

Table S1. SOLiD P1 and P2 barcoded adaptors were prepared following the SOLiD protocol (Applied Biosystems, Foster City, CA). Individual stocks of HPLC-purified oligonucleotides (IDT, Coralville, IA) were prepared at 1mM concentration. The adaptors were prepared by mixing equal molar amounts of each correspondent oligonucleotides per barcode with 5X ligase buffer. The mix was hybridized on a PCR machine by running the program: 95°C for 5 min, 72°C for 5 min, 60°C for 5 min, 50°C for 3 min, 40°C for 3 min, 30°C for 3 min, 20°C for 3 min, 10°C for 3 min, and 4°C forever.

Oligo Name	Oligo Sequence	Length
P1 Adaptor-5'-end	ATCACCGACTGCCCATAGAGAGGTT	25
P1 Adaptor-3'-end	CCTCTCTATGGGCAGTCGGTGAT	23
P2 Barcode-1-5'-end	CGCCTTGGCCGTACAGCAGGGGCTTAGAGAATGAGGAACCCGGGGCAGTT	50
P2 Barcode-1-3'-end	CTGCCCCGGGTTCTCATTCTCTAAGCCCCTGCTGTACGGCCAAGGCG	48
P2 Barcode-2-5'-end	CGCCTTGGCCGTACAGCAGGGTGTGAGAGAATGAGGAACCCGGGGCAGTT	50
P2 Barcode-2-3'-end	CTGCCCCGGGTTCTCATTCTCTCACACCCTGCTGTACGGCCAAGGCG	48
P2 Barcode-3-5'-end	CGCCTTGGCCGTACAGCAGAAGGGGAGAGAATGAGGAACCCGGGGCAGTT	50
P2 Barcode-3-3'-end	CTGCCCCGGGTTCTCATTCTCTCCCTTCTGCTGTACGGCCAAGGCG	48
P2 Barcode-4-5'-end	CGCCTTGGCCGTACAGCAGCCGATGAGAGAATGAGGAACCCGGGGCAGTT	50
P2 Barcode-4-3'-end	CTGCCCCGGGTTCTCATTCTCTCATCGGCTGCTGTACGGCCAAGGCG	48
P2 Barcode-5-5'-end	CGCCTTGGCCGTACAGCAGCAACGAAGAGAATGAGGAACCCGGGGCAGTT	50
P2 Barcode-5-3'-end	CTGCCCCGGGTTCTCATTCTCTTCGTTGCTGTACGGCCAAGGCG	48
P2 Barcode-6-5'-end	CGCCTTGGCCGTACAGCAGGTGCCAGAGAATGAGGAACCCGGGGCAGTT	50
P2 Barcode-6-3'-end	CTGCCCCGGGTTCTCATTCTCTGGGCACCTGCTGTACGGCCAAGGCG	48
P2 Barcode-7-5'-end	CGCCTTGGCCGTACAGCAGGTCTGGAGAGAATGAGGAACCCGGGGCAGTT	50
P2 Barcode-7-3'-end	CTGCCCCGGGTTCTCATTCTCTCCAGACCTGCTGTACGGCCAAGGCG	48
P2 Barcode-8-5'-end	CGCCTTGGCCGTACAGCAGACGGAGAGAGAATGAGGAACCCGGGGCAGTT	50
P2 Barcode-8-3'-end	CTGCCCCGGGTTCTCATTCTCTCTCCGTCTGCTGTACGGCCAAGGCG	48
P2 Barcode-9-5'-end	CGCCTTGGCCGTACAGCAGGAAGGGAGAGAATGAGGAACCCGGGGCAGTT	50
P2 Barcode-9-3'-end	CTGCCCCGGGTTCTCATTCTCTCCCTTCTGCTGTACGGCCAAGGCG	48
P2 Barcode-10-5'-end	CGCCTTGGCCGTACAGCAGGACCGCAGAGAATGAGGAACCCGGGGCAGTT	50
P2 Barcode-10-3'-end	CTGCCCCGGGTTCTCATTCTCTGCGGTCCTGCTGTACGGCCAAGGCG	48
P2 Barcode-11-5'-end	CGCCTTGGCCGTACAGCAGCTCAGGAGAGAATGAGGAACCCGGGGCAGTT	50
P2 Barcode-11-3'-end	CTGCCCCGGGTTCTCATTCTCTCTGAGCTGCTGTACGGCCAAGGCG	48
P2 Barcode-12-5'-end	CGCCTTGGCCGTACAGCAGAGCGTTAGAGAATGAGGAACCCGGGGCAGTT	50
P2 Barcode-12-3'-end	CTGCCCCGGGTTCTCATTCTCTAACGCTCTGCTGTACGGCCAAGGCG	48
P2 Barcode-13-5'-end	CGCCTTGGCCGTACAGCAGCGGGTCAGAGAATGAGGAACCCGGGGCAGTT	50
P2 Barcode-13-3'-end	CTGCCCCGGGTTCTCATTCTCTGACCCGCTGCTGTACGGCCAAGGCG	48
P2 Barcode-14-5'-end	CGCCTTGGCCGTACAGCAGCGTCTGAGAGAATGAGGAACCCGGGGCAGTT	50
P2 Barcode-14-3'-end	CTGCCCCGGGTTCTCATTCTCTCAGACGCTGCTGTACGGCCAAGGCG	48
P2 Barcode-15-5'-end	CGCCTTGGCCGTACAGCAGTAGCGTAGAGAATGAGGAACCCGGGGCAGTT	50
P2 Barcode-15-3'-end	CTGCCCCGGGTTCTCATTCTCTACGCTACTGCTGTACGGCCAAGGCG	48
P2 Barcode-16-5'-end	CGCCTTGGCCGTACAGCAGGCGTTTAGAGAATGAGGAACCCGGGGCAGTT	50
P2 Barcode-16-3'-end	CTGCCCCGGGTTCTCATTCTCTAAACGCCTGCTGTACGGCCAAGGCG	48
Primer PCR-1	CCACTACGCCTCCGCTTTCCTCTCTATGGGCAGTCGGTGAT	41
Primer PCR-2	CTGCCCCGGGTTCTCATTCT	21

Table S2. Mitochondrial candidate genes used in sample preparation

ENSEMBL-GENE-ID	ENSEMBL-PEPTIDE-ID	PEPTIDE-SEQUENCE	COUNT
ENSG00000005156	ENSP00000262327	MSLAFKIFFPQTLRALSRKELCLFRKH	949
ENSG00000005156	ENSP00000367787	MSLAFKIFFPQTLRALSRKELCLFRKH	1009
ENSG000000021574	ENSP00000320885	MNSPGGRGKKKGSGGASNPVPPRPPF	616
ENSG000000021574	ENSP00000340817	MNSPGGRGKKKGSGGASNPVPPRPPF	584
ENSG000000023228	ENSP00000233190	MLRIPVRKALVGLSKSPKGCVRTTAT/	727
ENSG000000025708	ENSP00000252029	MAALMTPGTGAPPAPGDFSGEGSQGI	482
ENSG000000025708	ENSP00000379036	MAALMTPGTGAPPAPGDFSGEGSQGI	482
ENSG000000025708	ENSP00000379037	MAALMTPGTGAPPAPGDFSGEGSQGI	482
ENSG000000025708	ENSP00000379038	MAALMTPGTGAPPAPGDFSGEGSQGI	487
ENSG000000029639	ENSP00000356134	MAASGKLSTCRLPPLPTIREIHKLLRLC	346
ENSG000000076248	ENSP00000242576	MIGQKTLYSFFSPSPARKRHAPSPEPA	313
