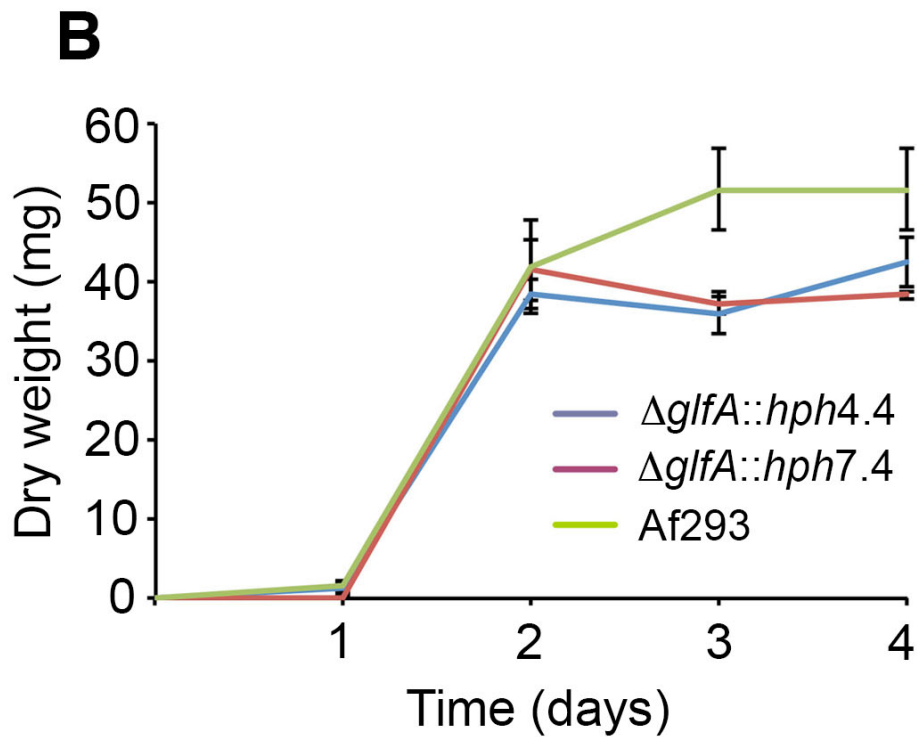
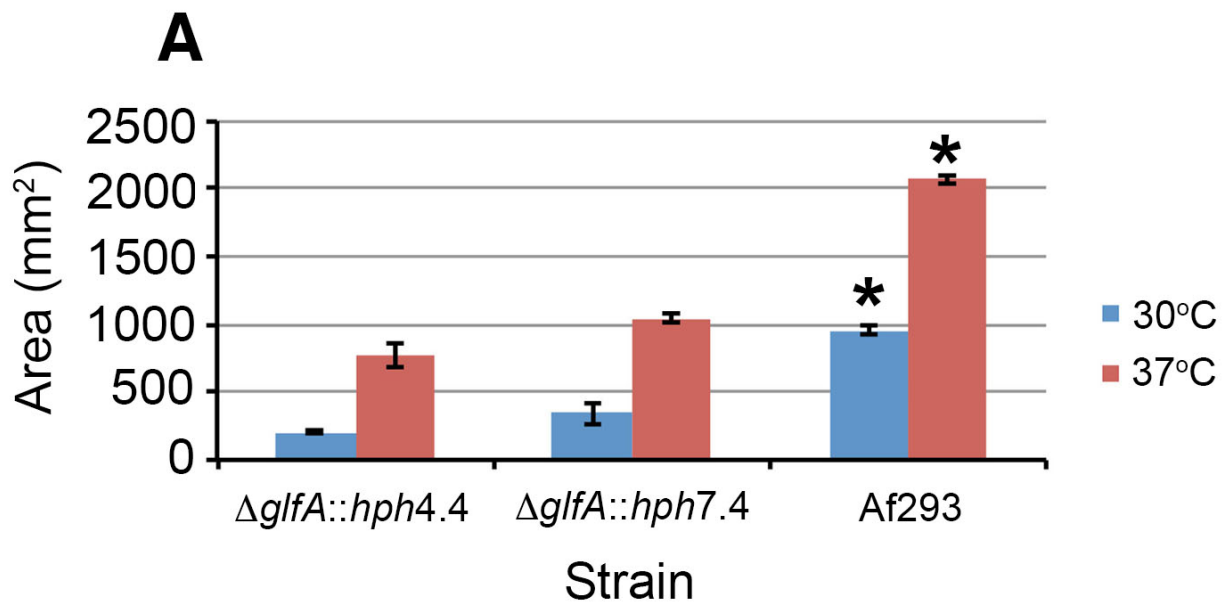


