

All sequences were checked by TRANSFAC to exclude other Transcription factor binding sites. Standard Restriction sites were excluded also.

BLUE series – only VDR

HB_0015

VDR (GGGKNARNRRGGWSA) V\$VDR_Q3

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-300  
-250 GCACTAGTAATAGCTGGGCAGTAAATGAAAGAAGCGCATGTAAAACCTATT TA  
-200 CCTCCGACCCGGTTAGTATCGACCGTACACAAGCACATAGTTGCGCAGGC  
-150 CTACAAAAGGGGATGCAAGGACATCAGCGTCTAACACATTCAGATGTCGC  
-100 GGGTATATCTACACGGCCTATGCACGTAGTAAGCTT GATC  
-50 TSS
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HB_0016

VDR (GGGKNARNRRGGWSA) V\$VDR_Q3

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TAGC ACTAGT  
AATAGCTGGGCAGTAAATGAAAGAAGCGCATGTAAAACCTATTCCTCCGACCCGGTTAGTATCGACCGT  
ACACAAGCACATAGTTGCGCAGGCCTACGAAGGGGGATGCAAGGACATCAGCGTCTAACACATTCAGA  
TGTGGGGATGCAAGGACAGCCCCATGCGTACTTGCC  
AAGCTT GATC
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HB_0017

VDR (GGGKNARNRRGGWSA) V\$VDR_Q3

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TAGC ACTAGT  
AATAGCTGGGCAGTAAATGAAAGAAGCGCATGTAAAACCTATTCCTCCGACCCGGTTAGTATCGACCGT  
ACACAAGCACATAGTTGCGCAGGCCTACGAAGGGGGATGCAAGGACATCAGCGTCTAACACATT  
CAGATGTCGCGGGTATATCTACACGGCCTATGCACGTAGTAACATTTTATTCGGT  
GCGAAGGATATCAAGCTCACAGCACCTGTCCCTACGCCTCAGATCGCTAGGATA  
TGTAAGTGCAGGCAGCTTCGCGGAAACATATCCATCGGAGGCATAGAGTACCT  
CGGTAGCATATCAAGTCCTGCCCCATGCGTACTTGCCCCTGCACACGGGGATG  
CAAGGACACCGATATCTGAGTATTTGACTAGAGGGGGATGCAAGGTCACCTAAT  
ACCATTTTCACT AAGCTT GATC
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HB_0018

VDR (GGGKNARNRRGGWSA) V\$VDR_Q3

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TAGC ACTAGT  
AATAGCTGGGCAGTAAATGAAAGAAGCGCATGTAAAACCTATTCCTCCGACCCGGTTAGTATCGACCGT  
ACACAAGCACATAGTTGCGCAGGCCTACGAAGGGGGATGCAAGGACATCAGCGTCTAACACATTCAGAT  
GTCGCGGGTATATCTACACGGCCTATGCACGTAGTAACATTTTATTCGGTGCGAAGGATATCAAGCTC  
ACAGCACCTGTCCCTACGCCTCAGATCGCTAGGATATGGTAAGTGCAGGCAGCTTCGCGGAAACATAT  
CCATCGGAGGCATAGAGTACCTGGGGATGCAAGGACACCGGGTGCATCGTAAATGCCCCATGCGTAC  
GGGGATGCAAGGACAGCTAGTCTTATGAGGGTAAAGAGTGGGGATGCAAGGTCATTGCCTACCATTTT  
CACT AAGCTT GATC
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RED series – VDR AND AP2

HB_0019

VDR (GGGKNARNRRGGWSA) V\$VDR_Q3

AP-2 (MKCCCSCNGGCG) V\$AP2_Q6

TCCC ACTAGT

AATAGCTGGGCAGTAAATGAAAGAAGCGCATGTAAAAC TATTCCTCCGACCCGGTTAGTATCGACCGT
ACACAAGCACATAGTTGCGCAGGCCTACGAA**GGGGATGCAAGGACA**TCAGCGTCTAACACATTCAGAT
GTCGCGGGTATATCTACACGGCCTATGCACGTAGTAACATTTTATTCGGTGCGAAGGATATCAAGCTC
ACAGCACCTGTCCCTACGCCTCAGATCGCTAGGATATGGTAAGTGCAGGCAGCTTCGCGGAAACATAT
CCATCGGAGGCATAGAGTACCT**GGGGATGCAAGGACA**CACGGGTGCATCGTAAATGCCCCATGCGTAC
TTG**AGCCCCCTGGCG**GTTAGTCTTATGAGGGTAAAGAGT**GGGGATGCAAGGTCA**TTGCCTACCATTTT
CACT AAGCTT GATC

