**Suppl Table 1 General information of the Müllerian adenosarcoma included in this study**

Case Age Size Procedure Site Grade SO Stage Recurrent WGS ENMS

AS01 29 3.3 TAH Cervix high Y IB y

AS02 45 6.2 TAH Uterus Low IB Y

AS03 86 15 BSO Ovary low y IIIB y y Y

AS04 48 5.0 TAH+BSO Uterus low y IB y

AS05 80 7.0 TAH+BSO Uterus low IA y

AS06 41 8.5 TAH+BSO Ovary high y IA y Y

AS07 43 6.0 TAH+BSO Uterus high y IB y

AS08 43 6.0 TAH+BSO Uterus high y IB y

AS09 49 4.0 TAH+BSO Ovary low y IIIB y y Y

AS10 41 12.0 TAH+BSO Uterus high IB y

AS11 22 5.5 TAH Cervix high y IB

AS12 44 7.0 TAH+BSO Uterus high y IA

AS13 38 9.6 TAH+BSO Ovary low y IIIC

AS14 34 3.0 TAH+BSO Uterus low IA

AS15 50 2.0 TAH+RSO Uterus low IA Y

AS16 51 0.7 TAH+BSO Cervix low IA

AS17 25 4.9 TAH Uterus high y IA Y

AS18 55 4.5 TAH+BSO Uterus high Y IA

AS19 41 5.9 TAH+BSO Uterus low y IB

AS20 69 11.4 TAH+BSO Uterus high y IA Y

AS21 41 3.0 TAH+BSO Cervix low IA Y

AS22 63 2.4 TAH+BSO Cervix low IA

AS23 72 2.5 TAH+BSO Uterus low IA

AS24 40 2.2 TAH+BSO Uterus low IA

AS25 41 3.2 TAH+BSO Cervix low IA

AS26 58 3.0 TAH+BSO Uterus low IA

AS27 68 7.0 EMC Uterus low Y IA

AS28 58 3.0 TAH+BSO Uterus low IA

AS29 44 5.2 TAH+BSO Uterus low IA

\* TAH: Total hysterectomy; BSO: bilateral salpingo-oophorectomy; SO: sarcomatous overgrowth; WGS: whole genomic sequencing. ENMS: endometriosis.