**Table S1.** Details of primer sequences used for amplification and targeted replacement of the UDP-galactopyranose mutase-encoding gene *glfA*. Sequences in bold are the reverse complement of the M13R/M13F overlap.

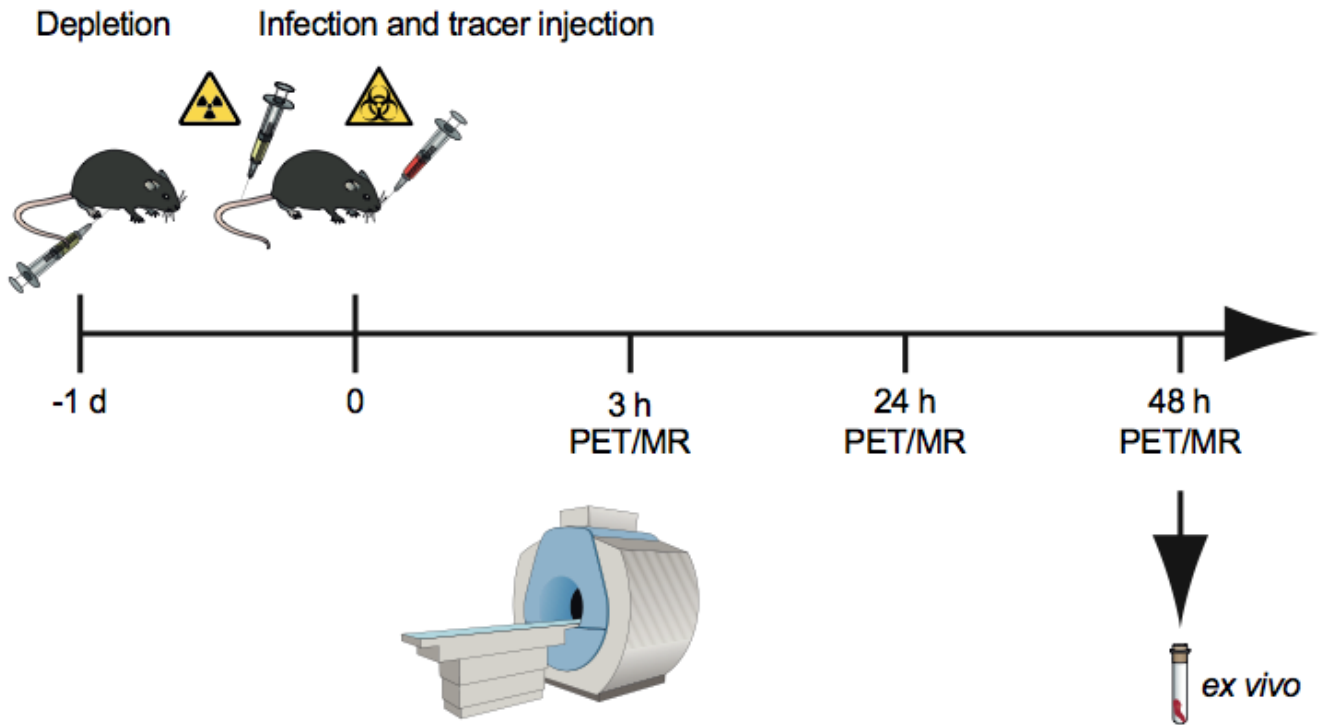
<b>Product</b>	<b>Primer</b>	<b>Sequence 5'→3'</b>
LF	glf50.1F	TCGCTAAGCTGCGGAGCGCATAGA
	glf50.1R	<b>GTCGTGACTGGGAAAACCCTGGCGCCTGCCTTGTAGGATATCCTGGAA</b>
RF	glf30.1F	<b>TCCTGTGTGAAATTGTTATCCGCTAATGTTTCCTTTCTCATGTACCACG</b>
	glf30.1R	TCGCCCCTGGACGCGTGTTGCTCA
HY	HY split	GGATGCCTCCGCTCGAAGTA
	M13F	CGCCAGGGTTTTCCAGTCACGAC
YG	YG split	CGTTGCAAGACCTGCCTGAA
	M13R	AGCGGATAACAATTCACACAGGA
LFHY	glf50.4F	GTATCATCTTGTGATCCGCAAAGG
	HY split	GGATGCCTCCGCTCGAAGTA
RFYG	glf30.1R	TCGCCCCTGGACGCGTGTTGCTCA
	nested YG split	CGCAAGGAATCGGTCAATACACTA
<i>glfA</i> ORF	PROBEF	ATTGGTGCCGGACCTACTGGTCTT
	PROBER	ACAGCTGCTTGGTGAGACCAACGA

