| mature          | structure       | chromoso | start       | stop       | strand |
|-----------------|-----------------|----------|-------------|------------|--------|
| p-hsa-miR-247   | novelmirna     | chr14    | 16057606    | 16057624   | +      |
| hsa-let-7a-5p   | miRNA          | chr22    | 46112752    | 46112773   | +      |
| hsa-miR-143-3p  | miRNA          | chr5     | 1.49E+08    | 1.49E+08   | +      |
| hsa-miR-142-5p  | miRNA          | chr17    | 58331283    | 58331303   | -      |
| hsa-miR-6823-3p | miRNA          | chr3     | 48549961    | 48549981   | -      |
| hsa-miR-660-5p  | miRNA          | chrX     | 50013256    | 50013277   | +      |
| hsa-miR-5096    | miRNA          | chr4     | 78820764    | 78820784   | +      |
| hsa-miR-140-3p  | miRNA          | chr16    | 69933142    | 69933162   | +      |
| hsa-miR-1246    | miRNA          | chr2     | 1.77E+08    | 1.77E+08   | -      |
| hsa-miR-423-3p  | miRNA          | chr17    | 30117131    | 30117153   | +      |
| hsa-miR-143-3p  | miRNA          | chr3     | 1.84E+08    | 1.84E+08   | +      |
| hsa-miR-181a-2-3p| miRNA        | chr9     | 95085505    | 95085525   | +      |
| hsa-miR-619-5p  | miRNA          | chr12    | 1.09E+08    | 1.09E+08   | -      |
| hsa-miR-1307-5p | miRNA          | chr10    | 94178841    | 94178862   | +      |
| hsa-miR-3182    | miRNA          | chr16    | 83508349    | 83508365   | +      |
| hsa-miR-24-3p   | miRNA          | chr19    | 13836289    | 13836310   | -      |
| hsa-let-7d-5p   | miRNA          | chr9     | 45200958    | 45200979   | -      |
| hsa-miR-6124    | miRNA          | chr11    | 12163692    | 12163711   | +      |
| hsa-miR-98-5p   | miRNA          | chr20    | 63919914    | 63919936   | +      |
| hsa-let-7d-3p   | miRNA          | chr9     | 52268336    | 52268357   | +      |
| hsa-miR-183-5p  | miRNA          | chr3     | 35744527    | 35744547   | +      |
| hsa-miR-106b-3p | miRNA          | chr7     | 1E+08       | 1E+08      | -      |
| hsa-miR-151a-5p | miRNA          | chr8     | 1.41E+08    | 1.41E+08   | -      |
| hsa-miR-144-3p  | miRNA          | chr17    | 28861583    | 28861604   | -      |
| hsa-miR-1307-5p | miRNA          | chr10    | 1.03E+08    | 1.03E+08   | -      |
| hsa-miR-29b-3p  | miRNA          | chr6     | 2.08E+08    | 2.08E+08   | -      |
| hsa-miR-183-5p  | miRNA          | chr3     | 91350797    | 91350819   | +      |
| hsa-miR-142-3p  | miRNA          | chr17    | 28861548    | 28861567   | -      |
| hsa-miR-19b-3p  | miRNA          | chr3     | 1.34E+08    | 1.34E+08   | -      |
| hsa-miR-21-5p   | miRNA          | chr17    | 59841273    | 59841294   | +      |
| hsa-miR-30e-5p  | miRNA          | chr3     | 40754371    | 40754392   | +      |
| hsa-miR-151a-5p | miRNA          | chr8     | 1.41E+08    | 1.41E+08   | -      |
| hsa-let-7d-3p   | miRNA          | chr9     | 94178895    | 94178916   | +      |
| hsa-miR-23a-3p  | miRNA          | chr19    | 13836595    | 13836615   | -      |
| hsa-miR-941     | miRNA          | chr20    | 63919914    | 63919936   | +      |
| hsa-miR-4497    | miRNA          | chr12    | 1.1E+08     | 1.1E+08    | +      |
| hsa-miR-185-5p  | miRNA          | chr22    | 20033153    | 20033174   | +      |
| hsa-miR-16-2-3p | miRNA          | chr3     | 1.6E+08     | 1.6E+08    | +      |
| hsa-let-7i-5p   | miRNA          | chr12    | 62603691    | 62603712   | +      |
| hsa-let-7i-3p   | miRNA          | chr12    | 62603747    | 62603768   | +      |
| p-hsa-miR-113   | novelmirna     | chr2     | 2.32E+08    | 2.32E+08   | +      |
| hsa-miR-98-5p   | miRNA          | chr19    | 53556299    | 53556320   | -      |
| hsa-miR-340-5p  | miRNA          | chr5     | 1.8E+08     | 1.8E+08    | -      |
| hsa-miR-128-3p  | miRNA          | chr3     | 35744527    | 35744547   | +      |
| hsa-miR-3609    | miRNA          | chr7     | 98881700    | 98881723   | +      |
| hsa-miR-106b-5p | miRNA          | chr7     | 1E+08       | 1E+08      | -      |
| hsa-miR-26b-5p  | miRNA          | chr2     | 2.18E+08    | 2.18E+08   | +      |
| hsa-miR-144-3p  | miRNA          | chr17    | 28861548    | 28861567   | -      |
| hsa-miR-20b-5p  | miRNA          | chrX     | 1.34E+08    | 1.34E+08   | -      |
| hsa-miR-21-5p   | miRNA          | chr17    | 59841273    | 59841294   | +      |
| hsa-miR-30e-5p  | miRNA          | chr1     | 40754371    | 40754392   | +      |
| hsa-miR-3960    | miRNA          | chr9     | 1.28E+08    | 1.28E+08   | +      |
| hsa-miR-151a-5p | miRNA          | chr8     | 1.41E+08    | 1.41E+08   | -      |
| hsa-miR-103     | novelmirna     | chr20    | 30514127    | 30514150   | -      |
| hsa-miR-4497    | miRNA          | chr12    | 1.1E+08     | 1.1E+08    | +      |
| hsa-miR-142-3p  | miRNA          | chr17    | 58331245    | 58331267   | -      |
| hsa-miR-183-5p  | miRNA          | chr7     | 1.3E+08     | 1.3E+08    | -      |
| miRNA       | Type     | Chromosome | start Position | end Position | strand |
|-------------|----------|------------|----------------|--------------|--------|
| hsa-miR-148a-3p | miRNA    | chr7       | 25949922       | 25949943     | -      |
| hsa-miR-324-3p  | miRNA    | chr17      | 7223308        | 7223327      | -      |
| hsa-miR-221-3p  | miRNA    | chrX       | 45746180       | 45746202     | -      |
| hsa-miR-10a-5p  | miRNA    | chr17      | 48579904       | 48579926     | -      |
| hsa-miR-374a-5p | miRNA    | chrX       | 74287325       | 74287346     | -      |
| hsa-miR-151a-3p | miRNA    | chr8       | 1,41E+08       | 1,41E+08     | +      |
| hsa-miR-192-3p  | miRNA    | chr17      | 64891159       | 64891180     | -      |
| hsa-miR-744-5p  | miRNA    | chr17      | 12081909       | 12081930     | +      |
| hsa-miR-7641   | miRNA    | chr14      | 75604211       | 75604229     | +      |
| hsa-miR-4732-3p | miRNA    | chr11      | 28861668       | 28861688     | -      |
| hsa-miR-4248    | miRNA    | chr7       | 73711327       | 73711344     | +      |
| hsa-miR-194-5p  | miRNA    | chr11      | 64891404       | 64891425     | -      |
| hsa-miR-92b-3p  | miRNA    | chr1       | 1,55E+08       | 1,55E+08     | +      |
| hsa-miR-192-5p  | miRNA    | chr11      | 64891203       | 64891223     | -      |
| hsa-miR-4508   | miRNA    | chr15      | 23562107       | 23562123     | -      |
| hsa-miR-5585-3p | miRNA    | chr1       | 32086986       | 32087007     | +      |
| hsa-miR-100-5p  | miRNA    | chr11      | 1,22E+08       | 1,22E+08     | -      |
| hsa-miR-1248   | miRNA    | chr3       | 1,87E+08       | 1,87E+08     | +      |
| hsa-miR-6073   | miRNA    | chr11      | 15969555       | 15969574     | -      |
| hsa-miR-126-5p  | miRNA    | chr9       | 1,37E+08       | 1,37E+08     | +      |
| hsa-miR-409-3p  | miRNA    | chr9       | 1,37E+08       | 1,37E+08     | +      |
| hsa-miR-17-5p  | miRNA    | chr13      | 91350618       | 91350640     | +      |
| hsa-miR-1273e  | miRNA    | chr17      | 64425136       | 64425157     | -      |
| hsa-miR-18a-5p  | miRNA    | chr13      | 91350756       | 91350778     | +      |
| hsa-miR-15a-5p  | miRNA    | chr13      | 50049167       | 50049188     | -      |
| hsa-miR-29c-3p  | miRNA    | chr3       | 2,08E+08       | 2,08E+08     | -      |
| hsa-miR-425-5p  | miRNA    | chr3       | 49020199       | 49020221     | -      |
| hsa-miR-424-5p  | miRNA    | chrX       | 1,35E+08       | 1,35E+08     | -      |
| hsa-miR-374a-3p | miRNA    | chrX       | 74287295       | 74287316     | -      |
| p-hsa-miR-335  | novelmirn | chr7       | 1,19E+08       | 1,19E+08     | -      |
| hsa-miR-30a-5p  | miRNA    | chr6       | 71403595       | 71403616     | -      |
| hsa-miR-3607-5p | miRNA    | chr5       | 86620508       | 86620529     | +      |
| p-hsa-miR-6  | novelmirn | chr10      | 42997630       | 42997651     | +      |
| hsa-miR-21-3p  | miRNA    | chr17      | 59841311       | 59841331     | +      |
| hsa-miR-210-3p  | miRNA    | chr11      | 5681122         | 5681332      | -      |
| hsa-miR-106a-5p | miRNA    | chrX       | 1,34E+08       | 1,34E+08     | -      |
| hsa-miR-652-3p  | miRNA    | chrX       | 1,1E+08        | 1,1E+08      | +      |
| hsa-miR-330    | novelmirn | chr7       | 1,49E+08       | 1,49E+08     | +      |
| hsa-miR-411-5p  | miRNA    | chr14      | 1,01E+08       | 1,01E+08     | +      |
| hsa-miR-502-3p  | miRNA    | chrX       | 50014649       | 50014670     | +      |
| hsa-miR-7704   | miRNA    | chr2       | 1,76E+08       | 1,76E+08     | +      |
| hsa-miR-3607-3p | miRNA    | chr5       | 86620547       | 86620566     | +      |
| hsa-miR-5100   | miRNA    | chr10      | 42997630       | 42997651     | +      |
| hsa-miR-339-3p  | miRNA    | chr7       | 10229552       | 10229772     | -      |
| hsa-miR-363-3p  | miRNA    | chrX       | 1,34E+08       | 1,34E+08     | -      |
| hsa-miR-139-5p  | miRNA    | chr11      | 72615102       | 72615124     | -      |
| p-hsa-miR-6   | novelmirn | chr10      | 1,02E+08       | 1,02E+08     | +      |
| hsa-miR-223-5p  | miRNA    | chrX       | 66018895       | 66018916     | +      |
| hsa-miR-15b-3p  | miRNA    | chr3       | 1,6E+08        | 1,6E+08      | +      |
| hsa-miR-16-5p  | miRNA    | chr3       | 1,6E+08        | 1,6E+08      | +      |
| ID               | Type      | Chromosome | Start | End   | Direction |
|------------------|-----------|------------|-------|-------|-----------|
| hsa-miR-532-5p   | miRNA     | chrX       | 50003167 | 50003188 | +         |
| hsa-miR-4286     | miRNA     | chr8       | 10666988 | 10667004 | +         |
| hsa-miR-29a-3p   | miRNA     | chr7       | 1.31E+08 | 1.31E+08 | -         |
| hsa-miR-3613-5p  | miRNA     | chr13      | 49996465 | 49996486 | -         |
| hsa-miR-196b-5p  | miRNA     | chr7       | 27169528 | 27169549 | -         |
| p-hsa-miR-232    | novelmiRNA| chr10      | 1.28E+08 | 1.28E+08 | +         |
| hsa-miR-20a-5p   | miRNA     | chr13      | 91351072 | 91351094 | +         |
| hsa-miR-4485-3p  | miRNA     | chr11      | 10508277 | 10508296 | -         |
| hsa-miR-26b-3p   | miRNA     | chr2       | 2.18E+08 | 2.18E+08 | +         |
| hsa-miR-30b-5p   | miRNA     | chr8       | 1.35E+08 | 1.35E+08 | -         |
| hsa-miR-1260b    | miRNA     | chr11      | 96341447 | 96341465 | +         |
| hsa-miR-3141     | miRNA     | chr5       | 1.55E+08 | 1.55E+08 | -         |
| hsa-miR-130a-3p  | miRNA     | chr11      | 57641252 | 57641273 | +         |
| hsa-miR-486-5p   | miRNA     | chr8       | 41660444 | 41660465 | +         |
| hsa-miR-99b-5p   | miRNA     | chr19      | 51692618 | 51692639 | +         |
| hsa-miR-451b     | miRNA     | chr17      | 28861377 | 28861398 | +         |
| hsa-miR-134-5p   | miRNA     | chr14      | 1.01E+08 | 1.01E+08 | +         |
| hsa-miR-342-5p   | miRNA     | chr14      | 1E+08   | 1E+08  | +         |
| hsa-miR-126-3p   | miRNA     | chr9       | 1.37E+08 | 1.37E+08 | +         |
| hsa-miR-181a-5p  | miRNA     | chr1       | 1.99E+08 | 1.99E+08 | +         |
| hsa-miR-6087     | miRNA     | chrX       | 1.09E+08 | 1.09E+08 | +         |
| hsa-miR-378a-3p  | miRNA     | chr5       | 1.5E+08  | 1.5E+08 | +         |
| hsa-miR-181c-5p  | miRNA     | chr19      | 13874725 | 13874746 | +         |
| hsa-miR-3653-5p  | miRNA     | chr22      | 29333226 | 29333245 | -         |
| hsa-miR-574-3p   | miRNA     | chr4       | 38868092 | 38868113 | +         |
| hsa-miR-27a-3p   | miRNA     | chr19      | 13836447 | 13836467 | -         |
| hsa-miR-30d-5p   | miRNA     | chr8       | 1.35E+08 | 1.35E+08 | -         |
| hsa-miR-942-5p   | miRNA     | chr1       | 1.17E+08 | 1.17E+08 | +         |
| hsa-miR-1273h-5p | miRNA     | chr16      | 24203148 | 24203168 | +         |
| hsa-miR-425-3p   | miRNA     | chr3       | 49020159 | 49020180 | -         |
| hsa-miR-1307-3p  | miRNA     | chr10      | 1.03E+08 | 1.03E+08 | -         |
| hsa-miR-221-5p   | miRNA     | chrX       | 45746221 | 45746242 | -         |
| hsa-miR-148b-5p  | miRNA     | chr12      | 54337240 | 54337261 | +         |
| hsa-miR-24-2-5p  | miRNA     | chr19      | 13836326 | 13836347 | -         |
| p-hsa-miR-338    | novelmiRNA| chr17      | 81346226 | 81346245 | -         |
| hsa-miR-301a-3p  | miRNA     | chr17      | 59151149 | 59151171 | -         |
| hsa-miR-28-5p    | miRNA     | chr3       | 1.89E+08 | 1.89E+08 | +         |
| hsa-miR-331-3p   | miRNA     | chr12      | 95308480 | 95308500 | +         |
| hsa-miR-582-5p   | miRNA     | chr5       | 59703666 | 59703688 | -         |
| hsa-miR-30c-5p   | miRNA     | chr1       | 40757300 | 40757322 | +         |
| hsa-miR-125a-5p  | miRNA     | chr19      | 51693268 | 51693291 | +         |
| hsa-miR-328-3p   | miRNA     | chr16      | 67202327 | 67202348 | -         |
| hsa-miR-3653-3p  | miRNA     | chr22      | 29333176 | 29333193 | -         |
| p-hsa-miR-225    | novelmiRNA| chr3       | 1.64E+08 | 1.64E+08 | -         |
| hsa-miR-574-5p   | miRNA     | chr4       | 38868056 | 38868078 | +         |
| hsa-miR-345-5p   | miRNA     | chr14      | 1E+08   | 1E+08  | +         |
| hsa-miR-150-5p   | miRNA     | chr19      | 49500832 | 49500853 | -         |
| hsa-miR-4732-5p  | miRNA     | chr17      | 28861700 | 28861722 | -         |
| hsa-miR-3184-5p  | miRNA     | chr17      | 30117128 | 30117151 | -         |
| hsa-miR-664a-3p  | miRNA     | chr1       | 2.2E+08  | 2.2E+08 | -         |
| hsa-miR-502-5p   | miRNA     | chrX       | 50014613 | 50014633 | +         |
| hsa-miR-7-1-3p   | miRNA     | chr9       | 83969771 | 83969792 | -         |
| hsa-miR-130b-3p  | miRNA     | chr22      | 21653354 | 21653375 | +         |
| hsa-miR-339-5p   | miRNA     | chr7       | 1022990 | 1023012 | -         |
| hsa-miR-629-5p   | miRNA     | chr15      | 70079427 | 70079447 | -         |
| ID          | Type     | Chromosome | Start | End   | Strand |
|-------------|----------|------------|-------|-------|--------|
| hsa-miR-4454 | miRNA    | chr4       | 1.63E+08 | 1.63E+08 | -      |
| hsa-miR-190a-5p | miRNA    | chr15      | 62823971 | 62823992 | +      |
| hsa-miR-324-5p | miRNA    | chr17      | 7223342  | 7223364  | -      |
| hsa-miR-1294  | miRNA    | chr5       | 1.54E+08 | 1.54E+08 | +      |
| hsa-miR-1304-3p | miRNA    | chr11      | 93733691 | 93733712 | -      |
| hsa-miR-33b-5p | miRNA    | chr8       | 41660486 | 41660506 | +      |
| hsa-miR-148b-3p | miRNA    | chr12      | 54337278 | 54337299 | +      |
| hsa-miR-4686-3p | miRNA    | chr22      | 30731610 | 30731631 | +      |
| hsa-miR-136-3p | miRNA    | chr14      | 1.01E+08 | 1.01E+08 | +      |
| hsa-miR-361-3p | miRNA    | chrX       | 85903641 | 85903663 | -      |
| hsa-miR-181c-3p | miRNA    | chr19      | 13874763 | 13874784 | +      |
| hsa-miR-2355-5p | miRNA    | chr2       | 2.07E+08 | 2.07E+08 | -      |
| hsa-miR-7706  | miRNA    | chr15      | 85380639 | 85380662 | +      |
| hsa-miR-454-5p | miRNA    | chr17      | 59137828 | 59137849 | -      |
| hsa-miR-5701  | miRNA    | chrX       | 50009735 | 50009756 | +      |
| p-hsa-miR-105 | novelmiRN| chr3       | 21372996 | 21373013 | +      |
| hsa-miR-501-5p | miRNA    | chrX       | 50009772 | 50009793 | +      |
| hsa-miR-1972  | miRNA    | chr4       | 1.16E+08 | 1.16E+08 | +      |
| miRNA         | chr  | start_position   | end_position   | strand |
|--------------|------|-----------------|----------------|--------|
| hsa-miR-454-3p | chr17 | 59137787         | 59137809       | -      |
| hsa-miR-3620-5p | chr1  | 2.28E+08          | 2.28E+08       | +      |
| hsa-miR-424-3p | chrX  | 1.35E+08          | 1.35E+08       | -      |
| hsa-miR-545-5p | chrX  | 74287164          | 74287185       | -      |
| hsa-miR-1285-3p | chr2  | 70252933          | 70252954       | -      |
| hsa-miR-152-3p | chr17 | 48037174          | 48037194       | -      |
| hsa-miR-4326 | chr20 | 63286818          | 63286837       | +      |
| hsa-miR-374b-3p | chrX  | 1167160           | 1167181        | +      |
| hsa-miR-484  | chr16 | 15643301          | 15643322       | +      |
| hsa-miR-181d-5p | chr19 | 13874910          | 13874932       | +      |
| hsa-miR-331-5p | chr12 | 95308445          | 95308466       | +      |
| hsa-miR-370-3p | chr14 | 1.01E+08          | 1.01E+08       | +      |
| hsa-miR-379-5p | chr14 | 1.01E+08          | 1.01E+08       | +      |
| hsa-miR-4668-5p | chrX  | 50008443          | 50008465       | +      |
| hsa-miR-3173-5p | chr13 | 91350655          | 91350676       | +      |
| hsa-miR-500a-5p | chr9  | 1.09E+08          | 1.09E+08       | -      |
| hsa-miR-103a-2-5p | chr14 | 3917504           | 3917526        | +      |
| hsa-miR-301b-3p | chr22 | 21653025          | 21653047       | +      |
| hsa-miR-369-3p | chr14 | 1.01E+08          | 1.01E+08       | +      |
| hsa-miR-335-5p | chr7  | 1.3E+08           | 1.3E+08        | +      |
| hsa-miR-542-3p | chrX  | 1.35E+08          | 1.35E+08       | -      |
| hsa-miR-370-3p | chr14 | 1.01E+08          | 1.01E+08       | +      |
| hsa-miR-379-5p | chr14 | 1.01E+08          | 1.01E+08       | +      |
| hsa-miR-4668-5p | chr9  | 1.12E+08          | 1.12E+08       | +      |
| hsa-miR-3173-5p | chr13 | 91350655          | 91350676       | +      |
| hsa-miR-500a-5p | chr9  | 1.09E+08          | 1.09E+08       | -      |
| hsa-miR-103a-2-5p | chr14 | 3917504           | 3917526        | +      |
| hsa-miR-301b-3p | chr22 | 21653025          | 21653047       | +      |
| hsa-miR-369-3p | chr14 | 1.01E+08          | 1.01E+08       | +      |
| hsa-miR-335-5p | chr7  | 1.3E+08           | 1.3E+08        | +      |
| hsa-miR-320b | chr1  | 2.24E+08          | 2.24E+08       | -      |
| hsa-miR-17-3p | chr13 | 91350655          | 91350676       | +      |
| hsa-miR-3173-5p | chr14 | 95137961          | 95137982       | -      |
| hsa-miR-8485 | chr2  | 50696172          | 50696192       | -      |
| hsa-miR-3651 | chr9  | 92292461          | 92292484       | -      |
| hsa-miR-6734-5p | chr1  | 43364688          | 43364710       | -      |
| hsa-miR-1299 | chr9  | 40929010          | 40929031       | -      |
| hsa-miR-1304-5p | chr11 | 93733724          | 93733745       | -      |
| hsa-miR-5001-3p | chr2  | 2.33E+08          | 2.33E+08       | -      |
| hsa-miR-495-3p | chr14 | 1.01E+08          | 1.01E+08       | +      |
| hsa-miR-651-5p | chrX  | 8126980           | 8127001        | +      |
| hsa-miR-25-3p | chr7  | 1E+08             | 1E+08          | -      |
| hsa-miR-362-5p | chrX  | 50008968          | 50008991       | +      |
| hsa-miR-548f-5p | chr10 | 54607926          | 54607947       | -      |
| p-hsa-miR-9 | novelmirna | chr10 | 31551106      | 31551126 |
| hsa-miR-378a-5p | chr2  | 1.5E+08           | 1.5E+08        | +      |
| hsa-miR-382-5p | chr14 | 1.01E+08          | 1.01E+08       | +      |
| hsa-miR-3656 | chr11 | 1.19E+08          | 1.19E+08       | +      |
| hsa-miR-1301-3p | chr2  | 25328651          | 25328674       | -      |
| hsa-miR-487b-3p | chr14 | 1.01E+08          | 1.01E+08       | +      |
| p-hsa-miR-135 | novelmirna | chr10 | 61012641      | 61012659 |
| hsa-miR-4781-3p | chr1  | 54054124          | 54054145       | +      |
| miRNA  | Chromosome | Start Position | End Position | Strand |
|--------|------------|----------------|--------------|--------|
| hsa-miR-15a-3p | chr13 | 50049130 | 50049151 | - |
| hsa-miR-18b-5p | chrX | 1.34E+08 | 1.34E+08 | + |
| hsa-miR-361-5p | chrX | 85903681 | 85903702 | - |
| hsa-miR-3143 | chr6 | 27147629 | 27147653 | + |
| p-hsa-miR-124 | chr22_KI270733v1_random | 167965 | 167985 | + |
| hsa-miR-493-5p | chr14 | 1.01E+08 | 1.01E+08 | + |
| hsa-miR-548at-5p | chr17 | 42494773 | 42494794 | + |
| hsa-miR-3127-5p | chr2 | 96798298 | 96798310 | - |
| hsa-miR-3143 | chr6 | 27147629 | 27147653 | + |
| p-hsa-miR-124 | chr22_KI270733v1_random | 167965 | 167985 | + |
| hsa-miR-493-5p | chr14 | 1.01E+08 | 1.01E+08 | + |
| hsa-miR-548at-5p | chr17 | 42494773 | 42494794 | + |
| hsa-miR-3127-5p | chr2 | 96798298 | 96798310 | - |
| hsa-miR-3143 | chr6 | 27147629 | 27147653 | + |
| p-hsa-miR-124 | chr22_KI270733v1_random | 167965 | 167985 | + |
| hsa-miR-493-5p | chr14 | 1.01E+08 | 1.01E+08 | + |
| hsa-miR-548at-5p | chr17 | 42494773 | 42494794 | + |
| hsa-miR-3127-5p | chr2 | 96798298 | 96798310 | - |
| hsa-miR-3143 | chr6 | 27147629 | 27147653 | + |
| p-hsa-miR-124 | chr22_KI270733v1_random | 167965 | 167985 | + |
| hsa-miR-493-5p | chr14 | 1.01E+08 | 1.01E+08 | + |
| hsa-miR-548at-5p | chr17 | 42494773 | 42494794 | + |
| hsa-miR-3127-5p | chr2 | 96798298 | 96798310 | - |
| hsa-miR-3143 | chr6 | 27147629 | 27147653 | + |
| p-hsa-miR-124 | chr22_KI270733v1_random | 167965 | 167985 | + |
| hsa-miR-493-5p | chr14 | 1.01E+08 | 1.01E+08 | + |
| hsa-miR-548at-5p | chr17 | 42494773 | 42494794 | + |
| hsa-miR-3127-5p | chr2 | 96798298 | 96798310 | - |
| hsa-miR-3143 | chr6 | 27147629 | 27147653 | + |
| p-hsa-miR-124 | chr22_KI270733v1_random | 167965 | 167985 | + |
| hsa-miR-493-5p | chr14 | 1.01E+08 | 1.01E+08 | + |
| hsa-miR-548at-5p | chr17 | 42494773 | 42494794 | + |
| hsa-miR-3127-5p | chr2 | 96798298 | 96798310 | - |
| miRNA        | chromosome | start      | end        | strand |
|--------------|------------|------------|------------|--------|
| p-hsa-miR-336 | novelmirna | chr6_GL00  | 97089      | -      |
| hsa-miR-23b-3p | miRNA      | chr9       | 95085265   | 95085285  | +     |
| hsa-miR-197-3p | miRNA      | chr1       | 1.1E+08    | 1.1E+08   | +     |
| hsa-miR-3157-5p | miRNA     | chr10      | 96064369   | 96064390  | -     |
| hsa-miR-193a-5p | miRNA     | chr17      | 31560016   | 31560037  | +     |
| hsa-miR-2110  | miRNA      | chr10      | 1.14E+08   | 1.14E+08  | -     |
| hsa-miR-330-5p | miRNA      | chr19      | 45639049   | 45639070  | -     |
| hsa-miR-1224-5p | miRNA     | chr19      | 55239912   | 55239933  | -     |
| hsa-miR-181a-3p | miRNA     | chr1       | 1.99E+08   | 1.99E+08  | -     |
| hsa-miR-3613-3p | miRNA     | chr13      | 49996426   | 49996449  | -     |
| hsa-miR-590-3p | miRNA      | chr7       | 74191253   | 74191273  | +     |
| p-hsa-miR-3117-3p | novelmiRNA | chr17     | 66628485   | 66628505  | +     |
| hsa-miR-326   | miRNA      | chr11      | 75335108   | 75335127  | -     |
| hsa-miR-3135a | miRNA      | chr10      | 20137574   | 20137595  | +     |
| hsa-miR-1285-5p | miRNA     | chr7       | 92204067   | 92204087  | -     |
| hsa-miR-2355-3p | miRNA     | chr2       | 2.07E+08   | 2.07E+08  | -     |
| hsa-miR-6513-3p | miRNA     | chr2       | 2.18E+08   | 2.18E+08  | -     |
| hsa-miR-376a-3p | miRNA     | chr14      | 1.01E+08   | 1.01E+08  | +     |
| hsa-miR-1229-3p | miRNA     | chr5       | 1.8E+08    | 1.8E+08   | -     |
| hsa-miR-4672  | miRNA      | chr9       | 1.28E+08   | 1.28E+08  | -     |
| hsa-miR-191-3p | miRNA      | chr3       | 49020631   | 49020652  | -     |
| hsa-miR-6803-3p | miRNA      | chr19      | 55245186   | 55245207  | +     |
| p-hsa-miR-3117 | novelmiRNA | chr17     | 75183156   | 75183173  | +     |
| hsa-miR-10b-5p | miRNA      | chr2       | 1.76E+08   | 1.76E+08  | +     |
| p-hsa-miR-208 | miRNA      | chr16      | 26874569   | 26874591  | +     |
| hsa-miR-1468-5p | miRNA     | chrX       | 63786055   | 63786075  | -     |
| hsa-miR-629-3p | miRNA      | chr15      | 70079387   | 70079408  | -     |
| hsa-miR-548e-3p | miRNA     | chr10      | 1.11E+08   | 1.11E+08  | +     |
| hsa-miR-485-3p | miRNA      | chr14      | 1.01E+08   | 1.01E+08  | +     |
| hsa-miR-6726-3p | miRNA     | chr1       | 1.29E+08   | 1.29E+08  | +     |
| hsa-miR-125b-5p | miRNA     | chr21      | 16590253   | 16590274  | +     |
| hsa-miR-192-3p | miRNA      | chr11      | 64891159   | 64891180  | -     |
| hsa-miR-664b-3p | miRNA     | chrX       | 1.55E+08   | 1.55E+08  | +     |
| hsa-miR-5189-5p | miRNA      | chr16      | 88468943   | 88468966  | +     |
| hsa-miR-584-5p | miRNA      | chr5       | 1.49E+08   | 1.49E+08  | -     |
| hsa-miR-582-3p | miRNA      | chr5       | 59703630   | 59703651  | -     |
| hsa-miR-6880-3p | miRNA     | chr12      | 1.24E+08   | 1.24E+08  | -     |
| hsa-miR-1287-5p | miRNA     | chr10      | 98395271   | 98395292  | -     |
| hsa-miR-579-3p | miRNA      | chr5       | 32394392   | 32394414  | -     |
| hsa-miR-362-3p | miRNA      | chrX       | 50009005   | 50009026  | +     |
| hsa-miR-4446-3p | miRNA     | chr3       | 1.14E+08   | 1.14E+08  | +     |
| hsa-miR-6723-5p | miRNA     | chr1       | 632382     | 632403    | -     |
| p-hsa-miR-4    | novelmiRNA | chr3       | 47488760   | 47488781  | -     |
| hsa-miR-1226-3p | miRNA      | chr3       | 47849608   | 47849629  | +     |
| hsa-miR-940   | miRNA      | chr16      | 2271806    | 2271826   | +     |
| hsa-miR-4511  | miRNA      | chr15      | 65719297   | 65719318  | -     |
| hsa-miR-4500  | miRNA      | chr13      | 87618671   | 87618687  | -     |
| hsa-miR-335-3p | miRNA      | chr7       | 1.3E+08    | 1.3E+08   | +     |
| hsa-miR-33a-5p | miRNA      | chr22      | 41900949   | 41900969  | +     |
| p-hsa-miR-249 | novelmiRNA | chr5       | 1.77E+08   | 1.77E+08  | +     |
| hsa-miR-1277-3p | miRNA     | chrX       | 1.18E+08   | 1.18E+08  | +     |
| hsa-miR-1180-3p | miRNA     | chr17      | 19344513   | 19344534  | +     |
| p-hsa-miR-106 | novelmiRNA | chrX       | 43277869   | 43277886  | +     |
| hsa-miR-146b-5p | miRNA     | chr10      | 1.02E+08   | 1.02E+08  | +     |
| miRNA ID       | Type   | Chromosome | Start Base | End Base |strand |
|---------------|--------|------------|------------|----------|-------|
| hsa-miR-6787-3p | miRNA  | chr17      | 82236707   | 82236728 | +     |
| hsa-miR-27b-5p  | miRNA  | chr9       | 95085463   | 95085484 | +     |
| hsa-miR-193a-3p | miRNA  | chr17      | 31560050   | 31560071 | +     |
| hsa-miR-29a-5p  | miRNA  | chr7       | 1.31E+08   | 1.31E+08 | -     |
| hsa-miR-1271-5p | miRNA  | chr5       | 1.76E+08   | 1.76E+08 | +     |
| hsa-miR-6842-3p | miRNA  | chr8       | 27433413   | 27433434 | +     |
| hsa-miR-33a-3p  | miRNA  | chr22      | 41900989   | 41901010 | +     |
| hsa-miR-483-3p  | miRNA  | chr11      | 2134142    | 2134162  | -     |
| hsa-miR-215-5p  | miRNA  | chr1       | 2.2E+08    | 2.2E+08  | -     |
| hsa-miR-3139   | miRNA  | chr4       | 1.43E+08   | 1.43E+08 | +     |
| p-hsa-miR-337   | novelmiRNA | chr1_KI270  | 6632       | 6654     | +     |
| hsa-miR-101-3p  | miRNA  | chr9       | 4850345    | 4850365  | +     |
| hsa-miR-1273a   | miRNA  | chr8       | 1E+08      | 1E+08    | -     |
| hsa-miR-6842-3p | miRNA  | chr6       | 1.31E+08   | 1.31E+08 | +     |
| hsa-miR-6511a-3p | miRNA  | chr16      | 1834015    | 18344036 | -     |
| hsa-miR-5684    | miRNA  | chr19      | 12787132   | 12787151 | +     |
| hsa-miR-548o-3p | miRNA  | chr20      | 38516607   | 38516628 | +     |
| hsa-miR-411-3p  | miRNA  | chr6       | 1.01E+08   | 1.01E+08 | +     |
| p-hsa-miR-576-3p | miRNA  | chr4       | 1.09E+08   | 1.09E+08 | -     |
| hsa-miR-4289    | miRNA  | chr9       | 88745877   | 88745895 | -     |
| hsa-miR-576-3p  | miRNA  | chr4       | 1.09E+08   | 1.09E+08 | +     |
| p-hsa-miR-337   | novelmiRNA | chr1_KI270 | 1.43E+08   | 1.43E+08 | +     |
| p-hsa-miR-138   | novelmiRNA | chr20      | 53741952   | 53741969 | -     |
| p-hsa-miR-877-5p | miRNA  | chr10      | 30584332   | 30584351 | +     |
| hsa-miR-877-5p  | miRNA  | chr10      | 30584332   | 30584351 | +     |
| hsa-miR-6505-3p | miRNA  | chr12      | 48132847   | 48132867 | +     |
| hsa-miR-1270    | miRNA  | chr19      | 20399320   | 20399342 | -     |
| hsa-miR-5581-3p | miRNA  | chr11      | 37500935   | 37500956 | -     |
| hsa-miR-411-3p  | miRNA  | chr20      | 62554351   | 62554372 | +     |
| p-hsa-miR-89    | novelmiRNA | chr17      | 82300934   | 82300951 | -     |
| p-hsa-miR-15b-5p | miRNA  | chr6       | 4.6E+08    | 4.6E+08  | +     |
| hsa-miR-5699-3p | miRNA  | chr12      | 48132847   | 48132867 | +     |
| hsa-miR-610     | miRNA  | chr11      | 28056830   | 28056850 | +     |
| hsa-miR-628-3p  | miRNA  | chr15      | 53572954   | 53572974 | -     |
| hsa-miR-5189-3p | miRNA  | chr16      | 88468984   | 88469004 | +     |
| hsa-miR-129-2-3p | miRNA  | chr11      | 43581450   | 43581471 | +     |
| p-hsa-miR-73    | novelmiRNA | chr16      | 43581450   | 43581471 | +     |
| hsa-miR-6686-3p | miRNA  | chr19      | 11113511   | 11113531 | +     |
| hsa-miR-548u    | miRNA  | chr6       | 57390180   | 57390202 | +     |
| hsa-miR-30c-1-3p | miRNA  | chr1      | 33350664   | 33350685 | +     |
| p-hsa-miR-73    | novelmiRNA | chr16      | 33350664   | 33350685 | +     |
| hsa-miR-6511b-3p | miRNA  | chr21      | 15134078   | 15134098 | -     |
| p-hsa-miR-73    | novelmiRNA | chr16      | 15134078   | 15134098 | -     |
| hsa-miR-129-1-3p | miRNA  | chr7       | 1.28E+08   | 1.28E+08 | +     |
| hsa-miR-3158-3p | miRNA  | chr10      | 1.02E+08   | 1.02E+08 | -     |
| hsa-miR-543     | miRNA  | chr14      | 9.01E+08   | 9.01E+08 | +     |
| hsa-miR-6516-5p | miRNA  | chr17      | 77089428   | 77089449 | +     |
| hsa-miR-130b-5p | miRNA  | chr22      | 21653316   | 21653336 | +     |
| hsa-miR-548aq-5p | miRNA  | chr3       | 1.66E+08   | 1.66E+08 | -     |
| hsa-miR-4676-3p | miRNA  | chr10      | 72721072   | 72721093 | +     |
