**S2 Table.** Analysis of transcription factors on *TK1* promoter by PROMO 3.0 and rVISTA 2.0.

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| --- | --- | --- | --- |
| **S.No.** | **Transcription factor** | **Predicted binding site on *TK1* promoter****(5’-3’ upstream of transcription start)** | **Consensus DNA binding sequence (5’-3’)** |
| 1 | AhR | -583 CCACGCCCGG -574 | GCACGCCAGC |
| 2 | Arnt | -583 CCACGCCCGG -574 | GCACGCCAGC |
| 3 | AP-1 | -1226 TGACTGAGC -1218 | GATGAGTCA |
| 4 | AP-2alphaA | -459 GCCTGG -454-1233 GCCTGG -1228-1410 GCCTGG -1405 | GCAGGC |
| 5 | AR | -1076 GATCTGTCC -1068 | GCACTGTCC |
| 6 | C/EBPalpha | -818 CATTGTG -812 | GATTGAG |
| 7 | C/EBPbeta | -172 TTGC -169-985 TTGC -982-1121 TTGC -1118-1267 TTGC -1264-1444 TTGC -1441-1516 TTGC -1513 | TTGC |
| 8 | c-Myb | -66 AAACTTGG -59 | CAACTGCC |
| 9 | COUP-TF1 | -1907 CCTGAGGTCAAAT -1895 | CGAGAGGTCAAAG |
| 10 | Egr-3 | -63 CTTGGTGGGCGGA -51 | TACACCCACTATA |
| 11 | Elk-1 | -1115 CTTCCTCCC -1107 | CTTCCTCCC |
| 12 | ER-alpha | -509 TATCTG -505-1888 TATCTG -1884 | TGACC |
| 13 | ETF | -237 GCCCCAGCCCC -227 | GCCCCCCGCAC |
| 14 | GATA-1 | -1166 GAGATA -1161 | TATCTG |
| 15 | GATA-2 | -1165 AGATAAAGC -1157 | GCCCTATCT |
| 16 | GR | -387 CAAAAAT -381-1671 CAAAAAT -1665 | CAAAAAA |
| 17 | HNF-1 | -1173 GTTAAAAG -1166 | ATATTAAC |
| 18 | HNF-4alpha | -237 TCTCAGCACTTTG -227 | TGTTTGGACTTTG |
| 19 | Ik-1 | -1323 TCCCAGCCACTCG -1311 | TCCCAGCACCTTG |
| 20 | LEF-1 | -990 CTTTGTTG -983 | CTTTGATC |
| 21 | MAZ | -223 GTCCCTCCCTGCA -211 | AACCCTCCCCCCC |
| 22 | NF-1 | -533 TTGGCCAG -526-1665 TTGGCCAG -1658 | TTGGCCCA |
| 23 | NF-kappaB | -167 TGGGAAACCCAC -156 | GGGAAATTCCCC |
| 24 | NF-Y | -1666 ATTGGCCA -1659 | ATTGGTCA |
| 25 | p53 | -312 CATGCCC -306 | CATGCCC |
| 26 | Pax-5 | -32 CAGGCCC -26-234 CCAGCCC -228-312 CATGCCC -306-1524 GGGCATG -1518-1800 CAGGCCC -1794 | CAAGCCC |
| 27 | PPAR-alpha | -1503 TAGTCCCAGCT -1493 | CTGACCCAGTG |
| 28 | PR | -1870 TACTGTT -1864 | AACAGTA |
| 29 | PXR-1 | -1725 GGAGTTCA -1718 | TGAACTAA |
| 30 | RBP-Jkappa | -171 TGCTTGGGAAAC -160 | GTTTCCCACGAC |
| 31 | SRY | -990 CTTTGTTGC -982 | AGAACAAAG |
| 32 | STAT4 | -266 ATTTCC -261 | ATTTCC |
| 33 | STAT5A | -558 TTAGTAGAAACGG -546 | TTACCAGAAAAGG |
| 34 | T3R-beta1 | -586 TCACCACGC -578 | TCACCACCG |
| 35 | USF2 | -476 CAGGTGTGAG -467-1026 GCCACACCTG -1017-1783 CTCACACCTG -1774 | AGGTCACCTG |
| 36 | VDR | -641 GTTCAAGCG -633 | CGGGTGAAC |
| 37 | XBP-1 | -1645 ATGCCT -1640 | ATGACG |
| 38 | YY1 | -7 CCAT -4-144 CCAT -141-358 CCAT -355-538 CCAT -535-994 CCAT -991-1558 CCAT -1553-1581 CCAT -1578-1689 CCAT -1686-1893 CCAT -1890-1949 CCAT -1946 | CCAT |