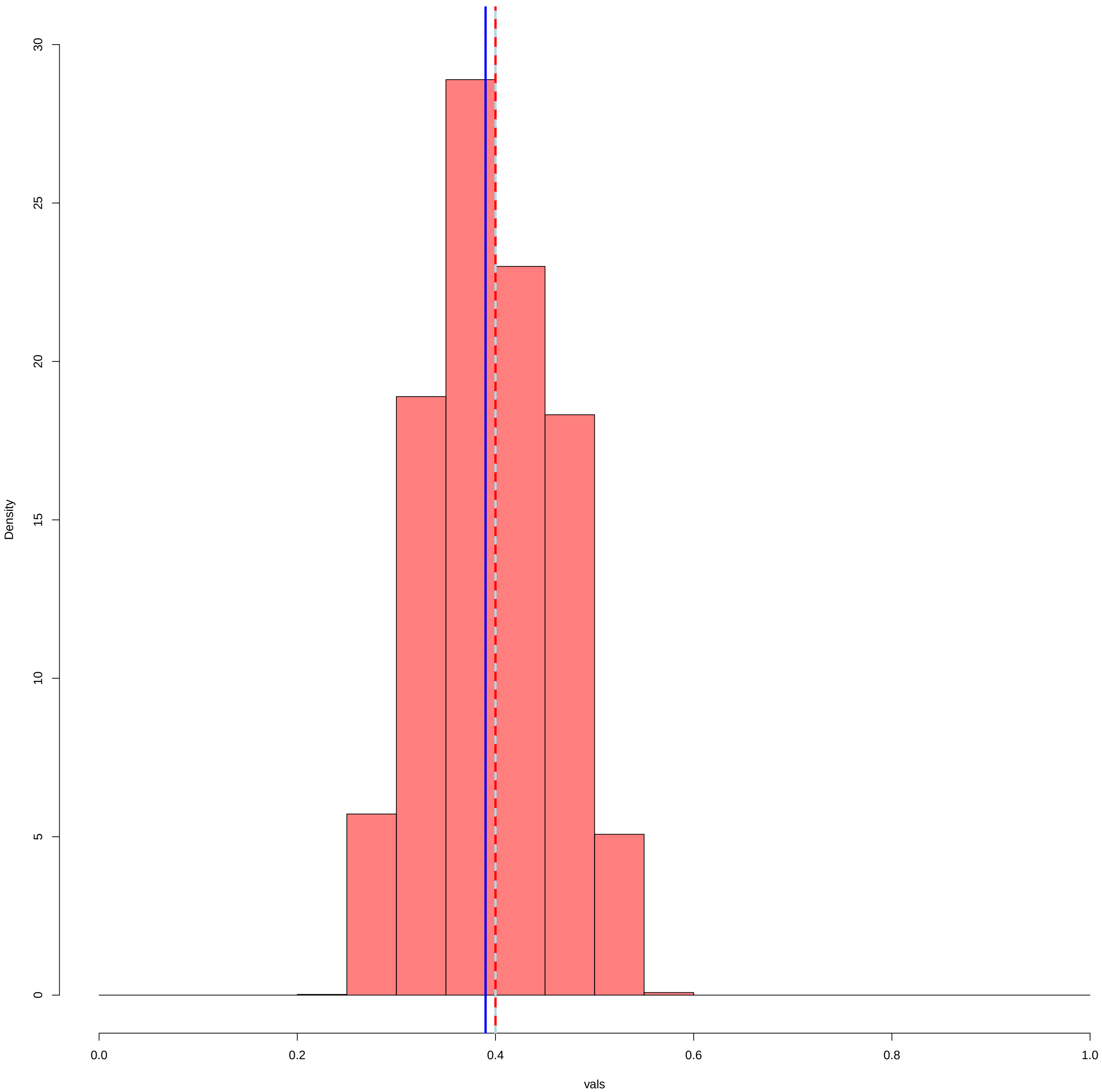
PCDH19: ExAC v1 MTR



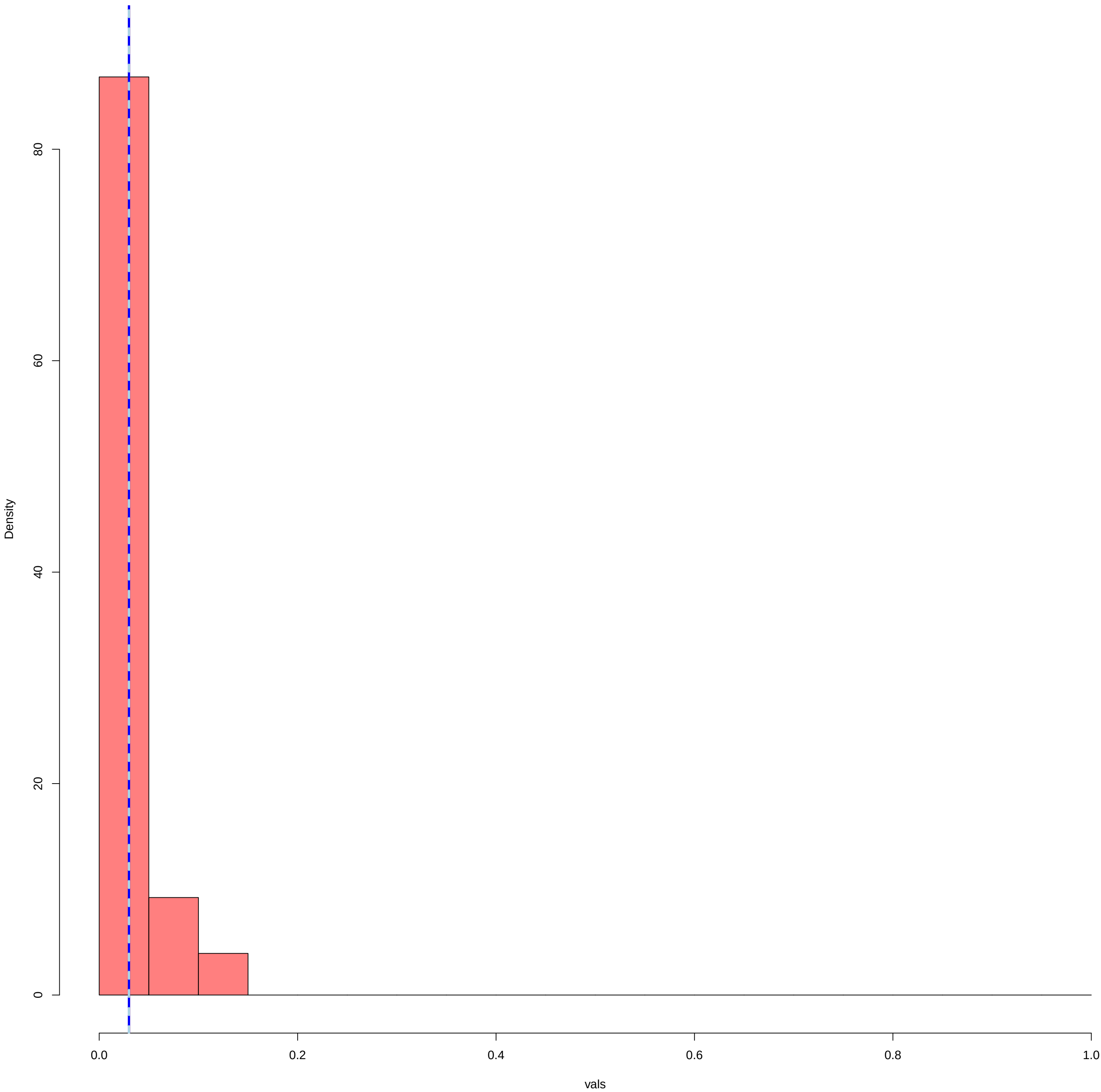
PCDH19: ExAC v2 & gnomAD MTR



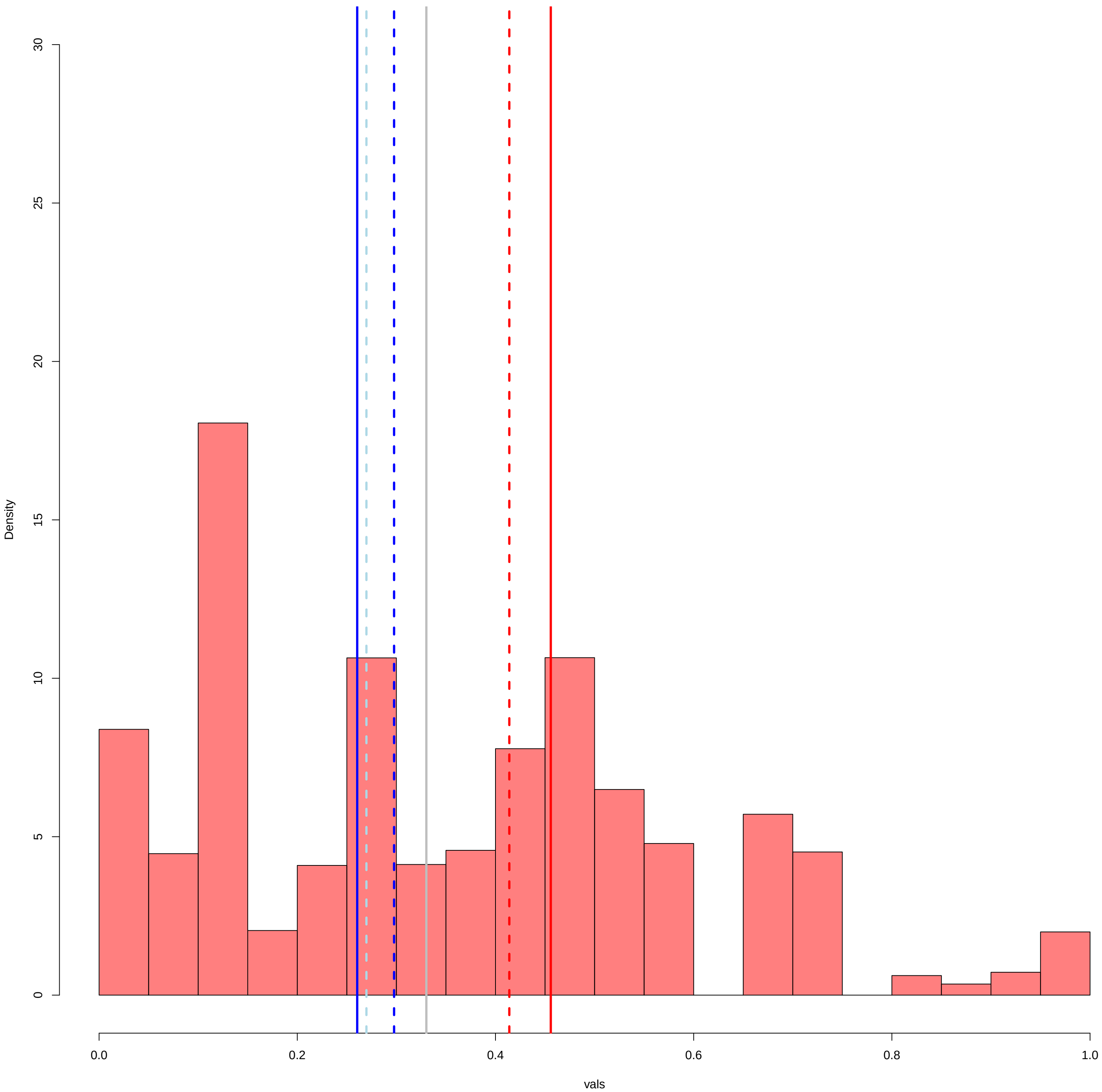
SCN1A: GC (Percent GC content in a window of ± 75 bp)



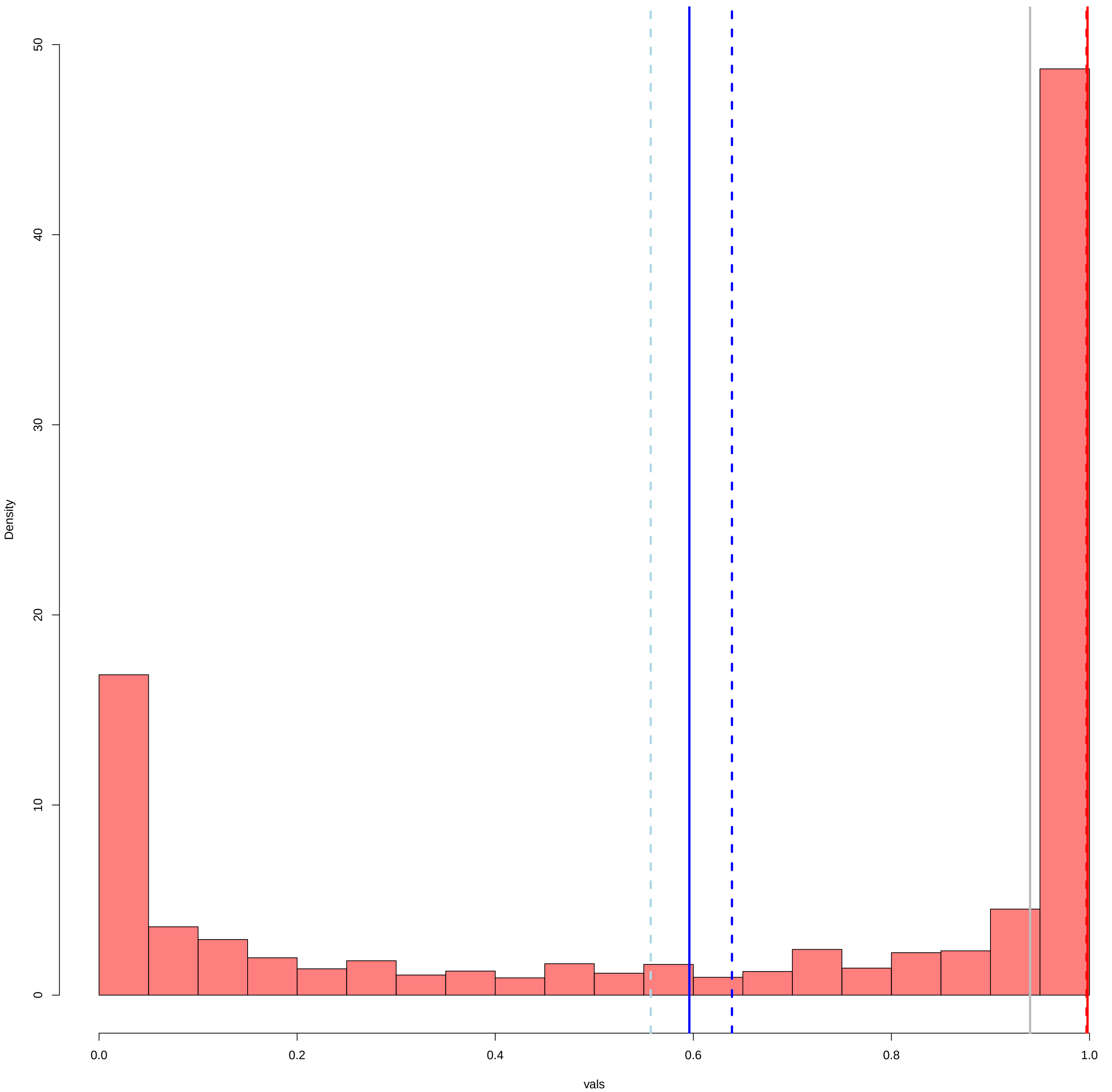
SCN1A: CpG (Percent CpG in a window of +/-75bp)



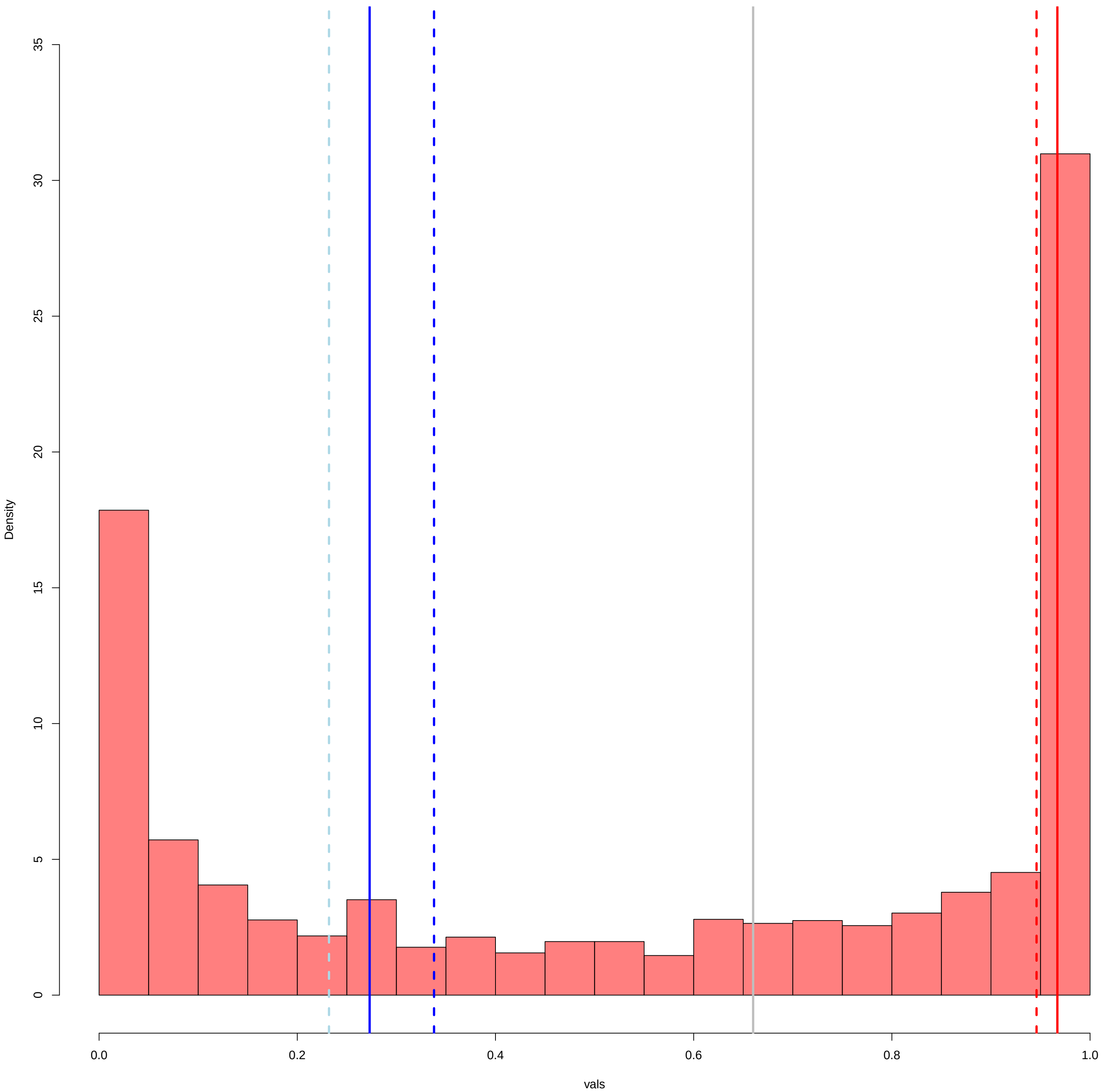
SCN1A: Grantham



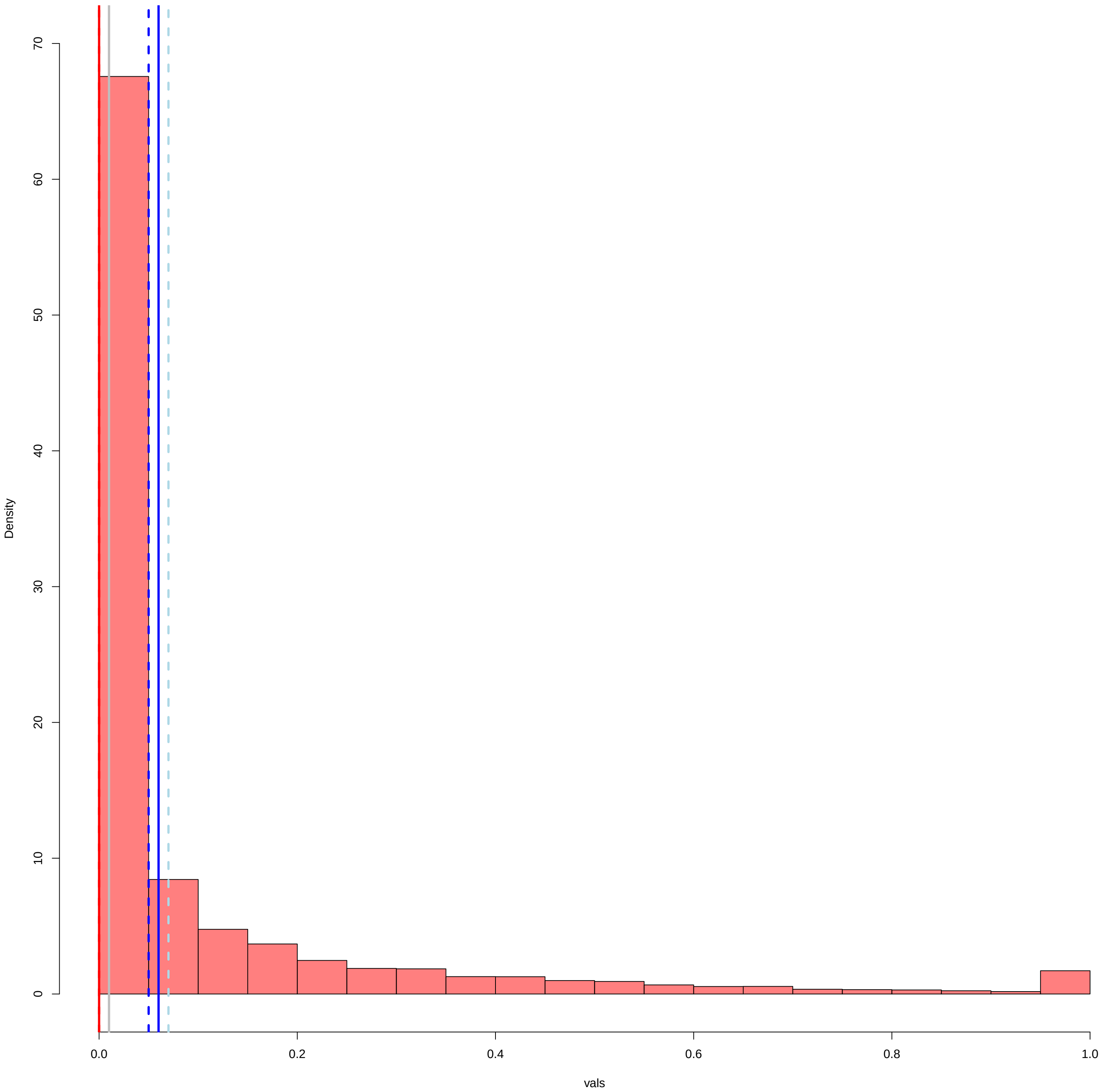
SCN1A: Hdiv quan



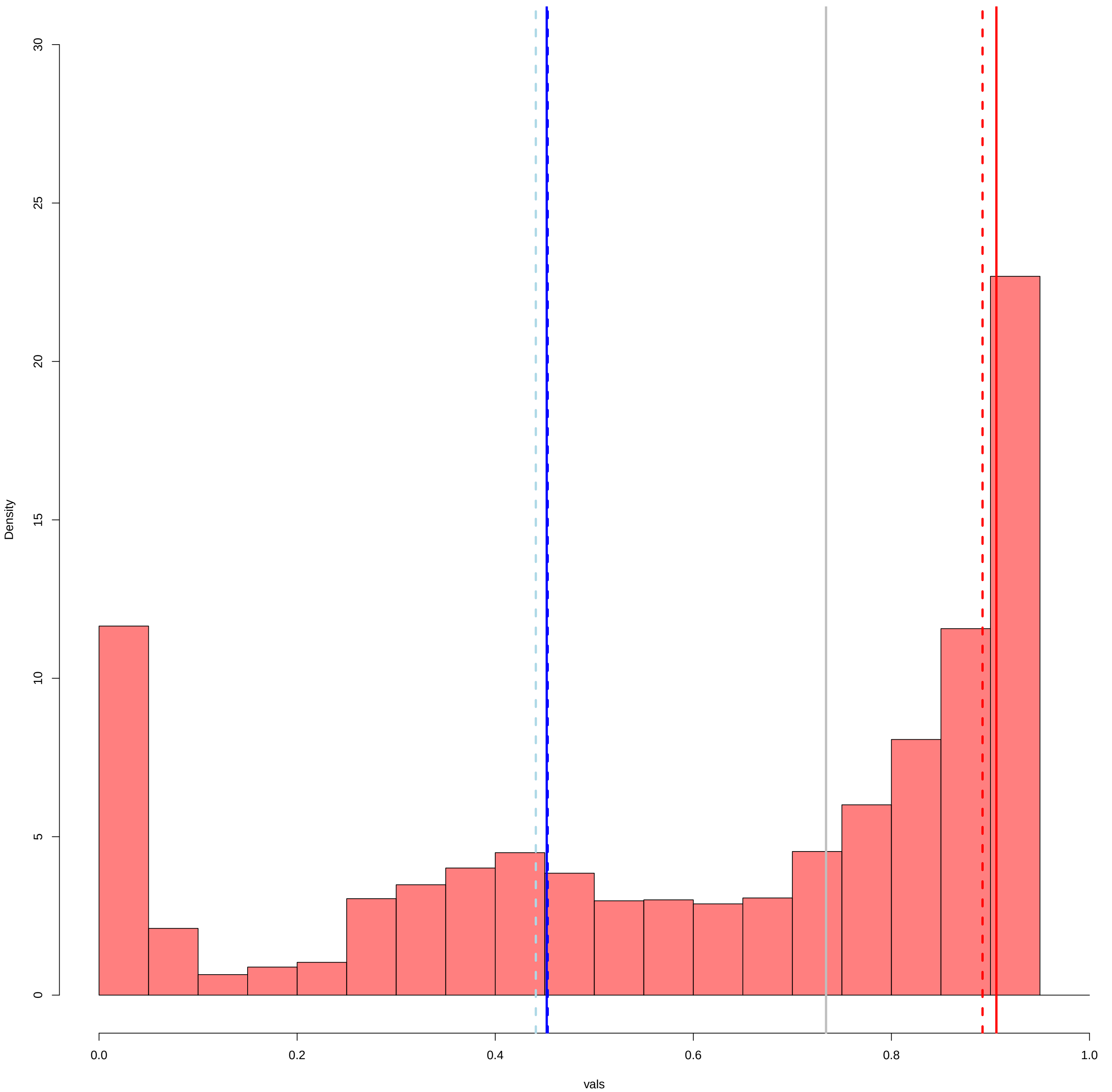
SCN1A: Hvar quan



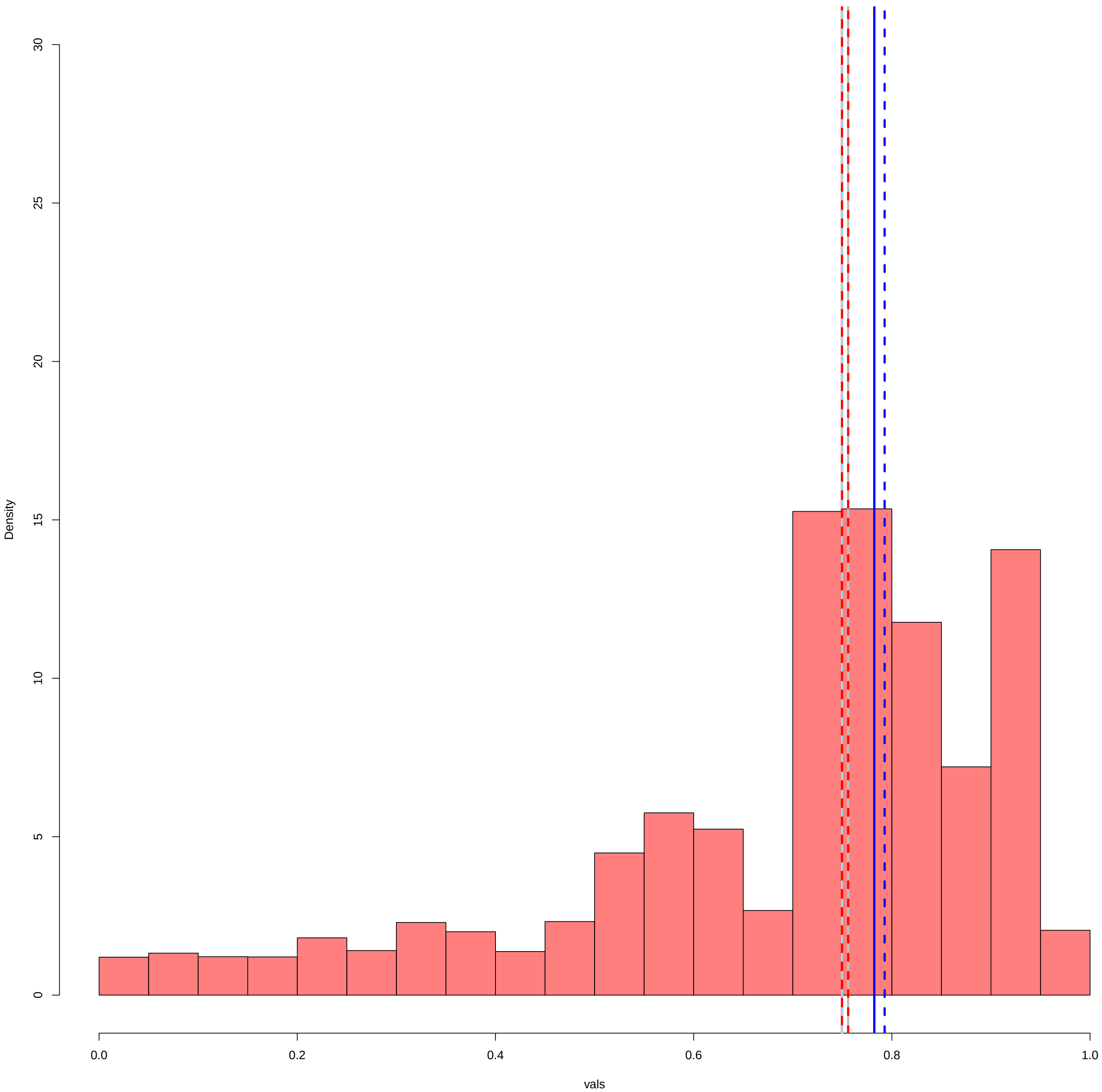
SCN1A: SIFT



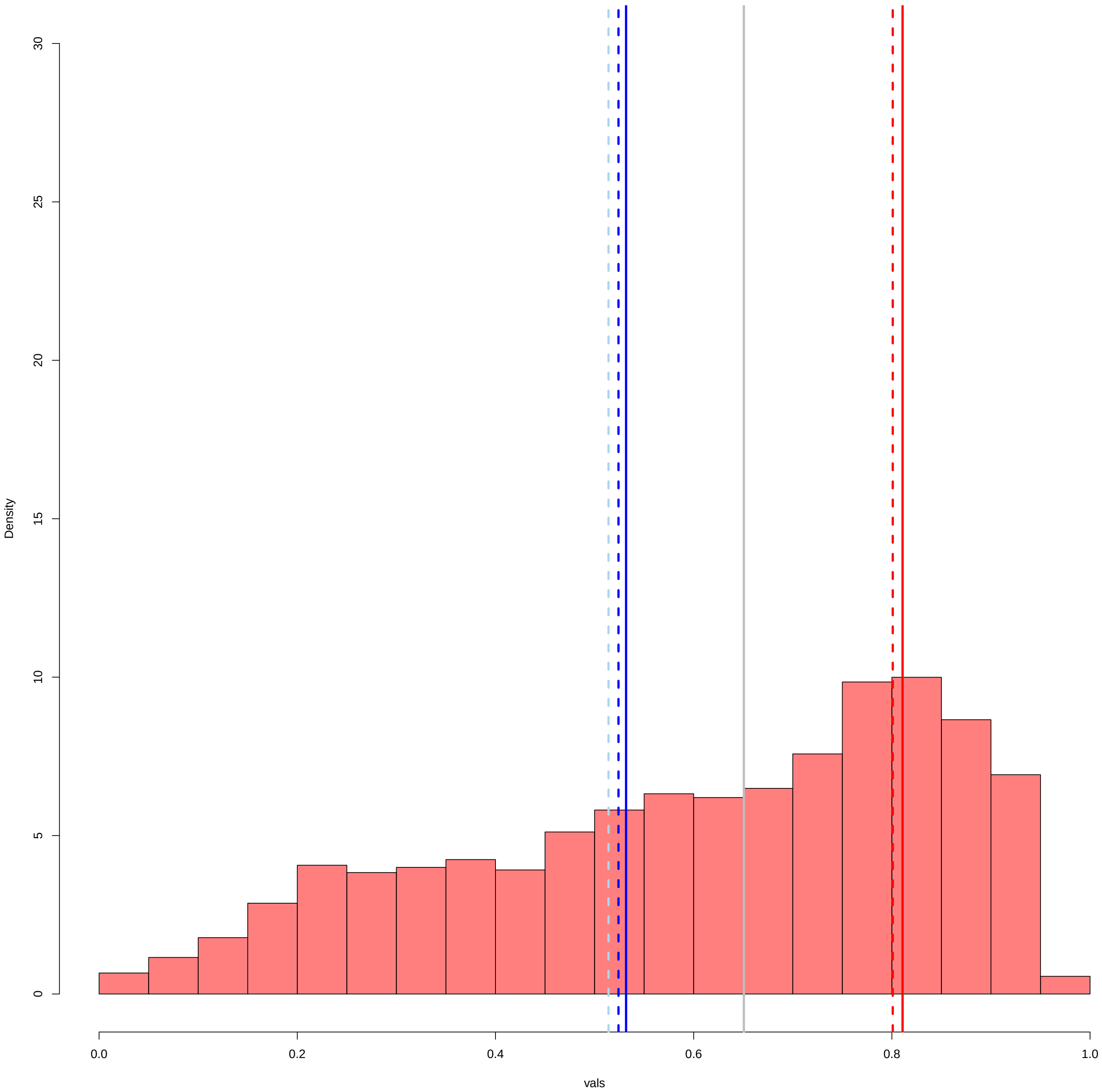
SCN1A: Condel



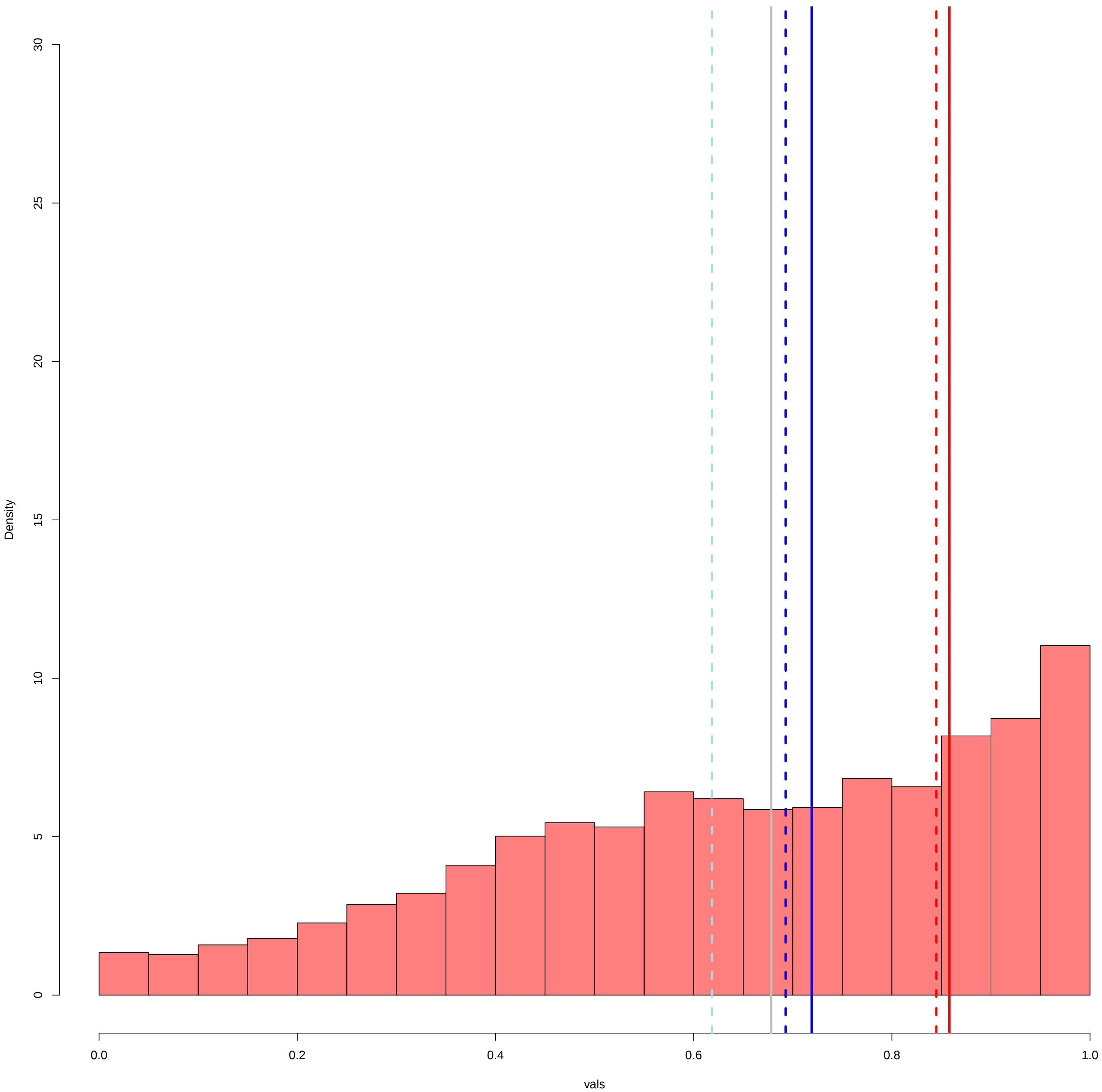
SCN1A: GERP++_RS_rankscore



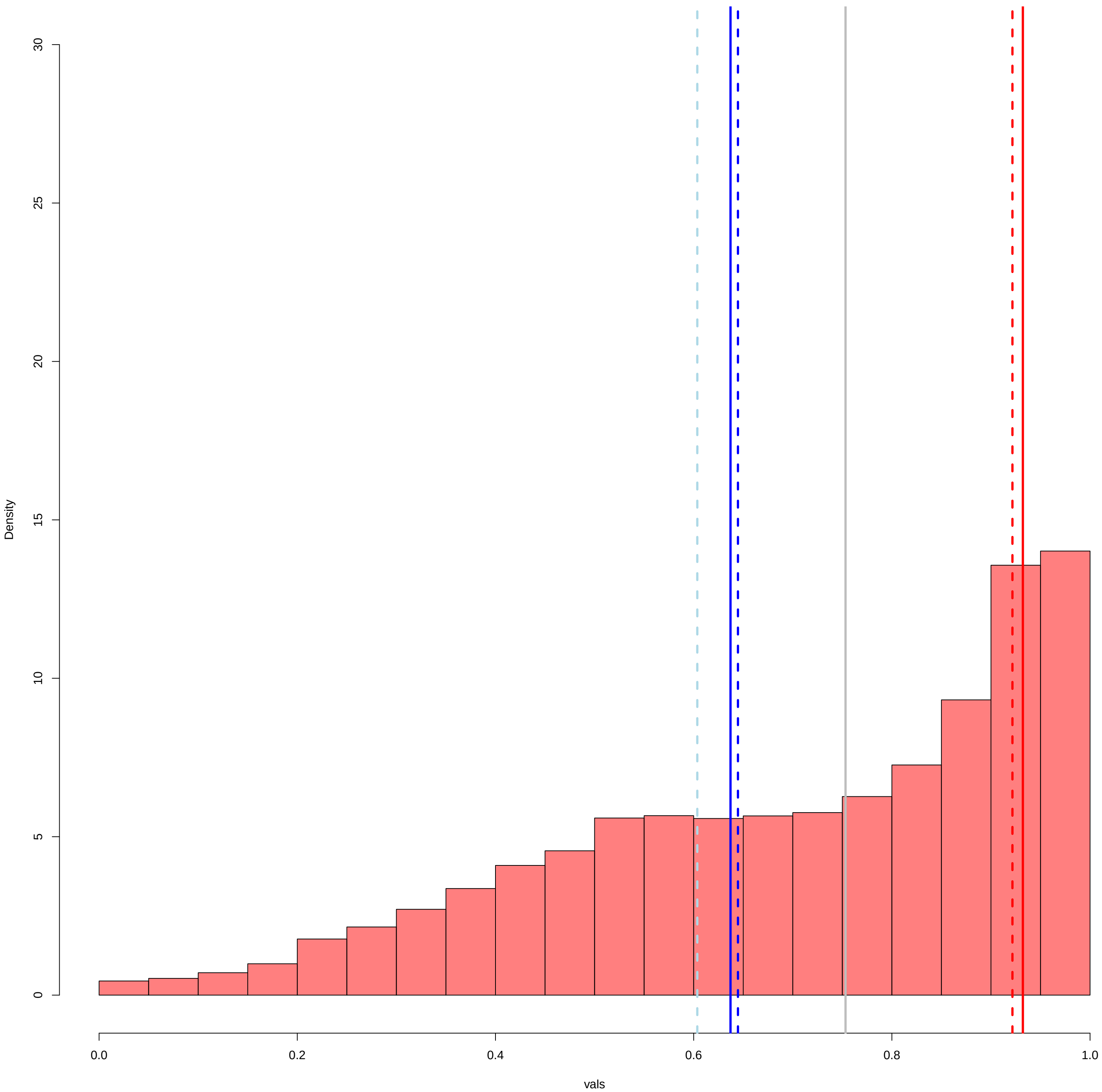
SCN1A: CADD_raw_rankscore



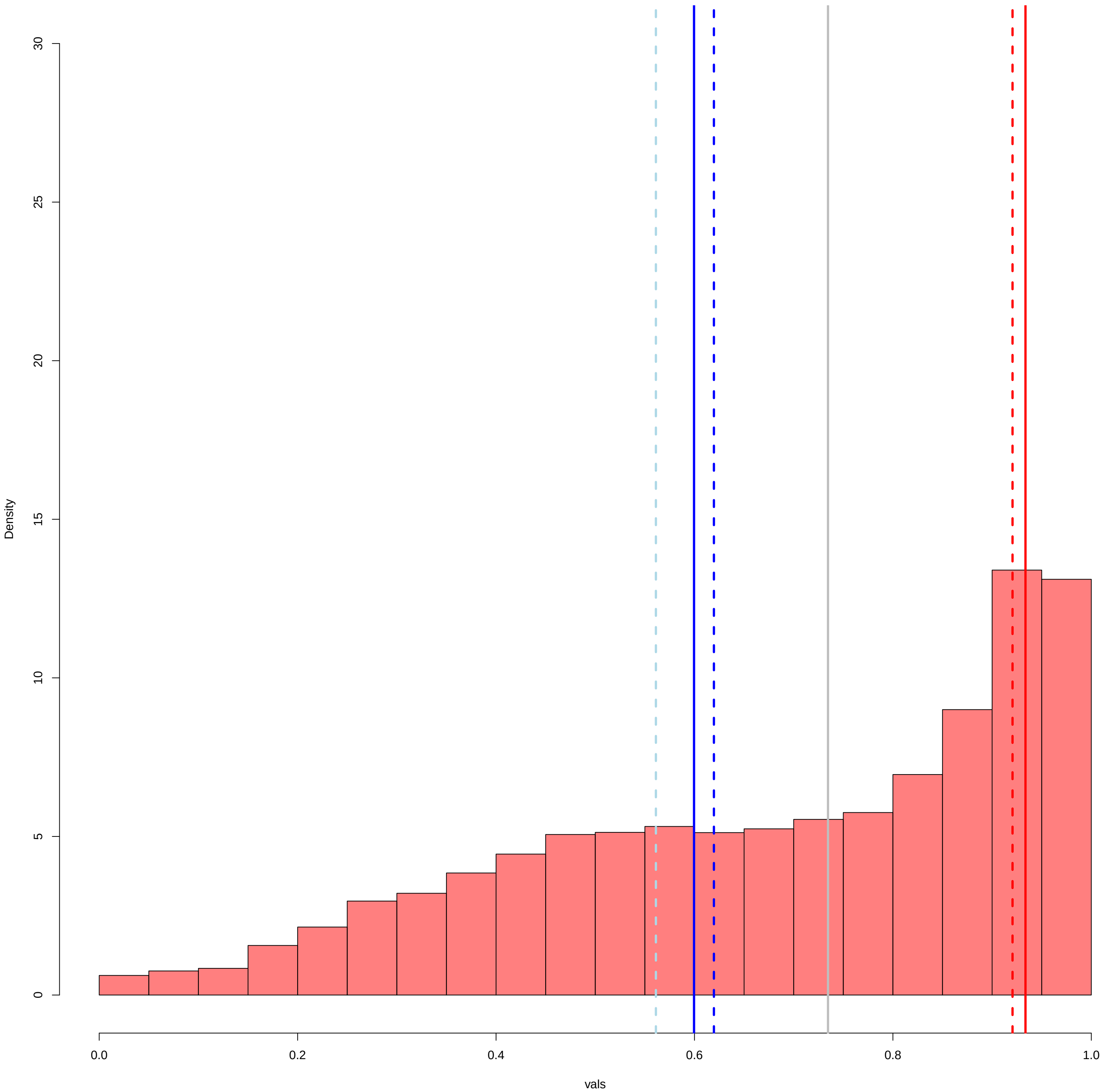
SCN1A: DANN_rankscore



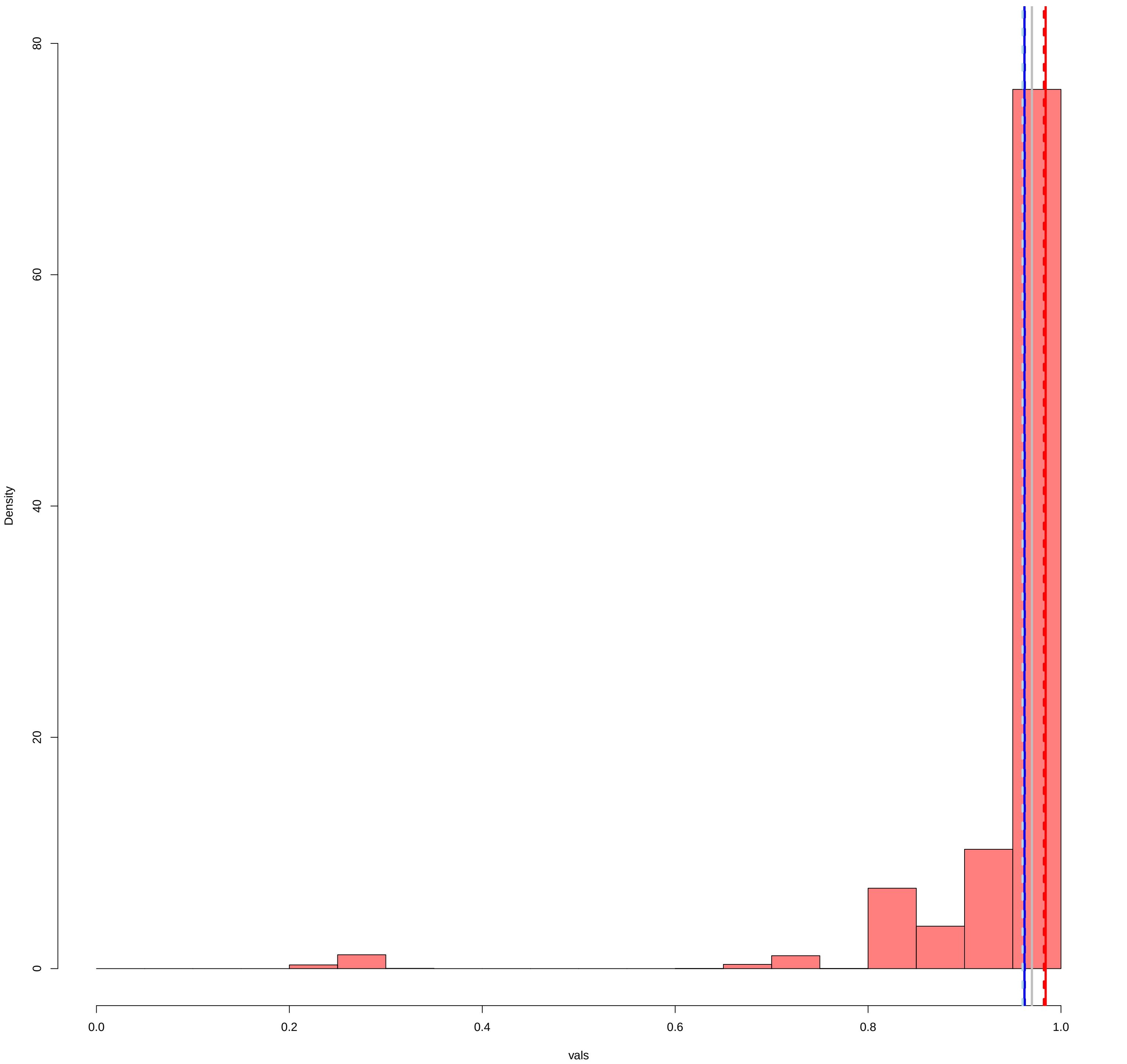
SCN1A: Eigen-PC-raw_rankscore



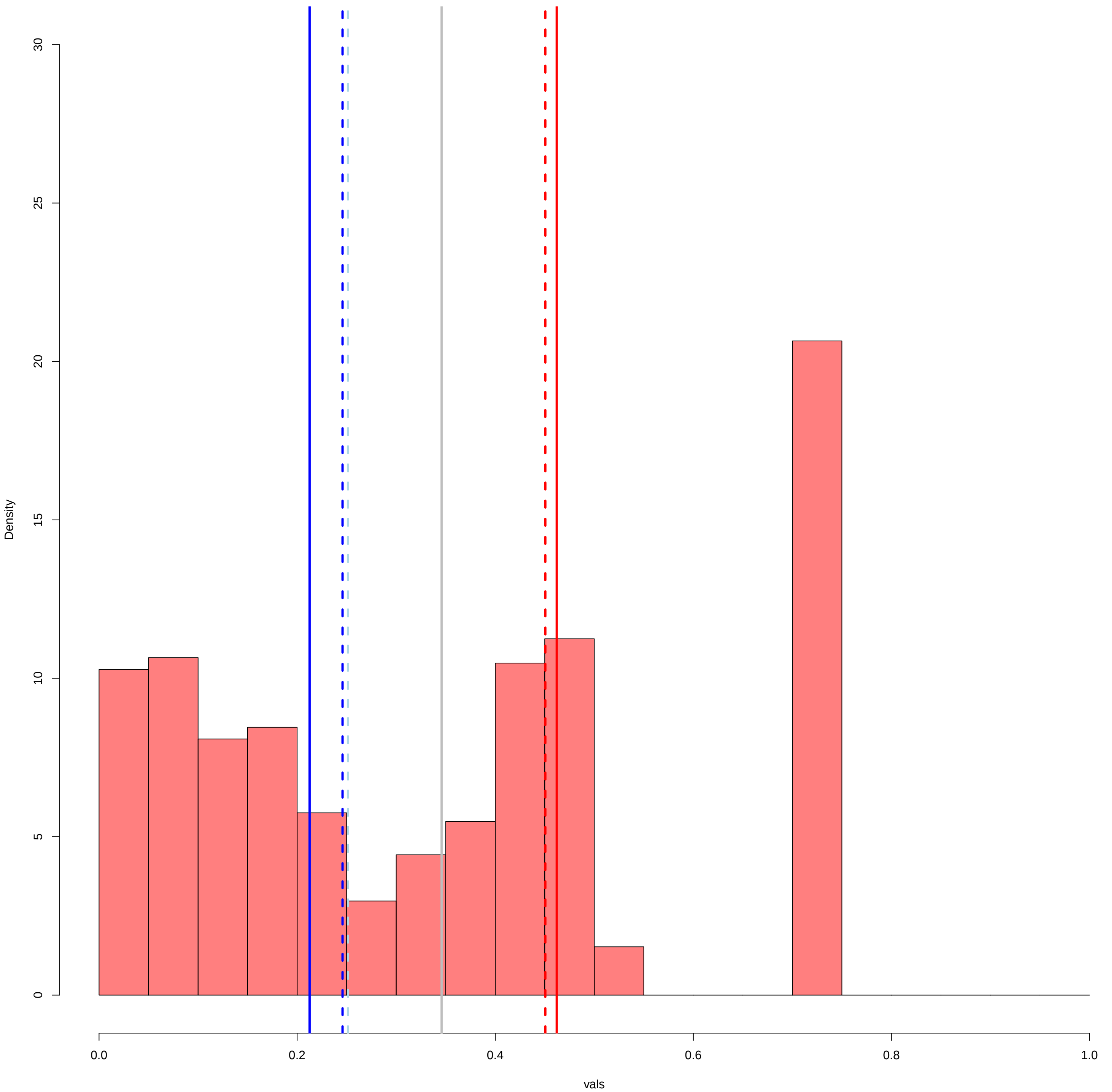
SCN1A: Eigen-row_rankscore



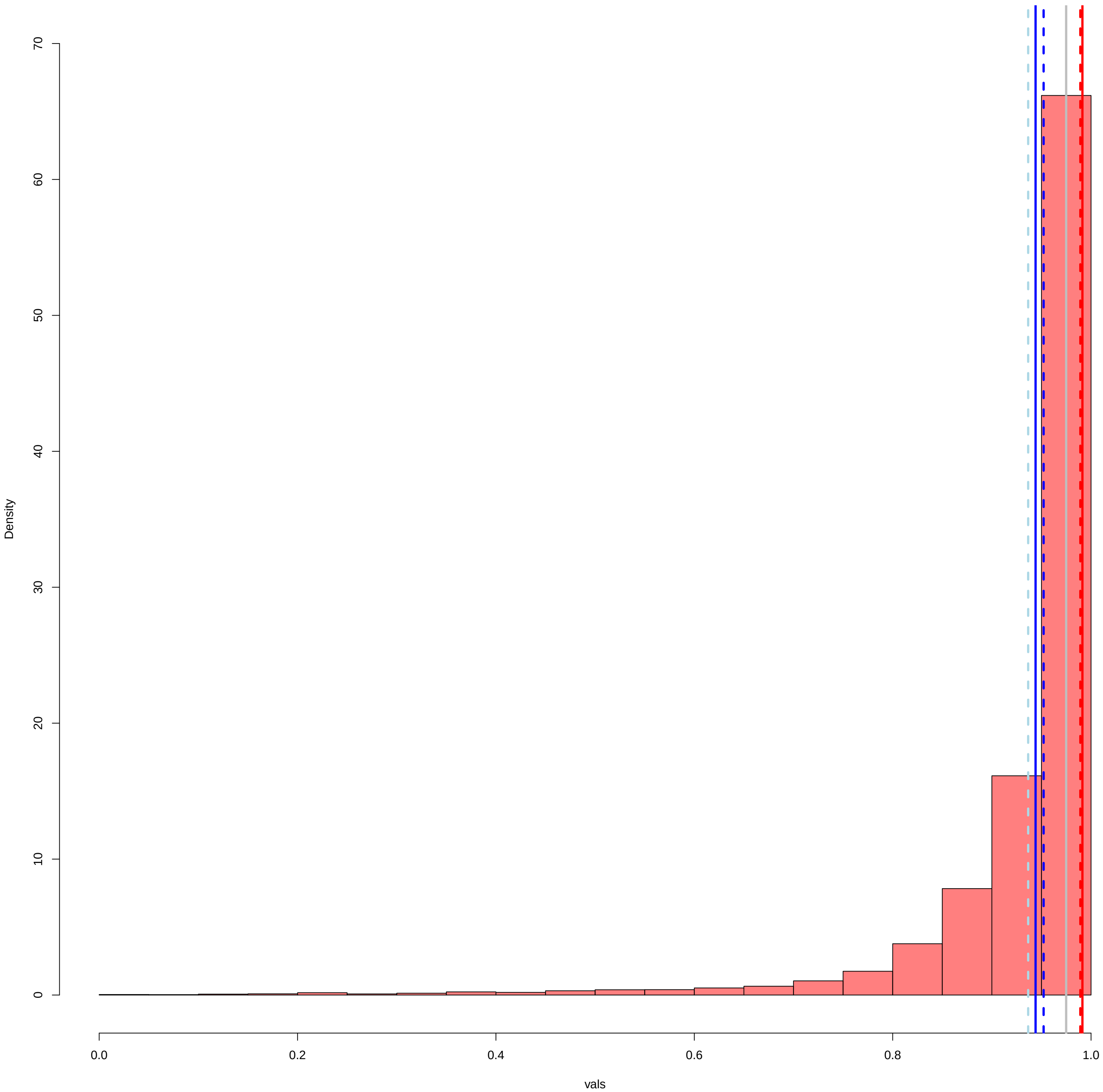
SCN1A: FATHMM_converted_rankscore



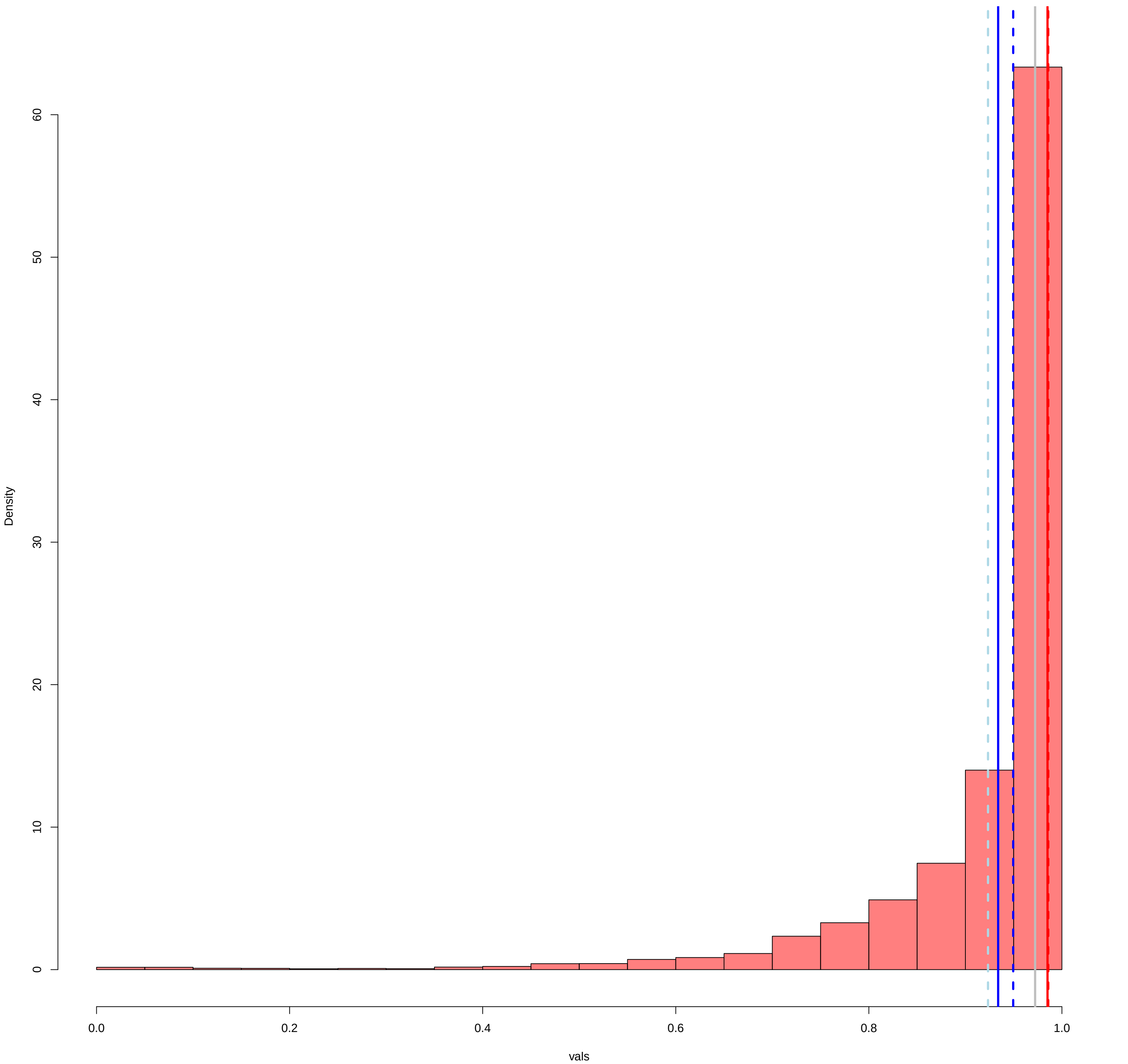
SCN1A: GenoCanyon_score_rankscore



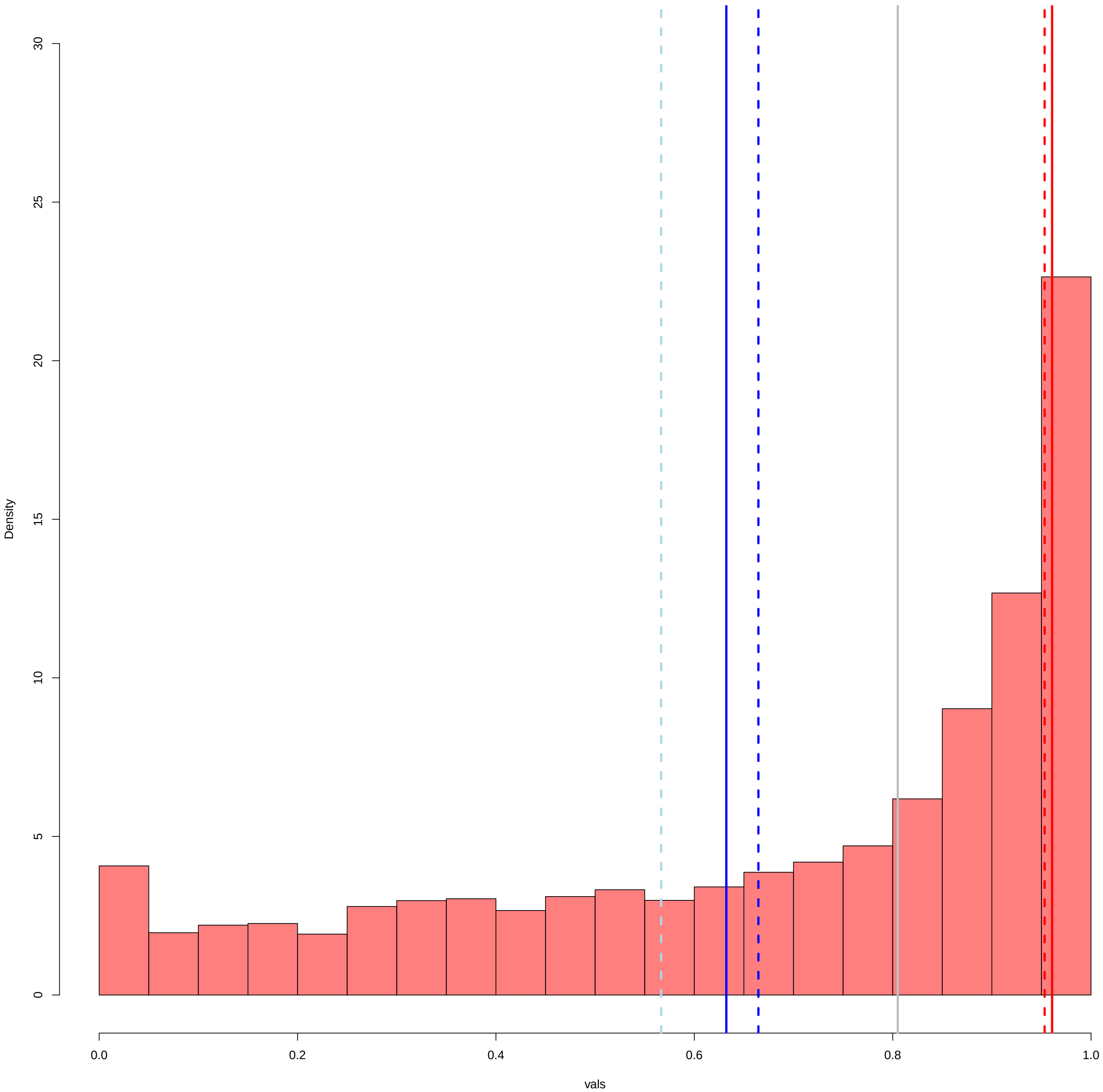
SCN1A: MetaLR_rankscore



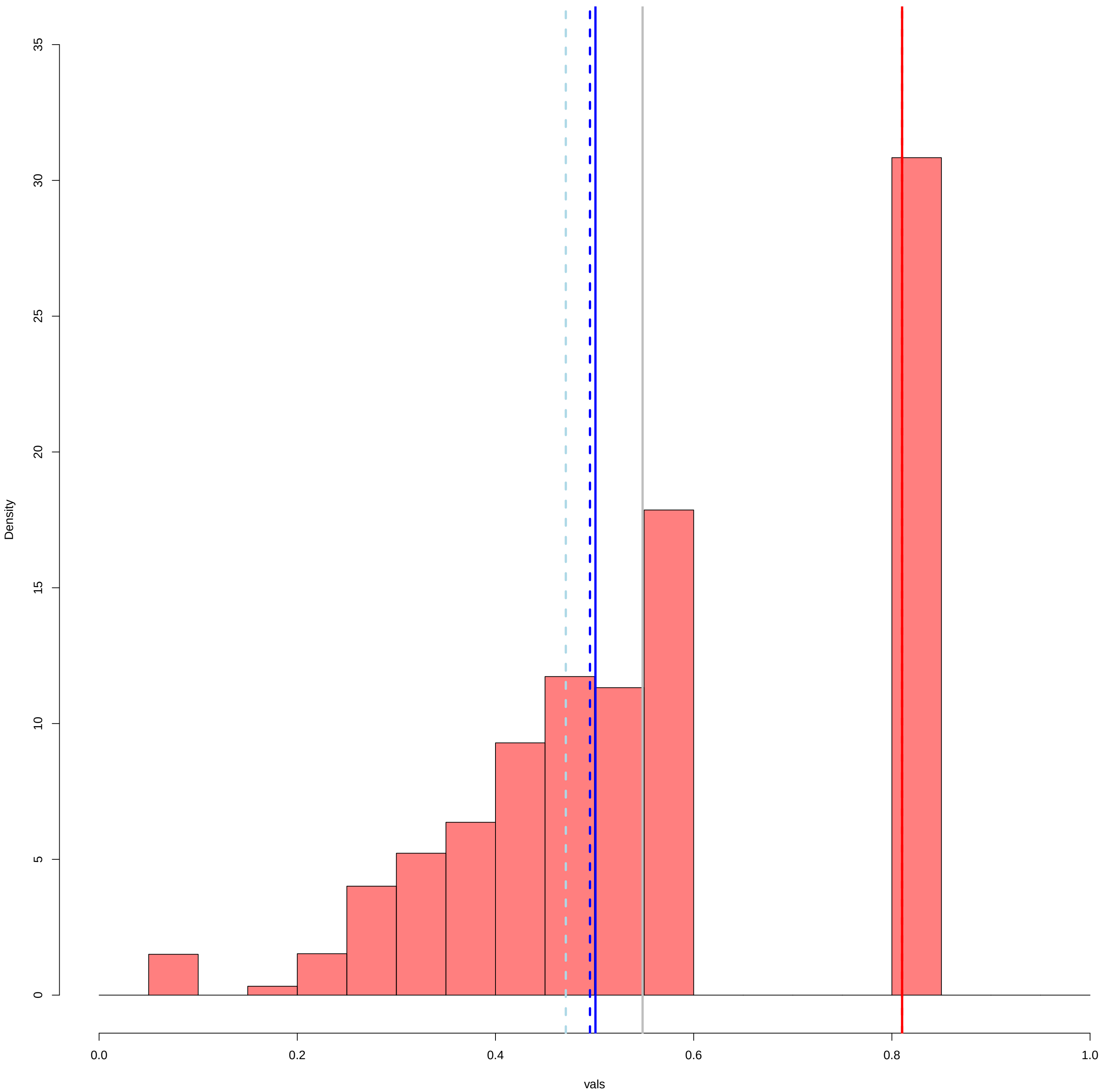
SCN1A: MetaSVM_rankscore



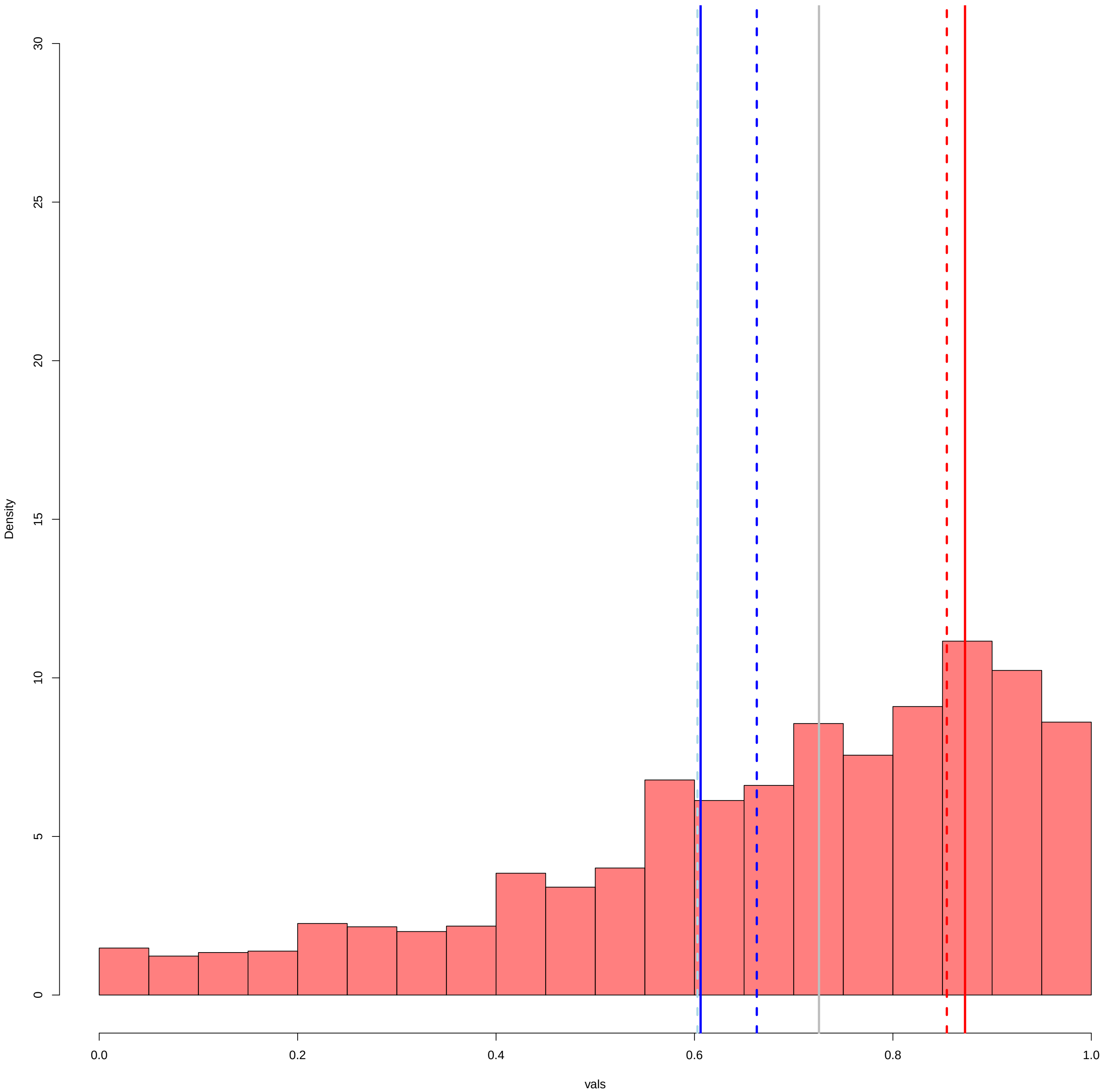
SCN1A: MutationAssessor_score_rankscore



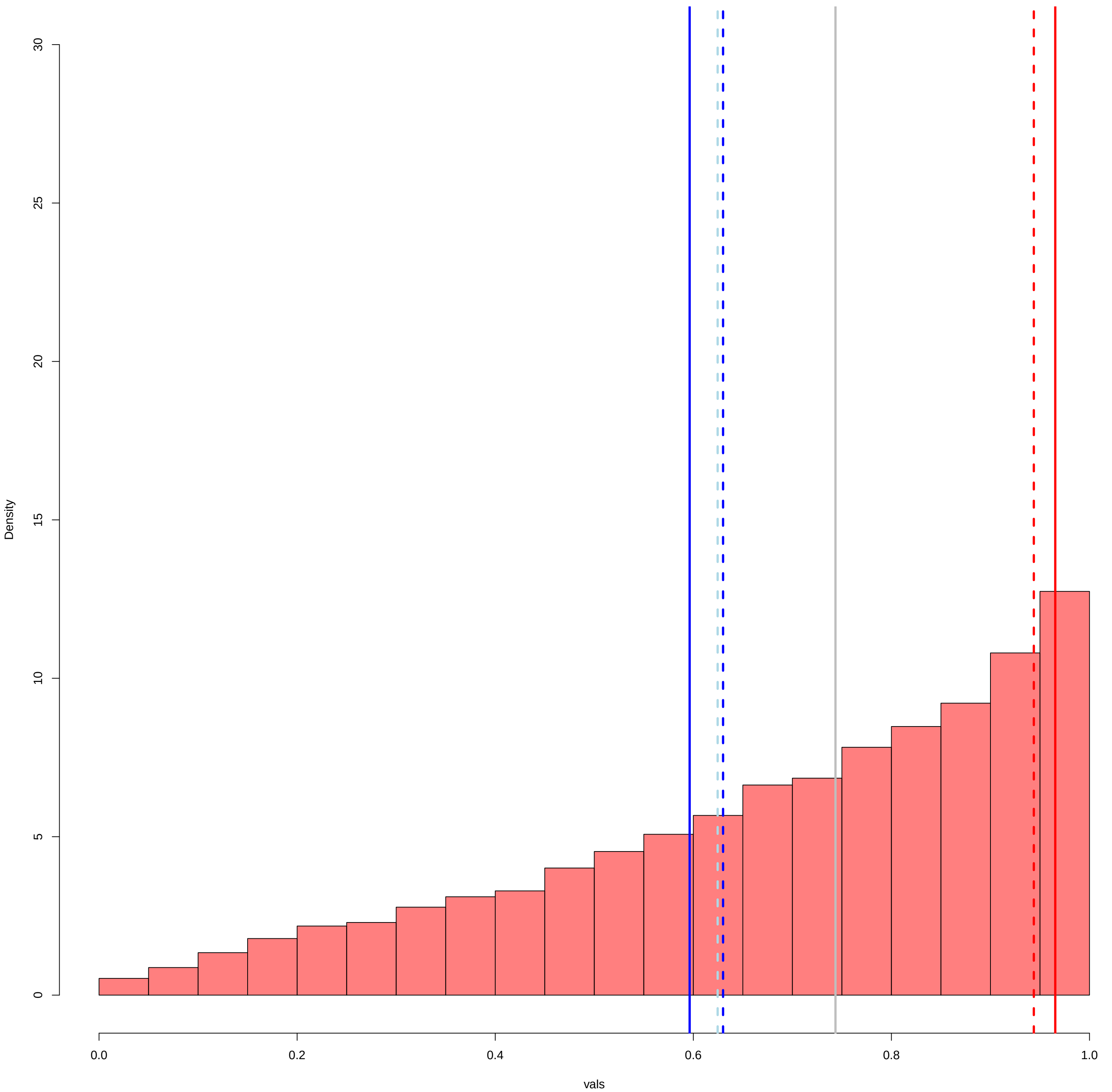
SCN1A: MutationTaster_converted_rankscore



