

## **Multi-bioinformatics revealed potential biomarkers and repurposed drugs for gastric adenocarcinoma-related gastric intestinal metaplasia**

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<b>Table S1: Pathways</b>	<b>GIM</b>	<b>GA</b>
Insulin Receptor Signaling	-0.25	0
Pyridoxal 5`-phosphate Savage Pathway	-0.27	0
UDP-N-acetyl-D-galactosamine Biosynthesis II	0	-0.28
Glucose and Glucose-1-phosphate Degradation	0	-0.28
Geramide Degradation	0	-0.28
Acute Myeloid Leukemia Signaling	0	+0.38
Blader Cancer Signaling	0	+0.15
PTEN Signaling	+0.27	-0.27
Dopamine Receptor Signaling	0	-0.57
Remodeling of Epithelial Adherens Junction	0	-0.52
BMP Signaling Pathway	0	-0.69
UVC-induced MAPK Signaling	+0.31	-0.69
Glioma Signaling	+0.28	-0.41
AMPK Signaling	-0.56	-0.07
Inhibition of Angiogenesis by TSP1	-0.42	-0.15
Estrogen-Dependent Breast Cancer Signaling	-0.59	-0.49
Amyloid Processing	-0.42	-0.42
Regulation of Cellular Mechanics by Calpain Protease	+0.80	+0.28
Ovarian Cancer Signaling	+0.74	+0.28
Pancreatic Cancer Signaling	+0.80	+0.27
Neuregulin Signaling	+0.81	+0.14
PhoA Signaling	+0.42	0
STAT3 Pathway	+0.56	0
IL-22 Signaling	+0.42	+0.15
Leukotriene Biosynthesis	+0.77	0
Rac Signaling	+0.79	+0.56
MIF Regulation of Innate Immunity	+0.83	+0.49
Fcy Receptor-Mediated Phagocytosis in Macrophages and Monocytes	+0.56	+0.53
Regulation of eIF4 and p70s6k Signaling	+0.56	+0.67
Salvage Pathways of Pyrimidine Ribonucleotides	+1.12	+0.65
NF-κB Signaling	-0.97	+0.96
Apoptosis Signaling	-0.96	+0.85
HIPPO Signaling	-1.12	+0.83
Small Cell Lung Cancer Signaling	-0.81	+0.59
B Cell Activating Factors Signaling	-0.98	+0.35
P53 Signaling	-0.96	+0.14
April Mediated Signaling	-0.98	0
IL-6 Signaling	0	0
Oncostatin M Signaling	0	+1.92
Chondroitin Sulfate Degradation (Metazoa)	0	+1.05
ATM Signaling	-0.25	+1.08
Folate Polyglutamylation	0	+0.78
Telomerase Signaling	-0.25	+0.77
IL-17A Signaling in Gastrin Cells	0	+0.42

Glycogen Degradation II	0	+0.56
HGF Signaling	+0.28	+0.56
ERK/MAPK Signaling	+0.35	+1.09
Wnt/ $\beta$ -catenin Signaling	+0.42	+1.12
P38 MAPK Signaling	+0.44	+1.01
Role of BRCA1 in DNA Damage Response	+4.34	+1.16
Sirtuin Signaling Pathway	+0.82	+1.26
Death Receptor Signaling	0	+1.89
Purine Nucleotides De NOVO Biosynthesis II	0	+1.83
Acute Phase Response Signaling	0	+1.82
Interferon Signaling	0	+2.08
Tetrahydrofolate Salvage from 5,10-methenyltetrahydrofolate	0	+1.65
Cell cycle Regulation by BTG Family Proteins	0	+1.54
Mitosis Roles of Polo-like Kinase	0	+1.68
Type 1 Diabetes Mellitus Signaling	+0.28	+1.96
Aging Interaction at Neuromuscular Junction	+0.26	+1.51
Guanosine Nucleotides Degradation	+1.96	0
Mevalonate Pathway	+1.96	0
Acyl-coA Hydrolysis	+1.96	0
Sucrose Degradation V(Mammalian)	+1.83	0
Cholesterol Biosynthesis II (via 24,25-dihydrolanosterol)	+2.24	0
Cholesterol Biosynthesis III (via Desmosterol)	+2.24	0
Cholesterol Biosynthesis I	+2.24	0
Citrulline Biosynthesis	+2.24	0
Superpathway of Citrulline Metabolism	+2.66	0
Stearate Biosynthesis I (Animal)	+2.52	-0.25
NRF2-Mediated Oxidative Stress Response	+1.59	+0.40
$\gamma$ -glutamyl Cycle	+1.61	+0.40
CDK5 Signaling	+1.54	+0.41
D-myo-inositol (1,4,5)-tris phosphate Degradation	+1.60	+0.28
Ceramide Signaling	+1.57	+0.25
Glycolysis	+2.05	+0.25
D-myo-inositol-5-phosphate Metabolism	+1.76	+0.25
Glycogen Degradation	+1.96	+0.56
$\gamma$ -linolenate Biosynthesis II (Animal)	+1.33	0
IGF-1 Signaling	+1.26	0
14-3-3-Mediated Signaling	+1.47	0
CD27 Signaling in Lymphocytes	+0.98	-0.37
Superpathway of D-myo-inositol(1,4,5)-tris phosphate Metabolism	+1.40	-0.54
D-myo-inositol(1,4,5,6)-tetrakisphosphate Biosynthesis	+1.75	+1.12
D-myo-inositol(3,4,5,6)-tetrakisphosphate Biosynthesis	+1.12	+1.12
3-phosphoinositide Degradation	+1.67	+0.91
Ephrin Receptor Signaling	+1.33	+1.19
mTOR Signaling	+1.33	+1.26

Induction of Apoptosis by HIV I	+1.24	+1.55
Pyrimidine Ribonucleotides De NOVO Biosynthesis	+2.27	+1.44
Pyrimidine Ribonucleotides Interconversion	+2.26	+1.28
Apelin Liver Signaling Pathway	+1.96	+1.96
IL-8 Signaling	+1.54	+2.38
2-oxobutanoate Degradation	0	-1.61
Methylmalonyl Pathway	0	-1.61
Leucine Degradation	0	-1.54
Oleate Biosynthesis II (Animal)	0	-1.54
Complement System	0	-1.68
Role of CHK Proteins in Cell Cycle Check-point control	+0.31	-1.40
Aldosterone Signaling in Epithelial Cells	+0.71	-1.96
Gluconeogenesis I	+1.38	-0.96
Cell cycle: G2/SM DNA Damage Checkpoint Regulation	+1.41	-0.98
Phenylalanine Degradation IV (Mammalin, via Side Chain)	+1.27	-1.26
Cell Cycle: G1/S Checkpoint Regulation	+0.84	-1.12
D-myo-inositol(1,3,4)-trisphosphate Biosynthesis	+0.81	-0.84
Methylglyoxal Degradation III	+1.96	-1.68
Valine Degradation	+2.02	-1.53
Glutathione-Mediated Detoxification	+1.61	-1.68
Colanic Acid Building Block Biosynthesis	+1.96	-1.26
Bile Biosynthesis, Neural Pathway	+2.24	-1.26
Acid Fatty Acid $\beta$ -Oxidation	+2.63	-1.54
Bupropion Degradation	+2.66	-1.82
Aceton Degradation (to Methylglyoxal)	+2.92	-1.68
Thyroid Hormone Metabolism II (via Conjugation and/or Degradation)	+3.36	-1.26
Glutaryl-coA Degradation	+2.24	-0.84
Superpathway of Cholesterol Biosynthesis	+2.94	-0.56
Granzyme B Signaling	0	+2.66
P13K/AKT Signaling	0	+2.66
Inflammasome Pathway	0	+2.73
GP6 Signaling Pathway	+0.72	+2.66
TREM 1 Signaling	0	+3.36
NER Pathway	-0.68	+1.75
EIF2 Signaling	-1.12	+1.67
Estrogen-Mediated S-Phase Entry	-0.99	+2.45
Cycling and Cell Cycle Regulation	-1.05	+2.52
Dematan Sulfate Degradation (Metaz)	-1.96	+0.70
LPS/IL-1- Mediated Inhibition of RXR Function	-2.38	+0.91
Ary Hydrocarbon Receptor Signaling	-1.54	+0.98
Toll-like Receptor Signaling	-2.1	+1.64
Nicotine Degradation III	+3.71	-2.31
Nicotine Degradation II	+3.85	-2.52
Estrogen Biosynthesis	+3.43	-2.03
Superpathway Of Melatonin Degradation	+4.76	-2.52

Melatonin Degradation	+4.2	-2.52
Serotonin Degradation	+4.2	-3.22
TCA Cycle II (Eukaryotic)	+2.632	-2.66

**Table S2: List of IPA genes in GA-related GIM**

1. AES
2. ANKRD6
3. ARID1A
4. ARR3
5. ARRB1
6. ARRB2
7. AXIN1
8. BCL9
9. BTRC
10. CDH1
11. CDH10
12. CDH11
13. CDH12
14. CDH13
15. CDH15
16. CDH16
17. CDH17
18. CDH18
19. CDH19
20. CDH2
21. CDH20
22. CDH22
23. CDH23
24. CDH24
25. CDH3
26. CDH4
27. CDH5
28. CDH6
29. CDH7
30. CDH8
31. CDH9
32. CDHR1
33. CDHR2
34. CELSR1
35. CELSR2
36. CELSR3
37. CER1
38. CHD1L
39. CREBBP
40. CSNK1A1

41.	CSNK1A1L
42.	CSNK1D
43.	CSNK1G2
44.	CSNK1G3
45.	CSNK2A1
46.	CSNK2A2
47.	CSNK2B
48.	CTBP1
49.	CTBP2
50.	CTNNA1
51.	CTNNA2
52.	CTNNA3
53.	CTNNAL1
54.	CTNNB1
55.	DACT1
56.	DCHS1
57.	DVL1
58.	DVL2
59.	DVL3
60.	EP300
61.	EP400
62.	FAT1
63.	FAT2
64.	FAT3
65.	FBXW11
66.	FRZB
67.	FZD1
68.	FZD10
69.	FZD2
70.	FZD3
71.	FZD4
72.	FZD5
73.	FZD6
74.	FZD7
75.	FZD8
76.	FZD9
77.	GNA11
78.	GNA14
79.	GNA15
80.	GNAQ
81.	GNB1
82.	GNB2
83.	GNB3
84.	GNB4
85.	GNG10
86.	GNG12

87.	GNG13
88.	GNG2
89.	GNG3
90.	GNG4
91.	GNG5
92.	GNG7
93.	GNG8
94.	GSK3B
95.	HDAC1
96.	HDAC2
97.	HDAC3
98.	HDAC8
99.	HELLS
100.	HLTF
101.	INO80
102.	ITPR1
103.	ITPR2
104.	ITPR3
105.	KREMEN1
106.	KREMEN2
107.	LEF1
108.	LRP5
109.	LRP6
110.	MAP3K7
111.	NFATC1
112.	NFATC2
113.	NFATC3
114.	NFATC4
115.	NKD1
116.	NKD2
117.	NLK
118.	PCDH1
119.	PCDH10
120.	PCDH11X
121.	PCDH11Y
122.	PCDH12
123.	PCDH15
124.	PCDH18
125.	PCDH19
126.	PCDH20
127.	PCDH7
128.	PCDH8
129.	PCDH9
130.	PCDHA1
131.	PCDHA10
132.	PCDHA11

133. PCDHA12
134. PCDHA13
135. PCDHA2
136. PCDHA3
137. PCDHA4
138. PCDHA5
139. PCDHA6
140. PCDHA7
141. PCDHA8
142. PCDHA9
143. PCDHAC1
144. PCDHAC2
145. PCDHB1
146. PCDHB10
147. PCDHB11
148. PCDHB12
149. PCDHB13
150. PCDHB14
151. PCDHB15
152. PCDHB16
153. PCDHB2
154. PCDHB3
155. PCDHB4
156. PCDHB5
157. PCDHB6
158. PCDHB7
159. PCDHB8
160. PCDHGA1
161. PCDHGA10
162. PCDHGA11
163. PCDHGA12
164. PCDHGA2
165. PCDHGA3
166. PCDHGA5
167. PCDHGA6
168. PCDHGA7
169. PCDHGA8
170. PCDHGB1
171. PCDHGB2
172. PCDHGB4
173. PCDHGB6
174. PCDHGB7
175. PCDHGC3
176. PCDHGC4
177. PCDHGC5
178. PLCB1



179. PLCB2
180. PLCB3
181. PLCB4
182. PPP2CA
183. PPP2CB
184. PPP2R5A
185. PPP2R5B
186. PPP2R5C
187. PPP2R5D
188. PPP2R5E
189. PPP3CA
190. PPP3CB
191. PPP3CC
192. PPP3R1
193. PPP3R2
194. PRKCA
195. PRKCB
196. PRKCD
197. PRKCE
198. PRKCG
199. PRKCH
200. PRKCI
201. PRKCQ
202. PRKCZ
203. PYGO1
204. PYGO2
205. SAG
206. SFRP1
207. SFRP2
208. SFRP4
209. SFRP5
210. SIAH1
211. SMAD1
212. SMAD4
213. SMARCA1
214. SMARCA2
215. SMARCA4
216. SMARCA5
217. SMARCAL1
218. SMARCB1
219. SMARCC1
220. SMARCC2
221. SMARCD1
222. SMARCD2
223. SMARCD3
224. SMARCE1

225. SRCAP
226. TBL1X
227. TBL1XR1
228. TBL1Y
229. TCF7L1
230. TCF7L2
231. TLE1
232. TLE2
233. TLE3
234. TLE4
235. TLE6
236. WNT1
237. WNT10A
238. WNT10B
239. WNT11
240. WNT16
241. WNT2
242. WNT2B
243. WNT3
244. WNT3A
245. WNT4
246. WNT5A
247. WNT5B
248. WNT6
249. WNT7A
250. WNT7B
251. WNT8A
252. WNT8B
253. WNT9A
254. WNT9B
255. ATF2
256. CDC42
257. CREB1
258. DDIT3
259. ELK1
260. H3F3A
261. H3F3B
262. HMGN1
263. HRAS
264. HSPB1
265. MAP2K4
266. MAP2K6
267. MAP3K1
268. MAP3K5
269. MAP3K9
270. MAPK14

271. MAPKAPK2
272. MAPKAPK5
273. MAX
274. MEF2A
275. MEF2BNB-MEF2B
276. MEF2C
277. MEF2D
278. MKNK1
279. MYC
280. NR2C2
281. PLA2G1B
282. RAC1
283. RPS6KA5
284. STAT1
285. ATM
286. ATR
287. BRCA1
288. BRCA2
289. CHEK1
290. CHEK2
291. FANCA
292. FANCC
293. FANCD2
294. FANCE
295. FANCF
296. FANCG
297. HUS1
298. MRE11A
299. NBN
300. RAD1
301. RAD17
302. RAD50
303. RAD51
304. RAD9A
305. TP53
306. TREX1
307. AKR7A2
308. CRYZ
309. FOS
310. FXRD2
311. GSTA2
312. HMOX1
313. HMOX2
314. JUN
315. KEAP1
316. MAFF

317. MAFG
318. MAFK
319. NFE2L2
320. POR
321. UGT1A6
322. CNDP2
323. GCLC
324. GCLM
325. GGCT
326. GGT5
327. GSS
328. OPLAH
329. ADCY1
330. ADRBK1
331. CAMK2B
332. CDK5
333. CDK5R1
334. DRD1
335. DRD2
336. GNAS
337. GNGT1
338. GRM1
339. NCS1
340. PPP1CA
341. PPP1R1B
342. PRKACB
343. PRKACG
344. ACTB
345. ACTG1
346. ACTR2
347. ACTR3
348. ADAM10
349. ANKS1A
350. AP2A1
351. AP2A2
352. AP2B1
353. AP2M1
354. AP2S1
355. APH1A
356. APH1B
357. ARHGEF28
358. ARHGEF7
359. ARPC1A
360. ARPC2
361. ARPC3
362. ARPC5

363. CFL1
364. CHN1
365. CRK
366. DNM1
367. EFNA1
368. EFNA2
369. EFNA3
370. EFNA4
371. EFNA5
372. EFNB1
373. EFNB2
374. EFNB3
375. EPHA1
376. EPHA10
377. EPHA2
378. EPHA3
379. EPHA4
380. EPHA5
381. EPHA6
382. EPHA7
383. EPHA8
384. EPHB1
385. EPHB2
386. EPHB3
387. EPHB4
388. EPHB6
389. FYN
390. GIT1
391. GRIN1
392. GRIN2B
393. ITSN1
394. KALRN
395. LIMK1
396. LYN
397. MMP2
398. MMP9
399. MYH10
400. MYH11
401. MYH14
402. MYH9
403. MYL12A
404. MYL12B
405. MYL6
406. MYL9
407. NCK2
408. NCSTN

409. NGEF
410. PAK1
411. PAK3
412. PSEN2
413. PSENEN
414. PTK2
415. PTPN11
416. RASA1
417. RHOA
418. ROCK1
419. ROCK2
420. SDC2
421. SDCBP
422. SIPA1L1
423. SRC
424. SS18
425. TIAM1
426. VAV2
427. VAV3
428. WASL
429. YES1
430. AKT1
431. EIF3A
432. EIF4A1
433. EIF4B
434. EIF4E
435. EIF4EBP1
436. EIF4G1
437. FKBP1A
438. GH1
439. GHR
440. IRS1
441. MTOR
442. PDK2
443. PDPK1
444. PIK3CA
445. PIK3R1
446. PTEN
447. RHEB
448. RPS6
449. RPS6KB1
450. TSC1
451. TSC2
452. ADIPOQ
453. AGTR1
454. APLN

455. APLNR
456. ATF4
457. AVP
458. BMPR2
459. COL1A1
460. CRP
461. GHRL
462. HIF1A
463. IGF1
464. LEP
465. MIR224
466. NAMPT
467. OPRK1
468. PPARG
469. RETN
470. AGR2
471. AMOT
472. AMOTL2
473. AREG
474. CTGF
475. DICER1
476. EGFR
477. FRMD6
478. GFER
479. HMMR
480. HPCA
481. ILK
482. LATS1
483. LATS2
484. MARK1
485. MIR31
486. MOB1A
487. NEK2
488. NEWENTRY
489. NF2
490. NPHP4
491. PHLPP1
492. PJA2
493. PKP2
494. PTPN14
495. RASSF1
496. RASSF6
497. RB1
498. SAV1
499. STK3
500. STK4

501. TEAD1
502. TEAD4
503. TGFB1
504. VPRBP
505. WWTR1
506. YAP1
507. YY1AP1
508. ABCF1
509. ATF5
510. BZW2
511. EEF1E1
512. EIF1
513. EIF1AX
514. EIF2A
515. EIF2AK2
516. EIF2B1
517. EIF2S1
518. EIF2S2
519. EIF2S3
520. EIF5
521. MCL1
522. VEGFA
523. CCNH
524. CDKN1A
525. CUL4A
526. CUL4B
527. DDB1
528. DDB2
529. E2F1
530. ERCC1
531. ERCC2
532. ERCC3
533. ERCC4
534. ERCC5
535. GLI1
536. GTF2H4
537. H2AFX
538. HMGB1
539. MDM2
540. MIR192
541. MMS19
542. PARP1
543. RNF2
544. RPA1
545. SIRT1
546. TP63



547. USP7
548. VCP
549. XPA
550. XPC
551. XRCC1
552. CDKN1B
553. CORO1B
554. CSPG5
555. ERBB2
556. ERBB3
557. ERBB4
558. L1CAM
559. MIR145
560. MUC4
561. NRG1
562. NRG3
563. NRG4
564. P2RY2
565. PRKD1
566. RNF41
567. SLC1A6
568. TNF
569. TRPV1
570. YY1
571. ABI1
572. ABL1
573. ADGRA2
574. AIRE
575. AJUBA
576. ARF6
577. ARHGAP24
578. ARHGAP32
579. AXL
580. BAIAP2
581. BAIAP2L1
582. BCAR1
583. BCAR3
584. BCL2
585. BCR
586. CADM1
587. CASP3
588. CCL2
589. CCL5
590. CCND1
591. CCR1
592. CCR5