### Supplementary figures and legends

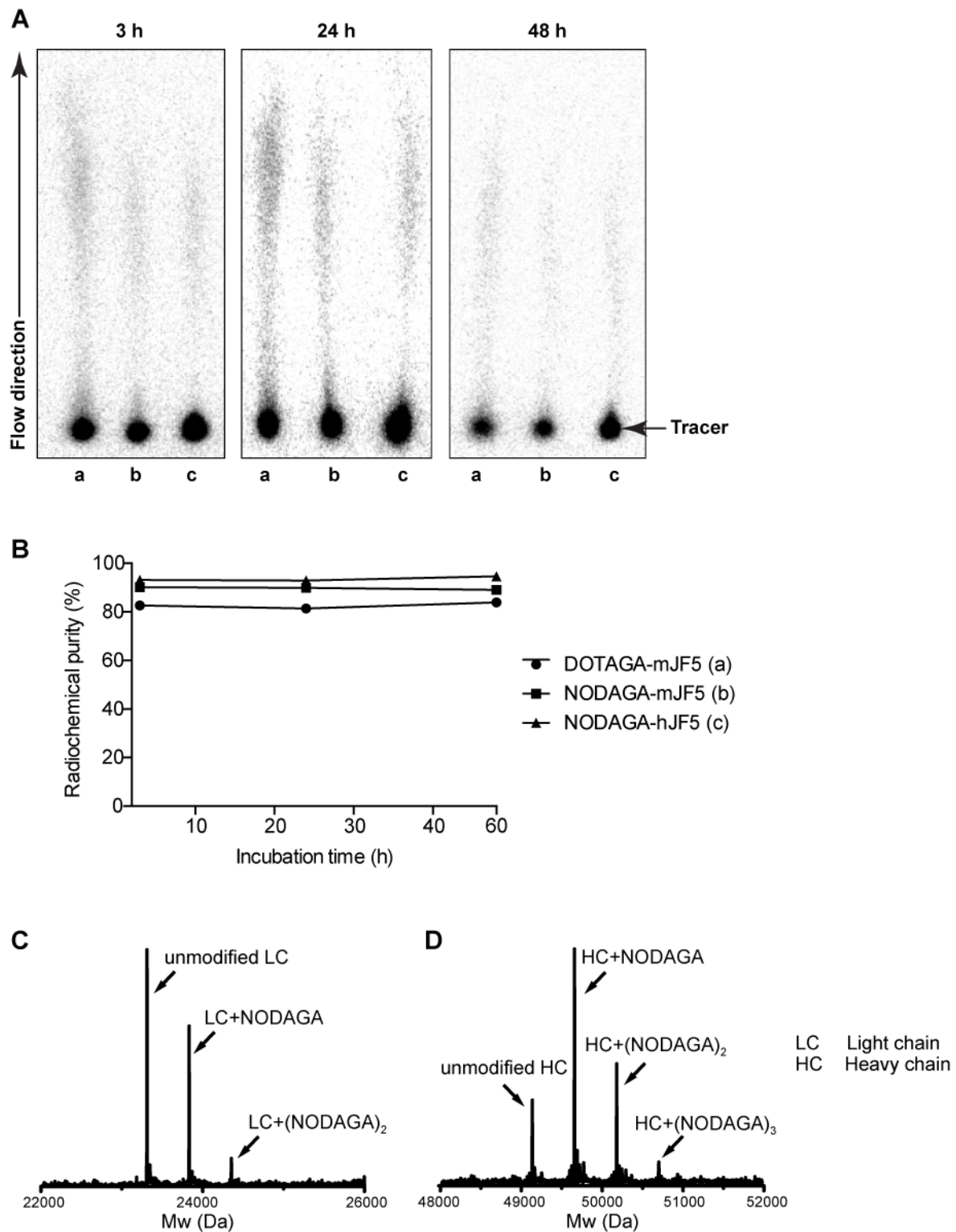


**Supplementary Figure 1. A.** Colony areas of wild-type Af293 and mutant *A. fumigatus* strains following 3 days growth on MEA at 30 °C and 37 °C. Each bar is the mean of 3 replicates  $\pm$  standard errors, and asterisks by Af293 bars denote significant differences ( $P < 0.05$ ) in mean areas compared to mutant strains at the two different temperatures. Note the

reductions in growth of the two mutant strains at both temperatures when compared to Af293. **B.** Biomass dry weights in mg of mutant and wild-type strains (n=3) over 4 days growth in MEB shake cultures. The growth of all three strains was similar on days 1 and 2, with no additional growth of the two mutants compared to Af293 thereafter. Culture filtrates were tested in ELISA for reactivity with mAbs mJF5 and hJF5 (see Fig 2B).

