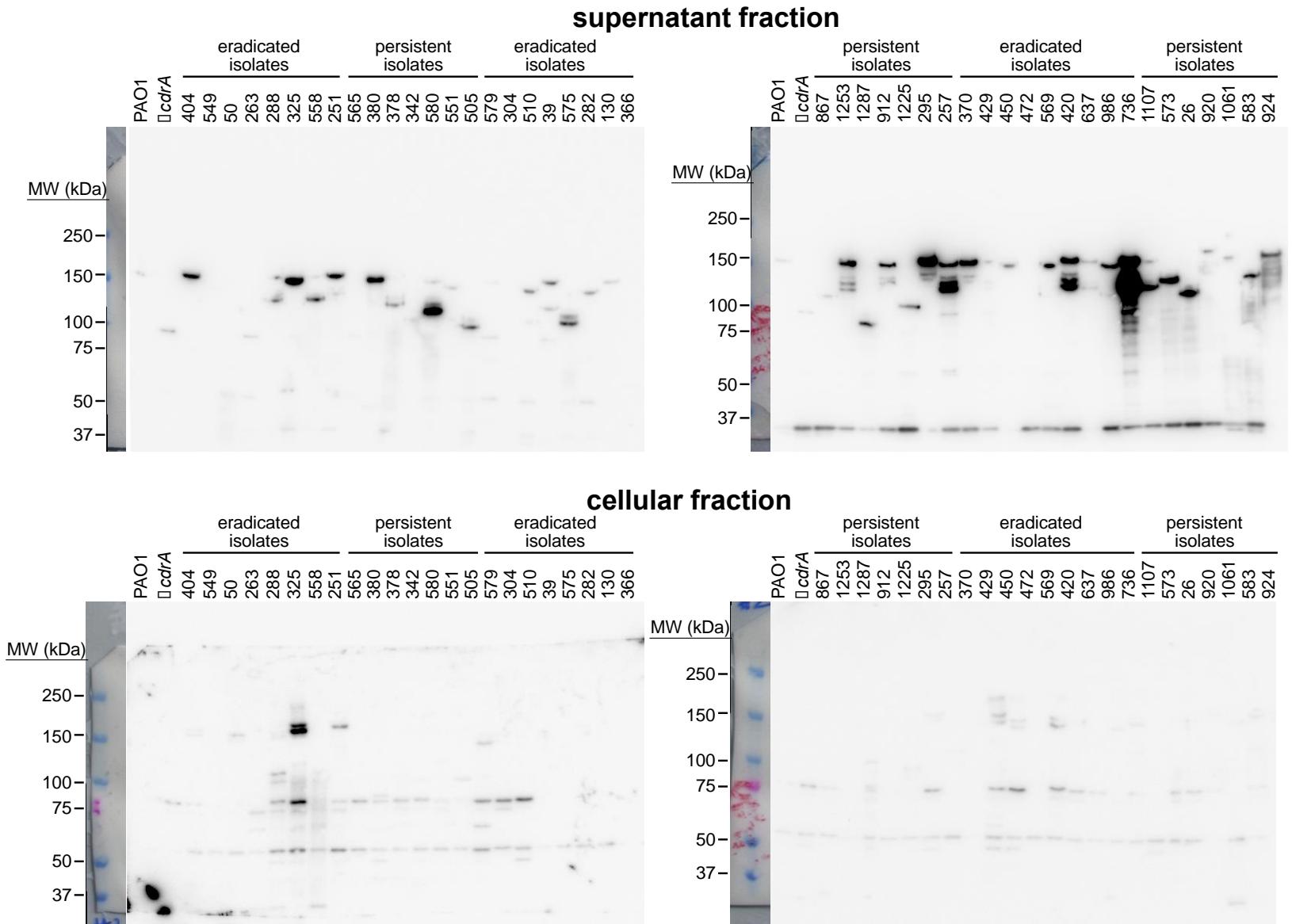


Supplemental Figure 1. SickKids *P. aeruginosa* isolates (N=7 Persistent; N=7 Eradicated) were grown as biofilms for 24 hrs after which antibodies (LB control, IgG or anti-Psl 0096) and tobramycin (or LB alone) were added for the following 24 hrs before plating for colony counts. The mean colony forming unit (CFU) per well for each isolate (done in triplicate) was calculated and the log transformed (log₁₀) mean of all isolates was plotted with standard error of the mean (SEM). Comparisons with and without tobramycin treatment were performed for each condition using non-parametric Mann-Whitney test ***p<0.001, **p<0.01

Strain	E/P	pslA	pslB	pslC	pslD	pslE	pslF	pslG	pslH	pslI	pslJ	pslK	pslL	pslM	pslN	pslO
263	E	0	1	1	0	0	2	0	1	1	0	3	2	1	1	0
288	E	0	1	1	0	0	2	0	1	1	1	1	1	2	1	0
325	E	0	2	2	0	1	1	0	3	2	0	2	0	1	0	1
549	E	0	0	1	0	0	2	0	1	1	1	1	1	1	1	0
558	E	0	0	1	0	0	2	0	1	1	1	1	1	1	1	0
404	E	0	2	2	0	1	1	0	3	2	0	2	0	1	0	1
50	E	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0
375	P	0	1	3	0	1	1	1	2	3	0	1	2	2	0	1
551	P	0	0	1	0	0	2	0	1	1	1	1	1	1	1	0
580	P	0	1	1	0	0	2	0	1	1	0	3	2	1	1	0
380	P	0	1	3	0	1	1	0	1	1	0	1	1	2	0	3
342	P	0	0	1	0	0	2	0	1	1	1	1	1	1	1	0
505	P	0	1	2	0	0	2	0	2	1	0	0	1	2	0	1
565	P	1	0	2	0	1	1	1	1	1	0	1	0	2	0	1
	Ttest	0.337	0.484	0.165	N/A	0.611	0.698	0.147	0.765	0.718	0.611	0.580	0.290	0.109	0.626	0.223

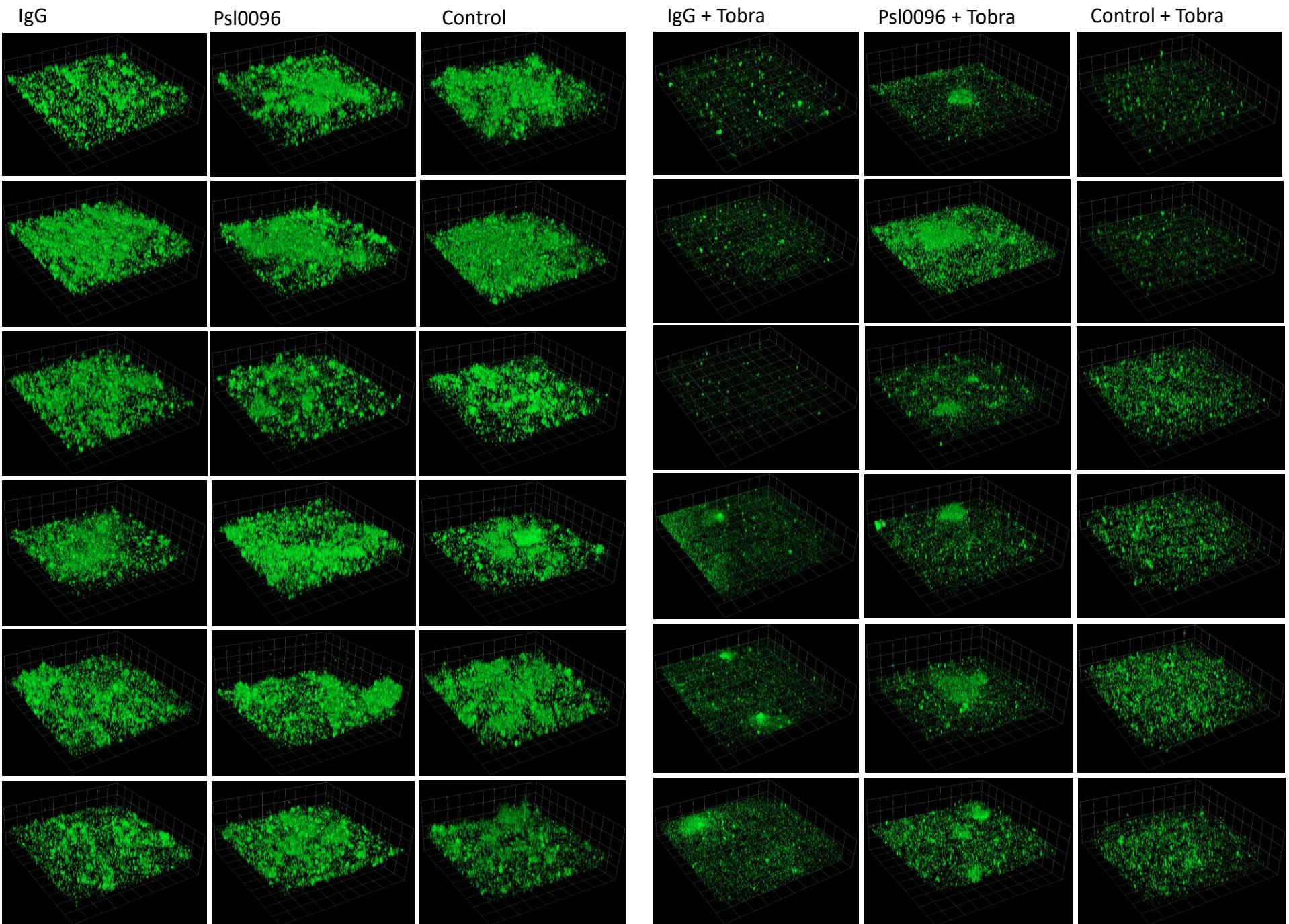
Supplemental Figure 2. The number of non-synonymous mutations in each Psl gene was counted for each of the 14 strains. T-test was used to determine whether there was a significant difference in the number of mutations between all 14 of the strains for each Psl gene as well as when all the Psl genes were considered together.



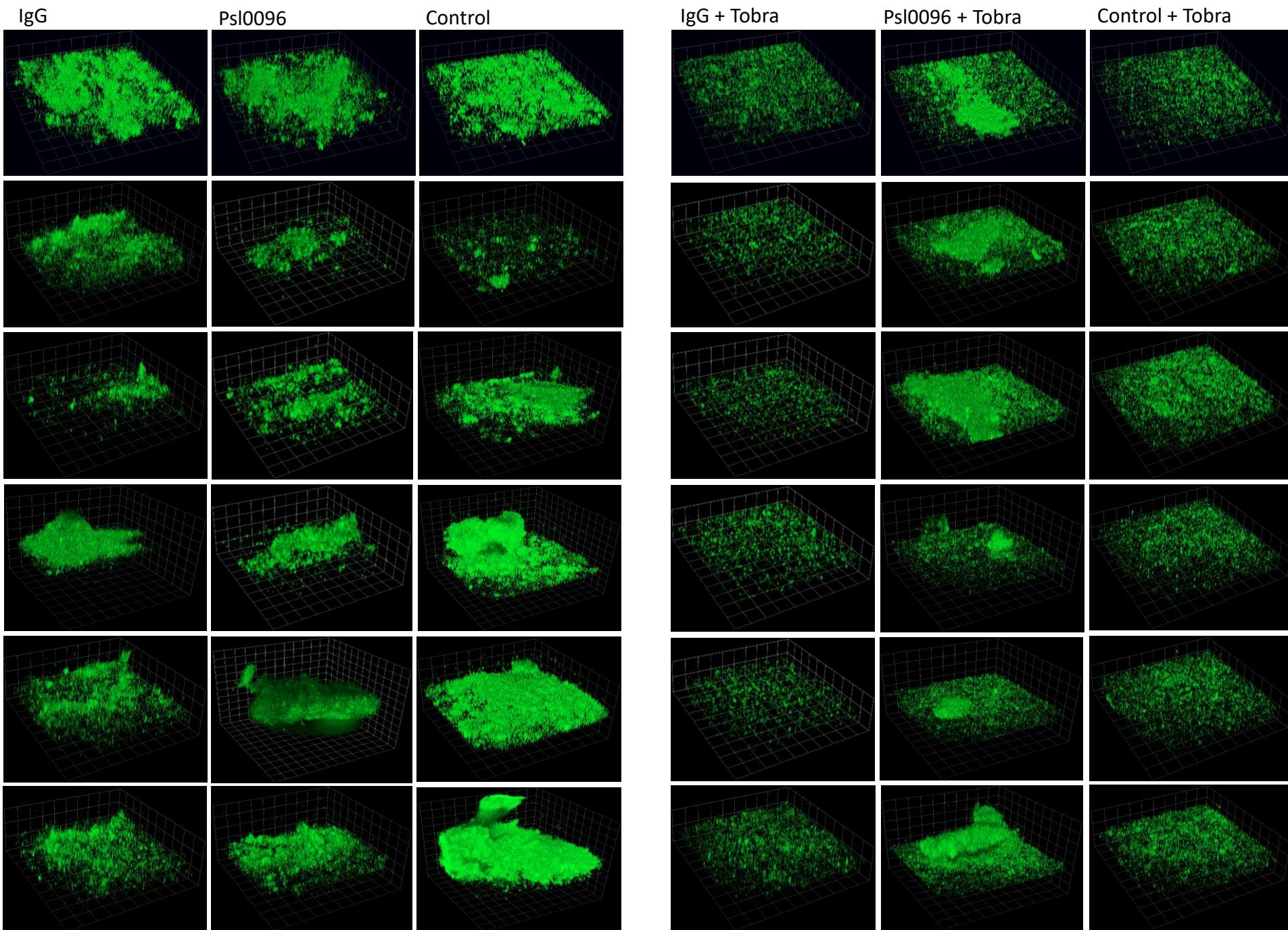
Supplemental Figure 3. SickKids *P. aeruginosa* isolates (N=21 Persistent; N=25 Eradicated) were grown as biofilms for 24 h then separated by centrifugation into supernatant and cellular fractions. Samples were then analyzed by western blot analysis using an anti-CdrA antibody. PAO1 was used as a positive control and the CdrA deletion strain (PAO1 Δcda) was used as a negative control. All blots derive from the same experiment and were processed in parallel.