| hsa-miR-145-5p  | miRNA  | chr5       | 1.49E+08   | 1.49E+08 | +     |
| hsa-miR-190b    | miRNA  | chr1       | 1.54E+08   | 1.54E+08 | -     |
| hsa-miR-329-3p  | miRNA  | chr14      | 1.01E+08   | 1.01E+08 | +     |
| hsa-miR-765     | miRNA  | chr1       | 1.57E+08   | 1.57E+08 | -     |
| hsa-miR-4466    | miRNA  | chr6       | 1.57E+08   | 1.57E+08 | -     |
| miRNA       | chromosome | start | end   | strand |
|-------------|------------|-------|-------|--------|
| hsa-miR-7847-3p | chr11      | 1880105 | 1880125 | +      |
| hsa-miR-4801   | chr4       | 37241911 | 37241932 | -      |
| hsa-miR-3688-3p | chr4      | 1.59E+08 | 1.59E+08 | +      |
| hsa-miR-5706   | chr5       | 1.19E+08 | 1.19E+08 | +      |
| hsa-miR-6836-3p | chr7      | 2257515  | 2257535  | -      |
| hsa-miR-25-5p  | chr7       | 1E+08    | 1E+08    | -      |
| hsa-miR-1234-3p | chr8      | 35732974 | 35732995 | +      |
| hsa-miR-3684   | chr4       | 98997434 | 98997454 | +      |
| hsa-miR-5689   | chr6       | 1.44E+08 | 1.44E+08 | -      |
| hsa-miR-6845-3p | chr6      | 1.55E+08 | 1.55E+08 | +      |
| hsa-miR-5706   | chr5       | 1.19E+08 | 1.19E+08 | +      |
| hsa-miR-6836-3p | chr7      | 27169493 | 27169514 | +      |
| hsa-miR-6698-5p | chrX      | 74399301 | 74399322 | +      |
| p-hsa-miR-264  | chr14      | 321681   | 321701   | -      |
| hsa-miR-616-5p  | chr12      | 57519223 | 57519244 | -      |
| hsa-miR-3173-3p | chr14     | 95137923 | 95137944 | -      |
| hsa-miR-433-3p  | chr14      | 1.01E+08 | 1.01E+08 | +      |
| hsa-miR-6775-5p | chr6      | 87834631 | 87834655 | -      |
| hsa-miR-4697-5p | chr6      | 1.34E+08 | 1.34E+08 | -      |
| hsa-miR-6790-5p | chr6      | 6392961  | 6392983  | -      |
| hsa-miR-6876-3p | chr8      | 25345451 | 25345474 | +      |
| hsa-miR-3907   | chr7       | 1.51E+08 | 1.51E+08 | -      |
| hsa-miR-7107-3p | chr12     | 1.21E+08 | 1.21E+08 | -      |
| p-hsa-miR-200  | chr7       | 78011578 | 78011596 | -      |
| hsa-miR-490-3p  | chr7       | 1.37E+08 | 1.37E+08 | +      |
| hsa-miR-5087   | chr7       | 1.48E+08 | 1.48E+08 | -      |
| hsa-miR-219b-5p | chr9      | 1.28E+08 | 1.28E+08 | +      |
| hsa-miR-6510-5p | chr17     | 41517194 | 41517215 | -      |
| hsa-miR-6834-5p | chr6      | 33290245 | 33290265 | +      |
| hsa-miR-4463   | chr6       | 75428446 | 75428462 | +      |
| hsa-miR-608    | chr10      | 1.01E+08 | 1.01E+08 | +      |
| hsa-miR-4653-3p | chr7      | 1.01E+08 | 1.01E+08 | +      |
| hsa-miR-5193   | chr3       | 49806165 | 49806186 | -      |
| hsa-miR-23a-5p  | chr19      | 13836630 | 13836651 | -      |
| hsa-miR-6509-3p | chr7      | 1.35E+08 | 1.35E+08 | -      |
| hsa-miR-4441   | chr2       | 2.39E+08 | 2.39E+08 | -      |
| hsa-miR-3195   | chr20      | 62064812 | 62064828 | +      |
| hsa-miR-22-5p  | chr17      | 1713952  | 1713973  | -      |
| p-hsa-miR-146  | chr5       | 54908782 | 54908799 | -      |
| hsa-miR-181b-2-3p | chr9     | 1.25E+08 | 1.25E+08 | +      |
| hsa-miR-450a-5p | chrX      | 1.35E+08 | 1.35E+08 | -      |
| hsa-miR-382-3p  | chr14      | 1.01E+08 | 1.01E+08 | +      |
| hsa-miR-548ax   | chrX      | 11318656 | 11318677 | -      |
| hsa-miR-4716-5p | chr15      | 49169121 | 49169142 | -      |
| hsa-miR-6856-5p | chr9       | 1.31E+08 | 1.31E+08 | +      |
| hsa-miR-6771-5p | chr16      | 50292621 | 50292642 | +      |
| hsa-miR-6804-5p | chr19      | 55230927 | 55230947 | -      |
| p-hsa-miR-224  | chr11      | 76436521 | 76436545 | +      |
| hsa-miR-3687   | chr21      | 8987404  | 8987427  | +      |
| hsa-miR-6733-3p | chr1       | 43171652 | 43171671 | -      |
| hsa-miR-612    | chr11      | 65444473 | 65444497 | +      |
| hsa-miR-493-3p  | chr14      | 1.01E+08 | 1.01E+08 | +      |
| hsa-miR-31-5p  | chr9       | 21512158 | 21512178 | -      |
| hsa-miR-5693   | chr13      | 51348576 | 51348597 | -      |
| miRNA         | Type | Chromosome | Start Position | End Position | Strand |
|---------------|------|------------|----------------|--------------|--------|
| hsa-miR-1289  | miRNA| chr5       | 1.33E+08       | 1.33E+08     | -      |
| hsa-miR-199a-5p | miRNA| chr1       | 1.72E+08       | 1.72E+08     | -      |
| p-hsa-miR-29  | novelmiRNA| chr19    | 55225520       | 55225541     | -      |
| hsa-miR-4742-3p | miRNA| chr1       | 2.24E+08       | 2.24E+08     | -      |
| hsa-miR-6804-3p | miRNA| chr19      | 55230885       | 55230906     | -      |
| hsa-miR-3192-5p | miRNA| chr20      | 18470624       | 18470646     | +      |
| hsa-miR-6854-5p | miRNA| chr9       | 98229189       | 98229212     | -      |
| hsa-miR-6777-5p | miRNA| chr17      | 17813518       | 17813540     | -      |
| hsa-miR-4449  | miRNA| chr4       | 52712720       | 52712741     | +      |
| hsa-miR-6503-5p | miRNA| chr11      | 60209118       | 60209140     | -      |
| p-hsa-miR-125 | novelmiRNA| chr9      | 1.26E+08       | 1.26E+08     | +      |
| hsa-miR-1908-5p | miRNA| chr11      | 61815209       | 61815229     | -      |
| hsa-miR-6793-3p | miRNA| chr19      | 43171686       | 43171707     | +      |
| hsa-miR-6733-5p | miRNA| chr1       | 1119E+08       | 1119E+08     | -      |
| hsa-miR-2277-5p | miRNA| chr5       | 31355228       | 31355248     | -      |
| hsa-miR-4492  | miRNA| chr11      | 62792702       | 62792722     | -      |
| p-hsa-miR-133 | novelmiRNA| chr1      | 3560710        | 3560730      | -      |
| hsa-miR-320a-3p | miRNA| chr14      | 4578271        | 4578293      | +      |
| p-hsa-miR-202 | novelmiRNA| chr12     | 64893363       | 6489383      | -      |
| hsa-miR-6891-3p | miRNA| chr6       | 1.04E+08       | 1.04E+08     | -      |
| hsa-miR-5092  | miRNA| chr9       | 79402032       | 79402053     | -      |
| hsa-miR-4493  | miRNA| chr19      | 1.51E+08       | 1.51E+08     | +      |
| hsa-miR-3142  | miRNA| chr5       | 8460933        | 8460951      | +      |
| hsa-miR-6815-5p | miRNA| chr21      | 45478271       | 45478293     | +      |
| hsa-miR-6750-3p | miRNA| chr11      | 5148286        | 5148308      | -      |
| hsa-miR-6833-5p | miRNA| chr6       | 25455692       | 25455710     | +      |
| hsa-miR-548ar-3p | miRNA| chr22      | 1.01E+08       | 1.01E+08     | +      |
| hsa-miR-4757-3p | miRNA| chr10      | 19348476       | 19348497     | +      |
| hsa-miR-369-5p | miRNA| chr14      | 35335710       | 35335731     | +      |
| hsa-miR-5585-5p | miRNA| chr16      | 32086949       | 32086970     | +      |
| hsa-miR-3820-3p | miRNA| chr20      | 2.28E+08       | 2.28E+08     | +      |
| hsa-miR-320c  | miRNA| chr18      | 2.652779       | 2.652803     | +      |
| hsa-miR-3691-5p | miRNA| chr6       | 5148286        | 5148308      | -      |
| hsa-miR-197-5p | miRNA| chr1       | 1.1E+08        | 1.1E+08      | +      |
| hsa-miR-8075  | miRNA| chr13      | 1.13E+08       | 1.13E+08     | +      |
| hsa-miR-708-3p | miRNA| chr11      | 79402032       | 79402053     | -      |
| hsa-miR-96-5p  | miRNA| chr7       | 1.3E+08        | 1.3E+08      | -      |
| miRNA       | chromosome | start position | end position | strand |
|-------------|------------|----------------|--------------|--------|
| hsa-miR-1268b | chr17       | 80098831       | 80098850     | +      |
| hsa-miR-200a-3p | chr1        | 1167916        | 1167937      | +      |
| hsa-miR-3605-5p | chr14     | 65471153       | 65471174     | +      |
| hsa-miR-4516 | chr16       | 2133120        | 2133136      | +      |
| hsa-miR-153-3p | chr7        | 1.58E+08       | 1.58E+08     | -      |
| hsa-miR-19a-5p | chr13      | 91350904       | 91350925     | +      |
| hsa-miR-659-5p | chr22      | 37847732       | 37847753     | -      |
| hsa-miR-4491 | chr11       | 1.11E+08       | 1.11E+08     | +      |
| hsa-miR-4298 | chr11       | 1859505        | 1859525      | -      |
| hsa-miR-548an | chrX        | 1.07E+08       | 1.07E+08     | +      |
| hsa-miR-127-3p | chr14      | 1.01E+08       | 1.01E+08     | +      |
| hsa-miR-548j-5p | chr22    | 26555239       | 26555259     | -      |
| hsa-miR-3163 | chr11       | 66934476       | 66934497     | -      |
| hsa-miR-7107-5p | chr12       | 1.21E+08       | 1.21E+08     | -      |
| hsa-miR-939-5p | chr8        | 1.44E+08       | 1.44E+08     | -      |
| hsa-miR-4435 | chr2        | 1.11E+08       | 1.11E+08     | -      |
| hsa-miR-7705 | chr8        | 1.01E+08       | 1.01E+08     | -      |
| hsa-miR-135b-5p | chr14      | 2.05E+08       | 2.05E+08     | -      |
| hsa-miR-1255b-5p | chr1       | 1.68E+08       | 1.68E+08     | +      |
| hsa-miR-6501-3p | chr21      | 33550705       | 33550727     | +      |
| hsa-miR-6766-3p | chr15      | 89326742       | 89326763     | -      |
| hsa-miR-4657 | chr7        | 44881778       | 44881800     | -      |
| hsa-miR-6882-5p | chr15      | 74840681       | 74840702     | -      |
| hsa-miR-6852-3p | chr9        | 35710684       | 35710700     | -      |
| hsa-miR-6796-3p | chr19       | 40369887       | 40369907     | +      |
| hsa-miR-663b | chr2        | 1.32E+08       | 1.32E+08     | -      |
| hsa-miR-186-3p | chr1        | 71067642       | 71067663     | -      |
| hsa-miR-6867-5p | chr17      | 40193602       | 40193624     | +      |
| hsa-miR-1273g-5p | chr1       | 52940339       | 52940360     | +      |
| hsa-miR-92b-5p | chr1        | 1.55E+08       | 1.55E+08     | +      |
| hsa-miR-7848-3p | chr8        | 1.33E+08       | 1.33E+08     | -      |
| hsa-miR-762 | chr16       | 30893951       | 30893972     | +      |
| p-hsa-miR-178 | chrX        | 14467325       | 14467344     | +      |
| hsa-miR-3124-5p | chr1        | 2.49E+08       | 2.49E+08     | +      |
| hsa-miR-6739-5p | chr1       | 2.02E+08       | 2.02E+08     | +      |
| hsa-miR-1249-5p | chr22      | 45200993       | 45201016     | -      |
| hsa-miR-378i | chr22       | 41923271       | 41923291     | -      |
| hsa-miR-6805-3p | chr19      | 55388220       | 55388242     | +      |
| hsa-miR-4795-5p | chr3       | 87226240       | 87226260     | -      |
| hsa-miR-4678 | chr10       | 87503890       | 87503911     | +      |
| hsa-miR-766-5p | chrX        | 1.2E+08        | 1.2E+08      | -      |
| hsa-miR-5091 | chr4        | 13627875       | 13627897     | +      |
| hsa-miR-2392 | chr14       | 25906384       | 25906403     | +      |
| hsa-miR-4434 | chr2        | 64525520       | 64525537     | +      |
| hsa-miR-6797-5p | chr19      | 41869632       | 41869656     | +      |
| miRNA          |_chr| start  | end    |
|----------------|----|--------|--------|
| hsa-miR-6788-3p |18  |10759584 |10759605 |
| hsa-miR-215-3p |1   |2,2E+08 |2,2E+08 |
| hsa-miR-555    |14  |1,55E+08 |1,55E+08 |
| hsa-miR-6717-5p|14  |21023355 |21023376 |
| hsa-miR-494-5p |14  |1,01E+08 |1,01E+08 |
| hsa-miR-1282   |15  |43793732 |43793751 |
| p-hsa-miR-63   |      |38086083 |38086104 |
| hsa-miR-1266-5p|15  |52277166 |52277188 |
| hsa-miR-520d-5p|19  |53720111 |53720130 |
| p-hsa-miR-109  |      |94731212 |94731233 |
| p-hsa-miR-160  |5   |1.8E+08  |1.8E+08 |
| hsa-miR-3169   |17  |61199849 |61199869 |
| hsa-miR-2117   |17  |43444856 |43444876 |
| hsa-miR-202-5p |15  |34528347 |34528368 |
| hsa-miR-6860   |11  |67045683 |67045704 |
| hsa-miR-4652-3p|15  |93716977 |93716998 |
| hsa-miR-6764-5p|14  |26908697 |26908715 |
| hsa-miR-1260a  |14  |77266231 |77266248 |
| hsa-miR-4760-5p|15  |40212401 |40212422 |
| hsa-miR-520d-3p|19  |53720149 |53720170 |
| hsa-miR-487a-3p|14  |1.01E+08 |1.01E+08 |
| hsa-miR-4307   |14  |26908697 |26908715 |
| hsa-miR-6730-3p|1   |12578958 |12578979 |
| hsa-miR-6782-3p|17  |44207772 |44207794 |
| hsa-miR-943    |15  |1986403  |1986423 |
| hsa-miR-6801-5p|12  |52222025 |52222047 |
| hsa-miR-6760-3p|15  |1.11E+08 |1.11E+08 |
| hsa-miR-5695   |19  |12920373 |12920394 |
| hsa-miR-4479   |17  |1.37E+08 |1.37E+08 |
| hsa-miR-607    |10  |96828684 |96828704 |
| hsa-miR-6808-3p|1  |1339650  |1339670 |
| hsa-miR-145-3p |5   |1.49E+08 |1.49E+08 |
| hsa-miR-95-3p  |4   |8005312  |8005333 |
| hsa-miR-3174   |15  |90006764 |90006786 |
| hsa-miR-3934-5p|6   |33698152 |33698173 |
| hsa-miR-1306-3p|22  |20086112 |20086129 |
| hsa-miR-3683   |7   |7067010  |7067031 |
| hsa-miR-3674   |8   |1801133  |1801154 |
| hsa-miR-135a-5p|12  |97563834 |97563856 |
| hsa-miR-6833-3p|6   |32179856 |32179876 |
| hsa-miR-4746-5p|19  |4445987  |4446009 |
| hsa-miR-561-5p |2   |1.88E+08 |1.88E+08 |
| hsa-miR-449c-5p|5   |55172313 |55172337 |
| hsa-miR-3667-5p|22  |49543437 |49543458 |
| hsa-miR-138-5p |3   |44114234 |44114256 |
| hsa-let-7i-2-3p|X   |53557196 |53557217 |
| hsa-miR-7110-3p|3   |1.23E+08 |1.23E+08 |
| hsa-miR-505-5p |2   |1.4E+08  |1.4E+08 |
| hsa-miR-196a-5p|12  |53991762 |53991783 |
| hsa-miR-136-5p |14  |1.01E+08 |1.01E+08 |
| hsa-miR-769-5p |15  |46018961 |46018982 |
| hsa-miR-627-3p |15  |42199593 |42199612 |
| hsa-miR-4467   |7   |1.02E+08 |1.02E+08 |
| hsa-miR-548q   |10  |12725325 |12725346 |
hsa-miR-99b-3p  miRNA  chr19  51692656  51692677  +
hsa-miR-618   miRNA  chr12  80935796  80935818  -
hsa-miR-548k  miRNA  chr11  70283986  70284007  +
hsa-miR-6857-3p miRNA  chrX  53405673  53405693  -
hsa-miR-671-5p miRNA  chr7  1.51E+08  1.51E+08  +
hsa-miR-6514-3p miRNA  chr11  62792749  62792771  -
hsa-miR-671-5p miRNA  chr7  1.51E+08  1.51E+08  +
hsa-miR-4775  miRNA  chr2  2.08E+08  2.08E+08  +
hsa-miR-485-5p miRNA  chr14  1.01E+08  1.01E+08  +
hsa-miR-5094  miRNA  chr15  89850690  89850711  -
hsa-miR-4775  miRNA  chr2  2.08E+08  2.08E+08  +
hsa-miR-485-5p miRNA  chr14  1.01E+08  1.01E+08  +
hsa-miR-5094  miRNA  chr15  89850690  89850711  -
hsa-miR-769-3p miRNA  chr19  46019000  46019022  +
hsa-miR-186-5p miRNA  chr1  71067681  71067702  -
hsa-miR-190a-3p miRNA  chr15  62824008  62824028  +
hsa-miR-627-5p miRNA  chr15  42199630  42199651  -
hsa-miR-2277-3p miRNA  chr5  93620710  93620730  -
hsa-miR-491-5p miRNA  chr9  20716120  20716141  +
hsa-miR-7152-3p miRNA  chr17  40161938  40161960  +
hsa-miR-4804-3p miRNA  chr5  72878635  72878655  +
hsa-miR-6886-5p miRNA  chr10  71790781  71790800  +
hsa-miR-4804-3p miRNA  chr5  72878635  72878655  +
hsa-miR-6747-3p miRNA  chr11  62567011  62567031  -
hsa-miR-4690-3p miRNA  chr11  65636348  65636368  +
hsa-miR-3928-3p miRNA  chr22  31160062  31160083  -
hsa-miR-655-3p miRNA  chr14  1.01E+08  1.01E+08  +
hsa-miR-2861  miRNA  chr9  1.28E+08  1.28E+08  +
hsa-miR-6781-3p miRNA  chr17  42823880  42823901  -
| miRNA ID     | Type   | Chromosome | Start Position | End Position | Strand |
|-------------|--------|------------|----------------|--------------|--------|
| hsa-miR-3157-3p | miRNA  | chr10      | 96064321       | 96064342     | -      |
| hsa-miR-539-5p  | miRNA  | chr14      | 1.01E+08       | 1.01E+08     | +      |
| hsa-miR-380-3p  | miRNA  | chr14      | 1.01E+08       | 1.01E+08     | +      |
| hsa-miR-7155-3p | miRNA  | chr11      | 64341849       | 64341867     | -      |
| hsa-miR-3177-3p | miRNA  | chr16      | 1735038        | 1735058      | +      |
| hsa-miR-1538   | miRNA  | chr16      | 69565808       | 69565830     | -      |
| hsa-miR-4785   | miRNA  | chr2       | 1.6E+08        | 1.6E+08      | -      |
| hsa-miR-556-3p  | miRNA  | chr1       | 1.62E+08       | 1.62E+08     | +      |
| hsa-miR-1255a  | miRNA  | chr4       | 1.01E+08       | 1.01E+08     | -      |
| hsa-miR-4662a-5p | miRNA  | chr8       | 1.25E+08       | 1.25E+08     | +      |
| hsa-miR-1284   | miRNA  | chr3       | 71542039       | 71542060     | -      |
| hsa-miR-3140-3p | miRNA  | chr4       | 1.52E+08       | 1.52E+08     | -      |
| hsa-miR-4638-3p | miRNA  | chr5       | 1.81E+08       | 1.81E+08     | -      |
| hsa-miR-616-3p  | miRNA  | chr14      | 57519183       | 57519204     | -      |
| p-hsa-miR-1    | novelmiRNA | chr8   | 98393667       | 98393688     | -      |
| hsa-miR-577    | miRNA  | chr4       | 1.15E+08       | 1.15E+08     | +      |
| hsa-miR-580-3p  | miRNA  | chr5       | 36147907       | 36147928     | -      |
| hsa-miR-548l   | miRNA  | chr11      | 94466545       | 94466566     | -      |
| hsa-miR-30b-3p  | miRNA  | chr2       | 1.36E+08       | 1.36E+08     | +      |
| p-hsa-miR-85   | novelmiRNA | chr16   | 173945         | 173967      | -      |
| hsa-miR-6513-5p | miRNA  | chr2       | 2.18E+08       | 2.18E+08     | -      |
| hsa-miR-2115-5p | miRNA  | chr3       | 48316418       | 48316439     | -      |
| hsa-miR-3675-5p | miRNA  | chr1       | 16858988       | 16859010     | -      |
| hsa-miR-760    | miRNA  | chr1       | 93846880       | 93846899     | +      |
| hsa-miR-548d-3p | miRNA  | chr17      | 67471504       | 67471525     | -      |
| p-hsa-miR-90   | novelmiRNA | chr11   | 76745548       | 76745569     | -      |
| hsa-miR-4521   | miRNA  | chr17      | 8186948        | 8186969      | +      |
| hsa-miR-4669   | miRNA  | chr9       | 1.34E+08       | 1.34E+08     | +      |
| hsa-miR-9-3p   | miRNA  | chr15      | 89368071       | 89368092     | +      |
| hsa-miR-3179   | miRNA  | chr16      | 18494504       | 18494525     | -      |
| hsa-miR-6741-5p | miRNA  | chr1       | 2.26E+08       | 2.26E+08     | -      |
| hsa-miR-4646-5p | miRNA  | chr6       | 31701070       | 31701091     | -      |
| hsa-miR-6791-3p | miRNA  | chr19      | 6736712        | 6736732      | -      |
| hsa-miR-4637   | miRNA  | chr5       | 14825932       | 14825953     | -      |
| hsa-miR-4433b-3p | miRNA  | chr2       | 64340769       | 64340789     | -      |
| hsa-miR-376b-3p | miRNA  | chr14      | 1.01E+08       | 1.01E+08     | +      |
| hsa-miR-452-5p  | miRNA  | chrX       | 1.52E+08       | 1.52E+08     | -      |
| hsa-miR-6503-3p | miRNA  | chr11      | 60209084       | 60209104     | -      |
| hsa-miR-3941   | miRNA  | chr10      | 1.22E+08       | 1.22E+08     | +      |
| hsa-miR-5582-3p | miRNA  | chr11      | 46753125       | 46753146     | -      |
| hsa-miR-6741-3p | miRNA  | chr1       | 2.26E+08       | 2.26E+08     | -      |
| hsa-miR-105-5p  | miRNA  | chrX       | 1.52E+08       | 1.52E+08     | -      |
| hsa-miR-6799-3p | miRNA  | chr19      | 49791912       | 49791934     | +      |
| p-hsa-miR-139  | novelmiRNA | chr3    | 1.91E+08       | 1.91E+08     | +      |
| hsa-miR-5006-3p | miRNA  | chr13      | 41568306       | 41568326     | -      |
| hsa-miR-125a-3p | miRNA  | chr19      | 51693306       | 51693327     | +      |
| hsa-miR-668-3p  | miRNA  | chr14      | 1.01E+08       | 1.01E+08     | +      |
| hsa-miR-6819-3p | miRNA  | chr22      | 36286847       | 36286867     | -      |
| hsa-miR-3074-5p | miRNA  | chr9       | 95086063       | 95086083     | -      |
| hsa-miR-7854-3p | miRNA  | chr16      | 81533942       | 81533962     | +      |
| hsa-miR-548a-3p | miRNA  | chr8       | 1.04E+08       | 1.04E+08     | -      |
| hsa-miR-6783-5p | miRNA  | chr17      | 44934655       | 44934676     | -      |
| hsa-miR-3175   | miRNA  | chr15      | 92904408       | 92904429     | +      |
| miRNA          | Type    | Chromosome | Position Start | Position End |strand |
|----------------|---------|------------|----------------|--------------|-------|
| hsa-miR-4665-5p| miRNA   | chr9       | 6007835        | 6007857      | +     |
| hsa-miR-497-5p | miRNA   | chr17      | 7017979        | 7017999      | -     |
| p-hsa-miR-14  | novelmiRNA | chr19     | 18284683       | 18284706     | +     |
| hsa-miR-29b-1-5p | miRNA | chr7      | 1,31E+08       | 1,31E+08     | -     |
| p-hsa-miR-96  | novelmiRNA | chr9     | 87796926       | 87796945     | -     |
| p-hsa-miR-496 | miRNA   | chr14      | 1,01E+08       | 1,01E+08     | +     |
| p-hsa-miR-146 | miRNA   | chr7       | 19705366       | 19705387     | -     |
| p-hsa-miR-4743-3p | miRNA | chr9        | 20502277      | 20502298       | -     |
| p-hsa-miR-3154 | miRNA   | chr9       | 1,28E+08       | 1,28E+08     | -     |
| hsa-miR-4440  | miRNA   | chr2       | 2,39E+08       | 2,39E+08     | -     |
| hsa-miR-655-3p | miRNA   | chr17      | 1,01E+08       | 1,01E+08     | +     |
| hsa-miR-4731-5p | miRNA | chr17      | 15251666       | 15251687     | -     |
| hsa-miR-570-3p | miRNA   | chr3       | 1,96E+08       | 1,96E+08     | +     |
| hsa-miR-6515-5p | miRNA | chr19     | 12940486       | 12940506     | +     |
| p-hsa-miR-92a-1-5p | miRNA | chr13   | 91351324       | 91351346     | -     |
| hsa-miR-314 | miRNA   | chr19      | 64164344       | 6416455     | +     |
| p-hsa-miR-182 | novelmiRNA | chr10 | 1,13E+08       | 1,13E+08     | -     |
| p-hsa-miR-92a-1-5p | miRNA | chr13 | 91351324       | 91351346     | -     |
| p-hsa-miR-146 | miRNA   | chr7       | 19705366       | 19705387     | -     |
| p-hsa-miR-4743-3p | miRNA | chr9        | 20502277      | 20502298       | -     |
| p-hsa-miR-3154 | miRNA   | chr9       | 1,28E+08       | 1,28E+08     | -     |
| p-hsa-miR-4440 | miRNA   | chr2       | 2,39E+08       | 2,39E+08     | -     |
| p-hsa-miR-655-3p | miRNA | chr17      | 1,01E+08       | 1,01E+08     | +     |
| hsa-miR-496  | miRNA   | chr14      | 1,01E+08       | 1,01E+08     | +     |
| p-hsa-miR-146 | miRNA   | chr7       | 19705366       | 19705387     | -     |
| p-hsa-miR-4743-3p | miRNA | chr9        | 20502277      | 20502298       | -     |
| p-hsa-miR-3154 | miRNA   | chr9       | 1,28E+08       | 1,28E+08     | -     |
| hsa-miR-4440  | miRNA   | chr2       | 2,39E+08       | 2,39E+08     | -     |
| hsa-miR-655-3p | miRNA   | chr17      | 1,01E+08       | 1,01E+08     | +     |
| hsa-miR-4731-5p | miRNA | chr17      | 15251666       | 15251687     | -     |
| hsa-miR-570-3p | miRNA   | chr3       | 1,96E+08       | 1,96E+08     | +     |
| hsa-miR-6515-5p | miRNA | chr19     | 12940486       | 12940506     | +     |
| p-hsa-miR-92a-1-5p | miRNA | chr13 | 91351324       | 91351346     | -     |
| hsa-miR-7155-5p | miRNA | chr11     | 64341866       | 64341904     | -     |
| hsa-miR-500b-3p | miRNA   | chrX       | 50010722       | 50010741     | +     |
| hsa-miR-3682-3p | miRNA | chr2       | 3349136        | 3349156      | +     |
| hsa-miR-296-3p | miRNA   | chr20      | 58817626       | 58817647     | +     |
| p-hsa-miR-146 | miRNA   | chr7       | 1844189        | 1844209      | -     |
| hsa-miR-6152 | miRNA   | chr12      | 62260418       | 62260437     | +     |
| hsa-miR-6843-3p | miRNA | chr8       | 27610601       | 27610621     | -     |
| hsa-miR-6805-5p | miRNA | chr19     | 55388186       | 55388207     | +     |
| hsa-miR-377-5p | miRNA   | chr14      | 1,01E+08       | 1,01E+08     | +     |
| hsa-miR-212-5p | miRNA   | chr17      | 2050328        | 2050350      | -     |
| hsa-miR-1281 | miRNA   | chr22      | 41092545       | 41092561     | +     |
| p-hsa-miR-74 | novelmiRNA | chr5   | 32314109       | 32314128     | +     |
| p-hsa-miR-222 | novelmiRNA | chr14_KI270846v1_alt | 333330 | 333353     |
| hs-miR-1469 | miRNA   | chr15      | 96333261       | 96333282     | +     |
| hsa-miR-551b-3p | miRNA | chr3       | 1,69E+08       | 1,69E+08     | +     |
| p-hsa-miR-265 | novelmiRNA | chr7       | 1,01E+08       | 1,01E+08     | +     |
| miRNA     | Type     | Chromosome | Start Position | End Position | Strand |
|-----------|----------|------------|----------------|--------------|--------|
| hsa-miR-3187-3p | miRNA    | chr19      | 813627         | 813646       | +      |
| hsa-miR-516b-5p  | miRNA    | chr19      | 53736860       | 53736881     | +      |
| hsa-miR-6719-3p  | miRNA    | chr19      | 39829726       | 39829747     | -      |
| hsa-miR-6754-3p  | miRNA    | chr11      | 71473546       | 71473567     | +      |
| hsa-miR-4259     | miRNA    | chr1       | 1.6E+08        | 1.6E+08      | -      |
| hsa-miR-4710     | miRNA    | chr14      | 1.05E+08       | 1.05E+08     | -      |
| hsa-miR-6868-3p  | miRNA    | chr17      | 76098019       | 76098039     | -      |
| hsa-miR-758-5p   | miRNA    | chr5       | 1.01E+08       | 1.01E+08     | +      |
| hsa-miR-580-5p   | miRNA    | chr5       | 36147946       | 36147967     | -      |
| hsa-miR-1273c   | miRNA    | chr6       | 1.55E+08       | 1.55E+08     | +      |
| p-hsa-miR-88     | novelmiRNA | chr22     | 50273275       | 50273295     | +      |
| hsa-miR-4444    | miRNA    | chr3       | 75214518       | 75214535     | +      |
| hsa-miR-146a-3p  | miRNA    | chr5       | 1.6E+08        | 1.6E+08      | +      |
| p-hsa-miR-68     | novelmiRNA | chr22     | 39994798       | 39994819     | -      |
| hsa-miR-5001-5p  | miRNA    | chr6       | 2.33E+08       | 2.33E+08     | -      |
| hsa-miR-3691-3p  | miRNA    | chr6       | 5148246        | 5148267      | -      |
| hsa-miR-375     | miRNA    | chr6       | 2.19E+08       | 2.19E+08     | -      |
| hsa-miR-452-3p  | miRNA    | chrX       | 1.52E+08       | 1.52E+08     | -      |
| hsa-miR-6767-5p  | miRNA    | chr16      | 2445397        | 2445419      | +      |
| hsa-miR-4644    | miRNA    | chr6       | 1.7E+08        | 1.7E+08      | +      |
| hsa-miR-877-3p  | miRNA    | chr6       | 30584397       | 30584417     | +      |
| hsa-miR-6789-5p  | miRNA    | chr19      | 2235899        | 2235922      | -      |
| hsa-miR-4783-3p  | miRNA    | chr2       | 1.27E+08       | 1.27E+08     | +      |
| hsa-miR-4429    | miRNA    | chr2       | 11540652       | 11540671     | -      |
| hsa-miR-6816-3p  | miRNA    | chr22      | 20114693       | 20114710     | -      |
| hsa-miR-6809-3p  | miRNA    | chr2       | 2.18E+08       | 2.18E+08     | -      |
| hsa-miR-5683    | miRNA    | chr6       | 6169343        | 6169366      | +      |
| hsa-miR-3138    | miRNA    | chr4       | 10078622       | 10078645     | -      |
| hsa-miR-4433a-5p | miRNA    | chr2       | 64340770       | 64340790     | +      |
| hsa-miR-206     | miRNA    | chr6       | 52144401       | 52144422     | +      |
| p-hsa-miR-84    | novelmiRNA | chr16     | 180208         | 180228       | +      |
| hsa-miR-34c-3p  | miRNA    | chr11      | 1.12E+08       | 1.12E+08     | +      |
| hsa-miR-5696    | miRNA    | chr2       | 1.01E+08       | 1.01E+08     | +      |
| hsa-miR-541-3p  | miRNA    | chr14      | 1.01E+08       | 1.01E+08     | +      |
| hsa-miR-1909-3p | miRNA    | chr19      | 1816169        | 1816190      | -      |
| hsa-miR-6625-3p  | miRNA    | chr3       | 1.28E+08       | 1.28E+08     | -      |
| hsa-miR-202-3p  | miRNA    | chr10      | 1.33E+08       | 1.33E+08     | -      |
| hsa-miR-3939    | miRNA    | chr6       | 1.67E+08       | 1.67E+08     | -      |
| hsa-miR-5586-5p | miRNA    | chr14      | 59646999       | 59647020     | -      |
| hsa-miR-1537-3p | miRNA    | chr1       | 2.36E+08       | 2.36E+08     | -      |
| p-hsa-miR-8085  | miRNA    | chr19      | 44758667       | 44758687     | +      |
| p-hsa-miR-86    | novelmiRNA | chr8      | 42052337       | 42052357     | -      |
| hsa-miR-6884-5p | miRNA    | chr17      | 40026383       | 40026404     | -      |
| hsa-miR-154-3p  | miRNA    | chr14      | 1.01E+08       | 1.01E+08     | +      |
| hsa-miR-6832-5p | miRNA    | chr6       | 31633792       | 31633814     | +      |
| hsa-miR-4695-3p | miRNA    | chr1       | 18883204       | 18883225     | -      |
| hsa-miR-4459    | miRNA    | chr5       | 54075560       | 54075581     | -      |
| p-hsa-miR-329-5p | miRNA    | chr14      | 1.01E+08       | 1.01E+08     | +      |
| p-hsa-miR-267   | novelmiRNA | chr8      | 1.3E+08        | 1.3E+08      | +      |
| p-hsa-miR-1247-5p| miRNA    | chr14      | 1.02E+08       | 1.02E+08     | -      |
| p-hsa-miR-4739  | miRNA    | chr17      | 79707216       | 79707240     | -      |
| p-hsa-miR-91    | novelmiRNA | chr17     | 7306833        | 7306853      | -      |
| hsa-miR-6810-3p | miRNA    | chr2       | 2.18E+08       | 2.18E+08     | +      |
| p-hsa-miR-319   | novelmiRNA | chr10     | 71962614       | 71962634     | -      |
| hsa-miR-6505-5p | miRNA    | chr12      | 48132800       | 48132821     | +      |
| p-hsa-miR-64-3p | miRNA    | chr11      | 64891368       | 64891389     | -      |
| miRNA   | chr | Start   | End     | Type |
|---------|-----|---------|---------|------|
| hsa-miR-876-5p | chr9 | 28863675 | 28863696 | -   |
| hsa-miR-4779   | chr2  | 86193037 | 86193058 | -   |
| p-hsa-miR-642a-5p | chr19 | 45674943 | 45674964 | +   |
| hsa-miR-4667-3p | chr9  | 35608139 | 35608159 | +   |
| hsa-miR-3186-5p | chr17 | 81451152 | 81451173 | -   |
| p-hsa-miR-315   | chr22 | 40652100 | 40652120 | +   |
| hsa-miR-4779   | chr2  | 86193037 | 86193058 | -   |
| hsa-miR-3944-3p | chr10 | 1.33E+08 | 1.33E+08 | -   |
| hsa-miR-412-5p  | chr14 | 1.01E+08 | 1.01E+08 | +   |
| p-hsa-miR-4779  | chr2  | 86193037 | 86193058 | -   |
| hsa-miR-412-5p  | chr14 | 1.01E+08 | 1.01E+08 | +   |
| hsa-miR-4442    | chr3  | 25664875 | 25664891 | -   |
| hsa-miR-412-5p  | chr14 | 1.01E+08 | 1.01E+08 | +   |
| hsa-miR-442     | chr3  | 25664875 | 25664891 | -   |
| hsa-miR-4442    | chr3  | 25664875 | 25664891 | -   |
| hsa-miR-1197    | chr14 | 1.01E+08 | 1.01E+08 | +   |
| hsa-miR-3123    | chr1  | 2.41E+08 | 2.41E+08 | +   |
| p-hsa-miR-107   | chr11 | 3841759  | 3841780  | +   |
| hsa-miR-442     | chr3  | 25664875 | 25664891 | -   |
| p-hsa-miR-107   | chr11 | 3841759  | 3841780  | +   |
| hsa-miR-1119    | chr15 | 88608121 | 88608141 | +   |
| hsa-miR-3652    | chr12 | 1.04E+08 | 1.04E+08 | +   |
| hsa-miR-599     | chr8  | 99536651 | 99536670 | -   |
| hsa-miR-605-3p  | chr10 | 51299623 | 51299644 | +   |
| hsa-miR-4787-5p | chr3  | 50675093 | 50675114 | +   |
