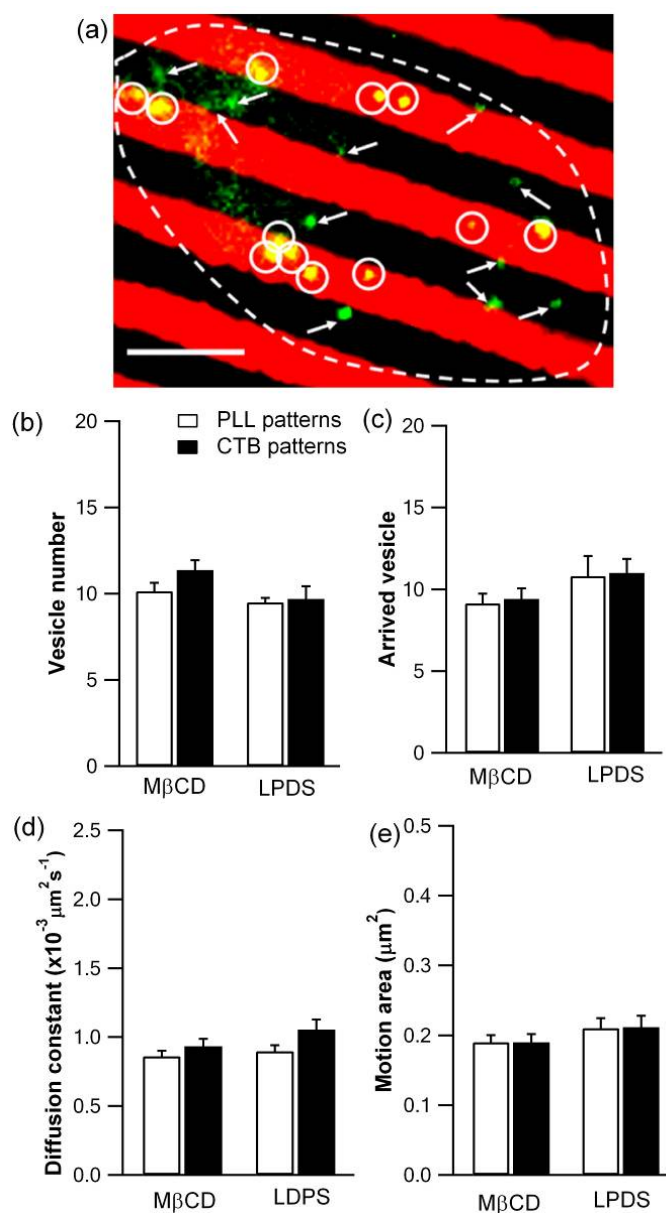


## Supplemental Data for:

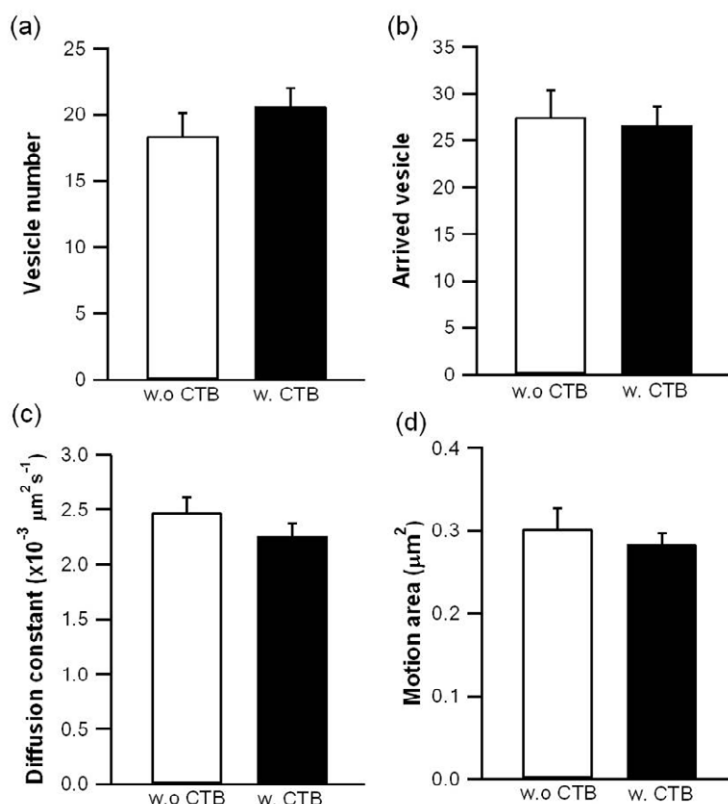
### Surface immobilized cholera toxin B subunit (CTB) facilitates vesicle docking, trafficking and exocytosis

