Characteristic	Number of patients (%)		
Age (range) in years	55.6 (23-79)		
Gender			
Male	35 (64.8)		
Female	19 (35.2)		
Tumor size (largest diameter, cm)	6.3 (3-12)		
Tumor location			
Sacral vertebra	42 (77.8)		
Cervical vertebra	6 (11.1)		
Thoracic vertebra	4 (7.4)		
Lumbar vertebra	2 (3.7)		
Surrounding muscle invasion			
Yes	35 (64.8)		
No	19 (35.2)		
Preoperative recurrence			
Yes	11 (20.4)		
No	43 (79.6)		
Tumor grade			
High	38 (70.4)		
Low	16 (29.6)		
Tumor stage			
IA	13 (24.1)		
IB	6 (11.1)		
IIA	4 (7.4)		
IIB	27 (50)		
III	4 (7.4)		
Type of resection			
EI	17 (31.5)		
EA	37 (68.5)		
Tumor hemorrhage			
No	10 (18.5)		
Yes	44 (81.5)		
Tumor necrosis			
Absent	13 (24.1)		
Mild	18 (33.3)		
Moderate	15 (27.8)		
Severe	8 (14.8)		
Level of overall TILs	~ /		
Absent	0 (0)		
Rare/few	23 (42.6)		

Supplementary Table 1 Summary of patient characteristics

Moderate	15 (27.8)
Prominent	16 (29.6)
Ki-67 staining index	
Low	25 (46.3)
High	29 (53.7)
Number of TILs subsets (cells/mm <sup>2</sup> )	
PD-1 <sup>+</sup> TILs, mean $\pm$ SD	$151.8\pm121.7$
PD-L1 <sup>+</sup> TILs, mean $\pm$ SD	$288.0\pm182.5$
$CD8^+$ TILs, mean $\pm$ SD	$311.0\pm274.8$
$Foxp3^+$ TILs, mean $\pm$ SD	$132.0\pm115.0$
$CD8^+/Foxp3^+$ ratio, mean $\pm$ SD	$3.3 \pm 3.1$
Survival during follow-up	
Death	24 (44.4%)
Alive	30 (55.6%)
Relapse during follow-up	
Yes	41 (75.9%)
No	13 (24.1%)

EI, Enneking inappropriate; EA, Enneking appropriate; TILs, tumor-infiltrating lymphocytes; PD-1, programmed cell death 1; PD-L1, programmed cell death-1 ligand 1; SD, standard deviation.

Gene	Forward	Reverse
miR-574-3p	5'-GGCGCACGCTCATGCACACA-3'	5'-GTGCAGGGTCCGAGGT-3'
miR-4731-3p	5'-GGCGCACACAAGTGGCCCCC-3'	5'-GTGCAGGGTCCGAGGT-3'
miR-4433-5p	5'-GGCGCGTCCCACCCCCAC-3'	5'-GTGCAGGGTCCGAGGT-3'
miR-671-5p	5'-GGCGAGGAAGCCCTGGAGGGG-3'	5'-GTGCAGGGTCCGAGGT-3'
miR-371b-5p	5'-GGCGACTCAAAAGATGGCGG-3'	5'-GTGCAGGGTCCGAGGT-3'
miR-1225-3p	5'-GGCGTGAGCCCCTGTGCCGC-3'	5'-GTGCAGGGTCCGAGGT-3'
U6	5'-CTCGCTTCGGCAGCACA-3'	5'-AACGCTTCACGAATTTGCGT-3'

Supplementary Table 2 List of the specific primers that were used in this study

Supplementary Table 3 Candidate miRNAs from microarray and boinformatical
analysis that could potentially regulate PD-L1 expression in spinal chordoma

miRNAs	<i>P</i> -value	Fold change	<b>FDR</b> <sup>a</sup>	Expression	Sequence
hsa-miR-574-3p	2.72E-02	4.98	0.03210	down	TGTGGGTGTGTGCATG
hsa-miR-4731-3p	5.41E-03	10.81	0.00782	down	AGTGTTGGGGGGCCA
hsa-miR-4433-5p	1.73E-02	3.82	0.02975	down	ACAGGAGTGGGGGG
hsa-miR-671-5p	6.43E-03	2.61	0.00684	down	CTCCAGCCCCT
hsa-miR-371b-5p	2.84E-02	2.30	0.00622	down	AAAGTGCCGCCATCT
hsa-miR-1225-3p	9.38E-03	12.08	0.02133	down	CTGGGGGGCGGC

miRNA, microRNA; FDR, false discovery rate; <sup>a</sup>FDR < 0.05

TIL a subturned	Frequency of infiltration pattern					
TILS subtypes	Absent	Rare/few	Moderate	Prominent		
PD-1 <sup>+</sup>	0	15	20	19		
PD-L1 <sup>+</sup>	0	24	18	12		
Foxp3 <sup>+</sup>	4	22	14	14		
$CD8^+$	10	17	14	13		

