

Supplementary Table 2. scRNA-seq PC9 filter, related to Figures 3 and S2

Sample_name	Gene expressed at least in N cells (>0.15%)	Genes expressed at exceptional level	nGene (aka nFeature) over all cells	Mito ratio	Ribo ratio	Original: nGene	Original: nCell	After filtering: nGene	After filtering: nCell	Retained Gene %	Retained Cell %
2214004_JCC287_PC9 MOCK2_GEX	>0.15%	Mito genes, ribosomal genes, FTH1, FTL, MALAT1	>3500 & < 10000	<25	>10	36601	8997	18632	3753	50.91%	41.71%
2214005_JCC287_PC9_1d_rel_GEX	>0.15%	Mito genes, ribosomal genes, FTH1, FTL, MALAT1	>1000 & < 10000	<10	>0	36601	15898	17618	15339	48.14%	96.48%
2214006_JCC287_PC9_3d_rel_GEX	>0.15%	Mito genes, ribosomal genes, FTH1, FTL, MALAT1	>1000 & < 10000	<20	>0	36601	16743	17470	16406	47.73%	97.99%
2214007_JCC287_PC9_1w_rel_GEX	>0.15%	Mito genes, ribosomal genes, FTH1, FTL, MALAT1	>1500 & < 9500	<20	>0	36601	13781	18080	9558	49.40%	69.36%