S4 Table. Putative SREs found in promoter regions of genes involved in ergosterol biosynthesis, *PdsreA* and *PdsreB*[a]

Gene	Putative SRE	Position	
		Start	Stop
ERG10A	GTCATGACATT	-751	-740
HMG2	ATGGAATGATG	-1763	-1752
ERG12	ATGTGCTGACC	-1903	-1892
	ATCATCCCACC	-1104	-1093
	ATAATCCCATC	-1091	-1080
IDI1	ATGGGCTGATA	-1954	-1943
	ATCTTGACACC	-311	-300
ERG1	ATCAGTCCACT	-239	-228
	GTCACGCCACC	-157	-146
CYP51A	GTGGGAAGATA	-1804	-1793
	TGGCACCATCC	-1758	-1747
	ATGATGCCAGC	-965	-954
	ATGGCCTGACC	-132	-121
CYP51B	GTGGCGTGATA	-391	-380
ERG25	GTGGGGTGATC	-480	-469
	GTGGCCTTACC	-447	-436
ERG27	GTCGCCTGACG	-965	-954
ERG3B	ATGAGTACACT	-1288	-1277
ERG4B	TTGTGCTGATC	-1001	-990
PdsreA	ATCATACGACC	-636	-626
PdsreB	GTCACCCCACT	-1793	-1783

[a] Sequences of putative SREs in the promoters of genes in egosterol biosynthetic pathway are listed together with their position relative to the start codon of ORF. The search was based on the SRE motif found in *A. fumigatus*.