

## Appendix 1

### Sequences of Primer Pairs Used to Construct the Human SCL Tiling Path Array

| Amplicon Name | Primer 1 (5'→3')            | Primer 2 (5'→3')          | Amplicon Size (bp) | Chrom 1 Co-ordinate Start | Chrom 1 Co-ordinate Finish |
|---------------|-----------------------------|---------------------------|--------------------|---------------------------|----------------------------|
| HSTAL.1       | CATGATATTCATCCCCTGCC        | TTCTGAATGATGACCATGCC      | 499                | 47262288                  | 47262786                   |
| HSTAL.2       | TTCAGCTCTCAAGGCCAAAT        | TCCTAAGTCCCCAAAAACCC      | 504                | 47262613                  | 47263116                   |
| HSTAL.3       | AATGACAAGTCAAGGGGGAA        | AAAAATGGCCTAAGCCTGAA      | 457                | 47267138                  | 47267594                   |
| HSTAL.4       | ATTTGAGCACCAGTCTCTACCA      | CCTTCCGGTCTCTGGATTACT     | 459                | 47271823                  | 47272281                   |
| HSSCL/M183A   | CCAGCGCCTTTTCTGAGTAGTAT     | TACTGTCCCTTACCAACTCAGGAAC | 218                | 47272114                  | 47272331                   |
| HSTAL.6       | GTCTTTTTCGAAGCCCACAA        | AGGTTGAAGATGCTTGGCAC      | 507                | 47272825                  | 47273331                   |
| HSTAL.7       | GCCAAGCATCTTCAACCTTT        | ATTTTGCAGTGCCCTGTTCT      | 447                | 47273314                  | 47273760                   |
| HSSCL/M182A   | TTTGCAGTGCCCTGTTCTTAGTA     | ATCTCATGCCATTTCCGTTGTAC   | 284                | 47273475                  | 47273758                   |
| HSTAL.8       | CTAAAACTGCCTGCAATCCC        | CAACAGAATTCAACTGGGCA      | 417                | 47276178                  | 47276594                   |
| HSTAL.9       | TCTGAAGCAGATCTCCAGGC        | GGCAGACTATTCTTTCCGCA      | 439                | 47276807                  | 47277245                   |
| HSSCL/M178A   | GTGATAAGGAAGAGGGGTGTGAAT    | AGCAGAGATGCCGAGATGAAAT    | 488                | 47276919                  | 47277406                   |
| HSTAL.10      | GTCACAGGAGCCCTGGAATA        | CCTCTTTCTCCCTCTCTGGG      | 539                | 47283559                  | 47284097                   |
| HSTAL.11      | ATCACCTTTCCAGATGGACG        | GCTACATCATGGCTCCAGGT      | 511                | 47283920                  | 47284430                   |
| HSSCL/M171A   | TGTTGCCCTTCAATCCATCTTG      | TGAGGGGGCCTTCGTGAA        | 405                | 47284183                  | 47284587                   |
| HSTAL.12      | CATTGGTGGAATGCAAGATG        | GCAAAGATCCCCATGATAGC      | 559                | 47284553                  | 47285111                   |
| HSTAL.13      | CACATAATATTCCGCCACC         | GCCTAAAACTGAGTCAGCCG      | 452                | 47285213                  | 47285664                   |
| HSSCL/M170A   | GAAAGCTCTGGAGGGCAAGAA       | TCCCCCGACCCATACAAAA       | 399                | 47285443                  | 47285841                   |
| HSTAL.14      | CTTTACATTCTTTCCGCCA         | AGCAAATGAAGAGAAGGGCA      | 561                | 47285797                  | 47286357                   |
| HSTAL.15      | CCTTCTCTTCATTTGCTGGC        | AAGTGGCAACAGAATCACCC      | 467                | 47286341                  | 47286807                   |
| HSSCL/M168B   | TGCAGCCACCCTCTCATTG         | TCTCAGTTATTGCCTTTGTCAATCT | 383                | 47286641                  | 47287023                   |
| HSTAL.16      | ATTCTGTTGCCACTTGTCCC        | TGGACATCCCCTTTTCTCTG      | 470                | 47286793                  | 47287262                   |
| HSSCL/M168A3  | AAAAAAGCATGCACATTATCTAACAAA | AAGGGGATGTCCACTCTGCTG     | 494                | 47287249                  | 47287742                   |
| HSSCL/M168A   | TTATTAGGGGATTTTCATGGAACAC   | ACAATGCAGATCCCTTTTCACTAA  | 625                | 47287327                  | 47287951                   |
| HSTAL.18      | TGGCCTAGTATGTGCCATGA        | CAGAACAGACTGCCCATTA       | 516                | 47287855                  | 47288370                   |
| HSSCL/M167A   | AATGGCAACTGGAACACCATAAC     | GAGACTCACCCAAAGGAGCTAATAA | 447                | 47288277                  | 47288723                   |
| HSTAL.20      | TTGCCACTAAAGCAGCATTC        | TCCTTTTCAGGGGCTCTACA      | 439                | 47289636                  | 47290074                   |
| HSSCL/M165B   | TTTTCAGGGGCTCTACAATTTTC     | ATCAGTTGGGGAAAGAATAAAAGAG | 324                | 47289748                  | 47290071                   |
| HSTAL.21      | TGTAGAGCCCCTGAAAAGGA        | CAGGGTGGAGATGATATGGG      | 521                | 47290055                  | 47290575                   |

| <b>Amplicon Name</b> | <b>Primer 1 (5'→3')</b>     | <b>Primer 2 (5'→3')</b> | <b>Amplicon Size (bp)</b> | <b>Chrom 1 Co-ordinate Start</b> | <b>Chrom 1 Co-ordinate Finish</b> |
|----------------------|-----------------------------|-------------------------|---------------------------|----------------------------------|-----------------------------------|
| HSTAL.22             | CAGAATCTTCGCTCATGCAC        | GAAAGCAGAGAGCAAGGTGG    | 400                       | 47293173                         | 47293572                          |
| HSSCL/M161A          | CCCAAAAGCCTACCACTGAAAA      | TGGGAAGTAGAGGGGTGTGATT  | 675                       | 47293506                         | 47294180                          |
| HSTAL.24             | CGGGTTTACTGTGAAGGGAA        | GTCAGCTAACTGAGGGCCTG    | 495                       | 47294020                         | 47294514                          |
| HSSCL/M160A          | TAAGCCCCGATCAGAAAGTCC       | CATGACAGGCCCAAAGACTACA  | 426                       | 47294670                         | 47295095                          |
| HSTAL.26             | CCACAGTTTGCAGGTCTTGA        | AAGCGGAGCAGAGTTAATGC    | 479                       | 47295048                         | 47295526                          |
| HSSCL/M159B          | AACTATGCTTGAAAGCCACTCTACC   | GCAGCATTTTGCCTAATTGAG   | 437                       | 47295470                         | 47295906                          |
| HSTAL.28             | GCCACCTTCTGAGTCCCATA        | CCCACCCTACAACCTCAAAA    | 479                       | 47296007                         | 47296485                          |
| HSSCL/M159A          | AACCTCTGCGTCCTAACTTGTA      | CCCCATGCTGGTGTGTGCT     | 509                       | 47296301                         | 47296809                          |
| HSTAL.30             | TCCAGCTGTCACTCATGGAT        | GCATGTGGGAAAGTGATAAAAG  | 583                       | 47305418                         | 47306000                          |
| HSSIL/M64A           | CACAAGCACACTTTTCTAAGAGTTACA | GCAGCCCCTAAACCTTCCAG    | 304                       | 47305922                         | 47306225                          |
| HSTAL.31             | GAGCTGCCCTGGATAGTGAG        | TCCCTACTTGGATCAGCACC    | 561                       | 47306091                         | 47306651                          |
| HSSIL/M65A           | GGGAGGTTGGGTGGAATGAA        | CTTGGGCCATTAGAGACAGAG   | 477                       | 47306728                         | 47307204                          |
| HSSCL/M148A          | GGGCCATTAGAGACAGAGAAG       | CCAGGATTTGAGGCAGAAAGAA  | 410                       | 47306792                         | 47307201                          |
| HSTAL.33             | GGATTAGGGAGCAGGAGGAA        | GCCATAGAAAACATAAATGGGG  | 572                       | 47306900                         | 47307471                          |
| HSSCL/M141A          | CCAAGCCCTGAATCATTACTTTT     | GCCAGGGAGGGTTAATTCATAG  | 558                       | 47314179                         | 47314736                          |
| HSTAL.35             | CCAGTCTCCCCAATGGAATA        | GGGAGAACAGCTTCATCAGC    | 448                       | 47314549                         | 47314996                          |
| HSSCL/M140A          | CTCCCCCACTGAGTTCCTCC        | ATGGACAGGGGAATGTGGTAGA  | 444                       | 47314953                         | 47315396                          |
| HSTAL.37             | ATCCAGGAGGTAGGGAGGAA        | ACTTAGCCAGTTGGTCCCCT    | 569                       | 47315364                         | 47315932                          |
| HSSCL/M139A          | ACAGGAAGGGGATGACATGCT       | GGAGGGCAATGCCTGATTG     | 521                       | 47315634                         | 47316154                          |
| HSTAL.38             | CCTCCAAGTGAGGAGACTGG        | GATAGCAGTGCACAGGGGAT    | 485                       | 47316032                         | 47316516                          |
| HSTAL.39             | ATCCCCTGTGCACTGCTATC        | AAAAGAGTCGGCCCTTCACT    | 456                       | 47316497                         | 47316952                          |
| HSTAL.40             | AGTGAAGGGCCGACTCTTTT        | TCTAATGTCTGCCCACCTCC    | 486                       | 47316933                         | 47317418                          |
| HSTAL.41             | GGAGGTGGGCAGACATTAGA        | CATATGGTGTGGTGTGGA      | 500                       | 47317399                         | 47317898                          |
| HSSCL/M137A          | AGTCAGCCATTGTCTTCATGTTGT    | GCAGGCAGCAGGGAGCTCA     | 448                       | 47317806                         | 47318253                          |
| HSSCL/M136B          | ATCTGGGGCAATTTACGTTTC       | CCTTCACTCCTGCTGCAAAGAC  | 479                       | 47318407                         | 47318885                          |
| HSTAL.45             | ACCAAGAAGTATGCTGCCT         | TGACTGGTGACAATTTGGGA    | 557                       | 47319185                         | 47319741                          |
| HSSCL/M135B5         | GGGCAATGCAGGAAAAGGA         | TCAGACCCGAAATCCCATGG    | 412                       | 47319258                         | 47319669                          |
| HSSCL/M135B3         | CTGCACGGACCTAGGGATGA        | ACAAATTCCTGGCTCCACGG    | 476                       | 47319283                         | 47319758                          |
| HSSCL/M135A5         | AAGGGCCTTGTGTTACCATG        | CTCCCTCCCAAATTGTCACCA   | 438                       | 47319716                         | 47320153                          |
| HSSCL/M135A3         | CTGTCCATGCTGCCACTGAAG       | CCCAGCCTTCCACAATGACAT   | 462                       | 47319857                         | 47320318                          |
| HSTAL.47             | AGAGGGTTCCCCAGAGTTGT        | AAGGGGCTAGTATGGGCACT    | 468                       | 47320067                         | 47320534                          |

| <b>Amplicon Name</b> | <b>Primer 1 (5'→3')</b>      | <b>Primer 2 (5'→3')</b>        | <b>Amplicon Size (bp)</b> | <b>Chrom 1 Co-ordinate Start</b> | <b>Chrom 1 Co-ordinate Finish</b> |
|----------------------|------------------------------|--------------------------------|---------------------------|----------------------------------|-----------------------------------|
| HSSCL/M134B          | GGGGGCATGGACCTTCTTAA         | TGCCCAGCACATTTTGATGA           | 493                       | 47320457                         | 47320949                          |
| HSTAL.49             | TCTCCTTGATGACCCTGGAC         | ATGGCCTGGATGTAGGACTG           | 465                       | 47321016                         | 47321480                          |
| HSSCL/M134A          | GGAGTCAGGGCAGGTACTTTCA       | ACCGCCACACAAAGGAAGAG           | 499                       | 47321175                         | 47321673                          |
| HSSCL/M133A          | CGTGGCCCTCAAACATGAA          | AAGAGGAGCCTCCATGAACTGT         | 470                       | 47321845                         | 47322314                          |
| HSSCL/M132A          | CCAGCCCTGCACATCTCAAG         | GGCCTCCTGGGTGATGGA             | 529                       | 47322401                         | 47322929                          |
| HSTAL.53             | ATGGGGTCAGTGCAAAAGAG         | CATGATACCTGTGGTGCAGG           | 592                       | 47322974                         | 47323565                          |
| HSSCL/M131B          | TCAGAGGGTTGACCAGAGACTTC      | TAGGTGTTTTGGGCCCTTCTTTT        | 448                       | 47323461                         | 47323908                          |
| HSSCL/M131A          | ACCGCAGCCATTCTGGAGT          | TCAAATGGGCAGCCTGAATT           | 665                       | 47324064                         | 47324728                          |
| HSTAL.56             | TCTTGAGAGAAAAAGCCCAA         | ATGTGTGTCTGGAGCACAGG           | 598                       | 47324602                         | 47325199                          |
| HSSCL/M130A          | TCCAGCCCACATCCTAGCC          | ATCATGTCGCTGCCACTAGAGAA        | 515                       | 47324950                         | 47325464                          |
| HSSCL/M129B          | GACAGGGCCAGGGCTCTAAG         | GATGCTGTCCCACCTGTGATG          | 503                       | 47325526                         | 47326028                          |
| HSSCL/M129A          | GAGTGGGGGTCAGGAAGACAG        | GCCAGGATGGGGTAGAAGTGT          | 401                       | 47326128                         | 47326528                          |
| HSTAL.60             | TCCCTGAATCTCCACCCAC          | GATGACAATCAGGTAGGGGC           | 591                       | 47327280                         | 47327870                          |
| HSSCL/M127A          | CTTAGCTCAGCCTTGCTGTGATT      | TCAGCCAGACAATCCCTCTATCT        | 407                       | 47327924                         | 47328330                          |
| HSTAL.62             | GAGGGAGAAGCTCACACCTG         | CTTTGAGGCTTTCCTGCTCA           | 576                       | 47328237                         | 47328812                          |
| HSSCL/M126B          | GCCCAGGGTCAGCAGTACC          | GAGGCTGCACTGAGCTGAGC           | 409                       | 47328778                         | 47329186                          |
| HSTAL.65             | GATCCCTCTCTCCTTGGGTT         | GTTGCTGGATGTTTCCTGGT           | 493                       | 47338055                         | 47338547                          |
| HSSCL/M116A          | GATGGCAGCCCCTAACTTTC         | CATCATCAACTGGCACAGTCCTC        | 446                       | 47338682                         | 47339127                          |
| HSTAL.67             | AGTCCCACAGTTTGCCATTC         | TCAGCACCTGTATTTACGC            | 593                       | 47338958                         | 47339550                          |
| HSSIL/M53A           | GGGAGGGAAAGCAAACTCAC         | CAAGGGCACCAATTCAGAACT          | 467                       | 47339446                         | 47339912                          |
| HSSCL/M115A          | GCCACCCAGCAAAGAAGAAA         | TGTCCCTACCCTTTGGCTTAGA         | 439                       | 47339676                         | 47340114                          |
| HSSIL/M53B           | TTGGTGCCCTTGGCTATGAC         | ATGTCACAGTTCAGTTGCTCAAGG       | 305                       | 47339901                         | 47340205                          |
| HSSCL/M113A          | GCAGGACCATTTCCTATTCTT        | CTCATTTTCATGTTTGTAGTGGAATAGT   | 298                       | 47342174                         | 47342471                          |
| HSSIL/M55A           | ATGATACAATGAAGATTGAAATGTGACA | TTCATCCCTAACTGAAGGAGAATGATAAC  | 325                       | 47342204                         | 47342528                          |
| HSSIL/M57A           | GTGGCCATGATGGGAAAATTA        | TTCCCTTATCTATGCCATATCCATTA     | 282                       | 47343276                         | 47343557                          |
| HSSCL/M105A          | TCGGGGTCACTGGGAAATG          | CTAAAGAGGGTCAAGTTATCTTCTGG     | 367                       | 47350069                         | 47350435                          |
| HSSCL/M104A          | TGATCGTCCCATGAATGTGAAGT      | GCCATCAGAGCTTCCATTTTAAT        | 471                       | 47351208                         | 47351678                          |
| HSTAL.71             | AGTCCATAACACCAGGGCAG         | AAACAGTGTGTGTGGAGGGG           | 575                       | 47351603                         | 47352177                          |
| HSSCL/M103A          | GGGGGTAAAGGGCACTTGTTT        | ATACAGAGAACAGGAAGTGGTATTACATAT | 391                       | 47352054                         | 47352444                          |
| HSSCL/M102A          | CGGGTCTCAGGATCTCCTTTT        | ACAGCCAGCCAGGATGCTT            | 418                       | 47352494                         | 47352911                          |
| HSTAL.73             | GACAATGGCTAGTGGGCAAT         | CAGCCATCGTGATTTTCCTT           | 504                       | 47352766                         | 47353269                          |

| <b>Amplicon Name</b> | <b>Primer 1 (5'→3')</b>  | <b>Primer 2 (5'→3')</b>   | <b>Amplicon Size (bp)</b> | <b>Chrom 1 Co-ordinate Start</b> | <b>Chrom 1 Co-ordinate Finish</b> |
|----------------------|--------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------|
| HSTAL.74             | TCCTCTCGCAGATGTGAATG     | TTTGTGAGGCAAAGACCACA      | 508                       | 47353496                         | 47354003                          |
| HSSCL/M101A          | ACCACCTGCCCTCAGCTCAT     | TGCAGGAGGGAGTGAGCT        | 271                       | 47353827                         | 47354097                          |
| HSTAL.76             | GAAAACAGCACCACCACCAT     | CAGAGTGAAGTGAATTGGATGC    | 509                       | 47355636                         | 47356144                          |
| HSTAL.77             | ACATTCTGTACCTGCCAGCC     | GAGTTCTGAAACAGCTGGGC      | 525                       | 47355951                         | 47356475                          |
| HSSCL/M98A           | TGCCGATTGGTTCAAATTCC     | CGGGACAGATGGCTGGAGT       | 498                       | 47357176                         | 47357673                          |
| HSTAL.80             | CAATTTTACCGCAAAGGAA      | GAGTTCCGTCTCCAGAGTGC      | 513                       | 47357585                         | 47358097                          |
| HSSCL/M97A           | GTGCCACCTCCTCTTTCTCT     | ACGGAAGTCCACAGCCTGTTT     | 491                       | 47358089                         | 47358579                          |
| HSTAL.82             | AAGGAAGCTTAGGAGGCAGG     | CTGGAGAAGGCTGATAACGC      | 540                       | 47358481                         | 47359020                          |
| HSSCL/M96B           | GCCCCCTTCTCATTCTGTCTT    | CTCCAGCCCCGCCCTAGT        | 447                       | 47358901                         | 47359347                          |
| HSSCL/M96A           | CGTGGCTGCCTGTGACTCA      | TGCTGGGGAGCAAGGTGA        | 491                       | 47359379                         | 47359869                          |
| HSTAL.84             | GAACCTTGGTTGGGTCAAGA     | TCACCTCTGTGACTGTTGGC      | 537                       | 47359783                         | 47360319                          |
| HSSCL/M95A           | ACGGCAGAGCTGGAGGAGA      | AAGCAAGGGGGCTGTGACA       | 351                       | 47360136                         | 47360486                          |
| HSTAL.85             | ACAGTCACAGAGGTGAGGGG     | CCACTCTACCTTGCTCCAG       | 523                       | 47360304                         | 47360826                          |
| HSSCL/M94B           | GCCAGGGTGAGGGTAAGAGAG    | GGGCTACTGGAGGGAGACAGA     | 485                       | 47360654                         | 47361138                          |
| HSSCL/M94A           | AGCACCCCGATGTAACCTTCT    | AGGGGCTTCCTGCATAATCC      | 479                       | 47361199                         | 47361677                          |
| HSSCL/M92A           | TTCAGGGAGAGCCCACACTG     | CCCCCTCGTCCAAGCAGA        | 427                       | 47362829                         | 47363255                          |
| HSTAL.92             | ACCAAGACTCCAAGAAGCGA     | AGGTGGGGTCCTTGAAGAGT      | 490                       | 47364722                         | 47365211                          |
| HSSCL/M90B           | CCTGCCTCCCCACAATGTC      | CCCACCCTGCCTGCTCAG        | 296                       | 47364972                         | 47365267                          |
| HSTAL.93             | ACTCTTCAAGGACCCACCT      | TGTCCTGGTCCACTCCTCTC      | 515                       | 47365192                         | 47365706                          |
| HSSCL/M90A           | TGGGGCCTCAACCTAATCTCT    | GGCAGCCCAGAGCCTCTTT       | 427                       | 47365419                         | 47365845                          |
| HSTAL.94             | GAGAGGAGTGGACCAGGACA     | AGAGGAAAGTCCTTTGGGGA      | 409                       | 47365687                         | 47366095                          |
| HSTAL.95             | AAGGACTTTCCTCTTCCCCA     | ACCTGAGGGAGCAGTCTGAA      | 470                       | 47366082                         | 47366551                          |
| HSSCL/M88B           | CAAGGTCTGGCTTTCATTCTACAC | AAGCAGTATTTGGGAGTCATTGTTT | 467                       | 47366498                         | 47366964                          |
| HSTAL.96             | CCCTGTTTCCTCTAGACCC      | GAGAACAGTGCCCAGTGTGA      | 578                       | 47366602                         | 47367179                          |
| HSSCL/M88A           | AGACTGAGCCCAGGTTGATTC    | TCACACTGGGCACTGTTCTCTATC  | 569                       | 47367160                         | 47367728                          |
| HSTAL.98             | AGTCTATTGGTGTCGCCTG      | AGGCACTGAAGCCGTAGTGT      | 574                       | 47367688                         | 47368261                          |
| HSSCL/M87A           | TTCAGGCCCTCTATTGAGATCTTT | GCTGGCATTGAGGTCATCT       | 463                       | 47367872                         | 47368334                          |
| HSTAL.99             | ACACTACGGCTTCAGTGCCT     | AGGAACTCTGGCCATTCTCA      | 536                       | 47368242                         | 47368777                          |
| HSSCL/M86A           | CCTGGGGACCTTCCATCTCT     | TCTTGGCCCCAGATGTGGT       | 505                       | 47368414                         | 47368918                          |
| HSTAL.100            | GAGAATGGCCAGAGTTCTCTG    | GCATCACTCAACTCCAAGCA      | 485                       | 47368759                         | 47369243                          |
| HSSCL/M85A           | TGTGGGGCTGCTGAGACCT      | CCTCCAACCACTGCCCTCA       | 411                       | 47370130                         | 47370540                          |

| <b>Amplicon Name</b> | <b>Primer 1 (5'→3')</b> | <b>Primer 2 (5'→3')</b>  | <b>Amplicon Size (bp)</b> | <b>Chrom 1 Co-ordinate Start</b> | <b>Chrom 1 Co-ordinate Finish</b> |
|----------------------|-------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------|
| HSSCL/M84A           | GCTCTTTGCCTGGATTCTCT    | AACCATCAGGCCCTTAGACA     | 457                       | 47370620                         | 47371076                          |
| HSTAL.103            | GCAGGCAAAGTTAGCCAGAG    | TTTAAGGGCTGATGAATGCC     | 555                       | 47371010                         | 47371564                          |
| HSTAL.104            | GCAAACCTTCTTGCATGGGT    | GTCCTTGCCCCACAGATAGA     | 581                       | 47371572                         | 47372152                          |
| HSTAL.106            | GATCAATCAACCCATCCTGC    | TTTCCAGTCCCATAGTAGCCA    | 471                       | 47374482                         | 47374952                          |
| HSSCL/M78A           | GGCACCTCCTTGATTGACTCTTT | TGGGTGCAGCCGTGGAG        | 520                       | 47376719                         | 47377238                          |
| HSTAL.108            | GCTGCATAGACGCAGAAGTG    | TGCTCACTGCACCCACTAAC     | 593                       | 47377186                         | 47377778                          |
| HSTAL.109            | GGAGCTCACAGGTTAGTGGG    | GACTCCACATGCCCTGAAAT     | 403                       | 47377748                         | 47378150                          |
| HSTAL.110            | ATTCAGGGCATGTGGAGTC     | GCTTCTTGACTGAGCAAGGG     | 445                       | 47378131                         | 47378575                          |
| HSSCL/M76A           | CTTCTCTCGCCACACTGTGCT   | CCCTCGGACCCTTTCACACT     | 559                       | 47378586                         | 47379144                          |
| HSTAL.112            | GTAATTGGAGGCTTCCCCTC    | GACTCCTTTCCTGGCATTCA     | 440                       | 47379037                         | 47379476                          |
| HSTAL.114            | TACAAGTCACATCCCTCCCC    | TCCATCCTCTTCTCCCTGAA     | 485                       | 47385593                         | 47386077                          |
| HSSCL/M69A           | GGCTGGCAGGCTGTGTGA      | GGGCAGGATGGGACCATTAG     | 634                       | 47385726                         | 47386359                          |
| HSSCL/M68B           | AGTCCCCAGCCAATCTTTCC    | GCCCCAACCCAGCAGATG       | 461                       | 47386420                         | 47386880                          |
| HSTAL.116            | GGTGCTTAGGGTGATGGA      | TATGCCTGGTGACAGCTCAG     | 586                       | 47386620                         | 47387205                          |
| HSTAL.117            | TGAGCTGTCACCAGGCATAG    | AGAATCCAGGGTAGAGGGGA     | 512                       | 47387187                         | 47387698                          |
| HSSCL/M67A           | CACAGCGAGGCTGCTTAGAGA   | AGGGAGGGAACAGCAGGACA     | 482                       | 47387699                         | 47388180                          |
| HSTAL.119            | ATAGCACCAGCAGTCTTGCTT   | TGGAGTGCTGCCCTAGAAGT     | 527                       | 47388080                         | 47388606                          |
| HSSCL/M66A           | CTGCCTGGGTCTCCCTCTG     | CACCAGCAGATCTAGTTCTAGCTT | 414                       | 47389245                         | 47389658                          |
| HSTAL.121            | CTTCGAACGGATCACATCCT    | ATACAGAGCCCTTCCACCCT     | 421                       | 47389762                         | 47390182                          |
| HSSCL/M65A           | TGCTTGGGAATGGCAGAAGA    | GCAAGTGGGGAGAGGTAGGAA    | 509                       | 47389839                         | 47390347                          |
| HSTAL.122            | AGGGTGGAAGGGCTCTGTAT    | GTCAGGGCAGTCAATTTGGT     | 500                       | 47390163                         | 47390662                          |
| HSTAL.123            | ATTGACTGCCCTGACTGTCC    | ATTGGGAGGCTGTTGATTG      | 575                       | 47390648                         | 47391222                          |
| HSSCL/M64A           | GGTGGGAGGCAGAATCATTGT   | GAGGGGGAACACTGGCTTCT     | 334                       | 47391105                         | 47391438                          |
| HSSCL/M63A           | GTCCTCCAGGGAAGAGCTG     | CTCCCACCATCTCCACTCTT     | 507                       | 47391431                         | 47391937                          |
| HSTAL.126            | ACCTCATCGTTTCTGCCTTG    | ATGGTGAGATTTAGCCGTGG     | 491                       | 47392128                         | 47392618                          |
| HSSCL/M62B           | GCCAAGAGGTGAGTTCAAGGAC  | CCCTCAAGCCCTTAACCACAG    | 369                       | 47392495                         | 47392863                          |
| HSTAL.127            | CCACGGCTAAATCTCACCAT    | GGCCATCAAGGTGAAAAAGA     | 584                       | 47392599                         | 47393182                          |
| HSSCL/M62A           | TTATGCCTGGCTCTTAAGGATTG | GGTGCCAGTTCACATGCTG      | 479                       | 47393085                         | 47393563                          |
| HSTAL.128            | GTGCCTGCATGACCTACTGA    | TCAGCAGACATCCCCTCTTT     | 404                       | 47393307                         | 47393710                          |
| HSSCL/M61B           | ATGAATTGCGTTGGTCTCTGC   | GGAAGCTCACCCCAACACAA     | 503                       | 47393673                         | 47394175                          |
| HSSCL/M61A           | CCAAAACAAGCCTGGTAGGAAA  | GCAGGGGGCAAGTCTTCAG      | 443                       | 47394243                         | 47394685                          |

| <b>Amplicon Name</b> | <b>Primer 1 (5'→3')</b>  | <b>Primer 2 (5'→3')</b>  | <b>Amplicon Size (bp)</b> | <b>Chrom 1 Co-ordinate Start</b> | <b>Chrom 1 Co-ordinate Finish</b> |
|----------------------|--------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------|
| HSTAL.131            | CCTGGCCTTGGAACAAGATA     | AATCTCAATCCTGCAGTGGG     | 503                       | 47394753                         | 47395255                          |
| HSSCL/M60A           | AGCTTGGGGCAACATTGTTT     | CAGGCCAAAGCGGTTTACAA     | 525                       | 47395143                         | 47395667                          |
| HSTAL.133            | AGGACAAGCCACTAGGCTGA     | TGCAGCTTTTGGTCATCAAG     | 463                       | 47395756                         | 47396218                          |
| HSSCL/M58B           | TTCGTGAGCCCCATCTTCAC     | CGTACGCCCATCAGCACAC      | 415                       | 47396529                         | 47396943                          |
| HSSCL/M58A           | GTGCTTTCCCCAACTCCA       | CTCCAGGCCAAAAGCAGTGA     | 461                       | 47397098                         | 47397558                          |
| HSTAL.137            | TCCTCCTCCTGGTCATTGAG     | GCCTCTTGGCACAAGTGAAT     | 547                       | 47397662                         | 47398208                          |
| HSTAL.138            | GCCAAGAGGCCTTACAGCTA     | GGCTGTTTCTTCACAGCCTC     | 462                       | 47398199                         | 47398660                          |
| HSSCL/M56A           | TCGATGTTAGGGAGAGAAGCAGT  | TCCACAGGGCCTTGCAGTAA     | 475                       | 47398789                         | 47399263                          |
| HSTAL.140            | CTTGAACCTTCTGGGCTGAGG    | CCTGCAGTTGTGCTGTGTTT     | 512                       | 47399219                         | 47399730                          |
| HSTAL.141            | GACAGAGAGCATCCCTCAGC     | CAGACATGTAGGCGAAGGGT     | 549                       | 47399791                         | 47400339                          |
| HSSCL/M55A           | GGGGCTGGGATCTGCACA       | ACAGGAATCCACATCAAGTCCTAA | 549                       | 47400200                         | 47400748                          |
| HSSCL/M54A           | CGATCCCCCATTCTAGGCAC     | CCTTGGGCAGCCTTCCTAC      | 475                       | 47400853                         | 47401327                          |
| HSSCL/M53B           | GGTGGGGGGCTCAAGACA       | GGGCTAAGCGCCATTATGTG     | 447                       | 47401442                         | 47401888                          |
| HSTAL.145            | GGGGAAGGTCTCCTCTTCAC     | GTGGTGACCAAGATGCACAC     | 538                       | 47401719                         | 47402256                          |
| HSSCL/M53A           | CCGCCTGAGGACTGACCTG      | CTCCCGCCCCAGAAACAA       | 473                       | 47402147                         | 47402619                          |
| HSSCL/M52B           | GGAGCGCAGGGAGAGGAG       | CCTCTGCCACCACCCTCAG      | 374                       | 47402649                         | 47403022                          |
| HSSCL/M52A           | CAGGCACCCCTCCCTTCTC      | ACGCCGTTTACGAGGACC       | 337                       | 47403471                         | 47403807                          |
| HSTAL.150            | AGGGAAGAGGAGGGAACAAA     | TCAGAGTCCAGCTGAGCAGA     | 446                       | 47403976                         | 47404421                          |
| HSSCL/M51A           | GGGGTCACAAGGTGGTTTCAC    | CGCCCAGCGGATCTTTACT      | 505                       | 47404306                         | 47404810                          |
| HSTAL.152            | TCACTTTGCTCAACCCTCCT     | CCTGGGTGTCTAGTGGCAAT     | 493                       | 47404756                         | 47405248                          |
| HSSCL/M50A           | TGGCATTCCCAAAGAAGGTGT    | GTGCTGGGGCTCTTCCATC      | 443                       | 47404857                         | 47405299                          |
| HSSCL/M50A5          | TCCCAAAGAAGGTGTACAGCAGTC | CTGGGGCTCTTCCATCACCT     | 434                       | 47404859                         | 47405292                          |
| HSSCL/M50A3          | TTCCAGTGGCCTTGGTGTCTT    | AAGGGCCAGAGTTTGTGAGTTG   | 529                       | 47404939                         | 47405467                          |
| HSTAL.153            | CCAGAAGGGAGAATGGATCA     | GCAGTGAGGTAGGGAACCAA     | 407                       | 47405181                         | 47405587                          |
| HSSCL/M49B           | TGGGGCATGGACCTCTGG       | CAAGGCCACTGGAAATGCAC     | 505                       | 47405455                         | 47405959                          |
| HSSCL/M49A           | GGTGGGGAGGCAGGAACA       | AAGGAACGCCCAGAGATTT      | 447                       | 47406027                         | 47406473                          |
| HSSCL/M48B           | AGATCGCCCAGGACCACAC      | ACAGCCGCCCCAAAGTTAC      | 462                       | 47406584                         | 47407045                          |
| HSTAL.156            | CTGTCCTGAGCCTTCCTCAC     | GAGGGGTGTTGTTGCTGTT      | 515                       | 47406802                         | 47407316                          |
| HSSCL/M48A           | CCCCTTCCCAACTCCATTTT     | CCCCGACCAACCAGTCCA       | 497                       | 47407155                         | 47407651                          |
| HSTAL.157            | AACAGCAACAACAACCCCTC     | ACCCCGAAAAATCGAAAATC     | 557                       | 47407297                         | 47407853                          |
| HSSCL/M47B           | CCGCTACAGCCGTTTTCTAAG    | TTCGGGGTTTAGACAGAGTAAGG  | 497                       | 47407846                         | 47408342                          |