**Supplementary Table 2 The data summary for the sequence quality in ten cases of Müllerian adenosarcoma**

Sample ID AS1-10 Mean

READS Total PF Reads 745,609,677.80

Total Aligned Reads-1 355,256,601.60

Total Aligned Reads-2 350,251,382.60

DEPTH OF COVERAGE Percent Q30 Bases 90%

READ LEVEL STATSITICS Percent Aligned Reads-1 95%

Percent Aligned Reads-2 94%

SNVs In Genes 1513193.20

In Exons 50869.20

In Coding Regions 21801.20

In UTR Regions 29068.00

In Splice Site Regions 2655.30

INSERTIONS In Genes 202765.70

In Exons 4164.20

In Coding Regions 199.20

In UTR Regions 3965.00

In Splice Site Regions 284.10

DELETIONS In Genes 209037.00

In Exons 4268.90

In Coding Regions 231.70

In UTR Regions 4037.20

In Splice Site Regions 324.90

STRUCTURE VARIANTS

TOTAL VARIANT TYPES CNVs 51.30

SV Insertions 1553.00

SV Deletions 3608.00

SV Tandem Duplications 74.50

SV Inversions 144.70

SV Breakends 398.40

VARIANT TYPES

CNVs 37.00

SV Insertions 702.40

SV Deletions 1655.00

SV Tandem Duplications 33.90

SV Inversions 86.20

SV Breakends 124.90

**Suppl Table 3A Primer sequence information for target validation of gene mutations**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Name** | **Exon** | **Amino acid change** | **5'-3' forward sequence** | **5'-3' reverse sequence** | **Product size (bp)** |
| ABCC12 | 24 | p.Pro1134His | CGACTGTCTGCCCACTTTGTAT | CTGTGTTCCTGAATGCACTCATC | 164 |
| ABCC12 | 22 | p.Thr1037Ala | GGCATTACCTGGATGATGTATGACA | AAAACTCCAGTCACCTCCTCTACT | 175 |
| ABCC12 | 21 | p.Ile1000Val | GGTGATGCAGCTCTCCTTCTTG | CAATTTTCTTCCAGCATTTTCCACAGA | 150 |
| ABCC12 | 21 | p.Leu915Phe | GGTGATGCAGCTCTCCTTCTTG | CAATTTTCTTCCAGCATTTTCCACAGA | 150 |
| ADAMTS8 | 7 | p.Phe638Leu | GGATCTGAGTCCCAGGGTGATT | AATTACACTGACATGGACGGGAAT | 156 |
| ADAMTS8 | 7 | p.Gly605Arg | CCTTGGCCTCGAACACTTTGAA | GCAGTGTGAGAAGTATAATGCCTACAATTA | 155 |
| ADAMTS8 | 5 | p.Arg442Cys | CGTCCTGAGCAGAGGTGTT | TCCTCTTTTCCCAGGAGACTGT | 161 |
| ADAMTS8 | 1 | p.Gly93Val | ATGGTGAACTCCTCGCCG | TCAAGATCGAGCGCCTCG | 166 |
| AHNAK | 5 | p.Ile3378Thr | CTTGGATCCTTTCACTTTTCCTTGG | AAAGAAATCTCGTTTTAAGCTTCCCAAATT | 166 |
| AHNAK | 5 | p.Thr2181Ala | GGGCCTTTCAAGTTTAAGTTCACA | TTTGCCAAAATTGGAGGGAGATTTAAC | 174 |
| ANKRD30A | 7 | p.Ser274Pro | GTGGAAAGAACACCTGACACG | TGACTGTTCGAACTTTCCAGATGT | 132 |
| ANKRD30A | 8 | p.Cys426Trp | CTTTTTATAGATCAGAGGTTCCCATCAGAA | GCCTCTGACTTTATATTTTCACATCACTCA | 144 |
| ANP32E | 7 | p.Gly47fs | CCCTTCTTCAACATAGTCATCATCATCT | AGGTTGTCAAAACACAGAATAACCATAGT | 153 |
| ANP32E | 7 | p.Tyr46fs | CCCTTCTTCAACATAGTCATCATCATCT | AGGTTGTCAAAACACAGAATAACCATAGT | 153 |
| ANP32E | 5 | p.Glu164= | CAGCAGAGGCTATAATTATGACACACT | GTGAGATCACAAACCTGGAAGATTATAGAG | 175 |
| ANP32E | 5 | p.Gln92= | CAGCAGAGGCTATAATTATGACACACT | GTGAGATCACAAACCTGGAAGATTATAGAG | 175 |
| ATRX | 26 | p.Arg2028\* | ATCTTTAGGAAGGAAGGAAAAGCAACA | AGCATTCTGGGAAAATGGTACTTCTC | 175 |
| ATRX | 20 | p.Gln1752Pro | ATCTGAGGAAATACCAATATTCTACTGCATA | CTGCTGTTTCTAAAGCTATGAATTCTATACGA | 137 |
| ATRX | 9 | p.His865Gln | GAAGAGAAAGTCTCTCTCTCTTGTTTTCT | GTGCTGCCAGAACCACCAAAAA | 175 |
| BARD1 | 11 | p.Ile738Val | GACATCACACAGTCTATAAACCAGCT | GTGACGTGACTCAGACCATCAA | 175 |
| BARD1 | 10 | p.Ser660Gly | AATCAGTCACCTGTAGCTGTTGAAA | GTGAACAGGAAGAAAAGTATGAAATTCCTG | 172 |
| BARD1 | 4 | p.Leu359\_Pro365del | GAAGGTGGTGTACCTGGTGAAA | CATTCTGAGCACCAGTGGAGAT | 174 |
| BCOR | Intron14-15 | c.4977-4G>T | ACGTTTGGAAAATTGCAGCGAA | TGGTCCACTTGGGTTGGTAGTTA | 174 |
| BRCA1 | 15 | p.Met1673Ile | ATTAGGGAGATACATATGGATACACTCACA | GAAGAAAGTGTGAGCAGGGAGAA | 131 |
| BRCA1 | 10 | p.Gln356Arg | TGAATGCTGCTATTTAGTGTTATCCAAGG | TGGAAGTAAGGAAACATGTAATGATAGGC | 174 |
| CSPG4 | 10 | p.Pro2294Leu | CACCCAGTACTGGCCATTCTT | TGGTGACACCGAGACCTTTC | 160 |
| CSPG4 | 3 | p.Ala863Val | AGAAATATGGTGGAGCTGTGACAC | TTCAACTACAGGGCACAAGGCT | 150 |
| DCHS2 | 25 | p.Pro2824Ala | GCATTCTTGGTGGGACTGCTTT | CAAAACTAAAGGATGAACATTTGCATATGC | 126 |
| DCHS2 | 25 | p.Val2820fs | GCATTCTTGGTGGGACTGCTTT | CAAAACTAAAGGATGAACATTTGCATATGC | 126 |
| DCHS2 | 18 | p.Thr1602Ala | AAACATTGACTGGGTCTCTGCAA | CCAGTTTTGGAACAGAACCCTTTTG | 147 |
| DCHS2 | 18 | p.Arg1438Leu | ACTGTGGTCATTGGCATCCAAA | GAGTGCTTTACTATAAATGAGATGTCAGGA | 171 |
| DNAH10 | 22 | p.Glu1186Lys | TTCACTTCCTGAGTAAAGACATTGAAAAAC | TTTATCAAGATCATCACCAACAGAACCA | 170 |
