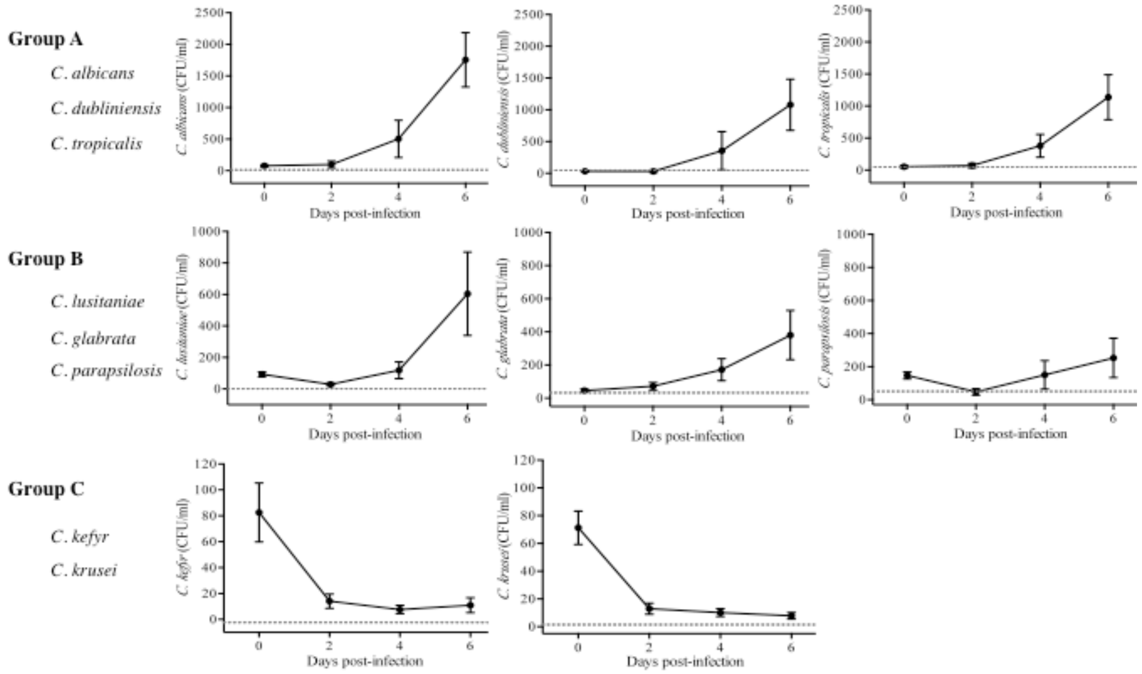

Fig. S1. Evolution profiles of the fungal burden within granulomatous structures of *Candida* spp. The fungal burden was followed at 0, 2, 4 and 6 days after infection of human peripheral blood mononuclear and polymorphonuclear cells with living yeasts from different *Candida* species. Results are expressed as colony-forming units per ml (CFU/ml). Data are represented as the mean + SEM of the fungal burden from ten healthy donors for each *Candida* species. Profiling was performed according to the two-way ANOVA statistical analysis ($\alpha = 0.05$). Three profiles were identified: profile A: *C. albicans*, *C. dubliniensis* and *C. tropicalis* showing “high” fungal burdens. Profile B: *C. lusitaniae*, *C. glabrata* and *C. parapsilosis* showing “intermediate” fungal burdens. Profile C: *C. kefyr* and *C. krusei* presenting “low” fungal burdens.

