

## Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our [Editorial Policies](#) and the [Editorial Policy Checklist](#).

### Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a Confirmed

- The exact sample size ( $n$ ) for each experimental group/condition, given as a discrete number and unit of measurement
- A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- The statistical test(s) used AND whether they are one- or two-sided  
*Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
- A description of all covariates tested
- A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- For null hypothesis testing, the test statistic (e.g.  $F$ ,  $t$ ,  $r$ ) with confidence intervals, effect sizes, degrees of freedom and  $P$  value noted  
*Give  $P$  values as exact values whenever suitable.*
- For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- Estimates of effect sizes (e.g. Cohen's  $d$ , Pearson's  $r$ ), indicating how they were calculated

*Our web collection on [statistics for biologists](#) contains articles on many of the points above.*

### Software and code

Policy information about [availability of computer code](#)

**Data collection** Imaging was done using the Leica Application Suite Software (4.1). Western blots were imaged using Amersham Imager 680. qRT-PCRs using Roche LightCycler480 II. ChIP libraries were sequenced as 75 bp Single-Read on Illumina NextSeq 550 platform High-Output. SS18-SSX and H2AK119ub1 CUT&RUN libraries were sequenced as 75 bp Paired-End reads on Illumina NextSeq 550 platform Mid-Output. HA-eGFP-SS18, HA-eGFP-SS18-SSX1 and HA-eGFP-SSX-C CUT&RUN libraries and Native H2AK119ub1 calibrated ChIP were sequenced as 50bp Paired-End reads on NovaSeq 6K SP. RNA libraries were sequenced on a NovaSeq 6K Paired-End 100 S4

**Data analysis** For ChIP-Seq analysis: Raw reads were trimmed for quality and Illumina adapter sequences using Trim Galore! (Galaxy Version 0.6.7+galaxy0), then aligned to the human genome assembly Hg38 using Bowtie2 (Galaxy Version 2.4.2+galaxy0). ChIP signals were normalised to their respective inputs using the pileup function from MACS2 callpeak (Galaxy Version 2.1.1.20160309.6) using corresponding input for background normalization. To visualize ChIP-Seq tracks, normalized bigWig files were generated with Wig/BedGraph-to-bigWig converter (Galaxy Version 1.1.1).

For the Cut and Run: Paired-end reads were aligned to the T2T or E.coli K12, MG1655 reference genome using Bowtie2 (Galaxy Version 2.4.2+galaxy0). Genome coverage files were generated using bamCoverage (Galaxy Version 3.5.1.0.0).

Image analysis was done using the Fiji software (2.9.0).  
 Statistics and graphs were done using Excel (16.75.2) or Prism (9.4.0).  
 R (versions 3.6.0 to 4.2.1; <https://www.r-project.org/>).  
 Flow Cytometry analysis: FlowJo (v10.9.0)  
 Gene editing efficiency: Tide (v3.3.0)  
 RNA-seq analysis: IDEP.93 <http://bioinformatics.sdstate.edu/idep93/>

Gene Tiling screen: MAGeCK (0.5.9) and ProTiler: (1.0.2) were run on Python (3.7.0)

I used python 3.7.0

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [guidelines for submitting code & software](#) for further information.

## Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

Re-analysed HA-SS18-SSX1 and KDM2B ChIP sequencing data originates from GEO accession number GSE108929. The GEO accession number for all data created in this paper is reported under GSE205955. Genome assembly used for ChIP and Cut&Run was hg38, for RNAseq hg19. Proteomic data is provided as a supplementary table.

## Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research](#).

Reporting on sex and gender	<a href="#">Sex and gender considerations where not relevant for the biological question addressed in this study.</a>
Population characteristics	Patients who underwent surgical excision specimens in the Vancouver General Hospital to which material was archived between 2007 and 2020.
Recruitment	N/A
Ethics oversight	Tissue Microarray construction from anonymized patient primary surgical excision specimens was performed under protocols H18-00524 and H18-02391, approved by the Clinical Research Ethics Board of the University of British Columbia and BC Cancer.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

## Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

Life sciences  Behavioural & social sciences  Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see [nature.com/documents/nr-reporting-summary-flat.pdf](https://nature.com/documents/nr-reporting-summary-flat.pdf)

## Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	The sample size was not predetermined statistically. The sample size, which is listed in the material and method section, was chosen based on expected variance of the experiments and technical limitations.
Data exclusions	No data exclusions was performed.
Replication	All experiments were repeated independently. The number of biological replicates are indicated in the figure legends.
Randomization	Not relevant because the samples were no grouped, as it includes only molecular assays performed in cell lines of known genotype.
Blinding	Blinding was not relevant for this study as there were no prior assumptions about experimental outcomes. All data was collected and processed uniformly regardless of treatment groups

## Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

## Materials &amp; experimental systems

## Methods

n/a	Involved in the study
<input type="checkbox"/>	<input checked="" type="checkbox"/> Antibodies
<input type="checkbox"/>	<input checked="" type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input type="checkbox"/>	<input checked="" type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern

n/a	Involved in the study
<input type="checkbox"/>	<input checked="" type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

## Antibodies

## Antibodies used

anti-NanoLuc, R&D Systems, MAB100261  
 BCoR (C10), Santa Cruz, sc-514576  
 EED (E4L6E) XP® Rabbit mAb, Cell Signaling, #85322  
 Ezh2 (D2C9) XP Rabbit mAb, Cell Signaling, #5246  
 GFP (D5.1) XP® Rabbit mAb, Cell Signaling, #2956  
 HA-tag, Abcam, #9110  
 HA-Tag (6E2) Mouse mAb, Cell Signaling, #23675  
 HA-Tag (C29F4) Rabbit mAb, Cell Signaling, #3724  
 Histone H3 (1B1B2), Cell Signaling, #14269  
 HP1 (E-6), Santa Cruz, sc- 515341  
 PCGF1 (E-8), Santa Cruz, sc-515371  
 SS18-SSX (E9X9V) XP, Cell Signaling, #72364  
 SS18/SSX Antibody, Cell Signaling, #70929  
 SSX (E5A2C), Cell Signaling, #23855  
 β-Actin HRP, Sigma, A3854  
 SYT (a-10), Santa Cruz, sc-365170  
 Tri-Methyl-Histone H3 (Lys27) (C36B11), Cell Signaling, #9733  
 Tri-Methyl-Histone H3 (Lys9) (D4W1U), Cell Signaling, #13969  
 Ubiquityl-Histone H2A (Lys119) (D27C4) XP® Rabbit mAb, Cell Signaling, #8240  
 Acetyl-Histone H3 (Lys27) (D5E4) XP, #8173  
 V5 Tag Monoclonal Antibody (2F11F7), Alexa Fluor 555, ThermoFisher, 2F11F7  
 v5-Probe (E10), Santa Cruz, sc-81594  
 V5-Tag (E9H8O) mAb, Cell Signaling, #80076  
 V5-Taq (D3H8Q) Rabbit mAb, Cell Signaling, #13202  
 Anti-TATA binding protein TBP antibody[mAbcam51841], Abcam, ab300656  
 SMARCC1/BAF155 (D7F8S) Rabbit mAb, Cell Signaling, #11956  
 BRM (D9E8B) XP® Rabbit mAb, Cell Signaling, #11966  
 p300 (D8Z4E), Cell Signaling, #86377S  
 Brg-1 (G-7), Santa Cruz, sc-17796  
 ARID1A/BAF250A (D2A8U) Rabbit, Cell Signaling, #12354  
 BCOR polyclonal antibody, Proteintech, 12107-1-AP

Secondary antibodies  
 ECL Anti-Mouse IgG  
 ECL Anti-Rabbit IgG

## Validation

All antibodies were validated by the manufacturers. Tag antibodies (HA, V5) have been extensively used in the literature. In addition, the majority of primary antibodies were further validated using target-specific knockouts (PCGF1 E-8, EZH2 D2C9, EEDE4L6E, BRM D9E8B) or over-expression of a tagged proteins (NanoLuc MAB100261, BCoR polyclonal antibody, Proteintech, 12107-1-AP, BCoR (C10), Santa Cruz, sc-514576).  
 Antibodies against SS18-SSX and SSX (SS18-SSX (E9X9V) XP, Cell Signaling, #72364 SS18/SSX Antibody, Cell Signaling, #70929 SSX (E5A2C), Cell Signaling, #23855) have been validated by Baranov et al (PMID: 32141887).

p300 (D8Z4E), Cell Signaling, #86377S, Brg-1 (G-7), Santa Cruz, sc-17796, ARID1A/BAF250A (D2A8U) Rabbit, Cell Signaling, #12354 have been used previously in many other studies. See for example PMID: 33651988 (EP300), PMID: 35732731 (BRG1) and PMID: 36435834 (ARID1A).