| DNAH10 | 27 | p.Met1518Val | CCTGTTCTGGGCTCAAGAACAG | CTGACGTTCTGTAGGTCACTGA | 160 |
| DNAH10 | 33 | p.Val1896Met | CCCTTGTCCTGACATGTCTTTCT | GTGGTTAACTGATGGATCAGAGCA | 175 |
| DNAH10 | 49 | p.Gln2735His | GTCCTTAAGTGGGCTTCTGTTTCA | GCCTCGTAGTCCTGGATGTCTT | 175 |
| DNAH10 | 56 | p.Lys3115Glu | CAGAGGAAAAGGCCATGGAGATA | ACTTGTCCAGCTTCTGCAGTTC | 135 |
| DNAH10 | 63 | p.Thr3620Ile | GGAACATGCTGGACAATGTGGA | TCATTGAGCAGACAGAGAAATGGAC | 149 |
| ERBB3 | 2 | p.Pro30Leu | GTAACTGGAAGAGGGCAACCAA | AGCTTGTACAGTGTCTGGTATTGG | 174 |
| ERBB3 | 28 | p.Arg1173Trp | CCCTACCCTCATGAAGTTCTTCAC | ACTCCTCATCTTCATCTTCTTCTTCAGTA | 139 |
| EXT2 | 2 | p.Arg161Trp | GATGTCTATCGCTGTGGCTTCA | CCCGGTTGATGTCATCAGTGTA | 175 |
| EXT2 | 7 | p.Val396Met | GTGAAATGAAACAAGACTGTGTGTAGAAA | CTGTCTCTGCATTTCTTCAATCTGTC | 175 |
| EXT2 | 8 | p.Arg426Gln | GCCTAACCTGGAGTTGACTATGATAGA | GGATAGATCCGGTCATTGATAATCTGC | 174 |
| FAT1 | 10 | p.Met2845Ile | AAGTTGTAATCCAGCCTGTTTCCA | ATGAGGCATTCATTGTTGAAAACCTG | 174 |
| FAT1 | 2 | p.Ile895Thr | GGTGGAATAAATGTAGGTGGGTTGT | CGTGACGGGTGTTGTTAACATC | 174 |
| FCGBP | 32 | p.Arg4950Gln | TGGGCATCGCCATCAAAGAG | TGGTTCTGTGAGTTCCTGACCTA | 169 |
| FCGBP | 16 | p.Glu2640Lys | CTGGAGAGGAGCCCACAGAACTC | CAGGCAACGCCAATGAGTTC | 172 |
| FCGBP | 8 | p.Ala1343Val | CCGAAGTCGGTCTCAATCACAA | CCCTACTCAAAGTCTACTTTCTGAAGC | 150 |
| FCGBP | 8 | p.Gly1333Arg | CCGAAGTCGGTCTCAATCACAA | CCCTACTCAAAGTCTACTTTCTGAAGC | 150 |
| FCGBP | 4 | p.Gly645Glu | CGGTCGCCCTCATAGTGTTG | GTGACCCAGCAGACGACTTCCT | 169 |
| GLI3 | 14 | p.Gly727Arg | CGATGGCACTGAGGTCTCCTAT | GTGACATTTCTTTCCTTTCCACTTGAC | 165 |
| GLI3 | 3 | p.Ser45Arg | CTGGACATTCTGTGGCTGCATA | CGAGAATGAGACCTAATTGATCATGGTTTT | 158 |
| GPLD1 | 14 | p.Asn422Ser | GGAAGCCTTCAAGGATCCTGT | CAGCTGACCTCAACCAGGAT | 174 |
| GPLD1 | 13 | p.Asp337Tyr | GACGTGCTTTTGTGACAACTGA | CACAAGTCCAATACTTTGGACAGGAA | 174 |
| ITIH5 | 13 | p.Glu757Lys | CCCACCATCCAAGATGACTCTG | ACAGTGAACGGAGAGTTAATTGGG | 150 |
| ITIH5 | 9 | p.Asn421His | GCCAATGGTGAAGATGCAGACT | ATCAGGCTCCTCAACAAGTACG | 171 |
| KDM6B | Intron6-7 | c.456+6A>G | ACTGTACGAGTCAGAGCACGATA | CTGAGCCAGAAGGCACAATCGT | 168 |
| KDM6B | Intron6-7 | c.457-8A>C | GGGACGGGATTGTACGATTGTG | TGTAGCAAGTTCCACACTTGCT | 167 |
| KDM6B | 8 | p.Pro203Ala | ACAAACGGAACTATGGAGCCAA | CTATACCCACACCTGTTCAGAGTTG | 173 |
| KDM6B | 8 | p.Glu221Asp | ACAAACGGAACTATGGAGCCAA | CTATACCCACACCTGTTCAGAGTTG | 173 |
| KDM6B | 11 | p.Ser444Gly | GGATGGGTGGAGCTTGTCTTG | CCCAAGAACGGTTTCCGAC | 161 |
| KDM6B | 11 | p.Pro482Ser | CAGTCGGAAACCGTTCTTGG | TTCTAAGATCTCTCCATCCTCTCGG | 175 |
| KDM6B | 11 | p.Pro511His | CCCGAGAGGATGGAGAGATCTT | AATCCTGAGTGCCCACAGAAAA | 138 |
| KMT2C | 8 | p.Cys391\* | ACCTCTATTATATTACACAAACCTTTAGCACC | GGATATAGCGGTTACTCCATTAAAACGT | 162 |
| KMT2C | 8 | p.Arg380Leu | GCACACTTTGCACTCAGGACAT | GTTAATTATAGCGAAGGAAGATGCAAACTG | 172 |
| KMT2C | 8 | p.Asp348Asn | GCACACTTTGCACTCAGGACAT | GTTAATTATAGCGAAGGAAGATGCAAACTG | 172 |
| KMT2C | 7 | p.Pro309Ser | CCGTAGTAAACTTACATCTTTCAGGAGC | GTGCATTTTGTAAGCACCTTGGA | 174 |
| LATS2 | 8 | p.Asp1006Gly | ACCTTCGCTGGCATCGTT | CCCTTCTTCAGCGCCATTGA | 141 |
| LATS2 | 8 | p.Ala955Val | CTTCCGGATGTCACTGGAGA | AGAACACGCTCCACATTCCA | 167 |
| MACF1 | 1 | p.Ile23Met | GATTAGGAGAGGAAGGAAATGGGAAATT | CTGAGGTTTCTTCCTGGTGAGATG | 175 |
| MACF1 | 1 | p.Cys242Tyr | GTGTGGAGGAAGGAACCAAGAGT | AGAAGTAGGCAGTCTGGAATCCT | 167 |
| MACF1 | 30 | p.Arg2850Ser | GCAAGAAGGGATTGAAGTGTGTG | CCCATCAGAAACTCTCACTTTAACCT | 175 |
| MACF1 | 30 | p.Glu2978Lys | TCTCATATGAAGCAGTCTACCTCATGT | TCATTGGTTGCTGCAAAACCTG | 142 |
| MAGEC1 | 4 | p.Val176Leu | CCAGTCTGTTCTCCAGATTCCTG | CTCAATAAAGTGGAGGAGAAGGAGC | 159 |
| MAGEC1 | 4 | p.Ile178Leu | CCAGTCTGTTCTCCAGATTCCTG | CTCAATAAAGTGGAGGAGAAGGAGC | 159 |
| MAGEC1 | 4 | p.Val447Gly | TTTATTGAGTATTTTACAGAGTTCTCCTGAGAG | GGAACTCTGGAAAAGACTCAATAAAGTGT | 130 |
| MCM9 | 13 | p.Met1096Val | GTAAAGTGAAGAGGGATTCTTTGGAAAC | CCATCGGAATCCAAATCAAAATCCC | 175 |
| MCM9 | 13 | p.Ser898Phe | GATCAGTTTTGACTTCTGCTTGAAAGT | CCATCCTCAGTCCACTCCTGTA | 175 |
| MCM9 | 13 | p.Glu816Asp | GGGACATGATGAGTCAGTACTGAG | CCAAAGGAGCAAAGTGGACATTG | 165 |
| MXRA5 | 7 | p.Val2688Ile | TCCGTCTCCATCCTGCATACA | CAGGGACGTTTCTCCTGGAC | 152 |
| MXRA5 | 7 | p.Glu2426Asp | GGGTTACCGTTGATCTTGGG | TATTCAGAAAGCCCAGCGTTCTG | 126 |
