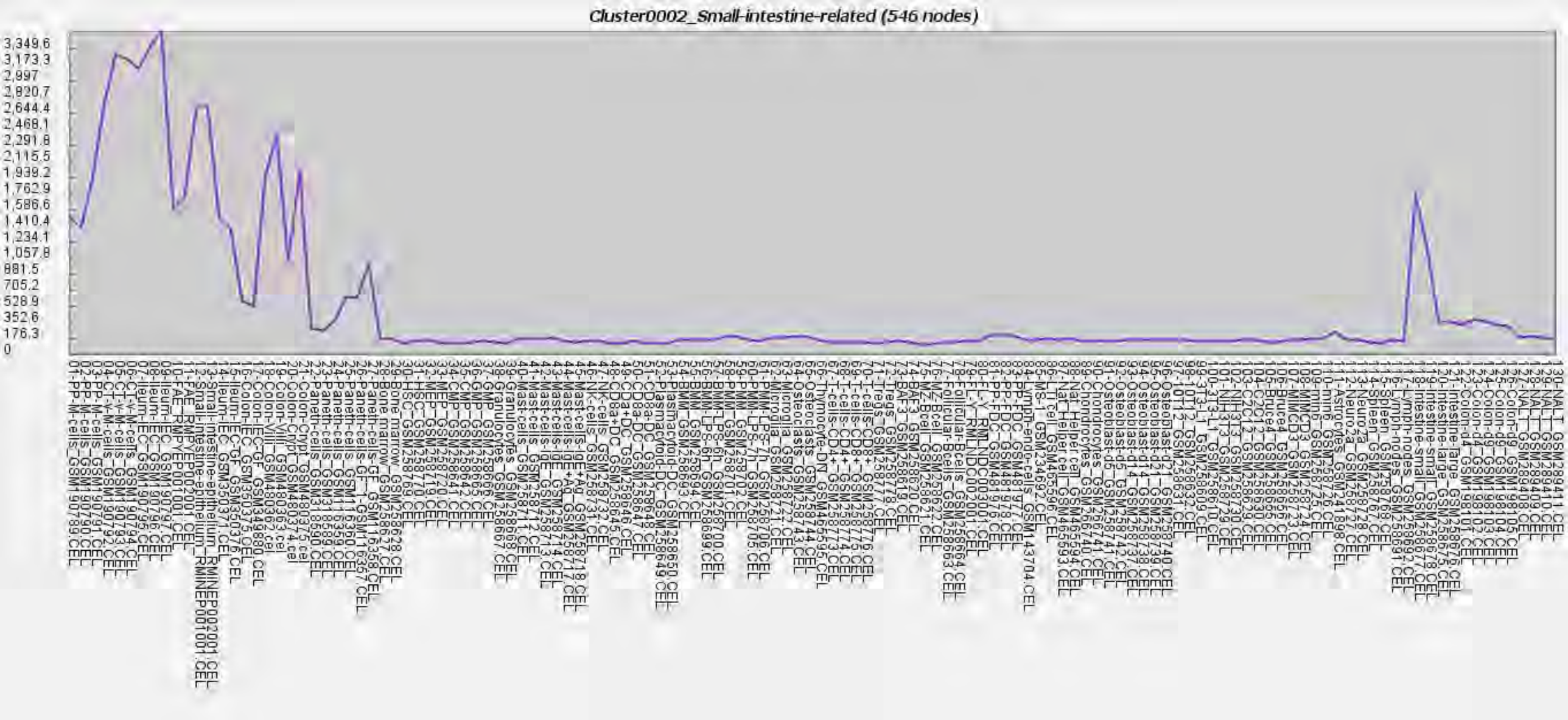
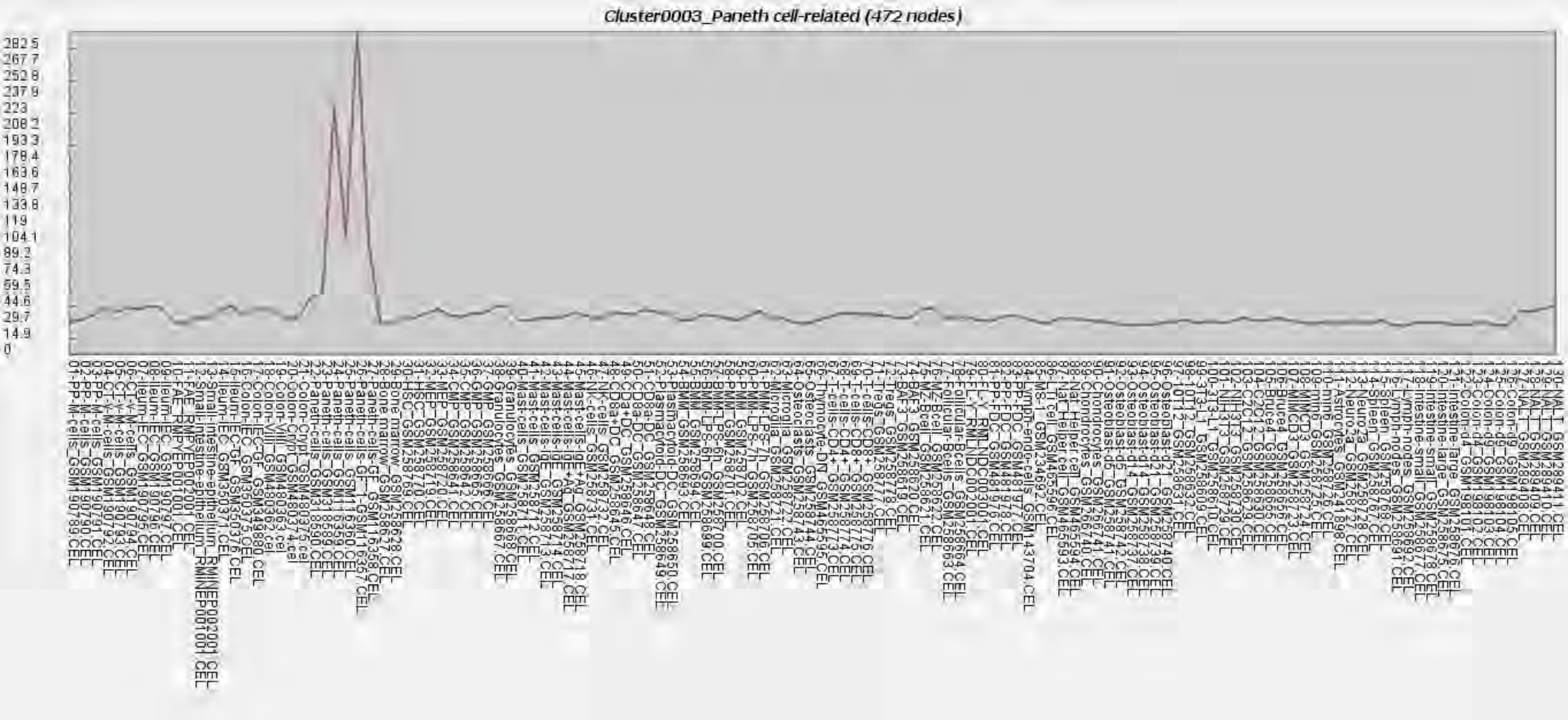
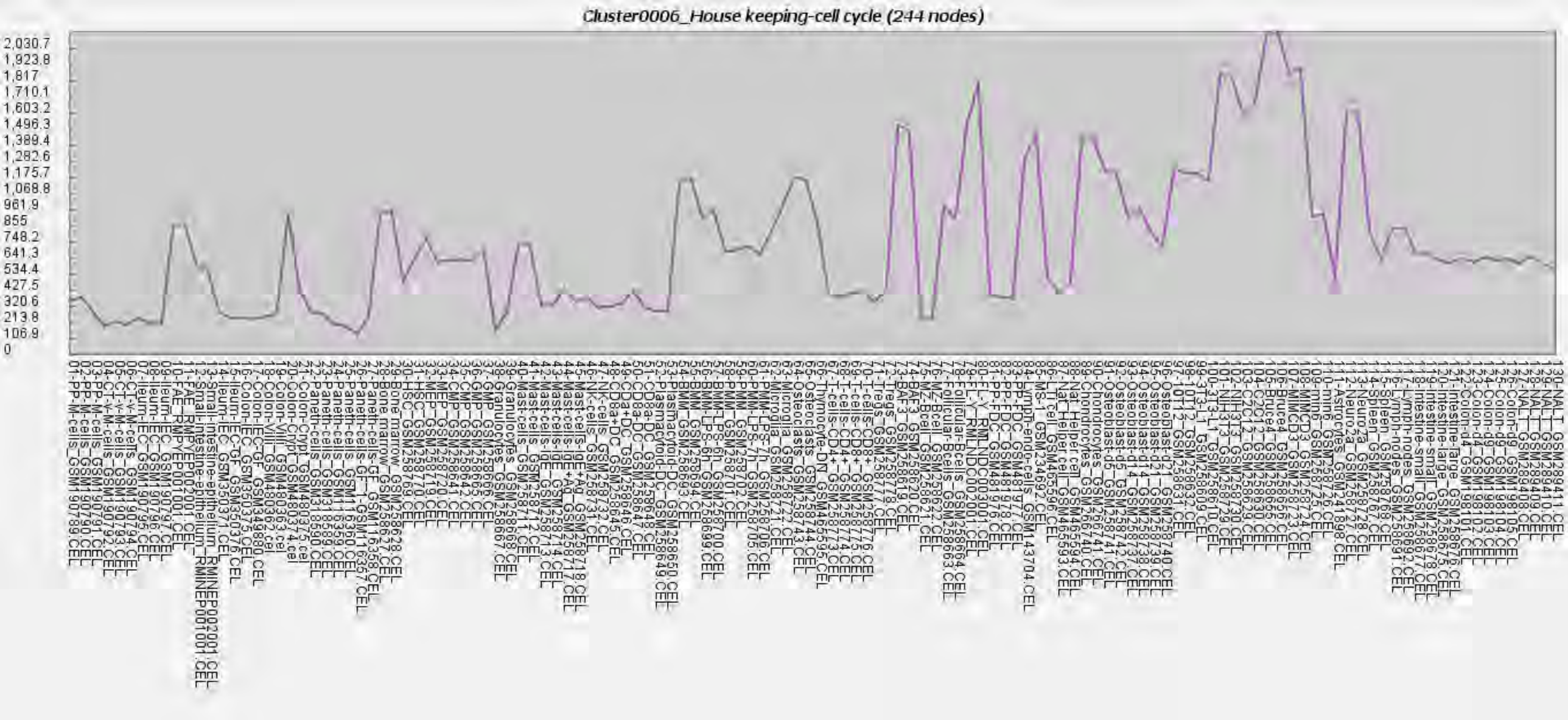
Cluster0001_Astrocyte-related (561 nodes)
2,087.2
1,977.4
1,867.5
1,757.7
1,647.8
1,538
1,428.1
1,318.2
1,208.4
1,098.5
988.7
878.8
769
659.1
549.3
439.4
329.6
219.7
109.9
0

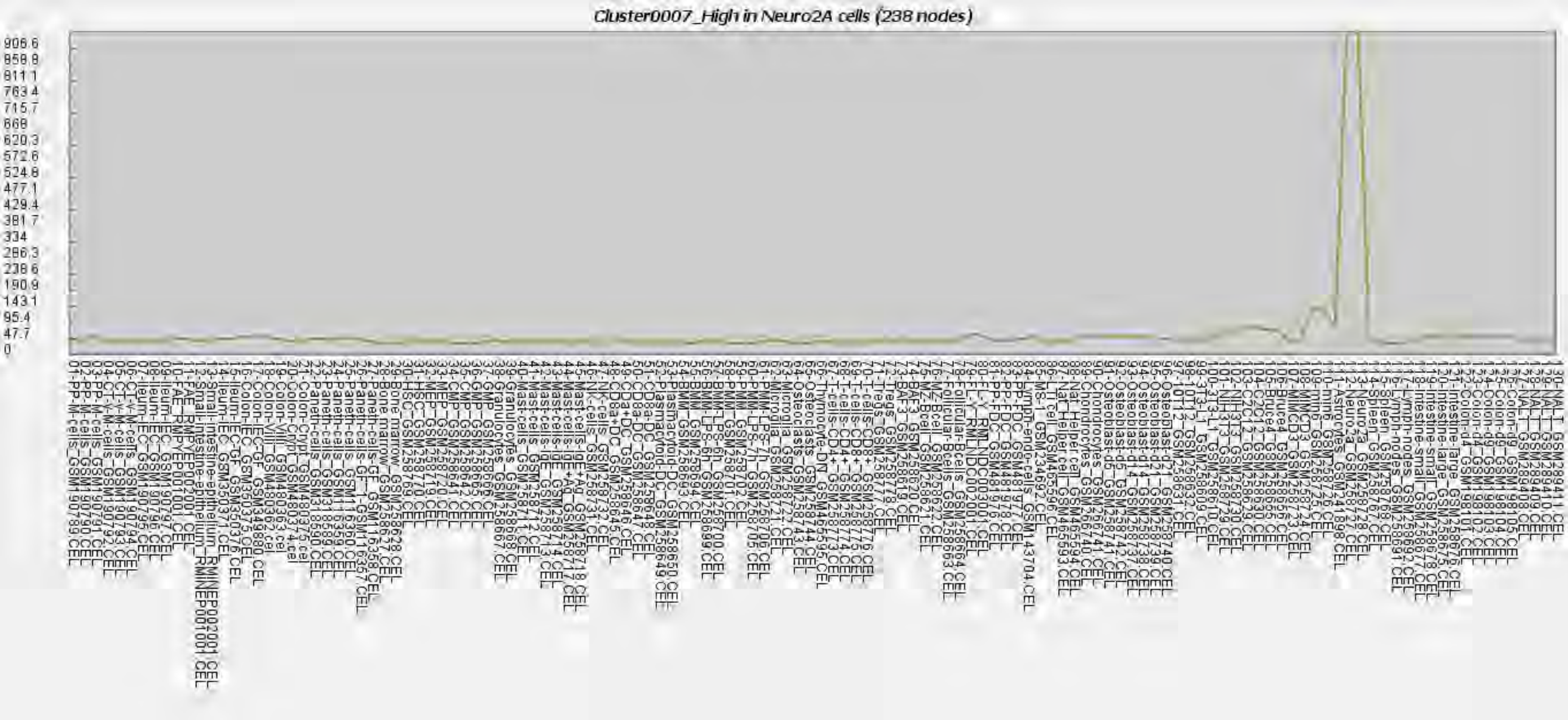

Cluster0002_Small-intestine-related (546 nodes)
3,349.6
3,173.3
2,997
2,820.7
2,644.4
2,468.1
2,291.8
2,115.5
1,939.2
1,762.9
1,586.6
1,410.4
1,234.1
1,057.8
881.5
705.2
528.9
352.6
176.3
0


Cluster0003_Paneth cell-related (472 nodes)
282.5
267.7
252.8
237.9
223
208.2
193.3
178.4
163.6
148.7
133.8
119
104.1
89.2
74.3
59.5
44.6
29.7
14.9
0

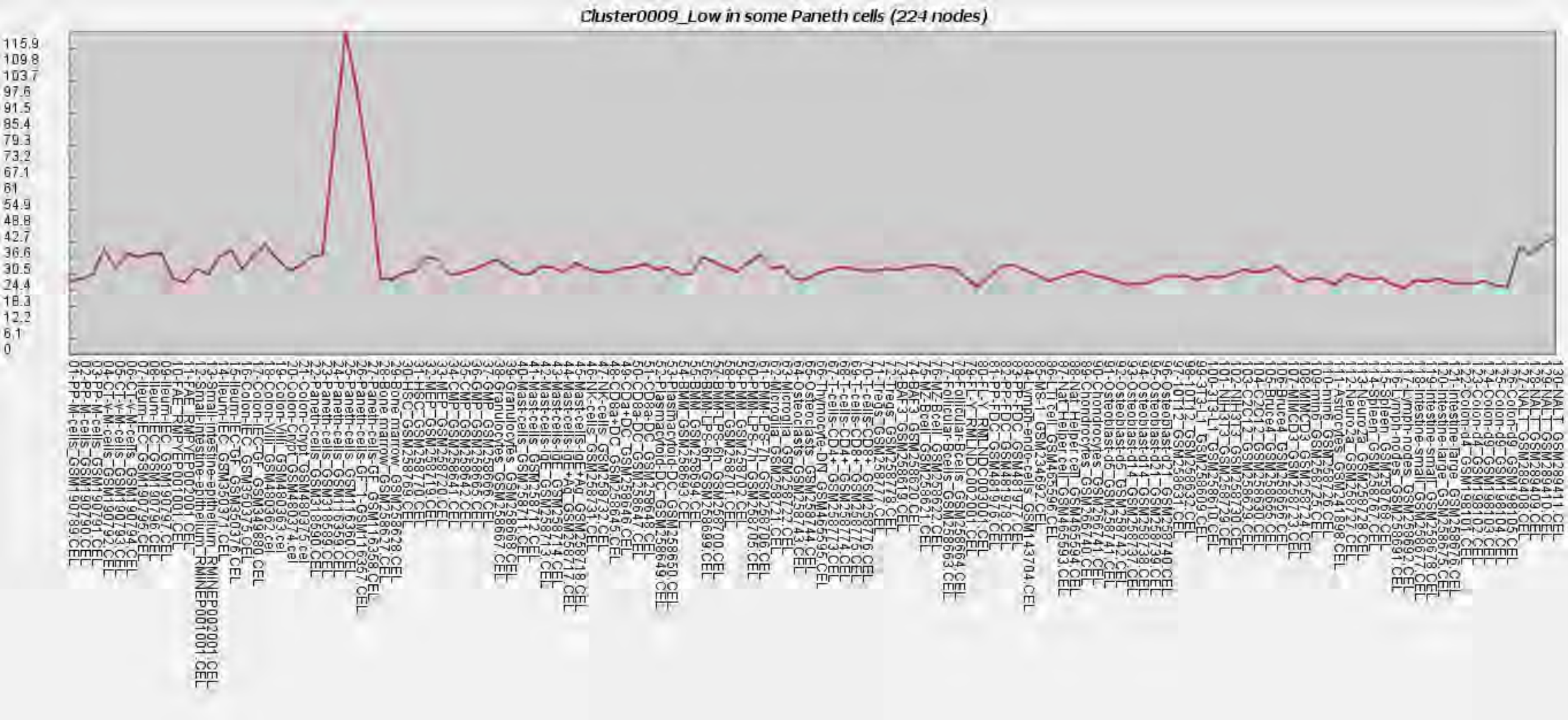
Cluster0004_High in MIN-6-Pancreatic beta cell, insulin secreting (410 nodes)
1,841.5
1,744.6
1,647.7
1,550.8
1,453.8
1,356.9
1,260
1,163.1
1,066.1
969.2
872.3
775.4
678.5
581.5
484.6
387.7
290.8
193.8
96.9
0

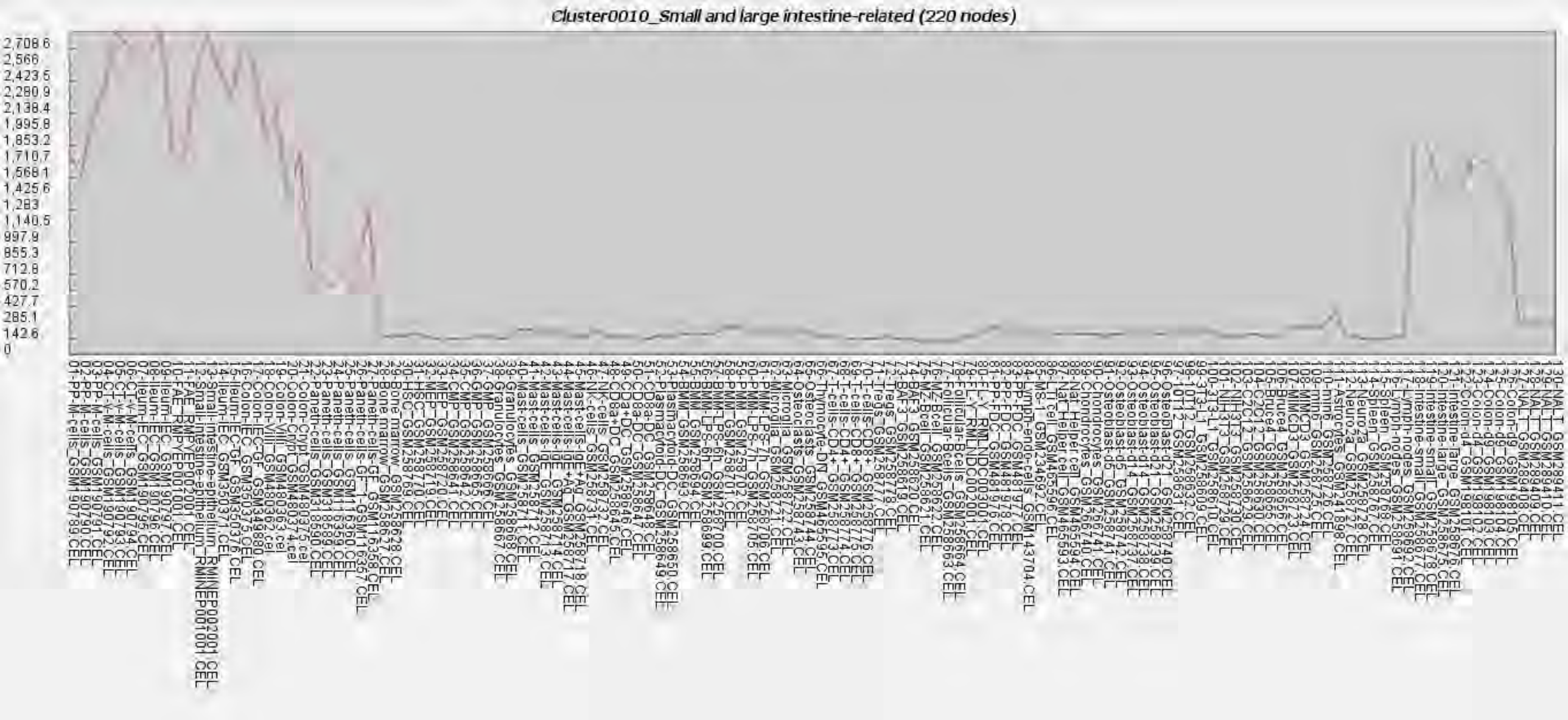
Cluster0005_High in NALT (350 nodes)
2,918.9
2,765.2
2,611.6
2,458
2,304.4
2,150.7
1,997.1
1,843.5
1,689.9
1,536.2
1,382.6
1,229
1,075.4
921.7
768.1
614.5
460.9
307.2
153.6
0

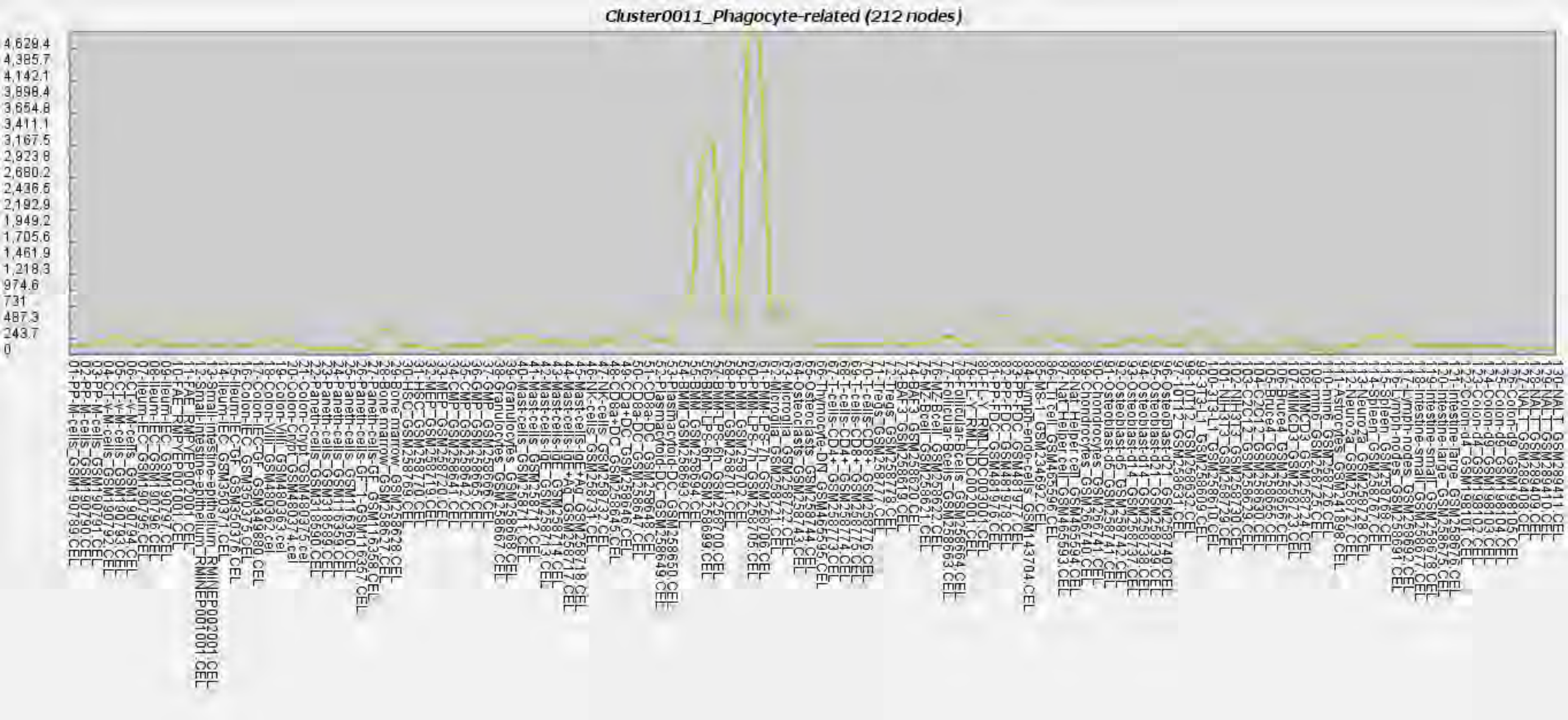

Cluster0006_House keeping-cell cycle (244 nodes)
2,030.7
1,923.8
1,817
1,710.1
1,603.2
1,496.3
1,389.4
1,282.6
1,175.7
1,068.8
961.9
855
748.2
641.3
534.4
427.5
320.6
213.8
106.9
0

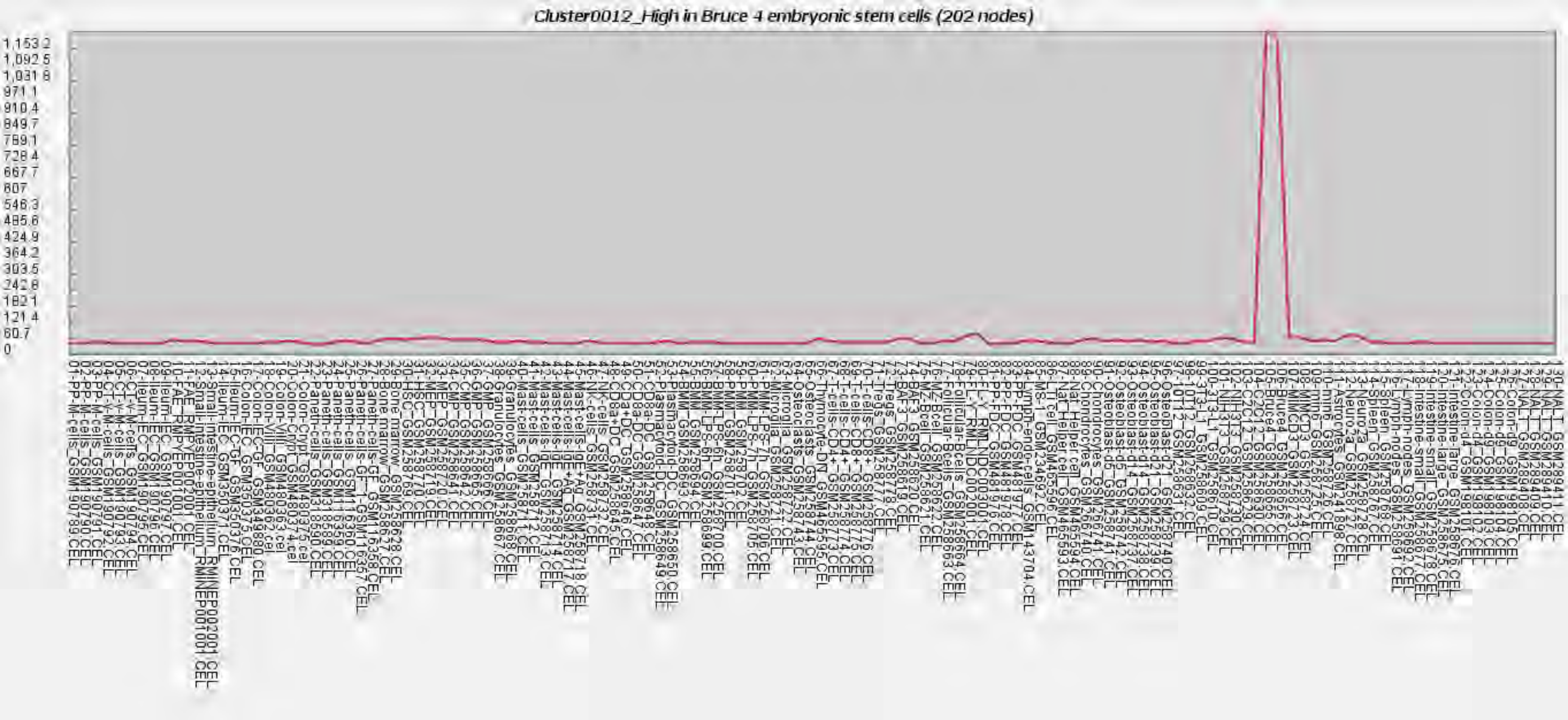

Cluster0007_High in Neuro2A cells (238 nodes)
906.6
858.8
811.1
763.4
715.7
668
620.3
572.6
524.8
477.1
429.4
381.7
334
286.3
238.6
190.9
143.1
95.4
47.7
0

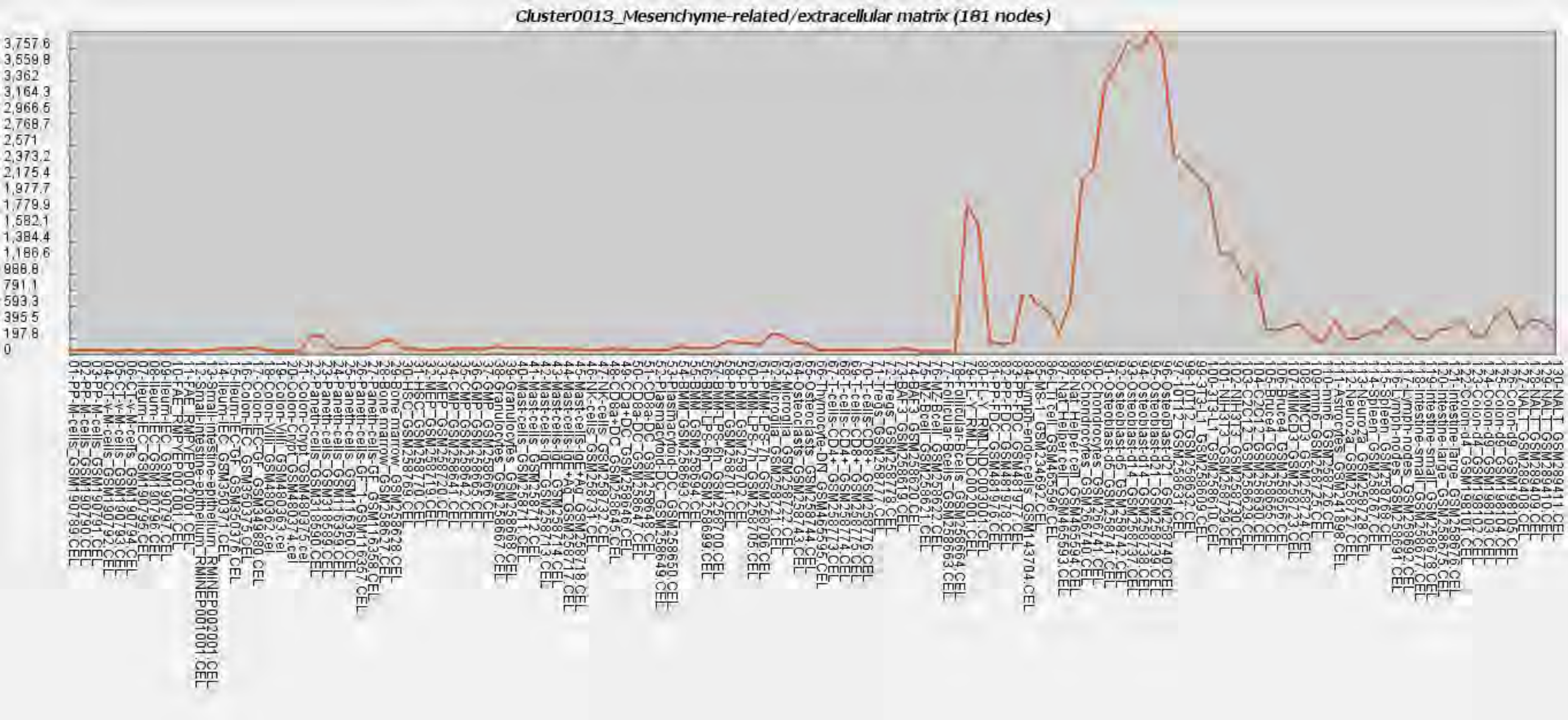
Cluster0008_High in differentiating osteoblasts (236 nodes)
2,445.8
2,317.1
2,188.4
2,059.6
1,930.9
1,802.2
1,673.5
1,544.7
1,416
1,287.3
1,158.6
1,029.8
901.1
772.4
643.6
514.9
386.2
257.5
128.7
0

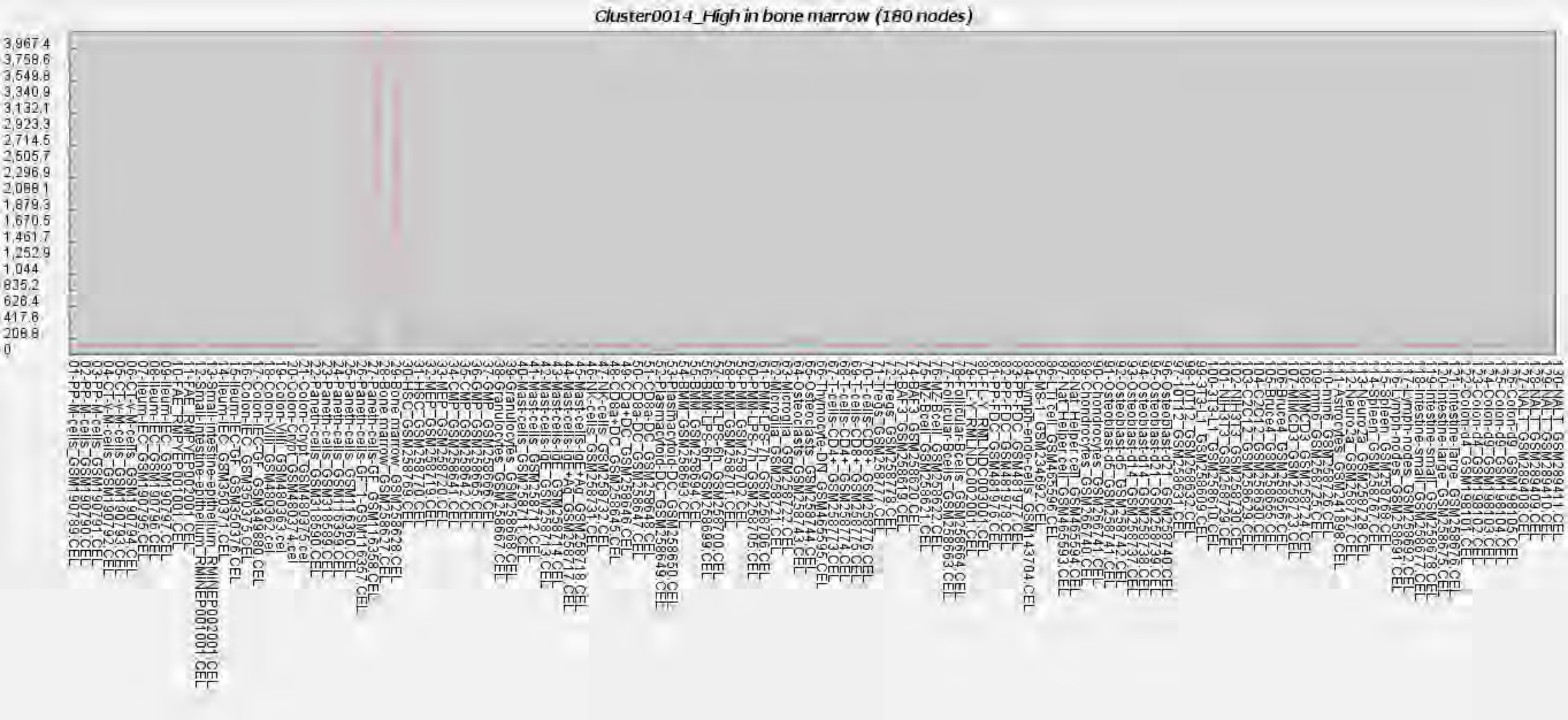

Cluster0009_Low in some Paneth cells (224 nodes)
115.9
109.8
103.7
97.6
91.5
85.4
79.3
73.2
67.1
61
54.9
48.8
42.7
36.6
30.5
24.4
18.3
12.2
6.1
0


Cluster0010_Small and large intestine-related (220 nodes)
2,708.6
2,566
2,423.5
2,280.9
2,138.4
1,995.8
1,853.2
1,710.7
1,568.1
1,425.6
1,283
1,140.5
997.9
855.3
712.8
570.2
427.7
285.1
142.6
0

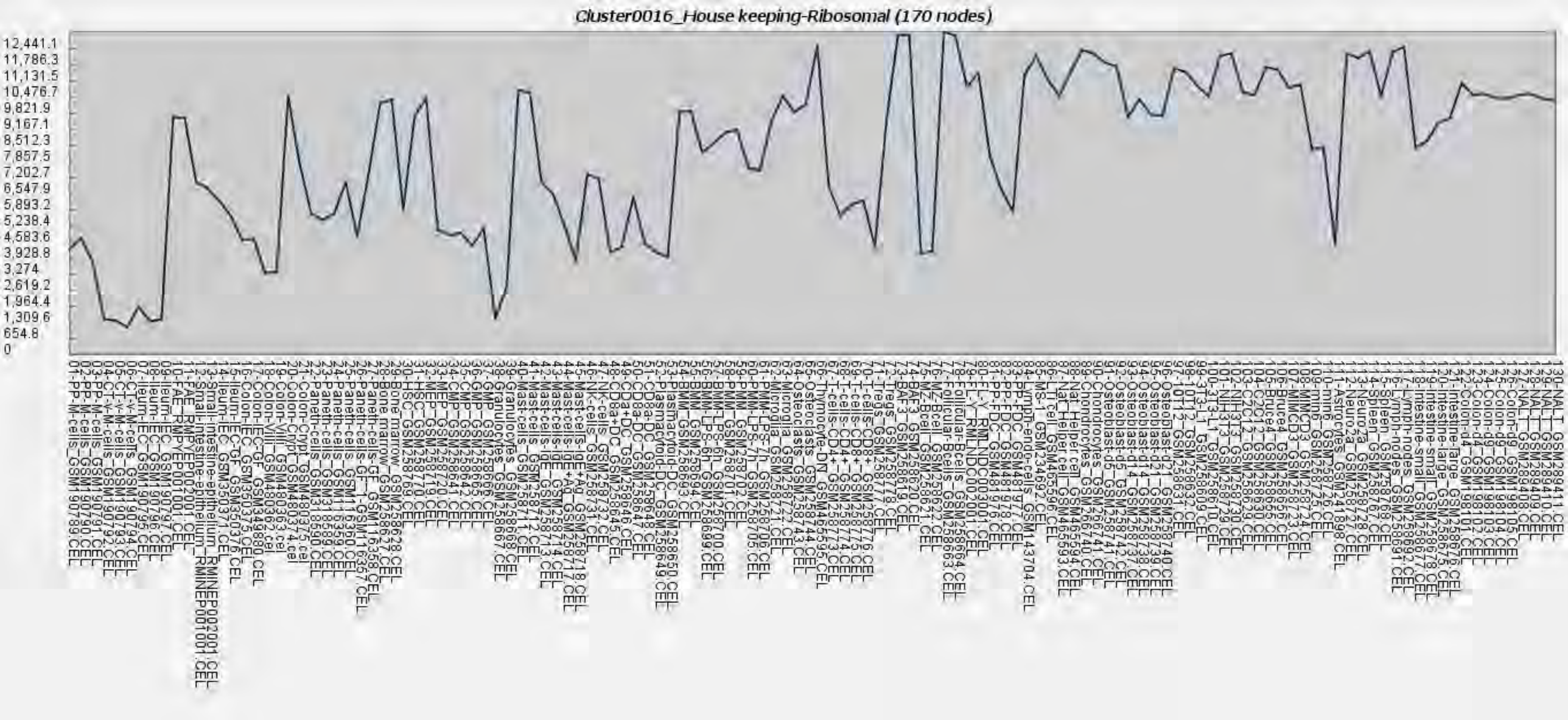

Cluster0011_Phagocyte-related (212 nodes)
4,629.4
4,385.7
4,142.1
3,898.4
3,654.8
3,411.1
3,167.5
2,923.8
2,680.2
2,436.6
2,192.9
1,949.2
1,705.6
1,461.9
1,218.3
974.6
731
487.3
243.7
0

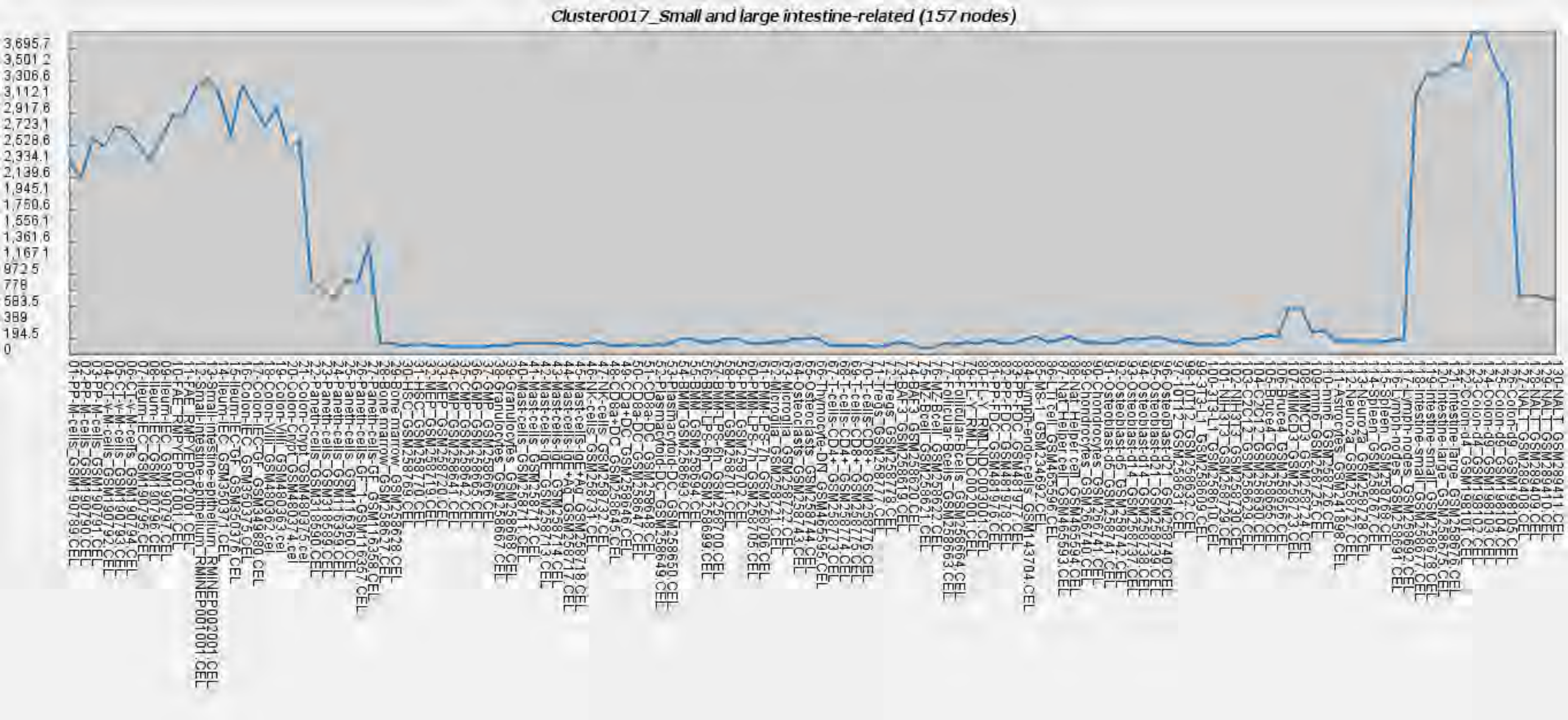

Cluster0012_High in Bruce 4 embryonic stem cells (202 nodes)
1,153.2
1,092.5
1,031.8
971.1
910.4
849.7
789.1
728.4
667.7
607
546.3
485.6
424.9
364.2
303.5
242.8
182.1
121.4
60.7
0

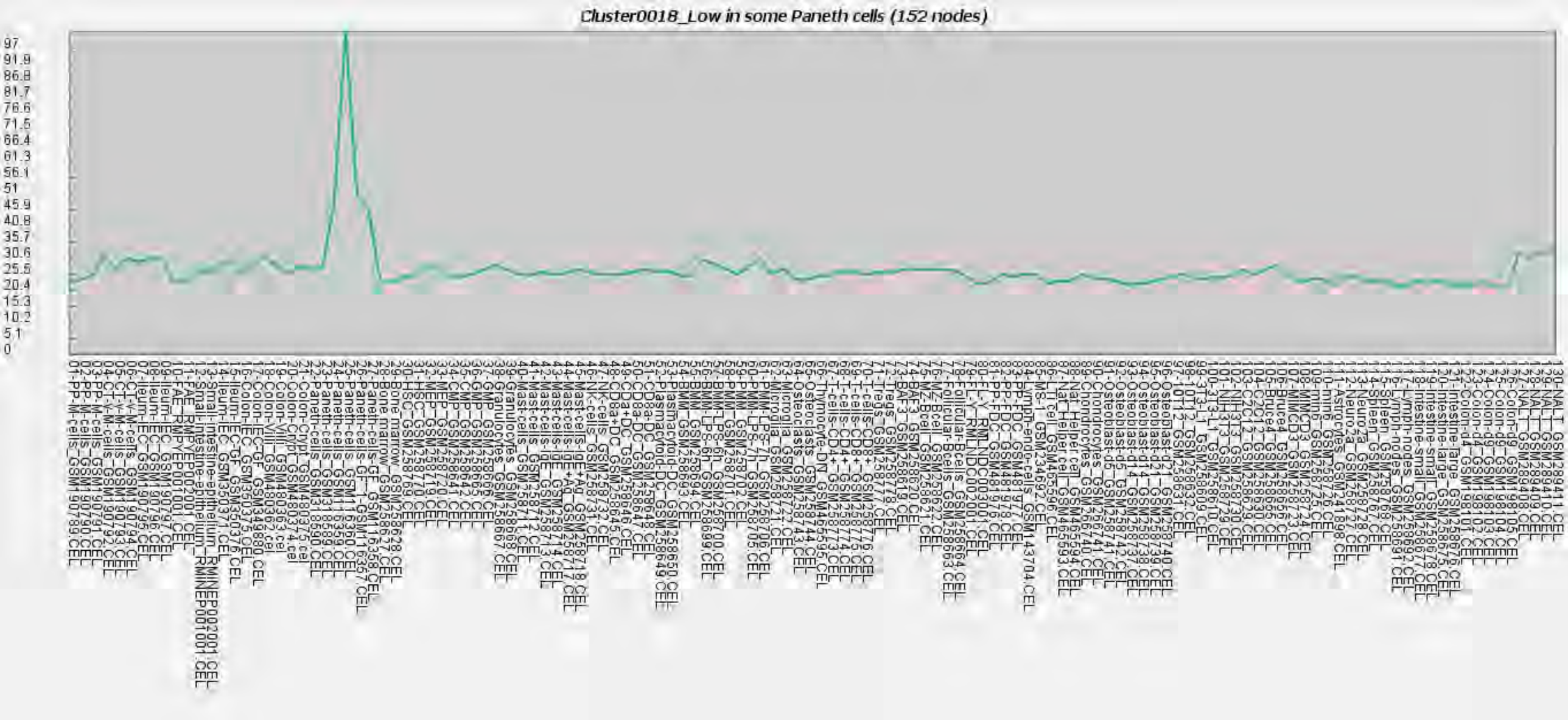

Cluster0013_Mesenchyme-related/extracellular matrix (181 nodes)
3,757.6
3,559.8
3,362
3,164.3
2,966.5
2,768.7
2,571
2,373.2
2,175.4
1,977.7
1,779.9
1,582.1
1,384.4
1,186.6
988.8
791.1
593.3
395.5
197.8
0

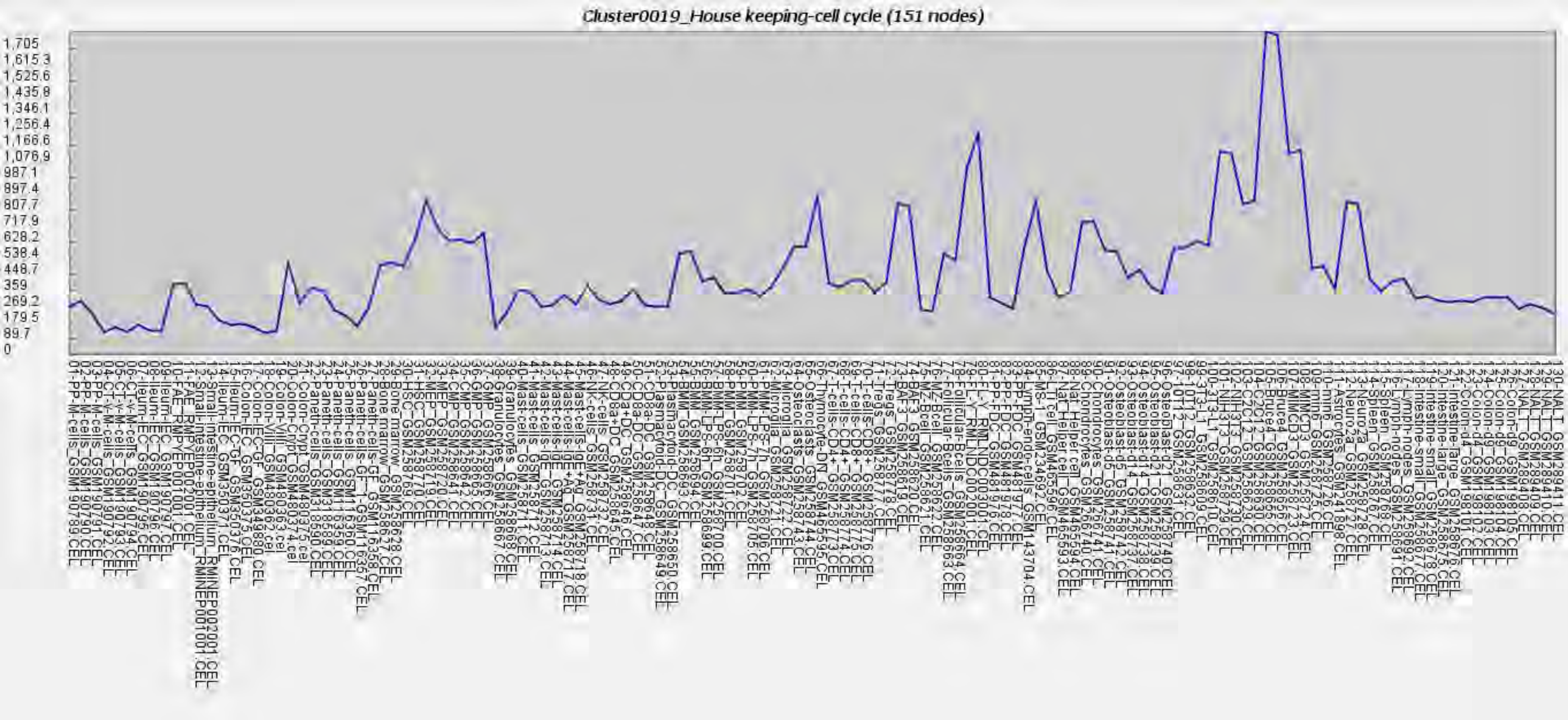

Cluster0014_High in bone marrow (180 nodes)
3,967.4
3,758.6
3,549.8
3,340.9
3,132.1
2,923.3
2,714.5
2,505.7
2,296.9
2,088.1
1,879.3
1,670.5
1,461.7
1,252.9
1,044
835.2
626.4
417.6
208.8
0

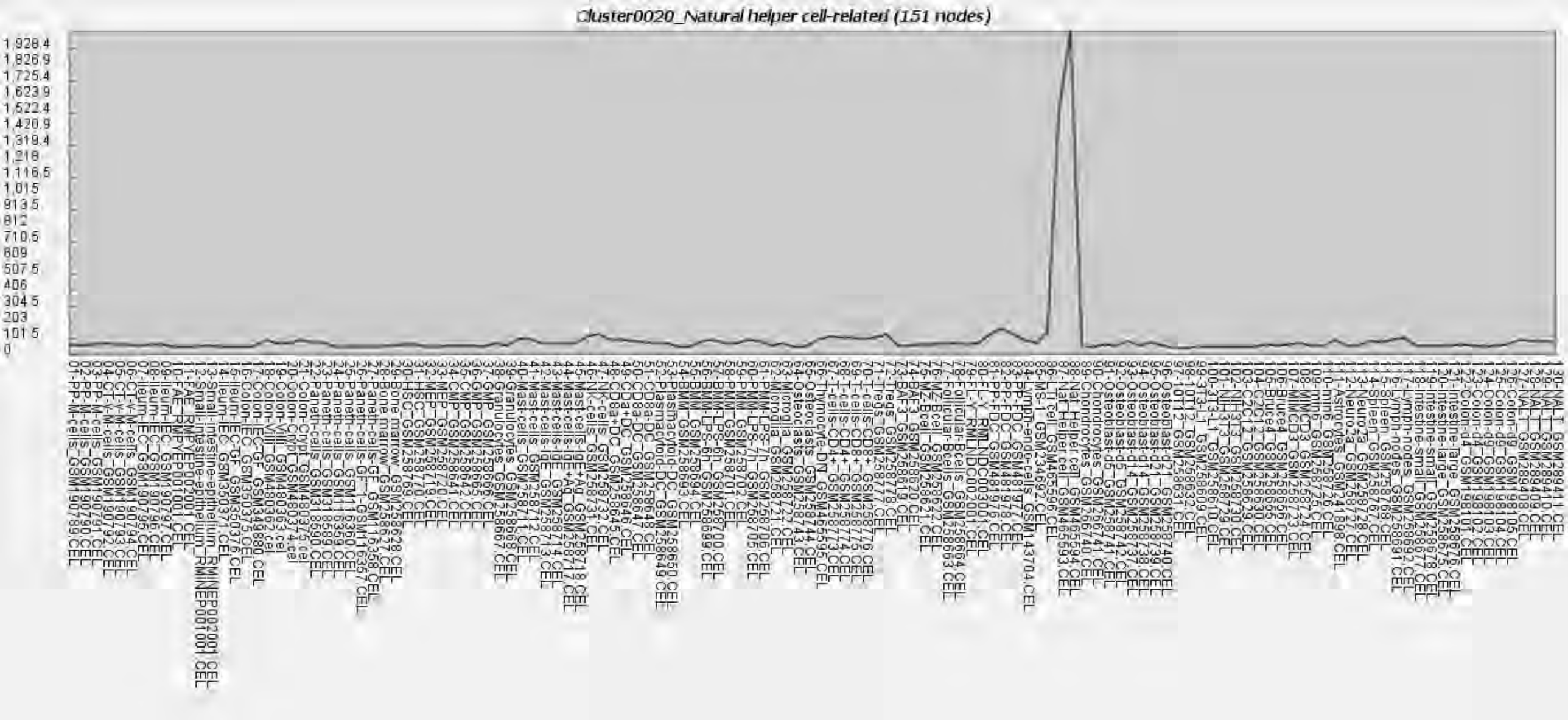
Cluster0015_Large intestine-related (171 nodes)
3,298.3
3,124.7
2,951.1
2,777.5
2,604
2,430.4
2,256.8
2,083.2
1,909.6
1,736
1,562.4
1,388.8
1,215.2
1,041.6
868
694.4
520.8
347.2
173.6
0

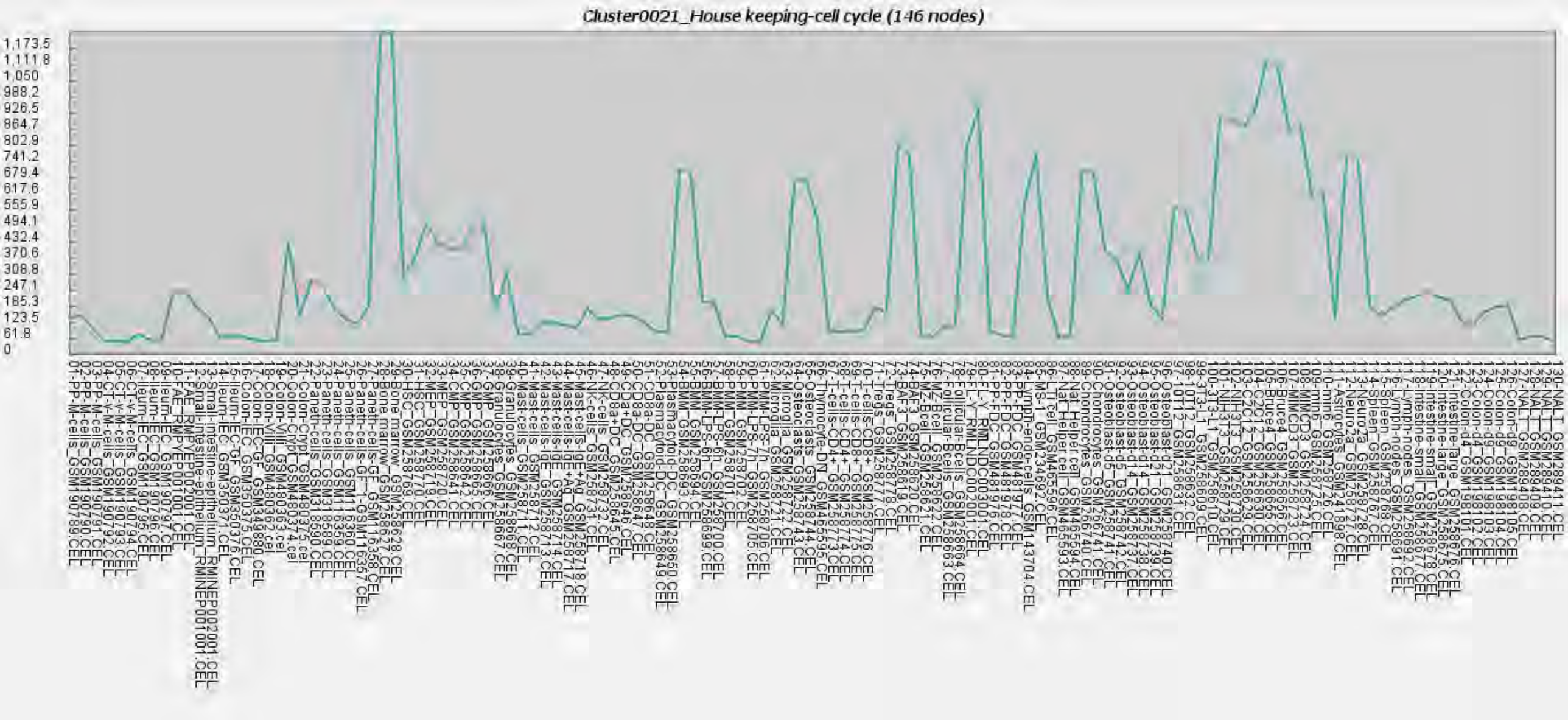

Cluster0016_House keeping-Ribosomal (170 nodes)
12,441.1
11,786.3
11,131.5
10,476.7
9,821.9
9,167.1
8,512.3
7,857.5
7,202.7
6,547.9
5,893.2
5,238.4
4,583.6
3,928.8
3,274
2,619.2
1,964.4
1,309.6
654.8
0

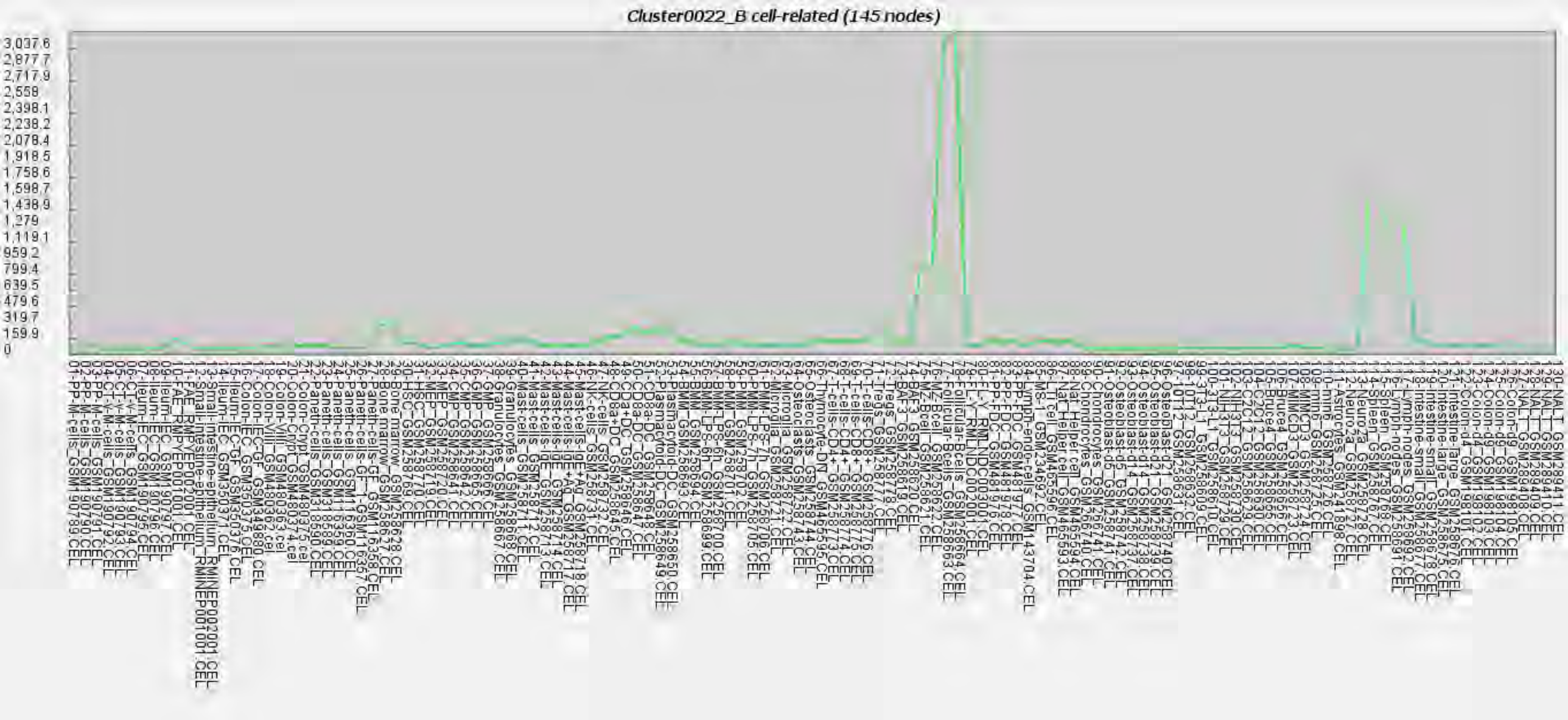

Cluster0017_Small and large intestine-related (157 nodes)
3,695.7
3,501.2
3,306.6
3,112.1
2,917.6
2,723.1
2,528.6
2,334.1
2,139.6
1,945.1
1,750.6
1,556.1
1,361.6
1,167.1
972.5
778
583.5
389
194.5
0

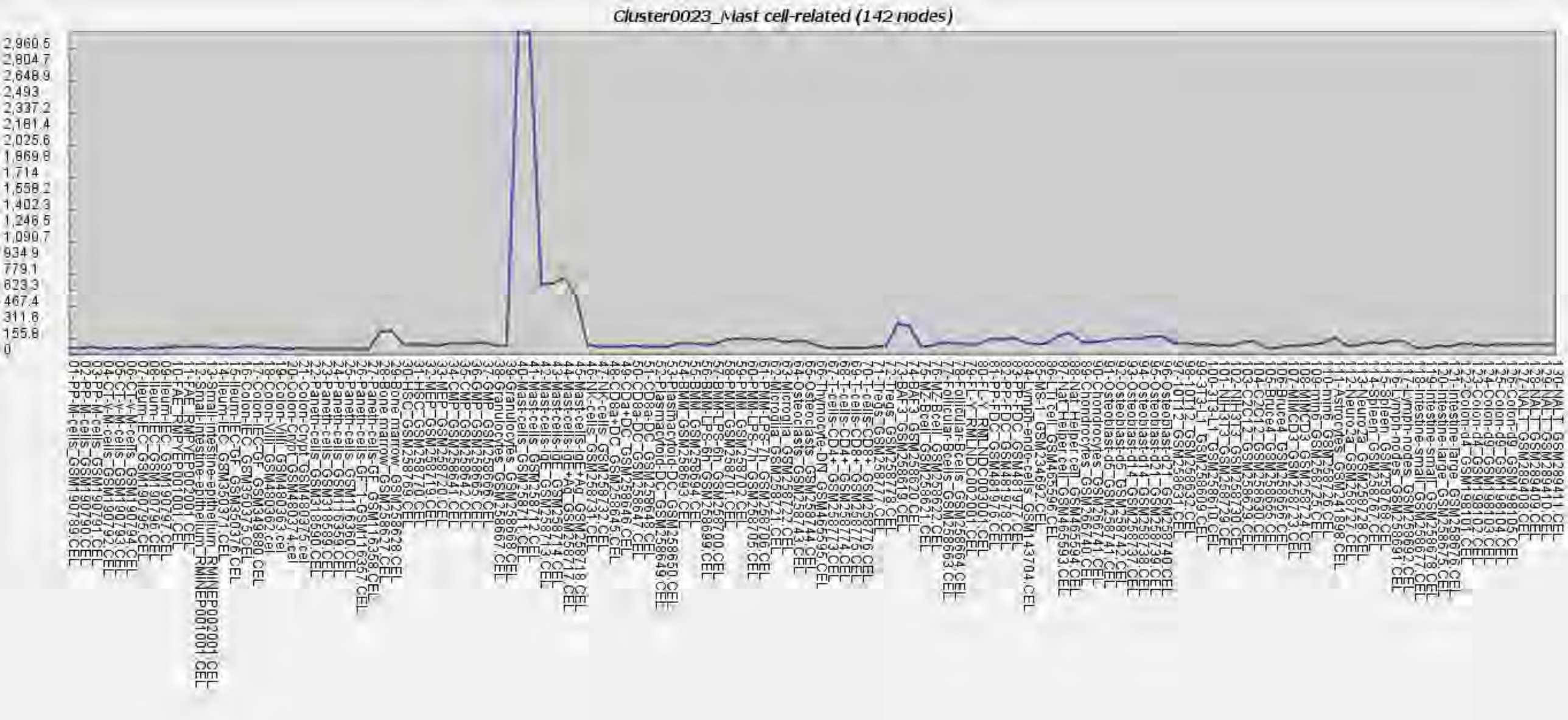

Cluster0018_Low in some Paneth cells (152 nodes)
97
91.9
86.8
81.7
76.6
71.5
66.4
61.3
56.1
51
45.9
40.8
35.7
30.6
25.5
20.4
15.3
10.2
5.1
0

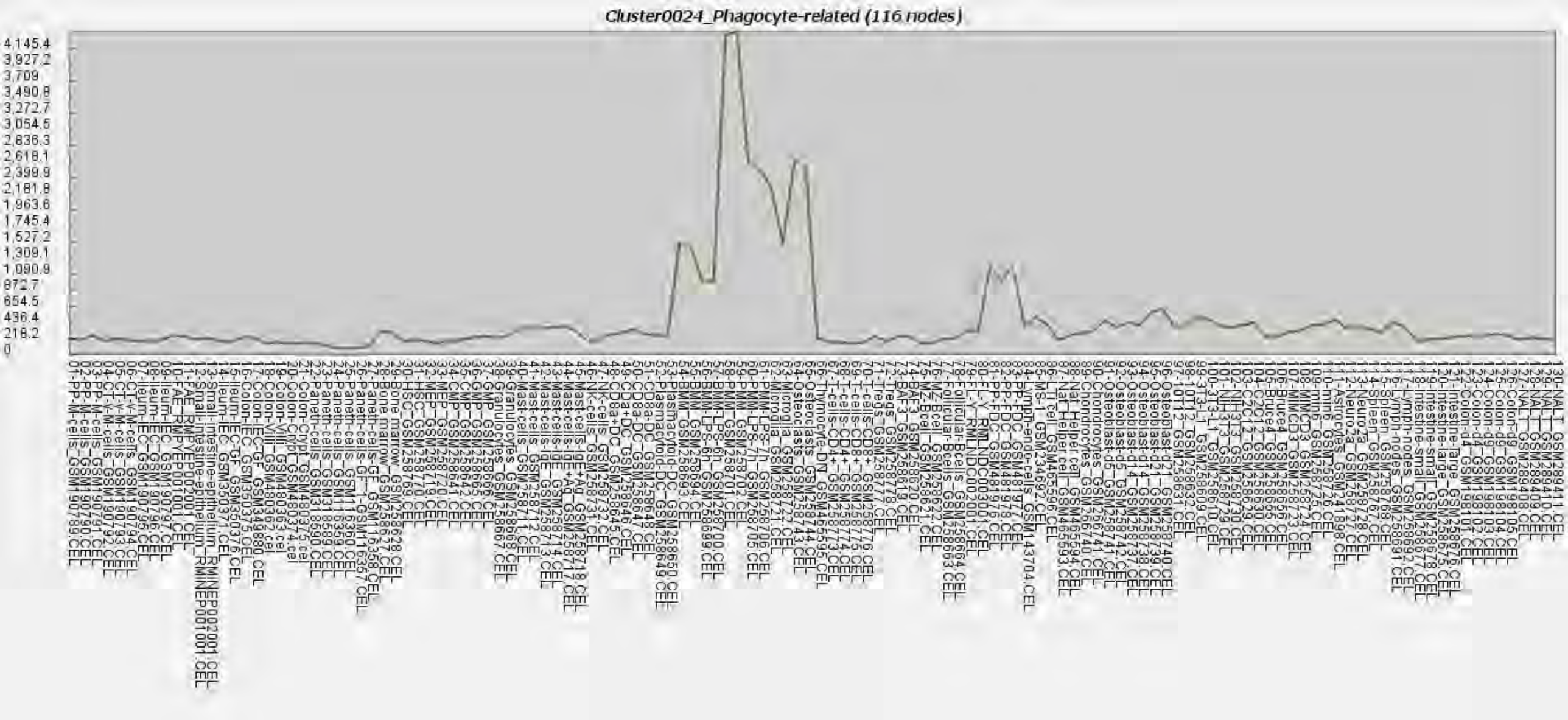

Cluster0019_House keeping-cell cycle (151 nodes)
1,705
1,615.3
1,525.6
1,435.8
1,346.1
1,256.4
1,166.6
1,076.9
987.1
897.4
807.7
717.9
628.2
538.4
448.7
359
269.2
179.5
89.7
0

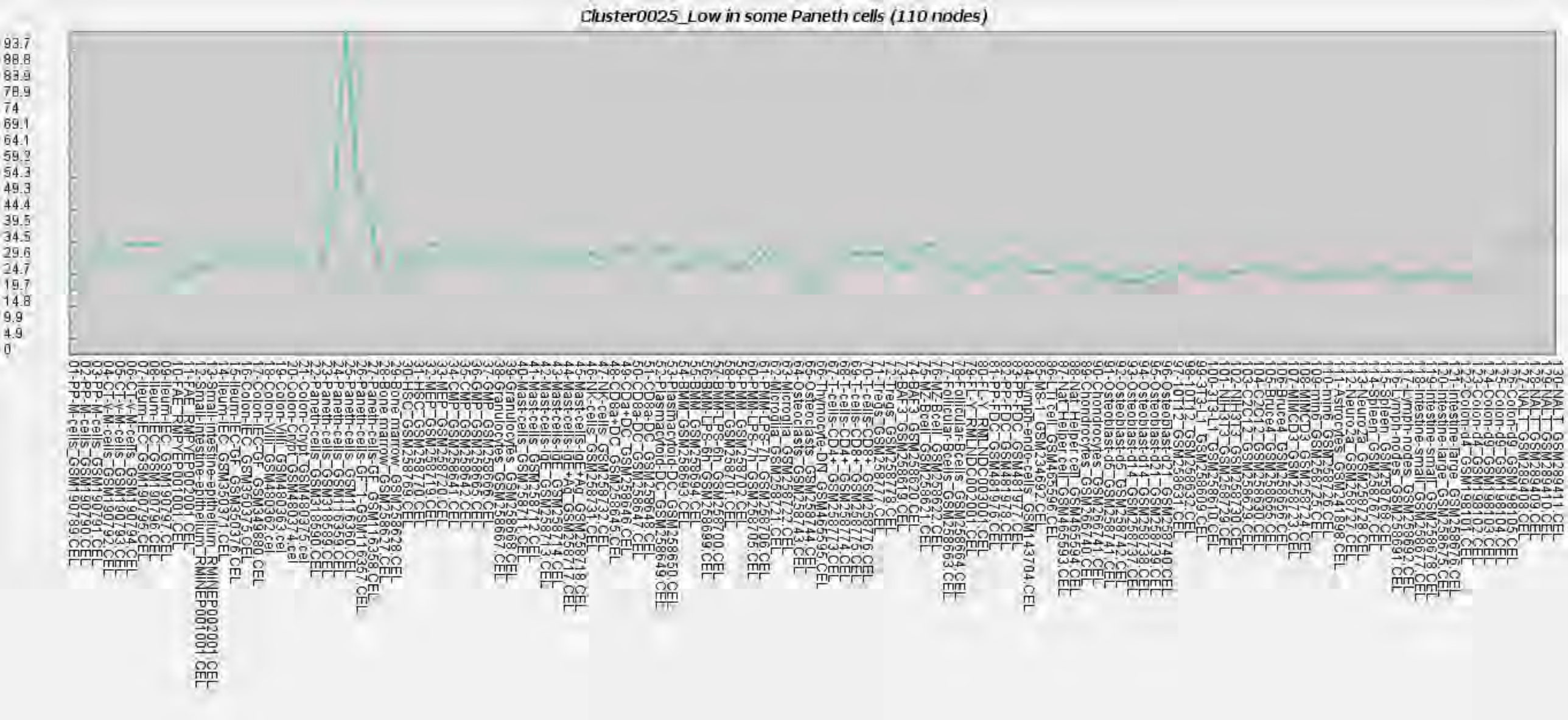

Cluster0020_Natural helper cell-related (151 nodes)
1,928.4
1,826.9
1,725.4
1,623.9
1,522.4
1,420.9
1,319.4
1,218
1,116.5
1,015
913.5
812
710.5
609
507.5
406
304.5
203
101.5
0


Cluster0021_House keeping-cell cycle (146 nodes)
1,173.5
1,111.8
1,050
988.2
926.5
864.7
802.9
741.2
679.4
617.6
555.9
494.1
432.4
370.6
308.8
247.1
185.3
123.5
61.8
0

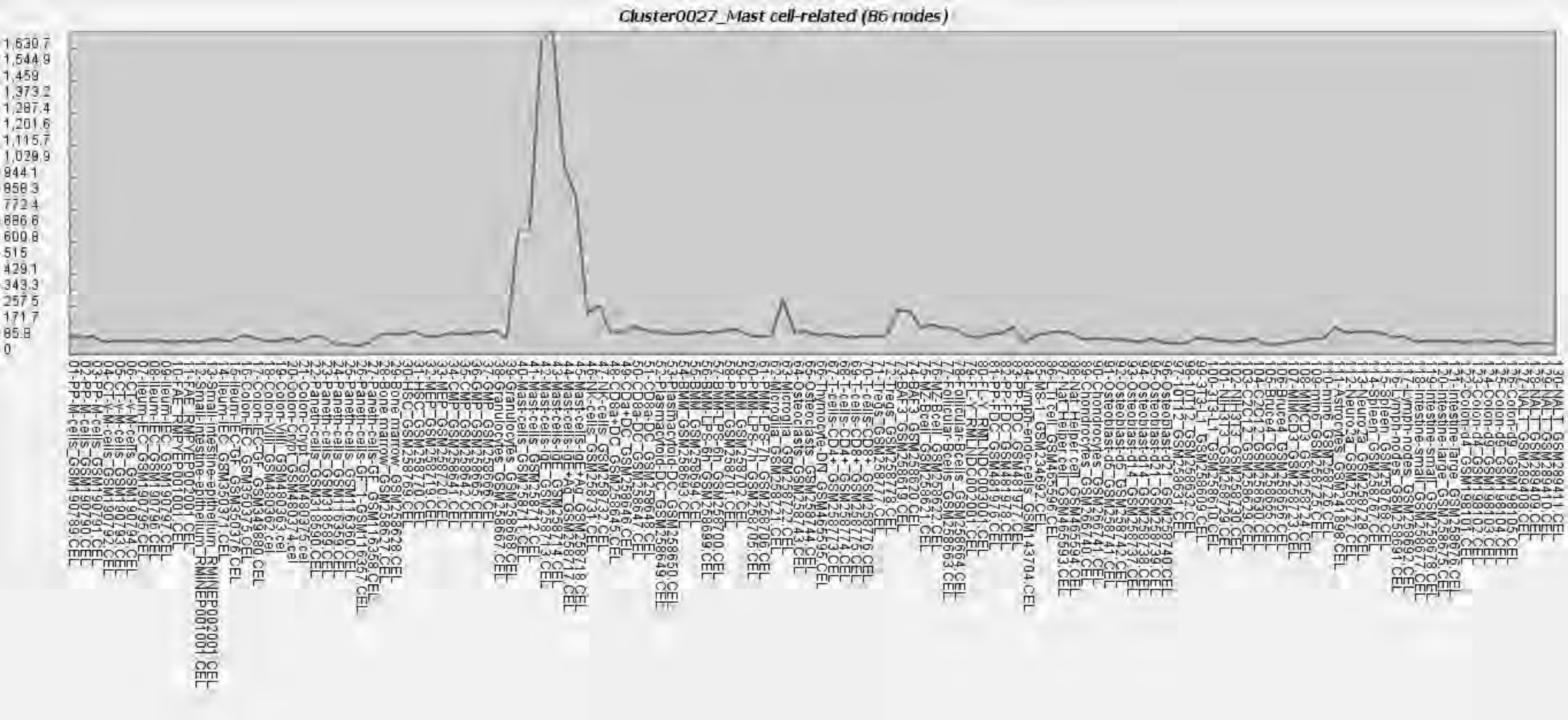

Cluster0022_B cell-related (145 nodes)
3,037.6
2,877.7
2,717.9
2,558
2,398.1
2,238.2
2,078.4
1,918.5
1,758.6
1,598.7
1,438.9
1,279
1,119.1
959.2
799.4
639.5
479.6
319.7
159.9
0

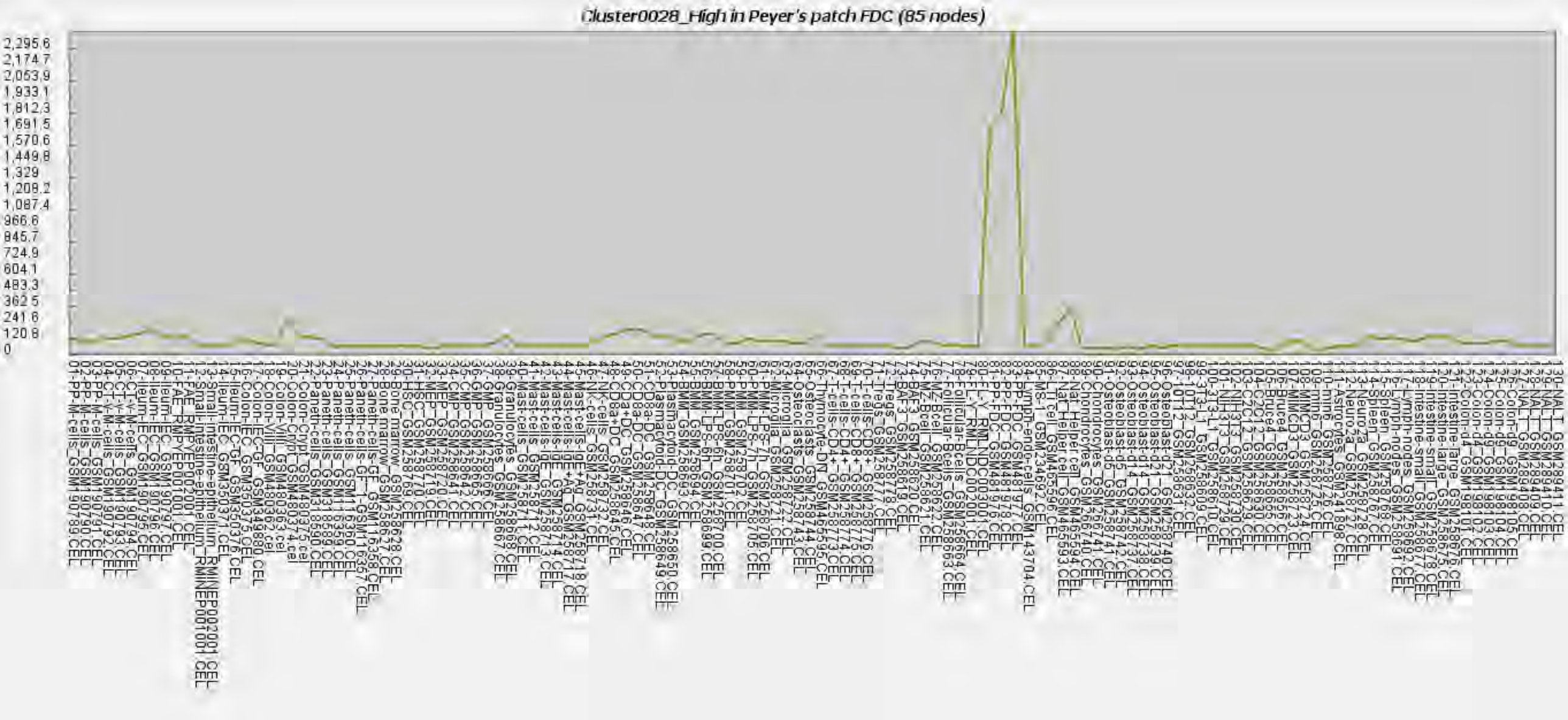

Cluster0023_Mast cell-related (142 nodes)
2,960.5
2,804.7
2,648.9
2,493
2,337.2
2,181.4
2,025.6
1,869.8
1,714
1,558.2
1,402.3
1,246.5
1,090.7
934.9
779.1
623.3
467.4
311.6
155.8
0

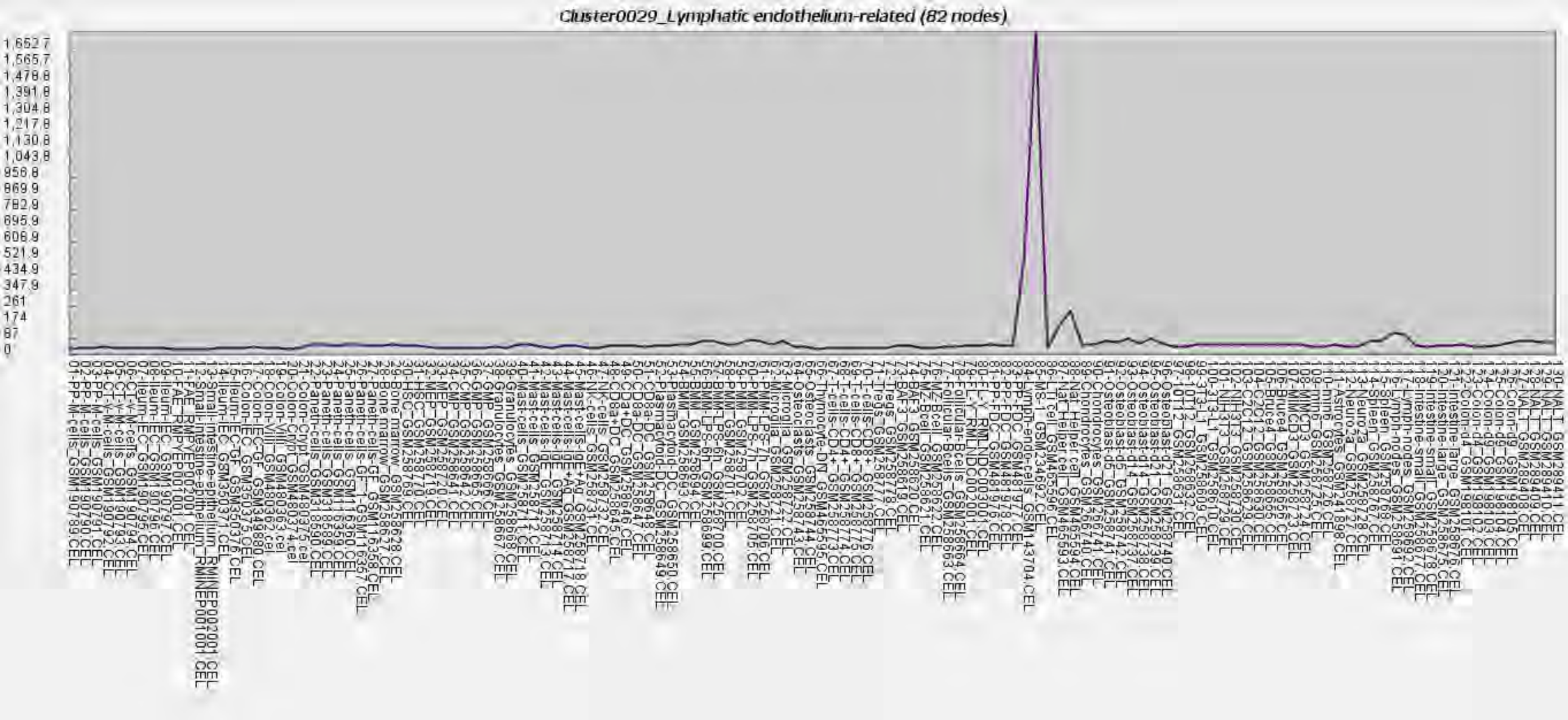

Cluster0024_Phagocyte-related (116 nodes)
4,145.4
3,927.2
3,709
3,490.8
3,272.7
3,054.5
2,836.3
2,618.1
2,399.9
2,181.8
1,963.6
1,745.4
1,527.2
1,309.1
1,090.9
872.7
654.5
436.4
218.2
0

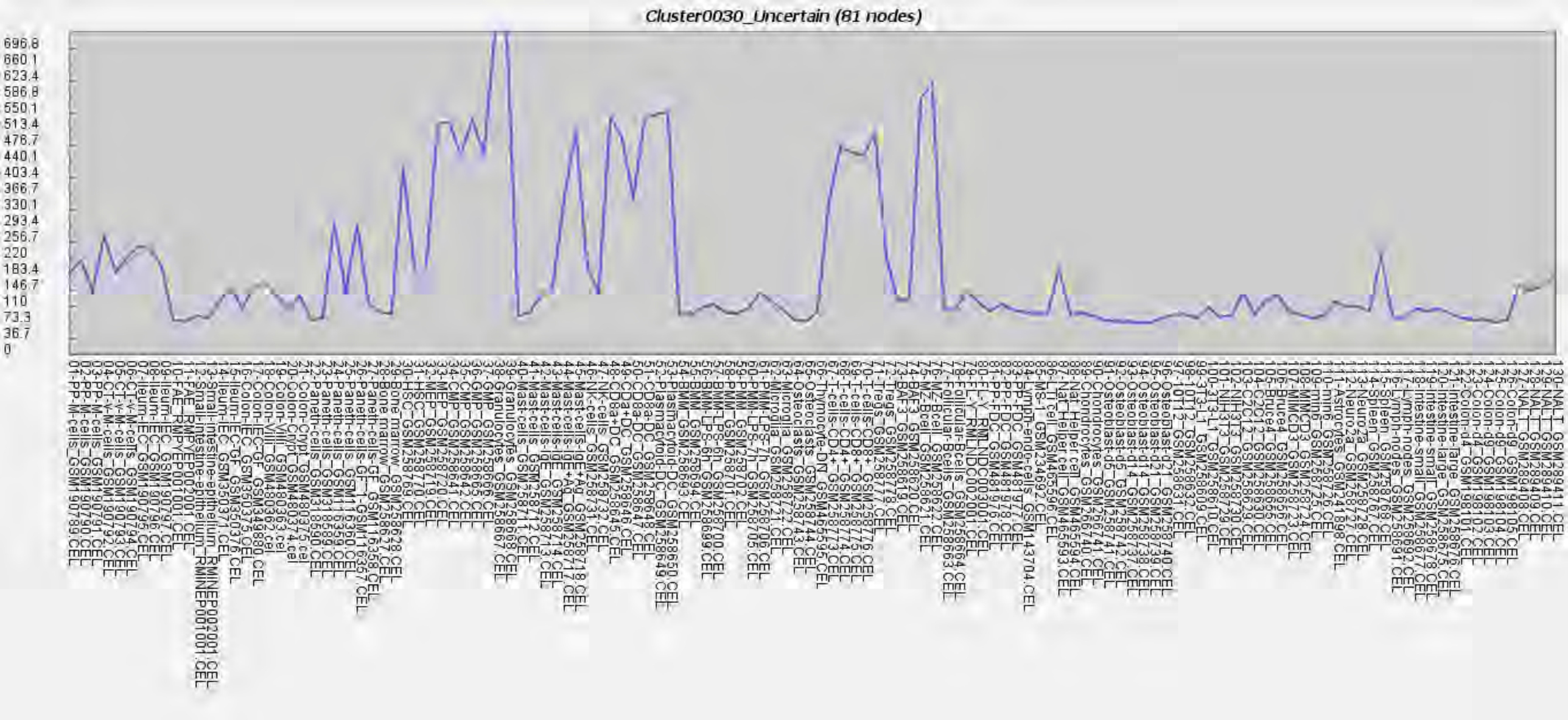

Cluster0025_Low in some Paneth cells (110 nodes)
93.7
88.8
83.9
78.9
74
69.1
64.1
59.2
54.3
49.3
44.4
39.5
34.5
29.6
24.7
19.7
14.8
9.9
4.9
0

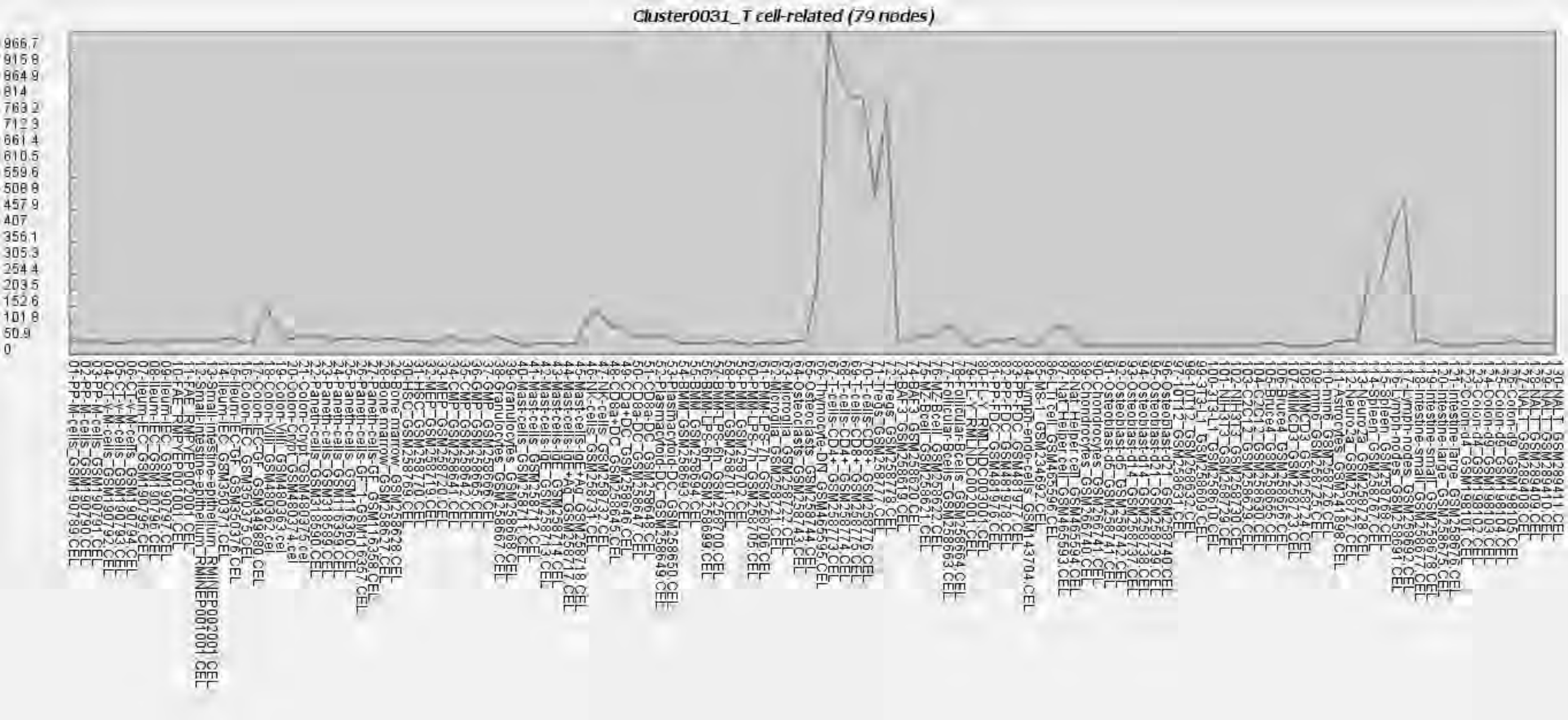
Cluster0026_High in Min6 & Neuro2A cells (98 nodes)
635.1
601.7
568.2
534.8
501.4
468
434.5
401.1
367.7
334.3
300.8
267.4
234
200.6
167.1
133.7
100.3
66.9
33.4
0

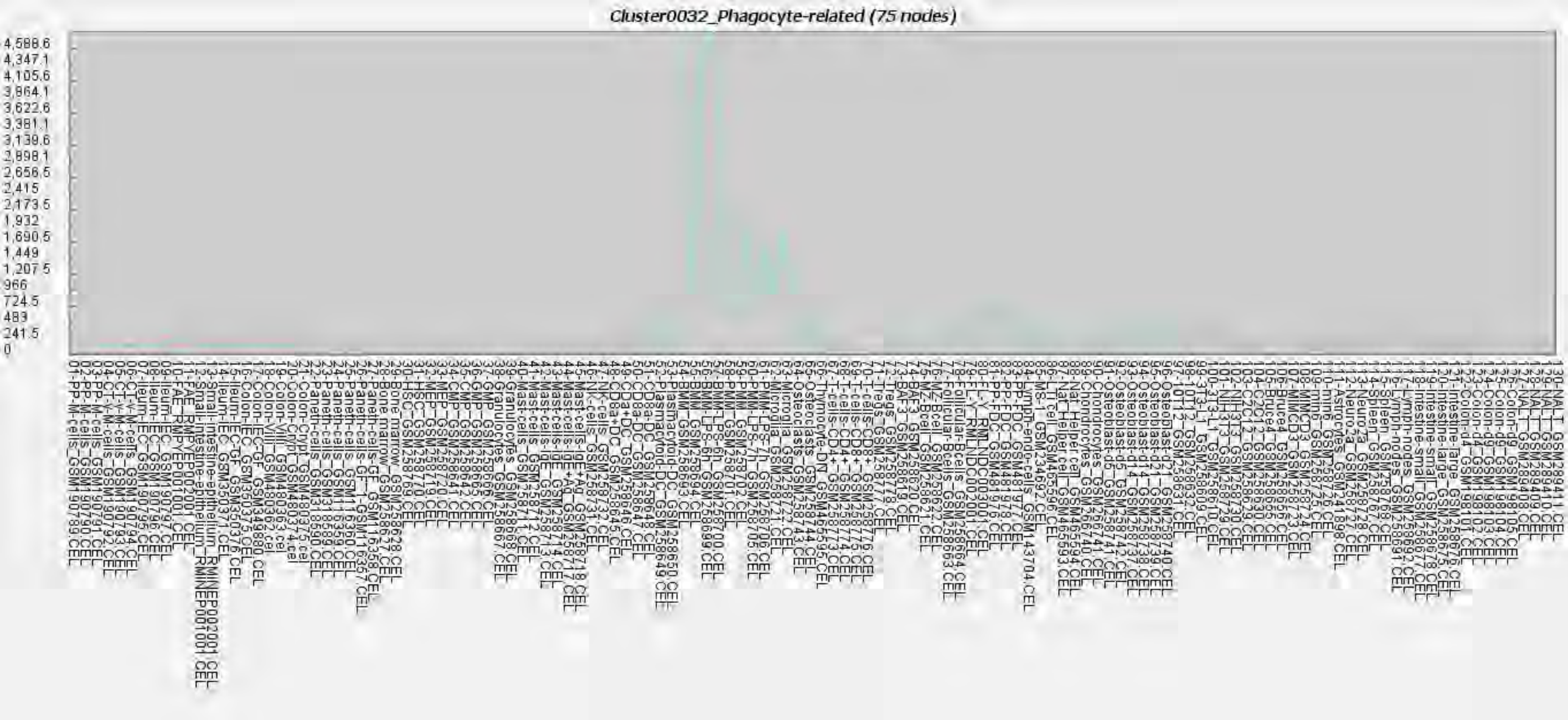

Cluster0027_Mast cell-related (86 nodes)
1,630.7
1,544.9
1,459
1,373.2
1,287.4
1,201.6
1,115.7
1,029.9
944.1
858.3
772.4
686.6
600.8
515
429.1
343.3
257.5
171.7
85.8
0

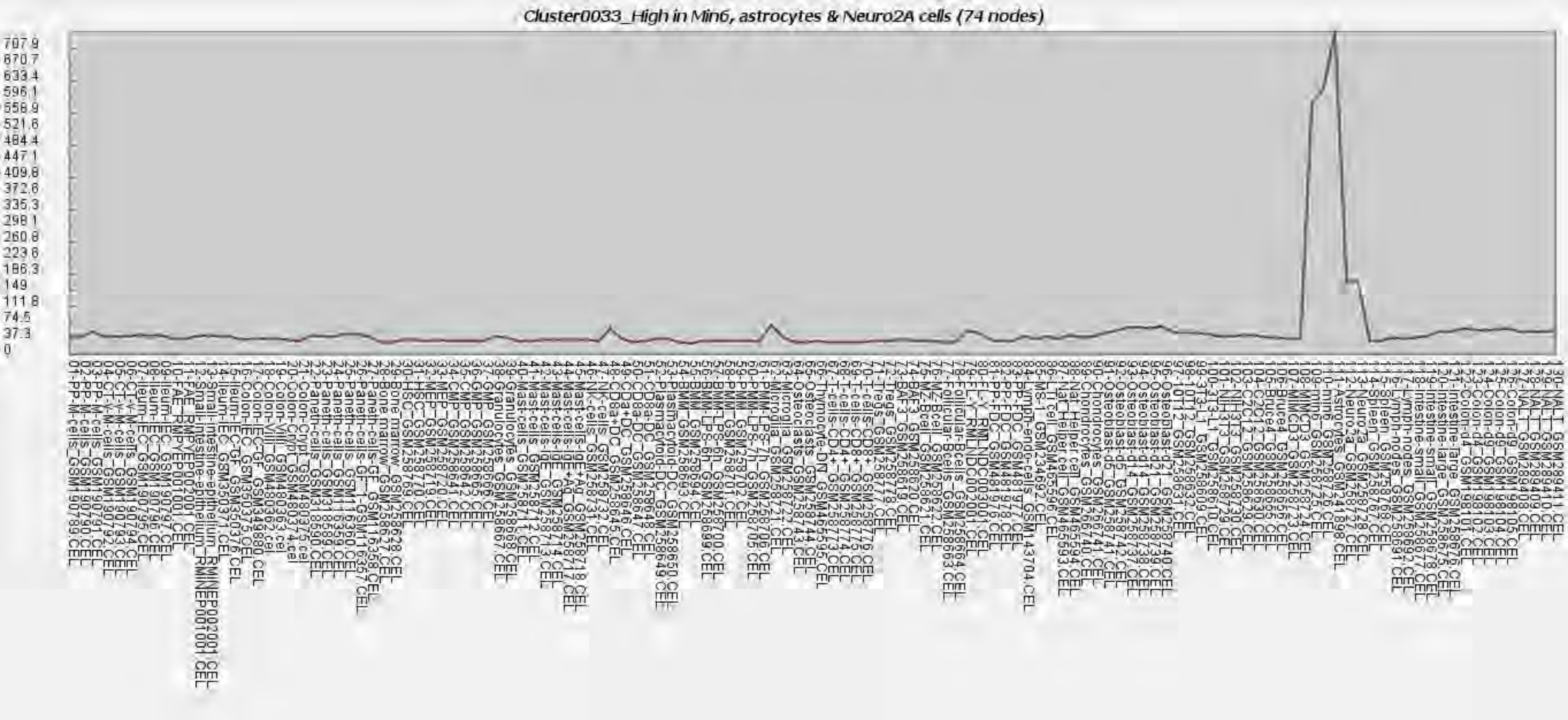

Cluster0028_High in Peyer's patch FDC (85 nodes)
2,295.6
2,174.7
2,053.9
1,933.1
1,812.3
1,691.5
1,570.6
1,449.8
1,329
1,208.2
1,087.4
966.6
845.7
724.9
604.1
483.3
362.5
241.6
120.8
0

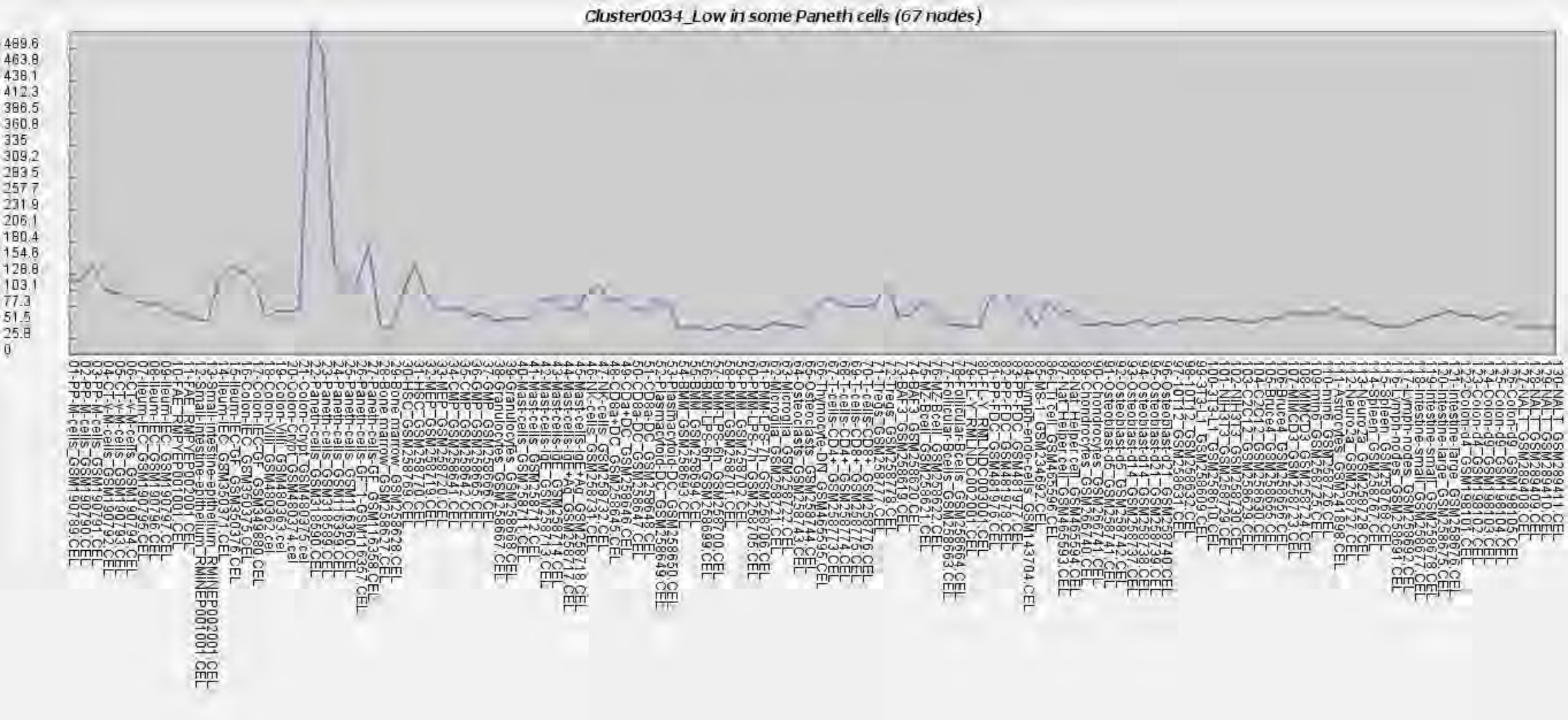

Cluster0029_Lymphatic endothelium-related (82 nodes)
1,652.7
1,565.7
1,478.8
1,391.8
1,304.8
1,217.8
1,130.8
1,043.8
956.8
869.9
782.9
695.9
608.9
521.9
434.9
347.9
261
174
87
0

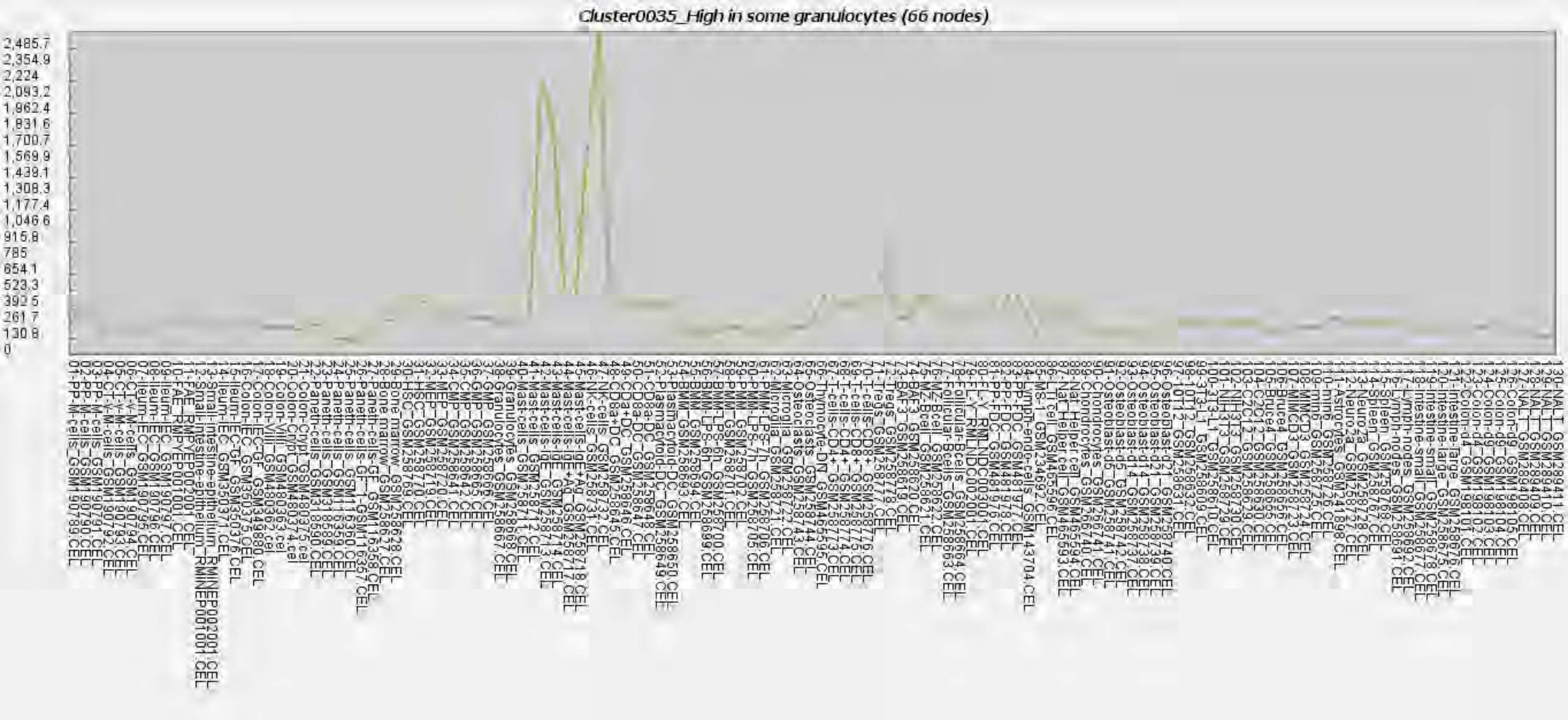

Cluster0030_Uncertain (81 nodes)
696.8
660.1
623.4
586.8
550.1
513.4
476.7
440.1
403.4
366.7
330.1
293.4
256.7
220
183.4
146.7
110
73.3
36.7
0

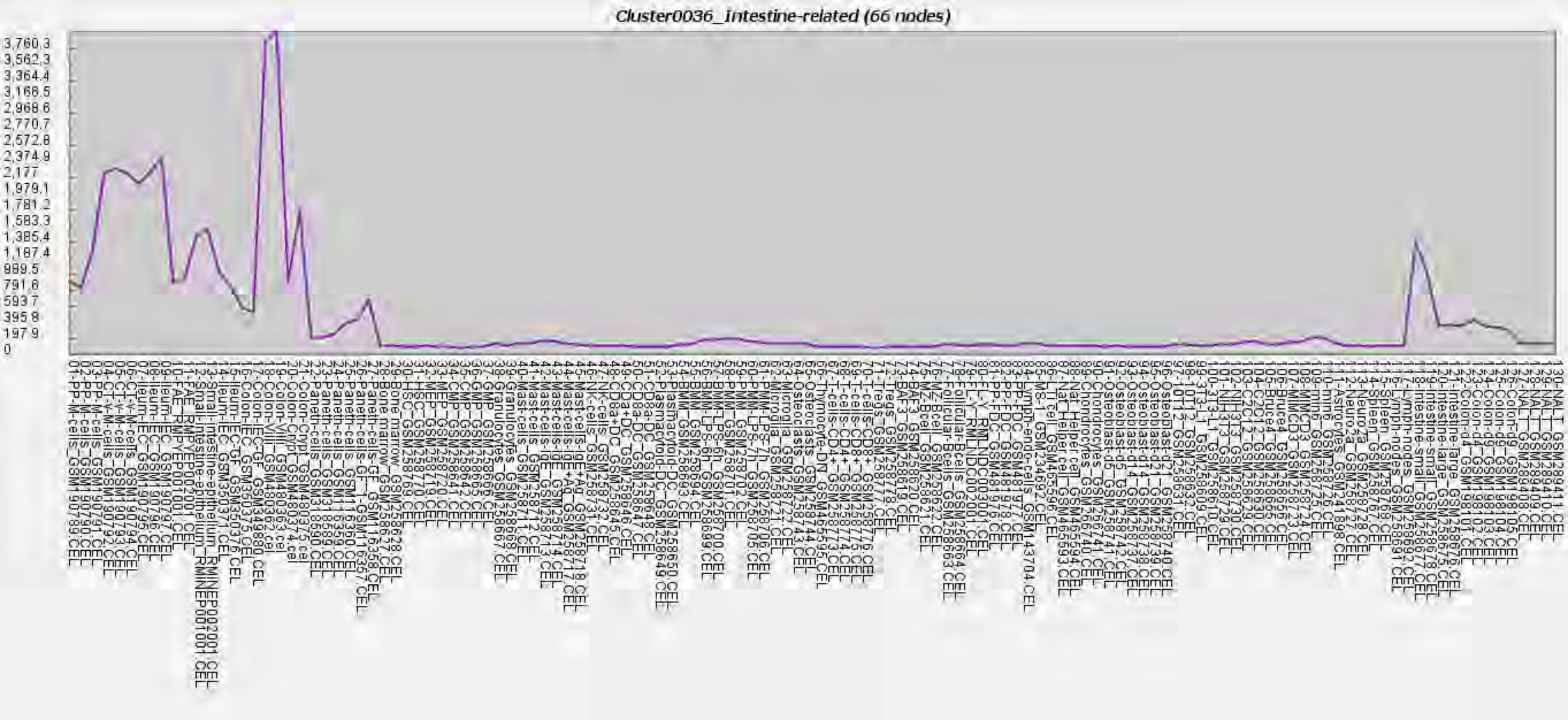

Cluster0031_T cell-related (79 nodes)
966.7
915.8
864.9
814
763.2
712.3
661.4
610.5
559.6
508.8
457.9
407
356.1
305.3
254.4
203.5
152.6
101.8
50.9
0

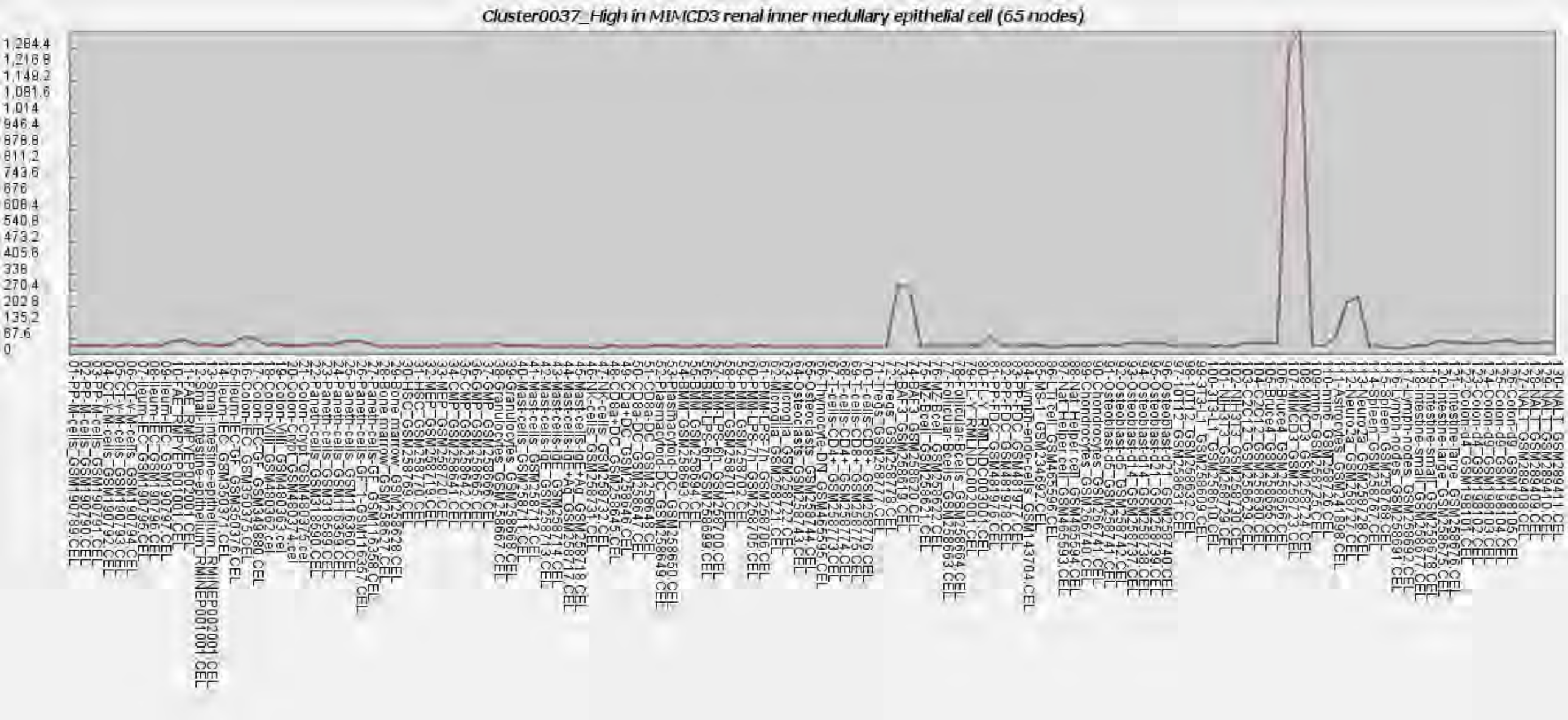

Cluster0032_Phagocyte-related (75 nodes)
4,588.6
4,347.1
4,105.6
3,864.1
3,622.6
3,381.1
3,139.6
2,898.1
2,656.5
2,415
2,173.5
1,932
1,690.5
1,449
1,207.5
966
724.5
483
241.5
0


Cluster0033_High in Min6, astrocytes & Neuro2A cells (74 nodes)
707.9
670.7
633.4
596.1
558.9
521.6
484.4
447.1
409.8
372.6
335.3
298.1
260.8
223.6
186.3
149
111.8
74.5
37.3
0

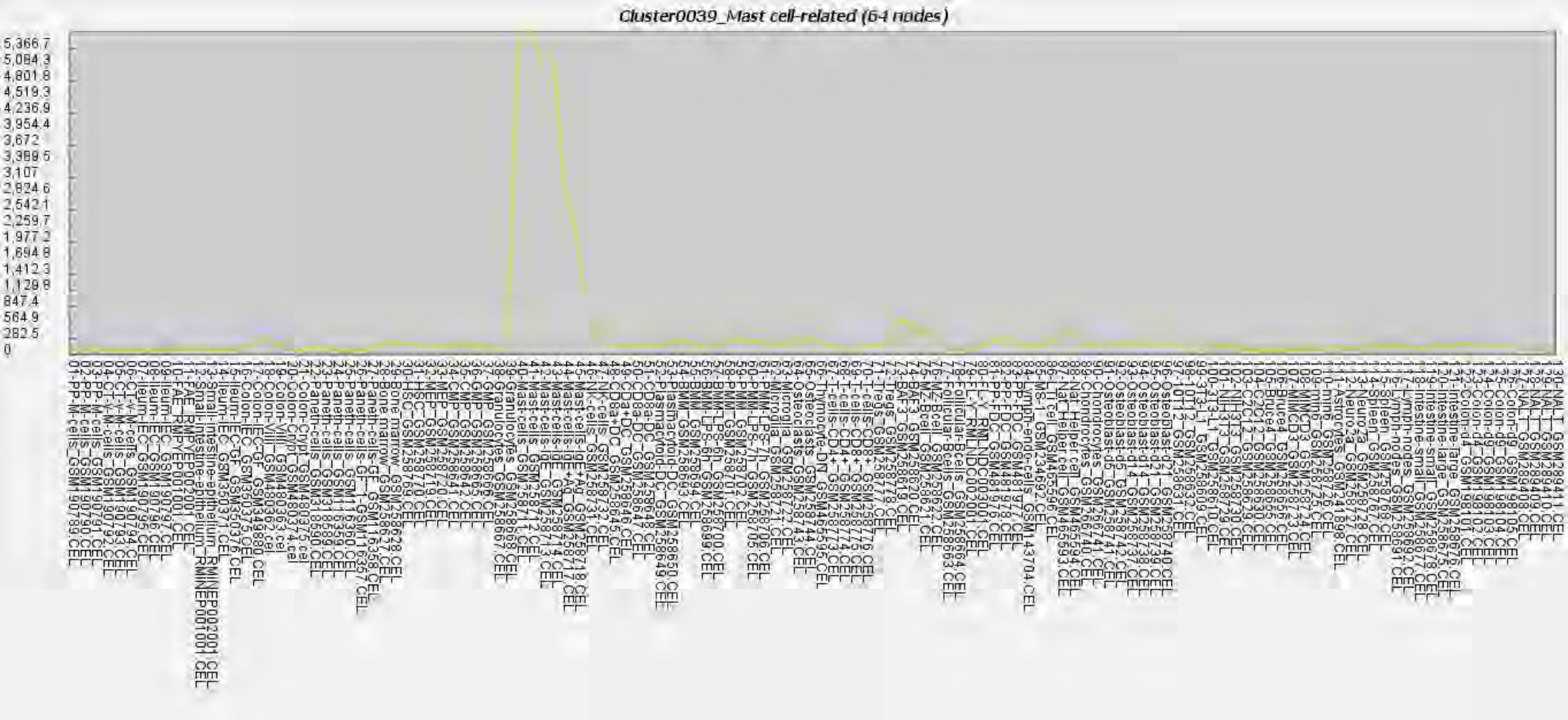

Cluster0034_Low in some Paneth cells (67 nodes)
489.6
463.8
438.1
412.3
386.5
360.8
335
309.2
283.5
257.7
231.9
206.1
180.4
154.6
128.8
103.1
77.3
51.5
25.8
0

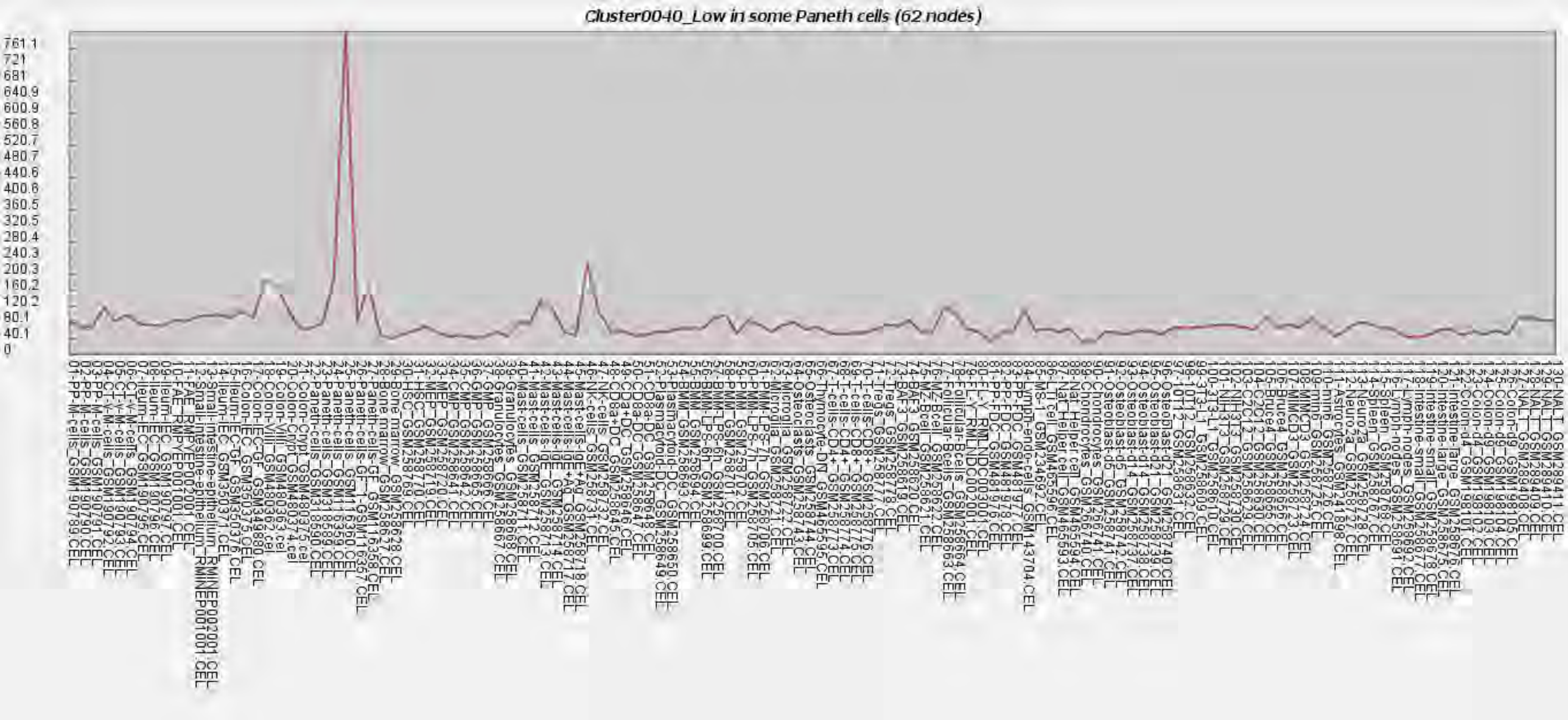

Cluster0035_High in some granulocytes (66 nodes)
2,485.7
2,354.9
2,224
2,093.2
1,962.4
1,831.6
1,700.7
1,569.9
1,439.1
1,308.3
1,177.4
1,046.6
915.8
785
654.1
523.3
392.5
261.7
130.8
0

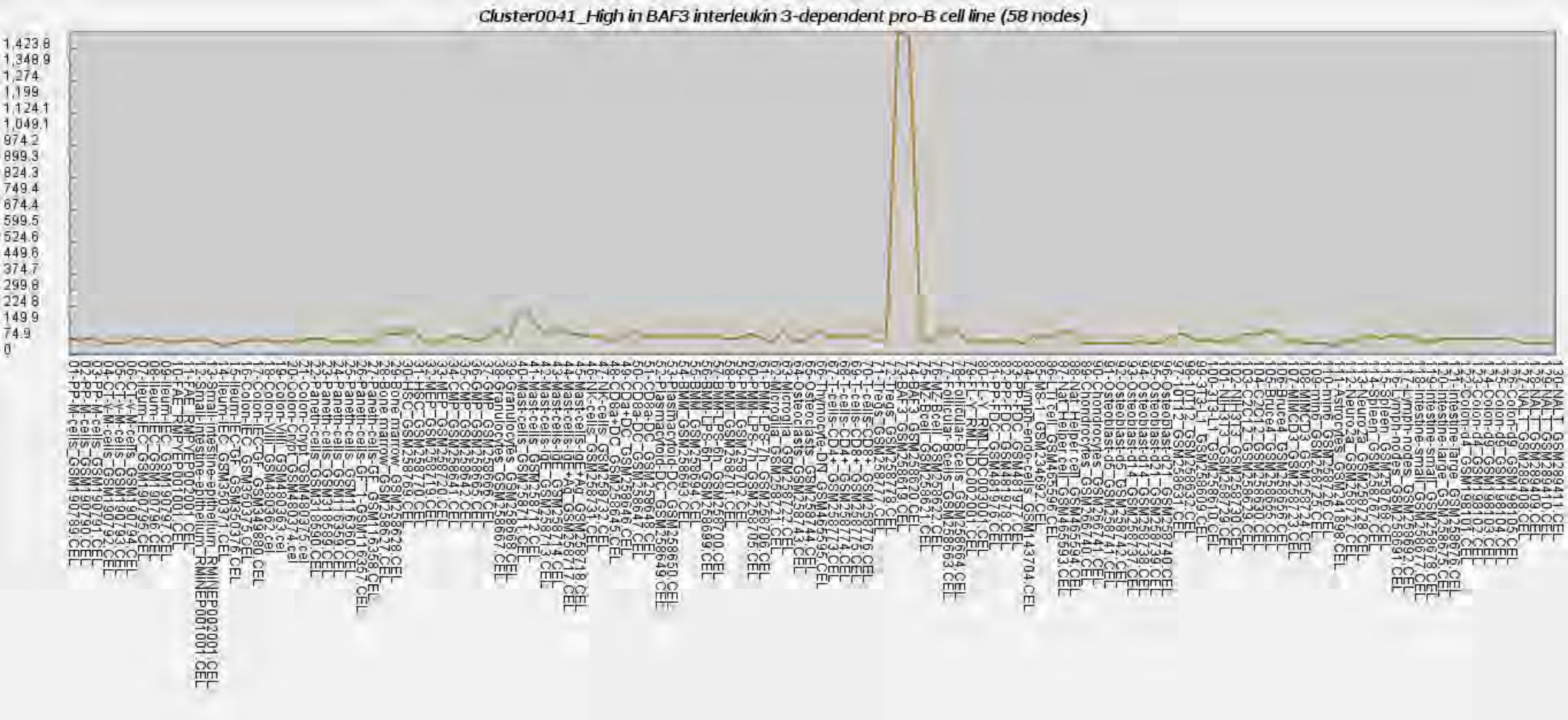

Cluster0036_intestine-related (66 nodes)
3,760.3
3,562.3
3,364.4
3,166.5
2,968.6
2,770.7
2,572.8
2,374.9
2,177
1,979.1
1,781.2
1,583.3
1,385.4
1,187.4
989.5
791.6
593.7
395.8
197.9
0


Cluster0037_High in MIMCD3 renal inner medullary epithelial cell (65 nodes)
1,284.4
1,216.8
1,149.2
1,081.6
1,014
946.4
878.8
811.2
743.6
676
608.4
540.8
473.2
405.6
338
270.4
202.8
135.2
67.6
0

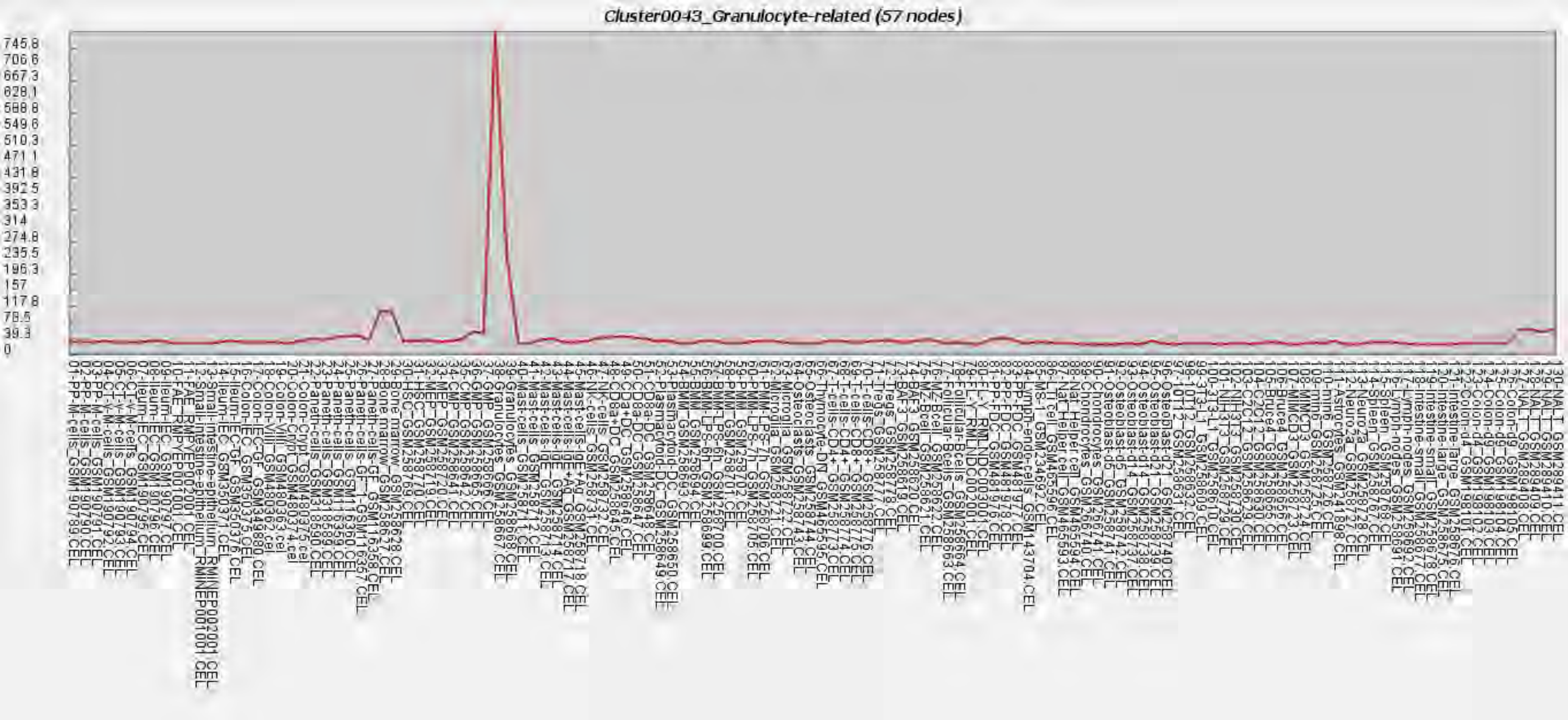
Cluster0038_Lymphatic endothelium-related (65 nodes)
2,519.1
2,386.5
2,253.9
2,121.4
1,988.8
1,856.2
1,723.6
1,591
1,458.4
1,325.8
1,193.3
1,060.7
928.1
795.5
662.9
530.3
397.8
265.2
132.6
0

