

**S4 Table.** Thirty-two genes that were differently expressed in the R1 (CR1, LR1, and CH1) or R2 (CR1LR1 and CR1CH1) groups compared to the parental H3122 cell line are described with the top 20 ranking genes with an absolute log<sub>2</sub> fold change

Symbol	Full name	Function	Group with top 20 ±log <sub>2</sub> FC	Log <sub>2</sub> FC	
				R1	R2
OR2W1	Olfactory receptor family 2 subfamily W member 1	G-protein-coupled receptor activity, olfactory receptor activity	Both	16.66	17.33
C1RL-AS1, RNU6-485P	C1RL antisense RNA 1, RNA, U6 small nuclear 485, pseudogene	Unknown	Both	-10.95	-15.42
PGLYRP4	Peptidoglycan recognition protein 4	Peptidoglycan binding, defense response to Gram-positive bacteria, innate immune response	Both	9.77	8.04
CCL20	C-C motif chemokine ligand 20	Extracellular region, T cell migration, cell chemotaxis, immune response	Both	7.98	7.12
DEFB4A	Defensin Beta 4A	Chemotaxis, immune response	Both	7.8	8.62
AB019440.1, AB019440.50	ENSG00000211945 (immunoglobulin heavy variable 1-18 (IGHV1-18), ENSG00000271201	Unknown	Both	-7.09	-8.03
LTB	Lymphotoxin beta	Plasma membrane, immune response	Both	6.91	8.05
CDH6	Cadherin 6	Plasma membrane, adherens junction organization	Both	6.52	8.69
PDZK1IP1	PDZK1 interacting protein 1	Extracellular exosome, integral component of membrane	R1	8.54	5.98
CD177	CD177 molecule	Plasma membrane, protein binding, leukocyte migration	R1	7.87	3.43
PIGR	Polymeric immunoglobulin receptor	Extracellular exosome, epidermal growth factor receptor signaling pathway, immunoglobulin transcytosis in epithelial cells mediated by polymeric immunoglobulin receptor	R1	7.85	3.04
RP11-583F2.6	Uncharacterized LOC105371863	Unknown	R1	-7.82	-2.17
ALPL	Alkaline phosphatase, liver/bone/kidney	Extracellular exosome, alkaline phosphatase activity	R1	7.56	3
NELL1	Neural EGFL like 1	Cell differentiation, extracellular region, negative regulation of osteoblast proliferation	R1	7.43	4.91
ASB2	Ankyrin repeat and SOCS box containing 2	Intracellular signal transduction, protein polyubiquitination, myoblast differentiation	R1	6.98	5.18
FCGBP	Fc fragment Of IgG binding protein	Extracellular exosome, protein binding	R1	6.95	3.95

S100A8	S100 calcium binding protein A8	Extracellular exosome, protein binding, inflammatory response, chemokine production, cytoskeleton, innate immune response, leukocyte migration involved in inflammatory response	R1	6.9	6.31
TMPRSS11D	Transmembrane protease, serine 11D	Extracellular exosome, proteolysis, respiratory gaseous exchange	R1	6.86	5.64
CTD-2319I12.1	WAP four-disulfide core domain 21, pseudogene (WFDC21P)	Unknown	R1	6.75	5.92
C2, CFB	Complement component 2, complement factor B	Protein binding, extracellular exosome, complement activation, phosphatidylinositol 3-kinase complex, plasma membrane	R1	6.6	5.94
GPIHBP1	Glycosylphosphatidylinositol anchored high density lipoprotein binding protein 1	Anchored component of external side of plasma membrane, cholesterol homeostasis	R2	-6.34	-8.56
ANKRD33B	Ankyrin repeat domain 33B	Unknown in <i>Homo sapiens</i>	R2	6.28	9.44
MAGEC1	MAGE family member C1	Protein binding	R2	5.19	7.68
RP4-555D20.2	ENSG00000261786	Unknown	R2	4.77	7.18
PAEP	Progestagen-associated endometrial protein	Apoptotic process, positive regulation of granulocyte macrophage colony-stimulating factor production, positive regulation of interleukin-13 secretion, positive regulation of interleukin-6 secretion	R2	-4.54	-7.2
BEST1	Bestrophin 1	Plasma membrane, ion transmembrane transport	R2	-4.37	-8.29
AQP5	Aquaporin 5	Water channel activity, plasma membrane, cellular water homeostasis	R2	-4.24	-8.02
RP11-346D6.6	Long intergenic non-protein coding RNA 1468 (LINC01468)	Unknown	R2	4.18	7.12
GABRB1	Gamma-aminobutyric acid type A receptor beta1 subunit	GABA-A receptor complex, cell junction, ion transmembrane transport	R2	-3.85	-7.56
FAM46C	Family with sequence similarity 46 member C	Unknown in <i>Homo sapiens</i>	R2	-3.77	-7.5
PPP1R1B	Protein phosphatase 1 regulatory inhibitor subunit 1B	Cytosol, D1-5 dopamine receptor binding, intracellular signal transduction, protein kinase inhibitor activity	R2	-3.04	-8.74
ARSD	Arylsulfatase D	Arylsulfatase activity, extracellular exosome, post-translational protein modification	R2	-2.43	-8.06

FC, fold change.