**Supplemental Table 1. Homozygous Sequence Variants in the Affected Cat**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Chr:Pos | Ref/Alt | Allele Counts | Allele Freq. | # Alleles | 99 Lives | 99 Lives Count | Allelic Depths | Read Depths | Genotype Qualities (GQ) | Gene | Effect | Coding Change | | HGVS p.  (Clinically Relevant) |
| A1:125848605 | G/C | 2 | 0.025 | 80 | 0.000 | 0.000 | 0,188 | 188 | 99 | CDC20B,GPX8 | missense\_variant | ENSFCAT00000054793:c.126+10486C>G,ENSFCAT00000029649:c.391G>C | | ,p.Gly131Arg |
| A1:91397399 | -/CT | 2 | 0.025 | 80 | 0.000 | 0.000 | 0,67 | 67 | 99 | BTNL9 | splice\_region\_variant | ENSFCAT00000034165:c.1001-8\_1001-7dupCT | |
| A2:122815907 | G/A | 2 | 0.025 | 80 | 0.000 | 0.000 | 0,141 | 141 | 99 | ENSFCAG00000008416 | splice\_region\_variant | ENSFCAT00000008417:c.1236-4G>A | |
| A2:146932854 | C/T | 2 | 0.025 | 80 | 0.000 | 0.000 | 0,44 | 44 | 99 | ENSFCAG00000027848 | splice\_region\_variant |  |
| A3:525353 | G/A | 2 | 0.025 | 80 | 0.000 | 0.000 | 0,16 | 16 | 47 | SOX18 | missense\_variant | ENSFCAT00000066037:c.596G>A | | p.Gly199Asp |
| B3:39334330 | G/A | 2 | 0.025 | 80 | 0.000 | 0.000 | 0,138 | 138 | 99 | CLN6 | stop\_gained | ENSFCAT00000025909:c.668G>A | | p.Trp223Ter |
| B4:36127005 | C/T | 2 | 0.025 | 80 | 0.000 | 0.000 | 0,183 | 183 | 99 | ENSFCAG00000031264 | missense\_variant | ENSFCAT00000035238:c.401C>T | | p.Ala134Val |
| B4:942385 | G/A | 2 | 0.025 | 80 | 0.000 | 0.000 | 0,389 | 389 | 99 | ENSFCAG00000000721,ENSFCAG00000035941 | missense\_variant | ENSFCAT00000055964:c.3593C>T,ENSFCAT00000048383:c.102-808G>A | | p.Pro1198Leu, |
| C2:151718791 | -/GCA | 2 | 0.025 | 80 | 0.000 | 0.000 | 0,154 | 156 | 99 | ULK4 | inframe\_insertion | ENSFCAT00000067277:c.476\_478dupCAG | | p.Ala159\_Glu160insAla |
| D1:112281089 | G/A | 2 | 0.025 | 80 | 0.000 | 0.000 | 0,127 | 127 | 99 | TBC1D10C | missense\_variant | ENSFCAT00000003393:c.1178G>A | | p.Arg393Gln |
| D2:13079966 | G/A | 2 | 0.025 | 80 | 0.000 | 0.000 | 0,107 | 107 | 99 | NID1 | missense\_variant | ENSFCAT00000011033:c.3436G>A | | p.Gly1146Arg |
| D3:96347187 | C/T | 2 | 0.025 | 80 | 0.000 | 0.000 | 0,32 | 32 | 96 | CTDP1 | missense\_variant | ENSFCAT00000000566:c.10C>T | | p.Pro4Ser |
| E1:57742047 | C/A | 2 | 0.025 | 80 | 0.000 | 0.000 | 0,162 | 162 | 99 | UNK | missense\_variant | ENSFCAT00000005759:c.1939C>A | | p.Leu647Met |
| E1:61754232 | GGGGGGGCCGGA/- | 2 | 0.025 | 80 | 0.000 | 0.000 | 0,112 | 112 | 99 | CEP131 | inframe\_deletion | ENSFCAT00000062174:c.31\_42delTCCGGCCCCCCC | | p.Ser11\_Pro14del |
| E1:6825122 | G/A | 2 | 0.025 | 80 | 0.000 | 0.000 | 0,145 | 145 | 99 | MYOCD | missense\_variant | ENSFCAT00000064311:c.2416G>A | | p.Ala806Thr |
| E2:36241154 | G/A | 2 | 0.025 | 80 | 0.000 | 0.000 | 0,34 | 34 | 99 | NLRC5 | missense\_variant | ENSFCAT00000002930:c.4033G>A | | p.Gly1345Ser |