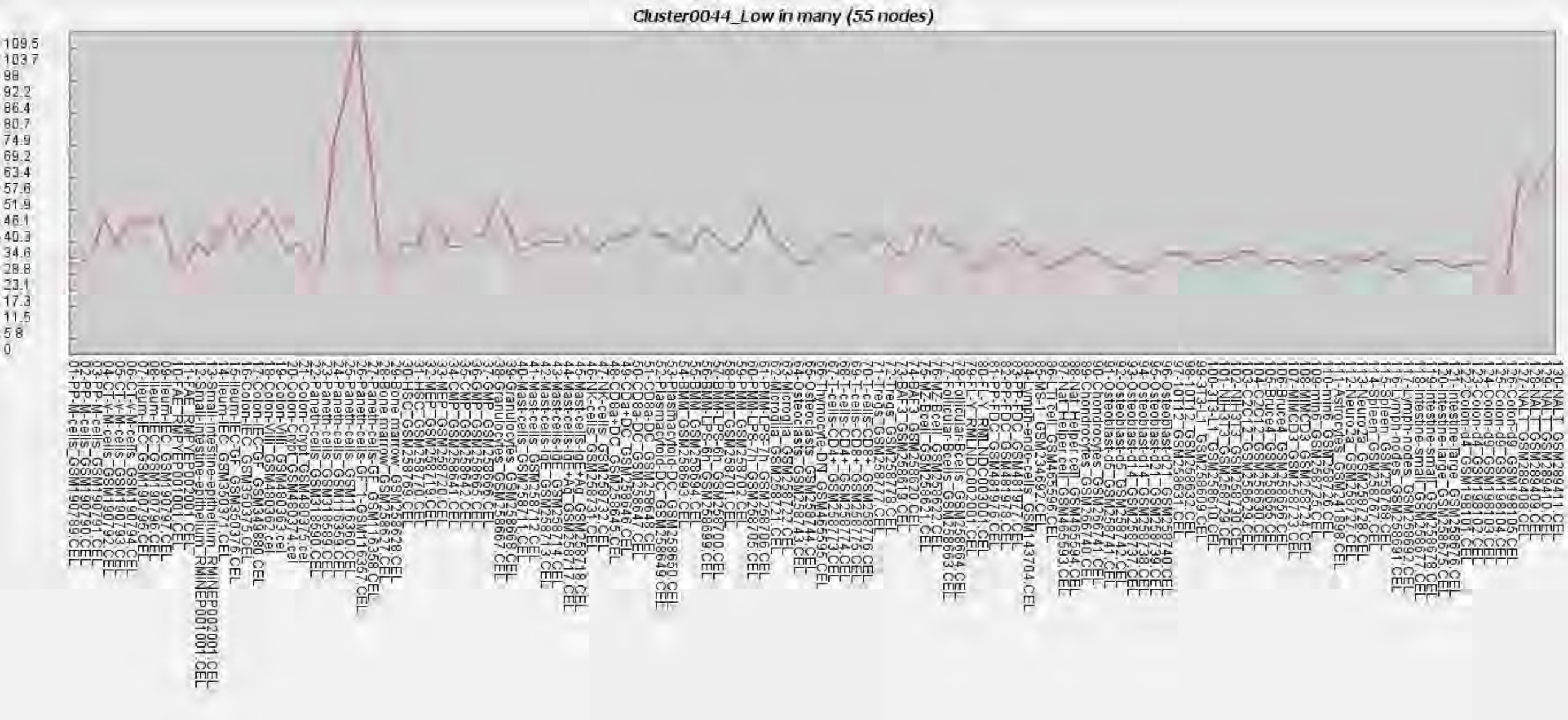

Cluster0039_Mast cell-related (64 nodes)
5,366.7
5,084.3
4,801.8
4,519.3
4,236.9
3,954.4
3,672
3,389.5
3,107
2,824.6
2,542.1
2,259.7
1,977.2
1,694.8
1,412.3
1,129.8
847.4
564.9
282.5
0


Cluster0040_Low in some Paneth cells (62 nodes)
761.1
721
681
640.9
600.9
560.8
520.7
480.7
440.6
400.6
360.5
320.5
280.4
240.3
200.3
160.2
120.2
80.1
40.1
0

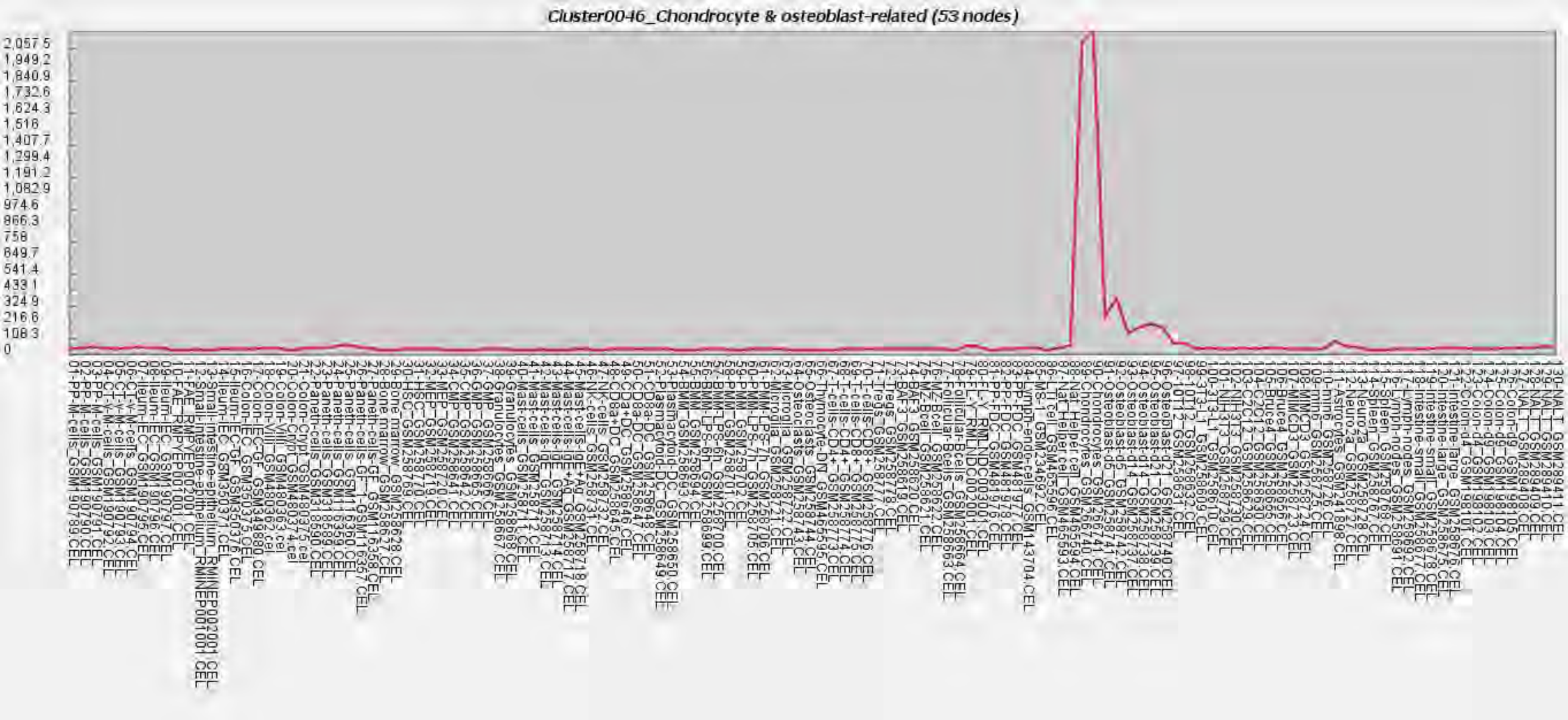

Cluster0041_High in BAF3 interleukin 3-dependent pro-B cell line (58 nodes)
1,423.8
1,348.9
1,274
1,199
1,124.1
1,049.1
974.2
899.3
824.3
749.4
674.4
599.5
524.6
449.6
374.7
299.8
224.8
149.9
74.9
0

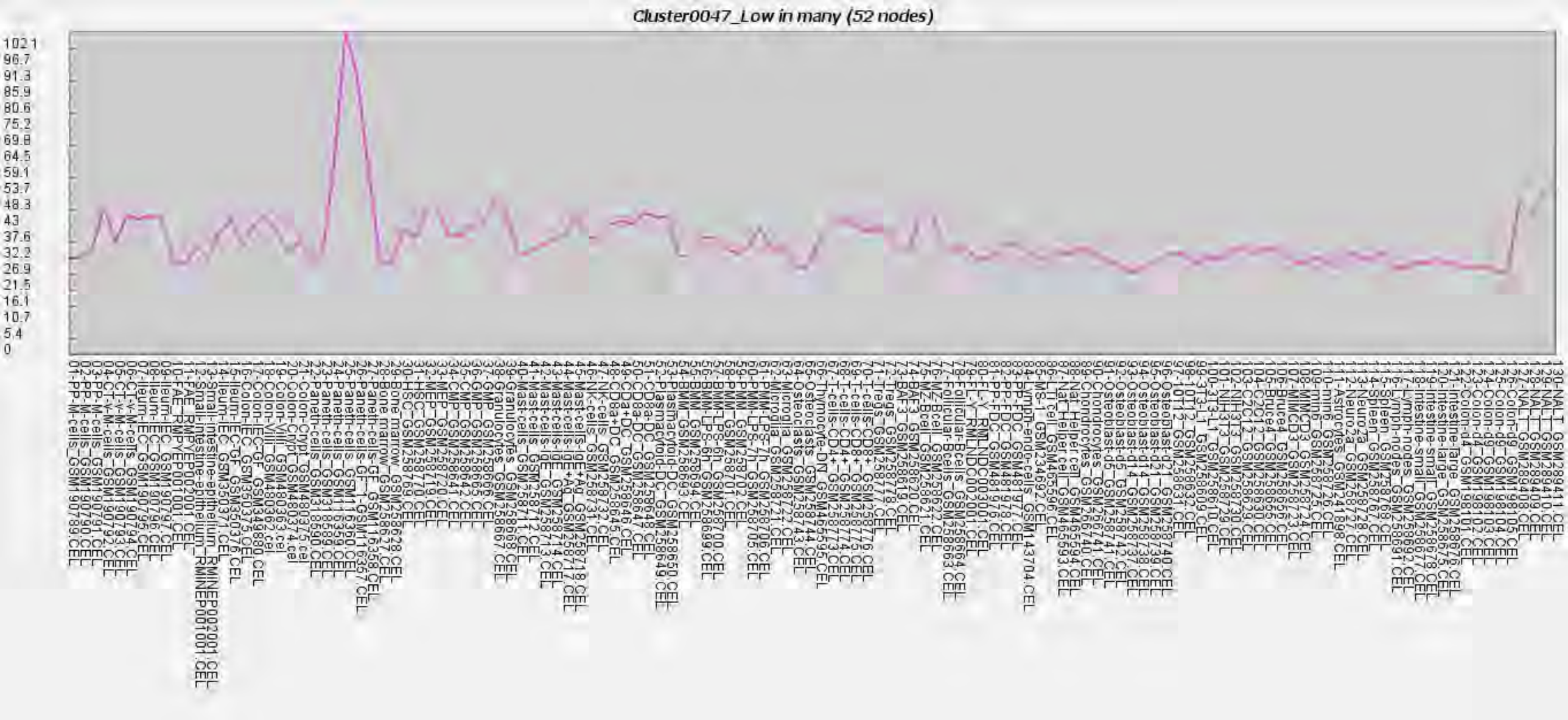
Cluster0042_NK cell-related (57 nodes)
3,537.6
3,351.4
3,165.2
2,979
2,792.8
2,606.7
2,420.5
2,234.3
2,048.1
1,861.9
1,675.7
1,489.5
1,303.3
1,117.1
930.9
744.8
558.6
372.4
186.2
0


Cluster0043_Granulocyte-related (57 nodes)
745.8
706.6
667.3
628.1
588.8
549.6
510.3
471.1
431.8
392.5
353.3
314
274.8
235.5
196.3
157
117.8
78.5
39.3
0

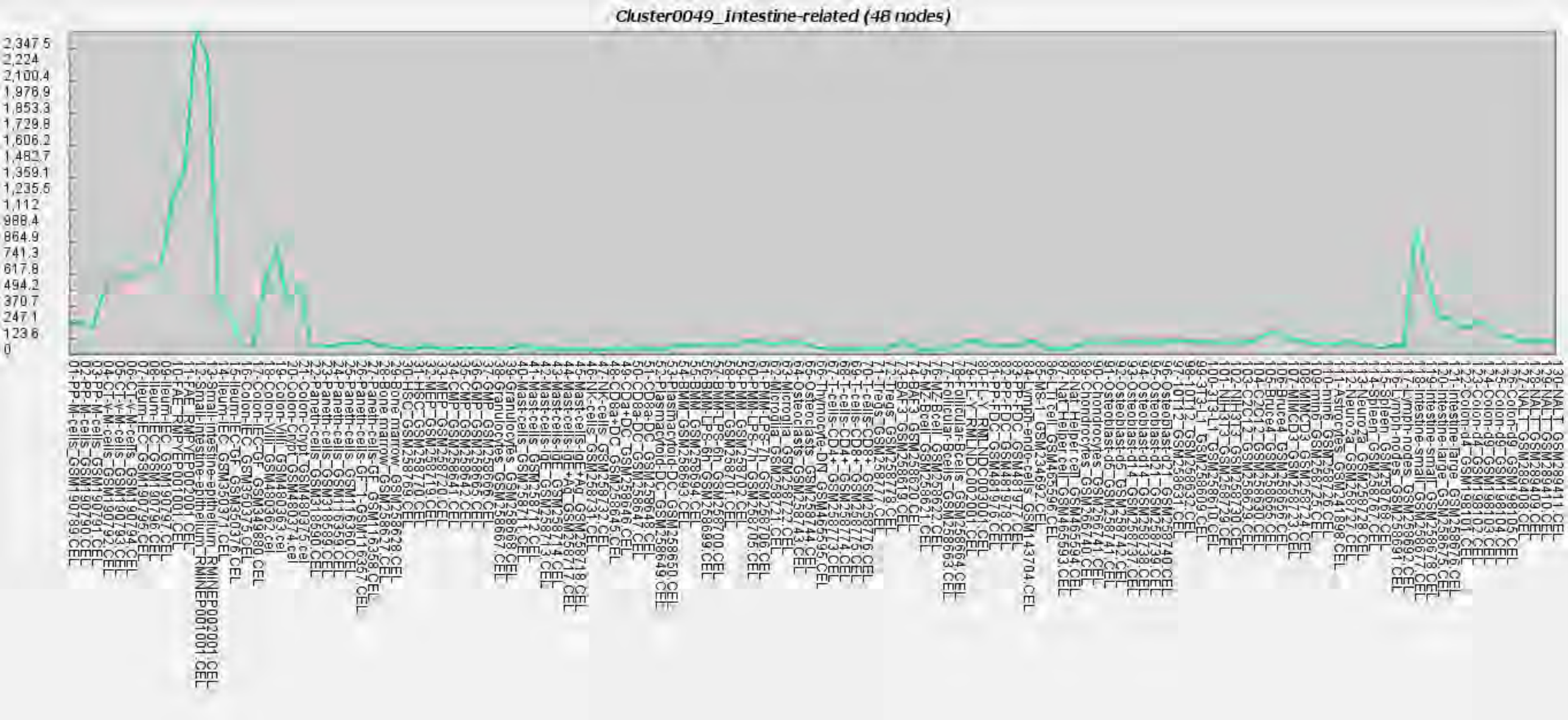

Cluster0044_Low in many (55 nodes)
109.5
103.7
98
92.2
86.4
80.7
74.9
69.2
63.4
57.6
51.9
46.1
40.3
34.6
28.8
23.1
17.3
11.5
5.8
0

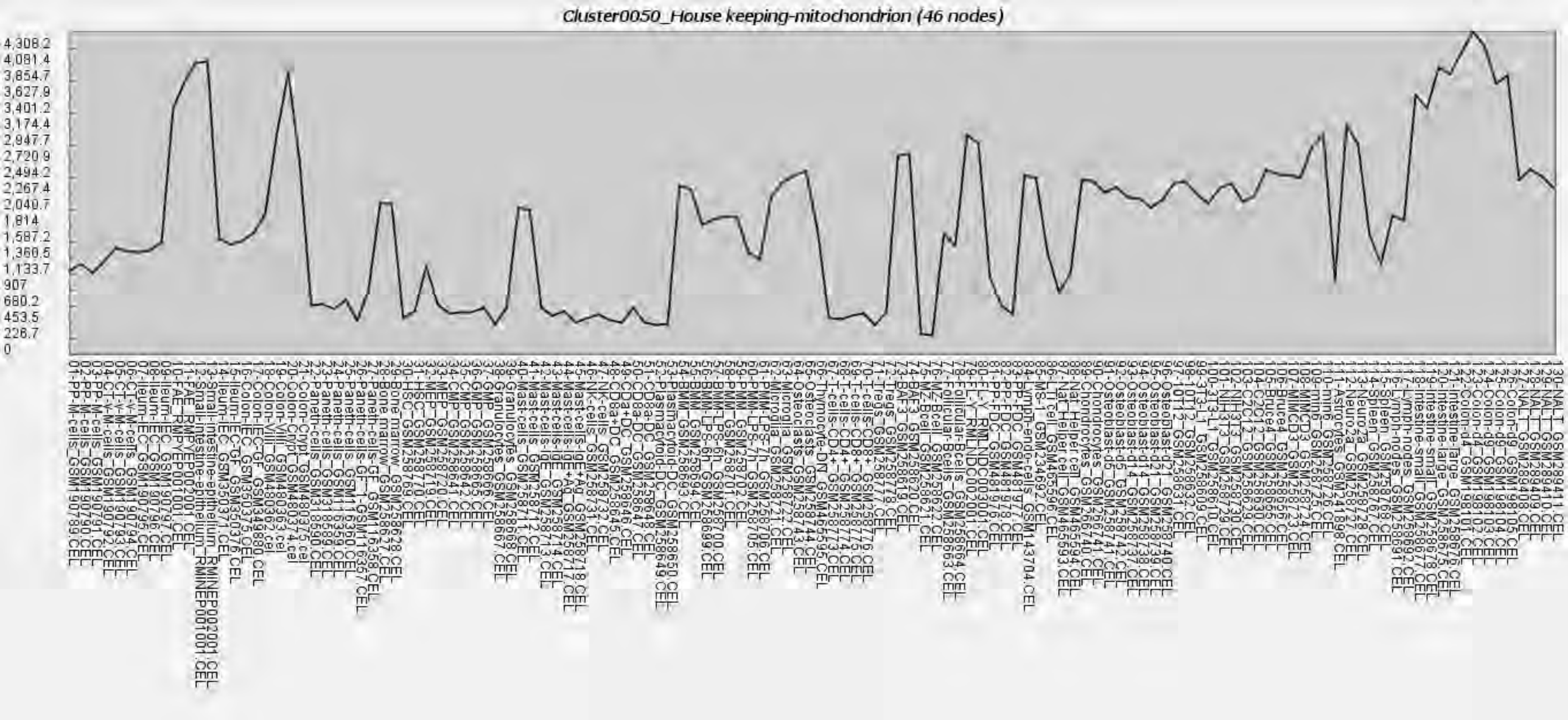
Cluster0045_Plasmacytoid DC-related (54 nodes)
827.3
783.8
740.3
696.7
653.2
609.6
566.1
522.5
479
435.4
391.9
348.4
304.8
261.3
217.7
174.2
130.6
87.1
43.5
0

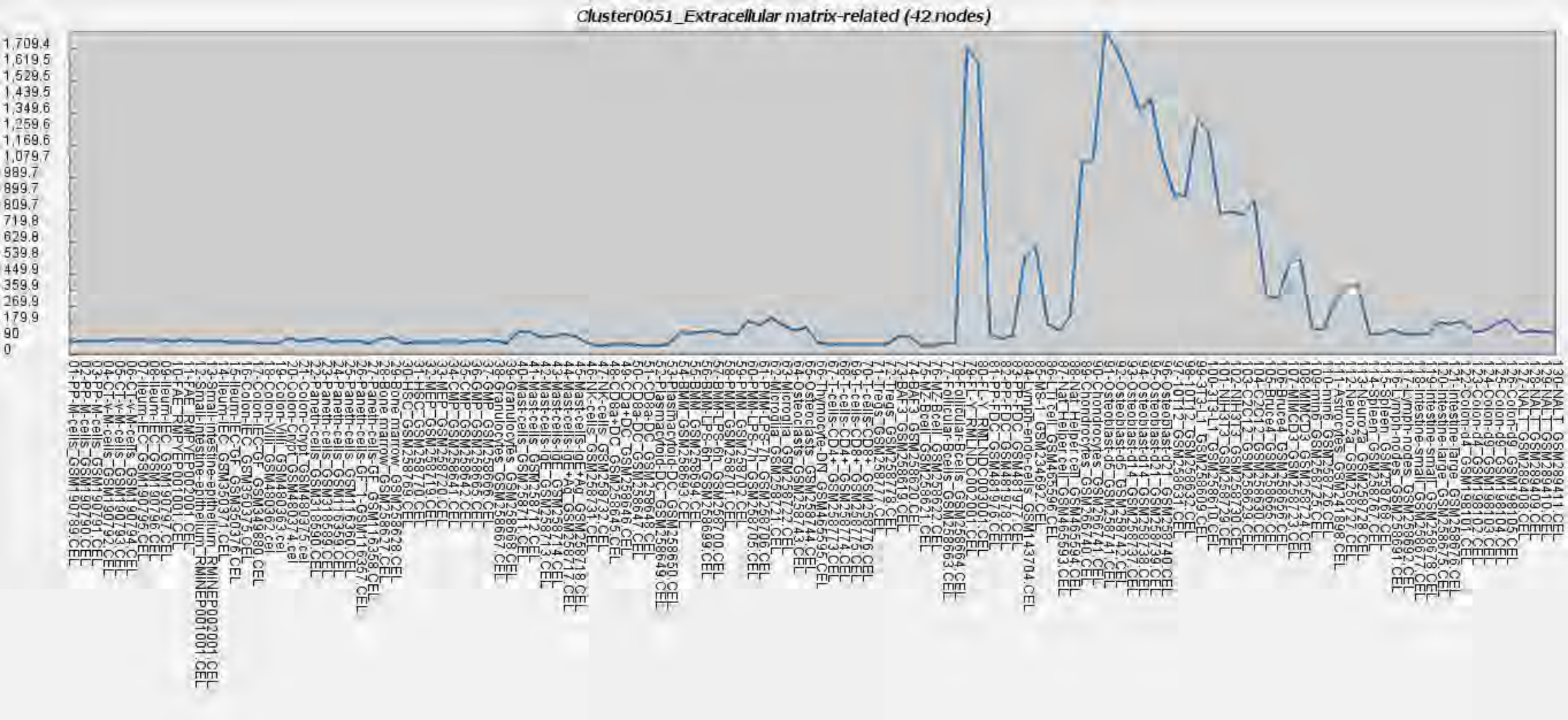

Cluster0046_Chondrocyte & osteoblast-related (53 nodes)
2,057.5
1,949.2
1,840.9
1,732.6
1,624.3
1,516
1,407.7
1,299.4
1,191.2
1,082.9
974.6
866.3
758
649.7
541.4
433.1
324.9
216.6
108.3
0

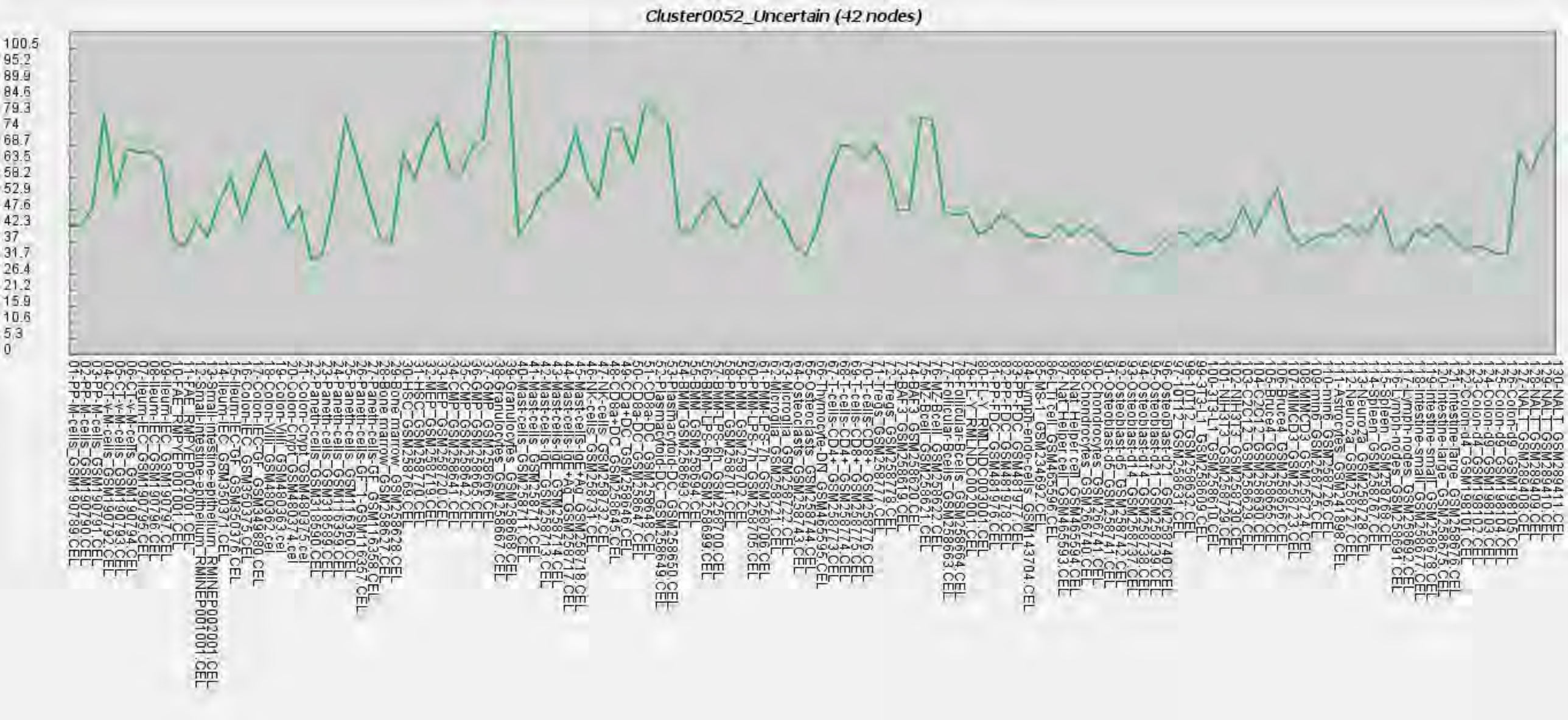

Cluster0047_Low in many (52 nodes)
102.1
96.7
91.3
85.9
80.6
75.2
69.8
64.5
59.1
53.7
48.3
43
37.6
32.2
26.9
21.5
16.1
10.7
5.4
0

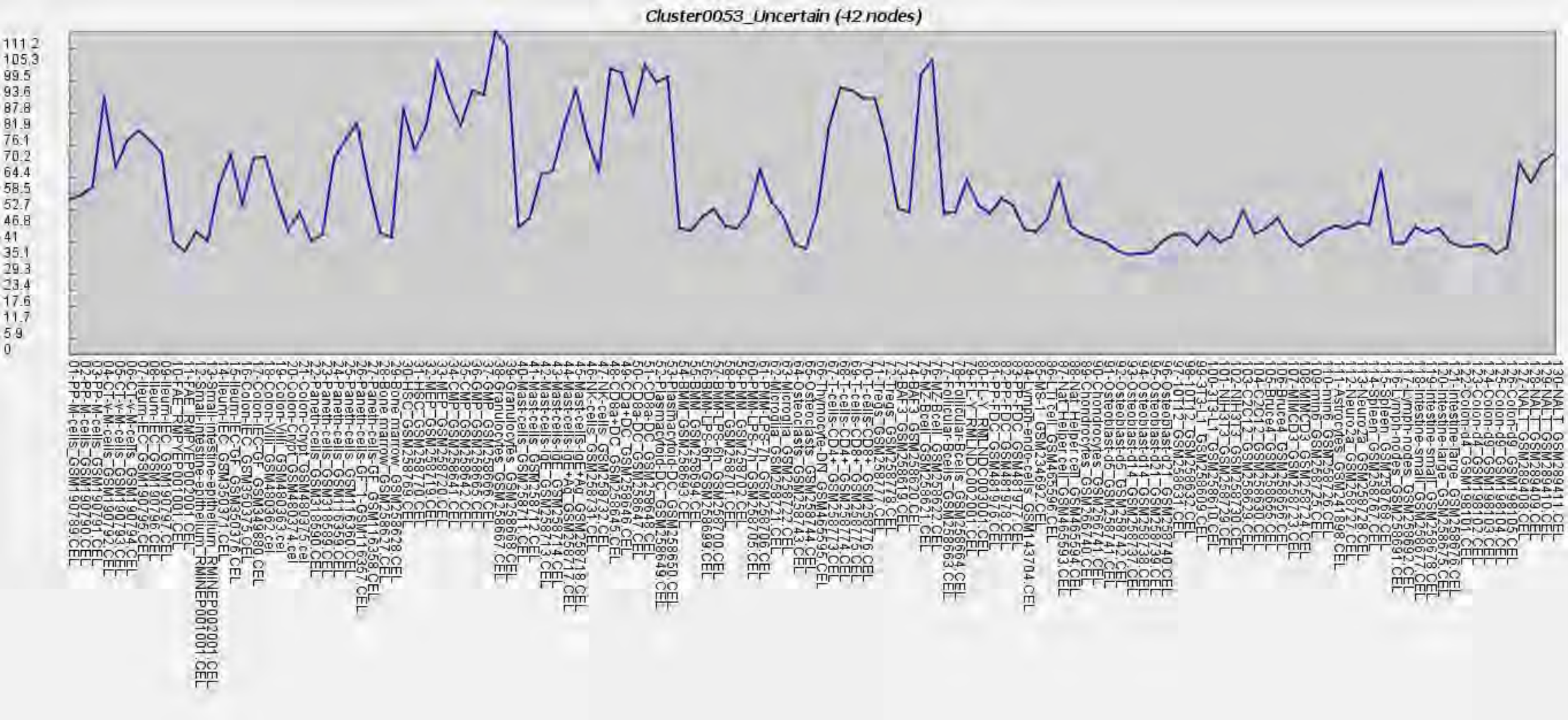
Cluster0048_Thymocyte-related (49 nodes)
1,041.8
987
932.2
877.3
822.5
767.7
712.8
658
603.2
548.3
493.5
438.7
383.8
329
274.2
219.3
164.5
109.7
54.8
0

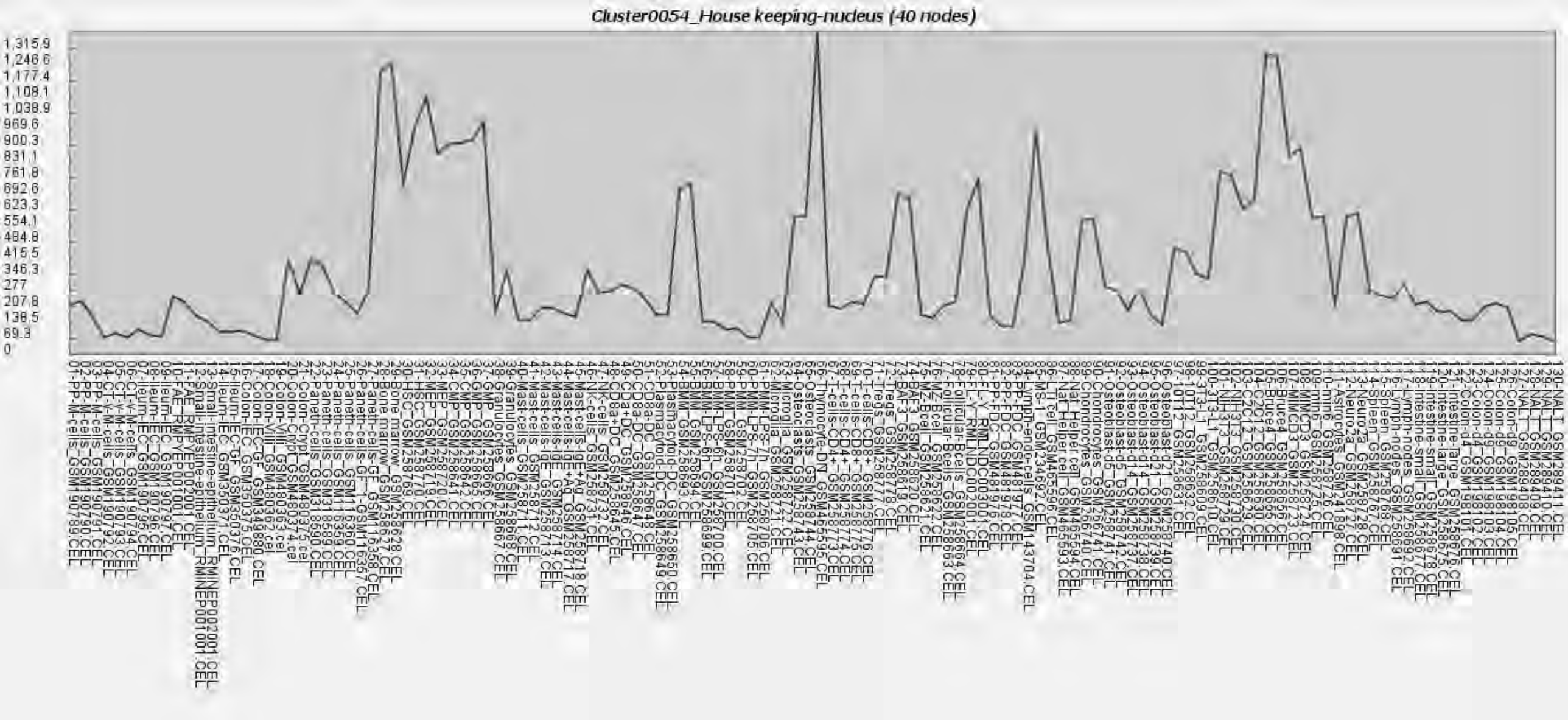

Cluster0049_intestine-related (48 nodes)
2,347.5
2,224
2,100.4
1,976.9
1,853.3
1,729.8
1,606.2
1,482.7
1,359.1
1,235.6
1,112
988.4
864.9
741.3
617.8
494.2
370.7
247.1
123.6
0

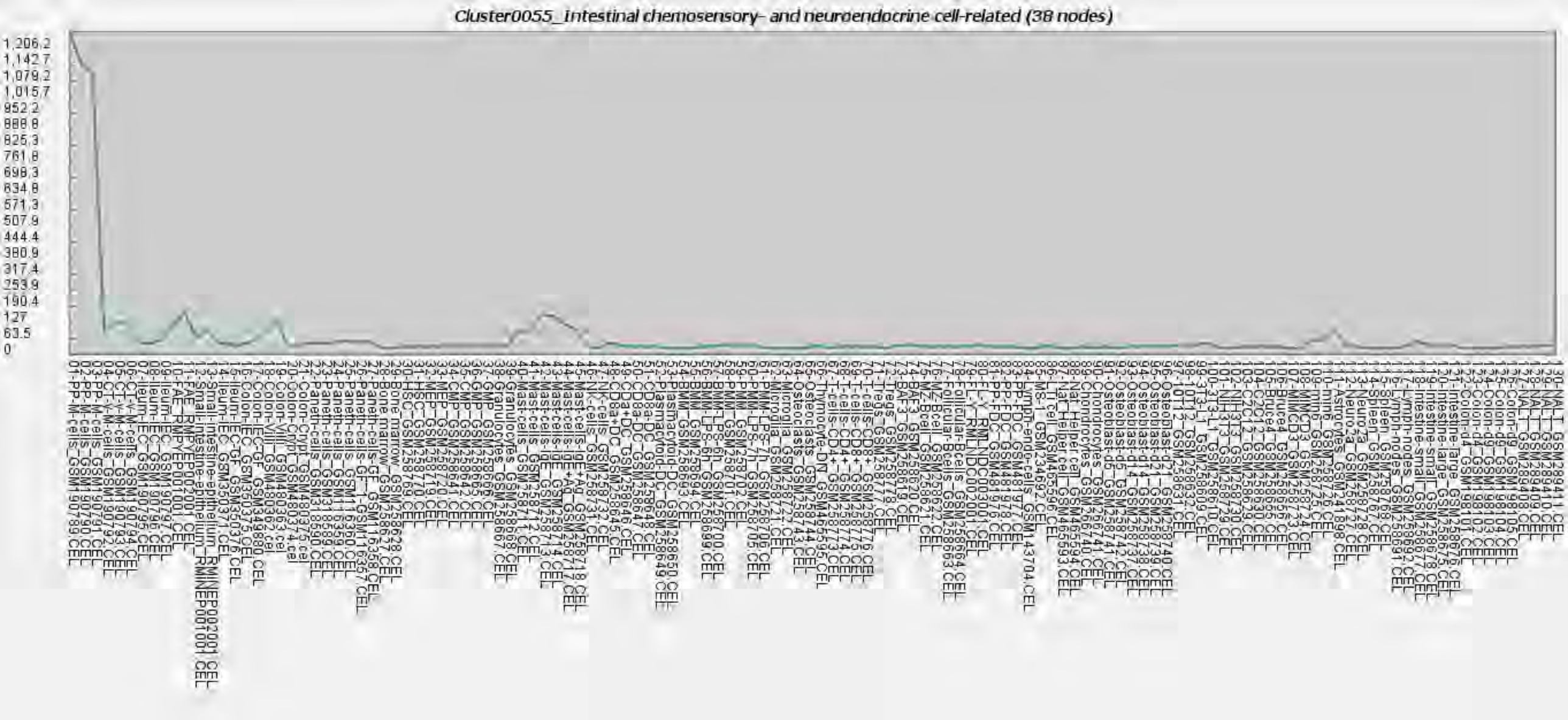

Cluster0050_House keeping-mitochondrion (46 nodes)
4,308.2
4,081.4
3,854.7
3,627.9
3,401.2
3,174.4
2,947.7
2,720.9
2,494.2
2,267.4
2,040.7
1,814
1,587.2
1,360.5
1,133.7
907
680.2
453.5
226.7
0

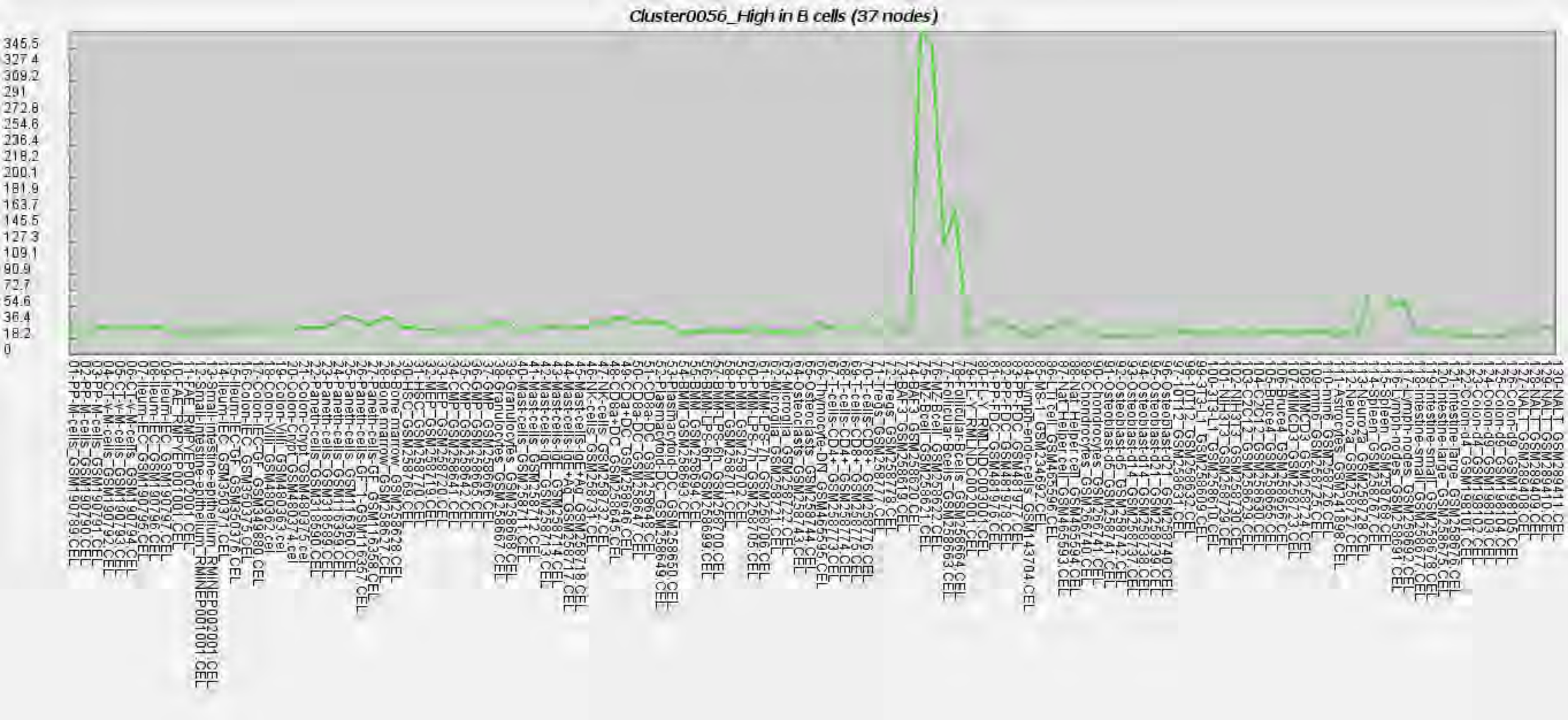

Cluster0051_Extracellular matrix-related (42 nodes)
1,709.4
1,619.5
1,529.5
1,439.5
1,349.6
1,259.6
1,169.6
1,079.7
989.7
899.7
809.7
719.8
629.8
539.8
449.9
359.9
269.9
179.9
90
0

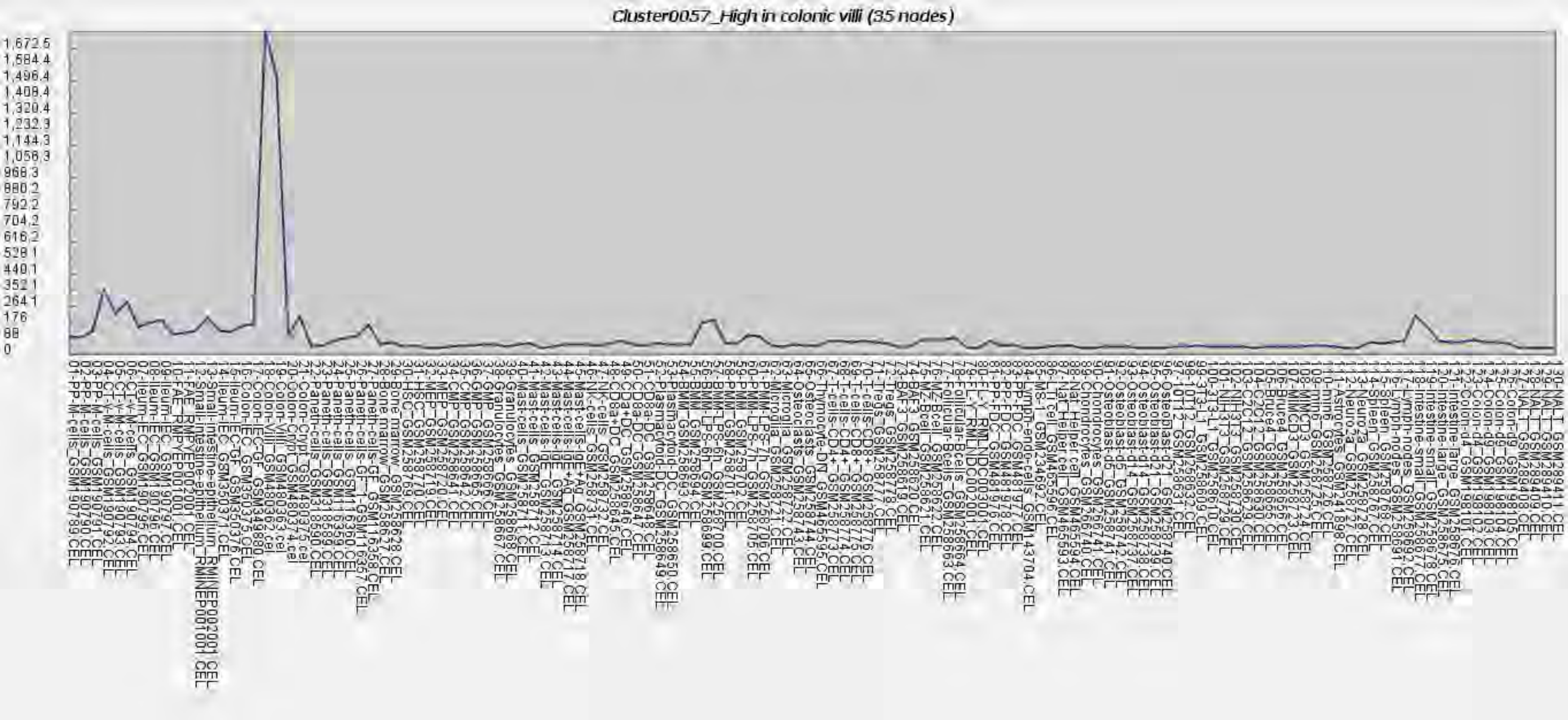

Cluster0052_Uncertain (42 nodes)
100.5
95.2
89.9
84.6
79.3
74
68.7
63.5
58.2
52.9
47.6
42.3
37
31.7
26.4
21.2
15.9
10.6
5.3
0

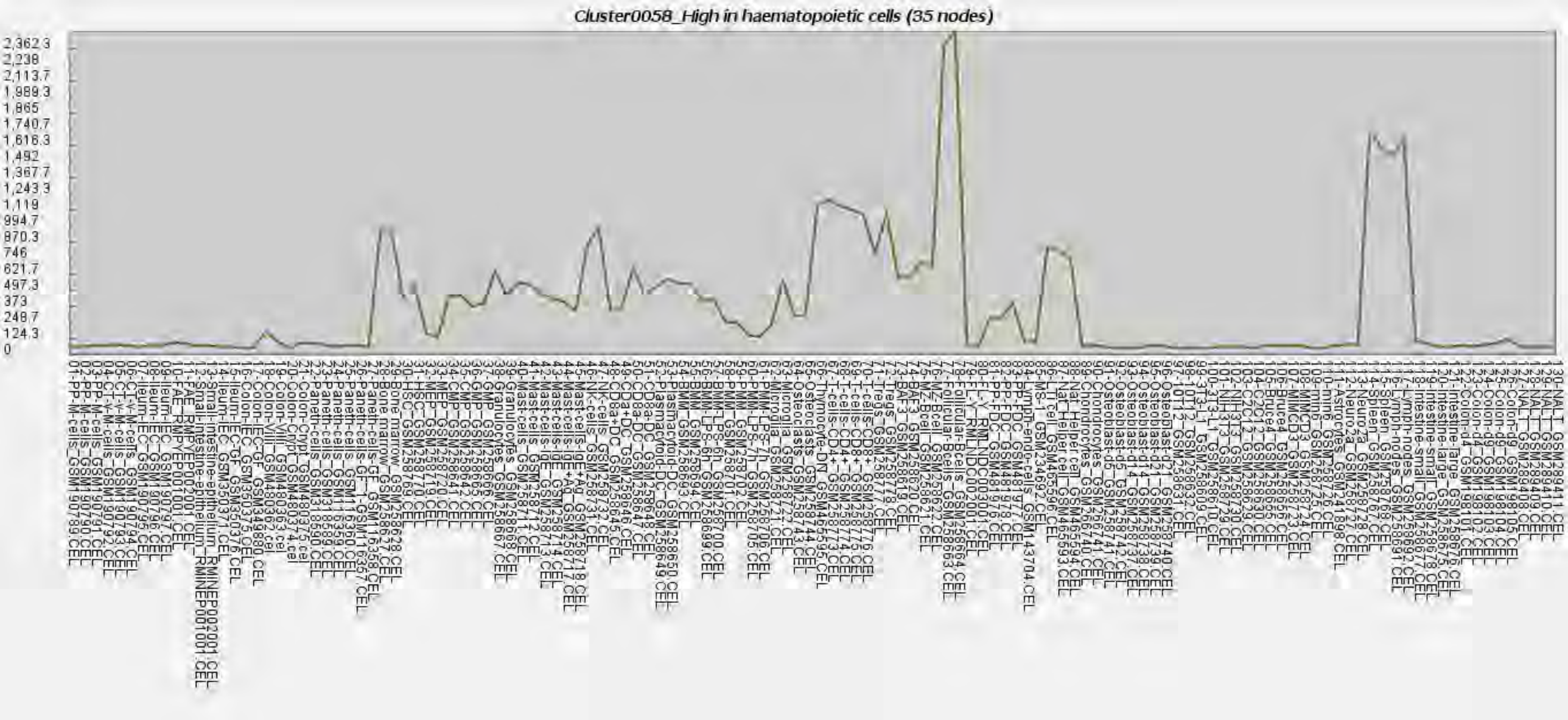

Cluster0053_Uncertain (42 nodes)
111.2
105.3
99.5
93.6
87.8
81.9
76.1
70.2
64.4
58.5
52.7
46.8
41
35.1
29.3
23.4
17.6
11.7
5.9
0


Cluster0054_House keeping-nucleus (40 nodes)
1,315.9
1,246.6
1,177.4
1,108.1
1,038.9
969.6
900.3
831.1
761.8
692.6
623.3
554.1
484.8
415.5
346.3
277
207.8
138.5
69.3
0

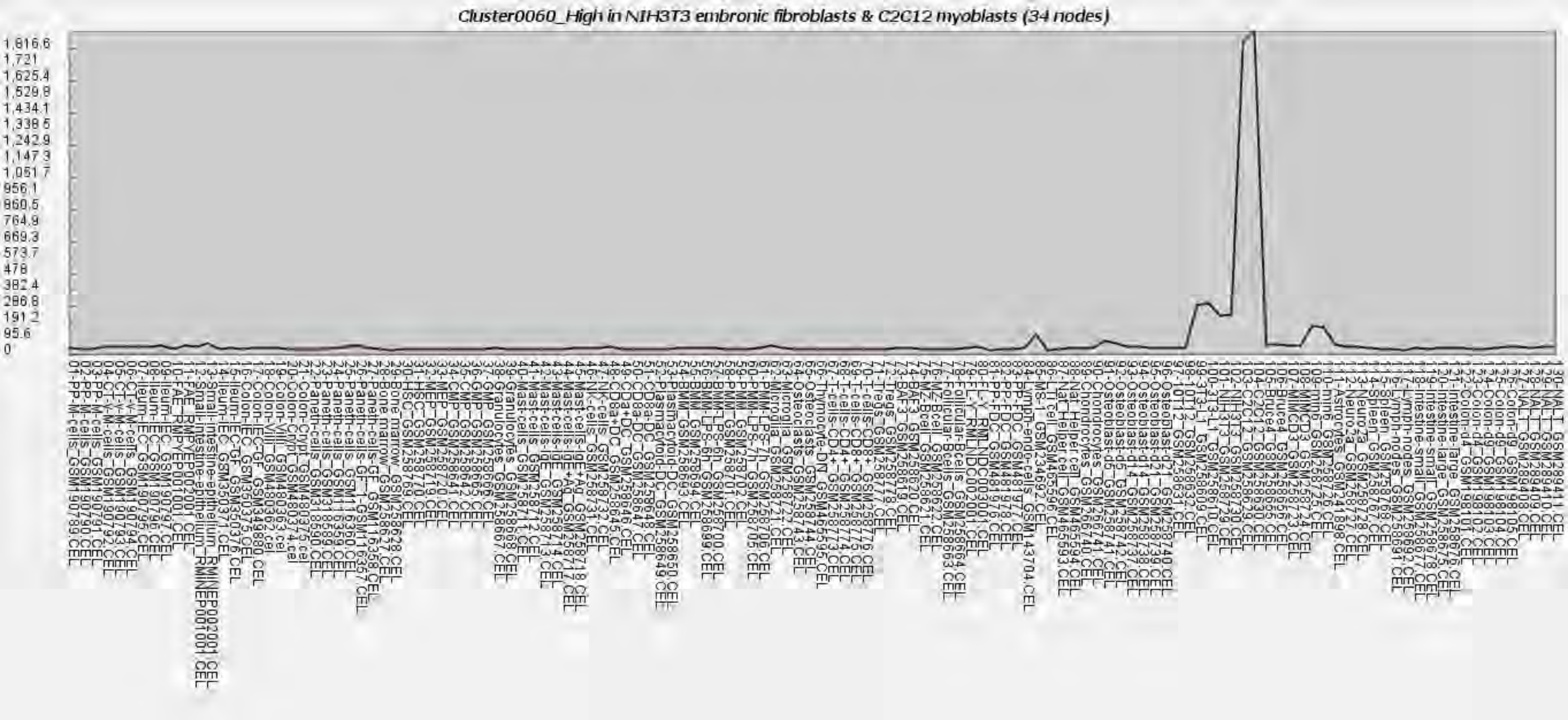

Cluster0055_Intestinal chemosensory- and neuroendocrine cell-related (38 nodes)
1,206.2
1,142.7
1,079.2
1,015.7
952.2
888.8
825.3
761.8
698.3
634.8
571.3
507.9
444.4
380.9
317.4
253.9
190.4
127
63.5
0

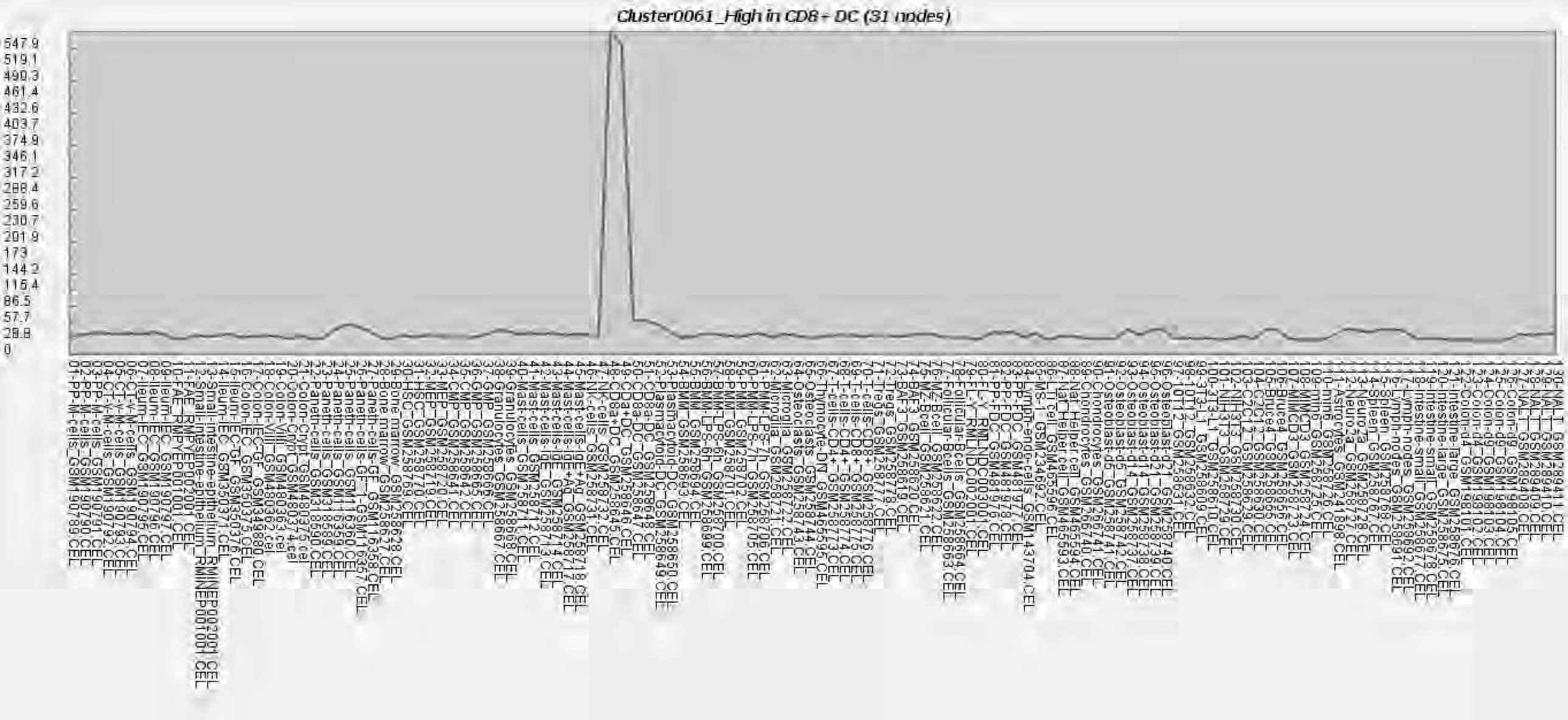

Cluster0056_High in B cells (37 nodes)
345.5
327.4
309.2
291
272.8
254.6
236.4
218.2
200.1
181.9
163.7
145.5
127.3
109.1
90.9
72.7
54.6
36.4
18.2
0

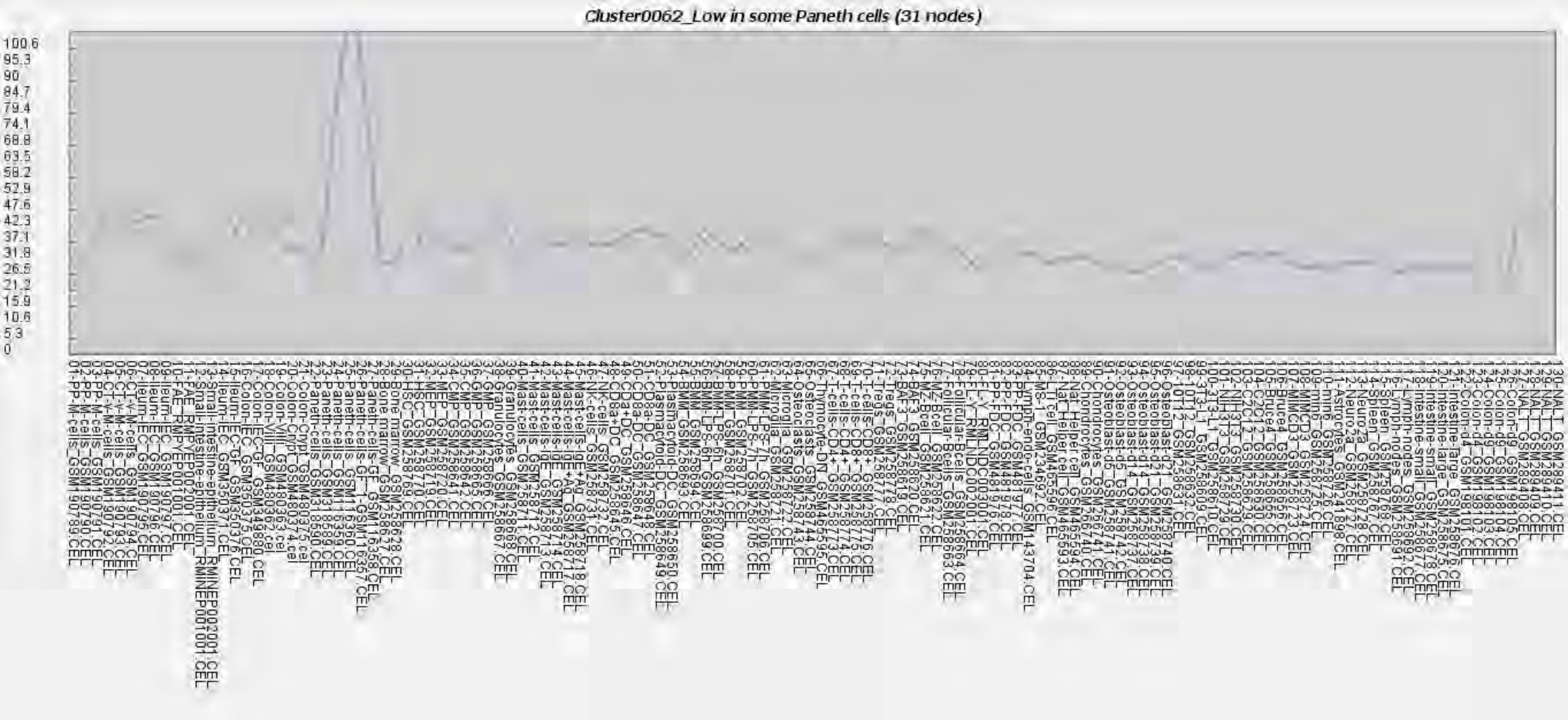

Cluster0057_High in colonic villi (35 nodes)
1,672.5
1,584.4
1,496.4
1,408.4
1,320.4
1,232.3
1,144.3
1,056.3
968.3
880.2
792.2
704.2
616.2
528.1
440.1
352.1
264.1
176
88
0


Cluster0058_High in haematopoietic cells (35 nodes)
2,362.3
2,238
2,113.7
1,989.3
1,865
1,740.7
1,616.3
1,492
1,367.7
1,243.3
1,119
994.7
870.3
746
621.7
497.3
373
248.7
124.3
0

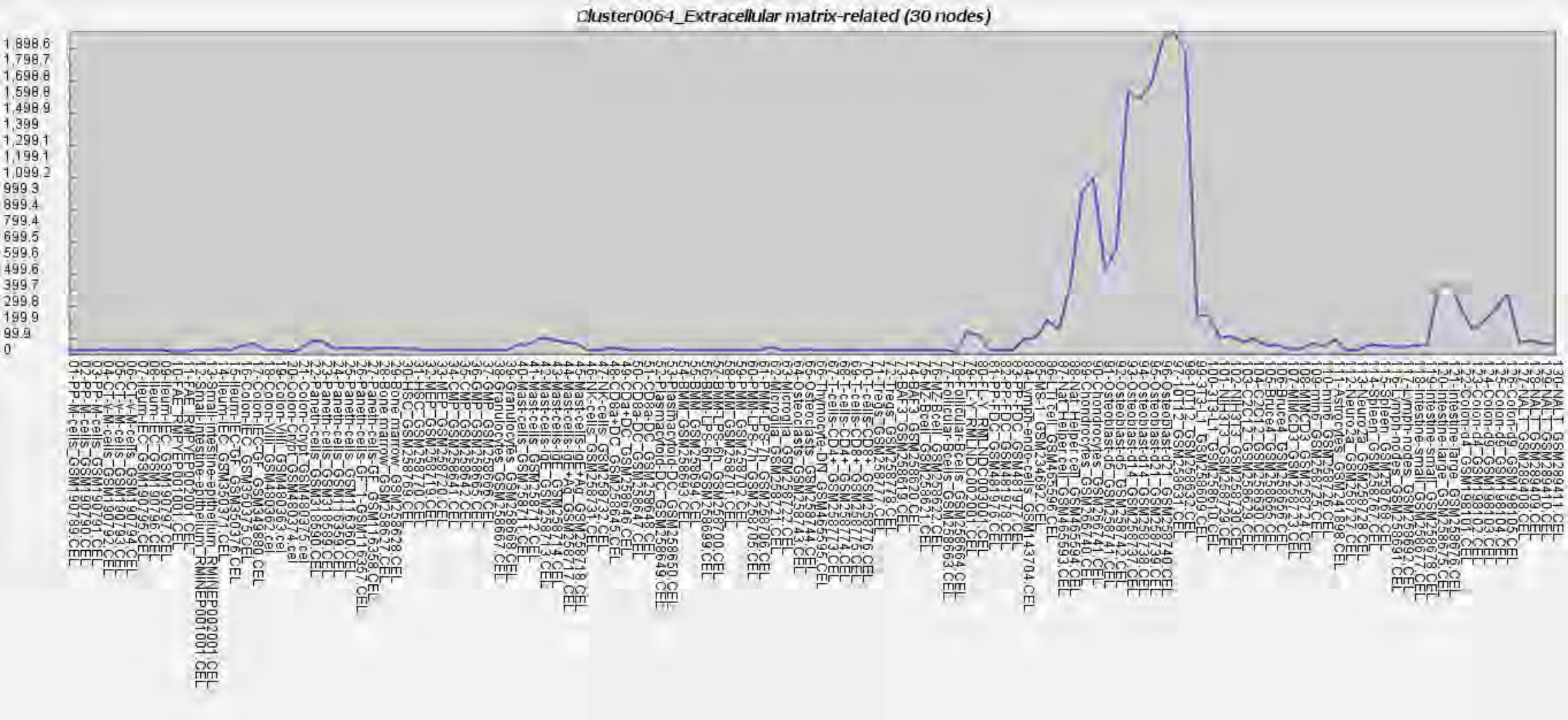
Cluster0059_Large intestine-related (34 nodes)
1,929.9
1,828.3
1,726.7
1,625.1
1,523.6
1,422
1,320.4
1,218.9
1,117.3
1,015.7
914.1
812.6
711
609.4
507.9
406.3
304.7
203.1
101.6
0


Cluster0060_High in NIH3T3 embronic fibroblasts & C2C12 myoblasts (34 nodes)
1,816.6
1,721
1,625.4
1,529.8
1,434.1
1,338.5
1,242.9
1,147.3
1,051.7
956.1
860.5
764.9
669.3
573.7
478
382.4
286.8
191.2
95.6
0

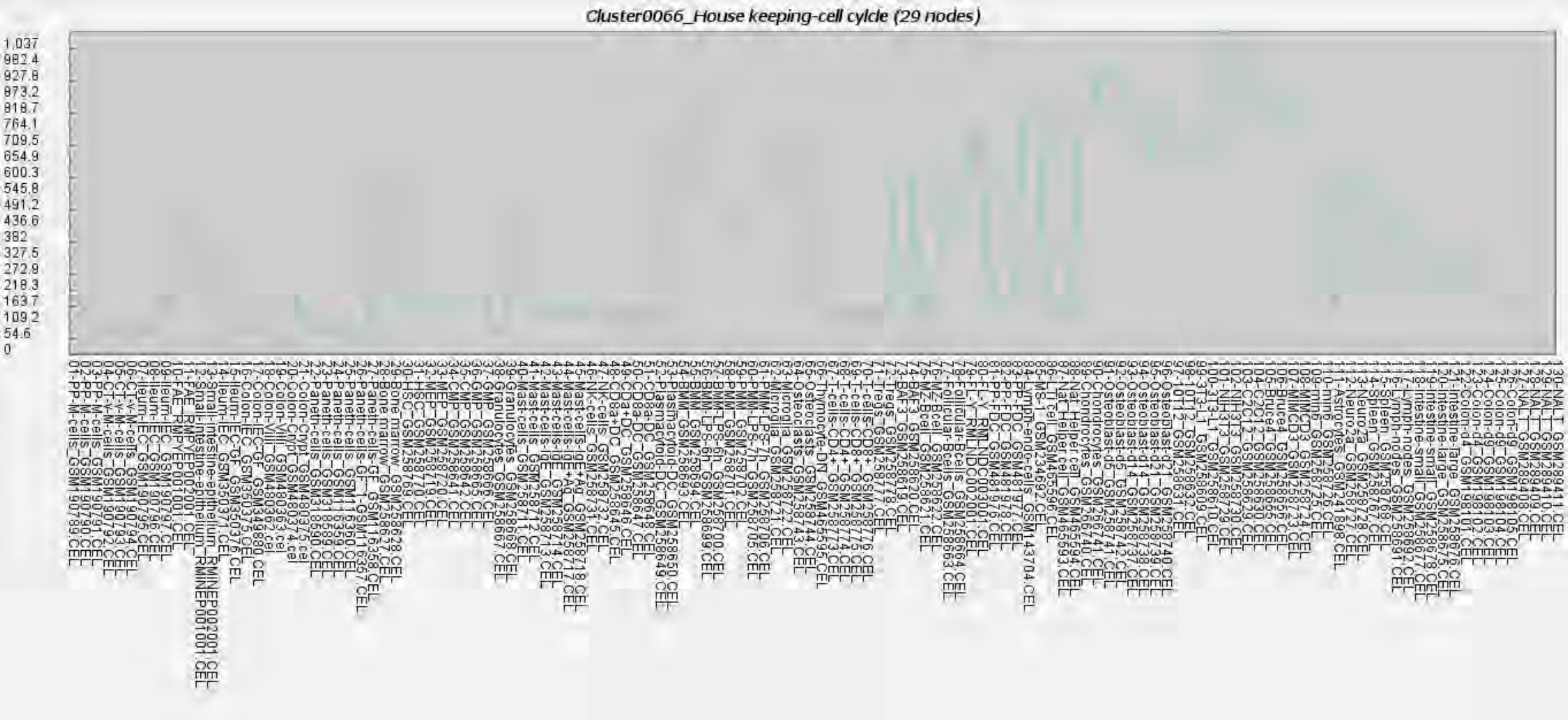

Cluster0061_High in CD8+ DC (31 nodes)
647.9
519.1
490.3
461.4
432.6
403.7
374.9
346.1
317.2
288.4
259.6
230.7
201.9
173
144.2
115.4
86.5
57.7
28.8
0


Cluster0062_Low in some Paneth cells (31 nodes)
100.6
95.3
90
84.7
79.4
74.1
68.8
63.5
58.2
52.9
47.6
42.3
37.1
31.8
26.5
21.2
15.9
10.6
5.3
0

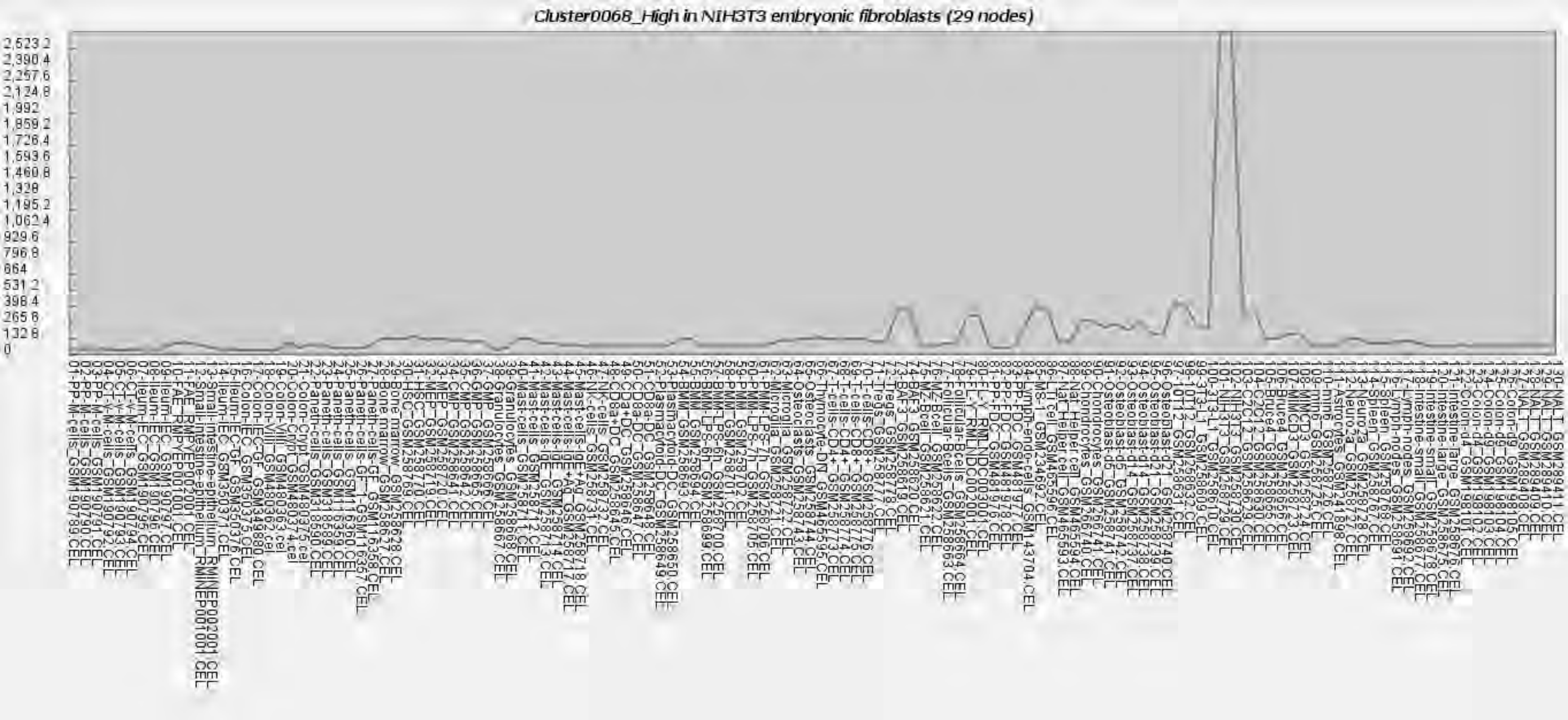
Cluster0063_Lymph node-related (30 nodes)
3,428.2
3,247.8
3,067.3
2,886.9
2,706.5
2,526.1
2,345.6
2,165.2
1,984.8
1,804.3
1,623.9
1,443.5
1,263
1,082.6
902.2
721.7
541.3
360.9
180.4
0


Cluster0064_Extracellular matrix-related (30 nodes)
1,898.6
1,798.7
1,698.8
1,598.8
1,498.9
1,399
1,299.1
1,199.1
1,099.2
999.3
899.4
799.4
699.5
599.6
499.6
399.7
299.8
199.9
99.9
0

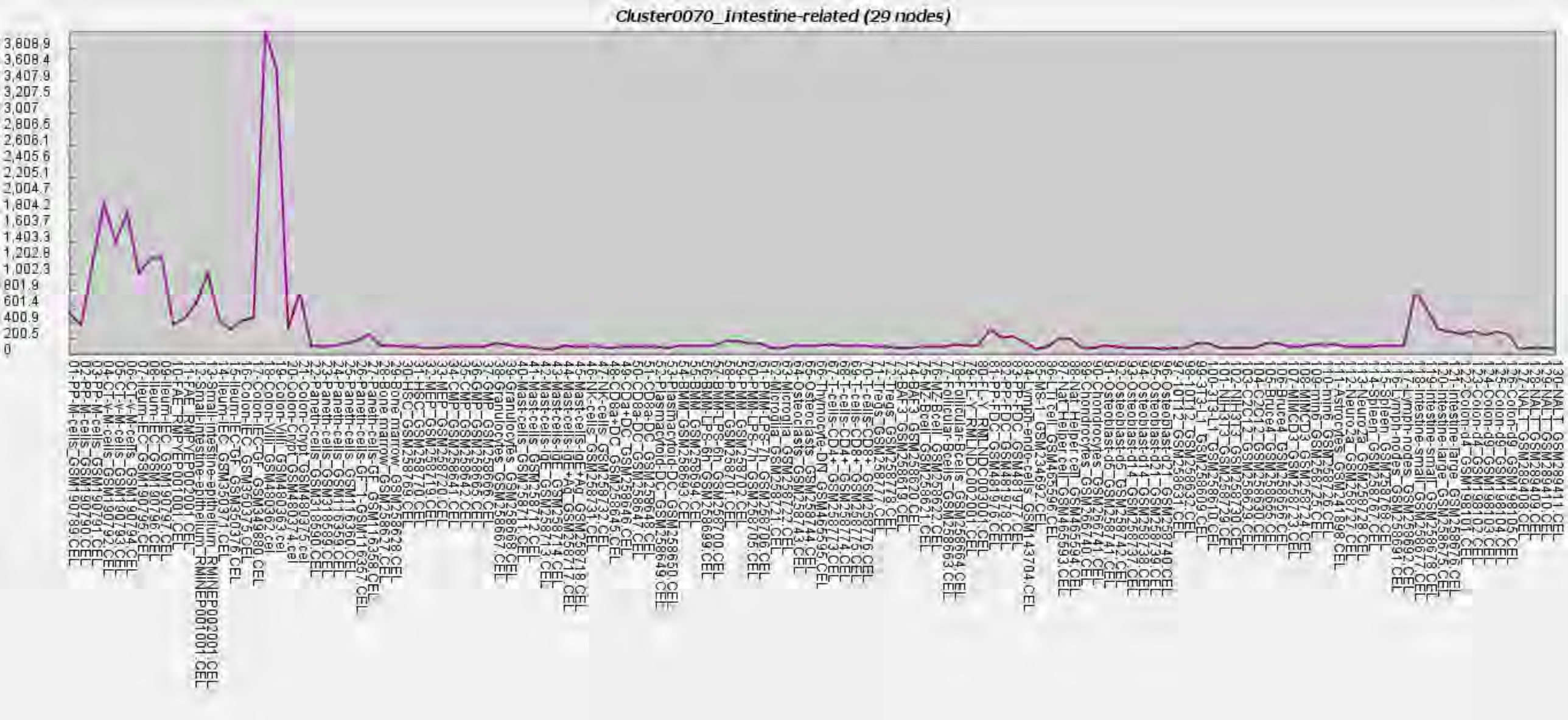
Cluster0065_FAE- and Peyer's patch M cell-related (29 nodes)
1,304.1
1,235.5
1,166.9
1,098.2
1,029.6
960.9
892.3
823.7
755
686.4
617.8
549.1
480.5
411.8
343.2
274.6
205.9
137.3
68.6
0

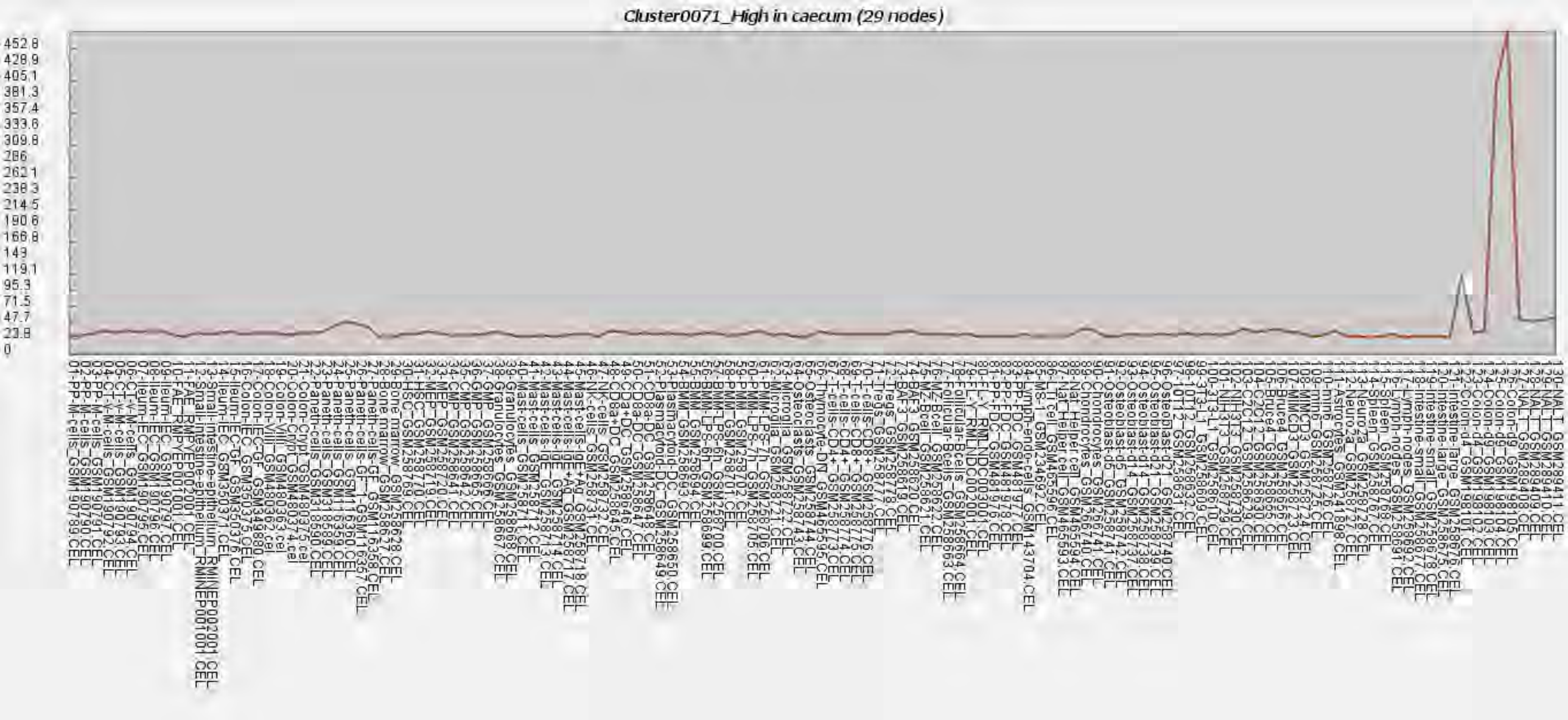

Cluster0066_House keeping-cell cylcle (29 nodes)
1,037
982.4
927.8
873.2
818.7
764.1
709.5
654.9
600.3
545.8
491.2
436.6
382
327.5
272.9
218.3
163.7
109.2
54.6
0

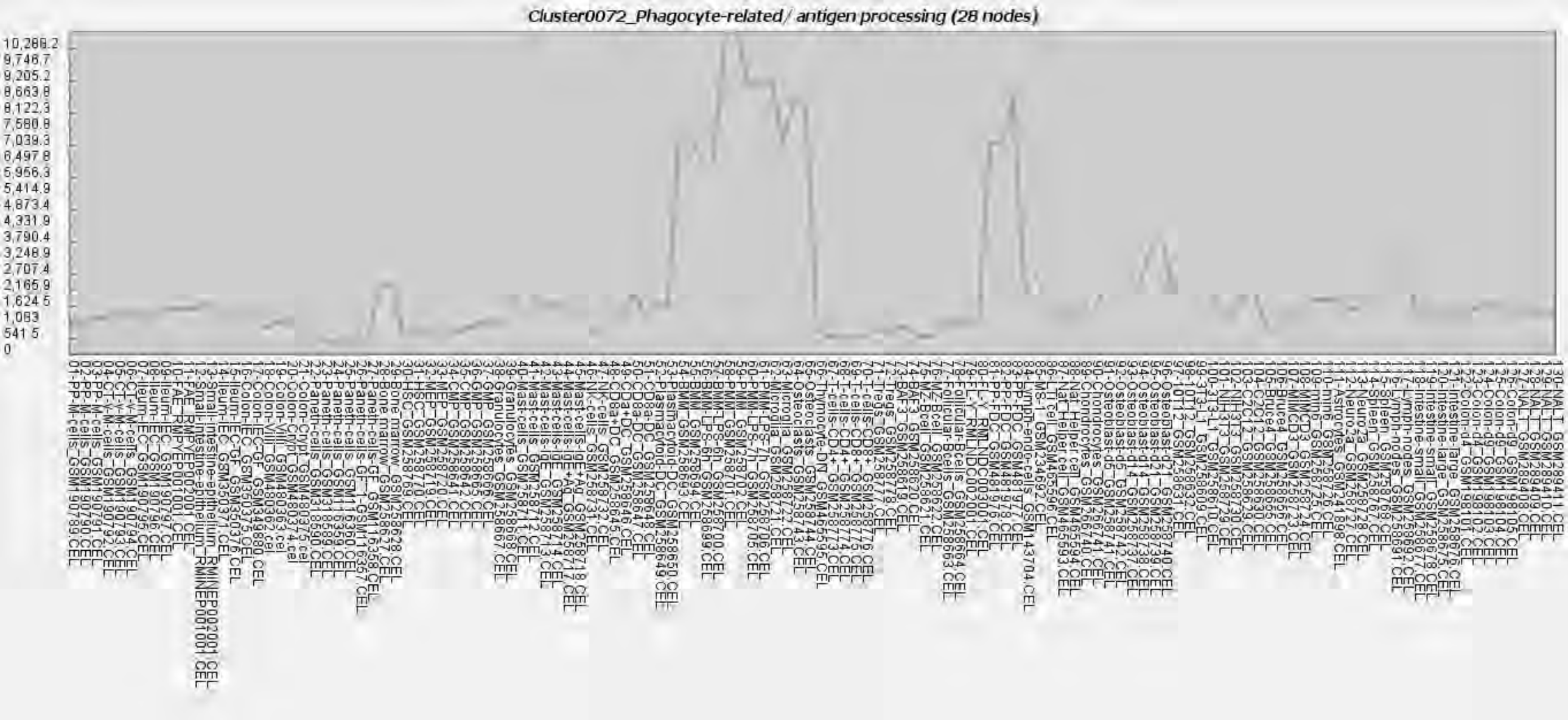
Cluster0067_Chondrocyte and osteoblast-related (29 nodes)
3,669.5
3,476.4
3,283.3
3,090.1
2,897
2,703.9
2,510.7
2,317.6
2,124.5
1,931.3
1,738.2
1,545.1
1,351.9
1,158.8
965.7
772.5
579.4
386.3
193.1
0

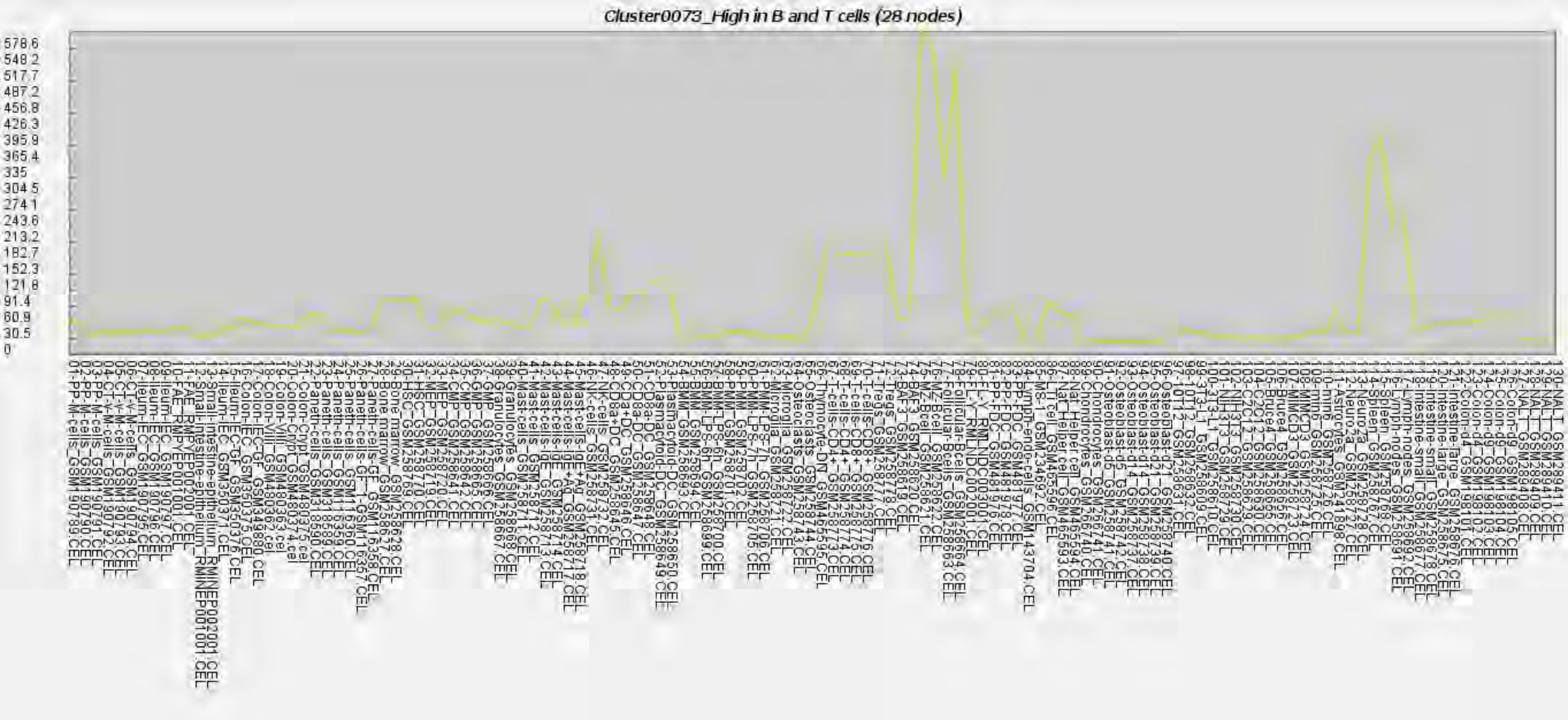

Cluster0068_High in NIH3T3 embryonic fibroblasts (29 nodes)
2,523.2
2,390.4
2,257.6
2,124.8
1,992
1,859.2
1,726.4
1,593.6
1,460.8
1,328
1,195.2
1,062.4
929.6
796.8
664
531.2
398.4
265.6
132.8
0

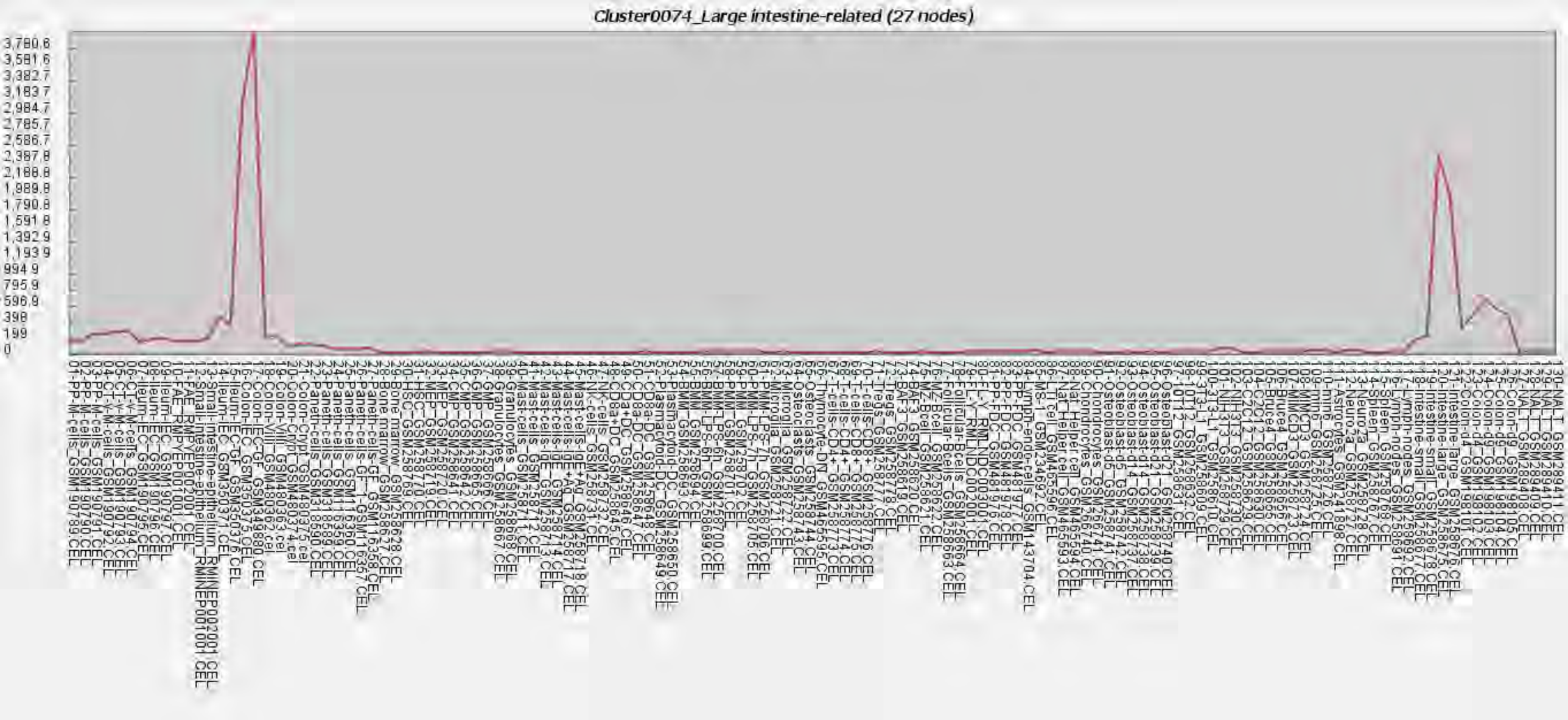
Cluster0069_Osteoblast-related (29 nodes)
792.3
750.6
708.9
667.2
625.5
583.8
542.1
500.4
458.7
417
375.3
333.6
291.9
250.2
208.5
166.8
125.1
83.4
41.7
0

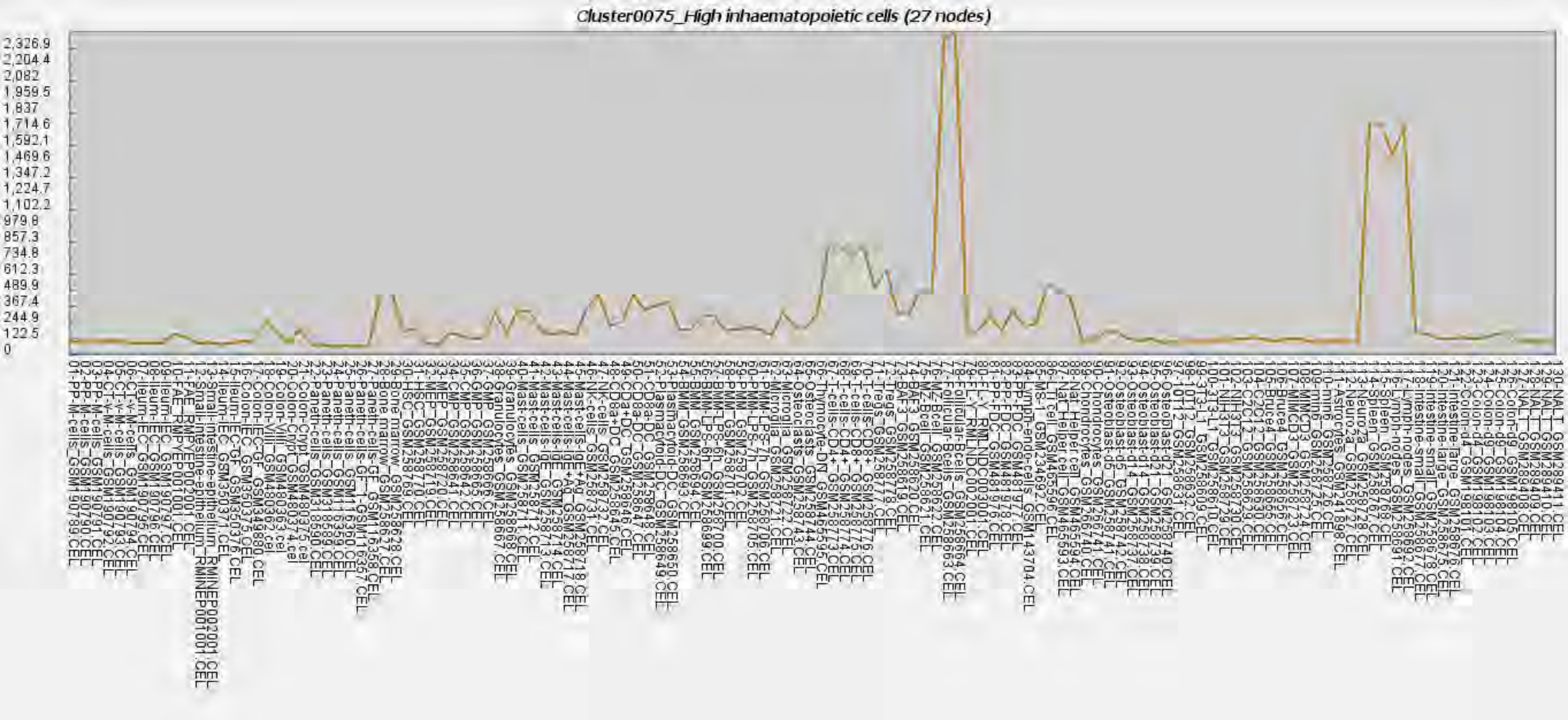

Cluster0070_intestine-related (29 nodes)
3,808.9
3,608.4
3,407.9
3,207.5
3,007
2,806.5
2,606.1
2,405.6
2,205.1
2,004.7
1,804.2
1,603.7
1,403.3
1,202.8
1,002.3
801.9
601.4
400.9
200.5
0


Cluster0071_High in caecum (29 nodes)
452.8
428.9
405.1
381.3
357.4
333.6
309.8
286
262.1
238.3
214.5
190.6
166.8
143
119.1
95.3
71.5
47.7
23.8
0

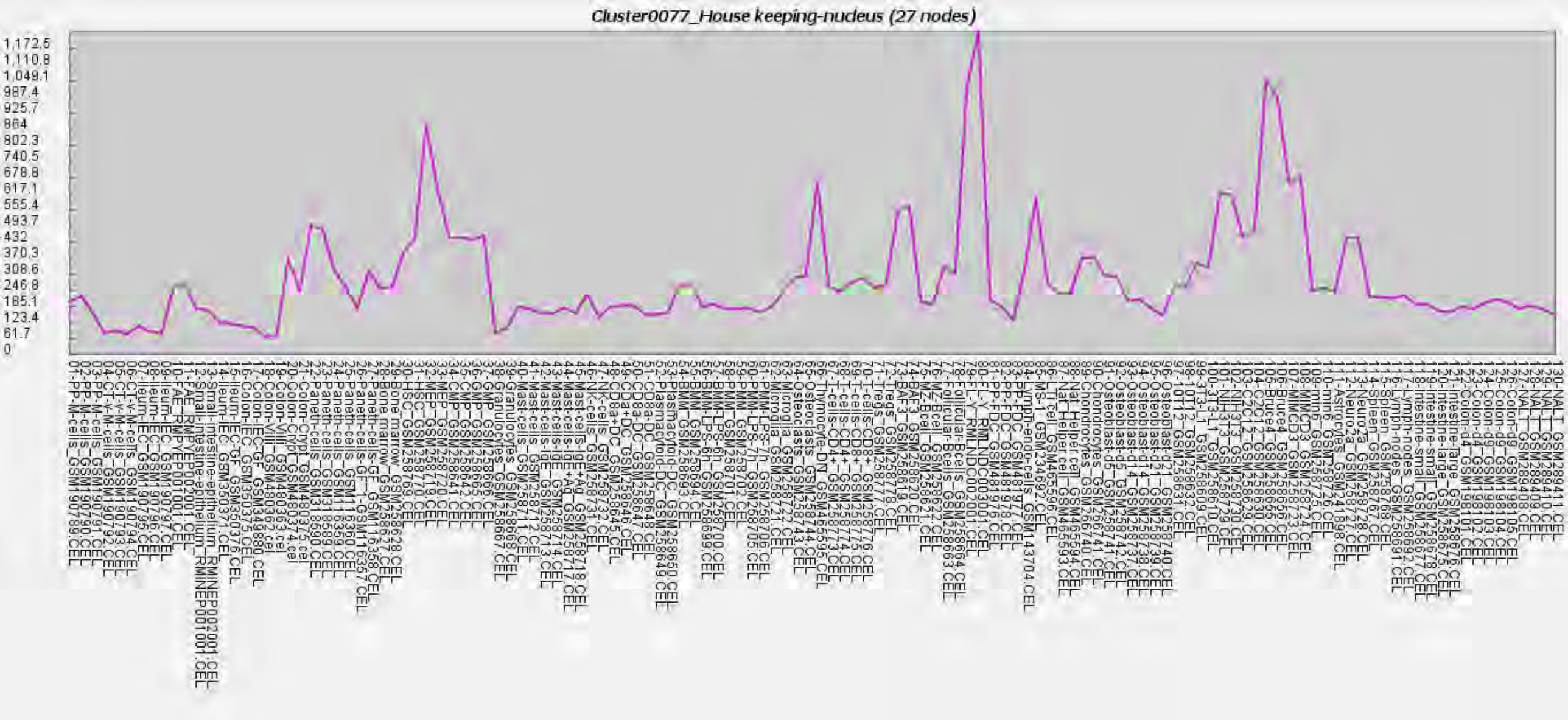

Cluster0072_Phagocyte-related / antigen processing (28 nodes)
10,288.2
9,746.7
9,205.2
8,663.8
8,122.3
7,580.8
7,039.3
6,497.8
5,956.3
5,414.9
4,873.4
4,331.9
3,790.4
3,248.9
2,707.4
2,165.9
1,624.5
1,083
541.5
0

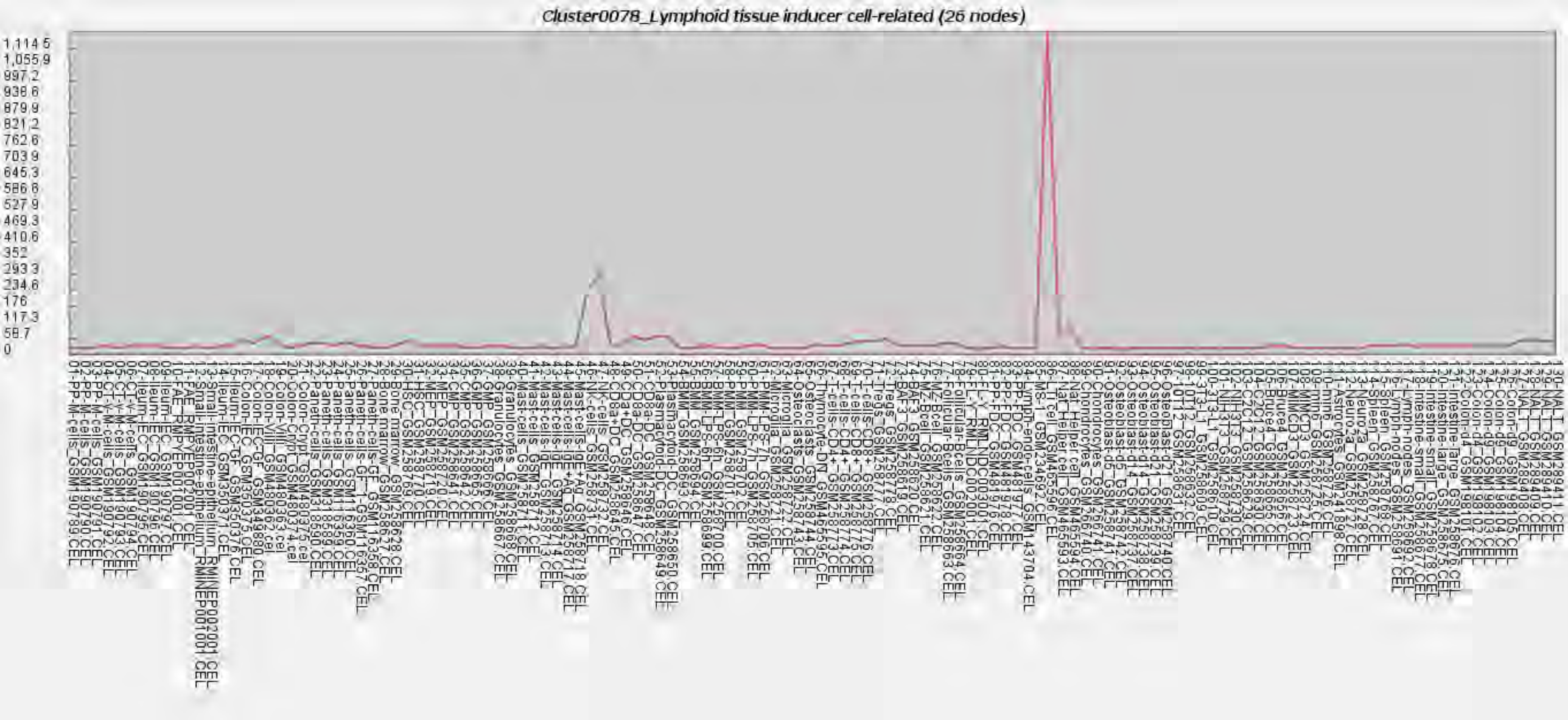

Cluster0073_High in B and T cells (28 nodes)
578.6
548.2
517.7
487.2
456.8
426.3
395.9
365.4
335
304.5
274.1
243.6
213.2
182.7
152.3
121.8
91.4
60.9
30.5
0


Cluster0074_Large intestine-related (27 nodes)
3,780.6
3,581.6
3,382.7
3,183.7
2,984.7
2,785.7
2,586.7
2,387.8
2,188.8
1,989.8
1,790.8
1,591.8
1,392.9
1,193.9
994.9
795.9
596.9
398
199
0


Cluster0075_High inhaematopoietic cells (27 nodes)
2,326.9
2,204.4
2,082
1,959.5
1,837
1,714.6
1,592.1
1,469.6
1,347.2
1,224.7
1,102.2
979.8
857.3
734.8
612.3
489.9
367.4
244.9
122.5
0

Cluster0076_House keeping-cell cycle (27 nodes)
2,018.4
1,912.1
1,805.9
1,699.7
1,593.5
1,487.2
1,381
1,274.8
1,168.5
1,062.3
956.1
849.8
743.6
637.4
531.2
424.9
318.7
212.5
106.2
0


Cluster0077_House keeping-nucleus (27 nodes)
1,172.5
1,110.8
1,049.1
987.4
925.7
864
802.3
740.5
678.8
617.1
555.4
493.7
432
370.3
308.6
246.8
185.1
123.4
61.7
0


Cluster0078_Lymphoid tissue inducer cell-related (26 nodes)
1,114.5
1,055.9
997.2
938.6
879.9
821.2
762.6
703.9
645.3
586.6
527.9
469.3
410.6
352
293.3
234.6
176
117.3
58.7
0

Cluster0079_House keeping-mitochondrion (26 nodes)

6,900.6
6,537.4
6,174.2
5,811
5,447.8
5,084.6
4,721.5
4,358.3
3,995.1
3,631.9
3,268.7
2,905.5
2,542.3
2,179.1
1,815.9
1,452.8
1,089.6
726.4
363.2
0

GSM2289411_CEL
GSM2289410_CEL
GSM2289409_CEL
GSM1981108_CEL
GSM1981107_CEL
GSM2586676_CEL
GSM2586675_CEL
GSM2586674_CEL
GSM2586673_CEL
GSM2586672_CEL
GSM2586671_CEL
GSM1981105_CEL
GSM1981104_CEL
GSM1981103_CEL
GSM1981102_CEL
GSM1981101_CEL
GSM2586669_CEL
GSM2586668_CEL
GSM2586667_CEL
GSM2586666_CEL
GSM2586665_CEL
GSM2586664_CEL
GSM2586663_CEL
GSM2586662_CEL
GSM2586661_CEL
GSM2586660_CEL
GSM2586659_CEL
GSM2586658_CEL
GSM2586657_CEL
GSM2586656_CEL
GSM2586655_CEL
GSM2586654_CEL
GSM2586653_CEL
GSM2586652_CEL
GSM2586651_CEL
GSM2586650_CEL
GSM2586649_CEL
GSM2586648_CEL
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GSM2586645_CEL
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GSM2586643_CEL
GSM2586642_CEL
GSM2586641_CEL
GSM2586640_CEL
GSM2586639_CEL
GSM2586638_CEL
GSM2586637_CEL
GSM2586636_CEL
GSM2586635_CEL
GSM2586634_CEL
GSM2586633_CEL
GSM2586632_CEL
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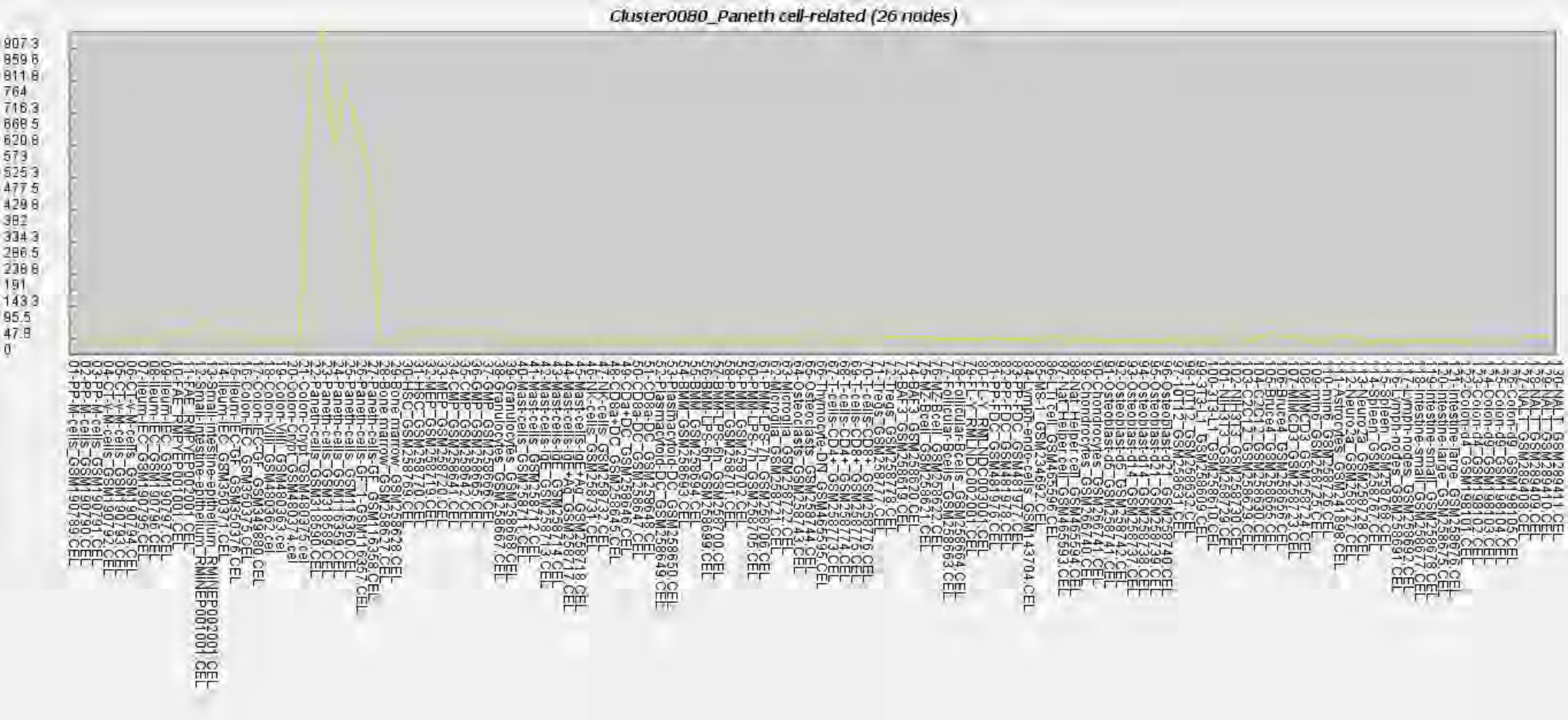
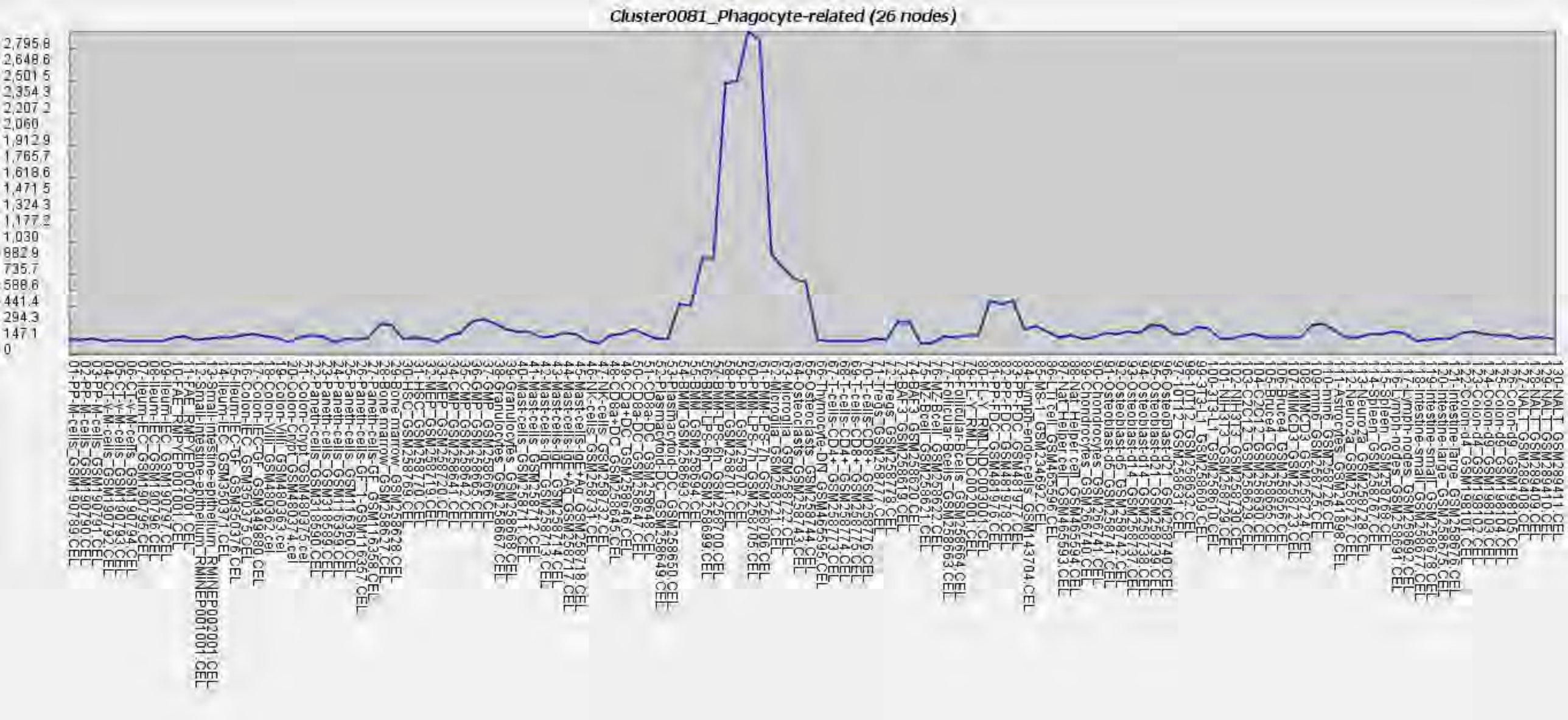
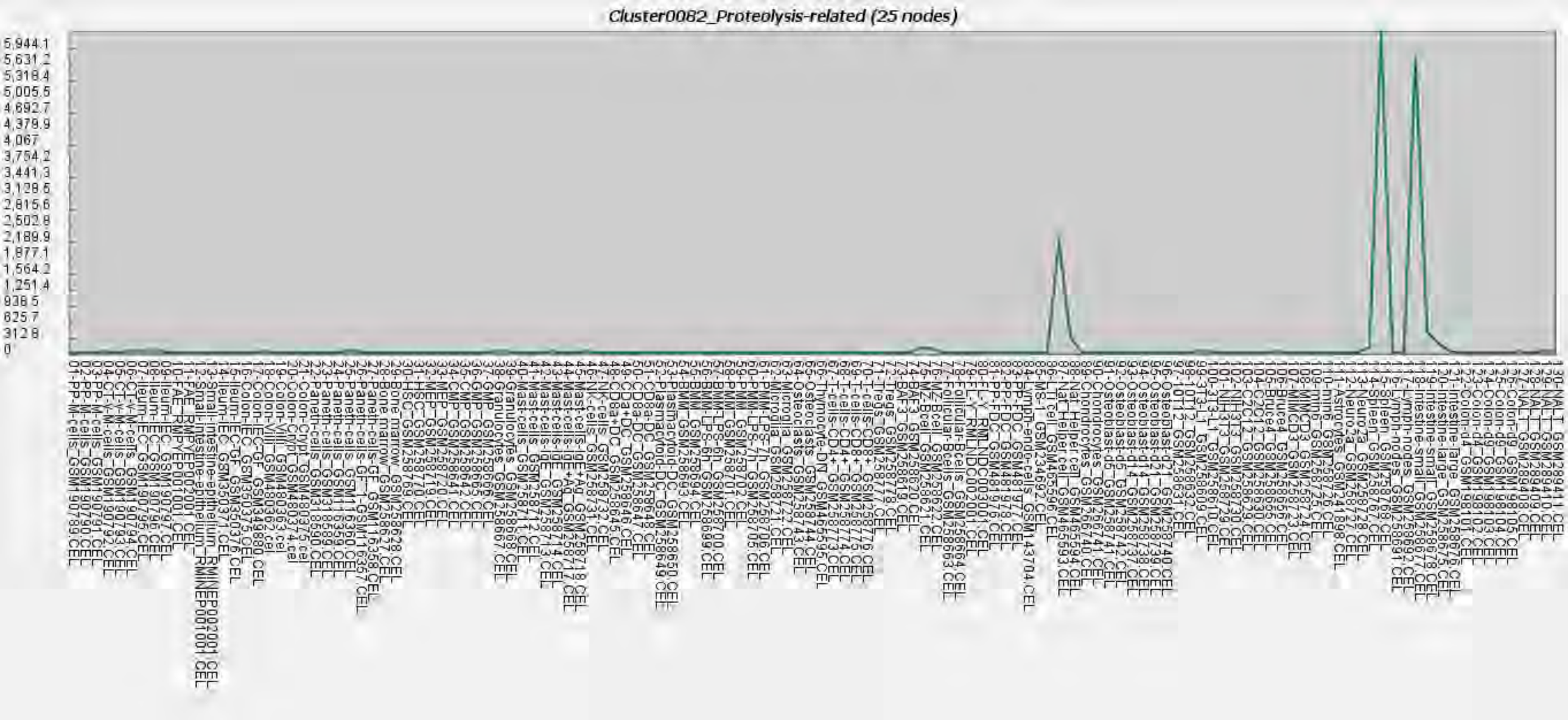
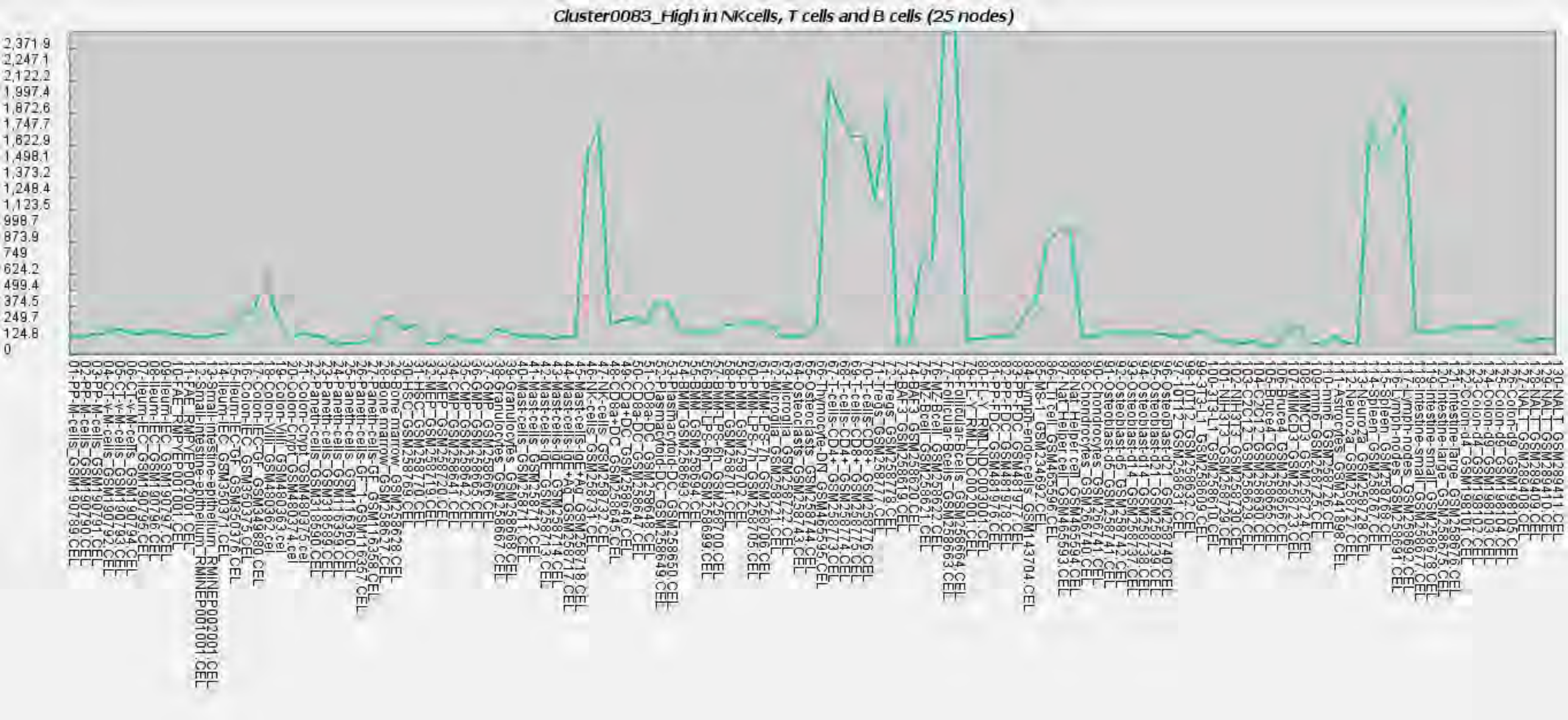
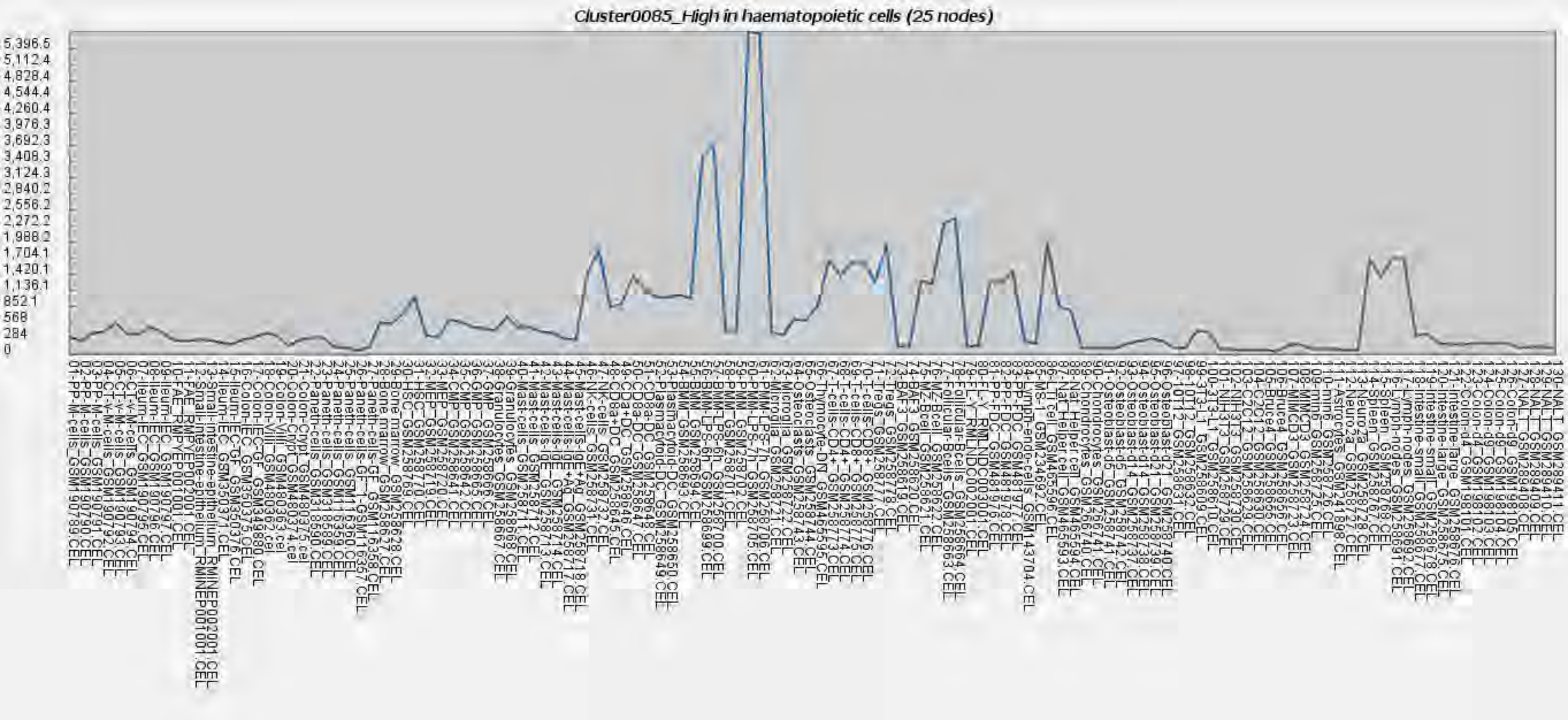

Cluster0080_Paneth cell-related (26 nodes)
907.3
859.6
811.8
764
716.3
668.5
620.8
573
525.3
477.5
429.8
382
334.3
286.5
238.8
191
143.3
95.5
47.8
0

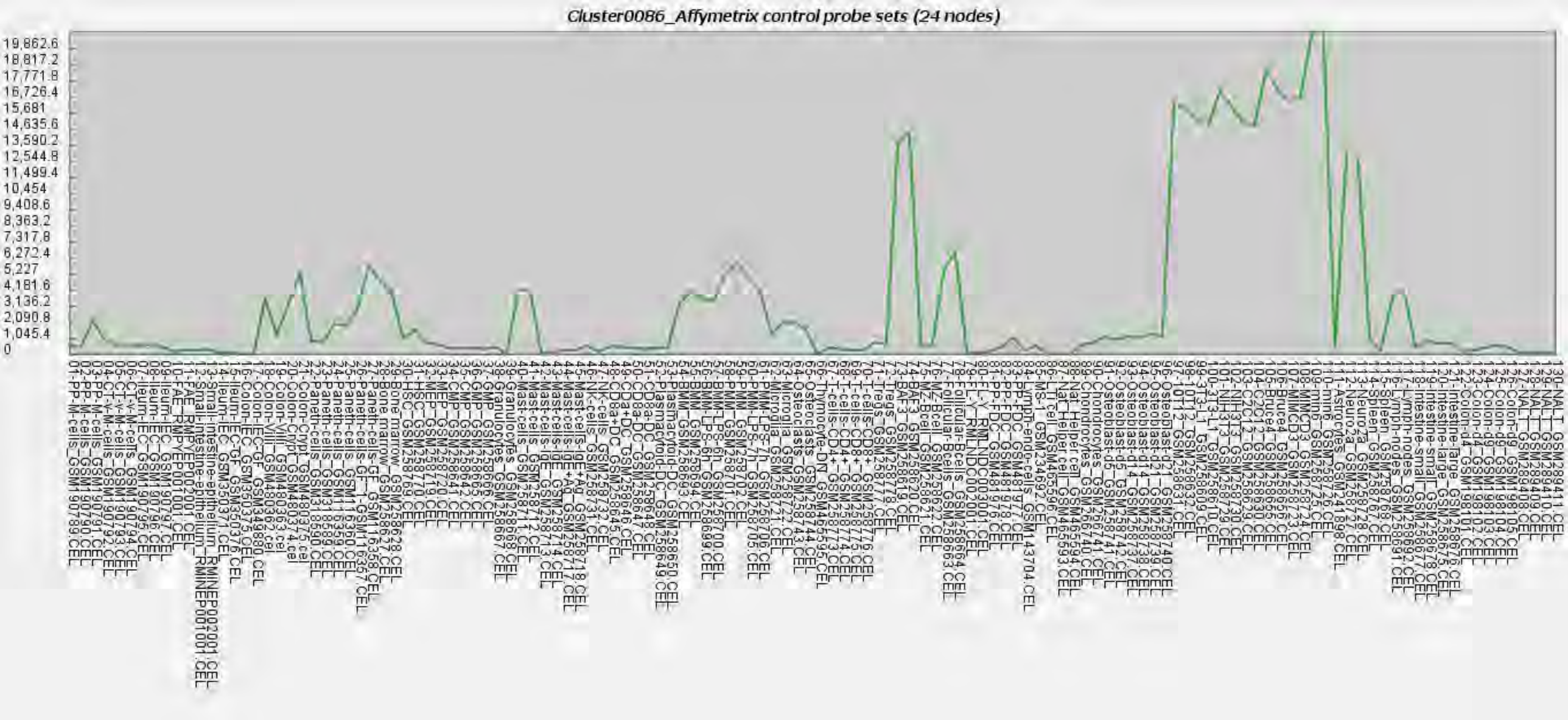

Cluster0081_Phagocyte-related (26 nodes)
2,795.8
2,648.6
2,501.5
2,354.3
2,207.2
2,060
1,912.9
1,765.7
1,618.6
1,471.5
1,324.3
1,177.2
1,030
882.9
735.7
588.6
441.4
294.3
147.1
0

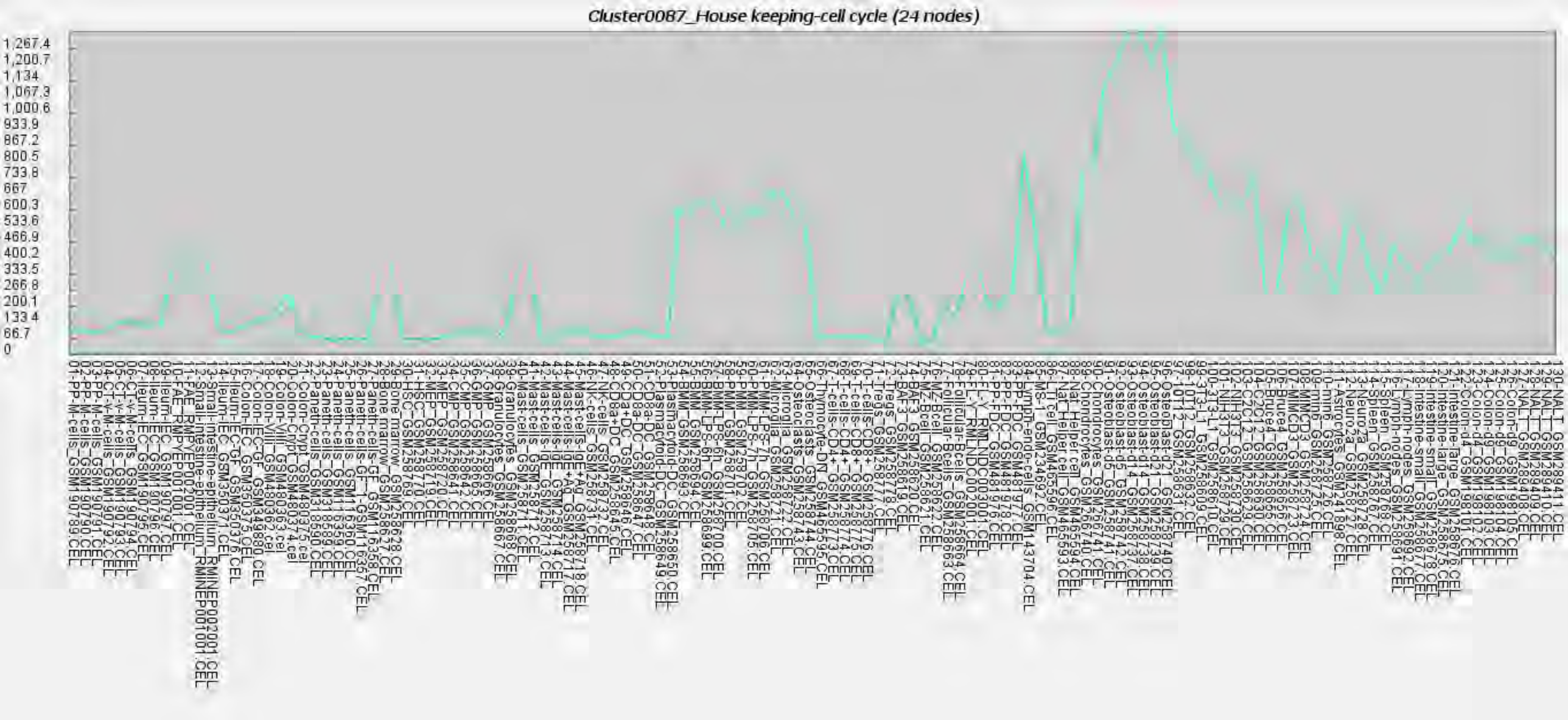

Cluster0082_Proteolysis-related (25 nodes)
5,944.1
5,631.2
5,318.4
5,005.5
4,692.7
4,379.9
4,067
3,754.2
3,441.3
3,128.6
2,815.6
2,502.8
2,189.9
1,877.1
1,564.2
1,251.4
938.5
625.7
312.8
0

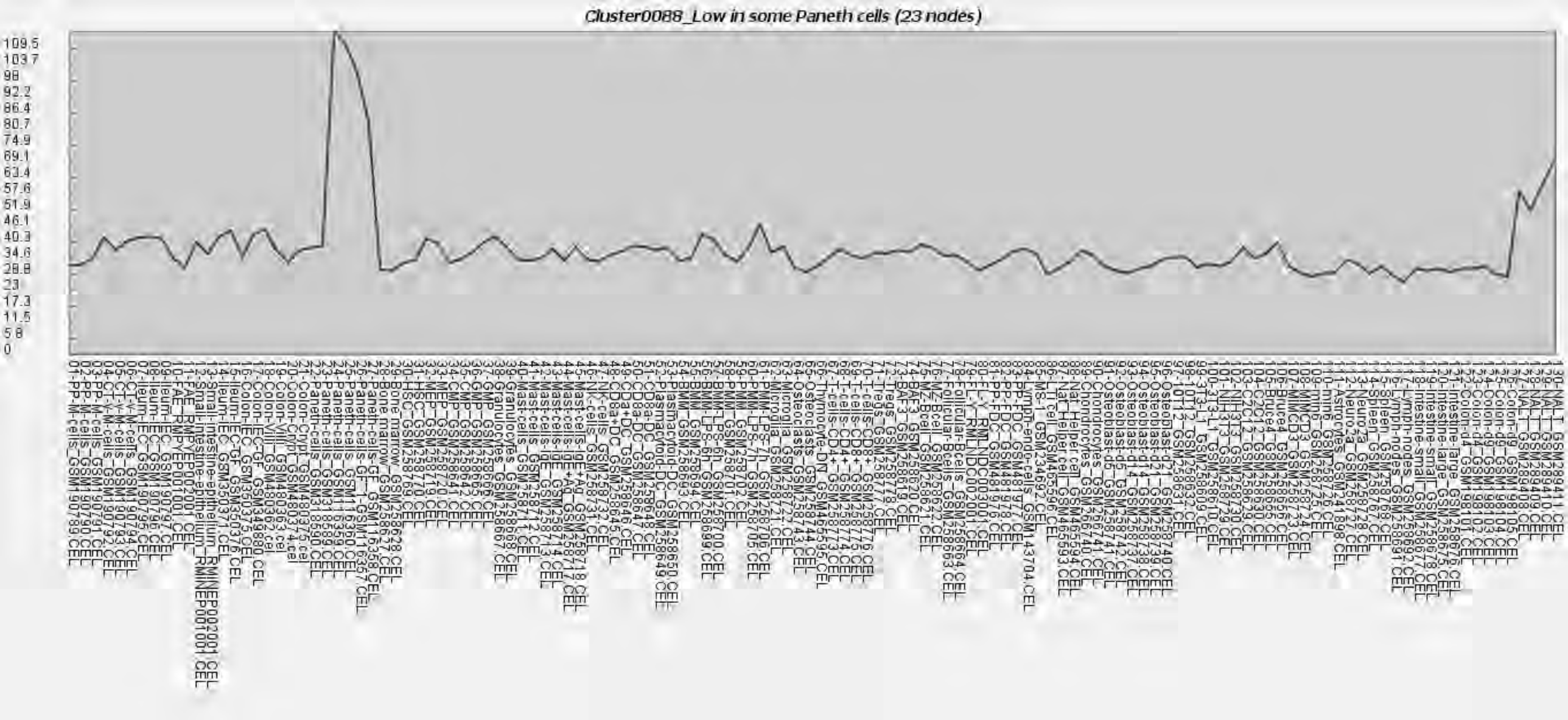

Cluster0083_High in NKcells, T cells and B cells (25 nodes)
2,371.9
2,247.1
2,122.2
1,997.4
1,872.6
1,747.7
1,622.9
1,498.1
1,373.2
1,248.4
1,123.5
998.7
873.9
749
624.2
499.4
374.5
249.7
124.8
0

