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Developmental expression patterns of chemokines CXCL11, CXCL12 and their receptor CXCR7 in testes of common marmoset and human testes

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Developmental expression patterns of the chemokines CXCL11, CXCL12 and its receptor CXCR7 in common marmoset and human testes

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Keywords:	CXCR7, CXCL12, CXCL11, primate testes, testicular development



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**To the Editor-in-Chief of
Cell and Tissue Research**

(via electronic submission)

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Münster, 21.02.2015

**Resubmission of the revised manuscript (CTR-14-0494.R1) entitled 'Developmental
expression patterns of the chemokines CXCL11, CXCL12 and its receptor CXCR7 in
common marmoset and human testes'.**

Dear Prof. Unsicker, dear Prof. Sutovsky,

thank you for the second review of our manuscript. We are delighted to see
that the paper is close to acceptance. We revised the manuscript in
accordance to the suggestions by referee 1. We herewith submit a slightly
revised version with some changes to the discussion.

We are grateful that you consider our work for publication in Cell and Tissue
Research.

Yours sincerely,

Prof. Dr. Stefan Schlatt

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3 **Response to Reviewer**
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6 Reviewer: 1

7 **I re-examined the revised version of the manuscript. The authors have addressed all of**
8 **my concerns and the manuscript has been modified accordingly.**
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10
11
12 Response: We thank the reviewer for this positive assessment.
13

14
15 **1) However, I have noted that the same group has recently published a paper on the**
16 **profiling of CXCR4 and CXCR7 during murine testis development (Westernstroer et al.**
17 **2014). The expression pattern of CXCR7 in the murine germ cells as well as the**
18 **expression profile of CXCL12 (assessed by qRT-PCR) is not perfectly in line with data**
19 **obtained on monkey and human testis. CXCR7 expression is retained in more**
20 **differentiated murine germ cells, and murine CXCL12 is stable up to 21 postnatal day**
21 **and increases after 37 postnatal days. In my opinion, the authors should discuss and**
22 **comment on this in more details (page 21, lane 354).**
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29 Response (lines 322 – 333, 362 – 367): We expanded the discussion as suggested.
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Cell and Tissue Research

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4 1 **Title:** Developmental expression patterns of the chemokines CXCL11, CXCL12 and its
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6 2 receptor CXCR7 in common marmoset and human testes
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10
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49
50 19 **Key words:** CXCR7, CXCL12, CXCL11, primate testes, testicular development
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21 **Abstract**

22 The chemokine receptor CXCR7 interacts with the chemokines CXCL11 and CXCL12.
23 During development this ligand receptor system (C-X-C) provokes cell type-specific
24 responses in terms of migration, adhesion or ligand sequestration. It is active in zebrafish
25 and rodents but no data are available for its presence or function in primate testes. Real-time
26 quantitative PCR was performed in the monkeys to detect CXCL11, CXCL12 and CXCR7. At
27 the protein level CXCL12 and CXCR7 were localized in marmoset (*Callitrix jacchus*) testes
28 whereas CXCR7 patterns were determined for various stages of human testes. Morphometry
29 and flow cytometry were applied to quantify CXCR7-positive cells in monkeys. Transcript
30 levels and protein expression of CXCR7 were detectable throughout testicular development.
31 In both species CXCR7 protein expression was restricted to premeiotic germ cells. In
32 immature marmoset testes 69.9 % \pm 9% of the total germ cell population were labelled for
33 CXCR7 whereas in the adult 4.7% \pm 2.7% were positive for CXCR7. CXCL12 mRNA was
34 detectable in all developmental stages of marmosets. The CXCL12 protein was exclusively
35 localized to Sertoli cells. This pattern of CXCL12/CXCR7 indicates its involvement in
36 regulatory processes that may concert the interaction between undifferentiated germ cells
37 and Sertoli cells.

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4 39 **Introduction:**
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7 40 The (C-X-C-motif) chemokine receptor type 7 (CXCR7) is a deorphanized G-protein-coupled
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9 41 seven-span transmembrane receptor which binds the chemokines CXCL12 (also called
10
11 42 stromal-derived factor-1, SDF-1) and CXCL11 (also called interferon-inducible T cell α -
12
13 43 chemoattractant, I-TAC) (Balabanian et al. 2005; Burns et al. 2006). Whereas CXCL12 is
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15 44 expressed under homeostatic conditions to modulate immune surveillance and development,
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17 45 the expression of CXCL11 is upregulated upon stimuli and therefore belongs to the
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19 46 inflammatory chemokines. In general, CXCL11 production is stimulated by interferons in a
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21 47 variety of cells, including leukocytes, fibroblasts and endothelial cells (reviewed in: Sánchez-
22
23 48 Martin et al. 2013) and therefore supports the massive cell infiltration in several inflamed
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25 49 tissues. The chemokines CXCL12 and CXCL11 bind also to the conventional chemokine
26
27 50 receptors CXCR4 and CXCR3, respectively (Balabanian et al. 2005). However, CXCR7
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29 51 binds CXCL12 and CXCL11 with higher affinity and belongs to the group of atypical
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31 52 chemokine receptors (ACKRs). Interestingly, ACKRs are unable to couple to G-proteins
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33 53 following ligand binding and therefore fail to induce the full spectrum of classical G-protein-
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35 54 coupled chemokine receptor signalling and cellular responses (Comerford et al. 2007;
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37 55 Ulvmar et al. 2011; Cancellieri et al. 2013; Nibbs et al. 2013). Instead, recent studies have
38
39 56 demonstrated that CXCR7 can signal through versatile adapter molecules and acts as an
40
41 57 endogenous β -arrestin-biased signalling receptor (Rajagopal et al. 2010). In addition,
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43 58 CXCR7 may serve as a co-receptor for CXCR4 and therefore enhances the classical
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45 59 CXCL12-mediated G-protein signalling (Levoye et al. 2009; Luker et al. 2009).

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49 60 In particular, the action of CXCR7 has been shown to be important for several steps in
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51 61 developing organs (Sánchez-Martin et al. 2013). Interestingly, expression of CXCR7 was
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53 62 detected in various cell types. For instance, expression was found on the cell surface of
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55 63 mesenchymal stem cells (Liu et al. 2010) as well as on renal progenitor cells (Mazzinghi et
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57 64 al. 2008). However, in the primordium of the zebrafish, CXCR7 expression was restricted to

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4 65 the somatic environment. More specifically, it has been demonstrated that a CXCL12
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6 66 gradient in the somatic tissue facilitates the directed migration of CXCR4-positive primordial
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8 67 germ cells (PGCs) towards the future gonad (Boldajipour et al. 2008; Mahabaleshwar et al.
9
10 68 2008; Staton et al. 2011; Mahabaleshwar et al. 2012). In this regard, expression of CXCR7 is
11
12 69 of particular importance as it acts as a scavenger for CXCL12 and is therefore responsible
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14 70 for the generation of a CXCL12 gradient (Boldajipour et al. 2008; Mahabaleshwar et al. 2008;
15
16 71 Staton et al. 2011; Mahabaleshwar et al. 2012). In addition, the CXCL12/CXCR4 interaction
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18 72 is also of importance for PGC migration in mice, suggesting a conserved mechanism (Ara et
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20 73 al. 2003; Molyneaux et al. 2003).

21
22
23 74 Moreover, recent studies in juvenile as well as in adult mouse and human testes have
24
25 75 revealed that CXCL12 is secreted by Sertoli cells and showed that this chemokine is required
26
27 76 for the migration and maintenance of undifferentiated spermatogonia within the stem cell
28
29 77 niche (Gilbert et al. 2009; Payne et al. 2010; Kanatsu-Shinohara et al. 2012; Yang et al.
30
31 78 2013). Transcripts of *Cxcr7* have been detected in developing mouse testes (Westernströer
32
33 79 et al. 2014) as well in testes obtained from adult rats and humans (Eva et al. 1993; McIver et
34
35 80 al. 2013). In addition, the cellular localization of *Cxcr7* in developing mouse testes has been
36
37 81 shown in premeiotic germ cells suggesting that *Cxcr7* may be involved in the regulation of
38
39 82 the spermatogonial population (Westernströer et al. 2014).

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42 83 Regarding testicular development and testicular stem cell physiology, the common marmoset
43
44 84 monkey is similar to the human (Li et al. 2005; Mitchell et al. 2008; Albert et al. 2010; Albert
45
46 85 et al. 2012; Lin et al. 2012; McKinnell et al. 2013) and is therefore an appropriate animal
47
48 86 model to study the CXCR7 axis in the developing testis further. Therefore, we used immature
49
50 87 and adult human testicular tissues and employed the marmoset monkey (*Callitrix jacchus*) as
51
52 88 a non-human primate animal model in order to elucidate the expression pattern of CXCR7
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54 89 and its ligands at distinct stages of testicular development.

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4 90 The primary aim of the present study was to investigate mRNA expression levels of *CXCL12*,
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6 91 *CXCL11* and *CXCR7* in marmoset monkeys during four different phases of testicular
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8 92 development. Based on these results, the second aim was to identify and to characterize the
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10 93 cellular localization of *CXCR7* protein expression during testicular development in the
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12 94 marmoset and human testis.
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96 **Material and Methods**

97 **Animals, collection and processing of testicular tissue**

98 All experimental procedures were performed in compliance with the German Federal Law on
99 the Care and Use of Laboratory Animals (animal license No. 84-02.05.20.12.0.18, LANUV
100 NRW, Germany). Common marmoset monkeys, *Callitrix jacchus*, were maintained at the
101 institutional breeding facilities under standardized conditions. Marmosets were fed with
102 pellets from Altromin (Lage, Germany) with daily supplement of fresh vegetables and fruits.
103 In addition, they had unlimited access to tap water and were kept under 12h light / 12h
104 darkness cycles.
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105 Monkeys (n = 4 / group) were sacrificed under anaesthesia (ketamine/xylazine solution in
106 saline; i.m.; 0.1 ml per 100 gram body weight) at the age of 16, 32, 52 and > 80 weeks *post-*
107 *partum (wpp)*. Testes were dissected and one half was snap-frozen for subsequent RNA
108 expression analysis, whereas the remaining tissue was fixed in Bouin's solution for 24 hrs,
109 transferred into 70% EtOH and embedded in paraffin for immunohistochemical analyses.

110 For flow cytometric analysis, adult marmosets (n = 3) were sacrificed as outlined above.
111 Testes were dissected and transferred into pre-cooled minimum essential medium-alpha
112 (MEM- α , Life Technologies, Gibco, Darmstadt, Germany), followed by enzymatic digestion
113 for flow cytometry.

114 **Human testicular tissues and preparation for histological analyses**

115 Human adult testicular tissues were obtained from patients attending the department of
116 Clinical Andrology due to treatment of testicular tumours. Of such patients testicular tissue
117 which was assessed to be unaffected by the tumour and with complete spermatogenesis
118 was used in this study (Ethics Committee of the Medical Faculty of Muenster and the State
119 Medical Board no. 2006-588-f-S). Status of spermatogenesis was assessed according to
120 Bergmann and Kliesch (2010).

121 Tissue was fixed in 4% paraformaldehyde (PFA) for 24 hrs, before it was transferred into an
122 increasing ethanol series (30%, 50% and 70%) and embedded in paraffin. For histological
123 evaluation, 3 µm sections were prepared and were stained using periodic acid Schiff's
124 reagent (PAS staining) followed by haematoxylin counterstaining as previously described
125 (Brinkworth et al. 1995). Based on the histological analysis, testicular tissues (n = 2) with
126 normal spermatogenesis were selected for this study.

127 In addition, human testicular tissues (age: 2 weeks and 6 months) from the Centre for
128 Reproductive Health at the University of Edinburgh were used. Testes were obtained at
129 autopsy with consent of their legal guardian from boys who died from various causes
130 (excluding reproductive and endocrine abnormalities). Testes were fixed in 10% Neutral
131 Buffered Formalin (NBF) for at least 24 hrs and transferred into 70% EtOH for processing.