| E3:22046090 | C/G | 2 | 0.025 | 80 | 0.000 | 0.000 | 0,71 | 71 | 99 | RABEP2 | missense\_variant | ENSFCAT00000063051:c.908G>C | | p.Ser303Thr |
| X:91111120 | C/T | 2 | 0.025 | 80 | 0.000 | 0.000 | 0,26 | 26 | 78 | COL4A5 | missense\_variant | ENSFCAT00000051940:c.953C>T | | p.Pro318Leu |
| X:92843364 | G/A | 2 | 0.025 | 80 | 0.000 | 0.000 | 0,175 | 175 | 99 | CHRDL1 | missense\_variant | ENSFCAT00000051331:c.709C>T | | p.Pro237Ser |
| A2:165112701 | A/T | 2 | 0.025 | 80 | 0.003 | 1.000 | 0,66 | 66 | 99 | NOS3 | missense\_variant | ENSFCAT00000013195:c.163A>T | | p.Ser55Cys |
| C1:157895258 | C/A | 2 | 0.025 | 80 | 0.003 | 1.000 | 0,69 | 69 | 99 | SCN9A | splice\_region\_variant | ENSFCAT00000051209:c.1600-4G>T | |
| D1:110377968 | G/A | 2 | 0.025 | 80 | 0.003 | 1.000 | 0,129 | 129 | 99 | CAPN1 | missense\_variant | ENSFCAT00000058310:c.1553G>A | | p.Arg518His |
| D1:110386110 | C/T | 2 | 0.025 | 80 | 0.003 | 1.000 | 0,15 | 15 | 45 | CAPN1,ENSFCAG00000001439 | 5\_prime\_UTR\_premature\_start\_codon\_gain\_variant | ENSFCAT00000058310:c.\*2372C>T,ENSFCAT00000001439:c.-103C>T | | ,p.Met1ext-34 |
| D1:110390721 | T/C | 2 | 0.025 | 80 | 0.003 | 1.000 | 0,181 | 181 | 99 | ENSFCAG00000001439 | splice\_region\_variant | ENSFCAT00000001439:c.635-7T>C | |
| D2:13223469 | G/A | 2 | 0.025 | 80 | 0.003 | 1.000 | 0,111 | 111 | 99 | LYST | missense\_variant | ENSFCAT00000006053:c.3593G>A | | p.Gly1198Asp |
| D2:72876254 | C/G | 2 | 0.025 | 80 | 0.003 | 1.000 | 0,148 | 148 | 99 | DCLRE1A | missense\_variant | ENSFCAT00000011836:c.3027G>C | | p.Met1009Ile |
| E1:17285119 | G/A | 2 | 0.025 | 80 | 0.003 | 1.000 | 0,119 | 119 | 99 | CORO6 | missense\_variant | ENSFCAT00000043362:c.398G>A | | p.Arg133His |
| E2:36535148 | C/T | 2 | 0.025 | 80 | 0.003 | 1.000 | 0,126 | 126 | 99 | ENSFCAG00000004695 | missense\_variant | ENSFCAT00000004696:c.760G>A | | p.Ala254Thr |
| E2:942326 | C/G | 2 | 0.025 | 80 | 0.003 | 1.000 | 0,175 | 175 | 99 | ENSFCAG00000045763 | missense\_variant | ENSFCAT00000051345:c.1970C>G | | p.? |
| F2:51065743 | G/C | 2 | 0.025 | 80 | 0.003 | 1.000 | 0,148 | 148 | 99 | BAALC | missense\_variant | ENSFCAT00000066309:c.287G>C | | p.Gly96Ala |
| D2:72893937 | T/G | 2 | 0.025 | 80 | 0.003 | 1.005 | 0,214 | 214 | 99 | DCLRE1A | missense\_variant | ENSFCAT00000011836:c.1345A>C | | p.Asn449His |
| B3:5427645 | G/A | 2 | 0.025 | 80 | 0.005 | 2.000 | 0,209 | 209 | 99 | BLM | missense\_variant | ENSFCAT00000006091:c.4133G>A | | p.Arg1378His |
| B4:37121994 | C/T | 2 | 0.025 | 80 | 0.005 | 2.000 | 0,204 | 204 | 99 | WNK1 | missense\_variant | ENSFCAT00000046718:c.7267G>A | | p.Ala2423Thr |
| C1:11181496 | C/T | 2 | 0.025 | 80 | 0.005 | 2.000 | 0,83 | 83 | 99 | ENSFCAG00000045927 | splice\_region\_variant |  |
| E1:29368925 | A/G | 2 | 0.025 | 80 | 0.005 | 2.000 | 0,44 | 44 | 99 | DHX40 | splice\_region\_variant | ENSFCAT00000001408:c.973+6T>C | |
| E1:40793528 | G/A | 2 | 0.025 | 80 | 0.005 | 2.000 | 0,57 | 57 | 99 | ERBB2 | missense\_variant | ENSFCAT00000062681:c.1150G>A | | p.Asp384Asn |
