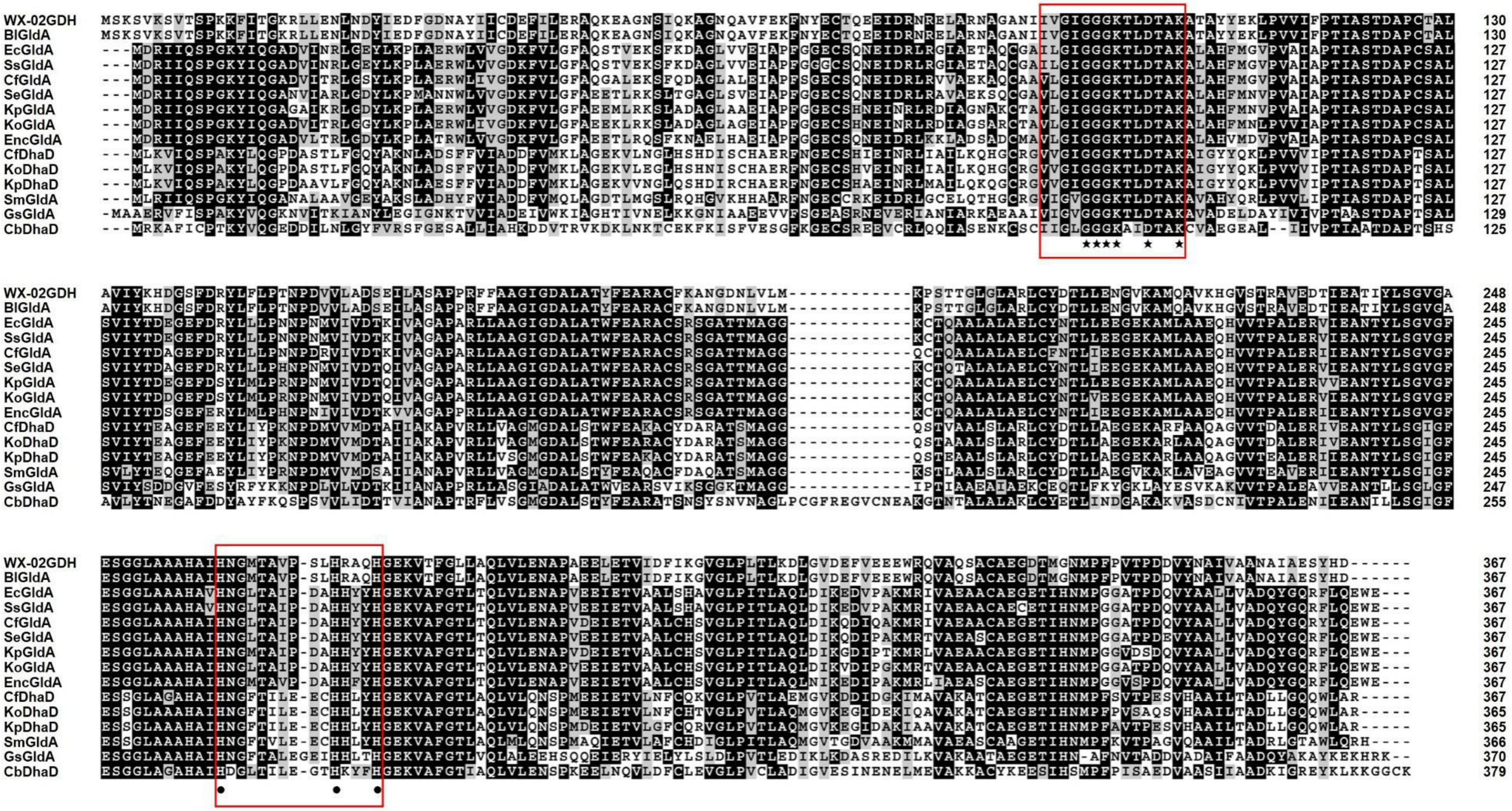

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BlGldA     MSKSVKSVTSPKKFITGKRLLENLNDYIEDFGDNAYIICDEFILERAQKEAGNSIQKAGNQAVFEKFNYECTQEEIDRNRELARNAGANIIVGIGGGKTLDTAKATAYYEKLPVVIFPTIASTDAPCTAL 130
EcGldA     ---MDRIIQSPGKYIQGADVINRLGEYLKPLAERWLVVGDKFVLGFAQSTVEKSFKDAGLVVEIAPFGGECSQNEIDRLRGIAETAQCGAILGIGGGKTLDTAKALAHFMGVPVAIAPTIASTDAPCSAL 127
SsGldA     ---MDRIIQSPGKYIQGADVINRLGEYLKPLAERWLVVGDKFVLGFAQSTVEKSFKDAGLVVEIAPFGGGCSQNEIDRLRGIAETAQCGAILGIGGGKTLDTAKALAHFMGVPVAIAPTIASTDAPCSAL 127
CfGldA     ---MDRIIQSPGKYIQGADVITRLGSYLKPLAERWLIVGDKFVLGFAQGALEKSFQDAGLALEIAPFSGECSQNEIDRLRVVAEKAQCAAVLGIGGGKTLDTAKALAHFMGVPVAIAPTIASTDAPCSAL 127
SeGldA     ---MDRIIQSPGKYIQGANVIARLGDYLKPMANNWLVVGDKFVLGFAEETLRKSLTGAGLSVEIAPFGGECSQNEIDRLRAVAEKSQCGAVLGIGGGKTLDTAKALAHFMNVPVAIAPTIASTDAPCSAL 127
KpGldA     ---MDRIIQSPGKYIQGAGAIKRLGDYLKPLAERWLVVGDKFVLGFAEEMLRKSLADAGLAAEIAPFGGECSHNEINRLRDIAGNAKCTAVLGIGGGKTLDTAKALAHFMNVPVAIAPTIASTDAPCSAL 127
KoGldA     ---MDRIIQSPGKYIQGADVITRLGGYLKPLAERWLIVGDKFVLGFAEEKLRKSLADAGLAGEIAPFGGECSHNEINRLRDIAGSARCTAVLGIGGGKTLDTAKALAHFMNLPVVIAPTIASTDAPCSAL 127
EncGldA    ---MDRIIQSPGKYIQGADVLTRLGDYLKPLATRWLVVGDKFVLGFAEETLRQSFKNAELHAEIAPFGGECSQNEIDRLKKLADSADCMAVLGIGGGKTLDTAKALAHVMDVPVAIAPTIASTDAPCSAL 127