133 **Immunofluorescence on testicular tissue**

134 Paraffin was removed using Pro Taqs Clear (Pro Taqs Clear, Quartett Immunodiagnostika &
135 Biotechnologie, Berlin, Germany) and sections were rehydrated in a decreasing ethanol
136 series. After washing with phosphate-buffered saline (PBS), sections were incubated with 5%
137 (w/v) bovine serum albumin (BSA) in Tris-buffered saline (TBS) for 20 min at room

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4 138 temperature (RT). Primary antibodies against CXCR7 (rabbit polyclonal anti-CXCR7, Abcam,
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6 139 dilution of 1:400, Cambridge, UK) and MAGE-A4 (mouse anti-MAGE-A4, provided by Prof.
7
8 140 G. C. Spagnoli from the University Hospital of Basel Switzerland, dilution of 1:20) were
9
10 141 applied to the sections and sections were incubated in a humid chamber at 4°C for 1 hr.
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12 142 Following two washing steps in PBS, the appropriate Alexa fluor 488-linked or 546-linked
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14 143 secondary antibodies, diluted in TBS/5% BSA, were applied for 45 min at RT in the dark.
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16 144 Incubation with non-specific immunoglobulin G (rabbit IgG and mouse IgG, dilution of
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18 145 1:1000) was used as negative control. Cells were counterstained with Hoechst (Sigma-
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20 146 Aldrich, Steinheim, Germany).
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26 148 **Immunohistochemistry on testicular tissue**

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29 149 Sections were dewaxed and rehydrated as described above. After rinsing with distilled water
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31 150 and TBS, non-specific peroxidases were blocked with 3% (v/v) H₂O₂ for 15 min at RT. In
32
33 151 order to block non-specific binding sites, sections were incubated with 5% (w/v) bovine
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35 152 serum albumin (BSA) for 20 min at RT. Subsequently, primary antibodies against CXCR7
36
37 153 (rabbit polyclonal anti-CXCR7, Abcam, dilution of 1:400, Cambridge, UK) and CXCL12
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39 154 (mouse monoclonal anti-CXCL12, R&D system, dilution of 1:50, Wiesbaden, Germany) were
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41 155 applied and sections were incubated overnight in a humid chamber at 4°C. Incubation with
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43 156 corresponding non-specific immunoglobulin G (rabbit IgG or mouse IgG, respectively)
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45 157 antibodies served as negative control. After three washing times with TBS, sections were
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47 158 incubated with biotin conjugated secondary antibodies and subsequently labeled with a
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49 159 streptavidin-conjugated horseradish peroxidase (Sigma-Aldrich, Steinheim, Germany).
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51 160 Staining was visualized using 3,3'-diaminobenzidine as chromogen (Sigma-Aldrich,
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53 161 Steinheim, Germany), and haematoxylin as counterstain.
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163 **Morphometric evaluation**

164 For morphometric evaluation of marmoset testicular tissues, 4- μ m sections were taken at 40-
165 μ m intervals. In tissue sections from infantile marmosets, a total of 100 seminiferous tubules
166 per animal (n = 3) were analyzed to determine labeling indices of CXCR7-positive germ cells.
167 In accordance with previous publications germ cell types were categorized into the following
168 three groups, cells with no observable contact with the basement membrane were classified
169 as gonocytes, those with some point of contact as pre-spermatogonia and those with full
170 contact with the basement membrane as spermatogonia (Sharpe et al. 2003b). Additionally,
171 the percentages of CXCR7-positive and negative gonocytes, pre-spermatogonia and
172 spermatogonia were determined.

173

174 **RNA isolation and relative gene expression analysis**

175 RNA extraction was performed using the miRNeasy Kit (Quiagen, Hilden, Germany) and
176 genomic DNA was removed by DNase treatment. cDNA was generated with the iScript
177 cDNA Synthesis Kit (Bio-Rad, Munich, Germany) using 200 ng of total RNA. Specific primers
178 were designed using Primer Express[®] 3.0 Software (Life Technologies, Darmstadt,
179 Germany). Optimal primer concentrations, primer specificity and PCR efficiency were
180 evaluated following the Power SYBR[®] Green PCR User Guide (Life Technologies,
181 Darmstadt, Germany). Primer sequences are summarized in Table 1. For quantitative real-
182 time PCR (qRT-PCR) analyses, cDNA was diluted 1:10 and 1.5 μ l were used for each 15 μ l
183 PCR reaction with Power SYBR[®] Green Mastermix (Life Technologies, Darmstadt,
184 Germany). The PCR programme consisted of initial steps of activation and denaturation
185 which were run once for 10 min at 95°C, followed by 40 cycles of denaturation (15 sec at
186 95°C), annealing and elongation (1 min at 60°C). qRT-PCRs were run on the StepOnePlus[™]
187 (Life Technologies, Darmstadt, Germany) and were subsequently analysed using the

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4 188 StepOne™ software 2.2 (Life Technologies, Darmstadt, Germany). To calculate relative
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6 189 expression levels of *CXCR7* (n = 4 / group), *CXCL12* (n = 4 / group) and *CXCL11* (n = 4 /
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8 190 group) in marmoset testes, the $2^{-\Delta\Delta CT}$ method (Livak et al. 2001) was applied, using *TOP1* as
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10 191 reference gene. Each sample was measured in duplicate.
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16 193 **Enzymatic digestion and flow cytometry of testicular cells**

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19 194 Single-cell suspension of testicular cells was prepared by sequential enzymatic digestion.
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21 195 The seminiferous tubules were digested in MEM- α with 1 mg/mL collagenase I (Sigma
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23 196 Aldrich, Steinheim, Germany) in a water bath at 37°C for 40 min. The digestion was stopped
24
25 197 by adding MEM- α containing 10% fetal bovine serum (FBS, Life Technologies, PAA,
26
27 198 Darmstadt, Germany). Afterwards, the seminiferous tubular fragments were isolated from
28
29 199 interstitial cells by sedimentation at unit gravity and the seminiferous tubular fragments were
30
31 200 further digested with 1 mg/mL collagenase I, 2.2 mg/mL DNase I (Sigma Aldrich, Steinheim,
32
33 201 Germany) and 0.5 mg/mL hyaluronidase (Sigma Aldrich, Steinheim, Germany) in MEM- α
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35 202 until a single-cell suspension was achieved. Finally, the single-cell suspension was
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37 203 centrifuged (1500 rpm, 4 min), the supernatant was removed and enzymatic digestion was
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39 204 stopped with FBS.

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41 205 For haematoxylin staining, testicular single cells were fixed on poly L-lysine coverslips with
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43 206 4% PFA for 15 min. After rinsing with PBS, cells were counterstained with haematoxylin at
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45 207 RT for 1 min and afterwards analyzed.

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48 208 For flow cytometric analysis, single-cell suspensions were filtered through a 30 μ m mesh and
49
50 209 washed with 5% (w/v) goat serum. Subsequently, cells were collected by centrifugation
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52 210 (1500 rpm, 5 min), the supernatant was removed and cells were incubated with the primary
53
54 211 antibody against *CXCR7* (rabbit polyclonal anti-*CXCR7*, Abcam, dilution of 1:200,
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56 212 Cambridge, UK) on ice for 30 min. Incubation with the corresponding non-specific
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4 213 immunoglobulin G (rabbit IgG, dilution of 1:2000) served as negative control. Following two
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6 214 washing steps in 5% (w/v) goat serum, cells were incubated on ice with an Alexa fluor 488-
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8 215 linked secondary antibody (goat anti-rabbit Alexa fluor 488, Life Technologies, Darmstadt,
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10 216 Germany, diluted in 5% goat serum for 30 min. Finally, stained cells were analysed using a
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12 217 BD FACSAria II (Becton Dickinson).
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219 **Immunofluorescence staining of testicular single cells**

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21 220 Fixed testicular single cells on poly L-lysine coverslips were rinsed with PBS. Cells were then
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23 221 incubated with 5% (w/v) BSA at RT for 30 min. Subsequently, primary antibodies against
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25 222 CXCR7 (rabbit polyclonal anti-CXCR7, Abcam, dilution of 1:400, Cambridge, UK) were
26
27 223 applied and cells were incubated in a humid chamber at 4 °C for 1 hr. Following two washing
28
29 224 steps in PBS, the appropriate Alexa fluor 546-linked secondary antibody, diluted in TBS/5%
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31 225 BSA, was applied for 30 min at RT in the dark. Incubation with non-specific immunoglobulin
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33 226 G (rabbit IgG, dilution of 1:2000) was performed as negative control. Cells were
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35 227 counterstained with Hoechst (Sigma-Aldrich, Steinheim, Germany).
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229 **Histological sample evaluations and image acquisition**

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43 230 Samples were analyzed using an Olympus BX61 microscope (Melville, NY, USA) with an
44
45 231 attached Retiga 400R camera (QImaging, Burnaby, BC, Canada). All images were acquired
46
47 232 digitally using cellSens imaging software (Olympus, Münster, Germany) and were processed
48
49 233 using Adobe Photoshop CS2 9.0 (Adobe Systems, CA, USA).
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4 236 **Statistical analysis**
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7 237 Statistical analyses were performed using Graph Pad Prism 5 (Graph Pad Software, USA).
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9 238 For analysis of qRT-PCR results the non-parametric Kruskal-Wallis test was performed
10

11 239 followed by the Dunn's multiple comparison test. For morphometric analyses the Student's t-
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13 240 test was applied. For these two tests, significant differences between the groups are marked
14

15 241 with * $P < 0.05$.
16
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18 242 Significant differences between the testis weights were determined using the "One way
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20 243 analysis of variance" followed by the "Tukey's multiple comparison test". Groups marked with
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22 244 different letters (a, b, c, d) are significantly different from each other ($P < 0.001$).
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4 246 **Results**

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7 247 **Testicular development, testis growth and expression pattern of *CXCL12*, *CXCL11* and**
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9 248 ***CXCR7* in postnatal marmoset testes.**

10
11 249 Testicular tissues from four phases of testicular development (16 *wpp*, 32 *wpp*, 52 *wpp* and >
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13 250 80 *wpp*) were selected to characterize the expression pattern of *CXCR7*, *CXCL12* and
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15 251 *CXCL11* in the marmoset monkey.

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19 252 Histological examination of testicular tissues of marmoset monkeys at the age of 16 *wpp*
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21 253 (Fig. 1a) revealed the presence of gonocytes, pre-spermatogonia and spermatogonia. At the
22
23 254 age of 32 *wpp*, differentiated germ cells up to spermatocytes were detected in seminiferous
24
25 255 tubules of marmoset monkeys (Fig. 1b). At the age of 52 *wpp* (Fig. 1c), round as well as
26
27 256 elongated spermatids were observed in the seminiferous tubules. Finally, spermatogenesis
28
29 257 was completed in the seminiferous tubules of marmoset monkeys at the age of > 80 *wpp*
30
31 258 (Fig. 1d). In these age groups, testis weights (Fig. 1e) increased significantly from 36.4 ± 6.3
32
33 259 mg (16 *wpp*) via 181.9 ± 35.7 mg (32 *wpp*) and 376.7 ± 72.0 mg (52 *wpp*) to 481.9 ± 36.5 mg
34
35 260 (> 80 *wpp*).

