

# Compare selected clusters

```
gene_fits <- fit_models(cds_subset[1:100,],  
                        model_formula_str = "~cluster")  
fit_coefs <- coefficient_table(gene_fits)  
  
head(fit_coefs)
```

# A tibble: 6 x 10

	gene_short_name	status	term	estimate	std_err	test_val	p_value	normalized_effect	model_component	q_value
	<fct>	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<chr>	<dbl>
1	aap-1	OK	(Intercept)	-4.75	0.578	-8.21	2.56e-16	0	count	1.51e-14
2	aap-1	OK	cluster35	0.109	1.08	0.101	9.20e- 1	0.0750	count	1.00e+ 0
3	aap-1	OK	cluster43	-13.6	536.	-0.0253	9.80e- 1	-0.900	count	1.00e+ 0
4	aap-1	OK	cluster45	0.789	0.688	1.15	2.51e- 1	0.640	count	1.00e+ 0
5	aap-1	OK	cluster54	0.157	0.783	0.200	8.41e- 1	0.109	count	1.00e+ 0
6	aap-1	OK	cluster60	1.31	0.643	2.03	4.25e- 2	1.17	count	1.00e+ 0

# 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

```
> |
```