chr12 100796196 100796298 AMPLP863907290 AGCAGCTCATCCAACAATATCCA TTCTGTAAGAAGGCAACACAATCACT AGCAGCTCAUCCAACAATAUCCA TTCTGUAAGAAGGCAACACAAUCACT TGAGGAGAAGACCTATATAGAGACAAGCATAGGAGAGGGGGCCAACGTGGTTAGTCTAAGTGTAAGTATAAAAAGTCAGATGAAGACTTACCTTTTTTCATA 28 42 4 4 1 0 1023 267 263 554.5 283 2 IAD78091\_236\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 46 0 44 50 0 0 0 0 1290 756 2

chr16 2121503 2121683 AMPL7153222961 CTCTGGCTTTCACCATCCTCTT ACATCCCTCAGACATGCAAACAG CTCTGGCTTUCACCATCCTCUT ACATCCCUCAGACAUGCAAACAG CTGACAGGCCTTTGACTTCCTGTTGCTGCTGCGGGCCGACTCACTGCACCGCCTGGGCCTGCCCAACAAGGATGGAGTCGTGCGGTTCAGCCCCTACTGCGTCTGCGACTACATGTACGCGGGACCTCGCCCACGGCCCATGAGGCTCAGGGCGTCAGAGGCGCTGGGGCTGTGGTGGCG 32 24 6 3 1 121 244 251 560.5 274 286.5 2 IAD53548\_124\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 495 7 1

chr12 112892322 112892540 AMPL7153022487 CATGAGAGTGCTTGAAAACACTAATGT TCTACCTCTGTATGTTTGCAAAATTCTCT CATGAGAGTGCUTGAAAACACTAAUGT TCTACCTCTGTAUGTTTGCAAAATTCUCT ACATAAAGGTAACAAATAATAAATGTCATGTGTTTATCTTGAAAGGAACTGAAATACGACGTTGGTGGAGGAGAACGGTTTGATTCTTTGACAGATCTTGTGGAACATTATAAGAAGAATCCTATGGTGGAAACATTGGGTACAGTACTACAACTCAAGCAGGTGAGCAGATTGGAAAGCTCAAGCTTTCTCCTTAAAAACTTAAAACAAATCCTAAt 34 34 5 8 1 78 270 224 650.5 342.5 308 2 IAD49522\_124\_primers\_U.txt 1 1 1 1 0.3666666316 0.166667 0 0 0 0 0 0 0 0 0 0 0 0 494 46 1

chr2 152380935 152381146 AMPL7153255600 TGGCTCTGTACTCCACCTGAA AAAAAGCCTCTCTCTTGAGTAAACATT TGGCTCTGUACTCCACCUGAA AAAAAGCCTCTCUCTTGAGTAAACAUT CAGAGAAAACCAAAATGGGCAACAGGTGATGGTTGCCTGGCATGCCTTGGCAATGGCTGTTGGGGACTGGGGACATTTTCATGACACCCTTACCTCACTGGCCTGTTTGGCTGCCTGTGTGGCCTTCTTGATGTCTGGTCGATCAGCCACTGTGGTGTAATGCAGGTTCTCTTTGGCATCTTTTCTGTAAGCGACCTTTATTGGGGAAGAA 26 34 5 6 1 107 104.5 410 1134.5 515 619.5 2 IAD59911\_183\_primers\_U.txt 1 1 0.1136885402 4.93267e-05 1 1 0 0 0 44 42 0 0 0 0 0 0 0 514.5 305.5 1

chr22 30064203 30064327 7153067409 GGCTTTGGTGTTTCACTCTATGC GATCATGGTTCCCGATACATAGCTG GGCTTTGGUGTTTCACTCTAUGC GATCATGGTUCCCGATACATAGCUG TTCATCTTCACGTTTACTGCTACCTGCAAGAGCTCAAACTGCTATGGCACTAGTGGGCCAGTAGGCAGTGAAGTAAATTTGTGGATATTAACCTTTTTGTCTGCTTCTGTGGCCACAGATTCTC 30 40 6 6 1 55 193 317.5 677 343 334 2 WG\_IAD51217.20140604\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 44 48 0 510.5 124.5 1

chr13 39263558 39263893 FREM2\_1.3.590413 CTACAGCGGTTTGTGATTCGT AGCTCGGTCTTCCACCTG CTACAGCGGUTTGTGATUCGT AGCTCGGUCTTCCACCUG TCCATCCTGTGGATCGCCTCCCTCCGGAGCTGGGCAGTGGCTGTCCCCTTCGTATGGTGGTACAGGAATCCCAGCTCACACCACTGAGGAAGAAGTGGCTGCGCTACACTGACCTGGACACAGATGACCGAGAACTACGTTACACAGTGACTCAGTCCCCCACAGACACAGACGAAAATCACCTGCCAGCCCCACTGGGTACCTTGGTCTTGACTGACAACCCCTCAGTCGTGGTGACCCATTTTACCCAAGCCCAGATCAACCATCATAAAATTGCTTACAGACCCCCGGGTCAAGAACTGGGCGTGGCTACTCGAGTGGCCCAGTTCCAGTTC 30 26 4 4 1 188 0 0 667 295 372 1 WG\_IAD76560.20150714\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 42 0 0 0 0 44 36 0 0 0 0

chr12 76742038 76742122 AMPL7154804609 GGGCTTCGTACACAAAACTTGC GGCCCAGATATGTTAAGTTCTATGG GGGCTTCGUACACAAAACTUGC GGCCCAGAUATGTTAAGTTCTAUGG GTCCCTCGGGCCCCACGCAGCAGCTCACGATGGCTTCCAGCACCTCGGCCACCTGCAACGCCGCCTTCACAGACCCTGCAGCGG 28 32 3 6 1 60 1 10 18 1 17 2 IAD67652\_152\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 44 0 44 44 0 0 0 0 11 9 0

chr3 37067348 37067508 AMPL7154913543 CCATTGTCACAGAGGATAAGACAGATATTT GAGGTAGGCTGTACTTTTCCCAA CCATTGTCACAGAGGAUAAGACAGATATUT GAGGTAGGCUGTACTTTUCCCAA TAGTGGCAGGGCTAGGCAGCAAGATGAGGAGATGCTTGAACTCCCAGCCCCTGCTGAAGTGGCTGCCAAAAATCAGAGCTTGGAGGGGGATACAACAAAGGGGACTTCAGAAATGTCAGAGAAGAGAGGACCTACTTCCAGCAACCCCAGGTATGGCCTT 48 30 5 4 1 86 562.5 575 1281.5 642 639.5 2 IAD86166\_188\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 60 0 0 0 0 0 0 0 1137.5 12.5 2

chr2 136543615 136543743 SP\_47.2839 ACATGGTAGAGAGAAACTAGGTTATGGA GGCTTTTCATGTATTTTGATGTTTTATGCATAC ACATGGUAGAGAGAAACTAGGTTAUGGA GGCTTTTCATGTATUTTGATGTTTTATGCAUAC AGTATTATCTGTGTTTTCCTTTATGACCTCCAGGTCTTGAGTCTTGCTTATAAATACCTTTCCCACTTCAAAAATTAATTTTTTTATATCCTAGGATTCTTATGGTTTCCTTTTTGTATGTTTAAATC 46 38 5 8 1 39 0 0 0 0 0 2 WG00043.3.20140613\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

chr5 112173809 112174016 AMPL7154393992 CCAGCTCCTCTTCATCAAGAGGA CATCTGTCACACAATGTAATTCAGTGG CCAGCUCCTCTTCAUCAAGAGGA CATCTGTCACACAAUGTAATTCAGUGG GCTTAGATAGTTCTCGTTCTGAAAAAGATAGAAGTTTGGAGAGAGAACGCGGAATTGGTCTAGGCAACTACCATCCAGCAACAGAAAATCCAGGAACTTCTTCAAAGCGAGGTTTGCAGATCTCCACCACTGCAGCCCAGATTGCCAAAGTCATGGAAGAAGTGTCAGCCATTCATACCTCTCAGGAAGACAGAAGTTCTGGGTCTA 24 40 4 7 1 95 0 1 1 0 1 1 IAD63279\_182\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 46 0 0 0 0 44 54 0 1 1 0

chr5 37310772 37310847 AMPL5044259876 TGATGTAGCAGTTGATAAGAGAAGCAAT TCTATAATTGTGATAGAAAAGTTTTATGCTCCT TGAUGTAGCAGTTGAUAAGAGAAGCAAT TCTATAATTGTGAUAGAAAAGTTTTATGCUCCT ATGCCCCTGTGAGTTCTTTGTCCCTGATTACAAGATCTTTAAAGGTGGTGATCTTCAGCTGCTCTTGAAGTTCCT 32 38 4 8 1 33 512 508 1075.5 554.5 521 2 IAD44795\_93\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 56 0 0 0 0 0 0 0 1020 4 2

chr7 153750122 153750303 DPP6\_2.19194 GCCCCGGTTCCAGTACCAG CGCGGTGACCGCGATCTG GCCCCGGUTCCAGUACCAG CGCGGUGACCGCGATCUG CGCGGAGCGATGGTGACGAGGAGGACGTAAGAGCTTCTcgggggcggggggcggcggcgggTTCTCCGGGCTGAGCGCGCAGCGAGACGCGTCGGCAGGGGAAATTTTTTTTGGGGGGGGAATCAGGCGCCCTCCCCCCGCCCACGACTCTCCGGGCGCCCCCAGACAGGCTCCGTGGCGC 28 34 2 3 1 132 3 1 43 25.5 17.5 2 IAD53887\_WG.20140521\_primers\_U.txt 0.5 0.5 0.75 0.5 0.75 0.5 0 0 0 44 38 0 0 0 0 0 0 0 4 2 0

chr11 26386548 26386701 SP\_117.10293 CAATGTGAAGAGTCTCAATGTGACAG TATTATTCAATCTGGAGAAGCCTGCTTT CAATGTGAAGAGUCTCAATGUGACAG TATTATTCAATCUGGAGAAGCCTGCTUT tataaattcaaaggcaggttatttacttccaagatacaatgggggtattggcattggtaaacatacccattccaaaaagaagaaatcaaccaaaacaaaggggctgcaggccacacacaagtttgaaacacagcagggcactcattaaatctt 34 42 6 6 1 60 0 0 0 0 0 2 WG00042.3.20140613\_primers\_U.txt 1 1 0.39791675 0.1 0.2112106803 0.00352113 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

