Supplementary materials

Supplementary images



Figure S1. STAT3 inhibition hampers scratch reoccupation in melanoma cell cultures. A Representative pictures and relative quantification of 1205Lu cells treated with vehicle, 5 μ M AZD1480 or 12.5 μ M PD98059 for 24 hours. B Representative pictures and relative quantification of B16F10 cells treated with vehicle, 5 μ M AZD1480 or 12.5 μ M PD98059 for 24 hours. Mean ± SEM. * p < 0.05, **p < 0.01.

Danio Xenopus Homo Mus	GNGGRTNSDASLIVTEELHLITFETEVYHQGLKIDLETHSLPVVVISNICQMPNAWASIL GNGGRANCDASLIVTEELHLITFETEVYHQGLKIDLETHSLPVVVISNICQMPNAWASIL GNGGRANCDASLIVTEELHLITFETEVYHQGLKIDLETHSLPVVVISNICQMPNAWASIL GNGGRANCDASLIVTEELHLITFETEVYHQGLKIDLETHSLPVVVISNICQMPNAWASIL *****:*.	479 478 478 478
Danio Xenopus Homo Mus	WYNMLTNHPKNVNFFTKPPVGTWDQVAEVLSWQFSSTTKRGLTIEQLTTLAEKLLGPCVN WYNMLTNNPKNVNFFTKPPIGTWDQVAEVLSWQFSSTTKRGLSIEQLTTLAEKLLGPGVN WYNMLTNNPKNVNFFTKPPIGTWDQVAEVLSWQFSSTTKRGLSIEQLTTLAEKLLGPGVN WYNMLTNNPKNVNFFTKPPIGTWDQVAEVLSWQFSSTTKRGLSIEQLTTLAEKLLGPGVN *******:*****************************	539 538 538 538
Danio Xenopus Homo Mus	YSGCQITWAKFCKENMAGKGFSFWVWLDNIIDLVKKYILALWNEGYIMGFISKERERAIL YSGCQITWAKFCKENMAGKGFSFWVWLDNIIDLVKKYILALWNEGYIMGFISKERERAIL YSGCQITWAKFCKENMAGKGFSFWVWLDNIIDLVKKYILALWNEGYIMGFISKERERAIL YSGCQITWAKFCKENMAGKGFSFWVWLDNIIDLVKKYILALWNEGYIMGFISKERERAIL ************************************	599 598 598 598
Danio Xenopus Homo Mus	SPKPPGTFLLRFSESSKEGGITFTWVEKDINGKTQIQSVEPYTKQQLNSMSFAEIIMGYK STKPPGTFLLRFSESSKEGGITFTWVEKDISGKTQIQSVEPYTKQQLNNMSFAEIIMGYK STKPPGTFLLRFSESSKEGGVTFTWVEKDISGKTQIQSVEPYTKQQLNNMSFAEIIMGYK STKPPGTFLLRFSESSKEGGVTFTWVEKDISGKTQIQSVEPYTKQQLNNMSFAEIIMGYK * ***********************************	659 658 658
Danio Xenopus Homo Mus	IMDATNILVSPLVYLYPDIPKEEAFGKYCRPETHPDTEFPDTGCVTQPYLKTKFICVTPC IMDATNILVSPLVYLYPDIPKEEAFGKYCRPESQEHQEPTDPG-STAPYLKTKFICVTPT IMDATNILVSPLVYLYPDIPKEEAFGKYCRPESQEHPE-ADPG-SAAPYLKTKFICVTPT IMDATNILVSPLVYLYPDIPKEEAFGKYCRPESQEHPE-ADPG-SAAPYLKTKFICVTPT ***********************************	719 717 716 716
Danio Xenopus Homo Mus	PSVFMDFPDSELLGNGFPGTNSGNTSDLFPMSPRTLDSLMHNEAAEANPGPLESL TCSSTLDLPMSPRTLDSLMQFPGEGADSSAGNQFETL TCSNTIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESL TCSNTIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESL . : :***********: : :*:*	774 754 755 755
Danio Xenopus Homo Mus	TLDMELSSDHASPMREGFAASTVSDMDTCRNA 806 TFDMELTSECASSPM 769 TFDMELTSECATSPM 770 TFDMDLTSECATSPM 770 *I**!*!*: *: *:	

Figure S2. Alignment of *Danio rerio, Xenopus laevis, Mus musculus* and *Homo sapiens* **STAT3 amino acid sequences.** The Y708, S729 and S751 phosphorylation sites are respectively highlighted in blue, orange and green. S729 belongs to a zebrafish-specific domain, whereas zebrafish S751 corresponds to S727 in frog, mouse and human.



Figure S3. Representative pictures and quantification of regenerated area of wild type zebrafish tail fins cut at 3-dpf and treated for 2 days either with vehicle or 0.1 μ M AZD1480. Mean \pm SEM. * p < 0.05.