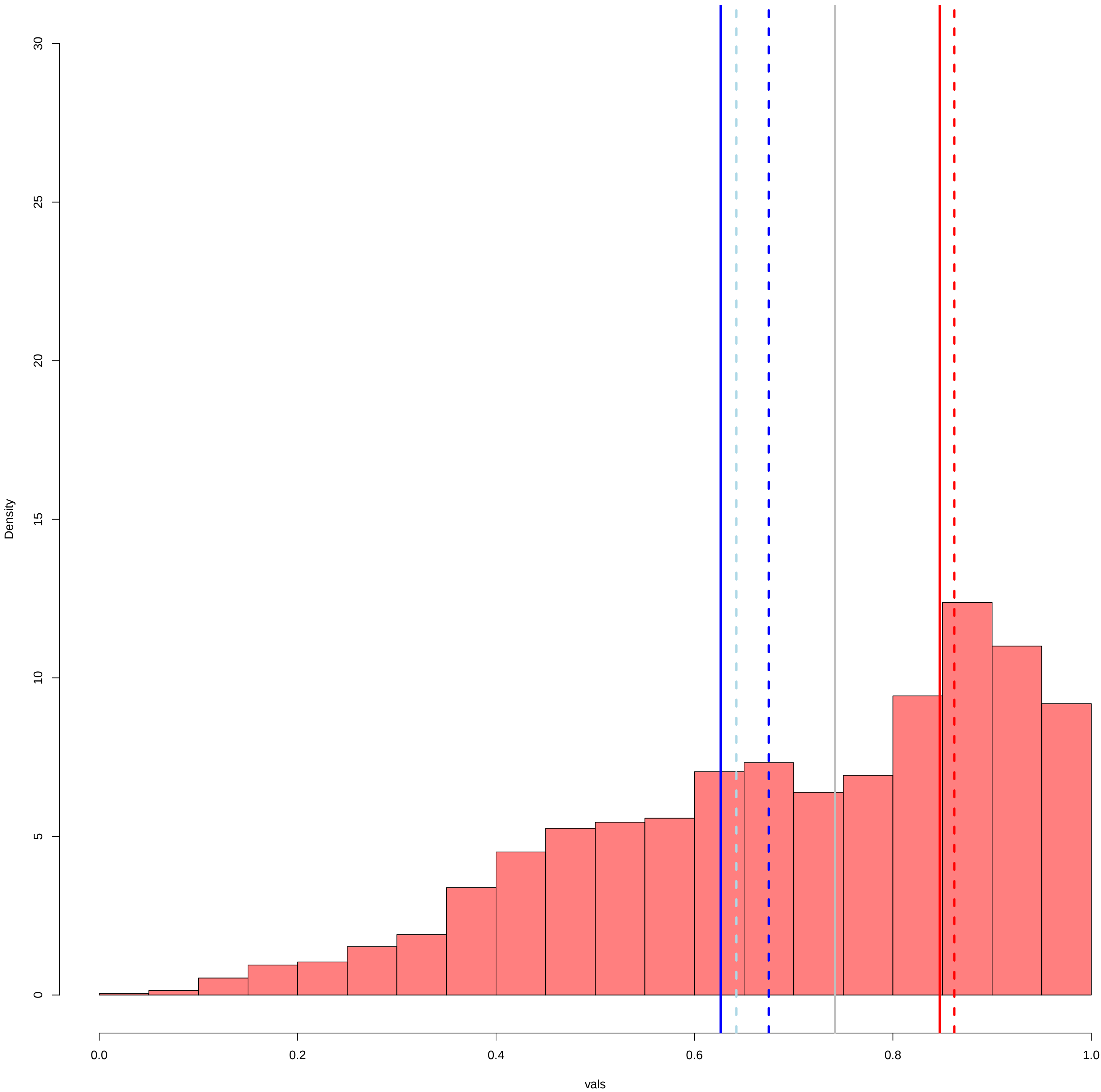
SCN1A: PROVEAN_converted_rankscore



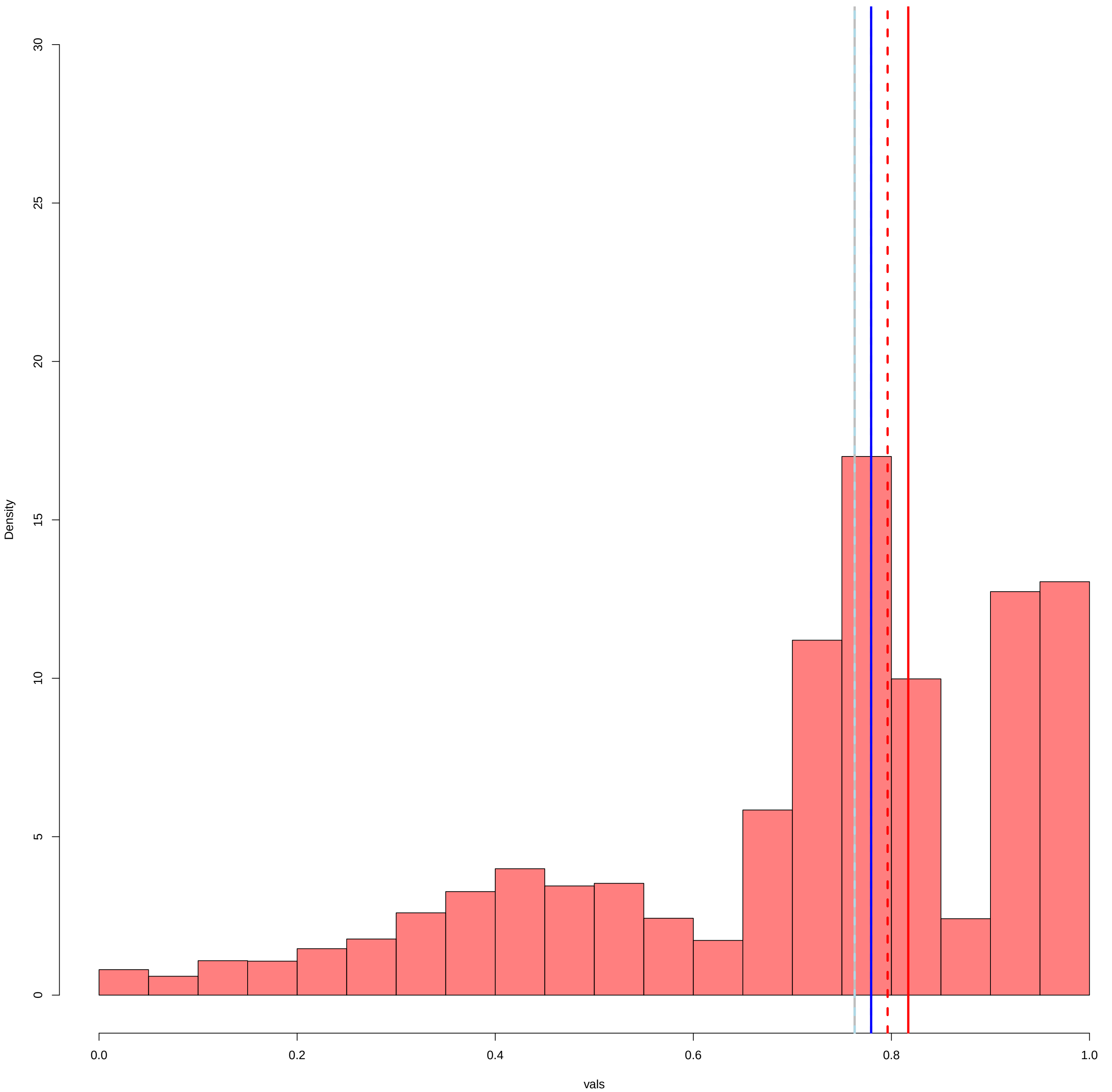
SCN1A: VEST3_rankscore



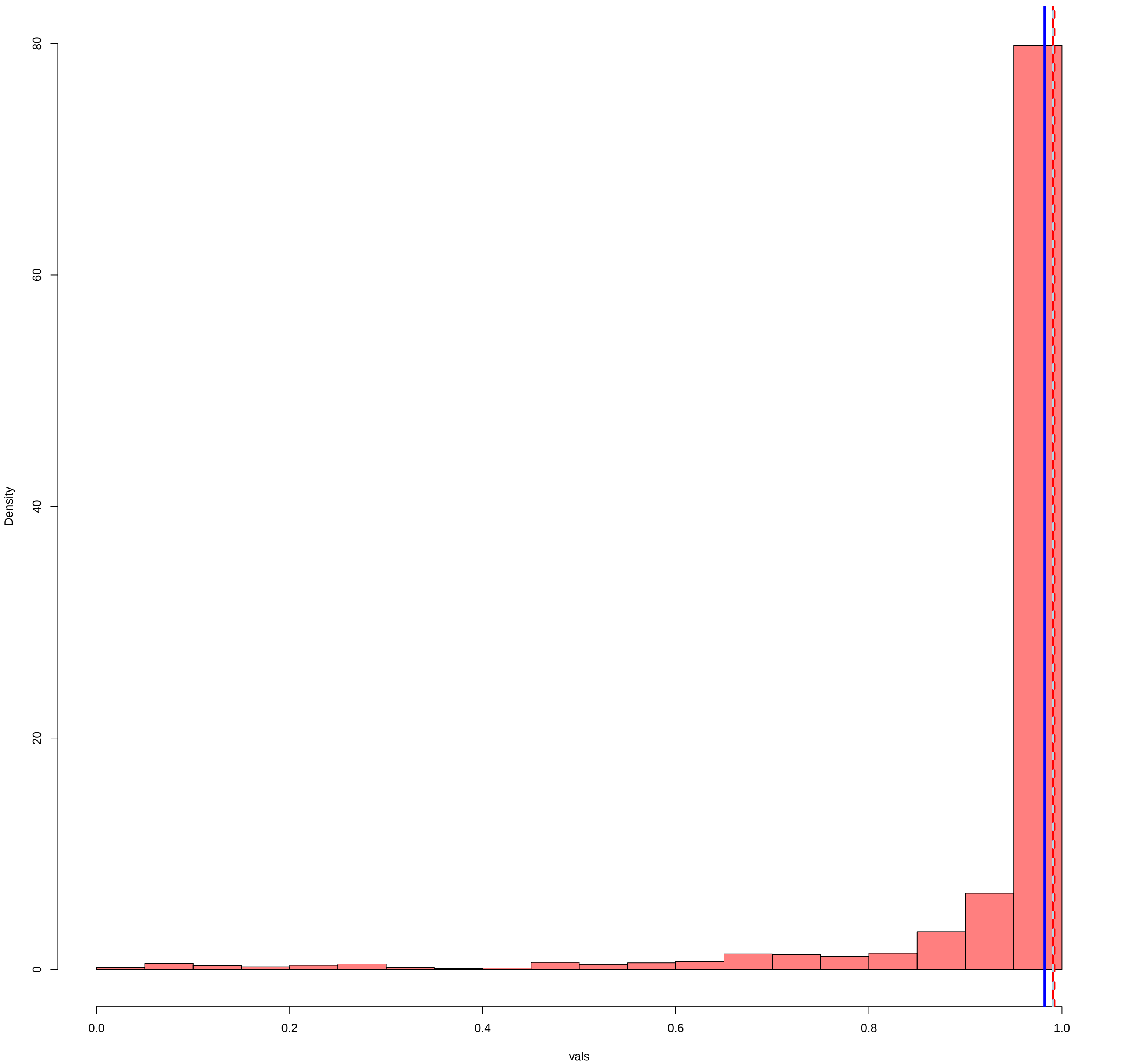
SCN1A: fathmm-MKL_coding_rankscore



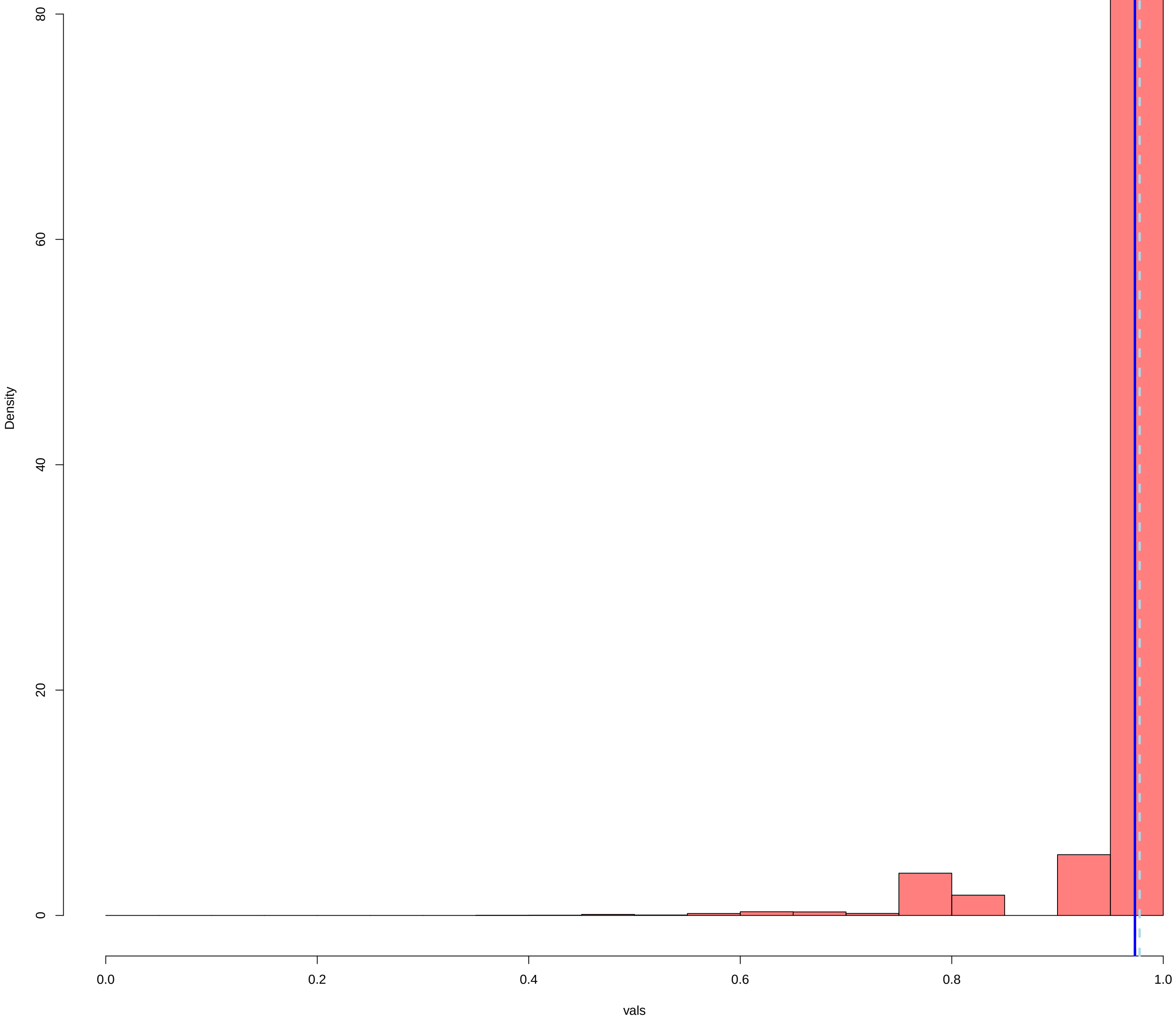
SCN1A: SiPhy_29way_logOdds_rankscore



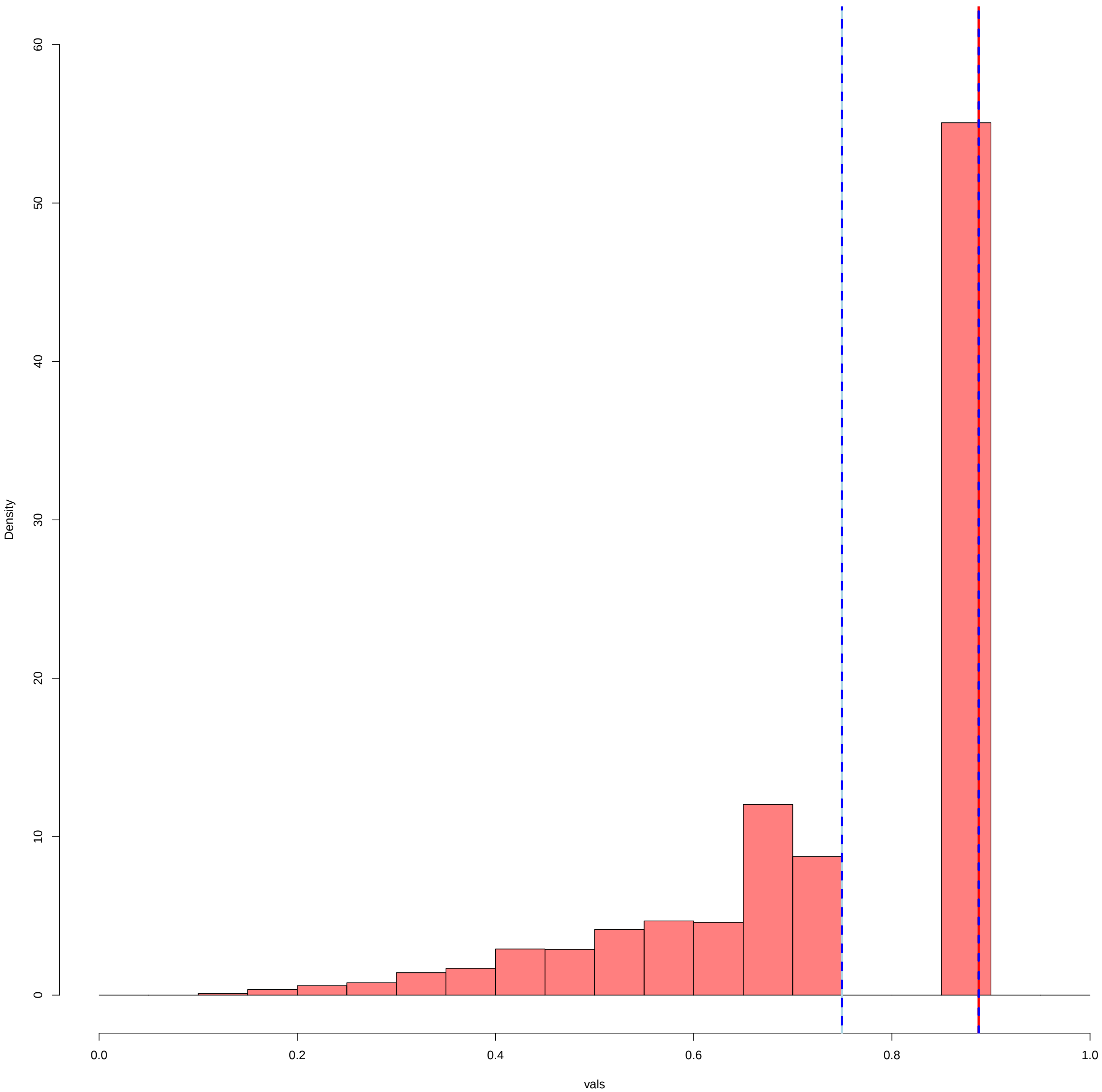
SCN1A: priPhCons



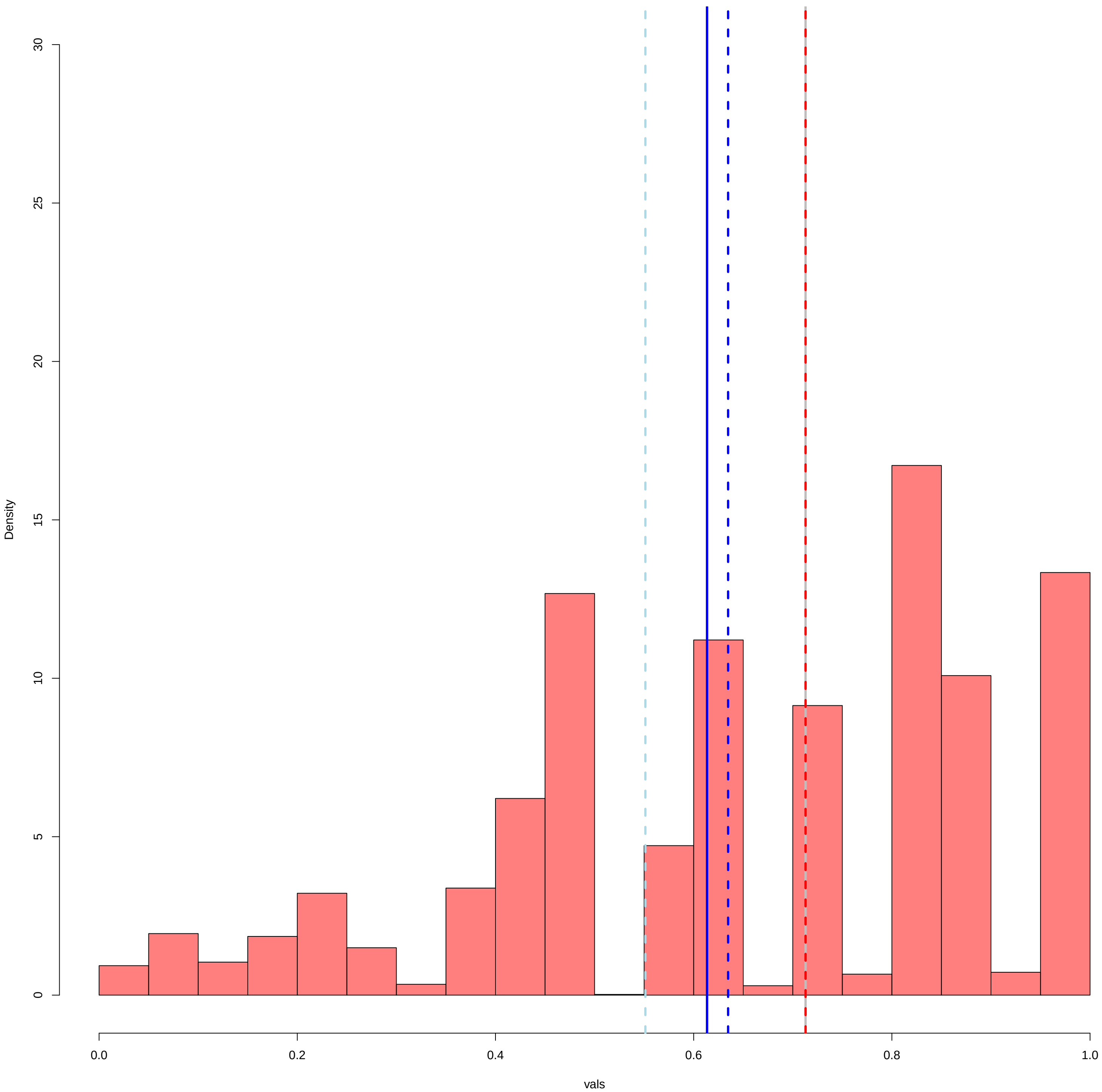
SCN1A: priPhyloP



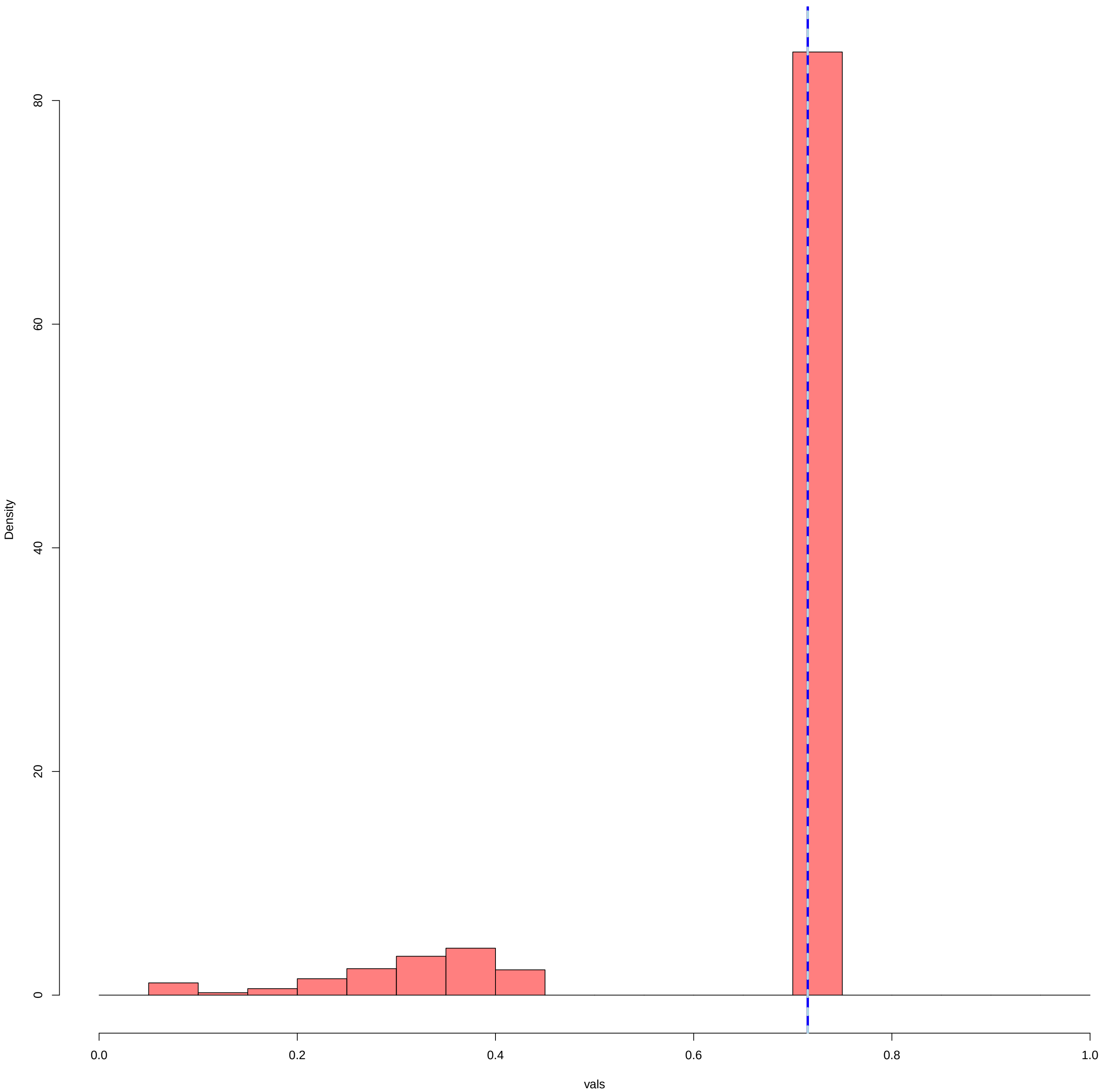
SCN1A: phastCons20way_mammalian_rankscore



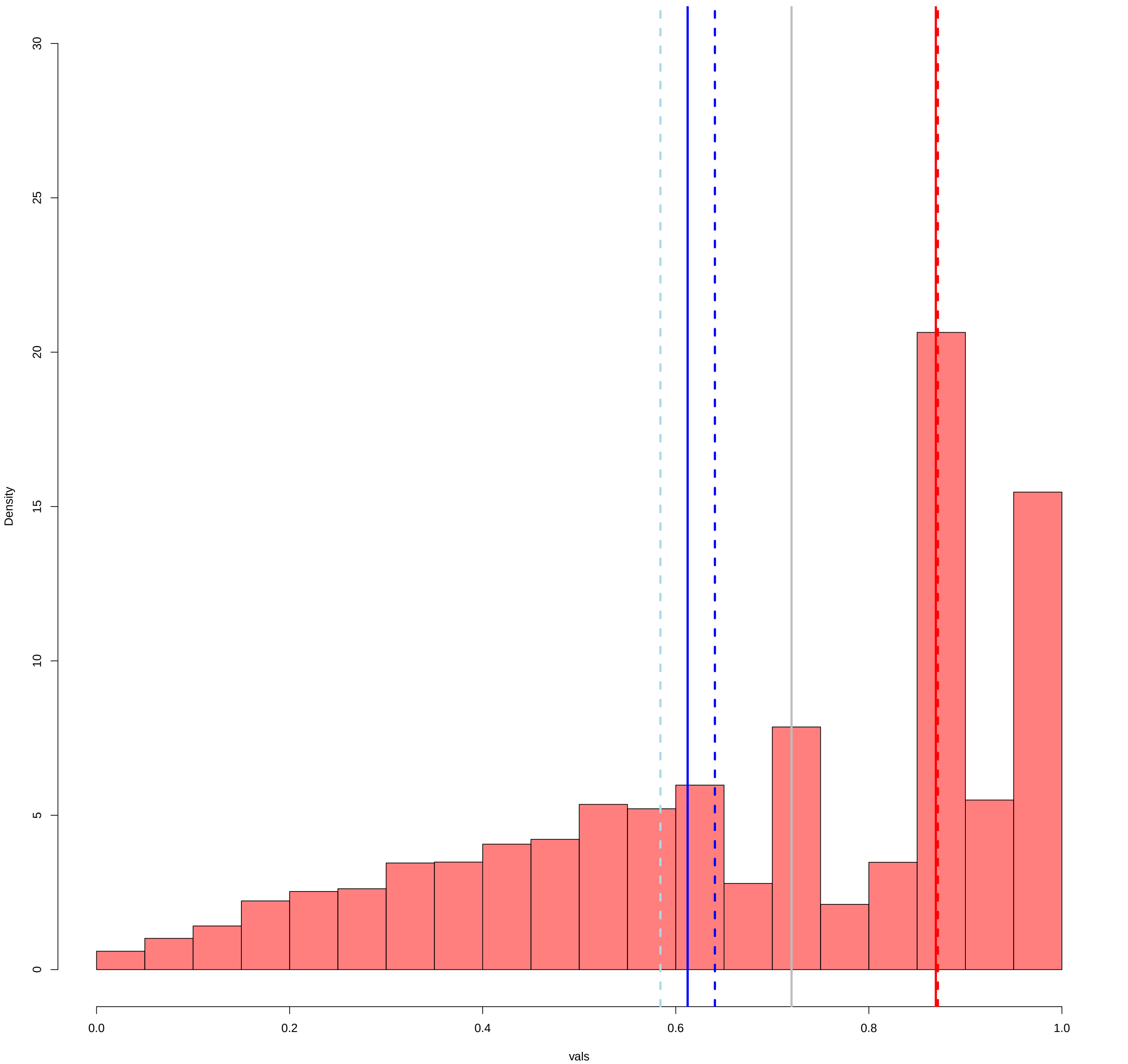
SCN1A: phyloP20way_mammalian_rankscore



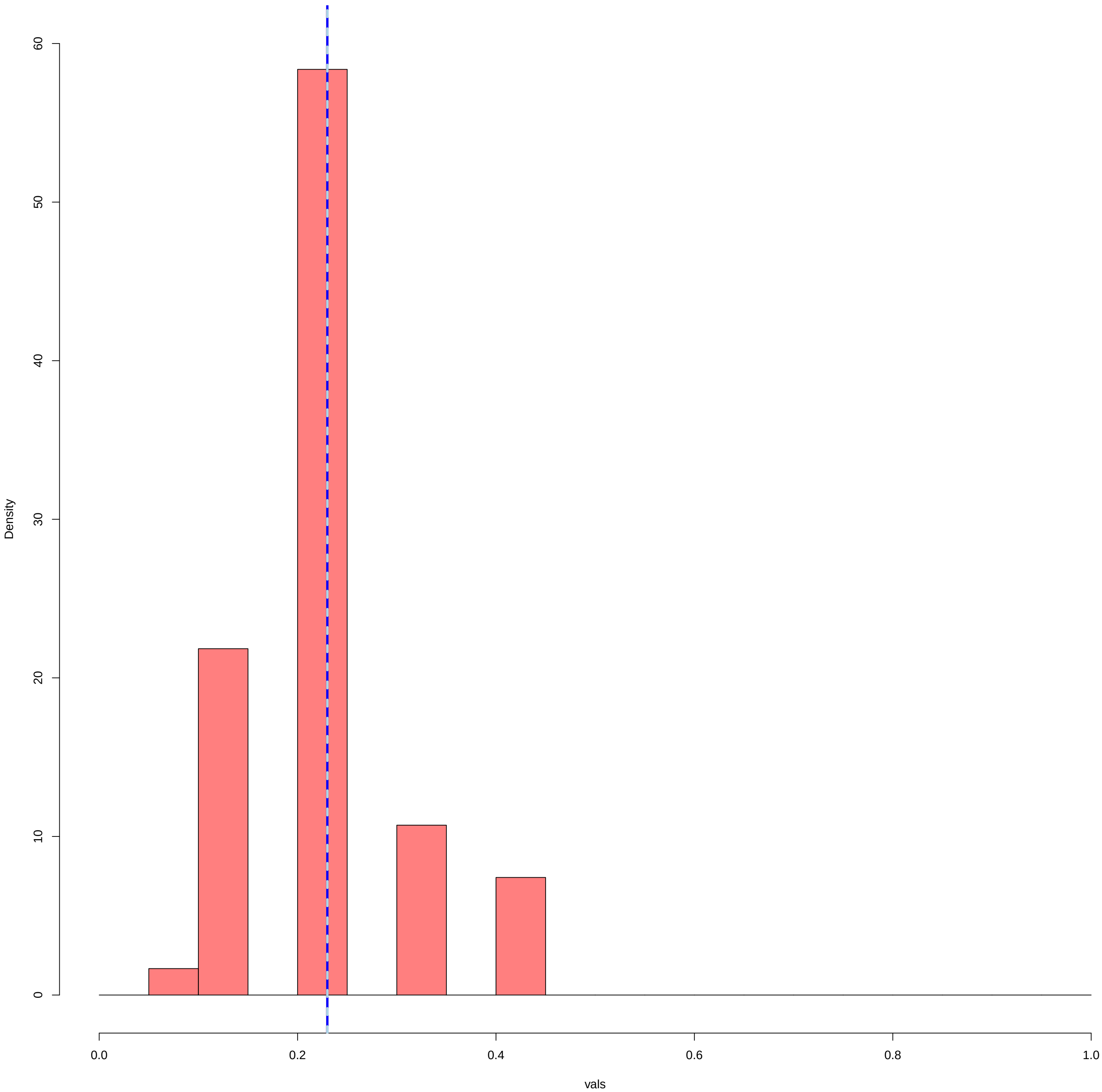
SCN1A: phastCons100way Vertebrate RankScore



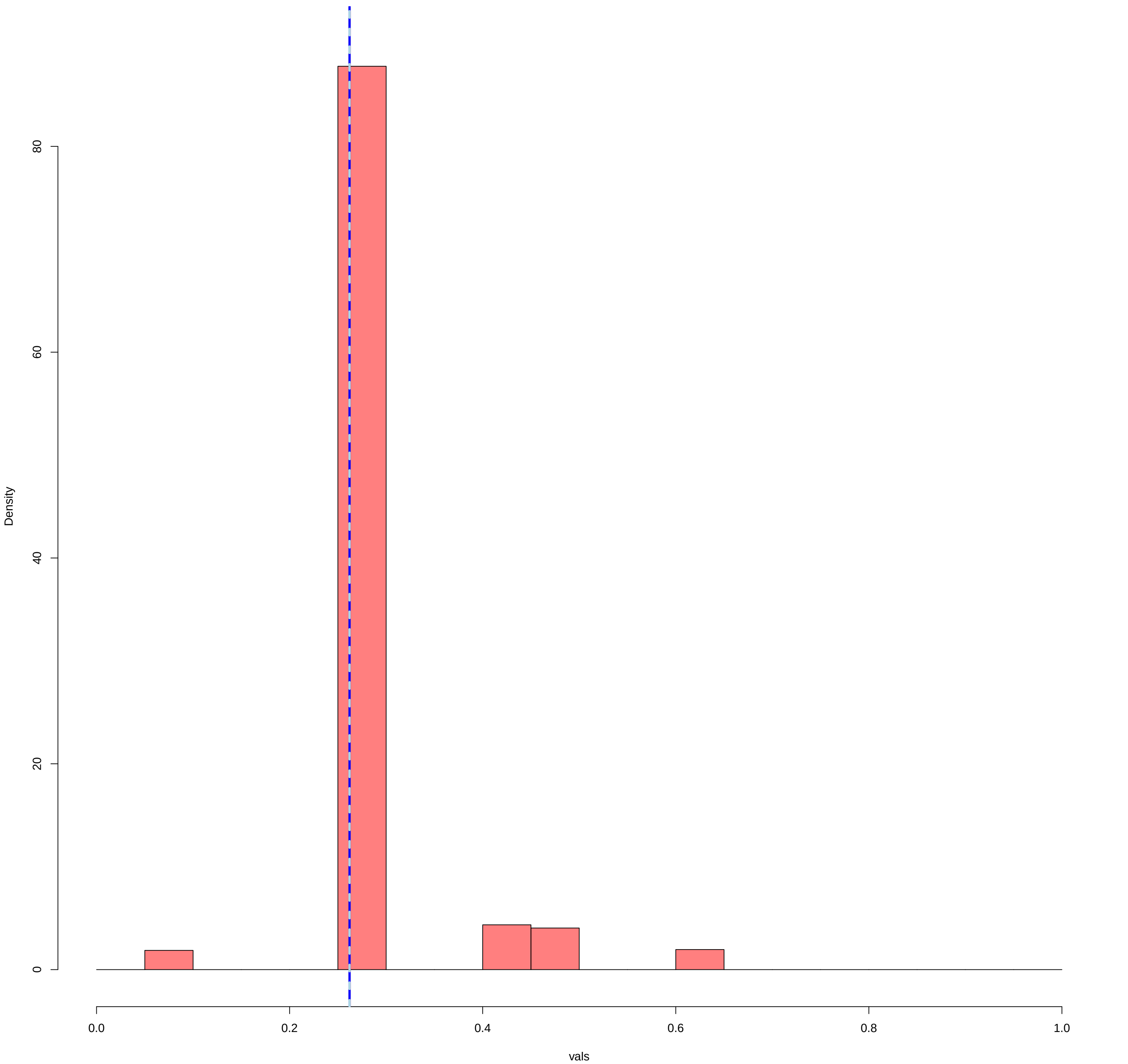
SCN1A: phyloP100way_vertebrate_rankscore



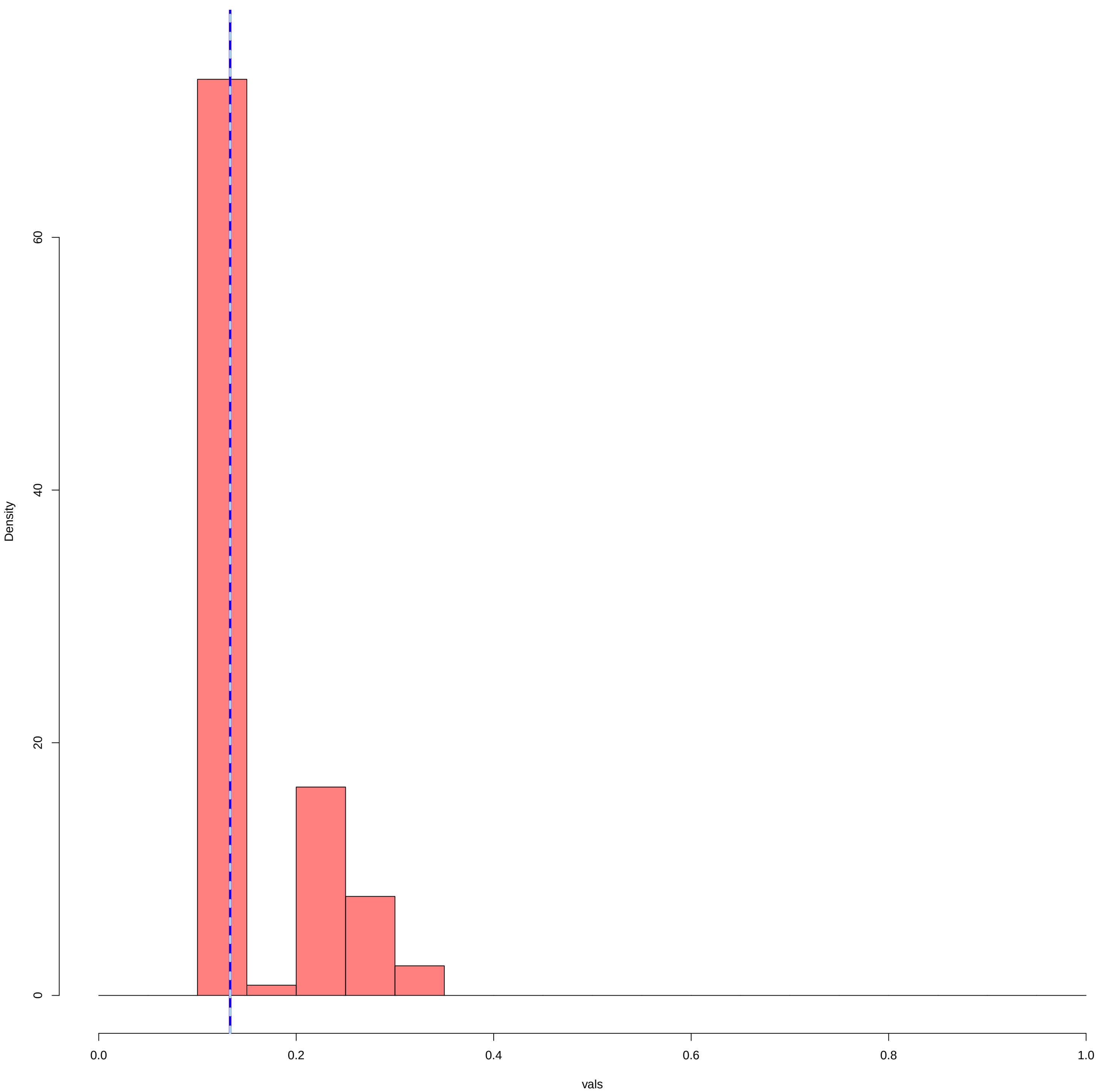
SCN1A: H1-hESC_fitCons_score_rankscore



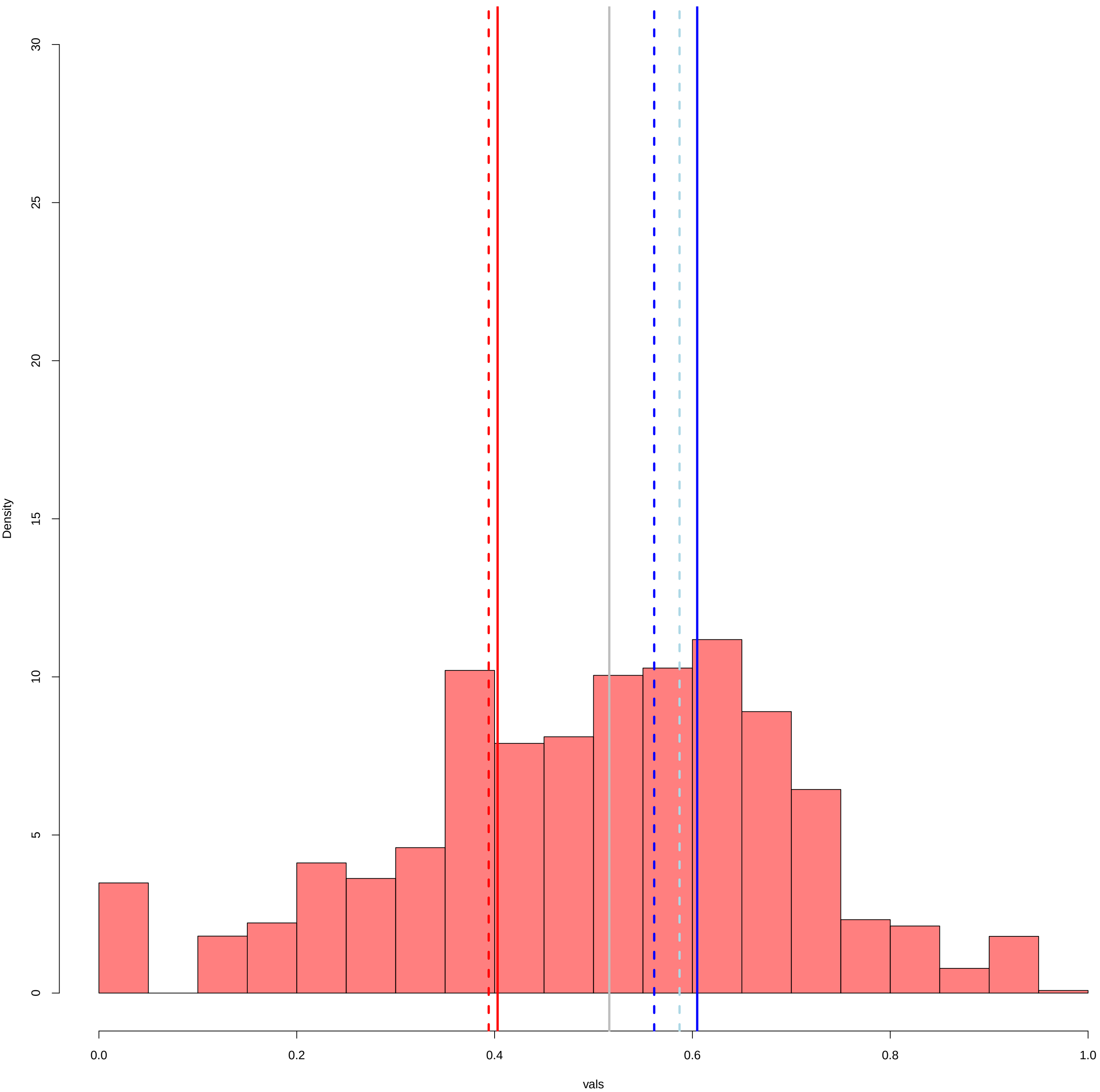
SCN1A: HUVEC_fitCons_score_rankscore



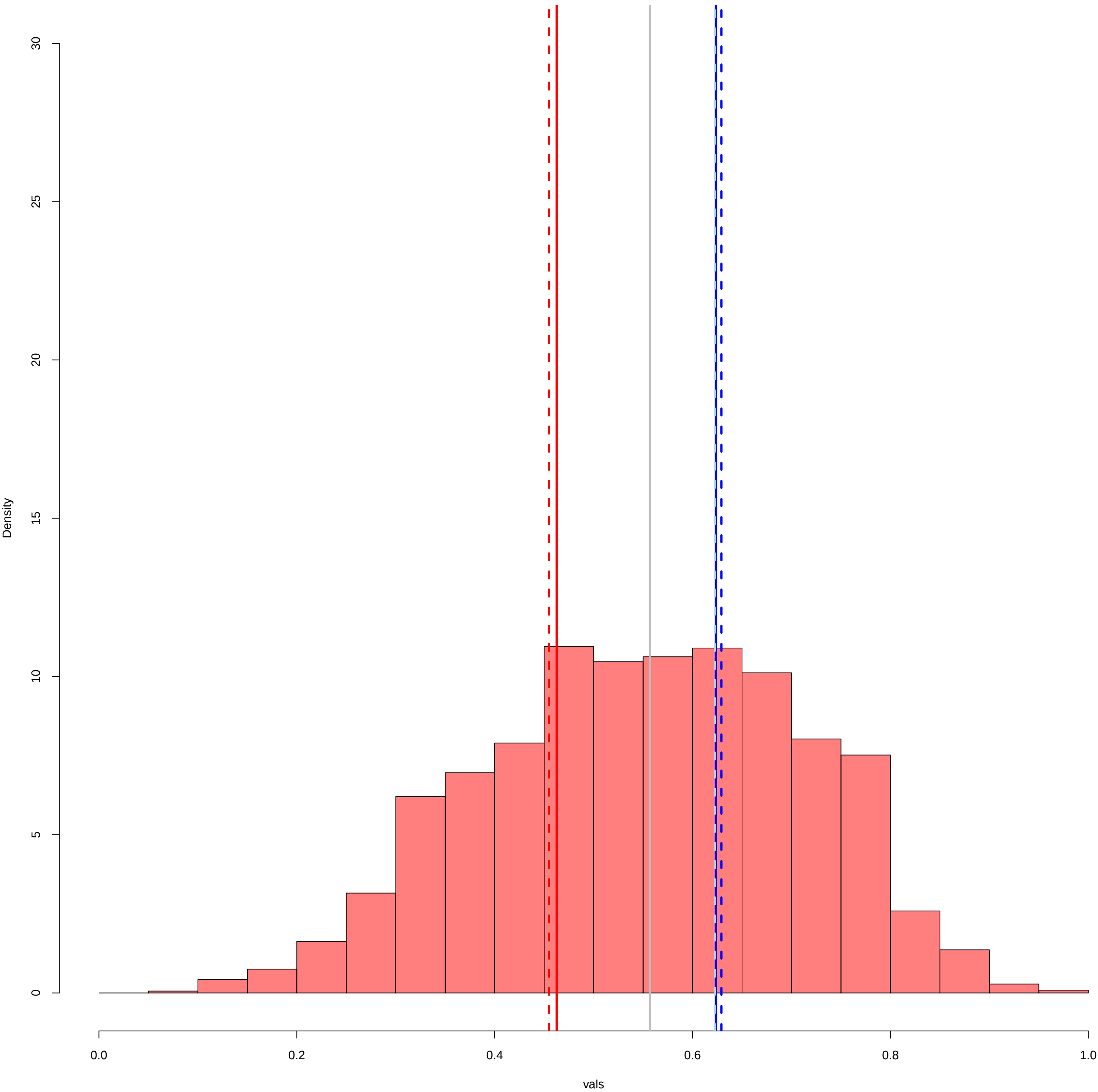
SCN1A: integrated_fitCons_score_rankscore



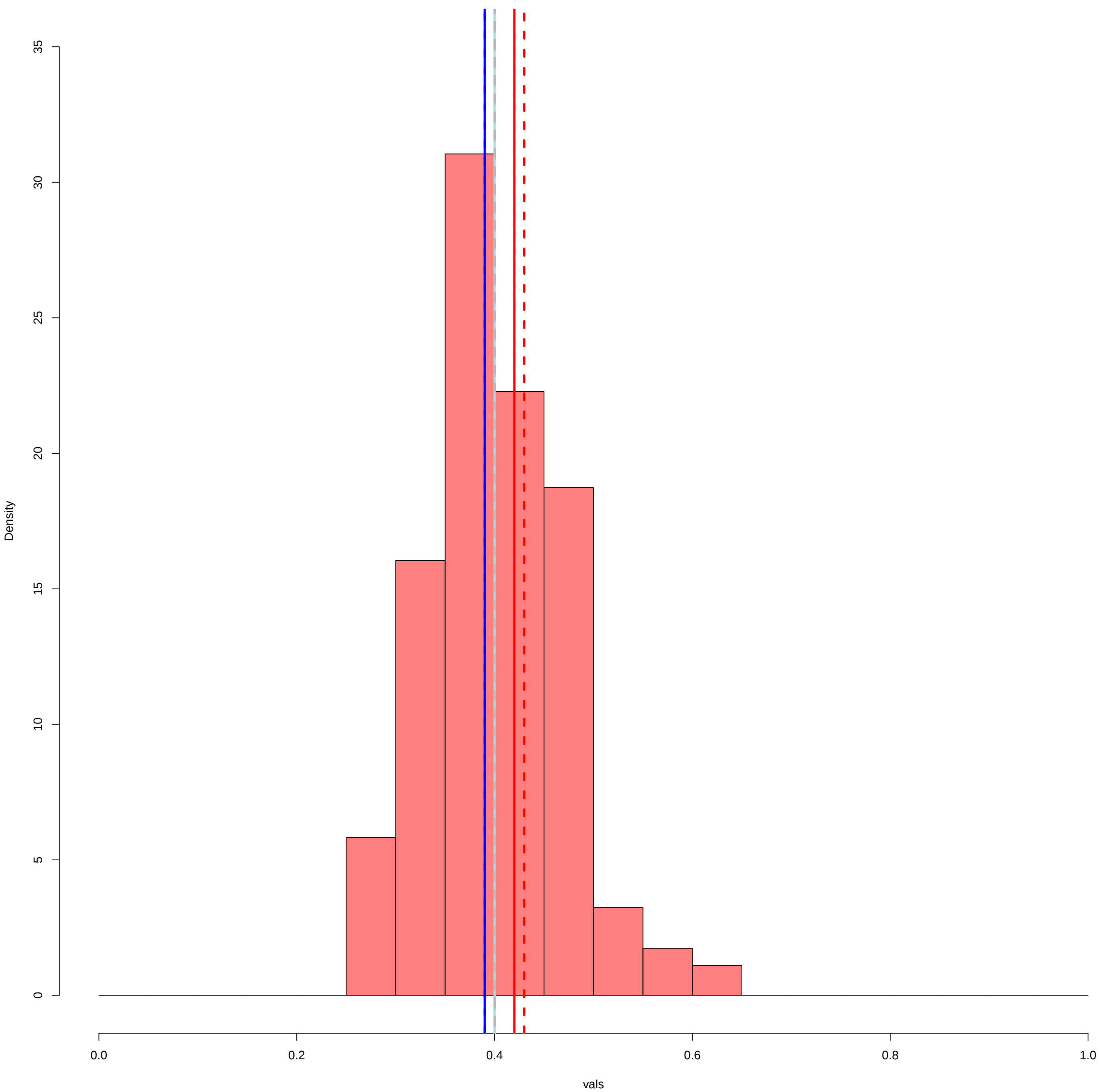
SCN1A: ExAC v1 MTR



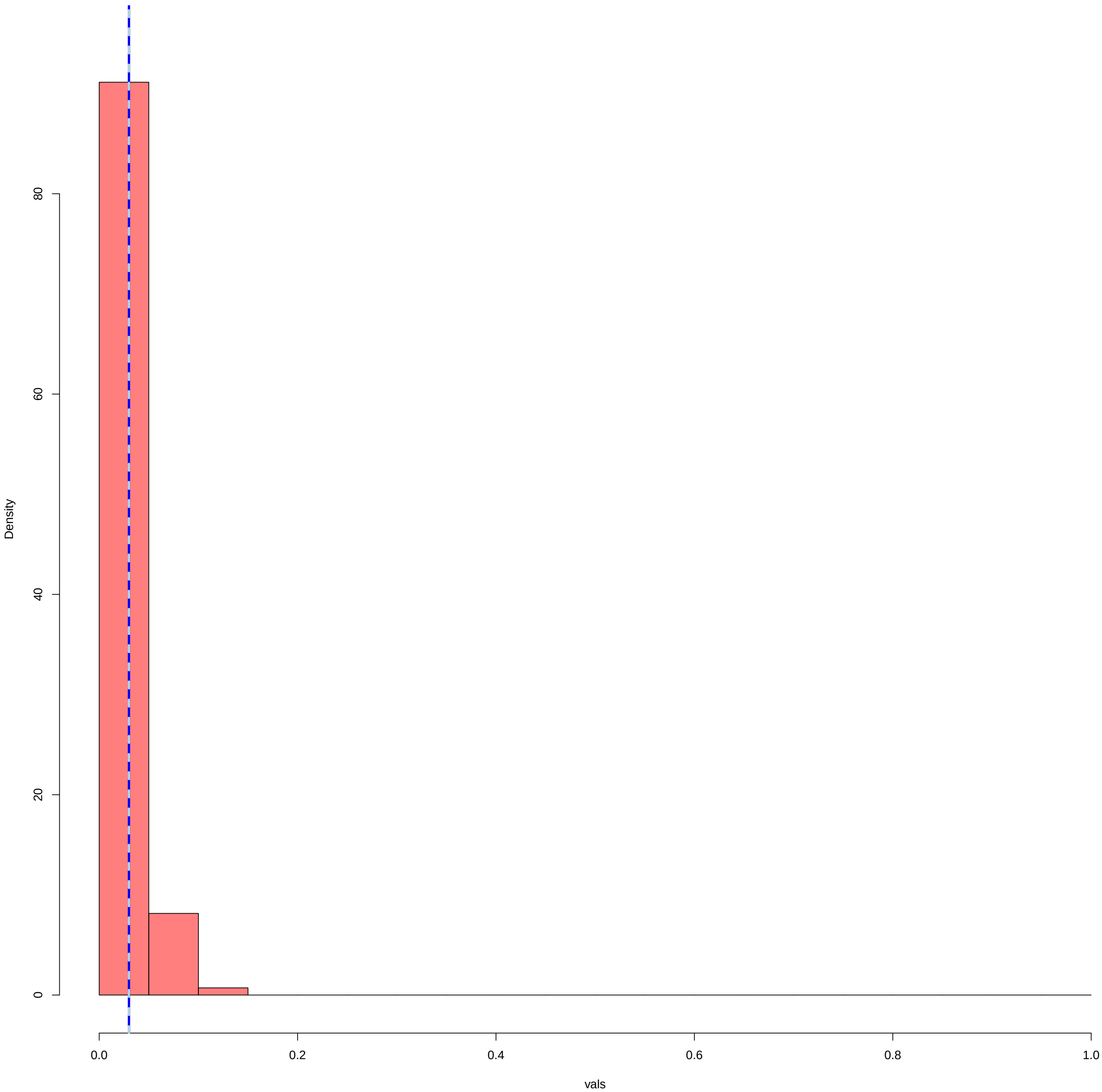
SCN1A: ExAC v2 & gnomAD MTR



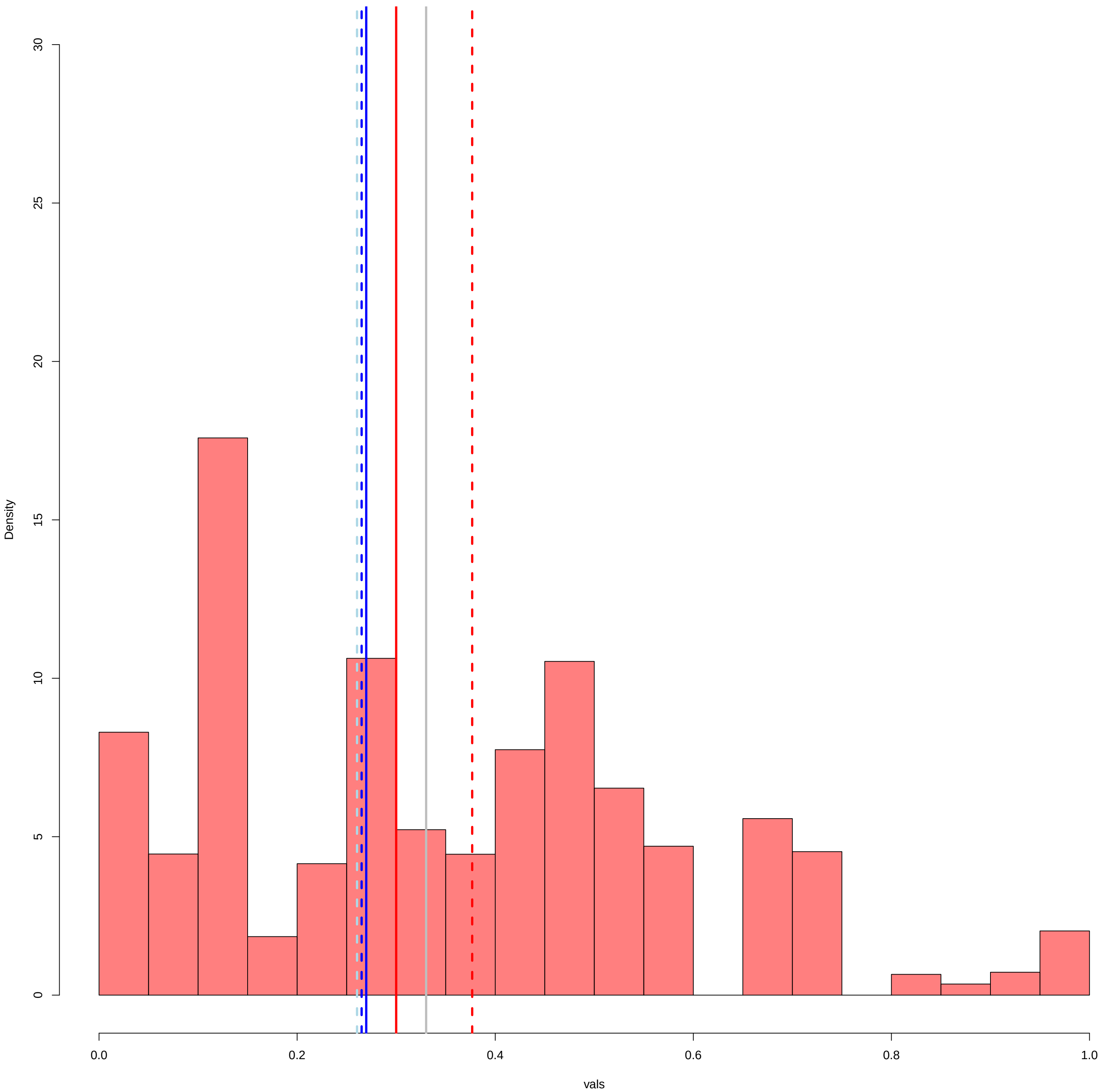
SCN2A: GC (Percent GC content in a window of +/-75bp)



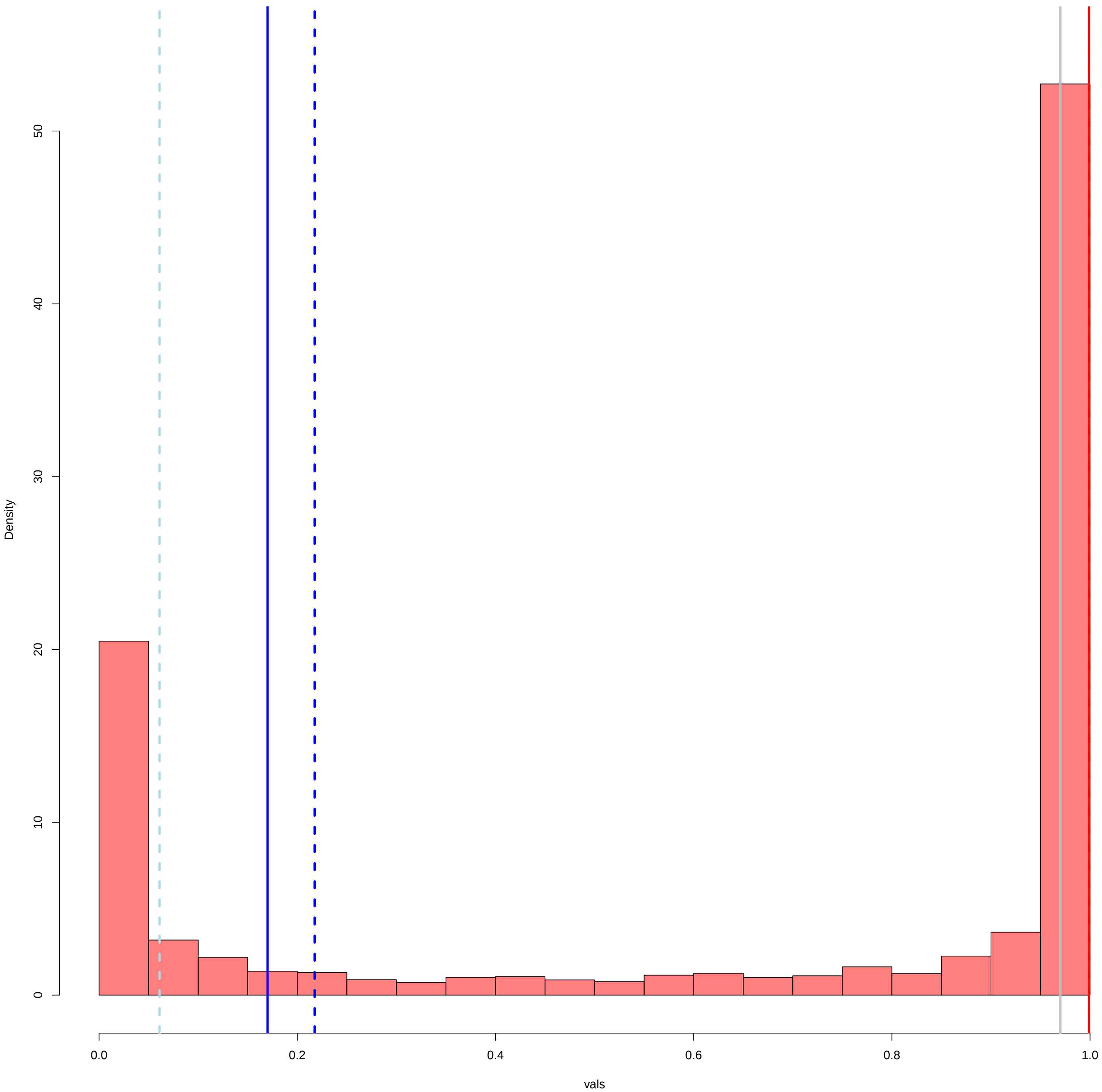
SCN2A: CpG (Percent CpG in a window of +/-75bp)



