



e







650-





500-



600·



600-







h

C

Responder





0.8 * * * * * * * * * * * * * * 0.6 * 0.4 0.2 L2 * * * * * * * * * * * * * * 0 18 * * -0.2 L9 P10 * * * * * LIF 🗴 MCP1.MCAF. MCP3 * * * -0.4 MCSF MIF * * * * * MIG * * * * * MIP1a * * * * * MIP1b * * * * * PD.L1 * * * * * * - -0.6 PD.L1.AREA PD.L2 PD.L2.AREA PDGFbb * * RANTES * * * * * * SCF * * * -0.8 SCGFb * * * * SDF1a * * * * TNFa * * * TNFb * * TRAIL * -1

SUP Figure 4

Responder

Non-responder



* * * * * * 0.8 * * * * * * * 0.6 * * * * * * 0.4 * * 0.2 0 * * -0.2 * * * * * * * LIF . . . MCP1.MCAF. * MCP3 * * -0.4 MCSF MIF * * * * * * * MIG * * * * * * * MIP1a \star 🛪 * * * * MIP1b 🔹 * * * * * * * * PD.L1 * * * * * * -0.6 PD.L1.AREA PD.L2 PD.L2.AREA PDGFbb * * * RANTES * * * * * * SCF * * * SCGFb * * * -0.8 SDF1a * * * * TNFa * * * TNFb * * TRAIL * -1

SUP Figure 5

Responder

Non-responder



* * * * * * 0.8 * 0.6 . . . * * * * 0.4 * * 0.2 0 -0.2 IP10 LIF MCP1.MCAF. MCP3 -0.4 MCSF MIF MIG * * MIP1a \star 🛪 MIP1b * * * * * PD.L1 * * -0.6 PD.L1.AREA PD.L2 PD.L2.AREA PDGFbb * * * RANTES * * * * * * -0.8 SCF * * * SCGFb * * * * SDF1a * * * * TNFa * * * TNFb *

TRAIL *

-1

SUP Figure 1

Supplementary Figure 1. NR and R CC patients presented higher CD8⁺ and higher CD4⁺ TILs respectively, when analyzed in stromal and intratumoral compartments. (a and e) Representative IHC images of CD8⁺ (a) and CD4⁺ (e) TILs distributed in stromal and intra-tumoral regions. (a) Scale bar = 200µm. (e) Scale bar = 50µm. (b and f) Morphometric analysis showed NR patients with a higher number of CD8⁺ TILs than in R patients (b, NR n=33, R n=34) and no difference in the number of CD4⁺ TILs (f, NR n=32, R n=33) in stromal and intra-tumoral regions. (c) Number of CD8⁺ TILs plotted in both regions (low R vs. NR and high R vs. NR, p < 0.001; NR low, n=16, NR high, n=17; R low, n=17 and R high, n=17). (g) Higher number of CD4⁺ TILs in the intra-tumoral region of R (high R vs. NR; NR low, n=16; NR high, n=15; R low, n=16 and R high, n=15). (d and h) Kaplan-Meier survival curves show a comparison of OS between low and high infiltration of CD8⁺ and CD4⁺, *p* values determined using the log-rank test. (d) Survival analysis of CC patients showed an association between a low level of CD8⁺TILs in R vs. NR (*p*=0.0061) and a high CD8⁺ R vs. NR (*p*=0.0002; NR low, n=21, NR high, n=15; R low, n=17 and R high, n=17). (h) Survival analysis of CC patients showed an association between a low level of CD4⁺TILs in R vs. NR (*p*=0.0006; NR low, n=16, NR high, n=15; R low, n=16 and R high, n=17). (h) Survival analysis of CC patients showed an association between a low level of CD4⁺TILs in R vs. NR (*p*=0.0006; NR low, n=16, NR high, n=15; R low, n=16 and R high, n=17). (h) Survival analysis of CC patients showed an association between a low level of CD4⁺ R vs. NR (*p*=0.0006; NR low, n=16, NR high, n=15; R low, n=16 and R high, n=15). Statistical differences are indicated by asterisks (*) $p \le 0.05$, (**) $p \le 0.01$, and (***) $p \le 0.001$. The *p* values were calculated using the Mann-Whitney test. CC, Cervical Cancer; NR, Non-responder (Red) patients; R, Responder (Blue) patients.

Supplementary Figure 2. NR CC patients presented a high number of stromal FoxP3+TILs and stromal CD68+ TAMs when analyzed in low and high densities. (a and e) Representative IHC images of FoxP3⁺ TILs (a) and CD68⁺ TAMs (e) distributed in stromal and intra-tumoral regions. Scale bar = 50µm. Morphometric analysis did not show a difference between the groups (b, NR, n=32; R, n=36 and f, NR, n=30; R, n=34). (c) Higher number of FoxP3⁺ TILs (low R vs. NR $p \le 0.01$; NR low, n=16; NR high, n=16; R low, n=19 and R high, n=17), and (g) CD68⁺ TAMs (low R vs. NR $p \le 0.05$; NR low, n=15, NR high, n=15; R low, n=19 and R high, n=15) in the stromal region of NR patients. (d) Survival analysis of CC patients showed association between low level of FoxP3⁺TILs in R vs. NR (p=0.0047) and high FoxP3⁺ R vs. NR (p=0.0003; NR low, n=16, NR high, n=15; R low, n=18 and R high, n=18). (h) Survival analysis of CC patients showed association between low level of CD68⁺TAMs in R vs. NR (p=0.0001; NR low, n=16, NR high, n=15; R low, n=18 and R high, n=16, NR high, n=15; R low, n=18 and R high, n=16, NR high, n=15; R low, n=18 and R high, n=16, NR high, n=15; R low, n=18 and R high, n=16, NR high, n=15; R low, n=18 and R high, n=16, NR high, n=15; R low, n=18 and R high, n=16, NR high, n=15; R low, n=18. (h) Survival analysis of CC patients showed association between low level of CD68⁺TAMs in R vs. NR (p=0.0001; NR low, n=16, NR high, n=15; R low, n=18. Statistical differences are indicated by asterisks (*) $p \le 0.05$, (**) $p \le 0.01$, and (***) $p \le 0.001$. The p values were calculated using the Mann-Whitney test. CC, Cervical Cancer; NR, Non-responder (Red) patients; R, Responder (Blue) patients.

