

**Table S1.****Capsule size differences in variable capsule inducing conditions.**

Medium	RC2 (SM)	RC2 $\Delta all1$	RC2 $\Delta all1$ + ALL1	H99	H99 $\Delta all1$	H99 $\Delta all1$ + ALL1
SAB	0.8±0.4	2.0±0.5	0.9±0.2	1.2±0.2	1.3±0.2	1.2 0.3
<i>In vivo</i> (d7-PI)	8.0±1.8	5.9±1.7	ND	12.2±4.8	6.0±3.4	ND
LIM	6.0±1.1	5.0±1.1	5.8±1.3	2.5±1.0	1.7±0.6	2.3±0.8
DMEM + FCS (10%), CO <sub>2</sub>	3.7±0.9	2.5±1.1	3.0±1.1	3.7±1.1	3.0±0.8	4.4±0.6
LIM + 5% CO <sub>2</sub>	7.2±2.0	6.3±2.0	7.4±1.8	3.3±1.0	2.5±0.6	3.5±0.4

**ND – Not done****Table S2. Capsule Size in mutants overexpressing ALL1**

	RC2 (SM)	RC2- $\Delta all1$	P <sub>CTR4-2</sub> -ALL1
Minimal media	2.94 ± 0.49	2.82 ± 0.38	3.31 ± 0.61
ASN + BCS	1.48 ± 0.42	ND	5.47 ± 1.86
LIM + BPS + BCS	7.04 ± 1.14	5.13 ± 0.64	7.74 ± 1.65
DMEM+10%FCS (5% CO <sub>2</sub> )	5.04 ± 0.81	4.37± 0.62	5.5 ± 1.05

ST1 and ST2: Capsule size is expressed in  $\mu\text{m} \pm$  standard deviation. LIM-low iron media, SAB-Sabroaud's Dextrose Broth, D7-post infection (PI)-Day 7, ASN-Asparagine Salt medium, BPS-Iron Chelator, BCS- Copper Chelator

**Table S3:** Gene ontology (GO) enrichment analysis on differentially expressed genes (at least 2-fold) with statistical significance (q value less than 0.05) in RC2- $\Delta all1$  mutant versus wild-type (RC2-SM).

GO_ID	GO_TERM	P_Value_Hypergeometric	P_Value_Hypergeometric_with_Bonferroni_Correction
GO:0016491	GO:oxidoreductase activity	3.97E-05	0.0021041
GO:0055114	GO:oxidation-reduction process	0.000286645	0.01519218
GO:0055085	GO:transmembrane transport	0.000411722	0.02182127
GO:0016021	GO:integral to membrane	0.001892841	0.10032057
GO:0005507	GO:copper ion binding	0.00326928	0.17327184
GO:0045735	GO:nutrient reservoir activity	0.00877193	0.46491229
GO:0022857	GO:transmembrane transporter activity	0.01421087	0.75317611
GO:0000042	GO:protein targeting to Golgi	0.01746781	0.92579393
GO:0006801	GO:superoxide metabolic process	0.01746781	0.92579393
GO:0016301	GO:kinase activity	0.02608829	1
GO:0031683	GO:G-protein beta/gamma-subunit complex binding	0.02608829	1
GO:0046872	GO:metal ion binding	0.02608829	1
GO:0070403	GO:NAD+ binding	0.04310564	1
GO:0006031	GO:chitin biosynthetic process	0.04310564	1
GO:0007186	GO:G-protein coupled receptor signaling pathway	0.04310564	1
GO:0004100	GO:chitin synthase activity	0.04310564	1
GO:0004871	GO:signal transducer activity	0.05150379	1
GO:0005840	GO:ribosome	0.05200313	1
GO:0006412	GO:translation	0.05604526	1
GO:0019001	GO:guanyl nucleotide binding	0.05982908	1
GO:0015693	GO:magnesium ion transport	0.05982908	1
GO:0015095	GO:magnesium ion transmembrane transporter activity	0.05982908	1
GO:0003735	GO:structural constituent of ribosome	0.06023334	1
GO:0008565	GO:protein transporter activity	0.07626363	1
GO:0004252	GO:serine-type endopeptidase activity	0.1003845	1
GO:0003964	GO:RNA-directed DNA polymerase activity	0.1003845	1
GO:0005509	GO:calcium ion binding	0.1003845	1
GO:0004672	GO:protein kinase activity	0.1003845	1
GO:0005543	GO:phospholipid binding	0.1082857	1
GO:0005643	GO:nuclear pore	0.1082857	1
GO:0016020	GO:membrane	0.1207823	1
GO:0016706	GO:oxidoreductase activity, acting on paired donors,	0.1392103	1
GO:0006351	GO:transcription, DNA-dependent	0.1741184	1
GO:0003677	GO:DNA binding	0.1806229	1