| p-hsa-miR-23    | chr19 | 5978996  | 5979018  | -   |
| p-hsa-miR-149   | chr15 | 57316657 | 57316678 | +   |
| hsa-miR-3165    | chr11 | 72072272 | 72072293 | -   |
| p-hsa-miR-97    | chr6  | 41223892 | 41223913 | +   |
| miRNA         | Type   | chr | Start (bp) | End (bp)  | Strand |
|--------------|--------|-----|-----------|----------|--------|
| hsa-miR-3064-5p | miRNA  | chr17 | 64500817  | 64500837 |        |
| p-hsa-miR-42  | novelmiRNA | chr1 | 1.5E+08   | 1.5E+08  | +      |
| hsa-miR-4506  | miRNA  | chr14 | 93948233  | 93948252 | -      |
| hsa-miR-7975  | miRNA  | chr19 | 55123225  | 55123242 | -      |
| hsa-miR-1537-5p | miRNA  | chr1  | 2.36E+08  | 2.36E+08 | -      |
| hsa-miR-3074-3p | miRNA  | chr9  | 95086024  | 95086045 | -      |
| hsa-miR-297   | miRNA  | chr4  | 1.11E+08  | 1.11E+08 | -      |
| hsa-miR-4745-3p | miRNA  | chr19 | 804977    | 804999   | +      |
| p-hsa-miR-329 | novelmiRNA | chr2 | 1.56E+08  | 1.56E+08 | -      |
| hsa-miR-181b-3p | miRNA  | chr13 | 98208533  | 98208554 | +      |
| hsa-miR-4800-3p | miRNA  | chr4  | 2250091   | 2250109  | -      |
| hsa-miR-1237-5p | miRNA  | chr11 | 10403505  | 10403525 | -      |
| hsa-miR-581   | miRNA  | chr5  | 53951564  | 53951584 | -      |
| hsa-miR-187-5p | miRNA  | chr18 | 35904871  | 35904892 | -      |
| hsa-miR-6750-5p | miRNA  | chr6  | 60890891  | 60891013 | -      |
| hsa-miR-3927  | miRNA  | chr1  | 1.44E+08  | 1.44E+08 | +      |
| p-hsa-miR-123 | novelmiRNA | chr1  | 2.08E+08  | 2.08E+08 | -      |
| hsa-miR-625-5p | miRNA  | chr14 | 65471116  | 65471136 | +      |
| hsa-miR-3065-3p | miRNA  | chr17 | 81125926  | 81125948 | +      |
| hsa-miR-6786-3p | miRNA  | chr17 | 81693844  | 81693866 | +      |
| hsa-miR-3972  | miRNA  | chr1  | 1.7277948 | 1.7277969 | +    |
| p-hsa-miR-137 | novelmiRNA | chr5  | 8910793   | 8910814  | +      |
| p-hsa-miR-331 | novelmiRNA | chr14 | 1.05E+08  | 1.05E+08 | +      |
| hsa-miR-3168  | miRNA  | chr13 | 41101076  | 41101092 | -      |
| hsa-miR-1181  | miRNA  | chr19 | 10403505  | 10403525 | -      |
| hsa-miR-4640-5p | miRNA  | chr6  | 30890891  | 30890913 | -      |
| hsa-miR-4701-5p | miRNA  | chr12 | 48772014  | 48772035 | -      |
| hsa-miR-6759-5p | miRNA  | chr12 | 57748660  | 57748682 | -      |
| hsa-miR-3922-3p | miRNA  | chr12 | 1.05E+08  | 1.05E+08 | +      |
| hsa-miR-3692-5p | miRNA  | chr6  | 1.58E+08  | 1.58E+08 | +      |
| hsa-miR-31-3p  | miRNA  | chr9  | 21512121  | 21512142 | -      |
| hsa-miR-7161-3p | miRNA  | chr6  | 1.59E+08  | 1.59E+08 | +      |
| hsa-miR-1290  | miRNA  | chr1  | 18897078  | 18897096 | -      |
| hsa-miR-920   | miRNA  | chr12 | 24212471  | 24212490 | +      |
| hsa-miR-548g-3p | miRNA  | chr4  | 1.47E+08  | 1.47E+08 | -      |
| hsa-miR-6762-3p | miRNA  | chr12 | 1.13E+08  | 1.13E+08 | +      |
| hsa-miR-6826-5p | miRNA  | chr3  | 1.29E+08  | 1.29E+08 | +      |
| hsa-miR-4321  | miRNA  | chr19 | 2250688   | 2250708  | +      |
| hsa-miR-513b-5p | miRNA  | chrX  | 1.47E+08  | 1.47E+08 | -      |
| hsa-miR-6849-3p | miRNA  | chr12 | 1.44E+08  | 1.44E+08 | -      |
| hsa-miR-933   | miRNA  | chr2  | 1.75E+08  | 1.75E+08 | -      |
| hsa-miR-4745-5p | miRNA  | chr19 | 804941    | 804963   | +      |
| hsa-miR-4277  | miRNA  | chr5  | 1708838   | 1708858  | -      |
| hsa-miR-6759-5p | miRNA  | chr12 | 57748656  | 57748677 | -      |
| hsa-miR-597-3p | miRNA  | chr5  | 9741729   | 9741751  | +      |
| hsa-miR-2116-3p | miRNA  | chr15 | 59171192  | 59171212 | +      |
| hsa-miR-6810-5p | miRNA  | chr6  | 43434600  | 43434620 | +      |
| hsa-miR-3115  | miRNA  | chr1  | 1.54E+08  | 1.54E+08 | -      |
| hsa-miR-593-3p | miRNA  | chr7  | 1.28E+08  | 1.28E+08 | +      |
| miRNA       | Type   | Chromosome | Start Base | End Base | Strand |
|------------|--------|------------|------------|----------|--------|
| hsa-miR-597-5p | miRNA  | chr8       | 9741687    | 9741708  | +      |
| hsa-miR-518b  | miRNA  | chr19      | 53702787   | 53702808 | +      |
| hsa-miR-96-3p  | miRNA  | chr7       | 1.3E+08    | 1.3E+08  | -      |
| hsa-miR-6870-3p | miRNA  | chr20      | 10649636   | 10649657 | -      |
| hsa-miR-548c-3p | miRNA  | chr12      | 64622569   | 64622590 | +      |
| hsa-miR-4662a-3p | miRNA  | chr8       | 1.25E+08   | 1.25E+08 | +      |
| hsa-miR-509-3-5p | miRNA  | chrX       | 1.47E+08   | 1.47E+08 | -      |
| hsa-miR-2278  | miRNA  | chr9       | 94809977   | 94809998 | +      |
| hsa-miR-6729-5p | miRNA  | chr1       | 12029163   | 12029184 | +      |
| hsa-miR-4781-5p | miRNA  | chr1       | 54054091   | 54054111 | +      |
| hsa-miR-2278  | miRNA  | chr9       | 94809977   | 94809998 | +      |
| hsa-miR-6729-5p | miRNA  | chr1       | 12029163   | 12029184 | +      |
| hsa-miR-4781-5p | miRNA  | chr1       | 54054091   | 54054111 | +      |
| miRNA   | chr | start       | end       | strand |
|---------|-----|-------------|-----------|--------|
| hsa-miR-6507-5p | chr10 | 98924543 | 98924563 | -      |
| hsa-miR-6877-3p | chr9  | 1.33E+08  | 1.33E+08  | +      |
| hsa-miR-4723-3p | chr17 | 28360712  | 28360733  | +      |
| hsa-miR-4728-3p | chr17 | 39726537  | 39726661  | +      |
| hsa-miR-4707-5p | chr14 | 22956998  | 22957020  | -      |
| hsa-miR-3943 | chr7  | 43150917  | 43150939  | +      |
| hsa-miR-193b-5p | chr16 | 14303980  | 14304001  | +      |
| hsa-miR-4525 | chr17 | 82668281  | 82668301  | -      |
| hsa-miR-5187-3p | chr1  | 1.61E+08  | 1.61E+08  | +      |
| p-hsa-miR-8 | chrY  | 1395424   | 1395444   | +      |
| hsa-miR-6802-5p | chr19 | 55239952  | 55239971  | -      |
| hsa-miR-4677-5p | chr1  | 2.43E+08  | 2.43E+08  | +      |
| hsa-miR-5589-5p | chr19 | 10038354  | 10038374  | +      |
| hsa-miR-548t-5p | chr4  | 1.73E+08  | 1.73E+08  | +      |
| hsa-miR-3192-3p | chr20 | 1.13E+08  | 1.13E+08  | -      |
| p-hsa-miR-12 | chr7  | 68920402  | 68920425  | -      |
| hsa-miR-1237-3p | chr11 | 64368683  | 64368703  | +      |
| hsa-miR-4530 | chr19 | 39409629  | 39409646  | -      |
| hsa-miR-4728-3p | chr17 | 6655481   | 6655502   | +      |
| hsa-miR-4682 | chr10 | 1.2E+08   | 1.2E+08   | +      |
| hsa-miR-6858-3p | chrX  | 1.54E+08  | 1.54E+08  | +      |
| p-hsa-miR-334 | novelmirna | 68920402 | 68920425 | -      |
| hsa-miR-1237-3p | chr11 | 64368683  | 64368703  | +      |
| hsa-miR-4306 | chr13 | 99643123  | 99643139  | +      |
| hsa-miR-346 | chr10 | 86260725  | 86260765  | +      |
| hsa-miR-6735-3p | chr1  | 1.37E+08  | 1.37E+08  | -      |
| p-hsa-miR-28 | novelmirna | 85473921 | 85473942 | +      |
| hsa-miR-508-3p | chrX  | 1.47E+08  | 1.47E+08  | -      |
| hsa-miR-7846-3p | chr1  | 12167010  | 12167030  | +      |
| hsa-miR-378c | chr10 | 1.31E+08  | 1.31E+08  | -      |
| hsa-miR-548as-5p | chr13 | 92490163  | 92490184  | +      |
| hsa-miR-6776-3p | chr17 | 2692861   | 2692863   | +      |
| p-hsa-miR-12 | chr7  | 28864130  | 28864150  | +      |
| hsa-miR-6835-5p | chr17 | 8145045   | 8145066   | +      |
| hsa-miR-6807-5p | chr19 | 58550285  | 58550306  | +      |
| hsa-miR-5942-5p | chr9  | 1.71E+08  | 1.71E+08  | -      |
| hsa-miR-6735-3p | chr1  | 43448590  | 43448611  | +      |
| hsa-miR-7315-5p | chr1  | 24919390  | 24919411  | -      |
| hsa-miR-381-5p | chr14 | 1.01E+08  | 1.01E+08  | +      |
| hsa-miR-4306 | chr13 | 99643123  | 99643139  | +      |
| hsa-miR-346 | chr10 | 86264747  | 86264769  | -      |
| hsa-miR-6075 | chr5  | 15107677  | 15107870  | -      |
| hsa-miR-6735-3p | chr1  | 8145045   | 8145066   | +      |
| hsa-miR-6835-5p | chr17 | 58550285  | 58550306  | +      |
| hsa-miR-3912-5p | chr5  | 1.71E+08  | 1.71E+08  | -      |
| hsa-miR-6735-3p | chr1  | 43448590  | 43448611  | +      |
| hsa-miR-7315-5p | chr1  | 24919390  | 24919411  | -      |
| hsa-miR-381-5p | chr14 | 1.01E+08  | 1.01E+08  | +      |
| hsa-miR-4306 | chr13 | 99643123  | 99643139  | +      |
| hsa-miR-346 | chr10 | 86264747  | 86264769  | -      |
| hsa-miR-6075 | chr5  | 15107677  | 15107870  | -      |
| hsa-miR-6735-3p | chr1  | 43448590  | 43448611  | +      |
| hsa-miR-7315-5p | chr1  | 24919390  | 24919411  | -      |
| hsa-miR-381-5p | chr14 | 1.01E+08  | 1.01E+08  | +      |
| hsa-miR-4306 | chr13 | 99643123  | 99643139  | +      |
| hsa-miR-346 | chr10 | 86264747  | 86264769  | -      |
| hsa-miR-6075 | chr5  | 15107677  | 15107870  | -      |
| hsa-miR-6735-3p | chr1  | 43448590  | 43448611  | +      |
| hsa-miR-7315-5p | chr1  | 24919390  | 24919411  | -      |
| hsa-miR-381-5p | chr14 | 1.01E+08  | 1.01E+08  | +      |
| hsa-miR-4306 | chr13 | 99643123  | 99643139  | +      |
| hsa-miR-346 | chr10 | 86264747  | 86264769  | -      |
| p-hsa-miR-316 | novelmirna | chr3 | 1.9E+08 | 1.9E+08 | + |
|----------------|------------|------|----------|----------|---|
| hsa-miR-4734  | miRNA      | chr17 | 38702270 | 38702291 | - |
| hsa-miR-450a-2-3p | miRNA       | chrX   | 1.35E+08 | 1.35E+08 | - |
| hsa-miR-6772-5p | miRNA      | chr16  | 57772326 | 57772347 | - |
| hsa-miR-6788-5p | miRNA      | chr18  | 10759624 | 10759644 | - |
| hsa-miR-105-3p | miRNA      | chr8   | 1.25E+08 | 1.25E+08 | - |
| hsa-miR-5008-3p | miRNA     | chr1   | 2.28E+08 | 2.28E+08 | - |
| hsa-miR-7160-5p | miRNA     | chr8   | 2076589 | 2076609 | + |
| hsa-miR-3940-5p | miRNA     | chr19  | 18883250 | 18883271 | - |
| hsa-miR-6791-5p | miRNA     | chr19  | 18883250 | 18883271 | - |
| hsa-miR-3939-3p | miRNA     | chr12  | 5632533 | 5632556 | + |
| hsa-miR-6763-3p | miRNA     | chr12  | 5632533 | 5632556 | + |
| hsa-miR-6756-3p | miRNA     | chr11  | 2173072 | 2173094 | + |
| hsa-miR-6685-5p | miRNA     | chr17  | 81693809 | 81693829 | + |
| hsa-miR-6861-5p | miRNA     | chr12  | 11206807 | 11206845 | + |
| hsa-miR-548az-5p | miRNA   | chr8   | 1.19E+08 | 1.19E+08 | + |
| hsa-miR-6727-3p | miRNA     | chr17  | 13611188 | 13611188 | + |
| hsa-miR-3129-5p | miRNA     | chr2   | 1.89E+08 | 1.89E+08 | - |
| hsa-miR-3920 | miRNA | chr11  | 1.02E+08 | 1.02E+08 | - |
| hsa-miR-4526 | miRNA | chr18  | 13611187 | 13611188 | + |
| hsa-miR-4690-5p | miRNA     | chr11  | 65636310 | 65636331 | + |
| hsa-miR-6786-5p | miRNA     | chr17  | 81693809 | 81693829 | + |
| hsa-miR-1256 | miRNA | chr1   | 20988377 | 20988398 | - |
| hsa-miR-7109-5p | miRNA     | chr22  | 31621506 | 31621526 | - |
| hsa-miR-3117-5p | miRNA     | chr17  | 38915017 | 38915037 | + |
| hsa-miR-3939-3p | miRNA     | chr12  | 11206807 | 11206845 | + |
| hsa-miR-3680-5p | miRNA     | chr16  | 29599231 | 29599232 | - |
| hsa-miR-3920 | miRNA | chr11  | 1.02E+08 | 1.02E+08 | - |
| hsa-miR-4677-5p | miRNA     | chr9   | 35608096 | 35608117 | + |
| hsa-miR-3675-3p | miRNA     | chr17  | 4970123 | 4970145 | - |
| hsa-miR-6784-3p | miRNA     | chr17  | 45114367 | 45114388 | - |
| hsa-miR-6727-3p | miRNA     | chr1   | 1312502 | 1312521 | - |
| hsa-miR-4478 | miRNA | chr9   | 1.22E+08 | 1.22E+08 | - |
| hsa-miR-6844 | miRNA | chr8   | 1.25E+08 | 1.25E+08 | - |
| p-hsa-miR-248 | novelmirna | chr2  | 96483588 | 96483609 | - |
| miRNA   | strand | chromosome | start | end   |
|---------|--------|------------|-------|-------|
| p-hsa-miR-252 | novelmirna | chr9      | 1.29E+08 | 1.29E+08 |
| hsa-miR-2276-3p | miRNA    | chr13     | 24162469 | 24162490 |
| hsa-miR-5003-5p | miRNA    | chr5      | 1.73E+08 | 1.73E+08 |
| hsa-miR-4655-5p | miRNA    | chr7      | 1844223  | 1844244  |
| hsa-miR-4330 | miRNA    | chrX      | 1.51E+08 | 1.51E+08 |
| hsa-miR-6785-3p | miRNA    | chr17     | 75498608 | 75498628 |
| hsa-miR-4325 | miRNA    | chr20     | 57321564 | 57321581 |
| hsa-miR-3136-3p | miRNA    | chr3      | 69048966 | 69048987 |
| hsa-miR-6801-3p | miRNA    | chr19     | 52222074 | 52222093 |
| hsa-miR-6716-3p | miRNA    | chr11     | 1.19E+08 | 1.19E+08 |
| hsa-miR-6759-3p | miRNA    | chr12     | 1.24E+08 | 1.24E+08 |
| hsa-miR-4758-5p | miRNA    | chr20     | 62332534 | 62332556 |
| hsa-miR-6880-5p | miRNA    | chr12     | 1.24E+08 | 1.24E+08 |
| hsa-miR-4701-3p | miRNA    | chr12     | 48771980 | 48771999 |
| hsa-miR-487a-5p | miRNA    | chr14     | 1.01E+08 | 1.01E+08 |
| hsa-miR-129-5p | miRNA    | chr11     | 43581408 | 43581428 |
| hsa-miR-3122 | miRNA    | chr1      | 2.12E+08 | 2.12E+08 |
| hsa-miR-422a | miRNA    | chr15     | 63870989 | 63871010 |
| hsa-miR-1185-2-3p | miRNA    | chr14     | 1.01E+08 | 1.01E+08 |
| hsa-miR-6794-3p | miRNA    | chr19     | 12852306 | 12852325 |
| hsa-miR-2682-3p | miRNA    | chr1      | 98045271 | 98045292 |
| hsa-miR-3159 | miRNA    | chr11     | 18387796 | 18387817 |
| hsa-miR-8081 | miRNA    | chr9      | 1.07E+08 | 1.07E+08 |
| hsa-miR-921 | miRNA    | chr1      | 1.66E+08 | 1.66E+08 |
| p-hsa-miR-196 | novelmirna | chr22     | 25257858 | 25257881 |
| hsa-miR-5690 | miRNA    | chr6      | 35664760 | 35664780 |
| hsa-miR-4757-5p | miRNA    | chr2      | 19348439 | 19348461 |
| hsa-miR-4665-3p | miRNA    | chr9      | 6007871  | 6007896  |
| hsa-miR-3606-3p | miRNA    | chr2      | 1.89E+08 | 1.89E+08 |
| hsa-miR-4755-5p | miRNA    | chr20     | 34049128 | 34049149 |
| hsa-miR-4709-3p | miRNA    | chr14     | 74480135 | 74480157 |
| p-hsa-miR-18 | novelmirna | chr14     | 36204593 | 36204614 |
| p-hsa-miR-4320 | miRNA    | chr18     | 50126509 | 50126526 |
| hsa-miR-873-3p | miRNA    | chr9      | 28888889 | 28888910 |
| hsa-miR-5584-5p | miRNA    | chr1      | 44545493 | 44545514 |
| hsa-miR-3924 | miRNA    | chr7      | 57304489 | 57304510 |
| hsa-miR-4446-5p | miRNA    | chr3      | 1.14E+08 | 1.14E+08 |
| hsa-miR-4802-3p | miRNA    | chr4      | 40502051 | 40502073 |
| hsa-miR-124-3p | miRNA    | chr20     | 63178552 | 63178571 |
| hsa-miR-1225-5p | miRNA    | chr16     | 2090263  | 2090284  |
| hsa-miR-4755-3p | miRNA    | chr20     | 34049162 | 34049183 |
| hsa-miR-6878-3p | miRNA    | chr1      | 1.5E+08  | 1.5E+08  |
| hsa-miR-1276 | miRNA    | chr15     | 85770548 | 85770567 |
| hsa-miR-1292-3p | miRNA    | chr20     | 2652819  | 2652838  |
| p-hsa-miR-43 | novelmirna | chr1      | 1.5E+08  | 1.5E+08  |
| hsa-miR-2113 | miRNA    | chr6      | 98024586 | 98024606 |
| hsa-miR-3191-3p | miRNA    | chr19     | 47226952 | 47226974 |
| hsa-miR-4254 | miRNA    | chr1      | 31758670 | 31758692 |
| p-hsa-miR-189 | novelmirna | chr8      | 76934580 | 76934600 |
| p-hsa-miR-72 | novelmirna | chr14     | 52177921 | 52177938 |
| hsa-miR-514b-5p | miRNA    | chrX      | 1.47E+08 | 1.47E+08 |
| hsa-miR-7843-5p | miRNA    | chr14     | 72516831 | 72516852 |
| hsa-miR-141-5p | miRNA    | chr12     | 6964113  | 6964134  |
| ID     | Type       | chr  | Start   | End     | Strand |
|--------|------------|------|---------|---------|--------|
| hsa-miR-4782-3p | miRNA     | chr2 | 1.14E+08 | 1.14E+08 | -      |
| hsa-miR-6845-5p  | miRNA     | chr8 | 1.44E+08 | 1.44E+08 | -      |
| p-hsa-miR-38     | novelmirna| chr22_KI2 | 152965  | 152984  | -      |
| hsa-miR-4654     | miRNA     | chr1 | 1.62E+08 | 1.62E+08 | +      |
| hsa-miR-4748     | miRNA     | chr19| 1.0780263 | 1.0780283 | +      |
| p-hsa-miR-332    | novelmirna| chr1 | 2.32E+08 | 2.32E+08 | +      |
| p-hsa-miR-98     | novelmirna| chr7  | 6.4946376 | 6.4946396 | +      |
| hsa-miR-1205     | miRNA     | chr8  | 1.28E+08 | 1.28E+08 | +      |
| hsa-miR-1206     | miRNA     | chr8  | 1.28E+08 | 1.28E+08 | +      |
| hsa-miR-4693-3p  | miRNA     | chr11 | 1.04E+08 | 1.04E+08 | +      |
| hsa-miR-6735-3p  | miRNA     | chr11 | 6.804932 | 6.804953 | +      |
| hsa-miR-1910-3p  | miRNA     | chr16 | 8.5741631 | 8.5741650 | -      |
| p-hsa-miR-181    | novelmirna| chr2  | 7.6187762 | 7.6187783 | +      |
| hsa-miR-6796-5p  | miRNA     | chr19 | 4.0369851 | 4.0369873 | +      |
| p-hsa-miR-17     | novelmirna| chr14 | 7.6956511 | 7.6956530 | -      |
| p-hsa-miR-170    | novelmirna| chr2  | 7.6187725 | 7.6187746 | +      |
| hsa-miR-6806-5p  | miRNA     | chr19 | 5.8334693 | 5.8334716 | +      |
| hsa-miR-3677-5p  | miRNA     | chr16 | 2.270715  | 2.270736 | +      |
| hsa-miR-4417     | miRNA     | chr1  | 5.564082  | 5.564099 | +      |
| hsa-miR-513c-5p  | miRNA     | chrX  | 1.47E+08  | 1.47E+08 | -      |
| hsa-miR-4683     | miRNA     | chr10 | 3.5641181 | 3.5641203 | -      |
| p-hsa-miR-263    | novelmirna| chr9  | 6.4451844 | 6.4451866 | +      |
| hsa-miR-6818-5p  | miRNA     | chr22 | 3.0007054 | 3.0007075 | +      |
| hsa-miR-5188     | miRNA     | chr12 | 1.25E+08  | 1.25E+08 | +      |
| hsa-miR-4496     | miRNA     | chr12 | 1.09E+08  | 1.09E+08 | +      |
| hsa-miR-8082     | miRNA     | chr4  | 1.13E+08  | 1.13E+08 | +      |
| hsa-miR-370-5p   | miRNA     | chr14 | 1.01E+08  | 1.01E+08 | +      |
| hsa-miR-2114-5p  | miRNA     | chrX  | 1.5E+08   | 1.5E+08 | +      |
| hsa-miR-4632-3p  | miRNA     | chr1  | 1.2191752 | 1.2191773 | +      |
| hsa-miR-5088-5p  | miRNA     | chr19 | 4.9682122 | 4.9682145 | +      |
| p-hsa-miR-80     | novelmirna| chr9  | 8.7796962 | 8.7796982 | -      |
| hsa-miR-5187-5p  | miRNA     | chr1  | 1.61E+08  | 1.61E+08 | +      |
| hsa-miR-7112-5p  | miRNA     | chr8  | 1.44E+08  | 1.44E+08 | -      |
| hsa-miR-6745     | miRNA     | chr11 | 4.7179615 | 4.7179635 | -      |
| p-hsa-miR-20     | novelmirna| chr1  | 5.6436546 | 5.6436568 | +      |
| hsa-miR-4518     | miRNA     | chr16 | 3.0503968 | 3.0503993 | +      |
| hsa-miR-4708-5p  | miRNA     | chr14 | 6.5335155 | 6.5335175 | -      |
| hsa-miR-5002-5p  | miRNA     | chr3  | 1.24E+08  | 1.24E+08 | +      |
| hsa-miR-512-3p   | miRNA     | chr19 | 5.3669213 | 5.3669234 | +      |
| hsa-miR-6767-3p  | miRNA     | chr16 | 2.445436  | 2.445457 | +      |
| p-hsa-miR-165    | novelmirna| chr2  | 1.76E+08  | 1.76E+08 | +      |
| p-hsa-miR-314    | novelmirna| chr17_KI2 | 2.621322 | 2.621343 | -      |
| hsa-miR-224-3p   | miRNA     | chrX  | 1.52E+08  | 1.52E+08 | -      |
| hsa-miR-3657     | miRNA     | chr12 | 1.12E+08  | 1.12E+08 | -      |
| hsa-miR-6747-5p  | miRNA     | chr11 | 6.2567043 | 6.2567066 | -      |
| hsa-miR-6748-5p  | miRNA     | chr11 | 6.2789820 | 6.2789841 | +      |
| hsa-miR-3183     | miRNA     | chr17 | 1.022529  | 1.022550 | -      |
| hsa-miR-4697-3p  | miRNA     | chr11 | 1.34E+08  | 1.34E+08 | -      |
| hsa-miR-4797-5p  | miRNA     | chr3  | 1.97E+08  | 1.97E+08 | -      |
| p-hsa-miR-83     | novelmirna| chr2  | 6.4763720 | 6.4763741 | +      |
| hsa-miR-7106-3p  | miRNA     | chr12 | 1.13E+08  | 1.13E+08 | -      |
| hsa-miR-3661     | miRNA     | chr5  | 1.34E+08  | 1.34E+08 | +      |
| hsa-miR-95-5p    | miRNA     | chr4  | 8.005347  | 8.005367 | -      |
| hsa-miR-548as-3p | miRNA     | chr13 | 9.2490199 | 9.2490220 | +      |
| hsa-miR-6069     | miRNA     | chr22 | 3.5336768 | 3.5336788 | -      |
| hsa-miR-2052     | miRNA     | chr8  | 7.4705694 | 7.4705713 | +      |
| ID               | Type   | Chromosome | Start   | End     | Strand |
|-----------------|--------|------------|---------|---------|--------|
| hsa-miR-6795-5p | miRNA  | chr19      | 15179322| 15179345| -      |
| p-hsa-miR-187   | novelmiRNA | chr5       | 1.55E+08| 1.55E+08| +      |
| hsa-miR-4687-3p | miRNA  | chr11      | 3856113 | 3856133 | +      |
| hsa-miR-4668-3p | miRNA  | chr9       | 1.12E+08| 1.12E+08| +      |
| hsa-let-7c-3p   | miRNA  | chr21      | 16539883| 16539904| +      |
| hsa-miR-1183    | miRNA  | chr7       | 21471105| 21471131| +      |
| hsa-miR-4438    | miRNA  | chr2       | 2.14E+08| 2.14E+08| +      |
| hsa-miR-4519    | miRNA  | chr16      | 30875301| 30875318| -      |
| hsa-miR-4792    | miRNA  | chr3       | 24521412| 24521429| -      |
| p-hsa-miR-874-5p| miRNA  | chr7       | 5711883 | 5711905 | -      |
| p-hsa-miR-223   | novelmiRNA | chr6       | 81765751| 81765771| -      |
| hsa-miR-499b-3p | miRNA  | chr10      | 32506305| 32506326| +      |
| hsa-miR-519d-3p | miRNA  | chr19      | 53713400| 53713421| +      |
| hsa-miR-538      | miRNA  | chr19      | 10718419| 10718443| +      |
| hsa-miR-548ay-3p| miRNA  | chr3       | 32506305| 32506326| +      |
| hsa-miR-5697    | miRNA  | chr1       | 9967390 | 9967411 | +      |
| hsa-miR-5790-3p | miRNA  | chr20      | 62564933| 62564954| +      |
| p-hsa-miR-179   | novelmiRNA | chr1       | 47180432| 47180451| +      |
| hsa-miR-1287-3p | miRNA  | chr10      | 98395232| 98395253| -      |
| hsa-miR-6780b-5p| miRNA  | chr6       | 43434547| 43434569| +      |
| hsa-miR-6809-5p | miRNA  | chr2       | 2.1E+08  | 2.1E+08  | +      |
| hsa-miR-6775-3p | miRNA  | chr16      | 87834592| 87834612| -      |
| hsa-miR-6924-5p | miRNA  | chr1       | 94745880| 94745899| -      |
| p-hsa-miR-279   | novelmiRNA | chr14      | 31208907| 31208929| +      |
| hsa-miR-6869-5p | miRNA  | chr20      | 1392940 | 1392961 | -      |
| hsa-miR-4722-5p | miRNA  | chr16      | 88716315| 88716337| -      |
| hsa-miR-6807-3p | miRNA  | chr19      | 58550354| 58550376| +      |
| hsa-miR-3120-5p | miRNA  | chr1       | 1.72E+08| 1.72E+08| +      |
| hsa-miR-6752-5p | miRNA  | chr11      | 67490250| 67490271| +      |
| hsa-miR-7114-3p | miRNA  | chr9       | 1.37E+08| 1.37E+08| -      |
| hsa-miR-7843-3p | miRNA  | chr14      | 72516866| 72516887| +      |
| hsa-miR-200b-5p | miRNA  | chr1       | 1167124 | 1167145 | +      |
| hsa-miR-4270    | miRNA  | chr3       | 15496279| 15496298| -      |
| hsa-miR-1272    | miRNA  | chr15      | 64762471| 64762496| -      |
| hsa-miR-548ab   | miRNA  | chr3       | 1.04E+08| 1.04E+08| -      |
| hsa-miR-455-5p  | miRNA  | chr9       | 1.14E+08| 1.14E+08| +      |
| hsa-miR-4773    | miRNA  | chr2       | 1.51E+08| 1.51E+08| -      |
| hsa-miR-6792-3p | miRNA  | chr19      | 7617439 | 7617459 | +      |
| p-hsa-miR-240   | novelmiRNA | chr8       | 80894029| 80894050| +      |
| p-hsa-miR-61    | novelmiRNA | chr14_KI270847v1_alt| 355123 | 355145 | -      |
| hsa-miR-4796-3p | miRNA  | chr3       | 1.15E+08| 1.15E+08| -      |
| hsa-miR-4726-5p | miRNA  | chr17      | 38719691| 38719713| +      |
| hsa-miR-4317    | miRNA  | chr18      | 6374399 | 6374415 | -      |
| hsa-miR-7110-5p | miRNA  | chr3       | 1.23E+08| 1.23E+08| +      |
| hsa-miR-3667-3p | miRNA  | chr22      | 49543401| 49543422| -      |
| Genomic ID   | Type     | Chromosome | Start Position | End Position | Strand |
|-------------|----------|------------|----------------|--------------|--------|
| hsa-miR-4726-3p | miRNA   | chr17      | 38719727       | 38719748     | +      |
| hsa-miR-6743-5p | miRNA   | chr11      | 209341         | 209362       | +      |
| hsa-miR-4539   | miRNA   | chr14      | 1.06E+08       | 1.06E+08     | -      |
| hsa-miR-4679   | miRNA   | chr10      | 89063381       | 89063402     | -      |
| hsa-miR-601    | miRNA   | chr9       | 1.23E+08       | 1.23E+08     | -      |
| hsa-miR-630    | miRNA   | chr15      | 72587277       | 72587298     | +      |
| hsa-miR-6742-3p | miRNA   | chr1       | 2.28E+08       | 2.28E+08     | -      |
| p-hsa-miR-110  | novelmiRNA | chr6   | 38662737       | 38662757     | +      |
| p-hsa-miR-308  | novelmiRNA | chr9   | 1.23E+08       | 1.23E+08     | +      |
| hsa-miR-6749-5p | miRNA   | chr11      | 64902429       | 64902450     | -      |
| hsa-miR-133a-3p | miRNA   | chr20      | 62564970       | 62564991     | +      |
| hsa-miR-690    | miRNA   | chrX       | 1.46E+08       | 1.46E+08     | -      |
| hsa-miR-1238-3p | miRNA   | chr19      | 10552183       | 10552202     | +      |
| hsa-miR-391    | miRNA   | chr9       | 1.28E+08       | 1.28E+08     | -      |
| hsa-miR-3918   | miRNA   | chr6       | 1.59E+08       | 1.59E+08     | -      |
| hsa-miR-6774-3p | miRNA   | chr16      | 85918396       | 85918416     | +      |
| p-hsa-miR-116  | novelmiRNA | chrX   | 94177629       | 94177650     | +      |
| hsa-miR-6742-3p | miRNA   | chr1       | 2.28E+08       | 2.28E+08     | -      |
| p-hsa-miR-110  | novelmiRNA | chr6   | 143137007      | 143137029    | +      |
| hsa-miR-3164   | miRNA   | chr11      | 69083185       | 69083206     | +      |
| hsa-miR-6799b-3p | miRNA   | chr1       | 2.06E+08       | 2.06E+08     | +      |
| hsa-miR-1914-3p | miRNA   | chr20      | 63941474       | 63941495     | -      |
| hsa-miR-3197   | miRNA   | chr21      | 41167564       | 41167586     | +      |
| hsa-miR-520f-5p | miRNA   | chr19      | 53682173       | 53682194     | +      |
| hsa-miR-523-3p | miRNA   | chr19      | 53698437       | 53698459     | +      |
| hsa-miR-548a-5p | miRNA   | chr13      | 1.14E+08       | 1.14E+08     | +      |
| hsa-miR-6068   | miRNA   | chr1       | 63326964       | 63326984     | -      |
| hsa-miR-6794-5p | miRNA   | chr19      | 12852265       | 12852284     | +      |
| hsa-miR-6816-5p | miRNA   | chr22      | 20114726       | 20114746     | -      |
| hsa-miR-6850-3p | miRNA   | chr8       | 1.45E+08       | 1.45E+08     | -      |
| p-hsa-miR-239  | novelmiRNA | chr9   | 18438312       | 18438330     | -      |
| hsa-miR-3180-3p | miRNA   | chr16      | 18402189       | 18402210     | -      |
| p-hsa-miR-157  | novelmiRNA | chr8_KI270 | 103532        | 103549       | -      |
| hsa-miR-34a-5p | miRNA   | chr1       | 9151735        | 9151756      | -      |
| hsa-miR-3682-5p | miRNA   | chr2       | 53849170       | 53849191     | -      |
| hsa-miR-4719   | miRNA   | chr16      | 76868988       | 76869009     | +      |
| hsa-miR-548v   | miRNA   | chr8       | 17681588       | 17681609     | -      |
| hsa-miR-4430   | miRNA   | chr2       | 33418519       | 33418536     | +      |
| p-hsa-miR-161  | novelmiRNA | chr8_KI270   | 2.3E+08        | 2.3E+08     | +      |
| p-hsa-miR-219  | novelmiRNA | chr2   | 69302094       | 69302115     | -      |
| hsa-miR-365a-5p | miRNA   | chr16      | 14309300       | 14309322     | +      |
| hsa-miR-1296-3p | miRNA   | chr10      | 63372969       | 63372990     | -      |
| hsa-miR-4480   | miRNA   | chr10      | 12578796       | 12578816     | +      |
| hsa-miR-8079   | miRNA   | chr13      | 44196171       | 44196190     | -      |
| hsa-miR-9-5p   | miRNA   | chr15      | 89368032       | 89368054     | +      |
| hsa-miR-3916   | miRNA   | chr1       | 2.47E+08       | 2.47E+08     | -      |
| hsa-miR-3622a-3p | miRNA   | chr8       | 27701726       | 27701747     | +      |
| hsa-miR-3153   | miRNA   | chr9       | 89312274       | 89312296     | +      |
| hsa-miR-1200   | miRNA   | chr7       | 36919403       | 36919424     | -      |
| hsa-miR-1203   | miRNA   | chr17      | 48156486       | 48156506     | -      |
| hsa-miR-1238-5p | miRNA   | chr19      | 10552122       | 10552144     | +      |
| hsa-miR-200c-5p | miRNA   | chr12      | 593703         | 593703       | -      |
| hsa-miR-34b-3p | miRNA   | chr11      | 1.12E+08       | 1.12E+08     | +      |
| hsa-miR-378b   | miRNA   | chr3       | 10330262       | 10330280     | +      |
| hsa-miR-3925-5p | miRNA   | chr6       | 36622480       | 36622501     | -      |
| hsa-miR-4271   | miRNA   | chr3       | 49274158       | 49274176     | +      |
| hsa-miR-4292   | miRNA   | chr9       | 1.37E+08       | 1.37E+08     | +      |
| miRNA       | chromosome | start position | end position | strand |
|-------------|------------|----------------|--------------|--------|
| hsa-miR-4296 | chr10      | 1,25E+08       | 1,25E+08     | -      |
| hsa-miR-4425 | chr1       | 25023552       | 25023573     | +      |
| hsa-miR-4520-3p | chr17   | 6655447        | 6655468      | -      |
| hsa-miR-4641  | chr6       | 41598764       | 41598787     | +      |
| hsa-miR-4661-3p | chr8    | 91205531       | 91205552     | +      |
| hsa-miR-4664-5p | chr8     | 1,44E+08       | 1,44E+08     | -      |
| hsa-miR-4673  | chr9       | 1,37E+08       | 1,37E+08     | -      |
| hsa-miR-4764-3p | chr22   | 33436588       | 33436609     | +      |
| hsa-miR-4790-5p | chr3     | 5250227        | 5250246      | -      |
| hsa-miR-515-3p | chr19    | 53685059       | 53685080     | +      |
| hsa-miR-639   | chr19      | 14529603       | 14529625     | +      |
| hsa-miR-6755-5p | chr14   | 1,05E+08       | 1,05E+08     | +      |
| hsa-miR-6838-3p | chr7     | 44073378       | 44073397     | -      |
| p-hsa-miR-270 | chr16      | 85868355       | 85868856     | -      |
| p-hsa-miR-339 | chr11      | 73238761       | 73238782     | +      |
| hsa-miR-373-5p | chr19    | 53788710       | 53788731     | +      |
| hsa-miR-6765-5p | chr18    | 28958587       | 28958611     | +      |
| hsa-miR-6506-3p | chr16    | 15611031       | 15611052     | -      |
| hsa-miR-514a-5p | chrX    | 1E+08          | 1E+08        | +      |
| hsa-miR-4437  | chr2       | 1,81E+08       | 1,81E+08     | -      |
| hsa-miR-6828-5p | chr7    | 641748         | 641769       | -      |
| hsa-miR-4512  | chr15      | 66496965       | 66496986     | -      |
| hsa-miR-6766-5p | chr12   | 1,11E+08       | 1,11E+08     | +      |
| hsa-miR-936   | chr10      | 1,04E+08       | 1,04E+08     | -      |
| p-hsa-miR-147 | chr16_KI270855v1_alt | 35107 | 35130 | +      |
| p-hsa-miR-295 | chr10      | 20502310       | 20502330     | -      |
| p-hsa-miR-3672 | chr10   | 45197734       | 45197755     | -      |
| miRNA       | chromosome | start | end   | strand |
|-------------|------------|-------|-------|--------|
| hsa-miR-6769a-5p | chr16     | 4671323 | 4671343 | +      |
| hsa-miR-6778-5p   | chr17     | 18340860 | 18340881 | -      |
| hsa-miR-600       | chr9      | 1.23E+08 | 1.23E+08 | -      |
| hsa-miR-4499      | chr13     | 20433830 | 20433846 | -      |
