

Supplementary Table 1: Demographics and Clinical Characteristics of Modified Intent-to-Treat (mITT)**Population**

Characteristic	N (%) [@]
Enrollment breakdown - Screened - Evaluable for safety (ITT) - Evaluable for radiographic and survival endpoints (mITT) - Evaluable for primary efficacy endpoint (PP)	43 34 31 30
Age, median in years (range)	62 (range 19-93)
Sex - Male - Female	17 (54.8%) 14 (45.2%)
AJCC 8th Edition Clinical Stage, n (%) - IIIB - IIIC - IIID	15 (48.4%) 14 (45.2%) 2 (6.5%)
Baseline lactate dehydrogenase (LDH) (IU/L), n (%) ≤upper limit of normal (ULN) >ULN	7 (22.6%) 24 (77.4%)
Number and nature of lesion - Size in mm, median (range) 1 lesion 2-3 lesions >3 lesions	25 (15–64) 18 (58.0%) 8 (25.8%) 5 (16.2%)
Tumor mutation status - BRAF[#] - NRAS[§] - NF1[§] - WT	8 (25.8%) 2 (25.8%) 2 (6.5%) 13 (41.9%)
Prior therapy - None - Immune therapy - BRAF/MEK targeted therapy	28 2 (1 – CTLA-4, 1 – IFN) 1
Location (injected lesion) - Head and neck - Trunk (inguinal, axillary) - Extremity	11 (35.5%) 16 (51.6%) 4 (12.9%)
Nature (injected lesion) - Lymph node (LN) - In-transit	26 (83.9%) 5 (16.1%)
Imaging response (RECIST v1.1) - Partial response (PR) - Stable disease (SD) - Progressive disease (PD)	14 (45.2%) 10 (32.3%) 7 (22.6%)

Notes:

[@]34 patients were enrolled.

- 3 withdrew consent after receiving 1 dose of intratumoral therapy but prior to completion of neoadjuvant therapy, restaging scans and surgery. These patients were evaluable for safety but unevaluable for primary (pathologic response) and secondary (radiographic response) endpoints. These patients were included in the intention-to-treat (ITT) analysis.
- 1 patient (UOP-029) completed neoadjuvant therapy but had systemic disease progression at restaging scans, and did not undergo planned surgery. This patient was evaluable for safety, evaluable for secondary (radiographic response) but not primary (pathologic response) endpoints, and was included in the modified ITT (mITT) analysis.
- 30 patients completed neoadjuvant therapy, and underwent restaging scans. These patients were evaluable for safety, primary (pathologic response) and secondary (radiographic response) endpoints and were included in the per-protocol (PP) analysis.

All percentages are reflective of the number of patients (31) who completed neoadjuvant therapy and included in mITT analyses.

[#]8 patients were BRAF mutant, of whom 7 had BRAF V600E mutations, and 1 (UOP-033) had a non-V600 mutation (E501K).[§]10 patients had either NRAS codon 61 (n=7) or NF1 (n=3) mutations; while 1 patient had both mutations in both NRAS codon 61 and NF1 (UOP-005; NRAS G13V, NF1 R1830C).

Supplementary Table 2: Incidence of Treatment-related Adverse Events (≥1% incidence) in Intent-to-Treat (ITT) Population (CTCAE v5.0)

	Grade 1 n (%)	Grade 2 n (%)	Grade 3 n (%)
Constitutional			
Arthralgia, myalgia, joint pain	8 (3.8%)	7 (3.3%)	2 (0.9%)
Fever	2 (0.9%)	6 (2.8%)	0 (0.0%)
Flu-like reaction (e.g., rigors, chills, flushing)	23 (10.8%)	19 (9.0%)	2 (0.9%)
Fatigue and malaise	10 (4.7%)	3 (1.4%)	0 (0.0%)
Immune-related adverse events			
Diarrhea/colitis	9 (4.2%)	4 (1.9%)	1 (0.5%)
Hypothyroidism	5 (2.4%)	1 (0.5%)	0 (0.0%)
Hyperthyroidism	6 (2.8%)	0 (0.0%)	0 (0.0%)
Rash (e.g., rash, maculopapular rash, vitiligo, pruritus)	11 (5.2%)	3 (1.4%)	0 (0.0%)
Cardiac			
Hypertension	3 (1.4%)	11 (5.2%)	3 (1.4%)
Tachycardia	6 (2.8%)	1 (0.5%)	0 (0.0%)
Dyspnea	0 (0.0%)	4 (1.9%)	0 (0.0%)
Fluid overload	0 (0.0%)	3 (1.4%)	0 (0.0%)
Electrolyte			
Hypokalemia	5 (2.4%)	0 (0.0%)	0 (0.0%)
Hypomagnesemia	5 (2.4%)	0 (0.0%)	0 (0.0%)
Hyponatremia	30 (14.2%)	0 (0.0%)	0 (0.0%)
Hypophosphatemia	11 (5.2%)	10 (4.7%)	4 (1.9%)
Hyperuricemia	3 (1.4%)	0 (0.0%)	0 (0.0%)
Gastrointestinal			
Mucositis	4 (1.9%)	2 (0.9%)	0 (0.0%)
Nausea and vomiting	10 (4.7%)	5 (2.4%)	0 (0.0%)
Aspartate transaminase (AST) increase	3 (1.4%)	1 (0.5%)	0 (0.0%)
Alanine transaminase (ALT) increase	5 (2.4%)	0 (0.0%)	0 (0.0%)
Hematologic			
Anemia	12 (5.7%)	1 (0.5%)	0 (0.0%)
Thrombocytopenia	9 (4.2%)	1 (0.5%)	0 (0.0%)
Leucopenia	22 (10.4%)	7 (3.3%)	0 (0.0%)
Other			
Injection site reaction	14 (6.6%)	4 (1.9%)	0 (0.0%)
Injection site infection	2 (0.9%)	3 (1.4%)	1 (0.5%)
Infusion related reactions	3 (1.4%)	5 (2.4%)	0 (0.0%)
Cytokine-release syndrome	2 (0.9%)	8 (3.8%)	0 (0.0%)

Supplementary Table 3: Histopathologic Features of Response to Neoadjuvant Vidutolimod/Nivolumab in Per-Protocol (PP) Population

Study ID	Nature of injected tumor (nature – LN vs. in-transit)	Total number of target/non-target lesions (LN + in-transit)			Histopathologic features in tumor bed					
		LN	In-transit	Total (LN + in-transit)	Necrosis (%)	Tumoral melanosis (%)	Hyalinized fibrosis (%)	Proliferative fibrosis (%)	RVT (%)	Pathologic response
UOP-001	LN	1	2	3	0	0	0	0	100%	pNR
UOP-002	In-transit	0	1	1	20	30	0	50	0	pCR
UOP-004	LN	3	0	3	70	30	0	0	0	pCR
UOP-005	LN	1	0	1	10	70	0	20	0	pCR
UOP-007	In-transit	0	1	1	0	20	0	80	0	pCR
UOP-008	LN	1	0	1	90	8	0	0	2	pMR
UOP-009	LN	1	0	1	90	0	0	10	0	pCR
UOP-010	LN	5	0	5	75	15	0	6	4	pMR
UOP-011	LN	2	0	2	80	5	3	12	0	pCR
UOP-012	LN	1	0	1	10	0	70	20	0	pCR
UOP-013	LN	1	0	1	20	0	0	10	70	pNR
UOP-014	LN	1	1	2	10	25	0	25	40	pPR
UOP-015	LN	1	0	1	80	5	0	15	0	pCR
UOP-016	LN	1	0	1	5	5	10	80	0	pCR
UOP-018	LN	2	0	2	20	5	1	4	70	pNR
UOP-019	In-transit	0	1	1	20	0	0	80	0	pCR
UOP-021	LN	2	0	2	70	20	0	10	0	pCR
UOP-022	LN	2	0	2	70	15	0	15	0	pCR
UOP-023	In-transit	0	1	1	30	10	0	25	35	pPR
UOP-024	LN	1	0	1	5	0	0	15	80	pNR
UOP-025	LN	4	0	4	15	5	2	8	70	pNR
UOP-026	In-transit	3	1	4	5	5	10	20	100%	pNR
UOP-027	LN	1	0	1	40	0	20	20	0	pPR
UOP-029	LN	1	0	1	N/A	N/A	N/A	N/A	N/A	Not evaluable
UOP-030	LN	4	0	4	75	20	0	5	0	pCR
UOP-032	LN	1	0	1	95	5	0	0	0	pCR
UOP-033	LN	1	0	1	10	0	0	0	90	pNR
UOP-034	LN	3	0	3	90	5	0	5	5	pMR
UOP-035	LN	1	0	1	10	0	0	0	90	pNR
UOP-036	LN	1	0	1	15	0	0	0	85	pNR
UOP-037	LN	1	3	4	10	5	0	5	80	pNR

Abbreviations: LN, lymph node; RVT, residual viable tumor; pNR, pathologic non-response; pCR, pathologic complete response; pMR, pathologic major response.

Supplementary Table 4: Univariate Models of Major Pathologic Response (pR) and Relapse-Free Survival (RFS) in Per-Protocol (PP) Population

	Univariate analysis for pR			Univariate analysis for RFS		
Variable	Odds ratio	95% CI	Odds ratio	95% CI	Odds ratio	95% CI
Tumor size						
• Longest dimension, target lesion(s)	1.06	0.98 - 1.15	0.1621	0.95	0.89 – 1.02	0.1975
• Cross-product sum, total, all targets	1.0003	0.9995 - 1.0012	0.4404	0.9996	0.9987 – 1.0005	0.3956
Laboratory values						
• Pre-treatment LDH ratio	0.44	0.01 – 21.08	0.6803	1.35	0.04 – 42.96	0.8663
• Pre-treatment NLR	2.18	0.81 – 5.87	0.1245	0.45	0.19 – 1.10	0.0796
Radiographic response						
• PR (vs. SD/PD)	13.20	2.11 - 82.50	0.0058	0.17	0.03 – 0.82	0.0274
Pathologic response						
• pR (pCR, pMR) vs. pNR (pPR, pNR)	N/A	N/A	N/A	0.12	0.03 – 0.60	0.0092

Abbreviations: LDH, lactate dehydrogenase; NLR, neutrophil-lymphocyte ratio; PD, progressive disease; PR, partial response; pR, pathologic reponse; pCR, pathologic complete response; pMR, pathologic major response; pNR, pathologic non-response; pPR, pathologic partial response; SD, stable disease

Supplementary Table 5: Multivariate Models of Major Pathologic Response (pR) and Relapse-Free Survival (RFS) in Per-Protocol (PP) Population

[illegible]

Supplementary Table 6: Immune Markers in Figure 3 and Extended Data Figure 3 by Compartment**[CD45⁺/CD303⁺, CD45⁺, or CD303⁺ regions of interest (ROI)]**

CD45+ and CD303+ ROIs (combined)			
Target Name	Log2 FC	P value	-log10 p value
MART1	-2.073313925	0.099337461	1.002886944
PTEN	0.715121205	0.415321138	0.381615965
S100B	-3.165163704	0.00052701	3.278181312
EpCAM	0.736894018	0.460033402	0.337210634
ER-alpha	0.455301665	0.609021094	0.215367665
PR	-0.314569799	0.834934466	0.078347611
NY-ESO-1	-0.383095993	0.460033402	0.337210634
Bcl-2	0.458332823	0.437348409	0.359172449
Her2	0.103259626	0.924539691	0.03407444
IDO1	-1.079574068	0.805477915	0.093946363
GITR	1.072312504	0.247866814	0.605781615
Tim-3	1.069502776	0.14466413	0.839639139
LAG3	1.722113652	0.029369666	1.532100991
VISTA	0.341160011	0.690769511	0.160666839
OX40L	-0.74016879	0.14466413	0.839639139
B7-H3	0.440870135	0.280243409	0.552464592
ARG1	1.143291575	0.091803333	1.037141551
STING	-0.204619186	0.805477915	0.093946363
4-1BB	0.669926173	0.315379009	0.501167216
FOXP3	0.878337908	0.280243409	0.552464592
CD34	-0.202990096	0.805477915	0.093946363
FAP-alpha	1.434110478	0.016136683	1.792185728
CD66b	0.901698969	0.460033402	0.337210634
CD45RO	0.563788303	0.247866814	0.605781615
CD163	0.631503399	0.107356959	0.969169799
CD14	2.115351875	0.001774078	2.751027181
PD-L2	1.651048713	0.032306145	1.490714858
CD127	0.338059024	0.507318817	0.294719029
CD25	0.324108025	0.232699842	0.633203911
ICOS	0.942320979	0.247866814	0.605781615
CD80	0.945057317	0.297464563	0.526564765
CD40	0.509083723	0.232699842	0.633203911
CD44	1.266885536	0.232699842	0.633203911
CD27	0.749422339	0.315379009	0.501167216
PD-1	0.300927843	0.437348409	0.359172449
Beta-2-microglobulin	0.536937347	0.218203298	0.661138689
CD3	0.920598116	0.191181036	0.71855519
Ki-67	-0.909730959	0.155388417	0.808581359
CD20	0.311409864	0.690769511	0.160666839
CD56	0.149332893	0.635796217	0.19668206
CD8	0.92194538	0.191181036	0.71855519
CD68	1.990478325	0.004764135	2.322015925
PanCk	0.362264269	0.609021094	0.215367665
GZMB	-0.133084188	0.805477915	0.093946363
Fibronectin	1.750959944	0.046695135	1.330728367
CTLA4	0.915786097	0.232699842	0.633203911
HLA-DR	1.17472637	0.507318817	0.294719029
CD11c	1.514097843	0.042668371	1.369893937
PD-L1	0.234092427	0.690769511	0.160666839
SMA	-0.073059306	0.894506834	0.048416337
CD45	0.968902276	0.178631682	0.748041512
CD4	0.544292881	0.166705713	0.778049516

CD45+ ROIs			
Target Name	Log2 FC	P value	-log10 p value
MART1	-1.375584849	5.39445E-05	4.268052746
PTEN	-0.478026852	0.002602973	2.584530361
S100B	-3.729891407	1.96311E-07	6.707056269
EpCAM	0.133867831	0.573617776	0.241377399
ER-alpha	0.192005817	0.379590624	0.420684524
PR	-0.515628591	0.016439333	1.784115805
NY-ESO-1	-0.773130361	4.41754E-06	5.354819638
Bcl-2	-0.213601991	0.62856218	0.201651754
Her2	-0.221932912	0.163916383	0.785377637
IDO1	-2.329383428	7.571E-07	6.120846925
GITR	0.323119109	0.33824902	0.470763453
Tim-3	0.172440321	0.459035423	0.3381538
LAG3	0.301808185	0.182602378	0.738493571
VISTA	-0.799782433	0.000168955	3.772230017
OX40L	-0.996329742	1.11666E-05	4.952077323
B7-H3	-0.084855375	0.264597509	0.577414249
ARG1	0.418556442	0.152284164	0.817345257
STING	-0.912567543	2.28252E-05	4.641584673
4-1BB	-0.831720713	2.28252E-05	4.641584673
FOXP3	0.094772862	0.40137902	0.396445332
CD34	-0.783687637	0.005534322	2.256935586
FAP-alpha	0.34938714	0.012498861	1.903129547
CD66b	1.018834345	0.015573601	1.807610965
CD45RO	-0.495869179	0.077199067	1.112387948
CD163	-0.218191791	0.685645308	0.163900491
CD14	0.542944403	0.030612519	1.514100937
PD-L2	0.750990467	0.000708519	3.14964825
CD127	-0.036390815	1	0
CD25	-0.247238458	0.195909032	0.707945541
ICOS	-0.373625969	0.042984696	1.366686141
CD80	0.31635707	0.080562918	1.093864812
CD40	-0.638622994	0.004605541	2.336719364
CD44	-0.004676935	0.976372153	0.010384615
CD27	-0.426754907	0.030612519	1.514100937
PD-1	-0.09789847	0.224627384	0.648537301
Beta-2-microglobulin	-0.387586094	0.012498861	1.903129547
CD3	-0.0002278	0.82037159	0.085989388
Ki-67	-1.414385523	1.75064E-05	4.756802381
CD20	-1.211335643	0.00213814	2.669963844
CD56	-0.151519777	0.24805754	0.605447568
CD8	-0.100906582	0.299917401	0.522998336
CD68	1.487820265	5.57612E-07	6.253667933
PanCk	0.649551952	0.002962361	2.528362015
GZMB	-0.265427549	0.047214748	1.325922322
Fibronectin	0.25708608	0.390392449	0.408498591
CTLA4	-0.323628001	0.379590624	0.420684524
HLA-DR	-0.039015413	0.789810271	0.102477223
CD11c	0.747621521	0.004898144	2.309968493
PD-L1	-0.380395921	0.152284164	0.817345257
SMA	-0.367439457	0.182602378	0.738493571
CD45	-0.399665861	0.073950563	1.131058517
CD4	-0.239943926	0.273146426	0.563604477

Neoadjuvant Intratumoral Vidutolimod and Nivolumab in High-Risk Resectable Melanoma

CD303+ ROIs			
Target Name	Log2 FC	P value	-log10 p value
MART1	-1.375584849	5.39445E-05	4.268052746
PTEN	-0.478026852	0.002602973	2.584530361
S100B	-3.729891407	1.96311E-07	6.707056269
EpCAM	0.133867831	0.573617776	0.241377399
ER-alpha	0.192005817	0.379590624	0.420684524
PR	-0.515628591	0.016439333	1.784115805
NY-ESO-1	-0.773130361	4.41754E-06	5.354819638
Bcl-2	-0.213601991	0.62856218	0.201651754
Her2	-0.221932912	0.163916383	0.785377637
IDO1	-2.329383428	7.571E-07	6.120846925
GITR	0.323119109	0.33824902	0.470763453
Tim-3	0.172440321	0.459035423	0.3381538
LAG3	0.301808185	0.182602378	0.738493571
VISTA	-0.799782433	0.000168955	3.772230017
OX40L	-0.996329742	1.11666E-05	4.952077323
B7-H3	-0.084855375	0.264597509	0.577414249
ARG1	0.418556442	0.152284164	0.817345257
STING	-0.912567543	2.28252E-05	4.641584673
4-1BB	-0.831720713	2.28252E-05	4.641584673
FOXP3	0.094772862	0.40137902	0.396445332
CD34	-0.783687637	0.005534322	2.256935586
FAP-alpha	0.34938714	0.012498861	1.903129547
CD66b	1.018834345	0.015573601	1.807610965
CD45RO	-0.495869179	0.077199067	1.112387948
CD163	-0.218191791	0.685645308	0.163900491
CD14	0.542944403	0.030612519	1.514100937
PD-L2	0.750990467	0.000708519	3.14964825
CD127	-0.036390815	1	0
CD25	-0.247238458	0.195909032	0.707945541
ICOS	-0.373625969	0.042984696	1.366686141
CD80	0.31635707	0.080562918	1.093864812
CD40	-0.638622994	0.004605541	2.336719364
CD44	-0.004676935	0.976372153	0.010384615
CD27	-0.426754907	0.030612519	1.514100937
PD-1	-0.09789847	0.224627384	0.648537301
Beta-2-microglobulin	-0.387586094	0.012498861	1.903129547
CD3	-0.0002278	0.82037159	0.085989388
Ki-67	-1.414385523	1.75064E-05	4.756802381
CD20	-1.211335643	0.00213814	2.669963844
CD56	-0.151519777	0.24805754	0.605447568
CD8	-0.100906582	0.299917401	0.522998336
CD68	1.487820265	5.57612E-07	6.253667933
PanCk	0.649551952	0.002962361	2.528362015
GZMB	-0.265427549	0.047214748	1.325922322
Fibronectin	0.25708608	0.390392449	0.408498591
CTLA4	-0.323628001	0.379590624	0.420684524
HLA-DR	-0.039015413	0.789810271	0.102477223
CD11c	0.747621521	0.004898144	2.309968493
PD-L1	-0.380395921	0.152284164	0.817345257
SMA	-0.367439457	0.182602378	0.738493571
CD45	-0.399665861	0.073950563	1.131058517
CD4	-0.239943926	0.273146426	0.563604477

Supplementary Table 7: Differentially Enriched Cytokines in Extended Data Figure 7 and Supplementary Data Figure 4

Differentially Upregulated Cytokines Post- vs. Pre- Treatment in pR and pNR			
Cytokines upregulated in tumors with pathologic response (pR)			
Target Name	Median Difference	P value	-log₁₀ p value
IL-17A	0.533114052	0.0012016296	2.92022
CXCL10	0.849482776	0.0086860657	2.061177
ITAC	0.591446343	0.0211388724	1.674918
Cytokines downregulated in tumors with pathologic response (pR)			
HMGB1	-0.638099515	0.0003433228	3.464297
Cytokines up- or down- regulated in tumors with pathologic non-response (pNR)			
None			

Supplementary Table 8: Significant Differentially Expressed Genes (DEGs) in Post-Treatment Samples
(pR vs. pNR) Plotted in Figure 5

Gene Name	Gene ID	Log2FC	Adjusted p value	FDR	Gene Name	Gene ID	Log2FC	Adjusted p value	FDR
DEGs upregulated in tumors with pathologic response (pR)									
<i>PRH1</i>	ENSG00000231887	7.49797415	1.0493E-09	1.013E-06	<i>FTL</i>	ENSG00000087086	2.41816345	0.00191925	0.03183117
<i>CHIT1</i>	ENSG00000133063	7.03291854	2.1748E-09	1.8786E-06	<i>SLC15A3</i>	ENSG00000110446	2.41162564	0.00022695	0.00774382
<i>MMP12</i>	ENSG00000262406	5.89693603	3.7171E-08	1.3865E-05	<i>LINC00426</i>	ENSG00000238121	2.41087903	7.9922E-05	0.00375839
<i>TCEAL7</i>	ENSG00000182916	5.44875568	1.2448E-07	3.7832E-05	<i>CEBPA</i>	ENSG00000245848	2.4088562	0.00019131	0.00681064
<i>TNNI2</i>	ENSG00000130598	5.33547773	9.1941E-09	5.3891E-06	<i>KCNJ5</i>	ENSG00000120457	2.4058457	0.00046923	0.01242641
<i>RNF112</i>	ENSG00000128482	5.11808421	3.9064E-06	0.0004714	<i>CTSS</i>	ENSG00000163131	2.40487258	1.7617E-05	0.00132629
<i>RBP4</i>	ENSG00000138207	5.08381484	4.3656E-06	0.00051919	<i>NKG7</i>	ENSG00000105374	2.40133218	0.00063964	0.01494409
<i>KCNH3</i>	ENSG00000135519	4.85368541	3.0581E-06	0.00040686	<i>RGS13</i>	ENSG00000127074	2.39480743	0.00116997	0.02264324
<i>TNNT3</i>	ENSG00000130595	4.73821093	7.2745E-08	2.4873E-05	<i>ITGAX</i>	ENSG00000140678	2.39367825	0.00018355	0.00662518
<i>IGHG3</i>	ENSG00000211897	4.70643038	8.4266E-07	0.00017287	<i>RHOBTB1</i>	ENSG00000072422	2.39239475	0.00029342	0.00915525
<i>LINC01871</i>	ENSG00000235576	4.64769965	7.0832E-08	2.4734E-05	<i>TNFRSF17</i>	ENSG00000048462	2.38995207	0.00072728	0.01634607
<i>HLA-DQB1-AS1</i>	ENSG00000223534	4.52703404	2.0937E-08	9.4588E-06	<i>CNN1</i>	ENSG00000130176	2.38845315	0.00024325	0.00812101
<i>FBP1</i>	ENSG00000165140	4.49689358	1.144E-08	6.4745E-06	<i>TMEM37</i>	ENSG00000171227	2.38297746	8.6955E-05	0.00398473
<i>RPL13P5</i>	ENSG00000240370	4.47383151	3.3059E-07	7.9788E-05	<i>SLAMF8</i>	ENSG00000158714	2.37270302	0.00025949	0.00844998
<i>MMP7</i>	ENSG00000137673	4.37901766	4.5641E-05	0.00247215	<i>MGST1</i>	ENSG00000008394	2.37098554	0.00238424	0.03677641
<i>APOC1</i>	ENSG00000130208	4.35086215	1.8774E-08	8.9901E-06	<i>CTSW</i>	ENSG00000172543	2.36996578	0.00024395	0.00812101
<i>G0S2</i>	ENSG00000123689	4.32036902	2.9954E-07	7.6814E-05	<i>PTPRCAP</i>	ENSG00000213402	2.36388613	0.00074958	0.01664696
<i>KLK1</i>	ENSG00000167748	4.24608525	2.1093E-06	0.00031188	<i>GADD45G</i>	ENSG00000130222	2.35705553	0.00062779	0.01478888
<i>HLA-DQA2</i>	ENSG00000237541	4.21390334	1.464E-05	0.00115759	<i>CXCR6</i>	ENSG00000172215	2.35631151	0.00013677	0.0053758
<i>HBB</i>	ENSG00000244734	4.0563803	5.7822E-06	0.00062432	<i>SERPINA1</i>	ENSG00000197249	2.35226911	0.00023525	0.0079442
<i>HLA-DRB6</i>	ENSG00000229391	4.05526156	1.523E-05	0.00118461	<i>IL4I1</i>	ENSG00000104951	2.34922505	0.00264463	0.03910235
<i>FABP4</i>	ENSG00000170323	4.03259765	1.0716E-05	0.00092773	<i>CPZ</i>	ENSG00000109625	2.34536929	0.00183674	0.0311089
<i>CXCL2</i>	ENSG00000081041	4.0207235	1.3725E-06	0.00024863	<i>SLC7A7</i>	ENSG00000155465	2.33003745	0.00013402	0.00532591
<i>CESI</i>	ENSG00000198848	4.01519135	4.415E-06	0.00052129	<i>SDS</i>	ENSG00000135094	2.32496558	0.00041315	0.01151195
<i>PLA2G7</i>	ENSG00000146070	4.01017959	1.7077E-08	8.4931E-06	<i>POLK</i>	ENSG00000122008	2.3214442	2.8855E-05	0.00181442
<i>CCL3L1</i>	ENSG00000276085	4.00916071	5.6436E-08	2.0136E-05	<i>PLAAT4</i>	ENSG00000133321	2.31735257	0.00030318	0.00933135
<i>DACH1</i>	ENSG00000276644	3.98113089	1.3872E-06	0.00024863	<i>RSPO3</i>	ENSG00000146374	2.31580675	0.00020702	0.00719843
<i>ACTG2</i>	ENSG00000163017	3.9364091	2.7627E-05	0.00177811	<i>CDC37L1</i>	ENSG00000106993	2.30707193	2.9433E-05	0.00181877
<i>IGHA1</i>	ENSG00000211895	3.85781563	4.8031E-06	0.00054742	<i>RARRES2</i>	ENSG00000106538	2.30480334	0.00203694	0.03303386
<i>CYP27B1</i>	ENSG00000111012	3.84100838	2.0248E-06	0.00031057	<i>PMS2P3</i>	ENSG00000127957	2.3037782	0.00129803	0.02437452
<i>SCN11A</i>	ENSG00000168356	3.82867465	0.00033422	0.00993691	<i>NPIPBA</i>	ENSG00000185864	2.30161953	5.4755E-05	0.00283481
<i>JSRP1</i>	ENSG00000167476	3.76064897	6.9869E-06	0.00069831	<i>CD2</i>	ENSG00000116824	2.29864414	0.00049527	0.012729
<i>ADAMDEC1</i>	ENSG00000134028	3.7436064	8.907E-07	0.00017956	<i>NCF2</i>	ENSG00000116701	2.29751119	0.00011196	0.00470846
<i>PRAM1</i>	ENSG00000133246	3.74239875	2.091E-06	0.00031188	<i>NUDT16L2P</i>	ENSG00000246082	2.29687042	0.00030401	0.00933135
<i>CAMP</i>	ENSG00000164047	3.73752252	1.3402E-05	0.00109431	<i>CLEC4E</i>	ENSG00000166523	2.29384487	0.00036094	0.01048449
<i>CFD</i>	ENSG00000197766	3.72857093	9.6334E-07	0.00018822	<i>NEXN</i>	ENSG00000162614	2.29121999	7.2451E-06	0.00071631
<i>CHI3L1</i>	ENSG00000133048	3.71137138	5.9705E-06	0.00063218	<i>JCHAIN</i>	ENSG00000132465	2.28968867	0.00175899	0.03010273
<i>HS3ST2</i>	ENSG00000122254	3.66585192	3.991E-07	9.2254E-05	<i>FXYD2</i>	ENSG00000137731	2.28850343	0.00121646	0.02335039
<i>ATP6V0D2</i>	ENSG00000147614	3.66098581	0.00031043	0.00943473	<i>POU2F2</i>	ENSG0000028277	2.28328281	0.00012775	0.00516409
<i>SORDP3</i>	ENSG00000259479	3.65771887	0.0002206	0.00757437	<i>IL32</i>	ENSG00000008517	2.28059736	0.00035369	0.01031026
<i>POPDC2</i>	ENSG00000132429	3.60891323	0.00108874	0.02155426	<i>FCGR1A</i>	ENSG00000150337	2.27384636	0.00109464	0.0126302
<i>CCL3</i>	ENSG00000277632	3.59117591	1.5613E-06	0.00026773	<i>GZMM</i>	ENSG00000197540	2.27329517	0.00148073	0.02667589
<i>SPP1</i>	ENSG00000118785	3.5756972	0.00105332	0.02116794	<i>NR2C1</i>	ENSG00000120798	2.27240101	0.00014851	0.00570816
<i>IFIT2</i>	ENSG00000119922	3.54443278	1.6729E-06	0.00027185	<i>CD300A</i>	ENSG00000167851	2.27159594	0.0001856	0.00666219
<i>HBA1</i>	ENSG00000206172	3.51915676	8.3441E-05	0.00386847	<i>NCF1C</i>	ENSG00000165178	2.26926806	0.00045608	0.01227454
<i>MUSTN1</i>	ENSG00000272573	3.51752317	5.8499E-05	0.00296321	<i>CLEC3B</i>	ENSG00000163815	2.26688645	0.00154853	0.02759447
<i>HTRA4</i>	ENSG00000169495	3.48469439	4.0067E-06	0.00047998	<i>TIMP4</i>	ENSG00000157150	2.26667361	0.00211907	0.03366714
<i>TRGC2</i>	ENSG00000227191	3.44733677	3.0445E-06	0.00040686	<i>HSBP1L1</i>	ENSG00000226742	2.26643362	0.00262004	0.03884383
<i>AKR1C3</i>	ENSG00000196139	3.43199548	3.9185E-05	0.00227246	<i>CAPG</i>	ENSG00000042493	2.26529795	0.00252458	0.03783872
<i>SFRP4</i>	ENSG00000106483	3.42991134	4.7149E-06	0.00054493	<i>CRACR2B</i>	ENSG00000177685	2.26238435	0.00028581	0.00895167
<i>ALOX15B</i>	ENSG00000179593	3.40765189	4.8686E-06	0.00055106	<i>CCR1</i>	ENSG00000163823	2.26145282	6.3346E-06	0.00066219
<i>CCL4L2</i>	ENSG00000276070	3.40340005	3.6588E-06	0.00045491	<i>CD14</i>	ENSG00000170458	2.26058263	0.00106763	0.02126446
<i>GNLY</i>	ENSG00000115523	3.38029158	2.2127E-06	0.00032137	<i>ALOX5</i>	ENSG00000012779	2.26030524	0.00016682	0.00615233
<i>CCL3-AS1</i>	ENSG00000277089	3.34568266	2.413E-06	0.00034139	<i>COL1A1</i>	ENSG00000108821	2.25649144	0.00045045	0.01219936
<i>GZMH</i>	ENSG00000100450	3.33916817	7.8849E-06	0.0007631	<i>KLRC1</i>	ENSG00000134545	2.25627504	0.00162468	0.02841674
<i>CCL18</i>	ENSG00000275385	3.31019415	2.9478E-05	0.00181877	<i>FOS</i>	ENSG00000170345	2.25614781	0.00016319	0.00607316
<i>GPD1</i>	ENSG00000176588	3.29476782	0.0040558	0.01133959	<i>ZBTB20</i>	ENSG00000181722	2.25441948	0.00156219	0.02772112
<i>DONSON</i>	ENSG00000159147	3.27182125	2.503E-06	0.00034813	<i>SFRP2</i>	ENSG00000145423	2.25030438	0.00297512	0.04222278
<i>SOS1-IT1</i>	ENSG00000229692	3.2713105	0.00011322	0.00471597	<i>LGMN</i>	ENSG00000100600	2.2482695	0.0001993	0.0070041
<i>IGKV1D-13</i>	ENSG00000276566	3.25142956	0.0004956	0.012729	<i>FANCB</i>	ENSG00000181544	2.24587381	0.00102786	0.02072397

Neoadjuvant Intratumoral Vidutolimod and Nivolumab in High-Risk Resectable Melanoma

