

The data set (file 'data050302sort.xls') is given as an Excel spread sheet where rows correspond to gene probes and columns correspond to samples. The samples (columns) are labeled '103', '104', etc. These labeling are referred to as `rat_id` in the table below. The table below identifies which `rat_id` (sample) were allocated to each of three factors in the $3 \times 2 \times 2$ factorial experiment:

1. Diet: CO (n6-PUFA), FO (n3-PUFA), OO (n9-MUFA)
2. Treatment: AOM, Saline
3. Time: 12 hours, 10 weeks.

The `rat_name` additional label (1 through 59) in the table identifies unique rats allocated to each factor combination. For example, rat 13 RNA were replicated twice (two hybridization runs; `rat_ids` or samples 202 and 207 respectively).

Table 1: First column in each factor combination level give the `rat_id`, immediately followed by the `rat_name` (1 through 59). The total number of arrays and the (effective) sample size for each combination level (in parenthesis) is also given.

12 hours						
Treatment						
Diet	AOM			Saline		
	CO	FO	OO	CO	FO	OO
	102 1	201 12	301 22	401 32	502 42	601 50
	103 2	202 13	307 22	402 33	506 42	602 51
	107 2	207 13	302 23	406 33	503 43	606 51
	104 3	203 14	304 24	403 34	504 44	603 52
	108 3	205 15	305 25	407 34	507 44	604 53
	105 4	206 16	306 26	404 35	505 45	605 54
	106 5	208 16		405 36		607 54
Total	7(5)	7(5)	6(5)	7(5)	6(4)	7(5)

10 weeks						
Treatment						
Diet	AOM			Saline		
	CO	FO	OO	CO	FO	OO
	131 6	232 17	332 27	421 37	522 46	621 55
	132 7	233 18	333 28	426 37	526 46	622 56
	133 8	237 18	334 29	422 38	523 47	626 56
	134 9	234 19	337 29	423 39	524 48	623 57
	134.1 9	238 19	335 30	424 40	527 48	627 57
	134.2 9	235 20	335.1 30	427 40	525 49	624 58
	135 10	236 21	336 31	425 41	525.1 49	625 59
	138 10	236.1 21	338 31		525.2 49	
	136 11	236.2 21			525.3 49	
	136.1 11	236.3 21				
	136.2 11					
	136.3 11					
Total	12(6)	10(5)	8(5)	7(5)	9(4)	7(5)