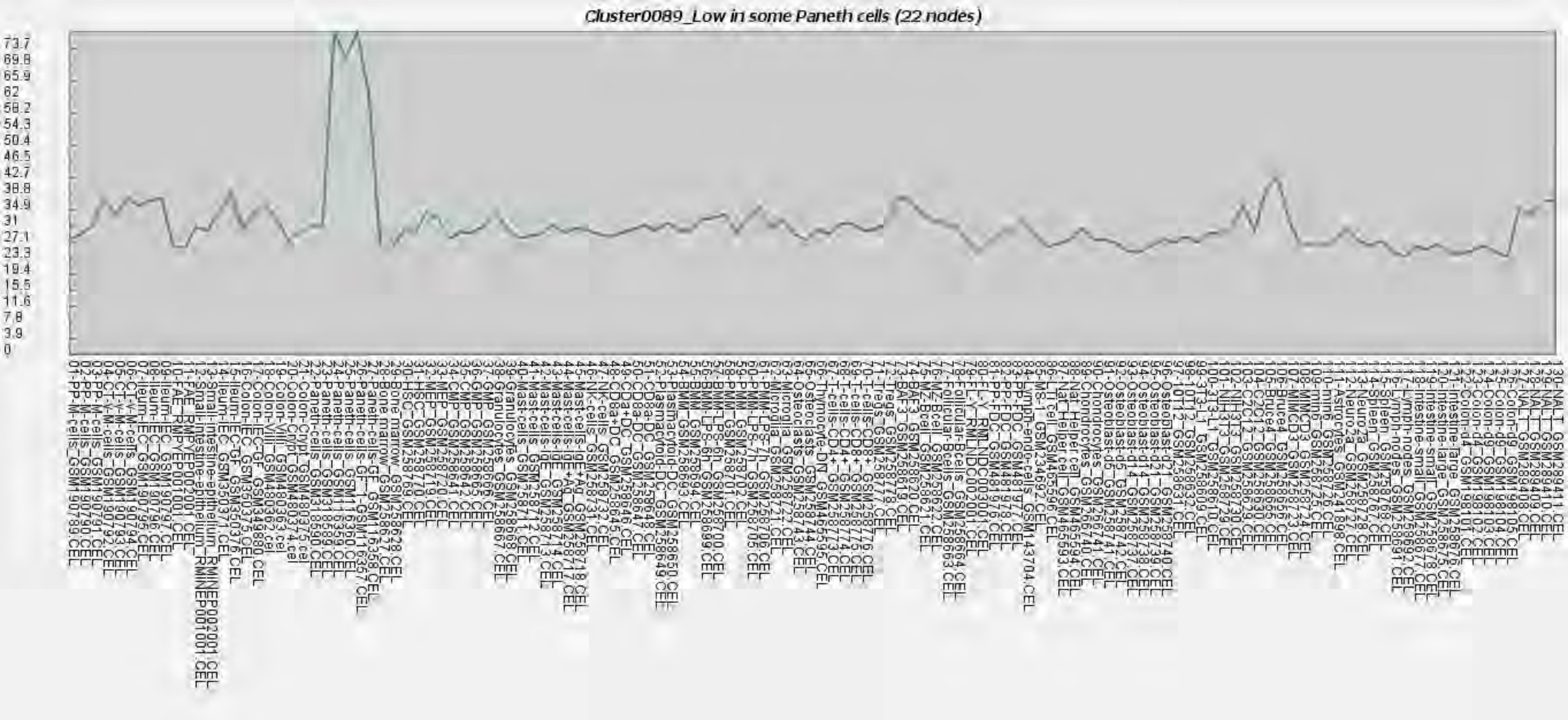
Cluster0084_intestine-related (25 nodes)
1,360.2
1,288.6
1,217
1,145.4
1,073.8
1,002.3
930.7
859.1
787.5
715.9
644.3
572.7
501.1
429.5
357.9
286.4
214.8
143.2
71.6
0

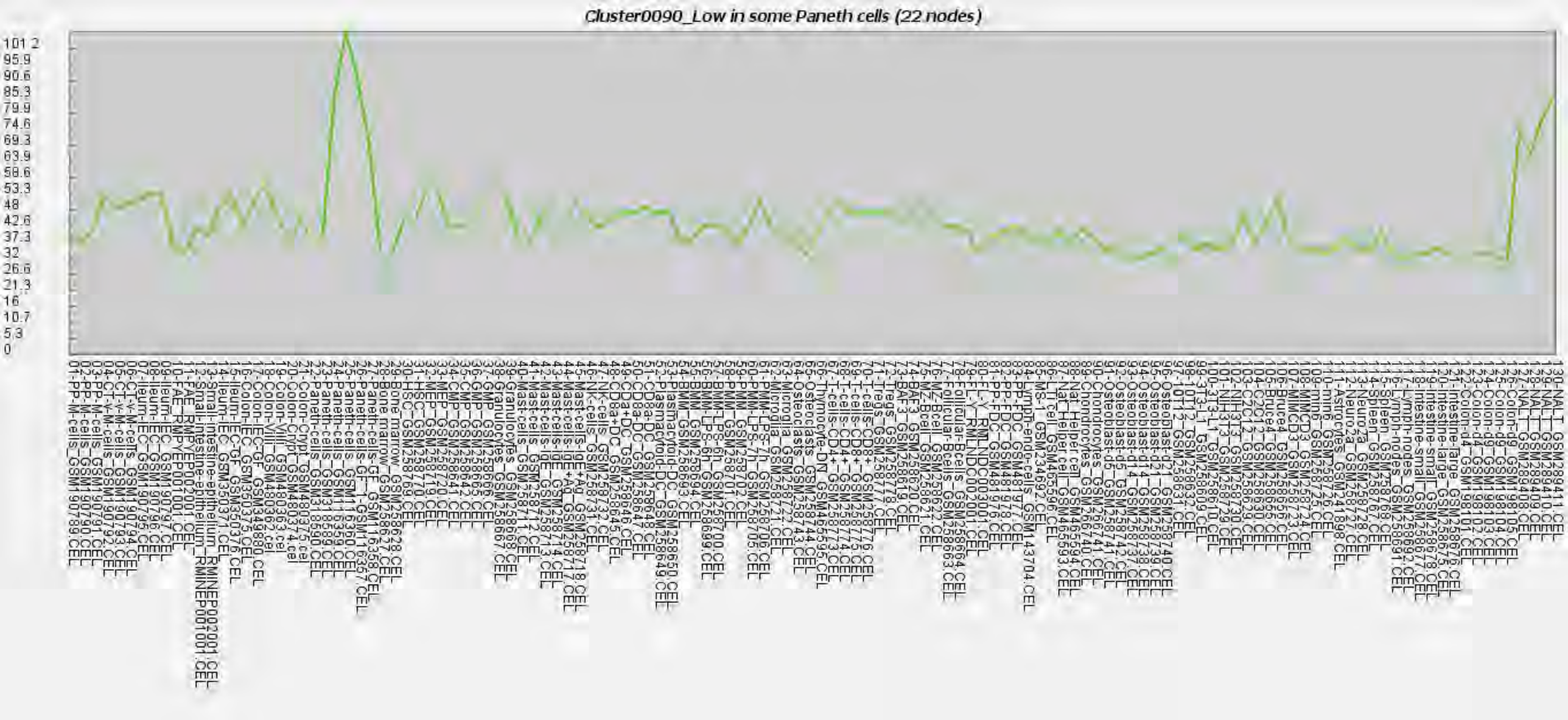

Cluster0085_High in haematopoietic cells (25 nodes)
5,396.5
5,112.4
4,828.4
4,544.4
4,260.4
3,976.3
3,692.3
3,408.3
3,124.3
2,840.2
2,556.2
2,272.2
1,988.2
1,704.1
1,420.1
1,136.1
852.1
568
284
0

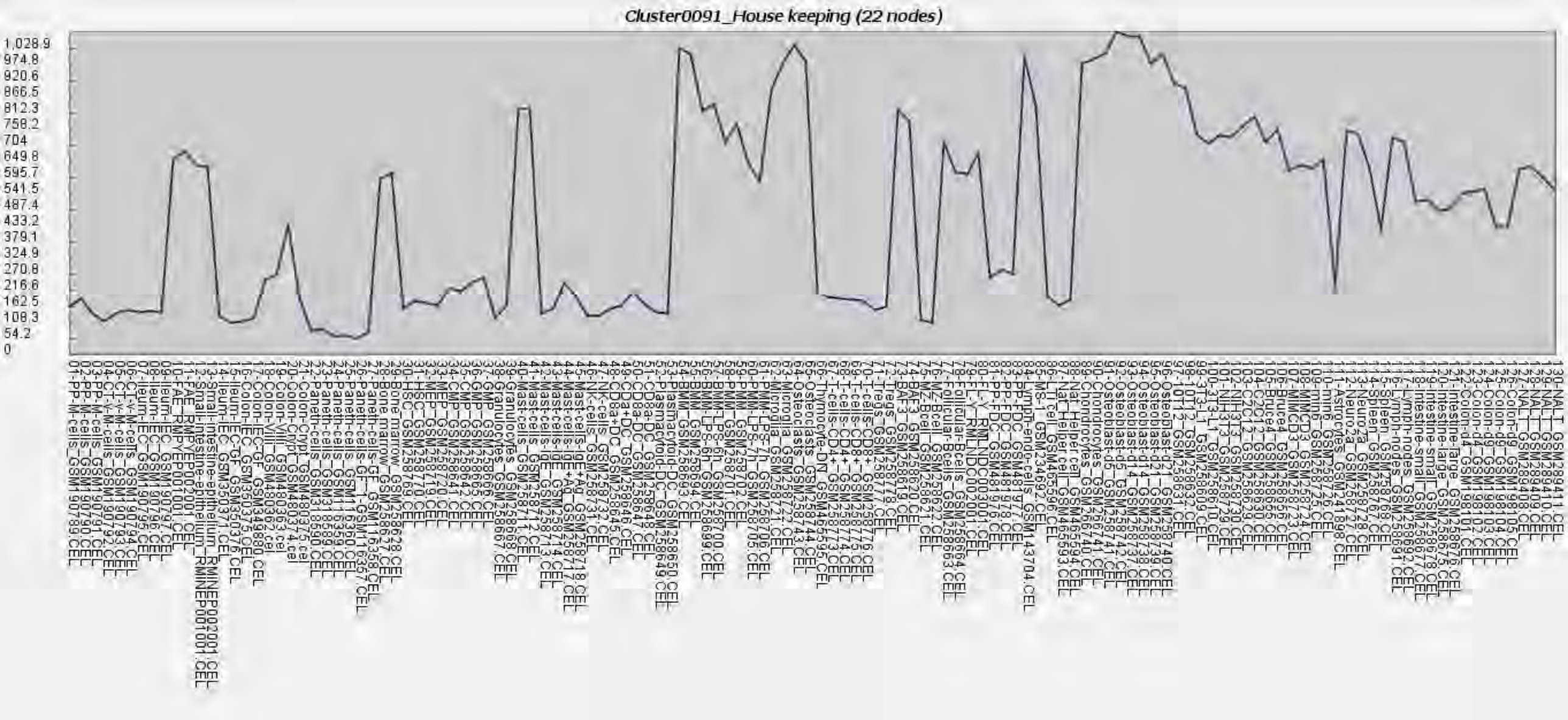

Cluster0086_Affymetrix control probe sets (24 nodes)
19,862.6
18,817.2
17,771.8
16,726.4
15,681
14,635.6
13,590.2
12,544.8
11,499.4
10,454
9,408.6
8,363.2
7,317.8
6,272.4
5,227
4,181.6
3,136.2
2,090.8
1,045.4
0

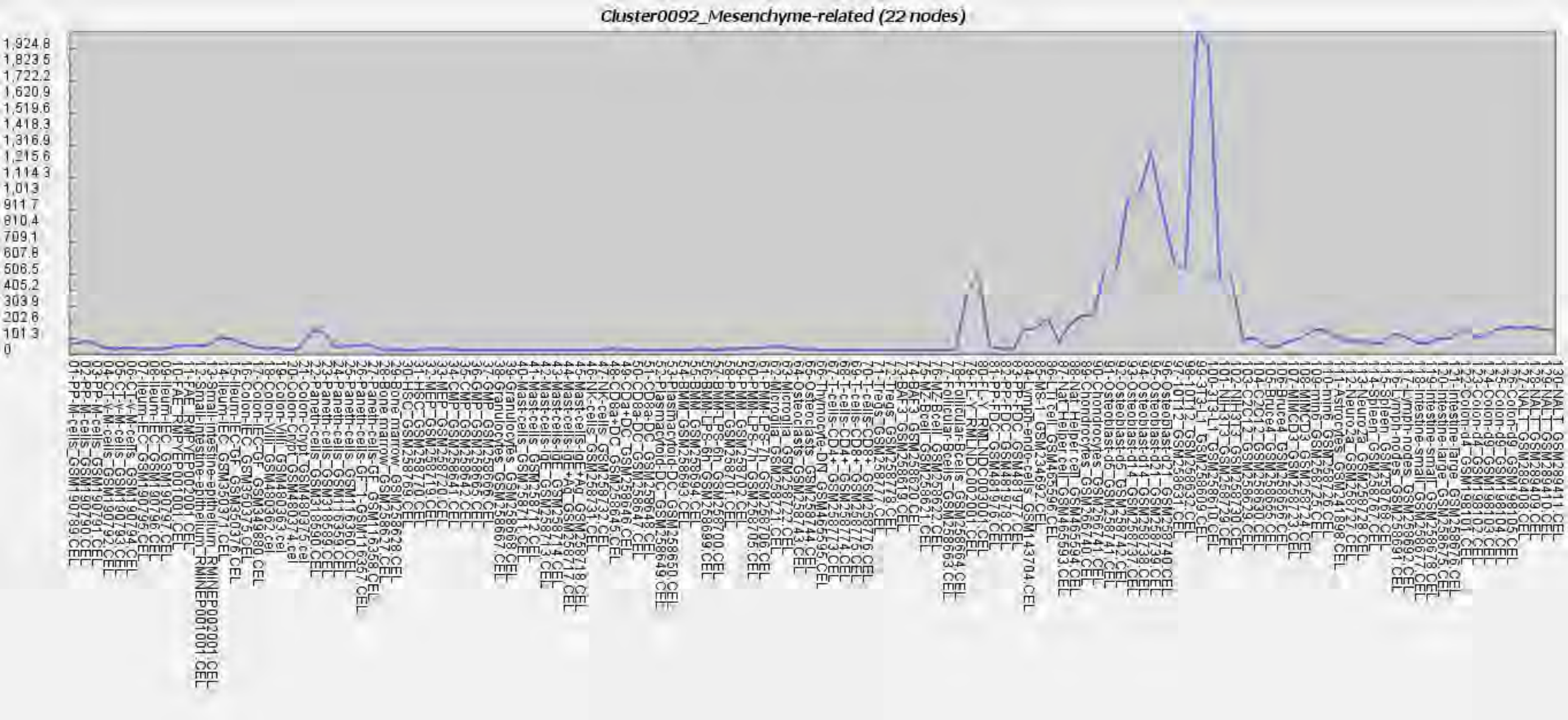

Cluster0087_House keeping-cell cycle (24 nodes)
1,267.4
1,200.7
1,134
1,067.3
1,000.6
933.9
867.2
800.5
733.8
667
600.3
533.6
466.9
400.2
333.5
266.8
200.1
133.4
66.7
0

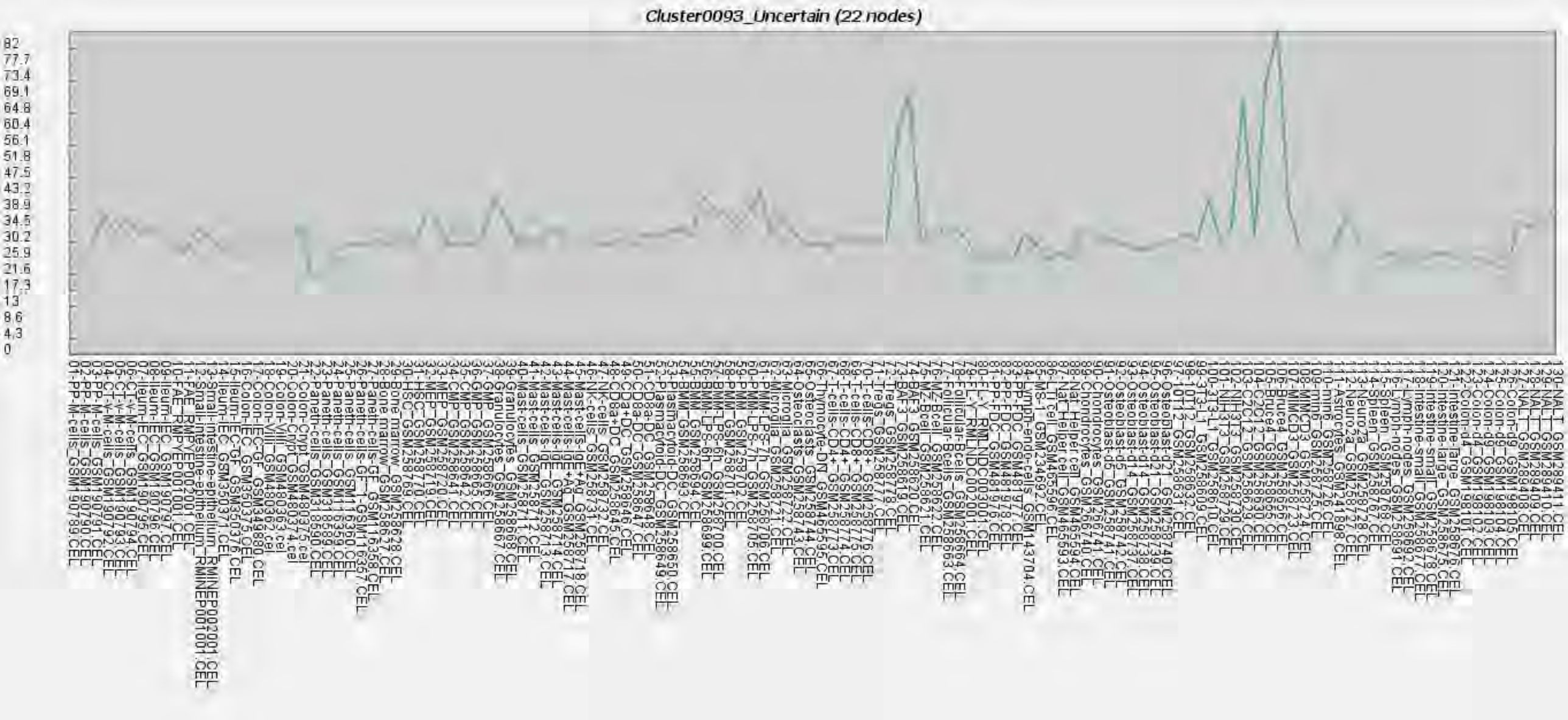

Cluster0088_Low in some Paneth cells (23 nodes)
109.5
103.7
98
92.2
86.4
80.7
74.9
69.1
63.4
57.6
51.9
46.1
40.3
34.6
28.8
23
17.3
11.5
5.8
0

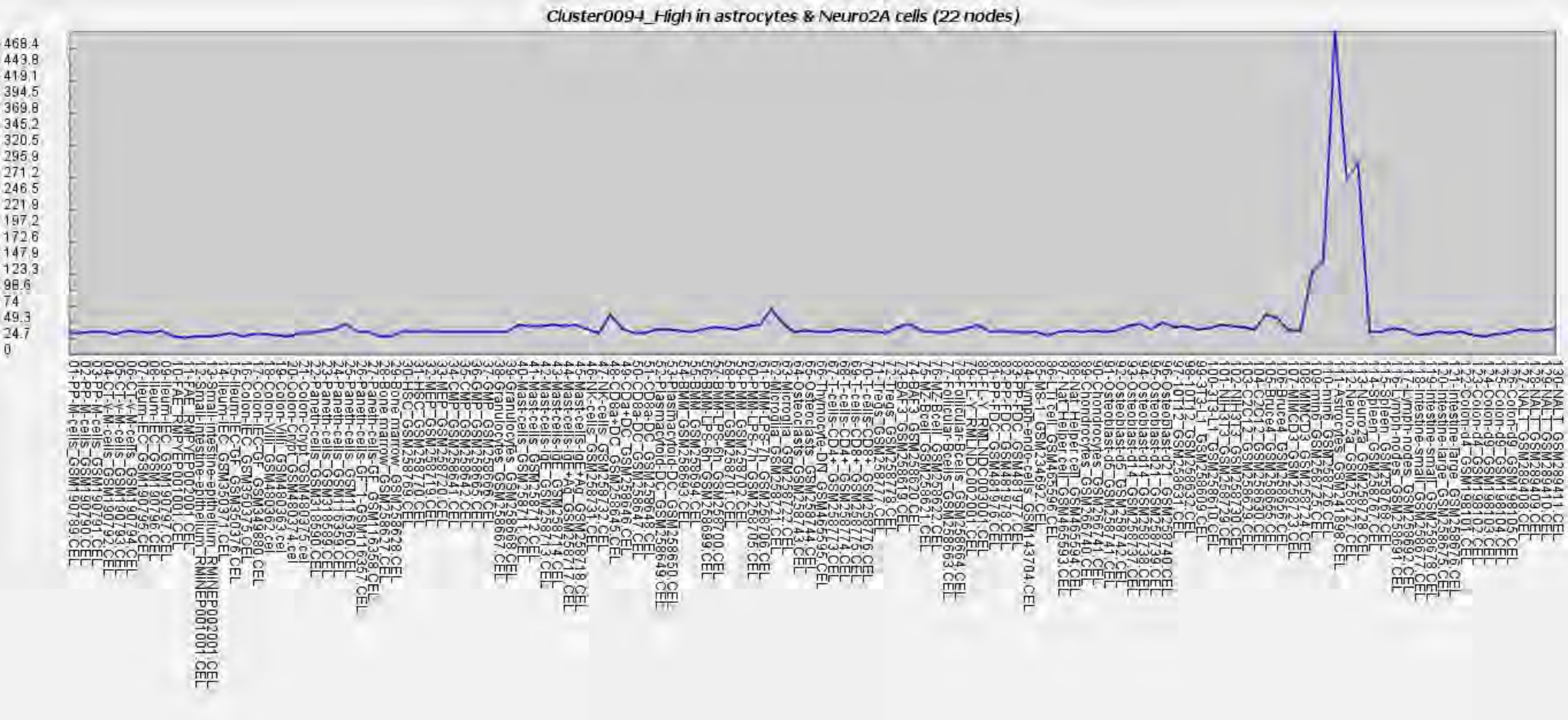

Cluster0089_Low in some Paneth cells (22 nodes)
73.7
69.8
65.9
62
58.2
54.3
50.4
46.5
42.7
38.8
34.9
31
27.1
23.3
19.4
15.5
11.6
7.8
3.9
0

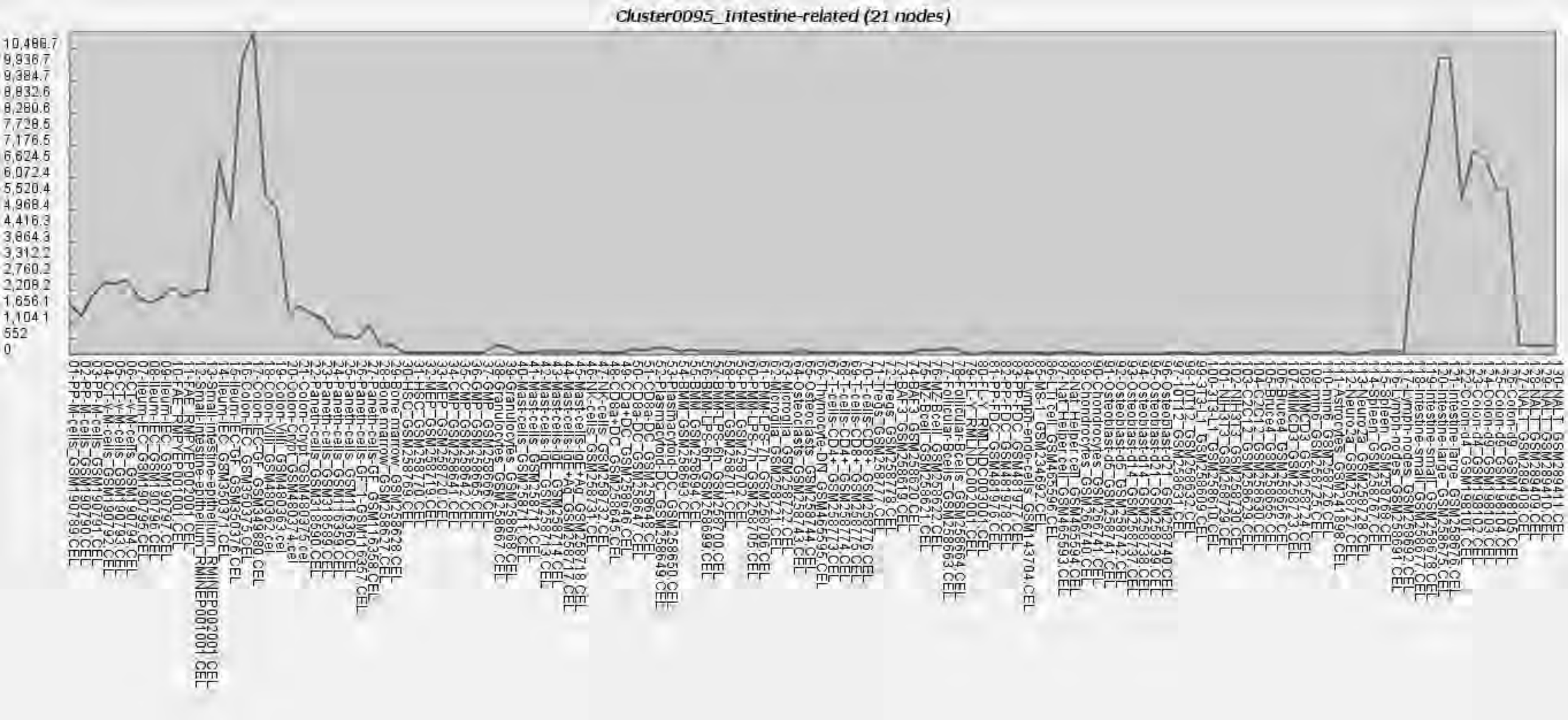

Cluster0090_Low in some Paneth cells (22 nodes)
101.2
95.9
90.6
85.3
79.9
74.6
69.3
63.9
58.6
53.3
48
42.6
37.3
32
26.6
21.3
16
10.7
5.3
0


Cluster0091_House keeping (22 nodes)
1,028.9
974.8
920.6
866.5
812.3
758.2
704
649.8
595.7
541.5
487.4
433.2
379.1
324.9
270.8
216.6
162.5
108.3
54.2
0

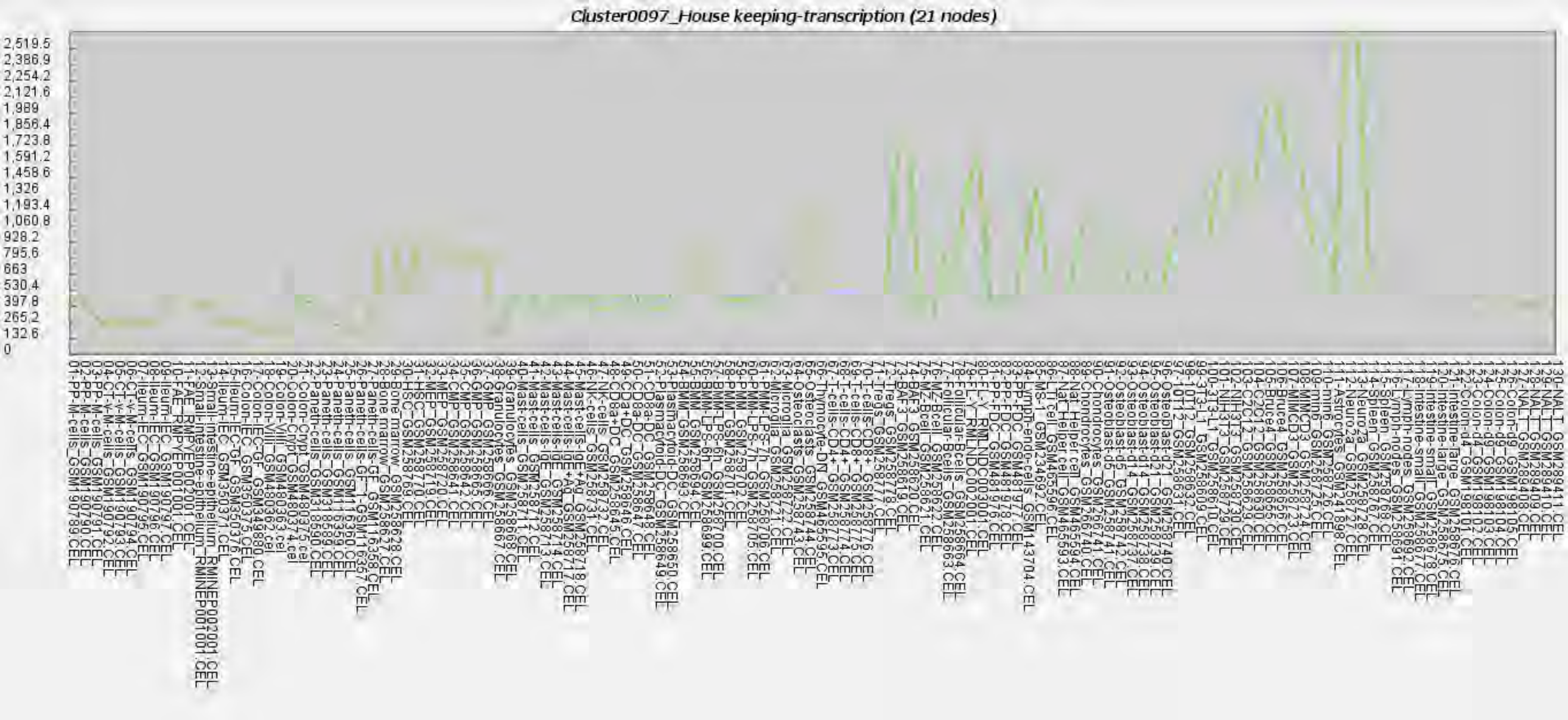

Cluster0092_Mesenchyme-related (22 nodes)
1,924.8
1,823.5
1,722.2
1,620.9
1,519.6
1,418.3
1,316.9
1,215.6
1,114.3
1,013
911.7
810.4
709.1
607.8
506.5
405.2
303.9
202.6
101.3
0

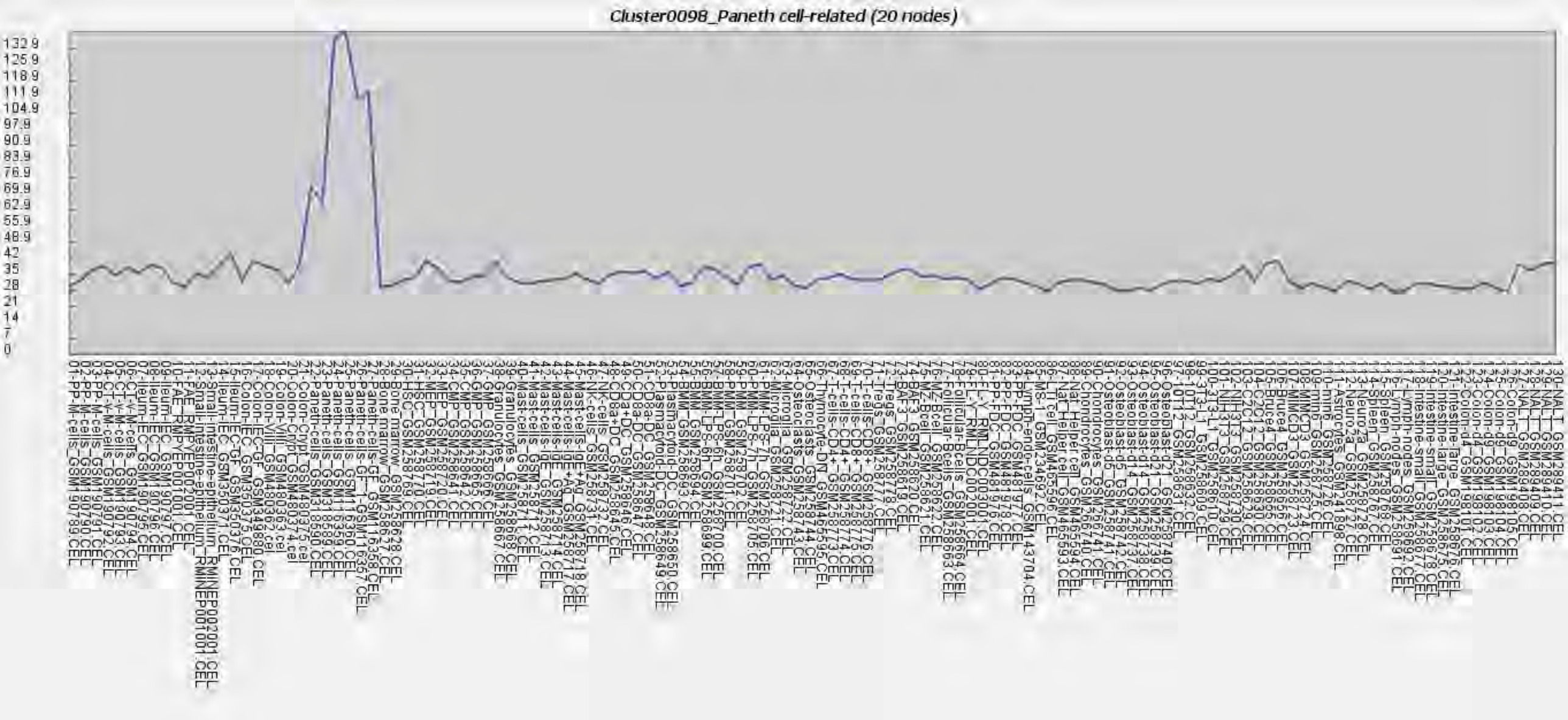

Cluster0093_Uncertain (22 nodes)
82
77.7
73.4
69.1
64.8
60.4
56.1
51.8
47.5
43.2
38.9
34.5
30.2
25.9
21.6
17.3
13
8.6
4.3
0

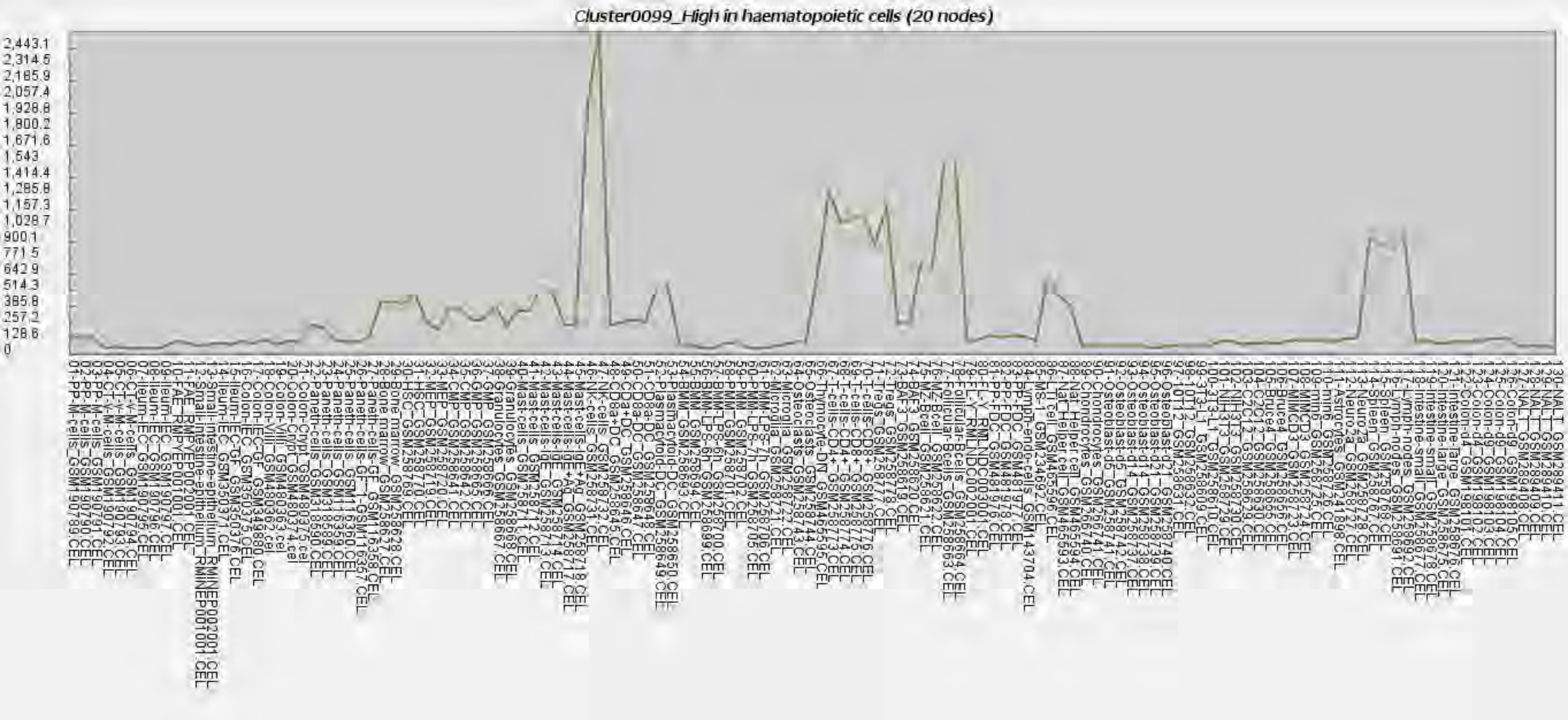

Cluster0094_High in astrocytes & Neuro2A cells (22 nodes)
468.4
443.8
419.1
394.5
369.8
345.2
320.5
295.9
271.2
246.5
221.9
197.2
172.6
147.9
123.3
98.6
74
49.3
24.7
0


Cluster0095_Intestine-related (21 nodes)
10,488.7
9,936.7
9,384.7
8,832.6
8,280.6
7,728.5
7,176.5
6,624.5
6,072.4
5,520.4
4,968.4
4,416.3
3,864.3
3,312.2
2,760.2
2,208.2
1,656.1
1,104.1
552
0

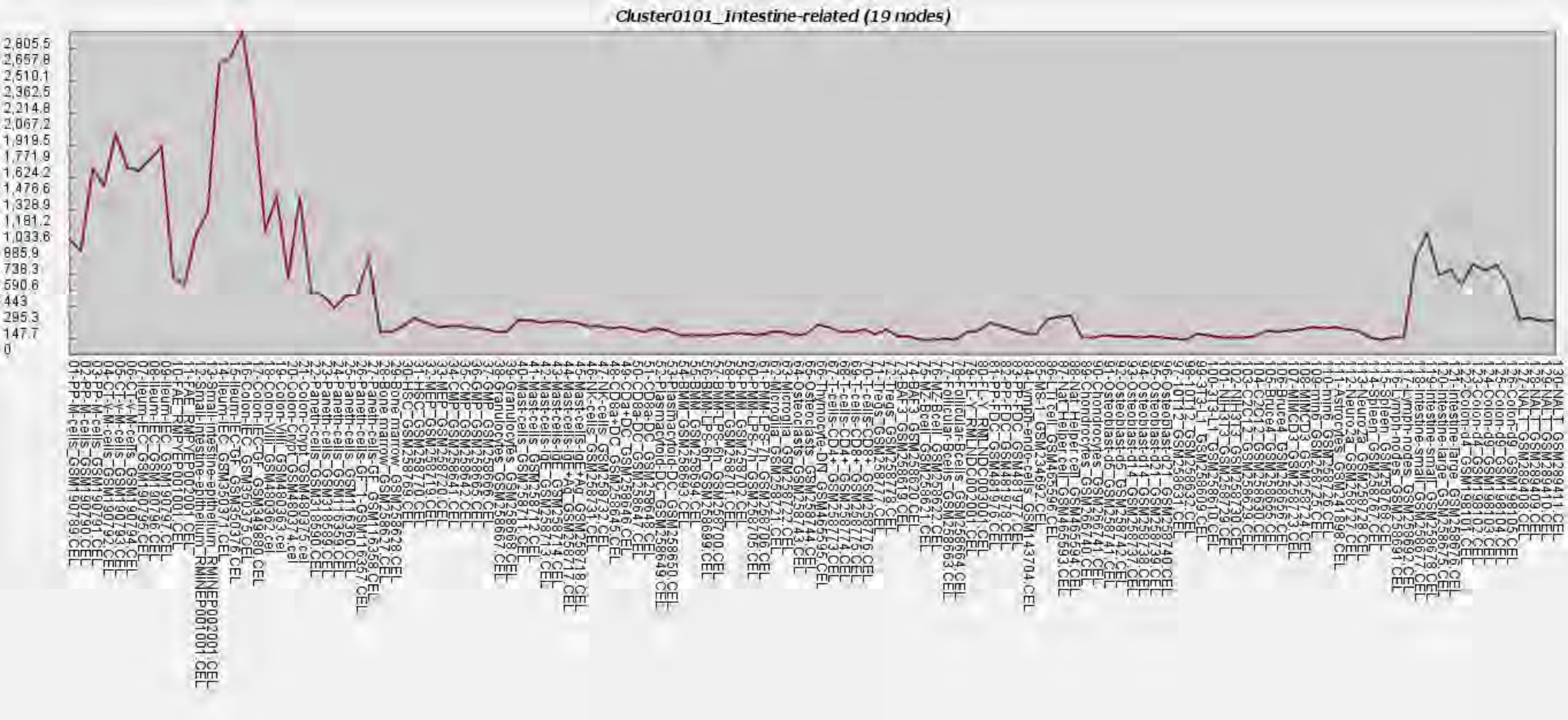
Cluster0096_High in NALT (21 nodes)
989.8
937.7
885.6
833.5
781.4
729.3
677.2
625.1
573
520.9
468.8
416.7
364.6
312.6
260.5
208.4
156.3
104.2
52.1
0

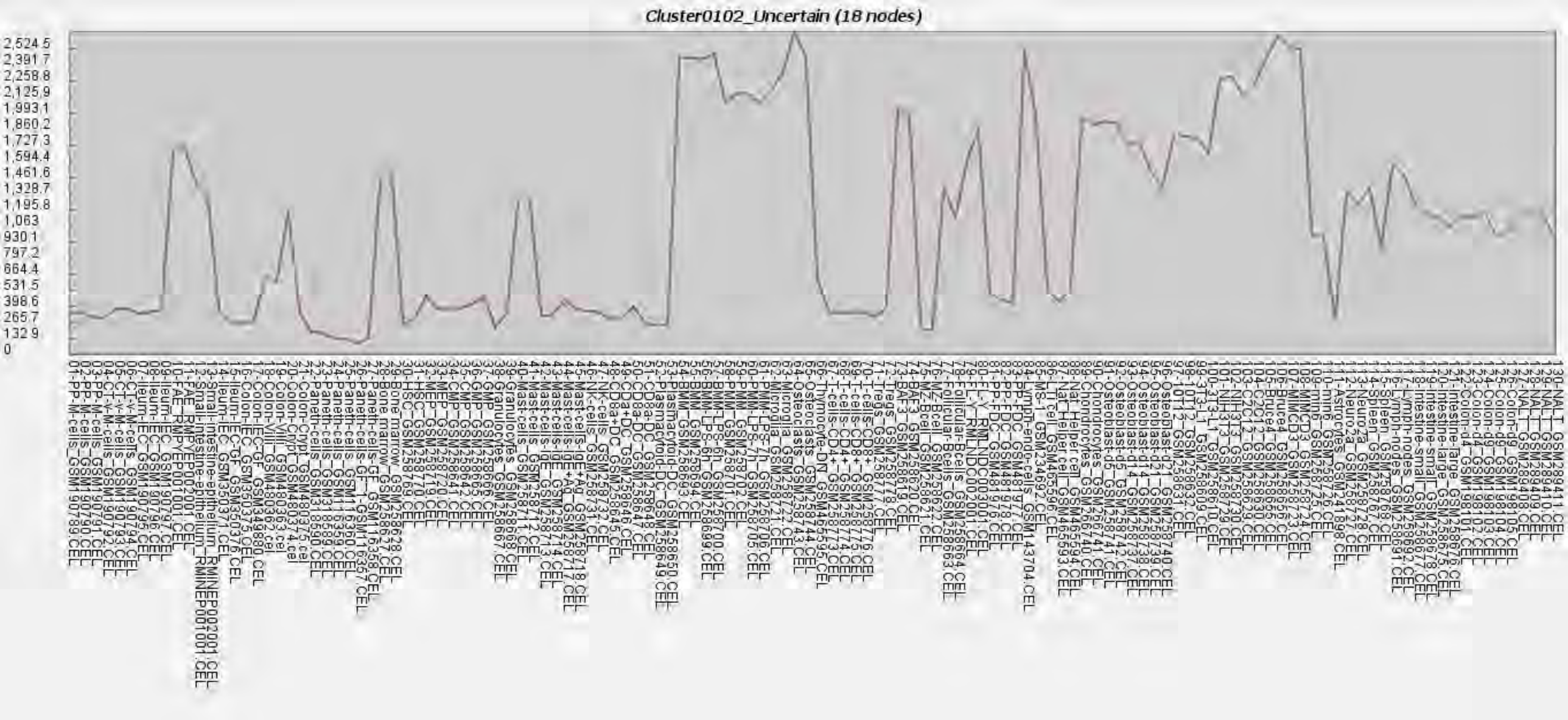

Cluster0097_House keeping-transcription (21 nodes)
2,519.5
2,386.9
2,254.2
2,121.6
1,989
1,856.4
1,723.8
1,591.2
1,458.6
1,326
1,193.4
1,060.8
928.2
795.6
663
530.4
397.8
265.2
132.6
0

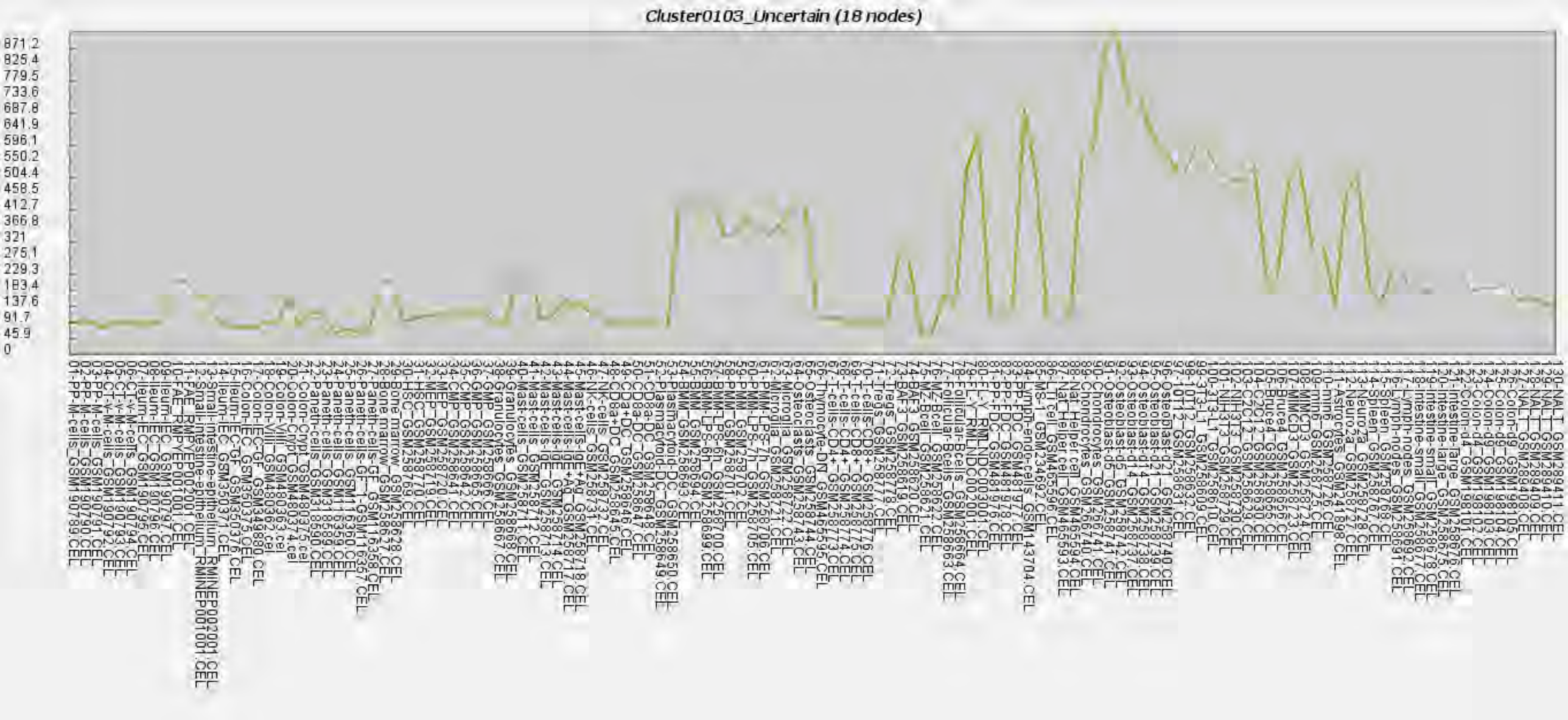

Cluster0098_Paneth cell-related (20 nodes)
132.9
125.9
118.9
111.9
104.9
97.9
90.9
83.9
76.9
69.9
62.9
55.9
48.9
42
35
28
21
14
7
0

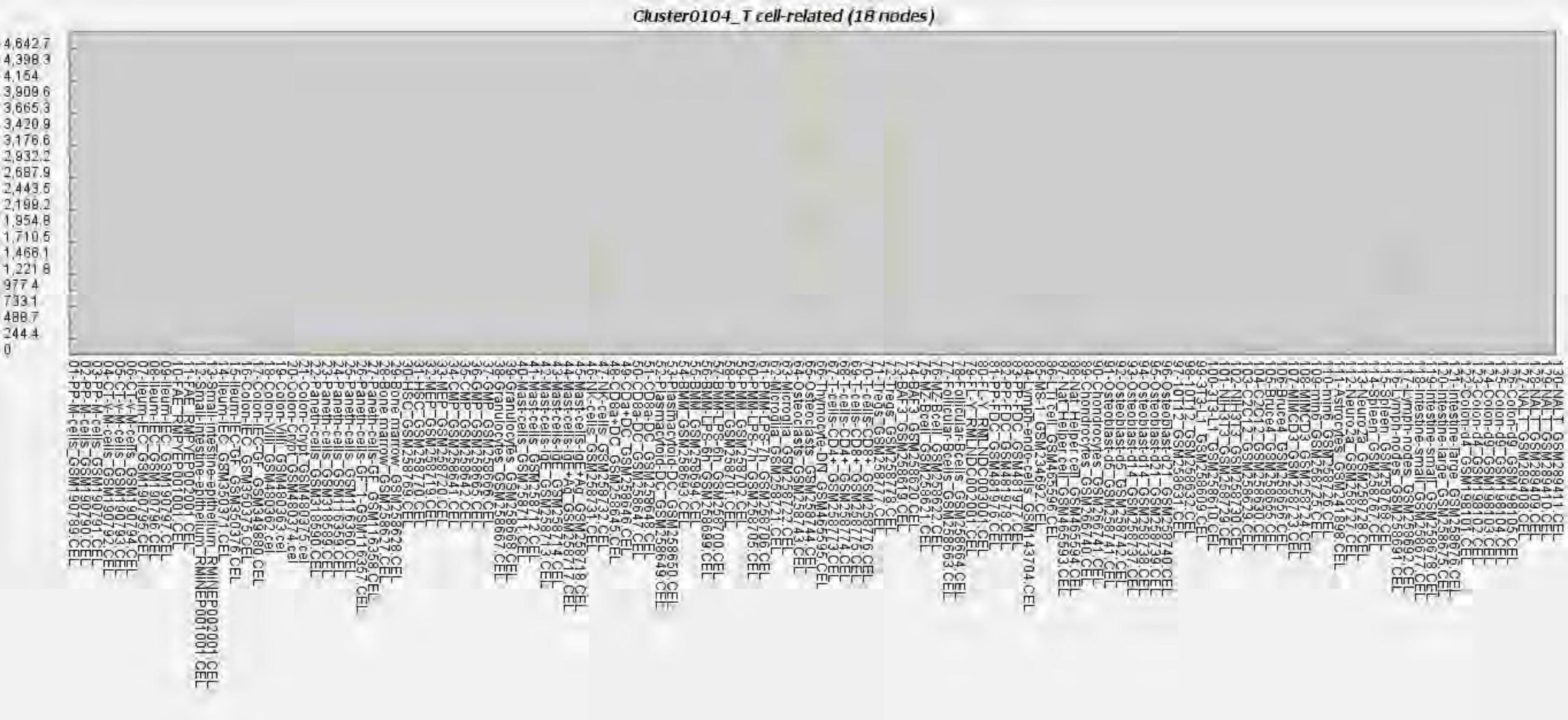

Cluster0099_High in haematopoietic cells (20 nodes)
2,443.1
2,314.5
2,185.9
2,057.4
1,928.8
1,800.2
1,671.6
1,543
1,414.4
1,285.8
1,157.3
1,028.7
900.1
771.5
642.9
514.3
385.8
257.2
128.6
0

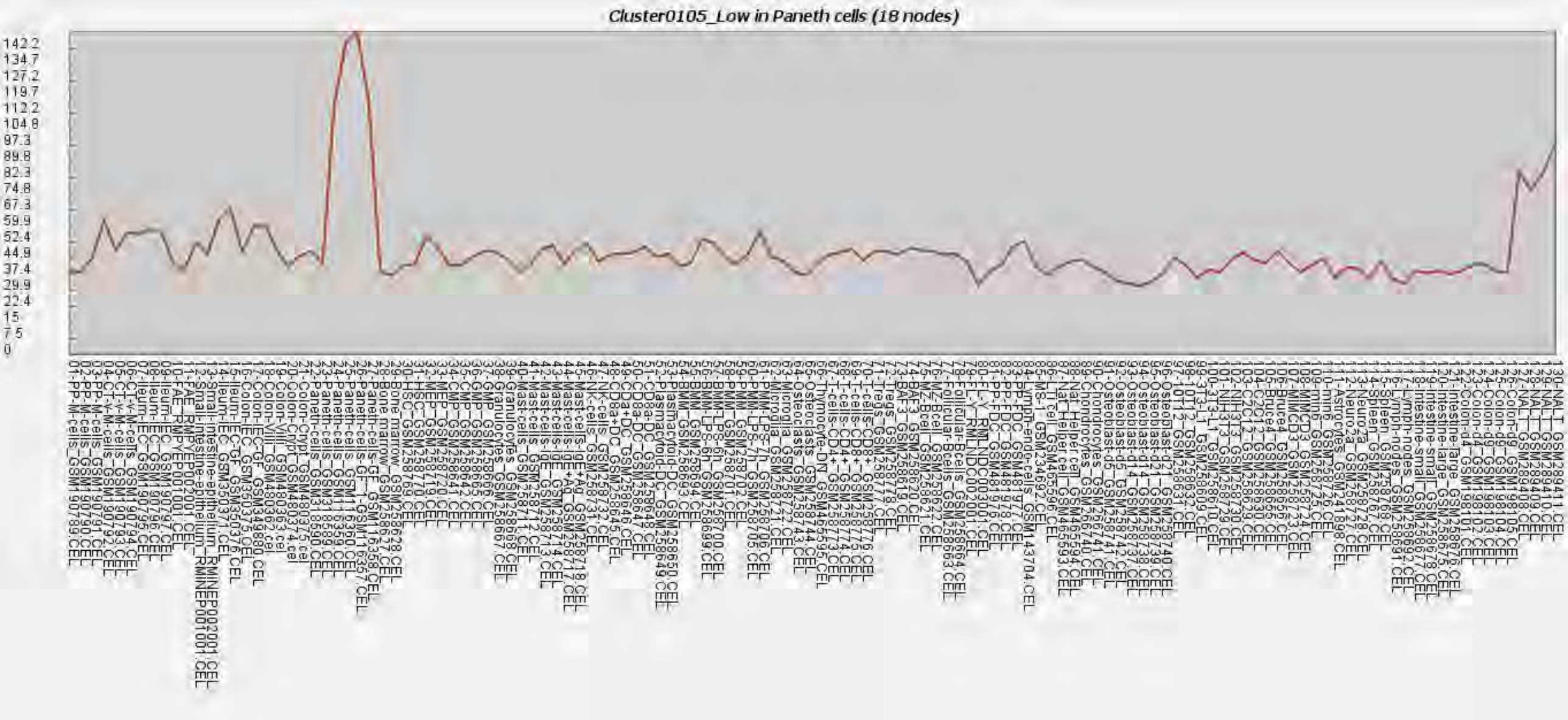
Cluster0100_High in astrocytes & NALT (20 nodes)
1,035.1
980.6
926.1
871.7
817.2
762.7
708.2
653.7
599.3
544.8
490.3
435.8
381.4
326.9
272.4
217.9
163.4
109
54.5
0


Cluster0101_intestine-related (19 nodes)
2,805.5
2,657.8
2,510.1
2,362.5
2,214.8
2,067.2
1,919.5
1,771.9
1,624.2
1,476.6
1,328.9
1,181.2
1,033.6
885.9
738.3
590.6
443
295.3
147.7
0


Cluster0102_Uncertain (18 nodes)
2,524.5
2,391.7
2,258.8
2,125.9
1,993.1
1,860.2
1,727.3
1,594.4
1,461.6
1,328.7
1,195.8
1,063
930.1
797.2
664.4
531.5
398.6
265.7
132.9
0

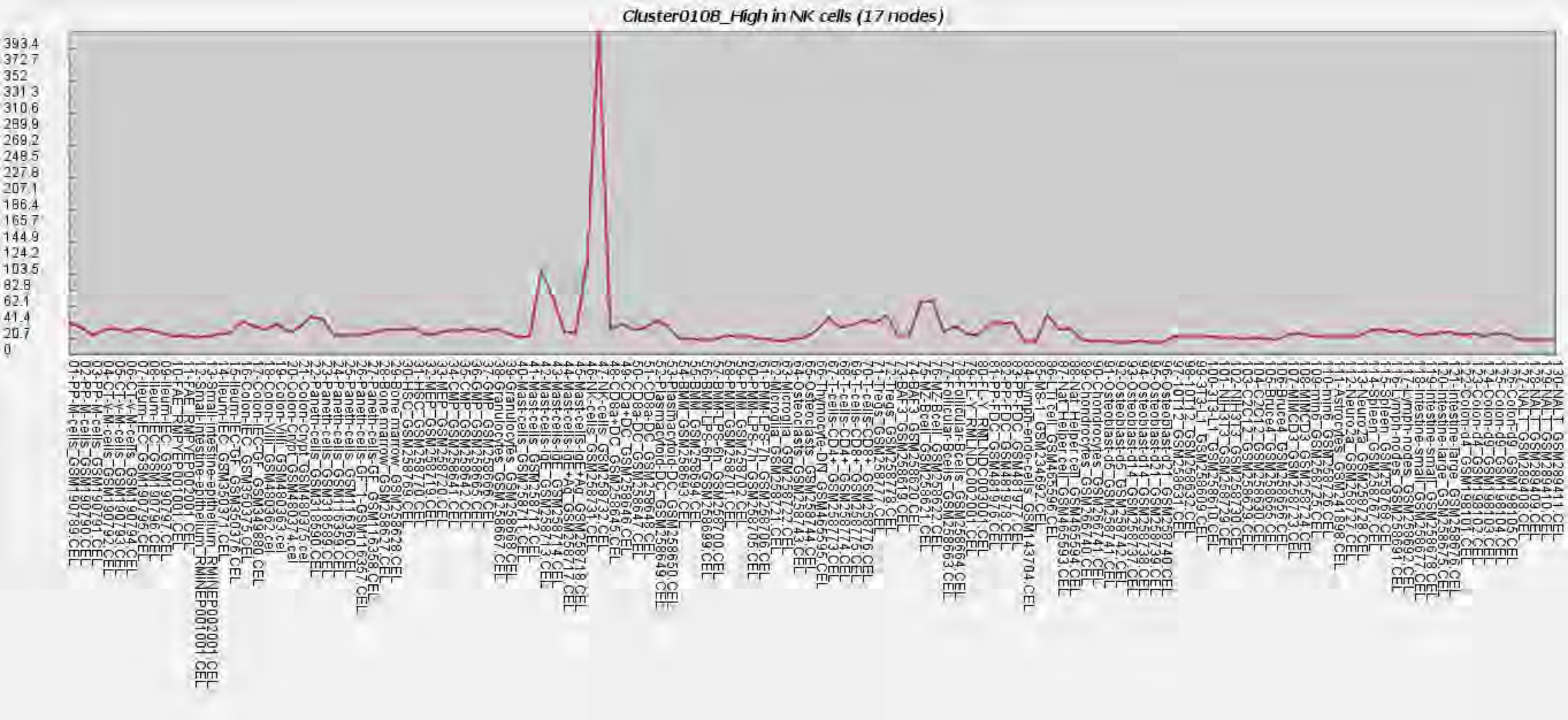

Cluster0103_Uncertain (18 nodes)
871.2
825.4
779.5
733.6
687.8
641.9
596.1
550.2
504.4
458.5
412.7
366.8
321
275.1
229.3
183.4
137.6
91.7
45.9
0

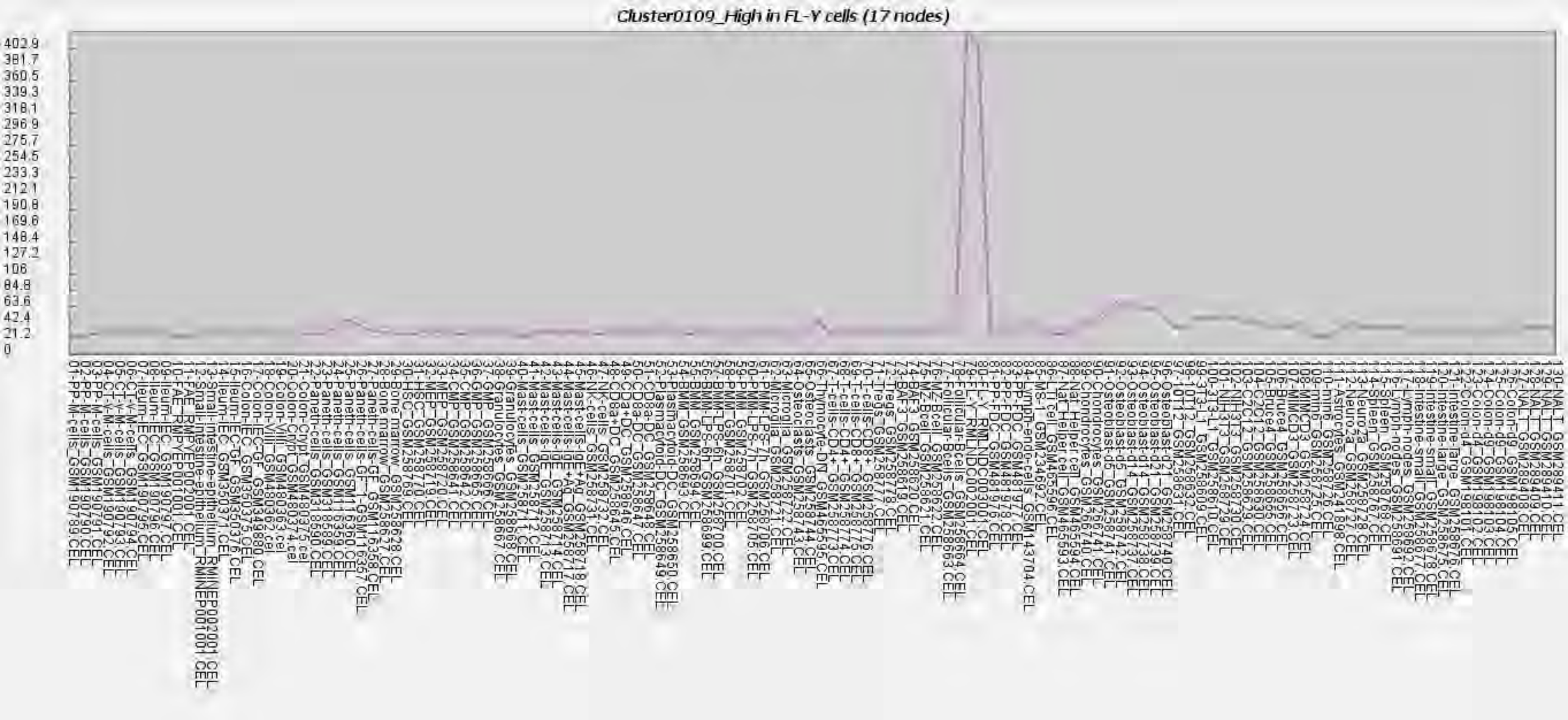

Cluster0104_T cell-related (18 nodes)
4,642.7
4,398.3
4,154
3,909.6
3,665.3
3,420.9
3,176.6
2,932.2
2,687.9
2,443.5
2,199.2
1,954.8
1,710.5
1,466.1
1,221.8
977.4
733.1
488.7
244.4
0


Cluster0105_Low in Paneth cells (18 nodes)
142.2
134.7
127.2
119.7
112.2
104.8
97.3
89.8
82.3
74.8
67.3
59.9
52.4
44.9
37.4
29.9
22.4
15
7.5
0

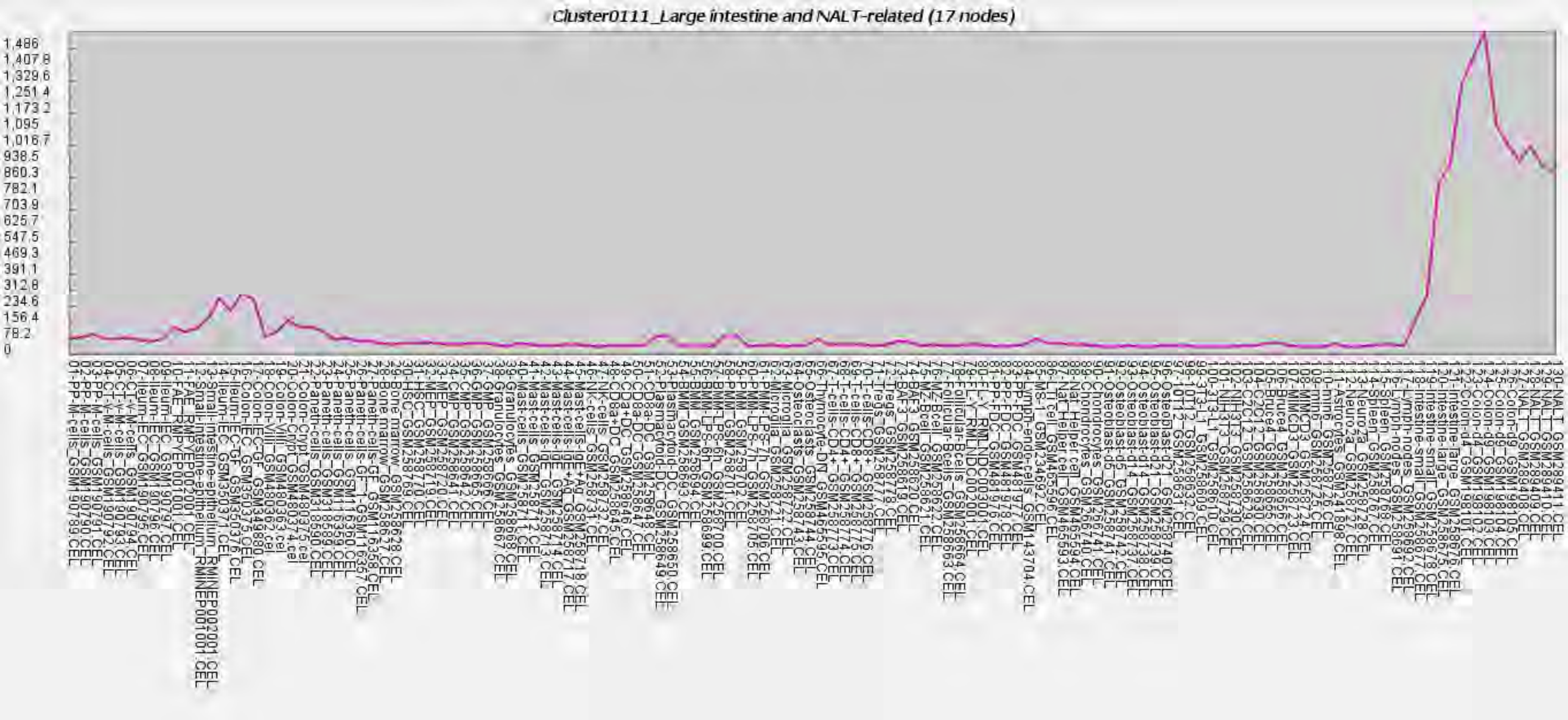
Cluster0106_Immunoglobulin-related (18 nodes)
2,642.2
2,503.2
2,364.1
2,225
2,086
1,946.9
1,807.8
1,668.8
1,529.7
1,390.6
1,251.6
1,112.5
973.5
834.4
695.3
556.3
417.2
278.1
139.1
0

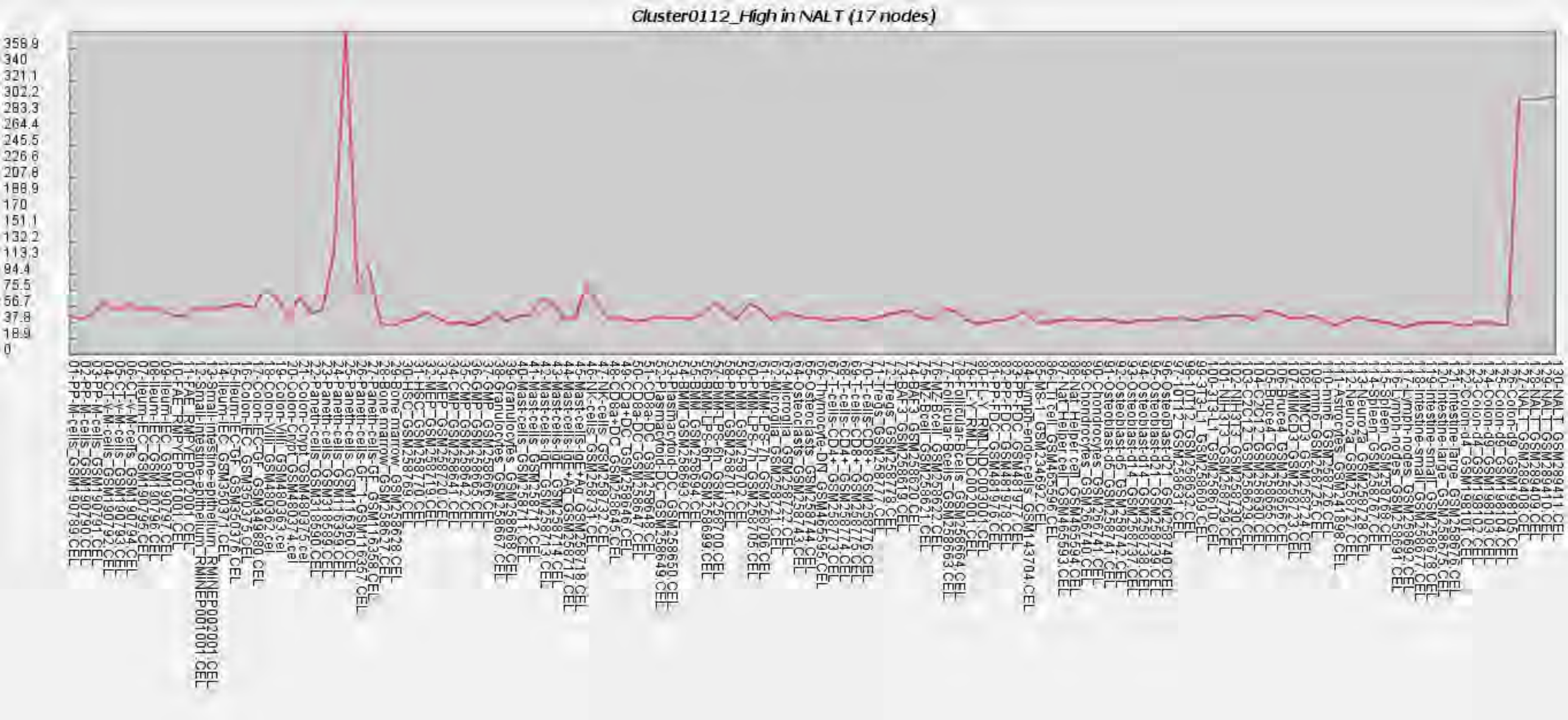
Cluster0107_High in 3T3L1 cells (17 nodes)
1,821
1,725.1
1,629.3
1,533.5
1,437.6
1,341.8
1,245.9
1,150.1
1,054.3
958.4
862.6
766.7
670.9
575
479.2
383.4
287.5
191.7
95.8
0


Cluster0108_High in NK cells (17 nodes)
393.4
372.7
352
331.3
310.6
289.9
269.2
248.5
227.8
207.1
186.4
165.7
144.9
124.2
103.5
82.8
62.1
41.4
20.7
0

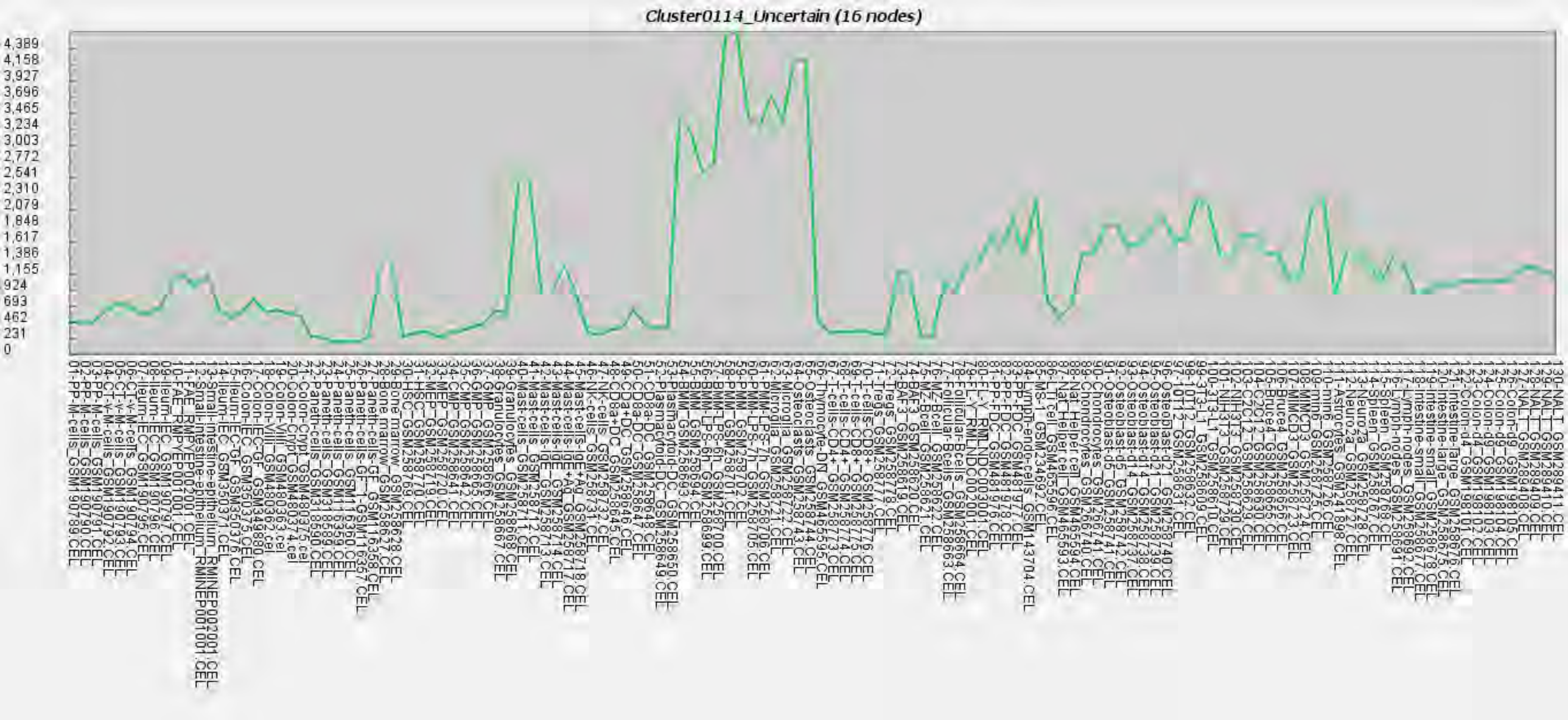

Cluster0109_High in FL-Y cells (17 nodes)
402.9
381.7
360.5
339.3
318.1
296.9
275.7
254.5
233.3
212.1
190.8
169.6
148.4
127.2
106
84.8
63.6
42.4
21.2
0

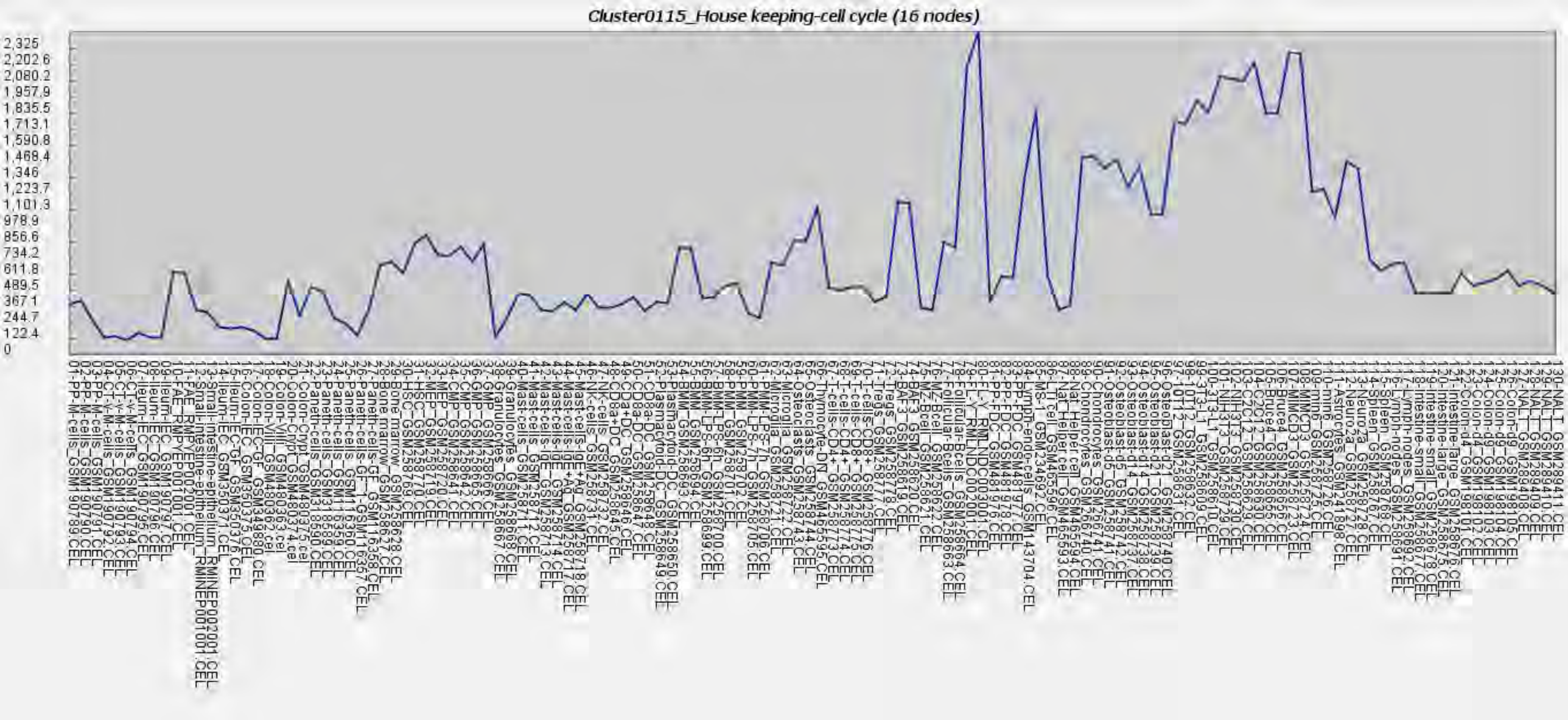
Cluster0110_High in NK cells and lymphocytes (17 nodes)
601.9
570.2
538.5
506.9
475.2
443.5
411.8
380.1
348.5
316.8
285.1
253.4
221.8
190.1
158.4
126.7
95
63.4
31.7
0

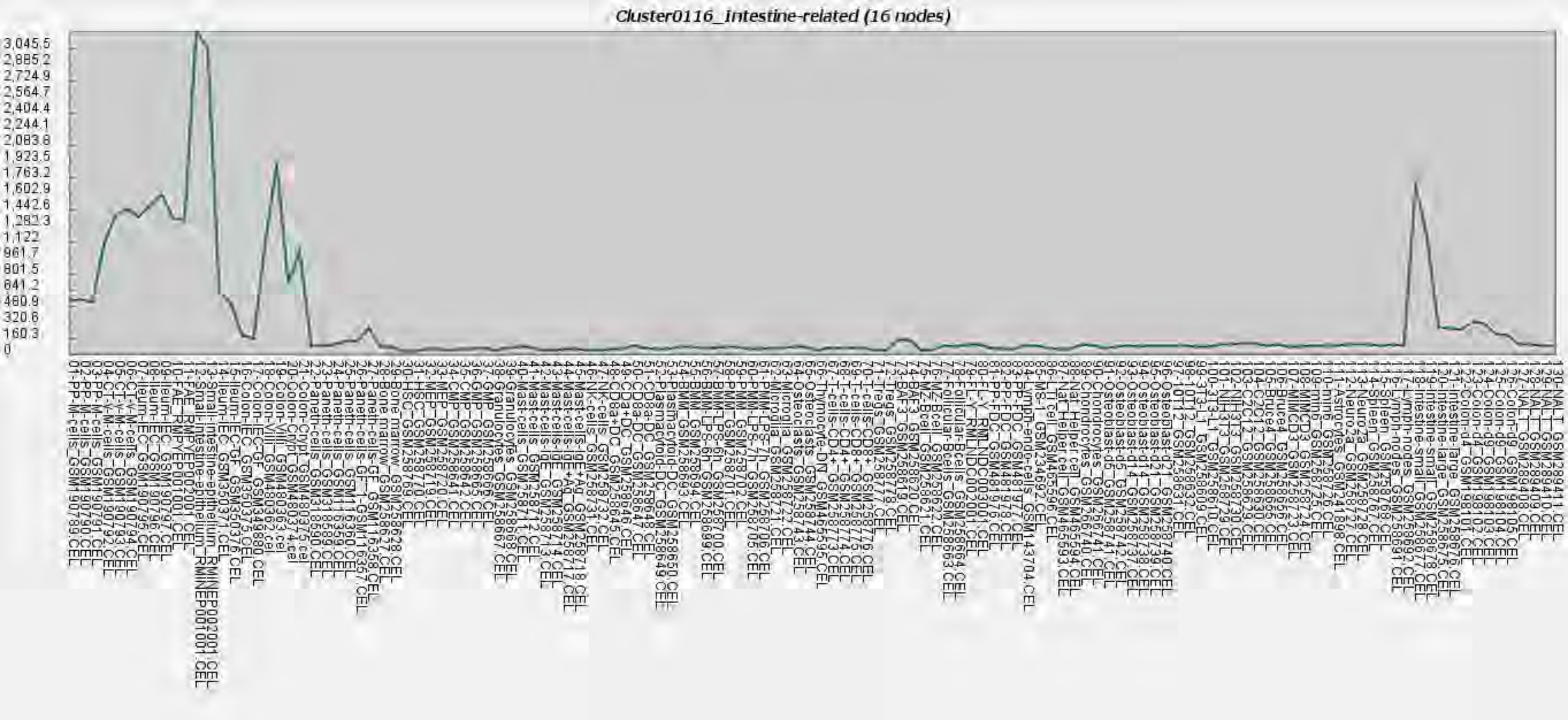

Cluster0111_Large intestine and NALT-related (17 nodes)
1,486
1,407.8
1,329.6
1,251.4
1,173.2
1,095
1,016.7
938.5
860.3
782.1
703.9
625.7
547.5
469.3
391.1
312.8
234.6
156.4
78.2
0

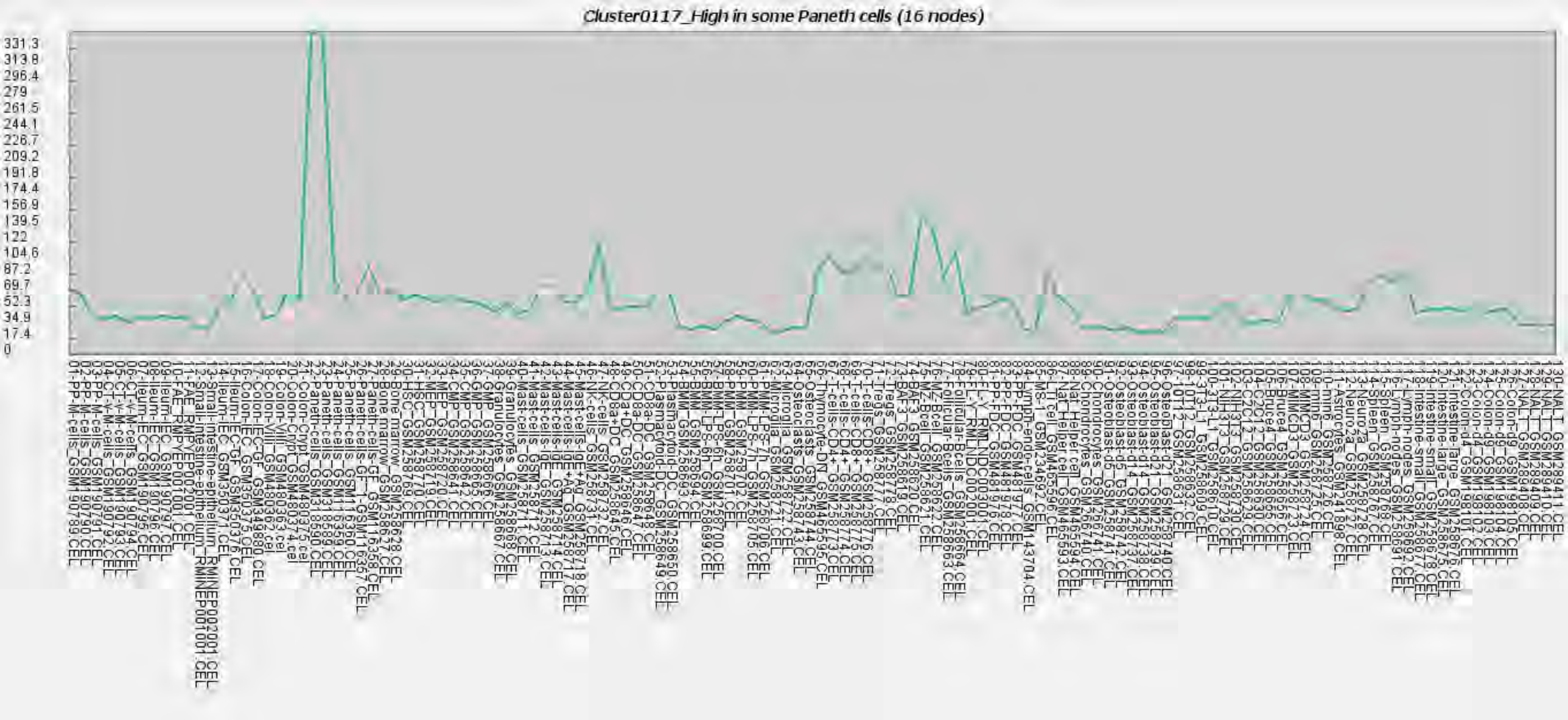

Cluster0112_High in NALT (17 nodes)
358.9
340
321.1
302.2
283.3
264.4
245.5
226.6
207.8
188.9
170
151.1
132.2
113.3
94.4
75.5
56.7
37.8
18.9
0

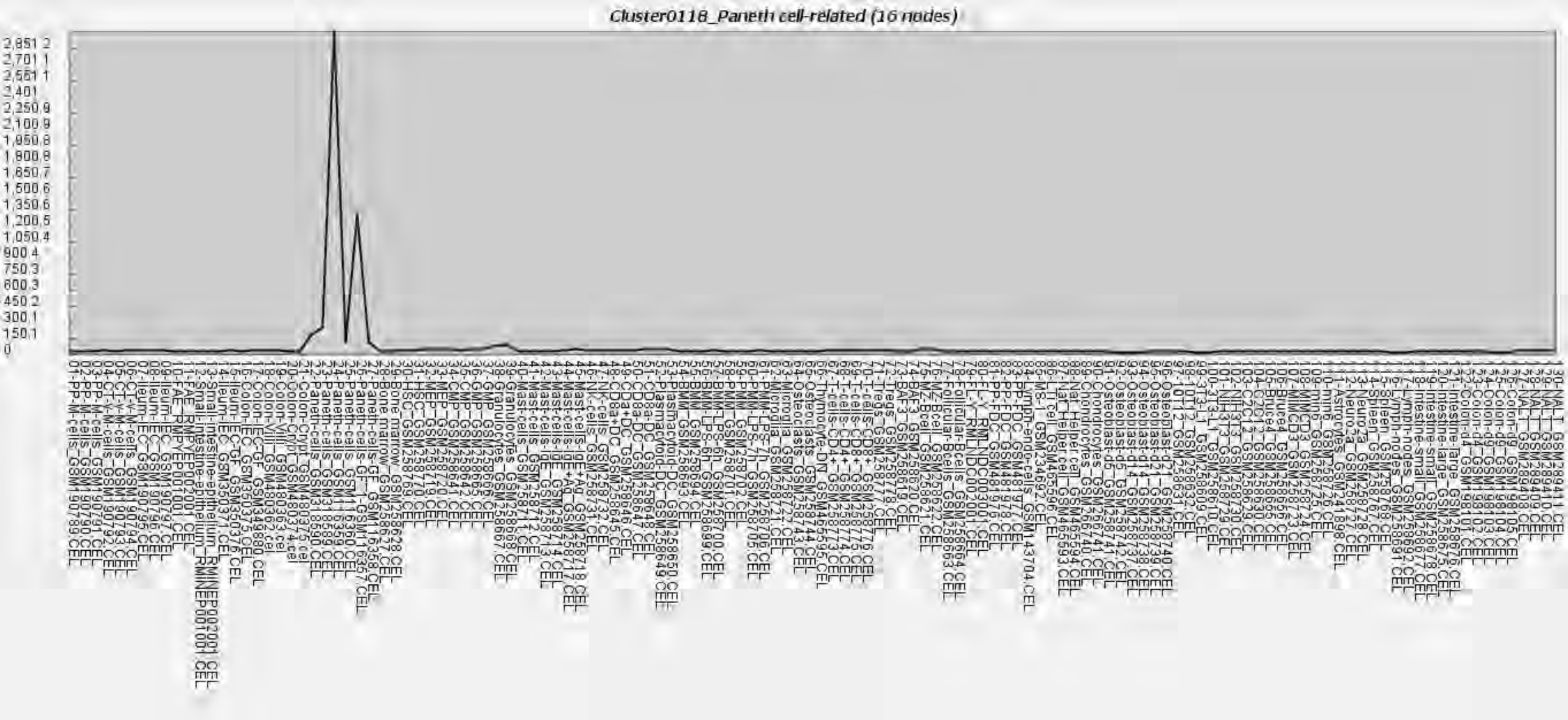
Cluster0113_Uncertain (16 nodes)
104.2
98.7
93.2
87.7
82.2
76.7
71.3
65.8
60.3
54.8
49.3
43.9
38.4
32.9
27.4
21.9
16.4
11
5.5
0

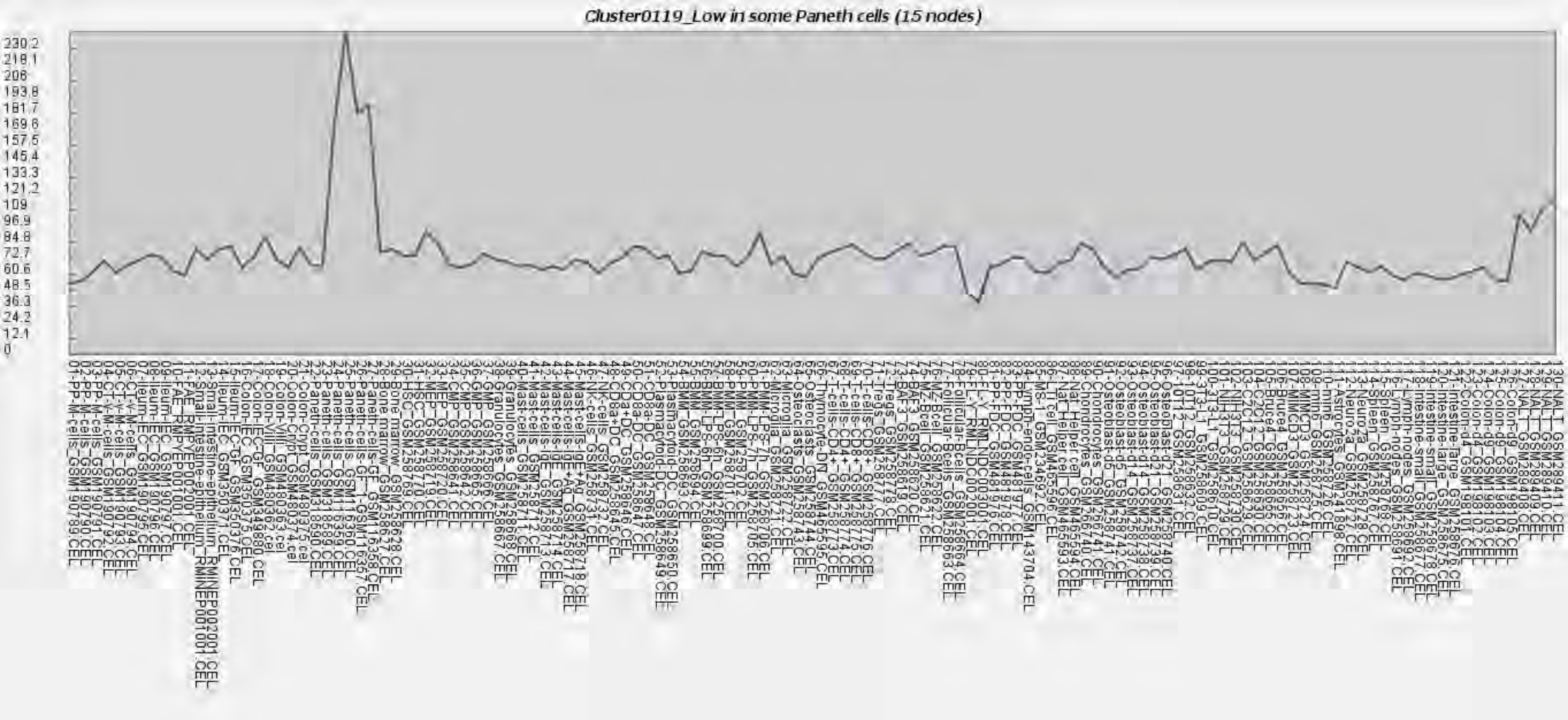

Cluster0114_Uncertain (16 nodes)
4,389
4,158
3,927
3,696
3,465
3,234
3,003
2,772
2,541
2,310
2,079
1,848
1,617
1,386
1,155
924
693
462
231
0

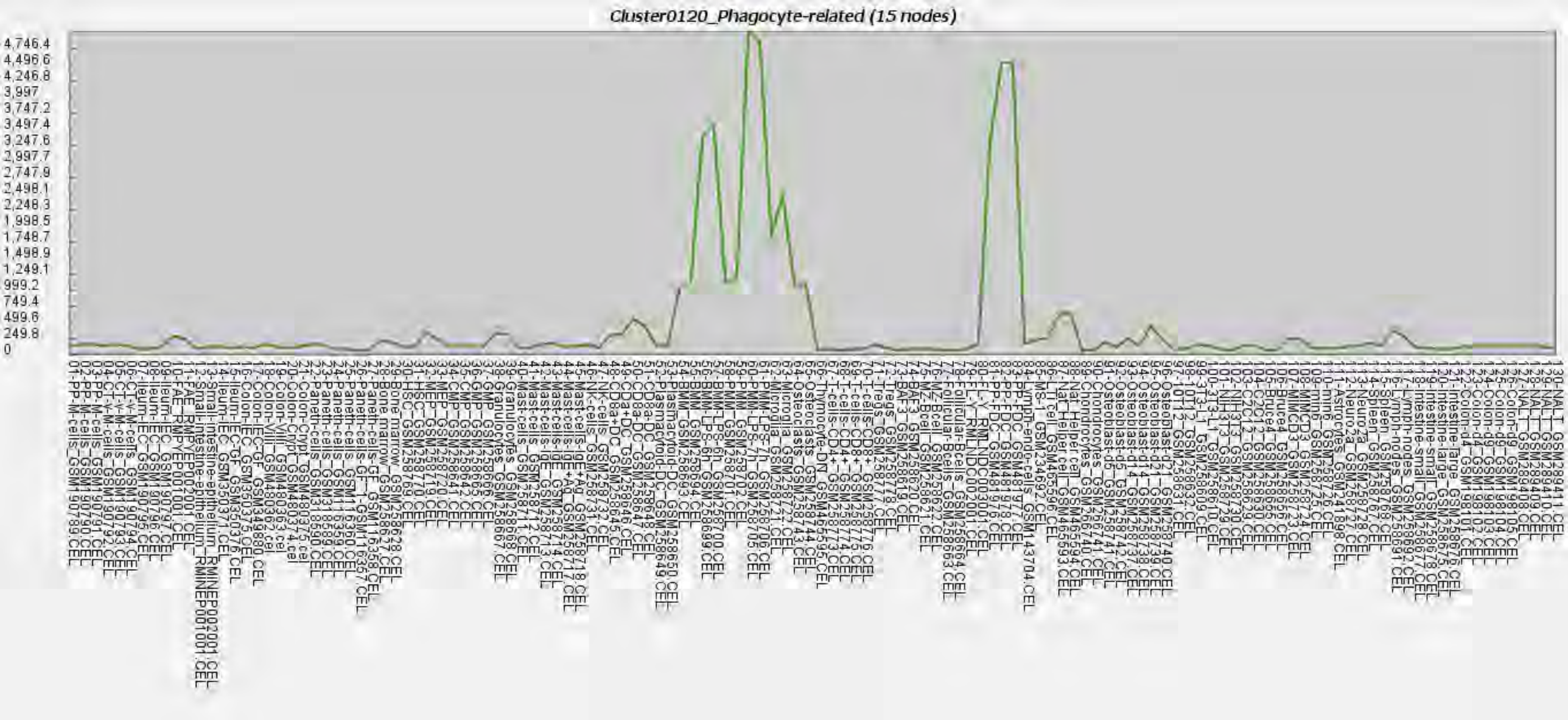

Cluster0115_House keeping-cell cycle (16 nodes)
2,325
2,202.6
2,080.2
1,957.9
1,835.5
1,713.1
1,590.8
1,468.4
1,346
1,223.7
1,101.3
978.9
856.6
734.2
611.8
489.5
367.1
244.7
122.4
0


Cluster0116_intestine-related (16 nodes)
3,045.5
2,885.2
2,724.9
2,564.7
2,404.4
2,244.1
2,083.8
1,923.5
1,763.2
1,602.9
1,442.6
1,282.3
1,122
961.7
801.5
641.2
480.9
320.6
160.3
0

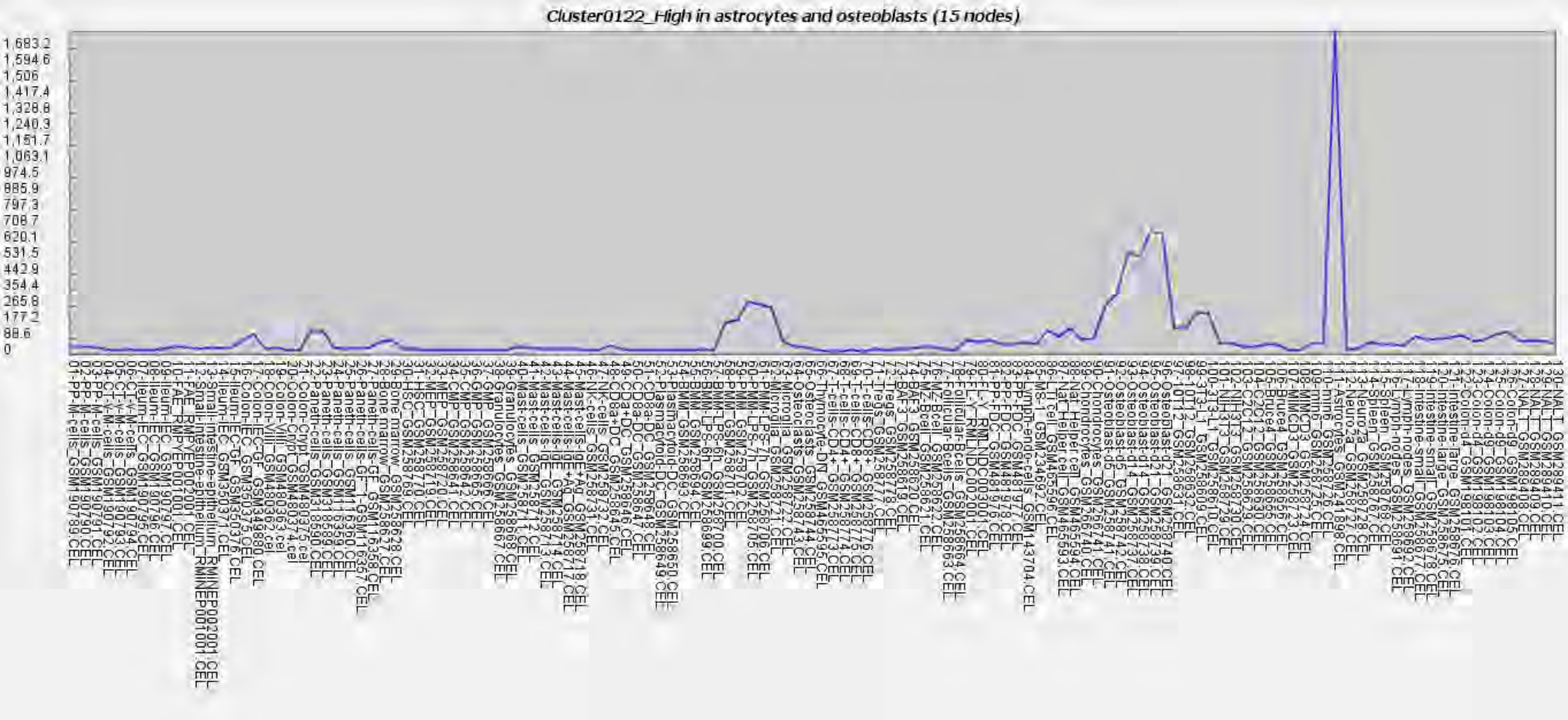

Cluster0117_High in some Paneth cells (16 nodes)
331.3
313.8
296.4
279
261.5
244.1
226.7
209.2
191.8
174.4
156.9
139.5
122
104.6
87.2
69.7
52.3
34.9
17.4
0

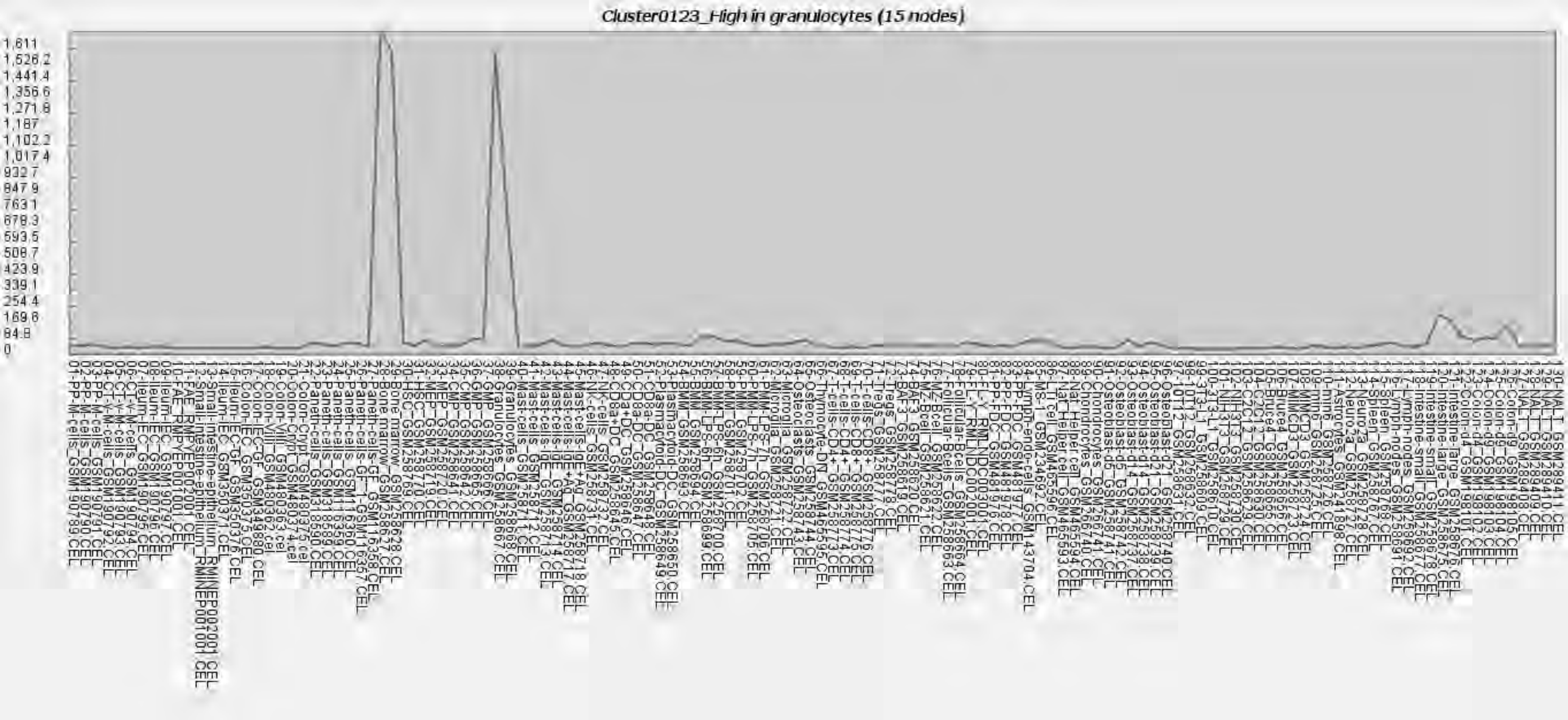

Cluster0118_Paneth cell-related (16 nodes)
2,851.2
2,701.1
2,551.1
2,401
2,250.9
2,100.9
1,950.8
1,800.8
1,650.7
1,500.6
1,350.6
1,200.5
1,050.4
900.4
750.3
600.3
450.2
300.1
150.1
0


Cluster0119_Low in some Paneth cells (15 nodes)
230.2
218.1
206
193.8
181.7
169.6
157.5
145.4
133.3
121.2
109
96.9
84.8
72.7
60.6
48.5
36.3
24.2
12.1
0

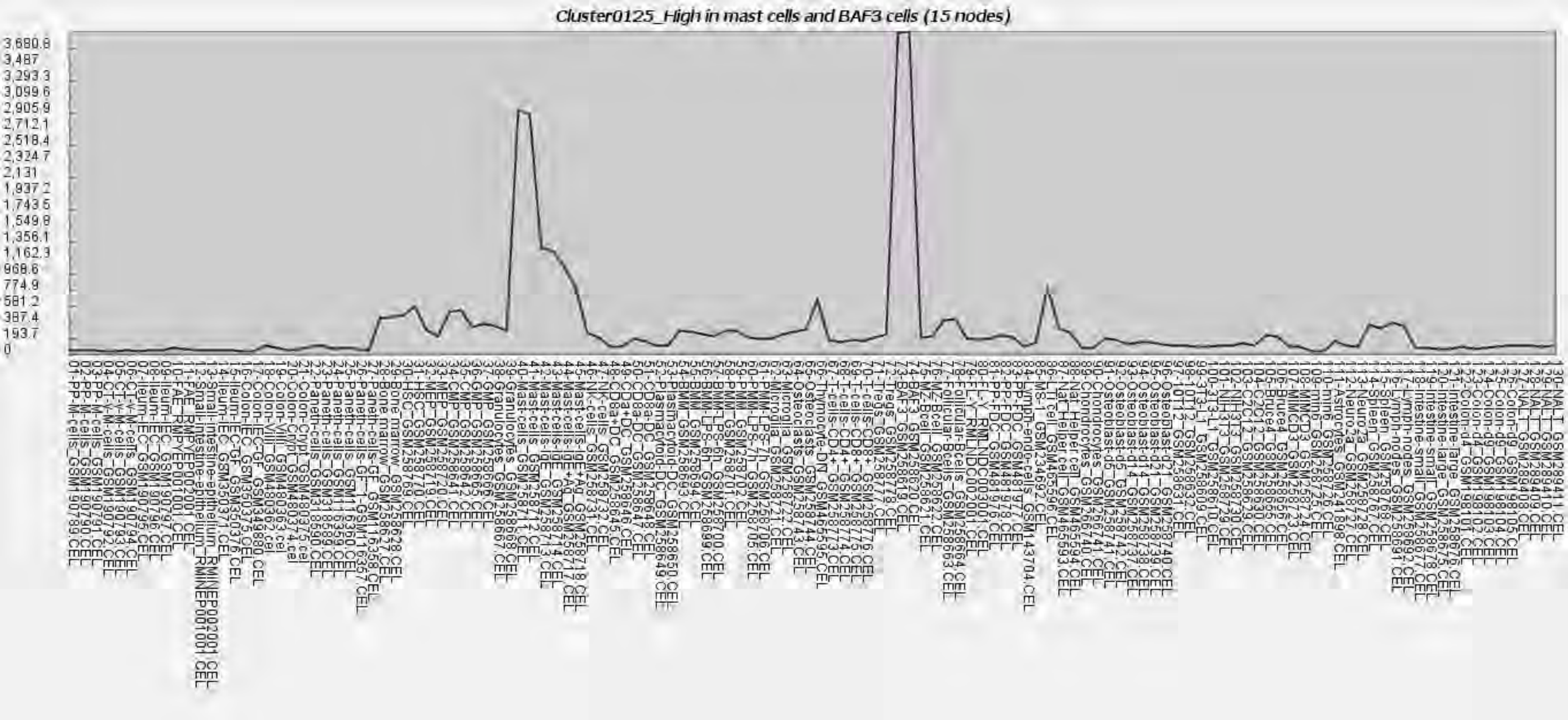

Cluster0120_Phagocyte-related (15 nodes)
4,746.4
4,496.6
4,246.8
3,997
3,747.2
3,497.4
3,247.6
2,997.7
2,747.9
2,498.1
2,248.3
1,998.5
1,748.7
1,498.9
1,249.1
999.2
749.4
499.6
249.8
0

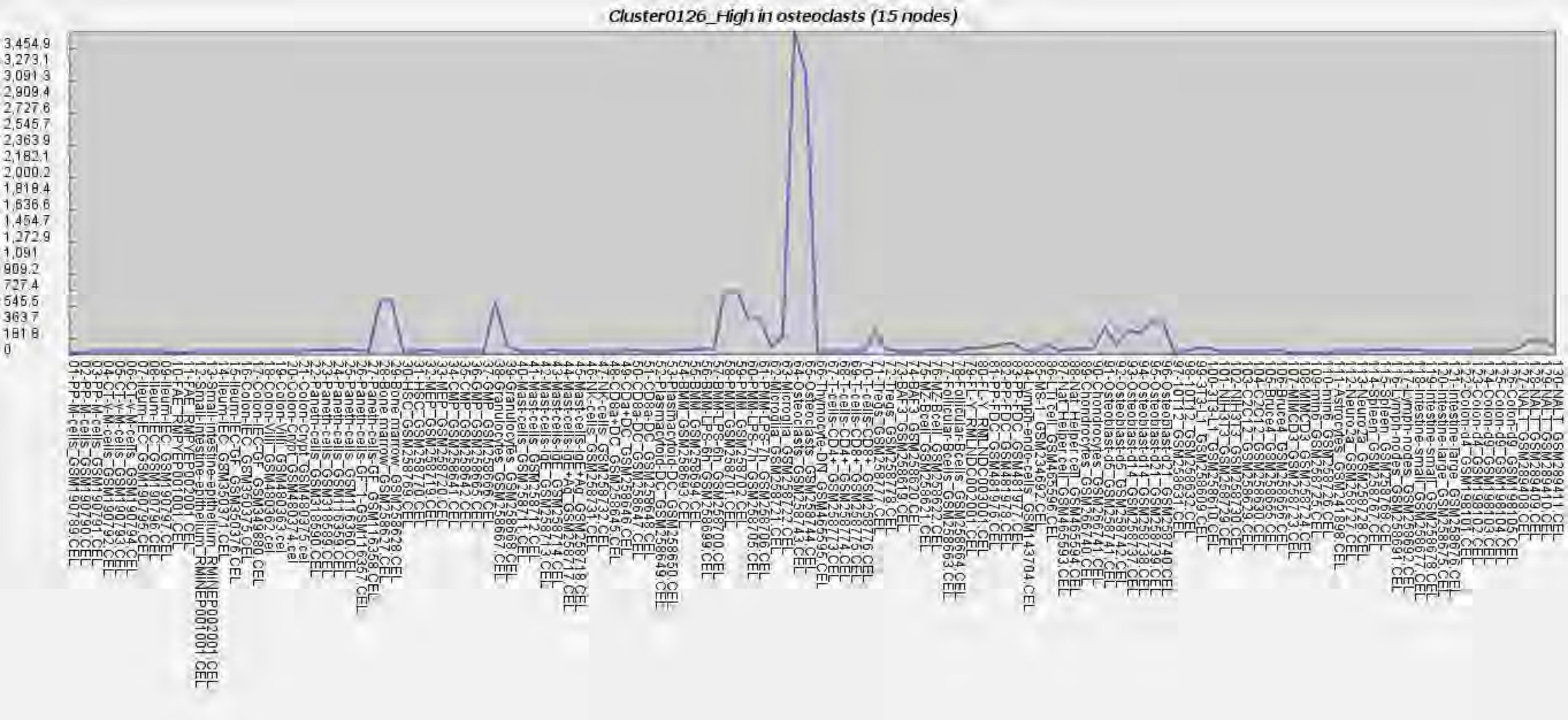
Cluster0121_Large intestine-related (15 nodes)
1,045.7
990.6
935.6
880.6
825.5
770.5
715.5
660.4
605.4
550.3
495.3
440.3
385.2
330.2
275.2
220.1
165.1
110.1
55
0

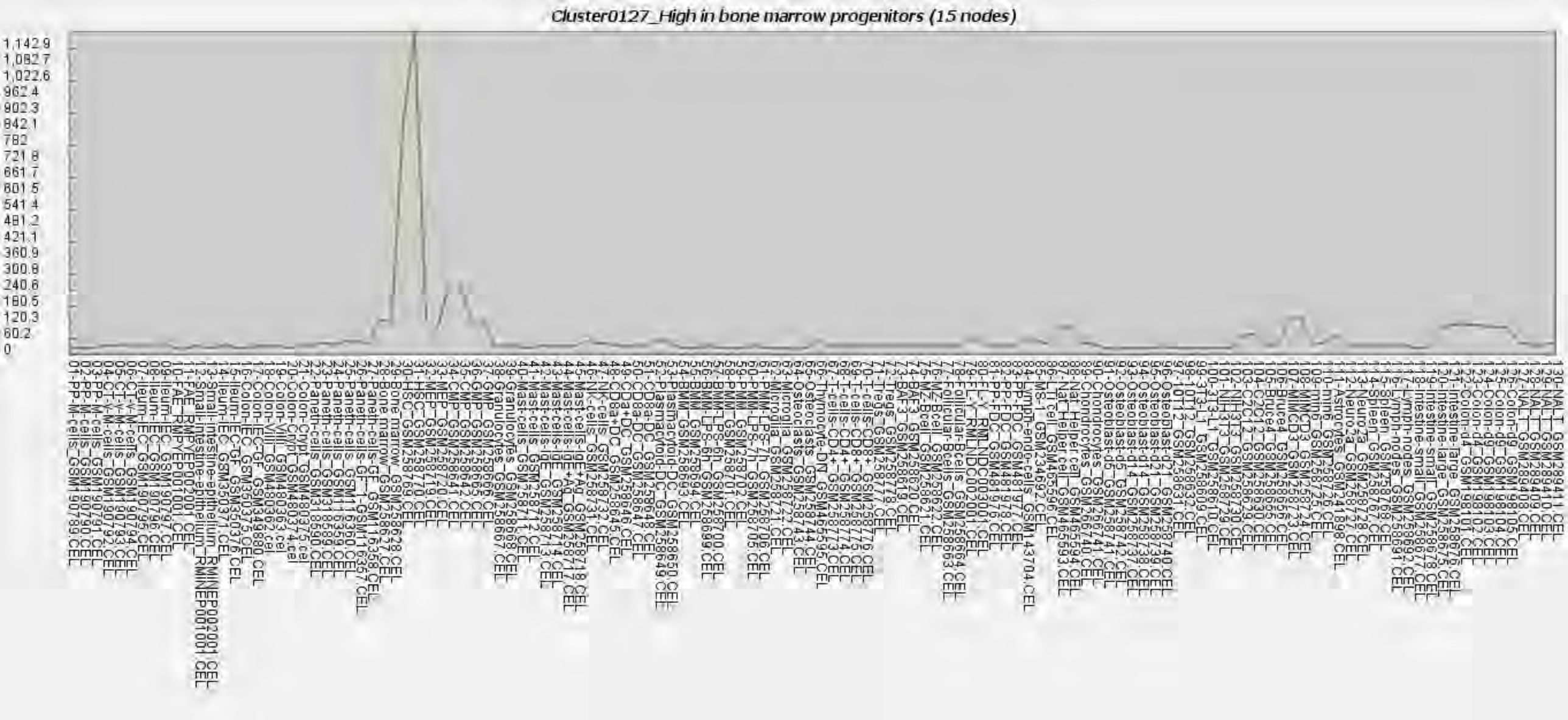

Cluster0122_High in astrocytes and osteoblasts (15 nodes)
1,683.2
1,594.6
1,506
1,417.4
1,328.8
1,240.3
1,151.7
1,063.1
974.5
885.9
797.3
708.7
620.1
531.5
442.9
354.4
265.8
177.2
88.6
0

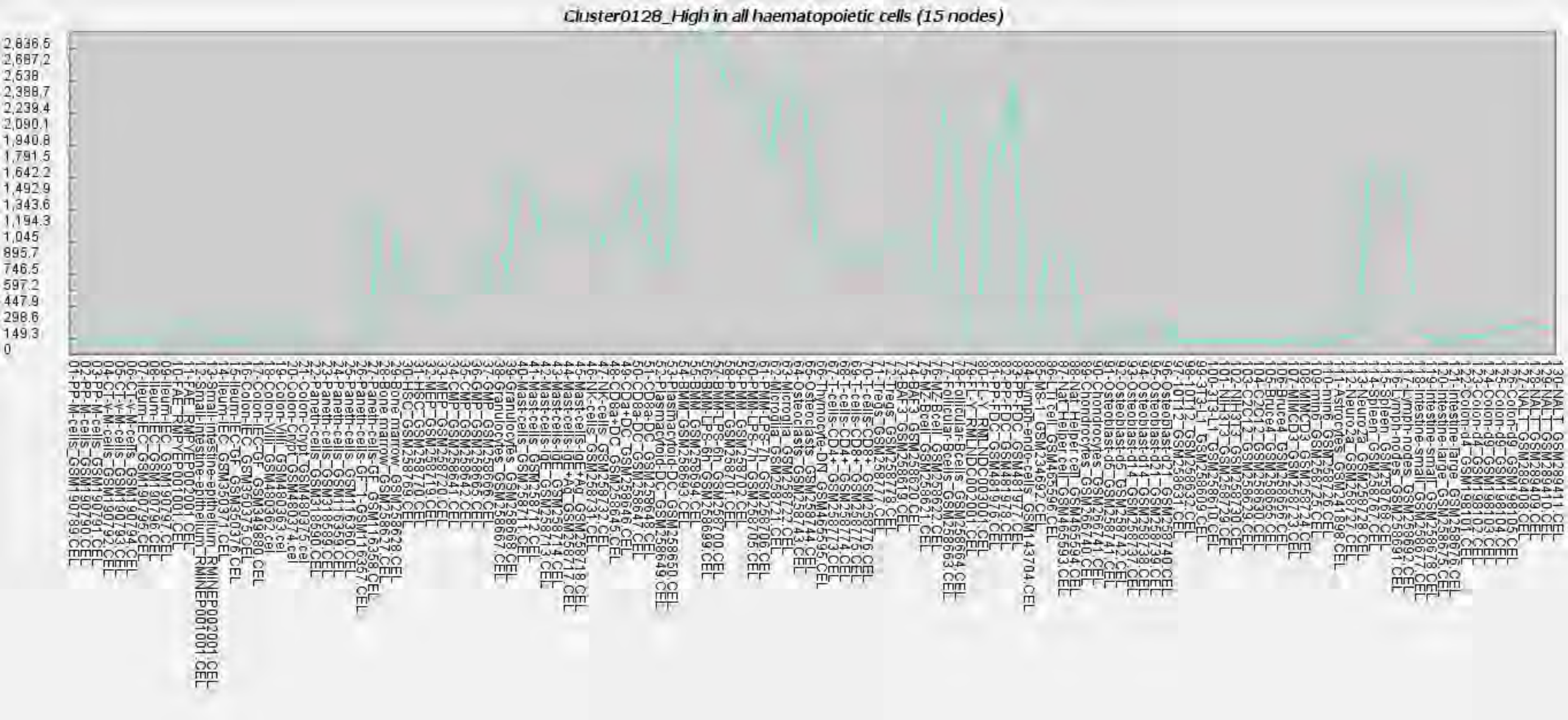

Cluster0123_High in granulocytes (15 nodes)
1,611
1,526.2
1,441.4
1,356.6
1,271.8
1,187
1,102.2
1,017.4
932.7
847.9
763.1
678.3
593.5
508.7
423.9
339.1
254.4
169.6
84.8
0

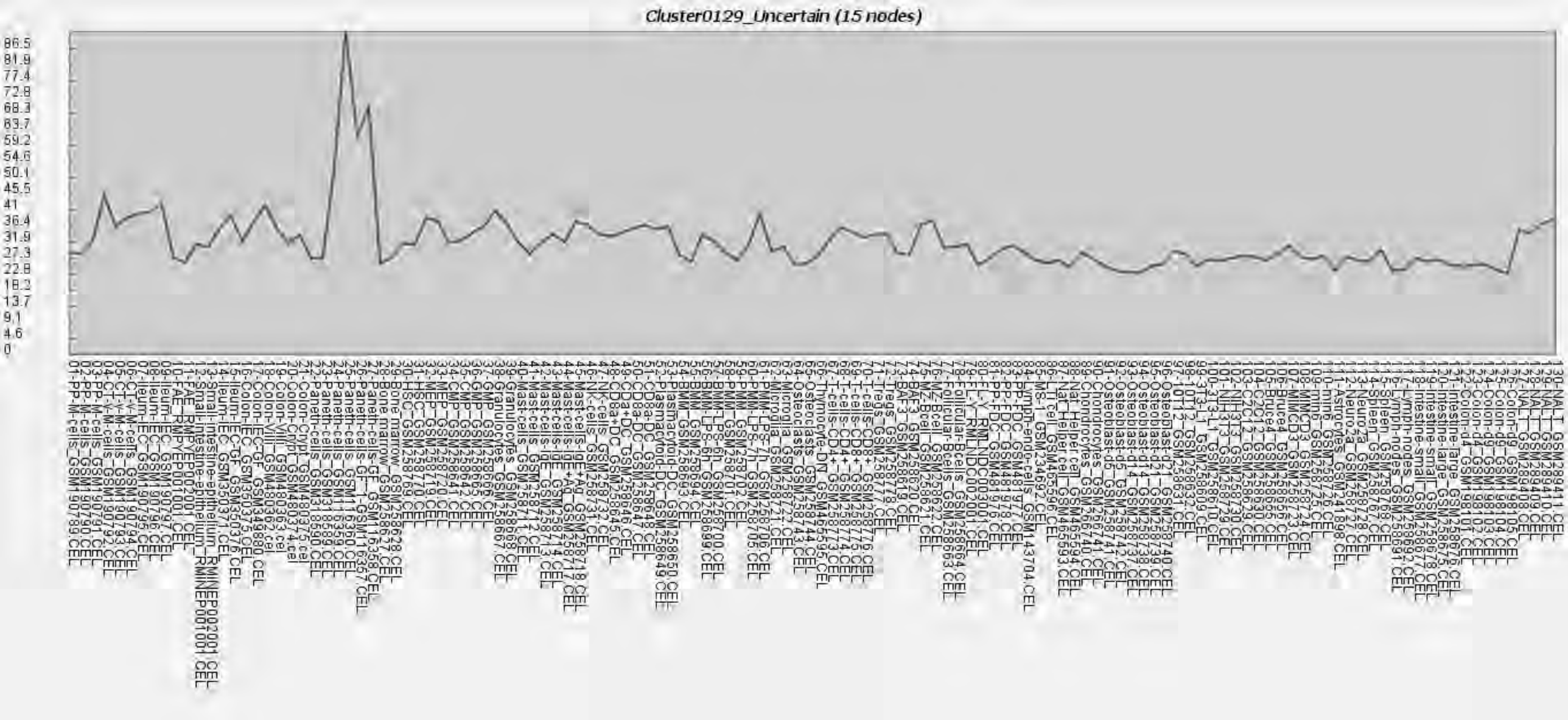
Cluster0124_intestine-related (15 nodes)
4,161.4
3,942.4
3,723.4
3,504.3
3,285.3
3,066.3
2,847.3
2,628.3
2,409.2
2,190.2
1,971.2
1,752.2
1,533.2
1,314.1
1,095.1
876.1
657.1
438
219
0


Cluster0125_High in mast cells and BAF3 cells (15 nodes)
3,680.8
3,487
3,293.3
3,099.6
2,905.9
2,712.1
2,518.4
2,324.7
2,131
1,937.2
1,743.5
1,549.8
1,356.1
1,162.3
968.6
774.9
581.2
387.4
193.7
0

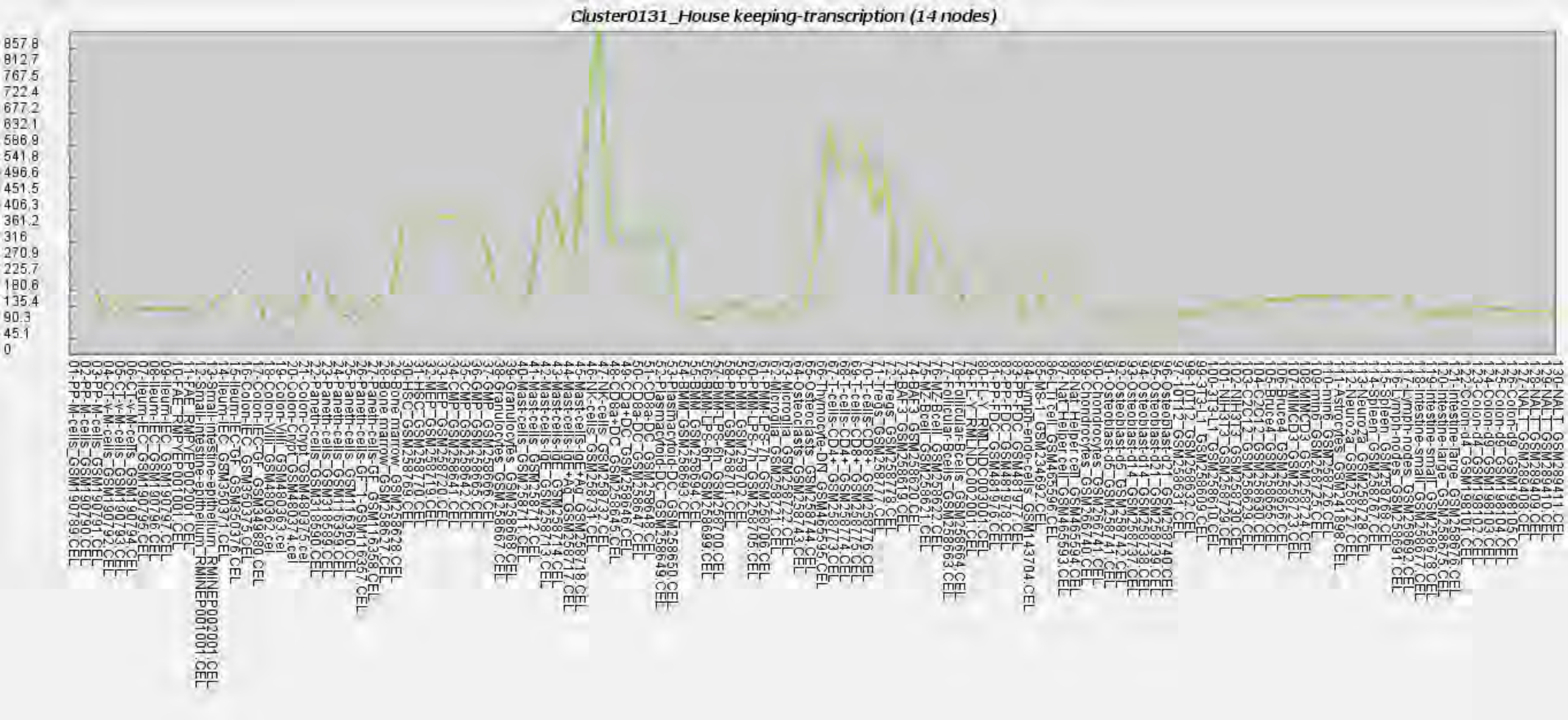

Cluster0126_High in osteoclasts (15 nodes)
3,454.9
3,273.1
3,091.3
2,909.4
2,727.6
2,545.7
2,363.9
2,182.1
2,000.2
1,818.4
1,636.6
1,454.7
1,272.9
1,091
909.2
727.4
545.6
363.7
181.8
0

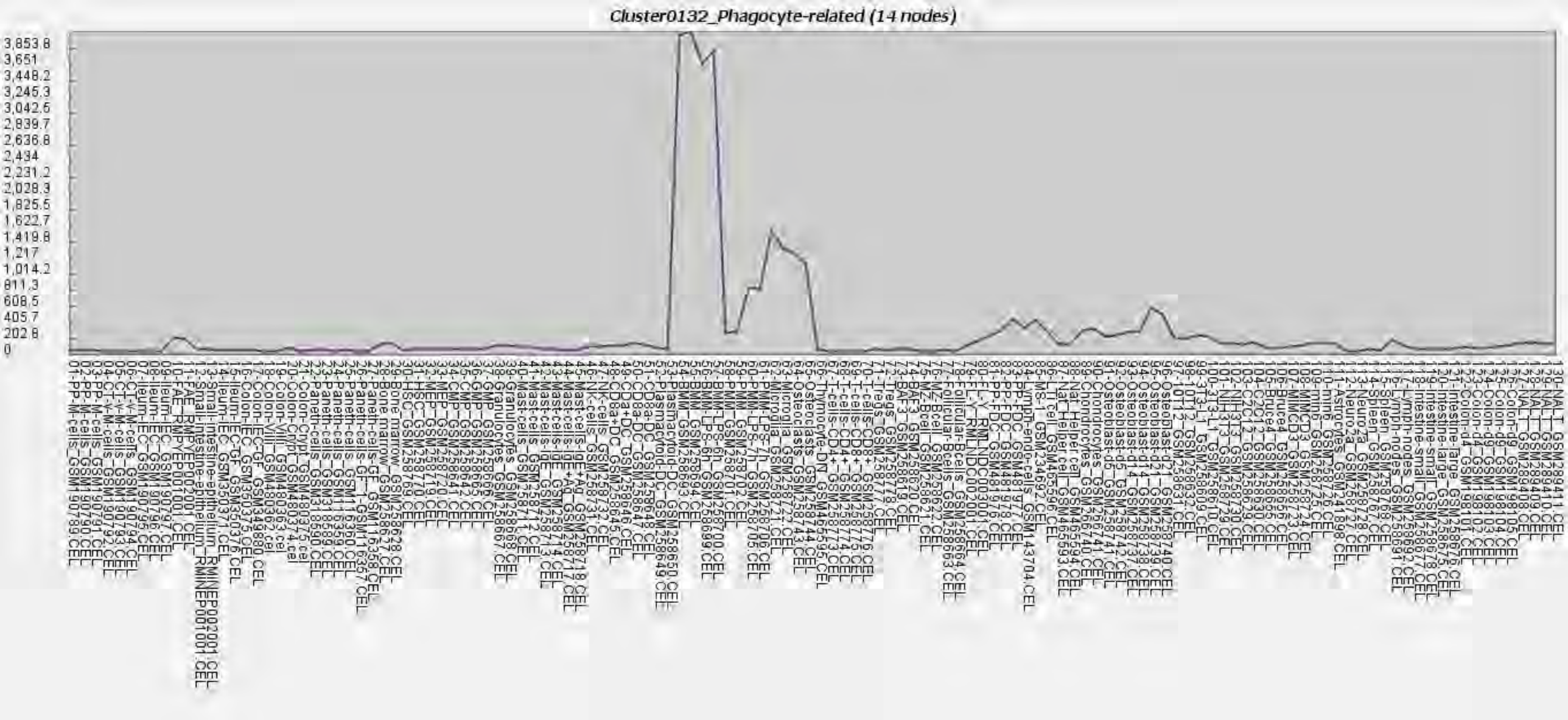

Cluster0127_High in bone marrow progenitors (15 nodes)
1,142.9
1,082.7
1,022.6
962.4
902.3
842.1
782
721.8
661.7
601.5
541.4
481.2
421.1
360.9
300.8
240.6
180.5
120.3
60.2
0