Supplementary Figure 4

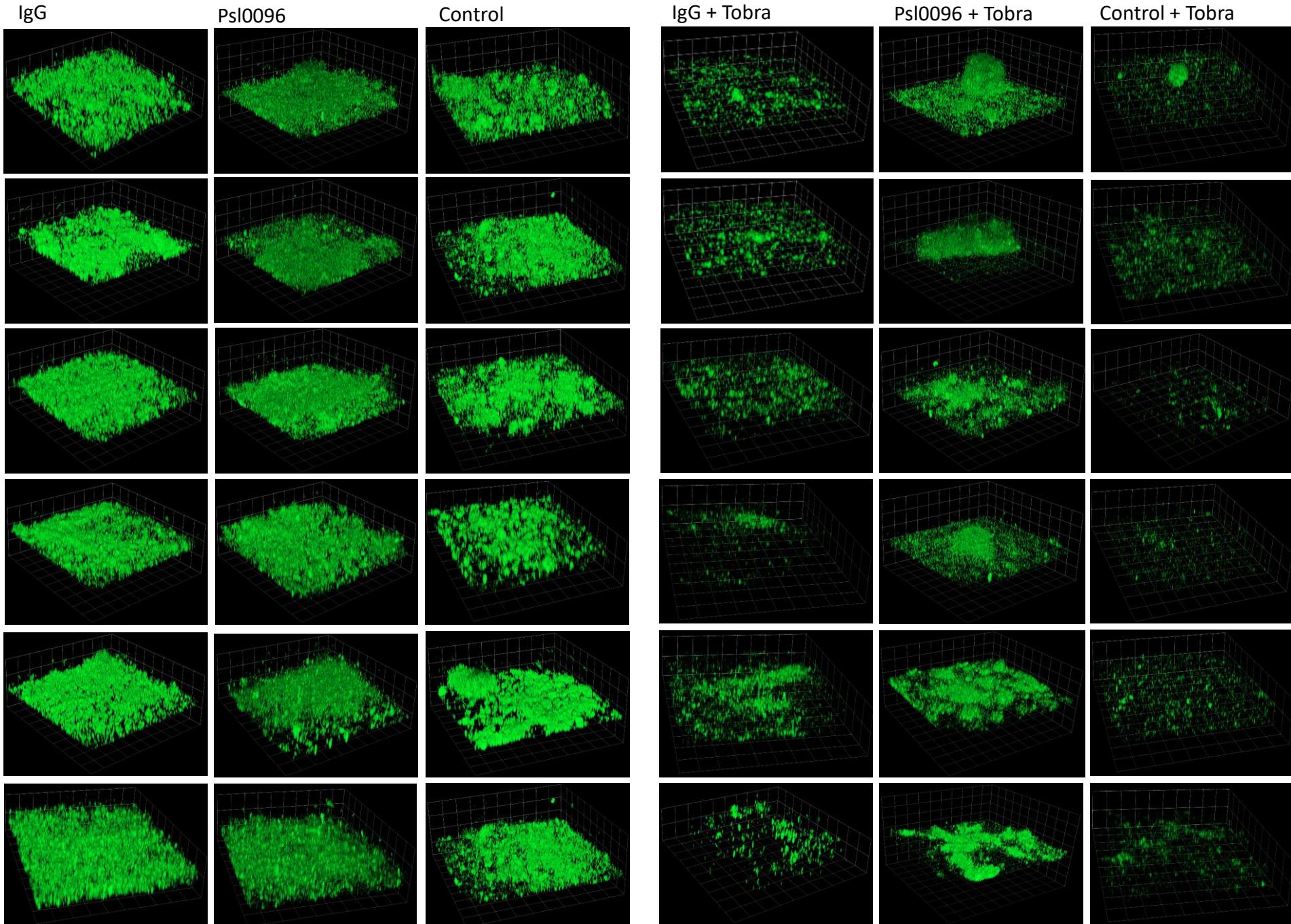
Pa342 (Persistent) Trial1



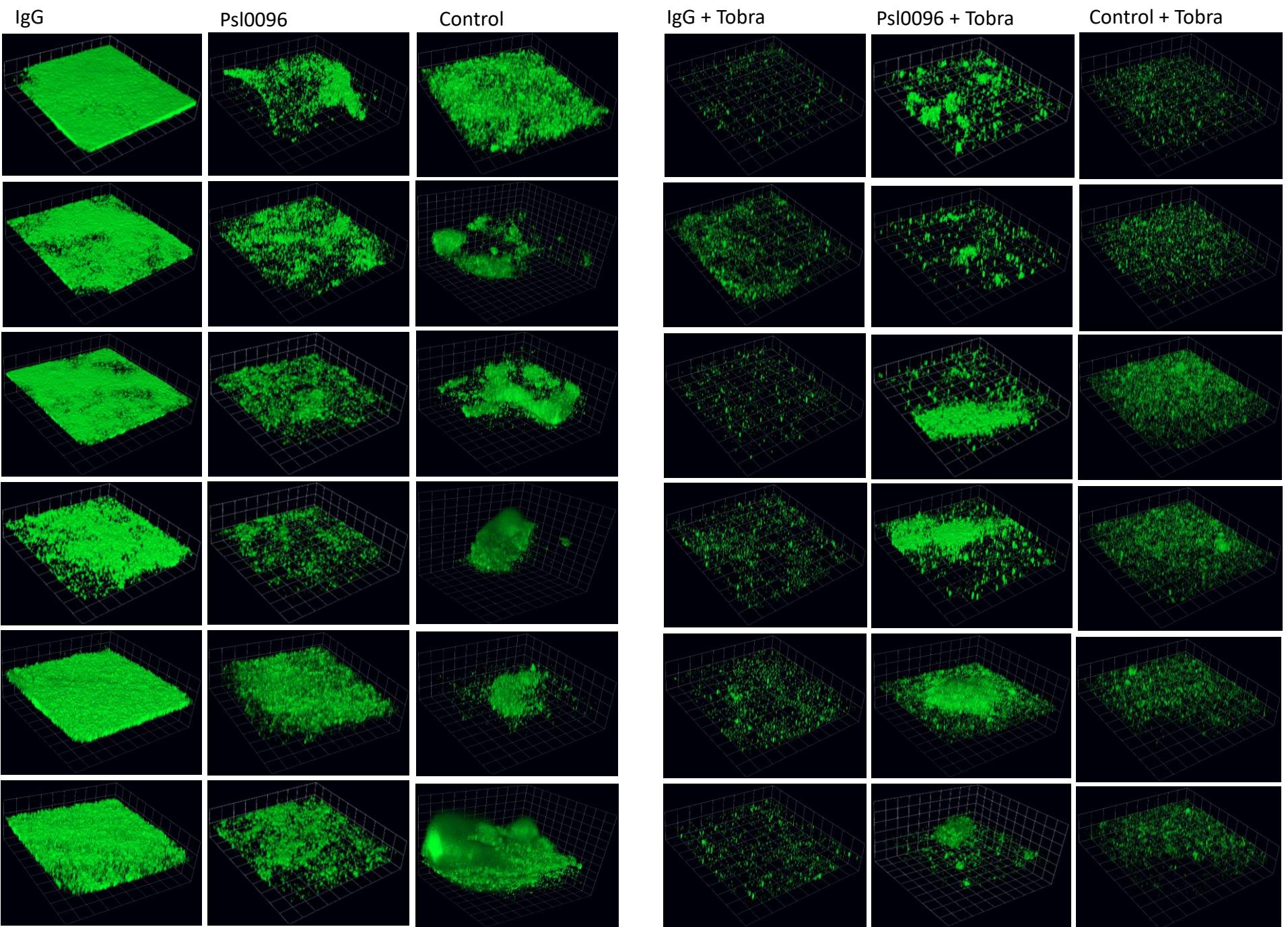
Pa342 (Persistent) Trial2



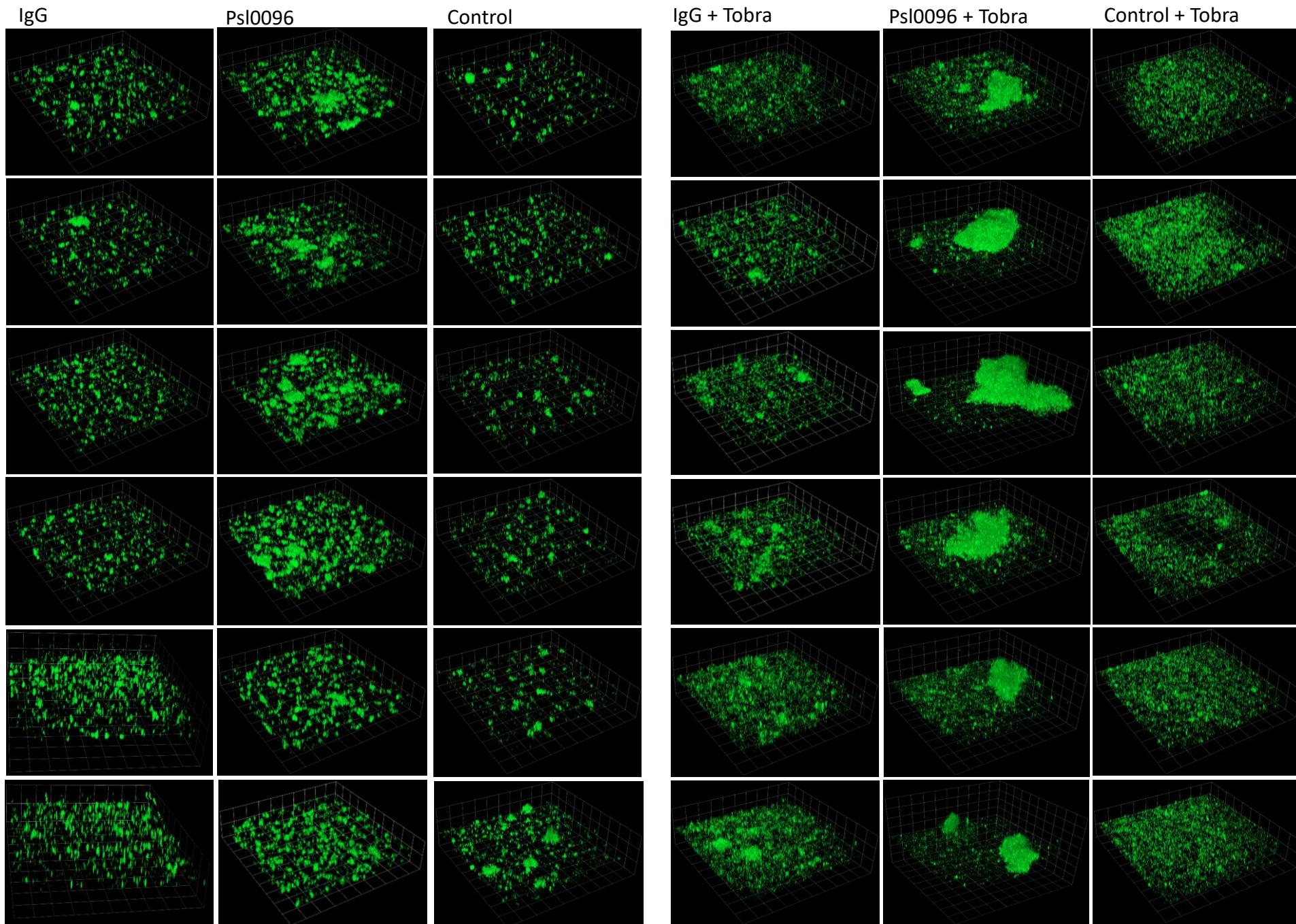
Pa342 (Persistent) Trial3



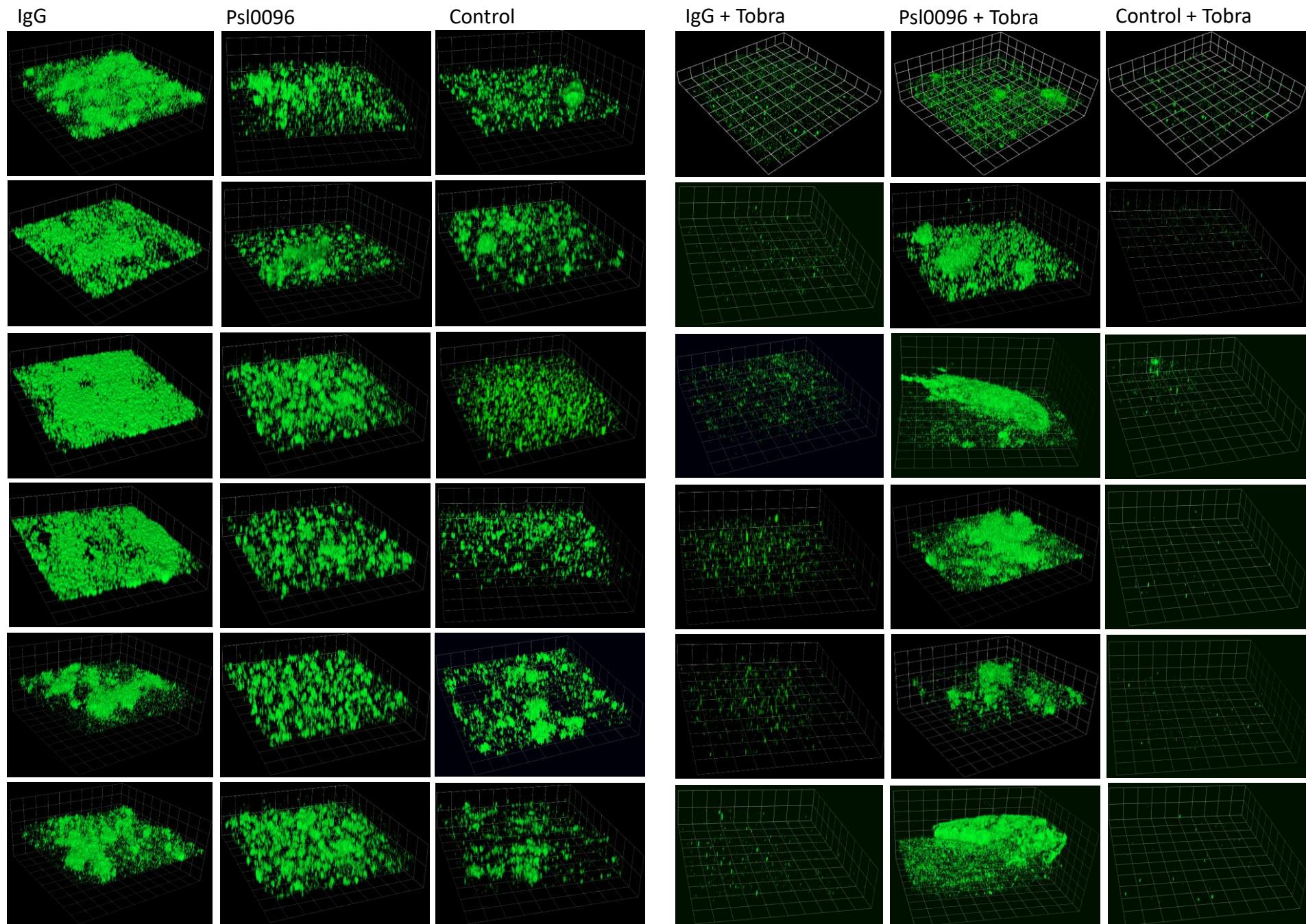
Pa375 (Persistent) Trial1



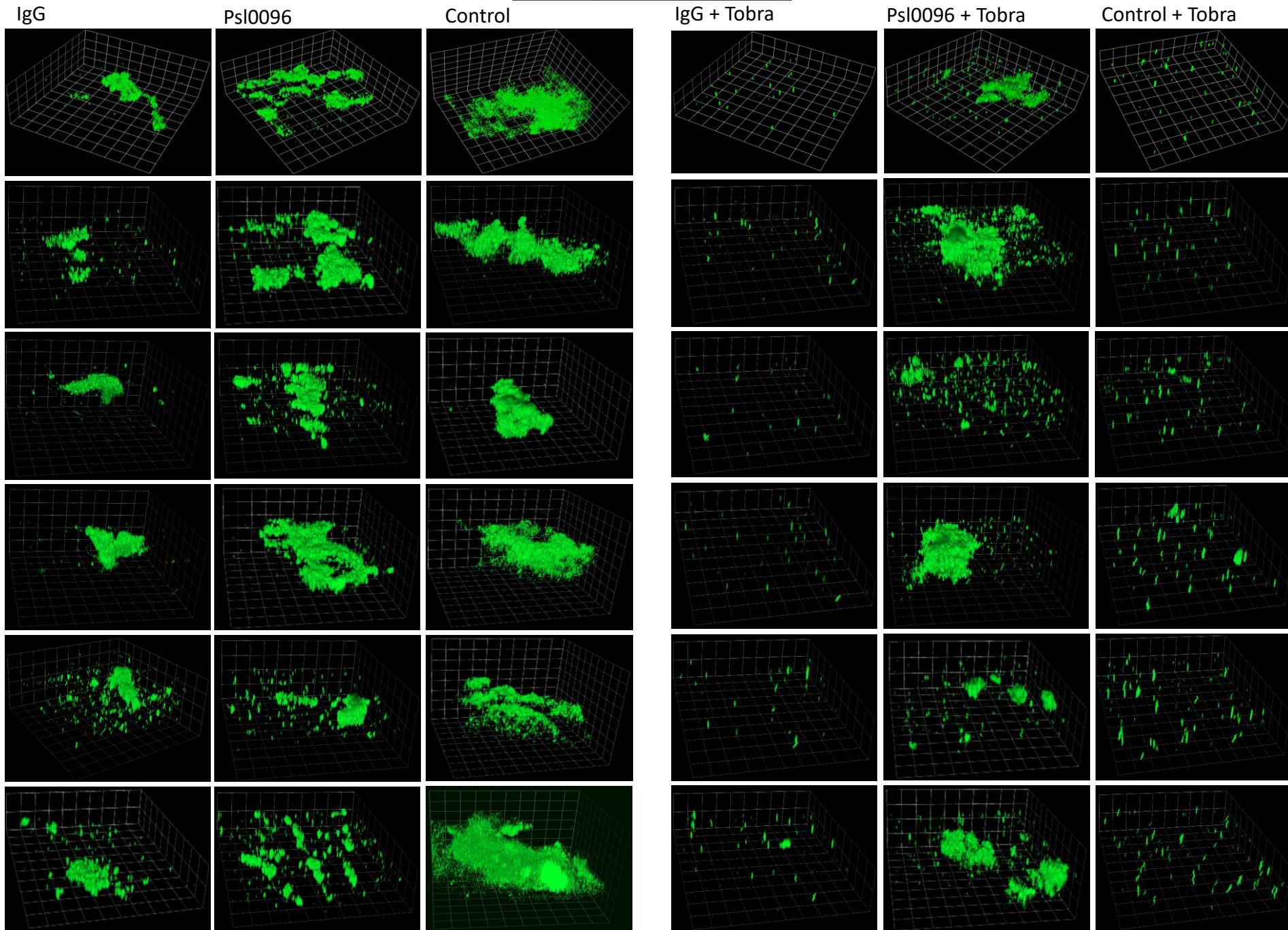
Pa375 (Persistent) Trial2



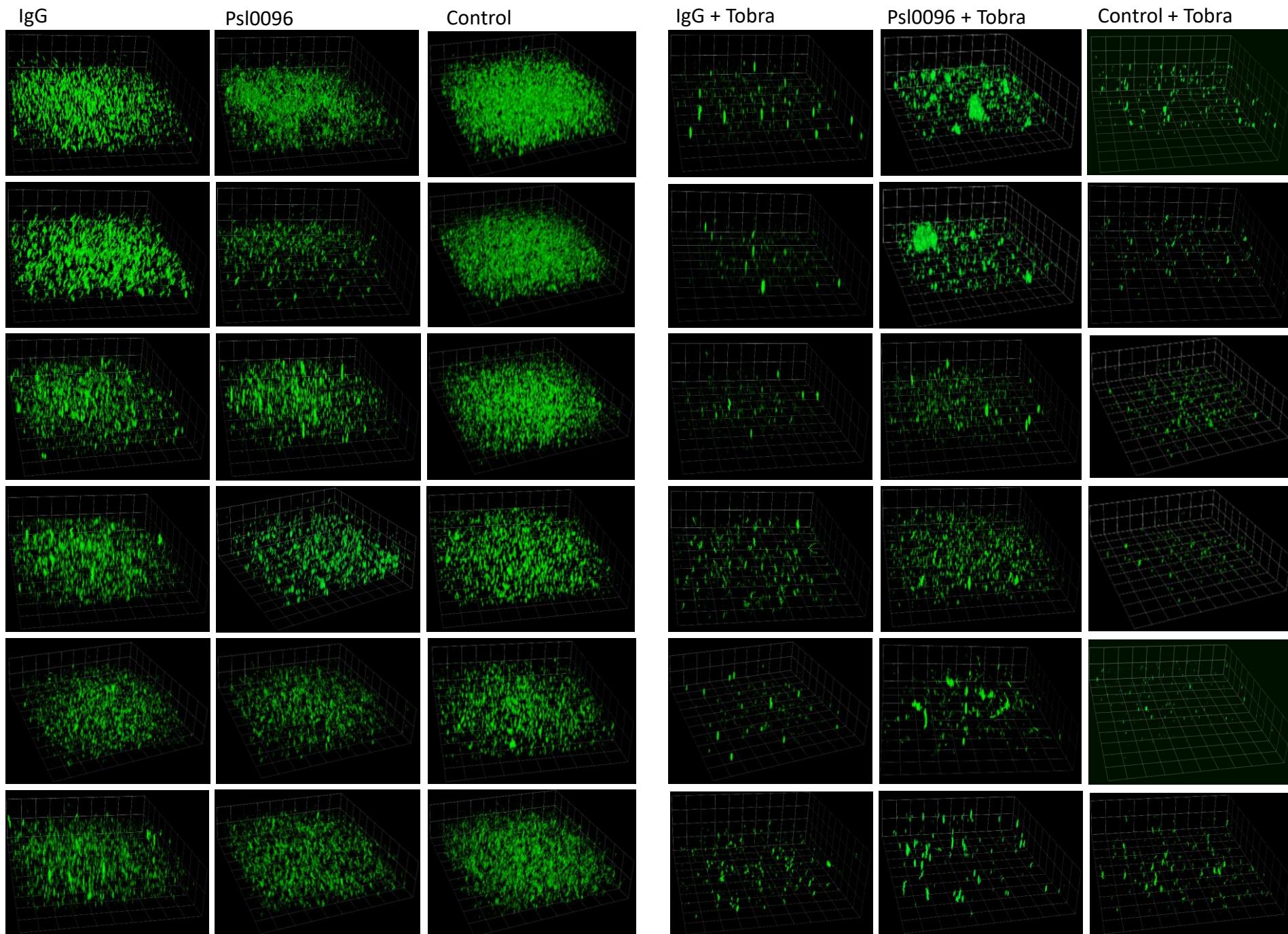
