## TABLE S1 Primers used in this study

Primer	Sequence
NAT-F	AGCGGATAACAATTTCACACAGGA
NAT-R	CGCCAGGGTTTTCCCAGTCACGAC
CAP60up-F	TGGCACCACAACATCTGGGA
CAP60up-R	ACAACGTCGTGACTGGGAAAACCCTGGCGATCGGTGACGGATGAGGGAT
CAP60down-F	CTGTTTCCTGTGTGAAATTGTTATCCGCTCGGGCTTCTAATGCACAGGT
CAP60down-R	GAAATGATGGTCACTCGACA
CAP60up-NotI-F	AAAAGCGGCCGCGCACCACAACATCTGGGA
CAP60down-SacII-R	AAAACCGCGGGAAATGATGGTCACTCGACA
CAP60rt-F	ACTCAACAACGCCGCCATGG
NATcheck-F1	GTCACCAACGTCAACGCACC
CAP60-downR1	GGAGGCGGAGTTAAAAGCAA





**FIG S1 Gene disruption and reintegration.** *CAP60* ORF, the region from the ATG start codon to the TAG stop codon, was completely deleted by homologous recombination. Deletant CAP60Δ was nourseothricin resistant, as it had nourseothricin resistant gene *NAT1* in its *CAP60* locus. Complement vector pJAF12-CAP60 was integrated into the *CAP60* locus of deletant CAP60Δ to generate revertant CAP60C. Because the complement vector harbored the geneticin resistant gene NeoR, revertant CAP60C was geneticin/nourseothricin double resistant. Two PCRs were used to confirm the intended recombination in transformants. The primers used for PCR were: (1) CAP60T+F and Cap60-downR1 and (2) NATcheck-F1 and Cap60-downR1; M: 1 kb ladder, W: wild type strain PNG18, Δ: deletant CAP60Δ, C: revertant CAP60C, N: non-template control.



**FIG S2 Several CAP60 Cells are engulfed by each BMDC.** Prior to incubation, heat-killed *C. gattii* cells were stained with acridine-orange (AO: green), which binds to nucleic acids. After 24 h incubation for phagocytosis, these cells were stained with calcofluor white (CFW: blue), which binds to chitin in the cell wall. Because this fluorescent dye did not enter BMDCs, engulfed fungal cells were not stained by calcofluor white.



**FIG S3 CAP60** $\Delta$  **induces BMDCs to express co-stimulatory molecules.** BMDCs (2 × 10<sup>6</sup> cells/ml) were incubated with heat-killed strain R265 cells, CAP60 $\Delta$  cells (MOI = 0.1), or 100 ng/ml of LPS for 24 h. BMDCs were collected and stained for CD11c, CD11b, CD86, CD40, and I-Ab. For flow cytometry analysis, gates were set for CD11c+ CD11b+ cells.



FIG S4 Vaccination using heat-killed fungal cells does not ameliorate pulmonary infection with highly virulent *C. gattii* strain R265. Heat-killed fungal cells, HK-R265 or HK-CAP60 $\Delta$ (5 × 10<sup>6</sup> cells/mouse), were administered intravenously to mice, both at 14 days and at 1 day prior to intratracheal infection with R265 (3 × 10<sup>3</sup> CFUs/mouse). Fungal burdens at day 14 post-infection (A) and survival rates (B) were determined as described in Figure 2. Median survivals: non-vaccination = 23 days; HK-CAP60 $\Delta$  transfer = 21.5 days.



**FIG S5 DC-based vaccine induces lung leukocyte recruitment and ameliorates lung pathology.** Lung leukocytes were stained using Diff-Quick (A-B) and cell numbers were determined (C) at day 7 post-transfer. Multi-nucleated cells were found in the lungs of CAP60 $\Delta$ / DC injected mice (B). Histograms show results expressed as means ± SD, \* *p* < 0.05 vs. control by unpaired *t*-test, # *p* < 0.05 vs. control by unpaired *t*-test with Welch's correction. Similar results were obtained at day 9 post-transfer (C). Gross pathology and lung sections were assessed at day 13 post-infection (D-E). Lung sections were stained with hematoxylin-eosin [HE] or alcian blue [AB], as described in Figure 3, and observed at a magnification of ×100.

## TABLE S2 Statistical analysis for lung sections

	Three mice per group for evaluation	non-transfer	CAP60∆/DC	<i>p</i> -value
A. /	Alveolar space (Cross point interval, um)	68.6 ± 38.0	52.4 ± 25.7	– <i>p</i> < 0.01
	Alveolar space (Cross point interval, pin)	n = 1072	n = 1038	
В.	Variance of alveolar space	38.0 ± 0.753	25.6 ± 1.06	– <i>p</i> < 0.01
	(Variance of cross point interval, µm)	n = 3	n = 3	
C. <sup>-</sup>	The number of MCCs (MCCs/mm <sup>2</sup> )	0.43 ± 0.14	1.1 ± 0.46	– <i>p</i> < 0.05
		n = 6	n = 6	
D.	The number of nuclei per MCC	3.7 ± 2.2	7.0 ± 5.5	– <i>p</i> < 0.01
	The number of nuclei per MGC	n = 273	n = 378	
E.	Nuclear density in MCC (nuclei/ $(1000 \text{ um}^2)$ )	4.2 ± 2.4	8.8 ± 4.4	– <i>p</i> < 0.01
		n = 116	n = 108	

Detail methods are described in Material and Methods. Values are means  $\pm$  SD. *P*-value in Column B was derived from unpaired *t*-test and the other *p*-values were derived from unpaired *t*-tests with Welch's correction.



FIG S6 Transferring CAP60 $\Delta$ /DCs induces cytokine production in lung. (A) Lung leukocytes were collected from three mice at 7 days posttransfer and stimulated with PMA and ionomycin for 3 h. For flow cytometry analysis, gates were set for CD3+ cells. Total numbers of CD4 T cells that expressed intracellular IL-17A, IFN $\gamma$ , or TNF $\alpha$  were determined. Representative data from two separate experiments are expressed as means ± SD, \* *p* < 0.05 vs. control by unpaired *t*-test, # *p* < 0.05 vs. control by unpaired *t*-test with Welch's correction. (B) Lungs were harvested from five mice at 14 days post-injection. Cytokine levels in lung homogenates were determined by ELISA. Representative data from three or four independent experiments are shown. Histogram results are means ± SD, \* *p* < 0.05 vs. control by unpaired *t*-test, # *p* < 0.05 vs. control by unpaired *t*-test, # *p* < 0.05 vs. control by unpaired *t*-test, # *p* < 0.05 vs. control by unpaired *t*-test, # *p* < 0.05 vs. control by unpaired *t*-test, # *p* < 0.05 vs. control by unpaired *t*-test, # *p* < 0.05 vs. control by unpaired *t*-test, # *p* < 0.05 vs. control by unpaired *t*-test, # *p* < 0.05 vs. control by unpaired *t*-test, # *p* < 0.05 vs. control by unpaired *t*-test, # *p* < 0.05 vs. control by unpaired *t*-test, # *p* < 0.05 vs. control by unpaired *t*-test with Welch's correction.