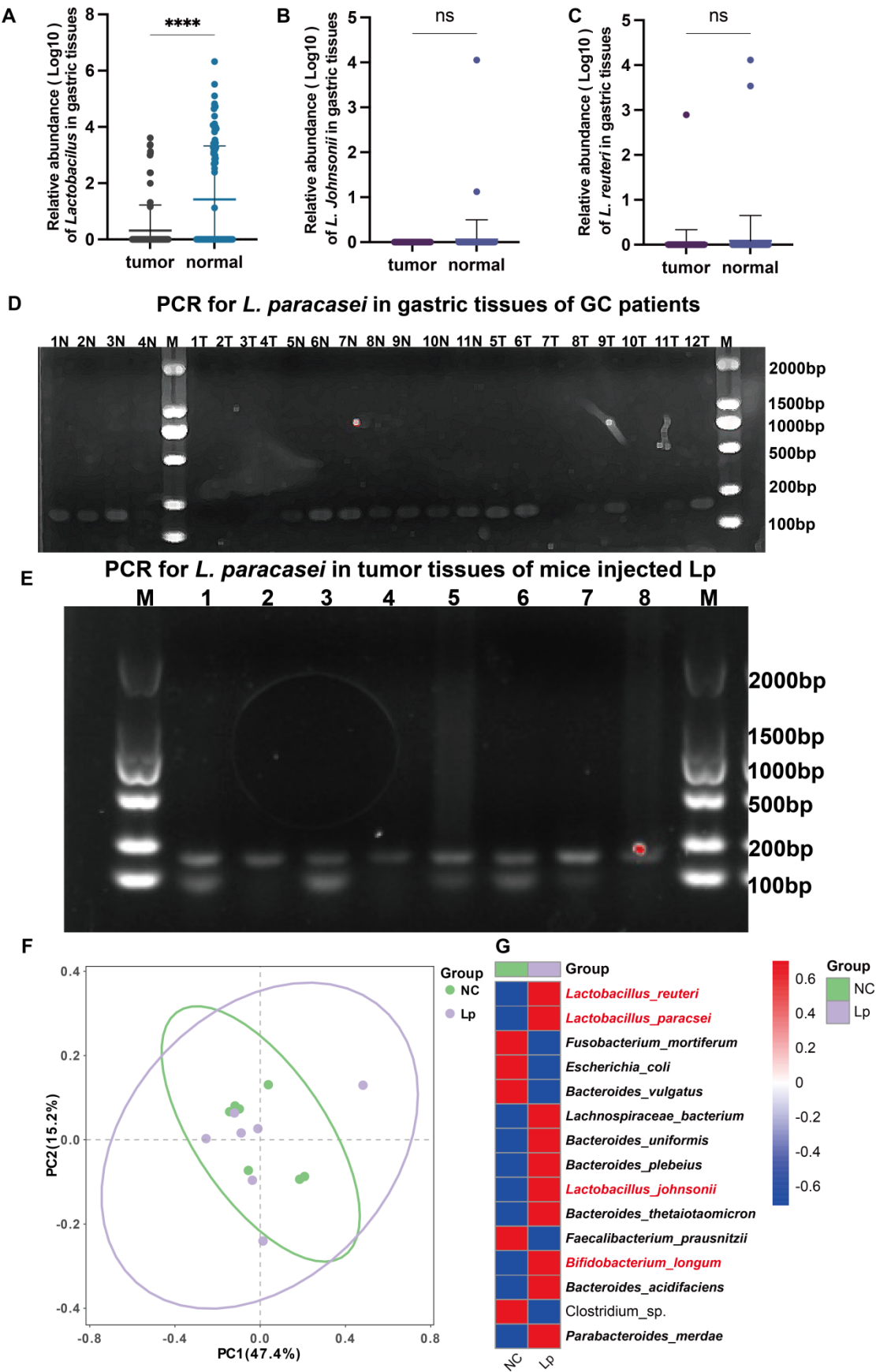


Supplementary information



Supplementary Figure 1

(A-C) The relative abundance of (A) *Lactobacillus* (B) *L. johnsonii* (C) *L. reuteri* in tumor tissues and normal tissues of GC patients. Data were analyzed by t tests; Means $\pm$ SD. ns $p \geq 0.05$, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.

