Supplementary File

Table S1. Radiological evaluation of fistula healing in stem cell sheet (SCS), magneto-fluorescent stem cell sheet (MFSCS) and control groups.

	Control n=10	**SCS n=10**	**MFSCS n=8**	**p value**
Hypointense MRI signals at the fistula transplantation site (n)				
D0	0	0	8	<0.05[†]
D7	4	2	4	-
D14	4	3	4	-
Peri-anastomosis collection (n)				
D0	8	9	8	-
D7	2	1	1	-
D14	0	0	0	-
Fistula orifice surface (cm^2)				
D0	0.082 ±0.014	0.081 ±0.023	0.083 ±0.025	-
D7	0.072 ±0.015	0.047 ±0.020	0.059 ±0.010	<0.05 [‡]
D14	0.056 ±0.012	0.022 ±0.011	0.032 ±0.011	<0.05 [‡]

[†]Comparison between MFSCS and other groups.

[‡]Comparison between Control and SCS or MFSCS. There was no significant difference between SCS and MFSCS.

Table S2. Quantitative reverse transcription polymerase chain reaction. mRNA synthesis comparison between control and bone marrow derived mesenchymal stem cell (BMMSC) sheet–treated mice at D5: cDNA samples were duplicated and factor expression was normalized relative to the mouse hypoxanthine phosphoribosyltransferase (HPRT) gene with ΔΔCT calculation.

EGF				
C D1	BMMSC D1	C D5	BMMSC D5	*p**
0.00477 ±0.00271	*0.00230 ±0.00040*	*0.00973 ±0.00247*	*0.02258 ±0.01341*	*0.007*
VEGF				
C D1	BMMSC D1	C D5	BMMSC D5	*p**
0.16176 ±0.18089	*0.15081 ±0.06198*	*0.09679 ±0.02167*	*0.50418 ±0.31000*	*0.042*
TGF-β2				
C D1	BMMSC D1	C D5	BMMSC D5	*p**
0.00008 ±0.00005	*0.00044 ±0.00035*	*0.00134 ±0.00060*	*0.005135 ±0.00167*	*0.008*
IL-10				
C D1	BMMSC D1	C D5	BMMSC D5	*p**
0.00013 ±0.00007	*0.00008 ±0.00005*	*0.00020 ±0.00015*	*0.00044 ±0.00015*	*0.033*
IL8				
C D1	BMMSC D1	C D5	BMMSC D5	*p**
1.39914 ±0.09455	*1.31164 ±0.61778*	*1.21391 ±0.55699*	*0.77003 ±0.10538*	*0.274*
TNFα				
C D1	BMMSC D1	C D5	BMMSC D5	*p**
0.02738 ±0.01304	*0.02958 ±0.01001*	*0.01569 ±0.00945*	*0.01009 ±0.00298*	*0.019*
IL6				
C D1	BMMSC D1	C D5	BMMSC D5	*p**
0.00266 ±0.00214	*0.001274 ±0.00058*	*0.00122 ±0.00071*	*0.00360 ±0.00169*	*0.065*
MIP1α				
C D1	BMMSC D1	C D5	BMMSC D5	*p**
0.04768 ±0.01335	*0.14415 ±0.08368*	*0.04963 ±0.00247*	*0.26026 ±0.15164*	*0.072*

*p value for comparison of mRNA synthesis between control and grafted mice at D5

Table S3. Histological evaluation at D14 showed two fistula closures. The inflammatory infiltrate surface evaluated at the tissue surrounding the fistula site was lower and the maximal size of the fistula orifice was smaller in the treated groups (stem cell sheet (SCS) and magneto-fluorescent stem cell sheet (MFSCS) groups).