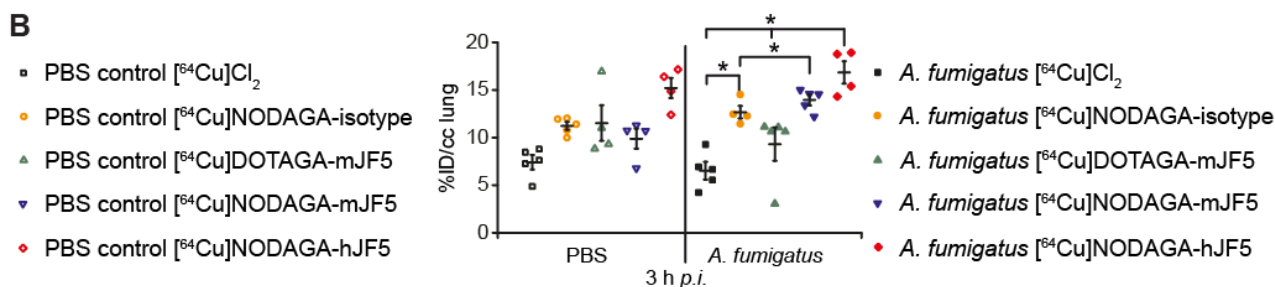
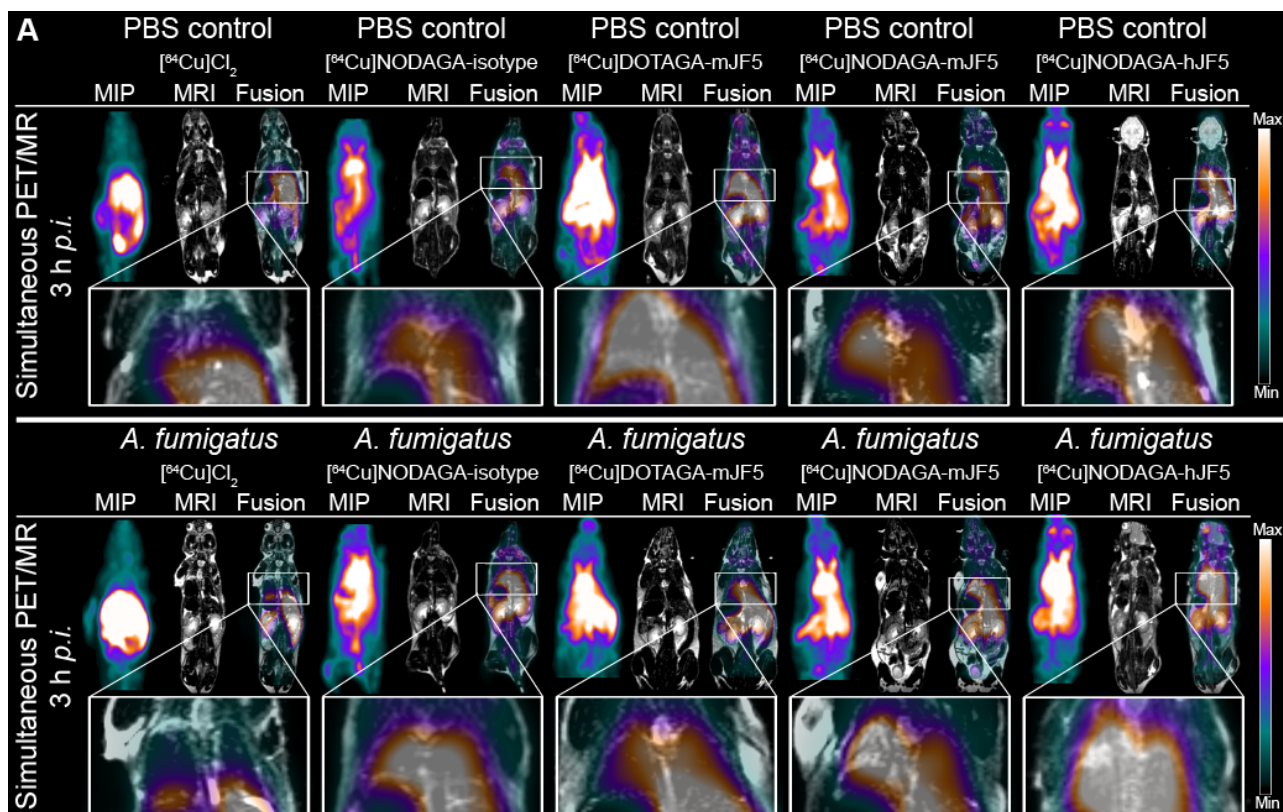


**Supplementary Figure 2.** Schematic representation of the imaging procedure. 24 h prior to the infection procedure with *A. fumigatus*, neutropenia was induced by the injection of 100  $\mu\text{g}$  per animal of the anti-Ly-6G/anti-Ly6C antibody RB6-8C5. 24 h later, mice were *i.t.* infected with an *A. fumigatus* spore solution for pulmonary fungal infection and the respective PET tracers were *i.v.* injected at the same time. Simultaneous PET/MR imaging of the animals was performed 3 h, 24 h and 48 h after the infection/tracer injection. *Ex vivo* biodistribution and autoradiography were conducted after the last PET scan at 48 h *p.i.*