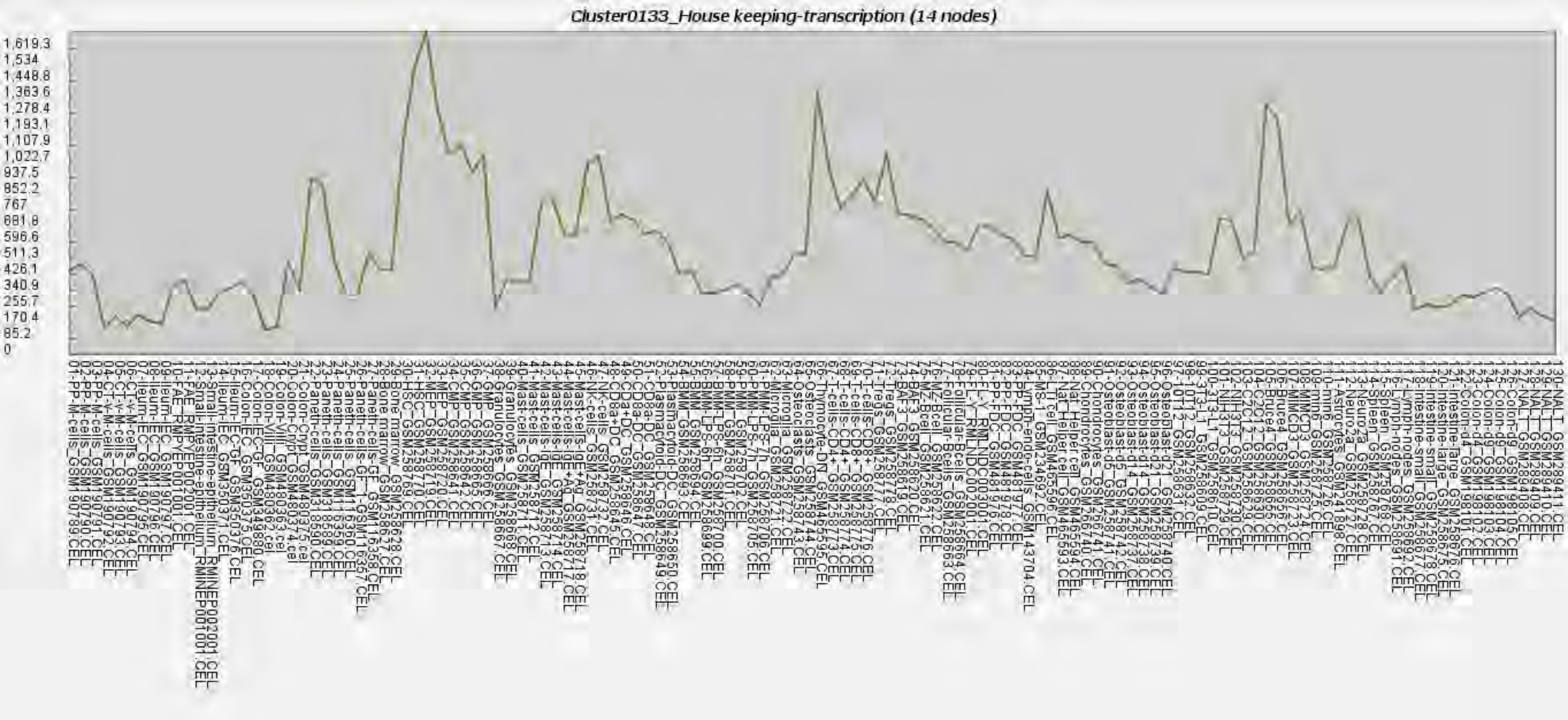

Cluster0128_High in all haematopoietic cells (15 nodes)
2,836.5
2,687.2
2,538
2,388.7
2,239.4
2,090.1
1,940.8
1,791.5
1,642.2
1,492.9
1,343.6
1,194.3
1,045
895.7
746.5
597.2
447.9
298.6
149.3
0


Cluster0129_Uncertain (15 nodes)
86.5
81.9
77.4
72.8
68.3
63.7
59.2
54.6
50.1
45.5
41
36.4
31.9
27.3
22.8
18.2
13.7
9.1
4.6
0

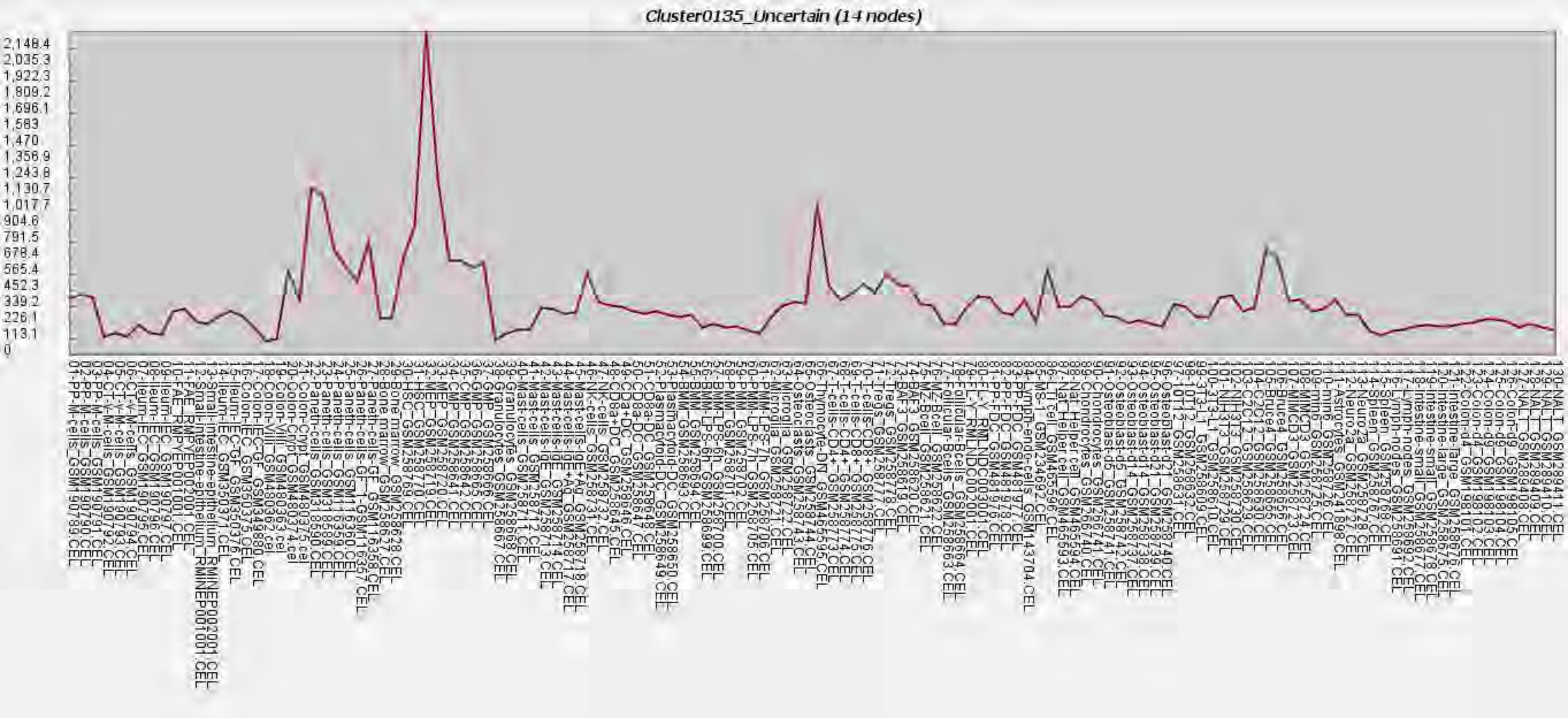
Cluster0130_Uncertain (14 nodes)
443.1
419.8
396.4
373.1
349.8
326.5
303.2
279.8
256.5
233.2
209.9
186.6
163.2
139.9
116.6
93.3
70
46.6
23.3
0

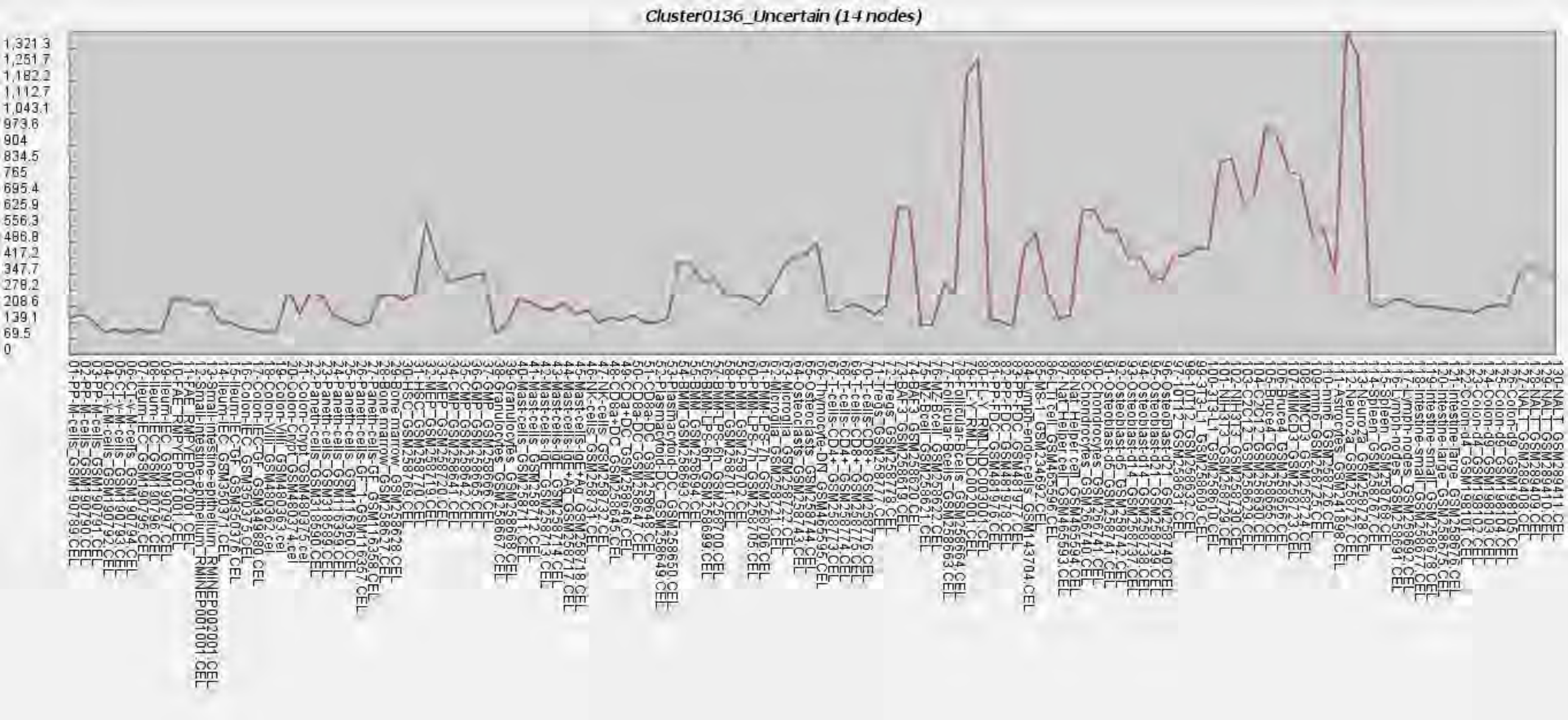

Cluster0131_House keeping-transcription (14 nodes)
857.8
812.7
767.5
722.4
677.2
632.1
586.9
541.8
496.6
451.5
406.3
361.2
316
270.9
225.7
180.6
135.4
90.3
45.1
0


Cluster0132_Phagocyte-related (14 nodes)
3,853.8
3,651
3,448.2
3,245.3
3,042.6
2,839.7
2,636.8
2,434
2,231.2
2,028.3
1,825.5
1,622.7
1,419.8
1,217
1,014.2
811.3
608.5
405.7
202.8
0

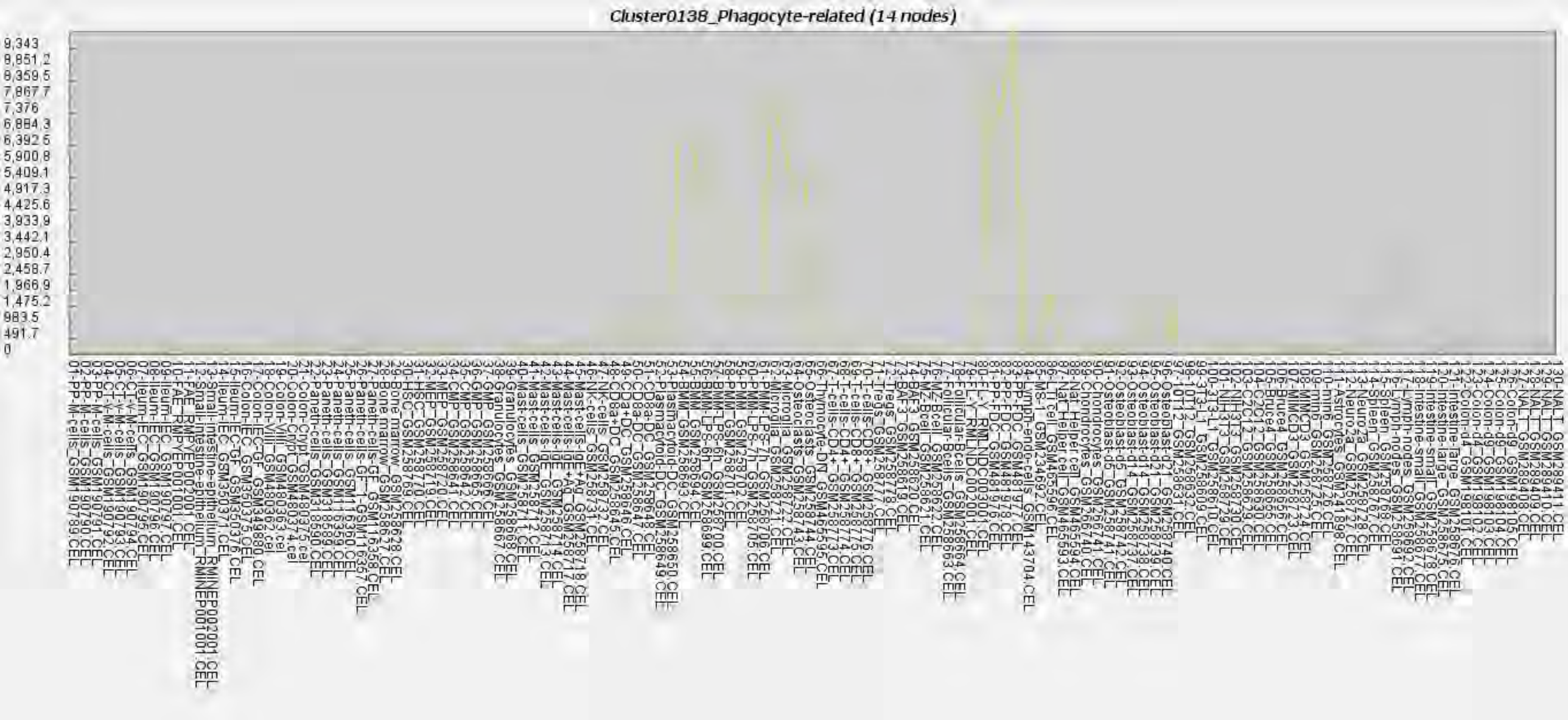

Cluster0133_House keeping-transcription (14 nodes)
1,619.3
1,534
1,448.8
1,363.6
1,278.4
1,193.1
1,107.9
1,022.7
937.5
852.2
767
681.8
596.6
511.3
426.1
340.9
255.7
170.4
85.2
0

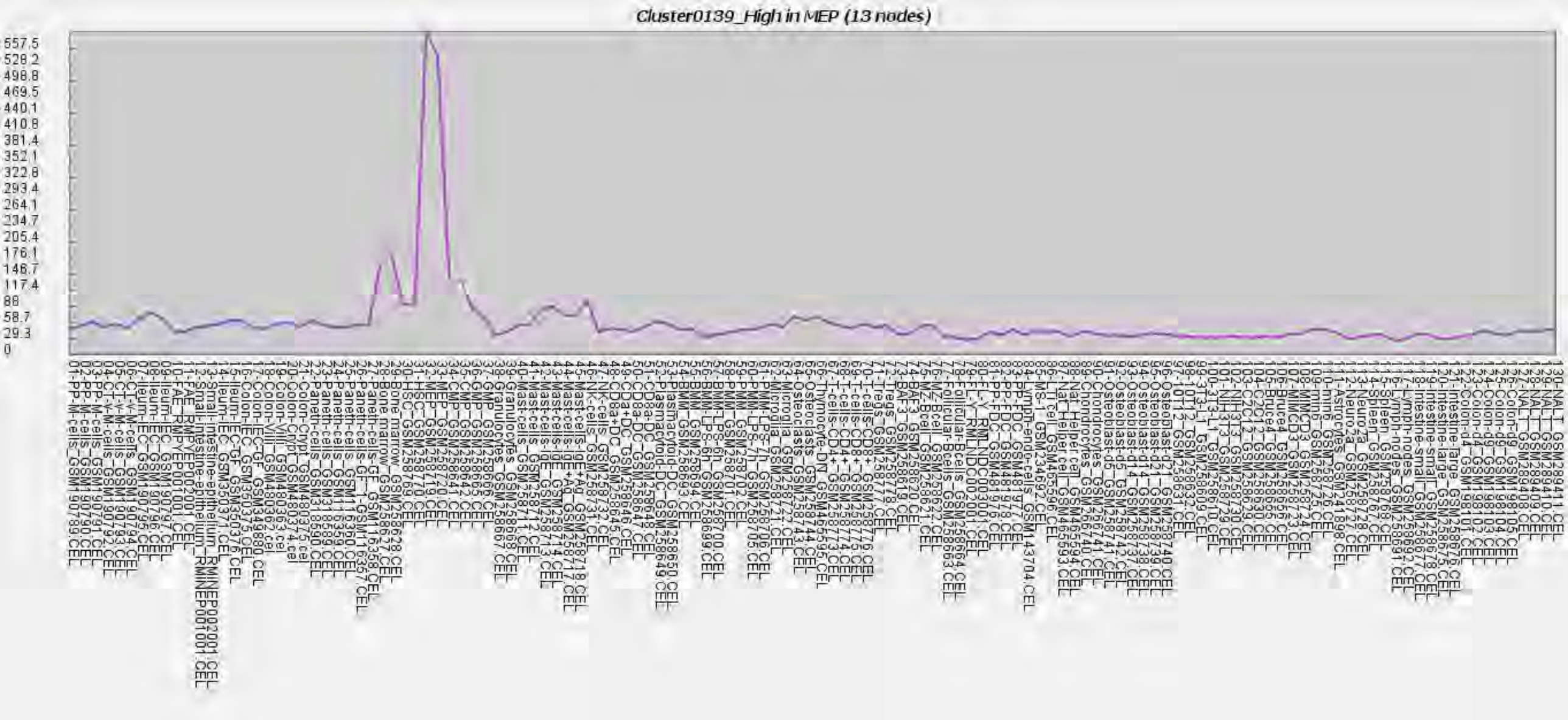
Cluster0134_intestine-related (14 nodes)
548.8
519.9
491
462.2
433.3
404.4
375.5
346.6
317.7
288.9
260
231.1
202.2
173.3
144.4
115.5
86.7
57.8
28.9
0


Cluster0135_Uncertain (14 nodes)
2,148.4
2,035.3
1,922.3
1,809.2
1,696.1
1,583
1,470
1,356.9
1,243.8
1,130.7
1,017.7
904.6
791.5
678.4
565.4
452.3
339.2
226.1
113.1
0


Cluster0136_Uncertain (14 nodes)
1,321.3
1,251.7
1,182.2
1,112.7
1,043.1
973.6
904
834.5
765
695.4
625.9
556.3
486.8
417.2
347.7
278.2
208.6
139.1
69.5
0

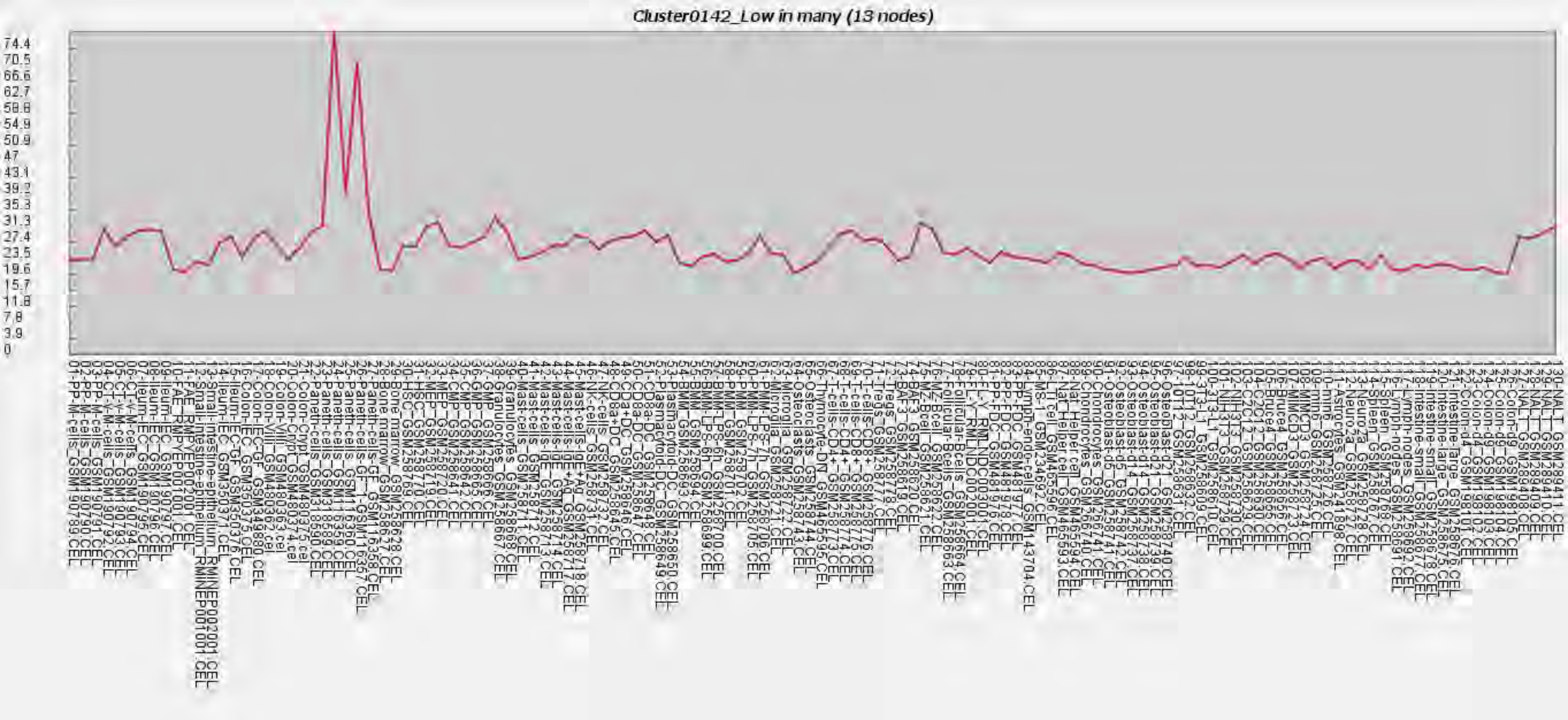
Cluster0137_Uncertain (14 nodes)
104.7
99.2
93.7
88.2
82.7
77.2
71.6
66.1
60.6
55.1
49.6
44.1
38.6
33.1
27.6
22
16.5
11
5.5
0

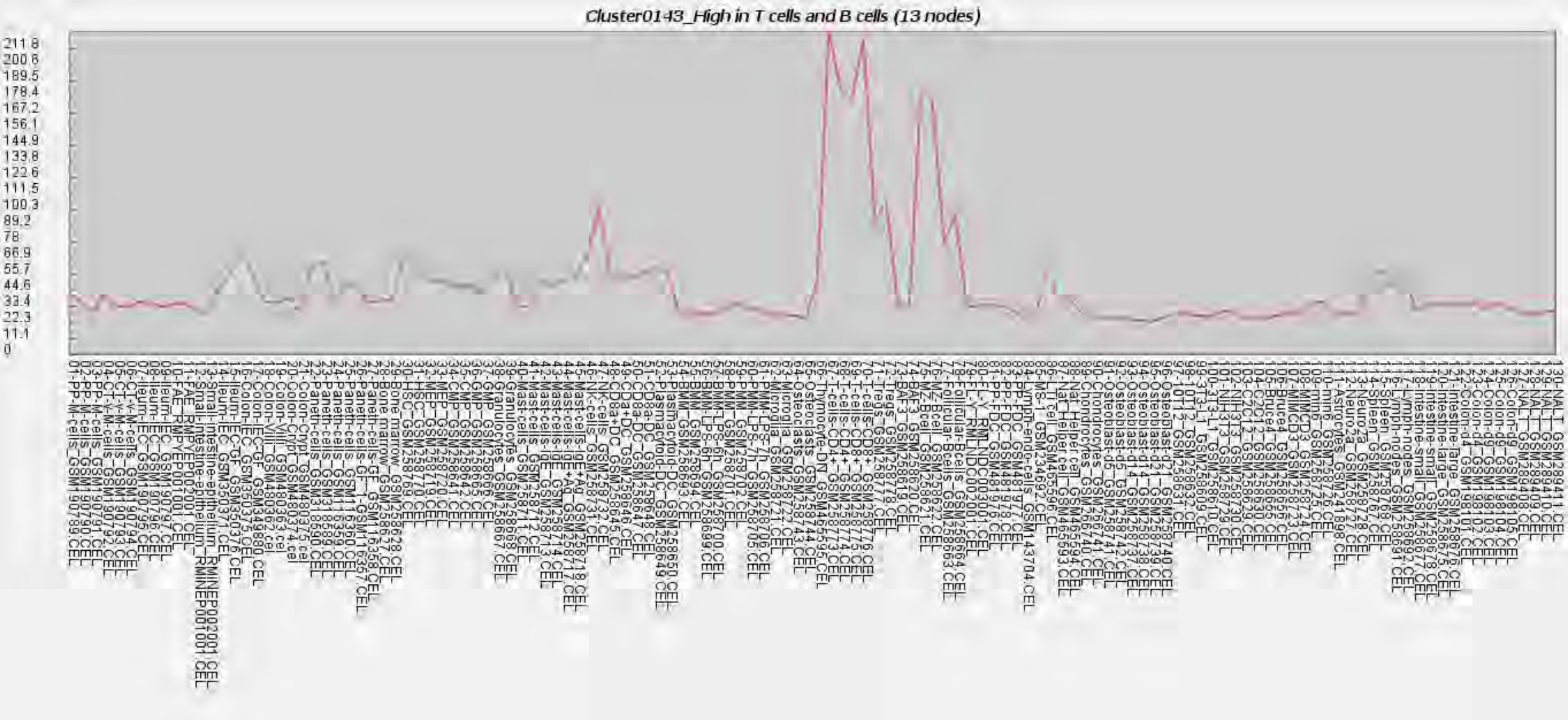

Cluster0138_Phagocyte-related (14 nodes)
9,343
8,851.2
8,359.5
7,867.7
7,376
6,884.3
6,392.5
5,900.8
5,409.1
4,917.3
4,425.6
3,933.9
3,442.1
2,950.4
2,458.7
1,966.9
1,475.2
983.5
491.7
0

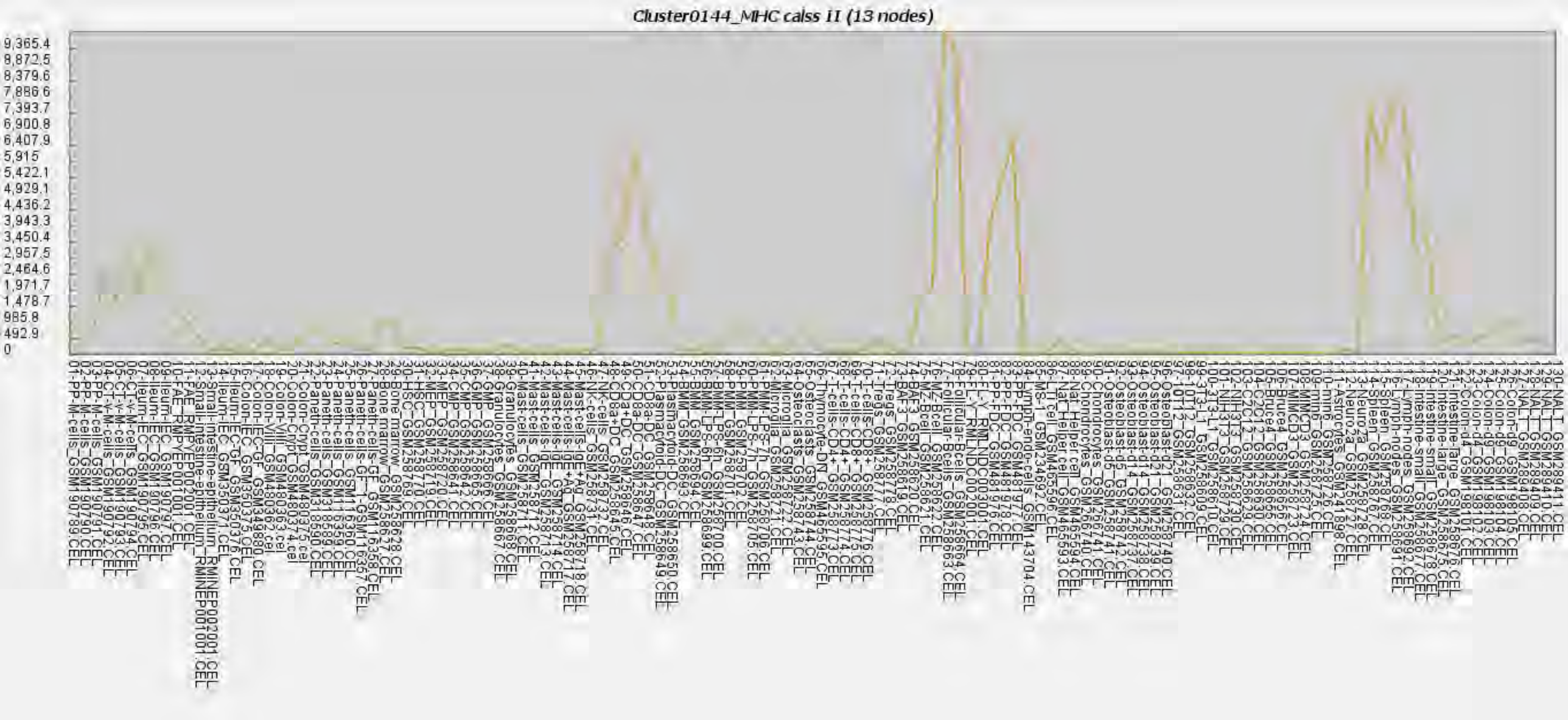

Cluster0139_High in MEP (13 nodes)
657.5
528.2
498.8
469.5
440.1
410.8
381.4
352.1
322.8
293.4
264.1
234.7
205.4
176.1
146.7
117.4
88
58.7
29.3
0

Cluster0140_intestine-related (13 nodes)
2,392
2,266.1
2,140.2
2,014.4
1,888.5
1,762.6
1,636.7
1,510.8
1,384.9
1,259
1,133.1
1,007.2
881.3
755.4
629.5
503.6
377.7
251.8
125.9
0

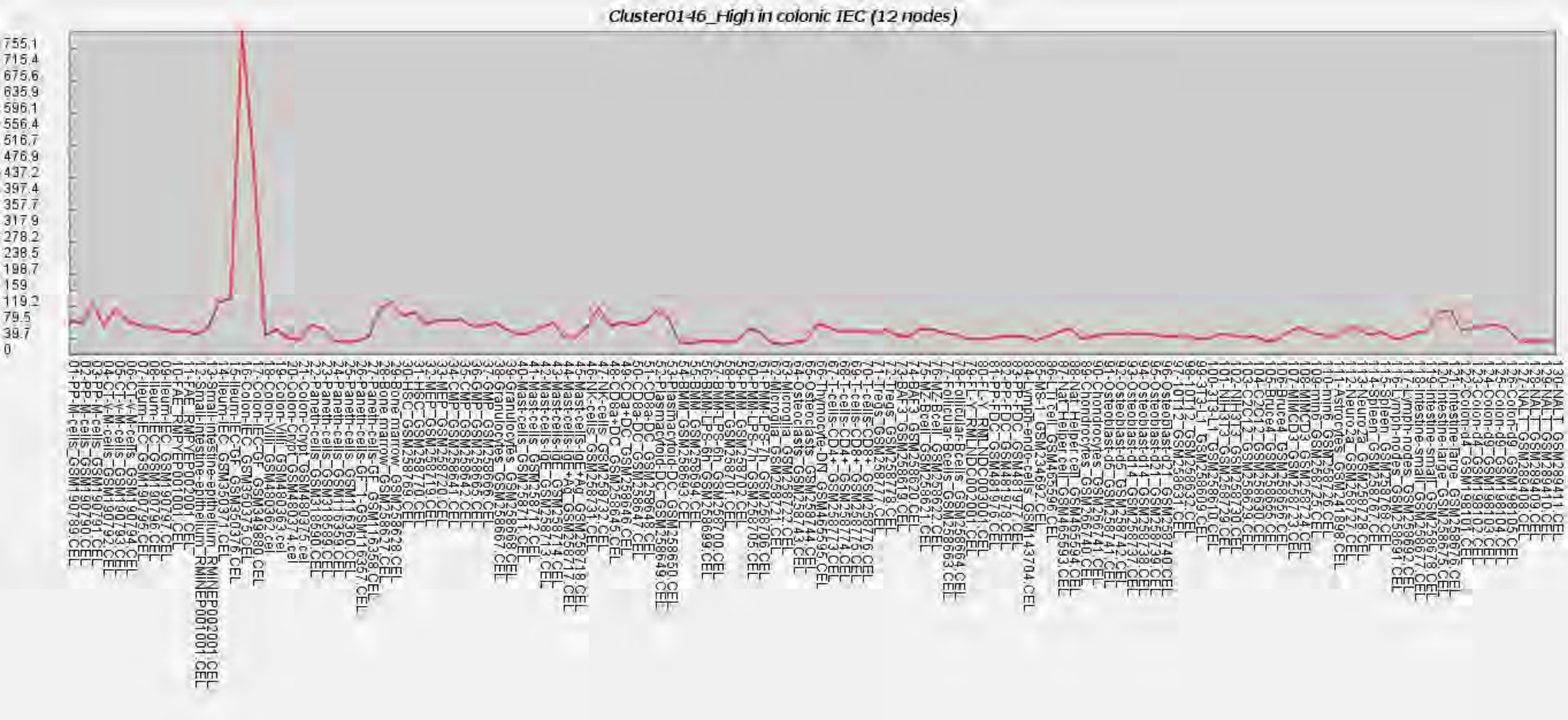
Cluster0141_High in min6 cells and NALT (13 nodes)
496.8
472.6
446.3
420.1
393.8
367.6
341.3
315
288.8
262.5
236.3
210
183.8
157.5
131.3
105
78.8
52.5
26.3
0

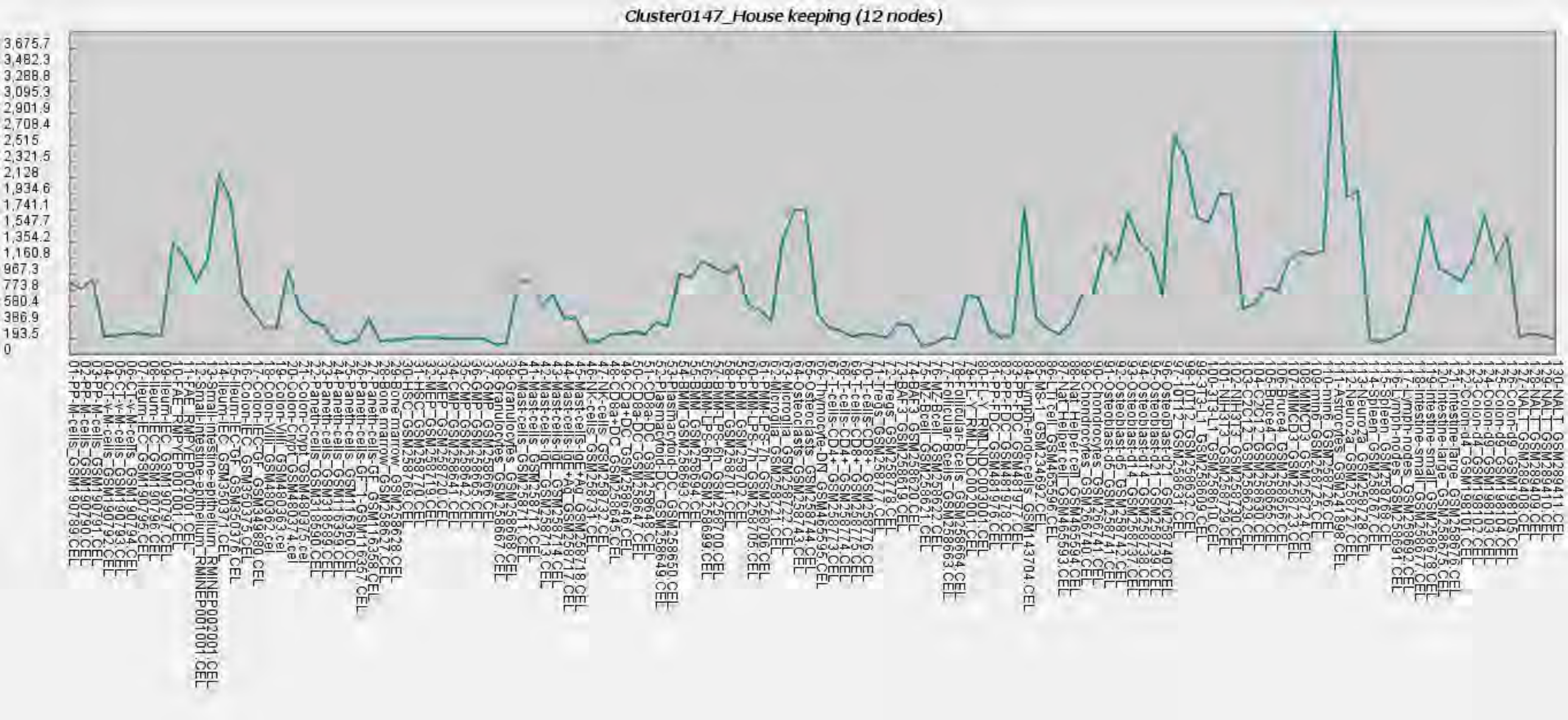

Cluster0142_Low in many (13 nodes)
74.4
70.5
66.6
62.7
58.8
54.9
50.9
47
43.1
39.2
35.3
31.3
27.4
23.5
19.6
15.7
11.8
7.8
3.9
0

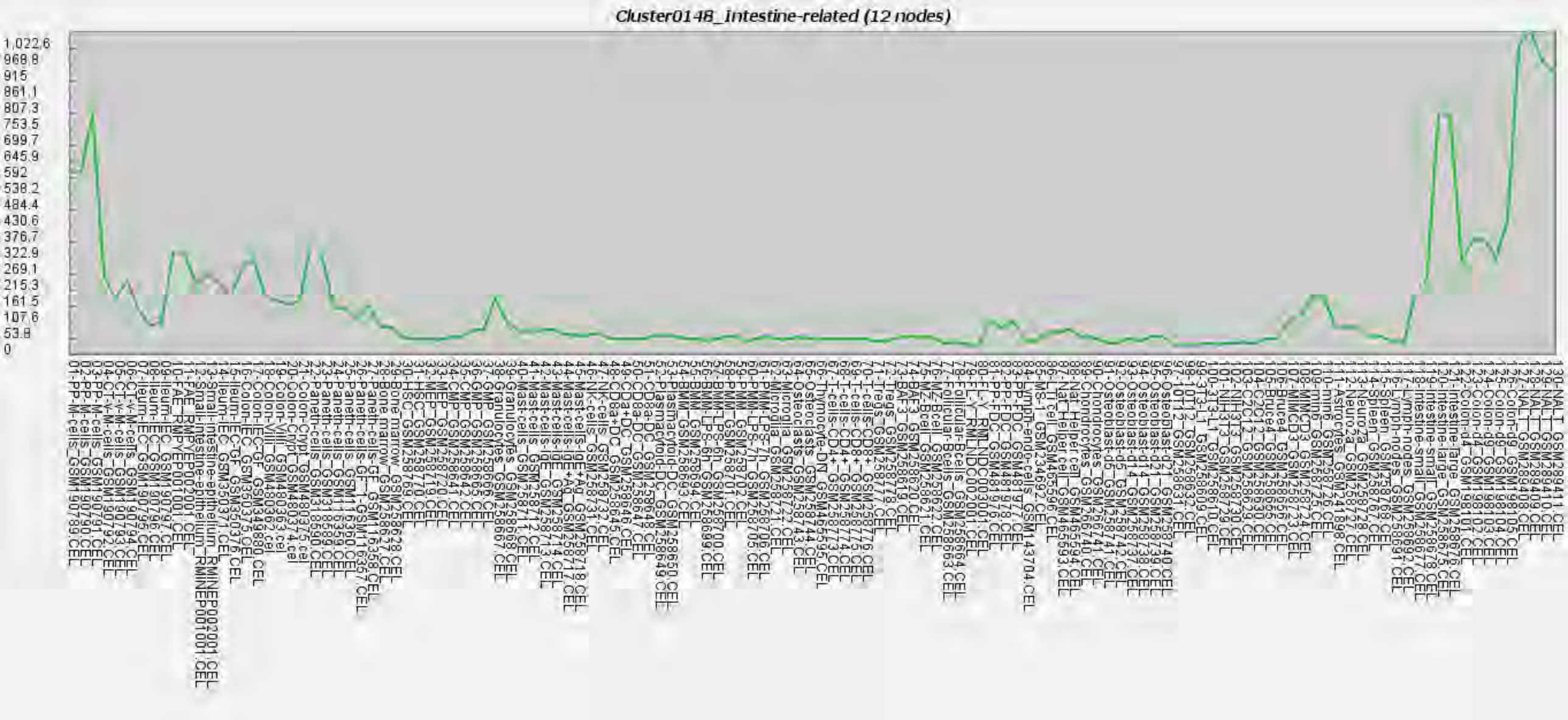

Cluster0143_High in T cells and B cells (13 nodes)
211.8
200.6
189.5
178.4
167.2
156.1
144.9
133.8
122.6
111.5
100.3
89.2
78
66.9
55.7
44.6
33.4
22.3
11.1
0

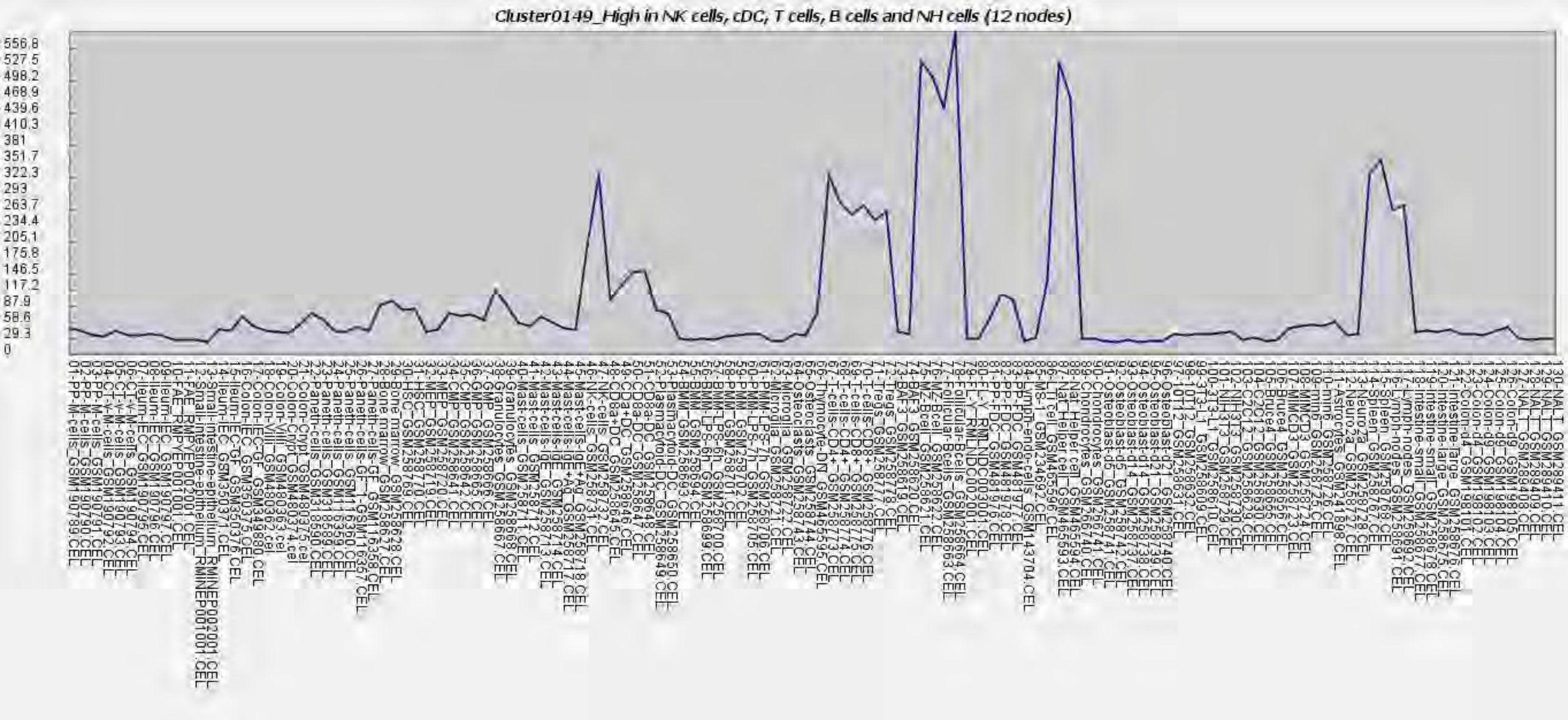

Cluster0144_MHC calss i1 (13 nodes)
9,365.4
8,872.5
8,379.6
7,886.6
7,393.7
6,900.8
6,407.9
5,915
5,422.1
4,929.1
4,436.2
3,943.3
3,450.4
2,957.5
2,464.6
1,971.7
1,478.7
985.8
492.9
0

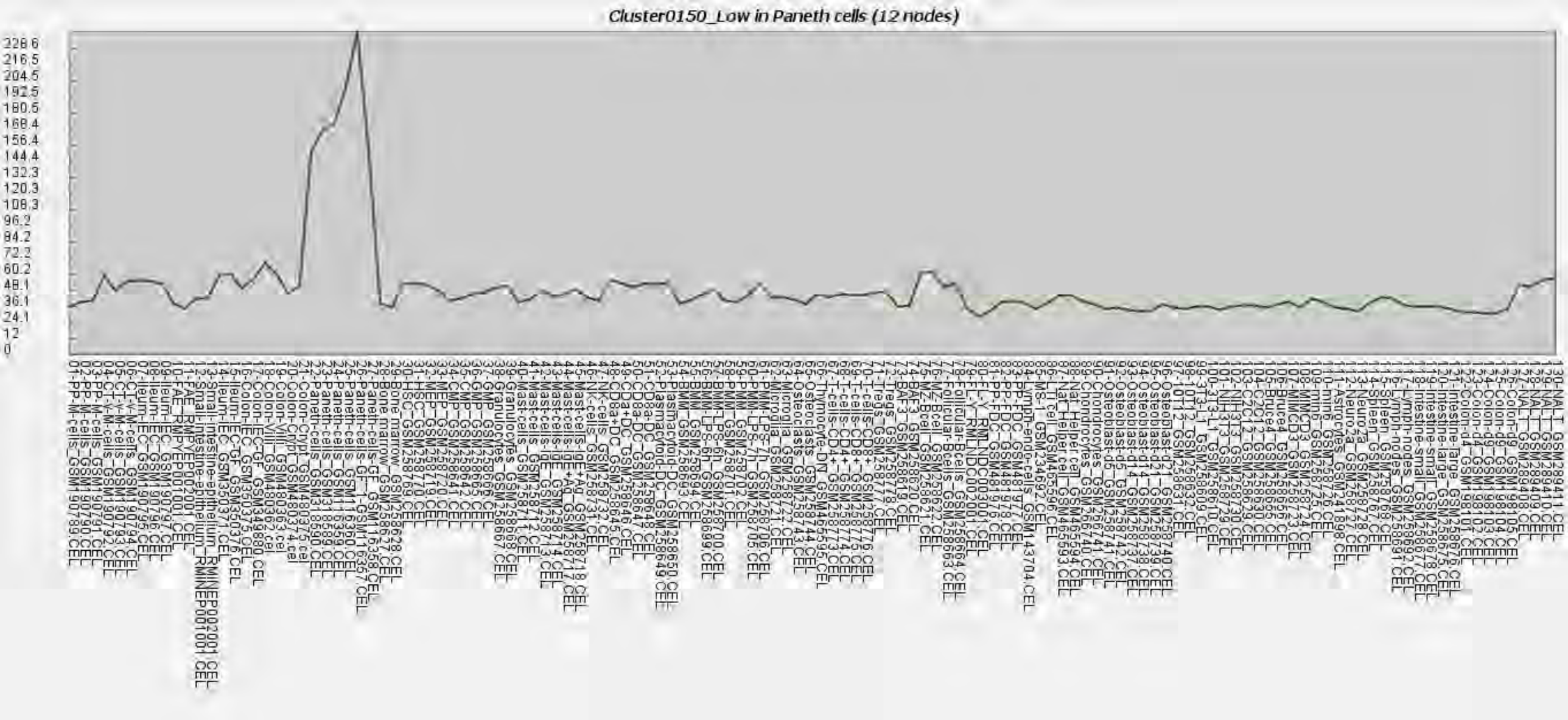
Cluster0145_intestine-related (13 nodes)
567.7
537.8
507.9
478
448.2
418.3
388.4
358.5
328.6
298.8
268.9
239
209.1
179.3
149.4
119.5
89.6
59.8
29.9
0


Cluster0146_High in colonic IEC (12 nodes)
755.1
715.4
675.6
635.9
596.1
556.4
516.7
476.9
437.2
397.4
357.7
317.9
278.2
238.5
198.7
159
119.2
79.5
39.7
0

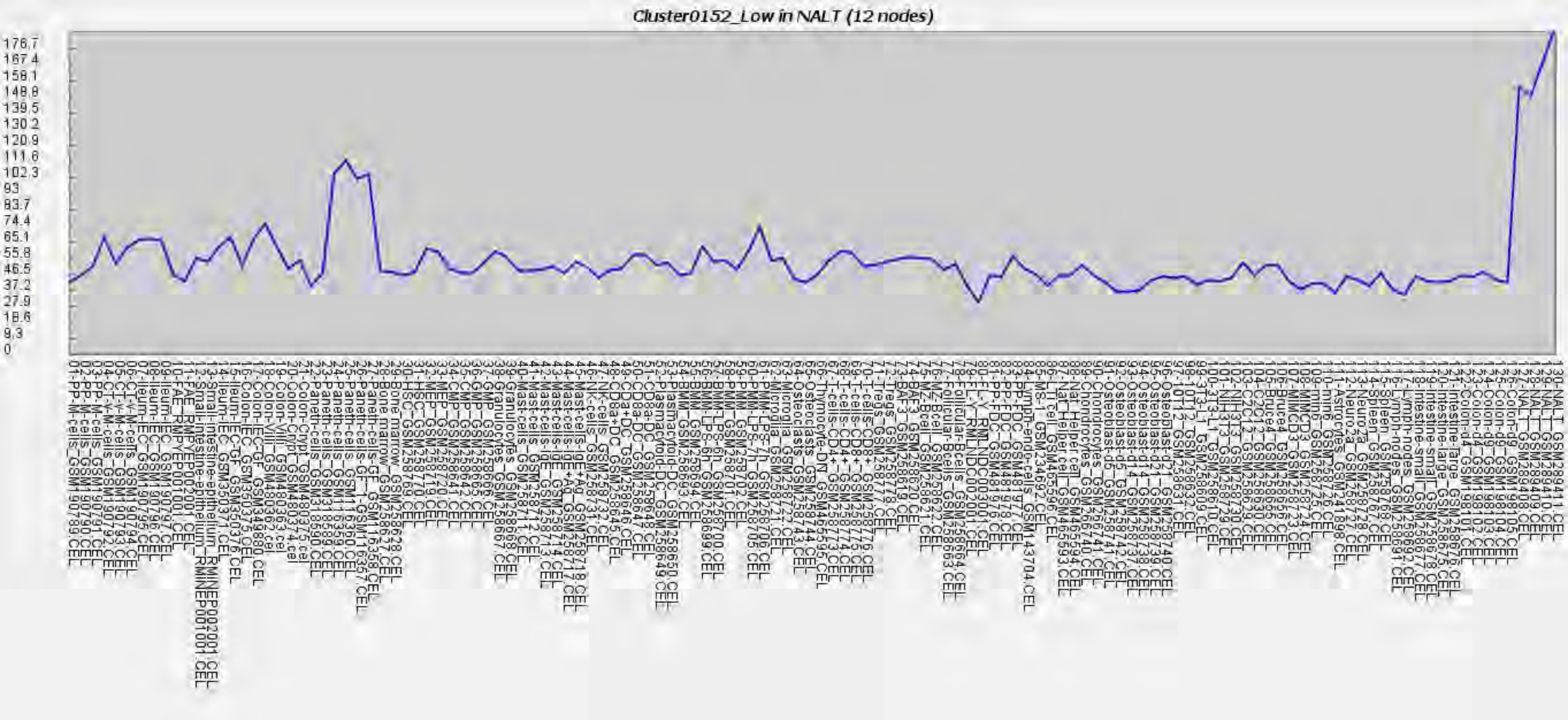

Cluster0147_House keeping (12 nodes)
3,675.7
3,482.3
3,288.8
3,095.3
2,901.9
2,708.4
2,515
2,321.5
2,128
1,934.6
1,741.1
1,547.7
1,354.2
1,160.8
967.3
773.8
580.4
386.9
193.5
0

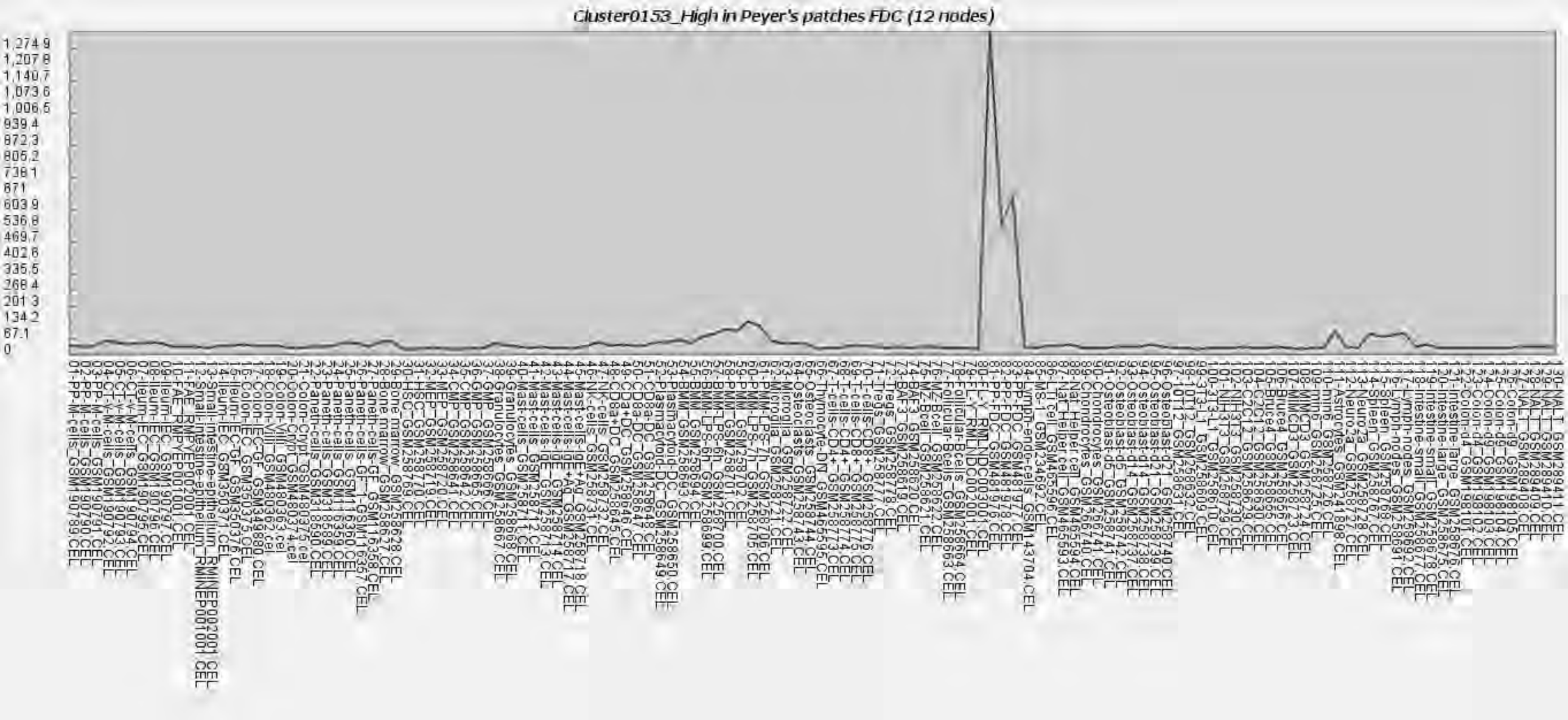

Cluster0148_intestine-related (12 nodes)
1,022.6
968.8
915
861.1
807.3
753.5
699.7
645.9
592
538.2
484.4
430.6
376.7
322.9
269.1
215.3
161.5
107.6
53.8
0

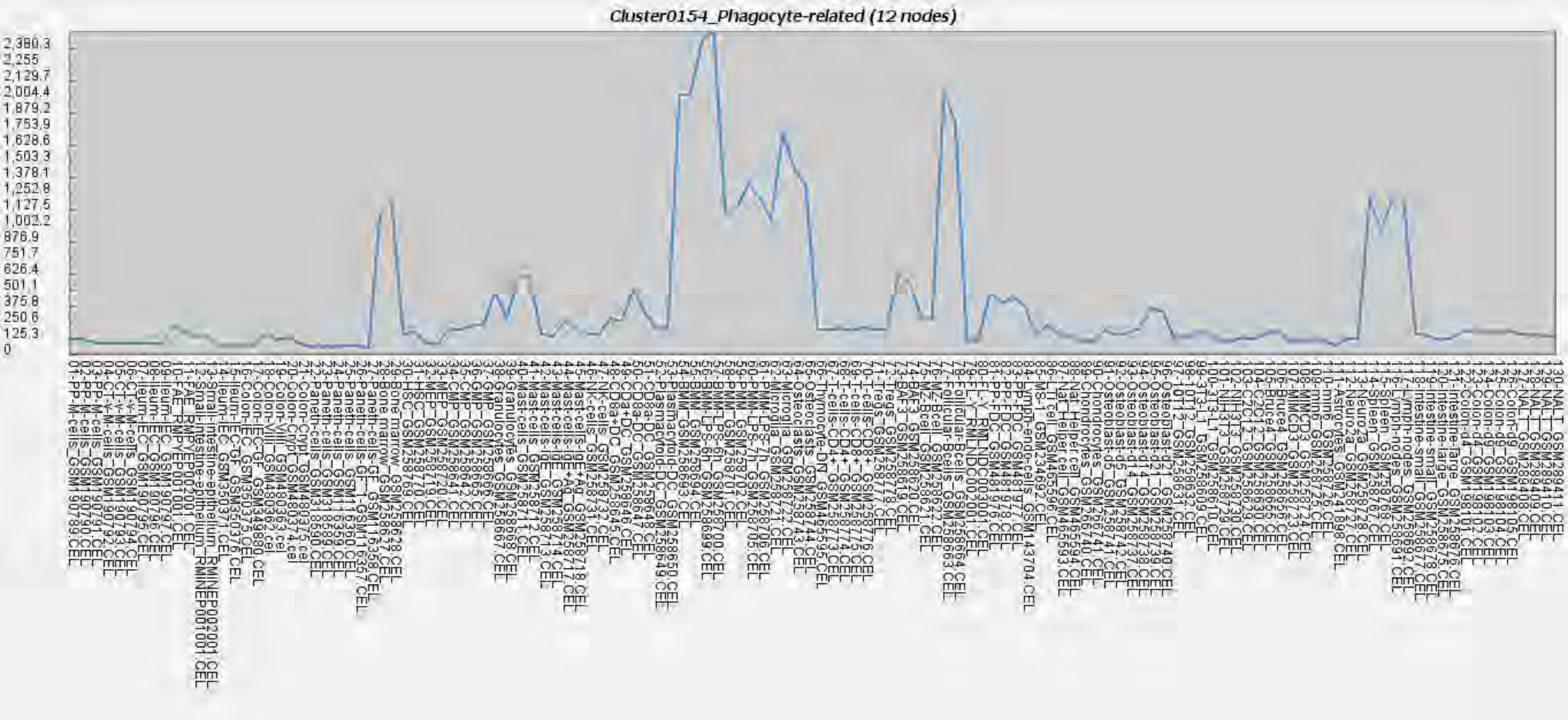

Cluster0149_High in NK cells, cDC, T cells, B cells and NH cells (12 nodes)
556.8
527.5
498.2
468.9
439.6
410.3
381
351.7
322.3
293
263.7
234.4
205.1
175.8
146.5
117.2
87.9
58.6
29.3
0


Cluster0150_Low in Paneth cells (12 nodes)
228.6
216.5
204.5
192.5
180.5
168.4
156.4
144.4
132.3
120.3
108.3
96.2
84.2
72.2
60.2
48.1
36.1
24.1
12
0

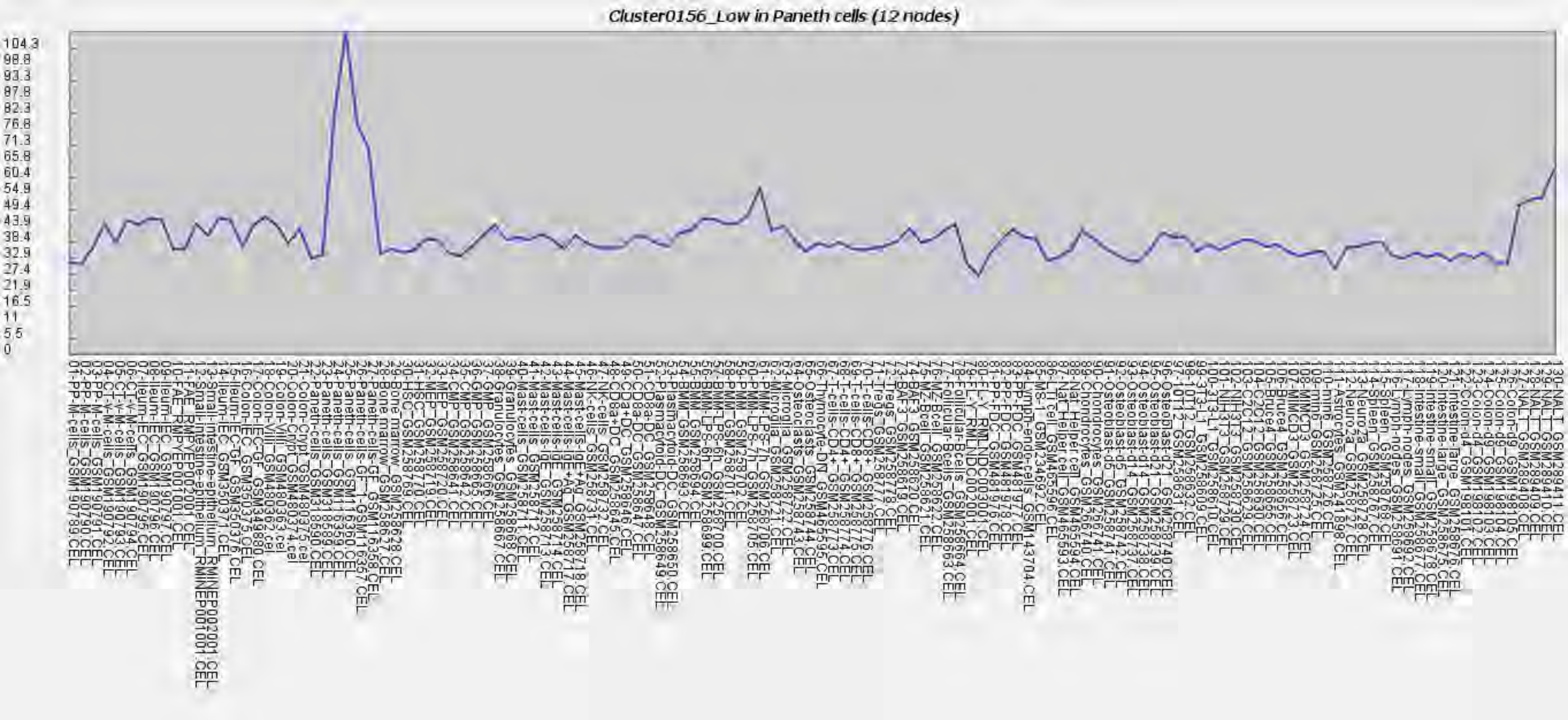
Cluster0151-Intestine-related (12 nodes)
817.5
774.5
731.5
688.4
645.4
602.4
559.3
516.3
473.3
430.3
387.2
344.2
301.2
258.2
215.1
172.1
129.1
86.1
43
0

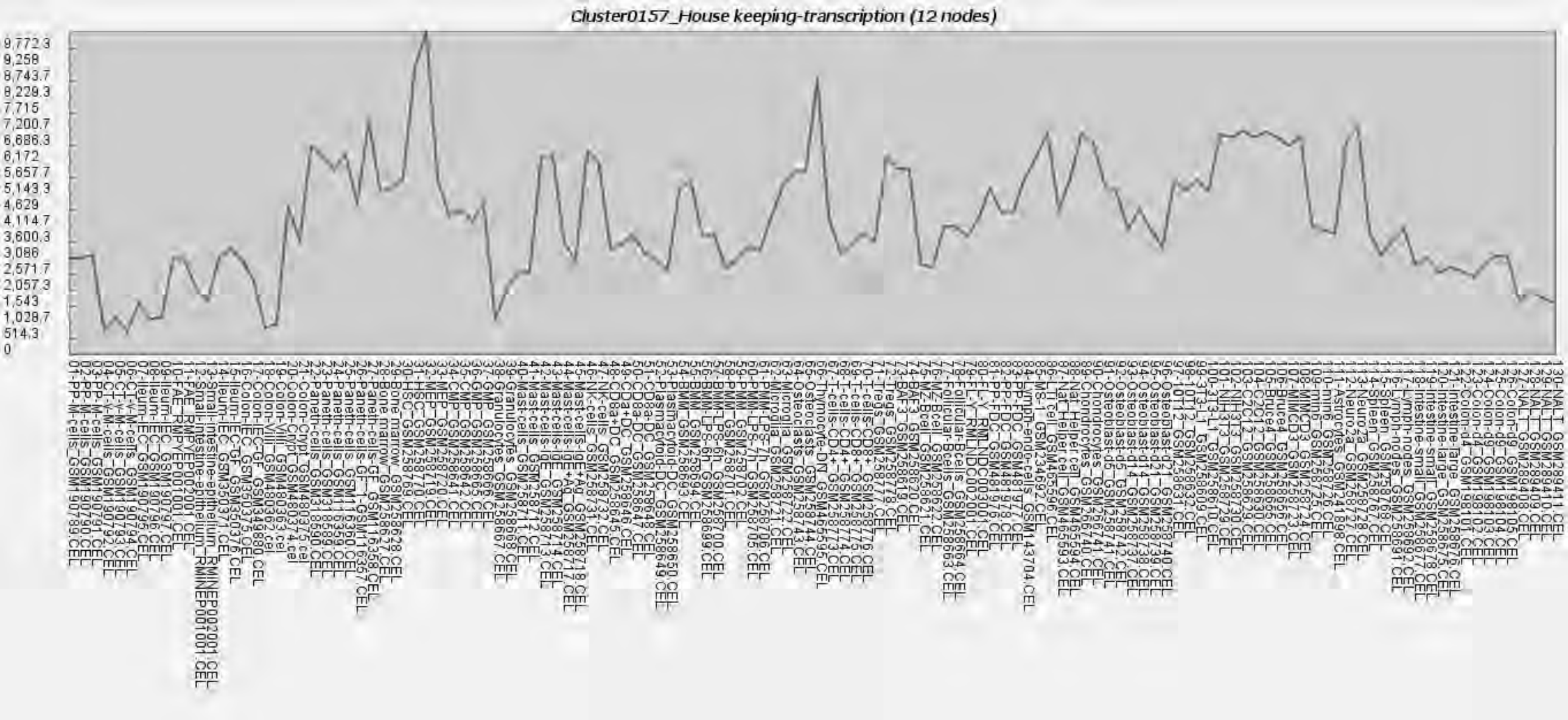

Cluster0152_Low in NALT (12 nodes)
176.7
167.4
158.1
148.8
139.5
130.2
120.9
111.6
102.3
93
83.7
74.4
65.1
55.8
46.5
37.2
27.9
18.6
9.3
0

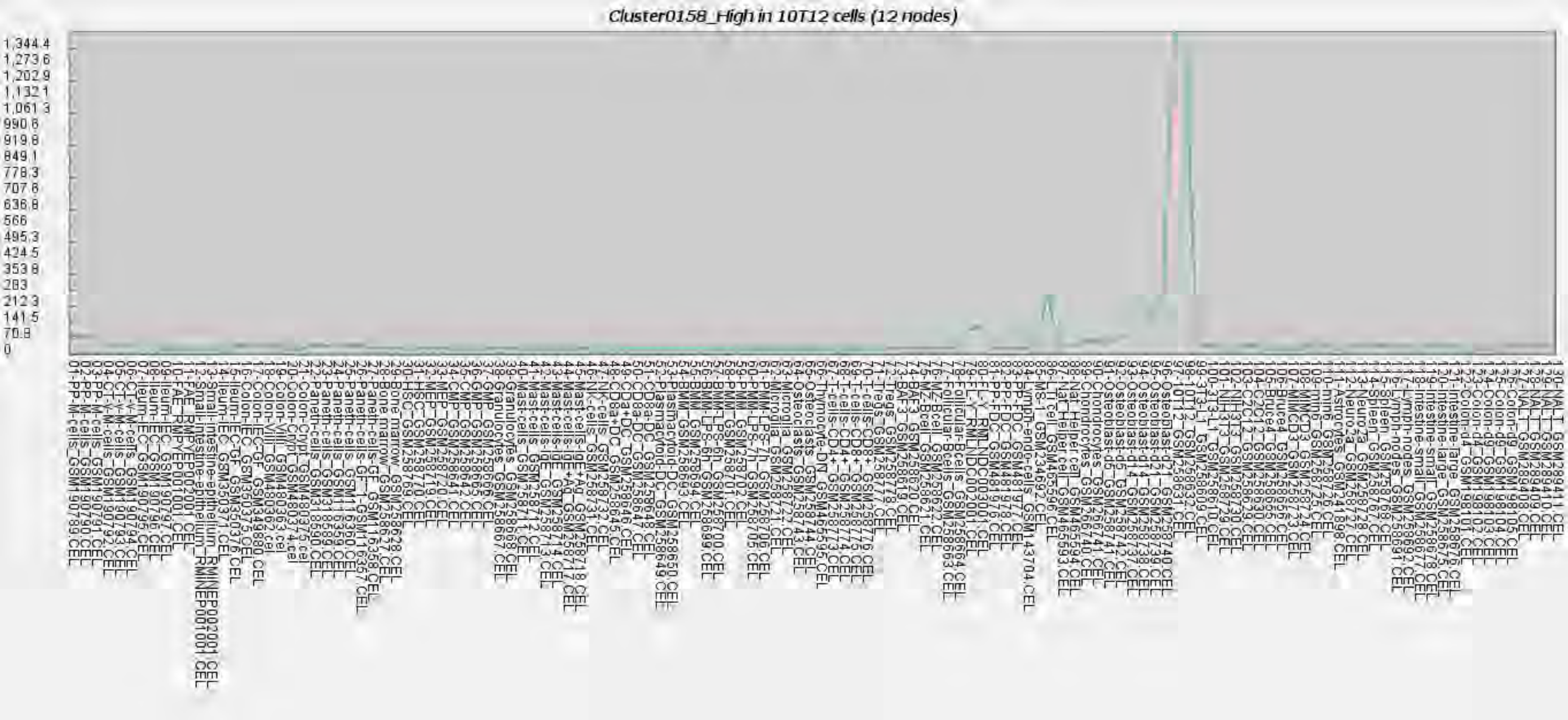

Cluster0153_High in Peyer's patches FDC (12 nodes)
1,274.9
1,207.8
1,140.7
1,073.6
1,006.5
939.4
872.3
805.2
738.1
671
603.9
536.8
469.7
402.6
335.5
268.4
201.3
134.2
67.1
0

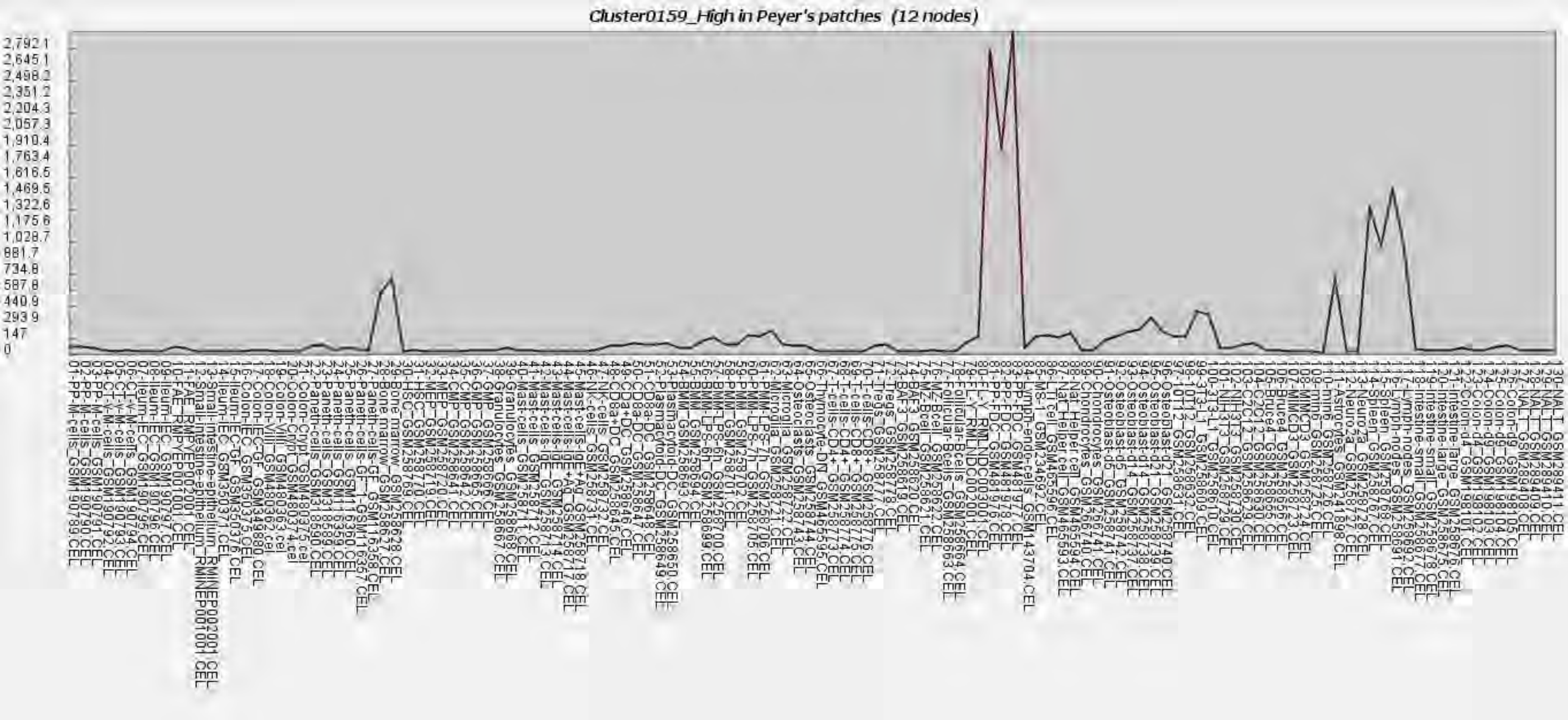

Cluster0154_Phagocyte-related (12 nodes)
2,380.3
2,255
2,129.7
2,004.4
1,879.2
1,753.9
1,628.6
1,503.3
1,378.1
1,252.8
1,127.5
1,002.2
876.9
751.7
626.4
501.1
375.8
250.6
125.3
0

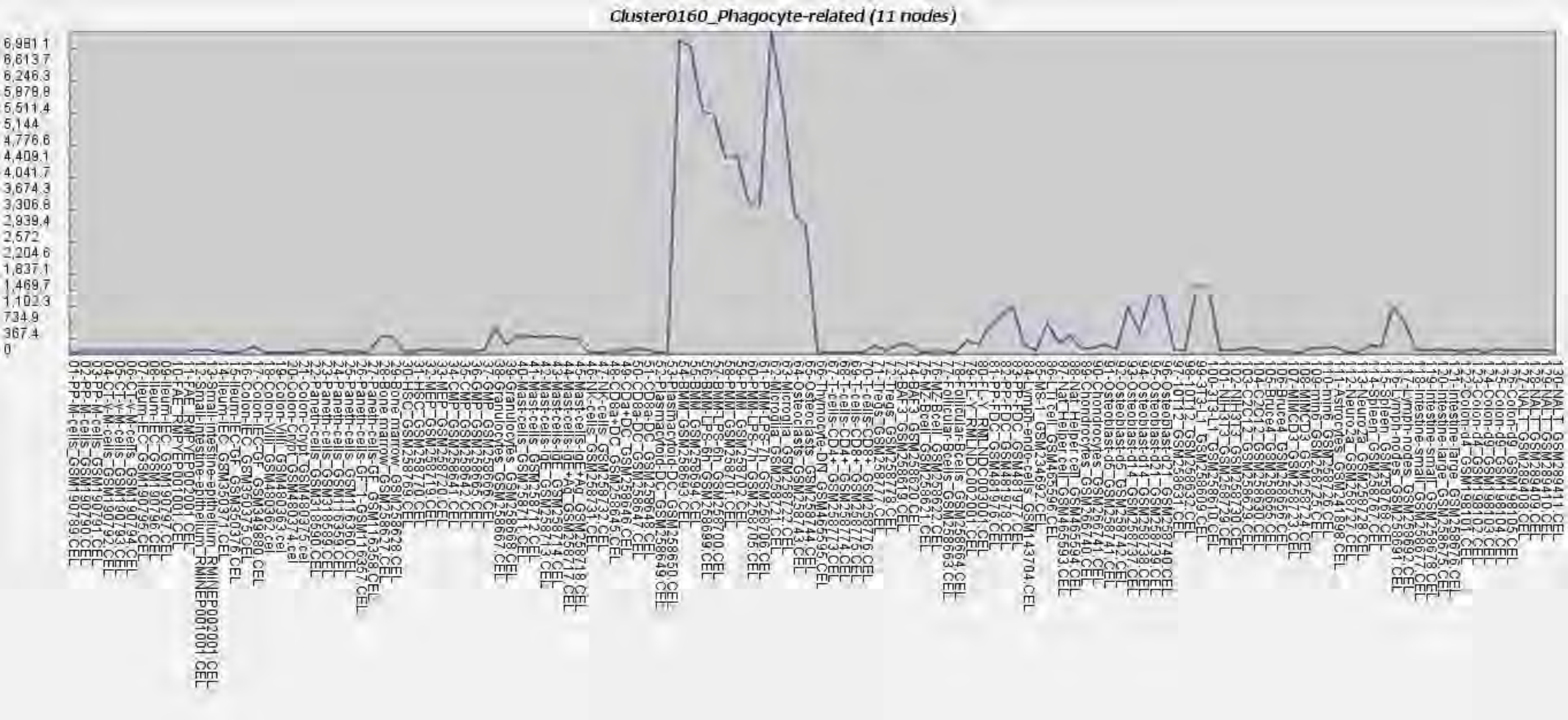
Cluster0155_Mesenchyme-related/extracellular matrix (12 nodes)
565.2
535.5
505.7
476
446.2
416.5
386.7
357
327.2
297.5
267.7
238
208.2
178.5
148.7
119
89.2
59.5
29.7
0

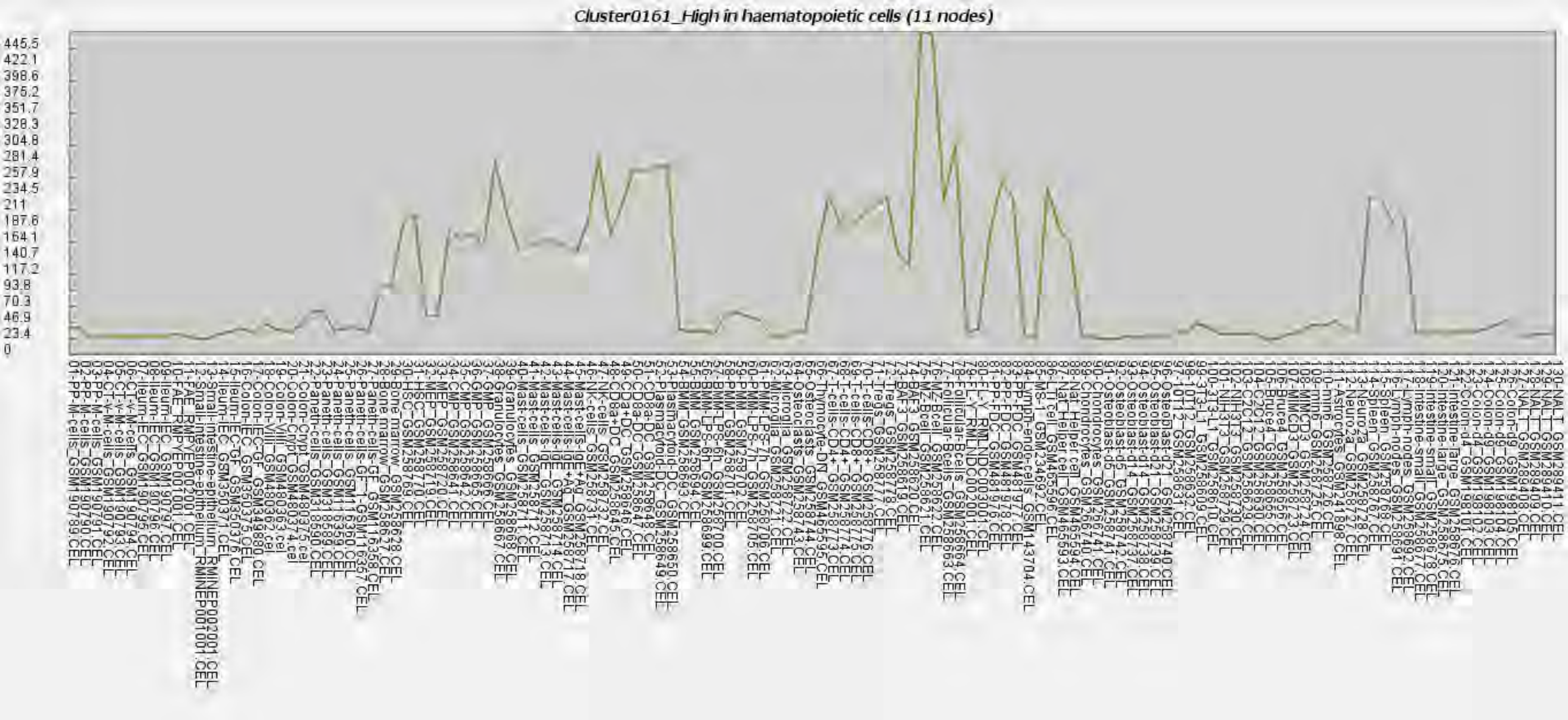

Cluster0156_Low in Paneth cells (12 nodes)
104.3
98.8
93.3
87.8
82.3
76.8
71.3
65.8
60.4
54.9
49.4
43.9
38.4
32.9
27.4
21.9
16.5
11
5.5
0


Cluster0157_House keeping-transcription (12 nodes)
9,772.3
9,258
8,743.7
8,229.3
7,715
7,200.7
6,686.3
6,172
5,657.7
5,143.3
4,629
4,114.7
3,600.3
3,086
2,571.7
2,057.3
1,543
1,028.7
514.3
0

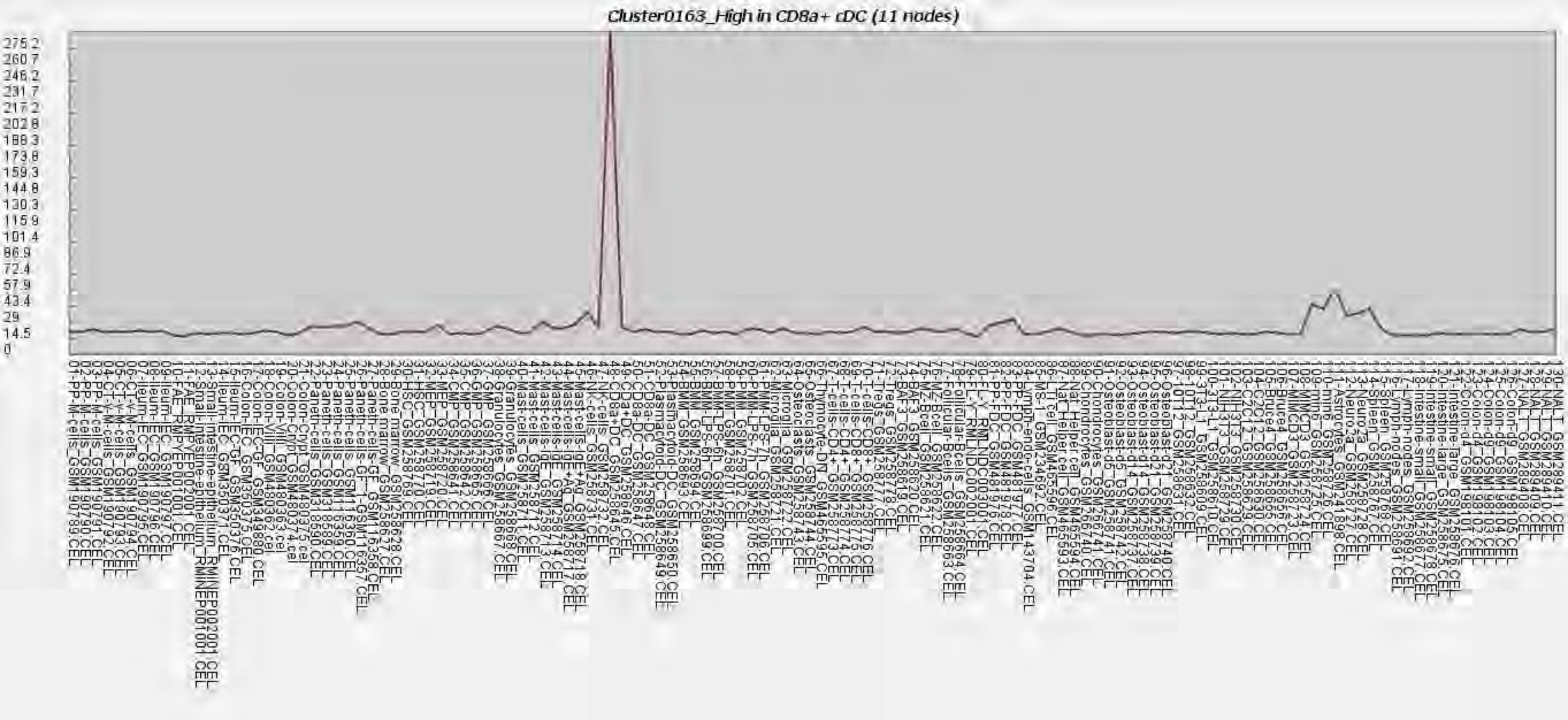

Cluster0158_High in 10T12 cells (12 nodes)
1,344.4
1,273.6
1,202.9
1,132.1
1,061.3
990.6
919.8
849.1
778.3
707.6
636.8
566
495.3
424.5
353.8
283
212.3
141.5
70.8
0

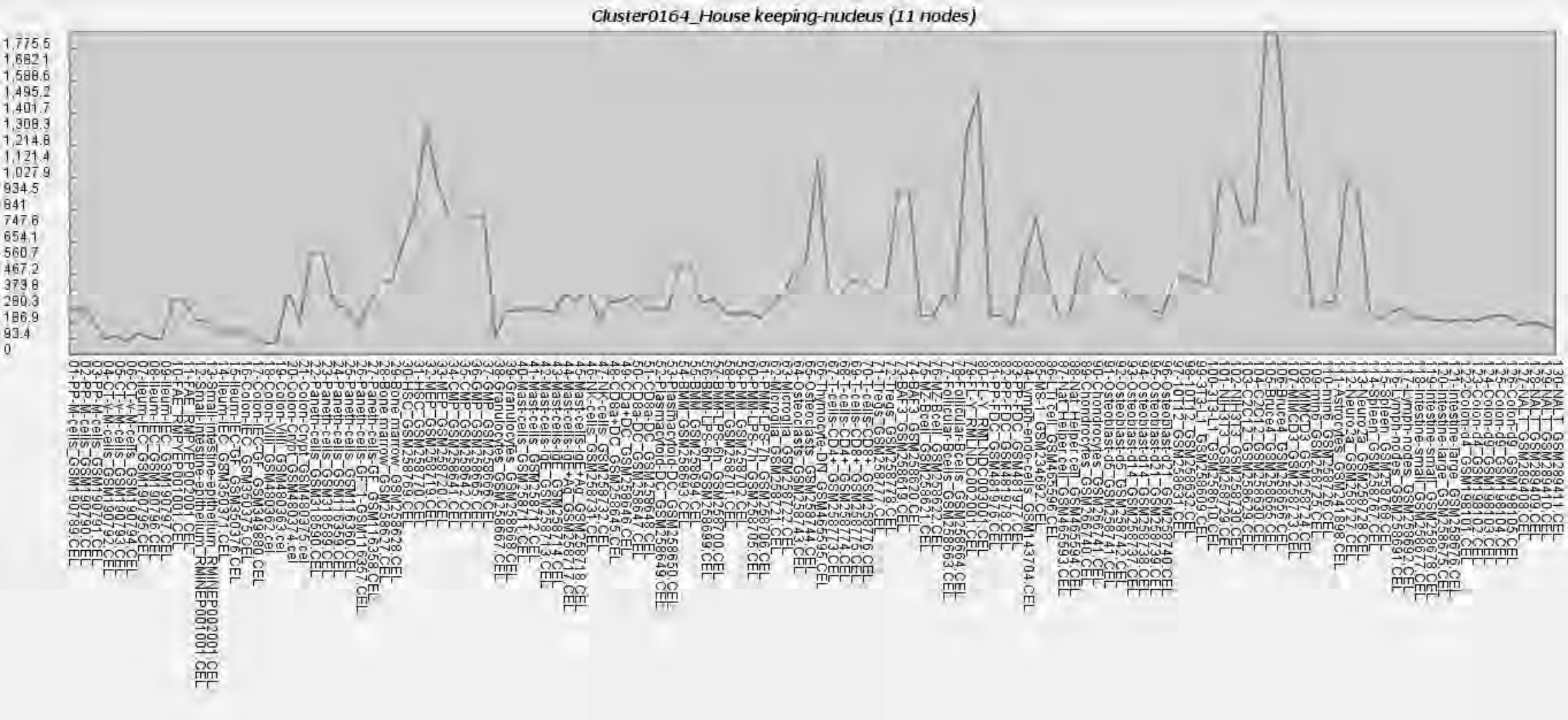

Cluster0159_High in Peyer's patches (12 nodes)
2,792.1
2,645.1
2,498.2
2,351.2
2,204.3
2,057.3
1,910.4
1,763.4
1,616.5
1,469.5
1,322.6
1,175.6
1,028.7
881.7
734.8
587.8
440.9
293.9
147
0

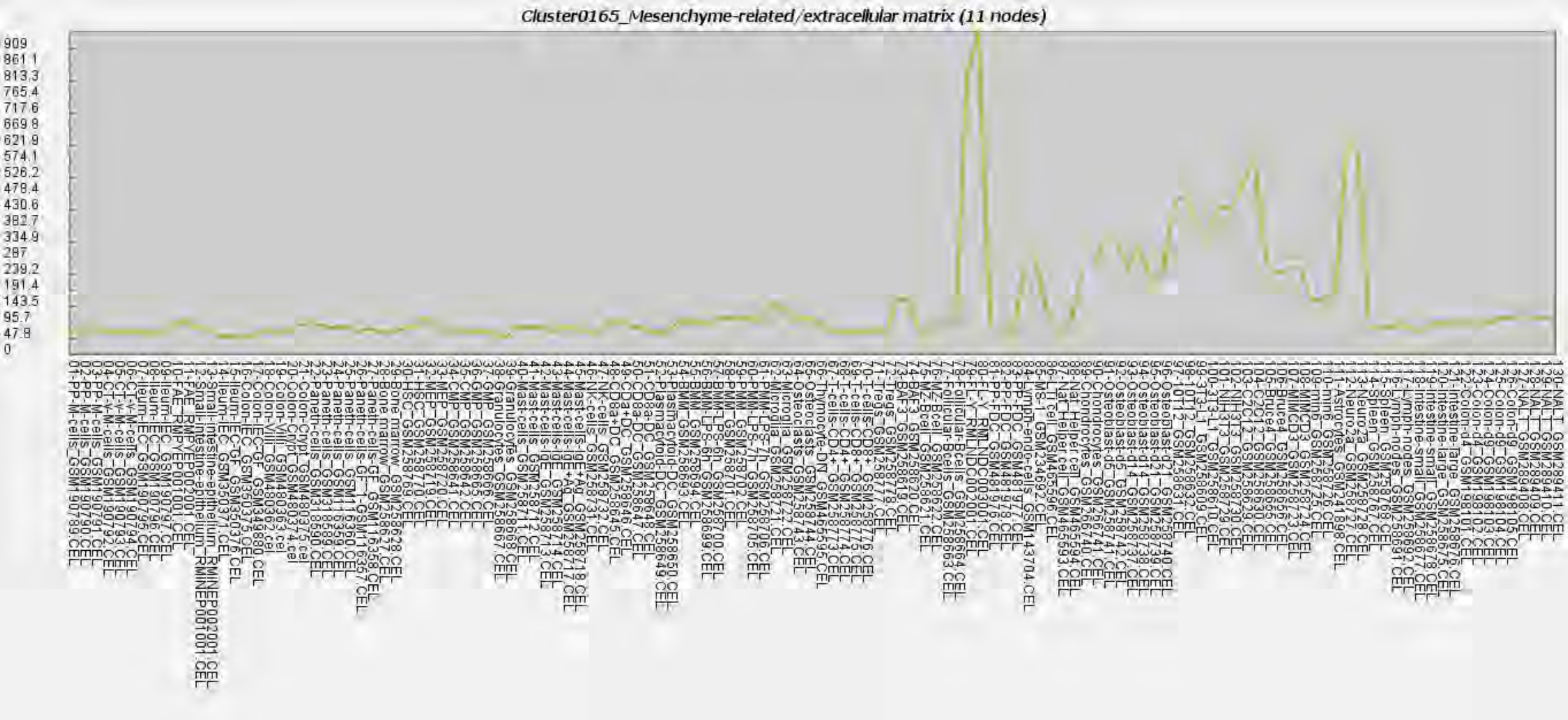

Cluster0160_Phagocyte-related (11 nodes)
6,981.1
6,613.7
6,246.3
5,878.8
5,511.4
5,144
4,776.6
4,409.1
4,041.7
3,674.3
3,306.8
2,939.4
2,572
2,204.6
1,837.1
1,469.7
1,102.3
734.9
367.4
0

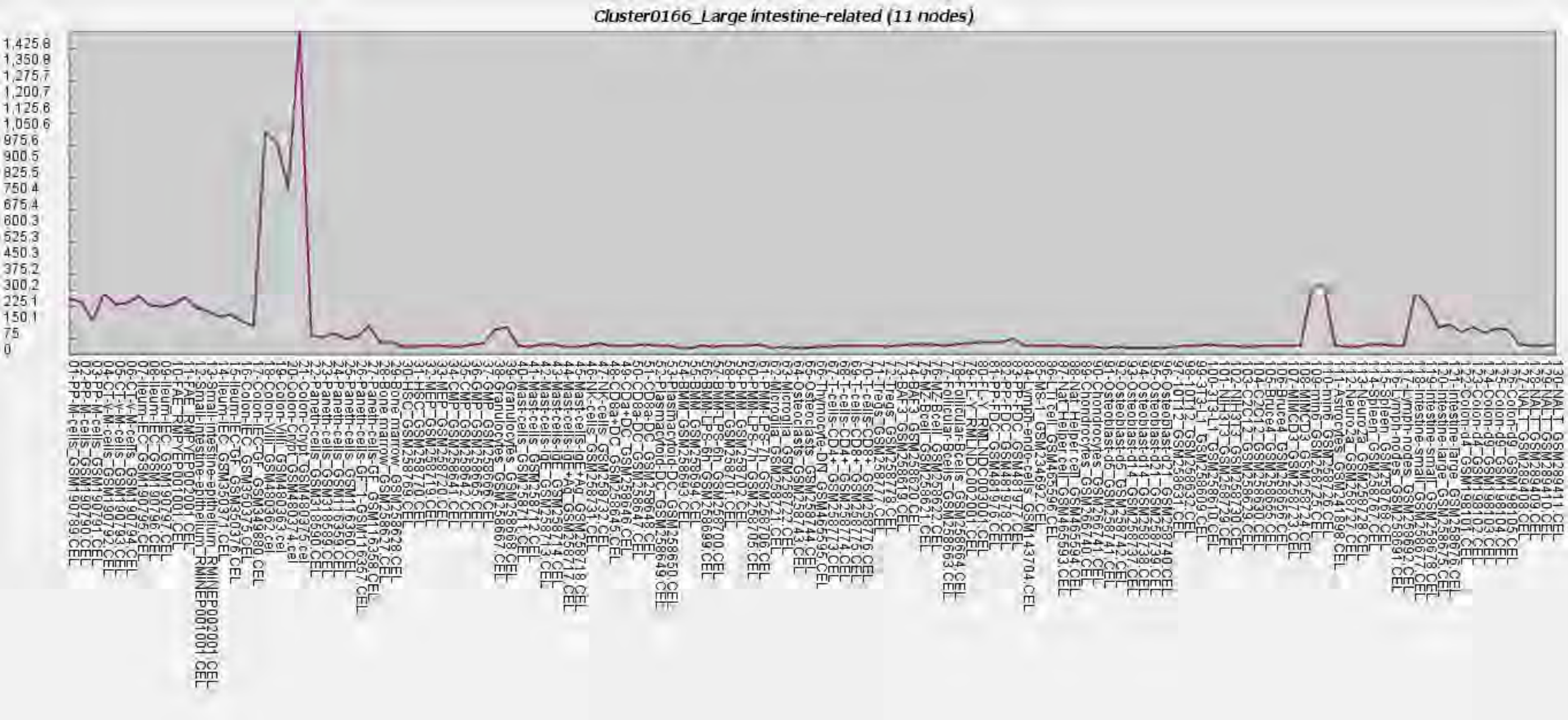

Cluster0161_High in haematopoietic cells (11 nodes)
445.5
422.1
398.6
375.2
351.7
328.3
304.8
281.4
257.9
234.5
211
187.6
164.1
140.7
117.2
93.8
70.3
46.9
23.4
0

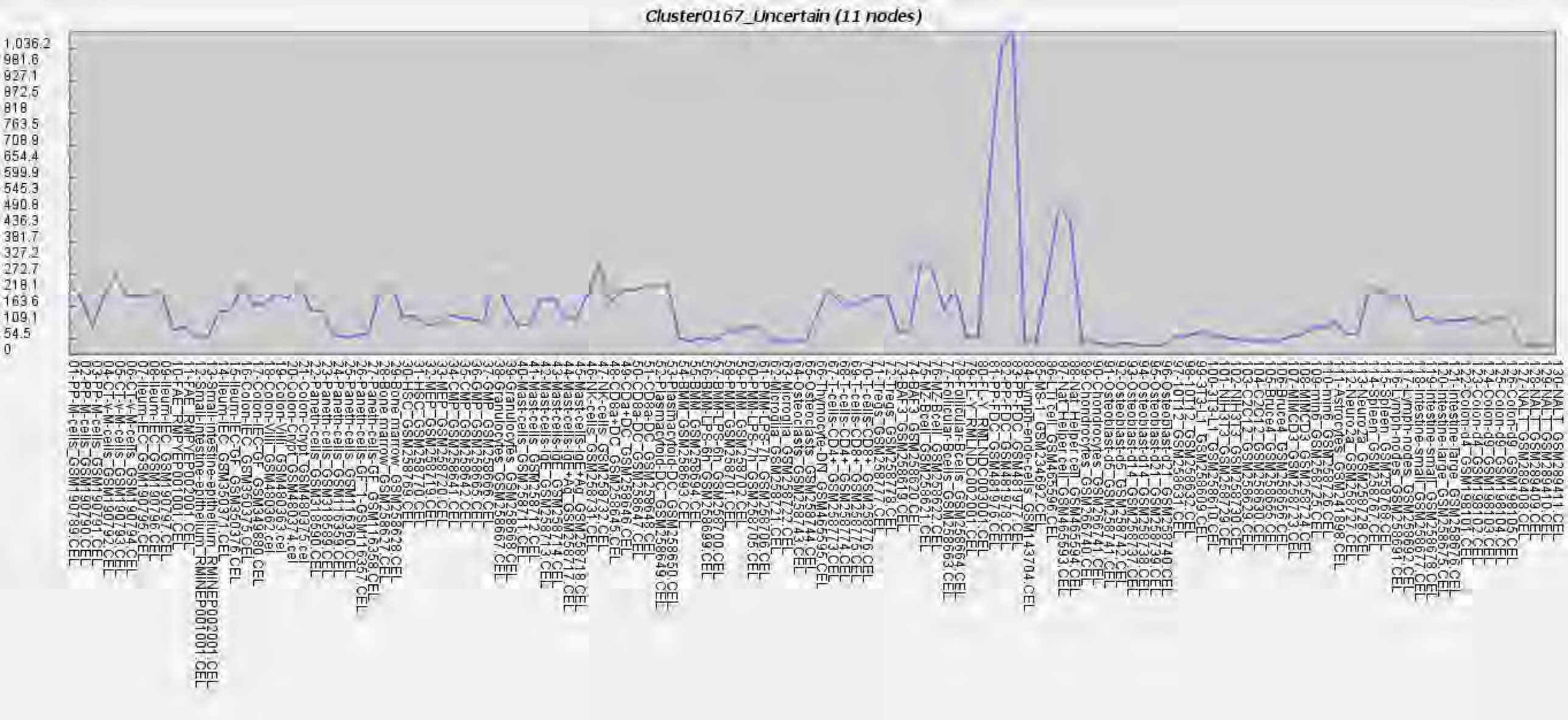
Cluster0162_Uncertain (11 nodes)
110.6
104.7
98.9
93.1
87.3
81.5
75.6
69.8
64
58.2
52.4
46.6
40.7
34.9
29.1
23.3
17.5
11.6
5.8
0


Cluster0163_High in CD8a+ cDC (11 nodes)
275.2
260.7
246.2
231.7
217.2
202.8
188.3
173.8
159.3
144.8
130.3
115.9
101.4
86.9
72.4
57.9
43.4
29
14.5
0


Cluster0164_House keeping-nucleus (11 nodes)
1,775.5
1,682.1
1,588.6
1,495.2
1,401.7
1,308.3
1,214.8
1,121.4
1,027.9
934.5
841
747.6
654.1
560.7
467.2
373.8
280.3
186.9
93.4
0

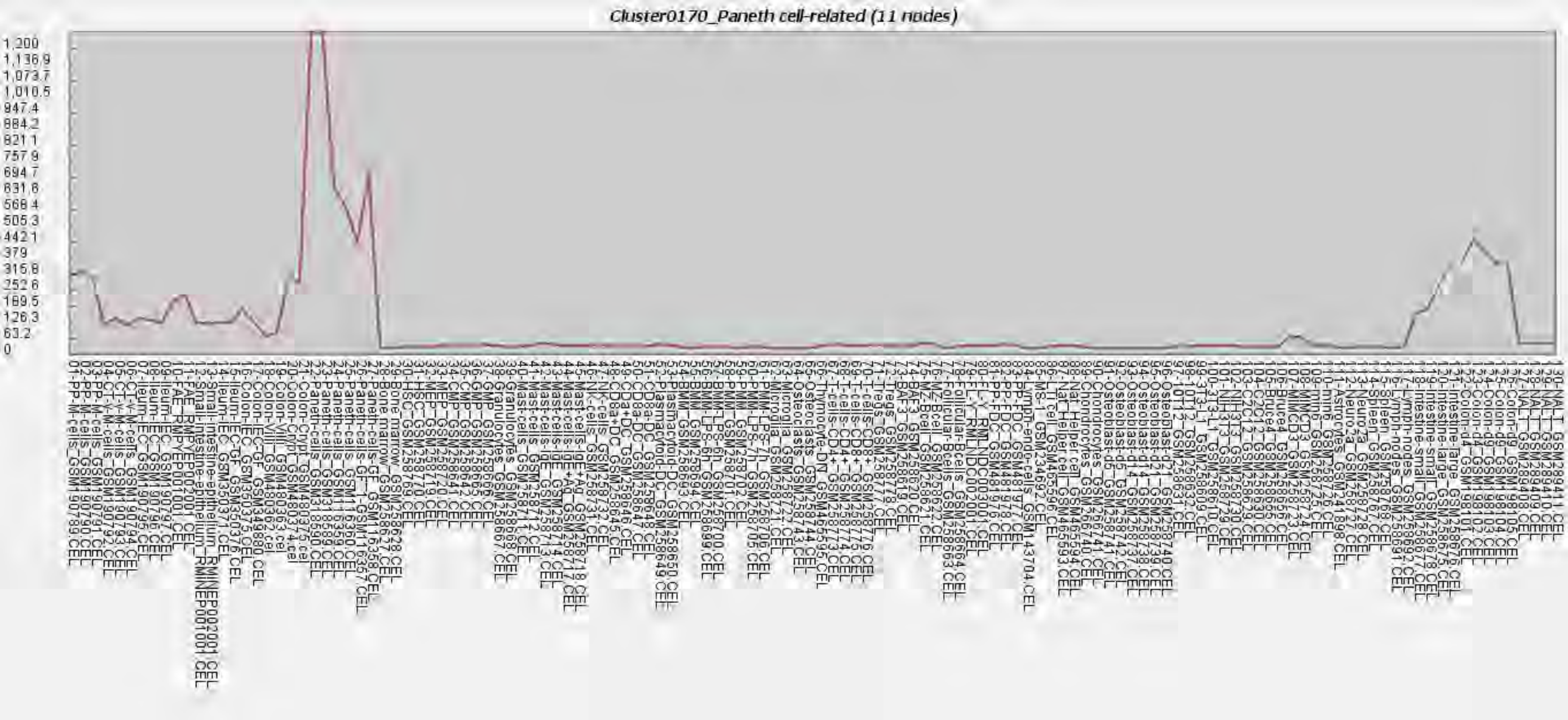

Cluster0165_Mesenchyme-related/extracellular matrix (11 nodes)
909
861.1
813.3
765.4
717.6
669.8
621.9
574.1
526.2
478.4
430.6
382.7
334.9
287
239.2
191.4
143.5
95.7
47.8
0

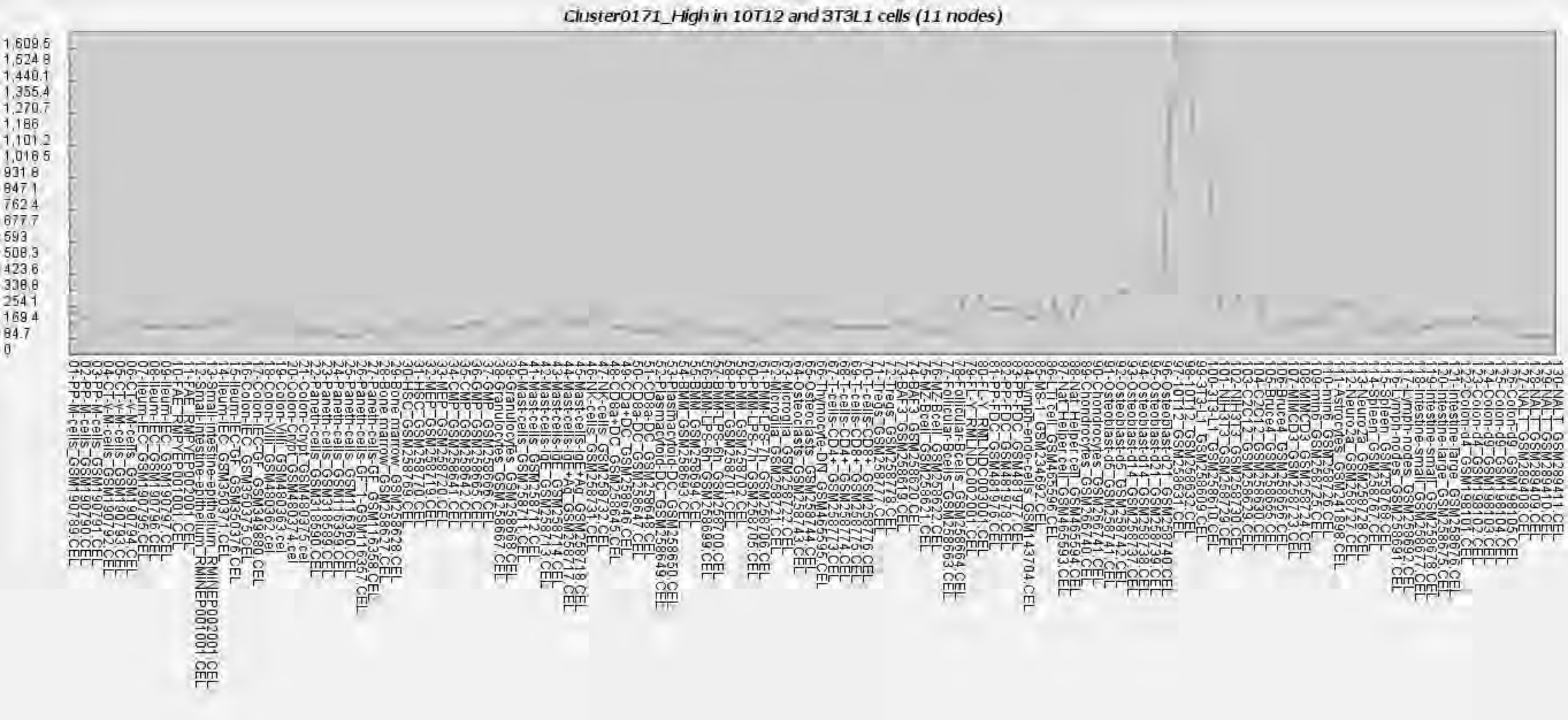

Cluster0166_Large intestine-related (11 nodes)
1,425.8
1,350.8
1,275.7
1,200.7
1,125.6
1,050.6
975.6
900.5
825.5
750.4
675.4
600.3
525.3
450.3
375.2
300.2
225.1
150.1
75
0


Cluster0167_Uncertain (11 nodes)
1,036.2
981.6
927.1
872.5
818
763.5
708.9
654.4
599.9
545.3
490.8
436.3
381.7
327.2
272.7
218.1
163.6
109.1
54.5
0

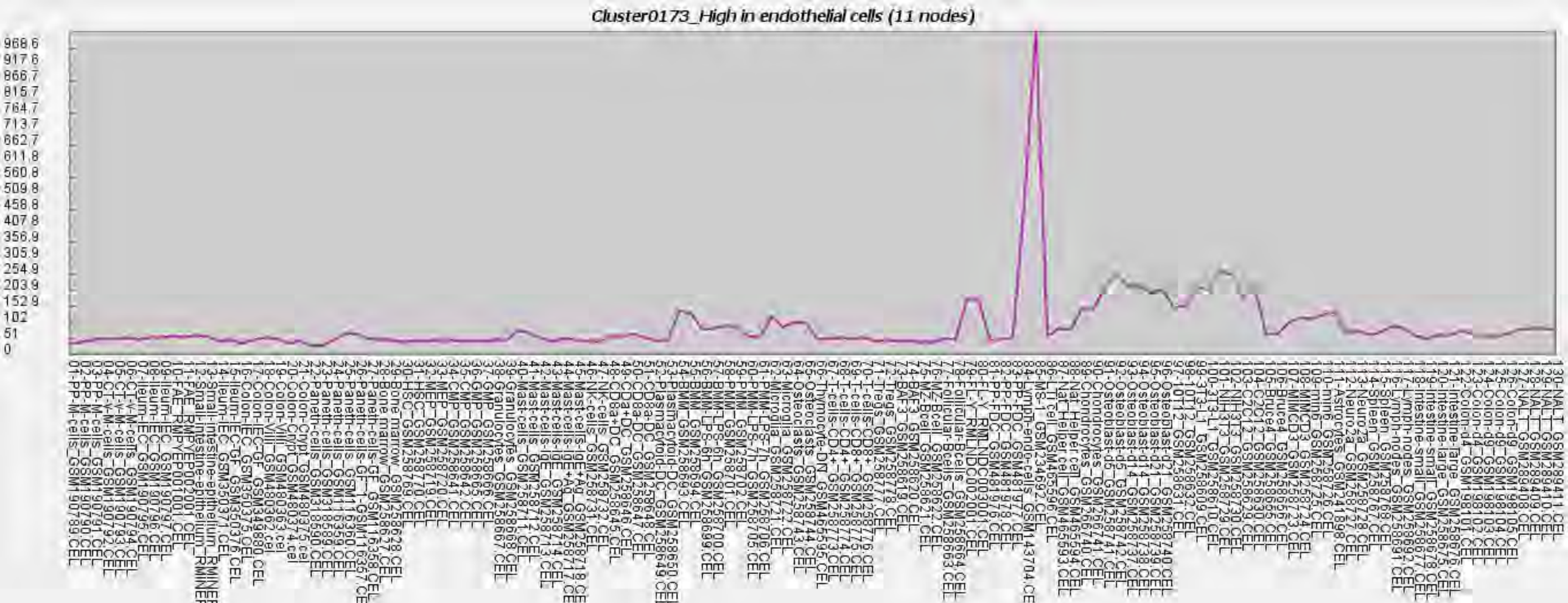
Cluster0168_High in classical DC (11 nodes)
317.3
300.6
283.9
267.2
250.5
233.8
217.1
200.4
183.7
167
150.3
133.6
116.9
100.2
83.5
66.8
50.1
33.4
16.7
0

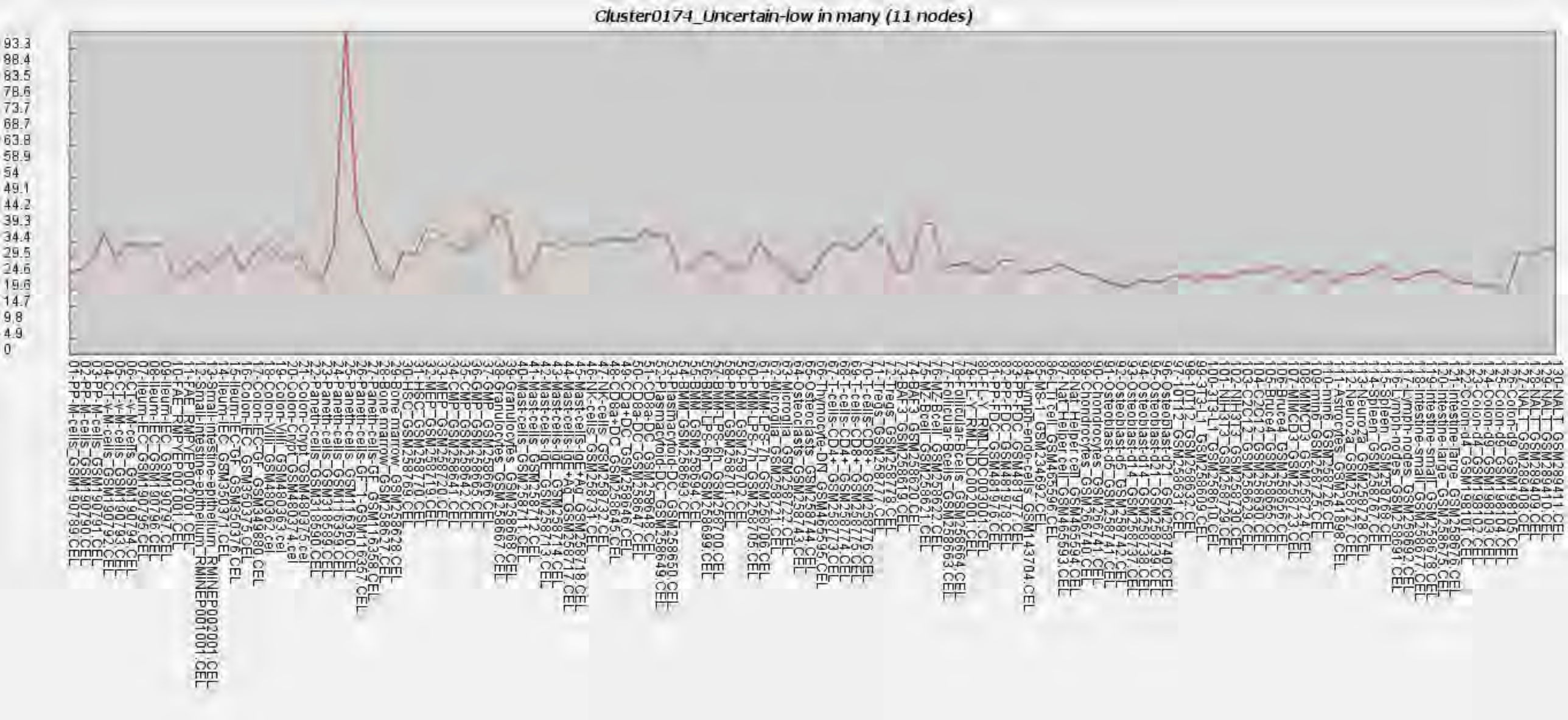
Cluster0169_High in NK cell, cDC, T cells and B cells (11 nodes)
374.5
354.8
335.1
315.4
295.7
276
256.3
236.5
216.8
197.1
177.4
157.7
138
118.3
98.6
78.8
59.1
39.4
19.7
0


Cluster0170_Paneth cell-related (11 nodes)
1,200
1,136.9
1,073.7
1,010.5
947.4
884.2
821.1
757.9
694.7
631.6
568.4
505.3
442.1
379
315.8
252.6
189.5
126.3
63.2
0

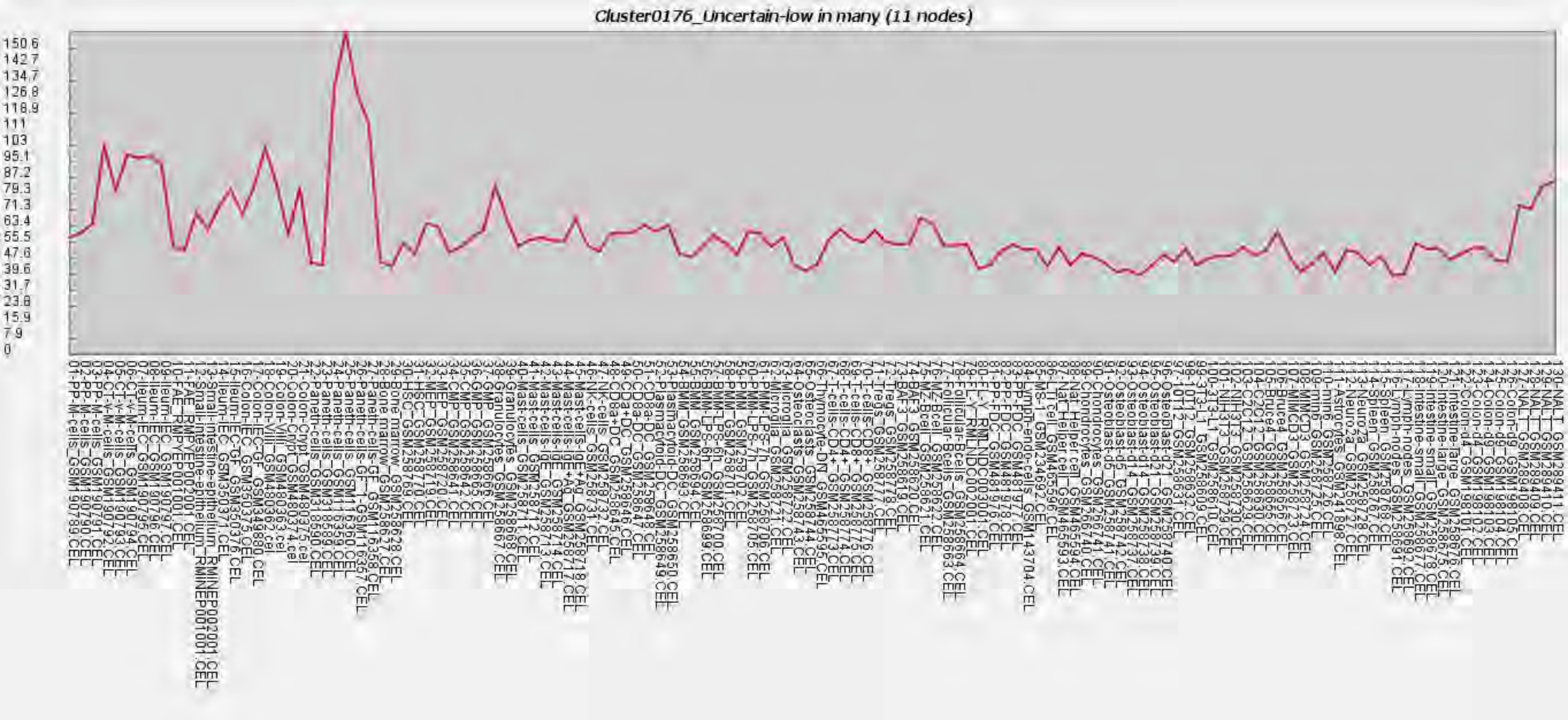

Cluster0171_High in 10T12 and 3T3L1 cells (11 nodes)
1,609.5
1,524.8
1,440.1
1,355.4
1,270.7
1,186
1,101.2
1,016.5
931.8
847.1
762.4
677.7
593
508.3
423.6
338.8
254.1
169.4
84.7
0

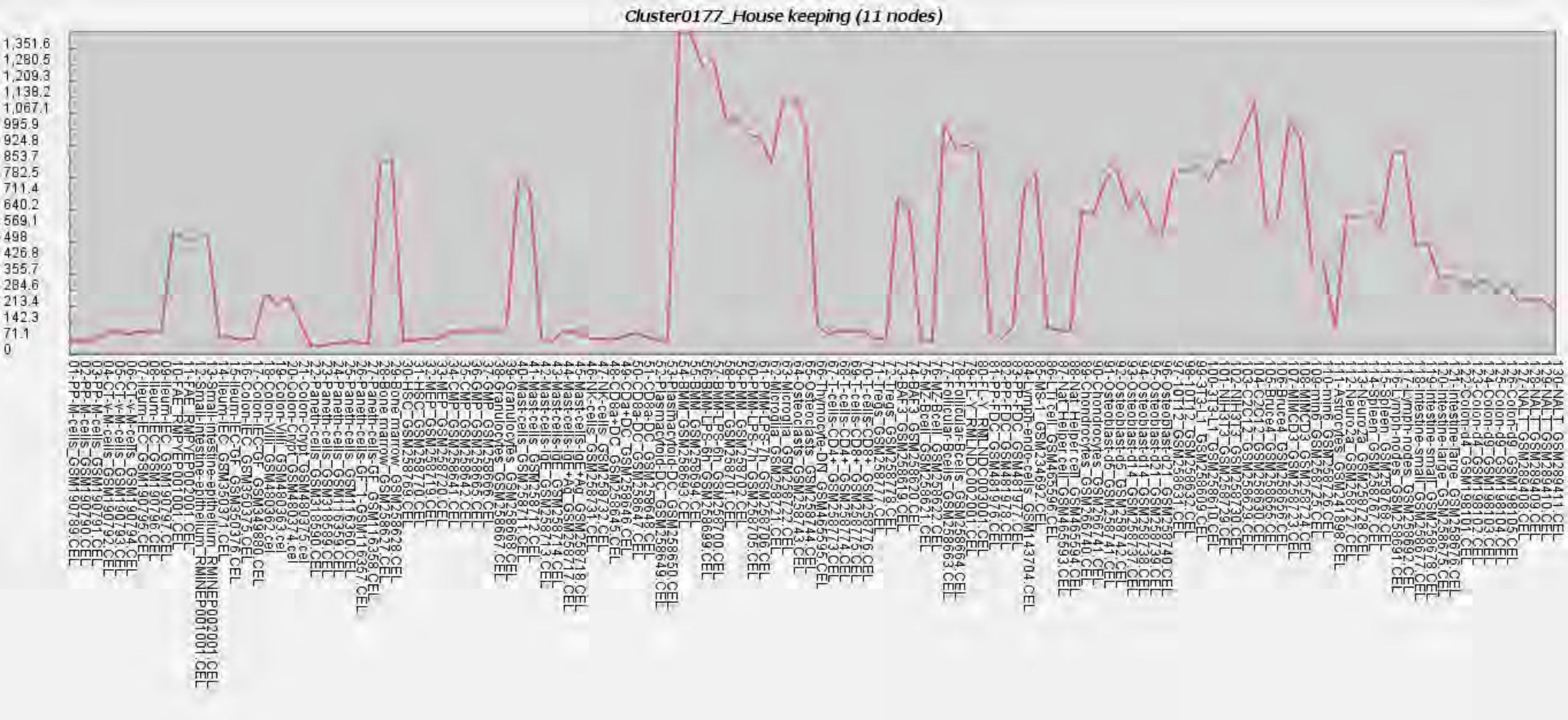
Cluster0172_House keeping-transcription (11 nodes)
289.1
273.9
258.7
243.5
228.3
213
197.8
182.6
167.4
152.2
137
121.7
106.5
91.3
76.1
60.9
45.7
30.4
15.2
0

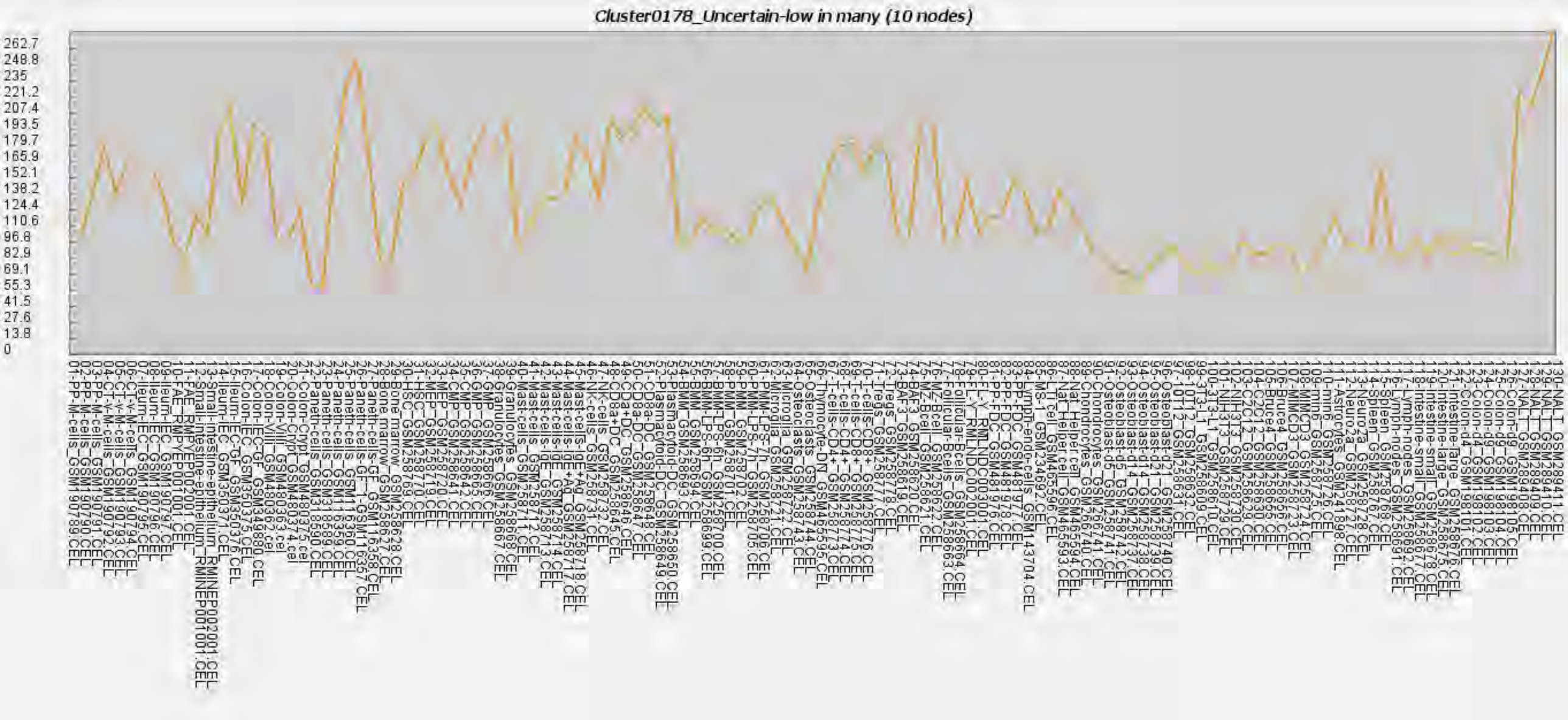

Cluster0173_High in endothelial cells (11 nodes)
968.6
917.6
866.7
815.7
764.7
713.7
662.7
611.8
560.8
509.8
458.8
407.8
356.9
305.9
254.9
203.9
152.9
102
51
0

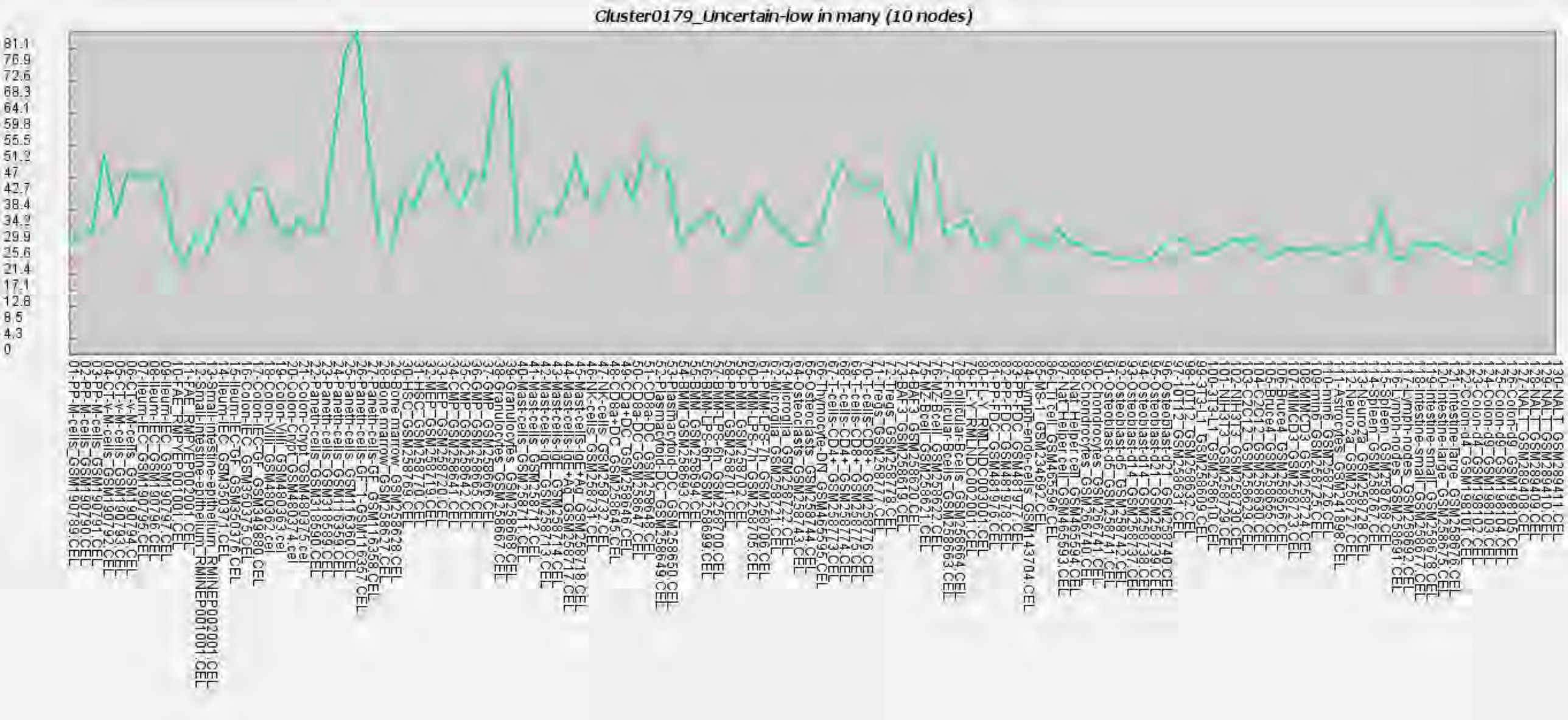

Cluster0174_Uncertain-low in many (11 nodes)
93.3
88.4
83.5
78.6
73.7
68.7
63.8
58.9
54
49.1
44.2
39.3
34.4
29.5
24.6
19.6
14.7
9.8
4.9
0

