

## Supplementary Information

**Table S1.** The sequence of primers used for real-time qPCR and amplifying the 3'UTR of Cav-1 mRNA.

Gene	Accession number	Sequence (5'-3')	Product size
<i>perilipin A</i>	NM_001038638.1	F: CAGCCAAGGAAGAGTCAGC R: CCTGGAAGGTGTGTTGAGAG	107 bp
<i>aP2</i>	HM453202	F: GAGCACCATAACCTTAGATGGA R: AAATTCTGGTAGCCGTGACA	121 bp
<i>PPAR<math>\gamma</math></i>	NM_214379	F: AGGACTACCAAAGTGCCATCAAA R: GAGGCTTTATCCCCACAGACAC	142 bp
<i>LPL</i>	NM_214286.1	F: GGAGAGAGGAAGGGAAAACAGAG R: AGACCGACCAATAAACTGCAAAG	150 bp
<i><math>\beta</math>-actin</i>	NM_007393	F: GGACTTCGAGCAGGAGATGG R: AGGAAGGAGGGCTGGAAGAG	138 bp
<i>Cav-1</i>	NM_214438.2	F: ATCCCAAGCATCTCAACG R: AAGAGGGCAGACAGCAAA	157 bp
<i>Cav-1</i> 3'UTR	-	F: CCGCTCGAGAGGCAGTAACGAAAGA R: ATTTGCGGCCGCGAAGGGTAAACTTTGG	708 bp

Figure S1. Original data of one independent flow cytometry assay.