| <b>Amplicon Name</b> | <b>Primer 1 (5'→3')</b>  | <b>Primer 2 (5'→3')</b> | <b>Amplicon Size (bp)</b> | <b>Chrom 1 Co-ordinate Start</b> | <b>Chrom 1 Co-ordinate Finish</b> |
|----------------------|--------------------------|-------------------------|---------------------------|----------------------------------|-----------------------------------|
| HSSCL/M47A           | CGCCTGTGCCTAGGTGTTTG     | GCTGCGCTCTGGGATGATTA    | 491                       | 47408395                         | 47408885                          |
| HSSCL/M46B           | GCGGTTGGGGTGTGTAGATG     | CCACAGAAGGGCAGCAAACA    | 308                       | 47409142                         | 47409449                          |
| HSSCL/M46A           | GGCCTCCCACCGAATTCTT      | CAGGCACACCACACTCGGA     | 368                       | 47409451                         | 47409818                          |
| HSSCL/M45A           | CCATGTGGGGAGCAGTGTTT     | GCCATTATGGGCCAAATGATT   | 534                       | 47410103                         | 47410636                          |
| HSTAL.164            | CCCTTCCCTACCTCTTCACC     | AAAGACCCTGGTCTCTGCAA    | 467                       | 47410476                         | 47410942                          |
| HSTAL.165            | ACTCATTGCAGAGACCAGGG     | CCAGTTCTCAGGCTCCAAAA    | 512                       | 47410918                         | 47411429                          |
| HSSCL/M44A           | CCTTATGGTAGGGGGAACTAGA   | TGCCAGGCTGATTTGTCCTT    | 316                       | 47411366                         | 47411681                          |
| HSTAL.166            | GGCTTCTCCTTGGTCATCAG     | CCCACCTTCAAACCAACAA     | 599                       | 47411507                         | 47412105                          |
| HSTAL.167            | CATTAAATGTCCCAGCCAG      | TGTTCTTGTCCTCTGCTCTT    | 569                       | 47412831                         | 47413399                          |
| HSSCL/M42A           | TCGGCTGCTCATCAGAGTGC     | GGCGCTGCTGAAATAGCA      | 444                       | 47413153                         | 47413596                          |
| HSTAL.168            | ATGCATGCACTCTGATGAGC     | TGGAAGCACAGACGTGACTC    | 595                       | 47413571                         | 47414165                          |
| HSSCL/M40A           | AAACCGGGGGATATCACAATG    | GCGGAAGACCAAGCATACAG    | 556                       | 47415098                         | 47415653                          |
| HSSCL/M38B           | GAATGCACATGCGCTTAAATAG   | TGGCCCCACATCAATCTTATG   | 389                       | 47416739                         | 47417127                          |
| HSTAL.170            | TGGCCCCACATCAATCTTAT     | GGAATGTGGCAAGAGAATC     | 574                       | 47416739                         | 47417312                          |
| HSSCL/M38A           | AGGAGAGGGCCACAGCTTTT     | CCCCATAGAAGCAAGGCATG    | 259                       | 47417271                         | 47417529                          |
| HSTAL.171            | TCACCGTTCAGGAGACACAC     | AAGGGATTCTCCTGCCTCTC    | 568                       | 47417423                         | 47417990                          |
| HSTAL.172            | GAGAGGCAGGAGAATCCCTT     | CCTCTAGCAGGCACACACCT    | 533                       | 47417971                         | 47418503                          |
| HSTAL.173            | AAGAATCCATTGCACTGCC      | AGTCCCAGGGCAACCTAACT    | 588                       | 47418453                         | 47419040                          |
| HSSCL/M36B           | TTTCCCTGTGGCTGGTTTCTA    | GGGGGAAGGGTGAACACCA     | 425                       | 47418970                         | 47419394                          |
| HSSCL/M36A           | TGGGAGCAGCAGGTTGAAAT     | CCAGCCACAGGGAAATGTGA    | 401                       | 47419380                         | 47419780                          |
| HSTAL.175            | GGTTTGGGGATGGGTAGACT     | CCCATGCTCTTAACCTGAACA   | 449                       | 47419510                         | 47419958                          |
| HSTAL.176            | TGTTCAGGTTAAGAGCATGGG    | CATTGGGGATCAGTAGGGTTT   | 451                       | 47419938                         | 47420388                          |
| HSSCL/M35A           | TCGGACTCATATGTGCAGAATCAT | CCAATGCGGCAAGCAAATA     | 320                       | 47420383                         | 47420702                          |
| HSTAL.178            | ACCAGAGAAAGCGCTATGGA     | AATCAAACCCAGGCCTCTCT    | 536                       | 47420920                         | 47421455                          |
| HSTAL.179            | TGGAGGCAAAGGGAGTAATG     | TCCTGGTCAGAGGCTGAACT    | 468                       | 47421331                         | 47421798                          |
| HSSCL/M33A           | GAGTTGGGCTTTGAAAGATTTTG  | CCCCAGACCTCCCATGAAGA    | 421                       | 47421718                         | 47422138                          |
| HSTAL.181            | CCCAACTCCAGTGCTCTCTC     | ACAGAGGCGGTGACATTTTC    | 422                       | 47422131                         | 47422552                          |
| HSTAL.182            | GAAAATGTCACCGCCTCTGT     | AAGGCAGAACCTTCCCTAGC    | 577                       | 47422533                         | 47423109                          |
| HSSCL/M32A           | TGCCCTTTAGCCAAGACCAG     | AGTGGCTGCATTGGGCTAGA    | 510                       | 47422804                         | 47423313                          |
| HSSCL/M31A           | TCCTCCAGTCCTGCAGCATAC    | TCATTCATGTTGGCTTTTCATCA | 394                       | 47424426                         | 47424819                          |
| HSTAL.184            | ACCTTCAGAGTAGGCTTCG      | CACTGGGAGCCCTGTAATGT    | 555                       | 47425549                         | 47426103                          |

| <b>Amplicon Name</b> | <b>Primer 1 (5'→3')</b>     | <b>Primer 2 (5'→3')</b>       | <b>Amplicon Size (bp)</b> | <b>Chrom 1 Co-ordinate Start</b> | <b>Chrom 1 Co-ordinate Finish</b> |
|----------------------|-----------------------------|-------------------------------|---------------------------|----------------------------------|-----------------------------------|
| HSSCL/M29A           | TAAGGCTTTTCTGATGAAGTTAAATTG | ATTACAGGGCTCCCAGTGATAAA       | 521                       | 47426086                         | 47426606                          |
| HSSCL/M27A           | CCAGCATGTTGCATCTCTGCA       | GACAACAAAGGAAAATAGTCAATCTAGAC | 387                       | 47427821                         | 47428207                          |
| HSTAL.186            | TACACCAAAACCAACCCACC        | TCCAGCTCTAAGTCTCAACTGC        | 587                       | 47427971                         | 47428557                          |
| HSSCL/M26C           | TAGGCACCTTCTTAGATGTAAAACG   | GCAGTTGAGACTTAGAGCTGGATAGTA   | 345                       | 47428536                         | 47428880                          |
| HSTAL.187            | AATGATCAGGAGCCTTGTGG        | GCTTGGTGGTCAGAAAGAGC          | 469                       | 47428735                         | 47429203                          |
| HSSCL/M26B           | CACAGTGGGGCTTAGTTTAATTTTC   | TCATCTGCTTAGCGTTTCAGAAG       | 488                       | 47428896                         | 47429383                          |
| HSSCL/M26A           | AGGACCATGAACTTAAAGCTGAAGA   | GGAGAAGGCTGAATGGGTCAC         | 328                       | 47429403                         | 47429730                          |
| HSTAL.189            | TTCAGCTTTAAGTTCATGGTCC      | TTGGGGCCTTGATTTTGTTTC         | 519                       | 47429708                         | 47430226                          |
| HSSCL/M25A           | CCATATCCAGAGACTGGTTGATGTT   | AATAATAGCCTAGAAGGTAATCCATGAT  | 349                       | 47430116                         | 47430464                          |
| HSTAL.190            | GGCCCCAAATGTAAAAGTCA        | TGCCAACATTAGCAAATGACA         | 485                       | 47430219                         | 47430703                          |
| HSTAL.191            | ATGGCTTTCTACATCATCCCA       | TGGCATCACTGGTTTCAGAG          | 505                       | 47431421                         | 47431925                          |
| HSTAL.192            | AAGAAAGCAGGTCTAATTTGGG      | TGGCTAGCTTGTTAGGCAT           | 436                       | 47432200                         | 47432635                          |
| HSTAL.193            | GCCTAACACAAGCTAGCCAA        | CCCATAAATTGTTGACATGTGG        | 414                       | 47432617                         | 47433030                          |
| HSTAL.194            | TTAGATGTGCAGCCACAAGG        | ATGGAGATTGTGGGTTTCGAG         | 512                       | 47432956                         | 47433467                          |
| HSSCL/M22A           | TCCGCCAGAAGAGTGGCTAA        | GTTTTTCAACTACTAAGCAGATAGCCA   | 288                       | 47433323                         | 47433610                          |
| HSSCL/M22A3          | AGAATGCCGCAGAGATTAAGAGA     | AGCCAGGAAGCAAGGTAAAGAAG       | 206                       | 47433344                         | 47433549                          |
| HSTAL.195            | CTCGAACCCACAATCTCCAT        | AGGTCATCACCGACGCTTAC          | 490                       | 47433448                         | 47433937                          |
| HSSCL/M21A5          | CCGACGCTTACAGTGAAGGTTTC     | TCTGCGGCATTCTATTAACAGGA       | 391                       | 47433537                         | 47433927                          |
| HSSCL/M21A3          | CTTAGTGGGCCTTCAATGAGTCA     | TCCCCTGCCTTAGCCACTCT          | 409                       | 47433581                         | 47433989                          |
| HSSCL/M21A           | AATCCTCATTGCCTCTACCACTAAC   | CTTCTGGCGGAATGATGTGC          | 415                       | 47433600                         | 47434014                          |
| HSTAL.197            | AGGGGCCATTTTGATGTAGA        | TCCTAACCCTTCCCCTCTTG          | 568                       | 47435305                         | 47435872                          |
| HSSCL/M17A           | GCCCATCATTGGCTAGATGAA       | CAGAAAATATGCCAGCCTTAATAATAT   | 492                       | 47437422                         | 47437913                          |
| HSSCL/M17A5          | TCAGGGCCTACCATATGCATG       | CATGACCAGTTGGGCACATTC         | 290                       | 47437526                         | 47437815                          |
| HSSCL/M17A3          | ATTGTGGCAATCTCATCAGAAAAGT   | TTAGATGGCACGACTGTGTAACGTGA    | 305                       | 47437573                         | 47437877                          |
| HSTAL.199            | TATCCAGCCAGGAGTCATCC        | CTCCAAGGAACTGAGCAGC           | 496                       | 47437707                         | 47438202                          |
| HSTAL.200            | CTGCTCAGTTTCCTTGGAGG        | TTCCCTGGCCTTGTTGTATC          | 447                       | 47438184                         | 47438630                          |
| HSSCL/M15C           | TTGTCCATTTGCGAGAAGGC        | GTAATTCTCCAAGTATTTTCGAGGAC    | 311                       | 47439625                         | 47439935                          |
| HSSCL/M15B5          | AAATGTGATCTGGGACTTAAAGGATAG | AATTAGGCCTTTATGATGTTACAGAG    | 286                       | 47439721                         | 47440006                          |
| HSTAL.201            | AGGCCTTTATGATGTTACAGA       | TGAGAGCCTAGGGGAAACAA          | 421                       | 47439726                         | 47440146                          |
| HSSCL/M15B3          | AAGGGGTAATTCTGGTTGGAGG      | TTTCTGCATATTTCAATCCCTGAG      | 249                       | 47439800                         | 47440048                          |
| HSSCL/M15B           | TTGAAAATTGGAAAGTAGTGGGATAT  | GCCTTCTCGCAAATGGACAA          | 380                       | 47439916                         | 47440295                          |



| <b>Amplicon Name</b> | <b>Primer 1 (5'→3')</b>        | <b>Primer 2 (5'→3')</b>      | <b>Amplicon Size (bp)</b> | <b>Chrom 1 Co-ordinate Start</b> | <b>Chrom 1 Co-ordinate Finish</b> |
|----------------------|--------------------------------|------------------------------|---------------------------|----------------------------------|-----------------------------------|
| HSSCL/M15A5          | TCCTTCCCAGCAGCTCTTCTCT         | CCTAGGCTCTCAAGGGCACAG        | 684                       | 47440134                         | 47440817                          |
| HSTAL.202            | CTCAAGGGCACAGAGTGTC            | AATGCAACCCTTGCTTCATC         | 510                       | 47440143                         | 47440652                          |
| HSSCL/M15A           | ACAACCAGGTGCTGCTTGAGTC         | TTTGGTTTGAATTAGGCATAATATCA   | 581                       | 47440333                         | 47440913                          |
| HSSCL/M15A3          | TGGGGTGTATGTAGCATCATC          | ACCTTCTCAAAAAGATGAAATGCT     | 396                       | 47440556                         | 47440951                          |
| HSTAL.203            | AGAGAAGAGCTGCTGGGAAG           | AGCTTGTTTTCCAGGCTTCA         | 559                       | 47440797                         | 47441355                          |
| HSTAL.204            | GAAGCCTGGAAAACAAGCTG           | TGCTTCCTAGGTTAGACACCAA       | 453                       | 47441337                         | 47441789                          |
| HSTAL.205            | TGGTGTCTAACCTAGGAAGCAA         | ATTTGCCTTGCAGCTTCATT         | 512                       | 47441769                         | 47442280                          |
| HSSCL/M13A           | CTCTGTGCATCCCAACACATAACTA      | AGGTATGCCCAAAGCACAGC         | 404                       | 47442151                         | 47442554                          |
| HSTAL.206            | GATCCCAGAGAAGCACCAA            | AATGGGGGTTTTTCAGATTGG        | 571                       | 47442428                         | 47442998                          |
| HSSCL/M11A           | GGGGCAGGCAGTGGATTACT           | ATATGGAAATTACTATGATCCTTACCCT | 263                       | 47443770                         | 47444032                          |
| HSTAL.207            | TCCTTACCCTGCAGGAAGCTC          | TCCCAGGATAATAGCACATGAA       | 538                       | 47443788                         | 47444325                          |
| HSSCL/M8A            | TTAACAAAGGTTTGGCAGAGTATTATT    | GGATACAGAAAGTGGCTGGTTAAAT    | 305                       | 47447329                         | 47447633                          |
| HSSIL/M70A           | AAAGTGGCTGGTTAAATTCTTCTTC      | AGGTTTGGCAGAGTATTATTTTTAAAG  | 290                       | 47447337                         | 47447626                          |
| HSSCL/M7A            | CCTGCCTGATATTACAGATATTACAGATG  | TCAGAAATGCCAGGAAGAGGTAG      | 313                       | 47448021                         | 47448333                          |
| HSSIL/M71A           | GCCAGGAAGAGGTAGGTGGAA          | ACCTGCCTGATATTACAGATATTACAGA | 306                       | 47448029                         | 47448334                          |
| HSSCL/M5B            | CTTCCCCTGGCTTGCACAT            | CCAGAATTGGGTCCAGCCTAG        | 289                       | 47449530                         | 47449818                          |
| HSSIL/M72A           | AATTGGGTCCAGCCTAGAAAAGT        | GGCGCTTTGTAATTCATTATTTAAAC   | 485                       | 47449534                         | 47450018                          |
| HSSCL/M5A            | AGTGATAATGGCTTTCTATATTGAATAAGT | CAAGCCAGGGGAAGACTGTG         | 307                       | 47449805                         | 47450111                          |
| HSTAL.213            | GACCACGGCCTGTGATCTAT           | CGCTTTGGATAGGAACACCT         | 452                       | 47456154                         | 47456605                          |
| HSTAL.214            | AGGTGTTCTATCCAAAGCG            | CTGACGTCCTTCCTCCACAT         | 557                       | 47456586                         | 47457142                          |
| HSTAL.215            | ATTGGTGCTGGGGAGAAAG            | TTTTTCAGAACCTCTGTTGCAG       | 400                       | 47457079                         | 47457478                          |
| HSSIL_GAP/M39A       | TTTTTGCCTCTAATGAAAAGTCTG       | GGTTCTGAAAAAGGGAACATTT       | 203                       | 47457467                         | 47457669                          |
| HSTAL.217            | AGCAAACCTGTGCCTGAAGT           | CCCCACTGCCATCTTACTGT         | 450                       | 47457926                         | 47458375                          |
| HSSIL_GAP/M38B       | ACCCTCCACACTTAATTCTAGGC        | GGAGATAGTCCCATCATTCATTAT     | 498                       | 47457991                         | 47458488                          |
| HSSIL/M81A           | TGCAACCCCAGCTTTATGATG          | CTGCCCATATCTCCCTGAGGT        | 625                       | 47458132                         | 47458756                          |
| HSSIL_GAP/M38A       | TGTTGGATGGCAATTTTCATAGAATC     | ATATCATGAGATGGCCATTATGAG     | 313                       | 47458549                         | 47458861                          |
| HSSIL/M80A           | CCAACCTGTGGGTCATTTTAGAA        | CTCTGCAAAAAATAAAATTGTCACAA   | 299                       | 47459241                         | 47459539                          |
| HSSIL_GAP/M37A       | TCACTAGAGCTTGACATTGGTTTTT      | AAATTGTCACAAGCAGAATGTTTTT    | 390                       | 47459255                         | 47459644                          |
| HSSIL_GAP/M36B       | AAAGAAAACACTGGATTACCAAAGG      | GGTCTCTAACCACAAAAGTGAATGC    | 213                       | 47459993                         | 47460205                          |
| HSSIL_GAP/M36A       | GCATGCCATCTGTGATACAATG         | GGACCAGCCAGCCTTAATAAAC       | 344                       | 47460327                         | 47460670                          |
| HSSIL_GAP/M35B       | GGGTGTTGGAGAAGAGCTTTGT         | TGCATCAGGCTTTTTTACATCCT      | 362                       | 47460757                         | 47461118                          |

| <b>Amplicon Name</b> | <b>Primer 1 (5'→3')</b>     | <b>Primer 2 (5'→3')</b>      | <b>Amplicon Size (bp)</b> | <b>Chrom 1 Co-ordinate Start</b> | <b>Chrom 1 Co-ordinate Finish</b> |
|----------------------|-----------------------------|------------------------------|---------------------------|----------------------------------|-----------------------------------|
| HSSIL_GAP/M35A       | GTCAACGGTTTTGTGTGTATATTCATC | AACACCCAAGGCAGCTTGAG         | 444                       | 47461112                         | 47461555                          |
| HSSIL/M78A           | AATTCCATGCCACAACCTCAGGT     | CACCCAAGGCAGCTTGAGATAC       | 395                       | 47461114                         | 47461508                          |
| HSTAL.223            | TACCTGAGTTGTGGCATGGA        | TGGCCTAAGCTTTAATGAGGA        | 540                       | 47461486                         | 47462025                          |
| HSTAL.224            | TGCTGACCCAAGAAGTCACA        | TTCCTCTCCTCAAGCTGCAT         | 579                       | 47463484                         | 47464062                          |
| HSTAL.225            | ATGCAGCTTGAGGAGAGGAA        | GGTCCTGAAATTGATCACCC         | 462                       | 47464043                         | 47464504                          |
| HSSIL_GAP/M31A       | GGACAGTTTACAAAAGAGGGTTACAGA | TTCTGCATTTTGGCTTTCAGC        | 208                       | 47465287                         | 47465494                          |
| HSTAL.229            | CTGAGTGGACACGTGGTTATTT      | TGTGTGGGAATAAGAAATGGTT       | 598                       | 47465838                         | 47466435                          |
| HSTAL.230            | TCCCACAAAGTTAACCTTCACA      | AGATTGGGAGACTCACATGAAG       | 556                       | 47466805                         | 47467360                          |
| HSSIL/M51B           | TTTATGAATGCTTCCCTTGATG      | CCCACAAAGTTAACCTTCACAAGT     | 407                       | 47466806                         | 47467212                          |
| HSTAL.231            | CTTCATGTGAGTCTCCCAATCT      | AGATTCACCCACTCCAGGTG         | 577                       | 47467339                         | 47467915                          |
| HSSIL_GAP/M28A       | CATCTTTTCATATTGCTTGCTAG     | AAAGTAGAACTCCAAAAGCATCTGA    | 276                       | 47467836                         | 47468111                          |
| HSTAL.232            | CCTGGAGTGGGTGAATCTTT        | CTCATCTTCCAGGAACTGCC         | 577                       | 47467898                         | 47468474                          |
| HSSIL_GAP/M26B       | CCATTCTCAGAGGCAATCACTGTAA   | CCAAGAGGTAATGATCTCCAAGGTA    | 189                       | 47470259                         | 47470447                          |
| HSSIL_GAP/M26A       | GAATTCACCTTGCCCTAACACAGAA   | TCAATTTATTACTATGTGCTTGACTGCC | 438                       | 47470505                         | 47470942                          |
| HSSIL/M47A           | TACTAAGGCTTTTTAATGTATGGCTG  | TCCAAACTCATTTGCAGTCATTTTC    | 551                       | 47470810                         | 47471360                          |
| HSSIL_GAP/M25B       | CTTTTAGTTGGCTGTCTGGAATTAC   | ATTCTTGGTATTTCCAGGTATACTG    | 305                       | 47470939                         | 47471243                          |
| HSTAL.236            | TGGCTTTTATCAGCCATACATT      | GGGAACCCATGTAAGGGAAT         | 508                       | 47471325                         | 47471832                          |
| HSSIL_GAP/M25A       | TAAAGTGACCAGTATGGAAAGTGAACA | ACAGGTAGTCAGAAAGAGAGAAGGCT   | 295                       | 47471671                         | 47471965                          |
| HSTAL.237            | TGTTCACTTTCCATACTGGTCA      | CACCCTAAAGAACTCAGGGC         | 593                       | 47471939                         | 47472531                          |
| HSSIL_GAP/M23A       | GTGCAAGACAACGTTCAATTTGAAT   | ACATTTGAACATTTGGCTGATAAGG    | 257                       | 47473407                         | 47473663                          |
| HSTAL.238            | TCCCACCAATGGTAGAGAATAA      | TATGGCACATGGAAGGTTGA         | 559                       | 47473459                         | 47474017                          |
| HSTAL.239            | CCTTCCATGTGCCATATTCC        | CATCAGTGGTACTGCCAAGG         | 564                       | 47474002                         | 47474565                          |
| HSSIL_GAP/M22A       | AAATTTATCAGATGGGCAAGACATG   | GTGATATAAAGCCTTGGCAGTACCA    | 191                       | 47474535                         | 47474725                          |
| HSTAL.240            | GCCTTGGCAGTACCACTGAT        | GGAAATCATGGAAAGCCTGA         | 532                       | 47474545                         | 47475076                          |
| HSTAL.241            | TCAGGCTTTCCATGATTTCC        | CCTATTCTCCTTGCCACTTCC        | 446                       | 47475057                         | 47475502                          |
| HSSIL_GAP/M21A       | TTTGCCAAAGTACACTCAATTCCA    | CGCCCAGCAGTCACAGATG          | 332                       | 47475546                         | 47475877                          |
| HSTAL.242            | AAAATCCCATGCTCCACTTG        | GGGTGGAGTTTCCTCACAGA         | 508                       | 47475656                         | 47476163                          |
| HSSIL_GAP/M20A       | AACCCAAGGGAGGCTAGAGAATT     | TGGAGTCACTGGGAAAGGAAAC       | 385                       | 47475913                         | 47476297                          |
| HSTAL.243            | TTTTGTAGGTGGTGGCACA         | TCCTTGGACTGTGGTAAGCTG        | 419                       | 47477396                         | 47477814                          |
| HSSIL_GAP/M19A       | ATGTAGCAAAGATTCTTGGACTGT    | TGTAGGTGGTGGCACAACCTAAA      | 428                       | 47477400                         | 47477827                          |
| HSSIL_GAP/M18B       | TCCCCAATAAGACTGAAGTGCTG     | GTGCCCATATCGCCAAAGTT         | 228                       | 47477887                         | 47478114                          |

| <b>Amplicon Name</b> | <b>Primer 1 (5'→3')</b>     | <b>Primer 2 (5'→3')</b>         | <b>Amplicon Size (bp)</b> | <b>Chrom 1 Co-ordinate Start</b> | <b>Chrom 1 Co-ordinate Finish</b> |
|----------------------|-----------------------------|---------------------------------|---------------------------|----------------------------------|-----------------------------------|
| HSTAL.244            | GCCCATATCGCCAAAGTTTA        | ATTCTCTGAGGCTCAATCGG            | 598                       | 47477889                         | 47478486                          |
| HSSIL/M31A           | TTGTCTGCCAGCCTGATGAAT       | TTCCGATTGAGCCTCAGAGAA           | 322                       | 47478465                         | 47478786                          |
| HSSIL_GAP/M18A       | TGTCTGCCAGCCTGATGAAT        | TTCCGATTGAGCCTCAGAGAATC         | 321                       | 47478465                         | 47478785                          |
| HSTAL.245            | CCGATTGAGCCTCAGAGAAT        | TGAATTTGTGGGCAGTCAGA            | 524                       | 47478467                         | 47478990                          |
| HSSIL_GAP/M17B       | GGGACTTTTTGATTCCATGCA       | ACTGCCACAAATTCAGCAA             | 373                       | 47478975                         | 47479347                          |
| HSSIL_GAP/M17A       | ATTCGGCCAACTATTGATTTGCT     | AGTCCCCAGGAAGAGAAGCAGT          | 403                       | 47479342                         | 47479744                          |
| HSTAL.247            | GACCAGGATCAAAGCGATCT        | TGGTTCTCTGACAGCAGACG            | 553                       | 47479396                         | 47479948                          |
| HSSIL_GAP/M15A       | CAAGAAAGAAAGTATTCGGGTTCAA   | TTAGATGGCAGCTAAGCACAGC          | 210                       | 47481287                         | 47481496                          |
| HSSIL_GAP/M14B       | TTGTGGAACGTTGAGAAGCTTG      | GCTAGGCTGACTCAAGGCTCTC          | 219                       | 47482073                         | 47482291                          |
| HSSIL/M27A           | CAACGCCAACTGGAGATTTTCA      | GCTCTCCCCGCCATAATCTAT           | 538                       | 47482089                         | 47482626                          |
| HSSIL_GAP/M14A       | GTACCTTTCCACTTTTCTCCATCA    | TCCACAAAGACACCATGCTGAC          | 385                       | 47482285                         | 47482669                          |
| HSTAL.250            | ACCAGGAGAATAGGCACTCAAA      | TTTGCTTTTCATAACTGTTGGG          | 548                       | 47483767                         | 47484314                          |
| HSSIL_GAP/M12A       | TGTGGTTTTCTCGTGTTATACACTCAT | TGAAGTATTTCAGATAATTGTTAGATAATAC | 282                       | 47484261                         | 47484542                          |
| HSSIL/M22B           | TGGTTGGGTTCTTCCCTCT         | GGCAGGGGGGTAGAACAACA            | 412                       | 47487145                         | 47487556                          |
| HSSIL_GAP/M9A        | GGTTCCTTCCCTCTTACAAATACTGA  | CAGGGGGGTAGAACAACAAGG           | 404                       | 47487147                         | 47487550                          |
| HSTAL.252            | CCAACCAATTTCCACTTGT         | TTCACCAGACATCATGGAGC            | 475                       | 47487550                         | 47488024                          |
| HSSIL_GAP/M8A        | GCCCCAAATAAATATCTAGCCCA     | GGCCCGTGCAAAAGGATATA            | 475                       | 47487982                         | 47488456                          |
| HSTAL.255            | ATCCTCCACTCCCATTGCTT        | AGATGGAAGTGTCCAGTGGG            | 445                       | 47488878                         | 47489322                          |
| HSTAL.256            | CCCACTGGACAGTTCCATCT        | GCACGTTTTCTCTGTCTTGAA           | 580                       | 47489303                         | 47489882                          |
| HSTAL.257            | TTCAAGACAGAGAAAAACGTGC      | CCATCTTTTACCCAAATGAA            | 541                       | 47489861                         | 47490401                          |
| HSSIL/M19A           | TAAGGTGGTGGGTATGGAAAGATAA   | AGCTTCCACAGAATGCAGGC            | 409                       | 47490209                         | 47490617                          |
| HSSIL_GAP/M6A        | TCTTCTAGCAGCATTATGGGGACT    | CCACAGAATGCAGGCTTTAAATC         | 464                       | 47490214                         | 47490677                          |
| HSTAL.258            | CATACCCACCACCTTAGTTGC       | GCATCCTGTGCAGATATTGAAA          | 600                       | 47490602                         | 47491201                          |
| HSSIL_GAP/M5B        | ACGGTGGGAATTTCTTGAGGACT     | ATGCCTCCCTTAACTTGGAATG          | 291                       | 47491198                         | 47491488                          |
| HSSIL_GAP/M5A        | CGCCCGCAGTTCTCCAAG          | AGCTCAGATGATACCCAAGGATTC        | 497                       | 47491542                         | 47492038                          |
| HSSIL/M18A           | CGGGTGTCCGCTTCCAGT          | CGCGGAGCTGAGGTCTGTT             | 495                       | 47491737                         | 47492231                          |
| HSSIL_GAP/M4A        | TGTCATAAAACAGATGGCTTCCTAG   | AGGATCCGAGGATTTAAACCTTT         | 360                       | 47492059                         | 47492418                          |
| HSTAL.261            | TTCTCAACACTCCACTTTTGT       | CAGGAAAGCAGAGAATGATGC           | 509                       | 47495016                         | 47495524                          |
| HSTAL.262            | GCATCATTCTCTGCTTTCCTG       | CATGTAACCAATGGCCGTC             | 401                       | 47495504                         | 47495904                          |
| HSTAL.263            | CAAGGTGAGAGCTGAGGCAT        | GGGTCAGATCCCCAAAGCTA            | 600                       | 47499089                         | 47499688                          |
| HSSIL/M10A           | TCAGTTCCCTTAATCTCTTTGAACA   | ACCACTGGACTTCTAAGCAGGATAT       | 417                       | 47499474                         | 47499890                          |

| <b>Amplicon Name</b> | <b>Primer 1 (5'→3')</b>  | <b>Primer 2 (5'→3')</b>      | <b>Amplicon Size (bp)</b> | <b>Chrom 1 Co-ordinate Start</b> | <b>Chrom 1 Co-ordinate Finish</b> |
|----------------------|--------------------------|------------------------------|---------------------------|----------------------------------|-----------------------------------|
| HSTAL.264            | GTGCTAGCTGGTATGGGGAG     | GCTTTTCTCTGTAAGGGCCA         | 573                       | 47500449                         | 47501021                          |
| HSTAL.265            | TGGCCCTTACAGAGAAAAGC     | TCATGTGGACAGGGACTGAA         | 584                       | 47501002                         | 47501585                          |
| HSTAL.266            | TCACCAGGAACAGGGAAGTT     | GGAATTTGGCATAAATTGACAG       | 558                       | 47501683                         | 47502240                          |
| HSSIL/M7A            | ACGCCCAGCCCATCTCAA       | CAATTTATGCCAAATTCCTTTTAGAC   | 431                       | 47502223                         | 47502653                          |
| HSSIL/M5A            | CCCACAAGGCAATAGATGACAA   | TAGGCAGCAAAGGGGAGTAGTC       | 418                       | 47504210                         | 47504627                          |
| HSTAL.269            | TCATCTATTGCCTTGTGGGG     | TACAGCCTTTCCAGTTGGGT         | 449                       | 47504609                         | 47505057                          |
| HSTAL.270            | ACCCAAGTGGAAAGGCTGTA     | TGCTAGATTGTGGGGAGGTC         | 419                       | 47505038                         | 47505456                          |
| HSTAL.271            | GACCTCCCCACAATCTAGCA     | TGTCTACTATGTGCCAGGCATT       | 426                       | 47505437                         | 47505862                          |
| HSTAL.272            | ATGCCTGGCACATAGTAGACA    | TTAGTGCTCCTTGAGGTGG          | 505                       | 47505842                         | 47506346                          |
| HSSIL/M3A            | CAAAGCCCTCTGTGGAACCT     | GAAATGCCCTTTACTGGGTG         | 512                       | 47506217                         | 47506728                          |
| HSTAL.273            | TGATCAAATAGGCCCAAAGC     | TAGAGACGGAAGCTGGAAA          | 566                       | 47506516                         | 47507081                          |
| HSSIL/M2A            | ACATGGGCAGCCAAGAACAA     | ATGGGTGTCTGGGTTTCAGTTTT      | 475                       | 47508028                         | 47508502                          |
| HSSIL/M33A           | TTTGGGGACCAGATTCGTCTC    | AGGCTGGGAGACAGGAAGTGA        | 471                       | 47512062                         | 47512532                          |
| HSTAL.277            | CACTGTCACCGAACGTGTCT     | TGGTCGCCTCTTCTGTTTCT         | 515                       | 47512283                         | 47512797                          |
| HSSIL/M34A           | GGTTGGTTAGCTGCATTGACACT  | AAATACATCTGTCCAACACATAATGACT | 342                       | 47512690                         | 47513031                          |
| HSTAL.278            | GCACACAGAGACAGATGCAGA    | TGCATTCAAATATAACACGCAT       | 484                       | 47514101                         | 47514584                          |
| HSTAL.279            | AATTGCTATTCCCTAGCTGGC    | AATTCAGGTGCCCTGTGAG          | 562                       | 47515265                         | 47515826                          |
| HSSIL/M37A           | CATAAATCCACGGTAAATTCTCCA | AATCCCAAACCTCCCTCCA          | 382                       | 47515758                         | 47516139                          |
| HSTAL.281            | GGTTTTGGGATTGATTTTGC     | GAAAGCAATTTGGCATGGTT         | 595                       | 47516128                         | 47516722                          |
| HSTAL.282            | TGCTTTCTGTAGCACCCAGA     | CCTCTGGGGATCGAATTTTT         | 591                       | 47516716                         | 47517306                          |
| HSTAL.283            | TGAGCAGATTCCAAGCTCC      | CTGAAGATCTCCCCTCCTCC         | 559                       | 47518205                         | 47518763                          |
| HSSIL/M38A           | ATTAAGGGTGCTTATGACATGGG  | TGAGAAAGAGATGGGAAAGCAGTT     | 220                       | 47518703                         | 47518922                          |

