

A

ReMOAT

CONVERT GENE ID'S

Paste gene ID's in box

ILMN_1705423
ILMN_1697642
ILMN_1788184
ILMN_1681845
ILMN_1889845
ILMN_1690979
ILMN_1811114
ILMN_1660729
ILMN_1705659
ILMN_1694630
ILMN_1819355
ILMN_1797055
ILMN_1713038
ILMN_1670547
ILMN_2342515
ILMN_1809425
ILMN_1728019
ILMN_1783852
ILMN_1882325
ILMN_1721344
ILMN_1691223
ILMN_1766219
ILMN_1679973

Select ID type:
Illumina

Species:
Human

Platform:
Illumina_Human_WG-6_V1_hg18

Please choose output ID type:
 Illumina
 Ensembl
 Entrez
 Gene Symbol
 Unigene
 Lumi
 CytoBand

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Convert Gene ID's

Search Probe Sequences

Probe Location

Second Matches

Transcript Information

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B

ID Converter

Illumina probe	Lumi id	Gene Symbol	Ensembl	Entrez	Unigene	Cyto Band	Description	iHOP	Wiki Genes
ILMN_1705423	Ed5J5UnfUnjp1E36qA	TBC1D29	ENSG00000197689	651450	Hs.241421	17q11.2	TBC1 domain family, member 29	iHop	wikigenes
ILMN_1697642	BU_IInUkheOXOBERI	BCAP29	ENSG00000057590	55973	Hs.303787	7q22.3	B-cell receptor-associated protein 29	iHop	wikigenes
ILMN_1788184	3Sm5Uom7k7HlP61NM	CIDEA	ENSG00000176194	1149	Hs.249129	18p11.21	Cell death-inducing DFPA-like effector a	iHop	wikigenes
ILMN_1681845	Ql8LF5 HR6JleKf6u4	PAPD4	ENSG00000164329	167153	Hs.418198	5q14.1	PAP associated domain containing 4	iHop	wikigenes
ILMN_1889845	uiT4gnlKel.dcOwf4o				Hs.542469	20p12.2		iHop	wikigenes
ILMN_1690979	rqJNCKP9ITJF7T7FR4	SLC17A3	ENSG00000124564	10786	Hs.327179	6p22.2	Solute carrier family 17 (sodium phosphate), member 3	iHop	wikigenes
ILMN_1811114	E_KBTdJTXVKCVFXhXw	SDS	ENSG00000135094	10993	Hs.654416	12q24.13	Serine dehydratase	iHop	wikigenes
ILMN_1660729	uFKnit46gofh1K5ljk	ATP6V1C2	ENSG00000143882	245973	Hs.580464	2p25.1	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C2	iHop	wikigenes
ILMN_1705659	HilE5uDqOglIq3eXj4	FAM71C	ENSG00000180219	196472	Hs.591011	12q23.1	Family with sequence similarity 71, member C	iHop	wikigenes
ILMN_1694630	BX11LxXl d3DNTepCo	AKO55082		645113	Hs.680609	22q12.3		iHop	wikigenes
ILMN_1819355	W3UuLHVT8SS7VQ95Do				Hs.558279	8q24.12		iHop	wikigenes
ILMN_1797055	Hqi3RRpw.jogr2KXEg	LIN52	ENSG00000205659	91750	Hs.612866	14q24.3	Lin-52 homolog (C. elegans)	iHop	wikigenes
ILMN_1713038	W5KEOeUil610idGwk0	PCOTH	ENSG00000205861	387911	Hs.707257	13q12.12	Prostate collagen triple helix	iHop	wikigenes
ILMN_1670547	rVzFCKlgHFRfs73JE	GRM1	ENSG00000152822	2911	Hs.32945	6q24.3	Glutamate receptor, metabotropic 1	iHop	wikigenes
ILMN_1800425	c12ITelNdd1OQue.qQ	SLC9A1	ENSG00000090020	6548	Hs.469116	1p36.11	Solute carrier family 9 (sodium/hydrogen exchanger), member 1 (antiporter, Na+/H+, amiloride sensitive)	iHop	wikigenes
ILMN_1728019	uBujoq7tKivqEikiCI	PML		5371	Hs.526464	15q24.1	Promyelocytic leukemia	iHop	wikigenes
ILMN_1783852	Tvl.5C3EDid_QSB0SU	CD164	ENSG00000135535	8763	Hs.520313	6q21	CD164 molecule, sialomucin	iHop	wikigenes
ILMN_1882325	3V1oo7pChEIRKHYHeY				Hs.576630	10q23.1		iHop	wikigenes
ILMN_1721344	K0dTUXaUV1VJSMaDA	MOBK12A	ENSG00000172081	126308	Hs.86912	19p13.3	MOB1, Mps One Binder kinase activator-like 2A (yeast)	iHop	wikigenes
ILMN_1691223	NKQOxX_FM1QKMLNLO	ZNF566	ENSG00000186017	84924	Hs.646371	19q13.12	Zinc finger protein 566	iHop	wikigenes
ILMN_1766219	BX3oJ0PNGJE66AG6lo	HGC6.1.1	ENSG00000153298	26236	Hs.225962	6q27	Homo sapiens HGC6.1.1 mRNA, complete cds.	iHop	wikigenes
ILMN_1679973	ivRLKrrrTxXIPTuzXo	OR1J2	ENSG00000197233	26740	Hs.460145	9q33.2	Olfactory receptor, family 1, subfamily J, member 2	iHop	wikigenes

