Table 1. Quantitative analysis of *Mrg* and sensory neuron marker coexpression within rat DRG neurons

	Percentage of cells that coexpress the indicated genes relative to the reference gene ± SEM							
Mrg*	IB4+Mrg*	IB4+Mrg*	Ret+Mrg*	Ret+Mrg*	VR1+Mrg*	VR1+Mrg*	P2X3+Mrg*	P2X3+Mrg*
	IB4	Mrg*	Ret	Mrg*	VR1	Mrg*	P2X3	Mrg*
rMrgB4	28.8 ± 0.9	97.3 ± 1.5	24.6 ± 2.4	97.5 ± 1.4	0	0	27.3 ± 2.3	98.4 ± 1.0
rMrgC	13.0 ± 2.2	97.4 ± 2.6	9.3 ± 2.7	100 ± 0	1.1 ±1.1	7.1 ± 7.1	14.3 ± 6.7	91.9 ± 4.9
rMrgD	48.0 ± 1.6	100 ± 0	44.1 ± 2.8	98.8 ± 0.7	50.9 ± 8.0	98.2 ± 1.1	50.6 ± 3.9	100 ± 0

At least three Sprague–Dawley adult DRGs were analyzed by confocal microscopy to determine the extent of colocalization between probe combinations. With the exception of c-Ret, all cells detected by the probes were included in the counts. For the c-Ret probe, very large and small diameter cells were clearly distinguishable. We did not include large-diameter c-Ret$^+$ cells in our counts. These cells represented a very small fraction of the total number of c-Ret$^+$ cells (≈2%) and were never *Mrg*$^+$.