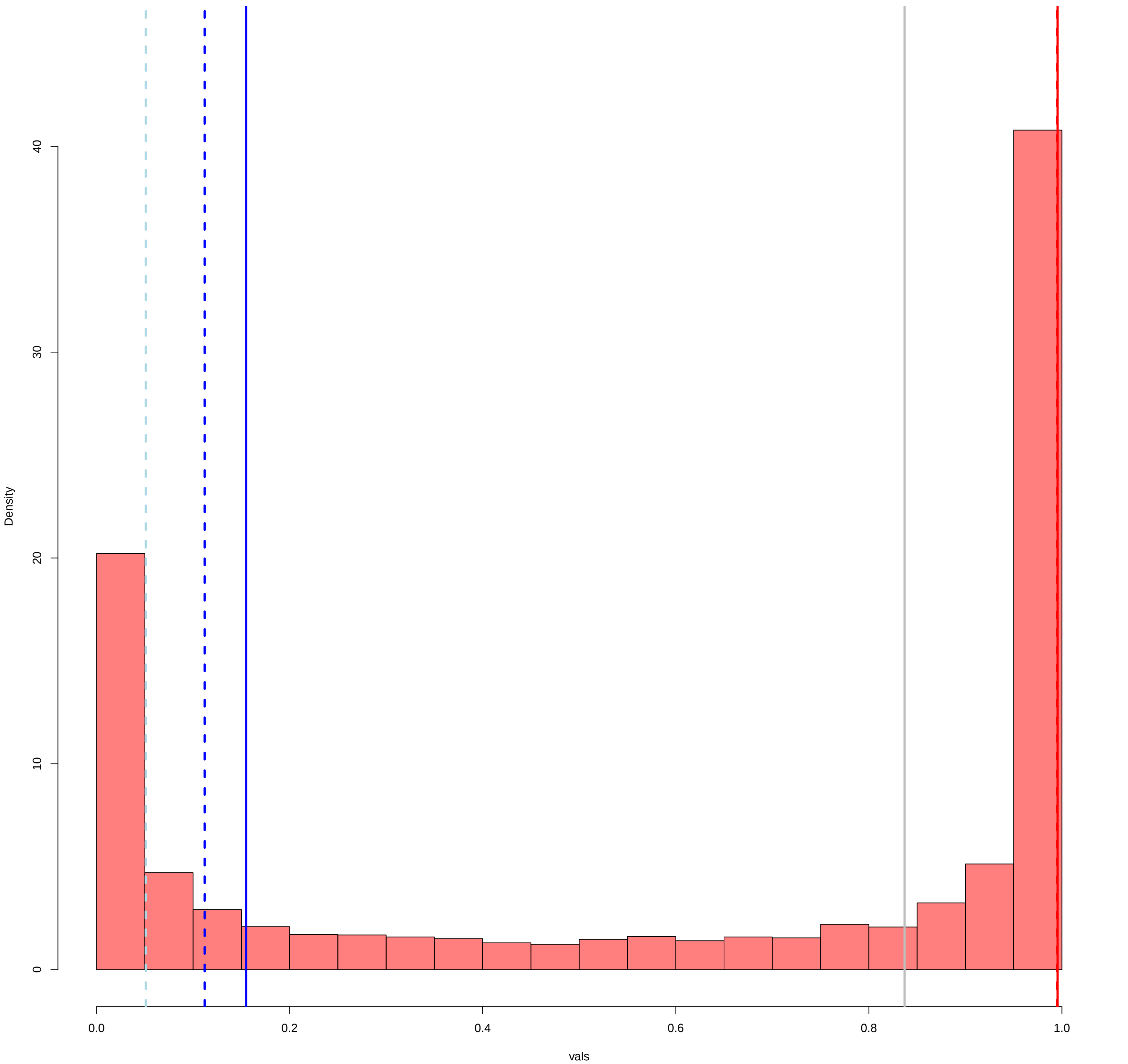
SCN2A: Grantham



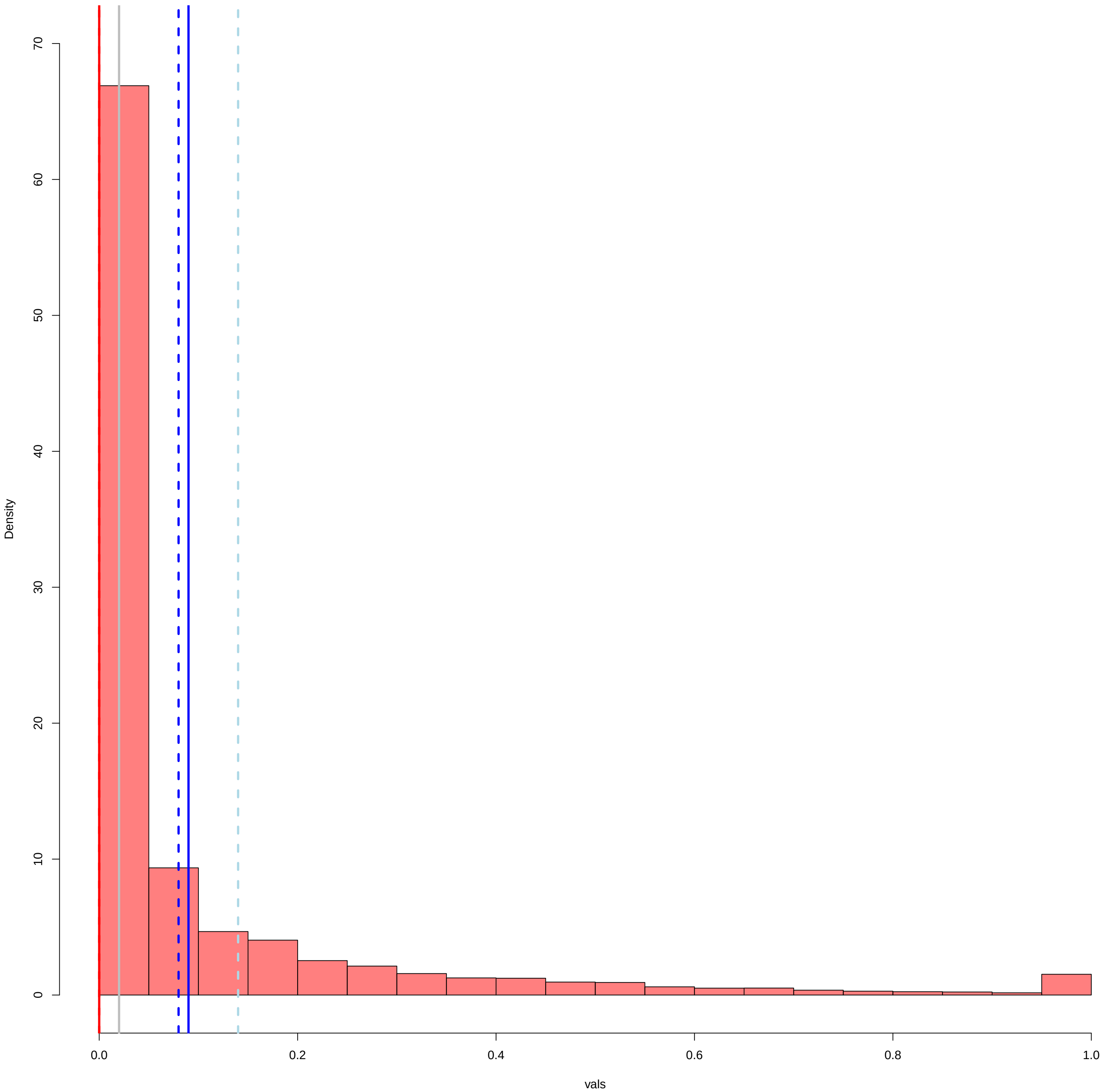
SCN2A: Hdiv quan



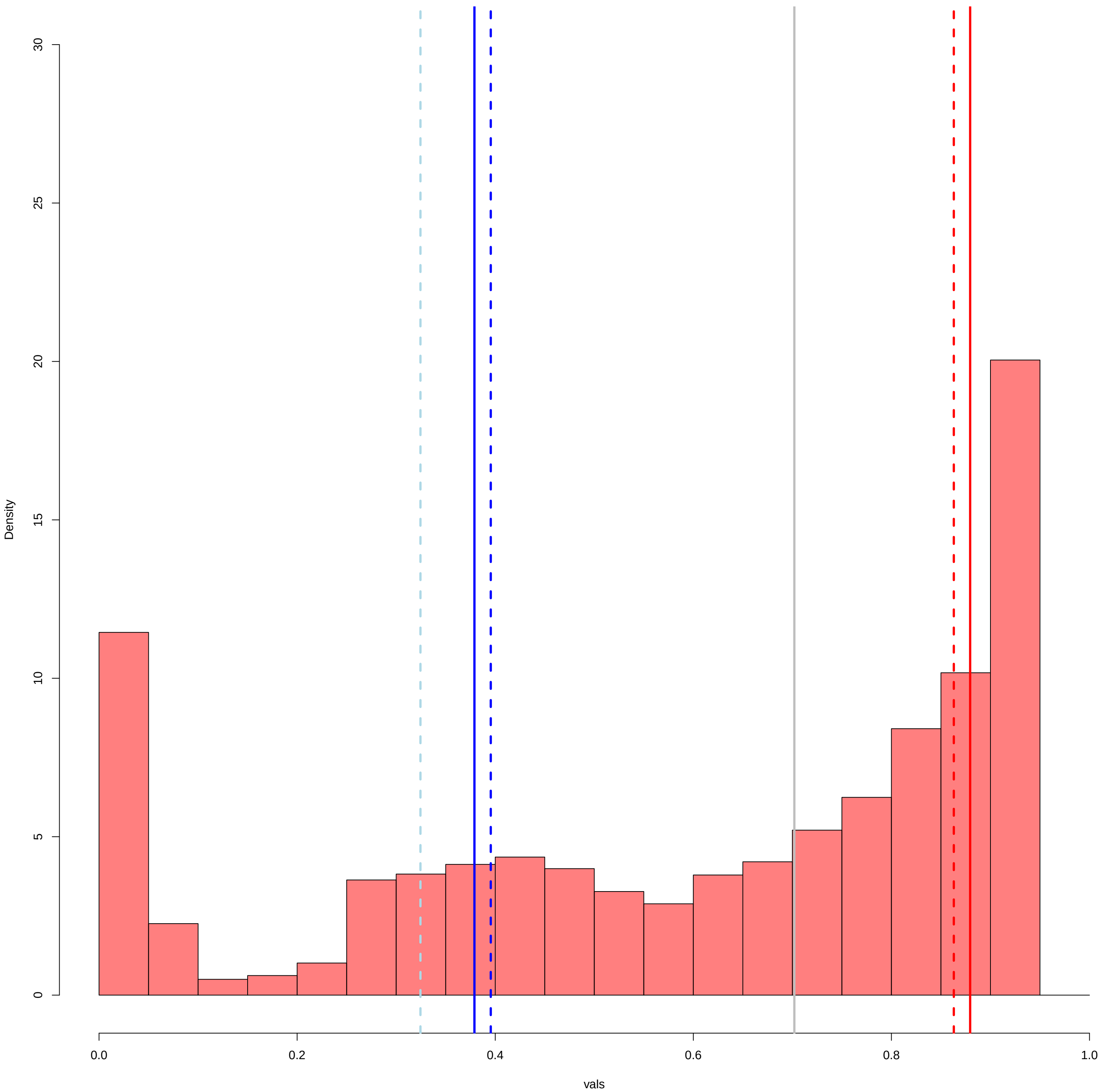
SCN2A: Hvar quan



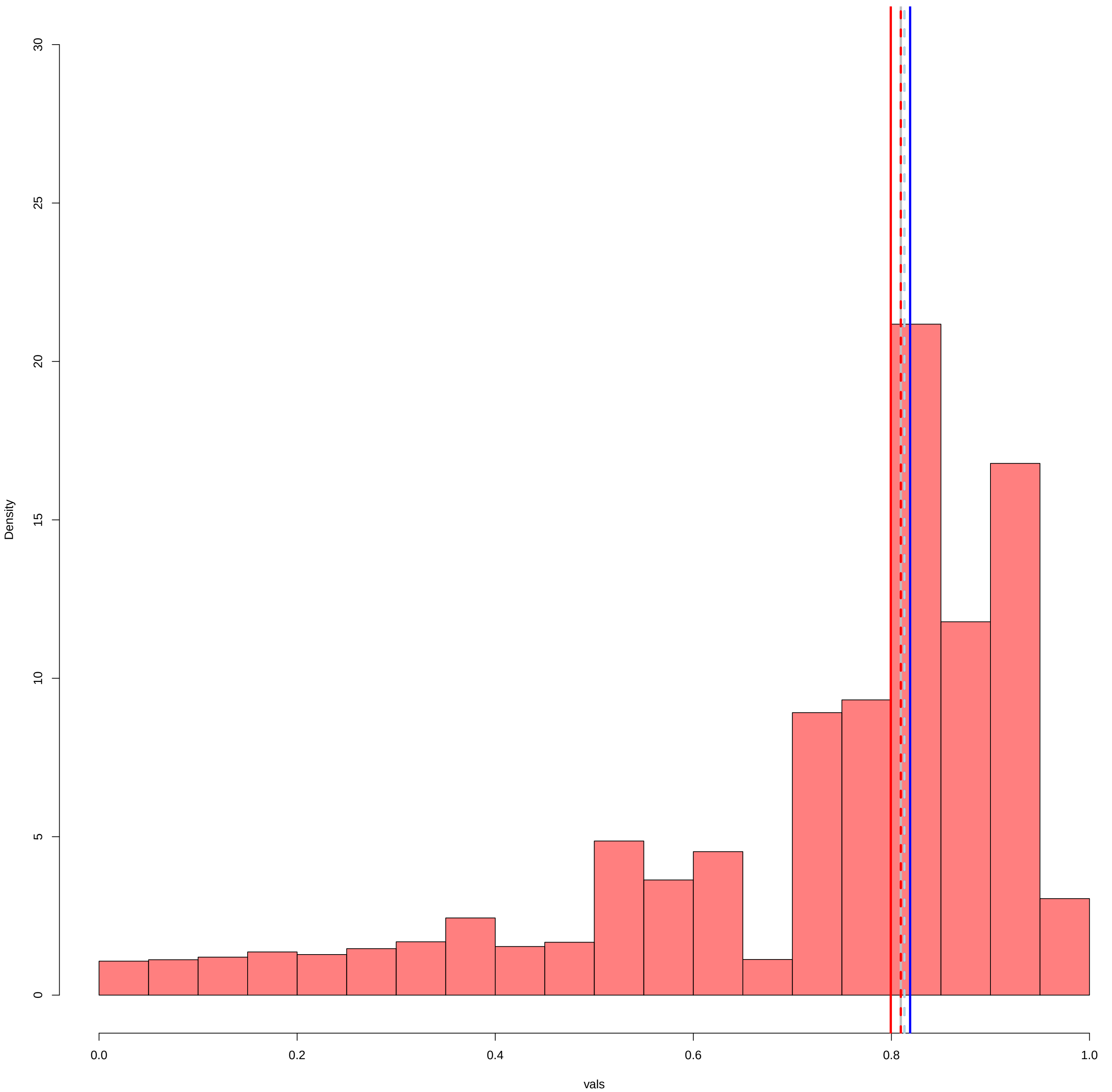
SCN2A: SIFT



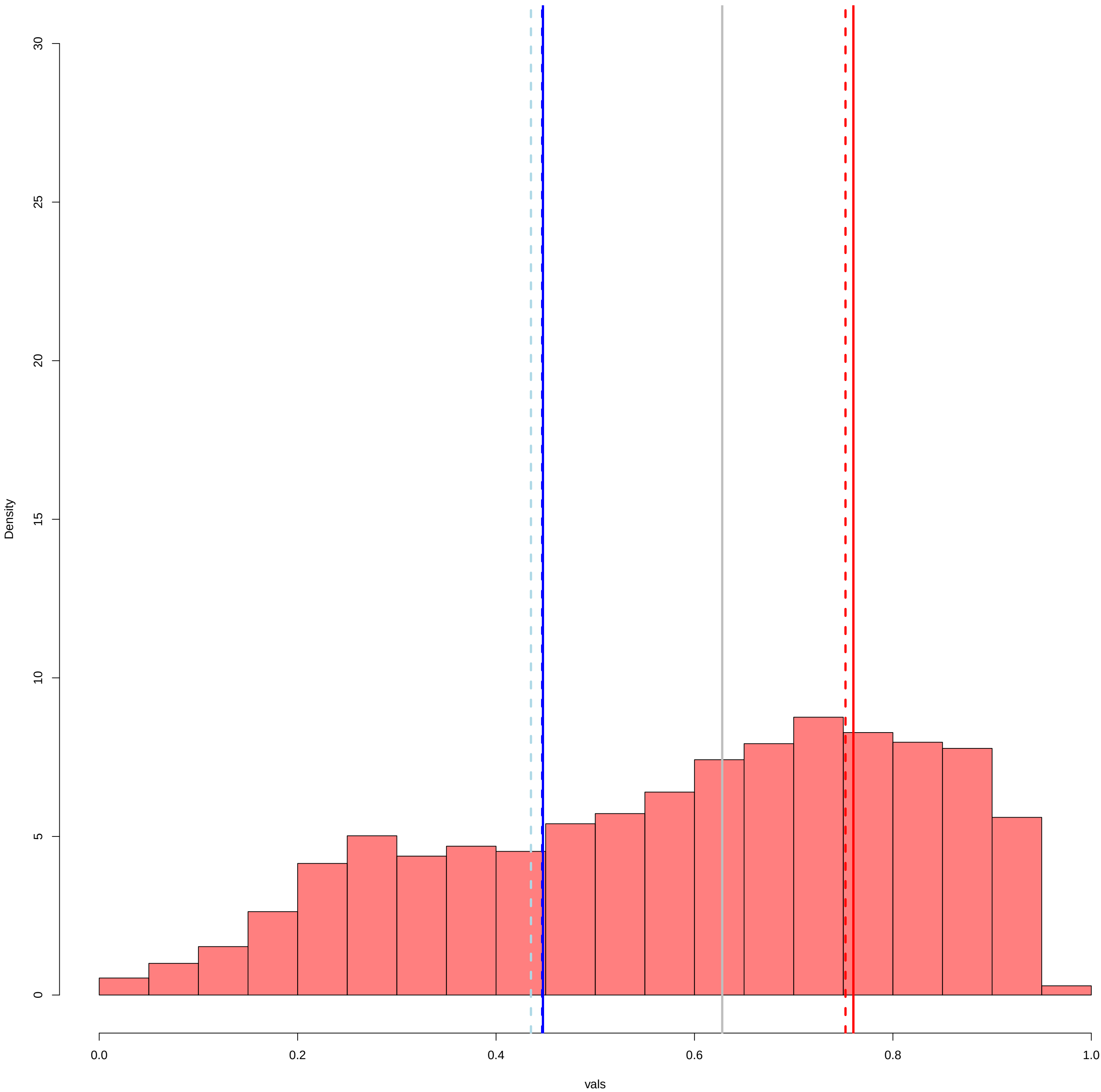
SCN2A: Condel



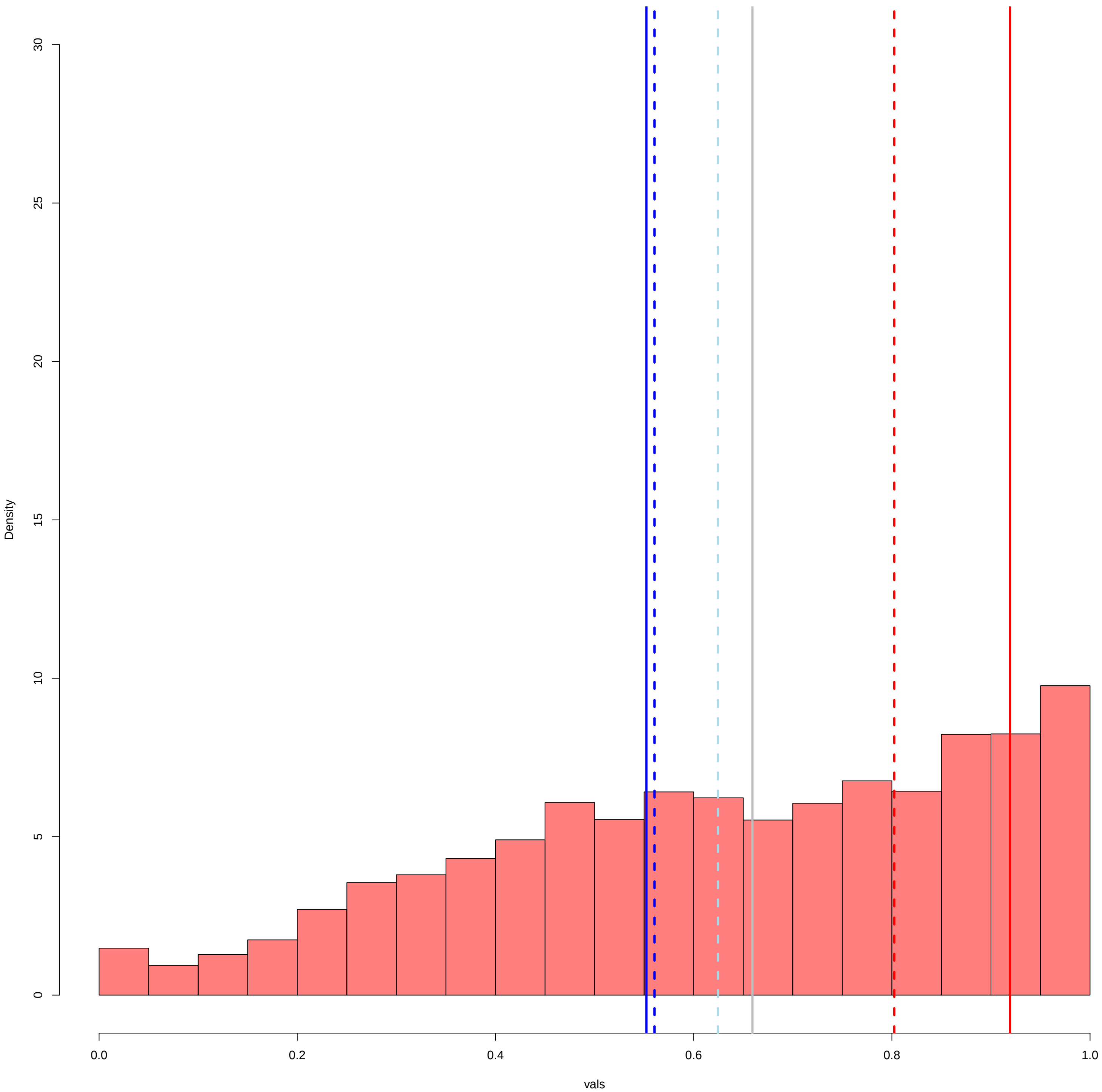
SCN2A: GERP++_RS_rankscore



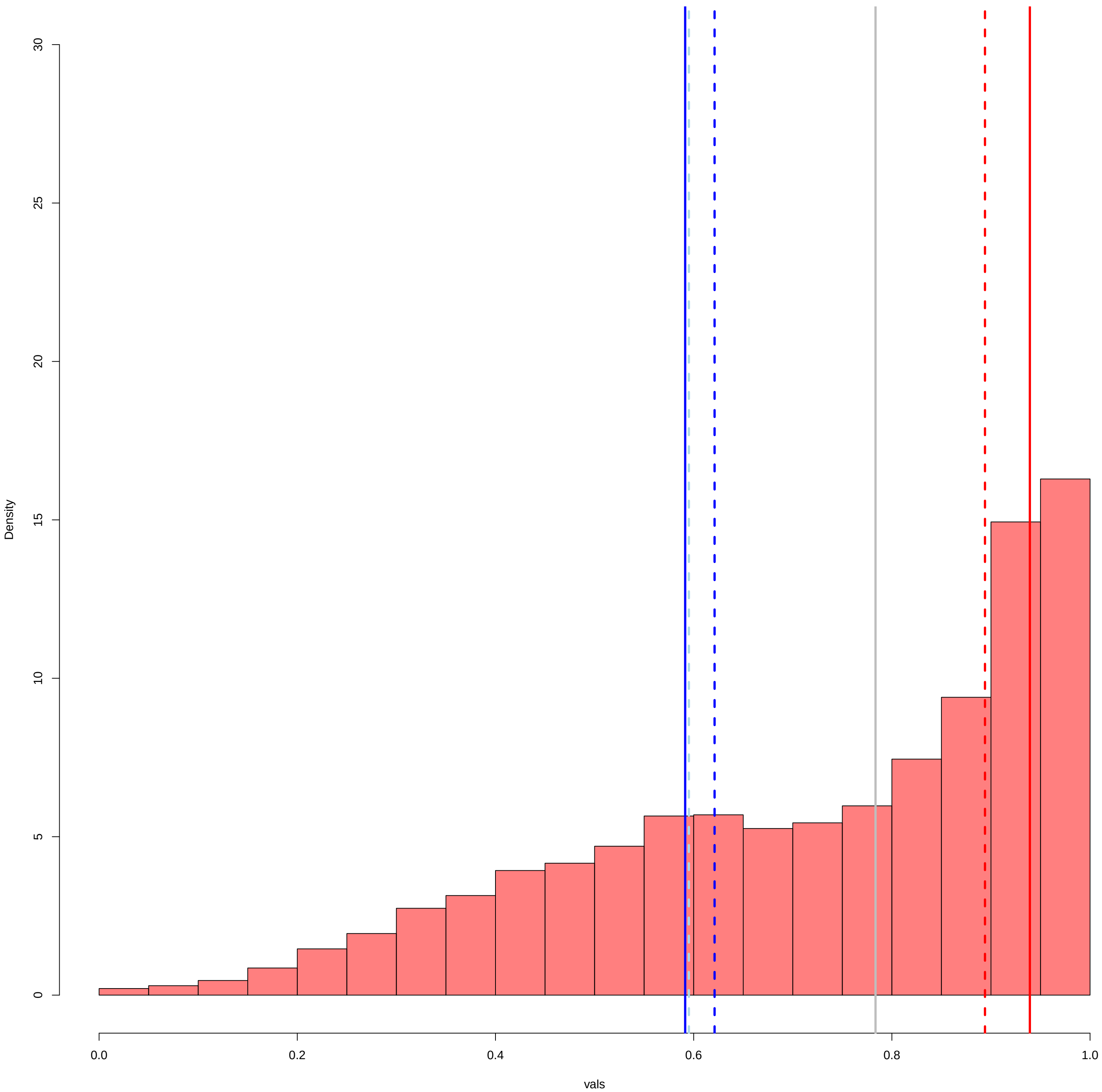
SCN2A: CADD_raw_rankscore



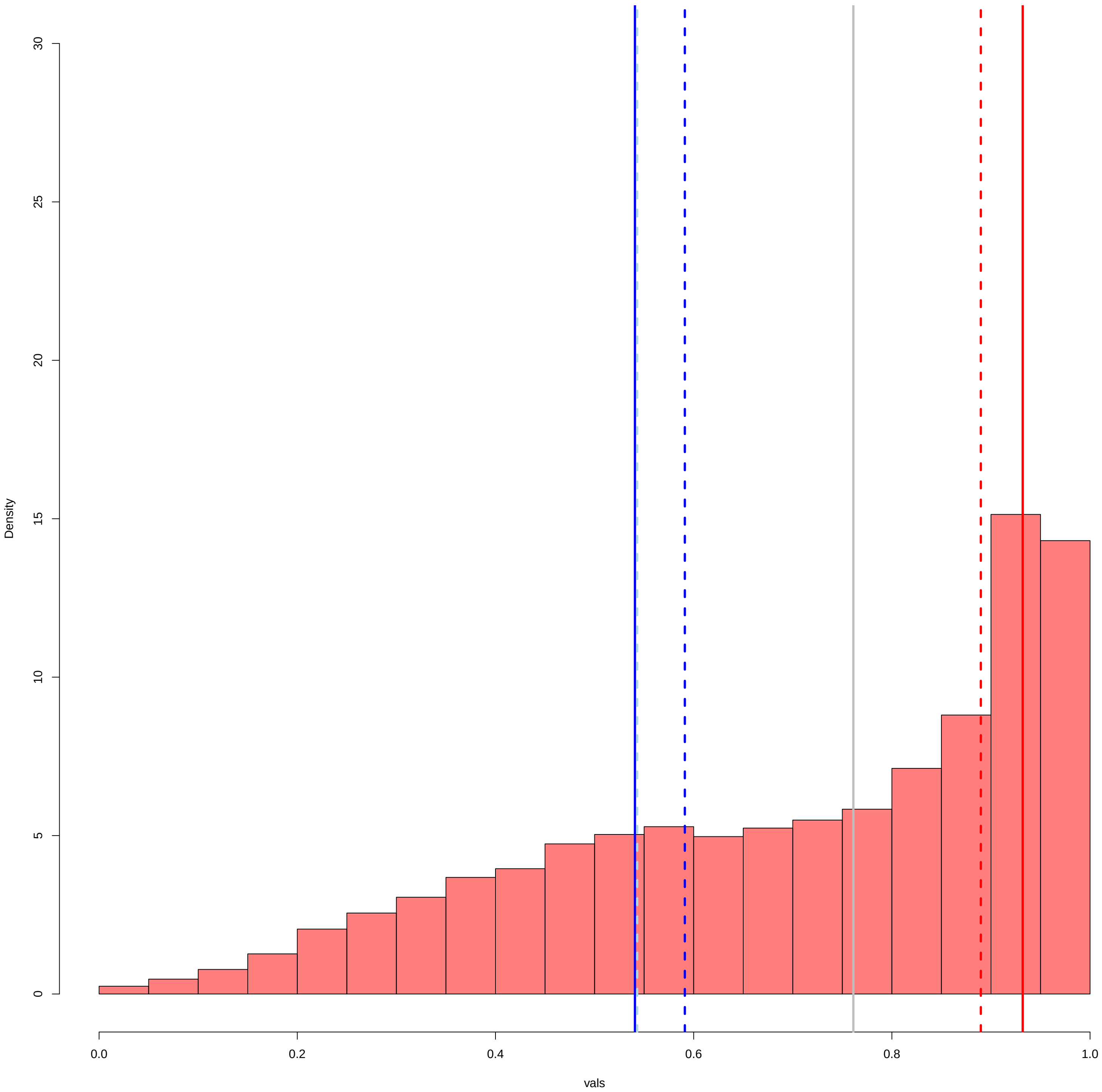
SCN2A: DANN_rankscore



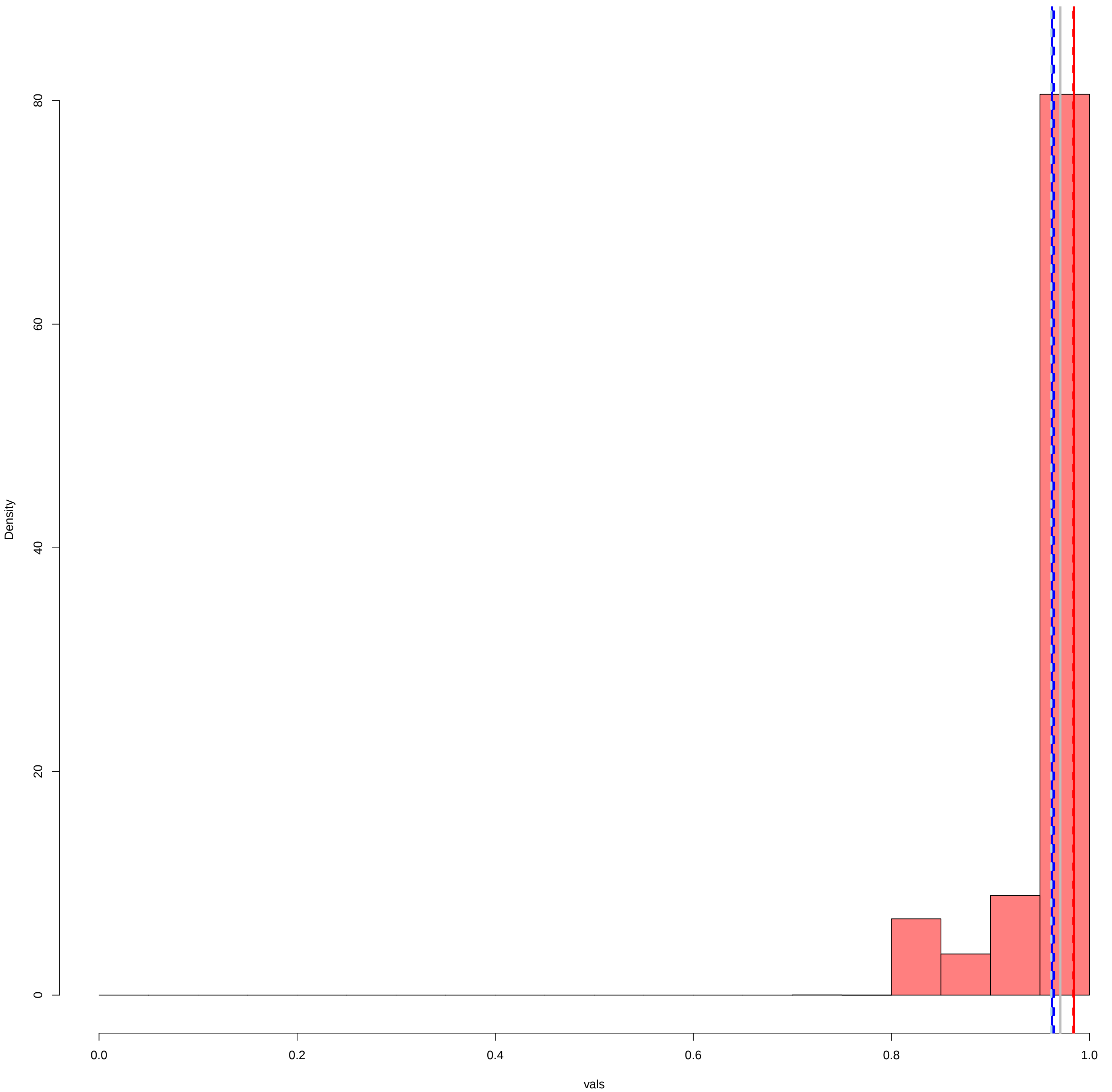
SCN2A: Eigen-PC-raw_rankscore



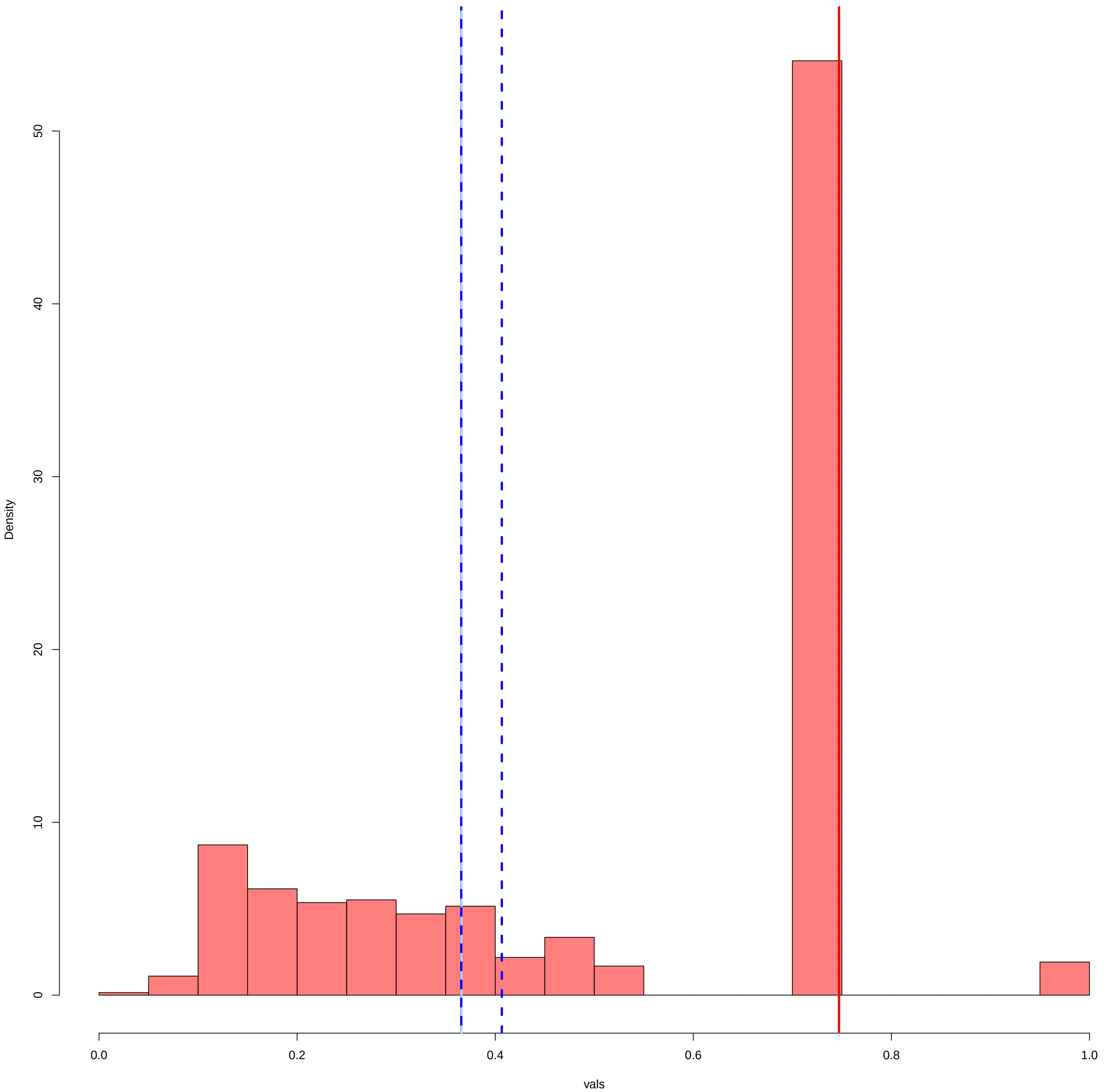
SCN2A: Eigen-row_rankscore



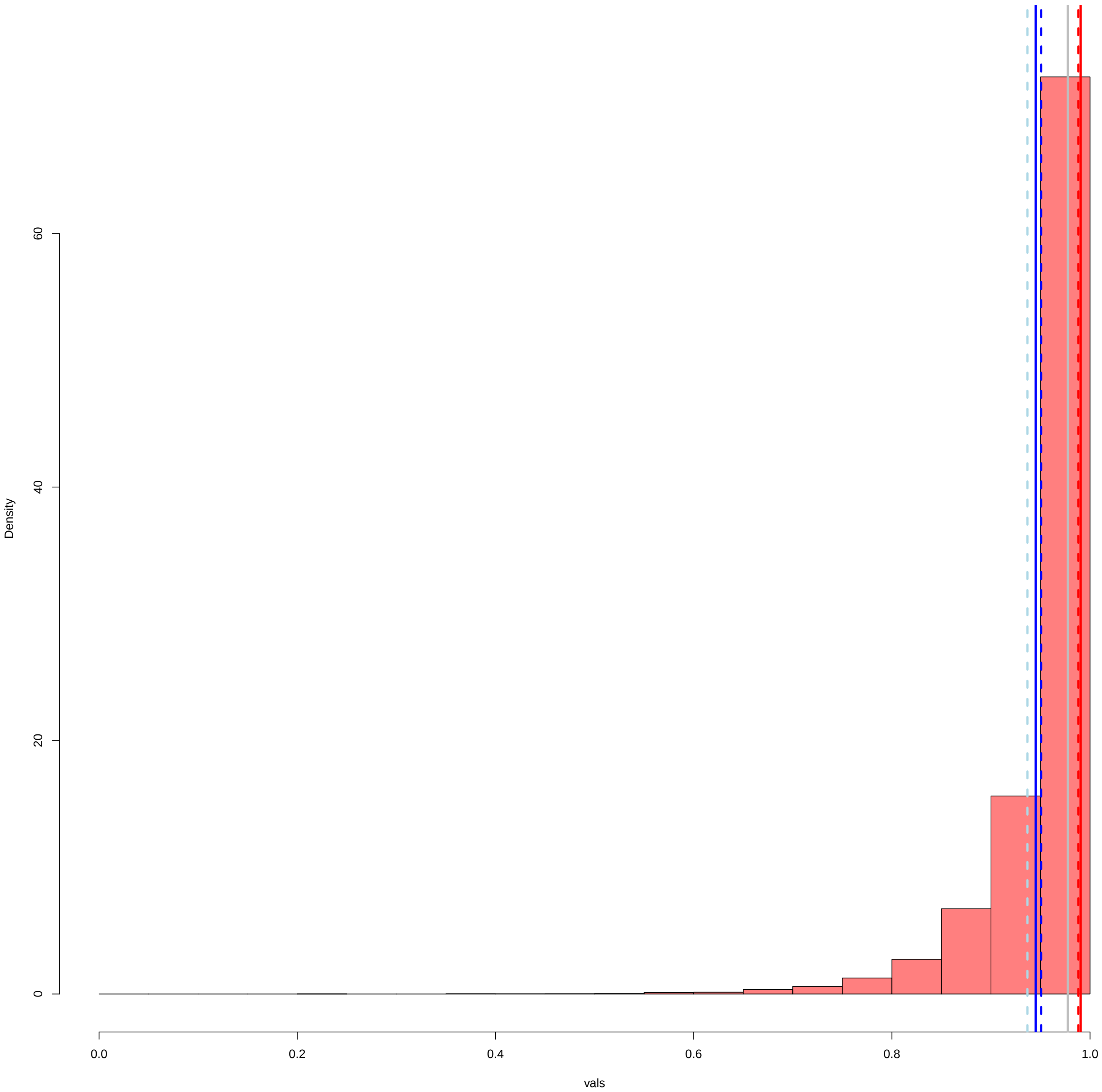
SCN2A: FATHMM_converted_rankscore



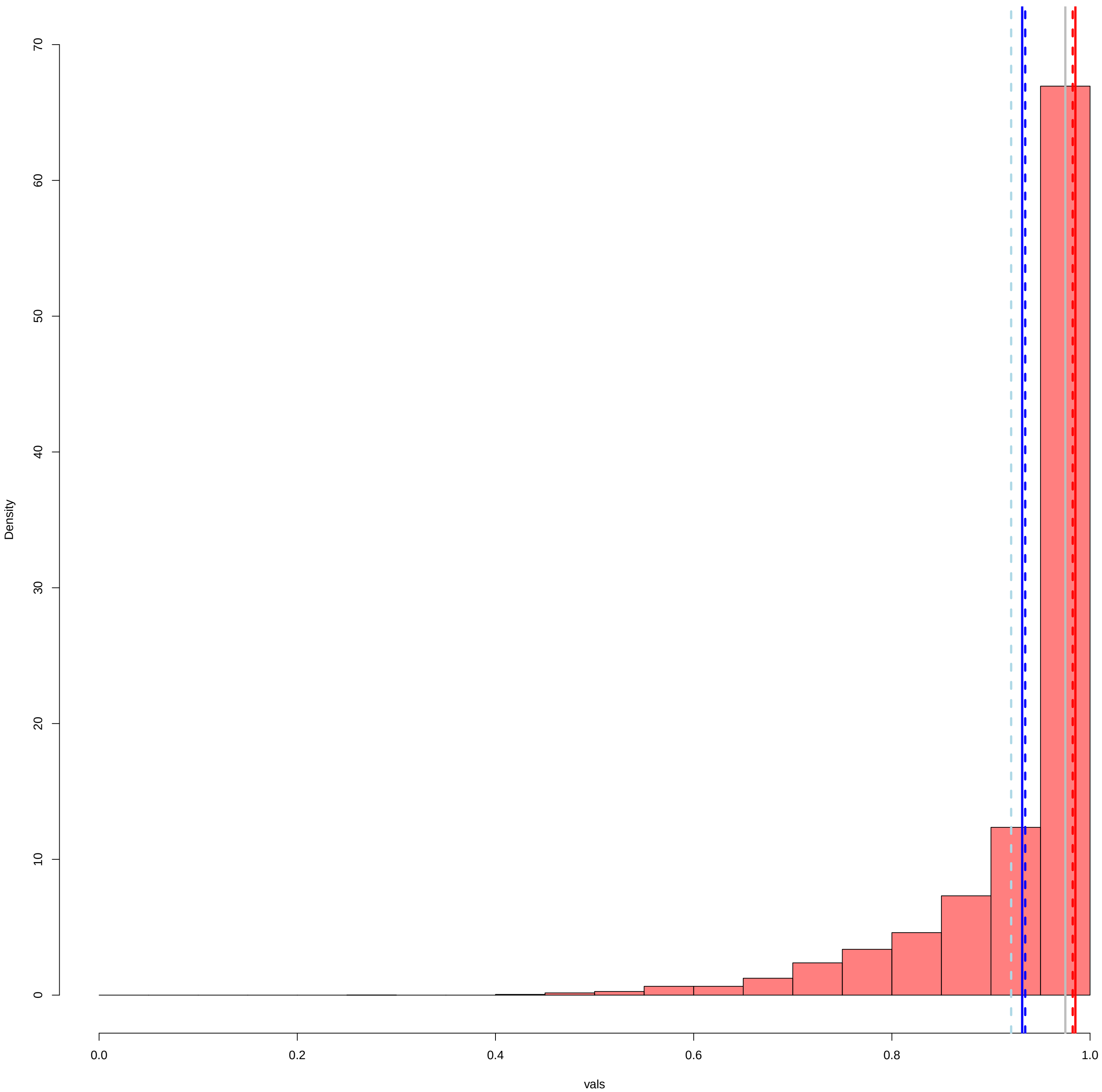
SCN2A: GenoCanyon_score_rankscore



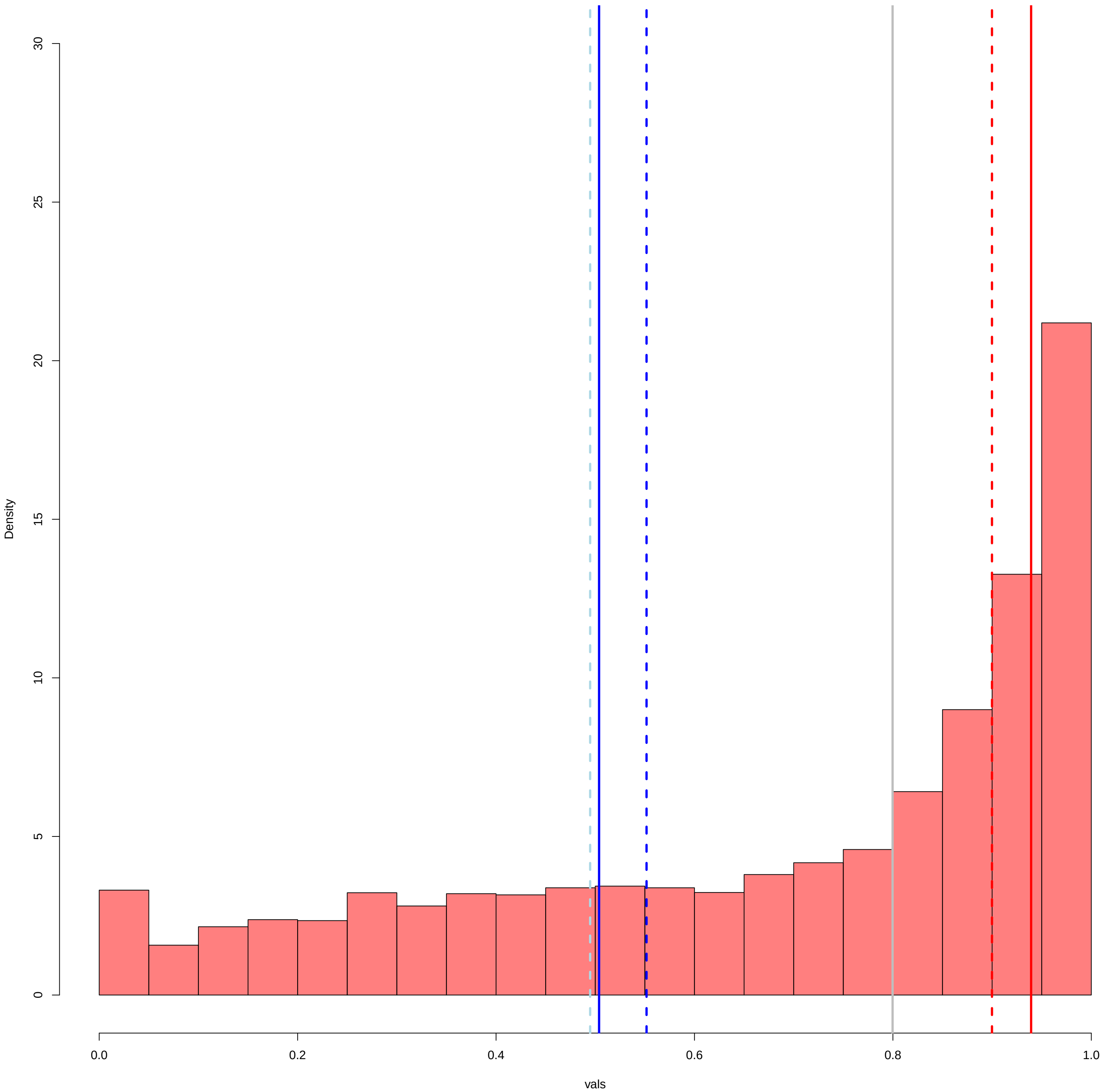
SCN2A: MetaLR_rankscore



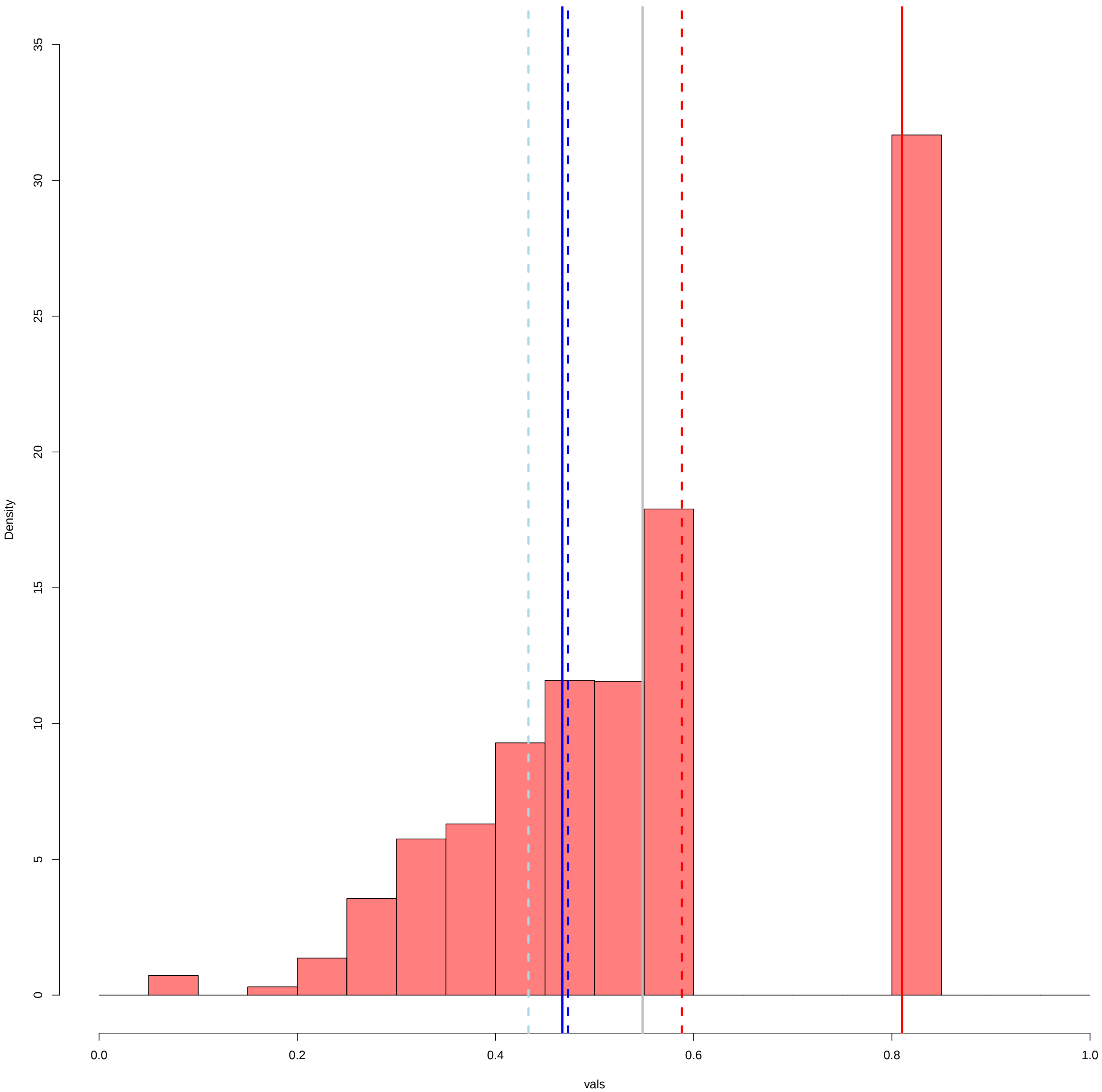
SCN2A: MetaSVM_rankscore



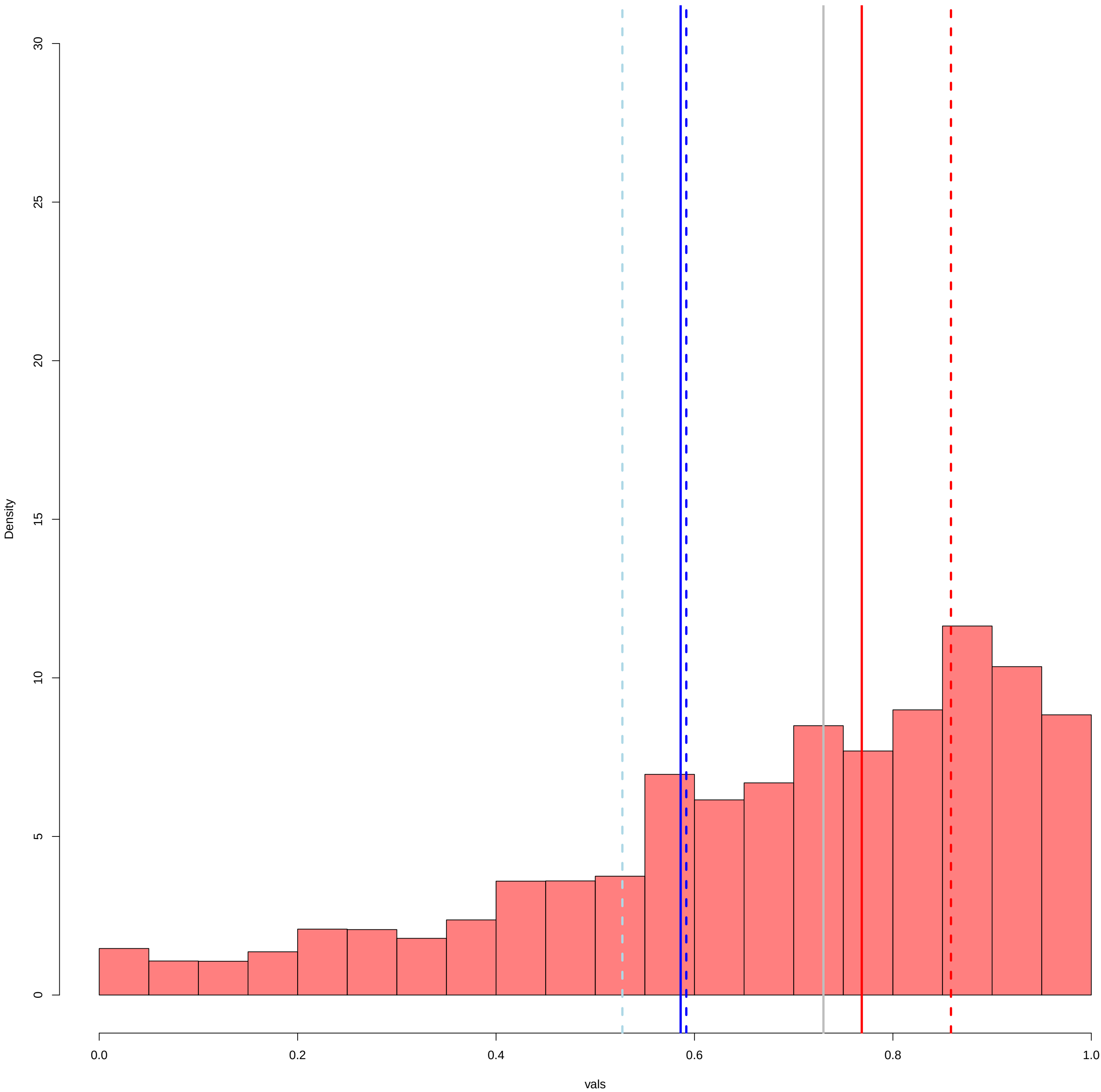
SCN2A: MutationAssessor_score_rankscore



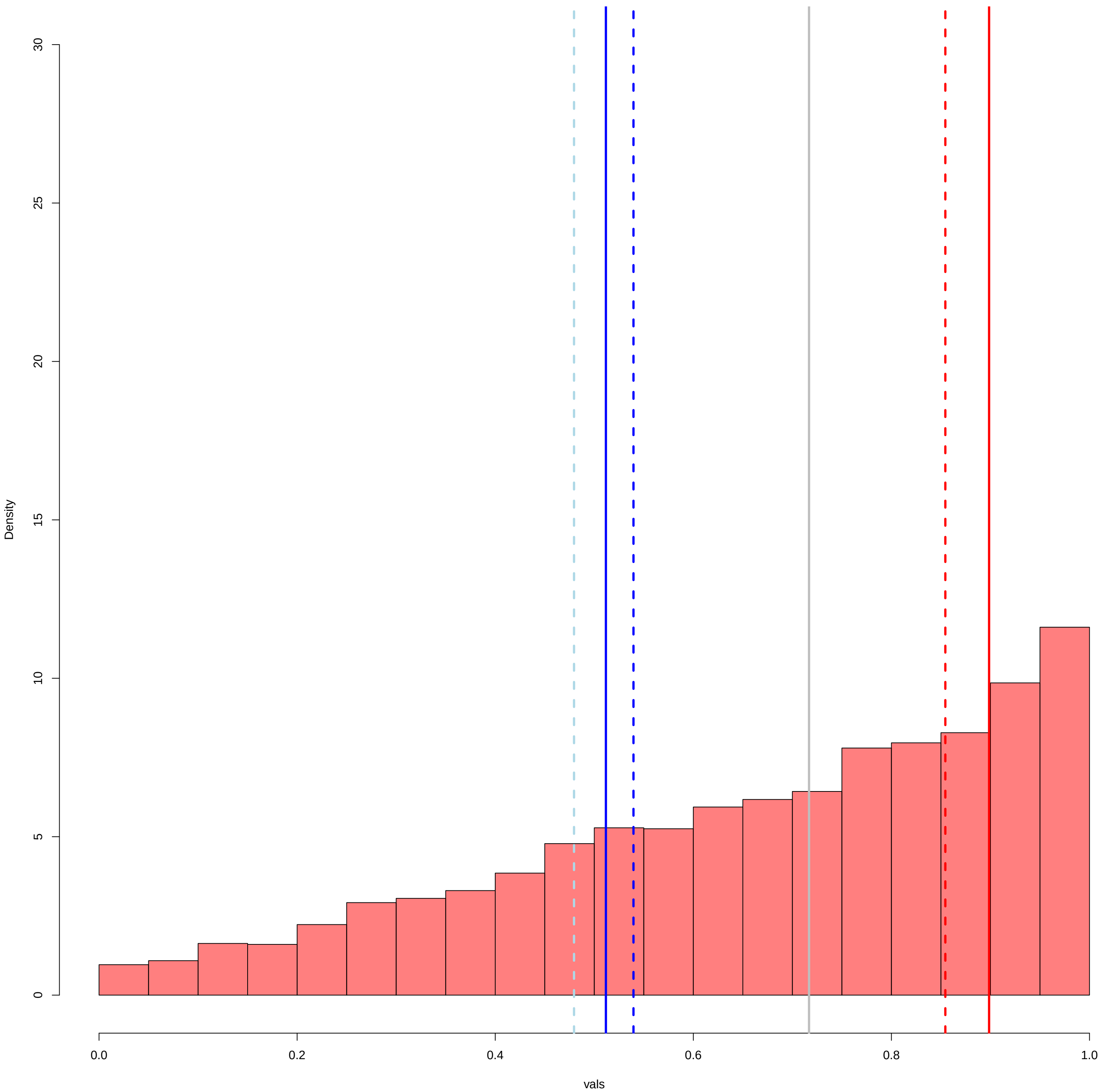
SCN2A: MutationTaster_converted_rankscore



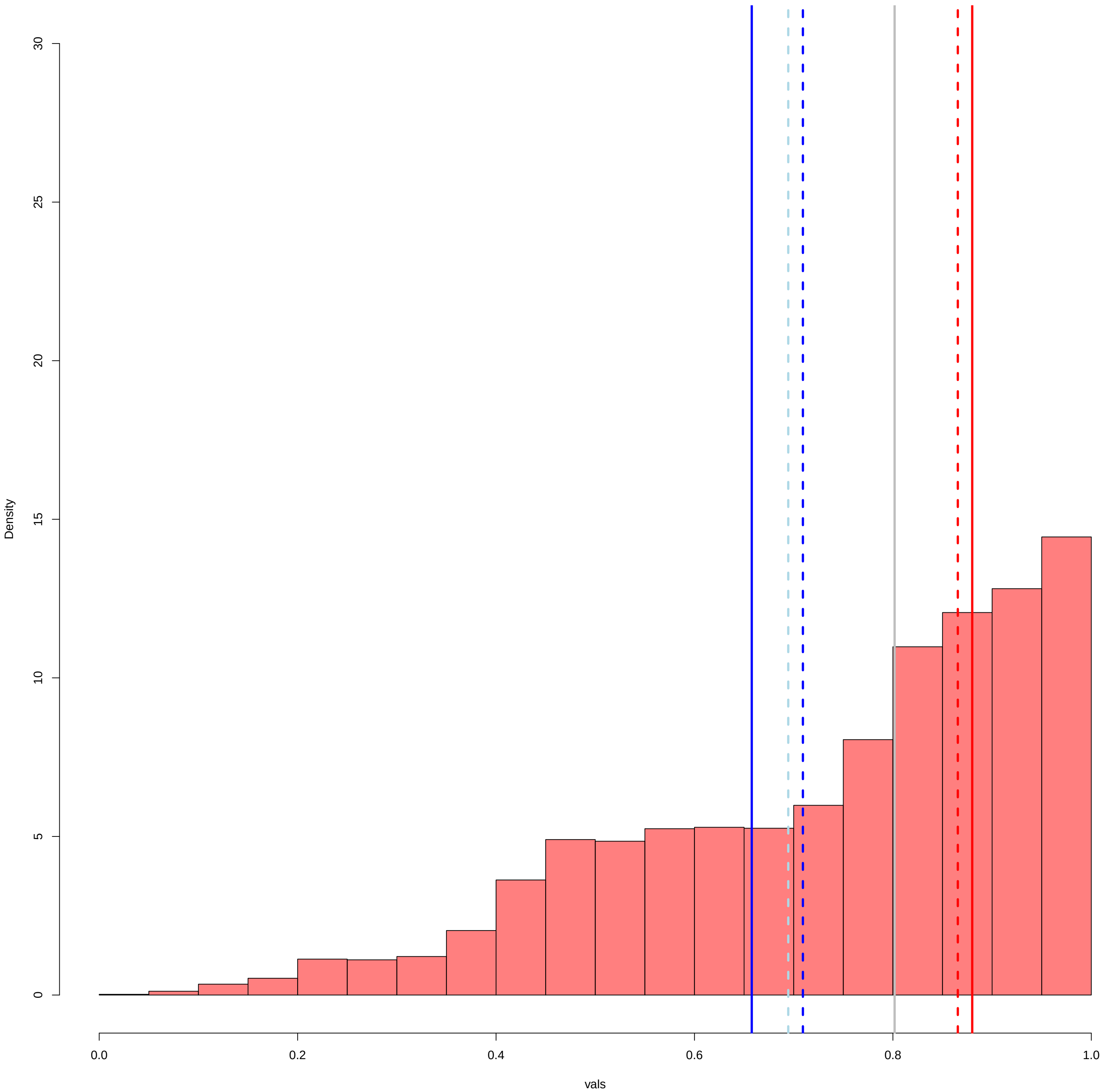
SCN2A: PROVEAN_converted_rankscore



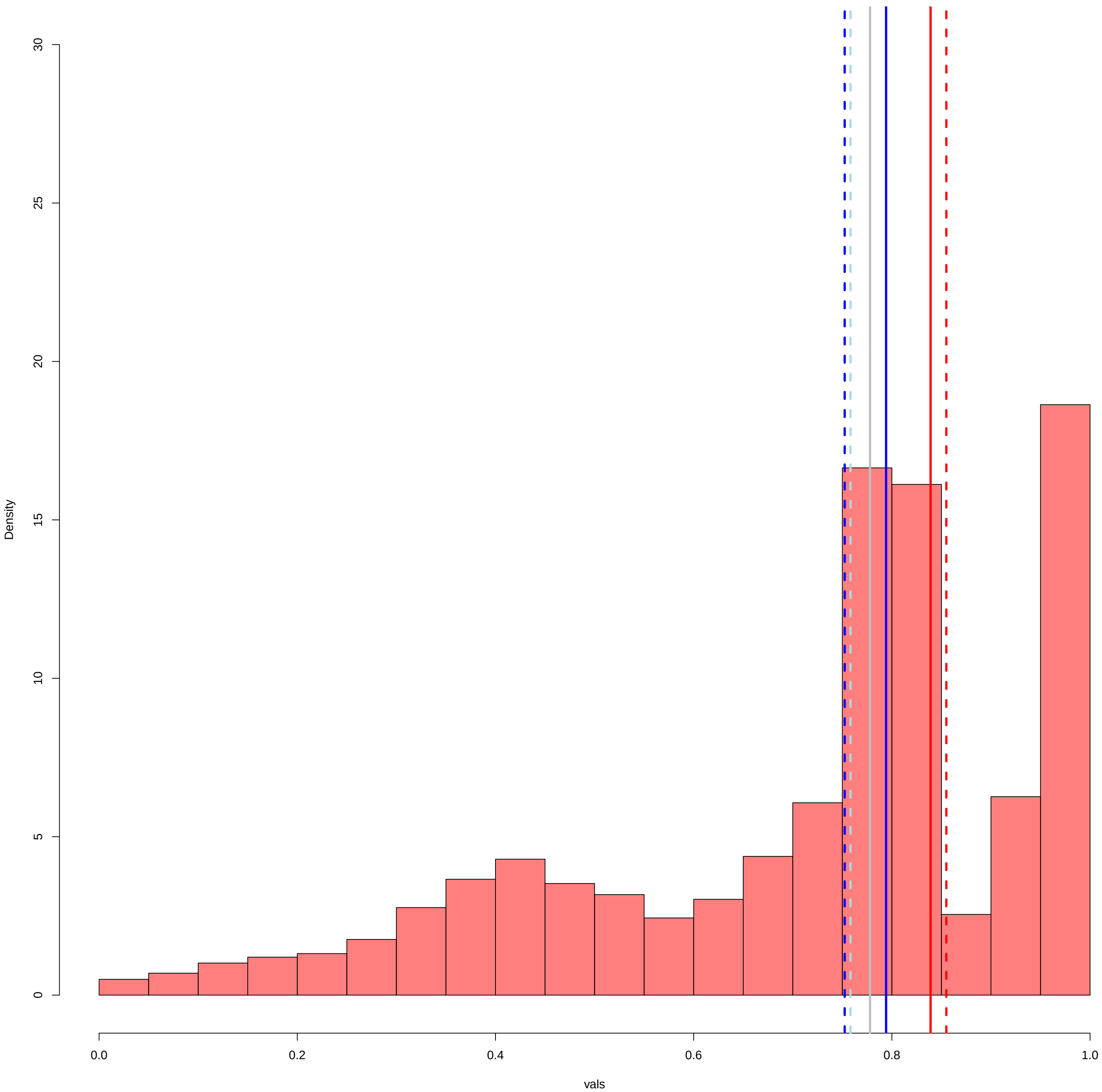
SCN2A: VEST3_rankscore



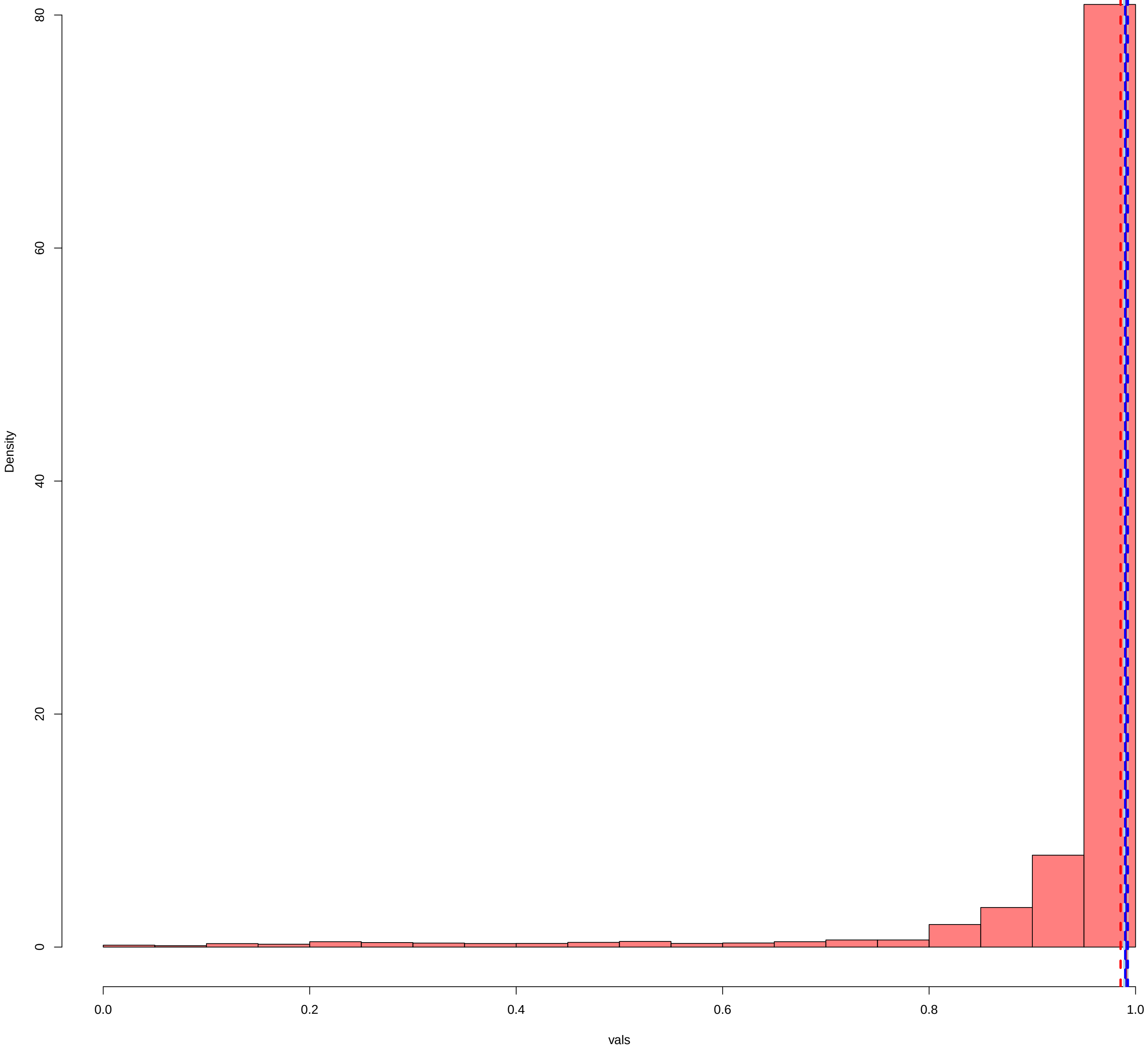
SCN2A: fathmm-MKL_coding_rankscore



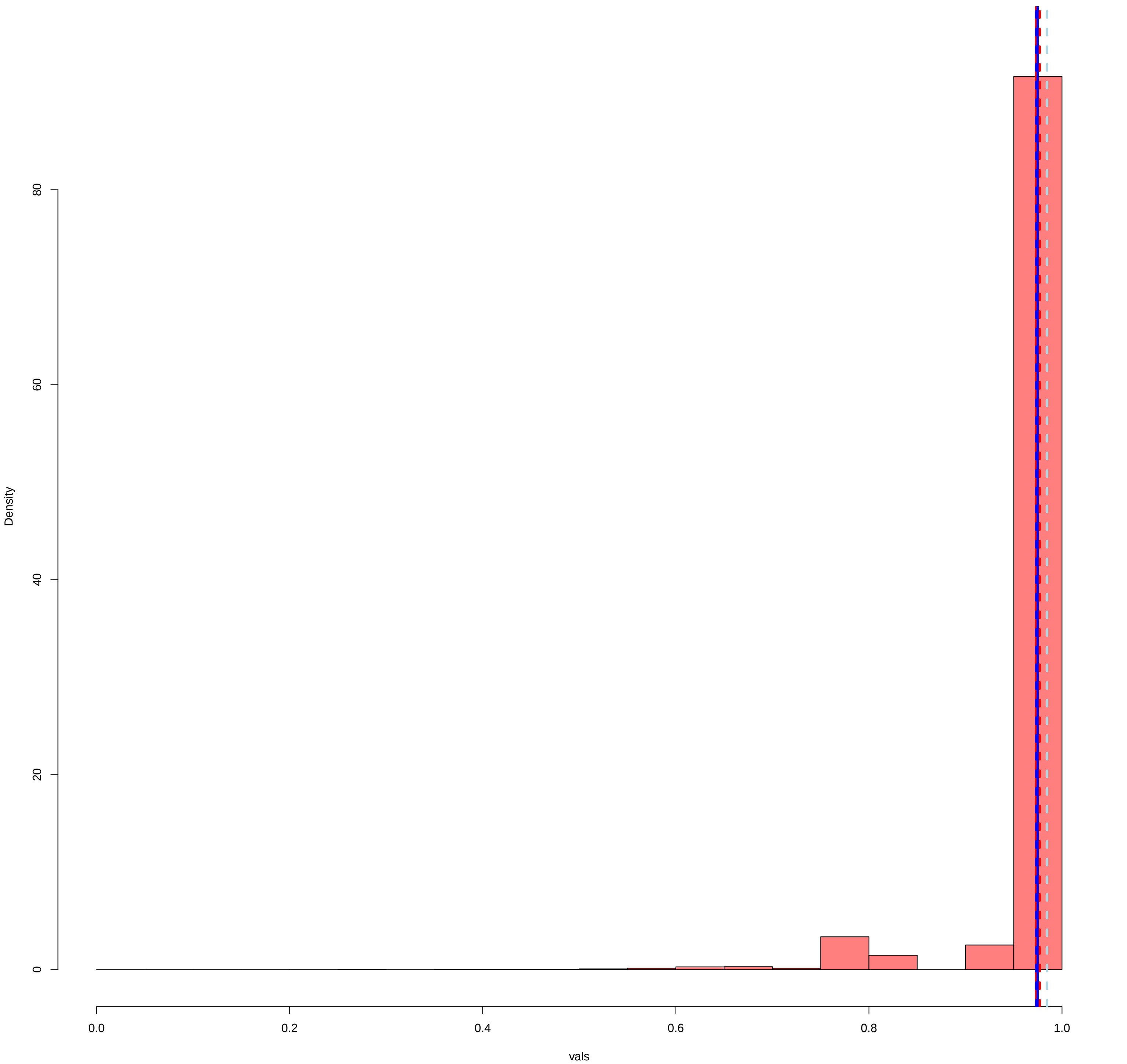
SCN2A: SiPhy_29way_logOdds_rankscore



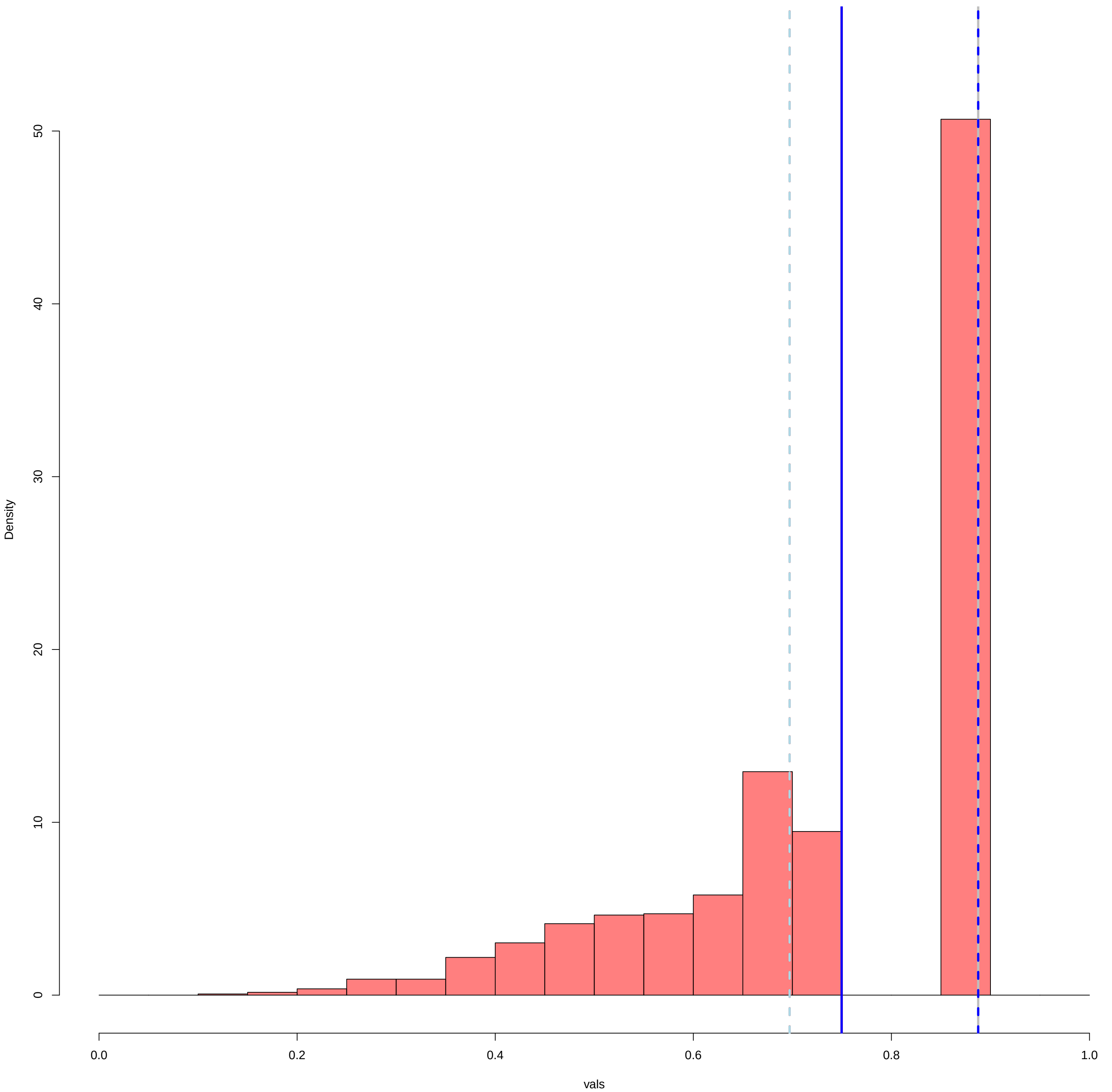
SCN2A: priPhCons



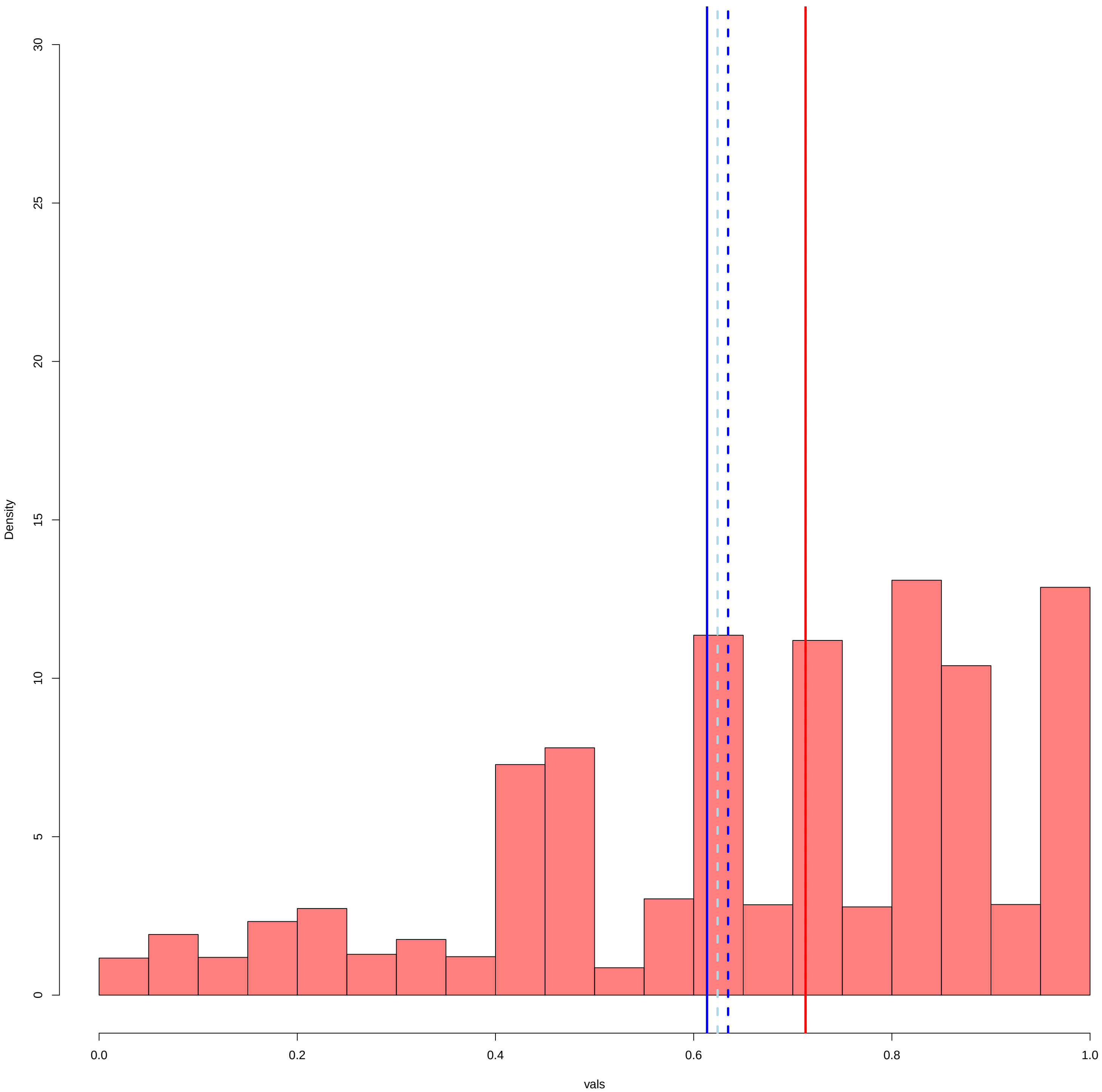
SCN2A: priPhyloP



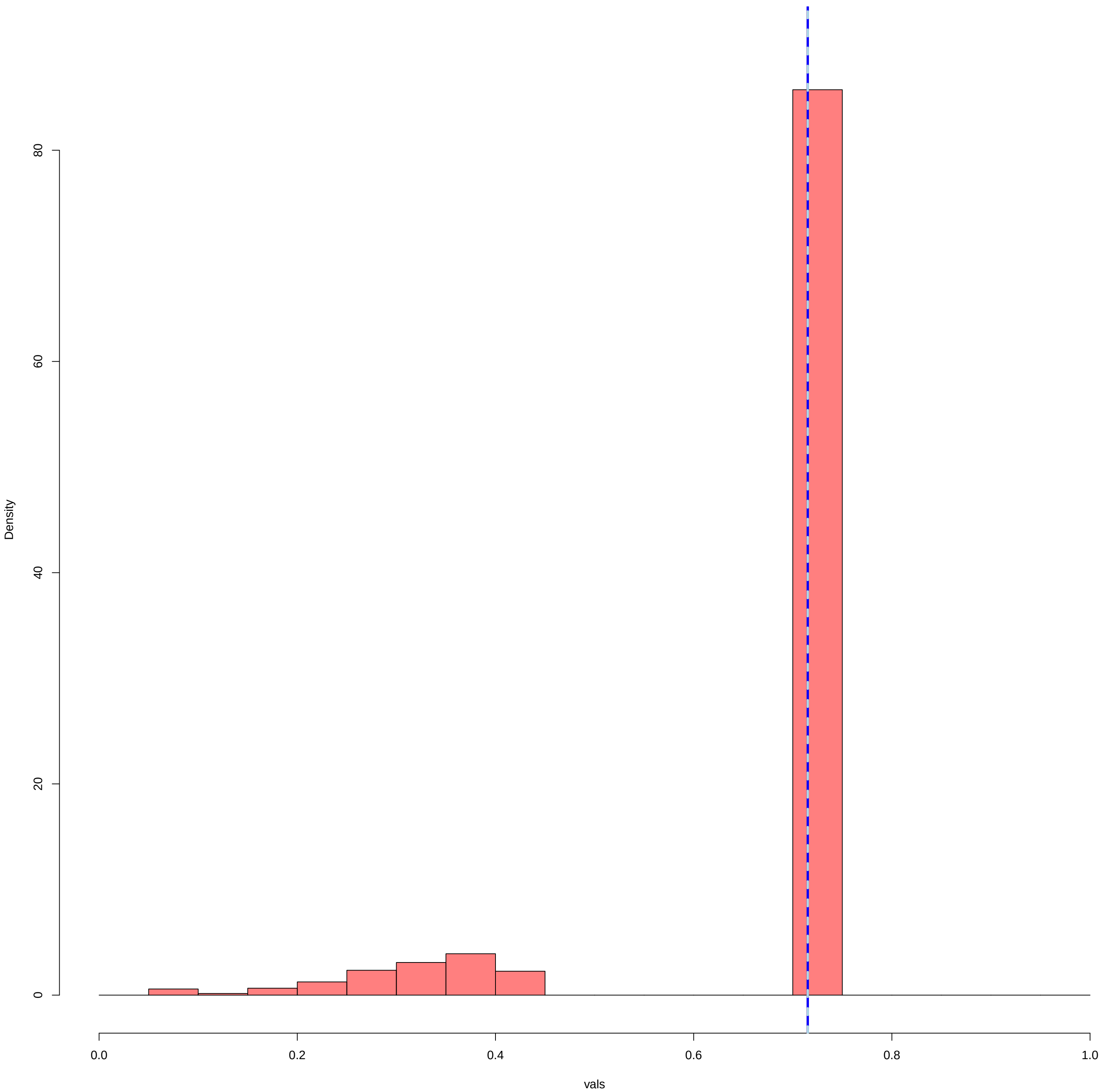
SCN2A: phastCons20way_mammalian_rankscore



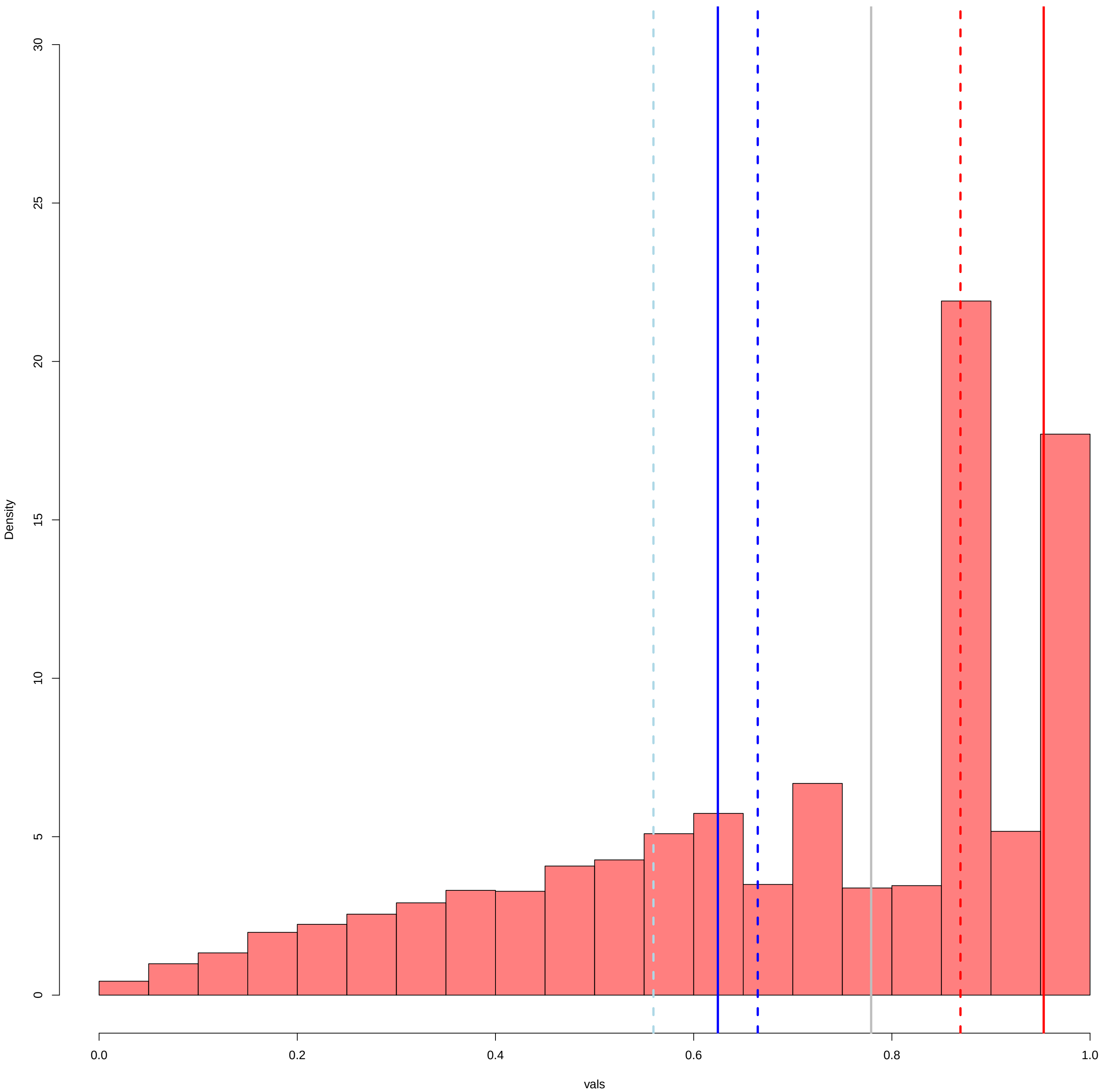
SCN2A: phyloP20way_mammalian_rankscore



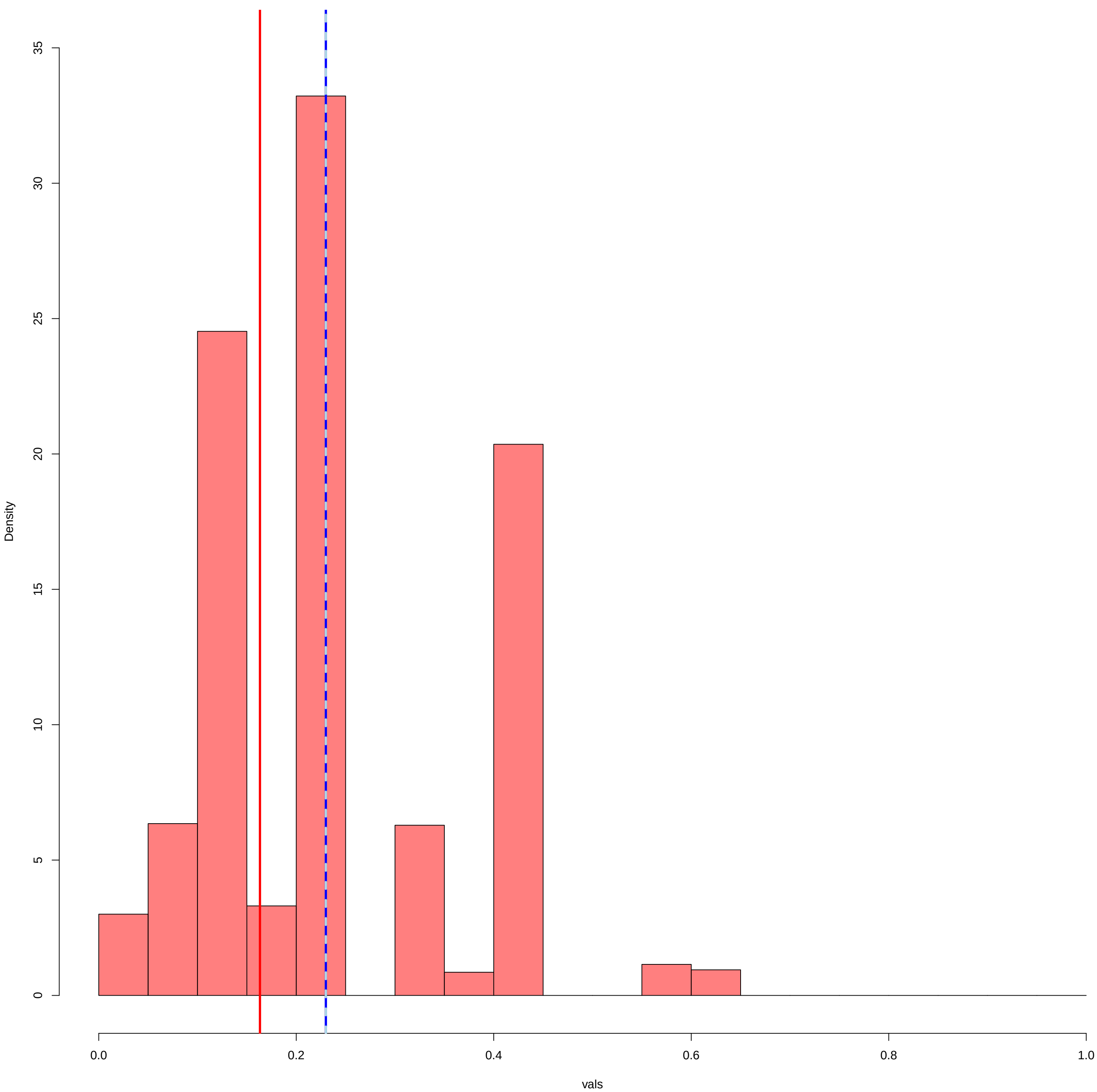
SCN2A: phastCons100way Vertebrate RankScore