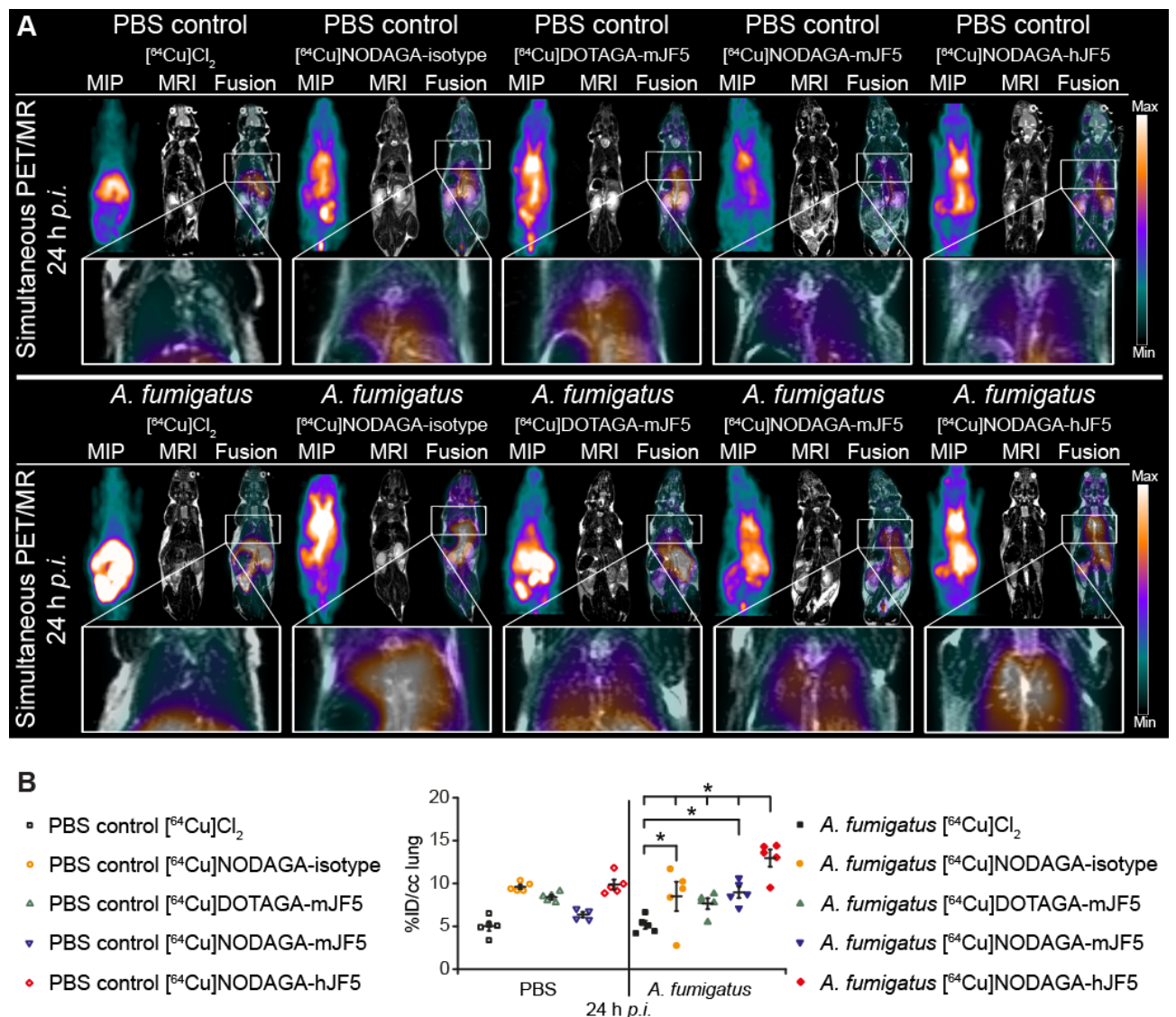
**Supplementary Figure 3. A.** Serum stability of the  $^{64}\text{Cu}$ -labeled, chelator-conjugated hJF5 and mJF5 determined by TLC. Samples were run on iTLC-SG paper and then analyzed by autoradiography. a = DOTAGA-mJF5, b = NODAGA-mJF5, c = NODAGA-hJF5. Arrow = direction of flow. **B.** Serum stability of the  $^{64}\text{Cu}$ -labelled, chelator-conjugated hJF5 and