chr13 32910325 32910478 223448105 CACTGTGCCCAAACACTACCT AGAACATTTCCTCAGAATTGTCCCAAA CACTGUGCCCAAACACUACCT AGAACATTTCCUCAGAATTGUCCCAAA TTTAACTTAGTGAAAAATATTTAGTGAATGTGATTGATGGTACTTTAATTTTGTCACTTTGTGTTTTTATGTTTAGGTTTATTGCATTCTTCTGTGAAAAGAAGCTGTTCACAGAATGATTCTGAAGAACCAACTTTGTCCTTAACTAGCTCT 32 30 3 4 1 46 592 683 1355.5 642 713.5 2 BioRef\_BRCA\_WG.20130906\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 44 54 0 1275 91 2

chr10 96072925 96073246 PLCE1\_28.715770 TTTTGCATTTACATGTTCCTATCCGTAC GGCATATCATCCACATGGACTTTTG TTTTGCATTTACAUGTTCCTATCCGUAC GGCATATCAUCCACATGGACTTTUG TCTAAGTACTAGCACCTCTGTATCAAATAGAGCTTAGAAATATGTGATTACGGATGAATGATCAGCCATGTGATCTTCTTGACAGATGTTTAATACAGAAGAAAGAAAATGTTTGCAGACTCACAGAGTCACGGTGCATGGGGTCCCAGGGCCAGAGCCCTTTACCGTTTTCACTATTAATGGAGGCACCAAGGCAAAGCAGCTTCTGCAGCAAGTAAGTCCACTGAGCCGTGGTTGGGAGAATCCAAAATCTAAGATGTATGGATGTATGTGTGTGTATAAATGCCTGTGTGTAAACATACACAGATGCACATGAATGCG 34 38 7 5 1 138 0 0 617 276 341 1 WG\_IAD76560.20150714\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

chr17 18051318 18051474 AMPLP387772519 AGCTAGCTTCAGATCCTTCTTGAT TGGCCTTCTCATAGGTCGCT AGCTAGCTUCAGATCCTTCTUGAT TGGCCTUCTCATAGGUCGCT CTGGCTCCAACTCCTACCCATCAGGTTTGTGTCTGATTATGGGCGGAATGGCTTCCAGGCTGTGTGTCAGCACCGCCTCATGCAGGCCATGGGCCGGGCCCAACAGCAGGGCTCGGGGGCTGCCCGCACCTTACCCCCGACCCAGCTCGAGTGGAC 32 24 5 4 1 0 1074 238.5 257 522 255 2 IAD78091\_236\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 1312.5 835.5 2

chr2 48025848 48026022 AMPL7154393686 GACACAAGGATCTAGGCGAAGTAG GCCATTTCCAGTCACCATTCTCTT GACACAAGGAUCTAGGCGAAGUAG GCCATTTCCAGUCACCATTCTCUT CGCCAAATAAAAAAACGAAGGGTCATATCAGATTCTGAGAGTGACATTGGTGGCTCTGATGTGGAATTTAAGCCAGACACTAAGGAGGAAGGAAGCAGTGATGAAATAAGCAGTGGAGTGGGGGATAGTGAGAGTGAAGGCCTGAACAGCCCTGTCAAAGTTGCTCGAAAGCGG 32 34 3 5 1 83 249.5 259 668 361.5 306.5 2 IAD93167\_182\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 48 0 0 0 0 44 48 0 508.5 9.5 1

chr1 155208262 155208487 AMPL7153252931 GACCTACCCTACAGTTTCTCAACC CAAGTGATAAGCAGAGTCCCATACT GACCTACCCUACAGTTTCUCAACC CAAGTGAUAAGCAGAGTCCCAUACT CCAGACATCAGGGCCCTCAGGGCCTGAAAAAGCTAGAATGCCTACCTTGAGCTTGGTATCTTCCTCTGGGAGGCTGAAGTTGTGCAACTGGAAATCATCAGGGGTGTCTGCATAGGTGTAGGTGCGGATGGAGAAGTCACAGCTGGCCATGGGTACCCGGATGATGTTATATCCGATTCCTACAGAAAAGGATGATCAAGATATGGTAGTCCGAGTCAATAGGAG 30 40 4 4 1 114 272 233 553 284 269 2 IAD50814\_124\_primers\_U.txt 0.5 0.5 0.5 0.5 0.5 0.5 0 0 0 0 0 0 0 0 0 0 0 0 505 39 1

chr7 117234941 117235106 AMPL7153017234 ATTAAAAATAAAACCACAATGGTGGCATGA AATACTTTACAATAGAACATTCTTACCTCTGC ATTAAAAATAAAACCACAAUGGTGGCAUGA AATACTTTACAAUAGAACATTCTTACCTCUGC ACTGTACTGTCTTATTGTAATAGCCATAATTCTTTTATTCAGGAGTGCTTTTTTGATGATATGGAGAGCATACCAGCAGTGACTACATGGAACACATACCTTCGATATATTACTGTCCACAAGAGCTTAATTTTTGTGCTAATTTGGTGCTTAGTAATTTTTCTG 44 44 5 7 1 57 242.5 268 646.5 318 328.5 2 IAD55165\_124\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 510.5 25.5 1

chr3 151999325 151999518 AMPL7156621396 GCCTAATCTGCCTGTGTGGTTT AGATTACAAGAGCATTTGAAACTCTTTTGG GCCTAATCUGCCTGTGTGGTUT AGATTACAAGAGCAUTTGAAACTCTTTUGG CTCAGTATTAGTTCTACTCATACCTAATACCCTCTGCCCCAGCACTCGCCAAGATCAGCAAAATCTACTTTTAGACTCAAAATCATTACCACCTGTGAAGTTTCTGATGTCGCTTCTGAGTGACATAGCACTCTGTCAATTGCTCTGTTGGATGGCTTTGCTGAATGGCACCTTTTAAGAAGTGCCTTGAGCC 36 38 7 4 1 86 0 0 1 1 0 1 IAD46040\_182\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 44 0 0 0 0 44 60 0 0 0 0

chr7 134719139 134719313 AMPL6910053118 GCAGAGAATAGGAGACCAAATCAAGTAT CGTGTGGCACAAAACACGTATT GCAGAGAAUAGGAGACCAAATCAAGUAT CGTGUGGCACAAAACACGTAUT TAGGAACAACCCAGGCCAAGATGGGCGCCATTATTTCTCTCTTACATGGACATTTCAATTTCCACACAACAAAGATACCTGCTACTTTGCTCATTGCTATCCATACACTTACACCAACCTGCAAGAATACCTTTCTGGCATCAATAATGATCCAGTACGGTCAAAGTTTTGTAA 46 44 3 4 1 71 494.5 580.5 1138 522 616 2 IAD48162\_93\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 56 0 0 0 0 44 40 0 1075 86 2

chr11 1272579 1272710 AMPL7154567231 CGGATCCTCACTGAGCTGAC CTGTTCCCAGAGTGGAGGAG CGGATCCUCACTGAGCUGAC CTGTUCCCAGAGUGGAGGAG ACAACAGCCACTACAACTGCAGCCACTGGATCCACGGCCACCCTGTCCTCCACCCCAGGGACCACCTGGATCCTCACAGAGCCGAGCACTATAGCCACCGTGATGGTGCCCACCGGTTCCACGGCCACCGC 26 24 4 3 1 85 17 20 701 350 351 1 IAD75762\_182\_primers\_U.txt 0.2083334 0.125 1 1 0.3743056667 0.1 0 0 0 44 40 0 0 0 0 44 40 0 37 3 0

chrX 107863515 107863700 AMPL7153077547 GGTTTACATGGAATACCAGGAGAGAAG TGGGAATTATCTACCAGAGTCGTATTAGTT GGUTTACATGGAAUACCAGGAGAGAAG TGGGAATTATCUACCAGAGTCGTATTAGUT GGGATCCAGGACCTCCTGGACTTGATGTTCCAGGACCCCCAGGTGAAAGAGGCAGTCCAGGGATCCCCGGAGCACCTGGTCCTATAGGACCTCCAGGATCACCAGGGCTTCCAGGAAAAGCAGGTGCCTCTGGATTTCCAGGTAATTTGTTTAAAGTTTTCTCTGATTTGGATTAAGGAAATTAA 40 46 3 7 1 95 276 227 543 300 243 1 IAD50452\_124\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 54 0 0 0 0 0 0 0 503 49 1

chr5 172662873 172663042 AMPL7153410511 GAGTTGCTGCCTCCTACAGTA GGATCGATGGCCTCCAAACAG GAGTTGCUGCCTCCTACAGUA GGATCGAUGGCCUCCAAACAG tgttatgcacagcacaactccagggggcatcagtcacTGCCAGTACCCTCCCAGGGAAATGCCTCTCCCCTTAATAATGAAATAAATCAGGAATCCCAGCTGGTAAGCTCAGCTTCCCAGGAGACACCTGTCTTGTGGAGTGCCCCAGCTACCAGCCACCTTGTTTCCC 36 24 5 3 1 1000 91 2090.5 134.5 321 777 2 IAD49353\_124\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 42 0 0 0 0 44 42 0 2181.5 1999.5 2

chr1 17326638 17326789 AMPL7153268579 GGAGTCCACCCACTCTTCCT ACAGCAAAGCCAGACTCTAAGG GGAGUCCACCCACTCTUCCT ACAGCAAAGCCAGACUCUAAGG TGCAGGCAGGCAGGAGAGGAGCTCAGCTAGGTGGGGCCAGCCCCAGCCATGCCCCCCCACCCTCCCACTCCTGCCCCCGCCCCCTGGGCCCTAGCTCCTCACCTCCCCCTGGCCGGCACACGCACACCCGCATGGACAACTTGACCATGTC 36 46 3 2 1 108 0 5 10 2.5 7.5 2 IAD50814\_124\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 40 0 0 0 0 44 42 0 5 5 0