593. CEP135
594. CHN2
595. CHUK
596. CTNND1
597. CTTN
598. CXCL12
599. CXCR4
600. DOCK1
601. DOCK2
602. ELMO1
603. ELMO2
604. ENOX2
605. F2
606. FER
607. FMNL1
608. FN1
609. FSCN1
610. GRASP
611. HRH1
612. IL10
613. IL1B
614. ITGA2B
615. ITGA4
616. ITGB1
617. ITGB3
618. KIT
619. LCK
620. LPAR1
621. MAPK8
622. MIR149
623. MIR21
624. MTSS1
625. NCF2
626. NCKIPSD
627. NFKB1
628. NISCH
629. NOX1
630. NOX5
631. NOXA1
632. OCRL
633. PARVB
634. PDGFB
635. PIK3CG
636. PIP5K1A
637. PIP5K1C
638. PLAU

639. PLAUR
640. PLCG2
641. F2RL1
642. KITLG
643. MIF
644. NME1
645. TXN
646. ADAM17
647. ANGPT2
648. ANKS1B
649. APC
650. AR
651. ARHGEF4
652. BIRC5
653. BMP7
654. BMPR1B
655. C3
656. CD40LG
657. CD44
658. CDKN2A
659. CFTR
660. CLIP1
661. CNKSR3
662. COL3A1
663. CSF1
664. CXCL8
665. CYP19A1
666. DLL4
667. EGF
668. EGR1
669. EREG
670. ETS1
671. EZR
672. FAS
673. FGF2
674. FGF7
675. FLT3LG
676. FPR2
677. FURIN
678. GAB1
679. GINGF3
680. GRP
681. HEY2
682. HGF
683. HGFAC
684. HLX

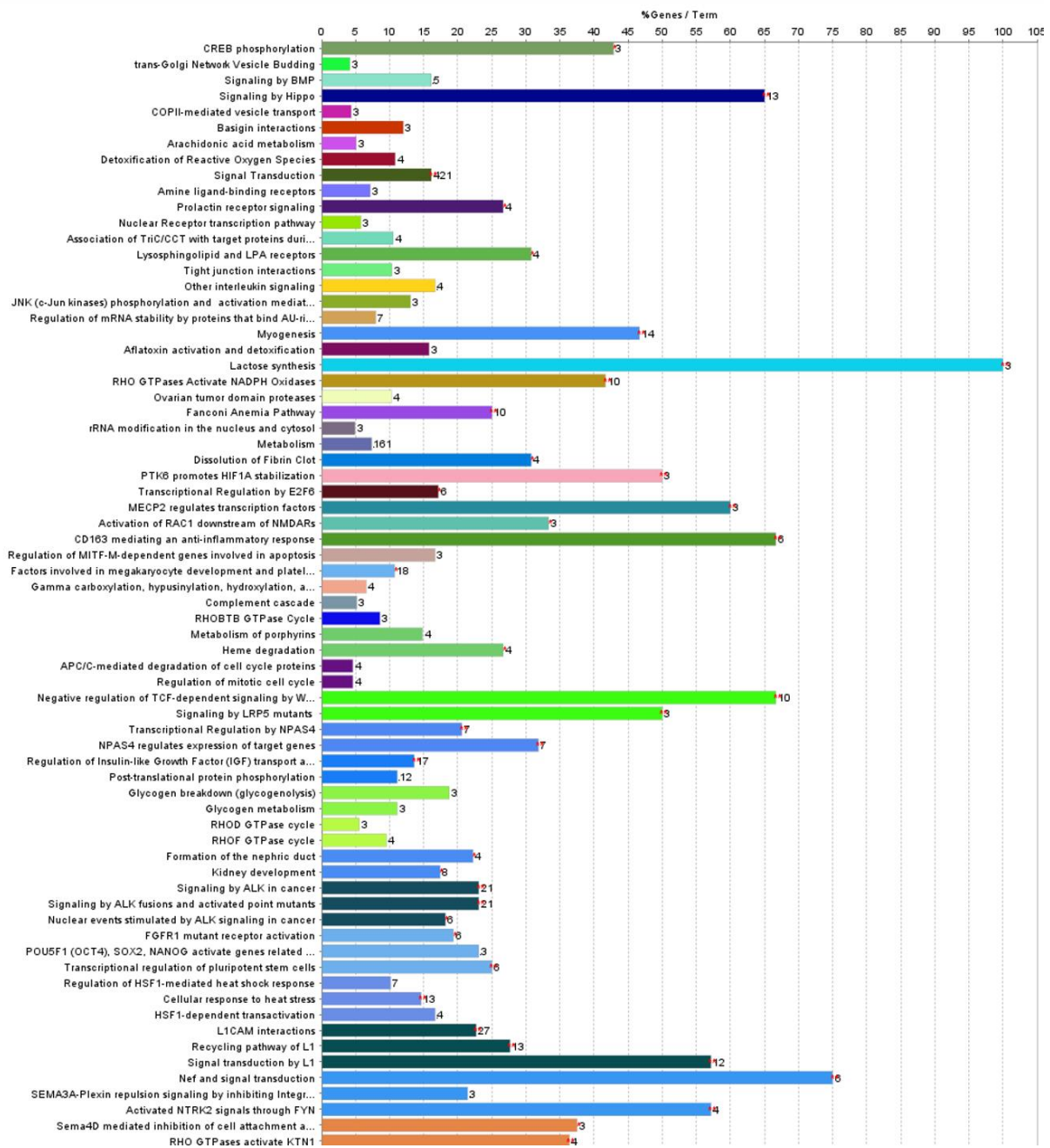
685. HPN
686. HPSE
687. ID1
688. IGF1R
689. IL11
690. IL1RN
691. IL32
692. IL6
693. IPCEF1
694. ITGA2
695. ITGB2
696. ITGB4
697. JUNB
698. KIF5B
699. KLF4
700. KLF6
701. KRAS
702. LIF
703. LUM
704. MACC1
705. MAPK1
706. MET
707. MIR199A1
708. MIR200C
709. MIR27B
710. MIR519C
711. MMP1
712. MMP3
713. MMP7
714. MMP8
715. MYD88
716. NFYC
717. NOTCH1
718. NOTCH3
719. NOX4
720. PAK2
721. PAK6
722. PDGFA
723. PGF
724. PLG
725. PROM1
726. PTGS2
727. PXN
728. RELA
729. RGMB
730. S1PR1

731. S1PR2
732. S1PR3
733. SDC1
734. SERPINE1
735. SHC1
736. SKIL
737. SLC2A4
738. SMAD2
739. SMYD3
740. SNAI1
741. SP1
742. SPINT1
743. SPINT2
744. SPP1
745. ST14
746. STAT3
747. TGIF1
748. THBS1
749. TICAM2
750. TIMP1
751. TLR4
752. WASF2
753. XIAP
754. AFP
755. ALDH1A1
756. CALB2
757. CD24
758. CLDN7
759. EPCAM
760. ERAP2
761. FOLR1
762. GPA33
763. GPNMB
764. IFNAR2
765. KRT19
766. MAML1
767. MLH1
768. MSH2
769. PTTG1
770. TSPAN8
771. VCAM1
772. WISP1
773. ABCA1
774. SREBF1
775. ADPGK
776. AGL

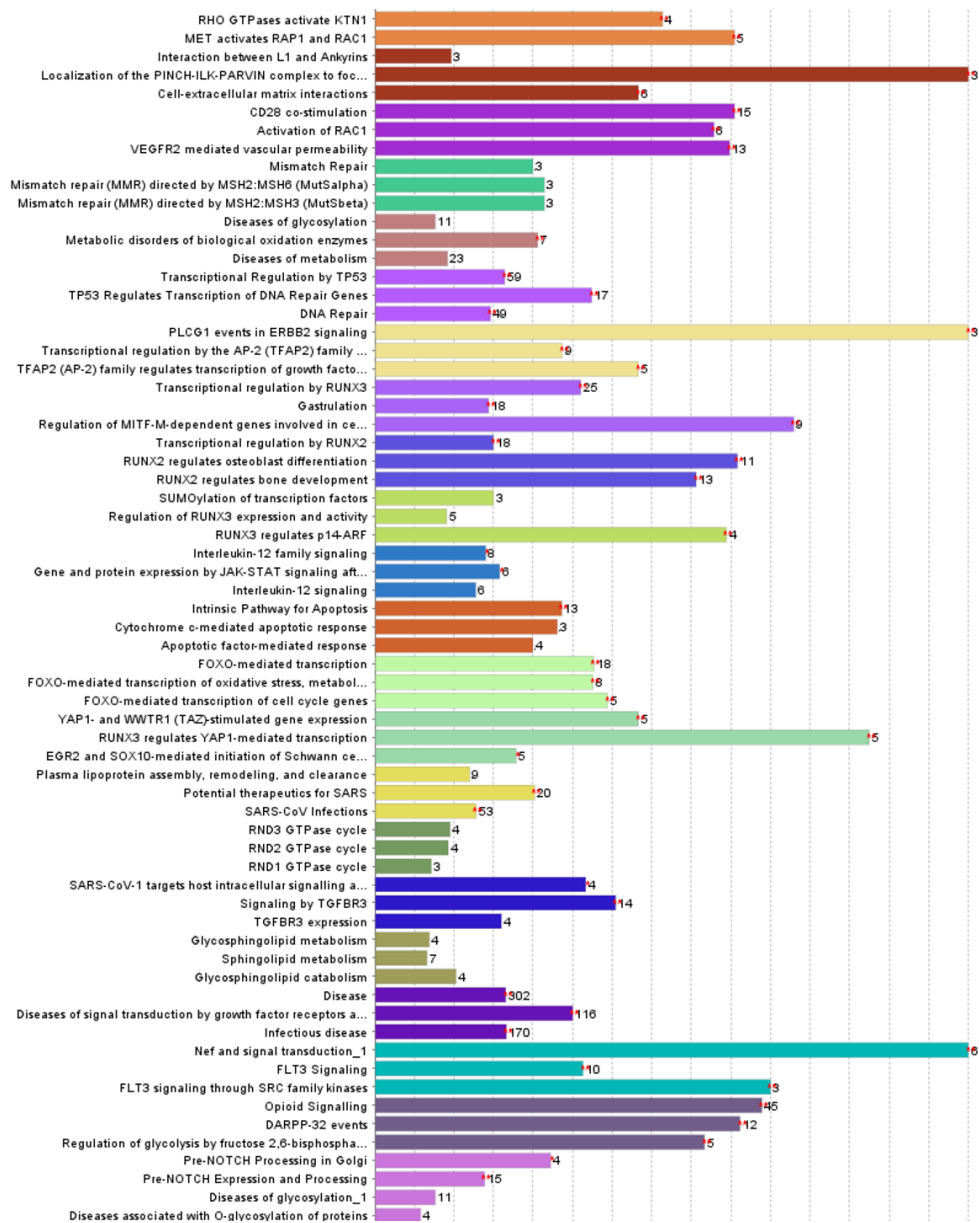
777. B4GALT1
778. B4GALT2
779. G6PC
780. G6PC2
781. G6PC3
782. GAA
783. GANAB
784. GANC
785. GBA
786. GBA2
787. GBA3
788. GCK
789. GCKR
790. GLA
791. GPI
792. HK1
793. HK2
794. HK3
795. HKDC1
796. LALBA
797. LCT
798. MGAM
799. MOGS
800. PGM1
801. SI
802. SLC2A1
803. TREH
804. HSD17B1
805. ADH1B
806. ADH6
807. ALDH2
808. ALDH3A2
809. MAOA
810. SULT1A1
811. SULT1A2
812. UGT2B11
813. ABCC2
814. CHST5
815. CYP3A4
816. PPP1R14D
817. SULT1A3/SULT1A4
818. UGT1A1
819. UGT2B7
820. UGT2B17
821. CLDN3
822. HLA-DPB1

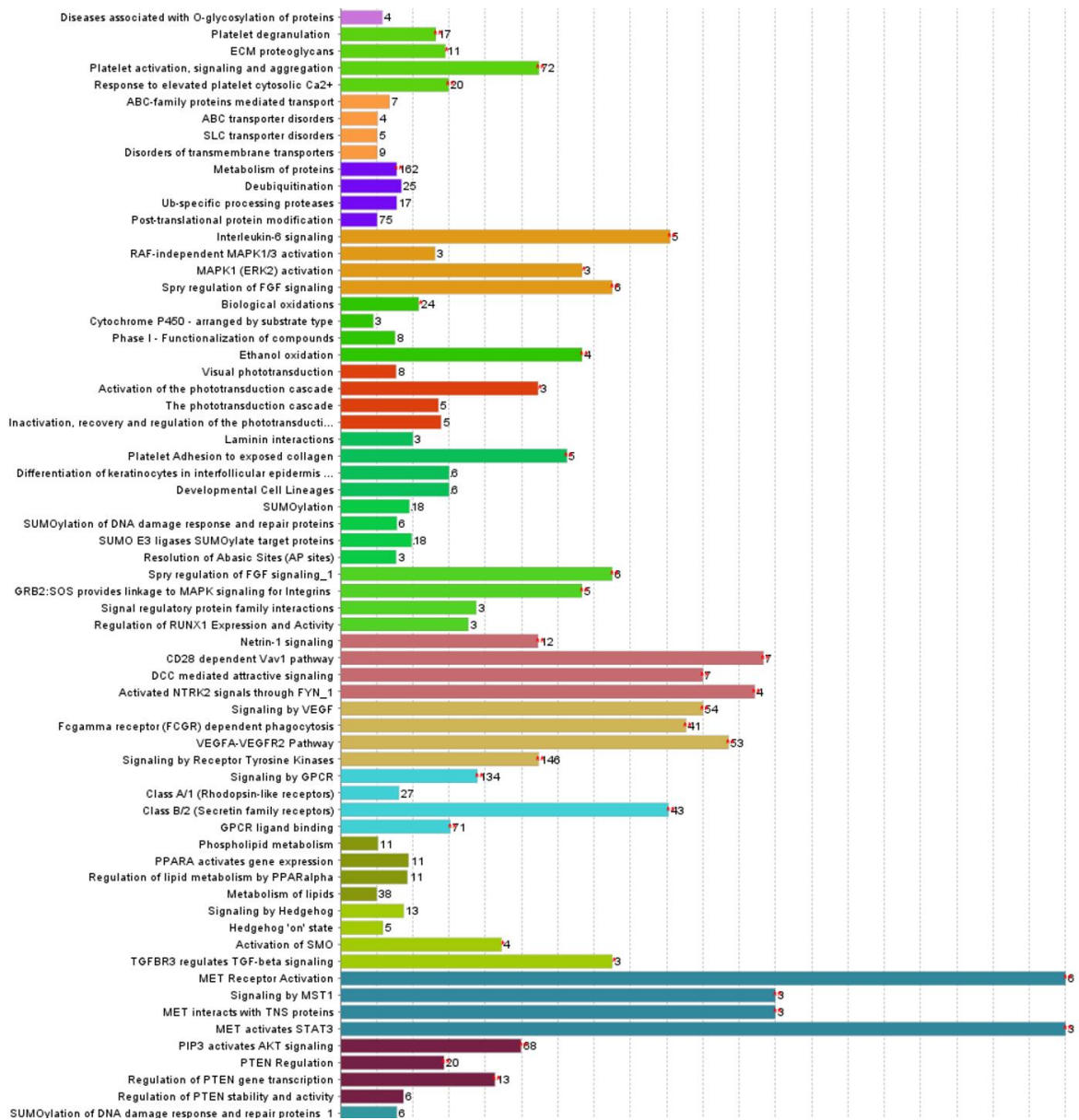
823. HLA-DQB1
824. HLA-DPA1
825. HLA-DMB
826. RPS13
827. RPL22
828. RPL13A
829. RPL11
830. RPL38
831. RPS7
832. RPL6
833. RPL26
834. RPL5
835. RPS3
836. PCBD1
837. RPL23
838. RPL10A
839. KLF5
840. RPL14
841. RPL1
842. RPS20
843. EEF1A1
844. RPS23
845. RPL15
846. FGFR4
847. RPL35A
848. RPL9
849. RPS15A
850. RPSA
851. SOCS3
852. RPS25
853. RPL37
854. RPL30
855. APP
856. RPLP1
857. RPS5
858. RPS24
859. RPL13
860. IGFBP4
861. CYSTM1
862. DDC
863. RPS14
864. WFDC2
865. RBM47

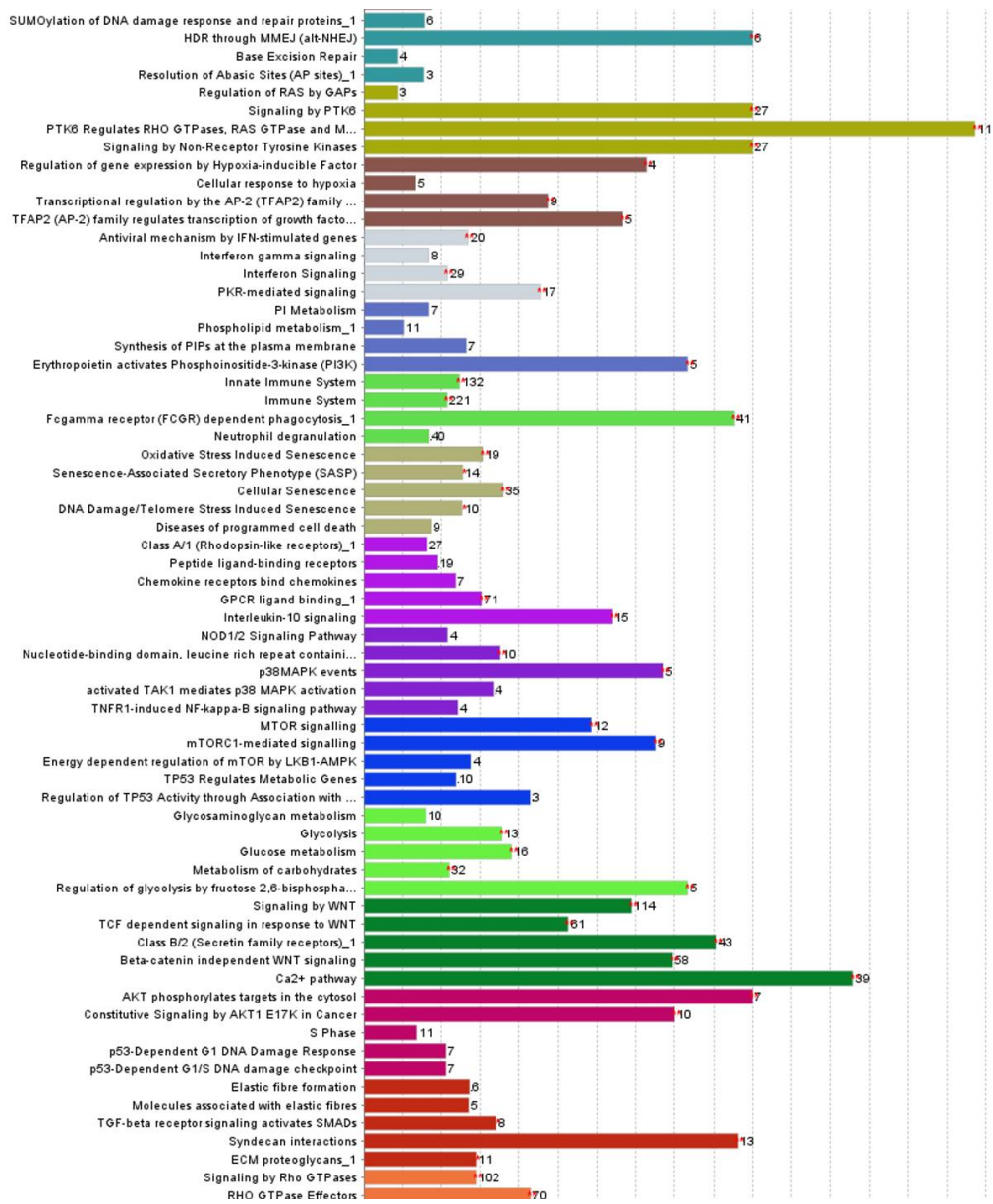
**Table S3 List of % genes per term in GA-related GIM**