| MXRA5 | 77 | p.Ile1819Leu | CTTTGAGCTGCTCTGGTGGAA | ACCTCCGTTGTTGCACACT | 148 |
| MXRA5 | 5 | p.Gly943Asp | CTCAGCCAAGGAGACAGCATCCA | CCTTATGAACCATCTCCTACTCTGCA | 165 |
| NACA | 3 | p.Asp1401Ala | GGGAGTGAGATCTCCTTTGGA | AAGGAGGTCCCGCTATGACT | 170 |
| NACA | 3 | p.Ser1377Pro | GATGGGATAGCTGGTCCTCTTTTG | CTCTAAAGGAGGCCCAACTACTC | 126 |
| NACA | 3 | p.Ser1304Pro | GGGTACCTGGGCTTCCTTTTG | CTCCCTCCCTAAAAGGAGGTCT | 168 |
| NACA | 3 | p.His1283Pro | GGGTACCTGGGCTTCCTTTTG | CTCCCTCCCTAAAAGGAGGTCT | 168 |
| NACA | 3 | p.Ser435Phe | ATGTTACTTATGGGACCTGATGACATTG | CTCTCCTAATGCCACTTATCATTATCCT | 174 |
| NACA | 3 | p.Ser435Phe | TTCCAACAGAAGAAACGGGCATT | CCCTTCTGGCTCCTTAAATGTAGC | 131 |
| NACA | 3 | p.Val381Asp | TGAGAATGAGAGAGGTTGTAGGAGATAATG | AGAAATGAGGTAGTTCCTGCTACTGT | 160 |
| NCOA2 | 20 | p.Gly1363Arg | TGTCACAGTGGCGGTATGAAAA | GTCCCATGATGCAACAGTCTCA | 133 |
| NCOA2 | 11 | p.Glu653Val | GTATCCGACAAAGAGCTGGCTAA | CTGGAGAGCAAAAGGAAACAAATGACC | 175 |
| NCOA2 | 11 | p.Ala407Ser | CCATTTGTTCCTTTGGGCCATT | AATGTGTGTGTGATGAATCCGGAT | 172 |
| NUMA1 | 22 | p.Tyr1836His | CTGAGTTGCCATAATCGGGAGAA | GCAACAGATTCACTCTGTCTTCCA | 167 |
| NUMA1 | 21 | p.Lys1766Arg | CAGGGATGGGAGTGAAGTAGAGA | AGGTTTCCTTTCCATAGCAAGCT | 139 |
| NUMA1 | 15 | p.Gln1089Glu | CCAGATGCGTGCTCCTTTTCT | ATGCCCTGACGGAAAAGGAAG | 151 |
| PER1 | 22 | p.Ala1196Val | CCCTTGAACTTGAGCTCAATTCT | CCTCGGTTTTCTGAGGACCA | 206 |
| PER1 | 19 | p.Thr866Pro | GAGAGAACACTGGGAGAGGGTA | CTGCCGATCCAAAGCCAAGC | 170 |
| PER1 | 6 | p.Val240Ile | GATGGAGCAGTGGAACCATAGAA | CCTGCCAGGATACCTTCTCAGT | 175 |
| RABL6 | 9 | p.Pro373Thr | GGCGCAGCATCATCTCTAGG | GCGCTCCGAAATCCAGGAC | 145 |
| RABL6 | 10 | p.Thr387Met | GTTCTGGTGCCGAGTGAAGA | GGTTGTGTCTTCCAGGAAGCTG | 141 |
| RABL6 | 15 | p.Arg375fs | CCGATGAGCTGGAGGCTTT | GCGATGGTACAGAGGCAAATG | 160 |
| ROS1 | 21 | p.Ser1054Arg | CCCATTTTCATGCTTAGGTTTGTTCC | CTCTACCTGTGCCTCTACTTTTCA | 138 |
| ROS1 | 18 | p.Arg894Trp | ACTGATTAAATCTGGCTGGTTCCAA | GGATACCACCATCACAGAATTTGC | 173 |
| ROS1 | 16 | p.Trp827Leu | CTGCTTTAAGTACTCACAATAAGCGAGA | CTCTATTCAGTGGAAAGCACCAGA | 175 |
| RRBP1 | 5 | p.Asn727Ile | CTCTGAGGACGGGAGAGGACAA | CTGGAAGAGAAGGAAAAACTGCTG | 131 |
| RRBP1 | 3 | p.Gln606His | CTCTGGGCCACATCTGTATTTCT | CACAAAGGTAGAGGGTATTACAAACCAG | 174 |
| RRBP1 | 3 | p.Gln606His | ATTTAAAGACAGCCTTTCCTTCTAAGTTCA | GGGTAAAAAGACAGAGTCAGCTTCT | 175 |
| RRBP1 | 3 | p.Lys210Arg | CTCTGCCTTTTTCCCTTGGTTTG | TGGCACTACTCAGGGCAAAAAG | 148 |
| RRBP1 | 3 | p.Asp85Glu | GGTTCTCGAAGGAGGACAGTCA | GTCGAGAAGAAAAAGAAGGAGAAAACAGTG | 128 |
| SCUBE2 | 21 | p.His107Arg | ATGTGTGCTTGTCAGCAGTTTG | GTCAAAGAAGCTGTGGATTCAGTTC | 175 |
| SCUBE2 | 20 | p.Asn835Asn | CTGGGTAATTGCCTGGGTAGTT | GGTGGTCAGGACAGAGATGACA | 138 |
| SCUBE2 | 19 | p.Asn790Thr | TTTTTCCAAATTCAGGCTGGTATGTT | CAAACTTTAAAATCTTTGTGCTGCATTTGA | 172 |
| SDHA | 11 | p.Thr508Ile | TTTTTGTTTTAGGAGATAAAGTCCCTCCAA | CGAGTCCAGGCTCTTACCTTCT | 148 |
| SDHA | 15 | p.Leu649fs | GCTTAACTTACCACTGACTCTTCTTTTCAA | CACATCTTGTCTCATCAGTAGGAGC | 132 |
| SDHA | 15 | p.Cys654Arg | GCTTAACTTACCACTGACTCTTCTTTTCAA | CACATCTTGTCTCATCAGTAGGAGC | 132 |
| SEC16A | 1 | p.Arg641Cys | GCTTCCGTGGTGGAGTTAAGAG | GCCAACGTGGTTGGTGAAGTAA | 170 |
| SEC16A | 1 | p.Arg346His | CCCTTGGAAAAACATCGCCAG | AGGAGTGAAGAATGAGCACCG | 172 |
| SH2B3 | 1 | p.Leu6Pro | GGTGGAGCTCAGAAGGACAT | GATTCAGAAGAAGAGGTGAGAGCAA | 130 |
| SH2B3 | 2 | p.Trp262Arg | AAGAGCATCAGGAACAAGCCTT | GGGTGTGAAAAGCCTTGTCACT | 173 |
| SH2B3 | 7 | p.Asn537Asp | TCTCCCAGGGCGATCCTCAC | GGATGAGTCCATTTCGTAGTCCG | 139 |
| SLC25A5 | 2 | p.Phe82Ile | CATTATAGACTGCGTGGTCCGTA | CCAAAACTGGGTTCTCTTGTCCA | 172 |
| SLC25A5 | 3 | p.Arg244Cys | GATGATCGCACAGACTGTCACT | CCCACGACTACAACTTTATCTTCTGC | 139 |
| TACC2 | 4 | p.Arg960Lys | AAGAGTCAGAATTGTCAGCACCAA | CCAGTGCAGCAAGTTTCCTTTC | 175 |
| TACC2 | 4 | p.Pro1563Arg | CTGGAGAGGAGCAGGCAGGAATT | GCTTTCCAGAAGGAATTCTGTCTTG | 151 |
| TNN | 6 | p.Arg440Ser | GGGACTGAGTATAAGATCACGGT | GAGAGGAGTCAGCCAAGAAAAATATGA | 154 |
| TNN | 15 | p.Val1073Ile | CCTTAAAATAGGAAGAAACTCCACCTCTT | GCCATGCAGGTAGATGGTGTAC | 168 |
| TNN | 16 | p.Val1130Met | TCATCTTCCTTCTCAGGTCTTCCA | GCTTGTCCTGGGAGAAATCACC | 172 |
| TNN | 16 | p.Asp1135Glu | TCATCTTCCTTCTCAGGTCTTCCA | GCTTGTCCTGGGAGAAATCACC | 172 |
| TNN | 17 | p.Arg1157Gln | TACTCGCACACATGGGTTGATT | CTGGAGGCCACTTGGAAGAAAT | 173 |