Pa375 (Persistent) Trial3



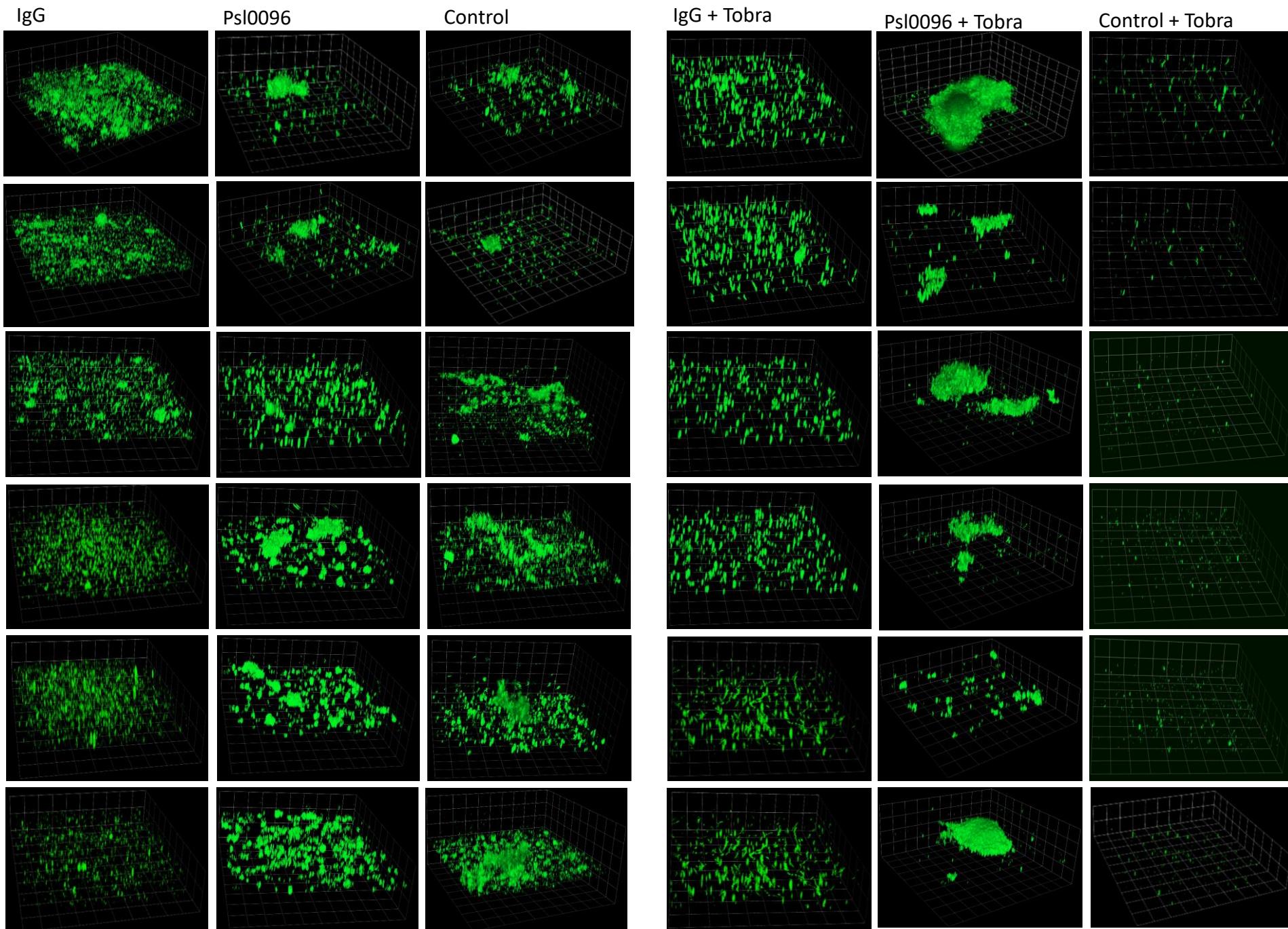
Pa380 (Persistent) Trial1



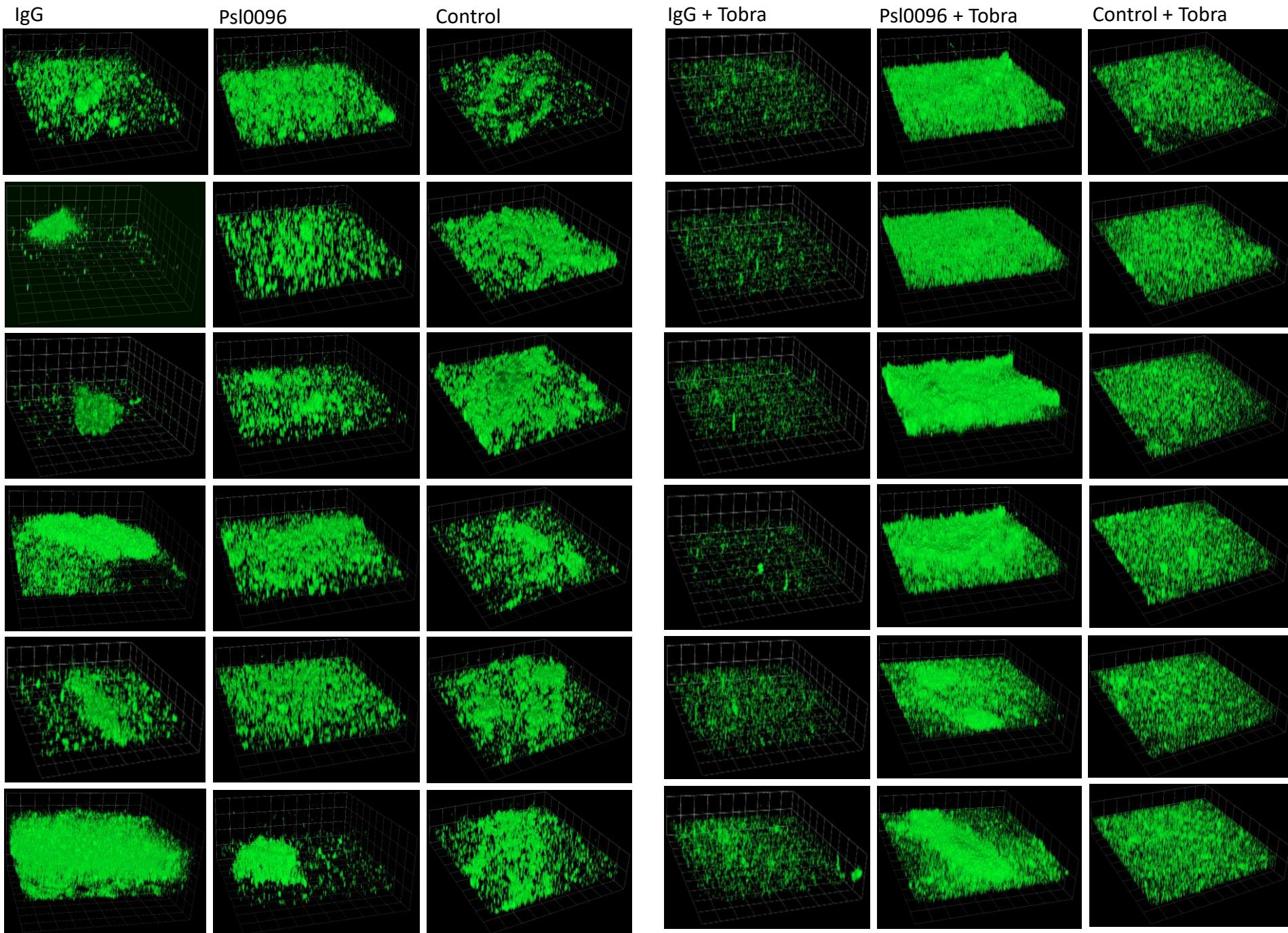
Pa380 (Persistent) Trial2



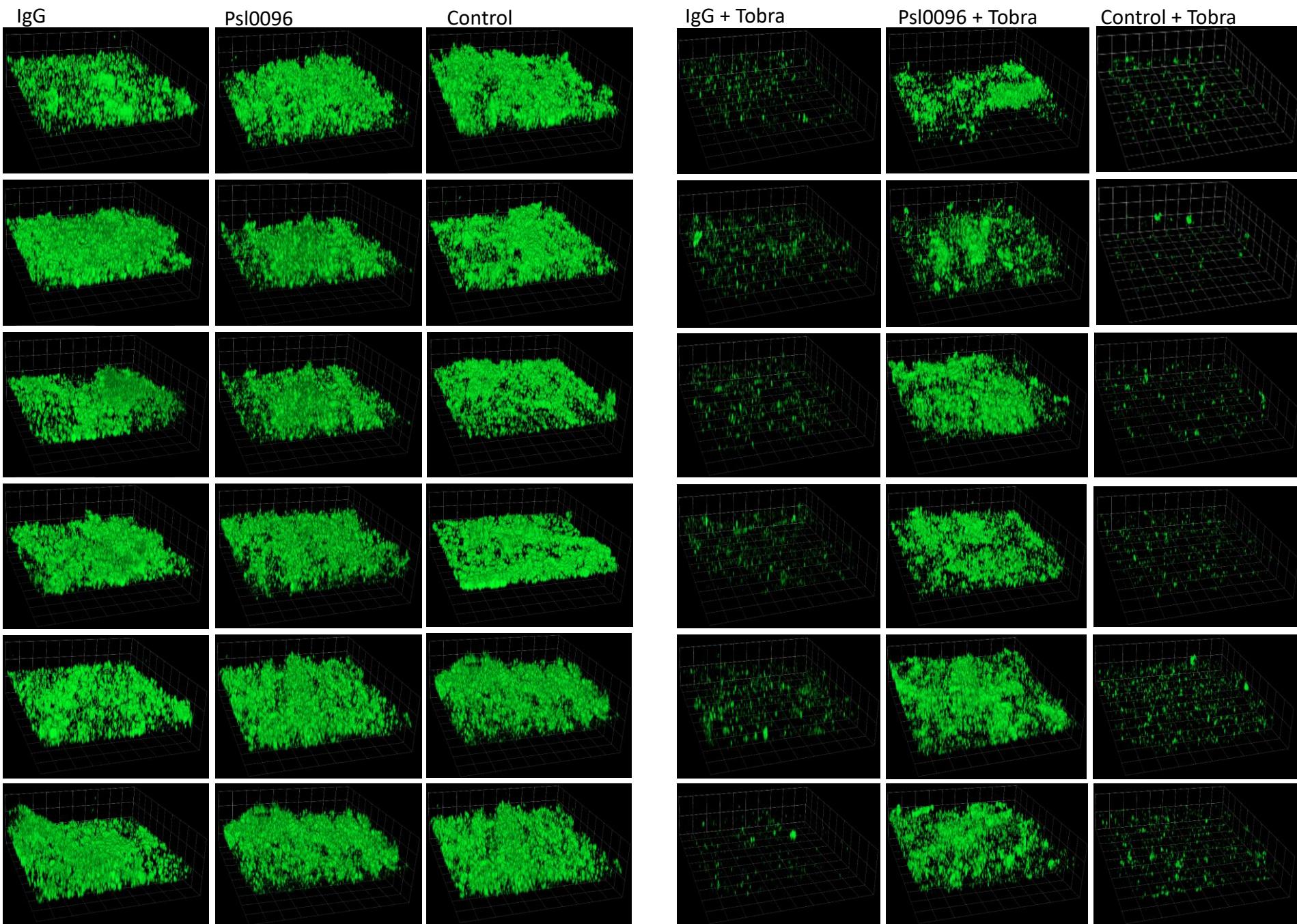
Pa380 (Persistent) Trial3



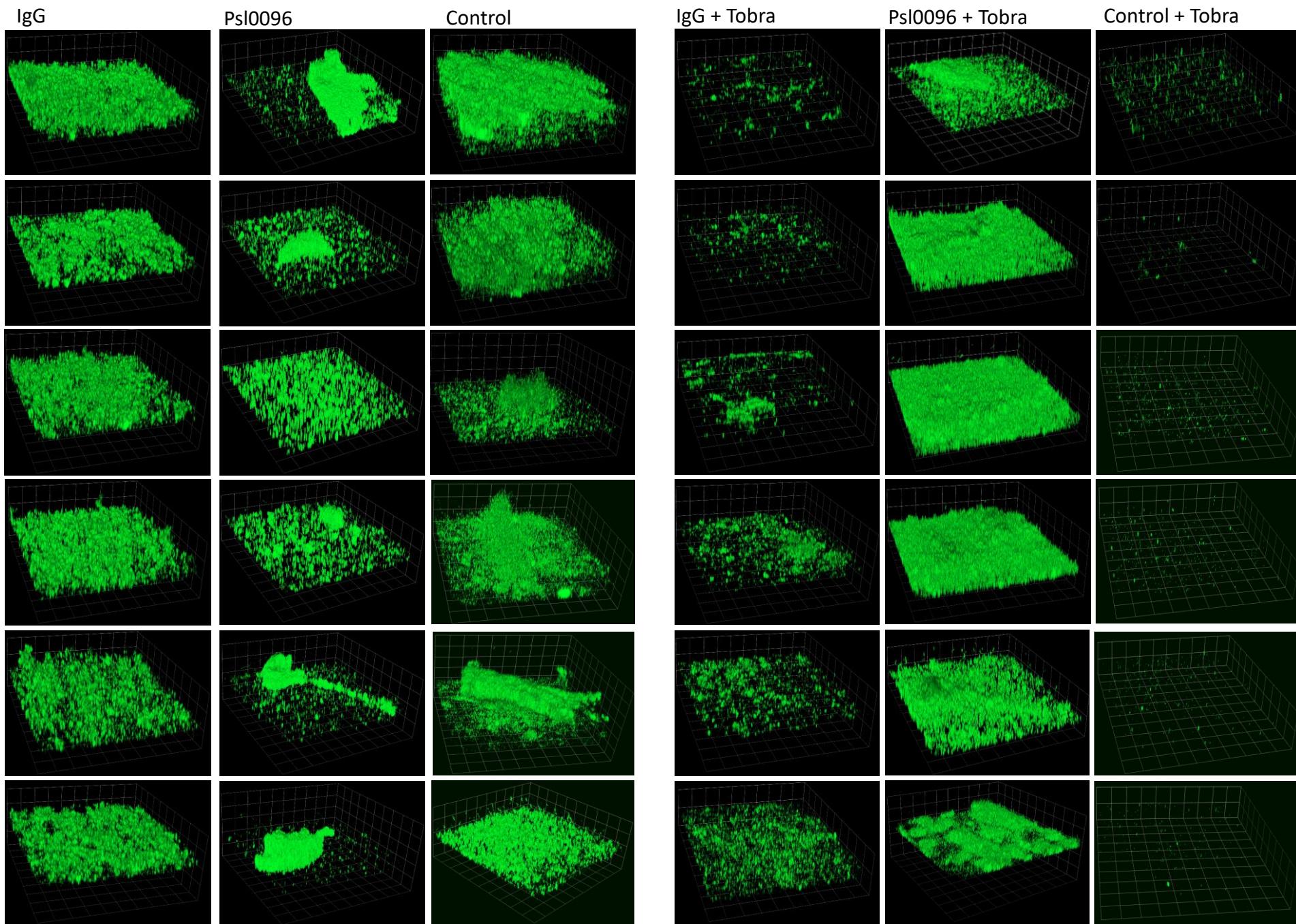
Pa565 (Persistent) Trial1



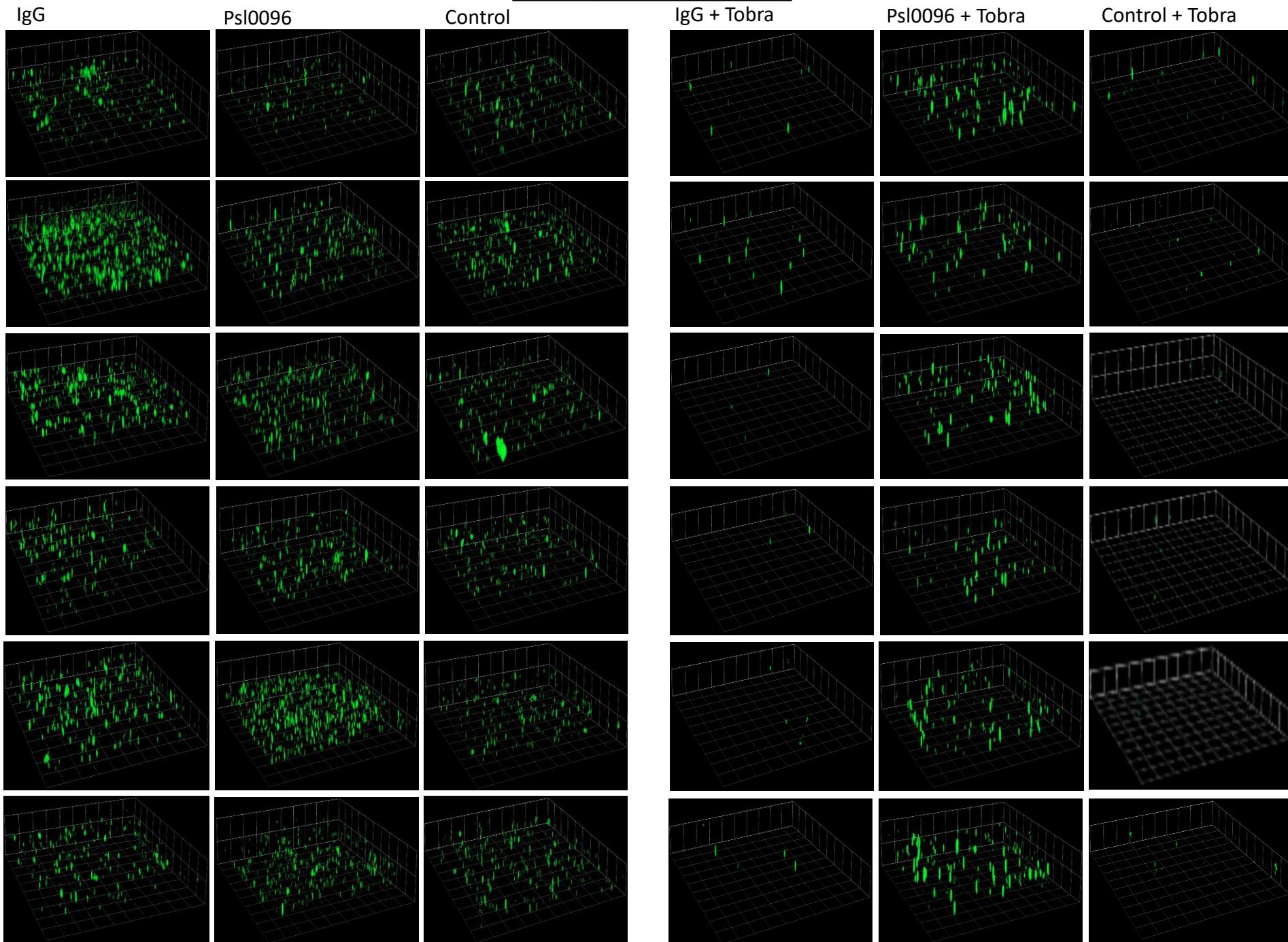
Pa565 (Persistent) Trial2