mJF5. The radiochemical purity over the time of 48 h shows no signs of proteolytic degradations, protein aggregations or copper transchelations to serum proteins. **C** and **D**. Conjugation of NODAGA-NCS to hJF5 analyzed by LC-MS-ESI (DTT was used to separate the light from the heavy chain). Representative de-convoluted LC-MS spectra of the hJF5 light chain (**C**) and heavy chain (**D**), with up to two and three NODAGA chelators being conjugated, respectively. From the peak intensities, a conjugation ratio of approximately three was estimated.



**Supplementary Figure 4. A.** *In vivo* biodistribution of  $[^{64}\text{Cu}]\text{Cl}_2$ ,  $[^{64}\text{Cu}]\text{NODAGA-isotype}$  control,  $[^{64}\text{Cu}]\text{DOTAGA-mJF5}$ ,  $[^{64}\text{Cu}]\text{NODAGA-mJF5}$  and  $[^{64}\text{Cu}]\text{NODAGA-hJF5}$  in PET/MR imaging at 3 h *p.i.* Coronal MIP, MR and fused PET/MR images of PBS treated mice and *A. fumigatus* infected mice injected with the respective tracers. **B.** Quantification of the *in vivo* PET insert images for the lung at 3 h *p.i.* in groups of n=4-5 mice. The graph shows the uptake of the various tracers in the lungs of infected animals and PBS controls at 3 h *p.i.* The quantification reveals higher tracer uptake in the lungs of animals injected with  $[^{64}\text{Cu}]\text{NODAGA-hJF5}$  and lower tracer uptake in lungs of animals which received

[<sup>64</sup>Cu]Cl<sub>2</sub>. Data are expressed as the mean ± SD %ID/cc. Group differences were examined using one-way ANOVA, followed by post hoc Tukey–Kramer, \**P* < 0.05.