**Suppl Table 3B Primer sequence information for SV validation**

|  |  |  |  |
| --- | --- | --- | --- |
| **Fusion gene** | **5'-3' forward sequence** | **5'-3' reverse sequence** | **Product size (bp)** |
| FSIP1-BAZ2A | GCTATATGGCAGACTAGATGT | ACTTGTTGGTGTTGATGGT | 214 |
| SET-DPP10 | CCTTGAGCAGAATACAATGG | CAAGACTATCCTGGCTAACA | 233 |
| MUC19-ORC5 | CTCAGAGAAGACAGGCATAT | GGTTCACGCCATTATCCT | 325 |

**Suppl Table 4 Antibody information**

|  |  |  |  |
| --- | --- | --- | --- |
| **Gene name** | **Vendor** | **Item number** | **titration** |

|  |  |  |  |
| --- | --- | --- | --- |
| CDK4 | Cell Signaling | 127905 | 1;50 |
| BRAP (D-5) | Santa Cruz Biotechnology,INC | sc-166012 | 1;100 |
| FOP (B-1) | Santa Cruz Biotechnology,INC | sc-374340 | 1;100 |
| TERT(A-6) | Santa Cruz Biotechnology,INC | sc-393013 | 1;100 |
| Limd1 (H-4) | Santa Cruz Biotechnology,INC | sc-271448 | 1;100 |
| Msi1(69-Q) | Santa Cruz Biotechnology,INC | sc-135721 | 1;100 |
| Y14(4C4) | Santa Cruz Biotechnology,INC | sc-32312 | 1;100 |
| TBRG1(D-9) | Santa Cruz Biotechnology,INC | sc-515620 | 1;100 |
| Mi2(B-4) | Santa Cruz Biotechnology,INC | sc-55606 | 1;100 |
| GADD153 (H-5) | Santa Cruz Biotechnology,INC | sc-166682 | 1;100 |
| Myosin X (C-1) | Santa Cruz Biotechnology,INC | sc-166720 | 1;100 |
| Epac (A-5) | Santa Cruz Biotechnology,INC | sc-28366 | 1;500 |
| ErbB-3 (RTJ.2) | Santa Cruz Biotechnology,INC | sc-415 | 1;200 |
| HDGF (E-7) | Santa Cruz Biotechnology,INC | sc-271344 | 1;1000 |
| KIF14 (E-3) | Santa Cruz Biotechnology,INC | sc-365553 | 1;500 |
| NDUFB6 (B-2) | Santa Cruz Biotechnology,INC | sc-515596 | 1;500 |
| cathepsin K (E-7) | Santa Cruz Biotechnology,INC | sc-48353 | 1;200 |
| PP2A-Aa/b (4G7) | Santa Cruz Biotechnology,INC | sc-13600 | 1;200 |
| 14-3-3 e (8C3) | Santa Cruz Biotechnology,INC | sc-23957 | 1;500 |
| BAP1 (C-4) | Santa Cruz Biotechnology,INC | sc-28383 | 1;200 |
| Atm (G-12) | Santa Cruz Biotechnology,INC | sc-377293 | 1;500 |
| B-catenin (12F7) | Santa Cruz Biotechnology,INC | sc-59737 | 1;200 |
| NF-1 (D-2) | Santa Cruz Biotechnology,INC | sc-74444 | 1;200 |
| NuMA (F-11) | Santa Cruz Biotechnology,INC | sc-365532 | 1;100 |
| Positive cofactor 4 (H-12) | Santa Cruz Biotechnology,INC | sc-166280 | 1;2000 |
| MDM2 IF2 | Invitrogen | 182403 | 1;200 |
| HDAC5 (HDAC5-35) | abcam | ab50001 | 1;1000 |
| Cyclin D1 | Epitomics | AC-0017 | 1;100 |
| ER (SP1) | Thermo scientific | RM-9101 | 1;200 |
| P16 | BIOCARE | ACR3007C | 1;50 |
| Ki67 | Dako/Agilent | M7240 | 1;100 |
| Bcl-2 | Dako/Agilent | M0887 | 1;50 |