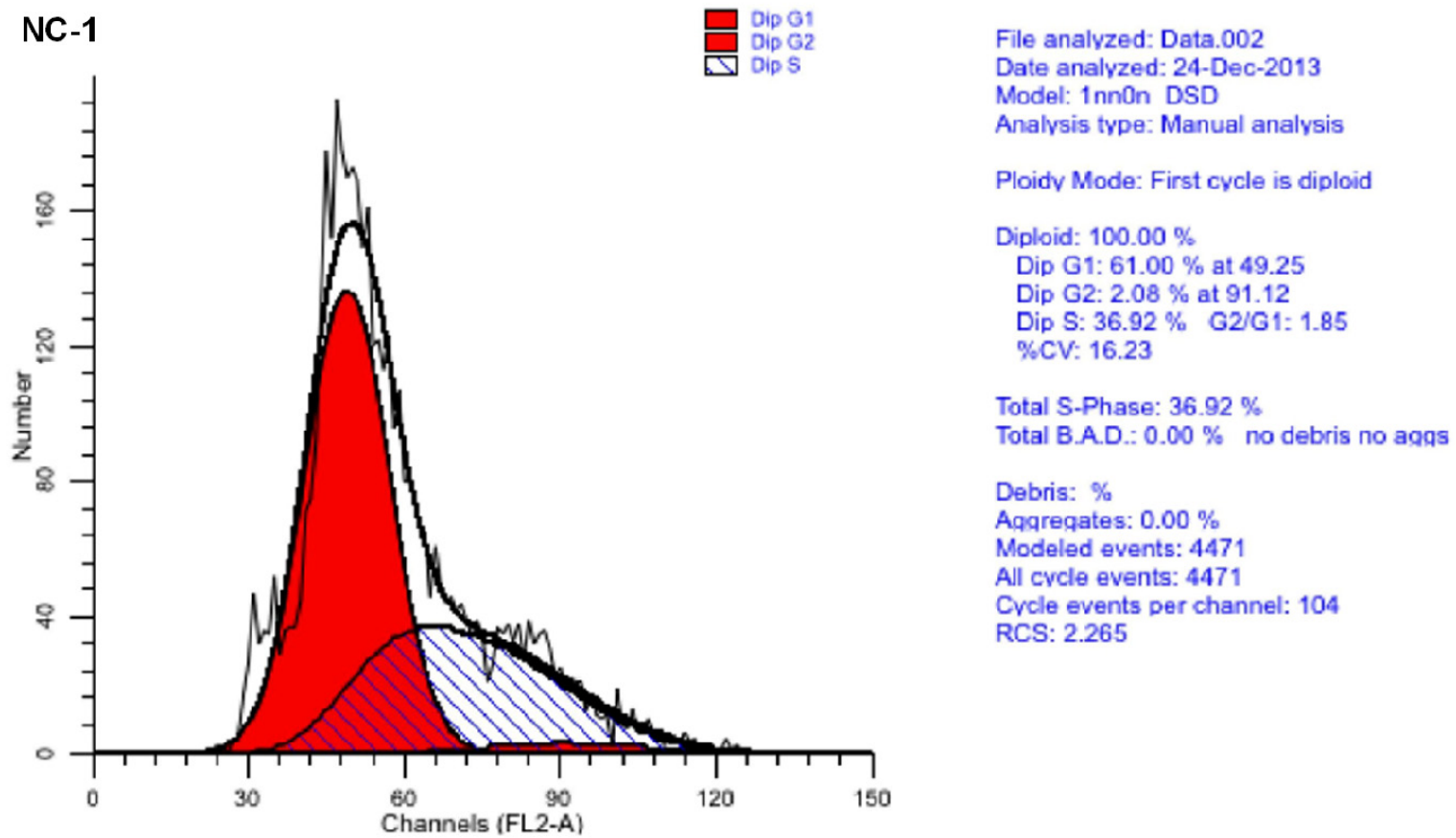


Figure S1. Cont.