SERPINA9	ENSG00000170054	3.21734584	0.00018794	0.00671531	CD74	ENSG00000019582	2.24206458	0.00065695	0.01520713
MMP9	ENSG00000100985	3.20556722	9.7357E-05	0.00427878	FRZB	ENSG00000162998	2.241615	1.3975E-05	0.00112982
MFAP4	ENSG00000166482	3.14837706	3.3105E-06	0.00042117	RAB42	ENSG00000188060	2.23870351	3.1663E-06	0.00041156
CELF6	ENSG00000140488	3.11929206	0.00026505	0.00857999	AQP9	ENSG00000103569	2.23770578	0.00241588	0.03705556
FUCA1	ENSG00000179163	3.11491074	3.0042E-05	0.00184536	CLK4	ENSG00000113240	2.23695189	2.7272E-05	0.00176215
IGHV4-31	ENSG00000231475	3.10620653	0.00177783	0.03033032	CYP11B1	ENSG00000138061	2.2365218	5.192E-07	0.00011835
TREM2	ENSG00000095970	3.09083797	9.2458E-05	0.00413468	DCN	ENSG00000011465	2.23478711	0.00027263	0.00868266
OLR1	ENSG00000173391	3.0888798	0.00023824	0.00801234	HSPB6	ENSG00000004776	2.23054687	0.00073202	0.01636773
CARF	ENSG00000138380	3.07118704	2.4044E-05	0.00165109	PTGDS	ENSG00000107317	2.22939616	0.00267925	0.0393536
HBA2	ENSG00000188536	3.04461118	0.00031675	0.00955301	SLC37A2	ENSG00000134955	2.22799499	0.00019433	0.00687344
ABCG1	ENSG00000160179	3.04322259	8.4536E-08	2.7748E-05	MBOAT1	ENSG00000172197	2.22528765	0.0004762	0.01253505
IGHD	ENSG00000211898	3.03567308	0.0005377	0.01341156	PSTPIP2	ENSG00000152229	2.2240128	0.00042825	0.01185239
ZNF230	ENSG00000159882	3.03134329	2.3285E-05	0.00162621	ZFP36	ENSG00000128016	2.2164337	0.00114601	0.02233767
CP	ENSG00000047457	3.02668665	3.017E-06	0.00040686	FPR3	ENSG00000187474	2.21418845	0.00031506	0.00955301
APOE	ENSG00000130203	3.02219418	9.873E-06	0.00087587	SLC35A5	ENSG00000138459	2.2136063	0.00034804	0.01019998
STMN2	ENSG00000104435	3.0017016	0.00147255	0.02662962	LAX1	ENSG00000122188	2.21341464	0.00089807	0.0190674
AKR1C2	ENSG00000151632	2.9978191	0.00051773	0.01307023	HLA-DRA	ENSG00000204287	2.21090174	0.00177647	0.03033032
TNXB	ENSG00000168477	2.98957085	0.00019776	0.00696483	SPNS3	ENSG00000182557	2.20574341	0.00135117	0.02514209
LINC02422	ENSG00000255760	2.98677898	0.00071893	0.01622975	BLNK	ENSG00000095585	2.20472347	7.3678E-05	0.00353566
TTN	ENSG00000155657	2.98521095	0.00045347	0.01224084	APOBEC3G	ENSG00000239713	2.2040799	7.2151E-05	0.00352005
FAM3B	ENSG00000183844	2.97694609	0.00213248	0.03374956	CD86	ENSG00000114013	2.20306295	4.2839E-05	0.00235142
LRRC2	ENSG00000163827	2.97592649	0.00194631	0.03209731	TMEM119	ENSG00000183160	2.1937803	1.0568E-06	0.00020406
CTSD	ENSG00000117984	2.89519748	2.5352E-05	0.00168442	MIR22HG	ENSG00000186594	2.19068947	0.00013692	0.0053758
HK3	ENSG00000160883	2.89300334	4.125E-05	0.00232777	LINC00861	ENSG00000245164	2.18969801	0.00211618	0.03365388
IGLC3	ENSG00000211679	2.88519587	0.0016411	0.02859204	ARL4C	ENSG00000188042	2.18283226	7.2494E-05	0.00352005
MIR155HG	ENSG00000234883	2.88409773	3.4956E-05	0.0020862	MAFB	ENSG00000204103	2.1802829	0.00011454	0.00475923
IGHA2	ENSG00000211890	2.86748198	0.00068544	0.01566782	TMEM42	ENSG00000169964	2.17567526	0.00114921	0.02237354
PTPRN2	ENSG00000155093	2.8636374	1.4695E-05	0.00115759	CD300LF	ENSG00000186074	2.17171088	0.00024346	0.00812101
PLIN1	ENSG00000166819	2.86157065	0.00327877	0.04506792	TMIGD3	ENSG00000121933	2.16449658	0.00049255	0.012729
OGN	ENSG00000106809	2.85202159	2.3525E-05	0.00162906	MS4A7	ENSG00000166927	2.1636995	4.1245E-05	0.00232777
GZMA	ENSG00000145649	2.85105032	5.5008E-05	0.00283894	HTRA1	ENSG00000166033	2.16174933	0.00063552	0.01487894
CREBRF	ENSG00000164463	2.84537003	5.3885E-07	0.00012115	DHR59	ENSG00000073737	2.16147596	0.00036547	0.01059737
CCL5	ENSG00000271503	2.84490379	3.7918E-05	0.00221464	PTGDR	ENSG00000168229	2.15842731	4.4095E-05	0.00239631
CCL4	ENSG00000275302	2.83325687	4.1968E-05	0.00232777	JAML	ENSG00000160593	2.15779488	4.1583E-05	0.00232777
MATK	ENSG00000007264	2.82657946	8.455E-06	0.00078707	KLRB1	ENSG00000111796	2.14598935	0.00014212	0.00552722
IGHG2	ENSG00000211893	2.8046578	0.00053982	0.01344398	TNFSF8	ENSG00000106952	2.14452821	2.8202E-05	0.00179403
TYROBP	ENSG00000011600	2.79787748	5.9814E-05	0.0029929	NPL	ENSG00000135838	2.14383936	1.9113E-05	0.00138922
SNHG22	ENSG00000267322	2.79737377	0.00054902	0.01354954	RASL10A	ENSG00000100276	2.14023249	0.00157331	0.02785463
FOXD1	ENSG00000251493	2.79606622	0.00132657	0.02479916	XPNPPE2	ENSG00000122121	2.13972071	0.0036688	0.04883218
CCL8	ENSG00000108700	2.7848351	0.00018539	0.00666219	GMPR	ENSG00000137198	2.13797166	0.00318967	0.044251
MTND2P28	ENSG00000225630	2.75065013	0.00194013	0.032059	MMP2	ENSG00000087245	2.13478561	0.0008695	0.01853282
SLC49A4	ENSG00000138463	2.74857096	2.5453E-05	0.00168442	SYNDIG1	ENSG00000101463	2.13213303	9.0412E-05	0.00407935
IGLC1	ENSG00000211675	2.74638829	0.00207264	0.03330026	THUMPD3-AS1	ENSG00000206573	2.1308675	0.00088683	0.01887772
LYZ	ENSG00000090382	2.74542653	0.00015349	0.00580704	TRG-AS1	ENSG00000281103	2.12557655	9.0475E-05	0.00407935
TREM1	ENSG00000124731	2.74216537	0.00034364	0.01010731	FCN1	ENSG00000085265	2.12283669	0.00082911	0.01797529
FGF7	ENSG00000140285	2.7191669	1.395E-05	0.00112982	HID1	ENSG00000167861	2.12010974	4.7074E-05	0.00251654
ALKAL2	ENSG00000189292	2.71460639	0.00332192	0.04554673	HLA-DPB1	ENSG00000223865	2.1196218	0.00072825	0.01634607
SMIM10	ENSG00000184785	2.71092626	4.2124E-05	0.00232777	MSR1	ENSG00000038945	2.11506081	0.00048711	0.01270985
NUDT18	ENSG00000275074	2.71084938	6.9117E-06	0.00069831	FAR1	ENSG00000197601	2.11502619	0.00035315	0.01031026
SUGT1-DT	ENSG00000273723	2.7099282	0.00228189	0.03570101	CTSH	ENSG00000103811	2.10816068	2.6806E-05	0.00174581
LTC4S	ENSG00000213316	2.70320648	0.00018203	0.00659475	SRGN	ENSG00000122862	2.1045553	0.00028555	0.00895167
USP30-AS1	ENSG00000256262	2.70223762	2.6071E-05	0.00171148	RESF1	ENSG00000174718	2.10236534	0.00018367	0.00662518
OSR2	ENSG00000164920	2.69844913	2.8827E-05	0.00181442	FBLN2	ENSG00000163520	2.10043205	0.00083183	0.01799908
ZFH2-AS1	ENSG00000157306	2.69239129	0.00065621	0.01520713	ZNF350	ENSG00000256683	2.09948894	1.4646E-05	0.00115759
PPP1R1A	ENSG00000135447	2.69178123	0.0027129	0.03968282	FUNDC1	ENSG00000069509	2.09670454	0.00297477	0.04222278
CIDEB	ENSG00000136305	2.68357627	7.3413E-05	0.00353566	PNP	ENSG00000198805	2.09341447	0.00057615	0.01395967
HCST	ENSG00000126264	2.68209678	5.9279E-05	0.00298432	PILRA	ENSG00000085514	2.089259	0.00067643	0.0155484
ADAM28	ENSG00000042980	2.67674672	3.1119E-06	0.00040859	CEP250-AS1	ENSG00000230155	2.08858084	0.00073952	0.01645181
ELN	ENSG000000049540	2.66121034	7.8311E-05	0.00371456	IL7R	ENSG00000168685	2.08325769	0.00294057	0.04203884
LINC01781	ENSG00000234184	2.65932871	0.00326026	0.04496034	TCF4	ENSG00000196628	2.07753846	5.5923E-07	0.00012237
SLC46A3	ENSG00000139508	2.65191298	6.2837E-06	0.00066108	LAPTM5	ENSG00000162511	2.07417542	0.0011338	0.02215226
SIGLEC8	ENSG00000105366	2.65055525	0.000271	0.00867533	CTLA4	ENSG00000163599	2.07011051	0.00094579	0.0196733
FGR	ENSG00000000938	2.64492679	5.0603E-05	0.00264489	TRBC2	ENSG00000211772	2.0688463	0.00157749	0.02789849
LY86	ENSG00000112799	2.64472889	2.486E-05	0.0016801	CD226	ENSG00000150637	2.06571486	0.00093206	0.01956143
GTF2E1	ENSG00000153767	2.63752573	1.5666E-05	0.00120709	RRAD	ENSG00000166592	2.063833	0.00161236	0.0283624
IFI30	ENSG00000216490	2.63495729	0.00016315	0.00607316	CD53	ENSG00000143119	2.06059224	0.00093841	0.01961927
CCDC152	ENSG00000198865	2.6349354	2.5077E-05	0.00168442	PDK4	ENSG00000004799	2.05852109	0.00049508	0.012729
CD68	ENSG00000129226	2.63062652	0.00032124	0.00960335	MXR48	ENSG00000162576	2.05717178	0.00065074	0.015146
FNDC1	ENSG00000164694	2.62889394	8.6001E-05	0.00396476	ZNF564	ENSG00000249709	2.05661423	0.00056853	0.01384385
ADIRF	ENSG00000148671	2.62710336	0.00201456	0.03283305	LAMTOR3	ENSG00000109270	2.05421983	0.00051417	0.01304252
MARCO	ENSG00000019169	2.61788879	0.00106006	0.0211909	PLAUR	ENSG00000011422	2.05312167	0.00198033	0.03240389

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<i>MCM9</i>	ENSG00000111877	2.61531604	0.00011893	0.00489182	<i>C3AR1</i>	ENSG00000171860	2.05264416	0.00021248	0.00734139
<i>CCL14</i>	ENSG00000276409	2.60884675	0.00011307	0.00471597	<i>PDGFRL</i>	ENSG00000104213	2.04979436	0.00080219	0.01759381
<i>ARL5B</i>	ENSG00000165997	2.60243008	9.5963E-05	0.00424514	<i>FBXL12</i>	ENSG00000127452	2.04691921	0.00136667	0.02534439
<i>SLC29A3</i>	ENSG00000198246	2.59876033	2.0833E-06	0.00031188	<i>KLRK1</i>	ENSG00000213809	2.04496771	4.75E-05	0.00252288
<i>INTS6L</i>	ENSG00000165359	2.59343775	0.00012614	0.00514982	<i>SIGLEC7</i>	ENSG00000168995	2.04473212	0.00016477	0.00610292
<i>PODN</i>	ENSG00000174348	2.58691438	3.021E-05	0.00184536	<i>ZNF75D</i>	ENSG00000186376	2.0443277	0.00046659	0.01241126
<i>PLEKHF1</i>	ENSG00000166289	2.58378563	2.6739E-05	0.00174581	<i>TM6SF1</i>	ENSG00000136404	2.04090013	0.00189632	0.03168431
<i>CTSB</i>	ENSG00000164733	2.58352777	4.1397E-05	0.00232777	<i>MYOM1</i>	ENSG00000101605	2.03773397	0.0004429	0.01209462
<i>EEF1AKMT4</i>	ENSG00000284753	2.56862417	0.00117598	0.0227329	<i>TREML1</i>	ENSG00000161911	2.03705059	0.00234739	0.03644424
<i>DPT</i>	ENSG00000143196	2.56011847	0.00047838	0.01256188	<i>ZNF736</i>	ENSG00000234444	2.02633396	0.00061445	0.01461509
<i>IGKC</i>	ENSG00000211592	2.55889379	0.00329562	0.04526167	<i>NCRI</i>	ENSG00000189430	2.02565487	0.00313142	0.04377581
<i>DPEP2</i>	ENSG00000167261	2.55621227	1.0073E-05	0.00088879	<i>ITGB2</i>	ENSG00000160255	2.0198346	0.00083822	0.01804239
<i>BASP1</i>	ENSG00000176788	2.5542088	1.9015E-06	0.00029584	<i>B3GNT8</i>	ENSG00000177191	2.01874854	0.00353453	0.04750915
<i>ZNF700</i>	ENSG00000196757	2.54902417	5.864E-06	0.00062494	<i>SOWAHD</i>	ENSG00000187808	2.01806625	0.00162049	0.02841674
<i>CCDC7</i>	ENSG00000216937	2.53477553	7.2458E-05	0.00352005	<i>ZBP1</i>	ENSG00000124256	2.0149392	0.00054519	0.0135349
<i>SH2D1A</i>	ENSG00000183918	2.53064715	8.6422E-05	0.003973	<i>VNN1</i>	ENSG00000112299	2.01469479	0.00242051	0.03709184
<i>LINC01857</i>	ENSG00000224137	2.52460493	0.00046944	0.01242641	<i>IGF1</i>	ENSG00000017427	2.01142169	0.00098674	0.02024294
<i>ADAMTS7P4</i>	ENSG00000218052	2.51872799	0.00038245	0.01089729	<i>SPACA6</i>	ENSG00000182310	2.0111205	0.00211532	0.03365388
<i>ADH1B</i>	ENSG00000196616	2.50106694	0.00210283	0.03354044	<i>METTL1</i>	ENSG00000037897	2.00976992	0.00361936	0.04825415
<i>NOTCH2NL A</i>	ENSG00000264343	2.4926952	4.4078E-05	0.00239631	<i>TATDN1</i>	ENSG00000147687	2.00952755	0.00082578	0.01795058
<i>IFNG</i>	ENSG00000111537	2.49268075	0.00105375	0.02116794	<i>FASLG</i>	ENSG00000117560	2.00706344	0.00246842	0.03740691
<i>ABCA1</i>	ENSG00000165029	2.4924359	9.1005E-07	0.00017995	<i>CTSK</i>	ENSG00000143387	2.00692022	9.5175E-05	0.00422163
<i>PLIN2</i>	ENSG00000147872	2.49141428	6.8686E-06	0.00069831	<i>GPNMB</i>	ENSG00000136235	2.00676457	0.00171257	0.02949285
<i>OSCAR</i>	ENSG00000170909	2.48581234	5.6076E-05	0.002876	<i>HNMT</i>	ENSG00000150540	2.00093512	1.199E-05	0.00101429
<i>LIPA</i>	ENSG000000107798	2.48357917	4.6723E-05	0.00251415					
<i>MEF2B</i>	ENSG00000213999	2.46882016	0.0014787	0.02666857					
<i>PIF1</i>	ENSG00000140451	2.45866977	0.0004836	0.01265846					
<i>CHRNA1</i>	ENSG00000138435	2.4580913	0.0012537	0.02381441					
<i>IGSF6</i>	ENSG00000140749	2.45316744	7.7297E-06	0.00075512					
<i>PRDM1</i>	ENSG00000057657	2.45288285	1.2852E-05	0.00105996					
<i>CD3D</i>	ENSG00000167286	2.43699134	0.00080615	0.01759381					
<i>GCHFR</i>	ENSG00000137880	2.42119364	0.00019357	0.00686141					
<i>LILRB4</i>	ENSG00000186818	2.42038579	0.0001178	0.00485902					
DEGs upregulated in tumors with pathologic non-response (pNR)									
<i>S100A2</i>	ENSG00000196754	8.6584E-06	0.00079386	-6.8877104	<i>MMP15</i>	ENSG00000102996	5.0053E-06	0.00055504	-2.6581988
<i>MPZ</i>	ENSG00000158887	5.3344E-10	6.2534E-07	-6.8002138	<i>GTF2IP13</i>	ENSG00000272556	0.00011547	0.00478574	-2.6554783
<i>S100B</i>	ENSG00000160307	1.5996E-10	2.3866E-07	-6.5958426	<i>OLMALINC</i>	ENSG00000235823	0.00045846	0.01227454	-2.6530992
<i>COL22A1</i>	ENSG00000169436	1.1361E-12	6.215E-09	-6.5606812	<i>CHRNA5</i>	ENSG00000169684	0.00010606	0.00453302	-2.6498282
<i>SCG2</i>	ENSG00000171951	3.0448E-08	1.2493E-05	-6.3631514	<i>AADAT</i>	ENSG00000109576	6.2252E-05	0.00308667	-2.6380196
<i>DCT</i>	ENSG00000080166	2.774E-06	0.00037939	-6.2830233	<i>ARHGEF16</i>	ENSG00000130762	0.00114052	0.02225717	-2.6334008
<i>S100A8</i>	ENSG00000143546	2.8197E-05	0.00179403	-6.2470023	<i>SRPX</i>	ENSG00000101955	0.00037857	0.01081911	-2.6257879
<i>MIA</i>	ENSG00000261857	6.229E-10	6.3894E-07	-6.1159876	<i>STRA6</i>	ENSG00000137868	0.00049943	0.01278727	-2.6212971
<i>CNFN</i>	ENSG00000105427	4.4842E-06	0.00052273	-5.9459042	<i>BRME1</i>	ENSG00000132016	2.9311E-08	1.2335E-05	-2.6200826
<i>LOXL4</i>	ENSG00000138131	2.1517E-13	1.7657E-09	-5.7471314	<i>NCAM1</i>	ENSG00000149294	3.7503E-05	0.00219823	-2.6155412
<i>RXRγ</i>	ENSG00000143171	6.2125E-12	2.0392E-08	-5.7116721	<i>HEY1</i>	ENSG00000164683	7.0109E-06	0.00069831	-2.6133418
<i>COL11A2</i>	ENSG00000204248	3.0245E-12	1.241E-08	-5.6529544	<i>AGRN</i>	ENSG00000188157	0.00046911	0.01242641	-2.6106118
<i>S100A9</i>	ENSG00000163220	1.0598E-05	0.00092515	-5.6345045	<i>RND2</i>	ENSG00000108830	0.00043231	0.011918	-2.6102602
<i>PTPRZ1</i>	ENSG00000106278	1.0604E-07	3.3469E-05	-5.5637099	<i>HES6</i>	ENSG00000144485	4.9202E-06	0.00055304	-2.5994107
<i>SERPINA3</i>	ENSG00000196136	2.6651E-11	6.2485E-08	-5.5482042	<i>CAPN5</i>	ENSG00000149260	1.3095E-06	0.00024702	-2.599318
<i>FXYD3</i>	ENSG00000089356	2.294E-06	0.00032843	-5.3805056	<i>DHH</i>	ENSG00000139549	0.00167242	0.029076	-2.5881291
<i>SERPINE2</i>	ENSG00000135919	5.9411E-15	9.7506E-11	-5.2798513	<i>PNMA8A</i>	ENSG00000182013	6.1558E-05	0.00306149	-2.5871966
<i>SHISA2</i>	ENSG00000180730	5.4351E-09	3.7167E-06	-5.2315002	<i>FHDC1</i>	ENSG00000137460	1.7575E-05	0.00132629	-2.5862482
<i>CSAG1</i>	ENSG00000198930	3.4814E-09	2.7208E-06	-5.1260617	<i>GLB1L2</i>	ENSG00000149328	0.00190266	0.03173417	-2.5851499
<i>FOXD3</i>	ENSG00000187140	1.9172E-08	8.9901E-06	-5.0326489	<i>FKBP10</i>	ENSG00000141756	0.00152669	0.02726448	-2.5840743
<i>GPRI43</i>	ENSG00000101850	1.3366E-07	3.9508E-05	-4.9873474	<i>REEP2</i>	ENSG00000132563	2.1717E-05	0.00155639	-2.5718905
<i>CDH19</i>	ENSG00000071991	1.2008E-06	0.00022915	-4.8878086	<i>ETV5</i>	ENSG00000244405	2.1324E-08	9.4588E-06	-2.5649842
<i>AGMO</i>	ENSG00000187546	1.3481E-07	3.9508E-05	-4.8242457	<i>IGFBP2</i>	ENSG00000115457	0.00025848	0.00844998	-2.5502894
<i>CSPG4</i>	ENSG00000173546	1.0156E-11	2.7779E-08	-4.7658842	<i>TMEM132A</i>	ENSG00000006118	7.9044E-06	0.0007631	-2.5478762
<i>COL9A3</i>	ENSG00000092758	7.4251E-11	1.354E-07	-4.6332573	<i>HOXB5</i>	ENSG00000120075	0.00188267	0.03158262	-2.5473911
<i>GAP43</i>	ENSG00000172020	8.3994E-06	0.00078707	-4.6285375	<i>AKAP6</i>	ENSG00000151320	0.00069997	0.01591121	-2.544802
<i>PLXNB3</i>	ENSG00000198753	3.6767E-08	1.3865E-05	-4.6276661	<i>CTXND1</i>	ENSG00000259417	0.00184195	0.03116503	-2.5438249
<i>FOXD3-AS1</i>	ENSG00000230798	7.7533E-09	4.8941E-06	-4.6260675	<i>P3H2</i>	ENSG00000090530	1.1196E-05	0.00095209	-2.5428845
<i>SCRGI</i>	ENSG00000164106	4.7998E-06	0.00054742	-4.5747128	<i>SYT1</i>	ENSG00000067715	0.00093749	0.01961927	-2.5340295
<i>DMKN</i>	ENSG00000161249	0.00025924	0.00844998	-4.5573271	<i>SLC26A2</i>	ENSG00000155850	1.9107E-06	0.00029584	-2.5294978
<i>GRIK3</i>	ENSG00000163873	2.218E-05	0.00156901	-4.5163527	<i>SLC6A8</i>	ENSG00000130821	5.1089E-06	0.0005627	-2.5215673
<i>BCHE</i>	ENSG00000114200	5.1985E-10	6.2534E-07	-4.5003703	<i>ADGRG1</i>	ENSG00000205336	1.913E-05	0.00138922	-2.5211986
<i>ADGRB1</i>	ENSG00000181790	8.1289E-08	2.7227E-05	-4.4425815	<i>SPRY2</i>	ENSG00000136158	1.1877E-07	3.6778E-05	-2.5183494
<i>CADM4</i>	ENSG00000105767	5.7903E-10	6.3353E-07	-4.4344869	<i>HOGA1</i>	ENSG00000241935	0.00321658	0.04447394	-2.5172981

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<i>CSPG5</i>	ENSG00000114646	1.9104E-06	0.00029584	-4.3812155	<i>CGREF1</i>	ENSG00000138028	0.00049027	0.012729	-2.5163076
<i>ETV4</i>	ENSG00000175832	8.939E-11	1.4671E-07	-4.3480185	<i>TTYH1</i>	ENSG00000167614	0.00238868	0.03681031	-2.5091209
<i>PLEKHB1</i>	ENSG00000021300	3.3454E-11	6.863E-08	-4.3369065	<i>RTKN</i>	ENSG00000114993	4.9535E-06	0.00055304	-2.5083596
<i>ASPRV1</i>	ENSG00000244617	0.00054126	0.01345935	-4.2949106	<i>TAF45</i>	ENSG00000219438	0.00015345	0.00580704	-2.5075767
<i>EDN3</i>	ENSG00000124205	0.00038693	0.01096762	-4.1764787	<i>SYNM</i>	ENSG00000182253	1.5507E-05	0.00120048	-2.497016
<i>TNFRSF19</i>	ENSG00000127863	7.0153E-09	4.6054E-06	-4.1472173	<i>FGFR4</i>	ENSG00000160867	0.00027229	0.00868266	-2.495242
<i>ITGA10</i>	ENSG00000143127	3.823E-07	9.0219E-05	-4.1341203	<i>EFNB3</i>	ENSG00000108947	0.00015039	0.00573154	-2.4827405
<i>SOX10</i>	ENSG00000100146	0.00011095	0.0046931	-4.113028	<i>DPYSL4</i>	ENSG00000151640	0.00043698	0.01197272	-2.4824742
<i>ALDH1A3</i>	ENSG00000184254	2.2022E-07	5.737E-05	-4.1103789	<i>MT-CO2</i>	ENSG00000198712	0.00024468	0.00812909	-2.4655863
<i>ITGB3</i>	ENSG00000259207	3.1801E-08	1.273E-05	-4.0956306	<i>PIK3CD-AS2</i>	ENSG00000231789	1.9233E-05	0.0013905	-2.4642856
<i>PLP1</i>	ENSG00000123560	8.2882E-06	0.00078707	-4.0861039	<i>BRSK1</i>	ENSG00000160469	0.00082876	0.01797529	-2.4464894
<i>LRP2</i>	ENSG00000081479	0.00055961	0.01371061	-4.0812873	<i>ANKS1A</i>	ENSG00000064999	1.0513E-05	0.00092263	-2.4447045
<i>SPRY4</i>	ENSG00000187678	4.9232E-10	6.2534E-07	-4.0627013	<i>DNAJC22</i>	ENSG00000178401	0.00196041	0.03214212	-2.4429255
<i>DIRAS1</i>	ENSG00000176490	1.1888E-08	6.5034E-06	-4.0626792	<i>MFAP3L</i>	ENSG00000198948	3.9979E-05	0.00230222	-2.4393817
<i>CAPS</i>	ENSG00000105519	1.5987E-06	0.00026773	-4.0525083	<i>PPFIA4</i>	ENSG00000143847	0.00013092	0.00525327	-2.4338967
<i>FAM27E3</i>	ENSG00000274026	3.074E-06	0.00040686	-4.0204442	<i>TFAP2C</i>	ENSG00000087510	0.00296179	0.04212977	-2.4332807
<i>WNK4</i>	ENSG00000126562	5.7694E-05	0.00293148	-4.0149268	<i>LINC00511</i>	ENSG00000227036	0.00146328	0.02656558	-2.4271688
<i>GJB1</i>	ENSG00000169562	5.4363E-06	0.00059086	-3.9932127	<i>CD320</i>	ENSG00000167775	0.00012692	0.00515142	-2.4258216
<i>UGDH-AS1</i>	ENSG00000249348	1.7559E-05	0.00132629	-3.9437503	<i>MDF1</i>	ENSG00000112559	0.00189774	0.03168431	-2.4234724
<i>GJB2</i>	ENSG00000165474	0.00011217	0.00470846	-3.930668	<i>SOX5</i>	ENSG00000134532	1.3594E-06	0.00024863	-2.4206616
<i>ERBB3</i>	ENSG00000065361	6.5535E-06	0.00068074	-3.9280303	<i>ITGA3</i>	ENSG00000005884	4.4909E-06	0.00052273	-2.4194745
<i>GPR37</i>	ENSG00000170775	9.7598E-05	0.00427878	-3.9057176	<i>COLEC11</i>	ENSG00000118004	0.00046122	0.01230908	-2.4193818
<i>PRIMA1</i>	ENSG00000175785	9.0956E-05	0.00408978	-3.9038658	<i>TRNP1</i>	ENSG00000253368	9.9587E-05	0.00432388	-2.4189007
<i>SHROOM2</i>	ENSG00000146950	4.4152E-09	3.2937E-06	-3.8934065	<i>NPAS2</i>	ENSG00000170485	5.921E-07	0.00012786	-2.4141049
<i>GPM6B</i>	ENSG00000046653	8.3155E-09	5.0546E-06	-3.8832442	<i>AFAP1L2</i>	ENSG00000169129	1.7547E-06	0.00028233	-2.4115876
<i>SLC24A5</i>	ENSG00000188467	0.00015356	0.00580704	-3.8615613	<i>PCBP4</i>	ENSG00000090097	8.3984E-06	0.00078707	-2.40993
<i>AZGP1</i>	ENSG00000160862	0.00041577	0.01154596	-3.8117344	<i>FAM131B</i>	ENSG00000159784	0.00181809	0.03085675	-2.4001226
<i>GLUD2</i>	ENSG00000182890	1.3616E-08	7.2084E-06	-3.8116163	<i>METR1</i>	ENSG00000103260	6.7505E-06	0.00069678	-2.3968247
<i>PRAME</i>	ENSG00000185686	1.4424E-05	0.00115759	-3.7882311	<i>SRCIN1</i>	ENSG00000277363	0.00015006	0.00573154	-2.3957101
<i>RAB17</i>	ENSG00000124839	8.6526E-06	0.00079386	-3.7758377	<i>PGF</i>	ENSG00000119630	0.00013043	0.00524679	-2.3921448
<i>SLITRK2</i>	ENSG00000185985	2.4781E-06	0.00034762	-3.7747482	<i>DPY19L2P2</i>	ENSG00000170629	9.1828E-05	0.0041177	-2.38832
<i>HOXC13</i>	ENSG00000123364	9.2433E-06	0.00082446	-3.7624258	<i>SOX8</i>	ENSG00000005513	0.00037905	0.01081911	-2.3877083
<i>GPCI</i>	ENSG00000063660	8.9715E-07	0.00017956	-3.7541442	<i>NANOS1</i>	ENSG00000188613	8.4884E-06	0.00078707	-2.3876131
<i>CERS1</i>	ENSG00000223802	1.478E-05	0.00115759	-3.7533944	<i>PLEKHH1</i>	ENSG00000054690	0.00045743	0.01227454	-2.3780789
<i>TF</i>	ENSG00000091513	0.00013471	0.00532731	-3.748805	<i>SLC44A5</i>	ENSG00000137968	0.00276169	0.04003961	-2.3749825
<i>ATPIB2</i>	ENSG00000129244	2.083E-06	0.00031188	-3.7041323	<i>TBC1D8B</i>	ENSG00000133138	0.00023916	0.00802676	-2.3711413
<i>MLLT1</i>	ENSG00000213190	1.3937E-06	0.00024863	-3.6701967	<i>PCDHGA10</i>	ENSG00000253846	0.00125571	0.02382508	-2.3669192
<i>NMNAT3</i>	ENSG00000163864	1.2522E-05	0.00104854	-3.6517917	<i>PBK</i>	ENSG00000168078	0.00018822	0.00671531	-2.3616554
<i>FREM1</i>	ENSG00000164946	3.5154E-06	0.00044381	-3.6437896	<i>GGT7</i>	ENSG00000131067	0.00027027	0.00867533	-2.3540772
<i>PI15</i>	ENSG00000137558	7.0206E-06	0.00069831	-3.6373688	<i>FGFBP2</i>	ENSG00000137441	0.00345927	0.04688152	-2.353284
<i>F12</i>	ENSG00000131187	2.7651E-08	1.1942E-05	-3.6133726	<i>COSMOC</i>	ENSG00000260552	0.00052774	0.01322332	-2.3525316
<i>SHC4</i>	ENSG00000185634	1.6639E-06	0.00027185	-3.6126417	<i>CHL1</i>	ENSG00000134121	0.00010839	0.00459649	-2.3516933
<i>RGS20</i>	ENSG00000147509	1.856E-05	0.00136734	-3.6007417	<i>GGH</i>	ENSG00000137563	5.3311E-05	0.00277757	-2.3404696
<i>PHLDA2</i>	ENSG00000181649	1.5964E-06	0.00026773	-3.5916506	<i>ACP3</i>	ENSG00000014257	0.001065	0.02123798	-2.3374412
<i>RIPK4</i>	ENSG00000183421	9.9034E-05	0.00431128	-3.5420596	<i>CTXN1</i>	ENSG00000178531	0.00107383	0.02133615	-2.3346952
<i>SLITRK6</i>	ENSG00000184564	1.8662E-05	0.00136734	-3.5404272	<i>ASB9</i>	ENSG00000102048	0.00062952	0.01480187	-2.3239451
<i>FABP5</i>	ENSG00000164687	0.00031955	0.00958752	-3.5338311	<i>ADGRG6</i>	ENSG00000112414	9.6763E-05	0.00426901	-2.3196781
<i>GDNF</i>	ENSG00000168621	0.00017456	0.00639483	-3.500103	<i>SPRED3</i>	ENSG00000188766	0.0018654	0.03143845	-2.3118756
<i>NRCAM</i>	ENSG00000091129	3.2233E-07	7.8956E-05	-3.4971247	<i>ITIH5</i>	ENSG00000123243	0.00101801	0.02060116	-2.3113677
<i>F2RL2</i>	ENSG00000164220	8.8638E-06	0.00080385	-3.4820913	<i>ABTB2</i>	ENSG00000166016	0.00030488	0.00933135	-2.3063932
<i>FREM2</i>	ENSG00000150893	0.00143539	0.02623337	-3.4738544	<i>TMEM45A</i>	ENSG00000181458	0.00313508	0.04378968	-2.3062365
<i>PCSK1N</i>	ENSG00000102109	3.3842E-05	0.0020571	-3.4605069	<i>PRR7</i>	ENSG00000131188	0.00031678	0.00955301	-2.3035471
<i>ROPN1B</i>	ENSG00000114547	7.3607E-05	0.00353566	-3.4441778	<i>MMP17</i>	ENSG00000198598	1.1111E-05	0.00094973	-2.2940827
<i>CIQTNF3</i>	ENSG00000082196	5.5436E-05	0.00285209	-3.4186661	<i>CEROX1</i>	ENSG00000260807	0.00026131	0.00849243	-2.2903108
<i>SEMA3D</i>	ENSG00000153993	2.459E-05	0.00167458	-3.3999316	<i>ST3GAL4</i>	ENSG00000110080	2.9239E-05	0.00181877	-2.2875868
<i>ZFPM2-AS1</i>	ENSG00000251003	0.0001296	0.00522619	-3.3912591	<i>PODXL2</i>	ENSG00000114631	0.00056304	0.01376984	-2.286711
<i>NSG1</i>	ENSG00000168824	1.7496E-05	0.00132629	-3.3905924	<i>MELTF</i>	ENSG00000163975	0.00097609	0.0201107	-2.281146
<i>MYH14</i>	ENSG00000105357	1.074E-05	0.00092773	-3.3890432	<i>MTATP6P1</i>	ENSG00000248527	0.00107045	0.02129489	-2.2734072
<i>APOD</i>	ENSG00000189058	4.1878E-05	0.00232777	-3.3844472	<i>LIF</i>	ENSG00000128342	4.189E-05	0.00232777	-2.2704559
<i>BAALC</i>	ENSG00000164929	5.0087E-09	3.574E-06	-3.3808321	<i>HSPA1B</i>	ENSG00000204388	0.00030246	0.00933135	-2.2686297
<i>LGI4</i>	ENSG00000153902	3.1848E-06	0.00041156	-3.3796672	<i>TUBB3</i>	ENSG00000258947	2.4876E-05	0.0016801	-2.2624119
<i>ASPHD1</i>	ENSG00000174939	3.1549E-07	7.8452E-05	-3.3793597	<i>GREB1</i>	ENSG00000196208	0.00050041	0.0127923	-2.2504602
<i>SEZGL2</i>	ENSG00000174938	2.0004E-07	5.4718E-05	-3.3612537	<i>H3C10</i>	ENSG00000278828	3.8141E-06	0.00046714	-2.2490391
<i>ELOVL2</i>	ENSG00000197977	7.6061E-06	0.00074749	-3.3516657	<i>TRIL</i>	ENSG00000255690	2.5227E-05	0.00168442	-2.236514
<i>LOXL3</i>	ENSG00000115318	9.4638E-08	3.0455E-05	-3.3386513	<i>IGFBP3</i>	ENSG00000146674	0.0003038	0.00933135	-2.235326
<i>BAMBI</i>	ENSG00000095739	1.8999E-07	5.285E-05	-3.3278603	<i>OBSL1</i>	ENSG00000124006	3.4867E-05	0.0020862	-2.2338454
<i>IGSF3</i>	ENSG00000143061	2.66E-06	0.00036686	-3.3269684	<i>CDK18</i>	ENSG00000117266	8.0751E-05	0.00378654	-2.2308525
<i>NLGN3</i>	ENSG00000196338	5.5874E-07	0.00012237	-3.3138854	<i>BFSPI</i>	ENSG00000125864	0.00014531	0.00561148	-2.2203441
<i>S100A1</i>	ENSG00000160678	0.00012712	0.00515142	-3.3123307	<i>HOXA4</i>	ENSG00000197576	8.113E-05	0.00379348	-2.2158686
<i>AATK</i>	ENSG00000181409	1.7052E-08	8.4931E-06	-3.3122806	<i>CHST10</i>	ENSG00000115526	2.2145E-05	0.00156901	-2.2146452
<i>PAX3</i>	ENSG00000135903	8.8676E-05	0.00403145	-3.2819414	<i>LINC02289</i>	ENSG00000258819	0.0009214	0.01941219	-2.2111366
<i>SEMA3B</i>	ENSG00000012171	2.8137E-05	0.00179403	-3.2628193	<i>ADCY1</i>	ENSG00000164742	0.00022163	0.00759385	-2.2081027