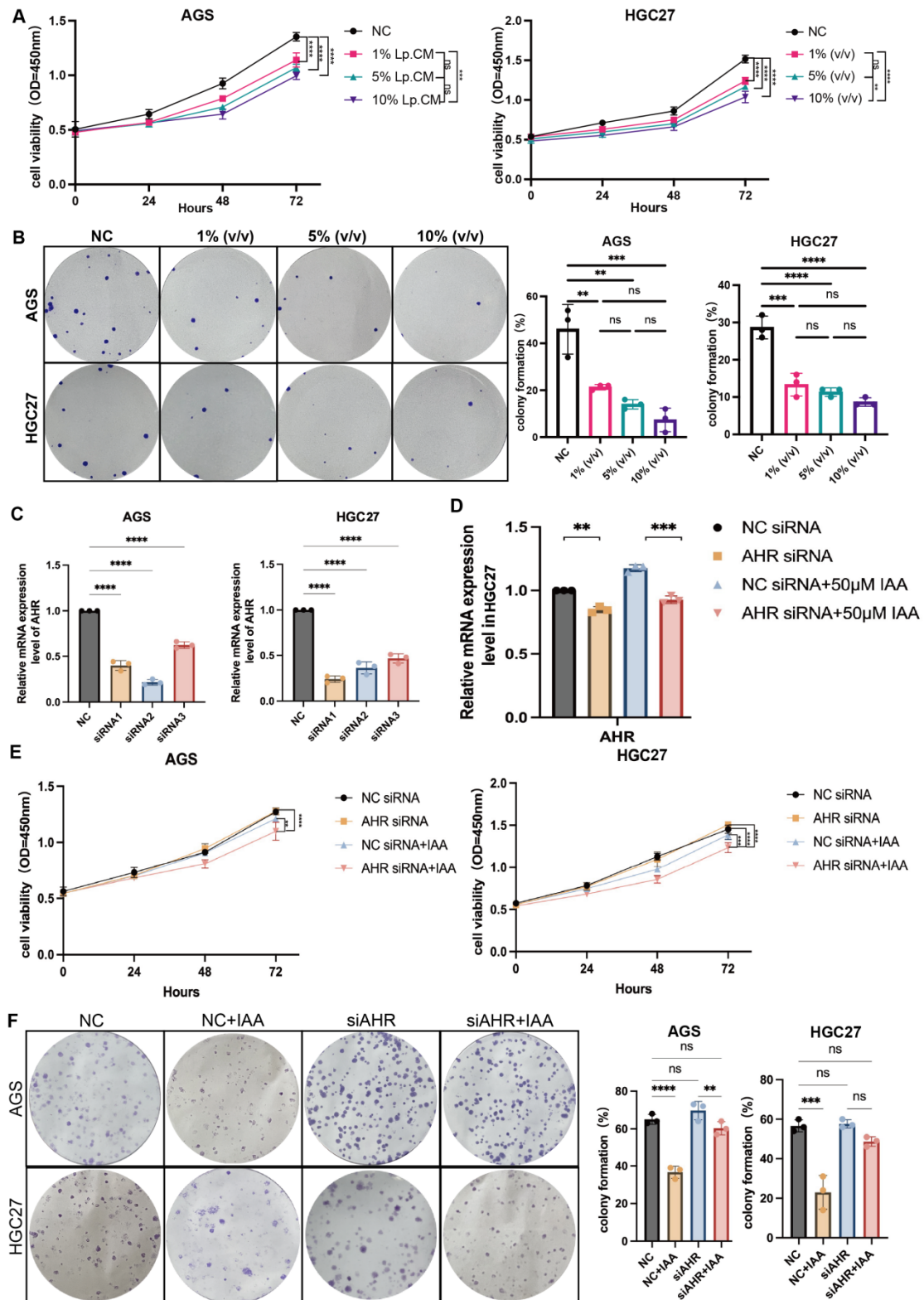
(D) PCR was used to determine the colonization of *L. paracasei* in both tumor or normal tissues of GC patients.