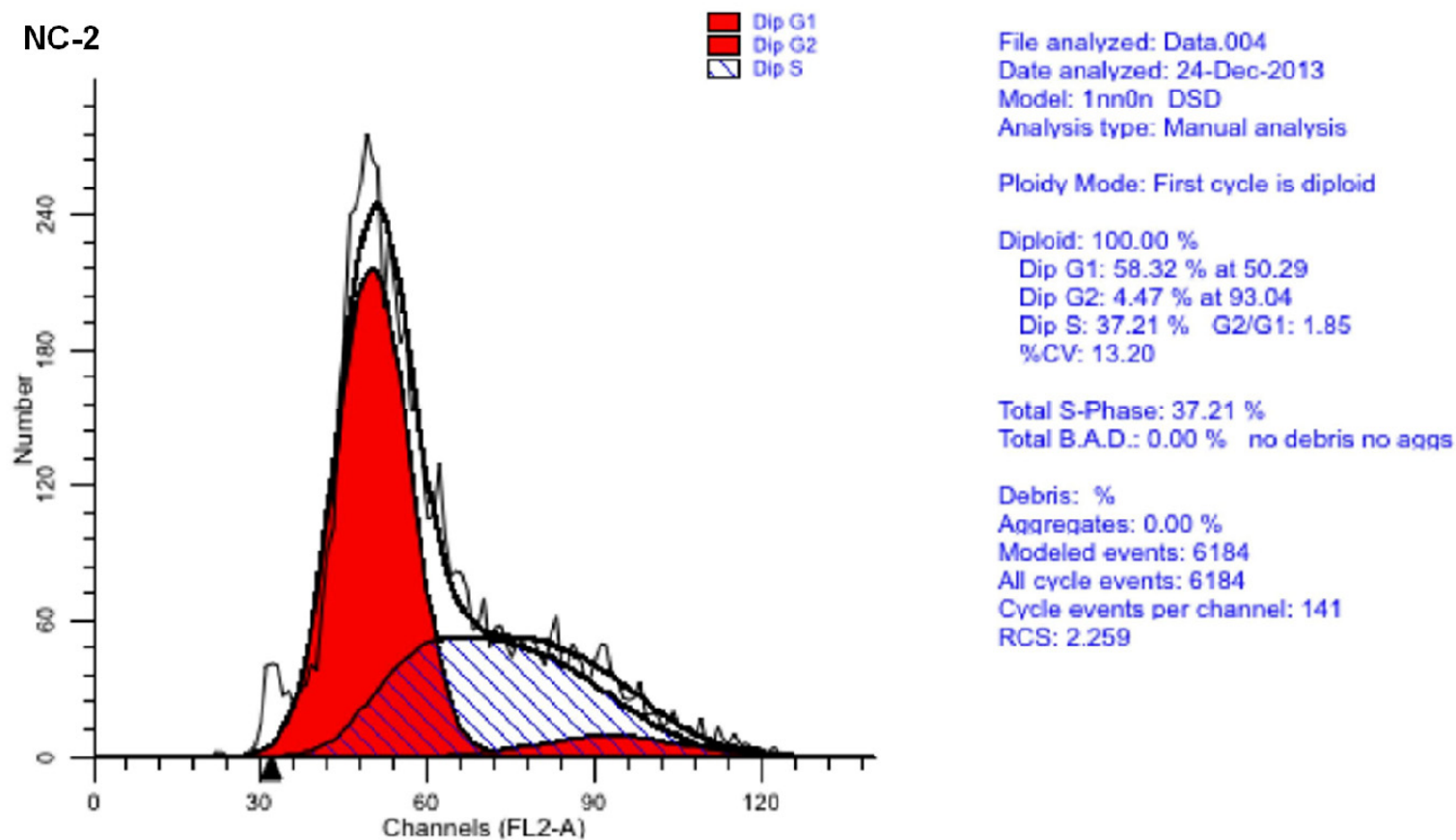


Figure S1. Cont.