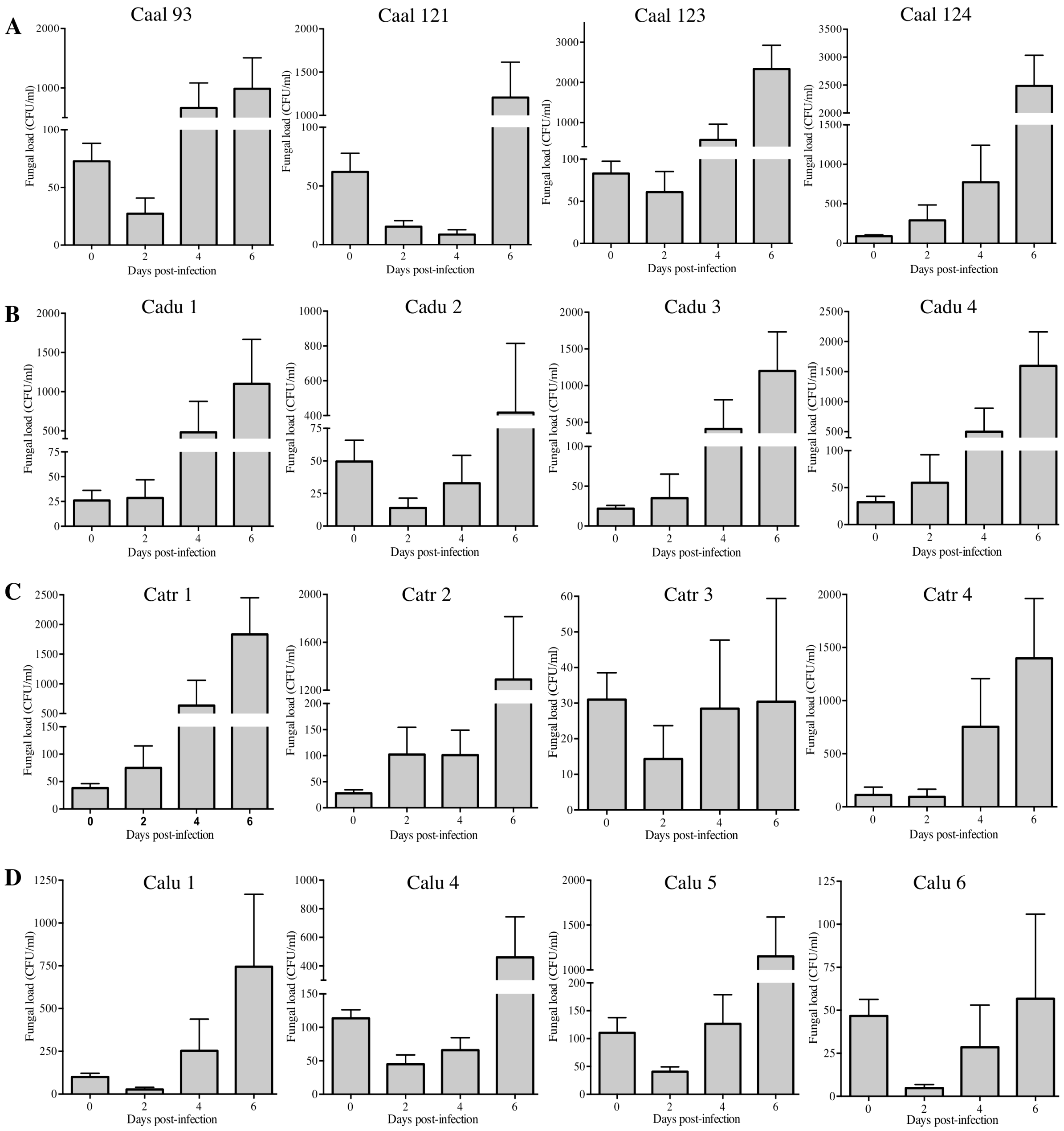

Fig. S2. Evolution of the fungal burden within granulomatous structures of 32 clinical isolates of *Candida* spp. The fungal burden was followed at 0, 2, 4 and 6 days after infection of human peripheral blood mononuclear and polymorphonuclear cells with living yeasts from different *Candida* species. Results are expressed as colony-forming units per ml (CFU/ml). Data are represented as the mean + SEM of the fungal burden from ten healthy donors for each *Candida* species: **(A)** *C. albicans*, **(C)** *C. dubliniensis*, **(C)** *C. tropicalis* and **(D)** *C. lusitaniae*.