| hsa-miR-1321      | chrX      | 85835832 | 85835849 | +      |
| hsa-miR-380-5p    | chr14     | 1.01E+08 | 1.01E+08 | +      |
| hsa-miR-4640-3p   | chr6      | 30890949 | 30890970 | +      |
| hsa-miR-4680-5p   | chr10     | 1.11E+08 | 1.11E+08 | +      |
| hsa-miR-6817-5p   | chr22     | 25455651 | 25455674 | +      |
| hsa-miR-6819-5p   | chr22     | 36286881 | 36286902 | -      |
| hsa-miR-6878-5p   | chr1      | 1.5E+08  | 1.5E+08  | +      |
| hsa-miR-328-5p    | chr16     | 67202367 | 67202389 | -      |
| hsa-miR-219b-3p   | chr9      | 1.28E+08 | 1.28E+08 | +      |
| hsa-miR-4747-5p   | chr19     | 4932687 | 4932708 | +      |
| hsa-miR-3659      | chr1      | 38089289 | 38089309 | +      |
| hsa-miR-3936      | chr5      | 1.32E+08 | 1.32E+08 | -      |
| hsa-miR-4462      | chr6      | 37555366 | 37555388 | -      |
| hsa-miR-4703-5p   | chr13     | 51552599 | 51552621 | +      |
| hsa-miR-6134      | chrX      | 28495575 | 28495593 | -      |
| hsa-miR-622       | chr13     | 90231242 | 90231262 | +      |
| hsa-miR-8066      | chr4      | 1.01E+08 | 1.01E+08 | -      |
| hsa-miR-885-3p    | chr3      | 10394499 | 10394520 | -      |
| p-hsa-miR-36      | novelmirna| 102413  | 102436  | +      |
| hsa-miR-6740-3p   | chr1      | 2.02E+08 | 2.02E+08 | +      |
| hsa-miR-4766-3p   | chr22     | 40813893 | 40813913 | -      |
| hsa-miR-6126      | chr16     | 3485422  | 3485439  | -      |
| hsa-miR-4721      | chr16     | 28843927 | 28843948 | -      |
| hsa-miR-3678-5p   | chr17     | 75406077 | 75406096 | +      |
| hsa-miR-4510      | chr15     | 35926863 | 35926884 | +      |
| hsa-miR-4666a-3p  | chr1      | 2.28E+08 | 2.28E+08 | +      |
| hsa-miR-4716-3p   | chr15     | 49169079 | 49169100 | -      |
| hsa-miR-5004-5p   | chr6      | 33438351 | 33438372 | +      |
| hsa-miR-518d-3p   | chr19     | 53734929 | 53734949 | +      |
| hsa-miR-5197-3p   | chr5      | 1.44E+08 | 1.44E+08 | +      |
| hsa-miR-6508-3p   | chr21     | 39447046 | 39447067 | +      |
| hsa-miR-7114-5p   | chr9      | 1.37E+08 | 1.37E+08 | -      |
| p-hsa-miR-236     | novelmirna| 2580021  | 25800240 | +      |
| p-hsa-miR-297     | novelmirna| 2.22E+08 | 2.22E+08 | -      |
| p-hsa-miR-327     | novelmirna| 78572428 | 78572448 | -      |
| hsa-miR-6515-3p   | chr19     | 12940521 | 12940540 | +      |
| hsa-miR-1324      | chr3      | 75630823 | 75630846 | +      |
| hsa-miR-568       | chr3      | 1.14E+08 | 1.14E+08 | -      |
| hsa-miR-656-5p    | chr14     | 1.01E+08 | 1.01E+08 | +      |
| hsa-miR-6811-5p   | chr2      | 2.38E+08 | 2.38E+08 | +      |
| hsa-miR-8057      | chr18     | 26591505 | 26591525 | -      |
| hsa-miR-149-5p    | chr2      | 2.4E+08  | 2.4E+08  | +      |
| hsa-miR-198       | chr3      | 1.2E+08  | 1.2E+08  | -      |
| hsa-miR-3121-5p   | chr1      | 1.8E+08  | 1.8E+08  | -      |
| hsa-miR-3150b-3p  | chr8      | 95072924 | 95072944 | -      |
| hsa-miR-3666      | chr7      | 1.15E+08 | 1.15E+08 | +      |
| hsa-miR-3685      | chr12     | 95309928 | 95309949 | +      |
| hsa-miR-378e      | chr5      | 1.7E+08  | 1.7E+08  | +      |
| hsa-miR-3935      | chr16     | 56245577 | 56245598 | +      |
| hsa-miR-4283      | chr7      | 63621100 | 63621116 | +      |
| hsa-miR-4453      | chr4      | 1.53E+08 | 1.53E+08 | +      |
| hsa-miR-4699-3p   | chr12     | 81158433 | 81158454 | +      |
| miRNA       | chromosome | start position | end position | strand |
|------------|------------|----------------|--------------|--------|
| hsa-miR-4724-5p | chr17      | 31534893       | 31534915     | +      |
| hsa-miR-4754    | chr19      | 58386827       | 58386849     | -      |
| hsa-miR-4786-3p | chr2       | 2.4E+08        | 2.4E+08      | +      |
| hsa-miR-4798-3p | chr4       | 7310496        | 7310517      | +      |
| hsa-miR-514b-3p | chrX       | 1.47E+08       | 1.47E+08     | +      |
| hsa-miR-5694    | chr14      | 67441902       | 67441922     | -      |
| hsa-miR-6081    | chr9       | 95065406       | 95065429     | +      |
| hsa-miR-6086    | chrX       | 13590293       | 13590312     | +      |
| hsa-miR-614     | chr12      | 12915882       | 12915904     | +      |
| hsa-miR-6871-3p | chr20      | 41169057       | 41169078     | +      |
| p-hsa-miR-111   | chr22      | 47512876       | 47512894     | +      |
| p-hsa-miR-328   | chr7       | 1.668014       | 1.668036     | +      |
| hsa-miR-449a    | chr5       | 55170586       | 55170607     | -      |
| hsa-miR-6837-5p | chr7       | 44051771       | 44051791     | +      |
| hsa-miR-4708-3p | chr14      | 65335123       | 65335144     | -      |
| hsa-miR-6746-3p | chr11      | 61878216       | 61878237     | -      |
| hsa-miR-124-5p  | chr20      | 63178514       | 63178535     | +      |
| hsa-miR-1267    | chr13      | 1.08E+08       | 1.08E+08     | +      |
| hsa-miR-205-5p  | chr1       | 2.09E+08       | 2.09E+08     | +      |
| hsa-miR-3155a   | chr10      | 6152247        | 6152267      | +      |
| hsa-miR-3185    | chr17      | 48724446       | 48724468     | -      |
| hsa-miR-3616-5p | chr20      | 47166985       | 47167006     | +      |
| hsa-miR-3919    | chr3       | 1.59E+08       | 1.59E+08     | +      |
| hsa-miR-3923    | chr3       | 79507937       | 79507958     | +      |
| hsa-miR-4265    | chr2       | 1.09E+08       | 1.09E+08     | +      |
| hsa-miR-4290    | chr9       | 90023451       | 90023469     | -      |
| hsa-miR-4310    | chr15      | 41866505       | 41866520     | -      |
| hsa-miR-4419a   | chr1       | 23057880       | 23057896     | -      |
| hsa-miR-4419b   | chr12      | 1.28E+08       | 1.28E+08     | +      |
| hsa-miR-4427    | chr1       | 2.34E+08       | 2.34E+08     | +      |
| hsa-miR-4436b-5p| chr2       | 1.1E+08        | 1.1E+08      | +      |
| hsa-miR-4456    | chr5       | 535861         | 535877       | -      |
| hsa-miR-4457    | chr5       | 1309314        | 1309335      | -      |
| hsa-miR-4486    | chr11      | 19575314       | 19575330     | +      |
| hsa-miR-455-3p  | chr9       | 1.14E+08       | 1.14E+08     | +      |
| hsa-miR-4645-5p | chr6       | 2854079        | 2854097      | -      |
| hsa-miR-4658    | chr7       | 1E+08          | 1E+08        | -      |
| hsa-miR-466     | chr3       | 31161714       | 31161736     | -      |
| hsa-miR-4681    | chr10      | 1.19E+08       | 1.19E+08     | +      |
| hsa-miR-4693-5p | chr11      | 1.04E+08       | 1.04E+08     | +      |
| hsa-miR-4722-3p | chr16      | 88716278       | 88716299     | -      |
| hsa-miR-4756-5p | chr20      | 54068452       | 54068474     | -      |
| hsa-miR-4793-3p | chr3       | 48644201       | 48644223     | -      |
| hsa-miR-489-5p  | chr7       | 93483985       | 93484006     | -      |
| hsa-miR-497-3p  | chr17      | 7017938        | 7017959      | -      |
| hsa-miR-5000-5p | chr2       | 75090835       | 75090856     | +      |
| hsa-miR-5196-5p | chr19      | 35345541       | 35345562     | +      |
| hsa-miR-548ah-5p| chr4       | 76575561       | 76575580     | +      |
| hsa-miR-548au-3p| chr9       | 93594874       | 93594894     | +      |
| hsa-miR-5680    | chr8       | 1.02E+08       | 1.02E+08     | +      |
| hsa-miR-5682    | chr3       | 1.21E+08       | 1.21E+08     | +      |
| hsa-miR-5692a   | chr8       | 12719134       | 12719155     | +      |
| hsa-miR-587     | chr6       | 1.07E+08       | 1.07E+08     | +      |
| hsa-miR-6084    | chr1       | 20633756       | 20633775     | +      |
| hsa-miR-6127    | chr1       | 22633328       | 22633346     | -      |
| miRNA  | Type    | Chromosome | Start Position | End Position | Orientation |
|--------|---------|------------|----------------|--------------|-------------|
| hsa-miR-6128 | miRNA  | chr11      | 56743943       | 56743961     | +           |
| hsa-miR-646  | miRNA  | chr20      | 60308534       | 60308552     | +           |
| hsa-miR-6499-3p | miRNA  | chr5       | 1.52E+08       | 1.52E+08     | -           |
| hsa-miR-661   | miRNA  | chr8       | 1.44E+08       | 1.44E+08     | -           |
| hsa-miR-6722-5p | miRNA  | chr9       | 1.37E+08       | 1.37E+08     | -           |
| hsa-miR-6790-3p | miRNA  | chr19      | 6392925        | 6392945      | +           |
| hsa-miR-6800-5p | miRNA  | chr19      | 49832022       | 49832042     | +           |
| hsa-miR-6821-3p | miRNA  | chr22      | 49962919       | 49962939     | +           |
| hsa-miR-6839-5p | miRNA  | chr7       | 64679069       | 64679090     | +           |
| hsa-miR-6846-3p | miRNA  | chr8       | 1.44E+08       | 1.44E+08     | -           |
| hsa-miR-7108-5p | miRNA  | chr19      | 2434980        | 2435000      | -           |
| hsa-miR-7154-5p | miRNA  | chr11      | 45691754       | 45691776     | -           |
| hsa-miR-7162-3p | miRNA  | chr10      | 89197694       | 89197715     | +           |
| p-hsa-miR-128 | novelmiRNA  | chr4       | 30368597       | 30368615     | -           |
| p-hsa-miR-158 | novelmiRNA  | chr10     | 89197694       | 89197715     | +           |
| p-hsa-miR-253 | novelmiRNA  | chr16     | 54326638       | 54326659     | -           |
| p-hsa-miR-280 | novelmiRNA  | chr17_KI270862v1_alt | 224858 | 224875 | - |
| p-hsa-miR-47  | novelmiRNA  | chr17_KI270861v1_alt | 74352 | 74373 | + |
| hsa-miR-410-5p | miRNA  | chr14      | 1.01E+08       | 1.01E+08     | +           |
| hsa-miR-5688  | miRNA  | chr3       | 85385761       | 85385782     | +           |
| hsa-miR-718   | miRNA  | chrX       | 1.54E+08       | 1.54E+08     | -           |
| hsa-miR-1251-5p | miRNA  | chr12      | 97491913       | 97491933     | +           |
| hsa-miR-1262  | miRNA  | chr1       | 68183576       | 68183597     | -           |
| hsa-miR-1322  | miRNA  | chr8       | 10825375       | 10825393     | -           |
| hsa-miR-196a-3p | miRNA  | chr12      | 53991799       | 53991820     | +           |
| hsa-miR-208b-3p | miRNA  | chr14      | 23417997       | 23418018     | -           |
| hsa-miR-218-1-3p | miRNA  | chr4       | 20528342       | 20528363     | +           |
| hsa-miR-302d-3p | miRNA  | chr4       | 1.13E+08       | 1.13E+08     | -           |
| hsa-miR-3144-3p | miRNA  | chr6       | 1.2E+08        | 1.2E+08      | +           |
| hsa-miR-3160-5p | miRNA  | chr11      | 46451817       | 46451838     | +           |
| hsa-miR-3162-3p | miRNA  | chr11      | 59595087       | 59595107     | -           |
| hsa-miR-3610  | miRNA  | chr8       | 1.17E+08       | 1.17E+08     | -           |
| hsa-miR-371b-5p | miRNA  | chr19      | 53787715       | 53787736     | -           |
| hsa-miR-4257  | miRNA  | chr1       | 1.51E+08       | 1.51E+08     | +           |
| hsa-miR-4269  | miRNA  | chr2       | 2.39E+08       | 2.39E+08     | +           |
| hsa-miR-4304  | miRNA  | chr12      | 1.23E+08       | 1.23E+08     | -           |
| hsa-miR-4445-5p | miRNA  | chr3       | 1.1E+08        | 1.1E+08      | +           |
| hsa-miR-4475  | miRNA  | chr9       | 36823542       | 36823563     | -           |
| hsa-miR-4477a | miRNA  | chr9       | 41233802       | 41233823     | +           |
| hsa-miR-450b-3p | miRNA  | chrX       | 1.35E+08       | 1.35E+08     | -           |
| hsa-miR-4515  | miRNA  | chr15      | 83067349       | 83067370     | +           |
| hsa-miR-4528  | miRNA  | chr18      | 53237156       | 53237177     | +           |
| hsa-miR-4534  | miRNA  | chr22      | 37988829       | 37988845     | +           |
| hsa-miR-4663  | miRNA  | chr8       | 1.23E+08       | 1.23E+08     | -           |
| hsa-miR-4709-5p | miRNA  | chr14      | 74480175       | 74480196     | -           |
| hsa-miR-4765  | miRNA  | chr2       | 32635300       | 32635321     | +           |
| hsa-miR-4776-3p | miRNA  | chr2       | 2.13E+08       | 2.13E+08     | -           |
| hsa-miR-4786-5p | miRNA  | chr2       | 2.4E+08        | 2.4E+08      | -           |
| hsa-miR-541-5p | miRNA  | chr14      | 1.01E+08       | 1.01E+08     | +           |
| hsa-miR-548ad-3p | miRNA  | chr2       | 35471453       | 35471474     | +           |
| hsa-miR-548ao-5p | miRNA  | chr8       | 41271102       | 41271123     | -           |
| miRNA        | Chromosome | Start Position | End Position | Orientation |
|-------------|------------|----------------|--------------|-------------|
| hsa-miR-5586-3p | chr14      | 59646962       | 59646983     | -           |
| hsa-miR-588   | chr6       | 1.26E+08       | 1.26E+08     | +           |
| hsa-miR-592   | chr7       | 1.27E+08       | 1.27E+08     | -           |
| hsa-miR-595   | chr7       | 1.59E+08       | 1.59E+08     | -           |
| hsa-miR-596   | chr8       | 1817246        | 1817266      | +           |
| hsa-miR-6076  | chr14      | 49966399       | 49966419     | +           |
| hsa-miR-6132  | chr7       | 1.17E+08       | 1.17E+08     | +           |
| hsa-miR-620   | chr12      | 1.16E+08       | 1.16E+08     | -           |
| hsa-miR-670-5p| chr11      | 43559675       | 43559694     | +           |
| hsa-miR-6737-5p| chr1      | 1.54E+08       | 1.54E+08     | -           |
| hsa-miR-6827-3p| chr3      | 1.34E+08       | 1.34E+08     | -           |
| hsa-miR-6887-5p| chr19     | 35122705       | 35122727     | +           |
| p-hsa-miR-144 | chr17      | 24134389       | 24134511     | -           |
| p-hsa-miR-234 | chr14      | 43331922       | 43331945     | +           |
| p-hsa-miR-274 | chr21      | 43762335       | 43762357     | +           |
| p-hsa-miR-281 | chr19      | 47850102       | 47850120     | -           |
| p-hsa-miR-298 | chr19      | 12541956       | 12541977     | +           |
| p-hsa-miR-322 | chr19      | 29989436       | 29989453     | -           |
| p-hsa-miR-33  | chr19      | 299923136      | 299923156    | -           |
| p-hsa-miR-39  | chr7       | 1.43E+08       | 1.43E+08     | +           |
| p-hsa-miR-50  | chr2       | 2.29E+08       | 2.29E+08     | -           |
| hsa-miR-6511a-5p| chr16     | 18344053       | 18344075     | -           |
| hsa-miR-6761-3p| chr12      | 1.12E+08       | 1.12E+08     | +           |
| hsa-miR-6743-3p| chr11      | 209383         | 209405       | +           |
| hsa-miR-1244  | chr12      | 12112006       | 12112031     | +           |
| hsa-miR-433-5p| chr14      | 1.01E+08       | 1.01E+08     | +           |
| hsa-miR-4639-3p| chr6       | 16141603       | 16141622     | +           |
| hsa-miR-671-3p| chr12      | 1.12E+08       | 1.12E+08     | +           |
| hsa-miR-6743-3p| chr11      | 209383         | 209405       | +           |
| hsa-miR-1298-5p| chrX       | 1.15E+08       | 1.15E+08     | +           |
| hsa-miR-1915-3p| chr10      | 21496576       | 21496595     | -           |
| hsa-miR-19b-2-5p| chrX      | 1.34E+08       | 1.34E+08     | -           |
| hsa-miR-203a-3p| chr14      | 1.04E+08       | 1.04E+08     | +           |
| hsa-miR-3713  | chr15      | 76586647       | 76586666     | +           |
| hsa-miR-376b-5p| chr14      | 1.01E+08       | 1.01E+08     | +           |
| hsa-miR-4258  | chr1       | 1.55E+08       | 1.55E+08     | +           |
| hsa-miR-4297  | chr10      | 1.3E+08        | 1.3E+08      | -           |
| hsa-miR-4314  | chr17      | 8088066        | 8088083      | +           |
| hsa-miR-4324  | chr19      | 49308807       | 49308826     | -           |
| hsa-miR-4633-3p| chr5       | 1.29E+08       | 1.29E+08     | +           |
| hsa-miR-4684-5p| chr1       | 22719530       | 22719551     | +           |
| hsa-miR-4715-5p| chr15      | 25848795       | 25848816     | -           |
| hsa-miR-4720-5p| chr16      | 81385021       | 81385042     | +           |
| hsa-miR-4729  | chr17      | 59366092       | 59366113     | +           |
| hsa-miR-4738-5p| chr17      | 75784567       | 75784588     | -           |
| hsa-miR-4768-5p| chrX       | 17425889       | 17425910     | +           |
| hsa-miR-4777-3p| chr2       | 2.31E+08       | 2.31E+08     | +           |
| hsa-miR-499a-5p| chr20      | 34990408       | 34990428     | +           |
| hsa-miR-511-5p| chr10      | 17845122       | 17845142     | +           |
| hsa-miR-5190  | chr18      | 13459993       | 13460013     | +           |
| hsa-miR-5195-5p| chr14      | 1.07E+08       | 1.07E+08     | +           |
| hsa-miR-5197-5p| chr5       | 1.44E+08       | 1.44E+08     | +           |
| hsa-miR-5581-5p| chr1       | 37500973       | 37500994     | -           |
| hsa-miR-5707  | chr7       | 1.59E+08       | 1.59E+08     | +           |
| hsa-miR-585-5p| chr5       | 1.69E+08       | 1.69E+08     | -           |
| hsa-miR-591   | chr7       | 96219722       | 96219741     | -           |
| miRNA        | chr   | start    | end     | strand |
|-------------|-------|----------|---------|--------|
| hsa-miR-676-3p | chrX  | 70022899 | 70022919 | +      |
| hsa-miR-6764-3p | chr14 | 1E+08    | 1E+08   | +      |
| hsa-miR-6839-3p | chr7  | 64679155  | 64679176  | +      |
| hsa-miR-6863 | chr16 | 56904327  | 56904349  | +      |
| hsa-miR-7160-3p | chr8  | 2076620   | 2076640   | +      |
| hsa-miR-8080 | chr2  | 79866551  | 79866573  | -      |
| hsa-miR-875-5p | chr8  | 99536830  | 99536851  | -      |
| p-hsa-miR-126 | chr17 | 81867174  | 81867197  | +      |
| p-hsa-miR-190 | chr13  | 81349508  | 81349529  | +      |
| p-hsa-miR-291 | chr1  | 8259682   | 8259704   | -      |
| p-hsa-miR-311 | chr11_KI270832v1_alt | 189404  | 189424  | -      |
| hsa-miR-6847-3p | chr8  | 1.44E+08  | 1.44E+08  | +      |
| p-hsa-miR-172 | chr13  | 51330783  | 51330803  | +      |
| p-hsa-miR-117 | chr20  | 63537682  | 63537702  | -      |
| hsa-miR-3618 | chr22  | 20085797  | 20085818  | +      |
| hsa-miR-548ag | chr20  | 60564565  | 60564585  | +      |
| p-hsa-miR-171 | chr20  | 12459891  | 12459911  | +      |
| hsa-miR-4647 | chr6   | 44254253  | 44254275  | -      |
| hsa-miR-4635 | chr5   | 1062904   | 1062924   | -      |
| hsa-miR-509-3p | chrX  | 1.47E+08  | 1.47E+08  | -      |
| hsa-miR-4538 | chr14  | 1.06E+08  | 1.06E+08  | -      |
| hsa-miR-3621 | chr9   | 1.37E+08  | 1.37E+08  | -      |
| hsa-miR-3121-3p | chr1  | 1.8E+08   | 1.8E+08   | -      |
| hsa-miR-214-3p | chr1  | 1.72E+08  | 1.72E+08  | -      |
| hsa-miR-566 | chr3   | 50173341  | 50173359  | +      |
| p-hsa-miR-119 | chr15_KI270850v1_alt | 218564  | 218588  | +      |
| hsa-miR-4505 | chr14  | 73758749  | 73758766  | +      |
| hsa-miR-6889-5p | chr22  | 41253023  | 41253045  | -      |
| hsa-miR-5191 | chr1   | 2.02E+08  | 2.02E+08  | +      |
| p-hsa-miR-548at-3p | chr17 | 42494810  | 42494830  | +      |
| hsa-miR-6859-5p | chr16  | 17092    | 17114    | -      |
| hsa-miR-1236-3p | chr6  | 31956839  | 31956860  | -      |
| p-hsa-miR-4714-3p | chr15  | 98784473  | 98784494  | +      |
| hsa-miR-6779-5p | chr17  | 38914984  | 38915004  | +      |
| hsa-miR-8060 | chr3   | 96360006  | 96360029  | +      |
| p-hsa-miR-201 | chr18  | 64706880  | 64706897  | +      |
| hsa-miR-3130-5p | chr2  | 2.07E+08  | 2.07E+08  | +      |
| p-hsa-miR-1271-3p | chr5  | 1.76E+08  | 1.76E+08  | +      |
| p-hsa-miR-222-5p | chrX  | 45747073  | 45747094  | -      |
| hsa-miR-4260 | chr1   | 2.1E+08   | 2.1E+08   | -      |
| hsa-miR-4731-3p | chr17  | 15251634  | 15251655  | -      |
| hsa-miR-6769-3p | chr11  | 67490295  | 67490315  | +      |
| hsa-miR-603 | chr10  | 24275745  | 24275766  | +      |
| hsa-miR-6769a-3p | chr16  | 4671370   | 4671390   | +      |
| p-hsa-miR-55 | chr8_KI270 | 68526    | 68547    | -      |
| hsa-miR-6808-5p | chr1  | 1339682  | 1339703  | -      |
| hsa-miR-6873-5p | chr6  | 33287263  | 33287284  | -      |
| hsa-miR-6078 | chr10  | 3991178   | 3991196   | +      |
| hsa-miR-6820-5p | chr22  | 37967568  | 37967586  | +      |
| p-hsa-miR-244 | chr6   | 836193    | 836215    | +      |
| p-hsa-miR-260 | chr6   | 5773674   | 5773694   | +      |
| p-hsa-miR-69 | chr17  | 19979440  | 19979461  | +      |
| hsa-miR-4703-3p | chr13  | 51552637  | 51552658  | +      |
| hsa-miR-3942-3p | chr15  | 35372280  | 35372300  | +      |
| hsa-miR-3158-5p | chr10  | 1.02E+08  | 1.02E+08  | -      |
| hsa-miR-6753-5p | chr11  | 68044794  | 68044815  | +      |
| miRNA    | Chromosome | Start | End   | Strandedness |
|----------|------------|-------|-------|--------------|
| hsa-miR-6849-5p | chr8 | 1.44E+08 | 1.44E+08 | - |
| hsa-miR-6891-5p | chr6 | 31355297 | 31355315 | - |
| hsa-miR-4281 | chr5 | 1.77E+08 | 1.77E+08 | - |
| hsa-miR-6881-5p | chr15 | 74411406 | 74411427 | - |
| p-hsa-miR-262 | chr19 | 12887469 | 12887491 | + |
| hsa-miR-1199-5p | chr19 | 14073381 | 14073400 | + |
| p-hsa-miR-272 | chr19_KI270819v1_alt | 102464 | 102487 | + |
| hsa-miR-548aw | chr9 | 1.33E+08 | 1.33E+08 | + |
| p-hsa-miR-34 | chr6 | 10722842 | 10722863 | + |
| hsa-miR-6829-5p | chr3 | 1.96E+08 | 1.96E+08 | - |
| p-hsa-miR-286 | chr1 | 1.59E+08 | 1.59E+08 | + |
| hsa-miR-6891-5p | chr6 | 32170106 | 32170128 | - |
| hsa-miR-1178-3p | chr12 | 1.2E+08 | 1.2E+08 | - |
| hsa-miR-217 | chr2 | 55983020 | 55983042 | - |
| hsa-miR-1199-3p | chr19 | 14073425 | 14073445 | - |
| hsa-miR-3148 | chr8 | 29957318 | 29957339 | - |
| hsa-miR-4445-3p | chr8 | 1.1E+08 | 1.1E+08 | - |
| hsa-miR-3129-3p | chr2 | 1.89E+08 | 1.89E+08 | - |
| hsa-miR-499a-3p | chr20 | 34990445 | 34990466 | + |
| hsa-miR-6746-5p | chr11 | 61792500 | 61792522 | - |
| p-hsa-miR-41 | chr18 | 9017284 | 9017305 | - |
| hsa-miR-5004-3p | chr6 | 33438397 | 33438418 | + |
| p-hsa-miR-213 | chr1 | 1.13E+08 | 1.13E+08 | + |
| hsa-miR-5583-3p | chr18 | 39676719 | 39676740 | - |
| hsa-miR-606 | chr10 | 75552518 | 75552538 | + |
| hsa-miR-4802-5p | chr4 | 40502086 | 40502107 | - |
| hsa-miR-1229-5p | chr1 | 1.8E+08 | 1.8E+08 | - |
| hsa-miR-1258 | chr2 | 1.8E+08 | 1.8E+08 | - |
| hsa-miR-4423-5p | chr1 | 85133806 | 85133827 | + |
| hsa-miR-4764-5p | chr22 | 33436640 | 33436660 | - |
| hsa-miR-5009-3p | chr15 | 89883949 | 89883970 | - |
| hsa-miR-611 | chr11 | 61792500 | 61792522 | - |
| hsa-miR-6848-3p | chr8 | 1.44E+08 | 1.44E+08 | - |
| hsa-miR-2054 | chr4 | 1.26E+08 | 1.26E+08 | + |
| hsa-miR-6828-3p | chr3 | 1.7E+08 | 1.7E+08 | + |
| hsa-miR-1178-3p | chr12 | 1.2E+08 | 1.2E+08 | - |
| hsa-miR-217 | chr2 | 55983020 | 55983042 | - |
| hsa-miR-1199-3p | chr19 | 14073425 | 14073445 | + |
| hsa-miR-3148 | chr8 | 29957318 | 29957339 | - |
| hsa-miR-4445-3p | chr3 | 1.1E+08 | 1.1E+08 | + |
| hsa-miR-3129-3p | chr2 | 1.89E+08 | 1.89E+08 | - |
| hsa-miR-499a-3p | chr20 | 34990445 | 34990466 | + |
| hsa-miR-6746-5p | chr11 | 61792500 | 61792522 | - |
| p-hsa-miR-41 | chr18 | 9017284 | 9017305 | - |
| hsa-miR-4753-5p | chr1 | 2.35E+08 | 2.35E+08 | - |
| p-hsa-miR-293 | chr9 | 35161429 | 35161446 | + |
| hsa-miR-6721-5p | chr6 | 32170084 | 32170106 | - |
| hsa-miR-4302 | chr12 | 25874052 | 25874069 | - |
| hsa-miR-4644-3p | chr8 | 1.44E+08 | 1.44E+08 | - |
| miRNA       | chromosome | start position | end position | strand |
|-------------|------------|----------------|--------------|--------|
| hsa-miR-6842-5p | chr8       | 27433375       | 27433396     | +      |
| hsa-miR-548n     | chr7       | 34940804       | 34940825     | -      |
| hsa-miR-1180-5p   | chr17      | 19344548       | 19344568     | -      |
| hsa-miR-1257      | chr20      | 61953621       | 61953641     | -      |
| hsa-miR-1297      | chr13      | 54311981       | 54311997     | -      |
| hsa-miR-1912      | chrX       | 1.15E+08       | 1.15E+08     | +      |
| hsa-miR-203b-3p   | chr14      | 1.04E+08       | 1.04E+08     | -      |
| hsa-miR-2682-5p   | chr1       | 98045307       | 98045329     | -      |
| hsa-miR-302a-5p   | chr4       | 1.13E+08       | 1.13E+08     | -      |
| hsa-miR-3131      | chr2       | 2.19E+08       | 2.19E+08     | -      |
| hsa-miR-3147      | chr7       | 57405030       | 57405053     | +      |
| hsa-miR-3686      | chr8       | 1.29E+08       | 1.29E+08     | -      |
| hsa-miR-4305      | chr13      | 39664108       | 39664125     | -      |
| hsa-miR-4309      | chr14      | 1.03E+08       | 1.03E+08     | +      |
| hsa-miR-4428      | chr1       | 2.37E+08       | 2.37E+08     | -      |
| hsa-miR-4490      | chr13      | 90555785       | 90555806     | -      |
| hsa-miR-4509      | chr15      | 28490807       | 28490828     | -      |
| hsa-miR-4527      | chr18      | 47380503       | 47380524     | +      |
| hsa-miR-4537      | chr14      | 1.06E+08       | 1.06E+08     | -      |
| hsa-miR-4650-3p   | chr7       | 72697948       | 72697968     | +      |
| hsa-miR-4700-5p   | chr12      | 1.21E+08       | 1.21E+08     | +      |
| hsa-miR-4740-5p   | chr17      | 81400753       | 81400774     | -      |
| hsa-miR-4789-3p   | chr3       | 1.75E+08       | 1.75E+08     | +      |
| hsa-miR-517c-3p   | chr19      | 53741369       | 53741390     | +      |
| hsa-miR-518c-5p   | chr19      | 53708758       | 53708780     | +      |
| hsa-miR-522-3p    | chr19      | 53751264       | 53751285     | +      |
| hsa-miR-548ae-3p  | chr5       | 58530047       | 58530067     | -      |
| hsa-miR-5739      | chr22      | 28459925       | 28459944     | +      |
| hsa-miR-6502-5p   | chr12      | 66251091       | 66251112     | +      |
| hsa-miR-6504-3p   | chr16      | 81611387       | 81611406     | +      |
| hsa-miR-6508-5p   | chr21      | 39447014       | 39447034     | +      |
| hsa-miR-6720-3p   | chr6       | 1390324        | 1390345      | -      |
| hsa-miR-6761-5p   | chr12      | 1.12E+08       | 1.12E+08     | +      |
| hsa-miR-6762-5p   | chr12      | 1.13E+08       | 1.13E+08     | +      |
| hsa-miR-6778-3p   | chr17      | 18340814       | 18340834     | -      |
| hsa-miR-6792-3p   | chr19      | 7617480       | 7617501      | +      |
| hsa-miR-6814-5p   | chr21      | 41746815       | 41746836     | -      |
| hsa-miR-6827-5p   | chr3       | 1.34E+08       | 1.34E+08     | -      |
| hsa-miR-6838-5p   | chr7       | 44073407       | 44073428     | -      |
| hsa-miR-6856-3p   | chr9       | 1.31E+08       | 1.31E+08     | +      |
| hsa-miR-6864-5p   | chr17      | 4969743        | 4969766      | -      |
| hsa-miR-7151-5p   | chr10      | 67403388       | 67403410     | -      |
| hsa-miR-7977      | chr3       | 1.77E+08       | 1.77E+08     | +      |
| hsa-miR-888-3p    | chrX       | 1.46E+08       | 1.46E+08     | -      |
| p-hsa-miR-101     | chr9       | 1.15E+08       | 1.15E+08     | +      |
| p-hsa-miR-127     | chr3       | 1.39E+08       | 1.39E+08     | +      |
| p-hsa-miR-131     | chr19      | 51682139       | 51682160     | +      |
| p-hsa-miR-163     | chr15_KI270850v1_alt | 14761 | 14782 | + |
| p-hsa-miR-211     | chr9       | 1.05E+08       | 1.05E+08     | -      |
| p-hsa-miR-22      | chr2       | 2E+08          | 2E+08        | +      |
| p-hsa-miR-275     | chr1       | 92668170       | 92668192     | -      |
| p-hsa-miR-304     | chr2       | 36658127       | 36658149     | -      |
| p-hsa-miR-307     | chr2       | 46269596       | 46269617     | -      |
| p-hsa-miR-35      | chr1       | 1.55E+08       | 1.55E+08     | +      |
| hsa-miR-1207-5p   | chr8       | 1.28E+08       | 1.28E+08     | +      |
| ID       | Type    | Chromosome | Start   | End     | Orientation |
|----------|---------|------------|---------|---------|-------------|
| hsa-miR-431-3p | miRNA   | chr14      | 1.01E+08| 1.01E+08| +           |
| hsa-miR-6768-5p | miRNA   | chr16      | 2463972 | 2463994 | +           |
| hsa-miR-6800-3p | miRNA   | chr19      | 49832076| 49832096| +           |
| hsa-miR-6887-3p | miRNA   | chr19      | 35122744| 35122764| +           |
| p-hsa-miR-95    | novelmiRNA | chr8   | 98393704| 98393724| -           |
| hsa-miR-4487    | miRNA   | chr11      | 47401023| 47401041| +           |
| hsa-miR-4725-5p | miRNA   | chr17      | 31575281| 31575301| +           |
| hsa-miR-6850-5p | miRNA   | chr19      | 35122744| 35122764| +           |
| p-hsa-miR-95    | novelmiRNA | chr3   | 16933196| 16933217| +           |
| hsa-miR-4976-5p | miRNA   | chr3       | 1.15E+08| 1.15E+08| -           |
| p-hsa-miR-82    | novelmiRNA | chr22  | 39456052| 39456074| +           |
| p-hsa-miR-277   | novelmiRNA | chr11_KI270857 | 17494 | 17514 | -           |
| p-hsa-miR-78    | novelmiRNA | chr17_KI270857 | 160391 | 160413 | +           |
| hsa-miR-1288-3p | miRNA   | chr17      | 16282058| 16282078| +           |
| hsa-miR-374c-5p | miRNA   | chrX       | 74218561| 74218582| +           |
| hsa-miR-6757-5p | miRNA   | chr12      | 31621473| 31621494| -           |
| hsa-miR-4659a-5p | miRNA   | chr8       | 6745177 | 6745198 | +           |
| hsa-miR-6887-3p | miRNA   | chr7       | 5711840 | 5711862 | -           |
| hsa-miR-6888-5p | miRNA   | chr7       | 1.59E+08| 1.59E+08| +           |
| p-hsa-miR-214   | novelmiRNA | chr17_KI270857 | 746450 | 746471 | -           |
| hsa-miR-7851-3p | miRNA   | chr12      | 42323740| 42323761| -           |
| p-hsa-miR-217   | novelmiRNA | chr15  | 70493038| 70493059| +           |
| hsa-miR-3689d   | miRNA   | chr9       | 75353650| 75353670| -           |
| hsa-miR-6770-3p | miRNA   | chr16      | 18379351| 18379371| -           |
| hsa-miR-6861-3p | miRNA   | chr12      | 1.12E+08| 1.12E+08| +           |
| hsa-miR-3692-3p | miRNA   | chr6       | 1.58E+08| 1.58E+08| +           |
| p-hsa-miR-95    | novelmiRNA | chr2   | 42953866| 42953887| +           |
| hsa-miR-6770-5p | miRNA   | chr16      | 18379351| 18379371| -           |
| hsa-miR-4632-5p | miRNA   | chr1       | 12191713| 12191735| +           |