(E) PCR was used to determine the colonization of *L. paracasei* in tumor tissues of HGC27 xenograft.

(F) Beta-diversity by PCoA based on Binary-jaccard dissimilarity matrix in stomach samples of nude mice.

(G) Heatmap of differential bacterial species ($p < 0.05$) in nude mice, compared with control groups.

PCoA, principal coordinate analysis.



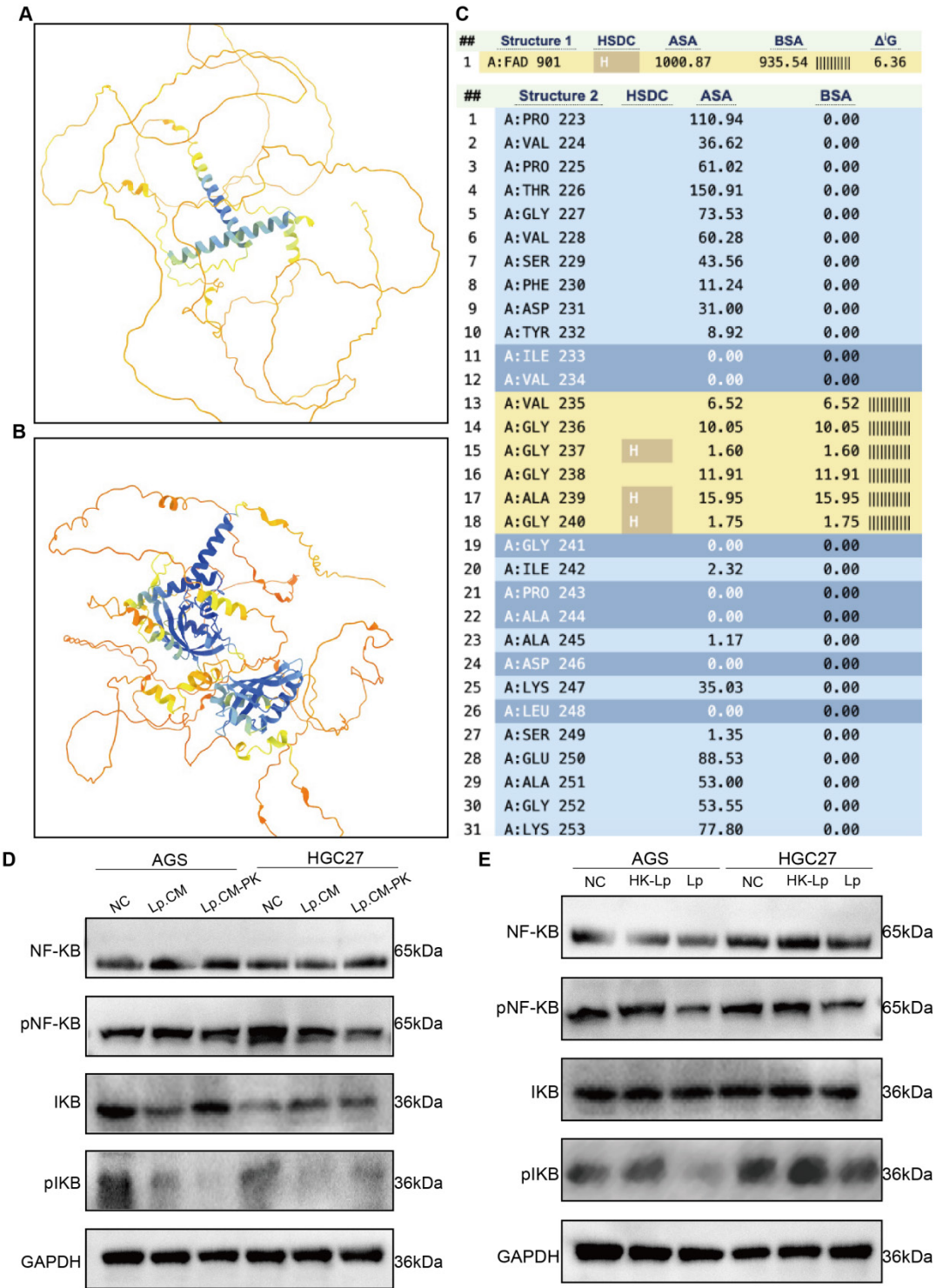
Supplementary Figure 2

(A, B) (A) Cell viability at OD450nm (B) colony formation of human GC cells with PBS, 1% Lp.CM, 5% Lp.CM and 10% Lp.CM.