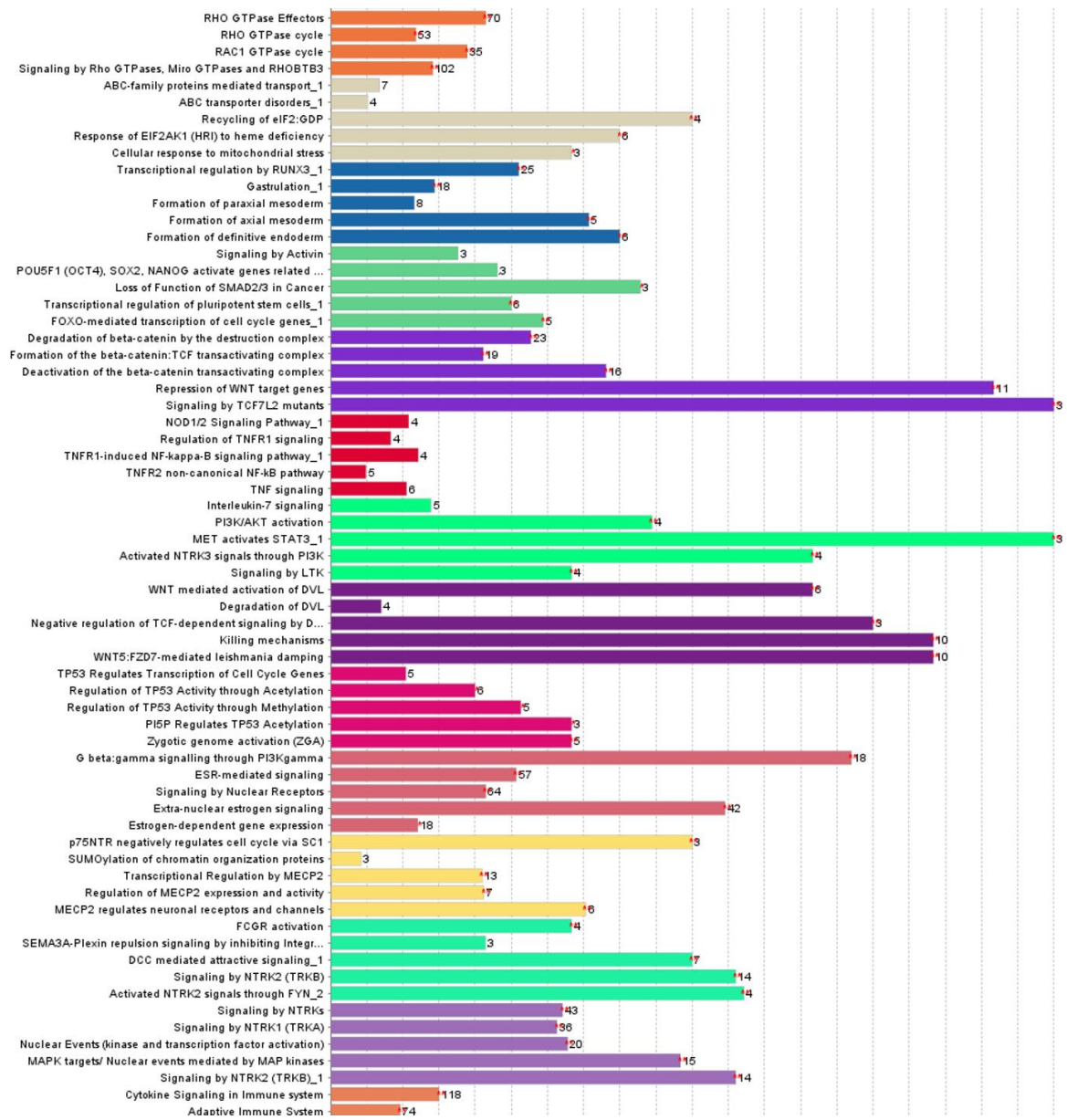


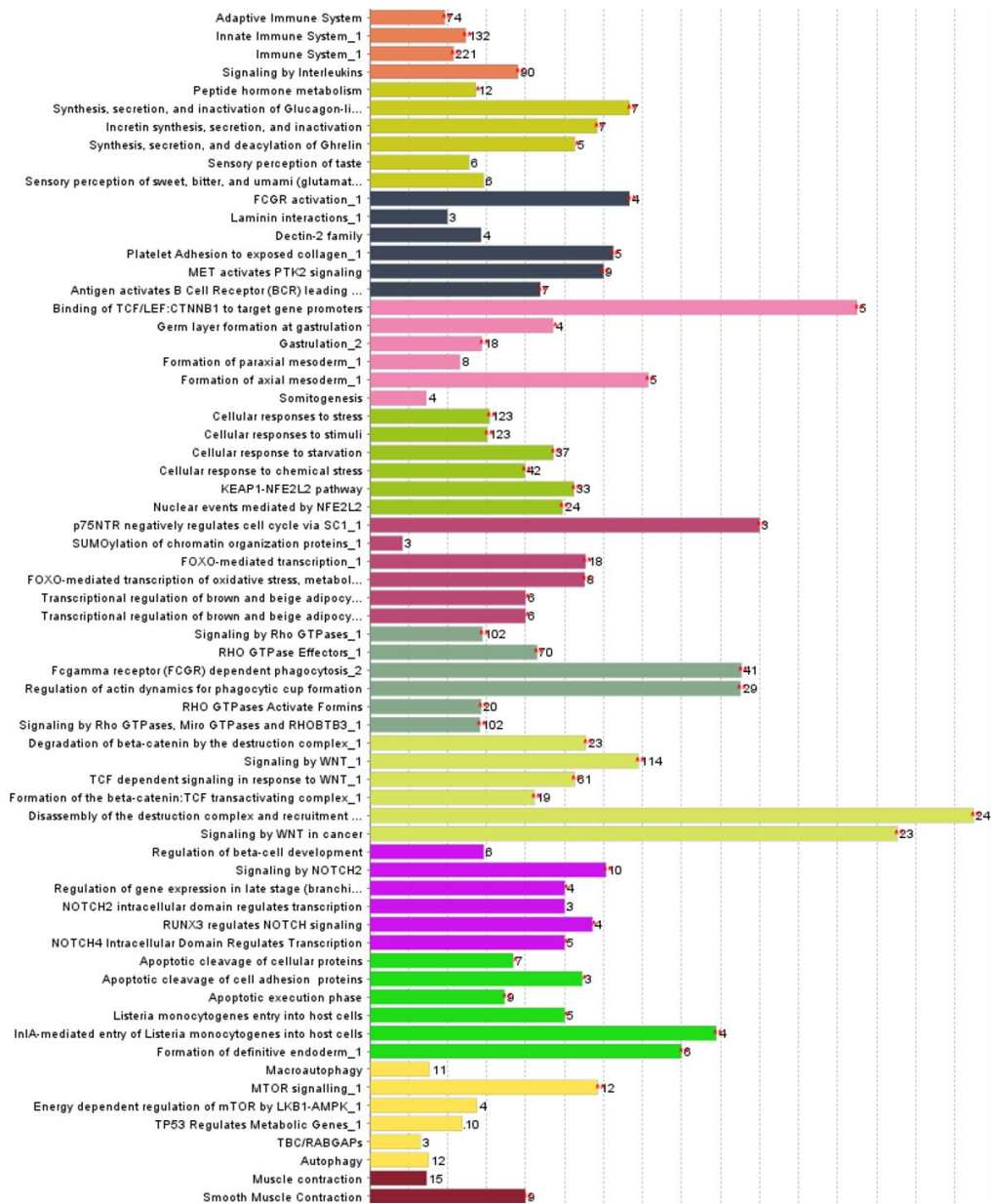


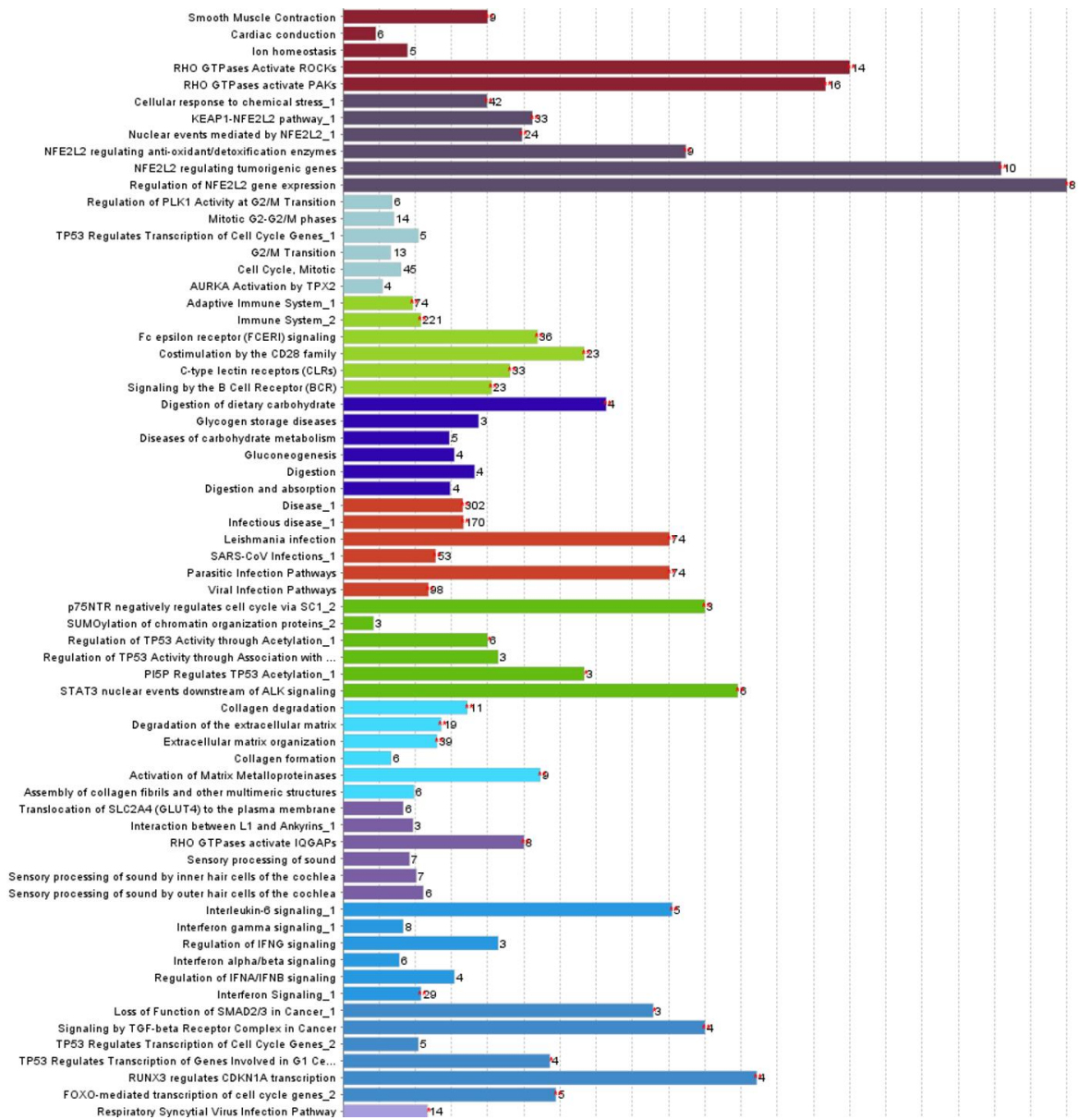


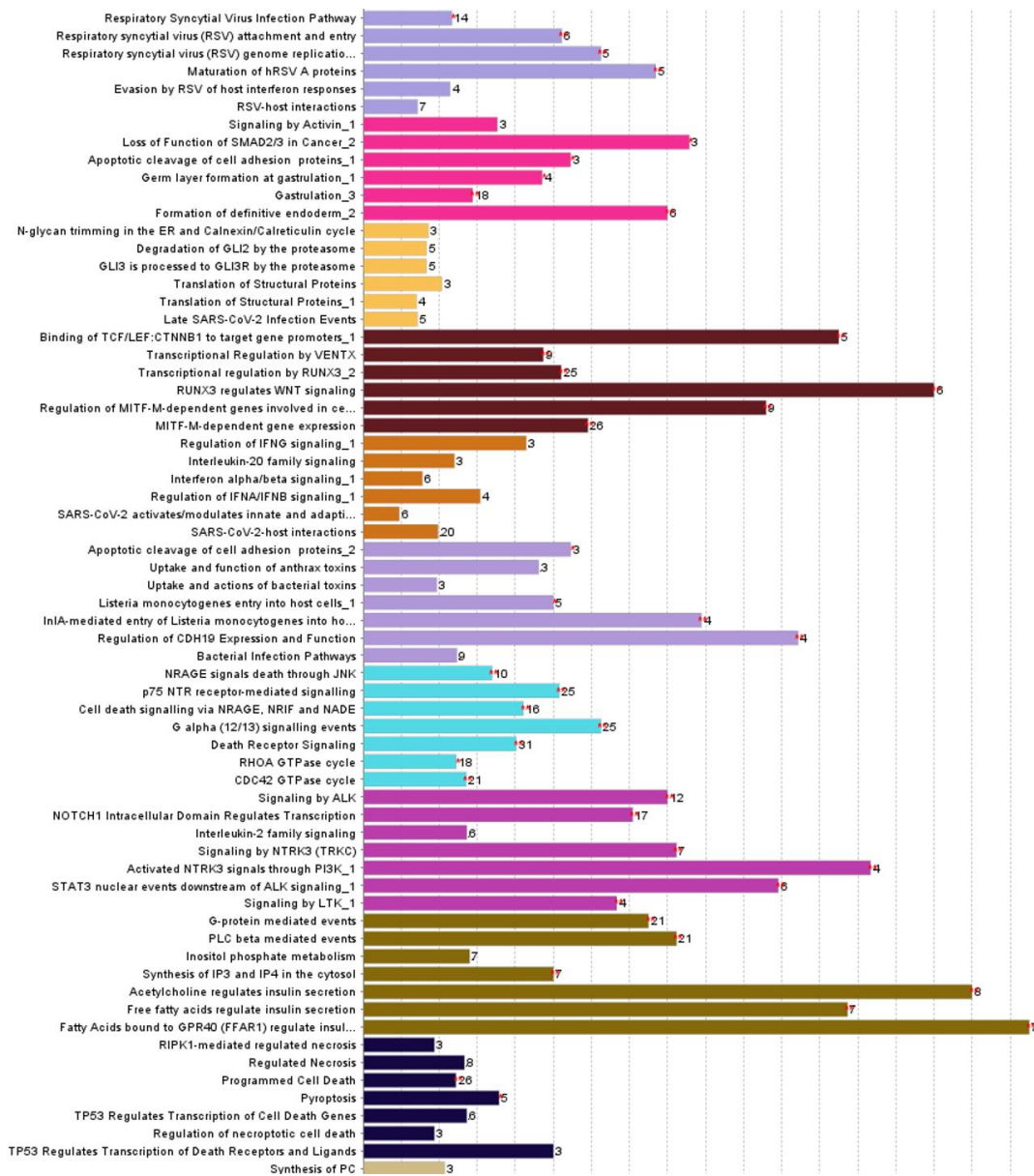






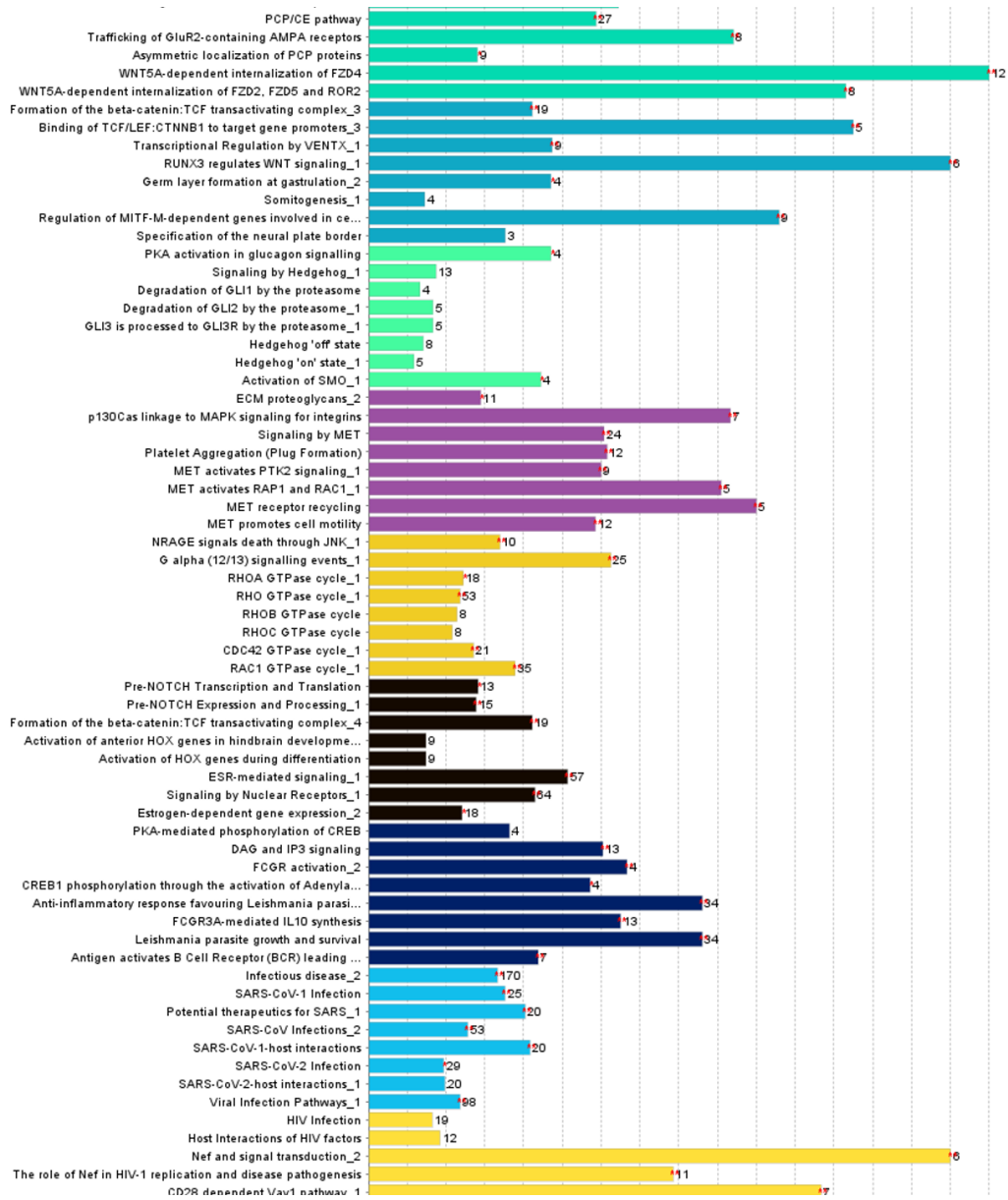


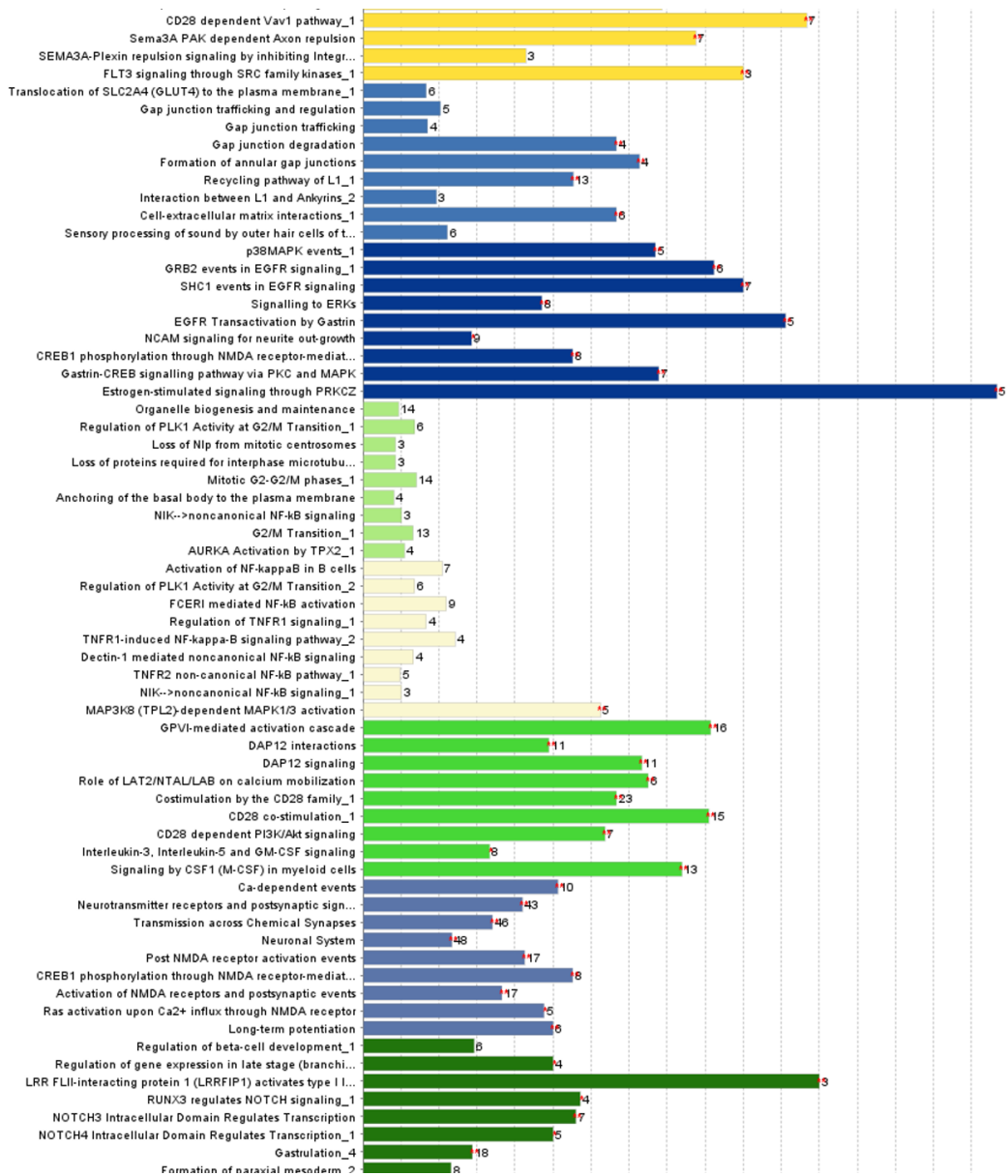






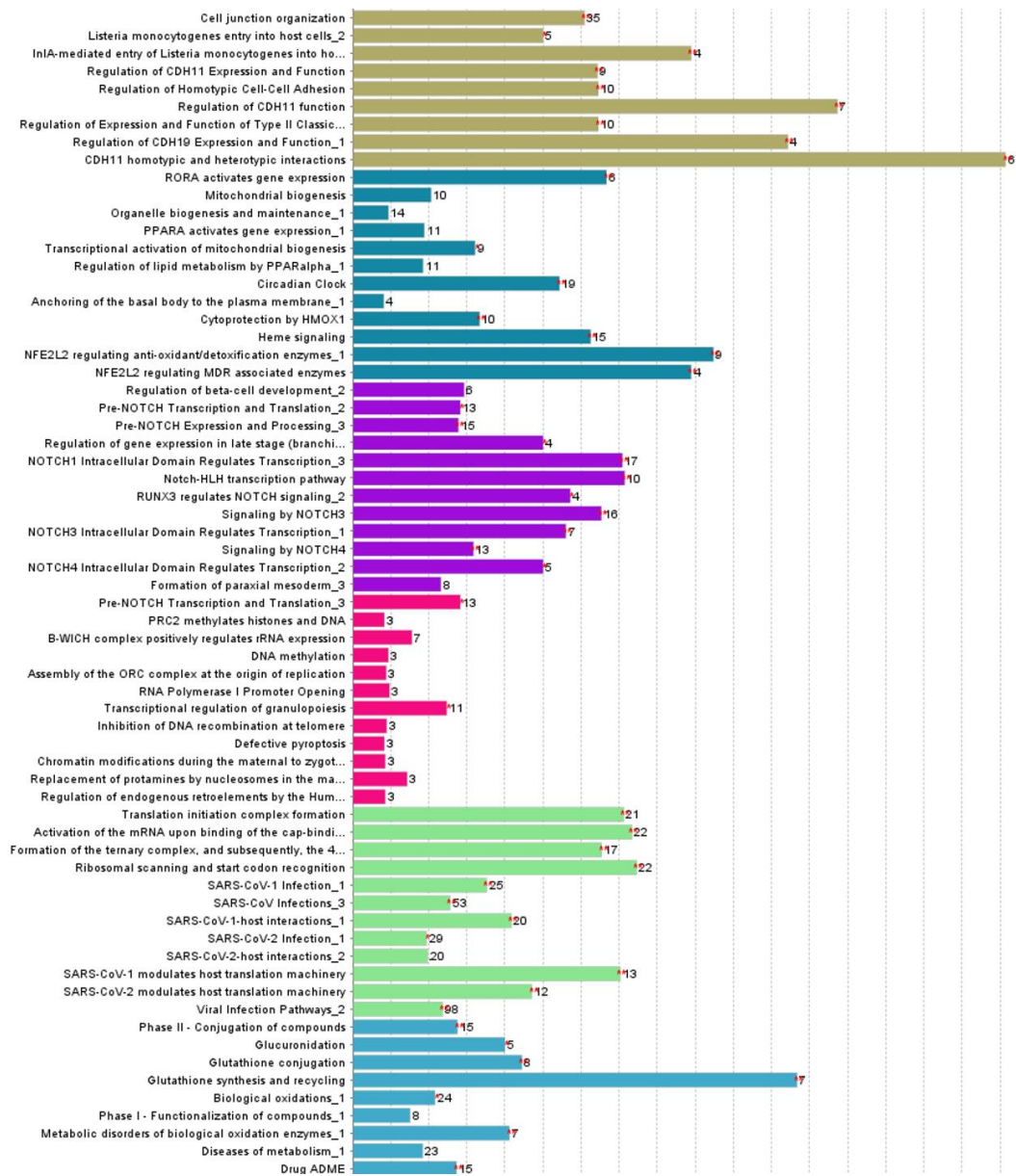


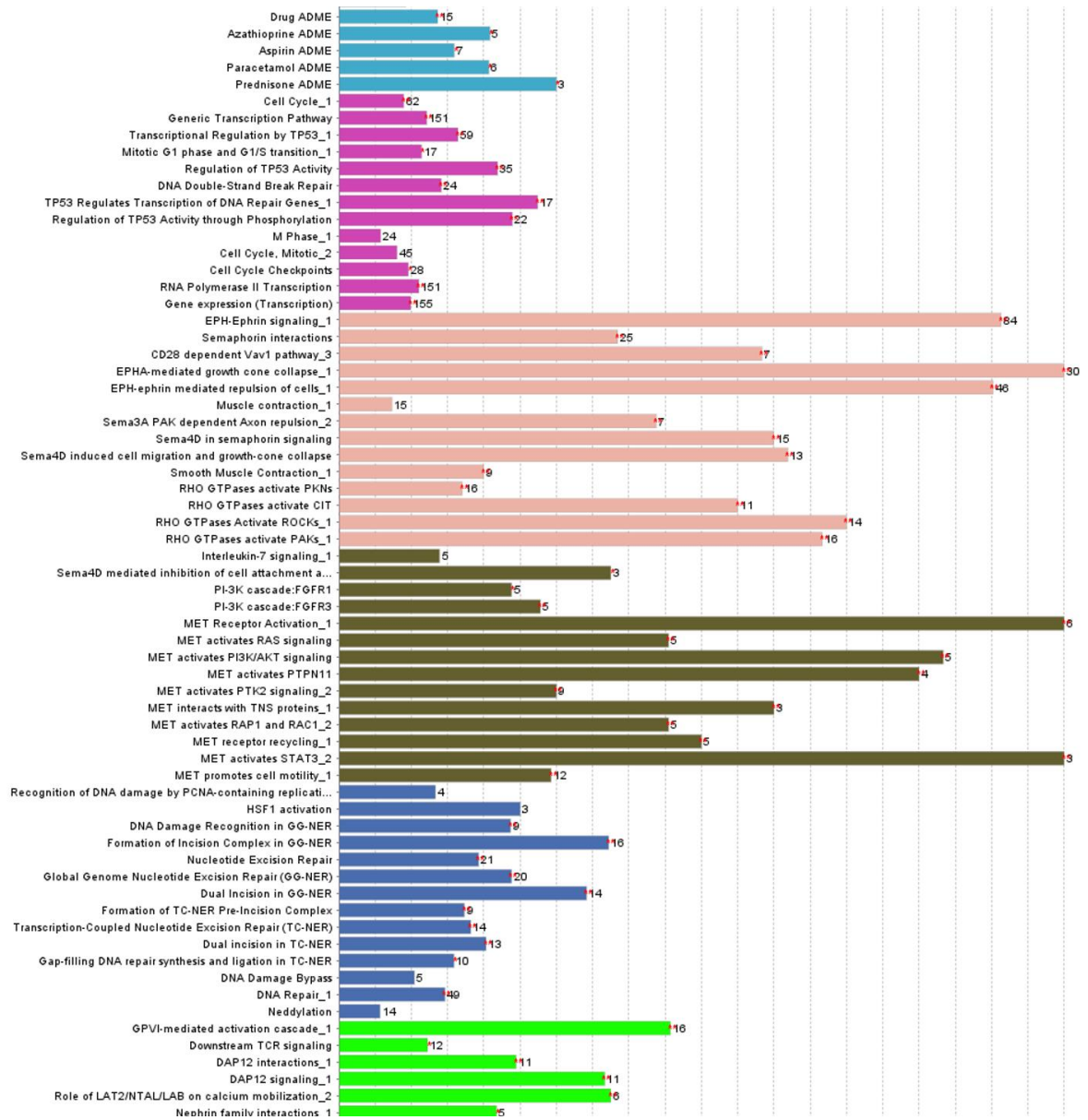


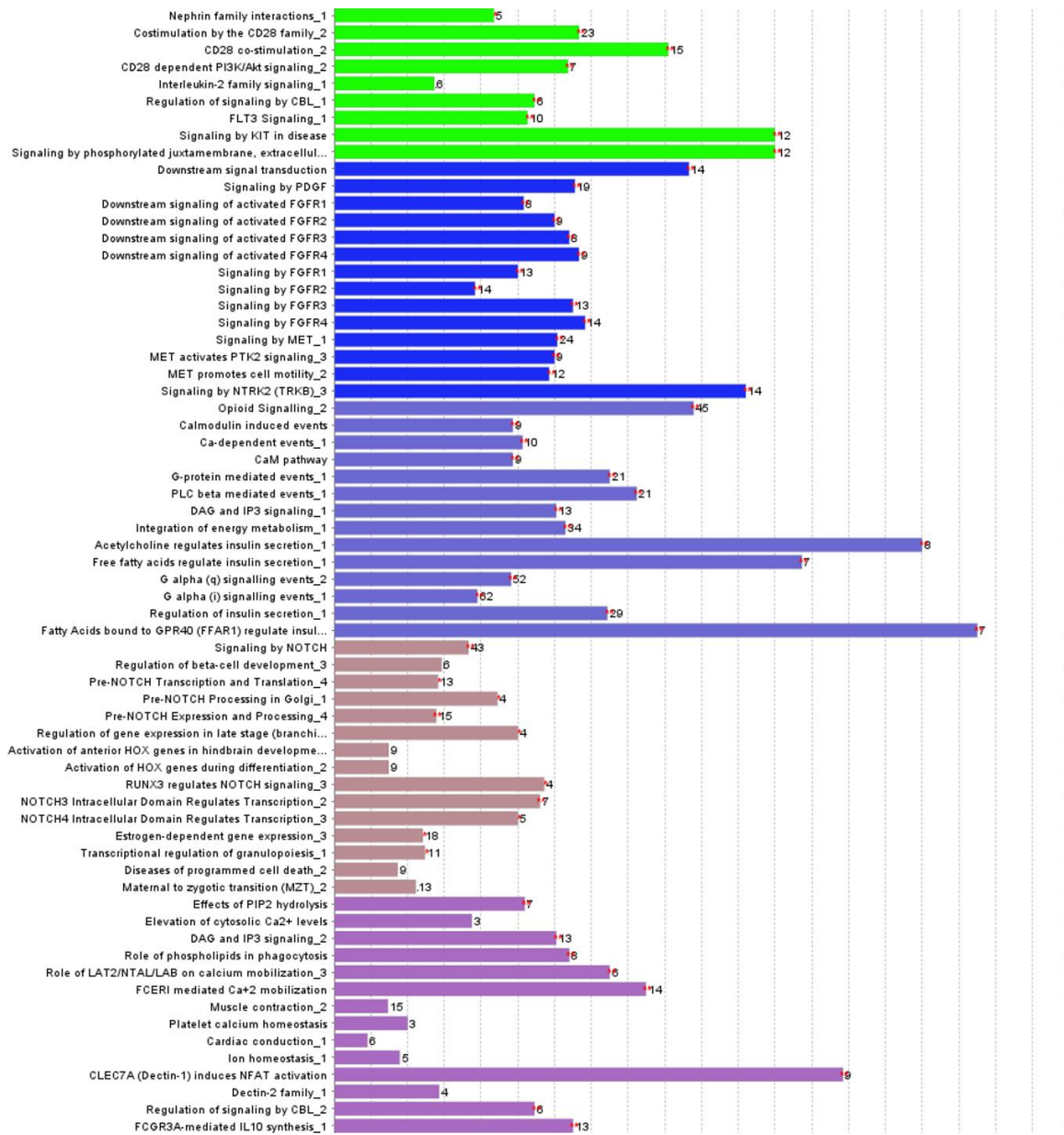


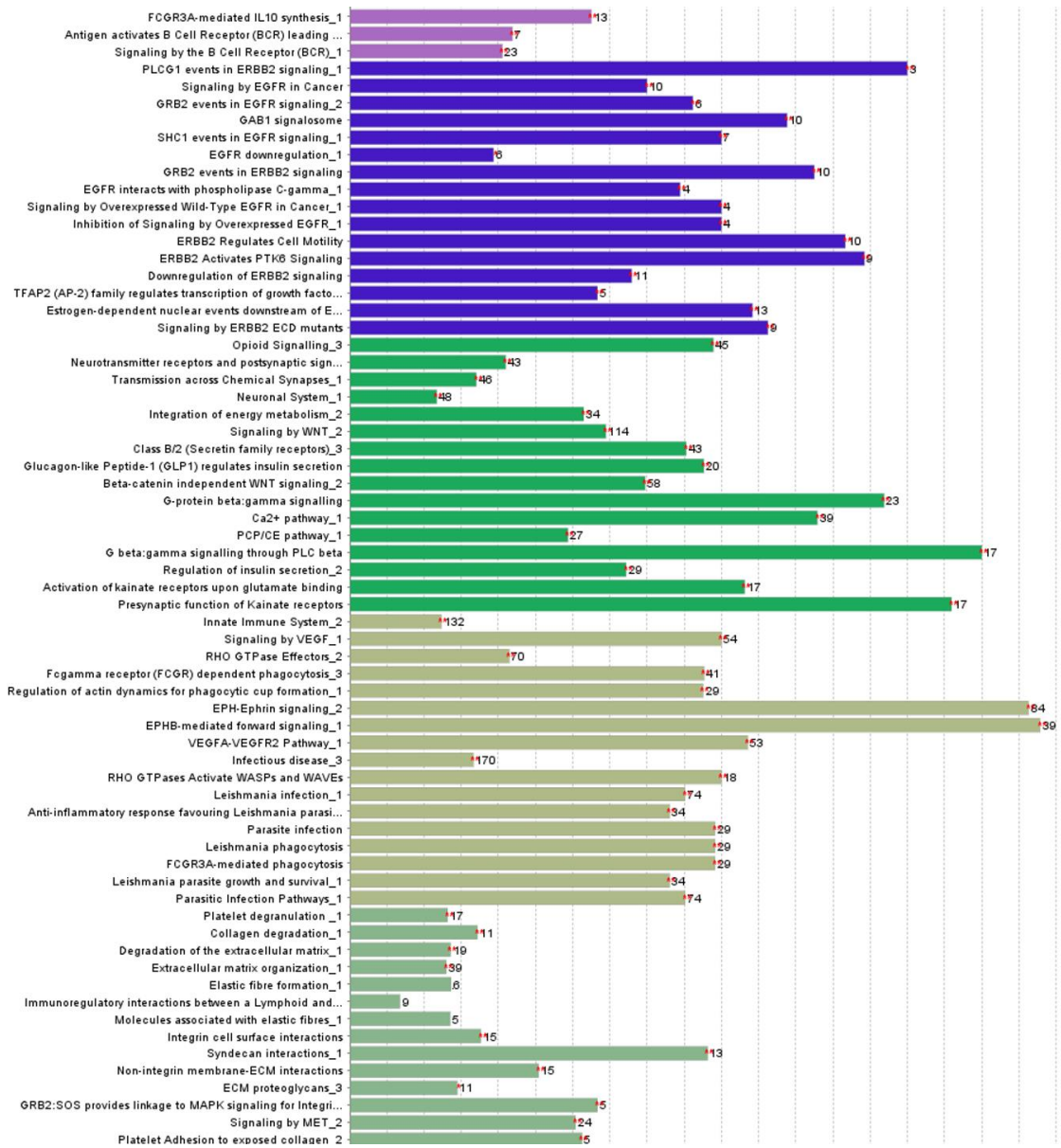






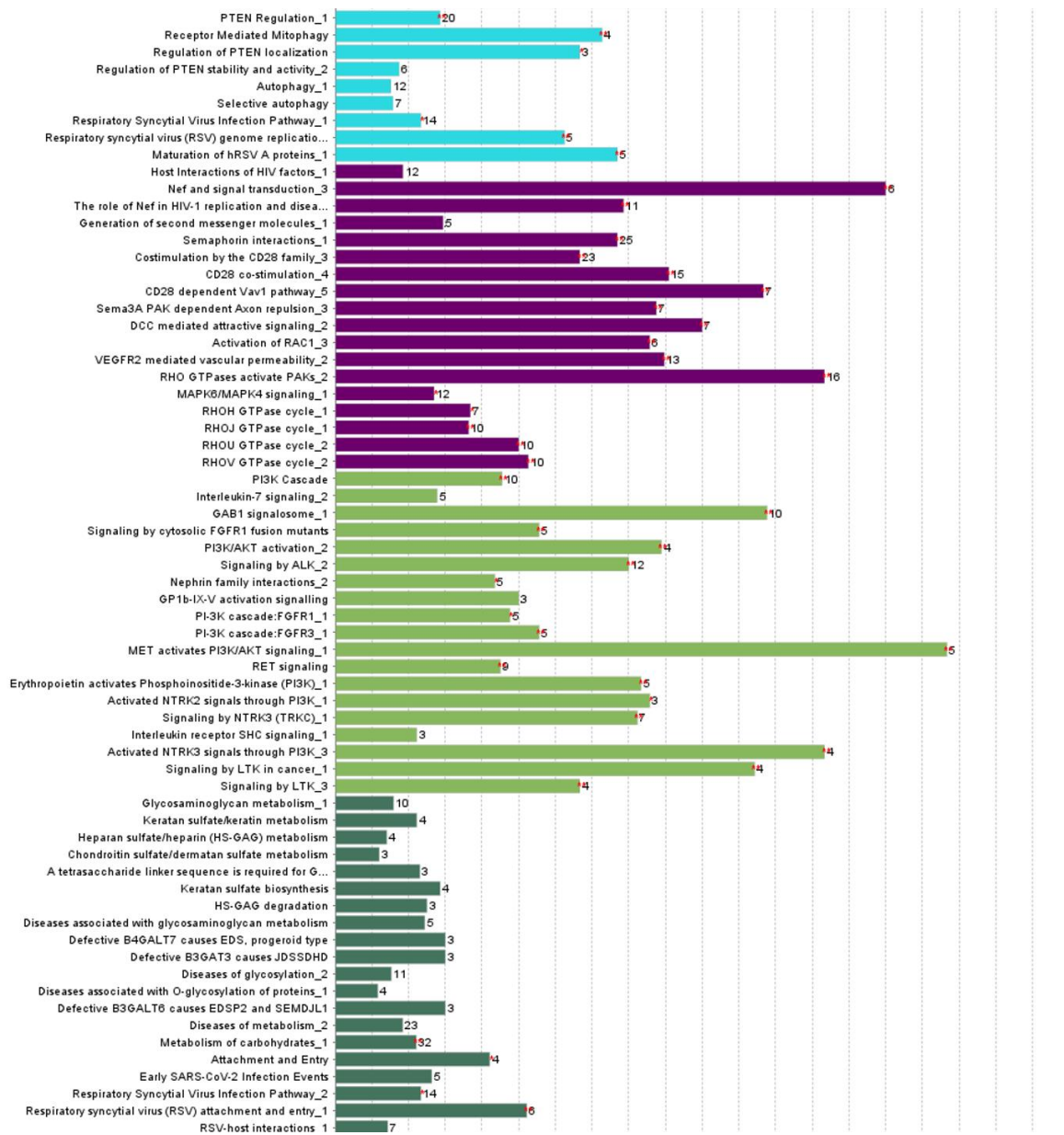


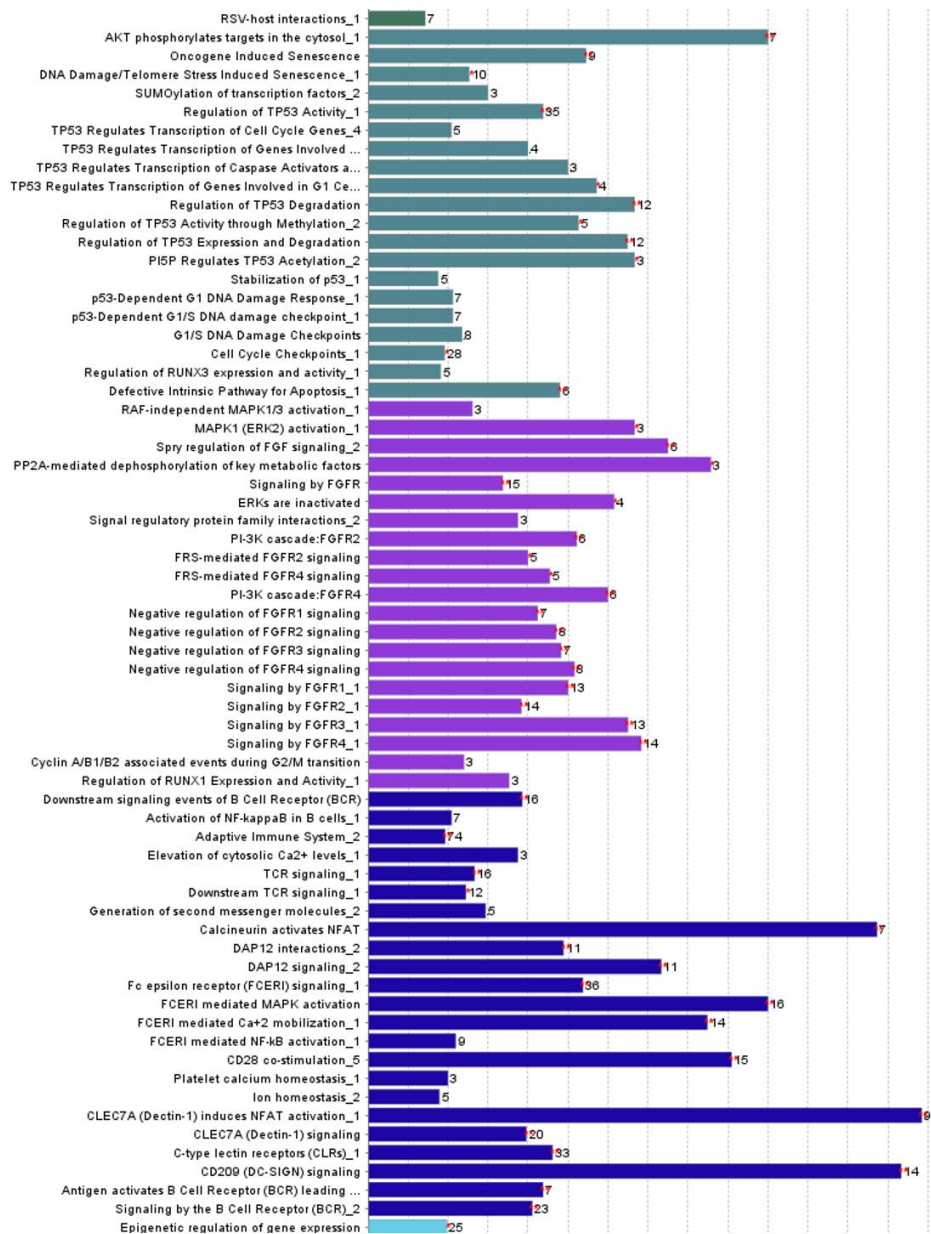


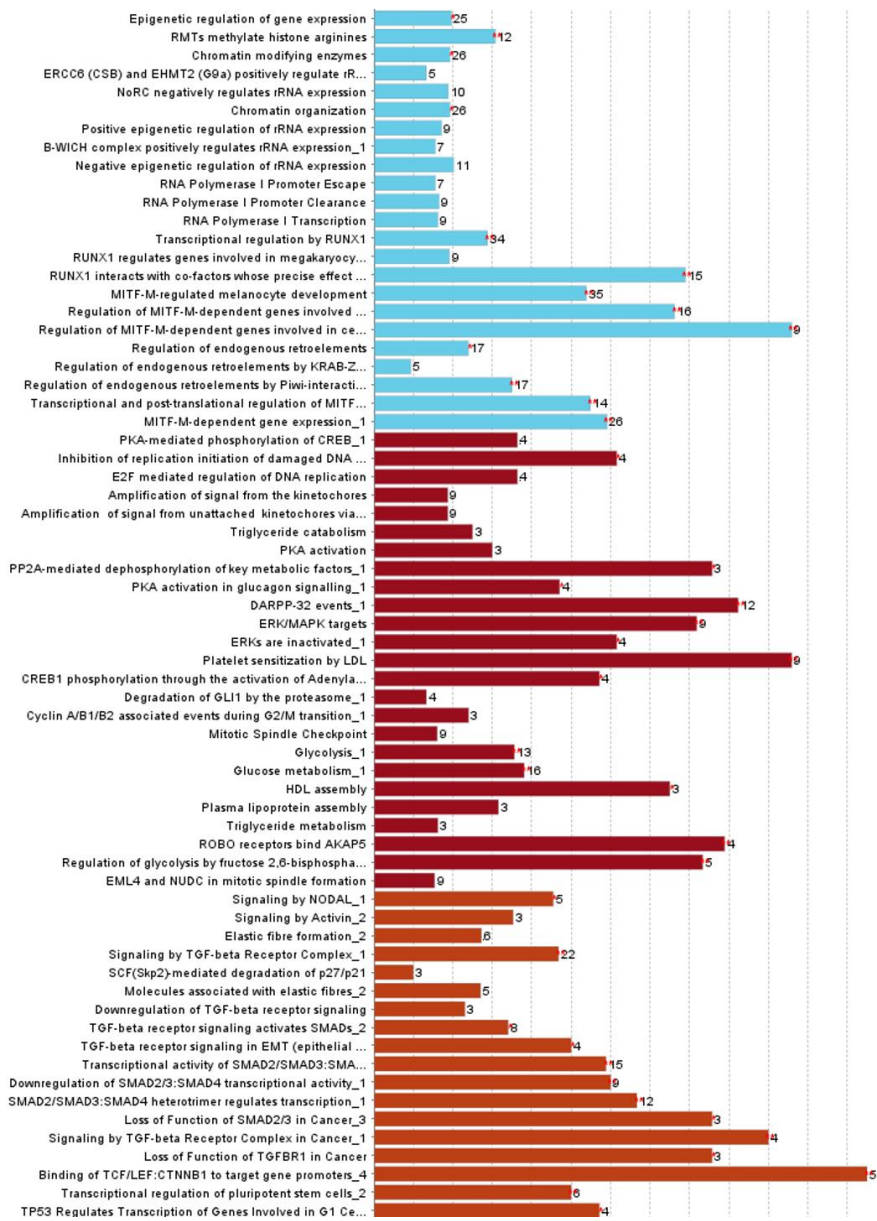


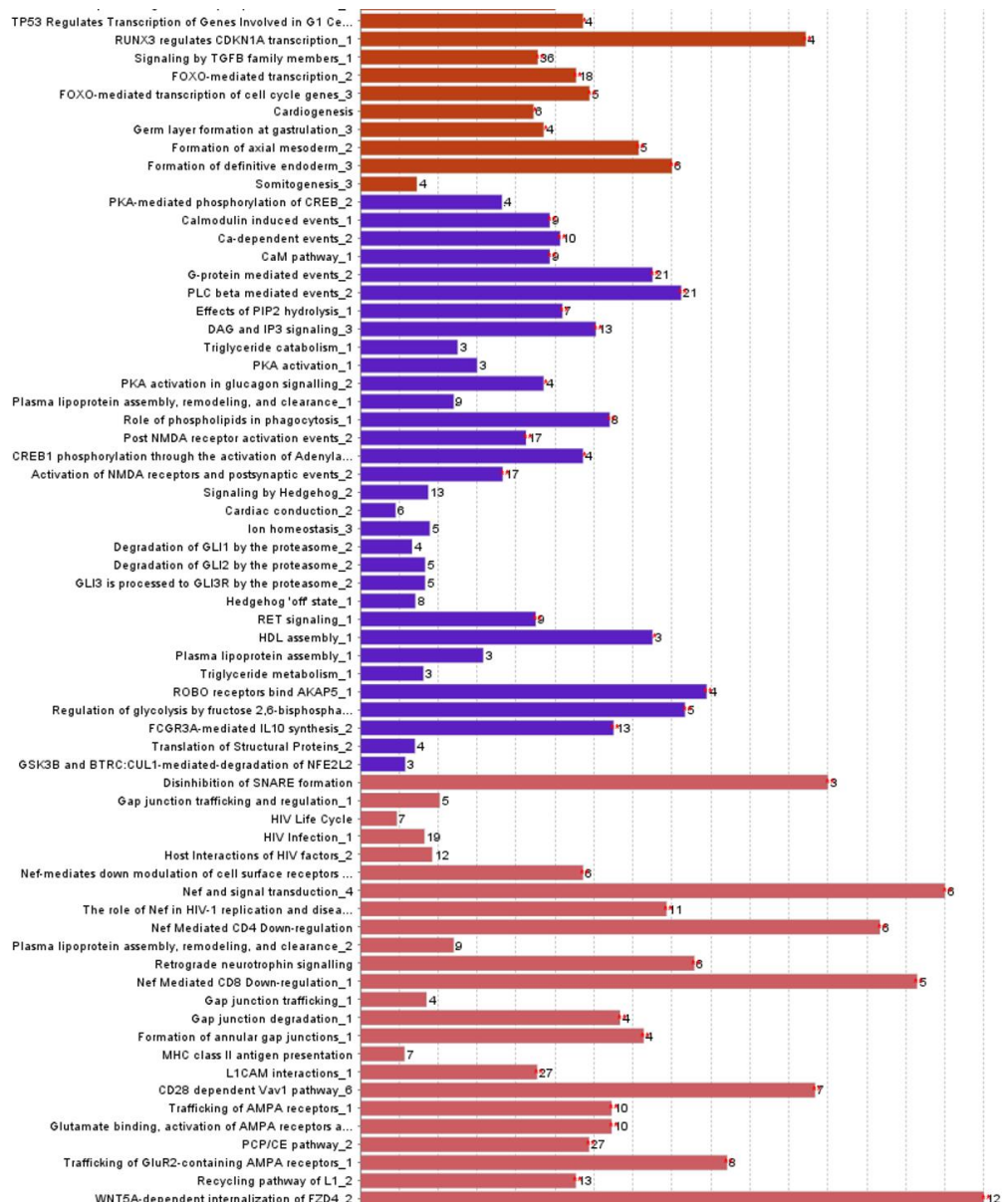


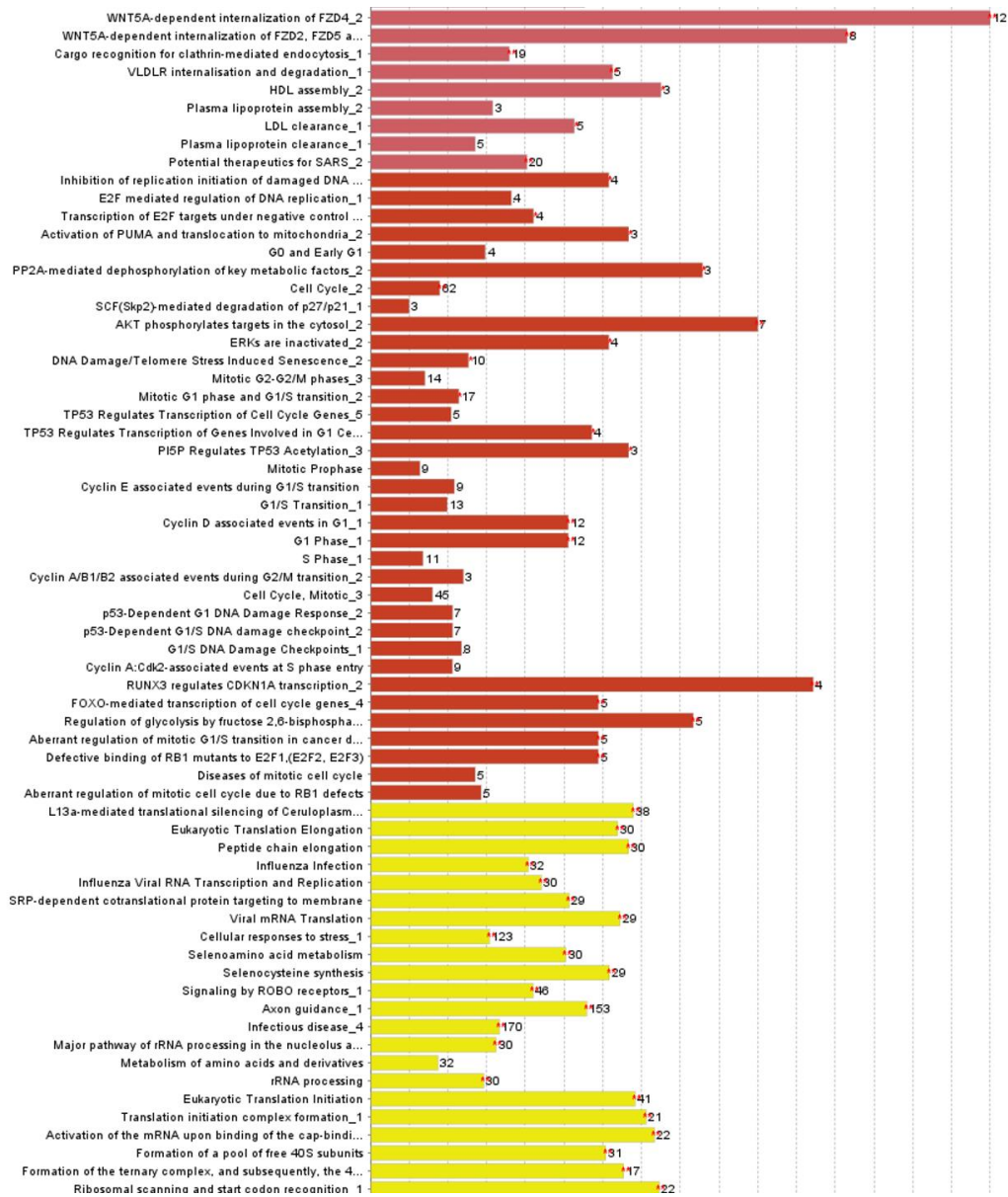


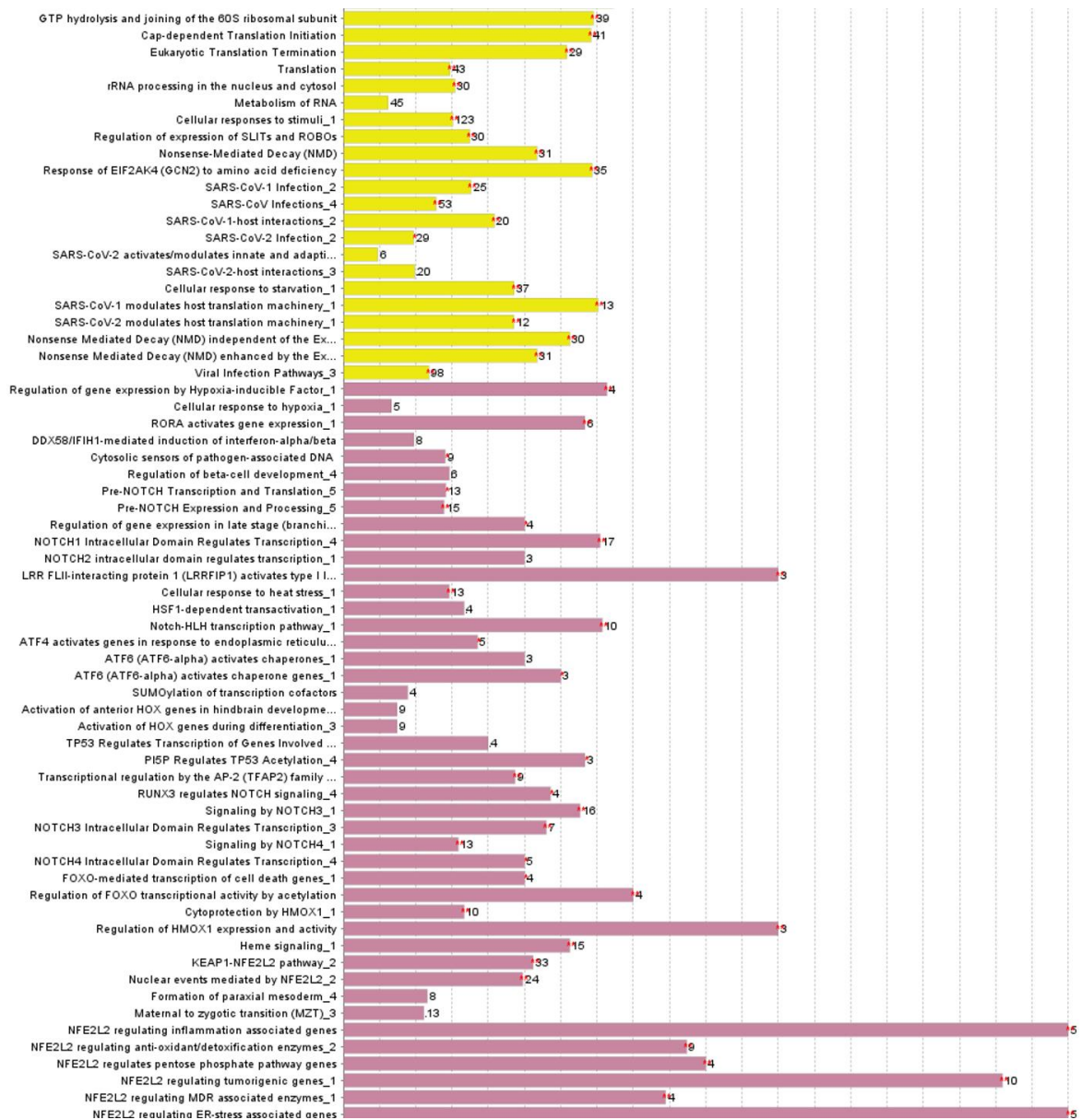


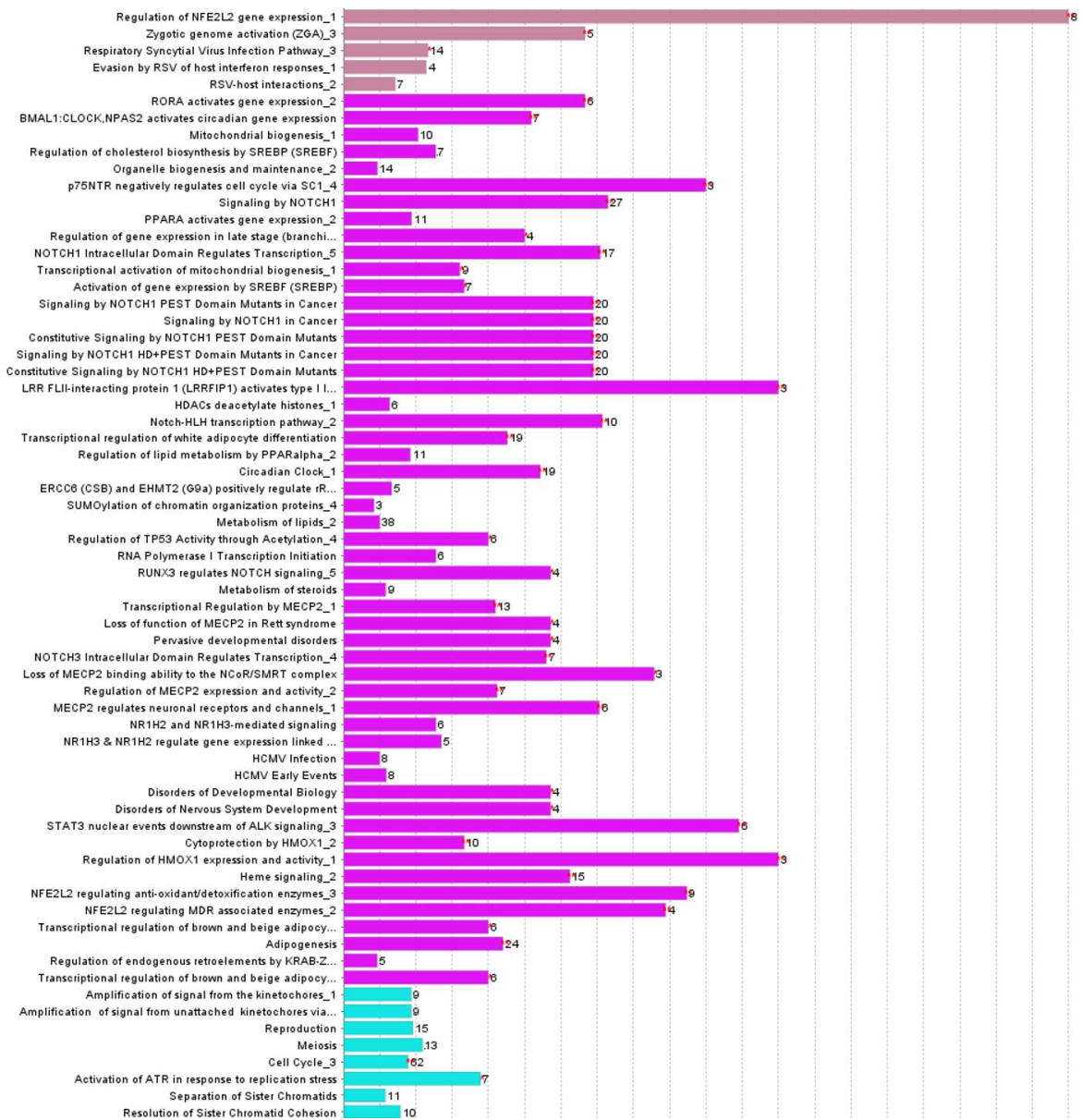




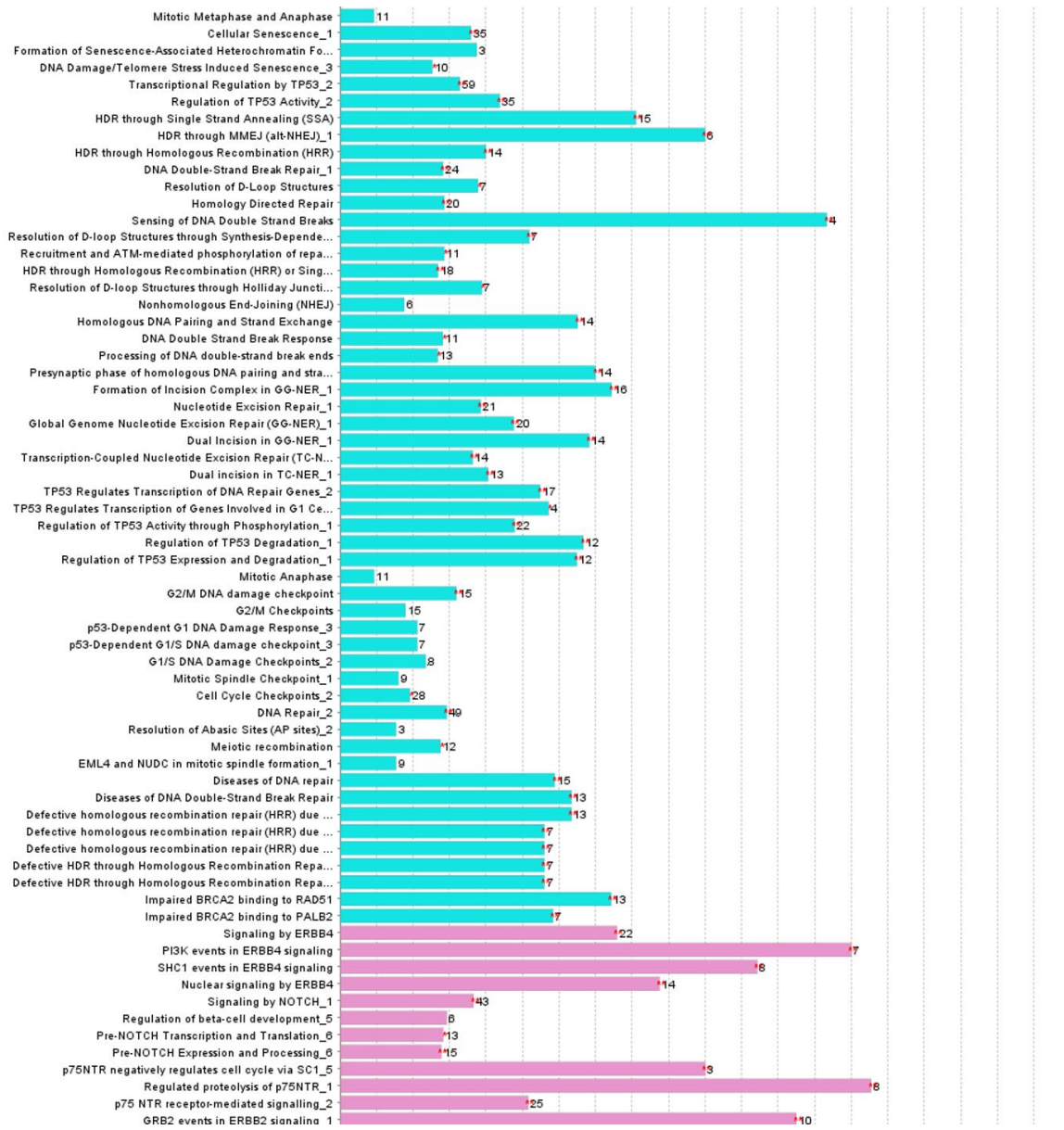


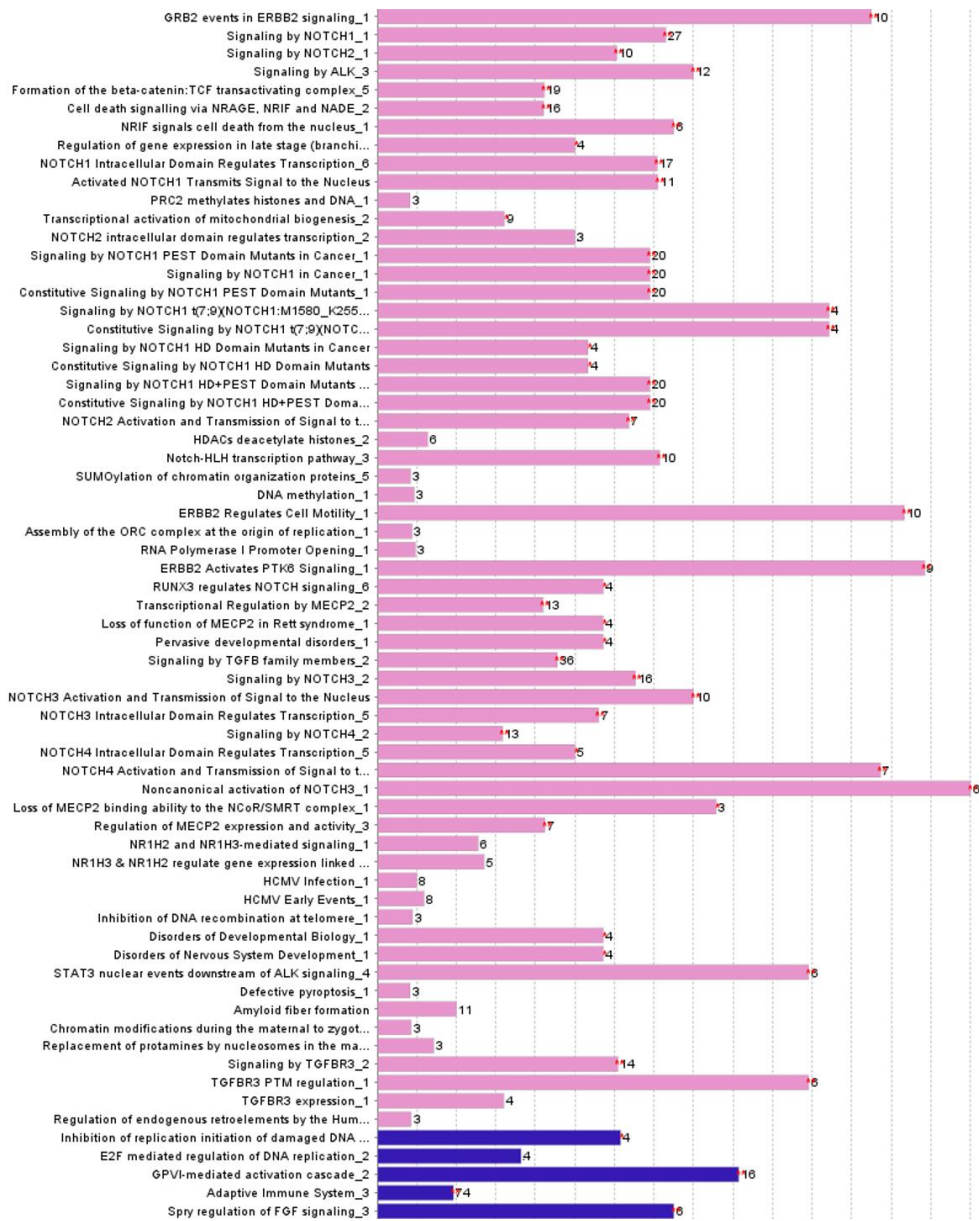


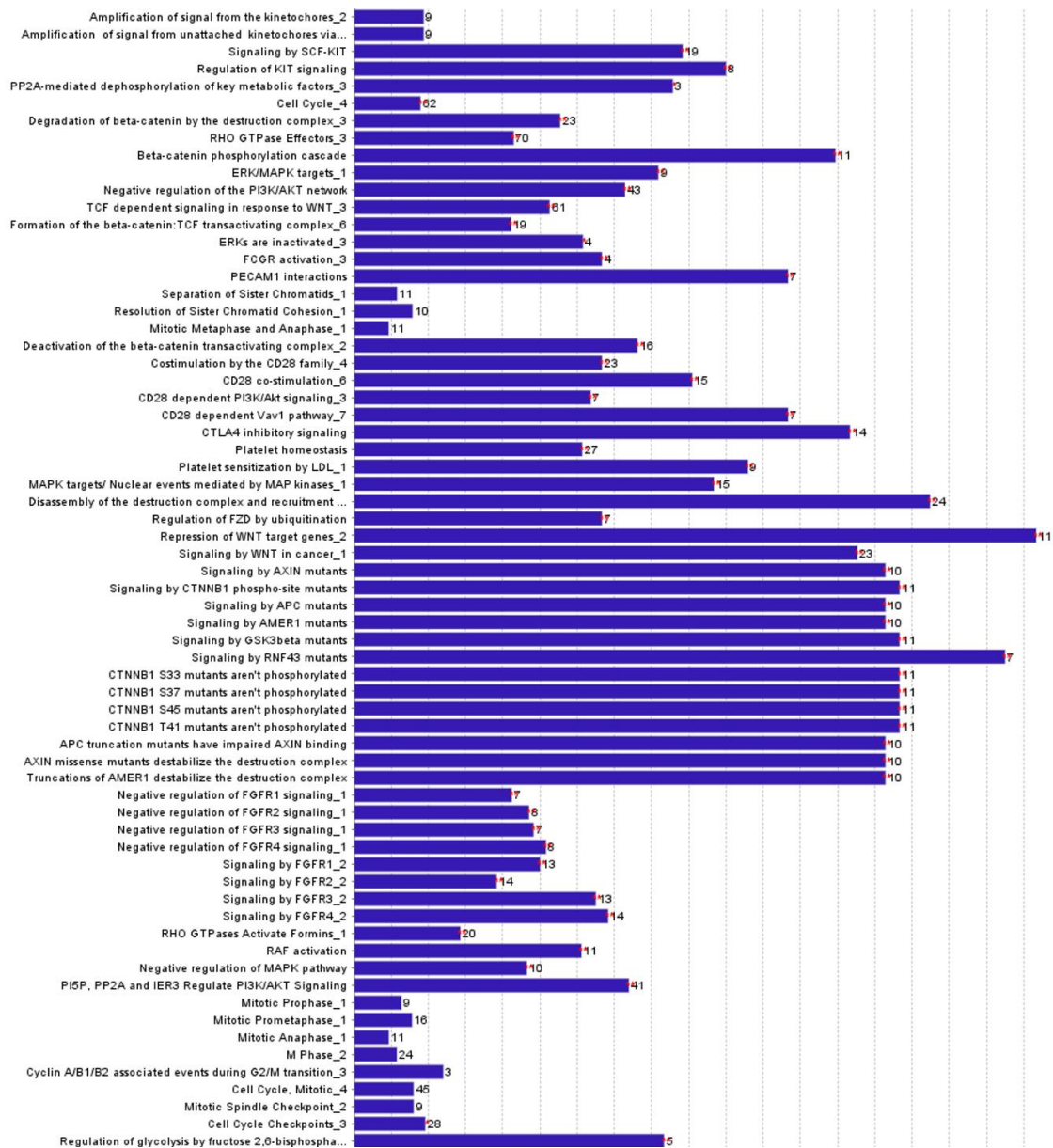


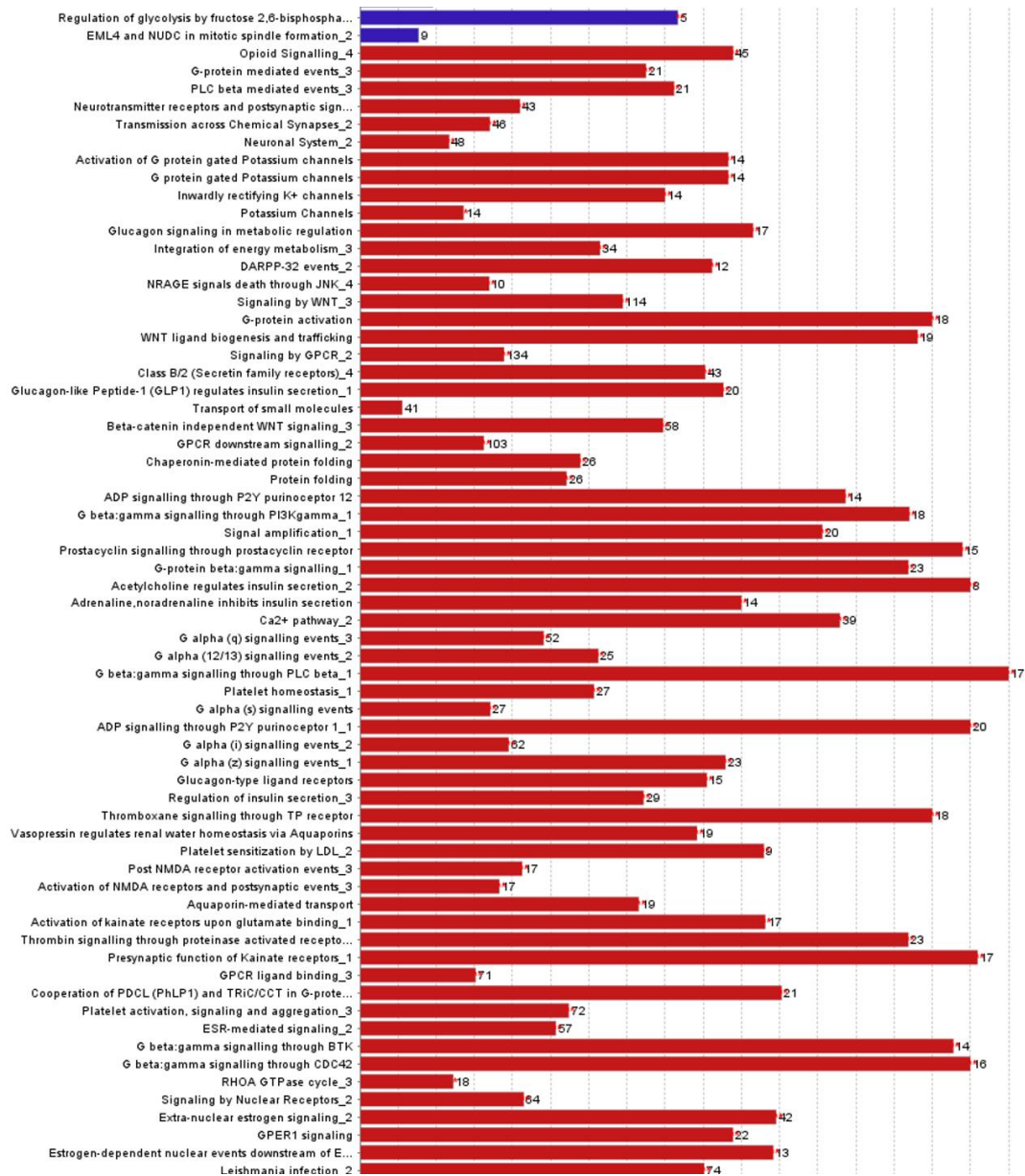


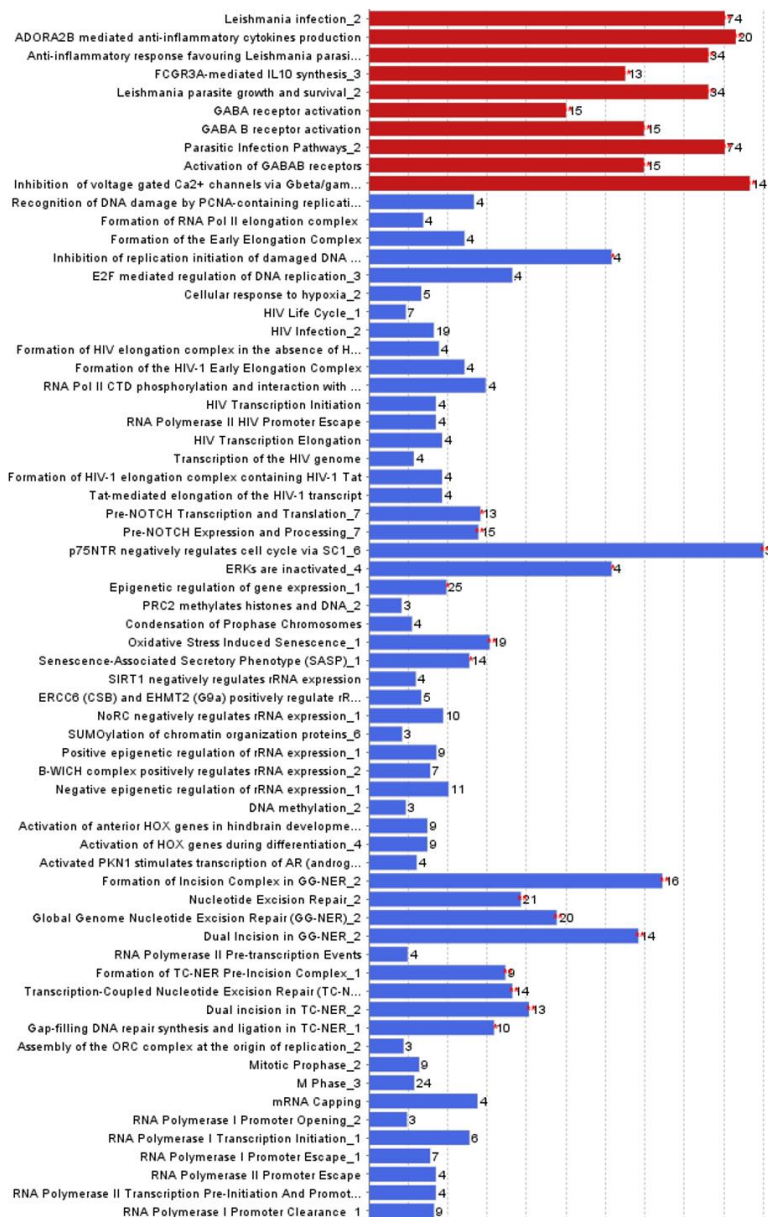


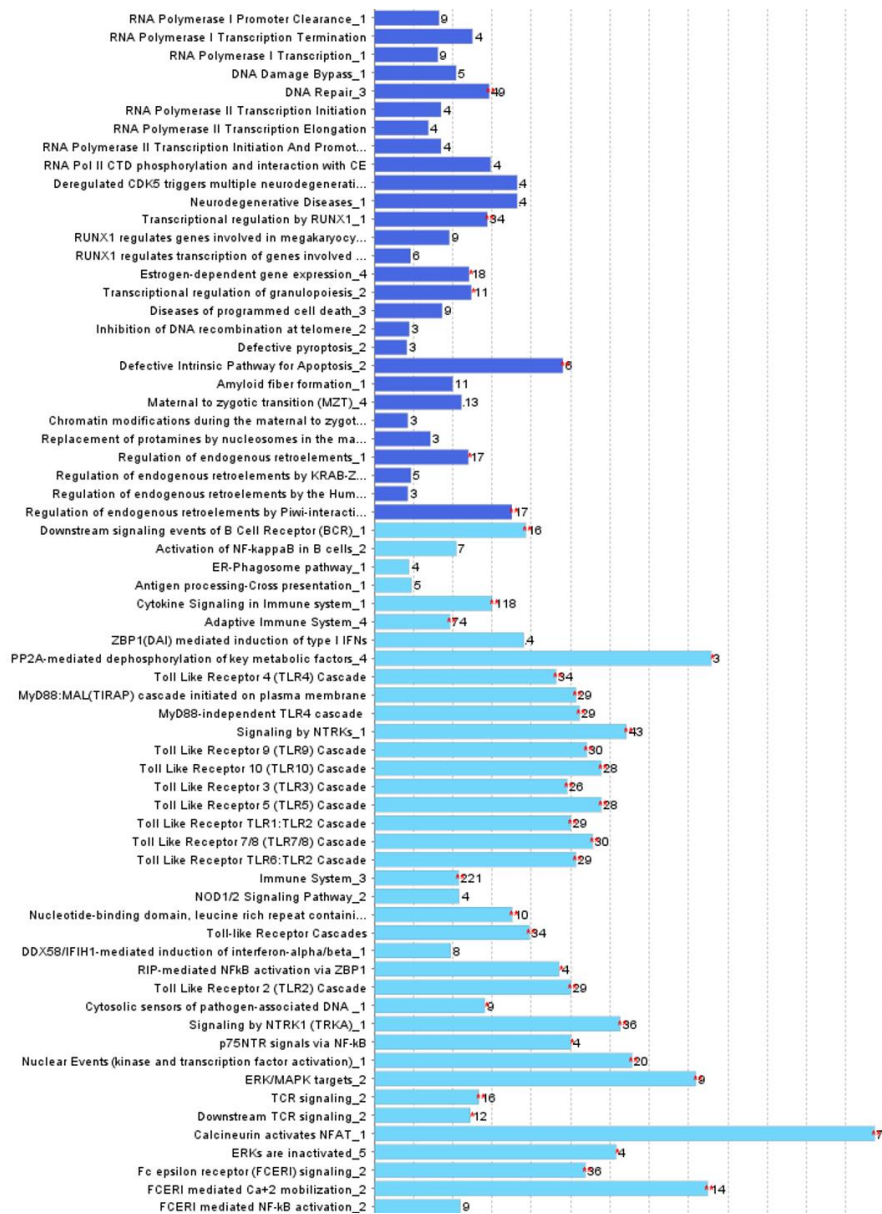


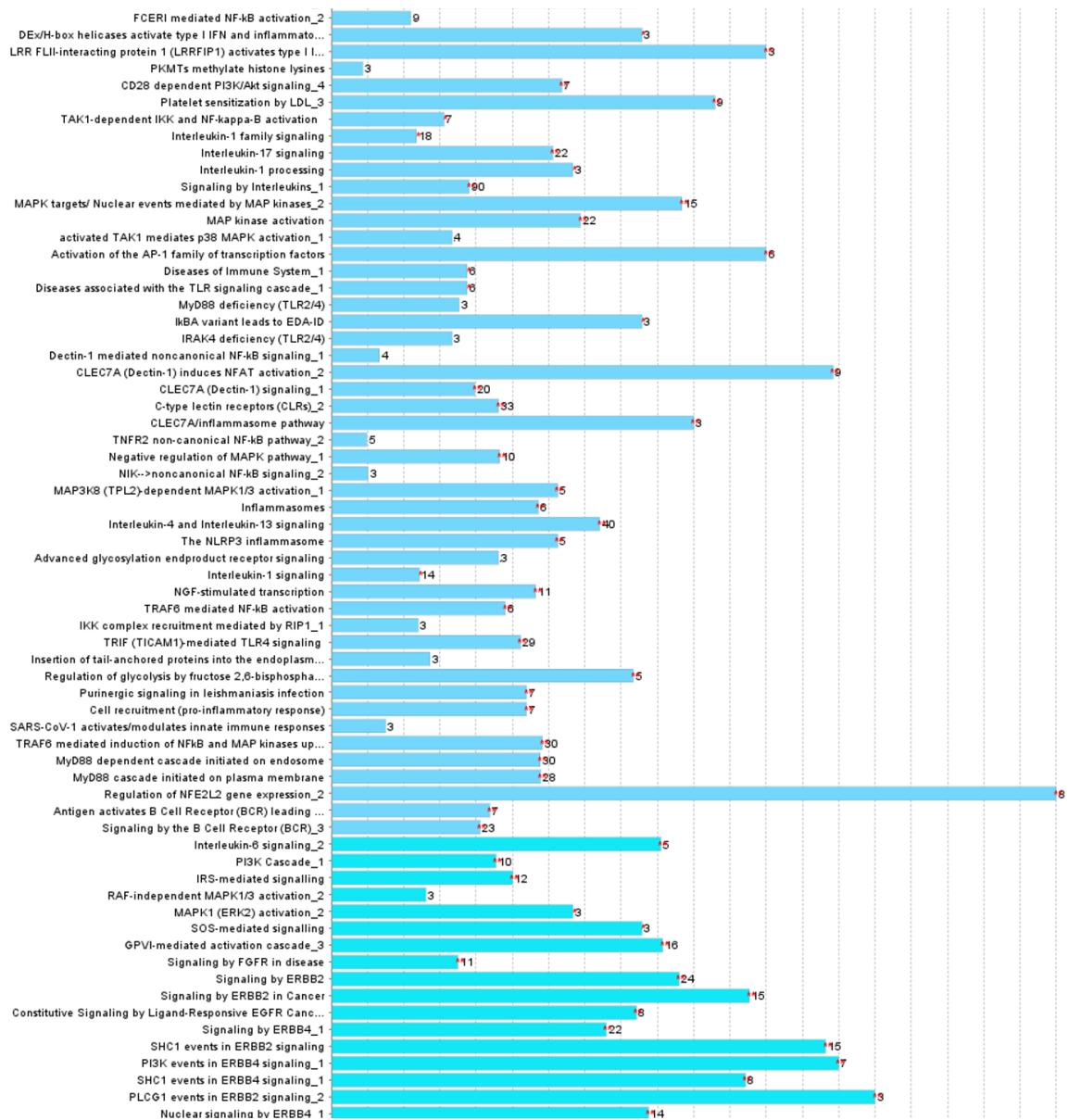


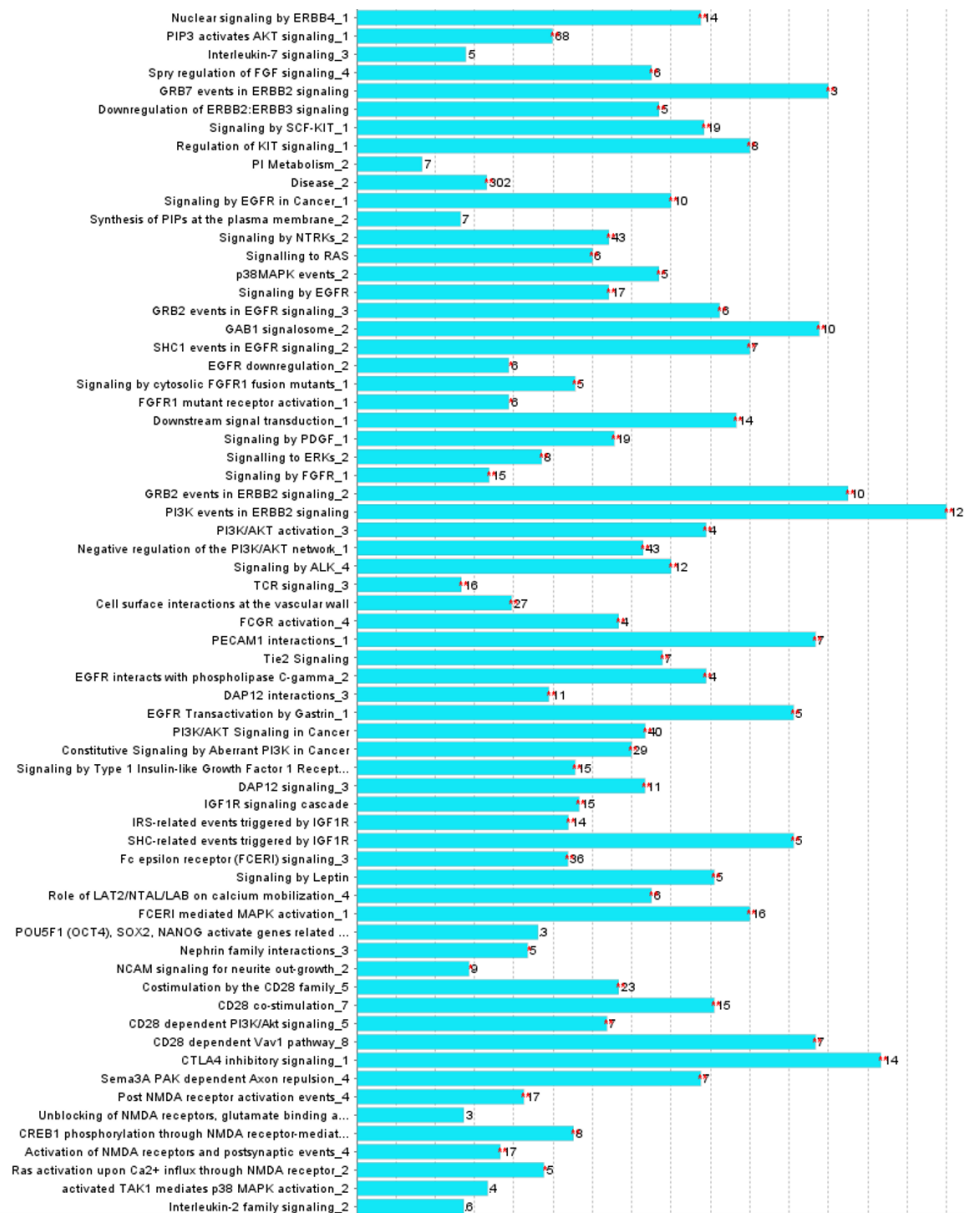






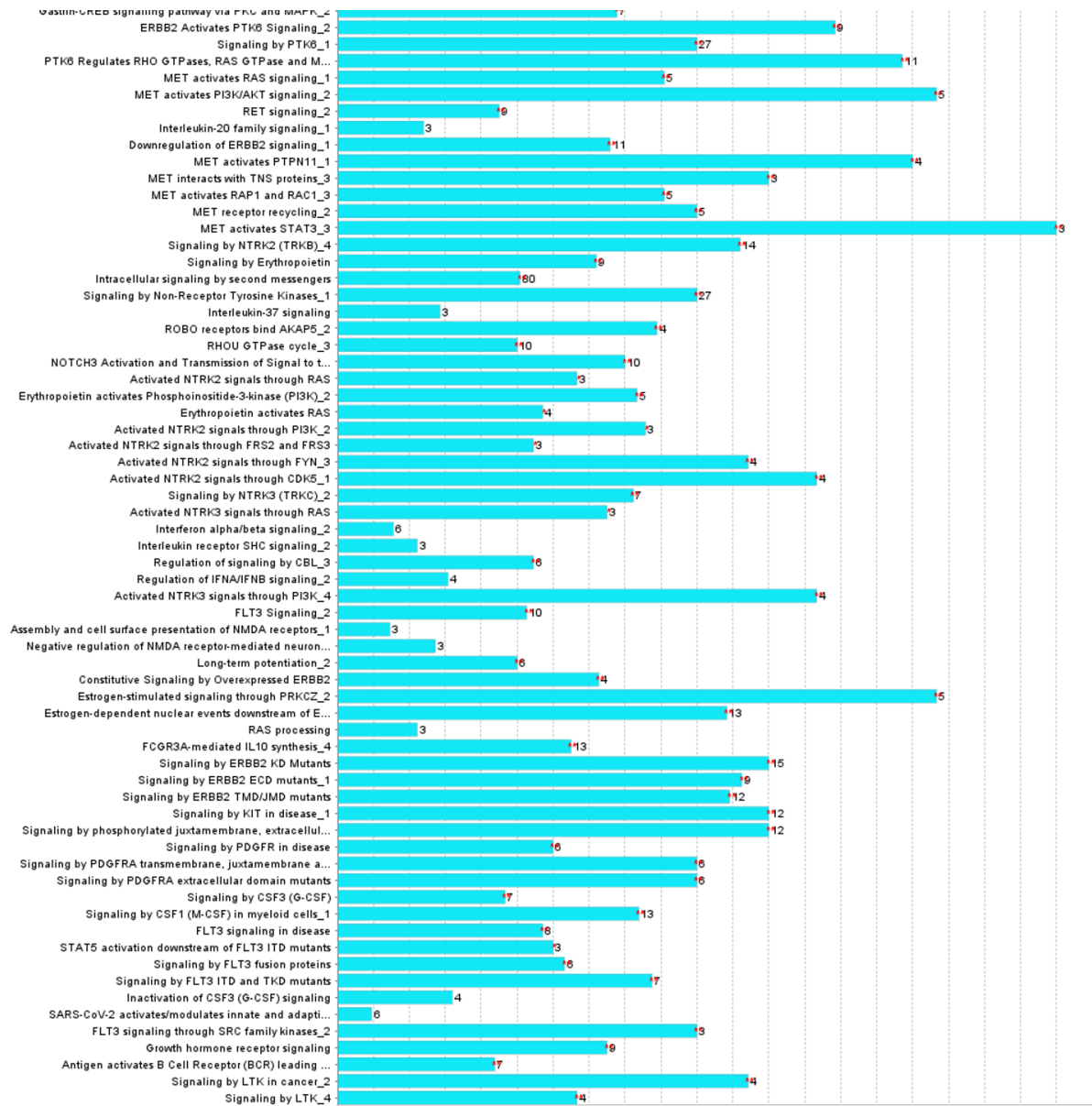












**Table 4S: Terms/signaling pathways in GA-related GIM (sorted by topological coefficient with p values corrected corrected with Benjamini-Hochberg)**

Term	Topological Coefficient	P value	UNIQUE_ID