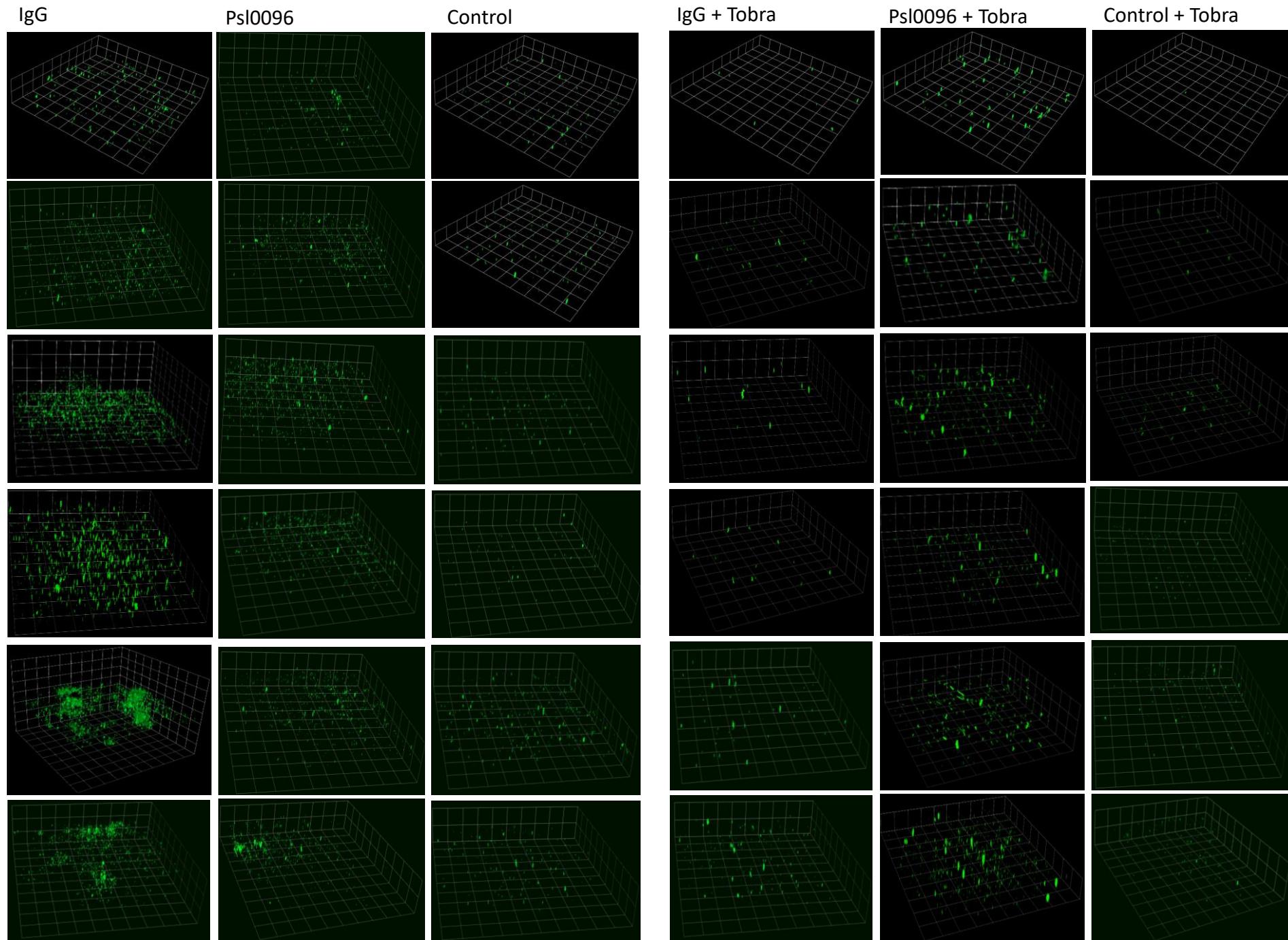
Pa565 (Persistent) Trial3



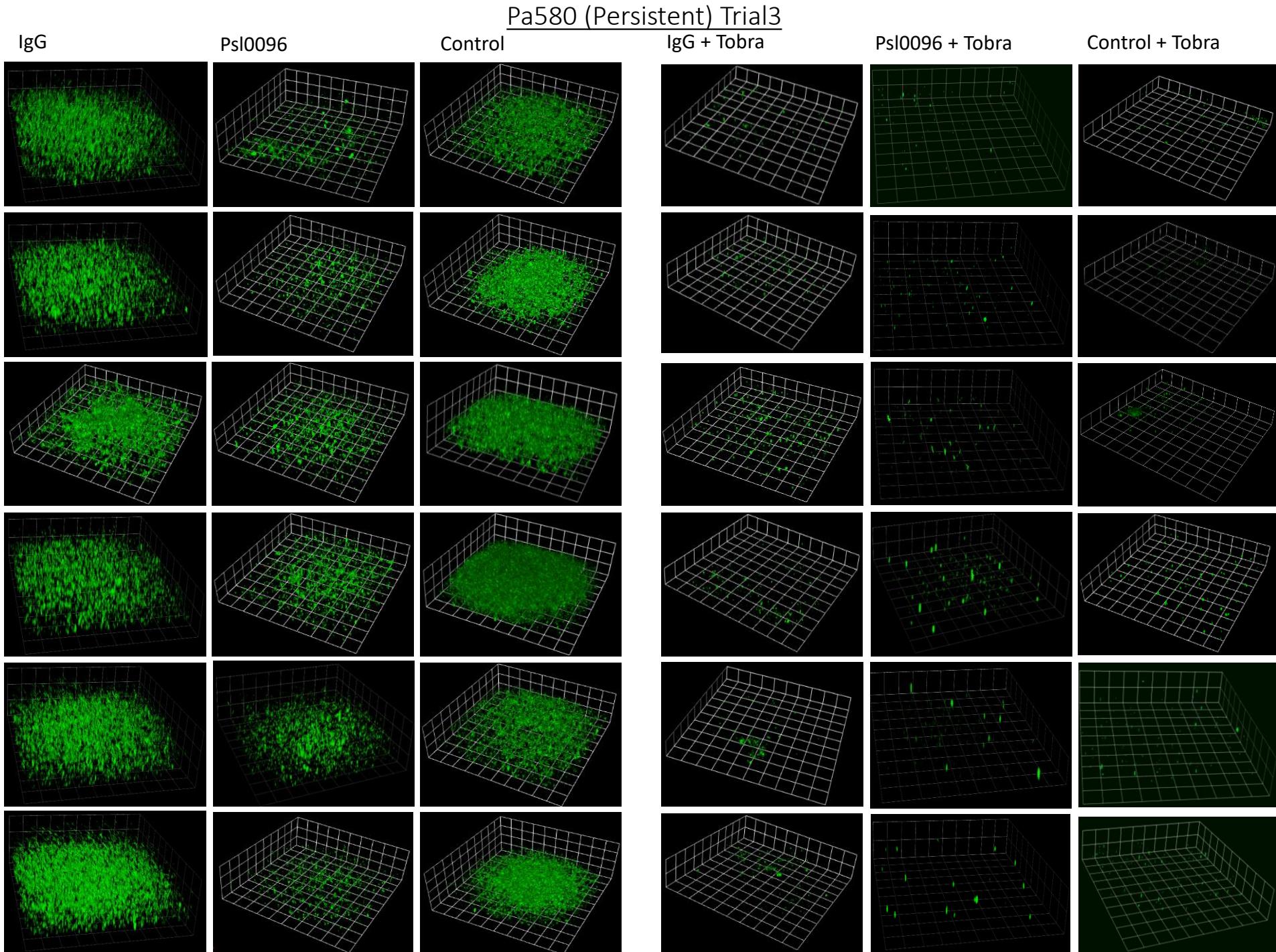
Pa580 (Persistent) Trial1



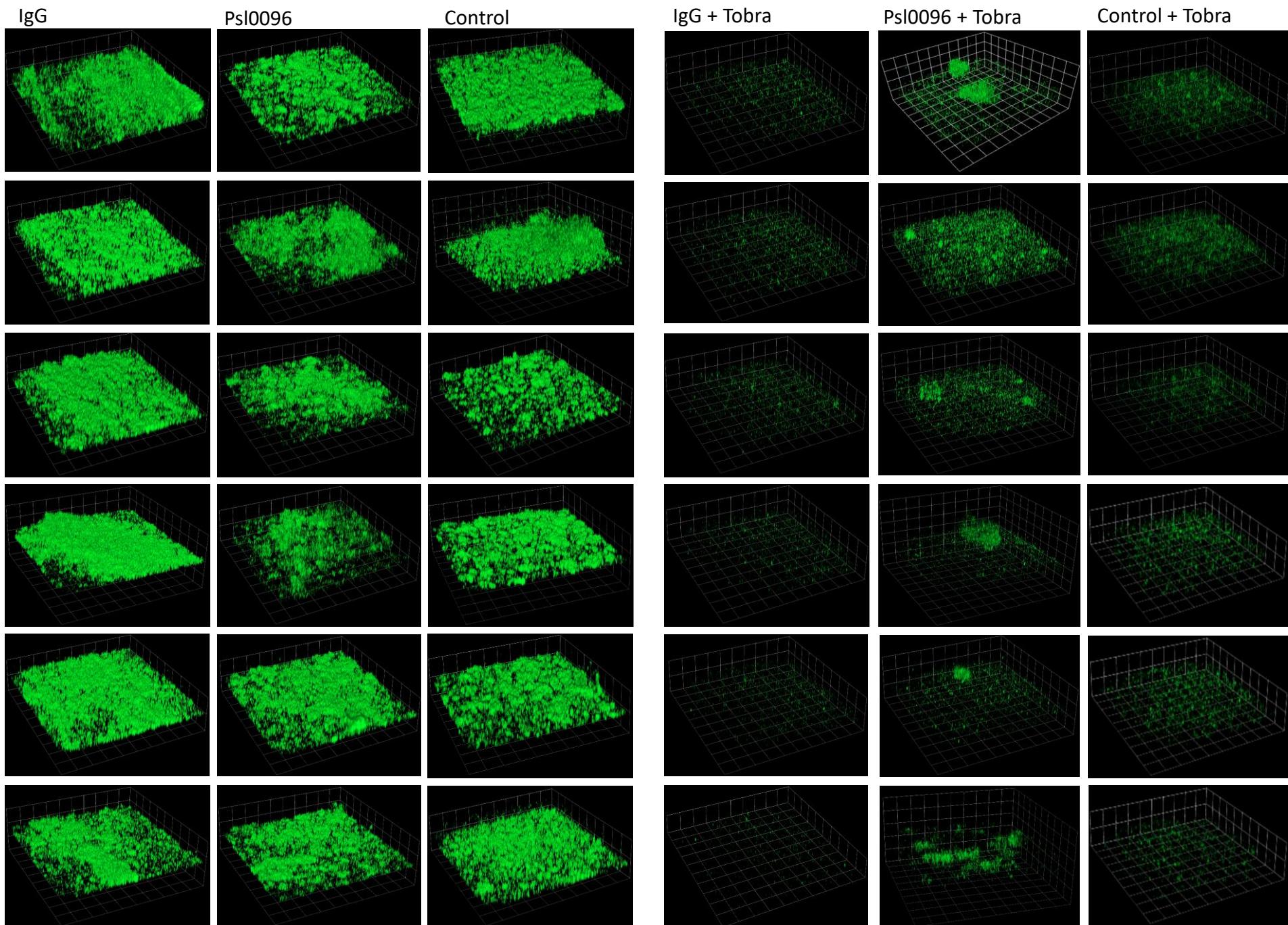
Pa580 (Persistent) Trial2



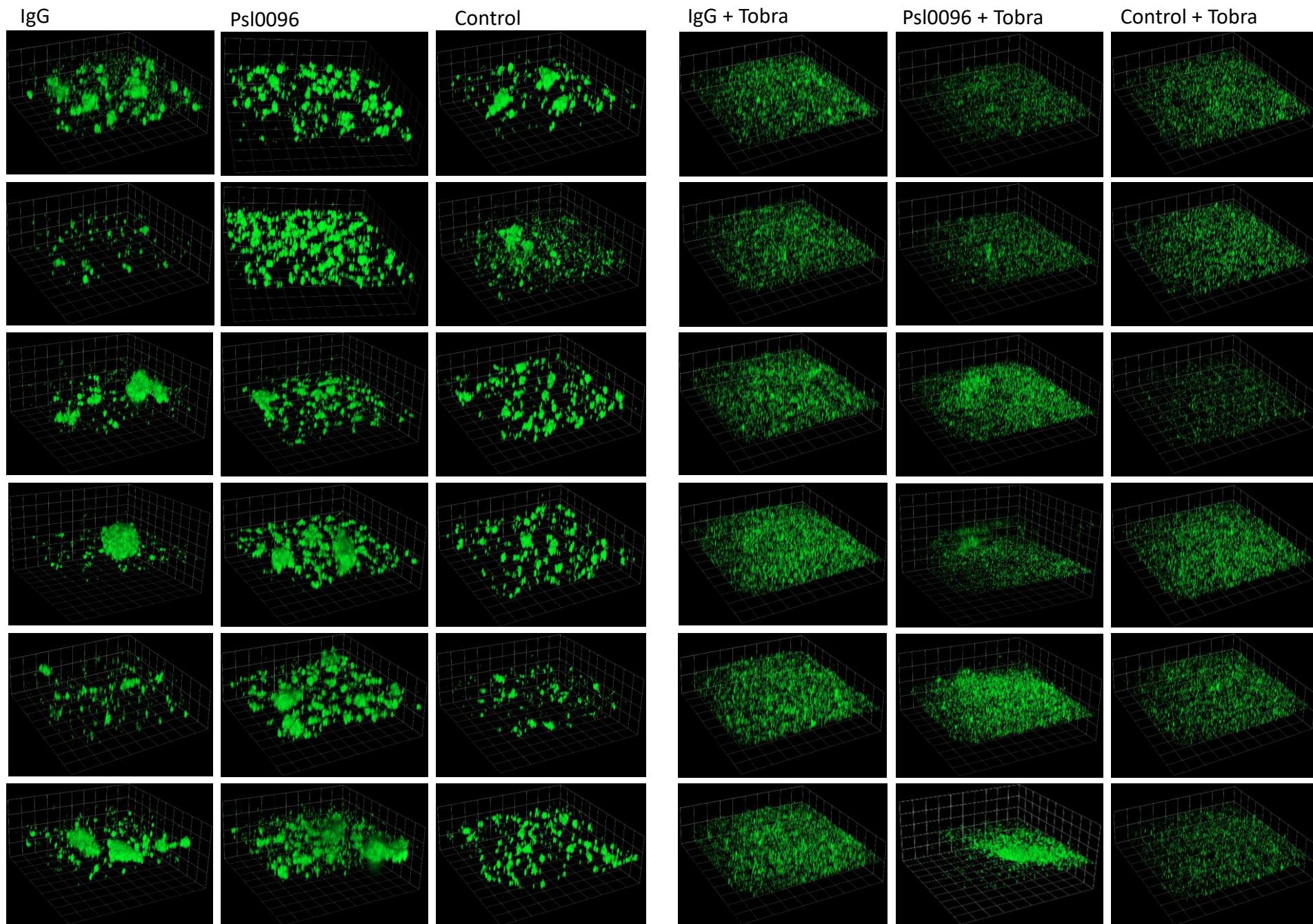
Pa580 (Persistent) Trial3



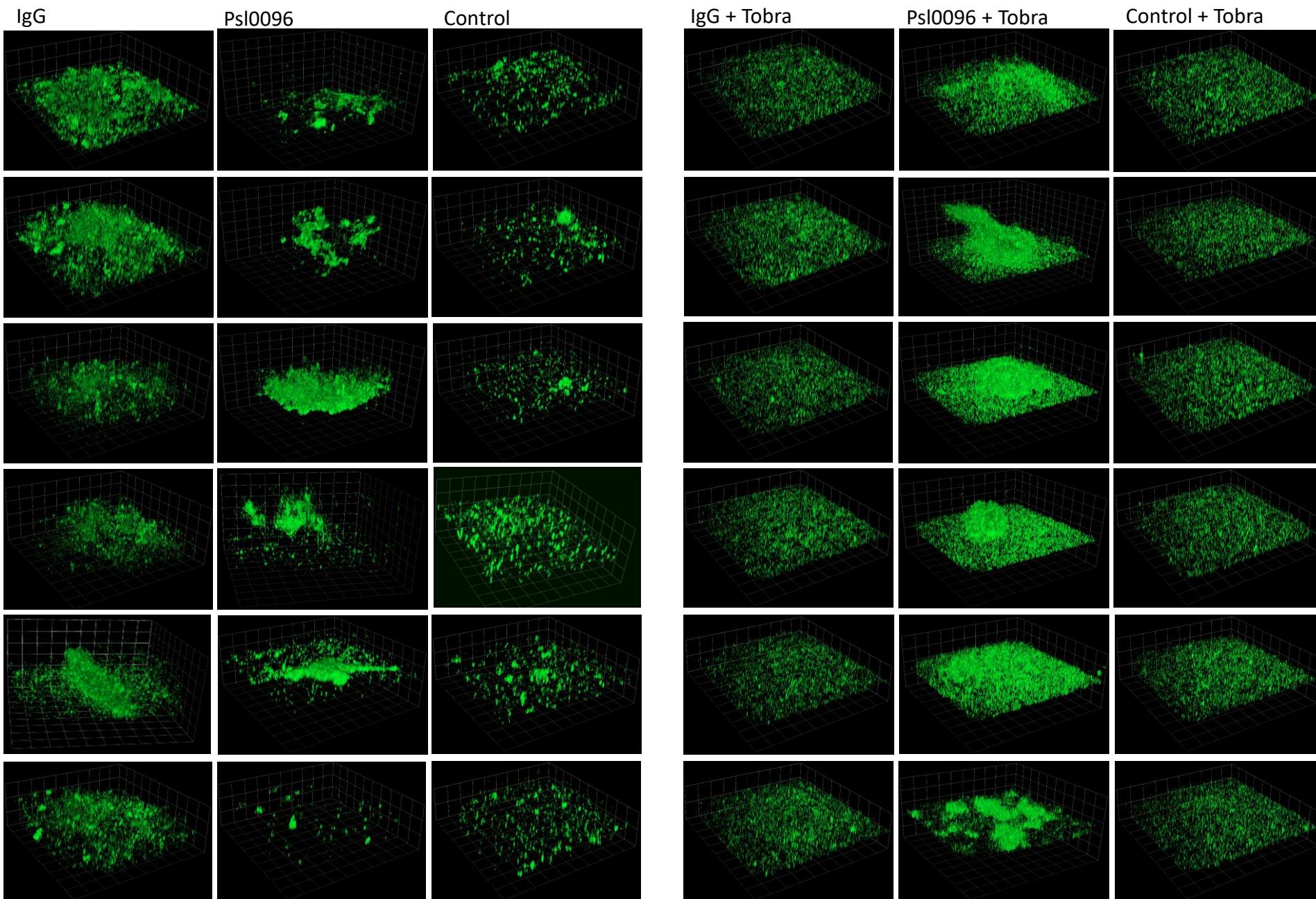
Pa505 (Persistent) Trial1



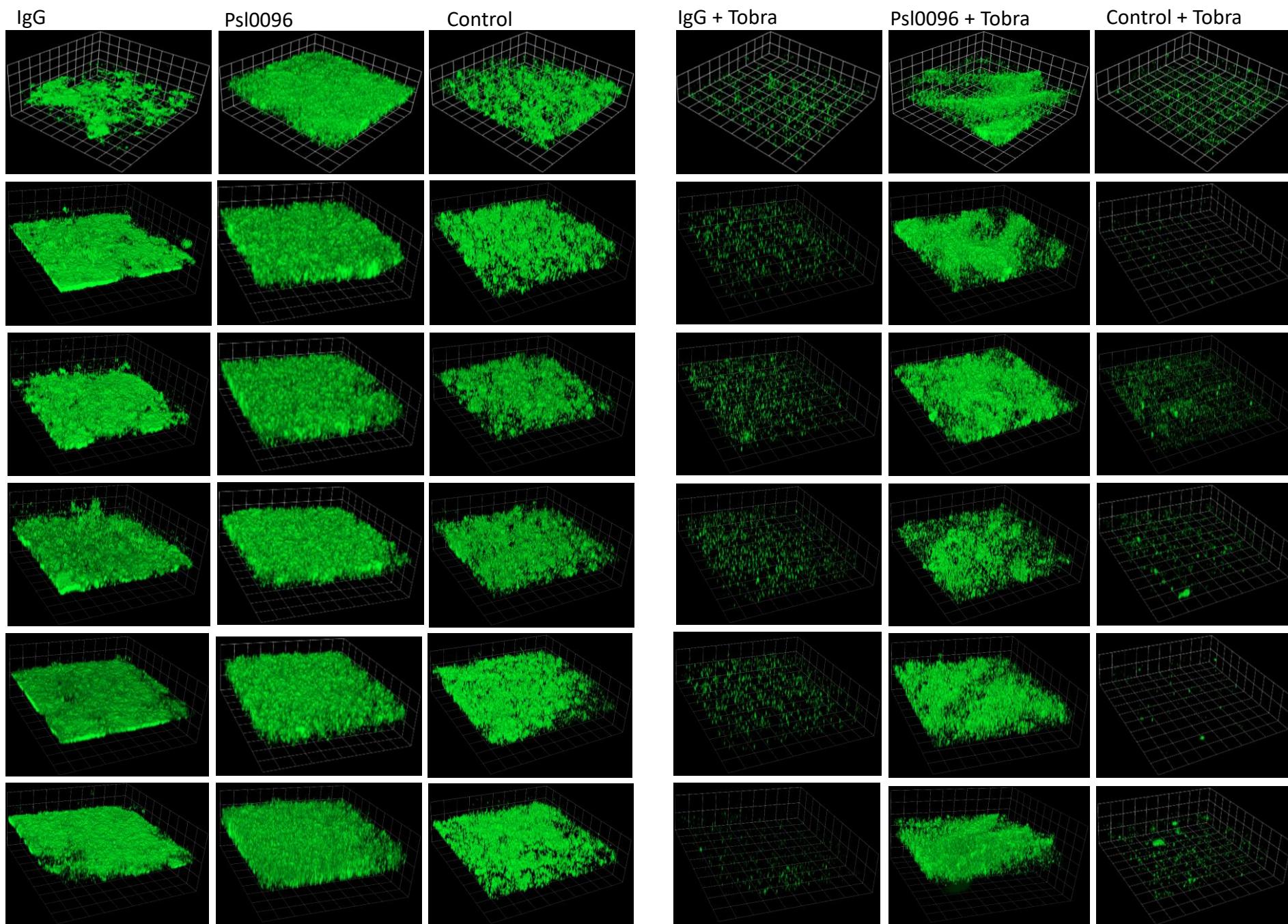
Pa505 (Persistent) Trial2