(C) The knockdown effect of AHR of human GC cells through qPCR.

(D) The mRNA level of AHR of HGC27 with siAHR and IAA.

(E, F) (E)Cell viability at OD450nm (F) colony formation of human GC cells with PBS, IAA, siAHR and siAHR+IAA. Data were analyzed by two-way ANOVA; Means $\pm$ SD.



Supplementary Figure 3

(A, B) The 3D structure of (A)MTDH and (B)AHR using ChimeraX.

(A) The receptor protein is located above, and the ligand protein is located below. Each row contains an amino acid residue, with the yellow region indicating the predicted binding region. HSDC is predicted for hydrogen bonding, BSA is the area of interaction encapsulation, and the more vertical lines there are, the higher the degree of encapsulation, indicating a tighter interaction.

(D) Western blot analysis of the inhibition of NF- κ B signaling pathway of AGS and HGC27 treated with Lp. CM and Lp. CM-PK.

Table 1 The proteins binding to AHR by COIP

Checked	Protein	FC Master	Accession	Descriptive	Exp. q-val	Sum	PEP	Coverage	# Peptide	# PSMs	# Unique	# AA	MW [k]	pI	calc.	Score	Seq	# Peptide	Biological	Cellular	Cy. Molecular	Plan	Id	Enrizz	Gen	Ensembl	Gene	Yip	Path	Reactome	# Protein	Found	In	# Protein
TRUE	High	Master Ph CON_P13	SWISS-PI		0	56.701	19	15	83	12	593	59.5	5.21	148.42	15																			
TRUE	High	Master Ph P04264	Keratin, ty		0	44.581	19	11	37	10	644	66	8.12	48.25	11				1 cell organ non-struct bone, toot	P00038														
TRUE	High	Master Ph P05509	Keratin, ty		0	26.204	21	14	35	11	639	65.4	8	60.47	14				14 cell cycle plasma m bone, toot	P00038														
TRUE	High	Master Ph CON_P02	SWISS-PI		0	27.935	17	10	11	10	607	69.2	6.18	16.15	10				10 stress resp non-struct nucleic ac	P00273														
TRUE	High	Master Ph P02553	Keratin, ty		0	24.795	17	8	36	5	472	51.5	5.16	51.39	8				8 cell organ plasma m cytoskelet	P00038														
TRUE	High	Master Ph P16403	Histone H		0	21.438	24	1	5	16	5	213	21.4	10.93	31.89	5				5 cell organ nucleotof nucleic ac	P00538													
TRUE	High	Master Ph CON_P05	SWISS-PI		0	20.055	13	8	14	8	603	62.1	5.3	11.88	8																			
TRUE	High	Master Ph P15401	Histone H		0	14.931	11	3	10	3	225	22.5	10.92	28.73	3																			
TRUE	High	Master Ph P48756	RNA-bind		0	13.595	6	4	4	4	843	100.1	6.32	5.59	4				4 RNA meta nucleotof nucleic ac	P00076														
TRUE	High	Master Ph P11387	DNA topoi		0	11.542	6	6	9	6	765	90.7	9.31	9.31	6				6 cell cycle nucleotof nucleic ac	P01028														
TRUE	High	Master Ph Q04761	ATP-deph		0	9.417	4	3	4	3	845	95.9	6.8	4.31	3				3 protein m cytosol tr translation	P00055														
TRUE	High	Master Ph Q05287	ATP-deph		0	8.863	5	4	5	4	859	96.3	9.06	6.29	4				4 RNA meta nucleic ac	P00270														
TRUE	High	Master Ph Q04088	Cyclin-deg		0	8.835	4	3	4	3	783	91.3	5.36	4.27	3				3 cell cycle nucleotof kinase ac	P00069														