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C

Probe Reannotation

Illumina probe	Probe Sequence	Probe Type	Repeats	CpG Islands	GC%	SNP's	quality score	quality comments
ILMN_1705423	CTCTGCAGCTGCCAGCTCTCCAGCTGATGGCTCCACATCTTGGGGAA	RefSeq_S			60.00	0	Perfect	
ILMN_1697642	CCATTGAGAAGAGCTCCACCAGCAGACTGATGCCTATGAACACACACAG	RefSeq_A			52.00	0	Perfect	
ILMN_1788184	CAGCGGTGCCAGGAGCGGTGTCATGTGTGACAGCCATTTGGTCCATCAT	RefSeq_A			58.00	0	Perfect	
ILMN_1681845	GCCTTAAGTCTTTGCTTGACTCACTGGGATAGACTGAGCGTTTGGGTGTG	RefSeq_S			50.00	0	Perfect	
ILMN_1889845	GAGCATTGAGAAGCTGCCAGGTGCCCTTCTCCTAATGTAACCTTTGAGG	Unigene_S			50.00	0	Perfect***	*** Check this probe manually, no CDS annotation
ILMN_1690979	GGGAGCATCAAGAGGATTTTCGAGCATAGCACCTGTCAATGTACCCACTG	RefSeq_S			50.00	0	Perfect	
ILMN_1811114	TTGAGGAACCATCTCAGCCATCTCCAGGAAGCCACCCCTGACCCCTTA	RefSeq_S			58.00	0	Perfect	
ILMN_1660729	ACCAGGGCTGAGGTCTGATGGGAAGACTTGACTCCAGGTGCAGAGATGC	RefSeq_S			58.00	0	Perfect	* Transcript match to reverse strand
ILMN_1705659	GAGGCCACATCGGTGAATGGATGGAAGCCAGAGGGTCTCTACTAGCTG	RefSeq_S			58.00	0	Perfect	
ILMN_1694630	CCTTCTCCAGTACCCCTTACTCCCTCTCTAATATCCATCTGGGCAAGGG	RefSeq_S			52.00	0	Perfect***	*** Check this probe manually, no CDS annotation
ILMN_1819355	TCTCCAGTGAGTACTCCCATTTACAGCAGGTGCCCAATTTGCAATGG	Unigene_S			50.00	0	Perfect***	*** Check this probe manually, no CDS annotation
ILMN_1797055	GGGAGTCTCACCACGGCTAATTTGATGGAGAAGGTTTCGAGGCCTACAGA	RefSeq_S			54.00	0	Perfect	
ILMN_1713038	TGCAGGACAATGCTGCAGAGGCCTGGTCTCAGAGCTCACGTAAGCATC	RefSeq_S			58.00	1	Perfect	* Transcript match to reverse strand
ILMN_1670547	CCCTATACCAAGAGGGCCGAAACTTTCACCTTGATGTATGTTCTGATAC	RefSeq_S			46.00	1	Perfect	
ILMN_1800425	TCCTCGCCCATCTGTCCATCTCTCTCCATGCAAGTGTGTTGGGCA	RefSeq_S			58.00	0	Perfect	* Transcript match to reverse strand
ILMN_1728019	AACGTGGATGGAGGGTGTGTGAGGGAGGTTGGGACAGAGGCAGAGAAGG	RefSeq_S			58.00	0	Perfect	* Transcript match to reverse strand
ILMN_1783852	GTTAGATTTGCAAGTCTACAAATGAGCTCTTGCAACAGAACTGCACAGC	RefSeq_S			42.00	0	Perfect	
ILMN_1882325	CCCAGAGGAGGATGGCAAGGACACAGACAGACTCGAACTCTGCG	Unigene_S			58.00	0	Perfect***	* Transcript match to reverse strand *** Check this probe manually, no CDS annotation
ILMN_1721344	TCACTCATCCACCTCGGAGACACCTCCCCAGCAGATACGGAATAA	RefSeq_S			58.00	1	Perfect	
ILMN_1691223	AGGCAAATGTACCCCTTGACCATATCCCAAAGGATAGTCTTATCAGTTC	RefSeq_S			40.00	0	Perfect	
ILMN_1766219	CCTTCTGGAGGCTCAATATACGAGCACATGGTGGAAAACGTTGGCCGG	RefSeq_S			54.00	0	Perfect	
ILMN_1679973	GTTCACAGTAGGGGTGGTGCATTACCTGCCATTCATGTATCTCTGG	RefSeq_S			52.00	0	Perfect	

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Figure S1