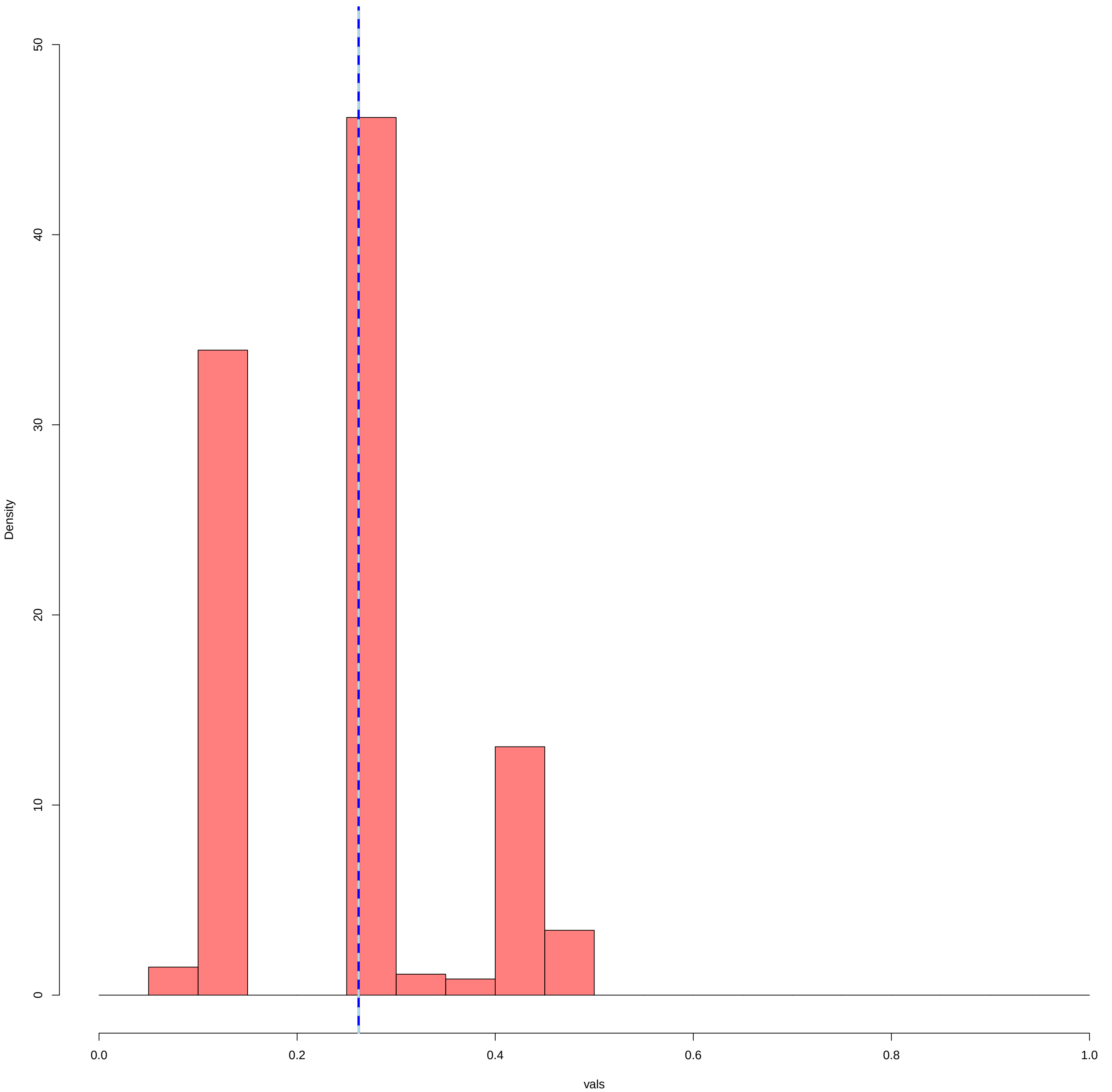
SCN2A: phyloP100way_vertebrate_rankscore



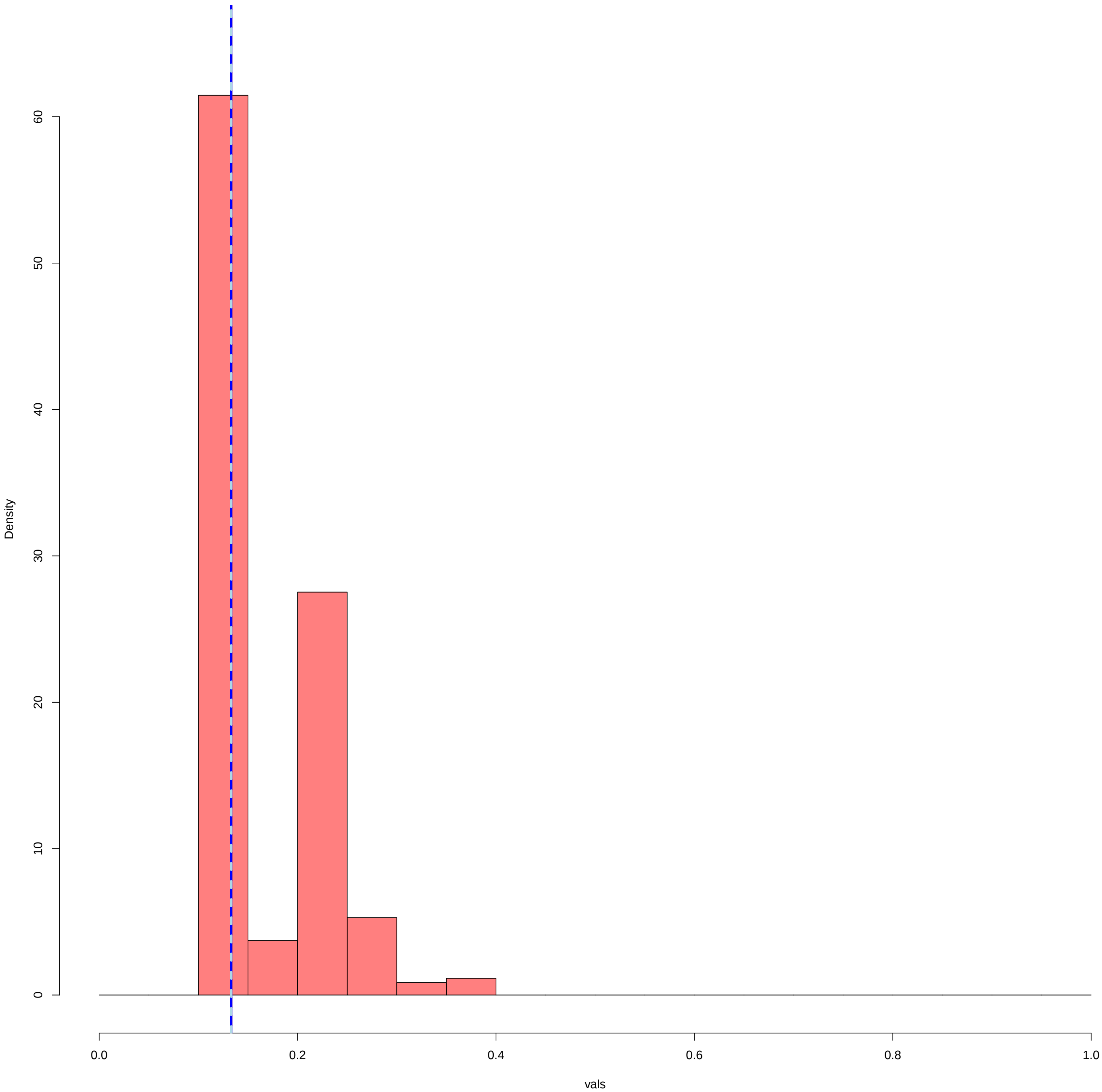
SCN2A: H1-hESC_fitCons_score_rankscore



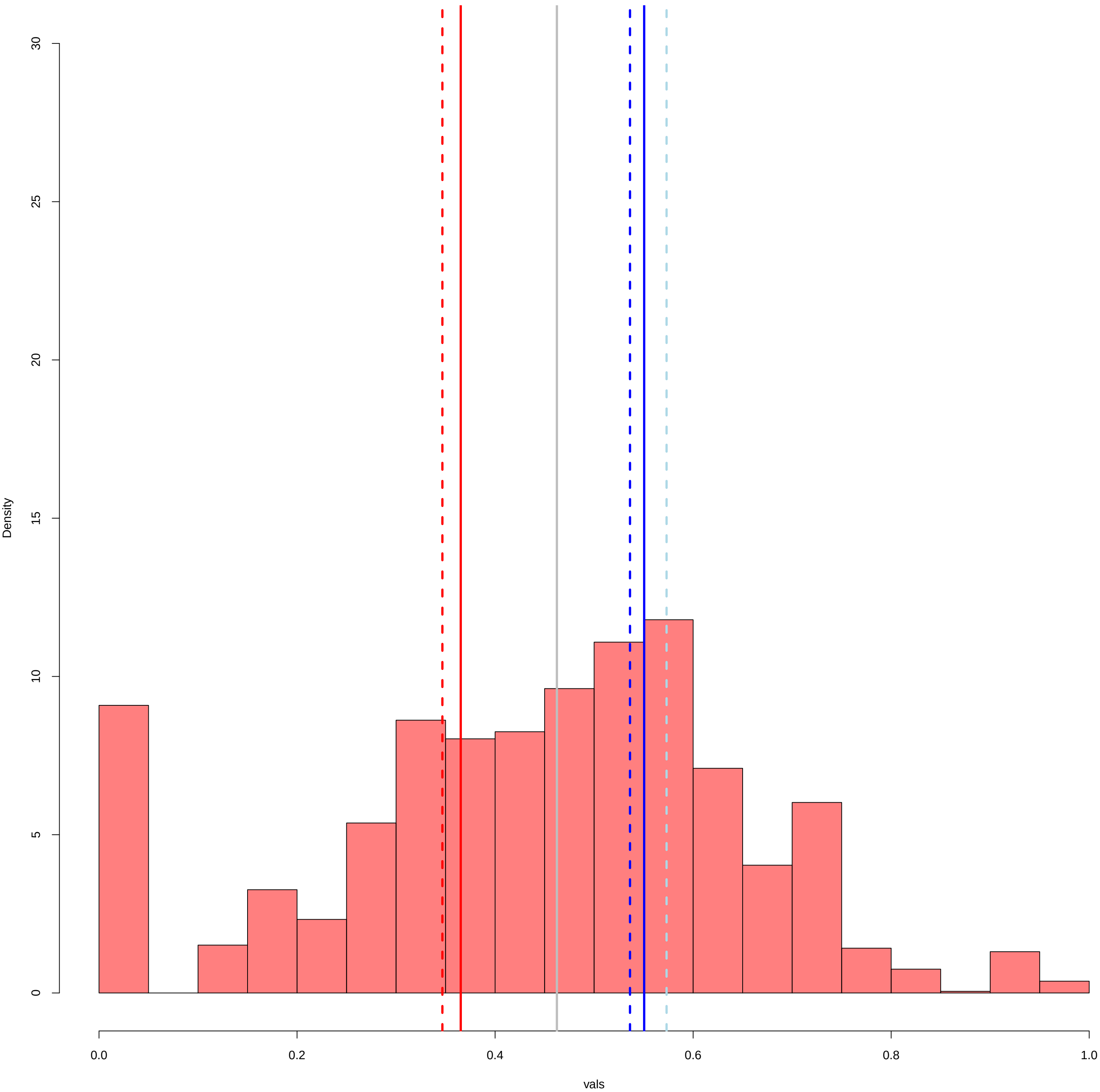
SCN2A: HUVEC_fitCons_score_rankscore



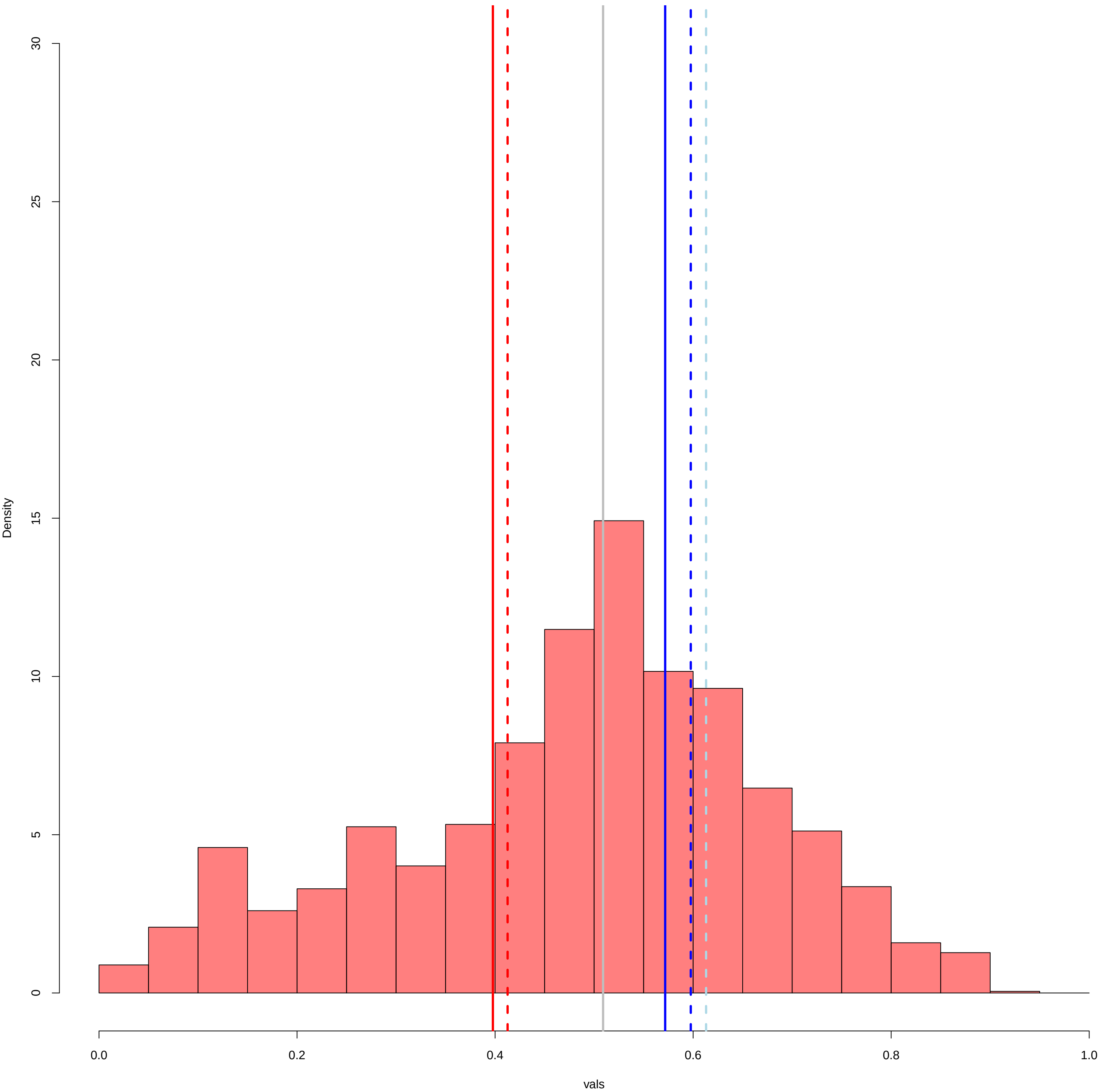
SCN2A: integrated_fitCons_score_rankscore



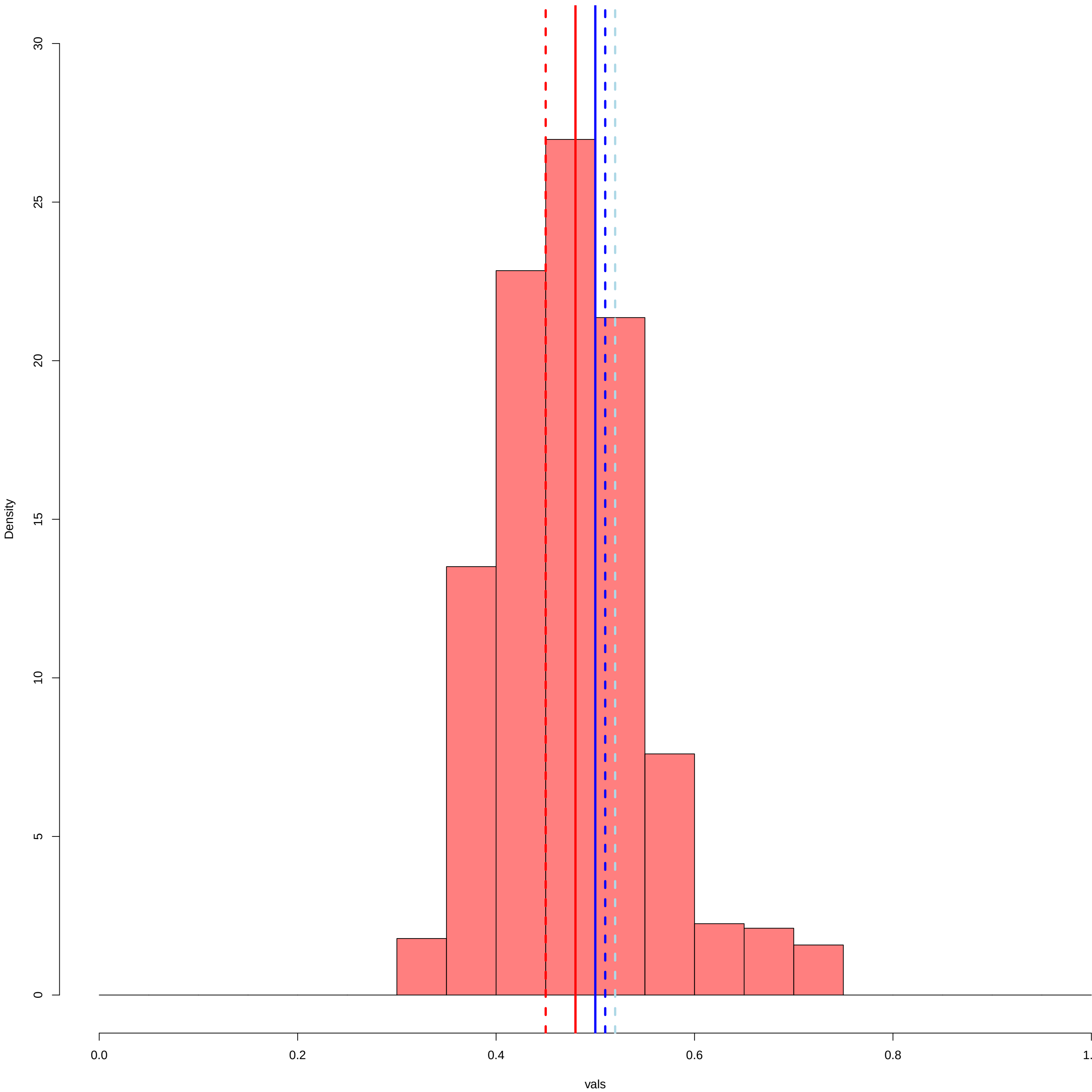
SCN2A: ExAC v1 MTR



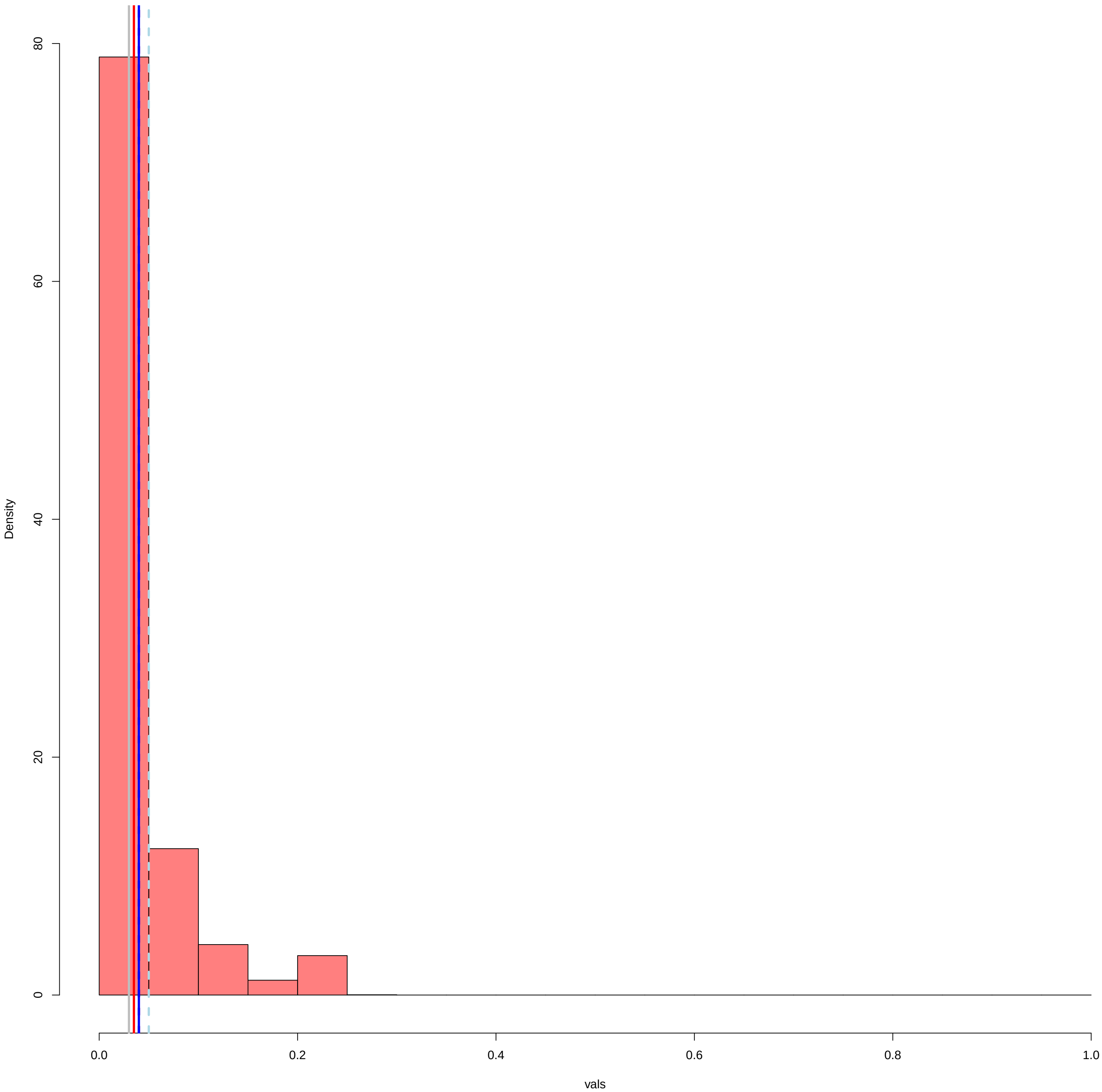
SCN2A: ExAC v2 & gnomAD MTR



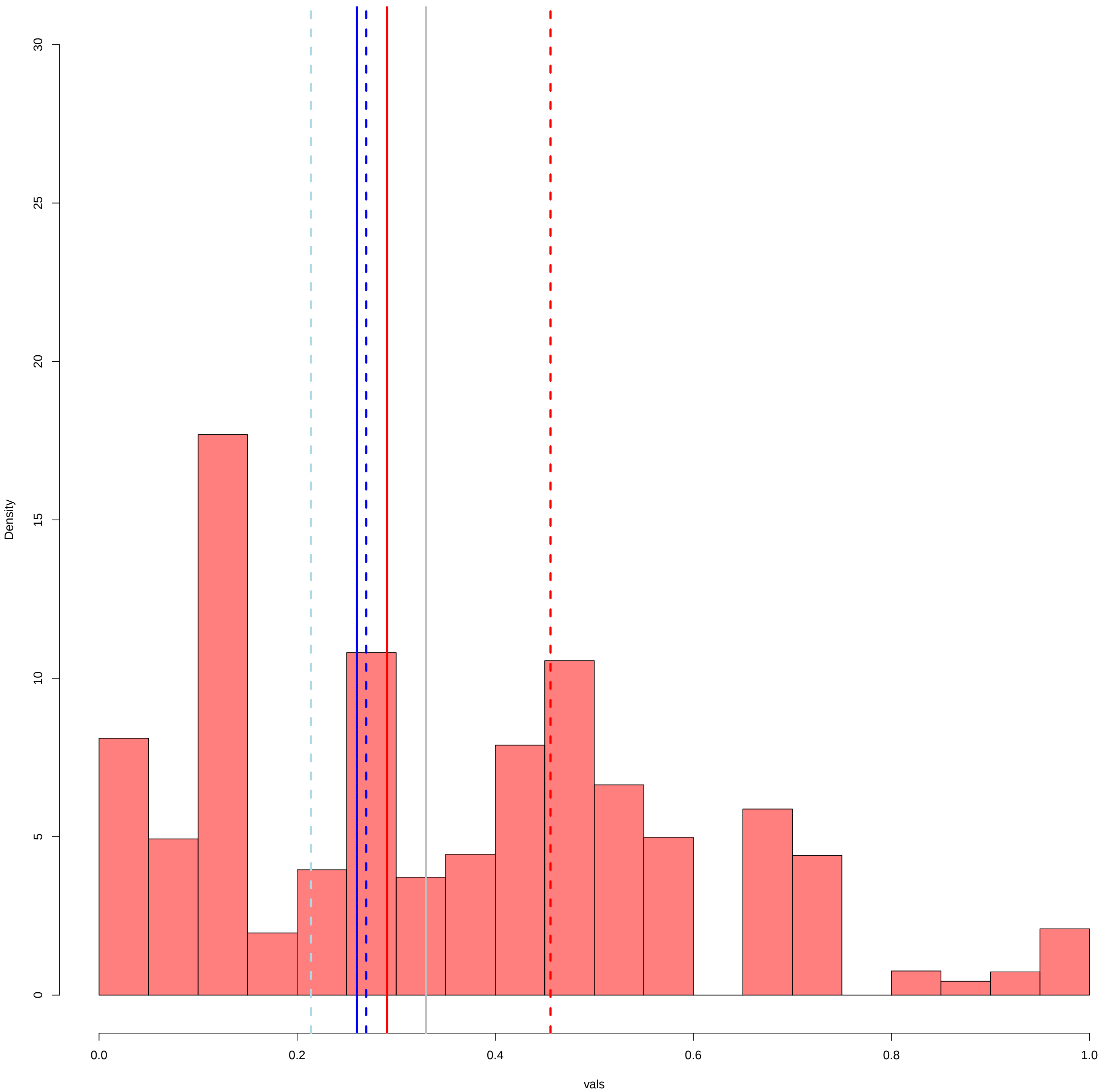
SCN8A: GC (Percent GC content in a window of +/-75bp)



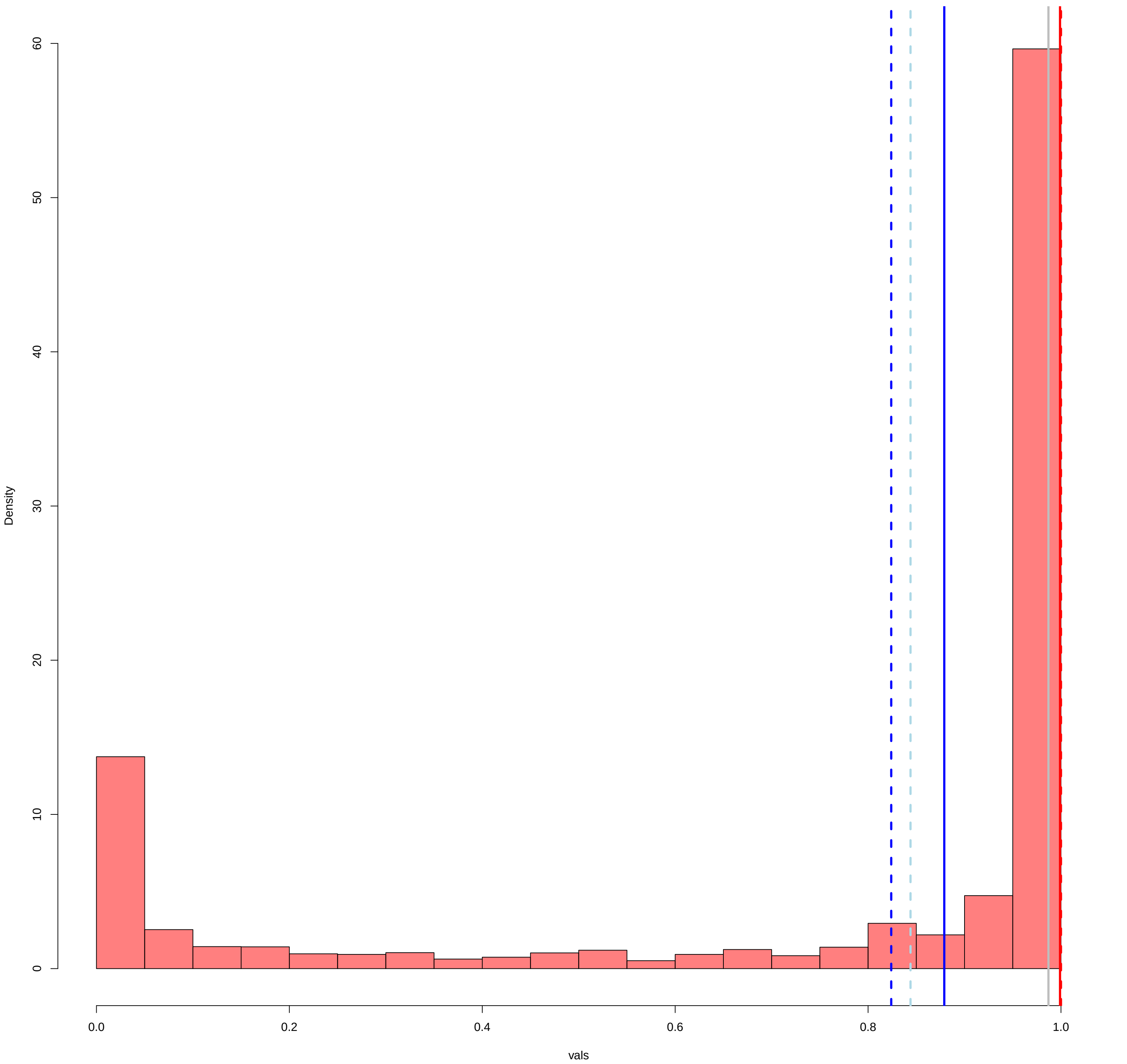
SCN8A: CpG (Percent CpG in a window of +/-75bp)