## Appendix 2

### Sequences of Primer Pairs Used to Construct the Mouse SCL Tiling Path Array

| Amplicon Name | Primer 1 (5'→3')          | Primer 2 (5'→3')           | Amplicon Size (bp) | Chrom 4 Co-ordinate Start | Chrom 4 Co-ordinate Finish |
|---------------|---------------------------|----------------------------|--------------------|---------------------------|----------------------------|
| MMTAL.3       | ATTGTCAGCAGCTGGTAGGT      | CATCACCCCCAACTATCCAC       | 498                | 113334279                 | 113334776                  |
| MMTAL/4ver2   | AGGATGGAGCGTGTACCAAG      | TAAGGGTTCCACAGGGAATG       | 641                | 113334608                 | 113335248                  |
| MMTAL/5ver2   | TCTGGACAGAGATTGCCCTT      | ACTGTGTGGGCTCCAGAGAT       | 543                | 113335309                 | 113335851                  |
| MMTAL.6       | CCAAACCTGGAGACCTGAGA      | TTTGTCTTGCCTCTGCTA         | 506                | 113335809                 | 113336314                  |
| MMTAL.10      | AGTGTTTCAGGGTGTTCGTC      | ATAGCATGCGGTTTCAGTCC       | 414                | 113338093                 | 113338506                  |
| MMTAL.11      | AGCTATTTCCTGGAGGCGTT      | CAAGTGCCTTTTAACCCCAA       | 592                | 113338592                 | 113339183                  |
| MMTAL.13      | AGTTCTCCCATGTCCTCT        | GCCTAGAGGCCAGTCTCTT        | 453                | 113339586                 | 113340038                  |
| MMTAL.14      | GGCAGAAATGGTTTTGGAGA      | CCTACACAAGGCTCAGCACA       | 459                | 113339959                 | 113340417                  |
| MMTAL.16      | GCACATGTTTTTAATCCCCG      | GGCATGAAGGCTGTCAAAAT       | 596                | 113341178                 | 113341773                  |
| MMTAL.17      | CATGCCAGCAGCTTAGGATGA     | GGATTGCCTGCCAGATTAATA      | 514                | 113341768                 | 113342281                  |
| MMSCL/M000A   | AAAGAATCGCACAGTATGAAGTCAG | AGCCCAATGGTGCCATTTAG       | 442                | 113342233                 | 113342674                  |
| MMSCL/M001A   | CATTGGGCTGGTTGCATTTAA     | CCAAATGGCCACCTGTAGA        | 524                | 113342666                 | 113343189                  |
| MMTAL.19      | AGATGTGGCATGCAAAATGAA     | ACCAGAAGAGGGCATAGGGT       | 539                | 113342906                 | 113343444                  |
| MMSCL/M001B   | TACAGGTGGGCCATTTGGG       | TCCCCTGCTCTGGTGCATAAT      | 520                | 113343172                 | 113343691                  |
| MMSCL/M002A   | TAGAAGTCCAGTGCCAATAAAATGT | AGGGTCCTGGGTTGAGTGACTAG    | 464                | 113344136                 | 113344599                  |
| MMTAL.22      | GCCTCCCGAAGAGTCTCAG       | TGGGAAATTCCTTCTCGTTG       | 447                | 113344641                 | 113345087                  |
| MMSCL/M003A   | CGTTTGCTACCTTCCCCTAACAC   | TCAGAGATAGAGGAGGTTAAATTTGC | 292                | 113344861                 | 113345152                  |
| MMTAL/23ver2  | CACCTCTTCAAAGCTGGGAC      | GAGTCAGGATCCAGGTAGCG       | 611                | 113345258                 | 113345868                  |
| MMTAL.24      | CCGTTGACCAATGAAGGTT       | TGAAGTCAATCTGAGGCACG       | 587                | 113345544                 | 113346130                  |
| MMTAL.25      | CATTGTGACGTGCCTCAGAT      | CCATCAAGTCACCTCACCT        | 574                | 113346103                 | 113346676                  |
| MMTAL.26      | GCATGAAAGGAGAGACAGGC      | ATCCTCAGACCTCCACATGC       | 435                | 113346835                 | 113347269                  |
| MMSCL/M005B   | TCGGCTCCTTCTGCCAGTAG      | GGCTTTCTGGGGATCATGTGT      | 453                | 113347282                 | 113347734                  |
| MMTAL/27ver2  | CTTCTGCCAGTAGGTCCTCG      | TTTCCTGTTTGGGCTTTCTG       | 457                | 113347289                 | 113347745                  |
| MMTAL.28      | GGAAGATCTCTGTCCCACA       | GGATGGAGCATTCTTGCCCTA      | 517                | 113347819                 | 113348335                  |
| MMSCL/M006A   | ATGAACGGAAGGAAGAGATTTGG   | GGAATTACAGGCTGAAGGAAGTACA  | 437                | 113348124                 | 113348560                  |
| MMTAL.30      | ATCTCTCCAGGACCCGTTTT      | TGCCTTCCACTTAATACGCC       | 489                | 113348812                 | 113349300                  |
| MMSCL/M007A   | TAGCTTGCGAAGGAATACTGGA    | CCAGCTCCTCCTCCCTACTCTAC    | 469                | 113349110                 | 113349578                  |

| <b>Amplicon Name</b> | <b>Primer 1 (5'→3')</b>      | <b>Primer 2 (5'→3')</b>   | <b>Amplicon Size (bp)</b> | <b>Chrom 4 Co-ordinate Start</b> | <b>Chrom 4 Co-ordinate Finish</b> |
|----------------------|------------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------|
| MMSCL/M008A          | GACAGCACTGAACACTTAACAATGAA   | ACCCTGGCTTGACCTGAAAAG     | 427                       | 113350226                        | 113350652                         |
| MMSCL/M009A          | CCCCTGGTGGAAGCCAAA           | GTGGATGCGCAGTAAGCTTCA     | 325                       | 113350767                        | 113351091                         |
| MMTAL.35             | TGGACCTCTGGAAGAGCAGT         | GGAAACCAGACTGGCCATAA      | 595                       | 113351530                        | 113352124                         |
| MMSCL/M010A          | TGCCTGCACCTCCTGAGTTC         | AGGAAATAGCCACATTAACAAAAAC | 412                       | 113351859                        | 113352270                         |
| MMSCL/M011A          | CATTGGTTTCAGCTGGCTATTG       | GGGGAAGATGGTGCAATTATGT    | 513                       | 113352531                        | 113353043                         |
| MMSCL/M011B          | CCCCTCACGCTCTGAAATTTAT       | CCACAACCTGATCAAAATGCAGAAA | 473                       | 113353074                        | 113353546                         |
| MMSCL/M012A          | TCTAGCCCCGGCATGACTTC         | CCCCTGAGCACTTCCTAGACC     | 495                       | 113353731                        | 113354225                         |
| MMTAL.40             | CGTTGTGGTGCTGTGAAAAAC        | TCTGACTTCAGTGAGCCTGC      | 477                       | 113353917                        | 113354393                         |
| MMSCL/M013A          | GGCTGAGTCATAATTGCGTCCTA      | GGCTTCACAGGCACACACTTG     | 485                       | 113354591                        | 113355075                         |
| MMTAL.43             | GTTGCCTGGAGACTTGCAAT         | TCCACACTAAGCCGAGAGGT      | 434                       | 113355399                        | 113355832                         |
| MMTAL.44             | ACCTCTCGGCTTAGTGTGGA         | GCCCTAACACAGAACCAAACA     | 555                       | 113355813                        | 113356367                         |
| MMSCL/M014A          | GGTCTCCAGCCTTCTCATTAAT       | GTTTTAAGCCCTAACACAGAACC   | 239                       | 113356136                        | 113356374                         |
| MMSCL/M014B          | TCACGAAAAAGAAAAGGTATTTGC     | AGCAAGGGCTACCCTGAGAAA     | 327                       | 113356454                        | 113356780                         |
| MMSCL/M015A          | AGTTGTGGGCATTTTCTTGTAAGG     | ATTCTAGGGTAGCAGGGCTACACA  | 468                       | 113356886                        | 113357353                         |
| MMTAL.46             | TTCTTTCCAGTCCATGCTC          | GTATCTCAAGCAGCAAGCCC      | 486                       | 113357010                        | 113357495                         |
| MMSCL/M015B          | GTATGGGCTTGCTGCTTGAGA        | TGGGCCACACACGGAGTTC       | 414                       | 113357472                        | 113357885                         |
| MMSCL/M016A          | GTGTGGCCAGATTGACTTTG         | CCGGGGGTACAGTGAGTGC       | 469                       | 113357876                        | 113358344                         |
| MMSCL/M016B          | CTAGCCCCAACCCCAAGGT          | TGCCCTCTTTCCATGAACAC      | 457                       | 113358447                        | 113358903                         |
| MMSCL/M017A          | CTGTGGGCGCTGGGTATG           | ATCTCAAGAATGCACACACAATCAC | 282                       | 113358947                        | 113359228                         |
| MMTAL/51ver2         | ATACTGGCTCTCTGCCTCCA         | CCAGACAACCATGCACAGAC      | 519                       | 113359480                        | 113359998                         |
| MMSCL/M018A          | ACTTACCCAGGAGATCTTTCATTATAAC | CCAGGGTAGCCAGGAAGTGAG     | 434                       | 113359643                        | 113360076                         |
| MMTAL.52             | GGGCTTCAGCCACTAAGATG         | ATGGCTGGGAACTAAACCC       | 532                       | 113360129                        | 113360660                         |
| MMSCL/M019A          | CGTGGGAGCGAGAGATATGG         | TGCCTGGCTCTCCTGGAAC       | 253                       | 113360579                        | 113360831                         |
| MMTAL.53             | CCAACCTGGGTCAGGCTTTTA        | TCTAGCACGGGGAAAATGAG      | 402                       | 113360742                        | 113361143                         |
| MMTAL.54             | TTATGGATGGTTGTGAGCCA         | GGTTTTTGCCAGAAGTTCA       | 513                       | 113361325                        | 113361837                         |
| MMTAL.55             | TGTTCCGATAAATGGGGTTC         | TTCAGGGTAGGGGTAAAGCA      | 416                       | 113361745                        | 113362160                         |
| MMTAL.56             | TTTTTAAATCATCGTGGCAGG        | TTCAGGGTTTGATTCTCTGGT     | 508                       | 113362336                        | 113362843                         |
| MMTAL.57             | CCAGGAATCAAACCTGAAC          | GGAGAGATGGCTCCAAGGTA      | 445                       | 113362825                        | 113363269                         |
| MMTAL.58             | TGGAGCCATCTCTCCAGTTC         | CATAACCTGGCTTTCCTGA       | 582                       | 113363255                        | 113363836                         |
| MMSCL/M022A          | AGGAAAGCCAGGGTTATGCA         | TGGTGGTGCTGGGATCAAAG      | 425                       | 113363819                        | 113364243                         |
| MMTAL.59             | TGCAGAGAAATGCTGTCTGG         | GAGAGCCAAAAATGGGTTGA      | 600                       | 113363835                        | 113364434                         |

| <b>Amplicon Name</b> | <b>Primer 1 (5'→3')</b>     | <b>Primer 2 (5'→3')</b>     | <b>Amplicon Size (bp)</b> | <b>Chrom 4 Co-ordinate Start</b> | <b>Chrom 4 Co-ordinate Finish</b> |
|----------------------|-----------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------|
| MMTAL.60             | TCAACCCATTTTGGCTCTC         | TCACAACGGTCTTTCTGTGC        | 548                       | 113364415                        | 113364962                         |
| MMSCL/M024A          | TGGGAGACAATGACTACAGCTGA     | TTGGTTTTCTGTTATGATAGCTACGTG | 283                       | 113365630                        | 113365912                         |
| MMTAL.63             | TTTCTCCGTGTATCCTTGCC        | TGCTTTACGTTTCCTGGTCC        | 579                       | 113366002                        | 113366580                         |
| MMSCL/M024B          | TGCCTGCTGTGCTGGAATTA        | AAGGGCCTGGCTGTGGAA          | 411                       | 113366240                        | 113366650                         |
| MMSCL/M025A          | GGGGGCATATCTGTCACACTG       | AGGACTAGGAATCGGTCTTGGAG     | 454                       | 113366759                        | 113367212                         |
| MMTAL.65             | CGATTCCTAGTCCTCACCCA        | GCATCGACTTCTCAAGGGAG        | 588                       | 113367199                        | 113367786                         |
| MMSCL/M026A          | TTGAAAGGGACGGAAAATTAATATAG  | GGTGGCCTCAATTTTAAACCTTT     | 426                       | 113367732                        | 113368157                         |
| MMTAL.67             | TTGAGGCCACCCTGATCTAC        | CTGGTCTTCGCTAACCTTCG        | 469                       | 113368147                        | 113368615                         |
| MMTAL.68             | AGGTTAGCGAAGACCAGCAA        | AACACGAGCGAAAGTTCAGG        | 568                       | 113368599                        | 113369166                         |
| MMSCL/M027A          | TTCCTGAACCTTCGCTCGTGT       | TGTGGCTGGGCTTGTGGA          | 421                       | 113369145                        | 113369565                         |
| MMSCL/M028A          | AGCCCAGCCACACAATCTTG        | GCTGCCTGTCTTGCTCTGTGA       | 485                       | 113369554                        | 113370038                         |
| MMTAL.71             | ATGGGACTGTCTCCTGATGC        | CCAATGCCCTCTTCTGATGT        | 439                       | 113369987                        | 113370425                         |
| MMTAL.74             | CCTGTGCCAGAGGAGGTA          | AGGAACAACATGTAAGGCCG        | 496                       | 113371813                        | 113372308                         |
| MMSCL/M030A          | ATGAATTTCTCCTCCTTTTAA       | CTCATTATCCTCTTCAGACATCTCAAC | 315                       | 113372212                        | 113372526                         |
| MMSCL/M031A          | ACGCATCGGCTCCCATTAC         | ACCTGGGCCTGGGGAAATA         | 294                       | 113372715                        | 113373008                         |
| MMTAL.76             | GGTTGCTGGGAAGTGAAGTCTC      | TGCTGGTACACTGTCTGCAA        | 567                       | 113372756                        | 113373322                         |
| MMTAL.77             | TGCAGACAGTGTACCAGCAA        | GGACCCATGTACTGGAAGGA        | 501                       | 113373304                        | 113373804                         |
| MMSCL/M032A          | CCTTAATGGAGTGGGCAGATGA      | CTGCAGTCCCAGGTGATCTAAAC     | 339                       | 113374027                        | 113374365                         |
| MMTAL.79             | ATGAGCGACAAAGCAAGGTT        | CTGGGGCTTGAGTGACAAGT        | 600                       | 113374326                        | 113374925                         |
| MMSCL/M033A          | ACTCAAGCCCCAGGGTATCTAAT     | GCTACTAAGGCCCGCTTTCAC       | 413                       | 113374913                        | 113375325                         |
| MMTAL.82             | GCAAAACAAATGGAGCTGGT        | CCCCTTTCTTTGGTGTGTGT        | 440                       | 113375591                        | 113376030                         |
| MMTAL.83             | CACACCAAAGAAAGGGGTTG        | TAATTCCTTTTGAATGGGC         | 549                       | 113376014                        | 113376562                         |
| MMSCL/M035A          | TCATGCCTAAAGTTCAAGTGCTG     | GGGCTGCACAGAAGGATCAC        | 443                       | 113376762                        | 113377204                         |
| MMSCL/M035B          | TGTGCAGCCCCAGATATTTATTC     | CAGAGCAGCAAATGAGAAGACAGA    | 294                       | 113377195                        | 113377488                         |
| MMTAL.86             | GGTCCTCATGCAAGCAGAAT        | TCTTGATCATCACCTGCTGC        | 588                       | 113377736                        | 113378323                         |
| MMSCL/M036A          | TTTCCTTTGCCACTGGTTTCTT      | TGGCTGATTAACCTCCTCCACA      | 403                       | 113378096                        | 113378498                         |
| MMSCL/M037A          | CCCACCCCATCCATCCT           | AAGACCCAACAAGCAGCTGAA       | 398                       | 113378615                        | 113379012                         |
| MMTAL.89             | CTATGTATCCTTGCGCTGC         | TGTACTGTCAATTTGGAAGCCTG     | 524                       | 113379132                        | 113379655                         |
| MMSCL/M037B          | AGCTTAGTGTATTTTCAATGACGTCTT | ATGCTGTTGTCTTTTCAAATATAATTG | 235                       | 113379447                        | 113379681                         |
| MMSCL/M038A          | AGGACAACCAGGGCTATACAGAGA    | ACAATCGGGAGCTCTGCTTTAC      | 296                       | 113379846                        | 113380141                         |
| MMTAL.91             | TGGGCAAAACAAAGTTGACA        | CGATTGCTCTCCAAGAGGAC        | 582                       | 113379902                        | 113380483                         |

| <b>Amplicon Name</b> | <b>Primer 1 (5'→3')</b>  | <b>Primer 2 (5'→3')</b>     | <b>Amplicon Size (bp)</b> | <b>Chrom 4 Co-ordinate Start</b> | <b>Chrom 4 Co-ordinate Finish</b> |
|----------------------|--------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------|
| MMSCL/M038B          | CCCAGGTCCTCCAGGTCTCTT    | TCAGGGCAGGGTTGTTCTATACA     | 349                       | 113380450                        | 113380798                         |
| MMSCL/M039A          | TGGTGGCTTCGGTGCTGTT      | GCTCCAACACTGTGCTCAAAAA      | 377                       | 113380858                        | 113381234                         |
| MMSCL/M039B          | TGCTGTGGGCTGTTGGTGAT     | GCATGGCCTGGCCTATACTG        | 345                       | 113381494                        | 113381838                         |
| MMTAL.94             | GCTTTAGGAATCTCCCAGGC     | CAAAAACAACAGGTTGCCCT        | 500                       | 113381670                        | 113382169                         |
| MMTAL.95             | AGGGCAACCTGTTGTTTTTG     | AAGCTGTCCAAACACTGGCT        | 554                       | 113382150                        | 113382703                         |
| MMSCL/M040A          | TTGGAGCACAGTGGGAGGAG     | GGTGCATGCCTTTAATCCCA        | 412                       | 113382167                        | 113382578                         |
| MMTAL.96             | AGGCATGCACCCATTATGTT     | CCATCTCTCCAACCTCCAAA        | 545                       | 113382568                        | 113383112                         |
| MMSCL/M041A          | GAGGCTGCAGTGAAGTCATGTG   | GAGCCAGAAAAAGAACCAGGATT     | 380                       | 113382769                        | 113383148                         |
| MMTAL.97             | TTTGGAGGTTGGAGAGATGG     | GGAGGAGCAGCACAAATAAGC       | 480                       | 113383093                        | 113383572                         |
| MMTAL.98             | GCTTATTGTGCTGCTCCTCC     | TGCTGTTACTGGCTCCCTCT        | 545                       | 113383553                        | 113384097                         |
| MMSCL/M042B          | TGTCCTTTGCAGCAGCTCTTC    | TGTCACAAGGAAGGCTAAATATTATCT | 531                       | 113383967                        | 113384497                         |
| MMSCL/M043A          | CCATAGGGCCAAGTGAACCA     | TGAGGGAAGGGGAACTTTGTGA      | 419                       | 113384703                        | 113385121                         |
| MMSCL/M043B          | GTTCCCTTCCCTCAAATTCCT    | TCGGCAAGCAGTGATAAAGCA       | 538                       | 113385107                        | 113385644                         |
| MMSCL/M044A          | AAGCCATCCCAGAAGCCCT      | AATGGGAGTCTTAATCATGCCTGTA   | 359                       | 113385883                        | 113386241                         |
| MMSCL/M044B          | GGGGTGTTGGGTGTTGGTTT     | GGCCAAAACACTGAAAGACACG      | 415                       | 113386410                        | 113386824                         |
| MMSCL/M045A          | AGCCCGGAAGCAGTGATCTC     | CTGCATGCTGGGTTTCTGTTC       | 389                       | 113386831                        | 113387219                         |
| MMSCL/M045C          | CCCAGCCACGCAGATAGTGA     | GAAGGTGCCACAGAATCCA         | 399                       | 113387164                        | 113387562                         |
| MMSCL/M046A          | GGCCATGACCTTTGGAATTC     | CCAGACGAGGAAGGCAGAATT       | 361                       | 113387819                        | 113388179                         |
| MMTAL.108            | GAACCCAGGTACCTCACACAA    | CTAAGTCCAGGACAGCGAGG        | 585                       | 113388340                        | 113388924                         |
| MMTAL.109            | CGCTGTCCTGGACTTAGCTC     | GGGAAACACCACTGTCACCT        | 400                       | 113388908                        | 113389307                         |
| MMTAL.110            | CTTTAAATCCCAGCAGGCAA     | CAGGACCTTTGGAAGAGCAG        | 492                       | 113389501                        | 113389992                         |
| MMSCL/M047A          | ACTTTGCCACCTGTTATCACATCT | GCTCCGGCCCAAAGATTTAT        | 349                       | 113389767                        | 113390115                         |
| MMSCL/M048A          | CCCAACAACCCCATGAAGC      | GGGACTGAGCACTGAGAAGGG       | 426                       | 113390173                        | 113390598                         |
| MMSCL/M048B          | GCTGGGGGCTCTGCACC        | AAGGCCCTCAATCTGGAAG         | 446                       | 113390724                        | 113391169                         |
| MMSCL/M049A          | GAGGGGCCTTTATGTCTGCA     | TGCATCACTCCCTACCAAGA        | 397                       | 113391160                        | 113391556                         |
| MMSCL/M049B          | GACGTTGGCACACTGGAGAAA    | CATCCTACCTGGCTCACGTCTT      | 369                       | 113391583                        | 113391951                         |
| MMSCL/M050A          | GTGCCGAAGAGAGGGAGGAG     | CAGGAAGTGGGGAAACAGGAT       | 417                       | 113392137                        | 113392553                         |
| MMSCL/M050B          | TTTCCCCACTTCCTGGCC       | TTTCCAGGATGTCAGGCTTCA       | 372                       | 113392539                        | 113392910                         |
| MMSCL/M051A          | GACCCCTGCATCATCTCCT      | GGCAGGGCAAGCCATACAA         | 389                       | 113393104                        | 113393492                         |
| MMSCL/M051B          | CCCCACCAGCACAAAGACT      | AGGGAATGGTAAGCACAAAGCA      | 475                       | 113393491                        | 113393965                         |
| MMTAL.118            | CAGCTCCATCAGTCTCCCTC     | CTCCCAACCTTGACACCAGT        | 532                       | 113393742                        | 113394273                         |



| <b>Amplicon Name</b> | <b>Primer 1 (5'→3')</b> | <b>Primer 2 (5'→3')</b>   | <b>Amplicon Size (bp)</b> | <b>Chrom 4 Co-ordinate Start</b> | <b>Chrom 4 Co-ordinate Finish</b> |
|----------------------|-------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------|
| MMTAL.119            | GGTGTCAAGGTTGGGAGAAA    | AAGTGGGTTTGTGAAGACGG      | 412                       | 113394257                        | 113394668                         |
| MMSCL/M052B          | TGGGTTTCTTTGCTTCATCCA   | AAAAGCACCATGTCTAGGGCA     | 347                       | 113394622                        | 113394968                         |
| MMSCL/M053A          | CTCCTGGCAACCCAAAGCT     | ATCTTAGGCTCAGGCAAACCTCTG  | 337                       | 113395186                        | 113395522                         |
| MMTAL.122            | TCTCAGTGAGCTGGAGCAGA    | TTACACCCTCTGTGCCCTTC      | 484                       | 113395398                        | 113395881                         |
| MMTAL.123            | GAAGGGCACAGAGGGGTGTAA   | GAGTTCCAGGACAGCCAGAG      | 485                       | 113395862                        | 113396346                         |
| MMSCL/M055A          | CAACAGGGGTGGAGAGGACA    | TGTGTCCCCAGTTTGTGTTC      | 392                       | 113396860                        | 113397251                         |
| MMTAL.126            | CTGAGGACAGAAAGCTTGGG    | AGCCCCTGCCATTCTAGTTT      | 479                       | 113397213                        | 113397691                         |
| MMSCL/M056A          | AGTCCCGACCTTCCCTACGT    | GCGCCGCCTGAAATAGCT        | 456                       | 113398031                        | 113398486                         |
| MMTAL.129            | GCATAACCTTTTCAAGCCCA    | CTTTCGGAGGGGAAACTAGG      | 457                       | 113398743                        | 113399199                         |
| MMSCL/M057C          | GACGCCTGGCTTTCCTGG      | GAAAGTAGGGGGCAAAGAGATG    | 376                       | 113399687                        | 113400062                         |
| MMTAL.132            | TTTGCCCCCTACTTTCCTTT    | CAAATCCAGGTCCTCCAGAA      | 454                       | 113400047                        | 113400500                         |
| MMSCL/M058A          | ACCTCCTATTACCCCTCATCTCC | GGGGGGGTGTTTCATGAGC       | 332                       | 113400372                        | 113400703                         |
| MMTAL.133            | TTCTGGAGGACCTGGATTTG    | CCTGCCTTGAAGCAGAAGAG      | 403                       | 113400481                        | 113400883                         |
| MMSCL/M058B          | GCTGTGAGTTGGTCCTTTTCTGA | CCAATGGGCTGAGGAGTATCTG    | 340                       | 113400781                        | 113401120                         |
| MMTAL.134            | AACAGCCAGTTTCCACCATC    | GGCCAAGGACTCAATTCTCA      | 576                       | 113401064                        | 113401639                         |
| MMSCL/M059A          | TTGAGTCCTTGGCCTTGAC     | CCGACCCATTCCCAACCA        | 400                       | 113401626                        | 113402025                         |
| MMSCL/M060A          | CCAAAGCCGCTGAACGAG      | ATAAGCGCCTCGGCCATT        | 242                       | 113402059                        | 113402300                         |
| MMSCL/M060B          | AACATGGCCACGCACACC      | AGACAGCGCAGGGTTTCACA      | 405                       | 113402419                        | 113402823                         |
| MMSCL/M061A          | GCGCTGTCTGGGTGTGGAG     | CCACCAGCGCCTCGATCT        | 424                       | 113402815                        | 113403238                         |
| MMSCL/M061B          | TATTCGGGAGCCAGTGTGG     | AAAACGCGATCCTTCTGTCC      | 456                       | 113403295                        | 113403750                         |
| MMSCL/M061C          | TCGCGTTTTCCCTTTTACTG    | TTGGCGGAAGCTCAGAAGT       | 406                       | 113403742                        | 113404147                         |
| MMTAL.140            | GCCTCAAGTAACAACGGGAA    | AGATTTTCGACTTTCGGGGT      | 405                       | 113404010                        | 113404414                         |
| MMSCL/M062B          | GGCAACCCGCATAGAGACG     | CGCCCAAAGCGAGTTTCC        | 361                       | 113404793                        | 113405153                         |
| MMSCL/M063A          | CCCGGTTCCGAGCACATT      | CCCCAGCCAGCAGGTGAC        | 421                       | 113405595                        | 113406015                         |
| MMSCL/M064A          | GCTGGGGCAACTGGAAGG      | CCCAGCTTCTAAATGACAAACATAC | 422                       | 113406009                        | 113406430                         |
| MMTAL.146            | CTCAAGGTAGGAGGACAGCG    | ACTAACCACCGACATGGAGC      | 468                       | 113406471                        | 113406938                         |
| MMSCL/M064B          | AGCAGGGAGGGAAGTCAGGA    | ACCACCGACATGGAGCACAC      | 391                       | 113406544                        | 113406934                         |
| MMTAL.147            | GCTCCATGTCGGTGGTTAGT    | CCCTGAGAAGGGGGTTAAAG      | 452                       | 113406919                        | 113407370                         |
| MMTAL.148            | AGGATCATGTGTAGCCCAGG    | GAGGGCATCAGATCCCATTA      | 455                       | 113407311                        | 113407765                         |
| MMSCL/M066A          | GGAGGGGAGCCCAGATTCT     | GCGGGGAATCTGTCCAGTG       | 361                       | 113408009                        | 113408369                         |
| MMSCL/M066B          | GCTTGCTCGGGGGATTAGTT    | CCGCTCCGTCATCCTGTAAC      | 385                       | 113408399                        | 113408783                         |

| <b>Amplicon Name</b> | <b>Primer 1 (5'→3')</b> | <b>Primer 2 (5'→3')</b> | <b>Amplicon Size (bp)</b> | <b>Chrom 4 Co-ordinate Start</b> | <b>Chrom 4 Co-ordinate Finish</b> |
|----------------------|-------------------------|-------------------------|---------------------------|----------------------------------|-----------------------------------|
| MMSCL/M067A          | CAGCCGCTCGCCTCACTAG     | ACCCTTTGTGGCGAACCTCA    | 384                       | 113409195                        | 113409578                         |
| MMSCL/M067B          | GGTGGGTGGACAGGCTGG      | CGTGAGGGATGGAAGTGCTAGTA | 375                       | 113409601                        | 113409975                         |
| MMSCL/M068A          | CTTGCCCTCCCATTATGTATT   | TCGCTCCAGGGTGAAGACT     | 434                       | 113410107                        | 113410540                         |
| MMTAL.155            | CACTTTAGGCTTGCTCCCTG    | CCCAGCTCTCTACATGCCTC    | 491                       | 113410592                        | 113411082                         |
| MMSCL/M069A          | AGGGGGACTCAGCATTCGTT    | AGAAAGAGGCGTGAGAAGCATC  | 438                       | 113410876                        | 113411313                         |
| MMTAL.156            | GAACCACAACAGCCAGAGT     | AGAGGGAAGGGAGGAAATCA    | 529                       | 113411187                        | 113411715                         |
| MMSCL/M069B          | TGCCCTGTCCACTTAGAAGCTC  | AACAGGCAGGCCAAGAGACC    | 370                       | 113411759                        | 113412128                         |
| MMSCL/M070A          | GACCCCTGGACCCAGACATT    | CACAGCCATGCCTCAGAAAAG   | 341                       | 113412168                        | 113412508                         |
| MMSCL/M070B          | TGGGGTTGGGGGACCTAG      | CAAAGGCAGGCTGGCAAGTA    | 328                       | 113412530                        | 113412857                         |
| MMTAL.159            | CCTTCCTGTGTCTGGATGGT    | GGTCACAGATGGTTTTGGCT    | 596                       | 113412710                        | 113413305                         |
| MMTAL.160            | GCCAAAACCATCTGTGACCT    | TGAGAAGCCAGGGAGCTAAA    | 573                       | 113413287                        | 113413859                         |
| MMSCL/M071A          | CTGCATAGCCCATAGGAGGTG   | CCTTCCTCCTCCTGGTCATTG   | 451                       | 113413675                        | 113414125                         |
| MMSCL/M072A          | TGGCATCCCCCTGAAGA       | GGCTTGGGAAAGGGAGAAGA    | 428                       | 113414189                        | 113414616                         |
| MMTAL.162            | GGTCTTCTCCCTTTCCCAAG    | AGGCAAGTCTCAGTGAGGGA    | 436                       | 113414595                        | 113415030                         |
| MMSCL/M072B          | CTGGCTGGGTGGCTTTTGT     | AAACCCAGTGCCCCAAACA     | 399                       | 113414758                        | 113415156                         |
| MMSCL/M073A          | CCAGCGCATCCCTGTTTGT     | AGGGGGCACTCGTTTCATG     | 409                       | 113415162                        | 113415570                         |
| MMSCL/M073B          | TTTCTCCCCTGTGTCAATCCA   | CACGCAATGGGAAAGAACCA    | 447                       | 113415695                        | 113416141                         |
| MMTAL.166            | CCATTGCGTGGGAGTTAGTT    | AAGACCAAAACCCTGGCTCT    | 597                       | 113416132                        | 113416728                         |
| MMSCL/M074A          | GCGGTGGACGGACTGTGAT     | CTGCCAGCCCCTTTAGAA      | 373                       | 113416333                        | 113416705                         |
| MMSCL/M074B          | AGCCAGGGTTTTGGTCTTTGT   | GGCTTGCCACAGACATGG      | 438                       | 113416711                        | 113417148                         |
| MMSCL/M075A          | CTGCGGGCGTGTGACTCTT     | ATGCAACCCCACTGAGTCA     | 491                       | 113417273                        | 113417763                         |
| MMTAL.170            | TTTGGTCTCCTGGGAGTTTG    | GCTGGGAATTAACGGTGAGA    | 557                       | 113417981                        | 113418537                         |
| MMSCL/M076A          | AAAGTGGGCAGATCAACAGGG   | CAAGGCCAAATCCTACCATCC   | 421                       | 113418281                        | 113418701                         |
| MMSCL/M076B          | TTTGGGGTGGAGGAAGTGG     | GGCCTCAGGGCACTTTTCTT    | 398                       | 113418794                        | 113419191                         |
| MMTAL.172            | CATTCTCCCTGTCCCAAGAA    | TCCCATGGAGTCAGGAAAAC    | 567                       | 113419111                        | 113419677                         |
| MMSCL/M077A          | CACCCACGCCTCACTCTT      | GCCAGGCCAGAGAGAAAAT     | 427                       | 113419484                        | 113419910                         |
| MMSCL/M078A          | CTGGGCCTGGCGTCTGAC      | CCTGTCTGGGCCTAAATTTG    | 491                       | 113419900                        | 113420390                         |
| MMTAL.174            | AGGAAGGACAGTTGGTGTGG    | CCTTCCTATTCCAGCTTCC     | 546                       | 113420453                        | 113420998                         |
| MMSCL/M079A          | AGACGAGGGAAGGACATGAGTG  | CCGCTCCACCACTGAAAAC     | 342                       | 113420838                        | 113421179                         |
| MMSCL/M079B          | TGCTCCCCACCTCACTTT      | GCTCCGGGCAGAAAACAAC     | 416                       | 113421248                        | 113421663                         |
| MMTAL.177            | CCAGCACTAGGTCATTGGGT    | CAAAGCACATCCCATTCTT     | 506                       | 113421894                        | 113422399                         |

| <b>Amplicon Name</b> | <b>Primer 1 (5'→3')</b>  | <b>Primer 2 (5'→3')</b>   | <b>Amplicon Size (bp)</b> | <b>Chrom 4 Co-ordinate Start</b> | <b>Chrom 4 Co-ordinate Finish</b> |
|----------------------|--------------------------|---------------------------|---------------------------|----------------------------------|-----------------------------------|
| MMSCL/M080A          | TGCCCTAGACACCAACCAGAAG   | AGCGGGCCATCATTCTGTG       | 436                       | 113422227                        | 113422662                         |
| MMSCL/M081A          | ATTGGTGGAGGACTTGTTCAAG   | GGCCTGCCTAACAAGAAGTACAT   | 437                       | 113423397                        | 113423833                         |
| MMSCL/M082A          | TTCCCCACACTGTTTATTCATAGG | GGCAAGGGGGTAGGCAAG        | 495                       | 113423971                        | 113424465                         |
| MMSCL/M082B          | CCCCCTTGCCACCCTGT        | GGGGATGGGAGTGCCTGTAG      | 422                       | 113424456                        | 113424877                         |
| MMSCL/M083A          | CCAGGACCGGCTGAGATCTTA    | CAACCCGGCAGATGTGGA        | 416                       | 113424898                        | 113425313                         |
| MMTAL.184            | GCCTTTGTCCTGCTCTTGTC     | GGATGCTGGGAGTTCAGAAA      | 404                       | 113425441                        | 113425844                         |
| MMSCL/M083B          | CCTTCCCTCAGCCAGTGTTG     | CAGGTCTTGGGGGTCTATTGAC    | 341                       | 113425765                        | 113426105                         |
| MMTAL.187            | ATGCTGGTATGATTGGAGGG     | GGTCTCAGCAGGGCAGATAG      | 585                       | 113426874                        | 113427458                         |
| MMSCL/M085A          | AGCCATGCCATCCTGAAGC      | TGATCCCTCTGCAACACACG      | 435                       | 113427369                        | 113427803                         |
| MMSCL/M086A          | ACCATCTCCCCAAAGCTCACT    | GGAGGGGGCAACTGGAAAG       | 488                       | 113427839                        | 113428326                         |
| MMSCL/M086B          | TGGCCTGAACCTGCAATGAT     | CAGGCCAGCAATGAACCAAG      | 439                       | 113428384                        | 113428822                         |
| MMSCL/M087A          | GTCTTGCCCCCTCCATACTTT    | GGCAGGTCCGCTCAAGGT        | 331                       | 113428908                        | 113429238                         |
| MMTAL.191            | TCTGCCCAGATCATAGTCCC     | ATCATCAAGGTGGGAGCATC      | 517                       | 113429133                        | 113429649                         |
| MMSCL/M087B          | TGCCCCAAGCTCCCCAAG       | CAGGCAGGCGTGGTACAGG       | 395                       | 113429235                        | 113429629                         |
| MMTAL.192            | GATGCTCCCACCTTGATGAT     | TTGTAAAGCCACAGCCCTCT      | 477                       | 113429630                        | 113430106                         |
| MMSCL/M088A          | TGAAGGGCAGCTGAGTGGG      | CCCCAGCCCCAAGTCTTCT       | 419                       | 113430196                        | 113430614                         |
| MMSCL/M088B          | GGGCTGGGGGAAGGTGA        | CACCTCCCAGCCCTCCAG        | 371                       | 113430606                        | 113430976                         |
| MMSCL/M089A          | GTGCGGCTCAGTGGTGGA       | AACTCACGCCCTGCTTCACA      | 349                       | 113430974                        | 113431322                         |
| MMTAL.195            | GGCTAACTTCCCCTCAGCTT     | CTCAGGCAGCTGTTCTACCC      | 474                       | 113431146                        | 113431619                         |
| MMTAL.196            | GGGTAGAACAGCTGCCTGAG     | GATGGGTGAACACTTGGCTT      | 442                       | 113431600                        | 113432041                         |
| MMSCL/M090A          | TGACCCGGGAGCTGTTTTCT     | GGGATCAAATAAAGGCCTAACATAC | 343                       | 113432097                        | 113432439                         |
| MMSCL/M090B          | TCACCCAATTGCCTAACTCAGA   | GGGCCTGTGACCATTCCAC       | 444                       | 113432545                        | 113432988                         |
| MMSCL/M091A          | CACAGGCCCACAGCACATG      | GTCCCTGTTGCTTGCATGGT      | 463                       | 113432980                        | 113433442                         |
| MMSCL/M091B          | GGGGTCTAGCCTGCTCTTGC     | GAGCCTGCTTCCCCTATGTGT     | 340                       | 113433479                        | 113433818                         |
| MMSCL/M092A          | CTGGTTGGAATGAAAGGAATGAG  | GCTGCCCCTTTTCCTTACA       | 387                       | 113433855                        | 113434241                         |
| MMSCL/M092B          | CAAGAAGCCCCACCCACTG      | CTGGAGGTCTGGGGTGTTTG      | 398                       | 113434331                        | 113434728                         |
| MMSCL/M092C          | GTTGGCCTTCAGTCTGCTCGT    | AGCCCCCATCCAGAGCAA        | 398                       | 113434789                        | 113435186                         |
| MMSCL/M093A          | GGCTAGGGGGTGGTGACATT     | GCTCAGGCATTGGGAACAAC      | 457                       | 113435183                        | 113435639                         |
| MMTAL.205            | TGTCACCCTTGGAACATCA      | CTGGGGTGTGGAGAGGTAAA      | 484                       | 113435818                        | 113436301                         |
| MMSCL/M094A5         | GGGTGGAATGATTCAGGCT      | AGGGCTGGCATCTGGAAGAT      | 501                       | 113435902                        | 113436402                         |
| MMTAL.206            | TTTACCTCTCCACACCCAG      | AACACAGCGACAGCAATGAG      | 553                       | 113436282                        | 113436834                         |

