

Each probe used is identified by the chromosome number where the sequence is located, followed by the probe size in base pairs. The PCR primer set corresponds to the first and last 24 nucleotides of each probe sequence, respectively. When the probes were shortened by restriction digests, the enzyme used is noted in parenthesis. Sequence files containing each probe can be accessed in the NCBI Human Genome Databank using BLASTN. The following is the list of probe sequences, ascending numerically, by chromosome number and probe size:

1-678:

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ACTGGTTAATCTGACGGAGGCCAAATTAAGTATTGATTAAAGCTGAATTTATTTATTGTACAGGA
GGAAATGTCGAGTGAGGCTTGTCACCTTTTACACTAGCCCATGTTTTAATTTGATACAGAACCTCATGAAAA
TGTATCATTATTTCAGGAGAGACAGTTGAACACAGCTTCAAGGAAATAATTTCCATACTCTCAGTTGCTTCT
CCTAGCTCTTTTCCAGTTGGATTAGTCCTCGAATTCATTCTCCAAAGTTACTAAGATTGCTTGAACATTTG
TTCTCACTCTTTGTTCAAAGGAGACTCTGTTTAAATTAATAAAAAAAAAATACTCTAGCCGTCATAAATGCCTCGT
CCTCCTCAAATCTGGTCTTCAATTCATTATAACAATTTCTAAGTGGAACACAAAAGTGTACTTAGTTTTTA
TATTGATTTTACCCAGTACTTCAAACCTCATCTCAACTCATATGCAAGAGAGATAGTCTACAGAAATATTT
ATCATCTACAAAATAAATCCTAAAATCCTGAGTTCATTAGATGTTTTTCAGGAATTAGTCTTATTATGAAGA
AATCAAAGTAGCTAATGATAGGATGCAATGATGAGTAAACTTCTAGGACAGCTGACAGGGATTTCCCTAGC
TATCTATGCTGAAAATGTCATGCCTCGTTCCTCCTTTCT
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2-375:

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GCACATGCCAGCTTGCTTCATAAGATGGCACCAGGAGTGCCCTGGGCAACGCTCAGCTTCCTCCAAAAA
GCTTTAACTGAACAAAAAGAGAGGAGTCTTAAAACATGTGTTGATATAGGAAGTAGCCAGTAATGGTGCCT
GCCCCACTTCACAGTTAATAGAAAAGAAGGACCTGTGCAGGCTGGCCAGCCATGCCCCAAGGCAGACATGCA
GGCCTGGCTAAACAGAGACCAGTGTGTGTACTCTGTGAGAACCATCTTTTAAAAATGTCTTCCAAGCTC
CTGCGCTATGCCAGGCTCCTCCTTAACCTACAGCTCAGAACAAAACATGCCCATATCCAACCTCTGAAAC
TTCCTCCTGAAGGGACCCAA
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2-450:

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AGCAGCCAGGTAAAGCATCCTACACACTCTCTCTAGCTATCACATCGAGCCAGGCATGGCATATTTCAG
CTTTCTCTGCTTGGCTTCTCCATTCAATTTGACGTACATTTGATTGCTCATTATTTGTGTATTAAGTGTTT
ATTCACCTAACAAATAAGGACCACCCGTGCCCTGAGCCAGGCGTCATGCTAGGTTCTGGAGACAGGGTGGC
AATATGATTTCTTGGTCTTGCAGAGTTCGAACTCAATGGAGATGGGGCAGCCACTCAACAATGTCATTTTG
TAGACTCATGCAAAAATTACATTGGAGGCCAGCACTTTAAGGCAAAAATGCCTGATAGTCTGAGGGAAGGGA
ATTAGGGAAGCAGAGACCTGCAAAGGAGATGGGAATTAATTAGGCAGAAGAGGCAGATAGACAAGAGGAAC
ATTGCATACCAGCCAAAGCTGCTG
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2-820:

