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Author Correction: Identification of oral cancer related candidate genes by integrating protein-protein interactions, gene ontology, pathway analysis and immunohistochemistry

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This Article contains errors.

In Table 1, incorrect values for ‘Consensus Ranking’ are given. The correct Table 1 appears below as Table 1.

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	Centrality	Degree	Closeness	Centroid	SPB	Eigen vector	Page rank	CFC	CFB	Stress	Vulnerability	Unique pooled genes	Consensus Ranking
Top 2%	Oral cancer genes [#]	2	22	18	24	26	13	27	21	23	21	37	30
	Total genes	4	67	46	76	90	47	90	71	74	84	152	91
	Precision*	50.00	32.84	39.13	31.58	28.89	27.66	30.00	29.58	31.08	25.00	24.34	30.77
Top 5%	Oral cancer genes [#]	5	41	31	43	46	32	51	43	44	45	71	56
	Total genes	9	170	109	193	221	121	221	181	180	211	359	227
	Precision*	55.56	24.12	28.44	22.28	20.81	26.45	23.08	23.76	24.44	21.33	19.77	24.67
Top 7%	Oral cancer genes [#]	7	55	37	59	68	42	65	56	56	58	94	68
	Total genes	13	237	157	269	309	168	308	252	251	295	517	313
	Precision*	61.54	23.21	23.57	21.93	22.01	25.00	21.10	22.22	22.31	19.66	18.18	23.85
Top 10%	Oral cancer genes [#]	10	75	52	77	85	53	83	71	73	70	118	88
	Total genes	18	354	230	383	442	239	440	359	357	423	762	443
	Precision*	44.44	21.19	22.61	20.10	19.23	22.18	18.86	19.78	20.45	16.55	15.48	19.87

Table 1. The distribution of oral cancer genes in HCGN in top ranked lists. *Precision is the percentage of oral cancer genes in total genes. *Common out of 297 oral cancer genes in HCGN.

As a result,

“The precision score for top 2%, 5%, 7%, and 10% of the consensus ranked genes was found to be 30.77, 24.67, 23.85 and 19.87 respectively (Table 1). This indicates that consensus ranking is clearly better than individual centralities or unique pooled genes (Table 1). The precision decreases as we move from top ranked 2% to top ranked 10% genes. Though the top ranked 2% genes comparatively showed greater fraction of oral cancer genes in HCGN, the total number of unique oral cancer genes was very less (28 out of total 91 genes, Table 1).”

should read:

“The precision score for top 2%, 5%, 7%, and 10% of the consensus ranked genes was found to be 32.97, 24.67, 21.73 and 19.86 respectively (Table 1). This indicates that consensus ranking is clearly better than individual centralities or unique pooled genes (Table 1). The precision decreases as we move from top ranked 2% to top ranked 10% genes. Though the top ranked 2% genes comparatively showed greater fraction of oral cancer genes in HCGN, the total number of unique oral cancer genes was very less (30 out of total 91 genes, Table 1).”

In Table 3, incorrect values for ‘HCGN Ranking’ and ‘Degree with known oral cancer genes’ are given. The correct Table 3 appears below as Table 2.

S. No.	Gene ID	Gene Symbol	HCGN Ranking	Degree with known oral cancer genes	Expression Atlas (mRNA)	Oncomine mRNA expression*
1	3320	HSP90AA1	1	55		Up
2	8452	CUL3	2	41		NA
3	2099	ESR1	3	59	Up	Down
4	3312	HSPA8	4	30	Up	Up
5	1499	CTNNB1	5	32		NA
6	6714	SRC	6	32		NA
7	4088	SMAD3	7	20	Up	NA
8	5071	PARK2	8	21	Down	Down
9	5970	RELA	9	23		NA
10	207	AKT1	10	28		NA
11	408	ARRB1	11	18		NA
12	7186	TRAF2	12	21		NA
13	1457	CSNK2A1	13	25		Up
14	7013	TERF1	14	15		Up
15	5591	PRKDC	15	25		Up
16	3064	HTT	15	15		NA
17	23411	SIRT1	17	20		NA
18	5518	PPP2R1A	18	14		NA
19	10014	HDAC5	19	21		NA
20	4176	MCM7	20	21		Up
21	3676	ITGA4	21	38		Up
22	1432	MAPK14	22	15		NA
23	808	CALM3	23	12		NA
24	805	CALM2	23	12		NA
25	801	CALM1	23	12		NA
26	4851	NOTCH1	26	10		NA
27	5515	PPP2CA	27	16		Up
28	2316	FLNA	28	14	Up	Up
29	5894	RAF1	29	19		NA
30	8841	HDAC3	30	12		NA
31	8826	IQGAP1	31	11	Down	NA
32	5747	PTK2	32	23		Up
33	6657	SOX2	33	7	Down	NA
34	6195	RPS6KA1	34	9		NA
35	5580	PRKCD	35	15		NA
36	3717	JAK2	36	15		NA
37	998	CDC42	37	5		Up
38	6709	SPTAN1	38	10		NA
39	3688	ITGB1	39	14	Down	NA

Table 2. The candidate oral cancer genes. *The mRNA expression status (oral cancer vs normal) of a gene as reported in the Oncomine database and expression ATLAS. NA = Not reported.

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