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<i>PIMREG</i>	ENSG00000129195	1.5513E-07	4.4666E-05	-3.2621338	<i>ANLN</i>	ENSG00000011426	3.5293E-05	0.00209867	-2.2075282
<i>SULT1B1</i>	ENSG00000173597	0.00137931	0.02546366	-3.2583928	<i>TMEM121</i>	ENSG00000184986	0.00025699	0.00841861	-2.2027042
<i>B4GALNT4</i>	ENSG00000182272	0.00014442	0.00559021	-3.2339688	<i>PACIN3</i>	ENSG00000165912	8.9134E-05	0.00404109	-2.2023568
<i>BMP8B</i>	ENSG00000116985	6.1334E-07	0.00013073	-3.2330305	<i>PCDHB11</i>	ENSG00000197479	0.00369662	0.04900562	-2.1999164
<i>LZTS1</i>	ENSG00000061337	2.042E-07	5.4939E-05	-3.203505	<i>CORO2B</i>	ENSG00000103647	0.00155363	0.02764487	-2.1983051
<i>DDR1</i>	ENSG00000204580	4.8923E-08	1.7843E-05	-3.1964915	<i>MLPH</i>	ENSG00000115648	0.0004444	0.01209535	-2.1922945
<i>BIRC7</i>	ENSG00000101197	0.00081923	0.01785543	-3.1738224	<i>LAPTM4B</i>	ENSG00000104341	1.0927E-05	0.00093888	-2.1908569
<i>SLC9A3</i>	ENSG00000066230	0.00034724	0.0101949	-3.1307611	<i>ETNK2</i>	ENSG00000143845	0.00014696	0.00566169	-2.1906502
<i>PSORS1C1</i>	ENSG00000204540	0.00080572	0.01759381	-3.1287804	<i>FCRLB</i>	ENSG00000162746	3.5438E-05	0.00209966	-2.186191
<i>SLC4A3</i>	ENSG00000114923	3.848E-07	9.0219E-05	-3.1272253	<i>CNR1</i>	ENSG00000118432	0.00337656	0.04614169	-2.1852023
<i>PLAT</i>	ENSG00000104368	3.3164E-08	1.2959E-05	-3.1173374	<i>HOXB6</i>	ENSG00000108511	0.00027117	0.00867533	-2.1806193
<i>LAD1</i>	ENSG00000159166	8.3966E-05	0.00388185	-3.116461	<i>MIR3681HG</i>	ENSG00000224184	0.00370931	0.0491342	-2.1797003
<i>GPR27</i>	ENSG00000170837	1.3725E-06	0.00024863	-3.100908	<i>TUSC3</i>	ENSG00000104723	1.4699E-05	0.00115759	-2.1723317
<i>ARSI</i>	ENSG00000183876	0.00014344	0.00556542	-3.0742793	<i>PPP1R9A</i>	ENSG00000158528	0.00135994	0.0252481	-2.1717859
<i>SHISA4</i>	ENSG00000198892	1.3266E-05	0.00108862	-3.0651618	<i>PABPC5</i>	ENSG00000174740	0.00023972	0.00802922	-2.1687028
<i>ARHGEF34</i>									
<i>P</i>	ENSG00000204959	0.00013562	0.00535065	-3.0585037	<i>B4GALT6</i>	ENSG00000118276	0.00020187	0.00706199	-2.16547
<i>PRR19</i>	ENSG00000188368	0.00039499	0.01111055	-3.0464299	<i>VPS37D</i>	ENSG00000176428	7.6096E-05	0.00361996	-2.159342
<i>SFRP1</i>	ENSG00000104332	0.00010248	0.00442879	-3.0331938	<i>NME1-NME2</i>	ENSG00000011052	0.00267949	0.0393536	-2.1589343
<i>RASAL2-AS1</i>	ENSG00000224687	9.0743E-06	0.00081589	-3.0270807	<i>WWTR1</i>	ENSG00000018408	8.28E-06	0.00078707	-2.157684
<i>INPP5F</i>	ENSG00000198825	1.3853E-09	1.263E-06	-3.0260526	<i>CYTL1</i>	ENSG00000170891	0.00125203	0.02381042	-2.1571132
<i>ARSL</i>	ENSG00000157399	8.8653E-06	0.00080385	-3.0229362	<i>IGSF8</i>	ENSG00000162729	3.4117E-05	0.00206618	-2.1512722
<i>SLC13A3</i>	ENSG00000158296	4.0831E-05	0.00232777	-3.0171311	<i>F5</i>	ENSG00000198734	0.00367164	0.04883218	-2.1492383
<i>S100A16</i>	ENSG00000188643	3.0246E-05	0.00184536	-3.0151039	<i>BAIAP3</i>	ENSG00000007516	0.00162413	0.02841674	-2.1486591
<i>TREX2</i>	ENSG00000183479	6.4824E-05	0.00320449	-3.0000425	<i>EFR3B</i>	ENSG00000084710	0.0026808	0.0393536	-2.1466099
<i>LINGO1</i>	ENSG00000169783	1.2753E-05	0.00105709	-2.981728	<i>LICAM</i>	ENSG00000198910	0.00171769	0.02951916	-2.1419809
<i>GPR39</i>	ENSG00000183840	6.8549E-05	0.00336832	-2.9790296	<i>RNF208</i>	ENSG00000212864	0.00015404	0.00581182	-2.1413853
<i>CBARP</i>	ENSG000000099625	3.2477E-06	0.00041642	-2.9760506	<i>IGF2BP2</i>	ENSG00000073792	1.5342E-06	0.00026773	-2.140849
<i>TUBB2B</i>	ENSG00000137285	6.6742E-07	0.00014043	-2.9643715	<i>LINC01852</i>	ENSG00000236914	0.00293442	0.04198759	-2.1391691
<i>TFAP2A-AS1</i>									
<i>AS1</i>	ENSG00000229950	8.3008E-06	0.00078707	-2.9623277	<i>PLEKHG4</i>	ENSG00000196155	5.9518E-05	0.00298717	-2.13415
<i>SORCSI</i>	ENSG00000108018	1.8313E-05	0.00135996	-2.9623007	<i>SOX12</i>	ENSG00000177732	2.228E-05	0.00156938	-2.1328323
<i>NGFR</i>	ENSG00000064300	1.7793E-05	0.00133342	-2.9488462	<i>DCBLD2</i>	ENSG00000057019	2.6941E-05	0.00174766	-2.124269
<i>TESC</i>	ENSG00000088992	3.4924E-05	0.0020862	-2.9365401	<i>H2AW</i>	ENSG00000181218	4.7843E-05	0.00252967	-2.1219094
<i>BEX3</i>	ENSG00000166681	6.7599E-05	0.00333161	-2.9334417	<i>LRP4</i>	ENSG00000134569	0.00336576	0.04605302	-2.1185679
<i>RBMS3-AS3</i>	ENSG00000235904	0.00029498	0.00918625	-2.9294507	<i>LAMC3</i>	ENSG00000050555	0.00221921	0.03495369	-2.1156406
<i>FOLH1</i>	ENSG00000086205	0.00034217	0.01008191	-2.9029106	<i>TEN1-CDK3</i>	ENSG00000261408	0.00109666	0.02163277	-2.0981283
<i>SMIM5</i>	ENSG00000204323	0.00016828	0.00619233	-2.8987801	<i>OSBP2</i>	ENSG00000184792	0.00047304	0.01248145	-2.093469
<i>APLP1</i>	ENSG00000105290	0.00026865	0.00866226	-2.8923642	<i>B4GALNT1</i>	ENSG00000135454	0.00045022	0.01219936	-2.0930417
<i>DUSP4</i>	ENSG00000120875	3.1816E-09	2.6108E-06	-2.8914526	<i>LDLRAD3</i>	ENSG00000179241	1.4812E-05	0.00115759	-2.0890904
<i>CEP170B</i>	ENSG00000099814	1.8232E-06	0.0002905	-2.8901285	<i>SMIM10L2A</i>	ENSG00000178947	0.00073979	0.01645181	-2.0875292
<i>FAM27C</i>	ENSG00000231527	0.00011296	0.00471597	-2.8619731	<i>MGC16275</i>	ENSG00000246731	0.00033606	0.0099621	-2.0858784
<i>FKBP9P1</i>	ENSG00000176826	0.00011783	0.00485902	-2.8570574	<i>GPSM1</i>	ENSG00000160360	7.2299E-05	0.00352005	-2.0855551
<i>ST6GALNA C2</i>									
<i>C2</i>	ENSG00000070731	0.00056541	0.01378822	-2.8568066	<i>STC1</i>	ENSG00000159167	0.00362338	0.04826861	-2.076828
<i>C10orf90</i>	ENSG00000154493	0.0018701	0.03145105	-2.8414674	<i>KIAA1549</i>	ENSG00000122778	0.00171638	0.02951916	-2.068997
<i>TRPM8</i>	ENSG00000144481	0.00048217	0.01264108	-2.8390216	<i>PYCR1</i>	ENSG00000183010	0.0002325	0.00786767	-2.0678048
<i>DAG1</i>	ENSG00000173402	3.5552E-06	0.0004454	-2.8370889	<i>TSPYL5</i>	ENSG00000180543	0.00051636	0.01307023	-2.0676663
<i>FRMD5</i>	ENSG00000171877	3.6071E-05	0.00212948	-2.8287997	<i>GNG4</i>	ENSG00000168243	9.0975E-06	0.00081589	-2.0662459
<i>NES</i>	ENSG00000132688	2.3013E-06	0.00032843	-2.8189804	<i>COL4A5</i>	ENSG00000188153	0.00055761	0.01369986	-2.0655105
<i>P2RX6</i>	ENSG00000099957	7.955E-05	0.00375167	-2.8165693	<i>RNF157</i>	ENSG00000141576	1.2625E-05	0.00105177	-2.0642882
<i>RBP1</i>	ENSG00000114115	0.00059587	0.01429738	-2.8094776	<i>TMEM54</i>	ENSG00000121900	0.00247919	0.03746885	-2.0605877
<i>CNIH3</i>	ENSG00000143786	6.9737E-06	0.00069831	-2.8077337	<i>FOXM1</i>	ENSG00000111206	0.00010287	0.00443111	-2.0599044
<i>FAM78B</i>	ENSG00000188859	1.6265E-06	0.00026963	-2.8029973	<i>RNF175</i>	ENSG00000145428	0.00066814	0.01540106	-2.05941
<i>CEACAM1</i>	ENSG00000079385	1.4364E-06	0.00025349	-2.8027061	<i>STEAP1B</i>	ENSG00000105889	0.00062235	0.0147499	-2.0579269
<i>TMEM169</i>	ENSG00000163449	6.1017E-05	0.00304379	-2.7930975	<i>TBX2-AS1</i>	ENSG00000267280	0.00132669	0.02479916	-2.05175
<i>IGSF11</i>	ENSG00000144847	0.00128261	0.02424309	-2.7927124	<i>BMS1P23</i>	ENSG00000286156	0.00326272	0.04496034	-2.0498737
<i>ARHGAP5-AS1</i>									
<i>AS1</i>	ENSG00000258655	3.1364E-07	7.8452E-05	-2.7832582	<i>TRO</i>	ENSG00000067445	0.00024801	0.00818037	-2.0490915
<i>KCTD15</i>	ENSG00000153885	1.7143E-07	4.8508E-05	-2.7792142	<i>MEIS3P1</i>	ENSG00000179277	0.00175323	0.03003552	-2.0488834
<i>DDIT3</i>	ENSG00000107984	0.00045158	0.01220965	-2.7773141	<i>DDIT3</i>	ENSG00000099974	0.00028936	0.00904563	-2.0447253
<i>MMP1</i>	ENSG00000196611	0.00037168	0.01068305	-2.7561067	<i>TLCDF1</i>	ENSG00000160606	0.00037611	0.01077726	-2.0384045
<i>HOXC10</i>	ENSG00000180818	2.3879E-05	0.00164667	-2.75253	<i>CHPF</i>	ENSG00000123989	0.00078273	0.01726633	-2.0349687
<i>ARNT2</i>	ENSG00000172379	2.1327E-07	5.6454E-05	-2.7449115	<i>CLTCL1</i>	ENSG00000070371	0.00208299	0.0333669	-2.0320815
<i>ARC</i>	ENSG00000198576	0.00096192	0.01988282	-2.7395556	<i>PCDH7</i>	ENSG00000169851	5.3934E-05	0.00280115	-2.0286971
<i>ESM1</i>	ENSG00000164283	0.00049231	0.012729	-2.734586	<i>ILIRAP</i>	ENSG00000196083	0.00013462	0.00532731	-2.0148797
<i>ARHGAP39</i>	ENSG00000147799	2.4458E-05	0.00167253	-2.7334872	<i>VEGFA</i>	ENSG00000112715	0.00012671	0.00515142	-2.0134777
<i>LYPD1</i>	ENSG00000150551	4.4076E-05	0.00239631	-2.7313175	<i>FAM83H</i>	ENSG00000180921	0.00079344	0.01744121	-2.009883
<i>FASN</i>	ENSG00000169710	0.00016504	0.00610292	-2.7259904	<i>PSATI</i>	ENSG00000135069	2.1978E-05	0.00156828	-2.0098439
<i>LRATD2</i>	ENSG00000168672	3.8703E-06	0.00047052	-2.7199108	<i>NME1</i>	ENSG00000239672	0.00044523	0.01209787	-2.0095328
<i>SLC26A4</i>	ENSG00000091137	0.0022951	0.03587352	-2.7064525	<i>TONSL</i>	ENSG00000160949	4.2058E-05	0.00232777	-2.0073833

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<i>GSTT2B</i>	ENSG00000133433	0.00024822	0.00818037	-2.6964425					
<i>TMEM198</i>	ENSG00000188760	5.9108E-05	0.00298432	-2.6931411					
<i>VSTM2L</i>	ENSG00000132821	0.0019069	0.03174353	-2.6868318					
<i>SERPINA5</i>	ENSG00000188488	0.0001389	0.00544078	-2.6850862					
<i>PCSK1</i>	ENSG00000175426	0.00069908	0.01591121	-2.6644673					
<i>CLDN1</i>	ENSG00000163347	0.00031626	0.00955301	-2.6626965					

Supplementary Table 9: Significant DEGs in Treatment-responsive Samples (Post- vs. Pre- Treatment) in**Figure 5**

Gene Name	Gene ID	Log2FC	Adjusted p value	FDR	Gene Name	Gene ID	Log2FC	Adjusted p value	FDR
DEGs that are upregulated post-treatment									
<i>IGKV1-9</i>	ENSG00000241755	7.0439247	8.3978E-07	0.00022582	<i>TNFRSF4</i>	ENSG00000186827	2.5672045	0.00020385	0.00834247
<i>TCEAL7</i>	ENSG00000182916	6.571394	1.9162E-08	2.1791E-05	<i>CARMIL2</i>	ENSG00000159753	2.5614242	0.00074096	0.01948559
<i>MMP12</i>	ENSG00000262406	6.2005806	4.4365E-08	3.4019E-05	<i>SEC31B</i>	ENSG00000075826	2.5588568	0.00234103	0.03955033
<i>SERPINA9</i>	ENSG00000170054	5.9636163	2.094E-08	2.1791E-05	<i>CD300A</i>	ENSG00000167851	2.5563361	0.00024788	0.00942916
<i>CXCL2</i>	ENSG00000081041	5.6197061	2.866E-07	9.9895E-05	<i>TMEM200C</i>	ENSG00000206432	2.5504459	0.00150094	0.03092948
<i>IGLV6-57</i>	ENSG00000211640	5.3660406	0.00025118	0.00945601	<i>NUGGC</i>	ENSG00000189233	2.5473799	0.00288978	0.04459251
<i>JSRP1</i>	ENSG00000167476	5.3418499	2.1902E-07	9.3591E-05	<i>PSTPIP1</i>	ENSG00000140368	2.5447578	0.00035243	0.01185823
<i>IGLV3-21</i>	ENSG00000211662	5.2758383	4.351E-05	0.0029347	<i>ANXA2R</i>	ENSG00000177721	2.5331636	0.00030017	0.01071869
<i>IGKV2-28</i>	ENSG00000244116	4.9536313	0.00011085	0.00536537	<i>LIPE-AS1</i>	ENSG00000213904	2.5302679	0.00238207	0.03976303
<i>DACH1</i>	ENSG00000276644	4.905867	2.383E-07	9.3591E-05	<i>VASH2</i>	ENSG00000143494	2.5301785	0.00058135	0.01687199
<i>RGS13</i>	ENSG00000127074	4.6490932	7.518E-07	0.00021063	<i>RHOH</i>	ENSG00000168421	2.5243356	0.00055311	0.0162464
<i>MEF2B</i>	ENSG00000213999	4.5879565	9.1891E-08	5.355E-05	<i>HSH2D</i>	ENSG00000196684	2.5215125	0.00075309	0.01961946
<i>IGLC3</i>	ENSG00000211679	4.5838729	1.3806E-06	0.00032812	<i>TRAF3IP3</i>	ENSG00000009790	2.5200022	0.00010958	0.00533706
<i>IGKV2D-28</i>	ENSG00000242534	4.4505963	9.9662E-05	0.00501981	<i>PLCXD2</i>	ENSG00000240891	2.518509	0.00126276	0.02794017
<i>CD52</i>	ENSG00000169442	4.4013117	2.2867E-07	9.3591E-05	<i>LINC01410</i>	ENSG00000238113	2.5161194	0.00257859	0.04174158
<i>PRH1</i>	ENSG00000231887	4.3926181	9.998E-05	0.00501981	<i>FTL</i>	ENSG00000087086	2.5149321	0.00049535	0.01509784
<i>IGKV3-11</i>	ENSG00000241351	4.3817623	0.00024892	0.00943873	<i>SPACA6</i>	ENSG00000182310	2.51345	0.00075548	0.01961946
<i>IGHM</i>	ENSG00000211899	4.3784158	1.1408E-06	0.00028171	<i>SMIM10</i>	ENSG00000184785	2.5095367	0.00218093	0.0376024
<i>CCL3L1</i>	ENSG00000276085	4.3323305	1.4189E-07	7.1282E-05	<i>CD27</i>	ENSG00000139193	2.5086985	0.00072587	0.01923231
<i>ITGAD</i>	ENSG00000156886	4.2308351	1.0814E-06	0.00027178	<i>PIK3IP1</i>	ENSG00000100100	2.4929176	0.00033519	0.01151756
<i>IGKV3-20</i>	ENSG00000239951	4.1995939	0.00024769	0.00942916	<i>PRKX</i>	ENSG00000183943	2.4890506	0.00047996	0.01466533
<i>IGKC</i>	ENSG00000211592	4.1696581	3.2641E-06	0.00054203	<i>PVRIG</i>	ENSG00000213413	2.4883866	0.00089288	0.0217895
<i>IGHG2</i>	ENSG00000211893	4.0991283	1.7029E-05	0.00162719	<i>ADA2</i>	ENSG00000093072	2.4782557	0.00029524	0.01066115
<i>IGLC1</i>	ENSG00000211675	4.040259	1.8505E-05	0.00166398	<i>MBOAT1</i>	ENSG00000172197	2.4778117	0.00120591	0.02707065
<i>TNFRSF17</i>	ENSG00000048462	4.0211164	2.684E-07	9.7759E-05	<i>INPP5D</i>	ENSG00000168918	2.4768512	8.1837E-05	0.00431988
<i>APOC1</i>	ENSG00000130208	4.0138442	6.3184E-07	0.00018786	<i>PSTPIP2</i>	ENSG00000152229	2.4768103	0.00100555	0.02378219
<i>VPREB3</i>	ENSG00000128218	4.0000909	1.4067E-05	0.0015069	<i>ITGAX</i>	ENSG00000140678	2.4700466	0.00013189	0.00615864
<i>BIK</i>	ENSG00000100290	3.9915556	2.4411E-07	9.3591E-05	<i>SH2D1A</i>	ENSG00000183918	2.4691812	0.00082854	0.02095665
<i>IGHV2-5</i>	ENSG00000211937	3.9523966	8.8029E-05	0.00459674	<i>SLC35A5</i>	ENSG00000138459	2.4623027	0.00112137	0.02580174
<i>GCSAM</i>	ENSG00000174500	3.9518182	1.976E-06	0.00038708	<i>C11orf21</i>	ENSG00000110665	2.4552092	0.00048015	0.01466533
<i>IGHG3</i>	ENSG00000211897	3.8936567	0.00012291	0.0058138	<i>RNASET2</i>	ENSG00000026297	2.4528053	9.8038E-05	0.00497786
<i>IGKV1-5</i>	ENSG00000243466	3.861017	0.00034776	0.01175516	<i>GID4</i>	ENSG00000141034	2.4424374	0.00054264	0.01610134
<i>ADAMDEC1</i>	ENSG00000134028	3.8477956	1.7374E-06	0.0003649	<i>MTERF4</i>	ENSG00000122085	2.4387105	0.0001483	0.0067309
<i>GZMH</i>	ENSG00000100450	3.843919	1.3977E-06	0.00032812	<i>FBXL12</i>	ENSG00000127452	2.433311	0.00101889	0.02401796
<i>GNLY</i>	ENSG00000115523	3.8379082	1.505E-06	0.00033732	<i>HCS7</i>	ENSG00000126264	2.4261308	0.00078402	0.02012452
<i>JCHAIN</i>	ENSG00000132465	3.8289922	2.9714E-06	0.00052156	<i>ADGRG5</i>	ENSG00000159618	2.425962	0.0004311	0.01353608
<i>CHIT1</i>	ENSG00000133063	3.7994902	0.00034879	0.01176291	<i>TNFSF8</i>	ENSG00000106952	2.4193681	6.2472E-05	0.00359745
<i>IGKV1D-33</i>	ENSG00000239975	3.7883785	0.00028164	0.01042482	<i>RPL2IP75</i>	ENSG00000213860	2.4183345	3.227E-05	0.00243776
<i>TNFRSF13B</i>	ENSG00000240505	3.7327559	1.446E-05	0.00151564	<i>C1orf131</i>	ENSG00000143633	2.4178353	0.00124327	0.02761167
<i>GCHFR</i>	ENSG00000137880	3.69822	2.0189E-07	9.1918E-05	<i>NOXA1</i>	ENSG00000188747	2.4157095	0.00062512	0.01758192
<i>HID1</i>	ENSG00000167861	3.6931403	2.0193E-08	2.1791E-05	<i>NSMCE4A</i>	ENSG00000107672	2.4120569	0.00023032	0.00903207
<i>GADD45G</i>	ENSG00000130222	3.6857989	1.6282E-06	0.00035941	<i>RAB39B</i>	ENSG00000155961	2.4067158	0.00014209	0.00657166
<i>RGL4</i>	ENSG00000159496	3.6503257	2.8665E-06	0.00050929	<i>ADORA2A</i>	ENSG00000128271	2.4031119	0.00053642	0.01594913
<i>CP</i>	ENSG00000047457	3.6445252	6.1841E-07	0.0001877	<i>SHROOM3</i>	ENSG00000138771	2.4025632	0.00199088	0.03600459
<i>ZNF230</i>	ENSG00000159882	3.6235619	4.4795E-05	0.00299294	<i>MRPL50</i>	ENSG00000136897	2.4019435	0.00138407	0.02935159
<i>IGLV3-10</i>	ENSG00000211669	3.6086822	1.4407E-05	0.00151564	<i>C7</i>	ENSG00000112936	2.4011607	0.00216855	0.03759433
<i>PRDM1</i>	ENSG00000057657	3.5776595	4.1963E-08	3.3965E-05	<i>IRF8</i>	ENSG00000140968	2.3984817	0.00037562	0.01233866
<i>FBP1</i>	ENSG00000165140	3.5619571	3.2294E-05	0.00243776	<i>LINC00426</i>	ENSG00000238121	2.3978346	0.00020633	0.00842009
<i>PTPRN2</i>	ENSG00000155093	3.5609973	3.5519E-06	0.00056247	<i>CCDC69</i>	ENSG00000198624	2.395112	0.00011533	0.00554559
<i>INTS6L</i>	ENSG00000165359	3.5451117	8.0633E-06	0.00103959	<i>ESR1</i>	ENSG00000091831	2.3904708	0.00238649	0.03976303
<i>CD69</i>	ENSG00000110848	3.5354363	4.4374E-07	0.00014684	<i>TNFRSF13C</i>	ENSG00000159958	2.3871013	0.00153485	0.0312744
<i>IGHA1</i>	ENSG00000211895	3.5289639	5.9286E-05	0.00354068	<i>HLA-DRB6</i>	ENSG00000229391	2.381882	0.00210116	0.03687805
<i>PRAM1</i>	ENSG00000133246	3.5160379	0.00010027	0.00501981	<i>CORO1A</i>	ENSG00000102879	2.3814912	0.0003795	0.01239657
<i>ZBP1</i>	ENSG00000124256	3.5079478	7.7426E-07	0.00021283	<i>LINC01197</i>	ENSG00000248441	2.3789438	0.00029563	0.01066115
<i>CD3D</i>	ENSG00000167286	3.5002543	2.0852E-05	0.001756	<i>CEACAM21</i>	ENSG00000007129	2.3681603	0.00030253	0.01077627
<i>TRGC2</i>	ENSG00000227191	3.4979401	1.6571E-05	0.00159881	<i>LGDN</i>	ENSG00000100600	2.3659125	0.00093434	0.02242562
<i>FAM30A</i>	ENSG00000226777	3.4915924	3.72E-06	0.00058276	<i>SDS</i>	ENSG00000135094	2.3635157	0.00301444	0.04559953
<i>IGLC7</i>	ENSG00000211685	3.489884	0.00034065	0.01165008	<i>GBGT1</i>	ENSG00000148288	2.3633814	0.00051418	0.01538222
<i>ZFP36</i>	ENSG00000128016	3.4394717	1.335E-06	0.00032417	<i>CYBA</i>	ENSG00000051523	2.356219	0.00066592	0.01822671
<i>FOSB</i>	ENSG00000125740	3.4389771	1.2373E-05	0.00136565	<i>SLC22A3</i>	ENSG00000146477	2.3533289	0.00198146	0.03595004
<i>STAP1</i>	ENSG00000035720	3.3915717	4.9218E-05	0.00314498	<i>COCH</i>	ENSG00000100473	2.3519338	0.00212747	0.03707836
<i>KCNJ5</i>	ENSG00000120457	3.3889858	1.5669E-05	0.00157385	<i>NKG7</i>	ENSG00000105374	2.3510498	0.00198068	0.03595004

Neoadjuvant Intratumoral Vidutolimod and Nivolumab in High-Risk Resectable Melanoma

LTC4S	ENSG00000213316	3.3844712	3.1976E-05	0.00243776	FCN1	ENSG00000085265	2.3449367	0.00167096	0.03296894
IGHD	ENSG00000211898	3.3814393	0.00086954	0.02147186	CLIC6	ENSG00000159212	2.3439298	0.0002783	0.01034312
DUSP1	ENSG00000120129	3.3701793	1.7533E-06	0.0003649	AN09	ENSG00000185101	2.3382967	0.00233861	0.03955033
CARF	ENSG00000138380	3.3682417	6.0803E-05	0.00355846	PRKCQ	ENSG00000065675	2.3378088	0.00150419	0.03095265
IGKV2-30	ENSG00000243238	3.3651715	0.00272443	0.04316543	IFI30	ENSG00000216490	2.333462	0.00115317	0.0263622
CD79B	ENSG00000007312	3.3628441	4.8648E-05	0.00312225	CD48	ENSG00000117091	2.3313837	0.00072614	0.01923231
CCL18	ENSG00000275385	3.3362249	8.0872E-05	0.00431582	ADAM33	ENSG00000149451	2.3287563	0.00167338	0.03296894
RPL13P5	ENSG00000240370	3.3201461	0.00043613	0.01366447	CXCL12	ENSG00000107562	2.3268491	0.00086319	0.02145626
MCM9	ENSG00000111877	3.3020521	4.2299E-05	0.00289022	CTSD	ENSG00000117984	2.3262214	0.00074687	0.01955012
PDE6G	ENSG00000185527	3.2942281	1.8547E-05	0.00166398	GTF3C5	ENSG00000148308	2.3230993	0.00148702	0.03087602
IGHG4	ENSG00000211892	3.2930636	0.00033984	0.0116496	RASAL3	ENSG00000105122	2.3224094	0.00149625	0.03087663
POU2AF1	ENSG00000110777	3.2768928	5.3872E-06	0.00075468	MYO1G	ENSG00000136286	2.3215226	6.1145E-05	0.00356331
ALOX15B	ENSG00000179593	3.2765167	6.1827E-05	0.0035887	TATDN1	ENSG00000147687	2.319886	0.00082427	0.02088473
AICDA	ENSG00000111732	3.2762868	0.00160703	0.03229357	SASH3	ENSG00000122122	2.3142643	0.00282307	0.04394164
TBC1D10C	ENSG00000175463	3.2663634	3.2167E-06	0.00054203	LAMTOR3	ENSG00000109270	2.3098896	0.00127542	0.02798426
CDH23	ENSG00000107736	3.2563863	1.0615E-05	0.00127805	KLRK1	ENSG00000213809	2.3089728	0.00023667	0.00914585
PTPRCAP	ENSG00000213402	3.255693	7.0983E-05	0.00396227	ACYPI	ENSG00000119640	2.3079634	0.00332993	0.04856232
ITGA8	ENSG00000077943	3.2534255	2.8443E-06	0.00050929	CARNS1	ENSG00000172508	2.3067438	0.0016894	0.03296894
TMEM42	ENSG00000169964	3.2438227	4.0617E-05	0.00281785	VAMP8	ENSG00000118640	2.3059436	0.00168993	0.03296894
RASSF6	ENSG00000169435	3.2382266	0.00014479	0.0066542	DTX1	ENSG00000135144	2.3045985	0.00218563	0.03763888
TIMD4	ENSG00000145850	3.2348277	0.00017156	0.00735336	PYM1	ENSG00000170473	2.3045578	0.00061217	0.01741923
EEF1AKMT4	ENSG00000284753	3.2334122	0.00047539	0.01461165	AFF2	ENSG00000155966	2.3041298	0.00210348	0.03687805
MS4A1	ENSG00000156738	3.2324932	0.0001074	0.00526822	ADAM28	ENSG00000042980	2.3034072	0.00040966	0.01305969
IGLL5	ENSG00000254709	3.2090871	0.00012051	0.00575657	P2RY8	ENSG00000182162	2.3000777	0.00167176	0.03296894
RAMP1	ENSG00000132329	3.2031289	0.00015715	0.00697101	BCL11B	ENSG00000127152	2.2990189	0.00076762	0.01989933
CFP	ENSG00000126759	3.1833827	2.1027E-05	0.00176056	VNN2	ENSG00000112303	2.2959098	0.00172099	0.03325349
TCL1A	ENSG00000100721	3.1605647	0.00037277	0.01228703	HFE	ENSG00000010704	2.2902462	0.00128635	0.02813936
KLHL6	ENSG00000172578	3.151248	8.525E-07	0.00022582	CR1	ENSG00000203710	2.2888754	8.1655E-05	0.00431988
IGLC2	ENSG00000211677	3.1495434	0.00014904	0.00674325	FGD2	ENSG00000146192	2.2886502	0.00047444	0.01461165
TMEM182	ENSG00000170417	3.1425987	0.00084427	0.02117068	ZNF350	ENSG00000256683	2.2861786	0.00032587	0.0113218
PMS2P3	ENSG00000127957	3.1415991	0.00021158	0.0085387	HTRA4	ENSG00000169495	2.2738726	0.00254577	0.04148693
IGLV2-8	ENSG00000278196	3.1415464	0.00160611	0.03229357	CD80	ENSG00000121594	2.2735999	0.00121372	0.02720405
KLRB1	ENSG00000111796	3.1167019	1.0365E-05	0.00125842	TP53INP1	ENSG00000164938	2.2727817	0.00041684	0.01317349
IGHG1	ENSG00000211896	3.1137467	0.00015416	0.0068895	SLC49A4	ENSG00000138463	2.2675266	0.0029117	0.04479669
GPR183	ENSG00000169508	3.1061096	4.5271E-05	0.00299294	LINC02384	ENSG00000251301	2.2674885	0.00241558	0.0401742
P2RX5	ENSG00000083454	3.1047291	4.0987E-05	0.00283007	ADCY5	ENSG00000173175	2.2670245	0.00119549	0.02693397
TSP0API	ENSG00000005379	3.101628	0.00011343	0.00547191	CLK4	ENSG00000113240	2.2667369	0.00165584	0.0328216
HMCN2	ENSG00000148357	3.0974087	0.00070477	0.01887449	NUDT16L2P	ENSG00000246082	2.2664313	0.00067486	0.01822671
BLNK	ENSG00000095585	3.0850606	5.6949E-06	0.00077541	CASP4LP	ENSG00000235505	2.2632395	0.00205182	0.0364025
IGLV2-23	ENSG00000211660	3.0847957	0.00119612	0.02693397	FAM124A	ENSG00000150510	2.2550142	0.00274216	0.04333027
GZMA	ENSG00000145649	3.0817903	4.7065E-05	0.00305608	SOWAHD	ENSG00000187808	2.2513005	0.00086679	0.02145626
NUDT18	ENSG00000275074	3.0729313	2.8117E-05	0.00220238	CD40LG	ENSG00000102245	2.2508418	0.00304708	0.04590785
FGR	ENSG00000000938	3.0699665	2.0674E-05	0.001756	TRAT1	ENSG00000163519	2.2494936	0.00272122	0.04316543
LGALS2	ENSG00000100079	3.0580506	6.0528E-05	0.00355846	IPCEF1	ENSG00000074706	2.2488247	0.00148374	0.03087602
USP30-AS1	ENSG00000256262	3.0558086	1.7427E-05	0.00164869	DOCK2	ENSG00000134516	2.2443516	0.00030347	0.01078362
EML6	ENSG00000214595	3.0406443	0.00163907	0.03271173	SIT1	ENSG00000137078	2.243339	0.00255351	0.04156657
GMFG	ENSG00000130755	3.0261937	5.2457E-05	0.00329418	CST7	ENSG00000077984	2.236812	0.00335366	0.04885947
OLR1	ENSG00000173391	3.0181153	0.00053195	0.01584863	CTSH	ENSG00000103811	2.2342143	0.00017275	0.00738049
CTSW	ENSG00000172543	3.0128879	2.9031E-05	0.00226178	FLT3	ENSG00000122025	2.2296069	0.00178133	0.03396885
ABCG1	ENSG00000160179	3.0085431	1.3358E-05	0.00145238	FAR1	ENSG00000197601	2.2249242	0.00112282	0.02580174
FXVD2	ENSG00000137731	2.9979745	1.2968E-05	0.00142051	SLC37A2	ENSG00000134955	2.2231485	0.00234004	0.03955033
FUNDC1	ENSG00000069509	2.993035	0.00018574	0.00770958	USP30	ENSG00000135093	2.222619	0.00199188	0.03600459
CLECL1	ENSG00000184293	2.9920636	1.1942E-05	0.0013383	GIMAP7	ENSG00000179144	2.2170012	0.00142787	0.03010512
TREM1	ENSG00000124731	2.965208	0.00066188	0.01822671	TRAC	ENSG00000277734	2.2145239	0.00262013	0.04222643
NPY1R	ENSG00000164128	2.9616748	0.00039157	0.0126517	MYH11	ENSG00000133392	2.212917	0.00301722	0.04559953
PIF1	ENSG00000140451	2.9614051	0.00055155	0.01623336	LINC02482	ENSG00000251580	2.2124138	0.00089509	0.02180686
PLCH2	ENSG00000149527	2.9561591	1.8916E-05	0.00168037	IL6	ENSG00000136244	2.2121246	0.00291183	0.04479669
CD19	ENSG00000177455	2.9533988	0.0002268	0.00895477	PASK	ENSG00000115687	2.2118102	0.00039368	0.0126517
LINC00861	ENSG00000245164	2.9524771	0.00019324	0.00799815	CLEC10A	ENSG00000132514	2.2088206	0.00341447	0.04936693
IRAG2	ENSG00000118308	2.9460679	1.92E-05	0.0016953	LYZ	ENSG00000090382	2.2054001	0.00294858	0.04494448
GTF2E1	ENSG00000153767	2.9460312	5.5696E-05	0.00342193	PIP5K1B	ENSG00000107242	2.203939	0.00095999	0.02283449
CD79A	ENSG00000105369	2.9451656	0.00059744	0.01716798	CD53	ENSG00000143119	2.1971375	0.00061951	0.01749566
TMSB4X	ENSG00000205542	2.9410679	0.00010443	0.00516855	NCF1C	ENSG00000165178	2.1954871	0.00183597	0.03464793
SKAP1	ENSG00000141293	2.9404022	7.648E-06	0.00101295	NR2C1	ENSG00000120798	2.1875215	0.00145206	0.03048287
MIR155HG	ENSG00000234883	2.9366952	0.00054741	0.01614422	SIRPB2	ENSG00000196209	2.1872252	0.00063916	0.01773706
CRACR2B	ENSG00000177685	2.9208709	0.00019551	0.00806899	PRF1	ENSG00000180644	2.1869702	0.00339925	0.04925532
DHRS9	ENSG00000073737	2.9082735	0.00012681	0.00597912	CHST15	ENSG00000182022	2.1861177	0.00087684	0.02159166
ARL5B	ENSG00000165997	2.9059224	0.00031614	0.01109826	SDK1	ENSG00000146555	2.185126	0.0021344	0.03712468
ZNF75D	ENSG00000186376	2.8950744	3.637E-05	0.00264935	FPR3	ENSG00000187474	2.1824193	0.00276126	0.04341964
FOS	ENSG00000170345	2.8912271	2.2724E-05	0.00186828	TBXAS1	ENSG00000059377	2.1766883	0.00071454	0.01899648
CYTIP	ENSG00000115165	2.8854629	5.9063E-05	0.00354068	RPRD1B	ENSG00000101413	2.1751368	0.00274014	0.04333027
FCRL2	ENSG00000132704	2.8778521	0.0015597	0.0316481	C5AR1	ENSG00000197405	2.1728494	0.00020827	0.00846615