AGCTTCCCCAAGACTTGGATCAGGAAGATGACAAAGTCCCTTAATGTAATAGCTGTTGAAAACACCATCT  
CCCAGAGATGCTTCCTTTGGGCCACACCTCTCCACATTCAGTGTAAAATCTCTGTCCAGGGTTTTTGTAT  
GAGAGCGAGCTATCCTACACTGTTGACACTTGGGCCATCTGAGAGCAGCCATACAAATGTAGATCTGTAGT  
CTAGACACATGGACTCTACAGAGCCCCTGCTTGTGGCCTCAGCTTTGTGAACAACGTGTCCACATAGGAC  
TGGCCAAATAAGGGATGGTCACCAAGACCCTTTCTAGAGGATCAGAAAGACGTAGTTGTCAATATGTTGCC  
TGGTAAGACGGGCCTGTCTAGCACCTGTTTGTGAAACAGAGCCTGGTATTTGTATATTTGCATTTACTTTG  
CAGTGTCTAAAGTTGGAGCACAGGGCCTTGACATGCAAATGTCACGTATGCCCCACTGGAGTCTTTTTATTT  
CGGTGTGTGTTTGTGAGCACACGTGCGTGTGAGTGCAGGTATGGGTGAGCGTGTCCATATGTGCCTGCATG  
TGAAGGCTAGAGGTGAGCATCACTCAAGTGCCACCCACCTTATTCTTTGAGACAGGGTCTCACACAGGGAT  
CTGGGGCTTATTGATTAGGCTAAACTGTTTGGCTAGTGAACCCAGGGACCCCCCCCCCATCTGCCCTCC  
TCTGGAATTACAGGTGTGCAGCCCCACACTTGATGTGATTGCTGCCTGAGCTCAGCTTGTACAGCAAGTAC  
CAAGCTATCTCCTAAGGCCCTGAGCCTGTGAGTCTGCA

3-342:

AACCCAGGCTGTTTCTCATTTGCCGCTGTGACACAGGGCATCACCATTCACGTTTTTTTTGAGATGCAGAG  
CATCCTTGAAGCTGAGCAACTGTTTAAAGCCCAGCTTGCTGCTATTTTAAATTGATATAAACATGAAAAGC  
GTCTGAGTGACCATCTGTGGCAGAATACAAAAATAATTGTGAGCTCATGTACTGAAAAATTATATAAAGTA  
GACAAAAGGCAAGCTACAATGATTAATAATATACCAACCCAACACTGACTAAAATAAACAGACTCAAAAC  
CATCCATAGTGCAAAGATCCCATCATAATCCATATAGCACAAAGCTTAGAGCCCATCA

3-413:

TCCTGAAGCTGTCACCAAACCTCAACATTCGCACCATGGTACTTGCACACTCACATACAACACATATAAAC  
ATGCTTACACACAGACGGTCAATAAGATGTAATCAAAATAAAAGTCAAAGCAGGCTTGTCTGAATAATGTA  
ATATCTTACAAAAACACCACTCTCCCAAGCTCTTTACCTGTCTATGGTCAATAAAAGTGAGTTCTTTGATGGA  
GTGATAGAGGTTTGTGTTGATTGGCGAACCTGACAGGTTTTTGGTTGGATTCTTGGAGTCACATATGCC  
TGGAGTGTGCCATACTGGCCTTCAATTGAACGAATCTGATAACATAAAAGGAAAAAGGAAAATTTAGCAGC  
ATAAATATATTTTCATATGTTTACTTAAAGTACAGAGTGCTTCAGTTGTCTGTCTGCTGGA

3-552:

ACCTCAGGCTCCCAGGAACATTTATCAAGCATGTTATCTGGTTCTTCACTGCAGTCAAGCTTGACCACCAT  
GAATCTCAAGGGGCTTTGTGAGGTATATAAGGGGCTTCTTAGGCAACAAGTGGACAAAAATATAGAACTTC  
CTTACTTTTTTATCTGTCTTCAGTTGGGGGAAGGAAGAAATTACATATATGTTTCATTGAAAGTCAGATGAGG  
AGAAATATGTGAAGAAAATACATCAATGTCCAGAAGTGGGTAAGAAAGTCAAATGAACATAAGGATTGCTA  
TGATCAGGCAGAGTGACAAACATTTTTCCCATCCTCATTCTCAGAGATCAAGCCATGCTGTTTTGAATGTG  
CTGAGTCACATAGAAAATGAAAATATCAAACACTGACAAGAATTTATTCTTTAGTTATCAATTGTTAAGAT  
TTTTCATGAAATGTGTTTTGGTTATATTTATACACTTAGCCTGCTACTTCACTATTCACCCAAATTTGTGTA  
TTTTTTTTCTACCTTTCACGACCAATTTGTACTGGTAGTGGATGTGTGGTCTTCCA