ENSG000000076248	ENSP00000337398	MGVFCLGPWGLGRKL RTPGKGPLQL	304
ENSG000000099817	ENSP00000215587	MDDEEETYRLWKIRKTIMQLCHDRG'	210
ENSG00000104936	ENSP00000291270	MSAEVRLRRLQQLVLDPGFLGLEPLL	629
ENSG00000104936	ENSP00000314954	MGGHFWPEPYTVFMWGWSPWEADSI	609
ENSG00000104936	ENSP00000342201	MSAEVRLRRLQQLVLDPGFLGLEPLL	629
ENSG00000104936	ENSP00000345997	MGGHFWPEPYTVFMWGWSPWEADSI	631
ENSG00000104936	ENSP00000346168	MGGHFWPEPYTVFMWGWSPWEADSI	575
ENSG00000106028	ENSP00000265304	MFRRPVLQVLRQFVRHESETTSLVLI	148
ENSG00000107815	ENSP00000309595	MWVLLRSGYPLRILLPLRGEWMGRR	684
ENSG00000107815	ENSP00000359248	MWVLLRSGYPLRILLPLRGEWMGRR	582
ENSG00000108064	ENSP00000363002	MAFLRSMWGVLSALGRSGAELCTGC	214
ENSG00000108064	ENSP00000363006	MAFLRSMWGVLSALGRSGAELCTGC	246
ENSG00000110025	ENSP00000301886	MSRQAKDDFLRHYTVSDPRTHPKGY'	342
ENSG00000110025	ENSP00000316410	MSRQAKDDFLRHYTVSDPRTHPKGY'	256
ENSG00000110025	ENSP00000366452	MSRQAKDDFLRHYTVSDPRTHPKGY'	342
ENSG00000113580	ENSP00000231509	MDSKESLTPGREENPSSVLAQERGDV	778
ENSG00000113580	ENSP00000343205	MDSKESLTPGREENPSSVLAQERGDV	777
ENSG00000113580	ENSP00000354274	MDSKESLTPGREENPSSVLAQERGDV	593
ENSG00000113580	ENSP00000377977	MDSKESLTPGREENPSSVLAQERGDV	777
ENSG00000113580	ENSP00000377979	MDSKESLTPGREENPSSVLAQERGDV	777
ENSG00000114026	ENSP00000303132	MPARALLPRRMGHRTLASTPALWASII	357
ENSG00000114026	ENSP00000305527	MPARALLPRRMGHRTLASTPALWASII	356
ENSG00000114026	ENSP00000305584	MPARALLPRRMGHRTLASTPALWASII	410
ENSG00000114026	ENSP00000306561	MPARALLPRRMGHRTLASTPALWASII	424
ENSG00000114026	ENSP00000341434	MVERLCQAFGPRLIQLDDV TYHG FPS	197
ENSG00000114026	ENSP00000342851	MPARALLPRRMGHRTLASTPALWASII	345
ENSG00000114026	ENSP00000344899	MLPWLNCITTGVPWTP TSKRWLRNSI	194
ENSG00000114026	ENSP00000345520	MPARALLPRRMGHRTLASTPALWASII	324
ENSG00000114026	ENSP00000352791	MPARALLPRRMGHRTLASTPALWASII	322
ENSG00000114026	ENSP00000373336	MVERLCQAFGPRLIQLDDV TYHG FPS	199
ENSG00000114026	ENSP00000373337	MPARALLPRRMGHRTLASTPALWASII	195
ENSG00000114956	ENSP00000264093	MAAGRLFLSRLRAPFSSMAKSPLGV	277
ENSG00000114956	ENSP00000306964	MAAGRLFLSRLRAPFSSMAKSPLGV	189
ENSG00000114956	ENSP00000345009	MAAGRLFLSRLRAPFSSMAKSPLGV	239
ENSG00000114956	ENSP00000349294	MAAGRLFLSRLRAPFSSMAKSPLGV	255
ENSG00000115204	ENSP00000233545	MALWRAYQRALAAHPWKVQVLTAG	176
ENSG00000115204	ENSP00000369383	MALWRAYQRALAAHPWKVQVLTAG	176
ENSG00000122971	ENSP00000242592	MAAALLARASGPARRALCPRAWRQL	412
ENSG00000123297	ENSP00000242983	MSLLRSLRVFLVARTGSYPAGSLLRQS	325
ENSG00000123297	ENSP00000313877	MSLLRSLRVFLVARTGSYPAGSLLRQS	346
ENSG00000132781	ENSP00000346354	MRKPRAAVGSGHRKQAASQEGRQKI	522
ENSG00000132781	ENSP00000347685	MRKPRAAVGSGHRKQAASQEGRQKI	521

ENSG00000132781	ENSP00000352239	SVFCCLHQRGPRAIMRKPRAAVGS	546
ENSG00000132781	ENSP00000361170	MTPLVSRLSRLWAIMRKPRAAVGS	546
ENSG00000132781	ENSP00000361172	MTPLVSRLSRLWEVNQLWAGLGYY	215
ENSG00000132781	ENSP00000361176	MRKPRAAVGSGHRKQAASQEGRQK	521
ENSG00000132781	ENSP00000361182	MTPLVSRLSRLWAIMRKPRAAVGS	536
ENSG00000132781	ENSP00000361187	MTPLVSRLSRLWAIMRKPRAAVGS	535
ENSG00000136143	ENSP00000367909	SGRGHPSEPPASDGPAGCCSGSKDV	393
ENSG00000136143	ENSP00000367912	MAASMFYGRVLAVATLRNHRPRTAQ	441
ENSG00000136143	ENSP00000367923	MAASMFYGRVLAVATLRNHRPRTAQ	463
ENSG00000136480	ENSP00000317618	MRSRVAVRACHKVCRCLLSGFGGRV	485
ENSG00000138095	ENSP00000260665	MAALLRSARWLLRAGAAPRLPLSLR	1394
ENSG00000140521	ENSP00000268124	MSRLLWRKVAGATVGPVPAPGRW	1239
ENSG00000148290	ENSP00000361042	MAAVAALQLGLRAAGLGRAPASAAW	300
ENSG00000151729	ENSP00000281456	MGDHAWSFLKDFLAGGVAAAVSKTA	298
ENSG00000166548	ENSP00000299697	MRPGLFKGQAPGSRRRPTAGLAVVR	307
ENSG00000167136	ENSP00000361725	MRALRAGLTLASGAGLGAVVEGWRR	297
ENSG00000167792	ENSP00000322450	MLATRLLGWSLPARVSVRFSGDTTA	464
ENSG00000168827	ENSP00000264263	MRLLGAAVAALGRGRAPASLGWQR	751
ENSG00000168827	ENSP00000327081	MFLEEKIPSISDLKLAIIRATLKRSFT	144
ENSG00000169188	ENSP00000364126	MLRVVSWNINGIRRPLQGVANQEPSN	518
ENSG00000171497	ENSP00000303754	MSHSPQAKPSNPSNPRVFFDVIDIGG	370