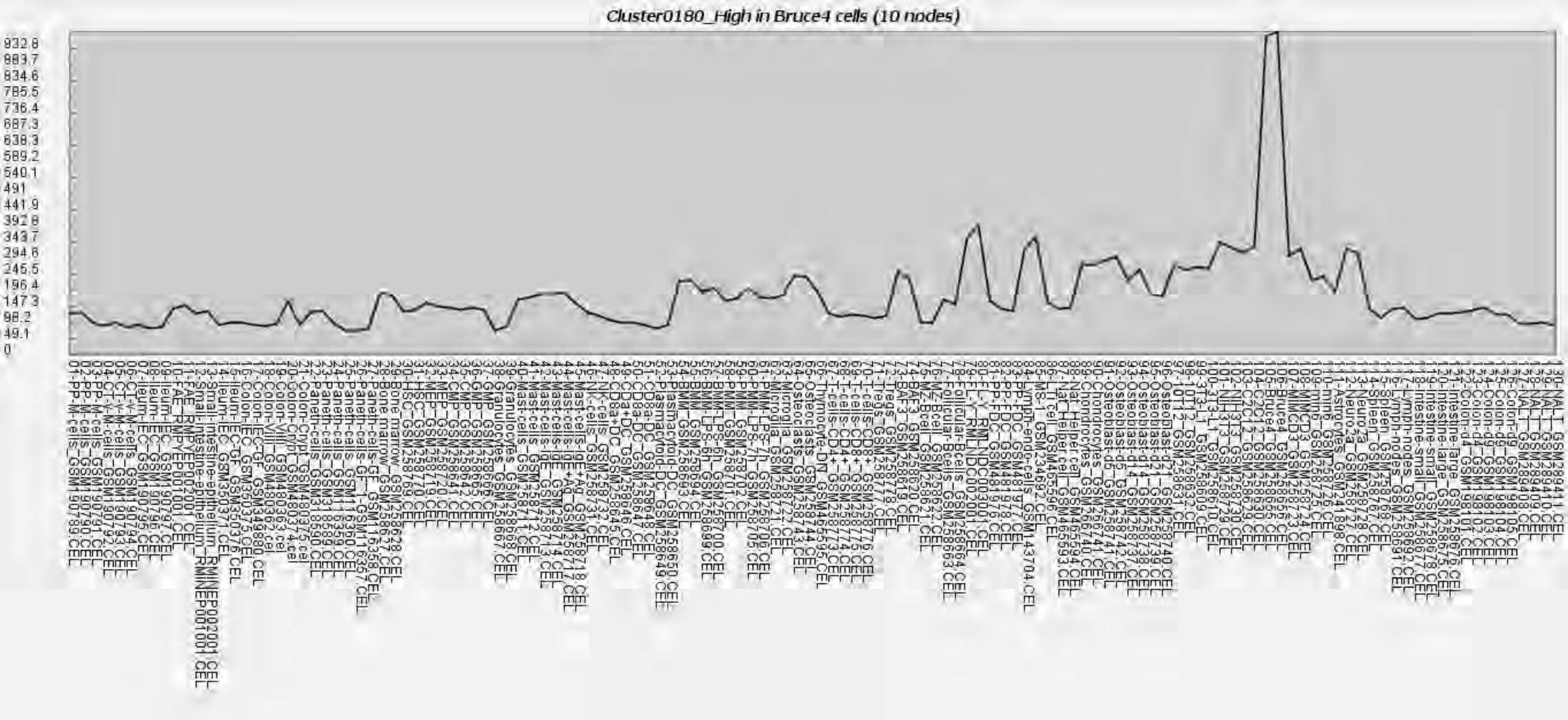
Cluster0175_Mast cells and phagocyte-related (11 nodes)
3,781.8
3,582.8
3,383.7
3,184.7
2,985.6
2,786.6
2,587.6
2,388.5
2,189.5
1,990.4
1,791.4
1,592.3
1,393.3
1,194.3
995.2
796.2
597.1
398.1
199
0

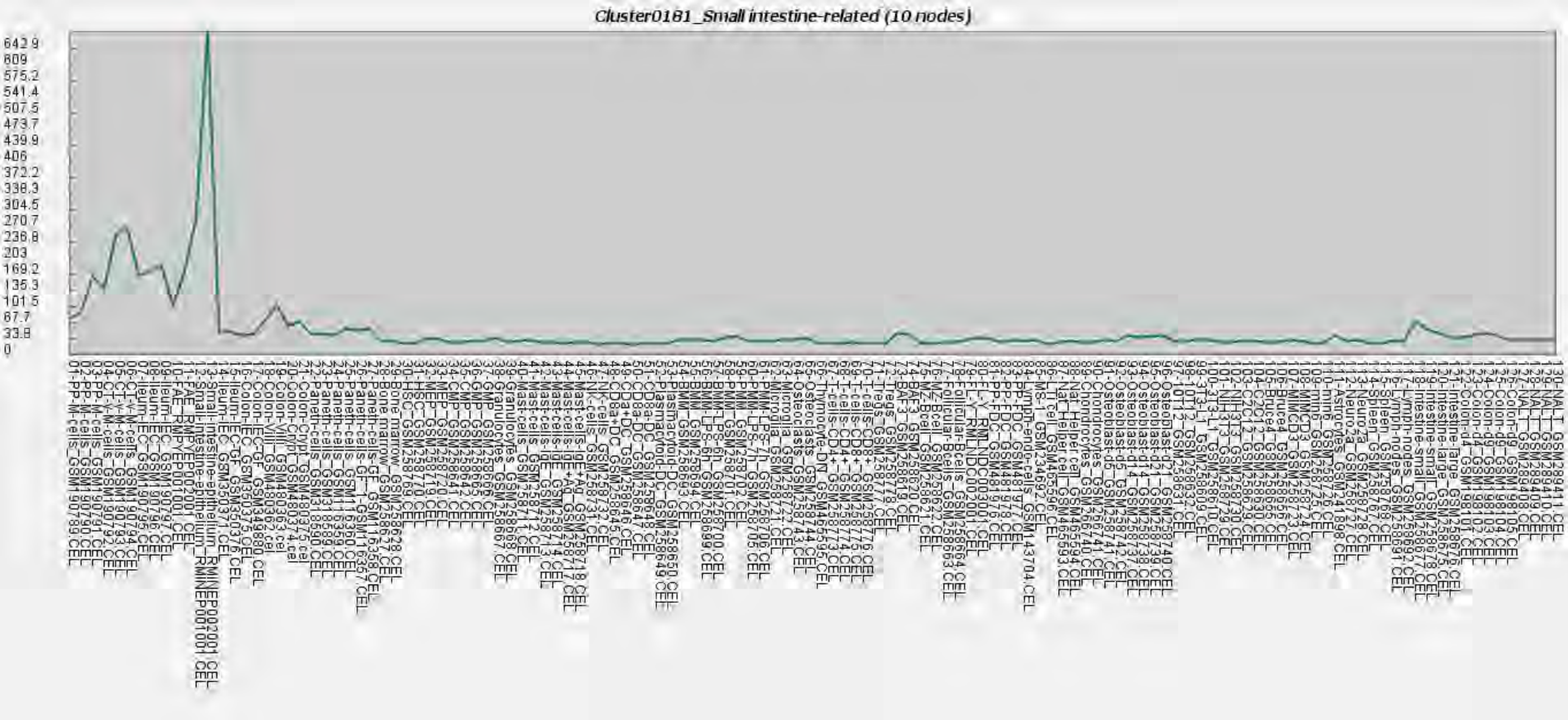

Cluster0176_Uncertain-low in many (11 nodes)
150.6
142.7
134.7
126.8
118.9
111
103
95.1
87.2
79.3
71.3
63.4
55.5
47.6
39.6
31.7
23.8
15.9
7.9
0

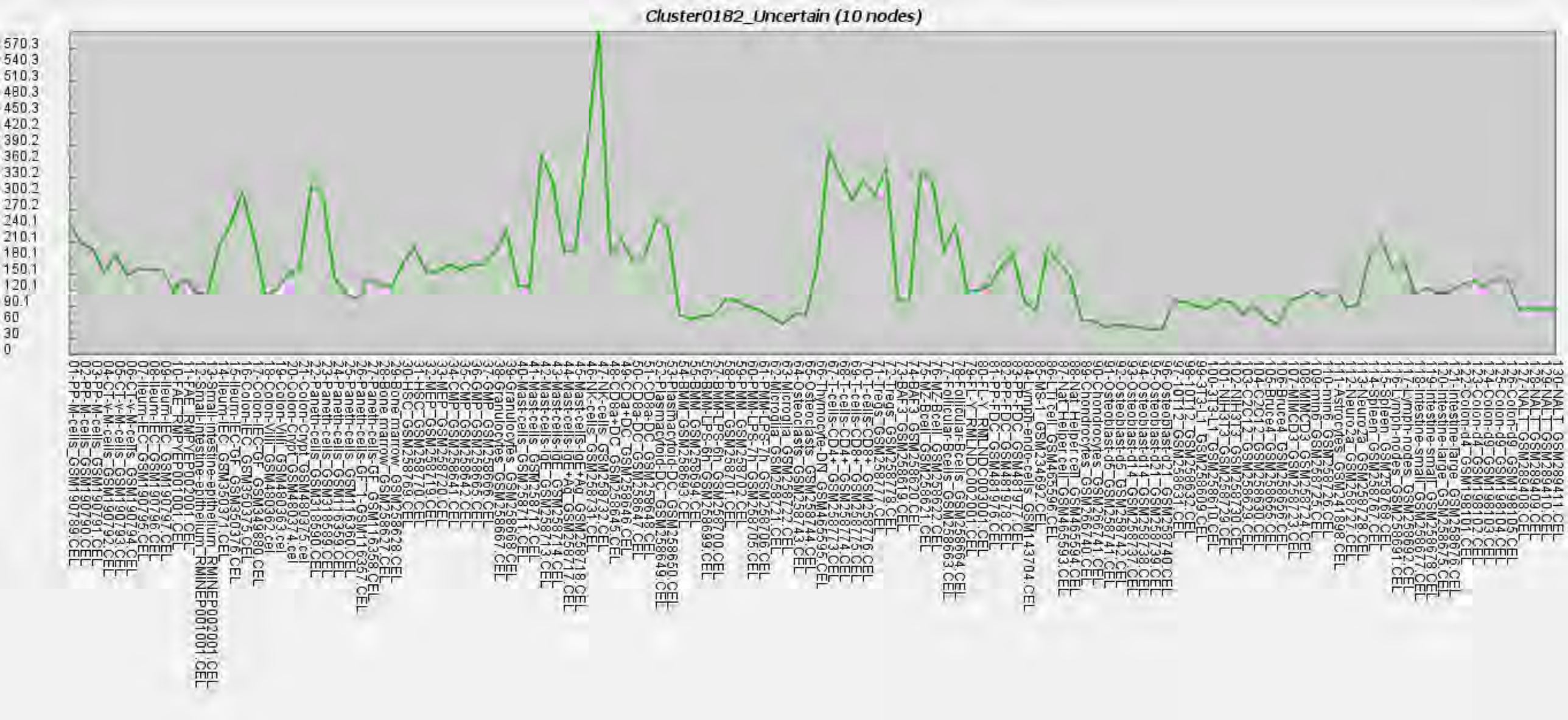

Cluster0177_House keeping (11 nodes)
1,351.6
1,280.5
1,209.3
1,138.2
1,067.1
995.9
924.8
853.7
782.5
711.4
640.2
569.1
498
426.8
355.7
284.6
213.4
142.3
71.1
0

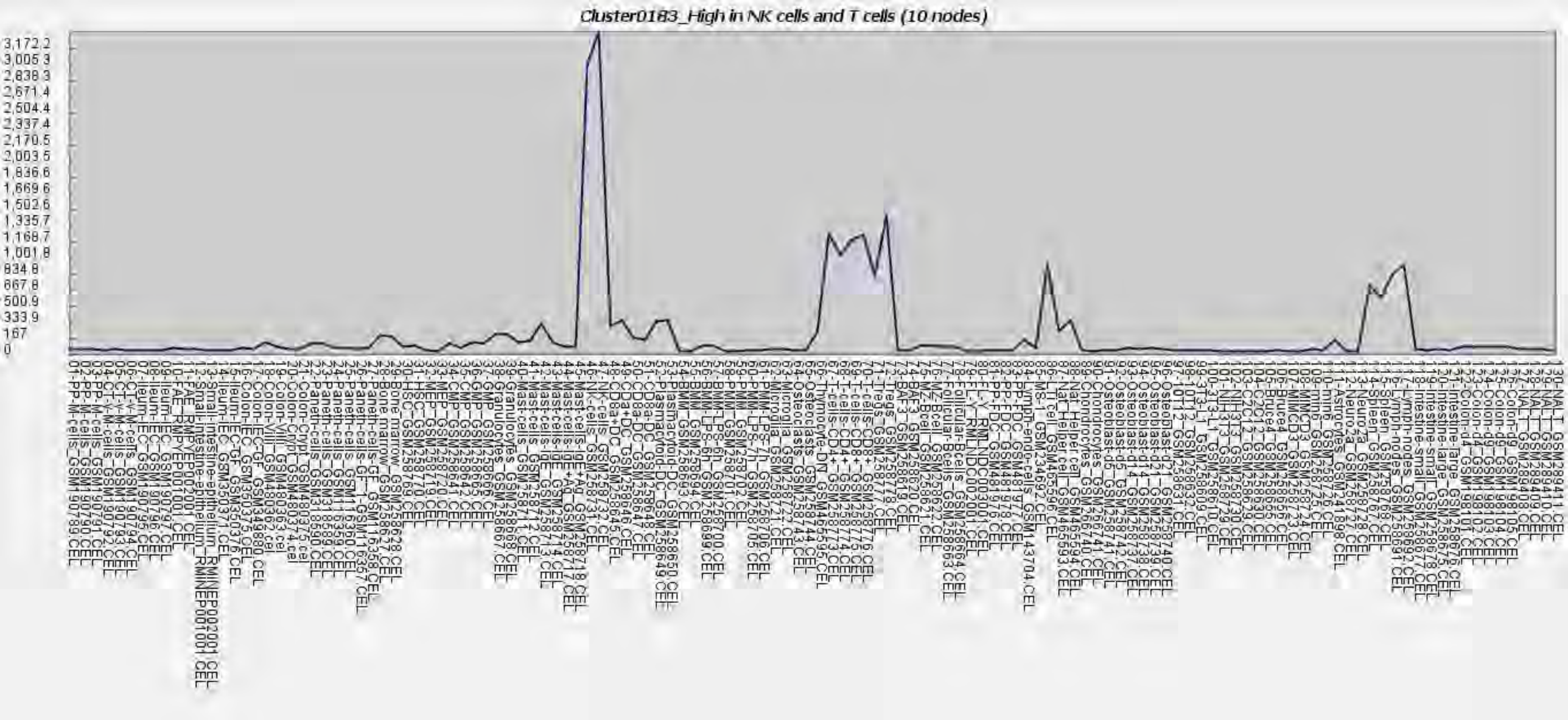

Cluster0178_Uncertain-low in many (10 nodes)
262.7
248.8
235
221.2
207.4
193.5
179.7
165.9
152.1
138.2
124.4
110.6
96.8
82.9
69.1
55.3
41.5
27.6
13.8
0

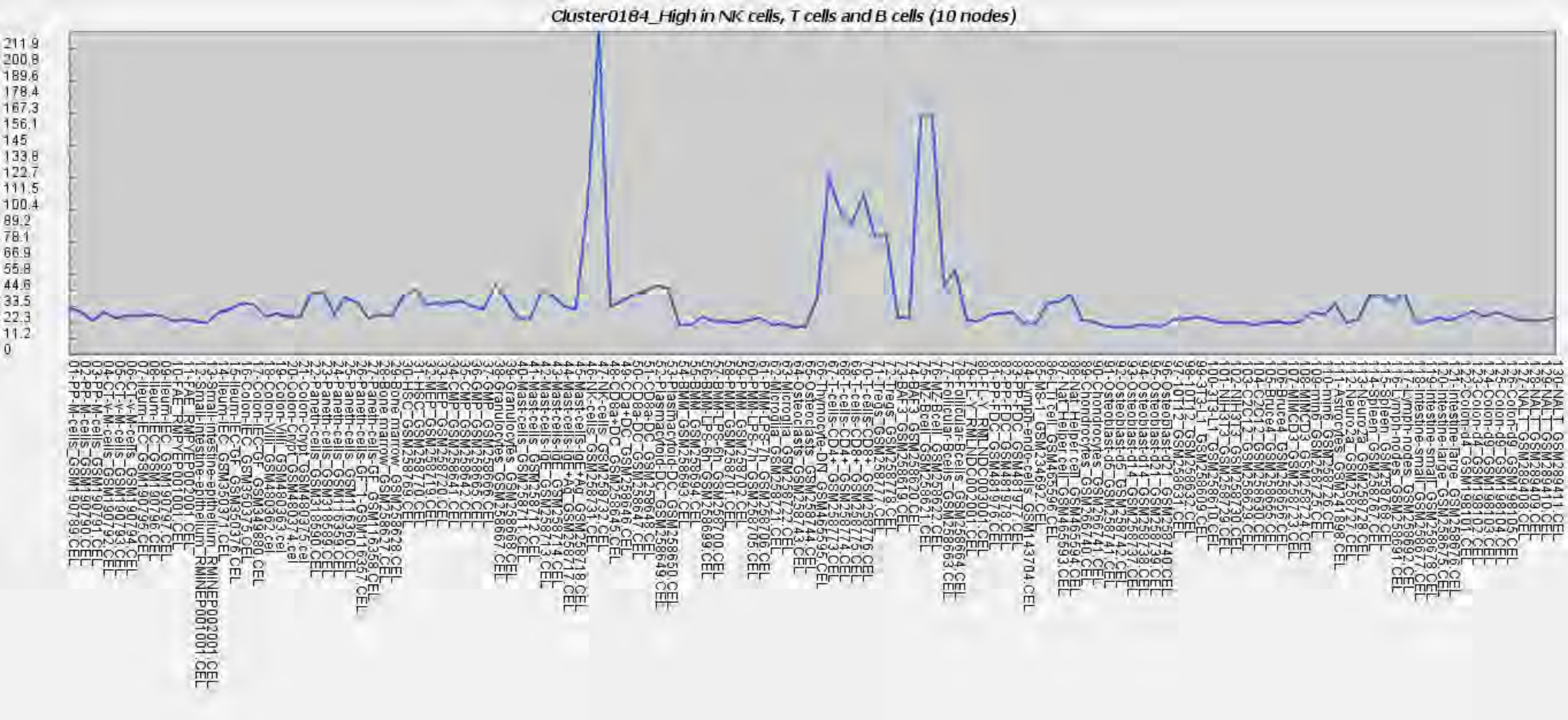

Cluster0179_Uncertain-low in many (10 nodes)
81.1
76.9
72.6
68.3
64.1
59.8
55.5
51.2
47
42.7
38.4
34.2
29.9
25.6
21.4
17.1
12.8
8.5
4.3
0

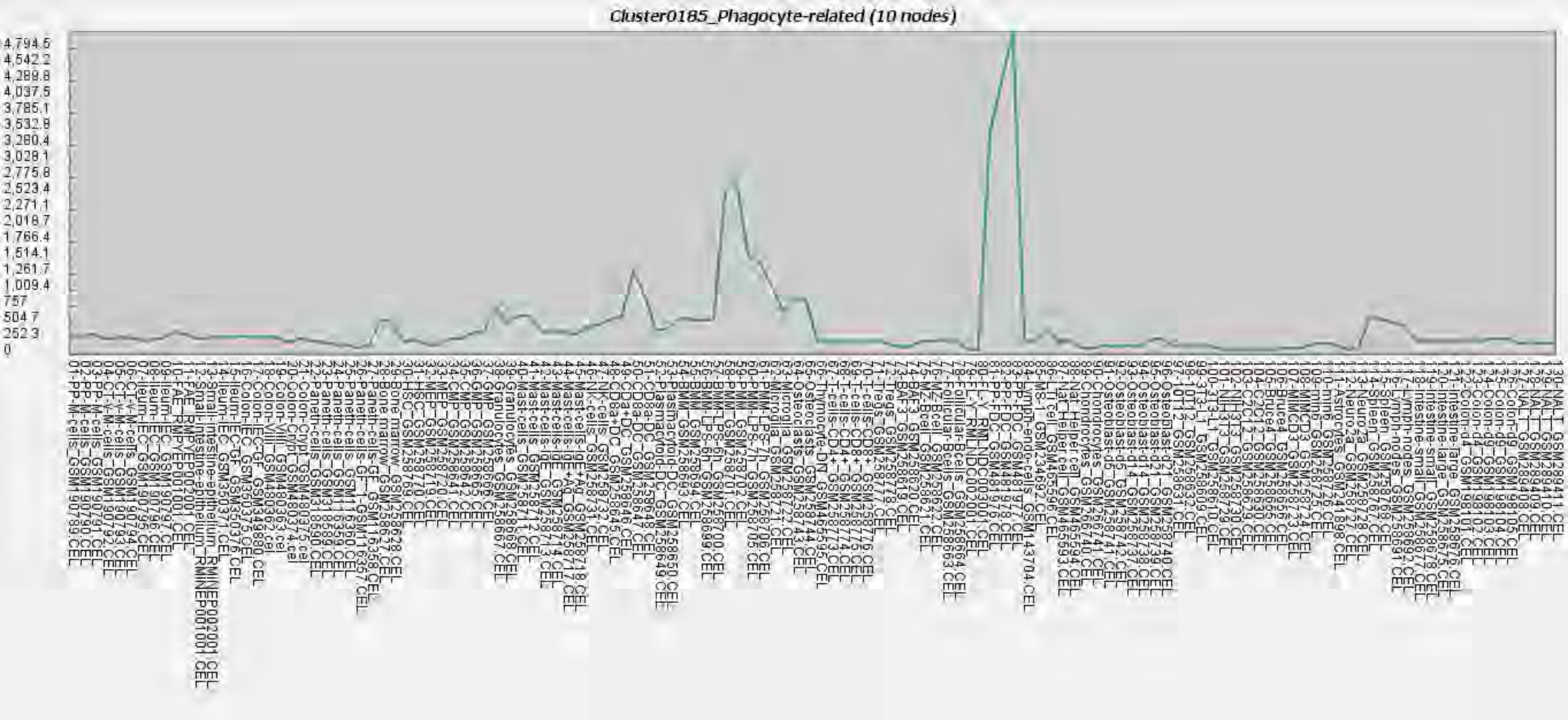

Cluster0180_High in Bruce4 cells (10 nodes)
932.8
883.7
834.6
785.5
736.4
687.3
638.3
589.2
540.1
491
441.9
392.8
343.7
294.6
245.5
196.4
147.3
98.2
49.1
0

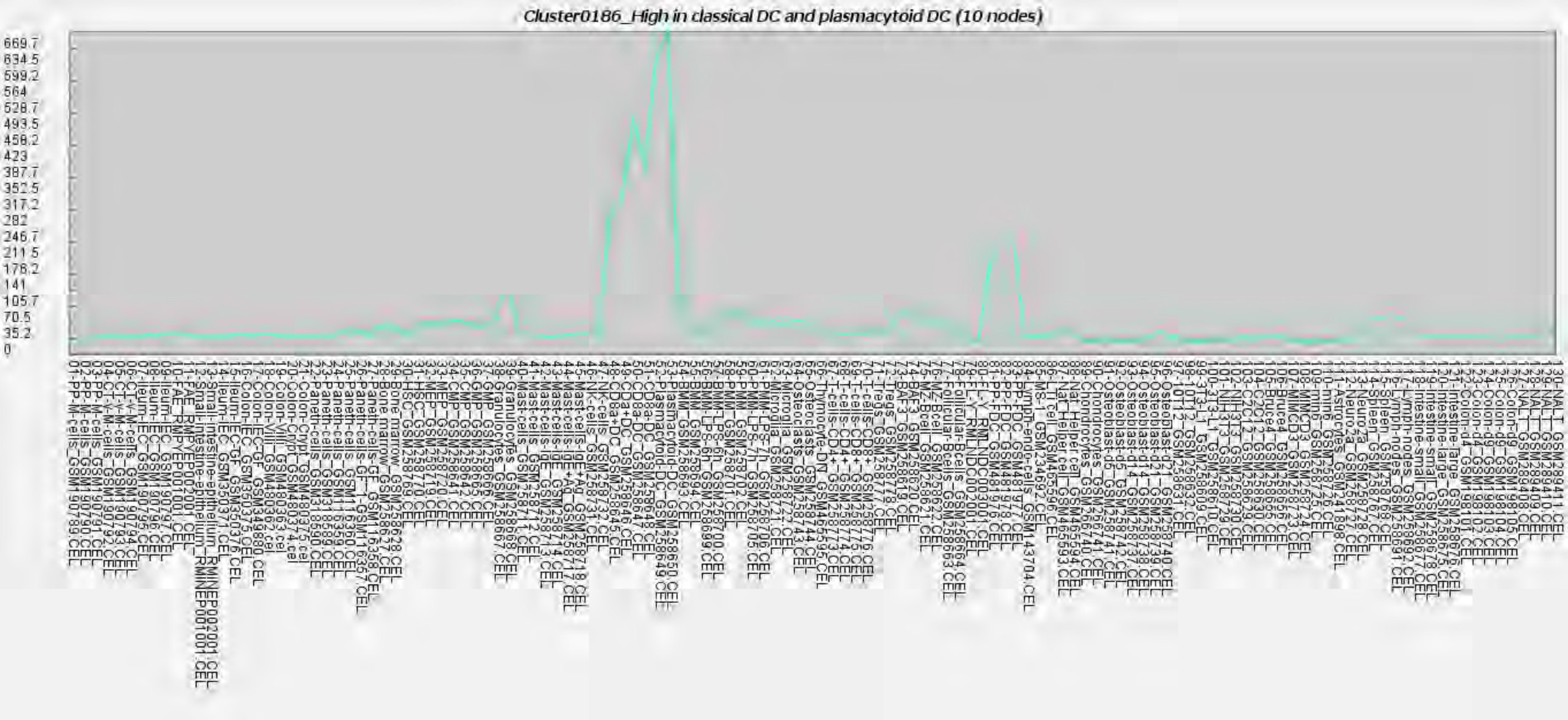

Cluster0181_Small intestine-related (10 nodes)
642.9
609
575.2
541.4
507.5
473.7
439.9
406
372.2
338.3
304.5
270.7
236.8
203
169.2
135.3
101.5
67.7
33.8
0


Cluster0182_Uncertain (10 nodes)
570.3
540.3
510.3
480.3
450.3
420.2
390.2
360.2
330.2
300.2
270.2
240.1
210.1
180.1
150.1
120.1
90.1
60
30
0

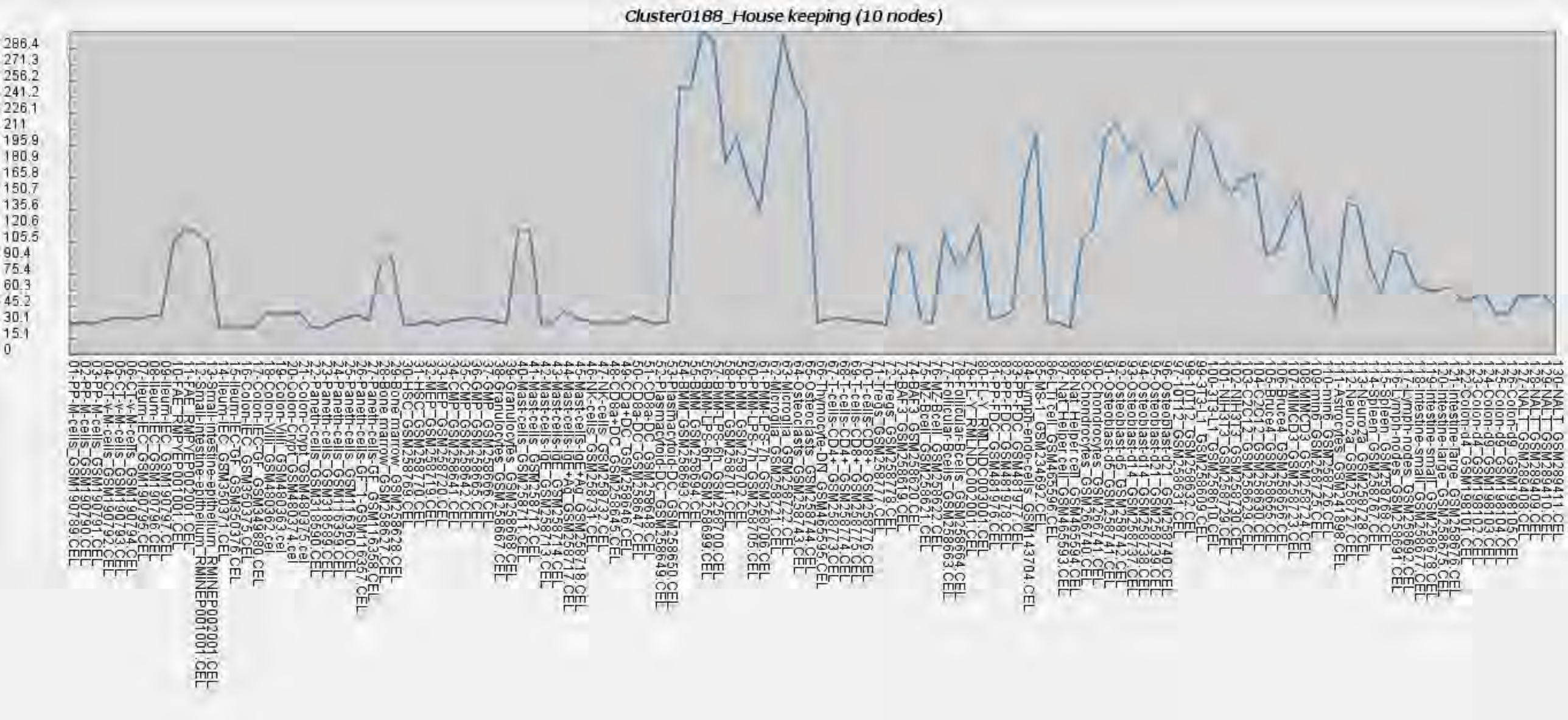

Cluster0183_High in NK cells and T cells (10 nodes)
3,172.2
3,005.3
2,838.3
2,671.4
2,504.4
2,337.4
2,170.5
2,003.5
1,836.6
1,669.6
1,502.6
1,335.7
1,168.7
1,001.8
834.8
667.8
500.9
333.9
167
0


Cluster0184_High in NK cells, T cells and B cells (10 nodes)
211.9
200.8
189.6
178.4
167.3
156.1
145
133.8
122.7
111.5
100.4
89.2
78.1
66.9
55.8
44.6
33.5
22.3
11.2
0


Cluster0185_Phagocyte-related (10 nodes)
4,794.5
4,542.2
4,289.8
4,037.5
3,785.1
3,532.8
3,280.4
3,028.1
2,775.8
2,523.4
2,271.1
2,018.7
1,766.4
1,514.1
1,261.7
1,009.4
757
504.7
252.3
0


Cluster0186_High in classical DC and plasmacytoid DC (10 nodes)
669.7
634.5
599.2
564
528.7
493.5
458.2
423
387.7
352.5
317.2
282
246.7
211.5
176.2
141
105.7
70.5
35.2
0

Cluster0187_Intestine-related (10 nodes)
1,575.8
1,492.9
1,409.9
1,327
1,244
1,161.1
1,078.2
995.2
912.3
829.4
746.4
663.5
580.6
497.6
414.7
331.7
248.8
165.9
82.9
0


Cluster0188_House keeping (10 nodes)
286.4
271.3
256.2
241.2
226.1
211
195.9
180.9
165.8
150.7
135.6
120.6
105.5
90.4
75.4
60.3
45.2
30.1
15.1
0

Cluster0189_Intestine-related (10 nodes)

3,166.9
3,000.2
2,833.5
2,666.9
2,500.2
2,333.5
2,166.8
2,000.1
1,833.5
1,666.8
1,500.1
1,333.4
1,166.7
1,000.1
833.4
666.7
500
333.4
166.7
0

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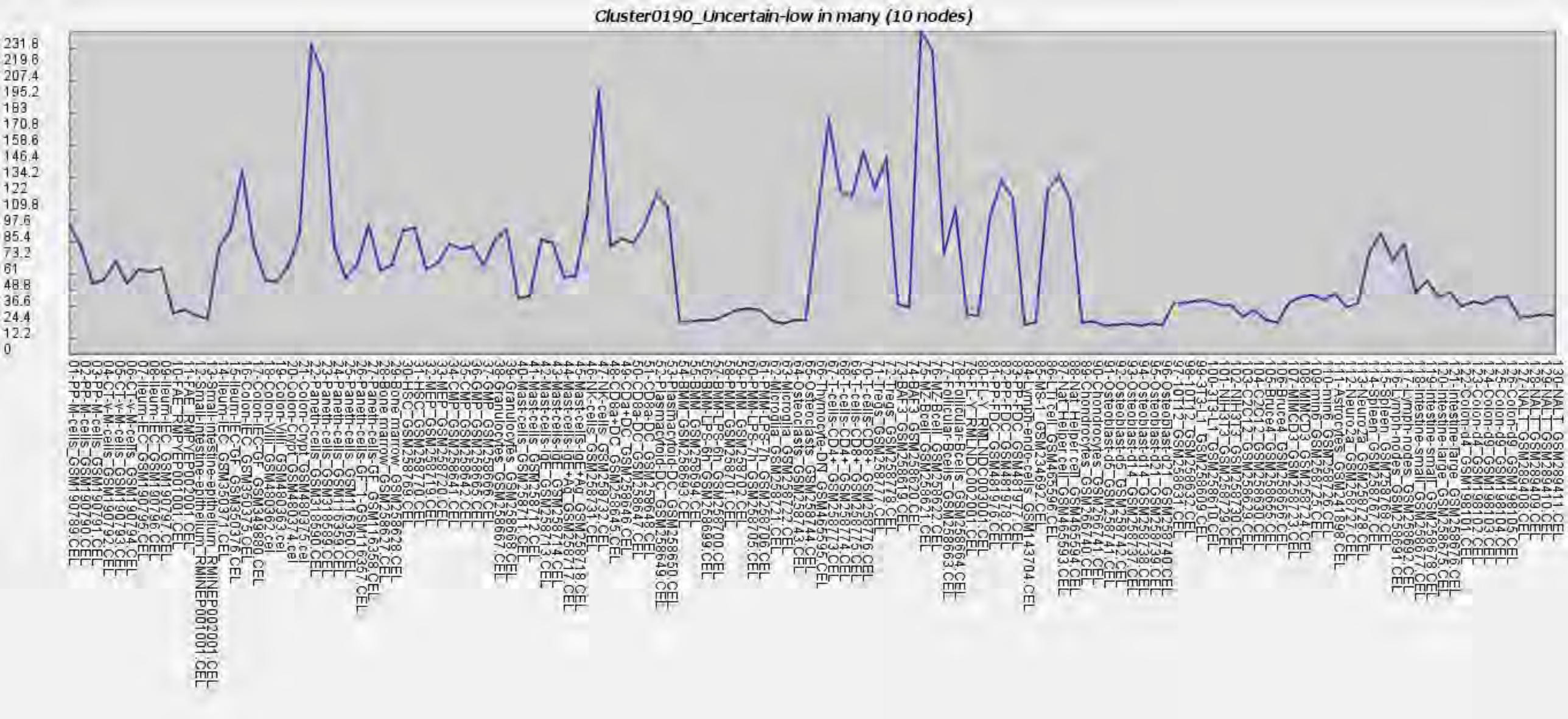
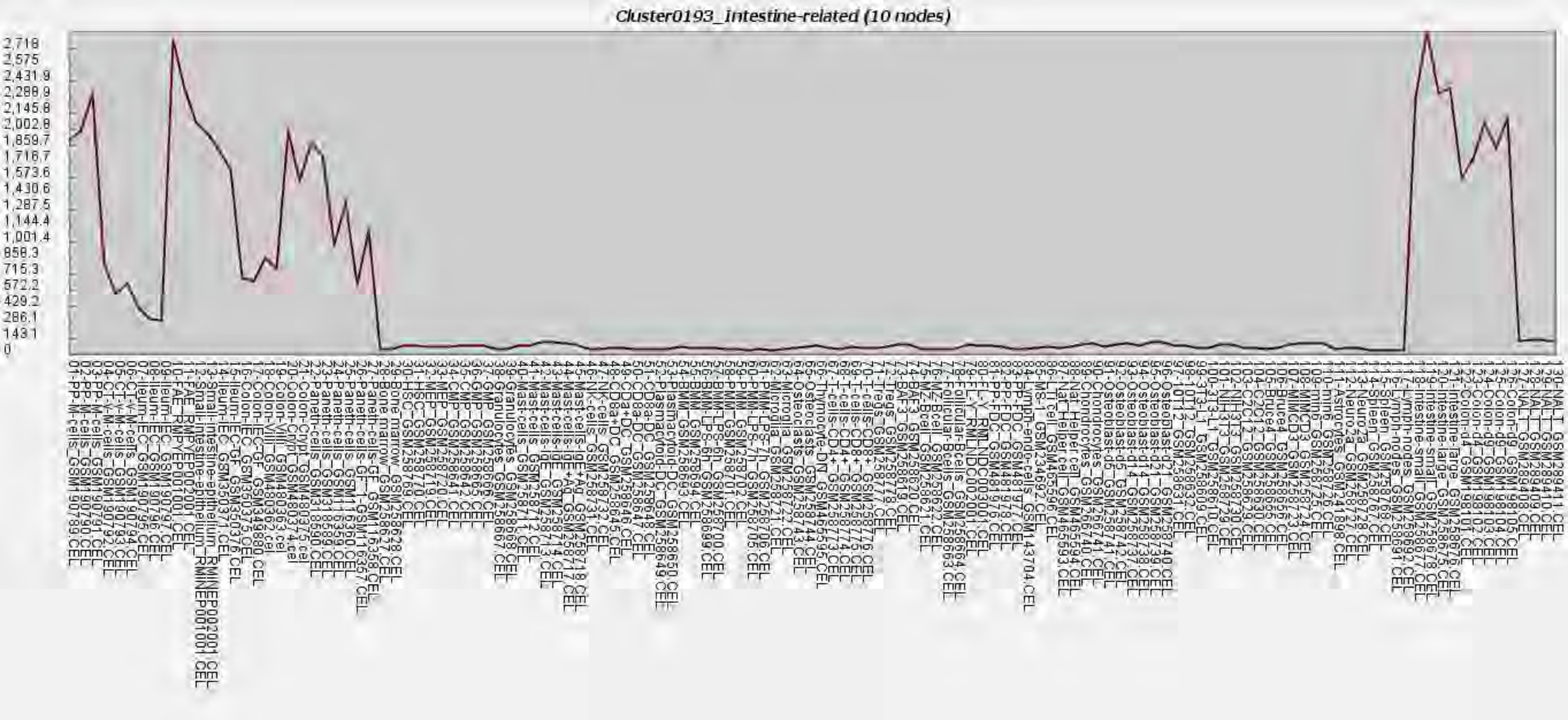
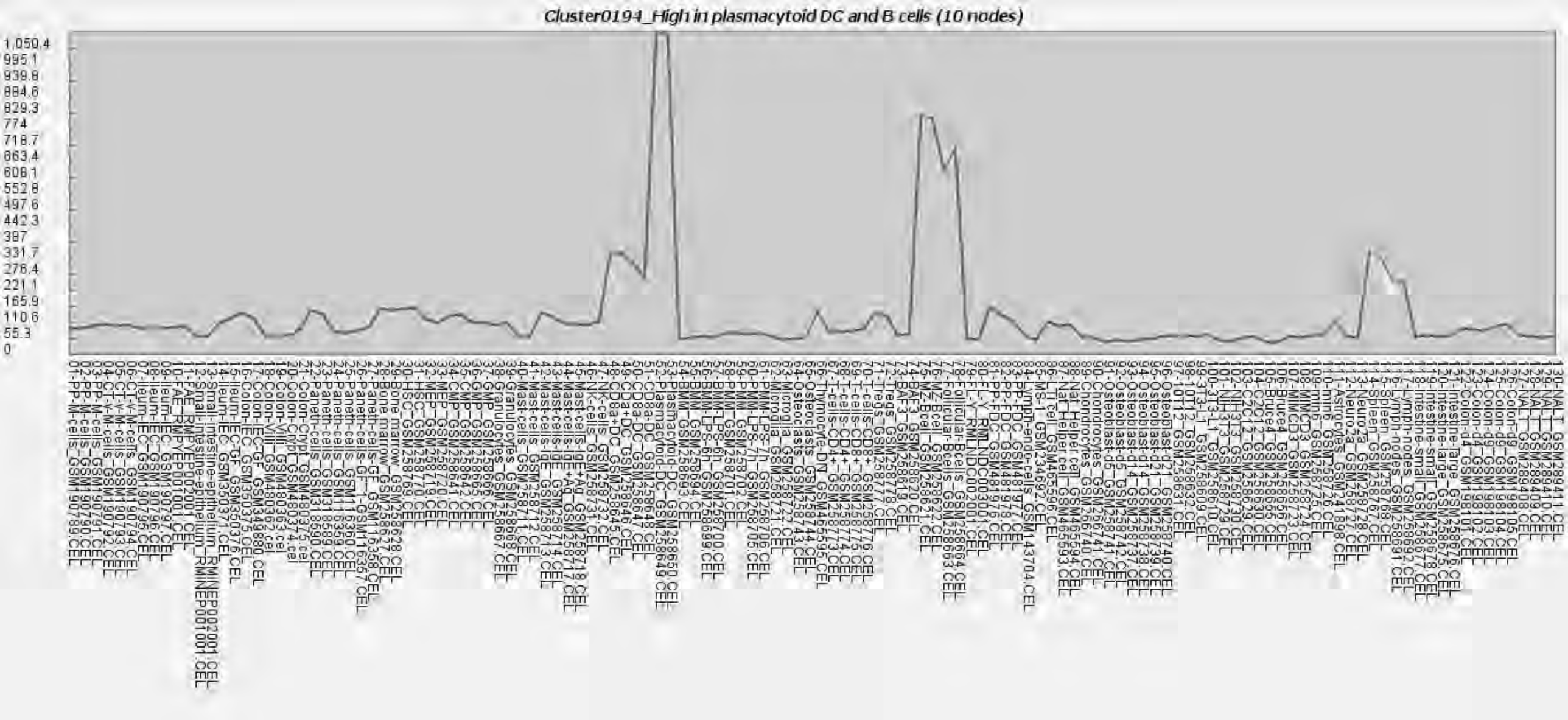
GSM2289410.CEL
GSM2289408.CEL
GSM2289409.CEL
GSM1981104.CEL
GSM1981103.CEL
GSM1981102.CEL
GSM1981101.CEL
GSM2586676.CEL
GSM2586675.CEL
GSM2586678.CEL
GSM2586677.CEL
GSM2586691.CEL
GSM2586692.CEL
GSM2586693.CEL
GSM2586694.CEL
GSM2586695.CEL
GSM2586696.CEL
GSM2586697.CEL
GSM2586698.CEL
GSM2587726.CEL
GSM2587725.CEL
GSM2587724.CEL
GSM2587723.CEL
GSM2587722.CEL
GSM2587721.CEL
GSM2587740.CEL
GSM2587739.CEL
GSM2587738.CEL
GSM2587737.CEL
GSM2587742.CEL
GSM2587741

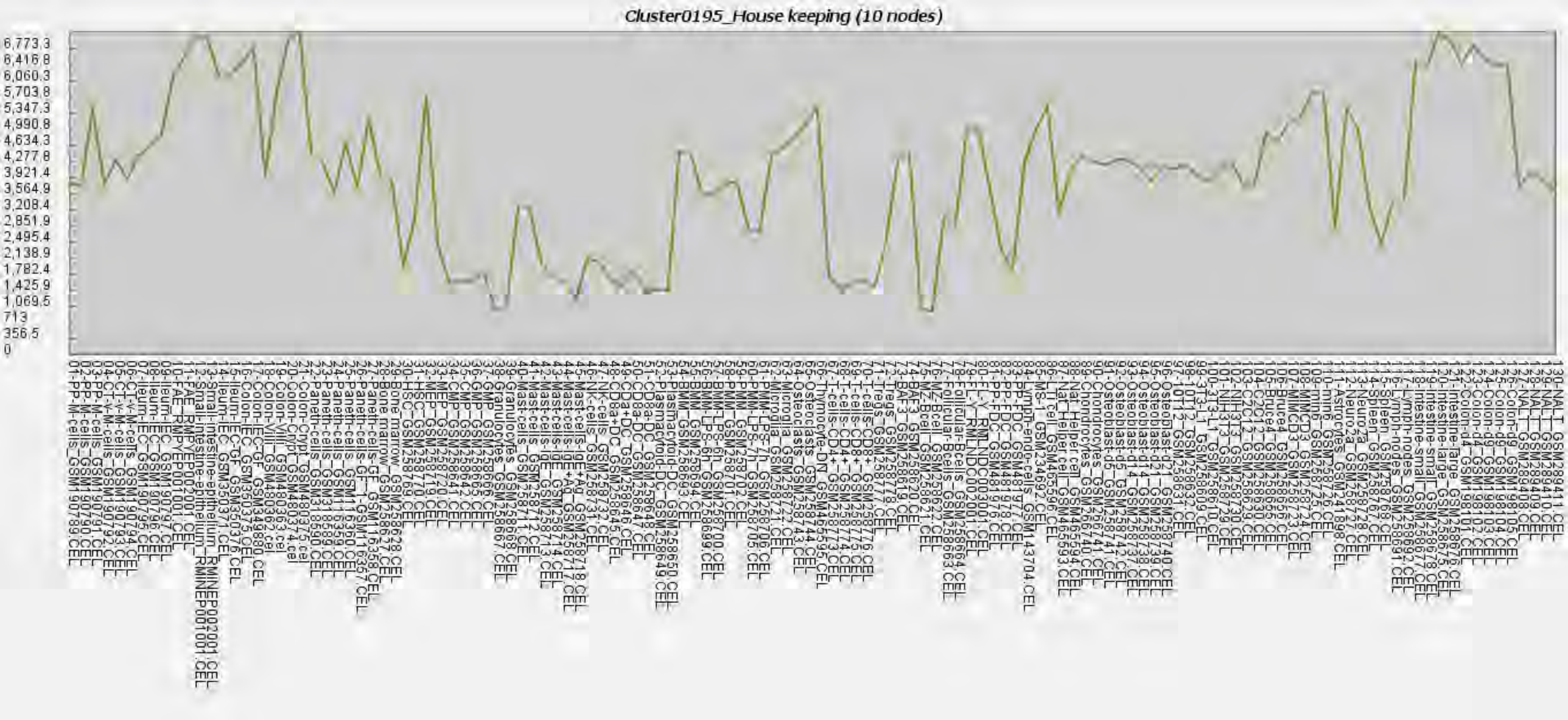

Cluster0190_Uncertain-low in many (10 nodes)
231.8
219.6
207.4
195.2
183
170.8
158.6
146.4
134.2
122
109.8
97.6
85.4
73.2
61
48.8
36.6
24.4
12.2
0

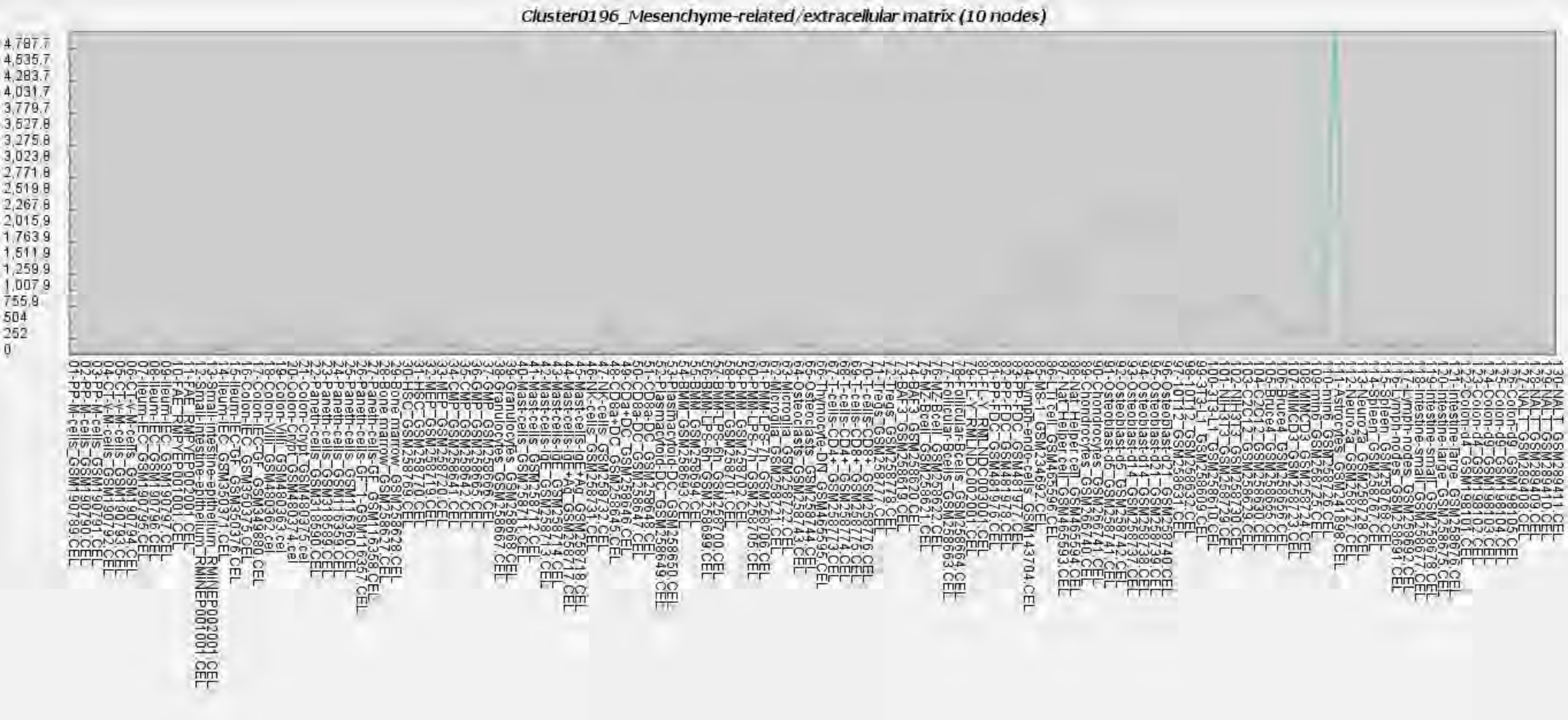
Cluster0191_High in Bruce4 and min6 cells (10 nodes)
345.1
327
308.8
290.7
272.5
254.3
236.2
218
199.8
181.7
163.5
145.3
127.2
109
90.8
72.7
54.5
36.3
18.2
0

Cluster0192_intestine-related (10 nodes)
4,143.2
3,925.2
3,707.1
3,489
3,271
3,052.9
2,834.8
2,616.8
2,398.7
2,180.7
1,962.6
1,744.5
1,526.5
1,308.4
1,090.3
872.3
654.2
436.1
218.1
0

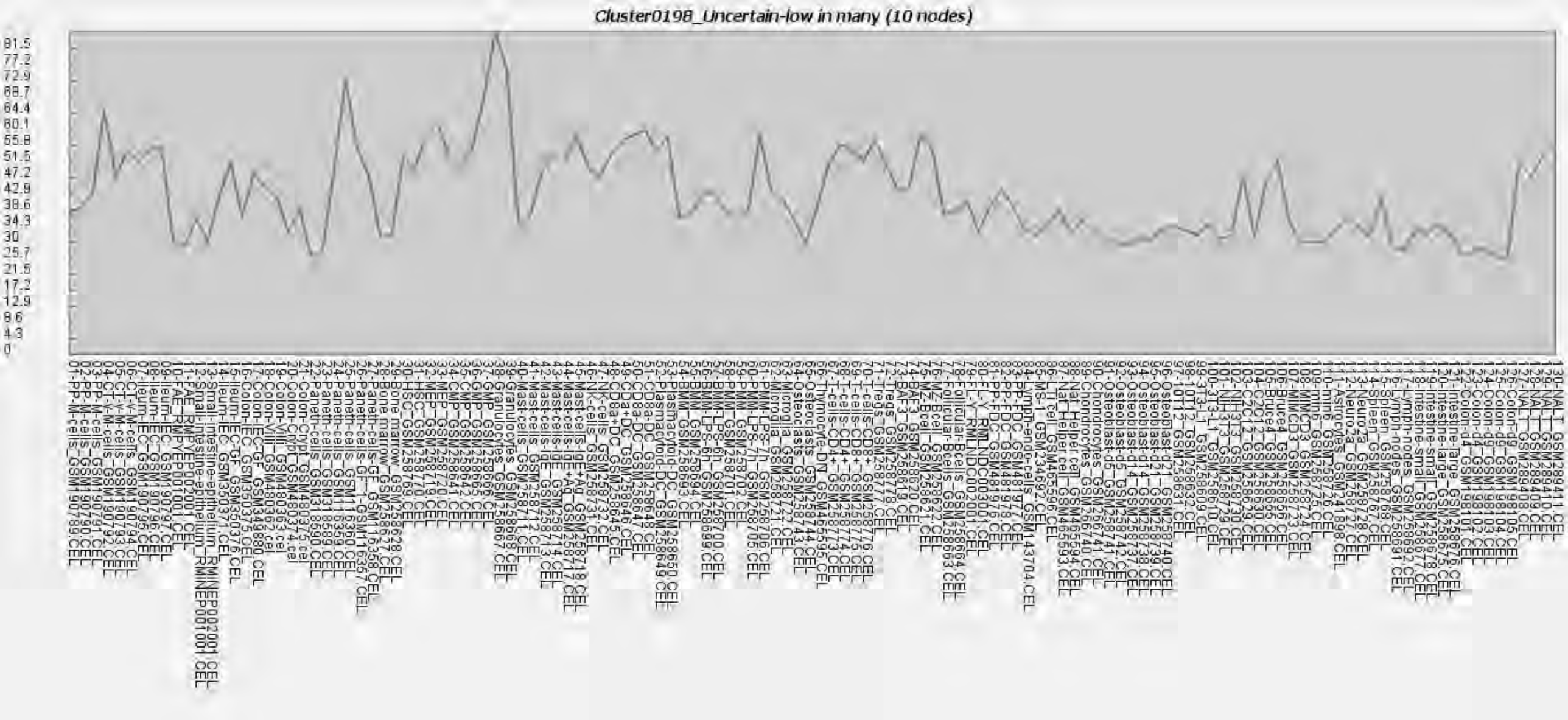

Cluster0193_intestine-related (10 nodes)
2,718
2,575
2,431.9
2,288.9
2,145.8
2,002.8
1,859.7
1,716.7
1,573.6
1,430.6
1,287.5
1,144.4
1,001.4
858.3
715.3
572.2
429.2
286.1
143.1
0


Cluster0194_High in plasmacytoid DC and B cells (10 nodes)
1,050.4
995.1
939.8
884.6
829.3
774
718.7
663.4
608.1
552.8
497.6
442.3
387
331.7
276.4
221.1
165.9
110.6
55.3
0

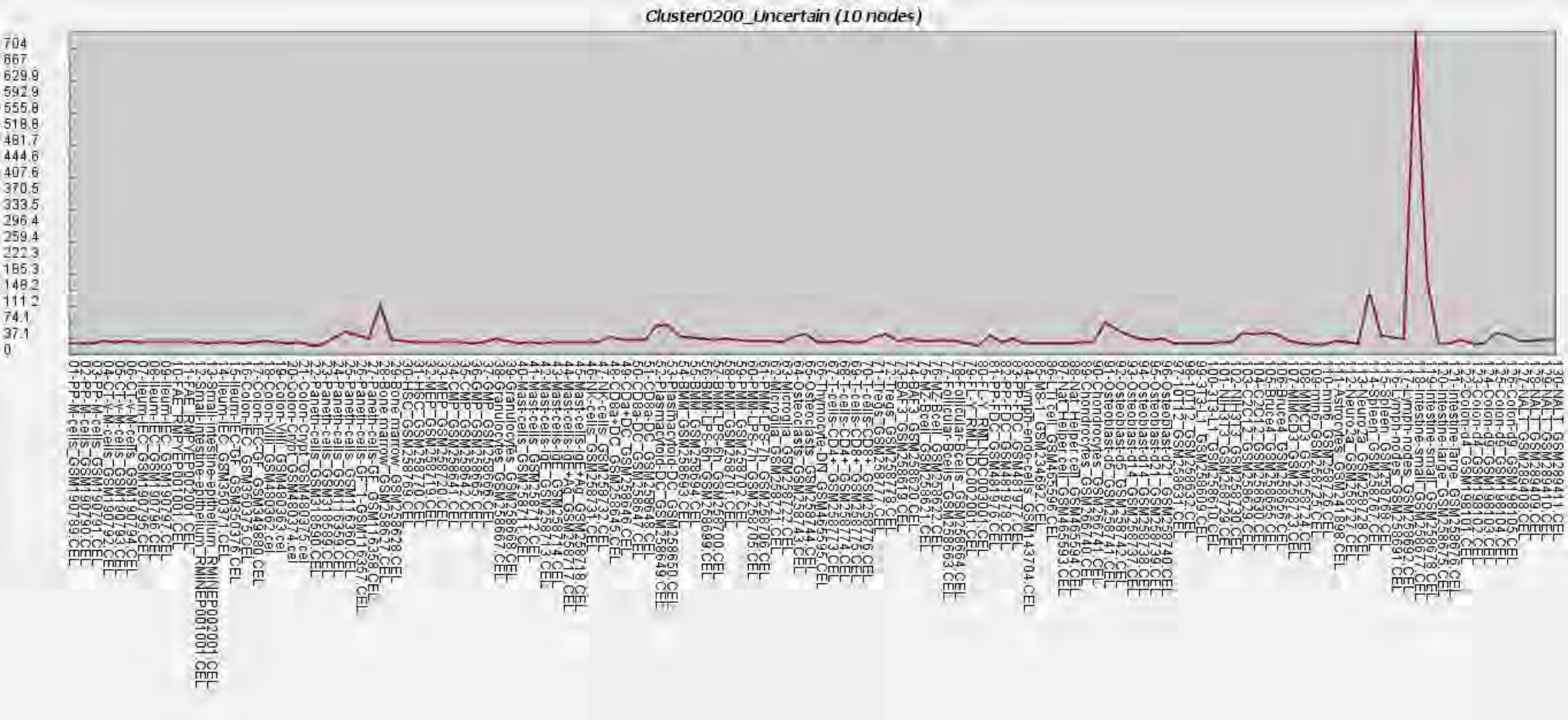

Cluster0195_House keeping (10 nodes)
6,773.3
6,416.8
6,060.3
5,703.8
5,347.3
4,990.8
4,634.3
4,277.8
3,921.4
3,564.9
3,208.4
2,851.9
2,495.4
2,138.9
1,782.4
1,425.9
1,069.5
713
356.5
0

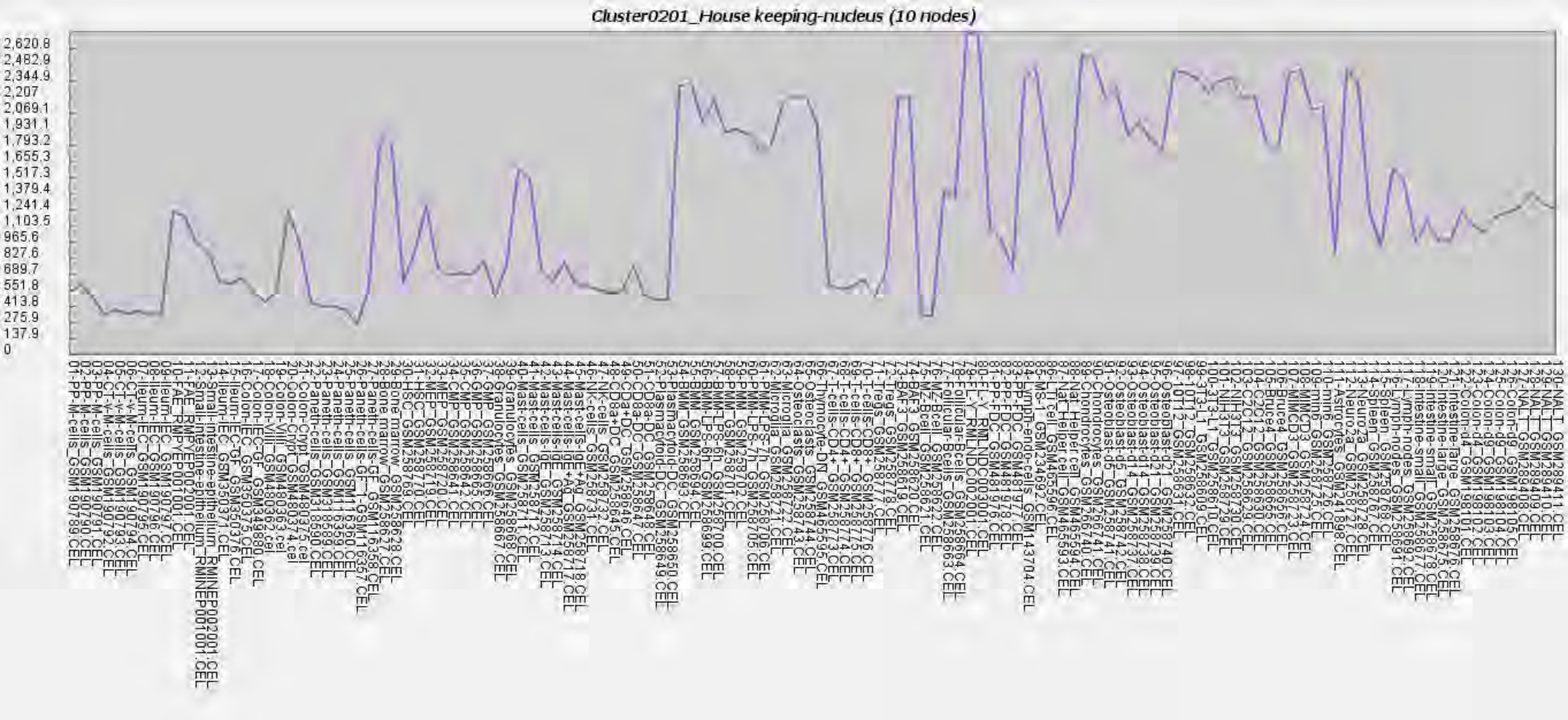

Cluster0196_Mesenchyme-related/extracellular matrix (10 nodes)
4,787.7
4,535.7
4,283.7
4,031.7
3,779.7
3,527.8
3,275.8
3,023.8
2,771.8
2,519.8
2,267.8
2,015.9
1,763.9
1,511.9
1,259.9
1,007.9
755.9
504
252
0

Cluster0197_Small intestine-related (10 nodes)
2,583.7
2,447.7
2,311.8
2,175.8
2,039.8
1,903.8
1,767.8
1,631.8
1,495.8
1,359.9
1,223.9
1,087.9
951.9
815.9
679.9
543.9
408
272
136
0


Cluster0198_Uncertain-low in many (10 nodes)
81.5
77.2
72.9
68.7
64.4
60.1
55.8
51.5
47.2
42.9
38.6
34.3
30
25.7
21.5
17.2
12.9
8.6
4.3
0

Cluster0199_Uncertain (10 nodes)
2,090.4
1,980.4
1,870.4
1,760.3
1,650.3
1,540.3
1,430.3
1,320.3
1,210.2
1,100.2
990.2
880.2
770.1
660.1
550.1
440.1
330.1
220
110
0


Cluster0200_Uncertain (10 nodes)
704
667
629.9
592.9
555.8
518.8
481.7
444.6
407.6
370.5
333.5
296.4
259.4
222.3
185.3
148.2
111.2
74.1
37.1
0


Cluster0201_House keeping-nucleus (10 nodes)
2,620.8
2,482.9
2,344.9
2,207
2,069.1
1,931.1
1,793.2
1,655.3
1,517.3
1,379.4
1,241.4
1,103.5
965.6
827.6
689.7
551.8
413.8
275.9
137.9
0

Cluster0202_House keeping (10 nodes)

5,951.8
5,638.6
5,325.3
5,012.1
4,698.8
4,385.6
4,072.3
3,759
3,445.8
3,132.5
2,819.3
2,506
2,192.8
1,879.5
1,566.3
1,253
939.8
626.5
313.3
0

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GSM2894410.CEL
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GSM2894408.CEL
GSM1981105.CEL
GSM1981104.CEL
GSM1981103.CEL
GSM1981102.CEL
GSM1981101.CEL
GSM2586676.CEL
GSM2586675.CEL
GSM2586674.CEL
GSM2586673.CEL
GSM2586672.CEL
GSM2586671.CEL
GSM2586670.CEL
GSM2586669.CEL
GSM2586668.CEL
GSM2586667.CEL
GSM2586666.CEL
GSM2586665.CEL
GSM2586664.CEL
GSM2586663.CEL
GSM2586662.CEL
GSM2586661.CEL
GSM2586660.CEL
GSM2586659.CEL
GSM2586658.CEL
GSM2586657.CEL
GSM2586656.CEL
GSM2586655.CEL
GSM2586654.CEL
GSM2586653.CEL
GSM2586652.CEL
GSM2586651.CEL
GSM2586650.CEL
GSM2586649.CEL
GSM2586648.CEL
GSM2586647.CEL
GSM2586646.CEL
GSM2586645.CEL
GSM2586644.CEL
GSM2586643.CEL
GSM2586642.CEL
GSM2586641.CEL
GSM2586640.CEL
GSM2586639.CEL
GSM2586638.CEL
GSM2586637.CEL

Cluster0203_intestine-related (10 nodes)
4,452.8
4,218.5
3,984.1
3,749.8
3,515.4
3,281
3,046.7
2,812.3
2,578
2,343.6
2,109.2
1,874.9
1,640.5
1,406.2
1,171.8
937.4
703.1
468.7
234.4
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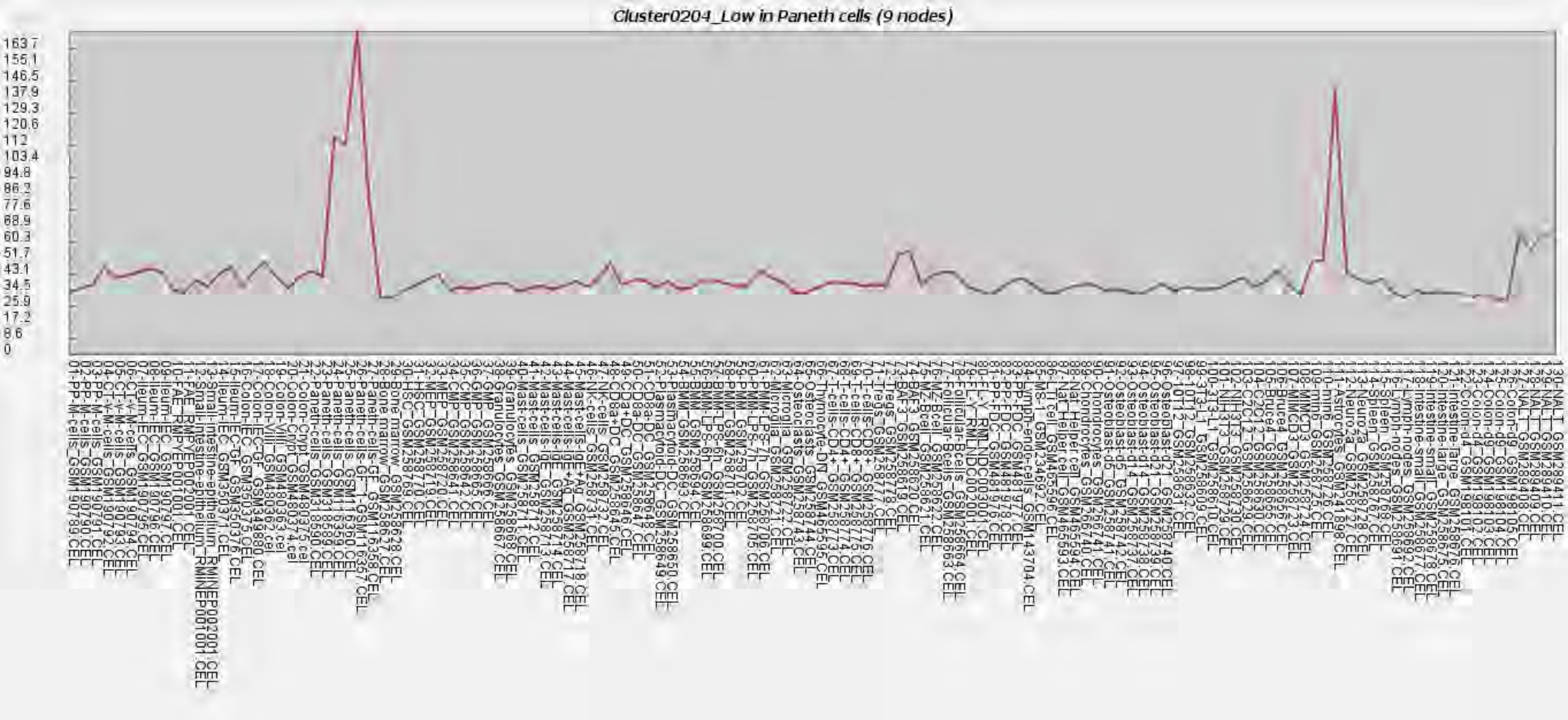
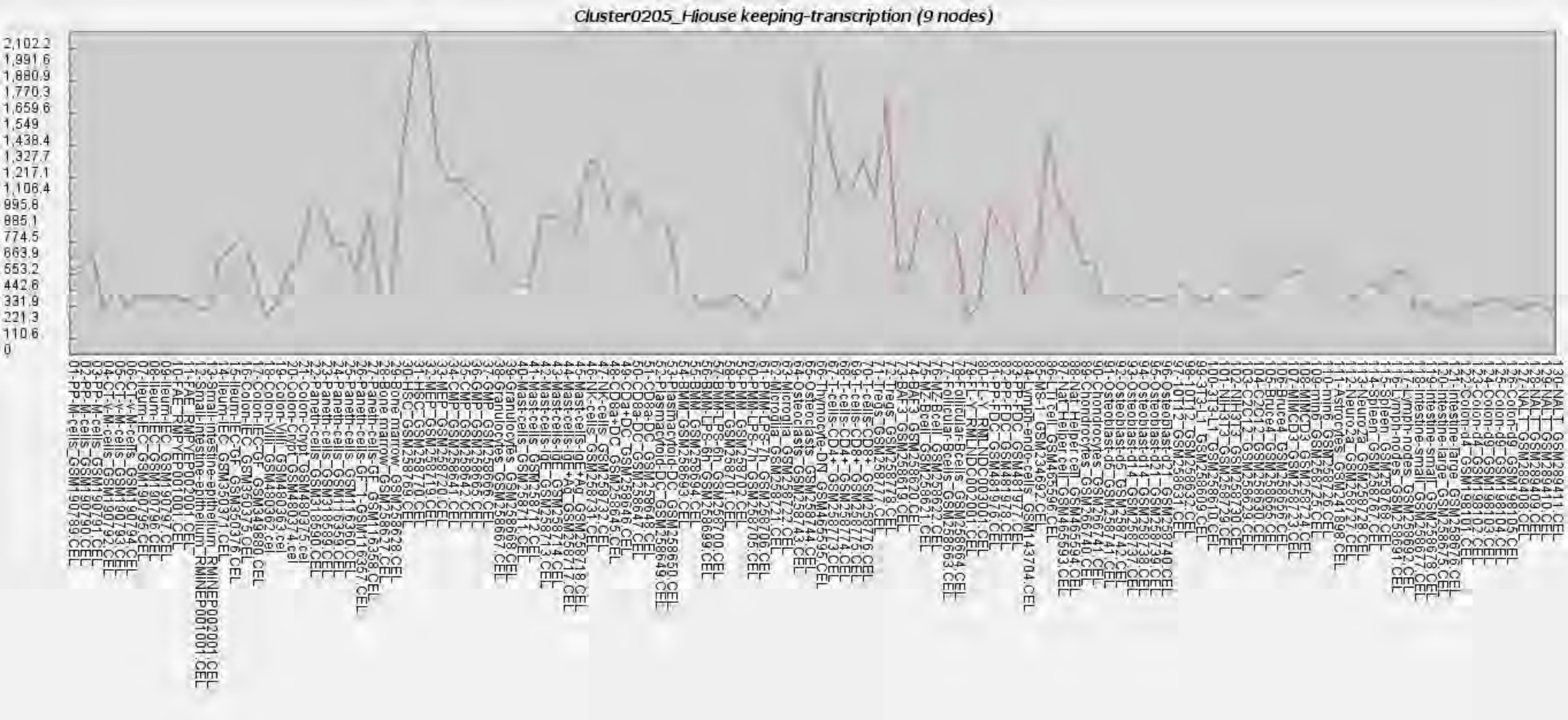
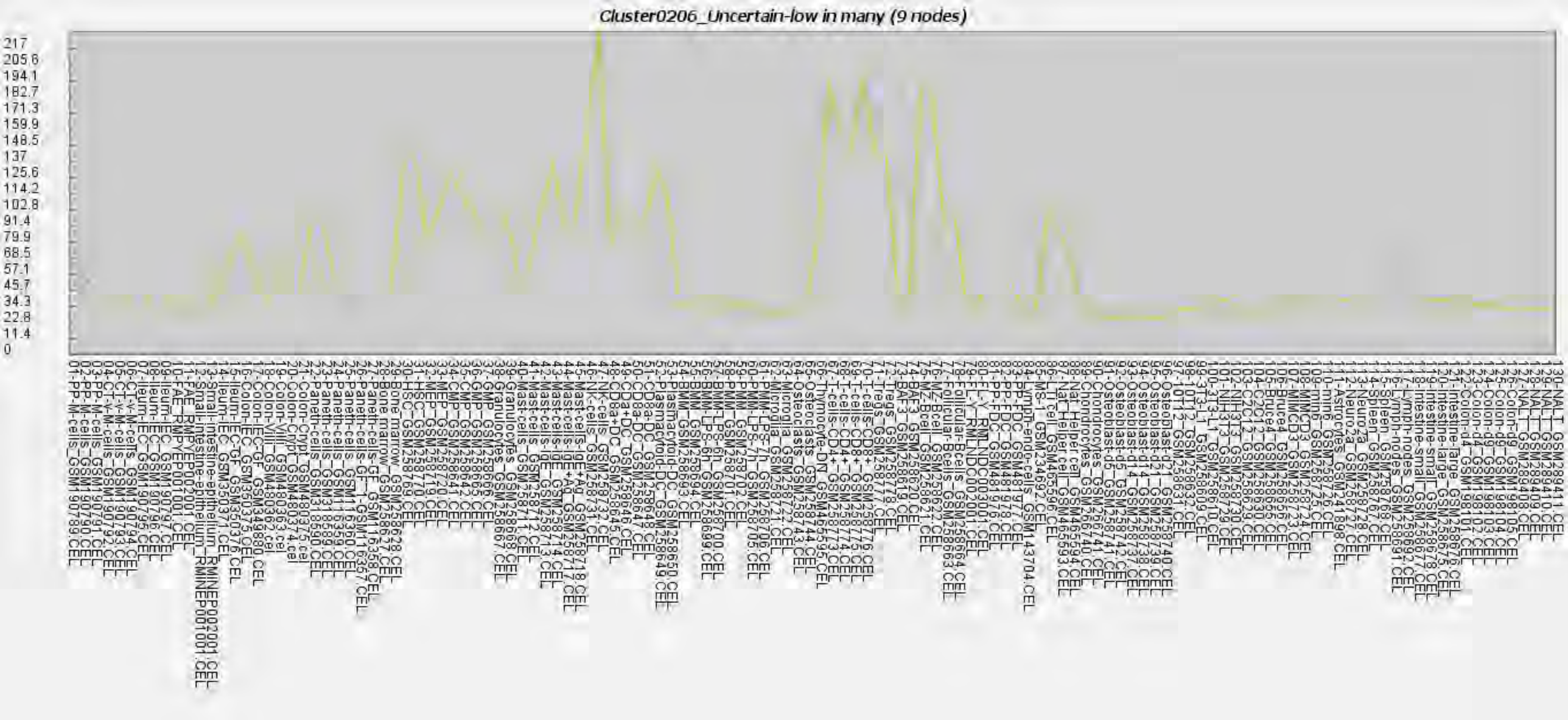
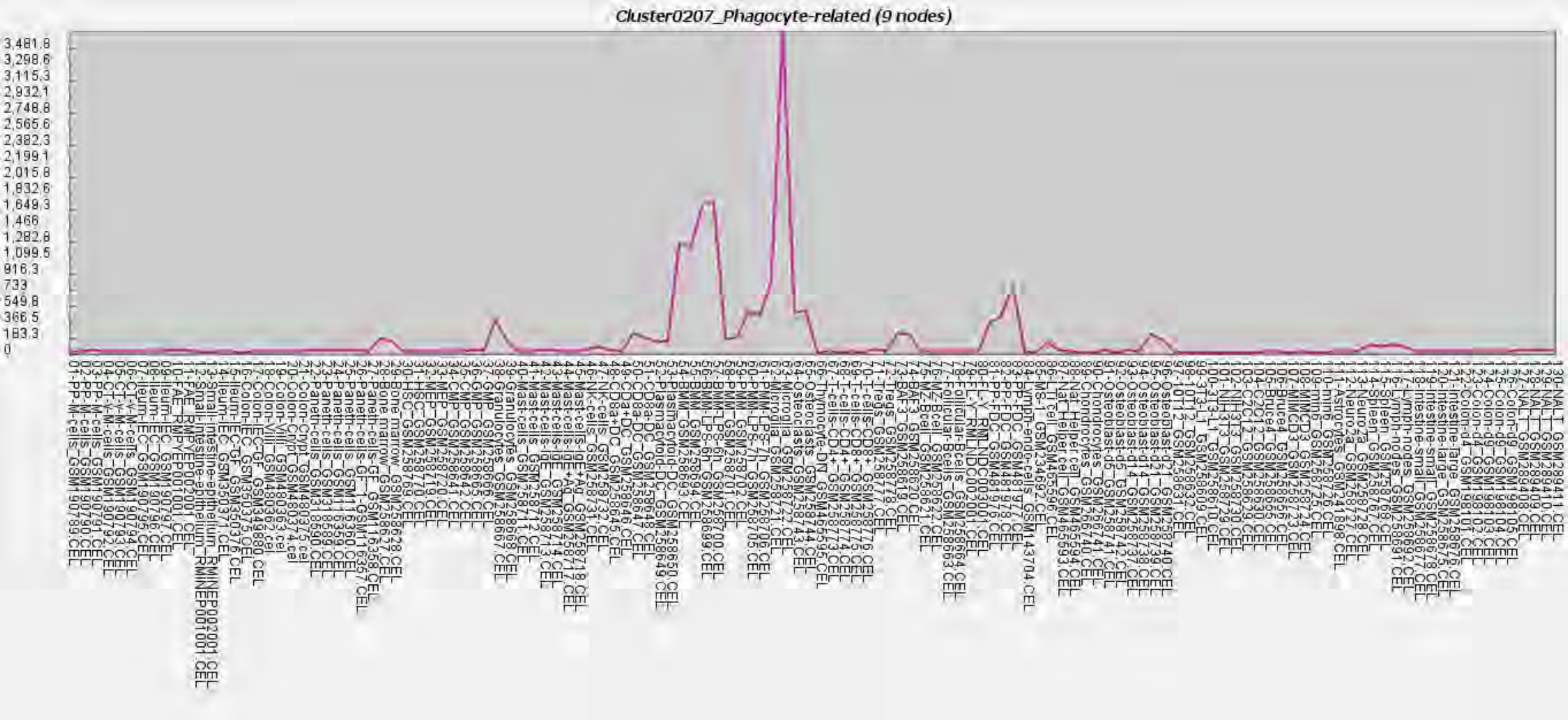
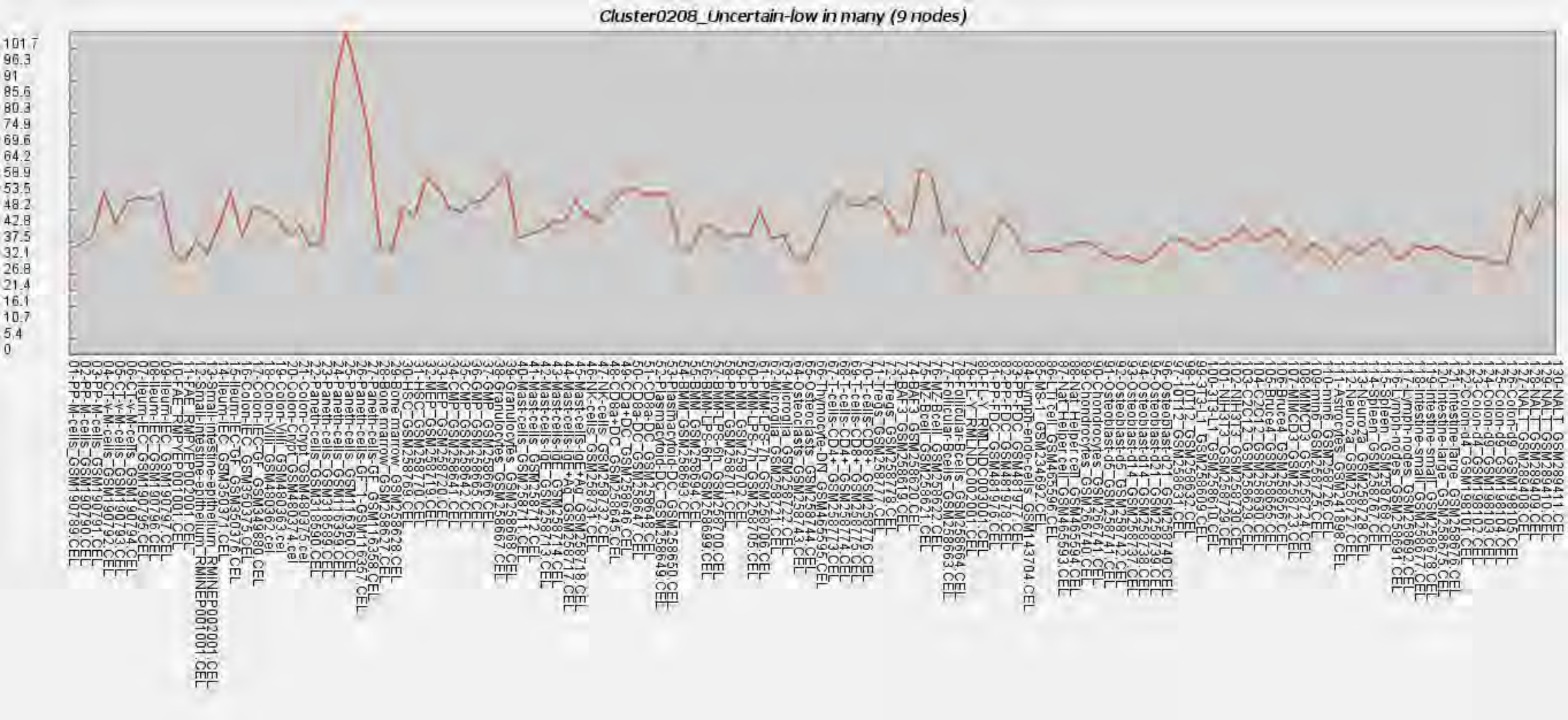

Cluster0204_Low in Paneth cells (9 nodes)
163.7
155.1
146.5
137.9
129.3
120.6
112
103.4
94.8
86.2
77.6
68.9
60.3
51.7
43.1
34.5
25.9
17.2
8.6
0

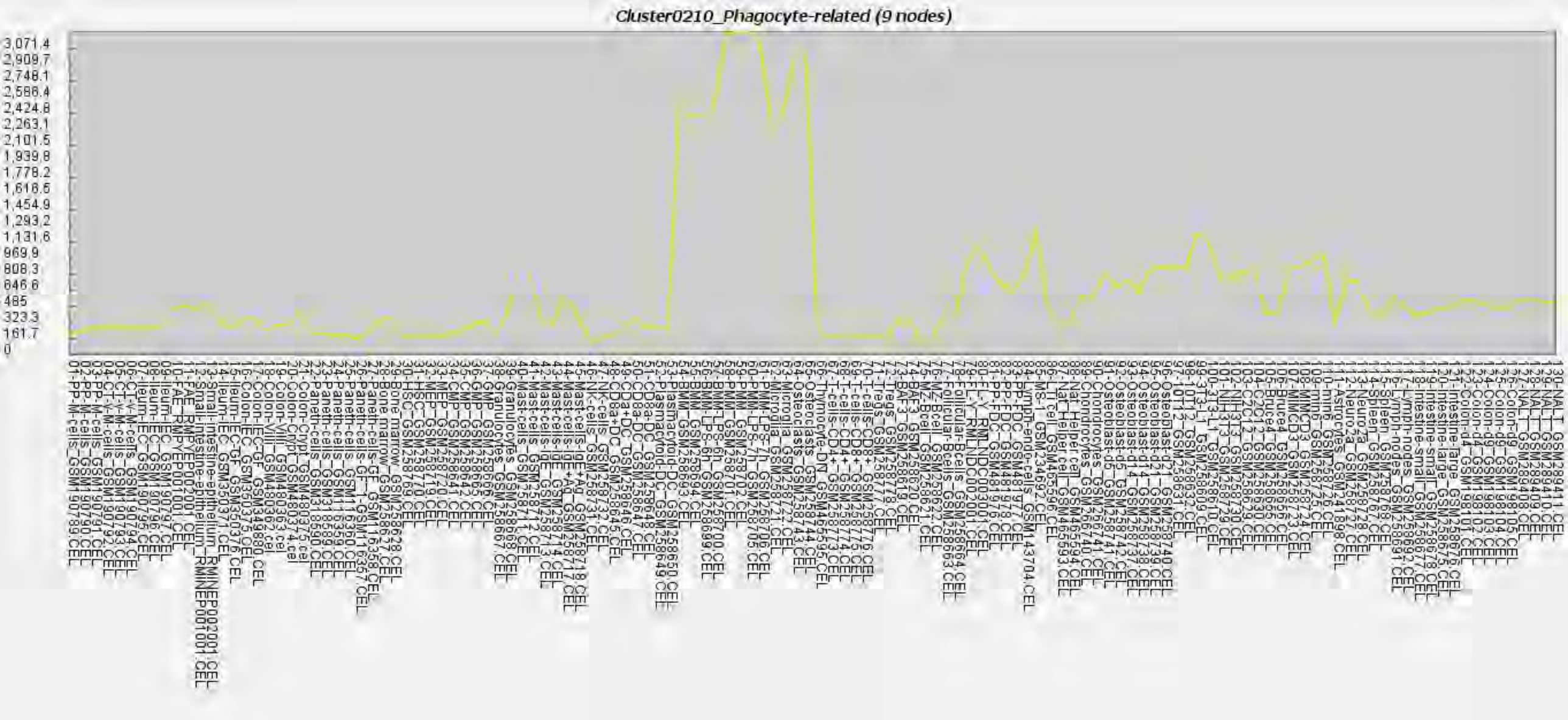

Cluster0205_Hiouse keeping-transcription (9 nodes)
2,102.2
1,991.6
1,880.9
1,770.3
1,659.6
1,549
1,438.4
1,327.7
1,217.1
1,106.4
995.8
885.1
774.5
663.9
553.2
442.6
331.9
221.3
110.6
0


Cluster0206_Uncertain-low in many (9 nodes)
217
205.6
194.1
182.7
171.3
159.9
148.5
137
125.6
114.2
102.8
91.4
79.9
68.5
57.1
45.7
34.3
22.8
11.4
0

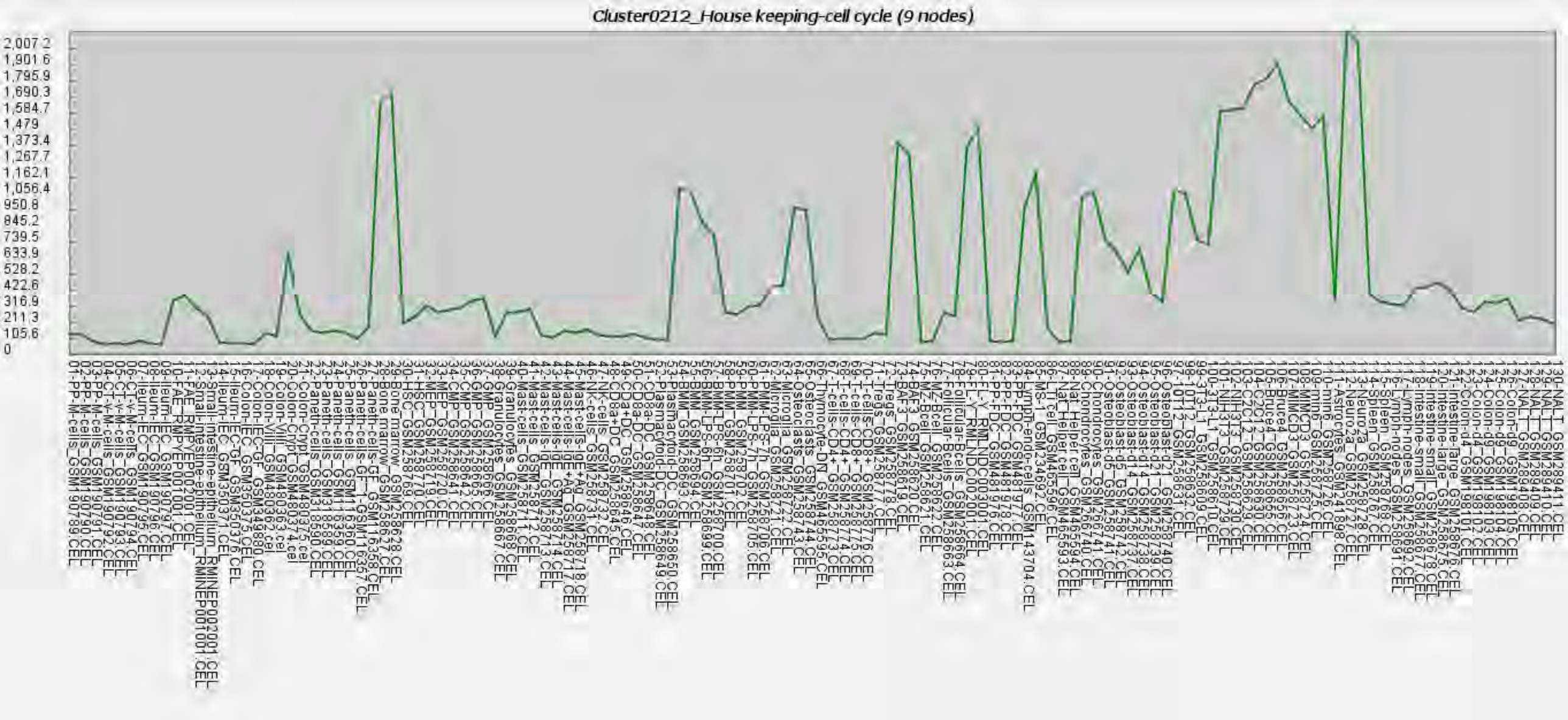

Cluster0207_Phagocyte-related (9 nodes)
3,481.8
3,298.6
3,115.3
2,932.1
2,748.8
2,565.6
2,382.3
2,199.1
2,015.8
1,832.6
1,649.3
1,466
1,282.8
1,099.5
916.3
733
549.8
366.5
183.3
0


Cluster0208_Uncertain-low in many (9 nodes)
101.7
96.3
91
85.6
80.3
74.9
69.6
64.2
58.9
53.5
48.2
42.8
37.5
32.1
26.8
21.4
16.1
10.7
5.4
0

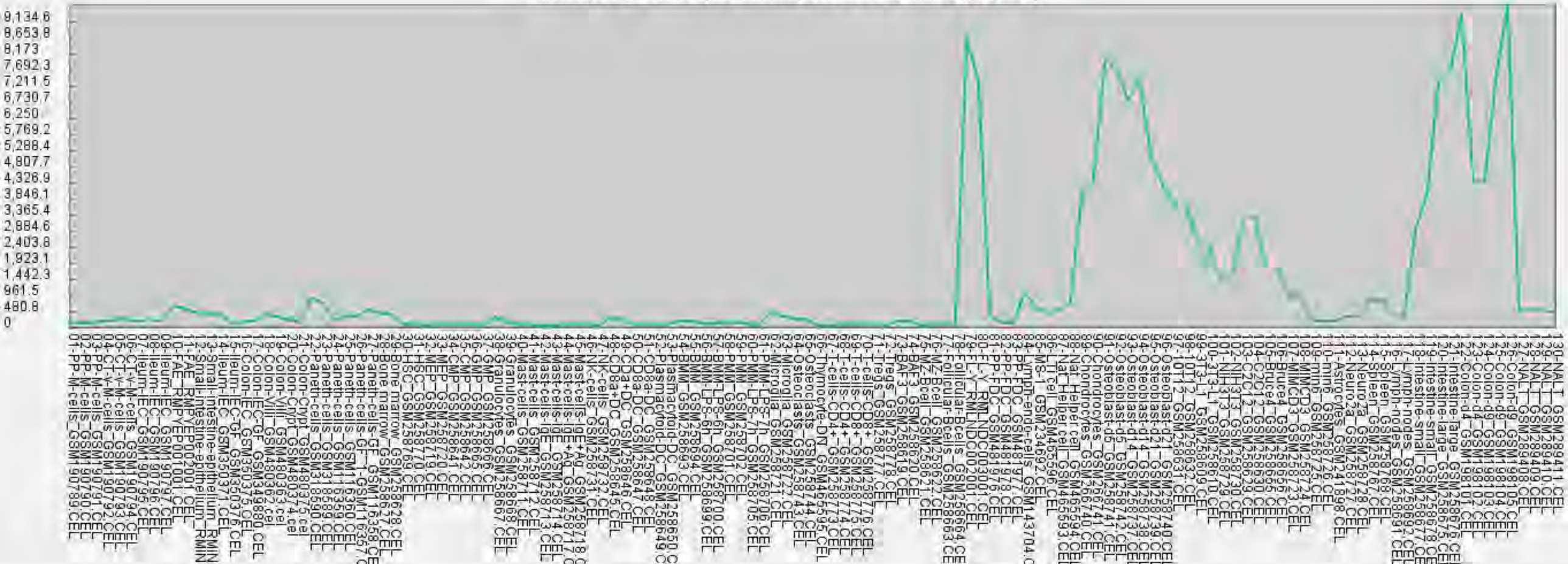
Cluster0209_High in osteoblasts, NIH3T3 and min6 cells (9 nodes)
3,555.8
3,368.7
3,181.5
2,994.4
2,807.2
2,620.1
2,432.9
2,245.8
2,058.6
1,871.5
1,684.3
1,497.2
1,310
1,122.9
935.7
748.6
561.4
374.3
187.1
0

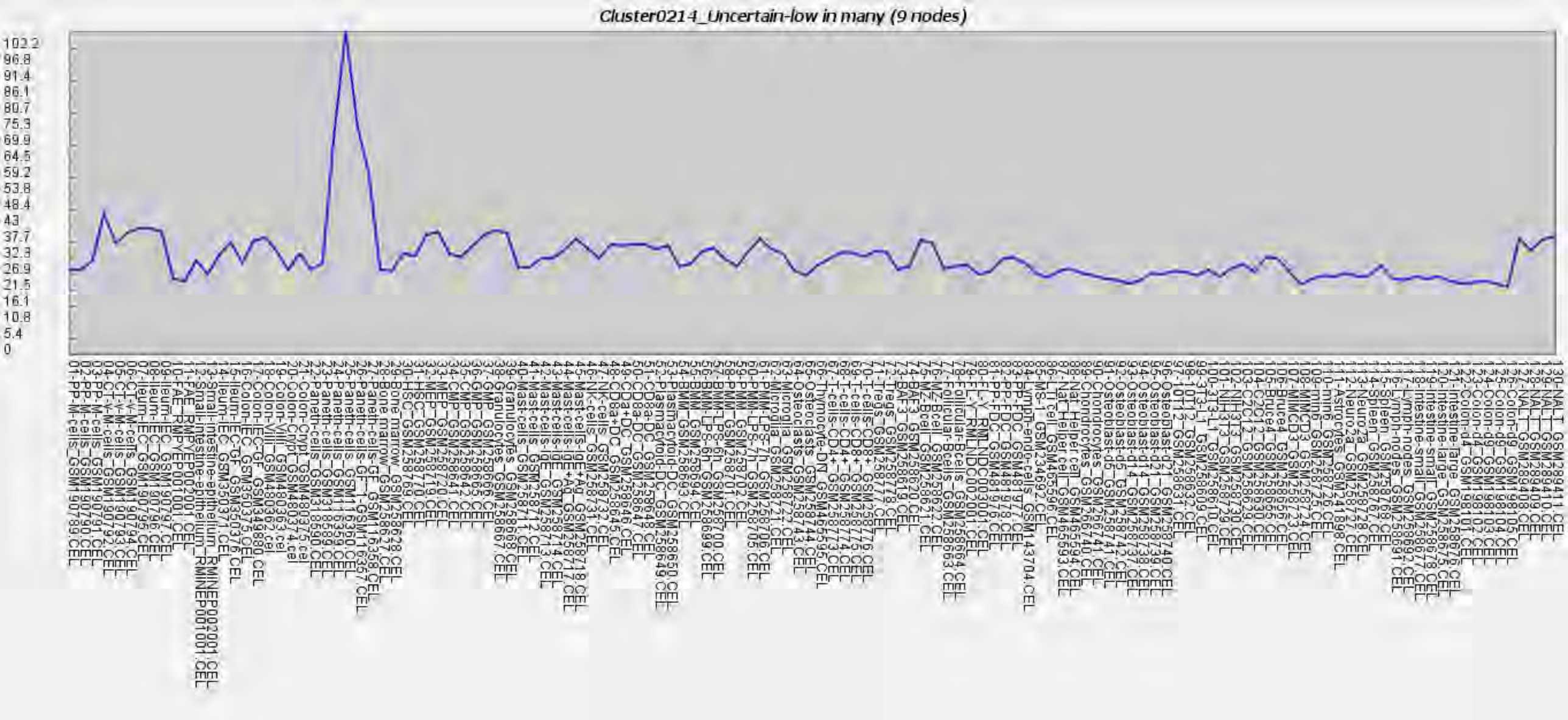

Cluster0210_Phagocyte-related (9 nodes)
3,071.4
2,909.7
2,748.1
2,586.4
2,424.8
2,263.1
2,101.5
1,939.8
1,778.2
1,616.5
1,454.9
1,293.2
1,131.6
969.9
808.3
646.6
485
323.3
161.7
0

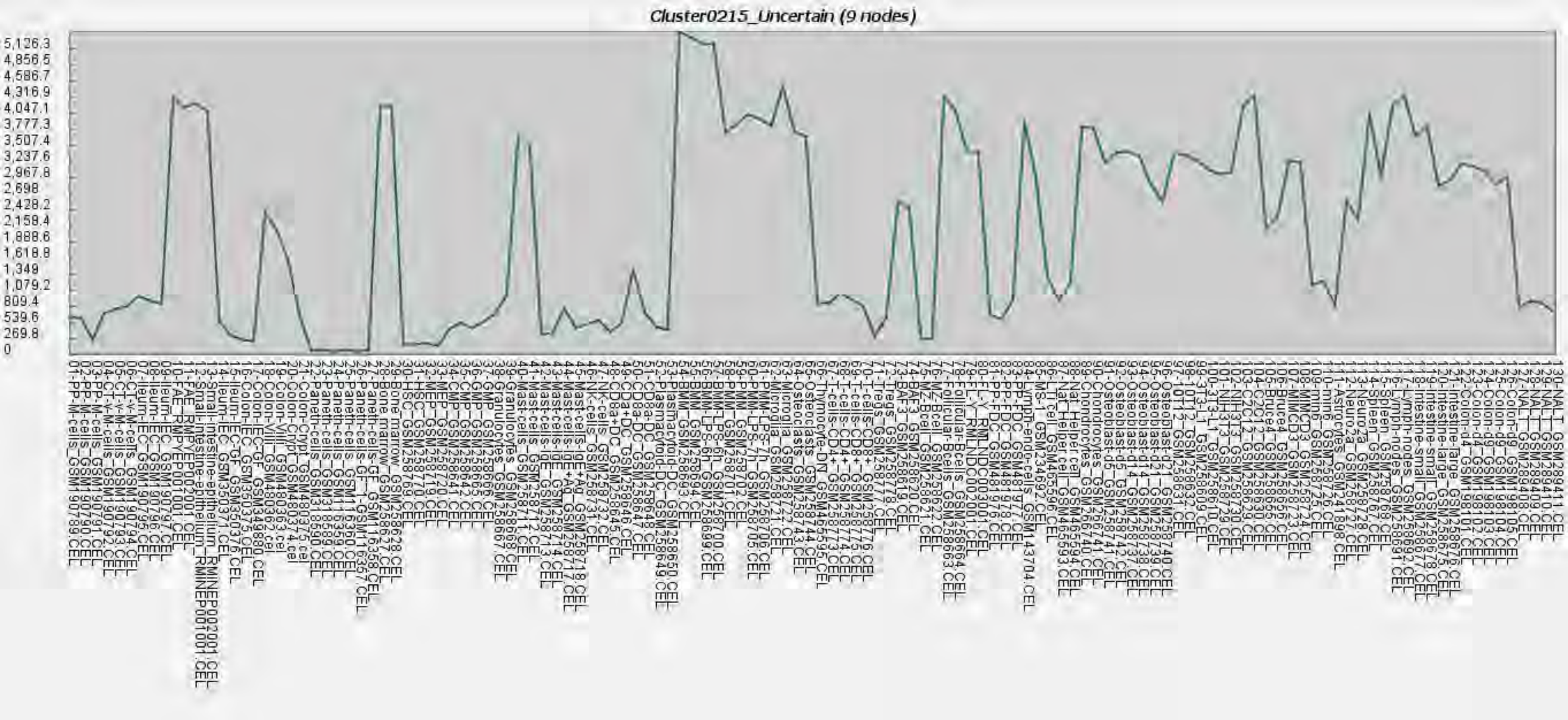
Cluster0211_intestine-related (9 nodes)
2,997.6
2,839.8
2,682.1
2,524.3
2,366.5
2,209.8
2,051
1,893.2
1,735.4
1,577.7
1,419.9
1,262.1
1,104.4
946.6
788.8
631.1
473.3
315.5
157.8
0

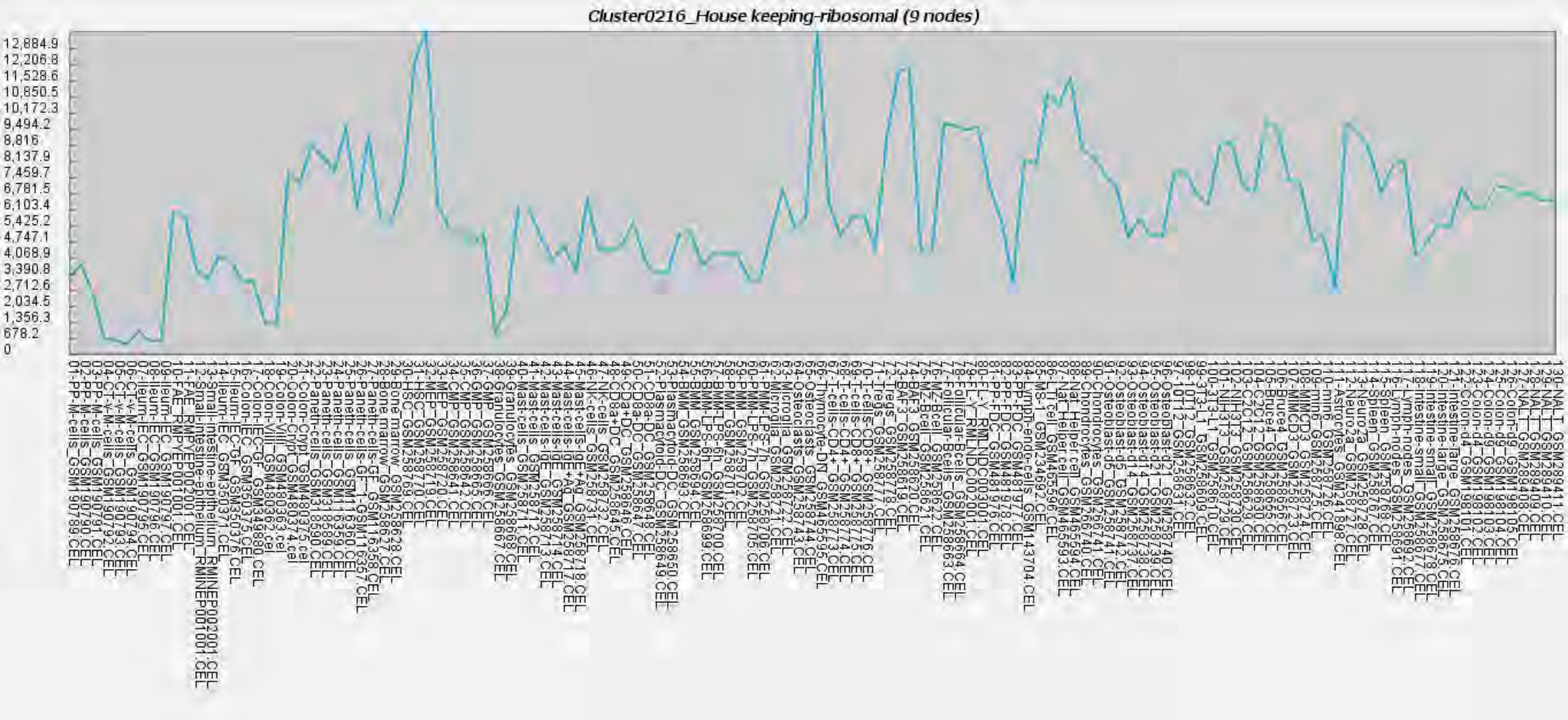

Cluster0212_House keeping-cell cycle (9 nodes)
2,007.2
1,901.6
1,795.9
1,690.3
1,584.7
1,479
1,373.4
1,267.7
1,162.1
1,056.4
950.8
845.2
739.5
633.9
528.2
422.6
316.9
211.3
105.6
0

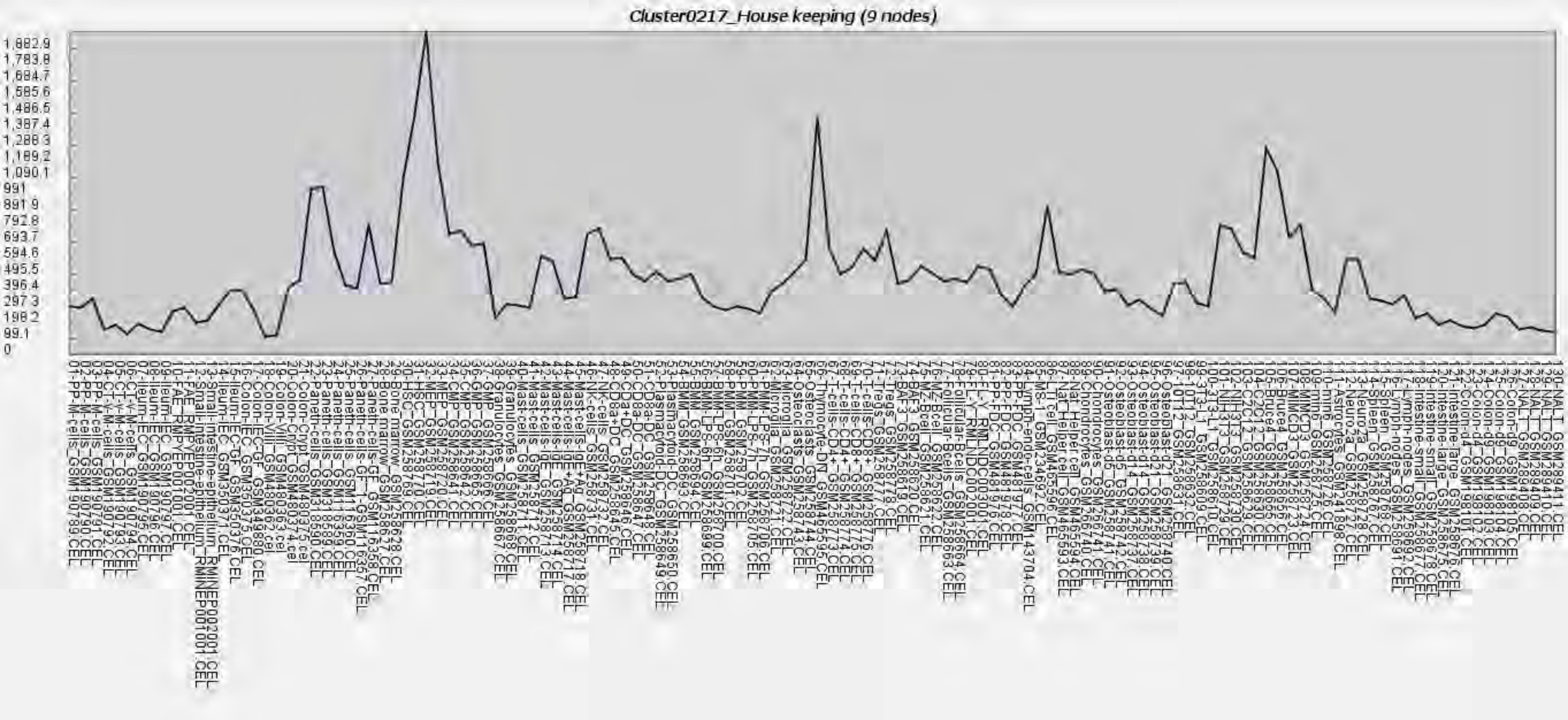
Cluster0213_Mesenchyme-related/extracellular matrix (9 nodes)

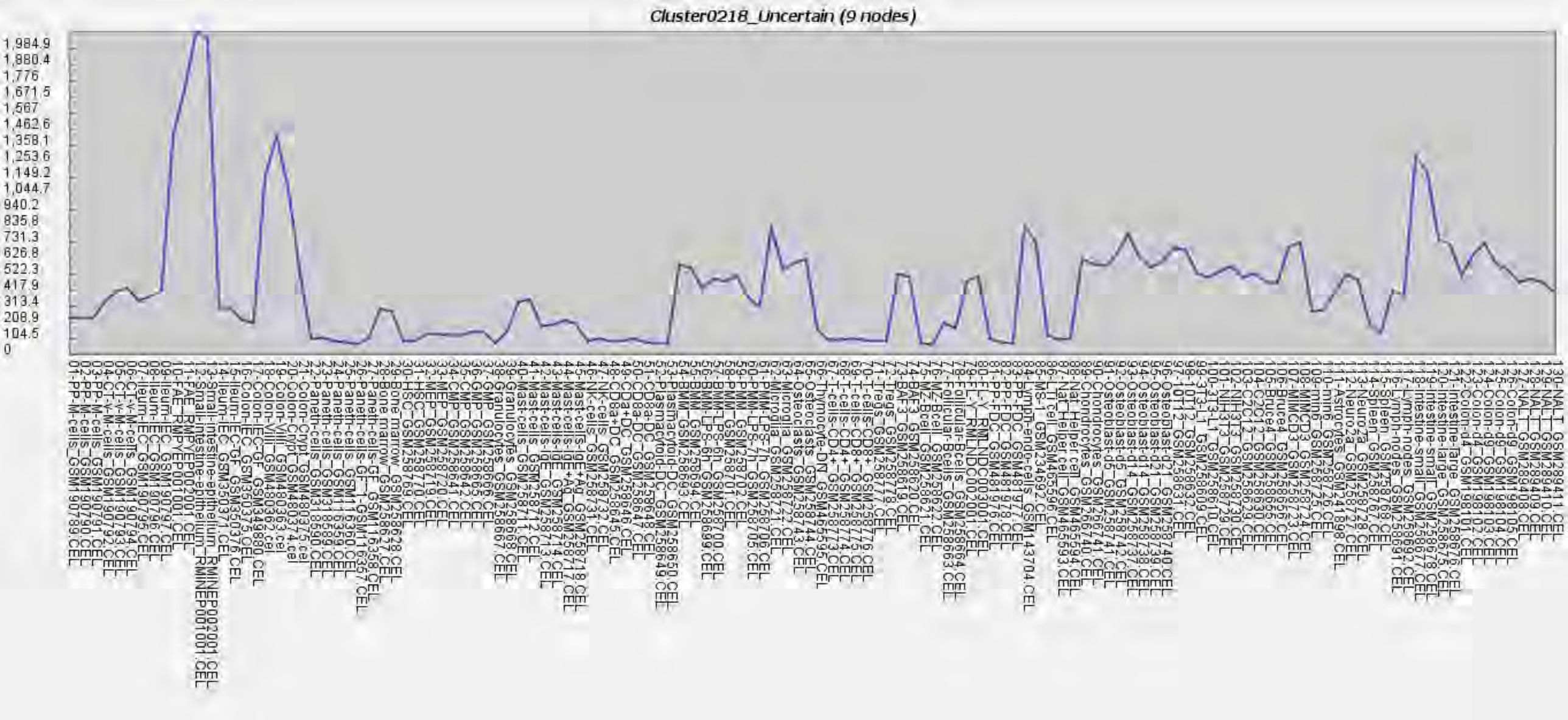



Cluster0214_Uncertain-low in many (9 nodes)
102.2
96.8
91.4
86.1
80.7
75.3
69.9
64.5
59.2
53.8
48.4
43
37.7
32.3
26.9
21.5
16.1
10.8
5.4
0

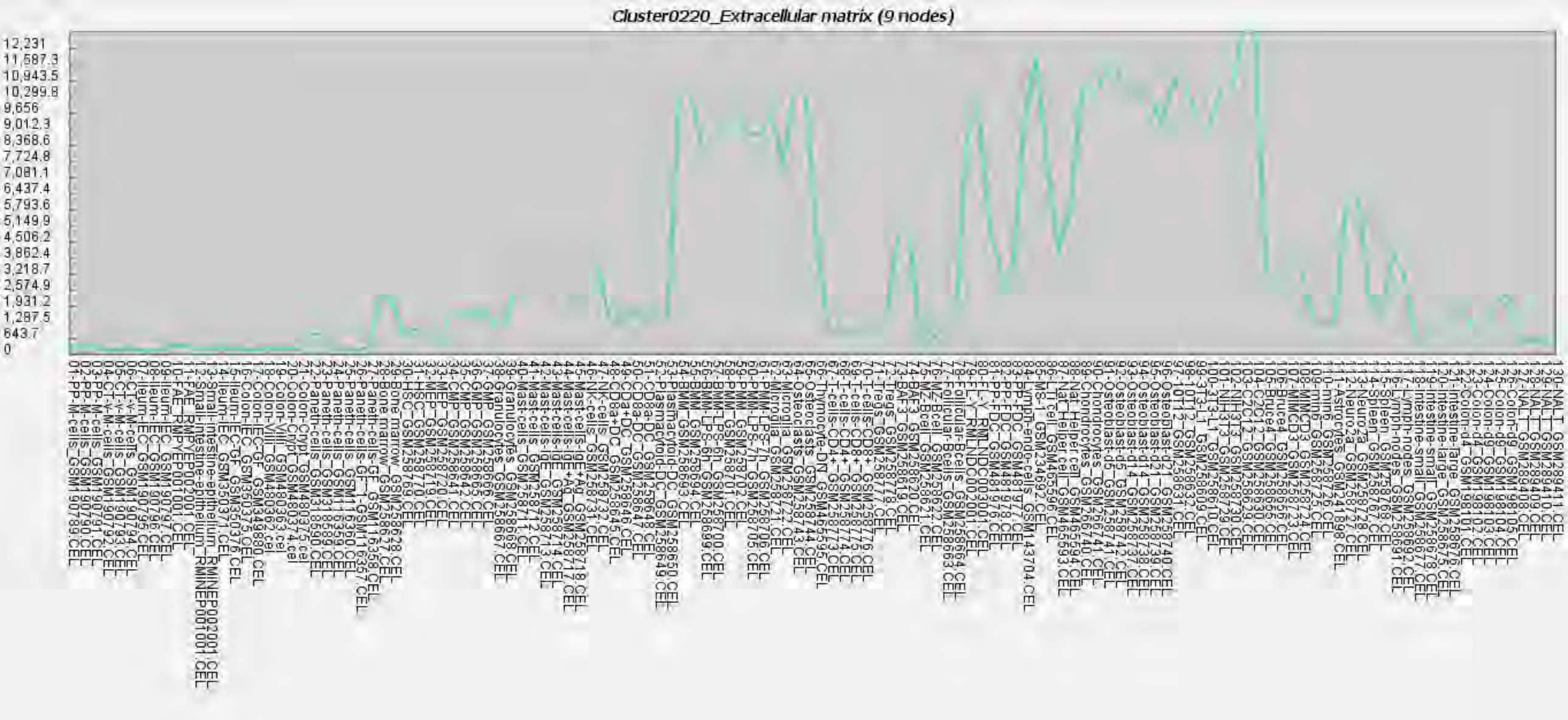

Cluster0215_Uncertain (9 nodes)
5,126.3
4,856.5
4,586.7
4,316.9
4,047.1
3,777.3
3,507.4
3,237.6
2,967.8
2,698
2,428.2
2,158.4
1,888.6
1,618.8
1,349
1,079.2
809.4
539.6
269.8
0

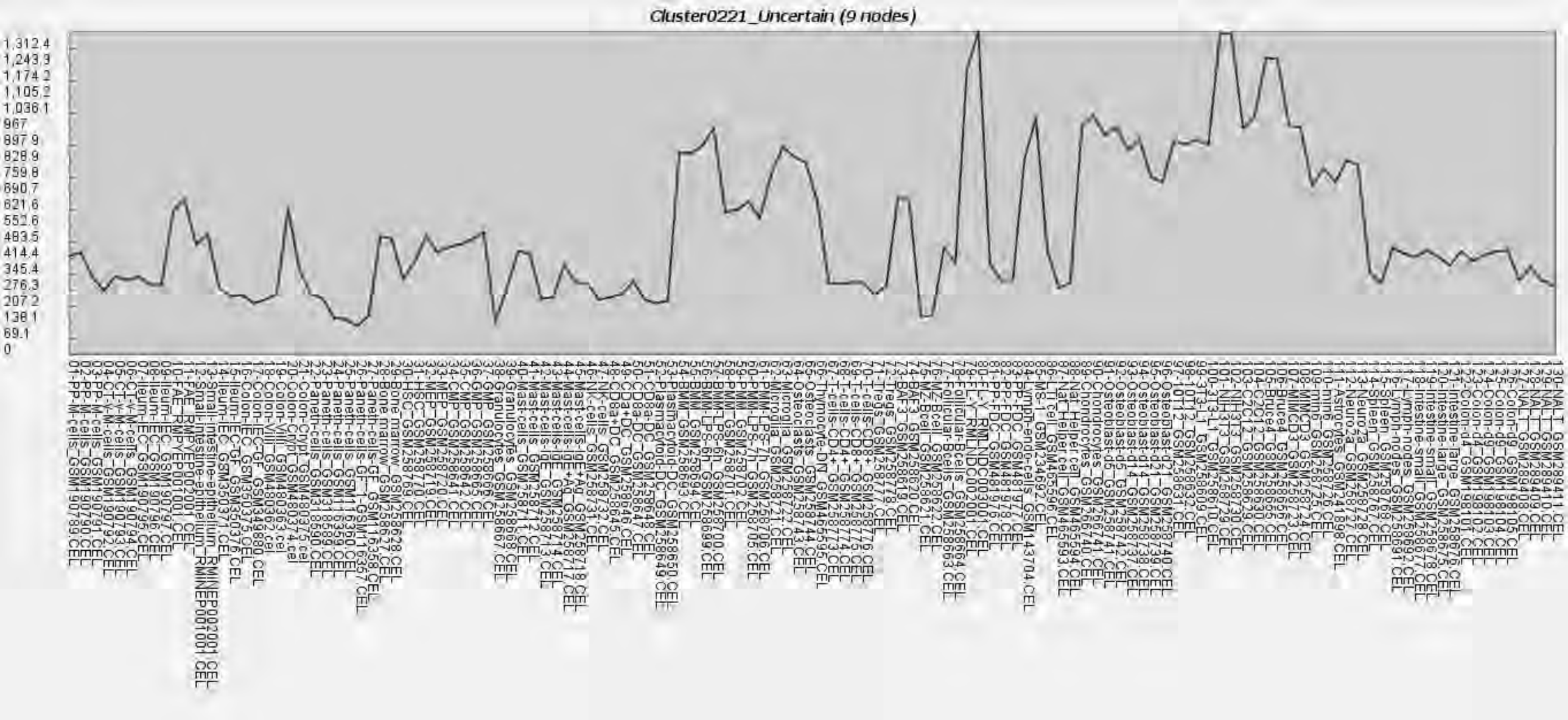

Cluster0216_House keeping-ribosomal (9 nodes)
12,884.9
12,206.8
11,528.6
10,850.5
10,172.3
9,494.2
8,816
8,137.9
7,459.7
6,781.5
6,103.4
5,425.2
4,747.1
4,068.9
3,390.8
2,712.6
2,034.5
1,356.3
678.2
0

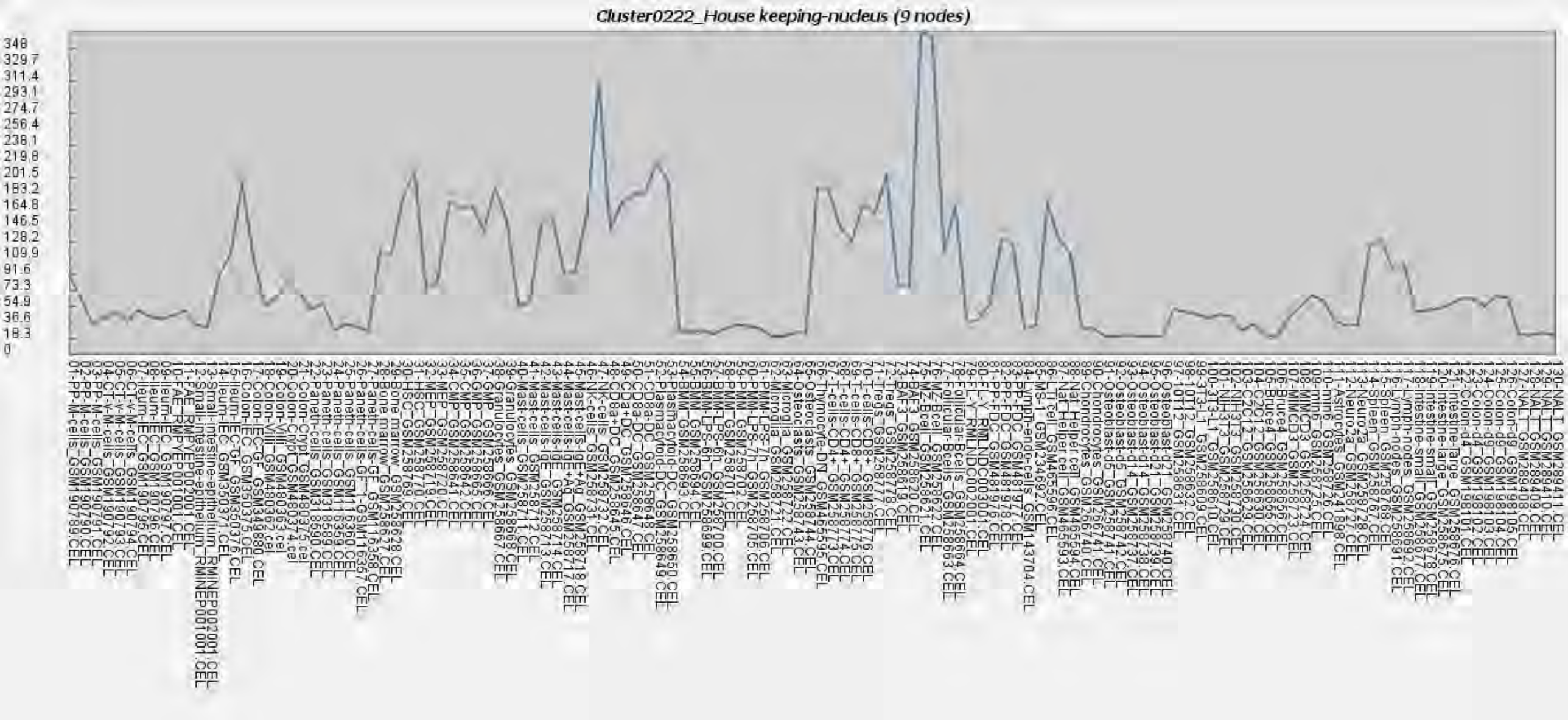

Cluster0217_House keeping (9 nodes)
1,882.9
1,783.8
1,684.7
1,585.6
1,486.5
1,387.4
1,288.3
1,189.2
1,090.1
991
891.9
792.8
693.7
594.6
495.5
396.4
297.3
198.2
99.1
0

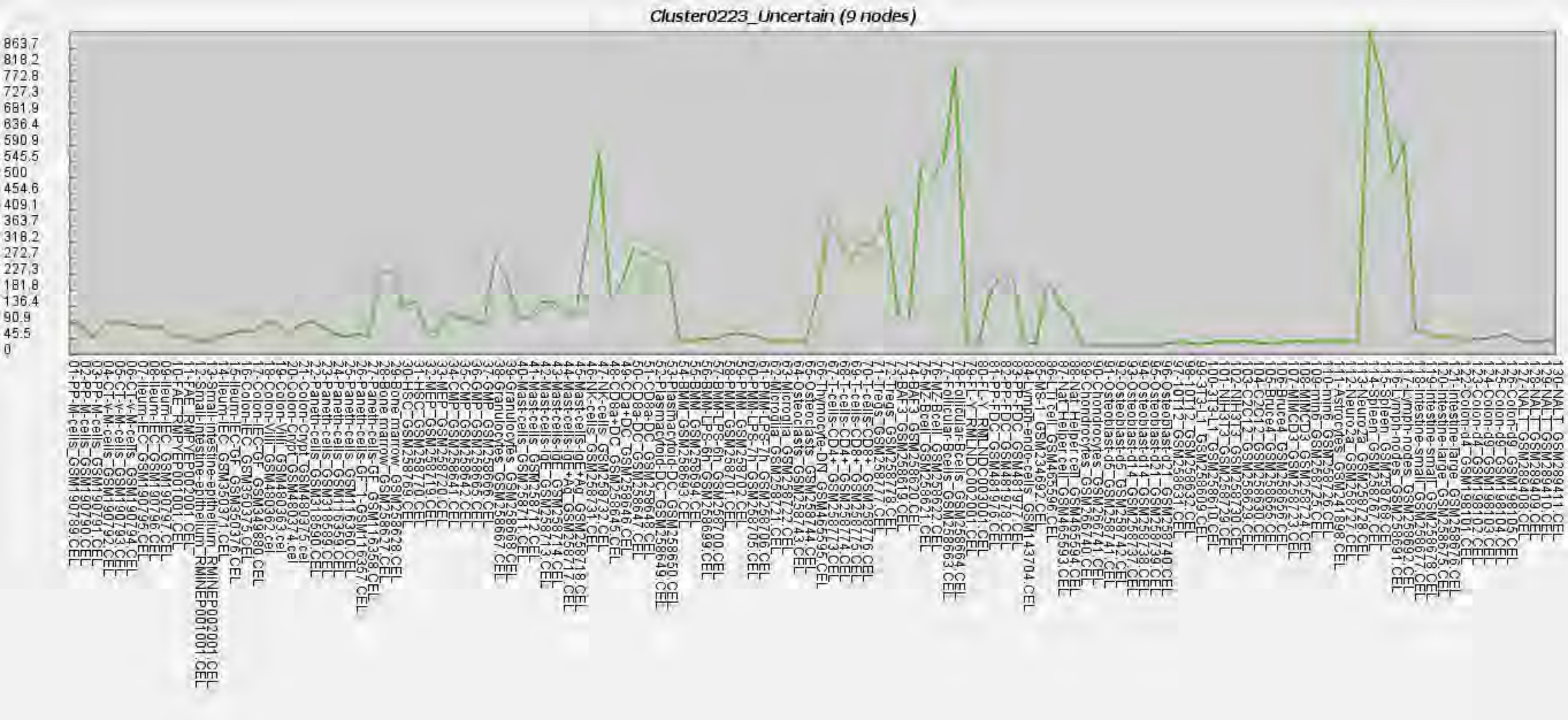

Cluster0218_Uncertain (9 nodes)
1,984.9
1,880.4
1,776
1,671.5
1,567
1,462.6
1,358.1
1,253.6
1,149.2
1,044.7
940.2
835.8
731.3
626.8
522.3
417.9
313.4
208.9
104.5
0

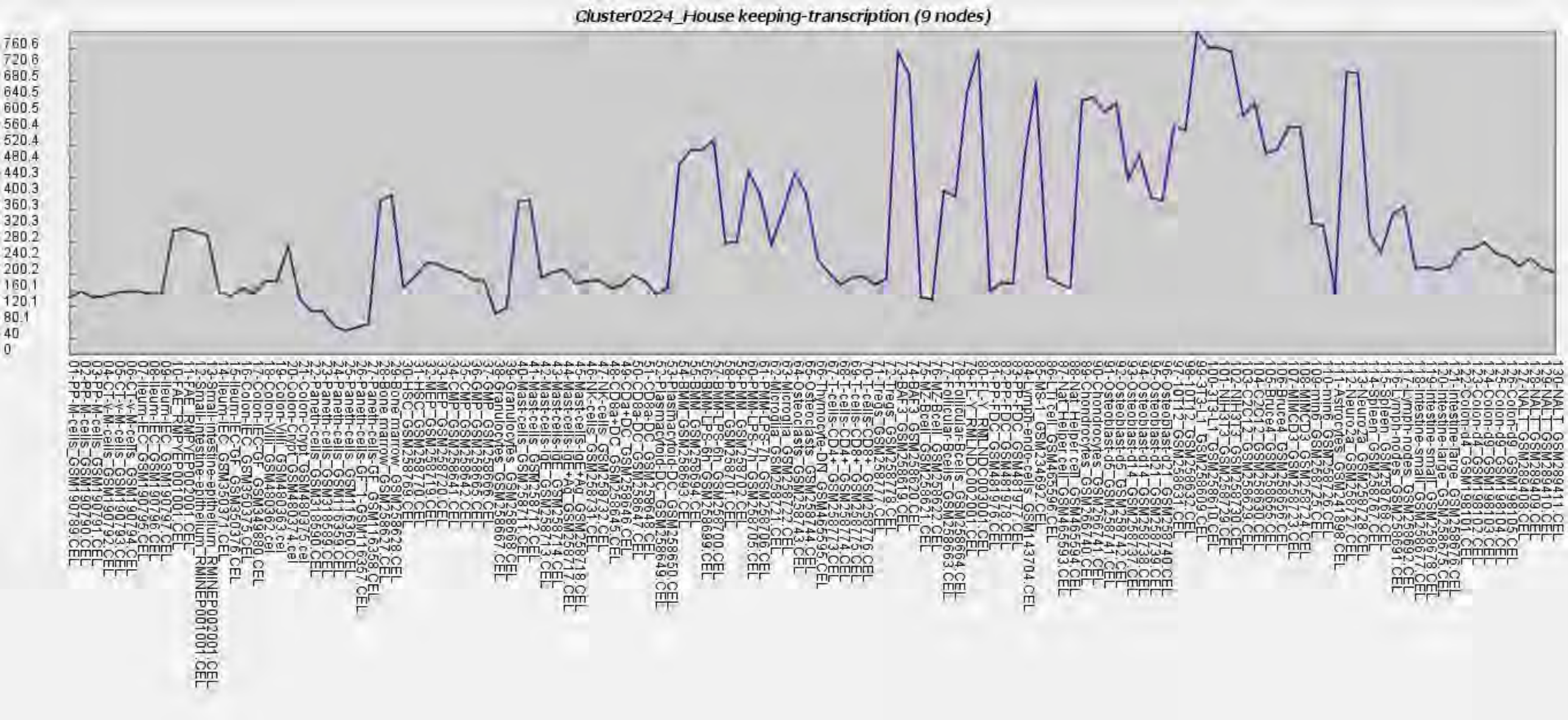
Cluster0219_Intestine-related (9 nodes)
6,922.1
5,610.4
5,298.7
4,987
4,675.3
4,363.6
4,052
3,740.3
3,428.6
3,116.9
2,805.2
2,493.5
2,181.8
1,870.1
1,558.4
1,246.8
935.1
623.4
311.7
0

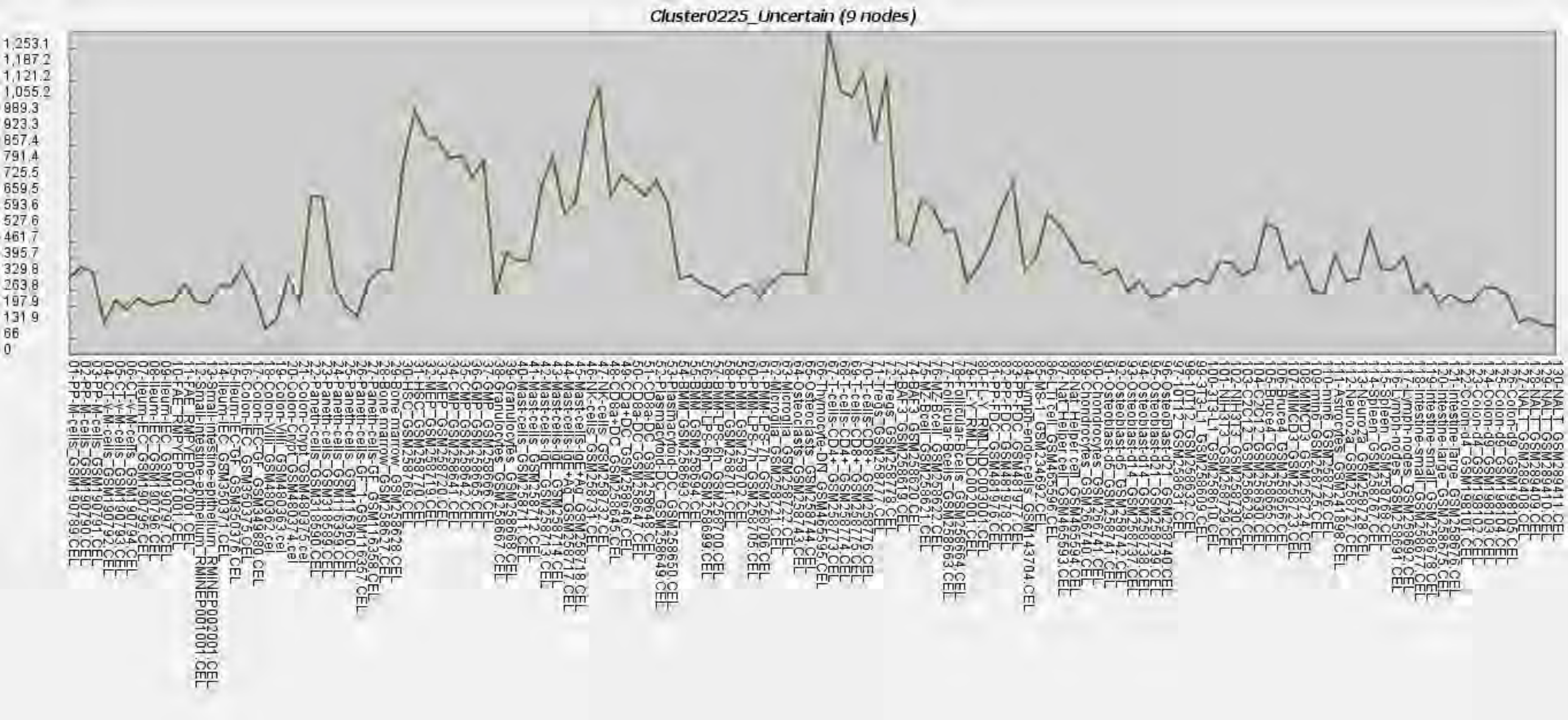

Cluster0220_Extracellular matrix (9 nodes)
12,231
11,587.3
10,943.5
10,299.8
9,656
9,012.3
8,368.6
7,724.8
7,081.1
6,437.4
5,793.6
5,149.9
4,506.2
3,862.4
3,218.7
2,574.9
1,931.2
1,287.5
643.7
0