	Control n=10	**SCS n=10**	**MFSCS n=8**	**P value**
Histological closure of the fistula	0	1	1	-
Abscess at the fistula site	1	0	0	-
Surface of fibrosis infiltration at the fistula orifice (mm^2)	2.05 ±0.40	0.66 ±0.17	0. 71 ±0.21	<0.05†
Maximal size of the fistula orifice (µm)	1055 ±371	342 ±298	412 ±343	<0.05†
Positive Perl's staining, n (%)	1 (10%)	1 (10%)	4 (50%)	-
Presence of BMMSC (CD90+)	0	0	0	-

†Comparison between Control and SCS or MFSCS. There was no significant difference between SCS and MFSCS.

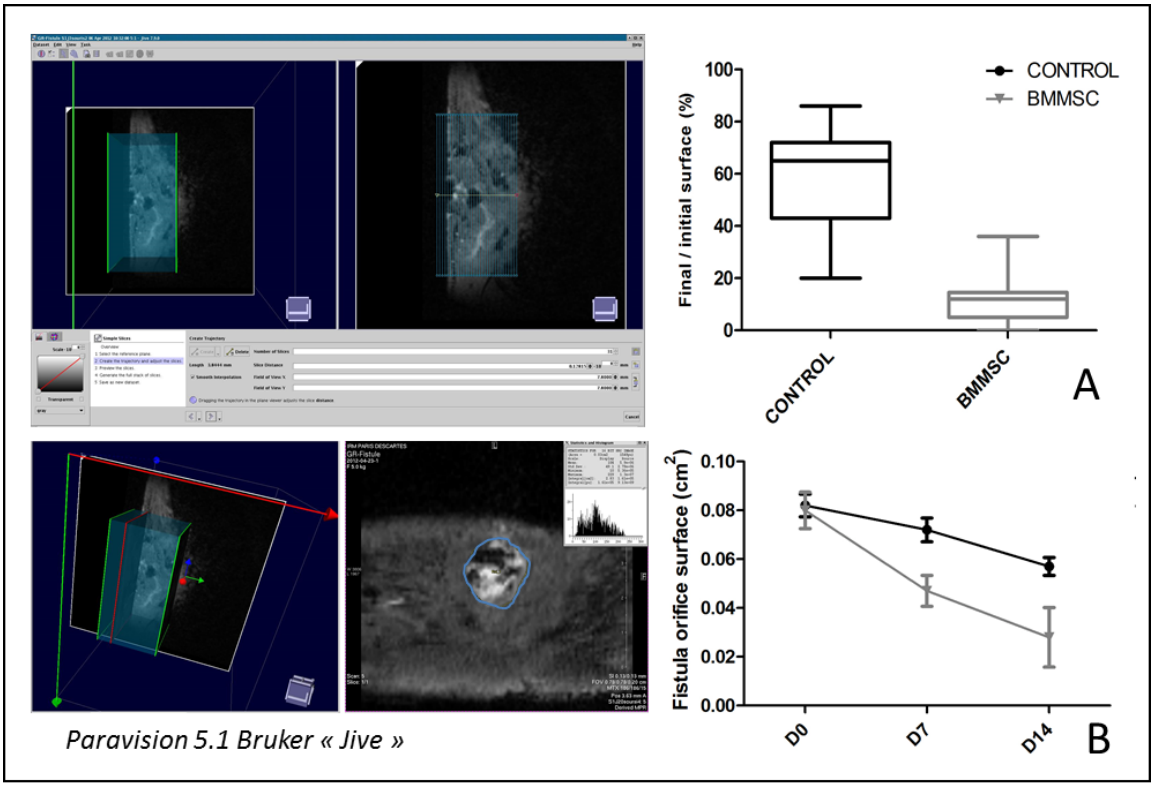

Figure S1. Measurement of fistula orifice surface by MRI for control and bone marrow derived mesenchymal stem cell (BMMSC) sheet–treated mice at D0, D7, and D14 (measured values were in cm^2). At D7, the orifice surface was smaller in treated mice in comparison with control mice. There was a major reduction in the median fistula orifice surface from D0 to D14 in treated mice, but not in control mice.