ENSG00000177192	ENSP00000324726	MAGNAEPPAGAACPDRRSCSGRA	399
ENSG00000177192	ENSP00000365837	MGLQLRALLGAFGRWTLRLGPRPSC	427
ENSG00000177302	ENSP00000321636	MIFPVARYALRWLRRPEDRAFSRAAM	1001
ENSG00000184428	ENSP00000328835	MRVVRLRLRAALTLLGEVPRRPASR	601
ENSG00000196365	ENSP00000351177	MAASTGYVRLWGAARCWVLRPML	895
ENSG00000196365	ENSP00000353826	MAASTGYVRLWGAARCWVLRPML	959
ENSG00000198836	ENSP00000354429	MWRLRRAAVACEVCQSLVKHSSGIK	978
ENSG00000198836	ENSP00000354681	MWRLRRAAVACEVCQSLVKHSSGIK	997
ENSG00000198836	ENSP00000354781	MWRLRRAAVACEVCQSLVKHSSGIK	961
ENSG00000198836	ENSP00000355311	MWRLRRAAVACEVCQSLVKHSSGIK	979
ENSG00000198836	ENSP00000355324	MWRLRRAAVACEVCQSLVKHSSGIK	1015
ENSG00000198836	ENSP00000376231	LLRIRLALIIEVCQSLVKHSSGIKSL	1015
ENSG00000198836	ENSP00000376232	MWRLRRAAVACEVCQSLVKHSSGIK	166
ENSG00000198836	ENSP00000376233	MWRLRRAAVACEVCQSLVKHSSGIK	960
ENSG00000065057	ENSP00000219066	MCSPQESGMTALSARMLTRSRLGPG	312
ENSG00000104936	ENSP00000366979	MVLPVQHVSARGAAEAAPAAGVGPGL	655
ENSG00000108064	ENSP00000378776	MAFLRSMWGVLSALGRSGAELCTGC	103
ENSG00000136143	ENSP00000367898	MAASMFYGRVLAVATLRNHRPRTAQ	154
ENSG00000171865	ENSP00000313350	MSWLLFLAHRVALAALPCRRGSRGFC	286

Table S3. Primer sequence used to amplify 438 exons present in the 32 samples used in this study

Exon ID	Gene_ID	Forward_primer	Reverse_primer
ENSE00000343045	ENSEG00000005156	CCAACTCCTTTTCTTGCTCTTATCTT	AGATCTCAGGGCTGGAATGTGAGACT
ENSE00000713843	ENSEG00000005156	GCTAGATCTGGTGTGTAGCAGTGAAGG	CTGTACCTCAAGCGGTACCTTCTAAAACA
ENSE00000713847	ENSEG00000005156	GCCTTCCACATGTTGTTCTATATCCTG	CCCACATGTACATACCTCACTCACACTCAT
ENSE000008087588	ENSEG00000005156	TCCAGAAGTGGACTGGTACTCTCTATTT	CTCACCCAGGAAATGAAAAACAGATTCT
ENSE00000887594	ENSEG00000005156	TTTGTATTTTTTTGTAGAGACGGGGTTG	AGAGGACATGTGAATGGCTCTAGATGCC
ENSE00000903608	ENSEG00000005156	CACAATACCCTATACCTACTACCCCCA	ACAGAATTTTCACTCTTTAGCCAAGATCC
ENSE00001106043	ENSEG00000005156	TCGTGTAGTTTCTTCTTCCCTTTCTT	AACATACAGCTCACATGCCCAAGGAAG
ENSE00001106059	ENSEG00000005156	ATCCACATAGGCACAGTATCTCAAAGAG	AACACTCATACCTTATCTGATCTCAGCC
ENSE00001106065	ENSEG00000005156	AGGTAACTACCTCTACTAACCCAGTTGC	TATTGTGTACCACAGCTGGAATGGCTA
ENSE00001160722	ENSEG00000005156	CAAACCTTGTGAGCTTAAGCAATTCTCC	AAACAGTATGTGCCCAACCAGAAAAA
ENSE00001331210	ENSEG00000005156	GACTATAAGACGCTGGCCTTTGGAA	AACCTCTATCCCTTTTTTCTCTCAGCAC
ENSE00001429066	ENSEG00000005156	TGAAAACACTCCCAACATCACAGGG	CACGTCACGGAGGGGTGTGCCCG
ENSE00000742217	ENSEG000000021574	GTTTGCTTGTCTTTATGTTACGTACAATT	AGCCTGGAAAAACAAGAGTCTCAAAAA
ENSE00000809459	ENSEG000000021574	TCATGTAACAATCTGGTAACACCTTGAG	GTGAAAACATGAACAATTAACACTCACCATT
ENSE00000809466	ENSEG000000021574	AAAGGATGCTTTTAGATGGCAAGAGT	GCAAGTCGTAATAATAGACTCAAGGACA
ENSE00000809468	ENSEG000000021574	ACACCTGGCCTCATAGCTTCAATTTTA	CAACACAAATGTACATAACTTCTACTCTGA
ENSE00000809475	ENSEG000000021574	CGATGCTAGTAGACGCCTAAACACTGAA	TGGTAACAAGAGGCTAGAGATAGTACTGGAA
ENSE00000809476	ENSEG000000021574	ACATTGATAACTACCAAAATGCATTCCA	TCAAGATGGTAGTCTTGTCTTCTGCTCT
ENSE00000809479	ENSEG000000021574	CGAGGCTATAGTGAGCTATGATTGTGC	GGAGGTAGAGGATGAGAGAAAGTCTCTG
ENSE00000809480	ENSEG000000021574	AACAAGAGCAAAACTCCATCTCAAAAAA	TTTGACTCTTAAACTTCTTAAGGTGGTA
ENSE00001070179	ENSEG000000021574	GACTGTGTCACAACTGTTTTTTATGT	GATCTGAAATCTGGACAATCATGTGAATA
ENSE00001070181	ENSEG000000021574	CCCCATGAAAGTAGTTTGGGTGATAAT	GGACCACATTTTCAACTACTGATCTATT
ENSE00000469826	ENSEG00000023228	TTCTAAATGGAAAAACATTCAGTTCACTA	GGGTTTTTTGACATGTGTAAGGAAATTA
ENSE00000784949	ENSEG00000023228	CACGTGAACTTGAATCTCTGTTCTGTA	TGAGGTGGGCTTAAATTTTATTACTTCAC
ENSE00000657760	ENSEG00000025708	GTGACTCATGAGTAACCTTGACCAAGTG	ATACTTTCCAATCCAGCTGCACCTCTA
ENSE00000657761	ENSEG00000025708	AGAAGCCTTGGTAGGGTCTTGGAG	GAGAGACTTTGGGTCCCTGGGGGTG
ENSE00000765449	ENSEG00000029639	AAGGTTCTCACTCTTAAAAAGTGCTGAG	ATGATCACACTATGCCACATATCATGC
ENSE00000813879	ENSEG00000029639	CCTACATAATCTTTGGTACCTTTGGGGT	TGATTGGGTAATGGCTGAATTTTATAG
ENSE00000813880	ENSEG00000029639	GAGTTCGTATACAAGAGGTCGAAGGAC	GTCTGACCAATGGGCTGACTCCGAGG