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37
38 261 Relative expression levels of *CXCR7* (n = 4 / group), *CXCL12* (n = 4 / group) and *CXCL11* (n
39
40 262 = 4 / group) during postnatal testis development in the marmoset were determined using
41
42 263 qRT-PCR analysis. Expression of *CXCL12* was high in marmoset testes at the age of 16 *wpp*
43
44 264 (0.214445 ± 0.112887) and then decreased significantly (0.088170 ± 0.012248 ; 2.4-fold; 52
45
46 265 *wpp*) during testicular development (Fig.1f). Compared to *CXCL12*, expression of *CXCL11*
47
48 266 was 56-fold (16 *wpp*), 76-fold (32 *wpp*), 21-fold (52 *wpp*) and 23-fold lower (> 80 *wpp*) and
49
50 267 did not change significantly during postnatal testis development (Fig. 1g). Expression of the
51
52 268 receptor *CXCR7* (Fig. 1h) was high in marmoset testes at the age of 16 *wpp* ($0.368448 \pm$
53
54 269 0.094921) and decreased significantly (0.092540 ± 0.013916 ; 4-fold; > 80 *wpp*) during
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56 270 postnatal development.

271 **CXCL12 and CXCR7 protein expression in postnatal marmoset testes**

272 Immunohistochemistry was performed to determine the expression of the homeostatic
273 chemokine CXCL12 and the corresponding receptor CXCR7 during postnatal testis
274 development in marmoset monkeys.

275 In the testes of marmoset monkeys at the age of 16 *wpp* (Fig. 2a), 32 *wpp* (Fig. 2c, d), 52
276 *wpp* (Fig. 2e, f) and > 80 *wpp* (Fig. 2g, h), CXCL12 was exclusively localized in the
277 cytoplasm of Sertoli cells. In contrast, expression of CXCR7 was restricted to the germ cell
278 population. More specifically, in marmoset testes at the age of 16 *wpp* the expression of
279 CXCR7 was found in a subset of gonocytes (Fig. 3c), pre-spermatogonia (Fig. 3e) and
280 spermatogonia (Fig. 3g). Furthermore, morphometric analyses revealed that the CXCR7
281 labelling index of the entire germ cell population was $69.9 \pm 9.0\%$ (Fig. 3i), which comprised
282 CXCR7-positive gonocytes (Fig. 3c), pre-spermatogonia (Fig. 3f) and spermatogonia (Fig.
283 3h) with the indices of $36.8 \pm 13.7\%$, $18.0 \pm 4.1\%$ and $15.1 \pm 9.8\%$, respectively (Fig. 3i).
284 Double immunofluorescence stainings (Fig. 4a-l) revealed subpopulations of MAGE-
285 A4⁺/CXCR7⁺ and MAGE-A4⁺/CXCR7⁻ gonocytes (Fig. 4d, e, f), pre-spermatogonia (Fig. 4g, h,
286 i) and spermatogonia (Fig. 4j, k, l). However, subsets of MAGE-A4⁺/CXCR7⁻ pre-
287 spermatogonia (Fig. 4g, h, i) were only rarely observed in tubules of marmoset testes at the
288 age of 16 *wpp*.

289 During postnatal development CXCR7 expression persisted in premeiotic germ cells located
290 at the basement membrane (Fig. 5a - f). CXCR7-positive A_{pale} (Fig. 5b, d) and A_{dark} (Fig. 5f)
291 spermatogonia were identified by morphological evaluation in marmoset monkeys at the age
292 of 32 *wpp*, 52 *wpp* and > 80 *wpp*.

293 Furthermore, adult marmoset testes (n = 3) were enzymatically digested and isolated single
294 cells were subjected to haematoxylin staining which showed cell types with different sizes
295 and morphology (Fig. 5g). Subsequent, flow cytometric assessment revealed expression of

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4 296 CXCR7 on the cell surface of $4.7 \pm 2.7\%$ of cells in the single cell suspension obtained from
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6 297 adult marmoset testes (Table S2) and CXCR7 protein expression was confirmed by
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8 298 immunofluorescence staining of cells fixed on poly L-lysine slides (Fig. 5h). The qualitative
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10 299 observations of CXCR7-positive cells following immunofluorescence staining were consistent
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12 300 with the data obtained by flow cytometry.
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18 302 **CXCR7 protein profiles in postnatal human testes**

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21 303 A panel of rare postnatal human testis samples (2 weeks, 6 months and adult) was
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23 304 immunohistochemically stained and revealed that a subset of gonocytes, pre-spermatogonia
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25 305 as well as spermatogonia was positive for CXCR7 in immature human testes (Fig. 6a-c).
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27 306 Moreover, the expression of CXCR7 in adult human testes (Fig. 6d) was found in premeiotic
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29 307 germ cells at the basement membrane.
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34 309 **Discussion**

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37 310 We have illustrated a schematic drawing of the localization patterns of CXCL12 and CXCR7
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39 311 which are pointing to a crucial role of this chemokine/receptor pair in the developing primate
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41 312 testis (Fig. 7). Interestingly, transcript levels of CXCL12 were constitutively expressed and
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43 313 immunohistochemical analyses further demonstrated protein expression of CXCL12 in the
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45 314 cytoplasm of Sertoli cells at all stages of postnatal testicular development which indicated a
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47 315 non-maturation-dependent expression of the homeostatic chemokine CXCL12 in the
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49 316 developing marmoset testis. After birth, the highest number of Sertoli cells per testis is
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51 317 established at around 4 month of age. Afterwards, the Sertoli cell population decreases and
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53 318 after 8 month of age Sertoli cells become morphologically mature (e.g. establishment of tight-
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55 319 junctions between adjacent Sertoli cells, formation of lumen in the seminiferous tubules) in

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4 320 marmoset testes (Sharpe et al. 2003a; Li et al. 2005). We therefore assume this
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6 321 phenomenon to explain the significantly decreased transcript levels of *CXCL12* in the
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8 322 developing marmoset testis. The Sertoli cell-specific expression pattern of *CXCL12*
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10 323 described in this study is in line with previous mouse (Payne et al. 2010; Yang et al. 2013,
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12 324 Westernströer et al. 2014) and human data (Gilbert et al. 2009). Here we describe for
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14 325 marmosets a decline of *CXCL12* from week 16-52 (prepuberty to postpuberty). This mRNA
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16 326 pattern is different from that previously observed in mice. The mRNA levels of *Cxcl12* in
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18 327 developing mouse testes remained constant from birth until day 21 and then increased until
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20 328 adulthood (Westernströer et al. 2014). The two methods for quantification of mRNA are
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22 329 different (mouse: luciferase based normalization; marmoset: reference gene based
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24 330 normalization) and the reported levels can therefore not be easily compared. However in
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26 331 mice and marmosets transcripts for *CXCL12* are detectable and appear to be modified
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28 332 throughout pubertal development. Current results therefore suggest that the action of
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30 333 *CXCL12* is evolutionarily conserved. Functions of *CXCL12* have been described to be organ
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32 334 or tissue specific. This includes a role for cell proliferation or survival (Kortesidis et al. 2005;
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34 335 Burns et al. 2006; Mazzinghi et al. 2008), differentiation (Lazarini et al. 2003), adhesion
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36 336 (Burns et al. 2006; Mazzinghi et al. 2008) and the regulation of cell migration (Bhakta et al.
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38 337 2006; Mazzinghi et al. 2008). Regarding germ cells, *CXCL12* has been shown to be secreted
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40 338 by the somatic environment thereby facilitating the colonization of the gonads by PGCs
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42 339 during mouse embryonic development (Doitsidou et al. 2002; Ara et al. 2003; Molyneaux et
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44 340 al. 2003; Dambly-Chaudiere et al. 2007; Boldajipour et al. 2008). Furthermore, recent studies
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46 341 in neonatal and adult mice revealed that *CXCL12* is required for maintenance of
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48 342 spermatogonial stem cells (SSCs) within their niches as well as for the homing and
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50 343 colonization process of SSCs into their niches following germ cell transplantation assays
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52 344 (Payne et al. 2010; Kanatsu-Shinohara et al. 2012; Yang et al. 2013). Moreover, we
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54 345 previously reported significantly increased transcript levels of *Cxcl12* following germ cell
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4 346 depletion in mice and suggested that Cxcl12 may stimulate the spermatogenic repopulation
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6 347 of the seminiferous tubules during testicular recovery (Westernströer et al. 2014).
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9 348 Whereas inflammatory chemokines (e.g. the C-X-C chemokine CXCL11) are mainly involved
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11 349 in the recruitment of leukocytes to inflamed tissue sites, homeostatic chemokines (e.g. the C-
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13 350 X-C chemokine CXCL12) are constitutively expressed in organs and have important
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15 351 functions in stem cell homing, tissue homeostasis and repair. Indications for testicular
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17 352 inflammation (e.g. massive cell infiltration by neutrophils, lymphocytes, macrophages and
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19 353 mast cells in the interstitium) (Guazzone et al. 2009) were not seen in the analyzed testes.
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21 354 Moreover, in contrast to *CXCL12*, only low transcript levels of *CXCL11* were detected in
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23 355 developing marmoset testes which confirmed that inflammatory C-X-C chemokines,
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25 356 especially *CXCL11* as a secondary ligand for CXCR7, is likely not of functional relevance for
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27 357 healthy marmoset testes.
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30 358 Transcript levels of CXCR7 were also constitutively expressed and immunohistochemical
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32 359 analyses further demonstrated that the atypical chemokine receptor CXCR7 is exclusively
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34 360 expressed by premeiotic germ cells (gonocytes, pre-spermatogonia, spermatogonia including
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36 361 A_{pale} and A_{dark} spermatogonia) throughout various phases of postnatal testicular development
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38 362 in the marmoset and the human testis. In agreement with these data we found that *Cxcr7*
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40 363 protein can be detected in gonocytes as well as in Sall4-positive undifferentiated
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42 364 spermatogonia of the developing mouse testis (Westernströer et al. 2014). Additionally,
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44 365 *Cxcr7* was also expressed on differentiated germ cells, spermatids and interstitial cells.
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46 366 These results reveal an evolutionarily conserved expression pattern of CXCR7 in premeiotic
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48 367 germ cells in the mouse and both analysed primate species (Westernströer et al. 2014). The
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50 368 morphometric evaluation in immature marmoset testes has shown additionally that
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52 369 approximately 80% of migrating germ cells (gonocytes and pre-spermatogonia) express
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54 370 CXCR7. In general, recent studies in marmoset monkeys indicated that the migration of
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56 371 gonocytes most likely begins postnatally between birth and 4 months of age (Rune et al.
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4 372 1991; Sharpe et al. 2003b). Interestingly, several MAGE-A4⁺/CXCR7⁻ gonocytes were
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6 373 observed, whereas subsets of MAGE-A4⁺/CXCR7⁻ pre-spermatogonia were only rarely seen
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8 374 in seminiferous tubules, suggesting that CXCR7 may be involved in migration and/or
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10 375 adhesion of germ cells in immature marmoset testes. In general, migration of centrally
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12 376 located germ cells into the basal part of the seminiferous epithelium is a cellular process
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14 377 critical for germ cell survival and establishment of A_{dark} and A_{pale} spermatogonia which
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16 378 represent the reserve and active SSC pool in adulthood in marmoset and human testis
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18 379 (McGuinness and Orth, 1992; Orth et al. 2000). Moreover, our morphometric evaluation in
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20 380 immature marmoset testes has shown that around 50% of the spermatogonia at the
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22 381 basement membrane express CXCR7. Furthermore, we demonstrated that A_{dark} and A_{pale}
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24 382 spermatogonia express CXCR7 in marmoset testes at the age of 32 *wpp*, 52 *wpp* and > 80
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26 383 *wpp*. Therefore, we assume different roles for the atypical chemokine receptor CXCR7 in the
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28 384 developing marmoset testes. Tissue- and cell type-specific functions of CXCR7 have been
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30 385 described and depend on the cell type and tissue. This includes a role for cell survival or
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32 386 adhesion as described for example for in the breast cancer cell line MCF-7 (Burns et al.
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34 387 2006) as well as in renal multipotent progenitor cells of the human kidney (Mazzeinghi et al.
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36 388 2008).