**Suppl Table 5 Chromosomal CNV and associated genes**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Chromosome and region | | | Start | End | Case number | Frequency(%) | Specific genes |
| Frequently Gained | | | | | | | |
| 1 | | 1q21.1 | 144000656 | 147380560 | AS3,AS6, | 20 | RNF115,LIX1L, PIAS3, **RBM8A**, CHD1L,BCL9, NBPF10 |
| 1q21.2-q21.3 | 149720001 | 151878880 | AS2,AS3,AS4,AS5,AS6,AS7 | 60 | ANP32E,BNIPL,**CTSK**,CTSS,ECM1,GOLPH3L, HORMAD1,MCL1,PLEKHO1, PRUNE, PSMB4, SELENBP1,SETDB1,SF3B4,THEM4,TUFT1 |
| 1q21.3-q23.1 | 153360001 | 157190000 | AS2,AS3,AS4,AS5,AS6,AS7 | 60 | ADAR,CCT3,**HDGF**,ILF2,IQGAP3,MEF2D,NPR1, NTRK1,PBXIP1,PRCC, PYGO2,RAB25,SCAMP3,SEMA4A,SLC39A1,UBE2Q1,YY1AP1 |
| 1q32.1,q32.2 | 199850001 | 207300000 | AS2,AS3,AS5,AS6 | 40 | CYB5R1,IKBKE,**KIF14**,KLHDC8A,LGR6,MAPKAPK2,MDM4,NFASC,NUAK2, NUCKS1,PIK3C2B,PKP1,PPFIA4,PTPN7,TIMM17A,UBE2T |
|  | | 1q42.2,q42.3 | 234450001 | 234910000 | AS1,AS3,AS6 | 30 | TARBP1 |
|  | | 1q44 | 244340001 | 247650000 | AS3,AS5,AS6 | 30 | DESI2,KIF26B,SMYD3 |
| 5 | | 5p15.33 | 10001 | 1960000 | AS1,AS2,AS7 | 30 | **TERT**,NKD2,CEP72,CLPTM1L,LPCAT1,SDHA,TPPP |
| 5p15.1 | 16490001 | 17670000 | AS2,AS4,AS5,AS7 | 40 | **MYO10**, BASP1, RETREG1 |
| 5p13.3 | 31300001 | 32650000 | AS2,AS4,AS5,AS7 | 40 | GOLPH3, PDZD2, **SUB1**, ZFR, CDH6 |
|  | | 5q13.1,q13.2 | 68260001 | 70900000 | AS2,AS7 | 20 | CCNB1,CDK7, CENPH, MARVELD2, RAD17,TAF9 |
| 6 | | 6q24.3-q25.2 | 148600001 | 154580000 | AS2,AS5 | 20 | SASH1, AKAP12, C6orf211, CCDC170, ESR1, PCMT1, ZBTB2, MYCT1, RGS17 |
|  | | 6q25.2-25.3 | 154580001 | 155590000 | AS2,AS5 | 20 | TIAM2 |
|  | | 6q25.3 | 157110001 | 159360000 | AS2,AS5 | 20 | ARID1B, EZR, GTF2H5, SNX9, SYNJ2, ZDHHC14 |
| 7 | | 7p22.3-p22.1 | 50001 | 7050000 | AS2,AS4,AS5,AS7 | 40 | MAFK, CYP2W1, GPER1, MICALL2, PDGFA |
|  | | 7p12.3 | 47200001 | 48010000 | AS2,AS4,AS7 | 30 | TNS3, HUS1 |
|  | | 7p12.2-12.1 | 50530001 | 51750000 | AS2,AS7 | 20 | GRB10 |
| 8 | | 8P11.22 | 37360001 | 39070000 | AS2,AS3,AS5,AS7 | 40 | ADAM9, BAG4, EIF4EBP1, **FGFR1**, GPR124, HTRA4, NSD3, PPAPDC1B, PROSC, RAB11FIP1, TACC1 |
|  | | 8q13.1 | 67320917 | 68343504 | AS2,AS3,AS4,AS5,AS7 | 50 | ARMC1,MYBL1,SGK3,CSPP1,COPS5 |
|  | | 8q13.3 | 70750001 | 71020000 | AS2,AS3,AS4,AS5,AS7 | 50 | PRDM14,NCOA2 |
|  | | 8q21.11 | 73902397 | 74954388 | AS2,AS3,AS4,AS5,AS7 | 50 | TERF1 |
|  | | 8q24.21 | 128671900 | 129171700 | AS2,AS3,AS4,AS5,AS7 | 50 | PVT1,MYC |
|  | | 8q24.21 | 131035000 | 131224400 | AS2,AS4,AS7 | 30 | ASAP1 |
| 12 | | 12p13.33-p13.31 | 150001 | 9130000 | AS2,AS3,AS5,AS7 | 40 | **CCND2**, **CHD4**, ERC1, KDM5A, TEAD4, RAD52, ACRBP, CDCA3, PTPN6, RAD51AP1, NANOG, WNT5B |
| 12q13.11-q13.13 | 48110001 | 54900000 | AS2,AS3,AS5,AS7 | 40 | ARF3, BCDIN3D, CCNT1, CERS5, FMNL3, GALNT6, HDAC7, ITGA5, MCRS1, NR4A1, PCBP2, **RAPGEF3**, RARG, SMAGP, TMBIM6 |
| 12q13.2-q14.1 | 56030001 | 58310000 | AS2,AS3,AS4,AS5,AS7 | 50 | CDK2, **CDK4**, **DDIT3**, DGKA, **ERBB3**, GLI1, ITGA7, MMP19, NABP2, PA2G4, RAB5B, SHMT2, STAT2, STAT6, TIMELESS, TSPAN31(SAS) |
| 12q14.1-q14.3 | 62810001 | 67700000 | AS2,AS4,AS5,AS7 | 40 | **HMGA2** |
| 12q15.1 | 68611133 | 70187177 | AS2,AS3,AS4,AS5,AS7 | 50 | **MDM2**, CPM, NUP107, RAP1B, SLC35E3, LYZ, FRS2, CCT2, YEATS4 |
| 12q23.3-q24.21 | 108970001 | 114480000 | AS2,AS3,AS5,AS7 | 40 | ALDH2, ANAPC7, **BRAP**, CORO1C, MAPKAPK5, PPP1CC, PTPN11, RPL6, SH2B3, TCTN1, TMEM119, TRPV4 |
| 12q24.21-q24.23 | 116670001 | 118970000 | AS2,AS3,AS5,AS7 | 40 | PEBP1, WSB2 |
| 12q24.23-q24.31 | 120080001 | 125670000 | AS2,AS3,AS4,AS5,AS7 | 50 | DENR, KDM2B, **MSI1**, PXN, RAB35, RNF34, SETD1B, SETD8, TRIAP1 |
| 12q24.33 | 128790001 | 133500000 | AS2,AS3,AS4,AS5,AS7 | 50 | DDX51, MMP17, **RAN**, ULK1 |
| 17 | | 17p13.3,p13.1 | 1 | 10300000 | AS2,AS4,AS5,AS7 | 40 | ARHGEF15, AURKB, C1QBP, DHX33, FAM57A, FBXO39, MINK1, NLRP1, NUP88, PELP1, RCVRN, RPAIN, SERPINF1, TAX1BP3, TRPV3, WDR16, WRAP53, **YWHAE** |
| 17p12,p11.2 | 15580001 | 21570000 | AS2,AS4,AS5,AS7 | 40 | ADORA2B, COPS3, EPN2, SHMT1, SPECC1, SREBF1, **TRPV2**, ULK2, USP22 |
| 17q12,q21.1 | 36290001 | 39850001 | AS2,AS4,AS7 | 30 | CDC6, CDK1, **ERBB2**, FBXL20, IGFBP4, KRT23, MIEN1, PIP4K2B, PLXDC1, RPL23, SMARCE1, TBC1D3, TNS4, TOP2A |
| 17q21.2 | 39850001 | 40530000 | AS2,AS4,AS5,AS7 | 40 | ACLY, **FKBP10**, LEPREL4, RAB5C, STAT3, STAT5A, STAT5B |
| 17q21.2,q21.31 | 40530001 | 43390000 | AS2,AS4,AS7 | 30 | ETV4, **HDAC5**, HSD17B1, KIF18B, NBR1, NMT1, RUNDC1, VAT1 |
| 17q21.32 | 45530001 | 46220000 | AS2,AS5 | 20 | CBX1, KPNB1, OSBPL7, SP2, CDK5RAP3 |
| 17q21.33 | 48060001 | 48410000 | AS1,AS2 | 20 | **ITGA3**, SAMD14, PDK2 |
| 17q22,q24.2 | 55450001 | 63200000 | AS2,AS5 | 20 | MSI2, **TRIM37**, APPBP2, BCAS3, BRIP1, CLTC, DDX5, GNA13, **MED13**, PPM1D, RPS6KB1, TBX2, TLK2, USP32, MAP3K3 |
| 17q23.2,q23.3 | 60710001 | 61220000 | AS1,AS2,AS5 | 30 | **MRC2** |
| 17q24.2 | 64620001 | 66440000 | AS2,AS5 | 20 | BPTF, **KPNA2**, PRKCA |
| 17q25.1,q25.3 | 70100001 | 81110000 | AS2,AS4,AS5,AS7 | 40 | MRPL58, RAB40B, SOX9, **BIRC5**, FOXK2, JMJD6, RAC3, TK1, TTYH2,USP36 |
| Frequently Lost | | | | | | | |
| 3 | 3p22.1-P21.1 | | 41110001 | 53310000 | AS3,AS6 | 20 | ACY1,ALS2CL,APEH,CISH,**CTNNB1**,CYB561D2,DAG1,**LIMD1**,MST1,PLXNB1,RASSF1,RNF123,SETD2,SMARCC1,TCTA,TMEM115,TUSC2,UBA7,USP4 |
| 3p21.1 | | 52420001 | 52670000 | AS2,AS3,AS5,AS6 | 40 | **BAP1**, NISCH, SEMA3G, PBRM1 |
| 3q13.31 | | 115230001 | 116910000 | AS5,AS6,AS8,AS9 | 40 | GAP43, LSAMP, LSAMP-AS1, TUSC7 |
| 3q22.3 | | 135730001 | 136370000 | AS5,AS6 | 20 | MSL2, STAG1 |
| 3q25.33,q26.1 | | 160390001 | 161120000 | AS3,AS5 | 20 | PPM1L |
| 9 | 9P23-22.3 | | 9530001 | 14800000 | AS5,AS6 | 20 | PTPRD, LURAP1L, MPDZ, **NFIB**, TYRP1 |
| 9  11 | 9p22.2-p22.1 | | 17680001 | 18890000 | AS5,AS6 | 20 | SH3GL2 |
| 9p22.1,p21.3 | | 19450001 | 23780000 | AS5,AS6 | 20 | **CDKN2A**, CDKN2B, MTAP |
| 9p21.1 | | 30900001 | 32870000 | AS5,AS6 | 20 | **NDUFB6** |
| 11q13.3-q22.3 | | 69360001 | 104810001 | AS5,AS6, | 20 | B3GNT6,**CCND1**,ENDOD1,**NUMA1**, USP35,UVRAG |
| 11 | 11q22.3-q23.3 | | 104810001 | 116180000 | AS4,AS5,AS6 | 30 | **ATM**,BCO2,BTG4,CUL5,**PPP2R1B**, SDHD, ZBTB16 |
| 11q23.3-q24.3, | | 120860001 | 127950000 | AS4,AS5,AS6 | 30 | BLID,EI24,HEPACAM,**TBRG1**,VWA5A,HEPN1 |