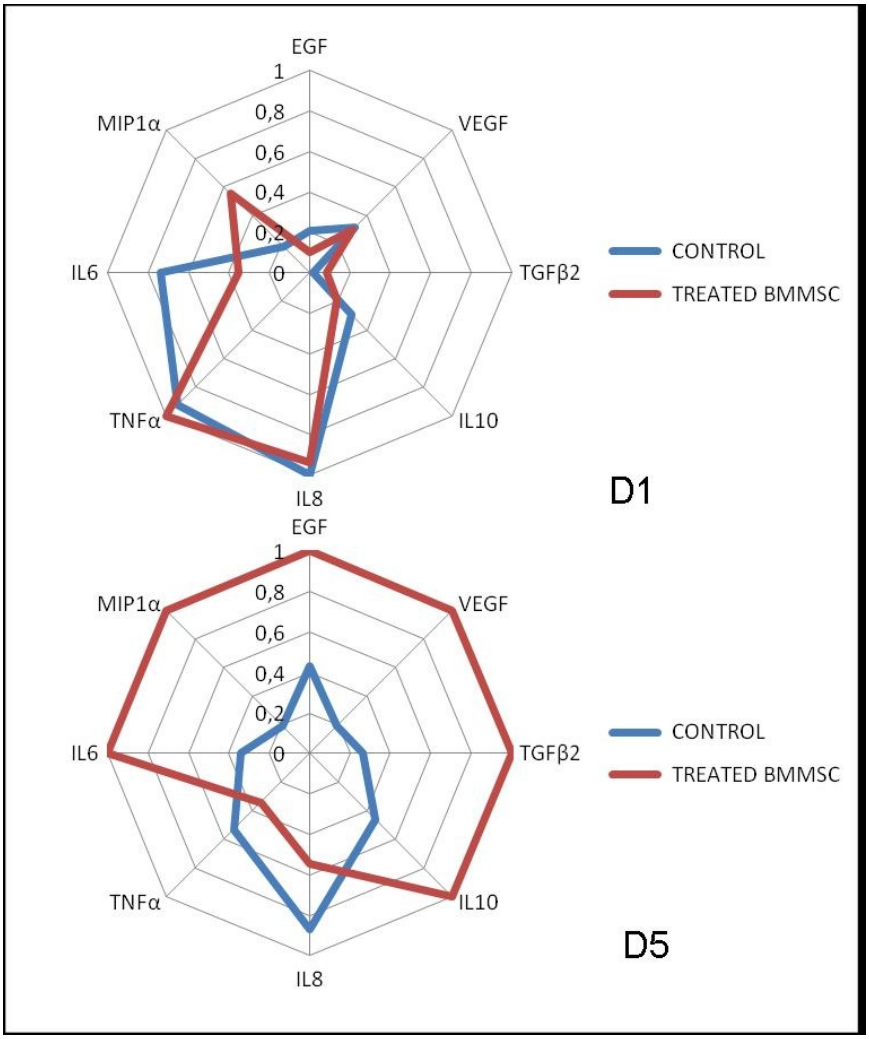

Figure S2. Chemokine factor profile in the intestinal mucosa of treated and control mice at D1 and D5. Results are presented for 8 cytokines as radar charts comparing the relative qRT-PCR (quantitative reverse transcription polymerase chain reaction) values in the fistulas of control (blue) and bone marrow derived mesenchymal stem cell (BMMSC) sheet–treated (red) mice at day 1 (D1) and day 5 (D5) after grafting. In order to compare the cytokine profiles between groups and, within each group, at the two different time points, qRT-PCR values, normalized by those of mouse (HPRT) gene, were divided by the highest value for that cytokine in both groups at both time points, i.e. for every radius corresponding to any

given cytokine, a value of 1 indicates that its qRT-PCR value was highest in that group at that time.