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39 389 In addition, using HEK-293 and MDA-MB-231 cells, it has been demonstrated that receptor
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41 390 heterodimerization between CXCR4 and CXCR7 may enhance CXCL12-induced cell
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43 391 migration (Levoye et al. 2009; Decaillot et al. 2011). Regarding the localization of CXCR4 in
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45 392 developing mammalian testes, different expression patterns have been shown for mouse and
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47 393 human (Gilbert et al. 2009; Yoon et al. 2009; Kanatsu-Shinohara et al. 2012; Yang et al.
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49 394 2013, McIver et al. 2013). Whilst expression of CXCR4 was found in gonocytes,
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51 395 undifferentiated spermatogonia, Sertoli cells and interstitial cells of neonatal and adult mouse
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53 396 testes (Yoon et al. 2009; Kanatsu-Shinohara et al. 2012; Yang et al. 2013), CXCR4 protein
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55 397 was detected throughout the seminiferous tubules of adult human testes (Gilbert et al. 2009).

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4 398 So far, the expression profile and the role of CXCR4 in developing marmoset testes remain
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6 399 unknown. Nevertheless, receptor heterodimerization between CXCR4 and CXCR7
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8 400 throughout testicular development in primate testes cannot be excluded but needs to be
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10 401 investigated in further studies.

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13 402 In conclusion, we show that CXCL12/CXCR7 network is present in primate testes. The
14
15 403 localization pattern suggests its involvement during migration, survival or adhesion in
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17 404 premeiotic germ cells.

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25 407 **Declaration of interest**

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28 408 The authors declare that there is no conflict of interest that could be perceived as prejudicing
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30 409 the impartiality of the research reported.

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32
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555 transcription factor in Sertoli cells. J Cell Physiol 220:245-256
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558 **Figures:**

559 **Fig. 1** Marmoset monkey testes after birth - age-related changes in histology, weight and
560 transcript levels. Micrographs showing PAS stained tissue sections of marmoset testes at the
561 age of 16 *wpp* (*wpp* = weeks *post partum*; a), 32 *wpp* (b), 52 *wpp* (c) and > 80 *wpp* (d).
562 Gonocytes (arrowhead), pre-spermatogonia (white arrow) and spermatogonia (black arrow)
563 are the predominant germ cells in marmoset testes at the age of 16 *wpp* (a). Meiotic cells
564 (primary spermatocytes) were present in the seminiferous tubules of marmosets at the age of
565 32 *wpp* (b), whilst germ cells up to the stage of elongated spermatids were detected in the
566 seminiferous epithelium of marmoset monkeys at the age of 52 *wpp* (c). Finally,
567 spermatogenesis was complete in all marmosets at the age of > 80 *wpp* (d). Scale bars
568 represent 50 μm . Changes in testis weight (e) are shown as mean \pm SEM. Groups marked
569 with different letters (a, b, c, d) are significantly different from each other ($p < 0.001$). Relative
570 mRNA levels of *CXCL12* (f), *CXCL11* (g) and *CXCR7* (h) in marmoset testes at the age of 16
571 *wpp*, 32 *wpp*, 52 *wpp* and > 80 *wpp* were normalized using the housekeeping gene *TOP1* (2
572 $^{-\Delta\text{Ct}}$) method). Results are shown as mean \pm SEM and significant differences between the
573 groups are marked with * $P < 0.05$.

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575 **Fig. 2** Immunohistochemical detection of *CXCL12* in marmoset testes at the age of 16 *wpp*
576 (*wpp* = weeks *post partum*; a), 32 *wpp* (c, d), 52 *wpp* (e, f) and > 80 *wpp* (g, h). Incubation
577 with non-specific IgG antibody was performed as control and a representative image of a
578 marmoset testis at the age of 16 *wpp* is shown in (b). During testicular development, the
579 chemokine *CXCL12* is exclusively localized in the cytoplasm of Sertoli cells (white arrow).
580 Neither relatively undifferentiated germ cells (gonocytes, arrow head; spermatogonia, black
581 arrow) nor differentiating germ cells showed expression of *CXCL12*. Scale bars represent 20
582 μm .

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4 583 **Fig. 3** Immunohistochemical detection of CXCR7 and labelling index of CXCR7-positive cells
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6 584 in marmoset testes at the age of 16 *wpp* (*wpp* = weeks *post partum*). A representative image
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8 585 is showing CXCR7 expression in marmoset testes at the age of 16 *wpp* (a). The staining
9
10 586 revealed that subsets of germ cells express CXCR7 (black arrow), whilst the remainder are
11
12 587 negative (arrow head) for CXCR7. Sertoli cells (white arrow) in the seminiferous tubules
13
14 588 showed no expression of CXCR7. Corresponding IgG antibody was used as negative control
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16 589 and a representative image is shown in (b). High magnification of CXCR7 stained tissue
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18 590 sections revealed CXCR7-positive and negative gonocytes (c, d), pre-spermatogonia (e, f)
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20 591 and spermatogonia (g, h). Scale bars represent 10 μm . Scores of CXCR7-positive and
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22 592 CXCR7-negative gonocytes (Gon+/Gon-), pre-spermatogonia (pre-SPG+/pre-SPG-) and
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24 593 spermatogonia (SPG+/SPG-) in marmoset testes at the age of 16 *wpp* are shown in (i).
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26 594 Results are shown as mean \pm SEM and significant differences between the groups are
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28 595 marked with * $P < 0.05$.

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34 597 **Fig. 4** Representative images for expression of MAGE-A4 (green) and CXCR7 (red) in testis
35
36 598 sections from marmosets at the age of 16 *wpp* (a - c). MAGE-A4 expression is seen in the
37
38 599 majority of germ cells including gonocytes (d), pre-spermatogonia (g) and spermatogonia (j).
39
40 600 Subpopulations of MAGE-A4⁺/CXCR7⁺ (arrow heads) and/or MAGE-A4⁺/CXCR7⁻ (arrows)
41
42 601 gonocytes (d - f), pre-spermatogonia (g - i) as well as spermatogonia (j - l) can be identified.
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44 602 Note that MAGE-A4⁺/CXCR7⁻ pre-spermatogonia are occasionally seen in the seminiferous
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46 603 tubules of marmoset testes at the age of 16 *wpp*. All sections were counterstained with
47
48 604 Hoechst (blue). Dotted lines indicate the basement membrane of the seminiferous tubules.
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50 605 Scale bars represent 10 μm .

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4 607 **Fig. 5** Immunohistochemical detection of CXCR7 in marmoset testes at the age of 32 *wpp*
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6 608 (*wpp* = weeks *post partum*; a, b), 52 *wpp* (c, d) and > 80 *wpp* (e, f). In marmoset testes at the
7
8 609 age of 32 *wpp*, 52 *wpp* and > 80 *wpp*, premeiotic germ cells (black arrow; including A_{pale} and
9
10 610 A_{dark} spermatogonia) located at the basement membrane are labelled for CXCR7 whereas
11
12 611 Sertoli cells (white arrow) showed no expression for CXCR7. Scale bars represent 20 μm (a
13
14 612 – f). Following enzymatic digestion of adult marmoset testes, haematoxylin-stained single
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16 613 cells showed cell types with different morphology (g) as well as immunofluorescence staining
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18 614 revealed CXCR7-positive cells in this single cell suspension (h). As negative control,
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20 615 incubation with nonspecific IgG antibody was performed and a representative image is
21
22 616 shown in (i). Scale bars represent 50 μm (g), 15 μm (h) and 60 μm (i).
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28 618 **Fig. 6** Immunohistochemical detection of CXCR7 in human testes at 2 weeks (a) and 6
29
30 619 months after birth (c) as well as in adult (d) human testes. Corresponding IgG antibody was
31
32 620 used as negative control and a representative image of an immature testis (2 weeks) is
33
34 621 shown in (b). In immature human testes (a; c), gonocytes (arrow head, no contact with the
35
36 622 basement membrane), pre-spermatogonia (white arrows, point contact with the basement
37
38 623 membrane) and spermatogonia (black arrows, full contact with the basement membrane)
39
40 624 were labelled for CXCR7. In adult human testes (d), premeiotic germ cells (red arrow)
41
42 625 located at the basement membrane were labelled for CXCR7. Scale bars represent 20 μm .
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48 627 **Fig. 7** Schematic drawing of CXCR7 (red) and CXCL12 (green) expression in seminiferous
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50 628 tubules of marmoset testes at the ages of 16 *wpp* (a), 32 *wpp* (b), 52 *wpp* (c) and > 80 *wpp*
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52 629 (*wpp* = weeks *post partum*, d). In marmoset testes at the age of 16 *wpp*, CXCL12 is highly
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54 630 expressed by Sertoli cells whereas the atypical chemokine receptor CXCR7 is expressed by
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56 631 few gonocytes, pre-spermatogonia and spermatogonia (a). In the seminiferous epithelium of
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632 marmoset testes at the ages of 32 wpp (b), 52 wpp (c) and > 80 wpp (d), CXCL12 is still
633 highly expressed by Sertoli cells whereas CXCR7 is expressed by premeitotic germ cells,
634 including A_{pale} and A_{dark} spermatogonia. The expression pattern of CXCL12 and CXCR7
635 indicates a CXCL12/CXCR7 network in primate testes.

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Cell and Tissue Research

1 **Title:** Developmental expression patterns of the chemokines CXCL11, CXCL12 and its
2 receptor CXCR7 in common marmoset and human testes

3
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19 **Key words:** CXCR7, CXCL12, CXCL11, primate testes, testicular development

20

21 **Abstract**

22 The chemokine receptor CXCR7 interacts with the chemokines CXCL11 and CXCL12.
23 During development this ligand receptor system (C-X-C) provokes cell type-specific
24 responses in terms of migration, adhesion or ligand sequestration. It is active in zebrafish
25 and rodents but no data are available for its presence or function in primate testes. Real-time
26 quantitative PCR was performed in the monkeys to detect CXCL11, CXCL12 and CXCR7. At
27 the protein level CXCL12 and CXCR7 were localized in marmoset (*Callitrix jacchus*) testes
28 whereas CXCR7 patterns were determined for various stages of human testes. Morphometry
29 and flow cytometry were applied to quantify CXCR7-positive cells in monkeys. Transcript
30 levels and protein expression of CXCR7 were detectable throughout testicular development.
31 In both species CXCR7 protein expression was restricted to premeiotic germ cells. In
32 immature marmoset testes 69.9 % \pm 9% of the total germ cell population were labelled for
33 CXCR7 whereas in the adult 4.7% \pm 2.7% were positive for CXCR7. CXCL12 mRNA was
34 detectable in all developmental stages of marmosets. The CXCL12 protein was exclusively
35 localized to Sertoli cells. This pattern of CXCL12/CXCR7 indicates its involvement in
36 regulatory processes that may concert the interaction between undifferentiated germ cells
37 and Sertoli cells.