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SmGldA     ---MLRIIQSPGKYIQGANALAAVGEYAKSLADHYFVIADDFVMQLAGDTLMGSLRQHGVKHHAARFNGECCRKEIDRLGCELQTHGCRGVIGVGGGKTLDTAKAVAHYQRLPVVLIPTIASTDAPTSAL 127
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CbDhaD     ---MRKAFICPTKYVQGEDDILNLGYFVRSFGESALLIAHKDDVTRVKDKLNKTCEKFKISFVESGFKGECSREEVCRLQQIASENKCSCIIGLGGGKAIDTAKCVAEGEAL--IIVPTIAATDAPTSHS 125
                                                                                                          ★★★★  ★  ★

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GsGldA     SVIYSDDGVFESYRFYKKNPDLVLVDTKIIANAPPRLLASGIADALATWVEARSVIKSGGKTMAGG------------IPTIAAEAIAEKCEQTLFKYGKLAYESVKAKVVTPALEAVVEANTLLSGLGF 247
CbDhaD     AVLYTNEGAFDDYAYFKQSPSVVLIDTTVIANAPTRFLVSGMGDALSTYFEARATSNSYSNVNAGLPCGFREGVCNEAKGTNTALALAKLCYETLINDGAKAKVASDCNIVTPALENIIEANILLSGIGF 255

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BlGldA     ESGGLAAAHAIHNGMTAVP-SLHRAQHGEKVTFGLLAQLVLENAPAEELETVIDFIKGVGLPLTLKDLGVDEFVEEEWRQVAQSACAEGDTMGNMPFPVTPDDVYNAIVAANAIAESYHD------ 367
EcGldA     ESGGLAAAHAVHNGLTAIP-DAHHYYHGEKVAFGTLTQLVLENAPVEEIETVAALSHAVGLPITLAQLDIKEDVPAKMRIVAEAACAEGETIHNMPGGATPDQVYAALLVADQYGQRFLQEWE--- 367
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CfGldA     ESGGLAAAHAIHNGLTAIP-DAHHYYHGEKVAFGTLTQLVLENAPVDEIETVAALCHSVGLPITLAQLDIKQDIQAKMRIVAEAACAEGETIHNMPGGATPDQVYAALLVADQYGQRYLQEWE--- 367