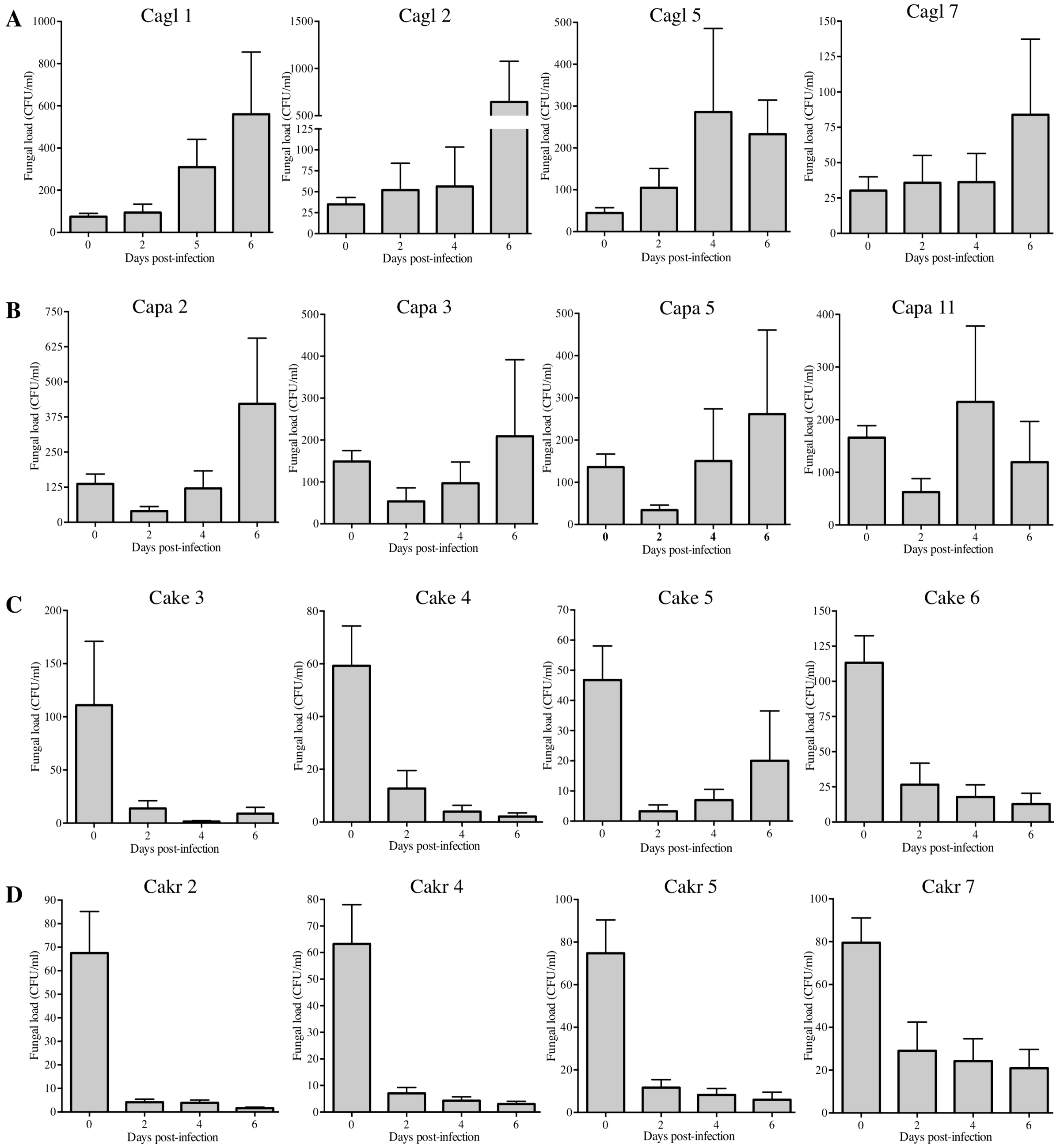

Fig. S3. Evolution of the fungal burden within granulomatous structures of 32 clinical isolates of *Candida* spp. The fungal burden was followed at 0, 2, 4 and 6 days after infection of human peripheral blood mononuclear and polymorphonuclear cells with living yeasts from different *Candida* species. Results are expressed as colony-forming units per ml (CFU/ml). Data are represented as the mean + SEM of fungal burden from ten healthy donors for each *Candida* species: **(A)** *C. glabrata*, **(B)** *C. parapsilosis*, **(C)** *C. kefyr* and **(D)** *C. krusei*.

Table S1. Distribution of granulocyte, monocyte and T cell subsets based on CD66, CD14, CD56, CD4 and CD8 from persistent-infection and controlled-infection granulomas after infection with *C. albicans*, *C. dubliniensis* and *C. tropicalis* (group A).

	Day 0				**Day 2**				**Day 4**				**Day 6**			
	Mean (SD) PI	**Mean (SD) CI**	***p***	**Mean Diff.**	**Mean (SD) PI**	**Mean (SD) CI**	***p***	**Mean Diff.**	**Mean (SD) PI**	**Mean (SD) CI**	***p***	**Mean Diff.**	**Mean (SD) PI**	**Mean (SD) CI**	***p***	**Mean Diff.**
CD66+	40.24 (9.95)	60.33 (13.96)	****	-20.1	26.26 (18.64)	46.78 (13.31)	****	-20.5	14.57 (6.32)	15.95 (5.206)	ns	-1.3	7.15 (7.77)	12.22 (6.41)	ns	-5.1