**Suppl Table 6 Immunohistochemistry analysis of selected oncogene/tumor suppressor genes product expression in Müllerian adenosarcoma**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | MAS | | EM | | | (MAS vs. EM) | (cervix vs. uterus vs. ovary) | |
| No Cases | 29 | | 8 | | |  |  |
| Markers | Median | Range (95% CI) | | Median | Range (95% CI) | P value | P value | | |
| ATM | 100 | 66-132 | | 80 | 38--137 | 0.89 | 0.86 | | |
| BAP1 | 100 | 93--168 | | 0 | 1--133 | 0.15 | 0.88 | | |
| BCL-2 | 100 | 46--121 | | 0 | 0-4 | **0.006** | 0.30 | | |
| CCND1 | 50 | 46--121 | | 0 | 3 | **0.002** | 0.21 | | |
| CDK4 | 30 | 42--107 | | 5 | 0--20 | **0.001** | 0.73 | | |
| EPAC | 140 | 90--186 | | 210 | 153--252 | 0.56 | 0.24 | | |
| ER | 100 | 68--123 | | 100 | 62--138 | **0.03** | 0.28 | | |
| ERBB3 | 100 | 95--182 | | 200 | 112--221 | 0.72 | 0.55 | | |
| FOPB1 | 200 | 182--250 | | 200 | 172--237 | 0.16 | 0.42 | | |
| HDGF | 50 | 13--79 | | 10 | 0--37 | 0.79 | 0.26 | | |
| HMGA2 | 10 | 9--21 | | 5 | 2--13 | **0.005** | 0.07 | | |
| Ki-67 | 100 | 74--132 | | 50 | 14--49 | **0.04** | 0.20 | | |
| KIF14 | 30 | 21--73 | | 0 | 17 | **<0.001** | 0.60 | | |
| MDM2 | 100 | 104--153 | | 160 | 60--168 | **0.02** | **0.05** | | |
| MSI1 | 50 | 27--104 | | 50 | 0-112 | 0.62 | 0.46 | | |
| MYOSIN X | 100 | 69--138 | | 50 | 14--88 | 0.79 | 0.26 | | |
| NDUFB6 | 150 | 123--199 | | 125 | 71--175 | 0.08 | **0.04** | | |
| NF1 | 200 | 129--199 | | 100 | 51-171 | 0.1 | 0.28 | | |
| NUMA | 300 | 231--282 | | 200 | 188--256 | 0.32 | 0.73 | | |
| PCO4 | 100 | 96--150 | | 100 | 95--172 | 0.17 | 0.69 | | |
| P16INK4a | 125 | 96--160 | | 50 | 4--96 | **0.04** | 0.17 | | |
| PP2A | 280 | 255--303 | | 267 | 228--305 | 0.37 | 0.37 | | |
| RAN | 170 | 138--200 | | 100 | 69--140 | 0.8 | 0.51 | | |
| YWHAE | 100 | 66-132 | | 80 | 38--137 | **0.006** | 0.91 | | |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  |  |  |  |  | 150 |