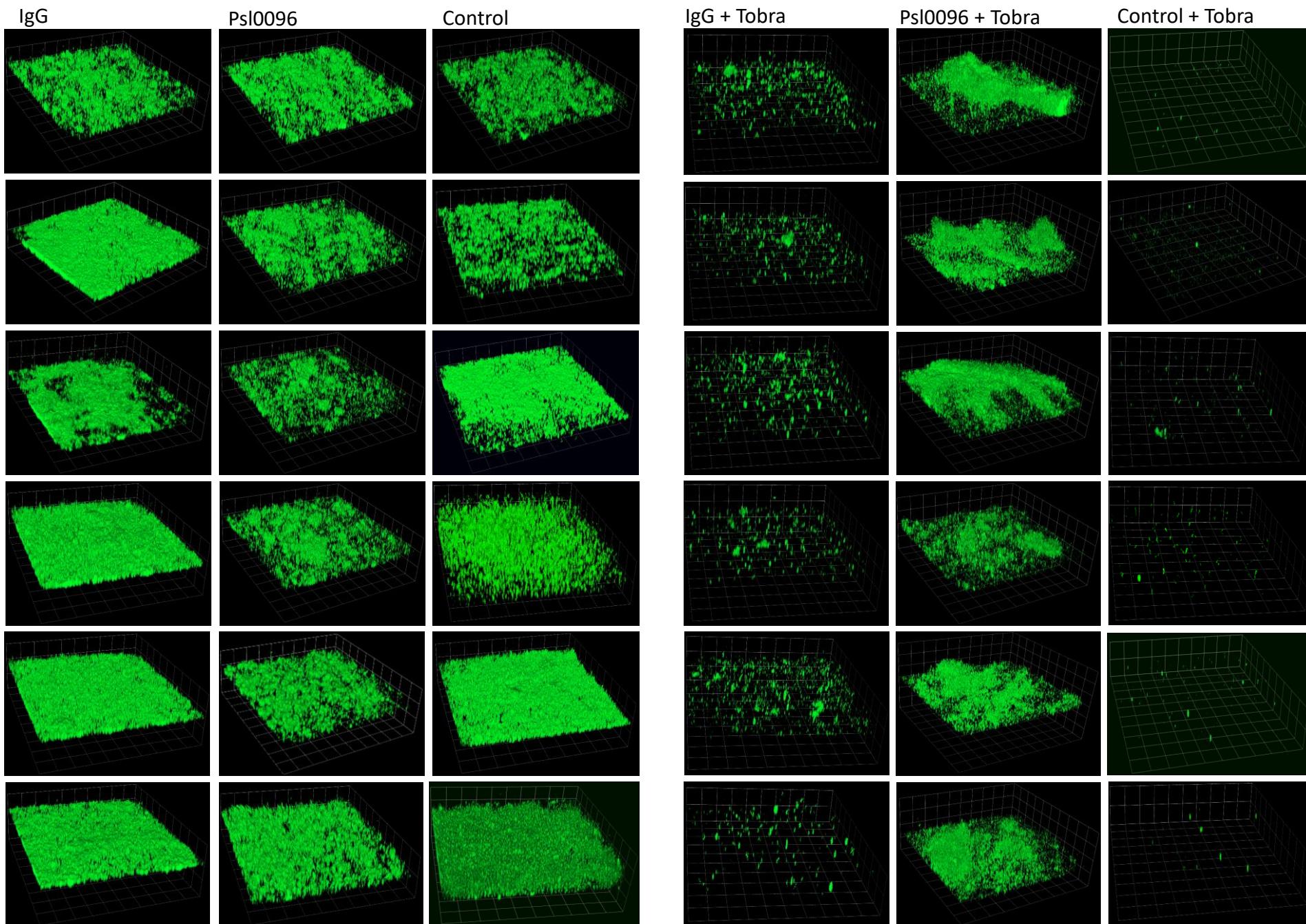
Pa505 (Persistent) Trial3



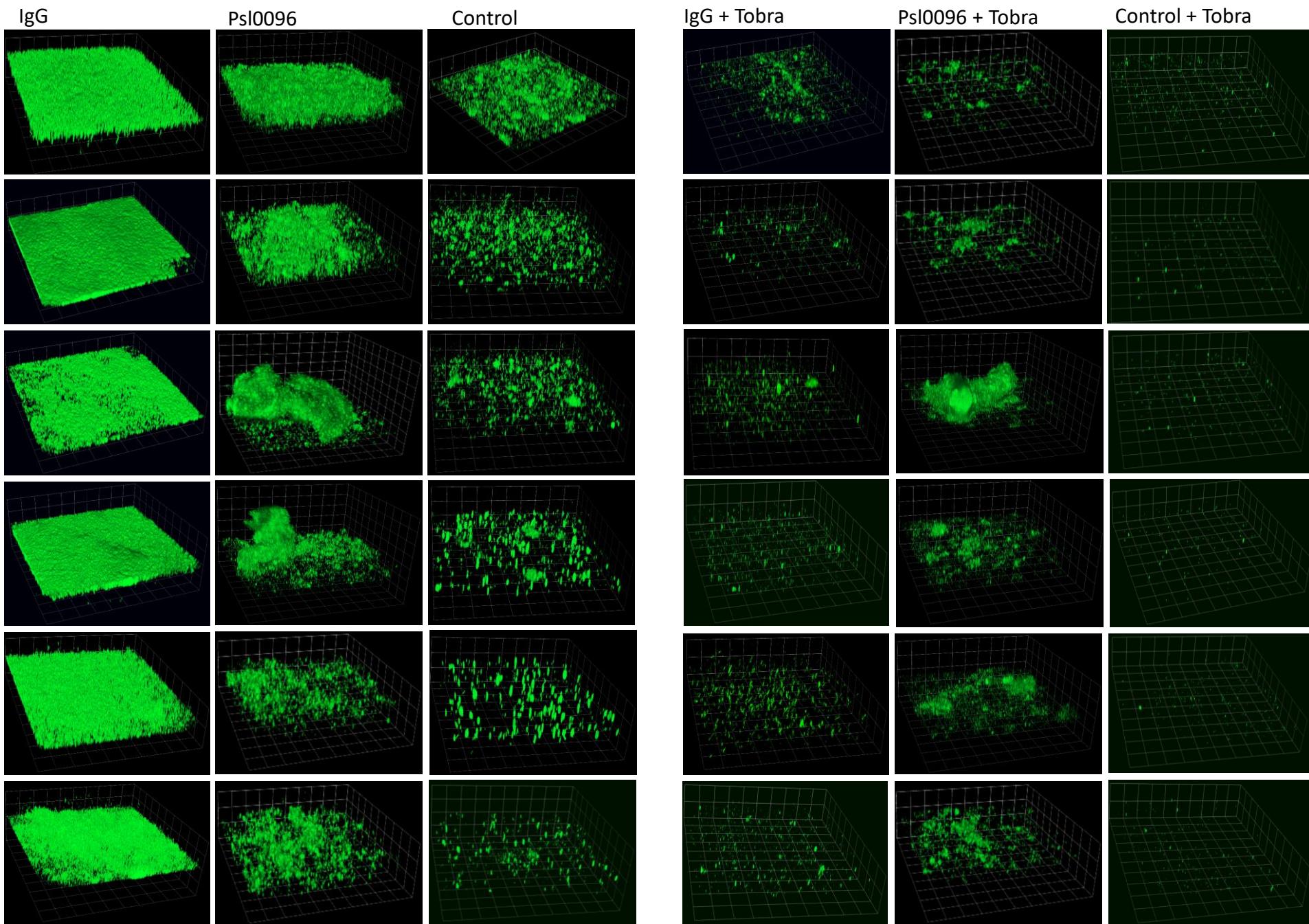
Pa551 (Persistent) Trial1



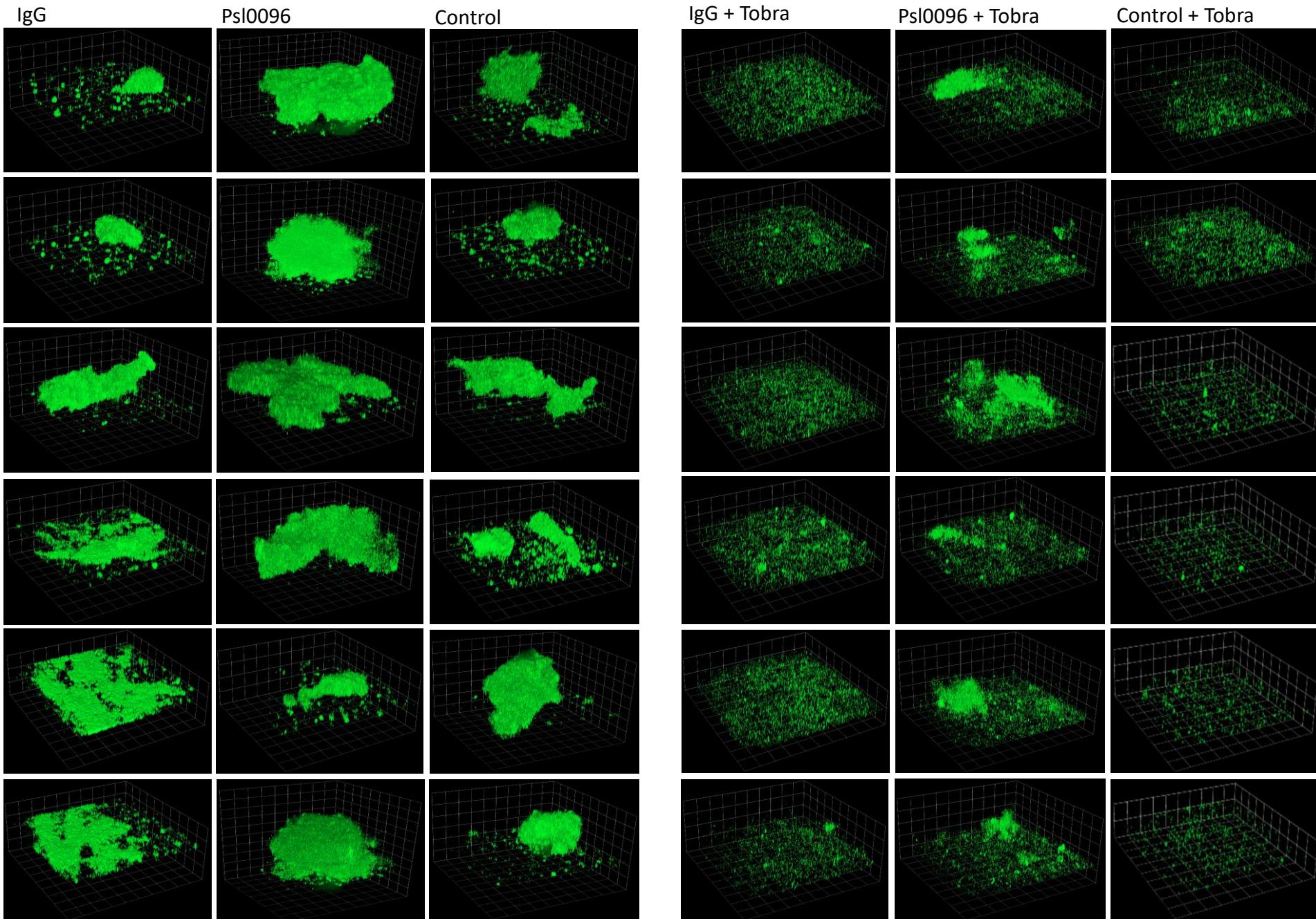
Pa551 (Persistent) Trial2



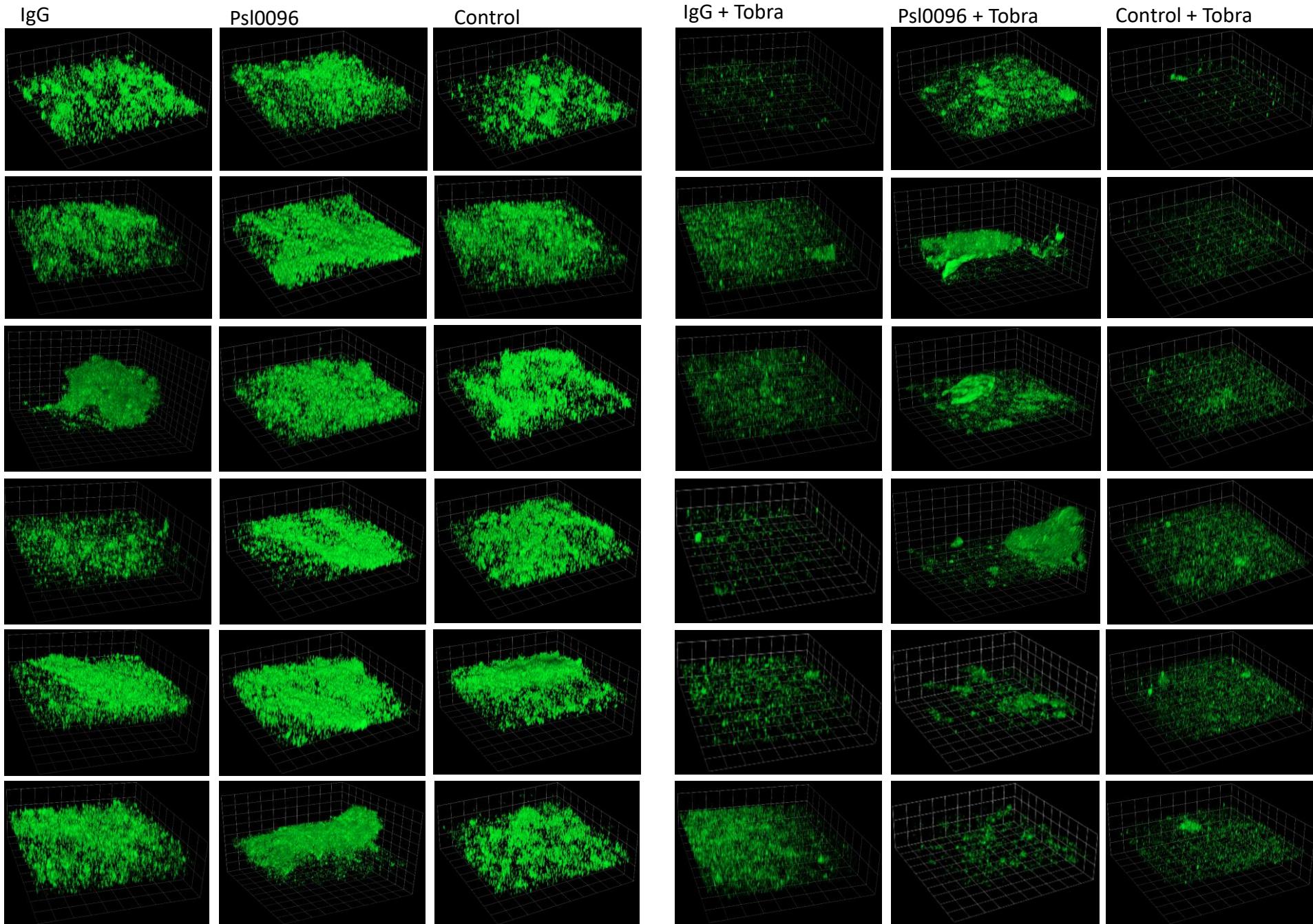
Pa551 (Persistent) Trial3



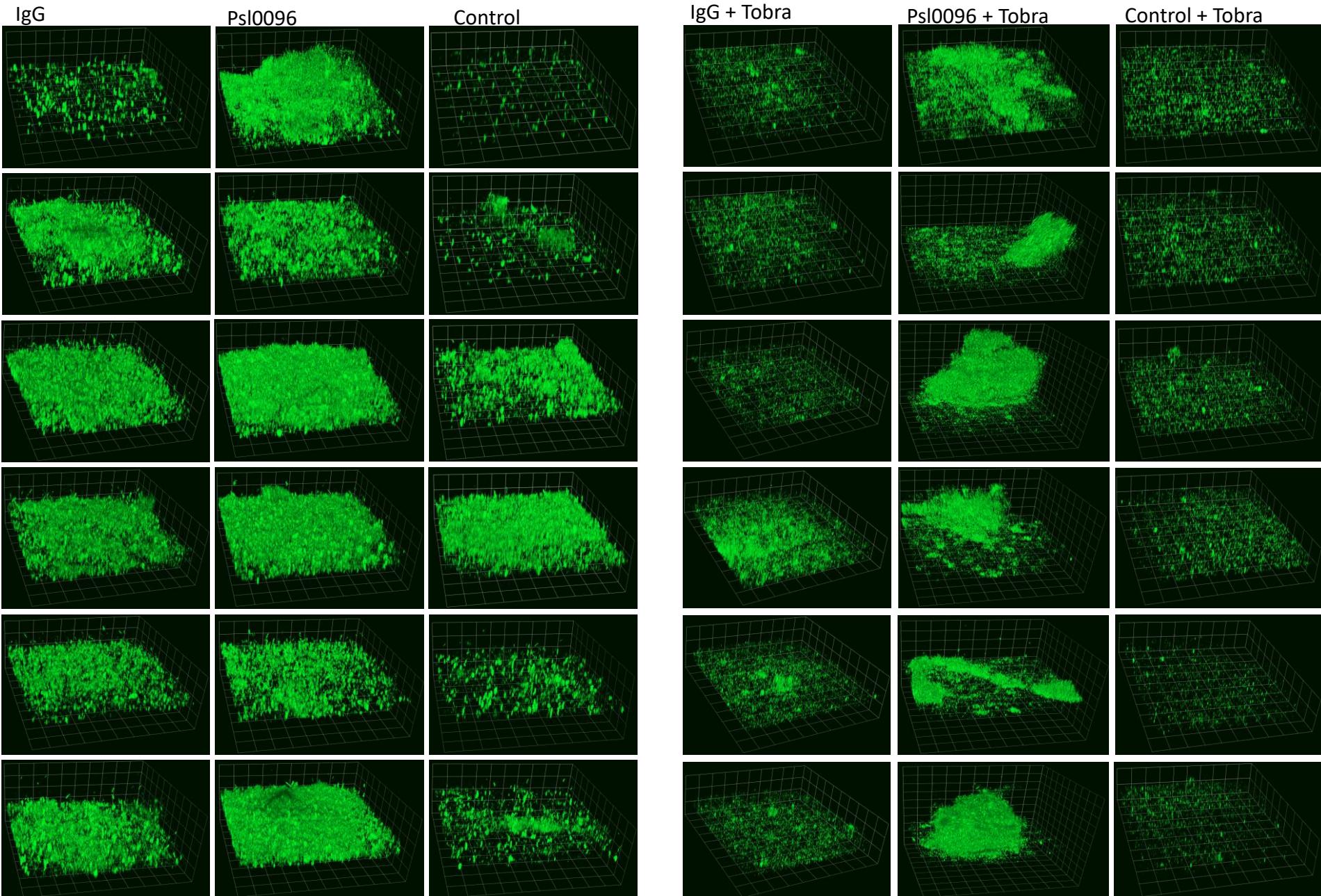
Pa549 (Eradicated) Trial1



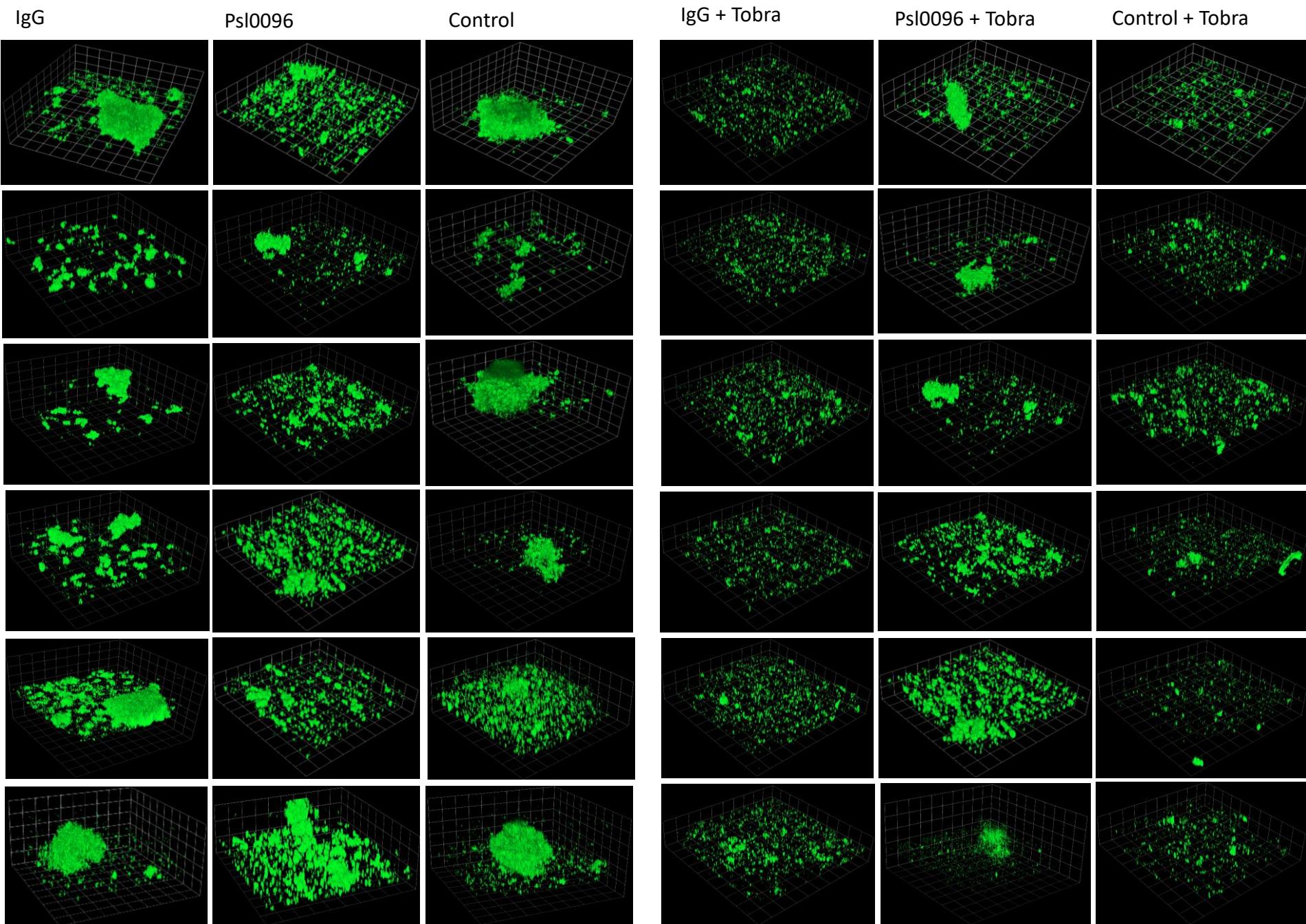
Pa549 (Eradicated) Trial2