Cytochrome c-mediated apoptotic response	1.0	0.03077941836978011	R-HSA:111461
COPI-mediated anterograde transport	1.0	0.032303979478631784	R-HSA:6807878
Membrane Trafficking	0.95	0.017147580936152578	R-HSA:199991
Vesicle-mediated transport	0.95	0.00996277877449441	R-HSA:5653656
Laminin interactions	0.9285714285714286	0.029830001939537696	R-HSA:3000157
Apoptosis	0.9166666666666666	0.032285379855300216	R-HSA:109581
Programmed Cell Death	0.9166666666666666	0.04872571128296693	R-HSA:5357801
Loss of function of MECP2 in Rett syndrome	0.8666666666666667	0.033001603260751265	R-HSA:9005891
Pervasive developmental disorders	0.8666666666666667	0.033001603260751265	R-HSA:9005895
Loss of MECP2 binding ability to the NCoR/SMRT complex	0.8666666666666667	0.032293221903259124	R-HSA:9022537
Regulation of MECP2 expression and activity	0.8666666666666667	0.018089301915738484	R-HSA:9022692
Disorders of Nervous System Development	0.8666666666666667	0.033001603260751265	R-HSA:9697154
ER to Golgi Anterograde Transport	0.84	0.017041728977493436	R-HSA:199977
Asparagine N-linked glycosylation	0.84	0.02818743056405486	R-HSA:446203
Transport to the Golgi and subsequent modification	0.84	0.03545172222555464	R-HSA:948021