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4 39 **Introduction:**
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7 40 The (C-X-C-motif) chemokine receptor type 7 (CXCR7) is a deorphanized G-protein-coupled
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9 41 seven-span transmembrane receptor which binds the chemokines CXCL12 (also called
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11 42 stromal-derived factor-1, SDF-1) and CXCL11 (also called interferon-inducible T cell α -
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13 43 chemoattractant, I-TAC) (Balabanian et al. 2005; Burns et al. 2006). Whereas CXCL12 is
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15 44 expressed under homeostatic conditions to modulate immune surveillance and development,
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17 45 the expression of CXCL11 is upregulated upon stimuli and therefore belongs to the
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19 46 inflammatory chemokines. In general, CXCL11 production is stimulated by interferons in a
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21 47 variety of cells, including leukocytes, fibroblasts and endothelial cells (reviewed in: Sánchez-
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23 48 Martín et al. 2013) and therefore supports the massive cell infiltration in several inflamed
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25 49 tissues. The chemokines CXCL12 and CXCL11 bind also to the conventional chemokine
26
27 50 receptors CXCR4 and CXCR3, respectively (Balabanian et al. 2005). However, CXCR7
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29 51 binds CXCL12 and CXCL11 with higher affinity and belongs to the group of atypical
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31 52 chemokine receptors (ACKRs). Interestingly, ACKRs are unable to couple to G-proteins
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33 53 following ligand binding and therefore fail to induce the full spectrum of classical G-protein-
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35 54 coupled chemokine receptor signalling and cellular responses (Comerford et al. 2007;
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37 55 Ulvmar et al. 2011; Cancellieri et al. 2013; Nibbs et al. 2013). Instead, recent studies have
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39 56 demonstrated that CXCR7 can signal through versatile adapter molecules and acts as an
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41 57 endogenous β -arrestin-biased signalling receptor (Rajagopal et al. 2010). In addition,
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43 58 CXCR7 may serve as a co-receptor for CXCR4 and therefore enhances the classical
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45 59 CXCL12-mediated G-protein signalling (Levoye et al. 2009; Luker et al. 2009).

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49 60 In particular, the action of CXCR7 has been shown to be important for several steps in
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51 61 developing organs (Sánchez-Martín et al. 2013). Interestingly, expression of CXCR7 was
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53 62 detected in various cell types. For instance, expression was found on the cell surface of
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55 63 mesenchymal stem cells (Liu et al. 2010) as well as on renal progenitor cells (Mazzinghi et
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57 64 al. 2008). However, in the primordium of the zebrafish, CXCR7 expression was restricted to

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4 65 the somatic environment. More specifically, it has been demonstrated that a CXCL12
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6 66 gradient in the somatic tissue facilitates the directed migration of CXCR4-positive primordial
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8 67 germ cells (PGCs) towards the future gonad (Boldajipour et al. 2008; Mahabaleshwar et al.
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10 68 2008; Staton et al. 2011; Mahabaleshwar et al. 2012). In this regard, expression of CXCR7 is
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12 69 of particular importance as it acts as a scavenger for CXCL12 and is therefore responsible
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14 70 for the generation of a CXCL12 gradient (Boldajipour et al. 2008; Mahabaleshwar et al. 2008;
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16 71 Staton et al. 2011; Mahabaleshwar et al. 2012). In addition, the CXCL12/CXCR4 interaction
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18 72 is also of importance for PGC migration in mice, suggesting a conserved mechanism (Ara et
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20 73 al. 2003; Molyneaux et al. 2003).

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23 74 Moreover, recent studies in juvenile as well as in adult mouse and human testes have
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25 75 revealed that CXCL12 is secreted by Sertoli cells and showed that this chemokine is required
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27 76 for the migration and maintenance of undifferentiated spermatogonia within the stem cell
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29 77 niche (Gilbert et al. 2009; Payne et al. 2010; Kanatsu-Shinohara et al. 2012; Yang et al.
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31 78 2013). Transcripts of *Cxcr7* have been detected in developing mouse testes (Westernströer
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33 79 et al. 2014) as well in testes obtained from adult rats and humans (Eva et al. 1993; McIver et
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35 80 al. 2013). In addition, the cellular localization of *Cxcr7* in developing mouse testes has been
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37 81 shown in premeiotic germ cells suggesting that *Cxcr7* may be involved in the regulation of
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39 82 the spermatogonial population (Westernströer et al. 2014).

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42 83 Regarding testicular development and testicular stem cell physiology, the common marmoset
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44 84 monkey is similar to the human (Li et al. 2005; Mitchell et al. 2008; Albert et al. 2010; Albert
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46 85 et al. 2012; Lin et al. 2012; McKinnell et al. 2013) and is therefore an appropriate animal
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48 86 model to study the CXCR7 axis in the developing testis further. Therefore, we used immature
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50 87 and adult human testicular tissues and employed the marmoset monkey (*Callitrix jacchus*) as
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52 88 a non-human primate animal model in order to elucidate the expression pattern of CXCR7
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54 89 and its ligands at distinct stages of testicular development.

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4 90 The primary aim of the present study was to investigate mRNA expression levels of *CXCL12*,
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6 91 *CXCL11* and *CXCR7* in marmoset monkeys during four different phases of testicular
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8 92 development. Based on these results, the second aim was to identify and to characterize the
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10 93 cellular localization of *CXCR7* protein expression during testicular development in the
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12 94 marmoset and human testis.
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96 **Material and Methods**

97 **Animals, collection and processing of testicular tissue**

98 All experimental procedures were performed in compliance with the German Federal Law on
99 the Care and Use of Laboratory Animals (animal license No. 84-02.05.20.12.0.18, LANUV
100 NRW, Germany). Common marmoset monkeys, *Callitrix jacchus*, were maintained at the
101 institutional breeding facilities under standardized conditions. Marmosets were fed with
102 pellets from Altromin (Lage, Germany) with daily supplement of fresh vegetables and fruits.
103 In addition, they had unlimited access to tap water and were kept under 12h light / 12h
104 darkness cycles.
105

106 Monkeys (n = 4 / group) were sacrificed under anaesthesia (ketamine/xylazine solution in
107 saline; i.m.; 0.1 ml per 100 gram body weight) at the age of 16, 32, 52 and > 80 weeks *post-*
108 *partum (wpp)*. Testes were dissected and one half was snap-frozen for subsequent RNA
109 expression analysis, whereas the remaining tissue was fixed in Bouin's solution for 24 hrs,
110 transferred into 70% EtOH and embedded in paraffin for immunohistochemical analyses.

111 For flow cytometric analysis, adult marmosets (n = 3) were sacrificed as outlined above.
112 Testes were dissected and transferred into pre-cooled minimum essential medium-alpha
113 (MEM- α , Life Technologies, Gibco, Darmstadt, Germany), followed by enzymatic digestion
114 for flow cytometry.

114 **Human testicular tissues and preparation for histological analyses**

115 Human adult testicular tissues were obtained from patients attending the department of
116 Clinical Andrology due to treatment of testicular tumours. Of such patients testicular tissue
117 which was assessed to be unaffected by the tumour and with complete spermatogenesis
118 was used in this study (Ethics Committee of the Medical Faculty of Muenster and the State
119 Medical Board no. 2006-588-f-S). Status of spermatogenesis was assessed according to
120 Bergmann and Kliesch (2010).

121 Tissue was fixed in 4% paraformaldehyde (PFA) for 24 hrs, before it was transferred into an
122 increasing ethanol series (30%, 50% and 70%) and embedded in paraffin. For histological
123 evaluation, 3 µm sections were prepared and were stained using periodic acid Schiff's
124 reagent (PAS staining) followed by haematoxylin counterstaining as previously described
125 (Brinkworth et al. 1995). Based on the histological analysis, testicular tissues (n = 2) with
126 normal spermatogenesis were selected for this study.

127 In addition, human testicular tissues (age: 2 weeks and 6 months) from the Centre for
128 Reproductive Health at the University of Edinburgh were used. Testes were obtained at
129 autopsy with consent of their legal guardian from boys who died from various causes
130 (excluding reproductive and endocrine abnormalities). Testes were fixed in 10% Neutral
131 Buffered Formalin (NBF) for at least 24 hrs and transferred into 70% EtOH for processing.

133 **Immunofluorescence on testicular tissue**

134 Paraffin was removed using Pro Taqs Clear (Pro Taqs Clear, Quartett Immunodiagnostika &
135 Biotechnologie, Berlin, Germany) and sections were rehydrated in a decreasing ethanol
136 series. After washing with phosphate-buffered saline (PBS), sections were incubated with 5%
137 (w/v) bovine serum albumin (BSA) in Tris-buffered saline (TBS) for 20 min at room

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4 138 temperature (RT). Primary antibodies against CXCR7 (rabbit polyclonal anti-CXCR7, Abcam,
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6 139 dilution of 1:400, Cambridge, UK) and MAGE-A4 (mouse anti-MAGE-A4, provided by Prof.
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8 140 G. C. Spagnoli from the University Hospital of Basel Switzerland, dilution of 1:20) were
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10 141 applied to the sections and sections were incubated in a humid chamber at 4°C for 1 hr.
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12 142 Following two washing steps in PBS, the appropriate Alexa fluor 488-linked or 546-linked
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14 143 secondary antibodies, diluted in TBS/5% BSA, were applied for 45 min at RT in the dark.
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16 144 Incubation with non-specific immunoglobulin G (rabbit IgG and mouse IgG, dilution of
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18 145 1:1000) was used as negative control. Cells were counterstained with Hoechst (Sigma-
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20 146 Aldrich, Steinheim, Germany).
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26 148 **Immunohistochemistry on testicular tissue**

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29 149 Sections were dewaxed and rehydrated as described above. After rinsing with distilled water
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31 150 and TBS, non-specific peroxidases were blocked with 3% (v/v) H₂O₂ for 15 min at RT. In
32
33 151 order to block non-specific binding sites, sections were incubated with 5% (w/v) bovine
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35 152 serum albumin (BSA) for 20 min at RT. Subsequently, primary antibodies against CXCR7
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37 153 (rabbit polyclonal anti-CXCR7, Abcam, dilution of 1:400, Cambridge, UK) and CXCL12
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39 154 (mouse monoclonal anti-CXCL12, R&D system, dilution of 1:50, Wiesbaden, Germany) were
40
41 155 applied and sections were incubated overnight in a humid chamber at 4°C. Incubation with
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43 156 corresponding non-specific immunoglobulin G (rabbit IgG or mouse IgG, respectively)
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45 157 antibodies served as negative control. After three washing times with TBS, sections were
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47 158 incubated with biotin conjugated secondary antibodies and subsequently labeled with a
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49 159 streptavidin-conjugated horseradish peroxidase (Sigma-Aldrich, Steinheim, Germany).
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51 160 Staining was visualized using 3,3'-diaminobenzidine as chromogen (Sigma-Aldrich,
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53 161 Steinheim, Germany), and haematoxylin as counterstain.
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163 Morphometric evaluation

164 For morphometric evaluation of marmoset testicular tissues, 4- μ m sections were taken at 40-
165 μ m intervals. In tissue sections from infantile marmosets, a total of 100 seminiferous tubules
166 per animal (n = 3) were analyzed to determine labeling indices of CXCR7-positive germ cells.
167 In accordance with previous publications germ cell types were categorized into the following
168 three groups, cells with no observable contact with the basement membrane were classified
169 as gonocytes, those with some point of contact as pre-spermatogonia and those with full
170 contact with the basement membrane as spermatogonia (Sharpe et al. 2003b). Additionally,
171 the percentages of CXCR7-positive and negative gonocytes, pre-spermatogonia and
172 spermatogonia were determined.