| p-hsa-miR-194   | novelmiRNA | chr2   | 42953866| 42953887| +           |
| hsa-miR-4656    | miRNA   | chr7       | 4788608 | 4788630 | -           |
| hsa-miR-1914-5p | miRNA   | chr20      | 63941511| 63941532| -           |
| p-hsa-miR-95    | novelmiRNA | chr17_KI270857 | 75353650 | 75353670 | -           |
| hsa-miR-6757-3p | miRNA   | chr12      | 53056949| 53056970| +           |
| p-hsa-miR-255   | novelmiRNA | chr3   | 1.88E+08| 1.88E+08| +           |
| hsa-miR-548ah-3p | miRNA   | chr17      | 44207810| 44207834| -           |
| hsa-miR-3914-3p | miRNA   | chr20      | 51452912| 51452933| -           |
| hsa-miR-4656    | miRNA   | chr7       | 4788608 | 4788630 | -           |
| hsa-miR-1914-5p | miRNA   | chr20      | 63941511| 63941532| -           |
| hsa-miR-6769b-5p | miRNA   | chr1      | 2.06E+08| 2.06E+08| +           |
| hsa-miR-4450    | miRNA   | chr4       | 76573572| 76573593| +           |
| hsa-miR-1228-3p | miRNA   | chr12      | 57194555| 57194574| +           |
| hsa-miR-6774-3p | miRNA   | chr16      | 85891352| 85891376| +           |
| hsa-miR-1182    | miRNA   | chr1       | 2.31E+08| 2.31E+08| +           |
| hsa-miR-122-5p  | miRNA   | chr18      | 58451088| 58451109| +           |
| hsa-miR-1470    | miRNA   | chr19      | 15449548| 15449568| +           |
| miRNA             | chromosome | start position | end position | strand |
|-------------------|------------|----------------|--------------|--------|
| hsa-miR-1471     | chr2       | 2.32E+08       | 2.32E+08     | -      |
| hsa-miR-3646     | chr20      | 44408177       | 44408198     | +      |
| hsa-miR-3655     | chr5       | 1.41E+08       | 1.41E+08     | +      |
| hsa-miR-373-3p   | chr19      | 53788748       | 53788770     | +      |
| hsa-miR-4794     | chr19      | 64579855       | 64579876     | +      |
| hsa-miR-5088-3p  | chr19      | 49682174       | 49682194     | +      |
| hsa-miR-5093     | chr16      | 85306236       | 85306258     | -      |
| p-hsa-miR-516a-5p| chr19      | 53761148       | 53761170     | +      |
| hsa-miR-6781-5p  | chr17      | 42823918       | 42823938     | -      |
| p-hsa-miR-3655   | chr5       | 1.41E+08       | 1.41E+08     | +      |
| hsa-miR-516a-5p  | chr19      | 53761148       | 53761170     | +      |
| hsa-miR-6781-5p  | chr17      | 42823918       | 42823938     | -      |
| p-hsa-miR-5093   | chr16      | 85306236       | 85306258     | -      |
| hsa-miR-373-3p   | chr19      | 64579855       | 64579876     | +      |
| hsa-miR-4794     | chr19      | 49682174       | 49682194     | +      |
| hsa-miR-5088-3p  | chr19      | 49682174       | 49682194     | +      |
| hsa-miR-5093     | chr16      | 85306236       | 85306258     | -      |
| hsa-miR-516a-5p  | chr19      | 53761148       | 53761170     | +      |
| hsa-miR-6781-5p  | chr17      | 42823918       | 42823938     | -      |
| hsa-miR-5088-3p  | chr19      | 49682174       | 49682194     | +      |
| hsa-miR-5093     | chr16      | 85306236       | 85306258     | -      |
| p-hsa-miR-516a-5p| chr19      | 53761148       | 53761170     | +      |
| hsa-miR-6781-5p  | chr17      | 42823918       | 42823938     | -      |
| p-hsa-miR-5093   | chr16      | 85306236       | 85306258     | -      |
| hsa-miR-373-3p   | chr19      | 64579855       | 64579876     | +      |
| hsa-miR-4794     | chr19      | 49682174       | 49682194     | +      |
| hsa-miR-5088-3p  | chr19      | 49682174       | 49682194     | +      |
| hsa-miR-5093     | chr16      | 85306236       | 85306258     | -      |
| hsa-miR-516a-5p  | chr19      | 53761148       | 53761170     | +      |
| hsa-miR-6781-5p  | chr17      | 42823918       | 42823938     | -      |
| miRNA         | chromosome | start base | end base | strand |
|---------------|------------|------------|----------|--------|
| hsa-miR-7151-3p | chr10      | 67403351   | 67403371 | -      |
| hsa-miR-483-5p  | chr11      | 2134181    | 2134202  | -      |
| hsa-miR-3619-3p | chr22      | 46091090   | 46091111 | +      |
| hsa-miR-4774-5p | chr2       | 1.69E+08   | 1.69E+08 | +      |
| hsa-miR-1204    | chr8       | 1.28E+08   | 1.28E+08 | +      |
| hsa-miR-1228-5p | chr12      | 57194504   | 57194524 | +      |
| hsa-miR-345-3p  | chr14      | 1E+08      | 1E+08    | +      |
| hsa-miR-1204    | chr12      | 57194504   | 57194524 | +      |
| hsa-miR-1235-3p | chr6       | 35470558   | 35470579 | +      |
| hsa-miR-4723-5p | chr17      | 28360660   | 28360683 | +      |
| hsa-miR-548p    | chr5       | 1.01E+08   | 1.01E+08 | +      |
| hsa-miR-379-3p  | chr14      | 42708084   | 42708104 | +      |
| hsa-miR-3145-3p | chr6       | 1.38E+08   | 1.38E+08 | +      |
| p-hsa-miR-259   | chr11      | 62003144   | 62003165 | +      |
| hsa-miR-2115-3p | chr3       | 48316381   | 48316402 | +      |
| hsa-miR-301a-5p | chr17      | 59151187   | 59151208 | +      |
| hsa-miR-548a-5p | chr8       | 1.04E+08   | 1.04E+08 | +      |
| hsa-miR-318-3p  | chr3       | 31378578   | 31378596 | +      |
| hsa-miR-7111-3p | chr6       | 35470558   | 35470579 | +      |
| hsa-miR-4723-5p | chr17      | 28360660   | 28360683 | +      |
| hsa-miR-548a-5p | chr8       | 1.04E+08   | 1.04E+08 | +      |
| hsa-miR-379-3p  | chr14      | 42708084   | 42708104 | +      |
| hsa-miR-3145-3p | chr6       | 1.38E+08   | 1.38E+08 | +      |
| p-hsa-miR-259   | chr11      | 62003144   | 62003165 | +      |
| hsa-miR-2115-3p | chr3       | 48316381   | 48316402 | +      |
| hsa-miR-301a-5p | chr17      | 59151187   | 59151208 | +      |
| hsa-miR-548a-5p | chr8       | 1.04E+08   | 1.04E+08 | +      |
| hsa-miR-318-3p  | chr3       | 31378578   | 31378596 | +      |
| hsa-miR-7111-3p | chr6       | 35470558   | 35470579 | +      |
| hsa-miR-4723-5p | chr17      | 28360660   | 28360683 | +      |
| hsa-miR-548a-5p | chr8       | 1.04E+08   | 1.04E+08 | +      |
| hsa-miR-379-3p  | chr14      | 42708084   | 42708104 | +      |
| hsa-miR-3145-3p | chr6       | 1.38E+08   | 1.38E+08 | +      |
| p-hsa-miR-259   | chr11      | 62003144   | 62003165 | +      |
| hsa-miR-2115-3p | chr3       | 48316381   | 48316402 | +      |
| hsa-miR-301a-5p | chr17      | 59151187   | 59151208 | +      |
| hsa-miR-548a-5p | chr8       | 1.04E+08   | 1.04E+08 | +      |
| hsa-miR-318-3p  | chr3       | 31378578   | 31378596 | +      |
| hsa-miR-7111-3p | chr6       | 35470558   | 35470579 | +      |
| hsa-miR-4723-5p | chr17      | 28360660   | 28360683 | +      |
| hsa-miR-548a-5p | chr8       | 1.04E+08   | 1.04E+08 | +      |
| hsa-miR-379-3p  | chr14      | 42708084   | 42708104 | +      |
| hsa-miR-3145-3p | chr6       | 1.38E+08   | 1.38E+08 | +      |
| p-hsa-miR-259   | chr11      | 62003144   | 62003165 | +      |
| hsa-miR-2115-3p | chr3       | 48316381   | 48316402 | +      |
| hsa-miR-301a-5p | chr17      | 59151187   | 59151208 | +      |
| hsa-miR-548a-5p | chr8       | 1.04E+08   | 1.04E+08 | +      |
| hsa-miR-318-3p  | chr3       | 31378578   | 31378596 | +      |
| hsa-miR-7111-3p | chr6       | 35470558   | 35470579 | +      |
| hsa-miR-4723-5p | chr17      | 28360660   | 28360683 | +      |
| hsa-miR-548a-5p | chr8       | 1.04E+08   | 1.04E+08 | +      |
| miRNA         | chromosome | start | end   | strand |
|--------------|------------|-------|-------|--------|
| hsa-miR-188-3p | chrX       | 50003556 | 50003576 | +      |
| hsa-miR-449b-5p | chr5       | 55170706 | 55170727 | -      |
| hsa-miR-4795-3p | chr3       | 87226199 | 87226220 | -      |
| hsa-miR-323a-5p | chr14      | 1.01E+08 | 1.01E+08 | +      |
| hsa-miR-4473   | chr9       | 20411161 | 20411182 | -      |
| hsa-miR-376a-5p | chr14      | 1.01E+08 | 1.01E+08 | +      |
| hsa-miR-6820-3p | chr22      | 37967603 | 37967624 | +      |
| hsa-miR-4642   | chr6       | 44435650 | 44435671 | +      |
| hsa-miR-4714-5p | chr15      | 98784435 | 98784456 | +      |
| hsa-miR-6851-5p | chr9       | 33467908 | 33467930 | -      |
| hsa-miR-675-5p | chr11      | 65129951 | 65129973 | -      |
| p-hsa-miR-49   | chr6       | 1.2E+08  | 1.2E+08  | +      |
| hsa-miR-100-3p | chr11      | 1.22E+08 | 1.22E+08 | -      |
| hsa-miR-3177-5p | chr16      | 1734995  | 1735017  | +      |
| hsa-miR-892c-3p | chrX       | 1.46E+08 | 1.46E+08 | -      |
| hsa-miR-99a-3p | chr21      | 16539138 | 16539159 | +      |
| hsa-miR-4688   | chr11      | 46376456 | 46376477 | +      |
| hsa-miR-4464   | chr6       | 90312753 | 90312773 | +      |
| hsa-miR-125b-1-3p | chr11    | 1.22E+08 | 1.22E+08 | -      |
| hsa-miR-3928-5p | chr22      | 31160095 | 31160117 | +      |
| hsa-miR-6754-5p | chr11      | 71473508 | 71473529 | +      |
| hsa-miR-548d-5p | chr17      | 67471540 | 67471561 | -      |
| hsa-miR-7849-3p | chr4       | 1.46E+08 | 1.46E+08 | +      |
| hsa-miR-7856-5p | chr1       | 86357665 | 86357685 | +      |
| hsa-miR-3678-3p | chr17      | 75406137 | 75406158 | +      |
| hsa-miR-6813-5p | chr20      | 64076983 | 64077005 | +      |
| hsa-miR-6892-5p | chr7       | 1E+08    | 1E+08    | +      |
| hsa-miR-4503   | chr14      | 36952358 | 36952379 | -      |
| hsa-miR-6882-3p | chr15      | 74840642 | 74840665 | +      |
| hsa-miR-4455   | chr4       | 1.85E+08 | 1.85E+08 | +      |
| hsa-miR-6894-5p | chrX       | 53198917 | 53198940 | -      |
| hsa-miR-559    | chr2       | 47377690 | 47377710 | +      |
| hsa-miR-299-5p | chr14      | 1.01E+08 | 1.01E+08 | +      |
| hsa-miR-6840-5p | chr7       | 1E+08    | 1E+08    | +      |
| hsa-miR-34c-5p | chr11      | 1.12E+08 | 1.12E+08 | -      |
| hsa-miR-548b-3p | chr6       | 1.19E+08 | 1.19E+08 | -      |
| hsa-miR-371b-3p | chr19      | 53787678 | 53787700 | -      |
| hsa-miR-3690   | chr8       | 96358736 | 96358756 | +      |
| hsa-miR-548w   | chr16      | 26025246 | 26025268 | +      |
| hsa-miR-4772-5p | chr2       | 1.02E+08 | 1.02E+08 | +      |
| hsa-miR-6894-5p | chrX       | 53198917 | 53198940 | -      |
| hsa-miR-559    | chr2       | 47377690 | 47377710 | +      |
| hsa-miR-299-5p | chr14      | 1.01E+08 | 1.01E+08 | +      |
| hsa-miR-66     | chr21      | 32523670 | 32523692 | -      |
| hsa-miR-944    | chr3       | 1.9E+08  | 1.9E+08  | +      |
| hsa-miR-6892-5p | chr7       | 1.43E+08 | 1.43E+08 | +      |
| hsa-miR-4503   | chr14      | 36952358 | 36952379 | -      |
| hsa-miR-6882-3p | chr15      | 74840642 | 74840665 | +      |
| hsa-miR-4455   | chr4       | 1.85E+08 | 1.85E+08 | +      |
| hsa-miR-548i   | chrX       | 84225797 | 84225818 | +      |
| hsa-miR-34c-5p | chr11      | 1.12E+08 | 1.12E+08 | +      |
| hsa-miR-6759-5p | chrX       | 47587436 | 47587459 | +      |
| p-hsa-miR-215  | chr1       | 19068658 | 19068679 | -      |
| hsa-miR-6738-5p | chr1       | 1.56E+08 | 1.56E+08 | -      |
| hsa-miR-7850-5p | chr19      | 2630723 | 2630743  | +      |
| miRNA       | ChR  | Start   | End     | Str   |
|-------------|------|---------|---------|-------|
| hsa-miR-4766-5p | chr22 | 40813927 | 40813947 | -     |
| hsa-miR-548ba   | chr2  | 49059603 | 49059624 | +     |
| hsa-miR-6879-5p | chr11 | 65018510 | 65018531 | +     |
| hsa-miR-6824-3p | chr3  | 48633636 | 48633656 | -     |
| hsa-miR-6739-3p | chr1  | 2.02E+08 | 2.02E+08 | +     |
| hsa-miR-6890-5p | chr3  | 49099889 | 49099909 | -     |
| hsa-miR-4999-5p | chr19 | 8389340  | 8389360  | -     |
| hsa-miR-7113-3p | chr11 | 68032900 | 68032922 | +     |
| hsa-miR-342-3p  | chr14 | 1E+08    | 1E+08    | +     |
| hsa-miR-4742-5p | chr1  | 2.24E+08 | 2.24E+08 | -     |
| p-hsa-miR-122   | novel | chr1    | 1.61E+08 | 1.61E+08 | -     |
| hsa-miR-6806-3p | chr19 | 58334730 | 58334751 | +     |
| hsa-miR-26a-1-3p | chr3  | 37969452 | 37969473 | +     |
| hsa-miR-542-5p  | chrX  | 1.35E+08 | 1.35E+08 | -     |
| hsa-miR-579-5p  | chr5  | 32394430 | 32394451 | -     |
| hsa-miR-193b-3p | chr16 | 14304017 | 14304038 | +     |
| hsa-miR-2467-5p | chr2  | 2.39E+08 | 2.39E+08 | -     |
| hsa-miR-744-3p  | chr17 | 12081966 | 12081987 | +     |
| hsa-miR-3202    | chrX  | 1.54E+08 | 1.54E+08 | -     |
| hsa-miR-147b    | chr15 | 45433098 | 45433119 | +     |
| hsa-miR-4772-3p | chr2  | 1.02E+08 | 1.02E+08 | +     |
| p-hsa-miR-122   | novel | chrX    | 53198889 | 53198909 | -     |
| hsa-miR-193b-3p | chr16 | 14304017 | 14304038 | +     |
| hsa-miR-2467-5p | chr2  | 2.39E+08 | 2.39E+08 | -     |
| hsa-miR-744-3p  | chr17 | 12081966 | 12081987 | +     |
| hsa-miR-3202    | chrX  | 1.54E+08 | 1.54E+08 | -     |
| hsa-miR-7974    | chr19 | 11495544 | 11495567 | -     |
| hsa-miR-6894-3p | chrX  | 53198889 | 53198909 | -     |
| hsa-miR-193b-3p | chr16 | 14304017 | 14304038 | +     |
| hsa-miR-2467-5p | chr2  | 2.39E+08 | 2.39E+08 | -     |
| hsa-miR-744-3p  | chr17 | 12081966 | 12081987 | +     |
| hsa-miR-3202    | chrX  | 1.54E+08 | 1.54E+08 | -     |
| hsa-miR-147b    | chr15 | 45433098 | 45433119 | +     |
| hsa-miR-4772-3p | chr2  | 1.02E+08 | 1.02E+08 | +     |
| hsa-miR-6859-3p | chr16 | 17052    | 17074    | -     |
| hsa-miR-590-5p  | chr7  | 74191213 | 74191234 | +     |
| hsa-miR-4313    | chr15 | 75762286 | 75762305 | -     |
| hsa-miR-5787    | chr3  | 50227438 | 50227457 | +     |
| hsa-miR-20a-3p  | chr13 | 91351108 | 91351129 | +     |
| hsa-miR-4482-3p | chr10 | 1.04E+08 | 1.04E+08 | -     |
| p-hsa-miR-12    | novel | chr7    | 458135   | 458155 | +     |
| hsa-miR-199b-5p | chr9  | 1.28E+08 | 1.28E+08 | -     |
| hsa-miR-143-5p  | chr5  | 1.49E+08 | 1.49E+08 | +     |
| hsa-miR-30d-3p  | chrX  | 1.4E+08  | 1.4E+08  | -     |
| hsa-miR-1277-5p | chrX  | 1.4E+08  | 1.4E+08  | -     |
| hsa-miR-6133    | miRNA | chr7    | 1.33E+08 | 1.33E+08 | +     |
| sequence                          | log2FoldChange | baseMean | baseMean_control |
|----------------------------------|----------------|----------|------------------|
| UGCCUGUCUGAGCGUCGU             | -1.00          | 18.17    | 21.23            |
| UGAGGUAGUAGGUUGUAUGAUU         | -0.56          | 471.50   | 598.07           |
| UGAGAUGAGACUGAGCU              | 0.70           | 15.25    | 13.00            |
| CAUAAGAUAGAAACGCAUCU           | 0.50           | 133.83   | 121.10           |
| UAGGCUCUCUUCCUCUCUCAG          | -0.88          | 17.97    | 22.80            |
| UACCCAUUGCAUUCGGAGUUUG         | 0.51           | 4.97     | 4.26             |
| GUUUCUGCAUGUUUGUCAGGC          | -0.90          | 6.62     | 7.40             |
| UACCCACAGGGUAGAAACCACGG        | -0.49          | 65.61    | 70.60            |
| AUAUGGAAUUUGGAGCAGG            | -0.70          | 47.43    | 52.43            |
| AGCUCGUCUGAGGGCCUCAGU          | -0.80          | 4.13     | 4.66             |
| GCUCGCUUGUCUGAGGGAUA           | -0.82          | 12.69    | 14.57            |
| ACCACUGACGGUAGACGUACC          | -0.61          | 1.66     | 1.45             |
| UUCACAGUGCCAUAGGUCUCUGC        | 0.40           | 11.48    | 10.29            |
| GGCGGAUACACGGCAUGAGCC          | -0.74          | 4.31     | 4.66             |
| AGAGGUAGUAGGUUGCAUGAUU         | -0.54          | 34.63    | 45.93            |
| GCUUCUGUAUGUGUCUC             | -0.75          | 331.14   | 388.59           |
| UGCUCAGUUCACAGGGACACAG        | -0.73          | 4.77     | 5.55             |
| UAGGGAGAUGGUGUGUUGGGUGU       | -0.45          | 116.92   | 174.51           |
| GGAUUAUCAGAUAUACUUGAAG        | 0.36           | 86.50    | 81.00            |
| UGACCGAGACCUGGACGCGC         | 0.69           | 2.05     | 1.15             |
| UAGCAGCAUUAAGGAACAUAGGU       | -0.66          | 2.15     | 2.60             |
| UAGCAGAUGCUUGACUAAACCCCA      | 0.45           | 39.10    | 34.89            |
| ACUGCUCACUAGGUUGCUUCUGG       | -0.61          | 0.66     | 0.79             |
| ACCACUGACACUGACCCUGAG        | -0.64          | 25.44    | 28.19            |
| ACCCGCUUCUCUCUCUCUCUCUCAC   | -0.70          | 1.81     | 2.29             |
| GGGAAAGGAGGAGGGGGAGGA        | -0.63          | 4.92     | 6.26             |
| CUAUACAGACCUGGCUCCUCUCC       | -0.59          | 5.20     | 5.84             |
| AUCAUACAGUCCUCGGAUUCUCC      | 0.50           | 1.49     | 7.02             |
| CACCAGGCUGUGUGCACAGUGGC      | 0.56           | 2.49     | 2.20             |
| UAGGGAGAUGGUGUGUAUGU         | -0.35          | 175.92   | 215.86           |
| UCCUCUCUCUCUCUCUCCUCUCAG     | -0.63          | 2.25     | 2.86             |
| UGAGAGAAGGAGCCAGUGUCCAG     | -0.52          | 7.43     | 10.63            |
| CCAUAUACAGUGCUUGCUUUACU     | -0.56          | 8.33     | 9.10             |
| UAGGGAGAUGGUGUGUUGGUGUGU     | -0.20          | 238.05   | 245.79           |
| CUGCCGCAAGCUAGCCUCUCUCU      | -0.49          | 2.28     | 2.67             |
| AGAGGUGUGGGGUGGUGAGA        | -0.52          | 15.42    | 16.67            |
| UAGGGAGAUGGUGUUGUAUGU        | -0.32          | 19.45    | 20.72            |
| UUAUAAGAAGCAUGAGACUGAUU      | 0.37           | 4.53     | 3.94             |
| UCAGUGAAACCGGUCUCUUUC        | -0.55          | 1.10     | 2.02             |
| UAAAGUGCCUCAGACUGAGCAU      | -0.34          | 53.03    | 55.82            |
| CAAAGAGGUGAUGAAUCAGUGCCUG    | -0.56          | 3.96     | 4.40             |
| CCGACUGGUGGUGCACUGUCUCG     | 0.23           | 23.42    | 22.18            |
| UUCAGAUAAUACAGGGAUGAGU      | 0.28           | 75.27    | 71.68            |
| UACGUAAUAGAUGAUGAUCU        | 0.21           | 224.02   | 216.19           |
| CAAAGUGCUCAGAGUCAGAGAG     | 0.33           | 4.75     | 4.54             |
| UGGACCCAUUACUGGAAAACUGA      | 0.31           | 45.92    | 43.49            |
| UAGCUUACAGACUGAGUGUGUA      | 0.28           | 107.38   | 102.19           |
| UGAUAACUCCUUAGCUGGAAGA     | 0.18           | 98.62    | 94.50            |
| GCGGCGGCCGGCGGCGGCGG        | -0.48          | 2.71     | 3.08             |
| UGGAGGAGCCACAUGAGCUAGU     | -0.35          | 17.71    | 18.71            |
| GUGCCACUGUUGGUGGAGUAGCAGA   | -0.48          | 7.38     | 8.04             |
| CUCCGCGACGCGCGGCGC         | -0.48          | 1.36     | 1.63             |
| UGUAGUUGUUCUCUACUUAAUGGA   | 0.27           | 15.67    | 14.75            |
| UAUUGCCACUGGUAGAAUUCACU    | -0.34          | 15.35    | 16.39            |
| Sequence                          | Score 1 | Score 2 | Score 3 |
|----------------------------------|---------|---------|---------|
| UCAGUGCCACUACAGAACUUUGU          | 0.22    | 19.82   | 19.60   |
| ACUGCCCGAGGGCUCCUGG             | -0.47   | 1.88    | 2.13    |
| AGCUACAUUGUCUGCCGGGUUUC         | 0.22    | 7.30    | 7.03    |
| UACCCUGUAGACUGAUAUUGUG          | 0.38    | 5.81    | 5.30    |
| UUAUUAACUAACCUGAUAGUGU          | 0.32    | 8.46    | 8.10    |
| CUAGACUAAGGCUCCUUGAGG           | 0.26    | 18.73   | 17.43   |
| UUAAGAGAGCGGGUCUUCUGCU          | 0.47    | 3.12    | 1.84    |
| CUGCCAUAUUCAGCUACAG             | -0.03   | 0.16    | 0.21    |
| UGGCGGCAUAGGCUACAGCA            | -0.43   | 0.90    | 0.91    |
| UUGAUCUCGGAAGCUGAAGC            | -0.45   | 4459.10 | 4907.48 |
| GCCCCUGACCUUGCCUGUGUGUG        | 0.40    | 0.89    | 0.69    |
| GGCGUCUACAUACACCACAU           | 0.44    | 16.67   | 10.66   |
| UGUAACAGCAUACUCCAGUGGA          | 0.32    | 4.28    | 4.17    |
| UAUUGCAUCUGCCGCGCUCUC          | 0.23    | 3.10    | 3.08    |
| CUGACCUAUGAAUUGACAGGC          | 0.36    | 83.37   | 79.24   |
| GCGGGCGUUGGGCGCGCG             | -0.41   | 4.21    | 4.70    |
| CUGAAUAGCUGGACUACAGGU           | -0.40   | 12.51   | 13.13   |
| AACCCGUAGUACUGGACUUGUG         | 0.41    | 2.27    | 2.17    |
| ACCUUCUUGUAUAAAGCAGUCUGUGUCU    | -0.40   | 62.04   | 69.50   |
| GGUAUGAGAGAUAAUCAGUAC          | 0.41    | 6.89    | 6.31    |
| CAUAAUACUUUUUGUAGCCG           | 0.24    | 117.89  | 113.35  |
| GAAGUGUUGCGGUAGAACCACU         | -0.37   | 0.93    | 1.01    |
| UGAGGAUAGUAGUUGUAAGGUAU         | -0.38   | 1.66    | 1.96    |
| CAAAGUAGCGUUACAGUGAGGUAG       | -0.38   | 15.82   | 16.67   |
| UUGCUUAAGACGCCAGGAUGGA          | -0.39   | 1.34    | 1.67    |
| UAAGGUGCAUUCUAGUGCACAGAUAG     | -0.27   | 11.91   | 12.01   |
| UAGCAGCAUAUAAUGGUUUGUG         | -0.12   | 107.55  | 109.32  |
| UAGCACCUAUUGUGAAGCGGUA         | 0.26    | 2.90    | 2.82    |
| AAUGACAGCAGUACCCUGCCUGUGA      | -0.20   | 22.57   | 23.57   |
| CAGCAGCAAAUAUCAUGUUGGAA        | 0.28    | 1.10    | 1.11    |
| CUUAAUCAGAUUGUAUUGUAAUU         | 0.27    | 1.61    | 1.65    |
| CACUAGAUGUUGAGACUCUCUGGA        | 0.32    | 1.90    | 1.70    |
| AAAAGCUGGGUGAGAGCGGCA          | -0.30   | 22.83   | 24.13   |
| UUGUAAUCCCAUCUUUCUGACACCA      | -0.33   | 1.21    | 1.28    |
| UUGUAAACAUCCUCAGAGGAAG         | -0.33   | 1.11    | 1.21    |
| GCAUGUGAGAAGGCAAAUACGU         | -0.36   | 22.41   | 35.10   |
| CAAACAGACGCGUGGCGUGU           | 0.28    | 3.76    | 3.62    |
| CUGUGCGUGAGACAGCGCGCGUAG        | 0.29    | 2.16    | 1.90    |
| CACUGCAACCCUGCCUUGUGUGU        | -0.33   | 4.64    | 4.55    |
| AAAAGUGCGUUCAGAGCAGCAGUAG      | -0.34   | 1.32    | 1.59    |
| AAUGGGGCCCAUCAGGGUGUGUGU       | -0.28   | 9.81    | 10.11   |
| AGUUGGUCAGGAGUUGUGU            | -0.32   | 514.93  | 550.03  |
| UAGUAGACGCAUAGCGUAGC            | -0.32   | 0.36    | 0.44    |
| AAUGCCACUUGGCGCAAGAUCA         | -0.33   | 0.20    | 0.25    |
| CUGGUGCGCGCGCGCGUGQG           | -0.31   | 1.66    | 1.66    |
| ACUGUAAAGCCUCCCCUGUAGU         | -0.32   | 1.22    | 0.98    |
| UUCAGUAUCCAGCGGGUGCCUCU        | -0.32   | 1.13    | 1.31    |
| UGAGCGCCCUGACGACAGCGCC         | -0.32   | 0.38    | 0.45    |
| AAUUGCAGCAUACAGCGUAGUA         | -0.13   | 56.41   | 57.40   |
| UUCAGACUCAGCGUGUGUCUCAGU       | 0.29    | 0.64    | 0.48    |
| AAACCGGUAACCUAAUCUGAGGU        | -0.11   | 4750.96 | 4827.78 |
| UAGGUGAGGAGUUGUGUAAGGU        | -0.29   | 0.70    | 1.08    |
| CAACAGAGCAACGCAUCAUCU         | -0.29   | 0.92    | 1.13    |
| CGUGUAUUGUGAGCAAGCGUGA         | 0.27    | 0.38    | 0.25    |
| CGAACAUAAUUUGUGCUCCUCA         | -0.23   | 5.03    | 5.40    |
| UAGCAGACGUGAAUAUUGGCG         | -0.09   | 1962.23 | 1989.76 |
| Nucleotide Sequence | Capacity | Height | Width |
|---------------------|----------|--------|-------|
| GGAUCCGAGUCAUGGCAGC | 0.12     | 2.11   | 2.21  |
| UGAUUAUGUUGAUAAAUUAGG | -0.12    | 1.88   | 2.04  |
| CGCAUCCCCUAGGCAGUUGG | 0.09     | 2.04   | 2.06  |
| UUGAGGUUGGCAUUGUGUG | -0.16    | 0.17   | 0.20  |
| UCUCACUGUAGCCCUGCAGCCC | 0.15     | 0.35   | 0.31  |
| GUGCAUUUCUGUGCAUUGC | -0.16    | 0.30   | 0.34  |
| CGGGGCAUCCUGAGCAUGGAU | -0.16    | 1.18   | 1.17  |
| UCAGUGCACAGCAGAUCUUUG | -0.08    | 9.14   | 9.75  |
| UCUCUCCUUCUGCCUGCAG | -0.15    | 0.31   | 0.38  |
| CAUCAUGUUCUCUCACCAUGCU | 0.15    | 0.14   | 0.05  |
| UCCGCCAGUGUGAUUCCUGAUU | -0.14    | 0.51   | 0.56  |
| AAACAUUGCCAGUUGAGUGGAC | 0.15     | 0.19   | 0.12  |
| AUCCCGAUAUAAUGGACAA | 0.15     | 0.13   | 0.08  |
| UGAAGCGCGCCUUGCUCUGCAGA | 0.15     | 0.10   | 0.05  |
| ACCUAUAUAUAUUGUCUUG | -0.12    | 0.36   | 0.40  |
| CUGAUAAGAACAGAGGCCCAGA | -0.10    | 1.44   | 1.84  |
| AUCAUGAUAUACUGUUCAAAACA | -0.13    | 0.54   | 0.69  |
| CUGCAGACUCGACCUCCCGAGC | -0.14    | 0.81   | 1.02  |
| ACUGCUGGGAGUACCGG | 0.14     | 0.14   | 0.09  |
| CUGCCUGGCCCGAGGAGCCG | -0.13    | 0.28   | 0.28  |
| UUCAAAGUAUCCAGGUAUGCU | -0.07    | 153.02 | 154.76 |
| CAAAGUGCUUGUCUGCAGUGAG | 0.05    | 149.03 | 147.48 |
| UAUUGCAUUUCUCCCGGCU | 0.05     | 569.72 | 565.01 |
| UUAUUUGUCAGUCUUGA | 0.13     | 40.43  | 38.83 |
| UAACGCAUAUAUUGGACAU | -0.13    | 0.10   | 0.12  |
| CACCUUUGCCUACUCAGGUCUG | -0.12    | 0.63   | 0.68  |
| UCUCUCCGCUCCUCGGGUCUC | 0.13     | 0.86   | 0.76  |
| UCAGAACAUAUGCCGGUUCCCGA | 0.12    | 0.19   | 0.01  |
| AAGCUGGCCAGUUGAAGACGU | 0.04     | 225.96 | 224.78 |
| UUGAGGGCGGGG | -0.09    | 0.19   | 0.37  |
| GACCCAGCCUGACCA | -0.12    | 0.77   | 0.95  |
| CUGUAACGGCCACUGCCUUUGC | 0.12     | 0.24   | 0.16  |
| AGCUACUCUGCUACUUGG | -0.10    | 2.07   | 1.72  |
| UAGCAGCGGAAACAGUUCUGCAG | -0.11    | 0.14   | 0.17  |
| UAGCCGUAUUCUCCUGGUGUC | -0.11    | 0.50   | 0.59  |
| CUUUCAGUGCGAUGUUUACAGC | 0.09     | 1.86   | 1.78  |
| CCUCCCACACCCAAGCUGCA | 0.10     | 0.34   | 0.35  |
| UCGGUCUCAUUACUUUAUAGG | -0.11    | 0.21   | 0.23  |
| AAUCUGAGAAGGCGACACAGU | -0.11    | 0.12   | 0.14  |
| CUAUACAACCACUCUGCCCUCCC | -0.11    | 0.15   | 0.16  |
| UAUACAGGGCAACUCUCUGU | 0.11     | 0.18   | 0.09  |
| UAGCAGCCAGCCACAGUGGUCA | -0.11    | 0.23   | 0.28  |
| AUGUCGCAUAUUUCUAGAGG | 0.10     | 0.20   | 0.12  |
| AAUCCUUUGUCUCCCUGGGUG | 0.11     | 0.11   | 0.07  |
| UUUCUAAUUCUCCACUGCUUU | -0.11    | 0.12   | 0.08  |
| UAACUGUCUUGUCUACUGUCA | -0.11    | 0.22   | 0.24  |
| UGGAUUAUGAGCUGAAA | -0.10    | 26.38  | 26.92 |
| ACCAGGAGCUGAGGCCCUC | -0.09    | 0.46   | 0.59  |
| GUGGGGGAGAGGUGUC | -0.09    | 0.25   | 0.41  |
| CCUCUGCCUCUCUUGCU | -0.10    | 0.19   | 0.22  |
| AUUCUAUUUUCUCCACUGCUUU | -0.09    | 0.80   | 0.87  |
| UAACUCUGUCUGUAAGAGG | 0.10     | 0.38   | 0.32  |
| AAUGCCACCCGGGCAAGGAAUUC | 0.07    | 1.50   | 1.85  |
| ACCGUGAAAGGUUGCA | 0.07     | 0.16   | 0.03  |
| AUCAACAGCAUAUAUUGGCCG | -0.06    | 1.35   | 1.33  |
| UAUUGUCUGCUAGCAUCACUU | 0.09     | 1.44   | 1.44  |
| Sequence                        | Score 1 | Score 2 | Score 3 |
|--------------------------------|---------|---------|---------|
| CAGGCCAUAUUGUGCUUGCCUCUGA      | -0.06   | 0.19    | 0.24    |
| UAAGGUGCAGAUAGUAGCCAUAGUAG     | 0.06    | 0.58    | 0.56    |
| UUAUCAGAAGUCCUCAGGCUAUCGAGA   | -0.07   | 0.44    | 0.45    |
| AUAACAUUGUCAAAACGCUUCCUUGCAG  | 0.06    | 0.05    | 0.04    |
| GACCUCGCUGCCUGCUGCUGCAG       | -0.06   | 0.35    | 0.39    |
| UUGUACAUGUGUAGCUGUUCAUCAGA    | -0.06   | 0.08    | 0.18    |
| AAAAGUUAUUGCUGUUUCUGCGAGA     | -0.06   | 0.07    | 0.08    |
| AUCUGUGUCUGUUGGAAUGGGAAGG     | -0.06   | 0.18    | 0.23    |
| UAGCAAAACAUUAUUAUGUGUGAGA     | 0.06    | 0.04    | 0.01    |
| AAGCAAAUCUGUACUACUGUAAGGUGA   | 0.06    | 0.03    | 0.01    |
| UGAGAACCAGUCUUGCUUGCAGUGA     | -0.05   | 8.89    | 9.08    |
| AGGUUCACCGAGCAGAUUUCUGAUCG    | -0.06   | 0.04    | 0.04    |
| CUAAACAAUCUGUUCUUGCCUUCAG     | -0.06   | 0.27    | 0.29    |
| UCUGUGAGACCAAGAACAUACUUCCAG   | -0.06   | 0.04    | 0.04    |
| CUGGUAUAGCUGGCUCUGGGGAGAGA    | -0.06   | 0.09    | 0.10    |
| CGGUGCAGUGGCGGUGGGCUGAAGA     | 0.05    | 0.17    | 0.22    |
| UUAUGUCUAUCUGUAGAUAGGUGG     | 0.05    | 1.15    | 1.07    |
| UCUCGUAUAGCCGCUCUCUGAC       | -0.05   | 0.08    | 0.10    |
| GGAGGUGCUGGUGGGGCGGCGGCGG    | -0.05   | 0.27    | 0.31    |
| ACUCAGCCCCACACUCUCAGCG       | -0.05   | 0.08    | 0.09    |
| UUUUGUUCUCAGCAUUCCCCGAG    | -0.05   | 0.16    | 0.18    |
| GAUUGAAGCUAGUAGGCGUAGGCGG    | 0.05    | 0.33    | 0.36    |
| CCCCAAACAGUGCUCAGGCAUCGACG   | -0.05   | 0.05    | 0.06    |
| UGGGCGAGUGACUAGGUGCGACAG     | -0.04   | 0.17    | 0.22    |
| CCUCUGUAGUACCUCUCUAGG       | 0.05    | 0.09    | 0.02    |
| UGAGAAGCUAAUUCAUGCGGUGU    | -0.04   | 24.42   | 23.38   |
| UUAACCGCGCUGCUCCACUUGCUG     | -0.05   | 0.03    | 0.03    |
| CUGUGGGCGUCUGGGCCACGCG     | -0.05   | 0.04    | 0.05    |
| ACUGUGACAGCGACACUUCCGG     | -0.05   | 0.61    | 0.71    |
| AGUGCCUGACGGAGUACAGAGC     | -0.05   | 0.06    | 0.07    |
| UAGAGAGGGAAGGGAUGUGAUGU     | -0.04   | 0.32    | 0.40    |
| CAAGCUCAAGUGUGGUCCGUUAU     | -0.04   | 0.09    | 0.19    |
| GAAGAUGAGACUGUGGUGCAUGA     | -0.04   | 0.10    | 0.12    |
| GAUCUGCGAGUGCUAGUCUGAGC    | -0.05   | 1.14    | 1.34    |
| UGAGUACUGCAUAUCUAUCUUCAU    | -0.04   | 0.05    | 0.06    |
| AGGUGCUGGCGCUCUGGCGCG     | -0.04   | 0.07    | 0.08    |
| UGAAACAUACACGGGAACACUC       | -0.04   | 0.06    | 0.07    |
| ACUGGCUAGGUGGGAAAAGAUUGGAU  | 0.05    | 0.14    | 0.15    |
| UGUGCCUGACUGGUGCCCGGCGCA    | -0.05   | 0.03    | 0.03    |
| CAGUUAACAGUAGUGCUAGUGCAG    | 0.05    | 0.49    | 0.49    |
| AAGCCGUGAGUACUGAUCUGUGUG    | -0.05   | 0.16    | 0.17    |
| CUGACUAGUAAAGUAGGCUCAU      | -0.05   | 0.03    | 0.04    |
| AACUUAUCUGUGGUACUGGAGGUU    | 0.04    | 1.59    | 1.57    |
| CUCUGCCCUCUAGUCCUGAGGCA     | -0.04   | 0.04    | 0.05    |
| GUGCCUGUGGCGUCUGAGGGCGG    | -0.03   | 0.17    | 0.22    |
| ACCCGCUCGCCCAUGUAGA      | -0.04   | 0.27    | 0.32    |
| UCAGCAUCAUUGGACCAAGAGA     | -0.04   | 0.80    | 0.43    |
| CUAAACAUACUUACUUUCACCC     | -0.04   | 0.14    | 0.17    |
|AACUAAGAAACUUCUUCACGAGU      | -0.04   | 0.04    | 0.05    |
| GAACGGAUCCCAACAGACGUGCUG    | -0.03   | 98.59   | 99.11   |
| AGCCAAGAUGGUGUGCUAUCAGA   | -0.02   | 0.52    | 0.66    |
| UUGGGCCUGGUGCCUGAGAUAUGC    | -0.04   | 0.04    | 0.05    |
| CUGGGCGCGGCGGCGGUGGCGG     | -0.03   | 0.05    | 0.07    |
| GCAAGAAGACAGGCCUGGACAGA     | -0.04   | 0.04    | 0.05    |
| UUGAGCAUUAGAGAUGAAACUGA    | -0.04   | 0.03    | 0.03    |
| GAACCAUGGAGGUUGAGGCUGCAUG  | -0.04   | 0.39    | 0.47    |
|                |       |       |       |
|----------------|-------|-------|-------|
| UGGUGGAGGUGGCCGGGA | -0.04 | 0.93  | 1.02  |
| AUCACAUUGCCAGGGAUACC | -0.04 | 0.94  | 1.38  |
| UUCACCCAUUCUCACCCACGC | 0.03  | 3.06  | 2.95  |
| UUCAGCGGAGCUGAGCGUGCU | -0.04 | 0.04  | 0.05  |
| UGGGUGUUUGGGGAGAGAUGA | -0.04 | 0.18  | 0.22  |
| UUGGGGAAAGCGGCCCCGUGAGUG | -0.04 | 0.12  | 0.13  |
| UCUCUGGCCUGUGUCUAGGC | -0.04 | 0.04  | 0.04  |
| GUGAGGACUCGGGAGGUGG | -0.03 | 0.06  | 0.08  |
| UUCACCCUCUCACCAGCGAG | 0.03  | 0.04  | 0.01  |
| AGCAUCAGCGGUGAGUGUGAC | 0.04  | 0.58  | 0.14  |
| ACGGUGAGCUGCGUGAGUACC | 0.04  | 0.06  | 0.06  |
| UAAUUCUUAUAGUAAGCUAGU | -0.04 | 0.50  | 0.57  |
| AUAGGACUCUAAUAGUGCCAG | -0.03 | 0.17  | 0.22  |
| CUCUGGCGCCUCUCUCUCAG | 0.04  | 0.41  | 0.35  |