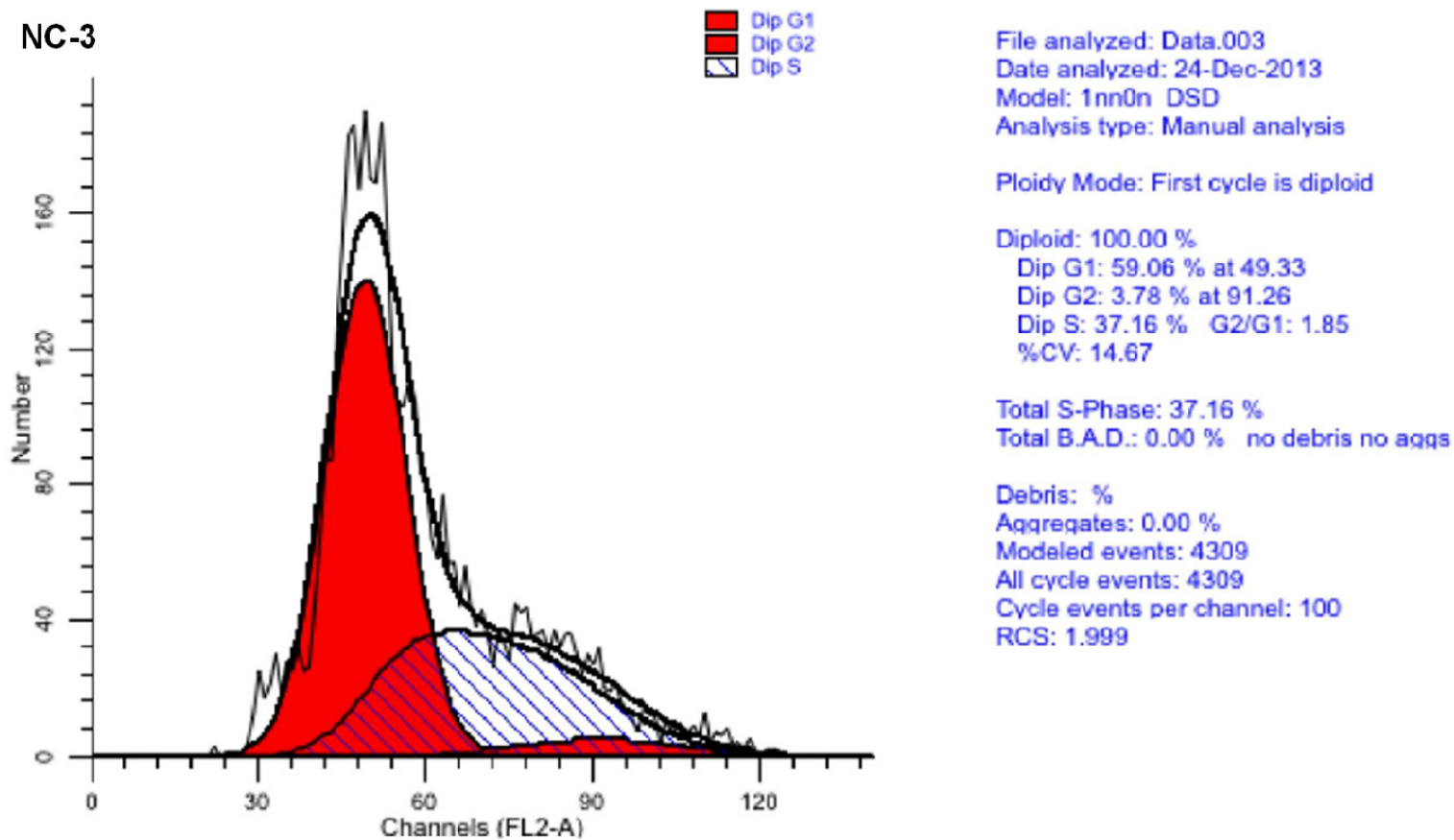
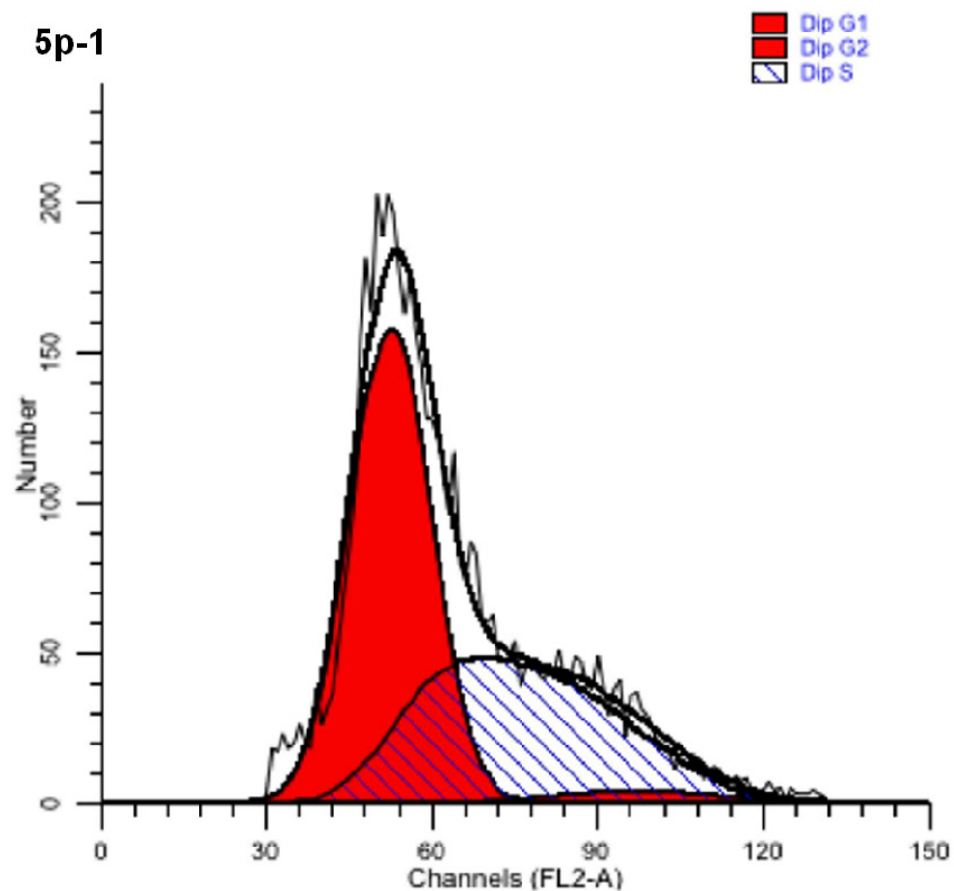


Figure S1. Cont.