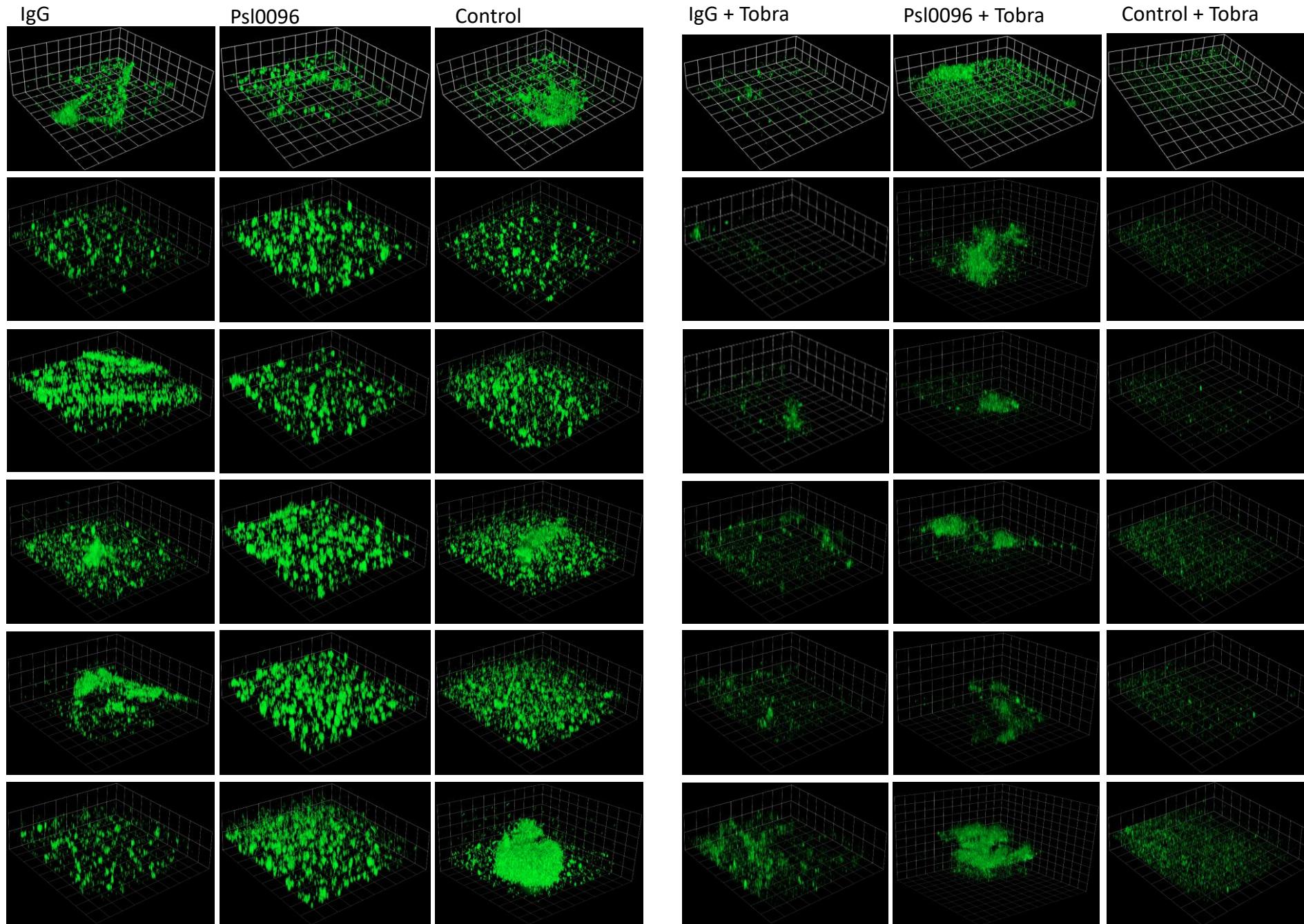
Pa549 (Eradicated) Trial3



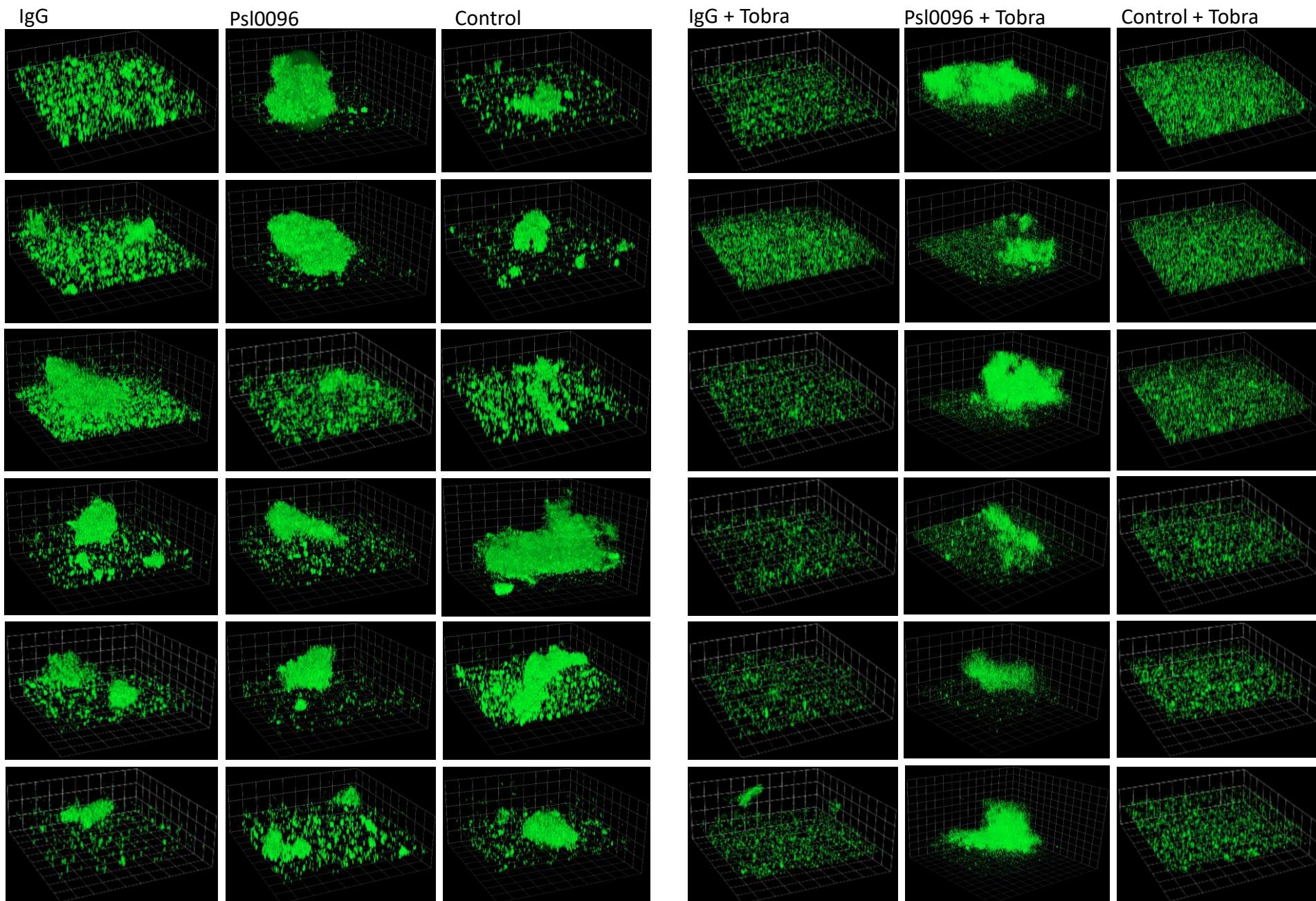
Pa404 (Eradicated) Trial1



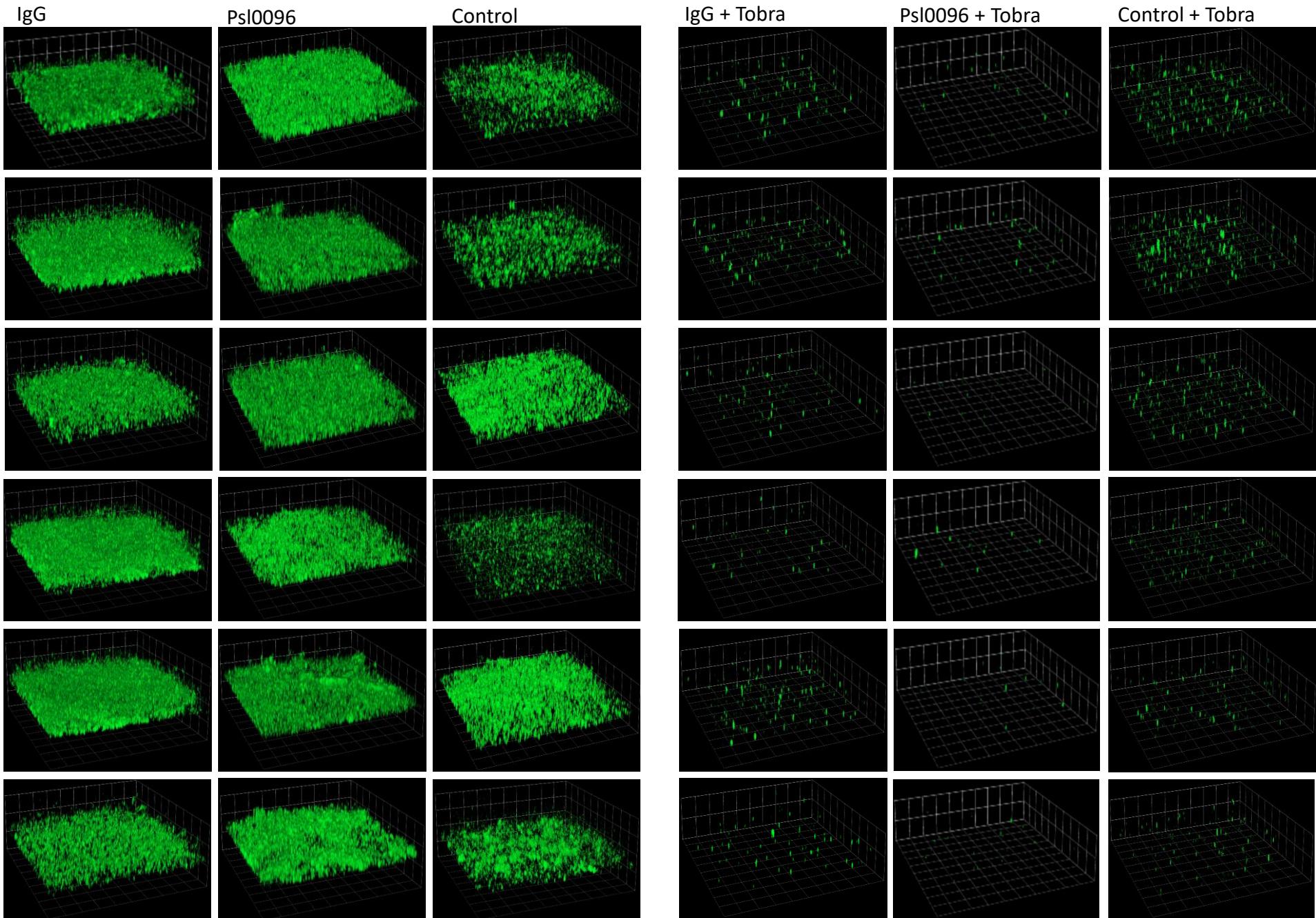
Pa404 (Eradicated) Trial2



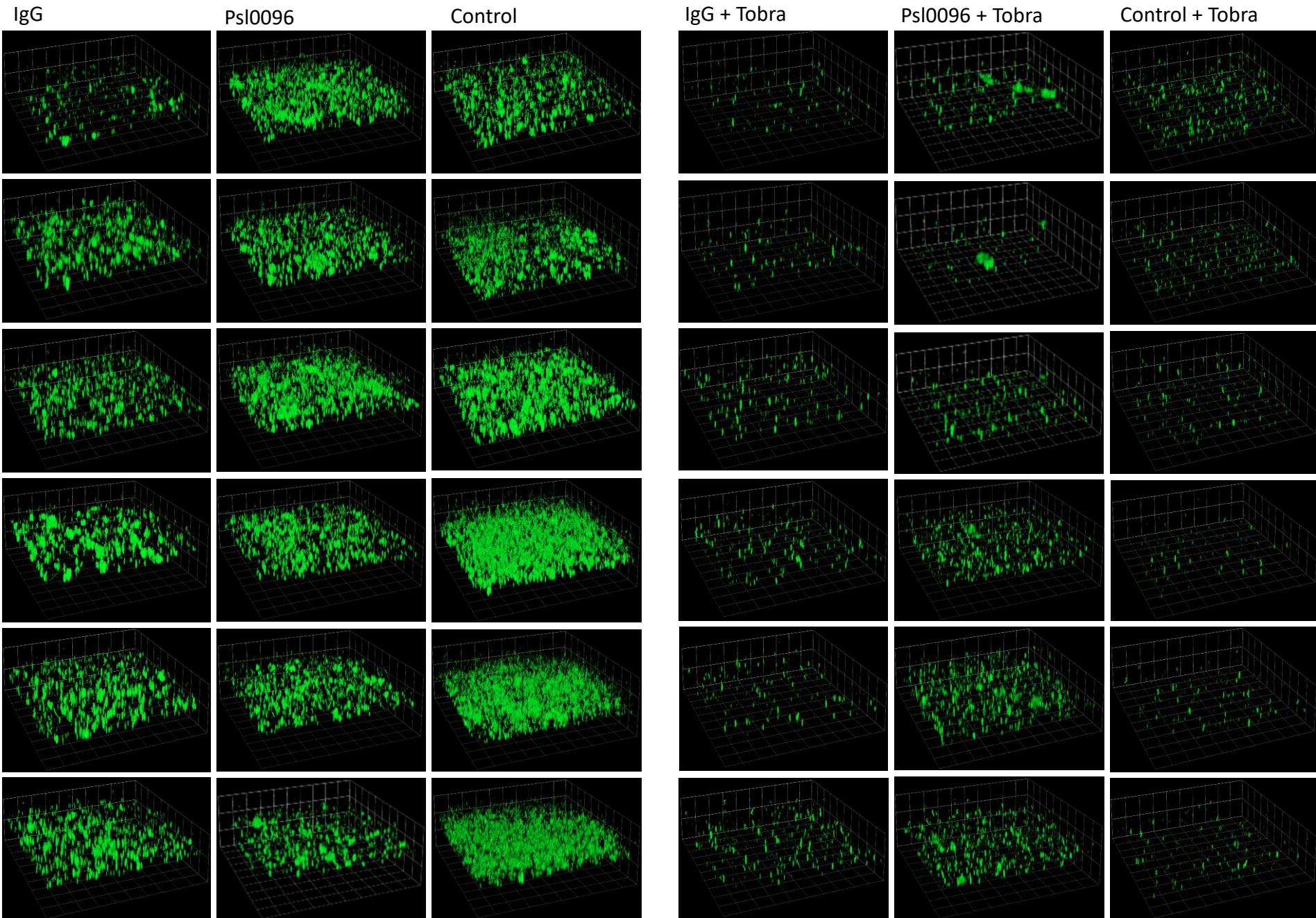
Pa404 (Eradicated) Trial3



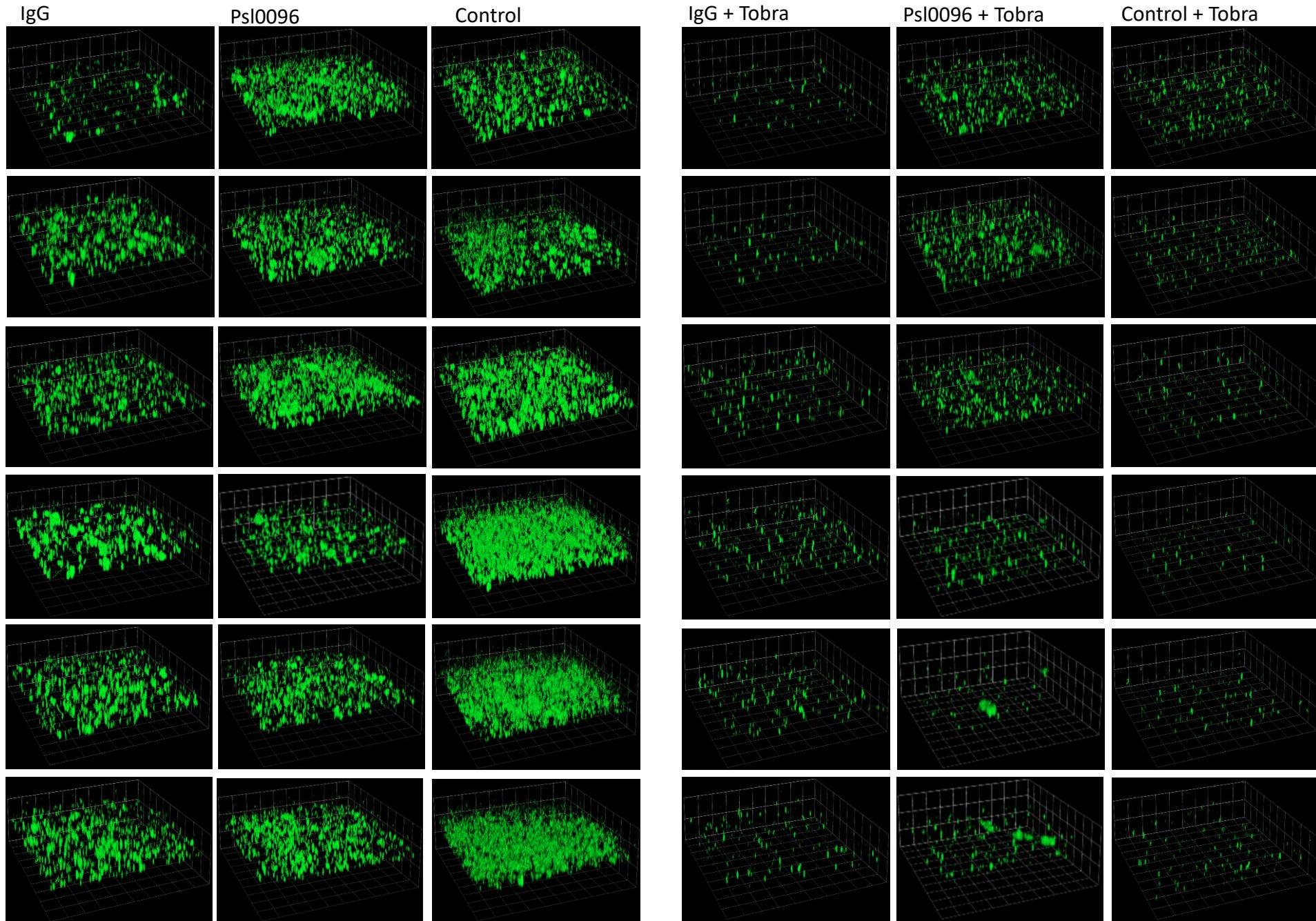
Pa288 (Eradicated) Trial1



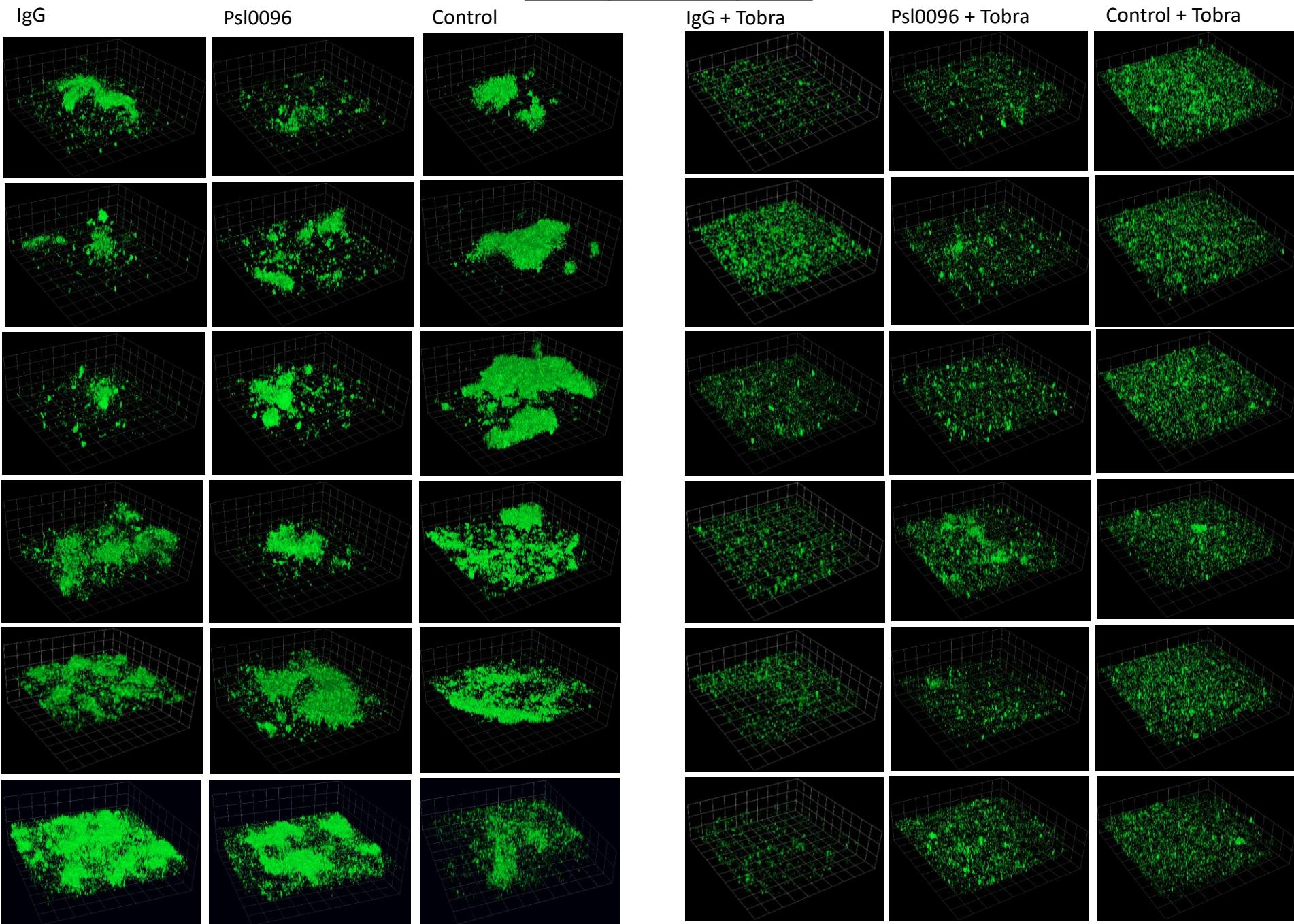