| UGGCUAGCGGAGCUGAGCAGUG | -0.04 | 0.03  | 0.03  |
| GAUCUCAUUUGUGUCGUGCAG | -0.04 | 0.03  | 0.04  |
| AUUGUCCUGUGCUUUUGAGAU | -0.03 | 0.12  | 0.16  |
| UCAAUGUGACUCUGAGCAG | -0.03 | 0.03  | 0.04  |
| AUCAAGUGAAAGAUAGCUAGU | -0.03 | 0.05  | 0.06  |
| CUCUCACAGUGCCCCCCCAG | -0.03 | 0.17  | 0.22  |
| CUGGUGUUCUCUGUGCUUAG | 0.04  | 0.28  | 0.30  |
| UUUCACAGUGGACAGAGGGA | 0.04  | 0.06  | 0.03  |
| GCUGCUGCUGAUUUGUGUCCC | -0.03 | 0.03  | 0.03  |
| UCCUCUCGCUUUCUCACCCAG | 0.03  | 0.06  | 0.04  |
| CGCCGCGGGGGCCGCGC | -0.03 | 0.05  | 0.06  |
| UACCCUGUAGAACGGAUUUUGUG | -0.03 | 0.09  | 0.10  |
| UGGUUUGAGCAGCGGACAGUCUGU | -0.03 | 0.05  | 0.06  |
| CUGCGGUCUGCUUGCGUGCU | -0.03 | 0.04  | 0.05  |
| GGUCCUCACGAUAGCCGCCG | 0.03  | 0.02  | 0.00  |
| AAAAUGAGACUACUUUGCA | -0.03 | 0.19  | 0.16  |
| GUCAUACAGGCUUCUCUCUCU | -0.03 | 0.03  | 0.04  |
| UCUCUGGCGUCUCGGUCUGAG | 0.03  | 0.03  | 0.01  |
| UCCCCAGACCCUAACUUUGGA | 0.03  | 0.15  | 0.14  |
| CUGGCGAUAUCAGUGUCACAG | -0.03 | 0.16  | 0.21  |
| UUCAUUCUGGCUCCAGGCUACA | -0.03 | 0.02  | 0.03  |
| UCGCGGACAGCGGGAUGGACAGG | -0.03 | 0.03  | 0.03  |
| UUAUGGGUUCGGCGGACUGAQ | 0.02  | 3.76  | 4.01  |
| UAACUGUUGAACAACUGAACC | 0.03  | 0.07  | 0.07  |
| CCGCCUUCUCUCUCGCCCGC | -0.02 | 0.68  | 0.87  |
| UCGUGGAUCAGUGGUUGAGUGUC | -0.03 | 0.02  | 0.02  |
| UUAACUGUGGUAAACCGCGAUU | -0.03 | 0.03  | 0.03  |
| AACACCAUUUCAAGGAAUUCA | 0.03  | 0.09  | 0.09  |
| CAGGCGUGGCAUGACAGUGGU | -0.03 | 0.03  | 0.04  |
| AUAGUGCGAUAACGUGGGGC | 0.03  | 0.56  | 0.60  |
| CAGUCCUUCUGUUCACACCAUG | 0.02  | 0.02  | 0.00  |
| UCACCGCCUGUGUGUCCCUAQ | -0.03 | 0.03  | 0.04  |
| AAGGCAAGGCGGCCCCGACCCC | -0.03 | 0.03  | 0.04  |
| GAAGAAGCCUGUCAUUGGCCC | -0.03 | 0.04  | 0.04  |
| UGAGUGAAGUUGUUUCUU | -0.02 | 0.07  | 0.09  |
| UUUUUCAUAUUGCUCUGAGACC | 0.03  | 0.15  | 0.14  |
| GUGCAUAGUAGGUGAUUGCA | -0.03 | 0.03  | 0.03  |
| AGCGAGGCCCCGUCUCUA | 0.02  | 0.03  | 0.00  |
| UACGUAGUAAUAUUGUAUUU | -0.02 | 0.26  | 0.32  |
| UUUCCGCGUCGGUGGGUGUGU | 0.03  | 0.36  | 0.32  |
| GCGGGCGGCAGAGGGGC | -0.02 | 0.05  | 0.06  |
| UGAGAUGAACUAUUGCAAGGC | -0.02 | 17.62 | 16.68 |
| RNA Sequence | Relative Abundance 1 | Relative Abundance 2 | Relative Abundance 3 |
|--------------|---------------------|---------------------|---------------------|
| UCUCCAGUGGCUGCCUCUCUCAG | 0.02 | 0.02 | 0.00 |
| AGAGCUUAGCUGAUUGUGAAGC | 0.03 | 0.13 | 0.09 |
| AACUGGCGCUCACAAUGUCGCGU | -0.03 | 0.09 | 0.16 |
| ACUGAUAUUCUUUGUGUGUUCAG | 0.02 | 0.03 | 0.00 |
| CUUGGCAUUCAGCAGCACUCAGU | 0.03 | 0.04 | 0.04 |
| UUUGCCUGUCCUCUCUCUCGCA | -0.03 | 0.03 | 0.03 |
| CAAUGUUUUCACAGUGCAUCUG | -0.03 | 0.02 | 0.02 |
| UCACUCUCUCUCUCUCGUCUU | 0.02 | 0.05 | 0.00 |
| AUGACCUUAUAGUGACAGACU | 0.02 | 0.33 | 0.27 |
| UAGGAGCUCAACAGAUGUCGUUU | -0.03 | 0.04 | 0.05 |
| GCAUUGUCAGGGCUAUCGA | 0.02 | 0.12 | 0.01 |
| AAAGAUGGAAAUUUGGAUCAUC | 0.03 | 0.11 | 0.07 |
| UCAGAGUCCAAGUGUCACCAU | -0.02 | 0.07 | 0.09 |
| UACAGAUACUGUAAUACUGA | 0.01 | 214.78 | 215.94 |
| GGGCGACAAAGCAAGACUCUUUCUUUCU | -0.02 | 0.06 | 0.07 |
| UUUCUCUUCAGCAGCAGUACCG | -0.03 | 0.03 | 0.03 |
| AUUGCCUCUCUCUCUCUCCAG | -0.02 | 0.13 | 0.16 |
| CUCACCAUUCUCUCUCGUC | -0.03 | 0.05 | 0.05 |
| AACUCUAGCGUGAGCAACAG | -0.02 | 0.03 | 0.04 |
| CCAAAACUGCAGUACUUUUGC | 0.03 | 0.12 | 0.12 |
| UAUGUAACAGGCUCCACUACC | -0.02 | 0.04 | 0.05 |
| ACCUUUUUCUCUUCUCCAG | -0.02 | 0.15 | 0.19 |
| GAGCCAGUGUGAGAGACAGUGA | 0.02 | 0.18 | 0.00 |
| UGACUUCUACCUUCCAAAG | 0.02 | 0.04 | 0.00 |
| CUGGAGAUAGGAAAGACUCGUUGU | -0.02 | 0.05 | 0.05 |
| UUCCAUCUCUUCAGAAGUUCU | 0.02 | 0.02 | 0.00 |
| UGGAAUGUAAAGGAUAGUUA | -0.02 | 0.04 | 0.14 |
| UGGUUGGGAGACCGCUGU | 0.02 | 0.17 | 0.23 |
| UAGCAGACAUCAUGUUUCUACA | -0.02 | 57.20 | 57.42 |
| UGCCCCUGUGGACUCAUCUCCUGG | -0.03 | 0.06 | 0.06 |
| AGGUUUUUGUGAGCAGG | 0.02 | 0.02 | 0.00 |
| GUAGAGGAGAUGGCGCAGGG | -0.02 | 0.05 | 0.05 |
| UGACUUAAUUGUGUCUGGGA | -0.02 | 0.02 | 0.03 |
| UCUCGUCUUUCCUCUGUGAC | -0.01 | 0.27 | 0.35 |
| UCUAGUAAGAUGGACUUCG | 0.03 | 0.10 | 0.10 |
| UGCCAACCGUCAGAACGCGAGA | -0.02 | 0.03 | 0.04 |
| AAGGCCUUACCCAAAAAGCAU | -0.02 | 0.68 | 0.75 |
| UGACCUCUGUGAAGCCACCCA | 0.02 | 0.07 | 0.02 |
| UGCCUCUCUCUCUCUGCCUC | -0.02 | 0.13 | 0.17 |
| CAAAGACUCAUCAUGUUCUCG | -0.02 | 0.14 | 0.17 |
| CUGGAGAAGGUGGUUGUUACUC | -0.02 | 0.01 | 0.01 |
| CAGGGCAGAGGGCACAGGAAUCUGA | -0.02 | 0.08 | 0.10 |
| AGUUGCACAGGGCGCUUUGGUGU | -0.02 | 0.02 | 0.02 |
| CUCACACCUCUCUCUGCCUGCA | -0.02 | 0.05 | 0.05 |
| AAGCCCUUACCCAAAAAGCAU | -0.01 | 0.27 | 0.35 |
| AAAGGCUUUCUCUCUGAGGAC | -0.02 | 0.03 | 0.03 |
| AAAACAUUCGCGUGACUCUUUU | -0.02 | 0.05 | 0.05 |
| UUUGCAGUAAAGGUGAGCA | 0.02 | 0.04 | 0.03 |
| ACUCUUUCCUGUGACUAC | -0.02 | 0.19 | 0.19 |
| GAAAGUAUUGCUGUUUUGGCC | -0.02 | 0.03 | 0.04 |
| CACUGUUUCCACAGCUGCUCUU | -0.02 | 0.02 | 0.02 |
| GUCCAGUUUUCCGAGAUAUCCCU | -0.02 | 0.15 | 0.13 |
| UGUAUUGUUGUAAUUGGGGUU | 0.02 | 0.02 | 0.01 |
| AACACCCUGGUUAAACUCUUU | -0.02 | 0.03 | 0.04 |
| UGGAGGAAGGAAUGUGAGUG | -0.02 | 0.03 | 0.04 |
| GGGUGCGGC CGCGGGG | 0.01 | 0.06 | 0.00 |
| Sequence                        | 0.01 | 0.02 | 0.03 | 0.04 | 0.05 | 0.06 | 0.07 | 0.08 | 0.09 |
|--------------------------------|------|------|------|------|------|------|------|------|------|
| CGUGGAGGACGAGGAGGAGGC          | 0.02 | 0.06 | 0.08 | 0.04 |
| UACACAAGAAAACCAAGCUCA          | -0.01| 0.07 | 0.09 |     |
| UAGGGAAAGACUUGGCAUCUCU         | 0.02 | 0.08 | 0.05 |     |
| UUCUGGAUAAACUGUGGAGACU         | 0.01 | 0.03 | 0.00 |     |
| AUGGCCUCCCGGCCGCGCAG           | -0.02| 0.02 | 0.02 |     |
| AGGCGGAGACUUGGGGCAUUUGG        | -0.02| 0.04 | 0.04 |     |
| UCGGCCUACCGACUUCUGCUCUCAC      | -0.02| 0.02 | 0.03 |     |
| UUCUCUGUGCUUUUCUCUCUCUCACAG    | 0.02 | 0.06 | 0.04 |     |
| UGGGCUAAGGGAAGUAGUUGGUAUUGGC   | -0.02| 0.03 | 0.04 |     |
| UCGACAGCAGCAGCAGCAGCUUCUC      | -0.02| 0.02 | 0.03 |     |
| UGUUCAUUGGAAACCUCGCGCAAGCG     | -0.01| 0.02 | 0.03 |     |
| UUAGACCUAGUACAGCUUCUU         | 0.01 | 0.04 | 0.00 |     |
| AGCAUACACCUGUAGUCCUAGA         | -0.01| 0.16 | 0.20 |     |
| CCUCUCUCUCUCUGCAGCCAGCAGC      | -0.01| 0.06 | 0.07 |     |
| AACGGCAUUGACUUUUUGUAACCA       | -0.02| 0.01 | 0.01 |     |
| GAUGUCACUCUCUCUCUCUCUUCUC      | -0.01| 0.04 | 0.06 |     |
| ACUCAAAACCCCUUCAGUAGACUUUC     | -0.02| 0.02 | 0.02 |     |
| AAAGGAGAAAAUGAGCGAGGCAAGGCA    | -0.01| 0.03 | 0.04 |     |
| AUCAUGACUGGCUCCUCUGGUGU        | -0.01| 0.02 | 0.02 |     |
| UCGGGGCAUGGGGGAGGGAGGCCGUG     | 0.01 | 0.45 | 0.00 |     |
| AGGGGGCAUGACUACUGAGCGUG        | 0.01 | 0.03 | 0.00 |     |
| GUGAGUGUGAUAUUGCAGGGG        | 0.01 | 0.02 | 0.00 |     |
| AGCUGUCUGUUGU UUCUUCUUCAG     | 0.01 | 0.02 | 0.00 |     |
| AGGUGUCAGGUGGGCGUCACCA        | 0.01 | 0.07 | 0.00 |     |
| UGGUCUGUUCAUUCUCUCUCUUUGG     | 0.01 | 0.02 | 0.00 |     |
| GCAGUGUGUGUUCUUCUGGG         | 0.01 | 0.07 | 0.00 |     |
| CAACCUGAGGACUCAUGCUG          | 0.01 | 0.07 | 0.00 |     |
| GGGUUGUAGCUUGCUUGCGAGCUG      | 0.01 | 0.04 | 0.00 |     |
| AGAUGUCACGCCCAUAAUCUCG        | 0.01 | 0.06 | 0.00 |     |
| CAGCAGGGAGAGAGAGAGACGAGAGUC   | 0.01 | 0.07 | 0.00 |     |
| GUGAGGACUGGAAUUGGUG           | 0.01 | 0.07 | 0.00 |     |
| GAGACUGUGGGUGUGGGCC           | 0.01 | 0.02 | 0.00 |     |
| AGGGUGUGUGUUGGAGCACGCUCCG     | 0.01 | 0.03 | 0.00 |     |
| UGGAGUUAAGGGUUGCUUGGAGA       | 0.01 | 0.02 | 0.00 |     |
| UCCUCUCUACCUCUAUCCAGU         | -0.01| 0.06 | 0.08 |     |
| GGGGUUCUGGGGAGGGGAUU         | -0.01| 0.03 | 0.03 |     |
| UUUCACUGCCACUACCUAUUU        | -0.01| 0.03 | 0.04 |     |
| ACAGGGAGGAGUAGUGA           | 0.01 | 0.12 | 0.01 |     |
| CGGCCGGCGGGCGGGG         | -0.02| 0.02 | 0.02 |     |
| AGUUUCUCAUGGGAAGCAGCUUUUA    | -0.02| 0.48 | 0.57 |     |
| UCAGGACUUUUUCUCUGA           | -0.01| 0.02 | 0.03 |     |
| CUCACUGUAACAGUAAGCA          | -0.01| 0.08 | 0.10 |     |
| UUUUGCAGUGUUGUUCCUAUU       | 0.02 | 0.11 | 0.10 |     |
| AAUCAUUCAGGCAAAACACU         | -0.01| 0.02 | 0.02 |     |
| AGAAAGUAUUCUGGGUUCUCAGCA    | -0.01| 0.02 | 0.03 |     |
| UCCAGUUUCUUCUCCCUUCUCU      | -0.01| 0.24 | 0.31 |     |
| AAGAGGAGGCAUGUGUGCUUGGUG    | -0.01| 0.05 | 0.06 |     |
| CUCGAGGGCAUGGGCCAGGC        | -0.01| 0.34 | 0.43 |     |
| UAGGGGUGUCAGGACAGGUGACG     | 0.01 | 0.01 | 0.00 |     |
| CCAGGGUUGUUGACUGUAGUGUG    | -0.01| 0.04 | 0.05 |     |
| CCCGGACAGGGCUUCUGGCGAGC     | -0.01| 0.03 | 0.04 |     |
| UCAGUGUGGGAUUUCUCUGA       | -0.01| 0.02 | 0.03 |     |
| GCUGGCCAGGCCUUCUAGACCUCCUL   | 0.01 | 0.01 | 0.00 |     |
| UGAAGGGUACUGUGUGGCAGAGC   | -0.02| 0.02 | 0.02 |     |
| AGGCAAGUGUGGCCAAGCAUGCU    | 0.02 | 0.08 | 0.04 |     |
| GCAGUGGUCUGGAAAGUAACUC       | 0.01 | 0.01 | 0.00 |     |
| RNA Sequence                        | ΔG (kcal/mol) | ΔS (kcal/mol K) | ΔH (kcal/mol) |
|------------------------------------|---------------|----------------|---------------|
| UGGAGUCCAGGAAUCUGCAUUUU            | -0.01         | 0.03           | 0.03          |
| CCCAGUUCAGACUACUCCUGUUC            | 0.02          | 0.70           | 0.78          |
| UGGAGGAGAACUCUGAAGGAGAUUGG         | -0.01         | 0.02           | 0.03          |
| UGGUAAUUCUCCUUUGCGUGCAUGAG         | -0.02         | 0.18           | 0.15          |
| CGCACCUGCUCUCACACCACAG             | -0.01         | 0.15           | 0.19          |
| UGGUGGAGGUUGAGGAGGUGGAA            | -0.01         | 0.02           | 0.03          |
| AAAGCUAGGUAUUGAGAAGCGUGA           | -0.01         | 0.17           | 0.21          |
| CGCAGGAGAUCAGGAGCGUGUGGA           | 0.01          | 0.01           | 0.00          |
| CGUGCCGGGUGCUGCGAGCGAGCA           | -0.01         | 0.03           | 0.04          |
| AGGUGCAUCAAAUUCCAGCAGA             | -0.02         | 0.01           | 0.01          |
| UACCACCAUCCAGGUAGA                | -0.01         | 0.16           | 0.20          |
| GGUGGUGGUGGCGGCGGC                | -0.01         | 0.18           | 0.22          |
| AGCCGGGCCUGAGCCUGCCAGUC           | -0.01         | 0.01           | 0.01          |
| CGUUGCCUGCUCCACUCCAG              | -0.01         | 0.06           | 0.07          |
| UGCGACACUGUGCAAGCCUUCA             | -0.01         | 0.04           | 0.05          |
| AAGGCUUACUGUUGAGCA                | 0.02          | 0.49           | 0.05          |
| AAGGCUUACUGUUGAGCA                | -0.01         | 0.01           | 0.01          |
| GAGGAAUGUAAGAAAGAA                | 0.01          | 0.01           | 0.00          |
| CCCUCUCUCCUCCUCCUUCUUC            | 0.01          | 0.05           | 0.04          |
| AAUCACCCUGAGCGUCCUGCAAGU          | 0.01          | 0.01           | 0.00          |
| AGAGGGCCUUUCUCCAGAUGAGGAGAUG      | -0.02         | 0.03           | 0.03          |
| AACCACUGCGCCUGAGGAGGAGCAUU        | -0.01         | 0.02           | 0.03          |
| UCCACUCUGCCUCGCCCGCAG             | -0.01         | 0.01           | 0.01          |
| AACCAUGGUGCUGAUGGAAAGAA          | -0.01         | 0.01           | 0.02          |
| CCCUGGGUUCUGAGCUGAGACUGA          | -0.02         | 0.03           | 0.03          |
| UCCGUGUCUCAGAGGUGUGUGCACC         | -0.01         | 0.02           | 0.02          |
| AGAGGUGAGUGUUGAGAAGAA            | 0.01          | 0.01           | 0.00          |
| GGAGGAGGAGGAGGAGGAGGAGCAUU        | -0.01         | 0.01           | 0.01          |
| CCCAGCCUACUUCUUGGCUUCA            | -0.01         | 0.04           | 0.05          |
| CUGGGUGCGGUCUGCGGUGGG             | -0.01         | 0.03           | 0.03          |
| CAUGACGUCAGAGGCAGCCUUCGC          | -0.01         | 0.03           | 0.03          |
| UGCCUCAUAGGUUGAGUGUGCAAGU        | -0.01         | 0.01           | 0.01          |
| AAAAGCUGGGUGUGAGGAGGU             | -0.01         | 0.03           | 0.03          |
| AGUGGAUGAUGAGACUCUGGUAC          | -0.01         | 0.01           | 0.01          |
| CGGGUGAAGAGGCGAGUGGAGGA           | -0.01         | 0.02           | 0.02          |
| UGGCGUGAUGAGGUGAGCUGUCUGAAG       | 0.01          | 0.01           | 0.00          |
| CACCCUCUAUCUUCUUUGGU              | -0.01         | 0.02           | 0.03          |
| UUGUGCCUACUCAUUUUUGGCU            | -0.01         | 8.24           | 8.12          |
| UGUCUUUCUUCUCCUUCCGCAG           | -0.01         | 0.17           | 0.21          |
| Sequence                      | Similarity | Identity | Coverage |
|-------------------------------|------------|----------|----------|
| CGGGCGUGGUGGUGGGGGUG          | -0.01      | 0.10     | 0.13     |
| UAACACUGUCUGGUACGAGU          | -0.01      | 0.70     | 0.84     |
| UGAGGGAGGGAUGCAAGGAGACGC      | -0.01      | 0.02     | 0.02     |
| GACUUAAGACUUUCCCCUCUCA        | 0.01       | 0.13     | 0.11     |
| GGGAGAAGGGUCUGGGGC            | -0.01      | 0.04     | 0.04     |
| UUGCAUAGUCACAAAGAUGAUC        | -0.01      | 0.01     | 0.01     |
| AAGUUUAUCAGUUGUCACUCA         | -0.01      | 0.01     | 0.01     |
| AGGCCAGUGCUAGAGAAAGAUGU       | -0.01      | 1.52     | 1.50     |
| AAAAGUAAUGGGGUGCUUUGGUGU      | -0.01      | 0.02     | 0.02     |
| AGCACAGUAGUUCUUGCUUGGGA       | -0.01      | 0.01     | 0.01     |
| CGGUGGACUGAGAGUGGUGG          | 0.01       | 0.62     | 0.73     |
| AUCAUAAGACAGAUAUUUCUUU        | -0.01      | 0.01     | 0.01     |
| UGGUGGGCCGAGAAGACUGUCG        | -0.01      | 0.01     | 0.02     |
| UGGCCAGAGGAGGAGGCAAGAGCA      | -0.01      | 0.07     | 0.08     |
| UUCUCUUUUUCUGCCUUUGUGU        | -0.01      | 0.01     | 0.02     |
| CUCUUAUAUGAGUUGCUUUCUCUCU     | -0.01      | 0.01     | 0.01     |
| CAAAACUGCAUAUUCUUUGGC         | -0.01      | 0.03     | 0.03     |
| UAAUAAAGUGGCGAGUAGAAGC        | -0.01      | 0.02     | 0.02     |
| UGGGCCUGGGAGGAGGAAGGGG        | -0.01      | 0.01     | 0.02     |
| UGGGGAGCUGAGGCUCUGGGGGGUGU    | -0.01      | 0.01     | 0.01     |
| AUGGCCAGACUGUCACACAGAGG       | -0.01      | 0.01     | 0.01     |
| AAUGAGCAGAUGUCAGUUGCUAGUCUG   | -0.01      | 0.03     | 0.03     |
| UAUUGGUCCUUGGUAGCUAGUGAAGCC   | -0.01      | 0.03     | 0.03     |
| CAGAUGAGCAGAUAUUUCUCACUCUA    | -0.01      | 0.02     | 0.03     |
| AAGUGAAGAGAGGUGUGUGUGAGGCAU   | -0.01      | 0.02     | 0.03     |
| UACAGAUCAGAGCGUGAGCAG         | -0.01      | 0.01     | 0.01     |
| UGGCCUCUGUUCUCUCACU           | -0.01      | 0.01     | 0.01     |
| GAACGUCUCCCCUCUCCCCGAGC       | -0.01      | 0.13     | 0.17     |
| GUGGCCCCGGCGCUGCCUGAGGG       | -0.01      | 0.02     | 0.03     |
| GCCCAAAGGUGAUAUUCUGGGG        | -0.01      | 0.00     | 0.01     |
| UUGUGUGUAGAGAAGAAGGGAAGGA     | -0.01      | 0.13     | 0.17     |
| GGUGGUGAGGCCAGCGAUAAGU        | -0.01      | 0.03     | 0.03     |
| AGGAGCGGAGCGGCGGCGAGCGAGUG    | -0.01      | 0.02     | 0.03     |
| AAUGCAGCUCUGCAGUAUC          | -0.01      | 0.03     | 0.03     |
| AAGGGAAGAGGCAGAAGGGAAGAGAUA   | -0.01      | 0.15     | 0.19     |
| AGGAGGGAGGAGAGAUUGGCAAGAUGU   | -0.01      | 0.15     | 0.19     |
| ACUGACAGUAGUAGCAAGAGG         | -0.01      | 0.02     | 0.02     |
| UUGCUCUGCUCCCCGGCCCCCAG       | -0.01      | 0.02     | 0.02     |
| AGAGAUGGGGUCAUAAUAAUUGAAGA    | -0.01      | 0.02     | 0.02     |
| AAGGGAUAUGUGUCAGACUAUGA       | -0.01      | 0.02     | 0.03     |
| AGGAGAACUAAGAAGGAAAGA          | -0.01      | 0.02     | 0.02     |
| AGGAGGAGGGGGGCGUGAGAAGCAGAAG  | -0.01      | 0.02     | 0.03     |
| UUCGCCACUUCCCUCCUGCAG | -0.01 | 0.02 | 0.22 |
|------------------------|-------|------|------|
| UCUGCACAUUCUUUAGGCAAUA | -0.01 | 0.02 | 0.02 |
| ACGGUAAGCAGACUCUUGAU | -0.01 | 0.02 | 0.03 |
| AGGCAUGUGGGAUGUAGAGA | -0.01 | 0.02 | 0.03 |
| AGUUUGUCGUUGUUUUCUCUCU | -0.01 | 0.02 | 0.03 |
| UCGUUUCCUUUUUUCUGCUU | -0.01 | 0.02 | 0.03 |
| ACCCGAAGCAGUAGUACACU | -0.01 | 0.02 | 0.03 |
| CCUCAGGCGUUGAAGACUGGCU | -0.01 | 0.03 | 0.03 |
| CUAACAGGGAAGCCUUUC | -0.01 | 0.03 | 0.03 |
| AAAACUAGGAGUCUGUGGUAGU | -0.01 | 0.03 | 0.03 |
| AAUCUCAUGACACUCACACU | -0.01 | 0.03 | 0.03 |
| UGCAUGUCUGUGUGCAU | -0.01 | 0.03 | 0.03 |
| UAGGACUGUGCUGGCAAUAG | -0.01 | 0.05 | 0.07 |
| UGUUCUUGCAGGGAAGCAG | -0.01 | 0.06 | 0.07 |
| UUCUAUGCAUAUCUUCUUG | -0.01 | 0.01 | 0.01 |
| AGUGGGAGGCGAGGCGAGGCA | -0.01 | 0.02 | 0.02 |
| ACUGGGCAGGGCGUGUGUGAGU | -0.01 | 0.03 | 0.03 |
| GUUUGUUAACCAUUCCCUCA | -0.01 | 0.15 | 0.19 |
| UCCCCAGGUGUCUGAGAUGUG | -0.01 | 0.02 | 0.03 |
| AUCCACACUCUGCCACCA | -0.01 | 0.02 | 0.02 |
| UUUAAGAUUAGCAAUGAAGUUAG | -0.01 | 0.02 | 0.03 |
| AAAUGUCUCUUCUUUUUGGGGU | -0.01 | 0.13 | 0.17 |
| AAUCUCAUGGAGCAUCCAGUU | -0.01 | 0.01 | 0.01 |
| AAUUUUUUCUCGUUUUC | -0.01 | 0.02 | 0.02 |
| CCUGACACCCCAUCUGCCCUCA | -0.01 | 0.03 | 0.03 |
| CACCUUUGUGUCCCCAUCCUGCA | -0.01 | 0.03 | 0.04 |
| CUGACUUGUGGCCGUCUCUCCCG | -0.01 | 0.15 | 0.19 |
| UGGUCAGAGCGAGCAGAAUUGA | -0.01 | 0.02 | 0.03 |
| ACACUGUCCUUUCCUCCCAG | -0.01 | 0.02 | 0.03 |
| ACUCAAAGAAGAAUCUAGACAG | -0.01 | 0.01 | 0.01 |
| CGCAGCGGCGGUGUCUCGAGCAG | -0.01 | 0.02 | 0.02 |
| GUUCAAUUCAGAUCUAUAAC | -0.01 | 0.02 | 0.03 |
| GUGUGACACGGCGUUCUGCGCAG | -0.01 | 0.03 | 0.03 |
| GGAUUUCUGAAAUCUGUUCU | 0.01 | 0.12 | 0.12 |
| UUCAACGGGUUAAUUUAGAGCA | -0.01 | 0.01 | 0.02 |
| UAGUGAGUAGAUGACAGGCC | -0.01 | 0.00 | 0.00 |
| UCAGGGUGGAAACUGAGGCAG | -0.01 | 0.01 | 0.01 |
| ACGUUGUUGCUGUGUGUG | -0.01 | 0.02 | 0.02 |
| UGCGACAUUGGAAUGAGUAAUCA | -0.01 | 0.10 | 0.13 |
| AUUGUGAACCUAUGAUGUGGCC | -0.01 | 0.03 | 0.03 |
| UAGGCGUUAUUGCUACUUGGAG | -0.01 | 0.01 | 0.02 |
| UUUCUCUCCACUCCUCCUCAG | -0.01 | 0.01 | 0.01 |
| CCGUCCAGGAGAACCUGCAGA | -0.01 | 0.01 | 0.01 |
| AUCAAAGAUCUAAACUUUGCC | -0.01 | 0.05 | 0.07 |
| UAGGCGAGUUAUUGCUACGCGCUGL | -0.01 | 0.03 | 0.04 |
| AAAGACCAGUGAGGAGAGU | -0.01 | 0.02 | 0.03 |
| AGCUGUGGUUGAAGAAGAGCG | -0.01 | 0.25 | 0.31 |
| CAUACAGUUCACUGCUUUC | -0.01 | 0.17 | 0.20 |
| UGUUCUCGACUUCUCCUCAG | -0.01 | 0.01 | 0.01 |
| GGGAGCCAGGAGAUAUGAUGU | -0.01 | 0.02 | 0.02 |
| UAGGUGUUAUCAUGUUGUG | -0.01 | 0.01 | 0.01 |
| ACUCACAUUGUUGUGUAGAUGA | -0.01 | 0.01 | 0.01 |
| UGAGACUCUGGCGUUCACUCU | -0.01 | 0.35 | 0.38 |
| UUUUUUGUUUGAAGACACU | -0.01 | 0.00 | 0.01 |
| UGGCGGCGUAGUUAUGGCUU | -0.01 | 0.01 | 0.02 |
| GCUGUGCAAAAGUAUGGCGG | -0.01 | 0.03 | 0.03 |
| Sequence          | Activity 1 | Activity 2 | Activity 3 |
|-------------------|------------|------------|------------|
| CAAGCUCGUUGUCUGUGGUCG | -0.01      | 0.01       | 0.01       |
| AAACUCUACUUGUCCUUCUGAGU | -0.01      | 0.01       | 0.01       |
| AAAAGUACUUGGGAUUUUGCU | -0.01      | 0.11       | 0.11       |
| UGACUGACGCUUCUCCCAAG | 0.01       | 0.38       | 0.34       |
| AGGAAGCCCUUGAGGCGUGGAG | -0.01      | 0.01       | 0.01       |
| UAGGAGUUGGACUUUCAGCUUGGC | -0.01      | 0.01       | 0.01       |
| UCUGGCAAGUAAAAACUCUCAU | -0.01      | 0.00       | 0.00       |
| UGGAGACGCGGCCCUUGUGAGAU | -0.01      | 0.01       | 0.01       |
| CAAAAGAUCUGGGUUUUGGC | -0.01      | 0.01       | 0.01       |
| UUAUUUUGUUGUUUCGUGCACU | -0.01      | 0.01       | 0.01       |
| AGAGGCUUGGCGUGAUGAAUCU | -0.01      | 0.01       | 0.01       |
| AAUACUGAAAUCGUUCAGGCU | -0.01      | 0.00       | 0.00       |
| CUGGGAUCUCGGGGUCUCUGGUU | -0.01      | 0.01       | 0.01       |
| CAUCCCUUGGCAUGGUGGAGGG | -0.01      | 0.04       | 0.04       |
| CAGGCCUUCGGCGACCCAA | -0.01      | 0.00       | 0.00       |
| AGGGCCUCCCCUCUAAUCUGCU | -0.01      | 0.01       | 0.01       |
| UUAGGAGCUGGAUAAGAAGAUUCU | -0.01      | 0.00       | 0.00       |
| CAAAAGAUCUCUUUUUUUGGCUC | -0.00      | 52.55      | 52.65      |
| CUAUAUAUCAAACAAUAUUCCU | -0.01      | 0.00       | 0.00       |
| GUGAGUCUCAUAGAAAAGAGGA | -0.01      | 0.02       | 0.02       |
| UGACACGCGCCUCUGCCUGGUC | -0.01      | 0.00       | 0.00       |
| AGUGGGAACCUUCUUCAUGAGG | -0.01      | 0.00       | 0.01       |
| UCUUGGUCGUCCAGAGGAGGC | -0.00      | 0.01       | 0.01       |
| UGCUUUACCUUGGCCUCUGAAA | -0.01      | 0.00       | 0.00       |
| CACCCGUAUGUGUGCUCC | -0.00      | 0.01       | 0.01       |
| UCCUGCCUUCUCUGCAACAG | -0.01      | 0.01       | 0.01       |
| GGAGGCCAGUGCGGCCUCUG | -0.01      | 0.00       | 0.00       |
| GGAGGAAUGCUUUGAGCGUCCG | -0.01      | 0.01       | 0.01       |
| AAUAAUCAUGGGUUAACCUUUU | -0.01      | 0.01       | 0.01       |
| GGGGCUUGGCGUUGGCGG | -0.00      | 0.01       | 0.01       |
| UGCCUCUUUUCACCGGCUCCAG | -0.00      | 0.01       | 0.01       |
| UAGCUGUUGGCAUGCAGCACCUCU | -0.00      | 0.01       | 0.01       |
| ACUUGUAUCAGCUCAGGUAG | -0.01      | 0.01       | 0.01       |
| UACUUUUCAGUUGUUGUGG | -0.01      | 0.00       | 0.00       |
| AUCACACAAGGCAACUUUUUGU | -0.01      | 0.00       | 0.00       |
| AGGGCCGAAGGGUGGAGACUCG | -0.01      | 0.00       | 0.00       |
| CUGCUCUCUCAUCCAGCCCA | -0.01      | 0.01       | 0.01       |
| AGAGUGAGAGUCUGAGCCUCG | -0.01      | 0.00       | 0.00       |
| CAAAACUAGGAGAGGGUGCCAUCA | -0.01      | 0.22       | 0.26       |
| UUGUGAAGAAAGAAAUUCUA | -0.01      | 0.00       | 0.00       |
| AAUACACGGGGAGACUCUUAU | -0.01      | 0.00       | 0.01       |
| ACUGUAGUAUGGCGACUUCACG | -0.01      | 0.01       | 0.01       |
| UUCACAUGUGUCUACUGUCUGC | -0.01      | 0.00       | 0.00       |
| ACCUGGCUUUUCAGAUUGUACU | -0.01      | 0.01       | 0.01       |
| CCCCGGAGGCCCGCGG | -0.01      | 0.00       | 0.00       |
| UUGUUCUUCUGUCCUCACACAG | -0.01      | 0.01       | 0.01       |
| GGGCCCGGCGCGGCAUCG | -0.00      | 0.01       | 0.01       |
| UCAGGACACUUCUGAAUUGGA | -0.01      | 0.01       | 0.01       |
| CUUUGCUUCUCUGCUCCCUAG | -0.01      | 0.00       | 0.00       |
| AAAGUUUGAGACACUCCGACU | 0.01       | 0.04       | 0.04       |
| CGGCCCAGCAGCAACAGGGUAAGA | -0.01      | 0.00       | 0.00       |
| CUUUCAGUUGGUAUGUUUGCACG | -0.01      | 0.00       | 0.00       |
| UGUUGUUGAGGCCCUGCAUGCA | 0.01       | 0.11       | 0.06       |
| AGGCCUGGAAGCUGGACUGCCUGAGU | -0.01      | 0.00       | 0.01       |
| CACAUUGCCGAACACAGGAAGAU | -0.01      | 0.00       | 0.01       |
| AAAAGGCGGAGAAGCCCCA | -0.01      | 0.00       | 0.01       |
CUGCCCUAGUCUAGCUAGCU -0.01 0.00 0.00
GGAGAAUUAUCUUGUGUGU -0.00 0.01 0.01
UAUGUAUAUGUGCACAUUCU -0.01 0.00 0.00
UGGCCAAGACUCUCAGACC -0.00 0.00 0.00
UGCAGCGACUGGGGACACGU -0.00 0.01 0.01
CGGCCGGGCUGUGCUUGUCCU -0.01 0.00 0.00
AGAGUCGCGAGCCCGCCACG -0.01 0.00 0.00
AUAUUAACUAGCUACUUCUU -0.00 0.01 0.01
AGGAUGACCAAAAGAAUGAAGAU -0.01 0.01 0.01
UUAGCCAAUUUGUCAUCUUAG -0.01 0.01 0.01
UCUAUACAGACCCUGCUUUCU -0.00 0.01 0.02
AGCUUUUGGAUUCAGGGAUG -0.01 0.01 0.01
CCUGGACACCGCUACCCGCCG -0.00 0.00 0.00
AGUCAUUGAGGUGUUUGAGCAG -0.00 0.01 0.01
UUUCAAGCAUGUAGACUAGGGA -0.01 0.00 0.00
UAGAUAAGAUAUGGUACUCUG -0.00 0.00 0.01
UUGGAUGAUGAAUCAUUAGG 0.01 0.18 0.08
AAAAGAUUUGCGGGUUUUGUC -0.01 0.01 0.01
CUGGGAGUGGUGUUUACUUC -0.00 0.01 0.01
UUUGGCAGGGAAGCAGCGUUGAGA -0.00 0.00 0.01
CGGUGCAGACUCUGUCUGAGA -0.00 0.00 0.00
GACUCUCUGAGUAGAACCUGGA -0.01 0.00 0.00
UUUGGCAUACGCACACAGUCU -0.01 0.00 0.00
AGCUUCAGAUGCCUCUGAUGGA -0.00 0.00 0.00
UAUGGGCUCUUCUGUAAGAU -0.00 0.00 0.01
CGGCUCUGGGCUUGUGGGA -0.00 0.00 0.00
CAAAAACCACUGUUCUUCUGC -0.00 0.00 0.00
UCAGUCCAGGCCAACCCAGCU -0.00 0.00 0.00
UGAGGUGUGUUUUCUGAGAgU -0.00 0.00 0.00
GCUAAGGAAGUGCUUGUCUCAG -0.00 0.00 0.00
UGUGUGGCUUGGAGCCUGUGUG -0.00 0.01 0.01
AUAAGCUGAUAAUCGCCAAGUG -0.00 0.01 0.01
AGAAGGGGGUGAAUUAAACACGU -0.00 0.00 0.00
GUGAGAUGUUGAUGGAG -0.00 0.00 0.00
ACUGGGAAGAGGUGAG -0.00 0.00 0.01
UGCCCUCUUUGUCUCGGCGAG -0.00 0.00 0.00
UACUAACUGCAUUCAAGUGA -0.01 0.00 0.00
CAGGAGUGGCGUUGGACGU -0.00 0.00 0.00
AUCAUGAGGAAAUAUCAUGUU -0.00 0.00 0.00
AACAGUUGCGAAGGAAACUGA -0.00 0.01 0.01
GGGAGAUGCAUGAGGACCUCC -0.00 0.00 0.00
UUACACAAACUGAGAUAUA -0.00 0.01 0.01
UAAAACUUUUGUGUCCUAGG -0.00 0.00 0.00
UCGCCUCUCCUCACCCUAG -0.00 0.00 0.00
UCUGAGCUGACUCCUGUGGU -0.00 0.01 0.01
UGGCUGACUGGCACCCACAG -0.00 0.00 0.00
GGAAUCAAGCAGAUAUCUACCAG -0.00 0.00 0.00
UUUCCUUUUCACCUGGCAG -0.00 0.00 0.00
AACAGGUGGAGGUCUGAGGACCC -0.00 0.00 0.00
UGUCAUGCGUCGGCCACUCAC -0.00 0.00 0.00
AAGCCUCUGUCCACCCACAG -0.00 0.01 0.01
GUUCUCUGUAAUGAGCAGCAG -0.00 0.00 0.00
UGAGGUGCCACAGAUUGGGA -0.00 0.00 0.00
CAAACUGGCAUAUCUUUUUGC -0.00 0.01 0.01
UAGGGAAAGUCCUAGUCCG -0.00 0.00 0.00
CGGGGAGAAGACGCGAUGACGU -0.00 0.00 0.00
| Sequence                                                   | Score 1 | Score 2 | Score 3 |
|------------------------------------------------------------|---------|---------|---------|
| UUGGCCAUUGGGCGUCGCGGG                                     | -0.00   | 0.01    | 0.01    |
| AUCUGAGGGAUAGAAGCAGCUUU                                   | -0.00   | 0.00    | 0.00    |
| UCUUGAGAUGCUGAUUUCUCUG                                    | -0.00   | 0.00    | 0.00    |
| UCCUUCAGCCAUCUGCCUCUGGA                                   | -0.00   | 0.00    | 0.00    |
| CAGUUUGUGCUAGGGGUCAGGA                                    | -0.00   | 0.00    | 0.00    |
| GGGUGAAGGGCGUCUGGGU                                      | -0.00   | 0.00    | 0.00    |
| UCUUUUGUGUCUGUCUGCAG                                      | -0.00   | 0.00    | 0.00    |
| GAUGGUUGAAGCAGACAGACAC                                    | -0.00   | 0.00    | 0.00    |
| UAAUGAUCAGAGACUCAUAGU                                     | -0.00   | 0.00    | 0.00    |
| GGGCGACAAAACAGAGACCUCCGUG                                 | -0.00   | 0.00    | 0.00    |
| CCCAUUGCUCUGCUGCGGGGUG                                    | -0.00   | 0.00    | 0.00    |
| CUCAGAUUUGAGAAGCGG                                       | -0.00   | 0.00    | 0.00    |
| CCUCUGAAAUCAUCUUCUCCAG                                    | -0.00   | 0.00    | 0.00    |
| CGGCCUGCGCGAGCGUGCGG                                     | -0.00   | 0.00    | 0.00    |
| AGGGCGUGAUCAGCGCGGCAGGUGAC                                   | -0.00   | 0.00    | 0.00    |
| ACCAGUUCUGCGGCUACUCCUCUCC                                 | -0.00   | 0.00    | 0.00    |
| UUUGUUCUGCUCCUGCGGU                                        | -0.00   | 0.01    | 0.01    |
| CUCAUCUGCAAAAGAUAUGAGG                                     | -0.00   | 0.00    | 0.00    |
| UCAGACACAGCCAGACAGACGAGA                                   | -0.00   | 0.00    | 0.00    |
| UGGAGAGAAGAAAAGAACGAGAG                                     | -0.00   | 0.00    | 0.00    |
| UCUCCUUCUCCUCCUCCUGCC                                    | -0.00   | 0.00    | 0.00    |
| UAAACACUCCCACCACACG                                       | -0.00   | 0.00    | 0.00    |
| GAAGGACCUCGACCUCUC                                        | -0.00   | 0.00    | 0.00    |
| CACUCUGACUCGCCGACCCCGG                                     | -0.00   | 0.00    | 0.00    |
| AAUCAUAACCACAGCGCCAG                                       | -0.00   | 0.00    | 0.00    |
| CUACAUUUAAGACUCUGAUGAGC                                    | -0.00   | 0.00    | 0.00    |
| UGGAGGCGACAGAAUCUCCAGC                                     | -0.00   | 0.00    | 0.00    |
| CGCAAGGGCGCGUGUCUCACCGG                                    | -0.00   | 0.00    | 0.00    |
| CCUCUGACCCCGCCCUCCUCCCGG                                  | -0.00   | 0.00    | 0.00    |
| AGAGGUAAAGGGCAUUGGA                                       | -0.00   | 0.00    | 0.00    |
| UAGCGCAGACACCAGACGACG                                     | -0.00   | 0.00    | 0.00    |
| UAUCCGACUUGGUAUUACUAGU                                      | -0.00   | 0.00    | 0.00    |
| CGUCACCCCCACUCACUCUGU                                      | -0.00   | 0.00    | 0.00    |
| UGGAGAGAAGAAGAUGAGG                                      | -0.00   | 0.00    | 0.00    |
| ACUCCUCUCUCUCCCGGGGUGG                                    | -0.00   | 0.00    | 0.00    |
| AGAGGCUAGAAGAUGGAGU                                       | -0.00   | 0.00    | 0.00    |
| AAUCAUAACGCUUGACCUAUU                                      | -0.00   | 0.00    | 0.00    |
| AGUAGAGAGAAAAGUAUGGAGG                                    | -0.00   | 0.00    | 0.00    |
| UGACUCGACUCUCCCUCUC                                       | -0.00   | 0.00    | 0.00    |
| CCAGGAGAGGACGCGGAGG                                        | -0.00   | 0.00    | 0.00    |
| UCCCUUCUCCUUGUCCUCAC                                      | -0.00   | 0.00    | 0.00    |
| UCUCAGAUCUCUCUGACUCC                                       | -0.00   | 0.00    | 0.00    |
| Sequence                        | Value 1 | Value 2 | Value 3 |
|--------------------------------|---------|---------|---------|
| UGGAUUUCUUGUGAAUCACCA          | -0.00   | 0.00    | 0.00    |
| UAGGAGGGAUAUAAGAAAGCAG         | -0.00   | 0.00    | 0.00    |
| GUCGCCUCUUCAAUGUGUCUUUG        | -0.00   | 0.00    | 0.00    |
| AGUCACCUCCUCUCUGGAGCCAG        | -0.00   | 0.00    | 0.00    |
| UCCUCUUCUGUCCCACAG            | -0.00   | 0.00    | 0.00    |
| CAGCGCUUCUCUACUGUGGCUU         | -0.00   | 0.00    | 0.00    |
| AGAAAGGGAGGGGUUGUGCAGA         | -0.00   | 0.00    | 0.00    |
| UGAAACUGGAGGCUGGAGGAGA         | -0.00   | 0.00    | 0.00    |
| UUCGGCCUGGCGGCUUGGUGGCGG       | -0.00   | 0.00    | 0.00    |
| UGGUGCACAGAUAAGGAAUAUA        | -0.00   | 0.00    | 0.00    |
| AAGAACAAAUACUCUCAGUCUUCCA      | -0.00   | 0.00    | 0.00    |
| UAGGACACAUCCGUACAUCUCUUCU      | -0.00   | 0.00    | 0.00    |
| CAGAGAAUGUUGUUAAAC             | -0.00   | 0.00    | 0.00    |
| GGCUUCAUCUCUGGUGCCUGGAGCCG    | -0.00   | 0.00    | 0.00    |
| AUUGCCCGAGACUCUAGUGUGAG       | -0.00   | 0.00    | 0.00    |
| GCCGGCACAGGAGGGAGG            | -0.00   | 0.00    | 0.00    |
| ACUCAUUUCUCCUCUGCCAG          | -0.00   | 0.00    | 0.00    |
| CGGGUGACAGUCCGAUUUU            | -0.00   | 0.00    | 0.00    |
| UUUGUCUGGCCUCUGUGAGU           | -0.00   | 0.00    | 0.00    |
| CUGAACUCAGAGGGCCUCUGUAU        | -0.00   | 0.00    | 0.00    |
| CCUCUCAGUGUACUCUGGUGCAG        | -0.00   | 0.00    | 0.00    |
| CGUGGGAGUGCCCGUGGGAGG          | -0.00   | 0.00    | 0.00    |
| AAGCAUUCUUCAUCUUAGUGG          | -0.00   | 0.00    | 0.00    |
| CGGCUGGAGGUGUAGGGA            | -0.00   | 0.00    | 0.00    |