**Supplementary Table 4** Frequency of infiltration pattern according to TILs subsets in the chordoma microenvironment

TILs, tumor-infiltrating lymphocytes; PD-1, programmed cell death 1; PD-L1, programmed cell death-1 ligand 1.

	miR-574-3p expression	PD-L1 expression (positive vs negative)	Extent of overall TILs (positive vs negative)	PD-1 <sup>+</sup> TILs number	PD-L1 <sup>+</sup> TILs number	CD8 <sup>+</sup> TILs number	Foxp3 <sup>+</sup> TILs number	CD8 <sup>+</sup> /Foxp3 <sup>+</sup> ratio
miR-574-3p expression		t = 3.435 P = 0.001	t = 1.345 P = 0.185	r = -0.102 P = 0.462	r = -0.203 P = 0.140	r = 0.156 P = 0.260	r = -0.125 P = 0.367	r = 0.503 <i>P</i> < 0.001
PD-L1 expression (positive vs negative)			$\chi^2 = 7.953$ <b>P</b> = 0.005	t = 2.718 <b>P</b> = <b>0.009</b>	t = 2.951 <b>P</b> = 0.005	t = 1.005 P = 0.320	t = 1.415 P = 0.163	t = 2.764 <b>P</b> = <b>0.008</b>
Extent of overall TILs (positive vs negative)				t = -0.555 P = 0.581	t = 1.022 P = 0.312	t = 0.054 P = 0.957	t = -0.285 P = 0.777	t = 0.084 P = 0.934
PD-1 <sup>+</sup> TILs number					r = -0.521 <b>P &lt; 0.001</b>	r = -0.188 P = 0.174	r = 0.031 P = 0.825	r = -0.383 P = 0.006
PD-L1 <sup>+</sup> TILs number						r = 0.234 P = 0.089	r = -0.013 P = 0.923	r = 0.181 P = 0.208
CD8 <sup>+</sup> TILs number							r = 0.595 <b>P &lt; 0.001</b>	r = 0.302 P = 0.033
Foxp3 <sup>+</sup> TILs number								r = -0.393 <b>P</b> = <b>0.005</b>

Supplementary Table 5 Correlations between tumor PD-L1 expression, miR-574-3p level and microenvironmental TILs in spinal chordoma (n = 54)

TILs, tumor-infiltrating lymphocytes; PD-1, programmed cell death 1; PD-L1, programmed cell death-1 ligand

Variables	Cut-off values		
Outcome parameter: LR	FS		
miRNA-574-3p	8.425		
PD-1 <sup>+</sup> TILs	88.5 cells/mm <sup>2</sup>		
PD-L1 <sup>+</sup> TILs	450 cells/mm <sup>2</sup>		
Foxp3 <sup>+</sup> TILs	$162.5 \text{ cells/mm}^2$		
CD8 <sup>+</sup> TILs	5 cells/mm <sup>2</sup>		
CD8 <sup>+</sup> /Foxp3 <sup>+</sup> ratio	1.090		
Outcome parameter: OS			
miRNA-574-3p	18.41		
PD-1 <sup>+</sup> TILs	80 cells/mm <sup>2</sup>		
PD-L1 <sup>+</sup> TILs	446.5 $cells/mm^2$		
Foxp3 <sup>+</sup> TILs	$196.5 \text{ cells/mm}^2$		
CD8 <sup>+</sup> TILs	$402.5 \text{ cells/mm}^2$		
CD8 <sup>+</sup> /Foxp3 <sup>+</sup> ratio	4.585		

**Supplementary Table 6** List of the cut-off points for miRNA-574-3p and TILs in prognosis analysis of LRFS and OS

TILs, tumor-infiltrating lymphocytes; PD-1, programmed cell death 1; PD-L1, programmed cell death-1 ligand 1; LRFS, local recurrence-free survival; OS, overall survival.

