Find cluster markers

```
marker_genes <- top_markers(cds)

tops_sig <- subset(marker_genes, marker_test_q_value < .05)
```

```
> head(tops_sig)
          gene_id gene_short_name cell_group specificity   pseudo_R2 marker_test_p_value marker_test_q_value
10 WBGene00000029           abu-6         87  0.30568790 0.024827862        1.086772e-31        9.889626e-27
11 WBGene00000030           abu-7         81  0.30616068 0.047979108        5.821295e-55        5.297378e-50
12 WBGene00000034          abu-11          3  0.18860409 0.101019149        4.085220e-17        3.717550e-12
15 WBGene00000045           acr-6         88  0.34506461 0.005105376        4.184526e-08        3.807919e-03
16 WBGene00000047           acr-8         84  0.17041092 0.003837754        3.099326e-08        2.820387e-03
19 WBGene00000063           act-1         19  0.04139546 0.313420714        0.000000e+00        0.000000e+00
>
```

The usual cell annotation workflow involves lots of manual labor