SeGldA     ESGGLAAAHAIHNGLTAIP-DAHHYYHGEKVAFGTLTQLVLENAPVEEIETVAALCHSVGLPITLAQLDIKQDIPAKMRTVAEASCAEGETIHNMPGGATPDEVYAALLVADQYGQRFLQEWE--- 367
KpGldA     ESGGLAAAHAIHNGMTAIP-DAHHYYHGEKVAFGTLTQLVLENAPVDEIETVAALCHSVGLPITLAQLDIKGDIPTKMRLVAEAACAEGETIHNMPGGVDSDQVYAALLVADQYGQRFLQEWE--- 367
KoGldA     ESGGLAAAHAIHNGLTAIP-DAHHYYHGEKVAFGTLTQLVLENAPVEEIETVAALCHSVGLPITLAQLDIKVDIPGKMRTVAEAACAEGETIHNMPGGATPDQVYAALLVADQYGQRFLQEWE--- 367
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CfDhaD     ESSGLAGAHAIHNGFTILE-ECHHLYHGEKVAFGTLAQLVLQNSPMEEIETVLNFCQKVGLPVTLAEMGVKDDIDGKIMAVAKATCAEGETIHNMPFSVTPESVHAAILTADLLGQQWLAR----- 367
KoDhaD     ESSGLAAAHAIHNGFTILE-ECHHLYHGEKVAFGTLAQLVLQNSPMEEIETVLNFCHTVGLPVTLAQMGVKEGIDEKIQAVAKATCAEGETIHNMPFPVSAQSVHAAILTADLLGQQWLAR----- 365
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SmGldA     ESSGLAAAHAIHNGFTVLE-ECHHLYHGEKVAFGTLAQLMLQNSPMAQIETVLAFCHDIGLPITLAQMGVTGDVAAKMMAVAEASCAAGETIHNMPFKVTPAGVQAAILTADRLGTAWLQRH---- 366
GsGldA     ESGGLAAAHAIHNGFTALEGEIHHLTHGEKVAFGTLVQLALEEHSQQEIERYIELYLSLDLPVTLEDIKLKDASREDILKVAKAATAEGETIHN-AFNVTADDVADAIFAADQYAKAYKEKHRK-- 370
CbDhaD     ESGGLAGAHAIHDGLTILE-GTHKYFHGEKVAFGTIAQLVLENSPKEELNQVLDFCLEVGLPVCLADIGVESINENELMEVAKKACYKEESIHSMPFPISAEDVAASIIAADKIGREYKLKKGGCK 379