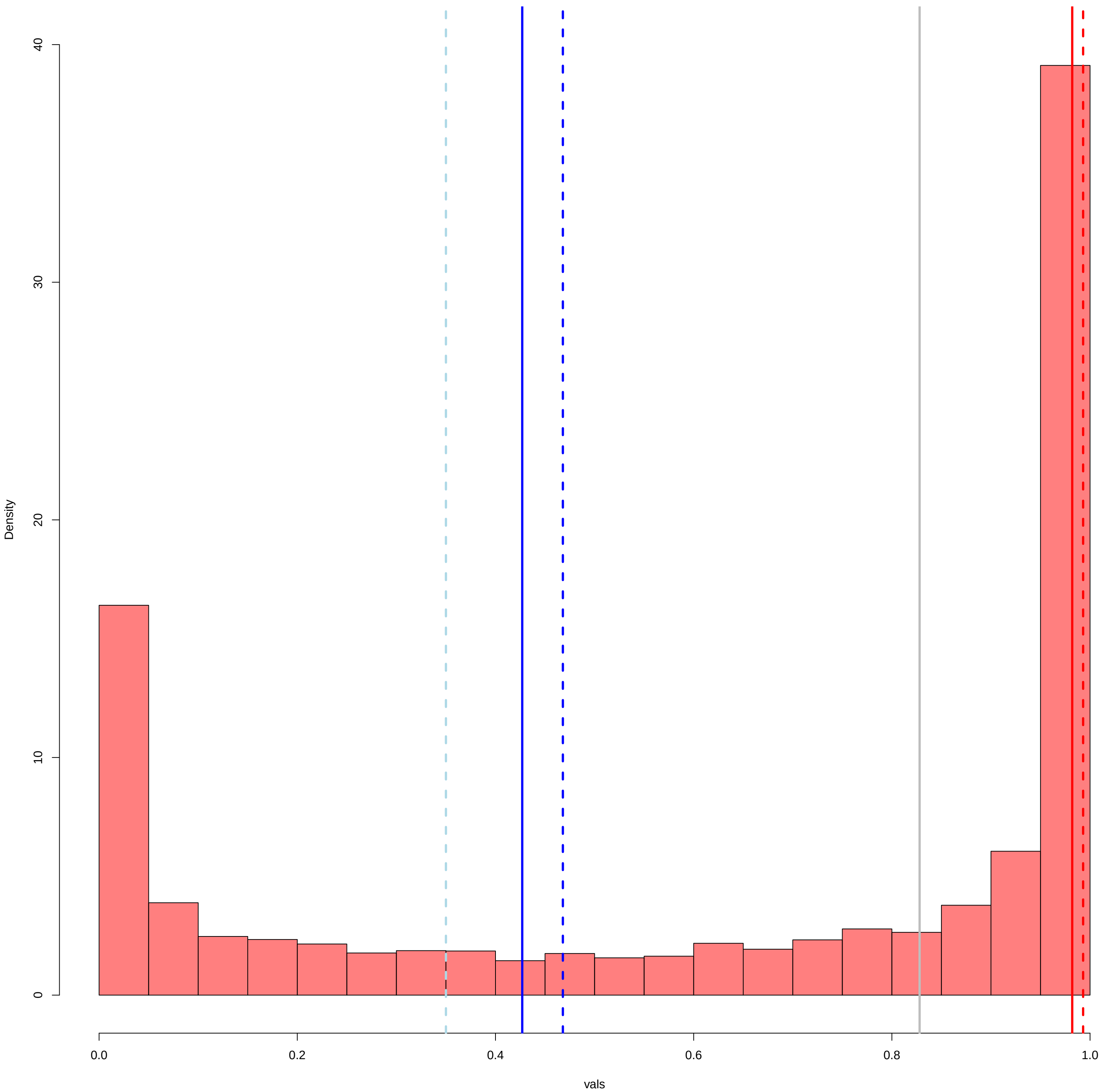
SCN8A: Grantham



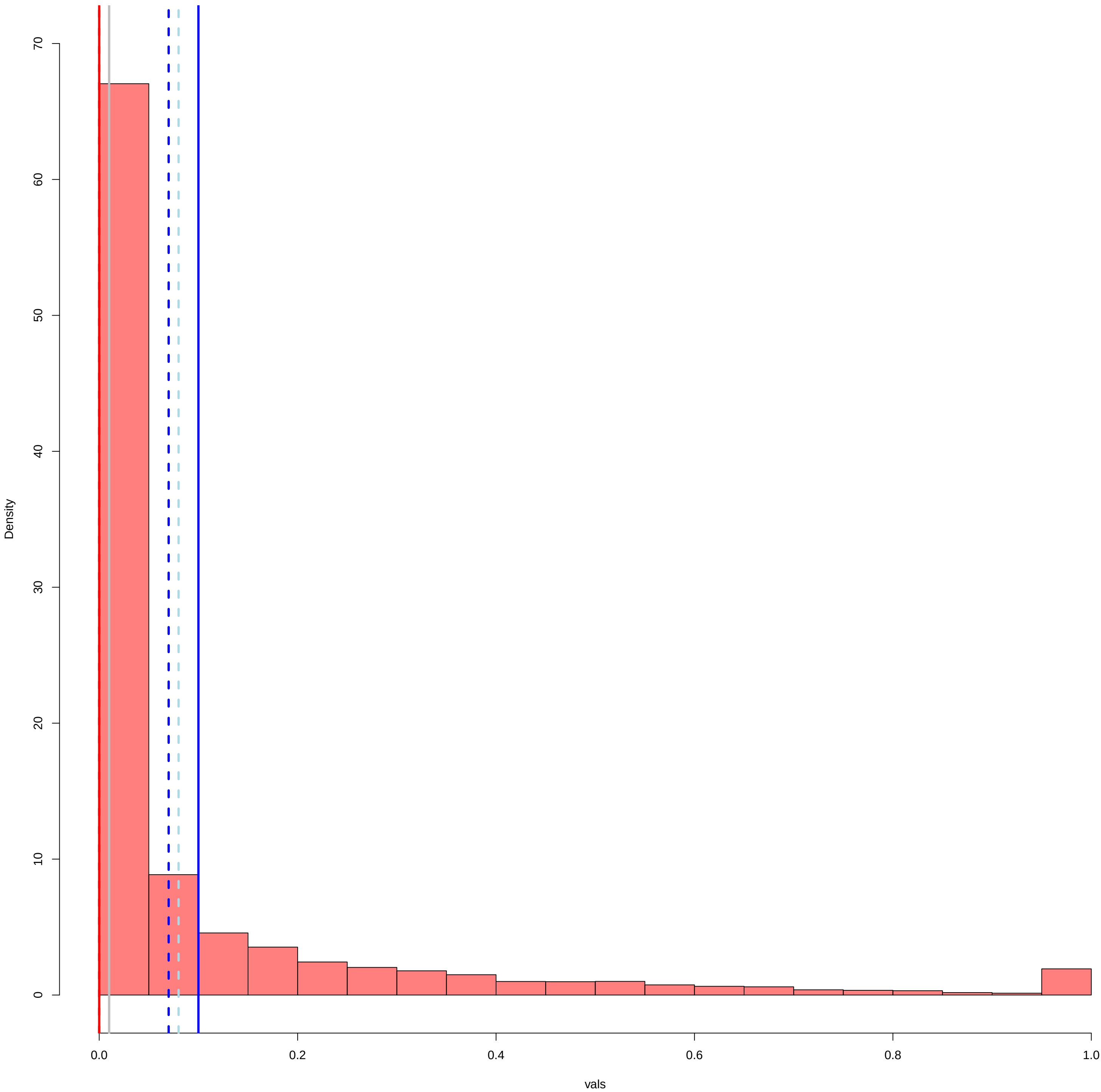
SCN8A: Hdiv quan



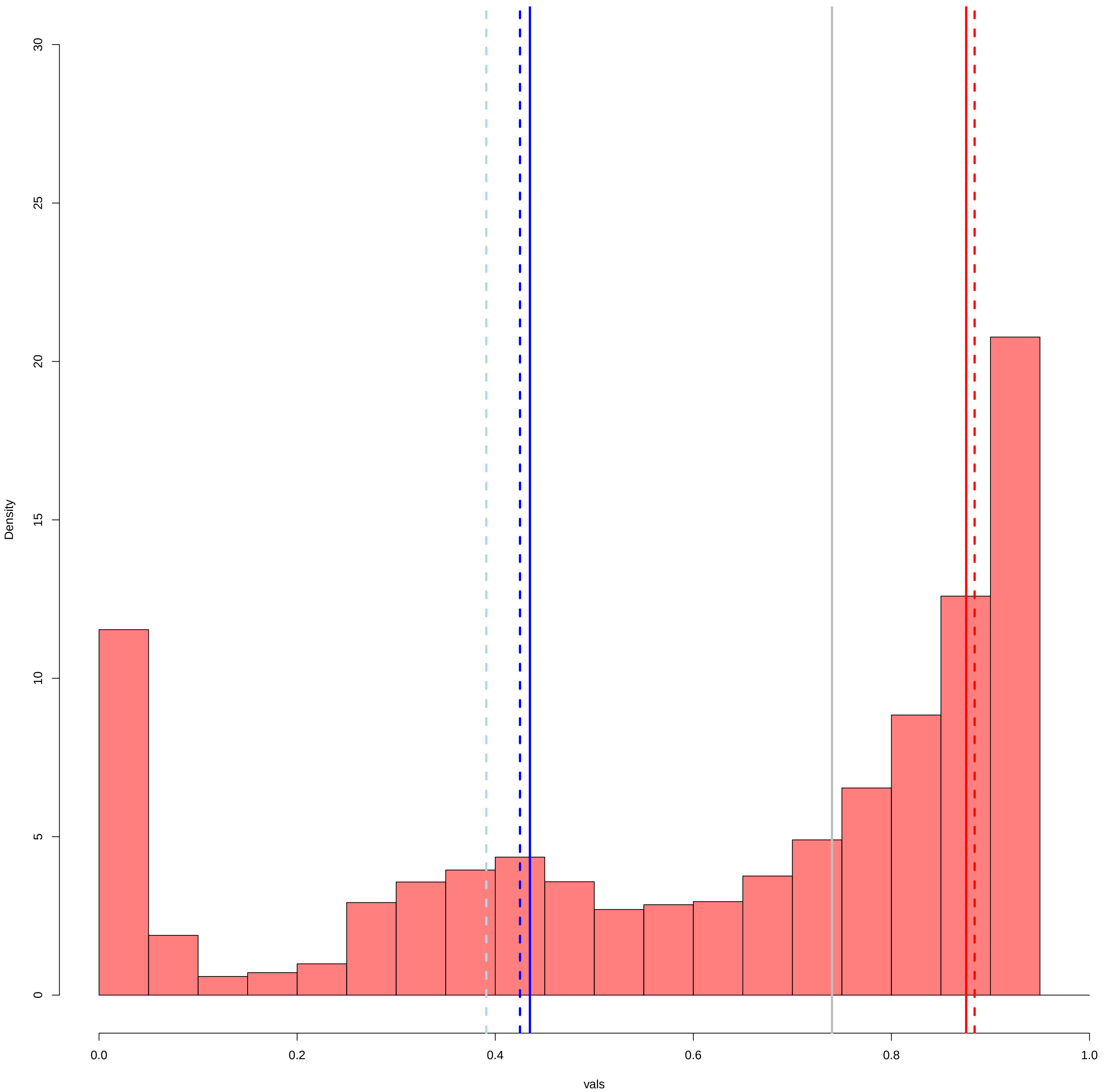
SCN8A: Hvar quan



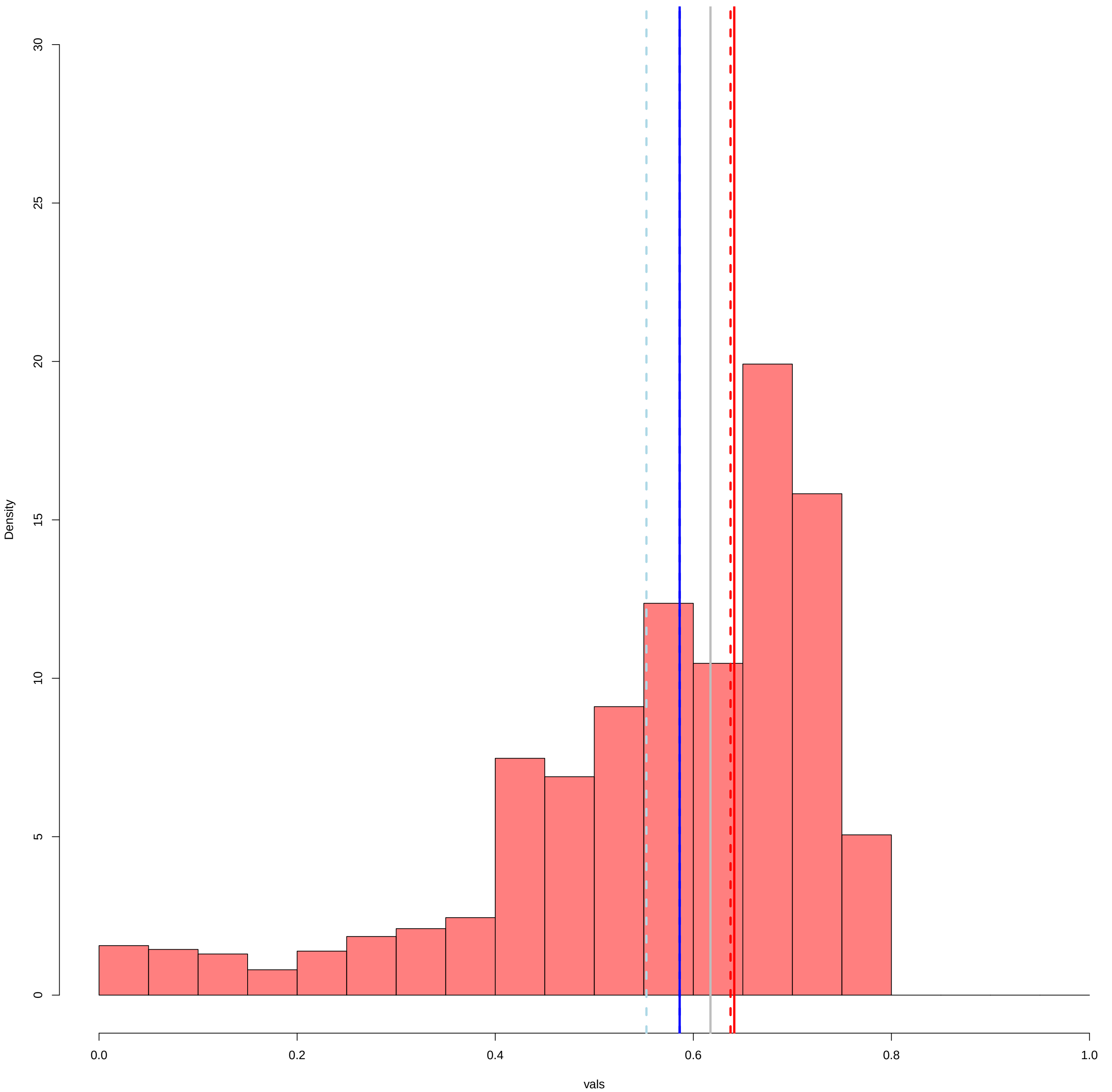
SCN8A: SIFT



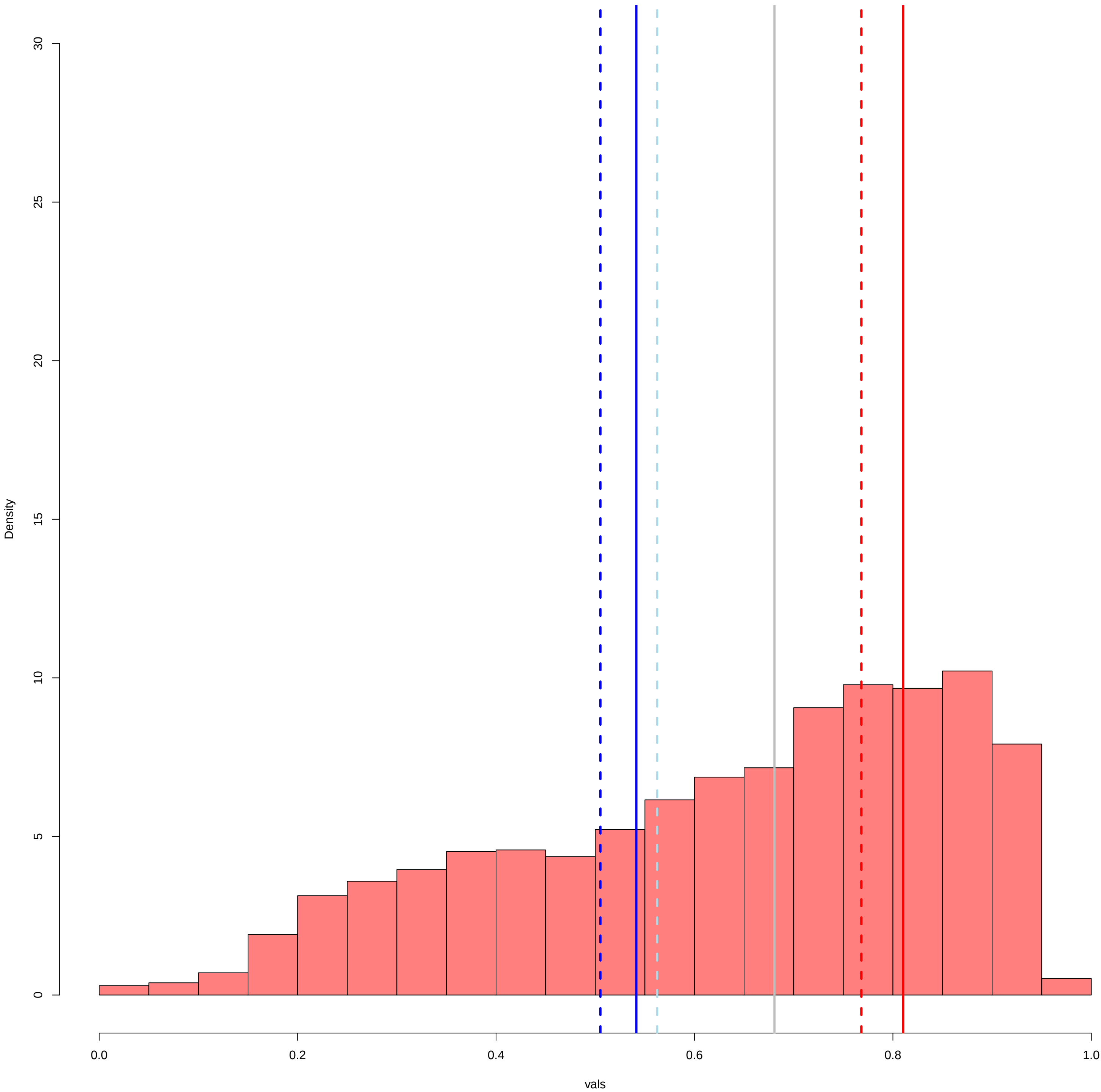
SCN8A: Condel



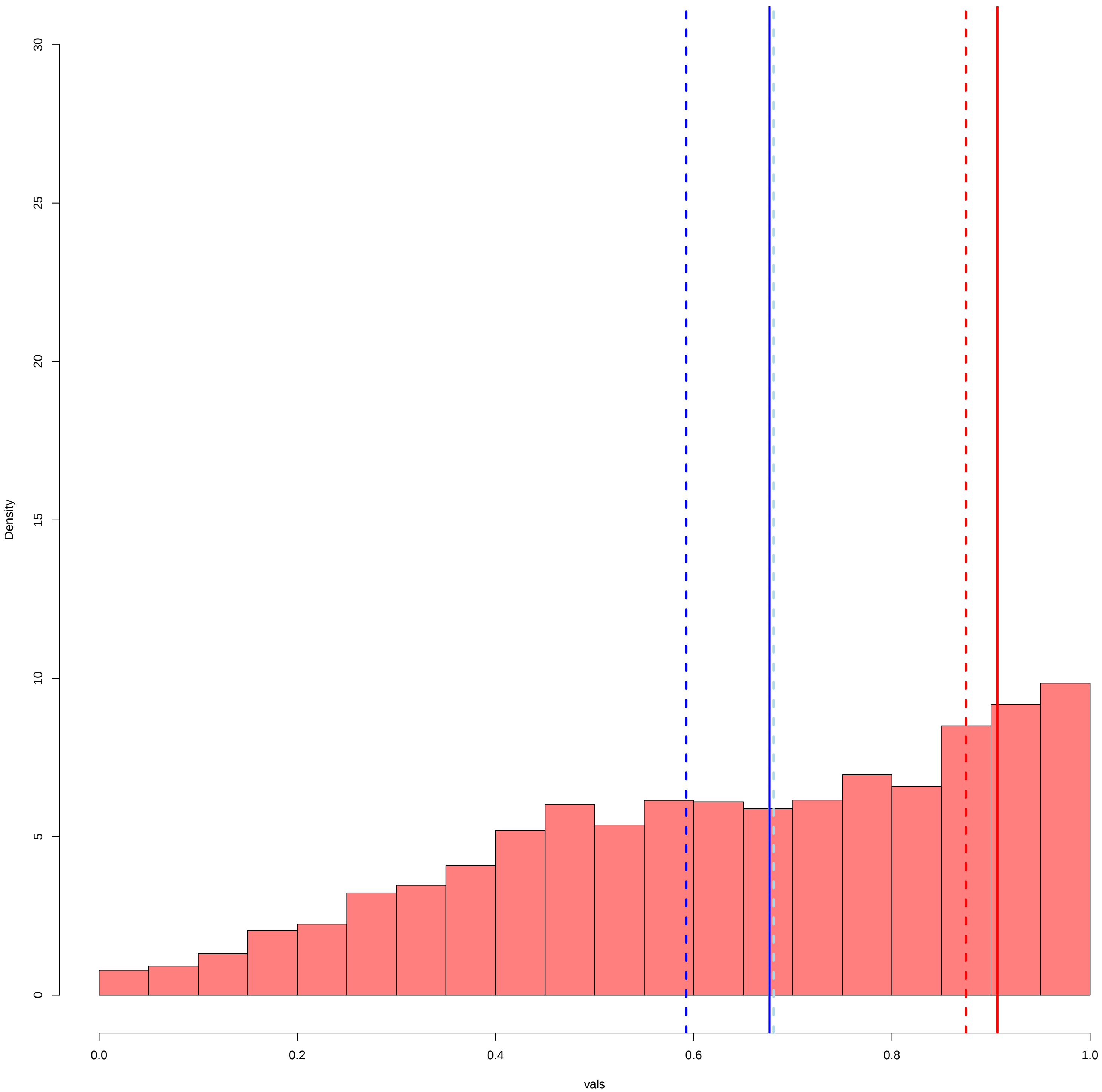
SCN8A: GERP++_RS_rankscore



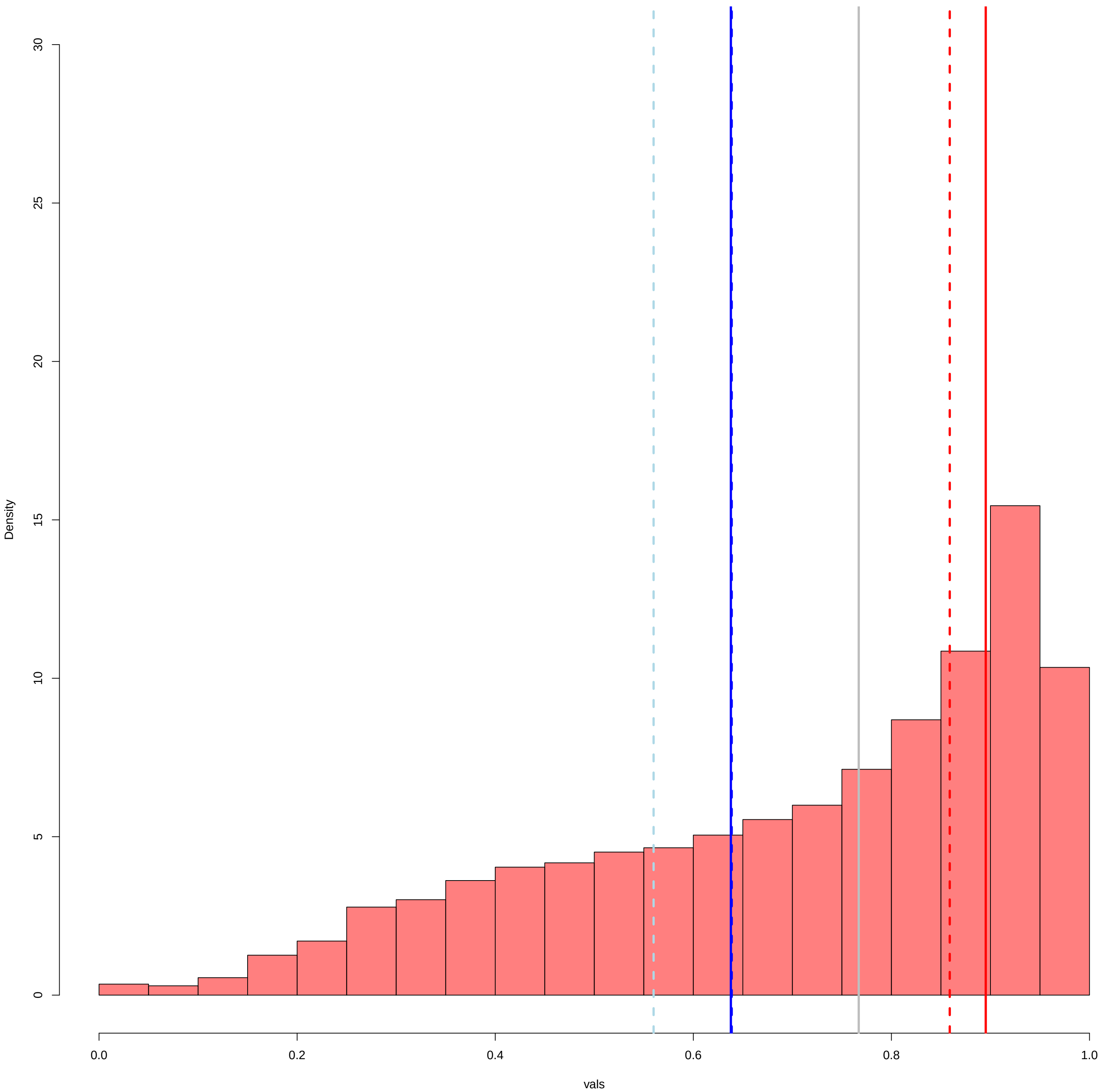
SCN8A: CADD_raw_rankscore



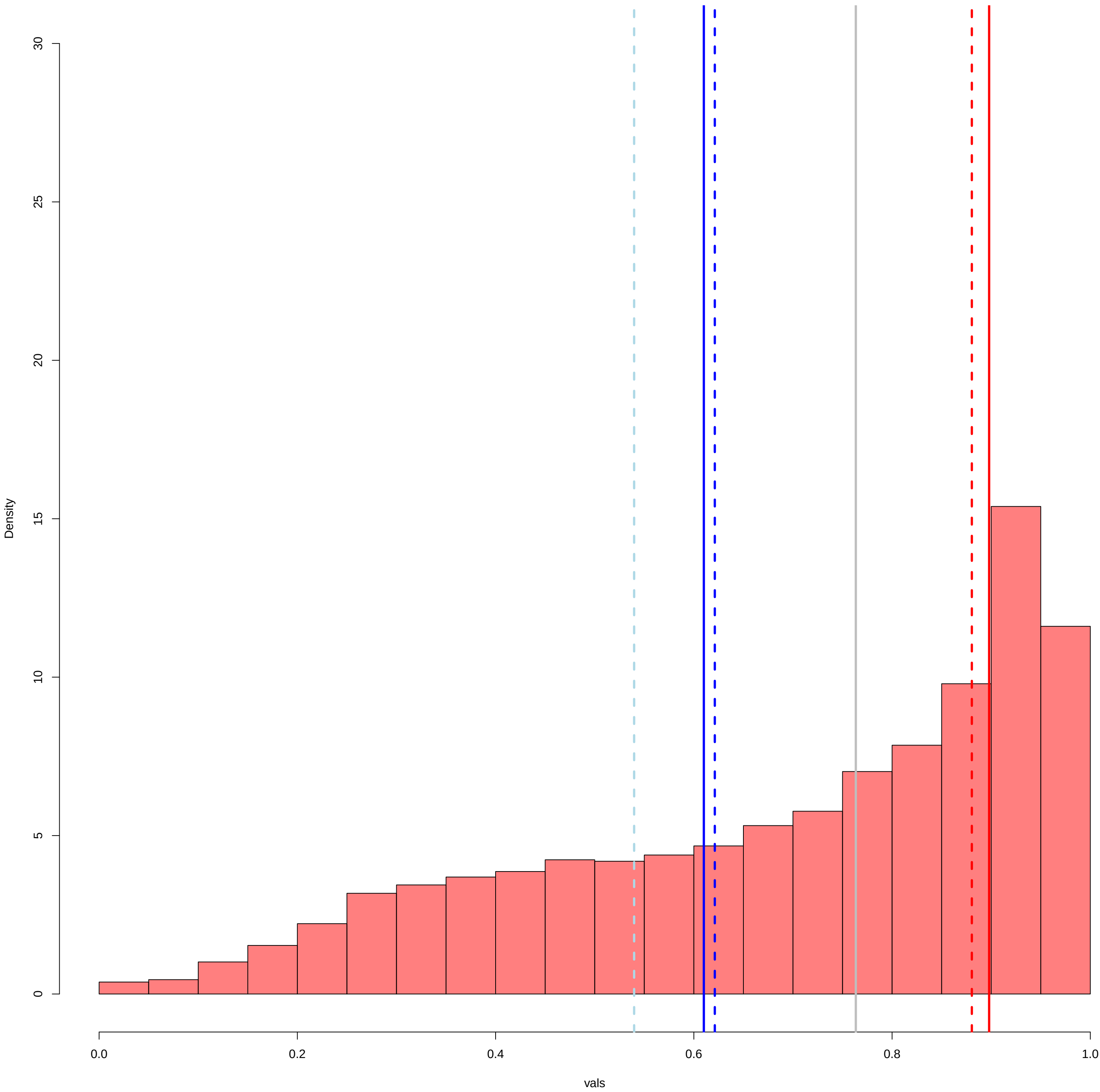
SCN8A: DANN_rankscore



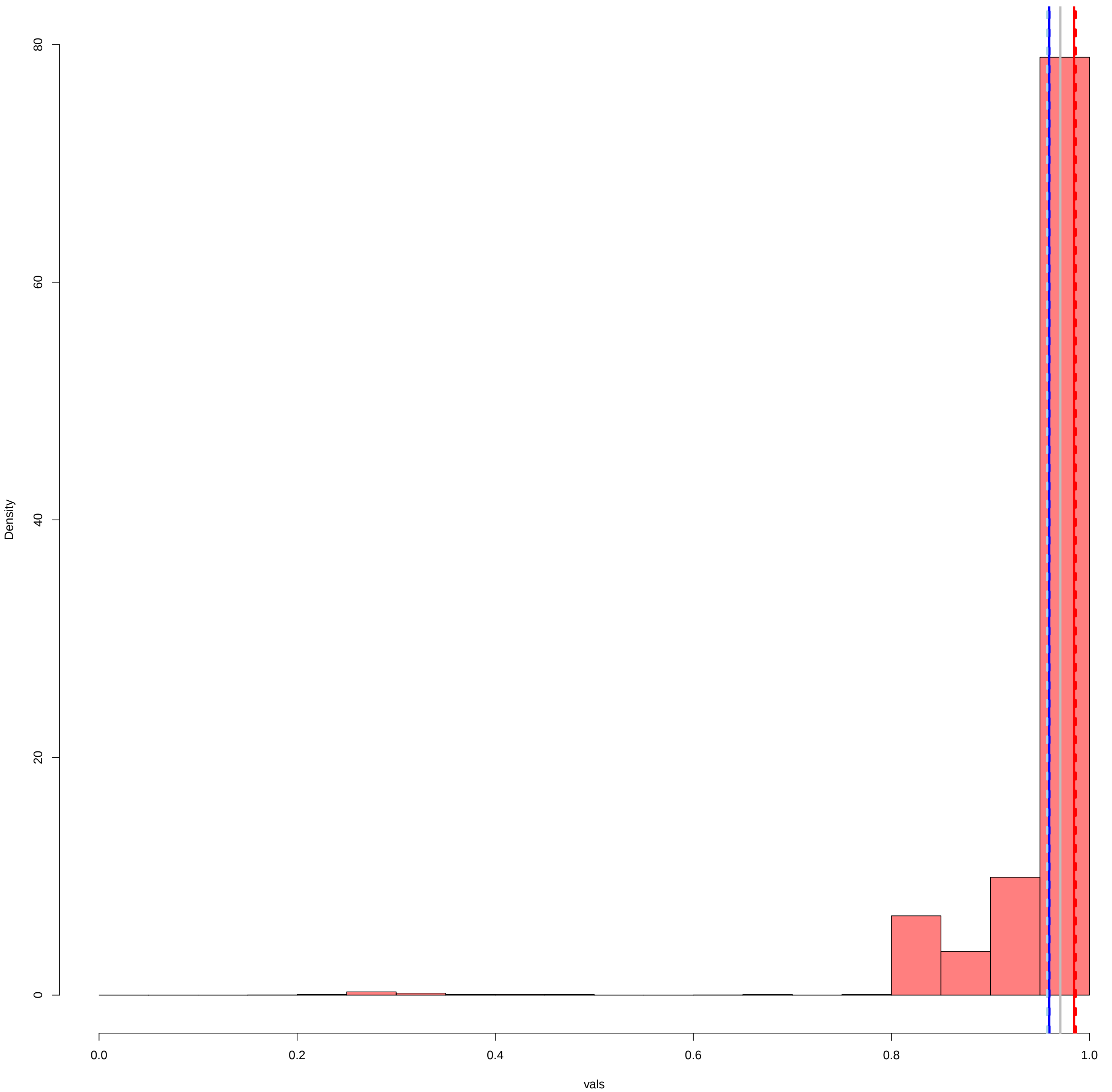
SCN8A: Eigen-PC-raw_rankscore



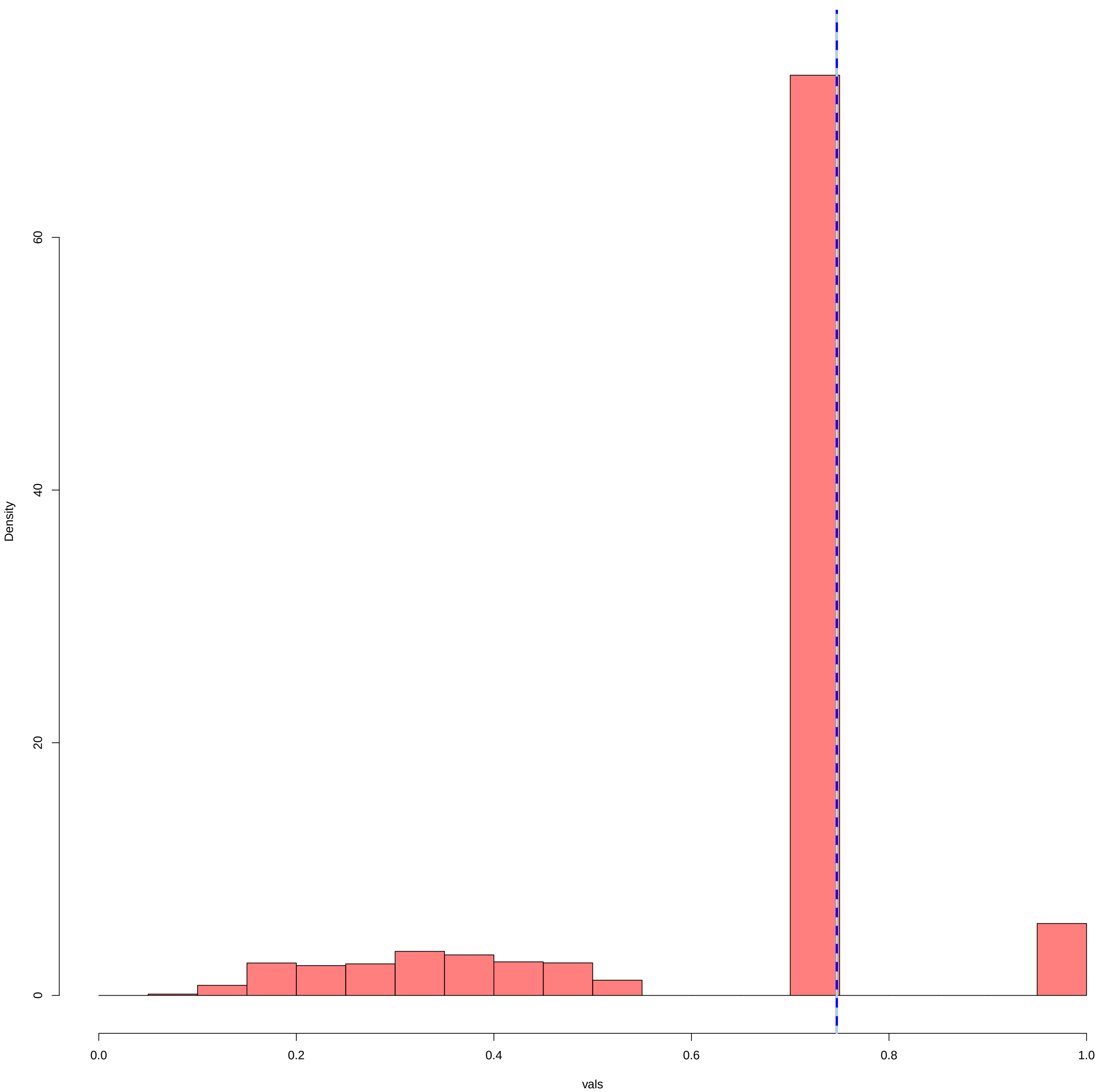
SCN8A: Eigen-row_rankscore



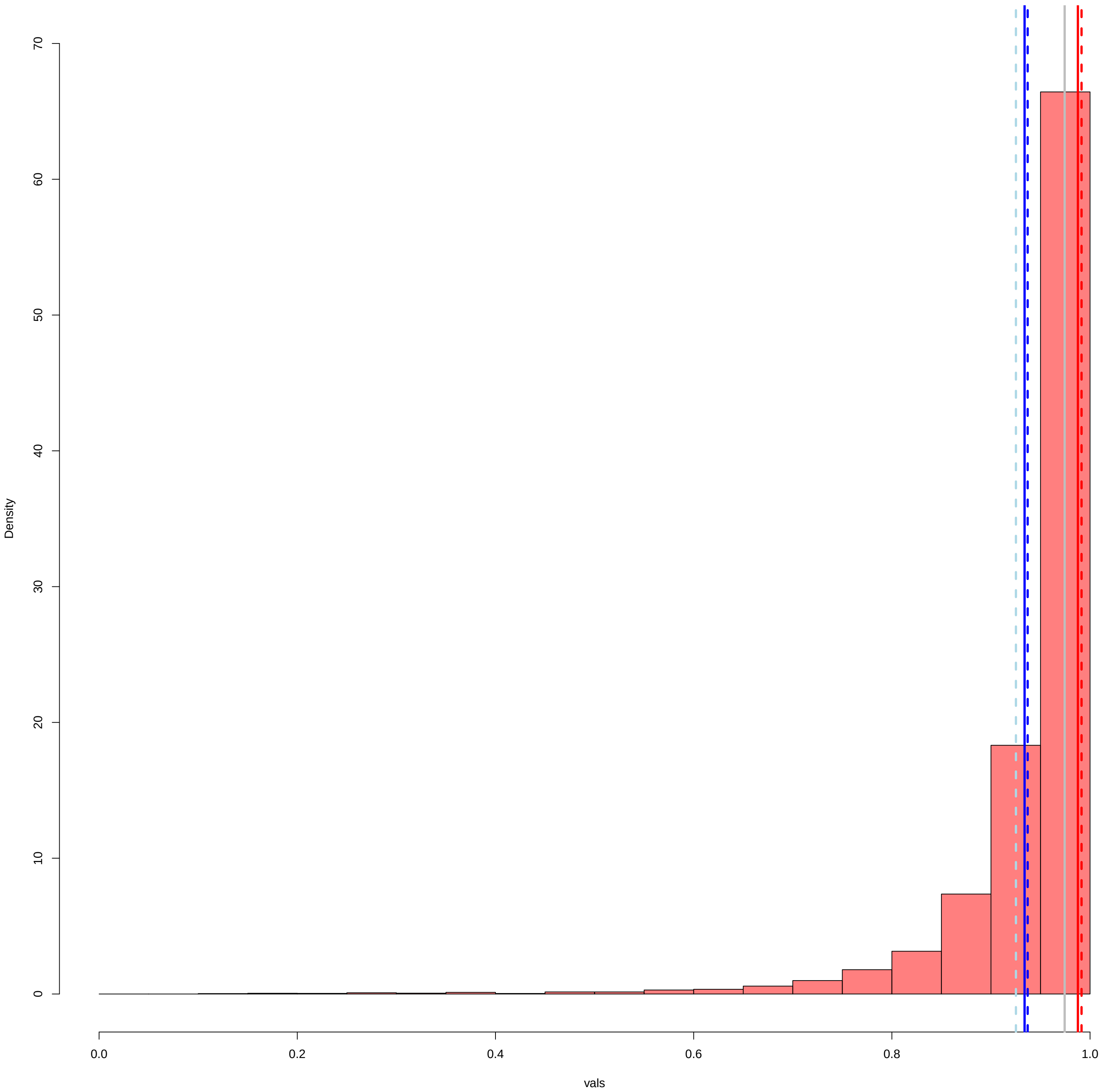
SCN8A: FATHMM_converted_rankscore



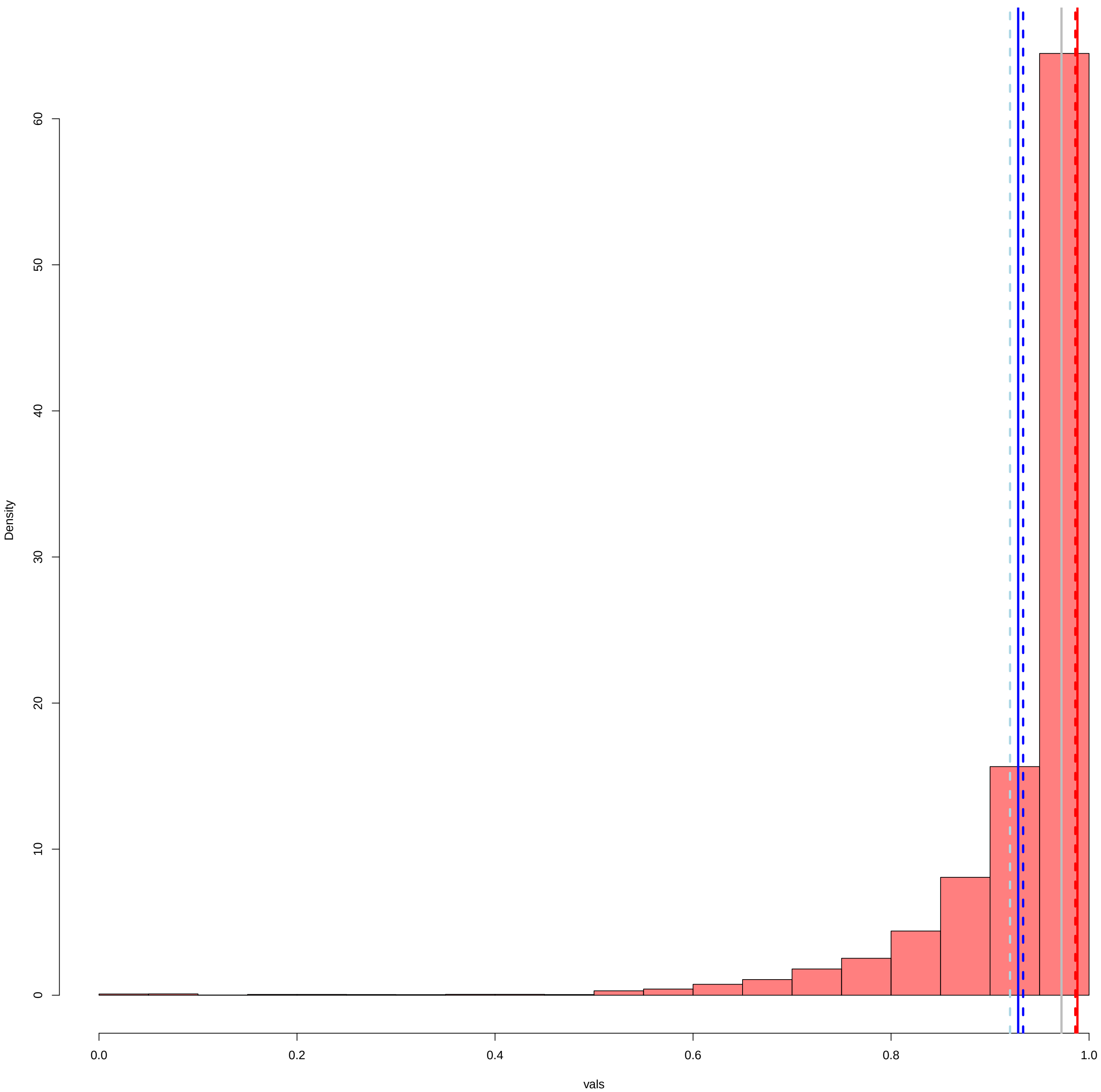
SCN8A: GenoCanyon_score_rankscore



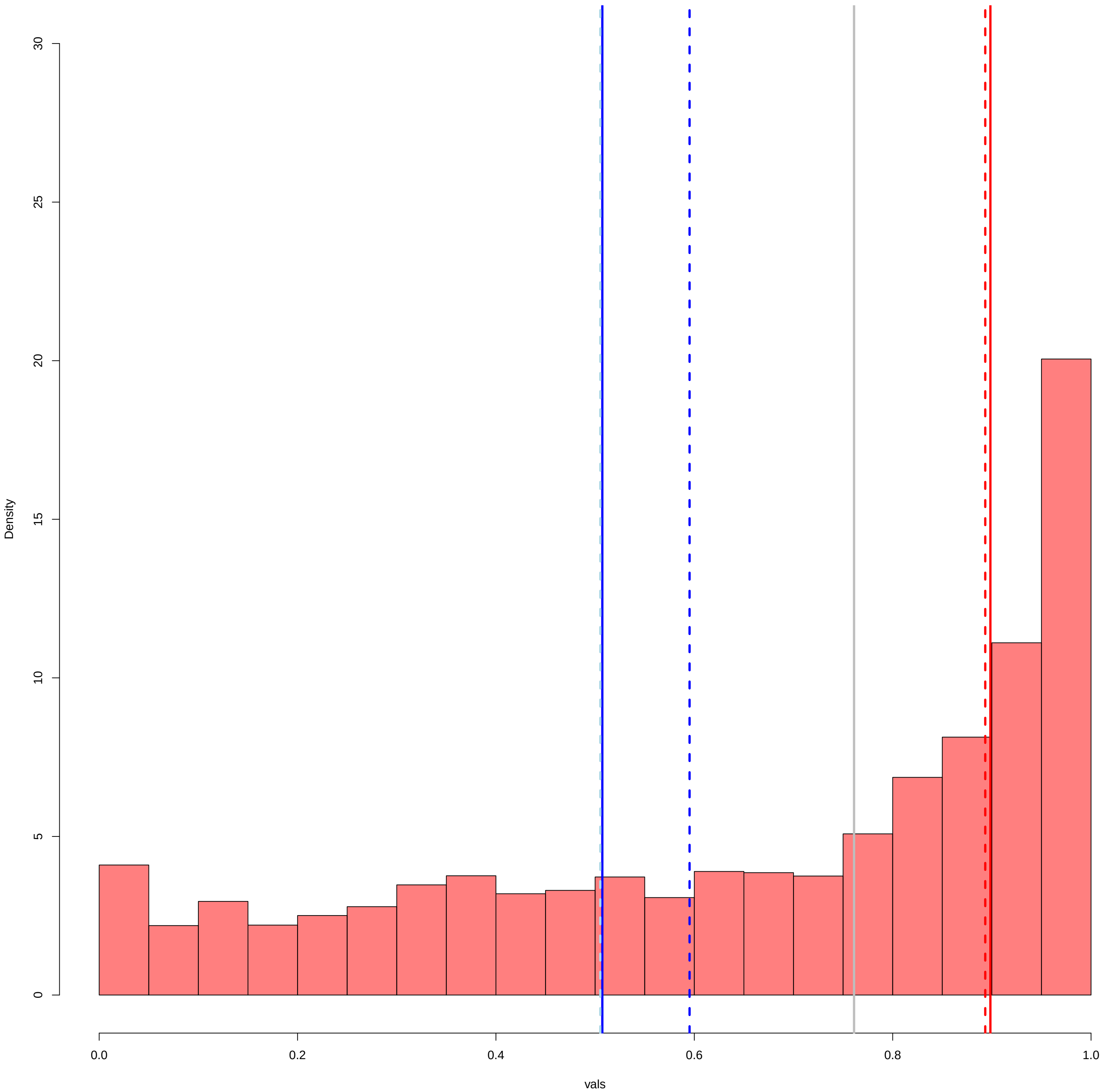
SCN8A: MetaLR_rankscore



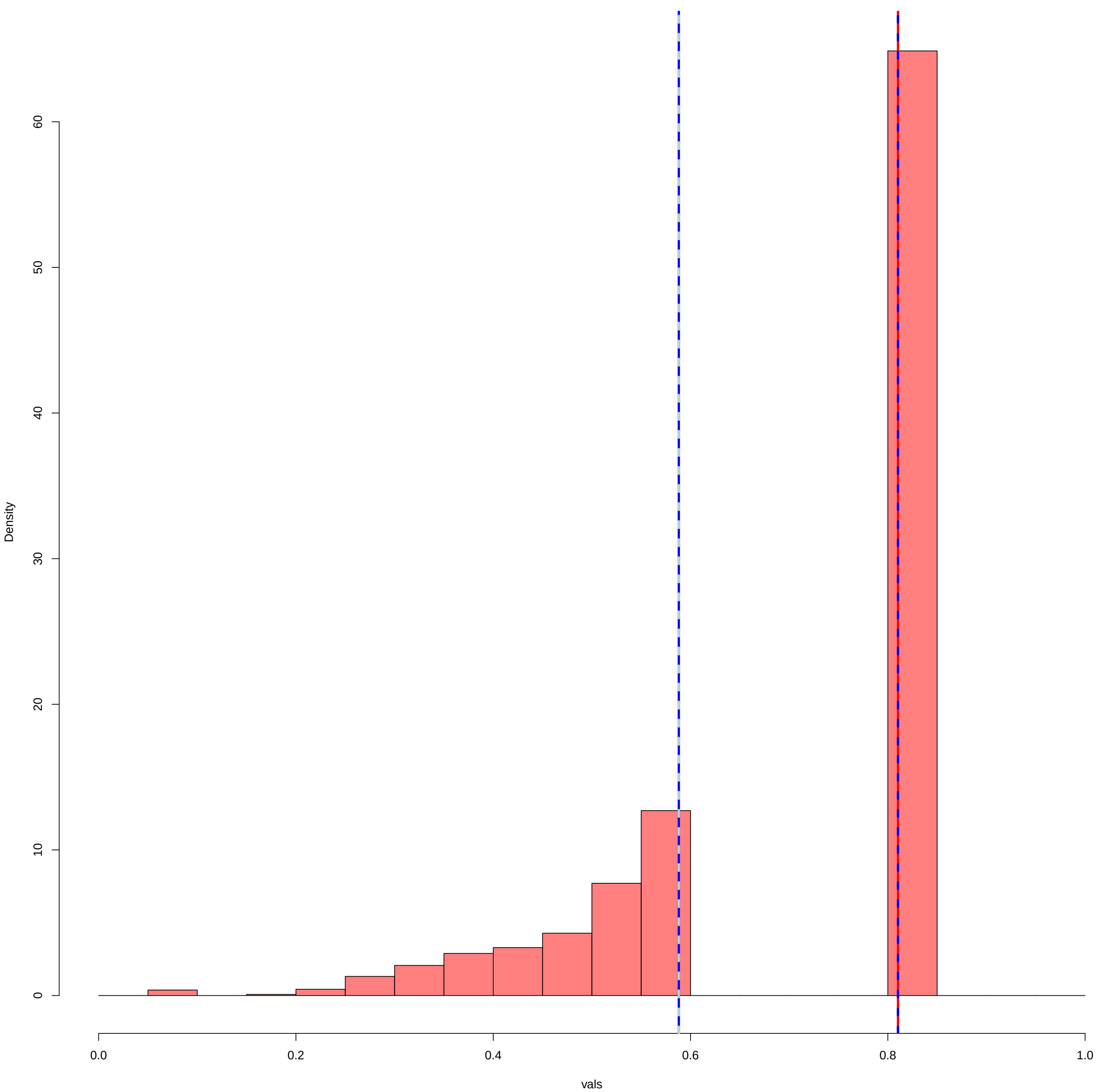
SCN8A: MetaSVM_rankscore



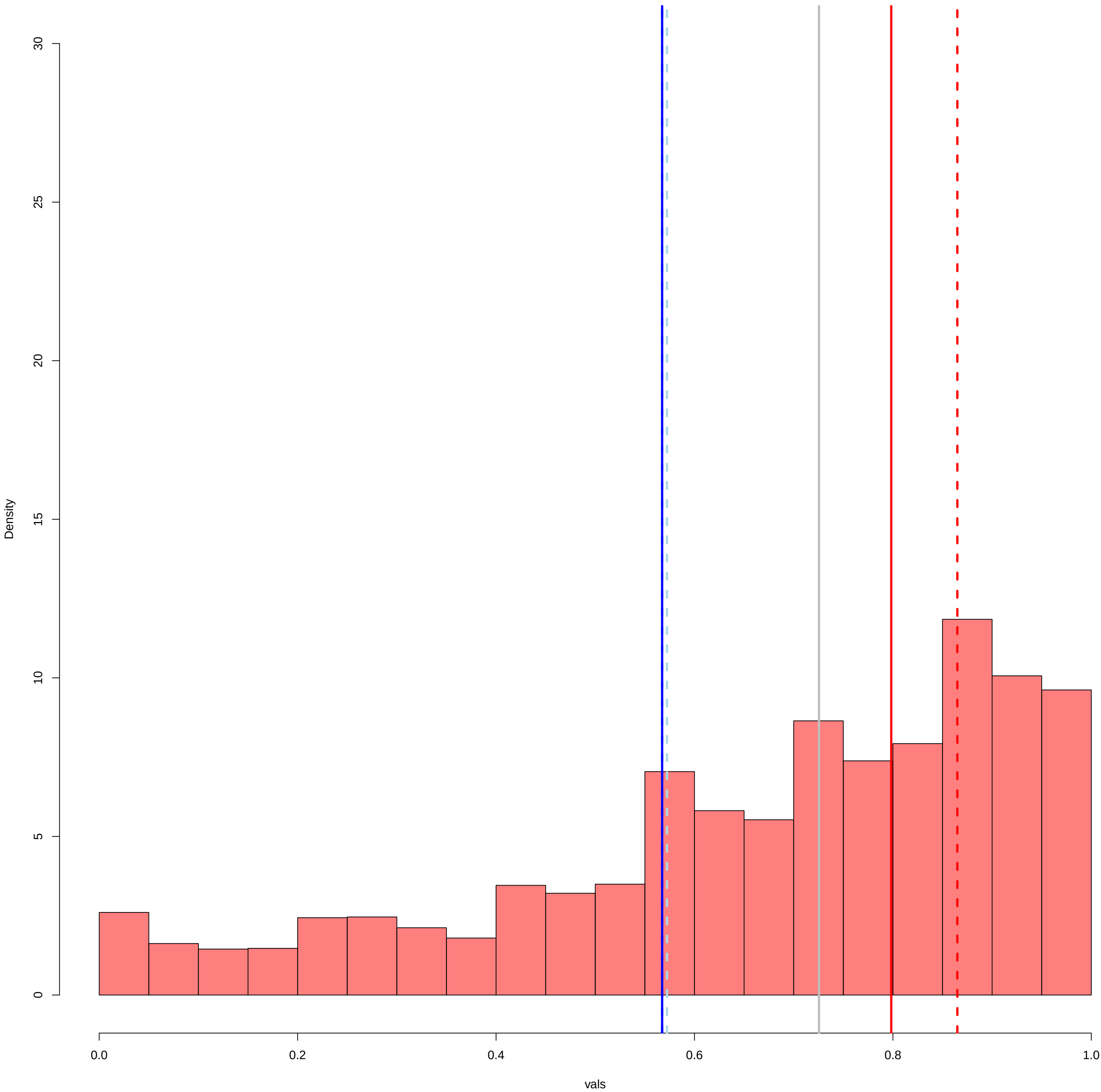
SCN8A: MutationAssessor_score_rankscore



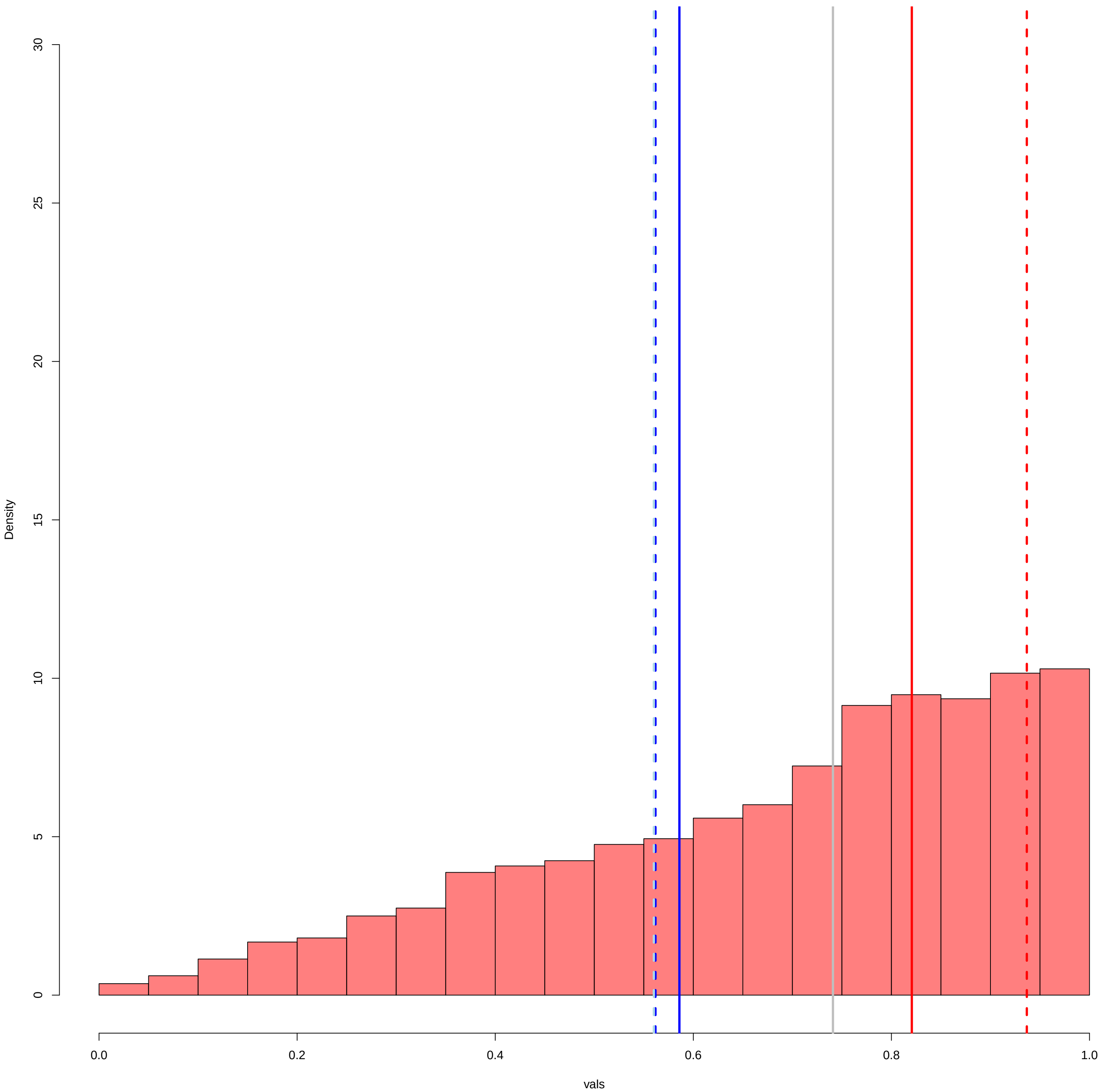
SCN8A: MutationTaster_converted_rankscore



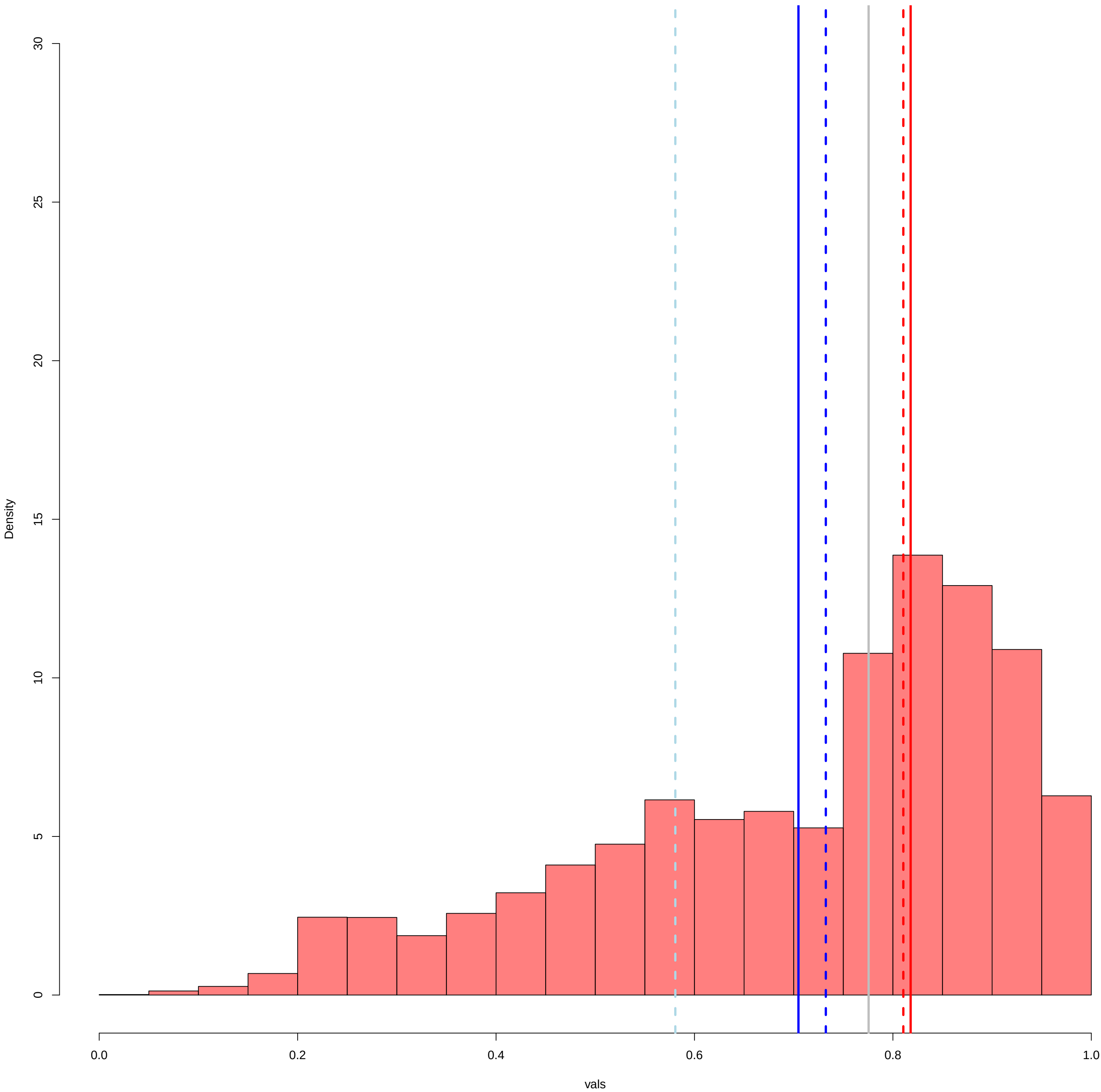
SCN8A: PROVEAN_converted_rankscore



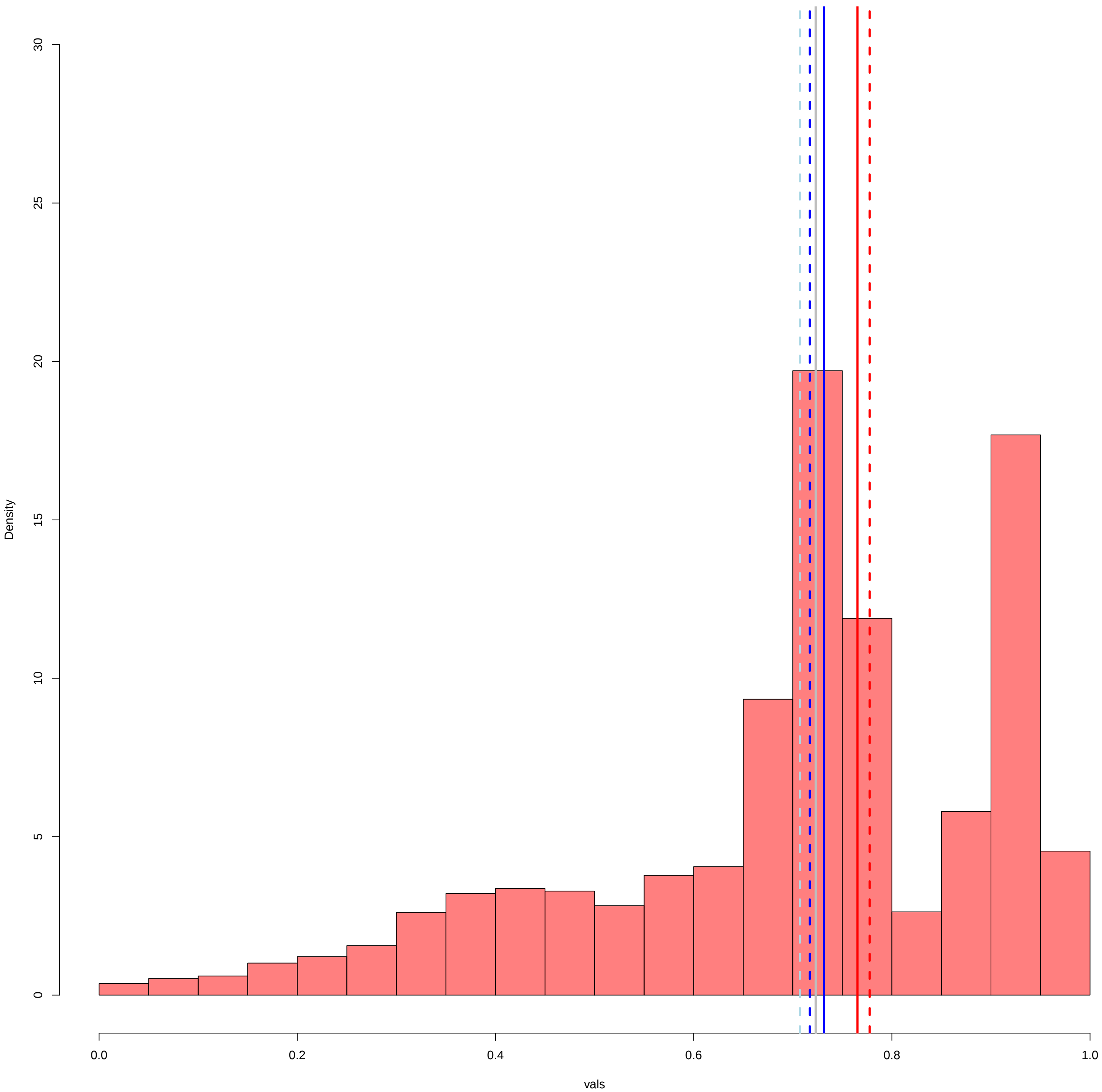
SCN8A: VEST3_rankscore



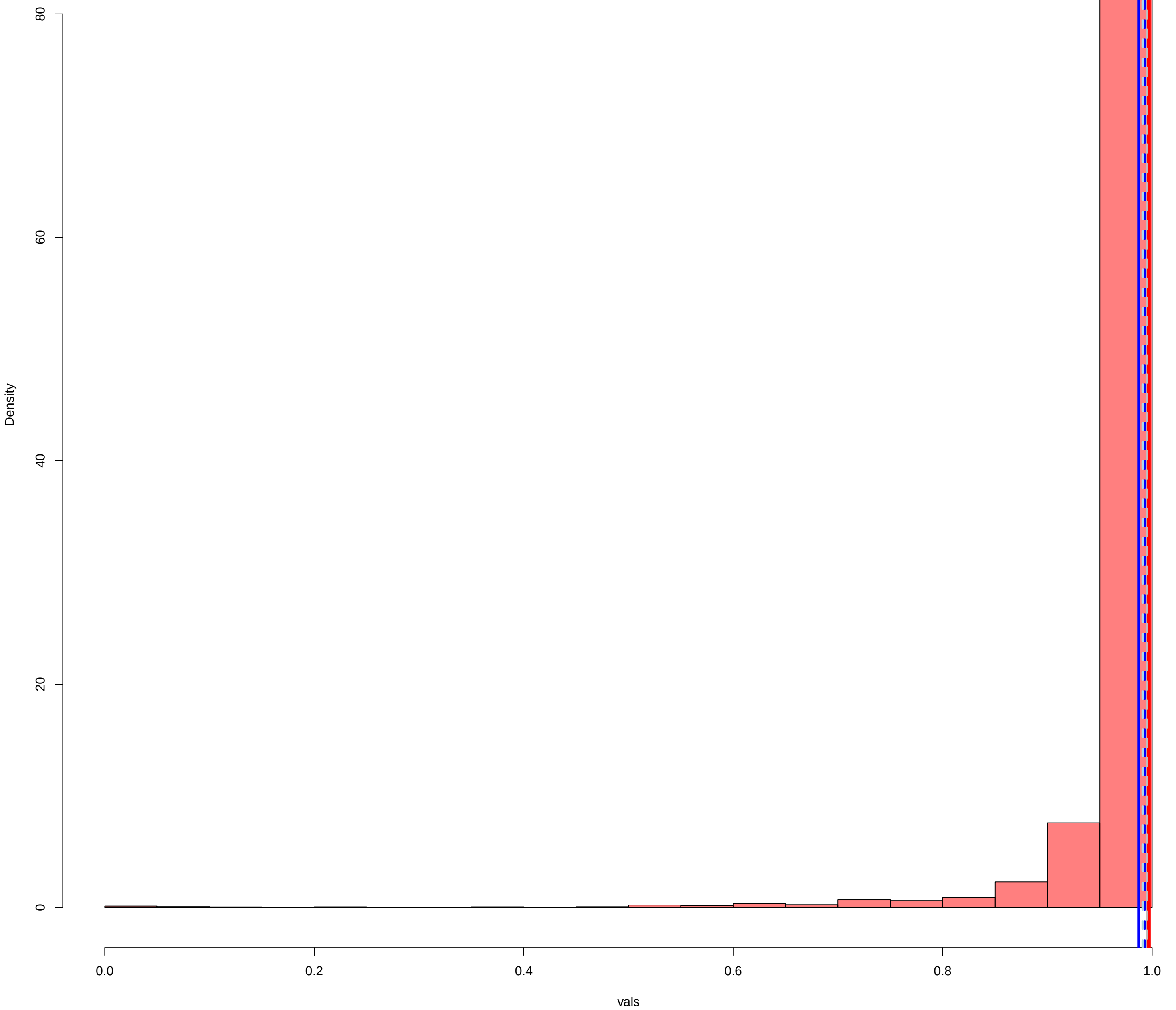
SCN8A: fathmm-MKL_coding_rankscore



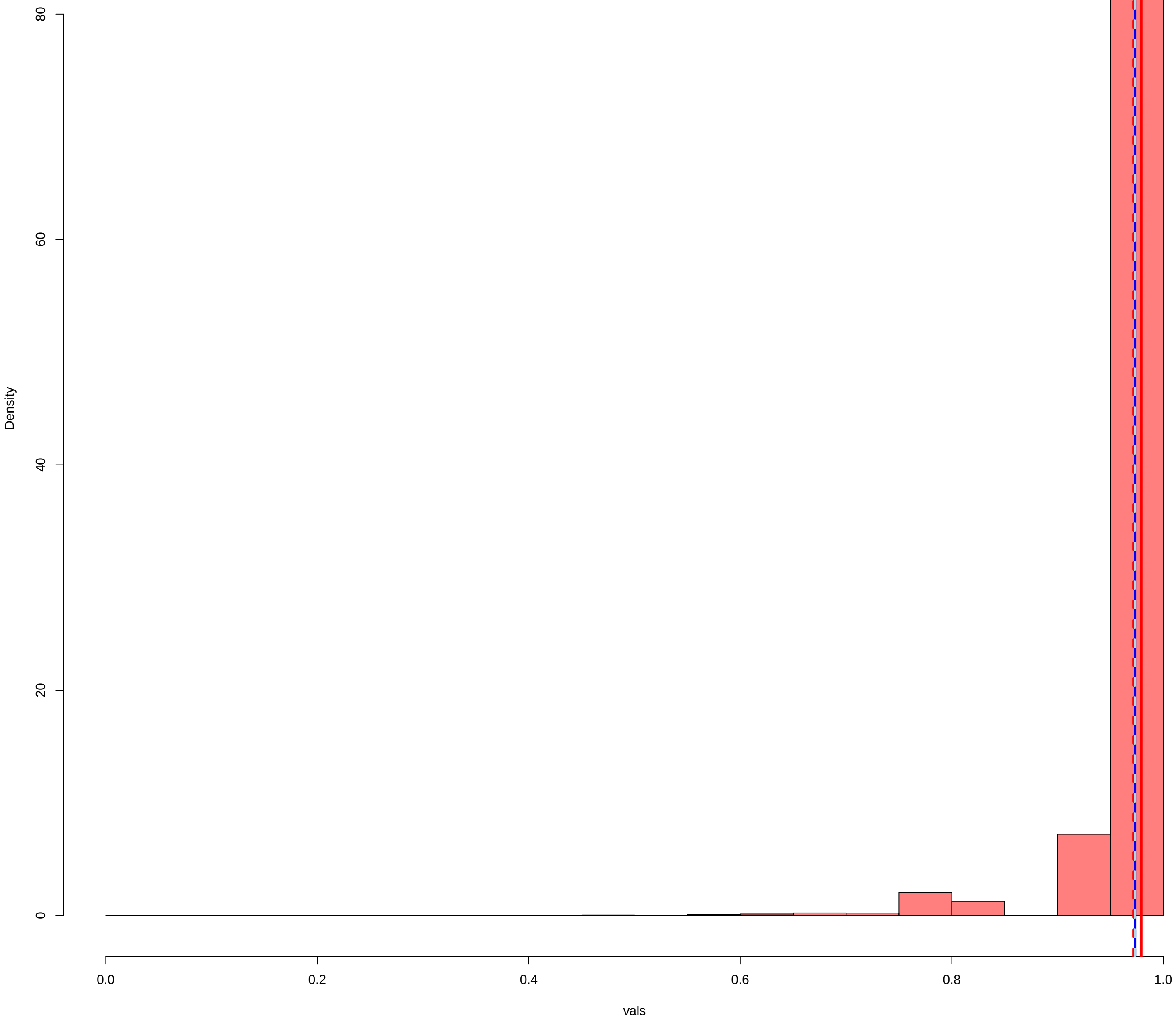
SCN8A: SiPhy_29way_logOdds_rankscore



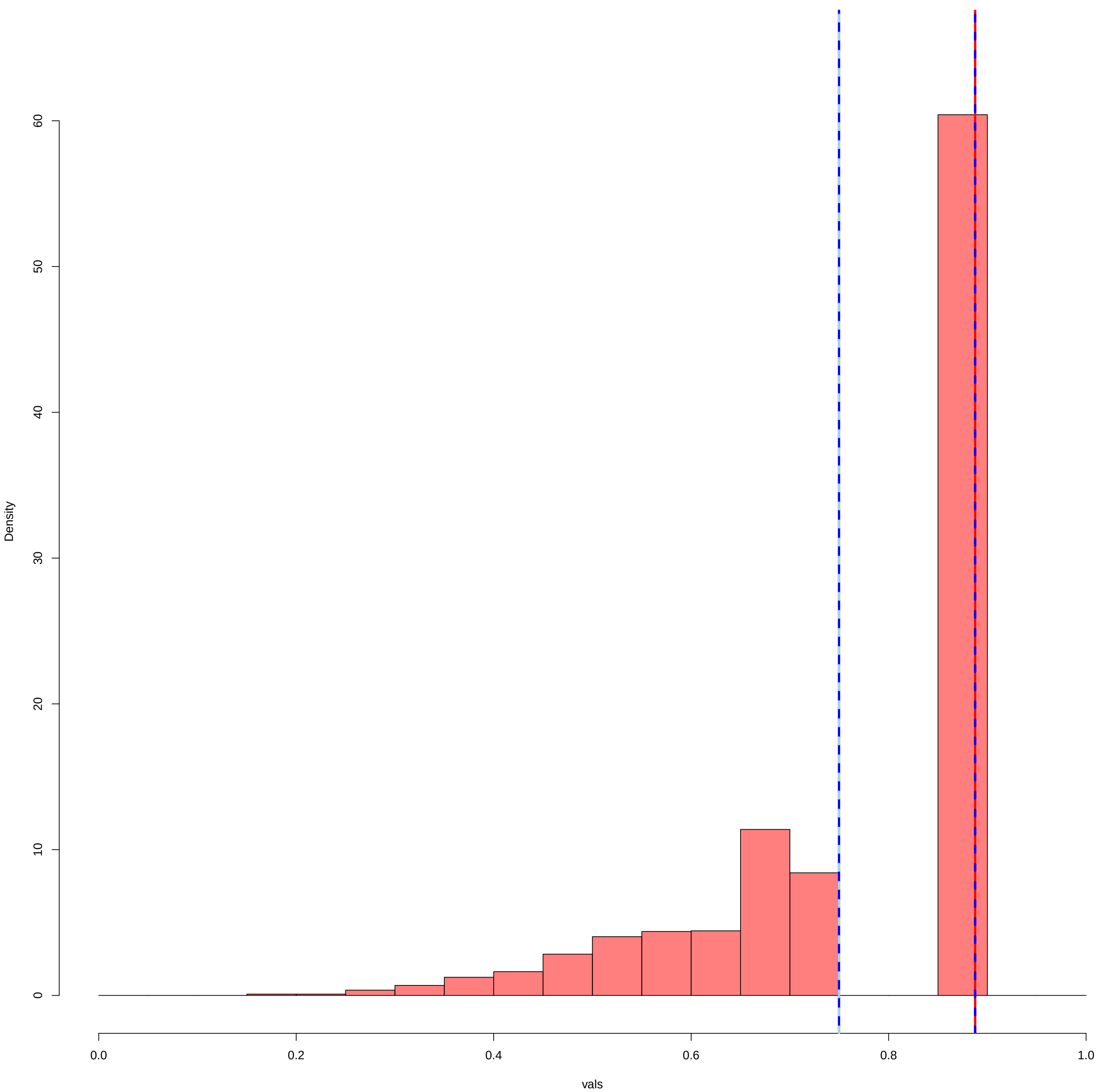
SCN8A: priPhCons



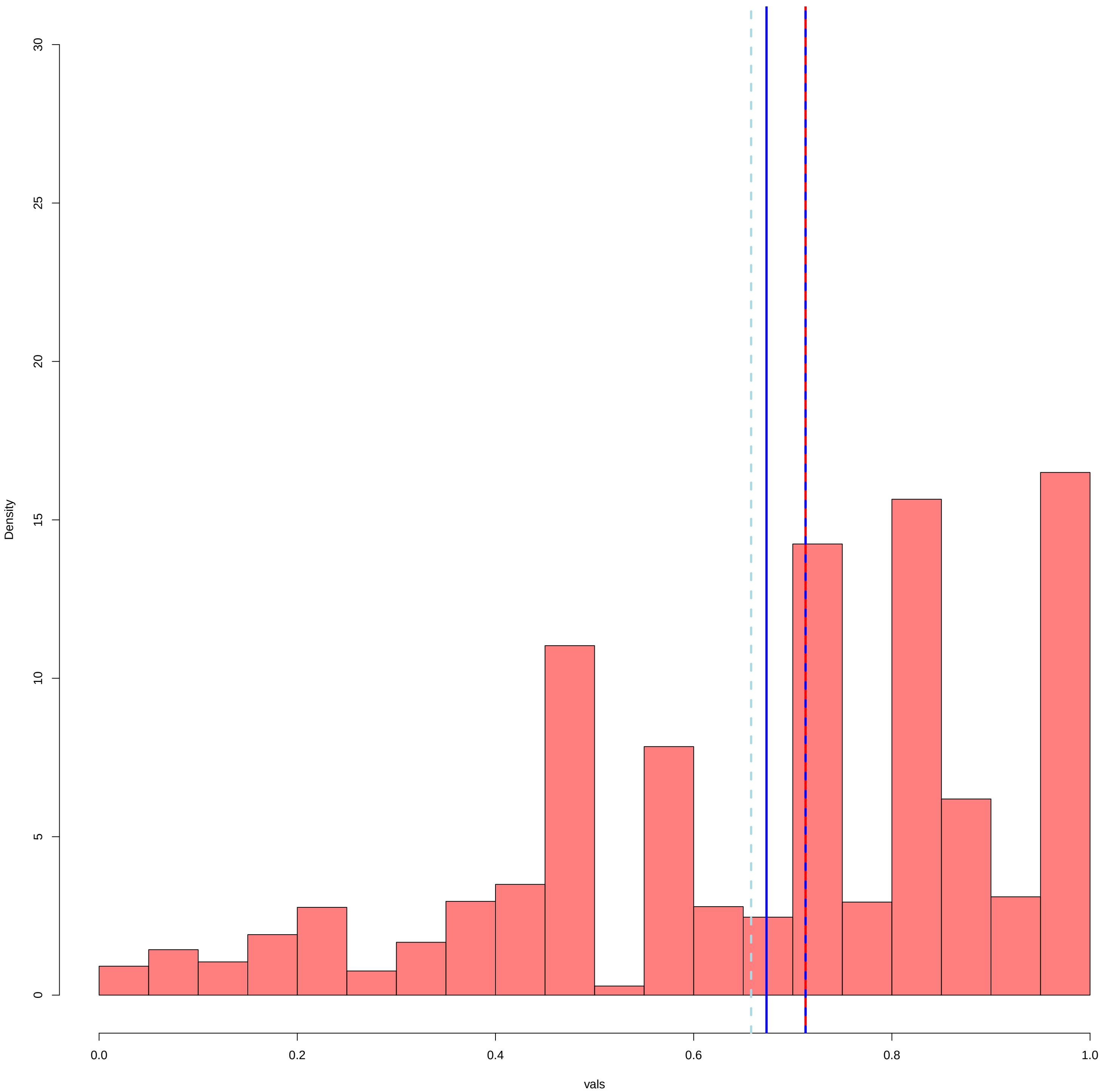
SCN8A: priPhyloP



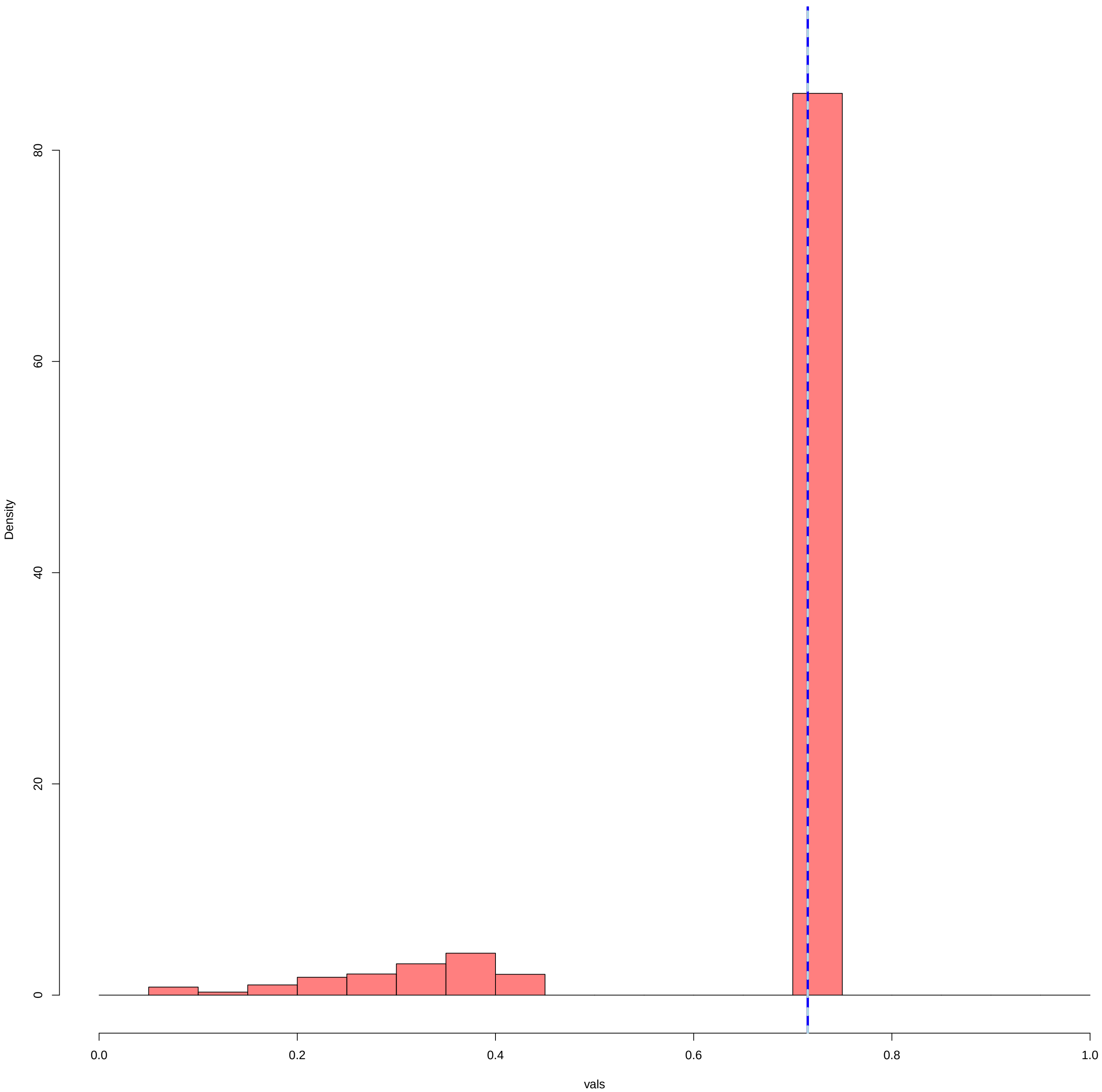
SCN8A: phastCons20way_mammalian_rankscore



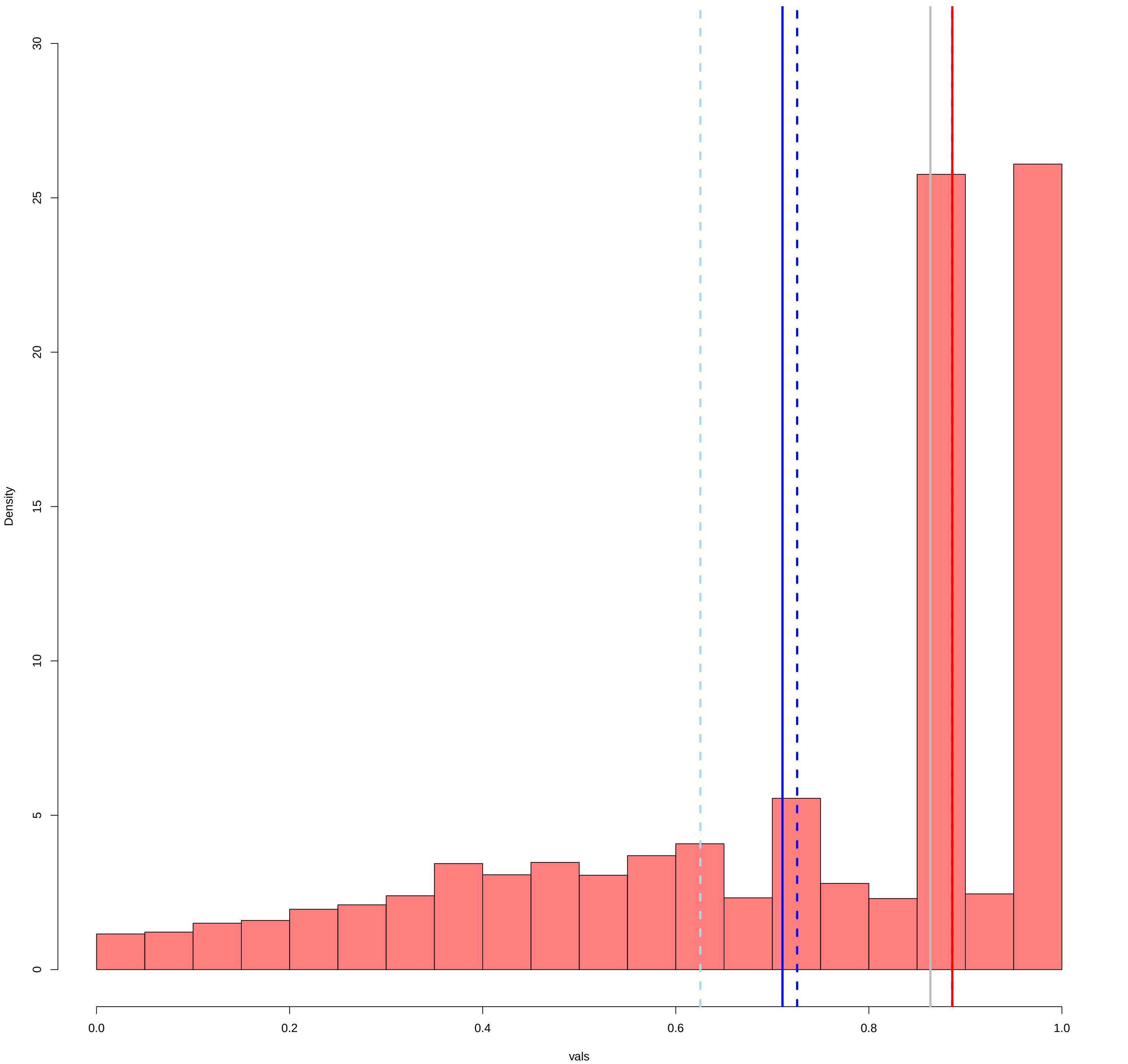
SCN8A: phyloP20way_mammalian_rankscore



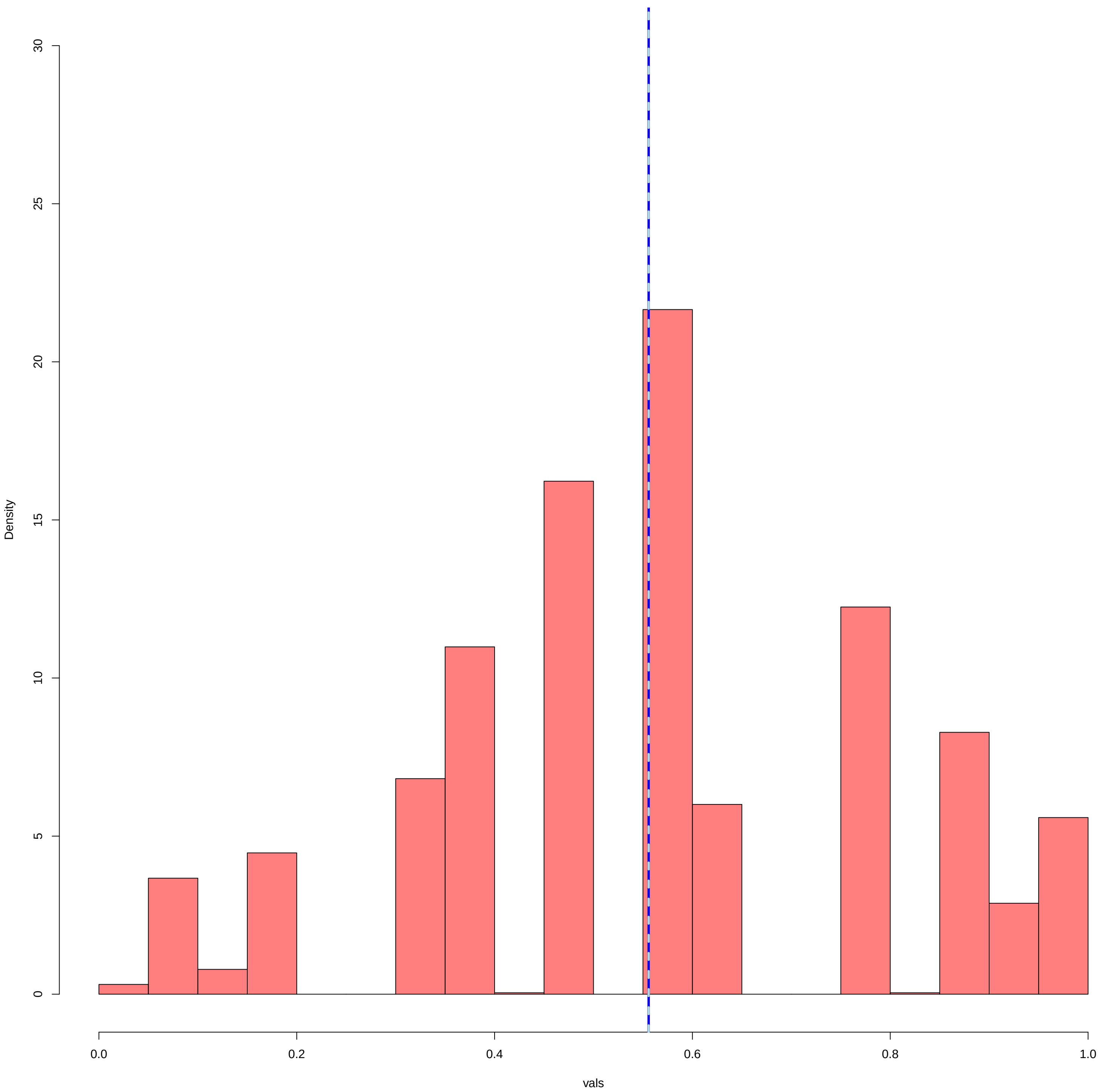
SCN8A: phastCons100way Vertebrate RankScore



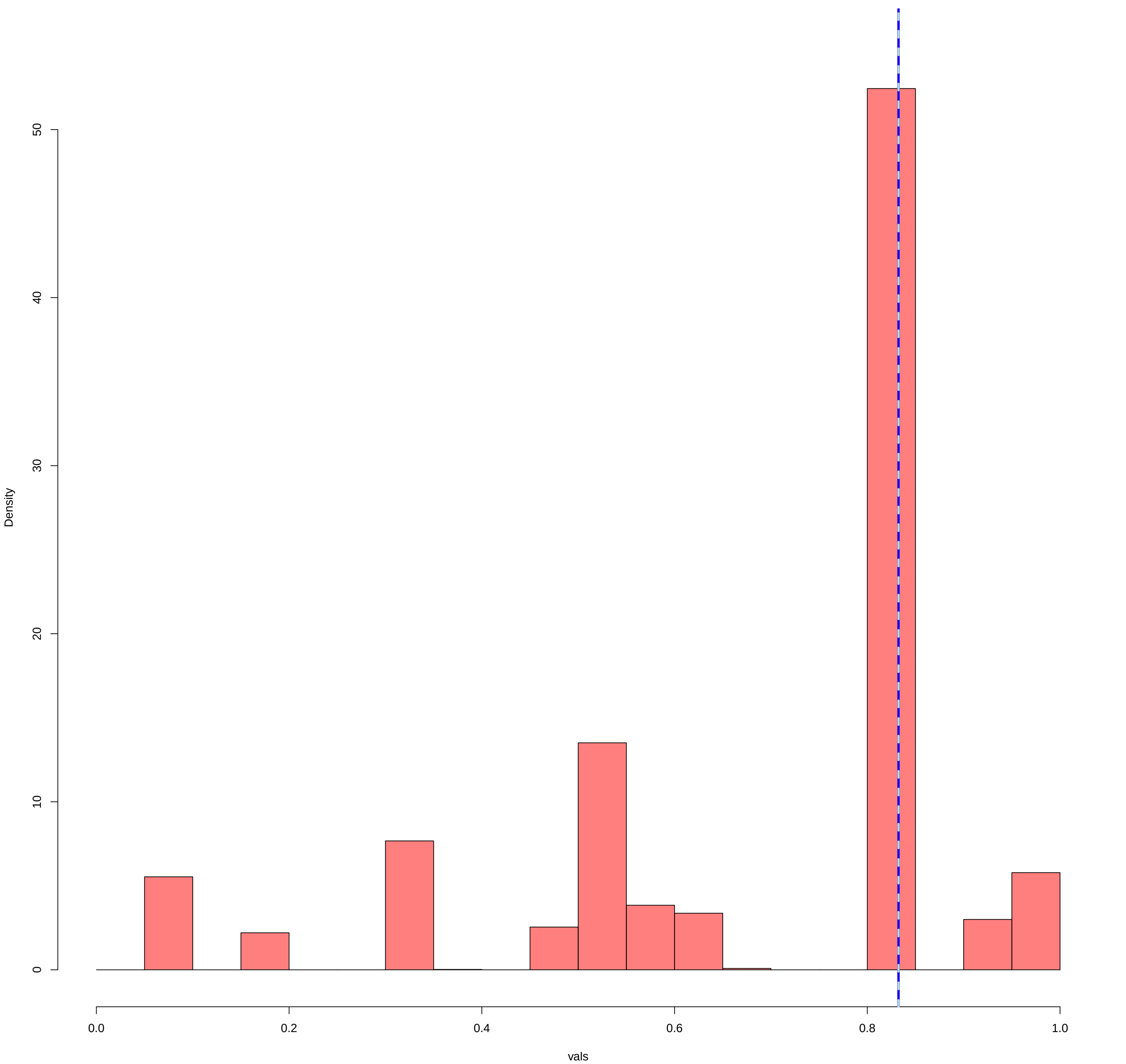
SCN8A: phyloP100way_vertebrate_rankscore



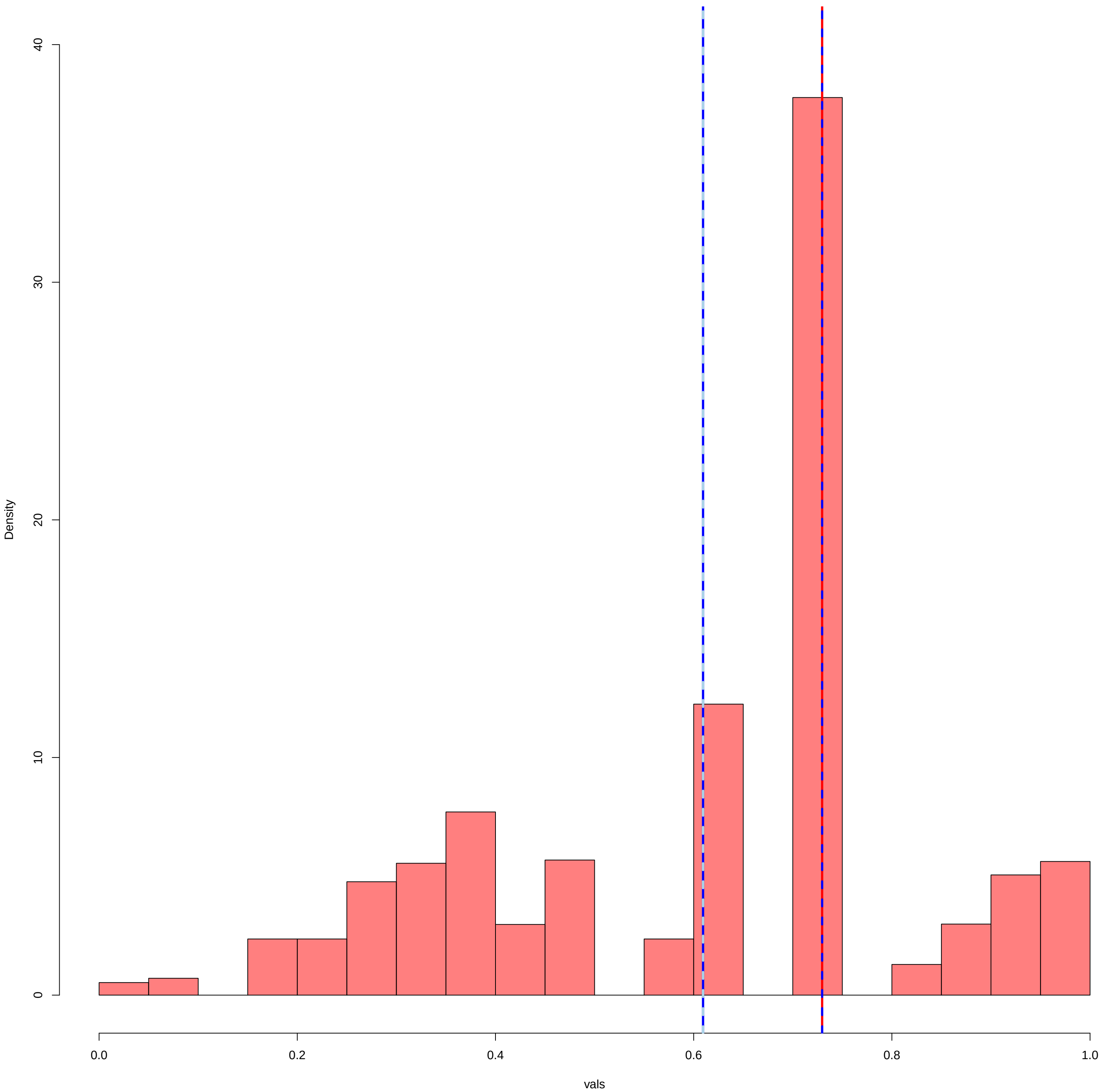
SCN8A: H1-hESC_fitCons_score_rankscore



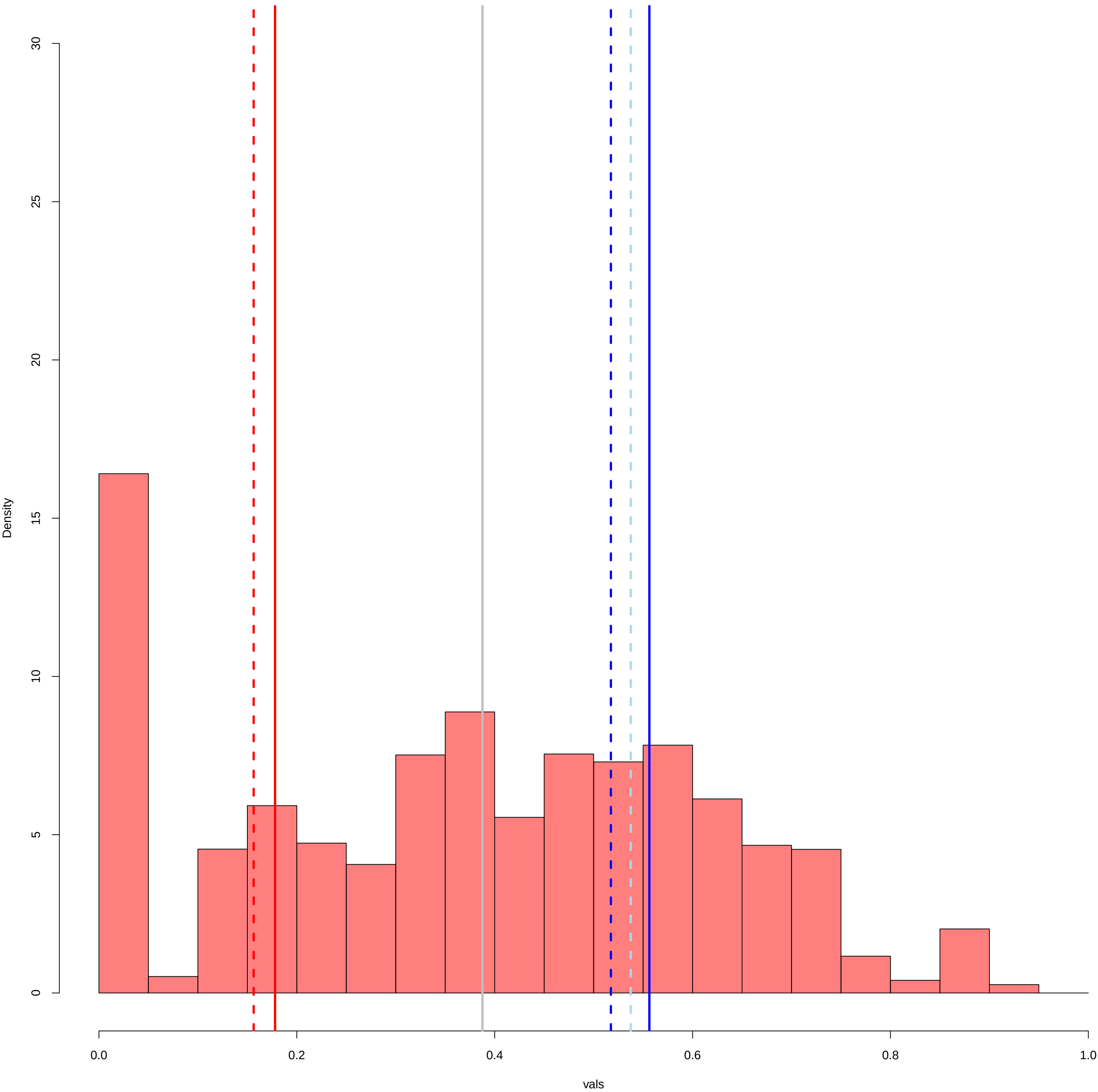
SCN8A: HUVEC_fitCons_score_rankscore



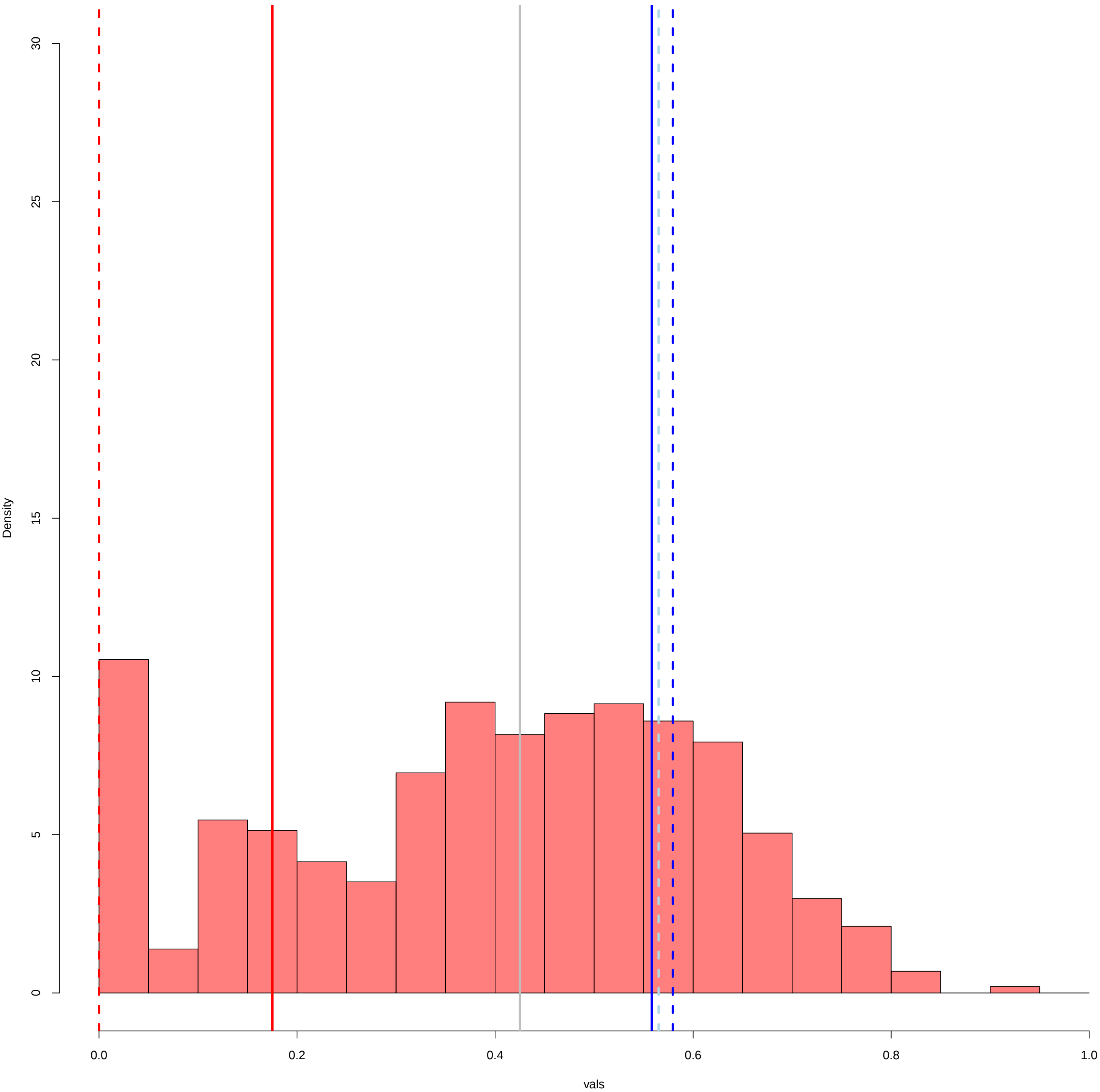
SCN8A: integrated_fitCons_score_rankscore



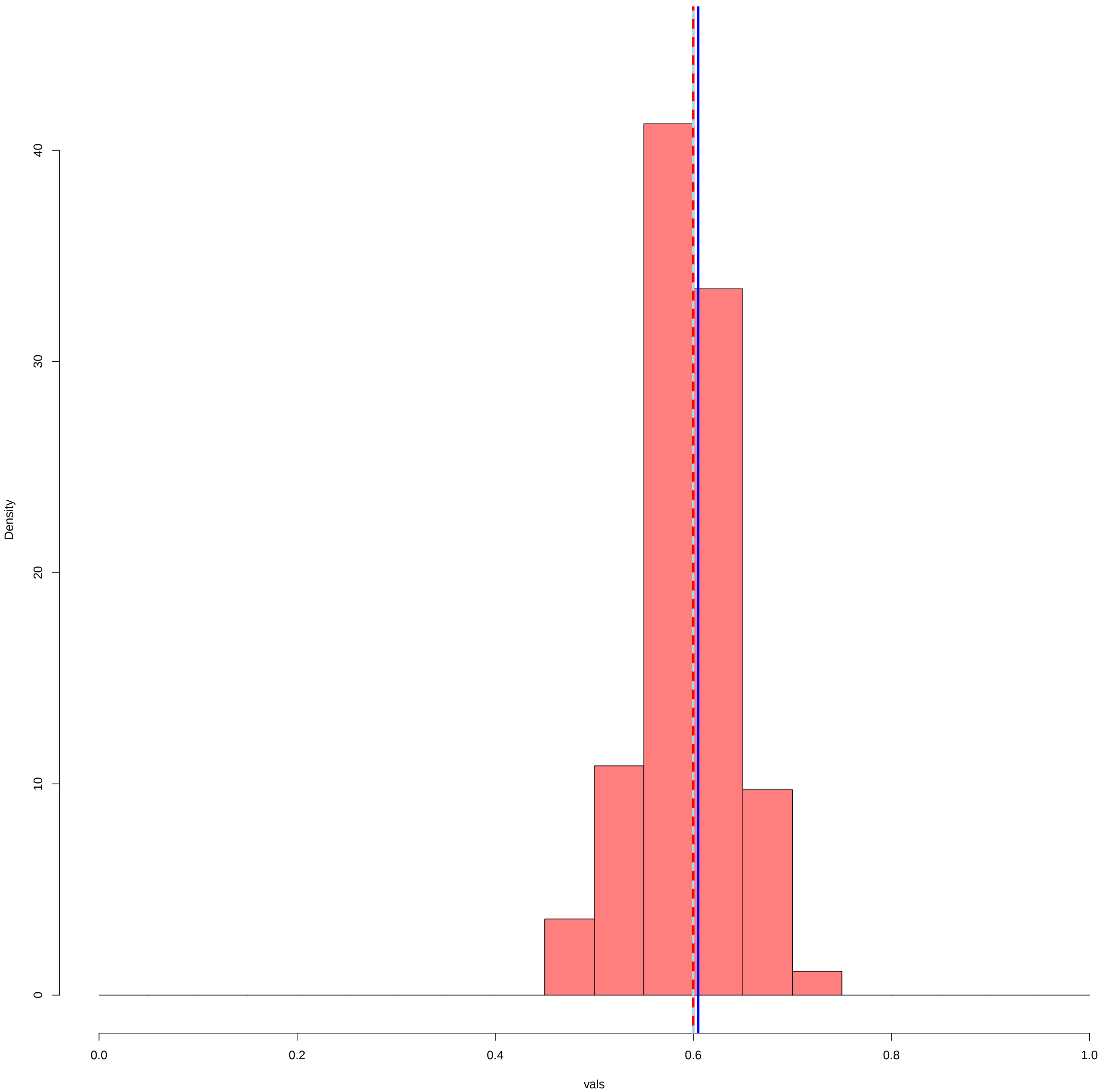
SCN8A: ExAC v1 MTR



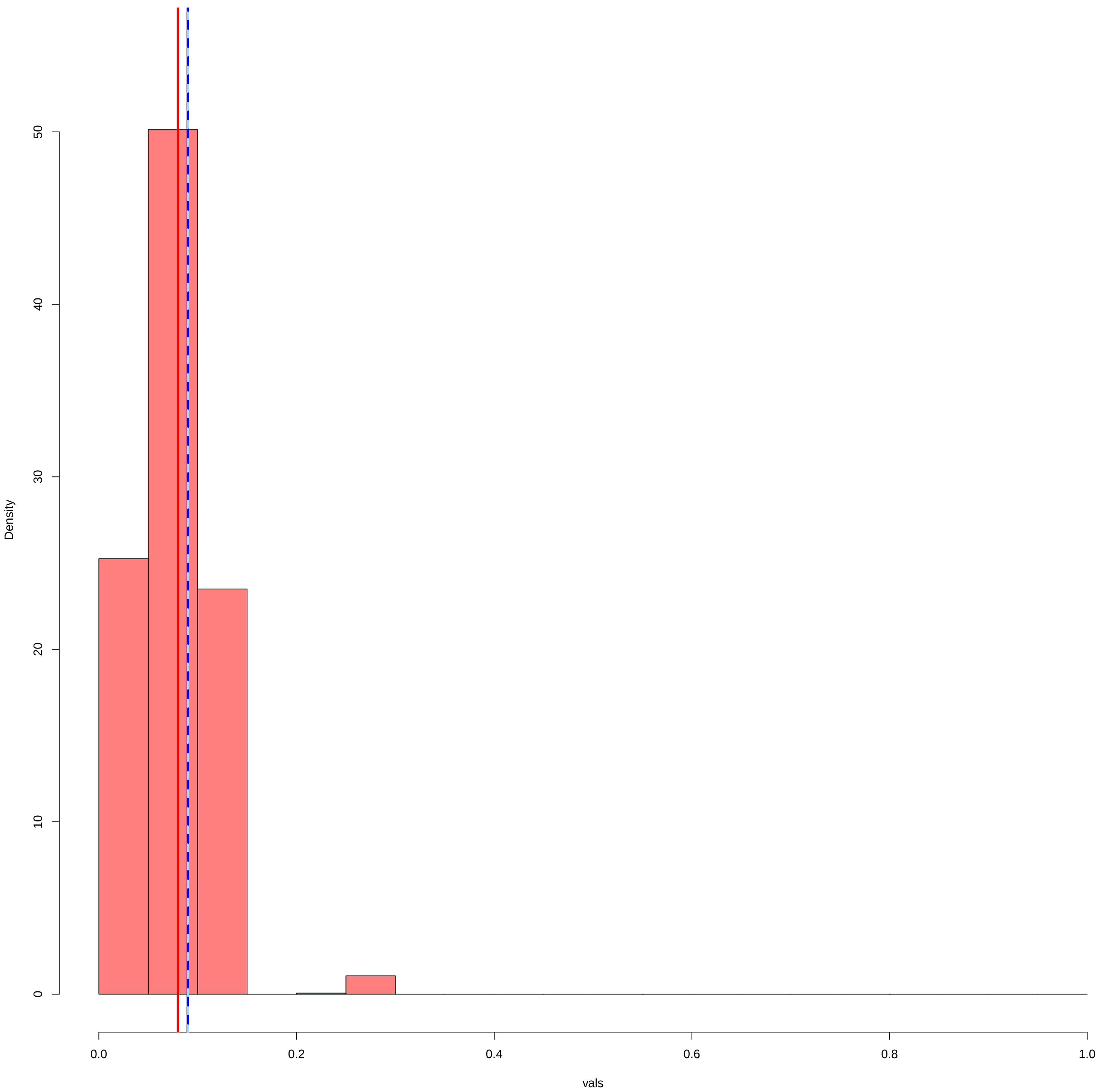
SCN8A: ExAC v2 & gnomAD MTR



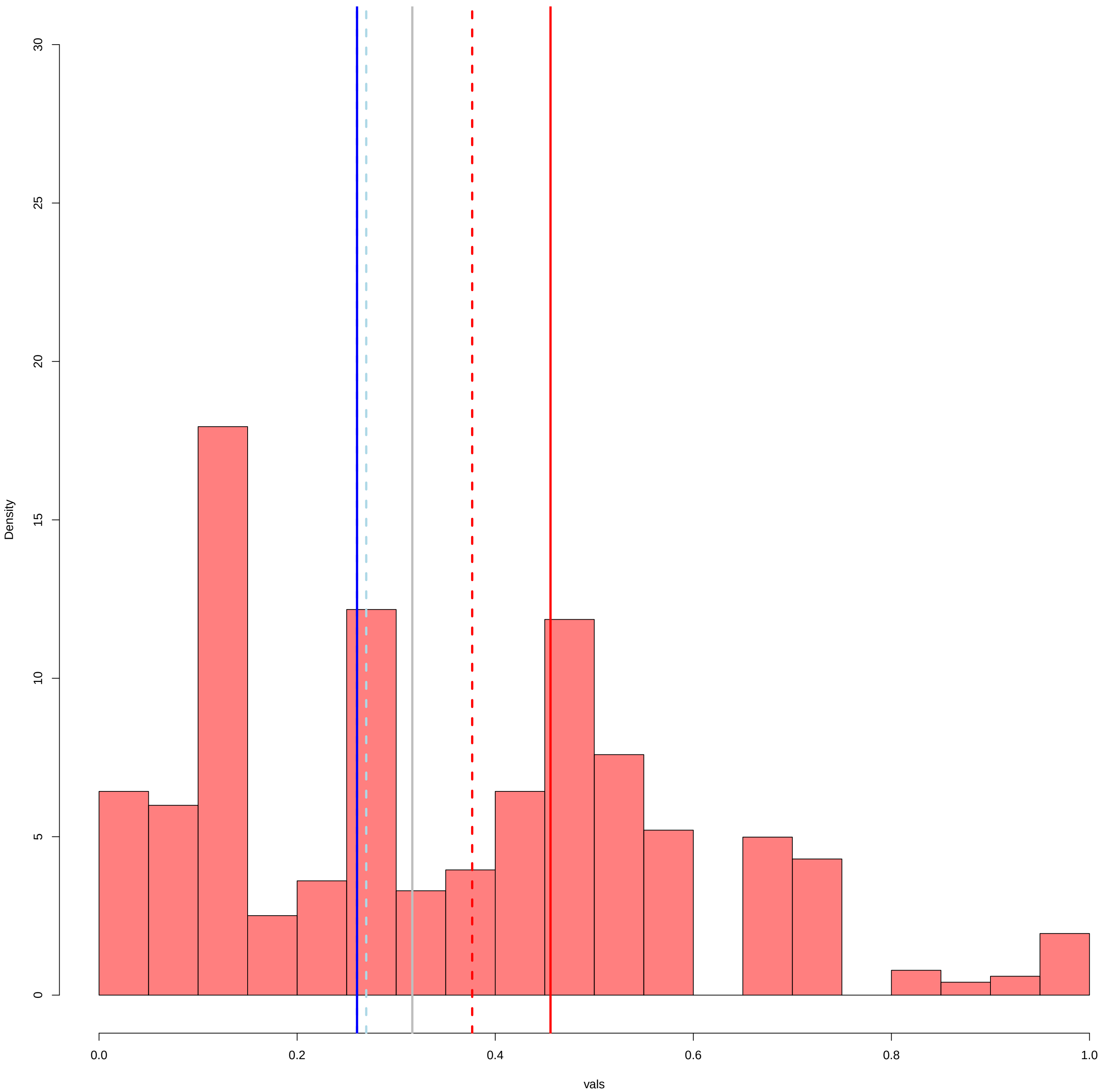
SLC2A1: GC (Percent GC content in a window of ± 75 bp)



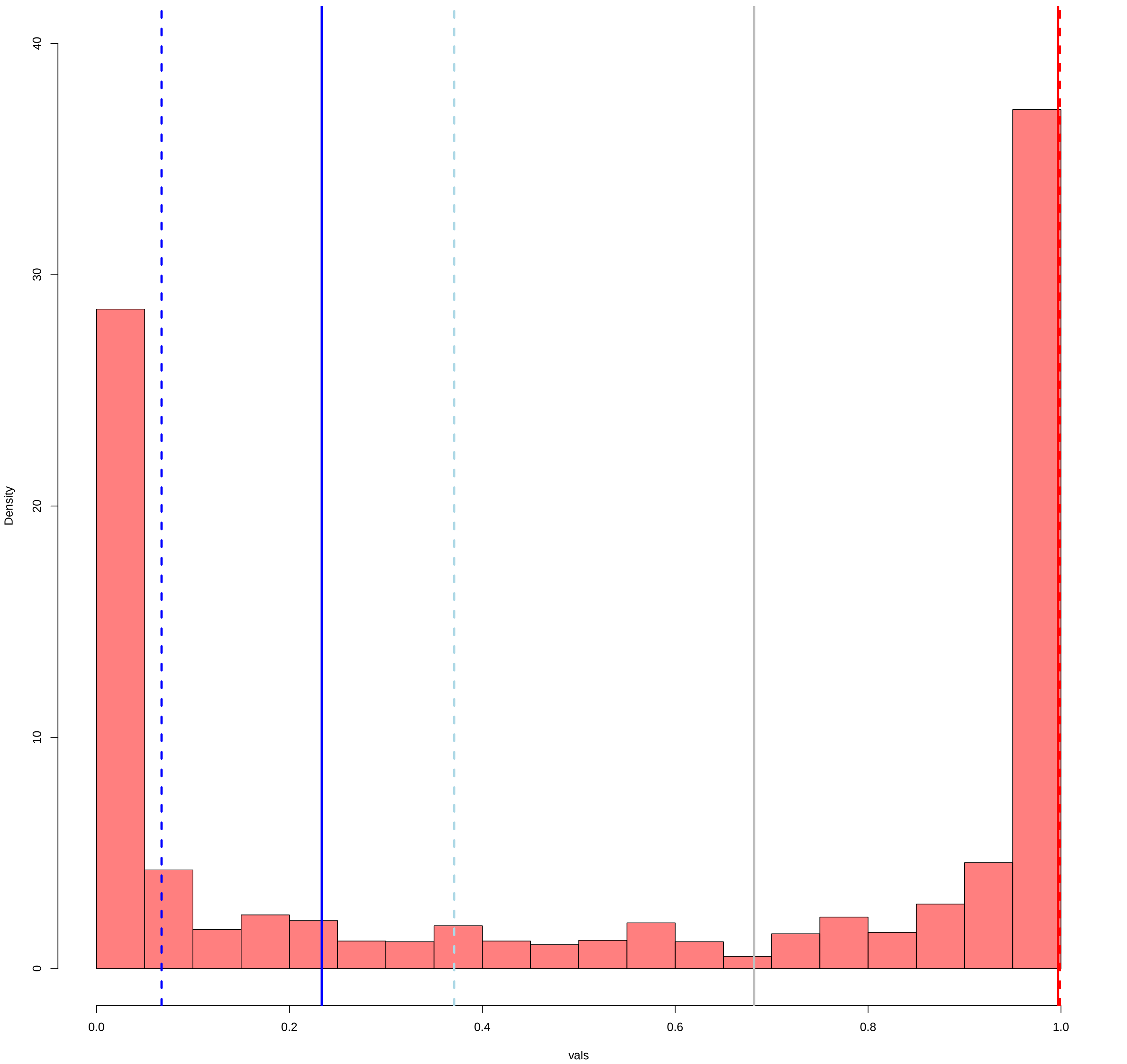
SLC2A1: CpG (Percent CpG in a window of +/-75bp)