Platelet degranulation	0.83	0.017316021878206047	R-HSA:114608
Response to elevated platelet cytosolic Ca <sup>2+</sup>	0.83	0.01790211946767316	R-HSA:76005
Regulation of TLR by endogenous ligand	0.83	0.03194047855949558	R-HSA:5686938

<b>Signaling by high-kinase activity BRAF mutants</b>	0.83	0.046466189073031405	R-HSA:6802948
<b>Signaling by BRAF and RAF1 fusions</b>	0.83	0.03641437116125538	R-HSA:6802952
<b>Intrinsic Pathway for Apoptosis</b>	0.75	0.03640015876644282	R-HSA:109606
<b>Apoptotic factor-mediated response</b>	0.75	0.02817738778075856	R-HSA:111471
<b>Cellular responses to stress</b>	0.75	0.005276693628432567	R-HSA:2262752
<b>Infectious disease</b>	0.75	0.03246340881112912	R-HSA:5663205
<b>Cellular responses to stimuli</b>	0.75	0.006796688699894478	R-HSA:8953897
<b>Viral Infection Pathways</b>	0.75	0.02974680918396593	R-HSA:9824446
<b>Extracellular matrix organization</b>	0.73	0.0322963648151965	R-HSA:1474244
<b>Integrin signaling</b>	0.70	0.02408799556758114	R-HSA:354192
<b>Signaling by PDGF</b>	0.70	0.04416119758411886	R-HSA:186797
<b>Cytoprotection by HMOX1</b>	0.70	0.04816227552410113	R-HSA:9707564
<b>MyD88:MAL(TIRAP) cascade initiated on plasma membrane</b>	0.69	0.04947705503115662	R-HSA:166058