Antibodies used for histone and histone marks have been extensively used in the literature:  
 Tri-Methyl-Histone H3 (Lys27) (C36B11), Cell Signaling, #9733 (1065 citations)  
 Tri-Methyl-Histone H3 (Lys9) (D4W1U), Cell Signaling, #13969 (112 citations)  
 Ubiquityl-Histone H2A (Lys119) (D27C4) XP® Rabbit mAb, Cell Signaling, #8240 (298 citations)  
 Histone H3 (1B1B2), Cell Signaling, #14269 (137 citations)  
 HP1 (E-6), Santa Cruz, sc- 515341 (more than 100 citations)

## Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

## Cell line source(s)

Human synovial sarcoma cell lines: HS-SY-II (RRID:CVCL\_8719) and SYO-1 (RRID:CVCL\_7146) were obtained from their original

Cell line source(s)	source laboratories. Human osteosarcoma KHOS-240S (RRID:CVCL_2544) and Human Embryonic Kidney HEK293T (RRID:CVCL_0063) were purchased from the American Type Culture Collection (ATCC). ASC52telo, hTERT immortalized adipose derived Mesenchymal stem cells were purchased from ATCC (SCRC-4000). Drosophila SG-4 cell line used for calibrated ChIP was provided by Angelika Feldmann (German Cancer Research Center).
Authentication	HS-SY-II and SYO-I were authenticated via classical STR profiling with the company Multiplexion and by western blot for SS18-SSX1/2 detection. The remaining cell lines (MSCs, HEK293-T, KHOS-240S and SG-4) were obtained authenticated by the manufacturer (ATCC) and by morphology.
Mycoplasma contamination	Cell lines were monthly tested against mycoplasma contamination and remained negative.
Commonly misidentified lines (See <a href="#">ICLAC</a> register)	No misidentified cell lines were used in this study.

## Animals and other research organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research, and [Sex and Gender in Research](#)

Laboratory animals	This study used <i>Mus musculus</i> (C57BL/6J) with a conditional SS18-SSX2-IRES-eGFP allele knocked into the Rosa26 locus. Tamoxifen treatment was performed on 8 weeks old mice. Mice were housed under standard conditions (12 h light/dark cycle) and provided food and water ad libitum. Animals were maintained in a controlled environment of between 21-24°C and 40-60% humidity, and experimental protocols were conducted in accordance with approved and ethical treatment standards of the Animal Care Committee at the University of British Columbia.
Wild animals	No wild animals were used.
Reporting on sex	No sex specific data was used.
Field-collected samples	No field-collected samples were used.
Ethics oversight	Animals were maintained and experimental protocols were conducted in accordance with approved and ethical treatment standards of the Animal Care Committee at the University of British Columbia.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

## ChIP-seq

### Data deposition

- Confirm that both raw and final processed data have been deposited in a public database such as [GEO](#).
- Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

Data access links <i>May remain private before publication.</i>	<a href="https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE205955">https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE205955</a>
Files in database submission	GSM6235997 HSSY, eGFP, input GSM6235998 HSSY, eGFP, HA GSM6235999 HSSY_S SX_input GSM6236000 HSSY_S SX_HA GSM6236001 HSSY_S SXDeltaRD_input GSM6236002 HSSY_S SXDeltaRD_HA GSM6236003 HSSY, IgG GSM6236004 HSSY, MacroH2A2 GSM6236005 HSSY, Control, H2Aub1 GSM6236006 HSSY, Control, HA (SS18-SSX1) GSM6236007 HSSY, PCGF1 knockout, H2Aub1 GSM6236008 HSSY, PCGF1 knockout, HA (SS18-SSX1) GSM6236009 SYOI, IgG GSM6236010 SYOI, Control, H2Aub1 GSM6236011 SYOI, Control, SS18-SSX2 GSM6236012 SYOI, PCGF1 knockout, H2Aub1 GSM6236013 SYOI, PCGF1 knockout, SS18-SSX2

Genome browser session  
(e.g. [UCSC](#))

Here is the link to the updated bigwigs:

