

**Table I: Transcription Hierarchy of Random-ITS Promoters**

| Promoter   | ITS (+1 - +20)         | 1<br>PY (%) | 2<br>RPY (%) | 3<br>RIF (%) | 4<br>APR  | 5<br>MSAT | 6<br>R |
|------------|------------------------|-------------|--------------|--------------|-----------|-----------|--------|
| DG146a     | ATTAAAAAAC CTGCTAGGAT  | 8.0 ± 2.4   | 154 ± 14     | 70 ± 33      | 13 ± 4    | 20        | 12     |
| N25/A1     | ATCGAGAGGG ACACGGCGAA  | 7.1 ± 0.9   | 150 ± 52     | 56 ± 16      | 13 ± 2    | 19        | 15     |
| DG122      | ATAAAGGAAA ACGGTCAGGT  | 7.0 ± 1.1   | 144 ± 31     | 76 ± 18      | 14 ± 1    | 18        | 15     |
| DG130a     | ATATAGTGAA CAAGGATTAA  | 6.9 ± 0.5   | 140 ± 42     | 73 ± 14      | 14 ± 1    | 18        | 14     |
|            |                        | *           | *            | *            | *         |           |        |
| DG131a     | ATAGGTTAAA AGCCAGACAT  | 5.1 ± 2.2   | 105 ± 41     | 125 ± 22     | 21 ± 9    | 16        | 13     |
| N25        | ATAAAATTGA GAGAGGAGTT  | 6.0 ± 1.9   | 100 ± 0      | 100 ± 0      | 18 ± 5    | 11        | 14     |
| DG151a     | ATCAGGATAC AAGAAGGTTT  | 6.0 ± 2.7   | 96 ± 23      | 99 ± 34      | 19 ± 9    | 16        | 13     |
|            |                        | *           | *            | *            | *         |           |        |
| DG161a     | ATAAAAGTAC TCAGTTCAAA  | 5.1 ± 2.1   | 81 ± 10      | 136 ± 32     | 22 ± 10   | 15        | 12     |
| DG159      | ATAACTAGGG AAAATAATAT  | 4.6 ± 2.2   | 74 ± 14      | 116 ± 14     | 26 ± 16   | 18        | 14     |
| DG121      | ATACACCATA AAGAAACAGT  | 3.4 ± 1.5   | 73 ± 31      | 104 ± 34     | 33 ± 17   | 17        | 13     |
| DG132a     | ATTCTAGTGA AAATCCCCAT  | 3.8 ± 1.5   | 72 ± 16      | 96 ± 27      | 30 ± 12   | 16        | 9      |
| DG115a     | ATCCCGCTCA AGAGCAACAT  | 3.5 ± 0.2   | 71 ± 17      | 105 ± 47     | 28 ± 2    | 18        | 10     |
| DG162      | ATGTAATAA GGTAGGCAAT   | 3.9 ± 1.1   | 70 ± 7       | 104 ± 19     | 27 ± 8    | 16        | 14     |
| DG128a     | ATCCCAGTAA GGAATGATAT  | 3.7 ± 1.4   | 69 ± 4       | 114 ± 27     | 30 ± 11   | 18        | 12     |
| DG126      | ATAAGCACAC GGATACCTTT  | 2.5 ± 0.7   | 57 ± 13      | 150 ± 41     | 40 ± 14   | 16        | 10     |
| DG163a     | ATTATACACG GTAATCGCTT  | 3.4 ± 1.4   | 54 ± 14      | 116 ± 48     | 34 ± 14   | 18        | 9      |
| DG164      | ATTAAGAAAA ATCTTCTATT  | 3.1 ± 0.6   | 51 ± 12      | 134 ± 50     | 34 ± 6    | 17        | 10     |
| DG149a     | ATAGCGGATG GTAACAGAAT  | 2.9 ± 1.2   | 49 ± 9       | 130 ± 16     | 38 ± 11   | 14        | 14     |
| DG165b     | ATCATCTGAA ATCATAGTGT  | 3.1 ± 0.9   | 48 ± 15      | 156 ± 47     | 33 ± 14   | 16        | 10     |