MAS: Müllerian adenosarcoma; EM: endometrium.

**Suppl Table 7 Frequent structure variation in Müllerian adenosarcoma**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Frequency | Case# | Breakend 1 Chrom | Breakend 1 Pos | Breakend 1 Gene Name | Breakend 2 Chrom | Breakend 2 Pos | Breakend 2 Gene Name | Breakend 1 Depth | Breakend 2 Depth |
| 2 | AS3,AS7 | chr1 | 17226400 | None | chr4 | 160898604 | None | 155 | 81 |
| 2 | AS5,AS7 | chr1 | 17784557 | None | chr2 | 210523447 | MAP2 | 105 | 99 |
| 2 | AS5.AS8 | chr1 | 88336599 | None | chr16 | 83666361 | CDH13 | 103 | 48 |
| 6 | AS3-5,AS8 | chr1 | 109494853 | CLCC1 | chr3 | 110413394 | None | 111 | 51 |
| 4 | AS1,AS2,AS4,AS9 | chr1 | 110191247 | None | chr3 | 155531847 | None | 111 | 47 |
| 6 | AS3-5,AS7,AS8,AS10 | chr1 | 121215018 | None | chr5 | 49771063 | None | 40 | 115 |
| 4 | AS2,AS5,AS6,AS8 | chr1 | 147855727 | None | chrX | 92418807 | None | 158 | 119 |
| 4 | AS5 | chr1 | 148928247 | None | chr2 | 91848017 | None | 200 | 84 |
| 6 | AS1,AS3,AS5,AS6-8 | chr1 | 149216152 | None | chr15 | 75867322 | PTPN9 | 205 | 146 |
| 2 | AS3,AS7 | chr1 | 163314432 | NUF2 | chr5 | 55384182 | None | 117 | 111 |
| 5 | AS3,AS5,AS6,AS8,AS10 | chr1 | 168024586 | DCAF6 | chr19 | 24033179 | ZNF254 | 111 | 55 |
| 3 | AS2,AS3,AS9 | chr1 | 168186489 | DCAF6 | chr3 | 53175885 | ZNF83 | 104 | 78 |
| 4 | AS1,AS4,AS5,AS7 | chr1 | 180903258 | KIAA1614 | chr3 | 48537167 | SHISA5 | 92 | 64 |
| 2 | AS6,AS10 | chr1 | 199440227 | None | chr5 | 33633345 | ADAMTS12 | 120 | 65 |
| 8 | AS2-8,AS10 | chr1 | 207579635 | None | chr6 | 57494241 | LOC100996486 | 95 | 169 |
| 5 | AS3,AS5,AS6,AS9,AS10 | chr1 | 214656661 | PTPN14 | chr5 | 115177797 | AP3S1 | 121 | 41 |
| 3 | AS3,AS6,AS7 | chr1 | 223293291 | TLR5 | chr5 | 54401983 | GZMA | 73 | 129 |
| 3 | AS3,AS4,AS7 | chr1 | 246565670 | SMYD3 | chr21 | 45327478 | AGPAT3 | 99 | 67 |
| 6 | AS2,AS4-8 | chr10 | 38908595 | None | chr22 | 16884260 | None | 28 | 176 |
| 4 | AS2,AS3,AS5,AS7 | chr10 | 42646416 | None | chr16 | 32097315 | None | 72 | 151 |
| 4 | AS1,AS3,AS4,AS5 | chr10 | 55983281 | PCDH15 | chr13 | 66704573 | None | 94 | 118 |
| 3 | AS4,AS5,AS7 | chr10 | 117006340 | ATRNL1 | chrX | 128670972 | None | 119 | 117 |
| 6 | AS1-3,AS5,AS8,AS10 | chr11 | 61841813 | None | chr14 | 81786774 | STON2 | 111 | 80 |
| 2 | AS7,AS8 | chr11 | 108585748 | DDX10 | chr13 | 21750661 | SKA3 | 82 | 129 |
| 2 | AS3,AS8 | chr12 | 14476864 | None | chrX | 38058552 | SRPX | 45 | 105 |
| 2 | AS5,AS8 | chr13 | 21490883 | None | chr17 | 7711989 | DNAH2 | 71 | 129 |
| 5 | AS1,AS3,AS4,AS7,AS8,AS10 | chr13 | 35686543 | NBEA | chr15 | 20873307 | None | 71 | 179 |
| 8 | AS1-4,AS6,AS8-10 | chr13 | 63621212 | None | chr17 | 21666609 | None | 156 | 67 |
| 10 | AS1-10 | chr13 | 63649022 | None | chr20 | 26149746 | None | 132 | 135 |
| 4 | AS3,AS6,AS7,AS10 | chr13 | 90550561 | None | chr15 | 52589547 | None | 103 | 115 |
| 3 | AS1,AS3,S4,AS9 | chr14 | 20301314 | None | chr15 | 22419158 | None | 123 | 56 |
| 2 | AS3,AS4 | chr14 | 106484215 | IGH | chr15 | 22486776 | LOC642131 | 106 | 71 |
| 4 | AS1.AS6,AS9,AS10 | chr15 | 20000101 | None | chr21 | 14345806 | None | 138 | 118 |
| 5 | AS3,AS4,AS7,AS9,AS10 | chr15 | 20014813 | None | chr21 | 14362821 | None | 187 | 162 |
| 8 | AS3,AS8,AS10 | chr15 | 20015855 | None | chr21 | 14363011 | None | 113 | 136 |
| 3 | AS3,AS4,AS7 | chr15 | 20452695 | RHPN2P1 | chr16 | 33406290 | None | 183 | 139 |
| 4 | AS4,AS5,AS8,AS9 | chr15 | 20470698 | RHPN2P1 | chr19 | 33506264 | None | 130 | 134 |
| 5 | AS3-5,AS8,AS9 | chr17 | 21525277 | None | chr20 | 26106896 | None | 188 | 112 |
| 9 | AS1,AS2, AS3-10 | chr19 | 19632427 | NDUFA13 | chr22 | 16347241 | NF1P6 | 122 | 93 |
| 7 | AS2,AS3,AS5-10 | chr2 | 13534907 | None | chr15 | 20609640 | None | 147 | 119 |
| 7 | AS2,AS3,AS5,AS6,AS8,AS10 | chr2 | 13534941 | None | chr15 | 20609594 | None | 111 | 63 |
| 7 | AS1,AS2,AS4-6,AS8,AS9 | chr2 | 13535013 | None | chr15 | 20609591 | None | 111 | 65 |
| 2 | AS3,AS7 | chr2 | 54111546 | PSME4 | chr14 | 40317376 | None | 112 | 79 |
| 5 | AS1-6 | chr2 | 71668034 | None | chr14 | 98494391 | None | 106 | 88 |
| 3 | AS2,AS5,AS10 | chr2 | 78091920 | None | chr4 | 174044215 | None | 123 | 100 |
| 2 | AS3,AS8 | chr2 | 91634988 | LOC101060169 | chr10 | 42645482 | None | 151 | 150 |
| 2 | AS9,AS10 | chr2 | 91694630 | None | chr22 | 17041903 | None | 157 | 85 |
| 4 | AS4-6,AS8 | chr2 | 117853382 | None | chr10 | 3138988 | PFKP | 100 | 54 |
| 2 | AS7,AS8 | chr2 | 132800294 | None | chr17 | 25285558 | None | 124 | 191 |
| 2 | AS4,AS5 | chr2 | 133011818 | None | chr16 | 33964361 | None | 166 | 177 |
| 4 | AS1,AS2,AS7,AS8 | chr2 | 242634320 | None | chr5 | 139347431 | NRG2 | 75 | 109 |
| 2 | AS2,AS3 | chr2 | 243052365 | LOC728323 | chr8 | 376926 | FBXO25 | 153 | 53 |
| 10 | AS1-10 | chr20 | 11281556 | None | chrX | 81651368 | None | 56 | 116 |
| 2 | AS7,AS10 | chr20 | 26252024 | None | chr22 | 17239016 | None | 105 | 105 |
| 3 | AS5-8 | chr3 | 49218384 | C3orf84 | chrX | 32001083 | DMD | 79 | 100 |
| 7 | AS3,AS4,AS7-10 | chr3 | 75994837 | ROBO2 | chr20 | 26203323 | None | 147 | 197 |
| 7 | AS1-5,AS7,AS9 | chr3 | 144687884 | None | chr22 | 18047371 | SLC25A18 | 114 | 60 |
| 3 | AS4-6 | chr3 | 151086531 | MED12L | chr12 | 118571033 | None | 80 | 61 |
| 8 | AS1-6,AS8,AS9 | chr3 | 151148544 | MED12L | chr5 | 39787751 | None | 59 | 133 |
| 2 | AS2,AS6 | chr4 | 33837359 | None | chr7 | 57608379 | None | 145 | 121 |
| 4 | AS5,AS6,AS8,AS10 | chr4 | 33837543 | None | chr20 | 26145998 | None | 115 | 109 |
| 3 | AS8-10 | chr4 | 33839916 | None | chr7 | 57610959 | None | 195 | 164 |
| 2 | AS1,AS4 | chr4 | 33857884 | None | chr20 | 26129184 | None | 97 | 113 |
| 5 | AS3,AS4,AS5,AS9,AS10 | chr4 | 33859622 | None | chr20 | 26128596 | None | 128 | 148 |
| 6 | AS2-5,AS7,AS10 | chr4 | 175884836 | ADAM29 | chr7 | 62473468 | None | 112 | 140 |
| 2 | AS3.AS6 | chr4 | 190897122 | None | chr9 | 141081917 | None | 130 | 148 |
| 4 | AS3,AS6-8 | chr5 | 5595243 | None | chr15 | 52589532 | None | 88 | 145 |
| 8 | AS1-3,AS5-7,AS9,AS10 | chr5 | 21573432 | GUSBP1 | chr6 | 57575919 | None | 77 | 120 |
| 2 | AS7,AS8 | chr5 | 39787751 | None | chr9 | 91774009 | SHC3 | 123 | 52 |
| 3 | AS2,AS3,AS10 | chr5 | 54402018 | GZMA | chr11 | 37466540 | None | 103 | 39 |
| 3 | AS4,AS7,AS8 | chr5 | 55931840 | None | chr6 | 57444972 | LOC100996481 | 66 | 160 |
| 8 | AS2-4,AS6-10 | chr5 | 141456960 | None | chr13 | 82367698 | None | 120 | 69 |
| 3 | AS2,AS5,AS7 | chr5 | 176753871 | None | chr7 | 157149907 | DNAJB6 | 129 | 48 |
| 7 | AS2-4,AS6,AS7,AS9,AS10 | chr6 | 382459 | None | chr16 | 33428528 | None | 117 | 101 |
| 3 | AS1,AS2,AS5 | chr6 | 147371567 | STXBP5-AS1 | chr19 | 13848429 | CCDC130 | 115 | 68 |
| 2 | AS7,AS8 | chr7 | 682398 | PRKAR1B | chr8 | 127865467 | None | 89 | 104 |
| 8 | AS2-8,AS10 | chr7 | 6616907 | None | chr9 | 132621533 | USP20 | 104 | 51 |
| 7 | AS2-8 | chr7 | 26241365 | CBX3 | chr15 | 40854180 | C15orf57 | 102 | 103 |
| 6 | AS2-6,AS8 | chr7 | 26252971 | CBX3 | chr15 | 40854194 | C15orf57 | 48 | 103 |
| 6 | AS1,AS6-10 | chr7 | 57606290 | None | chr13 | 63637902 | None | 105 | 179 |
| 7 | AS1-5,AS8,AS10 | chr7 | 57608639 | None | chr20 | 26145943 | None | 106 | 151 |
| 10 | AS1-10 | chr7 | 57638746 | None | chr17 | 21515211 | None | 148 | 91 |
| 2 | AS5,AS9 | chr7 | 57638967 | None | chr17 | 20772250 | CCDC144NL | 145 | 119 |
| 3 | AS4-6 | chr7 | 57706901 | None | chr20 | 25834871 | None | 100 | 121 |
| 7 | AS2-4,AS7 | chr7 | 57729226 | None | chr20 | 26248049 | None | 114 | 156 |
| 7 | AS6,AS7,AS9,AS10 | chr7 | 57730253 | None | chr20 | 25864477 | None | 118 | 108 |
| 4 | AS6,AS7,AS9,AS10 | chr7 | 57732769 | None | chr20 | 26244216 | None | 180 | 105 |
| 6 | AS1,AS8-10 | chr7 | 61891240 | None | chr16 | 32543549 | None | 122 | 82 |
| 6 | AS5,AS8,AS9 | chr7 | 61891341 | None | chr16 | 32543415 | None | 95 | 168 |
| 4 | AS2,AS3,AS5,AS6 | chr7 | 103814591 | ORC5 | chr12 | 40832785 | MUC19 | 142 | 98 |
| 4 | AS3,AS4,AS5,AS10 | chr7 | 105133270 | PUS7 | chr8 | 73095161 | None | 101 | 65 |
| 4 | AS3,AS5,AS7,AS10 | chr7 | 134901829 | None | chrX | 112537121 | LOC101928437 | 108 | 35 |
| 2 | AS5,AS8 | chr7 | 142475377 | TRB | chr9 | 33802794 | LOC101929665 | 104 | 81 |
| 4 | AS1,AS5,AS7,AS10 | chr7 | 148102947 | CNTNAP2 | chr17 | 21522349 | None | 67 | 173 |
| 4 | AS5,AS8,AS9,AS10 | chr7 | 151982283 | KMT2C | chr21 | 11069677 | BAGE2 | 140 | 187 |