

Table S3: Chimerically-mapping sequencing reads between sgRNA⁺ Cas9-expression construct and *T. gondii* genome (group A clones)

	contig A	contig A coordinate	contig A strand	contig B	contig B coordinate	contig B strand	CIGAR (contig A)	CIGAR (contig B)
clone A1c	AAQM03000805	5576	-	pBM006	10623	-	70S147M	70M147S
	pBM006	1762	-	TGGT1_chrVIIb	3940177	+	73S130M	130S73M
	pBM006	3617	-	TGGT1_chrXII	2563189	-	86S212M	86M212S
	pBM006	526	-	TGGT1_chrVIIb	2842781	+	189S92M19S	111S189M
	pBM006	526	-	TGGT1_chrVIIb	2842781	+	123S92M	92S123M
	pBM006	526	-	TGGT1_chrVIIb	2842781	+	127S88M	88S127M
	pBM006	526	-	TGGT1_chrVIIb	2842781	+	170S83M	83S170M
	pBM006	8059	-	AAQM03000001	145	-	108S193M	108M193S
	TGGT1_chrlb	950047	+	pBM006	4444	-	104M193S	193M104S
	TGGT1_chrlv	2264912	-	pBM006	1964	-	103S197M	103M197S
	TGGT1_chrVIIb	2842782	-	pBM006	525	+	30S178M	178S30M
	TGGT1_chrVIIb	2842782	-	pBM006	525	+	71S145M	145S71M
	TGGT1_chrVIIb	2842782	-	pBM006	525	+	45S189M	189S45M
	TGGT1_chrX	583086	+	pBM006	6495	-	185M103S	103M185S
	clone A2c	pBM006	11208	+	TGGT1_chrVIIb	2842782	+	177M124S
pBM006		6818	+	TGGT1_chrXI	3149611	+	248M48S	248S48M
pBM006		11209	+	TGGT1_chrVIIb	2842783	-	206M25S	25M206S
pBM006		11209	+	TGGT1_chrVIIb	2842783	-	31M182S	182M31S
pBM006		11208	+	TGGT1_chrVIIb	2842782	+	45M149S	45S149M
pBM006		11208	+	TGGT1_chrVIIb	2842782	+	160M55S	160S55M
pBM006		11208	+	TGGT1_chrVIIb	2842782	+	238M56S	238S56M
pBM006		11208	+	TGGT1_chrVIIb	2842782	+	246M55S	246S55M
TGGT1_chrVIIb		2842783	+	pBM006	11209	-	43M257S	257M43S
pBM006		11208	+	TGGT1_chrVIIb	2842782	+	266M35S	266S35M
pBM006		11209	+	TGGT1_chrVIIb	2842783	-	232M65S	65M232S
pBM006		4892	-	TGGT1_chrX	4509421	-	149S150M	149M150S
pBM006		11208	+	TGGT1_chrVIIb	2842782	+	103M134S	103S134M
pBM006		11208	+	TGGT1_chrVIIb	2842782	+	72M187S	72S187M
TGGT1_chrX		574673	+	pBM006	10134	+	108M80S	108S80M
pBM006		11208	+	TGGT1_chrVIIb	2842782	+	140M156S	140S156M
pBM006		7789	+	TGGT1_chrXII	4295071	-	146M148S	148M146S
pBM006		11209	+	TGGT1_chrVIIb	2842783	-	161M111S	111M161S
TGGT1_chrVIIb		2842783	+	pBM006	11209	-	174M126S	126M174S
TGGT1_chrVIIb		2842783	-	pBM006	11209	-	114S98M	114M98S
TGGT1_chrVIIb	2842783	+	pBM006	11209	-	36M118S	118M36S	
TGGT1_chrVIIb	2842783	+	pBM006	11209	-	145M154S	154M145S	
pBM006	11208	+	TGGT1_chrVIIb	2842782	+	258M43S	258S43M	
pBM006	11209	+	TGGT1_chrVIIb	2842783	-	105M117S	117M105S	
pBM006	7247	+	TGGT1_chrla	1490829	-	176M118S	118M176S	
pBM006	11208	+	TGGT1_chrVIIb	2842782	+	64M220S	64S220M	
pBM006	11209	+	TGGT1_chrVIIb	2842783	-	218M83S	83M218S	
clone A3c	AAQM03000805	5576	-	pBM006	10623	-	70S147M	70M147S
	pBM006	526	-	TGGT1_chrVIIb	2842781	+	189S92M19S	111S189M
	pBM006	4374	-	TGGT1_chrVIIb	2580925	+	204S95M	95S204M
	pBM006	526	-	TGGT1_chrVIIb	2842781	+	179S29M	29S179M
	TGGT1_chrVIIb	2842782	-	pBM006	525	+	107S192M	192S107M
	pBM006	526	-	TGGT1_chrVIIb	2842781	+	123S92M	92S123M
	pBM006	5370	+	AAQM03000741	5460	-	221M72S	72M221S
	pBM006	526	-	TGGT1_chrVIIb	2842781	+	127S88M	88S127M
	pBM006	10622	+	AAQM03000805	5575	+	168M131S	131M168S
	TGGT1_chrX	583086	+	pBM006	6495	-	185M103S	103M185S
	pBM006	8059	-	AAQM03000001	145	-	108S193M	108M193S
	pBM006	1762	-	TGGT1_chrVIIb	3940177	+	73S130M	130S73M
	pBM006	526	-	TGGT1_chrVIIb	2842781	+	146S70M	70S146M
	pBM006	3617	-	TGGT1_chrXII	2563189	-	86S212M	86M212S
	pBM006	526	-	TGGT1_chrVIIb	2842781	+	170S83M	83S170M
	TGGT1_chrVI	580409	+	pBM006	6125	+	194M106S	106M194S
	pBM006	526	-	TGGT1_chrVIIb	2842781	+	190S92M5S	97S190M
	pBM006	526	-	TGGT1_chrVIIb	2842781	+	239S62M	62S239M
	TGGT1_chrVIIb	2842782	-	pBM006	525	+	108S191M	191S108M
	pBM006	180	-	TGGT1_chrVIII	3081782	+	56S224M	224S56M
	pBM006	1964	+	TGGT1_chrlv	2264912	+	271M30S	30M271S
	pBM006	4444	+	TGGT1_chrlb	950047	-	205M95S	95M205S
	pBM006	526	-	TGGT1_chrVIIb	2842781	+	222S77M	77S222M