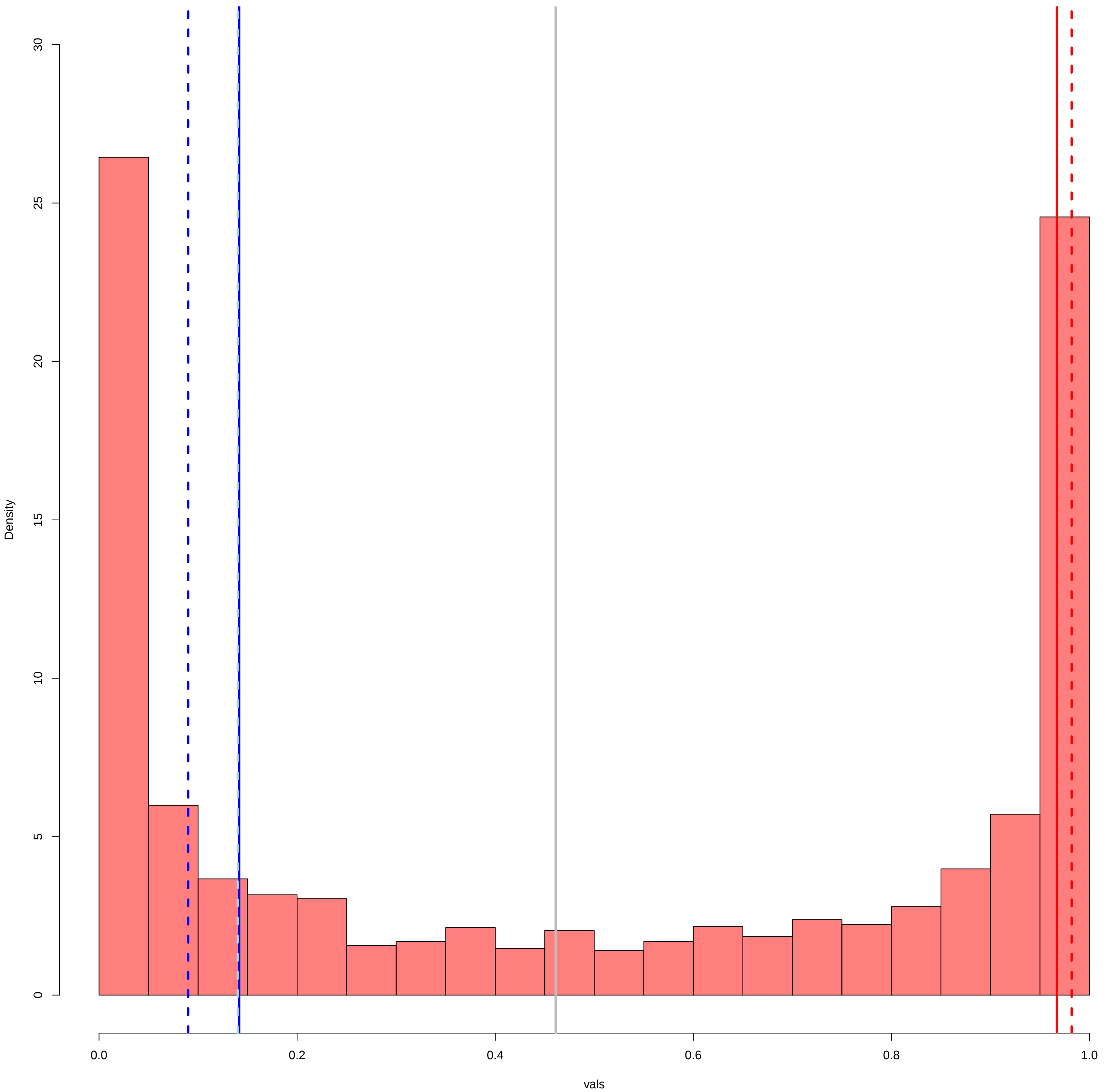
SLC2A1: Grantham



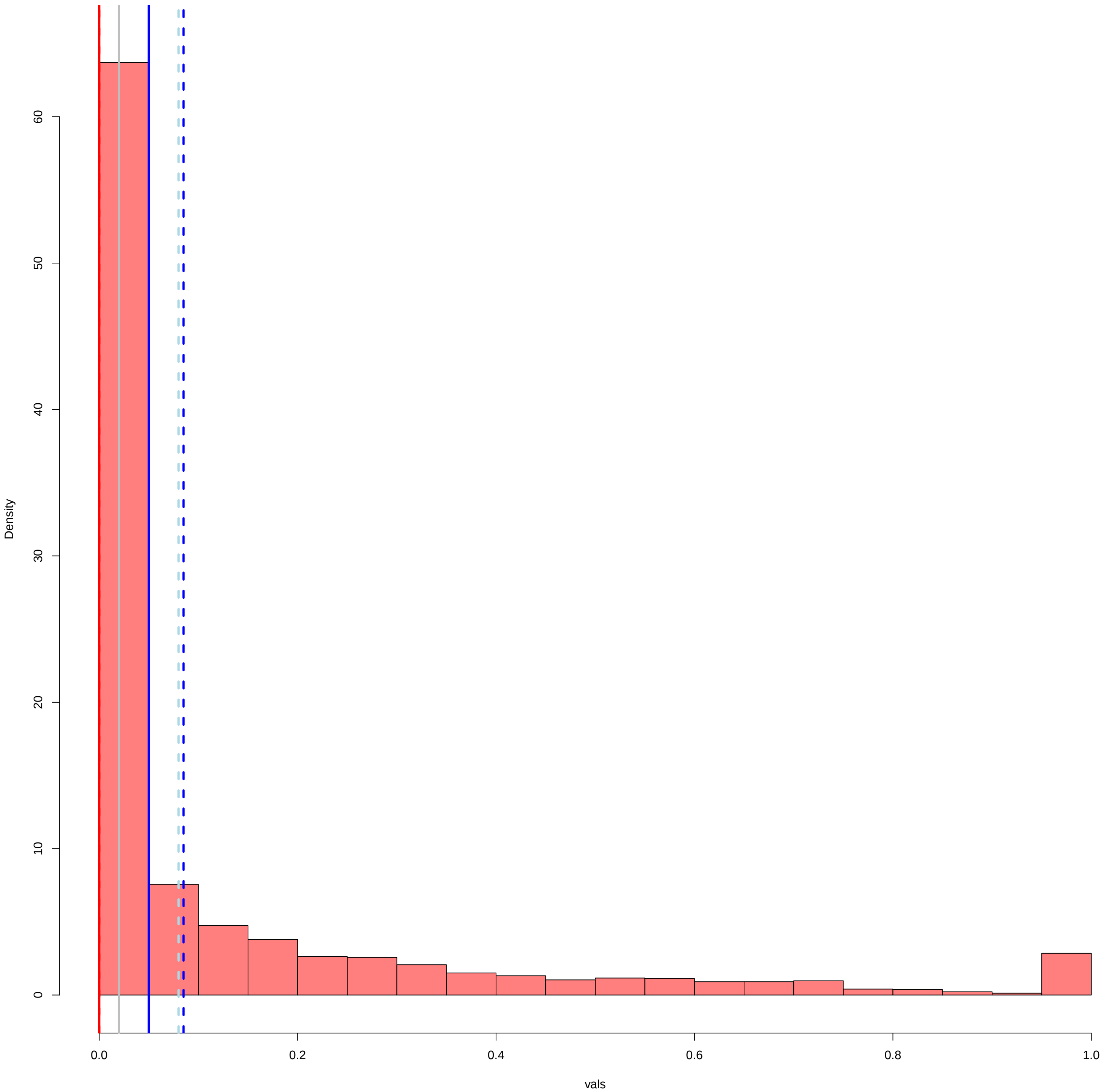
SLC2A1: Hdiv quan



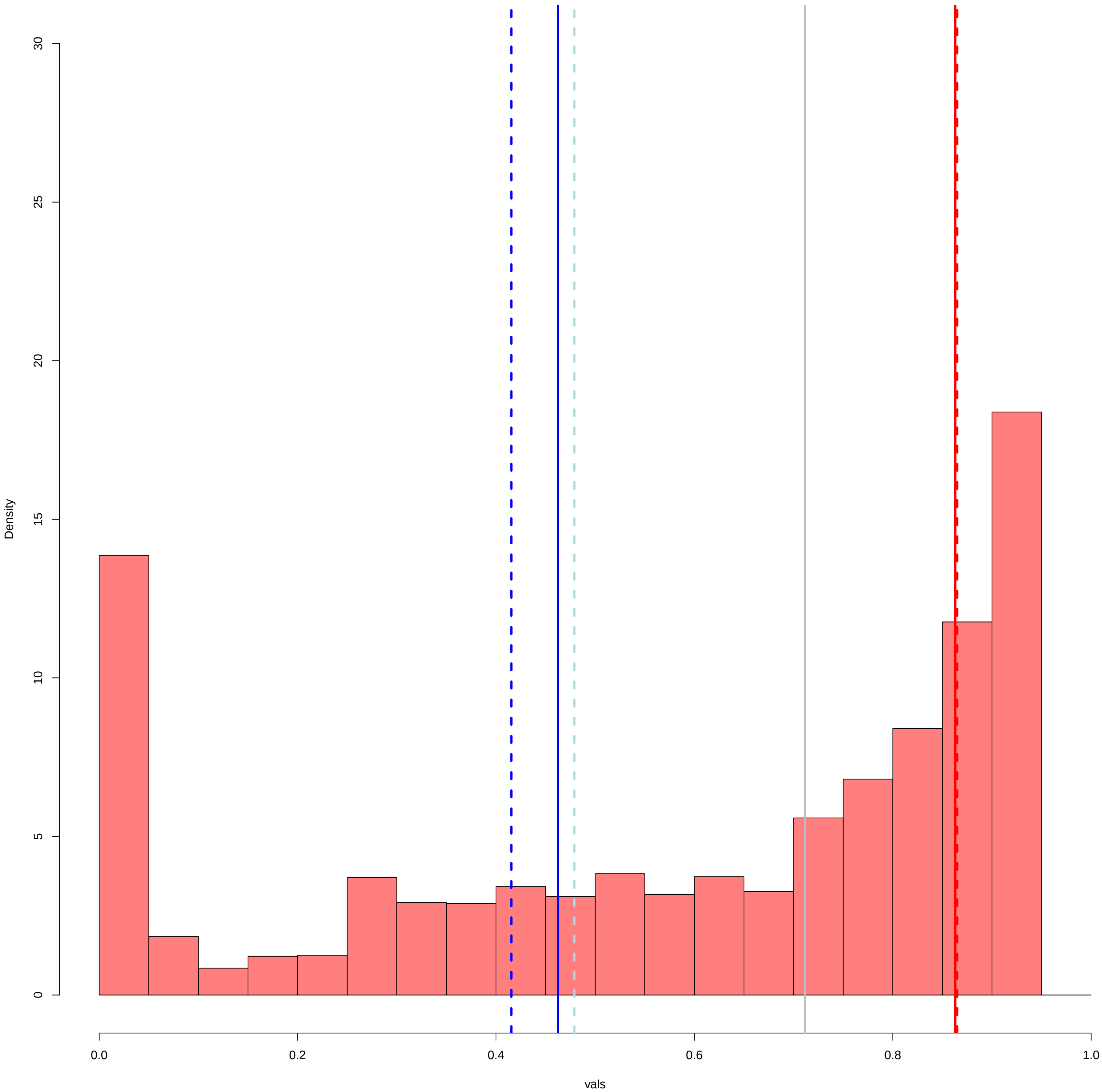
SLC2A1: Hvar quan



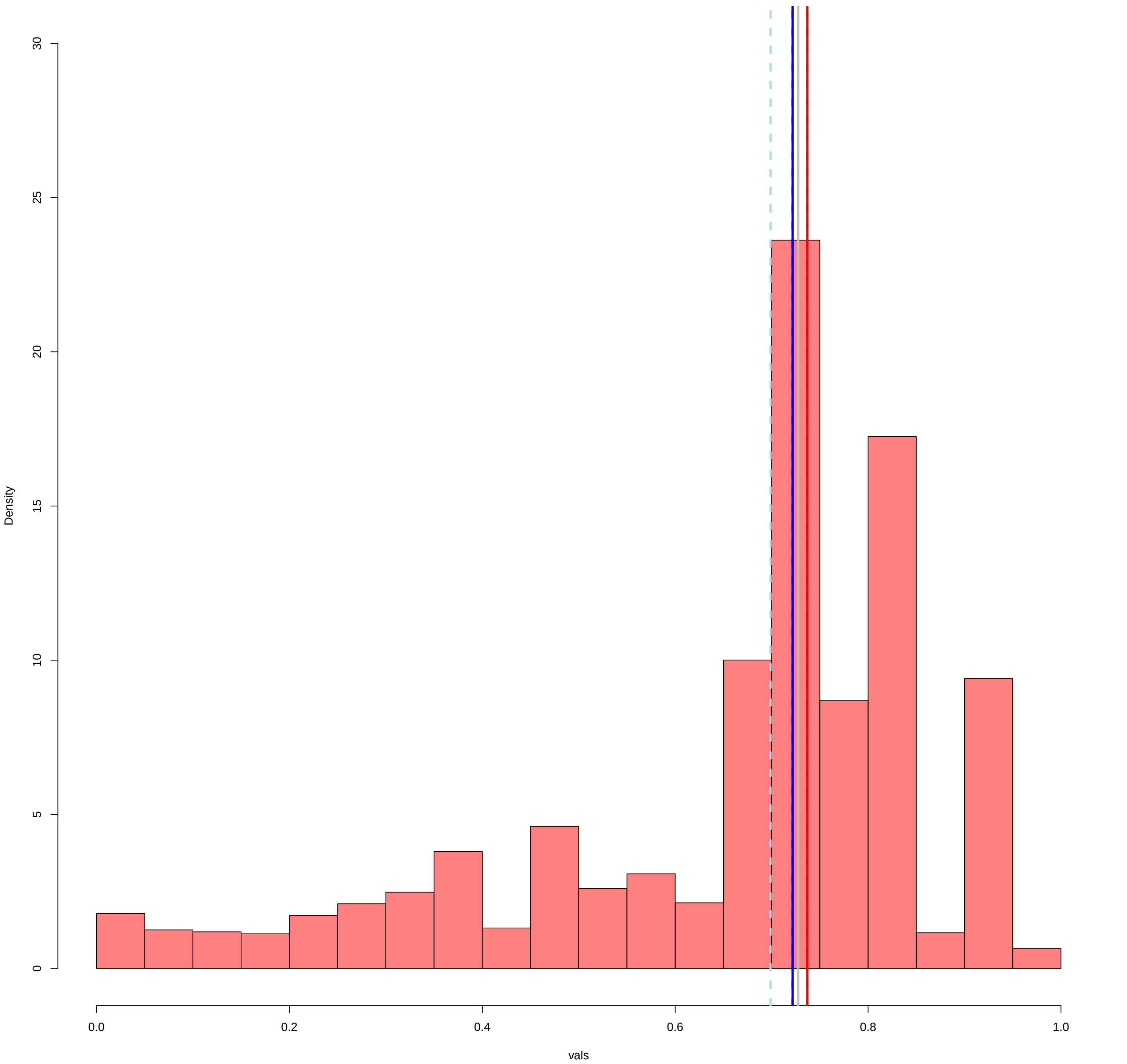
SLC2A1: SIFT



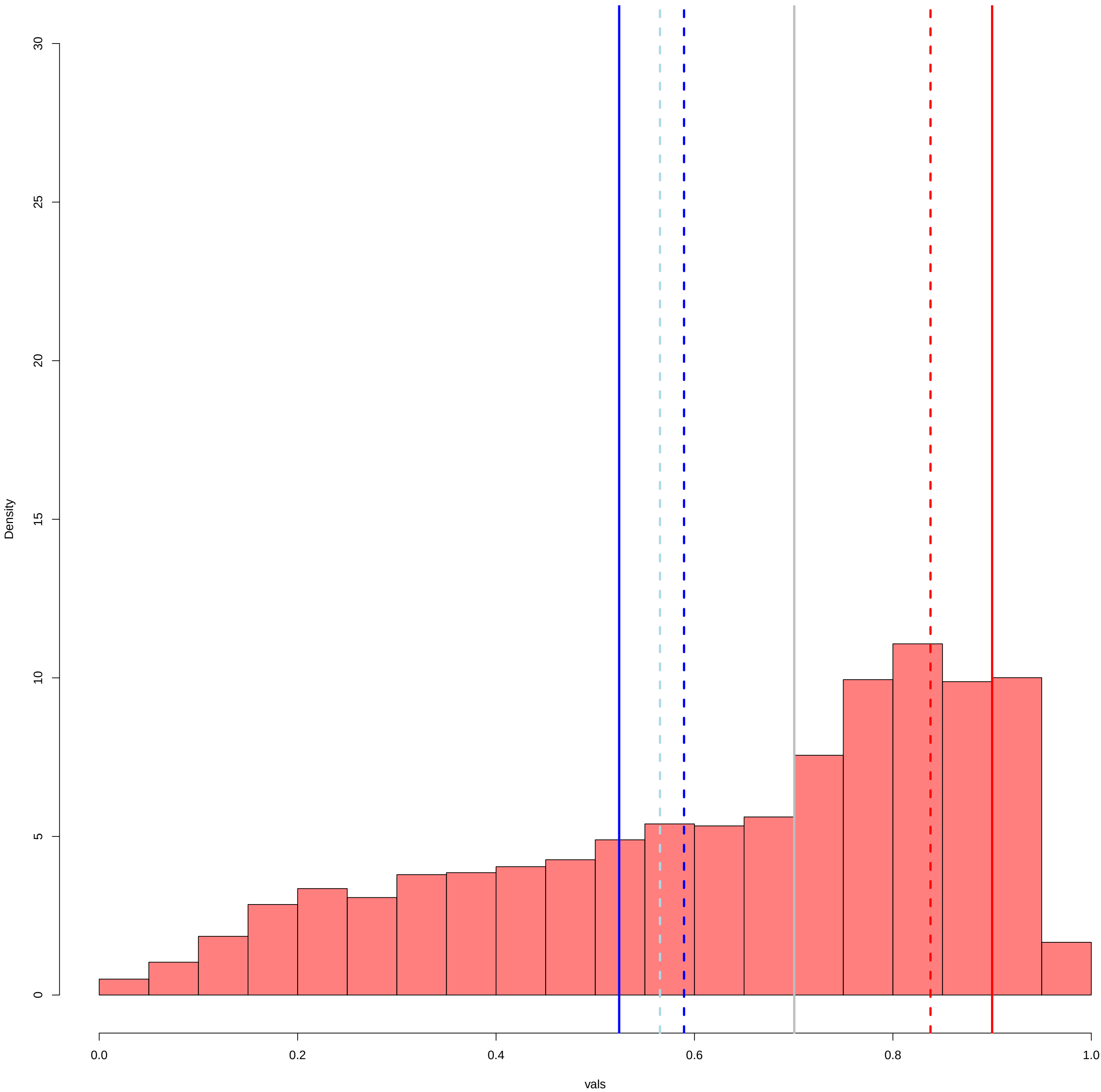
SLC2A1: Condel



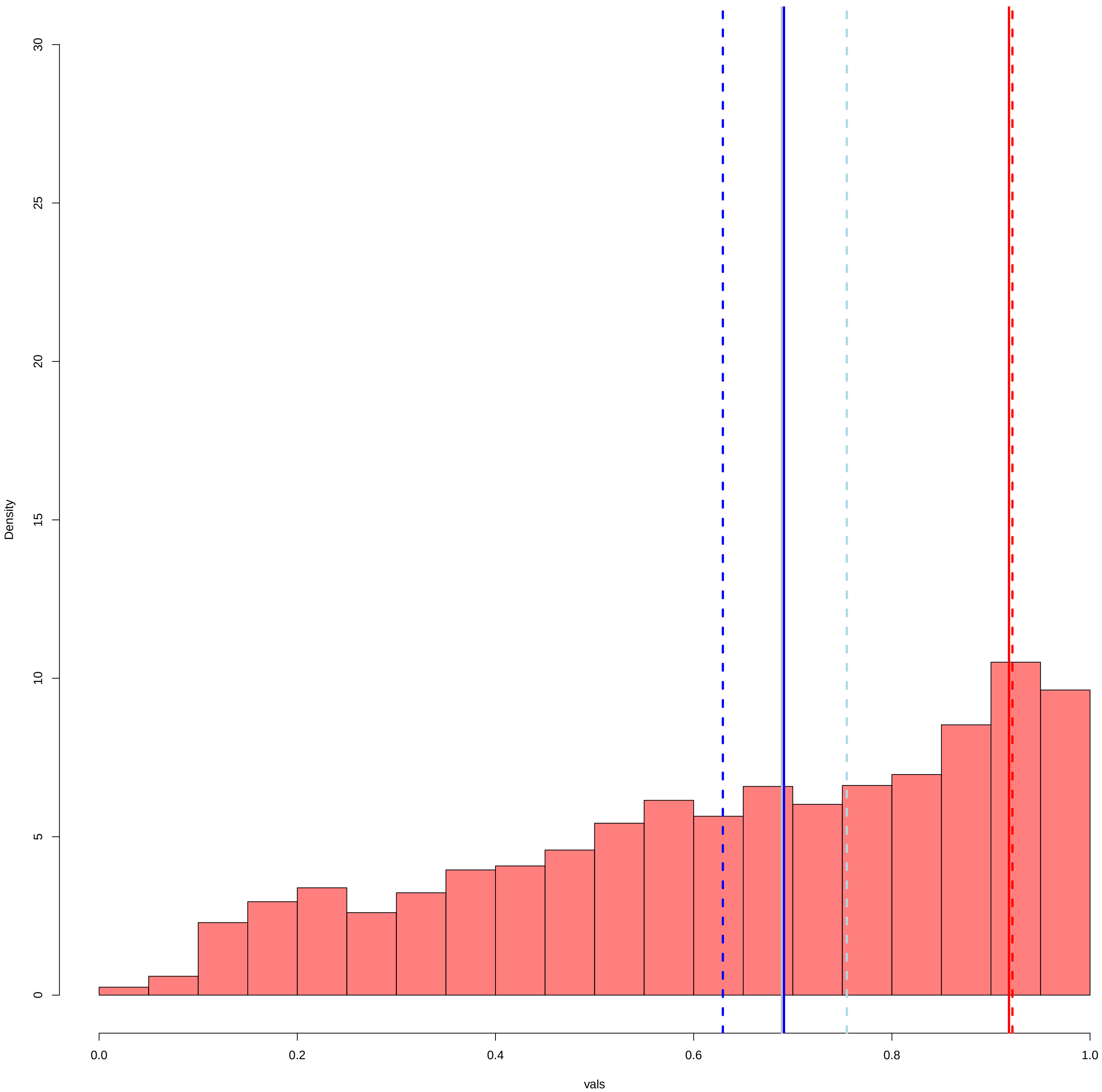
SLC2A1: GERP++_RS_rankscore



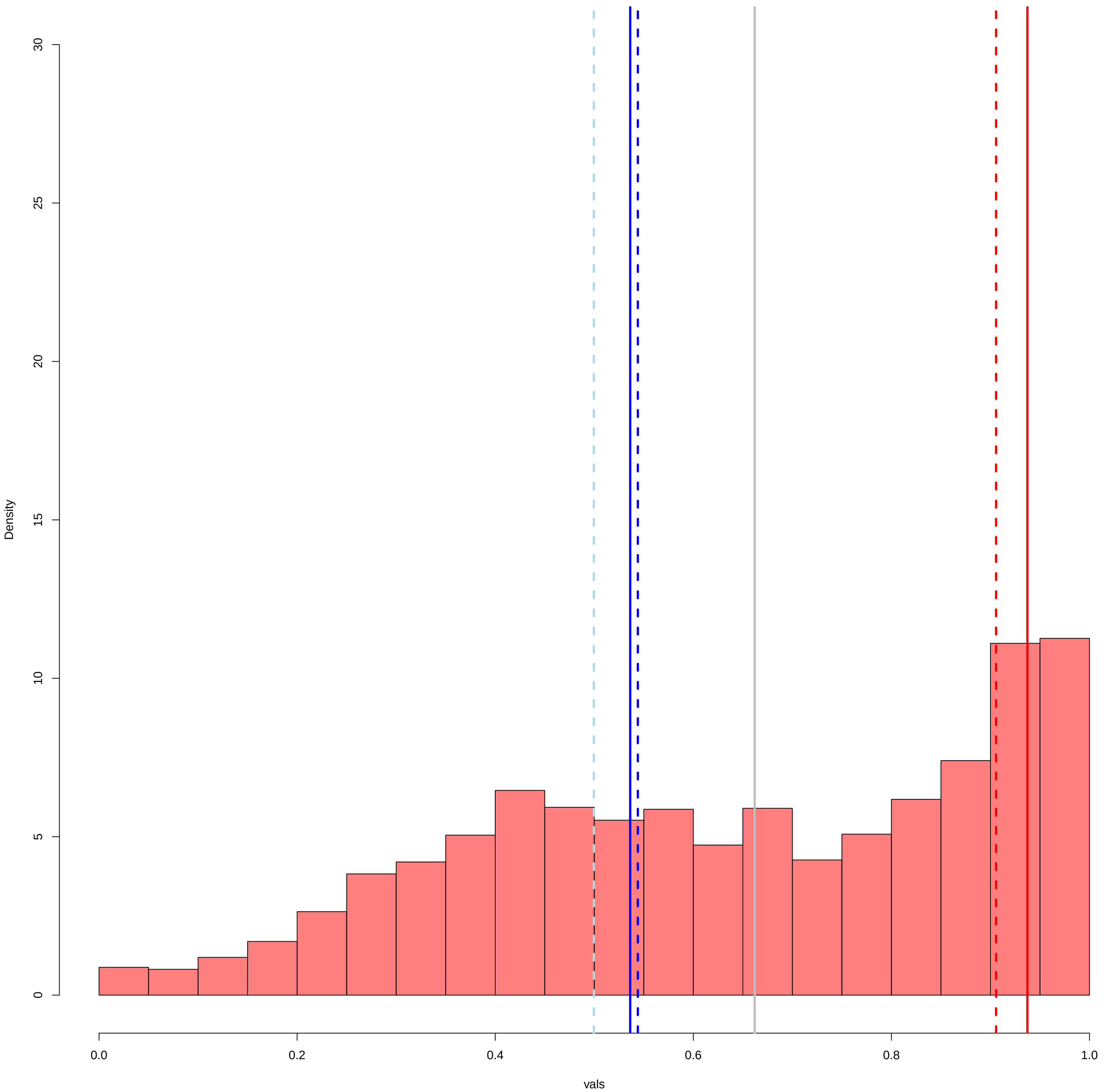
SLC2A1: CADD_raw_rankscore



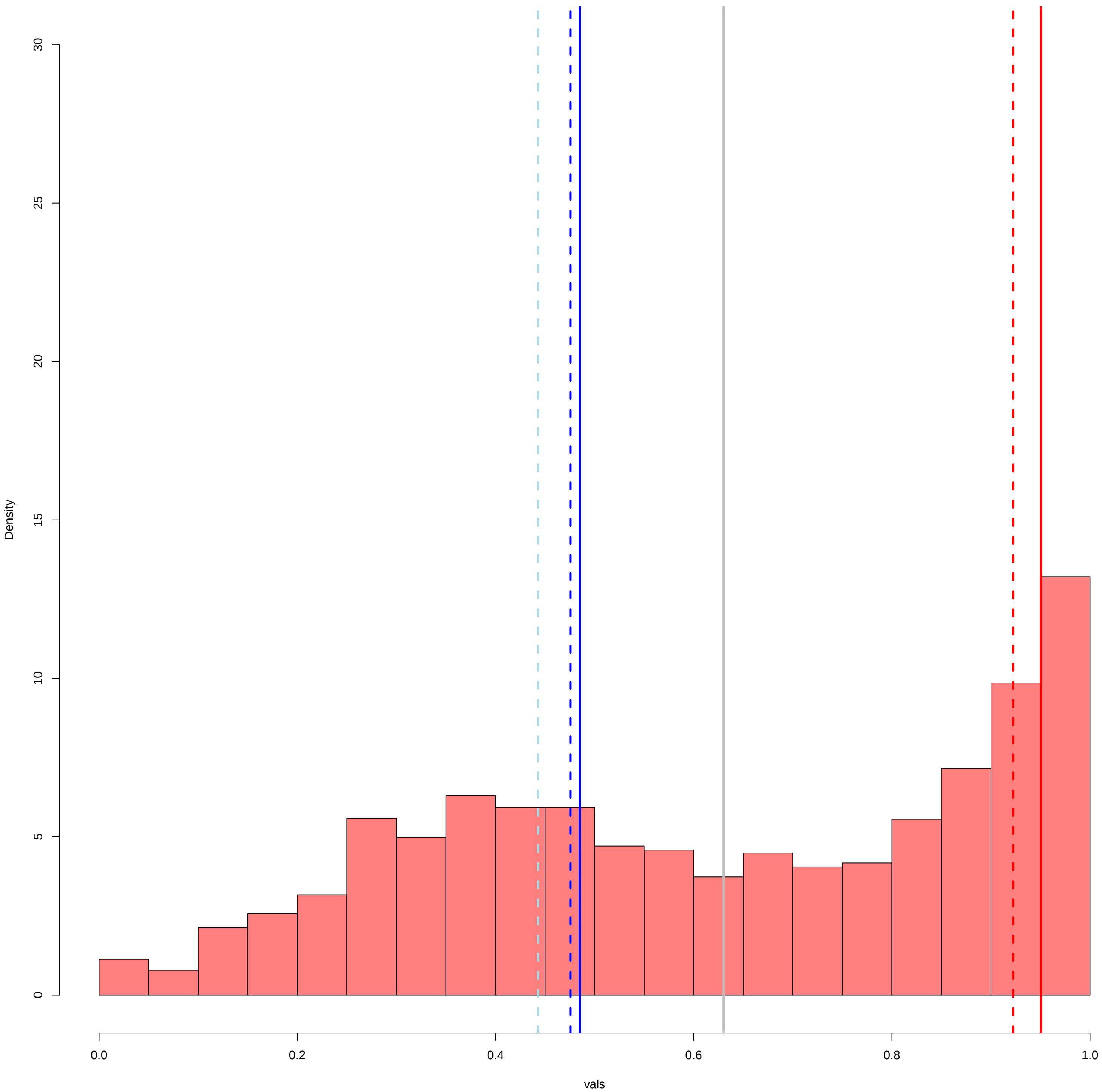
SLC2A1: DANN_rankscore



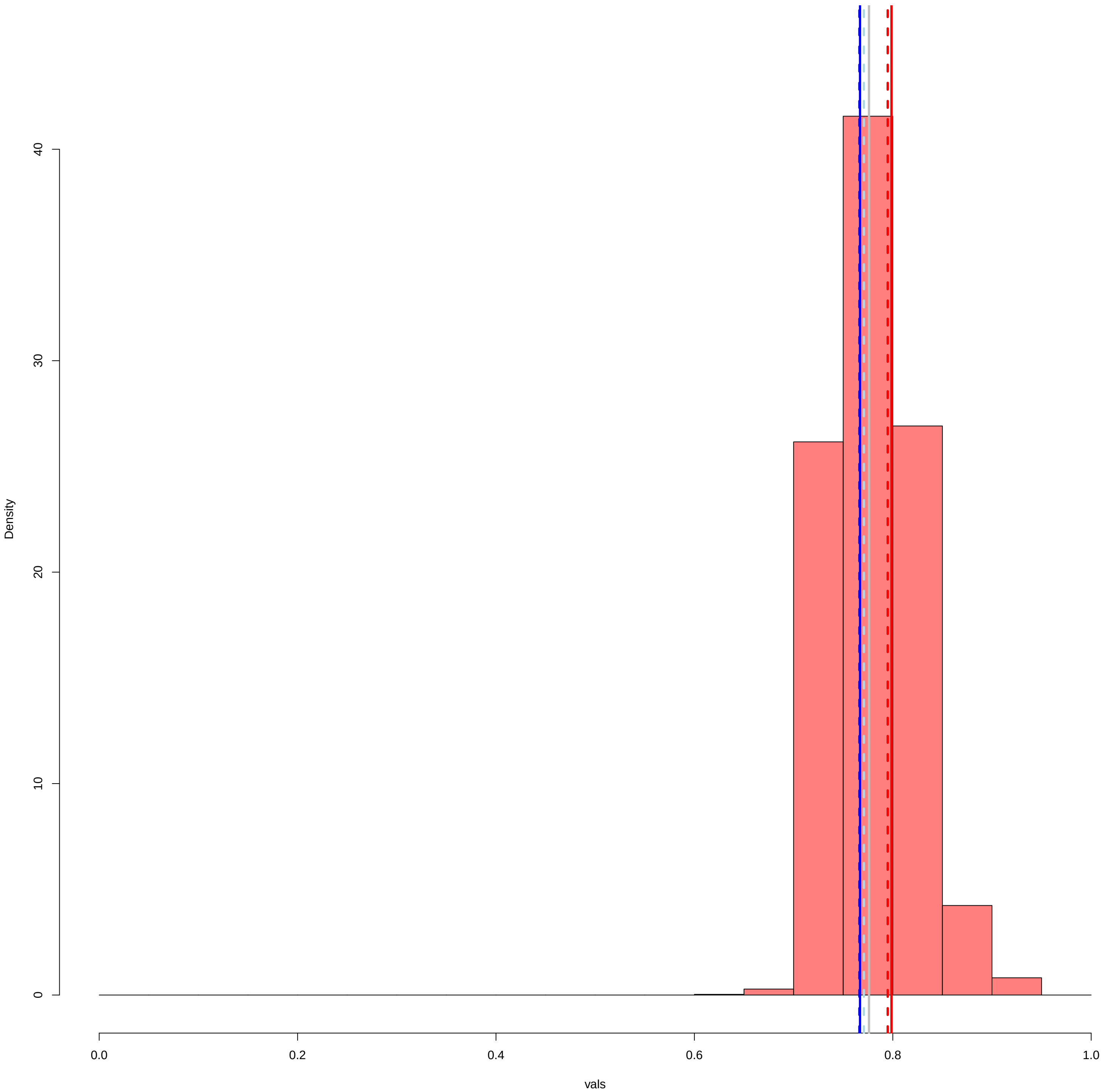
SLC2A1: Eigen-PC-raw_rankscore



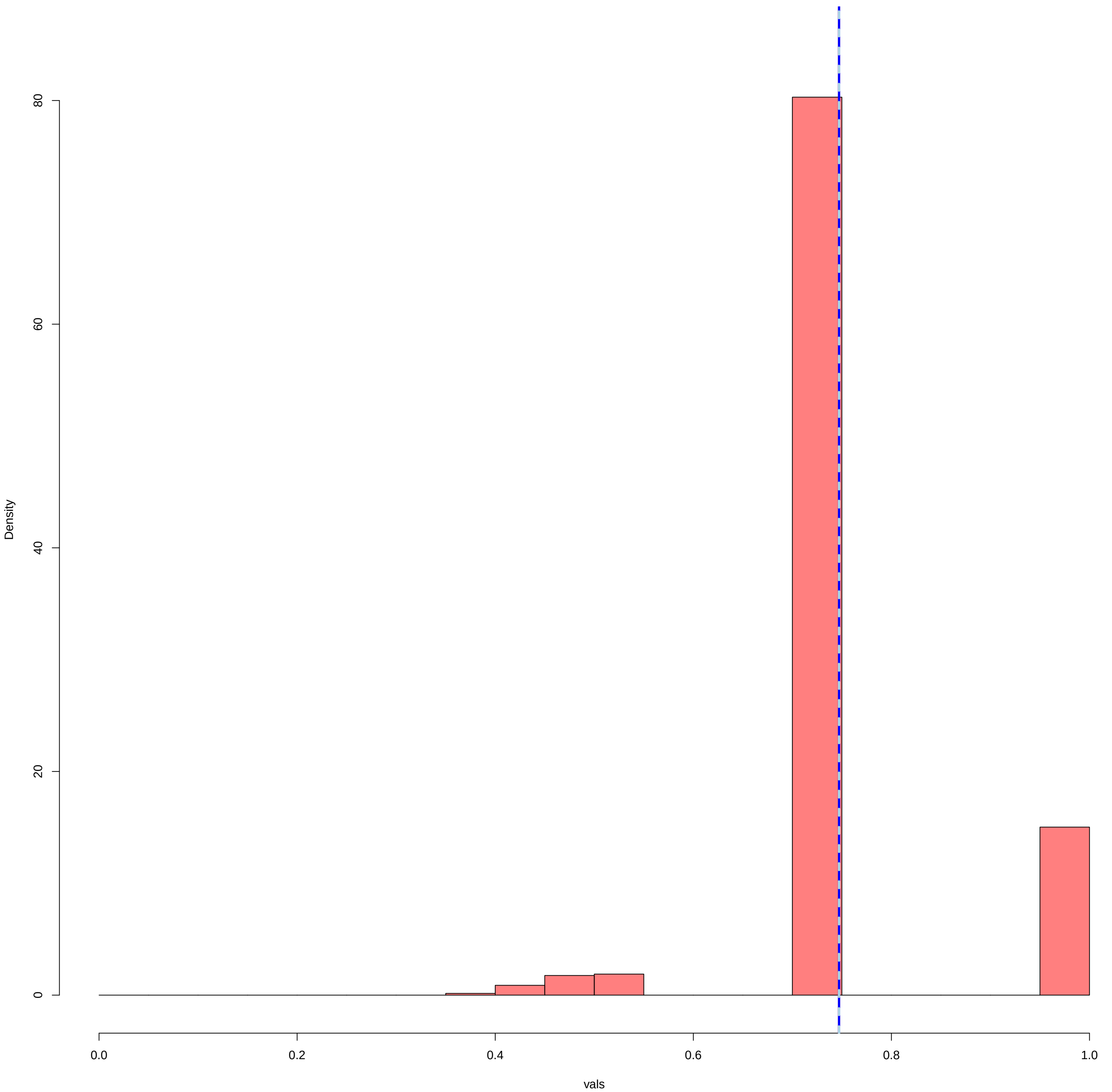
SLC2A1: Eigen-row_rankscore



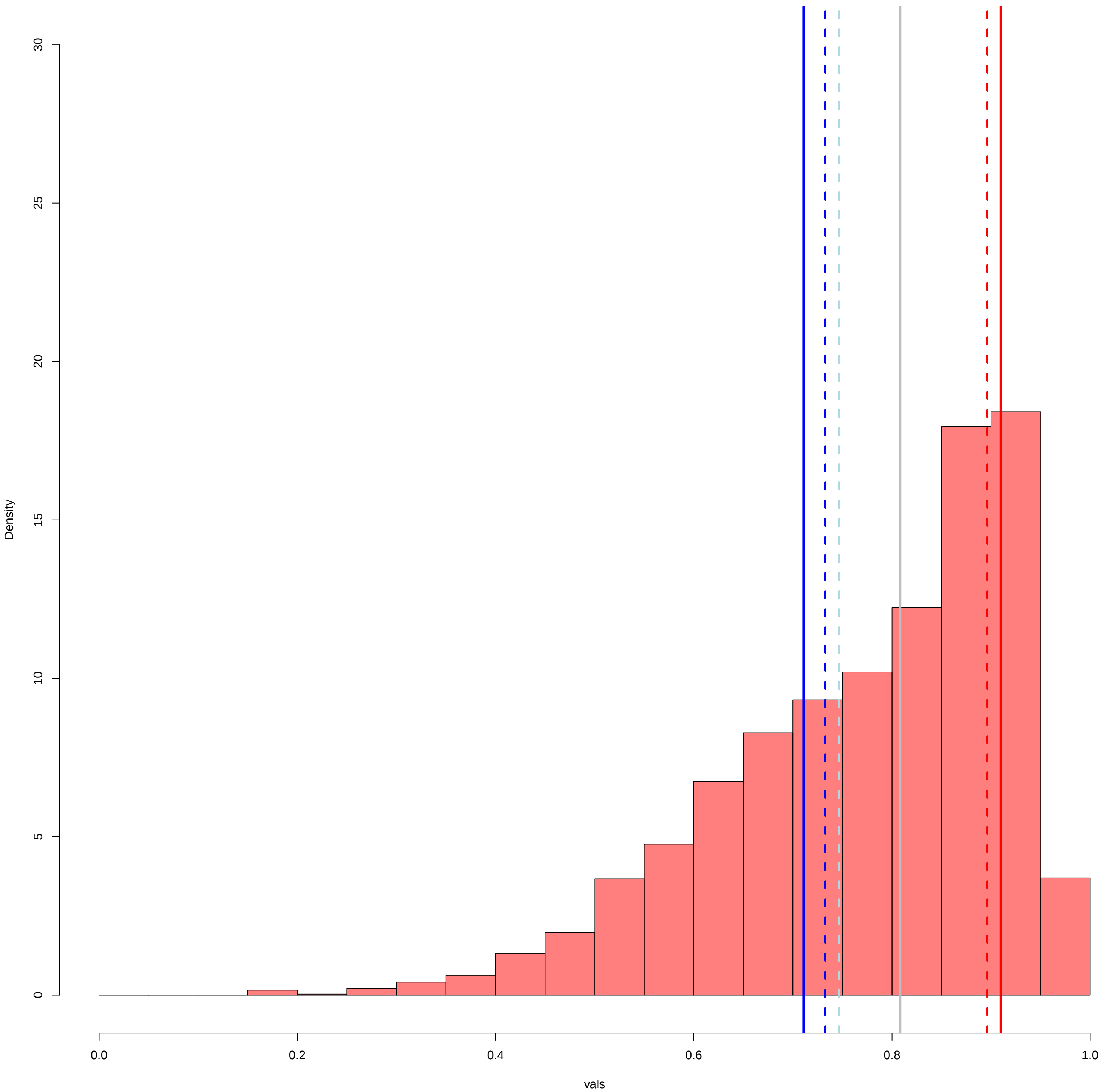
SLC2A1: FATHMM_converted_rankscore



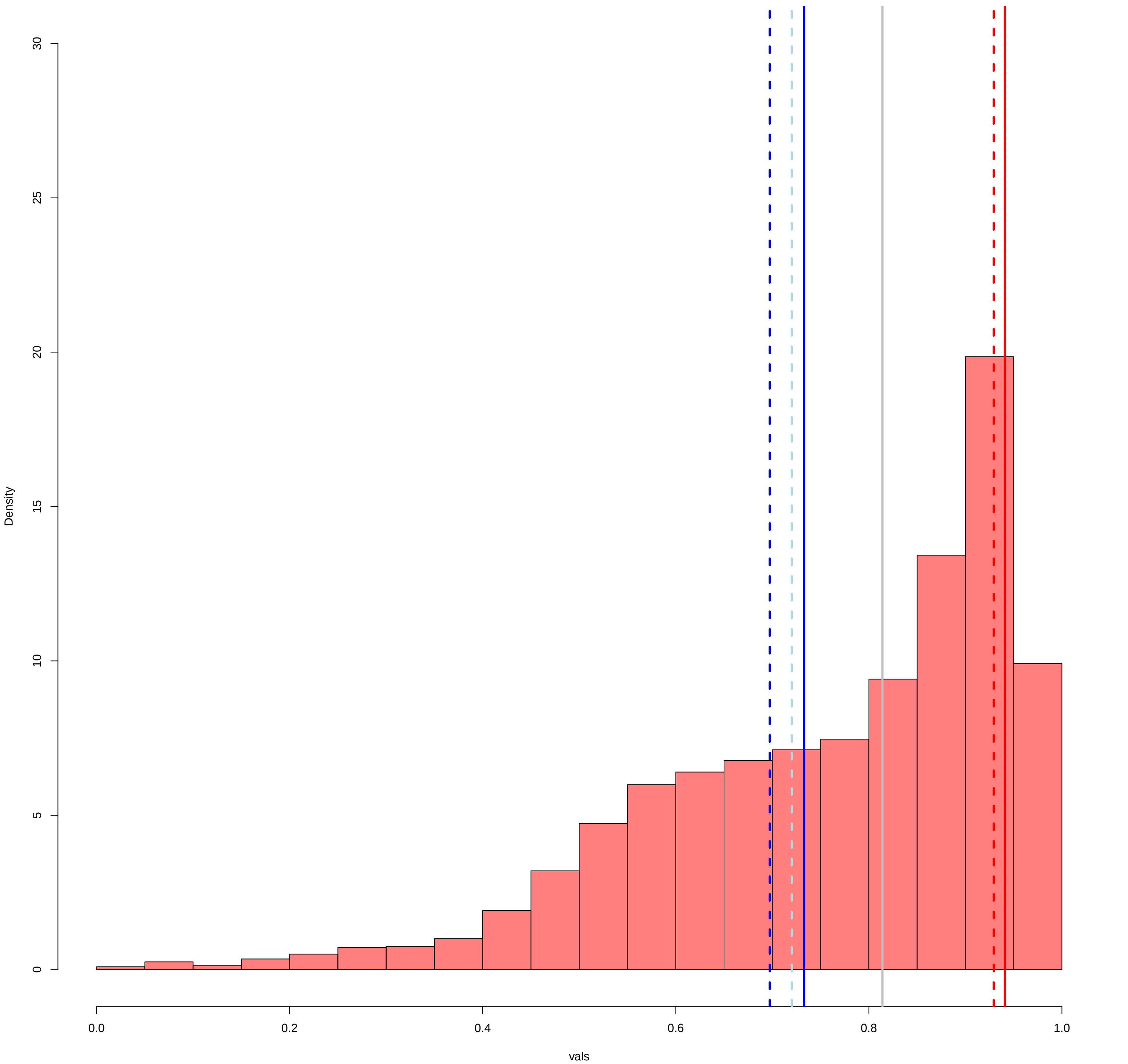
SLC2A1: GenoCanyon_score_rankscore



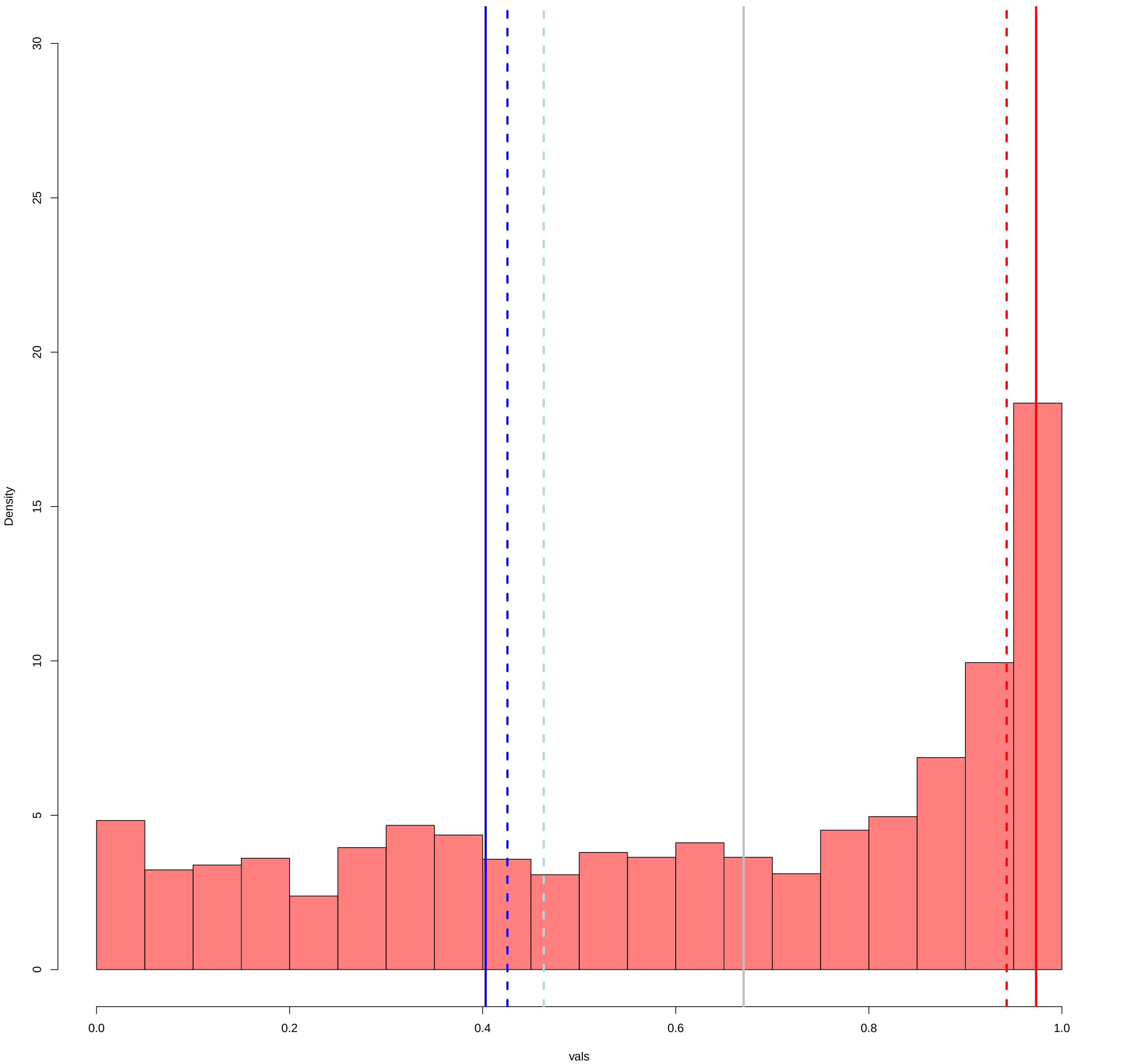
SLC2A1: MetaLR_rankscore



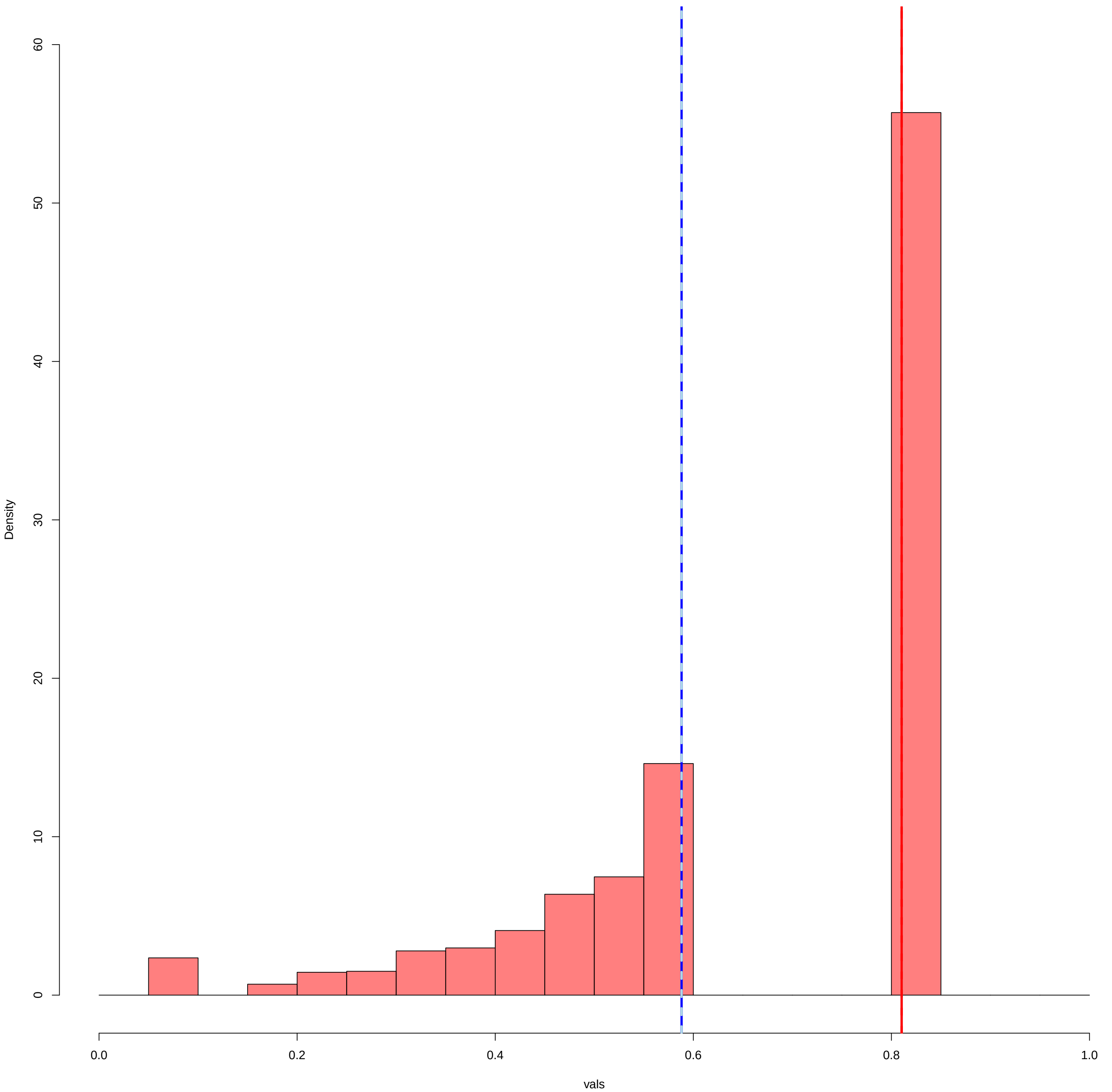
SLC2A1: MetaSVM_rankscore



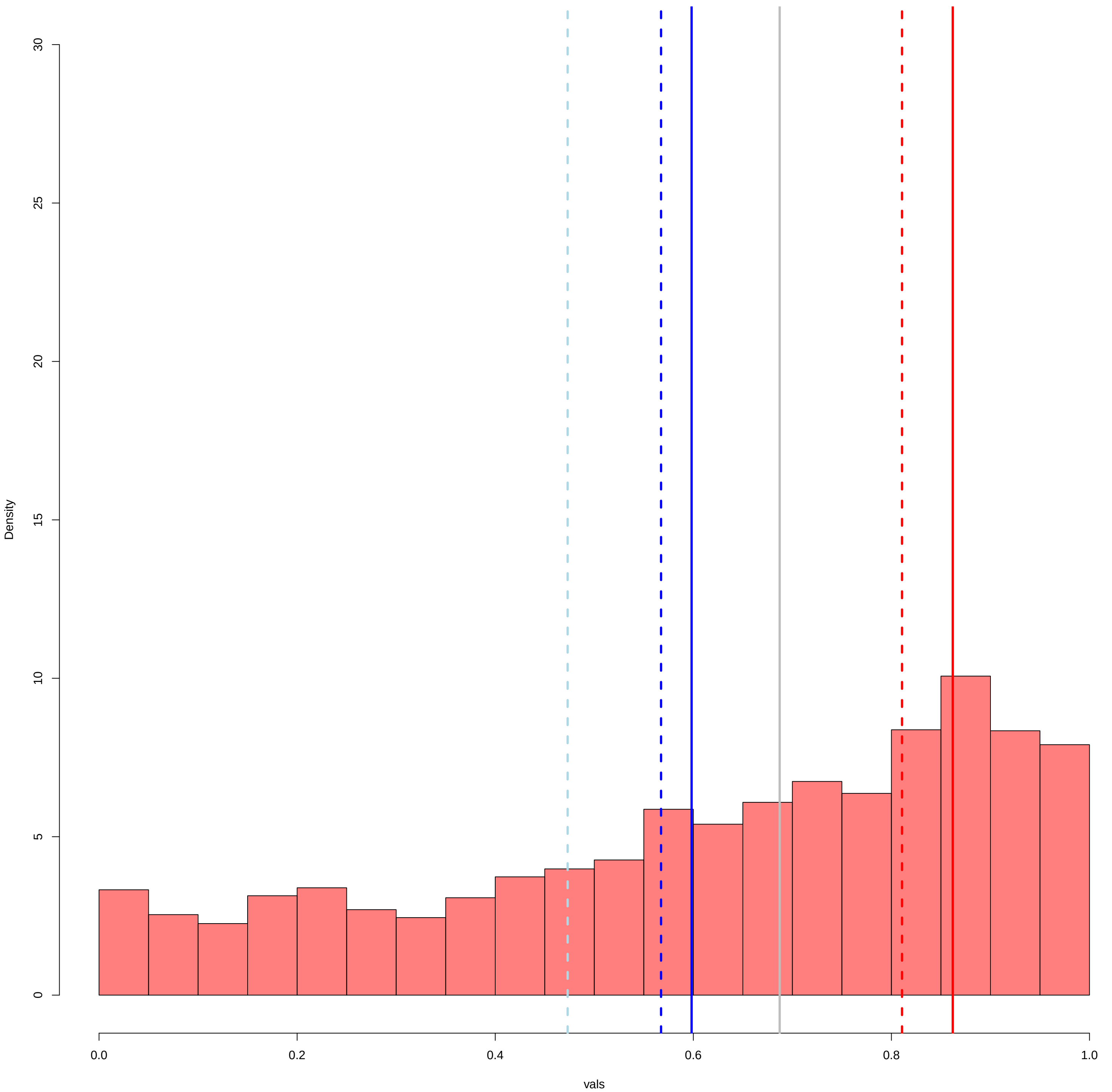
SLC2A1: MutationAssessor_score_rankscore



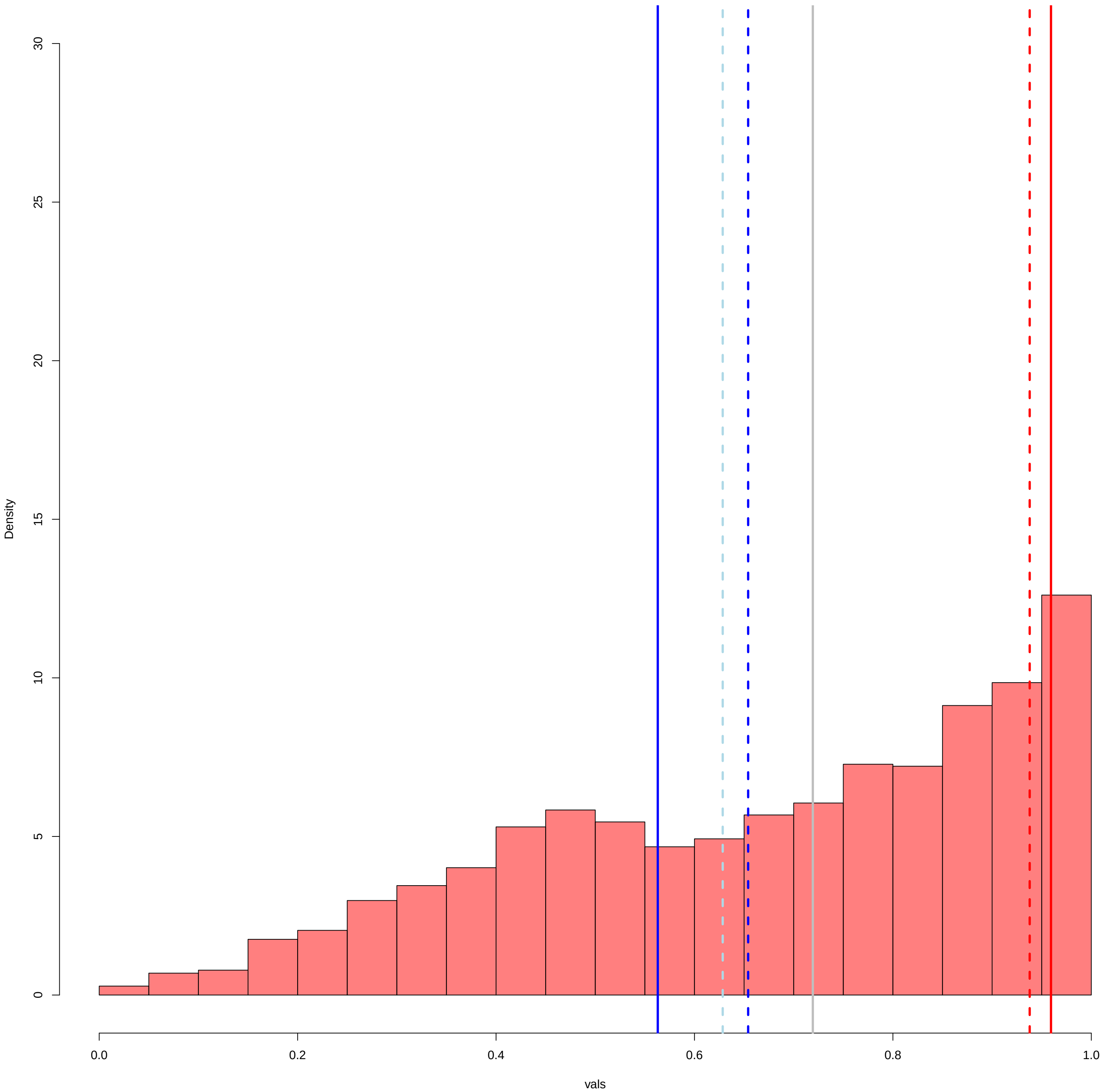
SLC2A1: MutationTaster_converted_rankscore



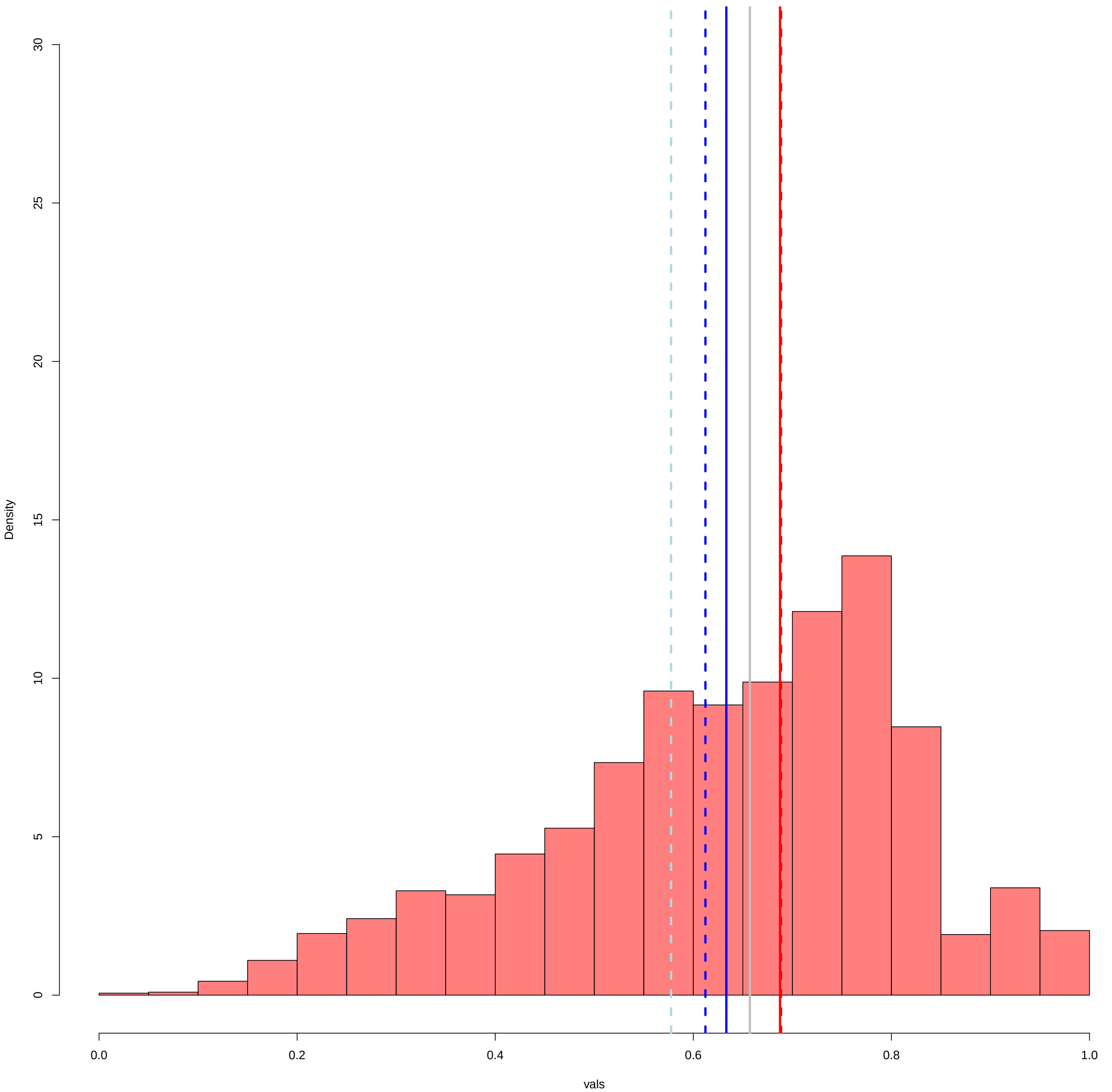
SLC2A1: PROVEAN_converted_rankscore



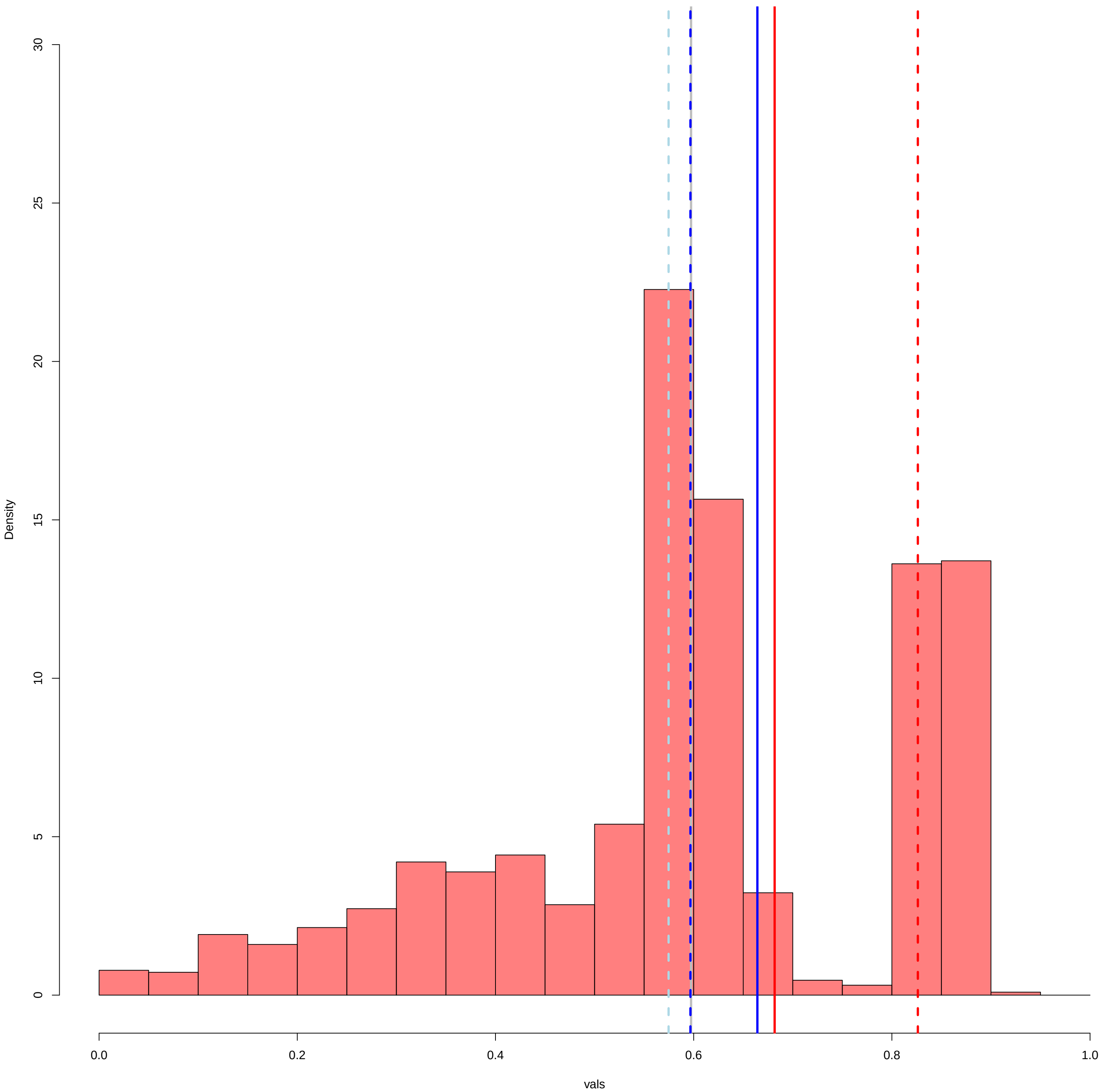
SLC2A1: VEST3_rankscore



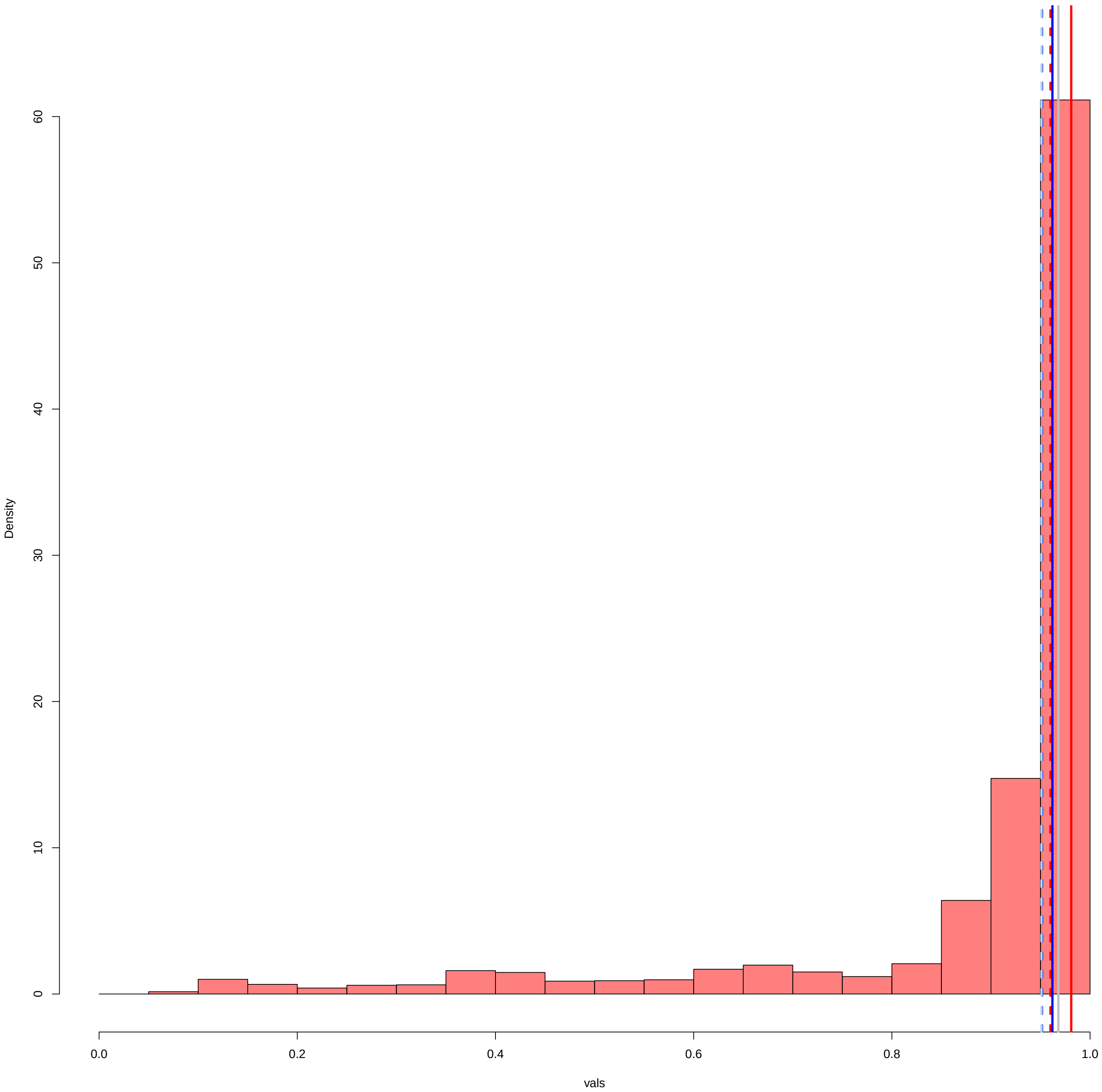
SLC2A1: fathmm-MKL_coding_rankscore



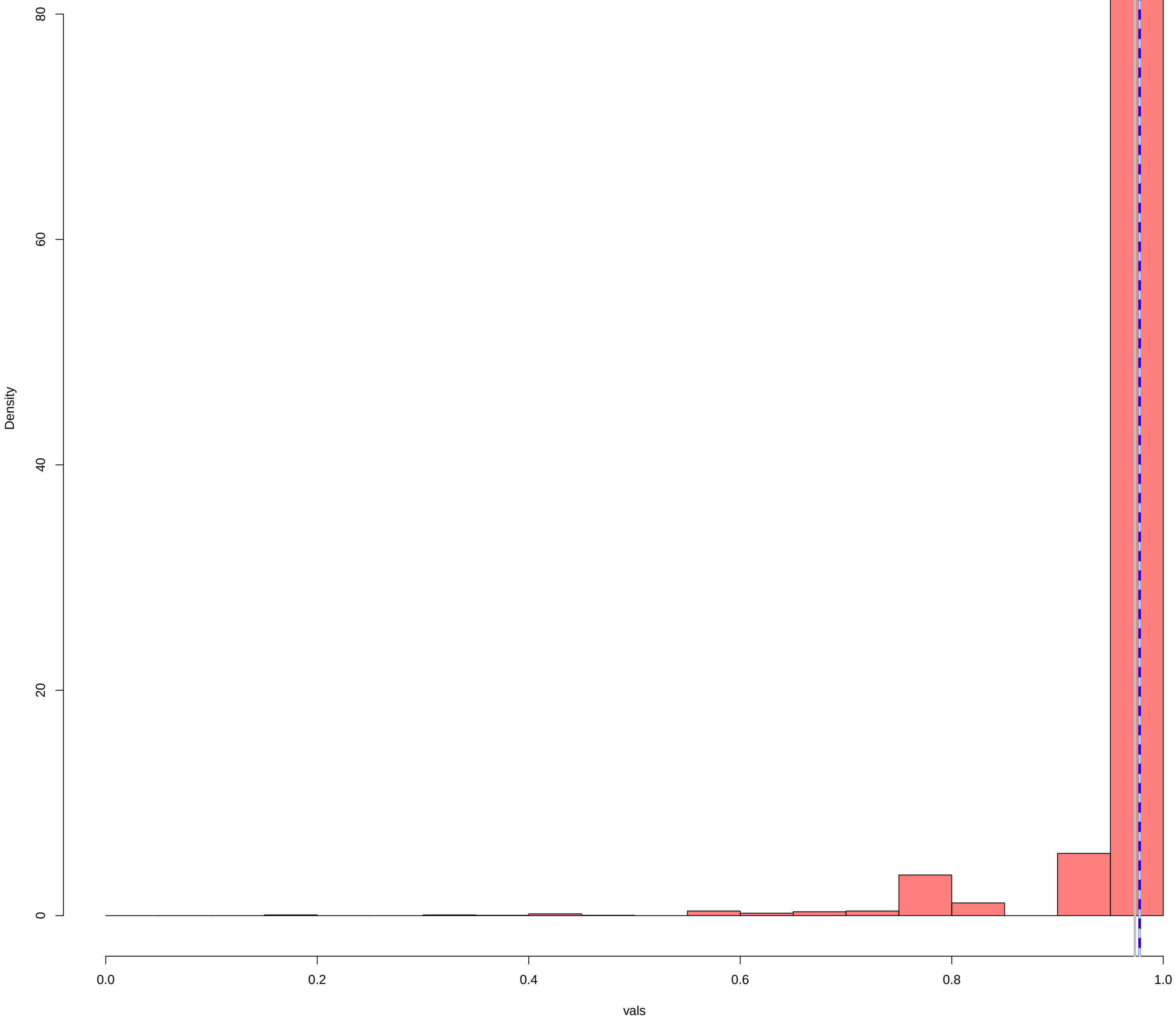
SLC2A1: SiPhy_29way_logOdds_rankscore



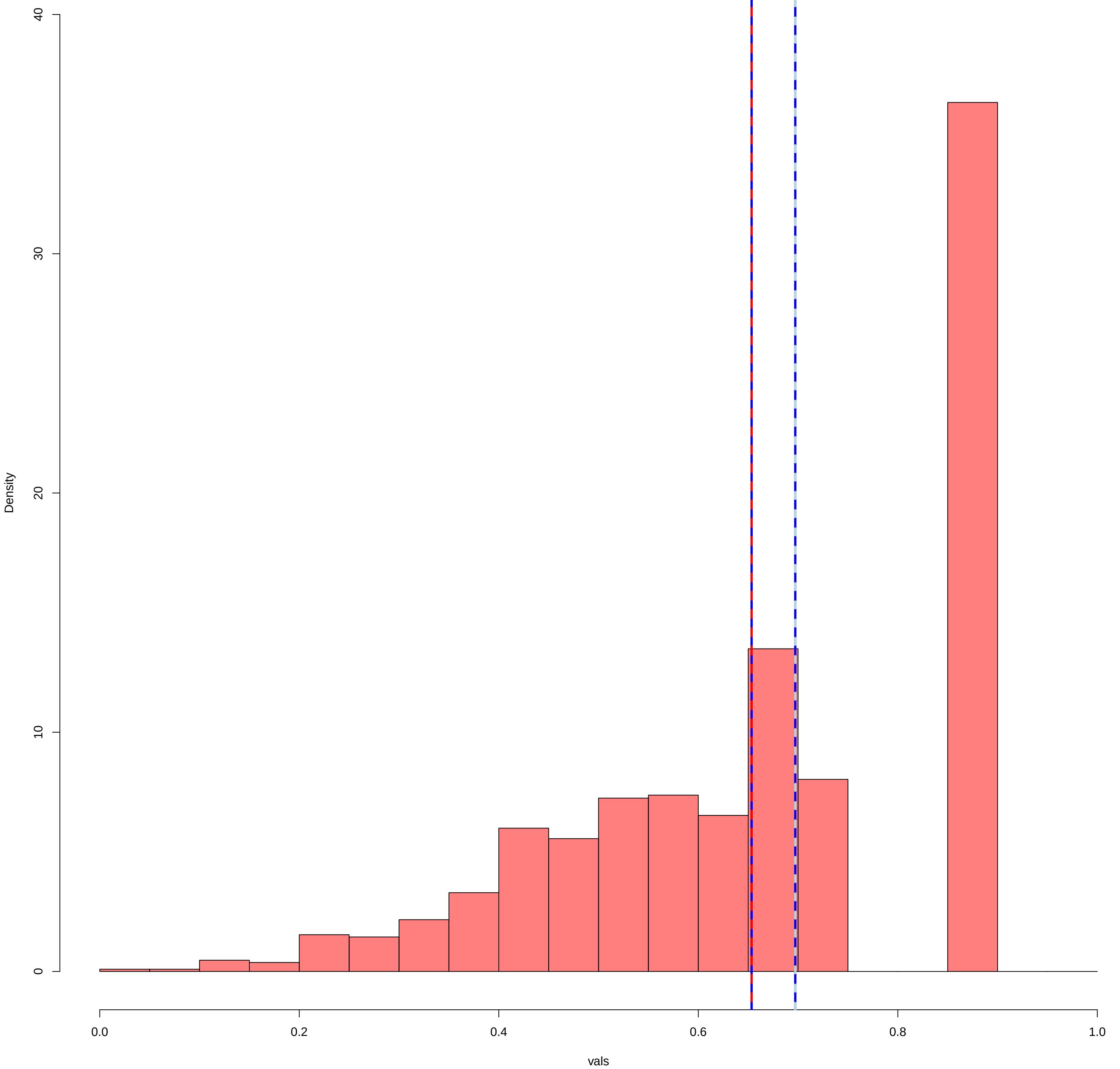
SLC2A1: priPhCons



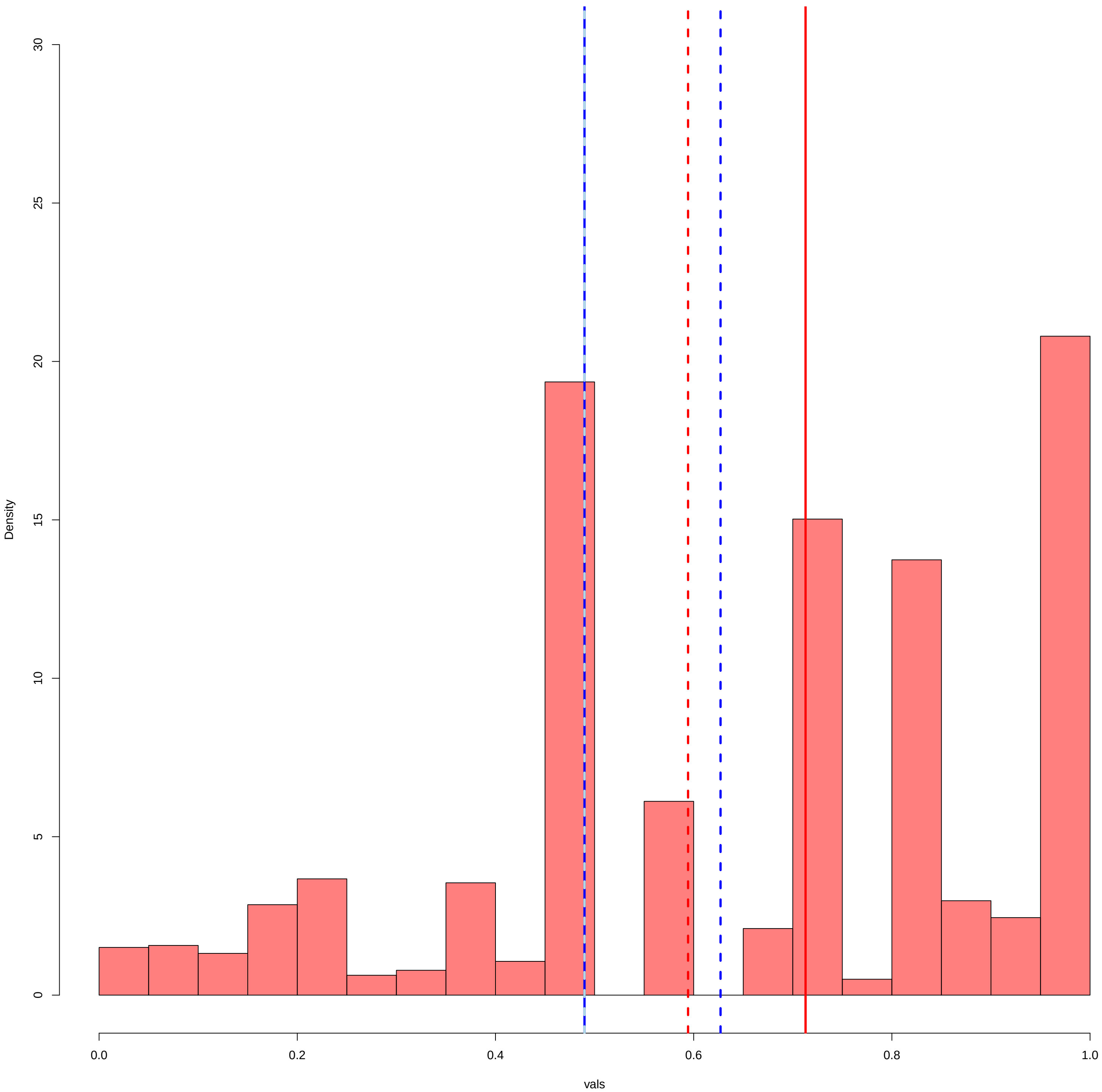
SLC2A1: priPhyloP



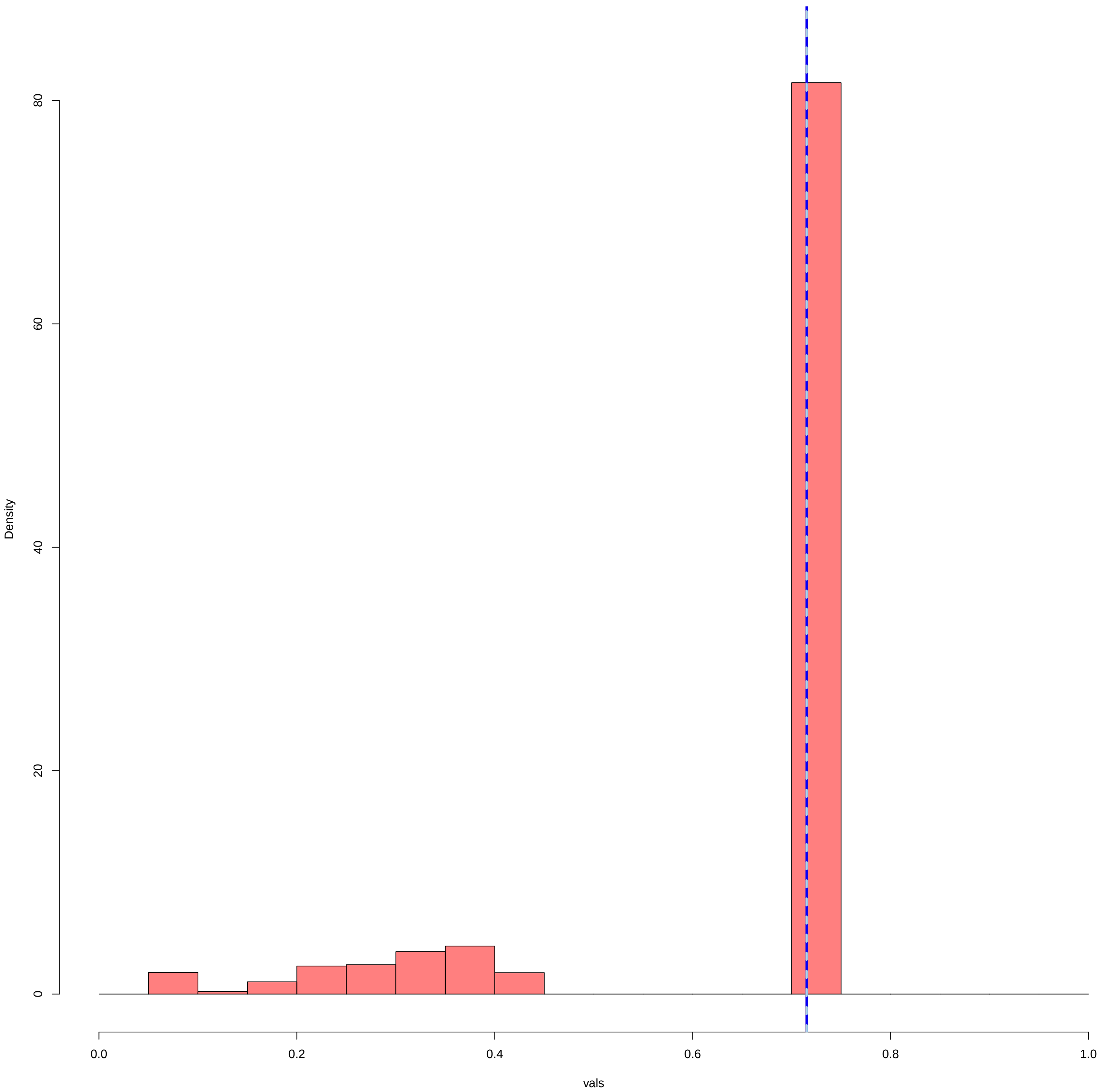
SLC2A1: phastCons20way_mammalian_rankscore