HB_0020

VDR (GGGKNARNRRGGWSA) V\$VDR_Q3

AP-2 (MKCCCSCNGGCG) V\$AP2_Q6

TCCC ACTAGT

AATAGCTGGGCAGTAAATGAAAGAAGCGCATGTAAAAC TATTCCTCCGACCCGGTTAGTATCGACCGT
ACACAAGCACATAGTTGCGCAGGCCTACGAA**AGCCCCCTGGCG**GCAGAATAGACACACGGGCCGCTTG
GCGAATTTGCAGGGTAGTTATTTGATCCTCAGTTCGCTATCTCACAGA**GGGGATGCAAGGACA**TCAG
CGTCTAACACATTCAGATGTCGCGGGTATATCTACACGGCCTATGCACGTAGTAACATTTTATTCGGT
GCGAAGGATATCAAGCTCACAGCACCTGTCCCTACGCCTCAGATCGCTAGGATATGGTAAGTGCAGGC
AGCTTCGCGGAAACATATCCATCGGAGGCATAGAGTACCT**GGGGATGCAAGGACA**CACGGGTGCATCG
TAAATGCCCCATGCGTACTTG**AGCCCCCTGGCG**TGCATCCTACAAGCGGAGAGCTAG**GGGGATGCAAG**
GACAGCGAGTCTTATGAGGGTA AAGCTT GATC

GREEN series – VDR AND WT1

HB_0021

VDR (GGGKNARNRRGGWSA) V\$VDR_Q3

WT1 (SMCNCCNSC) V\$WT1_Q6

TCCC ACTAGT

AATAGCTGGGCAGTAAATGAAAGAAGCGCATGTAAAAC TATTCCTCCGACCCGGTTAGTATCGACCGT
ACACAAGCACATAGTTGCGCAGGCCTACGAA**GGGGATGCAAGGACA**TCAGCGTCTAACACATTCAGAT
GTCGCGGGTATATCTACACGGCCTATGCACGTAGTAACATTTTATTCGGTGCGAAGGATATCAAGCTC
ACAGCACCTGTCCCTACGCCTCAGATCGCTAGGATATGGTAAGTGCAGGCAGCTTCGCGGAAACATAT
CCATCGGAGGCATAGAGTACCT**GGGGATGCAAGGACA**CACGGGTGCATCGTAAATGCCCCATGCGTAC
TTGCCCTGCATCC**ccctcctc**CGAGTACTACGCATCGA**GGGGATGCAAGGACA**TCTGTGCACACTA
TGGTT
AAGCTT GATC

HB_0022

VDR (GGGKNARNRRGGWSA) V\$VDR_Q3

WT1 (SMCNCCNSC) V\$WT1_Q6

TCCC ACTAGT

AATAGCTGGGCAGTAAATGAAAGAAGCGCATGTAAAAC TATTCCTCCGACCCGGTTAGTATCGACCGT
ACACAAGCACATAGTTGCGCAGGCCTACGAA**GGGGATGCAAGGA**
CATTCAGCGTCTAACACATTCAGATGTCGCGGGTATATCTACACGGCCTATGCACGTAGTAACATTTTA
TTCGGTGCGAAGGATATCAAGCTCACAGCACCTGTCCCTACGCCTCAGATCGCTAGGATATGGTAAGT
GCAGGCAGCTTCGCGGAAACATATCCATCGGAGGCATAGAGTACCT
GGGGATGCAAGGACACACGGGTGCATCGTAAATGCCCCATGCGTACTTGCCCTGCATCC**ccctcct**
cCGTACTACGCATCGAGT**GGGGATGCAAGGACA**TGCACCGG**ccccctgc**

AAGCTT GATC

ORANGE series – VDR AND WT1 AND AP-2

HB_0023

VDR (GGGKNARNRRGGWSA) V\$VDR_Q3

AP-2 (MKCCCSCNNGCG) V\$AP2_Q6

WT1 (SMCNCCNSC) V\$WT1_Q6

TCCC ACTAGT

AATAGCTGGGCAGTAAATGAAAGAAGCGCATGTAAAACCTATTCCTCCGACCCGGCCAGTAT**CCCTCC**
TCCTTCAGCGTCTAACACATTCAGATGTCGCGGGTATATCTACACGGCCTATGCACGTAGTAACATTTT
ATTCGGTGCGAAGGATATCAAGCTCACAGCACCTGTCCCTACGCCTCAGATCGCTAGGATATGGTAAG
TGCAGGCAGCTTCGCGGAAACATATCCATCGGAGGCATAGAGTACCTCGGTAGCATATCAAGTCGCAC
GGGTGCATCGTAAATGCCCATGCGTACTTGCCCCTGCATCCTACAAGCGGAGAGCTAGGTCTAAGAG
ATGACGAAGATATGTTCCCTGCTACGCTCCCCGCAACCTTGGCCCGGCCGGCCTCAAGGCG**AGCCCC**
CTGGCGTGCAGTCTTATGAGGGTAAAGAGTACTACGCATCGAGTCTAGCAAGTCGTTTCAGCTATGAG
ATCCAAGTCTGC**GGGGATGCAAGGTCA**TTGCCTACCATTTTCACTATGACCGTCTGTGCACACTATGG
TACTGGTCAAGACTACATCAAATCGAAGATAGCATTTGGAGCGACATCGTAATGCCCGGGTCATAAG
CCTCGTCCCGCGCAGCTACGATCACTGCATGGTCCAACCGAGAACGAATTTAGATACGATGGTTCCG
GAT**GGGGATGCAAGGACA**AGCCGATATCTGAGTATTTGACTAGACCTTAATCA**AGCCCCCTGGCG**TGTC
TAGCAGATATTTAGGCGACT**GGGGATGCAAGGACA**GTATGCCGG**CCCCCTGC**
AAGCTT GATC