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<i>WARS2-AS1</i>	ENSG00000231365	2.8749538	0.00063538	0.01773338	<i>SEPTIN1</i>	ENSG00000180096	2.1722354	0.00292942	0.04483053
<i>LTB</i>	ENSG00000227507	2.8702351	0.00018397	0.00765769	<i>MIAT</i>	ENSG00000225783	2.17188	0.00217226	0.03759433
<i>IL7R</i>	ENSG00000168685	2.8675153	9.5758E-05	0.00491233	<i>SOCS3</i>	ENSG00000184557	2.1678967	0.00223452	0.03829964
<i>LY86</i>	ENSG00000112799	2.8664304	5.1329E-05	0.00326556	<i>TREML1</i>	ENSG00000161911	2.1642924	0.00140298	0.02970942
<i>IGHV4-39</i>	ENSG00000211959	2.8584301	0.00308674	0.04610324	<i>ITGB2</i>	ENSG00000160255	2.1622352	0.00220104	0.03781475
<i>RASGRP2</i>	ENSG00000068831	2.8470194	6.3641E-05	0.00365033	<i>DPEP2</i>	ENSG00000167261	2.1584934	0.00066048	0.01822451
<i>NCR3</i>	ENSG00000204475	2.8373227	0.00014806	0.0067309	<i>FMNL1</i>	ENSG00000184922	2.1573637	0.00153182	0.0312564
<i>PKHD1L1</i>	ENSG00000205038	2.8367326	0.00206483	0.03646358	<i>TSPAN2</i>	ENSG00000134198	2.1573329	0.00111201	0.02571569
<i>CD247</i>	ENSG00000198821	2.8316357	4.5401E-05	0.00299294	<i>NUP42</i>	ENSG00000136243	2.1495833	0.00237539	0.03976303
<i>BHLHA15</i>	ENSG00000180535	2.8238392	0.00015834	0.00699063	<i>CD6</i>	ENSG00000013725	2.1447555	0.00256472	0.04165595
<i>GNGT2</i>	ENSG00000167083	2.8187759	5.6691E-05	0.0034558	<i>FUOM</i>	ENSG00000148803	2.1441159	0.00104358	0.02444352
<i>PRKCO-AS1</i>	ENSG00000237943	2.8151157	0.00010151	0.00504729	<i>ADORA3</i>	ENSG00000282608	2.1438736	0.00295014	0.04494448
<i>PNOC</i>	ENSG00000168081	2.813217	0.00012732	0.00598356	<i>IKZF3</i>	ENSG00000161405	2.1434402	0.00128929	0.02815476
<i>LIME1</i>	ENSG00000203896	2.8106609	0.00016705	0.00726508	<i>ALOX5</i>	ENSG00000012779	2.1380269	0.00280151	0.04372289
<i>CD226</i>	ENSG00000150637	2.8015896	8.0361E-05	0.00430435	<i>LCK</i>	ENSG00000182866	2.1375351	0.00152163	0.03115111
<i>VNN1</i>	ENSG00000112299	2.7983201	3.332E-05	0.00247675	<i>SMPD3</i>	ENSG00000103056	2.1365573	0.00204782	0.0364025
<i>CTLA4</i>	ENSG00000163599	2.7972781	0.00024594	0.00940428	<i>TRG-AS1</i>	ENSG00000281103	2.1300913	0.00138014	0.02935159
<i>LAX1</i>	ENSG00000122188	2.7971723	0.00044284	0.01381514	<i>ITGB7</i>	ENSG00000139626	2.12873	0.0020742	0.03658476
<i>EA2F</i>	ENSG00000145088	2.7909432	1.3593E-05	0.00146696	<i>CPAMD8</i>	ENSG00000160111	2.124619	0.00130947	0.03844382
<i>APOE</i>	ENSG00000130203	2.7874639	6.7793E-05	0.00382823	<i>CCL4</i>	ENSG00000275302	2.1242408	0.00322805	0.04747943
<i>PCED1B-AS1</i>	ENSG00000247774	2.782008	2.6552E-06	0.00048354	<i>FRAT1</i>	ENSG00000165879	2.1217813	0.00081543	0.02073306
<i>CCL21</i>	ENSG00000137077	2.7654808	0.00179498	0.0341397	<i>ATF3</i>	ENSG00000162772	2.1181261	0.001071	0.02504564
<i>CACNA1C</i>	ENSG00000151067	2.76067	4.5252E-05	0.00299294	<i>ATP2B1-AS1</i>	ENSG00000271614	2.1178255	0.00029955	0.01071869
<i>GZMB</i>	ENSG00000100453	2.7599408	0.00057812	0.01684527	<i>CD68</i>	ENSG00000129226	2.1159989	0.00285404	0.04418755
<i>ZNF700</i>	ENSG00000196757	2.758534	0.0001099	0.00533706	<i>PDE6B</i>	ENSG00000133256	2.110918	0.00083215	0.02101132
<i>BACH2</i>	ENSG00000112182	2.757126	9.8061E-05	0.00497786	<i>SMAD7</i>	ENSG00000101665	2.1082157	0.00168211	0.03296894
<i>HLA-DQA2</i>	ENSG00000237541	2.7545104	0.00134942	0.02908237	<i>DAPP1</i>	ENSG00000070190	2.1056705	0.00067532	0.01822671
<i>JAML</i>	ENSG00000160593	2.7527663	3.5363E-05	0.00261526	<i>TTC31</i>	ENSG00000115282	2.1009308	0.00276272	0.04341964
<i>SLC29A3</i>	ENSG00000198246	2.752093	7.1455E-05	0.0039734	<i>ZNF682</i>	ENSG00000197124	2.0987924	0.00265473	0.04256208
<i>TRBC2</i>	ENSG00000211772	2.7457088	0.00031794	0.01113472	<i>BASP1</i>	ENSG00000176788	2.0973387	0.00067557	0.01822671
<i>FCRL5</i>	ENSG00000143297	2.7417721	0.00041497	0.01314286	<i>SELPLG</i>	ENSG00000110876	2.0969274	0.00032758	0.01133625
<i>OTOAP1</i>	ENSG00000257838	2.7328584	0.0016755	0.03296894	<i>GAPT</i>	ENSG00000175857	2.0962931	0.00235496	0.03964513
<i>KLF2</i>	ENSG00000127528	2.7300052	0.00021766	0.00873572	<i>HS3ST3B1</i>	ENSG00000125430	2.0941708	0.0032545	0.04770098
<i>RAB37</i>	ENSG00000172794	2.7290123	0.00041489	0.01314286	<i>P2RY13</i>	ENSG00000181631	2.0926009	0.00066931	0.01822671
<i>TSPAN32</i>	ENSG00000064201	2.7260759	5.5901E-05	0.00342193	<i>PTPN7</i>	ENSG00000143851	2.0852389	0.00056712	0.01659107
<i>COL4A3</i>	ENSG00000169031	2.7177944	0.00092002	0.02233952	<i>AFF3</i>	ENSG00000144218	2.0850312	0.00060936	0.01737324
<i>PGGHG</i>	ENSG00000142102	2.7094169	0.00034502	0.01170953	<i>C1orf54</i>	ENSG00000118292	2.0800784	0.00323447	0.04747943
<i>XCR1</i>	ENSG00000173578	2.6985275	0.00080883	0.02060107	<i>RRAD</i>	ENSG00000166592	2.0772888	0.00292582	0.04482261
<i>LINC01857</i>	ENSG00000224137	2.6981517	0.00021429	0.00862416	<i>IL16</i>	ENSG00000172349	2.0737211	0.00135188	0.02909238
<i>P2RX1</i>	ENSG00000108405	2.6981274	4.8133E-05	0.00310287	<i>SLAMF1</i>	ENSG00000117090	2.0660079	0.00292299	0.04482261
<i>PIM2</i>	ENSG00000102096	2.6899734	3.9209E-05	0.00274635	<i>CD37</i>	ENSG00000104894	2.0598812	0.00225062	0.03839489
<i>POU2F2</i>	ENSG00000028277	2.683368	7.4611E-05	0.00407121	<i>ANKRD33B</i>	ENSG00000164236	2.0554989	0.00165014	0.03279787
<i>TRBC1</i>	ENSG00000211751	2.6716324	0.00077529	0.01999334	<i>PGM5</i>	ENSG00000154330	2.0531558	0.00305122	0.04592279
<i>SLC46A3</i>	ENSG00000139508	2.6680262	0.00013072	0.00612361	<i>TENT5C</i>	ENSG00000183508	2.0494636	0.00066704	0.01822671
<i>ACTA2-AS1</i>	ENSG00000180139	2.6670762	0.00078459	0.02012452	<i>FGD6</i>	ENSG00000180263	2.0455624	0.00042152	0.01329257
<i>CD300LF</i>	ENSG00000186074	2.6588226	8.9759E-05	0.00467033	<i>ABRACL</i>	ENSG00000146386	2.0369262	0.00203184	0.03632139
<i>BATF</i>	ENSG00000156127	2.6566163	0.00019924	0.00819982	<i>HDCC3</i>	ENSG00000184508	2.0340005	0.0020456	0.0364025
<i>CD3G</i>	ENSG00000160654	2.6558613	0.0001073	0.00526822	<i>FLI1</i>	ENSG00000151702	2.0322189	1.8519E-05	0.00166398
<i>RBP5</i>	ENSG00000139194	2.6469435	0.00026869	0.01001158	<i>MGRPRF</i>	ENSG00000172935	2.0320958	0.00265849	0.04256208
<i>PNP</i>	ENSG00000198805	2.6291157	0.00064305	0.01781113	<i>KIF21B</i>	ENSG00000116852	2.0273387	0.0018541	0.03470356
<i>PAX5</i>	ENSG00000196092	2.6278344	0.00126752	0.02794017	<i>FGD3</i>	ENSG00000127084	2.026885	0.00197837	0.03595004
<i>SNAI3</i>	ENSG00000185669	2.6133873	0.00018339	0.00765543	<i>PRKCB</i>	ENSG00000166501	2.0216505	0.00061455	0.01745285
<i>FCRL6</i>	ENSG00000181036	2.6114792	0.00033417	0.01151756	<i>KCNMA1</i>	ENSG00000156113	2.0215681	0.00074744	0.01955012
<i>COL13A1</i>	ENSG00000197467	2.606064	0.00188544	0.03494772	<i>ARHGAP44</i>	ENSG00000006740	2.0194694	0.00185559	0.03470356
<i>HLA-DOB</i>	ENSG00000241106	2.5928422	0.00115535	0.0263622	<i>MYO1F</i>	ENSG00000142347	2.0185929	0.00147116	0.03066292
<i>TREM2</i>	ENSG00000095970	2.588095	0.00170317	0.03305325	<i>ADAMTS15</i>	ENSG00000166106	2.0183674	0.00318706	0.04715758
<i>EFS</i>	ENSG00000100842	2.586832	0.00346767	0.04967593	<i>TAGAP</i>	ENSG00000164691	2.0084117	0.00191468	0.0351765
<i>APOBEC3G</i>	ENSG00000239713	2.5842094	0.0002092	0.00846615	<i>TMEM150C</i>	ENSG00000249242	2.005459	0.0016423	0.03273152
<i>SLC7A7</i>	ENSG00000155465	2.5828373	0.00051369	0.01538222	<i>GLIPR2</i>	ENSG00000122694	2.0017153	0.00280302	0.04372289
<i>NAPS7</i>	ENSG00000131401	2.5810323	0.0008379	0.02112012	<i>IL10</i>	ENSG00000136634	2.0016006	0.00195275	0.03569583
<i>ZNF736</i>	ENSG00000234444	2.5790651	0.0005969	0.01716798					
<i>CHEK2</i>	ENSG00000183765	2.5770937	0.00066564	0.01822671					
<i>NOTCH2NLA</i>	ENSG00000264343	2.5768862	0.00036382	0.01207404					
<i>OSM</i>	ENSG00000099985	2.5763588	0.00016805	0.00728506					
<i>GPR35</i>	ENSG00000178623	2.5738638	7.7331E-05	0.00420385					
<i>BANK1</i>	ENSG00000153064	2.5686592	0.00158095	0.03203451					
DEGs that are upregulated pre-treatment									
<i>DCT</i>	ENSG00000080166	5.95434331	6.5928E-07	0.0001921	<i>TBCC</i>	ENSG00000124659	2.70415814	0.00088607	0.02173254
<i>TRNP1</i>	ENSG00000253368	5.83839767	4.4618E-09	7.6422E-06	<i>RNF11</i>	ENSG00000123091	2.69291426	5.404E-05	0.00336458
<i>SHC4</i>	ENSG00000185634	5.42159542	1.3251E-07	6.895E-05	<i>ST3GAL4</i>	ENSG00000110080	2.68628238	5.9963E-05	0.0035512
<i>GPR143</i>	ENSG00000101850	5.30612346	8.2934E-10	4.0276E-06	<i>IFI6</i>	ENSG00000126709	2.68345916	1.0916E-05	0.00128976

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<i>CDH19</i>	ENSG00000071991	5.06564694	2.3409E-07	9.3591E-05	<i>TMEM158</i>	ENSG00000249992	2.67966266	6.2225E-05	0.00359742
<i>SERPINE2</i>	ENSG00000135919	5.02222961	4.1241E-16	6.0085E-12	<i>POU3F1</i>	ENSG00000185668	2.66904781	0.00071205	0.01896493
<i>MPZ</i>	ENSG00000158887	4.89856844	1.1368E-05	0.00130408	<i>CTTNBP2</i>	ENSG00000077063	2.66885417	8.7381E-05	0.00457931
<i>PTPRZ1</i>	ENSG00000106278	4.89544747	3.2606E-06	0.00054203	<i>PLXNA4</i>	ENSG00000221866	2.66709234	0.00275999	0.04341964
<i>RPPH1</i>	ENSG00000277209	4.89319776	3.1388E-06	0.00054203	<i>TOGARAM1</i>	ENSG00000198718	2.66519594	0.0001565	0.00697101
<i>C10orf90</i>	ENSG00000154493	4.88611984	2.8053E-05	0.00220238	<i>CBARP</i>	ENSG00000099625	2.66361239	0.0002867	0.01045044
<i>KRT7</i>	ENSG00000135480	4.84430443	6.4084E-05	0.00366131	<i>CDKN2A</i>	ENSG00000147889	2.66054847	6.9472E-05	0.00389285
<i>LICAM</i>	ENSG00000198910	4.81006124	5.7922E-08	4.2193E-05	<i>GAMT</i>	ENSG00000130005	2.65788644	0.00050903	0.01529097
<i>ABITRAM</i>	ENSG00000119328	4.80063505	3.5458E-06	0.00056247	<i>MIS18A</i>	ENSG00000159055	2.65315652	0.00080577	0.02055909
<i>TYR</i>	ENSG00000077498	4.76461083	0.00029845	0.01070955	<i>ATAD2</i>	ENSG00000156802	2.64665953	0.00018238	0.00764114
<i>FOXD3-AS1</i>	ENSG00000230798	4.74146963	1.0142E-07	5.5727E-05	<i>SNTA1</i>	ENSG00000101400	2.64424209	0.00124522	0.02761289
<i>ALX1</i>	ENSG00000180318	4.68490903	2.1417E-07	9.3591E-05	<i>SOX13</i>	ENSG00000143842	2.63720177	0.00026107	0.00980284
<i>MLA</i>	ENSG00000261857	4.66836443	6.3374E-09	9.233E-06	<i>ALDH1A3</i>	ENSG00000184254	2.62856912	0.00037936	0.01239657
<i>NSG1</i>	ENSG00000168824	4.61688386	4.0362E-08	3.3965E-05	<i>ACOT7</i>	ENSG00000097021	2.62796202	2.4993E-05	0.00201173
<i>PLXNB3</i>	ENSG00000198753	4.53875496	9.3643E-06	0.00116605	<i>EGFL8</i>	ENSG00000241404	2.62680992	7.3761E-05	0.00403994
<i>TPPP</i>	ENSG00000171368	4.53699353	1.761E-05	0.0016552	<i>GRAMD2B</i>	ENSG00000155324	2.61188222	0.0002393	0.00919878
<i>FAM149A</i>	ENSG00000109794	4.5210416	2.2682E-05	0.00186828	<i>MFS12</i>	ENSG00000161091	2.60700063	7.9334E-05	0.00426499
<i>SOX10</i>	ENSG00000100146	4.48818227	1.9589E-05	0.00170893	<i>PHACTR1</i>	ENSG00000112137	2.60010212	0.0003944	0.0126517
<i>PMEL</i>	ENSG00000185664	4.47648824	1.6514E-05	0.00159881	<i>TTC39A</i>	ENSG00000085831	2.59981477	0.00063738	0.01773706
<i>NECAB3</i>	ENSG00000125967	4.45566754	1.082E-06	0.00027178	<i>ATP2B4</i>	ENSG00000058668	2.59913303	0.000321	0.01121509
<i>DDK1</i>	ENSG00000107984	4.36701855	8.2615E-08	5.0151E-05	<i>ETV5</i>	ENSG00000244405	2.59859499	3.1896E-05	0.00243776
<i>PLP1</i>	ENSG00000123560	4.32573844	1.5561E-05	0.00157385	<i>DSN1</i>	ENSG00000149636	2.59670371	0.00092899	0.0223721
<i>CSPG4</i>	ENSG00000173546	4.30176932	3.6786E-08	3.3496E-05	<i>SPATA6</i>	ENSG00000132122	2.59342578	2.2826E-05	0.00186828
<i>ERBB3</i>	ENSG00000065361	4.27721757	5.6729E-06	0.00077541	<i>ATPIA1</i>	ENSG00000163399	2.58057306	6.9066E-07	0.0001973
<i>FOSL1</i>	ENSG00000175592	4.27263364	9.3895E-09	1.2436E-05	<i>MYCBP</i>	ENSG00000214114	2.57646079	0.0019038	0.03509527
<i>SLC24A5</i>	ENSG00000188467	4.26894619	5.9542E-05	0.00354068	<i>PLAT</i>	ENSG00000104368	2.57634441	4.2454E-05	0.00289022
<i>TSHR</i>	ENSG00000165409	4.25822171	0.00044893	0.01394551	<i>ABHD6</i>	ENSG00000163686	2.57059035	0.00015237	0.00685147
<i>PRAME</i>	ENSG00000185686	4.21316193	3.4368E-06	0.00055635	<i>CNIH3</i>	ENSG00000143786	2.56309574	0.00126436	0.02794017
<i>MIR3142HG</i>	ENSG00000253522	4.20799074	1.9696E-06	0.00038708	<i>VARS2</i>	ENSG00000137411	2.55818713	0.00102046	0.02401796
<i>GPM6B</i>	ENSG00000046653	4.20596835	4.0597E-09	7.6422E-06	<i>LAPTM4B</i>	ENSG00000104341	2.55188416	1.1234E-05	0.0012989
<i>SLC13A3</i>	ENSG00000158296	4.16727226	1.816E-05	0.00166398	<i>FHL3</i>	ENSG00000183386	2.55049871	0.0027067	0.04316543
<i>RAB17</i>	ENSG00000124839	4.16667362	9.5373E-06	0.00116764	<i>TUBB2B</i>	ENSG00000137285	2.54666738	0.00018252	0.00764114
<i>CACHD1</i>	ENSG00000158966	4.14583012	3.2783E-05	0.00244928	<i>MOK</i>	ENSG00000080823	2.53960876	0.00013703	0.00637817
<i>OPRL1</i>	ENSG00000125510	4.11214713	4.58E-05	0.00300166	<i>MFAP3L</i>	ENSG00000198948	2.53123692	0.00029192	0.01057968
<i>REEP6</i>	ENSG00000115255	4.09166981	2.4221E-06	0.00044994	<i>KIRREL1</i>	ENSG00000183853	2.53086537	0.00015742	0.00697101
<i>HARS2</i>	ENSG00000112855	4.06732083	1.1172E-05	0.0012989	<i>PHLDA1</i>	ENSG00000139289	2.52796054	3.274E-06	0.00054203
<i>SCN8A</i>	ENSG00000196876	4.05766399	6.0818E-05	0.00355846	<i>ARL4D</i>	ENSG00000175906	2.52680103	0.00176194	0.03368736
<i>NRCAM</i>	ENSG00000091129	4.02016054	1.7404E-06	0.0003649	<i>ARHGEF40</i>	ENSG00000165801	2.52386471	0.00029	0.01053606
<i>PAX3</i>	ENSG00000135903	4.00615269	1.9816E-05	0.00171846	<i>RTKN</i>	ENSG00000114993	2.51673861	9.4631E-06	0.00116764
<i>LYPD1</i>	ENSG00000150551	3.9921745	2.6125E-07	9.7592E-05	<i>LINGO1</i>	ENSG00000169783	2.51194648	0.0009304	0.0223721
<i>NPFFR1</i>	ENSG00000148734	3.95744425	0.00217321	0.03759433	<i>TRMT61B</i>	ENSG00000171103	2.51142016	0.00054651	0.01614422
<i>LZTS1</i>	ENSG00000061337	3.90249561	6.7653E-08	4.6935E-05	<i>TUBB3</i>	ENSG00000258947	2.50681527	0.00015923	0.00700839
<i>SLC22A4</i>	ENSG00000197208	3.9003379	0.00017633	0.00746808	<i>ARHGAP39</i>	ENSG00000147799	2.49899561	0.00092847	0.0223721
<i>ETV4</i>	ENSG00000175832	3.84058776	1.6748E-06	0.00036418	<i>PICK1</i>	ENSG00000100151	2.49533279	0.00059464	0.01715502
<i>RETRREG1</i>	ENSG00000154153	3.82991233	1.5772E-05	0.00157385	<i>DAG1</i>	ENSG00000173402	2.49129536	0.00014695	0.00671113
<i>ANLN</i>	ENSG00000011426	3.80305654	1.0718E-06	0.00027178	<i>ASB9</i>	ENSG00000102048	2.48834689	0.00165346	0.03281913
<i>SCG2</i>	ENSG00000171951	3.79527132	1.5376E-05	0.00157385	<i>ARNT2</i>	ENSG00000172379	2.48572616	0.00037603	0.01233866
<i>LRRC20</i>	ENSG00000172731	3.79420407	5.5588E-05	0.00342193	<i>GLMN</i>	ENSG00000174842	2.48415135	0.0003554	0.01187713
<i>LYRM4-AS1</i>	ENSG00000272142	3.79176298	1.7873E-05	0.00166398	<i>CDK2</i>	ENSG00000123374	2.48323216	0.0001428	0.00658369
<i>NGFR</i>	ENSG00000064300	3.78281615	1.4295E-05	0.00151564	<i>INPP5F</i>	ENSG00000198825	2.47909556	2.6572E-05	0.002114
<i>IGSF3</i>	ENSG00000143061	3.77397467	8.4462E-06	0.00107003	<i>MORN2</i>	ENSG00000188010	2.47830593	0.00028365	0.01042482
<i>BCHE</i>	ENSG00000114200	3.75636161	5.0333E-06	0.0007333	<i>ZNF561</i>	ENSG00000171469	2.46764405	0.00020307	0.00833374
<i>S100B</i>	ENSG00000160307	3.75345834	2.3052E-09	7.6422E-06	<i>ACACA</i>	ENSG00000278540	2.46739924	0.00047285	0.01459531
<i>MLANA</i>	ENSG00000120215	3.74575526	0.00022142	0.00883817	<i>SORCS1</i>	ENSG00000108018	2.46717846	0.00187804	0.03489936
<i>PC</i>	ENSG00000173599	3.7457036	2.3578E-05	0.00191905	<i>FAM161A</i>	ENSG00000170264	2.46556393	0.00149539	0.03087663
<i>BRPF3</i>	ENSG00000096070	3.74140306	2.9559E-05	0.00229064	<i>SHROOM2</i>	ENSG00000146950	2.46495795	0.00169175	0.03296894
<i>S100A1</i>	ENSG00000160678	3.71650816	7.803E-05	0.00422608	<i>SYCP2</i>	ENSG00000196074	2.464353	0.00162464	0.03252086
<i>NT5M</i>	ENSG00000205309	3.70864288	5.9387E-05	0.00354068	<i>BCKDHB</i>	ENSG00000083123	2.4609156	0.00094424	0.02255175
<i>BAALC</i>	ENSG00000164929	3.69521499	3.4581E-07	0.00011717	<i>UCK2</i>	ENSG00000143179	2.45671354	0.00036281	0.01206792
<i>MLPH</i>	ENSG00000115648	3.68233435	3.8739E-09	7.6422E-06	<i>GAREM2</i>	ENSG00000157833	2.45612451	0.00123697	0.02759784
<i>SHISA2</i>	ENSG00000180730	3.65773123	1.9359E-05	0.00169908	<i>MAPRE3</i>	ENSG00000084764	2.45556293	0.00024943	0.00943873
<i>TEX9</i>	ENSG00000151575	3.6510886	0.00014525	0.00665439	<i>CDK20</i>	ENSG00000156345	2.45453409	0.00183066	0.03461117
<i>MYO5B</i>	ENSG00000167306	3.65074579	0.00016113	0.00704956	<i>GEMIN8</i>	ENSG00000046647	2.45405608	0.00089017	0.02175996
<i>LTBR2</i>	ENSG00000213906	3.64723168	0.00012203	0.00579445	<i>EFNB3</i>	ENSG00000108947	2.45165186	0.00093057	0.0223721
<i>TRPM1</i>	ENSG00000134160	3.64600386	0.00033452	0.01151756	<i>EDA</i>	ENSG00000158813	2.44045472	0.00309169	0.04610324
<i>ASPHD1</i>	ENSG00000174939	3.61963429	1.0977E-05	0.00128976	<i>SGCD</i>	ENSG00000170624	2.43575286	0.00017344	0.0073886
<i>SEZ6L2</i>	ENSG00000174938	3.58163222	1.8253E-06	0.00037454	<i>SNCA</i>	ENSG00000145335	2.4340732	0.00015018	0.00677405
<i>SGCB</i>	ENSG00000163069	3.57773873	1.4189E-06	0.00032812	<i>METAP1D</i>	ENSG00000172878	2.4304816	0.00062231	0.01753668
<i>AATK</i>	ENSG00000181409	3.56723424	1.993E-06	0.00038708	<i>TMEM106C</i>	ENSG00000134291	2.42988182	0.0001624	0.00708397
<i>MELTF</i>	ENSG00000163975	3.55567533	3.5822E-05	0.0026226	<i>AIF1L</i>	ENSG00000126878	2.42475794	0.00039512	0.0126517
<i>PYGM</i>	ENSG00000068976	3.530298	0.0006168	0.01748272	<i>DUSP18</i>	ENSG00000167065	2.4128791	0.00093715	0.02245607
<i>PHLDA2</i>	ENSG00000181649	3.52001159	7.2381E-08	4.7933E-05	<i>B4GALT6</i>	ENSG00000118276	2.41095173	0.0003567	0.01189188

Neoadjuvant Intratumoral Vidutolimod and Nivolumab in High-Risk Resectable Melanoma

<i>GPRIN1</i>	ENSG00000169258	3.49427925	4.7161E-06	0.00070285	<i>SLC4A3</i>	ENSG00000114923	2.40948772	0.00032238	0.01123619
<i>TIMM44</i>	ENSG00000104980	3.49385578	1.6115E-05	0.00158686	<i>ST3GAL6</i>	ENSG00000064225	2.40693623	1.8234E-05	0.00166398
<i>KRT8</i>	ENSG00000170421	3.4931805	9.1025E-05	0.00471219	<i>STXBP6</i>	ENSG00000168952	2.39837504	0.00092697	0.0223721
<i>NLE1</i>	ENSG00000073536	3.48609865	5.3278E-06	0.00075468	<i>TTI2</i>	ENSG00000129696	2.39669965	0.00248079	0.04070108
<i>CADM4</i>	ENSG00000105767	3.47803963	3.9805E-06	0.00060915	<i>PARS2</i>	ENSG00000162396	2.3945248	0.0006723	0.01822671
<i>GJB1</i>	ENSG00000169562	3.46807862	0.00042845	0.01348194	<i>IL17RC</i>	ENSG00000163702	2.39395862	0.0019639	0.03585478
<i>TNNT1</i>	ENSG00000105048	3.45086641	0.00044764	0.01393506	<i>H1-2</i>	ENSG00000187837	2.38004343	0.00137452	0.02931964
<i>TFAP2A</i>	ENSG00000137203	3.44571235	4.2875E-05	0.00290533	<i>KCTD21</i>	ENSG00000188997	2.37795823	0.00085836	0.02145024
<i>TRIM63</i>	ENSG00000158022	3.42937451	0.00017546	0.00745262	<i>STX1A</i>	ENSG00000106089	2.3727325	0.00047732	0.01464008
<i>IGF2BP2</i>	ENSG00000073792	3.42904677	4.721E-09	7.6422E-06	<i>NEO1</i>	ENSG00000067141	2.37119072	0.00110794	0.02566221
<i>SEPTIN3</i>	ENSG00000100167	3.42019061	3.8306E-05	0.00270254	<i>SYNM</i>	ENSG00000182253	2.36378196	0.00039378	0.0126517
<i>TMEM99</i>	ENSG00000167920	3.41395243	4.5945E-05	0.00300166	<i>NRBP2</i>	ENSG00000185189	2.3567019	0.00057359	0.01674678
<i>CCN3</i>	ENSG00000136999	3.40907171	5.5547E-05	0.00342193	<i>MET</i>	ENSG00000105976	2.35357057	0.00054635	0.01614422
<i>PCDHGA12</i>	ENSG00000253159	3.40240299	0.00088472	0.02173254	<i>YIPF3</i>	ENSG00000137207	2.3516667	0.00032639	0.0113218
<i>STK32A</i>	ENSG00000169302	3.40207038	8.1605E-05	0.00431988	<i>AK1</i>	ENSG00000106992	2.35069137	0.00087736	0.02159166
<i>SEMA3B</i>	ENSG00000012171	3.39287076	0.00022404	0.0089079	<i>METRN</i>	ENSG00000103260	2.3503354	6.8553E-05	0.00385618
<i>TNFRSF19</i>	ENSG00000127863	3.38870701	3.8295E-05	0.00270254	<i>DBNDD1</i>	ENSG00000003249	2.34873297	0.00319153	0.04715758
<i>BMS1P23</i>	ENSG00000286156	3.38034144	5.9227E-05	0.00354068	<i>TGIF1</i>	ENSG00000177426	2.34048837	0.00094596	0.022556
<i>SAMD4A</i>	ENSG00000020577	3.37210782	5.0941E-06	0.00073481	<i>NIFK</i>	ENSG00000155438	2.33429546	0.00131003	0.02844382
<i>HAUS4</i>	ENSG00000092036	3.37061995	9.3942E-05	0.00483621	<i>ADCY1</i>	ENSG00000164742	2.33384375	0.00179881	0.03416807
<i>CYTH3</i>	ENSG00000008256	3.36312118	1.8617E-05	0.00166398	<i>ZFP41</i>	ENSG00000181638	2.33176552	0.00050128	0.01512699
<i>RCAN1</i>	ENSG00000159200	3.35388519	1.0328E-07	5.5727E-05	<i>EFNA4</i>	ENSG00000243364	2.33175105	0.00185323	0.03470356
<i>ADAM23</i>	ENSG00000114948	3.34787266	4.7278E-06	0.00070285	<i>IFT81</i>	ENSG00000122970	2.33067191	4.4643E-05	0.00299294
<i>ITGA3</i>	ENSG00000005884	3.34537477	2.3434E-06	0.0004434	<i>ACSL3</i>	ENSG00000123983	2.31948702	4.8636E-07	0.00015404
<i>SLC6A8</i>	ENSG00000130821	3.34396831	2.8798E-07	9.9895E-05	<i>TNIP2</i>	ENSG00000168884	2.31875943	0.00308102	0.04610324
<i>RIPK4</i>	ENSG00000183421	3.3173694	0.00035384	0.01187713	<i>ITGA2</i>	ENSG00000164171	2.31039465	3.7267E-05	0.00266146
<i>FRMD3</i>	ENSG00000172159	3.29758927	0.0001221	0.00579445	<i>MME</i>	ENSG00000196549	2.30588658	0.00323429	0.04747943
<i>ABCB6</i>	ENSG00000115657	3.29198102	0.00028203	0.01042482	<i>CTXN1</i>	ENSG00000178531	2.30525668	0.00233125	0.03953904
<i>TESC</i>	ENSG00000008892	3.27568461	0.00088873	0.02175996	<i>PYGB</i>	ENSG00000100994	2.30375714	0.00031384	0.01104446
<i>LINC01679</i>	ENSG00000237989	3.27457616	0.00013802	0.00640392	<i>QPCT</i>	ENSG00000115828	2.29796314	0.00063902	0.01773706
<i>FXYD3</i>	ENSG00000089356	3.26940112	0.00199927	0.03604872	<i>PPFIBP1</i>	ENSG00000110841	2.29593722	3.6663E-05	0.00265687
<i>IPO13</i>	ENSG00000117408	3.2680701	5.1946E-05	0.00329045	<i>CMBL</i>	ENSG00000164237	2.295711	0.0028347	0.04399455
<i>C12orf29</i>	ENSG00000133641	3.26462664	0.00010975	0.00533706	<i>EDNRB</i>	ENSG00000136160	2.29418608	0.00221109	0.03794265
<i>ST6GALNAC2</i>	ENSG000000070731	3.26009976	0.00049736	0.01512699	<i>PLK2</i>	ENSG00000145632	2.28639749	7.3389E-05	0.00403476
<i>SOX2</i>	ENSG00000181449	3.22773885	0.00170382	0.03305325	<i>GPR89B</i>	ENSG00000188092	2.28429709	0.00111508	0.02572358
<i>FHDC1</i>	ENSG00000137460	3.22344271	7.9236E-05	0.00426499	<i>UGDH</i>	ENSG00000109814	2.28422341	0.00024516	0.00939917
<i>IGSF11</i>	ENSG00000144847	3.21064903	0.00151953	0.03115111	<i>NUSAP1</i>	ENSG00000137804	2.28415762	0.0011361	0.02606583
<i>COL9A3</i>	ENSG00000092758	3.19793614	5.236E-05	0.00329418	<i>KCTD15</i>	ENSG00000153885	2.26865213	8.4949E-05	0.00446793
<i>SLITRK2</i>	ENSG00000185985	3.18241184	0.00061966	0.01749566	<i>ZNF106</i>	ENSG00000103994	2.26791782	1.8506E-05	0.00166398
<i>FAR2</i>	ENSG00000064763	3.18178929	5.3727E-06	0.00075468	<i>PIR</i>	ENSG00000087842	2.26621774	0.00034487	0.01170953
<i>KRT18</i>	ENSG00000111057	3.17857926	0.00076957	0.01991447	<i>AVEN</i>	ENSG00000169857	2.25861316	0.00187696	0.03489936
<i>PFN2</i>	ENSG00000070087	3.17101093	4.0279E-10	2.9341E-06	<i>HEATR1</i>	ENSG00000119285	2.24475467	0.00058134	0.01687199
<i>ABCB5</i>	ENSG00000004846	3.1573757	0.00038819	0.0126517	<i>MC1R</i>	ENSG00000258839	2.24049304	1.0736E-05	0.00128203
<i>DDR1</i>	ENSG00000204580	3.15498286	5.4754E-06	0.00075972	<i>SLC25A4</i>	ENSG00000151729	2.24035956	3.702E-05	0.00265687
<i>MYG1</i>	ENSG00000139637	3.15246993	9.7507E-05	0.00497786	<i>CAMK2N1</i>	ENSG00000162545	2.23818899	0.00023858	0.00919551
<i>PPP1R9A</i>	ENSG00000158528	3.14581088	0.00072919	0.01923231	<i>CTDSPL</i>	ENSG00000144677	2.23752726	2.4366E-05	0.00197213
<i>KCNN4</i>	ENSG00000104783	3.14077042	2.4398E-06	0.00044994	<i>CA5BP1</i>	ENSG00000186312	2.23597323	0.00142214	0.03007135
<i>APOD</i>	ENSG00000189058	3.13136787	3.5756E-05	0.0026226	<i>SRPX</i>	ENSG00000101955	2.23447174	0.00127149	0.02794017
<i>RAB38</i>	ENSG00000123892	3.12677943	2.0694E-05	0.001756	<i>SLC4A5</i>	ENSG00000188687	2.23288438	0.00257267	0.04169207
<i>TMEM17</i>	ENSG00000186889	3.11506823	0.00010466	0.00516855	<i>SERPINA3</i>	ENSG00000196136	2.23097504	0.0034156	0.04936693
<i>STXBP1</i>	ENSG00000136854	3.1021547	4.5354E-07	0.00014684	<i>ITGB3</i>	ENSG00000259207	2.22740204	0.00142665	0.03010512
<i>PERP</i>	ENSG00000112378	3.10084989	0.00102218	0.02401957	<i>LYST</i>	ENSG00000143669	2.22625208	6.4691E-06	0.00087267
<i>LOXL4</i>	ENSG00000138131	3.10073286	0.00010063	0.00502062	<i>SLC5A3</i>	ENSG00000198743	2.22512847	3.8398E-05	0.00270254
<i>KIF18A</i>	ENSG00000121621	3.07046429	7.1918E-05	0.00398391	<i>SLC26A2</i>	ENSG00000155850	2.21861781	1.1561E-05	0.00131585
<i>CABLES1</i>	ENSG00000134508	3.06281025	8.0116E-06	0.00103959	<i>KCNIP3</i>	ENSG00000115041	2.21521904	0.00247294	0.04066403
<i>DIPK1B</i>	ENSG00000165716	3.05788254	0.00022083	0.00883817	<i>NME1</i>	ENSG00000239672	2.21074068	0.00023202	0.00903207
<i>PDIA3P1</i>	ENSG00000180867	3.0559616	6.6414E-05	0.00376493	<i>WDSUB1</i>	ENSG00000196151	2.20828011	0.0018806	0.03490251
<i>ADGRG1</i>	ENSG00000205336	3.05219991	3.163E-08	3.0721E-05	<i>H2AC6</i>	ENSG00000180573	2.20620752	5.3617E-05	0.00335256
<i>SPRY4</i>	ENSG00000187678	3.03525081	1.7088E-05	0.00162719	<i>CEP170B</i>	ENSG00000099814	2.20551576	0.00259738	0.0419526
<i>TRIB3</i>	ENSG00000101255	3.0168858	3.2582E-05	0.00244683	<i>JRK</i>	ENSG00000234616	2.20533111	0.00116675	0.02651844
<i>DCBLD2</i>	ENSG00000057019	3.00945532	1.2154E-05	0.00135165	<i>VARSI</i>	ENSG00000204394	2.2042523	0.00138293	0.02935159
<i>DEPDC1</i>	ENSG00000024526	3.00527847	0.00090501	0.02201177	<i>DIS3L</i>	ENSG00000166938	2.20266999	0.00074254	0.01949213
<i>SHISA1</i>	ENSG00000138944	2.99550522	0.00217531	0.03759433	<i>KIF9</i>	ENSG00000088727	2.20102792	0.00235656	0.03964513
<i>PSPC1</i>	ENSG00000121390	2.99157609	0.00041357	0.01314286	<i>ZNF212</i>	ENSG00000170260	2.19969206	0.00209924	0.03687805
<i>GPR132</i>	ENSG00000183484	2.95964214	0.00251455	0.04116229	<i>KAZN</i>	ENSG00000189337	2.19401354	7.9987E-06	0.00103959
<i>CDI09</i>	ENSG00000156535	2.94266309	2.0192E-06	0.00038708	<i>BAE2</i>	ENSG00000182240	2.18892489	0.00017741	0.00749183
<i>NUF2</i>	ENSG00000143228	2.94153481	0.00028553	0.01045044	<i>CLDN12</i>	ENSG00000157224	2.18610372	0.00067819	0.01826339
<i>SLC2A13</i>	ENSG00000151229	2.94086958	0.0002676	0.0099965	<i>PDHX</i>	ENSG00000110435	2.17334279	0.00050446	0.01518479
<i>COL11A2</i>	ENSG00000204248	2.9322786	0.00018225	0.00764114	<i>ETNK2</i>	ENSG00000143845	2.1657703	0.00148935	0.03087602
<i>ITGB8</i>	ENSG00000105855	2.92821146	0.00022445	0.0089079	<i>ABHD17C</i>	ENSG000000136379	2.14924972	0.00347752	0.04971936
<i>NES</i>	ENSG00000132688	2.924094	9.121E-05	0.00471219	<i>C2orf88</i>	ENSG00000187699	2.14340733	0.00245698	0.04049291
<i>FAM72C</i>	ENSG00000263513	2.9223917	0.00182343	0.03454566	<i>KHDRBS3</i>	ENSG00000131773	2.12786379	0.00118257	0.02679445