4-419:

AATGAGCTGACCCTGGGAATCCATGGCAGAGCATGAGCCCTTGCTGTCTGTGATGCTTGTATCTGTGTTTC  
CCACACAGGTTTCTAGTTAACTGAGTTTAGGCCAAGTTGGGATTATTTCCAGCCTCAGCTTCTTTGCATG  
CCGTGCCAGGGTCTATATAATTATTAGACTGTTAGCTAGGTGTGACCAGCATTTCAAAAGGCAATAACT  
AAGGAGGACTGGAAACGGGCTCAGAGACCATCAGTAATGACCACACAGTTGTTTGTATCCCCTGGGGCTC  
TAGAACCTGCCTCTGGCTCATTTTCAGCAAGGGATCTCTGTCTCCTTAAGCCAAACATTCCATCCAGTTG  
TGTAACAACCTGCTTGGCCCATTCTTCTGCTTAGTCCCAGCACGCTCTGCACTCTTCCACTTTCT

7-474:

ACAGCAACATCAAGGTGCGAGTTGGCTGAGTTTTGTCCGTCCTACCTGATGGGACCTTCCATGCCTTATTG  
AGCAAGTGATGAAGACTTTCGAGACTCAGTGGAAGAAGGACTTACGGGACGGTGGAAGCGTGAGCTGGCCT  
GGAGTTAACATGCAGAATGTTCTACAACCTTGCTCACTAAGCCAGAGTAGCTTCAGTGTGCAACTCAGAGTC  
TGTGGAGTTGAAATGTGTTTTCGTTTTCGTATTACTCTGAACGGTATAATTTTCCACTATTTTTTCTGGAAG  
AAAGAAGGGAAACTCCACTCTTCCTCCCACCCCATCCTCTGCTAATGCTTTGGCATTGGTTTCAGGGTCTGA  
TGGAGTCTGTGAGGCACTAACAAGCTTCTTCTCTATCCTGTTTTGTGAAAATGCATCCTGCCAAATCCTGTT  
GTTAATGCAAAGGTCTCCAGGAGTTGACTGGTTTTATGCAGTGGGACGA

7-500:

TATGACCTGGGCACAGAGTGTGTTCTTTGCCACAAAAGGGTCACTGATAACATATCCTTTCTGCAGGTAGA  
ACTAGGAAATATGTATGTCTATAATGAAAGTCTATATACATCCATGTTTCAGGGTTTGTATCTTTATGCAG  
CTTACCTCGAGTTTATACTGTTTTCTGATTATCCTTACTTTGTCCTCAGCTCCCATTTTCTAGTATAGATAC  
TGGTTTGTATAATCCTTGATATACAGTACCCCTGTGTGAAACAAAATTATCTACAAGAATATTGTGTTTTAT  
GTCAGTATTTTTTCTCTAGGTTTTCTTTAGTCCAAACATTATTTTTTAAAGCAACGTTAGCAAGTTCCTCC  
TCCCCCAGACCCACCTTCTCTCTTCAGTGTCTATCATGTATTACACAACACACAGTCTACTCACCATAGT  
CTATTATCTGTCCCAGGATCCTCCAATATTCTAGTTGATTGCTGGACATTATTCCACTGCATAGGTGGGAC  
AGA

9-403 (Ava II digestion site is underlined; probe used is in bold):