Cluster0221_Uncertain (9 nodes)
1,312.4
1,243.3
1,174.2
1,105.2
1,036.1
967
897.9
828.9
759.8
690.7
621.6
552.6
483.5
414.4
345.4
276.3
207.2
138.1
69.1
0

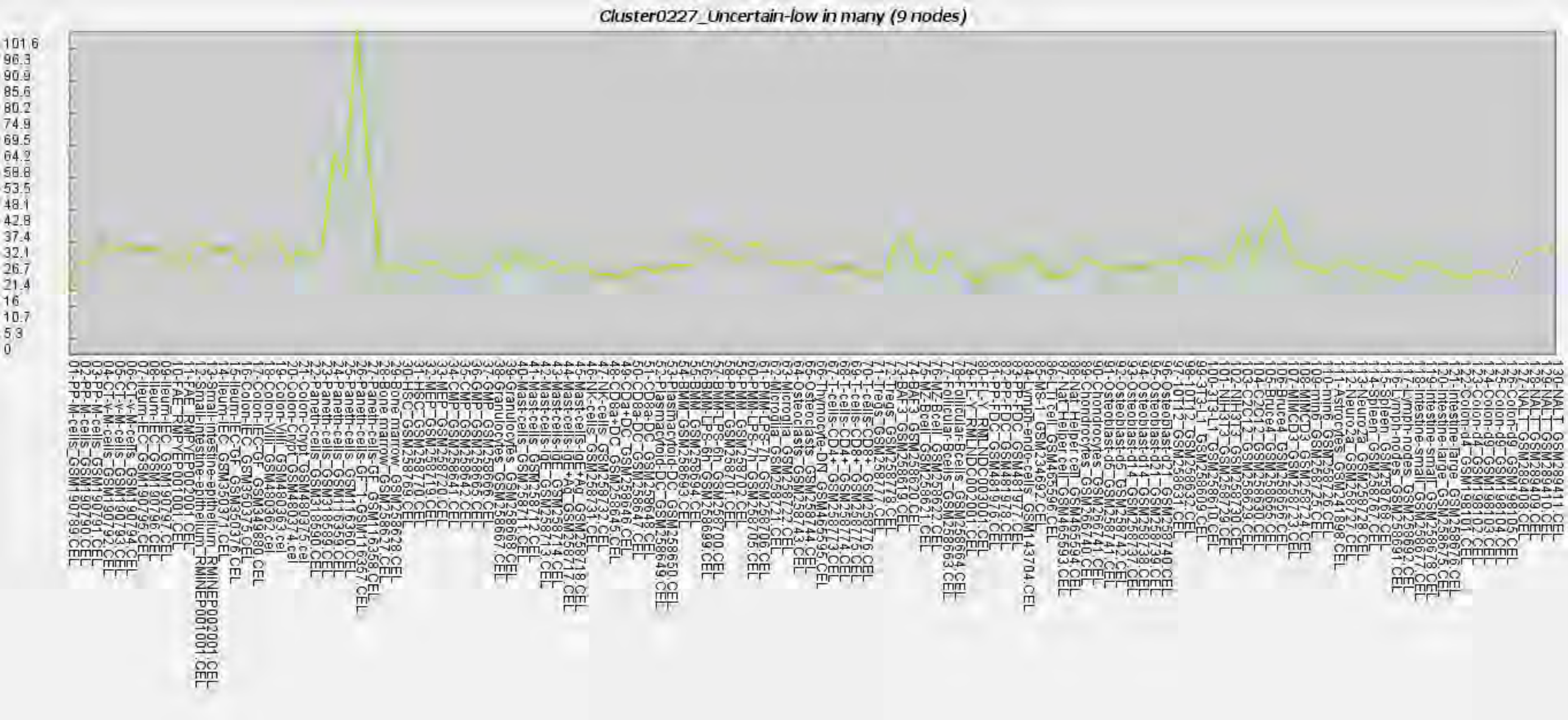

Cluster0222_House keeping-nucleus (9 nodes)
348
329.7
311.4
293.1
274.7
256.4
238.1
219.8
201.5
183.2
164.8
146.5
128.2
109.9
91.6
73.3
54.9
36.6
18.3
0


Cluster0223_Uncertain (9 nodes)
863.7
818.2
772.8
727.3
681.9
636.4
590.9
545.5
500
454.6
409.1
363.7
318.2
272.7
227.3
181.8
136.4
90.9
45.5
0

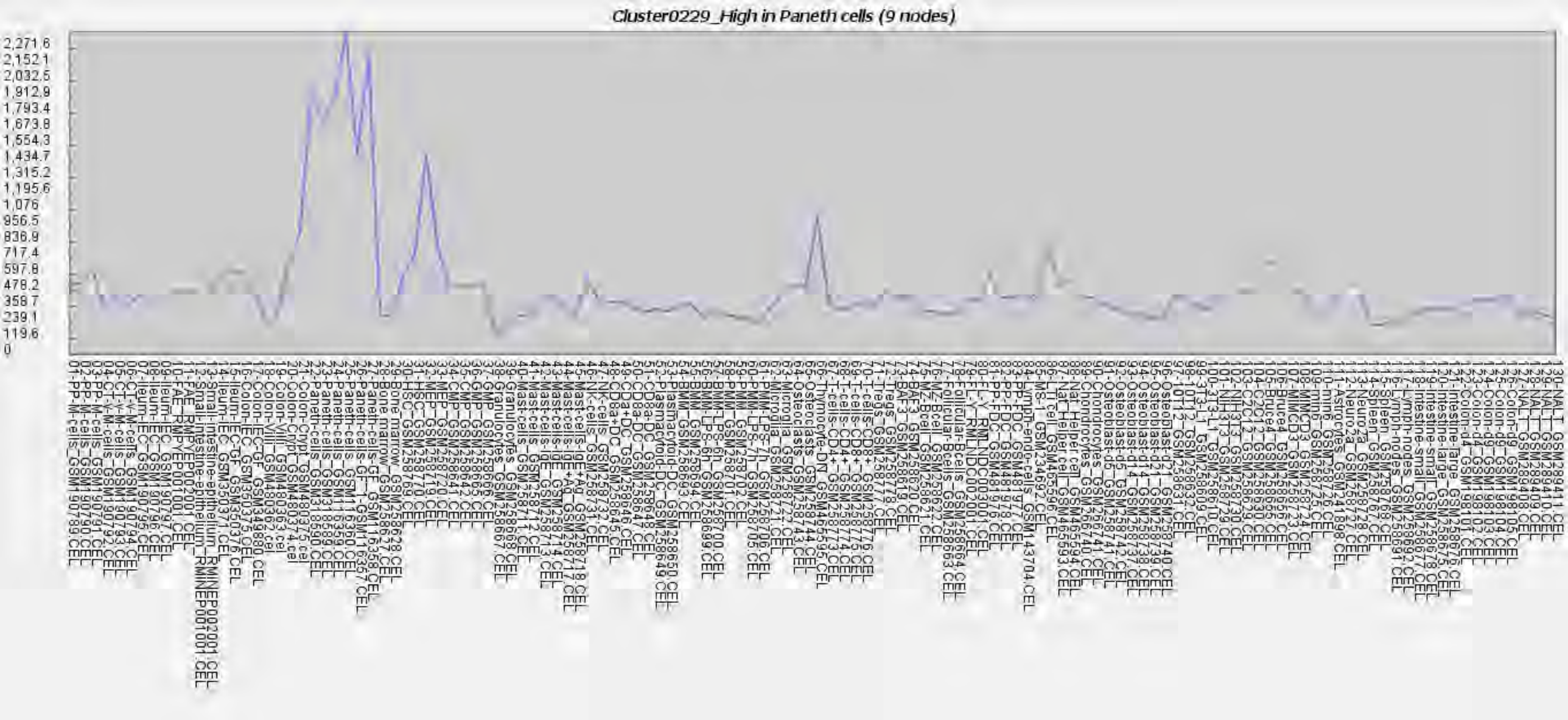

Cluster0224_House keeping-transcription (9 nodes)
760.6
720.6
680.5
640.5
600.5
560.4
520.4
480.4
440.3
400.3
360.3
320.3
280.2
240.2
200.2
160.1
120.1
80.1
40
0
130-NALT_GSM2289411.CEL
129-NALT_GSM2289410.CEL
128-NALT_GSM2289409.CEL
127-NALT_GSM2289408.CEL
126-Colon-d9_GSM1981105.CEL
125-Colon-d9_GSM1981104.CEL
124-Colon-d9_GSM1981103.CEL
123-Colon-d4_GSM1981102.CEL
122-Colon-d4_GSM1981101.CEL
121-Intestine-large_GSM2586676.CEL
120-Intestine-large_GSM2586675.CEL
119-Intestine-small_GSM2586678.CEL
118-Intestine-small_GSM2586677.CEL
117-Lymph-nodes_GSM2586692.CEL
116-Lymph-nodes_GSM2586691.CEL
115-Spleen_GSM2586688.CEL
114-Spleen_GSM2586687.CEL
113-Neuro2a_GSM2586728.CEL
112-Neuro2a_GSM2586727.CEL
111-Astrocytes_GSM2586726.CEL
110-mine_GSM2586725.CEL
109-mine_GSM2586724.CEL
108-MMCD3_GSM2586723.CEL
107-MMCD3_GSM2586722.CEL
106-Bruce4_GSM2586656.CEL
105-Bruce4_GSM2586630.CEL
104-C2C12_GSM2586629.CEL
103-C2C12_GSM2586628.CEL
102-NIH3T3_GSM2586627.CEL
101-NIH3T3_GSM2586626.CEL
100-3T3-L1_GSM2586610.CEL
99-3T3-L1_GSM2586609.CEL
98-10T1/2_GSM2586632.CEL
97-10T1/2_GSM2586631.CEL
96-Osteoblast-d21_GSM2586740.CEL
95-Osteoblast-d21_GSM2586739.CEL
94-Osteoblast-d14_GSM2586738.CEL
93-Osteoblast-d14_GSM2586737.CEL
92-Osteoblast-d5_GSM2586742.CEL
91-Osteoblast-d5_GSM2586741.CEL
90-Chondrocytes_GSM2586740.CEL
89-Chondrocytes_GSM2586739.CEL
88-Nat_Helper cell_GSM4655594.CEL
87-Nat_Helper cell_GSM4655593.CEL
86-LTi cell_GSM4655596.CEL
85-MS-1_GSM2346692.CEL
84-Lymph-endo-cells_GSM143704.CEL
83-PP-FDC_GSM4819778.CEL
82-PP-FDC_GSM4819777.CEL
81-PP-FDC_GSM4819776.CEL
80-FL-Y_RMLNDC002001.CEL
79-FL-Y_RMLNDC002001.CEL
78-Follicular-Bcells_GSM2586664.CEL
77-Follicular-Bcells_GSM2586663.CEL
76-MZ_Bcell_GSM2586621.CEL
75-MZ_Bcell_GSM2586620.CEL
74-BAF3_GSM2586619.CEL
73-BAF3_GSM2586618.CEL
72-Tregs_GSM2587778.CEL
71-Tregs_GSM2587777.CEL
70-T-cells-CD8+_GSM2587776.CEL
69-T-cells-CD8+_GSM2587775.CEL
68-T-cells-CD4+_GSM2587774.CEL
67-T-cells-CD4+_GSM2587773.CEL
66-Thymocyte-DN_GSM4655595.CEL
65-Osteoclasts_GSM2587744.CEL
64-Osteoclasts_GSM2587743.CEL
63-Microglia_GSM2587722.CEL
62-Microglia_GSM2587721.CEL
61-PMM-LPS-7h_GSM2587706.CEL
60-PMM-LPS-7h_GSM2587705.CEL
59-PMM_GSM2587702.CEL
58-PMM_GSM2587701.CEL
57-BMM-LPS-6h_GSM2588699.CEL
56-BMM-LPS-6h_GSM2588700.CEL
55-BMM_GSM2588693.CEL
54-BMM_GSM2588694.CEL
53-Plasmacytoid-DC_GSM2588649.CEL
52-Plasmacytoid-DC_GSM2588650.CEL
51-CD8a-DC_GSM2588647.CEL
50-CD8a-DC_GSM2588648.CEL
49-CD8a+DC_GSM2588645.CEL
48-CD8a+DC_GSM2588646.CEL
47-NK-cells_GSM2587732.CEL
46-NK-cells_GSM2587731.CEL
45-Mast-cells-IgE+Ag_GSM2587718.CEL
44-Mast-cells-IgE+Ag_GSM2587717.CEL
43-Mast-cells-IgE_GSM2587714.CEL
42-Mast-cells-IgE_GSM2587713.CEL
41-Mast-cells_GSM2587712.CEL
40-Mast-cells_GSM2587711.CEL
39-Granulocytes_GSM2586668.CEL
38-Granulocytes_GSM2586667.CEL
37-GMP_GSM2586666.CEL
36-GMP_GSM2586665.CEL
35-CMP_GSM2588642.CEL
34-CMP_GSM2588641.CEL
33-MEP_GSM2588720.CEL
32-MEP_GSM2588719.CEL
31-HSC_GSM2588670.CEL
30-HSC_GSM2588669.CEL
29-Bone marrow_GSM2586628.CEL
28-Bone marrow_GSM2586627.CEL
27-Paneth-cells-GF_GSM1163558.CEL
26-Paneth-cells-GF_GSM1163557.CEL
25-Paneth-cells_GSM1163560.CEL
24-Paneth-cells_GSM1163559.CEL
23-Paneth-cells_GSM3185889.CEL
22-Paneth-cells_GSM3185890.CEL
21-Colon-Crypt_GSM4803774.cel
20-Colon-Crypt_GSM4803775.cel
19-Colon-Villi_GSM4803763.cel
18-Colon-Villi_GSM4803762.cel
17-Colon-EC-GF_GSM3493880.CEL
16-Colon-EC-GF_GSM3503375.CEL
15-Ileum-EC-GF_GSM3503376.CEL
14-Ileum-EC-GF_GSM3503371.CEL
13-Small-Intestine-epithelium_RMINEP002001.CEL
12-Small-Intestine-epithelium_RMINEP001001.CEL
11-FAE_RMPYEP002001.CEL
10-FAE_RMPYEP001001.CEL
09-Ileum-EC_GSM1907797.CEL
08-Ileum-EC_GSM1907796.CEL
07-Ileum-EC_GSM1907795.CEL
06-CT-v-M-cells_GSM1907794.CEL
05-CT-v-M-cells_GSM1907793.CEL
04-CT-v-M-cells_GSM1907792.CEL
03-PP-M-cells_GSM1907791.CEL
02-PP-M-cells_GSM1907790.CEL
01-PP-M-cells_GSM1907789.CEL

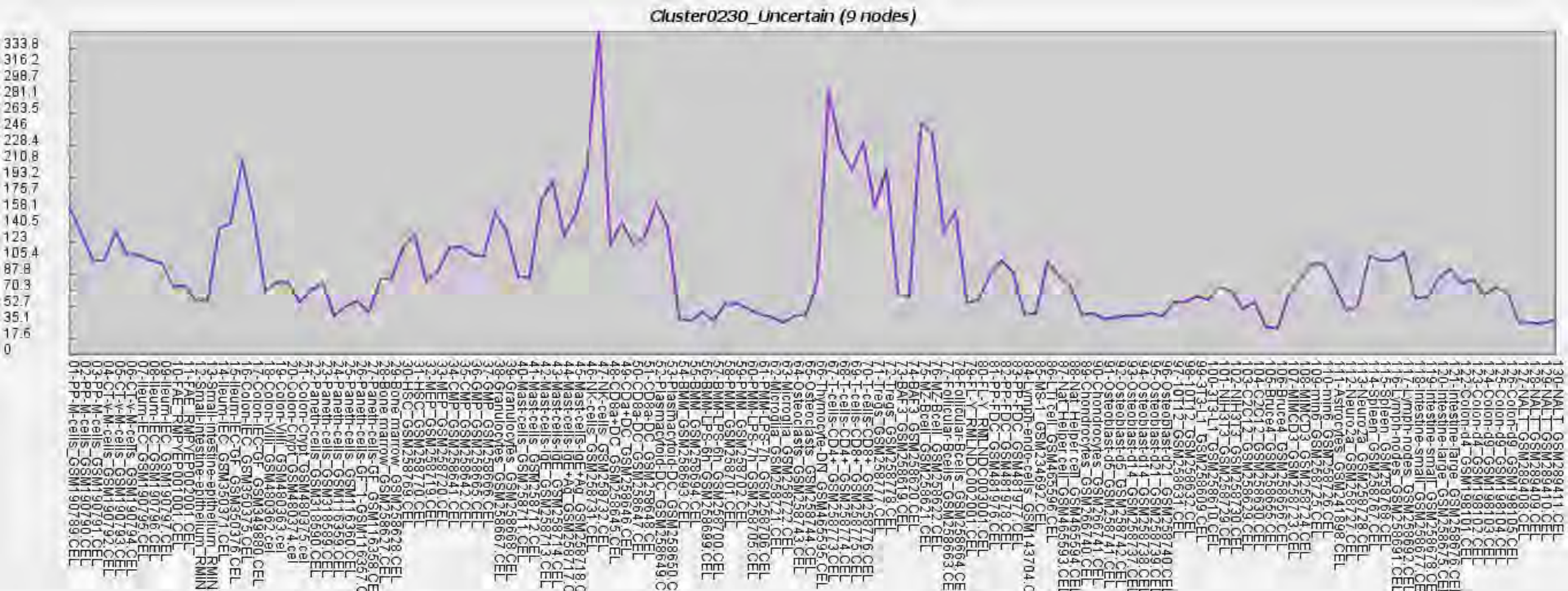

Cluster0225_Uncertain (9 nodes)
1,253.1
1,187.2
1,121.2
1,055.2
989.3
923.3
857.4
791.4
725.5
659.5
593.6
527.6
461.7
395.7
329.8
263.8
197.9
131.9
66
0

Cluster0226_House keeping (9 nodes)
4,137.1
3,919.4
3,701.6
3,483.9
3,266.2
3,048.4
2,830.7
2,612.9
2,395.2
2,177.4
1,959.7
1,742
1,524.2
1,306.5
1,088.7
871
653.2
435.5
217.7
0


Cluster0227_Uncertain-low in many (9 nodes)
101.6
96.3
90.9
85.6
80.2
74.9
69.5
64.2
58.8
53.5
48.1
42.8
37.4
32.1
26.7
21.4
16
10.7
5.3
0

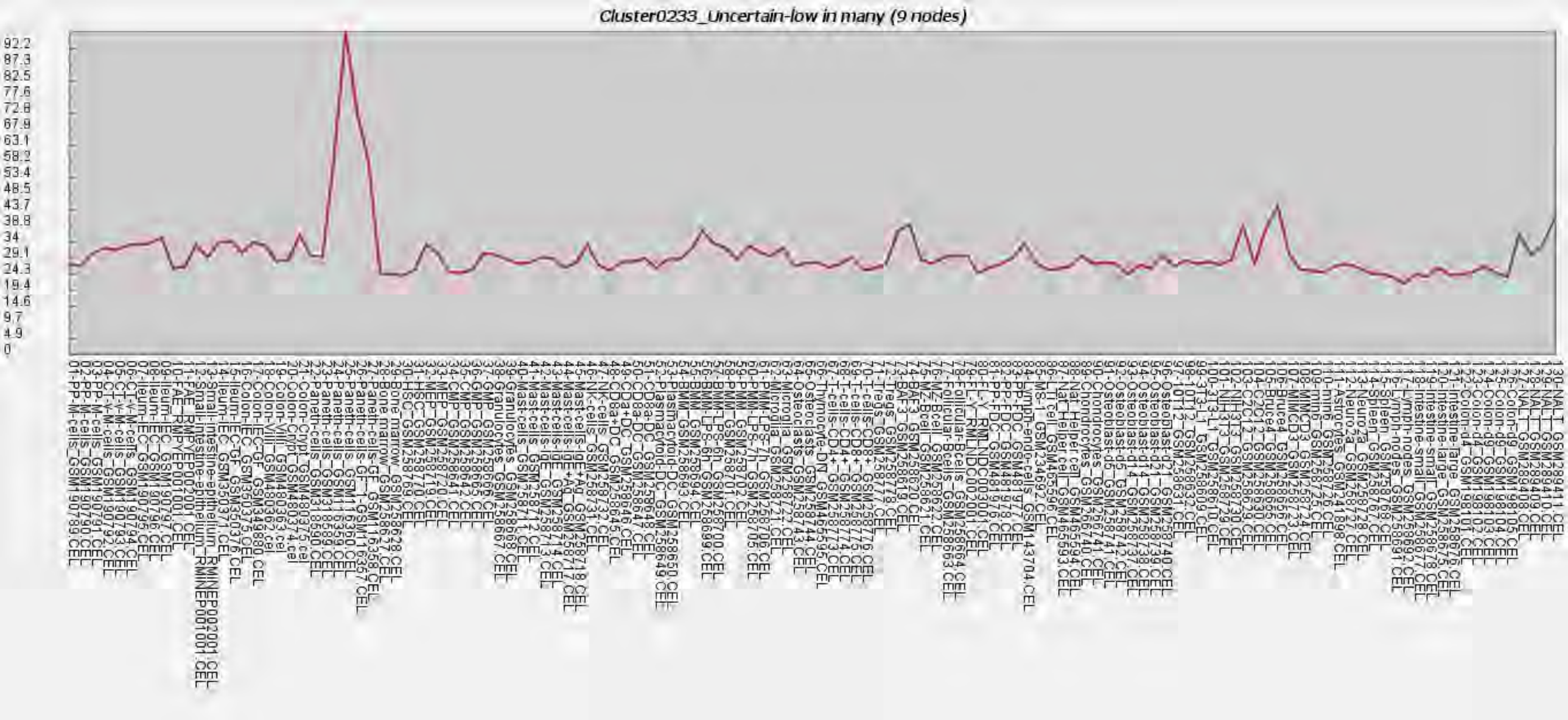
Cluster0228_Uncertain (9 nodes)
1,083.1
1,026.1
969.1
912.1
855
798
741
684
627
570
513
456
399
342
285
228
171
114
57
0

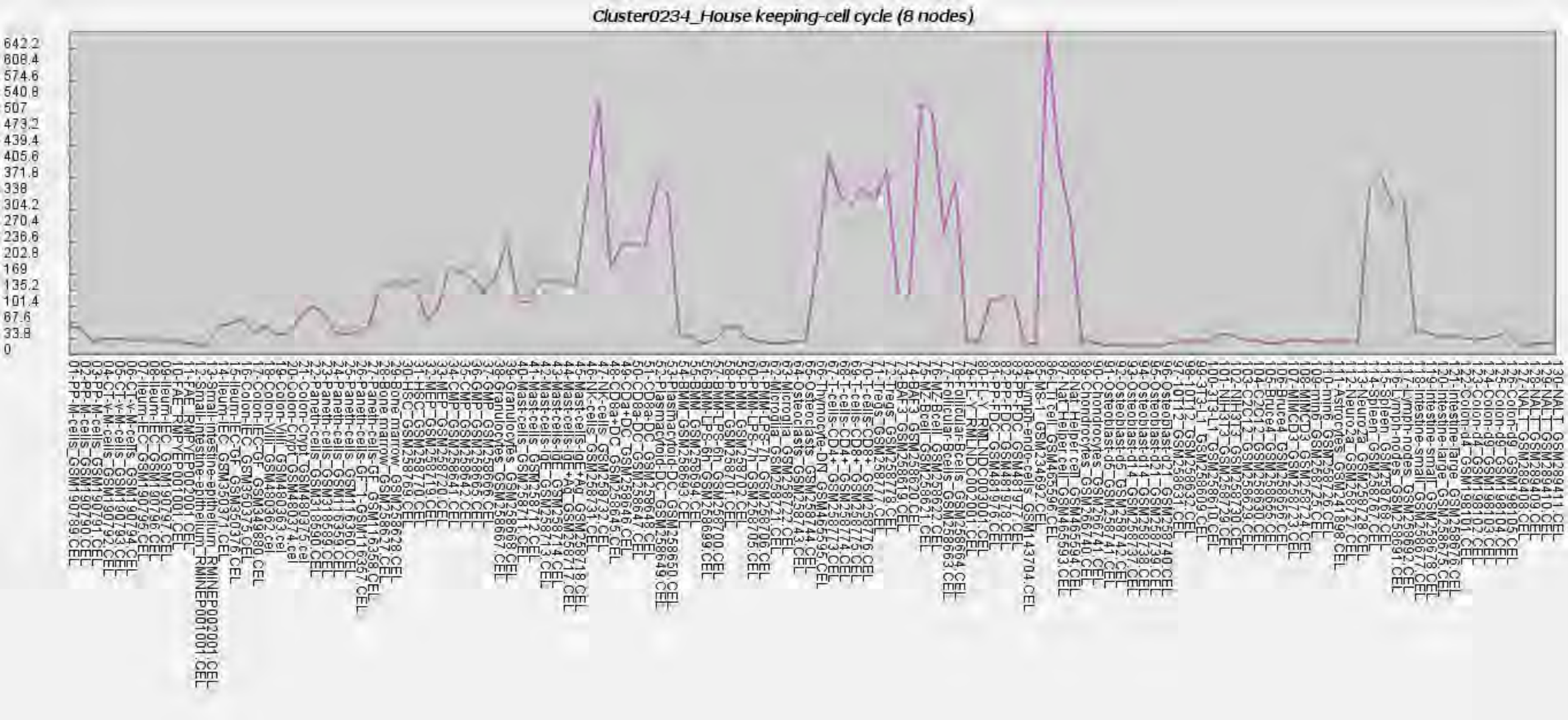

Cluster0229_High in Paneth cells (9 nodes)
2,271.6
2,152.1
2,032.5
1,912.9
1,793.4
1,673.8
1,554.3
1,434.7
1,315.2
1,195.6
1,076
956.5
836.9
717.4
597.8
478.2
358.7
239.1
119.6
0


Cluster0230_Uncertain (9 nodes)
333.8
316.2
298.7
281.1
263.5
246
228.4
210.8
193.2
175.7
158.1
140.5
123
105.4
87.8
70.3
52.7
35.1
17.6
0

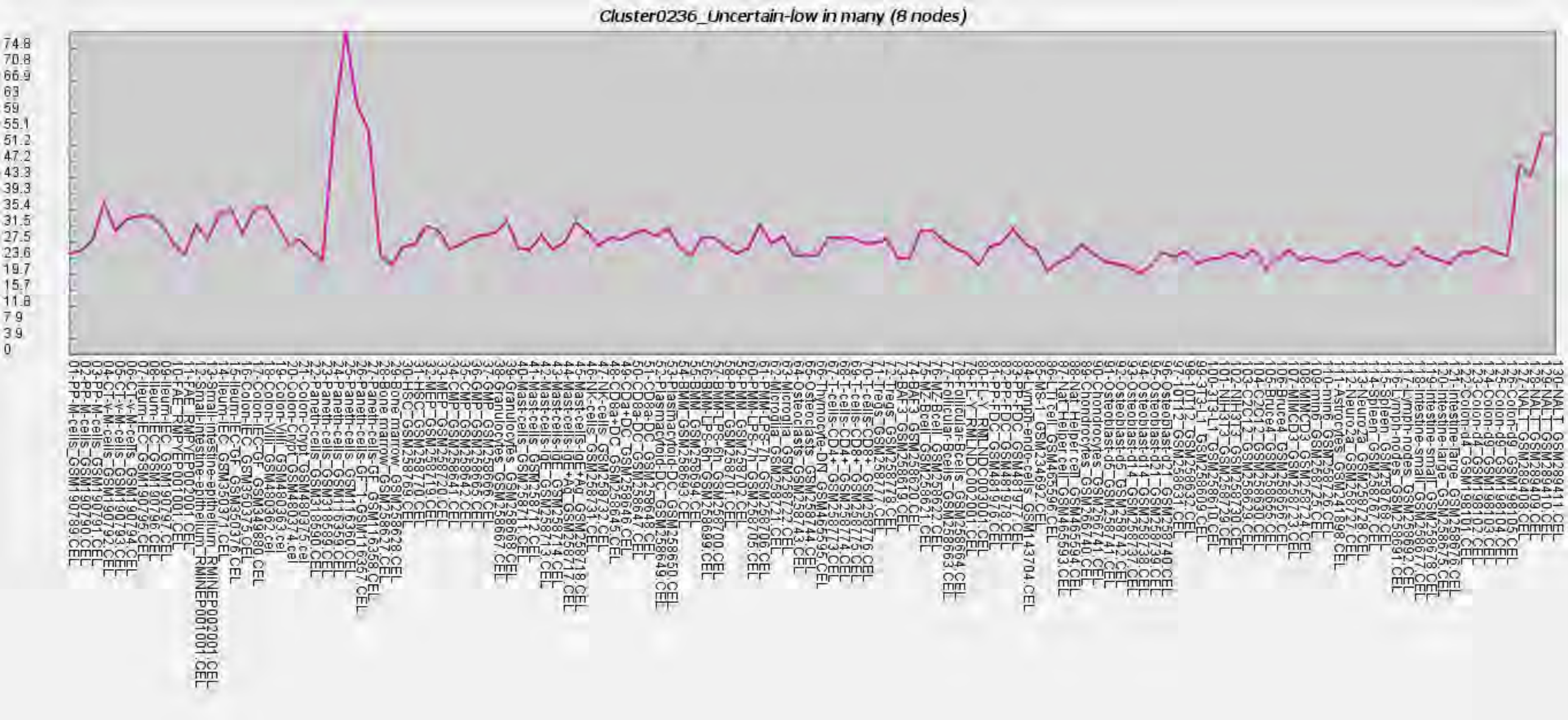
Cluster0231_intestine-related (9 nodes)
6,863.8
6,502.6
6,141.3
5,780.1
5,418.8
5,057.6
4,696.3
4,335.1
3,973.8
3,612.6
3,251.3
2,890
2,528.8
2,167.5
1,806.3
1,445
1,083.8
722.5
361.3
0

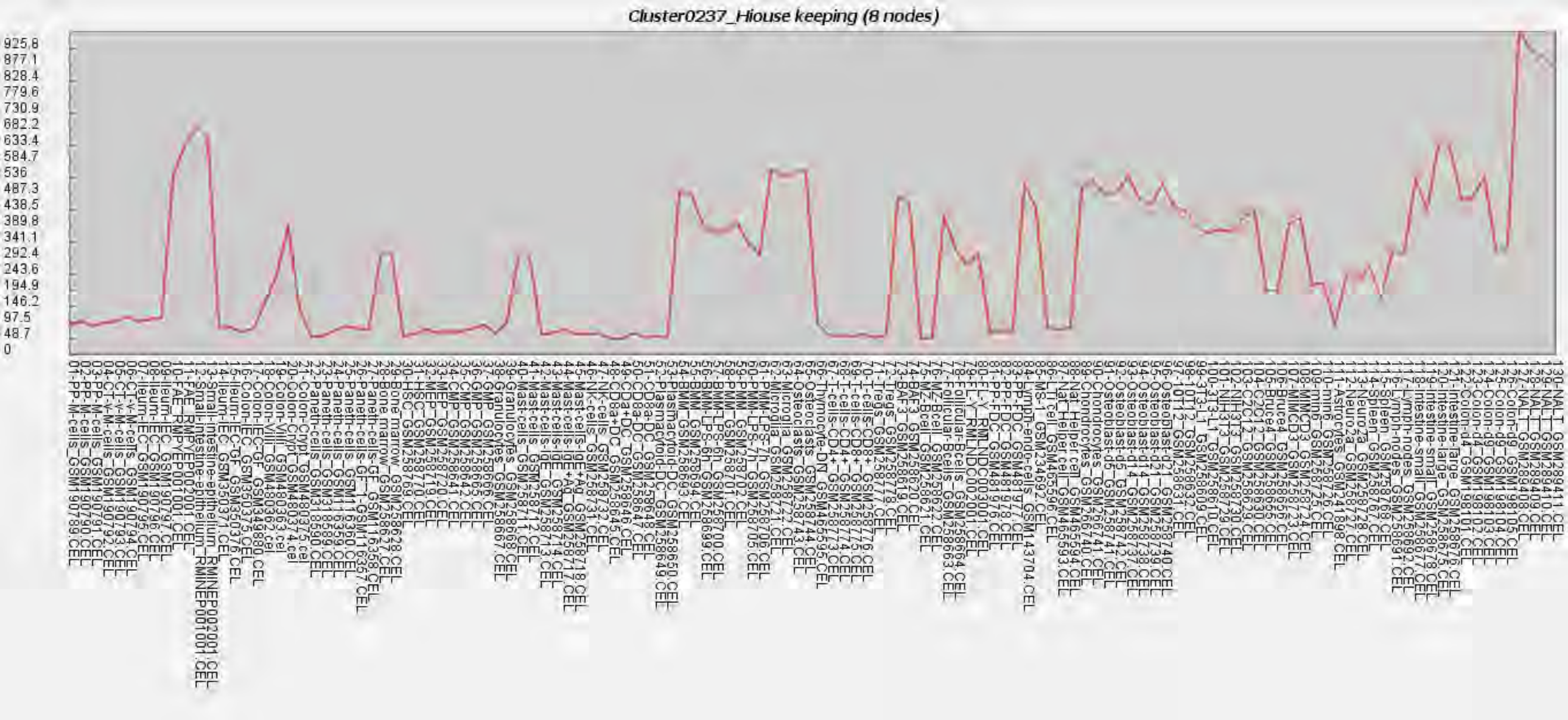
Cluster0232_Intestine-related (9 nodes)
801.7
759.5
717.3
675.1
632.9
590.7
548.5
506.3
464.1
421.9
379.7
337.5
295.4
253.2
211
168.8
126.6
84.4
42.2
0


Cluster0233_Uncertain-low in many (9 nodes)
92.2
87.3
82.5
77.6
72.8
67.9
63.1
58.2
53.4
48.5
43.7
38.8
34
29.1
24.3
19.4
14.6
9.7
4.9
0

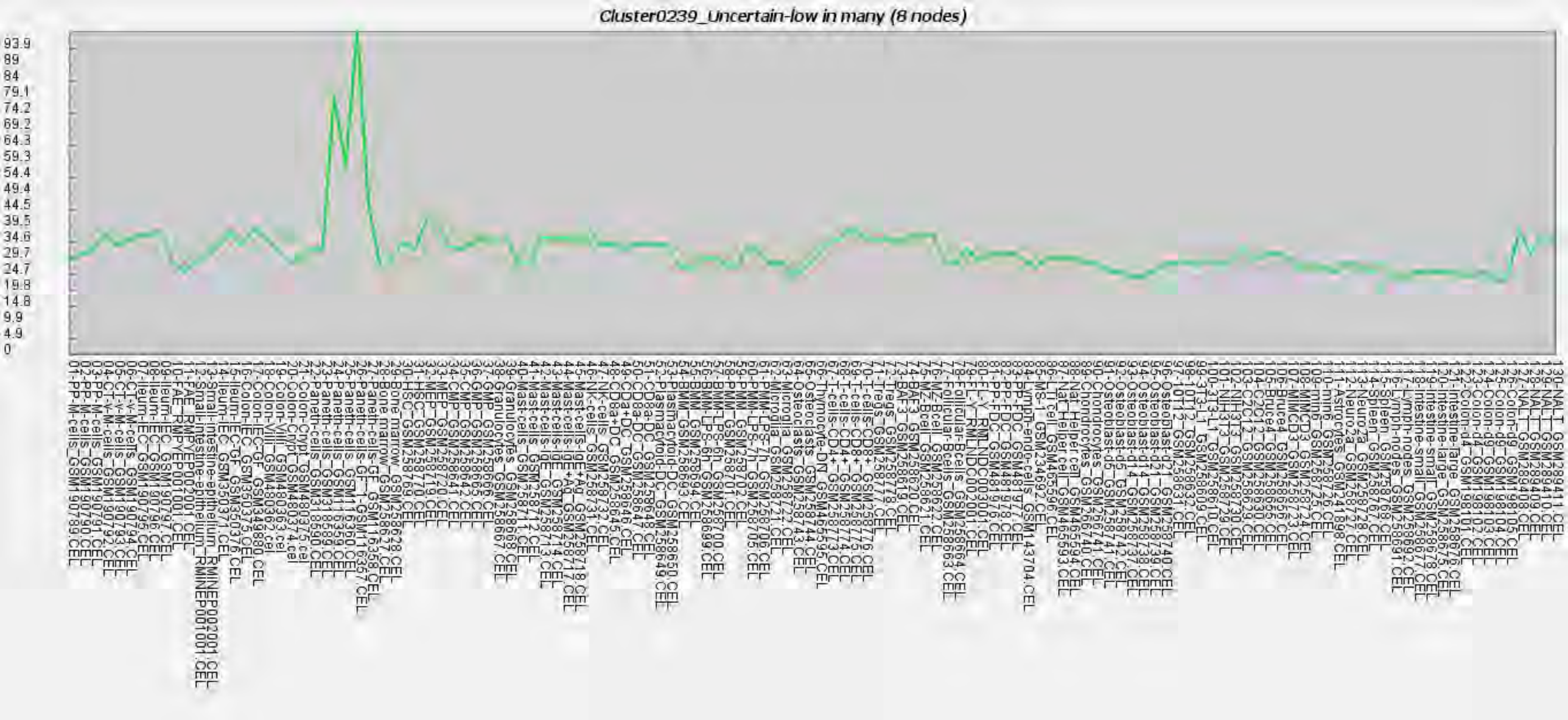

Cluster0234_House keeping-cell cycle (8 nodes)
642.2
608.4
574.6
540.8
507
473.2
439.4
405.6
371.8
338
304.2
270.4
236.6
202.8
169
135.2
101.4
67.6
33.8
0

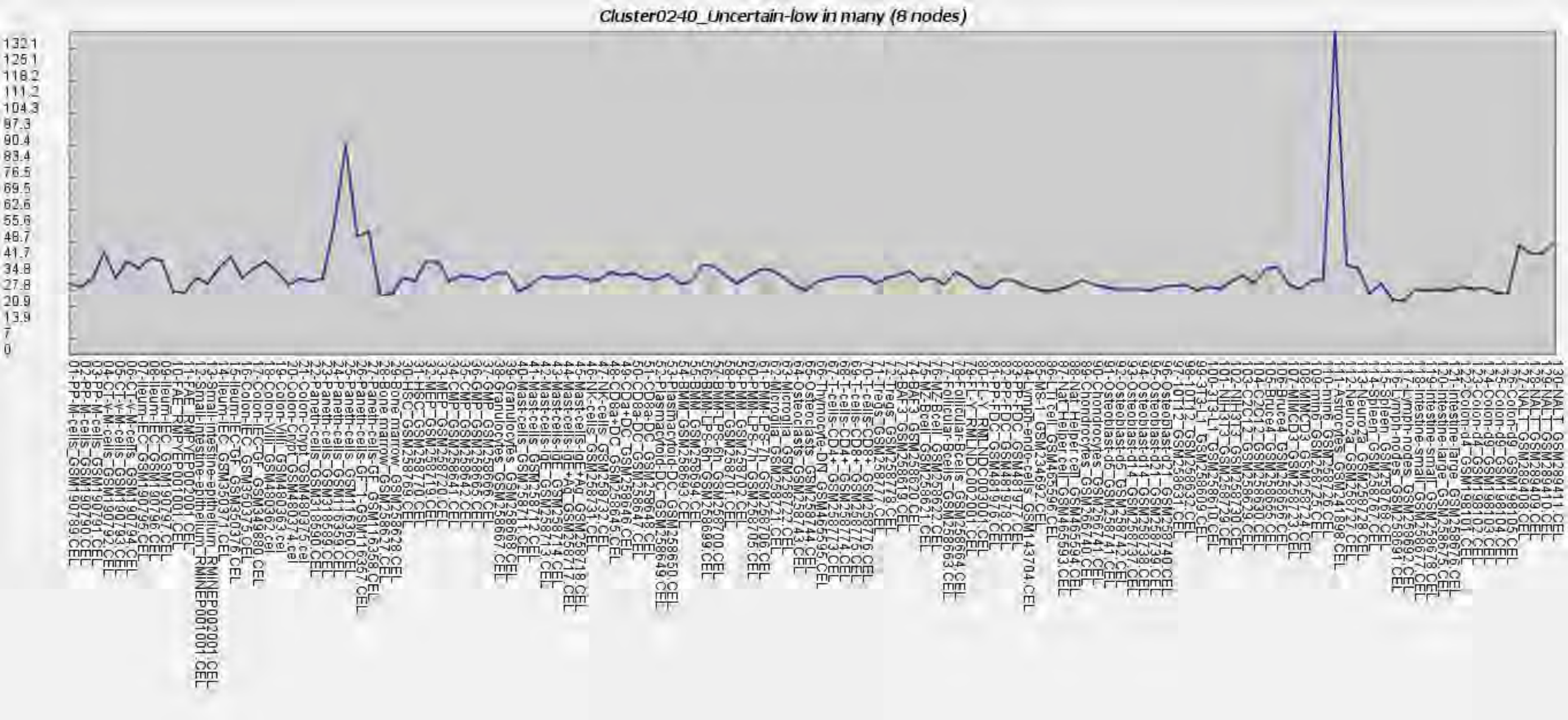
Cluster0235_Uncertain (8 nodes)
1,049.1
993.8
938.6
883.4
828.2
773
717.8
662.6
607.3
552.1
496.9
441.7
386.5
331.3
276.1
220.9
165.6
110.4
55.2
0

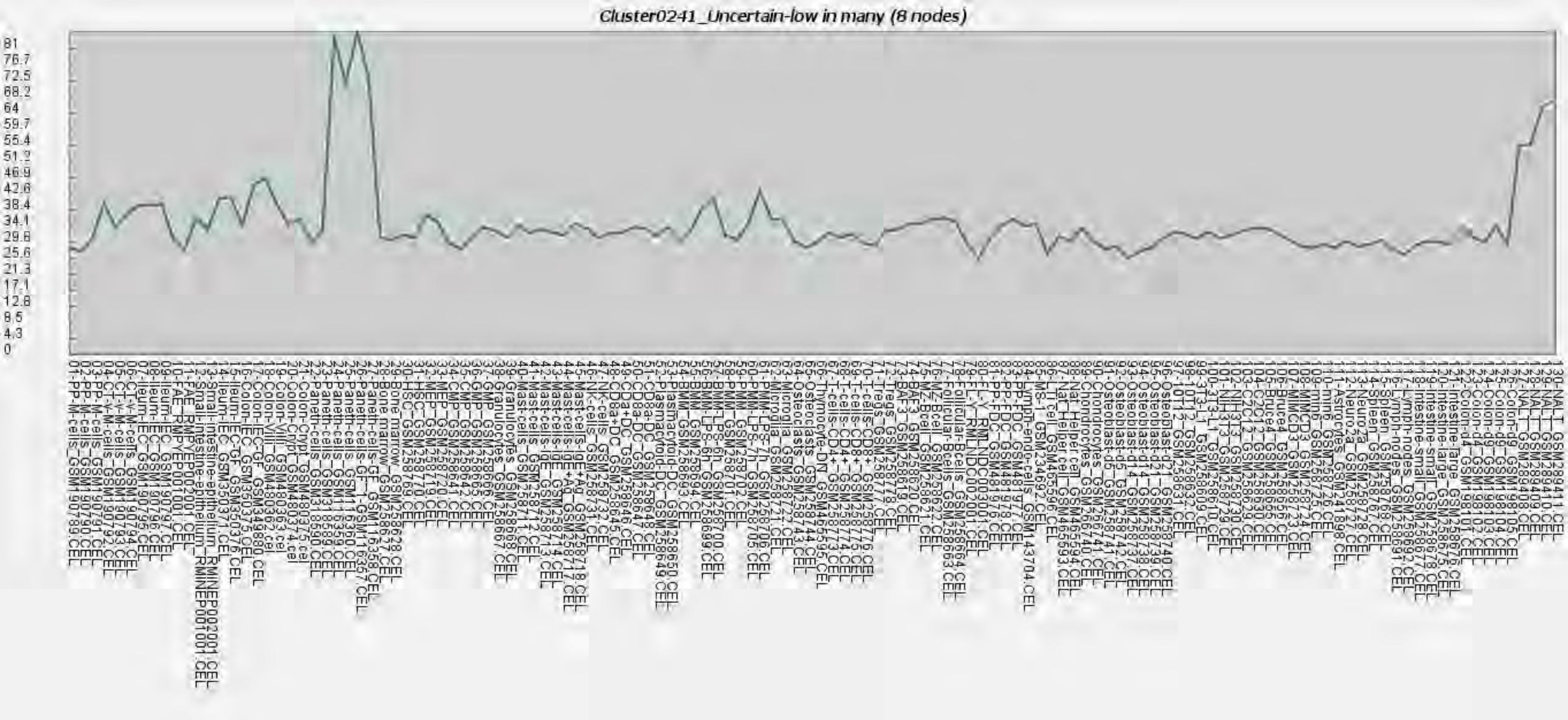

Cluster0236_Uncertain-low in many (8 nodes)
74.8
70.8
66.9
63
59
55.1
51.2
47.2
43.3
39.3
35.4
31.5
27.5
23.6
19.7
15.7
11.8
7.9
3.9
0


Cluster0237_Hiouse keeping (8 nodes)
925.8
877.1
828.4
779.6
730.9
682.2
633.4
584.7
536
487.3
438.5
389.8
341.1
292.4
243.6
194.9
146.2
97.5
48.7
0

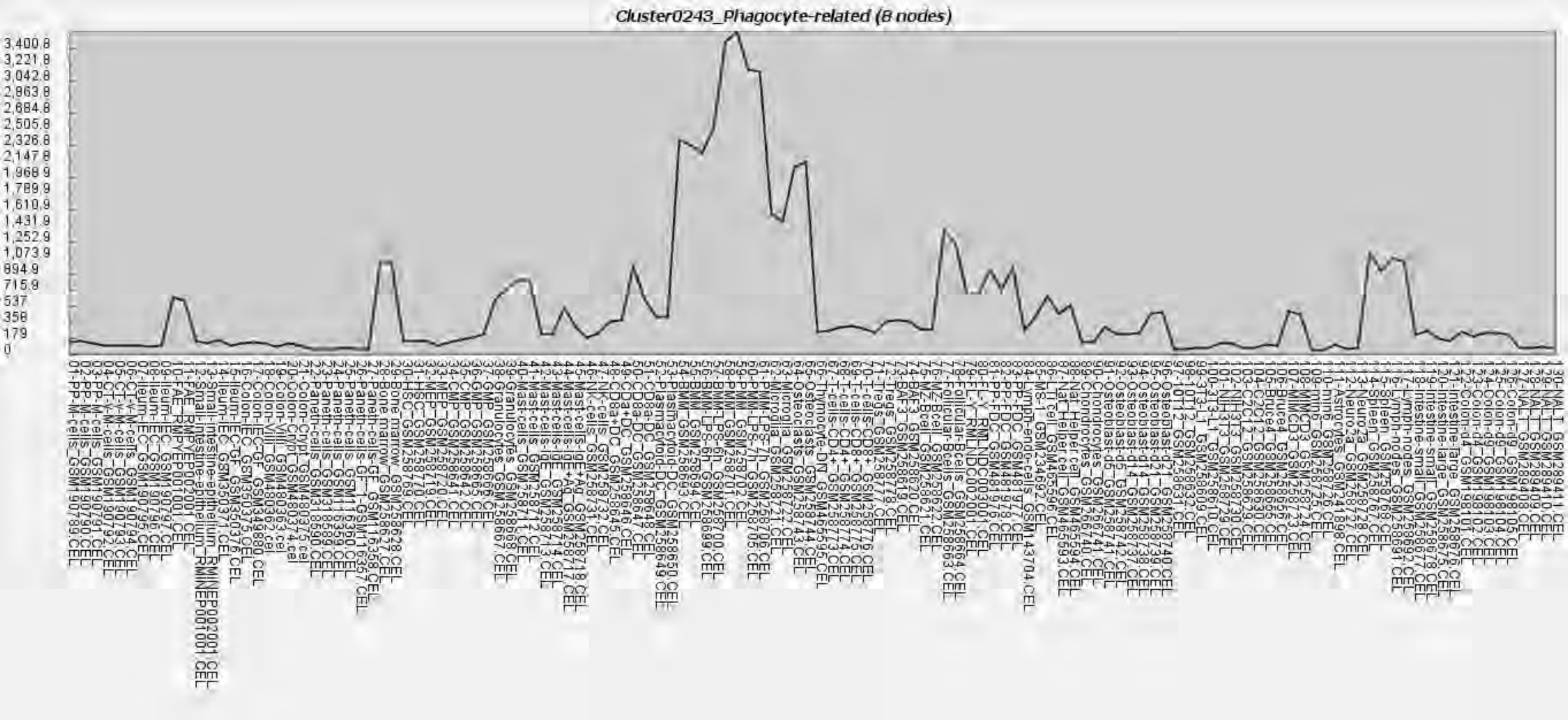
Cluster0238_High in B cells (8 nodes)
589
558
527
496
465
434
403
372
341
310
279
248
217
186
155
124
93
62
31
0

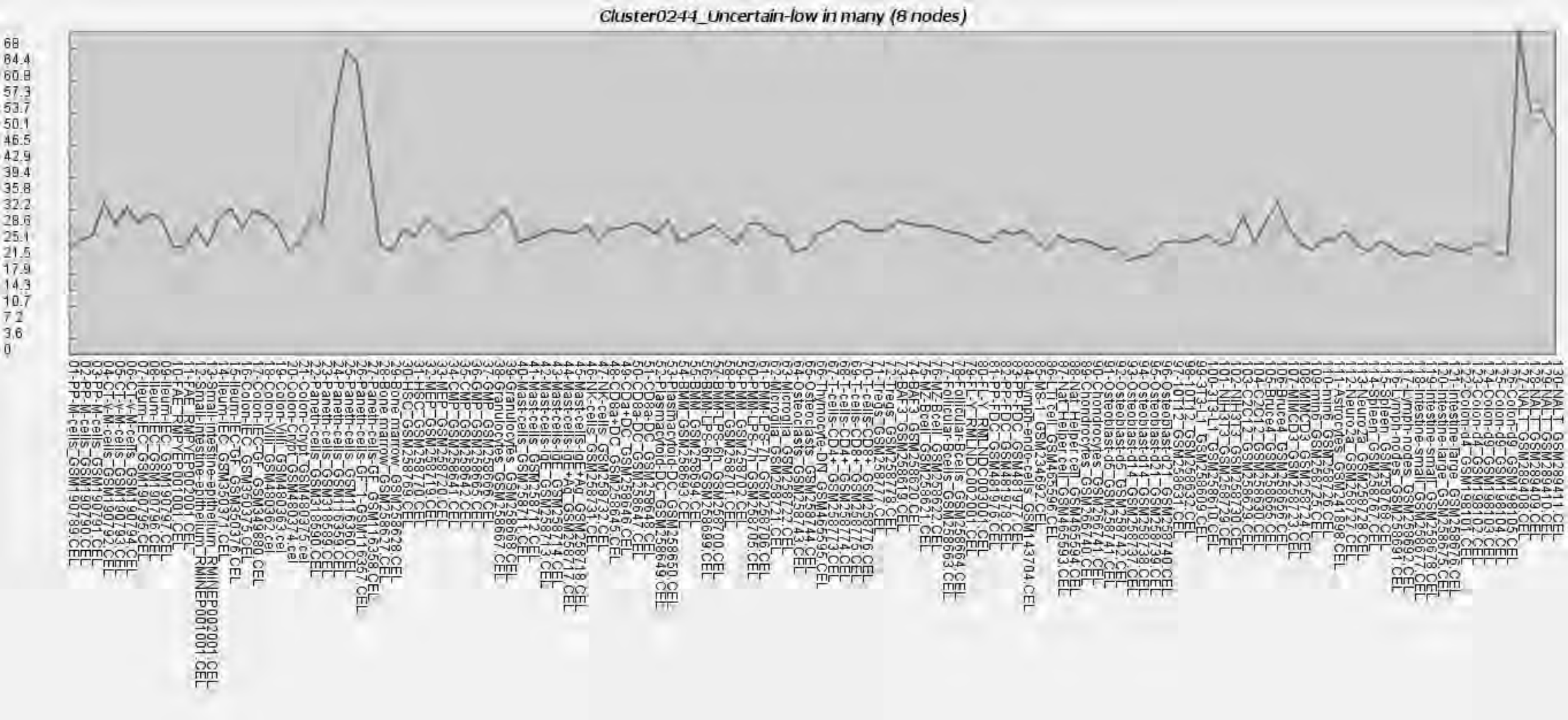

Cluster0239_Uncertain-low in many (8 nodes)
93.9
89
84
79.1
74.2
69.2
64.3
59.3
54.4
49.4
44.5
39.5
34.6
29.7
24.7
19.8
14.8
9.9
4.9
0

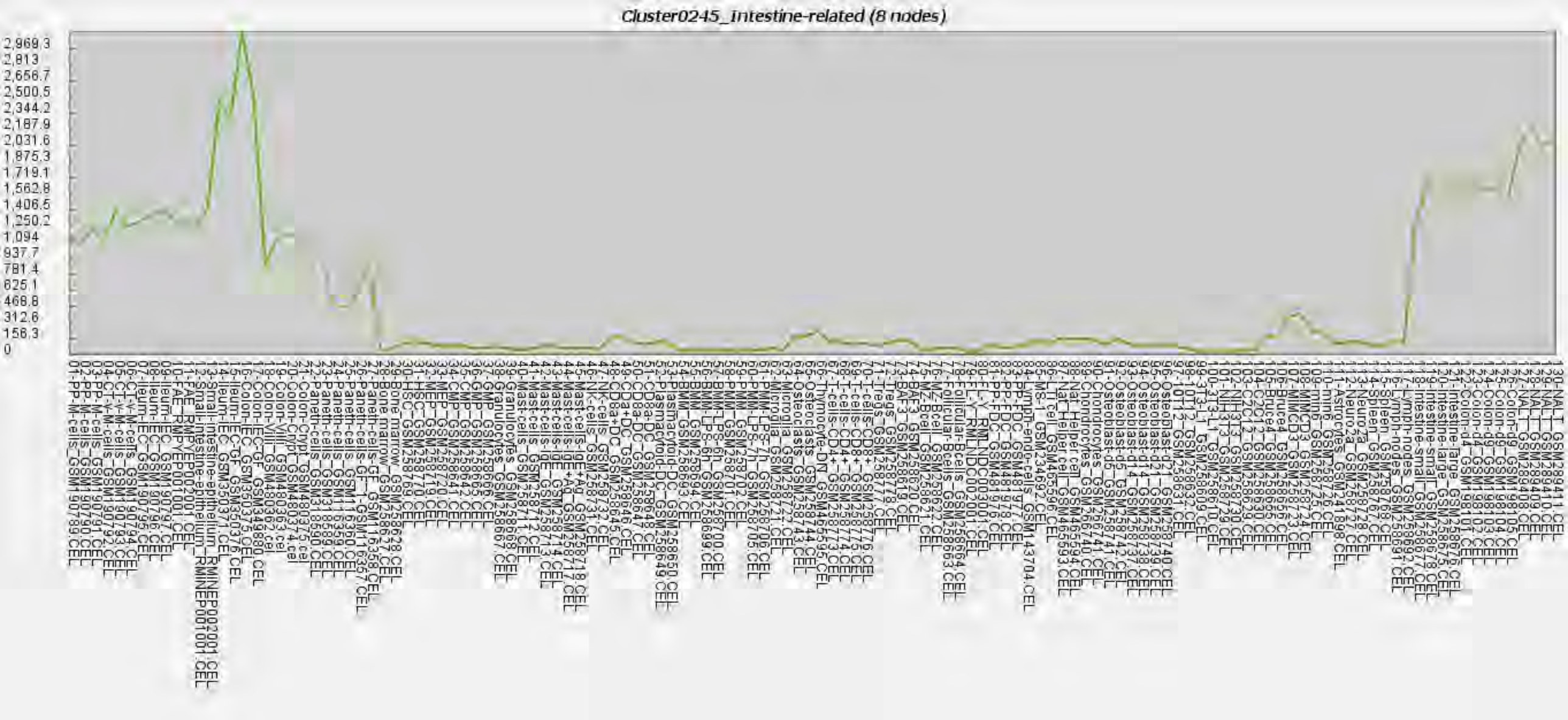

Cluster0240_Uncertain-low in many (8 nodes)
132.1
125.1
118.2
111.2
104.3
97.3
90.4
83.4
76.5
69.5
62.6
55.6
48.7
41.7
34.8
27.8
20.9
13.9
7
0

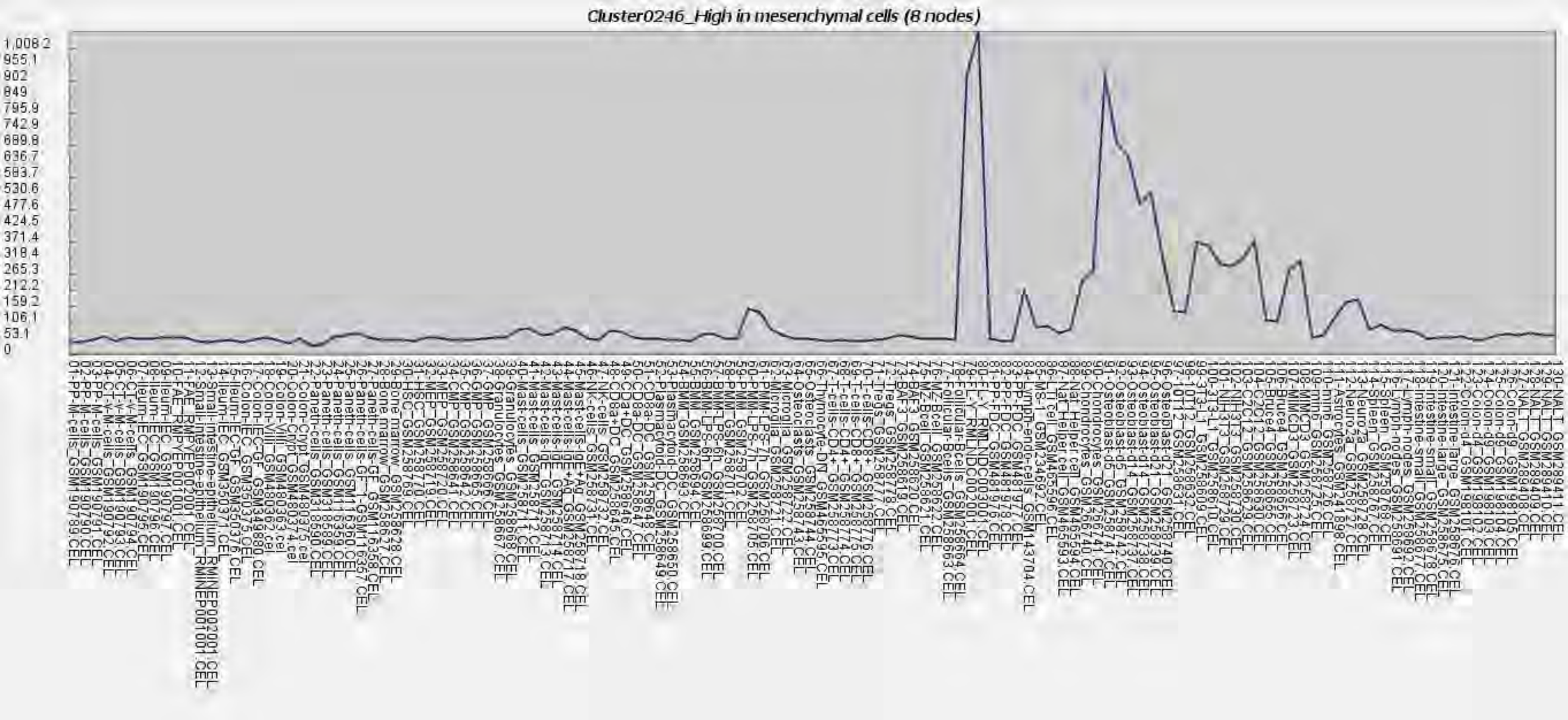

Cluster0241_Uncertain-low in many (8 nodes)
81
76.7
72.5
68.2
64
59.7
55.4
51.2
46.9
42.6
38.4
34.1
29.8
25.6
21.3
17.1
12.8
8.5
4.3
0

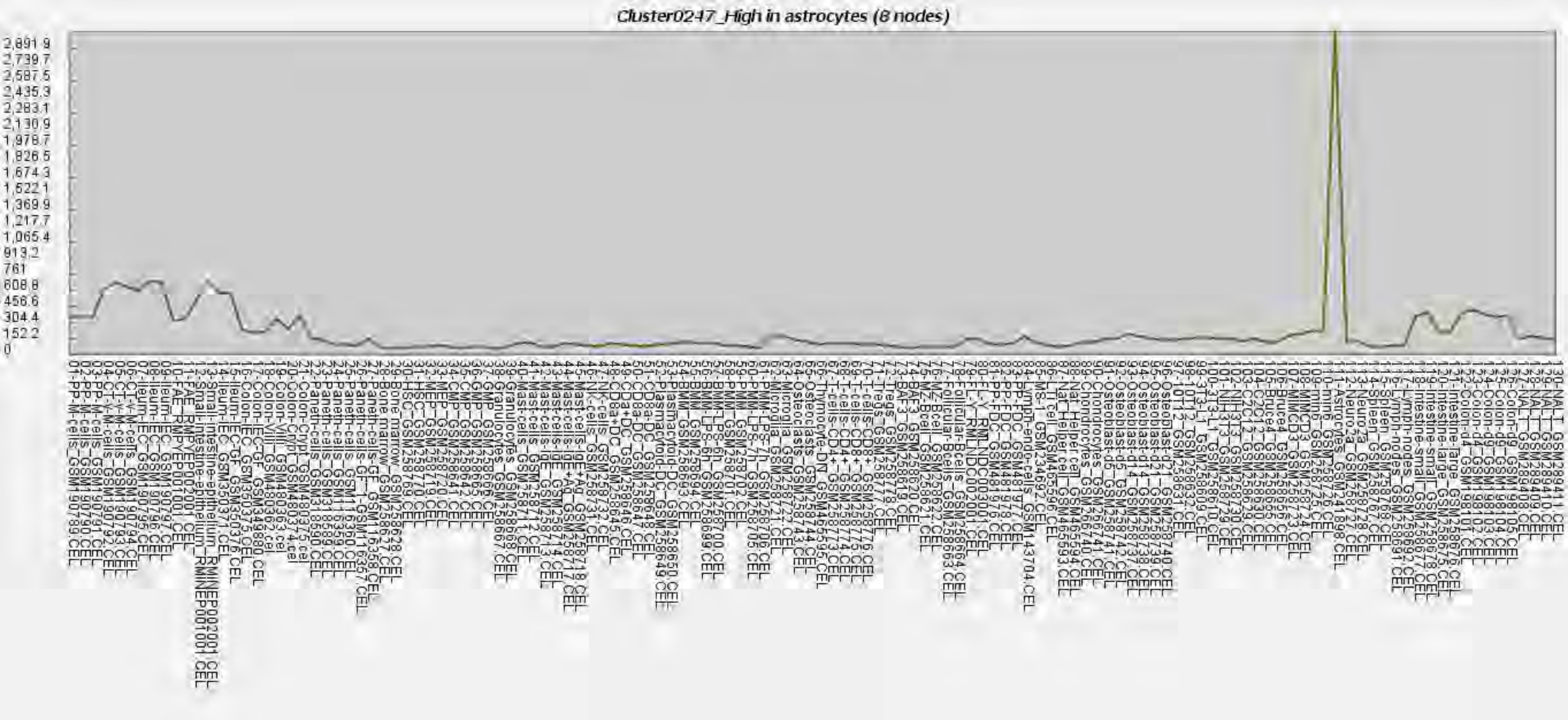
Cluster0242_Small intestine epithelium (8 nodes)
641.5
607.7
574
540.2
506.5
472.7
438.9
405.2
371.4
337.6
303.9
270.1
236.3
202.6
168.8
135.1
101.3
67.5
33.8
0

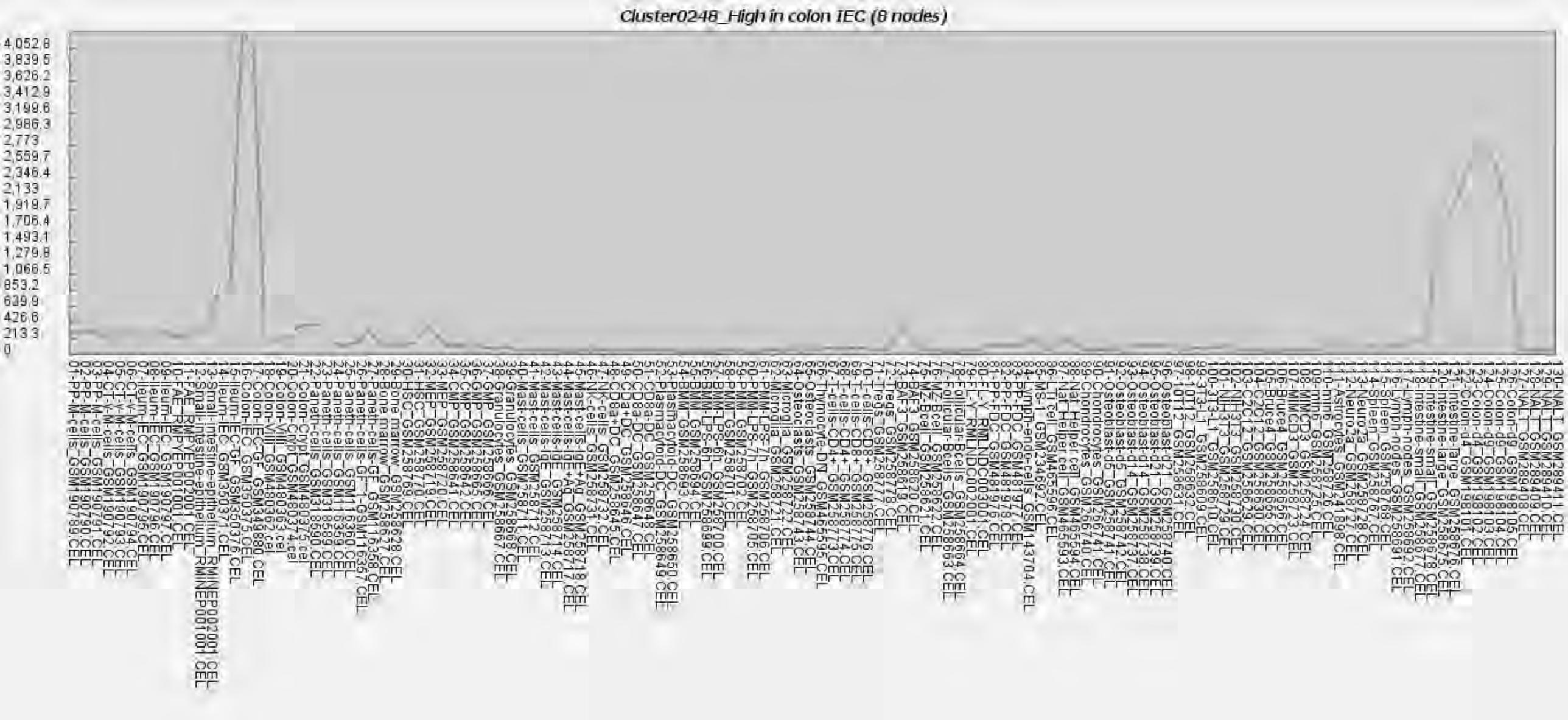

Cluster0243_Phagocyte-related (8 nodes)
3,400.8
3,221.8
3,042.8
2,863.8
2,684.8
2,505.8
2,326.8
2,147.8
1,968.9
1,789.9
1,610.9
1,431.9
1,252.9
1,073.9
894.9
715.9
537
358
179
0

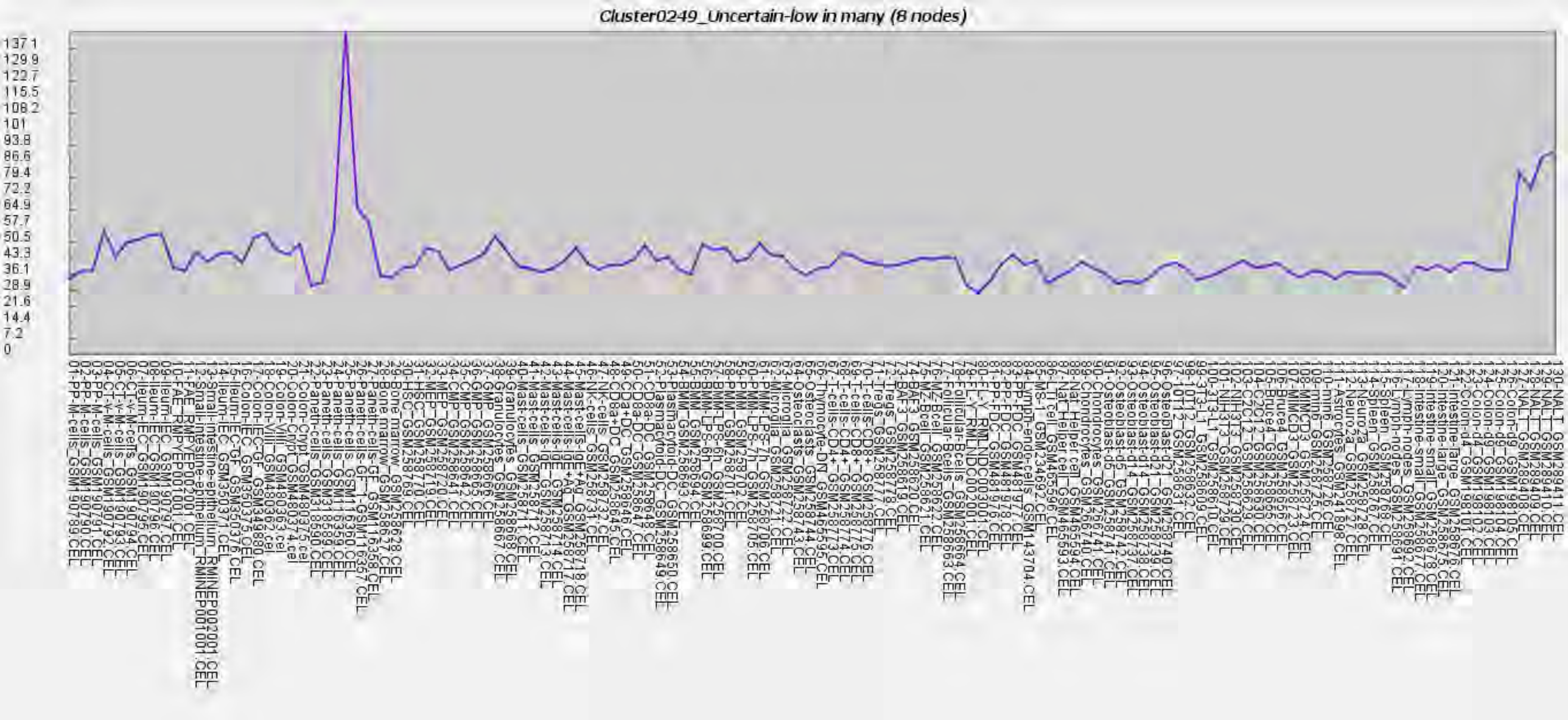

Cluster0244_Uncertain-low in many (8 nodes)
68
64.4
60.8
57.3
53.7
50.1
46.5
42.9
39.4
35.8
32.2
28.6
25.1
21.5
17.9
14.3
10.7
7.2
3.6
0

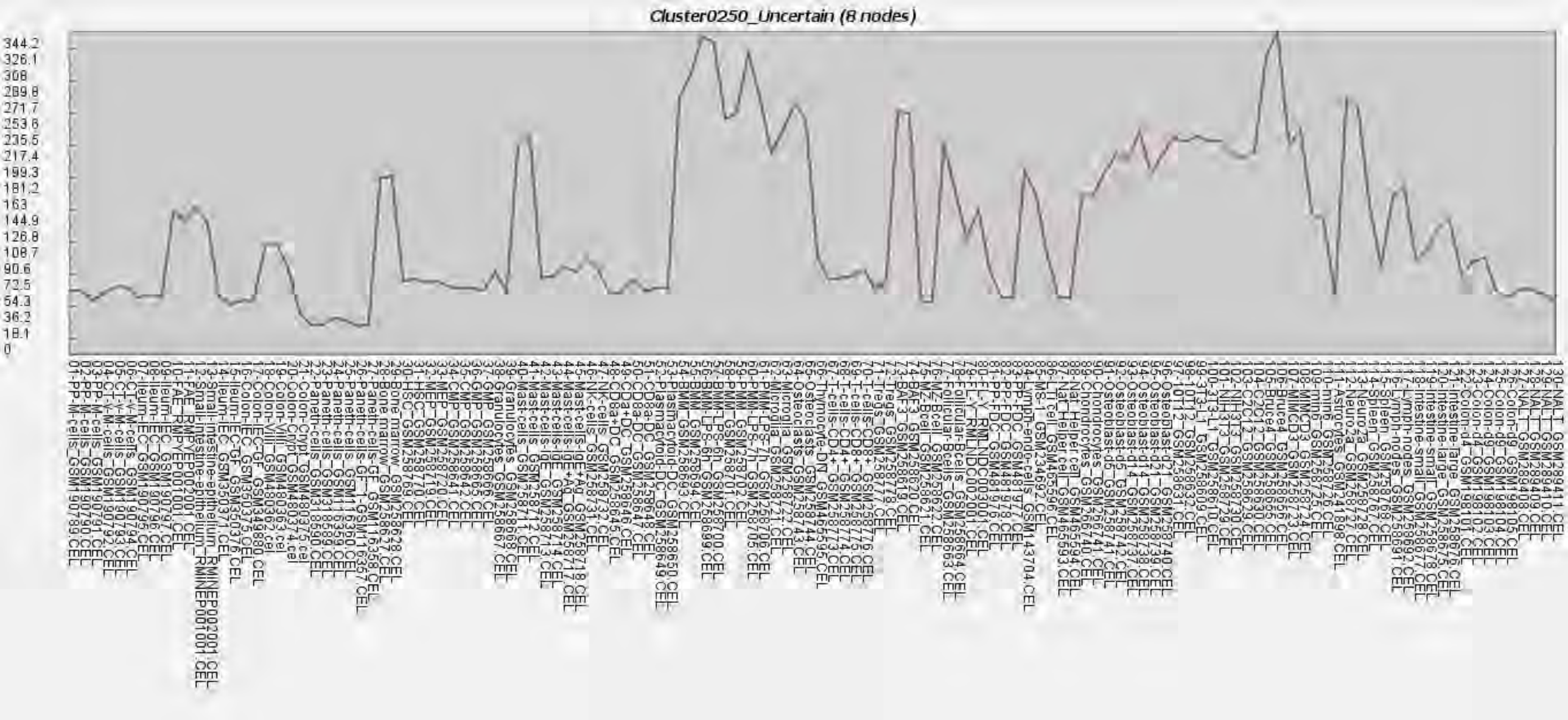

Cluster0245_Intestine-related (8 nodes)
2,969.3
2,813
2,656.7
2,500.5
2,344.2
2,187.9
2,031.6
1,875.3
1,719.1
1,562.8
1,406.5
1,250.2
1,094
937.7
781.4
625.1
468.8
312.6
156.3
0

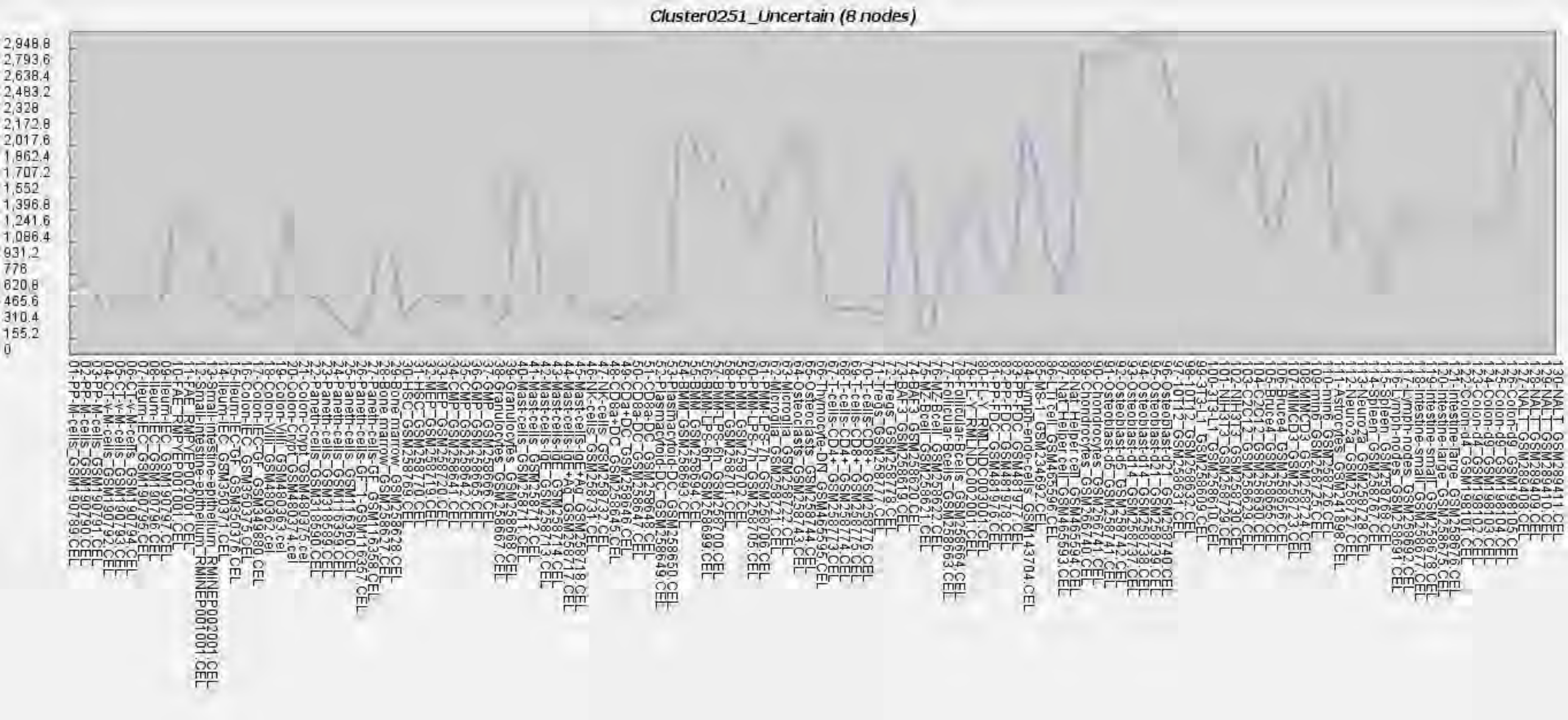

Cluster0246_High in mesenchymal cells (8 nodes)
1,008.2
955.1
902
849
795.9
742.9
689.8
636.7
583.7
530.6
477.6
424.5
371.4
318.4
265.3
212.2
159.2
106.1
53.1
0

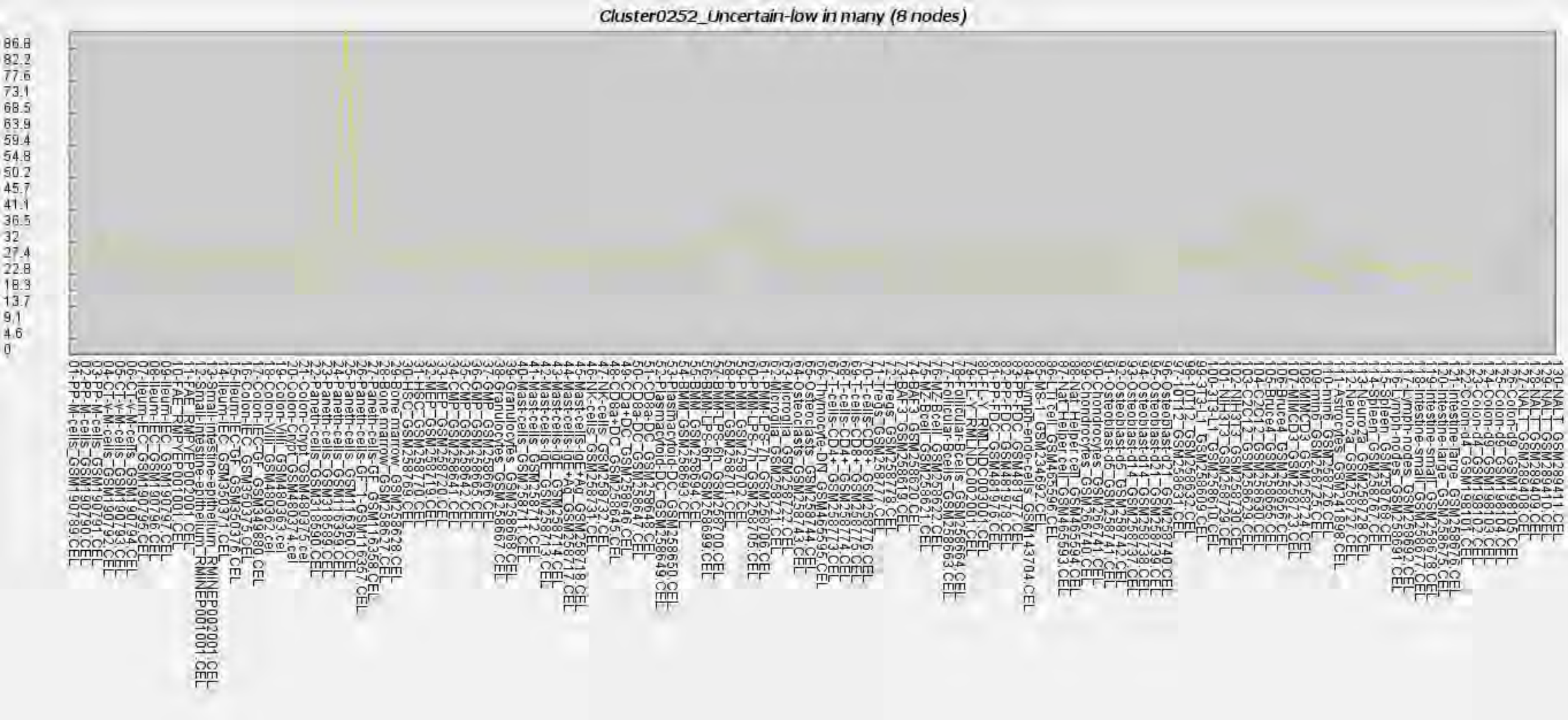

Cluster0247_High in astrocytes (8 nodes)
2,891.9
2,739.7
2,587.5
2,435.3
2,283.1
2,130.9
1,978.7
1,826.5
1,674.3
1,522.1
1,369.9
1,217.7
1,065.4
913.2
761
608.8
456.6
304.4
152.2
0

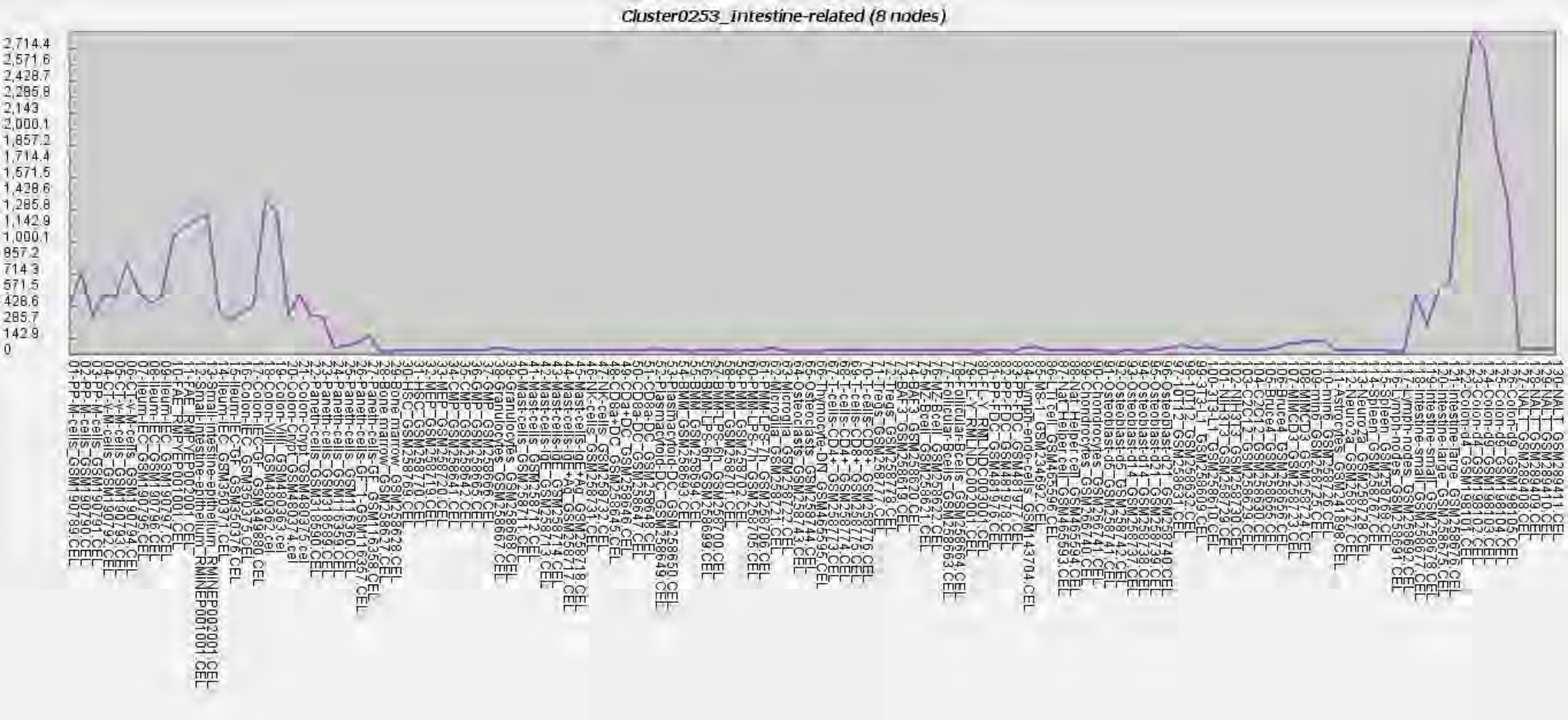

Cluster0248_High in colon IEC (8 nodes)
4,052.8
3,839.5
3,626.2
3,412.9
3,199.6
2,986.3
2,773
2,559.7
2,346.4
2,133
1,919.7
1,706.4
1,493.1
1,279.8
1,066.5
853.2
639.9
426.6
213.3
0

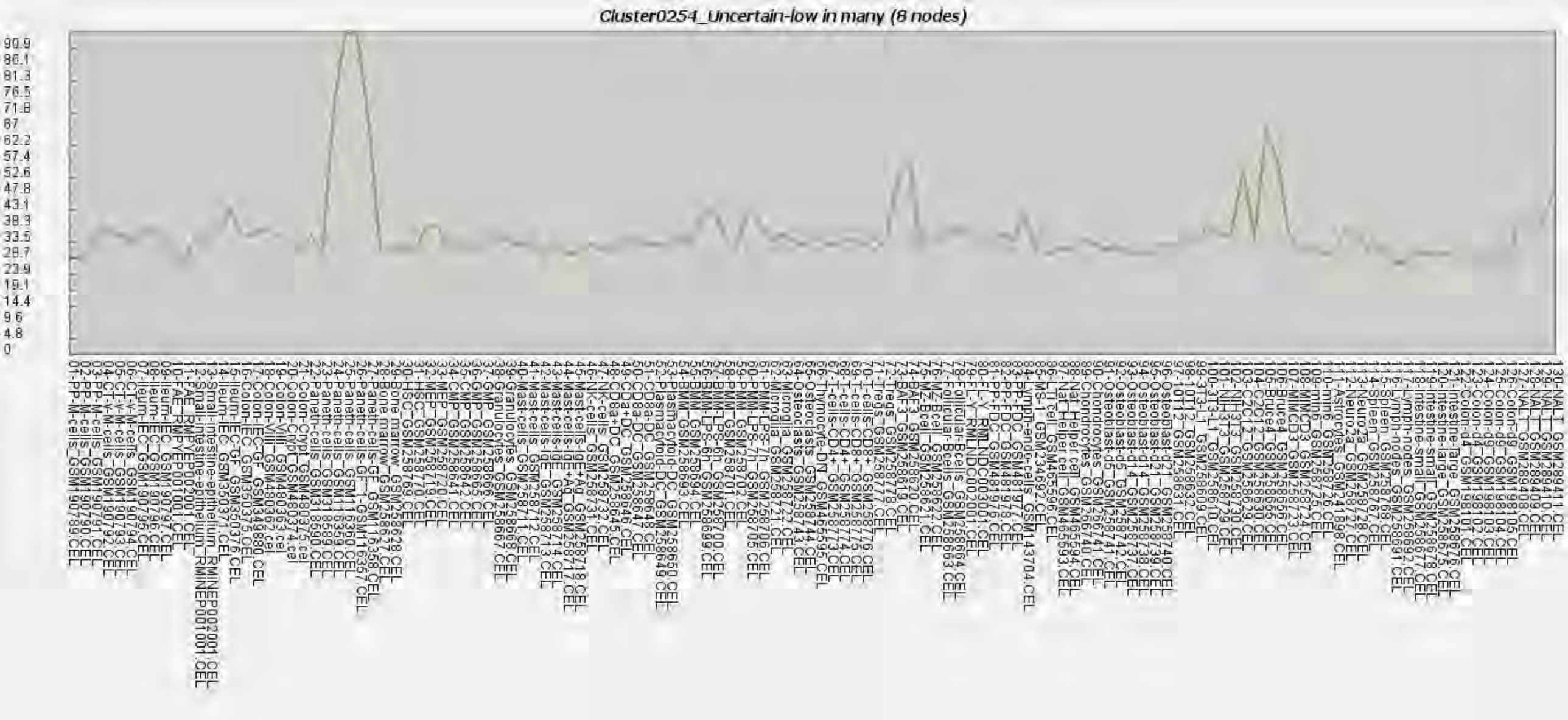

Cluster0249_Uncertain-low in many (8 nodes)
137.1
129.9
122.7
115.5
108.2
101
93.8
86.6
79.4
72.2
64.9
57.7
50.5
43.3
36.1
28.9
21.6
14.4
7.2
0


Cluster0250_Uncertain (8 nodes)
344.2
326.1
308
289.8
271.7
253.6
235.5
217.4
199.3
181.2
163
144.9
126.8
108.7
90.6
72.5
54.3
36.2
18.1
0

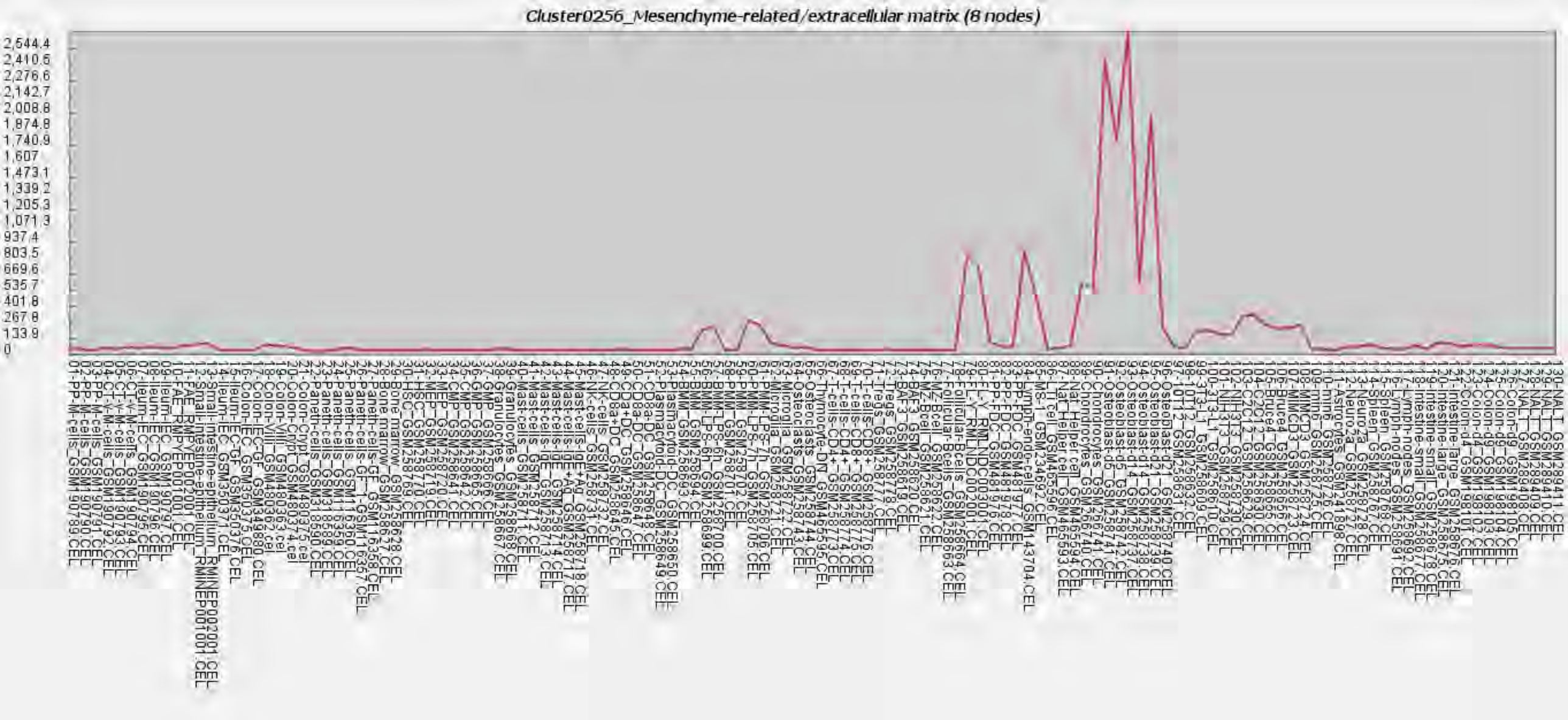

Cluster0251_Uncertain (8 nodes)
2,948.8
2,793.6
2,638.4
2,483.2
2,328
2,172.8
2,017.6
1,862.4
1,707.2
1,552
1,396.8
1,241.6
1,086.4
931.2
776
620.8
465.6
310.4
155.2
0

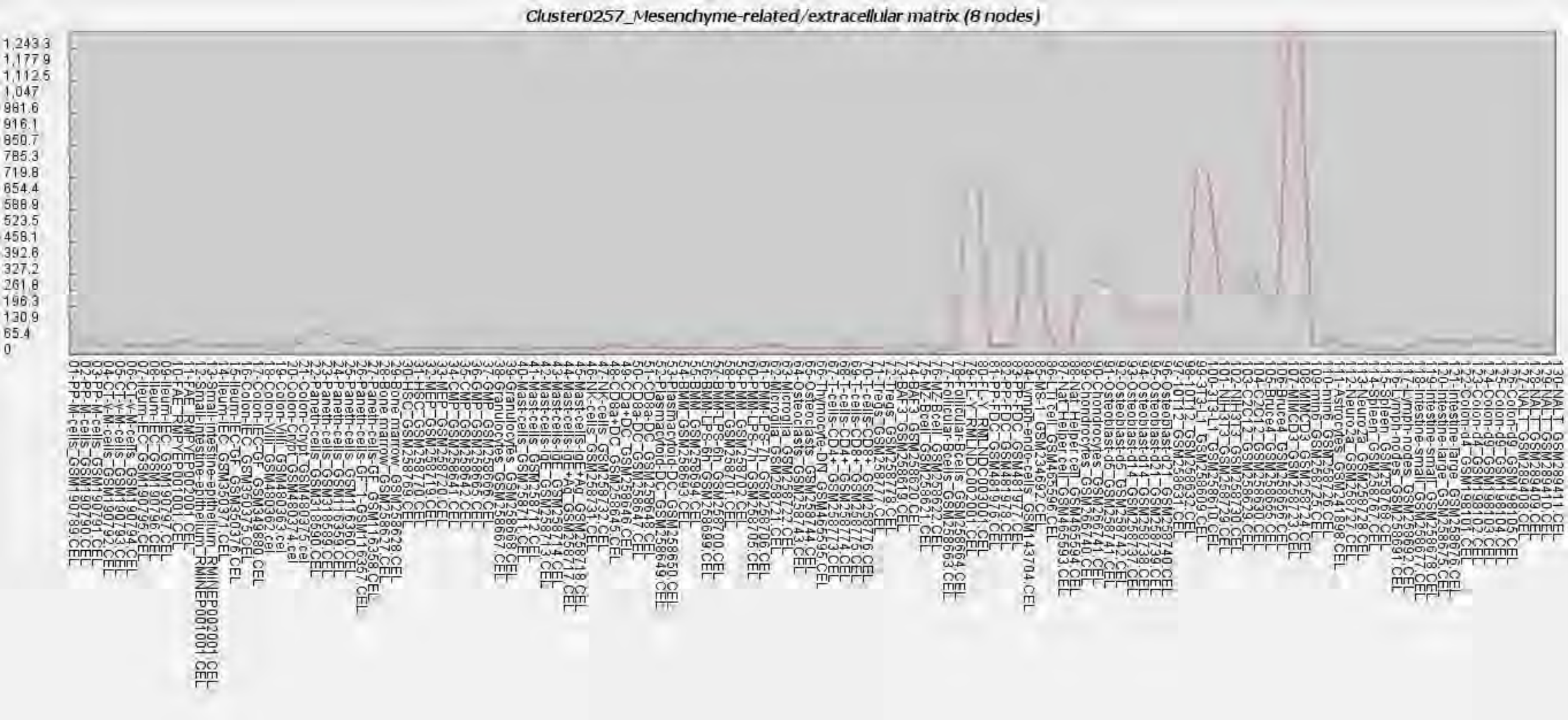

Cluster0252_Uncertain-low in many (8 nodes)
86.8
82.2
77.6
73.1
68.5
63.9
59.4
54.8
50.2
45.7
41.1
36.5
32
27.4
22.8
18.3
13.7
9.1
4.6
0

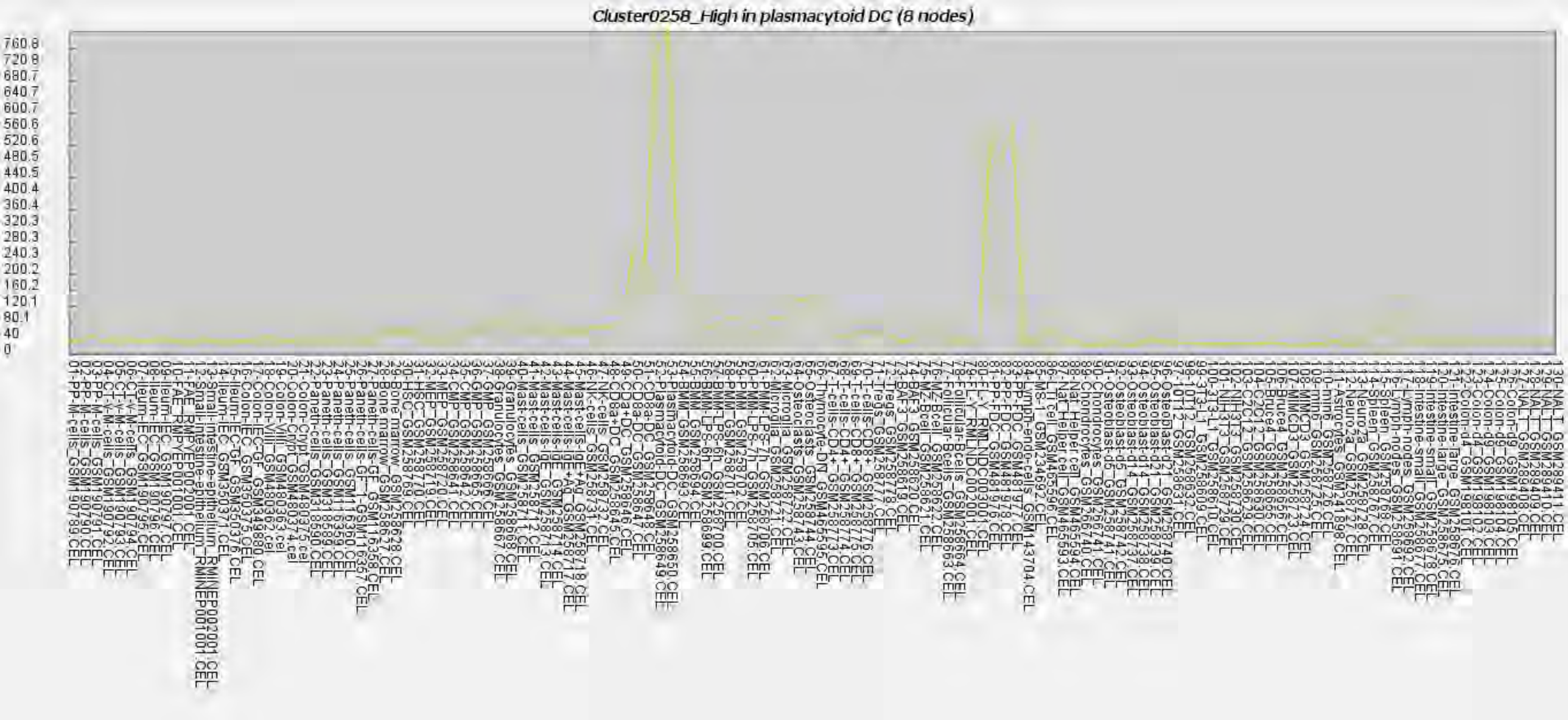

Cluster0253_Intestine-related (8 nodes)
2,714.4
2,571.6
2,428.7
2,285.8
2,143
2,000.1
1,857.2
1,714.4
1,571.5
1,428.6
1,285.8
1,142.9
1,000.1
857.2
714.3
571.5
428.6
285.7
142.9
0

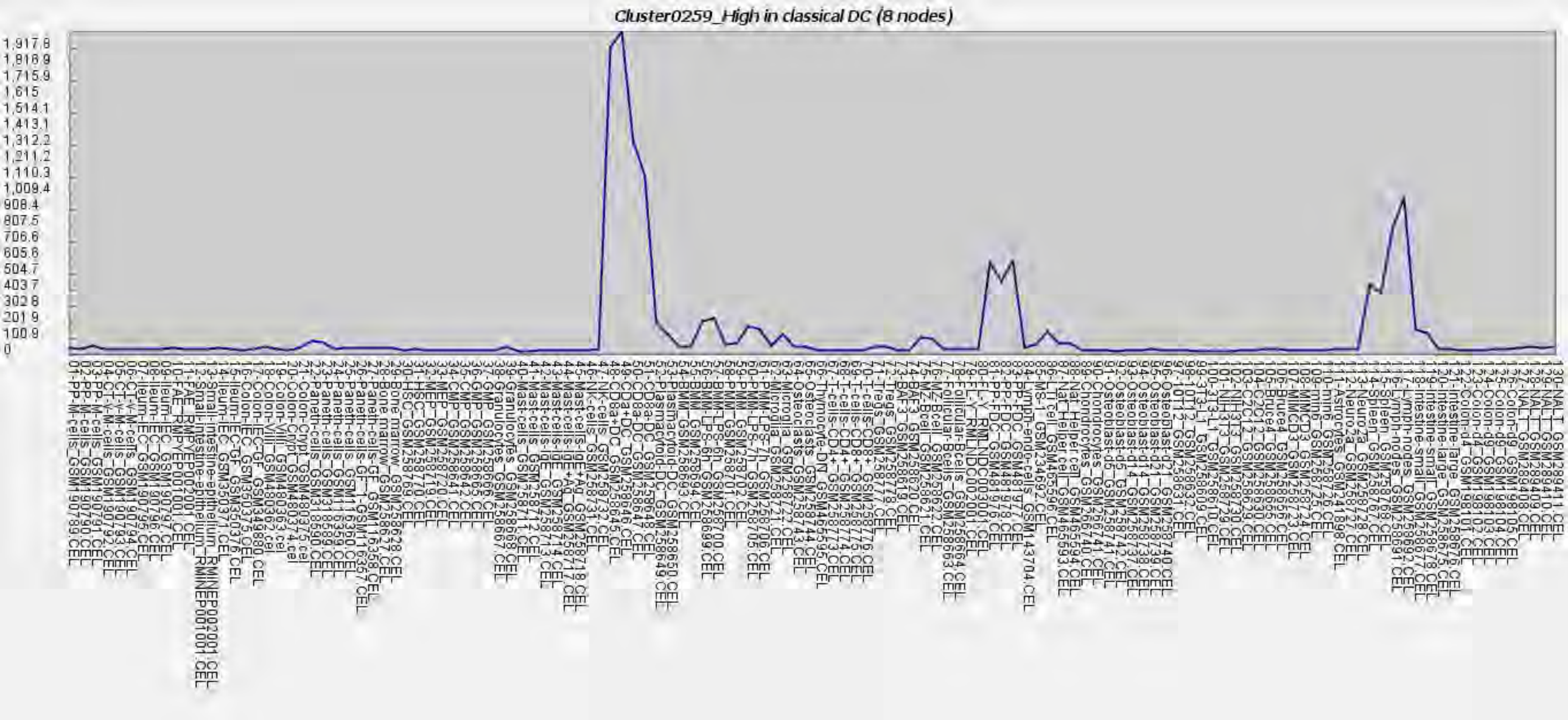

Cluster0254_Uncertain-low in many (8 nodes)
90.9
86.1
81.3
76.5
71.8
67
62.2
57.4
52.6
47.8
43.1
38.3
33.5
28.7
23.9
19.1
14.4
9.6
4.8
0

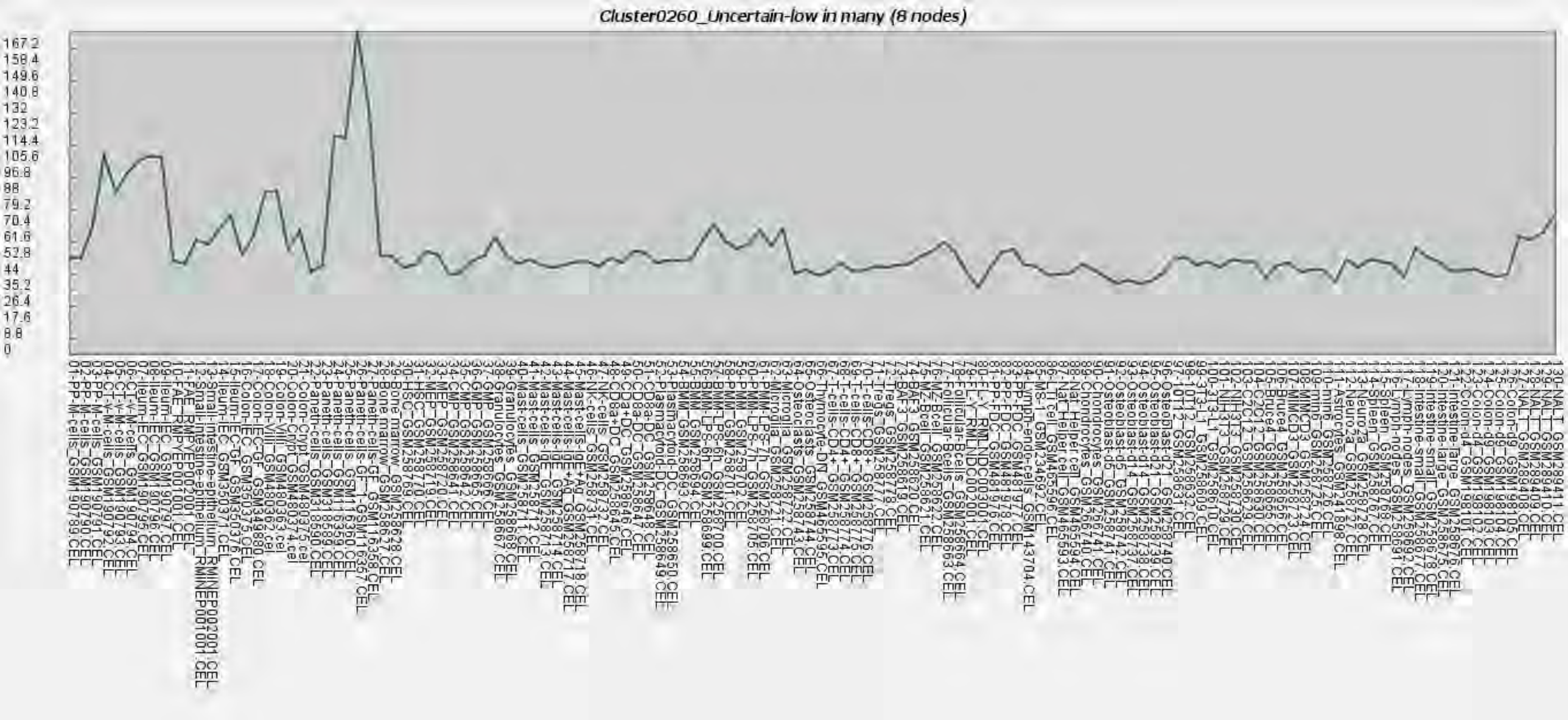
Cluster0255_High in bone marrow progenitors and mast cells (8 nodes)
678.4
642.7
607
571.3
535.5
499.8
464.1
428.4
392.7
357
321.3
285.6
249.9
214.2
178.5
142.8
107.1
71.4
35.7
0

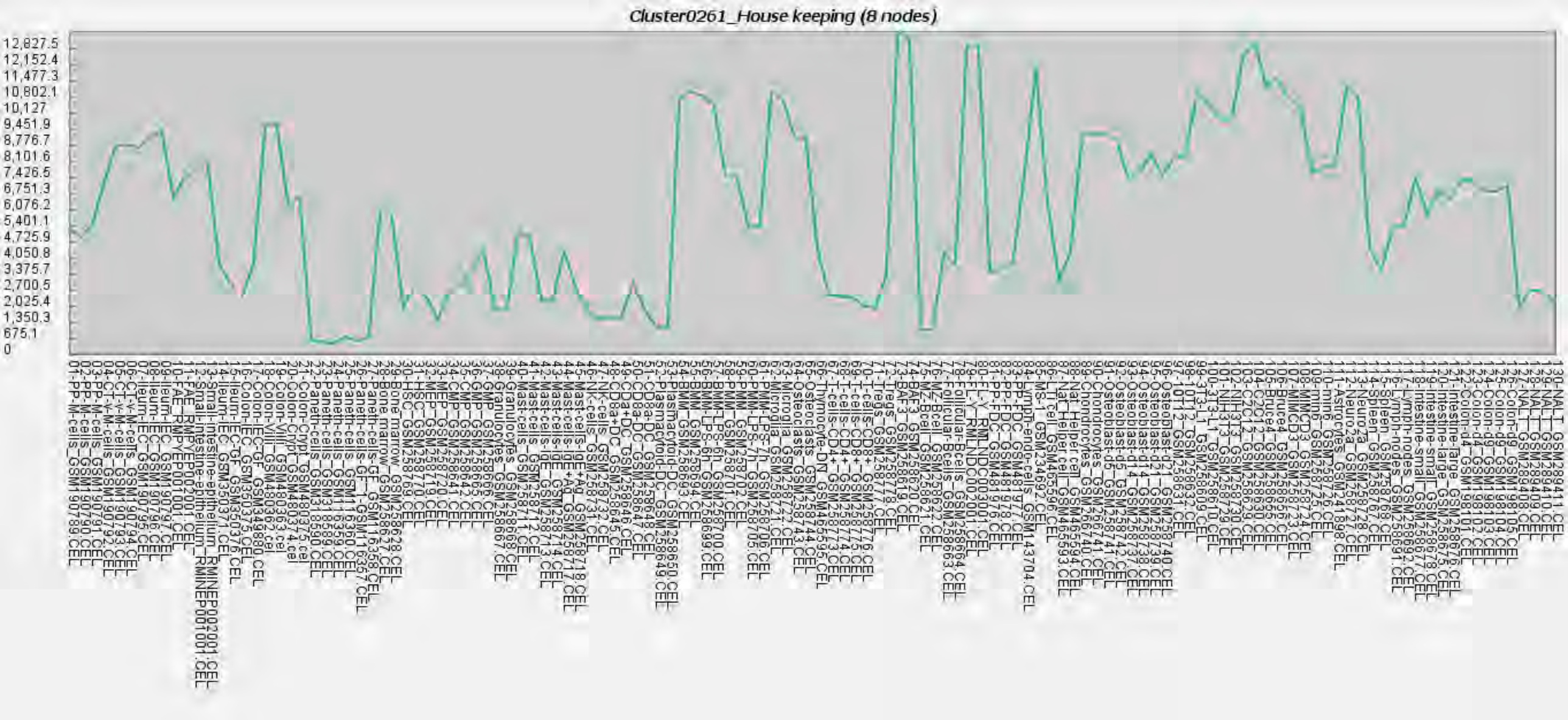

Cluster0256_Mesenchyme-related/extracellular matrix (8 nodes)
2,544.4
2,410.5
2,276.6
2,142.7
2,008.8
1,874.8
1,740.9
1,607
1,473.1
1,339.2
1,205.3
1,071.3
937.4
803.5
669.6
535.7
401.8
267.8
133.9
0

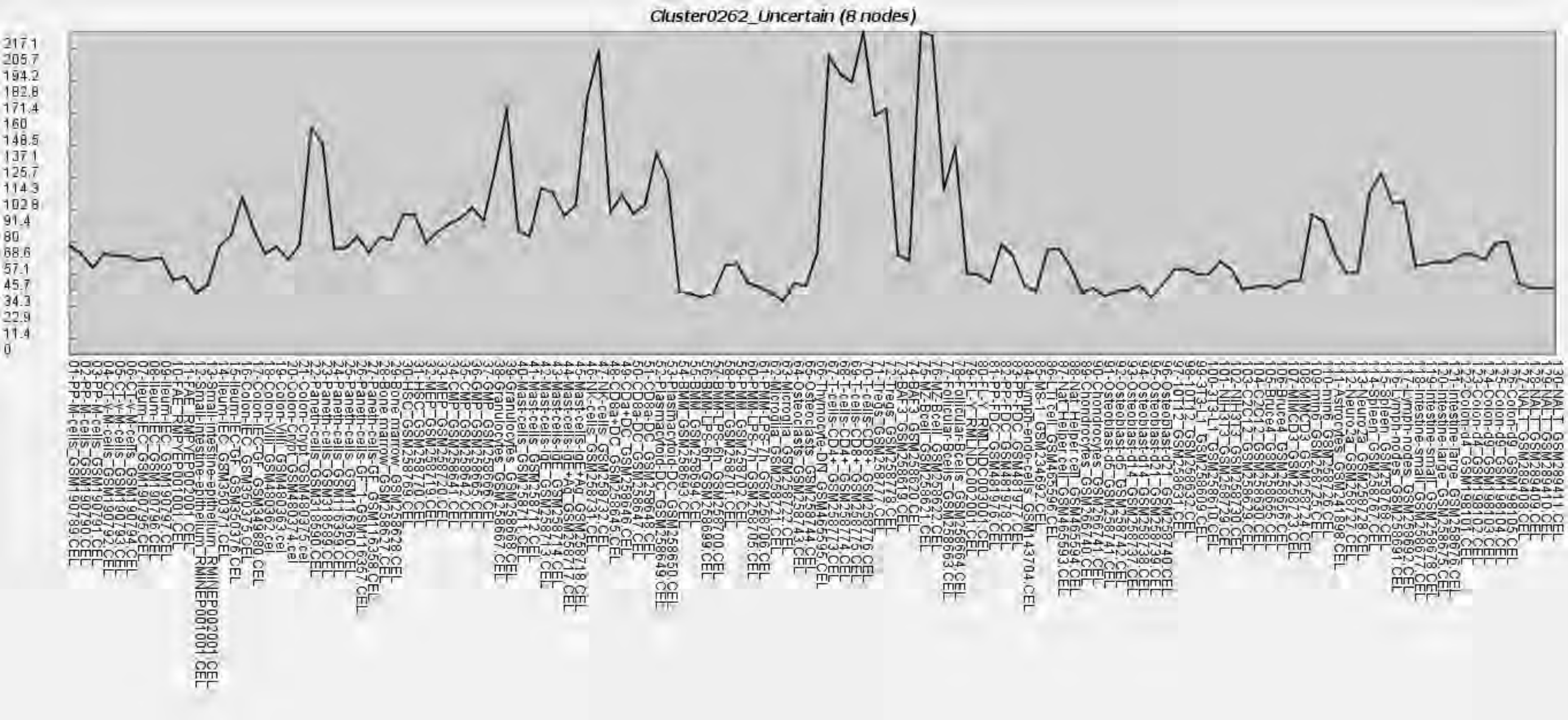

Cluster0257_Mesenchyme-related/extracellular matrix (8 nodes)
1,243.3
1,177.9
1,112.5
1,047
981.6
916.1
850.7
785.3
719.8
654.4
588.9
523.5
458.1
392.6
327.2
261.8
196.3
130.9
65.4
0

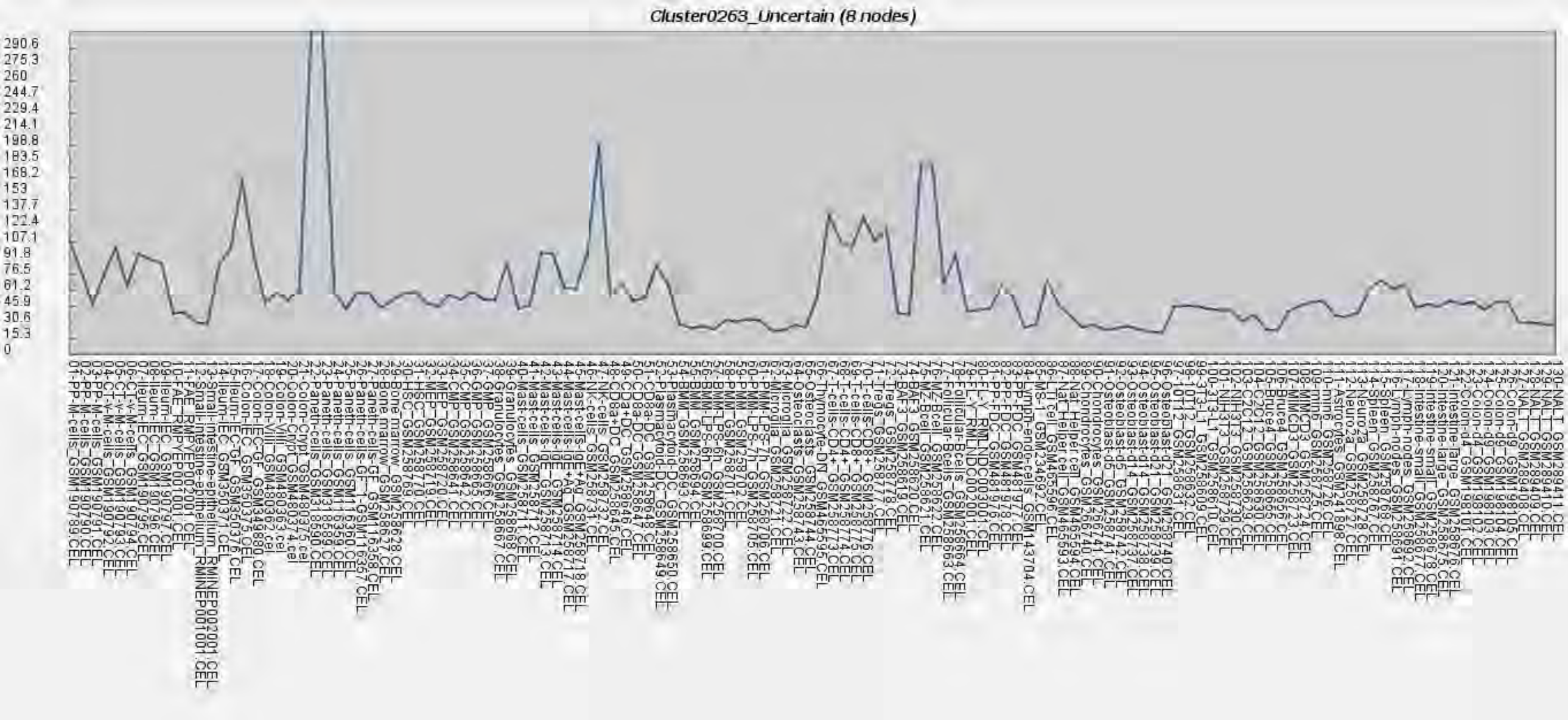

Cluster0258_High in plasmacytoid DC (8 nodes)
760.8
720.8
680.7
640.7
600.7
560.6
520.6
480.5
440.5
400.4
360.4
320.3
280.3
240.3
200.2
160.2
120.1
80.1
40
0

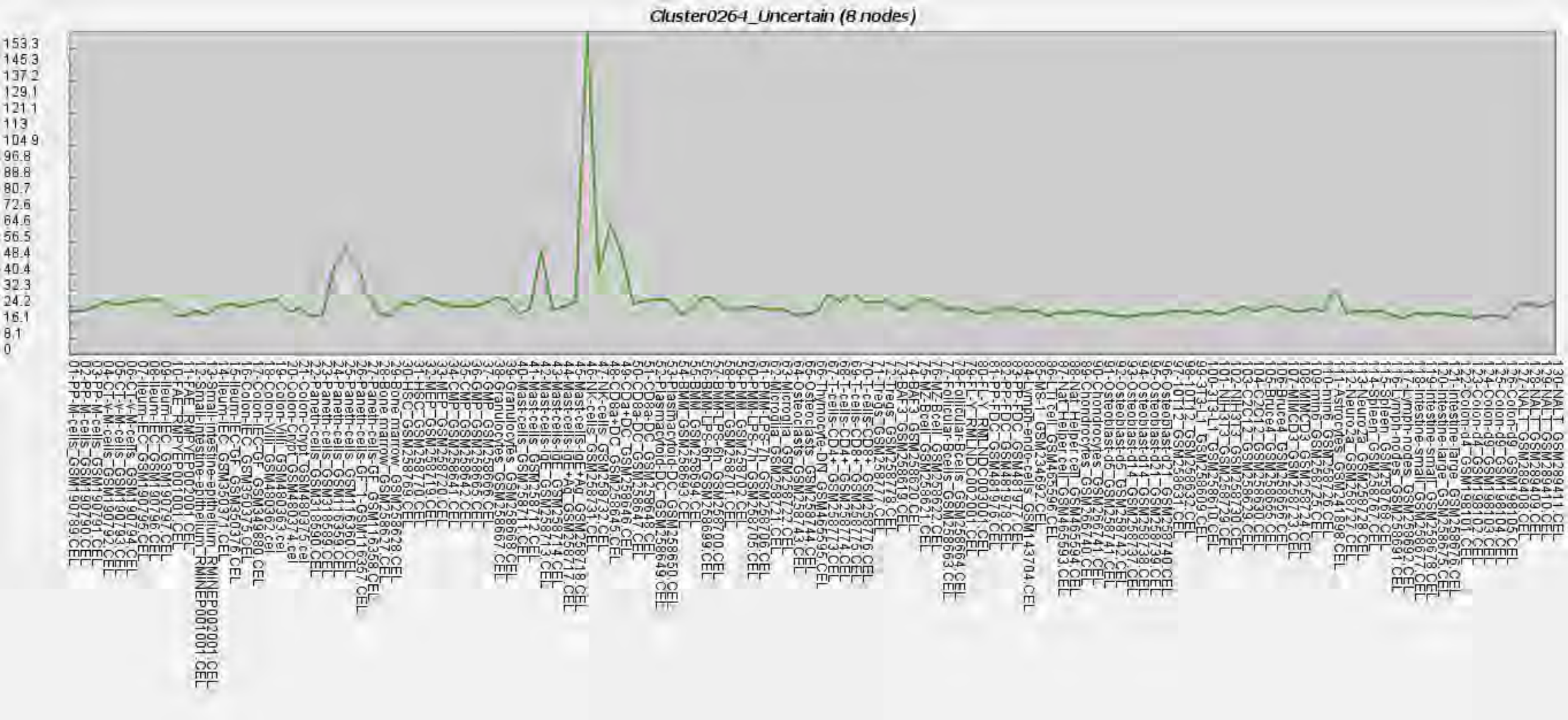

Cluster0259_High in classical DC (8 nodes)
1,917.8
1,816.9
1,715.9
1,615
1,514.1
1,413.1
1,312.2
1,211.2
1,110.3
1,009.4
908.4
807.5
706.6
605.6
504.7
403.7
302.8
201.9
100.9
0

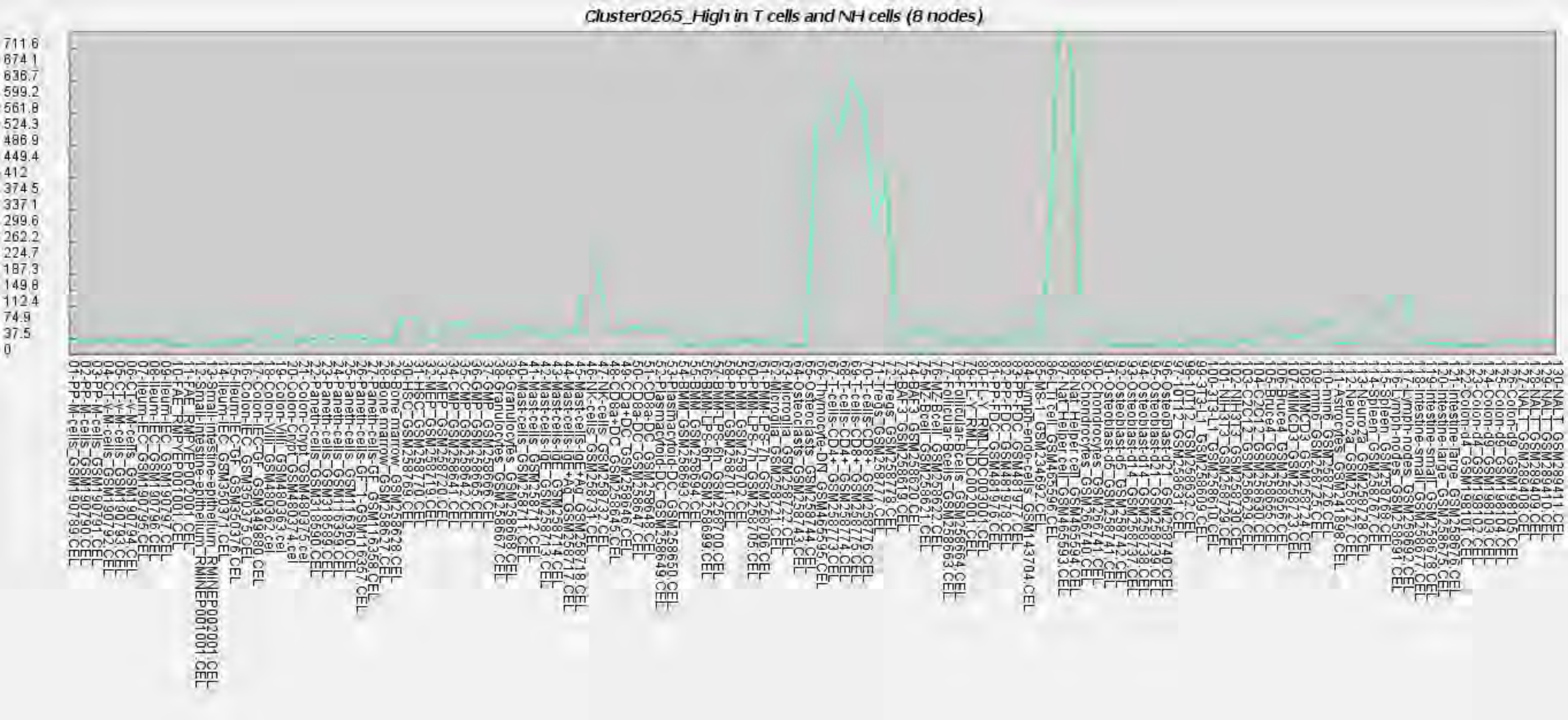

Cluster0260_Uncertain-low in many (8 nodes)
167.2
158.4
149.6
140.8
132
123.2
114.4
105.6
96.8
88
79.2
70.4
61.6
52.8
44
35.2
26.4
17.6
8.8
0

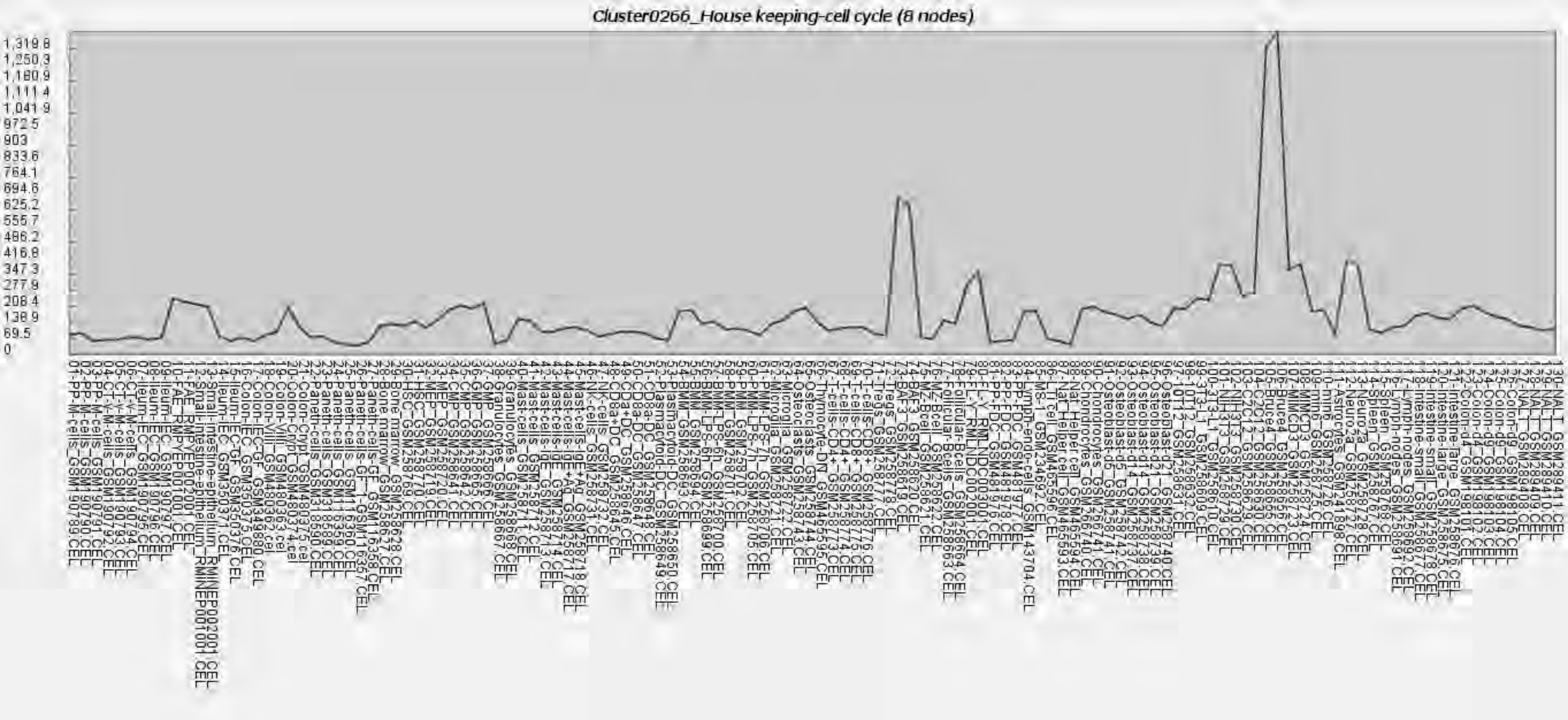

Cluster0261_House keeping (8 nodes)
12,827.5
12,152.4
11,477.3
10,802.1
10,127
9,451.9
8,776.7
8,101.6
7,426.5
6,751.3
6,076.2
5,401.1
4,725.9
4,050.8
3,375.7
2,700.5
2,025.4
1,350.3
675.1
0

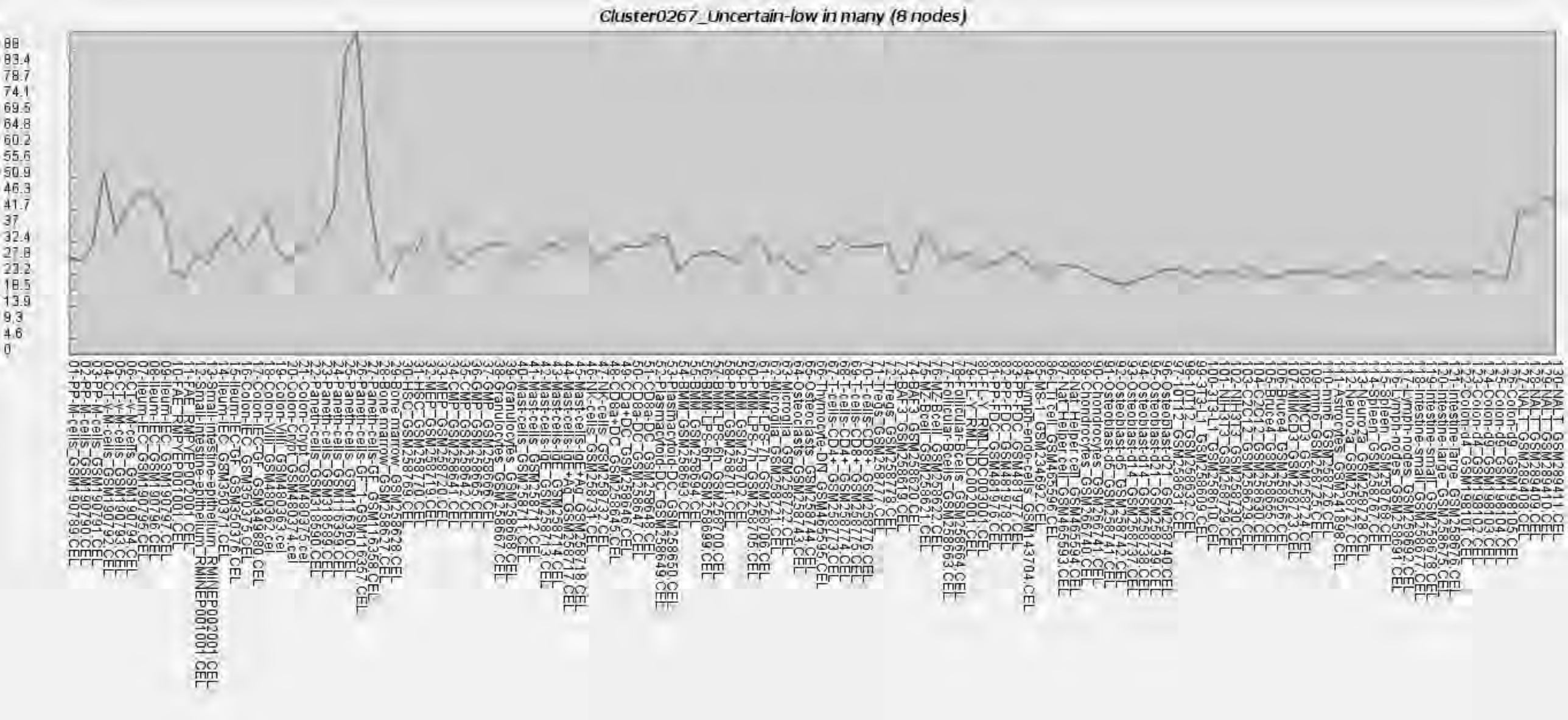

Cluster0262_Uncertain (8 nodes)
217.1
205.7
194.2
182.8
171.4
160
148.5
137.1
125.7
114.3
102.8
91.4
80
68.6
57.1
45.7
34.3
22.9
11.4
0