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<i>DUSP4</i>	ENSG00000120875	2.92004856	1.7697E-07	8.3168E-05	<i>PIMREG</i>	ENSG00000129195	2.12596688	0.00174922	0.03357633
<i>FBXO45</i>	ENSG00000174013	2.91774257	5.8359E-05	0.00354068	<i>TRAPPC13</i>	ENSG00000113597	2.12534669	0.00201671	0.03621414
<i>GDF15</i>	ENSG00000130513	2.91255009	0.00282946	0.04399407	<i>ARHGAP5-AS1</i>	ENSG00000258655	2.1248878	0.00123507	0.02759777
<i>NPTX2</i>	ENSG00000106236	2.88959402	0.00287544	0.04447161	<i>ZNF770</i>	ENSG00000198146	2.12035574	0.00077536	0.01999334
<i>GPR153</i>	ENSG00000158292	2.88129636	8.9179E-06	0.00112004	<i>MMP17</i>	ENSG00000198598	2.11712711	0.00137848	0.02935159
<i>DIRAS1</i>	ENSG00000176490	2.88119328	0.0005015	0.01512699	<i>PLEKHB1</i>	ENSG00000021300	2.10153279	0.00186762	0.03483904
<i>POMGNT1</i>	ENSG00000085998	2.88065773	1.4983E-06	0.00033732	<i>STX3</i>	ENSG00000166900	2.10141546	0.00023194	0.00903207
<i>NANOS1</i>	ENSG00000188613	2.88037531	3.0207E-05	0.00232851	<i>IGF1R</i>	ENSG00000140443	2.10105404	0.00051893	0.01549245
<i>RPAP1</i>	ENSG00000103932	2.86900583	0.00023095	0.00903207	<i>TRMT10A</i>	ENSG00000145331	2.09817289	0.00203081	0.03632139
<i>LDHD</i>	ENSG00000166816	2.86699948	0.00109209	0.02533537	<i>GNG12</i>	ENSG00000172380	2.09757694	2.6699E-05	0.002114
<i>PLEKHA4</i>	ENSG00000105559	2.85726977	1.1772E-05	0.00132954	<i>RND3</i>	ENSG00000115963	2.0919329	0.0002332	0.0090359
<i>MITF</i>	ENSG00000187098	2.84691454	3.255E-09	7.6422E-06	<i>NSMF</i>	ENSG00000165802	2.09175943	0.00164947	0.03279787
<i>GCNT2</i>	ENSG00000111846	2.83808362	4.0201E-05	0.00280235	<i>PRKD1</i>	ENSG00000184304	2.08808019	0.00185202	0.03470356
<i>PRKCI</i>	ENSG00000163558	2.82819615	4.181E-05	0.00287327	<i>DHCR24</i>	ENSG00000116133	2.08117379	0.0017086	0.03310192
<i>SPOCK1</i>	ENSG00000152377	2.82786287	1.652E-05	0.00159881	<i>FGD1</i>	ENSG00000102302	2.08000462	0.00295084	0.04494448
<i>ETHE1</i>	ENSG00000105755	2.82604067	0.00023248	0.00903207	<i>ILIRAP</i>	ENSG00000196083	2.0741351	0.00212271	0.03707836
<i>TFPI2</i>	ENSG00000105825	2.82461312	0.000313	0.01104157	<i>TIMP3</i>	ENSG00000100234	2.07008776	0.00086744	0.02145626
<i>ASAP2</i>	ENSG00000151693	2.82228674	0.00028692	0.01045044	<i>SNHG16</i>	ENSG00000163597	2.06719298	1.612E-05	0.00158686
<i>SLC7A5</i>	ENSG00000103257	2.81934812	0.00039254	0.0126517	<i>PNMA6A</i>	ENSG00000235961	2.06228888	0.00342292	0.04936723
<i>PIP4K2B</i>	ENSG00000276293	2.80952102	0.00016078	0.00704956	<i>ITPR3</i>	ENSG00000096433	2.05353155	0.00073001	0.01923231
<i>FZD6</i>	ENSG00000164930	2.80909116	9.9649E-05	0.00501981	<i>TRIB2</i>	ENSG00000071575	2.052549	0.00065171	0.01801666
<i>CELSR2</i>	ENSG00000143126	2.80715812	0.00011955	0.00572935	<i>RNF144A</i>	ENSG00000151692	2.05110674	0.00205229	0.0364025
<i>CCND1</i>	ENSG00000110092	2.80687795	1.4815E-05	0.00154172	<i>BEX3</i>	ENSG00000166681	2.04853743	0.00075427	0.01961946
<i>FMN1</i>	ENSG00000248905	2.79876297	6.1301E-07	0.0001877	<i>PLEKHG4</i>	ENSG00000196155	2.0484884	0.00345531	0.04954762
<i>TROAP</i>	ENSG00000135451	2.79459934	0.00062855	0.01764435	<i>PPIE</i>	ENSG00000084072	2.04536321	0.00185979	0.03473753
<i>SLC4A1AP</i>	ENSG00000163798	2.79247813	6.4415E-05	0.00366584	<i>NPAS2</i>	ENSG00000170485	2.03795794	0.00152238	0.03115111
<i>LMBR1</i>	ENSG00000105983	2.79054078	0.0003456	0.01170953	<i>GTF2H2C</i>	ENSG00000183474	2.03795685	0.00201839	0.03621414
<i>CENPA</i>	ENSG00000115163	2.78091732	0.00079404	0.02033097	<i>KRIT1</i>	ENSG00000001631	2.02753015	0.00234278	0.03955033
<i>PLEKHH1</i>	ENSG00000054690	2.75097044	0.00063309	0.01770894	<i>KANK1</i>	ENSG00000107104	2.02251914	0.00226718	0.03858703
<i>BMP8B</i>	ENSG00000116985	2.73942064	0.00046932	0.01451694	<i>SLC52A2</i>	ENSG00000185803	2.01610801	0.00299752	0.04544313
<i>IL17D</i>	ENSG00000172458	2.73281476	0.00023138	0.00903207	<i>PCBP4</i>	ENSG00000090097	2.00643573	0.00108826	0.02528697
<i>AJM1</i>	ENSG00000232434	2.73203104	0.00144072	0.03033209	<i>STAG3L2</i>	ENSG00000277072	2.00342511	0.00117376	0.0266362
<i>PPT2</i>	ENSG00000221988	2.72502032	4.0139E-06	0.00060915					
<i>FAM83H</i>	ENSG00000180921	2.7232849	0.00131823	0.02857935					
<i>LY6K</i>	ENSG00000160886	2.72326598	0.00276204	0.04341964					
<i>PEG10</i>	ENSG00000242265	2.7205267	0.00049914	0.01512699					
<i>MYO10</i>	ENSG00000145555	2.71154901	1.9211E-06	0.00038708					
<i>GPC1</i>	ENSG00000063660	2.70807479	3.7005E-05	0.00265687					

Supplementary Table 10: Significant DEGs in pNR Samples (Post- vs. Pre- Treatment) Plotted in Extended**Data Fig. 8**

Gene Name	Gene ID	Log2FC	Adjusted p value	FDR	Gene Name	Gene ID	Log2FC	Adjusted p value	FDR
DEGs that are upregulated post-treatment									
<i>IGLV6-57</i>	ENSG00000211640	6.559065	5.8268E-06	0.00391579	<i>MIR193BHG</i>	ENSG00000262454	3.0668823	0.00042976	0.03109571
<i>XACT</i>	ENSG00000241743	6.1581504	0.00013547	0.01815712	<i>MIR9-3HG</i>	ENSG00000255571	3.066773	0.00038015	0.02853325
<i>SI00A8</i>	ENSG00000143546	5.7128523	0.00071753	0.04107696	<i>MEIOC</i>	ENSG00000180336	3.0609634	0.00018319	0.01972548
<i>NMNAT3</i>	ENSG00000163864	5.2586305	2.0902E-08	0.00017649	<i>C5AR2</i>	ENSG00000134830	3.0502111	0.00016622	0.0192034
<i>UGDH-AS1</i>	ENSG00000249348	5.2385474	4.6181E-08	0.00025997	<i>WEE2-AS1</i>	ENSG00000228775	3.0216727	0.00015882	0.01902214
<i>ROCK1P1</i>	ENSG00000263006	5.200943	2.695E-06	0.00267723	<i>RTCA-AS1</i>	ENSG00000224616	3.0133698	0.00023452	0.0221281
<i>SULT1B1</i>	ENSG00000173597	5.1378509	2.4215E-06	0.0026629	<i>DRP2</i>	ENSG00000102385	2.9981602	0.0007054	0.04065787
<i>IGHV1-3</i>	ENSG00000211935	4.9078708	3.7577E-06	0.00334	<i>KLRD1</i>	ENSG00000134539	2.9972131	0.00010863	0.01638046
<i>LINC01608</i>	ENSG00000253877	4.8216485	9.8495E-05	0.01599145	<i>ARHGEF26-AS1</i>	ENSG00000243069	2.9898858	0.00079958	0.0428676
<i>IGHV4-39</i>	ENSG00000211959	4.7969139	6.0679E-05	0.01170389	<i>C2orf16</i>	ENSG00000221843	2.9754771	0.00011626	0.0172221
<i>ZNF556</i>	ENSG00000172000	4.661442	3.99E-05	0.009889	<i>FREM1</i>	ENSG00000164946	2.9439694	0.00080883	0.04295459
<i>GRIN2B</i>	ENSG00000273079	4.643724	0.00014072	0.0183303	<i>NUGGC</i>	ENSG00000189233	2.9417903	0.00075054	0.04140655
<i>PCDHA4</i>	ENSG00000204967	4.6243114	7.7259E-06	0.00432381	<i>HSPA1L</i>	ENSG00000204390	2.9417198	0.00014252	0.0183303
<i>CCDC26</i>	ENSG00000229140	4.5658676	7.6791E-05	0.01350876	<i>PYGM</i>	ENSG00000068976	2.9368735	0.00016715	0.0192034
<i>CFAP92</i>	ENSG00000114656	4.5157956	3.7892E-07	0.0015998	<i>AR</i>	ENSG00000169083	2.9367356	0.00031659	0.02533942
<i>IGHV4-61</i>	ENSG00000211970	4.3262979	0.00015838	0.01902214	<i>SSTR2</i>	ENSG00000180616	2.931287	0.00019228	0.01988309
<i>CDRT1</i>	ENSG00000241322	4.3128081	1.1208E-05	0.00512598	<i>PIFO</i>	ENSG00000173947	2.9209853	0.00019296	0.01988309
<i>NEFL</i>	ENSG00000277586	4.2932844	0.00055543	0.03580171	<i>SCOC-AS1</i>	ENSG00000196951	2.913712	0.0007298	0.04122038
<i>MUC3A</i>	ENSG00000169894	4.288927	4.9286E-05	0.01080953	<i>CSMD2</i>	ENSG00000121904	2.9027354	0.00099635	0.04819275
<i>MEFV</i>	ENSG00000103313	4.2793242	2.3223E-06	0.0026629	<i>USHBP1</i>	ENSG00000130307	2.8758739	5.3563E-05	0.01126376
<i>SLC6A1</i>	ENSG00000157103	4.2498798	8.7647E-06	0.00441636	<i>SV2B</i>	ENSG00000185518	2.8679954	0.00034934	0.02706289
<i>TSBP1-AS1</i>	ENSG00000225914	4.2313312	0.00015109	0.01862474	<i>DLG2</i>	ENSG00000150672	2.8519616	0.00091254	0.0453264
<i>SCUBE1</i>	ENSG00000159307	4.2305684	3.6464E-05	0.00959653	<i>MORN3</i>	ENSG00000139714	2.8383525	0.0010206	0.04896575
<i>IGHG4</i>	ENSG00000211892	4.2300996	0.00018247	0.01972548	<i>FAM241A</i>	ENSG00000174749	2.8345025	2.2173E-06	0.0026629
<i>CNTN2</i>	ENSG00000184144	4.2070604	2.2971E-05	0.00718388	<i>CXCL3</i>	ENSG00000163734	2.8275168	0.00096691	0.04700922
<i>SAMD12</i>	ENSG00000177570	4.1504415	6.2604E-06	0.00391579	<i>MAGIX</i>	ENSG00000269313	2.8233057	3.5901E-05	0.00959653
<i>OTOA</i>	ENSG00000155719	4.1404872	5.5369E-07	0.00187014	<i>FOSB</i>	ENSG00000125740	2.8166083	0.00061315	0.03820995
<i>EMBP1</i>	ENSG00000231752	4.120131	5.3688E-06	0.00391579	<i>LINC02731</i>	ENSG00000204241	2.8108321	0.00037601	0.02834827
<i>SCN7A</i>	ENSG00000136546	4.1061635	2.2441E-05	0.00715057	<i>ZC2HC1C</i>	ENSG00000119703	2.7938919	0.0001239	0.01763355
<i>FAM153CP</i>	ENSG00000204677	4.1028576	7.504E-05	0.01333979	<i>CLIC5</i>	ENSG00000112782	2.7733146	0.00019359	0.01988309
<i>LINC01002</i>	ENSG00000136881	4.1015866	2.1864E-05	0.00712062	<i>KIF6</i>	ENSG00000164627	2.7708584	0.00019839	0.01994247
<i>PLIN4</i>	ENSG00000167676	4.0512378	2.4721E-05	0.00726134	<i>LINC00910</i>	ENSG00000188825	2.7705375	0.00012324	0.01763355
<i>IGLC7</i>	ENSG00000211685	4.0232724	0.0007131	0.04096226	<i>TMEM121B</i>	ENSG00000183307	2.7669231	5.5962E-05	0.01138658
<i>EIF1B-AS1</i>	ENSG00000280739	4.0189194	1.7386E-06	0.0026629	<i>ZNF192P1</i>	ENSG00000226314	2.7654264	0.00034594	0.02704736
<i>CATSPERG</i>	ENSG00000099338	4.0029277	3.6964E-06	0.00334	<i>PPIL6</i>	ENSG00000185250	2.75304	0.00029631	0.02452725
<i>JPH2</i>	ENSG00000149596	3.9926016	6.0987E-05	0.01170389	<i>NRSN2-AS1</i>	ENSG00000225377	2.7511142	4.682E-05	0.01054263
<i>PRKAR2A-AS1</i>	ENSG00000224424	3.9901564	4.0932E-06	0.00338382	<i>CDKN2B-AS1</i>	ENSG00000240498	2.7413914	0.00062966	0.03822824
<i>HIF1A-AS3</i>	ENSG00000258667	3.9750657	0.0002757	0.02381501	<i>ADAMTSL3</i>	ENSG00000156218	2.7405954	0.00077544	0.0420836
<i>HELLPAR</i>	ENSG00000281344	3.9626286	0.00056607	0.03634888	<i>ZNF658B</i>	ENSG00000198416	2.7326921	0.00020654	0.02027948
<i>BAT</i>	ENSG00000136881	3.9536199	0.00066948	0.03981061	<i>GPR63</i>	ENSG00000112218	2.7319472	0.00083752	0.04392534
<i>TF</i>	ENSG00000091513	3.9489829	6.6169E-05	0.01227975	<i>PTOV1-AS1</i>	ENSG00000268006	2.7183619	0.00012812	0.01765601
<i>MIR99AHG</i>	ENSG00000215386	3.9381249	1.5782E-05	0.00664815	<i>PAPOLA-DT</i>	ENSG00000260806	2.7063984	0.00029773	0.02452725
<i>ZNF66</i>	ENSG00000160229	3.9262432	1.6636E-05	0.00664815	<i>XK</i>	ENSG00000047597	2.6950451	0.00086387	0.04478719
<i>MYO15A</i>	ENSG00000091536	3.9199416	5.9123E-06	0.00391579	<i>ZBTB16</i>	ENSG00000109906	2.6884655	0.00043086	0.03109571
<i>TRIM73</i>	ENSG00000178809	3.8957244	1.7092E-05	0.00664815	<i>GPD1</i>	ENSG00000167588	2.6735549	0.00025357	0.02319043
<i>LINC01012</i>	ENSG00000281706	3.8818719	0.00012444	0.01763355	<i>ALG1L9P</i>	ENSG00000248671	2.6715207	0.00026397	0.02342183
<i>TNNI1</i>	ENSG00000159173	3.841182	2.4938E-05	0.00726134	<i>POLRMTPI</i>	ENSG00000266066	2.6675134	0.00063155	0.03822824
<i>CACNA1A</i>	ENSG00000141837	3.8256295	9.4149E-07	0.00227142	<i>RNF165</i>	ENSG00000141622	2.6505715	0.00087303	0.04478719
<i>KIF19</i>	ENSG00000196169	3.7858931	4.2932E-06	0.00338382	<i>TAGAP-AS1</i>	ENSG00000271913	2.6464219	0.00068435	0.04004852
<i>STAR</i>	ENSG00000147465	3.6741216	0.00018664	0.01972548	<i>FAM182A</i>	ENSG00000125804	2.6392673	0.0006201	0.03822824
<i>ADAMTS9-AS2</i>	ENSG00000241684	3.6594467	0.00074917	0.04140655	<i>CECR2</i>	ENSG00000099954	2.6327569	0.00094756	0.04679085
<i>IGLV1-44</i>	ENSG00000211651	3.6231449	0.00087454	0.04478719	<i>RNF139-AS1</i>	ENSG00000245149	2.6071653	0.00035812	0.02744087
<i>TNIP3</i>	ENSG00000050730	3.6214882	9.0932E-05	0.0150555	<i>JSRP1</i>	ENSG00000167476	2.6042535	0.00029076	0.02442942
<i>COLCA1</i>	ENSG00000196167	3.6107303	0.0001391	0.0183303	<i>CCDC39</i>	ENSG00000284862	2.6035719	0.00028686	0.02430685
<i>DHH</i>	ENSG00000139549	3.5903679	9.376E-06	0.00452408	<i>ZBED3-AS1</i>	ENSG00000250802	2.5934151	0.00052662	0.03460524
<i>ESRRG</i>	ENSG00000196482	3.5733991	0.00095614	0.04700922	<i>TCL6</i>	ENSG00000187621	2.5925041	0.00045734	0.0320479
<i>RASSF6</i>	ENSG00000169435	3.5705705	0.00021192	0.02056875	<i>CRIP1</i>	ENSG00000213145	2.5898973	1.9445E-05	0.00684152
<i>DMC1</i>	ENSG00000100206	3.5694023	1.1231E-05	0.00512598	<i>LINC02202</i>	ENSG00000245812	2.586646	0.00049755	0.03361025
<i>EMX2OS</i>	ENSG00000229847	3.5618345	3.9628E-05	0.009889	<i>MEI1</i>	ENSG00000167077	2.5712286	0.00021124	0.02056875
<i>CFAP251</i>	ENSG00000158023	3.5469911	5.389E-05	0.01126376	<i>LINC02611</i>	ENSG00000226791	2.5683939	0.00043909	0.03123289

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<i>RND1</i>	ENSG00000172602	3.5444173	4.4081E-06	0.00338382	<i>TMED2-DT</i>	ENSG00000247373	2.5461831	0.00075271	0.04140655
<i>STXP5-AS1</i>	ENSG00000233452	3.5063995	0.00010663	0.01636323	<i>SRRM2-AS1</i>	ENSG00000205913	2.5374926	0.00082108	0.04333231
<i>ACBD7</i>	ENSG00000176244	3.489079	4.5909E-05	0.01054263	<i>LAMTOR5-AS1</i>	ENSG00000224699	2.5334572	0.00044756	0.03162518
<i>ASIC4</i>	ENSG00000072182	3.4826328	0.00067282	0.0398689	<i>DIO2</i>	ENSG00000211448	2.5303138	0.00089767	0.04489737
<i>NOX5</i>	ENSG00000255346	3.4821819	0.00027639	0.02381501	<i>ELAPOR1</i>	ENSG00000116299	2.5193035	0.00057137	0.03641264
<i>SOX2-OT</i>	ENSG00000242808	3.4634419	0.00092353	0.04573798	<i>H2BC8</i>	ENSG00000273802	2.515433	0.0007503	0.04140655
<i>HAND2-AS1</i>	ENSG00000237125	3.461093	0.0001763	0.01958835	<i>ESR1</i>	ENSG000000091831	2.5048485	0.0002012	0.02006665
<i>NEK5</i>	ENSG00000197168	3.4349419	3.9889E-05	0.009889	<i>LILRA2</i>	ENSG00000239998	2.5018336	0.00100569	0.04838775
<i>PLIN5</i>	ENSG00000214456	3.4297834	0.00012739	0.01765601	<i>PADI2</i>	ENSG00000117115	2.5009489	0.00046258	0.03228118
<i>CACNB4</i>	ENSG00000182389	3.4142732	5.4024E-05	0.01126376	<i>GPR85</i>	ENSG00000164604	2.5005382	0.00017444	0.01950961
<i>LINC01852</i>	ENSG00000236914	3.406099	6.1867E-05	0.01173948	<i>GRIN3A</i>	ENSG00000198785	2.4872013	0.00057794	0.03669274
<i>IHO1</i>	ENSG00000173421	3.4056852	0.00013496	0.01815712	<i>LINC00654</i>	ENSG00000205181	2.4777259	0.0006218	0.03822824
<i>LINC00882</i>	ENSG00000242759	3.3960902	0.00025404	0.02319043	<i>ZNNT1</i>	ENSG00000261087	2.4689099	0.00062364	0.03822824
<i>PDE4C</i>	ENSG00000105650	3.3935294	0.00051888	0.03460524	<i>PDPR2P</i>	ENSG00000214331	2.4638864	0.00012859	0.01765601
<i>FLJ40194</i>	ENSG00000177369	3.3778787	1.2778E-05	0.00567887	<i>VAMP8</i>	ENSG00000118640	2.4516571	0.00018538	0.01972548
<i>TMEM233</i>	ENSG00000224982	3.3765515	2.1498E-05	0.00712062	<i>PRR34</i>	ENSG00000182257	2.4415751	0.00062505	0.03822824
<i>KCNK12</i>	ENSG00000184261	3.3536768	0.00012007	0.01761618	<i>GTF2IP13</i>	ENSG00000272556	2.4306632	0.00015056	0.01862474
<i>ZNF774</i>	ENSG00000196391	3.3507426	4.0761E-05	0.009889	<i>ARHGAP44</i>	ENSG00000006740	2.4233091	0.00015481	0.0188086
<i>MLXIPL</i>	ENSG00000009950	3.337612	0.00017971	0.01972548	<i>KIF5C</i>	ENSG00000168280	2.4223957	0.00086873	0.04478719
<i>GIPC2</i>	ENSG00000137960	3.3294464	0.00010755	0.01636323	<i>ZNF843</i>	ENSG00000176723	2.4192281	0.00096869	0.04700922
<i>DNMIP51</i>	ENSG00000235370	3.3282834	0.00017179	0.0193409	<i>NR5A2</i>	ENSG00000116833	2.4059432	0.00033443	0.02639185
<i>LINC01694</i>	ENSG00000239922	3.3247595	0.00026102	0.02342183	<i>ODC1-DT</i>	ENSG00000257135	2.3568198	0.00018759	0.01972548
<i>FOXP2</i>	ENSG00000128573	3.3173865	0.00028786	0.02430685	<i>RALY-AS1</i>	ENSG00000285230	2.3362077	0.00014327	0.0183303
<i>HCAR1</i>	ENSG00000196917	3.3097102	2.439E-05	0.00726134	<i>ISG20</i>	ENSG00000172183	2.3356195	0.00026655	0.0234454
<i>AKRIC1</i>	ENSG00000187134	3.3064025	4.8845E-05	0.01080953	<i>MAPT</i>	ENSG00000186868	2.3025775	0.00058342	0.03690186
<i>LINC00891</i>	ENSG00000281852	3.2990746	0.00016251	0.0192034	<i>H4-16</i>	ENSG00000197837	2.2920684	0.00024881	0.02319043
<i>IGLC2</i>	ENSG00000211677	3.2984492	0.00051757	0.03460524	<i>TBC1D8B</i>	ENSG00000133138	2.2893263	0.00047078	0.03245093
<i>LINC02076</i>	ENSG00000220161	3.2965832	0.0001832	0.01972548	<i>PPM1F-AS1</i>	ENSG00000224086	2.2757081	0.00088312	0.04478719
<i>ABHD1</i>	ENSG00000143994	3.2821067	0.00023454	0.0221281	<i>KCNJ10</i>	ENSG00000177807	2.2597016	0.00080786	0.04295459
<i>SKIDA1</i>	ENSG00000180592	3.2668344	6.0269E-05	0.01170389	<i>CEBPA-DT</i>	ENSG00000267296	2.2325555	7.2605E-05	0.01304411
<i>ZNF788P</i>	ENSG00000214189	3.2660918	0.00014557	0.01848428	<i>KIAA1328</i>	ENSG00000150477	2.2310148	0.00034401	0.02702129
<i>FAM66D</i>	ENSG00000255052	3.263226	0.00010481	0.01623887	<i>FAIM2</i>	ENSG00000135472	2.2224209	0.00096358	0.04700922
<i>ACSL6</i>	ENSG00000164398	3.2594059	8.1098E-05	0.0139754	<i>MCTP2</i>	ENSG00000140563	2.2119508	0.00041218	0.03011883
<i>KLHL31</i>	ENSG00000124743	3.2525513	0.00013978	0.0183303	<i>SLX1A-SULT1A3</i>	ENSG00000213599	2.2078442	0.00035154	0.02710834
<i>STX1B</i>	ENSG00000099365	3.2522951	2.8977E-05	0.00815599	<i>DUX4L50</i>	ENSG00000232815	2.2059473	0.00041376	0.03011883
<i>FAM157C</i>	ENSG00000260528	3.2465733	8.5962E-05	0.01451723	<i>RFX2</i>	ENSG00000087903	2.1941621	0.00010107	0.01599145
<i>FRK</i>	ENSG00000111816	3.2247819	2.1925E-05	0.00712062	<i>ZNF554</i>	ENSG00000172006	2.1934989	0.00020408	0.02015521
<i>LINC01013</i>	ENSG00000228495	3.2080879	0.00016463	0.0192034	<i>E2F2</i>	ENSG00000007968	2.1862365	0.00021655	0.020898
<i>TPRG1</i>	ENSG00000188001	3.2064922	0.00019509	0.01988309	<i>DUSP1</i>	ENSG00000120129	2.1755772	0.00033014	0.02617597
<i>OLMALINC</i>	ENSG00000235823	3.1993886	6.8561E-05	0.01258541	<i>SEMA3G</i>	ENSG00000010319	2.1224795	0.00068189	0.04004852
<i>DNAH7</i>	ENSG00000118997	3.1965291	0.00052305	0.03460524	<i>SP2-DT</i>	ENSG00000264920	2.082219	0.000836	0.04392534
<i>DISP2</i>	ENSG00000140323	3.1795871	1.6782E-05	0.00664815	<i>RG59</i>	ENSG00000108370	2.0808523	0.00081771	0.04328996
<i>FAM131B</i>	ENSG00000159784	3.1716221	0.0002649	0.02342183	<i>GMFG</i>	ENSG00000130755	2.0781515	0.00067997	0.04004852
<i>INSYNI</i>	ENSG00000205363	3.1531562	0.00037575	0.02834827	<i>HECW2</i>	ENSG00000138411	2.0602526	0.00074416	0.04140655
<i>TRPM6</i>	ENSG00000119121	3.1441222	0.00010276	0.01606881	<i>P2RX5-TAX1BP3</i>	ENSG00000257950	2.0422362	0.0004803	0.03270689
<i>RPS6KA6</i>	ENSG00000072133	3.0929849	0.00066667	0.03978326					
<i>PPP5D1</i>	ENSG00000230510	3.089178	0.00046827	0.03241063					
<i>ADGRV1</i>	ENSG00000164199	3.0762133	0.00024175	0.02268152					
<i>FAM95B1</i>	ENSG00000223839	3.0745119	0.00013162	0.01792527					
<i>SLC4A8</i>	ENSG00000050438	3.0694772	0.00022069	0.02117644					
DEGs that are upregulated pre-treatment									
<i>MTND4P12</i>	ENSG00000247627	5.89085707	1.7835E-06	0.0026629	<i>NAA20</i>	ENSG00000173418	2.14470451	8.4587E-05	0.01442932
<i>RPPH1</i>	ENSG00000277209	4.7274237	1.7061E-05	0.00664815	<i>LMO4</i>	ENSG00000143013	1.77746873	5.5113E-05	0.01135059
<i>CHI3L1</i>	ENSG00000133048	4.62794544	7.1258E-06	0.00429785	<i>TAF13</i>	ENSG00000197780	1.72027241	7.4391E-06	0.00432381
<i>MTND1P23</i>	ENSG00000225972	4.61412278	5.8441E-05	0.01161117	<i>PIP4P2</i>	ENSG00000155099	1.668303	8.5583E-06	0.00441636
<i>DONSON</i>	ENSG00000159147	4.4662219	8.2747E-10	1.3974E-05	<i>UGCG</i>	ENSG00000148154	1.56542127	0.00096491	0.04700922
<i>MT-ATP8</i>	ENSG00000228253	4.16349405	7.1372E-07	0.00200889	<i>CENPQ</i>	ENSG00000031691	1.55521786	0.00034912	0.02706289
<i>ANKRD20A4P</i>	ENSG00000172014	3.77746445	0.000202	0.02006665	<i>RHOBTB3</i>	ENSG00000164292	1.49488343	0.00089294	0.04489737
<i>HBB</i>	ENSG00000244734	3.77327933	0.00025898	0.02338849	<i>DYNLT3</i>	ENSG00000165169	1.48981594	0.00102566	0.04906895
<i>SCARNA9</i>	ENSG00000254911	3.68652452	0.000452	0.03180594	<i>SLC16A4</i>	ENSG00000168679	1.48659082	9.32E-05	0.01528114
<i>NEAT1</i>	ENSG00000245532	3.52007391	1.5673E-06	0.0026629	<i>MPV17</i>	ENSG00000115204	1.48277094	0.00060253	0.03768721
<i>SPPI</i>	ENSG00000118785	3.49120524	2.1432E-05	0.00712062	<i>MINDY3</i>	ENSG00000148481	1.47867463	0.00052618	0.03460524
<i>RCC2-AS1</i>	ENSG00000227751	3.32883388	0.00078491	0.04235014	<i>RASSF8</i>	ENSG00000123094	1.47028809	0.00080296	0.04291243
<i>RN7SL2</i>	ENSG00000274012	3.21555177	6.1044E-06	0.00391579	<i>PURA</i>	ENSG00000185129	1.41124964	0.0002743	0.02381501
<i>CCN3</i>	ENSG00000136999	3.18712722	0.00014234	0.0183303	<i>RO60</i>	ENSG00000116747	1.39275722	0.00025697	0.02333218
<i>PRH1</i>	ENSG00000231887	3.17453911	7.9369E-06	0.00432381	<i>MYLIP</i>	ENSG00000007944	1.38128022	0.00085134	0.04451203
<i>IGF2R</i>	ENSG00000197081	3.13877908	1.7807E-05	0.00664815	<i>MAML2</i>	ENSG00000184384	1.30606344	0.00064208	0.03858865
<i>KIT</i>	ENSG00000157404	3.10508087	0.00011525	0.0172221	<i>TRMT13</i>	ENSG00000122435	1.29974252	0.00068885	0.040115