CD14+	6.31 (2.35)	5.94 (0.936)	ns	0.4	5.43 (3.767)	7.133 (1.94)	ns	-1.7	4.60 (4.51)	6.14 (3.11)	ns	-2	1.16 (1.41)	3.52 (2.55)	*	-2.4
CD3-CD56+	14.26 (4.93)	12.13 (4.864)	ns	2.2	15.2 (6.82)	12.96 (5.12)	ns	2.3	11.5 (4.952)	8.30 (3.969)	ns	3.2	13.55 (8.40)	4.81 (3.033)	****	8.7
CD3+CD56+	5.56 (6.13)	4.28 (1.27)	ns	1.2	4.01 (3.30)	2.923 (0.92)	ns	1.1	4.45 (4.44)	2.48 (1.348)	ns	2	4.53 (5.43)	2.36 (1.10)	ns	2.2
CD3+	60.49 (9.42)	68.53 (3.435)	ns	3.1	50.37 (16.17)	59.70 (7.75)	*	-9.1	61.55 (13.36)	63.51 (12.71)	ns	-1.9	50.92 (12.29)	65.88 (17.77)	****	-15
CD4+CD8-	45.85 (11.67)	58.85 (3.993)	****	-13	40.07 (11.96)	51.78 (6.931)	***	-11.7	45.65 (14.76)	58.31 (10.78)	****	-12.7	41.46 (12.16)	59.76 (15.08)	****	-18.3
CD4-CD8+	26.19 (8.76)	18.96 (3.263)	ns	4.8	23.83 (8.84)	15.67 (2.412)	***	8.1	23.46 (9.395)	10.59 (3.33)	****	12.9	20.15 (9.844)	11.29 (3.68)1	****	8.9
CD4+:CD8+ ratio	1.75	3.1			1.68	3.3			1.94	5.51			2.06	5.29		
CD4hiCD8hi	0.20 (0.17)	0.22 (0.04)	ns	0	0.33 (0.43)	0.15 (0.12)	ns	0.2	0.36 (0.50)	0.15 (0.11)	*	0.4	0.13 (0.17)	0.07 (0.06)	ns	0.1
CD4hiCD8lo	0.57 (0.55)	0.55 (0.30)	ns	0	0.47 (0.6434)	0.38 (0.30)	ns	0.1	0.59 (0.85)	0.35 (0.23)	ns	0.2	0.67 (0.80)	0.37 (0.36)	ns	0.3
CD4loCD8hi	0.93 (0.76)	0.47 (0.22)	ns	0.5	0.73 (0.89)	0.31 (0.18)	ns	0.4	1.02 (1.441)	0.23 (0.15)	**	0.8	1.32 (1.079)	0.46 (0.31)	***	0.9