| DG169a     | ATCCAGACGA ACTGGGGAAT  | 3.1 ± 0.3   | 47 ± 4       | 140 ± 56     | 31 ± 3    | 20        | 13     |
| DG155      | ATTAAAAATC CTTTCCTCTT  | 2.8 ± 0.4   | 45 ± 21      | 110 ± 38     | 38 ± 2    | 15        | 6      |
| DG168a     | ATCACGCAAC CGGACTAACT  | 2.7 ± 0.7   | 40 ± 8       | 165 ± 57     | 38 ± 10   | 16        | 10     |
| DG127      | ATCCTAGTAT ATGGAAGTGT  | 2.7 ± 1.2   | 40 ± 14      | 104 ± 20     | 40 ± 16   | 14        | 10     |
| DG135a     | ATAATGCTGT GAACGCGAGT  | 2.2 ± 0.6   | 39 ± 2       | 163 ± 10     | 53 ± 16   | 20        | 12     |
| DG160a     | ATATACTAGC AGCACC AATT | 2.4 ± 1.0   | 35 ± 3       | 137 ± 19     | 50 ± 17   | 15        | 10     |
| DG133      | ATATCGAATT ACTCAGATAT  | 1.8 ± 0.3   | 33 ± 6       | 269 ± 63     | 58 ± 14   | 16        | 10     |
| DG147a     | ATAATGGTCG GTTACACGAT  | 1.8 ± 1.0   | 31 ± 14      | 72 ± 17      | 70 ± 43   | 19        | 11     |
| DG125a     | ATATCGTTCC CTTGACCCAT  | 1.3 ± 0.1   | 25 ± 3       | 295 ± 86     | 76 ± 6    | 16        | 6      |
| N25anti    | ATCCGGAATC CTCTTCCCGG  | 1.4 ± 1.0   | 22 ± 14      | 115 ± 64     | 68 ± 31   | 15        | 7      |
| DG156-3    | ATCGCCGATA AATACGTAGT  | 1.4 ± 0.6   | 21 ± 7       | 243 ± 68     | 76 ± 25   | 15        | 11     |
| DG138a     | ATCTTCTTCG TAACTGGAGT  | 0.9 ± 0.3   | 15 ± 5       | 366 ± 62     | 121 ± 40  | 16        | 8      |
| DG142      | ATGATTTTCAT CTGACTCTAT | 0.9 ± 0.1   | 14 ± 5       | 340 ± 74     | 121 ± 5   | 16        | 7      |
| DG170a     | ATTACTGCAC ATTAATGAAT  | 0.8 ± 0.1   | 13 ± 2       | 288 ± 84     | 118 ± 25  | 16        | 10     |
| DG167      | ATTACATCTG CCGCCTTCCT  | 0.9 ± 0.5   | 13 ± 8       | 210 ± 72     | 151 ± 95  | 20        | 5      |
| DG166      | ATCTAATCTC TGATAATATT  | 0.8 ± 0.3   | 11 ± 3       | 273 ± 64     | 142 ± 60  | 17        | 8      |
| DG152a     | ATTACTATGC CCCATATCCT  | 0.8 ± 0.3   | 11 ± 5       | 234 ± 27     | 144 ± 52  | 15        | 6      |
| DG148      | ATAATTGTAC ATTTGAAACT  | 1.0 ± 0.5   | 11 ± 7       | 228 ± 29     | 135 ± 82  | 17        | 10     |
| DG145      | ATAACCCCTG ACTCCGAAAT  | 0.5 ± 0.2   | 10 ± 4       | 300 ± 72     | 202 ± 62  | 15        | 9      |
| DG141      | ATACATTATC AACGCATGCT  | 0.6 ± 0.2   | 10 ± 6       | 267 ± 77     | 169 ± 65  | 14        | 9      |
| DG124a     | ATCGCAACCT CCTAAATGAT  | 0.4 ± 0.2   | 9 ± 3        | 188 ± 52     | 205 ± 51  | 15        | 9      |
| N25/A1anti | ATATCTCTTT CACATTATCC  | 0.4 ± 0.1   | 7 ± 3        | 458 ± 113    | 255 ± 52  | 16        | 5      |
| DG154a     | ATGGTTCATT TTTCCACACT  | 0.5 ± 0.3   | 7 ± 5        | 287 ± 51     | 217 ± 101 | 17        | 6      |
| DG137a     | ATCGCTCTAC TAAATGTCCT  | 0.3 ± 0.1   | 6 ± 4        | 444 ± 99     | 386 ± 27  | 15        | 7      |