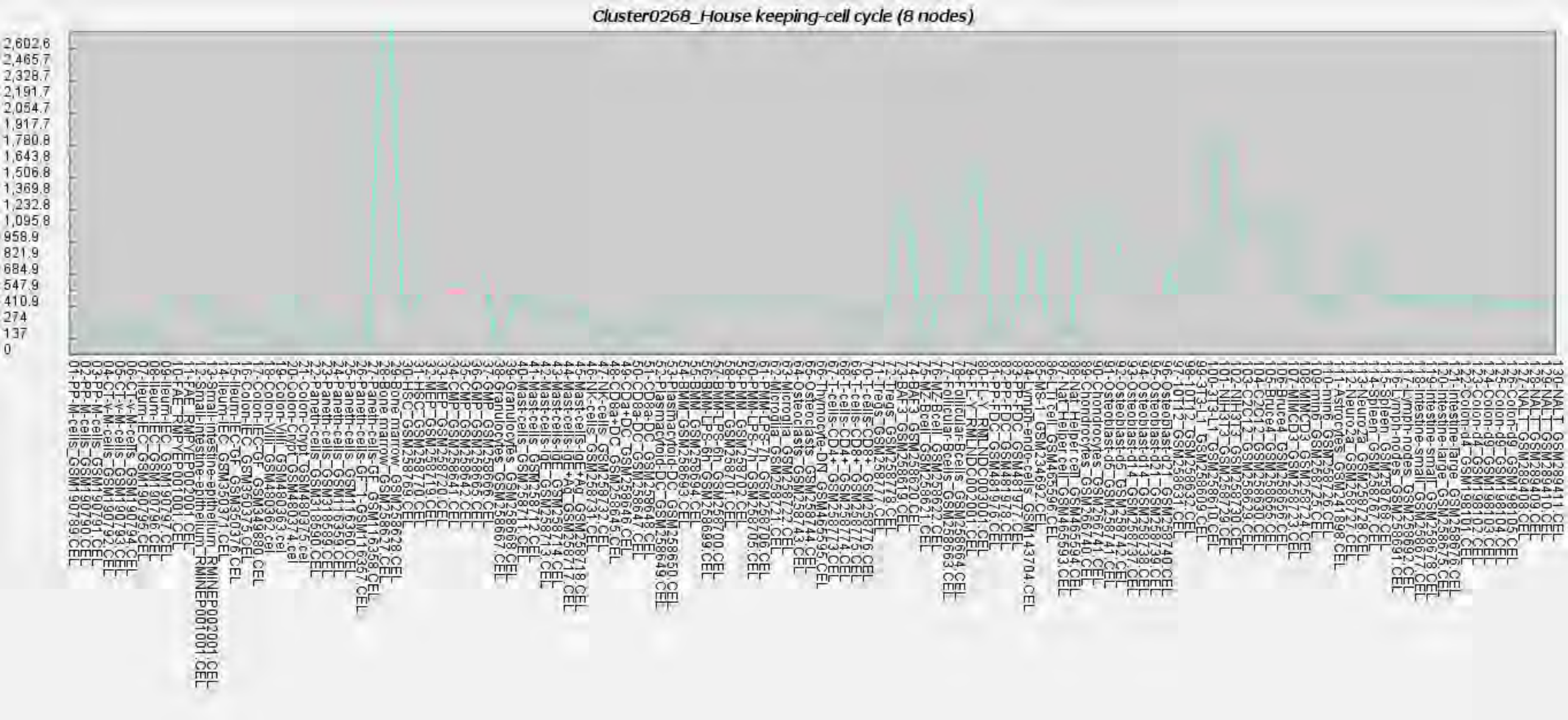

Cluster0263_Uncertain (8 nodes)
290.6
275.3
260
244.7
229.4
214.1
198.8
183.5
168.2
153
137.7
122.4
107.1
91.8
76.5
61.2
45.9
30.6
15.3
0

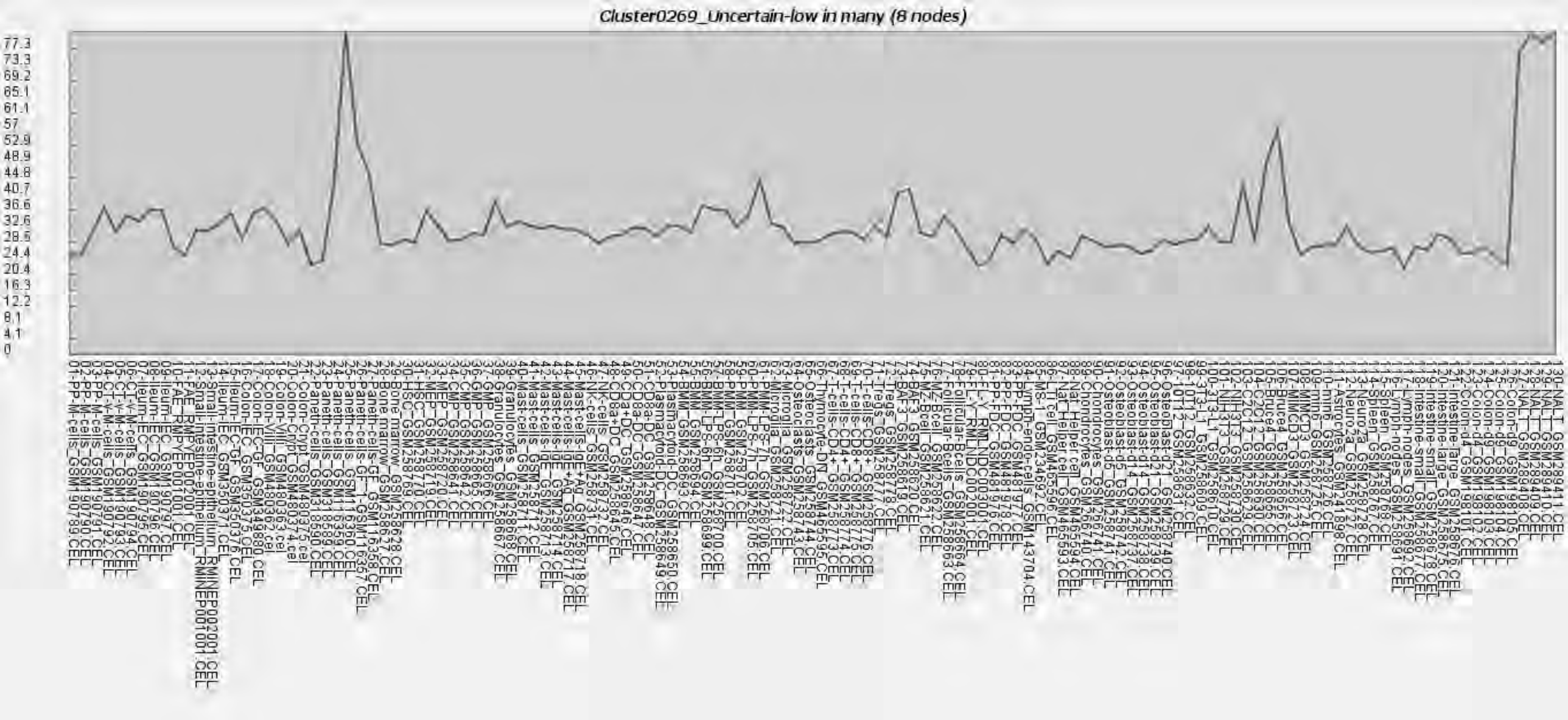

Cluster0264_Uncertain (8 nodes)
153.3
145.3
137.2
129.1
121.1
113
104.9
96.8
88.8
80.7
72.6
64.6
56.5
48.4
40.4
32.3
24.2
16.1
8.1
0


Cluster0265_High in T cells and NH cells (8 nodes)
711.6
674.1
636.7
599.2
561.8
524.3
486.9
449.4
412
374.5
337.1
299.6
262.2
224.7
187.3
149.8
112.4
74.9
37.5
0

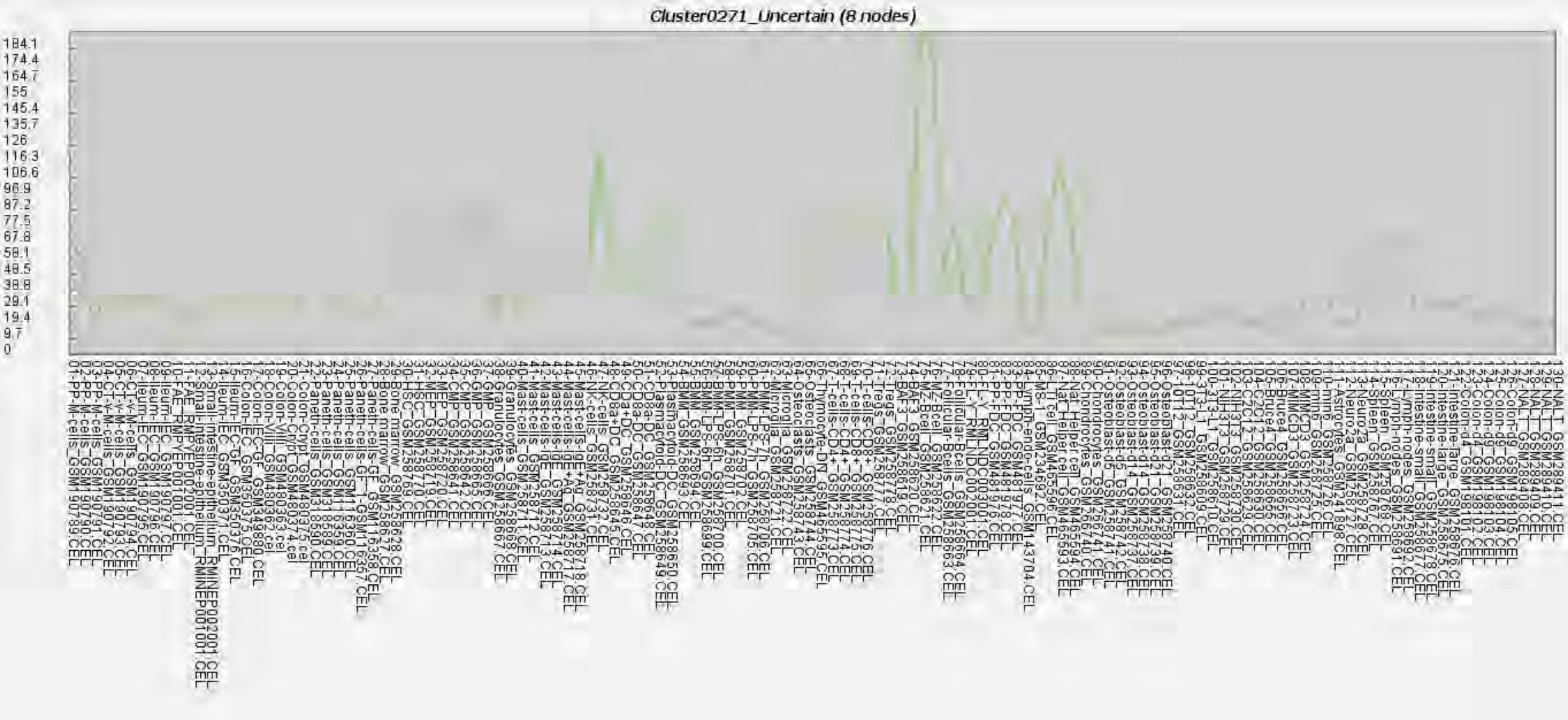

Cluster0266_House keeping-cell cycle (8 nodes)
1,319.8
1,250.3
1,180.9
1,111.4
1,041.9
972.5
903
833.6
764.1
694.6
625.2
555.7
486.2
416.8
347.3
277.9
208.4
138.9
69.5
0

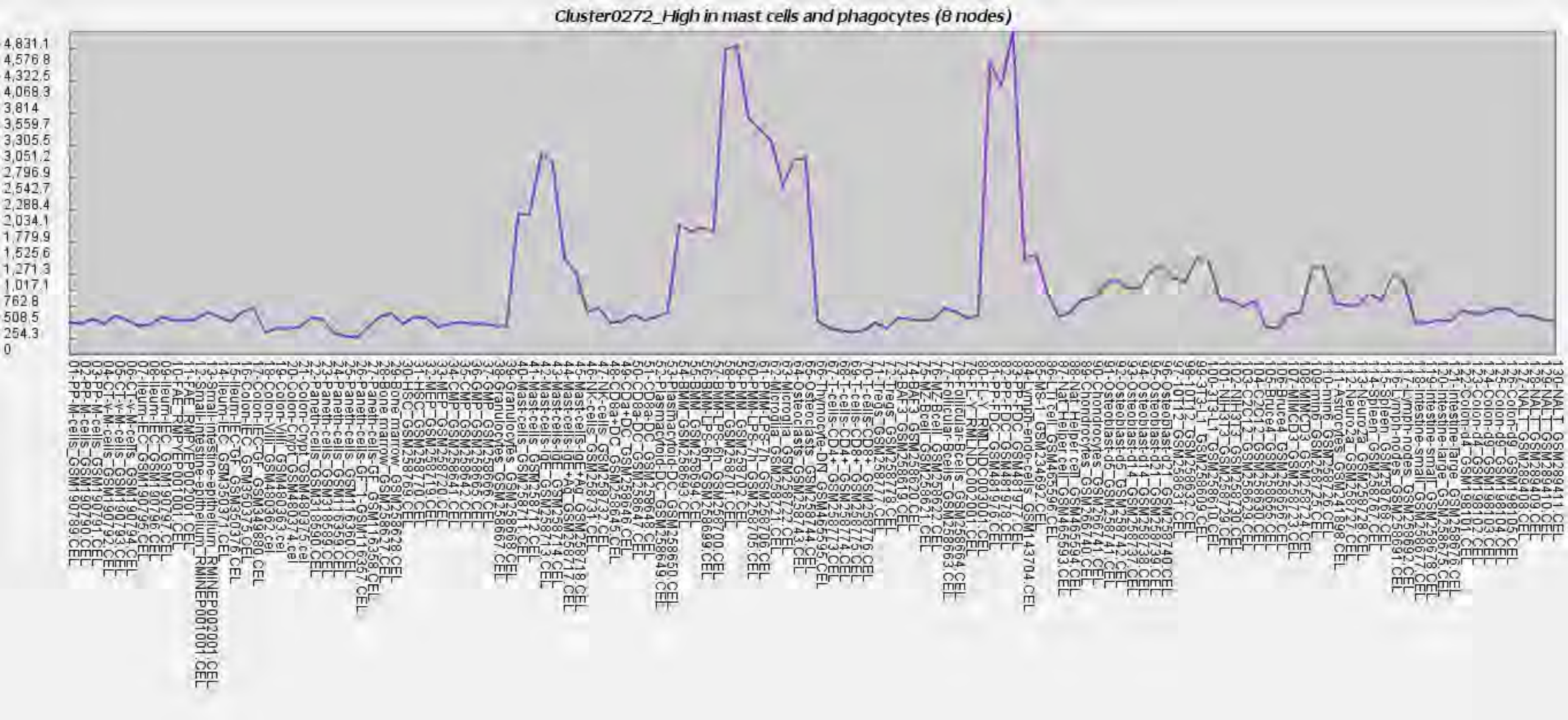

Cluster0267_Uncertain-low in many (8 nodes)
88
83.4
78.7
74.1
69.5
64.8
60.2
55.6
50.9
46.3
41.7
37
32.4
27.8
23.2
18.5
13.9
9.3
4.6
0

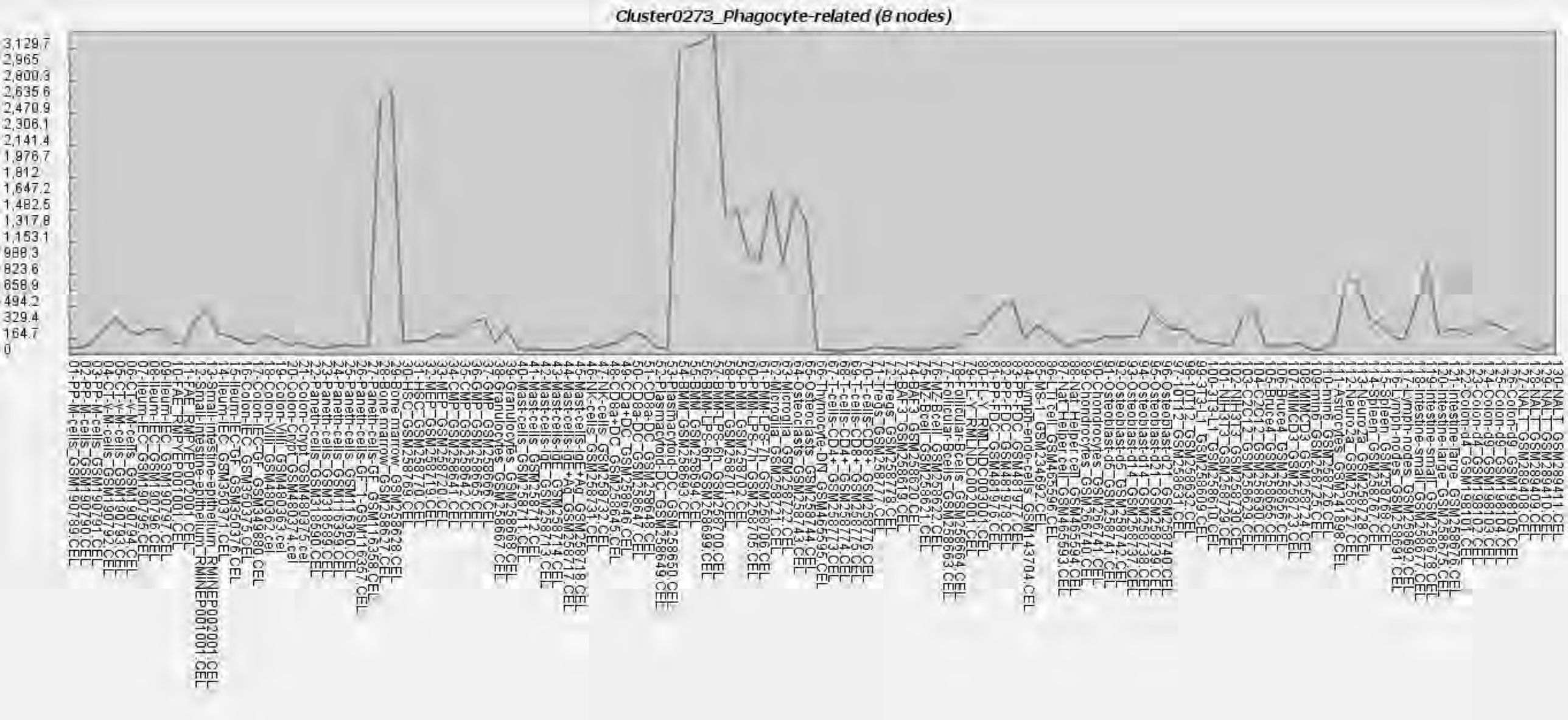

Cluster0268_House keeping-cell cycle (8 nodes)
2,602.6
2,465.7
2,328.7
2,191.7
2,054.7
1,917.7
1,780.8
1,643.8
1,506.8
1,369.8
1,232.8
1,095.8
958.9
821.9
684.9
547.9
410.9
274
137
0


Cluster0269_Uncertain-low in many (8 nodes)
77.3
73.3
69.2
65.1
61.1
57
52.9
48.9
44.8
40.7
36.6
32.6
28.5
24.4
20.4
16.3
12.2
8.1
4.1
0

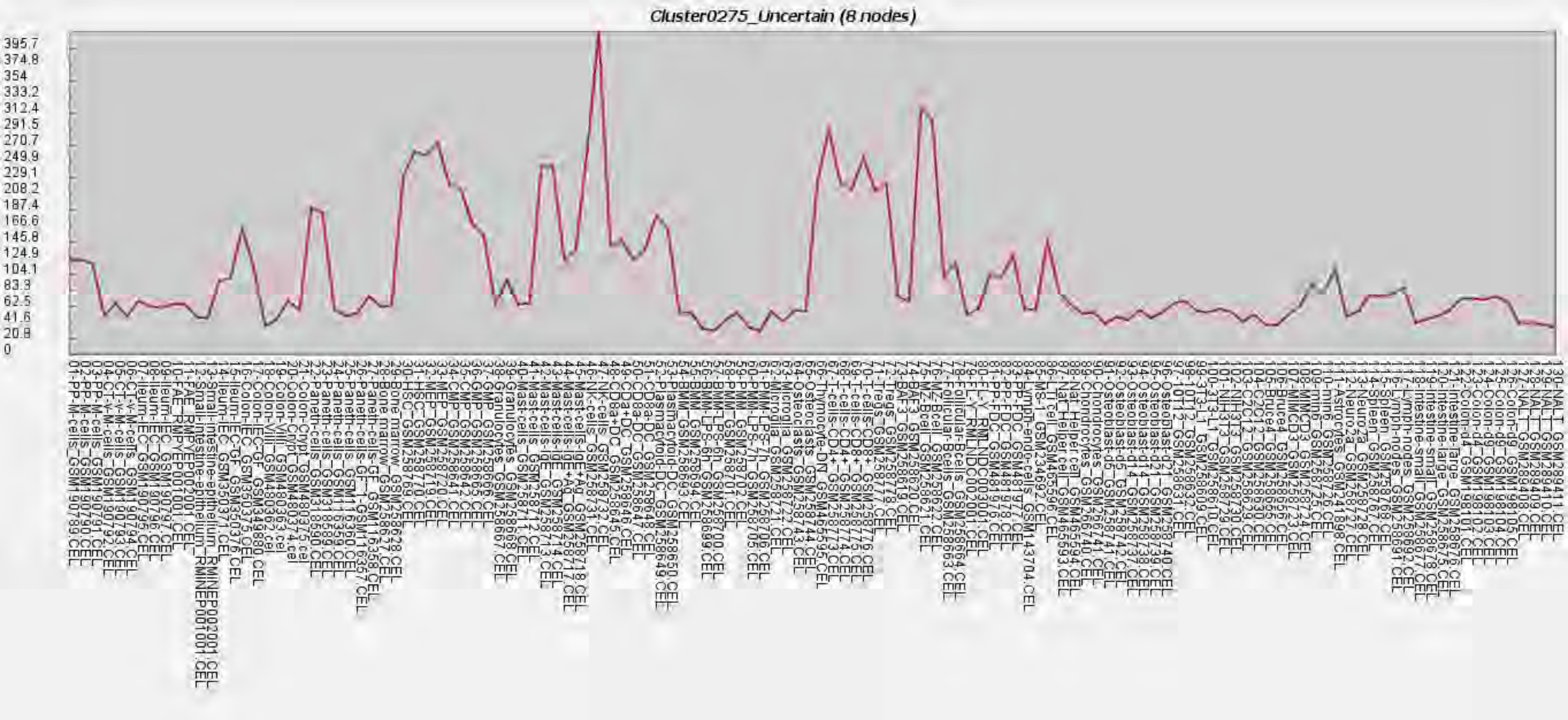
Cluster0270_High in spleen (8 nodes)
2,086.5
1,976.7
1,866.9
1,757
1,647.2
1,537.4
1,427.6
1,317.8
1,208
1,098.1
988.3
878.5
768.7
658.9
549.1
439.3
329.4
219.6
109.8
0

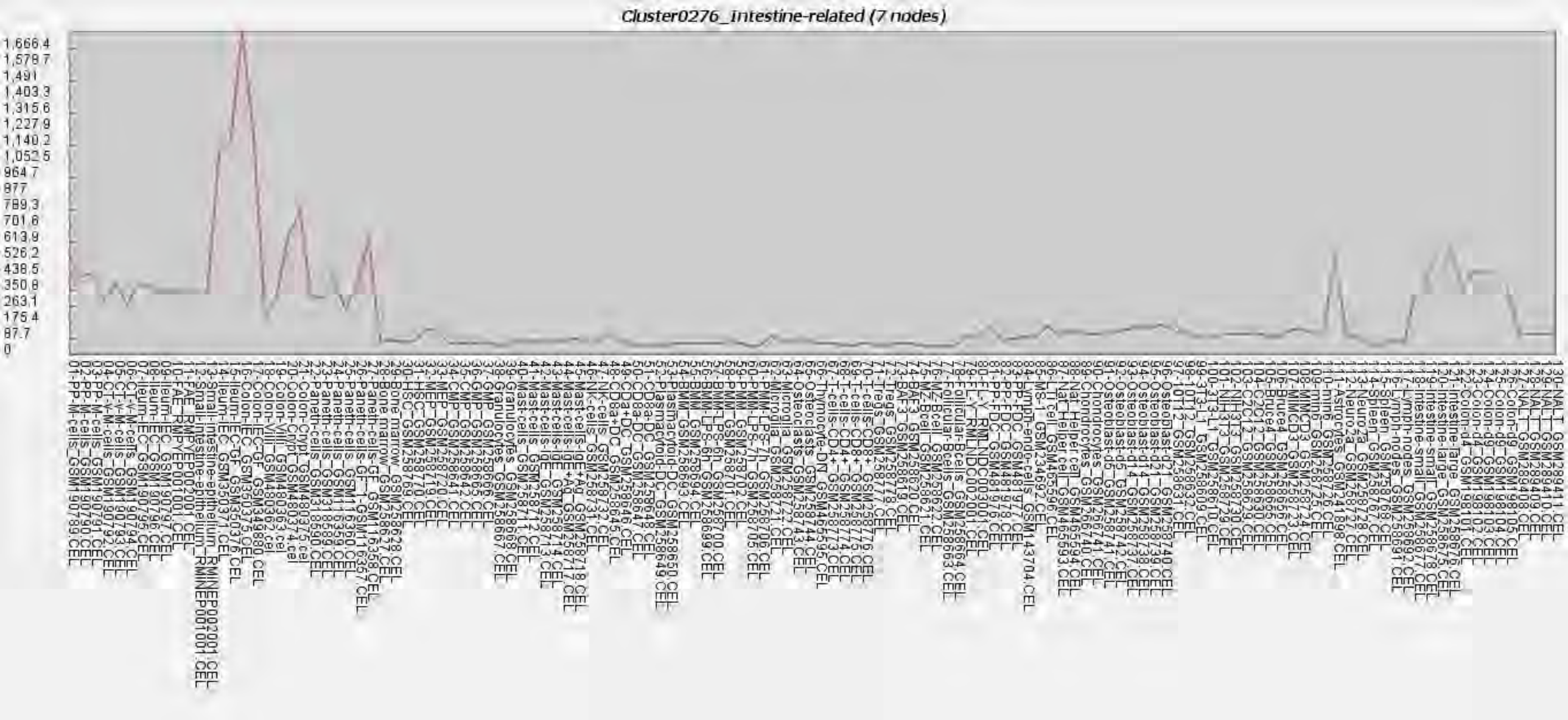

Cluster0271_Uncertain (8 nodes)
184.1
174.4
164.7
155
145.4
135.7
126
116.3
106.6
96.9
87.2
77.5
67.8
58.1
48.5
38.8
29.1
19.4
9.7
0

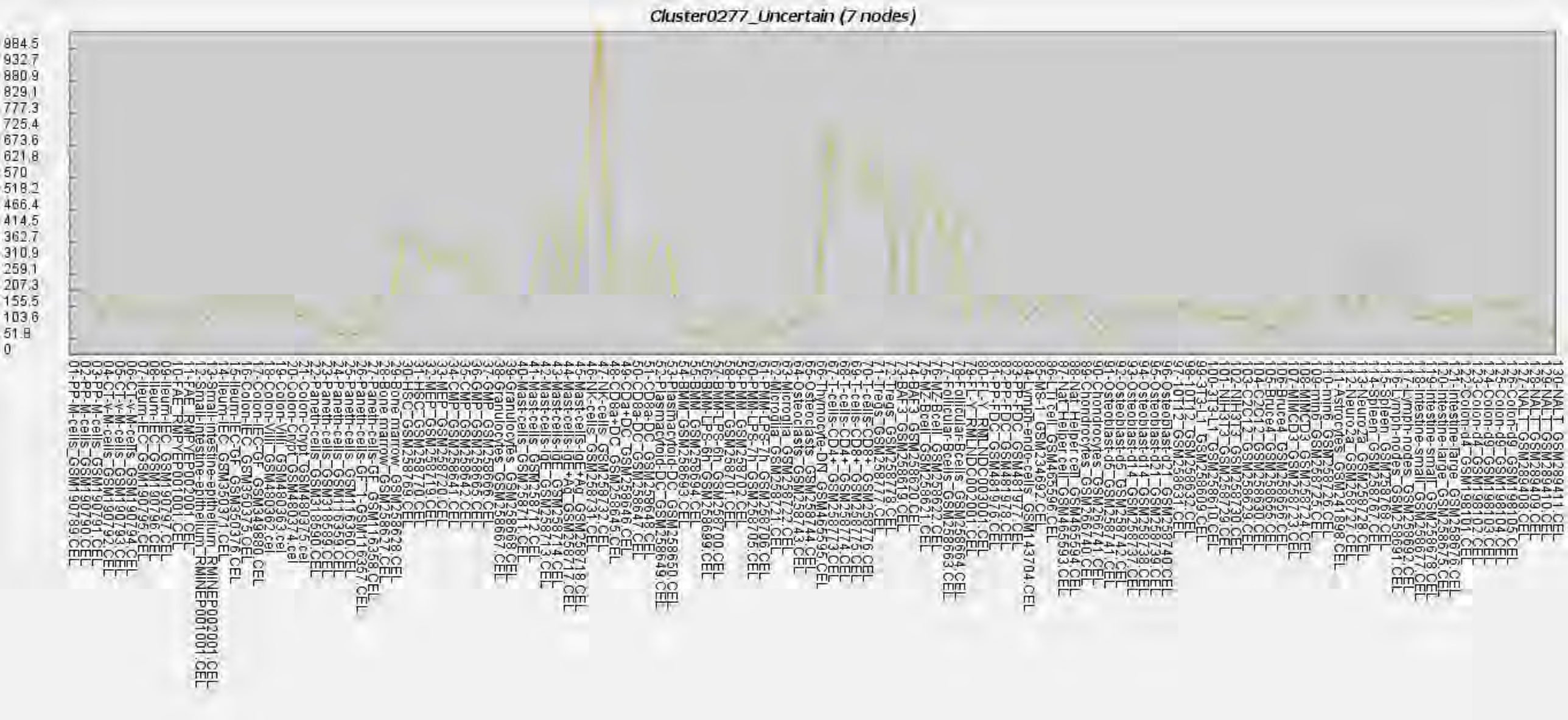

Cluster0272_High in mast cells and phagocytes (8 nodes)
4,831.1
4,576.8
4,322.5
4,068.3
3,814
3,559.7
3,305.5
3,051.2
2,796.9
2,542.7
2,288.4
2,034.1
1,779.9
1,525.6
1,271.3
1,017.1
762.8
508.5
254.3
0

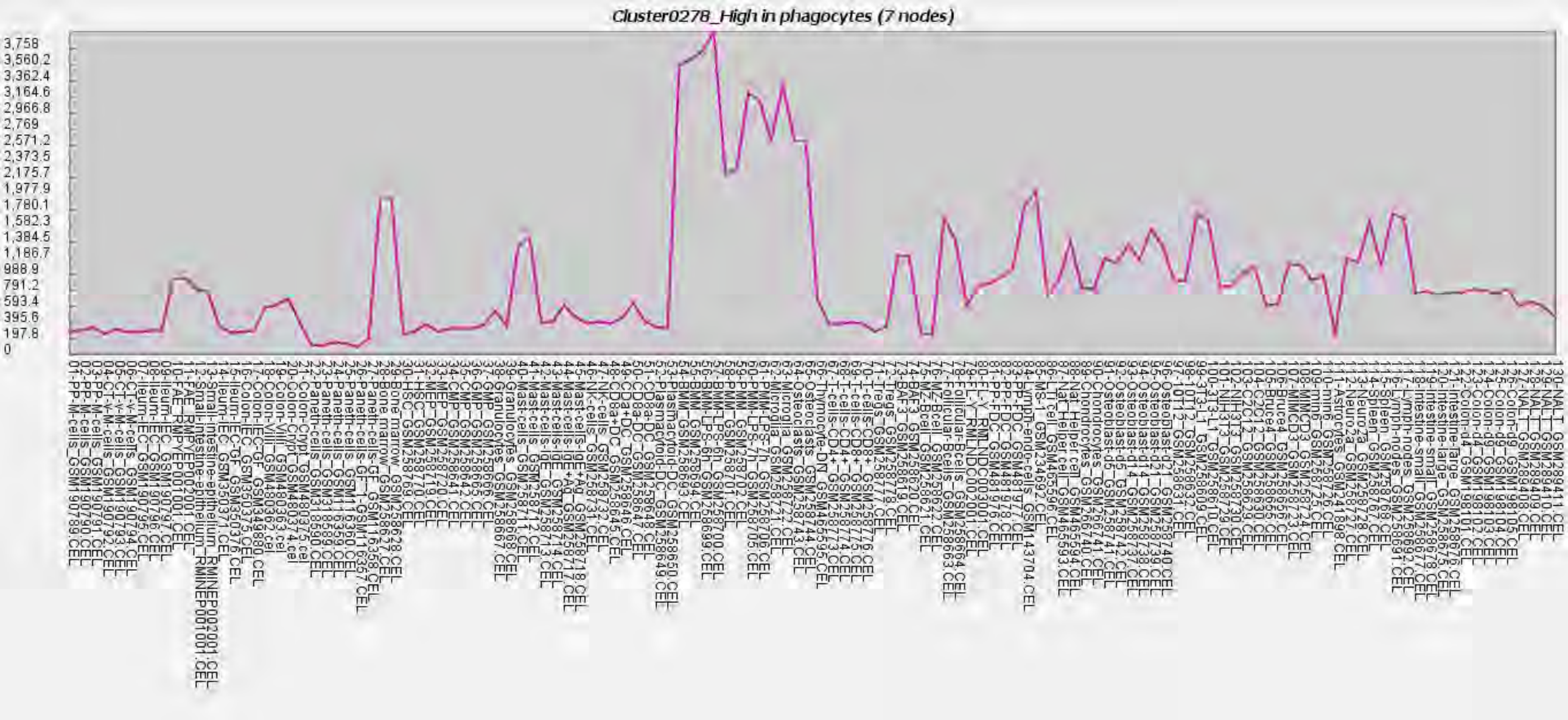

Cluster0273_Phagocyte-related (8 nodes)
3,129.7
2,965
2,800.3
2,635.6
2,470.9
2,306.1
2,141.4
1,976.7
1,812
1,647.2
1,482.5
1,317.8
1,153.1
988.3
823.6
658.9
494.2
329.4
164.7
0

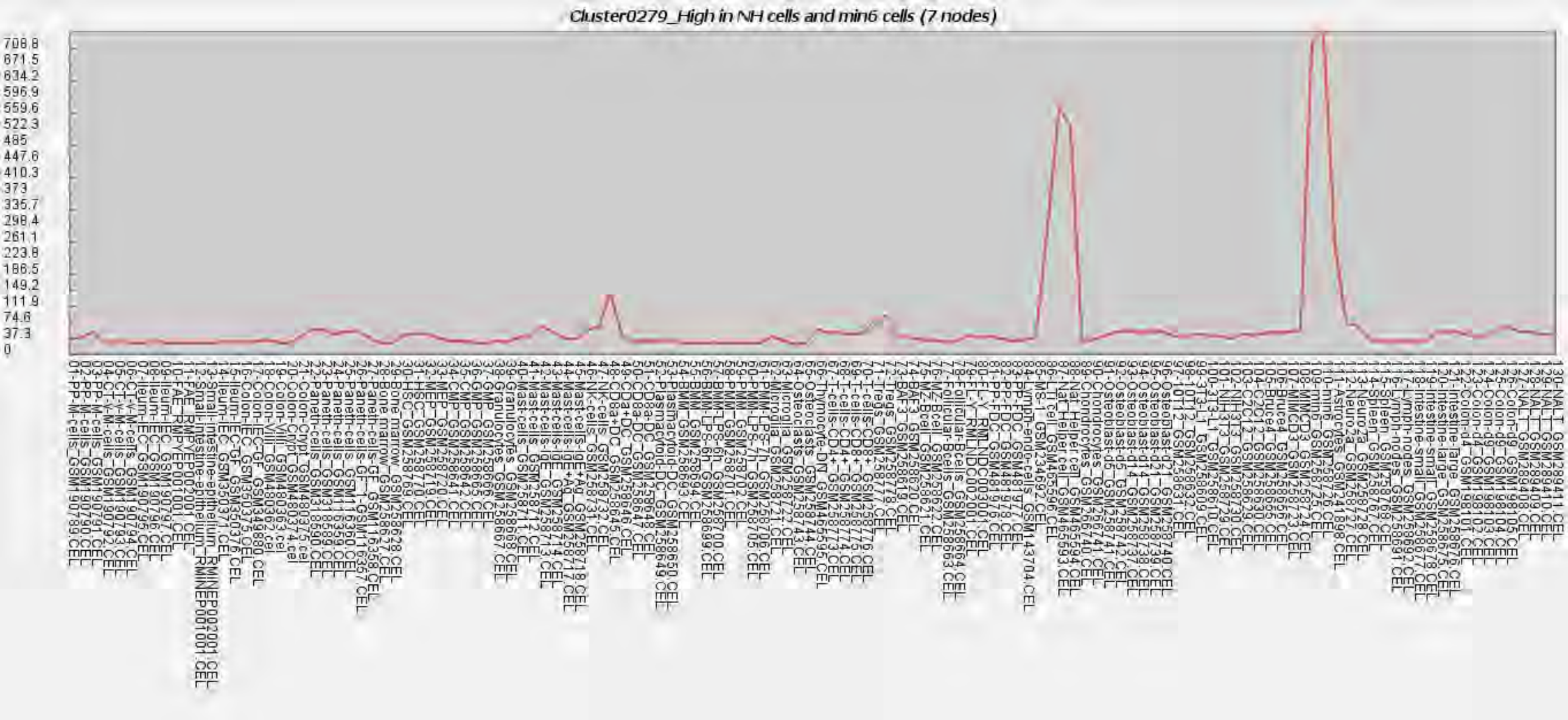
Cluster0274_Uncertain (8 nodes)
1,383.7
1,310.9
1,238.1
1,165.2
1,092.4
1,019.6
946.8
873.9
801.1
728.3
655.5
582.6
509.8
437
364.1
291.3
218.5
145.7
72.8
0

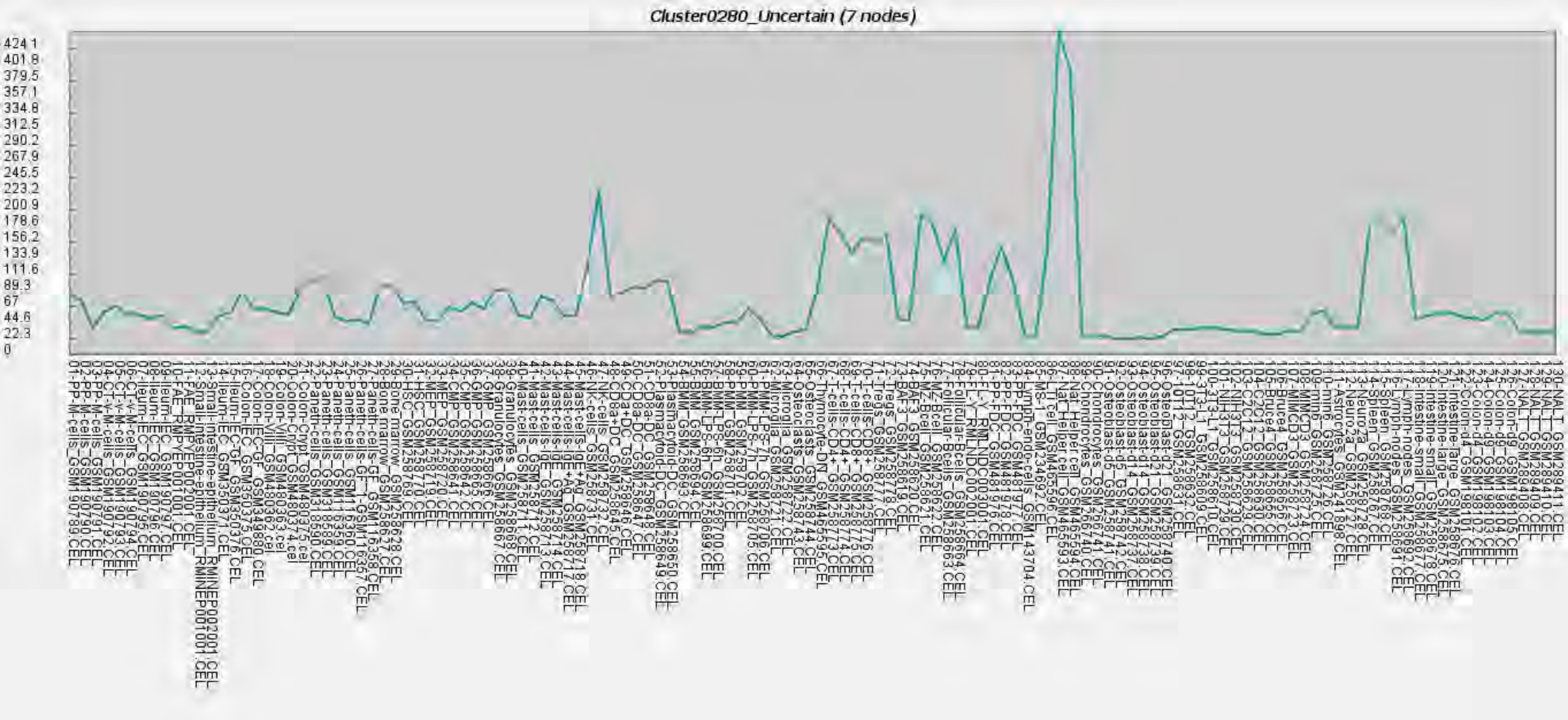

Cluster0275_Uncertain (8 nodes)
395.7
374.8
354
333.2
312.4
291.5
270.7
249.9
229.1
208.2
187.4
166.6
145.8
124.9
104.1
83.3
62.5
41.6
20.8
0

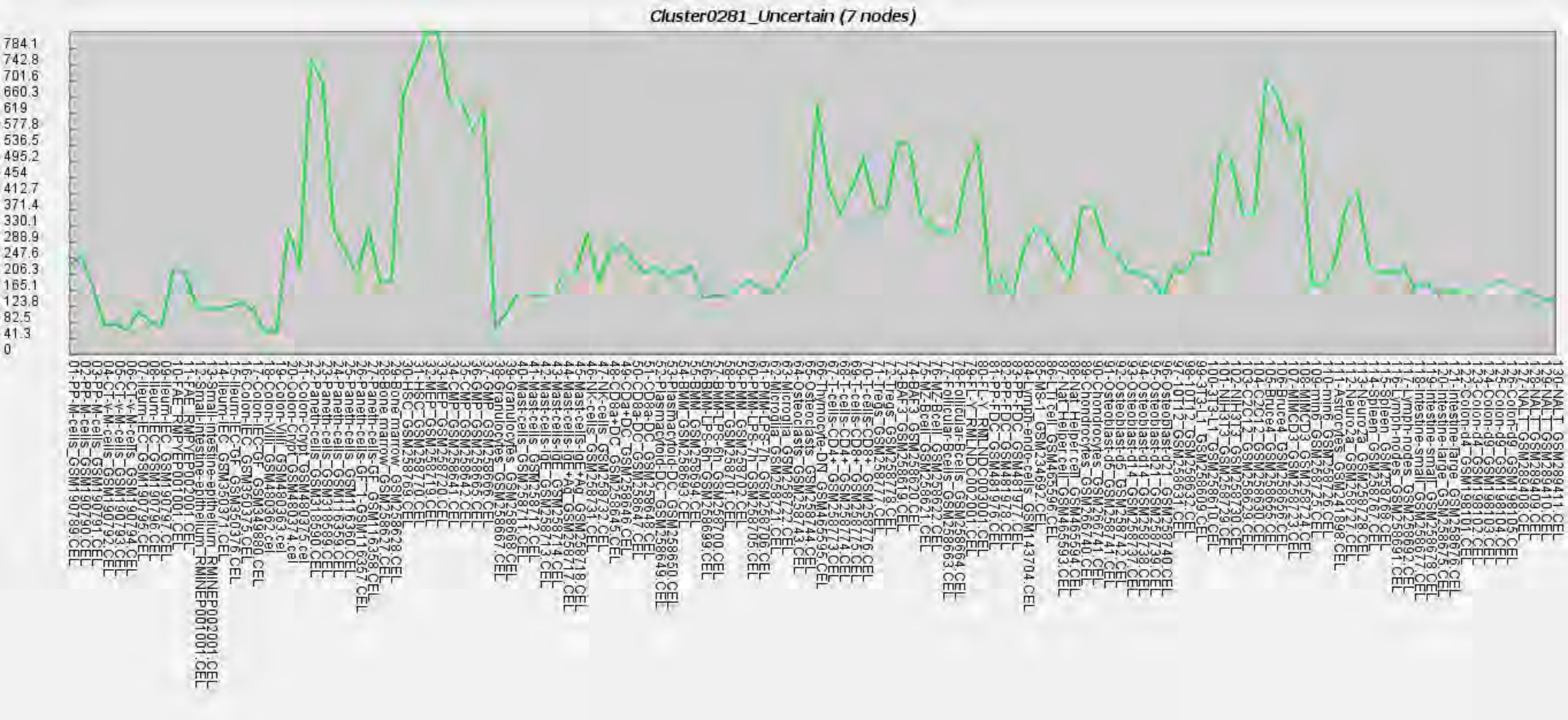

Cluster0276_Intestine-related (7 nodes)
1,666.4
1,578.7
1,491
1,403.3
1,315.6
1,227.9
1,140.2
1,052.5
964.7
877
789.3
701.6
613.9
526.2
438.5
350.8
263.1
175.4
87.7
0

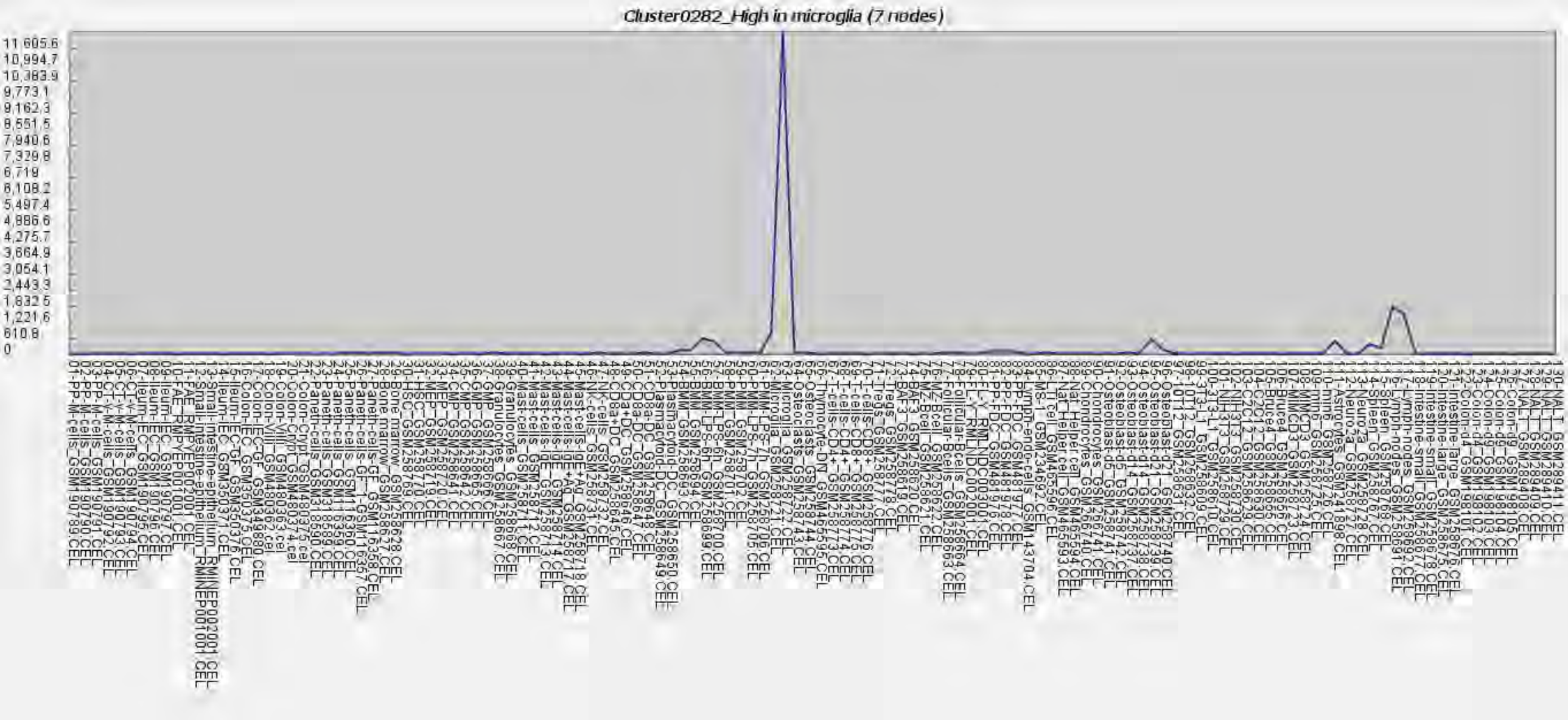

Cluster0277_Uncertain (7 nodes)
984.5
932.7
880.9
829.1
777.3
725.4
673.6
621.8
570
518.2
466.4
414.5
362.7
310.9
259.1
207.3
155.5
103.6
51.8
0

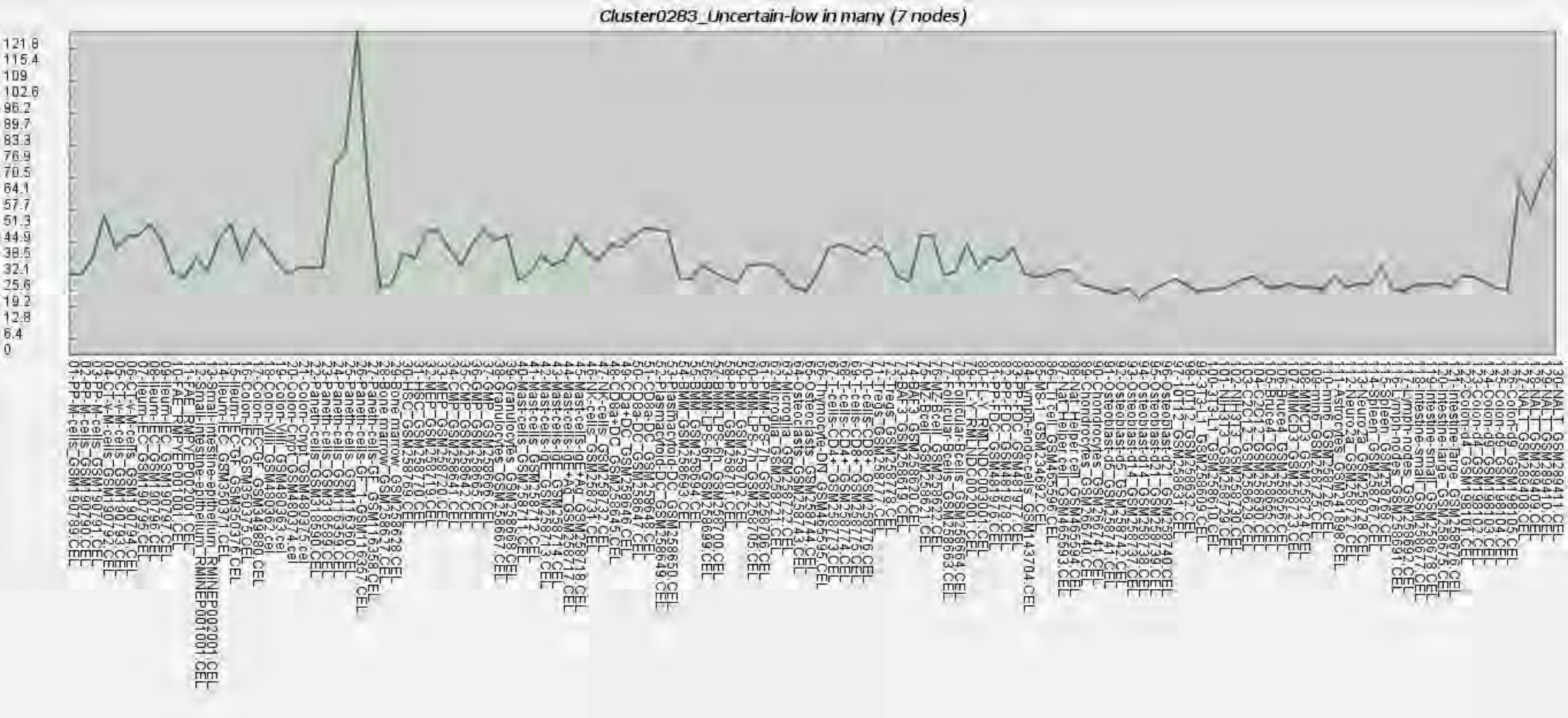

Cluster0278_High in phagocytes (7 nodes)
3,758
3,560.2
3,362.4
3,164.6
2,966.8
2,769
2,571.2
2,373.5
2,175.7
1,977.9
1,780.1
1,582.3
1,384.5
1,186.7
988.9
791.2
593.4
395.6
197.8
0

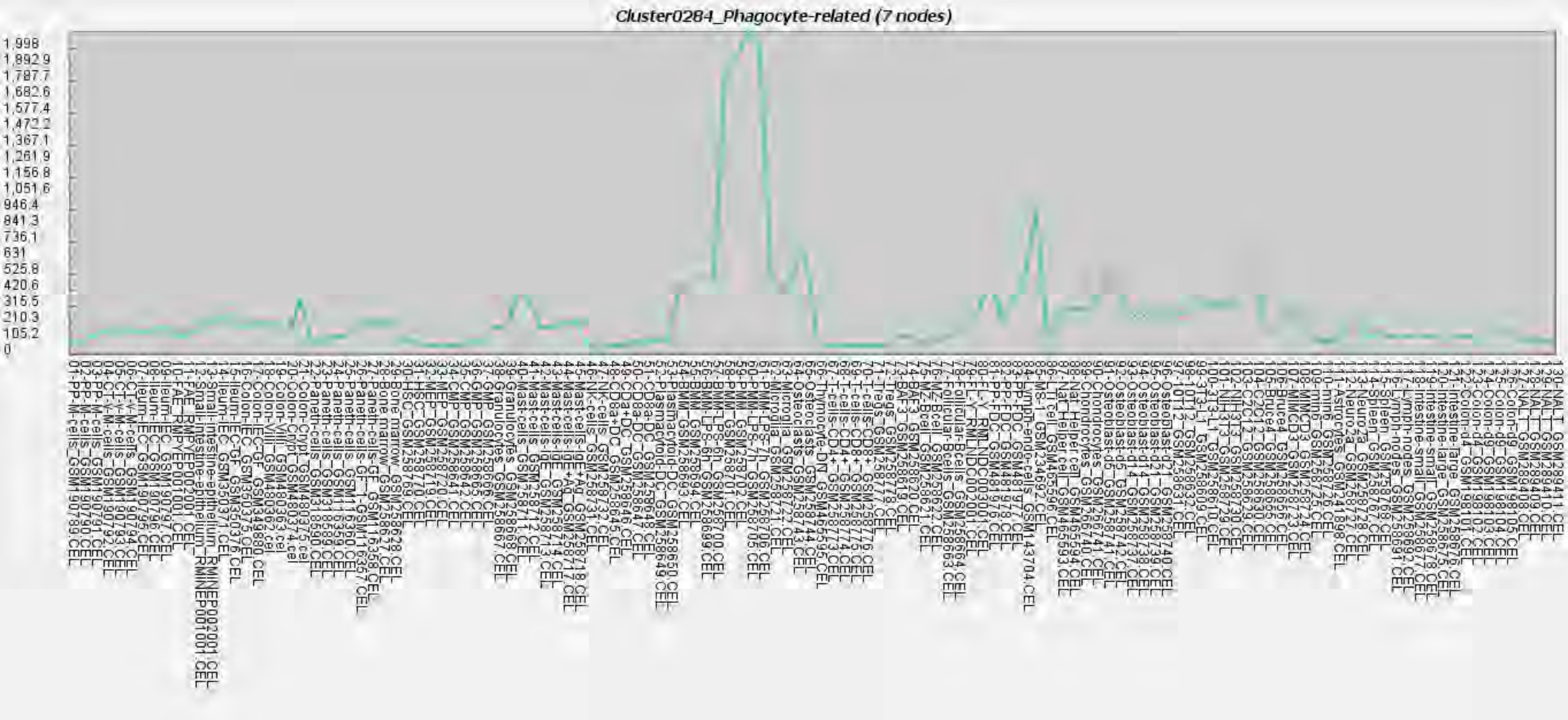

Cluster0279_High in NH cells and min6 cells (7 nodes)
708.8
671.5
634.2
596.9
559.6
522.3
485
447.6
410.3
373
335.7
298.4
261.1
223.8
186.5
149.2
111.9
74.6
37.3
0

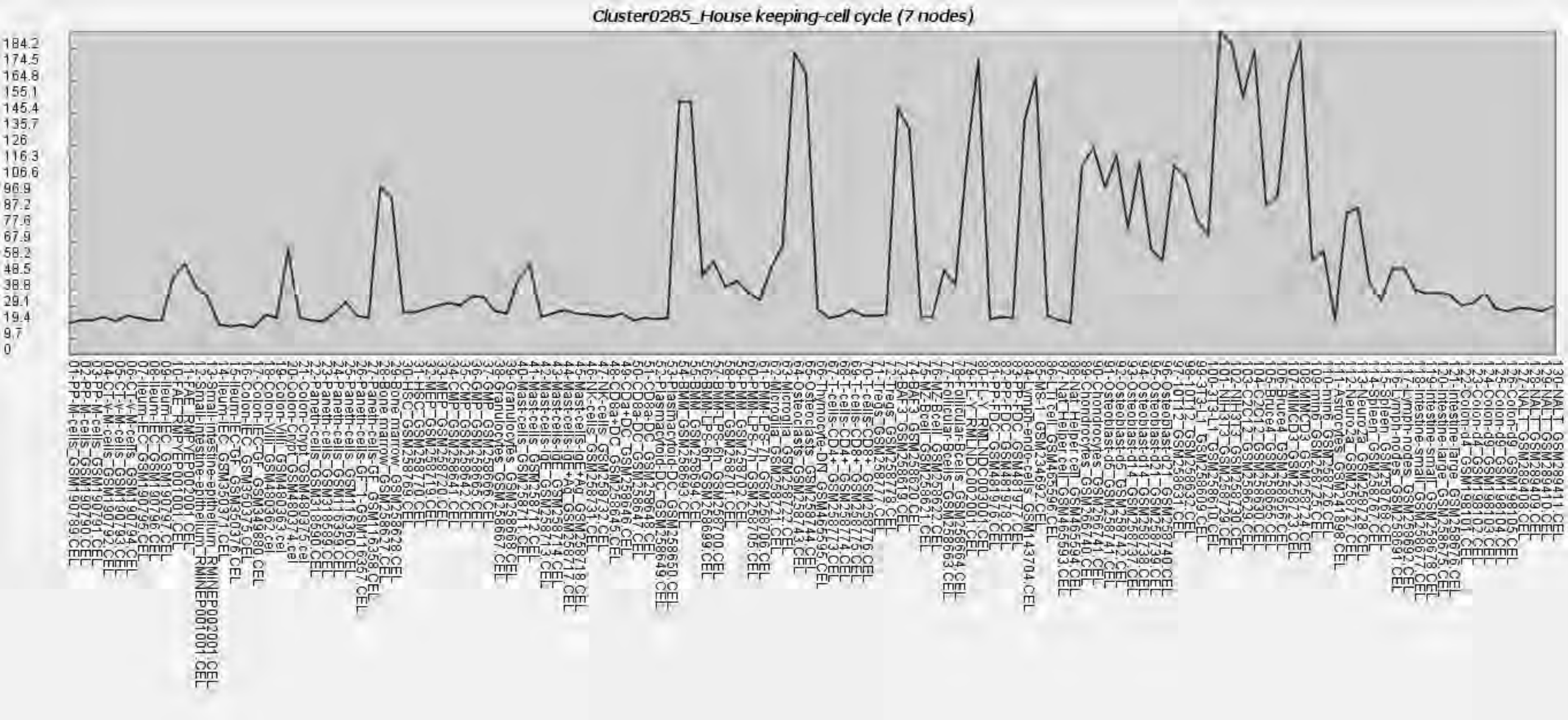

Cluster0280_Uncertain (7 nodes)
424.1
401.8
379.5
357.1
334.8
312.5
290.2
267.9
245.5
223.2
200.9
178.6
156.2
133.9
111.6
89.3
67
44.6
22.3
0

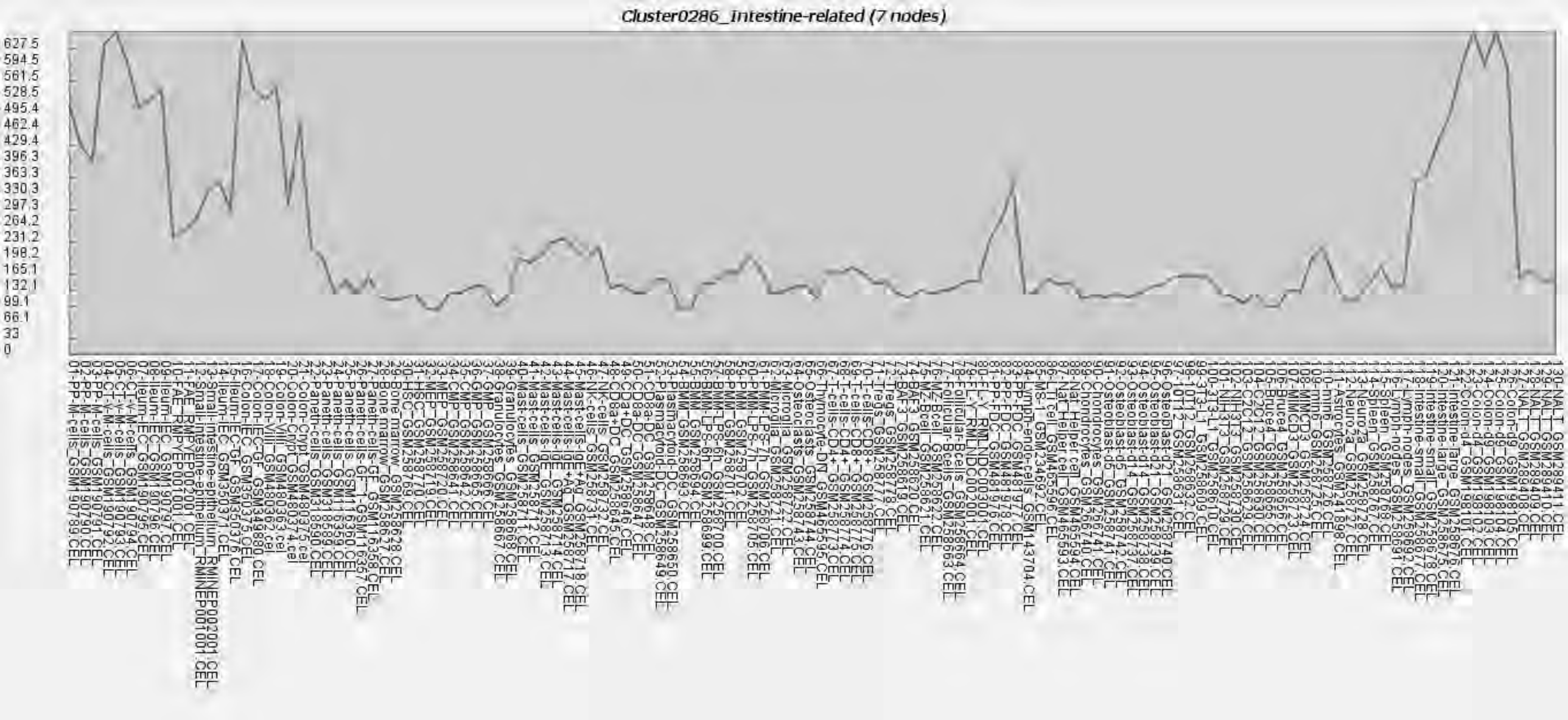

Cluster0281_Uncertain (7 nodes)
784.1
742.8
701.6
660.3
619
577.8
536.5
495.2
454
412.7
371.4
330.1
288.9
247.6
206.3
165.1
123.8
82.5
41.3
0

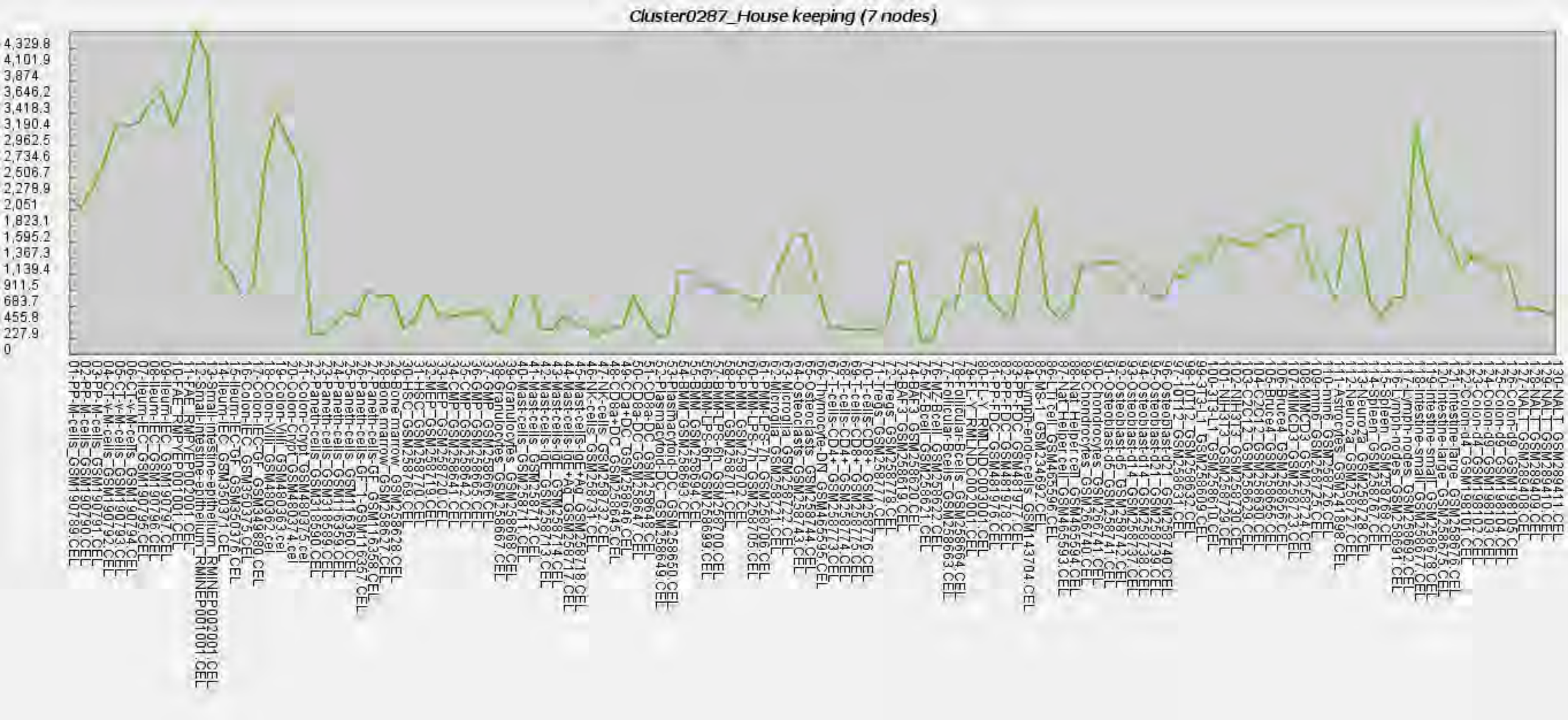

Cluster0282_High in microglia (7 nodes)
11,605.6
10,994.7
10,383.9
9,773.1
9,162.3
8,551.5
7,940.6
7,329.8
6,719
6,108.2
5,497.4
4,886.6
4,275.7
3,664.9
3,054.1
2,443.3
1,832.5
1,221.6
610.8
0

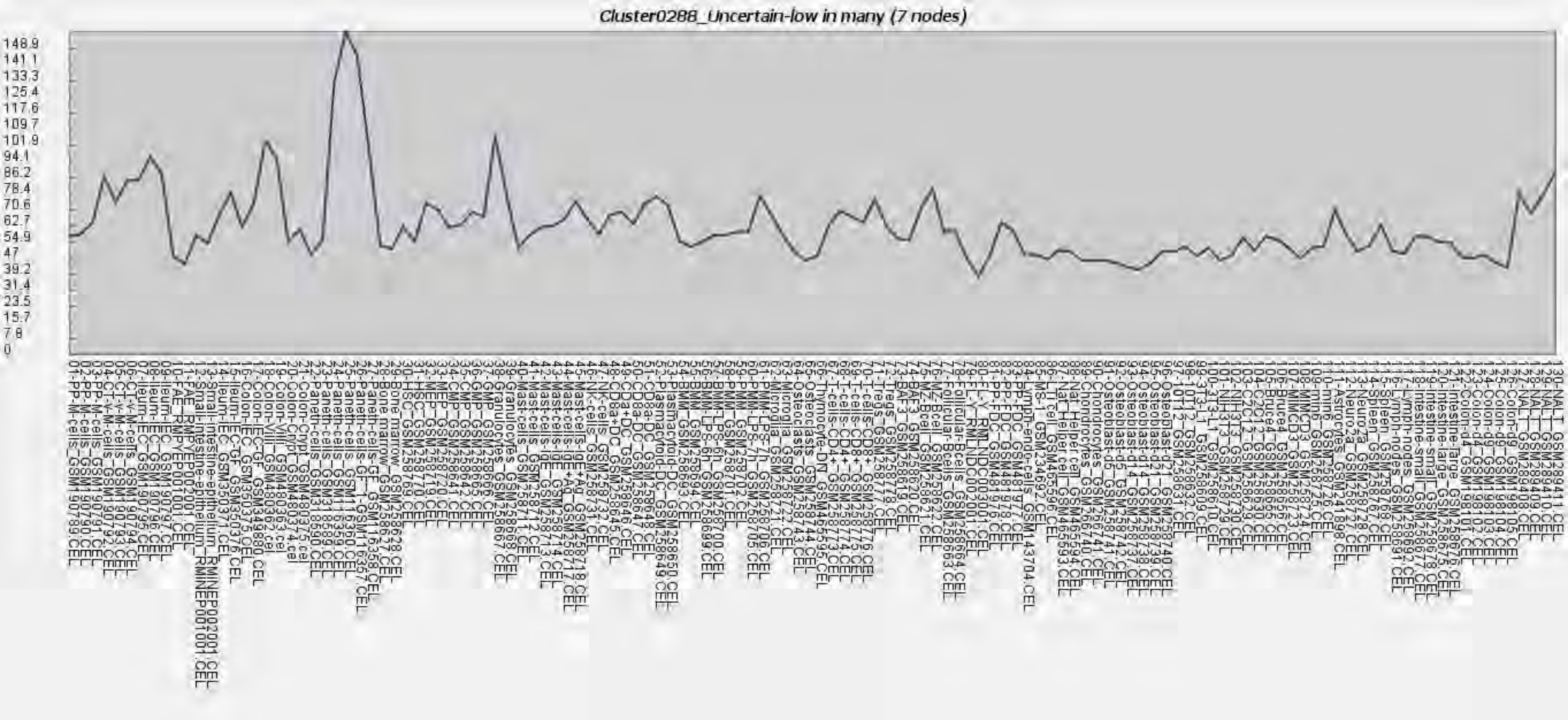

Cluster0283_Uncertain-low in many (7 nodes)
121.8
115.4
109
102.6
96.2
89.7
83.3
76.9
70.5
64.1
57.7
51.3
44.9
38.5
32.1
25.6
19.2
12.8
6.4
0

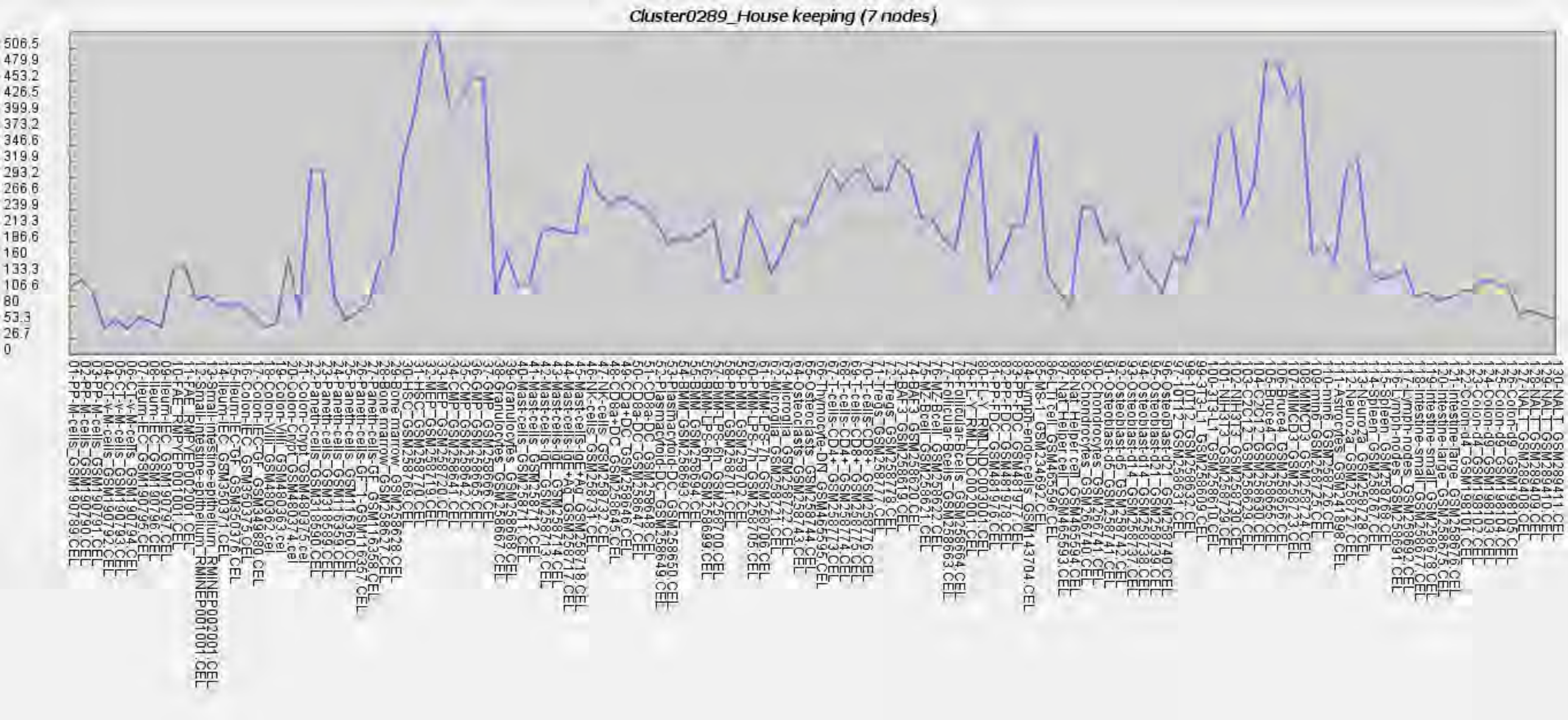

Cluster0284_Phagocyte-related (7 nodes)
1,998
1,892.9
1,787.7
1,682.6
1,577.4
1,472.2
1,367.1
1,261.9
1,156.8
1,051.6
946.4
841.3
736.1
631
525.8
420.6
315.5
210.3
105.2
0

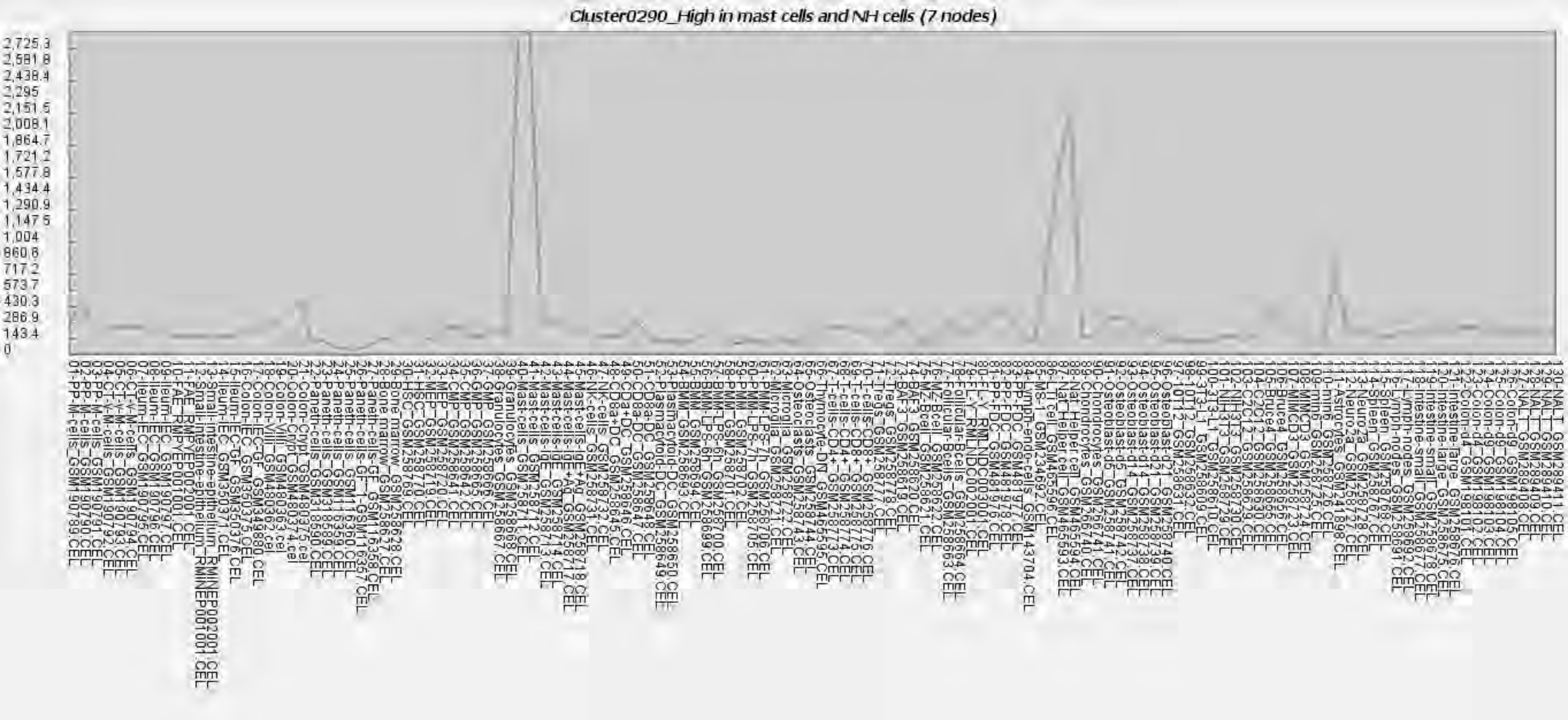

Cluster0285_House keeping-cell cycle (7 nodes)
184.2
174.5
164.8
155.1
145.4
135.7
126
116.3
106.6
96.9
87.2
77.6
67.9
58.2
48.5
38.8
29.1
19.4
9.7
0

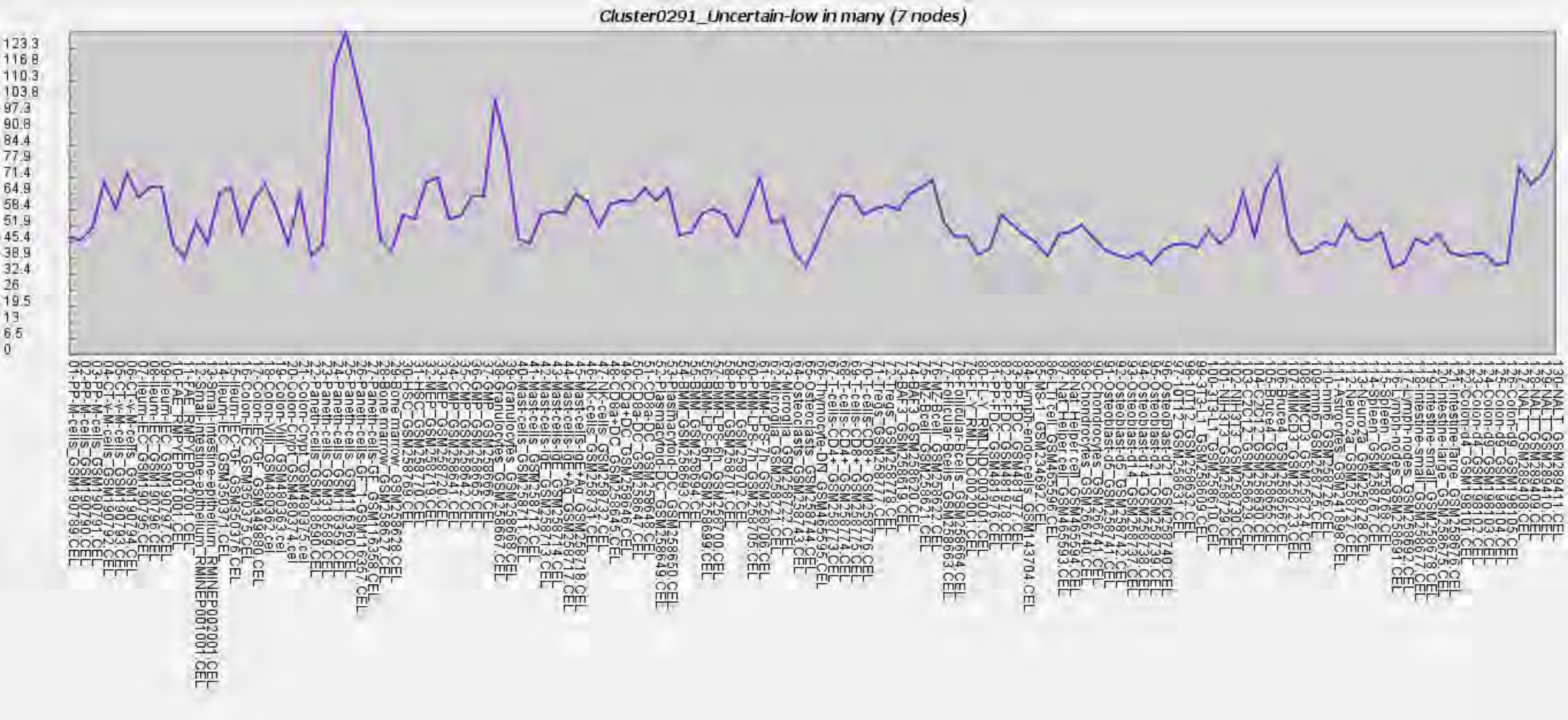

Cluster0286_Intestine-related (7 nodes)
627.5
594.5
561.5
528.5
495.4
462.4
429.4
396.3
363.3
330.3
297.3
264.2
231.2
198.2
165.1
132.1
99.1
66.1
33
0

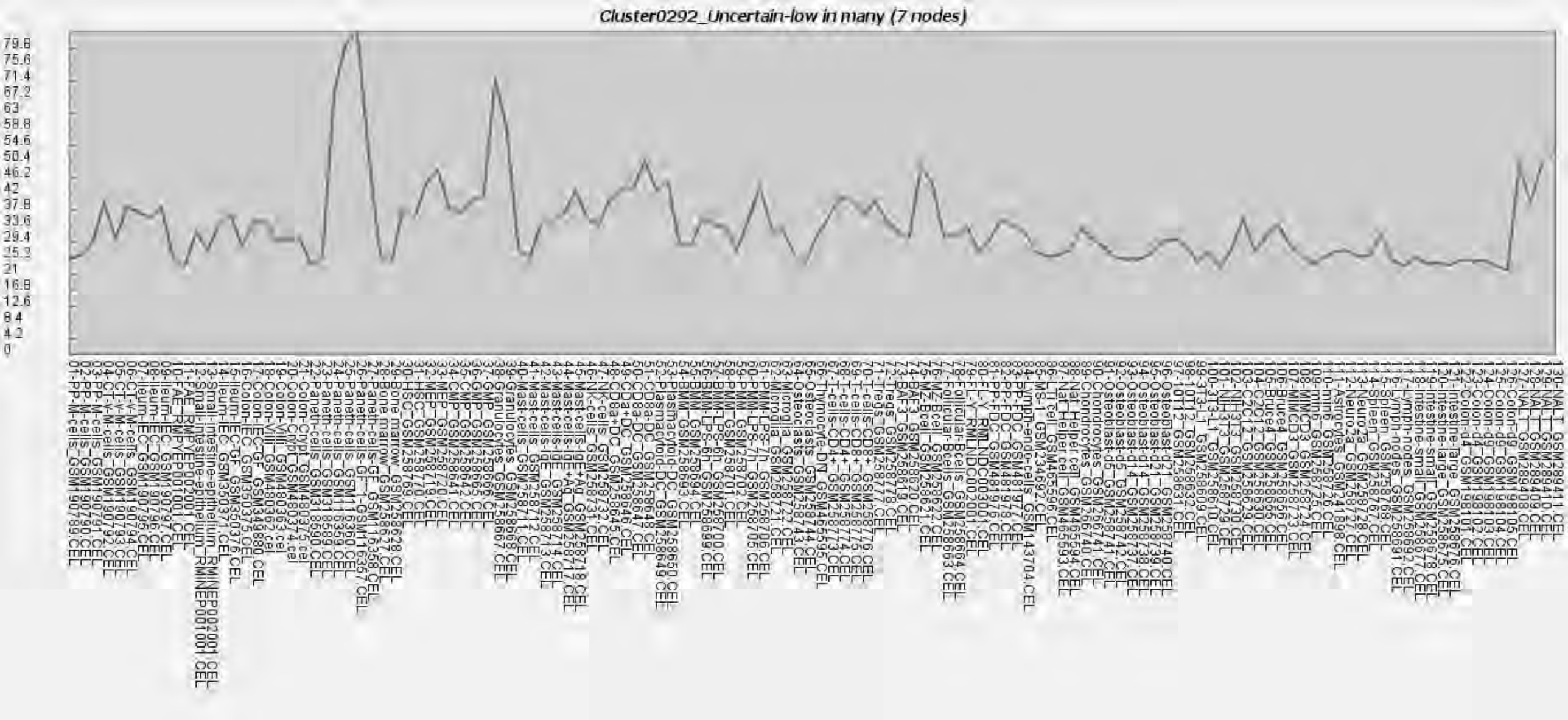

Cluster0287_House keeping (7 nodes)
4,329.8
4,101.9
3,874
3,646.2
3,418.3
3,190.4
2,962.5
2,734.6
2,506.7
2,278.9
2,051
1,823.1
1,595.2
1,367.3
1,139.4
911.5
683.7
455.8
227.9
0


Cluster0288_Uncertain-low in many (7 nodes)
148.9
141.1
133.3
125.4
117.6
109.7
101.9
94.1
86.2
78.4
70.6
62.7
54.9
47
39.2
31.4
23.5
15.7
7.8
0

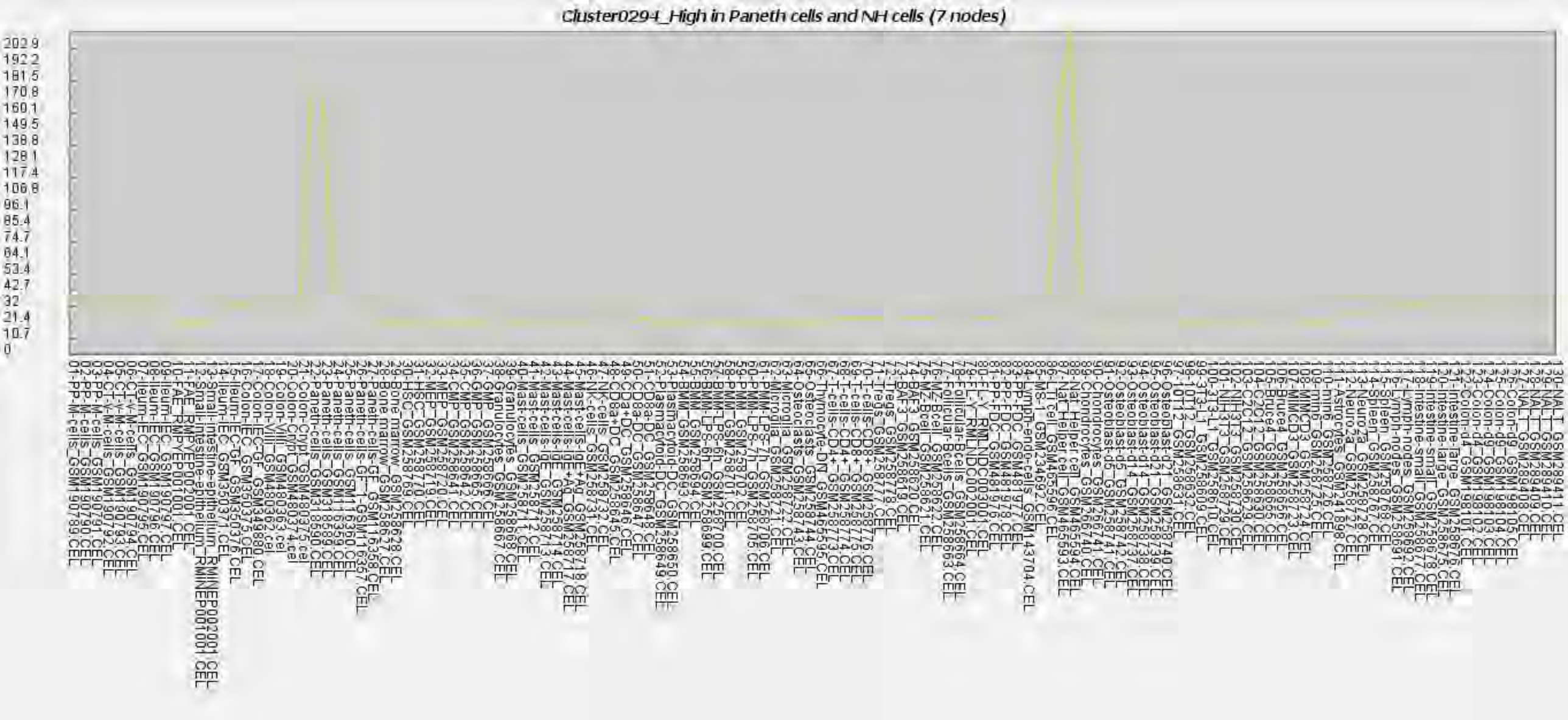

Cluster0289_House keeping (7 nodes)
506.5
479.9
453.2
426.5
399.9
373.2
346.6
319.9
293.2
266.6
239.9
213.3
186.6
160
133.3
106.6
80
53.3
26.7
0

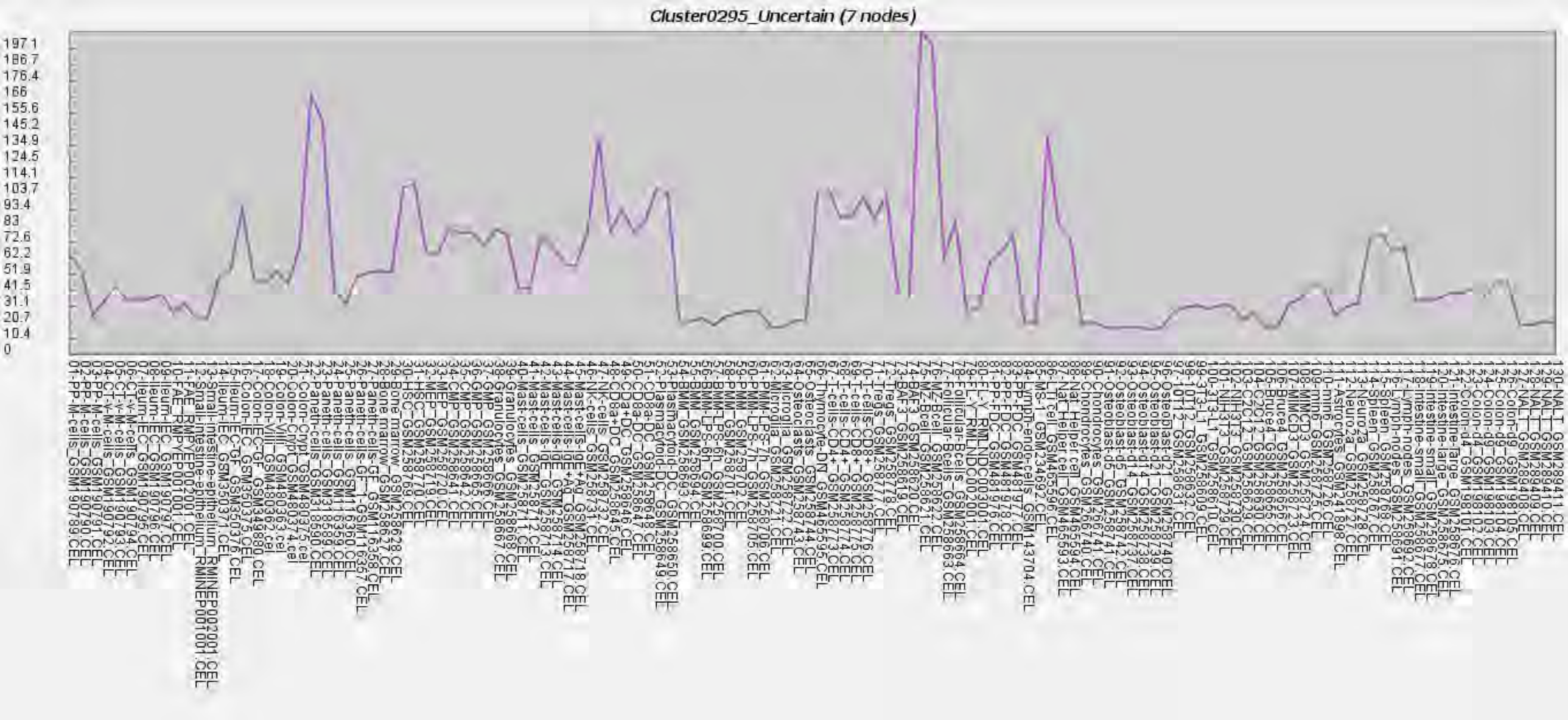

Cluster0290_High in mast cells and NH cells (7 nodes)
2,725.3
2,581.8
2,438.4
2,295
2,151.5
2,008.1
1,864.7
1,721.2
1,577.8
1,434.4
1,290.9
1,147.5
1,004
860.6
717.2
573.7
430.3
286.9
143.4
0

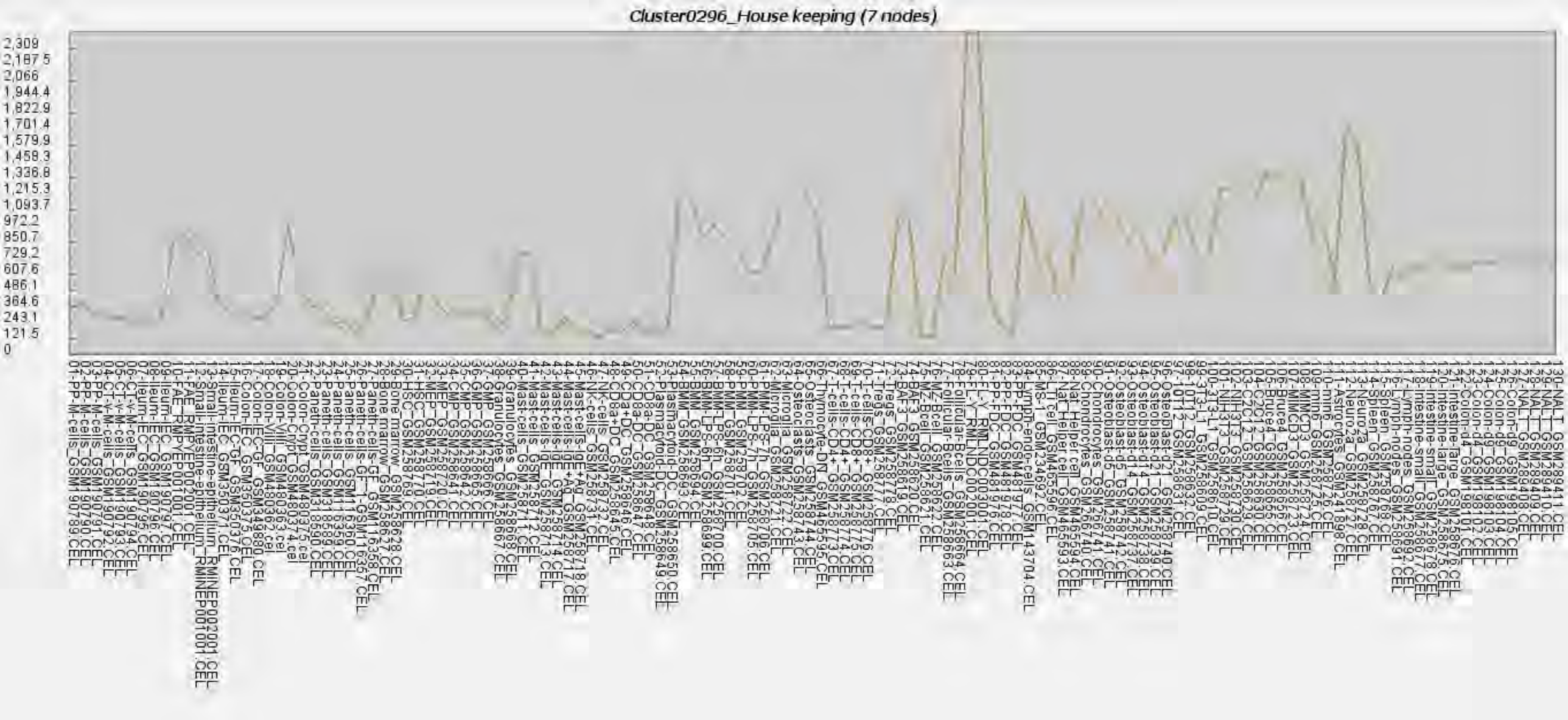

Cluster0291_Uncertain-low in many (7 nodes)
123.3
116.8
110.3
103.8
97.3
90.8
84.4
77.9
71.4
64.9
58.4
51.9
45.4
38.9
32.4
26
19.5
13
6.5
0

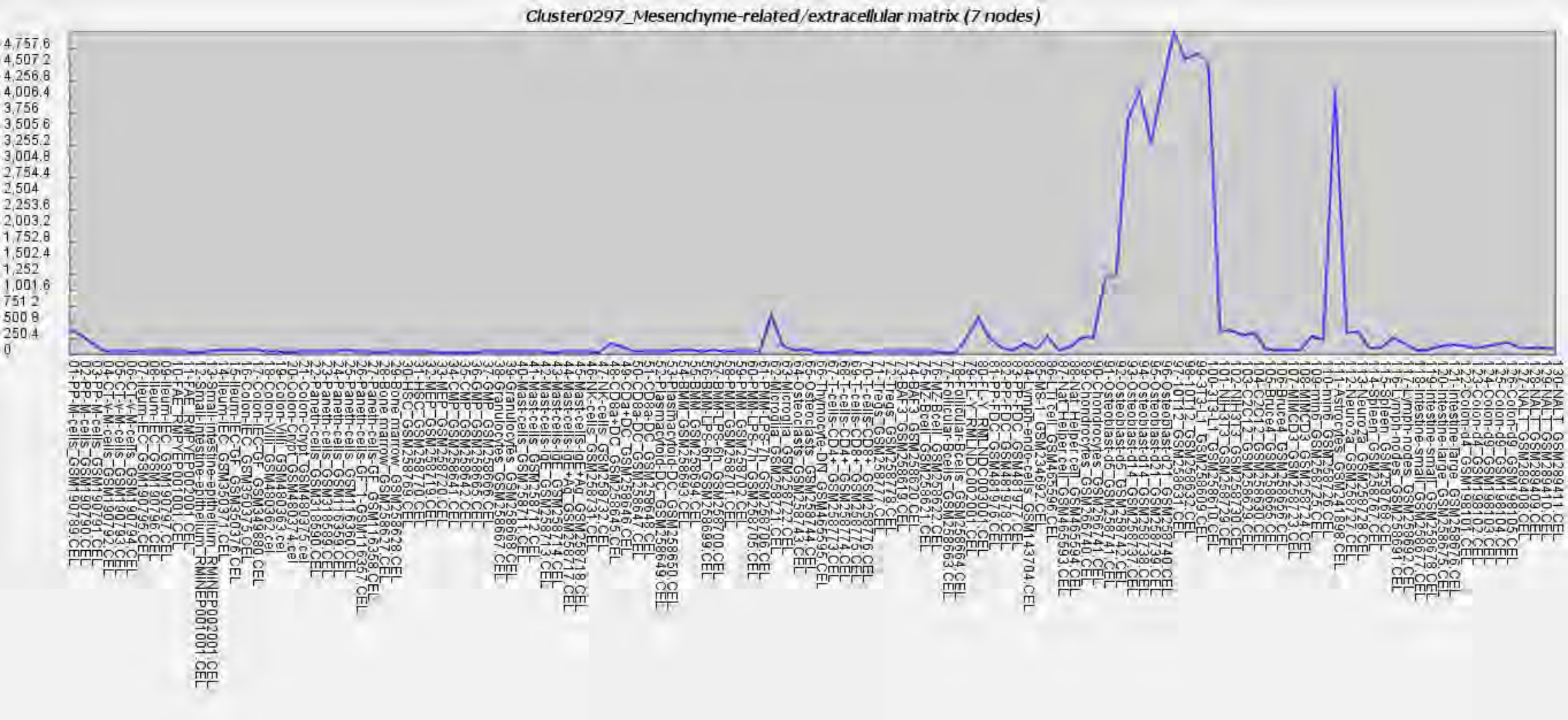

Cluster0292_Uncertain-low in many (7 nodes)
79.8
75.6
71.4
67.2
63
58.8
54.6
50.4
46.2
42
37.8
33.6
29.4
25.2
21
16.8
12.6
8.4
4.2
0

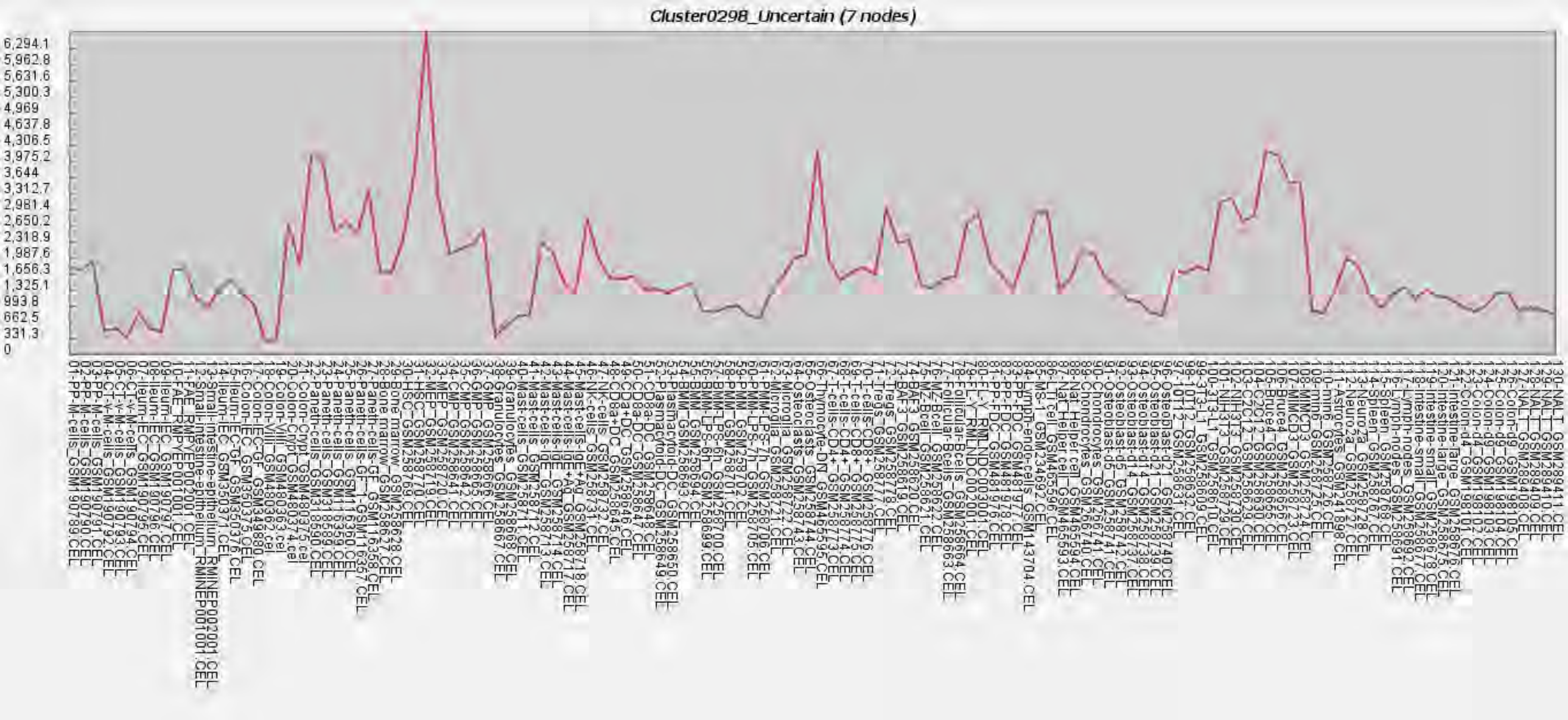
Cluster0293_House keeping (7 nodes)
13,695
12,974.2
12,253.4
11,532.6
10,811.8
10,091
9,370.3
8,649.5
7,928.7
7,207.9
6,487.1
5,766.3
5,045.5
4,324.7
3,603.9
2,883.2
2,162.4
1,441.6
720.8
0


Cluster0294_High in Paneth cells and NH cells (7 nodes)
202.9
192.2
181.5
170.8
160.1
149.5
138.8
128.1
117.4
106.8
96.1
85.4
74.7
64.1
53.4
42.7
32
21.4
10.7
0

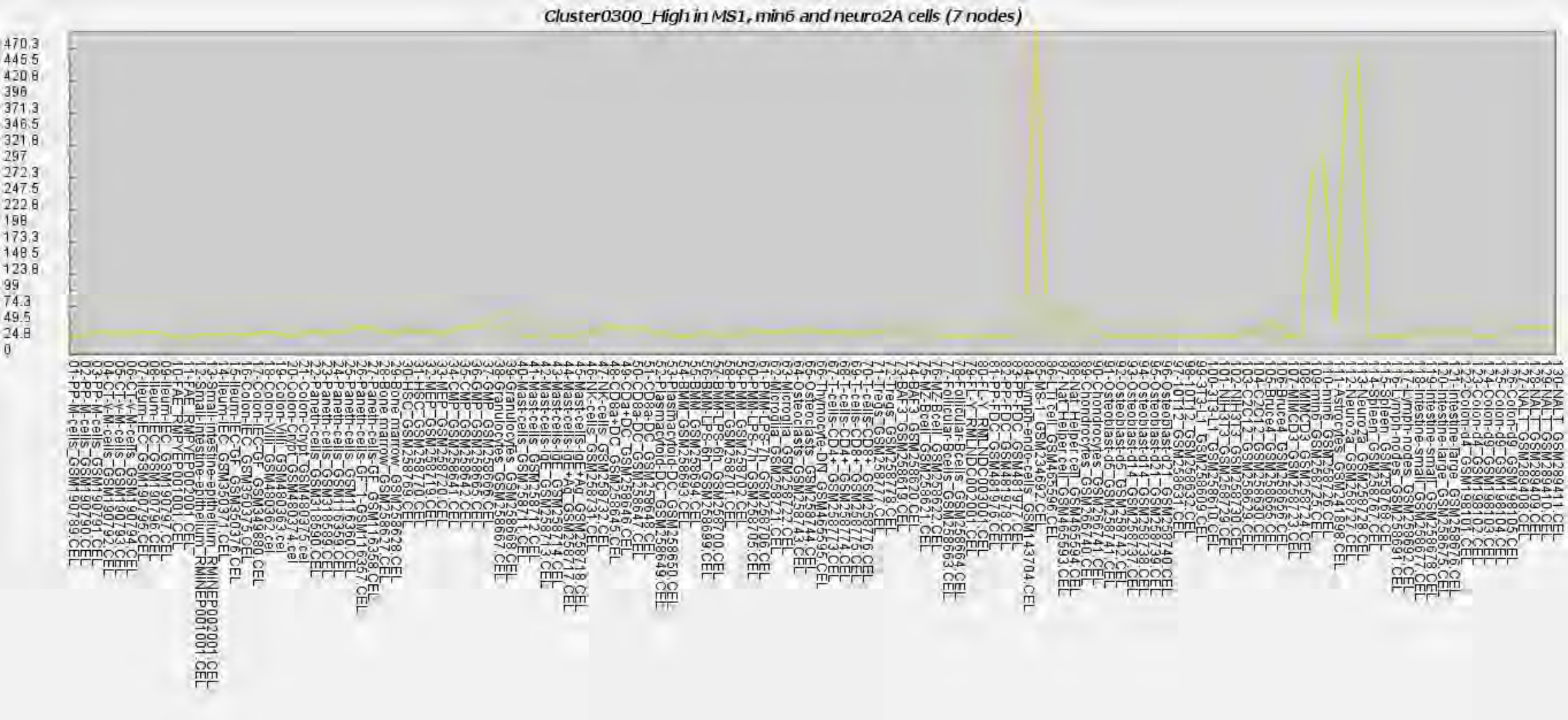

Cluster0295_Uncertain (7 nodes)
197.1
186.7
176.4
166
155.6
145.2
134.9
124.5
114.1
103.7
93.4
83
72.6
62.2
51.9
41.5
31.1
20.7
10.4
0

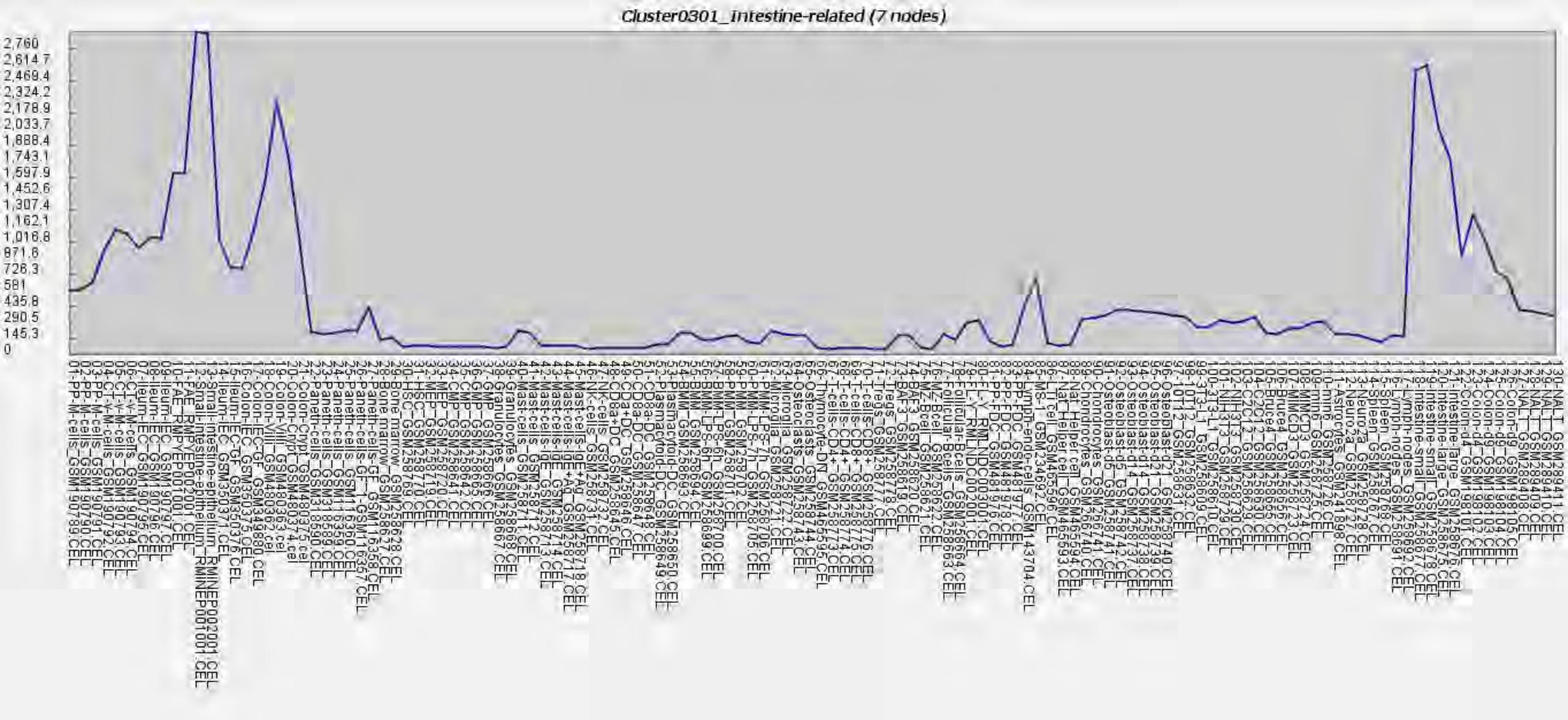

Cluster0296_House keeping (7 nodes)
2,309
2,187.5
2,066
1,944.4
1,822.9
1,701.4
1,579.9
1,458.3
1,336.8
1,215.3
1,093.7
972.2
850.7
729.2
607.6
486.1
364.6
243.1
121.5
0

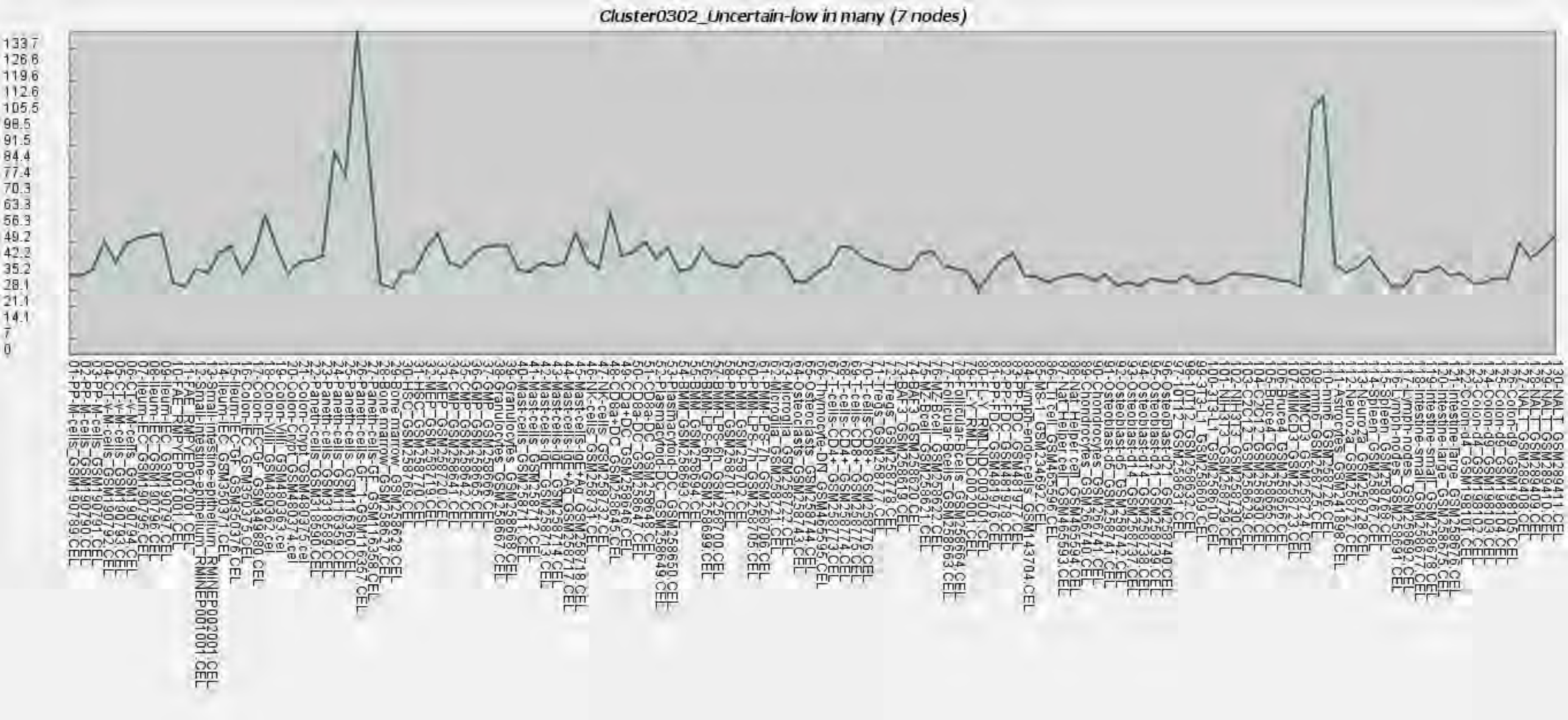

Cluster0297_Mesenchyme-related/extracellular matrix (7 nodes)
4,757.6
4,507.2
4,256.8
4,006.4
3,756
3,505.6
3,255.2
3,004.8
2,754.4
2,504
2,253.6
2,003.2
1,752.8
1,502.4
1,252
1,001.6
751.2
500.8
250.4
0

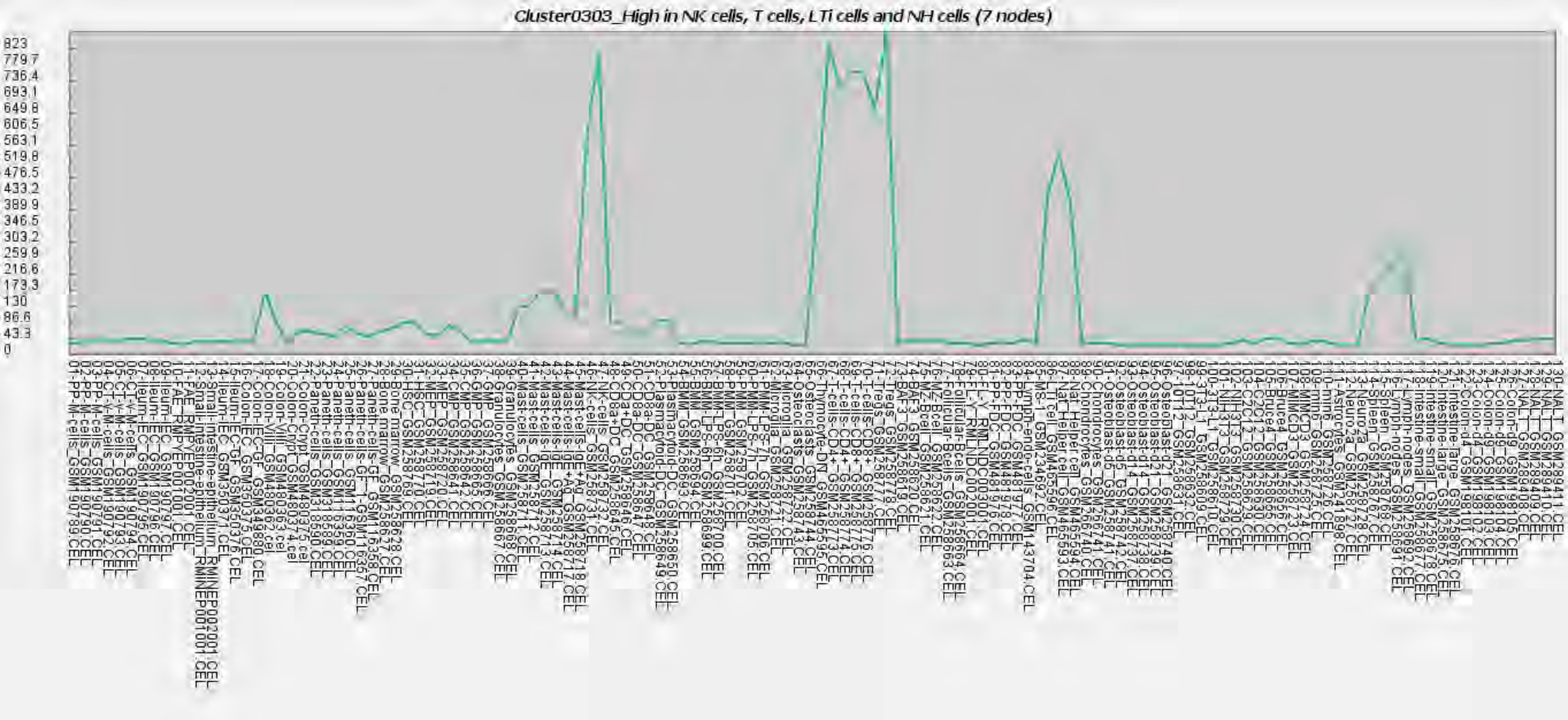

Cluster0298_Uncertain (7 nodes)
6,294.1
5,962.8
5,631.6
5,300.3
4,969
4,637.8
4,306.5
3,975.2
3,644
3,312.7
2,981.4
2,650.2
2,318.9
1,987.6
1,656.3
1,325.1
993.8
662.5
331.3
0

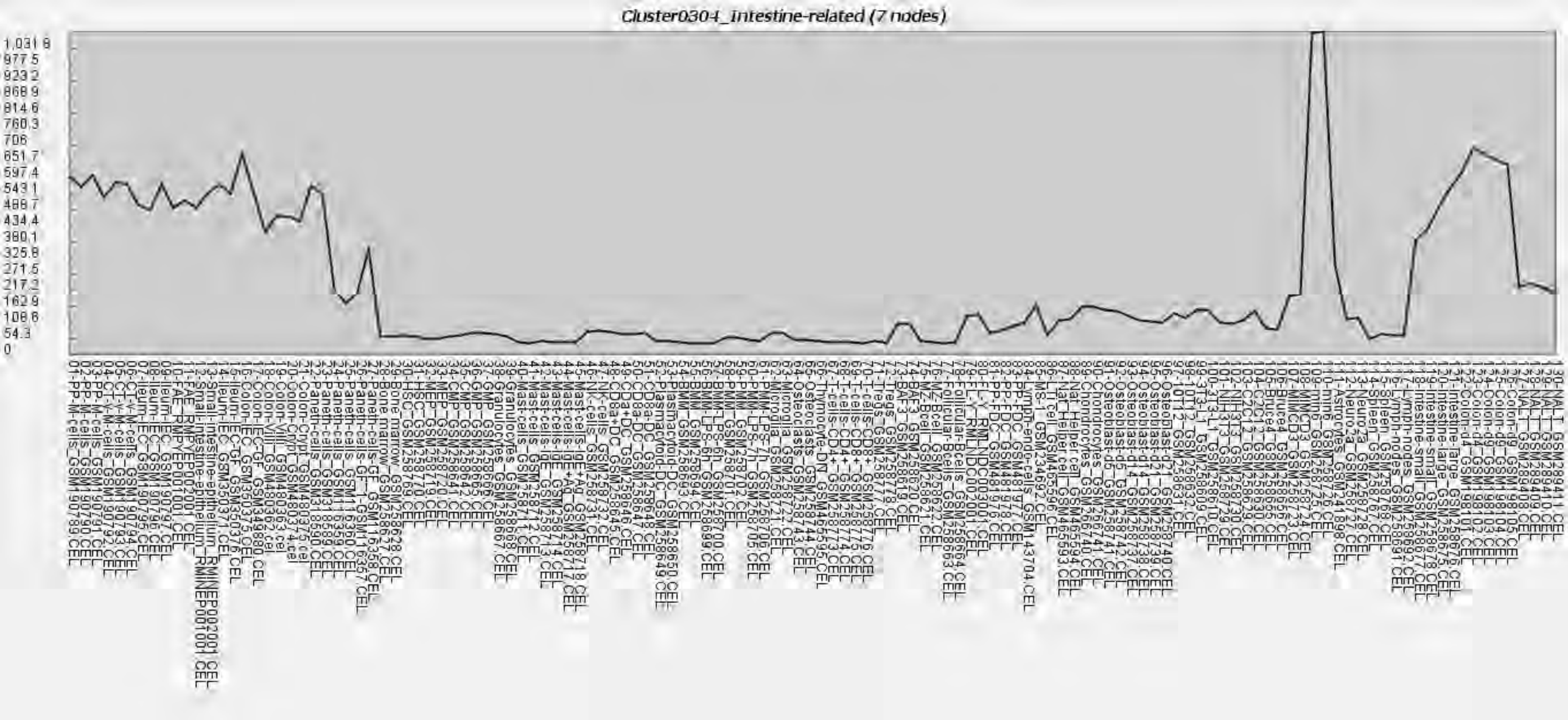
Cluster0299_Uncertain (7 nodes)
4,119.8
3,902.9
3,686.1
3,469.3
3,252.5
3,035.6
2,818.8
2,602
2,385.1
2,168.3
1,951.5
1,734.6
1,517.8
1,301
1,084.2
867.3
650.5
433.7
216.8
0

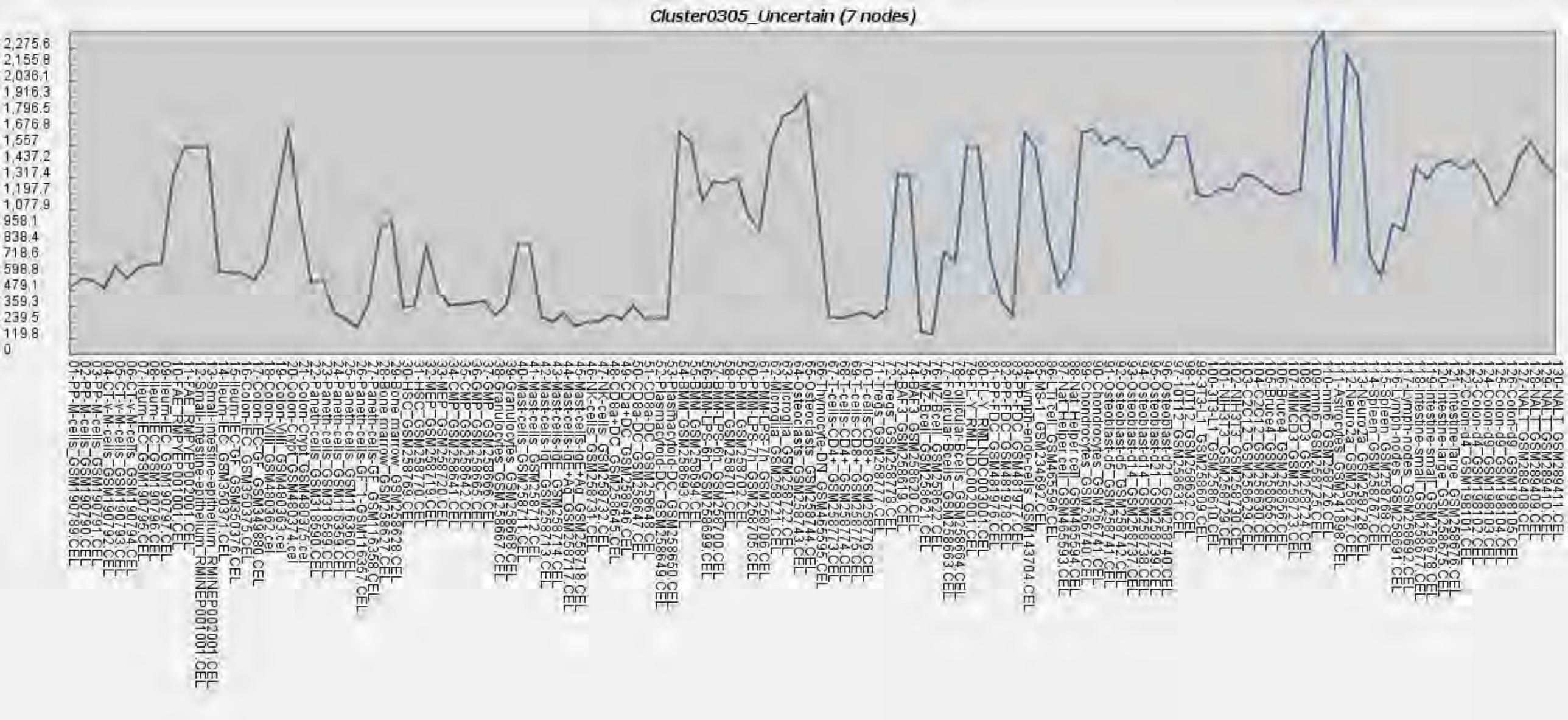

Cluster0300_High in MS1, min6 and neuro2A cells (7 nodes)
470.3
445.5
420.8
396
371.3
346.5
321.8
297
272.3
247.5
222.8
198
173.3
148.5
123.8
99
74.3
49.5
24.8
0

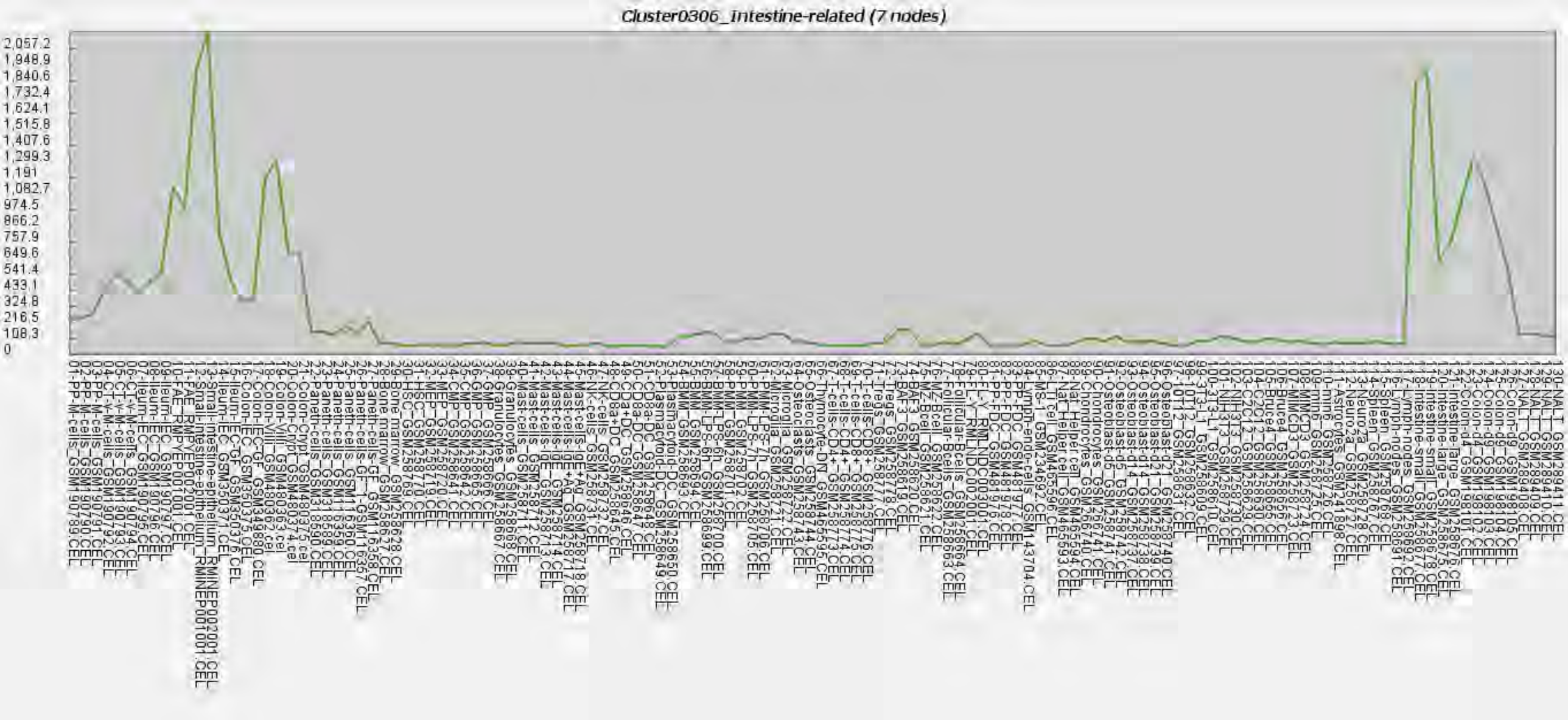

Cluster0301_Intestine-related (7 nodes)
2,760
2,614.7
2,469.4
2,324.2
2,178.9
2,033.7
1,888.4
1,743.1
1,597.9
1,452.6
1,307.4
1,162.1
1,016.8
871.6
726.3
581
435.8
290.5
145.3
0