| <b>Amplicon Name</b> | <b>Primer 1 (5'→3')</b>  | <b>Primer 2 (5'→3')</b> | <b>Amplicon Size (bp)</b> | <b>Chrom 4 Co-ordinate Start</b> | <b>Chrom 4 Co-ordinate Finish</b> |
|----------------------|--------------------------|-------------------------|---------------------------|----------------------------------|-----------------------------------|
| MMSCL/M094B          | GAGCTGCCCTTTGGTCCCT      | CACCCAGCCCTGAGCCTT      | 442                       | 113436482                        | 113436923                         |
| MMSCL/M095A          | TTGCCACCATGAGGAAGGAA     | CCAGCCCCCAAACCACTC      | 365                       | 113437003                        | 113437367                         |
| MMSCL/M095B          | GGGCTGGGAGGGGGTTAA       | TGCACCCACATGGAACAGCT    | 462                       | 113437361                        | 113437822                         |
| MMSCL/M096A          | GGAGGGGACAGAGGCAGTTC     | CAACCCTCCTACCTGATCCACA  | 476                       | 113437892                        | 113438367                         |
| MMSCL/M096B          | GCTGGGGGTGTTTTCTGCTT     | GGCACCCACTACCTCCTGAAC   | 374                       | 113438457                        | 113438830                         |
| MMSCL/M097A          | GGGGAGAAGGGGTTCATGT      | GGGGACTAGGGCCACAGAGA    | 383                       | 113438833                        | 113439215                         |
| MMSCL/M097B          | TCAGGCCAGGACTCAGACCA     | AACAGCCTCAGCCTCTCCAAC   | 361                       | 113439324                        | 113439684                         |
| MMSCL/M098A          | CCTGTGGGTGGCTCTTGATTC    | TGGGAAGGGAAGAGAGCTGG    | 313                       | 113439872                        | 113440184                         |
| MMTAL.215            | GTACAACACTCATGCCACG      | AGGCAAGCCTTAGACCACAA    | 547                       | 113440142                        | 113440688                         |
| MMSCL/M099A          | TTCCCTCTCTGGTCTTTAGCTTTA | GTGGGGAGAGGGGTGATT      | 382                       | 113440830                        | 113441211                         |
| MMSCL/M099B          | GGGCCAGGACGGAACCA        | CACCGTGC GGCTGACAGT     | 357                       | 113441235                        | 113441591                         |
| MMTAL.218            | CAGGGGCTAGGCTGATACTG     | GAATCAAGCTTGGGTGGAGA    | 574                       | 113441360                        | 113441933                         |
| MMSCL/M099C          | GGAGGGGACCCGGAGCT        | CACCTGCCACTCCATTCCAC    | 409                       | 113441730                        | 113442138                         |
| MMTAL.219            | GCTGTGGAGTAAACGGTGGT     | ACCTTCCCAGGTGCCTTACT    | 537                       | 113442092                        | 113442628                         |
| MMSCL/M100A          | ACCAGCCTCAAGACAAGCACA    | CCACTGGCGCACTGAAGC      | 424                       | 113442298                        | 113442721                         |
| MMSCL/M100B          | AGTGCGCCAGTGGGTACC       | CAGAGCTGCCGATTCCAAAA    | 294                       | 113442709                        | 113443002                         |
| MMTAL.221            | CACTCCATGGGAAAGGCTAA     | ATTGAAGCTGTGGGGATGAG    | 484                       | 113443022                        | 113443505                         |
| MMSCL/M101A          | CATCCCCACAGCTTCAATCC     | TGGGTGCTGGGAAGTGAATTA   | 434                       | 113443488                        | 113443921                         |
| MMSCL/M102A          | AAGAGCCCCTAGAATTGAAATGG  | TGGCGGTAGGGGTTTTAACA    | 415                       | 113444037                        | 113444451                         |
| MMTAL.223            | TGTCGTGAGATCCACCAGAG     | AGCTCCTTCATTGGGAACCT    | 599                       | 113444109                        | 113444707                         |
| MMSCL/M102B5         | TGCAGAAGCGGATGCTCAC      | GAATCCTTCCCTCCCTGCAC    | 501                       | 113444646                        | 113445146                         |
| MMTAL.224            | CAAGGAGCTGAAGGGATTTG     | CACCCTTGTAACCTCCTCCA    | 507                       | 113444720                        | 113445226                         |
| MMSCL/M102B          | AAGGAGCTGAAGGGATTTGCA    | TCCTTCCCTCCCTGCACC      | 423                       | 113444721                        | 113445143                         |
| MMSCL/M103A          | TGGGGTGGGGTGAACAGG       | ATGGAACGCACGGGATGTAC    | 388                       | 113445225                        | 113445612                         |
| MMSCL/M103B          | TCCCCTGAATCCCCTGAATC     | CATGGGCCTAGAGGAAAACAGA  | 459                       | 113445634                        | 113446092                         |
| MMTAL.227            | TAGTAGTTGGCCACTCCCGT     | TGCTGGAATAATCCAAAGGC    | 592                       | 113446173                        | 113446764                         |
| MMSCL/M104A          | CAAACCCAGAATAGCACTCAGCA  | CCAGCCTCACCATCCTTGTC    | 427                       | 113446375                        | 113446801                         |
| MMSCL/M105A          | TGGCACCAGGGAAAAGAATC     | GGCTCCAAACCCAAGTCCAG    | 398                       | 113446805                        | 113447202                         |
| MMTAL.229            | TTCTGGACTTGGGTTTGAG      | CCCACAGAAGGAAAACAGA     | 401                       | 113447181                        | 113447581                         |
| MMSCL/M105B          | GCCCCTCCAGGTTTTGCTTA     | CCCATGCCTAGACCTCACTGAA  | 455                       | 113447394                        | 113447848                         |
| MMTAL.231            | TGCTAATCCACATGGCAAAA     | TGCCCTCCACGTCCTATTTA    | 580                       | 113448011                        | 113448590                         |

| <b>Amplicon Name</b> | <b>Primer 1 (5'→3')</b>   | <b>Primer 2 (5'→3')</b>      | <b>Amplicon Size (bp)</b> | <b>Chrom 4 Co-ordinate Start</b> | <b>Chrom 4 Co-ordinate Finish</b> |
|----------------------|---------------------------|------------------------------|---------------------------|----------------------------------|-----------------------------------|
| MMSCL/M106A          | GGGGCGGAGAGCAATGTG        | CCACGTCCTATTTATTTCTTATTGA    | 478                       | 113448107                        | 113448584                         |
| MMSCL/M106B          | GGCACACACCTTTCTTTTGAT     | CCCCCTTCCTTCTCTGCATG         | 407                       | 113448587                        | 113448993                         |
| MMTAL.232            | CGCCTTGTGCACTAAACAAA      | CACTGCCCCAGATACTGGTT         | 597                       | 113448801                        | 113449397                         |
| MMSCL/M107A          | TGTGGGAGGGATGCTGAGTC      | AATCCCCCTTGCTTCACTGTGTAA     | 317                       | 113449299                        | 113449615                         |
| MMTAL.233            | GTATCTGGGGCAGTGCTGTT      | CTCTCACCAGCTGTCCATCA         | 570                       | 113449383                        | 113449952                         |
| MMSCL/M108A          | AATTTTGGCTCCTCCTTGCA      | TAGATGCTGCTTGCCAAGAGTG       | 313                       | 113449836                        | 113450148                         |
| MMTAL.235            | TTTGACACACATCCACACCC      | ATGCCCTCTTCTGGTGTGTC         | 573                       | 113450516                        | 113451088                         |
| MMTAL.236            | GAGCAGTCGGGTGCTCTTAC      | TGCCATGCTTTTCAGACAG          | 538                       | 113451157                        | 113451694                         |
| MMTAL.237            | GCCTCTGGCCTCTATATGCTT     | GGCTACTGCCCTGACAGAGT         | 405                       | 113451726                        | 113452130                         |
| MMSCL/M110A          | TATGCAGGAAAGAGTCAGGAAGAA  | TCGGGGCTACACTGGGATCT         | 331                       | 113452054                        | 113452384                         |
| MMTAL.239            | TGGGATTGAACTCTGGACC       | TCCCCAGATATGGCAGTCTC         | 455                       | 113452522                        | 113452976                         |
| MMTAL.240            | GAGACTGCCATATCTGGGGA      | AGTCCCCCATACCCTACCAC         | 424                       | 113452957                        | 113453380                         |
| MMSCL/M111A          | ACGCCAGGGCCAAAAAGT        | TGAAAGGGCATGGGGTGTT          | 428                       | 113453335                        | 113453762                         |
| MMSCL/M112A1         | TCTTCAGCAAAACAACCTCTCATG  | CCCATGGTCCAGGCAAGTG          | 419                       | 113453853                        | 113454271                         |
| MMSCL/M112B          | TGGTGAGGTCTGGAGCTACTTGA   | GCCCAAACCAGCACAAAGTGA        | 410                       | 113454406                        | 113454815                         |
| MMTAL.244            | ACCAGCTGTGCTACCCAGAG      | CATAAAGGGAAGCAAGGCAG         | 439                       | 113454707                        | 113455145                         |
| MMSCL/M113A          | GCTGCCTTGCTTCCCTTTATG     | GCTCACGGGCTCAAAGTCAC         | 397                       | 113455125                        | 113455521                         |
| MMSCL/M113B          | CACATGGGCCACGAGAGAAA      | ATGTGGCCAGCAGAATGTTTAA       | 307                       | 113455560                        | 113455866                         |
| MMTAL.246            | CAAGGGGTCAAAGACCTGAA      | TGACAACCTGAGCAATTTGGC        | 513                       | 113455738                        | 113456250                         |
| MMSCL/M114A          | GGGCTTATCTGGCTCTTGCTC     | TGGGGTGGAAAGAGTTAGGAGC       | 446                       | 113456278                        | 113456723                         |
| MMSCL/M115A          | GGCCCATCAGGTCTAGGTAAAG    | AGAGAGCGATGCGAGGTAAGTC       | 485                       | 113456746                        | 113457230                         |
| MMSCL/M115B          | AGGCTGCTGTAGTGTGCTCTCTG   | GGCAACCCTTCAACCTCTGTAA       | 471                       | 113457349                        | 113457819                         |
| MMTAL.251            | CAGTACTGTTCCCCGCCTTA      | GGTGTAAGTGCATGTGCAGG         | 521                       | 113461140                        | 113461660                         |
| MMTAL.253            | GTCTTAGCATCGATCAGGCA      | GTTGCCTCCAAACCTCACAT         | 417                       | 113463310                        | 113463726                         |
| MMSCL/M122A          | TGGGGATTAGATTCAGAACAGGC   | ACCTCACCAGACTTAATGTATCT      | 407                       | 113463761                        | 113464167                         |
| MMTAL.255            | GTCGTTGCCCTTACCACAGT      | CCTTAGGCTTGCACTTGAGAG        | 511                       | 113464281                        | 113464791                         |
| MMSCL/M123A          | GTTCAAAGGCCAAAGTCTACCC    | GATGCCGGACAGAGATCAGG         | 503                       | 113464629                        | 113465131                         |
| MMTAL.256            | CCAAGTGCAAGCCTAAGGTC      | GAACGAGCCTTCTCAGATGC         | 488                       | 113464774                        | 113465261                         |
| MMSCL/M123B          | GTCCGGCATCTGTCCTGATG      | GCAATGCTGAGGATAAAGATAACA     | 404                       | 113465122                        | 113465525                         |
| MMSCL/M124A          | TGCTATCCACACTTCCAACTTTTTC | TAGCTGTCCCTTTTGTAATGAA       | 411                       | 113465534                        | 113465944                         |
| MMSCL/M124B          | CCAAAGGGGACAGCTAAGTCAA    | CTTTTAGCTCCTTTAGTTTGATATGTTG | 351                       | 113465929                        | 113466279                         |

| <b>Amplicon Name</b> | <b>Primer 1 (5'→3')</b>      | <b>Primer 2 (5'→3')</b>    | <b>Amplicon Size (bp)</b> | <b>Chrom 4 Co-ordinate Start</b> | <b>Chrom 4 Co-ordinate Finish</b> |
|----------------------|------------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------|
| MMSCL/M125A          | TGTCTTAAGTGAAGTCAATTTTGCT    | GGTCCAGTCCCAACAGTAACCTTAGT | 331                       | 113466392                        | 113466722                         |
| MMTAL.260            | TGGGTTTAGCTTCTCATCCG         | CATTGCATGTGGCTTTCTTG       | 487                       | 113466510                        | 113466996                         |
| MMSCL/M125B          | TGCTCCCTTGCTATATATGTATTTGTAA | TTCTTGACAGCACCTATGAGTCTTAC | 414                       | 113467016                        | 113467429                         |
| MMSCL/M126A          | GCAAGAAGAAGCTGGAACAGTG       | CCATTTGCCAGACGTGAAGTG      | 419                       | 113467423                        | 113467841                         |
| MMSCL/M127A          | GAATGAGCCCCCTAAATGGTC        | CTTTGGGCAGTTTAGCAGTTAGAC   | 390                       | 113468293                        | 113468682                         |
| MMSCL/M127B          | GCCCAAAGTGCCCATCCT           | TTCCCTGCTCACATCCTTCCT      | 434                       | 113468675                        | 113469108                         |
| MMSCL/M127C          | ACAAGGGCCTGACAAGTGCA         | GCACCCCTATTACATGGCTTTC     | 425                       | 113469109                        | 113469533                         |
| MMSCL/M128A          | CCTTGCCAGTCCTTCATACC         | ACGATGGCCCACTCTGTGAA       | 400                       | 113469612                        | 113470011                         |
| MMSCL/M128B          | GGCCCATCTAAATTCAGGAGTC       | AAGGTTGGGTGTTTTGTATGTGTG   | 315                       | 113470082                        | 113470396                         |
| MMTAL.267            | AGATGAGGAACACAGGTGGC         | TCAGAGAGGGAGGATCAGGA       | 538                       | 113470159                        | 113470696                         |
| MMSCL/M129A          | GGCTTCCCCAACTTCTCCT          | GCCAGCGTTCTAAAAACACCA      | 437                       | 113470661                        | 113471097                         |
| MMTAL.268            | CGGTTGATCCACACAGTGAC         | TTTTCTCTGACGGGCAGTTT       | 506                       | 113470890                        | 113471395                         |
| MMSCL/M130A          | TCCTGGTCGAAAAATAACATCAAC     | AATTAAAGGTCAACCCAGTGTCAGG  | 313                       | 113471307                        | 113471619                         |
| MMTAL.269            | CCTTGACACTGGGTTGACCT         | GAGGCAGAGGGAGAAGGAGT       | 426                       | 113471594                        | 113472019                         |
| MMSCL/M130B          | GGACTGGGGGTTGAATTTGTG        | CTGCCCACTGTTTGCACTGA       | 460                       | 113471871                        | 113472330                         |
| MMTAL.270            | ACTCCTTCTCCCTCTGCCTC         | TCTGGAACTTGTCATCCCC        | 476                       | 113472000                        | 113472475                         |
| MMSCL/M131A          | TTCCCAGGACCTAAGCTCATATTC     | CCAGCAGCAGGGCCAGA          | 477                       | 113472393                        | 113472869                         |
| MMTAL.271            | GTTTCCAGAATGGGTGTTGG         | GCAAGTATGGAGAGGGGACA       | 508                       | 113472467                        | 113472974                         |
| MMSCL/M131B          | TGGGATTTATGGGTTCTGGA         | GACAAACCCCACTGACTCTAATCTC  | 392                       | 113472876                        | 113473267                         |
| MMSCL/M132A          | AGGGGGTGAGCTCGTGCTT          | TTACAGCCCCCAGGAGGATAG      | 393                       | 113473288                        | 113473680                         |
| MMSCL/M132B          | TGCATCCGTGTGAGTCAGTTG        | TGCTATCCTGGGACCTTGACTC     | 521                       | 113473743                        | 113474263                         |
| MMTAL.275            | GCCTTGGTCTCTTCTGCCTA         | TTTCTGTGCCCTCTGTTTCA       | 507                       | 113474172                        | 113474678                         |
| MMTAL.276            | TGAAACAGAGGGCACAGAAA         | GGCTCACAACCATCCGTAAT       | 492                       | 113474659                        | 113475150                         |
| MMTAL.277            | ATTACGGATGGTTGTGAGCC         | GGAAGAATGACTTCCAGGCA       | 518                       | 113475131                        | 113475648                         |
| MMSCL/M134A          | TTGGTCAAGGAGTGGCACTATTT      | AAGCATTTCTCACAGCATCTTCAA   | 471                       | 113475540                        | 113476010                         |
| MMSCL/M134B          | CCGATTGGGCTATGCAGACA         | AGGACCCACATGGCAGCTC        | 329                       | 113476102                        | 113476430                         |
| MMTAL.280            | GAGCATCAGATCCCCTGAAA         | ATCCTGGCACAAATAGGCAC       | 443                       | 113476372                        | 113476814                         |
| MMSCL/M135A          | TTGCGCAGTACAGGTTAAAAATATTC   | GATGTTTTTGCTAGTGTTCTGATG   | 463                       | 113476902                        | 113477364                         |
| MMTAL.282            | ATCTTGACCAACAACCCAGC         | TGTATAGTCCTGGATGCCCC       | 502                       | 113477206                        | 113477707                         |
| MMTAL.283            | GCCCTTGTTGCTGGGTAATA         | GTCCTGCCTGAACGTGTGTA       | 450                       | 113477581                        | 113478030                         |
| MMTAL.284            | TACACACGTTGAGGCAGGAC         | TGACTCGAGGTCCCTTCAGA       | 572                       | 113478011                        | 113478582                         |

| <b>Amplicon Name</b> | <b>Primer 1 (5'→3')</b>  | <b>Primer 2 (5'→3')</b>  | <b>Amplicon Size (bp)</b> | <b>Chrom 4 Co-ordinate Start</b> | <b>Chrom 4 Co-ordinate Finish</b> |
|----------------------|--------------------------|--------------------------|---------------------------|----------------------------------|-----------------------------------|
| MMSCL/M137A          | AATCCCCAGGGCAGACTTTC     | CCCCATTGCTCTGCGGAT       | 345                       | 113478669                        | 113479013                         |
| MMSCL/M137B          | GCCCCCTCCCGCTTTTACA      | TGCCGAGGAAGCCAATAGC      | 394                       | 113479018                        | 113479411                         |
| MMSCL/M138A          | TCAGGTCGCGCAGCAGTC       | CCGCGAACGAAGTCTGTCTG     | 384                       | 113479489                        | 113479872                         |
| MMTAL.288            | CAATCGCGGAAGATCTGAAT     | GGATGGGGACAGAGAAGTCA     | 501                       | 113479901                        | 113480401                         |
| MMSCL/M139A          | TCCCCACTCCTGACTTCTCTGT   | TTCCCTCGGCATTCTATCC      | 416                       | 113480372                        | 113480787                         |
| MMTAL.290            | CTGCTCTGGTCTCTGGTTCC     | CCTGATCAGCTTCAGGATCA     | 460                       | 113480674                        | 113481133                         |
| MMTAL.291            | TGTTTGCATGCACAGAGGAT     | GCAGGGTGTGGGTAGAAAAA     | 441                       | 113481347                        | 113481787                         |
| MMSCL/M140A          | TCCATCAGGTCCCTTGTCTCT    | TGGCAGGGTGTGGGTAGAAA     | 401                       | 113481389                        | 113481789                         |
| MMSCL/M141A          | GTCCCTCCTCTGCTTCTATGA    | CAAGACCGGAAACCATCAAATAG  | 469                       | 113482284                        | 113482752                         |
| MMSCL/M141C          | GGAGGGTTGGGGTAGGGTAA     | AGCAGGAGGCAGAAGGAGTTG    | 401                       | 113482770                        | 113483170                         |
| MMTAL.294            | CTGTGTGCAAGCCAACTT       | CGAGCTCTCAGGAACAATCC     | 589                       | 113483231                        | 113483819                         |
| MMSCL/M142A          | ATGTCTCGGCTGATTTAATTTGTC | GCCTGCCCCCTTACCTGACT     | 385                       | 113483612                        | 113483996                         |
| MMSCL/M142B          | GCAGGCAAGCCATCATTAGG     | GCATTGGGAAGCAACTAGCC     | 379                       | 113483991                        | 113484369                         |
| MMTAL.303            | GATGGATCCCATTGTGGAC      | CTCTGCCTCTTCCTTGTTG      | 551                       | 113484229                        | 113484779                         |
| MMSCL/M143A          | ACCCATCTCTGCTCCTGTGCT    | CGGGAGACTTAAGGATTCCAGA   | 455                       | 113484552                        | 113485006                         |
| MMSCL/M143B          | GTCTCCCGTTCTTAATGATCCTTC | GCTGGCCAATCATGAAGACC     | 342                       | 113484999                        | 113485340                         |
| MMSCL/M144A          | TGAGGGTGTAGGGCAGTGTTAA   | TCATGCTTTCCTGCCCTTCTC    | 456                       | 113485487                        | 113485942                         |
| MMTAL.296            | CGTTCAATGAGCTACAGAGGTG   | TGTAGCCACTGCCTGTTTTG     | 497                       | 113485531                        | 113486027                         |
| MMTAL.297            | AAGGACAAAACAGGCAGTGG     | TGGAAGGCATTTGACAAACC     | 404                       | 113486003                        | 113486406                         |
| MMTAL.307            | ACGATGCCTACCTCTGGATG     | CACCCATAACCAATGGAAGTG    | 522                       | 113486116                        | 113486637                         |
| MMTAL.298            | CCTTCCATGCACTGGAGAAT     | AACTGAACCCAAGCCCTCT      | 471                       | 113486400                        | 113486870                         |
| MMTAL.308            | AGAGGGCTTGGGTTCAGTTT     | ATTTACAGGGAACACCTGCAC    | 597                       | 113486851                        | 113487447                         |
| MMTAL.300            | GAAATGAAGCCCATCCTGAA     | GTTGTCAAGCTGAGGAAGGC     | 477                       | 113487443                        | 113487919                         |
| MMTAL.309            | GAAATGAAGCCCATCCTGAA     | GTTGTCAAGCTGAGGAAGGC     | 477                       | 113487443                        | 113487919                         |
| MMTAL.301            | GCCTTCCTCAGCTTGACAAC     | AGATTGCCCATGAACACACA     | 478                       | 113487900                        | 113488377                         |
| MMTAL.310            | GCCTTCCTCAGCTTGACAAC     | AGATTGCCCATGAACACACA     | 478                       | 113487900                        | 113488377                         |
| MMTAL.311            | GTGTGTTTCATGGGCAATCTG    | CAAAGAGACATGTGGGGCTT     | 419                       | 113488359                        | 113488777                         |
| MMTAL/302ver2        | CTTCGGCTATGGGAAGTCAG     | ATCACAGGACAAATGGGAGC     | 572                       | 113488395                        | 113488966                         |
| MMSCL/M147B          | TGGGGACAGAATCTTGCTTTTT   | GAAACAGGCATAGCAGTCCAAATA | 402                       | 113488717                        | 113489118                         |
| MMSCL/M148A          | ACCTTGCCAGCAGAGTCTCG     | TGGGGGGTAGCACTCTCCTT     | 403                       | 113489296                        | 113489698                         |
| MMSCL/M154A          | GGGGGCATCCTGATGTCAC      | TGGTCCTCCCTTGCTGGTT      | 273                       | 113495553                        | 113495825                         |

| <b>Amplicon Name</b> | <b>Primer 1 (5'→3')</b>   | <b>Primer 2 (5'→3')</b>    | <b>Amplicon Size (bp)</b> | <b>Chrom 4 Co-ordinate Start</b> | <b>Chrom 4 Co-ordinate Finish</b> |
|----------------------|---------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------|
| MMTAL.317            | ACACATGCTGCAACTTGGAA      | GGCAGATTCTGTGCAAGTGA       | 463                       | 113495858                        | 113496320                         |
| MMSCL/M155A          | CGACGATGCTGGAACCACTT      | GTGGCCTCTTCCCCTATTAT       | 431                       | 113496375                        | 113496805                         |
| MMSCL/M155C          | AGGAGGCCAAATAAAAGTGGG     | GGTGCCTGATTTGGAGAGTGTC     | 387                       | 113496989                        | 113497375                         |
| MMSCL/M156A          | GCCATGGTCCTTGCTGAATC      | TGGCAGCTAAAATATGGGAAGTT    | 414                       | 113497386                        | 113497799                         |
| MMSCL/M156B          | TTTAGCTGCCAATCTTCTGTCAT   | CCATGCTGCAGTTCCTCACA       | 373                       | 113497788                        | 113498160                         |
| MMTAL.322            | CCAGGTCATGGCATAAAGGT      | GGGATGGTTTTCTCTGGT         | 440                       | 113498181                        | 113498620                         |
| MMSCL/M157A          | TCTGCCAGCTCTTTGTGTTA      | CATCCTGGCTGCTTTCTGTCTT     | 475                       | 113498685                        | 113499159                         |
| MMSCL/M158A          | ATGCAGAAGGGATGGAGAGAGA    | CTCTGTGATGGTCCCTTGTTC      | 518                       | 113499157                        | 113499674                         |
| MMSCL/M158B          | GGAACAAGGGACCATCACAGAG    | CTTTGTCAATCCGAGGTGTTATATT  | 436                       | 113499653                        | 113500088                         |
| MMTAL.326            | CACCTCGGAATGACAAAAGGT     | TAAGGTGGTGATCCCAGAGC       | 537                       | 113500071                        | 113500607                         |
| MMSCL/M159A          | AGCTTTGGCCATTTCTTTGTGA    | AATGGCAGGAAAAATGAGGAA      | 384                       | 113500489                        | 113500872                         |
| MMSCL/M159B          | CTCCTTGCCTCTGACTCCTT      | GTTGGGGGACTCACATGGAGA      | 416                       | 113500971                        | 113501386                         |
| MMSCL/M160A          | GGGCTGCCTTGCTCTGGTCT      | GCGCAGCATCAATTCCTTTT       | 389                       | 113501447                        | 113501835                         |
| MMSCL/M160B          | GCTGCGCACTGTGAAGGATAT     | TGGGAAGGACAGTCTATGGGC      | 356                       | 113501829                        | 113502184                         |
| MMSCL/M161A          | GGGGGAAGACGGAGAACAGAT     | TTCAGGCAAGGAGATTTTACCAA    | 275                       | 113502247                        | 113502521                         |
| MMTAL.331            | AAACTCTGTCTCGACCCCT       | GTCTGATGCTCGACCTGACA       | 425                       | 113502688                        | 113503112                         |
| MMSCL/M161B          | TCAACCTGCCCTTACCTCCA      | TGGCTCCTGCAATACCTTTCA      | 430                       | 113502790                        | 113503219                         |
| MMSCL/M162A          | CAGGGGGTTTTACTCTTGGCA     | TTTCCATTCCCGCTTAGTCT       | 417                       | 113503307                        | 113503723                         |
| MMSCL/M162B          | ACTCTTTTGCCTCATGAACAGC    | CATTGATTGGGAAAAGACTAAAGC   | 409                       | 113503776                        | 113504184                         |
| MMSCL/M163A          | AGGTAAGGGGGTGACACAAATG    | ATGTTTTGCTGCGTATTAGAGTTAGG | 314                       | 113504196                        | 113504509                         |
| MMTAL.334            | GCGTTAACCTTTGCTTCCAA      | ATCTCCACCATGGGCTACAG       | 534                       | 113504305                        | 113504838                         |
| MMSCL/M163B          | ATGGCCAAAAACAATGTCTCTGA   | TTGGCACATGGCATGATCCT       | 365                       | 113504702                        | 113505066                         |
| MMTAL.335            | GAACAGGATCATGCCATGTG      | TTTGACCTATTGCATACCATCA     | 597                       | 113505043                        | 113505639                         |
| MMSCL/M164A          | GCACCACAGCAGCCTAAACTT     | TAAAGTTCTGGGGAGTAATTGTTGC  | 425                       | 113505700                        | 113506124                         |
| MMTAL.337            | GGAGCAACAATTACTCCCCA      | TGCAAGAGGGCCAAGATACT       | 588                       | 113506097                        | 113506684                         |
| MMSCL/M164C          | GCAACAATTACTCCCCAGAACTTTA | AGATCTACCCAGGTGTTGTTTCAAT  | 402                       | 113506100                        | 113506501                         |
| MMSCL/M165A          | AAGGCAGGGAGGGGTGAAGT      | CTAATGGCGCTCATTGGC         | 364                       | 113506535                        | 113506898                         |
| MMSCL/M165B          | CAAAGTGAGCGCCATTAGCA      | AAGCACAAACCAGCCCAGAA       | 427                       | 113506881                        | 113507307                         |
| MMSCL/M166A          | CTGGGCTGGTTTGTGCTTGT      | GGCCAAAAATCAAGCACAGC       | 416                       | 113507290                        | 113507705                         |
| MMTAL.339            | GCTGGTTTGTGCTTGTGTTGA     | ATCAAGCACAGCAGGAGAGG       | 404                       | 113507294                        | 113507697                         |
| MMTAL.340            | CTGCTGTGCTTGATTTTGG       | TGGAATGATGATGGCTTCAA       | 542                       | 113507684                        | 113508225                         |



| <b>Amplicon Name</b> | <b>Primer 1 (5'→3')</b>   | <b>Primer 2 (5'→3')</b>    | <b>Amplicon Size (bp)</b> | <b>Chrom 4 Co-ordinate Start</b> | <b>Chrom 4 Co-ordinate Finish</b> |
|----------------------|---------------------------|----------------------------|---------------------------|----------------------------------|-----------------------------------|
| MMTAL.341            | TTGAAGCCATCATCAGTCCA      | TATCTGTCCAGGCTGTGGTG       | 486                       | 113508206                        | 113508691                         |
| MMSCL/M167A          | CCATCTGCAAAACGCTCTCTACT   | CAGGCTGTGGTGGAGAGAAACT     | 436                       | 113508248                        | 113508683                         |
| MMTAL.347            | ATGGACACCTGTCTTCTGGC      | GAGAGGAAACACAAAAACCCC      | 543                       | 113515852                        | 113516394                         |
| MMSCL/M175A          | TTTTCCCATGTGACGGTGTATC    | CAGTCCCACAACACCAGAAGAA     | 414                       | 113516508                        | 113516921                         |
| MMTAL.349            | AGGAACCTGTGCCACTGGTC      | AAGGCACCACAGGTTTTTAC       | 585                       | 113516976                        | 113517560                         |
| MMSCL/M176A          | TGAGGTCCAAGGCAGCTAGG      | CTCCCCACACTGCTCAACCT       | 353                       | 113517314                        | 113517666                         |
| MMTAL.350            | GTGAAAACCTGTGGTGCCTT      | CACTGGAAAGAACACGCTCA       | 419                       | 113517541                        | 113517959                         |
| MMSCL/M176B          | GGACGGGGTTTTGCCATT        | CCACCACAATCCTCCCTCAA       | 383                       | 113517860                        | 113518242                         |
| MMTAL.351            | CGGGATAGAGCAGATCAAGG      | TTGCCTCAATGATGATGGTC       | 586                       | 113517972                        | 113518557                         |
| MMSCL/M177A          | TGTGGTGGCATTGGAATTTGG     | GCTGTGCTTCCTGCCATAATG      | 482                       | 113518235                        | 113518716                         |
| MMSCL/M177A5         | CTCAAAGCAGTGCAGGCCA       | TGCTGTGCTTCCTGCCATAAT      | 401                       | 113518317                        | 113518717                         |
| MMTAL.352            | TCATTATGGCAGGAAGCACA      | AAGGCCATTCTTCTTCTCC        | 448                       | 113518695                        | 113519142                         |
| MMSCL/M177B          | CTGGAGGAGCTGAGAGTTCTACAA  | GGCTGAACATTTGGCATTTAACA    | 453                       | 113518738                        | 113519190                         |
| MMTAL.353            | GGCCTTCTCCAGTAAGAGCA      | TTCAGATTCCCCTCTGGAA        | 419                       | 113519137                        | 113519555                         |
| MMTAL.354            | TTGTGGAGCACCCCTCATACA     | CCCACAGCCATCCTGTTACT       | 527                       | 113519486                        | 113520012                         |
| MMSCL/M178A          | TTGGAGTTTGGTTTTGCTTTGA    | ACCCCCACCATGAAGAACCT       | 418                       | 113519839                        | 113520256                         |
| MMTAL.355            | AGTAACAGGATGGCTGTGGG      | ATGTGGCACTGTGCTCTCTG       | 574                       | 113519993                        | 113520566                         |
| MMSCL/M179A          | GCAGGCAGAGGGTAAGAGAGG     | AGAGGCAGAGCACACTTCCAA      | 406                       | 113520455                        | 113520860                         |
| MMTAL.357            | AATGTGAGACTGTCCCTGG       | GGGCTAGTGAGATGGCTCAG       | 403                       | 113520952                        | 113521354                         |
| MMTAL.358            | CCCCCTGTTTTGTTTTCT        | AGCTCCTAGGCTTCTGGGAC       | 476                       | 113521352                        | 113521827                         |
| MMSCL/M180A          | TCCCCACTGCTCCAAGGTC       | AAGAAGGGAGCCAGGTGTAACTA    | 389                       | 113521792                        | 113522180                         |
| MMSCL/M181A          | GTCCCCACCTTCTTTTGATGTATAC | CAGGATGGCAGCAGAGTTGG       | 424                       | 113522196                        | 113522619                         |
| MMTAL.360            | GTTACCCACTGACGCCTTGT      | ACTTTGCACCCTACCTCCCT       | 466                       | 113522361                        | 113522826                         |
| MMSCL/M181B          | TCGGTCCACCCCAACATCTA      | TGGGGCTGGGAGGGAAA          | 393                       | 113522641                        | 113523033                         |
| MMSCL/M181C          | GCCTTTCCCCCTTGATCACT      | ACTTCTACCTGGTTACCTGTGTTTTT | 250                       | 113523170                        | 113523419                         |
| MMSCL/M187A          | GCCCAGAACTCAGAATACCCA     | AGGGAGCTCAAGGGATACTGGT     | 426                       | 113528151                        | 113528576                         |
| MMTAL.363            | TGGAATCTTCTGCACCTGAG      | TGCCTGCAGAGAATGTTTCA       | 585                       | 113532172                        | 113532756                         |
| MMSCL/M191A          | TTAGGTCTTGATGGTTTTGTTCA   | TCCCAGGTGAAAGAGGCTAACA     | 397                       | 113532312                        | 113532708                         |
| MMSCL/M191B          | TGCAGGGAAGGTACACAGAGGT    | AACCCTCAAGCTTCTGCCATAG     | 478                       | 113532768                        | 113533245                         |
| MMSCL/M192A          | TCACCTTCTCATTTCTCCAGTCT   | ATGGCCCTGTCTTCTTTGCA       | 409                       | 113533304                        | 113533712                         |
| MMSCL/M192B          | CAGGGCCATAATCATCAGGG      | TGGGGTCATGGTTTCACTTCC      | 426                       | 113533704                        | 113534129                         |

| <b>Amplicon Name</b> | <b>Primer 1 (5'→3')</b>  | <b>Primer 2 (5'→3')</b>     | <b>Amplicon Size (bp)</b> | <b>Chrom 4 Co-ordinate Start</b> | <b>Chrom 4 Co-ordinate Finish</b> |
|----------------------|--------------------------|-----------------------------|---------------------------|----------------------------------|-----------------------------------|
| MMTAL.367            | GGTCCAGATTTGGGAACTGA     | ATGCCTCCATGAGATCCAAC        | 474                       | 113534098                        | 113534571                         |
| MMSCL/M193C          | TCCTGGGCCTTCAATTACAAC    | GCCATTGCTGTTTTGATTGTGA      | 412                       | 113535111                        | 113535522                         |
| MMSCL/M193C5         | GGCTGCACCTTCACCAATG      | AAGATTCTGTAGTTCTGATTAGCTGGG | 367                       | 113535135                        | 113535501                         |
| MMSCL/M194A          | GCAATGGCCCTGAAAAGAGTC    | CCAGGAGAGGCAGGCTAGTAAAG     | 424                       | 113535515                        | 113535938                         |
| MMSCL/M194B          | GCCTTTCCCCCTTGATCACT     | TAAGCTGCCCCTGAGATGGA        | 420                       | 113536005                        | 113536424                         |
| MMSCL/M195A          | TCCAAGGGCACAGAACATAACA   | TTATCTGACCTCCCTGACTCTGG     | 440                       | 113536540                        | 113536979                         |
| MMSCL/M195B          | GTCAGGGAGGTCAGATAACAGCA  | TCCTGGATGGTTTTGTTCTCCTA     | 316                       | 113536962                        | 113537277                         |
| MMSCL/M197A          | ATTAGCCCAGAACTTAGGATACCC | GGGTTGCAGATTTCTTTAGCTCC     | 415                       | 113539004                        | 113539418                         |
| MMSCL/M198A          | CCCTGGGGATTGAAAGCC       | AGATATTTACTGGCTTTTGAGTTGG   | 256                       | 113539724                        | 113539979                         |
| MMTAL.376            | ACCCAAC TCAAAAAGCCAGT    | AAATACTCTCGGTGGGTCC         | 593                       | 113539952                        | 113540544                         |
| MMSCL/M199A          | GGGACCCCACCGAGAGTATT     | GGTGAGTGGTCTTGCTTTCTGTTAG   | 495                       | 113540524                        | 113541018                         |
| MMTAL.377            | GGACCCCACCGAGAGTATTT     | GGGTTCTGGTGATGGTGAGT        | 507                       | 113540525                        | 113541031                         |

