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

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`cds_subset <- chdse11s(cds)`

Compare selected clusters

Source



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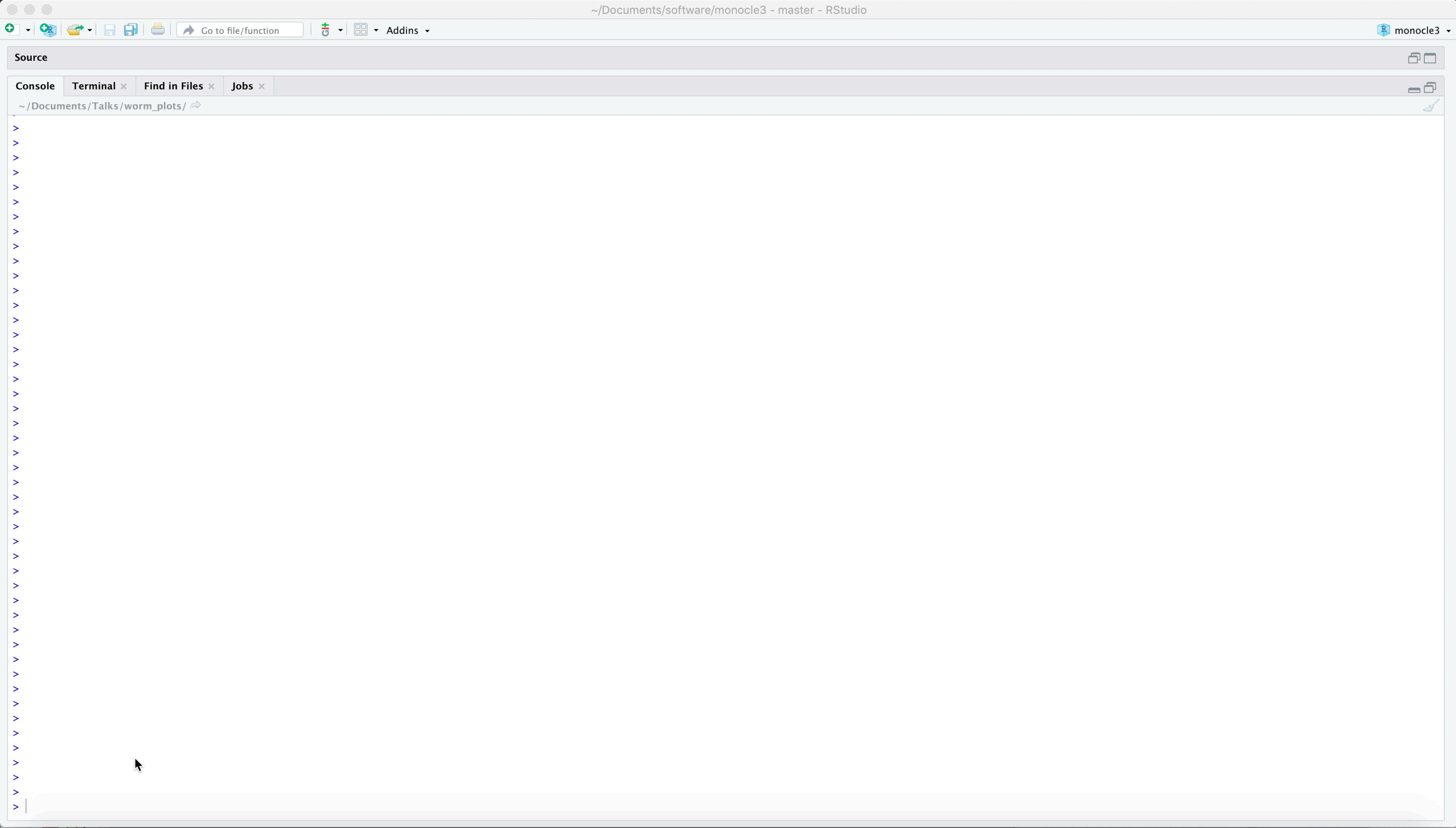