chr11 108127009 108127118 AMPL7154368972 GTGTCCTTGGCTGCTACTGTT GTCTTCCAAACAAATGTAATAATTTTCACAGGA GTGTCCTUGGCTGCTACTGUT GTCTTCCAAACAAAUGTAATAATTTUCACAGGA CATGGGTGTAATAGCTGAAGAGGAAGCATATAAGTCAGAATTATTCCAGAAAGCCAAGGTAGGAGAATTTATACTAATAAAGTTTCGGATAAATTTGAATGAAATGTAT 36 38 7 6 1 35 255 245.5 570 271 299 2 IAD93167\_182\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 42 0 0 0 0 0 0 0 500.5 9.5 1

chr4 154259203 154259349 AMPL7154512355 AACTTTAGTCTCCAGAACTAAACAAGTCC GTCAGTGCTAAGGATTCACAGATACT AACTTTAGTCUCCAGAACTAAACAAGUCC GTCAGTGCUAAGGATTCACAGAUACT TAAGTTTCCTTATTTTAATTTACTGTGACTAGATTTGAAGCAAATAAATACTCCAGATCCATGCAGCTAGAACACACTTGCTTCCACTACTAAATATACAGGGTATGTCCTAACATGGAGTTAACTGGAATAGCAGTACACTAGCA 42 36 5 5 1 53 499 501 1067 520 547 1 IAD75017\_236\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 58 0 0 0 0 44 52 0 1000 2 2

chr1 225765708 225765884 SP\_74.6730 AGAGAGAGAGCTTGAGAGAGAACTC CCTGCTGAGGGCTGTATGAC AGAGAGAGAGCUTGAGAGAGAACUC CCTGCUGAGGGCTGTAUGAC GTGACTCAGGCGGTAAAAAGAACCTGTCCCTATCTGCAACATACCTGGAGACAGAGAATAATAAAGACAATTAGAATGCACAATTTCCATATTCTTAGAACCATAAGAGAGACAGAGAAACTTGTAAAACTTACAAAAGCTCTGGAGACCGAAAAAAATAAAAAGAAACATTAACA 34 32 2 5 1 62 0 0 0 0 0 2 WG00042.3.20140613\_primers\_U.txt 1 1 0.8 0.5 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

chr7 103197449 103197656 AMPL7153093065 CCGTTATTATAAGGTTGCCAGAGTCT GCCTAAAGATTCAGCTAAGAACATACCATT CCGTTATTATAAGGUTGCCAGAGUCT GCCTAAAGATTCAGCUAAGAACATACCAUT AATCTTGTAGCATTGGTTTGGGCAGTGTATGGCAAGGGAACATTGATGAAAAGTATATTCGTTGTTTGAGGAAAGTAAAATTCATCCATCAGGTGCCAAGTGATTCCTCCACTGATGGAGAATTGTAACAGAATAGAGTGAGATCTCTCTGGGGTACCTAGGAAGAAGATAACACAGGTATAAAACATACTGTGATAAAAATGGGGA 38 44 5 5 1 82 115.5 389.5 1047 557 490 2 IAD59467\_182\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 52 0 0 0 0 0 0 0 505 274 1

chr1 155204450 155204662 AMPL7154789786 CAGCTTTCCTAGTCTCTTCTTTTCCT TGTGAGCTTACAGCGACGTAAG CAGCTTTCCUAGTCTCTTCTTTUCCT TGTGAGCTUACAGCGACGUAAG ACCCTCAGCCCTGATCTTGTGTTTGTACGGACAGTGAGCTCACCCTAGGCCTGGACCCAGGCCCAGTTTCCAAAGCAAGCAGCACACAGCGCATGTTCACATAAGCATGGGGGCTGGGGGGACACTGGGGCTTACTGATCTTTTTCTAGGGGCCTCCAGCCCCTGGCACCACCTAGAGGGGAAAGTGAGTCACCCAAACCATTGCCCCTGGG 32 30 6 3 1 124 0 0 0 0 0 1 IAD80412\_182\_primers\_U.txt 0.5 0.5 0.5 0.5 0.5 0.5 0 0 0 44 52 0 0 0 0 44 44 0 0 0 0

chr12 49426609 49426835 AMPL7154632996 GTTGAAACTGCTGCTGTTGTTGT GCAGAGTCTGATGTCACACAGT GTTGAAACTGCUGCTGTTGTUGT GCAGAGUCTGATGUCACACAGT gctgttgctgttgtagctgctgttgctgctgttgaagctgttgctgctgctgttgttgaagctgctgctgctgttgctgctgttgaagctgttgctgctgaagttgctgttgctgttgtagctgctgctgctgctgctgctgaagttgctgttgctgttgcagctgctgctgctgctgAAGCTGCTGTAAAGAGCCCATGGGCTGAGCGCTCAGTTTGGGCTGCCC 32 24 6 4 1 125 0 0 107 43 64 1 IAD72320\_182\_primers\_U.txt 0.8333333333 0.5 1 1 0.5980616429 0.0384615 0 0 0 44 46 0 0 0 0 44 44 0 0 0 0

chr16 2103240 2103374 TSC2\_3.18411 GGGCTCTCAGTCACAAGCC CTCCGGCTGCAACAGATCC GGGCUCTCAGUCACAAGCC CTCCGGCUGCAACAGAUCC CCGTTGTTCCTCCCTGTCCTCCGCTCACGGCACTGCTCCAGTTGCCGGGGCCAGGGTTCTTGGAGAGCACATCCTCACCGCTGTCCCCTCTGCTGGTGACAGCACGCAGTGGAAGCACTCTGGAAGGCGGTCGC 26 26 3 3 1 88 244 264 527 249 278 1 WG\_IAD68410.20150216\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 44 38 0 508 20 1

chrX 76944212 76944425 AMPL7153071976 TAGTAGAAGTCTTCCAAGGGCAGAT AAATGTGTGAATAATAGCCACTCCTTTCT TAGUAGAAGTCTUCCAAGGGCAGAT AAATGTGTGAATAAUAGCCACTCCTTUCT ccattttcatctttcttcaagactgtgccctcaaaggcctggtatatggtaagcattcaaatatttacggtatgaaATATCAACAGATCATTACATACCTTACAAATAAGAACTTGCAATGAAGGGTGTCTATAAATGGAATCTTTTTGAAAATGATTGACCTGTTGTCCACAAGCAGTGCAGCTCACAATCCCATGAAGCCCATCTTCTAGG 38 34 3 7 1 81 0 0 0 0 0 2 IAD93305\_183\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

chrY 6262097 6262320 AMPL7158191683 GTGCAAATAGTGGAATGTAGGGATTCA GGAGAGACAATAGCAATCCTGTCT GTGCAAATAGUGGAATGTAGGGATUCA GGAGAGACAAUAGCAATCCTGUCT TTGGAAGCATCTTCTGTGTCATTTGTCTTCACCTTATTTGCAGGTGAAGTTGTGAGACCCCATCCACCCCTCACAAGATTGTATCCCCACCCTGTCTGACCTTACTGCTGCTCAAACTATCTGTCCAAGGATGAAAACCCAGGACAAAGGAGGAGTAACCCTCATGATGTGAAGCACGTGTTCACCTGTGAATATAACCTGAGGTAAATTCAAGGGTTGTTGT 38 30 6 4 1 103 0 0 0 0 0 1 IAD69405\_185\_primers\_U.txt 0.3527776667 0.2 0.3666666 0.25 0.2967592222 0.1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

chr8 3267006 3267183 AMPL7154566311 CTGCTGACAGGTGATAACTCTCTC GCCACGTATTTACTTTCTAAGTTGTAGAGA CTGCTGACAGGUGATAACTCTCUC GCCACGTATTUACTTTCTAAGTTGUAGAGA CCCACCAGCTCAAAGGCCGCCGGGCATTCAAAGGTGAGTGTATCTCCATGGAGGAAACTGCTGCCCGTCCGCTTCCCATAGGCGGGGATTCCAGGATCCCCACACCCTCCCTTTTCAATTTCTGAAAATGGAAAAACAAATGAACCCTTAAAAAAACACACACAAGGAATATTTTTA 36 34 7 6 1 86 276 210 604 359.5 244.5 2 IAD57719\_182\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 48 0 0 0 0 0 0 0 486 66 1

chr1 201046933 201047136 AMPL7153568569 ACAGATCCCAGACCTCAGGAAAT CGCCAGTACTTCATGTCTATCTTCA ACAGAUCCCAGACCUCAGGAAAT CGCCAGTACUTCATGTCTATCTUCA AGATGGGTGTAGACCAGACCAGCCCGTGGTGCCTGCCGGGGACCCGGGAGTGCCAGCCGACCCCGGCACTCACTTGGTGATCTTGAAGATCCTCAGGAGGCGGATGCAGCGGAGCACGGAGATGCCCAGGGGTGTCATGGCACCCGACTCCACCAGCAGGATCTCCAGGATACCGCTACACACCACGAAGCAGTCGAAGCGGT 28 32 2 7 1 131 131 365 544 132 412 1 IAD59841\_185\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 44 50 0 496 234 1

chr1 215901588 215901753 AMPLP658099817 GTGTTAATGACCACAGACTCTCCAC GTTTTGAAGTGTGCAGCTGTCA GTGTTAAUGACCACAGACTCUCCAC GTTTTGAAGUGTGCAGCTGUCA GAACCCTTGGAGTTACAGGCTCTGACCCGATATTCGTAGAGTGTGAAAGGCCTCAGGGTGTCTCCTTCATCCATAAATTCAAGGGCTCCTTCTGACCAGACAAATAAAACAGACTCCTCTTCAATGCCAGCAGGGCGTCTGAAAGGAAACCAAGCAGGCAACCAG 38 30 5 5 1 0 1208 304.5 282 619 322 2 IAD78091\_236\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 50 0 0 0 0 0 0 0 1512.5 903.5 2