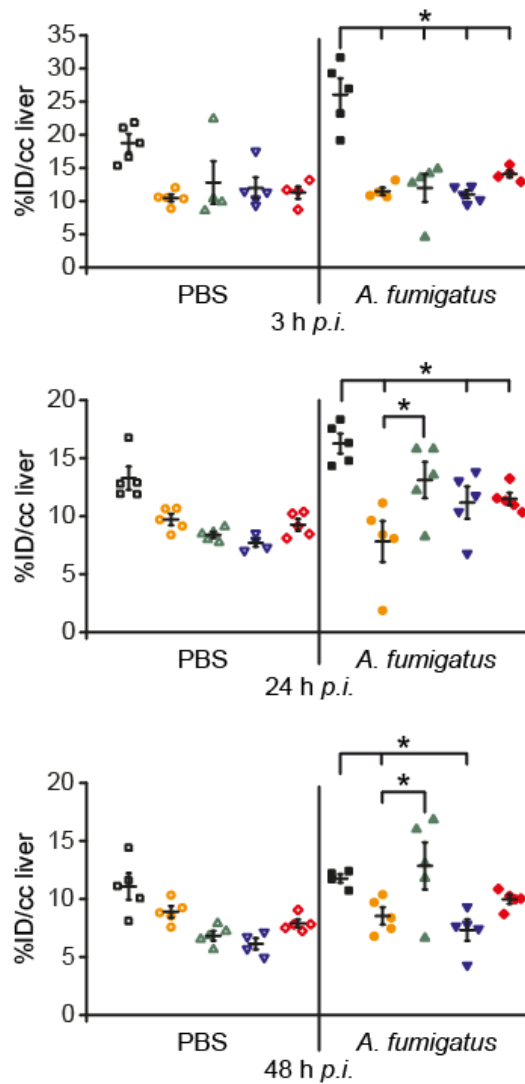


**Supplementary Figure 5. A.** *In vivo* biodistribution of [<sup>64</sup>Cu]Cl<sub>2</sub>, [<sup>64</sup>Cu]NODAGA-isotype control, [<sup>64</sup>Cu]DOTAGA-mJF5, [<sup>64</sup>Cu]NODAGA-mJF5 and [<sup>64</sup>Cu]NODAGA-hJF5 in PET/MR imaging at 24 h p.i. Coronal MIP, MR and fused PET/MR images of PBS treated mice and *A. fumigatus* infected mice injected with the respective tracers. The acquired images reveal the low lung uptake of [<sup>64</sup>Cu]Cl<sub>2</sub> in both infected and PBS treated mice, affirming the specificity of the <sup>64</sup>Cu-labeled, chelator conjugated JF5 antibody tracers as it



excludes perfusion effects derived from infection-related inflammation. The image further displays the specific and high lung uptake of the chelator-conjugated antibody-based tracers in infected animals compared to the PBS treated control groups. Additionally, the MR image of infected animals shows the beginning of hyphal growth of *A. fumigatus* in the lung (hyperintense structures). **B.** Quantification (n=4-5 mice) of the *in vivo* PET insert images for the lung 24 h *p.i.* The graph shows the uptake of the different tracers in the lungs of infected animals and the PBS controls at 24 h *p.i.* Lower uptake was observed in the lungs of infected and PBS treated animals receiving [<sup>64</sup>Cu]Cl<sub>2</sub>. Infected mice which received the [<sup>64</sup>Cu]NODAGA-hJF5 tracer show significantly higher lung uptakes compared to