File analyzed: Data.007  
 Date analyzed: 24-Dec-2013  
 Model: 1nn0n DSD  
 Analysis type: Manual analysis

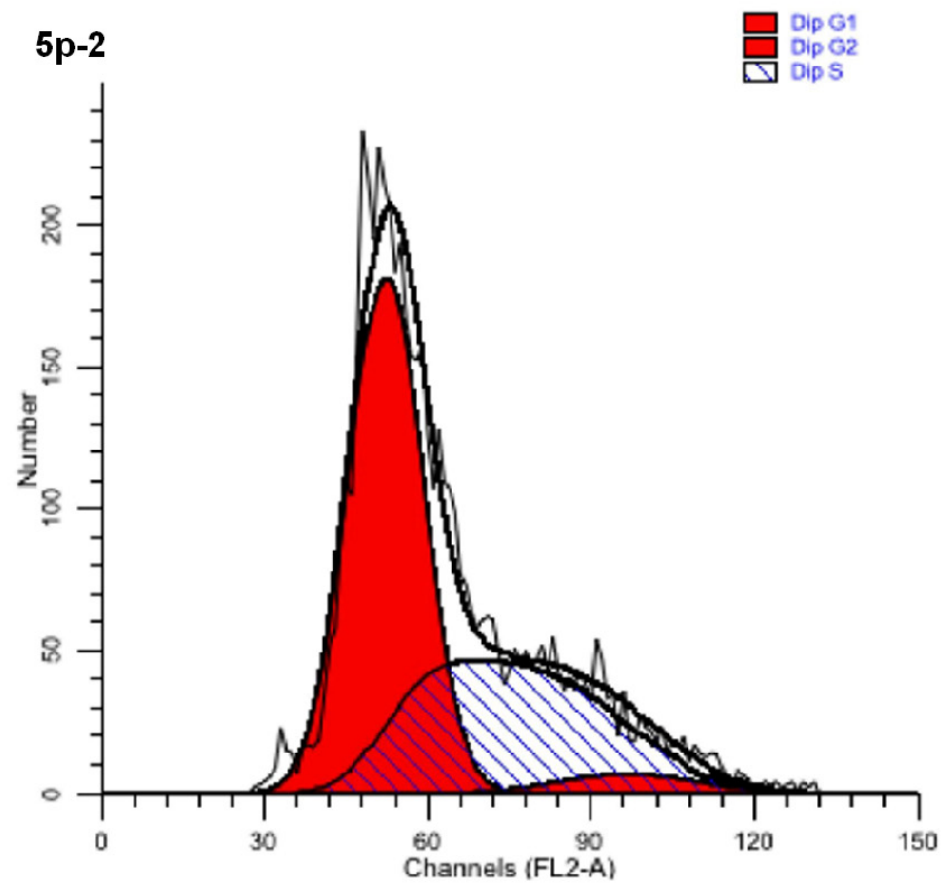
Ploidy Mode: First cycle is diploid

Diploid: 100.00 %  
 Dip G1: 55.25 % at 52.70  
 Dip G2: 2.72 % at 97.50  
 Dip S: 42.03 % G2/G1: 1.85  
 %CV: 13.86

Total S-Phase: 42.03 %  
 Total B.A.D.: 0.00 % no debris no aggs

Debris: %  
 Aggregates: 0.00 %  
 Modeled events: 5247  
 All cycle events: 5247  
 Cycle events per channel: 115  
 RCS: 1.449

Figure S1. Cont.



File analyzed: Data.006  
Date analyzed: 24-Dec-2013  
Model: 1nn0n DSD  
Analysis type: Manual analysis

Ploidy Mode: First cycle is diploid

Diploid: 100.00 %  
Dip G1: 56.59 % at 52.48  
Dip G2: 3.97 % at 97.09  
Dip S: 39.44 % G2/G1: 1.85  
%CV: 12.95

Total S-Phase: 39.44 %  
Total B.A.D.: 0.00 % no debris no aggs

Debris: %  
Aggregates: 0.00 %  
Modeled events: 5465  
All cycle events: 5465  
Cycle events per channel: 120  
RCS: 1.603

Figure S1. Cont.