Supplementary Figure 3. NR CC patients presented a high number of stromal PD-L2⁺TILs. (a and e) Representative IHC images of PD-L1⁺ (a) and PD-L2⁺ TILs (e) distributed in stromal and intra-tumoral regions. (a) Scale bar = 200µm. (e) Scale bar = 50µm. Morphometric analysis did not present a difference in the number of PD-L1⁺ TILs (b, NR, n=31; R n=34 and c, NR, n=17; NR high, n=14; R low, n=16 and R high, n=18). NR presented a higher number of PD-L2⁺ TILs than in R patients (f, NR, n=33, R n=34, p ≤ 0.05) and when compared low (R vs. NR, p ≤ 0.01) and high (R vs. NR, p ≤ 0.01) number of TILs in the stromal region (g, NR low, n=17; NR high, n=16; R low, n=17 and R high, n=17). (d) OS analysis revealed an association between a low level of PD-L1⁺ TILs in R vs. NR (p=0.0033) and a high PD-L1⁺ R vs. NR (p=0.0004; NR low, n=17, NR high, n=14; R low, n=17 and R high, n=17). (h) Survival analysis of CC patients showed an association between a low level of PD-L2⁺ TILs in R vs. NR (p=0.0004) and a high PD-L2⁺ R vs. NR (p=0.0018; NR low, n=18, NR high, n=15; R low, n=17 and R high, n=17). Statistical differences are indicated by asterisks (*) p ≤ 0.05, (**) p ≤ 0.01, and (***) p ≤ 0.001.

The *p* values were calculated using the Mann-Whitney test. CC, Cervical Cancer; NR, Non-responder (Red) patients; R, Responder (Blue) patients.

Supplementary Figure 4. Correlation matrix of all 48 cytokines and Total TILs (stromal with intratumoral). Evaluation in the R and NR groups. NR, Non-responder (n=21); R, Responder (n = 26). All statistical analyses were performed with Spearman's correlation Test (* $p \le 0.05$).

Supplementary Figure 5. Correlation matrix of all 48 cytokines and Stroma TILs. Evaluation in the R and NR groups. NR, Non-responder (n=21); R, Responder (n = 26). All statistical analyses were performed with Spearman's correlation Test (* $p \le 0.05$).

Supplementary Figure 6. Correlation matrix of all 48 cytokines and intratumoral TILs. Evaluation in the R and NR groups. NR, Non-responder (n=21); R, Responder (n = 26). All statistical analyses were performed with Spearman's correlation Test (* $p \le 0.05$).

Graphic Abstract. Mechanistic insights and biomarkers identified in locally advanced CC patients evaluated before chemoradiation therapy. With all results taken together, NR patients would present the highest levels of CD8⁺ TILs that collaborate with positive correlations between CD8 and VEGF, and IL-6 as well as the highest levels of these systemic soluble immune mediators. According to the literature, this scenario could promote tumor growth in CC patients as well as proliferation and invasion of CD8⁺ T cells. However, a dysfunctional state of TILs would be generated by PD-1/PD-L1 or PD-L2 interaction, since PD-1 scores were associated with NR outcome and PD-L1 IR area were highest in this group. In addition, immunosuppressive or unconventional macrophages expressing both CD4 and/or PD-L1 would participate in therapeutic failure perhaps by inducing T cell anergy, M2 polarization, and alterations in the cytokine's secretion. In contrast, R patients would have functional CD8⁺ TILs considering the correlations with IL-2 and PDGFbb. It is also suggested that after proper cooperation of different polarization profiles of CD4⁺ TILs, these cells are regulated by *Treg*. In addition, NR patients have cytokine levels closer to healthy individuals. All of this contributes to healthy tissue recovery. Finally, our findings also indicate promising biomarkers candidates that predict response to conventional treatment in CC. CC, Cervical Cancer; NR, Non-responder; R, Responder patients.

Marker	Group	Total Sum Cutoff	Stromal Cutoff	Intra-tumoral Cutoff
CD8	NR (n=33)	754.0	493.0	214.0
	R (n=34)	334.0	156.5	116.5
CD4	NR (n=32)	282.1	74.3	81.0
	R (n=33)	261.8	62.0	30.0
Foxp3	NR (n=32)	86.8	15.8	69.0
	R (n=36)	82.2	12.9	47.3
CD68	NR (n=30)	107.0	35.5	50.5
	R (n=34)	48.5	21.0	16.0
PD-L1	NR (n=31)	15.0	12.0	2.0
	R (n=34)	9.7	7.6	3.6
PD-L2	NR (n=33)	169.0	103.2	38.4
	R (n=34)	68.5	47.4	22.4

Supplementary Table 1. List of cutoff values for all cell markers.

The median cell density for each marker, in the stromal and intra-tumoral regions. These median values were subsequently used as cutoff values for low and high cell densities.