TRUE	High	Master Ph Q05359	Heterogen		0	8.673	5	4	7	4	822	90.5	6	4.28	4				4 cell cycle cytosolof cytoskelet	P00622														
TRUE	High	Master Ph Q04800	Nucleolar		0	8.537	6	4	5	4	783	87.3	9.28	4.34	4				4 cell organ cytosolof enzyme re	P00270														
TRUE	High	Master Ph Q04840	RNA cycl		0	8.402	4	4	8	4	1025	115.7	8.27	3.48	4				4 protein m nucleotof nucleic ac	P005127														
TRUE	High	Master Ph Q04361	Poly(ub-bi		0	8.336	3	3	3	3	559	59.8	5.29	6.48	3				3 cell organ cytosolof nucleic ac	P00076														
TRUE	High	Master Ph Q01020	60S ribos		0	7.426	10	4	4	3	188	21.5	11.72	3.39	3				3 protein m cytosolof nucleic ac	P01135														
TRUE	High	Master Ph CON_P12	SWISS-PI		0	7.4	7	2	4	2	359	38.4	5.5	5.16	2				2 stress resp non-struct enzyme re	P00031														
TRUE	High	Master Ph P46087	Probabli-1		0	7.257	4	3	4	3	812	89.2	9.23	4	3				3 cell organ nucleic ac	other mol	P01189													
TRUE	High	Master Ph P46087	Probabli-1		0	7.153	4	3	4	3	812	74.8	9.23	4	3				2 other bloc cytosolof nucleic ac	P00482														
TRUE	High	Master Ph Q06054	Nuclear en		0	6.223	3	3	5	3	1076	122.9	6.35	6.41	3				3 cell organ cytosol tr translation	P00470														
TRUE	High	Master Ph P15924	Desmopl		0	6.15	1	4	5	4	2871	331.6	6.81	0	4				4 cell adhes plasma m cytoskelet	P00681														
TRUE	High	Master Ph CON_P00	Yipson-1		0	6.024	8	2	124	2	231	24.4	7.18	103.2	2				2 protein m non-struct other mol	P00069														
TRUE	High	Master Ph Q04840	60S ribos		0	5.158	10	3	4	3	288	32.7	10.58	2.37	3				3 cell organ cytosolof nucleic ac	P01109														
TRUE	High	Master Ph P02914	60S ribos		0	5.531	11	2	3	2	215	23.4	10.93	5.03	2				2 protein m cytosol tr other mol	P01029														
TRUE	High	Master Ph P06578	60S ribos		0	5.454	10	4	4	4	427	47.7	11.06	0	4				4 protein m cytosolof other mol	P00573														
TRUE	High	Master Ph P01549	Caspase-1		0	5.397	9	2	2	2	242	27.7	5.56	6.08	2				2 protein m plasma m other mol	P00566														
TRUE	High	Master Ph Q7RT57	Keratin, ty		0	5.197	4	2	3	1	529	57.8	7.71	3.91	2				2 cell organ cytosolof bone, toot	P00038														
TRUE	High	Master Ph Q06841	Eukaryotic		0	5.058	1	1	3	1	1220	138.7	5.49	4.59	1				1 cell organ cytosolof nucleic ac	P00009														
TRUE	High	Master Ph Q05359	Heterogen		0	4.933	4	2	3	2	553	61.2	9.87	1.95	2				2 cell organ nucleotof nucleic ac	P00538														
TRUE	High	Master Ph CON_P05	SWISS-PI		0	4.816	6	2	4	2	401	43.9	5.35	5.29	2																			
TRUE	High	Master Ph Q13435	Splicing fa		0	4.414	2	2	3	2	895	100.2	5.87	0	2				2 cell organ nucleic ac	P00207														
TRUE	High	Master Ph Q01589	Suprabasi		0	4.389	2	2	2	2	1477	119.8	5.66	2.57	2				2 cell organ nucleic ac	other mol	P00557													
TRUE	High	Master Ph Q13435	Splicing fa		0	4.334	2	1	4	1	1184	132.5	8.41	5.3	1				1 other bloc non-struct	P00060														