                      •          •   •
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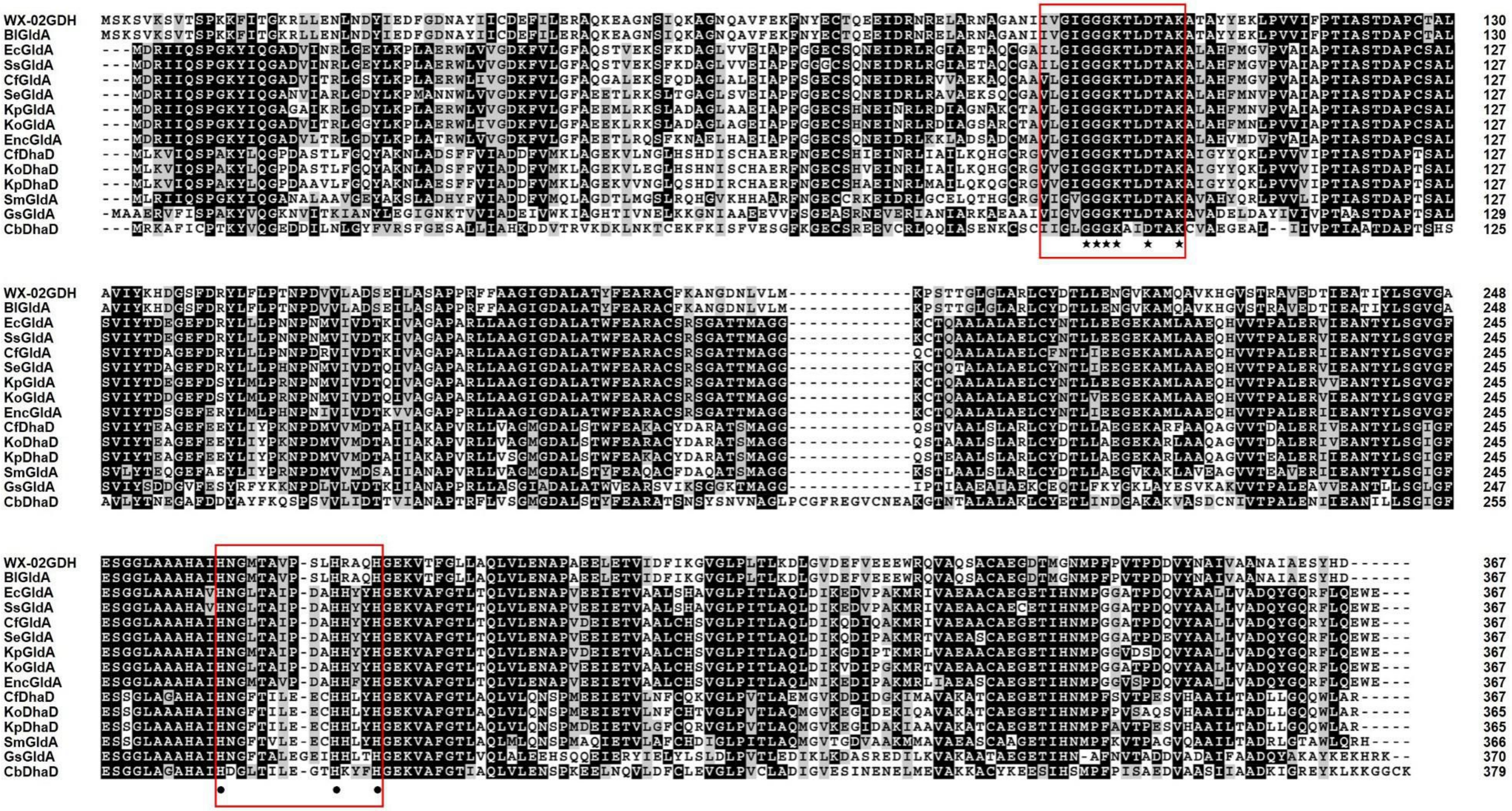

Figure S1. Multiple sequence alignments of GDH from *B. licheniformis* WX-02 (WX-02 GDH) with GDHs from other strains [*B. licheniformis* 10-1-A (BlGldA, AHW84748.1), *Escherichia coli* (EcGldA, P0A9S6), *Shigella sonnei* (SsGldA, YP_005459262.1), *Citrobacter freundii* (CfGldA, WP_003847842.1), *Salmonella enterica* (SeGldA, YP_006888481.1), *Klebsiella pneumoniae* 280_1220 (KpGldA, EPP12735.1), *Klebsiella oxytoca* (KoGldA, YP_005017437.1), *Enterobacter cloacae* (EncGldA, AFM62175), *Citrobacter freundii* (CfDhaD, P45511.1), *Klebsiella oxytoca* (KoDhaD, YP_005016612), *Klebsiella pneumoniae* CGMCC1.6366 (KpDhaD, KJ206474.1), *Serratia marcescens* H30 (SmGldA) [1], *Geobacillus stearothermophilus* (GsGldA, P32816), *Clostridium butyricum* (CbDhaD, AAN17729)]. The boxes indicate the putative coenzyme binding motif proposed as the signature of the iron-dependent ADH, and the box below indicates the residues involved in metal binding. The location of the conserved residues corresponding to coenzyme and metal binding sites are also marked with star and dot, respectively. Amino acid residues are numbered on the right.