| CUAAGACAGUGCCAGACUCUCUGA       | -0.00   | 0.00    | 0.00    |
| UUACAGCGCGUGAACACCUGCGG        | -0.00   | 0.00    | 0.00    |
| UGCCUGGAGACGGUUCUGACUGA        | -0.00   | 0.00    | 0.00    |
| UGGGCUCUGGCCUCUGGGUGG          | -0.00   | 0.00    | 0.00    |
| UGGACAGGAACUCUGAUAAGGGU        | -0.00   | 0.00    | 0.00    |
| GUUGUUGCACGUUUUAUCAAAC         | -0.00   | 0.00    | 0.00    |
| AGAAGGCACUAUGAGAUUAAGA         | -0.00   | 0.00    | 0.00    |
| GCCGCCGCGGCAGUCCCGGCGG         | -0.00   | 0.00    | 0.00    |
| UCACUGACAGUCCUCUGGCGU         | -0.00   | 0.00    | 0.00    |
| GCUGCCGGAGAGUGGCGACAG          | -0.00   | 0.00    | 0.00    |
| AUGGCCAAAACUGCAUGUUAAUUU       | -0.00   | 0.00    | 0.00    |
| CACCGACUCUGUCUCUGCAG           | -0.00   | 0.00    | 0.00    |
| UGGUGUCAUGUUUUUCUCUCUAG        | -0.00   | 0.00    | 0.00    |
| UUGGACUUUUUCAUGAUUUGGGAU       | -0.00   | 0.00    | 0.00    |
| CCCUGCUCCUCUACCCUCUGCCAG       | -0.00   | 0.00    | 0.00    |
| AACUCCAAAACACUCAAAAACUA        | -0.00   | 0.00    | 0.00    |
| CUCUCUGGCGCCGACUCUCGC         | -0.00   | 0.00    | 0.00    |
| UGGUUUCAGACUUGGCAACUA          | -0.00   | 0.00    | 0.00    |
| UCAAGGCCCAGAGGUCCACAGCA        | -0.00   | 0.00    | 0.00    |
| UCCCUUCUGCACGGCCUCUGCUGG       | -0.00   | 0.00    | 0.00    |
| CGAUAACUUGUGGCUUACCCUCUCC      | -0.00   | 0.00    | 0.00    |
| AAAAGUAACUCGUUUUUGGCC          | -0.00   | 0.00    | 0.00    |
| AUCUAAAUGCAGACUGCCAGUC         | -0.00   | 0.00    | 0.00    |
| GCGGGGUGGCGGGCGGGAUUCC         | -0.00   | 0.00    | 0.00    |
| CAUCUCCGCGCCCUUUUUCCGGCCG     | -0.00   | 0.00    | 0.00    |
| UCAUCCCGAAGGACGUUGGU          | -0.00   | 0.00    | 0.00    |
| AGUGGAGUCAUUGAGUACCUCAGAG     | -0.00   | 0.00    | 0.00    |
| UUGGUCUUCUCUGCCUCACGGC        | -0.00   | 0.00    | 0.00    |
| Sequence                        | Fill1 | Fill2 | Fill3 |
|--------------------------------|-------|-------|-------|
| GAAGAAUAGGAGGGACUUUGU          | 0.00  | 0.00  | 0.00  |
| CAGCCUCUGCCUUUGGCCUCC         | 0.00  | 0.00  | 0.00  |
| CCCUCUGCCUCCUCCGCCAAA        | 0.00  | 0.00  | 0.00  |
| CAUGCUGACCUCCUCCUGCAGG       | 0.00  | 0.00  | 0.00  |
| GCCCGGGCGGCGGGGGUUCUGG        | 0.00  | 0.00  | 0.00  |
| UAGGCCGCGAGCUUCUGCAGGCU       | 0.00  | 0.00  | 0.00  |
| CGGGGUGAUGGGGGAGAGAUGA        | 0.00  | 0.00  | 0.00  |
| GGGGGGAUGUGCAUGUGGUU          | 0.00  | 0.00  | 0.00  |
| ACUGAAUCCUCUUUUCUCAG         | 0.00  | 0.00  | 0.00  |
| CAGCAGGGUGUGGCGCUUCUGU        | 0.00  | 0.00  | 0.00  |
| CUAGGUGGGGGCGUGAAGGC          | 0.00  | 0.00  | 0.00  |
| UUGUUCUUGUGCUUCAGCAGGA       | 0.00  | 0.00  | 0.00  |
| GGGCCUGCGUCUUGUCAGGAGU       | 0.00  | 0.00  | 0.00  |
| CAAAAGUGAUCUGUGUUGUUGGAGU     | 0.00  | 0.00  | 0.00  |
| CUGACAGCCUCUCCUCCUCUCAC      | 0.00  | 0.00  | 0.00  |
| UUGUGGGAUGGGAUAAACCCUUCG      | 0.00  | 0.00  | 0.00  |
| UCCCAUCUACUCCUUCUGUGA        | 0.00  | 0.00  | 0.00  |
| GAAUACUAUGUAACAAACCAUGA       | 0.00  | 0.00  | 0.00  |
| UGGCCUCUGCAGGGCAAGGCGUGCUG    | 0.00  | 0.00  | 0.00  |
| UAGAGGAAGCUGUGGAGAGA          | 0.00  | 0.00  | 0.00  |
| UUUGGAGAGAAAACAGGAGGAGU       | 0.00  | 0.00  | 0.00  |
| UCUGCAUCUCCUCCUCCUCUCAC      | 0.00  | 0.00  | 0.00  |
| UCUAGAUCCUGGAGCUCUGGAGC       | 0.00  | 0.00  | 0.00  |
| CAGCCAGCCCUGCUCACCCCCU       | 0.00  | 0.00  | 0.00  |
| AAGGACAUUGUGAGCCAGGAGGAGU     | 0.00  | 0.00  | 0.00  |
| UCCUUCUGCCUCGGUCGCCAGGAGC    | 0.00  | 0.00  | 0.00  |
| CCCAGCAGGGAGGGAGGCGGAGG       | 0.00  | 0.00  | 0.00  |
| CCGGCCGCAGCGUCCGCCCCG        | 0.00  | 0.00  | 0.00  |
| AAGGGGCUUGGGGGAGAGCAAGA       | 0.00  | 0.00  | 0.00  |
| UGCGGGGAGAGCCAGGGAUUCUGG      | 0.00  | 0.00  | 0.00  |
| GCAUGACAGGCAGAAGUGGAU         | 0.00  | 0.00  | 0.00  |
| UGACACAUUGUAGAGUGACUCU        | 0.00  | 0.00  | 0.00  |
| AGCGGGGAGGAAUGGGGCCGUCGUCU    | 0.00  | 0.00  | 0.00  |
| UGCAGGGUGUGCGGUGGAGCCAGG      | 0.00  | 0.00  | 0.00  |
| AGGGGGCAGUCCAGCCCCUCUGAGA     | 0.00  | 0.00  | 0.00  |
| UGCAUUGAGCGUUUGACAGAAGUGAGU   | 0.00  | 0.00  | 0.00  |
| AGUUCAUAUGGGCAUCCUCCUCAGG     | 0.00  | 0.00  | 0.00  |
| AAAAAUAGAUUGGCUUGUUUGGCC      | 0.00  | 0.00  | 0.00  |
| CAAACACACAGUCUGUCUCCCGAG     | 0.00  | 0.00  | 0.00  |
| AACCUGACUCUGUGGAUCUGAC        | 0.00  | 0.00  | 0.00  |
| GCUCUGACCUUUGGAACCAAG         | 0.00  | 0.00  | 0.00  |
| AGGGAGGGUGUGGAUAGUAGGAGU      | 0.00  | 0.00  | 0.00  |
| CAGCGAGGGAGGGCAGGAGAAG        | 0.00  | 0.00  | 0.00  |
| AGUGACACAGUCAGAAGAGUGAGG      | 0.00  | 0.00  | 0.00  |
| AAAAGUAUUGGCUUGGUUUUGCC       | 0.00  | 0.00  | 0.00  |
| RNA Sequence | Start Position | End Position | Score |
|--------------|----------------|--------------|-------|
| GAAUUAUAACUCGGUGCUCUGU | -0.00 | 0.00 | 0.00 |
| GCUGCGGCUGCAGGCAGGCG | -0.00 | 0.00 | 0.00 |
| AUUGGGGACAUUUUGCAUUCAU | -0.00 | 0.00 | 0.00 |
| UGGGUGUAGGCUGCAGGCG | -0.00 | 0.00 | 0.00 |
| CUGGAGAAGAGUGUGAAGA | -0.00 | 0.00 | 0.00 |
| ACGGAAUGUUGACGAUGUGCAU | -0.00 | 0.00 | 0.00 |
| UGGUAGAGAAGGGAGCUCAGAGG | -0.00 | 0.00 | 0.00 |
| GAGGUGACAGGUGAGG | -0.00 | 0.00 | 0.00 |
| CCCUGGGGCUGGCGAGG | -0.00 | 0.00 | 0.00 |
| CAGUGCCUGGCAUGGCGCC | -0.00 | 0.00 | 0.00 |
| CCCAACUCGCAGGCUCCUCAG | -0.00 | 0.00 | 0.00 |
| CAGGAGGCAUGAGGGAGGAG | -0.00 | 0.00 | 0.00 |
| CCCUGGCGUCUGUCCCA | -0.00 | 0.00 | 0.00 |
| CUCUGGCGGCUGUGCCAG | -0.00 | 0.00 | 0.00 |
| GGCUGAUGAGGGUGUGGCGU | -0.00 | 0.00 | 0.00 |
| AAGAGAUUGUUGUUGUUGC | -0.00 | 0.00 | 0.00 |
| UAUUGCAAAAGGGCGAGUCA | -0.00 | 0.00 | 0.00 |
| UGACGAGCCAGGCGGCGAG | -0.00 | 0.00 | 0.00 |
| CCGUUGGCUAGUUGUCAGG | -0.00 | 0.00 | 0.00 |
| GGCUGUGUUCUCUCCCAA | -0.00 | 0.00 | 0.00 |
| AGGGACUUGGAGGGCGAGCUGU | -0.00 | 0.00 | 0.00 |
| UAUCUGUGGCUCUUUCUGGGU | -0.00 | 0.00 | 0.00 |
| AUCACAUUGCCAGUGAUUACC | -0.00 | 0.00 | 0.00 |
| UUGUUUUAACACUAAGAAUGGGU | -0.00 | 0.00 | 0.00 |
| GAGCAGCGCGUAGGCGGUGAA | -0.00 | 0.00 | 0.00 |
| CCGUUGGCUAGUUGUGGCGU | -0.00 | 0.00 | 0.00 |
| AGGCCAUUGACUUCACGAGC | -0.00 | 0.00 | 0.00 |
| CLUGGGGGAGGAGACCCUGCU | -0.00 | 0.00 | 0.00 |
| GCUGACAGCCAGGCGGCGCU | -0.00 | 0.00 | 0.00 |
| AAGCCCUUGCCUCCCAACU | -0.00 | 0.00 | 0.00 |
| CUAUCAGCCUCUGCUUUC | -0.00 | 0.00 | 0.00 |
| GCAGUAUGUGAGAUUGUUU | -0.00 | 0.00 | 0.00 |
| ACUGAUUAUCUUACUCUCUGA | -0.00 | 0.00 | 0.00 |
| ACUGGGUAGGGGGCGCCAAG | -0.00 | 0.00 | 0.00 |
| ACUGGGAGACGAAGAGAAC | -0.00 | 0.00 | 0.00 |
| UAAAAACUGCAUAUACUUU | -0.00 | 0.00 | 0.00 |
| UAGGGUGACAGAGGAGAUCUCA | -0.00 | 0.00 | 0.00 |
| CAUCUCUAGGAACUCGCCCAA | -0.00 | 0.00 | 0.00 |
| UCUCACCCCAACUCUGGCCCAAG | -0.00 | 0.00 | 0.00 |
| UCCUGACCCUCUCUCGCA | -0.00 | 0.00 | 0.00 |
| CUGGGGGUGGGGGCGGUGGC | -0.00 | 0.00 | 0.00 |
| CGCAAGCAUGCCUCUACUGCGU | -0.00 | 0.00 | 0.00 |
| UCCCCUUCCUCCUGCCCAAG | -0.00 | 0.00 | 0.00 |
| UCCAUAACACUCCUCUCUCUCU | -0.00 | 0.00 | 0.00 |
| UCCCCUUUGCUAUCCUAUGCU | -0.00 | 0.00 | 0.00 |
| GACUCACUCAAGAUUGUGCA | -0.00 | 0.00 | 0.00 |
| CACAGGACUGACUCUCACCCCA | -0.00 | 0.00 | 0.00 |
| UUGCAGAUGAAAUAUCUAGG | -0.00 | 0.00 | 0.00 |
| Sequence                        | Score | Charge | Mass |
|--------------------------------|-------|--------|------|
| ACCGAGGUUCCCUCCUGGGCCGGA        | -0.00 | 0.00   | 0.00 |
| AAGGGGACAGGGAGGGUGGCC           | -0.00 | 0.00   | 0.00 |
| GCUGAACUGGGCUAGCGUGGCC         | -0.00 | 0.00   | 0.00 |
| UGUUGUAGAGAUCUUCUUGCU          | -0.00 | 0.00   | 0.00 |
| UGGUCAUAGGUUGUCGGAGAG          | -0.00 | 0.00   | 0.00 |
| AGUAUCUGUCAAGCCAGGGAAGGU       | -0.00 | 0.00   | 0.00 |
| ACCUGGUGUUCCUCUCCUCUAG         | -0.00 | 0.00   | 0.00 |
| GCAAAACCUAAUUACCUUU            | -0.00 | 0.00   | 0.00 |
| UGAGAUCUCCUGACCCUGUGCU         | -0.00 | 0.00   | 0.00 |
| UCGGGCCUGGGGUUGGGGAGGAGC       | -0.00 | 0.00   | 0.00 |
| UUUGGUCUCUCCUCCUACCAGCUG       | -0.00 | 0.00   | 0.00 |
| UACUGGGAAGGCAUCAGUUG           | -0.00 | 0.00   | 0.00 |
| CUUCUCUGUCUGUCUGCC             | -0.00 | 0.00   | 0.00 |
| UGUGUAGAUCUCUGCAGAGGCA         | -0.00 | 0.00   | 0.00 |
| ACAGGGGCGCAUGAGGAGACU          | -0.00 | 0.00   | 0.00 |
| UCGUGUCCUCUUCUGUCACAG         | -0.00 | 0.00   | 0.00 |
| UAAACAGCAUCCUCUCCUCCAGA        | -0.00 | 0.00   | 0.00 |
| UGUGACUUUAAGGGAUUGCCG          | -0.00 | 0.00   | 0.00 |
| CCCUCUCUGUCCUCCCAUAG           | -0.00 | 0.00   | 0.00 |
| GGAGGGUGGUGGCGACUUGGAGG        | -0.00 | 0.00   | 0.00 |
| GGAGGGCCCGAGGCUCCGAAGGCG       | -0.00 | 0.00   | 0.00 |
| CCUCUAAAGGGAACGCUCUUUCU        | -0.00 | 0.00   | 0.00 |
| GAACGCGCUCCUAAAGGUGG           | -0.00 | 0.00   | 0.00 |
| AAAAGUAUUUGCAGUUUUGG           | -0.00 | 0.00   | 0.00 |
| CCUGCGAGUCUCCCGCGGUGG          | -0.00 | 0.00   | 0.00 |
| CAGGGGAGUGGUGGGGUGAGC          | -0.00 | 0.00   | 0.00 |
| UGGGGCCGGAGGCGUCCUCCGC         | -0.00 | 0.00   | 0.00 |
| CCCUCGGGAACCCCGCCCAUCCG        | -0.00 | 0.00   | 0.00 |
| GGAGCGUCCAUUUCUACCAG           | -0.00 | 0.00   | 0.00 |
| UGGGGCCGAGCUCCUCCGAGGCC        | -0.00 | 0.00   | 0.00 |
| UAGGUCAGGACCCUCUUGCCG          | -0.00 | 0.00   | 0.00 |
| UGGGAUCGUCAUAGCGUGGGUUGU       | -0.00 | 0.00   | 0.00 |
| CUACUUCCUACCGUGUAUCAU          | -0.00 | 0.00   | 0.00 |
| UGACCAAACUCAAUAUUGCGAGG        | -0.00 | 0.00   | 0.00 |
| AGCUAACGUUACUUULUGCACA          | -0.00 | 0.00   | 0.00 |
| AGGCUGUGAGUGACGGAGG            | -0.00 | 0.00   | 0.00 |
| AAGCCUCUGGCGUGUCUGUGU          | -0.00 | 0.00   | 0.00 |
| CUAUCUGAGAGGCGUCCUCAGU         | -0.00 | 0.00   | 0.00 |
| AGGGACUUCUGGGGAGGAGUGUG        | -0.00 | 0.00   | 0.00 |
| GAGUGGGCGUUCUGACCCUAACC        | -0.00 | 0.00   | 0.00 |
| AGCCAGUGGAGAAGUGUUACUU         | -0.00 | 0.00   | 0.00 |
| CAGUGAUCUGUCUGUCUGGC           | -0.00 | 0.00   | 0.00 |
| UCUUUGGUAUCCCUAGCUGUAGA        | -0.00 | 0.00   | 0.01 |
| AAGAGGAAGAAAGUGCGUUGUUCUCA     | -0.00 | 0.00   | 0.00 |
| UGACCUCUACCGUCCUUGCU          | -0.00 | 0.00   | 0.00 |
| GGAGGAAGAGCGAGUGGCAUUG         | -0.00 | 0.00   | 0.00 |
| CUCCUGAAGCUCUUCUGACCU          | -0.00 | 0.00   | 0.00 |
| CCCUGAGCCAGGAGUGACUC           | -0.00 | 0.00   | 0.00 |
| GUGAUGGGCGAGGCUGCCGAUGUGUG     | -0.00 | 0.00   | 0.00 |
| CGUCUUACCCAGCGAUGUUGG          | -0.00 | 0.00   | 0.00 |
| CAAGCUCUAAUCUCCACUGCGAAU       | -0.00 | 0.00   | 0.00 |
| AUCUGGACUUGAGCGCAGAA          | -0.00 | 0.00   | 0.00 |
| AAGGAACUGAAAAGUGGAGCCU         | -0.00 | 0.00   | 0.00 |
| GGGGGAAGGAAAAGGUGG             | -0.00 | 0.00   | 0.00 |
| CCCUGGGCGCGCCUUGG             | -0.00 | 0.00   | 0.00 |
| Sequence                        | Start | End  | Probability |
|--------------------------------|-------|------|-------------|
| ACUGGAAUUGGAGUCAAAAA           | -0.00 | 0.00 | 0.00        |
| AAGCAGCGCCUCUGAGGCG            | -0.00 | 0.00 | 0.00        |
| AGCAGUGUUUGUUUUGCCACACAG       | -0.00 | 0.00 | 0.00        |
| UGCCCCUGGGUCUCUGGCCGUGGAGG     | -0.00 | 0.00 | 0.00        |
| AGGGACACCGACACACAGG            | -0.00 | 0.00 | 0.00        |
| CGACCCUCGCCGACCCUCGCCAU       | -0.00 | 0.00 | 0.00        |
| GUAGGUGAGACUAGGGGGGCGG         | -0.00 | 0.00 | 0.00        |
| UGACCUCCCGCUGCGCACAG           | -0.00 | 0.00 | 0.00        |
| UGCGGAUUGAGAGACGACCAA         | -0.00 | 0.00 | 0.00        |
| UGACCUCUUCUGUUCUCCCAG        | -0.00 | 0.00 | 0.00        |
| GUGUGGGCGGACGGGGGUGG          | -0.00 | 0.00 | 0.00        |
| UUCUAGAAUGUGAGCUAGUUCG        | -0.00 | 0.00 | 0.00        |
| UCUAGAGUGGAGACACGACGC         | -0.00 | 0.00 | 0.00        |
| GCAGCGUGCCUCAGUCUUCCU        | -0.00 | 0.00 | 0.00        |
| CAGUAGAGAGCGAGAAAUCG          | -0.00 | 0.00 | 0.00        |
| UCCCGGCCCCGCGCCGGGCUG         | -0.00 | 0.00 | 0.00        |
| ACUAGUAGCCGACCCAGGGCG         | -0.00 | 0.00 | 0.00        |
| AGGGUGAAGUUCUGAGAAGGAU        | -0.00 | 0.00 | 0.00        |
| GUGACGCUUCACCUCCAGCGGC        | -0.00 | 0.00 | 0.00        |
| AAGGUGUUCUUGAUGAGUUUCG        | -0.00 | 0.00 | 0.00        |
| UAACGCAAGGAAUUGUGACG          | -0.00 | 0.00 | 0.00        |
| CUCGCGGCGCCGGCGCGUCU          | -0.00 | 0.00 | 0.00        |
| ACUGUACAGCGCCACACCUG          | -0.00 | 0.00 | 0.00        |
| AUAACGGUCCUUAGUAGUAGGAGU      | -0.00 | 0.00 | 0.00        |
| UAACGUAUUCGUCUCUCUUAAGU       | -0.00 | 0.00 | 0.00        |
| GGCUUUCAGUCUCUGGUUCEC        | -0.00 | 0.00 | 0.00        |
| UCCCUACCCUCUCCCACUUCCCA       | -0.00 | 0.00 | 0.00        |
| GAAUCGAGAAAAGGAGCGCCG         | -0.00 | 0.00 | 0.00        |
| ACUCAAAAAGUGCGGGCAGUUU        | -0.00 | 0.00 | 0.00        |
| CCGAGGGUGGGCAGUAGG           | -0.00 | 0.00 | 0.00        |
| GCAGGCCAGACAGACGACCGUGGC      | -0.00 | 0.00 | 0.00        |
| CCGCGAUGUCCAGGGCA             | -0.00 | 0.00 | 0.00        |
| AGAUUGGUUUCUUGUUGCCUGCA       | -0.00 | 0.00 | 0.00        |
| CAAGGGACCAAGCAUUCAUUA         | -0.00 | 0.00 | 0.00        |
| CUAUUAGGCAUUCAGUAGUUC         | -0.00 | 0.00 | 0.00        |
| UUGGGAUCAUUGUUCAGGCAUA        | -0.00 | 0.00 | 0.00        |
| AGGAUGAGACGUGCCGGAGCGGCAGC    | -0.00 | 0.00 | 0.00        |
| UCAUUAUGAUGAGUACUGGAC         | -0.00 | 0.00 | 0.00        |
| GGAUGAGAGGGGUGGUCU            | -0.00 | 0.00 | 0.00        |
| AGCCUGAGCUCACUGAGCUGAGCAGU    | -0.00 | 0.00 | 0.00        |
| ACAAGACAGACUGCGUCUCCAA        | -0.00 | 0.00 | 0.00        |
| UGAGAUGAUGAUGCUAUGUUC         | -0.00 | 0.00 | 0.00        |
| CUUGGCAUCUGCCUGGAGCGUAGA      | -0.00 | 0.00 | 0.00        |
| UGAGACAGACUGAGGACACC         | -0.00 | 0.00 | 0.00        |
| AAGGGAUUCUGUGUGUUGUCCACAU     | -0.00 | 0.00 | 0.00        |
| GAAAACGACAUUAGCUUUGGCA        | -0.00 | 0.00 | 0.00        |
| AGAAGUAAUCACGGGUUUGGCA        | -0.00 | 0.00 | 0.00        |
| Sequence                                    | Start | End  | Length |
|---------------------------------------------|-------|------|--------|
| GAGUGGAUAGGGGAGUGUGUGGA                   | -0.00 | 0.00 | 0.00   |
| UAAGGAGGGGAUGAGGGG                       | -0.00 | 0.00 | 0.00   |
| GGUGCCGGCGAGGGGGG                        | -0.00 | 0.00 | 0.00   |
| UGGGGUAAGGAUAGGAGGUGUCA                  | -0.00 | 0.00 | 0.00   |
| UUCCGCAGUUAACUUCUCCUGGA                  | -0.00 | 0.00 | 0.00   |
| CCGAGCCCGGCCCCGCAG                       | -0.00 | 0.00 | 0.00   |
| AGCCAGGGGCUUGUCUGGCGGG                    | -0.00 | 0.00 | 0.00   |
| CAUGGAGAGGAGAGGAGGG                      | -0.00 | 0.00 | 0.00   |
| UGGGUGCAGAGUGCGAGGCGAC                   | -0.00 | 0.00 | 0.00   |
| UUGAGCCACAGUUCUGGGCCCCGC                  | -0.00 | 0.00 | 0.00   |
| CGGAAAGUCUAUCGAGGU                      | -0.00 | 0.00 | 0.00   |
| CGUGAUGUGAGCCUGUGACUGUC                   | -0.00 | 0.00 | 0.00   |
| UUGUCUCUGAGUUUCC                        | -0.00 | 0.00 | 0.00   |
| GAUCUGAGUCAGGAGGCGGCUGUGUGU             | -0.00 | 0.00 | 0.00   |
| UGGGCUCUGAGAAAGGGCA                    | -0.00 | 0.00 | 0.00   |
| UAAUAUAUGUAGGACAGCCAGUV                 | -0.00 | 0.00 | 0.00   |
| AAACUCUGAGAAUAAUACGAU                    | -0.00 | 0.00 | 0.00   |
| GAUGAGGGAGCUAGUCAGAGU                  | -0.00 | 0.00 | 0.00   |
| AGUUGAGAGUAGUCUGGCA                     | -0.00 | 0.00 | 0.00   |
| AGUUGCCUUUUUGUUCCGAUC                    | -0.00 | 0.00 | 0.00   |
| UGGAGUGAAGGAUGUAAUCU                   | -0.00 | 0.00 | 0.00   |
| UCCUAAACUGAAACUGCCCCCCA                   | -0.00 | 0.00 | 0.00   |
| GGAGGACCCUCUGGGGGAGUGAC                 | -0.00 | 0.00 | 0.00   |
| UUGGUCUCUGGGCGCCCGA                     | -0.00 | 0.00 | 0.00   |
| CUGUAAUAUAUUAAUAAUAAU                    | -0.00 | 0.00 | 0.00   |
| AUCUGCUAGUCUGGCCAG                      | -0.00 | 0.00 | 0.00   |
| UUGUCACUGUUCUCUGCUAG                   | -0.00 | 0.00 | 0.00   |
| UACUGCAUGCAGAUCAGUUGGA                 | -0.00 | 0.00 | 0.00   |
| UGCGGCCGUGUCGACAGGC                    | -0.00 | 0.00 | 0.00   |
| UGGAUAAACUGUGUGAGCUU                   | -0.00 | 0.00 | 0.00   |
| CACGCGAAAAAGAACAAUCCA                   | -0.00 | 0.00 | 0.00   |
| AAACUAAUCUCACUCUGCUC                    | -0.00 | 0.00 | 0.00   |
| AACUAACAGCAGUCUGUCGU                   | -0.00 | 0.00 | 0.00   |
| CCGGGAAGGAGGGUGCGGCGUCC                | -0.00 | 0.00 | 0.00   |
| UGGUAGAAACUAGAUCUGAGG                 | -0.00 | 0.00 | 0.00   |
| CAAGGCGAAAAGAACAGAACAG                 | -0.00 | 0.00 | 0.00   |
| AUCCUCGUGGUGUACCA                      | -0.00 | 0.00 | 0.00   |
| UGGGAGGGGGCUAUAUUGUGAGG                 | -0.00 | 0.00 | 0.00   |
| CCAGUGCGUCAGAGGAG                     | -0.00 | 0.00 | 0.00   |
| CUUCCGCAGUUGAGGACGCCGUC                 | -0.00 | 0.00 | 0.00   |
UGGGGGUGGUCUCUAGCCAAGG
CAAAAGUAAUUGUGGAUUUUGU
GGACCCACCCGGCCGGGAAUA
AGUGAAUGAUGGGUUCUGACC
UUCAGUAUUUCAGGUG
UACCCAGACGCAUGCAGUGAA
UUACACUGUUUAGAAACCACUGGA
CAGCAGUGACUGUCUGACAGUC
ACUUAAACUGGAUGUACUUGCU
UCGAGACUGUGGGAAGGGCUCU
GGUUGGGAGUGAGGAGGGUGUGA
AUCUGUAAGAGAAAGUAAAUGA
CCUAGACACCUCAGUUUC
CUGGAGUCUAGGAUUCCA
CAAGGAGACGGGAACAUGGAGC
UCUGGAAGAUUUGGCCUA
ACUAAGGGAUAUGAAGGCUUU
UGUCUGCAAAGAAGAUGACUG
UGAGCCGAGUGACUUGACUG
AGGUAGAUGGCCUGACAU
UCUGGGAUGAGACAGUGU
AGGACUGAUUCCUCUCCGAGG
CACACAUACGAGGGUGUAUA
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UCUCUGGAGAGAAGCACUUCUG
AAAAUGGCUCCUUUAUGAGGUG
CAAACACUGAAUACUUUC
GGGAGAGAAGAUGGGAGGC
AGCUCAUAAAGUGUUUGAC
CAUACAGACGCAUGCAUUC
UCUAAGAAUGCAUGACCCACC
CGGCGCUAGAAGCAUCUUAGA
UCUGAGAGAUGGCAUGGCA
CGGGCCAAGAGCGAGGCUUGU
UGCCUCUGGACAUUUCACAG
CUCCUCACAGCCUCUCGCAU
UCCCAAGGGUGAGAUGGCAGCA
UGGGCUAGCAGAGCUGUGU
UCACCGUUGCCAGCGCACG
UCUGGGAUGAGGAAGGCUUU
UCUGGCGAGAGCGGACUCU
ACGAAUCAUAAAGAUAACCU
UACUGUGAGCUUGAGAUGA
UUCUGUGAAGAGUGCGCAUA
UCGGGAGUAGGCGGUGGCGG
UGCGGGAGGCGCGGCGGCG
| Sequence                           | Start | End   | Length |
|-----------------------------------|-------|-------|--------|
| CUACAGGCUUGGAAUGGGCUCA            | -0.00 | 0.00  | 0.00   |
| AAGACGGGAGAAGAAGGAG              | -0.00 | 0.00  | 0.00   |
| GGGACCAUCUGCUCUCUGUGG            | -0.00 | 0.00  | 0.00   |
| UCUGCUGAUGAUGAUGUUAAA            | -0.00 | 0.00  | 0.00   |
| UCGUGGCUCUGUCCAUUU               | -0.00 | 0.00  | 0.00   |
| GUGGCGGCCGGAUUGUGUGUG            | -0.00 | 0.00  | 0.00   |
| GCCUGUAACAGAGGGGUCUGG            | -0.00 | 0.00  | 0.00   |
| CCAAUCACCUUUUCCGUCUCCCCU         | -0.00 | 0.00  | 0.00   |
| UCCUGUCCCCUGUCCUACAG             | -0.00 | 0.00  | 0.00   |
| CUGUCUUACAUCCUCAAAGGA            | -0.00 | 0.00  | 0.00   |
| AUUGCCAGCGGAGGGGCCUGCUGC         | -0.00 | 0.00  | 0.00   |
| GAGCUUUGGCCCGGGUUUAAC            | -0.00 | 0.00  | 0.00   |
| UUUCGUCCUCCUCCAACCAGAC           | -0.00 | 0.00  | 0.00   |
| UGCAAAGAUGAUUGGCGUUUUGU          | -0.00 | 0.00  | 0.00   |
| UAGCAAAACACUGAGUUUACU             | -0.00 | 0.00  | 0.00   |
| CUCUCUUGUUUUUCUCUCAUG            | -0.00 | 0.00  | 0.00   |
| UUCAGGAAUACUGAGGAGGA             | -0.00 | 0.00  | 0.00   |
| AUCCUCUCUUCCUCCUCCCCAG           | -0.00 | 0.00  | 0.00   |
| UGGGGGAGCCAUAGAUAAGAGCA          | -0.00 | 0.00  | 0.00   |
| AAAAGUAUUUUGCGAUUUUACC           | -0.00 | 0.00  | 0.00   |
| AUUGGGAAACUUUUGCAUGUA            | -0.00 | 0.00  | 0.00   |
| UAGUAACAUUGGUCUCUAA             | -0.00 | 0.00  | 0.00   |
| AGAUUUUUUGAGUGUUUGGAAUGG         | -0.00 | 0.00  | 0.00   |
| UUUCUUCUUCAGCUUUCUCCU            | -0.00 | 0.00  | 0.00   |
| CAUCAGAAUCAUGGAGCUAG             | -0.00 | 0.00  | 0.00   |
| GCUCUGACUUUAUUGCAUCU             | -0.00 | 0.00  | 0.00   |
| AGGGGACUGCUGCCGCAAGCAAGGGC       | -0.00 | 0.00  | 0.00   |
| ACCUGAAAUUCAAAAAAGCUU            | -0.00 | 0.00  | 0.00   |
| UAAUACUGUCUGUAAACACGU            | -0.00 | 0.00  | 0.00   |
| CGCCUGCCGAGGCCUCUCUGC           | -0.00 | 0.00  | 0.00   |
| CUGCAAGCAGAGGUGGGGCUGACA         | -0.00 | 0.00  | 0.00   |
| UCACCGGGAGAUGGCUUUG              | -0.00 | 0.00  | 0.00   |
| CUGGGGAGCCGGCGCUUGGAGCCG         | -0.00 | 0.00  | 0.00   |
| AGCCCCUGCCACCUGCACAGUC           | -0.00 | 0.00  | 0.00   |
| UAGCCUUCAGAUUCUUGGUGUUU          | -0.00 | 0.00  | 0.00   |
| CCCUCCUCCUCACUCUUCUCUCAG         | -0.00 | 0.01  | 0.01   |
| GAUUGCGCGCCACCUGCCCCCAGGC        | -0.00 | 0.00  | 0.00   |
| UAAACGGUUCGCUCCUCUCUCUCAG        | -0.00 | 0.00  | 0.00   |
| AGACCGUGUUCUGACUUAUC             | -0.00 | 0.00  | 0.00   |
| AGGUCUGUAGAUCACUCCCCGAC          | -0.00 | 0.00  | 0.00   |
| GAUGACGUCAUUGUAAUUGAG            | -0.00 | 0.00  | 0.00   |
| UUUCUGGGCUUCCUCUCUGUAG           | -0.00 | 0.00  | 0.00   |
| CUGUGACUCCUCUCUCUGUCU            | -0.00 | 0.00  | 0.00   |
| GUUCUCUCACUCUCUCAGCA            | -0.00 | 0.00  | 0.00   |
| UCGGUCCCCUAAACCCCUCCCGGAC        | -0.00 | 0.00  | 0.00   |
| UUUCUUCUUAACAUCCGAGCU            | -0.00 | 0.01  | 0.01   |
| UCCUCUCUCCACCCCUUGCA             | -0.00 | 0.00  | 0.00   |
| UAAUCCACAGGUGCUUCUCCU            | -0.00 | 0.00  | 0.00   |
| UGGGCUAGUAGUAGCAGGAGC            | -0.00 | 0.00  | 0.00   |
| UGAGAUGAAGCGCUUUGUGG             | -0.00 | 0.00  | 0.00   |
| UUCUCUACUCACUCUCCUCACAG          | -0.00 | 0.00  | 0.00   |
| UCGUGUCCUGUGUGCGACG              | -0.00 | 0.00  | 0.00   |
| UUGGUGAGGACCCAAAGCUGG            | -0.00 | 0.00  | 0.00   |
| AUUGACACUUCUGUGAGUAGA            | -0.00 | 0.00  | 0.00   |
| AUUCACAUUCUGGCUCUGCU             | -0.00 | 0.00  | 0.00   |
| CUGCAUGUAAACGACUCCUUAC          | -0.00 | 0.01  | 0.01   |
| Sequence                        | 0.00 | 0.00 | 0.00 |
|--------------------------------|------|------|------|
| CUCCCACAUGCAGGGGCUUGCA         | -0.00| 0.00 | 0.00 |
| AGGCAGUGUAUGUGUAGCUGGC         | -0.00| 0.00 | 0.00 |
| AUAAUAAUGCCACUUCUGGAU          | -0.00| 0.00 | 0.00 |
| AGUGUGCGCGUGCGCGUUGC           | -0.00| 0.00 | 0.00 |
| CUAGUGCUCUCCGUACAGGAUA         | -0.00| 0.01 | 0.01 |
| GUAGAUUUCUCCUUAUGAGGAUA        | -0.00| 0.00 | 0.00 |
| UGUGACUUCUCCUCGCCCCACAG        | -0.00| 0.00 | 0.00 |
| AUGGCAUGCUCUCCGUUGGCUGCU       | -0.00| 0.00 | 0.00 |
| AACUCUGACCCCUAGGUUGAU          | -0.00| 0.00 | 0.00 |
| AGAGGUGGUACUAGGGGGCCACAG       | -0.00| 0.00 | 0.00 |
| UUGUGGCAGAGGGGCCCAGAGUG        | -0.00| 0.00 | 0.00 |
| UUGGUGGUGAGGGUUGGUGUCUGG       | -0.00| 0.00 | 0.00 |
| AUCUGCCAGCUUCACAGUGG           | -0.00| 0.00 | 0.00 |
| UUGGGGCAUAUUCUGCUAA            | -0.00| 0.00 | 0.00 |
| AUCUCUCUUCUGCCUUCGCACU         | -0.00| 0.00 | 0.00 |
| GGGGUAUUUGUUUGGGCCAGCCG        | -0.00| 0.00 | 0.00 |
| UUGAGCAAGUGAAAGGAUGUGGU        | -0.00| 0.00 | 0.00 |
| CCAGGGCGCCUCUGCCGCGCGCC        | -0.00| 0.00 | 0.00 |
| CAAGCUUAGUACUAAUGGUAUG         | -0.00| 0.00 | 0.00 |
| UGUGUACACAGUGUGCAGGCCGCU       | -0.00| 0.00 | 0.00 |
| CACUGUUUCCUUUCUGAGUGA          | -0.00| 0.00 | 0.00 |
| CAACUGCCGUUCAUUGGGGCUG         | -0.00| 0.00 | 0.00 |
| UIAGGGGCAUCAGGAGCCACUUG        | -0.00| 0.00 | 0.00 |
| AAGGUAUUGGGAUUGGUGCUAUA        | -0.00| 0.00 | 0.00 |
| ACGGGGUAACGUUCUGGGAGCU         | -0.00| 0.00 | 0.00 |
| UGAGGCUUACAGUGUUCGCUGGC        | -0.00| 0.00 | 0.00 |
| CCAGGGAGCCUGGUUGGGAGGA         | -0.00| 0.00 | 0.00 |
| UAGGUAUCCGUGUUGCCUUCG          | -0.00| 0.00 | 0.00 |
| AAAAGUAUUUGGGGUGUUGUUGCC       | -0.00| 0.00 | 0.00 |
| GCAAAUUGGUAUCUUGGGCCG          | -0.00| 0.00 | 0.00 |
| UUUUAAAGCAGACUGAGGGAU          | -0.00| 0.00 | 0.00 |
| CUGCAGAUUUGUACGCCGACCG         | -0.00| 0.00 | 0.00 |
| CAGGGGUGGGGUGUUGGAGGUUCU       | -0.00| 0.00 | 0.00 |
| ACCCCGGGGCAAGACUCUGCAAGAU      | -0.00| 0.00 | 0.00 |
| UCGAGGAUUGGAGCCUGGAGUC         | -0.00| 0.00 | 0.00 |
| CAAAGAACUGAUUGGUUUUGU          | -0.00| 0.00 | 0.00 |
| AAGUGGCCCAAGAGGGUGAGUQG        | -0.00| 0.00 | 0.00 |
| ACGUAGAUUGUCUUCUCCGUGG         | -0.00| 0.00 | 0.00 |
| ACCUGGACCAGCGGUAGCAAAAG        | -0.00| 0.00 | 0.00 |
| AAAAGUAACUGCGGUUUUGGCC         | -0.00| 0.00 | 0.00 |
| UGAGUCAGGCAAAAUUGCAGACU        | -0.00| 0.00 | 0.00 |
| AGGAGGUAUGGAGCCUGGAGGGAGCA     | -0.00| 0.00 | 0.00 |
| UAAAGUAAAUUGCAGCAAAAA          | -0.00| 0.00 | 0.00 |
| UGGUUUACCUGCCCAUCAAU           | -0.00| 0.00 | 0.00 |
| CUGGCCUGUGGUUCCUUAUCUGU        | -0.00| 0.00 | 0.00 |
| AAAUUAUUGCCACUGGGAUGGAG        | -0.00| 0.00 | 0.00 |
| GUAAGGGACCGGAGAUGGAQGA         | -0.00| 0.00 | 0.00 |
| UUAACAGGCAAAGAAAGGAUU         | -0.00| 0.00 | 0.00 |
| UGCUGCUCUCUCUCUGCGAGCAG        | -0.00| 0.00 | 0.00 |
| AGGGUGUGUGUGUUU                | -0.00| 0.00 | 0.00 |
| AAAAGUAAUUGCGGAUUUGGCG         | -0.00| 0.00 | 0.00 |
| AGGCAGUUGAUUGAUUGCUGGAUG        | -0.00| 0.00 | 0.00 |
| GGUGGGAUGGAGAGAAAAGUAUGAG      | -0.00| 0.00 | 0.00 |
| UCACUCUAGGUGGUGGACAGG          | -0.00| 0.00 | 0.00 |
| CGAGGGGUAAGAGAAGCAGAGGG        | -0.00| 0.00 | 0.00 |
| GUUUGGACAUAGUGUGGCCGG         | -0.00| 0.00 | 0.00 |
| Sequence | U  | C  | G  | A  | I  |
|----------|----|----|----|----|----|
| UCUGAAAGACAGUUGGUGUU | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| AAAGGUAACUGUGAUAUUUGCU | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| CAGGCGAGGGGAAGGUGGAGAG | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| UCUCUGUCUUGCCACCCCAG | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| AUUUGUCUGCUUUCUCCAGCAG | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| CAUGGGGUAGGGCAGAGUAGG | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| UCUGUAAUUGUCAGGUAGU | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| CCCUCUGCAGCCGCCUCCUCUGCAG | -0.00 | 3.46 | 3.52 | 0.00 | 0.00 |
| UCUCACAGAAAUCCGCAACCUGU | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| UCAGGCAAAGGGAUAAUUUACAGA | -0.00 | 0.01 | 0.00 | 0.00 | 0.00 |
| GCAGGAACUUGAGUCUGCCU | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| CCAAACUCUGAUCAGAAGCCU | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| AAAAGCAUCAGGAAAGUACCCA | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| AGGGGAACUUGAGGAGGCGAGGAG | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| UGAAGCGUCAGAUAUCUCUGCAG | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| CCUAUUCUGGUUACUGGCGACG | -0.00 | 0.01 | 0.00 | 0.00 | 0.00 |
| UCUGGGAUCAUCAUGUCAGAGA | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| UCUCGGUUUUGUGCCAGAUGACG | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| AACUGGCCUCUAAAAGUCCGCCU | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| UGAGGUCUGUUAACCUUGGCUUC | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| CUGUUUGCCACUAAACCUCACCU | 0.00 | 0.31 | 0.29 | 0.00 | 0.00 |
| UGAAGGGAAGAGGCUUUAUAU | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| GUGUGCGAAAGCUUGUCGUA | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| CCUGCAACUUGGCGUACAGA | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| UUGCCUGCCUCUCUCCUCACG | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| AGUUUUGCAAGGUUGCAUCCAGC | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| ACUCACUCUAAAUCUCUCUUG | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| CAGUGGCUUUAACCUUGGUGAG | 0.00 | 0.49 | 0.45 | 0.00 | 0.00 |
| AGCCCGCGGCGACGAGGUUCUC | -0.00 | 0.01 | 0.00 | 0.00 | 0.00 |
| AGCGUGAAGCGUCUCUCUGAGGCC | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| UGACCCCCGAUGUCGCCUCUGUAG | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| GAGCUUAUCAUAAAAGUGCCAG | -0.00 | 0.01 | 0.01 | 0.00 | 0.00 |
| AGCCCCCGUCCGCCAAAACC | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| GGGCUGGGGCGCGGGGAGGUGU | 0.00 | 0.39 | 0.39 | 0.00 | 0.00 |
| ACUGCAUAAUGAGCAGCUUUAG | -0.00 | 0.02 | 0.02 | 0.00 | 0.00 |
| UUUCUAAUUCUCAGUGGGGCUC | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| UCUGGUGCUGUAUCUCUGUGC | 0.00 | 0.17 | 0.19 | 0.00 | 0.00 |
| CCCAGUGUUUAGACUUCUGUUC | -0.00 | 0.09 | 0.09 | 0.00 | 0.00 |
| GGUGCACUGUGCAUCUCUGGU | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| CUUCUCAGUCAUGGUUUCUCGC | -0.00 | 0.05 | 0.05 | 0.00 | 0.00 |
| CCUAUUCUGUAUUACUGGUUC | -0.00 | 0.02 | 0.01 | 0.00 | 0.00 |
| CACAAGGUAUGUGUAAUACC | -0.00 | 0.01 | 0.01 | 0.00 | 0.00 |
| AAAUUAUAAUAUAAUAUGACGUAU | 0.00 | 0.17 | 0.11 | 0.00 | 0.00 |
| AAAAGCAUAGGAGAGUCACCCU | 0.00 | 0.08 | 0.08 | 0.00 | 0.00 |
| CUAUCAAUCUAUlGCUCUCUC | 0.00 | 0.03 | 0.02 | 0.00 | 0.00 |
| CGUCAACAUCUGCUGGCUUUC | 0.00 | 0.54 | 0.51 | 0.00 | 0.00 |
| AAGGACUUAACAUCUACGUGG | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| CCACCUCCCUUGCAACGUC | 0.00 | 0.04 | 0.03 | 0.00 | 0.00 |
| CUUAUGGAGAUUCCUCUUCAC | -0.00 | 0.11 | 0.10 | 0.00 | 0.00 |
| UCUUGGAGUAGGCUAUGGGUGG | 0.00 | 0.10 | 0.08 | 0.00 | 0.00 |
| CCACUCUGUCAUGCAGCUGCC | -0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| CCUCUUCUCUCUGGCGCUUCC | 0.00 | 0.21 | 0.23 | 0.00 | 0.00 |
| UGAGGGAGGAGGUUUGGUA | -0.00 | 0.09 | 0.07 | 0.00 | 0.00 |
| baseMean_treatment | lfcSE | stat  | pvalue   |
|-------------------|------|-------|---------|
| 6.97              | 0.39 | -2.56 | 1.03E-02|
| 481.16            | 0.24 | -2.35 | 1.88E-02|
| 23.47             | 0.32 | 2.21  | 2.73E-02|
| 180.50            | 0.25 | 2.00  | 4.60E-02|
| 0.26              | 0.44 | -1.98 | 4.72E-02|
| 7.58              | 0.26 | 1.97  | 4.89E-02|
| 3.76              | 0.46 | -1.94 | 5.27E-02|
| 47.31             | 0.27 | -1.84 | 6.61E-02|
| 29.10             | 0.38 | -1.82 | 6.85E-02|
| 2.18              | 0.45 | -1.77 | 7.64E-02|
| 5.82              | 0.47 | -1.75 | 7.96E-02|
| 2.41              | 0.37 | -1.62 | 1.05E-01|
| 15.86             | 0.25 | 1.62  | 1.05E-01|
| 3.02              | 0.46 | -1.60 | 1.09E-01|
| 42.51             | 0.34 | -1.60 | 1.10E-01|
| 120.46            | 0.47 | -1.59 | 1.12E-01|
| 1.88              | 0.46 | -1.57 | 1.16E-01|
| 151.94            | 0.28 | -1.57 | 1.17E-01|
| 106.68            | 0.23 | 1.55  | 1.21E-01|
| 5.35              | 0.45 | 1.55  | 1.22E-01|
| 0.50              | 0.43 | -1.52 | 1.28E-01|
| 54.56             | 0.30 | 1.51  | 1.30E-01|
| 0.38              | 0.40 | -1.51 | 1.31E-01|
| 15.35             | 0.42 | -1.51 | 1.31E-01|
| 0.08              | 0.47 | -1.49 | 1.35E-01|
| 0.00              | 0.43 | -1.48 | 1.39E-01|
| 2.87              | 0.40 | -1.47 | 1.42E-01|
| 3.03              | 0.35 | 1.46  | 1.45E-01|
| 3.58              | 0.38 | 1.46  | 1.45E-01|
| 188.62            | 0.25 | -1.36 | 1.74E-01|