ENSE00000900737	ENSEG00000029639	ATAATTTGGAAGCAAGTAGCAAGAGAAA	CCCTGGTCTCTGACTTTTTTAAGTGAATT
ENSE00000900739	ENSEG00000029639	ATCAAGGTTTTAACTTTTGGCTGAGCTG	CAGCTGATTTTACTGCTCACTGAAATGT
ENSE00000900741	ENSEG00000029639	AGTGTGAGTTTGCACATAAACAAGGTT	CTCTTTTCACTAATCAGGCTGGACTAA
ENSE00000514467	ENSEG00000065057	TTCTGAGGCTCTCTCAGGCCACT	AGATGACCAAAACATACCAAAACAGAC
ENSE00000665105	ENSEG00000065057	GAAAGAAAAACAAGGACCTTGCTAAGATG	CACCCCTACCCCTACTCTCACTGT
ENSE00000665121	ENSEG00000065057	GAGCACCTTTCTGACTCTATGGGCT	GTAGCTCTGGCCACTGTGGGGTCTCCT
ENSE00000754701	ENSEG00000076248	CAGGCACGTTTTTGTGTGTGTGT	TGTGGCTTAACCTCAGTGTCCCTAATT
ENSE00000754703	ENSEG00000076248	TGTTTGTGTATGTTTGTGTGAGGCAG	AAGCTAAGTACACATCTGAAAGGAATCATGT
ENSE00000754705	ENSEG00000076248	GGCTGGCTGTAACCTTCAACCTTTTCA	ACAGAGTGAGACTCGGCTCTAAAAAA
ENSE00001130047	ENSEG00000076248	GAAGGCACAAAGCGAATGAAAGAAATAG	AACACGTGGAGGCTAATTTGGAAGGC
ENSE00001345324	ENSEG00000076248	GGACCCAGAGGGAGGTTTTTTGC	CTAAGCCTACGGAACATGAACCTTGG
ENSE00000665196	ENSEG00000099817	CCACGCTTTATCCAAAGTAGC	CTCTTGCTCGCTGGAAGGCGCAG
ENSE00000665197	ENSEG00000099817	GTCTCCATGCACTAATAGGAACACCT	GTAGCTTAGGCGAGGAAATGGGGTTG
ENSE00000665199	ENSEG00000099817	GTACTGCTTGGGGAGGAGGCTG	GAGAGACACCTGTGTGGAATGGGG
ENSE00000892419	ENSEG00000099817	GACTGAGAGGGAACTAGAAAGAAGCTG	GTTTGCTGTTCACTCTGCTCTCGC
ENSE00000892420	ENSEG00000099817	CTCCGACGAGAGTACGAGGAGAC	GTTAGGCGGAGGGGGCTGATTC
ENSE00001055171	ENSEG00000099817	AAGAGACAGACACGCTCACGCCCTA	CTGTCTGGGCATACTGGATCTGC
ENSE00001112731	ENSEG00000104936	CAAAACAGTAAGGTTCCAAGACTGATCC	GTAAGCCAAGATCAAAAAGCAGTGAGG
ENSE00001112739	ENSEG00000104936	AAGCCCTCACCTTTTCTTCCCAAT	TCTGGTTCTCCACAGAGAATCAGCAAT
ENSE00001475019	ENSEG00000104936	CTTGACTCCAGGTGACAGTTCAAGT	ACTTGAGTCTGGGATATGTGACCATGCTA
ENSE00001475022	ENSEG00000104936	CTACAAGGACCCCTCGAGGCCCTG	GAGTCCCAGGAGCCAAATCAGAGG
ENSE00001475052	ENSEG00000104936	TAAGGCTCGGTCAATCATCAATTTCTAA	CCGTTACCCAGGACATTTCAATGA
ENSE00000727732	ENSEG00000106028	TGAGTAATCTTCTGTGTGCAATTTGCCT	ACAACACATTTGAGATTGGCAAATTA
ENSE00000872183	ENSEG00000106028	TATCCAAGTCTGTTTGGCACTCTGTTT	GCCAAGCTTTTAAAAAGAAAAGGAGAAA
ENSE00001043132	ENSEG00000106028	AACTTGTAGTCCACTTATGCCAACTG	GATTATACCACAAAAAGGAGAGCGAGAAC
ENSE00001090027	ENSEG00000106028	CTGGTGAGTTGTAATTTTGGCCATAAGAG	AAGTCTTCTGATCACTGTGGCTGATAGT
ENSE00001206769	ENSEG00000106028	AAACTTGAACCTTCCAAACTCACCCT	ACCTACACAGAAACACCTCCCGAC
ENSE00000721463	ENSEG00000107815	CTTCACAGGTAACCTTTGAGAAATCAC	CTAAGGAGATGGGGAGTTCCTACTG
ENSE00000721468	ENSEG00000107815	AGTTTTCAGGATGCTAGTTCTTCTGCCT	TGAGAAGTGTGTGTGTATGTCCAAGC
ENSE00000705087	ENSEG00000108064	AATCCATATACATCTCATCCAGAGCAC	TCTGCCTAACTGAAGAATACTTGATGACA
ENSE00000833891	ENSEG00000108064	AAAATTTGACCGCAAGATGTAATAATCA	CATGGCACTTAGAGATTTTCTGCTTAAATA
ENSE00000985817	ENSEG00000108064	ATGGATTGTGCTTTCTGATGATCTTT	ATGACAATTGCTCTCAACTGCAGAAATAC
ENSE00001274058	ENSEG00000108064	ATTTCTGTGAAGCGTTTGGATACATAG	CATTGGTATTTAACTGCTTAATGGCAATTT
ENSE00000729668	ENSEG00000110025	ACCTTGATCTTCCAGGTGATCCTTCAC	GCACCCAGCCTTTTGGTTATTTTAAAT
ENSE00000863754	ENSEG00000110025	ACGAGCGCTCGGCCAATGCACTAT	GTGACGCCAGGGGCACTGGGACGC
ENSE00001119977	ENSEG00000110025	CTGGGGCTGCACAAACTCTCCCT	ATTCCTTCTCTGCCCTGCTAGATTAG
ENSE00001169473	ENSEG00000110025	GTCTTCTTCTTCTGTGTCTACAGTTT	TGAGGAGACGCTCTCTCCCTGATCT
ENSE00001169520	ENSEG00000110025	AATAAGAGTTGGGTGGATGAACGAAAG	ATTCTGTGCTCTAAAAAGGGAGCAGTG
ENSE00000910346	ENSEG00000113580	TCCCATTTTATTGGGCAAGTAACTTAT	TATATTCCACCGGAAACAAGACAGAGG
ENSE00001082911	ENSEG00000113580	TGGCTCTAGGAAAAATGTCTACAAAACT	TGACACAGTGAGACCTTATCTATCTAAAA
ENSE00001082912	ENSEG00000113580	TTCTGGTGTCACTTACTGTGCCCTTTCTA	CTTTTTGGGGGGAAGTAGCAGTATT
ENSE00001082913	ENSEG00000113580	AGGATTGTTTCACTCTGAATTTATCACA	TTTTGACAGGGGCTAATTGATCTAATTG
ENSE00001082914	ENSEG00000113580	GCATAATGATTGAAAAGCAGGGAGTAA	TTGAATAAACTGTGTAGCGCAGACCTTC
ENSE00001165146	ENSEG00000114026	AGAAAACATGTGTAGAGGGACAGGACC	CATTCTCTGCTCTCTCTTAAGTGCAGT
ENSE00001295658	ENSEG00000114026	CTATTGTAGGATAGGAGGGACCCCAA	TGGCAAAACTGAGTCTAGAGAAGTGAC