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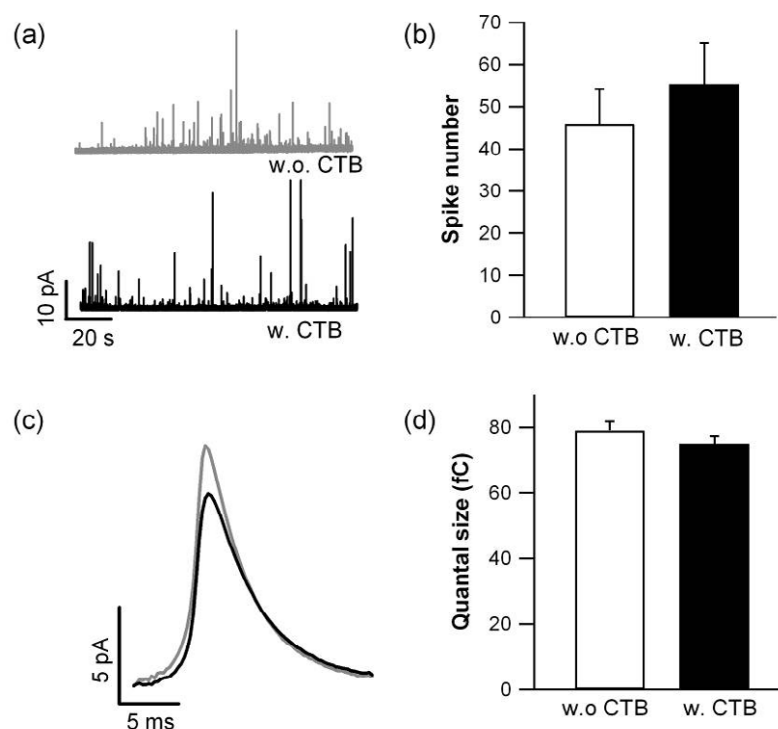


**Fig. S1** Similar to MβCD treatment, deprivation of membrane cholesterol by culturing the cells in the lipoprotein deficient serum (LPDS, Sigma) for 5 days eliminated effects of CTB patterns on vesicle docking and trafficking. (a) A typical TIRFM image showing

that the secretory vesicles in PC12 cells did not show preferential colocalization with CTB patterns. Scale bar = 5  $\mu\text{m}$ . (b)-(e) The statistics of average vesicle number in the subplasmalemmal region (b), vesicles arrived from cytosol (c), diffusion constant (d), and motion coverage area (e) for cells colocalized with PLL-(open columns) or CTB-patterns (dark columns) after culturing the cells in LPDS medium, in comparison to the results from M $\beta$ CD treatment as presented in Fig. 5. Data for LPDS medium culturing is analyzed from 10 cells with 203 vesicles on PLL patterns and 207 vesicles on CTB patterns. The error bars indicate SE.



**Fig. S2** Vesicle trafficking of PC12 cells revealed by TIRFM after 1 day incubation with (w., dark column) or without (w.o, open column) 10  $\mu\text{g}/\text{ml}$  CTB in culture medium. Statistical analysis includes average vesicle number in the subplasmalemmal region (a), the number of vesicles arrived from the cytosol (b), diffusion constant (c), and motion coverage area (d). Each data is analyzed from 2 min time-lapse images with 0.5s interval from 10 cells with 459 vesicles (w.o CTB) and 10 cells with 472 vesicles (w. CTB). The error bars indicate SEM.



**Fig. S3** Amperometric measurement of secretion of PC12 cells induced by high  $K^+$  stimulation after 1 day incubation with (w., dark traces, dark columns) or without (w.o., gray traces, open columns)  $10\mu\text{g/ml}$  CTB in culture medium. (a) Typical recordings with 2 mins high  $K^+$  stimulation from cells incubated without or with CTB. (b) The average number of amperometric spikes from 15 cells in each case. The averaged amperometric spike (c) and quantal size (d) from 687 events (w.o CTB) and 831 events (w. CTB). The error bars indicate SEM.