173

174 RNA isolation and relative gene expression analysis

175 RNA extraction was performed using the miRNeasy Kit (Quiagen, Hilden, Germany) and
176 genomic DNA was removed by DNase treatment. cDNA was generated with the iScript
177 cDNA Synthesis Kit (Bio-Rad, Munich, Germany) using 200 ng of total RNA. Specific primers
178 were designed using Primer Express[®] 3.0 Software (Life Technologies, Darmstadt,
179 Germany). Optimal primer concentrations, primer specificity and PCR efficiency were
180 evaluated following the Power SYBR[®] Green PCR User Guide (Life Technologies,
181 Darmstadt, Germany). Primer sequences are summarized in Table 1. For quantitative real-
182 time PCR (qRT-PCR) analyses, cDNA was diluted 1:10 and 1.5 μ l were used for each 15 μ l
183 PCR reaction with Power SYBR[®] Green Mastermix (Life Technologies, Darmstadt,
184 Germany). The PCR programme consisted of initial steps of activation and denaturation
185 which were run once for 10 min at 95°C, followed by 40 cycles of denaturation (15 sec at
186 95°C), annealing and elongation (1 min at 60°C). qRT-PCRs were run on the StepOnePlus[™]
187 (Life Technologies, Darmstadt, Germany) and were subsequently analysed using the

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4 188 StepOne™ software 2.2 (Life Technologies, Darmstadt, Germany). To calculate relative
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6 189 expression levels of *CXCR7* (n = 4 / group), *CXCL12* (n = 4 / group) and *CXCL11* (n = 4 /
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8 190 group) in marmoset testes, the $2^{-\Delta\Delta CT}$ method (Livak et al. 2001) was applied, using *TOP1* as
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10 191 reference gene. Each sample was measured in duplicate.
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16 193 **Enzymatic digestion and flow cytometry of testicular cells**

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19 194 Single-cell suspension of testicular cells was prepared by sequential enzymatic digestion.
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21 195 The seminiferous tubules were digested in MEM- α with 1 mg/mL collagenase I (Sigma
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23 196 Aldrich, Steinheim, Germany) in a water bath at 37°C for 40 min. The digestion was stopped
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25 197 by adding MEM- α containing 10% fetal bovine serum (FBS, Life Technologies, PAA,
26
27 198 Darmstadt, Germany). Afterwards, the seminiferous tubular fragments were isolated from
28
29 199 interstitial cells by sedimentation at unit gravity and the seminiferous tubular fragments were
30
31 200 further digested with 1 mg/mL collagenase I, 2.2 mg/mL DNase I (Sigma Aldrich, Steinheim,
32
33 201 Germany) and 0.5 mg/mL hyaluronidase (Sigma Aldrich, Steinheim, Germany) in MEM- α
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35 202 until a single-cell suspension was achieved. Finally, the single-cell suspension was
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37 203 centrifuged (1500 rpm, 4 min), the supernatant was removed and enzymatic digestion was
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39 204 stopped with FBS.

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41 205 For haematoxylin staining, testicular single cells were fixed on poly L-lysine coverslips with
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43 206 4% PFA for 15 min. After rinsing with PBS, cells were counterstained with haematoxylin at
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45 207 RT for 1 min and afterwards analyzed.

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48 208 For flow cytometric analysis, single-cell suspensions were filtered through a 30 μ m mesh and
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50 209 washed with 5% (w/v) goat serum. Subsequently, cells were collected by centrifugation
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52 210 (1500 rpm, 5 min), the supernatant was removed and cells were incubated with the primary
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54 211 antibody against *CXCR7* (rabbit polyclonal anti-*CXCR7*, Abcam, dilution of 1:200,
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56 212 Cambridge, UK) on ice for 30 min. Incubation with the corresponding non-specific
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4 213 immunoglobulin G (rabbit IgG, dilution of 1:2000) served as negative control. Following two
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6 214 washing steps in 5% (w/v) goat serum, cells were incubated on ice with an Alexa fluor 488-
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8 215 linked secondary antibody (goat anti-rabbit Alexa fluor 488, Life Technologies, Darmstadt,
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10 216 Germany, diluted in 5% goat serum for 30 min. Finally, stained cells were analysed using a
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12 217 BD FACSAria II (Becton Dickinson).

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18 219 **Immunofluorescence staining of testicular single cells**

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21 220 Fixed testicular single cells on poly L-lysine coverslips were rinsed with PBS. Cells were then
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23 221 incubated with 5% (w/v) BSA at RT for 30 min. Subsequently, primary antibodies against
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25 222 CXCR7 (rabbit polyclonal anti-CXCR7, Abcam, dilution of 1:400, Cambridge, UK) were
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27 223 applied and cells were incubated in a humid chamber at 4 °C for 1 hr. Following two washing
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29 224 steps in PBS, the appropriate Alexa fluor 546-linked secondary antibody, diluted in TBS/5%
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31 225 BSA, was applied for 30 min at RT in the dark. Incubation with non-specific immunoglobulin
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33 226 G (rabbit IgG, dilution of 1:2000) was performed as negative control. Cells were
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35 227 counterstained with Hoechst (Sigma-Aldrich, Steinheim, Germany).

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40 229 **Histological sample evaluations and image acquisition**

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43 230 Samples were analyzed using an Olympus BX61 microscope (Melville, NY, USA) with an
44
45 231 attached Retiga 400R camera (QImaging, Burnaby, BC, Canada). All images were acquired
46
47 232 digitally using cellSens imaging software (Olympus, Münster, Germany) and were processed
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49 233 using Adobe Photoshop CS2 9.0 (Adobe Systems, CA, USA).

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4 236 **Statistical analysis**
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7 237 Statistical analyses were performed using Graph Pad Prism 5 (Graph Pad Software, USA).
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9 238 For analysis of qRT-PCR results the non-parametric Kruskal-Wallis test was performed
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11 239 followed by the Dunn's multiple comparison test. For morphometric analyses the Student's t-
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13 240 test was applied. For these two tests, significant differences between the groups are marked
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15 241 with * $P < 0.05$.
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17
18 242 Significant differences between the testis weights were determined using the "One way
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20 243 analysis of variance" followed by the "Tukey's multiple comparison test". Groups marked with
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22 244 different letters (a, b, c, d) are significantly different from each other ($P < 0.001$).
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4 246 **Results**

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7 247 **Testicular development, testis growth and expression pattern of *CXCL12*, *CXCL11* and**
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9 248 ***CXCR7* in postnatal marmoset testes.**

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11 249 Testicular tissues from four phases of testicular development (16 *wpp*, 32 *wpp*, 52 *wpp* and >
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13 250 80 *wpp*) were selected to characterize the expression pattern of *CXCR7*, *CXCL12* and
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15 251 *CXCL11* in the marmoset monkey.

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19 252 Histological examination of testicular tissues of marmoset monkeys at the age of 16 *wpp*
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21 253 (Fig. 1a) revealed the presence of gonocytes, pre-spermatogonia and spermatogonia. At the
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23 254 age of 32 *wpp*, differentiated germ cells up to spermatocytes were detected in seminiferous
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25 255 tubules of marmoset monkeys (Fig. 1b). At the age of 52 *wpp* (Fig. 1c), round as well as
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27 256 elongated spermatids were observed in the seminiferous tubules. Finally, spermatogenesis
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29 257 was completed in the seminiferous tubules of marmoset monkeys at the age of > 80 *wpp*
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31 258 (Fig. 1d). In these age groups, testis weights (Fig. 1e) increased significantly from 36.4 ± 6.3
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33 259 mg (16 *wpp*) via 181.9 ± 35.7 mg (32 *wpp*) and 376.7 ± 72.0 mg (52 *wpp*) to 481.9 ± 36.5 mg
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35 260 (> 80 *wpp*).

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38 261 Relative expression levels of *CXCR7* (n = 4 / group), *CXCL12* (n = 4 / group) and *CXCL11* (n
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40 262 = 4 / group) during postnatal testis development in the marmoset were determined using
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42 263 qRT-PCR analysis. Expression of *CXCL12* was high in marmoset testes at the age of 16 *wpp*
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44 264 (0.214445 ± 0.112887) and then decreased significantly (0.088170 ± 0.012248 ; 2.4-fold; 52
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46 265 *wpp*) during testicular development (Fig.1f). Compared to *CXCL12*, expression of *CXCL11*
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48 266 was 56-fold (16 *wpp*), 76-fold (32 *wpp*), 21-fold (52 *wpp*) and 23-fold lower (> 80 *wpp*) and
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50 267 did not change significantly during postnatal testis development (Fig. 1g). Expression of the
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52 268 receptor *CXCR7* (Fig. 1h) was high in marmoset testes at the age of 16 *wpp* ($0.368448 \pm$
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54 269 0.094921) and decreased significantly (0.092540 ± 0.013916 ; 4-fold; > 80 *wpp*) during
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56 270 postnatal development.

271 **CXCL12 and CXCR7 protein expression in postnatal marmoset testes**

272 Immunohistochemistry was performed to determine the expression of the homeostatic
273 chemokine CXCL12 and the corresponding receptor CXCR7 during postnatal testis
274 development in marmoset monkeys.

275 In the testes of marmoset monkeys at the age of 16 *wpp* (Fig. 2a), 32 *wpp* (Fig. 2c, d), 52
276 *wpp* (Fig. 2e, f) and > 80 *wpp* (Fig. 2g, h), CXCL12 was exclusively localized in the
277 cytoplasm of Sertoli cells. In contrast, expression of CXCR7 was restricted to the germ cell
278 population. More specifically, in marmoset testes at the age of 16 *wpp* the expression of
279 CXCR7 was found in a subset of gonocytes (Fig. 3c), pre-spermatogonia (Fig. 3e) and
280 spermatogonia (Fig. 3g). Furthermore, morphometric analyses revealed that the CXCR7
281 labelling index of the entire germ cell population was $69.9 \pm 9.0\%$ (Fig. 3i), which comprised
282 CXCR7-positive gonocytes (Fig. 3c), pre-spermatogonia (Fig. 3f) and spermatogonia (Fig.
283 3h) with the indices of $36.8 \pm 13.7\%$, $18.0 \pm 4.1\%$ and $15.1 \pm 9.8\%$, respectively (Fig. 3i).
284 Double immunofluorescence stainings (Fig. 4a-l) revealed subpopulations of MAGE-
285 A4⁺/CXCR7⁺ and MAGE-A4⁺/CXCR7⁻ gonocytes (Fig. 4d, e, f), pre-spermatogonia (Fig. 4g, h,
286 i) and spermatogonia (Fig. 4j, k, l). However, subsets of MAGE-A4⁺/CXCR7⁻ pre-
287 spermatogonia (Fig. 4g, h, i) were only rarely observed in tubules of marmoset testes at the
288 age of 16 *wpp*.

289 During postnatal development CXCR7 expression persisted in premeiotic germ cells located
290 at the basement membrane (Fig. 5a - f). CXCR7-positive A_{pale} (Fig. 5b, d) and A_{dark} (Fig. 5f)
291 spermatogonia were identified by morphological evaluation in marmoset monkeys at the age
292 of 32 *wpp*, 52 *wpp* and > 80 *wpp*.