chr11 46900359 46900569 AMPL7154443738 CCTCTAGAAGCAGCAGGACTCAT CCAGTGTCTACACCATGTGCTATG CCTCUAGAAGCAGCAGGACUCAT CCAGTGTCUACACCATGTGCTAUG GTTTCTCAGACCACATTGGAGCCCATCTGCAAGGAAGGAAGAGAGCCATTGCCCCCTCCCAGAGAGGCTGCATCTAGATCTGTGATGCTTTCACTCACCTGGTGAGCAGGTCTTGCCATCAGACAGCAGGTTGATGCCTGTGGGGCAGGTACAGCTGAATCCGCTTGGATTTGGGGACCTAAGACACAGGTGGCTACAGCCGCCATTCTC 44 38 3 7 1 117 220.5 290.5 618.5 272.5 346 2 IAD85185\_182\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 44 48 0 511 70 1

chr2 39499434 39499616 AMPL7156325577 GGATGTACCCTTACCTTGGCAGTA ACAATTGCTTGCTATCAATATCTGGTAAGT GGATGTACCCUTACCTTGGCAGUA ACAATTGCTTGCUATCAATATCTGGUAAGT TCTGTCAGGGAGTTTGTGTGCTGGAATAGCAACAGGTAACTTTTGCATTTGTCTTGCATAATCAAAAAGCCCTGGTAAATTATGGGAATAAAGCTGAGAAGCTTTACCTATAAAGAAAAACAGATATGACATAAAAGCTAATAATAAATAGTAACAATTGTAAGGTATTTAAAAACTAATAT 34 34 5 8 1 56 176.5 308.5 757 349.5 407.5 2 IAD90522\_185\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 48 0 0 0 0 44 60 0 485 132 1

chr11 101323654 101323869 AMPL7153230195 TCAGAAAATAATATGGCTTCAAGTGGACA CACTAGTTTTTCCGCATTGCGTATTTA TCAGAAAATAATAUGGCTTCAAGUGGACA CACTAGTTTTUCCGCATTGCGTATTUA ATAAATATGAATTTCTAAGGAAGTCTTCGCATTATCTATTGGTTTCCTCTTGATTTGGTTCCATGGATAATTTCTCTCCAAGTTCTCTAATAAGTTCTGCTAGGTCTTCTGTATTCTGAGATTTTTCTTCAAGGAGTTCATAGCGGAGACTTGAGATGTCCTGCTTAATTTCCTTCAGTTCCCCTTTGAAAGCAAGAGTGATAAGAAGTCAACTA 30 42 5 5 1 78 184 304 623 276 347 1 IAD50452\_124\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 488 120 1

chr5 150922710 150922828 AMPL7156016271 CCTCCATCTTGGGCTTTGATGA GATGAAGGTCAGAACGCAGATGT CCTCCATCTUGGGCTTTGAUGA GATGAAGGUCAGAACGCAGAUGT GAAGTCAAGGGTCTGATTTTCCAATCCCACCAGGCTGTCTTTCACCTTGACCACACCAGTGACTGGGTTAATTTCAATGACATCTTTAACTAGGTCCTCTGGGTTCACTGAGTAGGTG 28 34 5 3 1 55 615 551 1225 638 587 1 IAD92582\_188\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 44 0 0 0 0 44 46 0 1166 64 2

chr4 55953776 55953860 CHP2\_KDR\_7 GGGATGTTAGGCCATATACAGTACCT GCATGGAAGAGGATTCTGGACT GGGATGTUAGGCCATATACAGUACCT GCAUGGAAGAGGATTCUGGACT ATTCCTGCTGTGTTGTCATAATGGAATTTGGGGTCACATACTTCCTCCTCCTCCATACAGGAAACAGGTGAGGTAGGCAGAGAG 38 36 5 3 1 41 250.5 239.5 522 273.5 248.5 2 WG00029\_CHP2.20131216\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 490 11 1

chr2 238242029 238242254 AMPL7153031984 GCTAAGACTTAGAACCCAGGAAGTT GCAGGCAACCTTATATCAGTCACT GCTAAGACTUAGAACCCAGGAAGUT GCAGGCAACCUTATATCAGUCACT AATTGGAATCAAGATGGGTATTTTCTTAGTGCCATTAATGGACCTAATAGTTTCACAACTCACCTGTTTCAGTGAGAGCCAATGGTTCTGTGCTCACCATTAGATTGATGGTTGAACTAGAAGCTGACCTTGCTGGCTGTGGAGGTGGGGGCTGAGATTTCTCTATAAAAGAAAAATATATGCAACTCGTAGGTAAATCAGAAACAGGAGGGCTTGGGAATCCTT 40 34 3 4 1 94 0.5 0 1 0.5 0.5 2 IAD51407\_124\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0.5 0.5 0

chr11 46337716 46337877 AMPL7153146674 GCAGGAGGTGACCTTTCCTATC CTTGTAAGGTCTGGAGATCTTGTTGG GCAGGAGGUGACCTTTCCTAUC CTTGTAAGGTCUGGAGATCTTGTUGG TGACTGAAACGGGCACCTGGCGTGGAGGCCAAGTCTGGAGCCAGCCCCCTAGGAGAGCTCCAGGAGGCAGAGATGCCTGCGGGGTCAAAGCCTGCCAGCTGACTGCTGTGCCCTCCTCAGGACCCTGCTCCAGCAGCTGCAGAAACTCCAGACTCTGGTCA 32 32 4 7 1 102 253.5 243 551.5 283 268.5 2 IAD52217\_124\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 44 50 0 496.5 10.5 1

chr1 120484223 120484387 AMPL7153103210 CCTGGCACTTGCAAGTGTAACT GCTACTCTTCAGAGGTCTAATTCTTTTGT CCTGGCACUTGCAAGTGUAACT GCTACTCTUCAGAGGTCTAATTCTTTUGT TTGACGTAGTCAGAGCAGGTCCCTCCATTCTTACAGGGTTCACTCAGACACTCATTCATGTCTGTCTGGCACTTATCCCCAGTGAAACCCGGAAGGCAGAGGCAGGAGAAAGTATTCACTCCATCCATACAGGAACCTCCATTCTGGCAAGGATCTAAGCCATT 28 46 4 7 1 82 245 246.5 577.5 309.5 268 2 IAD49670\_124\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 44 0 0 0 0 0 0 0 491.5 1.5 1

chr10 124214349 124214571 AMPL7153390871 TGGTTCCTGTGTCCTTCATTTCC CACTCCAGAATTTCTGATTCAATAGGTCT TGGTTCCTGUGTCCTTCATTUCC CACTCCAGAATTUCTGATTCAATAGGUCT CTCTGCGAGAGTCTGTGCTGGACCCTGGAGTTGGTGGAGAAGGAGCCAGTGACAAGCAGAGGAGCAAACTGTCTTTATCACACTCCATGATCCCAGCTGCTAAAATCCACACTGAGCTCTGCTTACCAGCCTTCTTCTCTCCTGCTGGAACCCAGAGGAGGTTccagcagcctcagcaccacctgacactggtaagaaatgcagatgatcaggccttacccc 28 36 6 6 1 120 288 217 639 316 323 1 IAD53091\_133\_primers\_U.txt 1 1 1 1 0.8 0.5 0 0 0 0 0 0 0 0 0 0 0 0 505 71 1

chr7 99264338 99264659 AMPL7155255368 CATCTAAGCACAAAACAGATCAGTACCT TAGGCCCAGTGGGATTTATGAAAAG CATCUAAGCACAAAACAGATCAGUACCT TAGGCCCAGUGGGATTTAUGAAAAG TAGTTAAATGTGCAGACTCAAGTCCCAGAAGGATATGGCTTTCTCCAGCATGGAGCAGTAAGTGACATTTTGTAATGAATTTTGTGATGTCTTTTCTGTACATAAAGATAAAAGACCATTTTTAGGAAGCTCGAACTCAGTGGACTACCCCTTGGAAACGGACTGTGATCTTACTTTCTACCTGTCCCCAGATTCATTCTTTACATTTCTAATTAAGACTCATCTTATTTTCATACCTCCTTGAGTTTTCCGCTGGTGAAGGTTGGAGACAGCAATGACCGTATTCTCTTCCATTCTTCATCCTCAGCTAAAGAGATGGCA 50 30 4 3 0 129 1 2 545 222 323 1 IAD67569\_196\_primers\_U.txt 1 1 1 1 0.6388888333 0.333333 0 0 0 0 0 0 0 0 0 0 0 0 3 1 0

chr11 89010941 89011255 AMPL7156686598 TCAGTTGTACTGCTTGGATTTCCA TGGAAGTATGCGACAAATTCAAGGAA TCAGTTGTACUGCTTGGATTUCCA TGGAAGTAUGCGACAAATUCAAGGAA acatcatctattttcctggacatcattttctcactgatttctttatccccctgatgcgtgcatatccaccaactcctactcttcctcagtcccttctctgcaacgaaatctgtgtggtcttttacaaatgataatctgttcgtgttatcattcaccttcccagatacaaacagtgactttctgttaggaaaaaaacacaaatctccctaacatggcctctgctacccttcatgatttggcctcagttcaccttcctagcctcatctggagctatttgctccttgatccctatagacatattggtcaatttttaa 28 26 5 3 1 130 0 0 347 143 204 1 IAD90086\_197\_primers\_U.txt 0.8333333333 0.5 0.75 0.5 0.7857142857 0.5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

chr10 55591001 55591168 AMPLP657860416 TGCACCATCAATATTTTACAACGCAAA ACCAGCATTAAAAAGAGAGGAGAAAGTC TGCACCAUCAATATTTUACAACGCAAA ACCAGCATUAAAAAGAGAGGAGAAAGUC CCATGTTACCAGAGATGGTTTTCTGCAATGACTTCTGAGGAACTATCCAGGTTTACCATCCTTGAATACTTACTGTCTGTAGCTGACCAAAACCACCAAGATGGCAGGAATGCAGCAGAGGATGATGATGAAGGCCAGAGCCAACAAGGCCCCTTCTGTGTATCCTA 28 46 3 2 1 0 1009 227 288 558 253 2 IAD78091\_236\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 44 54 0 1236 782 2