| 0.00              | 0.46 | -1.35 | 1.77E-01|
| 13.26             | 0.39 | -1.34 | 1.80E-01|
| 10.78             | 0.42 | -1.33 | 1.85E-01|
| 209.67            | 0.15 | -1.32 | 1.86E-01|
| 0.84              | 0.38 | -1.29 | 1.98E-01|
| 10.83             | 0.40 | -1.29 | 1.99E-01|
| 14.79             | 0.25 | -1.26 | 2.06E-01|
| 6.68              | 0.30 | 1.24  | 2.16E-01|
| 1.44              | 0.45 | -1.21 | 2.28E-01|
| 42.80             | 0.28 | -1.20 | 2.28E-01|
| 2.33              | 0.47 | -1.20 | 2.31E-01|
| 28.00             | 0.19 | 1.20  | 2.32E-01|
| 88.45             | 0.24 | 1.18  | 2.37E-01|
| 252.72            | 0.18 | 1.15  | 2.50E-01|
| 5.53              | 0.29 | 1.13  | 2.59E-01|
| 54.84             | 0.28 | 1.11  | 2.66E-01|
| 126.40            | 0.25 | 1.11  | 2.69E-01|
| 113.72            | 0.17 | 1.09  | 2.75E-01|
| 1.33              | 0.45 | -1.08 | 2.78E-01|
| 14.04             | 0.33 | -1.08 | 2.82E-01|
| 4.97              | 0.45 | -1.07 | 2.83E-01|
| 0.39              | 0.45 | -1.05 | 2.92E-01|
| 19.06             | 0.26 | 1.05  | 2.95E-01|
| 11.55             | 0.33 | -1.05 | 2.96E-01|
|            |       |       |             |          |
|------------|-------|-------|-------------|----------|
|            | 20.64 | 0.21  | 1.04        | 2.99E-01 |
|            | 0.99  | 0.46  | -1.03       | 3.02E-01 |
|            | 8.32  | 0.22  | 1.02        | 3.06E-01 |
|            | 7.67  | 0.37  | 1.02        | 3.06E-01 |
|            | 9.75  | 0.32  | 1.02        | 3.10E-01 |
|            | 23.52 | 0.26  | 1.01        | 3.12E-01 |
|            | 7.83  | 0.47  | 1.01        | 3.13E-01 |
|            | 0.00  | 0.41  | -0.07       | 9.42E-01 |
|            | 0.86  | 0.44  | -0.97       | 3.33E-01 |
| 2815.01    | 0.46  | -0.97 | 3.34E-01    |          |
|            | 1.64  | 0.41  | 0.96        | 3.37E-01 |
|            | 15.37 | 0.46  | 0.95        | 3.41E-01 |
|            | 4.69  | 0.34  | 0.94        | 3.49E-01 |
|            | 3.16  | 0.25  | 0.93        | 3.52E-01 |
|            | 98.55 | 0.29  | 0.90        | 3.67E-01 |
|            | 2.42  | 0.46  | -0.89       | 3.71E-01 |
|            | 10.23 | 0.45  | -0.89       | 3.72E-01 |
|            | 2.63  | 0.46  | 0.88        | 3.79E-01 |
|            | 44.26 | 0.46  | -0.88       | 3.81E-01 |
|            | 9.46  | 0.47  | 0.87        | 3.85E-01 |
|            | 134.55| 0.27  | 0.87        | 3.86E-01 |
|            | 0.63  | 0.43  | -0.85       | 3.93E-01 |
|            | 0.53  | 0.45  | -0.85       | 3.94E-01 |
|            | 12.66 | 0.45  | -0.84       | 3.99E-01 |
|            | 0.12  | 0.47  | -0.83       | 4.06E-01 |
|            | 11.56 | 0.32  | -0.82       | 4.10E-01 |
|            | 101.08| 0.15  | -0.82       | 4.11E-01 |
|            | 3.19  | 0.32  | 0.82        | 4.14E-01 |
|            | 18.91 | 0.25  | -0.80       | 4.21E-01 |
|            | 1.04  | 0.35  | 0.80        | 4.23E-01 |
|            | 1.45  | 0.33  | 0.80        | 4.24E-01 |
|            | 2.64  | 0.40  | 0.80        | 4.27E-01 |
|            | 18.07 | 0.38  | -0.78       | 4.33E-01 |
|            | 0.94  | 0.42  | -0.78       | 4.34E-01 |
|            | 0.77  | 0.42  | -0.78       | 4.34E-01 |
|            | 15.06 | 0.46  | -0.77       | 4.39E-01 |
|            | 4.28  | 0.36  | 0.77        | 4.39E-01 |
|            | 3.13  | 0.38  | 0.76        | 4.50E-01 |
|            | 4.98  | 0.45  | -0.73       | 4.65E-01 |
|            | 0.30  | 0.47  | -0.73       | 4.66E-01 |
|            | 8.72  | 0.39  | -0.72       | 4.69E-01 |
|            | 386.22| 0.45  | -0.71       | 4.80E-01 |
|            | 0.09  | 0.45  | -0.70       | 4.82E-01 |
|            | 0.22  | 0.47  | -0.70       | 4.84E-01 |
|            | 1.69  | 0.45  | -0.69       | 4.87E-01 |
|            | 2.09  | 0.46  | -0.69       | 4.89E-01 |
|            | 0.46  | 0.47  | -0.68       | 4.94E-01 |
|            | 0.16  | 0.46  | -0.68       | 4.94E-01 |
|            | 52.79 | 0.20  | -0.67       | 5.06E-01 |
|            | 1.21  | 0.45  | 0.64        | 5.20E-01 |
|            | 4469.28| 0.17  | -0.63       | 5.26E-01 |
|            | 0.34  | 0.46  | -0.62       | 5.36E-01 |
|            | 0.15  | 0.47  | -0.62       | 5.38E-01 |
|            | 0.85  | 0.45  | 0.61        | 5.43E-01 |
|            | 3.64  | 0.37  | -0.61       | 5.44E-01 |
|            | 1861.29| 0.15  | -0.60       | 5.46E-01 |
|      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
|    |     |     |     |      |    |
|----|-----|-----|-----|------|----|
| 1.74| 0.34| 0.36| 7.16E-01|    |
| 1.31| 0.33|-0.36| 7.19E-01|    |
| 1.96| 0.25| 0.35| 7.29E-01|    |
| 0.05| 0.47|-0.34| 7.30E-01|    |
| 0.49| 0.43| 0.34| 7.31E-01|    |
| 0.16| 0.46|-0.34| 7.33E-01|    |
| 1.21| 0.47|-0.34| 7.38E-01|    |
| 6.90| 0.25|-0.33| 7.40E-01|    |
| 0.06| 0.46|-0.32| 7.48E-01|    |
| 0.47| 0.46| 0.32| 7.48E-01|    |
| 0.35| 0.44|-0.32| 7.48E-01|    |
| 0.44| 0.47| 0.32| 7.52E-01|    |
| 0.30| 0.47| 0.32| 7.53E-01|    |
| 0.27| 0.47| 0.31| 7.53E-01|    |
| 0.21| 0.39|-0.31| 7.60E-01|    |
| 0.00| 0.34|-0.30| 7.61E-01|    |
| 0.00| 0.41|-0.30| 7.62E-01|    |
| 0.02| 0.46|-0.30| 7.65E-01|    |
| 0.32| 0.47| 0.30| 7.66E-01|    |
| 0.27| 0.45|-0.29| 7.69E-01|    |
| 146.67| 0.24|-0.29| 7.69E-01|    |
| 154.71| 0.17| 0.29| 7.72E-01|    |
| 586.96| 0.19| 0.29| 7.74E-01|    |
| 46.28| 0.44| 0.29| 7.75E-01|    |
| 0.04| 0.47|-0.28| 7.76E-01|    |
| 0.43| 0.42|-0.28| 7.77E-01|    |
| 1.22| 0.45| 0.28| 7.81E-01|    |
| 0.85| 0.45| 0.28| 7.83E-01|    |
| 230.28| 0.16| 0.27| 7.91E-01|    |
| 0.21| 0.36|-0.26| 7.92E-01|    |
| 0.09| 0.45|-0.26| 7.92E-01|    |
| 0.52| 0.45| 0.26| 7.93E-01|    |
| 3.33| 0.40|-0.26| 7.96E-01|    |
| 0.22| 0.41|-0.26| 7.98E-01|    |
| 0.18| 0.45|-0.25| 7.99E-01|    |
| 2.15| 0.38| 0.25| 8.03E-01|    |
| 0.32| 0.42| 0.25| 8.05E-01|    |
| 0.12| 0.46|-0.24| 8.07E-01|    |
| 0.06| 0.47|-0.24| 8.08E-01|    |
| 0.08| 0.47|-0.24| 8.10E-01|    |
| 0.52| 0.47| 0.24| 8.10E-01|    |
| 0.06| 0.46|-0.24| 8.12E-01|    |
| 0.51| 0.45| 0.23| 8.16E-01|    |
| 0.28| 0.45| 0.23| 8.16E-01|    |
| 0.27| 0.47| 0.23| 8.18E-01|    |
| 0.13| 0.46|-0.23| 8.19E-01|    |
| 24.42| 0.44|-0.23| 8.20E-01|    |
| 0.01| 0.41|-0.23| 8.20E-01|    |
| 0.01| 0.41|-0.22| 8.23E-01|    |
| 0.08| 0.47|-0.22| 8.23E-01|    |
| 0.05| 0.43|-0.22| 8.25E-01|    |
| 0.02| 0.46| 0.22| 8.27E-01|    |
| 2.07| 0.33| 0.22| 8.27E-01|    |
| 0.65| 0.33| 0.22| 8.28E-01|    |
| 1.41| 0.28|-0.22| 8.29E-01|    |
| 1.42| 0.44| 0.21| 8.31E-01|    |
|      |      |      |       |       |
|------|------|------|-------|-------|
| 12.79| 0.24 | 0.21 | 8.37E-01 |
| 0.03 | 0.47 | -0.20 | 8.38E-01 |
| 0.19 | 0.46 | 0.20 | 8.38E-01 |
| 3.64 | 0.24 | -0.20 | 8.42E-01 |
| 0.02 | 0.47 | -0.20 | 8.43E-01 |
| 0.83 | 0.40 | 0.20 | 8.44E-01 |
| 0.58 | 0.46 | 0.20 | 8.45E-01 |
| 0.01 | 0.46 | -0.19 | 8.46E-01 |
| 0.02 | 0.47 | -0.19 | 8.47E-01 |
| 19.54| 0.20 | -0.19 | 8.47E-01 |
| 0.04 | 0.47 | -0.19 | 8.49E-01 |
| 0.04 | 0.46 | -0.19 | 8.49E-01 |
| 0.03 | 0.47 | -0.19 | 8.53E-01 |
| 0.09 | 0.47 | -0.18 | 8.55E-01 |
| 0.07 | 0.47 | -0.18 | 8.55E-01 |
| 0.37 | 0.44 | 0.18 | 8.56E-01 |
| 0.04 | 0.44 | -0.18 | 8.56E-01 |
| 0.43 | 0.44 | 0.18 | 8.56E-01 |
| 0.00 | 0.42 | -0.18 | 8.57E-01 |
| 0.01 | 0.46 | -0.18 | 8.58E-01 |
| 0.27 | 0.47 | 0.18 | 8.58E-01 |
| 0.14 | 0.42 | 0.18 | 8.59E-01 |
| 0.35 | 0.47 | 0.18 | 8.59E-01 |
| 0.03 | 0.42 | -0.18 | 8.59E-01 |
| 0.02 | 0.40 | -0.18 | 8.60E-01 |
| 0.00 | 0.42 | -0.18 | 8.60E-01 |
| 0.02 | 0.46 | -0.18 | 8.60E-01 |
| 0.03 | 0.46 | -0.18 | 8.61E-01 |
| 0.55 | 0.37 | 0.17 | 8.64E-01 |
| 1.23 | 0.45 | -0.17 | 8.64E-01 |
| 0.43 | 0.47 | 0.17 | 8.64E-01 |
| 0.56 | 0.47 | 0.17 | 8.64E-01 |
| 0.02 | 0.45 | -0.17 | 8.64E-01 |
| 1.10 | 0.45 | -0.17 | 8.65E-01 |
| 0.06 | 0.42 | -0.17 | 8.68E-01 |
| 1.66 | 0.30 | 0.17 | 8.69E-01 |
| 0.04 | 0.44 | -0.16 | 8.69E-01 |
| 0.01 | 0.41 | -0.16 | 8.70E-01 |
| 0.97 | 0.30 | 0.16 | 8.74E-01 |
| 0.20 | 0.41 | 0.16 | 8.75E-01 |
| 0.00 | 0.43 | -0.16 | 8.76E-01 |
| 0.02 | 0.44 | -0.16 | 8.77E-01 |
| 0.02 | 0.46 | -0.15 | 8.78E-01 |
| 0.03 | 0.42 | -0.15 | 8.78E-01 |
| 0.05 | 0.47 | -0.15 | 8.78E-01 |
| 255.11| 0.12 | 0.15 | 8.79E-01 |
| 0.53 | 0.44 | -0.15 | 8.80E-01 |
| 0.25 | 0.47 | 0.15 | 8.81E-01 |
| 0.04 | 0.47 | -0.15 | 8.81E-01 |
| 0.04 | 0.47 | -0.15 | 8.82E-01 |
| 0.01 | 0.44 | -0.14 | 8.85E-01 |
| 0.25 | 0.47 | 0.14 | 8.86E-01 |
| 0.65 | 0.45 | 0.14 | 8.86E-01 |
| 0.02 | 0.39 | -0.14 | 8.86E-01 |
| 0.01 | 0.44 | -0.14 | 8.87E-01 |
| 0.00 | 0.44 | -0.14 | 8.88E-01 |
|   |   |   |   |   |
|---|---|---|---|---|
| 0.00 | 0.45 | -0.14 | 8.89E-01 |
| 0.64 | 0.46 | 0.14 | 8.89E-01 |
| 0.40 | 0.47 | -0.14 | 8.90E-01 |
| 0.12 | 0.45 | 0.14 | 8.90E-01 |
| 0.20 | 0.47 | -0.14 | 8.91E-01 |
| 0.03 | 0.40 | -0.14 | 8.91E-01 |
| 0.02 | 0.46 | -0.14 | 8.92E-01 |
| 0.01 | 0.44 | -0.13 | 8.94E-01 |
| 0.17 | 0.45 | 0.13 | 8.95E-01 |
| 0.10 | 0.45 | 0.13 | 8.98E-01 |
| 8.20 | 0.42 | -0.13 | 9.00E-01 |
| 0.01 | 0.46 | -0.12 | 9.01E-01 |
| 0.20 | 0.47 | -0.12 | 9.01E-01 |
| 0.03 | 0.47 | -0.12 | 9.02E-01 |
| 0.06 | 0.46 | -0.12 | 9.04E-01 |
| 0.02 | 0.45 | -0.12 | 9.04E-01 |
| 1.43 | 0.43 | 0.12 | 9.05E-01 |
| 0.03 | 0.44 | -0.12 | 9.07E-01 |
| 0.14 | 0.46 | -0.12 | 9.07E-01 |
| 0.06 | 0.46 | -0.12 | 9.08E-01 |
| 0.09 | 0.47 | -0.12 | 9.08E-01 |
| 0.23 | 0.42 | 0.11 | 9.09E-01 |
| 0.01 | 0.43 | -0.11 | 9.09E-01 |
| 0.00 | 0.37 | -0.11 | 9.09E-01 |
| 0.33 | 0.42 | 0.11 | 9.10E-01 |
| 28.26 | 0.31 | -0.11 | 9.10E-01 |
| 0.01 | 0.46 | -0.11 | 9.11E-01 |
| 0.01 | 0.46 | -0.11 | 9.11E-01 |
| 0.25 | 0.42 | -0.11 | 9.11E-01 |
| 0.05 | 0.46 | -0.11 | 9.12E-01 |
| 0.00 | 0.37 | -0.11 | 9.13E-01 |
| 0.05 | 0.40 | -0.11 | 9.13E-01 |
| 0.00 | 0.37 | -0.11 | 9.13E-01 |
| 0.41 | 0.42 | 0.11 | 9.15E-01 |
| 0.01 | 0.41 | -0.11 | 9.15E-01 |
| 0.03 | 0.41 | -0.11 | 9.15E-01 |
| 0.02 | 0.39 | -0.11 | 9.15E-01 |
| 0.11 | 0.46 | 0.11 | 9.16E-01 |
| 0.02 | 0.46 | -0.10 | 9.16E-01 |
| 0.48 | 0.43 | 0.10 | 9.17E-01 |
| 0.10 | 0.47 | -0.10 | 9.18E-01 |
| 0.01 | 0.46 | -0.10 | 9.21E-01 |
| 1.69 | 0.37 | 0.10 | 9.21E-01 |
| 0.01 | 0.46 | -0.10 | 9.22E-01 |
| 0.00 | 0.35 | -0.10 | 9.22E-01 |
| 0.06 | 0.40 | -0.10 | 9.22E-01 |
| 2.15 | 0.45 | -0.10 | 9.22E-01 |
| 0.03 | 0.42 | -0.10 | 9.23E-01 |
| 0.02 | 0.42 | -0.10 | 9.24E-01 |
| 96.69 | 0.31 | -0.09 | 9.25E-01 |
| 0.00 | 0.26 | -0.09 | 9.25E-01 |
| 0.00 | 0.39 | -0.09 | 9.26E-01 |
| 0.00 | 0.37 | -0.09 | 9.27E-01 |
| 0.01 | 0.40 | -0.09 | 9.27E-01 |
| 0.01 | 0.44 | -0.09 | 9.27E-01 |
| 0.12 | 0.45 | -0.09 | 9.28E-01 |
| 0.63 | 0.46 | -0.09 | 9.29E-01 |
| 1.02 | 0.45 | -0.09 | 9.29E-01 |
| 3.45 | 0.31 | 0.09 | 9.30E-01 |
| 0.01 | 0.45 | -0.09 | 9.31E-01 |
| 0.03 | 0.44 | -0.09 | 9.31E-01 |
| 0.09 | 0.43 | -0.08 | 9.32E-01 |
| 0.03 | 0.47 | -0.08 | 9.32E-01 |
| 0.01 | 0.39 | -0.08 | 9.33E-01 |
| 0.16 | 0.41 | 0.08 | 9.33E-01 |
| 2.18 | 0.46 | 0.08 | 9.33E-01 |
| 0.03 | 0.44 | -0.08 | 9.33E-01 |
| 0.26 | 0.46 | -0.08 | 9.33E-01 |
| 0.00 | 0.39 | -0.08 | 9.34E-01 |
| 0.61 | 0.45 | 0.08 | 9.35E-01 |
| 0.00 | 0.43 | -0.08 | 9.35E-01 |
| 0.01 | 0.43 | -0.08 | 9.35E-01 |
| 0.01 | 0.42 | -0.08 | 9.35E-01 |
| 0.01 | 0.42 | -0.08 | 9.35E-01 |
| 0.00 | 0.39 | -0.08 | 9.37E-01 |
| 0.01 | 0.37 | -0.08 | 9.37E-01 |
| 0.19 | 0.46 | 0.08 | 9.37E-01 |
| 0.18 | 0.45 | 0.08 | 9.37E-01 |
| 0.00 | 0.40 | -0.08 | 9.38E-01 |
| 0.10 | 0.42 | 0.08 | 9.38E-01 |
| 0.01 | 0.34 | -0.08 | 9.38E-01 |
| 0.03 | 0.45 | -0.08 | 9.38E-01 |
| 0.01 | 0.39 | -0.08 | 9.38E-01 |
| 0.01 | 0.40 | -0.08 | 9.38E-01 |
| 0.09 | 0.33 | 0.08 | 9.39E-01 |
| 0.31 | 0.45 | -0.08 | 9.39E-01 |
| 0.02 | 0.41 | -0.07 | 9.41E-01 |
| 0.13 | 0.34 | 0.07 | 9.41E-01 |
| 0.18 | 0.47 | 0.07 | 9.41E-01 |
| 0.00 | 0.41 | -0.07 | 9.42E-01 |
| 0.01 | 0.45 | -0.07 | 9.42E-01 |
| 0.01 | 0.42 | -0.07 | 9.42E-01 |
| 2.83 | 0.27 | 0.07 | 9.43E-01 |
| 0.08 | 0.46 | 0.07 | 9.43E-01 |
| 0.00 | 0.29 | -0.07 | 9.43E-01 |
| 0.01 | 0.45 | -0.07 | 9.43E-01 |
| 0.01 | 0.41 | -0.07 | 9.44E-01 |
| 0.12 | 0.45 | 0.07 | 9.44E-01 |
| 0.01 | 0.39 | -0.07 | 9.44E-01 |
| 0.44 | 0.44 | 0.07 | 9.45E-01 |
| 0.09 | 0.34 | 0.07 | 9.45E-01 |
| 0.01 | 0.41 | -0.07 | 9.45E-01 |
| 0.00 | 0.39 | -0.07 | 9.45E-01 |
| 0.01 | 0.43 | -0.07 | 9.46E-01 |
| 0.02 | 0.33 | -0.07 | 9.46E-01 |
| 0.19 | 0.47 | 0.07 | 9.46E-01 |
| 0.01 | 0.44 | -0.07 | 9.47E-01 |
| 0.13 | 0.32 | 0.07 | 9.47E-01 |
| 0.01 | 0.38 | -0.07 | 9.48E-01 |
| 0.53 | 0.47 | 0.07 | 9.48E-01 |
| 0.01 | 0.33 | -0.06 | 9.48E-01 |
| 21.04 | 0.28 | -0.06 | 9.49E-01 |
| 0.08 | 0.33 | 0.06 | 9.49E-01 |
|------|------|------|-----------|
| 0.27 | 0.47 | 0.06 | 9.49E-01 |
| 0.01 | 0.43 | -0.06| 9.50E-01 |
| 0.16 | 0.31 | 0.06 | 9.50E-01 |
| 0.07 | 0.47 | 0.06 | 9.50E-01 |
| 0.02 | 0.44 | -0.06| 9.50E-01 |
| 0.02 | 0.46 | -0.06| 9.50E-01 |
| 0.24 | 0.31 | 0.06 | 9.50E-01 |
| 0.54 | 0.39 | 0.06 | 9.50E-01 |
| 0.01 | 0.41 | -0.06| 9.50E-01 |
| 0.53 | 0.31 | 0.06 | 9.50E-01 |
| 0.28 | 0.44 | 0.06 | 9.51E-01 |
| 0.00 | 0.26 | -0.06| 9.51E-01 |
| 210.55| 0.16 | 0.06 | 9.51E-01 |
| 0.00 | 0.31 | -0.06| 9.52E-01 |
| 0.02 | 0.42 | -0.06| 9.52E-01 |
| 0.01 | 0.40 | -0.06| 9.52E-01 |
| 0.03 | 0.45 | -0.06| 9.52E-01 |
| 0.00 | 0.34 | -0.06| 9.52E-01 |
| 0.15 | 0.46 | 0.06 | 9.53E-01 |
| 0.01 | 0.36 | -0.06| 9.54E-01 |
| 0.00 | 0.30 | -0.06| 9.54E-01 |
| 0.86 | 0.29 | 0.06 | 9.54E-01 |
| 0.17 | 0.29 | 0.06 | 9.54E-01 |
| 0.03 | 0.41 | -0.06| 9.55E-01 |
| 0.09 | 0.28 | 0.06 | 9.55E-01 |
| 0.00 | 0.28 | -0.06| 9.55E-01 |
| 0.21 | 0.37 | 0.06 | 9.55E-01 |
| 56.40| 0.34 | -0.06| 9.56E-01 |
| 0.04 | 0.47 | -0.06| 9.56E-01 |
| 0.08 | 0.28 | 0.05 | 9.56E-01 |
| 0.05 | 0.44 | -0.05| 9.56E-01 |
| 0.01 | 0.39 | -0.05| 9.57E-01 |
| 0.00 | 0.23 | -0.05| 9.57E-01 |
| 0.13 | 0.47 | 0.05 | 9.57E-01 |
| 0.00 | 0.36 | -0.05| 9.57E-01 |
| 0.42 | 0.38 | -0.05| 9.57E-01 |
| 0.24 | 0.38 | 0.05 | 9.57E-01 |
| 0.00 | 0.35 | -0.05| 9.57E-01 |
| 0.01 | 0.41 | -0.05| 9.57E-01 |
| 0.94 | 0.38 | -0.05| 9.57E-01 |
| 0.01 | 0.42 | -0.05| 9.58E-01 |
| 0.03 | 0.45 | -0.05| 9.58E-01 |
| 0.00 | 0.25 | -0.05| 9.58E-01 |
| 0.02 | 0.42 | -0.05| 9.58E-01 |
| 0.02 | 0.31 | -0.05| 9.59E-01 |
| 0.09 | 0.35 | 0.05 | 9.59E-01 |
| 0.18 | 0.46 | -0.05| 9.59E-01 |
| 0.01 | 0.39 | -0.05| 9.59E-01 |
| 0.00 | 0.36 | -0.05| 9.59E-01 |
| 0.21 | 0.47 | -0.05| 9.60E-01 |
| 0.05 | 0.43 | 0.05 | 9.60E-01 |
| 0.01 | 0.31 | -0.05| 9.60E-01 |
| 0.00 | 0.33 | -0.05| 9.61E-01 |
| 0.26 | 0.27 | 0.05 | 9.61E-01 |
| 0.16 | 0.38 | 0.05 | 9.61E-01 |
| 0.00 | 0.28 | -0.05 | 9.61E-01 |
| 0.17 | 0.35 | 0.05 | 9.62E-01 |
| 0.16 | 0.24 | 0.05 | 9.63E-01 |
| 0.01 | 0.37 | -0.05 | 9.63E-01 |
| 0.03 | 0.42 | -0.05 | 9.63E-01 |
| 0.00 | 0.33 | -0.05 | 9.63E-01 |
| 0.12 | 0.35 | 0.05 | 9.64E-01 |
| 0.00 | 0.34 | -0.05 | 9.64E-01 |
| 0.01 | 0.36 | -0.05 | 9.64E-01 |
| 0.01 | 0.33 | -0.04 | 9.64E-01 |
| 0.17 | 0.23 | 0.04 | 9.64E-01 |
| 0.00 | 0.33 | -0.04 | 9.65E-01 |
| 0.00 | 0.32 | -0.04 | 9.65E-01 |
| 0.00 | 0.40 | -0.04 | 9.65E-01 |
| 0.00 | 0.25 | -0.04 | 9.65E-01 |
| 0.02 | 0.45 | -0.04 | 9.65E-01 |
| 0.00 | 0.31 | -0.04 | 9.65E-01 |
| 0.00 | 0.32 | -0.04 | 9.65E-01 |
| 2.09 | 0.23 | 0.04 | 9.65E-01 |
| 0.12 | 0.23 | 0.04 | 9.65E-01 |
| 0.08 | 0.23 | 0.04 | 9.65E-01 |
| 0.08 | 0.23 | 0.04 | 9.65E-01 |
| 0.31 | 0.23 | 0.04 | 9.65E-01 |
| 0.08 | 0.23 | 0.04 | 9.65E-01 |
| 0.31 | 0.23 | 0.04 | 9.65E-01 |
| 0.31 | 0.23 | 0.04 | 9.65E-01 |
| 0.17 | 0.23 | 0.04 | 9.65E-01 |
| 0.26 | 0.23 | 0.04 | 9.65E-01 |
| 0.31 | 0.23 | 0.04 | 9.65E-01 |
| 0.31 | 0.23 | 0.04 | 9.65E-01 |
| 0.08 | 0.23 | 0.04 | 9.65E-01 |
| 0.12 | 0.23 | 0.04 | 9.65E-01 |
| 0.08 | 0.23 | 0.04 | 9.66E-01 |
| 0.00 | 0.32 | -0.04 | 9.66E-01 |
| 0.00 | 0.28 | -0.04 | 9.66E-01 |
| 0.00 | 0.27 | -0.04 | 9.66E-01 |
| 0.53 | 0.27 | 0.04 | 9.66E-01 |
| 0.01 | 0.37 | -0.04 | 9.66E-01 |
| 0.15 | 0.47 | -0.04 | 9.67E-01 |
| 0.00 | 0.30 | -0.04 | 9.67E-01 |
| 0.00 | 0.32 | -0.04 | 9.67E-01 |
| 0.11 | 0.47 | 0.04 | 9.67E-01 |
| 0.01 | 0.33 | -0.04 | 9.67E-01 |
| 0.00 | 0.31 | -0.04 | 9.67E-01 |
| 0.00 | 0.23 | -0.04 | 9.68E-01 |
| 0.00 | 0.23 | -0.04 | 9.68E-01 |
| 0.00 | 0.23 | -0.04 | 9.68E-01 |
| 0.06 | 0.25 | 0.04 | 9.68E-01 |
| 0.00 | 0.23 | -0.04 | 9.68E-01 |
| 0.00 | 0.23 | -0.04 | 9.68E-01 |
| 0.00 | 0.30 | -0.04 | 9.68E-01 |
| 0.06 | 0.25 | 0.04 | 9.69E-01 |
| 0.01 | 0.40 | -0.04 | 9.69E-01 |
| 0.25 | 0.44 | 0.04 | 9.69E-01 |
| 0.06 | 0.25 | 0.04 | 9.69E-01 |
|   |   |   |   |
|---|---|---|---|
| 0.00 | 0.30 | -0.04 | 9.69E-01 |
| 0.73 | 0.42 | 0.04 | 9.69E-01 |
| 0.00 | 0.30 | -0.04 | 9.69E-01 |
| 0.28 | 0.47 | -0.04 | 9.69E-01 |
| 0.00 | 0.30 | -0.04 | 9.69E-01 |
| 0.00 | 0.30 | -0.04 | 9.70E-01 |
| 0.06 | 0.25 | 0.04 | 9.70E-01 |
| 0.00 | 0.31 | -0.04 | 9.70E-01 |
| 0.01 | 0.41 | -0.04 | 9.70E-01 |
| 0.00 | 0.30 | -0.04 | 9.70E-01 |
| 0.01 | 0.35 | -0.04 | 9.70E-01 |
| 0.13 | 0.47 | 0.04 | 9.70E-01 |
| 0.07 | 0.40 | 0.04 | 9.70E-01 |
| 0.00 | 0.30 | -0.04 | 9.71E-01 |
| 0.01 | 0.30 | -0.04 | 9.71E-01 |
| 0.06 | 0.44 | 0.04 | 9.71E-01 |
| 0.00 | 0.24 | -0.04 | 9.71E-01 |
| 0.03 | 0.33 | -0.04 | 9.71E-01 |
| 0.00 | 0.37 | -0.04 | 9.71E-01 |
| 0.00 | 0.29 | -0.04 | 9.71E-01 |
| 0.00 | 0.31 | -0.04 | 9.72E-01 |
| 2.09 | 0.45 | 0.04 | 9.72E-01 |
| 0.01 | 0.39 | -0.03 | 9.72E-01 |
| 0.06 | 0.23 | 0.03 | 9.72E-01 |
| 0.12 | 0.28 | 0.03 | 9.72E-01 |
| 0.06 | 0.23 | 0.03 | 9.72E-01 |
| 0.06 | 0.23 | 0.03 | 9.72E-01 |
| 0.00 | 0.27 | -0.03 | 9.72E-01 |
| 0.01 | 0.38 | -0.03 | 9.72E-01 |
| 0.00 | 0.31 | -0.03 | 9.72E-01 |
| 0.03 | 0.45 | -0.03 | 9.72E-01 |
| 0.02 | 0.41 | -0.03 | 9.73E-01 |
| 0.06 | 0.23 | 0.03 | 9.73E-01 |
| 0.01 | 0.28 | -0.03 | 9.73E-01 |
| 0.00 | 0.30 | -0.03 | 9.73E-01 |
| 0.06 | 0.23 | 0.03 | 9.73E-01 |
| 0.00 | 0.28 | -0.03 | 9.73E-01 |
| 0.01 | 0.30 | -0.03 | 9.73E-01 |
| 0.01 | 0.35 | -0.03 | 9.73E-01 |
| 0.02 | 0.41 | -0.03 | 9.73E-01 |
| 0.00 | 0.31 | -0.03 | 9.73E-01 |
| 0.00 | 0.28 | -0.03 | 9.73E-01 |
| 0.00 | 0.27 | -0.03 | 9.73E-01 |
| 0.01 | 0.40 | -0.03 | 9.74E-01 |
| 0.53 | 0.39 | 0.03 | 9.74E-01 |
| 0.00 | 0.36 | -0.03 | 9.74E-01 |
| 0.01 | 0.30 | -0.03 | 9.74E-01 |
| 0.00 | 0.27 | -0.03 | 9.74E-01 |
| 0.00 | 0.34 | -0.03 | 9.74E-01 |
| 0.00 | 0.26 | -0.03 | 9.75E-01 |
| 2.09 | 0.26 | 0.03 | 9.75E-01 |
| 0.00 | 0.27 | -0.03 | 9.75E-01 |
| 8.70 | 0.28 | -0.03 | 9.75E-01 |
| 0.00 | 0.27 | -0.03 | 9.75E-01 |
|    |    |    |    |    |
|----|----|----|----|----|
| 0.00 | 0.26 | -0.03 | 9.75E-01 |
| 0.17 | 0.40 | -0.03 | 9.75E-01 |
| 0.02 | 0.40 | -0.03 | 9.75E-01 |
| 0.19 | 0.47 | 0.03 | 9.76E-01 |
| 0.04 | 0.43 | -0.03 | 9.76E-01 |
| 0.01 | 0.39 | -0.03 | 9.76E-01 |
| 0.01 | 0.38 | -0.03 | 9.76E-01 |
| 0.00 | 0.34 | -0.03 | 9.76E-01 |
| 0.01 | 0.39 | -0.03 | 9.76E-01 |
| 0.47 | 0.22 | 0.03 | 9.76E-01 |
| 0.00 | 0.26 | -0.03 | 9.76E-01 |
| 0.00 | 0.24 | -0.03 | 9.77E-01 |
| 1.57 | 0.45 | -0.03 | 9.77E-01 |
| 0.01 | 0.32 | -0.03 | 9.77E-01 |
| 0.00 | 0.35 | -0.03 | 9.77E-01 |
| 0.24 | 0.23 | 0.03 | 9.77E-01 |
| 0.00 | 0.32 | -0.03 | 9.77E-01 |
| 0.00 | 0.27 | -0.03 | 9.77E-01 |
| 0.00 | 0.25 | -0.03 | 9.77E-01 |
| 0.00 | 0.28 | -0.03 | 9.77E-01 |
| 0.00 | 0.30 | -0.03 | 9.77E-01 |
| 0.01 | 0.39 | -0.03 | 9.77E-01 |
| 0.02 | 0.39 | -0.03 | 9.77E-01 |
| 0.00 | 0.26 | -0.03 | 9.77E-01 |
| 0.00 | 0.34 | -0.03 | 9.78E-01 |
| 0.00 | 0.34 | -0.03 | 9.78E-01 |
| 0.02 | 0.36 | -0.03 | 9.78E-01 |
| 0.00 | 0.24 | -0.03 | 9.78E-01 |
| 0.00 | 0.23 | -0.03 | 9.78E-01 |
| 0.00 | 0.24 | -0.03 | 9.78E-01 |
| 0.00 | 0.28 | -0.03 | 9.78E-01 |
| 0.00 | 0.32 | -0.03 | 9.78E-01 |
| 0.00 | 0.24 | -0.03 | 9.78E-01 |
| 0.00 | 0.23 | -0.03 | 9.78E-01 |
| 0.00 | 0.33 | -0.03 | 9.78E-01 |
| 0.00 | 0.24 | -0.03 | 9.78E-01 |
| 0.00 | 0.24 | -0.03 | 9.78E-01 |
| 0.01 | 0.27 | -0.03 | 9.78E-01 |
| 0.00 | 0.23 | -0.03 | 9.79E-01 |
| 0.00 | 0.23 | -0.03 | 9.79E-01 |
| 0.00 | 0.23 | -0.03 | 9.79E-01 |
| 0.00 | 0.23 | -0.03 | 9.79E-01 |
| 0.00 | 0.23 | -0.03 | 9.79E-01 |
| 0.00 | 0.23 | -0.03 | 9.79E-01 |
| 0.00 | 0.23 | -0.03 | 9.79E-01 |
| 0.00 | 0.23 | -0.03 | 9.79E-01 |
| 0.00 | 0.23 | -0.03 | 9.79E-01 |
| 0.00 | 0.23 | -0.03 | 9.79E-01 |
| 0.00 | 0.23 | -0.03 | 9.79E-01 |
| 0.00 | 0.23 | -0.03 | 9.79E-01 |
| 0.00 | 0.23 | -0.03 | 9.79E-01 |
| 0.00 | 0.23 | -0.03 | 9.79E-01 |
| 0.00 | 0.23 | -0.03 | 9.79E-01 |
| 0.00 | 0.23 | -0.03 | 9.79E-01 |
| 0.00 | 0.23 | -0.03 | 9.79E-01 |
| Time  | Value1 | Value2 | Value3 | Value4 |
|-------|--------|--------|--------|--------|
| 0.00  | 0.23   | -0.03  | 9.79E-01 |
| 0.00  | 0.23   | -0.03  | 9.79E-01 |
| 0.00  | 0.23   | -0.03  | 9.79E-01 |
| 0.00  | 0.23   | -0.03  | 9.79E-01 |
| 0.00  | 0.23   | -0.03  | 9.79E-01 |
| 0.00  | 0.23   | -0.03  | 9.79E-01 |
| 0.00  | 0.23   | -0.03  | 9.79E-01 |
| 0.00  | 0.23   | -0.03  | 9.79E-01 |
| 0.00  | 0.23   | -0.03  | 9.79E-01 |
| 0.00  | 0.23   | -0.03  | 9.79E-01 |
| 0.00  | 0.23   | -0.03  | 9.79E-01 |
| 0.00  | 0.23   | -0.03  | 9.79E-01 |
| 0.00  | 0.23   | -0.03  | 9.79E-01 |
| 0.00  | 0.23   | -0.03  | 9.79E-01 |
| 0.00  | 0.23   | -0.03  | 9.79E-01 |
| 0.00  | 0.23   | -0.03  | 9.79E-01 |
| 0.00  | 0.23   | -0.03  | 9.79E-01 |
| 0.00  | 0.23   | -0.03  | 9.79E-01 |
| 0.00  | 0.23   | -0.03  | 9.79E-01 |
| 0.02  | 0.42   | -0.03  | 9.79E-01 |
| 0.00  | 0.23   | -0.03  | 9.79E-01 |
| 0.00  | 0.23   | -0.03  | 9.80E-01 |
| 0.00  | 0.23   | -0.03  | 9.80E-01 |
| 0.12  | 0.47   | 0.03   | 9.80E-01 |
| 0.00  | 0.26   | -0.03  | 9.80E-01 |
| 0.00  | 0.35   | -0.03  | 9.80E-01 |
| 0.01  | 0.37   | -0.03  | 9.80E-01 |
| 0.02  | 0.35   | -0.03  | 9.80E-01 |
| 0.00  | 0.23   | -0.02  | 9.80E-01 |
| 0.00  | 0.23   | -0.02  | 9.80E-01 |
| 0.01  | 0.32   | -0.02  | 9.80E-01 |
| 0.01  | 0.34   | -0.02  | 9.80E-01 |
| 0.01  | 0.39   | -0.02  | 9.80E-01 |
| 0.00  | 0.23   | -0.02  | 9.80E-01 |
| 0.00  | 0.23   | -0.02  | 9.80E-01 |
| 0.00  | 0.23   | -0.02  | 9.81E-01 |
| 0.00  | 0.23   | -0.02  | 9.81E-01 |
| 0.04  | 0.46   | -0.02  | 9.81E-01 |
| 0.00  | 0.25   | -0.02  | 9.81E-01 |
| 0.02  | 0.30   | -0.02  | 9.81E-01 |
| 0.00  | 0.31   | -0.02  | 9.81E-01 |
| 0.00  | 0.29   | -0.02  | 9.81E-01 |
| 0.22  | 0.47   | -0.02  | 9.81E-01 |
| 0.00  | 0.31   | -0.02  | 9.81E-01 |
| 0.00  | 0.23   | -0.02  | 9.81E-01 |
| 0.03  | 0.38   | -0.02  | 9.81E-01 |
| 0.00 | 0.27 | -0.02 | 9.81E-01 |
| 0.00 | 0.31 | -0.02 | 9.81E-01 |
| 0.11 | 0.47 | -0.02 | 9.82E-01 |
| 0.53 | 0.40 | 0.02 | 9.82E-01 |
| 0.01 | 0.34 | -0.02 | 9.82E-01 |
| 0.00 | 0.31 | -0.02 | 9.82E-01 |
| 0.00 | 0.33 | -0.02 | 9.82E-01 |
| 0.00 | 0.26 | -0.02 | 9.82E-01 |
| 0.01 | 0.38 | -0.02 | 9.82E-01 |
| 0.01 | 0.39 | -0.02 | 9.82E-01 |
| 0.00 | 0.26 | -0.02 | 9.82E-01 |
| 0.00 | 0.31 | -0.02 | 9.82E-01 |
| 0.00 | 0.26 | -0.02 | 9.82E-01 |
| 0.04 | 0.44 | -0.02 | 9.82E-01 |
| 0.00 | 0.33 | -0.02 | 9.82E-01 |
| 0.02 | 0.42 | -0.02 | 9.82E-01 |
| 0.00 | 0.31 | -0.02 | 9.83E-01 |
| 52.19 | 0.20 | -0.02 | 9.83E-01 |
| 0.00 | 0.30 | -0.02 | 9.83E-01 |
| 0.03 | 0.44 | -0.02 | 9.83E-01 |
| 0.00 | 0.32 | -0.02 | 9.83E-01 |
| 0.00 | 0.31 | -0.02 | 9.83E-01 |
| 0.00 | 0.23 | -0.02 | 9.83E-01 |
| 0.00 | 0.29 | -0.02 | 9.83E-01 |
| 0.00 | 0.23 | -0.02 | 9.83E-01 |
| 0.01 | 0.36 | -0.02 | 9.83E-01 |
| 0.00 | 0.31 | -0.02 | 9.84E-01 |
| 0.00 | 0.31 | -0.02 | 9.84E-01 |
| 0.00 | 0.29 | -0.02 | 9.84E-01 |
| 0.00 | 0.23 | -0.02 | 9.84E-01 |
| 0.00 | 0.23 | -0.02 | 9.84E-01 |
| 0.00 | 0.31 | -0.02 | 9.84E-01 |
| 0.00 | 0.29 | -0.02 | 9.84E-01 |
| 0.00 | 0.31 | -0.02 | 9.84E-01 |
| 0.02 | 0.40 | -0.02 | 9.84E-01 |
| 0.01 | 0.34 | -0.02 | 9.84E-01 |
| 0.08 | 0.47 | -0.02 | 9.84E-01 |
| 0.00 | 0.28 | -0.02 | 9.84E-01 |
| 0.00 | 0.26 | -0.02 | 9.84E-01 |
| 0.01 | 0.40 | -0.02 | 9.84E-01 |
| 0.00 | 0.32 | -0.02 | 9.84E-01 |
| 0.00 | 0.31 | -0.02 | 9.84E-01 |
| 0.01 | 0.34 | -0.02 | 9.84E-01 |
| 0.01 | 0.34 | -0.02 | 9.84E-01 |
| 0.01 | 0.23 | -0.02 | 9.85E-01 |
| 0.01 | 0.35 | -0.02 | 9.85E-01 |
| 0.00 | 0.28 | -0.02 | 9.85E-01 |
| 0.06 | 0.45 | 0.02 | 9.85E-01 |
| 0.01 | 0.34 | -0.02 | 9.85E-01 |
| 0.00 | 0.30 | -0.02 | 9.85E-01 |
| 0.33 | 0.45 | 0.02 | 9.85E-01 |
| 0.01 | 0.32 | -0.02 | 9.85E-01 |
| 0.00 | 0.28 | -0.02 | 9.85E-01 |
| 0.00 | 0.28 | -0.02 | 9.85E-01 |
| 0.00 | 0.31 | -0.02 | 9.85E-01 |
|------|------|-------|----------|
| 0.00 | 0.26 | -0.02 | 9.85E-01 |
| 0.00 | 0.31 | -0.02 | 9.86E-01 |
| 0.00 | 0.27 | -0.02 | 9.86E-01 |
| 0.00 | 0.26 | -0.02 | 9.86E-01 |
| 0.01 | 0.33 | -0.02 | 9.86E-01 |
| 0.00 | 0.29 | -0.02 | 9.86E-01 |
| 0.00 | 0.23 | -0.02 | 9.86E-01 |
| 0.01 | 0.31 | -0.02 | 9.86E-01 |
| 0.01 | 0.28 | -0.02 | 9.86E-01 |
| 0.01 | 0.27 | -0.02 | 9.86E-01 |
| 0.00 | 0.28 | -0.02 | 9.86E-01 |
| 0.00 | 0.25 | -0.02 | 9.86E-01 |
| 0.01 | 0.34 | -0.02 | 9.86E-01 |
| 0.00 | 0.27 | -0.02 | 9.86E-01 |
| 0.55 | 0.47 | 0.02  | 9.86E-01 |
| 0.01 | 0.32 | -0.02 | 9.86E-01 |
| 0.00 | 0.25 | -0.02 | 9.86E-01 |
| 0.00 | 0.28 | -0.02 | 9.86E-01 |
| 0.00 | 0.25 | -0.02 | 9.86E-01 |
| 0.00 | 0.32 | -0.02 | 9.86E-01 |
| 0.01 | 0.34 | -0.02 | 9.86E-01 |
| 0.00 | 0.28 | -0.02 | 9.86E-01 |
| 0.00 | 0.23 | -0.02 | 9.87E-01 |
| 0.00 | 0.28 | -0.02 | 9.87E-01 |
| 0.00 | 0.28 | -0.02 | 9.87E-01 |
| 0.00 | 0.28 | -0.02 | 9.87E-01 |
| 0.00 | 0.27 | -0.02 | 9.87E-01 |
| 0.00 | 0.28 | -0.02 | 9.87E-01 |
| 0.00 | 0.23 | -0.02 | 9.87E-01 |
| 0.00 | 0.23 | -0.02 | 9.87E-01 |
| 0.00 | 0.23 | -0.02 | 9.87E-01 |
| 0.00 | 0.27 | -0.02 | 9.87E-01 |
| 0.00 | 0.25 | -0.02 | 9.87E-01 |
| 0.00 | 0.24 | -0.02 | 9.87E-01 |
| 0.01 | 0.33 | -0.02 | 9.87E-01 |
| 0.00 | 0.23 | -0.02 | 9.87E-01 |
| 0.00 | 0.28 | -0.02 | 9.87E-01 |
| 0.01 | 0.29 | -0.02 | 9.87E-01 |
| 0.00 | 0.28 | -0.02 | 9.87E-01 |
| 0.00 | 0.23 | -0.02 | 9.87E-01 |
| 0.00 | 0.28 | -0.02 | 9.87E-01 |
| 0.00 | 0.23 | -0.02 | 9.87E-01 |
| 0.00 | 0.27 | -0.02 | 9.87E-01 |
| 0.00 | 0.27 | -0.02 | 9.87E-01 |
| 0.00 | 0.23 | -0.02 | 9.87E-01 |
| 0.00 | 0.28 | -0.02 | 9.87E-01 |
| 0.00 | 0.27 | -0.02 | 9.87E-01 |
| 0.00 | 0.26 | -0.02 | 9.87E-01 |
| 0.00 | 0.27 | -0.02 | 9.87E-01 |
| 0.00 | 0.23 | -0.02 | 9.87E-01 |
| 0.00 | 0.23 | -0.02 | 9.87E-01 |
| 0.00 | 0.23 | -0.02 | 9.87E-01 |
| 0.00 | 0.27 | -0.02 | 9.87E-01 |
| 0.00 | 0.26 | -0.02 | 9.87E-01 |
| 0.00 | 0.27 | -0.02 | 9.87E-01 |
| 0.00 | 0.23 | -0.02 | 9.87E-01 |
| 0.00 | 0.27 | -0.02 | 9.87E-01 |
| 0.00 | 0.26 | -0.02 | 9.87E-01 |
| 0.00 | 0.23 | -0.02 | 9.87E-01 |
| 0.00 | 0.28 | -0.02 | 9.87E-01 |
| 0.00 | 0.23 | -0.02 | 9.87E-01 |
| 0.00 | 0.24 | -0.02 | 9.87E-01 |
| 0.01 | 0.28 | -0.02 | 9.87E-01 |
| 0.00 | 0.28 | -0.02 | 9.87E-01 |
| 0.00 | 0.23 | -0.02 | 9.87E-01 |
| 0.00 | 0.28 | -0.02 | 9.87E-01 |
| 0.00 | 0.23 | -0.02 | 9.87E-01 |
|     |     |     |     |     |
|-----|-----|-----|-----|-----|
| 0.00 | 0.23 | -0.01 | 9.88E-01 |
| 0.01 | 0.34 | -0.01 | 9.88E-01 |
| 0.00 | 0.23 | -0.01 | 9.88E-01 |
| 0.00 | 0.23 | -0.01 | 9.88E-01 |
| 0.02 | 0.34 | -0.01 | 9.88E-01 |
| 0.00 | 0.23 | -0.01 | 9.88E-01 |
| 0.00 | 0.23 | -0.01 | 9.88E-01 |
| 0.00 | 0.27 | -0.01 | 9.88E-01 |
| 0.00 | 0.23 | -0.01 | 9.88E-01 |
| 0.00 | 0.23 | -0.01 | 9.88E-01 |
| 0.00 | 0.23 | -0.01 | 9.88E-01 |
| 0.01 | 0.31 | -0.01 | 9.88E-01 |
| 0.00 | 0.23 | -0.01 | 9.88E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.16 | 0.46 | 0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.03 | 0.33 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 179.03 | 0.18 | 0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.01 | 0.34 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.25 | -0.01 | 9.89E-01 |
|------|------|-------|----------|
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.24 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.24 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
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| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
|   |   |   |          |
|---|---|---|----------|
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
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| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
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| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
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| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
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| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| 0.00 | 0.23 | -0.01 | 9.89E-01 |
| Time | Value 1 | Value 2 | Value 3 |
|------|---------|---------|---------|
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.03 | 0.38 | 0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
|------|------|-------|----------|
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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|    |    |    |    |    |
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| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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| 0.00 | 0.23 | -0.01 | 9.90E-01 |
|   |   |   |   |
|---|---|---|---|
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| Time | Value 1 | Value 2 | Value 3 |
|------|---------|---------|---------|
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
| 0.00 | 0.23    | -0.01   | 9.90E-01 |
|   |   |   |   |
|---|---|---|---|
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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| 0.00 | 0.23 | -0.01 | 9.90E-01 |
| 0.00 | 0.23 | -0.01 | 9.90E-01 |
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|     |     |     |     |
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|    |    |    |    |    |
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|------|------|-------|-----------|
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| 0.02 | 0.37 | -0.01 | 9.91E-01 |