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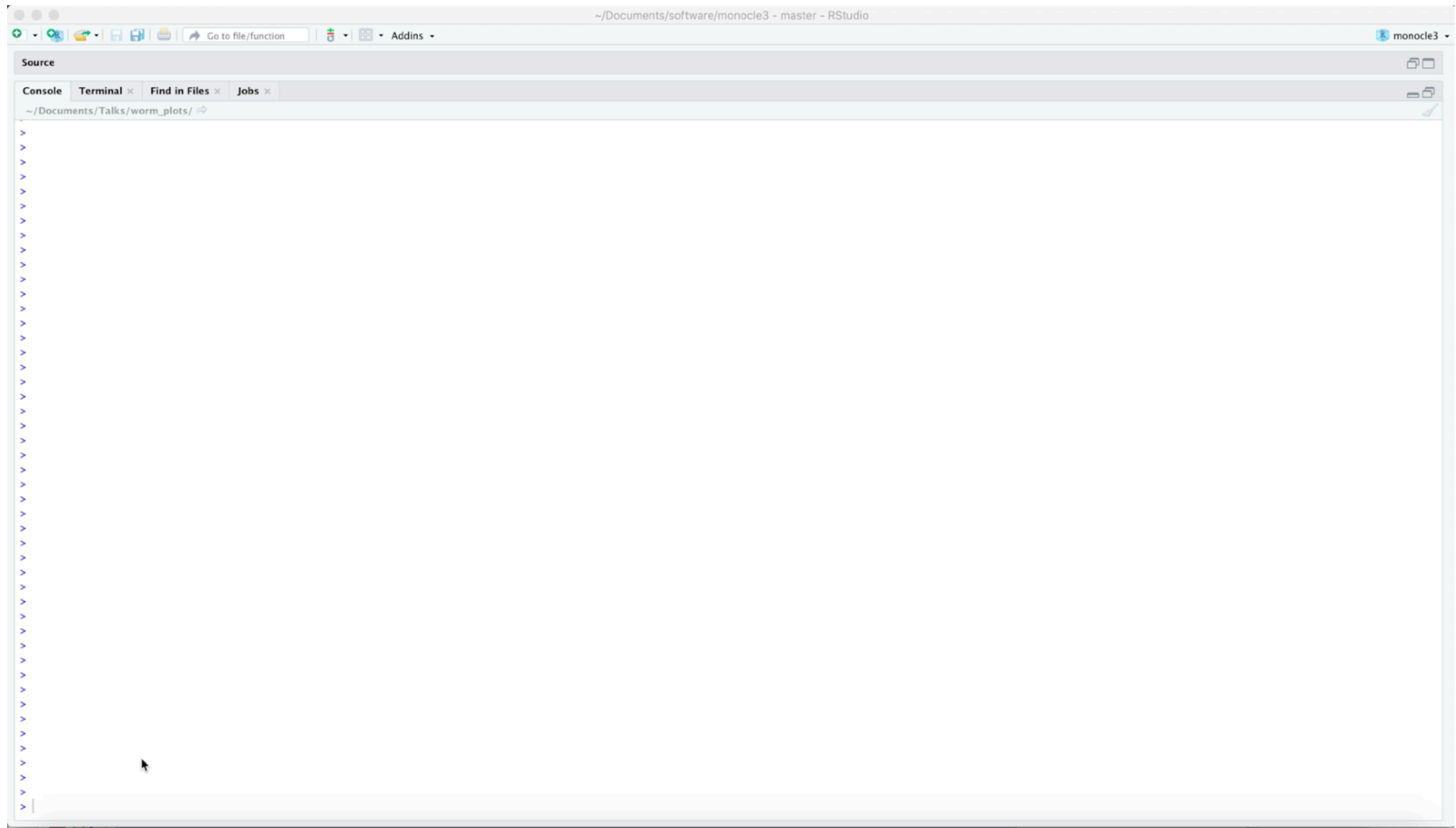
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# Compare selected clusters

```
cds_subset <- choose_cells(cds)
```





# 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