chr15 90208915 90209150 AMPL5136627054 CCCTGCGCTTTGGCTTCT CAGGCTGTCGCTGATGGA CCCTGCGCUTTGGCTUCT CAGGCTGUCGCTGAUGGA GCGGGGCACGGCCGGGAAGCCCGGGCGCGGCGCTGCGGGCGTGGCGACTTCGTCCTCCAggcccgggccggggggcgcgccggggcTCTGCGCGCTGCGCAGGCTGCGGCGGGGCTGTGCGAGAcgcggggcgggctccgggccggcggacggcgccccAGACGCTCTGCGCTCCGCCTCCCGGCGCTCGACCTCGGCTGGTGGGTTGTCGATGTCCCGGAATTCGCTCTCGGGC 30 24 3 4 1 191 0 0 0 0 0 2 IAD42964\_95\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 36 0 0 0 0 44 36 0 0 0 0

chr15 90627368 90627555 AMPL7153002228 GGGAAACACACATATGCTTTTAAAAACATC TGAACGAGCACTTCCTGAACAC GGGAAACACACAUATGCTTTTAAAAACAUC TGAACGAGCACUTCCUGAACAC GGCTTATAAAAAAACATCCCCTAGAAAGGCCTCCAGAGAGGGGCTGTGAGGCTCACCCTCTGCCGCGCTCAGGAGGACCCGCCGGCTCAGCCCTGGCCCCTCCACTGCAGCCATGGGTGGCGCCTCCCCCTACTGCCTGCCCAGGGCTCTGTCCAGGTTGCTCTTGATGGTGTCGAGGAAGTCCGTG 36 34 4 2 1 120 259 232 529 282 247 1 IAD72320\_182\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 44 44 0 491 27 1

chr7 107356704 107356772 AMPL7157535380 AGTCTATAGAAATGATCATTGCATGGAGG CATTTTAATCACCATGGTTATGTAAGCACA AGTCTATAGAAAUGATCATTGCAUGGAGG CATTTTAATCACCAUGGTTATGUAAGCACA ATGTATAGGTATGATCTGTGTAAAATCTGACATAAAAACAGTGCTATTCTGAGTGAAAATTTTTTTGA 30 36 7 6 1 20 32.5 0 40.5 40 0.5 2 IAD67652\_152\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 54 0 0 0 0 44 60 0 32.5 32.5 0

chr1 17282517 17282713 AMPL7153906871 GAAGCTTGCCAATGAGGACAAG GGGTAGAAACGTAATTCCAGAAAGG GAAGCUTGCCAAUGAGGACAAG GGGUAGAAACGTAATUCCAGAAAGG AGCAGAAGCTGGCACTCCTAGAGGAGGCACGGACAGCTGTGGGCAAGGAGGCCGGGGAGCTGCGAACTGGGCTGCAGGAGGTGGAGCGCTCACGGCTGGAGGCTCGGCGGGAGCTGCAGGAGCTCCGGCGTCAGGTACTCTCCCTGTGCCACCCCTTAGCCTGGGGcttgctgtgtgccccgggccaatagctccc 28 28 2 3 1 135 269 238 540 280 260 1 IAD93779\_182\_primers\_U.txt 0.75 0.5 1 1 0.8333333333 0.5 0 0 0 44 44 0 0 0 0 0 0 0 507 31 1

chr22 30060918 30061120 AMPL7153068430 TGGTTGCGCATTTGTGGAATTT CTTCACAAGATGTCACTCTGATATCCTTT TGGTTGCGCAUTTGTGGAATUT CTTCACAAGATGUCACTCTGATATCCTUT CAATTGCTGGTAACATTCCAGGCTGTCGGACTGAAACTGTGTTCTGCTTCATTCTTCCAGTTTACTATTAAACCACTGGATAAGAAAATTGATGTCTTCAAGTTTAACTCCTCAAAGCTTCGTGTTAATAAGCTGGTAAGTTGAGATCCTGGTTTTCATTACTGATAATGGTAGCTTTTCTGAGAATTGAATACTTCTTTTT 32 40 4 8 1 74 253.5 248.5 649.5 344.5 305 2 IAD59586\_182\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 502 5 1

chr2 26950927 26951161 KCNK3\_2.38454 AGTACGTGGCCTTCAGCTTC GCACATGGACTGGAAGTGCA AGTACGUGGCCTTCAGCTUC GCACAUGGACTGGAAGUGCA TCTACATCCTTACGGGCCTCACGGTCATCGGCGCCTTCCTCAACCTCGTGGTGCTGCGCTTCATGACCATGAACGCCGAGGACGAGAAGCGCGACGCCGAGCACCGCGCGCTGCTCACGCGCAACGGGCAGGCGGGCGGCGGCGGAGGGGGTGGCAGCGCGCACACTACGGACACCGCCTCATCCACGGCGGCAGCGGGCGGCGGCGGCTTCCGCAACGTCTACGCGGAGGTGC 36 32 4 3 1 167 30.5 1.5 472 265 207 2 IAD53887\_WG.20140521\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 40 0 0 0 0 44 40 0 32 29 0

chr10 131565711 131565794 AMPL6611858178 TGTGATGGCATTCTCCACTCAG CCTTTTTGGCAGGTAGGAAACAA TGTGATGGCAUTCTCCACUCAG CCTTTUTGGCAGGUAGGAAACAA GTTCCTAGCATCCCACACCCAGGTCTCACTGAAAGAAAGGGGAACAGGCCATGGCAGTCAGTGCTTACAGAGGTTTTCTAGCT 30 24 5 2 1 43 282.5 219.5 516.5 290.5 226 2 IAD46485\_87\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 44 0 0 0 0 0 0 0 502 63 1

chr16 2134781 2135007 AMPL7153043463 GGAACCTGGTGCCTCACTT CTCATTGGGCAGCAGGATTG GGAACCTGGUGCCTCACUT CTCATUGGGCAGCAGGATUG CCCCAGGCCGAGCGGGCTGGGGTGGGGTCCTCGCCTGTGCCCTAGGGCTGGCTGGAACCCCTGGGAGGGCGGTGGAGTGGGAGATGGCCAGGCTCTGTGTTCCTCCCTGTGGGCTGTGGCTGCCCTGGCCAGGCCCTCACCTGGGTGCCCACCATCCCCTCCCTGTGCAGTTTCGTGTTCCTGCAGCTCTACCATTCCCCCTTCTTTGGCGACGAGTCAAACAAGC 30 40 4 3 1 153 250 238.5 577.5 289.5 288 2 IAD50465\_124\_primers\_U.txt 1 1 1 1 1 1 1 38 38 0 0 0 0 0 0 44 40 0 488.5 11.5 1

chr1 16263592 16263817 AMPL7153212114 TGTGGCCCTTTGGGTCATT GGCTGCTCTACTCCCGTCT TGTGGCCCUTTGGGTCAUT GGCTGCTCUACTCCCGUCT GTTGGTCTCAGGGGCTTGTGCACAACAGACTGACTCTGTCCCTTTGCCTTCCTTCCCTACACCAGGGCCCTCCTCCTGAAGGTGAGCCCCTGCAGCCTCCTCAGCCTGTGCAGTCCACACAGCCTGCCCAGCCTGCACCACCCTGCCCGCCCTCCCAGCTCGGTCAGCCCGGCCAGCCACCAAGCAGCAAGATGCCTCAAGTGTCCCAGGAGGCAAAGGGGACCC 28 28 4 5 1 146 140 371 699 247 452 1 IAD91552\_182\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 44 38 0 511 231 1

chr1 17313454 17313687 AMPL7153268540 CTGTTCAGAGGCACGAACCT ACAGTGGCAGTGCTCATGAG CUGTUCAGAGGCACGAACCT ACAGTGGCAGUGCTCAUGAG GGGGTACAGGGATGGGGGTCAGGGAACGAACGTGGGGTGGACAGGGAAGGGGCGGGATGGGGGTGGTCAGTCAGCTCCCTACTCACCATGGCTGGGCCAGGGTCAGGAAGTAGCCCCCTAGCTGCACGCCGGTCACCAGGACCATCTGCAGCAGCAGGCTGCTGAGCACGGGCACGCTGAGCAGCGCCCCCGGTGGCCGCACCCGTCCCAGGACCAGCGCTGGCCCCGTGCGG 48 32 2 4 1 165 34 3 171 105 66 1 IAD70128\_182\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 40 0 0 0 0 0 0 0 37 31 0

chrX 70347781 70348008 AMPL7154716420 GGTGAAGAACACCATCTACTGCA TCAGCCCTCCCTATCTCAGATG GGTGAAGAACACCAUCTACUGCA TCAGCCCUCCCTATCTCAGAUG CGTGGAGCCATCGGAATCAAATATGCGCTGGGCACCTGAGTTCATGATCGACACTCTAGAGAACCCTGCAGCTCACACCTTCACCTACACGGGGCTAGGCAAGAGTCTTAGTGAGAACCCTGCTAACCGCTACAGCTTTGTCTGCAATGCCCTTATGCACGTCTGTGTGGGGCACCATGATCCCGATAGGTATGGGGTGTACTGAGTGAGGAAGGGCACCATGCCCC 42 36 4 5 1 125 213 280 600 293.5 306.5 2 IAD83650\_182\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 46 0 0 0 0 0 0 0 493 67 1

chr1 36941161 36941370 AMPL7160535910 GCTCCCAGTCTCCACAGAATCT CATATCTTGAAGGGTGAGACAGGAA GCTCCCAGUCTCCACAGAAUCT CATAUCTTGAAGGGUGAGACAGGAA TGGCTCCGGGTCCAGATGGCTGCAGTTCTGCTTGATGATGCAGGAGGCTGTGATGGGATCCCCCAGGTGGACGATGGGGGCTGAGACACTGATGTGCCCGCACTCCTCCAGACCTGGGGTGGAAGAGAATGGGCCAGGAACGACGCCTCTGCCtagcagagctgggctataatctaggcctttgtactcctagACTCAGAGGCCTCACC 30 30 4 4 1 126 300 200 565 328 237 1 IAD89639\_236\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 500 100 1