<b>Toll Like Receptor TLR6:TLR2 Cascade</b>	0.69	0.04947705503115662	R-HSA:168188
<b>Mitotic Metaphase and Anaphase</b>	0.68	0.021731129328632234	R-HSA:2555396
<b>Mitotic Anaphase</b>	0.68	0.021905342301370867	R-HSA:68882
<b>rRNA modification in the nucleus and cytosol</b>	0.66	0.01716009127428512	R-HSA:6790901
<b>rRNA processing in the nucleus and cytosol</b>	0.66	0.010071008918313544	R-HSA:8868773
<b>Assembly of collagen fibrils and other multimeric structures</b>	0.60	0.03110394719900843	R-HSA:2022090
<b>ECM proteoglycans</b>	0.60	0.03283706291377266	R-HSA:3000178
<b>Collagen chain trimerization</b>	0.60	0.036675012554702416	R-HSA:8948216
<b>Cell Cycle</b>	0.59	0.018467376538773828	R-HSA:1640170
<b>Cell Cycle, Mitotic</b>	0.59	0.02168314406519144	R-HSA:69278
<b>DARPP-32 events</b>	0.58	0.02205908844509303	R-HSA:180024

<b>Platelet sensitization by LDL</b>	0.58	0.006716243284585191	R-HSA:432142
<b>NCAM signaling for neurite out-growth</b>	0.58	0.033035631927149575	R-HSA:375165
<b>mRNA 3'-end processing</b>	0.58	0.047197336404730485	R-HSA:72187
<b>Transport of Mature Transcript to Cytoplasm</b>	0.58	0.01733189514184999	R-HSA:72202
<b>Disorders of Developmental Biology</b>	0.58	0.033001603260751265	R-HSA:9675151