TTTATTTGGGCTGCTGGCAGGAAGTCTTTGAGAGAGGGCTTCCAGCTGGGCTCTAATTCACAGTTTTCTTG  
TCTGCTTTCTTTTCTCTTGATGCTGTGAGAAAATGCCTAAGAGAATAGAAACAGGAGTTATTTTGAGAAGG  
GATATG**GTCCATTCTGACAGGAAGGACTGGTGGCTGGAAAGGCAGACAGTTGATCACACTGTATCCACAGT**  
**TACACAGAAAGAGCTAAACAACCACTTTACAATATCCTTATCATCTCAACATATAGATCAAAATGTACAGA**  
**GCCAATCACATTTAAAGGAAAATACTAGATAAAAAGTGGGGCTAGAGAGATGGTTCAGGAGGTAAAGCACTT**  
**GCTGCATGACCAGGAGTTTAGCTCTGCAATAGTGGACTGAAAATCTCTCACATTCTAAGCGGCTGGAACCTT**  
**TTGCTGCACCTCGCAGCCAGAATTAATAGTACACATGGAGGTCCTCTGAAACTTCACTCTGTACTCAGCC**  
**TGTTTAACTTCTGTTAAGAGAACAATGGAACCATCAGCCTTACTTGCCTTGA**

10-336 (Pst I digestion site is underlined; probe used is in bold):

GCAAGTGGAAAGCCAGTGTGGAAAACATAATCTGGTGGCTAGGACATGAAACGAAAGATATAATATGGCCC  
AAGCAAGCTTCCAAAGGCTAAACTCTTACTAGGCAGAAACATATGCTTTTATGGAATCTAAGTCCAGCAGT  
ACTGGTCTGACACAACAGTACGGGAGTAGCAAGGGGTAAACATTAAGGACTCCTGTTTGCAAGCTGTC  
GATCACTGGCATGCAAAGAGATCAGAAAAGGGCGTTATTAGCAGGCATCTTCACTTTCCTATGCCTGCAGT  
**GCTCTCTACAAAGATGAGGAGTCTGACCTTGGGGAATGTTTTGTACCTGGTGAGCAACTGAGATGGAAGC**  
**CTGGGGACAGAAAGTGCCCAATCCCGCTCAGAGCAAAGGCAGCAGAGCTCTTTTCTTTGGGGTGATTGAGG**  
**ATCCCCACAAGGAGAAGTCATCCACCTGGGTCCTTTGAGAAGAGAATCTTAGGCAGAGGGAGTAACCTAA**  
**ACAGAGACAGCTCAGAGAGGCATAGCCAGGGTGTGGTGAGAGACTACCCTCAGCCAGGCTGTGGGCAGCTG**  
**AGCCTGGGAGCAGTGGGGGTTGGAAGACCTTGACCATGCTGGGAGATCAA**

12-573:

ACCAGCACATTGGCATGAGAACACCCCATGTTCTCATAACAATTTACCAATGAGCTAAACGTGTCTAAATT  
 ACAACTGAGGACCAAGACAGGAAGAGTGGAATACGACAAAGCTTATATGAAGTCCTGTATCTCAAAGATGG  
 CCGAGACTGTCTGACTCCAAACCCTGACCTCTGTCTTAGCACATCAGAGGCAGATGCCAGGAACCAAAGGC  
 CAGCCAGTATGTGCTAACAGTGGGGACATACTGTGTGTCTTAAGAGAGAAAGATGGCAAGTTCTAGGAAAG  
 CCATTGATCTAACCTCGGAGGAAAGCGTAGGGCCTGTCTCACATCTGAGTTGACAGCTTCTTTGGTTTTTG  
 TATCTCCTCATATCTGCTAAGAGAAGAAACACTCTTCTTTCTGAGAAAGGGTTGAGCAATGGGACAAATAT  
 CAGTGAGACAGAGTTCTCACCAGAGAACTCTGGACTCTGGGTGCTGGCCCAAAGCTGTGCTTGACCTACCC  
 TCCACTCCCACCTCCACCCCTACCCCACTCCACATCTCATCTCAGGACCTCATCCCTGTCTGAGAATTG  
 GTGCA

15-407 (Xmn I digestion site is underlined; probe used is in bold):