[https://dl.dropboxusercontent.com/s/b9ordhxtpcac3gf/HSS\\_cChIP\\_EV\\_H2A.bigwig?dl=0](https://dl.dropboxusercontent.com/s/b9ordhxtpcac3gf/HSS_cChIP_EV_H2A.bigwig?dl=0)  
[https://dl.dropboxusercontent.com/s/xlvs7fhu6uwrrk4/HSS\\_cChIP\\_sgPCGF1\\_H2A.bigwig?dl=0](https://dl.dropboxusercontent.com/s/xlvs7fhu6uwrrk4/HSS_cChIP_sgPCGF1_H2A.bigwig?dl=0)  
[https://dl.dropboxusercontent.com/s/zdv5a4l7zlkpw01/HSS\\_CR\\_EV\\_H2Aub.bigwig?dl=0](https://dl.dropboxusercontent.com/s/zdv5a4l7zlkpw01/HSS_CR_EV_H2Aub.bigwig?dl=0)  
[https://dl.dropboxusercontent.com/s/htjf4d0n9czyfan/HSS\\_CR\\_EV\\_SS18-SSX.bigwig?dl=0](https://dl.dropboxusercontent.com/s/htjf4d0n9czyfan/HSS_CR_EV_SS18-SSX.bigwig?dl=0)  
[https://dl.dropboxusercontent.com/s/yi8cjf4lejxjr5/HSS\\_CR\\_sgPCGF1\\_H2Aub.bigwig?dl=0](https://dl.dropboxusercontent.com/s/yi8cjf4lejxjr5/HSS_CR_sgPCGF1_H2Aub.bigwig?dl=0)  
[https://dl.dropboxusercontent.com/s/8wfyomyzam0rnev/HSS\\_CR\\_sgPCGF1\\_SS18-SSX.bigwig?dl=0](https://dl.dropboxusercontent.com/s/8wfyomyzam0rnev/HSS_CR_sgPCGF1_SS18-SSX.bigwig?dl=0)  
[https://dl.dropboxusercontent.com/s/ecklriqyjtyjh68/HSS\\_CR\\_SXX-C\\_Dox.bigwig?dl=0](https://dl.dropboxusercontent.com/s/ecklriqyjtyjh68/HSS_CR_SXX-C_Dox.bigwig?dl=0)  
[https://dl.dropboxusercontent.com/s/j4n6197q8p8e0yi/HSS\\_CR\\_SXX-C\\_NoDox.bigwig?dl=0](https://dl.dropboxusercontent.com/s/j4n6197q8p8e0yi/HSS_CR_SXX-C_NoDox.bigwig?dl=0)  
[https://dl.dropboxusercontent.com/s/01lv1a8shce6kaz/KHOS\\_CR\\_EV.bigwig?dl=0](https://dl.dropboxusercontent.com/s/01lv1a8shce6kaz/KHOS_CR_EV.bigwig?dl=0)  
[https://dl.dropboxusercontent.com/s/j4kmdt4su6t9w31/KHOS\\_CR\\_SS18.bigwig?dl=0](https://dl.dropboxusercontent.com/s/j4kmdt4su6t9w31/KHOS_CR_SS18.bigwig?dl=0)  
[https://dl.dropboxusercontent.com/s/mzqs2x99k4grdst/KHOS\\_CR\\_SS18-SSX.bigwig?dl=0](https://dl.dropboxusercontent.com/s/mzqs2x99k4grdst/KHOS_CR_SS18-SSX.bigwig?dl=0)  
[https://dl.dropboxusercontent.com/s/rqmxm3e18wuovvd/KHOS\\_CR\\_SXX.bigwig?dl=0](https://dl.dropboxusercontent.com/s/rqmxm3e18wuovvd/KHOS_CR_SXX.bigwig?dl=0)  
[https://dl.dropboxusercontent.com/s/rbop41e9on1l4im/SYOI\\_CR\\_EV\\_H2Aub.bigwig?dl=0](https://dl.dropboxusercontent.com/s/rbop41e9on1l4im/SYOI_CR_EV_H2Aub.bigwig?dl=0)  
[https://dl.dropboxusercontent.com/s/a022ih0b4jv4fj6/SYOI\\_CR\\_EV\\_SS18-SSX.bigwig?dl=0](https://dl.dropboxusercontent.com/s/a022ih0b4jv4fj6/SYOI_CR_EV_SS18-SSX.bigwig?dl=0)  
[https://dl.dropboxusercontent.com/s/efiruly66pvvyy/SYOI\\_CR\\_sgPCGF1\\_H2Aub.bigwig?dl=0](https://dl.dropboxusercontent.com/s/efiruly66pvvyy/SYOI_CR_sgPCGF1_H2Aub.bigwig?dl=0)  
[https://dl.dropboxusercontent.com/s/hurzbo8lfdauhn/SYOI\\_CR\\_sgPCGF1\\_SS18-SSX.bigwig?dl=0](https://dl.dropboxusercontent.com/s/hurzbo8lfdauhn/SYOI_CR_sgPCGF1_SS18-SSX.bigwig?dl=0)

## Methodology

### Replicates

The ChIP sequencing was performed in a unique biological replicate. Cut and Run sequencing of endogenous SS18-SSX and H2AK119ub1 was performed in two independent cell lines HS-SY-II and SYO-I. Native H2AK119ub1 calibrated ChIP was performed in biological triplicates. Cut and Run of overexpressed constructs was done in one replicate.

