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Ca_CAT1 -----MAPFTTNSNGQPIPEPFATQRVGQHGPLLLQDFNLIDSLAHFDRERIP
Cg_CTA1 MSANPTNTSDVRGDRVVTNSTGYPYNDPFATQRVGQHGPLLLQDANLIDSLAHFNRRERIP
Cl_CLUG_04072 -----MAPFTTNSNGCPIPEPFATQRVGKHGPLLLQDFNLIDSLAHFDRERIP
Cau_QG37_05843_05842 -----MAPPTYTNSQGCPPEPFATQRVGQHGPLLLQDFNLIDSLAHFDRERIP
          . *** * * :*****:*****:* *****:*****
          QG37_05843
Ca_CAT1 ERVVHAKGSGAYGVFEVTDITDICAAKFLDVGKKTRIFTRFSTVGGELGSADTARDPR
Cg_CTA1 ERNPHAHSGAFGYFEVTDITDICGSAMFSEIGKRTRFLTRFSTVGGEGKSADTARDPR
Cl_CLUG_04072 ERVVHAKGSGAYGVFEVTDITDICSSKFLDVGKKTKVFTRFSTVGGESGSPDTARDPR
Cau_QG37_05843_05842 ERVVHAKGSGAYGVFEVTDITDICSSKMFHVGGKTRFTTRFSTVGGESGSADTARDPR
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Ca_CAT1 GFATKIFYTEEGNLDLVYNNTPVFFIRDPSKFPFHIHTQKRNPETHLKDANMFWDYLTNSNE
Cg_CTA1 GFATKIFYTEEGNLDWVYNNTPIFFIRDPSKFPFHIHTQKRNPQTNLKDPMFWDYLTTPPE
Cl_CLUG_04072 GFSTKLYTEEGNLDLVYNNTPVFFIRDPSKFPFHIHTQKRNPQTHLKDANMFWDYLTNSNE
Cau_QG37_05843_05842 GFSTKIFYTEEGNLDWVYNNTPVFFIRDPSKFPFHIHTQKRNPETNLKDANMFWDYLCNNP
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Ca_CAT1 --ESIHQVMVLFSDRGTTPASYREMNGYSGHYKWSNKKGEWFYVQVHFISDQGIKTLTNE
Cg_CTA1 NQVAVHQMLILFSDRGTTPASYRHMNGYSGHYKWSNKKGEWHYVQVHILTDQGIKNLTND
Cl_CLUG_04072 --ESVHQVTTLFSDRGTTPRSYREMNGYSGHYKWSTKDGNWHYVQVHFISDQGVKTLTNE
Cau_QG37_05843_05842 --ESIHQVVILFSDRGTTPASYREMNGYSGHYKWSTKDGNWHYVQVHMISDQGNKGLTNE
: :. **: ***** **.******: :. **:***** : :. ** * ** :
          QG37_05842
Ca_CAT1 EAGALAGSNPDYAQEDLFKNIAGNPSWTAYIQTMTEAEAKEAEFSVFDLTKVWPHKDY
Cg_CTA1 EAVEIAGKNPDYCOQDLYENIAKGNPSWTVYIQTMTEAQAKLPFSVFDLTKVWPHKDF
Cl_CLUG_04072 EAGELAGSNPDHAQEDLFRNIAGNFPSWTCYIQTMTEAQAKEAPFSVFDLTKVWPHKDY
Cau_QG37_05843_05842 EATELAGTNPDHAQEDLFKNIAGNFPSWTCYIQTMTEAQAKQAPFSVFDLTKVWPHKDY
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Ca_CAT1 PLRRFGKFTLNENPKNYFAEVEQAASFPAHTVPYMEPSADPVLQSRFLSYADTHRRLGT
Cg_CTA1 PLRRVKGMMNENPLNYFASIEQAASFPAHTVPYQEPSADPVLQSRFLFAYADAHRYRLGA
Cl_CLUG_04072 PLRRFGKFTLNENPKNYFAEVEQAASFPAHTVPYMEPSADPVLQSRFLSYADTHRRLGP
Cau_QG37_05843_05842 PMRRFGKFTLNENPKNYFAEVEQAASFPSHTVPYQEASADPVLQSRFLSYPDTHRRLGT
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Ca_CAT1 NYTQIPVNCPTGAVFNPHMRDGMTVNGNLGSHPNYLASDKPVEF--KQFSLOEDQEVW
Cg_CTA1 NFHQIPVNCPYASKFFNPVIRDGPMNVVDGNFNEPNYASNKQYQIPNQDRPIQHQEVW
Cl_CLUG_04072 NYTQIPVNCPTIG--VYNPHMRDGMNVNGNLGSAPNYLATSEPIEF--RQFSIQEDQEVW
Cau_QG37_05843_05842 NYSQIPVNCPVASQVYAPHIRNGAMTVNGNLGSTPNYVSSFNPMQF--REFSQQDQEVW
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Ca_CAT1 NGAATPFHWKATPA--DFKQAOELWVKLRYPNQOEHLAHNIAVHAAGADAAIQDRVFAY
Cg_CTA1 NGPAQPFHWATSPGIDFVQARDLYKVLGKQKQDQOEHLAYNIGTHVAGADPEIQORVIDM
Cl_CLUG_04072 NGAACPFHWKATED--EFTQATALYNVLGRYPGQKLNLAHNVAHVSAADKPIQERVIKY
Cau_QG37_05843_05842 TGAACPFHWKATDA--EYTOATALYHVLAKYPNQQRNLAHNVAVHAAGADPSVQDRVFEL
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Ca_CAT1 FGKVSQDLADAIKKEVLELSPRK*----
Cg_CTA1 FSRVDEGLGANIRKEIEKNASAPTAKI*
Cl_CLUG_04072 FGKVSPELAANIRKELEAN*-----
Cau_QG37_05843_05842 FTRVHPDLGAAIKKEVLELSPRK*----
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Figure S1. Alignment to compare the catalase protein sequences of *C. lusitaniae*, *C. glabrata* and *C. auris* to *Candida albicans* Cat1. Protein sequences were retrieved from the *Candida* genome database or NCBI and sequences were aligned using the Clustal Omega multiple sequence alignment tool. The two *C. auris* ORF annotations that made up the *CAT1* gene are indicated in red (QG37_05843) or blue (QG37_05842).