### Appendix 3A

#### Sequences of Primer Pair used to Amplify PCR Amplicons Containing GATA-1 Binding Sites (included as controls on the SCL tiling path array)

| PCR amplicon | Forward primer sequence (5'→3') | Reverse primer sequence (5'→3') |
|--------------|---------------------------------|---------------------------------|
| HB009BG      | TGACCATGTGATTCTGCCGCTTCTAGGT    | GACCTCCCATAGTCCAAGCA            |
| HB032BG_1    | TGACCATGAGCAACAGTTTCAGTGCAGG    | CATGAATACTTCCTGCCATGTT          |
| HB032BG_2    | TGACCATGGCCACTTAACATGGCAGGAA    | GGAACCCAACCAGACTCTCA            |

### Appendix 3B

#### Sequences of Primer Pairs used to in Real-Time PCR to Analyse SCL Expression in K562, Jurkat, HL-60 and HPB-ALL

| Gene    | Forward primer sequence (5'→3') | Reverse primer sequence (5'→3') |
|---------|---------------------------------|---------------------------------|
| β-Actin | AGAAGGAGATCACTGCCCTGG           | CACATCTGCTGGAAGGTGGAC           |
| SCL     | TTTTGTGAAGACGGCACGG             | TGAGAGCTGACAACCCCAGG            |
| SIL     | ATGCACATAACGTGGATCACG           | TCCATGCTCAAATCCACACC            |

## Appendix 4

### Sequences of Primer Pairs used to in the Real-Time PCR Verification of ChIP-chip data for Histone H3 K9/14 diacetylation

| Region Name | Amplicon Name  | Primer 1 (5'→3')           | Primer 2 (5'→3')           | Amplicon Size (bp) | Chrom 1 Co-ordinate Start |
|-------------|----------------|----------------------------|----------------------------|--------------------|---------------------------|
| KCY +1      | HSTAL.277q     | TGGTTGGTTAGCTGCATTGAC      | CCTTCTTTCCCAAGCATTCC       | 75                 | 47512689                  |
|             | HSSIL/M33Aq    | GCGCAGAGGTTAGCGTGTC        | GCCTCTAACCCAAATCCGC        | 71                 | 47512136                  |
| KCY -4      | HSSIL/M2Aq     | AGTCTTTGTTGTTTCCATGATAGAAC | GGTTTACTAGGAAGTTTCAGACCC   | 80                 | 47508213                  |
| NC i        | HSSIL/M10Aq    | TCTCTTTGAACACAGGGCAATG     | TATTAGTCTAGGTGTACTGGCAGTTG | 71                 | 47499807                  |
| SIL -1/+1   | HSSIL/GAP/M4Aq | CAGTCGCCGACCAATGATC        | GCTAGGTAGACGGAGGAGCG       | 73                 | 47492145                  |
|             | HSSIL_GAP/M5Aq | GCTCCTACCCTGCAAACAGAC      | GGAAACCAGGAGCACAAAGC       | 71                 | 47491699                  |
| NC ii       | HSSIL/M51Bq    | TGAATGCTTCCCTTGTGATG       | GTAATGTTTCCTTACTGGTTAGCAAC | 71                 | 47467138                  |
| NC iii      | HSSCL/M15Bq    | GTGCCCTTGAGAGCCTAGGG       | CCTCAACAGCCTGTCTTATAATTG   | 71                 | 47440083                  |
| SCL -9/-10  | HSTAL.175q     | GGCCAGAGTTCAAATCCTGAC      | CAAGCGTAAAGTGACATGCC       | 71                 | 47419831                  |
|             | HSSCL/M36Bq    | AGAGGAAGGACCTTCAGCTCC      | TCCTCAAGGCAGAGAGAGCC       | 71                 | 47418997                  |
| SCL +1      | HSSCL/M46Aq    | TTCCCCCTTTTCCTTACGC        | CGCACTCTCACAATCCCACC       | 102                | 47409535                  |
|             | HSSCL/M46Bq    | CCGTTGGTGTCTCAGCAGG        | CACCCAAACACAGTCGCAG        | 71                 | 47409309                  |
| SCL +2      | HSSCL/M47Aq    | AGGCCCGGAAAGGACAATG        | CAGGAGGTGATCCCGAATG        | 73                 | 47408628                  |
|             | HSSCL/M47Bq    | AGCCGTTTTCTAAGTTGCTGG      | CCAAGTCTCTGTGTCCGTGC       | 71                 | 47408265                  |
| SCL +3      | HSTAL.157q     | TTTGAACCCCTCCAATG          | CAACCGCGTAGACACCTCC        | 72                 | 47407338                  |
|             | HSSCL/M48Aq    | ACTGAACCAGACCGATCCCAG      | AACAACAACCCCTCCCGAC        | 71                 | 47407303                  |
| SCL +4/+5   | HSSCL/M48Bq    | ACCGCAGCGTAACTGCAGG        | CGAGGAAGAGGATGCACACC       | 73                 | 47406956                  |
|             | HSTAL.156q     | GAAGCCGAGGAAGAGGATGC       | CGTAACTGCAGGCCTCTCAG       | 71                 | 47406951                  |
|             | HSSCL/M49Bq    | GGAGAGGACATTTGTGGCCAG      | CGGTGGATTCTGAGAGGC         | 71                 | 47405741                  |
| SCL +8/+9   | HSSCL/M53Aq    | CAGTCAATGAACCTGGCGG        | CCTAGCTCTCTGCCCTCACC       | 73                 | 47402359                  |
|             | HSSCL/M53Bq    | CACCCTGCAGCTGAGCTAGG       | TGCAGGACTGTGAGTGTGGTC      | 71                 | 47401484                  |
| NC iv       | HSTAL.138q     | CATCACCTGCAAAATGGAGG       | TAAGCTGAGGCAGGCATTGTC      | 103                | 47398315                  |
| SCL +19     | HSSCL/M63Aq    | CACGTGCGATCTATCTCTTCG      | GGCAAATGCTGAAAGGAACC       | 71                 | 47391506                  |
|             | HSSCL/M64Aq    | TCTGCTGTAGCCATGGTCCTG      | GCAACAAAAGCAGTGCAAGG       | 71                 | 47391323                  |
| SCL +20/+22 | HSTAL.122q     | CCCAGTGGTCTGACTCCAAAG      | GCACAGAAGGCAGTGAATGG       | 74                 | 47390543                  |
|             | HSSCL/M65Aq    | GATACAGAGCCCTTCCACCC       | CAGAGCAGGATCTCCCGTG        | 74                 | 47390110                  |
|             | HSTAL.121q     | TTCGAACGGATCACATCCTG       | TTGGTCCGAGCTCTGCCTC        | 76                 | 47389763                  |

| Region Name | Amplicon Name | Primer 1 (5'→3')               | Primer 2 (5'→3')         | Amplicon Size (bp) | Chrom 1 Co-ordinate Start |
|-------------|---------------|--------------------------------|--------------------------|--------------------|---------------------------|
|             | HSSCL/M66Aq   | CCTCACCTCTAGGCAGCCAG           | GCTTTGGATCAGACACACGTG    | 71                 | 47389401                  |
|             | HSTAL.119q    | CTTTGCAGCATTCAAGGCC            | GCAGCTGGTAAGGCACCTG      | 71                 | 47388329                  |
|             | HSSCL/M67Aq   | CGAGGCTGCTTAGAGAGAGGC          | GGACCATAGCACCCGAGTC      | 101                | 47388075                  |
| NC v        | HSTAL.108q    | GGATTGAGGAGAGGGCATGTG          | GCACGGCTGTGGAGCTATG      | 101                | 47377642                  |
| NC vi       | HSTAL.106q    | CAGCAGAGGTCCCAAAGCC            | CAGTACTCCCAGCTTGCTTCC    | 101                | 47374561                  |
| SCL +43/+45 | HSSCL/M87Aq   | CTTTCCCTAGAATCCAGCCCC          | GGAGAGTCCCAGCCTCACC      | 71                 | 47367938                  |
|             | HSTAL.98q     | GCATTGAGGTCATCTTCCAG           | GGACTCTCCCACATCTGCTTG    | 71                 | 47367876                  |
|             | HSSCL/M88Aq   | GCCTGTCACCTGTTTTCAACG          | CAAATCCTGTTCTCCCTGAG     | 73                 | 47367324                  |
|             | HSSCL/M88Bq   | TGTCTCCCAGGTCTTGGAAGC          | TCTTGCCGTGCTCTGTGAC      | 71                 | 47366737                  |
|             | HSTAL.95q     | TGGCTCACTCCTGCTCAAATG          | GAGAAGAGGTCAGGCCTCCAC    | 78                 | 47366287                  |
|             | HSSCL/M90Aq   | GGTCCCCAAGACCCAGAGTAG          | CAGAGAGAGGAGTGGACCAGG    | 76                 | 47365683                  |
|             | HSTAL.93q     | GCCCATCTGACCCACTTATGC          | TGTTGTTCTCCAGCTCCC       | 71                 | 47365279                  |
| SCL +51     | HSTAL.84q     | TTAAGCCGAAGCCCAGAGAG           | GCTCCAGGCCTATCCTTGC      | 71                 | 47359910                  |
|             | HSSCL/M96Aq   | CACATTTCTCCAGCTCTGC            | GGCTGGTGGAGTGACCTGAC     | 76                 | 47359505                  |
|             | HSSCL/96Bq    | TGACCTTACAGCCCTTCACCC          | AGCTCCCTGCTCCCAGCAC      | 72                 | 47359190                  |
| SCL +52/+53 | HSTAL.82q     | TGGAGGAGGAGAAAGGCAAAC          | CCATCCATCTCTGTCTCCCTG    | 96                 | 47358590                  |
|             | HSSCL/M97Aq   | GCTCTCAGCCCAGAATGTCC           | CAAGGTGCAAGCCCTGTTC      | 71                 | 47358287                  |
|             | HSSCL/M98Aq   | TCCATGATCAGCGTAGATGCC          | GGAGGAAGTGCTGAACCCAG     | 71                 | 47357425                  |
| NC vii      | HSTAL.77q     | TTCTGTACCTGCCAGCCAAG           | CCCGACGAGCGTTATGTAAG     | 71                 | 47355954                  |
| NC viii     | HSSIL/M55Aq   | TCATGATGATATTTAGCATACTCAGCAAAG | GGAGAATGATAACTTGTGTCAGGC | 91                 | 47342423                  |
| NC ix       | HSSCL/M137Aq  | TCTCTGGAAGTCATAAATACAACA       | AATCTGCTCATCAAGTAATACG   | 71                 | 47318153                  |
| NC x        | HSSCL/M182Aq  | TTTGCAGTGCCCTGTTCTTAG          | TGTTGGCTACCTTGATCATGTG   | 71                 | 47273688                  |
| NC xi       | HSTAL.7q      | TCATGCCATTTCCGTTGTAC           | TTGAACACTTGGAGATGATGATG  | 71                 | 47273478                  |

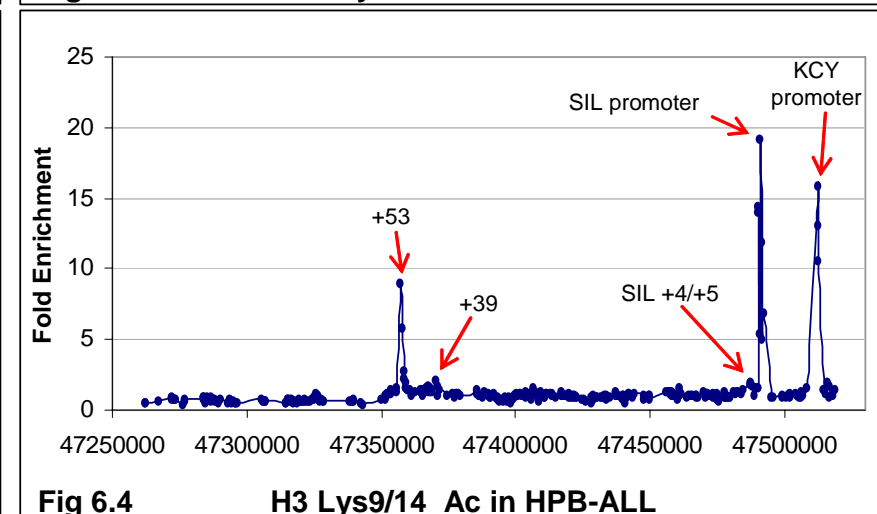
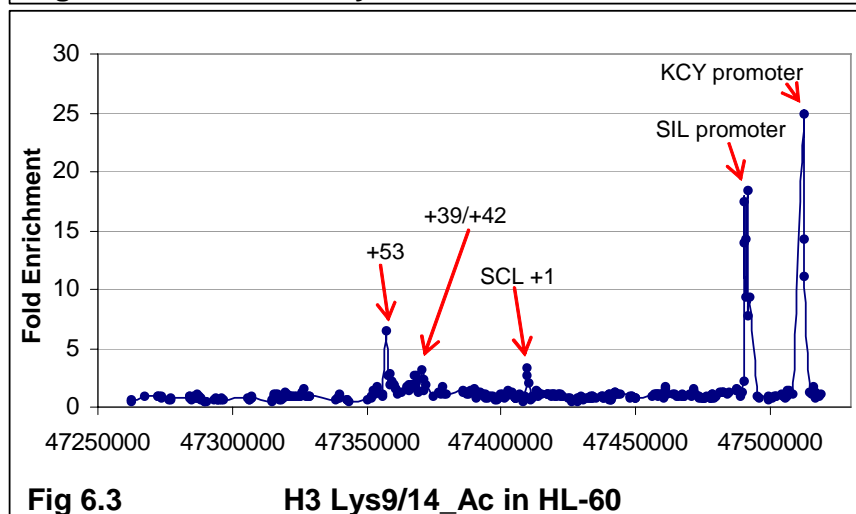
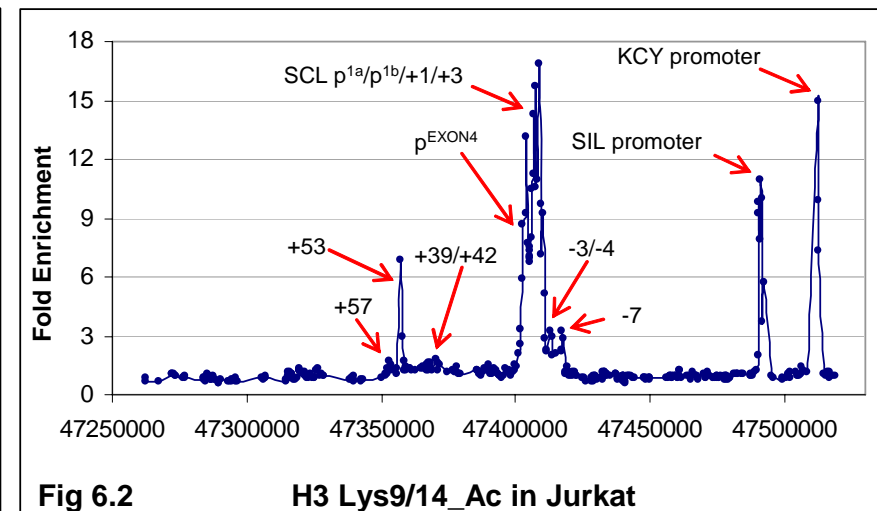
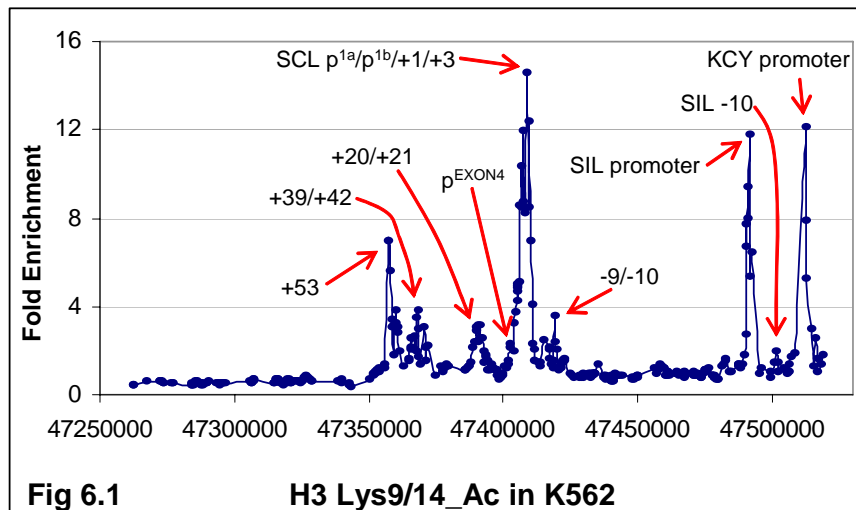
## Appendix 5

### Sequences of Primer Pairs used to in the Real-Time PCR Verification of ChIP-chip data for GATA-1

| Amplicon Name | Alternative Name | Primer 1 (5'→3')           | Primer 2 (5'→3')         | Amplicon Size (bp) | Chrom 1 Co-ordinate Start | Chrom 1 Co-ordinate Finish |
|---------------|------------------|----------------------------|--------------------------|--------------------|---------------------------|----------------------------|
| SIL -13       | HSSIL/M5Aq       | CAGGGTATATCTATGTTCCCTAGCAC | GATTGATGAATGGTGACAAAGC   | 71                 | 47504296                  | 47504366                   |
| NC i          | HSSCL/M15Bq      | GTGCCCTTGAGAGCCTAGGG       | CCTCAACAGCCTGTCTTATAATTG | 71                 | 47440083                  | 47440153                   |
| SCL -9/-10a   | HSTAL.175q       | GGCCAGAGTTCAAATCCTGAC      | CAAGCGTAAAGTGACATGCCC    | 71                 | 47419831                  | 47419901                   |
| SCL -9/-10b   | HSSCL/M36Aq      | GGCCTGTGCTGTGACTCTCC       | CCACAGATGGTCTCTGTGCTG    | 71                 | 47419540                  | 47419610                   |
| SCL -7        | HSSCL/M38Bq      | TTTGTGCCCTGTGTGCCTG        | TGATTAGCATACCCTGGAGCC    | 73                 | 47416835                  | 47416907                   |
| SCL Prom 1a   | HSSCL/M45Aq      | GGATAGGGGAGACTGCCCATTTG    | CACCTCCCAGGGCTTCTTTC     | 76                 | 47410385                  | 47410460                   |
| SCL +3        | HSTAL.156q       | GAAGCCGAGGAAGAGGATGC       | CGTAACTGCAGGCCTCTCAG     | 71                 | 47406951                  | 47407021                   |
| SCL +7/+8     | HSSCL/M53Aq      | CAGTCAATGAACCTGGCGG        | CCTAGCTCTCTGCCCTCACC     | 73                 | 47402359                  | 47402431                   |
| NC ii         | HSTAL.108q       | GGATTGAGGAGAGGGCATGTG      | GCACGGCTGTGGAGCTATG      | 101                | 47377642                  | 47377742                   |
| SCL +51       | HSSCL/M96Bq      | TGACCTTACAGCCCTTCACCC      | AGCTCCCTGCTCCCAGCAC      | 72                 | 47359190                  | 47359261                   |
| NC iii        | HSSCL/M182Aq     | TTTGCAGTGCCCTGTTCTTAG      | TGTTGGCTACCTTGATCATGTG   | 71                 | 47273688                  | 47273758                   |

## Appendices 6 to 11

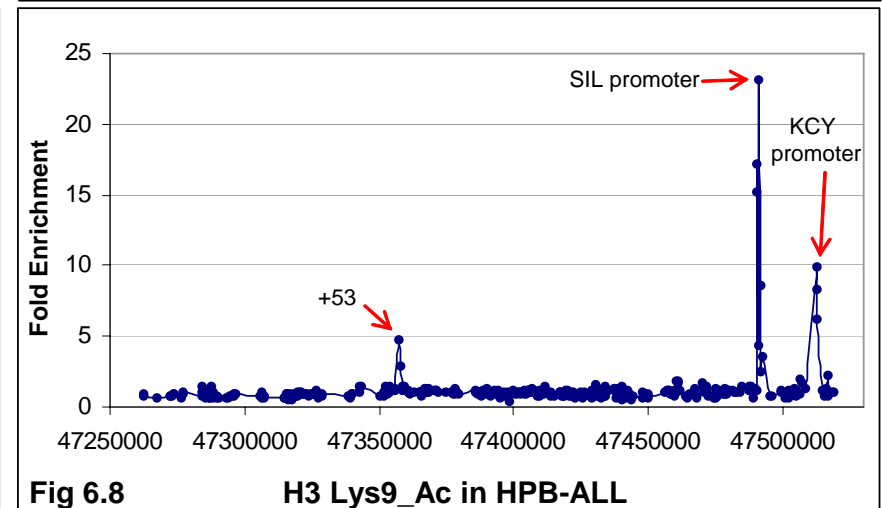
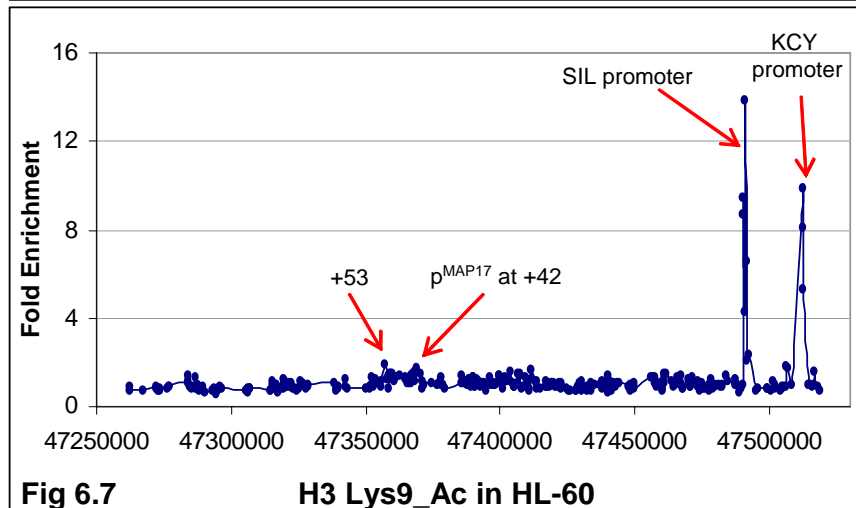
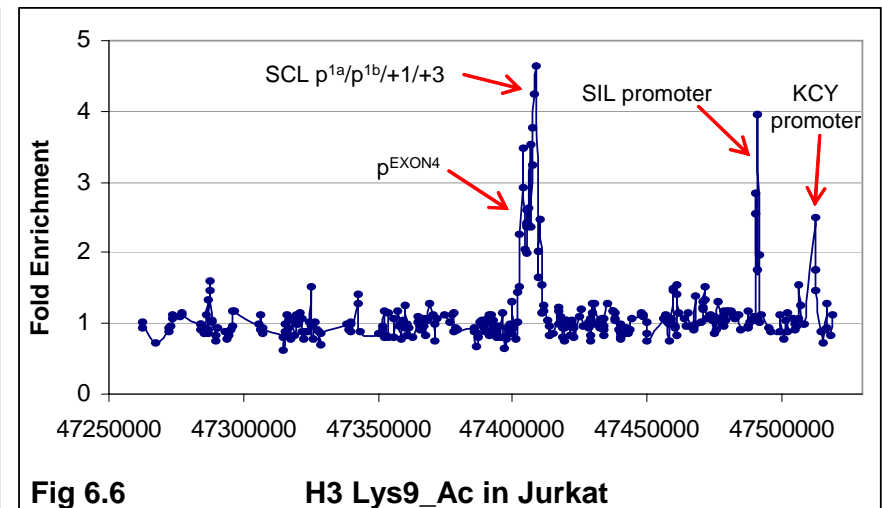
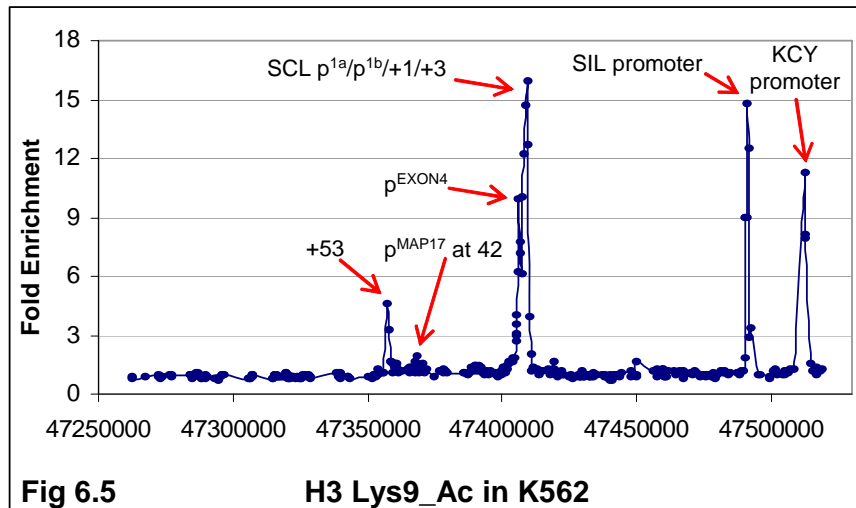
|             |  |     |
|-------------|--|-----|
| Appendix 6  | ChIP-chip profiles of histone H3 acetylation at specific lysine residues in K562, Jurkat, HL60 and HPB-ALL ..... | 315 |
|             | <b>Figures 6.1 to 6.22</b>   |     |
| Appendix 7  | ChIP-chip profiles of histone H4 acetylation at specific lysine residues in K562, Jurkat, HL60 and HPB-ALL ..... | 321 |
|             | <b>Figures 7.1 to 7.20</b>   |     |
| Appendix 8  | ChIP-chip profiles of histone H4 K5/8/12/16 tetraacetylation in K562, Jurkat, HL60 and HPB-ALL .....             | 326 |
|             | <b>Figures 8.1 to 8.4</b>  |     |
| Appendix 9  | ChIP-chip profiles of histone H3 methylation at specific residues in K562, Jurkat, HL60 and HPB-ALL .....        | 327 |
|             | <b>Figures 9.1 to 9.23</b>   |     |
| Appendix 10 | ChIP-chip profiles of histone H3 phosphorylation at serine 10 residue in K562, Jurkat, HL60 and HPB-ALL .....    | 332 |
|             | <b>Figures 10.1 to 10.4</b>  |     |
| Appendix 11 | ChIP-chip profiles of histone H3 modifications at specific residues in 416B and mouse E14 ES cell lines .....    | 333 |
|             | <b>Figures 11.1 to 11.8</b>  |     |



 CYP4Z1
  CYP4A22
  MAP17
  SCL
  SIL
  KCY

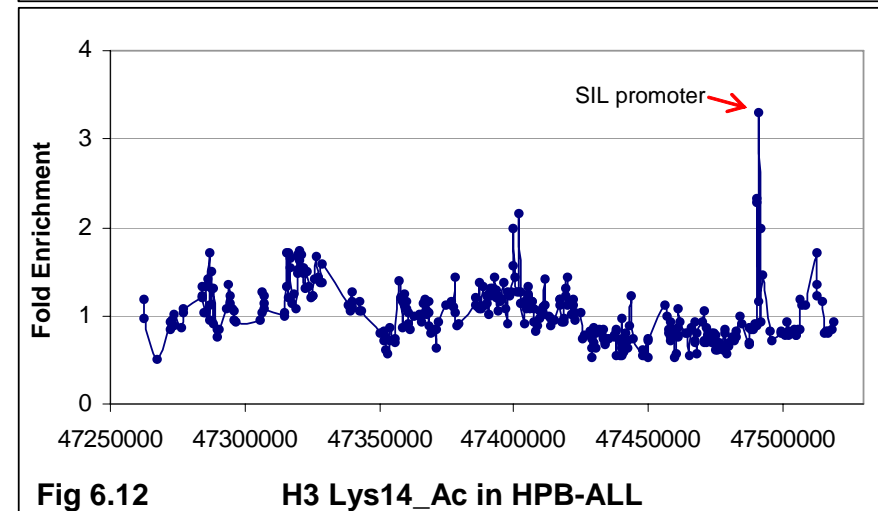
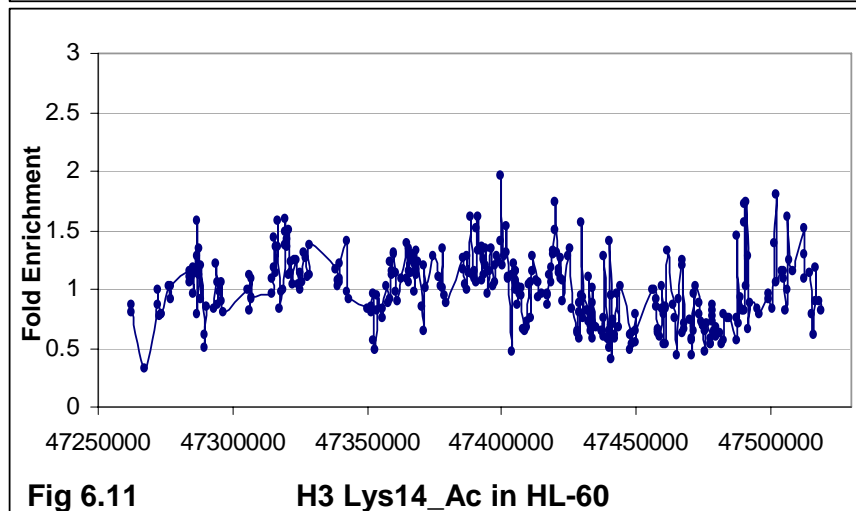
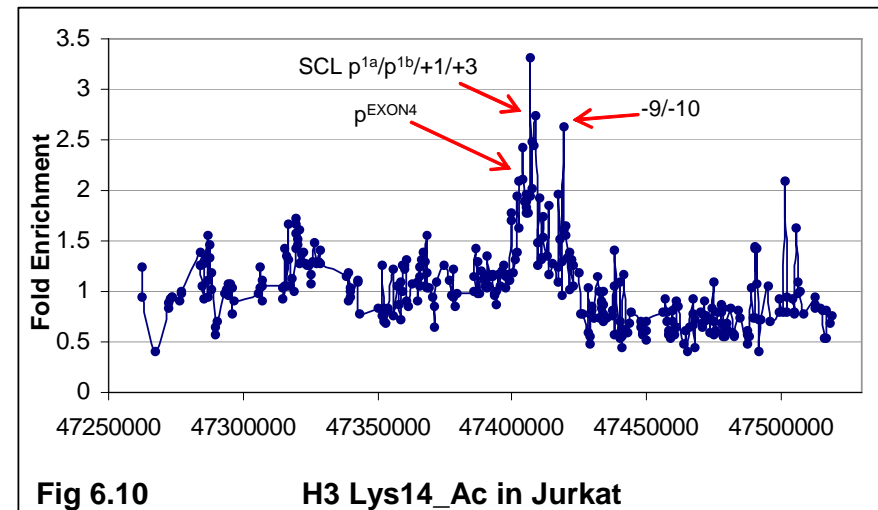
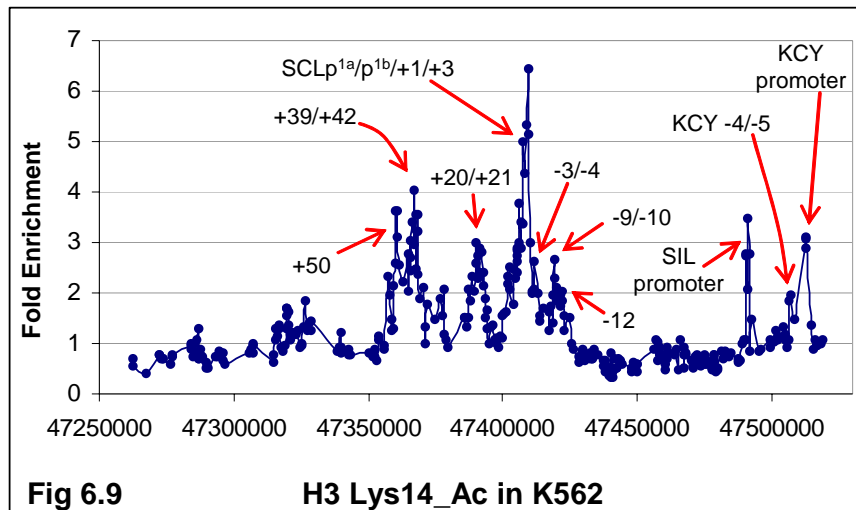
 CYP4Z1
  CYP4A22
  MAP17
  SCL
  SIL
  KCY