ENSE00001316654	ENSEG00000114026	AGTTTGTGTAACCTAGGATCTGACCTGTG	AGAAATGAACAGATCTGAAAGCTGATGG
ENSE00001498801	ENSEG00000114026	CTTCCACCTCCCAACACTGTCACTA	GGAGTTTCTCTGCCCTCTCCCT
ENSE00000761859	ENSEG00000114956	CTGATTGCATAAGAAAAACAAGACAGCAG	TATATTCTGAACCTCTCTACAGGGGGCT
ENSE00000846663	ENSEG00000114956	TTTTCTCCCTTATGGCTGTATTCAITA	GGATACTCAACCTGGGCTACTTTACTCA
ENSE00001121693	ENSEG00000114956	TGAGTAAGACTTGGCGAGTATGTGAAAC	GGCCAGAAAGATAAAAGTACACAAGGGA
ENSE00001200448	ENSEG00000114956	CCTTCACTCAACGCTCTTTTACAACAT	AAAACAAGGAGGCAAGATACACAGTGC
ENSE00001409499	ENSEG00000114956	CTTAGTACTGAGCAGGGAGGAGATAG	CTTGGAGAATGTCACTTCTTAGGTTTCA
ENSE00001411597	ENSEG00000114956	CCACATTTCTTCTCCATGCCTATTATT	TCTAGAGGTGAATTAGAGCAAGCACC
ENSE00001474840	ENSEG00000114956	TTCTCCAGGCTATTCTTACTCTGAAG	CAGCAAAAACTCTCAATAGGCATGATA
ENSE00000733143	ENSEG00000115204	TCAGAAATAGGGGAAGTGGACACTAAGAA	TAGTCAATTGTTTCCACAATGAAGCCCT
ENSE00001179981	ENSEG00000115204	CAACTACGCAATACCCCTTAAAAACAGC	CTTTAAGTCAATTTGGAAGTGGGAAGGG
ENSE00001483572	ENSEG00000115204	CAGCTCTAGAAATGACTCCCAATAGTT	ACCTAAACCTGCCAATCCTTTGTCTAT
ENSE00001127023	ENSEG00000122971	TGAGTTAGTGGGTCACTAGGATCTCTGG	AACCTCCAGAGCAATTTCTGGGTTCT
ENSE00001191815	ENSEG00000122971	TGTGTAGCAATTTTGATTAACGAATGTGG	AGAAGTGGGGCAAGGCCGTGAG
ENSE00001245851	ENSEG00000122971	ACTGAGAGCTTTGGGACCTCTCATCT	AGAAGGCCCTAGAAAAAGAAATGACAGC
ENSE00000920433	ENSEG00000123297	CATAAATCACTTCAITCTGTTCCAGGC	AATAGGAACAGCAAAAGACCAATGAG
ENSE00000920434	ENSEG00000123297	ACCTGATTTTGGCATTAGTGGTAGAC	CTACTACAAGCTTTTACACCCAAGGGACAG
ENSE00001180179	ENSEG00000123297	CACACCATTTGGATTGTACCAATTTTGC	CTTTTTAGTGGAGACAGGGTTTCACT
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ENSE00000962641-0962642	ENSG00000138095	TCTATCTCCACCAACGCCTATGTCTA	GGTTTCAGTTCGCTAGTGTTAATTGGTT
ENSE00001069565_1	ENSG00000138095	CCTCATCTCCAGTTAGGTCAATATCCA	TTCCCTGCTCTGTCTCATTTATTTCAITA
ENSE00001069565_2	ENSG00000138095	CTGTAGCTCTCTAGTGCCAACATTTAAC	AAGTTATGTACCACTACCTCTGCTGG
ENSE00001159316-1159309	ENSG00000138095	AATGAAAAAGCTTCGTTTAAATGGCTGT	AATCTTGATAACATGACAGTCTCGGTAA
ENSE00000943530_1	ENSG00000140521	CCACATAAACAGGGGCTAGTCTCTAAT	AGCAGCCGCAAGTGTATCTCCG
ENSE00000943530_2	ENSG00000140521	CTGTGCCAGGTTGTCCCGTAGAG	TCAAGGAATGATGATTATGGATACACCTAT
ENSE00000943531	ENSG00000140521	AAAGGAGTACCTCCCTTAACCACTGA	TTGTTGTGGAGTGGAAAGTTAATGTCTC
ENSE00000943533-0943534	ENSG00000140521	TTCTTTCAGCCTAGAAAAGTCAAGGTCC	ATAGTGCTTGGGACCCCTCTCAC
ENSE00000943536-0943537	ENSG00000140521	CAAAATGAGAATAGGACTGGAAAGACAGTG	CTCTCTCAGGAGAGAGGTAGCCAG
ENSE00000943540-0943541	ENSG00000140521	TAGTCATTCCCAACAAAAGGAAAGTCTC	GTGTCTGAGTACCATGACAGGGAGG
ENSE00000943543-0943544	ENSG00000140521	TGTCGCCAGAACATATTTACTGAAGGAGT	TAATGGAGTATAGCAGTCTGGAGGTGG
ENSE00000943545-0943546	ENSG00000140521	AGTTCAGTAATGGGCAGGAGATAGAAC	TAGCTCTTTCTCAGTCAACTCTGGCTC
ENSE00000943548-0943549	ENSG00000140521	TCTAGGGGGATGAAAAGTCAAAACTG	GCTTTGTTTTTTATGCTTTGAGATGCTGA
ENSE00000984111-0984112	ENSG00000148290	AGCCCAACAGATGACTGATAATGAGAG	CAGTACTGGAGTCTGTCTTGGAAACGG
ENSE00000984114-0984115	ENSG00000148290	AGTACTTGCCTAGGTTCTTTGCTGAGTT	TGAGTGACTGTCTTTAGTCAAAAACCTT
ENSE00000984116-1456594	ENSG00000148290	CCACCCCTTAAATACATTTTAAACCAGG	GTAAGGGCCATACAGGACTTCCAACCTG
ENSE00001456605-0984110	ENSG00000148290	AGCATTTTAAATACGGAACATGTCTACTCT	CTCGCAGAACCTGGAGCCGGGGG
ENSE00001001421	ENSG00000151729	GTGTGTCAGATATGTTTTCAGGGGAAAAA	TAGAAGCTTGGCTGCTGACTGATACAT
ENSE00001328829	ENSG00000166548	TCTTCATCCAGAACCAAGCCGA	TACCTAATCTCTGAGGACAAGCTCGGA
ENSE00001329349_1	ENSG00000166548	TAATCCTTTCCAGGGTTTGCATCTAGT	ACTTCCAAAAATATGCTGCATTTTG
ENSE00001329349_2	ENSG00000166548	CACAGACTTTTCAGTAATTCGAAGCAAA	TTTGCTAGTGTCTTTGCTATGCGTCTCT
ENSE00001329349_3	ENSG00000166548	AACTTTCTGAGCTTCAAACTCTCATC	CTTTTATCTGCTGCAACCTTCTGTG
ENSE00001458291_1	ENSG00000167136	AGATAAAAGCTTTTCGACAGTGTCTGACC	CACGTACGACTCGGGCTCTTGA
ENSE00001458291_2	ENSG00000167136	CTCTTTTAAAGGCCTCGCGGGTCCG	TCTGCAGAAAGACAAACCGAGGCC
ENSE00001170831-117088	ENSG00000167792	GAGGAAGGCTGCTCTGAGGAGATAA	AAACAGAGTCCAAAATCCCCAACAC
