Supplementary Data 5: Identification of evolutionary dynamics in multiple myeloma.

PID	Type	Mutations [≥5% VAF]	Mutations [VAF 0.12-0.24]	R^2	Unshared mutations [CCF≥0.8]	Shared-diff mutations [CCF≥0.8]
1	FNAS	90	5	-	25	27
1	RNAS	48	5	-	7	0
2	FNAS	71	7	-	2	33
2	RNAS	89	15	0.92	8	0
3	FNAS	49	2	-	12	10
3	RNAS	57	29	0.94	0	0
4	FNAS	143	25	0.57	54	11
4	RNAS	128	36	0.87	7	0
5	FNAS	128	15	0.92	9	26
5	RNAS	54	10	-	0	0
6	FNAS	53	7	-	6	8
6	RNAS	63	13	0.92	0	0
7	FNAS 1	44	3	-	8	0
7	FNAS 2	44	9	-	9	0
7	RNAS	45	5	-	1	0
8	FNAS 1	59	0	-	3	0
8	FNAS 2	63	1	-	11	1
8	FNAS 3	75	1	-	11	1
8	RNAS	69	5	-	6	0
9	FNAS	64	14	0.88	1	1
9	RNAS	61	7	-	0	0
10	FNAS	85	20	0.97	0	4
10	RNAS	63	5	-	1	3
11	FNAS	82	19	0.96	0	0
11	RNAS	60	13	0.68	0	0
12	FNAS 1	64	4	-	14	3
12	FNAS 2	62	4	-	9	1
12	FNAS 3	62	5	-	9	2
12	FNAS 4	64	5	-	10	3
12	RNAS	63	25	0.64	5	0
13	FNAS	68	2	-	0	5
13	RNAS	85	15	0.8	0	5
14	FNAS	78	0	-	12	10
14	RNAS	88	28	0.9	0	0
15	FNAS 1	68	6	-	4	3
15	FNAS 2	69	9	-	2	2
15	RNAS	95	27	0.97	0	0
16	FNAS	62	3	-	3	3
16	RNAS	77	6	-	0	0
17	FNAS	99	13	0.95	0	0
17	RNAS	56	28	0.89	0	0
18	FNAS	68	7	-	9	0

PID	Type	Mutations [≥5% VAF]	Mutations [VAF 0.12-0.24]	R^2	Unshared mutations [CCF≥0.8]	Shared-diff mutations [CCF≥0.8]
18	RNAS	62	12	0.73	0	0
19	FNAS	205	8	-	22	7
19	RNAS	191	22	0.75	5	0
20	FNAS 1	88	15	0.64	6	2
20	FNAS 2	93	13	0.87	0	0
20	FNAS 3	86	8	-	0	0
20	RNAS	90	8	-	0	0
21	FNAS	29	2	-	0	0
21	RNAS	31	1	-	0	0
22	FNAS	773	463	0.87	0	0
22	RNAS	716	65	0.9	0	0
23	FNAS	71	3	-	2	0
23	RNAS	77	13	0.72	0	0
24	FNAS	80	13	0.8	0	0
24	RNAS	80	9	-	0	2
25	FNAS 1	72	8	-	0	0
25	FNAS 2	70	16	0.93	0	0
25	FNAS 3	71	17	0.92	0	0
25	RNAS	66	12	0.9	0	0
26	FNAS	33	2	-	0	4
26	RNAS	35	1	-	0	0
27	FNAS	77	18	0.91	0	0
27	RNAS	74	13	0.97	0	0
28	FNAS 1	50	2	-	1	1
28	FNAS 2	50	0	-	1	0
28	RNAS	46	3	-	0	0
29	FNAS	166	27	0.76	0	0
29	RNAS	141	36	0.78	0	0
30	FNAS	63	2	-	0	1
30	RNAS	73	5	-	1	1
31	FNAS 1	87	3	-	0	0
31	FNAS 2	165	6	-	0	0
31	FNAS 3	144	6	-	0	0
31	RNAS	99	6	-	0	0
32	FNAS	56	3	-	0	0
32	RNAS	71	14	0.73	0	0
33	FNAS	66	4	-	0	0
33	RNAS	62	28	0.85	0	0
34	FNAS	124	4	-	0	0
34	RNAS	146	11	-	0	0
35	FNAS 1	57	7	-	0	0
35	FNAS 2	55	8	-	0	0

PID	Type	Mutations [≥5% VAF]	Mutations [VAF 0.12-0.24]	R^2	Unshared mutations [CCF≥0.8]	Shared-diff mutations [CCF≥0.8]
35	RNAS	55	7	-	0	0
36	FNAS	131	0	-	0	4
36	RNAS	134	7	-	0	0
37	FNAS	43	2	-	0	0
37	RNAS	45	2	-	0	0
38	FNAS	37	3	-	0	0
38	RNAS	38	6	-	0	0
39	FNAS	160	2	-	0	0
39	RNAS	149	1	-	0	0
40	FNAS	61	1	-	0	0
40	RNAS	66	8	-	0	0
41	FNAS	70	15	0.69	1	0
41	RNAS	64	13	0.69	0	0
42	FNAS	81	16	0.78	1	0
42	RNAS	86	19	0.88	0	0

Abbreviations: RNAS: random aspirate, FNAS: fine needle aspirate, VAF: variant allele frequency, CCF: cancer clonal fraction, R^2: goodness-of-fit measure for cumulative distribution of subclonal mutations