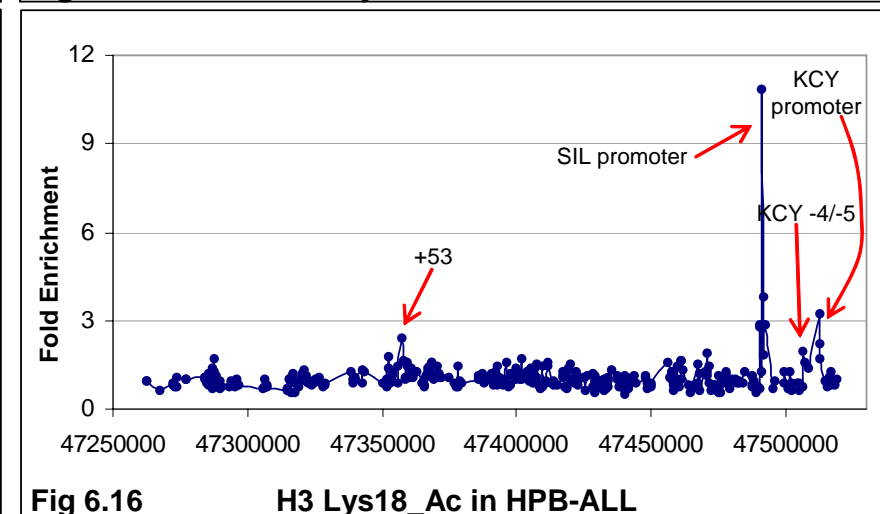
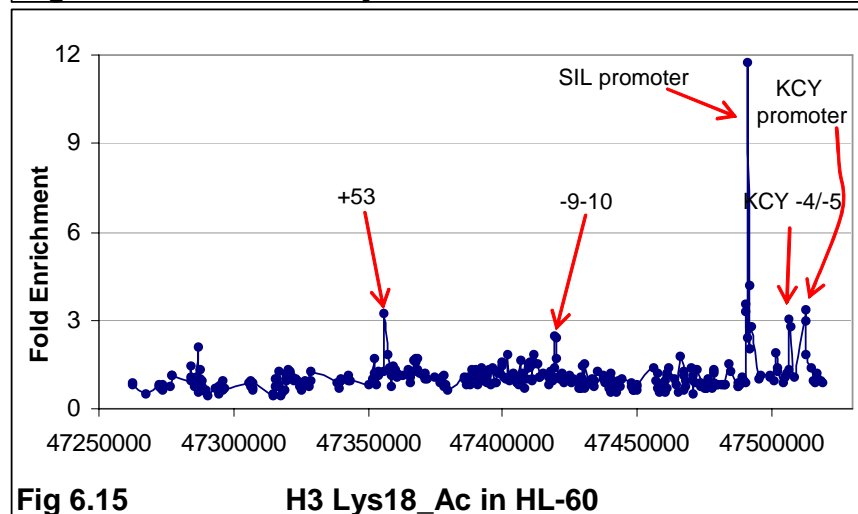
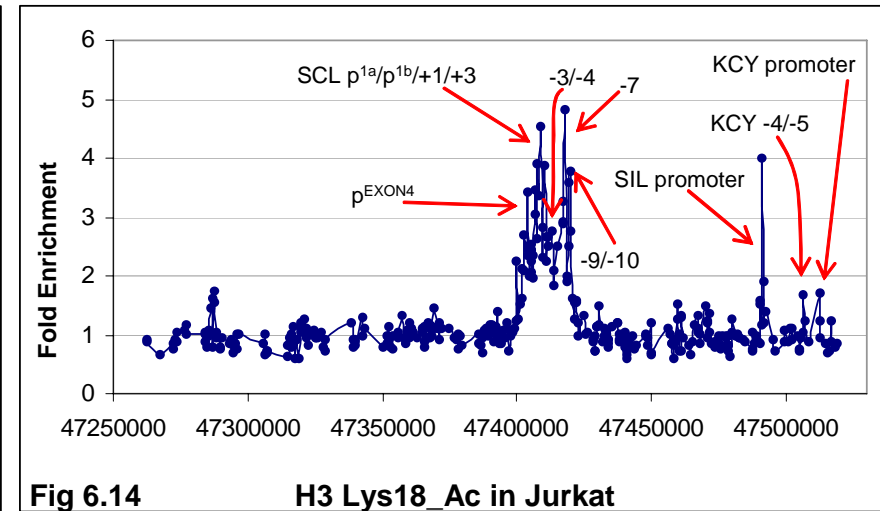
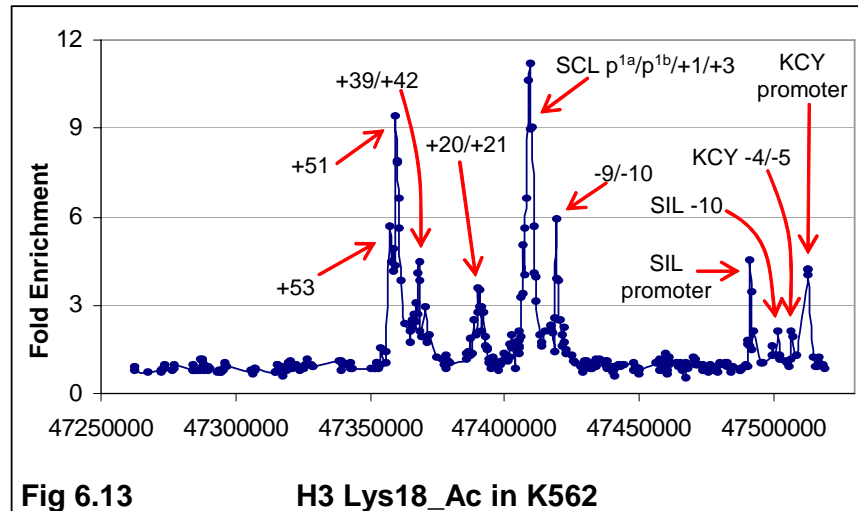
 CYP4Z1  
  CYP4A22  
  MAP17  
  SCL  
  SIL  
  KCY

 CYP4Z1  
  CYP4A22  
  MAP17  
  SCL  
  SIL  
  KCY



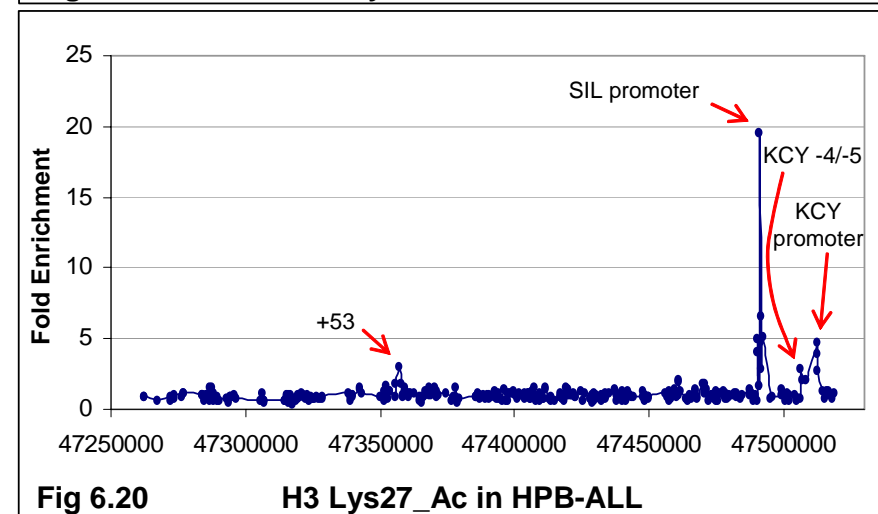
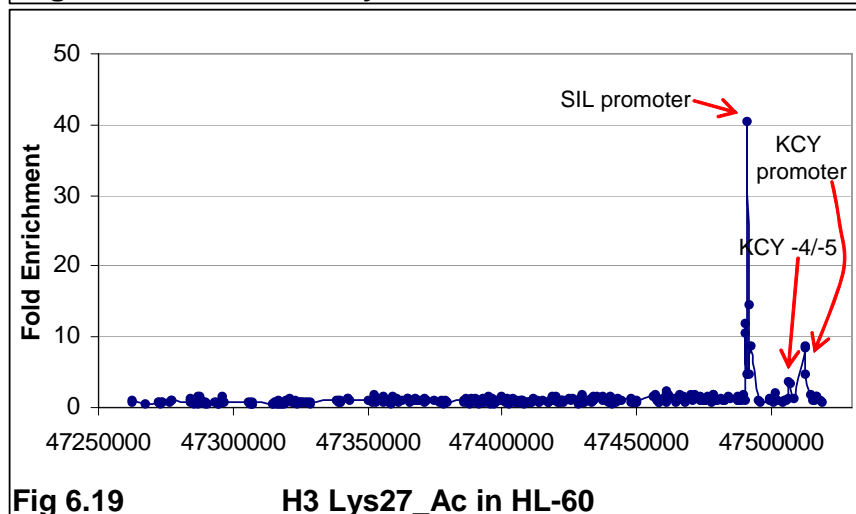
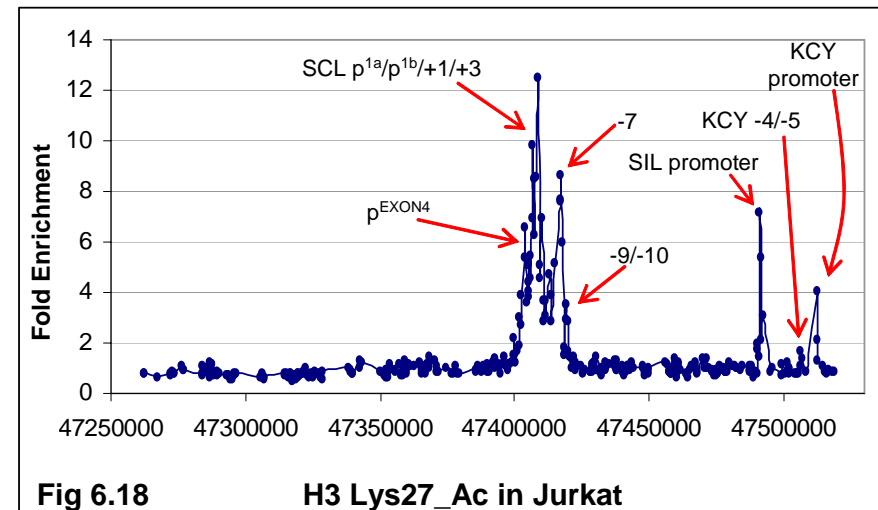
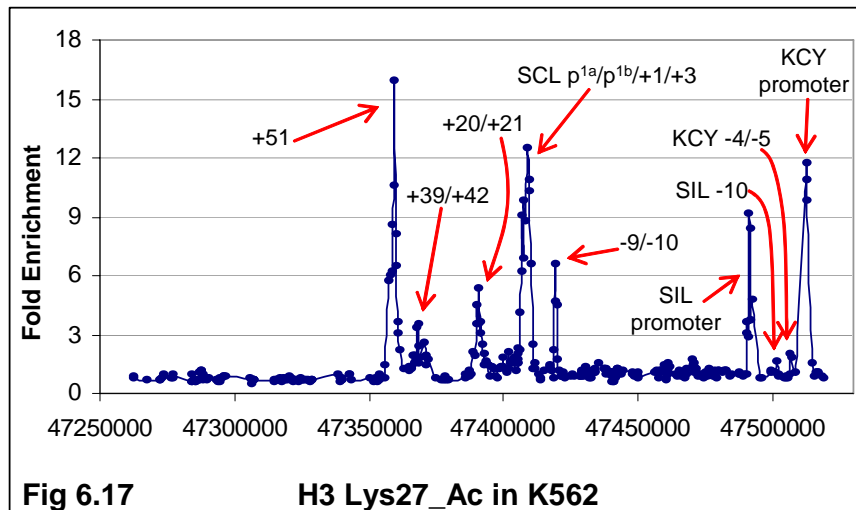
CYP4Z1  
 CYP4A22  
 MAP17  
 SCL  
 SIL  
 KCY

CYP4Z1  
 CYP4A22  
 MAP17  
 SCL  
 SIL  
 KCY



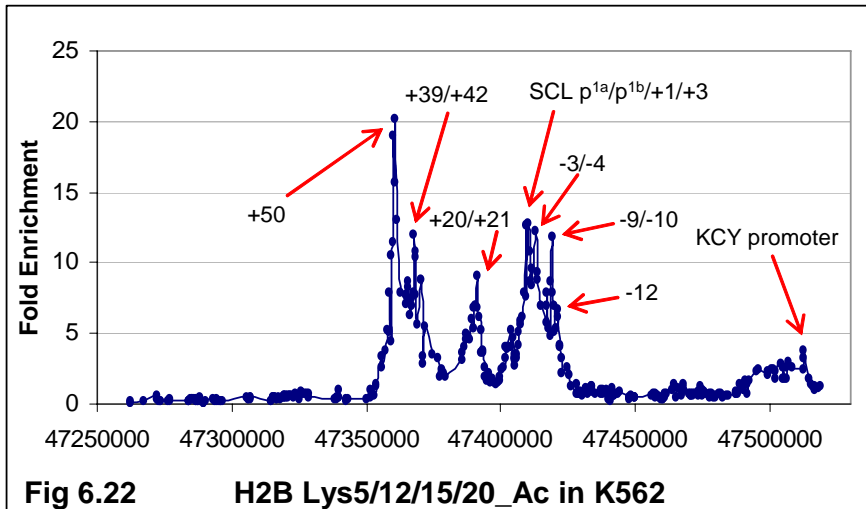
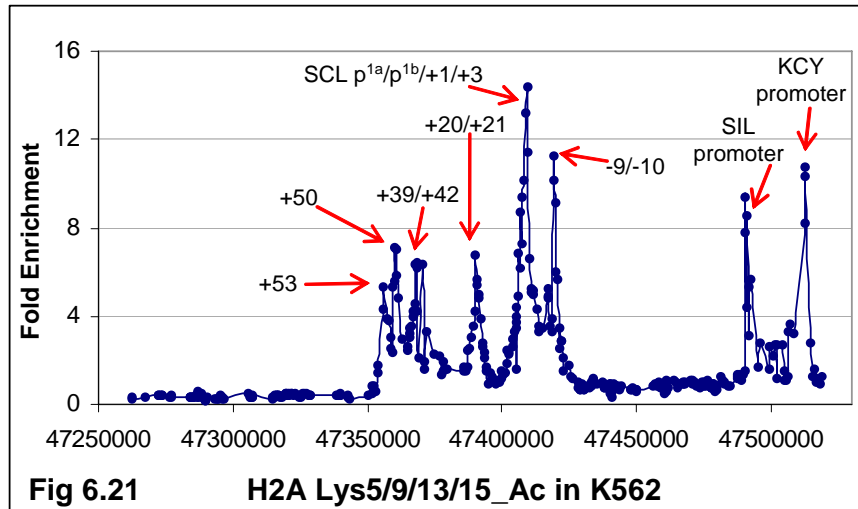
 CYP4Z1  
  CYP4A22  
  MAP17  
  SCL  
  SIL  
  KCY

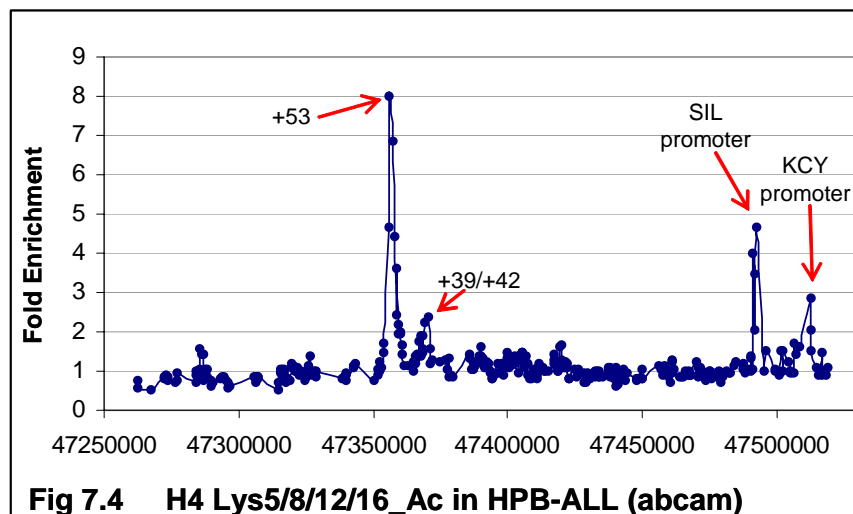
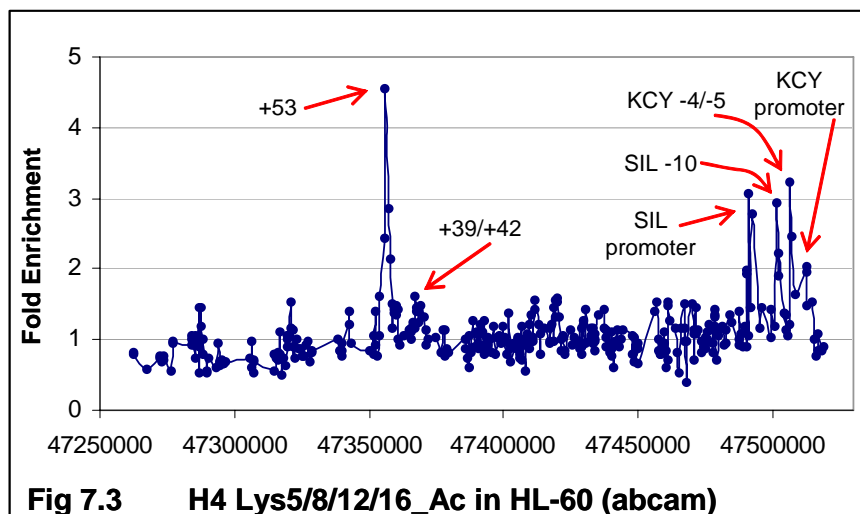
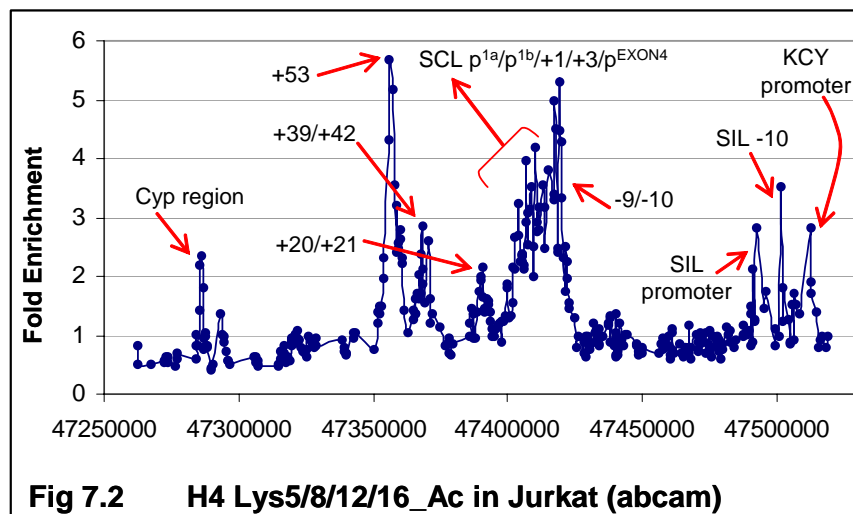
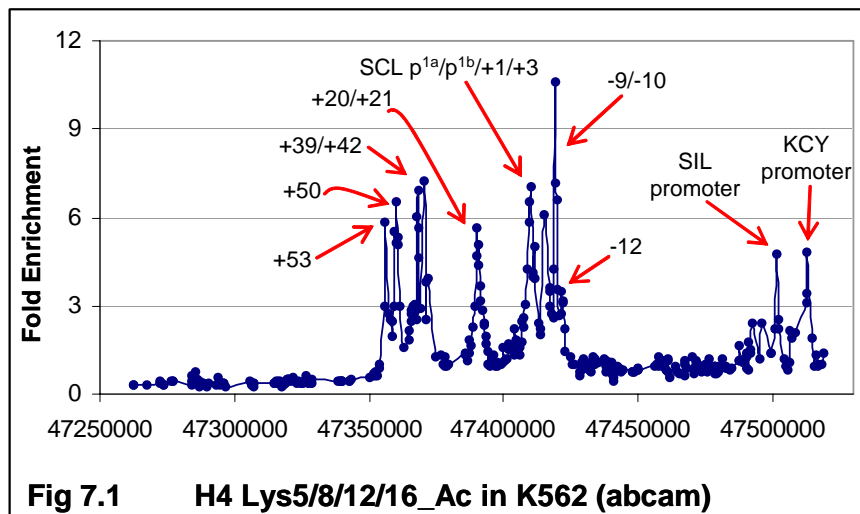
 CYP4Z1  
  CYP4A22  
  MAP17  
  SCL  
  SIL  
  KCY



 CYP4Z1
  CYP4A22
  MAP17
  SCL
  SIL
  KCY

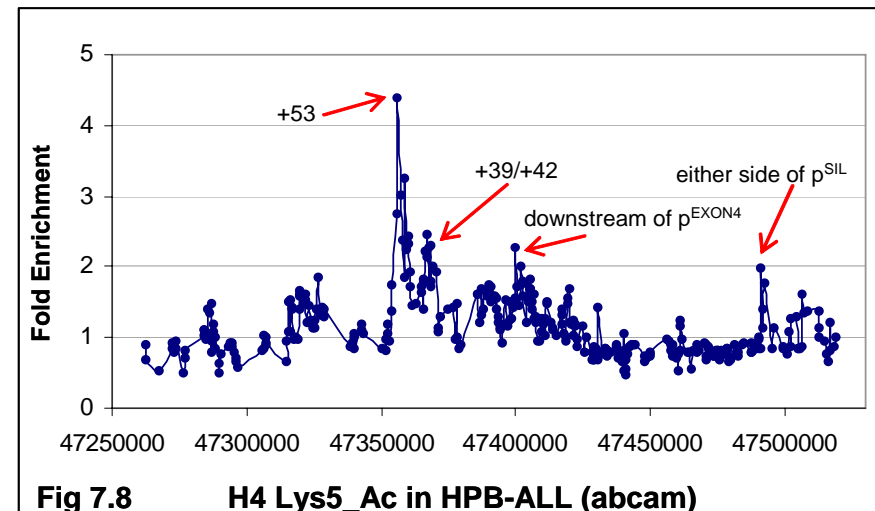
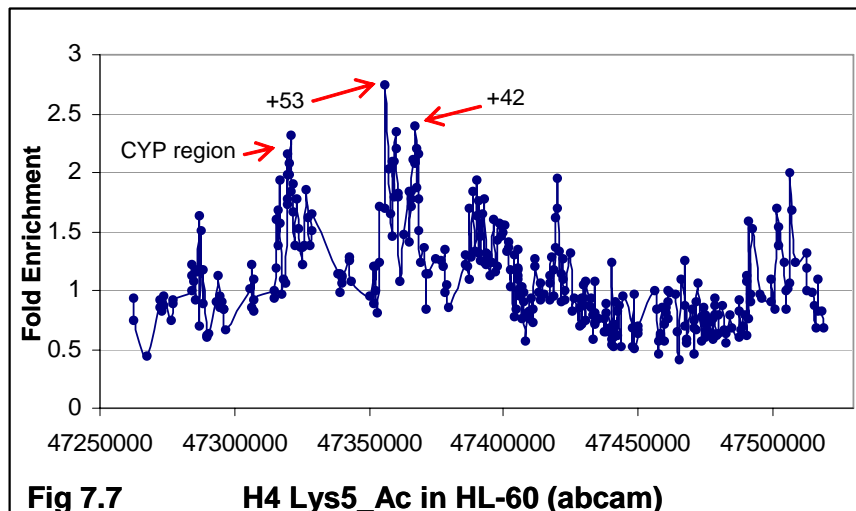
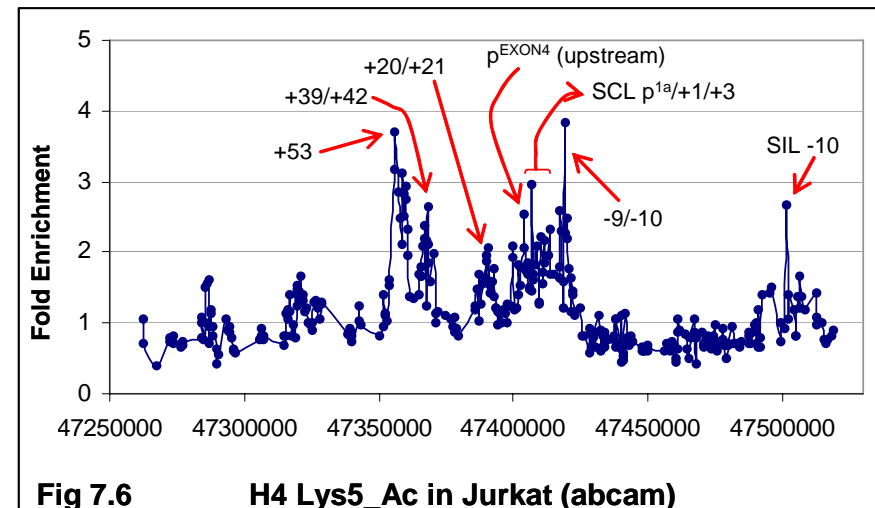
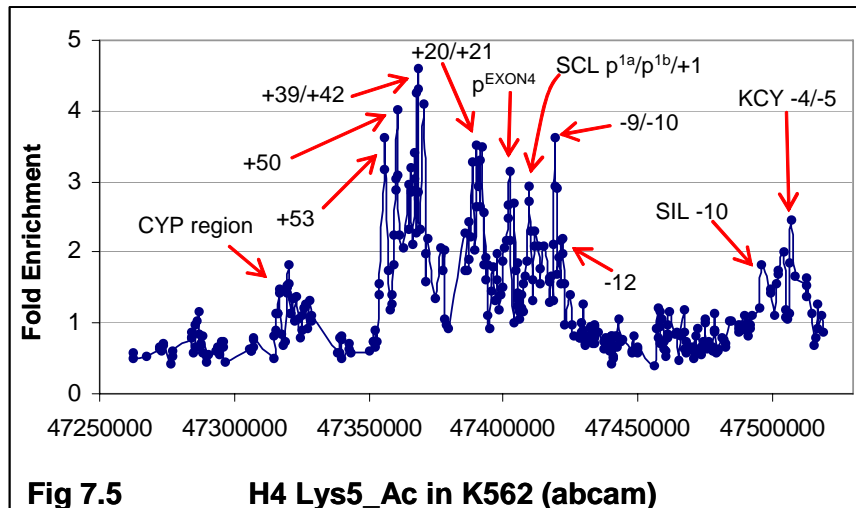
 CYP4Z1
  CYP4A22
  MAP17
  SCL
  SIL
  KCY





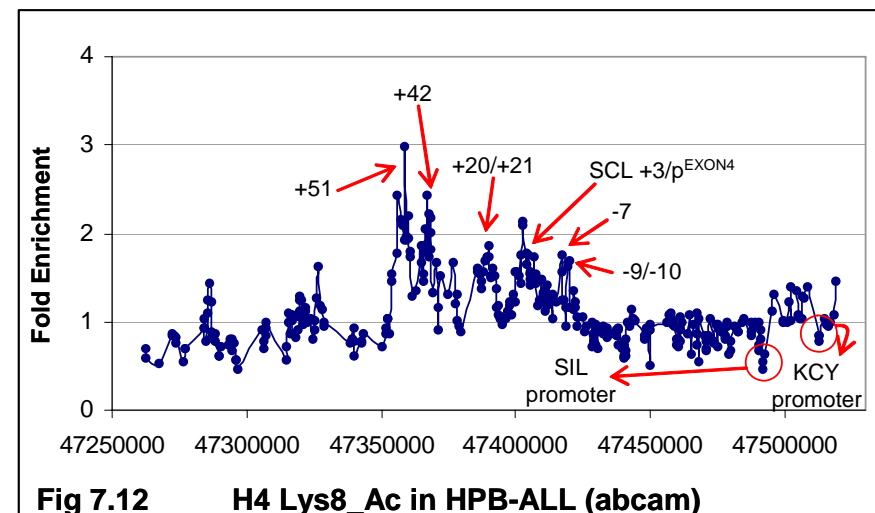
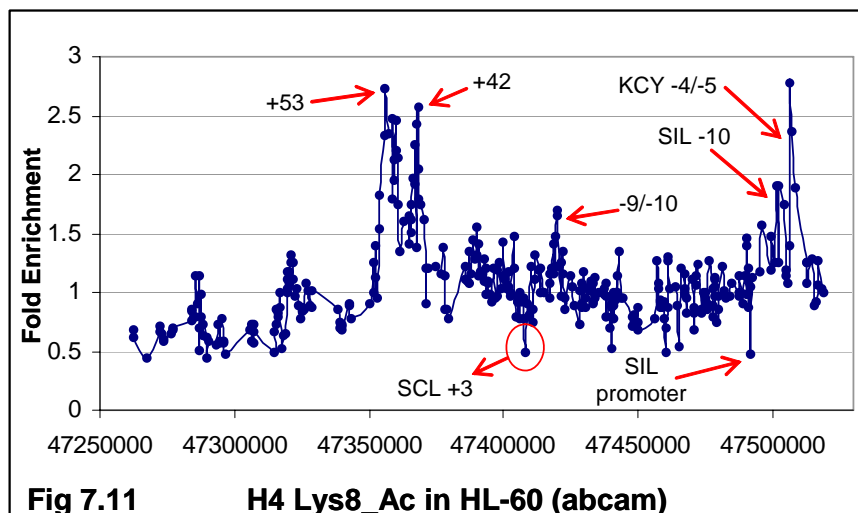
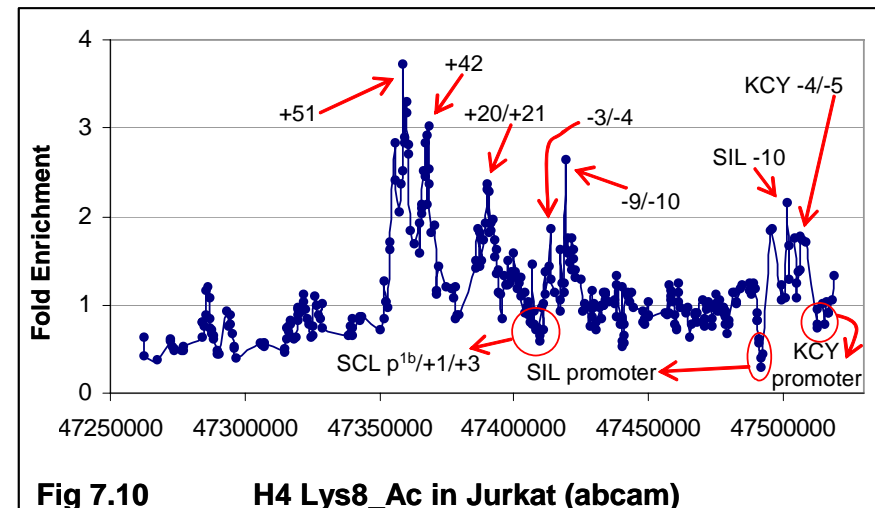
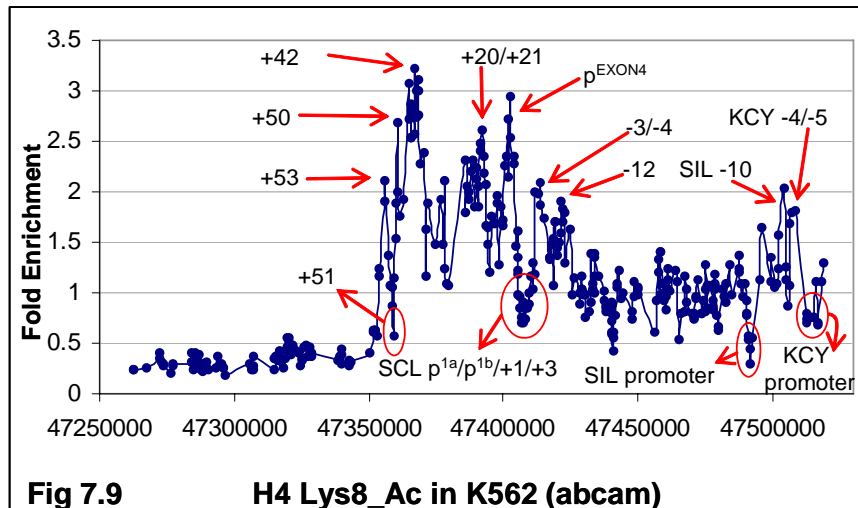
 CYP4Z1
  CYP4A22
  MAP17
  SCL
  SIL
  KCY

 CYP4Z1
  CYP4A22
  MAP17
  SCL
  SIL
  KCY



CYP4Z1  
 CYP4A22  
 MAP17  
 SCL  
 SIL  
 KCY

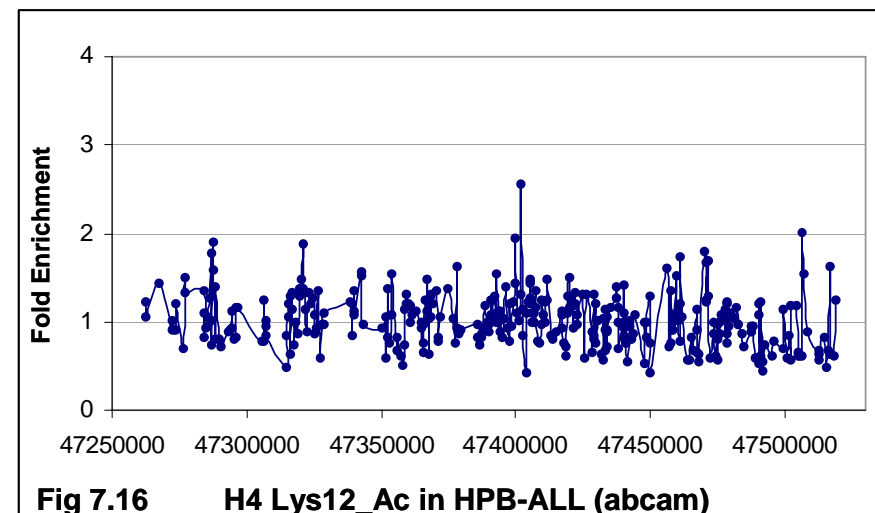
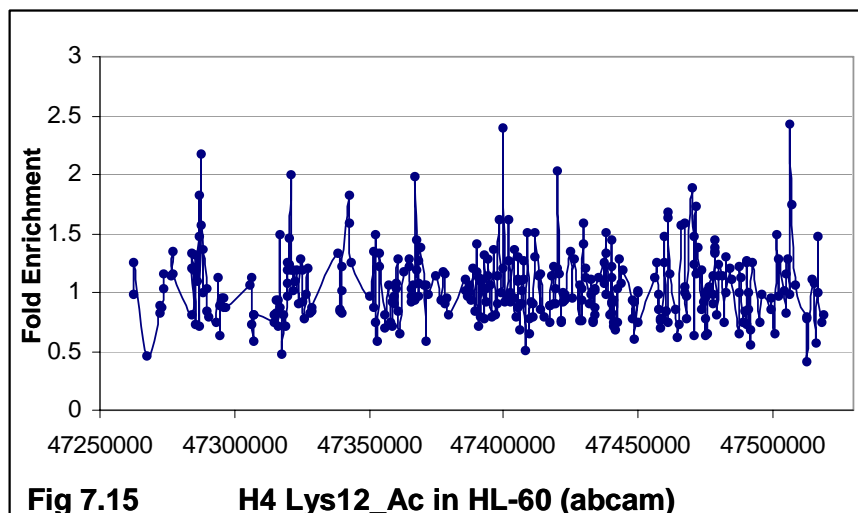
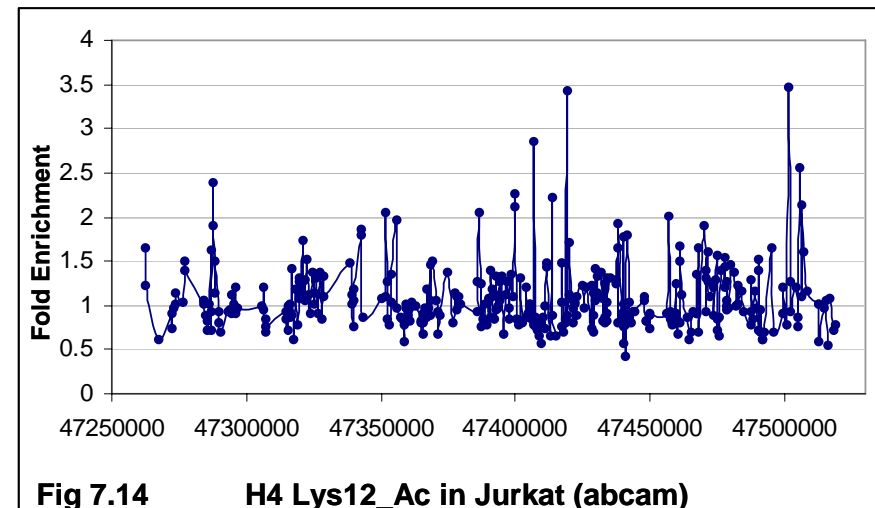
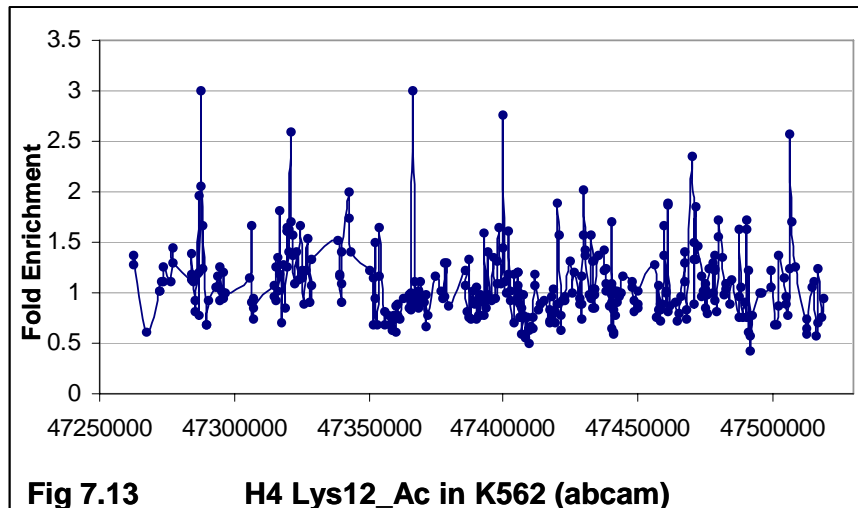
CYP4Z1  
 CYP4A22  
 MAP17  
 SCL  
 SIL  
 KCY