ENSE0000117084-1283609	ENSG00000167792	CAAAAGAGCAAGAGTCTGTCTCAAAAAA	TAAGTTTCTAAGGAAAGAGCCCAAGGC
ENSE0000126987-1270109_1	ENSG00000168827	AAAGGAATTAATGGCTAAATGCGTCT	CCAATCAATAGAGTTGAGATAGACATAGAA
ENSE0000126987-1270109_2	ENSG00000168827	ACTTCTGTGTAAAAAGGAAAAGCCAAG	CAGAAACCAAACTGAAATAAACAGACACA
ENSE0000126987-1270109_3	ENSG00000168827	GAATCGCATATATCATGACACTTCTTGG	TTTTAAAGATCTTTTCCCTAGAAACC
ENSE00001493945-1269936	ENSG00000168827	ATACTTGGAGGGAGTTATGAAGCTTTCC	AACTTGGCCCTTGAGAAAATATAGC
ENSE00001138109	ENSG00000169188	AGATATGAAAGGCAGCAAGTTTGTGGTA	TAAGAAATAGTATTGCAAGCCAAGTCCG
ENSE00001465324_1	ENSG00000169188	ATCAGTAAGGATGAAAATCAGAAATCCCA	CTAGGCAGCTCTATGTACAGGAGAGGCTT
ENSE00001465324_2	ENSG00000169188	TCTAGTTCTCTCTCGAACAAAGTCTCG	AACAAGGAGCTAGGTAGGAAGGAAAGC
ENSE00001465324_3	ENSG00000169188	GTACTGTGAAGAAGCCAGGACCCAACCT	GATACTACTTCTAAGGAGGCAATCGTCC
ENSE00001465324_4	ENSG00000169188	AAAGGGTTCTCTGCTCAGTTGAGGAAT	TCTTCTCAATCCATATCTCTCTCC
ENSE00001465324_5	ENSG00000169188	CTGTAATCCAAGTACTTAGGAGGCTGA	GTCTTCTGCTTTGTGTGCTCTTACG
ENSE00001126569-1126560	ENSG00000171497	TGAACAAACATCTAAATCTGGCAAAAGT	TAGGCAATGAATTGAAATCTGGCATATAA
ENSE00001126597-1126587	ENSG00000171497	CAACACACCTGGTTATTTCCAAGTAAT	TGCACATGACTTCAGCTGTATAGCTTTTAT
ENSE00001170868_1	ENSG00000171497	CTAAAAACTTTATGATCTGGCCCTTGC	TTTGTTTTCTTTGAGATGGAGTCTTGCT
ENSE00001170868_2	ENSG00000171497	CTAAAAATACAAAATTAGCTGGGCGTG	ACTTTGTAGAGAAGTTTCTTCAAGGGGT
ENSE00001168868-1168860	ENSG00000171865	CAAGAAATAAGCATGTGGAAACATCA	TCGTTATCCATTAGAAGAATCACTTTGA
ENSE00001253775_1	ENSG00000171865	GTGGACACAAAGGTATTCACTTTACAA	ATTTACCCTCCAGTTGACAGGTTTGAGT
ENSE00001253775_2	ENSG00000171865	TTTATGCTTCTTGGTCTTTATGATGTCG	CTGTTCTGAATGGTTTTTTATGATGACAA
ENSE00001223953_1	ENSG00000177192	CTTATAGAGCACTGCACCTGTCCCTC	ACTTCTCGAAGTGACCCCTTCCAGGAC
ENSE00001223953_2	ENSG00000177192	GTACTACCTCGGAGATGTACTGCGAG	CTCTGTACAATGGGAACAATGTGGG
ENSE00001223961	ENSG00000177192	TAGTCCTTCTTCTCAGAGACACAGC	GTGTCTCTGCAAGACCATCAACAAC
ENSE00001330883	ENSG00000177192	CTGTTTAAAGAGAATGACCGAGAACAAAC	GTGCTCATCTCTGTGGACGAAAAAA
ENSE00001281407_1	ENSG00000177302	AAGTGATCAAGTGAGGAAAAGTGAGGGTG	AAAGCAATTCGTGACCTGCAACTGTG
ENSE00001281407_2	ENSG00000177302	GTCTATATGCCAAGGCAGGAGGC	CTAAGGAGAAGCTGGCATCTGGTTGT
ENSE00001281439-1281433	ENSG00000177302	AAAGAAAAGGGGTATGTGGAAAACCTC	AAATGAAGGCATCTTACCTGCATAGGCT
ENSE00001281452-1281446	ENSG00000177302	TAGCAGCTGCATTAGAGAATGGTTTGA	GCTCTGTCTCTGAGAGGTGATATCTTA
ENSE00001281490-1281484	ENSG00000177302	CTTCCCTTTTCTTTTATGCTGTCTCTC	AGCCCTGGACTCTCATATCCATCAIT
ENSE00001281545_1	ENSG00000177302	AGAGACAAGGTCTAACTATGTGCCCAG	GCTGTTAGCAGAGGATTTGGTGCAGTC
ENSE00001281545_2	ENSG00000177302	TGAAGTCTTCTCTGAAGGATCAGTGTTA	CTAAAGTGCTGGGATACAGGCATGAG
ENSE00001304637-1327107	ENSG00000184428	TTTATCTACAATCTCTGCTCCGCAC	CTTGTGCTGTGGTTTAAAGACGCTGG
ENSE00001305900-1326407	ENSG00000184428	CACCCGAGGCTCACTCAACAAG	GTCTCACTGGATTGGGTTTTTTT
ENSE00000951714-1158972	ENSG00000196365	AAGCGTCTGGTGTGTCTCTCACG	CCAGCCCTGACCTGGGGTCTCCCCACT
ENSE00001158952-1158945	ENSG00000196365	AGGCTCAGAATGTCTCCACAAGACT	CTAAACTGGGGCAGGAGCGGTACAGGTG
ENSE00001158962-1158957	ENSG00000196365	CTTGTCTCGGGTAGAAATGGGAA	GTCTAGACTGAGCTGGTGGGCAAGGTC
ENSE00000924375-0924374	ENSG00000198836	AGTAGTGTGAAGGGAAGTCTGGATTTGT	GATAGCAGCAATCTAAACATCAATACCT
ENSE00000924377-0924376	ENSG00000198836	ACCATTTTTGTGAGCGTCTTATCTGAAT	AGCTTGGATTGTCAAAGAAGAAAAACATA
ENSE00000924380-0924379	ENSG00000198836	GGTTTTCGATACGTGTGTTTAAAT	CAGTTCAATTTAAGCTACTCTCTACTGT
ENSE00001267213_1	ENSG00000198836	TTATGCCAATATTGTATAGTTCGGTGATA	TAGGTAAGCTGGTACTGACTTGGCTTCC
ENSE00001267213_2	ENSG00000198836	TCTTAATCCCAAGAACTATTTGACCATGA	AAACAATAAAATGGGGATAGCAATGG
ENSE00001267213_3	ENSG00000198836	AAATGTCTATCTCAITTTGCTGCTTTTTC	TCAGGACTCTCATGTGGGACTTTTATGAT
ENSE00001267213_4	ENSG00000198836	GAAAGAAAGACCTTCAGCTGTAATTCGA	CAGAAAGAAGTCTCGGGAACCAACTGT
ENSE00001267213_5	ENSG00000198836	ATCCAAACTTAAITGGCTAGGACTTCA	ACAGGTTTCTCTTCCCTGTTAAACA