chr16 88788990 88789199 PIEZO1\_17.153489 GGGTCACCCCCGCACCTA GTCCCTGCTCTGCCTGACTA GGGUCACCCCCGCACCUA GTCCCTGCUCTGCCTGACUA CTGGACACGGTGCTTGGGGCATTGGGGGCCTCGGTGGGGCCTGGCAGCGTGGCCTCGGCCTGGCTTGTGTACAGCTGATCCAGCACGCCCCTGTGCACTTCGCCGCCCTGCAGGGCACAGCAGGGGGCTCAGGGCTGCGTCCAGCTCTTGTCCCCACACGGGGTTTCGTGCAGTGGGCGCGGGACTAGGCTGTTAAGCAGGCAGGGGCG 44 30 2 6 1 146 235 254 524 256 268 1 WG\_IAD65791.20150710\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 36 0 0 0 0 0 0 0 489 19 1

chr6 33141716 33141836 AMPL7153732094 CGTGGACCCTACAGAGGGAA GTAATGTTCTCTCTGCTTCATTCCCA CGUGGACCCUACAGAGGGAA GTAATGTTCTCUCTGCTTCATUCCCA AGGAGTTGTCAGAGAAACCCAAATGCCCCCCTCTGGACCTTGAGCCACCTGTTTCTCTCCCCTGCACTCACCGTGGGGCCCCGTTCTCCCCGAGGCCCTGACTTCCCCGACAGGCCCTGG 30 30 2 8 1 78 290.5 210 592.5 360.5 232 2 IAD55055\_124\_primers\_U.txt 1 1 1 1 0.83333325 0.333333 0 0 0 44 40 0 44 46 0 0 0 0 500.5 80.5 1

chr1 157252552 157252719 SP\_53.25445 CTTCCTTCCTCCCTCCTACTACTC TTTCCTTTGTCTTGACTTTAGATAACCTGATTA CTTCCTTCCUCCCTCCTACTACUC TTTCCTTTGTCTTGACUTTAGATAACCTGATUA tgggtgtaaacctgaggatattccagaatatagaggttagagagataagaaagaaactagcaaggaaactaaggagcagcctctaagtagaaggaaaagaatggtgagttgtaattggaggtgaagacagtttcaagggagggtatgttaattgctgctgacacatc 38 44 7 8 1 69 0 0 0 0 0 2 WG00042.3.20140613\_primers\_U.txt 1 1 0.6203703333 0.25 0.8333333333 0.5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

chr2 29543568 29543795 AMPL7153083413 CCCTGAGTCTCCCATCTGTCTA TCGACTTGGCATTGGCATATTTTG CCCTGAGTCUCCCATCTGTCUA TCGACTTGGCAUTGGCATATTTUG GTGGGCATGAAGATGGGCACCAGAGAGAAGGCAGGAGAGCAGTAGTACCTTGGTGGTCCTGGAACCGGGCATCCTTTAGGGTCCTGACCTGCCATTGAGGAGTGTGGGGTGACAGTGTGCCTTGGGTCCAGCCACAGAAGCCATCTTCAAAGTTGCAGTAAAAACCCACAGGCAGTTTCCCTATGGAGAGAGCAGAGAGGCACCATCATTTTCAGGACCACTAAAGG 32 34 7 4 1 123 555 518 1210 597 613 1 IAD77279\_182\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 1073 37 2

chr16 53720364 53720494 AMPL7153173893 TTTAACATACCTTTGATCTGTAGCTTGCT CAAACTACAAGTTCTTACAGAGGCTCTTTA TTTAACATACCTTUGATCTGTAGCTUGCT CAAACTACAAGTTCUTACAGAGGCTCTTUA TTCTCGAAGCTGAAGAAGAGATAACTCAATTTCATTTTCTTTTCTCCTCAACTGAGTTTTCAGGATCTCAGCCAAGTGCTCTAACTCCTCTATCTGGCCTCTTTGTGACTGAATAACGTTTTCTCTGAAA 32 38 7 5 1 52 240 263 548.5 263 285.5 2 IAD49379\_124\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 58 0 0 0 0 0 0 0 503 23 1

chr2 26698236 26698408 AMPL7155401729 GCCCACCCATACCATGGAATC GTGGCTTCTGTTTGTGCATCTG GCCCACCCAUACCATGGAAUC GTGGCTTCUGTTTGTGCATCUG TGGTCATAGATTTCAATGACAATGATGGGCGGATCGTCCCTCAGCTCATGAGCTTCACCATAGAGCTCCAGGTTGTCGAACACCAGCATCTGGTCCCAGGTGGGACACAGGGTCTCATTCAGCACCTGCAGCATGGGATGGGGAGACAGGGGACAAGTGACAGAGGGGGGGG 32 32 3 7 1 98 0 0 0 0 0 1 IAD87983\_185\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 42 0 0 0 0 0 0 0 0 0 0

chr21 36259847 36260069 AMPL7153218836 GTTCCAGTAGTTAATGCCTGTCAGT AAAAATCTGCAGCGTACATTAATGGAT GTTCCAGTAGUTAATGCCTGUCAGT AAAAATCUGCAGCGTACATTAAUGGAT TTTTGCAGGTGAGTTTTGTCTAAAGTCCCAACAGAACACAATTATCTCCCGTAACAAGGCCACTTTTATCATGCAAAACTGGCTTCAGTCCCGAAAAGCAAGAGCTGAGACTTCCAAAGGTAGTGCTACTAATGTATGTGCACGTATATATAAATATATACATATGCTCTACTTCATAAAATATTTACAATACAATCTGTGGAGAATTTAAACACAACAGAA 30 40 6 5 1 79 641.5 630.5 1379.5 704.5 675 2 IAD52176\_124\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 50 0 0 0 0 44 52 0 1272 11 2

chr5 149435462 149435618 AMPL7153009440 CACGATGCTGGGTTTCGAGA GAGCGACGTCTGGTCCTATG CACGAUGCTGGGTTUCGAGA GAGCGACGUCTGGTCCTAUG CCCTTGCCCATTCCTGCACTCTCACCAACCCTCGCTGTGTCCTGGGCACCAAACAGCTTTGTCCACCAGTGGGGCAACCAGAGGAGCCAGCCCCAGGCTCTGCCTGGAGTGGGCCCAGTGGCTCACCAAGTGAGAAGATCTCCCAGAGGAGGATGC 26 28 3 5 1 98 598 496.5 1388.5 733 655.5 2 IAD85185\_182\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 44 40 0 1094.5 101.5 2

chr17 41199644 41199740 223552235 AAGGACCCCATATAGCACAGGTA AGTCCTACTTTGACACTTTGAATGCTC AAGGACCCCAUATAGCACAGGUA AGTCCTACTTUGACACTTTGAATGCUC ATGCAGGCACCTTACCATGGAAGCCATTGTCCTCTGTCCAGGCATCTGGCTGCACAACCACAATTGGGTGGACACCCTGGATCCCCAGGAAGGAAA 32 40 3 6 1 54 569.5 754 1387.5 606.5 781 2 BioRef\_BRCA\_WG.20130906\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 46 0 0 0 0 0 0 0 1323.5 184.5 2

chr12 88478212 88478402 AMPL7154371493 CATGTACACAAACTTCCAGTTTTACTGAC GCAAGCAAGGTTAAATCAAAAAGAAGAAGT CATGTACACAAACUTCCAGTTTTACUGAC GCAAGCAAGGUTAAAUCAAAAAGAAGAAGT GAGGTGTAATCCAATCACATGCAAGTAACAATTCTTAAATAGAATCATTTGAAAGCAAGAAAAGAAATACCACTTTAGGGTAAAATAATATTTAGCATTTGCTTAAAAAAACTAATGGATAACAGCATAACTCATAATATAATAAAATACCTCTCTGGCTTTTTCTAGAAGACGTTGATACTTCTTTAAT 36 36 5 2 1 53 249 244 536 270 266 1 IAD64229\_194\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 44 60 0 493 5 1

chr19 46280521 46280650 AMPL7156619643 CCAGAAGGTAGGCACTGTCCTTA CCTTTACACCGGATTTCGAAGGT CCAGAAGGUAGGCACTGTCCTUA CCTTUACACCGGATTUCGAAGGT TCCAACTTTATGGAGGGAGCATGGGGAGGTTCCCGCAGCCGAGCAGGGGCCACAGGTACCTACCCCGCCCCCGCTCACCATGGCAGTGAGCCCGTCCTCCACCAAGTCGAAGTTGCATGTGTCGGTGGC 38 30 4 2 1 84 0 0 0 0 0 1 IAD46040\_182\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 46 0 0 0 0 44 46 0 0 0 0

chr14 77770983 77771198 AMPL7153026908 CCTTGAATGTACTGATTTTCAGCTACATTC CTTAAATGTTAGGTTGTACTGAGTCCAGT CCTTGAATGTACUGATTTTCAGCTACATUC CTTAAATGTTAGGUTGTACTGAGUCCAGT CGGAGTGGCAGCCCATTTCCCAAAAGCCATGGTATGGCTAAGACAACTTACCAAAGGTGAGGAGGGCAGCTGTGAGCAGTGCTGCCGAGAGGGACTTGGACAGATCCAGTACAGTGAGGTAGGCAAAGGGGACCAGCCAGGAGCCAAGGAATGCACAGAACTGTGGGAGGAATAGAGAAGCTGTCAAATAACAAGCTGAGCTAGGTCAGCGACCT 40 34 7 7 1 116 0.5 0.5 2.5 1 1.5 2 IAD62265\_182\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0

chrX 76937798 76937888 AMPL7154459358 TTTTTCTTCAGTTCCCTTTTTGCTCT GAGCAAGCATCTCAAAACCAAAACA TTTTTCTTCAGTUCCCTTTTTGCUCT GAGCAAGCAUCUCAAAACCAAAACA CTTTTTATCATCTTCAGAAGTTTCATCGCTCTGGTCTTTCTTTAGGAATTTCTCTGCAATATCAGATAAGCCATCCTGTACTTTTTTACA 30 34 5 2 1 32 260 232 507 262 245 1 IAD70902\_231\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 52 0 0 0 0 44 50 0 492 28 1