Pa288 (Eradicated) Trial2



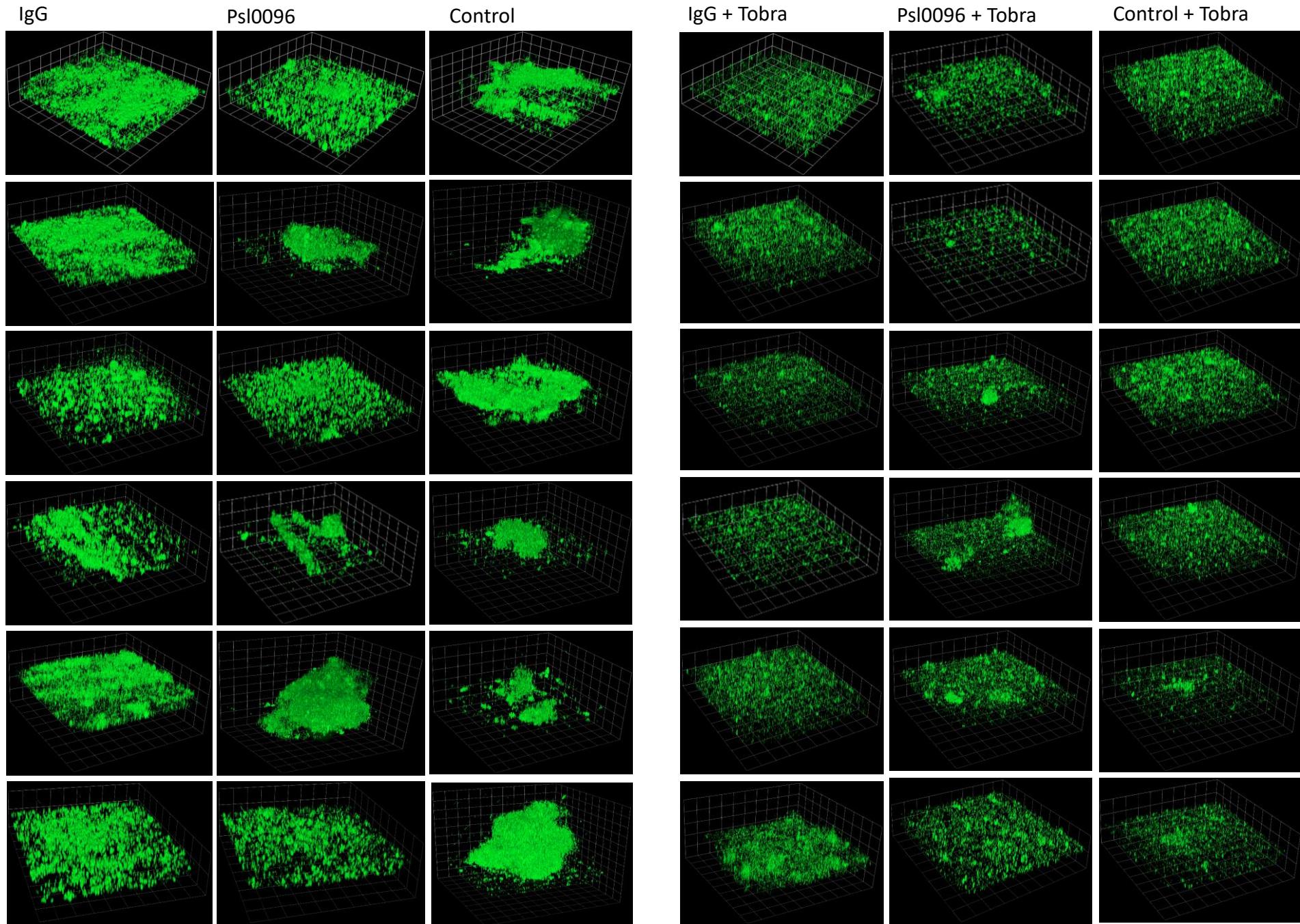
Pa288 (Eradicated) Trial3



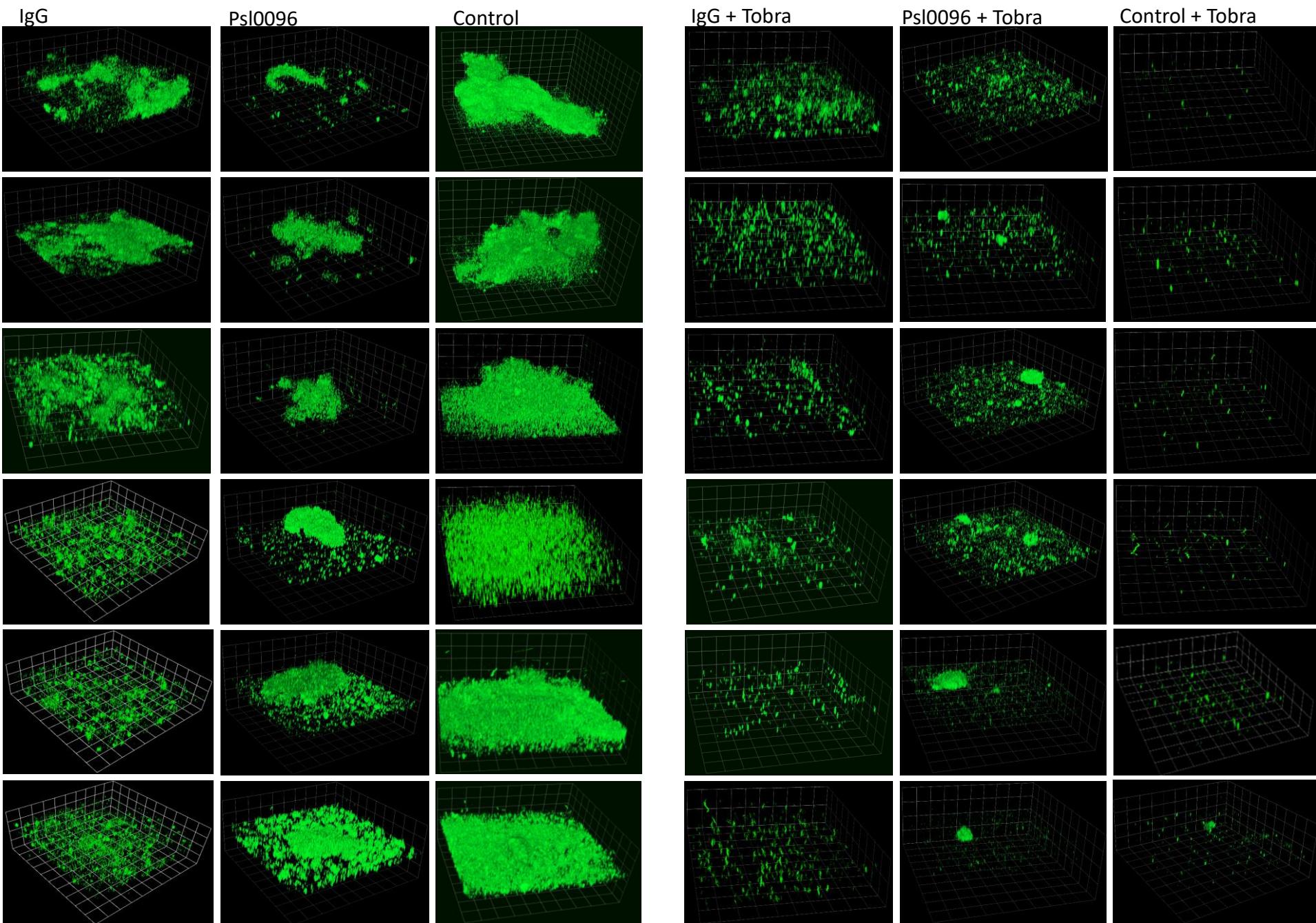
Pa325 (Eradicated) Trial1



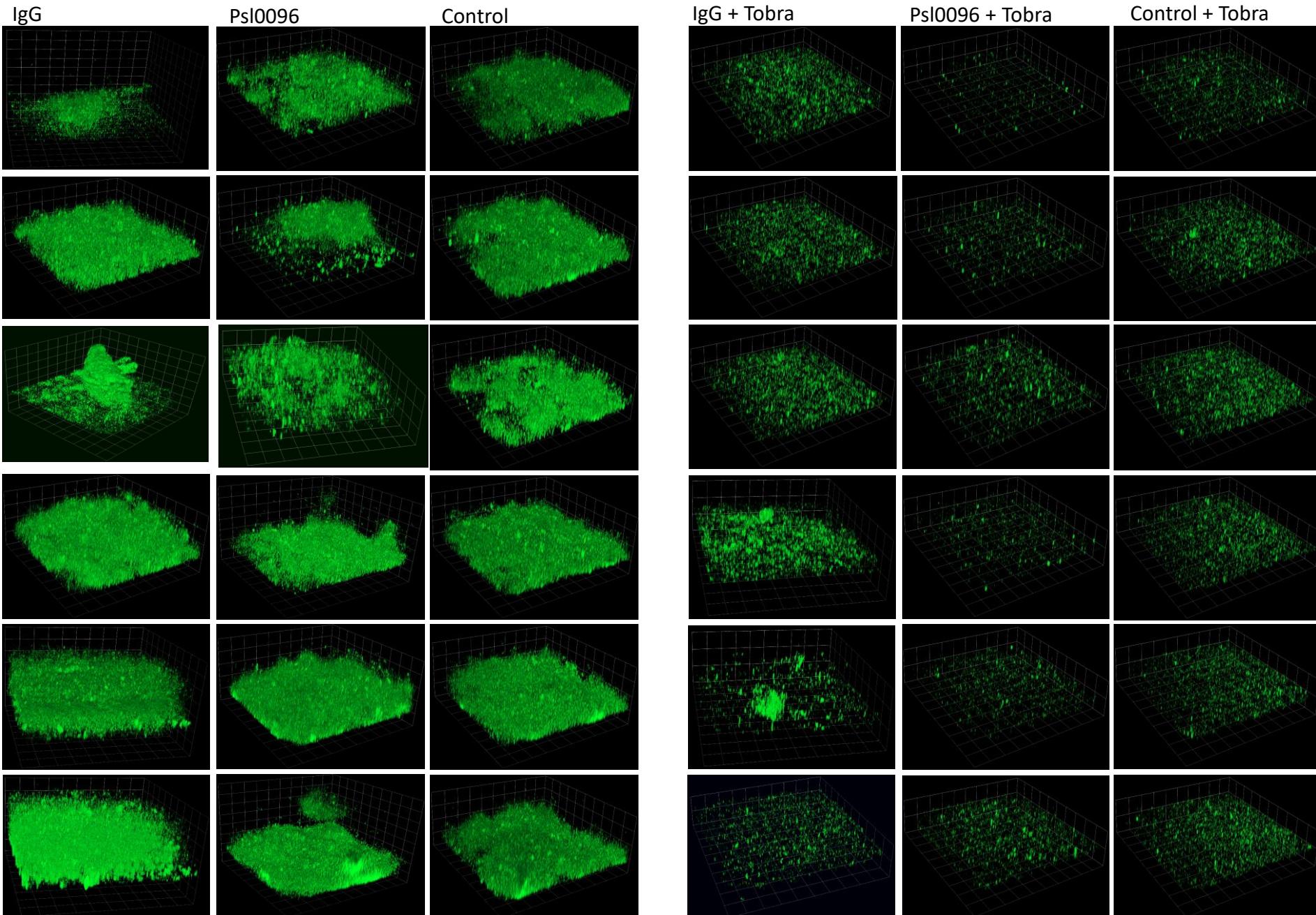
Pa325 (Eradicated) Trial2



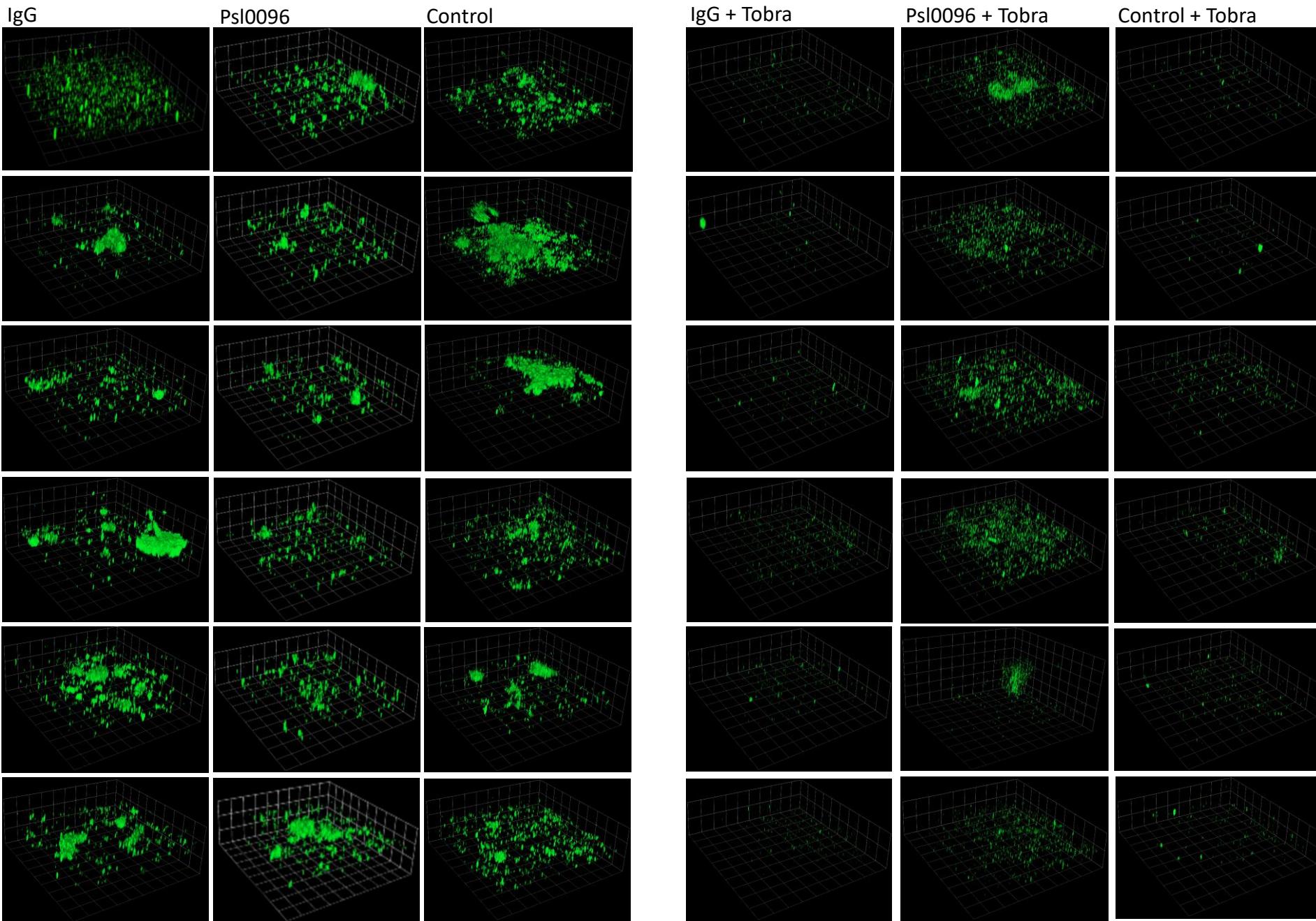
Pa325 (Eradicated) Trial3



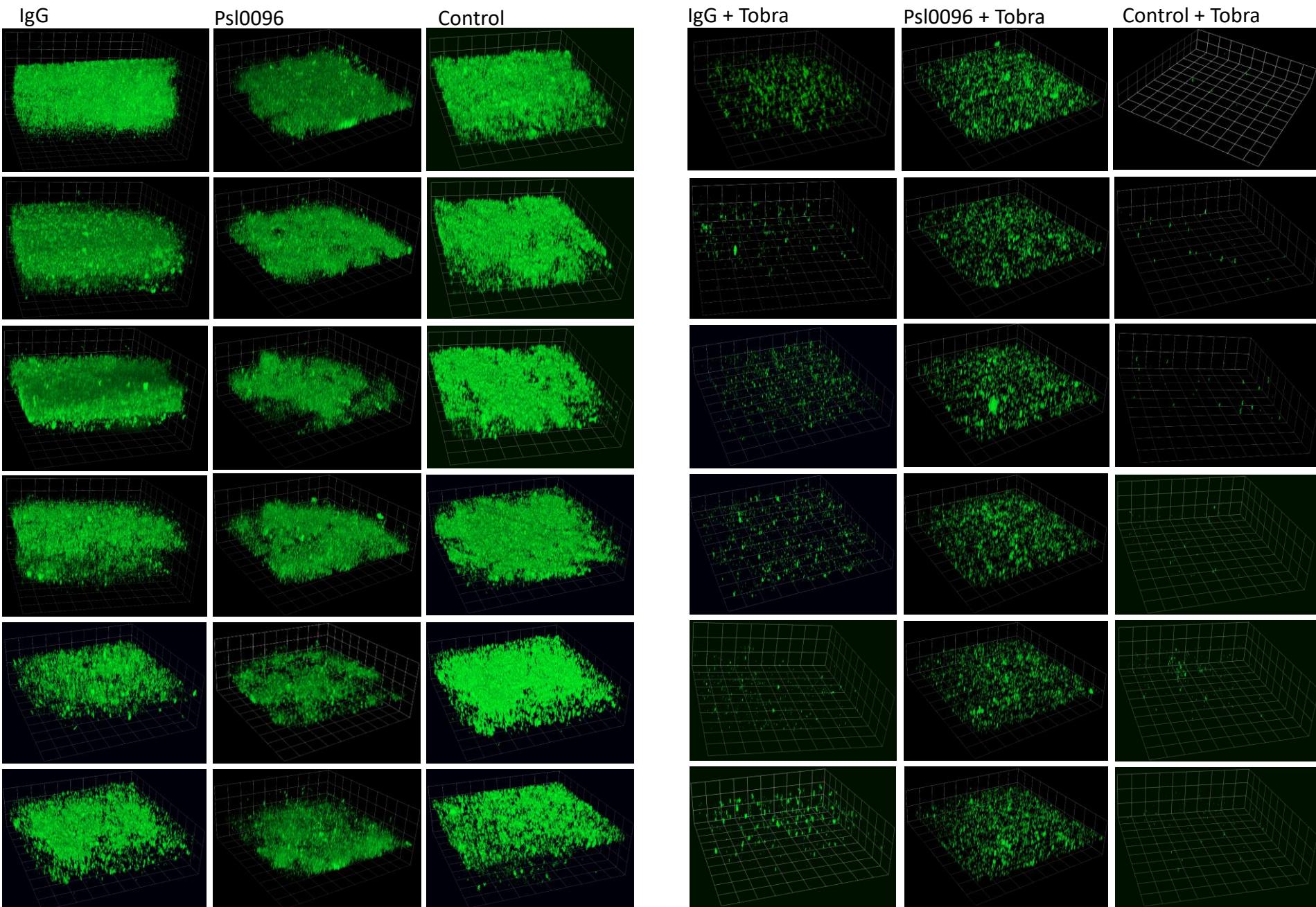
Pa263 (Eradicated) Trial1



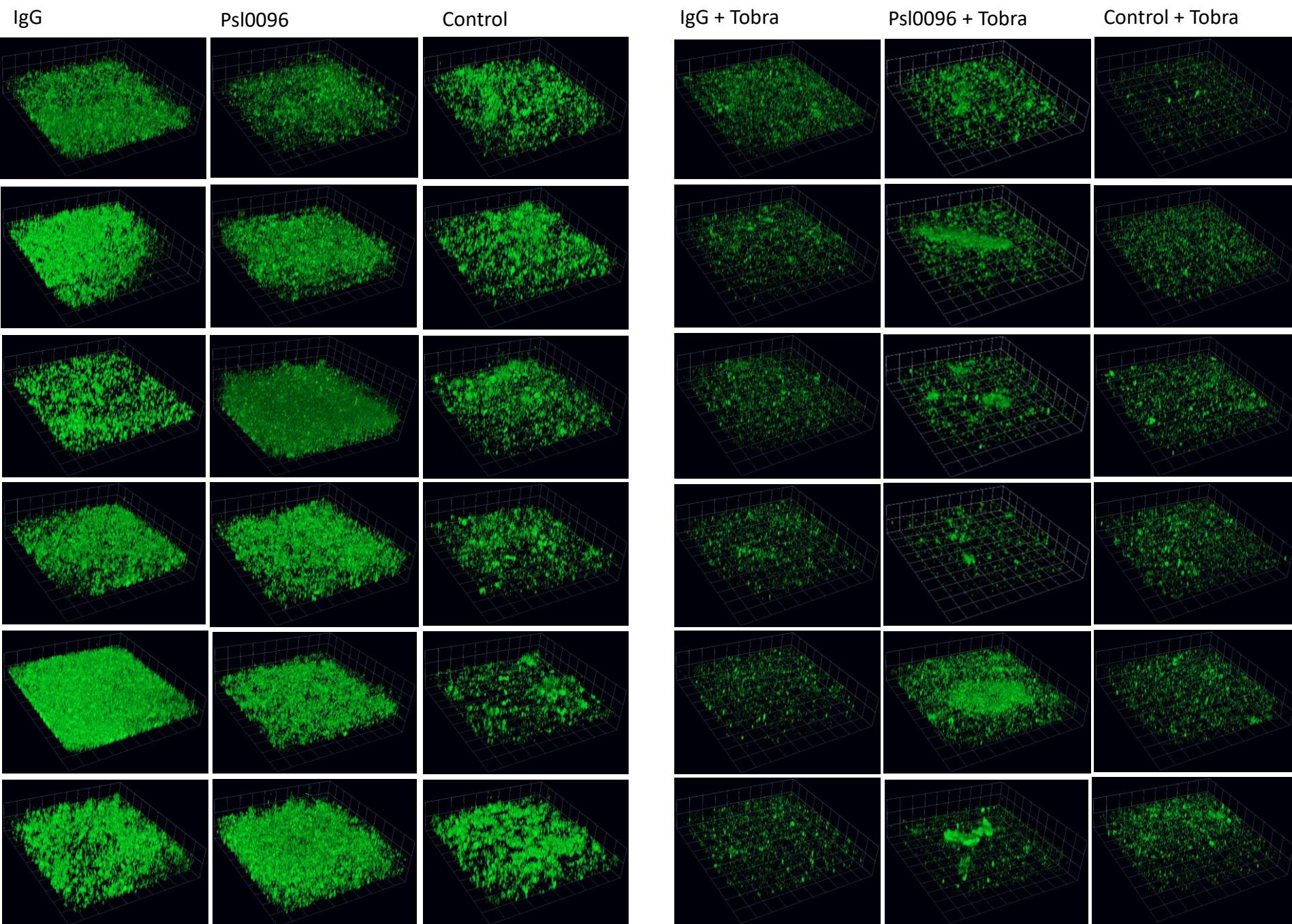