Figure S4. Generation of *stat3*^{s→A729} **zebrafish knock-in line. A** Sequence of the donor DNA used to generate the KI. The mutation (gcg) is highlighted in red and is flanked by a 27-nt and a 97-nt homology arms. **B** Representative picture of allele-specific PCRs routinely performed to genotype KI fish: heterozygotes are positive for both alleles, whereas homozygotes are positive for only one. **C** Fluorescence quantification of *Tg*(*7xStat3-Hsv.Ul23:EGFP*)^{*ia28*} intestines of 6-dpf *stat3*^{S729/S729}, *stat3*^{S729/A729} and *stat3*^{A729/A729} larvae. Scale bar: 100 µm. **D** Fluorescent image of *Tg*(*7xStat3-Hsv.Ul23:EGFP*)^{*ia28*} intestines of 12.5 µM PD98059 for 3 days. Scale bar: 100 µm. **E** Expression level of *stat3*, *socs3a*, *cebpb*, and *mt-nd2* in 6-dpf *stat3*^{S729/S729} larvae. **F** Regeneration rate of 6-dpf *stat3*^{S729/S729} and *stat3*^{A729/A729} larvae. **F** Regeneration rate of 6-dpf *stat3*^{S729/S729} and *stat3*^{A729/A729} larvae.



Figure S5. Schematic representation of samples collected for vitamin D effects on zebrafish larvae. A <u>Whole body samples</u>: we cut 3-dpf zebrafish larvae tail fins and we treated them for 2 days with 0.5 nM vitamin D, at the end of the treatment larvae were homogenized to extract RNA. B <u>Tail</u> <u>samples</u>: we treated 3-dpf larvae with 0.5 nM vitamin D for 2 days and at the end of the treatment we cut the tail (from the anus to the distal part of tail fin) of each treated larva; we pooled 20 tails for each condition. C <u>Regenerated tail samples</u>: we cut 3-dpf zebrafish larvae tail fins and we treated them for 2 days with 0.5 nM vitamin D, at the end of the treatment we cut the tail (from the anus to the distal part of tail fin) of each treated larva; we pooled 20 tails for each condition. D. Fluorescence quantification of *Tg(7xStat3-Hsv.Ul23:EGFP)^{ia28}* intestines of 5-dpf treated with vitamin D for 48h and relative control. Scale bar: 200 µm. Mean ± SEM.



Figure S6. Western blot images. A Western blot analysis of ERK 1/2, pERK1/2, STAT3, pSTAT3 (Y705 and S727) protein in L929 cells treated either with vehicle or 200 nM vitamin D for 24 hours. n=3 biological replicates. **B** Expression level of *Mapk1* and *Mapk3* in L929 cells treated either with vehicle or 200 nM vitamin D for 24 hours. Mean \pm SEM. * p < 0.05.

Supplementary tables

Table 1. Primers for RT-qPCR

Gene	Forward	Reverse
z-actb	TGGGTATGGAATCTTGCGGT	GTGGGGCAATGATCTTGATCT
z-stat3	TGCCACCAACATCCTAGTGT	GCTTGTTTGCACTTTTGACTGA
z-socs3a	GGAAGACAAGAGCCGAGACT	GCGATACACACCAAACCCTG
z-vegfa	AAAAGAGTGCGTGCAAGACC	TTTCGTGTCTCTGTCGGGAC
z-cebpb	CCAAAAGTAACGGGCGACAC	ATCTTCCCTTACCTGACGGC
z-ucmaa	GTTTTCGTGCCAGCATCTG	GTGTTCGTTGCTCTGTTCCT
z-cyp26b1	GCTGTCAACCAGAACATTCCC	GGTTCTGATTGGAGTCGAGGC
z-sp7	AACCCAAGCCCGTCCCGACA	CCGTACACCTTCCCGCAGCC
z-mpx	AGGTGTTGCTGAGCCTTTTG	ACCACAACCTATCGCCATCT
z-il4	GCAGGAATGGCTTTGAAGGG	TCCTTCATTGTGCATTCCCC
z-il21	AGTGCAAATCATGTGAAGCGT	GACTCTTCAGGTCTCTACGCT
z-cyp24a1	GCCTGTTGAGCTCCACAAAA	CTGCAGGTTCTTGTCGATGT
z-vdrb	AGACTCAAGCGTTGCCTAGA	GCCTCCTCATCCTTCCTTCT
z-vdra	GGACCAGACTTCAAATACTGCA	TCAGCTTCTTCAGACCAACCT
z-rarga	ATTCCGCCAGAGAGCTATGA	TAGGCCCAGGTCTAGCTGAA
z-mt-nd2	GCAGTAGAAGCCACCACAAA	GCTAGACCGATTTTGAGAGCC

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m-Actb	CTAAGGCCAACCGTGAAAAG	ACCAGAGGGCATACAGGGACA
m-Stat3	TGTTGGAGCAGCATCTTCAG	GAGGTTCTCCACCACCTTCA
m-Socs3a	ATTTCGCTTCGGGACTAGC	AACTTGCTGTGGGTGACCAT
m-Mapk1	CGCTACACCAACCTCTCGTA	AGGTCTGGTGCTCAAAAGGA
m-Mapk3	ATAGGCATCCGAGACATCCT	ATGTGGTCATTGCTCAGCTG

Table 2. Primers for genotyping PCR

Locus	Forward	Reverse
stat3 ex14	GGCCTCTCTGATAGTGACCG	AGTTGTGCTTAGACGCGATC
stat3 ex23	GCGATTTGTTCCCAATGTCG (FW WT)	CGTCATGACTCACCGAGAGG
	GCGATTTGTTCCCAATGgca (FW AA)	
stat3 ex22	TCATGGACTTCCCGGACAGT (FW WT)	CCCCCTCATGGACAAAAGAAC
	TCATGGACTTtCCGGACgcg (FW AA)	

Table 3. Sequences of gRNA used to generate *stat3* KI lines

Locus	Forward
stat3 ex23	AUGAGAGAGUCGAGCGUGCG
stat3 ex22	AGUGAGCUGCUUGGGAA