GAAACTGCACAGCACACTGAAGCAGAGCCTGGGCTAGCAGACTCGAGGTCTGGGATGCACCTCCCCAGAG  
 GCACCATTGAGCCAAAGAACTCTACCACATCGACACATTTGGGCACACATTCTATCTCATCTGACCCAG  
 AAATAAGGAGGCTCAGTCCCGGTTGGCACTTAGATGGGAGAAATATTTATAAAAAGTGTCTGCCATATG  
 CCAAAGCCTGGATCTCTGGAGACCCAGTAGGCAAGGCTCAGCTCACAAGAGCCTGGCTTCCAAGAAAGC  
**CTTCCACACTGGCCAGGACTGCTTAAATCTTGAGGCTTTTATTCAAAGGGTTTGGTTAAAGTGTTCCT**  
**CCACTCCTCTGCTCCTTCCAACTTACATGAGTCACCTGTTGGTTCAGACCCAGGGGTGGGGCTGAAGGC**  
**TCACACAGACTGGGCATGGTCACCAAGACCTCAGCACCAGGCTCTCCAGTACAGTAGGAGCACTATCTGA**  
**GAAGAAGATGCTGGGAGAGCCATGACTTACTTAGCCTGTGCAACTATATACTAACCAGAAGGGATAGCCT**  
**GTGTTTCGGATGGCCTTGTCTCTCTGACTCTCTTCCGAAGCTGTAGAACAGGGGGCAGGAGTTCCTCTT**  
**ACACAGCTAGGCACCTTGTGAGGCACCAGGTTTGTGGGTCCAGGAATTGAACTCA**

18-735:

AGAGCATGCTAGCTGGTCAAGTGTTAGCTTCCGTAGAGTTGGGGGATGCCAGGAGGTAAGTGTGAGTGTGT  
 CCACCATGGCATTTCAAATAAATGTCAAAGCCTCTGACCTAATGAGGTCATTGTTTGCTTGACAGATTCTA  
 AATGTAACAACATTGTTGGGATGTGGTGAAAGTTAGGAGCCAGGGCCTAGTTGAACAAAGTAGGATACTGA  
 AGTAAGGGGGTTTTGGTCCGACCTCTTCCATATATTTTTTCTCAGTTTCTAGGCCATGAGCCATGAAGTGT  
 TCAACATGCCATTCTATCATAATGGATTGACCTTTGATACCATGAGCTGAAATAAATGATCCTTTCTTTT  
 AAGTTGTTTGTAGACATTAGGTCACAATTAGGTCACAATGGCAAGAAAGTTGATGGACACAGGACAAAGG  
 GAAGAATGGGATAATTTGTCCAGTAGAACTGTCTCTACTAATGTCACTGTTTGTGTTAATGTCCACT  
 GGATGAACTTCAGTGGAGACTATGAAGTCTGTAGATAGCAACATTTGCATCCAATCCATACTGTGGTATTA  
 ATGGAGTAATTTATTTAAAAGAACCAGAAAAGTGTGAATAGAATTATTTTTAAATACAGAGTAGTAAAA  
 AGGAAATTTTTCAGGATATGAAATTTCCAGAGCAAACCATTAGGATGCAGTCAATCCCCTGGGAGTGAG  
 CATTGCCAGCCAGAGTTCATGAGA

19-395:

TCCAGTTAACCTCTTCTGTGGCTTCATAGGTTGTGTCTTTCTCTCTTCTGCTCATAGGAGTATGTATATA  
 GGGTTTCTGTAGCCCTAGCTTAGTCAGGAATTCCTTTAGTTTGTGCTTATCATGGAAAGTTTTTCATTCTT  
 TACTTAGGAATCAATTTGCTGGGTAAACAGTTACCATCTTTCAAAGCTTGACATTAAGCATCCTATGTTCT  
 CCTGGCATTATGATTTCTGTTAAGAAATTTGATGTCAAAAAGAAAGAAATTTGCTGTCTGTTCTGGGTTTAT  
 ATAGTCTTTCTTATTCTTTTTTTTTTTTTTTTTTACTACAGTATGATGTTAGGAGGTTCTTTTCTGGTCTC  
 ATTCATTTTGCATTATAAATGCCTCCTCTACTTGCAGGGA