NEGATIVE CONTROLS

HB_0024

VDR (GGGKNARNRRGGWSA) V\$VDR_Q3

TCCC ACTAGT

CCGGTTAGTATCGACCGTACACAAGCACATAGTTGCGAGTCC**GGGGATGCAAGGACA**CTACGAAGCAG
AATAGACACACGGGCCGCTTGGCGAATTTGCAGGGTAGTTATTTGATCCTCAGTTTCGCTATCTCACAG
AAAAAATTCAGCCTGCGCTAGGGCTCAGCGTCTAACACATTCAGATGTCGCGGGTATATCTACACGG
CCTATGCACGTAGTAACATTTTATTCGGTGCGAAGGATATCAAGCTCACAGCACCTGTCCCTACGCCT
CAGATCGCTAGGATATGGTAAGTGCAGGCAGCTTCGCGGAAACATATCCATCGGAGGCATAGAGTACC
TCGGTAGCATATCAAGTCC**GGGGAAGCAAGGACA**CACGGGTGCATCGTAAATGCCCATGCGTACTTG
CCCCTGCATCCTACAAGCGGAGAGCTAGGTCTAAGAGATGACGAAGATATGTTCCCTGCTACGCTCCC
CGCAACCTTGGCCCGGCCGGCCTCAAGGCGTGTGGAGCTCTGTACATGTCCAATCAGGGTCCAATG
CGATCCTGCATTGTTCCGCTGGCTGTAGGGTTAGTCTTATGAGGGTAAAGAGTACTACGCATCGAGTC
TAGCAAGTCGTTTCAGCTATGAGATCCAAGTCTGCGCCGATATCTGAGTATTTGACTAGACCTTAATC
ATGTCTAGCAGATATTTAGGCGTCTGTATGATCAGTCTTTGCATCGGGCATATACGTATCTCCCGGAT
ACGCTATATGTTTCGCAAGGGAGAGGTTGAATACCATTTTCACTATGACCGTCTGTGCACACTATGGTT
ACTGGTCAAGACTACATCAAATCGAAGATAGCATTTGGAGCGACATCGTAATGCCCGGGTCATAAGCC
TCGTCCCGCGCAGCTACGATCACTGCATGGTCCAACCGAGAACGAATTTAGATACGATGGTTCCG
AAGCTT GATC

HB_0025

TCCC ACTAGT

AATAGCTGGGCAGTAAATGAAAGAAGCGCATGTAAAACCTATTCCTCCGACCCGGTTAGTATCGACCGT
ACACAAGCACATAGTTGCGCAGGCCTACGAAGCAGAATAGACACACGGGCCGCTTGGCGAATTTGCAG
GGTAGTTATTTGATCCTCAGTTCGCTATCTCACAGAAAAAATT CAGCCTGCGCTAGGGCTAGGTCAG
CGAATGGGGATGCAAGGACA AACACATT CAGATGTCGCGGGTATATCTACACGGCCTATGCACGTAGT
AACATTTTATTCGGTGCGAAGGATATCAAGCTCACAGCACCTGTCCCTACGCCTCAGATCGCTAGGAT
ATGGTAAGTGCAGGCAGCTTCGCGGAAACATATCCATCGGAGGCATAGAGTACCTCGGTAGCATATCA
AGTCCGTGCGGTGCATCGTAAATGCCCATGCGTACTTGCCCCTGCATCCTACAAGCGGAGAGCTAGG
TCTAAGAGATGACGAAGATATGTTCCCTGCTACGCTCCCCGCAACCTTGGCCC GGCCGGGCCTCAAGG
CGTGTGGGAGCTCTGTACATGTCCAATCAGGGTCCAATGCGATCCTGCATTGTTCCGCTGGCTGTAGG
GTTAGTCTTATGAGGGTCTAAAGAGTACTACGCATCGAGTCTAGCAAGTCGTTTCAGCTATGAGATCC
AAGTCTGCGCCGATATCTGAGTATTTGACTAGACCTTAATCATGTCTAGCAGATATTTAGGCGTCTGT
ATGATCAGTCTTTGCATCGGGCATATACGTATCTCCCGGATAAACTATATGTTC
AAGCTT GATC