 CYP4Z1  
  CYP4A22  
  MAP17  
  SCL  
  SIL  
  KCY

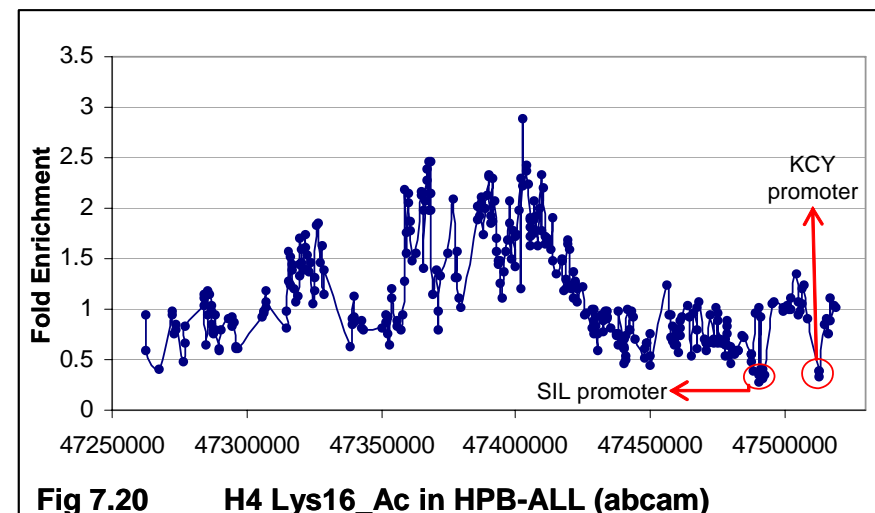
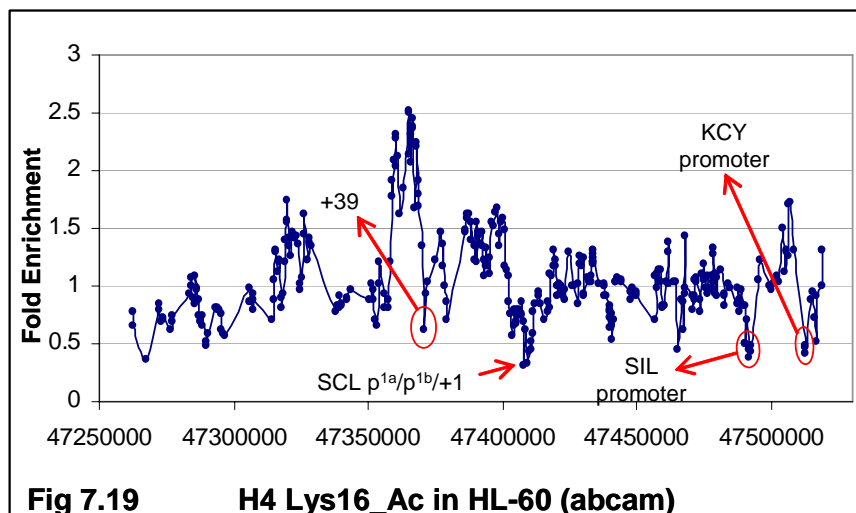
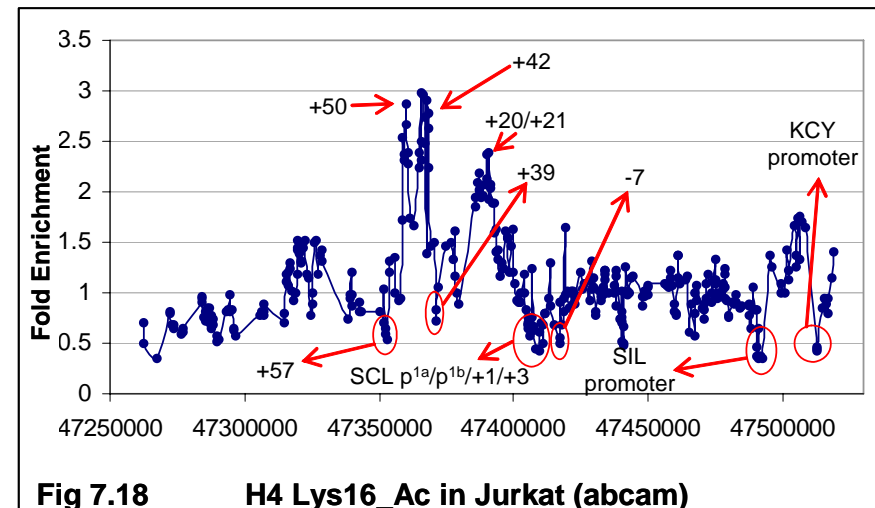
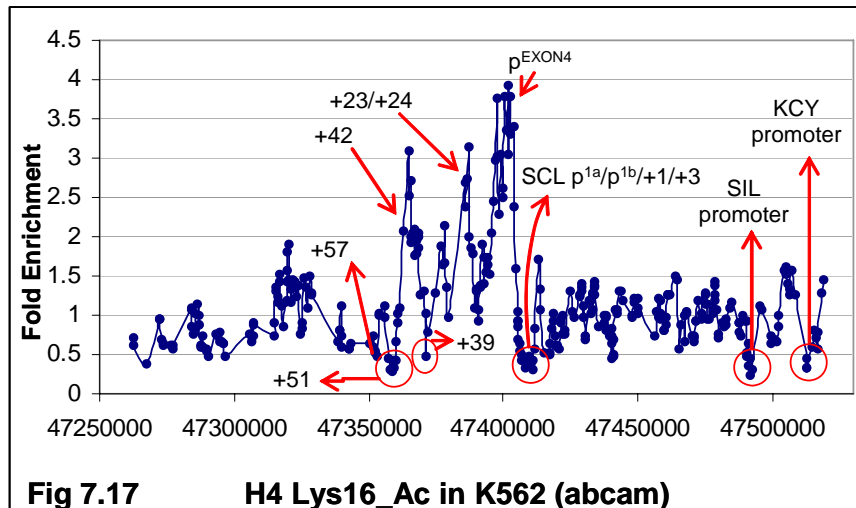
 CYP4Z1  
  CYP4A22  
  MAP17  
  SCL  
  SIL  
  KCY





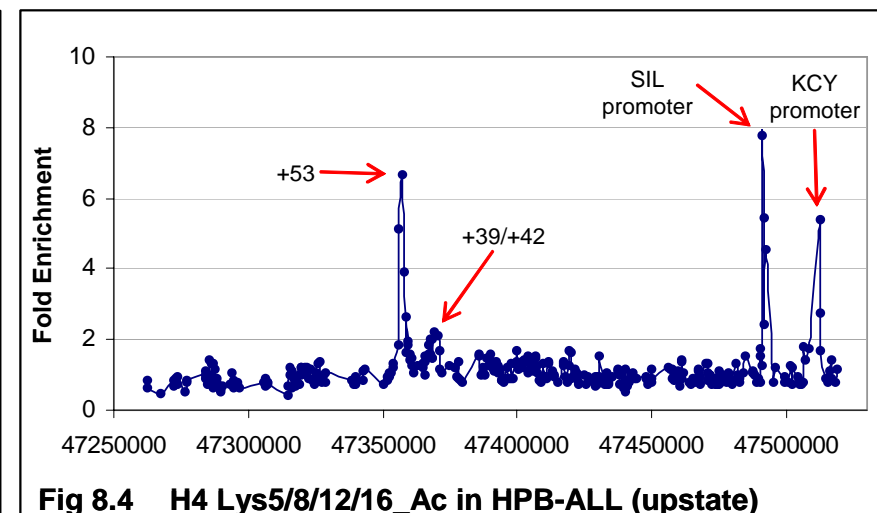
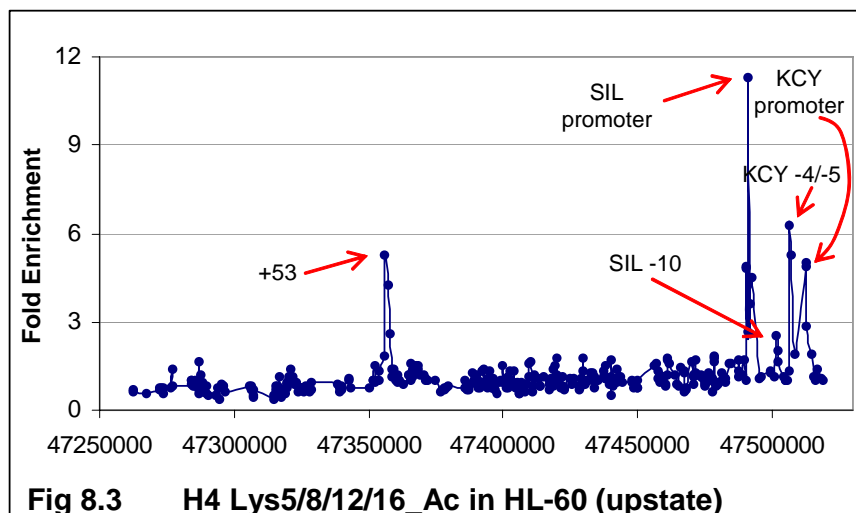
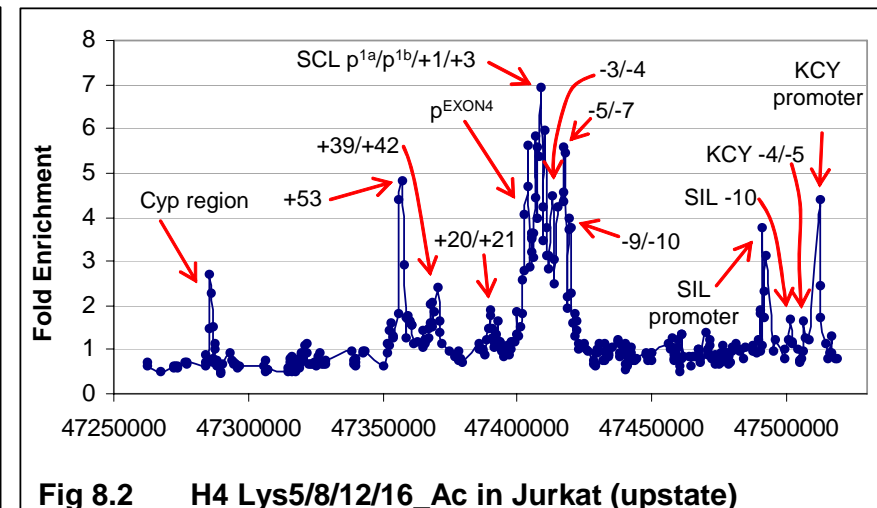
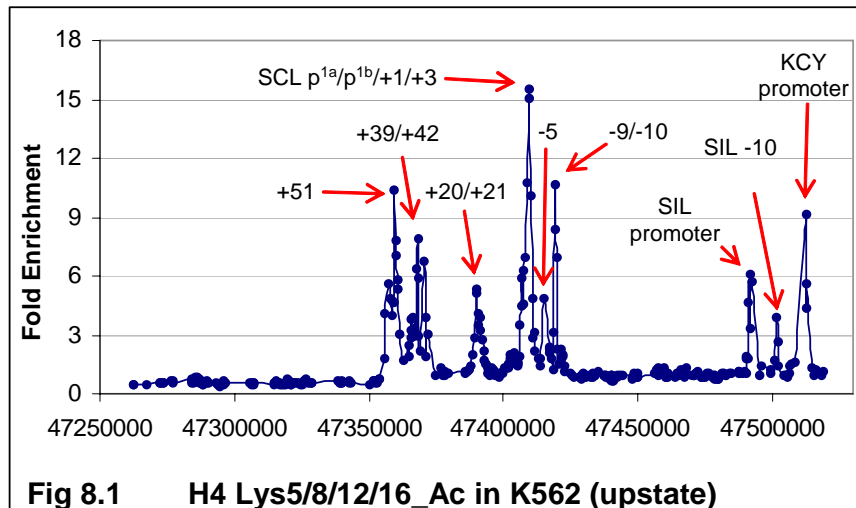
➡ CYP4Z1   
 ➡ CYP4A22   
 ➡ MAP17   
 ➡ SCL   
 ➡ SIL   
 ➡ KCY

➡ CYP4Z1   
 ➡ CYP4A22   
 ➡ MAP17   
 ➡ SCL   
 ➡ SIL   
 ➡ KCY



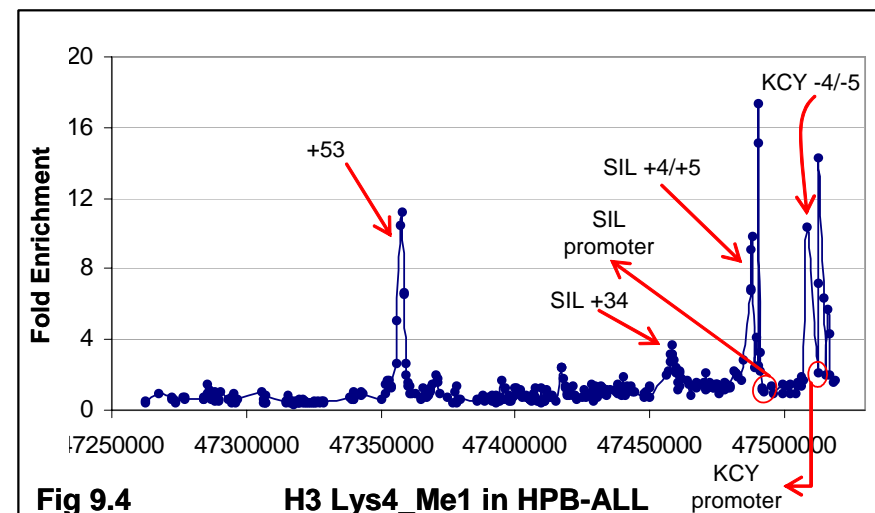
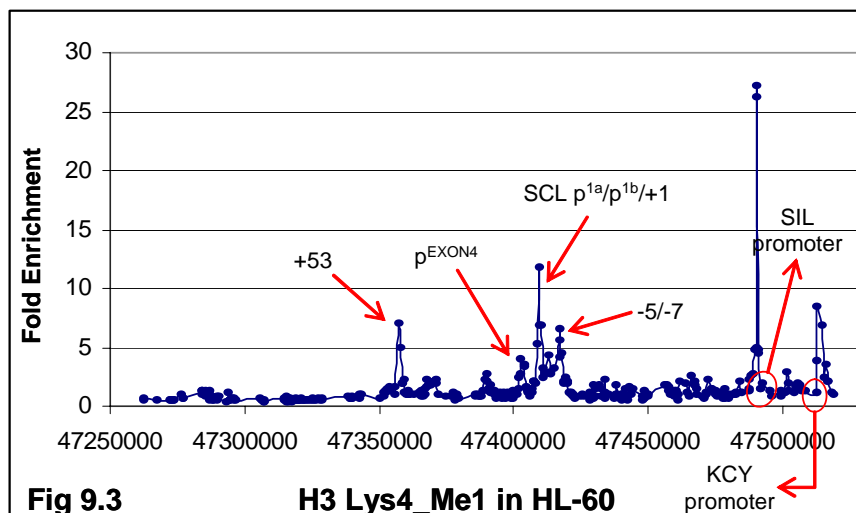
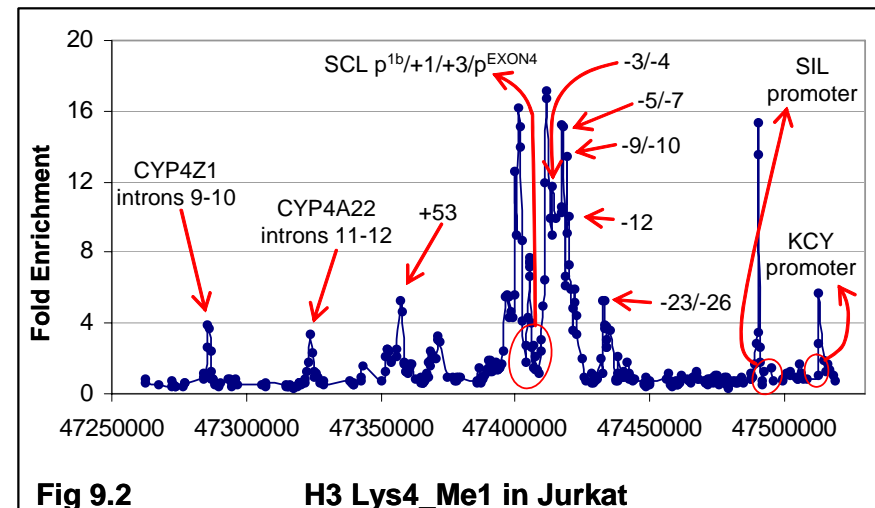
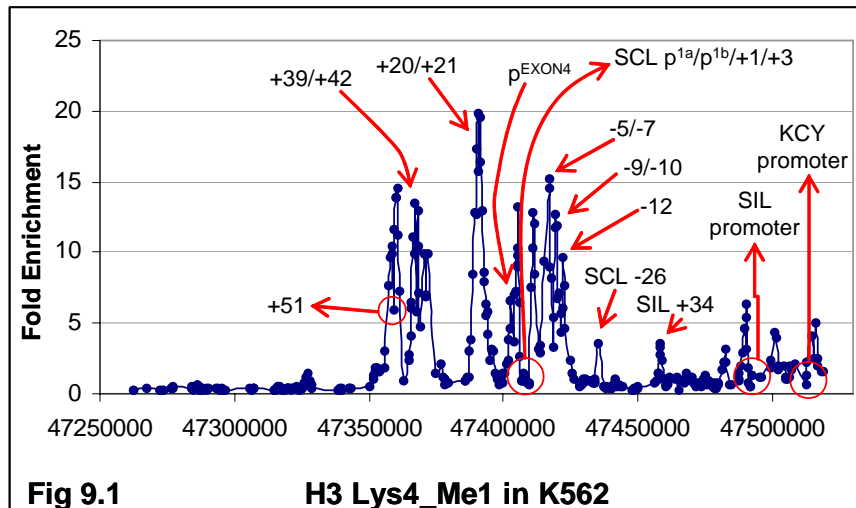
➡ CYP4Z1   
 ➡ CYP4A22   
 ➡ MAP17   
 ➡ SCL   
 ➡ SIL   
 ➡ KCY

➡ CYP4Z1   
 ➡ CYP4A22   
 ➡ MAP17   
 ➡ SCL   
 ➡ SIL   
 ➡ KCY



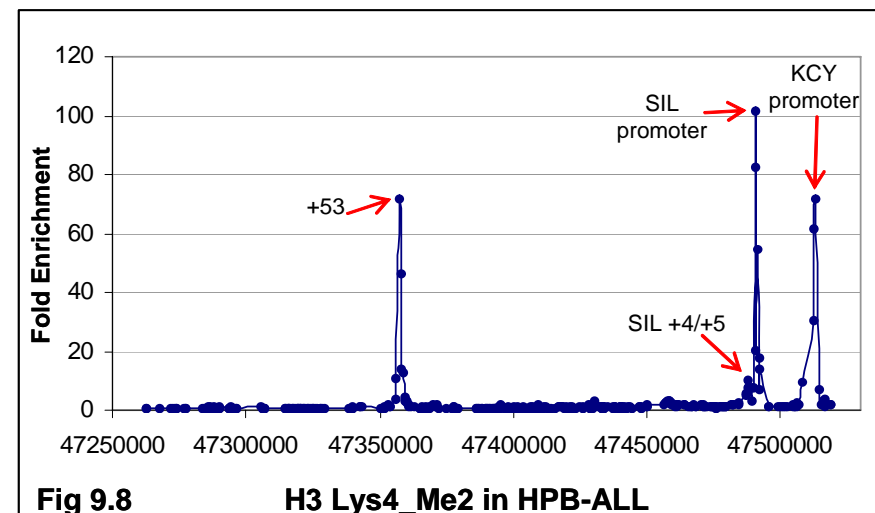
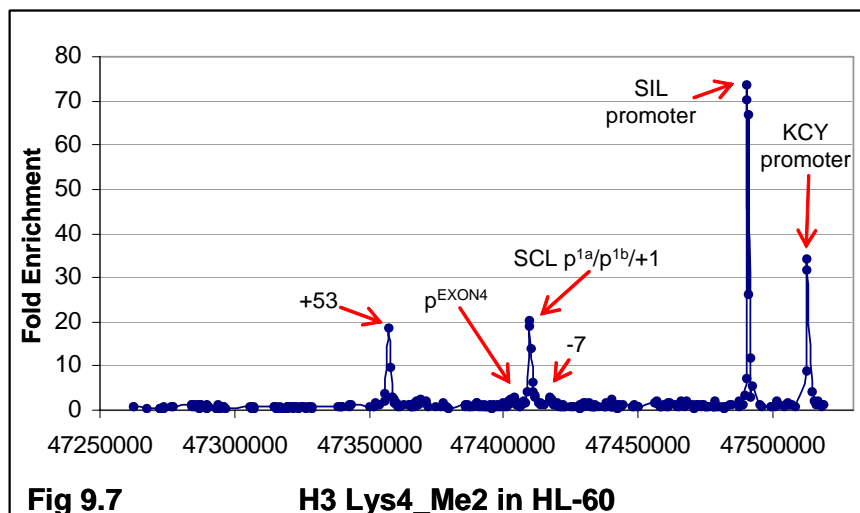
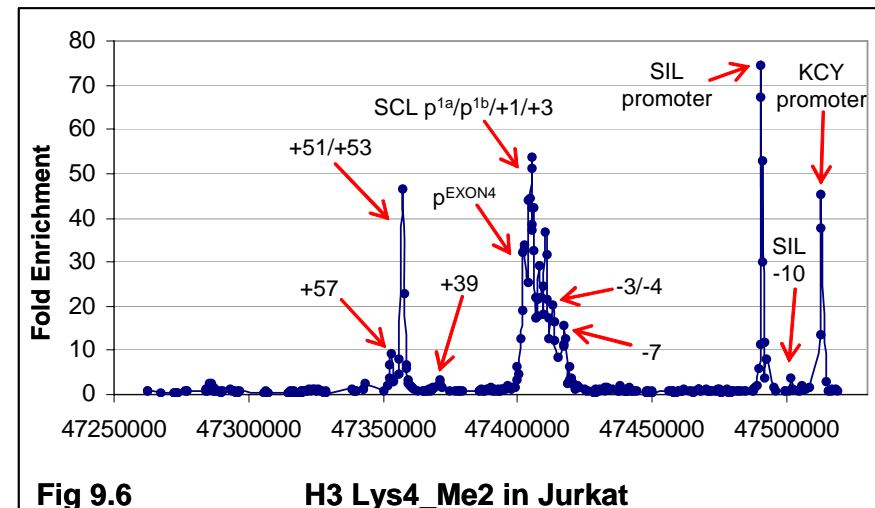
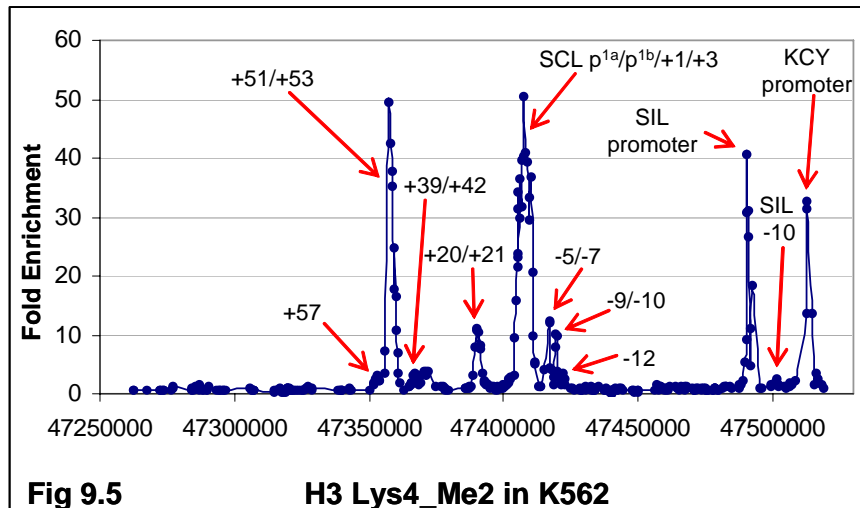
 CYP4Z1
  CYP4A22
  MAP17
  SCL
  SIL
  KCY

 CYP4Z1
  CYP4A22
  MAP17
  SCL
  SIL
  KCY



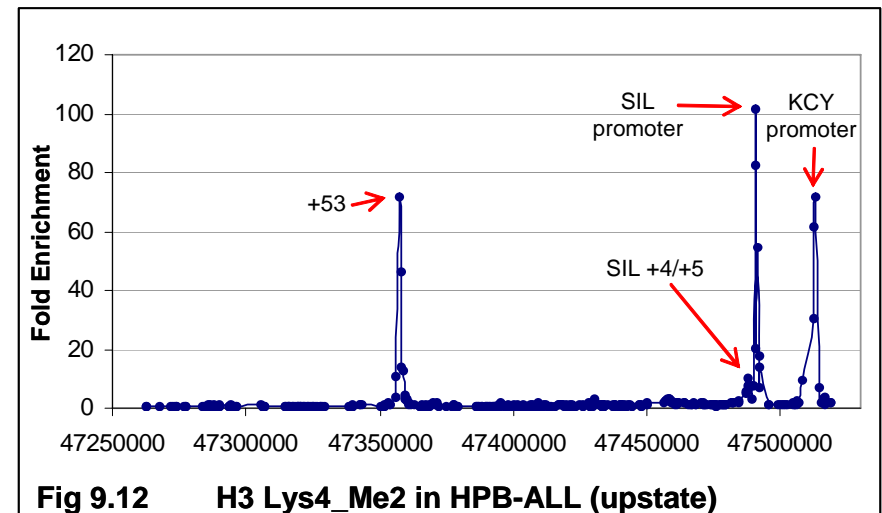
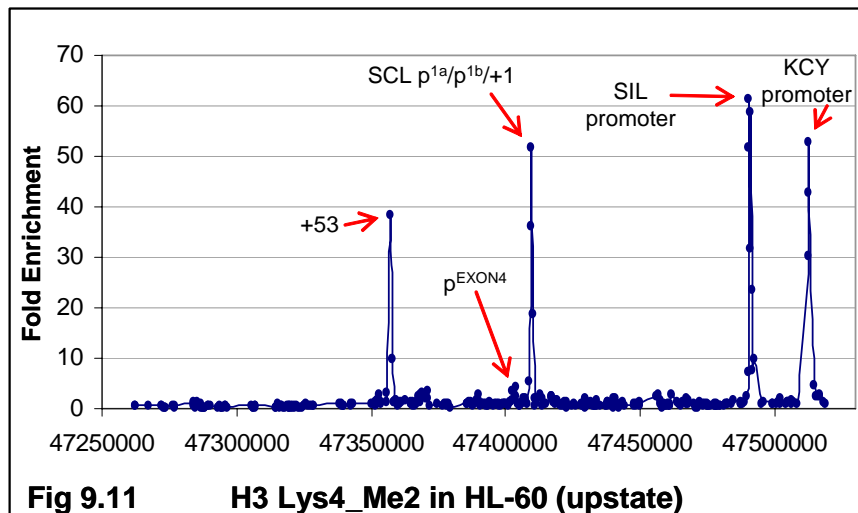
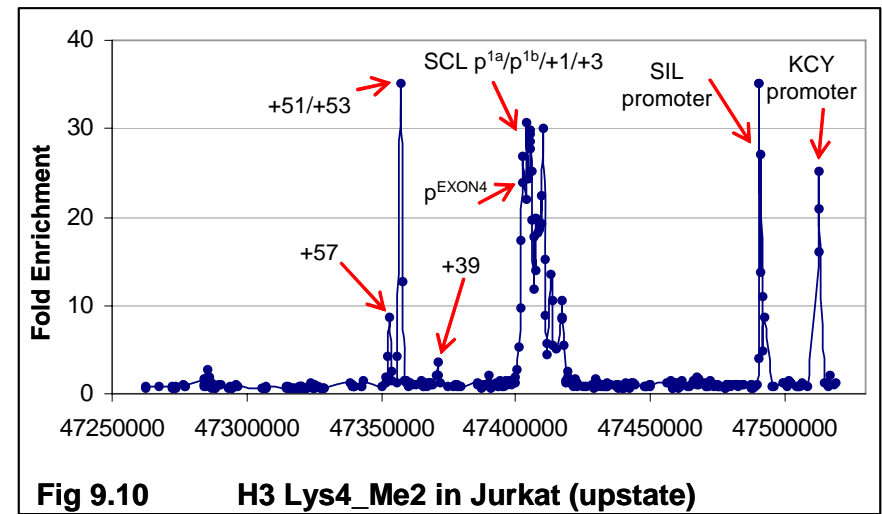
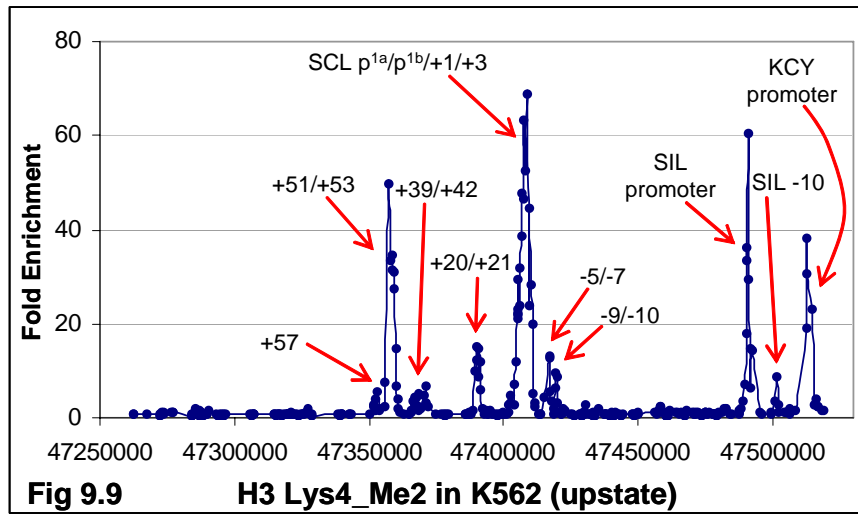
 CYP4Z1
  CYP4A22
  MAP17
  SCL
  SIL
  KYC

 CYP4Z1
  CYP4A22
  MAP17
  SCL
  SIL
  KYC



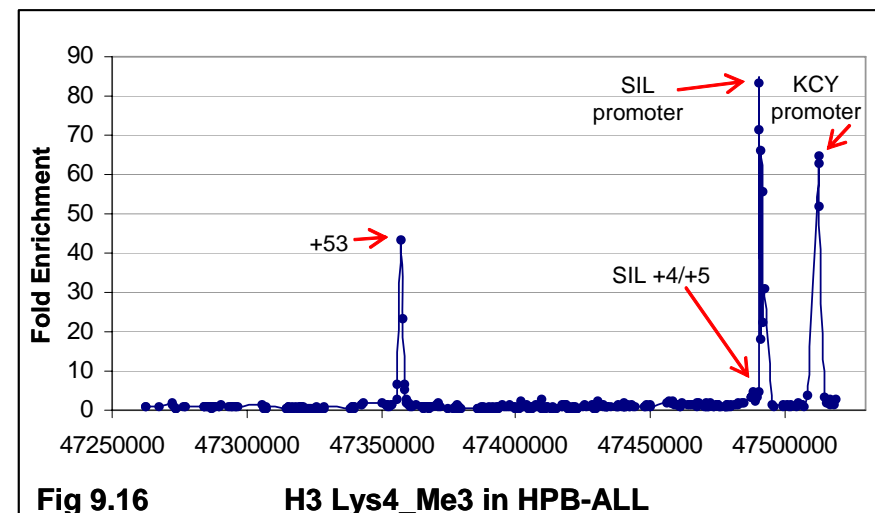
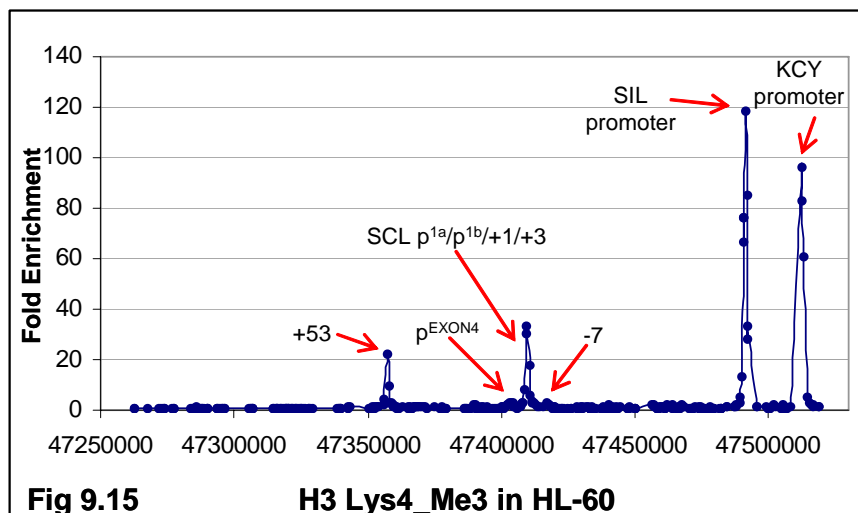
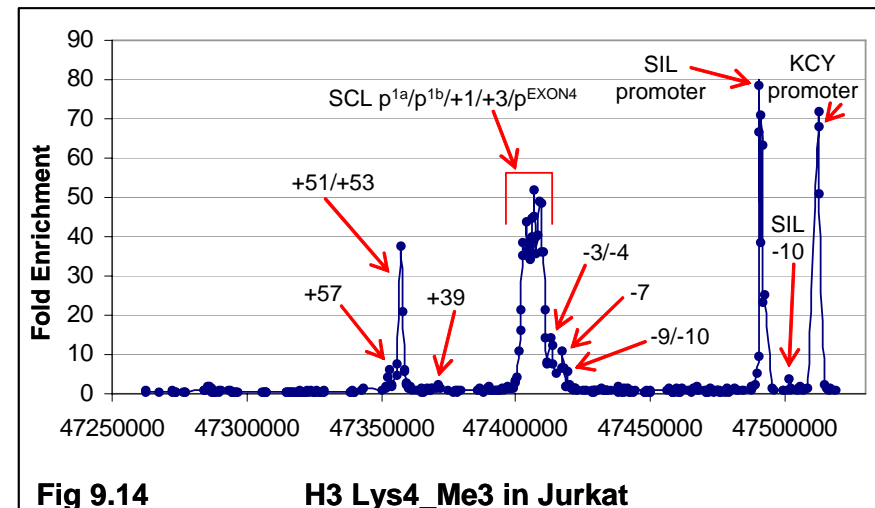
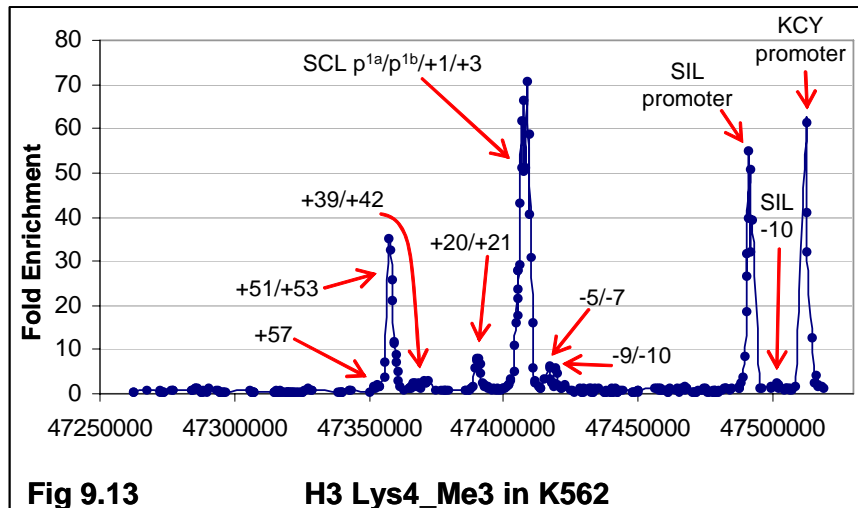
 CYP4Z1
  CYP4A22
  MAP17
  SCL
  SIL
  KCY