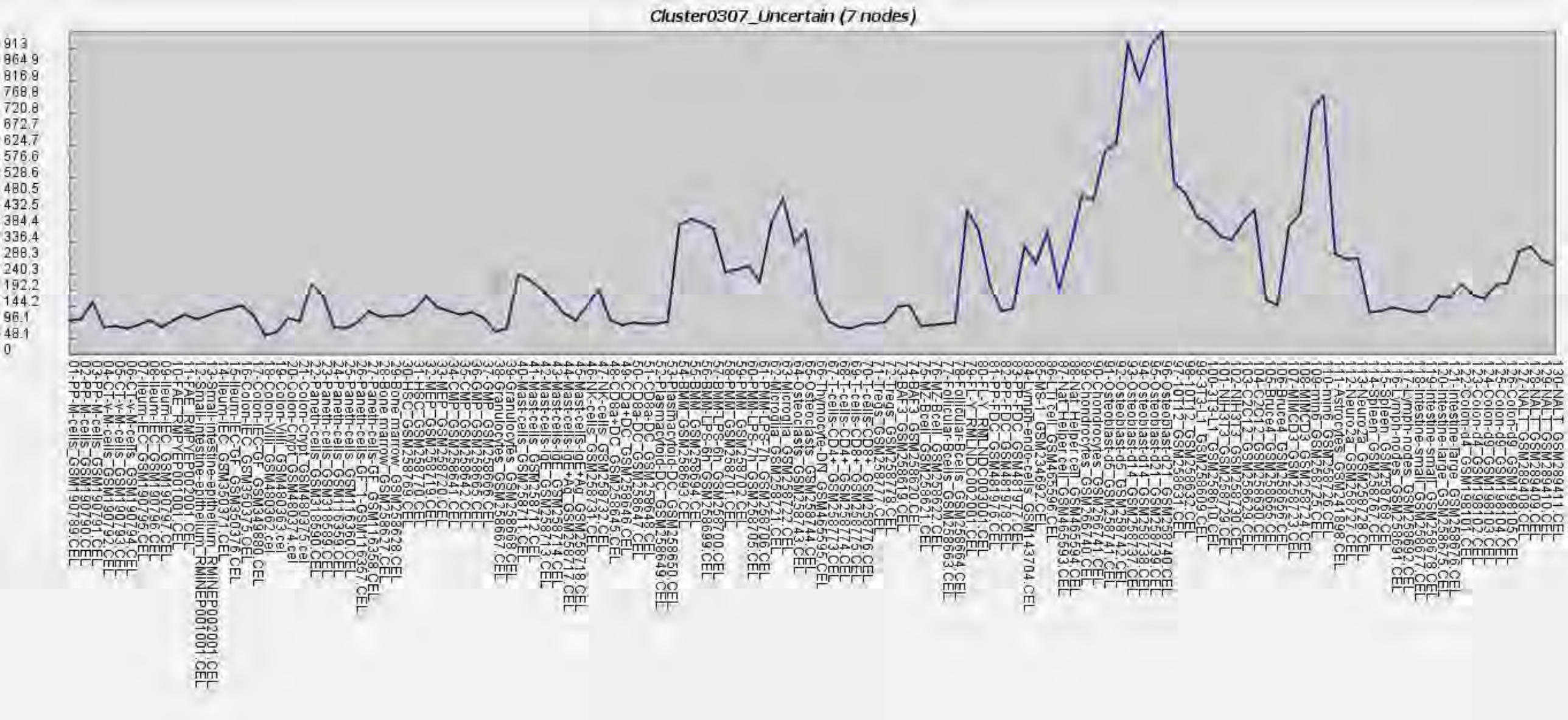

Cluster0302_Uncertain-low in many (7 nodes)
133.7
126.6
119.6
112.6
105.5
98.5
91.5
84.4
77.4
70.3
63.3
56.3
49.2
42.2
35.2
28.1
21.1
14.1
7
0

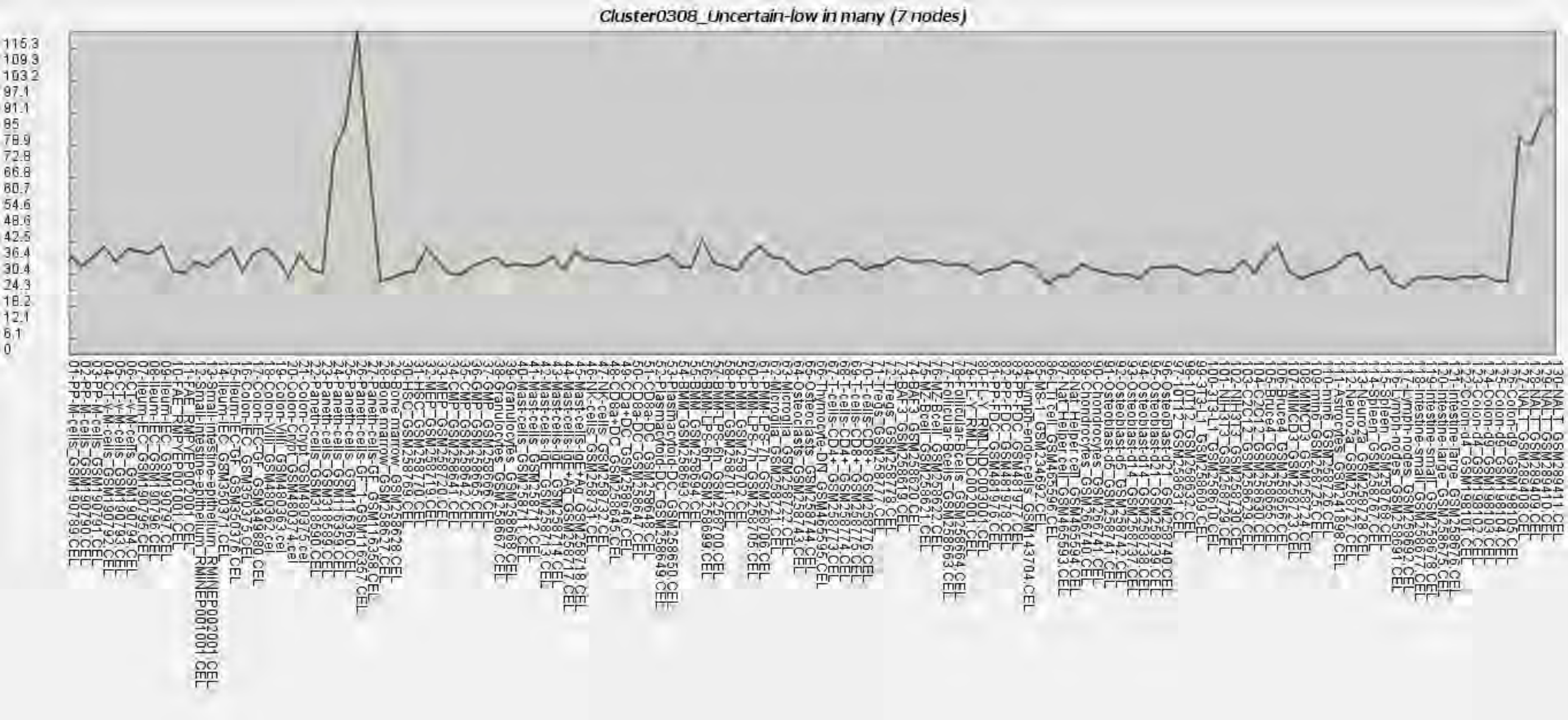

Cluster0303_High in NK cells, T cells, LTi cells and NH cells (7 nodes)
823
779.7
736.4
693.1
649.8
606.5
563.1
519.8
476.5
433.2
389.9
346.5
303.2
259.9
216.6
173.3
130
86.6
43.3
0

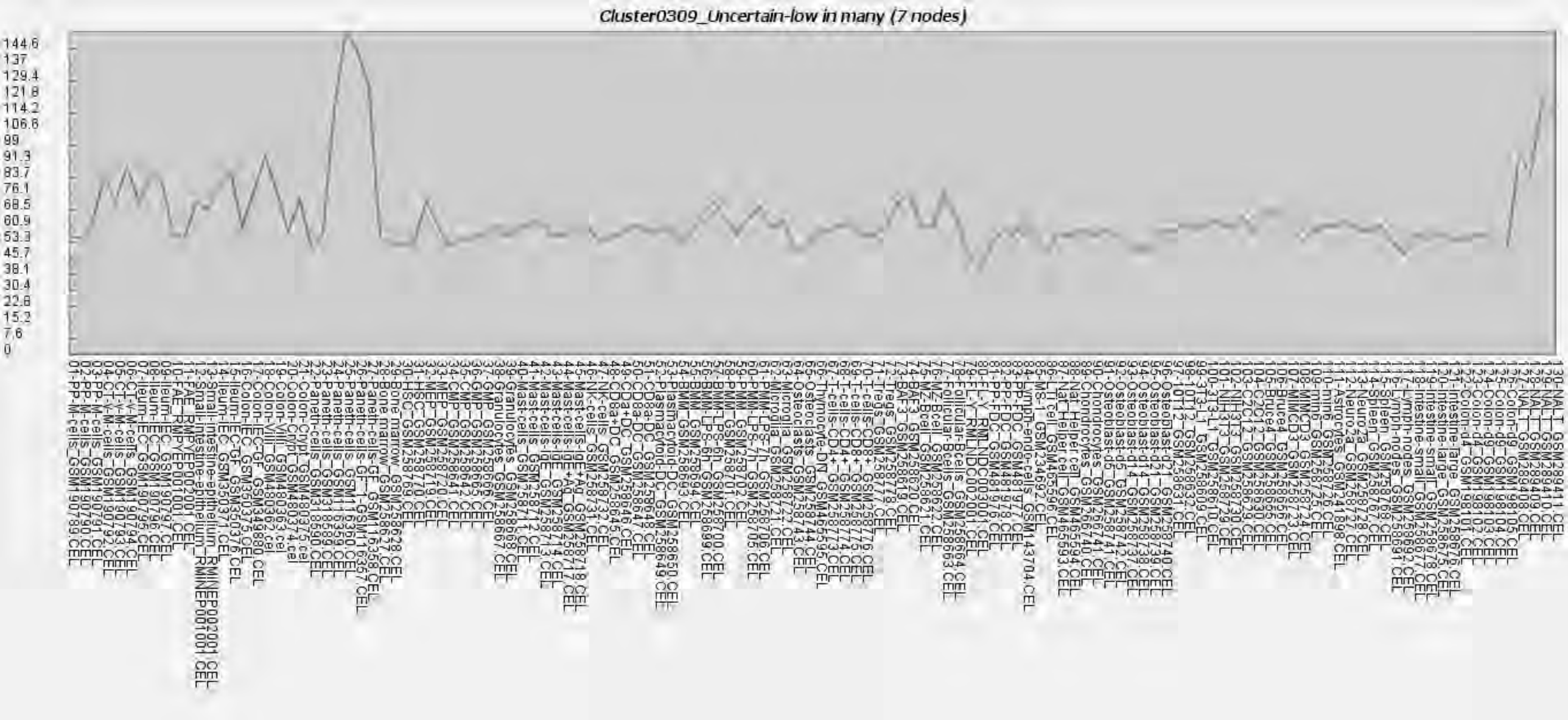

Cluster0304_Intestine-related (7 nodes)
1,031.8
977.5
923.2
868.9
814.6
760.3
706
651.7
597.4
543.1
488.7
434.4
380.1
325.8
271.5
217.2
162.9
108.6
54.3
0

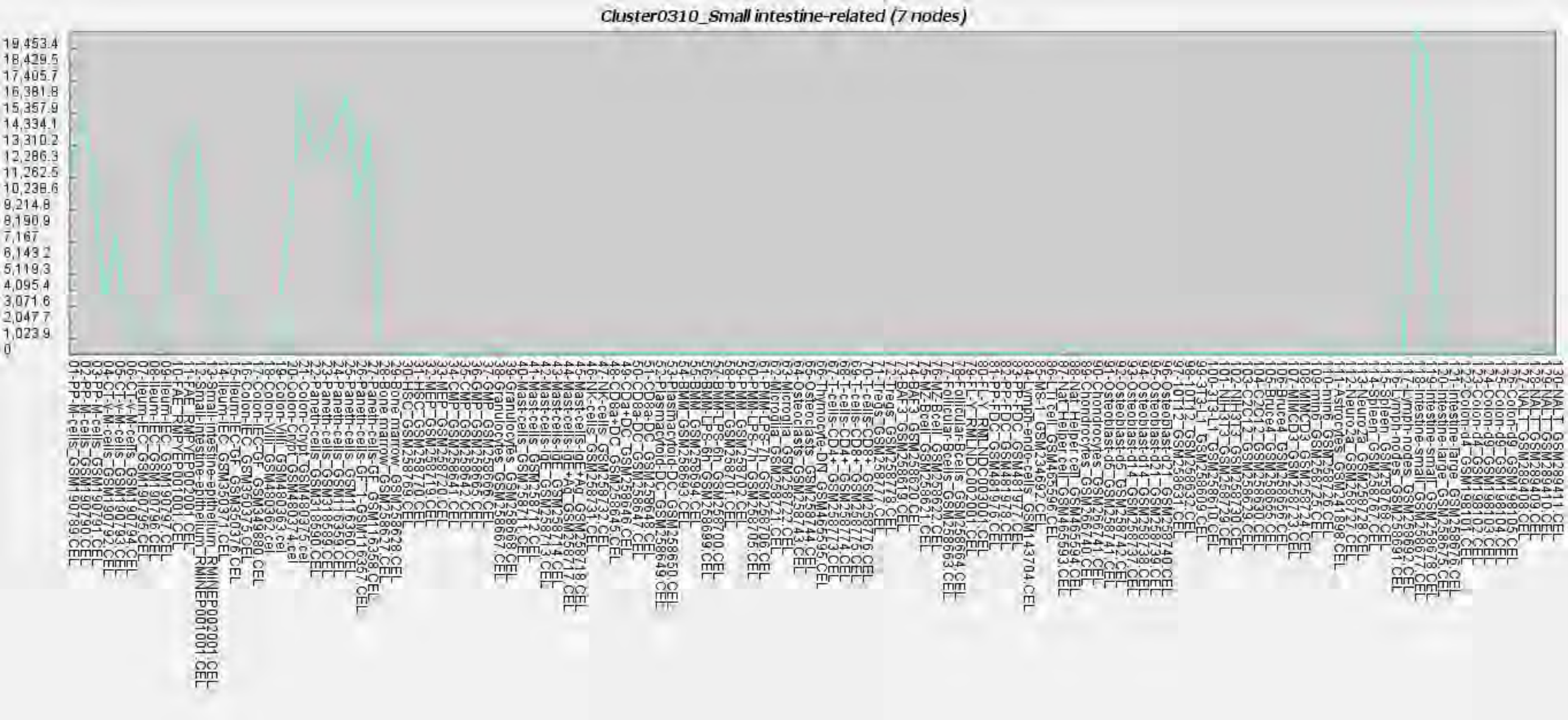

Cluster0305_Uncertain (7 nodes)
2,275.6
2,155.8
2,036.1
1,916.3
1,796.5
1,676.8
1,557
1,437.2
1,317.4
1,197.7
1,077.9
958.1
838.4
718.6
598.8
479.1
359.3
239.5
119.8
0

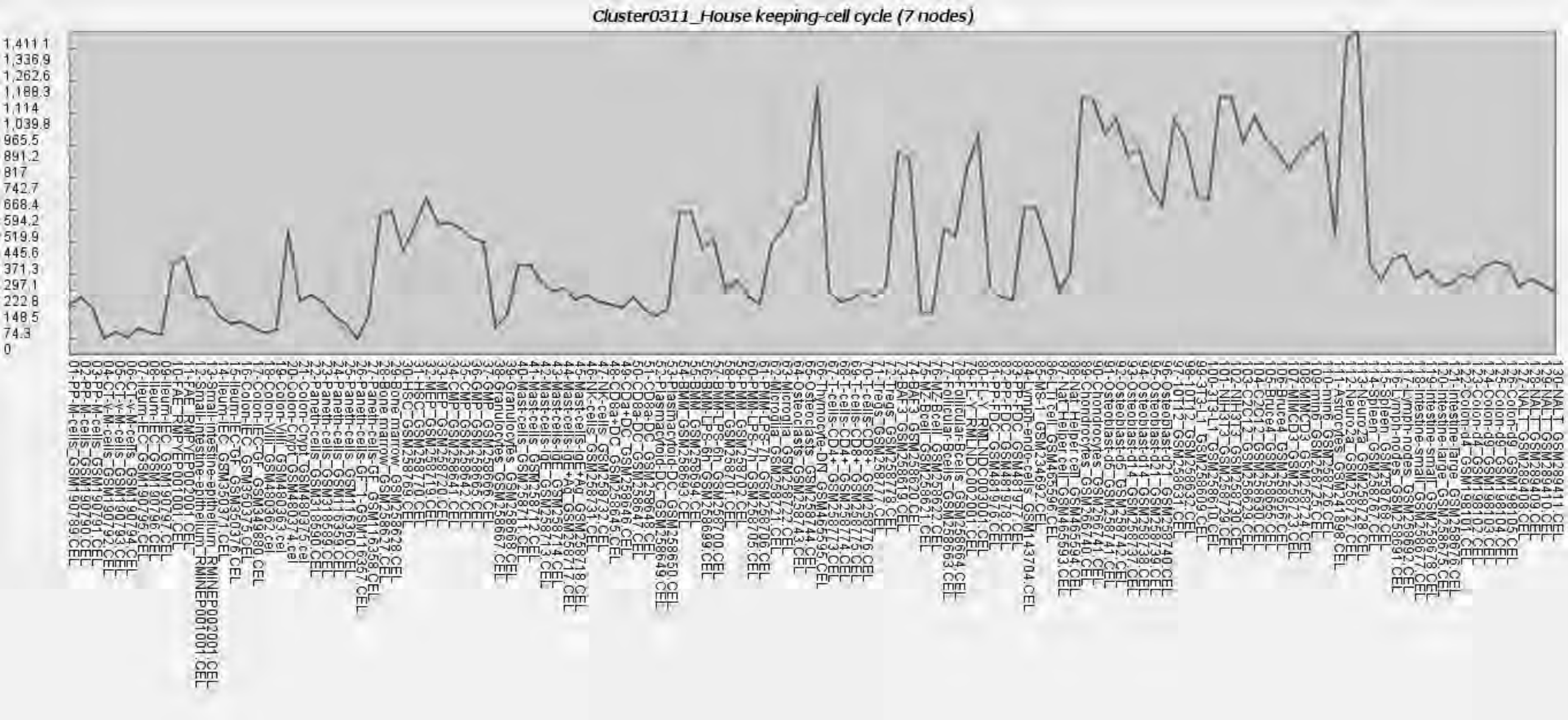

Cluster0306_Intestine-related (7 nodes)
2,057.2
1,948.9
1,840.6
1,732.4
1,624.1
1,515.8
1,407.6
1,299.3
1,191
1,082.7
974.5
866.2
757.9
649.6
541.4
433.1
324.8
216.5
108.3
0

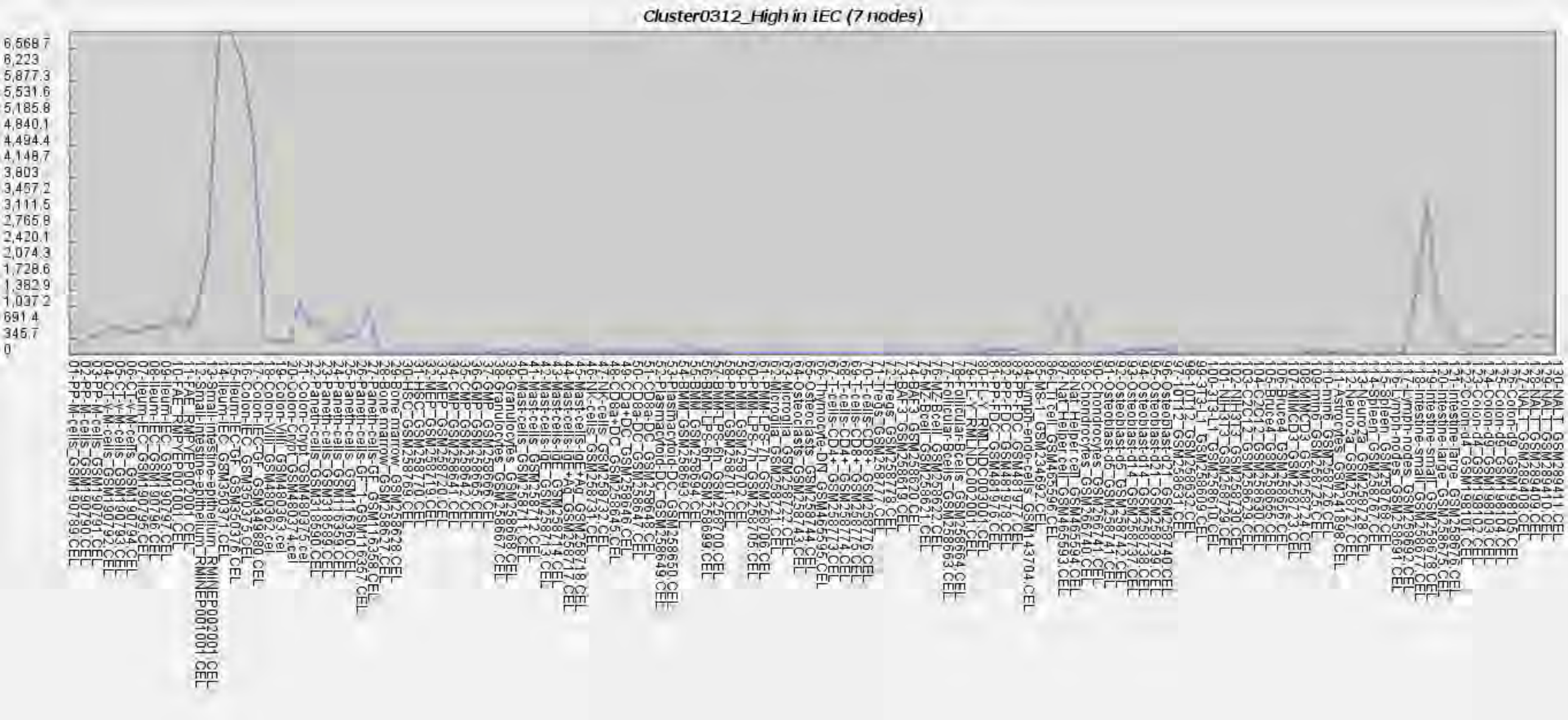

Cluster0307_Uncertain (7 nodes)
913
864.9
816.9
768.8
720.8
672.7
624.7
576.6
528.6
480.5
432.5
384.4
336.4
288.3
240.3
192.2
144.2
96.1
48.1
0

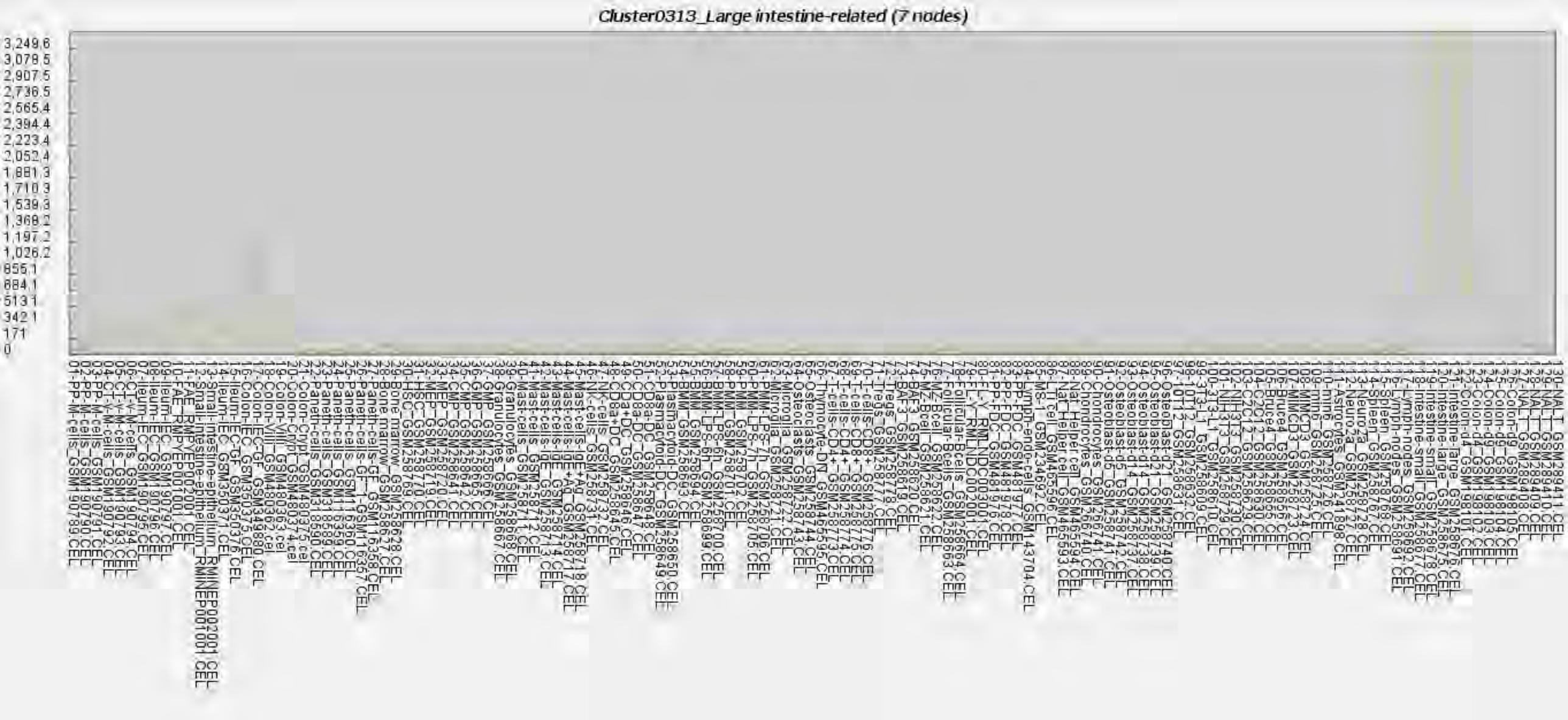

Cluster0308_Uncertain-low in many (7 nodes)
115.3
109.3
103.2
97.1
91.1
85
78.9
72.8
66.8
60.7
54.6
48.6
42.5
36.4
30.4
24.3
18.2
12.1
6.1
0

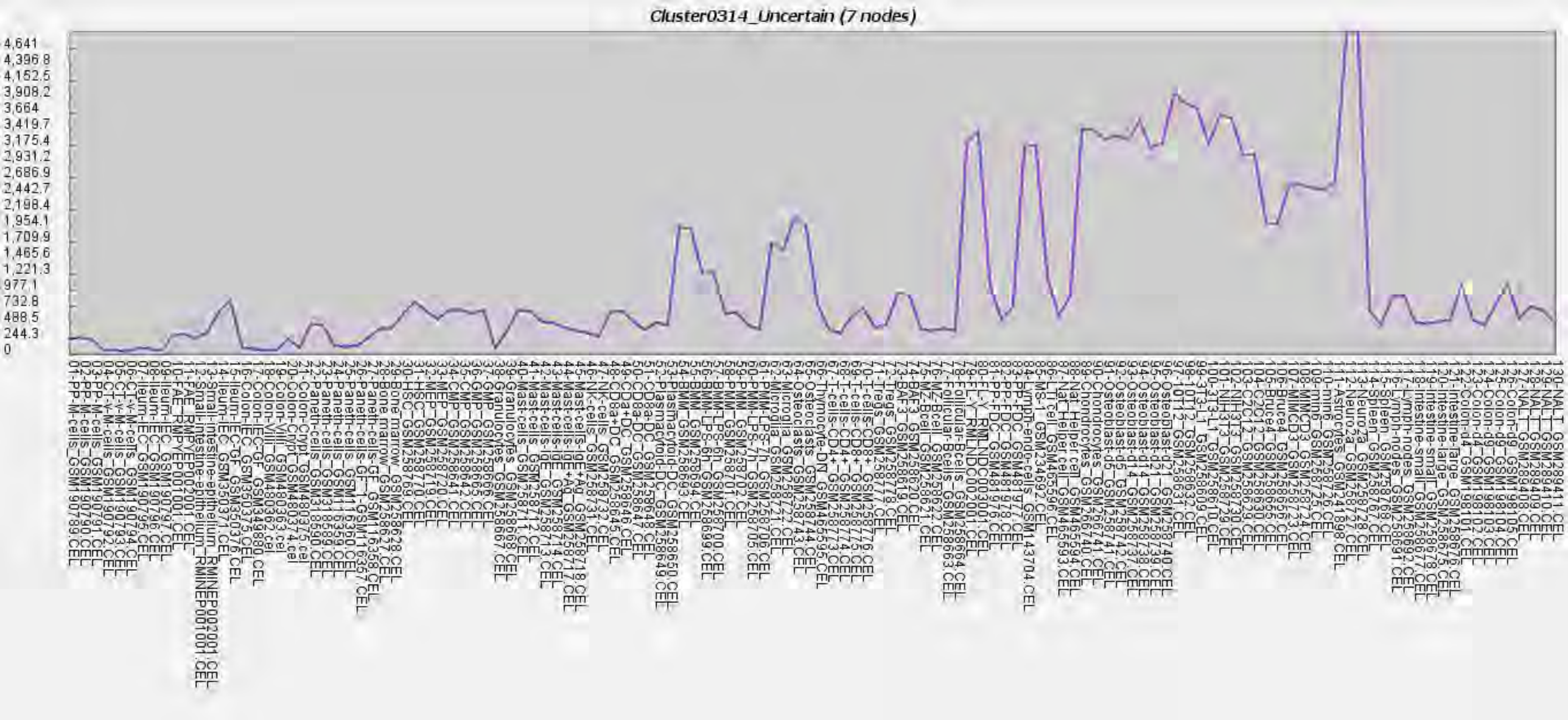

Cluster0309_Uncertain-low in many (7 nodes)
144.6
137
129.4
121.8
114.2
106.6
99
91.3
83.7
76.1
68.5
60.9
53.3
45.7
38.1
30.4
22.8
15.2
7.6
0

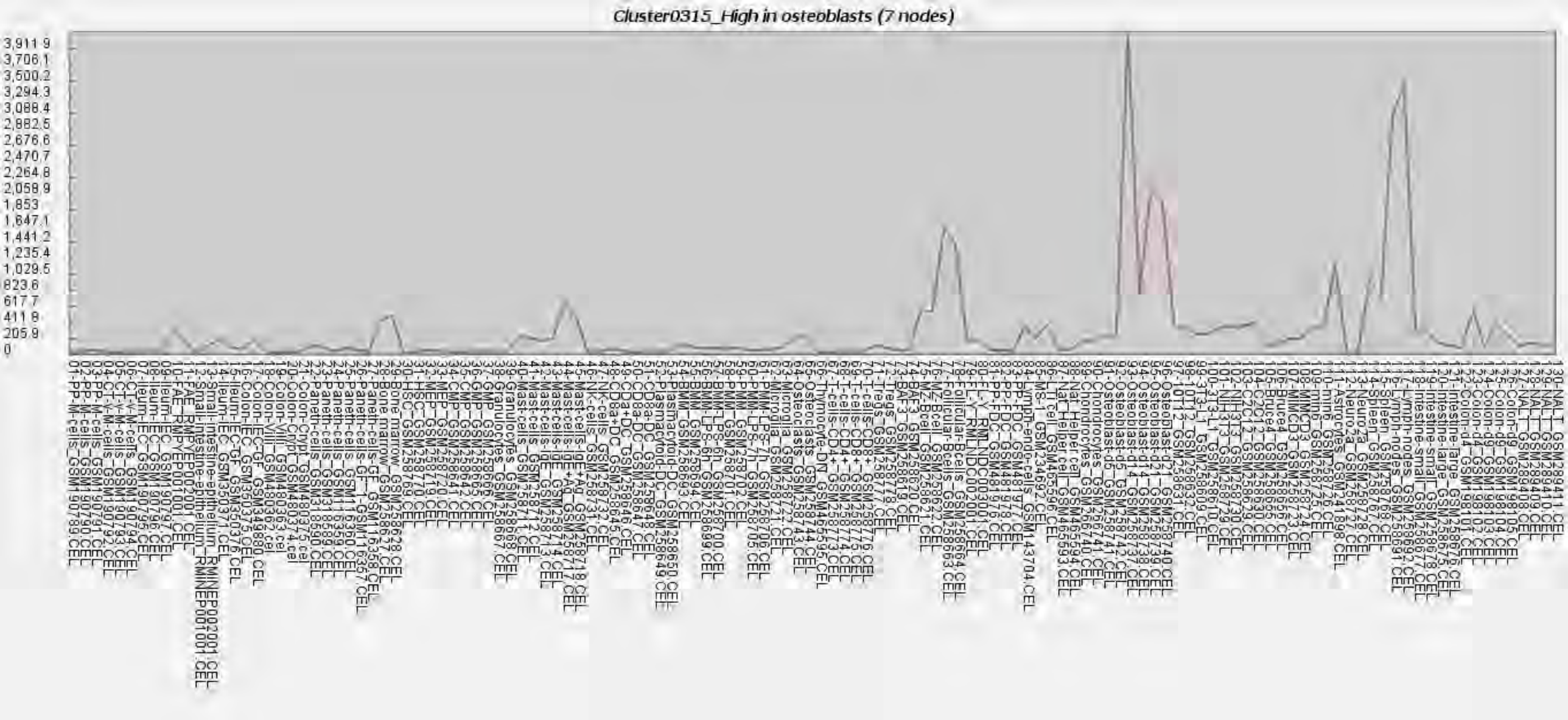

Cluster0310_Small intestine-related (7 nodes)
19,453.4
18,429.5
17,405.7
16,381.8
15,357.9
14,334.1
13,310.2
12,286.3
11,262.5
10,238.6
9,214.8
8,190.9
7,167
6,143.2
5,119.3
4,095.4
3,071.6
2,047.7
1,023.9
0


Cluster0311_House keeping-cell cycle (7 nodes)
1,411.1
1,336.9
1,262.6
1,188.3
1,114
1,039.8
965.5
891.2
817
742.7
668.4
594.2
519.9
445.6
371.3
297.1
222.8
148.5
74.3
0

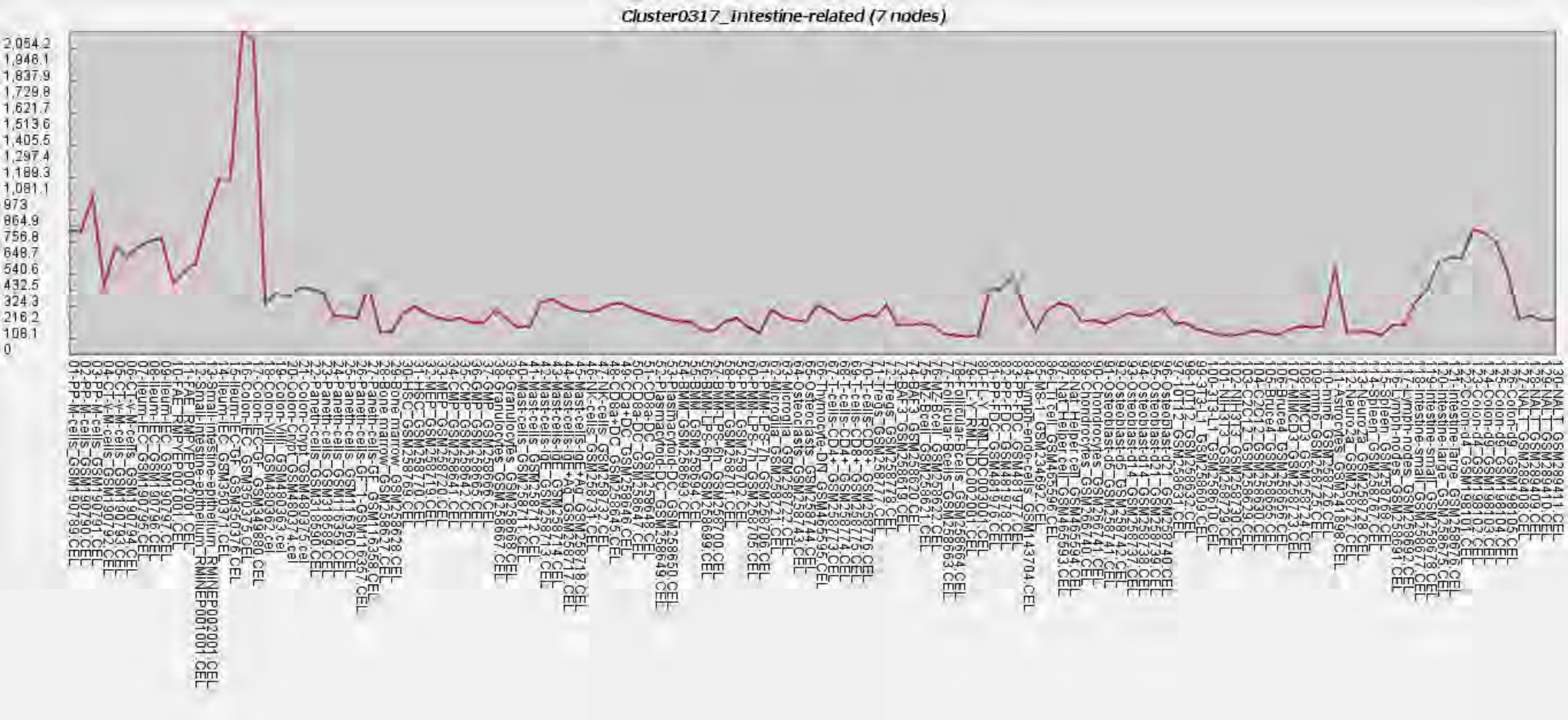

Cluster0312_High in iEC (7 nodes)
6,568.7
6,223
5,877.3
5,531.6
5,185.8
4,840.1
4,494.4
4,148.7
3,803
3,457.2
3,111.5
2,765.8
2,420.1
2,074.3
1,728.6
1,382.9
1,037.2
691.4
345.7
0


Cluster0313_Large intestine-related (7 nodes)
3,249.6
3,078.5
2,907.5
2,736.5
2,565.4
2,394.4
2,223.4
2,052.4
1,881.3
1,710.3
1,539.3
1,368.2
1,197.2
1,026.2
855.1
684.1
513.1
342.1
171
0


Cluster0314_Uncertain (7 nodes)
4,641
4,396.8
4,152.5
3,908.2
3,664
3,419.7
3,175.4
2,931.2
2,686.9
2,442.7
2,198.4
1,954.1
1,709.9
1,465.6
1,221.3
977.1
732.8
488.5
244.3
0

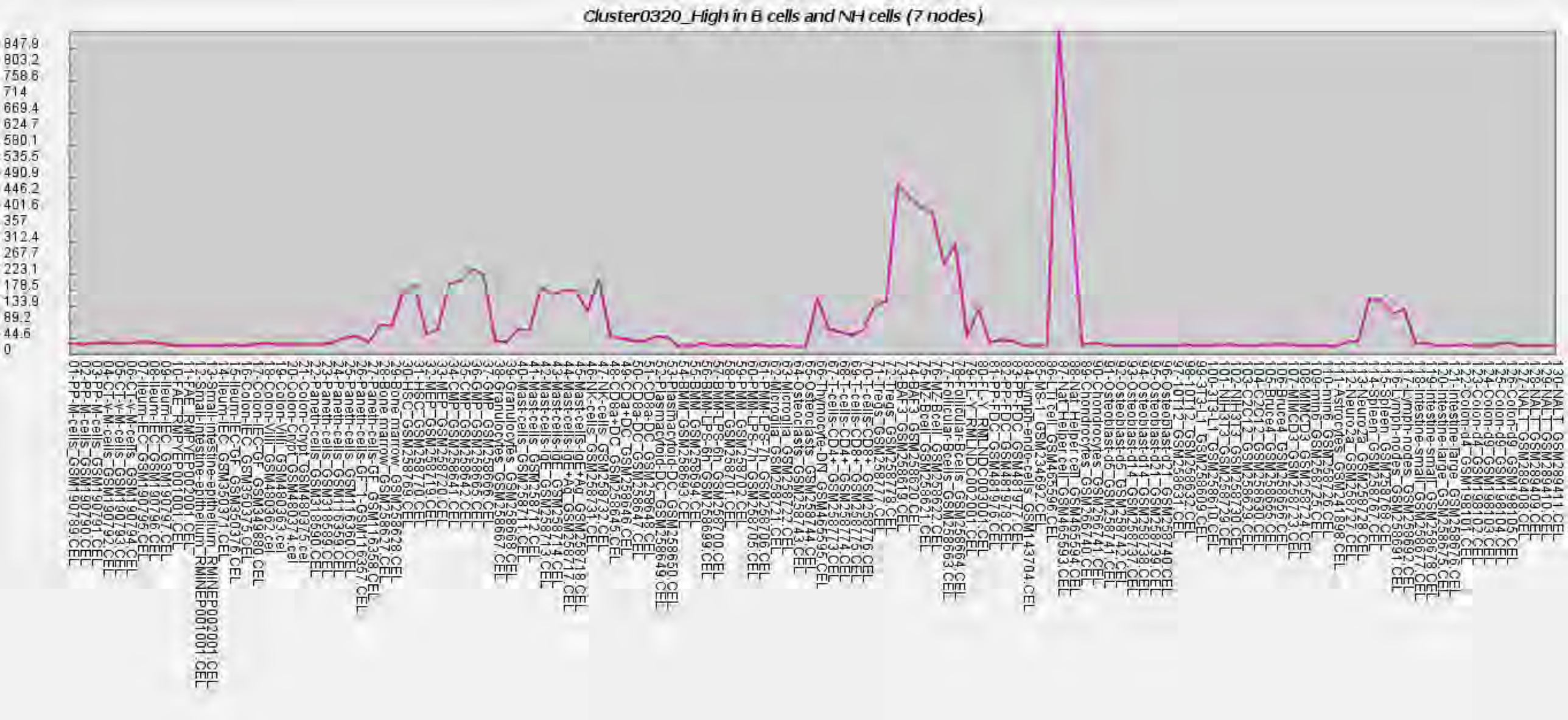

Cluster0315_High in osteoblasts (7 nodes)
3,911.9
3,706.1
3,500.2
3,294.3
3,088.4
2,882.5
2,676.6
2,470.7
2,264.8
2,058.9
1,853
1,647.1
1,441.2
1,235.4
1,029.5
823.6
617.7
411.8
205.9
0

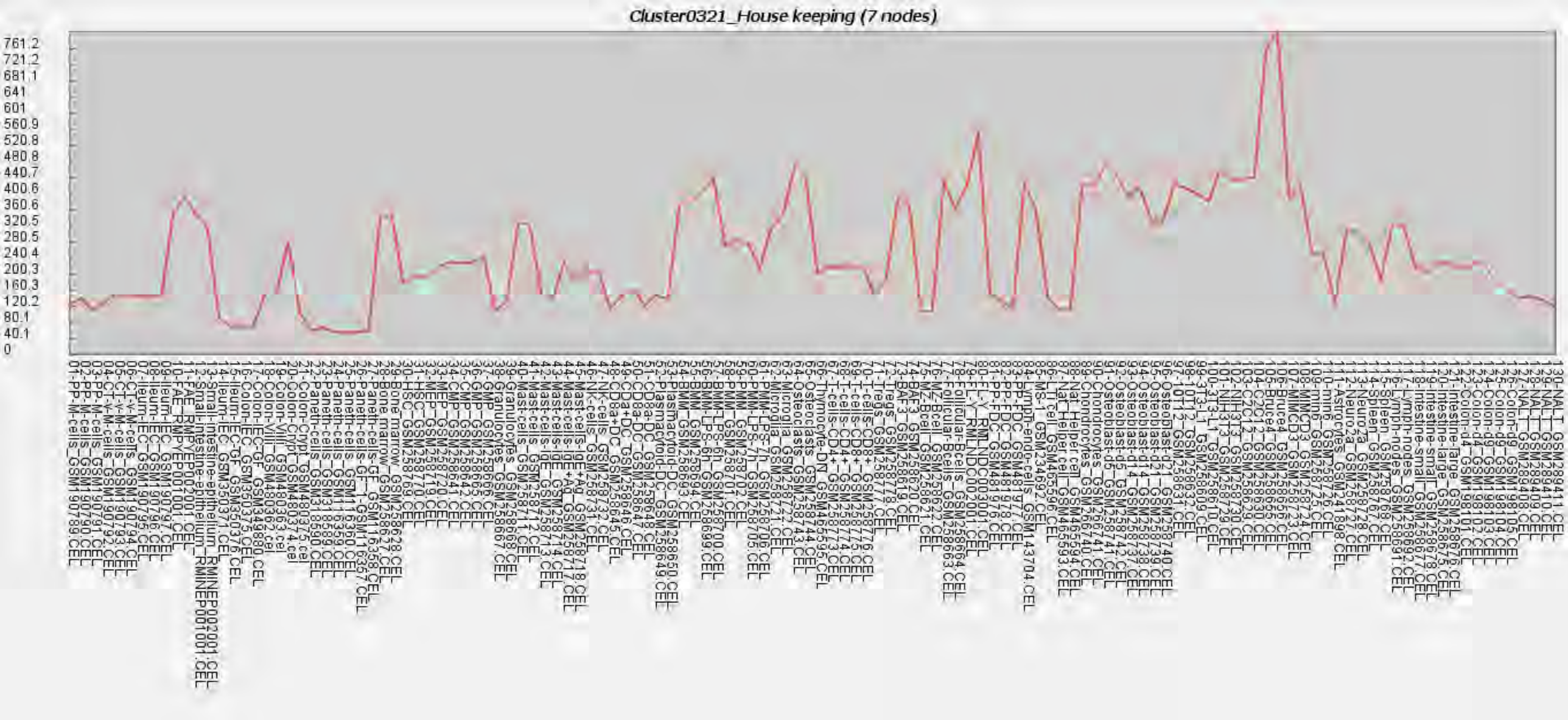
Cluster0316_High in 10T12 cells and astrocytes (7 nodes)
662.5
827.7
592.8
557.9
523.1
488.2
453.3
418.5
383.6
348.7
313.8
279
244.1
209.2
174.4
139.5
104.6
69.7
34.9
0

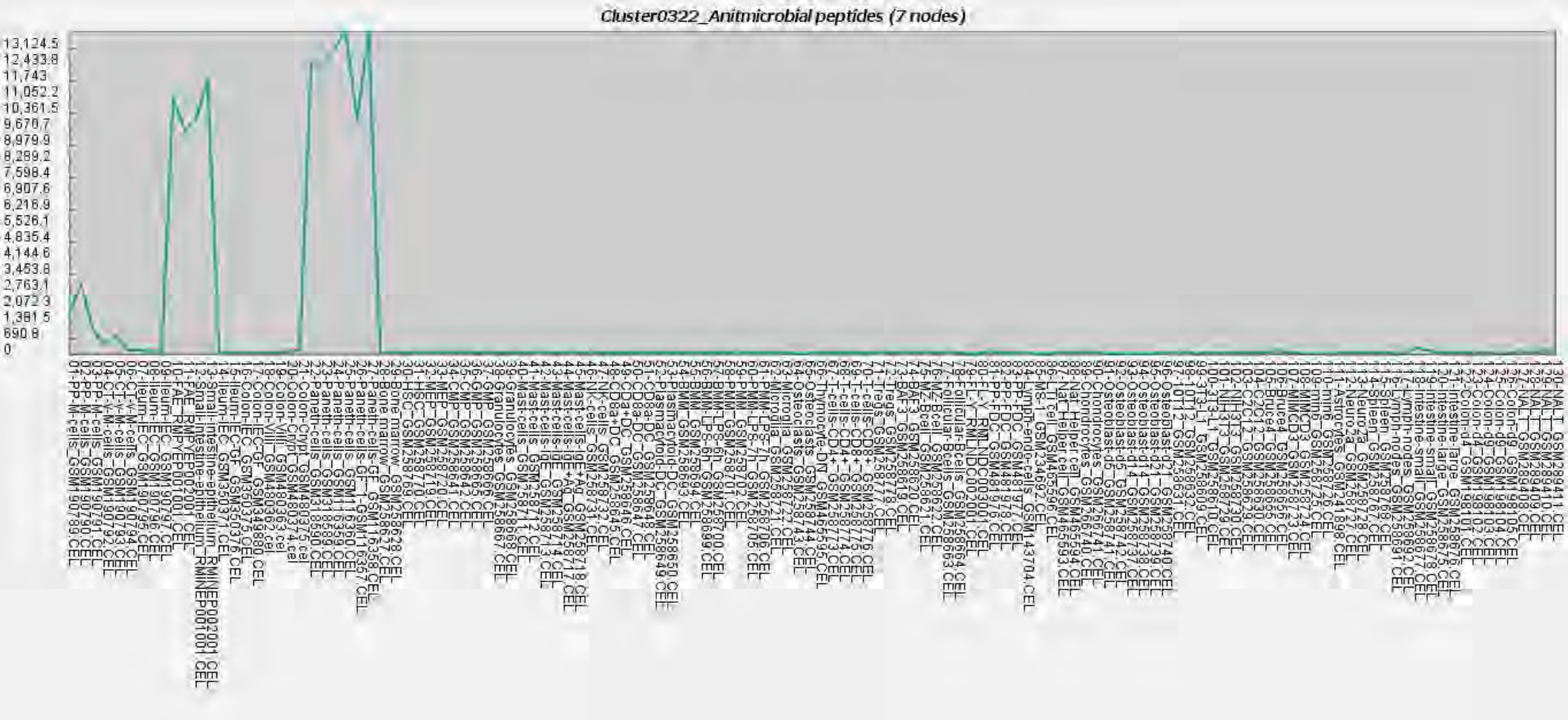

Cluster0317_Intestine-related (7 nodes)
2,054.2
1,946.1
1,837.9
1,729.8
1,621.7
1,513.6
1,405.5
1,297.4
1,189.3
1,081.1
973
864.9
756.8
648.7
540.6
432.5
324.3
216.2
108.1
0

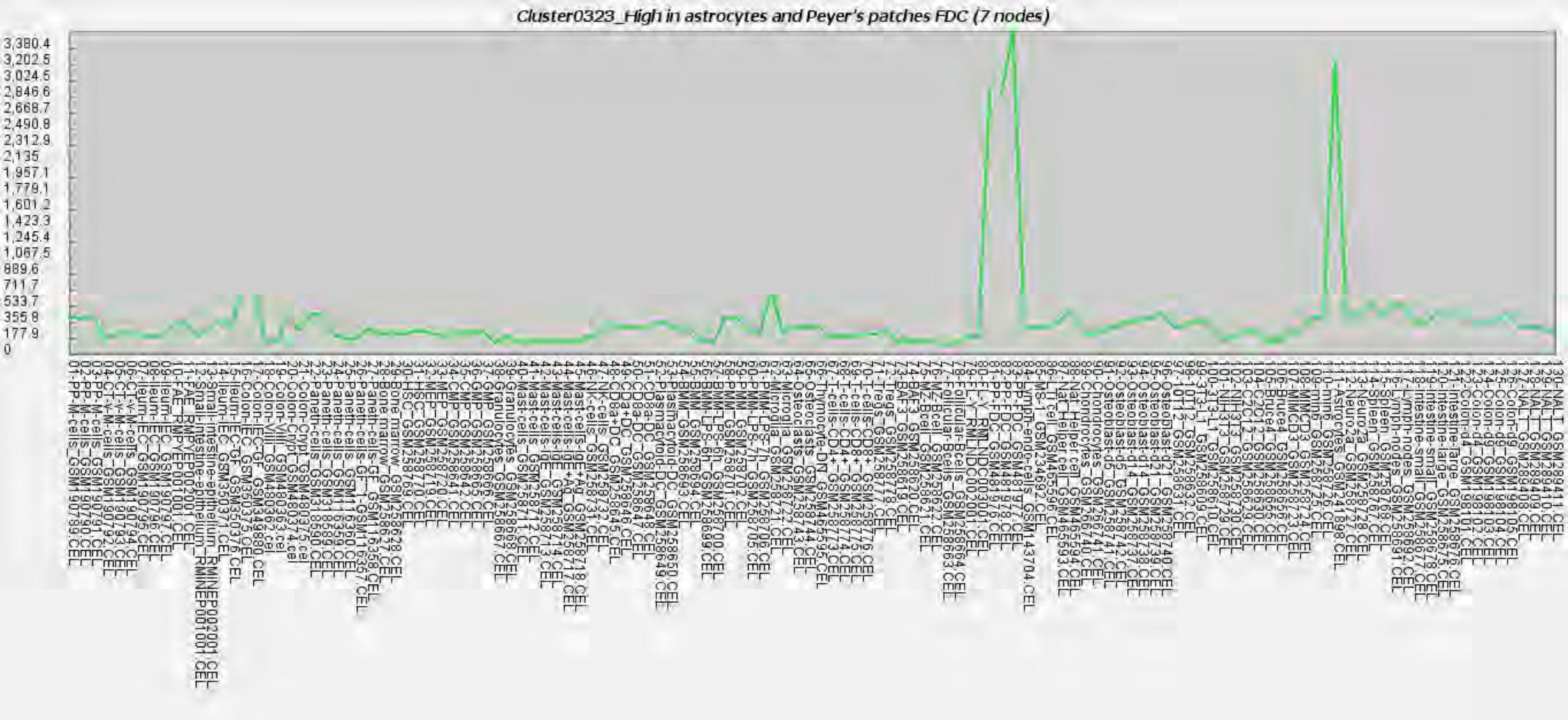
Cluster0318_High in Peyer's patches FDC (7 nodes)
406.6
385.2
363.8
342.4
321
299.6
278.2
256.8
235.4
214
192.6
171.2
149.8
128.4
107
85.6
64.2
42.8
21.4
0

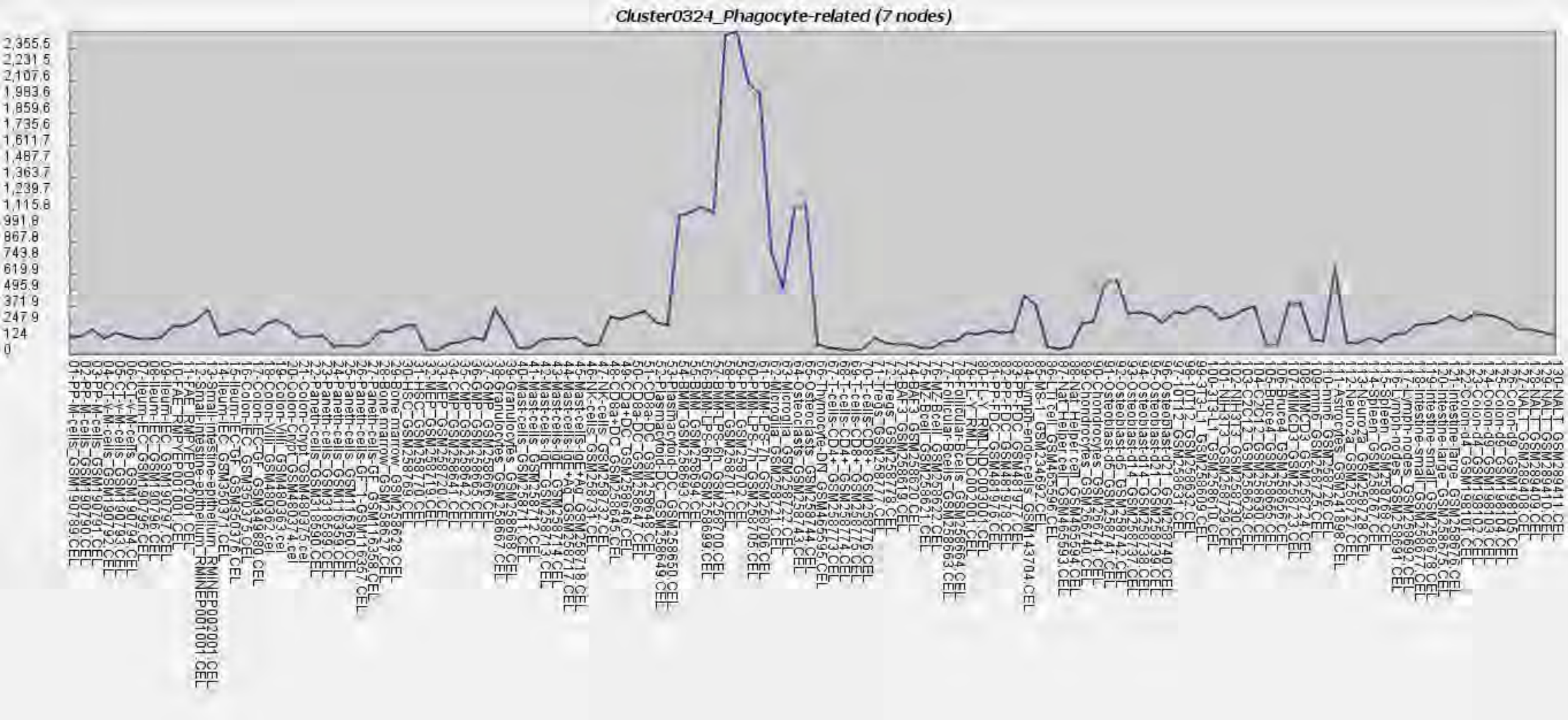
Cluster0319_Uncertain (7 nodes)
787.6
746.1
704.7
663.2
621.8
580.3
538.9
497.4
456
414.5
373.1
331.6
290.2
248.7
207.3
165.8
124.4
82.9
41.5
0

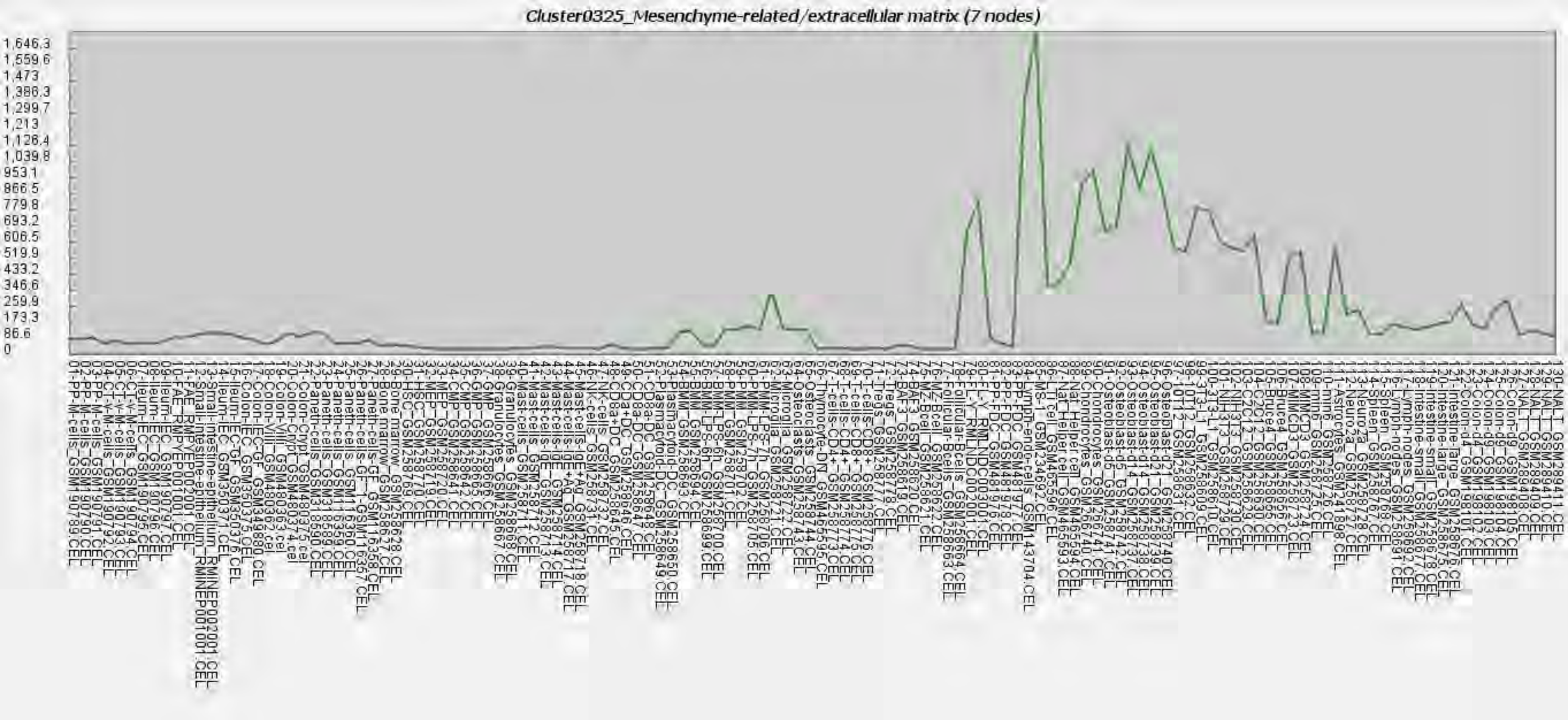

Cluster0320_High in B cells and NK cells (7 nodes)
847.9
803.2
758.6
714
669.4
624.7
580.1
535.5
490.9
446.2
401.6
357
312.4
267.7
223.1
178.5
133.9
89.2
44.6
0

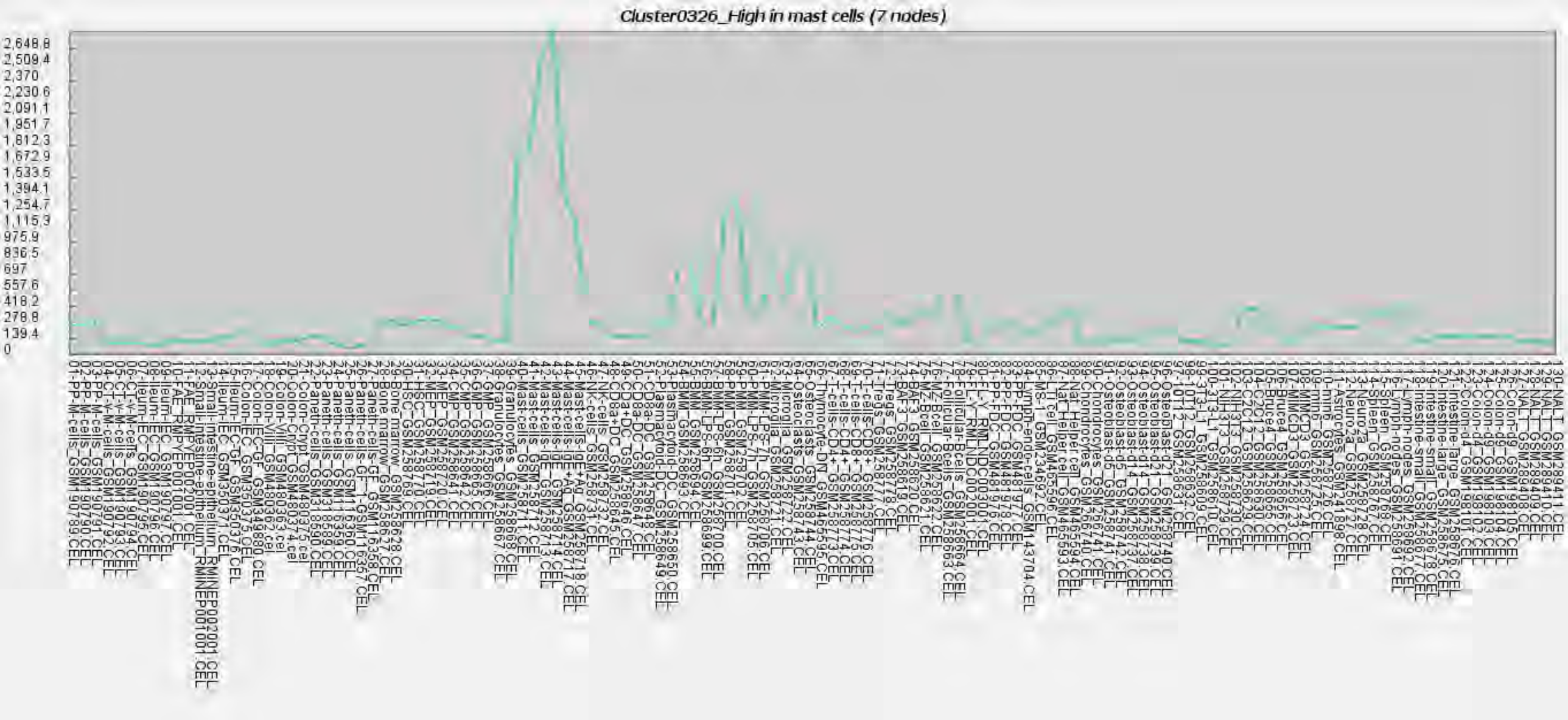

Cluster0321_House keeping (7 nodes)
761.2
721.2
681.1
641
601
560.9
520.8
480.8
440.7
400.6
360.6
320.5
280.5
240.4
200.3
160.3
120.2
80.1
40.1
0

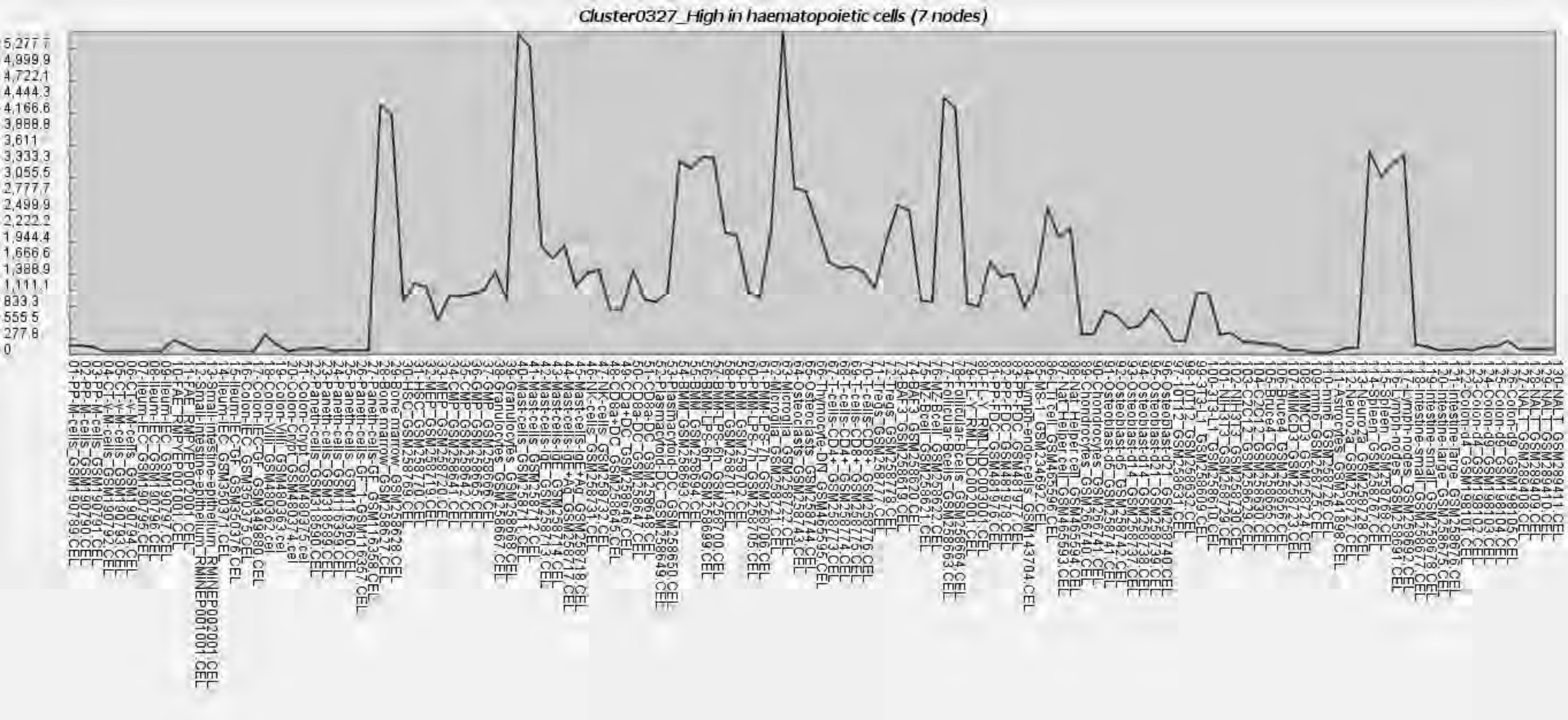

Cluster0322_Anitmicrobial peptides (7 nodes)
13,124.5
12,433.8
11,743
11,052.2
10,361.5
9,670.7
8,979.9
8,289.2
7,598.4
6,907.6
6,216.9
5,526.1
4,835.4
4,144.6
3,453.8
2,763.1
2,072.3
1,381.5
690.8
0


Cluster0323_High in astrocytes and Peyer's patches FDC (7 nodes)
3,380.4
3,202.5
3,024.5
2,846.6
2,668.7
2,490.8
2,312.9
2,135
1,957.1
1,779.1
1,601.2
1,423.3
1,245.4
1,067.5
889.6
711.7
533.7
355.8
177.9
0

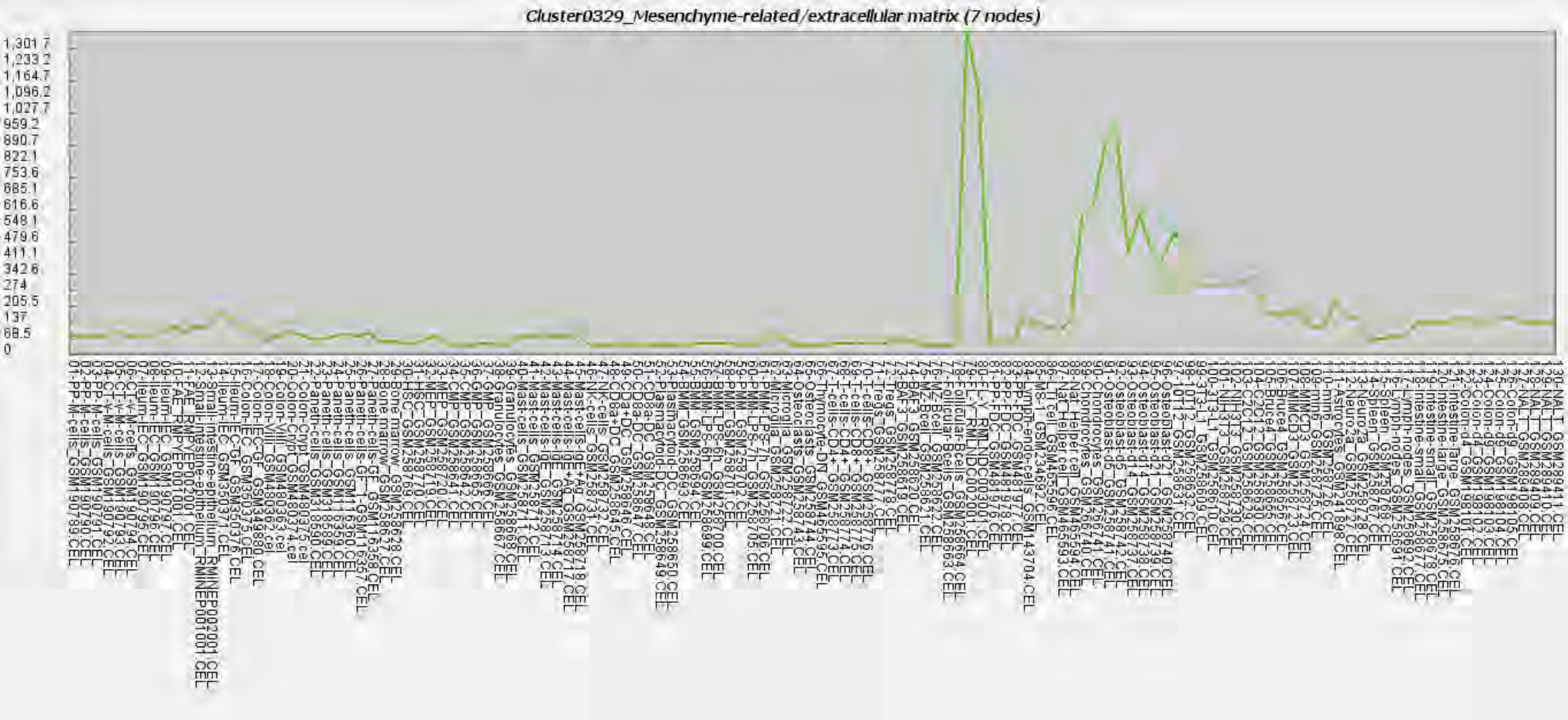

Cluster0324_Phagocyte-related (7 nodes)
2,355.5
2,231.5
2,107.6
1,983.6
1,859.6
1,735.6
1,611.7
1,487.7
1,363.7
1,239.7
1,115.8
991.8
867.8
743.8
619.9
495.9
371.9
247.9
124
0

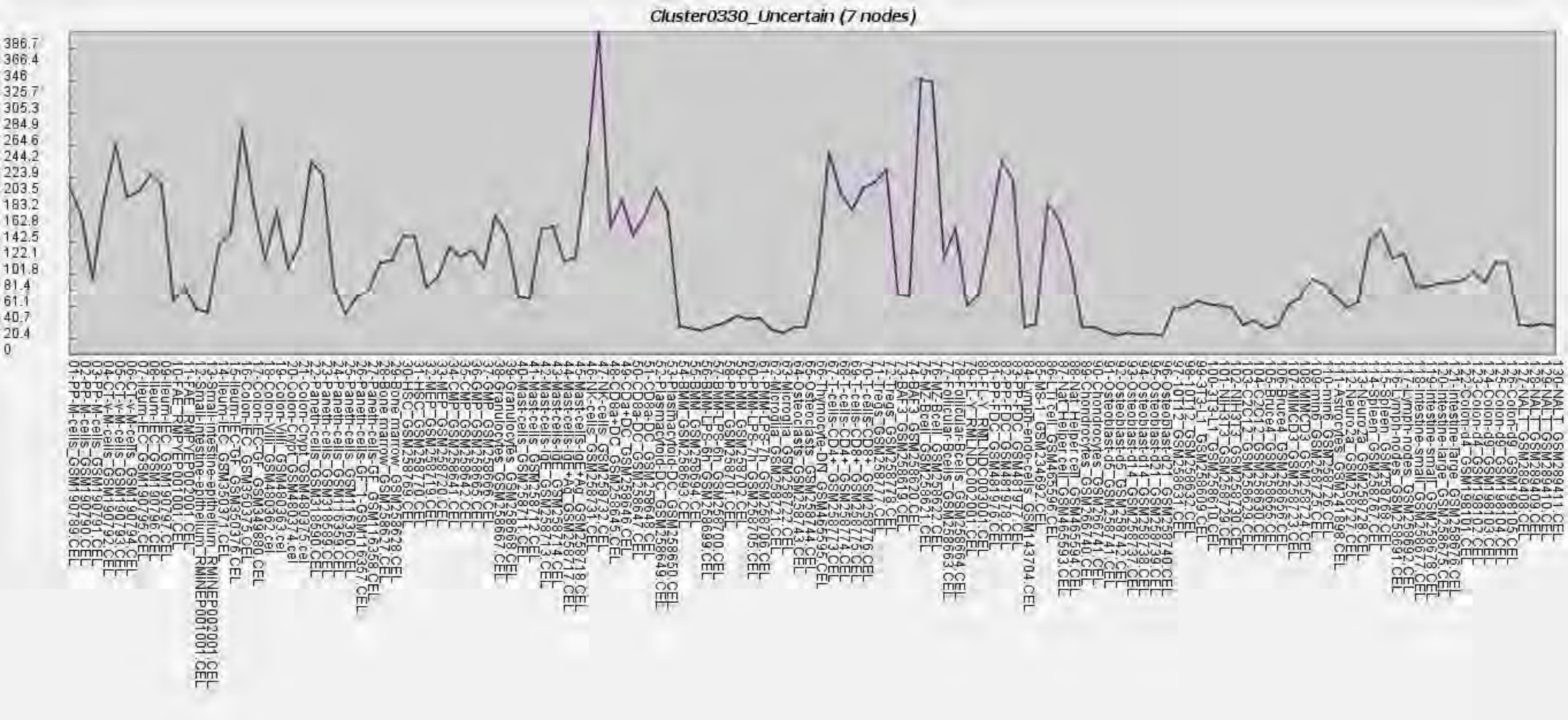

Cluster0325_Mesenchyme-related/extracellular matrix (7 nodes)
1,646.3
1,559.6
1,473
1,386.3
1,299.7
1,213
1,126.4
1,039.8
953.1
866.5
779.8
693.2
606.5
519.9
433.2
346.6
259.9
173.3
86.6
0

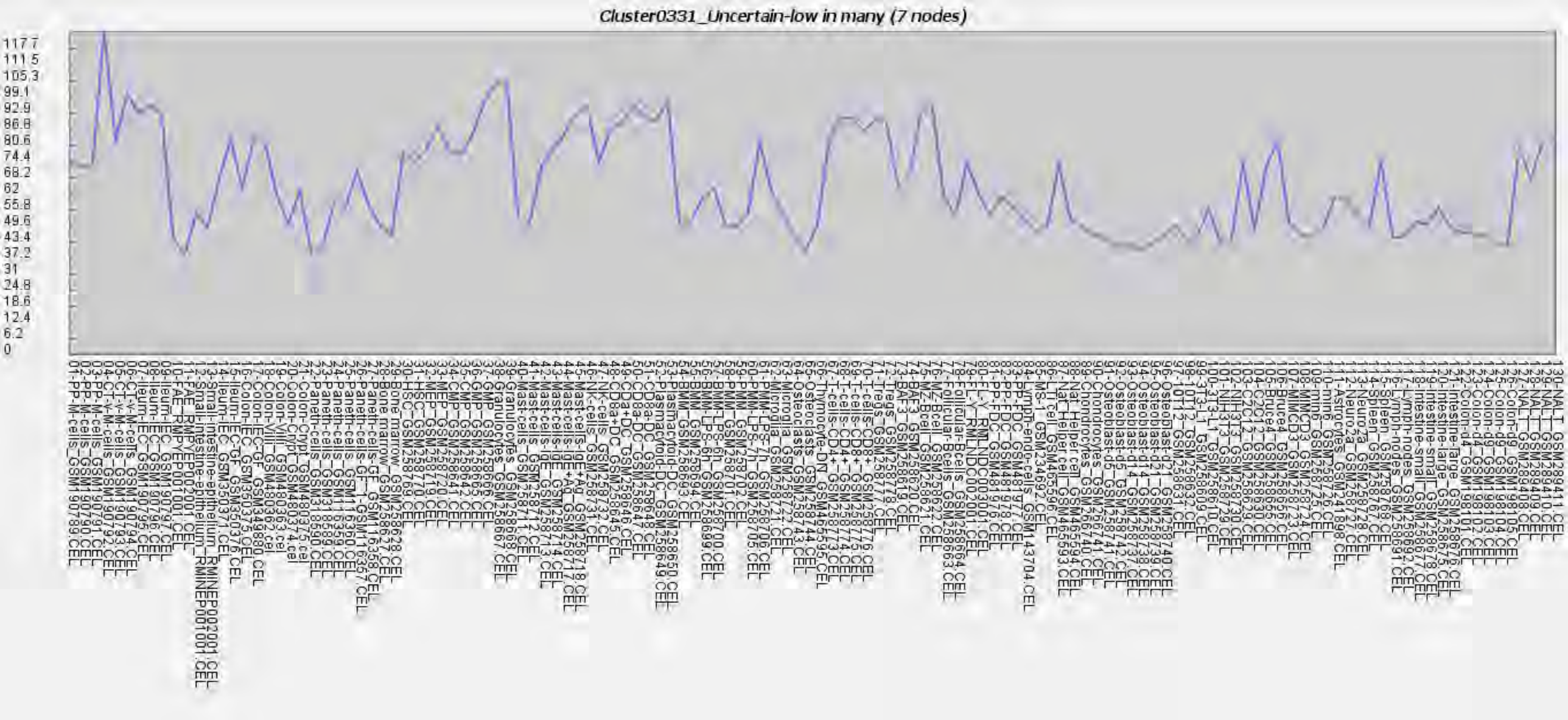

Cluster0326_High in mast cells (7 nodes)
2,648.8
2,509.4
2,370
2,230.6
2,091.1
1,951.7
1,812.3
1,672.9
1,533.5
1,394.1
1,254.7
1,115.3
975.9
836.5
697
557.6
418.2
278.8
139.4
0

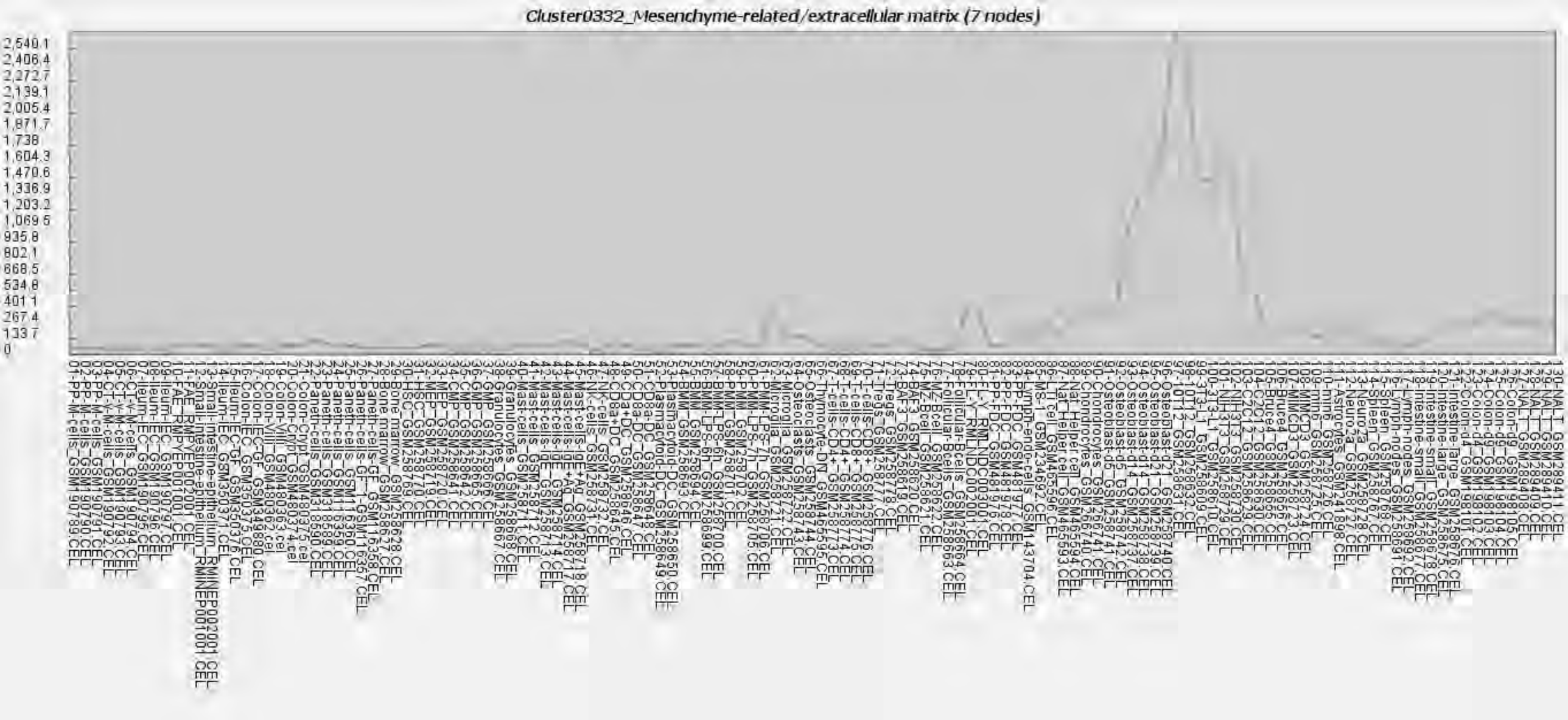

Cluster0327_High in haematopoietic cells (7 nodes)
5,277.7
4,999.9
4,722.1
4,444.3
4,166.6
3,888.8
3,611
3,333.3
3,055.5
2,777.7
2,499.9
2,222.2
1,944.4
1,666.6
1,388.9
1,111.1
833.3
555.5
277.8
0

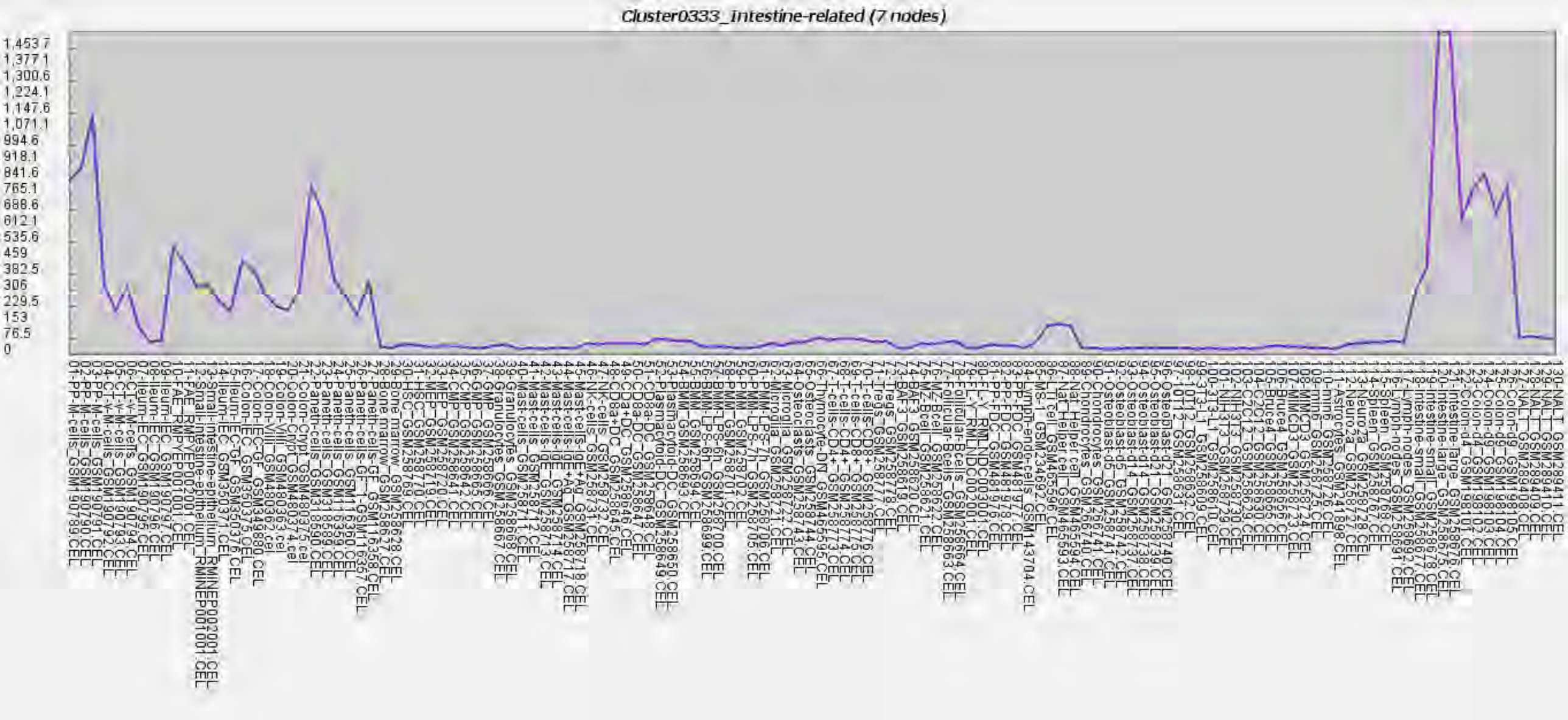
Cluster0328_Intestine-related (7 nodes)
4,281.7
4,056.3
3,831
3,605.6
3,380.3
3,154.9
2,929.6
2,704.2
2,478.9
2,253.5
2,028.2
1,802.8
1,577.5
1,352.1
1,126.8
901.4
676.1
450.7
225.4
0

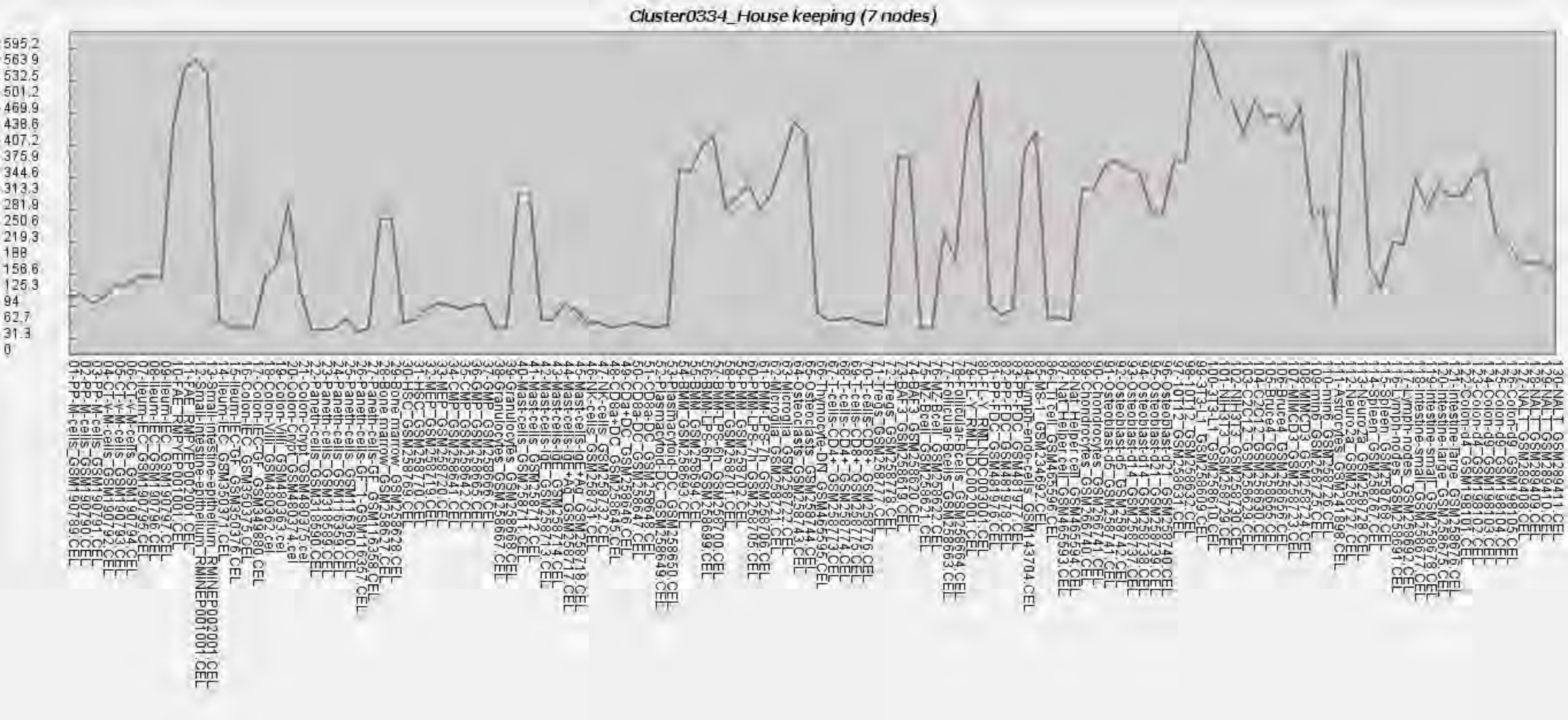

Cluster0329_Mesenchyme-related/extracellular matrix (7 nodes)
1,301.7
1,233.2
1,164.7
1,096.2
1,027.7
959.2
890.7
822.1
753.6
685.1
616.6
548.1
479.6
411.1
342.6
274
205.5
137
68.5
0


Cluster0330_Uncertain (7 nodes)
386.7
366.4
346
325.7
305.3
284.9
264.6
244.2
223.9
203.5
183.2
162.8
142.5
122.1
101.8
81.4
61.1
40.7
20.4
0

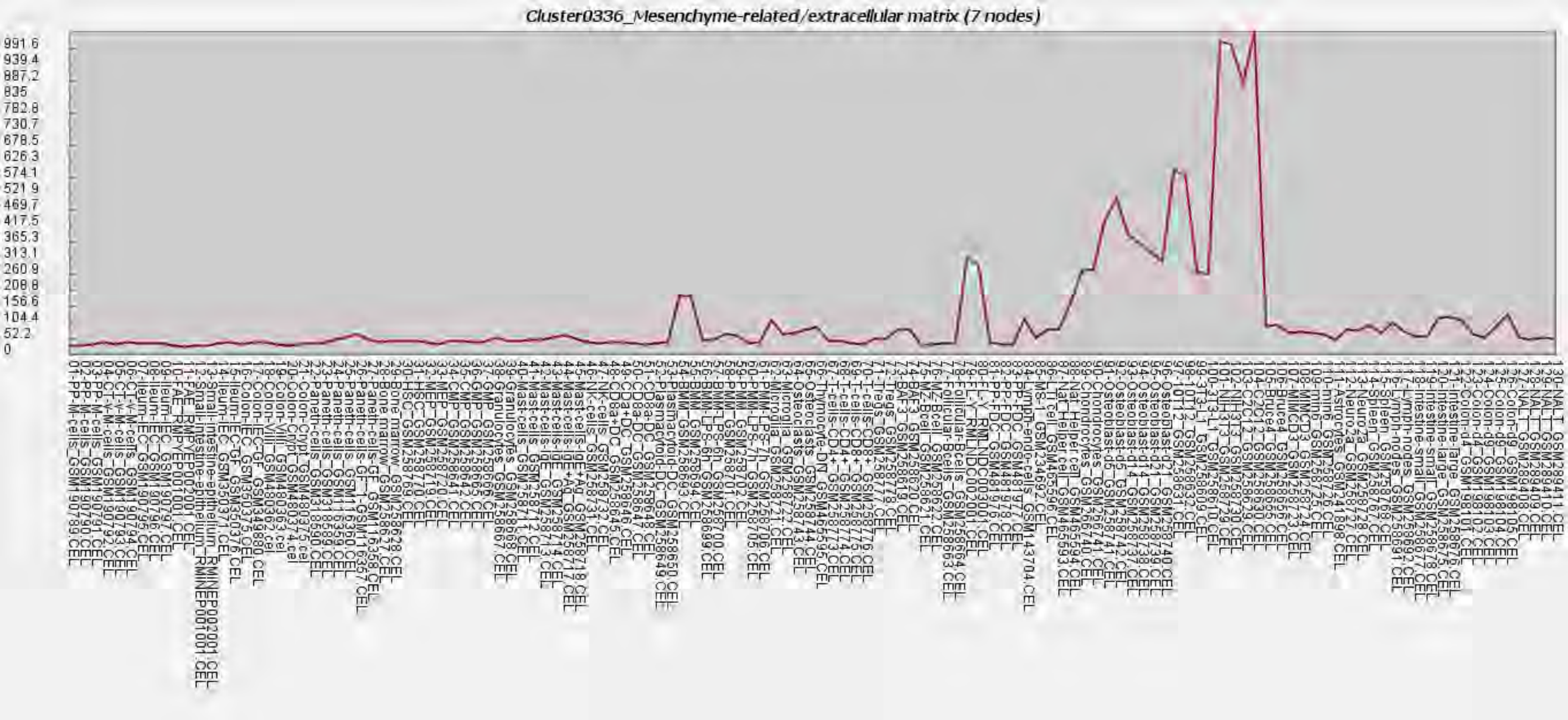

Cluster0331_Uncertain-low in many (7 nodes)
117.7
111.5
105.3
99.1
92.9
86.8
80.6
74.4
68.2
62
55.8
49.6
43.4
37.2
31
24.8
18.6
12.4
6.2
0

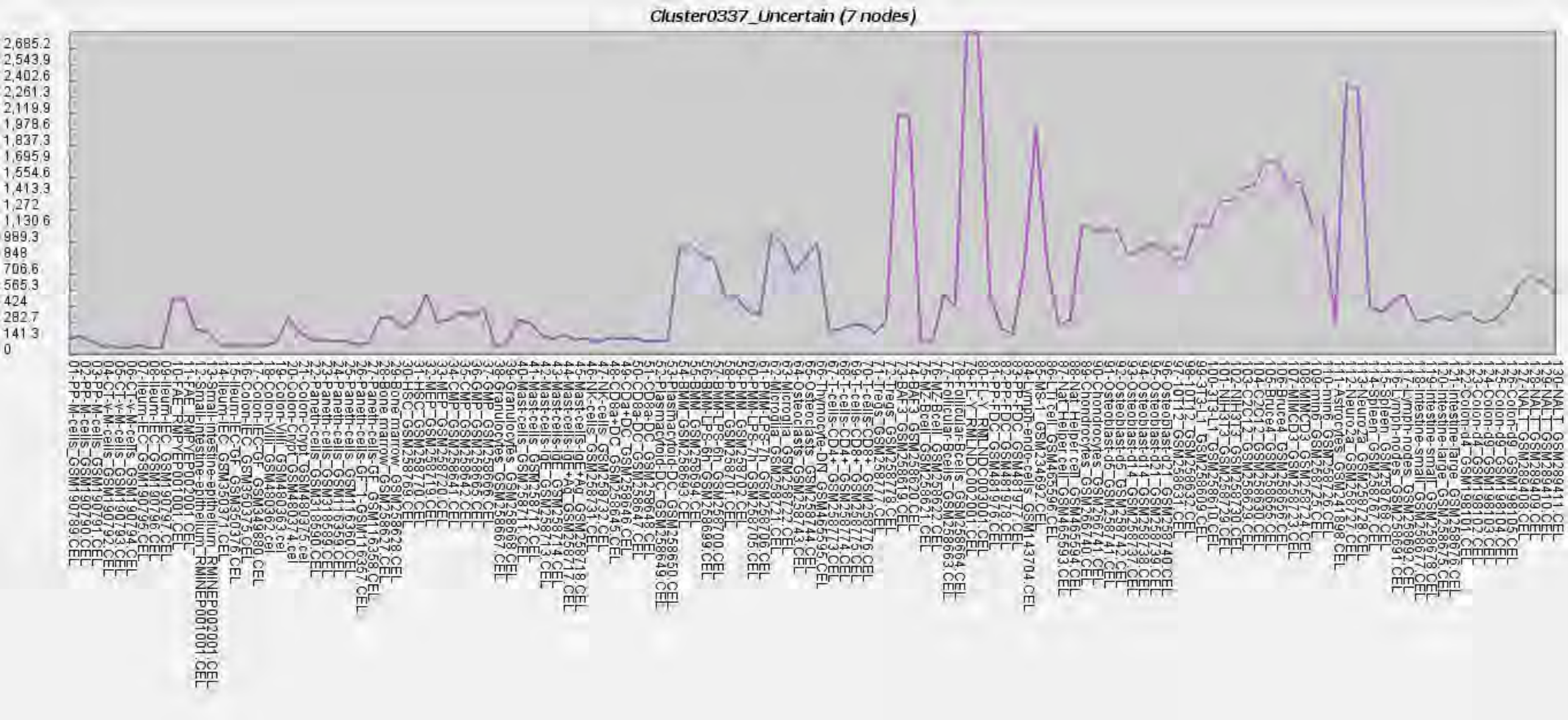

Cluster0332_Mesenchyme-related/extracellular matrix (7 nodes)
2,540.1
2,406.4
2,272.7
2,139.1
2,005.4
1,871.7
1,738
1,604.3
1,470.6
1,336.9
1,203.2
1,069.5
935.8
802.1
668.5
534.8
401.1
267.4
133.7
0

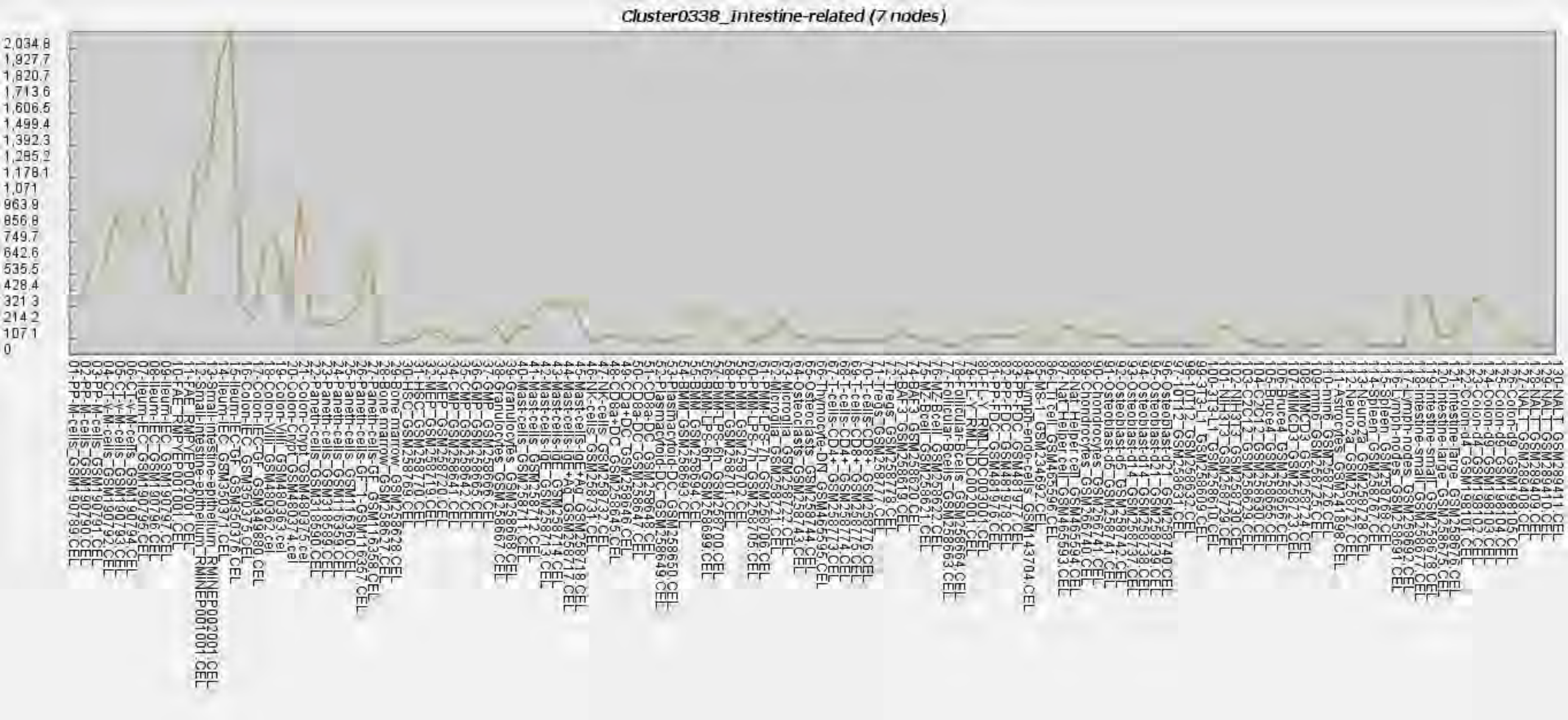

Cluster0333_Intestine-related (7 nodes)
1,453.7
1,377.1
1,300.6
1,224.1
1,147.6
1,071.1
994.6
918.1
841.6
765.1
688.6
612.1
535.6
459
382.5
306
229.5
153
76.5
0


Cluster0334_House keeping (7 nodes)
595.2
563.9
532.5
501.2
469.9
438.6
407.2
375.9
344.6
313.3
281.9
250.6
219.3
188
156.6
125.3
94
62.7
31.3
0

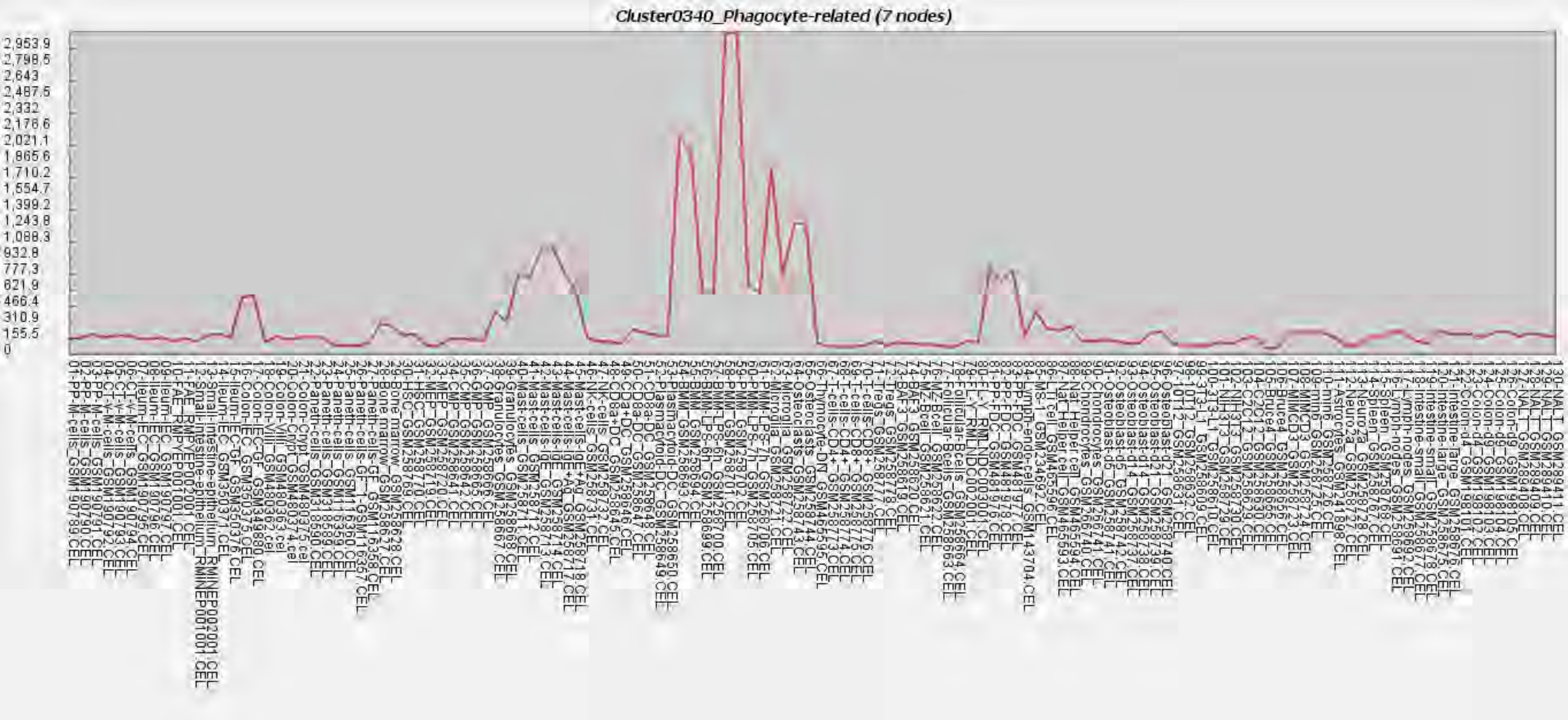
Cluster0335_Small intestine-related (7 nodes)
10,675.4
10,113.5
9,551.7
8,989.8
8,428
7,866.1
7,304.2
6,742.4
6,180.5
5,618.6
5,056.8
4,494.9
3,933
3,371.2
2,809.3
2,247.5
1,685.6
1,123.7
561.9
0


Cluster0336_Mesenchyme-related/extracellular matrix (7 nodes)
991.6
939.4
887.2
835
782.8
730.7
678.5
626.3
574.1
521.9
469.7
417.5
365.3
313.1
260.9
208.8
156.6
104.4
52.2
0

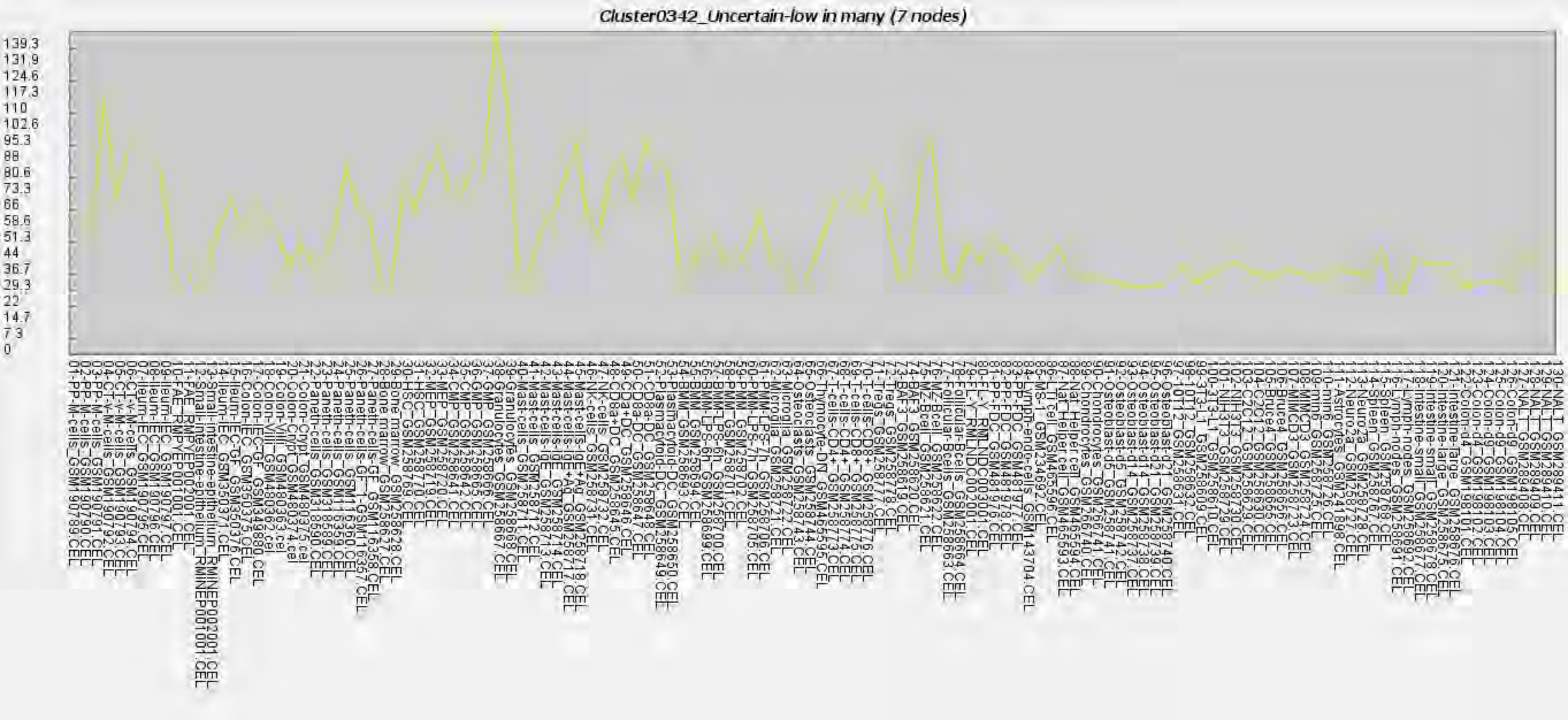

Cluster0337_Uncertain (7 nodes)
2,685.2
2,543.9
2,402.6
2,261.3
2,119.9
1,978.6
1,837.3
1,695.9
1,554.6
1,413.3
1,272
1,130.6
989.3
848
706.6
565.3
424
282.7
141.3
0

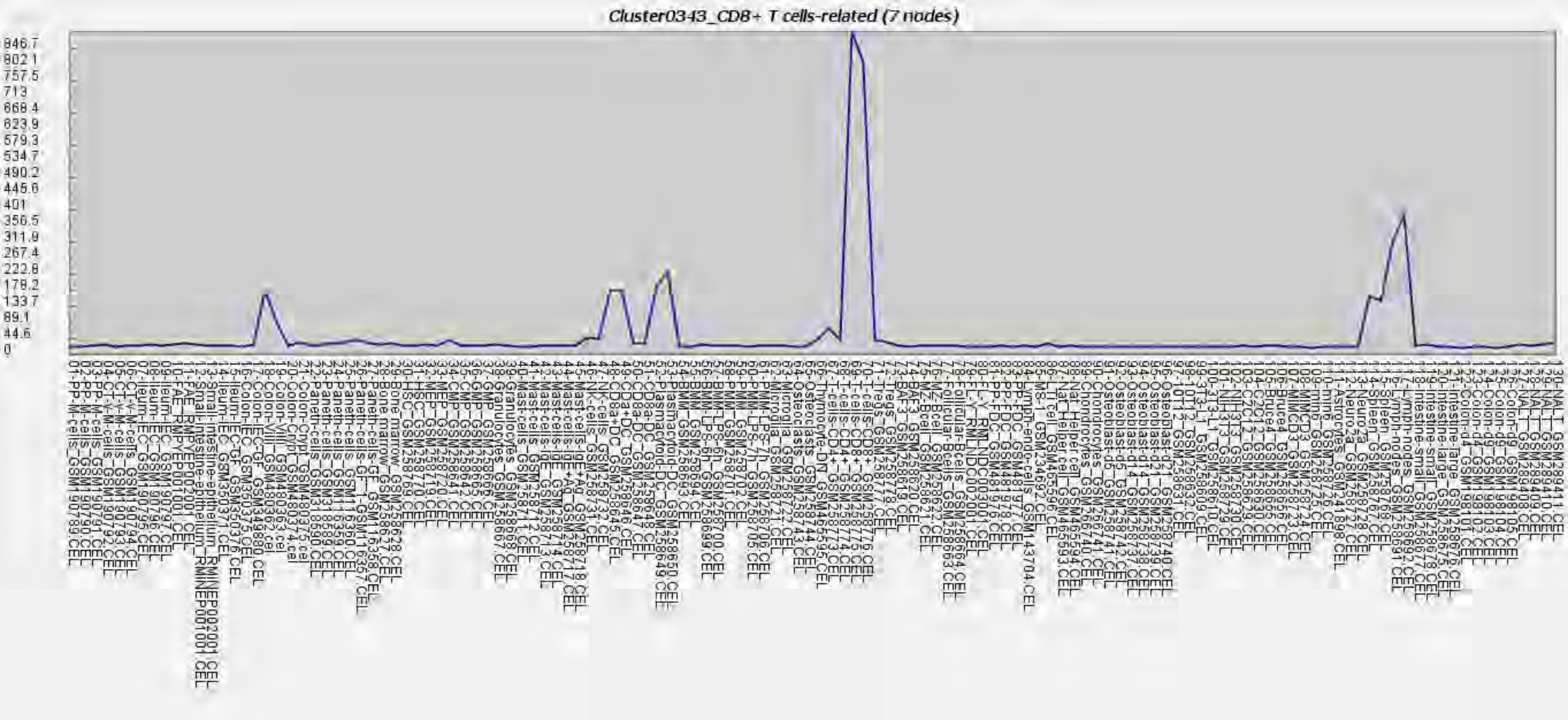

Cluster0338_Intestine-related (7 nodes)
2,034.8
1,927.7
1,820.7
1,713.6
1,606.5
1,499.4
1,392.3
1,285.2
1,178.1
1,071
963.9
856.8
749.7
642.6
535.5
428.4
321.3
214.2
107.1
0

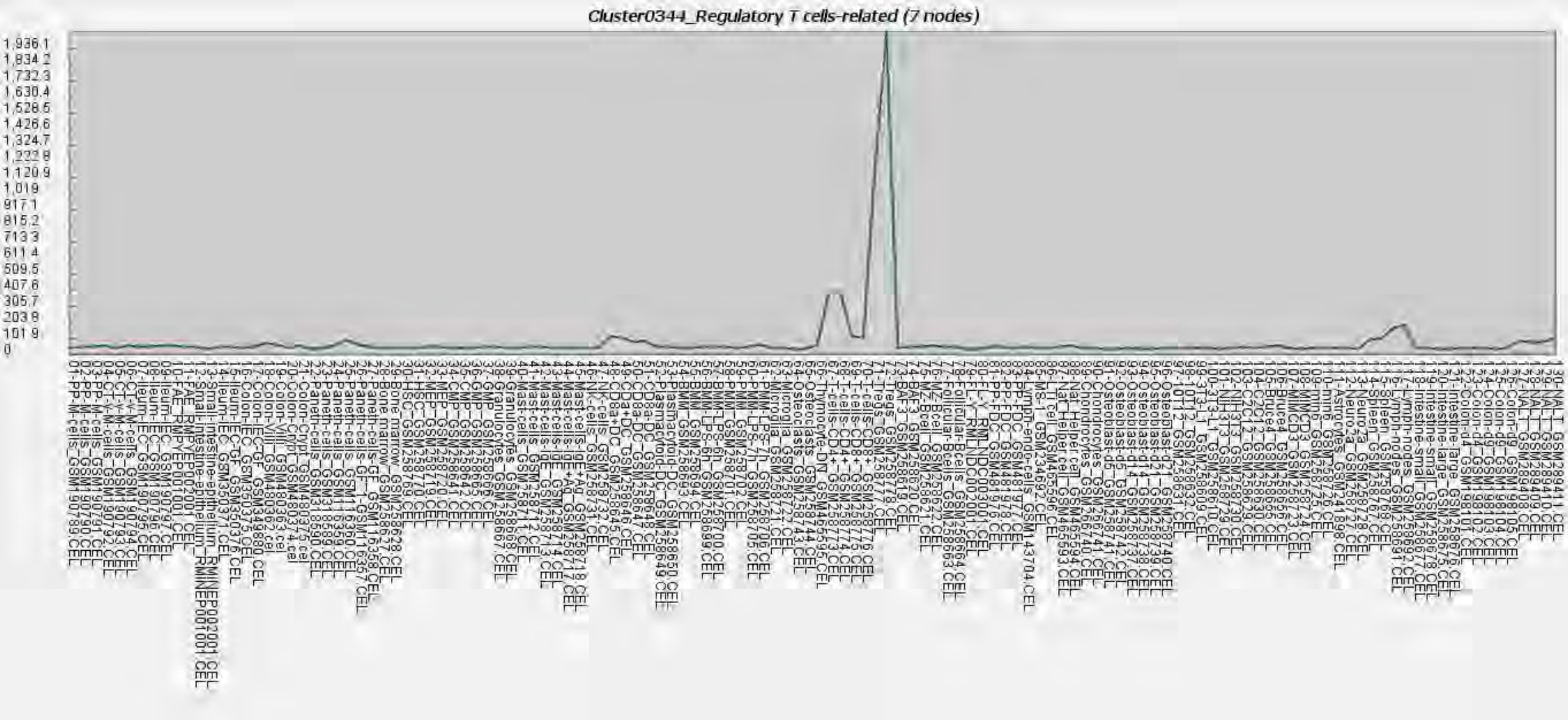
Cluster0339_House keeping (7 nodes)
2,588.8
2,452.5
2,316.3
2,180
2,043.8
1,907.5
1,771.3
1,635
1,498.8
1,362.5
1,226.3
1,090
953.8
817.5
681.3
545
408.8
272.5
136.3
0


Cluster0340_Phagocyte-related (7 nodes)
2,953.9
2,798.5
2,643
2,487.5
2,332
2,176.6
2,021.1
1,865.6
1,710.2
1,554.7
1,399.2
1,243.8
1,088.3
932.8
777.3
621.9
466.4
310.9
155.5
0

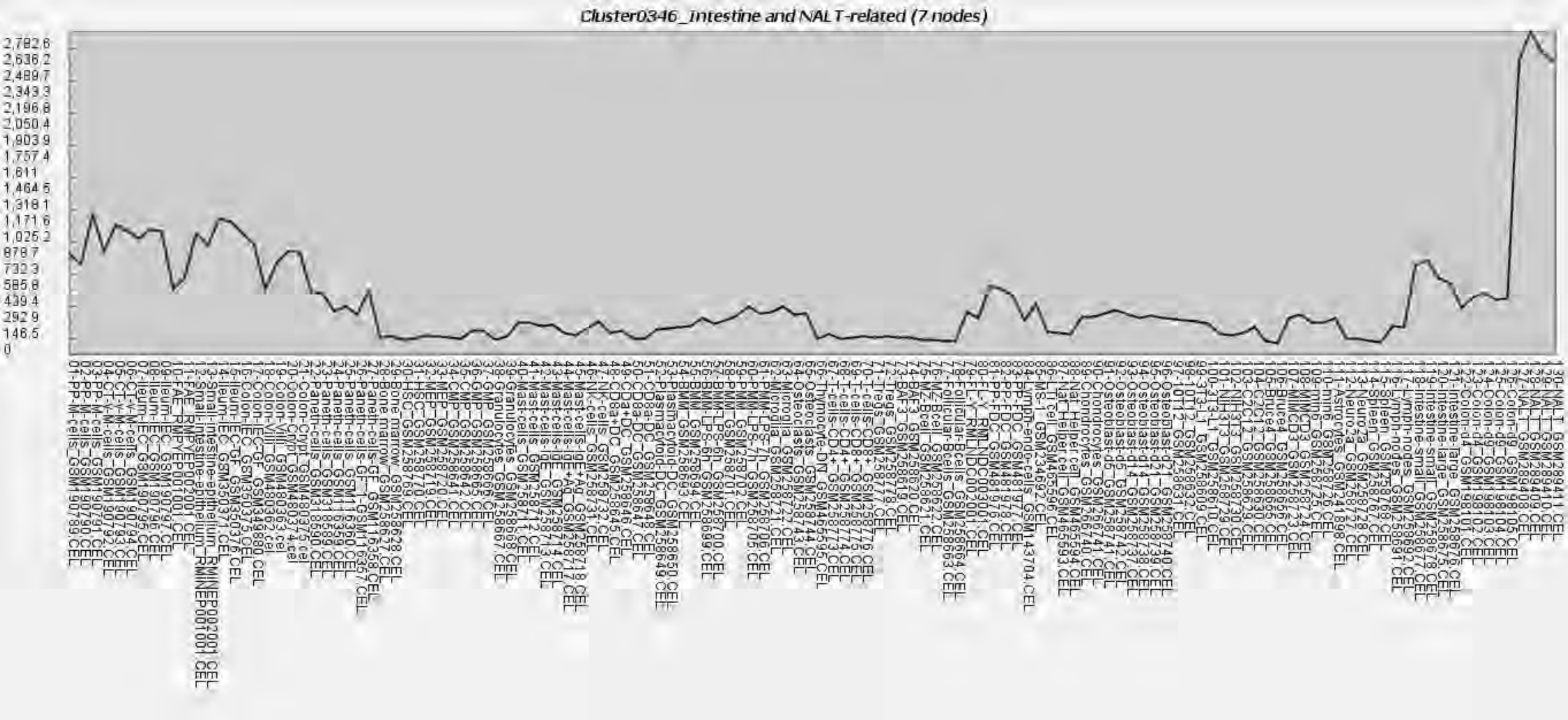
Cluster0341_Mesenchyme-related/extracellular matrix (7 nodes)
765.2
724.9
684.7
644.4
604.1
563.8
523.6
483.3
443
402.7
362.5
322.2
281.9
241.6
201.4
161.1
120.8
80.5
40.3
0

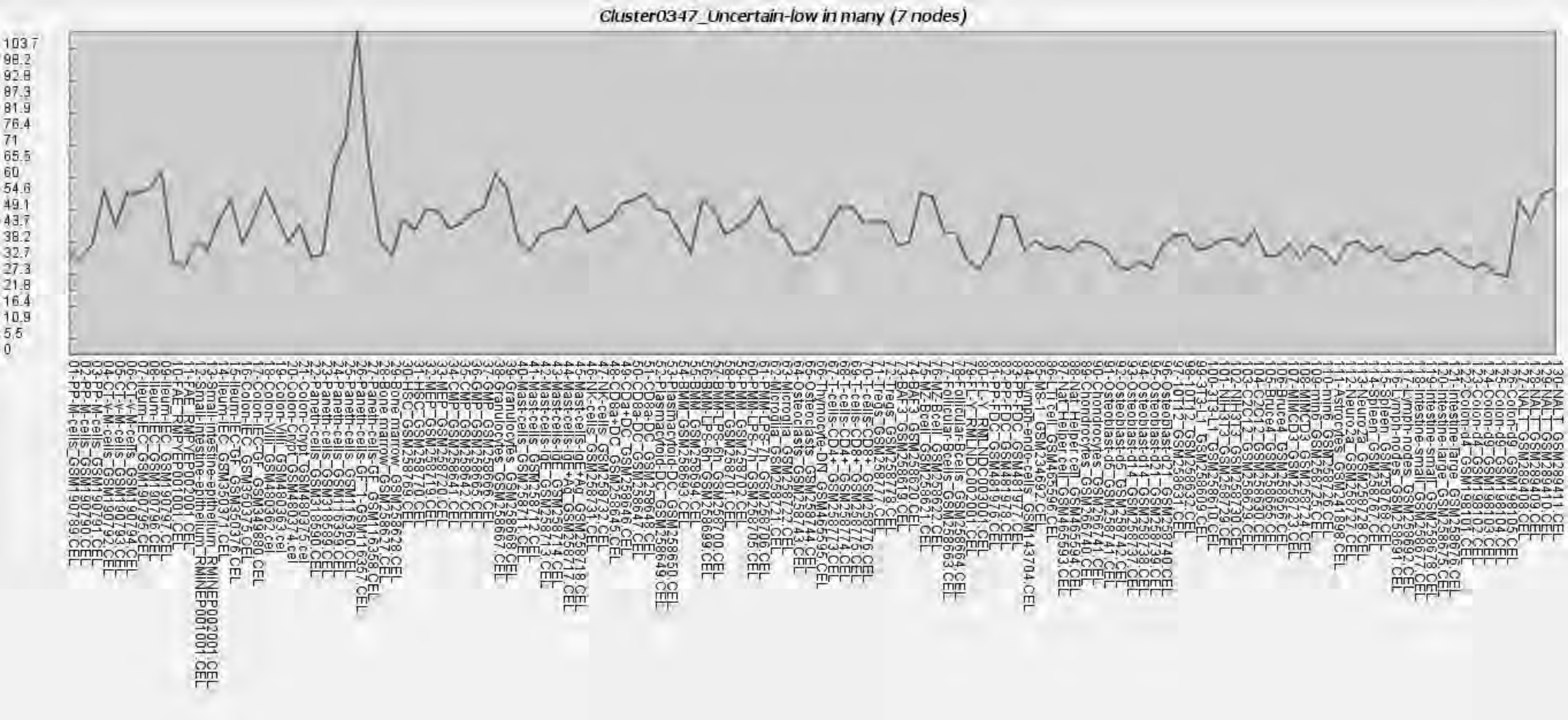

Cluster0342_Uncertain-low in many (7 nodes)
139.3
131.9
124.6
117.3
110
102.6
95.3
88
80.6
73.3
66
58.6
51.3
44
36.7
29.3
22
14.7
7.3
0

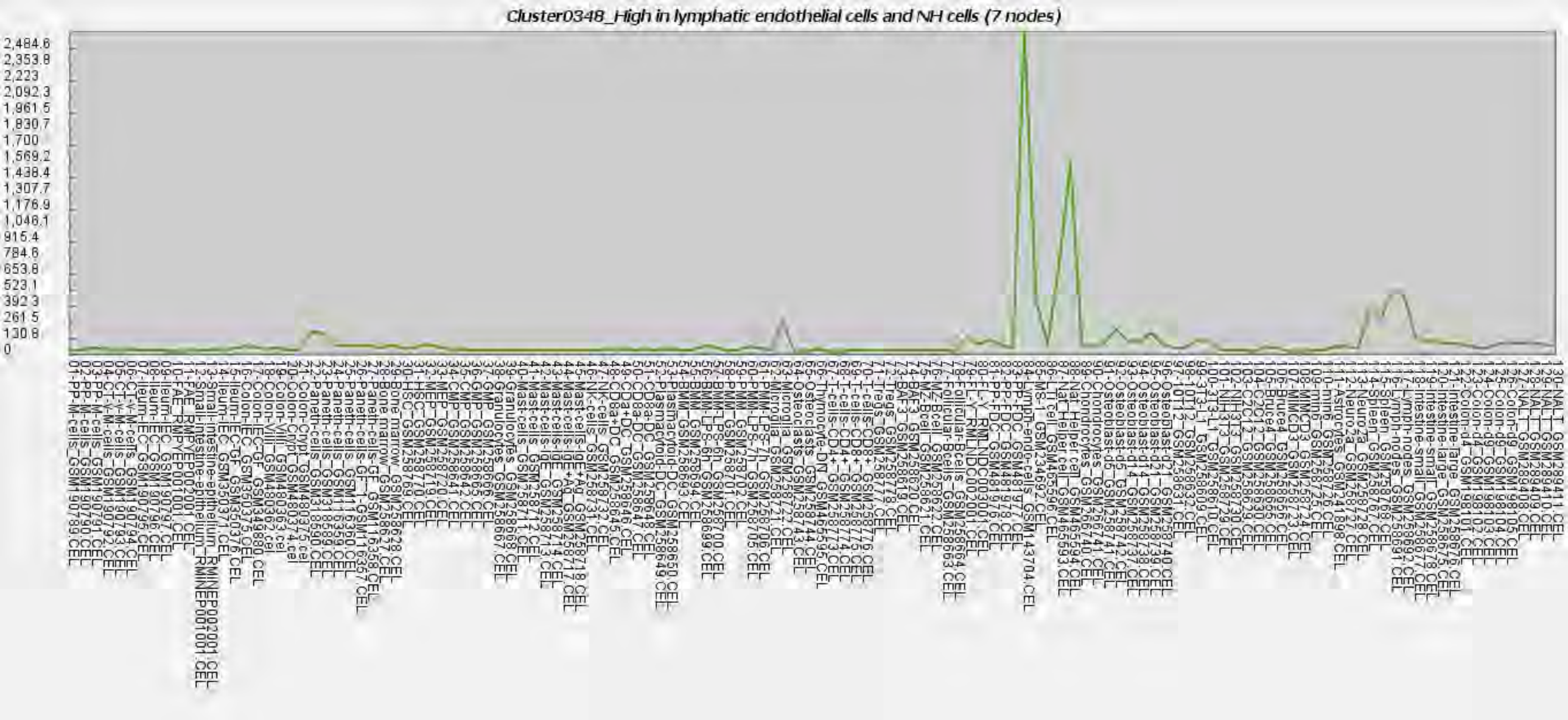

Cluster0343_CD8+ T cells-related (7 nodes)
846.7
802.1
757.5
713
668.4
623.9
579.3
534.7
490.2
445.6
401
356.5
311.9
267.4
222.8
178.2
133.7
89.1
44.6
0

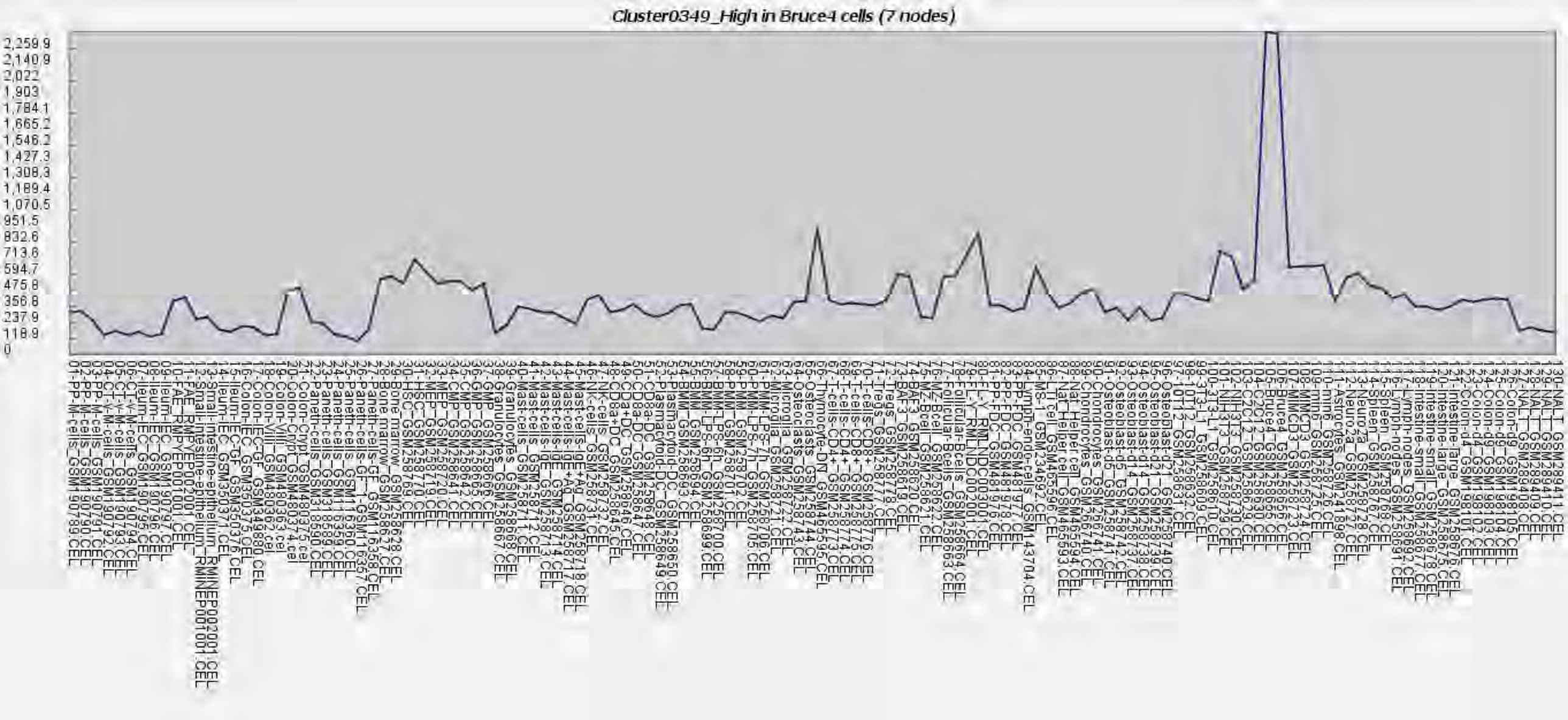

Cluster0344_Regulatory T cells-related (7 nodes)
1,936.1
1,834.2
1,732.3
1,630.4
1,528.5
1,426.6
1,324.7
1,222.8
1,120.9
1,019
917.1
815.2
713.3
611.4
509.5
407.6
305.7
203.8
101.9
0

Cluster0345_Uncertain (7 nodes)
1,362.5
1,290.8
1,219.1
1,147.4
1,075.6
1,003.9
932.2
860.5
788.8
717.1
645.4
573.7
502
430.3
358.5
286.8
215.1
143.4
71.7
0


Cluster0346_intestine and NALT-related (7 nodes)
2,782.6
2,636.2
2,489.7
2,343.3
2,196.8
2,050.4
1,903.9
1,757.4
1,611
1,464.5
1,318.1
1,171.6
1,025.2
878.7
732.3
585.8
439.4
292.9
146.5
0


Cluster0347_Uncertain-low in many (7 nodes)
103.7
98.2
92.8
87.3
81.9
76.4
71
65.5
60
54.6
49.1
43.7
38.2
32.7
27.3
21.8
16.4
10.9
5.5
0


Cluster0348_High in lymphatic endothelial cells and NH cells (7 nodes)
2,484.6
2,353.8
2,223
2,092.3
1,961.5
1,830.7
1,700
1,569.2
1,438.4
1,307.7
1,176.9
1,046.1
915.4
784.6
653.8
523.1
392.3
261.5
130.8
0


Cluster0349_High in Bruce4 cells (7 nodes)
2,259.9
2,140.9
2,022
1,903
1,784.1
1,665.2
1,546.2
1,427.3
1,308.3
1,189.4
1,070.5
951.5
832.6
713.6
594.7
475.8
356.8
237.9
118.9
0