| E1:40984412 | G/A | 2 | 0.025 | 80 | 0.005 | 2.000 | 0,156 | 156 | 99 | LRRC3C | missense\_variant | ENSFCAT00000014993:c.139G>A | | p.? |
| A2:8622192 | G/C | 2 | 0.025 | 80 | 0.008 | 3.000 | 0,103 | 103 | 99 | EPOR | missense\_variant | ENSFCAT00000004913:c.207C>G | | p.Ser69Arg |
| B4:16507409 | C/T | 2 | 0.025 | 80 | 0.008 | 3.000 | 0,41 | 41 | 99 | HACD1 | missense\_variant | ENSFCAT00000014224:c.529G>A | | p.Val177Met |
| C1:11486122 | G/A | 2 | 0.025 | 80 | 0.008 | 3.000 | 0,17 | 17 | 51 | TMEM82 | missense\_variant | ENSFCAT00000028472:c.349G>A | | p.Ala117Thr |
| D2:47375878 | C/A | 2 | 0.025 | 80 | 0.008 | 3.000 | 0,117 | 117 | 99 | ENSFCAG00000000311 | missense\_variant | ENSFCAT00000000311:c.804G>T | | p.Glu268Asp |
| E1:20234895 | G/A | 2 | 0.025 | 80 | 0.008 | 3.000 | 0,204 | 204 | 99 | RHOT1,RNF135 | missense\_variant | ENSFCAT00000044207:c.-27+111G>A,ENSFCAT00000009134:c.941G>A | | ,p.Gly314Glu |
| E1:40759996 | C/T | 2 | 0.025 | 80 | 0.008 | 3.000 | 0,85 | 85 | 99 | PGAP3 | splice\_region\_variant | ENSFCAT00000009905:c.695-8G>A | |
| E1:40761442 | G/C | 2 | 0.025 | 80 | 0.008 | 3.000 | 0,97 | 97 | 99 | PGAP3 | splice\_region\_variant | ENSFCAT00000009905:c.495+8C>G | |
| E1:43019421 | G/C | 2 | 0.025 | 80 | 0.008 | 3.000 | 0,217 | 217 | 99 | CAVIN1 | missense\_variant | ENSFCAT00000060905:c.804C>G | | p.His268Gln |
| E1:55695215 | C/T | 2 | 0.025 | 80 | 0.008 | 3.000 | 0,263 | 263 | 99 | SDK2 | missense\_variant | ENSFCAT00000004749:c.835G>A | | p.Ala279Thr |
| E3:9893651 | A/G | 2 | 0.025 | 80 | 0.008 | 3.000 | 0,72 | 72 | 99 | HIP1 | missense\_variant | ENSFCAT00000060987:c.2017A>G | | p.Lys673Glu |
| E1:57533233 | C/T | 2 | 0.025 | 80 | 0.010 | 3.900 | 0,124 | 124 | 99 | LLGL2 | missense\_variant | ENSFCAT00000005749:c.595C>T | | p.Arg199Cys |
| D1:15076123 | G/A | 2 | 0.025 | 80 | 0.013 | 5.070 | 0,200 | 200 | 99 | BACE1,CEP164 | missense\_variant | ENSFCAT00000064840:c.173+196C>T,ENSFCAT00000000182:c.959G>A | | ,p.Ser320Asn |
| E1:62048388 | C/T | 2 | 0.025 | 80 | 0.013 | 5.070 | 0,81 | 81 | 99 | FAAP100 | missense\_variant | ENSFCAT00000012922:c.1342G>A | | p.Glu448Lys |
| E1:62049873 | G/A | 2 | 0.025 | 80 | 0.013 | 5.070 | 0,105 | 105 | 99 | FAAP100 | missense\_variant | ENSFCAT00000012922:c.980C>T | | p.Pro327Leu |
| E1:62050562 | G/A | 2 | 0.025 | 80 | 0.013 | 5.070 | 0,95 | 95 | 99 | FAAP100 | splice\_region\_variant | ENSFCAT00000012922:c.298-7C>T | |
| E2:36951300 | G/C | 2 | 0.025 | 80 | 0.013 | 5.070 | 0,60 | 60 | 99 | ENSFCAG00000002691 | splice\_region\_variant | ENSFCAT00000002691:c.1440-7C>G | |
| B1:205970916 | G/A | 2 | 0.025 | 80 | 0.015 | 5.850 | 0,110 | 110 | 99 | HTT | splice\_region\_variant | ENSFCAT00000004610:c.2375-3C>T | |
| D2:16911323 | C/T | 2 | 0.025 | 80 | 0.015 | 5.850 | 0,311 | 311 | 99 | DISC1 | missense\_variant | ENSFCAT00000002498:c.1879G>A | | p.? |
