

split_yaml_batches
i: 1

run_zUMIs

read_separation_sub_pipeline

SNP_distribution_per_gene

CCID_all

```
graph TD; A["split_yaml_batches<br/>i: 1"] --> B["run_zUMIs"]; A --> C["read_separation_sub_pipeline"]; B --> C; C --> D["CCID_all"]; E["SNP_distribution_per_gene"] --> D;
```

The diagram is a flowchart with five nodes. The first node, 'split_yaml_batches i: 1', is at the top left and has a cyan border. It has two outgoing arrows: one straight down to 'read_separation_sub_pipeline' and one diagonal down to 'run_zUMIs'. 'run_zUMIs' is a smaller node with a green border. An arrow points from 'run_zUMIs' to 'read_separation_sub_pipeline'. 'read_separation_sub_pipeline' is a wide node with a green border. An arrow points from it to 'CCID_all' at the bottom center. 'SNP_distribution_per_gene' is a wide node with a yellow border to the right of 'read_separation_sub_pipeline'. An arrow points from it to 'CCID_all'. 'CCID_all' is a small node with a red border at the bottom center.