TRUE	High	Master Ph P02805	Histone H		0	4.247	21	2	2	2	103	11.4	11.36	1.83	2				2 cell organ non-struct nucleic ac	P01551														
TRUE	High	Master Ph P02841	Histone H		0	4.237	9	2	2	2	266	30	10.61	1.82	2				2 protein m other reat other mol	P01248														
TRUE	High	Master Ph P02841	Histone H		0	4.185	2	2	2	2	1341	151.8	6.43	0	2				2 RNA meta nucleotof other mol	P00270														
TRUE	High	Master Ph Q70021	Ribosome		0	4.115	5	2	2	2	490	54.9	10.13	1.92	2				2 RNA meta cytosol tr nucleic ac	P00687														
TRUE	High	Master Ph P02241	60S ribos		0	4.114	11	2	3	2	208	24.2	10.32	2.34	2				2 protein m cytosolof other mol	P01201														
TRUE	High	Master Ph P47914	60S ribos		0	4.023	9	1	3	1	159	17.7	11.66	7.09	1				1 protein m cytosol tr other mol	P01179														
TRUE	High	Master Ph P02553	Probabli-1		0	3.824	4	3	3	3	786	89.8	9.28	0	3				3 RNA meta nucleotof other mol	P00573														
TRUE	High	Master Ph P02346	Splicing fa		0	3.737	4	2	2	2	707	76.1	9.44	2.12	2				2 cell organ cytosolof nucleic ac	P00076														
TRUE	High	Master Ph Q04JW9	Suprabasi		0	3.324	3	1	2	1	690	60.5	7.01	2.01	1				1 P01009	747487														
TRUE	High	Master Ph P04840	60S ribos		0	3.296	1	1	1	1	877	72.6	8.6	5.15	1				1 cell organ cytosolof signal tran	P00076														
TRUE	High	Master Ph Q05854	SERP prot		0	3.194	2	1	2	1	655	74.3	6.16	3.71	1				1 cell cycle plasma m cytoskelet	P00069														
TRUE	High	Master Ph Q04W36	Calcium h		0	3.175	1	1	1	1	916	103.6	9.04	0	1				1 RNA meta other reat other mol	P01585														
TRUE	High	Master Ph Q04JW9	Translaci		0	1.842	1	1	1	1	670	75.4	9.5	2.53	1				1 RNA meta nucleotof other mol	P00270														
TRUE	High	Master Ph Q13429	Transac		0	2.893	2	2	2	2	1488	152	9.04	0	2				2 RNA meta cytosolof other mol	P00346														
TRUE	High	Master Ph Q04W36	Calcium h		0	2.728	2	1	1	1	759	85.7	9.22	0	1				1 RNA meta nucleic ac	P00076														
TRUE	High	Master Ph P02753	60S ribos		0	2.531	3	1	1	1	249	28.7	10.84	1.76	1				1 cell cycle cytosolof other mol	P01092														
TRUE	High	Master Ph P02753	60S ribos		0	2.527	1	1	1	1	125	13.7	11.18	0	1				1 protein m cytosolof other mol	P01092														
TRUE	High	Master Ph Q04W36	Calcium h		0	2.295	2	1	1	1	492	57.2	5.92	0	1				1 cytosolof other mol	P00076														
TRUE	High	Master Ph Q04W36	Calcium h		0	2.164	1	1	1	1	881	98.5	10.02	0	1				1 protein m ER/Golgi/ signal tran	P00070														
TRUE	High	Master Ph Q04W36	Calcium h		0	2.087	1	1	1	1	335	38	9.46	0	1				1 cell organ cytosolof enzyme re	P00076														
TRUE	High	Master Ph Q14776	Transcrip		0	1.969	1	1	1	1	1098	123.8	8.65	0	1				1 RNA meta nucleic ac	other mol	P00397													
TRUE	High	Master Ph P04040	Catalase		0	1.961	2	1	1	1	527	59.7	7.39	0	1				1 protein m non-struct other mol	P00199		</												