| C1:1135799 | G/C | 2 | 0.025 | 80 | 0.018 | 7.020 | 0,79 | 79 | 99 | MORN1 | splice\_region\_variant | ENSFCAT00000009519:c.1251-341C>G | |
| E2:36720605 | A/T | 2 | 0.025 | 80 | 0.018 | 7.020 | 0,195 | 195 | 99 | ADGRG1 | missense\_variant | ENSFCAT00000006655:c.1050A>T | | p.Gln350His |
| C1:216516966 | A/G | 2 | 0.025 | 80 | 0.021 | 8.190 | 0,76 | 76 | 99 | ENSFCAG00000009701 | splice\_region\_variant | ENSFCAT00000034945:c.2078-7A>G | |
| E1:19933725 | C/T | 2 | 0.025 | 80 | 0.021 | 8.190 | 0,156 | 156 | 99 | COPRS | missense\_variant | ENSFCAT00000058020:c.208G>A | | p.Gly70Ser |
| E1:8172037 | A/G | 2 | 0.025 | 80 | 0.021 | 8.190 | 0,215 | 215 | 99 | HS3ST3B1 | missense\_variant | ENSFCAT00000065000:c.569A>G | | p.Lys190Arg |
| E2:44436159 | T/C | 2 | 0.025 | 80 | 0.021 | 8.190 | 0,231 | 231 | 99 | CMTM2 | missense\_variant | ENSFCAT00000015253:c.185T>C | | p.Val62Ala |
| E3:6807957 | G/A | 2 | 0.025 | 80 | 0.021 | 8.190 | 0,211 | 211 | 99 | ZKSCAN5 | missense\_variant | ENSFCAT00000042616:c.902G>A | | p.Ser301Asn |
| E3:9488525 | C/T | 2 | 0.025 | 80 | 0.021 | 8.190 | 0,146 | 146 | 99 | STYXL1 | missense\_variant | ENSFCAT00000022573:c.248C>T | | p.Thr83Ile |
| C1:1187003 | G/A | 2 | 0.025 | 80 | 0.026 | 10.140 | 0,47 | 47 | 99 | ENSFCAG00000033807,MORN1 | missense\_variant | ENSFCAT00000043644:c.274G>A,ENSFCAT00000009519:c.26C>T | | p.Gly92Arg,p.? |
| E2:1315191 | C/T | 2 | 0.025 | 80 | 0.026 | 10.140 | 0,196 | 196 | 99 | ENSFCAG00000030721 | missense\_variant | ENSFCAT00000028127:c.506G>A | | p.Gly169Glu |
| B1:70829802 | A/G | 2 | 0.025 | 80 | 0.028 | 10.920 | 0,105 | 105 | 99 | RAPGEF2 | missense\_variant | ENSFCAT00000060426:c.556T>C | | p.Phe186Leu |
| C1:8728697 | C/T | 2 | 0.025 | 80 | 0.028 | 10.920 | 0,269 | 269 | 99 | KIAA2013 | missense\_variant | ENSFCAT00000024996:c.1477G>A | | p.Val493Ile |
| E1:37170780 | A/G | 2 | 0.025 | 80 | 0.028 | 10.920 | 0,120 | 120 | 99 | MYCBPAP | missense\_variant | ENSFCAT00000012339:c.907T>C | | p.Cys303Arg |
| E1:42289359 | A/G | 2 | 0.025 | 80 | 0.041 | 15.990 | 0,67 | 67 | 99 | ENSFCAG00000001928 | missense\_variant | ENSFCAT00000057604:c.611T>C | | p.Ile204Thr |
| F2:76537248 | C/T | 2 | 0.025 | 80 | 0.067 | 26.130 | 0,126 | 126 | 99 | TG | missense\_variant | ENSFCAT00000011957:c.2788C>T | | p.Pro930Ser |
| A2:159259844 | G/A | 2 | 0.025 | 80 | 0.072 | 28.080 | 1,182 | 183 | 99 | TCAF1 | missense\_variant | ENSFCAT00000007288:c.1973C>T | | p.Pro658Leu |
| A2:106328617 | C/A | 2 | 0.025 | 80 | 0.079 | 30.810 | 0,155 | 155 | 99 | THSD7A | missense\_variant | ENSFCAT00000033904:c.3241G>T | | p.Val1081Leu |
| C2:1992713 | G/A | 2 | 0.025 | 80 | 0.121 | 47.190 | 0,13 | 13 | 39 | ENSFCAG00000046465,TSPEAR | splice\_region\_variant | ,ENSFCAT00000001772:c.86-38291G>A | | , |
| B3:13140795 | G/T | 2 | 0.025 | 80 | .0077, .0026 |  | 0,187 | 187 | 99 | MCTP2 | missense\_variant | ENSFCAT00000001135:c.331G>T | | p.Gly111Cys |