<b>mRNA Splicing - Major Pathway</b>	0.55	3.1770569039773987E-7	R-HSA:72163
<b>mRNA Splicing</b>	0.55	6.383198641071852E-7	R-HSA:72172
<b>GRB2:SOS provides linkage to MAPK signaling for Integrins</b>	0.55	0.03646864389235669	R-HSA:354194
<b>p130Cas linkage to MAPK signaling for integrins</b>	0.55	0.03646864389235669	R-HSA:372708
<b>Mitotic G2-G2/M phases</b>	0.53	0.04904359332420217	R-HSA:453274
<b>G2/M Transition</b>	0.53	0.04842934856210643	R-HSA:69275
<b>CTLA4 inhibitory signaling</b>	0.52	0.03043086994374417	R-HSA:389513
<b>Nuclear Envelope (NE) Reassembly</b>	0.52	0.018627279867871778	R-HSA:2995410
<b>Signaling by moderate kinase activity BRAF mutants</b>	0.51	0.045986472185865504	R-HSA:6802946
<b>Signaling by RAS mutants</b>	0.51	0.045986472185865504	R-HSA:6802949
<b>Paradoxical activation of RAF signaling by kinase inactive BRAF</b>	0.51	0.045986472185865504	R-HSA:6802955
<b>Signaling downstream of RAS mutants</b>	0.51	0.045986472185865504	R-HSA:9649948
<b>Signaling by RAF1 mutants</b>	0.51	0.03510154802392978	R-HSA:9656223
<b>M Phase</b>	0.51	0.021703782367382473	R-HSA:68886
<b>Aerobic respiration and respiratory electron transport</b>	0.50	0.03502850716909681	R-HSA:1428517
<b>snRNP Assembly</b>	0.50	0.03254398990402931	R-HSA:191859

