



## *Supplementary materials*

# **Contribution of the STAT family of transcription factors to the expression of the serotonin 2B (HTR2B) receptor in human uveal melanoma**

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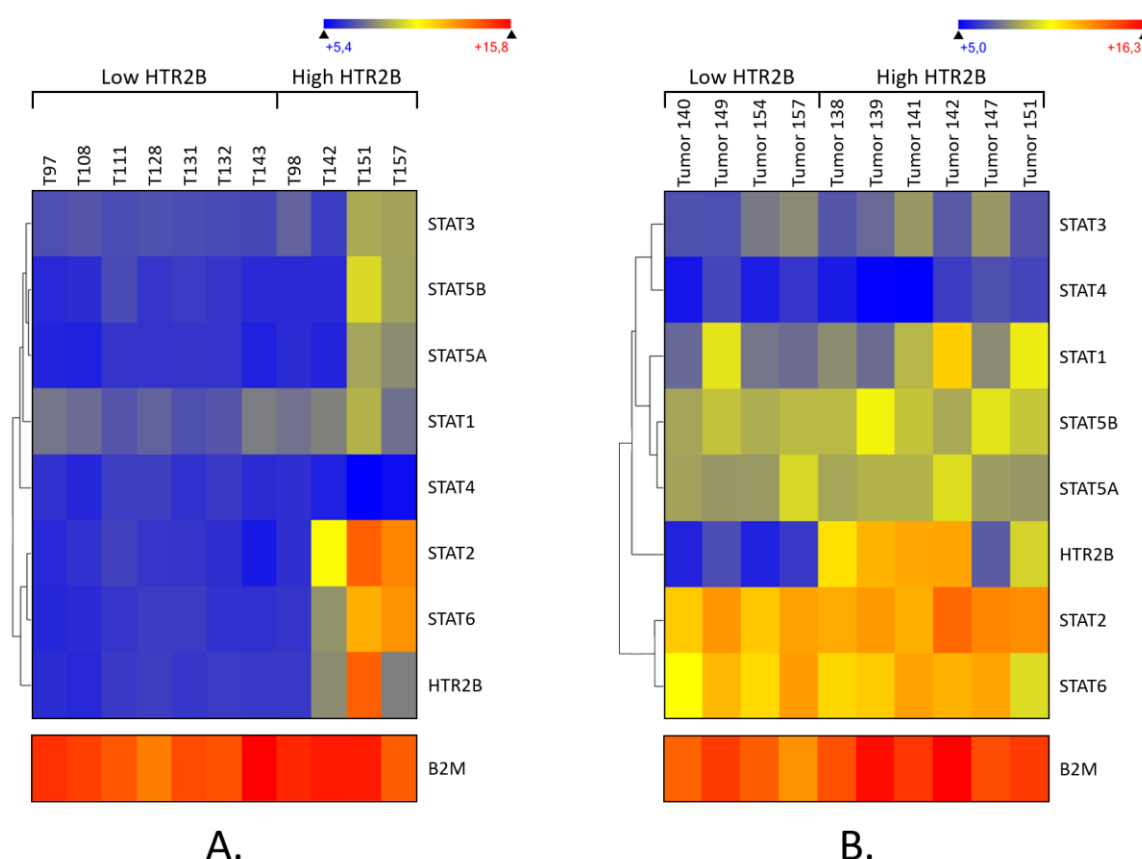
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**Supplementary Figures**

- A.** STAT DRE: TTC (N)<sub>2-4</sub> GAA
- 1862...TACT **TTC TACT tAA** AGTG...-1846  
 -1890...TACG **TTC CTTA GAc** ATTA... -1673  
 -1742...ATGC **TTC CCA tAA** CTTG... -1726  
 -1491...TTAT **TTC ATA cAA** GTCT... -1475  
 -1473...TCTT **TTC ACT GgA** TATA... -1457  
 -1409...TGCC **TTC ATAA GcA** CAGA... -1392  
 -1244...CAGG **TTC ATG cAA** TCCT... -1228  
 -602...CCAA **TTt TCT GAA** ATAA... -686  
 -559...TATT **TTC TC cAA** CGTA... -545  
 -244...ATTT **TTC TC aAA** TGTG... -229
- B.** STAT DRE: TTC (N)<sub>2-4</sub> GAA
- 990...CATA **TTC CT GAA** TAGA... -975  
 -950...TGAT **TTC TCTT GAA** TATT... -933  
 -288...AATC **TTC AAA GAA** TGAA... -272

**Supplementary Figure S1.** Putative target sites for STAT proteins identified in the promoter and 5'-flanking sequence of the HTR2B gene. **(A)** Predicted sites (red sequences) that diverge from the consensus DRE by one base pair (identified in blue). **(B)** Putative sites that perfectly match the canonical STAT DRE. Numbers refer to the position of the sequences relative to the HTR2B putative mRNA start site. Thirteen STAT target sites could be identified along the entire promoter and 5'-flanking sequence of the HTR2B gene of which three (at positions -982, -942 and -280 relative to the HTR2B mRNA start site) perfectly match the STAT consensus sequence.



**Supplementary Figure S2.** Supplementary figure. Expression of STAT genes in uveal melanoma. **(A)** Heatmap representation of HTR2B and all the STAT genes expressed by UM cell lines. Data show the individual transcriptome profile extracted from UM cell lines that express either low (T97, T108, T111, T128, T131, T132 and T143 cell lines) or high levels of HTR2B (T98, T142, T151 and T157 cell lines). Moderate to high levels of STAT gene expression could only be observed in HTR2B-expressing UM cell lines. **(B)** Heatmap representation of HTR2B and all the STAT genes expressed by UM primary tumors. Data show the individual transcriptome profile extracted from UM primary tumors with either low (tumors 140, 149, 154 and 157) or high HTR2B levels (tumors 138, 139, 141, 142, 147 and 151). A dark blue color corresponds to a very low level of expression whereas high levels appear in yellow/red. Data are also presented for the housekeeping gene  $\beta$ -2-microglobulin (B2M; control).

## Supplementary Tables

### Supplementary Table S1. DNA sequence of synthetic oligonucleotides

#### Oligonucleotides used as labeled probes or competitors in the EMSAs

Oligonucleotide	Top strand (5'-3')
	Bottom strand (5'-3')
AP-1	GATCCCCGCGTTGAGTCATTCGCCTC GATCGAGGCGAATGACTCAACGCGGG
NFI	TTATTTTGGATTGAAGCCAATATGAG CTCATATTGGCTTCAATCCAAAATAA
Sp1	GATCATATCTGCGGGGCGGGGCAGACACAG GATCCTGTGTCTGCCCCGCCCCGCAGATAT
STAT -280	GATCGGCAGAATCTTCAAAGAATGAAACC GATCGGTTTCATTCTTTGAAGATTCTGCC
STAT 280 mutant	GATCGGCAGAATCAACAAATAATGAAACC GATCGGTTTCATTATTTGTTGATTCTGCC

#### Oligonucleotides used for site-directed mutagenesis

##### WT Sequence

5' GGC TTT TAA AAC GGC AGA ATC **TTC** AAA **G**AA TGA AAC CTC TAA AAT AGC 3'

##### Mutated STAT putative binding Site

5' GGC TTT TAA AAC GGC AGA ATC **AAC** AAA **T**AA TGA AAC CTC TAA AAT AGC 3'