293 Furthermore, adult marmoset testes (n = 3) were enzymatically digested and isolated single
294 cells were subjected to haematoxylin staining which showed cell types with different sizes
295 and morphology (Fig. 5g). Subsequent, flow cytometric assessment revealed expression of

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4 296 CXCR7 on the cell surface of $4.7 \pm 2.7\%$ of cells in the single cell suspension obtained from
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6 297 adult marmoset testes (Table S2) and CXCR7 protein expression was confirmed by
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8 298 immunofluorescence staining of cells fixed on poly L-lysine slides (Fig. 5h). The qualitative
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10 299 observations of CXCR7-positive cells following immunofluorescence staining were consistent
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12 300 with the data obtained by flow cytometry.
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302 **CXCR7 protein profiles in postnatal human testes**

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18 303 A panel of rare postnatal human testis samples (2 weeks, 6 months and adult) was
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20 304 immunohistochemically stained and revealed that a subset of gonocytes, pre-spermatogonia
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22 305 as well as spermatogonia was positive for CXCR7 in immature human testes (Fig. 6a-c).
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24 306 Moreover, the expression of CXCR7 in adult human testes (Fig. 6d) was found in premeiotic
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26 307 germ cells at the basement membrane.
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309 **Discussion**

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37 310 We have illustrated a schematic drawing of the localization patterns of CXCL12 and CXCR7
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39 311 which are pointing to a crucial role of this chemokine/receptor pair in the developing primate
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41 312 testis (Fig. 7). Interestingly, transcript levels of CXCL12 were constitutively expressed and
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43 313 immunohistochemical analyses further demonstrated protein expression of CXCL12 in the
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45 314 cytoplasm of Sertoli cells at all stages of postnatal testicular development which indicated a
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47 315 non-maturation-dependent expression of the homeostatic chemokine CXCL12 in the
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49 316 developing marmoset testis. After birth, the highest number of Sertoli cells per testis is
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51 317 established at around 4 month of age. Afterwards, the Sertoli cell population decreases and
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53 318 after 8 month of age Sertoli cells become morphologically mature (e.g. establishment of tight-
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55 319 junctions between adjacent Sertoli cells, formation of lumen in the seminiferous tubules) in

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4 320 marmoset testes (Sharpe et al. 2003a; Li et al. 2005). We therefore assume this
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6 321 phenomenon to explain the significantly decreased transcript levels of *CXCL12* in the
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8 322 developing marmoset testis. The Sertoli cell-specific expression pattern of *CXCL12*
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10 323 described in this study is in line with previous mouse (Payne et al. 2010; Yang et al. 2013,
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12 324 Westernströer et al. 2014) and human data (Gilbert et al. 2009). Here we describe for
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14 325 marmosets a decline of *CXCL12* from week 16-52 (prepuberty to postpuberty). This mRNA
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16 326 pattern is different from that previously observed in mice. The mRNA levels of *Cxcl12* in
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18 327 developing mouse testes remained constant from birth until day 21 and then increased until
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20 328 adulthood (Westernströer et al. 2014). The two methods for quantification of mRNA are
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22 329 different (mouse: luciferase based normalization; marmoset: reference gene based
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24 330 normalization) and the reported levels can therefore not be easily compared. However in
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26 331 mice and marmosets transcripts for *CXCL12* are detectable and appear to be modified
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28 332 throughout pubertal development. Current results therefore suggest that the action of
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30 333 *CXCL12* is evolutionarily conserved. Functions of *CXCL12* have been described to be organ
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32 334 or tissue specific. This includes a role for cell proliferation or survival (Kortesidis et al. 2005;
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34 335 Burns et al. 2006; Mazzinghi et al. 2008), differentiation (Lazarini et al. 2003), adhesion
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36 336 (Burns et al. 2006; Mazzinghi et al. 2008) and the regulation of cell migration (Bhakta et al.
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38 337 2006; Mazzinghi et al. 2008). Regarding germ cells, *CXCL12* has been shown to be secreted
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40 338 by the somatic environment thereby facilitating the colonization of the gonads by PGCs
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42 339 during mouse embryonic development (Doitsidou et al. 2002; Ara et al. 2003; Molyneaux et
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44 340 al. 2003; Dambly-Chaudiere et al. 2007; Boldajipour et al. 2008). Furthermore, recent studies
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46 341 in neonatal and adult mice revealed that *CXCL12* is required for maintenance of
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48 342 spermatogonial stem cells (SSCs) within their niches as well as for the homing and
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50 343 colonization process of SSCs into their niches following germ cell transplantation assays
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52 344 (Payne et al. 2010; Kanatsu-Shinohara et al. 2012; Yang et al. 2013). Moreover, we
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54 345 previously reported significantly increased transcript levels of *Cxcl12* following germ cell
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4 346 depletion in mice and suggested that *Cxcl12* may stimulate the spermatogenic repopulation
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6 347 of the seminiferous tubules during testicular recovery (Westernströer et al. 2014).
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9 348 Whereas inflammatory chemokines (e.g. the C-X-C chemokine *CXCL11*) are mainly involved
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11 349 in the recruitment of leukocytes to inflamed tissue sites, homeostatic chemokines (e.g. the C-
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13 350 X-C chemokine *CXCL12*) are constitutively expressed in organs and have important
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15 351 functions in stem cell homing, tissue homeostasis and repair. Indications for testicular
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17 352 inflammation (e.g. massive cell infiltration by neutrophils, lymphocytes, macrophages and
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19 353 mast cells in the interstitium) (Guazzone et al. 2009) were not seen in the analyzed testes.
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21 354 Moreover, in contrast to *CXCL12*, only low transcript levels of *CXCL11* were detected in
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23 355 developing marmoset testes which confirmed that inflammatory C-X-C chemokines,
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25 356 especially *CXCL11* as a secondary ligand for *CXCR7*, is likely not of functional relevance for
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27 357 healthy marmoset testes.
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30 358 Transcript levels of *CXCR7* were also constitutively expressed and immunohistochemical
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32 359 analyses further demonstrated that the atypical chemokine receptor *CXCR7* is exclusively
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34 360 expressed by premeiotic germ cells (gonocytes, pre-spermatogonia, spermatogonia including
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36 361 A_{pale} and A_{dark} spermatogonia) throughout various phases of postnatal testicular development
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38 362 in the marmoset and the human testis. In agreement with these data we found that *Cxcr7*
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40 363 protein can be detected in gonocytes as well as in *Sall4*-positive undifferentiated
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42 364 spermatogonia of the developing mouse testis (Westernströer et al. 2014). Additionally,
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44 365 *Cxcr7* was also expressed on differentiated germ cells, spermatids and interstitial cells.
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46 366 These results reveal an evolutionarily conserved expression pattern of *CXCR7* in premeiotic
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48 367 germ cells in the mouse and both analysed primate species (Westernströer et al. 2014). The
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50 368 morphometric evaluation in immature marmoset testes has shown additionally that
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52 369 approximately 80% of migrating germ cells (gonocytes and pre-spermatogonia) express
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54 370 *CXCR7*. In general, recent studies in marmoset monkeys indicated that the migration of
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56 371 gonocytes most likely begins postnatally between birth and 4 months of age (Rune et al.
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4 372 1991; Sharpe et al. 2003b). Interestingly, several MAGE-A4⁺/CXCR7⁻ gonocytes were
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6 373 observed, whereas subsets of MAGE-A4⁺/CXCR7⁻ pre-spermatogonia were only rarely seen
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8 374 in seminiferous tubules, suggesting that CXCR7 may be involved in migration and/or
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10 375 adhesion of germ cells in immature marmoset testes. In general, migration of centrally
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12 376 located germ cells into the basal part of the seminiferous epithelium is a cellular process
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14 377 critical for germ cell survival and establishment of A_{dark} and A_{pale} spermatogonia which
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16 378 represent the reserve and active SSC pool in adulthood in marmoset and human testis
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18 379 (McGuinness and Orth, 1992; Orth et al. 2000). Moreover, our morphometric evaluation in
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20 380 immature marmoset testes has shown that around 50% of the spermatogonia at the
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22 381 basement membrane express CXCR7. Furthermore, we demonstrated that A_{dark} and A_{pale}
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24 382 spermatogonia express CXCR7 in marmoset testes at the age of 32 *wpp*, 52 *wpp* and > 80
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26 383 *wpp*. Therefore, we assume different roles for the atypical chemokine receptor CXCR7 in the
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28 384 developing marmoset testes. Tissue- and cell type-specific functions of CXCR7 have been
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30 385 described and depend on the cell type and tissue. This includes a role for cell survival or
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32 386 adhesion as described for example for in the breast cancer cell line MCF-7 (Burns et al.
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34 387 2006) as well as in renal multipotent progenitor cells of the human kidney (Mazzeinghi et al.
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36 388 2008).

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39 389 In addition, using HEK-293 and MDA-MB-231 cells, it has been demonstrated that receptor
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41 390 heterodimerization between CXCR4 and CXCR7 may enhance CXCL12-induced cell
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43 391 migration (Levoye et al. 2009; Decaillot et al. 2011). Regarding the localization of CXCR4 in
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45 392 developing mammalian testes, different expression patterns have been shown for mouse and
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47 393 human (Gilbert et al. 2009; Yoon et al. 2009; Kanatsu-Shinohara et al. 2012; Yang et al.
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49 394 2013, McIver et al. 2013). Whilst expression of CXCR4 was found in gonocytes,
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51 395 undifferentiated spermatogonia, Sertoli cells and interstitial cells of neonatal and adult mouse
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53 396 testes (Yoon et al. 2009; Kanatsu-Shinohara et al. 2012; Yang et al. 2013), CXCR4 protein
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55 397 was detected throughout the seminiferous tubules of adult human testes (Gilbert et al. 2009).

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4 398 So far, the expression profile and the role of CXCR4 in developing marmoset testes remain
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6 399 unknown. Nevertheless, receptor heterodimerization between CXCR4 and CXCR7
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8 400 throughout testicular development in primate testes cannot be excluded but needs to be
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10 401 investigated in further studies.

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13 402 In conclusion, we show that CXCL12/CXCR7 network is present in primate testes. The
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15 403 localization pattern suggests its involvement during migration, survival or adhesion in
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17 404 premeiotic germ cells.

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25 407 **Declaration of interest**

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28 408 The authors declare that there is no conflict of interest that could be perceived as prejudicing
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30 409 the impartiality of the research reported.

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558 **Figures:**

559 **Fig. 1** Marmoset monkey testes after birth - age-related changes in histology, weight and
560 transcript levels. Micrographs showing PAS stained tissue sections of marmoset testes at the
561 age of 16 *wpp* (*wpp* = weeks *post partum*; a), 32 *wpp* (b), 52 *wpp* (c) and > 80 *wpp* (d).
562 Gonocytes (arrowhead), pre-spermatogonia (white arrow) and spermatogonia (black arrow)
563 are the predominant germ cells in marmoset testes at the age of 16 *wpp* (a). Meiotic cells
564 (primary spermatocytes) were present in the seminiferous tubules of marmosets at the age of
565 32 *wpp* (b), whilst germ cells up to the stage of elongated spermatids were detected in the
566 seminiferous epithelium of marmoset monkeys at the age of 52 *wpp* (c). Finally,
567 spermatogenesis was complete in all marmosets at the age of > 80 *wpp* (d). Scale bars
568 represent 50 μm . Changes in testis weight (e) are shown as mean \pm SEM. Groups marked
569 with different letters (a, b, c, d) are significantly different from each other ($p < 0.001$). Relative
570 mRNA levels of *CXCL12* (f), *CXCL11* (g) and *CXCR7* (h) in marmoset testes at the age of 16
571 *wpp*, 32 *wpp*, 52 *wpp* and > 80 *wpp* were normalized using the housekeeping gene *TOP1* (2
572 $^{-\Delta\text{Ct}}$) method). Results are shown as mean \pm SEM and significant differences between the
573 groups are marked with * $P < 0.05$.

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575 **Fig. 2** Immunohistochemical detection of *CXCL12* in marmoset testes at the age of 16 *wpp*
576 (*wpp* = weeks *post partum*; a), 32 *wpp* (c, d), 52 *wpp* (e, f) and > 80 *wpp* (g, h). Incubation
577 with non-specific IgG antibody was performed as control and a representative image of a
578 marmoset testis at the age of 16 *wpp* is shown in (b). During testicular development, the
579 chemokine *CXCL12* is exclusively localized in the cytoplasm of Sertoli cells (white arrow).
580 Neither relatively undifferentiated germ cells (gonocytes, arrow head; spermatogonia, black
581 arrow) nor differentiating germ cells showed expression of *CXCL12*. Scale bars represent 20
582 μm .