Pa263 (Eradicated) Trial2



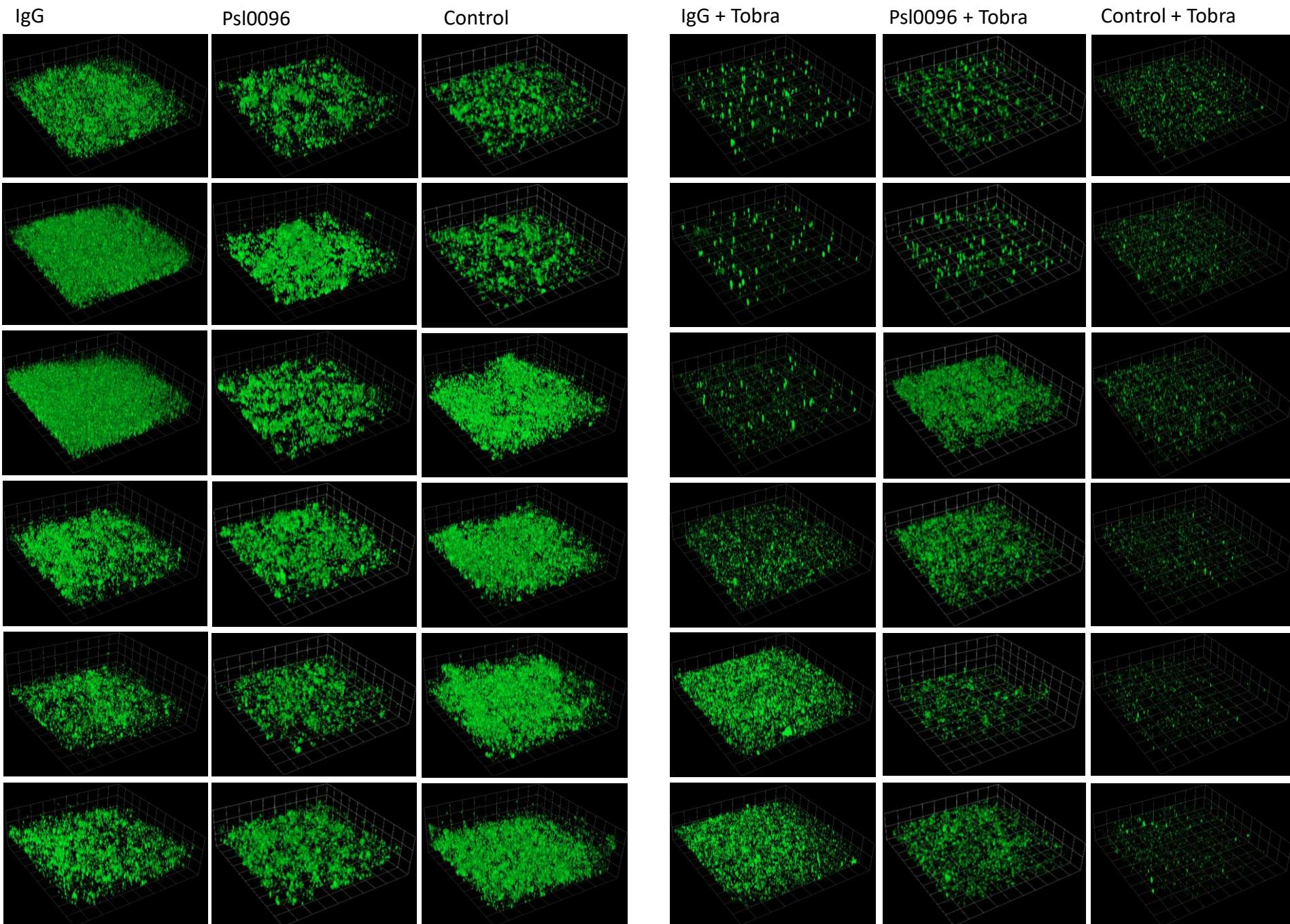
Pa263 (Eradicated) Trial3



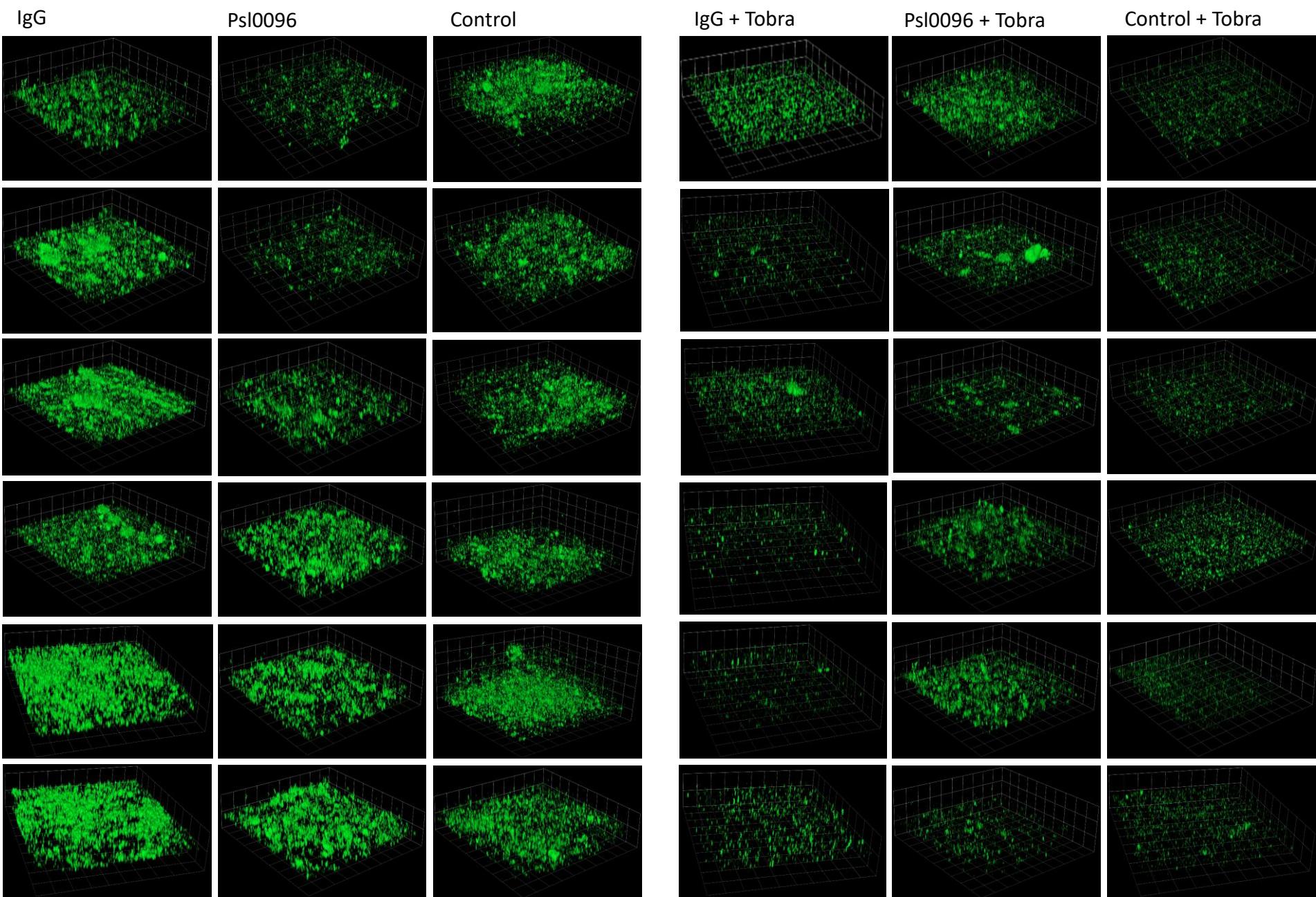
Pa50 (Eradicated) Trial1



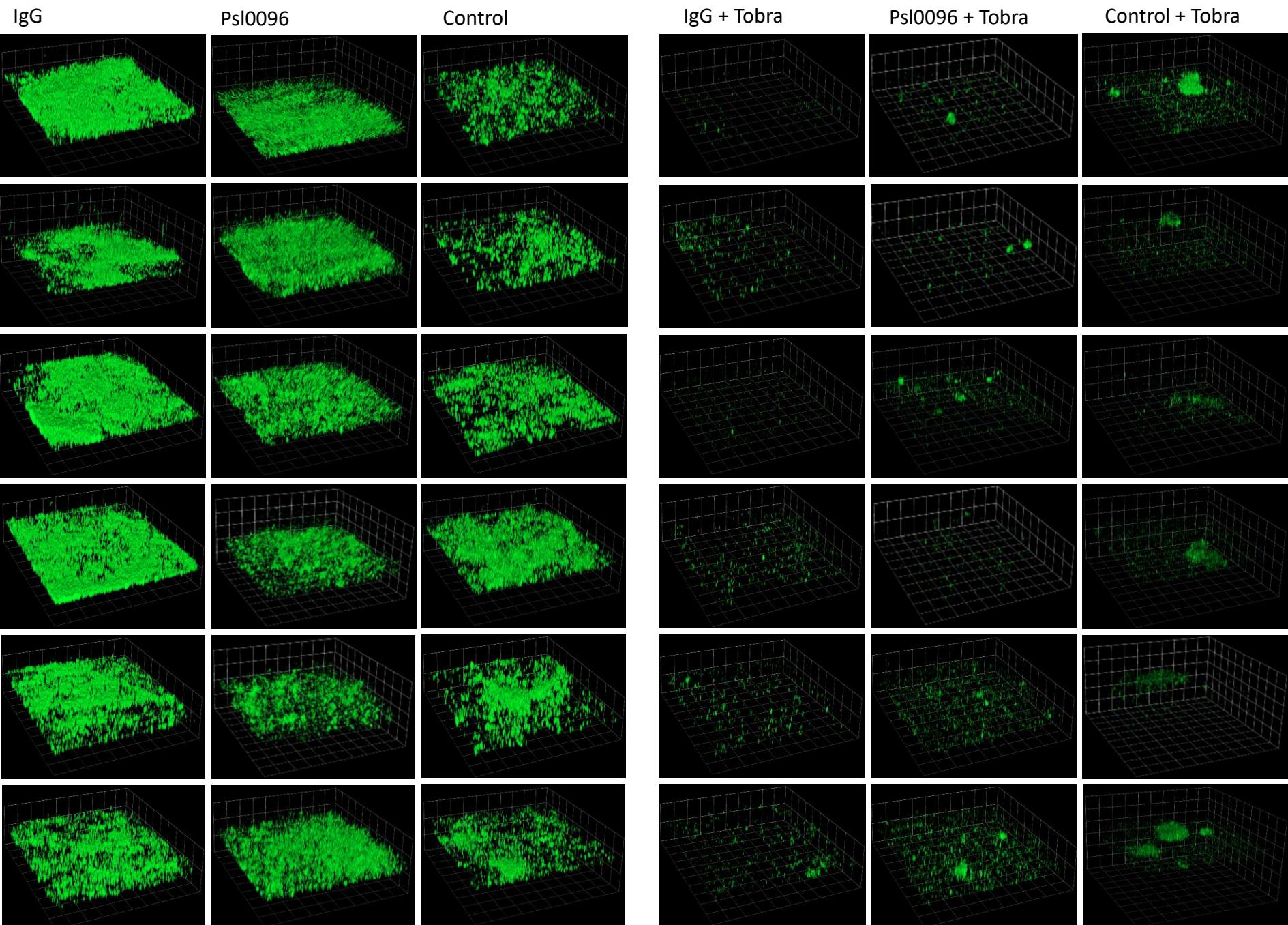
Pa50 (Eradicated) Trial2



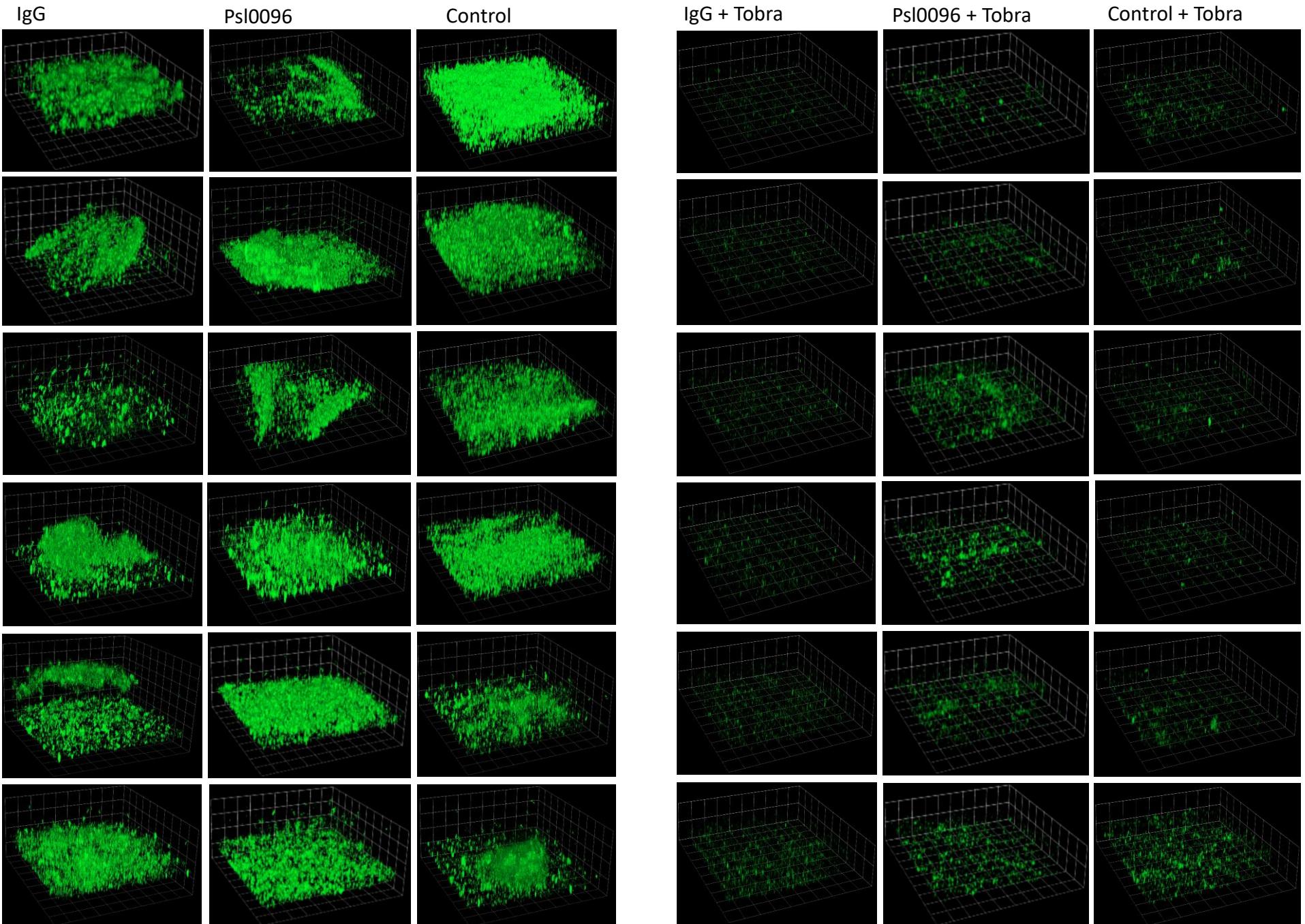
Pa50 (Eradicated) Trial3



Pa558 (Eradicated) Trial1



Pa558 (Eradicated) Trial2



Pa558 (Eradicated) Trial3