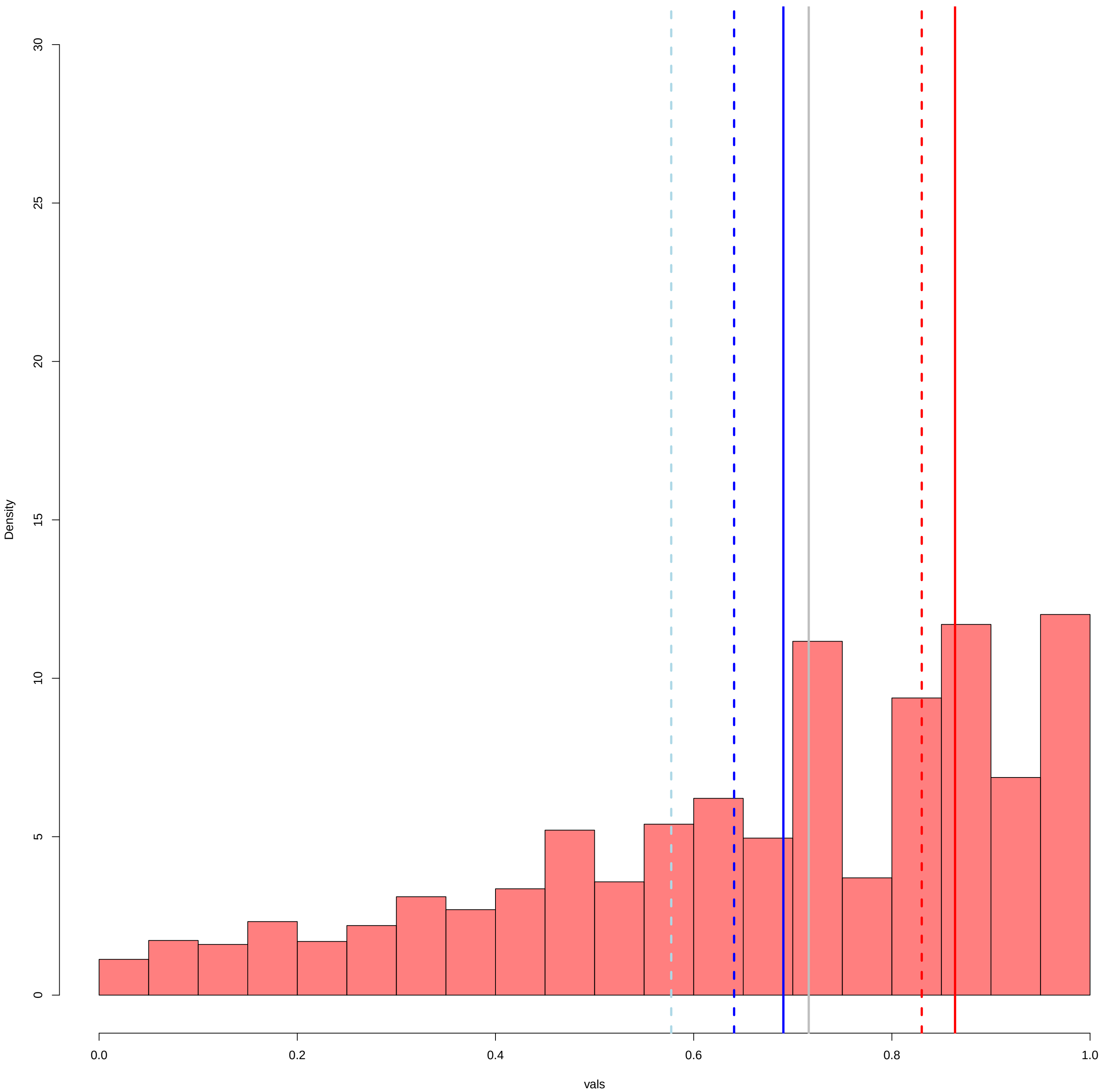
SLC2A1: phyloP20way_mammalian_rankscore



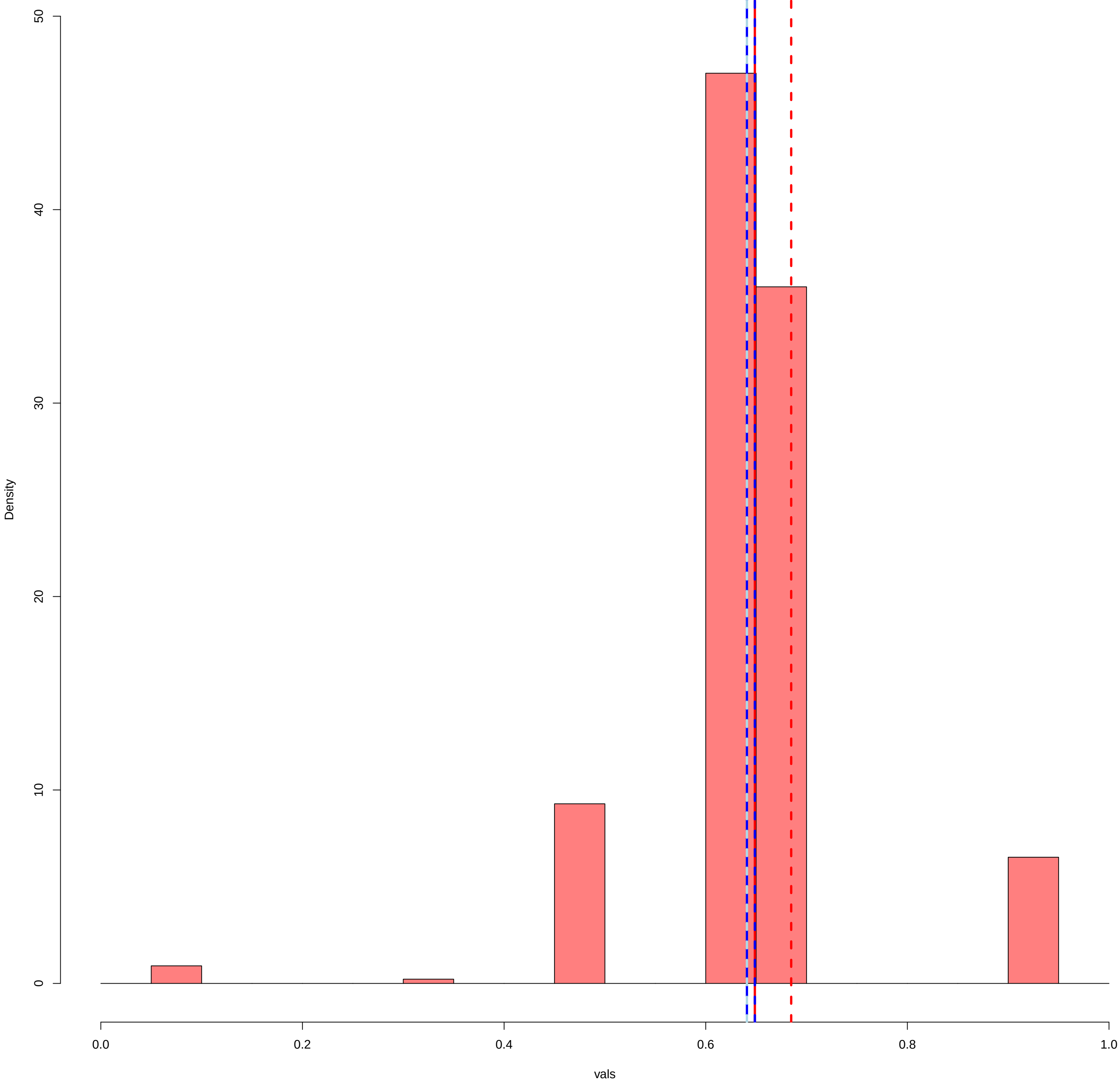
SLC2A1: phastCons100way_vertebrate_rankscore



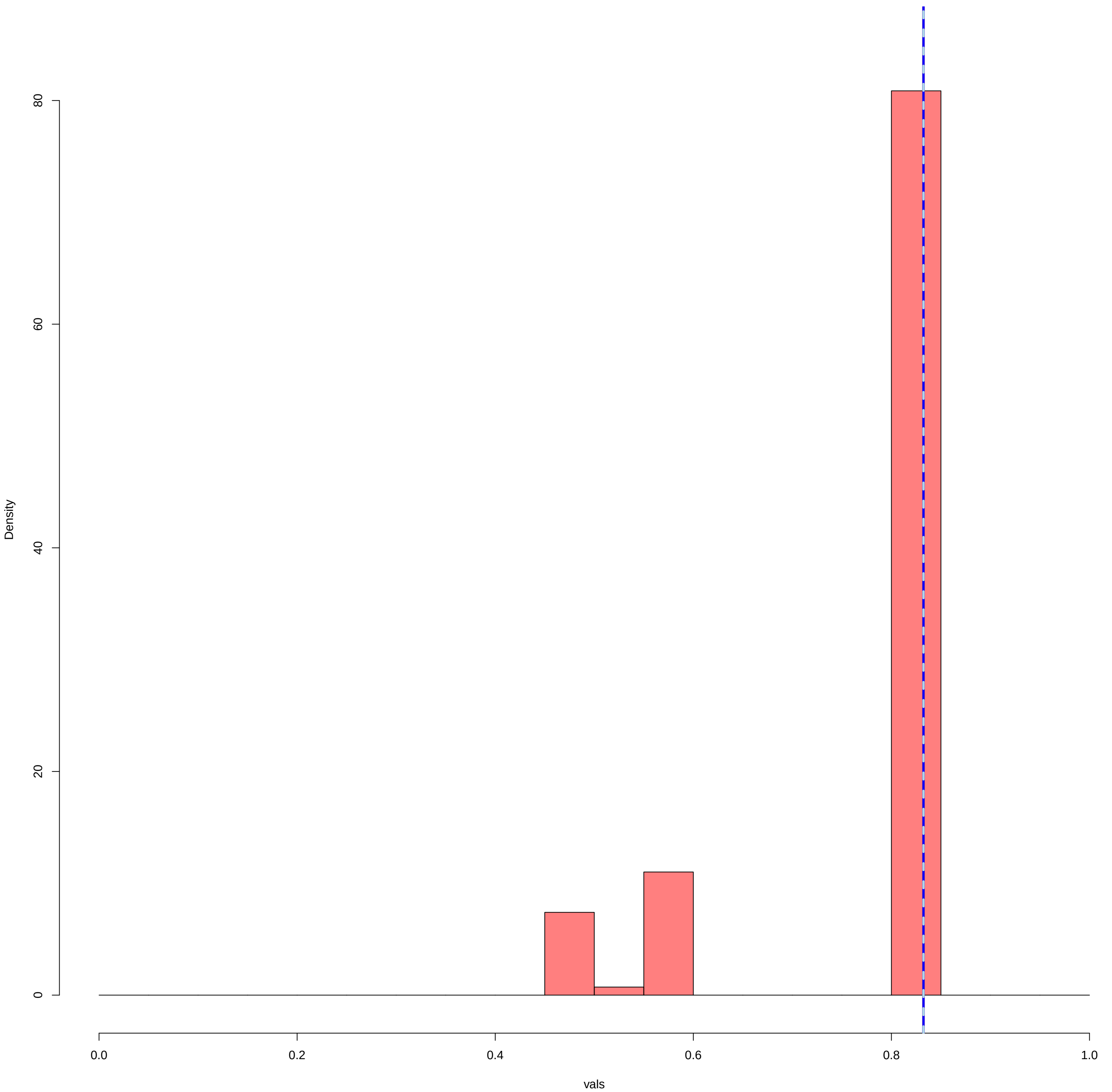
SLC2A1: phyloP100way_vertebrate_rankscore



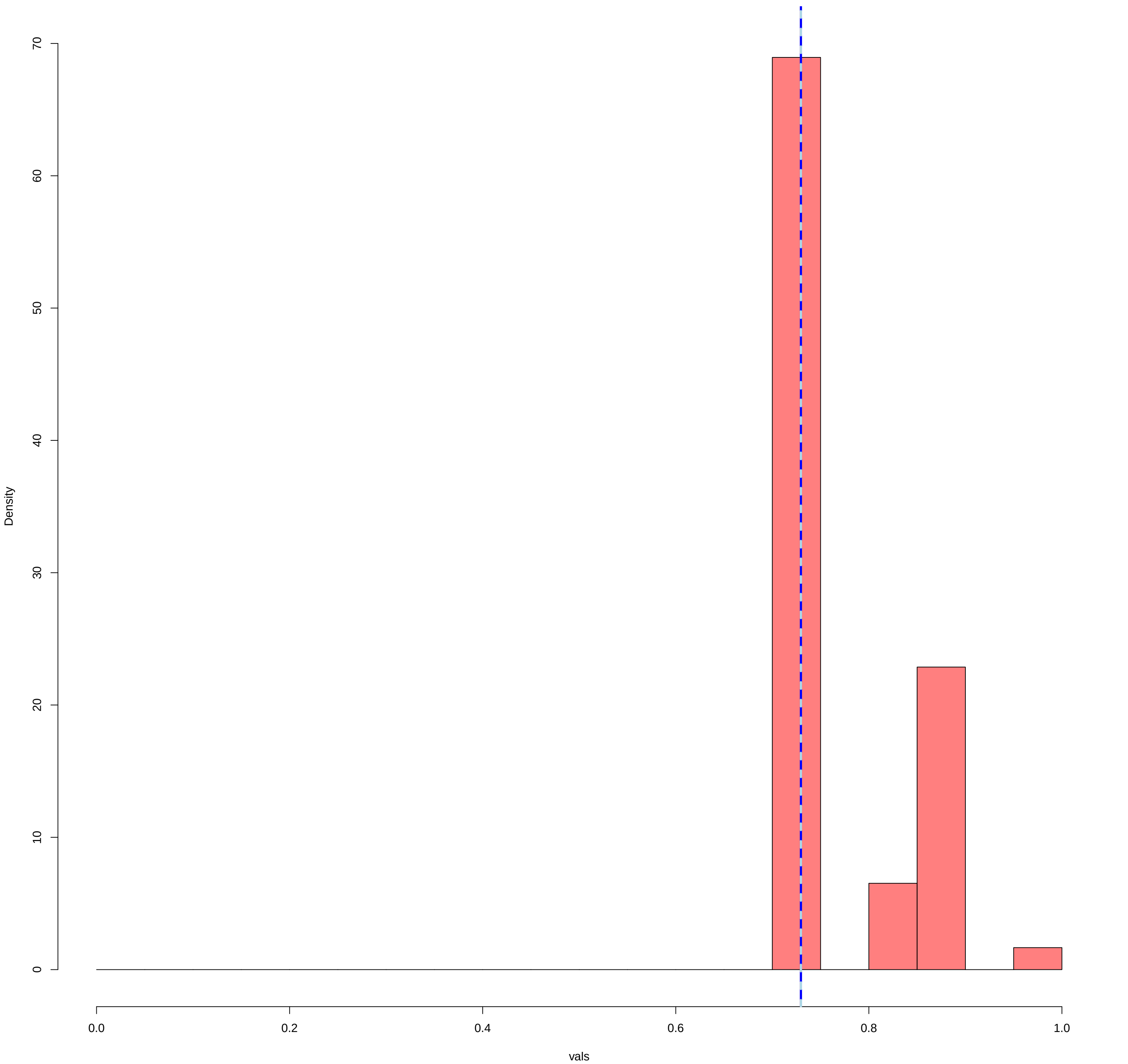
SLC2A1: H1-hESC_fitCons_score_rankscore



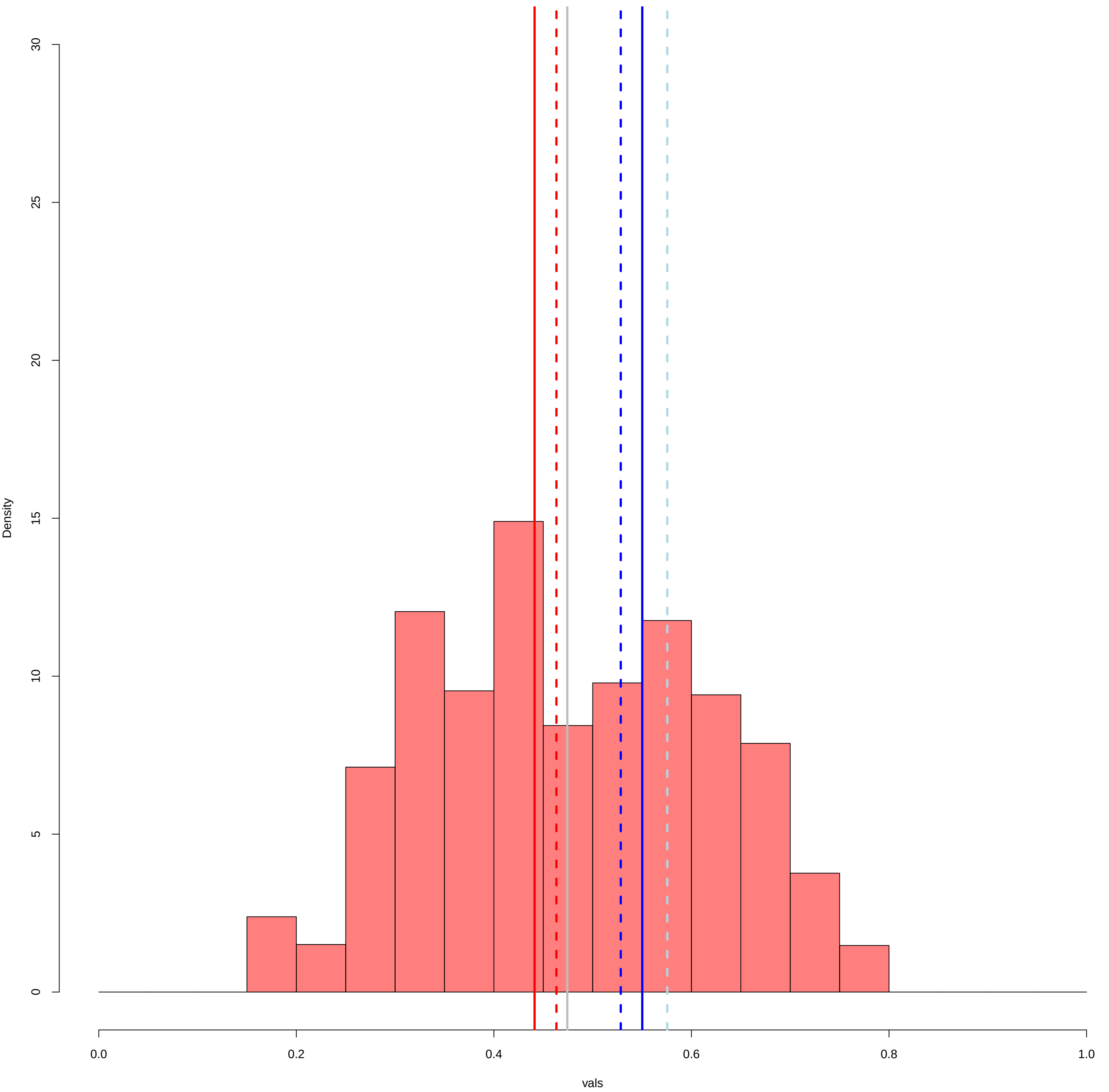
SLC2A1: HUVEC_fitCons_score_rankscore



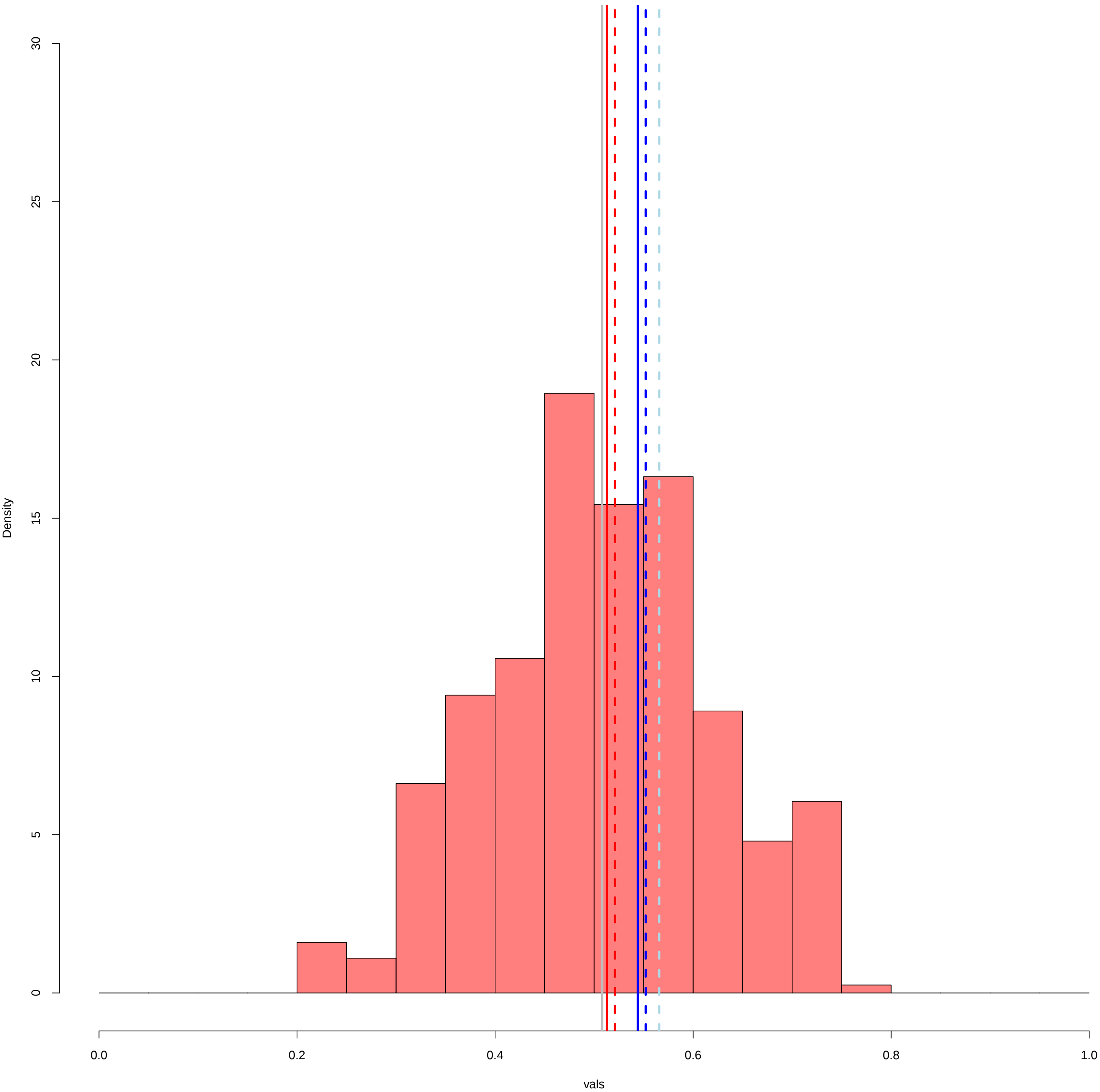
SLC2A1: integrated_fitCons_score_rankscore



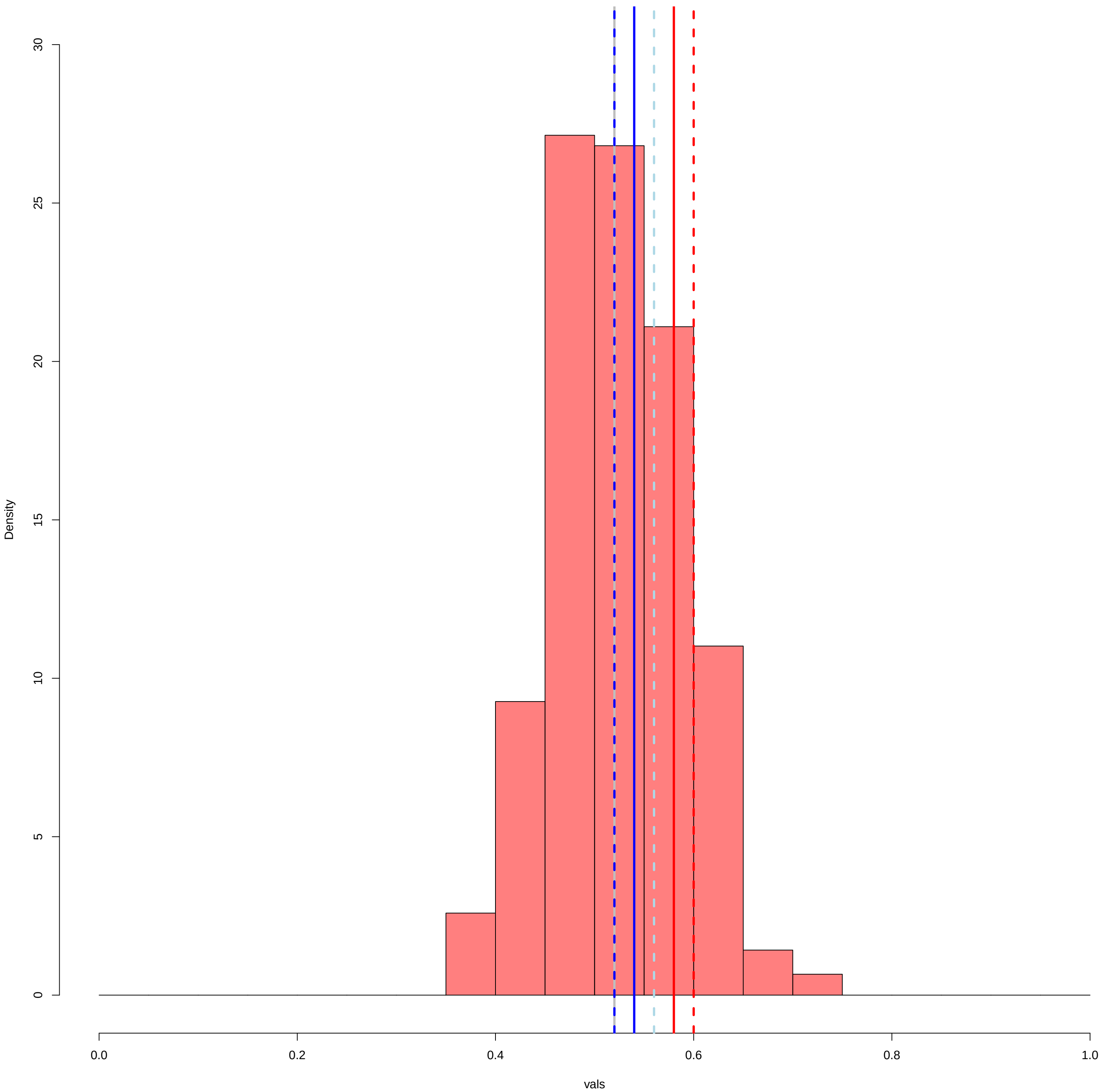
SLC2A1: ExAC v1 MTR



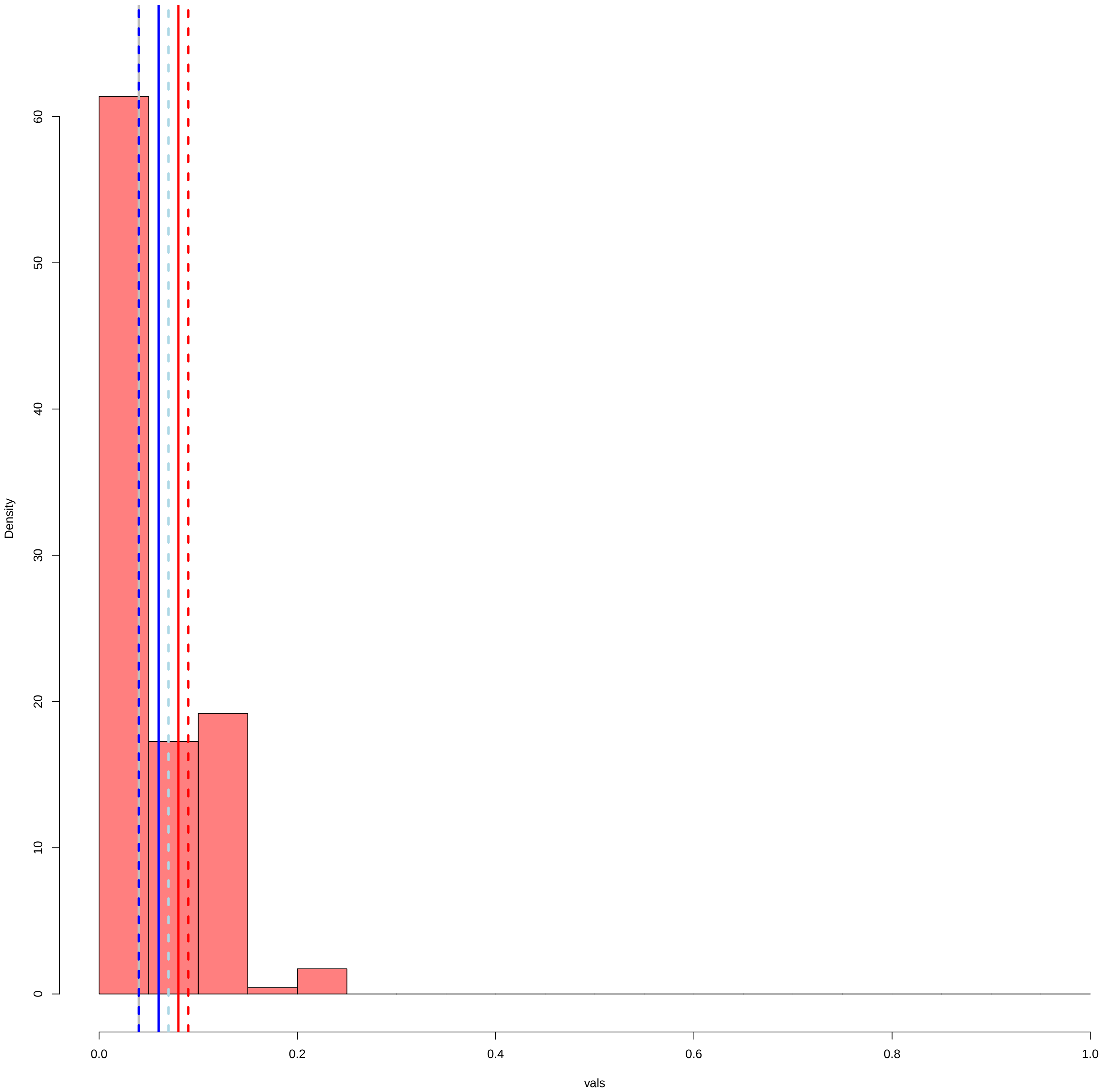
SLC2A1: ExAC v2 & gnomAD MTR



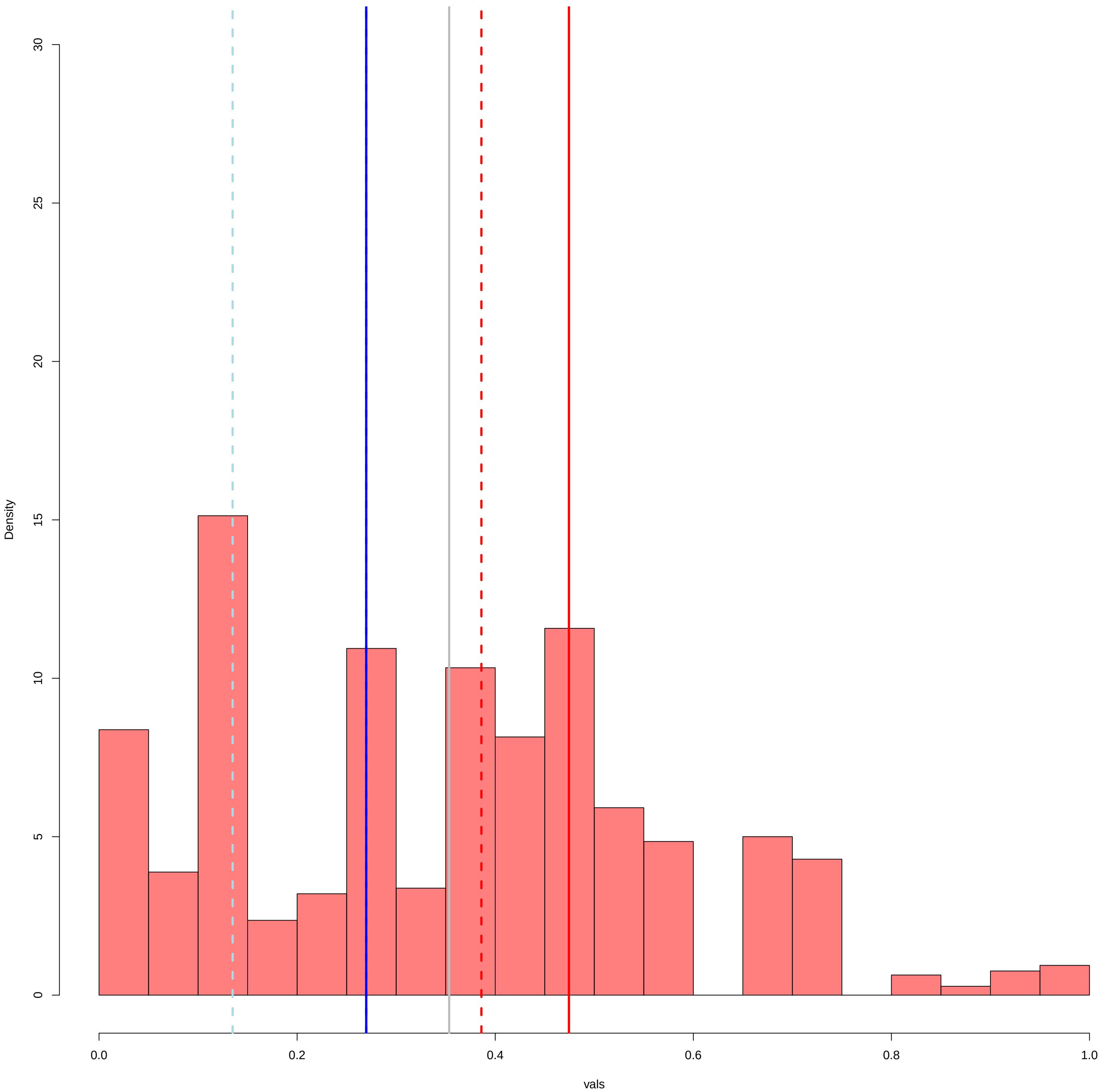
STXBP1: GC (Percent GC content in a window of +/-75bp)



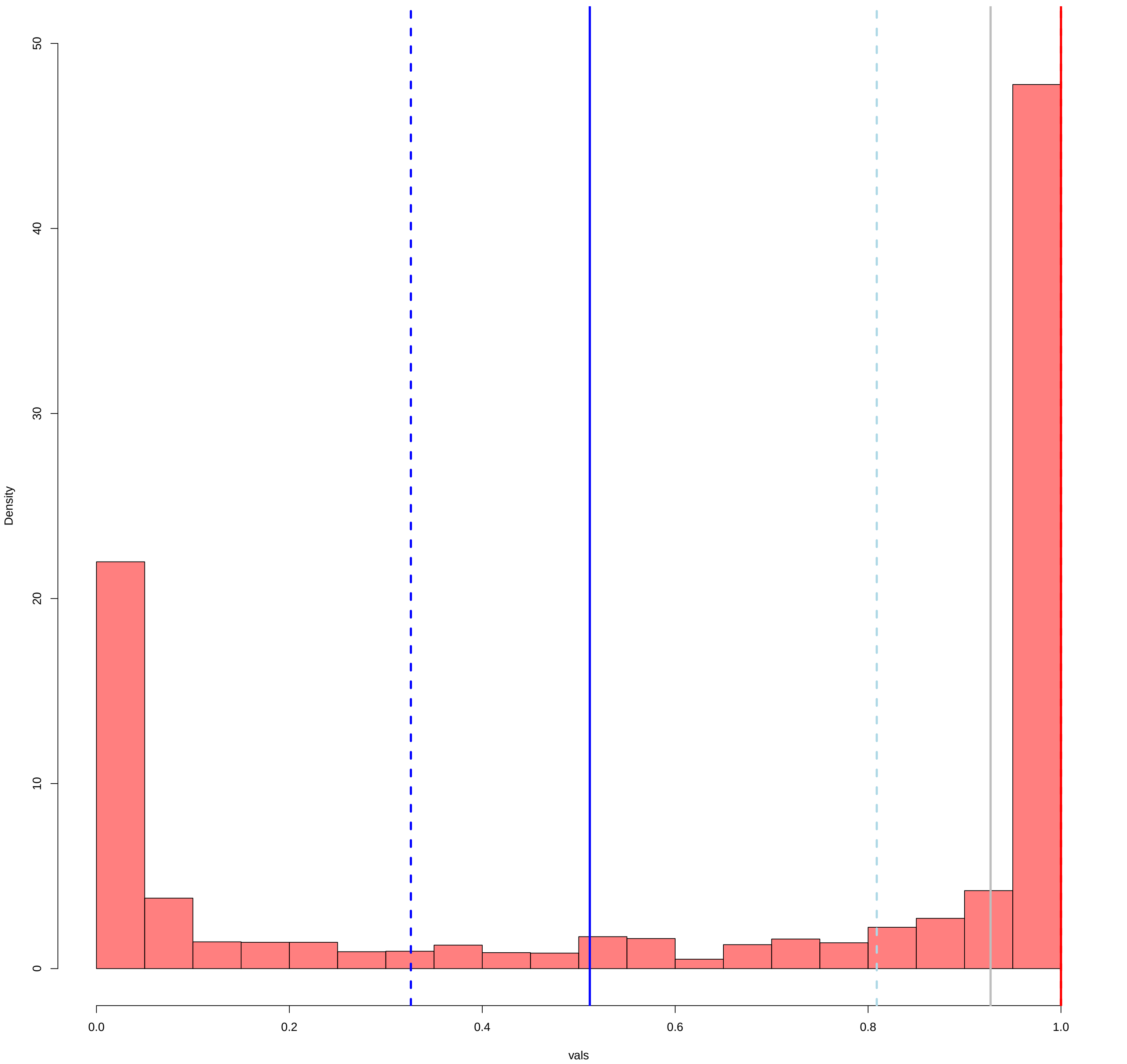
STXBP1: CpG (Percent CpG in a window of +/-75bp)