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4 583 **Fig. 3** Immunohistochemical detection of CXCR7 and labelling index of CXCR7-positive cells
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6 584 in marmoset testes at the age of 16 *wpp* (*wpp* = weeks *post partum*). A representative image
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8 585 is showing CXCR7 expression in marmoset testes at the age of 16 *wpp* (a). The staining
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10 586 revealed that subsets of germ cells express CXCR7 (black arrow), whilst the remainder are
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12 587 negative (arrow head) for CXCR7. Sertoli cells (white arrow) in the seminiferous tubules
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14 588 showed no expression of CXCR7. Corresponding IgG antibody was used as negative control
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16 589 and a representative image is shown in (b). High magnification of CXCR7 stained tissue
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18 590 sections revealed CXCR7-positive and negative gonocytes (c, d), pre-spermatogonia (e, f)
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20 591 and spermatogonia (g, h). Scale bars represent 10 μm . Scores of CXCR7-positive and
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22 592 CXCR7-negative gonocytes (Gon+/Gon-), pre-spermatogonia (pre-SPG+/pre-SPG-) and
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24 593 spermatogonia (SPG+/SPG-) in marmoset testes at the age of 16 *wpp* are shown in (i).
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26 594 Results are shown as mean \pm SEM and significant differences between the groups are
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28 595 marked with * $P < 0.05$.
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34 597 **Fig. 4** Representative images for expression of MAGE-A4 (green) and CXCR7 (red) in testis
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36 598 sections from marmosets at the age of 16 *wpp* (a - c). MAGE-A4 expression is seen in the
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38 599 majority of germ cells including gonocytes (d), pre-spermatogonia (g) and spermatogonia (j).
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40 600 Subpopulations of MAGE-A4⁺/CXCR7⁺ (arrow heads) and/or MAGE-A4⁺/CXCR7⁻ (arrows)
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42 601 gonocytes (d - f), pre-spermatogonia (g - i) as well as spermatogonia (j - l) can be identified.
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44 602 Note that MAGE-A4⁺/CXCR7⁻ pre-spermatogonia are occasionally seen in the seminiferous
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46 603 tubules of marmoset testes at the age of 16 *wpp*. All sections were counterstained with
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48 604 Hoechst (blue). Dotted lines indicate the basement membrane of the seminiferous tubules.
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50 605 Scale bars represent 10 μm .
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4 607 **Fig. 5** Immunohistochemical detection of CXCR7 in marmoset testes at the age of 32 *wpp*
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6 608 (*wpp* = weeks *post partum*; a, b), 52 *wpp* (c, d) and > 80 *wpp* (e, f). In marmoset testes at the
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8 609 age of 32 *wpp*, 52 *wpp* and > 80 *wpp*, premeiotic germ cells (black arrow; including A_{pale} and
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10 610 A_{dark} spermatogonia) located at the basement membrane are labelled for CXCR7 whereas
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12 611 Sertoli cells (white arrow) showed no expression for CXCR7. Scale bars represent 20 μm (a
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14 612 – f). Following enzymatic digestion of adult marmoset testes, haematoxylin-stained single
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16 613 cells showed cell types with different morphology (g) as well as immunofluorescence staining
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18 614 revealed CXCR7-positive cells in this single cell suspension (h). As negative control,
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20 615 incubation with nonspecific IgG antibody was performed and a representative image is
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22 616 shown in (i). Scale bars represent 50 μm (g), 15 μm (h) and 60 μm (i).
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28 618 **Fig. 6** Immunohistochemical detection of CXCR7 in human testes at 2 weeks (a) and 6
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30 619 months after birth (c) as well as in adult (d) human testes. Corresponding IgG antibody was
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32 620 used as negative control and a representative image of an immature testis (2 weeks) is
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34 621 shown in (b). In immature human testes (a; c), gonocytes (arrow head, no contact with the
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36 622 basement membrane), pre-spermatogonia (white arrows, point contact with the basement
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38 623 membrane) and spermatogonia (black arrows, full contact with the basement membrane)
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40 624 were labelled for CXCR7. In adult human testes (d), premeiotic germ cells (red arrow)
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42 625 located at the basement membrane were labelled for CXCR7. Scale bars represent 20 μm .
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48 627 **Fig. 7** Schematic drawing of CXCR7 (red) and CXCL12 (green) expression in seminiferous
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50 628 tubules of marmoset testes at the ages of 16 *wpp* (a), 32 *wpp* (b), 52 *wpp* (c) and > 80 *wpp*
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52 629 (*wpp* = weeks *post partum*, d). In marmoset testes at the age of 16 *wpp*, CXCL12 is highly
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54 630 expressed by Sertoli cells whereas the atypical chemokine receptor CXCR7 is expressed by
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56 631 few gonocytes, pre-spermatogonia and spermatogonia (a). In the seminiferous epithelium of
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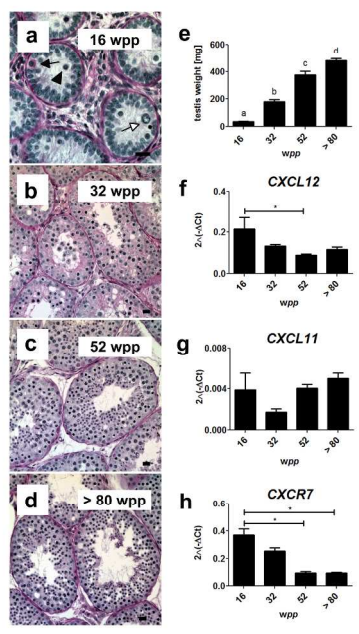
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4 632 marmoset testes at the ages of 32 wpp (b), 52 wpp (c) and > 80 wpp (d), CXCL12 is still
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6 633 highly expressed by Sertoli cells whereas CXCR7 is expressed by premeitotic germ cells,
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8 634 including A_{pale} and A_{dark} spermatogonia. The expression pattern of CXCL12 and CXCR7
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10 635 indicates a CXCL12/CXCR7 network in primate testes.
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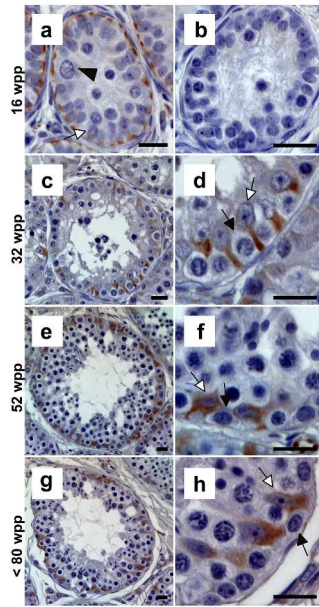
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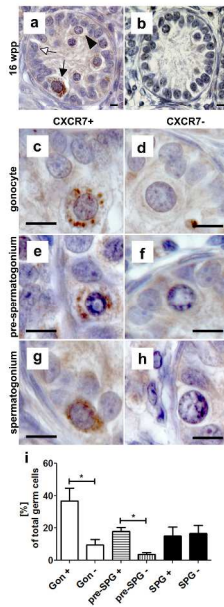
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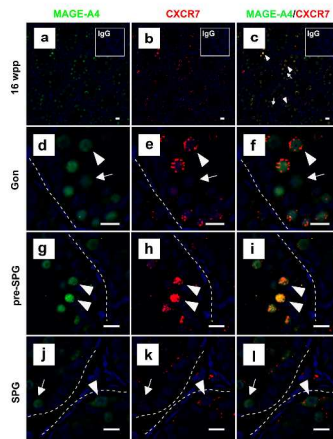
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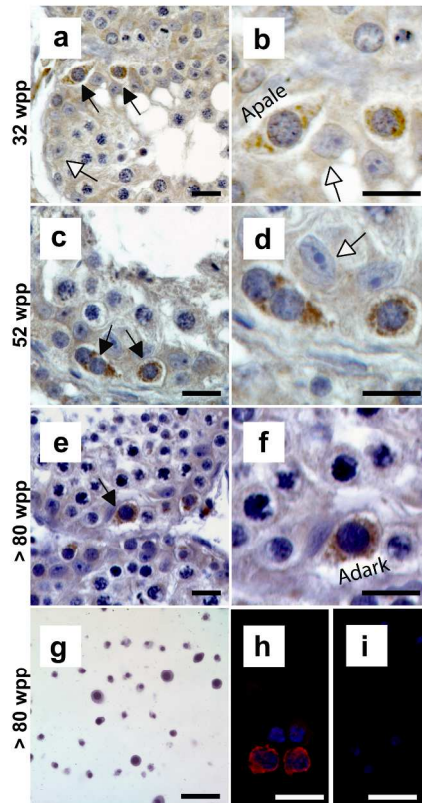
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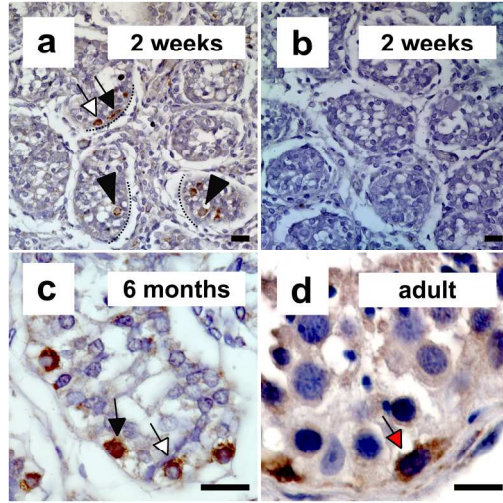
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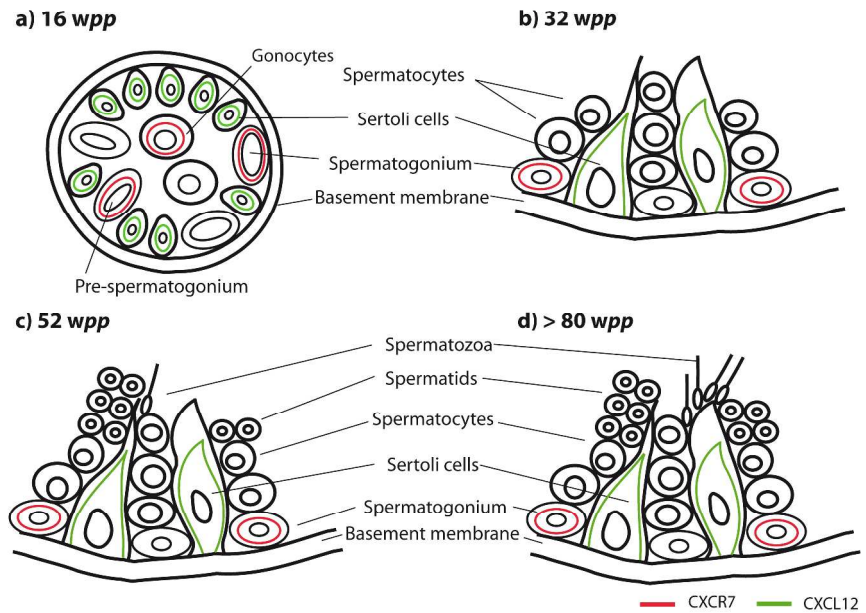
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Review

1 **Supplemental Table 1:** Westernströer *et al.*

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Primer sequences used for real-time quantitative PCR		
Target	Forward Primer (5' - 3')	Reverse Primer (5' - 3')
<i>calCXCR7</i>	CGTCATCGGCATGATTGC	TCTTGGCCTGGACGTTAC
<i>calCXCR4</i>	GGAGGGCATCAGTATATACACTTCAG	AAGCAGGGTTCCTTTATGGAGTC
<i>calCXCL12</i>	CACTCCAAACTGTGCCCTTCA	TGCACACTTGTCTGTTGTTGTTCT
<i>calCXCL11</i>	GCTGTGATATTCTGCGCTATGG	AGACAGCGTCCTCTGTTGAACA
<i>calTOP1</i>	CCGAAGGGACCTGAAAAGTG	CAGTCTCTGCACAGCCTTCTTCT
<i>cal</i> = <i>Callitrix jacchus</i>		

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Supplemental Table 2: Westernströer *et al.*

Flow cytometric assessment of CXCR7-positive cells in adult marmoset testes (n = 3)		
Animal Nr.:	Alexa ⁺ [%]	
	CXCR7	Rabbit IgG
1	7.6	0.5
2	2.4	0.9
3	4.0	0.3
Average ± SD	4.7 ± 2.7	0.6 ± 0.3

SD = Standard derivation

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