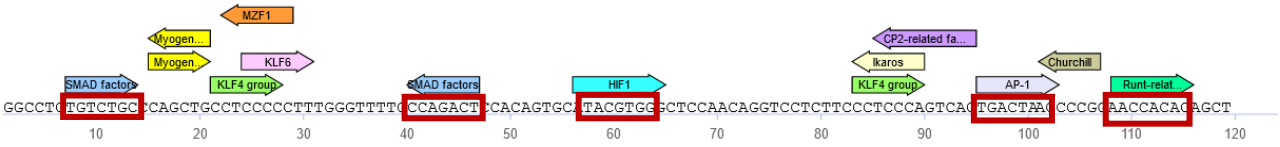
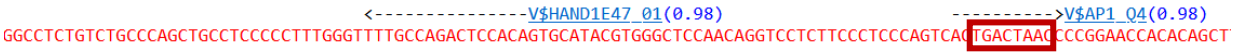
Transcription factor binding site prediction with MATCH™: TRANSFAC® professional (A) vs. TRANSFAC® public (B)

A: Analysis result with the MATCH™ tool in TRANSFAC® prof.:



B: Analysis result with the MATCH™ tool on gene-regulation.com using TRANSFAC® public data :



Analysis of 120 nucleotides of the human VEGFA promoter with the MATCH™ tool in TRANSFAC professional predicts fourteen sites for eleven different transcription factors **(Fig. A).** At least for four of these factors, **SMAD, HIF1, AP-1 and Runx2** (predicted binding sites framed in red in the figure above), supporting evidence has been published as referenced in the TRANSFAC® professional database: "Our findings indicate that **Smad** directly binds to Vegfa chromatin and represses Vegfa transcriptional activity." (PMID: 23863481) **"**Site-directed mutational analysis of the VEGF gene promoter revealed that an **HIF-1** binding site (HBS) and its downstream HIF-1 ancillary sequence (HAS) within the HRE are required as cis-elements for the transcriptional activation of VEGF by either hypoxia or nitric oxide (NO).**"** (PMID: 11056166) **"**A gel mobility shift assay showed that the inhibitory effect of CSA was associated with decreased **AP-1** binding activity to the VEGF promoter, in a cAMP-dependent manner." (PMID: 12215224) **"**Physical and functional interactions between **Runx2** and HIF-1α induce vascular endothelial growth factor gene expression." (PMID: 21793044)

With MATCH™ on the public website, at the same cut-offs, only one of these sites (**AP-1**) is detected **(Fig. B).**

Parameters:
Analyzed sequence: chr6:43769178..43769297 (hg38)
Cut-offs: matrix similarity = 0.97; core similarity = 1.00; Exclusion of low-quality matrices
Fig. A: MATCH™ in TRANSFAC® Release 2022.1; Profile: vertebrate_non_redundant.prf
Fig. B: MATCH™ public 1.0 with library of positional weight matrices of TRANSFAC® public from 2005; Profile: vertebrate matrices