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<i>IFI6</i>	ENSG00000126709	3.10219131	1.8016E-05	0.00664815	<i>GORAB</i>	ENSG00000120370	1.22992844	0.00025397	0.02319043
<i>REP15</i>	ENSG00000174236	3.02763802	0.0002742	0.02381501	<i>STEEP1</i>	ENSG00000018610	1.22887927	0.00076433	0.04163879
<i>DNAI3</i>	ENSG00000162643	2.98708495	0.00069798	0.04050658	<i>MAP4K5</i>	ENSG00000012983	1.21761261	0.00025401	0.02319043
<i>SPOCK1</i>	ENSG00000152377	2.6640242	1.8108E-05	0.00664815	<i>ERGIC2</i>	ENSG000000087502	1.21153433	0.00018805	0.01972548
<i>RN7SL1</i>	ENSG00000276168	2.45033235	0.00062941	0.03822824	<i>CTBS</i>	ENSG000000117151	1.14459767	0.00104418	0.04981403
<i>MDK</i>	ENSG00000110492	2.3816469	0.00073476	0.0413623	<i>HSD17B12</i>	ENSG000000149084	1.12479901	0.00030606	0.02484948
<i>MT-ND6</i>	ENSG00000198695	2.37630531	9.9713E-05	0.01599145	<i>YIPF5</i>	ENSG000000145817	1.06076663	0.00088217	0.04478719
<i>PCCA</i>	ENSG00000175198	2.35420543	0.00074501	0.04140655	<i>GOLT1B</i>	ENSG000000111711	1.05783815	0.00068534	0.04004852
<i>TGFB1</i>	ENSG00000120708	2.24183075	0.00030463	0.02484948					

Supplementary Table 11: Differentially Expressed Gene Ontology Biological Process (GO:BP) Terms**Plotted in Figure 5**

Significantly Changed Terms in Post-treatment Samples (pR vs. pNR)			
GO:BP ID	GO:BP Term	Term	-log10 of adjusted p value
Terms that are increased in pR			
GO:0006955	immune response	1.36E-32	31.8679029
GO:0002376	immune system process	1.41E-31	30.8502556
GO:0045321	leukocyte activation	8.03E-27	26.0953075
GO:0001775	cell activation	1.43E-25	24.8446992
GO:0002682	regulation of immune system process	5.38E-22	21.269406
GO:0002274	myeloid leukocyte activation	8.59E-22	21.0661657
GO:0006952	defense response	4.23E-21	20.3732896
GO:0002252	immune effector process	2.44E-19	18.6133303
GO:0002443	leukocyte mediated immunity	1.66E-18	17.7811103
GO:0002366	leukocyte activation involved in immune response	7.91E-18	17.1019448
GO:0002263	cell activation involved in immune response	1.09E-17	16.9622046
GO:0009607	response to biotic stimulus	1.51E-17	16.8214242
GO:0002275	myeloid cell activation involved in immune response	4.75E-17	16.3235706
GO:0050776	regulation of immune response	4.87E-17	16.3122285
GO:0043299	leukocyte degranulation	2.92E-16	15.5344698
GO:0051707	response to other organism	5.84E-16	15.2332729
GO:0043207	response to external biotic stimulus	6.13E-16	15.2125045
GO:0002444	myeloid leukocyte mediated immunity	1.76E-15	14.754011
GO:0036230	granulocyte activation	9.84E-15	14.007081
GO:0044419	biological process involved in interspecies interaction between organisms	1.73E-14	13.7620589
GO:0098542	defense response to other organism	1.82E-14	13.7390027
GO:0042119	neutrophil activation	2.41E-14	13.6177099
GO:0009605	response to external stimulus	2.92E-14	13.534701
GO:0045087	innate immune response	4.09E-14	13.3886959
GO:0045055	regulated exocytosis	6.87E-14	13.1629345
GO:0043312	neutrophil degranulation	9.21E-14	13.0358316
GO:0002283	neutrophil activation involved in immune response	1.44E-13	12.8420665
GO:0006950	response to stress	2.28E-13	12.6423259
GO:0002446	neutrophil mediated immunity	4.09E-13	12.3880047
GO:0006887	exocytosis	6.63E-13	12.1782939
GO:0032940	secretion by cell	1.22E-12	11.912167
GO:0048584	positive regulation of response to stimulus	2.24E-12	11.6502988
GO:0046903	secretion	3.88E-12	11.411
GO:0050896	response to stimulus	5.07E-12	11.2952463
GO:0140352	export from cell	7.22E-12	11.1414365
GO:0002684	positive regulation of immune system process	8.46E-12	11.0725269
GO:0002694	regulation of leukocyte activation	4.90E-11	10.3096548
GO:0006954	inflammatory response	4.97E-11	10.3037167
GO:0016192	vesicle-mediated transport	9.18E-11	10.0373257
GO:0034097	response to cytokine	1.01E-10	9.99576864
GO:0050865	regulation of cell activation	2.67E-10	9.57290805
GO:0050900	leukocyte migration	2.94E-10	9.53204793
GO:0071345	cellular response to cytokine stimulus	1.92E-09	8.71562065
GO:0007166	cell surface receptor signaling pathway	2.25E-09	8.64737176
GO:0046649	lymphocyte activation	2.37E-09	8.62509644
GO:0051240	positive regulation of multicellular organismal process	4.14E-09	8.38352178
GO:0002683	negative regulation of immune system process	6.50E-09	8.18716562
GO:0048583	regulation of response to stimulus	6.80E-09	8.16780545
GO:0034341	response to interferon-gamma	7.04E-09	8.15248485
GO:1902105	regulation of leukocyte differentiation	7.67E-09	8.11503177
GO:0002521	leukocyte differentiation	1.30E-08	7.88500353
GO:0070887	cellular response to chemical stimulus	1.43E-08	7.8436775
GO:0019221	cytokine-mediated signaling pathway	2.42E-08	7.61563104
GO:0030595	leukocyte chemotaxis	3.75E-08	7.42637624

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GO:0051239	regulation of multicellular organismal process	8.40E-08	7.07562408
GO:0071346	cellular response to interferon-gamma	1.07E-07	6.97246039
GO:0050778	positive regulation of immune response	1.88E-07	6.72513595
GO:2000026	regulation of multicellular organismal development	2.18E-07	6.6611043
GO:0060326	cell chemotaxis	2.19E-07	6.6599349
GO:1903706	regulation of hemopoiesis	3.55E-07	6.44977711
GO:0051249	regulation of lymphocyte activation	4.18E-07	6.37900003
GO:0097529	myeloid leukocyte migration	4.76E-07	6.32275391
GO:0048518	positive regulation of biological process	5.27E-07	6.2785796
GO:0051716	cellular response to stimulus	7.45E-07	6.12767291
GO:0002764	immune response-regulating signaling pathway	7.62E-07	6.11821922
GO:0071310	cellular response to organic substance	1.032E-06	5.98632944
GO:0002697	regulation of immune effector process	1.0558E-06	5.97642981
GO:0002548	monocyte chemotaxis	1.1769E-06	5.92925951
GO:0042127	regulation of cell population proliferation	1.5371E-06	5.81329575
GO:0002768	immune response-regulating cell surface receptor signaling pathway	2.1078E-06	5.67617128
GO:0002696	positive regulation of leukocyte activation	2.369E-06	5.6254383
GO:0071674	mononuclear cell migration	3.6994E-06	5.43186665
GO:1990868	response to chemokine	4.7357E-06	5.32461941
GO:1990869	cellular response to chemokine	4.7357E-06	5.32461941
GO:0002253	activation of immune response	4.9766E-06	5.30306595
GO:0002703	regulation of leukocyte mediated immunity	5.167E-06	5.28676348
GO:0050867	positive regulation of cell activation	5.1937E-06	5.28452451
GO:0016477	cell migration	5.38E-06	5.26921908
GO:0007165	signal transduction	5.3833E-06	5.26895429
GO:0030097	hemopoiesis	5.9839E-06	5.2230173
GO:0070098	chemokine-mediated signaling pathway	6.7848E-06	5.16846019
GO:0007159	leukocyte cell-cell adhesion	9.0827E-06	5.04178335
GO:0048534	hematopoietic or lymphoid organ development	1.0618E-05	4.97396105
GO:0030334	regulation of cell migration	1.0755E-05	4.96840827
GO:0001816	cytokine production	1.578E-05	4.80189707
GO:0006935	chemotaxis	1.7052E-05	4.76823359
GO:0002695	negative regulation of leukocyte activation	1.8496E-05	4.73292249
GO:0042330	taxis	1.9677E-05	4.7060474
GO:0097530	granulocyte migration	2.273E-05	4.64340444
GO:0002688	regulation of leukocyte chemotaxis	2.7507E-05	4.56056268
GO:0002757	immune response-activating signal transduction	2.9964E-05	4.52340145
GO:0002429	immune response-activating cell surface receptor signaling pathway	2.9964E-05	4.52340145
GO:0001817	regulation of cytokine production	3.0474E-05	4.51606822
GO:0050866	negative regulation of cell activation	3.5197E-05	4.45349676
GO:1903037	regulation of leukocyte cell-cell adhesion	3.6962E-05	4.43224264
GO:0002250	adaptive immune response	3.7059E-05	4.43111091
GO:0010647	positive regulation of cell communication	3.8816E-05	4.41099292
GO:0071621	granulocyte chemotaxis	4.066E-05	4.39082879
GO:1903131	mononuclear cell differentiation	4.1006E-05	4.3871525
GO:0023056	positive regulation of signaling	4.4359E-05	4.3530202
GO:0009617	response to bacterium	4.7111E-05	4.32688059
GO:0002573	myeloid leukocyte differentiation	5.5025E-05	4.25943615
GO:0023052	signaling	6.3868E-05	4.19471601
GO:0070371	ERK1 and ERK2 cascade	6.7555E-05	4.17034139
GO:0030593	neutrophil chemotaxis	7.3022E-05	4.13654893
GO:0002520	immune system development	7.4946E-05	4.12524899
GO:0032101	regulation of response to external stimulus	8.3303E-05	4.07933817
GO:0009967	positive regulation of signal transduction	8.6286E-05	4.06406176
GO:0042110	T cell activation	8.9664E-05	4.04738114
GO:2000145	regulation of cell motility	0.00010096	3.9958355
GO:0002685	regulation of leukocyte migration	0.00010961	3.96014111
GO:0051094	positive regulation of developmental process	0.00012992	3.8863342
GO:0010033	response to organic substance	0.00013219	3.87880016
GO:0070374	positive regulation of ERK1 and ERK2 cascade	0.00014231	3.84677153
GO:0007154	cell communication	0.00014903	3.82671236
GO:1990266	neutrophil migration	0.00016574	3.78056873

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GO:0008283	cell population proliferation	0.00016776	3.77532404
GO:0002761	regulation of myeloid leukocyte differentiation	0.00018729	3.72748419
GO:0040011	locomotion	0.00021074	3.67626241
GO:0006909	phagocytosis	0.00021413	3.66932325
GO:0048522	positive regulation of cellular process	0.00021484	3.66789181
GO:0010942	positive regulation of cell death	0.00024491	3.61099411
GO:0045088	regulation of innate immune response	0.00031416	3.50284628
GO:0001909	leukocyte mediated cytotoxicity	0.000319	3.49620451
GO:0010628	positive regulation of gene expression	0.00032678	3.48574111
GO:0051674	localization of cell	0.00034356	3.4640012
GO:0048870	cell motility	0.00034356	3.4640012
GO:0071675	regulation of mononuclear cell migration	0.0003614	3.44201402
GO:0051250	negative regulation of lymphocyte activation	0.00038795	3.41122542
GO:0040012	regulation of locomotion	0.00041655	3.38032998
GO:0002699	positive regulation of immune effector process	0.00041712	3.37973776
GO:0001910	regulation of leukocyte mediated cytotoxicity	0.00042594	3.3706519
GO:0050863	regulation of T cell activation	0.0004512	3.34563508
GO:0050793	regulation of developmental process	0.00056919	3.24474587
GO:0002831	regulation of response to biotic stimulus	0.00058005	3.23653228
GO:0045670	regulation of osteoclast differentiation	0.00061463	3.21138891
GO:0070372	regulation of ERK1 and ERK2 cascade	0.00074104	3.13015838
GO:0002704	negative regulation of leukocyte mediated immunity	0.0008258	3.08312578
GO:0002886	regulation of myeloid leukocyte mediated immunity	0.0008258	3.08312578
GO:0001819	positive regulation of cytokine production	0.00089483	3.04825845
GO:0050869	negative regulation of B cell activation	0.00098652	3.00589319
GO:0045600	positive regulation of fat cell differentiation	0.00102749	2.98822111
GO:0065007	biological regulation	0.00105351	2.97735955
GO:0042116	macrophage activation	0.00113958	2.94325489
GO:0042113	B cell activation	0.00117503	2.9299507
GO:0030198	extracellular matrix organization	0.00120831	2.91782099
GO:0043300	regulation of leukocyte degranulation	0.00123595	2.90799743
GO:0051270	regulation of cellular component movement	0.00126171	2.89904052
GO:0043062	extracellular structure organization	0.00127345	2.8950196
GO:0006911	phagocytosis, engulfment	0.00130572	2.8841501
GO:0090025	regulation of monocyte chemotaxis	0.00131782	2.8801439
GO:0045785	positive regulation of cell adhesion	0.00133827	2.87345551
GO:0045229	external encapsulating structure organization	0.00141361	2.8496717
GO:0050851	antigen receptor-mediated signaling pathway	0.00147536	2.83110153
GO:0030316	osteoclast differentiation	0.00150918	2.82125874
GO:0010324	membrane invagination	0.00152956	2.81543461
GO:0030574	collagen catabolic process	0.00153	2.81530902
GO:1902563	regulation of neutrophil activation	0.0017232	2.76366441
GO:0007155	cell adhesion	0.00182275	2.73927366
GO:0030098	lymphocyte differentiation	0.00201002	2.69679967
GO:0032963	collagen metabolic process	0.00205016	2.68821285
GO:0097242	amyloid-beta clearance	0.00210917	2.6758883
GO:0022610	biological adhesion	0.00217726	2.66208996
GO:0001906	cell killing	0.00218096	2.66135202
GO:0032103	positive regulation of response to external stimulus	0.00227671	2.64269277
GO:0002495	antigen processing and presentation of peptide antigen via MHC class II	0.00249201	2.60345083
GO:0060333	interferon-gamma-mediated signaling pathway	0.00287323	2.54162937
GO:0030099	myeloid cell differentiation	0.00287414	2.54149139
GO:0030155	regulation of cell adhesion	0.00309107	2.50989136
GO:0099024	plasma membrane invagination	0.00335863	2.47383766
GO:0048247	lymphocyte chemotaxis	0.00345293	2.46181259
GO:0042221	response to chemical	0.00346436	2.46037643
GO:0002504	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	0.00357004	2.44732632
GO:1902106	negative regulation of leukocyte differentiation	0.00450324	2.34647473
GO:0031347	regulation of defense response	0.00455766	2.34125847
GO:1903039	positive regulation of leukocyte cell-cell adhesion	0.00480282	2.31850356
GO:0002687	positive regulation of leukocyte migration	0.00497611	2.3031101
GO:0045597	positive regulation of cell differentiation	0.00502089	2.29921949

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GO:0022407	regulation of cell-cell adhesion	0.00563965	2.2487477
GO:0051251	positive regulation of lymphocyte activation	0.00599777	2.22200985
GO:0045595	regulation of cell differentiation	0.00613354	2.21228908
GO:0050920	regulation of chemotaxis	0.00620627	2.20716957
GO:0031341	regulation of cell killing	0.00631267	2.19978703
GO:0022409	positive regulation of cell-cell adhesion	0.0063981	2.19394881
GO:0002690	positive regulation of leukocyte chemotaxis	0.00695321	2.15781462
GO:1903707	negative regulation of hemopoiesis	0.00704584	2.15206696
GO:0030335	positive regulation of cell migration	0.00738822	2.13146021
GO:0050921	positive regulation of chemotaxis	0.00796431	2.09885212
GO:1902107	positive regulation of leukocyte differentiation	0.00811632	2.09064076
GO:1903708	positive regulation of hemopoiesis	0.00811632	2.09064076
GO:0006690	icosanoid metabolic process	0.00814939	2.08887498
GO:0050777	negative regulation of immune response	0.00862953	2.06401305
GO:0034612	response to tumor necrosis factor	0.00891077	2.05008473
GO:0050864	regulation of B cell activation	0.00938387	2.02761782
GO:0046456	icosanoid biosynthetic process	0.00986025	2.00611195
GO:1901700	response to oxygen-containing compound	0.01256496	1.90083901
GO:0046394	carboxylic acid biosynthetic process	0.01273782	1.89490476
GO:0006959	humoral immune response	0.01424762	1.8462576
GO:0002237	response to molecule of bacterial origin	0.01443582	1.84055859
GO:0045637	regulation of myeloid cell differentiation	0.01444217	1.84036762
GO:0097028	dendritic cell differentiation	0.01680454	1.77457333
GO:0071402	cellular response to lipoprotein particle stimulus	0.0177913	1.74979244
GO:1905523	positive regulation of macrophage migration	0.01824985	1.73874062
GO:2000147	positive regulation of cell motility	0.01889053	1.72375588
GO:0016053	organic acid biosynthetic process	0.01962297	1.7072353
GO:0048513	animal organ development	0.02204285	1.65673219
GO:0048002	antigen processing and presentation of peptide antigen	0.02658663	1.57533678
GO:0001501	skeletal system development	0.02770315	1.55747083
GO:0009893	positive regulation of metabolic process	0.02818661	1.54995711
GO:0050670	regulation of lymphocyte proliferation	0.02867634	1.54247631
GO:0051272	positive regulation of cellular component movement	0.03056105	1.51483175
GO:0070663	regulation of leukocyte proliferation	0.03125857	1.50503085
GO:0032944	regulation of mononuclear cell proliferation	0.03252733	1.48775159
GO:0040017	positive regulation of locomotion	0.03285493	1.48339946
GO:0019882	antigen processing and presentation	0.03683706	1.43371498
GO:1902533	positive regulation of intracellular signal transduction	0.03750082	1.42595922
GO:0032496	response to lipopolysaccharide	0.03827071	1.41713352
GO:0001774	microglial cell activation	0.03908619	1.40797666
GO:0042269	regulation of natural killer cell mediated cytotoxicity	0.03979856	1.40013265
GO:0031214	biomineral tissue development	0.04601558	1.33709509
GO:0019886	antigen processing and presentation of exogenous peptide antigen via MHC class II	0.04726159	1.32549164
GO:2001301	lipoxin biosynthetic process	0.04795288	1.31918534
GO:0043313	regulation of neutrophil degranulation	0.04795288	1.31918534
GO:0045619	regulation of lymphocyte differentiation	0.04860647	1.31330592
GO:0050870	positive regulation of T cell activation	0.04877314	1.31181927
Terms that are decreased in pR			
GO:0007275	multicellular organism development	4.42E-14	13.3544096
GO:0048856	anatomical structure development	6.42E-14	13.1926352
GO:0007399	nervous system development	8.18E-14	13.0870397
GO:0032502	developmental process	1.14E-13	12.9433124
GO:0022008	neurogenesis	6.77E-12	11.1695977
GO:0048731	system development	1.27E-11	10.8963954
GO:0048699	generation of neurons	1.16E-10	9.93601156
GO:0048666	neuron development	1.35E-10	9.87017672
GO:0032501	multicellular organismal process	2.91E-10	9.53677564
GO:0032990	cell part morphogenesis	3.15E-10	9.501179
GO:0048858	cell projection morphogenesis	3.79E-10	9.42088585
GO:0031175	neuron projection development	9.29E-10	9.03183249
GO:0048812	neuron projection morphogenesis	1.46E-09	8.83450129
GO:0030182	neuron differentiation	1.67E-09	8.77754042
GO:0000904	cell morphogenesis involved in differentiation	1.70E-09	8.76900019

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GO:0120039	plasma membrane bounded cell projection morphogenesis	3.39E-09	8.46961892
GO:0048468	cell development	6.96E-09	8.15740869
GO:0000902	cell morphogenesis	8.13E-09	8.08975167
GO:0061564	axon development	1.02E-08	7.99070087
GO:0048667	cell morphogenesis involved in neuron differentiation	1.40E-08	7.85470674
GO:0032989	cellular component morphogenesis	5.28E-08	7.2775754
GO:0030030	cell projection organization	2.16E-07	6.66629501
GO:0007409	axonogenesis	3.03E-07	6.51843093
GO:0120036	plasma membrane bounded cell projection organization	1.5797E-06	5.80143711
GO:0009653	anatomical structure morphogenesis	1.6403E-06	5.78508416
GO:0010001	glial cell differentiation	1.748E-06	5.75745563
GO:0042063	gliogenesis	1.7662E-06	5.75295639
GO:0051960	regulation of nervous system development	8.1747E-06	5.08752705
GO:0048513	animal organ development	7.3719E-05	4.13242074
GO:0048869	cellular developmental process	0.00012735	3.89500939
GO:0030154	cell differentiation	0.00017086	3.76736699
GO:0071526	semaphorin-plexin signaling pathway	0.00030818	3.51119736
GO:0051962	positive regulation of nervous system development	0.00037987	3.42035968
GO:0007155	cell adhesion	0.00043612	3.36039556
GO:0097485	neuron projection guidance	0.00046823	3.32954196
GO:0022610	biological adhesion	0.00052659	3.27852767
GO:0007267	cell-cell signaling	0.00070544	3.15153814
GO:0040007	growth	0.00123293	2.90906
GO:0007411	axon guidance	0.00156747	2.80480146
GO:0099536	synaptic signaling	0.00220762	2.65607581
GO:0032989	cellular component morphogenesis	5.28E-08	7.2775754
GO:0050808	synapse organization	0.00236254	2.62662078
GO:0050767	regulation of neurogenesis	0.0028968	2.5380818
GO:0009888	tissue development	0.00433761	2.36274914
GO:0007417	central nervous system development	0.00648834	2.18786616
GO:0010975	regulation of neuron projection development	0.00714654	2.14590432
GO:0007422	peripheral nervous system development	0.00728795	2.13739468
GO:0099537	trans-synaptic signaling	0.01141161	1.94265325
GO:0048762	mesenchymal cell differentiation	0.01323011	1.87843665
GO:0034330	cell junction organization	0.0140361	1.85275351
GO:0050793	regulation of developmental process	0.01490277	1.8267331
GO:0051588	regulation of neurotransmitter transport	0.02436144	1.61329709
GO:0022603	regulation of anatomical structure morphogenesis	0.02481075	1.60536014
GO:0014033	neural crest cell differentiation	0.02507318	1.60079059
GO:0021782	glial cell development	0.02692506	1.56984339
GO:0030198	extracellular matrix organization	0.02806664	1.55180951
GO:0071679	commissural neuron axon guidance	0.02905823	1.53673078
GO:0043062	extracellular structure organization	0.02935493	1.53231898
GO:2000026	regulation of multicellular organismal development	0.03149687	1.5017326
GO:0050770	regulation of axonogenesis	0.03186496	1.49668664
GO:0045229	external encapsulating structure organization	0.03209471	1.49356658
GO:0060485	mesenchyme development	0.03664131	1.43602896
GO:0031344	regulation of cell projection organization	0.03917142	1.40703068
GO:0040011	locomotion	0.04444814	1.35214645

Significantly Changed Terms in Post- vs. Pre-Treatment Samples			
GO:BP Id	GO:BP Term	Adjusted p value	-log10 of adjusted p value
Terms that are increased in pR			
GO:0006955	immune response	1.51E-35	34.8208392
GO:0002376	immune system process	1.75E-30	29.7580111
GO:0045321	leukocyte activation	4.32E-28	27.3647756
GO:0002682	regulation of immune system process	2.61E-27	26.5826068
GO:0001775	cell activation	5.26E-25	24.2786088
GO:0050776	regulation of immune response	1.17E-24	23.932136
GO:0002443	leukocyte mediated immunity	9.01E-24	23.0454032
GO:0002684	positive regulation of immune system process	1.90E-23	22.7223719
GO:0002252	immune effector process	3.10E-23	22.5080816
GO:0002250	adaptive immune response	2.63E-22	21.5793312
GO:0046649	lymphocyte activation	3.70E-22	21.4317636
GO:0002764	immune response-regulating signaling pathway	3.84E-21	20.4153833
GO:0002757	immune response-activating signal transduction	4.36E-21	20.3602211
GO:0002429	immune response-activating cell surface receptor signaling pathway	4.36E-21	20.3602211
GO:0002768	immune response-regulating cell surface receptor signaling pathway	1.93E-20	19.7136433
GO:0050778	positive regulation of immune response	6.45E-20	19.1905623
GO:0002253	activation of immune response	3.32E-19	18.4782706
GO:0050900	leukocyte migration	7.49E-18	17.1253236
GO:0002683	negative regulation of immune system process	3.48E-17	16.4589442
GO:0002694	regulation of leukocyte activation	1.75E-16	15.7557643
GO:0042113	B cell activation	8.80E-16	15.0557452
GO:0050865	regulation of cell activation	1.55E-15	14.8101193
GO:0006954	inflammatory response	1.79E-15	14.7476474
GO:0002449	lymphocyte mediated immunity	2.06E-15	14.6858567
GO:0002697	regulation of immune effector process	9.59E-15	14.0180123
GO:0051249	regulation of lymphocyte activation	1.03E-14	13.9880148
GO:0050851	antigen receptor-mediated signaling pathway	2.18E-14	13.6619737
GO:0006952	defense response	5.05E-14	13.2966934
GO:0050853	B cell receptor signaling pathway	9.65E-14	13.0155072
GO:0006959	humoral immune response	3.11E-13	12.507809
GO:0030449	regulation of complement activation	3.55E-13	12.4497464
GO:0050777	negative regulation of immune response	3.68E-13	12.4336589
GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	6.14E-13	12.2118694
GO:0006956	complement activation	9.40E-13	12.0270369
GO:0002366	leukocyte activation involved in immune response	1.20E-12	11.919203
GO:0002263	cell activation involved in immune response	1.57E-12	11.8047129
GO:0002431	Fc receptor mediated stimulatory signaling pathway	2.08E-12	11.6809275
GO:0002696	positive regulation of leukocyte activation	2.96E-12	11.5290627
GO:0006909	phagocytosis	4.04E-12	11.3935019
GO:0016064	immunoglobulin mediated immune response	6.74E-12	11.171335
GO:0050867	positive regulation of cell activation	8.74E-12	11.0586767
GO:0019724	B cell mediated immunity	8.95E-12	11.0480543
GO:0042110	T cell activation	1.05E-11	10.9805941
GO:0002920	regulation of humoral immune response	1.31E-11	10.8842415
GO:0018149	peptide cross-linking	1.35E-11	10.8689353
GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis	1.49E-11	10.8261465
GO:0002433	immune response-regulating cell surface receptor signaling pathway involved in phagocytosis	1.49E-11	10.8261465
GO:0038094	Fc-gamma receptor signaling pathway	1.94E-11	10.711422
GO:0006958	complement activation, classical pathway	2.86E-11	10.5428862
GO:0008228	opsonization	4.01E-11	10.3968403
GO:0002862	negative regulation of inflammatory response to antigenic stimulus	5.18E-11	10.2854543
GO:0030098	lymphocyte differentiation	8.80E-11	10.05538

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GO:0002455	humoral immune response mediated by circulating immunoglobulin	1.39E-10	9.85758211
GO:0006910	phagocytosis, recognition	1.78E-10	9.74975414
GO:0002861	regulation of inflammatory response to antigenic stimulus	3.24E-10	9.48949305
GO:0002437	inflammatory response to antigenic stimulus	3.87E-10	9.41187977
GO:1903131	mononuclear cell differentiation	3.89E-10	9.41053676
GO:0051251	positive regulation of lymphocyte activation	4.04E-10	9.39390649
GO:0050864	regulation of B cell activation	5.61E-10	9.25128971
GO:0002274	myeloid leukocyte activation	6.05E-10	9.2180737
GO:0007159	leukocyte cell-cell adhesion	9.36E-10	9.02883516
GO:0048584	positive regulation of response to stimulus	1.81E-09	8.74299741
GO:0050863	regulation of T cell activation	3.76E-09	8.42488368
GO:1903037	regulation of leukocyte cell-cell adhesion	3.76E-09	8.42488368
GO:0002444	myeloid leukocyte mediated immunity	4.00E-09	8.39805541
GO:0046651	lymphocyte proliferation	5.31E-09	8.2751298
GO:0002521	leukocyte differentiation	6.40E-09	8.19395377
GO:0032943	mononuclear cell proliferation	7.07E-09	8.15062898
GO:0002275	myeloid cell activation involved in immune response	9.96E-09	8.0015851
GO:0051707	response to other organism	1.27E-08	7.89480308
GO:0043207	response to external biotic stimulus	1.32E-08	7.87923554
GO:0043299	leukocyte degranulation	1.48E-08	7.82931296
GO:0070661	leukocyte proliferation	1.92E-08	7.71562516
GO:0009607	response to biotic stimulus	2.12E-08	7.6733019
GO:0031348	negative regulation of defense response	2.53E-08	7.59642577
GO:0038093	Fc receptor signaling pathway	3.00E-08	7.52289495
GO:0008037	cell recognition	3.55E-08	7.45027151
GO:0050728	negative regulation of inflammatory response	4.92E-08	7.30816992
GO:0002446	neutrophil mediated immunity	6.25E-08	7.20378992
GO:0043312	neutrophil degranulation	7.60E-08	7.11932879
GO:0002283	neutrophil activation involved in immune response	1.05E-07	6.97736898
GO:0044419	biological process involved in interspecies interaction between organisms	1.30E-07	6.88703181
GO:0031347	regulation of defense response	1.39E-07	6.85608826
GO:0050727	regulation of inflammatory response	1.75E-07	6.75699686
GO:0032101	regulation of response to external stimulus	1.82E-07	6.73977099
GO:0007166	cell surface receptor signaling pathway	2.34E-07	6.63151057
GO:0042119	neutrophil activation	2.57E-07	6.59090778
GO:0036230	granulocyte activation	3.95E-07	6.40355258
GO:1903039	positive regulation of leukocyte cell-cell adhesion	5.20E-07	6.28379442
GO:0009605	response to external stimulus	5.42E-07	6.26626881
GO:0042100	B cell proliferation	7.35E-07	6.13355423
GO:0022409	positive regulation of cell-cell adhesion	1.18E-06	5.92833901
GO:0098542	defense response to other organism	1.47E-06	5.83272169
GO:0030595	leukocyte chemotaxis	6.25E-06	5.20440509
GO:0016192	vesicle-mediated transport	6.46E-06	5.18990782
GO:0030097	hemopoiesis	7.20E-06	5.14288581
GO:0050870	positive regulation of T cell activation	7.21E-06	5.14233426
GO:0002703	regulation of leukocyte mediated immunity	7.55E-06	5.12215131
GO:0022407	regulation of cell-cell adhesion	1.08E-05	4.96726892
GO:0048534	hematopoietic or lymphoid organ development	1.25E-05	4.90465026
GO:0032102	negative regulation of response to external stimulus	1.27E-05	4.89664513
GO:0050670	regulation of lymphocyte proliferation	1.74E-05	4.75985841
GO:0050871	positive regulation of B cell activation	2.02E-05	4.69473812
GO:0060326	cell chemotaxis	2.06E-05	4.6850935
GO:0032944	regulation of mononuclear cell proliferation	2.07E-05	4.68376951
GO:0030217	T cell differentiation	3.07E-05	4.51347064
GO:0002520	immune system development	3.21E-05	4.49311197
GO:0009617	response to bacterium	3.72E-05	4.4290925
GO:0050854	regulation of antigen receptor-mediated signaling pathway	4.03E-05	4.39417227
GO:0006887	exocytosis	4.81E-05	4.31756582
GO:0030183	B cell differentiation	5.46E-05	4.26269854
GO:0045055	regulated exocytosis	6.05E-05	4.21809169
GO:0071674	mononuclear cell migration	7.97E-05	4.09862352
GO:0045087	innate immune response	9.48E-05	4.0232404

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GO:0070663	regulation of leukocyte proliferation	9.93E-05	4.00287804
GO:0046631	alpha-beta T cell activation	0.00011119	3.95393079
GO:0038095	Fc-epsilon receptor signaling pathway	0.00011419	3.9423723
GO:0071345	cellular response to cytokine stimulus	0.00011446	3.9413415
GO:0016477	cell migration	0.000132	3.87942603
GO:0006911	phagocytosis, engulfment	0.00014836	3.82868758
GO:0050869	negative regulation of B cell activation	0.00015223	3.81749913
GO:0042742	defense response to bacterium	0.00019316	3.71408481
GO:0002695	negative regulation of leukocyte activation	0.00019768	3.70404676
GO:0051250	negative regulation of lymphocyte activation	0.00025381	3.59549138
GO:0050866	negative regulation of cell activation	0.00028154	3.55045993
GO:0099024	plasma membrane invagination	0.00032127	3.49312994
GO:0019221	cytokine-mediated signaling pathway	0.00035965	3.44411651
GO:0006897	endocytosis	0.00044025	3.35630305
GO:0050855	regulation of B cell receptor signaling pathway	0.00046199	3.33536393
GO:0010324	membrane invagination	0.00060741	3.2165157
GO:0030155	regulation of cell adhesion	0.00067654	3.16970681
GO:0034097	response to cytokine	0.00071946	3.14299612
GO:0042098	T cell proliferation	0.0007226	3.14110424
GO:0048583	regulation of response to stimulus	0.00089065	3.05029332
GO:0097529	myeloid leukocyte migration	0.00117038	2.93167466
GO:0007165	signal transduction	0.0014259	2.8459122
GO:0006898	receptor-mediated endocytosis	0.00181517	2.74108326
GO:1902105	regulation of leukocyte differentiation	0.0018344	2.73650712
GO:0045785	positive regulation of cell adhesion	0.00217192	2.66315701
GO:0002699	positive regulation of immune effector process	0.00245107	2.61064408
GO:0042102	positive regulation of T cell proliferation	0.00258956	2.58677429
GO:0098609	cell-cell adhesion	0.00264773	2.57712609
GO:0030888	regulation of B cell proliferation	0.00283578	2.54732803
GO:0045576	mast cell activation	0.00352681	2.45261861
GO:0070665	positive regulation of leukocyte proliferation	0.00354954	2.44982854
GO:0045619	regulation of lymphocyte differentiation	0.00452581	2.34430384
GO:0050671	positive regulation of lymphocyte proliferation	0.0045978	2.33745017
GO:0002335	mature B cell differentiation	0.00461439	2.33588591
GO:0051480	regulation of cytosolic calcium ion concentration	0.00472689	2.32542441
GO:0032946	positive regulation of mononuclear cell proliferation	0.00505193	2.29654273
GO:0042129	regulation of T cell proliferation	0.00526973	2.27821128
GO:0002312	B cell activation involved in immune response	0.00546204	2.26264546
GO:0032940	secretion by cell	0.0055614	2.25481603
GO:1902107	positive regulation of leukocyte differentiation	0.00683535	2.16523958
GO:1903708	positive regulation of hemopoiesis	0.00683535	2.16523958
GO:0030889	negative regulation of B cell proliferation	0.00692694	2.15945886
GO:0007204	positive regulation of cytosolic calcium ion concentration	0.00762086	2.11799602
GO:0046634	regulation of alpha-beta T cell activation	0.00894091	2.04861835
GO:0050852	T cell receptor signaling pathway	0.00912834	2.03960839
GO:0007155	cell adhesion	0.00927993	2.03245526
GO:0031295	T cell costimulation	0.00996093	2.0017003
GO:0051674	localization of cell	0.01045852	1.98052959
GO:0048870	cell motility	0.01045852	1.98052959
GO:0022610	biological adhesion	0.01094575	1.96075448
GO:0023052	signaling	0.0120135	1.92033048
GO:0002706	regulation of lymphocyte mediated immunity	0.01210751	1.91694507
GO:0140352	export from cell	0.01268798	1.89660747
GO:0031294	lymphocyte costimulation	0.01369381	1.86347565
GO:0001819	positive regulation of cytokine production	0.01469504	1.83282913
GO:0006874	cellular calcium ion homeostasis	0.01685735	1.77321073
GO:1903706	regulation of hemopoiesis	0.02383581	1.62277009
GO:0035590	purinergic nucleotide receptor signaling pathway	0.02464227	1.6083193
GO:0046632	alpha-beta T cell differentiation	0.02639991	1.57839763
GO:0055074	calcium ion homeostasis	0.02690162	1.5702216
GO:0007154	cell communication	0.02697844	1.56898311
GO:0006875	cellular metal ion homeostasis	0.03070067	1.5128521
GO:0002704	negative regulation of leukocyte mediated immunity	0.03594709	1.44433628
GO:0045580	regulation of T cell differentiation	0.0366814	1.43555405