### Sequencing depth

ChIP libraries were sequenced as 75 bp Single-Read on Illumina NextSeq 550 platform High-Output.

total reads:

eGFP input: 31465378

eGFP HA: 35710039

SSX-C input: 39821585

SSX-C HA: 35710039

DeltaRD input: 38916894

DeltaRD HA: 27970228

CUT&RUN libraries were sequenced as 75 bp Paired-End reads on Illumina NextSeq 550 platform Mid-Output.

total reads:

HSS IgG: 13526884

HSS EV H2Aub: 19510962

HSS EV SS18-SSX: 11610526

HSS sgPCGF1 H2Aub: 15938066

HSS sgPCGF1 SS18-SSX: 13320300

SYOI IgG: 23814054

SYOI EV H2Aub: 23120676

SYOI EV SS18-SSX: 20301480

SYOI sgPCGF1 H2Aub: 25397092

SYOI sgPCGF1 SS18-SSX: 15248120

CUT&RUN for overexpression were sequenced as 50bp Paired-End reads on NovaSeq 6K SP.

total reads:

KHOS IgG 27488012

KHOS EV 55388126

KHOS SS18 45457932

KHOS SS18-SSX 41549600

KHOS SSX-C 46110250

Native H2AK119ub1 calibrated ChIP were sequenced as 50bp Paired-End reads on NovaSeq 6K SP.

total reads:

HSS EV R1 23109716

HSS EV R2 29247779:

HSS EV R3 29882136:

HSS sgPCF1 R1 29064591

	HSS sgPCF1 R2 39902391 HSS sgPCF1 R3 49357058
Antibodies	The ChIP sequencing has been done using the HA-tag antibody #9110 from Abcam. For the Cut and Run we used HA-Tag (C29F4) Rabbit mAb #3724 Cell Signaling, SS18-SSX (E9X9V) XP #72364 Cell Signaling, Ubiquityl-Histone H2A (Lys119) (D27C4) XP® Rabbit mAb #8240 Cell Signaling. Native H2AK119ub1 calibrated ChIP was done using Ubiquityl-Histone H2A (Lys119) (D27C4) XP® Rabbit mAb #8240 Cell Signaling.
Peak calling parameters	For ChIP sequencing HA-SS18-SSX1 peaks (n=26805) were generated with the MACS2 function (with "--no model", "--qvalue 0.05", "--broad" options) and normalized to input. For H2AK119ub1 (n=11099) and SS18-SSX2 (n= 27686) peak calling, the MACS2 callpeak function was used on the aligned BAM files and IgG as control (with "--nomodel", "--qvalue 0.01", "--broad" options, "--keep-dup all"). For HA peak calling in KHOS-240S, HA-SS18, HA-SS18-SSX1 and HA-eGFP-SSX1 were combined in MACS2 to compute all the HA peaks (n=58843).
Data quality	We assessed the quality of the sequencing using FastQC and Plotfingerprint. For Cut and Run, the percentage of reads mapped to E.Coli was also an indication of the success of assay. As an indication, histone H2Aub pull down has a percentage of E.Coli reads between 0.5 and 1. For SS18-SSX the percentage is between 1.5 and 3.5 % and IgG around 15%. Therefore a Cut and Run sequencing that shows abnormally high E.Coli content is a sign that the pull down did not work.
Software	We used Galaxy program for the analysis of the ChIP sequencing and the Cut and Run. For ChIP sequencing: Raw reads were trimmed for quality and Illumina adapter sequences using Trim Galore! (Galaxy Version 0.6.7 +galaxy0), then aligned to the human genome assembly Hg38 using Bowtie2 (Galaxy Version 2.4.2+galaxy0). ChIP signals were normalised to their respective inputs using the pileup function from MACS2 callpeak (Galaxy Version 2.1.1.20160309.6) using corresponding input for background normalization. To visualize ChIP-Seq tracks, normalized bigWig files were generated with Wig/BedGraph-to-bigWig converter (Galaxy Version 1.1.1). For the Cut and Run: Paired-end reads were aligned to the T2T or E.coli K12, MG1655 reference genome using Bowtie2 (Galaxy Version 2.4.2+galaxy0). Genome coverage files were generated using bamCoverage (Galaxy Version 3.5.1.0.0).