-4.0 CH-1	CH-2	0.0 CH-3	NP-1	NP-2	4.0 NP-3	
						hsa-miR-4652-3p
						hsa-miR-4701-5p
						hsa-miR-23c
						hsa-miR-6507-3
						hsa-miR-149-5p
						hsa-miR-1238-3
						hsa-miR-1825
						hsa-miR-3162-3
						hsa-miR-425-3p
						hsa-miR-4313
						hsa-miR-1304-3
						hsa-miR-4649-3
						hsa-miR-191-3p
						hsa-miR-6508-5
						hsa-let-7b-3p
						hsa-let-7f-1-3p
						hsa-miR-4725-5
						hsa-miR-3676-3
						hsa-miR-4758-3
						hsa-miR-4769-3
						hsa-miR-4646-3
						hsa-miR-634
						hsa-miR-4436b-
						hsa-miR-4/6/
						hsa-miR-6069
						hsa-miR-33b-3p
						hsa-miR-1225-3
						hsa-miR-6515-3
						hsa-miR-4/28-3
						nsa-miR-483-3p
						hsa-miR-1539
						nsa-miR-1237-3
						nsa-miR-4749-3
						1158-1111R-4310
						haa miD 2190 E
						hsa-miP-4323
						hsa-miP-4323
						hsa-miP-033
						hsa-miP-4433-5
						hsa-miP-1281
						hsa-miR-4665-3
						hsa-miR-1234-3
						hsa-miR-4664-3
						hsa-miR-296-5p
						hsa-miR-550a-5
						hsa-miR-574-3n
						hsa-miR-766-3n
						hsa-miR-877-3n
						hsa-miR-4634
						hsa-miR-4687-3
						hsa-miR-557
						hsa_miP_1015_3



hsa-miR-1229-5p hsa-miR-371b-5p hsa-miR-5195-3p hsa-miR-3679-5p hsa-miR-1207-5p hsa-miR-6724-5p hsa-miR-4433-3p hsa-miR-1228-3p hsa-miR-4787-3p hsa-miR-193b-3p hsa-miR-103a-3p hsa-miR-151a-5p hsa-miR-181a-5p hsa-miR-378a-3p hsa-miR-193a-3p hsa-miR-193b-5p hsa-miR-4793-3p hsa-miR-1306-3p





**Supplementary Figure 1** A heat-map representation of the differentially expressed miRNAs patterns in chordoma (CH) versus nucleus pulposus tissues (NP). Relative expression is presented as a colorgram (*red*: high expression).



**Supplementary Figure 2** Identification of six cadidate miRNAs that could potentially regulate PD-L1 expression in chordoma tissues by microarray and bioinformatical analysis.



**Supplementary Figure 3** (a) Comparison of six cadidate miRNAs expression by qRT-PCR in 54 chordoma and 20 nucleus pulposus tissues; (b) Association of cadidate miRNAs expression and PD-L1 level in chordoma tissues.



**Supplementary Figure 4** The pattern of overall TILs,  $PD-1^+$  TILs and  $PD-L1^+$  TILs in chordoma tissues (*red arrow*). (a) Rare/few TILs (HE × 400); (b) Moderate TILs (HE × 400); (c) Prominent TILs (HE × 400); (d) Rare/few TILs that expressed PD-1; (e) Moderate TILs that expressed PD-1; (f) Prominent TILs that expressed PD-1; (g) Rare/few TILs expressing PD-L1; (h) Moderate TILs expressing PD-L1; (i) Prominent TILs expressing PD-L1 (×400).



**Supplementary Figure 5** The pattern of CD8<sup>+</sup> TILs and Foxp3<sup>+</sup> TILs in chordoma tissues (*red arrow*). (**a**) Lack of TILs that expressed CD8 in chordoma tissues; (**b**) Rare/few TILs with CD8 expression; (**c**) Moderate TILs with CD8 expression; (**d**) Prominent TILs with CD8 expression; (**e**) Lack of TILs that expressed Foxp3 in chordoma tissues; (**f**) Rare/few TILs that expressed Foxp3; (**g**) Moderate TILs that expressed Foxp3; (**h**) Prominent TILs expressing Foxp3 (×400).



**Supplementary Figure 6** Association of PD-L1 expression and PD-1<sup>+</sup> TILs density (a), PD-L1<sup>+</sup> TILs density (b), CD8<sup>+</sup>/Foxp3<sup>+</sup> ratio (c), Foxp3<sup>+</sup> TILs density (d) and CD8<sup>+</sup> TILs density (e). Association of miR-574-3p expression and overall TILs level (f).



**Supplementary Figure 7 (a)** Association of miR-574-3p expression and CD8<sup>+/</sup> Foxp3<sup>+</sup> ratio via Pearson correlation test; (b) Association of PD-1<sup>+</sup> TILs and PD-L1<sup>+</sup> TILs densities; (c) Association of CD8<sup>+</sup> TILs and Foxp3<sup>+</sup> TILs densities. Association of CD8<sup>+</sup>/Foxp3<sup>+</sup> ratio and PD-1<sup>+</sup> TILs density (d), Foxp3<sup>+</sup> TILs density (e) and CD8<sup>+</sup> TILs density (f).