Results were expressed as the median fraction of cells expressing the marker(s) +/- SD among specific gates. Significant differences were evaluated by comparison between persistent-infection (PI) and controlled-infection (CI) status over time using one-way ANOVA with Tukey's multiple comparisons test.*, $p < 0.05$; **, $p < 0.001$; ***, $p < 0.0001$; ****, $p < 0.00001$, ns: not significant.

Table S2. Distribution of granulocyte, monocyte and T cell subsets based on CD66, CD14, CD56, CD4 and CD8 from persistent-infection and controlled-infection granulomas after infection with *C. lusitaniae*, *C. parapsilosis* and *C. glabrata* (group B).

	Day 0				**Day 2**				**Day 4**				**Day 6**			
	Mean (SD) PI	**Mean (SD) CI**	***p***	**Mean Diff.**	**Mean (SD) PI**	**Mean (SD) CI**	***p***	**Mean Diff.**	**Mean (SD) PI**	**Mean (SD) CI**	***p***	**Mean Diff.**	**Mean (SD) PI**	**Mean (SD) CI**	***p***	**Mean Diff.**
CD66+	41.25 (12.93)	53.87 (14.91)	****	-12.6	31.33 (18.40)	42.06 (16.82)	****	-22.5	15.96 (4.730)	16.67 (4.73)	ns	-0.7	6.73 (6.82)	9.48 (7.70)	ns	-2.7
CD14+	6.11 (2.075)	6.579 (1.054)	ns	-0.3	6.10 (3.70)	6.48 (3.22)	ns	-1.8	3.88 (2.77)	5.71 (3.76)	ns	-1.1	2.70 (2.61)	2.53 (2.81)	ns	-0.1
CD3-CD56+	13.98 (4.79)	13.12 (5.19)	ns	0.8	15.32 (6.80)	13.37 (6.50)	ns	10.5	13.32 (6.03)	9.11 (4.42)	**	4.2	9.86 (5.404)	5.95 (3.53)	*	3.9
CD3+CD56+	5.91 (5.733)	4.618 (4.402)	ns	1.2	4.35 (3.317)	3.03 (2.33)	ns	1.3	4.14 (3.88)	3.50 (3.01)	ns	0.6	4.27 (4.98)	3.38 (4.67)	ns	0.8
CD3+	62.31 (10.05)	64.03 (7.316)	ns	-1.7	52.68 (13.42)	52.32 (13.01)	ns	0.3	59.47 (11.41)	65.06 (11.33)	ns	-5.5	53.30 (13.61)	56.87 (17.85)	ns	-3.5
CD4+CD8-	48.30 (12.44)	52.06 (10.36)	ns	-3.7	41.24 (12.71)	43.66 (10.93)	ns	-2.4	46.34 (13.71)	53.64 (14.49)	ns	-7.3	43.31 (14.01)	47.93 (18.15)	ns	-4.6
CD4-CD8+	26.21 (8.43)	21.35 (7.107)	ns	4.8	24.75 (9.74)	17.84 (8.23)	**	6.9	22.19 (10.52)	16.65 (8.96)	ns	5.6	19.15 (8.60)	14.83 (9.287)	ns	4.3
CD4+:CD8+ ratio	1.84	2.44			1.67	2.45			2.08	3.22			2.26	3.23		
CD4hiCD8hi	0.20 (0.13)	0.23 (0.16)	ns	0	0.28 (0.36)	0.26 (0.43)	ns	0	0.28 (0.34)	0.33 (0.45)	ns	-0.1	0.11 (0.12)	0.11 (0.13)	ns	0
CD4hiCD8lo	0.44 (0.32)	0.52 (0.36)	ns	-0.1	0.32 (0.29)	0.39 (0.35)	ns	-0.1	0.36 (0.29)	0.40 (0.32)	ns	0	0.45 (0.36)	0.43 (0.45)	ns	0
CD4loCD8hi	0.70(0.58)	0.88 (0.78)	ns	-0.2	0.62 (0.75)	0.66 (0.10)	ns	0	0.72 (0.91)	0.83 (1.31)	ns	-0.1	0.94 (0.82)	0.10 (1.14)	ns	0