ENSE00001306402	ENSG00000198836	GACTCATATTTTCTTTTCCCGCAAT	AGCAGGATGTAATGAAGCAGATGATAA
ENSE00001437809	ENSG00000199916	CAGGTGAAAATCCGTCTCTACAAAAAT	CAACTTCTCACCTAATCATAAAAACAA

Sample Coverage	A1	A2	A3	A4	A5	A6	A7	A8	A9	A10	A11	A12	A13	A14	A15	A16	SUM of A	Avg of Each A	Min A	max A	Count=0	% no coverage	count=1	% =1	count>=1	% =1	count>=10	% =10	count>=20	% =20
ENR000004935: 42	32	2	1	25	46	17	2	128	77	9	108	165	14	25	82	673	48.3125	1	85	0	0	0	1	6.25	15	93.75	12	75	10	67.5
ENR000010011: 30	16	22	31	8	26	21	27	58	79	50	54	80	77	22	40	701	49.375	10	78	0	0	0	1	6.25	16	100	10	62.5	14	87.5
ENR000004936: 30	16	22	31	8	26	21	27	58	79	50	54	80	77	22	40	701	49.375	10	78	0	0	0	1	6.25	16	100	10	62.5	14	87.5
ENR000010012: 30	16	22	31	8	26	21	27	58	79	50	54	80	77	22	40	701	49.375	10	78	0	0	0	1	6.25	16	100	10	62.5	14	87.5
ENR000011127: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011128: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011129: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011130: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011131: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011132: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011133: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011134: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011135: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011136: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011137: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011138: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011139: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011140: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011141: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011142: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011143: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011144: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011145: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011146: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011147: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011148: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011149: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011150: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011151: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011152: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011153: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011154: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011155: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011156: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011157: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011158: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011159: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011160: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011161: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011162: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011163: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011164: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011165: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011166: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011167: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011168: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011169: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011170: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011171: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011172: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011173: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011174: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011175: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011176: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011177: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011178: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011179: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011180: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ENR000011181: 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		