infected animals injected with [<sup>64</sup>Cu]DOTAGA-mJF5, [<sup>64</sup>Cu]NODAGA-mJF5 or [<sup>64</sup>Cu]Cl<sub>2</sub>. Data are expressed as the mean ± SD %ID/cc. Group differences were examined using one-way ANOVA, followed by post hoc Tukey–Kramer, \**P* < 0.05.

- PBS control [<sup>64</sup>Cu]Cl<sub>2</sub>
- PBS control [<sup>64</sup>Cu]NODAGA-isotype
- ▲ PBS control [<sup>64</sup>Cu]DOTAGA-mJF5
- ▼ PBS control [<sup>64</sup>Cu]NODAGA-mJF5
- ◊ PBS control [<sup>64</sup>Cu]NODAGA-hJF5
- *A. fumigatus* [<sup>64</sup>Cu]Cl<sub>2</sub>
- *A. fumigatus* [<sup>64</sup>Cu]NODAGA-isotype
- ▲ *A. fumigatus* [<sup>64</sup>Cu]DOTAGA-mJF5
- ▼ *A. fumigatus* [<sup>64</sup>Cu]NODAGA-mJF5
- ◊ *A. fumigatus* [<sup>64</sup>Cu]NODAGA-hJF5



**Supplementary Figure 6.** Quantification of the *in vivo* PET insert data for the liver (n=4-5) at 3, 24 and 48 h *p.i.* The graphs display the uptake of the different antibody-based PET tracers in the liver of *A. fumigatus* infected and PBS treated control animals in groups of n=5 mice. Higher uptake of [<sup>64</sup>Cu]Cl<sub>2</sub> is observed in healthy and infected animals 3 h *p.i.*

suggesting fast clearance of  $^{64}\text{Cu}$  by the liver. Also, DOTAGA-conjugated mJF5 revealed higher uptake in the liver of *A. fumigatus* infected animals compared to the NODAGA-labeled antibodies 48 h *p.i.* Data are expressed as the mean  $\pm$  SD %ID/cc. Group differences were examined using one-way ANOVA, followed by post hoc Tukey–Kramer,  $*P < 0.05$ .