Results were expressed as the median fraction of cells expressing the marker(s) +/- SD among specific gates. Significant differences were evaluated by comparison between persistent-infection (PI) and controlled-infection (CI) status over time using one-way ANOVA with Tukey's multiple comparisons test.*, $p < 0.05$; **, $p < 0.001$; ***, $p < 0.0001$; ****, $p < 0.00001$, ns: not significant.

Table S3. Distribution of granulocyte, monocyte and T cell subsets based on CD66, CD14, CD56, CD4 and CD8 from persistent-infection and controlled-infection granulomas after infection with *C. krusei* and *C. kefyr* (group C).

	Day 0			**Day 2**			**Day 4**			**Day 6**		
	Mean (SD) CI	***p* vs. group A CI**	***p* vs. group B CI**	**Mean (SD) IC**	***p* vs. group A CI**	***p* vs. group B CI**	**Mean (SD) CI**	***p* vs. group A CI**	***p* vs. group B CI**	**Mean (SD) CI**	***p* vs. group A CI**	***p* vs. group B CI**
CD66+	48.61 (15.42)	***	ns	36.35 (18.29)	**	ns	16.13 (5.17)	ns	ns	8.50 (7.41)	ns	ns
CD14+	5.9 (2.172)	ns	ns	6.50 (3.41)	ns	ns	4.94 (4.03)	ns	ns	2.48 (2.22)	ns	ns
CD3-CD56+	13.55 (5.00)	ns	ns	15.98 (7.10)	*	ns	10.28 (4.58)	ns	ns	7.79 (4.32)	**	ns
CD3+CD56+	5.14 (5.10)	ns	ns	3.619 (2.90)	ns	ns	3.74 (3.62)	ns	ns	3.79 (4.71)	ns	ns
CD3+	63.17 (8.81)	ns	ns	52.58 (13.12)	ns	ns	63.05 (11.30)	ns	ns	56.01 (14.63)	**	ns
CD4+CD8-	50.18 (11.58)	ns	ns	42.79 (11.84)	ns	ns	50.76 (14.04)	ns	ns	46.16 (15.00)	****	ns
CD4-CD8+	23.78 (8.15)	ns	ns	22.24 (9.20)	*	ns	18.84 (9.82)	***	ns	17.65 (9.46)	*	ns
CD4+:CD8+ ratio	2.11			1.92			2.69			2.61		
CD4hiCD8hi	0.21 (0.15)	ns	ns	0.28 (0.37)	ns	ns	0.29 (0.43)	ns	ns	0.11 (0.12)	ns	ns
CD4hiCD8lo	0.49 (0.35)	ns	ns	0.34 (0.35)	ns	ns	0.40 (0.34)	ns	ns	0.51 (0.49)	ns	ns
CD4loCD8hi	0.79 0.69)	ns	ns	0.65 (0.888)	ns	ns	0.79 (1.17)	ns	ns	1.00 (1.00)	ns	ns

Results are expressed as median fraction of cells expressing the marker(s) +/- SD among specific gates. Significant differences were evaluated by comparison of controlled-infection (CI) status between profile A and B over time using one-way ANOVA with Tukey's multiple comparisons test.*, $p < 0.05$; **, $p < 0.001$; ***, $p < 0.0001$; ****, $p < 0.00001$, ns: not significant.