[illegible]

Figure 1. Coverage of the 131,000 bp region of the *hprt* gene. The bar chart shows the coverage of the region for each of the 131,000 bp regions. The y-axis represents Coverage (bp) from 0 to 2000. The x-axis represents the region (p8 to p13). The bars are colored red and blue. The table below shows the average and maximum coverage for each region.

Region	Average	Max
p8	43.39	527
p10	9.32	138
p11	20.69	297
p12	19.45	244
p14	23.75	513
p17	25.13	418
p18	10.29	234
p20	23.08	515
p21	8.233	185
p24	8.537	168
p25	27.79	447
p27	9.174	127
c4	30.83	448
c11	13.61	204
c12	16.2	317
c13	17.2	252

Series	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Series 1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Series 2	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Series 3	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Series 4	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Series 5	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Series 6	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Series 7	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Series 8	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Series 9	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Series 10	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Series 11	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Series 12	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Series 13	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Series 14	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Series 15	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Series 16	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Series 17	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58																																										

SNR	33971	24826	10801	17371	17693	41882	13833	10820	12854	12100	13103	148516	121201	129300	120201	1284256
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AVERAGE	75.594	56.68	40.5564	39.68	40.395	111.16	123.33	100.29	247.43	299.03	208.84	236.75	219.625	238.025	235.025	235.025
STDEV	3.94	3.22	4.71	3.62	4.71	3.24	3.005	2.97	2.92	3.94	2.97	3.03	2.94	3.1	3.1	3.1
COUNT=0	0	0	15	13	13	5	4	4	4	4	4	4	4	4	4	4
COUNT=1	3.6597	1.03	1.924	2.5142	2.5142	2.968	1.414	0.9132	1.82408	0.9132	0.65662	1.3009	2.04765	1.143152	1.143152	1.143152
COUNT=2	22	24	34	41	25	22	10	17	17	18	11	20	12	20	21	13
COUNT=3	5.02	14.54	9.7626	9.9807	5.9778	2.19	4.379	3.813	3.6378	4.038	2.6662	2.79728	4.74761	2.6662	2.6662	2.6662
COUNT=4	440	388	397	388	402	403	416	417	514	420	420	412	411	412	400	400
COUNT=5	91.242	80.43	81.8	91.1968	92.228	90.12	91.221	95.205	95.435	91.221	95.435	91.221	95.435	91.221	95.435	91.221
COUNT=6	83.516	83.333	80.594	75.224	75.445	82.416	80.5	80.868	82.904	80.509	82.27	84.7480	80.1	81.22744	80.8678	82.8806373
%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
%-2SD	74.7493	57.968	47.175	44.984	43.954	79.724	87	87	87	88.611	86.714	86	86	87.668	84.7633	84.7633
%-1SD	76.538	58.908	46.392	46.202	46.392	80.928	89.338	89.338	89.338	90.546	88.688	87.668	86.714	87.668	86.714	86.714
%0	64.3836	59.961	50	49.772	48.0001	71.233	75.71	71.689	83.105	81.5068	83.333	80.073	80.822	81.5068	80.93631	83.1052223
%1	76.538	58.908	46.392	46.202	46.392	80.928	89.338	89.338	89.338	90.546	88.688	87.668	86.714	87.668	86.714	86.714
%2	74.7493	57.968	47.175	44.984	43.954	79.724	87	87	87	88.611	86.714	86	86	87.668	84.7633	84.7633
%3	5.02	14.54	9.7626	9.9807	5.9778	2.19	4.379	3.813	3.6378	4.038	2.6662	2.79728	4.74761	2.6662	2.6662	2.6662
%4	440	388	397	388	402	403	416	417	514	420	420	412	411	412	400	400
%5	91.242	80.43	81.8	91.1968	92.228	90.12	91.221	95.205	95.435	91.221	95.435	91.221	95.435	91.221	95.435	91.221
%6	83.516	83.333	80.594	75.224	75.445	82.416	80.5	80.868	82.904	80.509	82.27	84.7480	80.1	81.22744	80.8678	82.8806373

