

Additional file 2: Table S2. Mapped and paired reads by sample against *Bos taurus* genome.

Sample	Total reads	Mapped reads	% mapped reads	High quality reads	% high quality reads	Splice reads	% splice reads
MØC R1	57978010	57066703	98.43	39294793	67.78	12982893	22.39
MØC R2	48884602	48177970	98.55	33370638	68.26	10548504	21.58
MØC R3	49634030	48097516	96.90	32464469	65.41	9432877	19.00
MØ1H R1	45726510	38902639	85.08	26406712	57.75	7926380	17.33
MØ1H R2	49810014	45221494	90.79	29675634	59.58	9187373	18.44
MØ1H R3	46709092	42000811	89.92	30077799	64.39	9428874	20.19
MØ7 R1	50818888	42614504	83.86	26894321	52.92	8298603	16.33
MØ7 R2	59129224	51174478	86.55	32684186	55.28	10153185	17.17
MØ7 R3	48795612	39459440	80.87	28423812	58.25	8812206	18.06
MØHK R1	45889532	45436847	99.01	31928506	69.58	10123030	22.06
MØHK R2	36301526	36482426	100.00	16726768	46.08	5510135	15.18
MØHK R3	51781248	48520326	93.70	32549263	62.86	10305755	19.90

MØC: Non-infected macrophages; MØ1H: macrophages inoculated with Nc-Spain1H; MØ7: macrophages inoculated with Nc-Spain7; MØHK: macrophages inoculated with *N. caninum* heat-killed tachyzoites; R1-R3: Biological replicates 1-3 collected from three independent experiments.