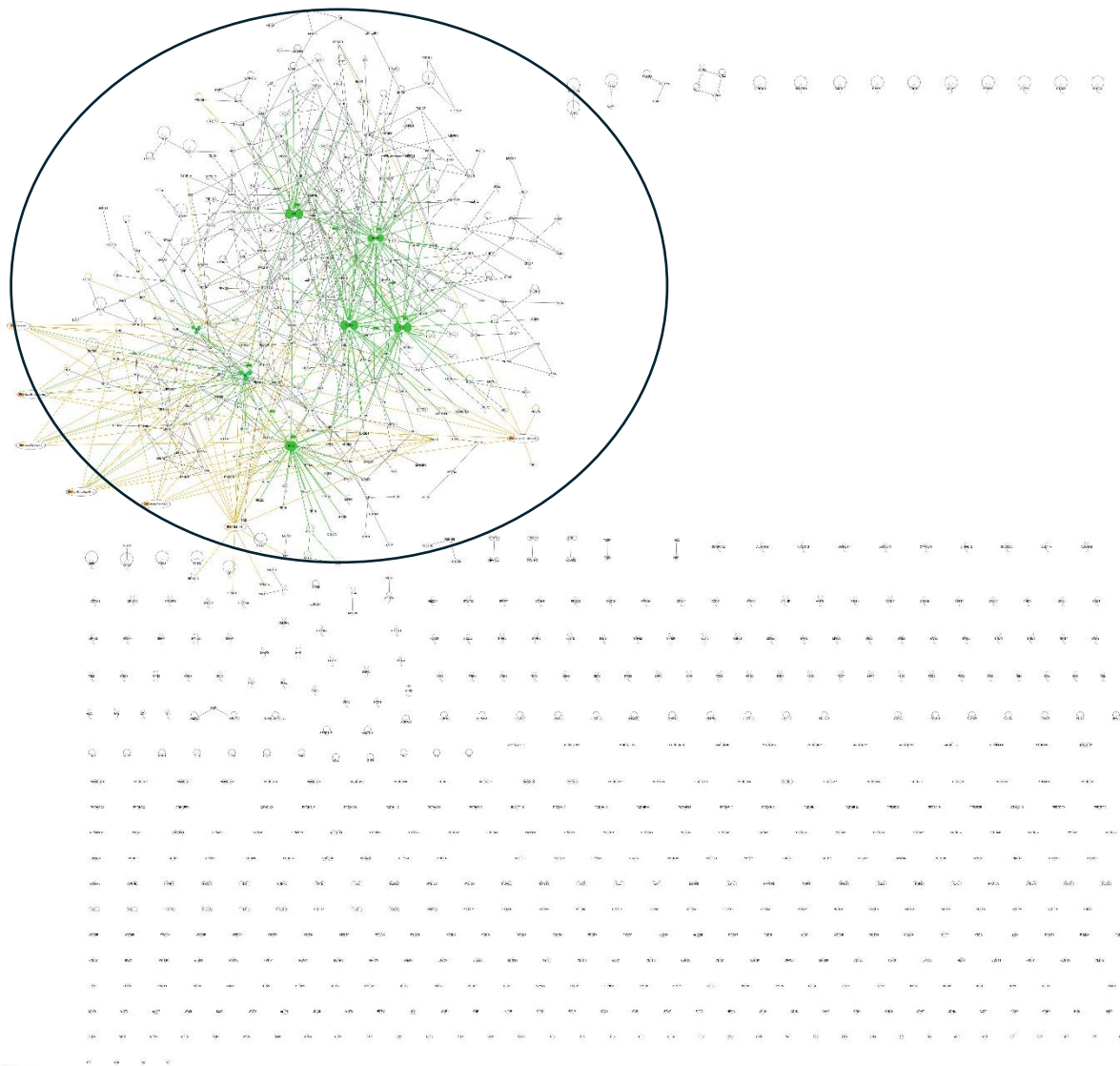
<b>MASTL Facilitates Mitotic Progression</b>	0.50	0.017717009334540117	R-HSA:2465910
<b>Metabolism of proteins</b>	0.50	0.009207695633988296	R-HSA:392499
<b>Axon guidance</b>	0.50	0.016785594278522928	R-HSA:422475
<b>mRNA decay by 3' to 5' exoribonuclease</b>	0.50	0.04195902417660218	R-HSA:429958
<b>MAPK targets/ Nuclear events mediated by MAP kinases</b>	0.50	0.03284753842766893	R-HSA:450282
<b>TP53 Regulates Metabolic Genes</b>	0.50	0.04723898496996881	R-HSA:5628897
<b>Metabolism of amino acids and derivatives</b>	0.50	0.006803327675130781	R-HSA:71291
<b>Translation</b>	0.50	0.036856802790047424	R-HSA:72766
<b>Glycogen metabolism</b>	0.50	0.049312230020330465	R-HSA:8982491
<b>ERK/MAPK targets</b>	0.45	0.03194047855949558	R-HSA:198753
<b>Cellular response to chemical stress</b>	0.45	0.0236541804627481	R-HSA:9711123
<b>Cyclin A/B1/B2 associated events during G2/M transition</b>	0.44	0.041876234163061854	R-HSA:69273
<b>SRP-dependent cotranslational protein targeting to membrane</b>	0.42	0.0326069815374156	R-HSA:1799339
<b>Selenoamino acid metabolism</b>	0.42	0.025768346695481757	R-HSA:2408522
<b>RAF activation</b>	0.42	0.046466189073031405	R-HSA:5673000
<b>Transport of Mature mRNA derived from an Intron-Containing Transcript</b>	0.42	0.018627279867871778	R-HSA:159236
<b>Major pathway of rRNA processing in the nucleolus and cytosol</b>	0.40	0.025460446702795705	R-HSA:6791226
<b>rRNA processing</b>	0.40	0.017418965543868823	R-HSA:72312
<b>Platelet activation, signaling and aggregation</b>	0.38	0.036958991533182606	R-HSA:76002
<b>Integrin cell surface interactions</b>	0.38	0.04840319342321396	R-HSA:216083
<b>Processing of Capped Intron-</b>	0.38	1.2863864573279597E-7	R-HSA:72203

<b>Containing Pre-mRNA</b>			
<b>PP2A-mediated dephosphorylation of key metabolic factors</b>	0.38	0.032293221903259124	R-HSA:163767
<b>Regulation of glycolysis by fructose 2,6-bisphosphate metabolism</b>	0.38	0.026713025026585815	R-HSA:9634600
<b>Metabolism of non-coding RNA</b>	0.375	0.03254398990402931	R-HSA:194441
<b>Mitotic Prophase</b>	0.35	0.032184383060804116	R-HSA:68875
<b>ERKs are inactivated</b>	0.34	0.03077941836978011	R-HSA:202670
<b>Metabolism of carbohydrates</b>	0.33	0.04825103104814824	R-HSA:71387
<b>Disease</b>	0.32	0.04175717465660903	R-HSA:1643685
<b>Glycolysis</b>	0.31	0.030479583649003734	R-HSA:70171
<b>Glucose metabolism</b>	0.31	0.04723898496996881	R-HSA:70326
<b>Metabolism</b>	0.25	2.783842857413548E-4	R-HSA:1430728
<b>Deadenylation-dependent mRNA decay</b>	0.25	1.8880161142073435E-4	R-HSA:429914
<b>Metabolism of RNA</b>	0.24	1.653600516017647E-12	R-HSA:8953854
<b>Glutathione conjugation</b>	0.0	0.046466189073031405	R-HSA:156590
<b>Metabolism of nucleotides</b>	0.0	0.04890606133035483	R-HSA:15869
<b>HIV Life Cycle</b>	0.0	0.04157605624452897	R-HSA:162587
<b>Late Phase of HIV Life Cycle</b>	0.0	0.030698987338338448	R-HSA:162599
<b>Innate Immune System</b>	0.0	0.047184009545942	R-HSA:168249
<b>Initiation of Nuclear Envelope (NE) Reformation</b>	0.0	0.024990348646255302	R-HSA:2995383
<b>Scavenging by Class A Receptors</b>	0.0	0.024990348646255302	R-HSA:3000480
<b>Glycogen synthesis</b>	0.0	0.033001603260751265	R-HSA:3322077
<b>Transcriptional Regulation by TP53</b>	0.0	0.03194405399919193	R-HSA:3700989
<b>mRNA decay by 5' to 3' exoribonuclease</b>	0.0	0.017586923244728072	R-HSA:430039
<b>Smooth Muscle Contraction</b>	0.0	0.03943813508117212	R-HSA:445355

<b>Synthesis of GDP-mannose</b>	0.0	0.026335567668901057	R-HSA:446205
<b>Butyrate Response Factor 1 (BRF1) binds and destabilizes mRNA</b>	0.0	0.04730442120502561	R-HSA:450385
<b>Fructose metabolism</b>	0.0	0.032293221903259124	R-HSA:5652084
<b>Diseases of signal transduction by growth factor receptors and second messengers</b>	0.0	0.03543770700709452	R-HSA:5663202
<b>Respiratory electron transport</b>	0.0	0.017519376237775018	R-HSA:611105
<b>Signaling by PTK6</b>	0.0	0.020093446265703075	R-HSA:8848021
<b>Signaling by Non-Receptor Tyrosine Kinases</b>	0.0	0.020093446265703075	R-HSA:9006927
<b>Nervous system development</b>	0.0	0.017784086016500188	R-HSA:9675108
<b>M-decay: degradation of maternal mRNAs by maternally stored factors</b>	0.0	0.03675061929732784	R-HSA:9820841
<b>Respiratory syncytial virus (RSV) genome replication, transcription and translation</b>	0.0	0.04195902417660218	R-HSA:9820965
<b>Maturation of hRSV A proteins</b>	0.0	0.03077941836978011	R-HSA:9828806
<b>Mitochondrial protein degradation</b>	0.0	0.04848782603948083	R-HSA:9837999



**Table S5: 330 out of 865 hub proteins with PPI >3 in GA-related GIM**



- ABI1
- ABL1
- ACTB
- ACTG1
- ACTR2
- ACTR3
- AIRE
- AKT1
- AP2A2
- AP2B1
- AP2M1
- AP2S1
- APC

APP  
AR  
AREG  
ARHGEF7  
ARPC2  
ARPC5  
ARR3  
ARRB1  
ARRB2  
ATF2  
ATF4  
ATM  
ATR  
AXIN1  
AXL  
BCAR1  
BCL2  
BCR  
BMP7  
BMPR2  
BMPR1B  
BRCA1  
BRCA2  
BTRC  
CASP3  
CCN2  
CCND1  
CCNH  
CD44  
CD40LG  
CDC42  
CDH1  
CDH5  
CDKN1A  
CDKN1B  
CDKN2A  
CFL1  
CHEK1  
CHEK2  
CHUK  
COL1A1  
CREB1  
CREBBP  
CRK  
CSF1  
CSNK1A1  
CSNK1D  
CSNK1G3

CSNK2A1  
CSNK2A2  
CSNK2B  
CTBP1  
CTNNA1  
CTNNB1  
CTNND1  
CTTN  
CUL4A  
CUL4B  
CXCL12  
CXCR4  
DCAF1  
DDB1  
DDB2  
DDIT3  
DNM1  
DOCK1  
DRD1  
DVL1  
DVL2  
DVL3  
E2F1  
EEF1A1  
EEF1E1  
EFNA1  
EFNA3  
EFNA4  
EFNA5  
EFNB1  
EFNB2  
EGF  
EGFR  
EGR1  
EIF2AK2  
EIF2B1  
EIF2S1  
EIF2S2  
EIF4A1  
EIF4E  
EIF4EBP1  
EIF4G1  
ELK1  
ELMO1  
EP300  
EP400  
EPHA2  
EPHA3

EPHA4  
EPHA6  
EPHA7  
EPHA10  
EPHB1  
EPHB2  
ERBB2  
ERBB3  
ERBB4  
ERCC1  
ERCC2  
ERCC3  
ERCC4  
ERCC5  
ETS1  
EZR  
FANCA  
FANCC  
FANCD2  
FANCE  
FANCF  
FANCG  
FBXW11  
FER  
FKBP1A  
FN1  
FOS  
FRMD6  
FYN  
GAB1  
GH1  
GHR  
GNB1  
GNB2  
GNB3  
GNG2  
GNG4  
GNG13  
GNGT1  
GPNMB  
GRIN1  
GRIN2B  
GRK2  
GRM1  
GSK3B  
H3-3A/H3-3B  
HDAC1  
HDAC2

HDAC3  
HGF  
HGFAC  
HIF1A  
HMGB1  
HMGN1  
HRAS  
IGF1  
IGF1R  
IGFBP4  
ILK  
IRS1  
ITGA2  
ITGA2B  
ITGB1  
ITGB2  
ITGB3  
ITPR1  
ITSN1  
JUN  
JUNB  
KEAP1  
KIT  
KLF6  
KRT19  
LATS1  
LCK  
LEF1  
LIMK1  
LYN  
MAFG  
MAFK  
MAML1  
MAP2K4  
MAP2K6  
MAP3K1  
MAP3K5  
MAPK1  
MAPK8  
MAPK14  
MAPKAPK2  
MAX  
MCL1  
MDM2  
MET  
MKNK1  
MLH1  
MRE11

MSH2  
MTOR  
MYC  
MYH9  
MYL6  
NBN  
NCF2  
NF2  
NFATC1  
NFATC2  
NFE2L2  
NFKB1  
NFYC  
NGEF  
NOTCH1  
NR2C2  
NRG1  
NRG3  
PAK1  
PAK3  
PARP1  
PCBD1  
PDPK1  
PGF  
PHLPP1  
PIK3CA  
PIK3CG  
PIK3R1  
PIP5K1A  
PLAUR  
PLCB2  
POR  
PPP1CA  
PPP2CA  
PPP3CA  
PPP3R1  
PRKCA  
PRKCB  
PRKCD  
PRKCE  
PRKCG  
PRKCH  
PRKCI  
PRKCQ  
PRKCZ  
PRKD1  
PSEN2  
PTEN

PTK2  
PTPN11  
PTTG1  
PXN  
RAC1  
RAD50  
RAD51  
RAD9A  
RASA1  
RB1  
RELA  
RHEB  
RHOA  
RNF41  
ROCK1  
ROCK2  
RPA1  
RPL5  
RPL6  
RPL9  
RPL11  
RPL13  
RPL15  
RPL22  
RPL23  
RPL26  
RPL38  
RPS6  
RPS7  
RPS14  
RPS23  
RPS24  
RPS6KA5  
RPSA  
SDC1  
SDC2  
SDCBP  
SHC1  
SIAH1  
SIRT1  
SKIL  
SMAD1  
SMAD2  
SMAD4  
SMARCA4  
SMARCA5  
SMARCE1  
SNAI1

SOCS3  
SP1  
SPINT1  
SRC  
SREBF1  
STAT1  
STAT3  
TAMALIN  
TBL1X  
TCF7L2  
TIAM1  
TLE1  
TLE5  
TP53  
TP63  
TREX1  
TSC1  
TSC2  
TXN  
USP7  
VAV2  
VCP  
VEGFA  
WASF2  
XIAP  
XPA  
XPC  
YES1  
YY1



**Table S6: Immunohistochemistry of the hub proteins and cell types (by scRNAseq) at Human Protein Atlas and RNA expression. Note: quantities of immunostaining from none (0), <25%, 25-75% and >75% shown under each protein. \*\*, \*\*\*:  $q < 0.05$ ,  $0.01$ .**

Protein	Antibody	Diagnosis	Patient information	URL	Quantity	Cell types	RNA (Log2FC)
EGFR	CAB000035	Normal/GIM	Male, age 72, id: 301	v23.proteinatlas.org/ENSG00000146648-EGFR/tissue/stomach#img	25-75%	Goblet cells and fibroblasts	0.009
		GA	Female, age 50, id: 664	v23.proteinatlas.org/ENSG00000146648-EGFR/pathology/stomach+cancer#img	>75%		0.032
SRC	HPA030875	Normal/GIM	Female, age 81, id: 526	v23.proteinatlas.org/ENSG00000197122-SRC/tissue/stomach#img	25-75%	Goblet cells	0.027
		GA	Male, age 59, id: 2378	v23.proteinatlas.org/ENSG00000197122-SRC/pathology/stomach+cancer#img	>75%		0.497***
PXN	CAB003841	Normal/GIM	Male, age 56, id: 338	v23.proteinatlas.org/ENSG00000089159-PXN/tissue/stomach#img	0	Goblet cells, fibroblasts, T cells, and macrophages	0.276***
		GA	Female, age 86, id: 549	v23.proteinatlas.org/ENSG00000089159-PXN/pathology/stomach+cancer#img	>75%		0.371**
JUN	HPA066898 HPA066898	Normal/GIM	Female, age 57, id: 1467	v23.proteinatlas.org/ENSG00000177606-JUN/tissue/stomach#img	25-75%	Goblet cells, fibroblasts, plasma cells and T cells	0.256***
		GA	Male, age 54, id: 319	v23.proteinatlas.org/ENSG00000177606-JUN/pathology/stomach+cancer#img	>75%		-0.693***

<b>BRCA1</b>	CAB0019 46	Normal/G IM	Female, age 56, id: 2130	v23.proteinatla s.org/ENSG00 000012048- BRCA1/tissue/ stomach#img	<25%	Plasm a cells and B cells	-0.020
		GA	Male, age 71, id: 703	v23.proteinatla s.org/ENSG00 000012048- BRCA1/pathol ogy/stomach+ cancer#img	>75%		-0.012
<b>p53</b>	CAB0392 38	Normal/G IM	Female, age 57 id: 1467	v23.proteinatla s.org/ENSG00 000141510- TP53/tissue/st omach#img	25-75%	Goblet cells, T cells, macro phages , B cells, and plasm a cells	0.011
		GA	Male, age 48, id: 3044	v23.proteinatla s.org/ENSG00 000141510- TP53/patholog y/stomach+ca ncer#img	>75%		-0.046
<b>MDM2</b>	CAB0000 86	Normal/G IM	Female, age 56, id: 3233	v23.proteinatla s.org/ENSG00 000135679- MDM2/tissue/s tomach#img	>75%	Plasm a cells, T cells, macro phages , goblet cells, fibrobl asts	0.060
		GA	Male, age 59, id: 2473	v23.proteinatla s.org/ENSG00 000135679- MDM2/patholo gy/stomach+c ancer#img	>75%		0.065
<b>CTNNB1</b>	CAB0019 50	Normal/ IM	Female, age 81, id: 526	V23.proteinatl as.org/ENSG00 000168036- CTNNB1/tissu e/stomach#im g	25-75%	T cells, macro phages , B cells, plasm a cells, fibrobl asts and goblet cells	0.1134
		GA	Male, age 63, id: 1207	V23.proteinatl as.org/ENSG00 000168036- CTNNB1/patho logy/stomach+ cancer#img	>75%		0.3326**
<b>CD44</b>	HPA0057 85	Normal/G IM	Female, age 56, id: 2130	v23.proteinatla s.org/ENSG00 000026508- CD44/tissue/st omach#img	0	T cells, macro phages , B cells,	0.839***

		GA	Male, age 76, id: 2066	v23.proteinatlas.org/ENSG0000026508-CD44/pathology/stomach+cancer#img	0	plasma cells, fibroblasts, goblet cells	1.483***
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