chr6 129635761 129635989 AMPL5369006829 TCAGGGTGATTTCTCCCCTAACT GCCTGACTAAAAGACACCAGCA TCAGGGTGAUTTCTCCCCUAACT GCCUGACUAAAAGACACCAGCA GCCGTTATAAACTCTGAGGGTCTCTTGTCTTTCCTCAGGTGAATGTGGAAGGCATCCACTGTGACAGATGCCGGCCTGGCAAATTCGGACTCGATGCCAAGAATCCACTTGGCTGCAGCAGCTGCTATTGCTTCGGCACTACTACCCAGTGCTCTGAAGCAAAAGGACTGATCCGGACGTGGGTGAGTAGGGAACTGCTGAGCCATGTAATGGTATAATGTTAGTTCC 28 40 4 2 1 117 266.5 224.5 537.5 290.5 247 2 IAD44951\_93\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 491 42 1

chr5 145718642 145718806 AMPLP862576123 CAAGCTAGACAAGCCTGATTCCA GTGCCTTAGAGCGGTAATTATGCT CAAGCUAGACAAGCCTGATUCCA GTGCCTUAGAGCGGTAATTAUGCT GTCACCCGCTGCCACCCTGCCAGGAGCGCGAAGATGATGGCCATGAACTCCAAGCAGCCTTTCGGCATGCACCCGGTGCTGCAAGAACCCAAATTCTCCAGTCTGCACTCTGGCTCCGAGGCCATGCGCCGAGTCTGTCTCCCAGCCCCGCAGGTACGTAGTGG 38 36 3 5 1 0 690 337.5 281 690 382 2 IAD78091\_236\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 1027.5 352.5 2

chr1 236900409 236900620 AMPL7153008220 ACAGAGCCGTCCTGTTTACCTA ACTTTCATCCTATCTGAGATGAAAAATGCA ACAGAGCCGUCCTGTTTACCUA ACTTTCATCCTAUCTGAGATGAAAAAUGCA TGTGTTTTACAGGCCGAGACAGCGGCTAACAGGATATGTAAGGTTCTTGCTGTGAATCAAGAGAATGAGAGGCTGATGGAAGAATATGAGAGGCTAGCGAGTGAGGTAAAGGAAACTGGTGACCTGCAGTTCTGTCCATCCTCACGCAGGGGCTGAGGCACAGAGGGTGAAAAAATACTCCGTGGGGGCatatatatatatatatatatTT 30 34 4 7 1 96 8 3.5 20.5 13.5 7 2 IAD50560\_124\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 11.5 4.5 0

chr1 154248026 154248243 AMPL7153159468 GGGAAGGGAAATCTTACTCTTCTACC CTGAGGTGGCAAGAGAAGCTAA GGGAAGGGAAAUCTTACTCTTCUACC CTGAGGUGGCAAGAGAAGCUAA TTGTCCTTTGCTTCTGCCTAGTCTCTTTCATTTAGCCTATTTACGTGTATGACTTTCTTCCTTAGATCCAGAATCACCAAGACCTCCAGCCCTGGATGATGCCTTTTCCATCCTGGACTTATTCCTGGGACGTTGGTTCCGGTCCCGGTAGCCTTGTTAACCCTCAGAGGCCTTCAAGTCCTTTCCACCTCTCACCCATTGCCCACCATTAATAAGC 34 38 5 3 1 106 537 782 1411 601 810 1 IAD91552\_182\_primers\_U.txt 1 1 1 1 0.7857142857 0.5 0 0 0 44 44 0 0 0 0 0 0 0 1319 245 2

chr15 80696856 80697055 AMPL7155731567 CGCCTATCCTCTCCGAGCA CGATTGGGATGCAGATGCC CGCCUATCCTCUCCGAGCA CGATTGGGAUGCAGAUGCC GATGGCAACCCCGGCGGCGGTCAACCCTCCGGGTGAGTAGCGGCCTgggccccgccgcccgccgcagcccgcaggccttgcccggggccggagcggaccaggcgcgccgggcgcccccgggggcgcggAGCCGCAGCTCGGCGCGGTGGGTGGTGGAGCGGCTGTCACTACGCGGCAGCCGCAGCATCAGCACCAGAGC 24 28 4 3 1 159 0 0 1 1 0 1 IAD61275\_182\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

chr1 165386198 165386364 AMPL7153458045 TGACTTTGGGCACCATGACTTC CCTCATCTACACGTGTCGGGATAATA TGACTTUGGGCACCATGACTUC CCTCATCTACACGUGTCGGGATAAUA CGTGTATTGCAGTTGAATGTCCCCTTGCCTAGGAAATGCCTCTCTCCGGACACGAGTTTTGGAACTGAATGTGTCTCACCTTCCCTCTTCATGCCCATGACAAGGCACTTCTGATAGCGACAGTACTGGCAGCGGTTGCGCTGACGCTTGTCAATGAGGCAGTCTT 42 40 3 7 1 86 5.5 18.5 41.5 15.5 26 2 IAD49670\_124\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 44 50 0 24 13 0

chr8 2964053 2964214 AMPL7155309298 GTAGTTTTAGTATCGAACAGTGCATACCTT CCTACATGTGTCACACCTTCACA GTAGTTTTAGTAUCGAACAGTGCATACCUT CCTACATGUGTCACACCTUCACA ACATGTTGGGAGAGAACCCTCAAACTGCAACTGGGAACTGAGCTTGCAAGTCAGAATGTCGGTCCCCACCAAGGTGTACCCGGGGTGGCACTGGTACTTCACAAAATCTCCTAGAAGAGTCAATGCAACAAACCAGGAAATTGTGTGTGACCTTCTGAGTG 46 28 7 5 1 81 630 559.5 1246.5 659.5 587 2 IAD57719\_182\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 60 0 0 0 0 0 0 0 1189.5 70.5 2

chr2 189866923 189867239 AMPL7156587335 GTTTATTGGCTACTCTGCACATTTCC AGGTGTTTTTATTTCCATCTTTCAAAGAGC GTTTATTGGCUACTCTGCACATTUCC AGGTGTTTTUATTTCCATCTTUCAAAGAGC GCTTAAAGGAAAGAAAAGATAAGATGATAAGATGACATTTCCTGCCTAAAGGAGATGACGCACACTTCACTGTGACTAAGGAGGATATTTTTCTCTTCAGGGTGAGAGAGGTGAAACTGGCCCTCCAGGACCTGCTGGTTTCCCTGGTGCTCCTGTAAGTGTGAATATTTATACATACATGTCCCATAGCCCAGGATCTCTATCTTGCTGAAAAATTACAAAAGTATAGTCAAGTTTGGTTTCTAGTCTCATTTTAGCTGCTCATTCCCTATAGGATTATTGTACCCCTATTTTGTTTTACTTTACCCCTATTGTC 34 28 6 5 1 127 0 0 508 245 263 1 IAD72098\_236\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

chr18 2784370 2784478 AMPL7153461764 CTACTGTGATCCTGTCATTTCTAATCTCAG GAATTCGATCTCCATCTCTGGTCA CTACTGTGATCCUGTCATTTCTAATCUCAG GAATTCGATCUCCATCTCTGGUCA AACTTTAAATTATTTCTCCTTTTTTGGAGCAGTTGAAATAAGTTGCTCACTACTTACTATTCACTTATTTACAATAGGTTGTTAAAATTACACACTGTCCTACACTGC 36 32 10 7 1 33 717.5 718 1549.5 748 801.5 2 IAD49633\_124\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 44 46 0 1435.5 0.5 2

chr7 72634708 72634878 AMPL7156890736 GGACACCTTCATCCGTCACATC GTAGATCCAGGCTCAAAGACCA GGACACCTUCATCCGTCACAUC GTAGAUCCAGGCUCAAAGACCA CCCTGCTGGGCTTTGAGAAGCGCTTCGTACCCAGCCAGCACTATGTGAGTAGCTGGTGGAGGGCATCCCGTGGGGGGAATACGGGAGGGACAGCACGGCCACCCTTGCAGTCCCAGGGCCAACCAGCTCCAGTGAGGACTAACGGGGCAGGGTCTTGGGCACCTGGTCCC 34 26 4 3 1 111 0 0 0 0 0 1 IAD63499\_185\_primers\_U.txt 0.333333 0.333333 0.333333 0.333333 0.333333 0.333333 0 0 0 1 44 44 0 0 0 44 44 0 0 0 0

chr12 133252672 133252797 AMPL7153015022 CCGGGTAGTTTCCCAAGTGATAC TGACTTGTGCTGATTGCTAATGAACT CCGGGTAGTUTCCCAAGTGAUAC TGACTTGTGCUGATTGCTAAUGAACT TCCTTACCTCATCGGGTTCATTGAAGACACAAAAGGGGCCTTCATATTCTGGCTTGGGGGTGAACTCAAAATCTTCAATATCTTCTGAAACAATCTCCCTGTTGGTGATGAGGTAGCCCTAGCCA 30 30 4 6 1 0 58 2141.5 325.5 292.5 705 2 IAD85873\_236\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 46 0 0 0 0 0 0 0 2199.5 2083.5 2

chr1 3348471 3348625 AMPL7153418637 TGGGCTTGCAGCATCAGAG TAAGGTGGAATTAAGCACATCTTTAACTTCA TGGGCTUGCAGCAUCAGAG TAAGGTGGAATUAAGCACATCTTTAACTUCA GGCGGCCAAGGCCAGGCTGCTGACAGCAGGCCTTCCCTCTCCCCGGTCATTGGTGCAGGTGTGCTGAGGACCACGAAGGCGGTCTGTTAGCTTTGGAGCCGATGCCGACTTTTGGGAAGGGGCTGGACCTCCGCAGAGCAGCTGAGGAAGCATT 20 42 2 5 1 97 235.5 279 564 253 311 2 IAD50560\_124\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 44 60 0 514.5 43.5 1

chr3 53842652 53842853 AMPL7153470578 GCAGAGAACTTGCTTCACAGCT AGGAGAAGGGAGTGACCTGATG GCAGAGAACUTGCTUCACAGCT AGGAGAAGGGAGUGACCTGAUG TGTGATGCCCTTTGCTTTCCCAGCCCACCGGAGATCCTCCTTCAACTTTGAGTGCCTGCGCCGGCAGAGCAGCCAGGAAGAGGTCCCGTCGTCTCCCATCTTCCCCCATCGCACGGCCCTGCCTCTGCATCTAATGCAGCAACAGGTGAGCGGCCCACCTGGCCTTGCCCCCACACCTAGGGGCACCCCACATAGGACCCC 28 38 2 3 1 129 467 549 1138 555 583 1 IAD66059\_182\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 1016 82 2