 CYP4Z1
  CYP4A22
  MAP17
  SCL
  SIL
  KCY



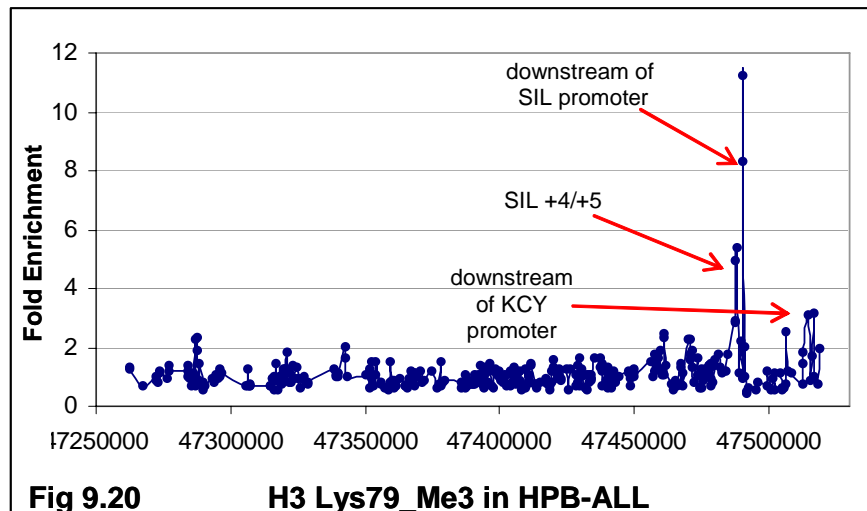
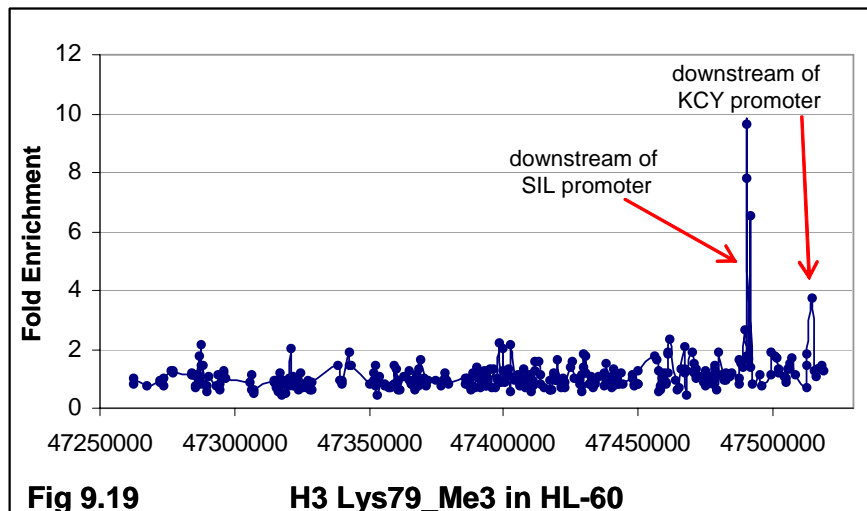
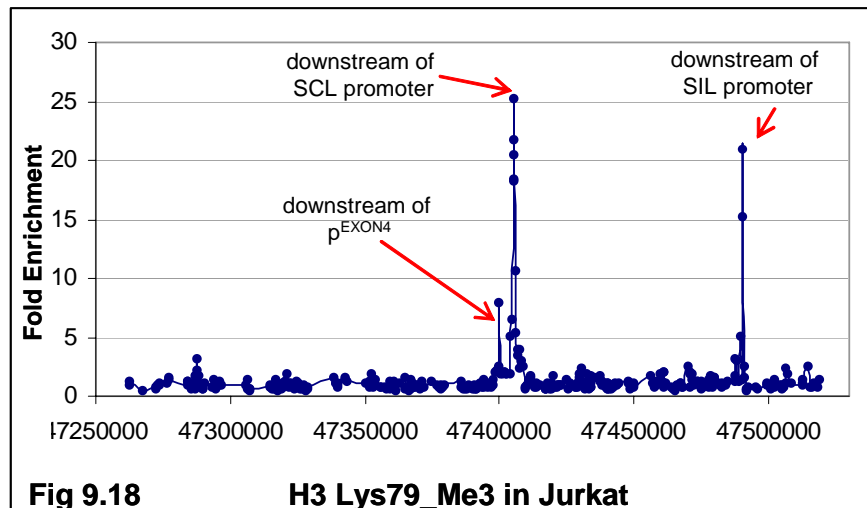
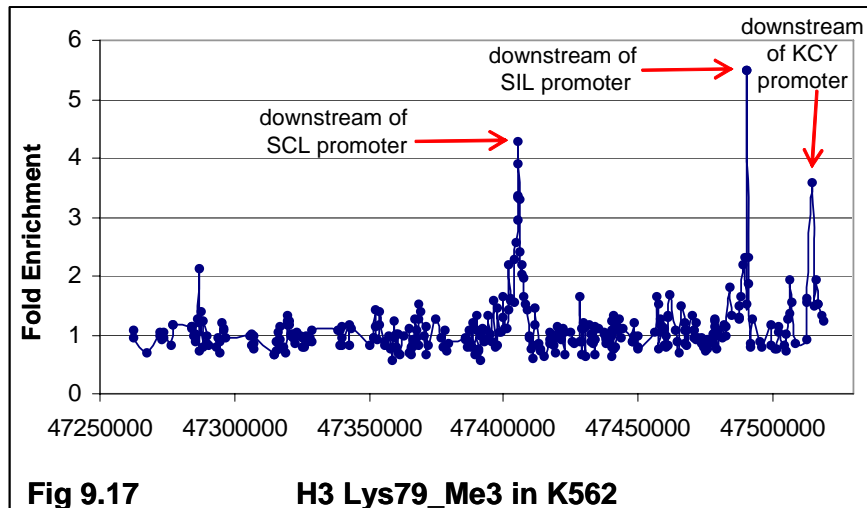
 CYP4Z1
  CYP4A22
  MAP17
  SCL
  SIL
  KCY

 CYP4Z1
  CYP4A22
  MAP17
  SCL
  SIL
  KCY



 CYP4Z1
  CYP4A22
  MAP17
  SCL
  SIL
  KCY

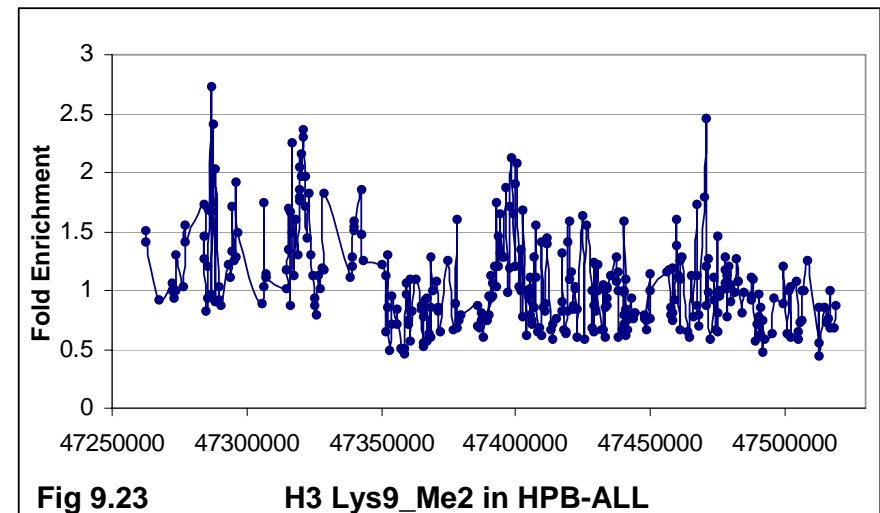
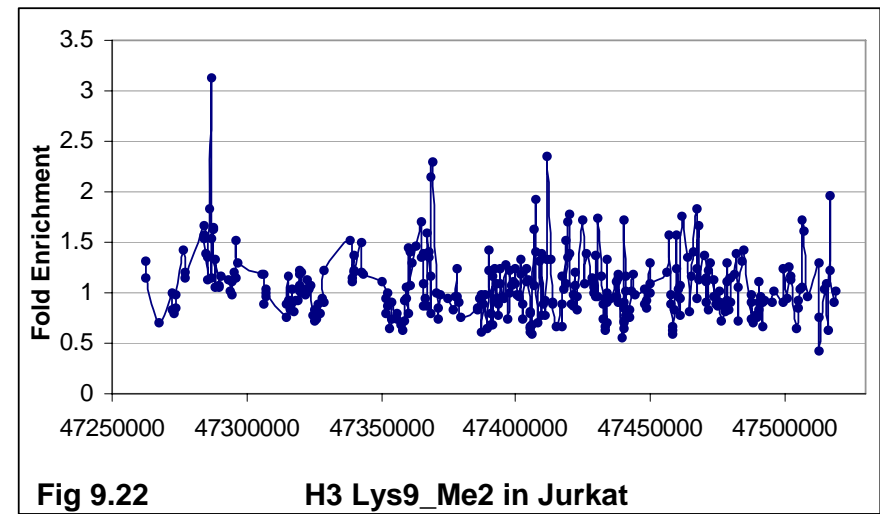
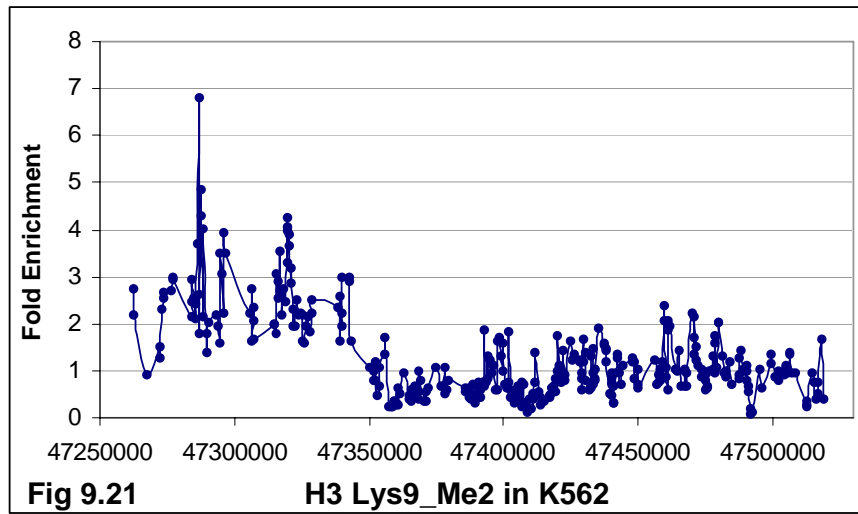
 CYP4Z1
  CYP4A22
  MAP17
  SCL
  SIL
  KCY



CYP4Z1  
 CYP4A22  
 MAP17  
 SCL  
 SIL  
 KCY

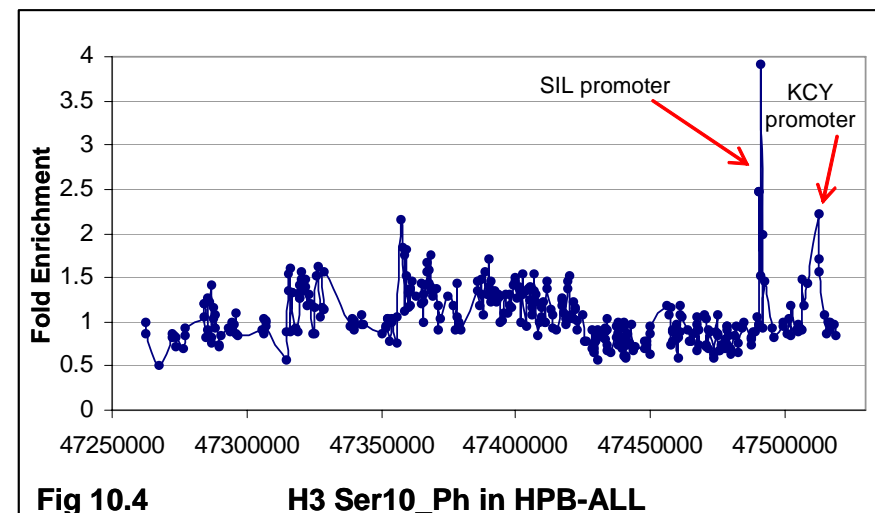
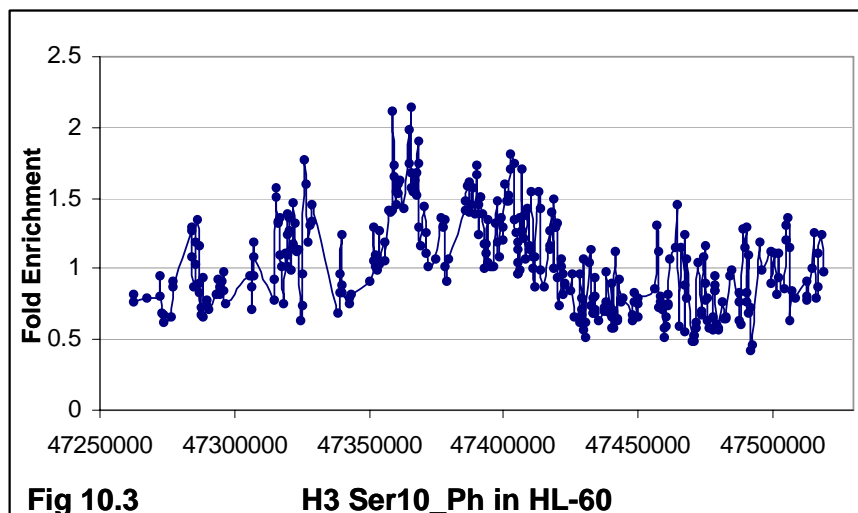
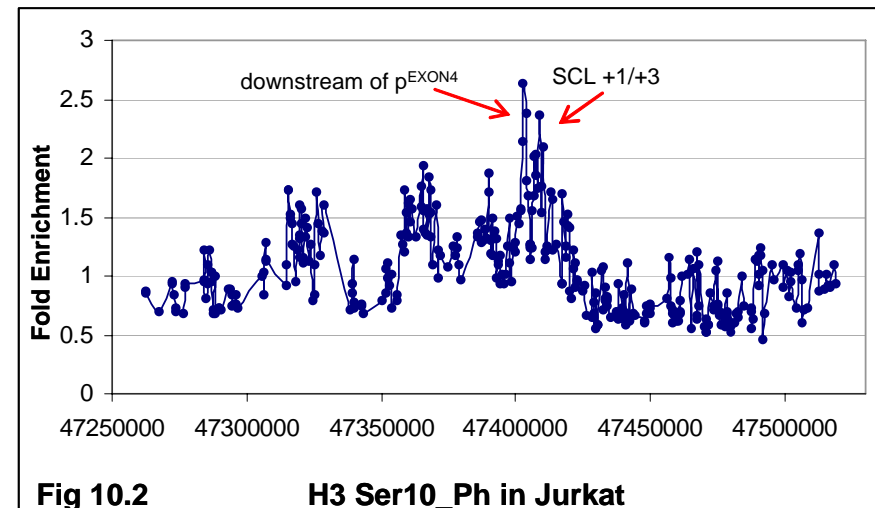
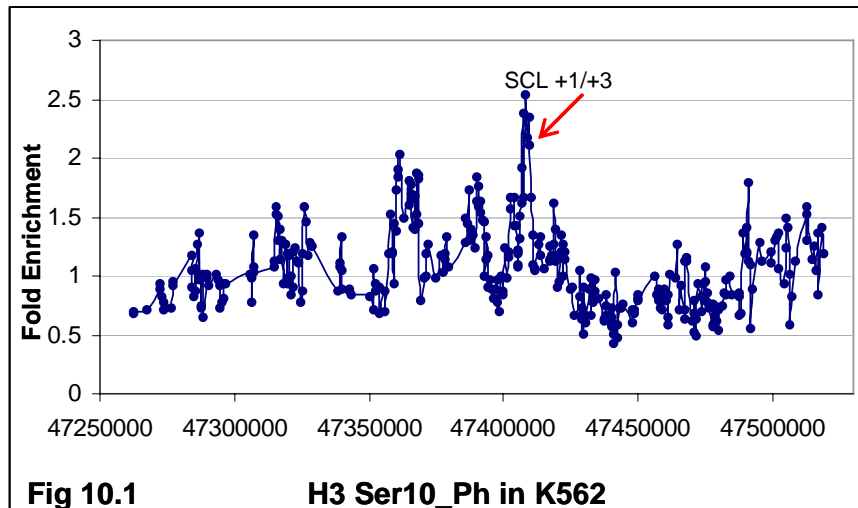
CYP4Z1  
 CYP4A22  
 MAP17  
 SCL  
 SIL  
 KCY





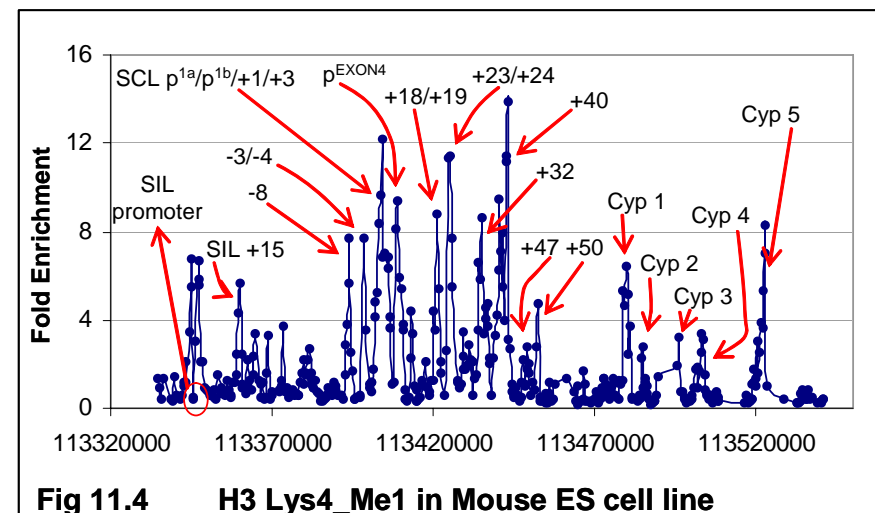
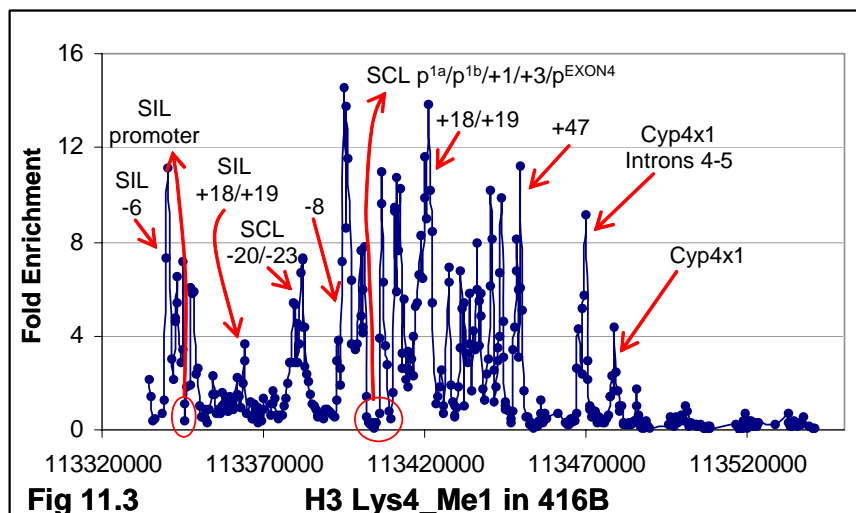
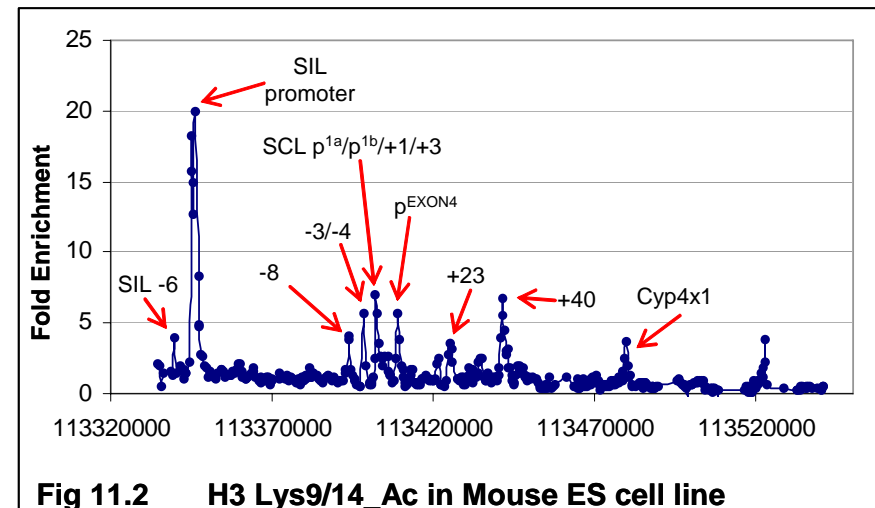
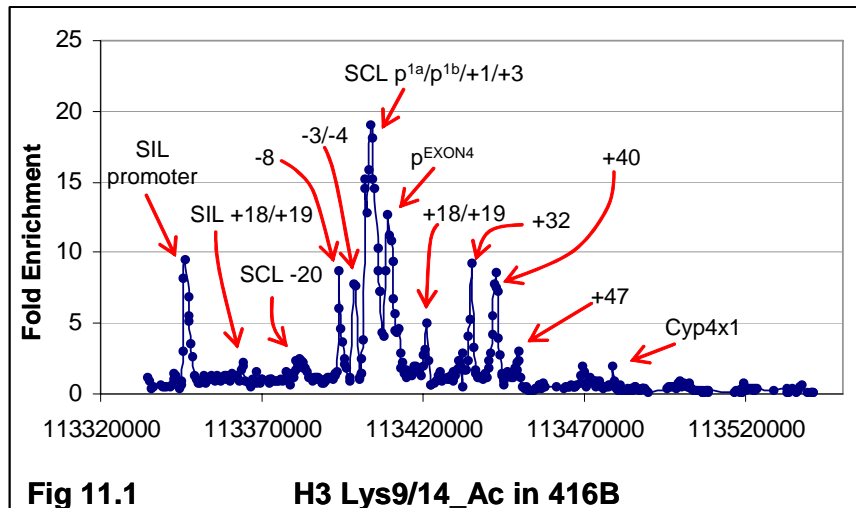
 CYP4Z1  
  CYP4A22  
  MAP17  
  SCL  
  SIL  
  KCY

 CYP4Z1  
  CYP4A22  
  MAP17  
  SCL  
  SIL  
  KCY



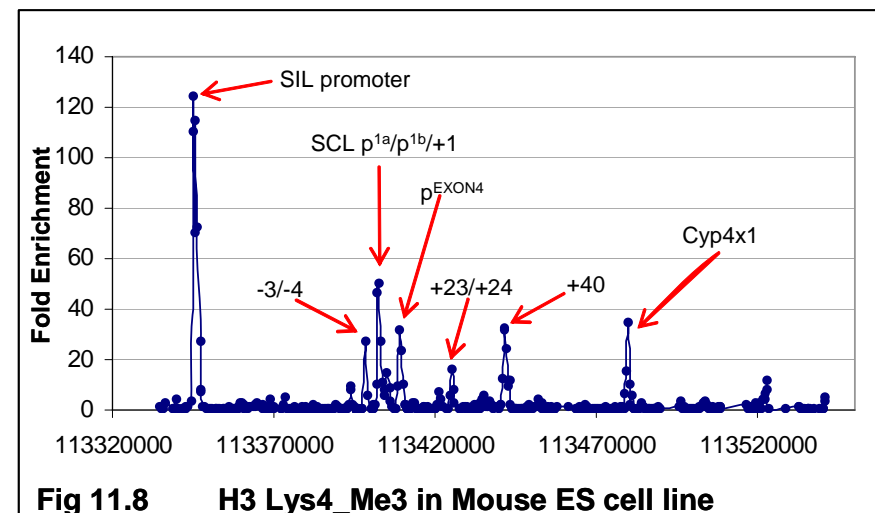
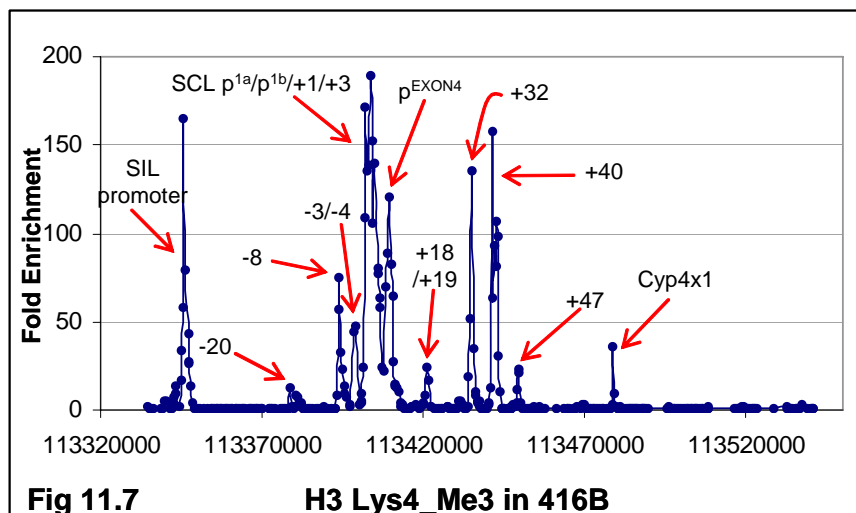
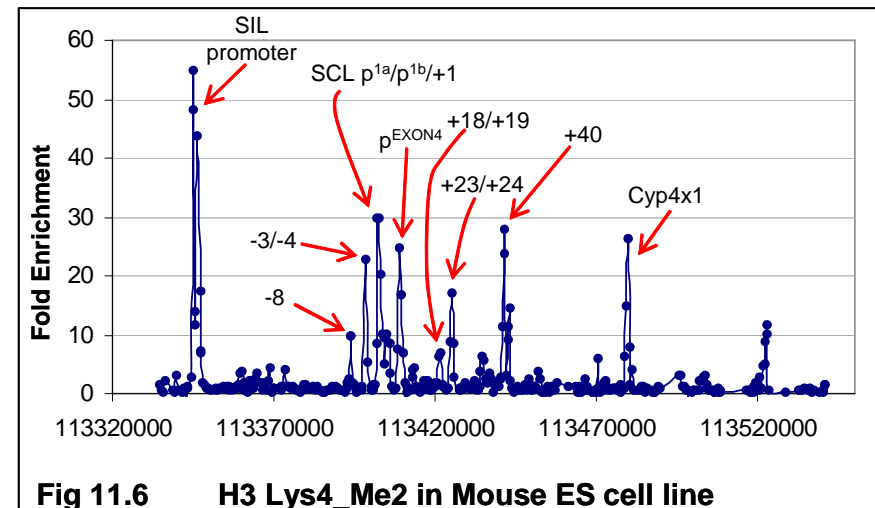
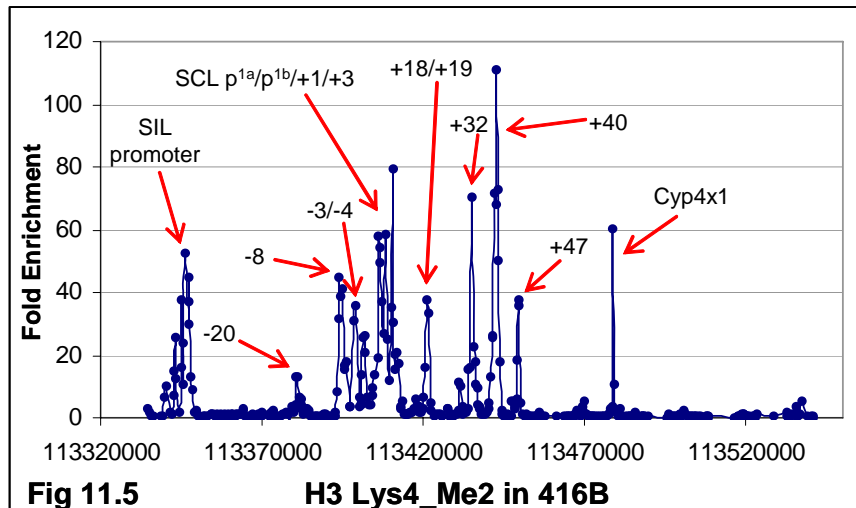
 CYP4Z1  
  CYP4A22  
  MAP17  
  SCL  
  SIL  
  KCY

 CYP4Z1  
  CYP4A22  
  MAP17  
  SCL  
  SIL  
  KCY



← KCY   
 → SIL   
 → SCL   
 → MAP17   
 ← Cyp4x1

← KCY   
 → SIL   
 → SCL   
 → MAP17   
 ← Cyp4x1







  
 KCY      SIL      SCL      MAP17      Cyp4x1

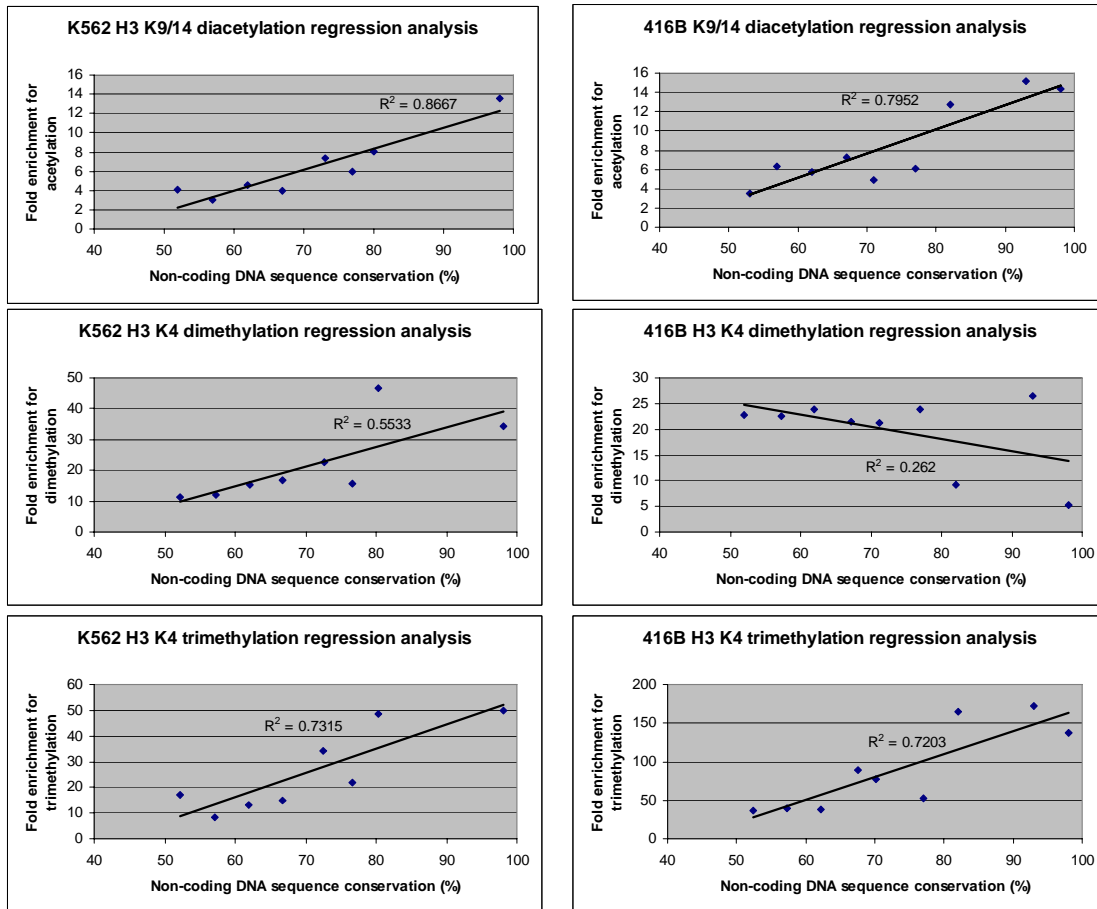




  
 KCY      SIL      SCL      MAP17      Cyp4x1

## Appendix 12

### Correlation graphs of non-coding sequence conservation with histone H3 acetylation and methylation



## Appendix 13

### Sequences of Primer Pairs used to generate constructs for transfection assays

| <b>Amplicon Name</b> | <b>Alternative Name</b> | <b>Primer 1 (5'→3')</b>                | <b>Primer 2 (5'→3')</b>               | <b>Amplicon Size (bp)</b> | <b>Chrom 1 Co-ordinate Start</b> | <b>Chrom 1 Co-ordinate Finish</b> |
|----------------------|-------------------------|--|---------------------------------------|---------------------------|----------------------------------|-----------------------------------|
| SV40/-12b            | HSSCL/M33Aet-b          | (CGGGATCCCG)CAGGAGCATTGAGCAGATCT       | (CGGGATCCCG)TGACGTTTGCAGACTCCTTCA     | 2235                      | 47420799                         | 47423033                          |
| SV40/ -12s           | HSSCL/M33Aet-s          | (CGGGATCCCG)TCTTTCCGTTGTGTTTGTGATCA    | (CGGGATCCCG)AAGATTTTGAAGGATTTCCACAGG  | 453                       | 47421672                         | 47422124                          |
| SV40/ -7             | HSTAL.170et             | (CGGGATCCCG)TTGACCTCAGATGATCCGCC       | (CGGGATCCCG)TCATTTCCTTCTCCCCAG        | 952                       | 47416433                         | 47417384                          |
| SV40/+51             | HSSCL/M96Bet            | (CGGGATCCCG)AAAGGTTGGGAAGAGAGCAGG      | (CGGGATCCCG)GGGTCAGGCCTCTGCTAAGG      | 936                       | 47358744                         | 47359679                          |
| SV40/neutral         | HSTAL.20et              | (CGGGATCCCG)ACTTTCCTTTTAAGTACACCAGCAAC | (CGGGATCCCG)TTTCAATGAGCTATTGGATTATGTG | 951                       | 47289370                         | 47290320                          |