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GO:1903038	negative regulation of leukocyte cell-cell adhesion	0.03692844	1.43263908
GO:0002548	monocyte chemotaxis	0.04482906	1.34844038
GO:0001817	regulation of cytokine production	0.04606889	1.33659227
Terms that are decreased in pR			
GO:0043473	pigmentation	1.77E-09	8.7531086
GO:0007399	nervous system development	3.02E-09	8.5206085
GO:0022008	neurogenesis	4.89E-07	6.31025916
GO:0048699	generation of neurons	1.13E-05	4.9487062
GO:0007417	central nervous system development	2.30E-05	4.63753449
GO:0030030	cell projection organization	2.65E-05	4.57720951
GO:0007275	multicellular organism development	4.10E-05	4.38748934
GO:0030182	neuron differentiation	4.84E-05	4.31520046
GO:0048731	system development	5.43E-05	4.26499627
GO:0048666	neuron development	8.22E-05	4.08518974
GO:0031175	neuron projection development	9.02E-05	4.04501973
GO:0120036	plasma membrane bounded cell projection organization	9.15E-05	4.03863769
GO:0032502	developmental process	0.0001002	3.9991258
GO:0048856	anatomical structure development	0.00017024	3.76894315
GO:0040011	locomotion	0.00030048	3.52218038
GO:0033059	cellular pigmentation	0.00056469	3.24819354
GO:0042063	gliogenesis	0.00057084	3.2434879
GO:0022610	biological adhesion	0.00058133	3.23557965
GO:0042438	melanin biosynthetic process	0.00076279	3.1175974
GO:0007155	cell adhesion	0.00100395	2.99828849
GO:0006582	melanin metabolic process	0.00100654	2.99716853
GO:0009653	anatomical structure morphogenesis	0.0012435	2.90535578
GO:0044550	secondary metabolite biosynthetic process	0.00131072	2.88249118
GO:0000904	cell morphogenesis involved in differentiation	0.00165958	2.78000218
GO:0046189	phenol-containing compound biosynthetic process	0.00282604	2.5488221
GO:0048066	developmental pigmentation	0.00282604	2.5488221
GO:0010001	glial cell differentiation	0.00304703	2.51612276
GO:0032501	multicellular organismal process	0.00327743	2.48446646
GO:0021675	nerve development	0.0033356	2.47682608
GO:0061564	axon development	0.00361612	2.44175695
GO:0031646	positive regulation of nervous system process	0.00379374	2.42093241
GO:0051674	localization of cell	0.0039937	2.39862421
GO:0048870	cell motility	0.0039937	2.39862421
GO:0042552	myelination	0.00446684	2.34999992
GO:0016477	cell migration	0.0045972	2.33750663
GO:0008366	axon ensheathment	0.00509203	2.29310924
GO:0007272	ensheathment of neurons	0.00509203	2.29310924
GO:0000902	cell morphogenesis	0.00593018	2.22693236
GO:0048167	regulation of synaptic plasticity	0.00827364	2.08230329
GO:0031589	cell-substrate adhesion	0.00905647	2.04304117
GO:0048858	cell projection morphogenesis	0.00930254	2.0313984
GO:0048468	cell development	0.01024785	1.98936726
GO:0032989	cellular component morphogenesis	0.0107718	1.96771155
GO:0006928	movement of cell or subcellular component	0.01130235	1.9468313
GO:0048667	cell morphogenesis involved in neuron differentiation	0.01192813	1.92342777
GO:0048812	neuron projection morphogenesis	0.01359505	1.86661929
GO:0050769	positive regulation of neurogenesis	0.01486927	1.82771032
GO:0032990	cell part morphogenesis	0.01588579	1.79899114
GO:0043474	pigment metabolic process involved in pigmentation	0.01969629	1.70561565
GO:0120039	plasma membrane bounded cell projection morphogenesis	0.01971886	1.70511823
GO:0031641	regulation of myelination	0.02214367	1.65475031
GO:0050808	synapse organization	0.02239215	1.64990418
GO:0001764	neuron migration	0.02355656	1.62788817
GO:0048513	animal organ development	0.02467037	1.6078243
GO:0007010	cytoskeleton organization	0.03183032	1.49715903
GO:0010810	regulation of cell-substrate adhesion	0.0328662	1.48325057
GO:0031106	septin ring organization	0.03870146	1.41227268
GO:0042440	pigment metabolic process	0.03905013	1.4083775
GO:0007611	learning or memory	0.03938575	1.40466088
GO:0046148	pigment biosynthetic process	0.04556698	1.34134973

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GO:0032438	melanosome organization	0.04592971	1.33790628
Terms that are increased in pNR			
GO:0031133	regulation of axon diameter	0.00597682	2.22352999
GO:0050896	response to stimulus	0.02673958	1.57284542
GO:0007154	cell communication	0.03383986	1.47057148

Supplementary Table 12: Differentially Enriched Gut Bacteria Plotted in Figure 6

Species name	Cleaned names	Class count	Effect at timepoint (pre)	LDA effect size	P value	Effect at timepoint (D+21)	LDA effect size	P value	Effect at timepoint (D+63)	LDA effect size	P value	Effect at timepoint (D+84)	LDA effect size	P value
k_Bacteria	NA	1		NA	-		NA	-	Bad	3.848332109	0.089679345		NA	-
k_Bacteria.p_Actinobacteria.c_Actinomycetia.o_Bifidobacteriales.f_Bifidobacteriaceae.g_Bifidobacterium.s_Bifidobacterium_adolescentis	Bifidobacterium adolescentis	1	Favorable	4.03158827	0.04069303		NA	-		NA	-		NA	-
k_Bacteria.p_Actinobacteria.c_Actinomycetia.o_Bifidobacteriales.f_Bifidobacteriaceae.g_Bifidobacterium.s_Bifidobacterium_bifidum	Bifidobacterium bifidum	2	Favorable	3.3947816	0.01962501	Favorable	3.212806857	0.061701274		NA	-		NA	-
k_Bacteria.p_Actinobacteria.c_Actinomycetia.o_Bifidobacteriales.f_Bifidobacteriaceae.g_Bifidobacterium.s_Bifidobacterium_dentium	Bifidobacterium dentium	2	Favorable	2.90061853	0.00697466	Favorable	3.072766799	0.040483999		NA	-		NA	-
k_Bacteria.p_Actinobacteria.c_Actinomycetia.o_Bifidobacteriales.f_Bifidobacteriaceae.g_Bifidobacterium.s_Unclassified_LKT_g_Bifidobacterium	NA	1	Favorable	2.99347308	0.0441636		NA	-		NA	-		NA	-
k_Bacteria.p_Actinobacteria.c_Actinomycetia.o_Unclassified	NA	4		NA	-		NA	-	Favorable	3.025134668	0.062698116	Favorable	2.36645696	0.098960154
k_Bacteria.p_Actinobacteria.c_Actinomycetia.o_Unclassified.f_Unclassified	NA	4		NA	-		NA	-	Favorable	3.025134668	0.062698116	Favorable	2.36714318	0.098960154
k_Bacteria.p_Actinobacteria.c_Actinomycetia.o_Unclassified.f_Unclassified.g_Unclassified	NA	4		NA	-		NA	-	Favorable	3.025134668	0.062698116	Favorable	2.36638134	0.098960154
k_Bacteria.p_Actinobacteria.c_Actinomycetia.o_Unclassified.f_Unclassified.g_Unclassified.s_Unclassified_LKT_c_Actinomycetia	NA	4		NA	-		NA	-	Favorable	3.025134668	0.062698116	Favorable	2.37735851	0.098960154
k_Bacteria.p_Actinobacteria.c_Coriobacteriia.o_Coriobacteriales.f_Coriobacteriaceae.g_Collinsella.s_Collinsella_Unclassified_AM3410	Collinsella sp. AM34-10	2		NA	-		NA	-		NA	-	Unfavorable	3.36016917	0.083550565
k_Bacteria.p_Actinobacteria.c_Coriobacteriia.o_Coriobacteriales.f_Coriobacteriaceae.g_Senegalimassilia	NA	2		NA	-		NA	-		NA	-	Favorable	2.73513936	0.091268752
k_Bacteria.p_Actinobacteria.c_Coriobacteriia.o_Coriobacteriales.f_Coriobacteriaceae.g_Senegalimassilia.s_Senegalimassilia_anacrobina	Senegalimassilia anacrobina	2		NA	-		NA	-		NA	-	Favorable	2.74540711	0.091268752
k_Bacteria.p_Actinobacteria.c_Coriobacteriia.o_Eggerthellales.f_Eggerthellaceae.g_Eggerthella.s_Unclassified_LKT_g_Eggerthella	NA	1	Unfavorable	2.90738813	0.03389485		NA	-		NA	-		NA	-

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[illegible]

Neoadjuvant Intratumoral Vidutolimod and Nivolumab in High-Risk Resectable Melanoma

[illegible]

Neoadjuvant Intratumoral Vidutolimod and Nivolumab in High-Risk Resectable Melanoma

nerellaceae.g__Parabacteroides.s__Parabacteroides_johnsonii_LKT__s__Parabacteroides_johnsonii														
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Tanerellaceae.g__Parabacteroides.s__Parabacteroides_merdae	Parabacteroides merdae	1	Favorable	3.47055286	0.06837759		NA	-		Favorable	3.100456678	0.008595046		NA -
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Unclassified	NA	3		NA	-	Favorable	3.017150143	0.028539064		Favorable	3.100456678	0.008595046		NA -
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Unclassified.g__Unclassified	NA	3		NA	-	Favorable	3.017150143	0.028539064		Favorable	3.100456678	0.008595046		NA -
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Unclassified.g__Unclassified.s__Unclassified_LKT_o__Bacteroidales	NA	3		NA	-	Favorable	3.017150143	0.028539064		Favorable	3.100456678	0.008595046		NA -
k__Bacteria.p__Firmicutes	NA	5		NA	-	Unfavorable	4.732002448	0.062698116		Unfavorable	4.864025161	0.028539064	Unfavorable	4.89919043 0.098960154
k__Bacteria.p__Firmicutes.c__Bacilli	NA	1	Favorable	4.44590082	0.0644064		NA	-			NA	-		NA -
k__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales	NA	1	Favorable	4.44590082	0.0644064		NA	-			NA	-		NA -
k__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae	NA	2		NA	-		NA	-			NA	-	Favorable	2.69549481 0.033894854
k__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Lacticaseibacillus	NA	2		NA	-		NA	-			NA	-	Favorable	2.58895593 0.057040882
k__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Lacticaseibacillus.s__Lacticaseibacillus_rhamnosus	Lacticaseibacillus rhamnosus	2		NA	-		NA	-			NA	-	Favorable	2.58895426 0.057040882
k__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Limosilactobacillus	NA	1	Favorable	4.04395106	0.03620653		NA	-			NA	-		NA -
k__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Limosilactobacillus.s__Limosilactobacillus_fermentum	Limosilactobacillus fermentum	1	Favorable	4.0437805	0.03620653		NA	-			NA	-		NA -
k__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae	NA	1	Favorable	4.23107204	0.0644064		NA	-			NA	-		NA -
k__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae.g__Streptococcus	NA	1	Favorable	4.23107204	0.0644064		NA	-			NA	-		NA -
k__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae.g__Streptococcus.s__Streptococcus_parasanguinis	Streptococcus parasanguinis	1	Favorable	3.53149476	0.01234695		NA	-			NA	-		NA -
k__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae.g__Streptococcus.s__Streptococcus_salivarius	Streptococcus salivarius	1	Favorable	4.13352677	0.03874098		NA	-			NA	-		NA -
k__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae.g__Streptococcus.s__Unclassified_LKT_g__Streptococcus	NA	3	Favorable	2.90181185	0.02234223		NA	-			NA	-	Unfavorable	2.4553967 0.098960154

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k_Bacteria.p_Firmicutes.c_Clostridia	NA	2		NA	-		NA	-	Unfavorable	4.885369047	0.042809798		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales	NA	2		NA	-		NA	-	Unfavorable	4.885369047	0.042809798		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridia.ceae.g_Butyricicoccus	NA	1		NA	-		NA	-	Favorable	2.954152091	0.021488739		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridia.ceae.g_Butyricicoccus.s_Butyricicoccus Unclassified AF10 3	Butyricicoccus sp. AF10-3	2	Favorable	3.04939726	0.08058463		NA	-	Favorable	2.981270362	0.079743983		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridia.ceae.g_Butyricicoccus.s_Butyricicoccus Unclassified AM28 25	Butyricicoccus sp. AM28-25	1		NA	-		NA	-	Favorable	3.358915148	0.089679345		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridia.ceae.g_Butyricicoccus.s_Butyricicoccus Unclassified BIOML A1	Butyricicoccus sp. BIOML-A1	1		NA	-		NA	-	Favorable	2.971590738	0.089679345		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridia.ceae.g_Butyricicoccus.s_Unclassified LKT g_Butyricicoccus	NA	1		NA	-		NA	-	Favorable	3.21225426	0.024797646		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridia.ceae.g_Clostridium.s_Clostridium saudiense	Clostridium saudiense	1	Favorable	2.7932418	0.01041046		NA	-		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridia.ceae.g_Clostridium.s_Clostridium Unclassified AT4	Clostridium sp. AT4	3		NA	-	Unfavorable	3.033589943	0.062698116		NA	-	Unfavorable	4.10093174	0.059346439
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridia.ceae.g_Clostridium.s_Clostridium Unclassified AT4_LKT_s_Clostridium Unclassified AT4	Clostridium sp. AT4	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridia.ceae.g_Clostridium.s_Clostridium Unclassified MCC344	Clostridium sp. MCC344	2	Unfavorable	3.02129215	0.02223916	Unfavorable	3.217991689	0.079801929		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridia.ceae.g_Clostridium.s_Clostridium Unclassified OM08 29	Clostridium sp. OM08-29	2		NA	-		NA	-		NA	-	Favorable	3.10908961	0.091268752
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridia.ceae.g_Clostridium.s_Unclassified LKT g_Clostridium	NA	2		NA	-		NA	-		NA	-	Unfavorable	2.85653058	0.098960154
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridia.ceae.g_Hungatella	NA	1	Favorable	3.11406828	0.09176158		NA	-		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridia.ceae.g_Hungatella.s_Hungatella_hathewayi	Hungatella hathewayi	1	Favorable	3.11406828	0.09176158		NA	-		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Eubacteriaceae.g_Eubacterium.s_Eubacterium coprostanoligenes	Eubacterium coprostanoligenes	2		NA	-		NA	-		NA	-	Favorable	2.67702614	0.091268752

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k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Eubacteriaceae.g_Eubacterium.s_Eubacterium_coprostanoligenes_LKT_s_Eubacterium_coprostanoligenes	Eubacterium coprostanoligenes	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Eubacteriaceae.g_Eubacterium.s_Eubacterium_ventricosum_LKT_s_Eubacterium_ventricosum	Eubacterium ventriosum	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Eubacteriaceae.g_Eubacterium.s_Unclassified_LKT_g_Eubacterium	NA	2		NA	-		NA	-		NA	-	Favorable	2.34269765	0.098960154
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae	NA	6	Unfavorable	4.87151137	0.0644064	Unfavorable	4.851177979	0.016006155	Unfavorable	4.756641265	0.062698116	Unfavorable	4.96703034	0.098960154
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Anaerostipes	NA	1		NA	-		NA	-		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Anaerostipes.s_Anaerostipes_hadrus_LKT_s_Anaerostipes_hadrus	Anaerostipes hadrus	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia	NA	6	Unfavorable	4.62507309	0.08175889	Unfavorable	4.540073292	0.048744921	Unfavorable	4.322143909	0.089679345	Unfavorable	4.8910678	0.059346439
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_caecimuris	Blautia caecimuris	1		NA	-	Unfavorable	4.122440599	0.016006155		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_caecimuris_LKT_s_Blautia_caecimuris	Blautia caecimuris	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_hansenii	Blautia hansenii	1		NA	-	Unfavorable	3.750631028	0.055356039		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_hansenii_LKT_s_Blautia_hansenii	Blautia hansenii	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_luti	Blautia luti	1		NA	-	Unfavorable	2.82909601	0.079801929		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_luti_LKT_s_Blautia_luti	Blautia luti	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_producta_LKT_s_Blautia_producta	Blautia producta	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.sp.	Blautia sp.	2		NA	-		NA	-		NA	-	Unfavorable	2.9073659	0.098960154

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raceae.g_Blautia.s_Blautia_Unclassified BIOML A1														
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_Unclassified DFI 4 84	Blautia sp. DFI.4.84	2		NA	-		NA	-		NA	-	Favorable	3.08148971	0.098960154
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_Unclassified Marseille P3087	Blautia sp. Marseille-P3087	1		NA	-	Favorable	3.174637928	0.055168507		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_Unclassified Marseille P3201T	Blautia sp. Marseille-P3201T	1		NA	-	Unfavorable	2.972569013	0.016006155		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_Unclassified_Marseille_P3201T_LKT_s_Blautia_Unclassified_Marseille_P3201T	Blautia sp. Marseille-P3201T	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_Unclassified MSK22 86	Blautia sp. MSK22 86	1	Unfavorable	3.33597892	0.06789937		NA	-		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_Unclassified MSK22 86 LKT_s_Blautia_Unclassified MSK22 86	Blautia sp. MSK22 86	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Unclassified_LKT_g_Blautia	NA	3		NA	-		NA	-		NA	-	Unfavorable	3.44054938	0.033894854
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Coproccoccus	NA	2		NA	-		NA	-		NA	-	Unfavorable	3.78120695	0.059346439
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Coproccoccus.s_Coproccoccus catus	Coproccoccus catus	2		NA	-	Unfavorable	3.209101939	0.028539064	Unfavorable	3.167587537	0.055356039		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Coproccoccus.s_Coproccoccus comes	Coproccoccus comes	1		NA	-		NA	-	Unfavorable	3.631718912	0.048744921		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Coproccoccus.s_Coproccoccus Unclassified AM27 12LB	Coproccoccus sp. AM27-12LB	1		NA	-	Unfavorable	2.990100423	0.024686779		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Coproccoccus.s_Coproccoccus Unclassified HPP0074	Coproccoccus sp. HPP0074	2		NA	-		NA	-		NA	-	Unfavorable	2.49805108	0.09588827
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Dorea.s_Dorea_formicigenans_LKT_s_Dorea_formicigenans	Dorea formicigenans	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Dorea.s_Dorea_formicigenans	Dorea sp. AGR2135	3		NA	-	Unfavorable	3.399647461	0.089679345		NA	-	Unfavorable	2.98916669	0.033894854

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raceae.g_Dorea.s_Dorea_Unclassified_AGR2135														
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Dorea.s_Unclassified_LKT_g_Dorea	NA	1		NA	-		NA	-		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Eisenbergiella.s_Eisenbergiella_massiliensis	Eisenbergiella massiliensis	2		NA	-		NA	-		NA	-	Unfavorable	3.24484013	0.098960154
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Enterocloster.s_Enterocloster_aldenensis	Enterocloster aldenensis	1		NA	-		NA	-	Unfavorable	3.210658732	0.028539064		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Enterocloster.s_Enterocloster_asparagiformis	Enterocloster asparagiformis	1		NA	-	Favorable	3.429837388	0.032756868		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Fusicatenibacter	NA	1		NA	-		NA	-		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Fusicatenibacter.s_Fusicatenibacter_saccharivorans_LKT_s_Fusicatenibacter_saccharivorans	Fusicatenibacter saccharivorans	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Lachnoclostridium.s_Clostridium_symbiosum	[Clostridium] symbiosum	2		NA	-		NA	-		NA	-	Favorable	2.49434077	0.098960154
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Lachnoclostridium.s_Lachnoclostridium_Unclassified_210928_DF1.6.3	Lachnoclostridium sp. 210928-DF1.6.3	1		NA	-	Unfavorable	3.442329536	0.079801929		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Lacrimispora	NA	1	Unfavorable	3.52511361	0.08175889		NA	-		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Lacrimispora.s_Lacrimispora_celerecrescens	Lacrimispora celerecrescens	2		NA	-		NA	-		NA	-	Favorable	2.19452157	0.033894854
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Mediterraneibacter.s_Ruminococcus_gnavus_LKT_s_Ruminococcus_gnavus	[Ruminococcus] gnavus	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Mediterraneibacter.s_Ruminococcus_lactaris	[Ruminococcus] lactaris	1	Unfavorable	3.33113967	0.03389485		NA	-		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Mediterraneibacter.s_Unclassified_LKT_g_Mediterraneibacter	NA	2		NA	-		NA	-		NA	-	Favorable	2.47660186	0.059346439
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Roseburia	NA	3	Unfavorable	4.18414366	0.0441636		NA	-	Unfavorable	4.280930106	0.070827576		NA	-

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k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Lachnospiraceae.g__Roseburia.s__Unclassified LKT__g__Roseburia	NA	1		NA	-		NA	-		NA	-		NA	-
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Lachnospiraceae.g__Tyzzerella	NA	2		NA	-		NA	-		NA	-	Unfavorable	3.78537985	0.059346439
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Lachnospiraceae.g__Tyzzerella.s__Tyzzerella nexilis	Tyzzerella nexilis	2		NA	-		NA	-		NA	-	Unfavorable	3.78149233	0.059346439
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Lachnospiraceae.g__Unclassified	NA	4		NA	-	Unfavorable	3.226946211	0.021488739	Unfavorable	3.228400292	0.055356039	Unfavorable	3.22913456	0.059346439
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Lachnospiraceae.g__Unclassified.s__Unclassified LKT__f__Lachnospiraceae	NA	4		NA	-	Unfavorable	3.226946211	0.021488739	Unfavorable	3.228400292	0.055356039	Unfavorable	3.22349223	0.059346439
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Lachnospiraceae.g__Waltera.s__Waltera Unclassified CLA_AA_H273	Waltera sp. CLA-AA-H273	2		NA	-	Unfavorable	3.05976376	0.055309147	Unfavorable	3.11765319	0.062698116		NA	-
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Missing.g__Evtepia	NA	3	Favorable	3.01585645	0.05675211		NA	-		NA	-	Favorable	3.13667449	0.098960154
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Missing.g__Evtepia.s__Evtepia gabavorous	Evtepia gabavorous	3	Favorable	3.01585645	0.05675211		NA	-		NA	-	Favorable	3.13671489	0.098960154
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Missing.g__Intestinimonas	NA	3	Favorable	2.9333302	0.0644064	Favorable	2.895084054	0.028539064	Favorable	3.010723921	0.089679345		NA	-
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Missing.g__Intestinimonas.s__Intestinimonas butyriciproducens	Intestinimonas butyriciproducens	1	Favorable	NA	-	Favorable	2.743185518	0.070827576		NA	-		NA	-
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Missing.g__Intestinimonas.s__Intestinimonas massiliensis	Intestinimonas massiliensis	4	Favorable	3.18803266	0.05003673		NA	-	Favorable	3.396930252	0.032756868	Favorable	2.31798558	0.059346439
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Missing.g__Intestinimonas.s__Intestinimonas Unclassified MSJ_38	Intestinimonas sp. MSJ-38	4	Favorable	2.77588731	0.0638934	Favorable	3.024537066	0.021488739		NA	-	Favorable	2.33800182	0.059346439
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Missing.g__Neglecta.s__Unclassified LKT__g__Neglecta	NA	4		NA	-	Favorable	3.325998015	0.058883518	Favorable	3.308277963	0.070773367	Favorable	2.25041491	0.033894854
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Oscillospiraceae.g__Acutalibacter	NA	3		NA	-	Favorable	2.926864424	0.048571513		NA	-	Favorable	2.46543511	0.057040882
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Oscillospiraceae.g__Acutalibacter.s__Acutalibacter Unclassified 1XD8_33	Acutalibacter sp. 1XD8-33	3		NA	-	Favorable	2.926864424	0.048571513		NA	-	Favorable	2.46579266	0.057040882
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Oscillospiraceae.g__Anaerofilum	NA	3		NA	-	Favorable	2.875606565	0.037350882		NA	-	Favorable	2.15386296	0.033894854
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Oscillospiraceae.g__Anaerofilum	Anaerofilum sp. An201	3		NA	-	Favorable	2.875606565	0.037350882		NA	-	Favorable	2.15401615	0.033894854

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k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Oscillospiraceae.g__Oscillibacter.s__Oscillibacter_valericigenes	Oscillibacter valericigenes	1		NA	-	Favorable	2.864632601	0.048744921		NA	-	NA	-
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Oscillospiraceae.g__Oscillibacter.s__Unclassified_LKT_g__Oscillibacter	NA	1		NA	-		NA	-	Favorable	3.276166828	0.037497491	NA	-
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Oscillospiraceae.g__Ruminococcus	NA	2		NA	-		NA	-		NA	-	4.20874499	0.098960154
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Oscillospiraceae.g__Ruminococcus.s__Ruminococcus_bicirculans	Ruminococcus bicirculans	2		NA	-		NA	-		NA	-	2.89853808	0.098960154
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Oscillospiraceae.g__Ruminococcus.s__Ruminococcus_bromii	Ruminococcus bromii	2		NA	-		NA	-		NA	-	3.85866441	0.098960154
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Oscillospiraceae.g__Ruminococcus.s__Ruminococcus_callidus	Ruminococcus callidus	2		NA	-		NA	-		NA	-	3.43260596	0.076428036
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Oscillospiraceae.g__Ruminococcus.s__Ruminococcus_Unclassified_AM31_32	Ruminococcus sp. AM31-32	1		NA	-	Favorable	3.055022207	0.091484211		NA	-	NA	-
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Oscillospiraceae.g__Ruminococcus.s__Ruminococcus_Unclassified_AM31_32_LKT_s__Ruminococcus_Unclassified_AM31_32	Ruminococcus sp. AM31-32	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Oscillospiraceae.g__Ruminococcus.s__Ruminococcus_Unclassified_M6_2020	Ruminococcus sp. M6(2020)	1	Favorable	2.9915574	0.03375771		NA	-		NA	-	NA	-
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Oscillospiraceae.g__Ruminococcus.s__Ruminococcus_Unclassified_Marseille_P6503	Ruminococcus sp. Marseille-P6503	1		NA	-	Favorable	3.095660124	0.076558582		NA	-	NA	-
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Oscillospiraceae.g__Ruminococcus.s__Ruminococcus_Unclassified_Marseille_P6503_LKT_s__Ruminococcus_Unclassified_Marseille_P6503	Ruminococcus sp. Marseille-P6503	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Oscillospiraceae.g__Ruthenibacterium	NA	3	Favorable	3.10772025	0.03389485		NA	-		NA	-	3.26087767	0.059346439
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Oscillospiraceae.g__Ruthenibacterium.s__Ruthenibacterium_lactatiformans	Ruthenibacterium lactatiformans	3	Favorable	3.10772025	0.03389485		NA	-		NA	-	3.26042166	0.059346439
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Oscillospiraceae.g__Unclassified	NA	2		NA	-		NA	-		NA	-	3.00416386	0.098960154

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k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Oscillospiraceae.g__Unclassified.s__Unclassified LKT f__Oscillospiraceae	NA	2		NA	-		NA	-		NA	-	Favorable	3.02225908	0.098960154
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Oscillospiraceae.g__Vescimonas	NA	5	Favorable	3.48212327	0.05694288	Favorable	3.221863333	0.055356039	Favorable	3.458925522	0.089679345	Favorable	3.36678462	0.033894854
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Oscillospiraceae.g__Vescimonas.s__Vescimonas coprocola	Vescimonas coprocola	5	Favorable	3.31372032	0.0470644	Favorable	3.179654463	0.042809798	Favorable	3.368293339	0.089617652	Favorable	3.28475668	0.033894854
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Oscillospiraceae.g__Vescimonas.s__Vescimonas fastidiosa	Vescimonas fastidiosa	5	Favorable	3.03507962	0.03355228	Unfavorable	2.709271816	0.084564286	Favorable	2.986292843	0.018571098	Favorable	2.64012909	0.033894854
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Peptostreptococcaceae.g__Intestinibacter	NA	1		NA	-	Unfavorable	2.878685615	0.036765962		NA	-		NA	-
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Peptostreptococcaceae.g__Intestinibacter.s__Intestinibacter bartlettii	Intestinibacter bartlettii	1		NA	-	Unfavorable	2.878685615	0.036765962		NA	-		NA	-
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Peptostreptococcaceae.g__Terrisporobacter	NA	3	Favorable	2.97966956	0.02985292		NA	-		NA	-	Favorable	2.31174392	0.057040882
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Peptostreptococcaceae.g__Terrisporobacter.s__Terrisporobacter mayombe	Terrisporobacter mayombe	3	Favorable	2.98441747	0.02985292		NA	-		NA	-	Favorable	2.31034243	0.057040882
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Unclassified	NA	1		NA	-		NA	-		NA	-		NA	-
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Unclassified.g__Unclassified	NA	1		NA	-		NA	-		NA	-		NA	-
k__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Unclassified.g__Unclassified.s__Unclassified LKT o__Eubacteriales	NA	1		NA	-		NA	-		NA	-		NA	-
k__Bacteria.p__Firmicutes.c__Erysipelotrichia.o__Erysipelotrichales.f__Coprobacillaceae.g__Catenibacterium.s__Catenibacterium mitsuokai	Catenibacterium mitsuokai	1	Unfavorable	3.28623409	0.09921206		NA	-		NA	-		NA	-
k__Bacteria.p__Firmicutes.c__Erysipelotrichia.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Erysipelotrichium.s__Clostridium_spiroforme	[Clostridium] spiroforme	1		NA	-	Unfavorable	2.972905169	0.02841693		NA	-		NA	-
k__Bacteria.p__Firmicutes.c__Erysipelotrichia.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Faecalibacillus	NA	1		NA	-	Unfavorable	3.618512352	0.06779652		NA	-		NA	-
k__Bacteria.p__Firmicutes.c__Erysipelotrichia.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Faecalibacillus.s__Faecalibacillus Unclassified MSK20_93	Faecalibacillus sp. MSK20_93	1		NA	-	Unfavorable	3.389539156	0.045212505		NA	-		NA	-
k__Bacteria.p__Firmicutes.c__Erysipelotrichia.o__Erysipelotrichales.f	Longicatena caecimuris	2		NA	-		NA	-		NA	-	Favorable	2.94450377	0.091268752

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_Erysipelotrichaceae.g_Longicaten a.s_Longicaten caecimuris														
k_Bacteria.p_Firmicutes.c_Uncl assified	NA	2		NA	-		NA	-		NA	-	Unfavorable	2.618211 19	0.0989601 54
k_Bacteria.p_Firmicutes.c_Uncl assified.o_Unclassified	NA	2		NA	-		NA	-		NA	-	Unfavorable	2.645495 23	0.0989601 54
k_Bacteria.p_Firmicutes.c_Uncl assified.o_Unclassified.f_Unclass ified	NA	2		NA	-		NA	-		NA	-	Unfavorable	2.533908 49	0.0989601 54
k_Bacteria.p_Firmicutes.c_Uncl assified.o_Unclassified.f_Unclass ified.g_Unclassified	NA	2		NA	-		NA	-		NA	-	Unfavorable	2.639297 39	0.0989601 54
k_Bacteria.p_Firmicutes.c_Uncl assified.o_Unclassified.f_Unclass ified.g_Unclassified.s_Unclassifie d LKT p_Firmicutes	NA	2		NA	-		NA	-		NA	-	Unfavorable	2.619830 27	0.0989601 54
k_Bacteria.p_Proteobacteria	NA	1		NA	-	Favorable	3.774530 164	0.055356 039		NA	-		NA	-
k_Bacteria.p_Proteobacteria.c__ Deltaproteobacteria	NA	1		NA	-		NA	-		NA	-		NA	-
k_Bacteria.p_Proteobacteria.c__ Deltaproteobacteria.o_Desulfovibri onales	NA	1		NA	-		NA	-		NA	-		NA	-
k_Bacteria.p_Proteobacteria.c__ Deltaproteobacteria.o_Desulfovibri onales.f_Desulfovibrionaceae	NA	1		NA	-		NA	-		NA	-		NA	-
k_Bacteria.p_Proteobacteria.c__ Deltaproteobacteria.o_Desulfovibri onales.f_Desulfovibrionaceae.g__ Bilophila	NA	1		NA	-		NA	-		NA	-		NA	-
k_Bacteria.p_Proteobacteria.c__ Deltaproteobacteria.o_Desulfovibri onales.f_Desulfovibrionaceae.g__ Bilophila.s_Bilophila_wadsworthia LKT s_Bilophila_wadsworthia	Bilophila wadsworthia	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
k_Bacteria.p_Proteobacteria.c__ Gammaproteobacteria	NA	3	Favorable	3.91109 031	0.022342 23	Favorable	3.805417 692	0.000561 435	Favorable	3.582812 193	0.01600615 5		NA	-
k_Bacteria.p_Proteobacteria.c__ Gammaproteobacteria.o_Enterobac terales	NA	3	Favorable	3.91109 031	0.022342 23	Favorable	3.805417 692	0.000561 435	Favorable	3.582812 193	0.01600615 5		NA	-
k_Bacteria.p_Proteobacteria.c__ Gammaproteobacteria.o_Enterobac terales.f_Enterobacteriaceae	NA	3	Favorable	3.91109 031	0.022342 23	Favorable	3.805417 692	0.000561 435	Favorable	3.582812 193	0.01600615 5		NA	-
k_Bacteria.p_Proteobacteria.c__ Gammaproteobacteria.o_Enterobac terales.f_Enterobacteriaceae.g_Es cherichia	NA	5	Favorable	3.86907 255	0.029451 58	Favorable	3.790011 992	0.000561 435	Favorable	3.564870 881	0.02148873 9	Favorable	4.231690 92	0.0338948 54
k_Bacteria.p_Proteobacteria.c__ Gammaproteobacteria.o_Enterobac terales.f_Enterobacteriaceae.g_Es cherichia.s_Escherichia coli	Escherichia coli	5	Favorable	3.86907 255	0.029451 58	Favorable	3.790011 992	0.000561 435	Favorable	3.564870 881	0.02148873 9	Favorable	4.231691 67	0.0338948 54
k_Bacteria.p_Proteobacteria.c__ Gammaproteobacteria.o_Enterobac terales.f_Enterobacteriaceae.g_U nclassified	NA	3	Favorable	2.96574 099	0.050169 2	Favorable	2.796462 946	0.009938 198	Favorable	3.149119 734	0.00615603 3		NA	-
k_Bacteria.p_Proteobacteria.c__ Gammaproteobacteria.o_Enterobac terales.f_Enterobacteriaceae.g_U	NA	3	Favorable	2.96574 099	0.050169 2	Favorable	2.796462 946	0.009938 198	Favorable	3.149119 734	0.00615603 3		NA	-