chr7 86479664 86479786 GRM3\_4.37317 GACTGAATGTACAGCCAGACACTT CAGTCTGTGTGTGACAACATTCTTC GACTGAATGUACAGCCAGACACUT CAGTCTGTGTGUGACAACATTCTUC CTAGCCAACCTTCTCTTGTAGGTGCAGACGACAACCATGTGCATCTCTGTCAGCCTGAGTGGCTTTGTGGTCTTGGGCTGTTTGTTTGCACCCAAGGTTCACATCATCCTGTTTCAACCCCA 38 34 4 7 1 62 273 224 514 278 236 1 WG\_IAD68410.20150216\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 44 50 0 497 49 1

chr3 37031732 37031849 AMPL7155574617 GAATGTGTACGACAGTTCCAAATTTTAGAA CAGGATTAGGAGGTGTGAGATATTTTAGC GAATGTGTACGACAGUTCCAAATTTUAGAA CAGGATTAGGAGGUGTGAGATATTTUAGC AAATCCATTTCTAGCATCTAACAAAATCTGATACTGTATCATTTTAAAACAAAGTGTTTACTTTAGGCAGGATTTTTTAAAATAAAGCAGCAATACCCACGCAGATAAGACAAAAAA 44 40 5 5 1 34 697 794 1682 805 877 1 IAD46040\_182\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 60 0 0 0 0 44 58 0 1491 97 2

chr10 26409673 26409789 AMPLP808971794 ATGTTGGCAACATTGAATTTTCTTCTGT TGCTTGAAATGGTCCTTATGTGATACTT ATGTTGGCAACAUTGAATTTTCTTCUGT TGCTTGAAATGGUCCTTATGTGATACUT GCAACTGAACACCAGATTGACAAGAGCCACATTTCTAATCATACAGCCCTGGAGAACTGTAAGTTTTATTACCTTCTATTCAAAACTGAAATCTTTCAAATCTTATGACATACCAT 34 36 6 8 1 0 999.5 244 234 498 251 2 IAD78091\_236\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 56 0 0 0 0 0 0 0 1243.5 755.5 2

chr18 28671976 28672124 AMPL7153082952 TTCATTCGTCTTTAAGCCAAACTATACCA CTCGGAGAAGAGAAGTTTTACCATATTACT TTCATTCGTCTUTAAGCCAAACTAUACCA CTCGGAGAAGAGAAGUTTTACCATATUACT atcctttCTGATTTCATATCTTCCCTGGTAATGTTGATTACGTCTGAAGAAAAGATATCATTTCTTCATTTATGTAGCCTTGTATACCTTTGTTTGATGCTCCAAAAAGACAAATATTTTCTTCTTTTCTTGGTTCTCAGTGTTGGAA 32 46 6 4 1 48 218.5 289 608 282 326 2 IAD34879\_124\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 507.5 70.5 1

chr3 165547835 165547904 AMPL7154989642 TCCAAGTTCAAGTAATATGTCTGGCAT CCCAAGAAATTCTTCTGAATGAAGCATT TCCAAGTUCAAGTAATATGTCUGGCAT CCCAAGAAATTCUTCTGAATGAAGCAUT TCAGTGAGAAAATCACCATCCACGGTCGGACCAAAGTTTACTGACAAAGGAGTCCCATAGGGGACAACA 34 36 6 5 1 34 0 7 60 0.5 59.5 2 IAD67652\_152\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 54 0 0 0 0 44 56 0 7 7 0

chr17 71403737 71403907 SP\_417.38193 TCAGTAGCATCCTGAATTAGGAAAGC CCTCAAAAGGAACTAGAAGAAAGCAGAG TCAGTAGCAUCCTGAATUAGGAAAGC CCUCAAAAGGAACUAGAAGAAAGCAGAG ttttagaaatagagatagcgggggcgggggagtctcactatattgcctaggctggtcttgaactcctggcctcaagcaagcctctgcctcatcctcccaaagtgttgggattacaggtgtgatacaccatgcccggccAgaaccaattcattatacgaaaaatttggtaa 26 40 4 2 1 82 0 0 0 0 0 2 WG00042.3.20140613\_primers\_U.txt 1 1 1 1 0.1489116908 3.89196e-05 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

chr4 55592007 55592232 AMPL5112281978 TCCTAGAGTAAGCCAGGGCTTT GAGCCTAAACATCCCCTTAAATTGGA TCCTAGAGUAAGCCAGGGCTUT GAGCCTAAACAUCCCCTTAAATUGGA TTTTCTTCCCTTTAGATGCTCTGCTTCTGTACTGCCAGTGGATGTGCAGACACTAAACTCATCTGGGCCACCGTTTGGAAAGCTAGTGGTTCAGAGTTCTATAGATTCTAGTGCATTCAAGCACAATGGCACGGTTGAATGTAAGGCTTACAACGATGTGGGCAAGACTTCTGCCTATTTTAACTTTGCATTTAAAGGTAACAACAAAGGTATATTTCTTTTTAA 36 32 3 4 1 92 242.5 262.5 554.5 272.5 282 2 IAD48187\_93\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 505 20 1

chr18 19751699 19751897 AMPL1700857242 CGCGTGGGTTCCATGCT GGCGGGCTGGGAGAGTA CGCGUGGGTTCCAUGCT GGCGGGCUGGGAGAGUA CCCGGCCTACCGTACCACCTGCAGGGGTCGGGCAGTGGGCCAGCCAACCAcgcgggcggcgcgggcgcgcaccccggcTGGCCTCAGGCCTCGGCCGACAGCCCTCCATACGGCAGCGGAggcggcgcggctggcggcggggccgcggggcctggcggcgcTGGCTCAGCCGCGGCGCACGTCTCGGCGCGCTTCCCC 26 28 3 2 1 162 0 0 0 0 0 2 IAD42964\_95\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 34 0 0 0 0 44 34 0 0 0 0

chr7 139876325 139876559 AMPL7157392205 GTTGTGGCGACTCTTCGC TCGAGTGCGATATCTGCAAGG GTTGUGGCGACTCTUCGC TCGAGUGCGATATCUGCAAGG CGGGCCAGGCGAGCCCACCGGCTCCCCTCTGGAGCCCGCCCGGCGAACCCGGGGCACCGCGCGCCCCACTGCCCGGCCGGGGGGCTAGGCACCGGGGCCCCCTGAAAGCTGGGCgcggcgcggcggcccggcccgagggaggcgcgggcggccggcggcggcggcggttggtcggtggccggcggtggcggctgcggGGCTGGAGGGGGTTTATTTACCTGCCGTGGAACCAGT 30 24 4 4 1 191 0 0 0.5 0 0.5 2 IAD89694\_182\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

chr9 71844067 71844212 AMPLP861691346 ATTTAGAAACGCACTCTTGTTAGTCCA ACTCTTCTGGATTTCAGTTACAGAGACA ATTTAGAAACGCACUCTTGTTAGUCCA ACTCTTCUGGATTTCAGTUACAGAGACA ATTGATAACAGTAGATGTTTCTTAACCTACAGCTCCTCAACCAAAAGCAGCCCCGAGAACTTTTCTTCGTCCTAGTCCTGAAGATGAAGCAATATATGGGTATGTATTTCCGTCTCTCTTTGTTTTCCCTTCTTCCTTACAGCTC 38 28 5 5 1 0 886.5 423 345.5 886.5 475 2 IAD78091\_236\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 1309.5 463.5 2

chr3 170805025 170805146 AMPL6758478657 AGTAGCTCTATGGTAGAAACCAACCA TCTCAACCCATTCCCAGGAGAT AGUAGCTCTATGGUAGAAACCAACCA TCUCAACCCATUCCCAGGAGAT CAAGTTTCAAGGAGCTTGGCGAAGCCTCATTCTTGAAGAGATCATGGTTTTAGAACCCCAGGAAGGACAGCAGAACTGTCATGTCAGCTGTTGCCCAGCACCTACTTCAGTCCCAGAGTCC 34 32 5 2 1 61 689 664 1527 725 802 2 IAD48279\_93\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 44 40 0 1353 25 2

chr9 135771765 135771908 AMPL7154418755 CAAGTCTTTGCCCAGTTCTGTCT TGGGAGACGACTATGGGAGAAG CAAGTCTTUGCCCAGTTCTGUCT TGGGAGACGACUAUGGGAGAAG TAGGCTCTCAGAAAGGCTACTGGTCATGCCGTCCTCATCACACTGGCTCTCGCTCTTATTACGAAATAACTCTCGAGCCTTCATACCCAGGAAGCTTTTTGAACTGGGAAGTGAGCCCACAGTGGTGGGGATGCTGGCAGACG 36 36 5 2 1 75 491.5 588.5 1188.5 548.5 640 2 IAD59586\_182\_primers\_U.txt 1 1 1 1 1 1 0 0 0 44 46 0 0 0 0 44 44 0 1080 97 2

chr10 122666198 122666426 AMPL7153048130 CAGTATGCAGGTTTCCAGGGAA AGGCAGCACAACTAAGGGAAATT CAGUATGCAGGTTUCCAGGGAA AGGCAGCACAACUAAGGGAAAUT ATGTGTAAATGTCTTTATACCCTTCGATGCTGCTGCCCACCAGTGATGTAAATCACAAAGCATAACTCTTGTTTTGTTCTGTTGAGCAGCATGAGATACTTTGATAGAGCAGCCTTATTTGTGGAAGCTTGCCTCAAGTATGGAGCATTTGAAGTCACTGAGGACACAGATATCCTTTGCAAGGTTGTTTGTAGTGACGAGGAAGAAAGTGACATGCATGGGTTTTGG 26 38 3 2 1 96 706 738 1538 752 786 1 IAD69405\_185\_primers\_U.txt 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 1444 32 2