GO:0003924	GO:GTPase activity	0.1979146	1
GO:0050660	GO:flavin adenine dinucleotide binding	0.2049686	1
GO:0006278	GO:RNA-dependent DNA replication	0.2090652	1
GO:0006468	GO:protein phosphorylation	0.2122815	1
GO:0005634	GO:nucleus	0.228065	1
GO:0006457	GO:protein folding	0.2325769	1
GO:0043565	GO:sequence-specific DNA binding	0.2393296	1
GO:0020037	GO:heme binding	0.2657581	1
GO:0003700	GO:sequence-specific DNA binding transcription fact	0.3037084	1
GO:0006355	GO:regulation of transcription, DNA-dependent	0.3388221	1
GO:0006886	GO:intracellular protein transport	0.3397192	1
GO:0008270	GO:zinc ion binding	0.3786665	1
GO:0005622	GO:intracellular	0.4324039	1
GO:0005515	GO:protein binding	0.4582816	1
GO:0003676	GO:nucleic acid binding	0.4591595	1
GO:0003723	GO:RNA binding	0.5028527	1
GO:0016787	GO:hydrolase activity	0.5328346	1
GO:0005524	GO:ATP binding	0.6710678	1
GO:0008152	GO:metabolic process	0.8374141	1

**Table S4: Primers used in the study**

Primer	SEQUENCE (5'-3')	Function/ restriction site
H99AII1-NF	<u>CCATAGATTGGT</u> GTCTCAAGTGCTTGTCCA	<i>ALL1</i> gene knock out cassette/ <i>van91I</i>
H99AII1-NR	<u>CCATCATTTGGAT</u> GAATTGGAGCGGAAAGTG	<i>ALL1</i> gene knock out cassette/ <i>van91I</i>
H99AII1-CF	<u>CCATTTCTTGGGGT</u> ATTTGAAGGTTAAAGGAGA CTTC	<i>ALL1</i> gene knock out cassette/ <i>van91I</i>
H99AII1-CR	<u>CCATAAATTGGT</u> GGACTTTACAGATGACAACAC AA	<i>ALL1</i> gene knock out cassette/ <i>van91I</i>
H99AII1-RecF	<u>TCTAGATGTCAAGT</u> GCTTGTCCA	<i>ALL1</i> gene reconstitution in H99 $\Delta$ <i>all1/XbaI</i>
H99AII1-RecR	<u>CTCGAGCTGGGT</u> TCTGTGCTAAG	<i>ALL1</i> gene reconstitution in H99 $\Delta$ <i>all1/XhoI</i>
H99AII1-RTf	AAGGCGAGGGT GAGCACT	Real time PCR <i>ALL1</i>
H99AII1-RTr	TTAGAGAGCCTGGGTCTTGC	Real time PCR <i>ALL1</i>
P <sub>CTR4-2</sub> For	<u>CCATTTCTTGGG</u> ACCAATTGGATATTGCTGTTTC TAC	<i>CTR4</i> promoter for Overexpression (OX) Construct/ <i>van91</i>
P <sub>CTR4-2</sub> Rev	<u>CATATGGATTGGT</u> GAAGTCGTTG	<i>CTR4</i> promoter for OX Construct/ <i>NdeI</i>
ALL1-For	<u>CATATGTCCGGC</u> GTTACCCAAGGTGTC	<i>ALL1</i> gene for OX Construct
ALL1-Rev	<u>CCATAAATTGGT</u> TAAAGAGCCTGGGTCTTGCTG	
CNC05700	GCGTATCAAGCTTTCCGAAG CCTTCTTCTTCATGGCTTGC	Real time PCR
CNC05690	ATTCCTCCAGGGGAGACACT GGAGCTCTCAAGCCATCAAC	Real time PCR
CNM02430	GCCTTCCTCAAAATGGACAG AGACATCTTTTCACGGGCGAGC	Real time PCR
CNM02420	GTGATCATCGTTCACGCAAC GGAATGGGACATTGGTTGAC	Real time PCR
CNB02540	GGGCATGTGAGTCGAGAGAT CTCTCGAAGAACCCCTTCT	Real time PCR
CNG00120	ACAGCGGAACCTAAGCAAGA AAGCAACAATGAGCGAGGTT	Real time PCR
CNC01660- JEC21	GGCAATCACTGACTTCGACA CACCGGACAAAGGGTAAGAA	Real time PCR