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[illegible]

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Species Name	Cleaned Names	Class Count	Effect at Time Point (D+84)	LDA effect size	P value	Effect at Pre-Treatment Time Point (PD-1 cohort)	LDA effect size	P value
k_Bacteria	NA	1		NA	-		NA	-
k_Bacteria.p_Actinobacteria.c_Actinomycetia.o_Bifidobacteriales.f_Bifidobacteriaceae.g_Bifidobacterium.s_Bifidobacterium_adolescentis	Bifidobacterium adolescentis	1		NA	-	NA	NA	NA
k_Bacteria.p_Actinobacteria.c_Actinomycetia.o_Bifidobacteriales.f_Bifidobacteriaceae.g_Bifidobacterium.s_Bifidobacterium_bifidum	Bifidobacterium bifidum	2		NA	-	NA	NA	NA
k_Bacteria.p_Actinobacteria.c_Actinomycetia.o_Bifidobacteriales.f_Bifidobacteriaceae.g_Bifidobacterium.s_Bifidobacterium_dentium	Bifidobacterium dentium	2		NA	-	NA	NA	NA
k_Bacteria.p_Actinobacteria.c_Actinomycetia.o_Bifidobacteriales.f_Bifidobacteriaceae.g_Bifidobacterium.s_Unclassified_LKT_g_Bifidobacterium	NA	1		NA	-	NA	NA	NA
k_Bacteria.p_Actinobacteria.c_Actinomycetia.o_Unclassified	NA	4	Favorable	2.36645696	0.09896015	Unfavorable	2.11081029	0.03773018
k_Bacteria.p_Actinobacteria.c_Actinomycetia.o_Unclassified.f_Unclassified	NA	4	Favorable	2.36714318	0.09896015	Unfavorable	2.11081029	0.03773018
k_Bacteria.p_Actinobacteria.c_Actinomycetia.o_Unclassified.f_Unclassified.g_Unclassified	NA	4	Favorable	2.36638134	0.09896015	Unfavorable	2.11081029	0.03773018
k_Bacteria.p_Actinobacteria.c_Actinomycetia.o_Unclassified.f_Unclassified.g_Unclassified.s_Unclassified_LKT_c_Actinomycetia	NA	4	Favorable	2.37735851	0.09896015	Unfavorable	2.11081029	0.03773018
k_Bacteria.p_Actinobacteria.c_Coriobacteriia.o_Coriobacteriales.f_Coriobacteriaceae.g_Collinsella.s_Collinsella_Unclassified_AM34_10	Collinsella sp. AM34-10	2	Unfavorable	3.36016917	0.08355057	NA	NA	NA
k_Bacteria.p_Actinobacteria.c_Coriobacteriia.o_Coriobacteriales.f_Coriobacteriaceae.g_Senegalimassilia	NA	2	Favorable	2.73513936	0.09126875	NA	NA	NA
k_Bacteria.p_Actinobacteria.c_Coriobacteriia.o_Coriobacteriales.f_Coriobacteriaceae.g_Senegalimassilia.s_Senegalimassilia_anaerobia	Senegalimassilia anaerobia	2	Favorable	2.74540711	0.09126875	NA	NA	NA
k_Bacteria.p_Actinobacteria.c_Coriobacteriia.o_Eggerthellales.f_Eggerthellaceae.g_Eggerthella.s_Unclassified_LKT_g_Eggerthella	NA	1	Favorable	NA	-		NA	-
k_Bacteria.p_Actinobacteria.c_Coriobacteriia.o_Eggerthellales.f_Eggerthellaceae.g_Gordonibacter	NA	2	Favorable	2.24906674	0.07642804		NA	-
k_Bacteria.p_Actinobacteria.c_Coriobacteriia.o_Eggerthellales.f_Eggerthellaceae.g_Gordonibacter.s_Gordonibacter_urolithinfaciens	Gordonibacter urolithinfaciens	2	Favorable	2.24481411	0.07642804	NA	NA	NA
k_Bacteria.p_Bacteroidetes	NA	3		NA	-	Unfavorable	4.73414477	0.00110031
k_Bacteria.p_Bacteroidetes.c_Bacteroidia	NA	3		NA	-	Unfavorable	4.73414477	0.00110031
k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales	NA	3		NA	-	Unfavorable	4.73414477	0.00110031
k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Bacteroidaceae	NA	1		NA	-	Unfavorable	NA	-
k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Bacteroidaceae.g_Bacteroides	NA	2		NA	-	Unfavorable	4.37301831	0.04963031
k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Bacteroidaceae.g_Bacteroides.s_Bacteroides_caccae	Bacteroides caccae	3	Favorable	3.87852952	0.03389485	NA	NA	NA
k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Bacteroidaceae.g_Bacteroides.s_Bacteroides_cellulosilyticus	Bacteroides cellulosilyticus	1		NA	-	NA	NA	NA

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k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_cellulosilyticus_LKT__s__Bacteroides_cellulosilyticus	Bacteroides cellulosilyticus	1	NA	NA	NA	Unfavorable	3.81765109	0.0463928
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_eggerthii	Bacteroides eggerthii	2	Unfavorable	4.03586405	0.09896015	NA	NA	NA
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_faecis	Bacteroides faecis	1		NA	-	NA	NA	NA
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_finegoldii	Bacteroides finegoldii	2		NA	-	NA	NA	NA
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_fragilis_LKT__s__Bacteroides_fragilis	Bacteroides fragilis	1	NA	NA	NA	Unfavorable	3.36381344	0.04296637
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_intestinalis	Bacteroides intestinalis	2		NA	-	NA	NA	NA
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_intestinalis_LKT__s__Bacteroides_intestinalis	Bacteroides intestinalis	1	NA	NA	NA	Unfavorable	3.78779748	0.00514475
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_nordii_LKT__s__Bacteroides_nordii	Bacteroides nordii	1	NA	NA	NA	Favorable	2.5438369	0.02520965
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_ovatus	Bacteroides ovatus	1		NA	-	NA	NA	NA
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_thetaiotaomicron	Bacteroides thetaiotaomicron	1		NA	-	NA	NA	NA
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_uniformis	Bacteroides uniformis	1		NA	-	NA	NA	NA
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides.s__Unclassified_LKT__g__Bacteroides	NA	1		NA	-		NA	-
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Phocaeicola.s__Phocaeicola_coprocola_LKT__s__Phocaeicola_coprocola	Phocaeicola coprocola	1	NA	NA	NA	Unfavorable	3.04163796	0.00403103
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Phocaeicola.s__Phocaeicola_dorei	Phocaeicola dorei	1		NA	-	NA	NA	NA
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Phocaeicola.s__Phocaeicola_massiliensis_LKT__s__Phocaeicola_massiliensis	Phocaeicola massiliensis	1	NA	NA	NA	Unfavorable	3.43167671	0.02037791
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Phocaeicola.s__Phocaeicola_plebeius	Phocaeicola plebeius	3	Favorable	3.14553812	0.03389485	NA	NA	NA
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Unclassified	NA	1		NA	-		NA	-
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Unclassified.s__Unclassified_LKT__f__Bacteroidaceae	NA	1		NA	-		NA	-
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Odoribacteraceae	NA	1		NA	-	Unfavorable	2.99119001	0.03216521

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k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Odoribacteraceae.g__Odoribacter	NA	1		NA	-	Unfavorable	2.93290398	0.04203936
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Odoribacteraceae.g__Odoribacter.s__Odoribacter_splanchnicus_LKT_s__Odoribacter_splanchnicus	Odoribacter splanchnicus	1	NA	NA	NA	Unfavorable	2.93290398	0.04203936
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae	NA	2		NA	-	Unfavorable	4.10906216	0.00745001
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotella	NA	2		NA	-	Unfavorable	4.07225007	0.0021657
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotella.s__Prevotella_copri	Prevotella copri	3	Favorable	4.34144567	0.09896015	NA	NA	NA
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotella.s__Prevotella_copri_LKT_s__Prevotella_copri	Prevotella copri	1	NA	NA	NA	Unfavorable	4.05998491	6.51E-05
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotella.s__Unclassified_LKT_g__Prevotella	NA	1		NA	-	Unfavorable	2.58486776	0.01734841
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae	NA	1		NA	-	Unfavorable	4.07826543	0.00824141
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae.g__Alistipes	NA	1		NA	-	Unfavorable	4.07826543	0.00824141
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae.g__Alistipes.s__Alistipes_communis_LKT_s__Alistipes_communis	Alistipes communis	1	NA	NA	NA	Unfavorable	2.81899042	0.04406945
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae.g__Alistipes.s__Alistipes_finegoldii_LKT_s__Alistipes_finegoldii	Alistipes finegoldii	1	NA	NA	NA	Unfavorable	3.57645805	0.00380584
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae.g__Alistipes.s__Alistipes_onderdonkii	Alistipes onderdonkii	1		NA	-	NA	NA	NA
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae.g__Alistipes.s__Alistipes_senegalensis_LKT_s__Alistipes_senegalensis	Alistipes senegalensis	1	NA	NA	NA	Unfavorable	2.10766342	0.0230947
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae.g__Alistipes.s__Alistipes_shahii_LKT_s__Alistipes_shahii	Alistipes shahii	1	NA	NA	NA	Unfavorable	3.33126654	0.01410255
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae.g__Alistipes.s__Alistipes_Unclassified_CHKCI003_LKT_s__Alistipes_Unclassified_CHKCI003	Alistipes sp. CHKCI003	1	NA	NA	NA	Unfavorable	2.82033847	0.03411917
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae.g__Alistipes.s__Unclassified_LKT_g__Alistipes	NA	2		NA	-	Unfavorable	2.37387591	0.03835087
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Tannerellaceae.g__Parabacteroides.s__Parabacteroides_johnsonii_LKT_s__Parabacteroides_johnsonii	Parabacteroides johnsonii	1	NA	NA	NA	Unfavorable	3.14792023	0.03149123
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Tannerellaceae.g__Parabacteroides.s__Parabacteroides_merdae	Parabacteroides merdae	1		NA	-	NA	NA	NA
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Unclassified	NA	3		NA	-	Unfavorable	2.89362727	0.04408416
k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__Unclassified.g__Unclassified	NA	3		NA	-	Unfavorable	2.89362727	0.04408416

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k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Unclassified.g_Unclassified.s_Unclassified LKT_o_Bacteroidales	NA	3		NA	-	Unfavorable	2.89362727	0.04408416
k_Bacteria.p_Firmicutes	NA	5	Unfavorable	4.89919043	0.09896015	Favorable	4.7213788	0.00071091
k_Bacteria.p_Firmicutes.c_Bacilli	NA	1		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales	NA	1		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Lactobacillaceae	NA	2	Favorable	2.69549481	0.03389485		NA	-
k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Lactobacillaceae.g_Lactacaseibacillus	NA	2	Favorable	2.58895593	0.05704088		NA	-
k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Lactobacillaceae.g_Lactacaseibacillus.s_Lactacaseibacillus_rhamnosus	Lactacaseibacillus rhamnosus	2	Favorable	2.58895426	0.05704088	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Lactobacillaceae.g_Limosilactobacillus	NA	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Lactobacillaceae.g_Limosilactobacillus.s_Limosilactobacillus_fermentum	Limosilactobacillus fermentum	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Streptococcaceae	NA	1		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Streptococcaceae.g_Streptococcus	NA	1		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Streptococcaceae.g_Streptococcus.s_Streptococcus_parasanguinis	Streptococcus parasanguinis	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Streptococcaceae.g_Streptococcus.s_Streptococcus_salivarius	Streptococcus salivarius	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Streptococcaceae.g_Streptococcus.s_Unclassified LKT_g_Streptococcus	NA	3	Unfavorable	2.4553967	0.09896015		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia	NA	2		NA	-	Favorable	4.65120894	0.00350449
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales	NA	2		NA	-	Favorable	4.65120894	0.00350449
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridiaceae.g_Butyricococcus	NA	1		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridiaceae.g_Butyricococcus.s_Butyricococcus_Unclassified AF10_3	Butyricococcus sp. AF10-3	2		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridiaceae.g_Butyricococcus.s_Butyricococcus_Unclassified AM28_25	Butyricococcus sp. AM28-25	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridiaceae.g_Butyricococcus.s_Butyricococcus_Unclassified BIOML_A1	Butyricococcus sp. BIOML-A1	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridiaceae.g_Butyricococcus.s_Unclassified LKT_g_Butyricococcus	NA	1		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridiaceae.g_Clostridium.s_Clostridium_saudiense	Clostridium saudiense	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridiaceae.g_Clostridium.s_Clostridium_Unclassified AT4	Clostridium sp. AT4	3	Unfavorable	4.10093174	0.05934644	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridiaceae.g_Clostridium.s_Clostridium	Clostridium sp. AT4	1	NA	NA	NA	Favorable	2.53174347	0.01737387

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m_Unclassified_AT4_LKT_s_Clostridium_Unclassified_AT4								
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridiaceae.g_Clostridium.s_Clostridium_Unclassified_MCC344	Clostridium sp. MCC344	2		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridiaceae.g_Clostridium.s_Clostridium_Unclassified_OM08_29	Clostridium sp. OM08-29	2	Favorable	3.10908961	0.09126875	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridiaceae.g_Clostridium.s_Unclassified_d_LKT_g_Clostridium	NA	2	Unfavorable	2.85653058	0.09896015		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridiaceae.g_Hungatella	NA	1		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridiaceae.g_Hungatella.s_Hungatella_hathewayi	Hungatella hathewayi	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Eubacteriaceae.g_Eubacterium.s_Eubacterium_coprostanoligenes	Eubacterium coprostanoligenes	2	Favorable	2.67702614	0.09126875	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Eubacteriaceae.g_Eubacterium.s_Eubacterium_coprostanoligenes_LKT_s_Eubacterium_coprostanoligenes	Eubacterium coprostanoligenes	1	NA	NA	NA	Unfavorable	2.82622369	0.00287641
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Eubacteriaceae.g_Eubacterium.s_Eubacterium_ventriosum_LKT_s_Eubacterium_ventriosum	Eubacterium ventriosum	1	NA	NA	NA	Favorable	2.38990944	0.03940633
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Eubacteriaceae.g_Eubacterium.s_Unclassified_LKT_g_Eubacterium	NA	2	Favorable	2.34269765	0.09896015		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae	NA	6	Unfavorable	4.96703034	0.09896015	Favorable	4.55129516	0.00148521
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Anaerostipes	NA	1		NA	-	Favorable	3.3429232	0.02423972
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Anaerostipes.s_Anaerostipes_hadrus_LKT_s_Anaerostipes_hadrus	Anaerostipes hadrus	1	NA	NA	NA	Favorable	3.3429232	0.02423972
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia	NA	6	Unfavorable	4.8910678	0.05934644	Favorable	3.99626684	0.00901342
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_caecimuris	Blautia caecimuris	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_caecimuris_LKT_s_Blautia_caecimuris	Blautia caecimuris	1	NA	NA	NA	Favorable	3.02154397	0.00330686
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_hansenii	Blautia hansenii	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_hansenii_LKT_s_Blautia_hansenii	Blautia hansenii	1	NA	NA	NA	Favorable	2.60214906	0.01806118
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_luti	Blautia luti	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_luti_LKT_s_Blautia_luti	Blautia luti	1	NA	NA	NA	Favorable	2.33515375	0.02145508
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_producta_LKT_s_Blautia_producta	Blautia producta	1	NA	NA	NA	Favorable	2.8954433	0.00163881

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k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_Unclassified BIOML A1	Blautia sp. BIOML-A1	2	Unfavorable	2.9073659	0.09896015	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_Unclassified DFI 4 84	Blautia sp. DFI.4.84	2	Favorable	3.08148971	0.09896015	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_Unclassified Marseille P3087	Blautia sp. Marseille-P3087	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_Unclassified Marseille P3201T	Blautia sp. Marseille-P3201T	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_Unclassified_Marseille_P3201T_LKT_s_Blautia_Unclassified Marseille P3201T	Blautia sp. Marseille-P3201T	1	NA	NA	NA	Favorable	2.39243359	0.0070597
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_Unclassified MSK22 86	Blautia sp. MSK22 86	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Blautia_Unclassified_MSK22_86_LKT_s_Blautia_Unclassified_MSK22_86	Blautia sp. MSK22 86	1	NA	NA	NA	Favorable		
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Blautia.s_Unclassified_LKT_g_Blautia	NA	3	Unfavorable	3.44054938	0.03389485	Favorable		
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Coprococcus	NA	2	Unfavorable	3.78120695	0.05934644		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Coprococcus.s_Coprococcus catus	Coprococcus catus	2		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Coprococcus.s_Coprococcus comes	Coprococcus comes	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Coprococcus.s_Coprococcus Unclassified AM27 12LB	Coprococcus sp. AM27-12LB	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Coprococcus.s_Coprococcus Unclassified HPP0074	Coprococcus sp. HPP0074	2	Unfavorable	2.49805108	0.09588827	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Dorea.s_Dorea formicigenerans LKT_s_Dorea formicigenerans	Dorea formicigenerans	1	NA	NA	NA	Favorable	2.82752572	0.01529735
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Dorea.s_Dorea Unclassified AGR2135	Dorea sp. AGR2135	3	Unfavorable	2.98916669	0.03389485	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Dorea.s_Unclassified_LKT_g_Dorea	NA	1		NA	-	Favorable	2.41824963	0.04798898
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Eisenbergiella.s_Eisenbergiella massiliensis	Eisenbergiella massiliensis	2	Unfavorable	3.24484013	0.09896015	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Enterocloster.s_Enterocloster aldenensis	Enterocloster aldenensis	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Enterocloster.s_Enterocloster asparagiformis	Enterocloster asparagiformis	1		NA	-	NA	NA	NA

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k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Fusicatenibacter	NA	1		NA	-	Favorable	3.38744933	0.00258875
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Fusicatenibacter.s_Fusicatenibacter_saccharivorans_LKT_s_Fusicatenibacter_saccharivorans	Fusicatenibacter saccharivorans	1	NA	NA	NA		3.38744933	0.00258875
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Lachnoclostridium.s_Clostridium symbiosum	[Clostridium] symbiosum	2	Favorable	2.49434077	0.09896015	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Lachnoclostridium.s_Lachnoclostridium Unclassified 210928 DFI 6 3	Lachnoclostridium sp. 210928-DFI.6.3	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Lacrimispora	NA	1		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Lacrimispora.s_Lacrimispora celerecrescens	Lacrimispora celerecrescens	2	Favorable	2.19452157	0.03389485	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Mediterraneibacter.s_Ruminococcus gnavus_LKT_s_Ruminococcus_gnavus	[Ruminococcus] gnavus	1	NA	NA	NA	Favorable	3.4363902	0.01877179
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Mediterraneibacter.s_Ruminococcus lactaris	[Ruminococcus] lactaris	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Mediterraneibacter.s_Unclassified LKT_g_Mediterraneibacter	NA	2	Favorable	2.47660186	0.05934644		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Roseburia	NA	3		NA	-	Favorable	4.12453039	0.00024757
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Roseburia.s_Roseburia faecis_LKT_s_Roseburia faecis	Roseburia faecis	1	NA	NA	NA	Favorable	3.67292941	0.00837362
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Roseburia.s_Roseburia intestinalis	Roseburia intestinalis	4	Unfavorable	4.29490075	0.05934644	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Roseburia.s_Roseburia intestinalis_LKT_s_Roseburia intestinalis	Roseburia intestinalis	1	NA	NA	NA	Favorable	3.54699347	0.0401021
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Roseburia.s_Roseburia inulinivorans_LKT_s_Roseburia inulinivorans	Roseburia inulinivorans	1	NA	NA	NA	Favorable	3.33504637	0.03454979
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Roseburia.s_Roseburia Unclassified 831b	Roseburia sp. 831b	3	Favorable	2.34835805	0.09896015	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Roseburia.s_Roseburia Unclassified_831b_LKT_s_Roseburia_Unclassified_831b	Roseburia sp. 831b	1	NA	NA	NA	Favorable	2.77606267	0.00210116
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Roseburia.s_Roseburia Unclassified_BX0805_LKT_s_Roseburia_Unclassified_BX0805	Roseburia sp. BX0805	1	NA	NA	NA	Favorable	2.42950831	0.01686921
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Roseburia.s_Roseburia Unclassified_BX1005_LKT_s_Roseburia_Unclassified_BX1005	Roseburia sp. BX1005	1	NA	NA	NA	Favorable	2.7034391	0.00491983
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Roseburia.s_Roseburia Unclassified CLA_AA_H204	Roseburia sp. CLA-AA-H204	1		NA	-	NA	NA	NA

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k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Roseburia.s_Roseburia_Unclassified_CLA_AA_H204_LKT_s_Roseburia_Unclassified_CLA_AA_H204	Roseburia sp. CLA-AA-H204	1	NA	NA	NA	Favorable	2.90259155	0.04132633
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Roseburia.s_Roseburia_Unclassified_CLA_AA_H209_LKT_s_Roseburia_Unclassified_CLA_AA_H209	Roseburia sp. CLA-AA-H209	1	NA	NA	NA	Favorable	2.69164874	0.03491194
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Roseburia.s_Roseburia_Unclassified_MSJ_14_LKT_s_Roseburia_Unclassified_MSJ_14	Roseburia sp. MSJ-14	1	NA	NA	NA	Favorable	2.23842255	0.04132892
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Roseburia.s_Unclassified_LKT_g_Roseburia	NA	1		NA	-	Favorable	2.80129161	0.00435048
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Tyzzereella	NA	2	Unfavorable	3.78537985	0.05934644		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Tyzzereella.s_Tyzzereella_nexilis	Tyzzereella nexilis	2	Unfavorable	3.78149233	0.05934644	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Unclassified	NA	4	Unfavorable	3.22913456	0.05934644		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Unclassified.s_Unclassified_LKT_f_Lachnospiraceae	NA	4	Unfavorable	3.22349223	0.05934644		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Lachnospiraceae.g_Waltera.s_Waltera_Unclassified_CLA_AA_H273	Waltera sp. CLA-AA-H273	2		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Missing.g_Evtepia	NA	3	Favorable	3.13667449	0.09896015		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Missing.g_Evtepia.s_Evtepia_gabavorous	Evtepia gabavorous	3	Favorable	3.13671489	0.09896015	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Missing.g_Intestinimonas	NA	3		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Missing.g_Intestinimonas.s_Intestinimonas_butyriciproducens	Intestinimonas butyriciproducens	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Missing.g_Intestinimonas.s_Intestinimonas_massiliensis	Intestinimonas massiliensis	4	Favorable	2.31798558	0.05934644	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Missing.g_Intestinimonas.s_Intestinimonas_Unclassified_MSJ_38	Intestinimonas sp. MSJ-38	4	Favorable	2.33800182	0.05934644	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Missing.g_Neglecta.s_Unclassified_LKT_g_Neglecta	NA	4	Favorable	2.25041491	0.03389485	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Acutalibacter	NA	3	Favorable	2.46543511	0.05704088	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Acutalibacter.s_Acutalibacter_Unclassified_1XD8_33	Acutalibacter sp. 1XD8-33	3	Favorable	2.46579266	0.05704088	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Anaerofilum	NA	3	Favorable	2.15386296	0.03389485	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Anaerofilum.s_Anaerofilum_Unclassified_An201	Anaerofilum sp. An201	3	Favorable	2.15401615	0.03389485	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Anaeromassilibacillus	NA	2		NA	-		NA	-

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k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Anaeromassilibacillus.s_Anaeromassilibacillus Unclassified An200	Anaeromassilibacillus sp. An200	3		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Anaerotruncus.s_Unclassified LKT g_Anaerotruncus	NA	4		NA	-	Unfavorable	2.39712139	0.01278098
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Dysosmobacter	NA	5	Favorable	2.77253808	0.03389485	Unfavorable	2.6867727	0.04010194
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Dysosmobacter.s_Dysosmobacter Unclassified BX15	Dysosmobacter sp. BX15	4	Favorable	2.6712606	0.03389485	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Dysosmobacter.s_Dysosmobacter welbionis	Dysosmobacter welbionis	4	Favorable	2.31385888	0.09896015	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Faecalibacterium.s_Faecalibacterium Unclassified An58	Faecalibacterium sp. An58	2		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Faecalibacterium.s_Faecalibacterium Unclassified CLA_AA_H233	Faecalibacterium sp. CLA-AA-H233	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Massiliimalia.s_Massiliimalia massiliensis	Massiliimalia massiliensis	3	Favorable	2.72681987	0.05704088	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Oscillibacter	NA	6	Favorable	3.78873813	0.09896015	Unfavorable	3.00724062	0.01720612
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Oscillibacter.s_Oscillibacter Unclassified ER4	Oscillibacter sp. ER4	3		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Oscillibacter.s_Oscillibacter Unclassified MCC667	Oscillibacter sp. MCC667	5	Favorable	2.75546917	0.03389485	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Oscillibacter.s_Oscillibacter Unclassified MSJ_31	Oscillibacter sp. MSJ-31	4	Favorable	2.98068394	0.05934644	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Oscillibacter.s_Oscillibacter Unclassified MSJ_31_LKT_s_Oscillibacter Unclassified MSJ_31	Oscillibacter sp. MSJ-31	1	NA	NA	NA	Unfavorable	2.8547942	0.01426782
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Oscillibacter.s_Oscillibacter valericigenes	Oscillibacter valericigenes	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Oscillibacter.s_Unclassified LKT g_Oscillibacter	NA	1		NA	-		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Ruminococcus	NA	2	Favorable	4.20874499	0.09896015		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Ruminococcus.s_Ruminococcus bicirculans	Ruminococcus bicirculans	2	Favorable	2.89853808	0.09896015	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Ruminococcus.s_Ruminococcus bromii	Ruminococcus bromii	2	Favorable	3.85866441	0.09896015	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Ruminococcus.s_Ruminococcus callidus	Ruminococcus callidus	2	Favorable	3.43260596	0.07642804	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Ruminococcus.s_Ruminococcus Unclassified AM31_32	Ruminococcus sp. AM31-32	1		NA	-	NA	NA	NA

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k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Ruminococcus.s_Ruminococcus Unclassified AM31_32_LKT_s_Ruminococcus Unclassified AM31_32	Ruminococcus sp. AM31-32	1	NA	NA	NA	Unfavorable	2.59152189	0.04412754
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Ruminococcus.s_Ruminococcus Unclassified M6_2020	Ruminococcus sp. M6(2020)	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Ruminococcus.s_Ruminococcus Unclassified Marseille P6503	Ruminococcus sp. Marseille-P6503	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Ruminococcus.s_Ruminococcus Unclassified Marseille_P6503_LKT_s_Ruminococcus Unclassified Marseille P6503	Ruminococcus sp. Marseille-P6503	1	NA	NA	NA	Unfavorable	2.56265569	0.0011284
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Ruthenibacterium	NA	3	Favorable	3.26087767	0.05934644		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Ruthenibacterium.s_Ruthenibacterium lactatiformans	Ruthenibacterium lactatiformans	3	Favorable	3.26042166	0.05934644	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Unclassified	NA	2	Favorable	3.00416386	0.09896015		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Unclassified.s_Unclassified LKT_f_Oscillospiraceae	NA	2	Favorable	3.02225908	0.09896015		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Vescimonas	NA	5	Favorable	3.36678462	0.03389485		NA	-
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Vescimonas.s_Vescimonas coprocola	Vescimonas coprocola	5	Favorable	3.28475668	0.03389485	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Oscillospiraceae.g_Vescimonas.s_Vescimonas fastidiosa	Vescimonas fastidiosa	5	Favorable	2.64012909	0.03389485	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Peptostreptococcaceae.g_Intestinibacter	NA	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Peptostreptococcaceae.g_Intestinibacter.s_Intestinibacter bartlettii	Intestinibacter bartlettii	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Peptostreptococcaceae.g_Terrisporobacter	NA	3	Favorable	2.31174392	0.05704088	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Peptostreptococcaceae.g_Terrisporobacter.s_Terrisporobacter mayombeii	Terrisporobacter mayombeii	3	Favorable	2.31034243	0.05704088	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Unclassified	NA	1		NA	-	Favorable	3.20377361	0.02379191
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Unclassified.g_Unclassified	NA	1		NA	-	Favorable	3.20377361	0.02379191
k_Bacteria.p_Firmicutes.c_Clostridia.o_Eubacteriales.f_Unclassified.g_Unclassified.s_Unclassified LKT_o_Eubacteriales	NA	1		NA	-	Favorable	3.20377361	0.02379191
k_Bacteria.p_Firmicutes.c_Erysipelotrichia.o_Erysipelotrichales.f_Coprobaillaceae.g_Catenibacterium.s_Catenibacterium mitsuokai	Catenibacterium mitsuokai	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Erysipelotrichia.o_Erysipelotrichales.f_Erysipelotrichaceae.g_Erysipelatoclostridium.s_Clostridium spiroforme	[Clostridium] spiroforme	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Erysipelotrichia.o_Erysipelotrichales.f_Erysipelotrichaceae.g_Faecalibacillus	NA	1		NA	-		NA	-

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k_Bacteria.p_Firmicutes.c_Erysipelotrichia.o_Erysipelotrichales.f_Erysipelotrichaceae.g_Faecalibacillus.s_Faecalibacillus Unclassified MSK20 93	Faecalibacillus sp. MSK20 93	1		NA	-	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Erysipelotrichia.o_Erysipelotrichales.f_Erysipelotrichaceae.g_Longicatena.s_Longicatena caecimuris	Longicatena caecimuris	2	Favorable	2.94450377	0.09126875	NA	NA	NA
k_Bacteria.p_Firmicutes.c_Unclassified	NA	2	Unfavorable	2.61821119	0.09896015		NA	-
k_Bacteria.p_Firmicutes.c_Unclassified.o_Unclassified	NA	2	Unfavorable	2.64549523	0.09896015		NA	-
k_Bacteria.p_Firmicutes.c_Unclassified.o_Unclassified.f_Unclassified	NA	2	Unfavorable	2.53390849	0.09896015		NA	-
k_Bacteria.p_Firmicutes.c_Unclassified.o_Unclassified.f_Unclassified.g_Unclassified	NA	2	Unfavorable	2.63929739	0.09896015		NA	-
k_Bacteria.p_Firmicutes.c_Unclassified.o_Unclassified.f_Unclassified.g_Unclassified.s_Unclassified LKT p_Firmicutes	NA	2	Unfavorable	2.61983027	0.09896015		NA	-
k_Bacteria.p_Proteobacteria	NA	1		NA	-		NA	-
k_Bacteria.p_Proteobacteria.c_Deltaproteobacteria	NA	1		NA	-	Unfavorable	2.83502037	0.03495086
k_Bacteria.p_Proteobacteria.c_Deltaproteobacteria.o_Desulfovibrionales	NA	1		NA	-	Unfavorable	2.83502037	0.03495086
k_Bacteria.p_Proteobacteria.c_Deltaproteobacteria.o_Desulfovibrionales.f_Desulfovibrionaceae	NA	1		NA	-	Unfavorable	2.83502037	0.03495086
k_Bacteria.p_Proteobacteria.c_Deltaproteobacteria.o_Desulfovibrionales.f_Desulfovibrionaceae.g_Bilophila	NA	1		NA	-	Unfavorable	2.83502037	0.03495086
k_Bacteria.p_Proteobacteria.c_Deltaproteobacteria.o_Desulfovibrionales.f_Desulfovibrionaceae.g_Bilophila.s_Bilophila wadsworthia LKT_s_Bilophila wadsworthia	Bilophila wadsworthia	1	NA	NA	NA	Unfavorable	2.83502037	0.03495086
k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria	NA	3		NA	-		NA	-
k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Enterobacterales	NA	3		NA	-		NA	-
k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Enterobacterales.f_Enterobacteriaceae	NA	3		NA	-		NA	-
k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Enterobacterales.f_Enterobacteriaceae.g_Escherichia	NA	5	Favorable	4.23169092	0.03389485		NA	-
k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Enterobacterales.f_Enterobacteriaceae.g_Escherichia.s_Escherichia coli	Escherichia coli	5	Favorable	4.23169167	0.03389485	NA	NA	NA
k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Enterobacterales.f_Enterobacteriaceae.g_Unclassified	NA	3		NA	-		NA	-
k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Enterobacterales.f_Enterobacteriaceae.g_Unclassified.s_Unclassified LKT_f_Enterobacteriaceae	NA	3		NA	-		NA	-
k_Bacteria.p_Proteobacteria.c_Unclassified	NA	1		NA	-	Unfavorable	2.25635059	0.02683551
k_Bacteria.p_Proteobacteria.c_Unclassified.o_Unclassified	NA	1		NA	-	Unfavorable	2.25635059	0.02683551
k_Bacteria.p_Proteobacteria.c_Unclassified.o_Unclassified.f_Unclassified	NA	1		NA	-	Unfavorable	2.25635059	0.02683551
k_Bacteria.p_Proteobacteria.c_Unclassified.o_Unclassified.f_Unclassified.g_Unclassified	NA	1		NA	-	Unfavorable	2.25635059	0.02683551
k_Bacteria.p_Proteobacteria.c_Unclassified.o_Unclassified.f_Unclassified.g_Unclassified.s_Unclassified LKT p_Proteobacteria	NA	1		NA	-	Unfavorable	2.25635059	0.02683551

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k_Bacteria.p_Unclassified	NA	1		NA	-		NA	-
k_Bacteria.p_Unclassified.c_Unclassified	NA	1		NA	-		NA	-
k_Bacteria.p_Unclassified.c_Unclassified.o_Unclassified	NA	1		NA	-		NA	-
k_Bacteria.p_Unclassified.c_Unclassified.o_Unclassified.f_Unclassified	NA	1		NA	-		NA	-
k_Bacteria.p_Unclassified.c_Unclassified.o_Unclassified.f_Unclassified.g_Unclassified	NA	1		NA	-		NA	-
k_Bacteria.p_Unclassified.c_Unclassified.o_Unclassified.f_Unclassified.g_Unclassified.s_Unclassified_LKT_k_Bacteria	NA	1		NA	-		NA	-
k_Bacteria.p_Verrucomicrobia	NA	1		NA	-	Unfavorable	3.68917171	0.00185549
k_Bacteria.p_Verrucomicrobia.c_Verrucomicrobiae	NA	1		NA	-	Unfavorable	3.68917171	0.00185549
k_Bacteria.p_Verrucomicrobia.c_Verrucomicrobiae.o_Verrucomicrobiales	NA	1		NA	-	Unfavorable	3.68917171	0.00185549
k_Bacteria.p_Verrucomicrobia.c_Verrucomicrobiae.o_Verrucomicrobiales.f_Akkermansiaceae	NA	1		NA	-	Unfavorable	3.68917171	0.00185549
k_Bacteria.p_Verrucomicrobia.c_Verrucomicrobiae.o_Verrucomicrobiales.f_Akkermansiaceae.g_Akkermansia	NA	1		NA	-	Unfavorable	3.68917171	0.00185549
k_Bacteria.p_Verrucomicrobia.c_Verrucomicrobiae.o_Verrucomicrobiales.f_Akkermansiaceae.g_Akkermansia.s_Akkermansia_muciniphila_LKT_s_Akkermansia_muciniphila	Akkermansia muciniphila	1	NA	NA	NA	Unfavorable	3.68917171	0.00185549