

Figure S5

Consensus MAS.LGTSSI AVLPSR..SS .SSKPSIHTL SLTSGQ.YGR KFYGGIGIHG 50  
Gma ChlI1a ...A..... ....YF.. S..... ....N...  
Gma ChlI1b ...T..... ....CI.. F..... ....S...

Consensus IKGR.QLSV. NVATEVNSVE QAQSIASKES QRPVYPFSAI VGQDEMKLCL 100  
Gma ChlI1a ....A....T .. .... .. .... ..  
Gma ChlI1b ....S....A .. .... .. .... ..

Consensus LLNVIDPKIG GVMIMGDRGT GKSTTVRSLV DLLPEIKVVA GDPYNNSDPQD 150  
Gma ChlI1a ..... .... .. .... .. .... ..  
Gma ChlI1b ..... .... .. .... .. .... ..

Consensus PEFMGVEVRE RVLQGEELSV VLTKINMVDL PLGATEDRVC GTIDIEKALT 200  
Gma ChlI1a ..... .... .. .... .. .... ..  
Gma ChlI1b ..... .... .. .... .. .... ..

Consensus EGVKAEPGL LAKANRGILY VDEVNLDDH LVDVLLDSAA SGWNTVEREG 250  
Gma ChlI1a ..... .... .. .... .. .... ..  
Gma ChlI1b ..... .... .. .... .. .... ..

Consensus ISISHPARFI LIGSGNPEEG ELRPQLLDRF GMHAQVGTVR DAELRVKIVE 300  
Gma ChlI1a ..... .... .. .... .. .... ..  
Gma ChlI1b ..... .... .. .... .. .... ..

Consensus ERGRFDKNPK EFRDSYKAEQ EKLQQQITSA RSVLSSVQID QDLKVKISKV 350  
Gma ChlI1a ..... .... .. .... .. .... ..  
Gma ChlI1b ..... .... .. .... .. .... ..

Consensus CAELNVDGLR GDIVTNRAAK ALAALK.RD. VSAEDIATVI PNCLRHLRK 400  
Gma ChlI1a ..... .... .. .... .. G..N .. .... ..  
Gma ChlI1b ..... .... .. .... .. E..K .. .... ..

Consensus DPLESIDSGL LVTEKFYEVF S 421  
Gma ChlI1a ..... .... .. .... ..  
Gma ChlI1b ..... .... .. .... ..

**Figure S5** Amino acid sequence comparison of ChlI1a (Glyma13g30560) to ChlI1b (Glyma15g08680) showing the high degree of similarity between the two Mg-chelatase subunits. The two boxed residues indicate the positions of the *y11-2* (R273Q) mutation and *y11* and CD-5 (Q275R) mutations.