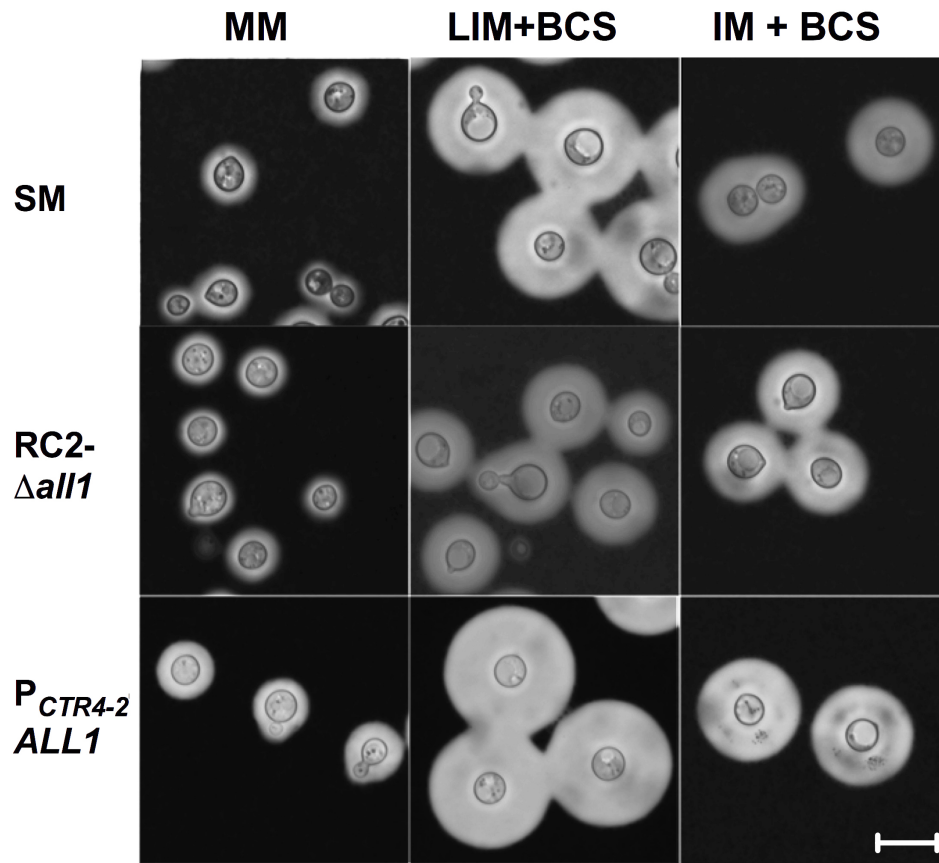
---

CNC01660-H99	CCTATGAGCGGTGGTGAGAT GATCTCGCGGATAGAGTTGG	Real time PCR
CNK02840-JEC21	ACCTTGGCTTCTGGTCTGTG TTTCCTCAATGGGGAGATTG	Real time PCR
CNK02840-H99	CCATCGAGGAAAGGAAATCA GTGGGCTTTGAAGATGTCGT	Real time PCR
CNG00950	CAGACGACCACGACTCTCAA CGTGCGAAGAATAGTGTGGA	Real time PCR
CNI01980	GACACGTCGATGTGGATGAG CCCCACTGACATTTCTGCTT	Real time PCR
CNB00400	TATCATGGCTGGTGTGGCTA GAAGCAGCAACGACGATGTA	Real time PCR
CNH01230	GCTTAGTAGATCCCGCGACA GTCAGGCAATCCGATGATTT	Real time PCR
CNG00110	TCTGGGTATTTCGACCGATTC GGAGCTGGTGACAGTAAGAC	Real time PCR
CNH00490	CAGACTGCCGCTGTTGATTA GTGGGGTTTGGAAACATTCAC	Real time PCR

---

**Figure S1: Effect of *ALL1* overexpression on capsule induction**

Under Capsule inducing conditions,  $\Delta all1$  mutant has impaired capsule induction. Cells  $P_{CTR4-2}$ -*ALL1* overexpressing *ALL1* under promoter-inducing conditions (200 $\mu$ M BCS) have enhanced capsular induction. LIM-Low Iron Medium+100 $\mu$ M BPS, IM (DMEM+10%FCS+1%NCTC in 5% CO<sub>2</sub>). All capsules were measured after 18h. Bar represent 10 $\mu$ m.



**Figure S2.** Antibody mediated phagocytosis of RC2-SM, RC2- $\Delta all1$ , H99 and H99- $\Delta all1$ . Reduction in percentage of phagocytosis was observed for  $\Delta all1$  mutants relative to the parental and reconstitution strains. Data are mean +/- SD of 3 independent experiments of triplicate wells