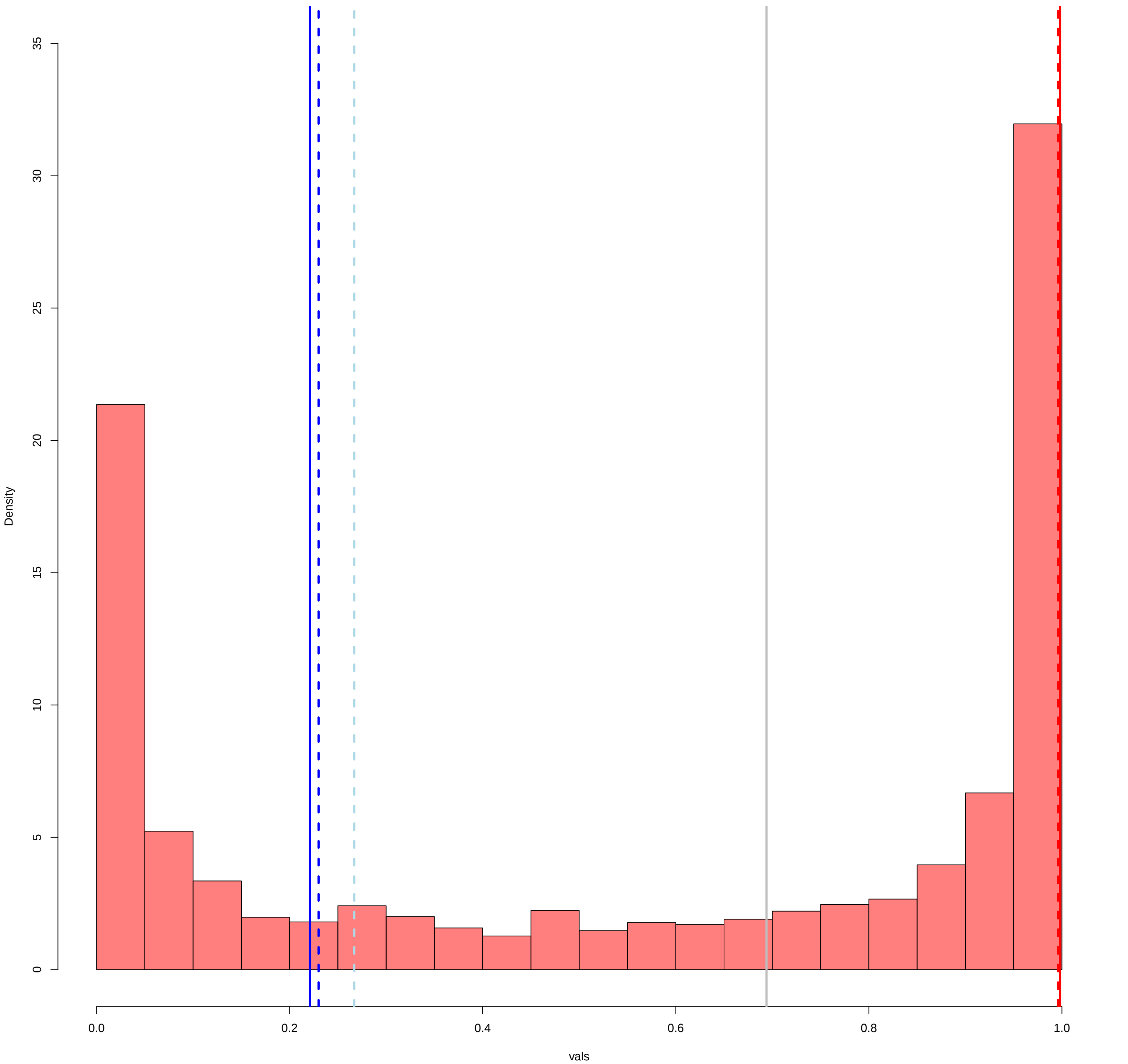
STXBP1: Grantham



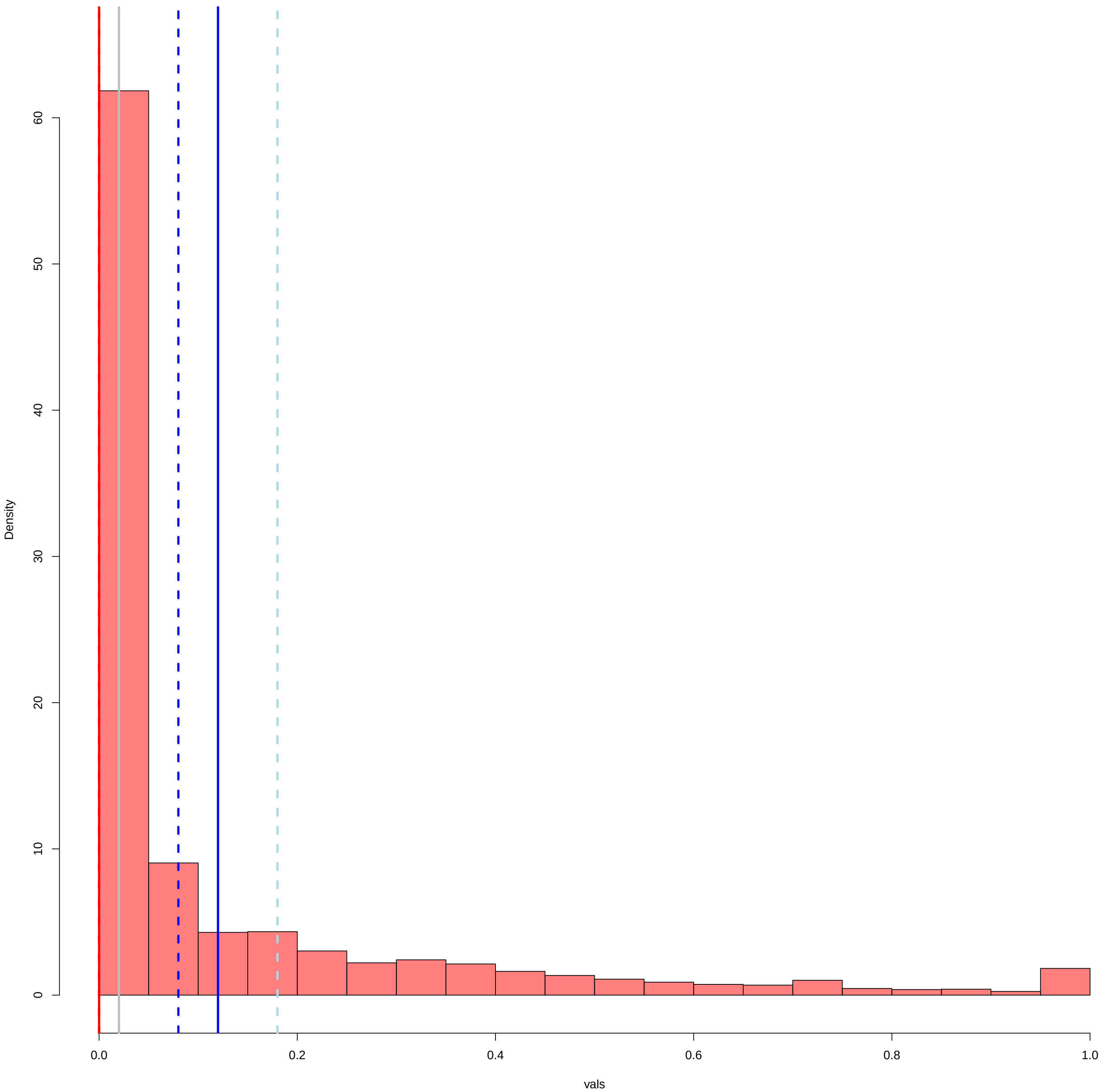
STXBP1: Hdiv quan



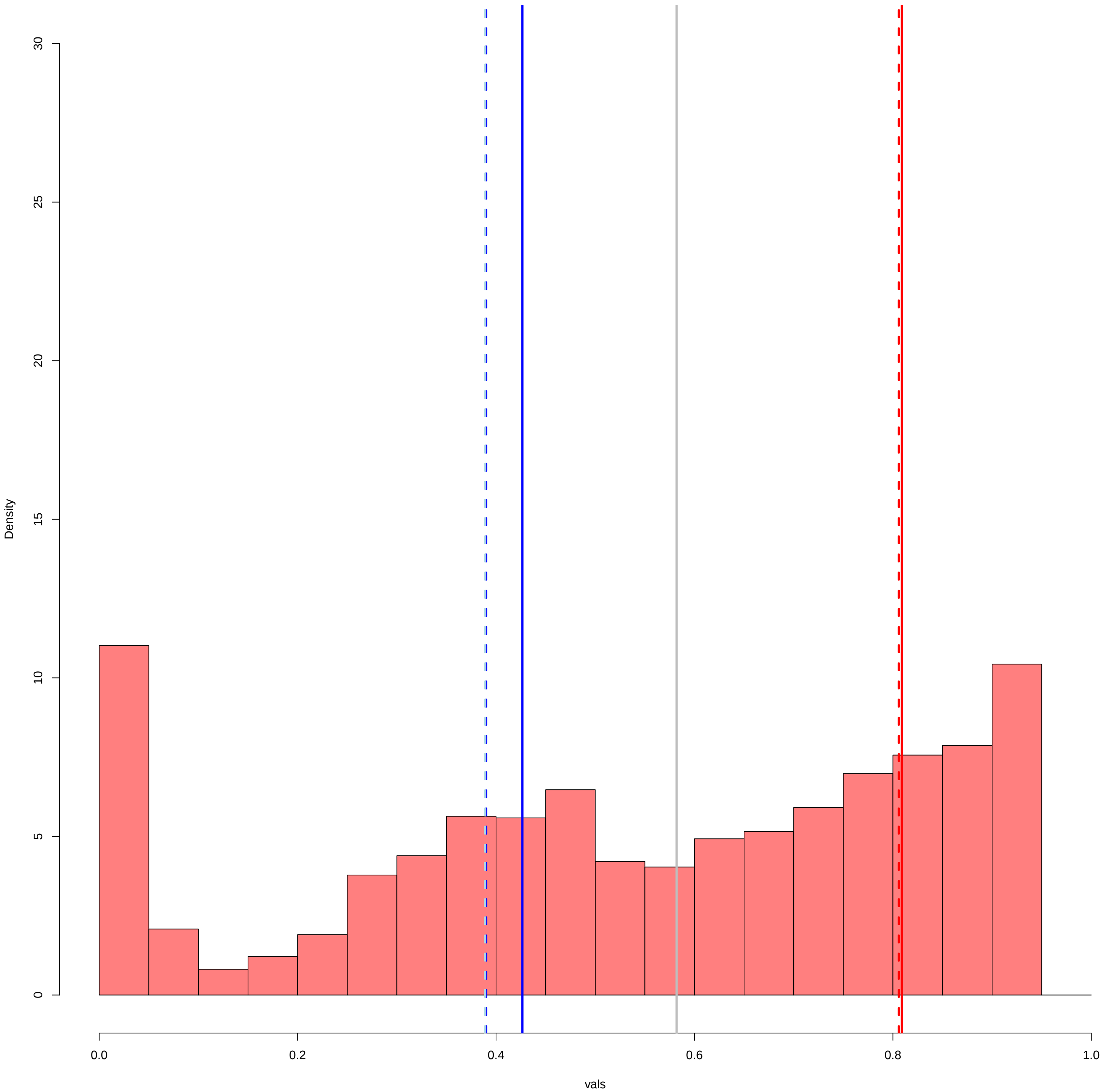
STXBP1: Hvar quan



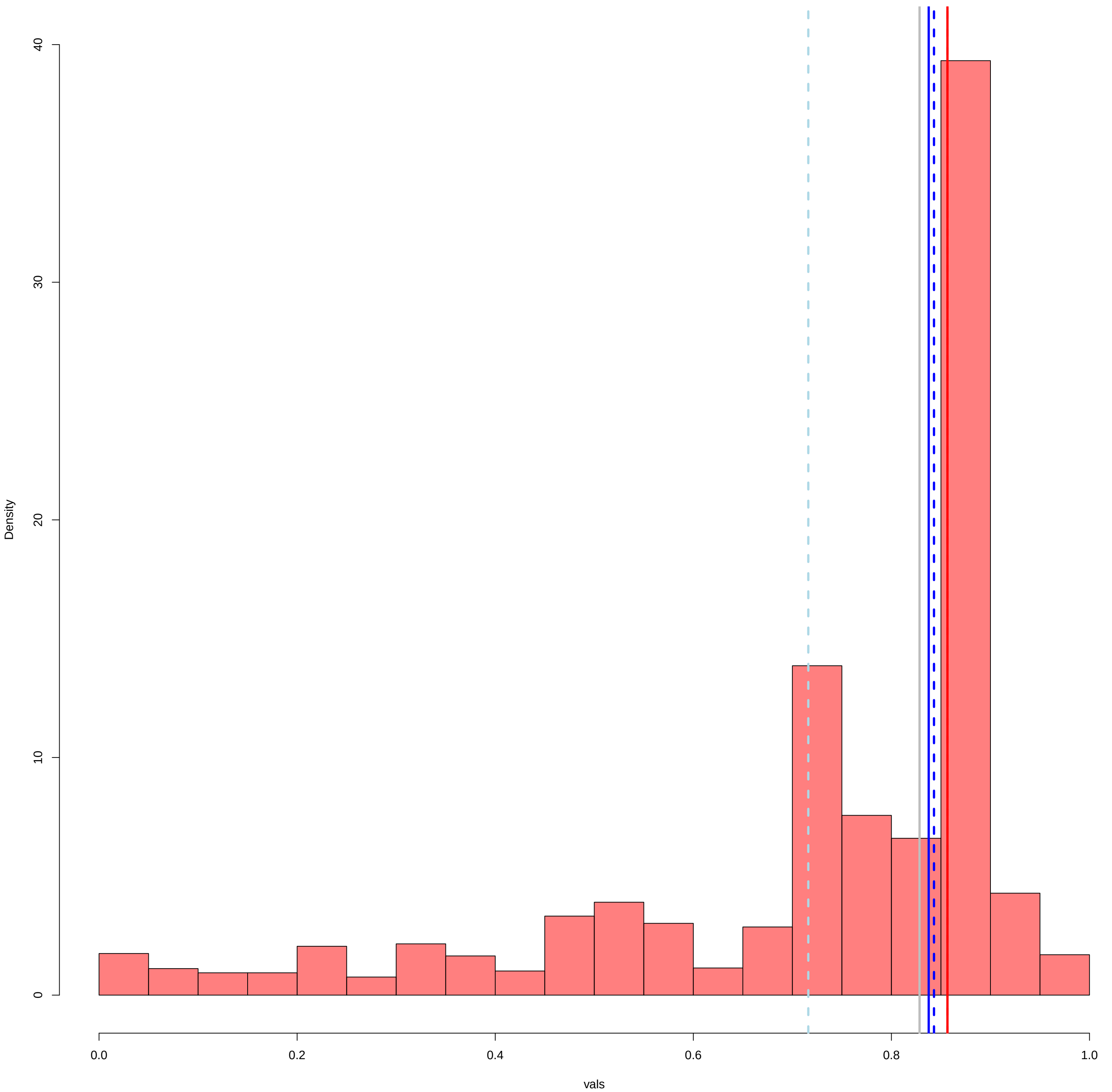
STXBP1: SIFT



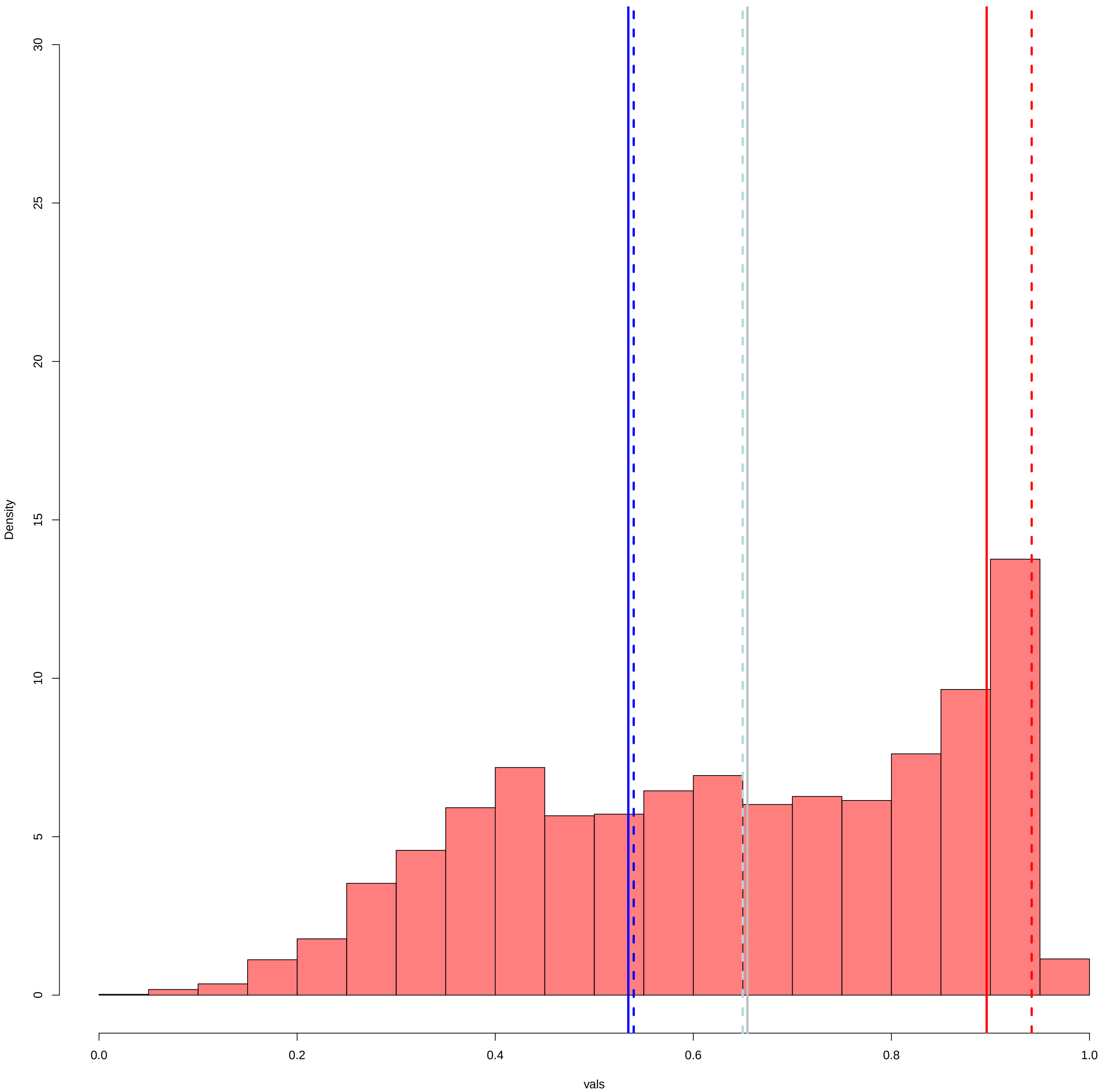
STXBP1: Condel



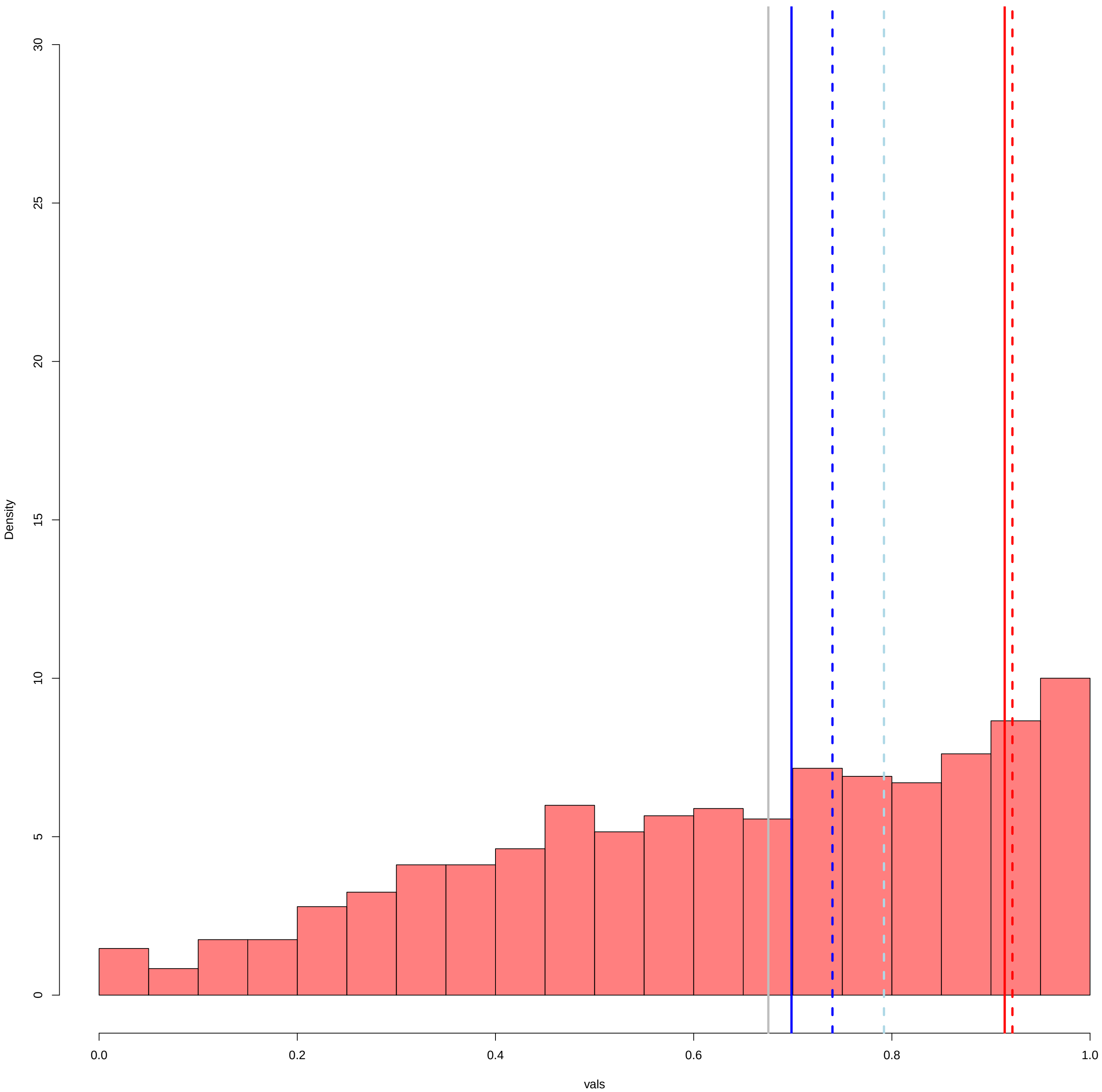
STXBP1: GERP++_RS_rankscore



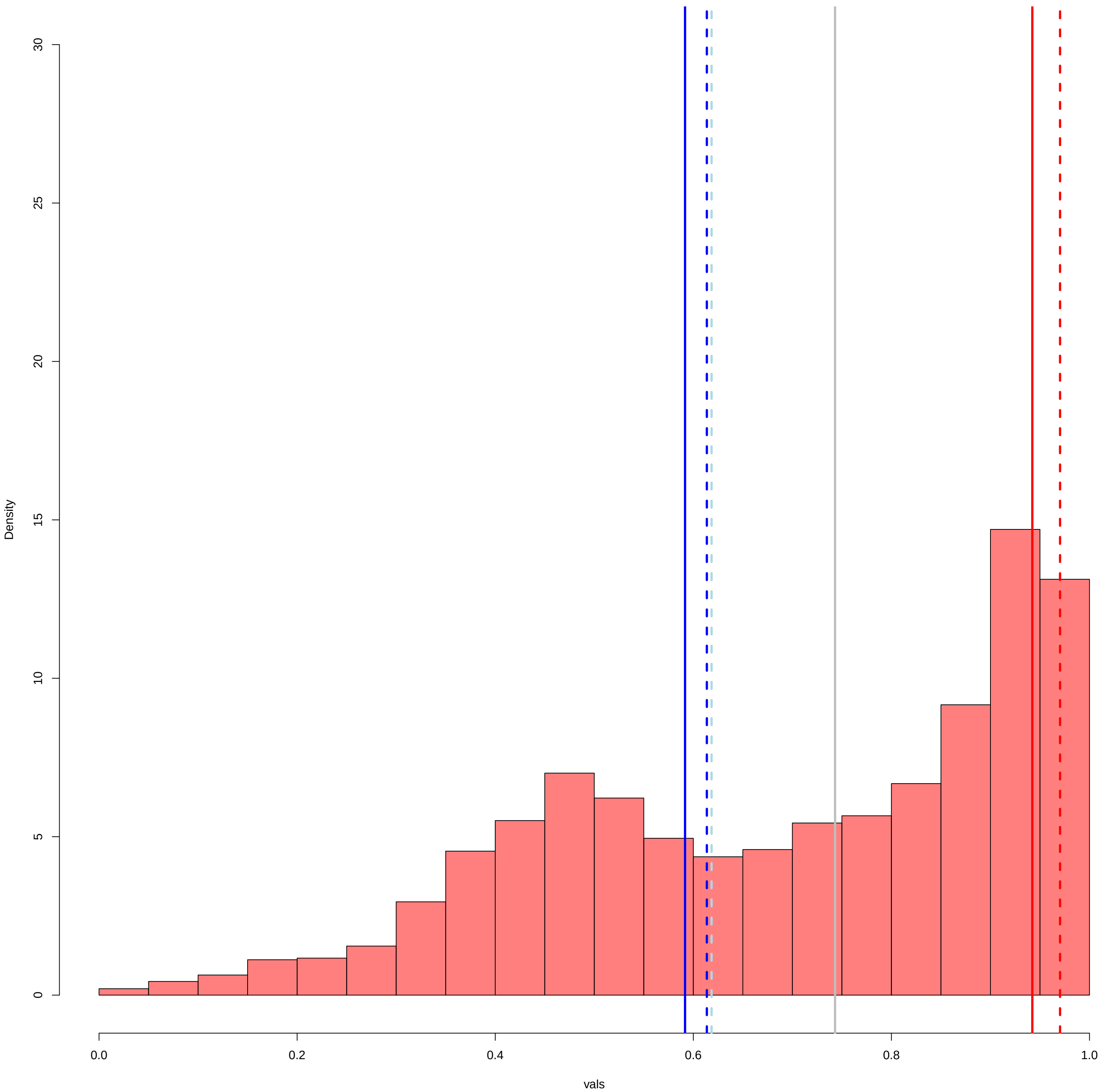
STXBP1: CADD_raw_rankscore



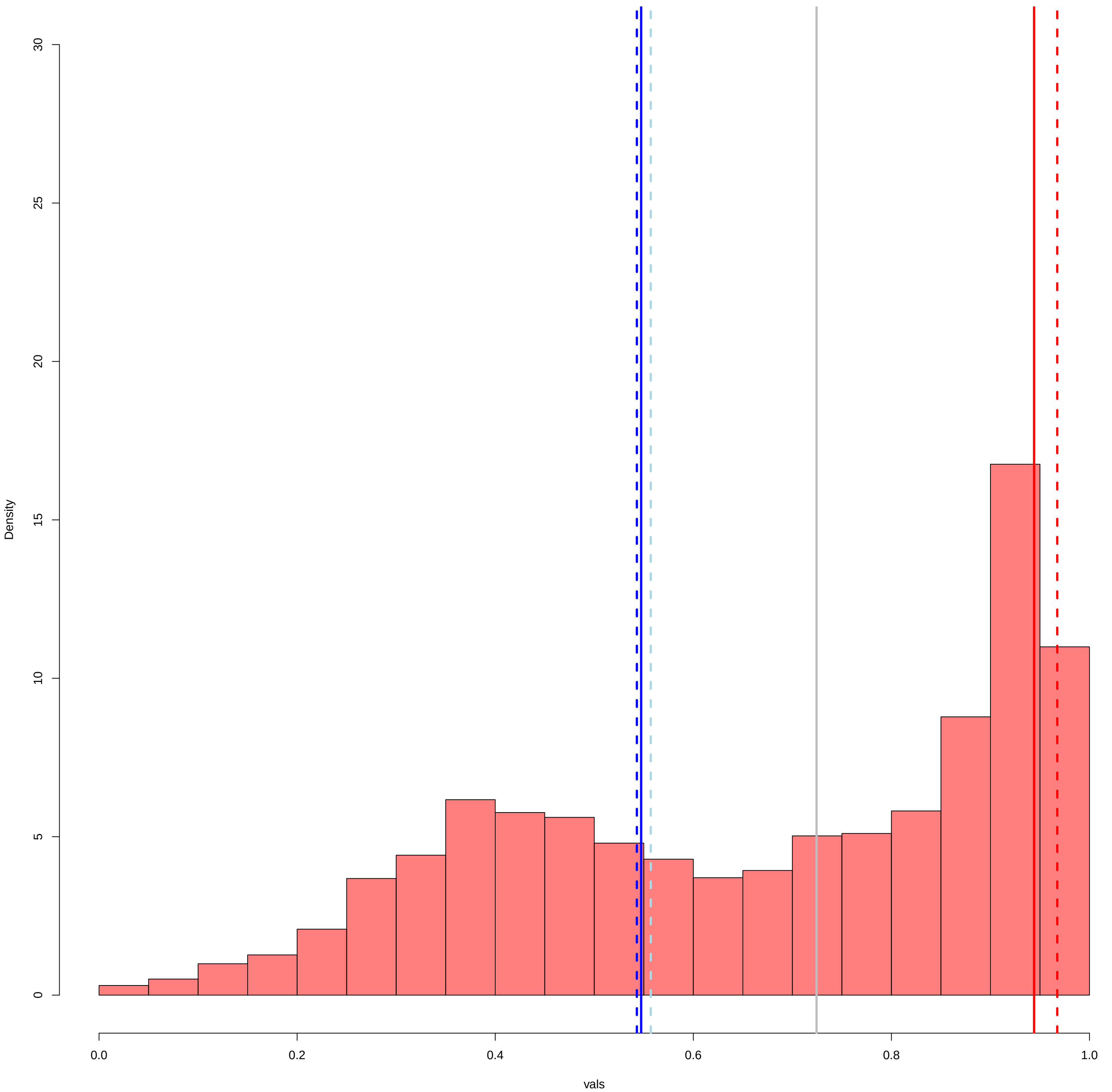
STXBP1: DANN_rankscore



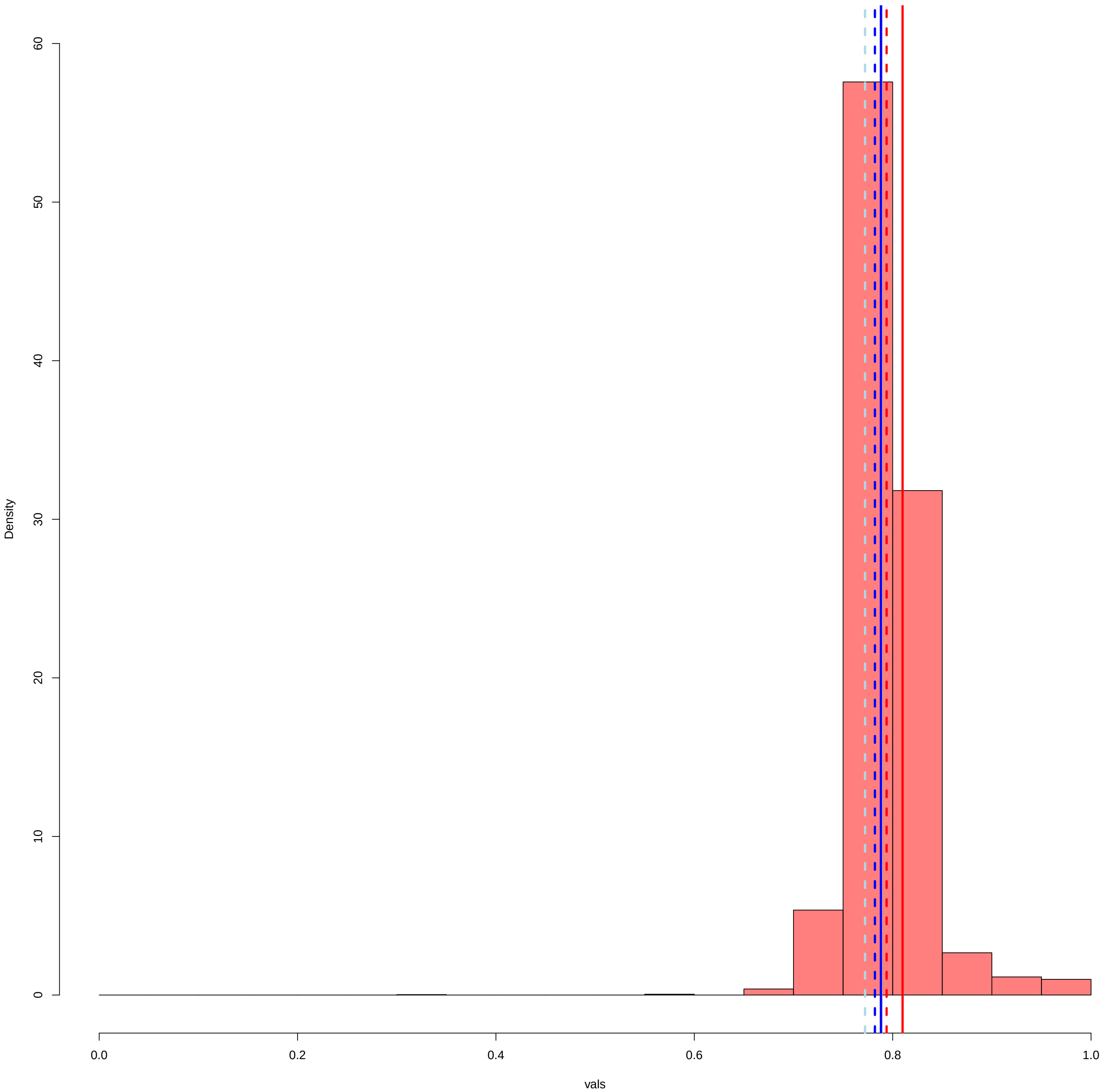
STXBP1: Eigen-PC-raw_rankscore



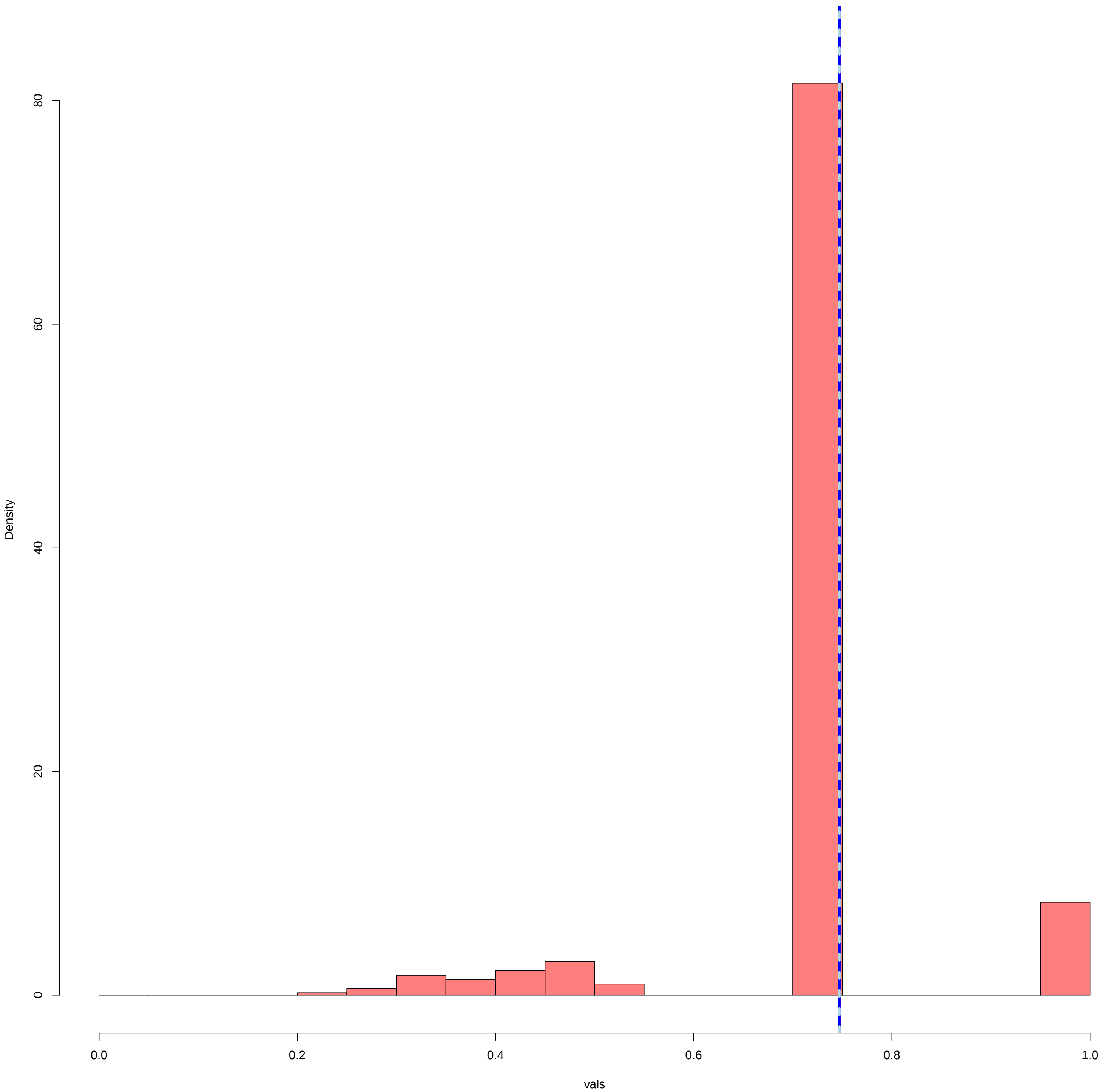
STXBP1: Eigen-raw_rankscore



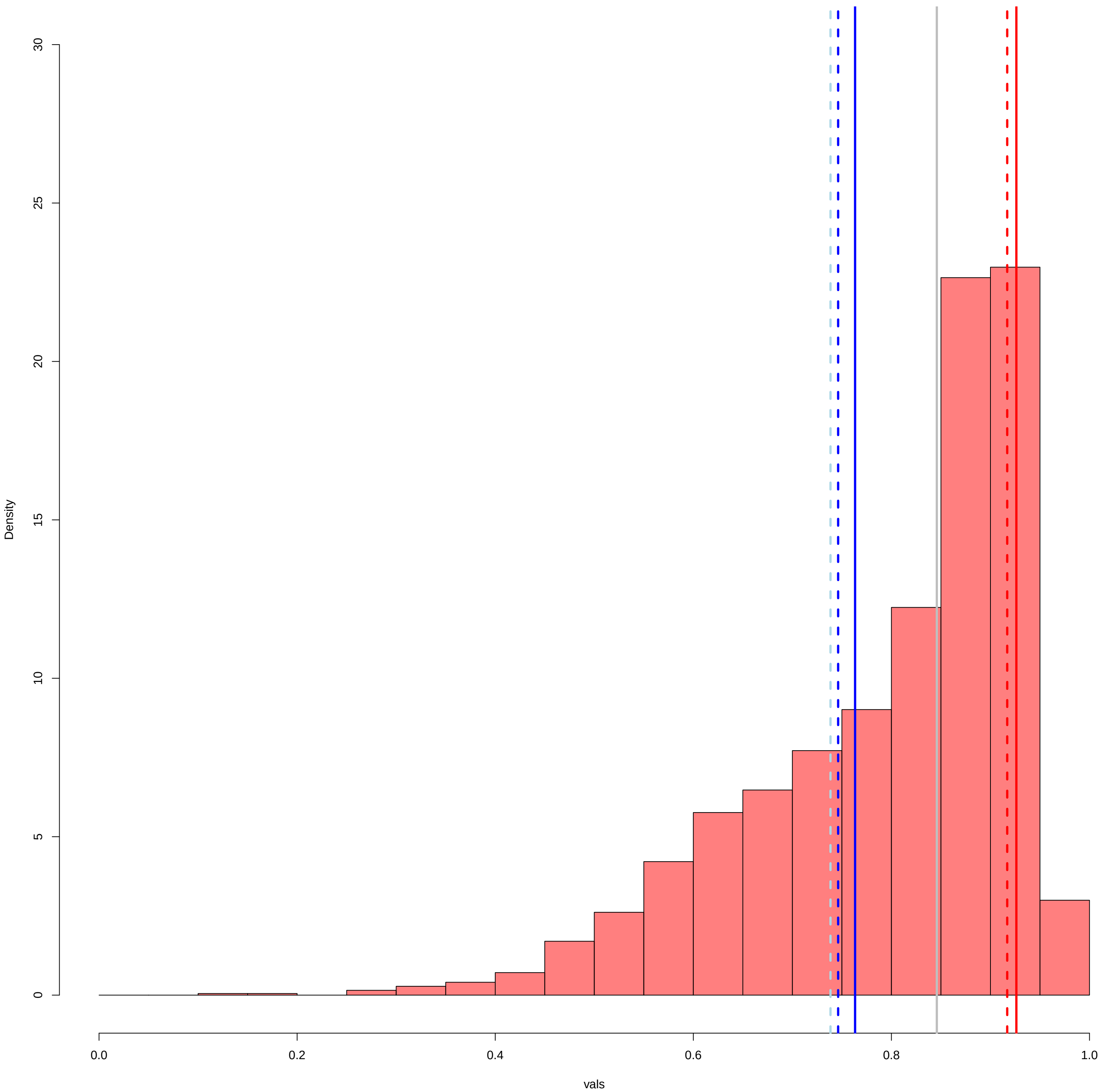
STXBP1: FATHMM_converted_rankscore



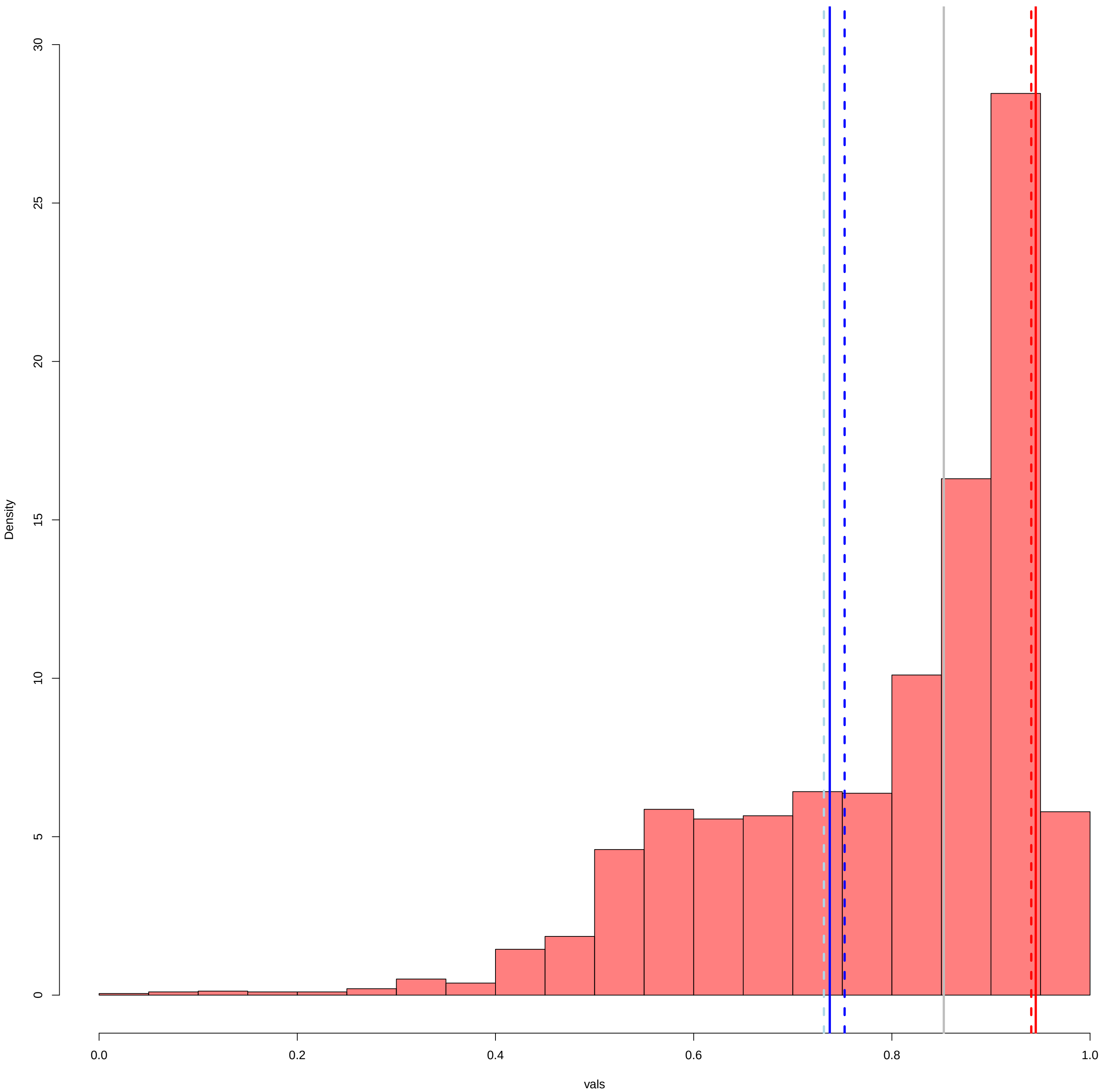
STXBP1: GenoCanyon_score_rankscore



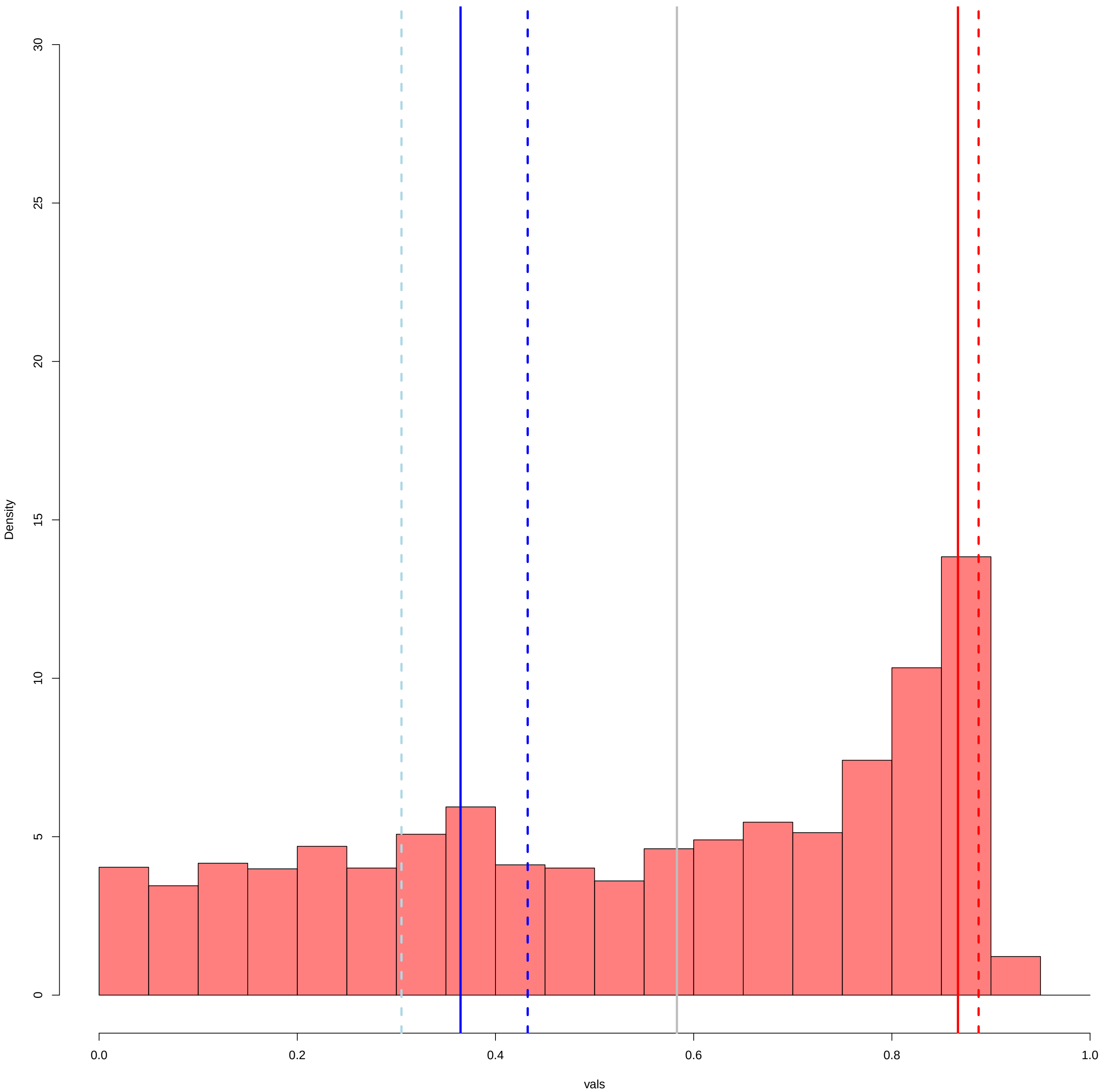
STXBP1: MetaLR_rankscore



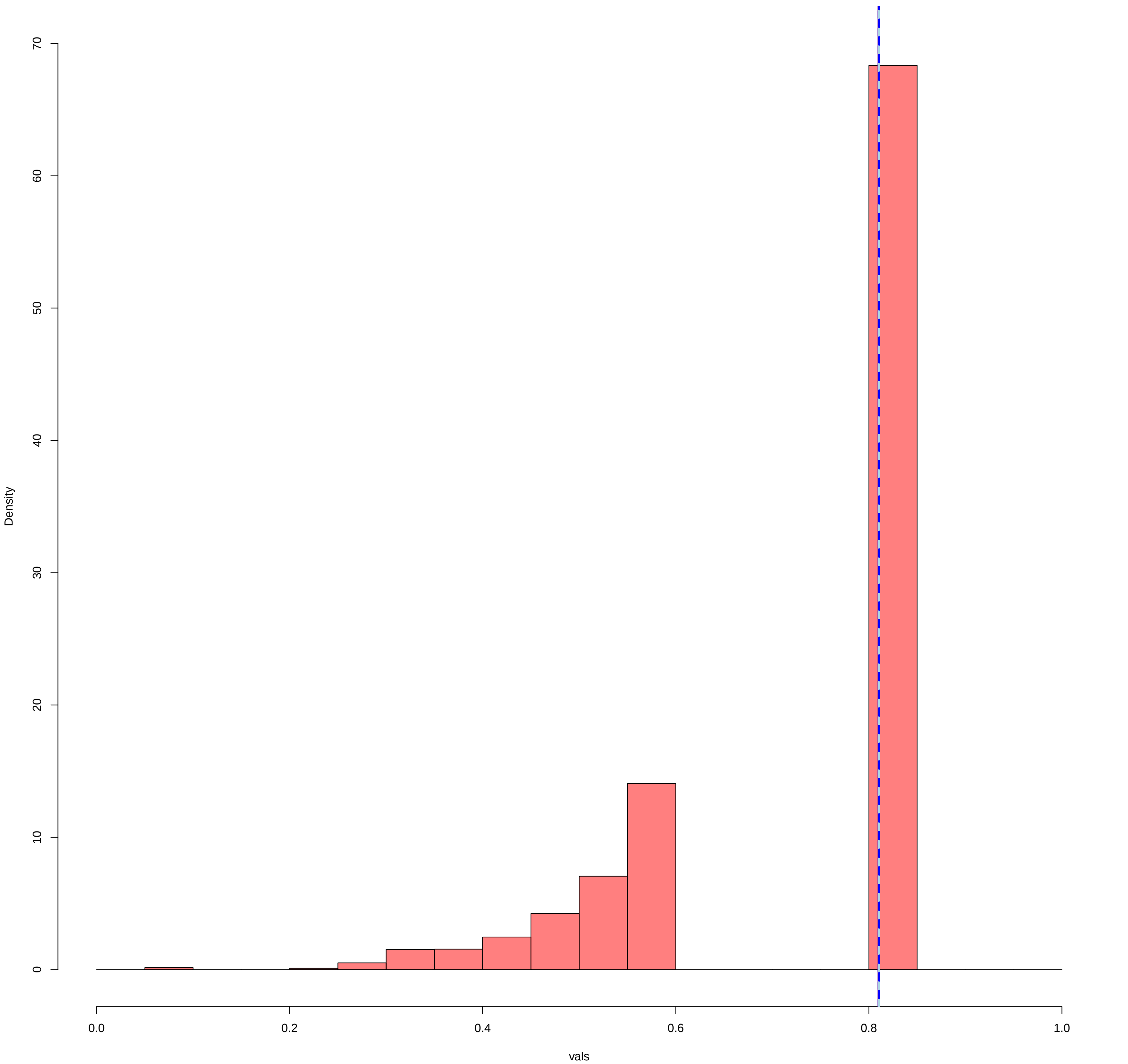
STXBP1: MetaSVM_rankscore



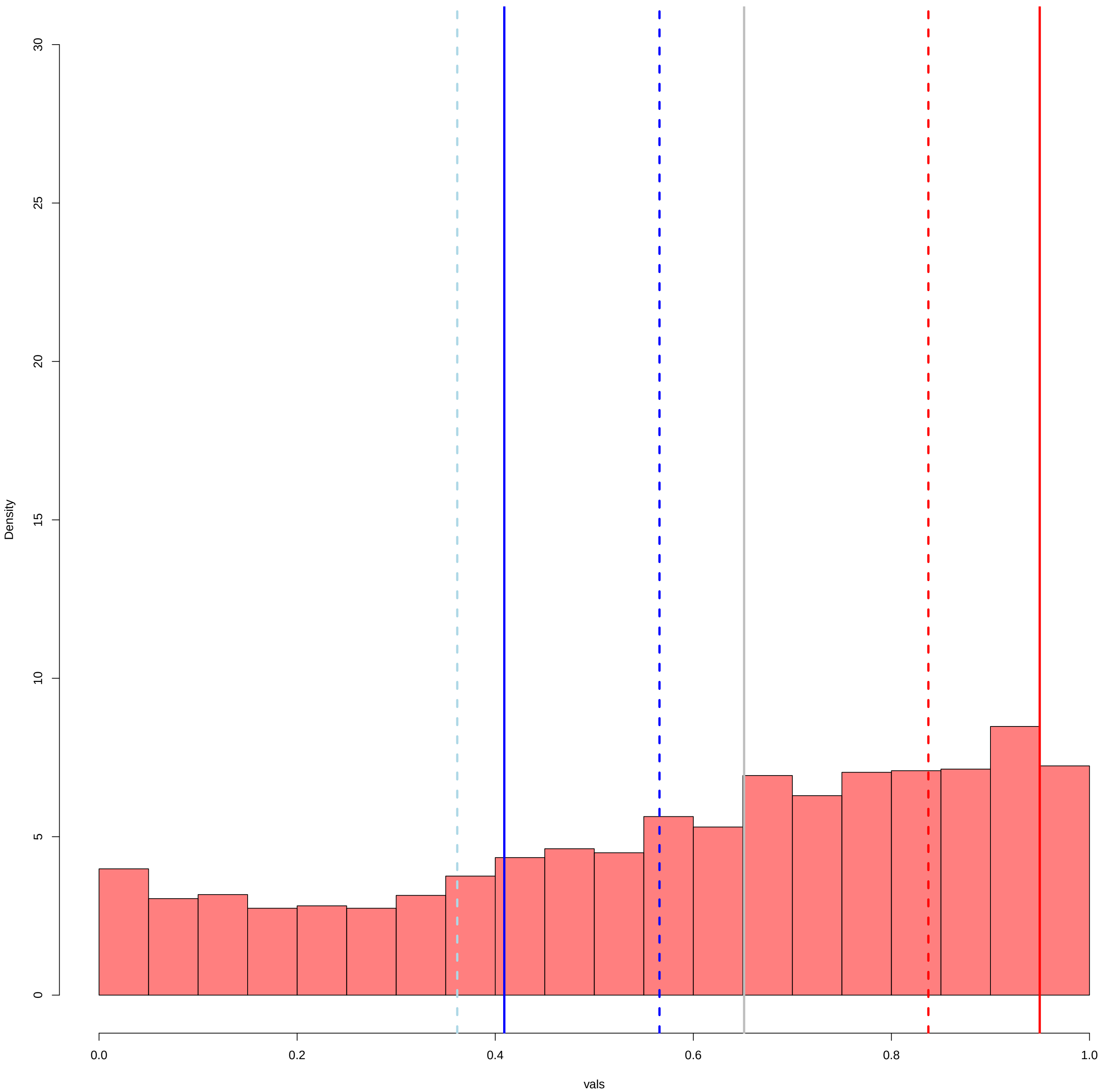
STXBP1: MutationAssessor_score_rankscore



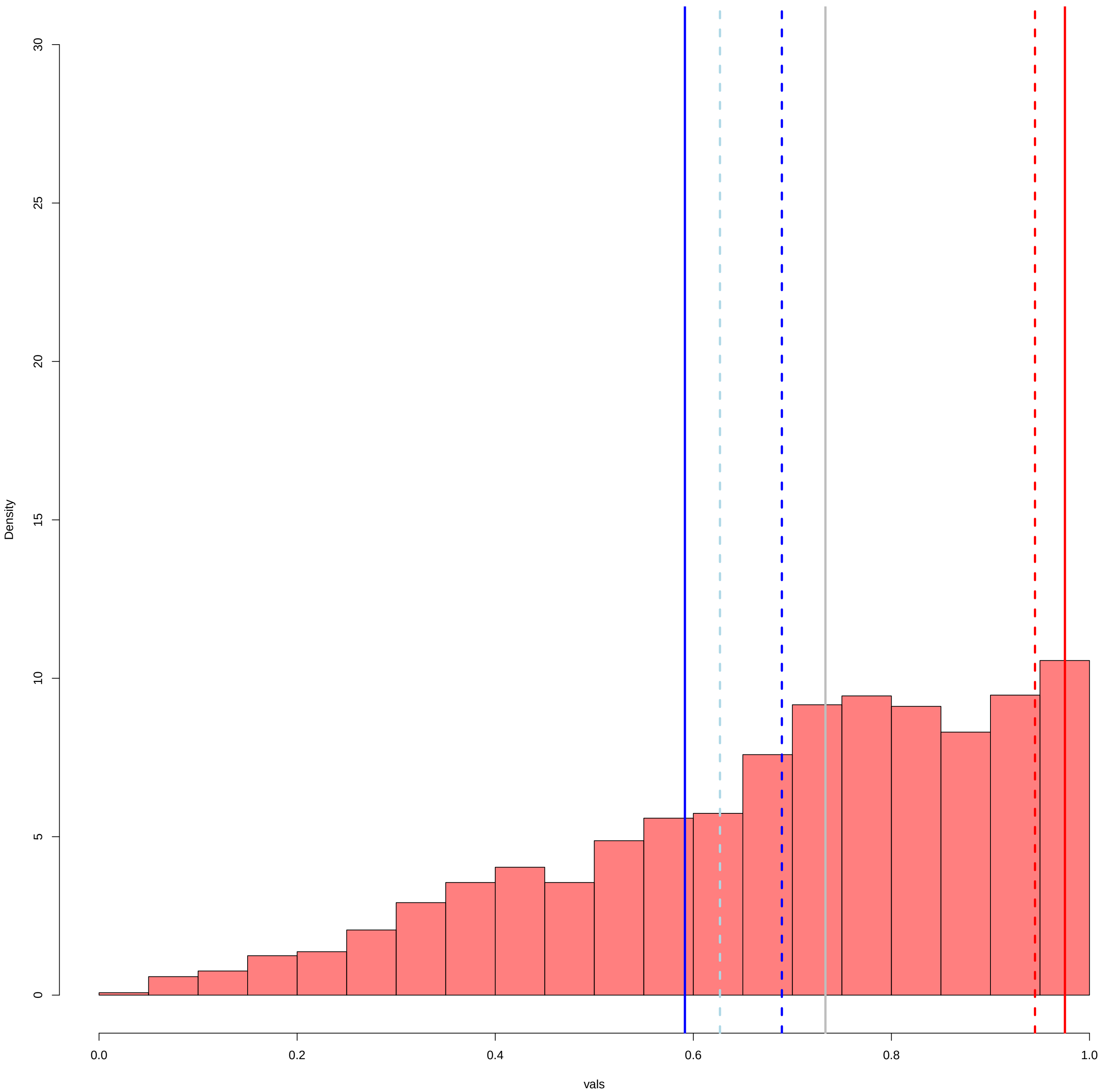
STXBP1: MutationTaster_converted_rankscore



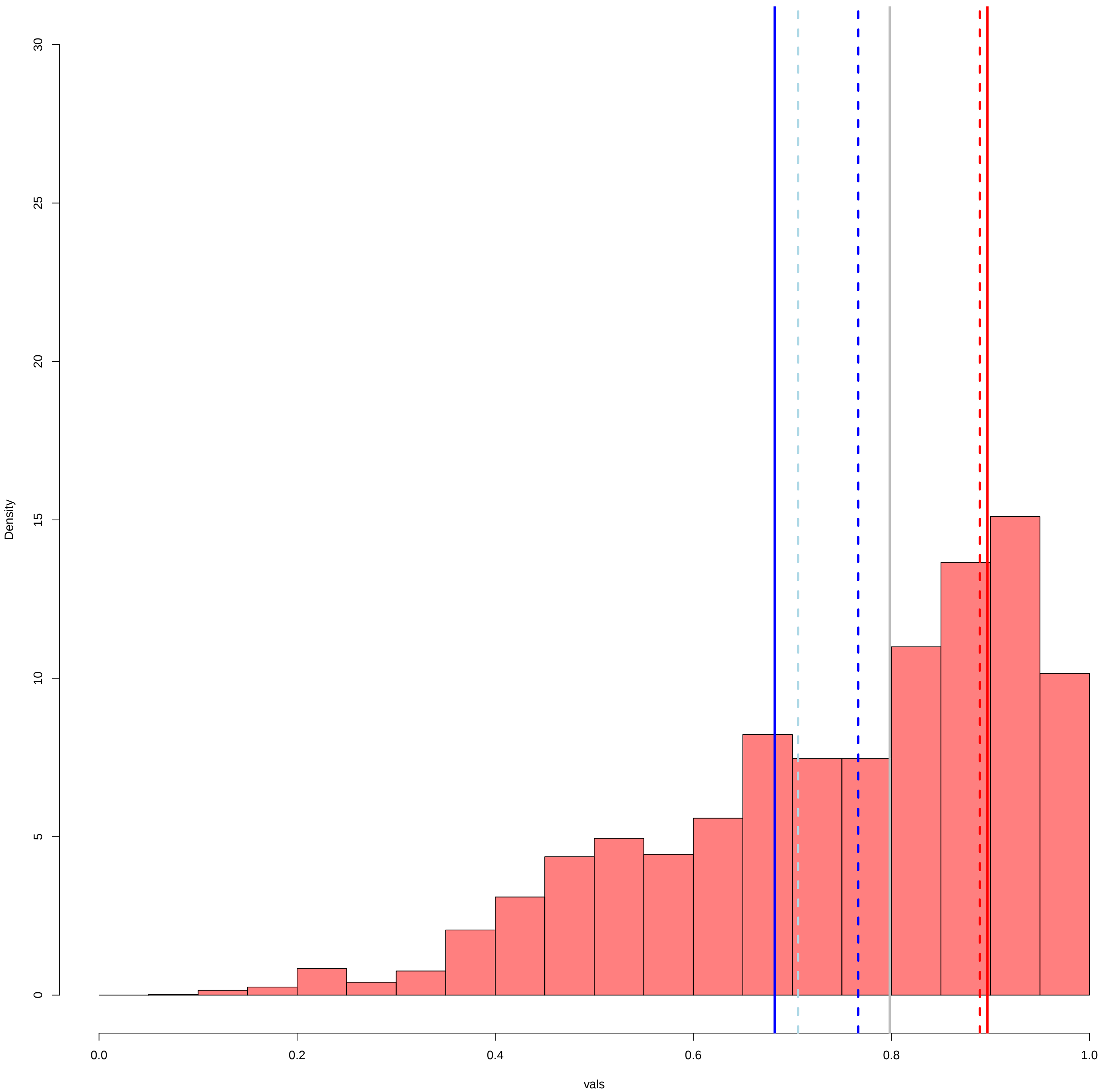
STXBP1: PROVEAN_converted_rankscore



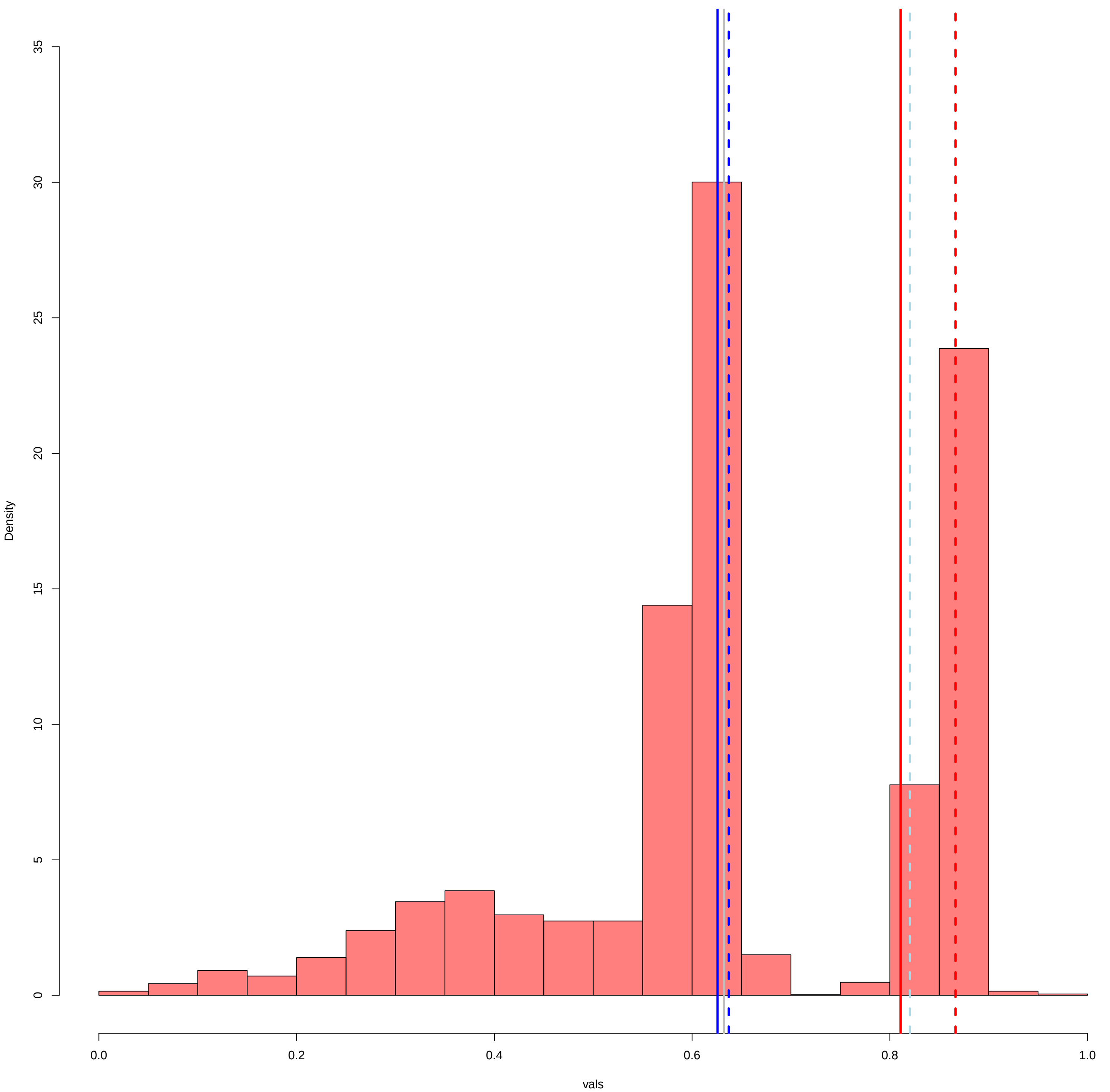
STXBP1: VEST3_rankscore



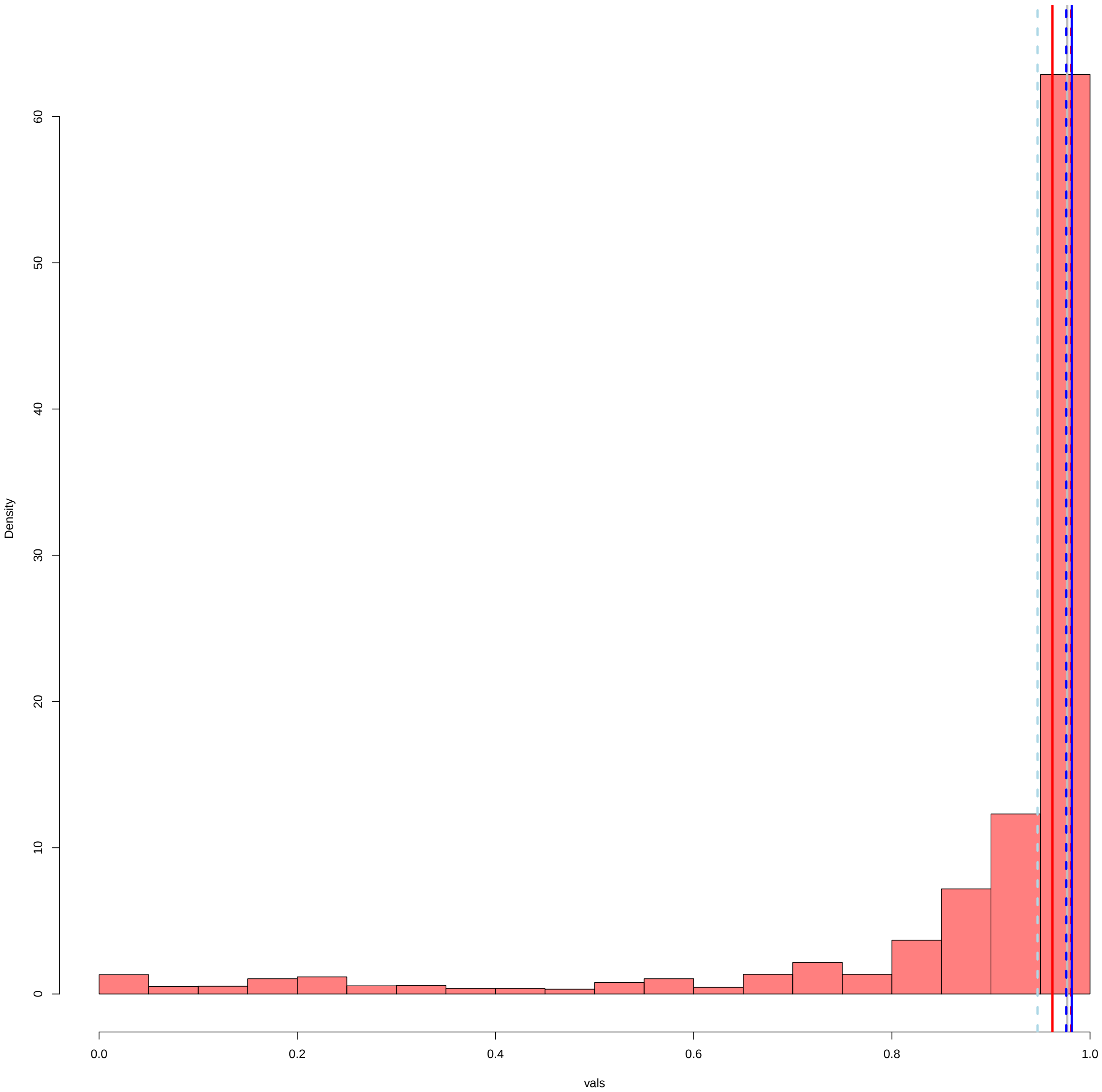
STXBP1: fathmm-MKL_coding_rankscore



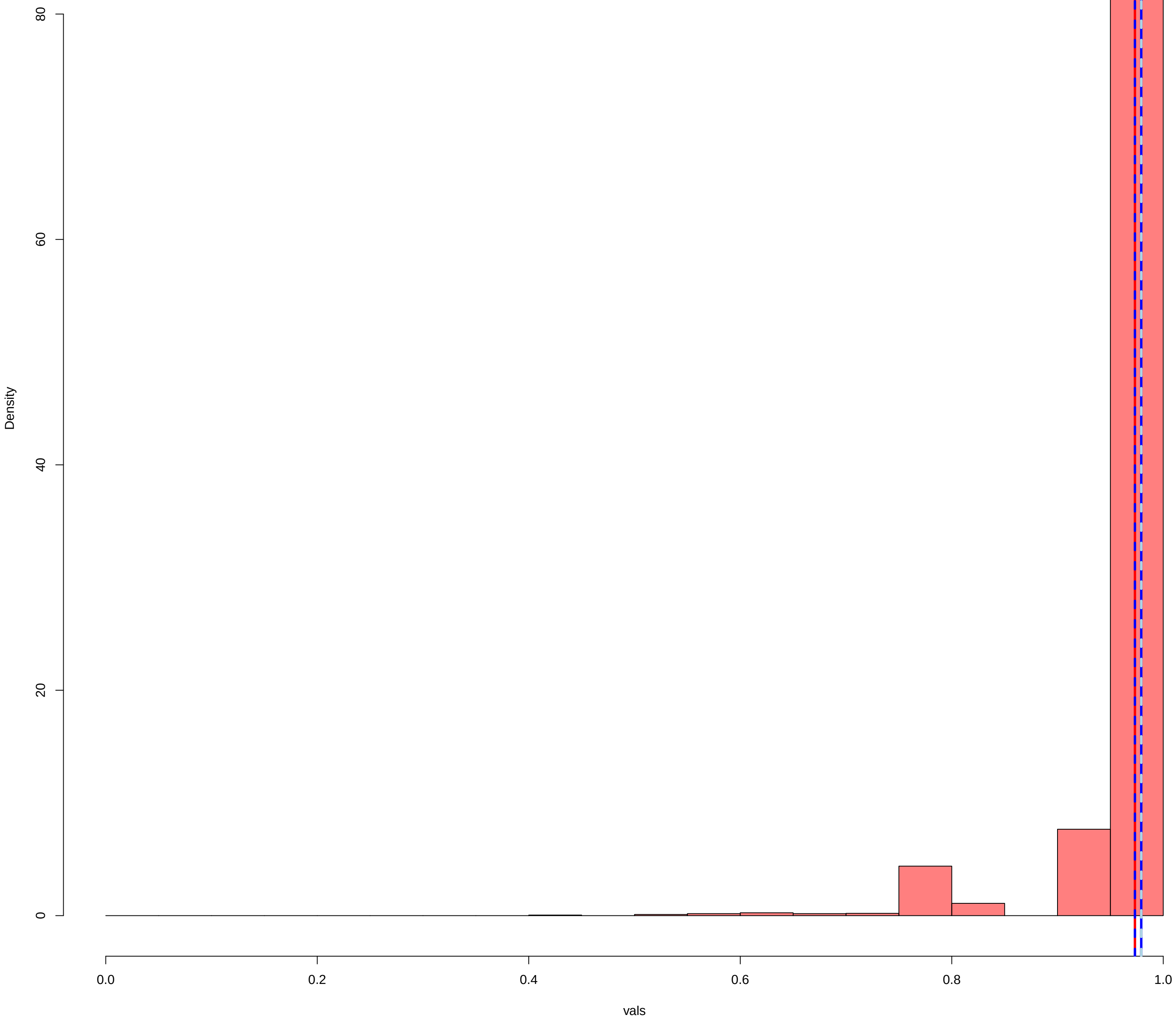
STXBP1: SiPhy_29way_logOdds_rankscore



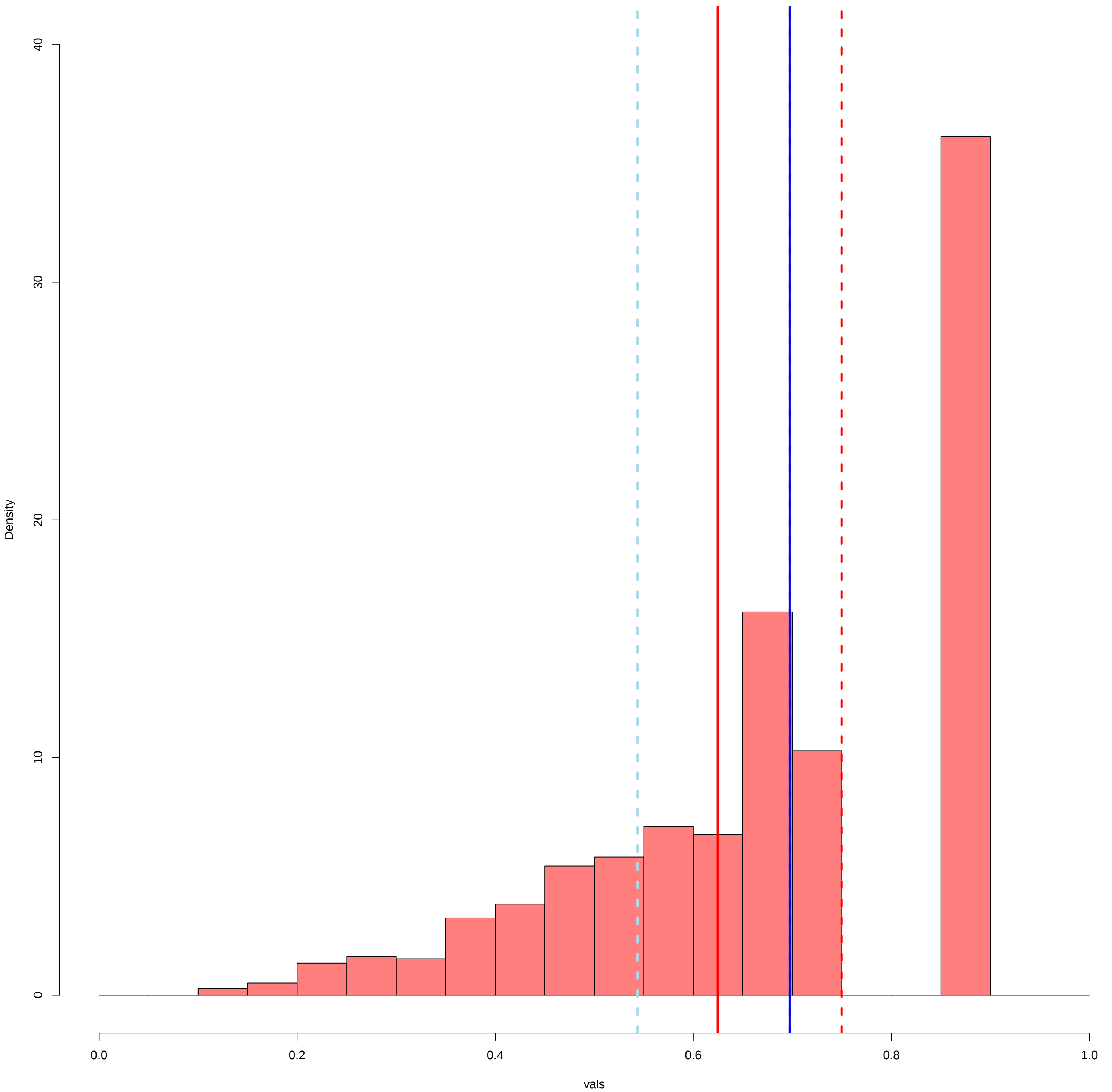
STXBP1: priPhCons



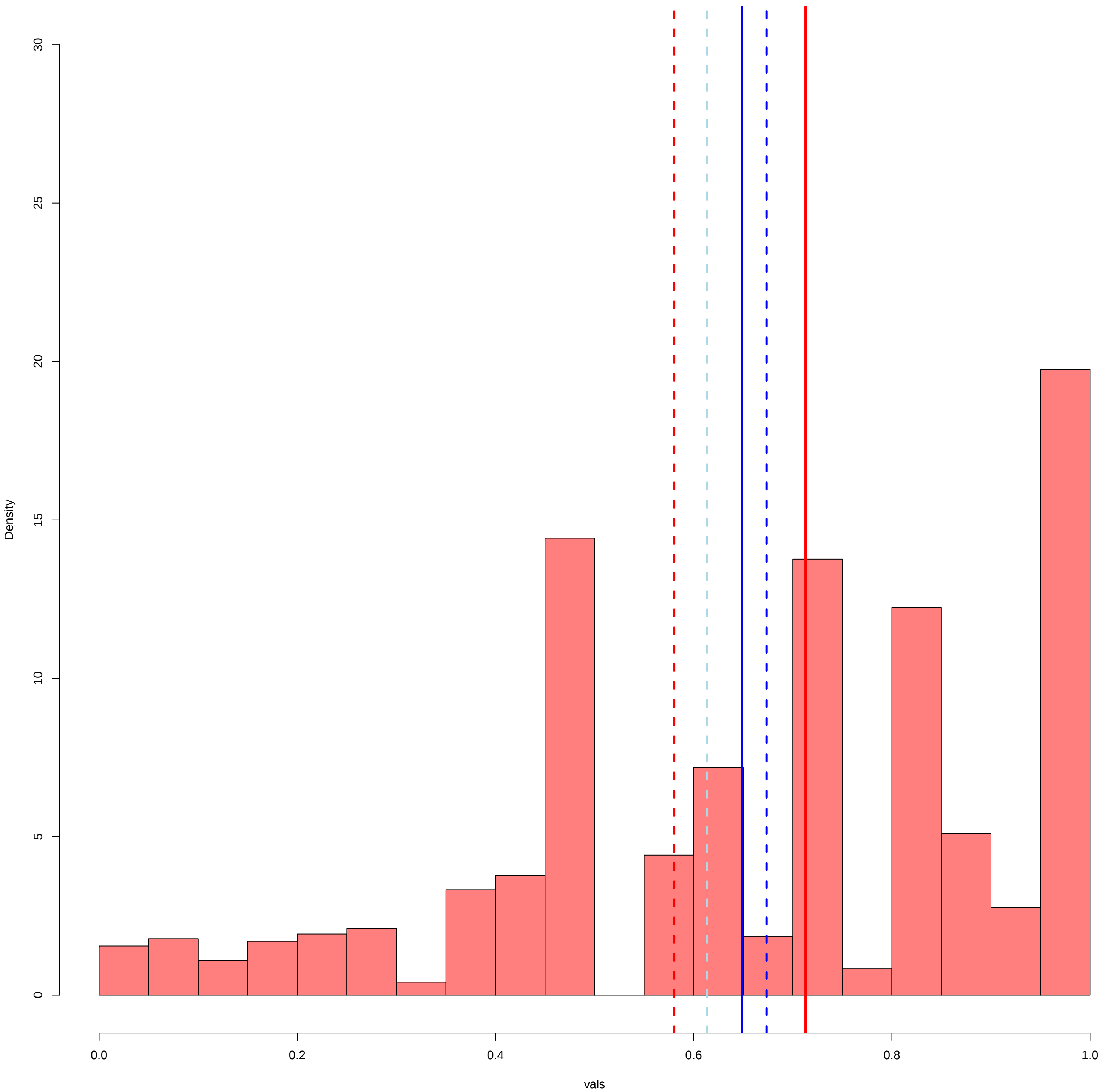
STXBP1: priPhyloP



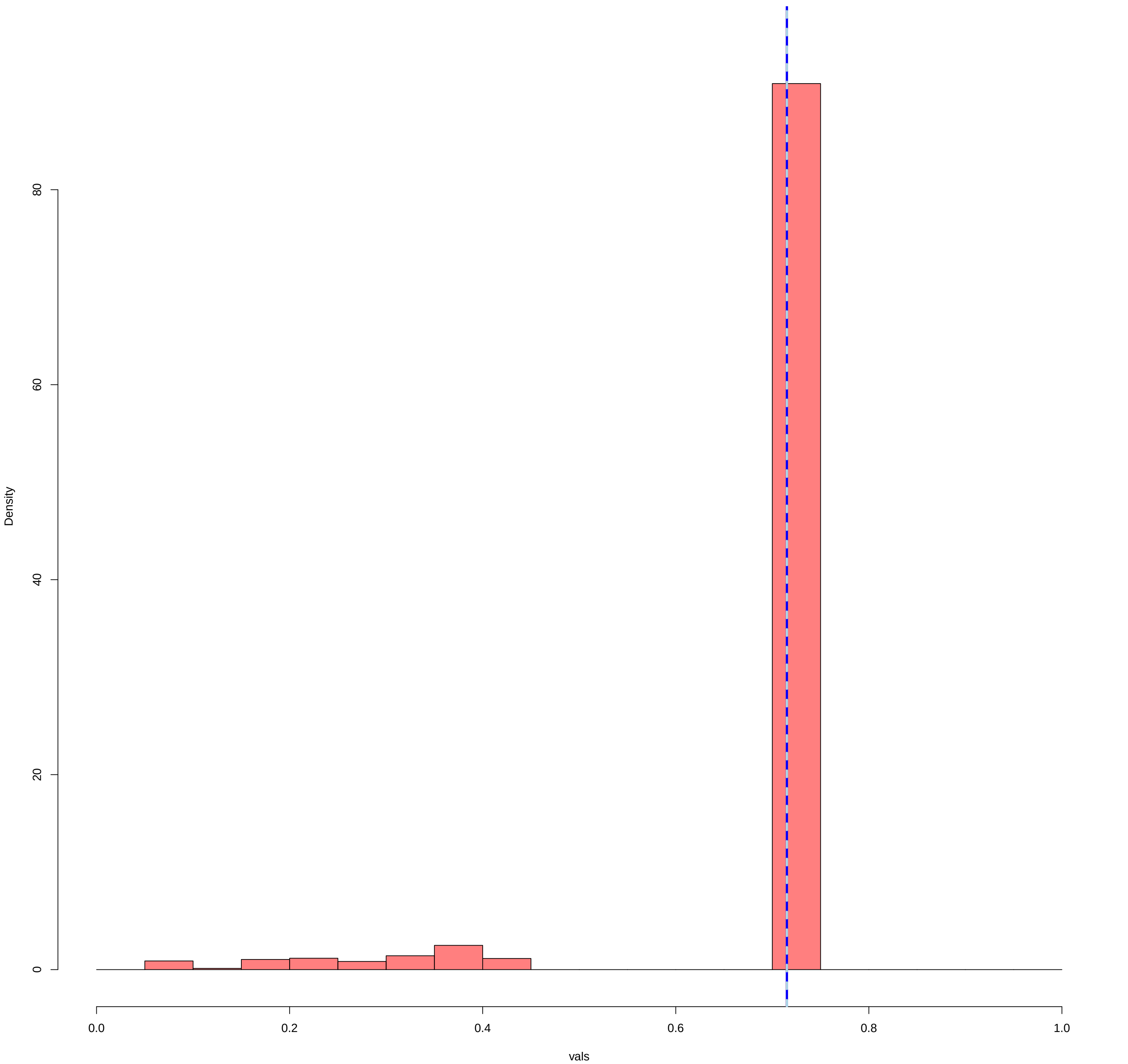
STXBP1: phastCons20way_mammalian_rankscore



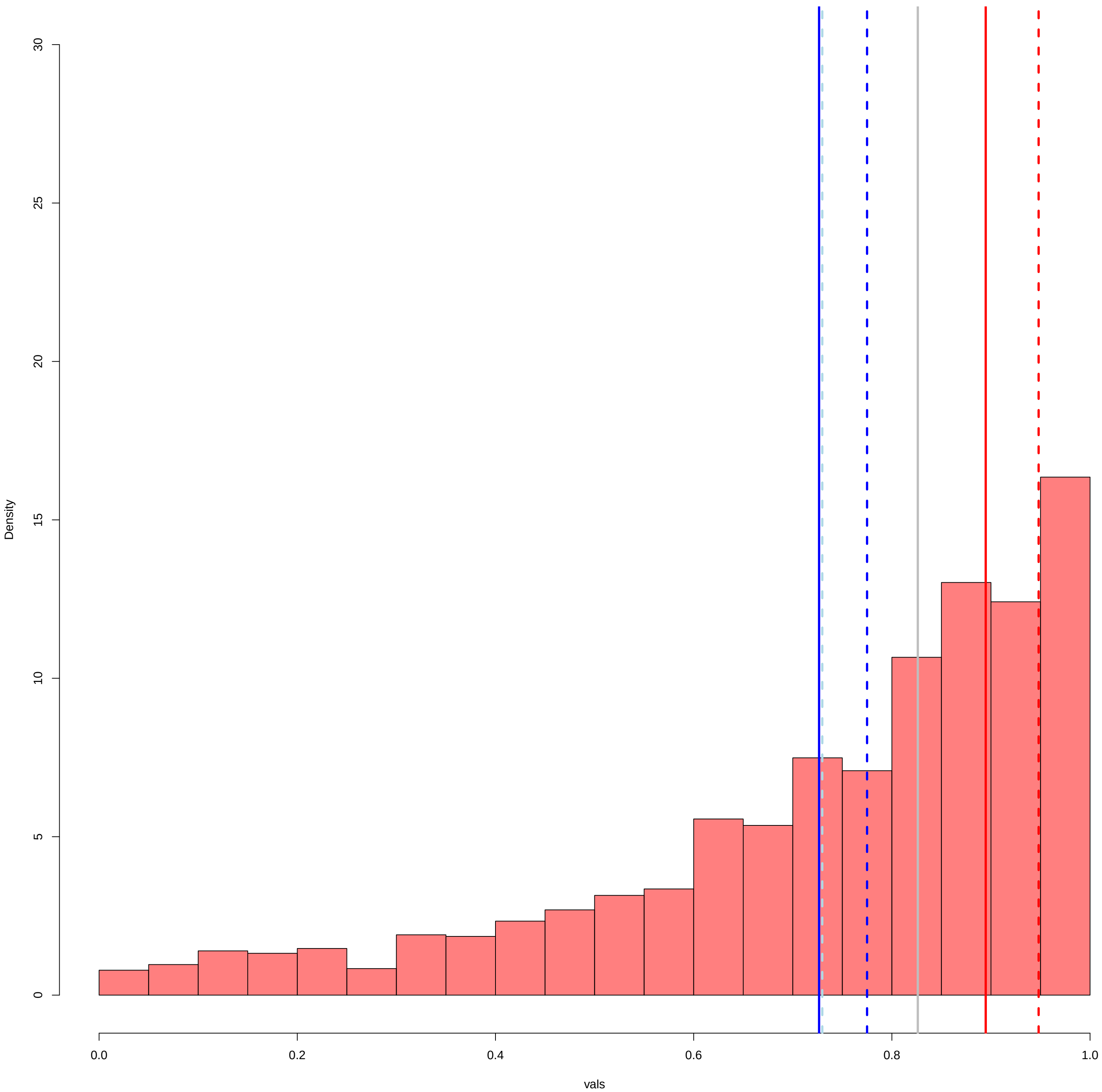
STXBP1: phyloP20way_mammalian_rankscore



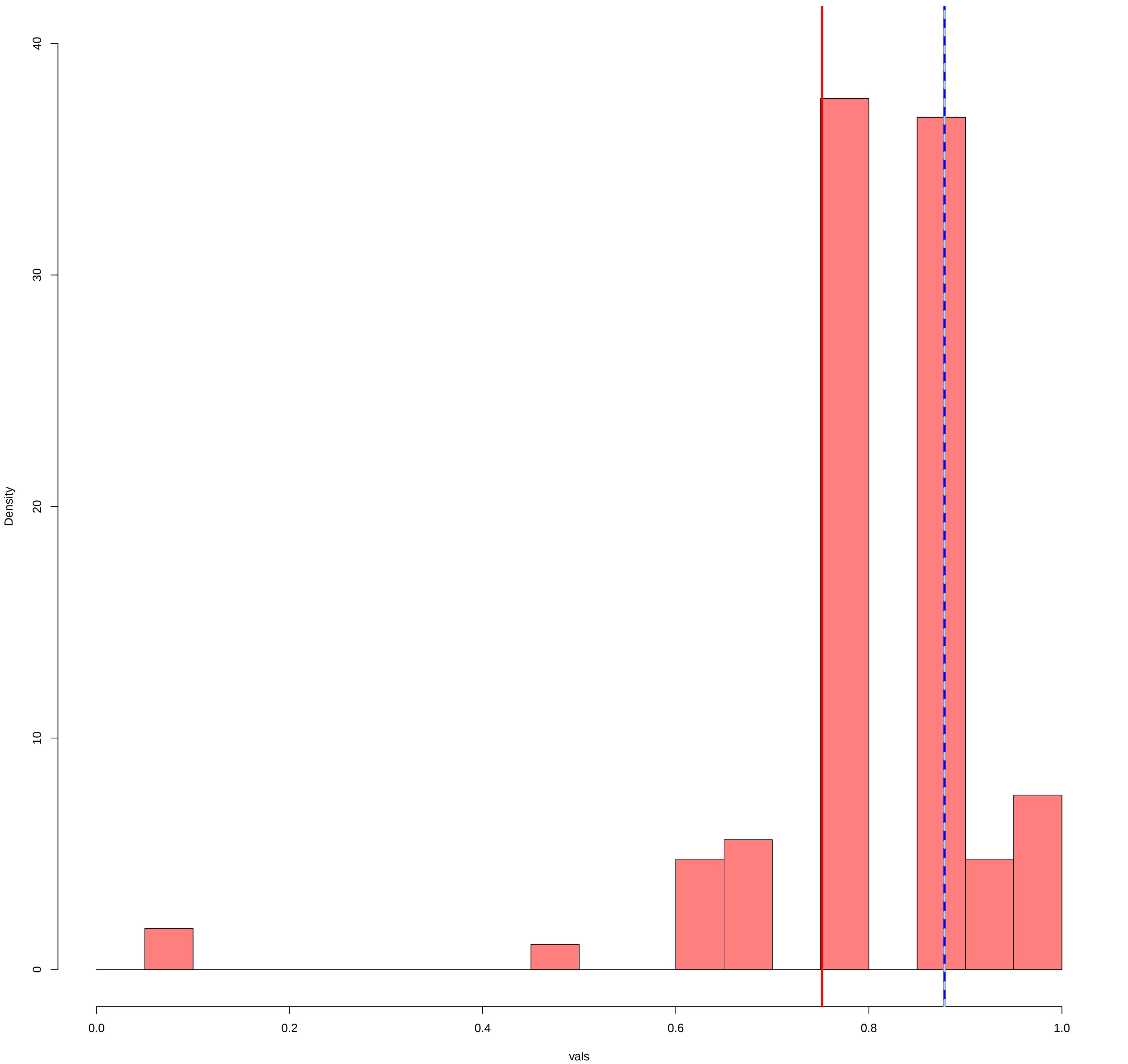
STXBP1: phastCons100way_vertebrate_rankscore



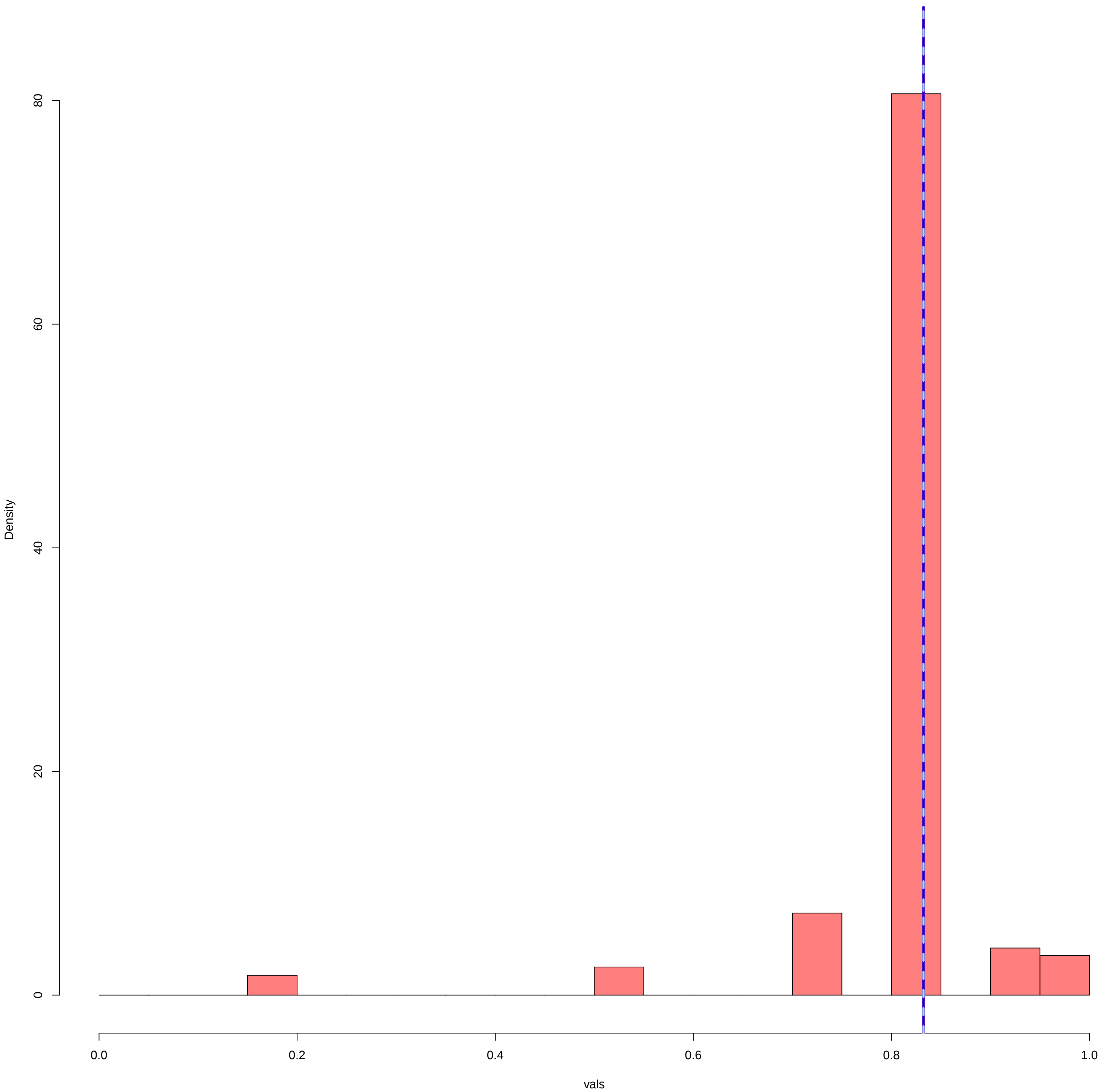
STXBP1: phyloP100way_vertebrate_rankscore



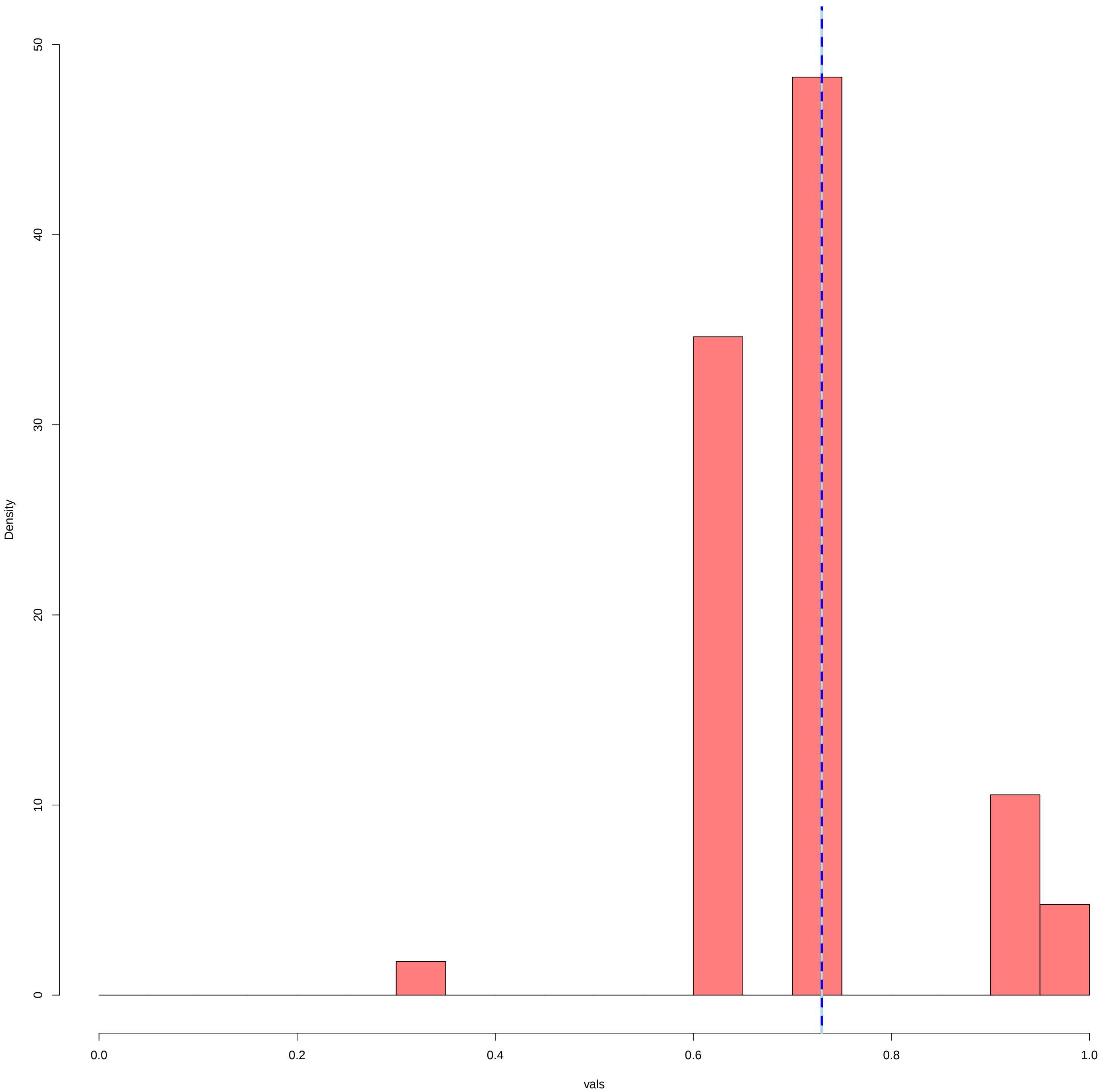
STXBP1: H1-hESC_fitCons_score_rankscore



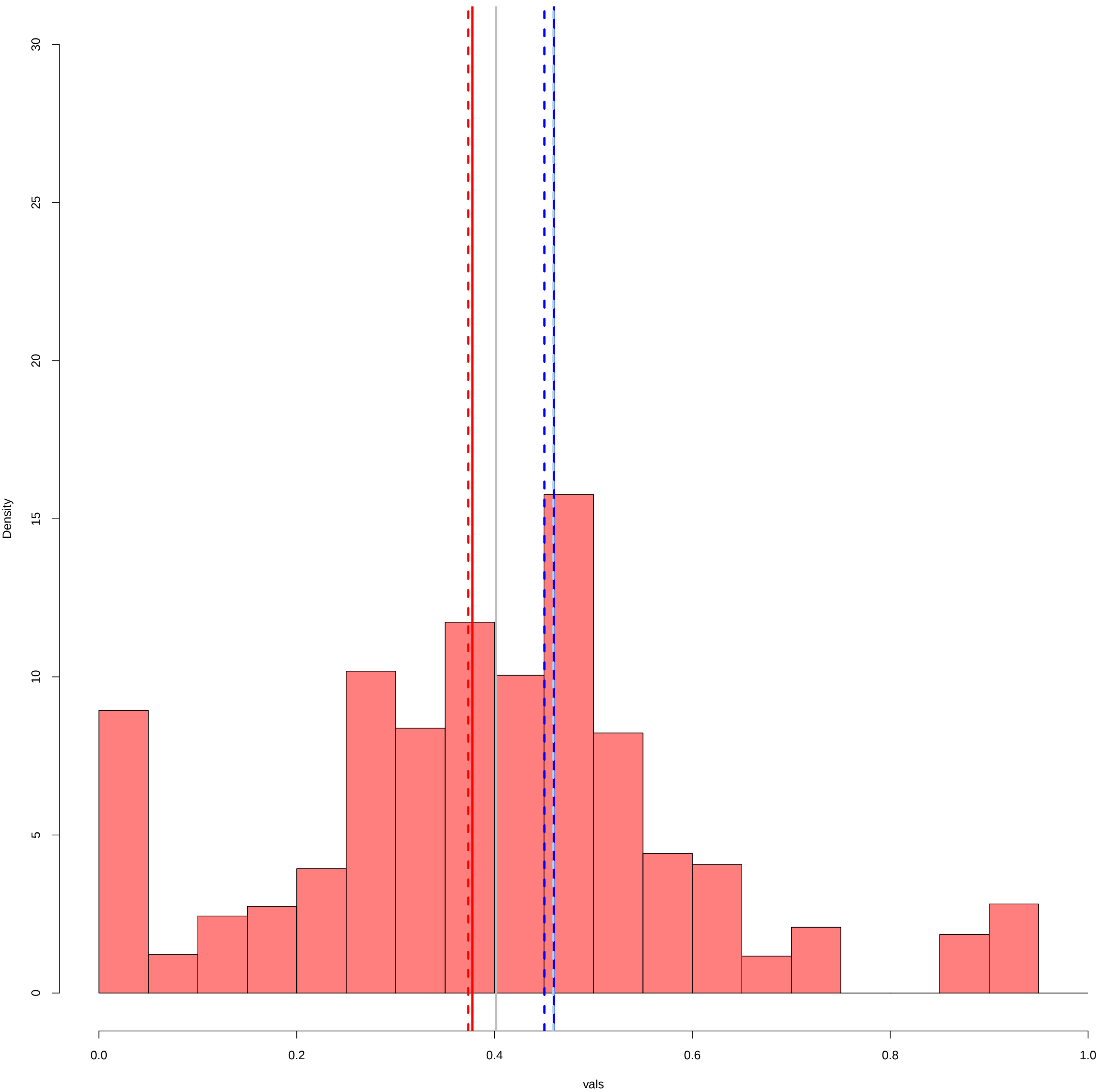
STXBP1: HUVEC_fitCons_score_rankscore



STXBP1: integrated_fitCons_score_rankscore



STXBP1: ExAC v1 MTR



STXBP1: ExAC v2 & gnomAD MTR

